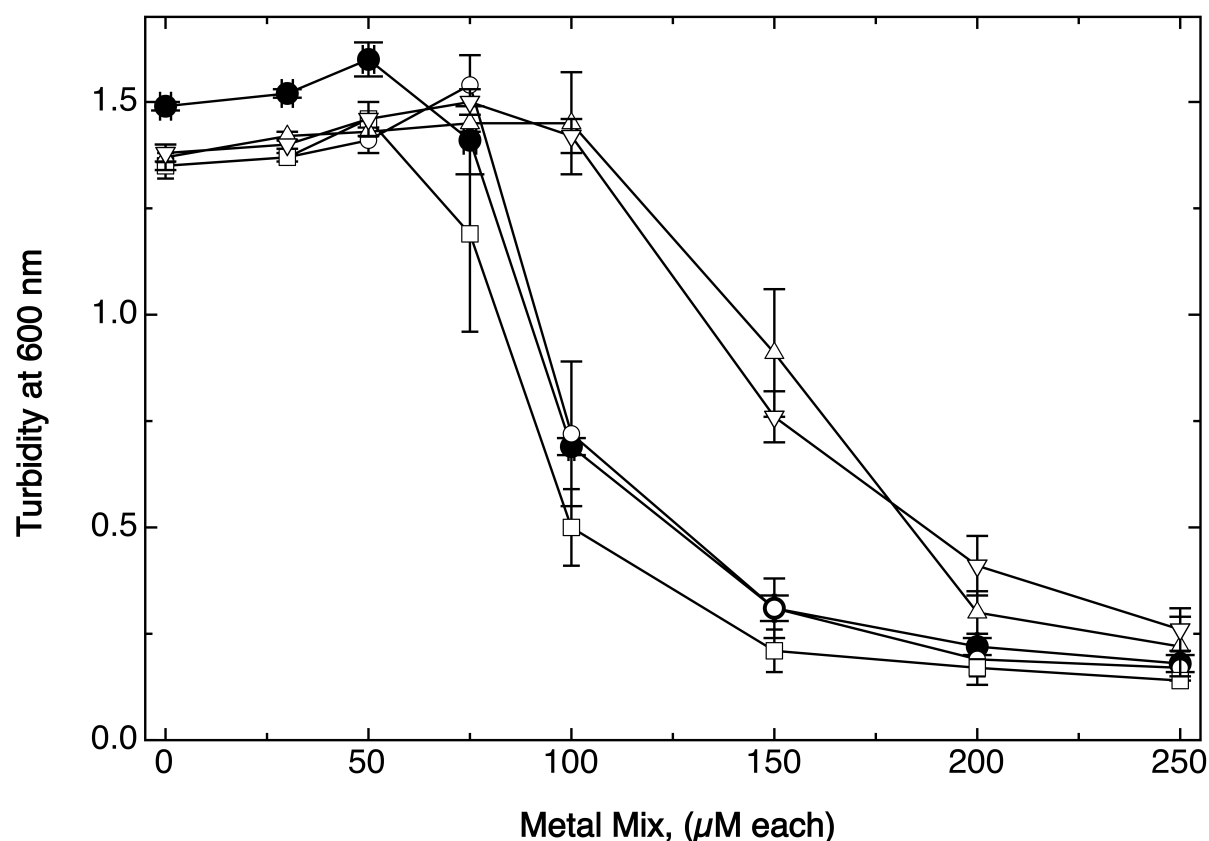


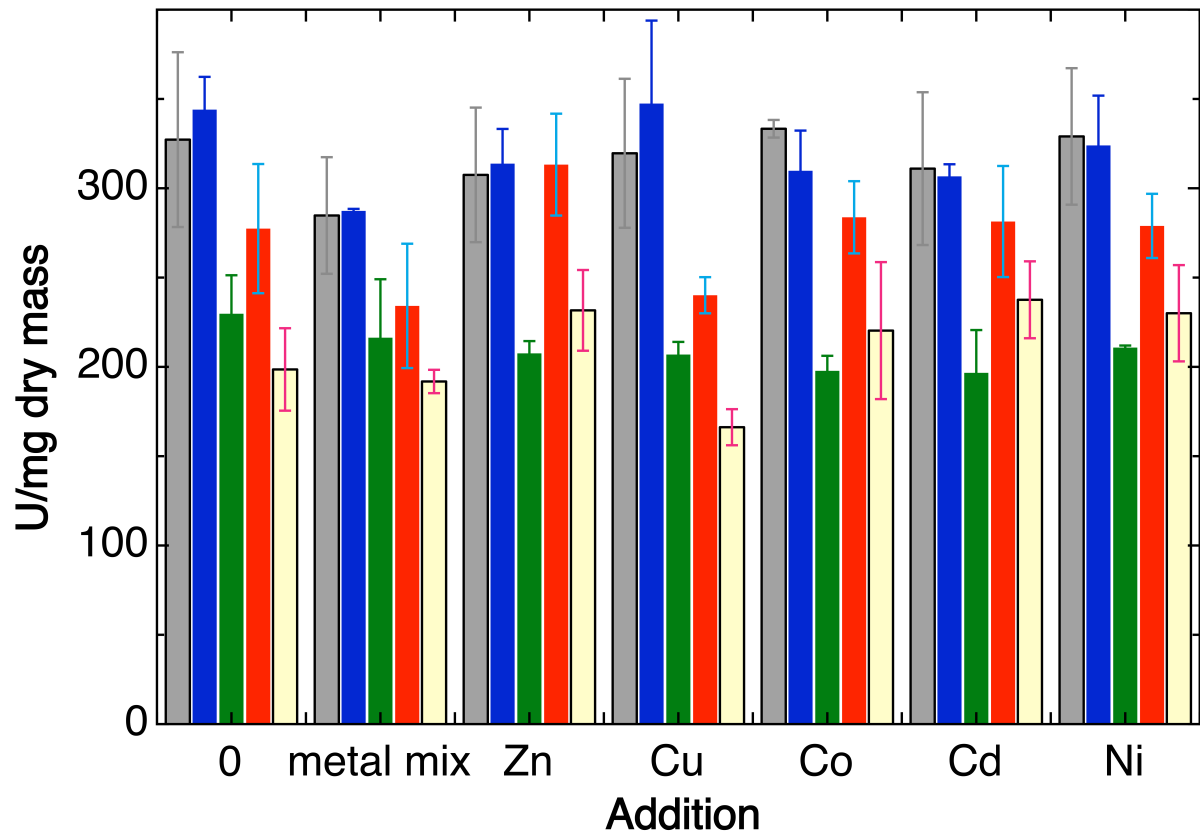
The third pillar of metal homeostasis in *Cupriavidus metallidurans* CH34:

Preferences are controlled by extracytoplasmic functions sigma factors

Supplementary Material



Supplementary Figure S1. Response of *C. metallidurans* wild type and sigma factor mutants to metal mix containing the indicated concentration of Co(II), Ni(II), Cu(II), Zn(II) and Cd(II) each. Precultures of *C. metallidurans* CH34 (closed circle, ●), DN553 (open circle, ○), DN554 (open square, □), DN555 (open triangle, △) and DN546 (open inverted triangle, ▽) were diluted 10-fold into fresh TMM and incubation was continued with shaking for 20 h at 30°C. The turbidity was determined at 600 nm against TMM as blank. Deviations shown, n = 3.



Supplementary Figure S2. Activity of a *pitA-lacZ* fusion in various *C. metallidurans* strains. Mutant cells carrying a *pitA-lacZ* fusion of *C. metallidurans* CH34 (grey), DN486 ($\Delta rpoJ$, blue), DN488 ($\Delta rpoI$, green), DN490 ($\Delta rpoK$, red) and of the triple mutant strain DN553 (light yellow) were cultivated for 3 h at 30°C with shaking in the presence of no added metal, a metal mix containing 30 μ M Zn, Cu, Co, Cd, Ni, or in the presence of 30 μ M of each metal separately, and the beta-galactosidase activity was determined.

Supplementary Table S1. RNA_Seq results. *C. metallidurans* CH34 wild type was cultivated in Tris-buffered mineral salts medium. The cells were harvested, RNA was isolated and sequenced, three biological repeats. The mean NPKM (nucleotide activities per kilobase of exon model per million mapped reads) values as measure for the transcriptional activities of the identified regions were calculated, normalized against the total number of reads of the respective experiment. Moreover, the 3' and 5' un-translated regions (3UTR, 5UTR) and possible transcriptional start sites (TSS) were determined.

Rows:

- Signal: NPKM signal for an open reading frame, 3UTR or 5UTR connected to an open reading frame.
- Start, S, Stop: Position and strand of the signal.
- Locus tag: Name of the open reading frame, Rmet = *Ralstonia metallidurans*, old name of *C. metallidurans*.
- Gene name, if available.
- Mean and DEV: NPKM signal strength as measure of the number of transcript in an open reading frame.
- Operon: All open reading frames on the same DNA strand that were not interrupted by reading frames on the other DNA strand were grouped into one operon region from Op0001f on the chromosome to Op1918f on plasmid pMOL28. Operon regions beginning with Op2000 were annotated in a later step to accommodate additional small open reading frames and non-coding RNAs. "f" are operon regions on the "+" strand (blue), "r" on the "-" strand (red). Within an operon region, a two-fold increase in the NPKM value from a downstream open reading frame to an upstream open reading frame indicated the beginning of a new operon. These were numerated with the name of the operon region plus "_1", "_2", etc.
- KO: KEGG orthology. First level: GIP, genetic information processing, Metabolism; EIP, environmental information processing; DIV, cell division and motility. Second level: GIP-REP, DNA replication and repair; GIP-TK, transcription; GIP-TL, translation; GIP-PTL, post-translation; DIV-Division, cell division; DIV-MOT, motility; EIP-TRA, transport; EIP-SIG, signal transduction; MET-AA, amino acid metabolism; MET-CAH, carbohydrates; MET-COF, cofactors; MET-EN, energy; MET-GLYC, glycans; MET-LIP, lipids; MET-Nglyc, N-glycans; MET-NUC, nucleotides; MET-OAA, other amino acids; MET-SecMetab, secondary metabolites; MET-XEN, xenobiotica; NA, not assigned. Third level gives the sub-category of the second.
- Description of the predicted gene product.

Signal	Start	S	Stop	Locus tag	Gene	Mean	DEV	Operon	KO	Description
Chromosome (replicon CP000352)										
5UTR_882		1 +	103	Rmet_0001	<i>dnaA</i>			Op0001f_1		
NPKM_2508		103 +	1843	Rmet_0001	<i>dnaA</i>	127.33	4.16	Op0001f_1	GIP-REP-Complex	Q1LSI9 Chromosomal replication initiator protein dnaA
NPKM_2509		2219 +	3335	Rmet_0002	<i>dnaN</i>	563.67	3.21	Op0001f_2	GIP-REP-DNA_Pol	Q1LSI8 DNA polymerase III, beta subunit
NPKM_2510		3520 +	6046	Rmet_0003	<i>gyrB</i>	258.67	8.33	Op0001f_2	GIP-REP-Complex	Q1LSI7 DNA gyrase subunit B
3UTR_1083		6047 +	6165	Rmet_0003	<i>gyrB</i>			Op0001f_2		
5UTR_883		6685 +	6989	Rmet_0004				Op0001f_2		
NPKM_2511		6989 +	8099	Rmet_0004		68.33	3.51	Op0001f_2	NA	Q1LSI6 Putative uncharacterized protein
3UTR_2081		7700 -	8365	Rmet_0005				Op0002r_3		
3UTR_1084		8100 +	9392	Rmet_0004				Op0001f_2		
NPKM_2512		8366 -	10121	Rmet_0005		49.67	6.03	Op0002r_3	NA	Q1LSI5 Twin-arginine translocation pathway signal
NPKM_2513		10259 -	11189	Rmet_0006		2.33	0.58	Op0002r_2	NA	Q1LSI4 Putative uncharacterized protein
NPKM_2514		11294 -	12113	Rmet_0007		36.67	2.08	Op0002r_2	NA	Q1LSI3 Transcriptional regulator, AraC family
5UTR_1751		12114 -	12145	Rmet_0007				Op0002r_2		
3UTR_2080		12148 -	12149	Rmet_0008				Op0002r_1		
NPKM_2515		12150 -	13038	Rmet_0008		1.00	0.00	Op0002r_1	EIP-TRA-ABC	Q1LSI2 Binding-protein-dependent transport systems inner membrane component
NPKM_2516		13039 -	13972	Rmet_0009		1.00	0.00	Op0002r_1	EIP-TRA-ABC	Q1LSI1 Binding-protein-dependent transport systems inner membrane component
NPKM_2517		13968 -	15006	Rmet_0010	<i>ugpC</i>	1.67	0.58	Op0002r_1	EIP-TRA-ABC	Q1LSI0 ABC transporter-related protein
5UTR_1750		15007 -	15024	Rmet_0010	<i>ugpC</i>			Op0002r_1		
NPKM_2518		15025 -	16420	Rmet_0011		2.33	0.58	Op0002r_1	EIP-TRA-ABC	Q1LSH9 Twin-arginine translocation pathway signal
NPKM_2519		16617 -	17277	Rmet_0012		7.00	1.73	Op0002r_1	NA	Q1LSH8 Isoprenylcysteine carboxyl methyltransferase
5UTR_1749		17278 -	17303	Rmet_0012				Op0002r_1		
5UTR_884		17386 +	17395	Rmet_0013	<i>mazG</i>			Op0003f_1		
NPKM_2520		17395 +	17752	Rmet_0013	<i>mazG</i>	24.33	0.58	Op0003f_1	NA	Q1LSH7 Putative uncharacterized protein
NPKM_2521		17883 +	18834	Rmet_0014		33.00	1.73	Op0003f_1	NA	Q1LSH6 Putative uncharacterized protein
NPKM_2522		18847 +	19531	Rmet_0015	<i>dbpA</i>	11.00	1.00	Op0003f_1	NA	Q1LSH5 DEAD/DEAH box helicase-like protein
NPKM_2523		19720 +	20161	Rmet_0016		59.00	4.36	Op0003f_2	NA	Q1LSH4 Putative signal-transduction protein with CBS domains
NPKM_2524		20368 +	21955	Rmet_0017		23.67	0.58	Op0003f_2	NA	Q1LSH3 Drug resistance transporter EmrB/QacA subfamily
NPKM_2525		22065 +	22692	Rmet_0018		51.33	4.04	Op0003f_3	MET-LIP-Others	Q1LSH2 Glutathione peroxidase
NPKM_2526		22852 +	23626	Rmet_0019		35.67	3.21	Op0003f_3	NA	Q1LSH1 Beta-lactamase-like protein
NPKM_2527		23691 +	24558	Rmet_0020		249.00	9.17	Op0003f_4	MET-AA-Tyr	Q1LSH0 Fumarylacetoacetate (FAA) hydrolase
NPKM_2528		24790 +	26068	Rmet_0021		114.67	9.87	Op0003f_4	MET-AA-Phe	Q1LSG9 Peptidase M20D, amidohydrolase
3UTR_2079		25240 -	26082	Rmet_0022				Op0004r_1		
NPKM_2529		26083 -	26902	Rmet_0022		26.33	1.53	Op0004r_1	NA	Q1LSG8 Transcriptional regulator, AraC family
5UTR_1748		26903 -	27122	Rmet_0022				Op0004r_1		
NPKM_2530		27027 +	28257	Rmet_0023	<i>fsr</i>	22.33	7.57	Op0005f_1	NA	Q1LSG7 Major facilitator superfamily MFS_1
3UTR_2078		27323 -	28318	Rmet_0024				Op0006r_1		
3UTR_1085		28258 +	28672	Rmet_0023	<i>fsr</i>			Op0005f_1		
NPKM_2531		28319 -	29636	Rmet_0024		89.67	4.04	Op0006r_1	NA	Q1LSG6 Peptidase dimerisation
5UTR_1747		29637 -	29924	Rmet_0024				Op0006r_1		
5UTR_885		29733 +	29808	Rmet_0025				Op0007f_1		
NPKM_2532		29808 +	30120	Rmet_0025		34.33	3.51	Op0007f_1	NA	Q1LSG5 Putative uncharacterized protein

NPKM_2533	30160 +	31252 Rmet_0026	<i>bug</i>	81.00	3.46	Op0007f_2	NA	Q1LSG4 Uncharacterized protein UPF0065
3UTR_2077	30723 -	31309 Rmet_0027				Op0008r_1		
NPKM_2534	31310 -	32078 Rmet_0027		20.67	0.58	Op0008r_1	NA	Q1LSG3 Two component transcriptional regulator, winged helix family
NPKM_2535	32263 +	33070 Rmet_0028		3.67	0.58	Op0009f_1	NA	Q1LSG2 Two component transcriptional regulator, winged helix family
3UTR_2076	33058 -	33081 Rmet_0029				Op0010r_1		
3UTR_1086	33071 +	33136 Rmet_0028				Op0009f_1		
NPKM_2536	33082 -	33916 Rmet_0029		22.00	2.00	Op0010r_1	NA	Q1LSG1 Porin, Gram-negative type
5UTR_1746	33917 -	33965 Rmet_0029				Op0010r_1		
NPKM_2537	33979 +	34276 Rmet_0030	<i>tnpA</i>	0.00	0.00	Op2000f_1	NA	NA
NPKM_2538	34272 +	35166 Rmet_0031	<i>tnpB</i>	0.00	0.00	Op2000f_1	NA	NA
3UTR_2075	35158 -	35206 Rmet_0032				Op0012r_3		
3UTR_1087	35167 +	36878 Rmet_0031	<i>tnpB</i>			Op2000f_1		
NPKM_2539	35207 -	35498 Rmet_0032		2280.00	189.17	Op0012r_3	NA	Q1LSF8 Porin, gram-negative type
NPKM_2540	35584 -	35794 Rmet_6403		16.00	1.73	Op0012r_2	NA	NA
NPKM_2541	35918 -	36173 Rmet_0033	<i>minE</i>	361.33	21.55	Op0012r_2	DIV-Division	Q1LSF7 Cell division topological specificity factor
NPKM_2542	36188 -	37001 Rmet_0034	<i>minD</i>	225.33	12.50	Op0012r_2	DIV-Division	Q1LSF6 Septum site-determining protein MinD
NPKM_2543	37049 -	37898 Rmet_0035	<i>minC</i>	106.00	8.00	Op0012r_1	DIV-Division	Q1LSF5 Probable septum site-determining protein minC
5UTR_886	37895 +	37985 Rmet_0036	<i>corA1</i>			Op0013f_1		
NPKM_2544	37985 +	39068 Rmet_0036	<i>corA1</i>	68.00	2.00	Op0013f_1	EIP-TRA-Ion	Q1LSF4 Mg2+ transporter protein, CorA-like protein
NPKM_2545	39291 +	39453 Rmet_0037		3.00	1.00	Op0014f_1	NA	Q1LSF3 Putative uncharacterized protein
NPKM_2546	39541 +	41374 Rmet_0038	<i>kdpA</i>	1.00	0.00	Op0015f_1	MET-EN-P_ATPase	Q1LSF2 Potassium-transporting ATPase, A subunit
NPKM_2547	41392 +	43624 Rmet_0039	<i>kdpB</i>	2.67	0.58	Op0015f_2	MET-EN-P_ATPase	Q1LSF1 Potassium-translocating P-type ATPase, B subunit
NPKM_2548	43645 +	44257 Rmet_0040	<i>kdpC</i>	2.67	0.58	Op0015f_2	MET-EN-P_ATPase	Q1LSF0 Potassium-transporting ATPase, C subunit
3UTR_1088	44258 +	44381 Rmet_0040	<i>kdpC</i>			Op0015f_2		
5UTR_887	44396 +	44405 Rmet_0041	<i>kdpD</i>			Op0015f_3		
NPKM_2549	44405 +	47309 Rmet_0041	<i>kdpD</i>	31.00	1.00	Op0015f_3	EIP-SIG-2Comp	Q1LSE9 Sensor protein
NPKM_2550	47310 +	48006 Rmet_0042	<i>kdpE</i>	29.67	2.08	Op0015f_3	EIP-SIG-2Comp	Q1LSE8 Two component transcriptional regulator, winged helix family
NPKM_2551	48144 +	48855 Rmet_0043		18.67	2.52	Op0015f_3	NA	Q1LSE7 Sel1
NPKM_2552	48932 +	51581 Rmet_0044		29.67	1.53	Op0015f_3	NA	Q1LSE6 Putative uncharacterized protein
NPKM_2553	51577 +	52480 Rmet_0045		18.00	2.00	Op0015f_3	NA	Q1LSE5 Transglutaminase-like protein
3UTR_2074	51660 -	52550 Rmet_0046	<i>gatB</i>			Op0016r_2		
3UTR_1089	52481 +	52662 Rmet_0045				Op0015f_3		
NPKM_2554	52551 -	54006 Rmet_0046	<i>gatB</i>	254.00	4.36	Op0016r_2	GIP-TL-Ass	Q1LSE4 Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B
NPKM_2555	54085 -	55156 Rmet_0047		179.33	7.77	Op0016r_2	NA	Q1LSE3 Dienelactone hydrolase
NPKM_2556	55189 -	55663 Rmet_0048		256.67	11.68	Op0016r_2	NA	Q1LSE2 Putative lipoprotein
NPKM_2557	55670 -	57170 Rmet_0049	<i>gatA1</i>	279.67	9.45	Op0016r_2	NA	NA
NPKM_2558	57221 -	57521 Rmet_0050	<i>gatC</i>	259.00	5.29	Op0016r_2	GIP-TL-Ass	Q1LSE0 Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit C
NPKM_2559	57749 -	58019 Rmet_6404		17.33	2.08	Op0016r_1	NA	NA
5UTR_1745	58020 -	58109 Rmet_6404				Op0016r_1		
5UTR_888	58231 +	58486 Rmet_0051	<i>mreB</i>			Op0017f_1		
NPKM_2560	58486 +	59530 Rmet_0051	<i>mreB</i>	514.00	13.45	Op0017f_1	DIV-Division	Q0KFF6 Rod shape-determining protein MreB
NPKM_2561	59672 +	60683 Rmet_0052	<i>mreC</i>	75.00	4.58	Op0017f_1	DIV-Division	Q1LSD8 Rod shape-determining protein MreC
NPKM_2562	60679 +	61192 Rmet_0053	<i>mreD</i>	55.33	3.79	Op0017f_1	DIV-Division	Q1LSD7 Rod shape-determining protein MreD

NPKM_2563	61235 +	63617 Rmet_0054	<i>mrdA</i>	41.67	1.15	Op0017f_1	NA	Q1LSD6 Peptidoglycan glycosyltransferase
NPKM_2564	63630 +	64773 Rmet_0055	<i>mrdB</i>	39.00	2.00	Op0017f_1	DIV-Division	Q1LSD5 Rod shape-determining protein RodA
NPKM_2565	64825 +	65497 Rmet_0056		211.33	6.43	Op0017f_2	NA	Q1LSD4 Putative uncharacterized protein
NPKM_2566	65516 +	66626 Rmet_0057	<i>xerC</i>	68.00	2.65	Op0017f_2	GIP-REP-Recomb	Q1LSD3 Tyrosine recombinase XerC subunit
3UTR_2073	66090 -	66621 Rmet_0058	<i>gcvA</i>			Op0018r_1		
NPKM_2567	66622 -	67516 Rmet_0058	<i>gcvA</i>	32.00	1.73	Op0018r_1	NA	Q1LSD2 Transcriptional regulator, LysR family
5UTR_1744	67517 -	67554 Rmet_0058	<i>gcvA</i>			Op0018r_1		
NPKM_2568	67772 +	68141 Rmet_0059		41.33	6.03	Op0019f_1	NA	Q1LSD1 Putative uncharacterized protein
NPKM_2569	68213 +	69008 Rmet_0060	<i>lipB</i>	175.67	8.74	Op0019f_2	NA	Q1LSD0 Lipoate-protein ligase B
NPKM_2570	69084 +	70077 Rmet_0061	<i>lipA</i>	321.67	6.03	Op0019f_2	NA	Q1LSC9 Lipoyl synthase
3UTR_1090	70078 +	70151 Rmet_0061	<i>lipA</i>			Op0019f_2		
5UTR_889	70354 +	70417 Rmet_0062				Op0019f_2		
NPKM_2571	70417 +	71068 Rmet_0062		41.33	2.52	Op0019f_2	NA	Q1LSC8 Putative uncharacterized protein
NPKM_2572	71064 +	72084 Rmet_0063		27.33	1.53	Op0019f_2	NA	Q1LSC7 Allophanate hydrolase subunit 2
NPKM_2573	72160 +	72901 Rmet_0064	<i>lamB</i>	42.00	1.73	Op0019f_2	NA	Q1LSC6 UPF0271 protein Rmet_0064
NPKM_2574	72968 +	73703 Rmet_0065		64.00	4.58	Op0019f_2	NA	Q1LSC5 Putative uncharacterized protein
NPKM_2575	73706 +	74657 Rmet_0066		63.33	4.04	Op0019f_2	NA	Q1LSC4 Putative uncharacterized protein
3UTR_2072	74334 -	75349 Rmet_0068				Op0020r_1		
NPKM_2576	74670 +	75339 Rmet_0067	<i>pcp1</i>	57.00	8.66	Op0019f_2	GIP-PTL-Fold	Q1LSC3 Pyroglutamyl-peptidase I. Cysteine peptidase. MEROPS family C15
3UTR_1091	75340 +	76216 Rmet_0067	<i>pcp1</i>			Op0019f_2		
NPKM_2577	75350 -	76673 Rmet_0068		35.67	2.08	Op0020r_1	NA	Q1LSC2 VanZ like protein
NPKM_2578	76724 -	77372 Rmet_0069		72.00	5.29	Op0020r_1	NA	Q1LSC1 Putative lipoprotein
NPKM_2579	77416 -	78358 Rmet_0070		67.00	5.29	Op0020r_1	EIP-TRA-ABC	Q1LSC0 Mammalian cell entry related
NPKM_2580	78357 -	79197 Rmet_0071		89.00	4.36	Op0020r_1	EIP-TRA-ABC	Q1LSB9 ABC transporter-related protein
NPKM_2581	79193 -	80324 Rmet_0072		111.67	4.04	Op0020r_1	EIP-TRA-ABC	Q1LSB8 Putative uncharacterized protein
5UTR_1743	80325 -	80390 Rmet_0072				Op0020r_1		
5UTR_890	80398 +	80484 Rmet_0073	<i>birA</i>			Op0021f_1		
NPKM_2582	80484 +	81342 Rmet_0073	<i>birA</i>	101.33	6.43	Op0021f_1	NA	Q1LSB7 Biotin--acetyl-CoA-carboxylase ligase
NPKM_2583	81338 +	82172 Rmet_0074		66.33	1.53	Op0021f_1	NA	Q1LSB6 Type III pantothenate kinase
NPKM_2584	82214 +	83009 Rmet_0075		70.00	2.00	Op0021f_1	NA	Q1LSB5 Sporulation related
3UTR_2071	82316 -	83131 Rmet_0076	<i>hldC</i>			Op0022r_3		
3UTR_1092	83010 +	83705 Rmet_0075				Op0021f_1		
NPKM_2585	83132 -	83624 Rmet_0076	<i>hldC</i>	52.67	4.16	Op0022r_3	NA	Q1LSB4 RfaE bifunctional protein, domain II
NPKM_2586	83701 -	84562 Rmet_0077		403.00	8.89	Op0022r_3	NA	Q1LSB3 Putative uncharacterized protein
NPKM_2587	84691 -	85948 Rmet_0078	<i>rssA</i>	106.00	7.00	Op0022r_2	NA	Q1LSB2 Patatin
NPKM_2588	85944 -	86844 Rmet_0079		192.33	6.51	Op0022r_2	NA	Q1LSB1 Putative uncharacterized protein
NPKM_2589	86898 -	87726 Rmet_0080		65.33	6.03	Op0022r_1	MET-CAH-Prop	Q1LSB0 Enoyl-CoA hydratase/isomerase
NPKM_2590	88107 -	89148 Rmet_0081	<i>mhpD2</i>	61.67	0.58	Op0022r_1	NA	Q1LSA9 Fumarylacetoacetate (FAA) hydrolase
5UTR_891	89170 +	89191 Rmet_0082				Op0023f_1		
NPKM_2591	89191 +	90049 Rmet_0082		62.00	6.00	Op0023f_1	NA	Q1LSA8 Transcriptional regulator, IclR family
NPKM_2592	90101 +	91106 Rmet_0083		42.00	1.00	Op0023f_1	NA	Q1LSA7 Putative prolin-rich signal peptide protein
NPKM_2593	91160 +	92009 Rmet_0084		36.33	1.53	Op0023f_1	MET-XEN-Benz	Q1LSA6 3-oxoadipate enol-lactonase
NPKM_2594	92244 +	92502 Rmet_0085		391.00	23.52	Op0023f_2	NA	Q1LSA5 Putative uncharacterized protein

3UTR_2070	92320 -	92619 Rmet_0086				Op0024r_1		
NPKM_2595	92620 -	93013 Rmet_0086		114.67	5.13	Op0024r_1	NA	Q1LSA4 Rhodanese-like protein
5UTR_1742	93014 -	93090 Rmet_0086				Op0024r_1		
NPKM_2596	93236 +	94304 Rmet_0087	<i>bhmT</i>	139.00	6.08	Op0025f_1	MET-AA-Met	Q1LSA3 Methionine synthase (B12-dependent)
NPKM_2597	94332 +	97080 Rmet_0088	<i>metH</i>	153.00	10.15	Op0025f_1	MET-AA-Met	Q1LSA2 Methionine synthase (B12-dependent)
3UTR_1093	97081 +	97344 Rmet_0088	<i>metH</i>			Op0025f_1		
5UTR_892	97348 +	97385 Rmet_0089				Op0025f_1		
NPKM_2598	97385 +	97724 Rmet_0089		91.00	13.89	Op0025f_1	NA	Q1LSA1 Cell wall surface anchor family protein
3UTR_2069	97847 -	99238 Rmet_0092				Op0026r_1		
NPKM_2599	97973 +	98606 Rmet_0090		960.67	51.39	Op0025f_2	NA	Q1LSA0 Two component transcriptional regulator, LuxR family
NPKM_2600	98766 +	99174 Rmet_0091		347.33	35.92	Op0025f_2	NA	Q1LS99 Response regulator receiver domain protein (CheY-like)
NPKM_2601	99239 -	100625 Rmet_0092		31.00	1.73	Op0026r_1	NA	Q1LS98 Histidine kinase
NPKM_2602	100776 +	101070 Rmet_0093		180.33	22.68	Op0027f_1	NA	Q1LS97 UPF0391 membrane protein Rmet_0093
NPKM_2603	101100 +	101535 Rmet_0094		486.00	13.53	Op0027f_2	NA	Q1LS96 Putative uncharacterized protein
NPKM_2604	101946 -	102267 Rmet_0095		197.67	9.24	Op0028r_1	NA	Q1LS95 Putative uncharacterized protein
5UTR_1741	102268 -	102419 Rmet_0095				Op0028r_1		
NPKM_2605	102444 +	104253 Rmet_0096	<i>argS</i>	230.33	3.06	Op0029f_1	MET-AA-ArgPro	Q1LS94 Arginyl-tRNA synthetase
NPKM_2606	104392 +	105133 Rmet_0097		343.33	17.47	Op0029f_1	NA	Q1LS93 Sporulation related
NPKM_2607	105278 +	105917 Rmet_0098	<i>dsbA</i>	602.33	51.50	Op0029f_1	GIP-PTL-Fold	Q1LS92 DSBA oxidoreductase
NPKM_2608	106008 +	106806 Rmet_0099		79.33	8.50	Op0029f_1	NA	Q1LS91 Short-chain dehydrogenase/reductase SDR
NPKM_2609	106805 +	107648 Rmet_0100		62.00	8.72	Op0029f_1	NA	Q1LS90 Putative uncharacterized protein
3UTR_2068	106876 -	107647 Rmet_0101				Op0030r_1		
NPKM_2610	107648 -	108728 Rmet_0101		95.00	8.89	Op0030r_1	NA	Q1LS89 Beta-lactamase-like protein
5UTR_1740	108729 -	108912 Rmet_0101				Op0030r_1		
NPKM_2611	108860 +	109295 Rmet_0102		28.67	0.58	Op0031f_1	NA	Q1LS88 Transcriptional regulator, MerR family
NPKM_2612	109417 +	110599 Rmet_0103	<i>ivd1</i>	64.67	3.51	Op0031f_2	MET-AA-ValLeulle	Q1LS87 Isovaleryl-CoA dehydrogenase
NPKM_2613	110725 +	112549 Rmet_0104	<i>aceK</i>	42.67	2.89	Op0031f_2	NA	Q1LS86 Isocitrate dehydrogenase kinase/phosphatase
NPKM_2614	112545 +	113217 Rmet_0105	<i>can</i>	126.33	5.69	Op0031f_3	MET-EN-Nitrog	Q1LS85 Carbonic anhydrase
NPKM_2615	113258 +	114443 Rmet_0106	<i>atoB</i>	162.33	9.61	Op0031f_3	MET-CAH-Pyr	Q1LS84 Thiolase
NPKM_2616	114492 +	115173 Rmet_0107		164.67	1.53	Op0031f_3	NA	Q1LS83 Short-chain dehydrogenase/reductase SDR
NPKM_2617	115188 +	116319 Rmet_0108		113.33	4.62	Op0031f_3	NA	Q1LS82 Acyl-CoA dehydrogenase-like protein
NPKM_2618	116408 +	117068 Rmet_0109		214.67	19.01	Op0031f_3	NA	Q1LS81 DSBA oxidoreductase
NPKM_2619	117064 +	117748 Rmet_0110		189.00	17.06	Op0031f_3	NA	Q1LS80 HAD-superfamily hydrolase subfamily IA, variant 3
NPKM_2620	117744 +	118170 Rmet_0111		135.00	17.09	Op0031f_3	NA	Q1LS79 UPF0225 protein Rmet_0111
NPKM_2621	118230 +	119160 Rmet_0112		52.67	7.51	Op0031f_3	NA	Q1LS78 Conserved hypothetical signal peptide protein
NPKM_2622	119220 +	120009 Rmet_0113		115.33	12.50	Op0031f_4	NA	Q1LS77 Enoyl-CoA hydratase/isomerase
NPKM_2623	120228 +	121695 Rmet_0114	<i>bioA</i>	388.00	156.94	Op0031f_5	MET-COF-Biotine	Q1LS76 Adenosylmethionine-8-amino-7-oxononanoate aminotransferase
NPKM_2624	121684 +	122905 Rmet_0115	<i>bioF</i>	395.00	162.34	Op0031f_5	MET-COF-Biotine	Q1LS75 8-amino-7-oxononanoate synthase
NPKM_2625	122901 +	123666 Rmet_0116	<i>bioD</i>	336.67	135.71	Op0031f_5	MET-COF-Biotine	Q1LS74 Dethiobiotin synthase
NPKM_2626	123667 +	124744 Rmet_0117	<i>bioB</i>	501.00	219.64	Op0031f_5	MET-COF-Biotine	Q1LS73 Biotin synthase
NPKM_2627	124893 +	125835 Rmet_0118	<i>ycdW</i>	387.00	78.08	Op0031f_5	NA	Q1LS72 D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding
NPKM_2628	125869 +	126367 Rmet_0119		318.00	49.27	Op0031f_5	NA	Q1LS71 YbaK/prolyl-tRNA synthetase associated region
NPKM_2629	126363 +	126618 Rmet_0120		233.00	33.18	Op0031f_5	NA	Q1LS70 Putative uncharacterized protein

NPKM_2630	126614 +	127544 Rmet_0121		169.00	24.00	Op0031f_5	Met-SecMetab	Q1LS69 Beta-lactamase-like protein
3UTR_2067	127431 -	128151 Rmet_0123				Op0032r_3		
NPKM_2631	127546 +	128098 Rmet_0122		122.00	20.66	Op0031f_5	NA	Q1LS68 GCN5-related N-acetyltransferase
3UTR_1094	128099 +	129384 Rmet_0122				Op0031f_5		
NPKM_2632	128152 -	130312 Rmet_0123		28.00	2.00	Op0032r_3	EIP-TRA-Pores	Q1LS67 TonB-dependent receptor
NPKM_2633	130426 -	130825 Rmet_0124		85.33	3.79	Op0032r_3	NA	Q1LS66 Putative uncharacterized protein
NPKM_2634	130814 -	131990 Rmet_0125	<i>cobW3</i>	172.67	1.15	Op0032r_3	NA	Q1LS65 Cobalamin synthesis CobW-like protein
NPKM_2635	132182 -	132872 Rmet_0126	<i>dksA1</i>	1311.67	78.49	Op0032r_3	NA	Q1LS64 Transcriptional regulators, TraR/DksA family
NPKM_2636	133190 -	134282 Rmet_0127	<i>cobW2</i>	222.67	17.04	Op0032r_2	NA	Q1LS63 Cobalamin synthesis protein, P47K
5UTR_893	134256 +	134974 Rmet_0129	<i>dehH2</i>			Op0033f_1		
NPKM_2637	134332 -	134842 Rmet_0128	<i>zur</i>	52.67	1.53	Op0032r_1	NA	Q1LS62 Putative ferric uptake regulator, FUR family
NPKM_2638	134974 +	135874 Rmet_0129	<i>dehH2</i>	18.33	1.53	Op0033f_1	MET-XEN-Hex	Q1LS61 Alpha/beta hydrolase fold
NPKM_2639	136125 +	137112 Rmet_0130	<i>bug</i>	3698.33	119.93	Op0033f_2	NA	Q1LS60 Uncharacterized protein UPF0065
NPKM_2640	137307 +	137844 Rmet_0131	<i>hslV</i>	157.00	14.18	Op0033f_2	GIP-PTL-Fold	Q1LS59 ATP-dependent protease hslV
NPKM_2641	137874 +	139194 Rmet_0132	<i>hslU</i>	237.67	20.01	Op0033f_2	GIP-PTL-Fold	Q1LS58 Heat shock protein HslVU, ATPase subunit HslU
3UTR_2066	137982 -	139270 Rmet_0133				Op0034r_1		
3UTR_1095	139195 +	139720 Rmet_0132	<i>hslU</i>			Op0033f_2		
NPKM_2642	139271 -	139799 Rmet_0133		1378.67	1167.22	Op0034r_1	NA	Q1LS57 Nuclear export factor GLE1
NPKM_2643	139938 +	140412 Rmet_0134		31.00	2.00	Op0035f_1	NA	Q1LS56 Putative uncharacterized protein
NPKM_2644	140453 -	141017 Rmet_0135	<i>regA</i>	424.33	338.31	Op0036r_1	NA	Q1LS55 Response regulator receiver domain protein (CheY-like)
NPKM_2645	141046 -	142426 Rmet_0136	<i>regB</i>	245.00	192.35	Op0036r_1	NA	Q1LS54 Sensor protein
NPKM_2646	142607 +	143096 Rmet_0137		1262.67	890.65	Op0037f_1	NA	Q1LS53 Putative uncharacterized protein
NPKM_2647	143181 -	144117 Rmet_0138		152.00	2.65	Op0038r_2	NA	Q1LS52 Transcriptional regulator, LysR family
NPKM_2648	144171 -	144480 Rmet_0139		68.67	6.81	Op0038r_1	NA	Q1LS51 Putative uncharacterized protein
5UTR_1739	144481 -	144529 Rmet_0139				Op0038r_1		
NPKM_2649	144494 +	145529 Rmet_0140	<i>argB</i>	608.33	73.00	Op0039f_1	MET-AA-Urea	Q1LS50 Acetylglutamate kinase
NPKM_2650	145593 +	146598 Rmet_0141		139.67	16.65	Op0039f_1	NA	Q1LS49 Pyrimidine 5-nucleotidase
NPKM_2651	146594 +	147245 Rmet_0142	<i>ttk</i>	215.67	20.55	Op0039f_1	NA	Q1LS48 Cell division inhibitor SlmA
NPKM_2652	147515 +	148688 Rmet_0143	<i>metX</i>	121.00	6.56	Op0039f_1	MET-EN-Sulf	Q1LS47 Homoserine O-acetyltransferase
NPKM_2653	148684 +	149296 Rmet_0144	<i>metW</i>	68.67	11.50	Op0039f_1	NA	Q1LS46 Methionine biosynthesis MetW
3UTR_2065	149374 -	150207 Rmet_0146	<i>ampG</i>			Op0040r_1		
NPKM_2654	149388 +	150207 Rmet_0145		77.67	7.57	Op0039f_1	NA	Q1LS45 Putative uncharacterized protein
3UTR_1096	150208 +	151173 Rmet_0145				Op0039f_1		
NPKM_2655	150208 -	151489 Rmet_0146	<i>ampG</i>	61.00	3.46	Op0040r_1	NA	Q1LS44 Major facilitator superfamily MFS_1
5UTR_894	151185 +	151707 Rmet_0147				Op0041f_1		
5UTR_1738	151490 -	151500 Rmet_0146	<i>ampG</i>			Op0040r_1		
NPKM_2656	151707 +	152562 Rmet_0147		72.00	6.08	Op0041f_1	NA	Q1LS43 Peptidase M48, Ste24p
3UTR_1097	152563 +	153309 Rmet_0147				Op0041f_1		
3UTR_2064	152563 -	152634 Rmet_0148	<i>argC1</i>			Op0042r_2		
NPKM_2657	152635 -	153643 Rmet_0148	<i>argC1</i>	664.67	40.41	Op0042r_2	MET-AA-Urea	Q1LS42 N-acetyl-gamma-glutamyl-phosphate reductase
NPKM_2658	153808 -	154585 Rmet_0149	<i>xthA1</i>	102.00	8.19	Op0042r_1	GIP-REP-Recomb	Q1LS41 Exodeoxyribonuclease III (Xth)
5UTR_1737	154586 -	154763 Rmet_0149	<i>xthA1</i>			Op0042r_1		
5UTR_895	154599 +	154615 Rmet_0150	<i>pyrE</i>			Op0043f_1		

NPKM_2659	154615 +	155293 Rmet_0150	<i>pyrE</i>	171.00	10.15	Op0043f_1	MET-NUC-Pyr	Q1LS40 Orotate phosphoribosyltransferase
3UTR_2063	155330 -	156692 Rmet_0152				Op0044r_3		
NPKM_2660	155340 +	156669 Rmet_0151		79.33	2.31	Op0043f_1	NA	Q1LS39 Patatin
3UTR_1098	156670 +	158629 Rmet_0151				Op0043f_1		
NPKM_2661	156693 -	157503 Rmet_0152		250.00	14.18	Op0044r_3	NA	Q1LS38 Polyphosphate:AMP phosphotransferase
NPKM_2662	157558 -	158425 Rmet_0153	<i>dapF</i>	113.00	6.56	Op0044r_2	MET-AA-Lys_Syn	Q1LS37 Diaminopimelate epimerase
NPKM_2663	158439 -	159333 Rmet_0154	<i>lpxL</i>	28.67	4.73	Op0044r_1	MET-GLYC-LPS	Q1LS36 Lipid A biosynthesis acyltransferase
NPKM_2664	159329 -	160250 Rmet_0155		31.33	1.53	Op0044r_1	MET-GLYC-LPS	Q1LS35 Lipid A biosynthesis acyltransferase
5UTR_1736	160251 -	160380 Rmet_0155				Op0044r_1		
5UTR_896	160253 +	160509 Rmet_0156	<i>metK</i>			Op0045f_1		
NPKM_2665	160509 +	161673 Rmet_0156	<i>metK</i>	1093.67	40.61	Op0045f_1	MET-AA-Met	Q1LS34 S-adenosylmethionine synthetase
NPKM_2666	161815 +	162709 Rmet_0157		142.00	5.20	Op0045f_1	NA	Q1LS33 Putative uncharacterized protein
3UTR_2062	162621 -	162753 Rmet_0158				Op0046r_1		
NPKM_2667	162754 -	164158 Rmet_0158		37.67	1.53	Op0046r_1	NA	Q1LS32 Aldehyde dehydrogenase
5UTR_1735	164159 -	164356 Rmet_0158				Op0046r_1		
NPKM_2668	164405 +	166088 Rmet_0159	<i>betA1</i>	31.00	2.65	Op0047f_1	NA	Q1LS31 Glucose-methanol-choline oxidoreductase
3UTR_2061	165943 -	166138 Rmet_0160				Op0048r_2		
3UTR_1099	166089 +	169776 Rmet_0159	<i>betA1</i>			Op0047f_1		
NPKM_2669	166139 -	167681 Rmet_0160		2.33	0.58	Op0048r_2	DIV-MOT-Chemotax	Q1LS30 Methyl-accepting chemotaxis sensory transducer
5UTR_1734	167682 -	167779 Rmet_0160				Op0048r_2		
3UTR_2060	167808 -	167865 Rmet_0161	<i>aidB</i>			Op0048r_2		
NPKM_2670	167866 -	169552 Rmet_0161	<i>aidB</i>	10.33	0.58	Op0048r_2	NA	Q1LS29 Acyl-CoA dehydrogenase-like protein
5UTR_1733	169553 -	169559 Rmet_0161	<i>aidB</i>			Op0048r_2		
NPKM_2671	169600 -	169945 Rmet_6405		0.33	0.58	Op0048r_1	NA	NA
5UTR_1732	169946 -	169956 Rmet_6405				Op0048r_1		
NPKM_2673	170010 +	171888 Rmet_0162	<i>thiC</i>	413.00	19.29	Op0049f_1	MET-COF-Thia	Q1LS28 Thiamine biosynthesis protein thiC
NPKM_2674	172043 +	173276 Rmet_0163	<i>thiO</i>	157.67	2.52	Op0049f_1	MET-COF-Thia	Q1LS27 FAD dependent oxidoreductase
NPKM_2675	173289 +	173487 Rmet_0164	<i>thiS</i>	137.33	13.20	Op0049f_1	MET-COF-Thia	Q1LS26 Thiamine biosynthesis protein ThiS
NPKM_2676	173494 +	174343 Rmet_0165	<i>thiG</i>	188.33	3.51	Op0049f_1	MET-COF-Thia	Q1LS25 Thiazole biosynthesis protein thiG
NPKM_2677	174339 +	175470 Rmet_0166	<i>thiE</i>	134.00	3.46	Op0049f_1	MET-COF-Thia	Q1LS24 Thiamine monophosphate synthase
3UTR_2059	175588 -	176036 Rmet_0168				Op0050r_1		
NPKM_2678	175606 +	176041 Rmet_0167		85.67	3.21	Op0049f_1	NA	Q1LS23 Phenylacetic acid degradation-related protein
NPKM_2679	176037 -	176481 Rmet_0168		86.00	1.73	Op0050r_1	NA	Q1LS22 Putative uncharacterized protein
3UTR_1100	176042 +	176480 Rmet_0167				Op0049f_1		
NPKM_2680	176501 -	177332 Rmet_0169	<i>thiD</i>	98.67	2.31	Op0050r_1	MET-COF-Thia	Q1LS21 Phosphomethylpyrimidine kinase
5UTR_1731	177333 -	177396 Rmet_0169	<i>thiD</i>			Op0050r_1		
5UTR_897	177471 +	177629 Rmet_0170	<i>ahcY</i>			Op0051f_1		
NPKM_2681	177629 +	179048 Rmet_0170	<i>ahcY</i>	828.33	9.29	Op0051f_1	MET-AA-Met	Q1LS20 Adenosylhomocysteinase
NPKM_2682	179181 +	179529 Rmet_0171		376.67	19.01	Op0051f_1	NA	Q1LS19 Putative uncharacterized protein
NPKM_2683	179576 +	180407 Rmet_0172	<i>metF</i>	346.67	3.06	Op0051f_1	MET-EN-Methane	Q1LS18 Methylene-tetrahydrofolate reductase
NPKM_2684	180413 +	180776 Rmet_0173		178.33	7.51	Op0051f_1	NA	Q1LS17 TfoX-like protein
NPKM_2685	180827 +	181628 Rmet_0174		36.67	2.89	Op0051f_1	NA	Q1LS16 Putative uncharacterized protein
3UTR_2058	181210 -	181632 Rmet_0175				Op0052r_1		

3UTR_1101	181629 +	181856 Rmet_0174				Op0051f_1		
NPKM_2686	181633 -	182368 Rmet_0175		24.33	1.53	Op0052r_1	MET-COF-C1	Q1LS15 5-formyltetrahydrofolate cyclo-ligase
5UTR_898	181869 +	182380 Rmet_0176				Op0053f_1		
5UTR_1730	182369 -	182371 Rmet_0175				Op0052r_1		
NPKM_2687	182380 +	184348 Rmet_0176		213.33	4.51	Op0053f_1	NA	Q1LS14 Lytic transglycosylase, catalytic
NPKM_2688	184448 +	185471 Rmet_0177		50.00	2.65	Op0053f_1	MET-EN-OxPhos	Q1LS13 NAD-dependent epimerase/dehydratase
NPKM_2689	185639 +	186329 Rmet_0178	<i>gst</i>	121.00	7.21	Op0053f_2	MET-OAA-GSH	Q1LS12 Glutathione S-transferase-like protein
NPKM_2690	186332 +	187577 Rmet_0179	<i>cca</i>	164.33	7.77	Op0053f_2	GIP-TL-Ass	Q1LS11 Multifunctional CCA protein
3UTR_2057	186552 -	187616 Rmet_0180				Op0054r_1		
NPKM_2691	187617 -	187812 Rmet_0180		45.67	1.53	Op0054r_1	NA	Q1LS10 Putative membrane protein
NPKM_2692	187837 -	189034 Rmet_0181		91.00	1.73	Op0054r_1	NA	Q1LS09 Putative uncharacterized protein
5UTR_1729	189035 -	189129 Rmet_0181				Op0054r_1		
NPKM_2693	189068 +	189869 Rmet_0182		97.67	2.08	Op0055f_1	NA	Q1LS08 Short-chain dehydrogenase/reductase SDR
NPKM_2694	189890 +	190289 Rmet_0183	<i>folB</i>	150.33	8.74	Op0055f_1	MET-COF-Folate	Q1LS07 Dihydroneopterin aldolase
NPKM_2695	190404 +	191349 Rmet_0184		118.33	3.21	Op0055f_1	NA	Q1LS06 tRNA 2-thiocytidine biosynthesis protein ttcA
3UTR_2056	190624 -	191377 Rmet_0185				Op0056r_1		
NPKM_2696	191378 -	192458 Rmet_0185		32.67	0.58	Op0056r_1	NA	Q1LS05 Putative uncharacterized protein
5UTR_1728	192459 -	192897 Rmet_0185				Op0056r_1		
NPKM_2697	192472 +	193837 Rmet_0186	<i>glmU</i>	146.33	1.53	Op0057f_1	MET-CAH-AminSug	Q1LS04 Bifunctional protein glmU
NPKM_2698	193851 +	195690 Rmet_0187	<i>glmS</i>	211.00	4.58	Op0057f_1	MET-CAH-AminSug	Q1LS03 Glutamine--fructose-6-phosphate transaminase
NPKM_2699	196165 +	196834 Rmet_0188		221.33	2.08	Op0057f_1	NA	Q1LS02 Pilus assembly protein
NPKM_2700	196824 +	197367 Rmet_0189		151.67	9.87	Op0057f_1	GIP-PTL-T2S	Q1LS01 Type-4 fimbrial biogenesis pilV transmembrane protein
NPKM_2701	197378 +	198107 Rmet_0190		156.00	12.00	Op0057f_1	GIP-PTL-T2S	Q1LS00 Type-4 fimbrial biogenesis transmembrane protein
NPKM_2702	198103 +	198700 Rmet_0191		124.67	6.66	Op0057f_1	GIP-PTL-T2S	Q1LRZ9 Putative type-4 fimbrial biogenesis transmembrane protein
NPKM_2703	198696 +	202080 Rmet_0192		189.67	8.08	Op0057f_1	GIP-PTL-T2S	Q1LRZ8 Putative type-4 fimbrial biogenesis pily1-related protein
NPKM_2704	202082 +	202526 Rmet_0193		222.00	16.64	Op0057f_1	GIP-PTL-T2S	Q1LRZ7 Pilus assembly protein PilE
NPKM_2705	202544 +	202721 Rmet_6406		165.33	14.22	Op0057f_1	NA	NA
NPKM_2706	202935 +	203532 Rmet_0194	<i>ribA</i>	146.33	10.21	Op0057f_1	MET-COF-Ribo	Q1LRZ6 GTP cyclohydrolase-2
3UTR_1102	203533 +	203578 Rmet_0194	<i>ribA</i>			Op0057f_1		
5UTR_899	203581 +	203745 Rmet_0195	<i>bfr</i>			Op0057f_1		
NPKM_2707	203745 +	204222 Rmet_0195	<i>bfr</i>	21.00	2.65	Op0057f_1	NA	Q1LRZ5 Bacterioferritin
NPKM_2708	204306 +	204381 Rmet_R0002		23.00	1.00	Op0057f_1	NA	NA
NPKM_2709	204743 +	205187 Rmet_0196		92.00	4.58	Op0057f_2	MET-AA-Urea	Q1LRZ4 GCN5-related N-acetyltransferase
NPKM_2710	205267 +	206251 Rmet_0197	<i>qor</i>	187.00	2.65	Op0057f_3	NA	Q1LRZ3 Alcohol dehydrogenase, zinc-binding
3UTR_2055	205577 -	206272 Rmet_0198	<i>dmeF</i>			Op0058r_2		
3UTR_1103	206252 +	207294 Rmet_0197	<i>qor</i>			Op0057f_3		
NPKM_2711	206273 -	207422 Rmet_0198	<i>dmeF</i>	38.00	2.65	Op0058r_2	EIP-TRA-Ion	Q1LRZ2 Cation diffusion facilitator family transporter
NPKM_2712	207471 -	208398 Rmet_0199		11.33	0.58	Op0058r_1	NA	Q1LRZ1 Transcriptional regulator, LysR family
5UTR_1727	208399 -	208449 Rmet_0199				Op0058r_1		
NPKM_2713	208469 +	209951 Rmet_0200	<i>leuC</i>	4.67	0.58	Op0059f_1	MET-AA-ValLeulle	Q1LRZ0 3-isopropylmalate dehydratase, large subunit
NPKM_2714	209943 +	210597 Rmet_0201	<i>leuD</i>	4.00	1.00	Op0059f_1	MET-AA-ValLeulle	Q1LKH6 3-isopropylmalate dehydratase, small subunit
NPKM_2715	210610 +	211489 Rmet_0202	<i>dehH1</i>	51.00	2.65	Op0059f_2	MET-XEN-Hex	Q1LRY8 Alpha/beta hydrolase fold
NPKM_2716	211951 +	212632 Rmet_0203		331.00	20.30	Op0059f_3	NA	Q1LRY7 Putative signal peptide protein

3UTR_2054	212048 -	212648 Rmet_0204				Op0060r_1		
NPKM_2717	212649 -	214095 Rmet_0204		23.67	1.15	Op0060r_1	NA	Q1LRY6 Transcriptional regulator, GntR family
NPKM_2718	214385 +	215717 Rmet_0205	<i>aptA</i>	40.33	3.21	Op0061f_1	MET-CAH-Prop	Q1LRY5 Aminotransferase
NPKM_2719	215757 +	217275 Rmet_0206	<i>mmsA</i>	159.33	7.37	Op0061f_2	MET-CAH-Prop	Q1LRY4 Methylmalonate-semialdehyde dehydrogenase (Acylation)
3UTR_1104	217276 +	217316 Rmet_0206	<i>mmsA</i>			Op0061f_2		
5UTR_900	217368 +	217472 Rmet_0207				Op0061f_2		
NPKM_2720	217472 +	218882 Rmet_0207		9.33	0.58	Op0061f_2	EIP-TRA-Ion	Q1LRY3 Amino acid permease-associated region
3UTR_2053	217968 -	218881 Rmet_0208				Op0062r_1		
NPKM_2721	218882 -	220283 Rmet_0208		23.00	1.73	Op0062r_1	NA	Q1LRY2 Transcriptional regulator, GntR family
3UTR_1105	218883 +	219146 Rmet_0207				Op0061f_2		
5UTR_1726	220284 -	220295 Rmet_0208				Op0062r_1		
5UTR_901	220371 +	220443 Rmet_0209				Op0063f_1		
NPKM_2722	220443 +	220782 Rmet_0209		27.00	1.00	Op0063f_1	NA	Q1LRY1 Putative uncharacterized protein
NPKM_2723	221031 +	224313 Rmet_0210	<i>sbm</i>	60.67	1.53	Op0063f_2	NA	Q1LRY0 Methylmalonyl-CoA mutase
NPKM_2724	224402 +	224840 Rmet_0211		182.33	10.79	Op0063f_3	EIP-TRA-ABC	Q1LRX9 Histidine triad (HIT) protein
3UTR_2052	224860 -	225857 Rmet_0213	<i>crp1</i>			Op0064r_1		
NPKM_2725	224896 +	225751 Rmet_0212	<i>hbdA</i>	354.33	12.22	Op0063f_3	MET-CAH-But	Q1LRX8 3-hydroxyacyl-CoA dehydrogenase
3UTR_1106	225752 +	226558 Rmet_0212	<i>hbdA</i>			Op0063f_3		
NPKM_2726	225858 -	226638 Rmet_0213	<i>crp1</i>	30.00	2.00	Op0064r_1	NA	Q1LRX7 Cyclic nucleotide-binding protein
5UTR_1725	226639 -	226645 Rmet_0213	<i>crp1</i>			Op0064r_1		
5UTR_902	226671 +	226792 Rmet_0214				Op0065f_1		
NPKM_2727	226792 +	228757 Rmet_0214		8.67	0.58	Op0065f_1	MET-LIP-FAMet	Q1LRX6 AMP-dependent synthetase and ligase
NPKM_2728	228773 +	229715 Rmet_0215	<i>livG8</i>	6.33	0.58	Op0065f_1	EIP-TRA-ABC	Q1LRX5 ABC transporter-related protein
NPKM_2729	229755 +	230670 Rmet_0216		3.67	0.58	Op0065f_1	EIP-TRA-ABC	Q1LRX4 Inner-membrane translocator
NPKM_2730	230682 +	231759 Rmet_0217		2.67	0.58	Op0065f_1	EIP-TRA-ABC	Q1LRX3 Inner-membrane translocator
NPKM_2731	231823 +	233161 Rmet_0218		8.00	0.00	Op0065f_2	EIP-TRA-ABC	Q1LRX2 Putative branched-chain amino acid transport system substrate-binding protein
5UTR_903	233163 +	233223 Rmet_0219	<i>livF8</i>			Op0065f_2		
NPKM_2732	233223 +	234039 Rmet_0219	<i>livF8</i>	8.67	0.58	Op0065f_2	EIP-TRA-ABC	Q1LRX1 ABC transporter-related protein
NPKM_2733	234053 +	235316 Rmet_0220	<i>paaK</i>	11.33	0.58	Op0065f_2	MET-AA-Tyr	Q1LRX0 Putative phenylacetate-CoA ligase
3UTR_2051	234785 -	235365 Rmet_0221				Op0066r_1		
3UTR_1107	235317 +	236372 Rmet_0220	<i>paaK</i>			Op0065f_2		
NPKM_2734	235366 -	235819 Rmet_0221		119.00	16.70	Op0066r_1	NA	Q1LRW9 Putative uncharacterized protein
NPKM_2735	235859 -	236837 Rmet_0222	<i>nppD</i>	195.33	27.02	Op0066r_1	MET-EN-Nitrogen	Q1LRW8 2-nitropropane dioxygenase, NPD
NPKM_2736	237240 -	238434 Rmet_0223		199.67	8.39	Op0066r_1	NA	Q1LRW7 SAM-dependent methyltransferase
NPKM_2737	238438 -	238747 Rmet_0224		261.33	17.93	Op0066r_1	NA	Q1LRW6 Putative uncharacterized protein
NPKM_2738	238764 -	239958 Rmet_0225	<i>dac</i>	188.00	7.00	Op0066r_1	NA	Q1LRW5 Penicillin-binding protein 6. Serine peptidase. MEROPS family S11
NPKM_2739	240001 -	240646 Rmet_0226		159.00	2.00	Op0066r_1	NA	Q1LRW4 Putative transmembrane protein
NPKM_2740	240780 -	241185 Rmet_0227		191.33	17.90	Op0066r_1	NA	Q1LRW3 Ferredoxin-like protein
5UTR_904	241491 +	241550 Rmet_0228	<i>dctA</i>			Op0067f_1		
NPKM_2741	241550 +	242840 Rmet_0228	<i>dctA</i>	11.33	2.52	Op0067f_1	NA	Q1LRW2 C4-dicarboxylate transport protein 1
NPKM_2742	242958 +	244965 Rmet_0229	<i>dctB</i>	17.67	1.53	Op0067f_1	NA	Q1LRW1 Sensor protein
NPKM_2743	245001 +	246336 Rmet_0230	<i>dctD</i>	32.33	2.52	Op0067f_1	NA	Q1LRW0 Two component, sigma54 specific, transcriptional regulator, Fis family
NPKM_2744	246472 +	248074 Rmet_0231	<i>hutH</i>	10.67	0.58	Op0067f_1	MET-EN-Nitrogen	Q1LRV9 Histidine ammonia-lyase

3UTR_2050	247555 -	248110 Rmet_0232				Op0068r_2			
3UTR_1108	248075 +	248495 Rmet_0231	<i>hutH</i>			Op0067f_1			
NPKM_2745	248111 -	250220 Rmet_0232		53.33	2.52	Op0068r_2	GIP-REP-Recomb	Q1LRV8 UvrD/REP helicase	
3UTR_2049	250227 -	250372 Rmet_0233				Op0068r_2			
NPKM_2746	250373 -	250913 Rmet_0233		267.33	136.62	Op0068r_2	NA	Q1LRV7 Thioredoxin-like protein	
NPKM_2747	251041 -	251539 Rmet_0234		60.33	8.50	Op0068r_1	NA	Q1LRV6 Putative uncharacterized protein	
5UTR_905	251203 +	251569 Rmet_0235				Op0069f_1			
5UTR_1724	251540 -	251597 Rmet_0234				Op0068r_1			
NPKM_2748	251569 +	252259 Rmet_0235		76.00	11.53	Op0069f_1	NA	Q1LRV5 Putative uncharacterized protein	
NPKM_2749	252301 +	252946 Rmet_0236	<i>rhtB</i>	163.67	29.87	Op0069f_2	EIP-TRA-Ion	Q1LRV4 Lysine exporter protein (LYSE/YGGA)	
3UTR_1109	252947 +	253196 Rmet_0236	<i>rhtB</i>			Op0069f_2			
NPKM_2750	253219 -	254758 Rmet_0237		3.00	0.00	Op0070r_1	GIP-PTL-Fold	Q1LRV3 Mg chelatase-related protein	
NPKM_2751	254840 -	255098 Rmet_0238		356.67	29.57	Op0070r_1	NA	Q1LRV2 Putative uncharacterized protein	
5UTR_1723	255099 -	255458 Rmet_0238				Op0070r_1			
5UTR_906	255593 +	255650 Rmet_0239				Op0071f_1			
NPKM_2752	255650 +	256451 Rmet_0239		2.00	0.00	Op0071f_1	NA	Q1LRV1 Putative uncharacterized protein	
NPKM_2753	256503 +	256842 Rmet_0240	<i>glnK</i>	10.67	1.15	Op0071f_2	NA	Q1LRV0 Nitrogen regulatory protein P-II (GlnB, GlnK)	
NPKM_2754	256873 +	258406 Rmet_0241	<i>amtB</i>	14.00	1.00	Op0071f_2	EIP-TRA-Ion	Q1LRU9 Ammonium transporter	
3UTR_2048	258309 -	258546 Rmet_6407				Op0072r_1			
3UTR_1110	258407 +	258469 Rmet_0241	<i>amtB</i>			Op0071f_2			
NPKM_2755	258547 -	258613 Rmet_6407		1.33	0.58	Op0072r_1	NA	NA	
5UTR_907	258591 +	258868 Rmet_0242	<i>gshA</i>			Op0071f_3			
NPKM_2756	258868 +	260164 Rmet_0242	<i>gshA</i>	363.00	13.23	Op0071f_3	MET-AA-GluGSH	Q1LRU8 Glutamate--cysteine ligase GshA	
NPKM_2757	260188 +	261142 Rmet_0243	<i>gshB</i>	407.33	22.14	Op0071f_3	MET-AA-GluGSH	Q1LRU7 Glutathione synthase	
NPKM_2758	261266 +	261722 Rmet_0244		318.67	17.79	Op0071f_3	EIP-TRA-Pts	Q1LRU6 PTS system fructose subfamily IIA component	
NPKM_2759	261690 +	261960 Rmet_0245	<i>ptsH</i>	395.33	11.24	Op0071f_3	NA	Q1LRU5 HPrNtr	
NPKM_2760	262010 +	263768 Rmet_0246	<i>ptsI</i>	225.00	4.36	Op0071f_3	EIP-TRA-Pts	Q1LRU4 Phosphoenolpyruvate--protein phosphotransferase	
NPKM_2761	264004 +	264310 Rmet_0247	<i>bfd</i>	143.33	11.37	Op0071f_3	NA	Q1LRU3 BFD-like (2Fe-2S)-binding region	
3UTR_2047	264416 -	265150 Rmet_0249	<i>moeB</i>			Op0072r_1			
NPKM_2762	264455 +	264935 Rmet_0248	<i>bfr</i>	1437.67	76.29	Op0071f_4	NA	Q1LRU2 Bacterioferritin	
3UTR_1111	264936 +	266471 Rmet_0248	<i>bfr</i>			Op0071f_4			
NPKM_2763	265151 -	265904 Rmet_0249	<i>moeB</i>	69.00	1.73	Op0072r_1	NA	Q1LRU1 UBA/THIF-type NAD/FAD binding fold	
NPKM_2764	266027 -	267635 Rmet_0250	<i>ctpA</i>	393.00	16.09	Op0072r_1	NA	Q1LRU0 Carboxyl-terminal protease	
NPKM_2765	267832 -	268579 Rmet_0251	<i>gpmA</i>	248.33	1.53	Op0072r_1	MET-CAH-FbP	Q1LRT9 Phosphoglycerate mutase	
5UTR_1722	268580 -	268988 Rmet_0251	<i>gpmA</i>			Op0072r_1			
5UTR_908	268650 +	268723 Rmet_6408				Op0073f_1			
NPKM_2766	268723 +	269137 Rmet_6408		319.00	17.69	Op0073f_1	NA	NA	
NPKM_2767	269215 +	269473 Rmet_0252	<i>grxC</i>	213.67	7.09	Op0073f_1	GIP-PTL-Fold	Q1LRT8 Glutaredoxin, GrxC	
NPKM_2768	270721 +	272437 Rmet_0253		662.67	33.01	Op0073f_2	GIP-REP-Recomb	Q1LRT7 RNA-directed DNA polymerase	
NPKM_2769	272595 +	273114 Rmet_0254	<i>secB</i>	846.67	24.34	Op0073f_2	GIP-PTL-Exp	Q1LRT6 Protein-export protein secB	
NPKM_2770	273232 +	274261 Rmet_0255	<i>gpsA</i>	82.67	4.16	Op0073f_2	MET-LIP-GlycPLip	Q1LRT5 Glycerol-3-phosphate dehydrogenase [NAD(P)+]	
3UTR_2046	274060 -	275263 Rmet_0257	<i>yibK</i>			Op0074r_1			
NPKM_2771	274267 +	275251 Rmet_0256	<i>bug</i>	73.67	4.04	Op0073f_2	NA	Q1LRT4 Uncharacterized protein UPF0065	

3UTR_1112	275252 +	276167 Rmet_0256	<i>bug</i>			Op0073f_2		
NPKM_2772	275264 -	275735 Rmet_0257	<i>yibK</i>	58.33	2.31	Op0074r_1	GIP-TL-Ass	Q1LRT3 RNA methyltransferase TrmH, group 2
NPKM_2773	275787 -	276627 Rmet_0258	<i>gntX</i>	56.33	2.52	Op0074r_1	NA	Q1LRT2 Amidophosphoribosyltransferases-like protein
5UTR_909	276183 +	276651 Rmet_0259				Op0075f_1		
5UTR_1721	276628 -	277180 Rmet_0258	<i>gntX</i>			Op0074r_1		
NPKM_2774	276651 +	277554 Rmet_0259		90.33	4.04	Op0075f_1	NA	Q1LRT1 Methyltransferase type 11
NPKM_2775	277817 +	278333 Rmet_0260		731.33	451.15	Op0075f_2	NA	Q1LRT0 Putative transmembrane protein
NPKM_2776	278394 +	279663 Rmet_0261	<i>coxB</i>	746.33	437.13	Op0075f_2	MET-EN-OxPhos	Q1LRS9 Cytochrome c oxidase subunit 2
NPKM_2777	279705 +	281316 Rmet_0262	<i>coxA</i>	910.33	547.18	Op0075f_2	MET-EN-OxPhos	Q1LRS8 Cytochrome c oxidase, subunit I
NPKM_2778	281381 +	281534 Rmet_6409		344.67	203.81	Op0075f_2	NA	NA
NPKM_2779	281570 +	282167 Rmet_0263	<i>ctaG</i>	322.33	175.70	Op0075f_2	MET-EN-OxPhos	Q1LRS7 Cytochrome c oxidase assembly protein CtaG/Cox11
3UTR_2045	282112 -	283454 Rmet_0266				Op0076r_1		
NPKM_2780	282169 +	282397 Rmet_0264		234.33	117.39	Op0075f_2	NA	Q1LRS6 Putative transmembrane protein
NPKM_2781	282494 +	283355 Rmet_0265	<i>coxC</i>	539.00	309.19	Op0075f_3	MET-EN-OxPhos	Q1LRS5 Cytochrome c oxidase, subunit III
NPKM_2782	283455 -	283665 Rmet_0266		37.00	5.00	Op0076r_1	NA	Q1LRS4 Putative transmembrane protein
NPKM_2783	283665 +	284484 Rmet_0267		119.00	51.97	Op0077f_1	NA	Q1LRS3 Putative uncharacterized protein
5UTR_1720	283666 -	283709 Rmet_0266				Op0076r_1		
NPKM_2784	284470 +	285148 Rmet_0268		136.00	46.77	Op0077f_1	NA	Q1LRS2 Putative transmembrane protein
NPKM_2785	285153 +	286257 Rmet_0269	<i>ctaA</i>	99.00	34.66	Op0077f_1	MET-EN-OxPhos	Q1LRS1 Cytochrome oxidase assembly
3UTR_2044	285472 -	287943 Rmet_0272	<i>rpoH</i>			Op0078r_1		
NPKM_2786	286253 +	287192 Rmet_0270	<i>ctaB</i>	133.67	18.77	Op0077f_1	MET-EN-OxPhos	Q1LRS0 Protoheme IX farnesyltransferase
NPKM_2787	287276 +	287891 Rmet_0271	<i>sco2</i>	562.33	367.58	Op0077f_2	NA	Q1LRR9 Electron transport protein SCO1/SenC
3UTR_1113	287892 +	288436 Rmet_0271	<i>sco2</i>			Op0077f_2		
NPKM_2788	287944 -	288880 Rmet_0272	<i>rpoH</i>	563.00	10.00	Op0078r_1	GIP-TK-RNAP	Q1LRR8 RNA polymerase sigma factor
5UTR_1719	288881 -	289074 Rmet_0272	<i>rpoH</i>			Op0078r_1		
5UTR_910	289010 +	289211 Rmet_0273				Op0079f_1		
NPKM_2789	289211 +	290087 Rmet_0273		208.00	11.53	Op0079f_1	NA	Q1LRR7 Pirin-like protein
3UTR_2043	289334 -	290126 Rmet_0274				Op0080r_3		
3UTR_1114	290088 +	291143 Rmet_0273				Op0079f_1		
NPKM_2790	290127 -	291117 Rmet_0274		77.33	3.21	Op0080r_3	MET-AA-PheTyrTrp	Q1LRR6 Glycosyl transferase, family 3
NPKM_2791	291215 -	292019 Rmet_0275	<i>nasD</i>	1.00	0.00	Op0080r_2	EIP-TRA-ABC	Q1LRR5 Nitrate transport ATP-binding subunits C and D
NPKM_2792	292035 -	292947 Rmet_0276	<i>nasE</i>	0.00	0.00	Op0080r_1	EIP-TRA-ABC	Q1LRR4 Nitrate transport permease
3UTR_2042	292977 -	293014 Rmet_0277	<i>nasF</i>			Op0080r_1		
NPKM_2793	293015 -	294320 Rmet_0277	<i>nasF</i>	0.00	0.00	Op0080r_1	EIP-TRA-ABC	Q1LRR3 Putative nitrate transporter protein
5UTR_1718	294321 -	294346 Rmet_0277	<i>nasF</i>			Op0080r_1		
3UTR_2041	294653 -	294682 Rmet_0278				Op0080r_1		
NPKM_2794	294683 -	295343 Rmet_0278		1.33	0.58	Op0080r_1	NA	Q1LRR2 Response regulator receiver (CheY-like) and ANTAR domain protein
5UTR_911	295324 +	295394 Rmet_0279				Op0081f_1		
NPKM_2795	295394 +	296195 Rmet_0279		1002.00	59.23	Op0081f_1	MET-AA-Tyr	Q1LRR1 Fumarylacetoacetate (FAA) hydrolase
NPKM_2796	296199 +	296847 Rmet_0280	<i>maiA</i>	823.00	54.44	Op0081f_1	MET-AA-Tyr	Q1LRR0 Maleylacetoacetate isomerase
3UTR_2040	296571 -	296917 Rmet_0281	<i>ftsY</i>			Op0082r_1		
3UTR_1115	296848 +	296890 Rmet_0280	<i>maiA</i>			Op0081f_1		
NPKM_2797	296918 -	297941 Rmet_0281	<i>ftsY</i>	158.67	13.05	Op0082r_1	GIP-PTL-Exp	Q1LRQ9 Signal recognition particle-docking protein FtsY

5UTR_912	297705 +	297879 Rmet_6410				Op0083f_1		
NPKM_2798	297879 +	298245 Rmet_6410		4.67	1.15	Op0083f_1	NA	NA
5UTR_1717	297942 -	298498 Rmet_0281	<i>ftsY</i>			Op0082r_1		
NPKM_2799	298241 +	299756 Rmet_0282		254.33	5.51	Op0083f_2	NA	Q1LRQ8 Peptidase M16-like protein
NPKM_2800	299764 +	301129 Rmet_0283		163.33	3.79	Op0083f_2	NA	Q1LRQ7 Peptidase M16-like protein
NPKM_2801	301237 +	301870 Rmet_0284		123.00	1.00	Op0083f_2	NA	Q1LRQ6 Putative uncharacterized protein
NPKM_2802	302081 +	302567 Rmet_0285	<i>coaD</i>	854.00	52.09	Op0083f_3	MET-COF-Pant	Q1LRQ5 Phosphopantetheine adenylyltransferase
NPKM_2803	302633 +	302894 Rmet_0286	<i>fdx</i>	811.00	64.90	Op0083f_3	NA	Q1LRQ4 4Fe-4S ferredoxin, iron-sulfur binding
3UTR_2039	302782 -	303016 Rmet_0287	<i>pth</i>			Op0084r_4		
3UTR_1116	302895 +	303706 Rmet_0286	<i>fdx</i>			Op0083f_3		
NPKM_2804	303017 -	303614 Rmet_0287	<i>pth</i>	120.67	4.62	Op0084r_4	GIP-TL-Ass	Q1LRQ3 Peptidyl-tRNA hydrolase
NPKM_2805	303788 -	304400 Rmet_0288	<i>rplY</i>	2856.33	113.81	Op0084r_4	GIP-TL-Ribo	Q1LRQ2 50S ribosomal protein L25
NPKM_2806	304570 -	305524 Rmet_0289	<i>prs</i>	984.33	34.30	Op0084r_3	MET-CAH-PP_KDPG	Q1LRQ1 Ribose-phosphate pyrophosphokinase
NPKM_2807	305619 -	305696 Rmet_R0003		369.33	71.86	Op0084r_2	NA	NA
NPKM_2808	305763 -	306642 Rmet_0290	<i>ispE</i>	376.67	41.63	Op0084r_2	MET-LIP-Ster	Q1LRQ0 4-diphosphocytidyl-2-C-methyl-D-erythritol kinase
NPKM_2809	306638 -	307253 Rmet_0291	<i>lolB</i>	87.33	4.04	Op0084r_1	MET-COF-Porph	Q1LRP9 Outer-membrane lipoprotein lolB
NPKM_2810	307338 -	309246 Rmet_0292		208.00	6.56	Op0084r_1	NA	Q1LRP8 Tetratricopeptide TPR_2
5UTR_1716	309247 -	309423 Rmet_0292				Op0084r_1		
5UTR_913	309306 +	309516 Rmet_0293	<i>mutM</i>			Op0085f_1		
NPKM_2811	309516 +	310410 Rmet_0293	<i>mutM</i>	34.67	1.15	Op0085f_1	NA	Q1LRP7 Formamidopyrimidine-DNA glycosylase
NPKM_2812	310667 +	312686 Rmet_0294		326.33	14.57	Op0085f_2	NA	Q1LRP6 Putative uncharacterized protein
NPKM_2813	312750 +	313968 Rmet_0295	<i>mutY</i>	49.00	3.61	Op0085f_2	GIP-REP-Recomb	Q1LRP5 A/G-specific DNA-adenine glycosylase
3UTR_2038	312812 -	313988 Rmet_0296				Op0086r_3		
3UTR_1117	313969 +	314492 Rmet_0295	<i>mutY</i>			Op0085f_2		
NPKM_2814	313989 -	314643 Rmet_0296		87.33	2.08	Op0086r_3	NA	Q1LRP4 Peptidase S16, lon-like protein
NPKM_2815	314689 -	315580 Rmet_0297		166.33	7.51	Op0086r_3	NA	Q1LRP3 UPF0042 protein Rmet_0297
NPKM_2816	315694 -	316066 Rmet_0298		306.33	12.22	Op0086r_3	NA	Q1LRP2 Conserved hypothetical signal peptide protein
NPKM_2817	316241 -	317213 Rmet_0299	<i>hprK</i>	171.67	7.23	Op0086r_3	NA	Q1LRP1 HPr kinase/phosphorylase
NPKM_2818	317281 -	317776 Rmet_0300	<i>ptsN</i>	292.00	17.00	Op0086r_3	EIP-TRA-Pts	Q1LRP0 PTS IIA-like nitrogen-regulatory protein PtsN
NPKM_2819	317850 -	318141 Rmet_0301		136.33	16.50	Op0086r_2	NA	Q1LRN9 Putative uncharacterized protein
NPKM_2820	318213 -	318567 Rmet_0302	<i>rpoX</i>	1992.67	177.58	Op0086r_2	GIP-TL-Ass	Q1LRN8 SSU ribosomal protein S30P / sigma 54 modulation protein
NPKM_2821	318617 -	320096 Rmet_0303	<i>rpoN</i>	188.67	10.02	Op0086r_1	GIP-TK-RNAP	Q1LRN7 Sigma-54 (RpoN)
NPKM_2822	320219 -	321011 Rmet_0304	<i>lptB</i>	228.00	7.81	Op0086r_1	NA	Q1LRN6 ABC transporter-related protein
NPKM_2823	321036 -	321681 Rmet_0305		171.67	4.51	Op0086r_1	NA	Q1LRN5 OstA-like protein
NPKM_2824	321743 -	322370 Rmet_0306		143.33	7.23	Op0086r_1	NA	Q1LRN4 Putative uncharacterized protein
NPKM_2825	322373 -	323357 Rmet_0307	<i>kdsD2</i>	228.00	5.29	Op0086r_1	NA	Q1LRN3 KpsF/GutQ family protein
5UTR_1715	323358 -	323445 Rmet_0307	<i>kdsD2</i>			Op0086r_1		
5UTR_914	323372 +	323462 Rmet_0308				Op0087f_1		
NPKM_2826	323462 +	325487 Rmet_0308		41.33	2.08	Op0087f_1	EIP-TRA-Ion	Q1LRN2 Sodium/hydrogen exchanger
3UTR_2037	324772 -	325475 Rmet_0309				Op0088r_1		
NPKM_2827	325476 -	325905 Rmet_0309		502.67	58.73	Op0088r_1	NA	Q1LRN1 Putative uncharacterized protein
NPKM_2828	325963 -	326593 Rmet_0310		1173.00	149.92	Op0088r_1	GIP-PTL-Fold	Q1LRN0 Peptidase C56, Pfpl
5UTR_1714	326594 -	326762 Rmet_0310				Op0088r_1		

NPKM_2829	326668 +	327241 Rmet_0311	<i>apt</i>	147.00	2.65	Op0089f_1	MET-NUC-Pur	Q1LRM9 Adenine phosphoribosyltransferase
NPKM_2830	327520 +	329197 Rmet_0312		128.33	2.52	Op0089f_1	EIP-TRA-Ion	Q1LRM8 Na/Pi cotransporter II-related
3UTR_2036	328600 -	329249 Rmet_0313	<i>uvrA1</i>			Op0090r_1		
3UTR_1118	329198 +	330593 Rmet_0312				Op0089f_1		
NPKM_2831	329250 -	332118 Rmet_0313	<i>uvrA1</i>	77.00	4.00	Op0090r_1	GIP-REP-Recomb	Q1LRM7 Excinuclease ABC subunit A
5UTR_915	331424 +	332392 Rmet_0314				Op0091f_1		
5UTR_1713	332119 -	332199 Rmet_0313	<i>uvrA1</i>			Op0090r_1		
NPKM_2832	332392 +	333649 Rmet_0314		110.00	3.61	Op0091f_1	NA	Q1LRM6 Major facilitator superfamily MFS_1
NPKM_2833	333924 +	334470 Rmet_0315	<i>ssb1</i>	237.67	5.69	Op0091f_2	GIP-REP-Complex	Q1LRM5 Single-stranded DNA-binding protein
3UTR_1119	334471 +	334586 Rmet_0315	<i>ssb1</i>			Op0091f_2		
5UTR_916	334662 +	334702 Rmet_0316				Op0091f_2		
NPKM_2834	334702 +	335569 Rmet_0316		31.00	0.00	Op0091f_2	NA	Q1LRM4 Putative uncharacterized protein
NPKM_2835	335756 +	336953 Rmet_0317	<i>int</i>	15.67	0.58	Op0091f_2	NA	Q1LRM3 Phage integrase
NPKM_2836	336949 +	337462 Rmet_0318		12.00	2.00	Op0091f_2	NA	Q1LRM2 Putative uncharacterized protein
NPKM_2837	337640 -	337856 Rmet_0319	<i>tnmC</i>	0.00	0.00	Op0092r_1	NA	Q58AJ2 Putative uncharacterized protein RMe0313 (Putative uncharacterized protei
NPKM_2838	337909 -	338743 Rmet_0320	<i>gspA</i>	0.00	0.00	Op0092r_1	NA	Q5NUU5 Hypothetical general secretion pathway protein A (ATPase) (General secre
NPKM_2839	338739 -	340179 Rmet_0321	<i>tnmA</i>	0.00	0.00	Op0092r_1	NA	Q5NUU4 ISRme2 transposase protein (Integrase, catalytic region) (Insertion eleme
NPKM_2840	340290 -	340860 Rmet_0322	<i>tnmB</i>	0.00	0.00	Op0092r_1	NA	Q1L9I3 Putative uncharacterized protein
NPKM_2841	341082 +	342111 Rmet_0323		15.00	1.73	Op0093f_1	NA	Q1LRL7 Phage integrase
NPKM_2842	342115 +	344119 Rmet_0324		9.00	1.00	Op0093f_1	NA	Q1LRL6 Putative uncharacterized protein
NPKM_2843	344105 +	344498 Rmet_0325		6.33	0.58	Op0093f_1	NA	Q1LRL5 Putative uncharacterized protein
3UTR_2035	344271 -	344938 Rmet_0326				Op0094r_4		
3UTR_1120	344499 +	344558 Rmet_0325				Op0093f_1		
5UTR_917	344570 +	344621 Rmet_6411				Op0093f_1		
NPKM_2844	344621 +	344747 Rmet_6411		5.00	3.61	Op0093f_1	NA	NA
3UTR_1121	344748 +	344970 Rmet_6411				Op0093f_1		
NPKM_2845	344939 -	345692 Rmet_0326		11.33	0.58	Op0094r_4	NA	Q1LRL4 Putative uncharacterized protein
5UTR_1712	345693 -	345781 Rmet_0326				Op0094r_4		
3UTR_2034	346100 -	346252 Rmet_0327	<i>arsP</i>			Op0094r_3		
NPKM_2846	346253 -	347447 Rmet_0327	<i>arsP</i>	5.00	0.00	Op0094r_3	NA	Q1LRL3 Major facilitator superfamily MFS_1
NPKM_2847	347465 -	348230 Rmet_0328	<i>arsH</i>	13.00	0.00	Op0094r_3	NA	Q1LRL2 NADPH-dependent FMN reductase
NPKM_2848	348226 -	348649 Rmet_0329	<i>arsC1</i>	13.67	2.31	Op0094r_3	NA	Q1LRL1 Arsenate reductase
NPKM_2849	348658 -	349723 Rmet_0330	<i>arsB</i>	8.67	0.58	Op0094r_3	EIP-TRA-Ion	Q1LRL0 Bile acid:sodium symporter
NPKM_2850	349719 -	350232 Rmet_0331	<i>arsC2</i>	8.67	1.53	Op0094r_3	NA	Q1LRK9 Protein tyrosine phosphatase
NPKM_2851	350297 -	350786 Rmet_0332	<i>arsI</i>	25.00	2.00	Op0094r_3	NA	Q1LRK8 Glyoxalase/bleomycin resistance protein/dioxygenase
NPKM_2852	350789 -	351119 Rmet_0333	<i>arsR</i>	8.00	1.00	Op0094r_2	NA	Q1LRK7 Transcriptional regulator, ArsR family
NPKM_2853	351312 -	352131 Rmet_0334	<i>arsM</i>	1.00	0.00	Op0094r_1	NA	Q1LRK6 Methyltransferase type 11
3UTR_2033	352326 -	352359 Rmet_0335				Op0094r_1		
NPKM_2854	352360 -	353860 Rmet_0335		2.33	0.58	Op0094r_1	NA	Q1LRK5 Lytic transglycosylase, catalytic
NPKM_2855	354043 -	354850 Rmet_0336		51.00	5.57	Op0094r_1	NA	Q1LRK4 Transcriptional regulator, IclR family
NPKM_2856	354846 -	355632 Rmet_0337		51.33	4.51	Op0094r_1	NA	Q1LRK3 Transcriptional regulator, IclR family
5UTR_1711	355633 -	355766 Rmet_0337				Op0094r_1		
NPKM_2857	355849 +	356809 Rmet_0338		9.00	1.00	Op0095f_1	NA	Q1LRK2 Beta-lactamase-like protein

NPKM_2858	356912 +	358667 Rmet_0339		9.00	0.00	Op0095f_1	MET-AA-Phe	Q1LRK1 Monooxygenase, FAD-binding
NPKM_2859	358692 +	358902 Rmet_0340		9.33	1.53	Op0095f_1	NA	Q1LRK0 Putative uncharacterized protein
3UTR_1122	358903 +	358967 Rmet_0340				Op0095f_1		
NPKM_2860	358985 +	360347 Rmet_0341		1.00	0.00	Op0095f_1	NA	Q1LRJ9 Major facilitator superfamily MFS_1
3UTR_1123	360348 +	360355 Rmet_0341				Op0095f_1		
NPKM_2861	360491 +	361400 Rmet_0342	<i>gltI</i>	6.67	0.58	Op0095f_2	NA	Q1LRJ8 Extracellular solute-binding protein, family 3
3UTR_2032	360682 -	361411 Rmet_0343				Op0096r_1		
3UTR_1124	361401 +	361423 Rmet_0342	<i>gltI</i>			Op0095f_2		
NPKM_2862	361412 -	362309 Rmet_0343		35.00	2.00	Op0096r_1	NA	Q1LRJ7 Transcriptional regulator, RpiR family
NPKM_2863	362512 +	363838 Rmet_0344		8.67	0.58	Op0097f_1	NA	Q1LRJ6 Aminotransferase
NPKM_2864	363849 +	364719 Rmet_0345		8.67	0.58	Op0097f_1	NA	Q1LRJ5 Putative uncharacterized protein
NPKM_2865	364799 +	365999 Rmet_0346		25.33	1.53	Op0097f_2	NA	Q1LRJ4 Aminotransferase
3UTR_1125	366000 +	366294 Rmet_0346				Op0097f_2		
3UTR_2031	366046 -	366069 Rmet_0347				Op0098r_1		
NPKM_2866	366070 -	367537 Rmet_0347		10.67	0.58	Op0098r_1	NA	Q1LRJ3 RND efflux system, outer membrane lipoprotein, NodT
NPKM_2867	367549 -	368704 Rmet_0348		6.00	0.00	Op0098r_1	NA	Q1LRJ2 ABC-type multidrug transport system permease component
NPKM_2868	368700 -	369687 Rmet_0349		11.33	0.58	Op0098r_1	EIP-TRA-ABC	Q1LRJ1 ABC transporter-related protein
NPKM_2869	369683 -	370646 Rmet_0350		10.33	1.53	Op0098r_1	EIP-TRA-ABC	Q1LRJ0 Secretion protein HlyD
NPKM_2870	370663 -	371356 Rmet_0351		10.67	2.08	Op0098r_1	NA	Q1LRJ9 Transcriptional regulator, TetR family
5UTR_918	371461 +	371485 Rmet_0352	<i>oprB</i>			Op0099f_1		
NPKM_2871	371485 +	372964 Rmet_0352	<i>oprB</i>	11.67	0.58	Op0099f_1	EIP-TRA-Pores	Q1LRJ8 Carbohydrate-selective porin OprB
3UTR_2030	372335 -	372975 Rmet_0353	<i>queF</i>			Op0100r_1		
3UTR_1126	372965 +	373468 Rmet_0352	<i>oprB</i>			Op0099f_1		
NPKM_2872	372976 -	373810 Rmet_0353	<i>queF</i>	113.67	4.04	Op0100r_1	NA	Q1LRJ7 NADPH-dependent 7-cyano-7-deazaguanine reductase
NPKM_2873	373821 -	375519 Rmet_0354	<i>ilvA</i>	94.67	3.79	Op0100r_1	MET-AA-GlySerThr	Q1LRJ6 L-threonine ammonia-lyase
5UTR_919	375490 +	375532 Rmet_0355	<i>otsB</i>			Op0101f_1		
5UTR_1710	375520 -	375522 Rmet_0354	<i>ilvA</i>			Op0100r_1		
NPKM_2874	375532 +	376351 Rmet_0355	<i>otsB</i>	533.33	51.29	Op0101f_1	MET-CAH-Starch	Q1LRJ5 HAD-superfamily hydrolase subfamily IIB
NPKM_2875	376347 +	378210 Rmet_0356		345.67	19.01	Op0101f_1	NA	Q1LRJ4 Glycoside hydrolase 15-related
NPKM_2876	378241 +	379636 Rmet_0357	<i>otsA</i>	213.33	6.03	Op0101f_1	MET-CAH-Starch	Q1LRJ3 Alpha,alpha-trehalose-phosphate synthase
3UTR_2029	378969 -	379681 Rmet_0358				Op0102r_2		
3UTR_1127	379637 +	384054 Rmet_0357	<i>otsA</i>			Op0101f_1		
NPKM_2877	379682 -	380279 Rmet_0358		51.67	5.51	Op0102r_2	NA	Q1LRJ2 Putative uncharacterized protein
NPKM_2878	380275 -	381313 Rmet_0359	<i>coxI</i>	59.00	2.00	Op0102r_2	GIP-PTL-Fold	Q1LRJ1 Predicted sulfurylase large subunit, molybdopterin cytosine dinucleotide bio:
NPKM_2879	381294 -	381858 Rmet_0360	<i>coxG</i>	32.67	5.86	Op0102r_2	NA	Q1LRJ0 Carbon monoxide dehydrogenase subunit G
NPKM_2880	381854 -	383141 Rmet_0361	<i>coxE</i>	9.67	0.58	Op0102r_1	NA	Q1LRH9 VWA containing CoxE-like protein
NPKM_2881	383143 -	384040 Rmet_0362	<i>coxD</i>	11.67	0.58	Op0102r_1	NA	Q1LRH8 ATPase associated with various cellular activities, AAA_5
5UTR_920	384058 +	388067 Rmet_0366				Op0103f_1		
NPKM_2882	384116 -	384917 Rmet_0363	<i>coxM</i>	23.67	0.58	Op0102r_1	MET-EN-Methane	Q1LRH7 Molybdopterin dehydrogenase, FAD-binding
NPKM_2883	384933 -	387312 Rmet_0364	<i>coxL</i>	30.00	1.73	Op0102r_1	NA	Q1LRH6 Xanthine dehydrogenase, molybdenum binding subunit apoprotein
NPKM_2884	387323 -	387845 Rmet_0365	<i>coxS</i>	73.67	2.89	Op0102r_1	MET-EN-Methane	Q1LRH5 (2Fe-2S)-binding
5UTR_1709	387846 -	387989 Rmet_0365	<i>coxS</i>			Op0102r_1		
NPKM_2885	388067 +	388646 Rmet_0366		51.67	6.03	Op0103f_1	NA	Q1LRH4 Putative membrane protein

NPKM_2886	388815 +	392790 Rmet_0367		264.67	10.41	Op0103f_2	NA	Q1LRH3 FAD linked oxidase-like protein
NPKM_2887	392868 +	393303 Rmet_0368		180.00	9.17	Op0103f_2	NA	Q1LRH2 Histidine triad (HIT) protein
NPKM_2888	393453 +	395364 Rmet_0369		81.00	3.61	Op0103f_2	EIP-TRA-ABC	Q1LRH1 ABC transporter-like protein
NPKM_2889	395434 +	395851 Rmet_0370		246.67	15.70	Op0103f_3	NA	Q1LRH0 Putative uncharacterized protein
NPKM_2890	395886 +	396618 Rmet_0371	<i>ubiE</i>	220.67	5.51	Op0103f_3	MET-COF-CoQ	Q1LRG9 Ubiquinone/menaquinone biosynthesis methyltransferase ubiE
NPKM_2891	396680 +	397670 Rmet_0372		2986.33	43.02	Op0103f_4	NA	Q1LRG8 Import inner membrane translocase, subunit Tim44
NPKM_2892	397790 +	398462 Rmet_0373		250.33	6.81	Op0103f_4	NA	Q1LRG7 Putative uncharacterized protein
NPKM_2893	398503 +	400081 Rmet_0374	<i>ubiB</i>	135.33	3.06	Op0103f_4	MET-COF-CoQ	Q1LRG6 2-octaprenylphenol hydroxylase
NPKM_2894	400090 +	400324 Rmet_6412		81.33	4.04	Op0103f_4	NA	NA
NPKM_2895	400415 +	401852 Rmet_0375		65.33	3.51	Op0103f_4	NA	Q1LRG5 Na+/solute symporter
NPKM_2896	402075 +	402405 Rmet_0376		388.67	17.47	Op0103f_5	NA	Q1LRG4 Putative uncharacterized protein
NPKM_2897	402419 +	403127 Rmet_0377		264.00	4.00	Op0103f_5	NA	Q1LRG3 Putative uncharacterized protein
NPKM_2898	403175 +	404984 Rmet_0378	<i>aspS</i>	516.67	12.01	Op0103f_5	MET-AA-AlaAsp	Q1LRG2 Aspartyl-tRNA synthetase
NPKM_2899	405162 +	406098 Rmet_0379		85.00	11.53	Op0103f_5	NA	Q1LRG1 Putative transmembrane protein
NPKM_2900	406144 +	406666 Rmet_0380	<i>ntpA</i>	66.33	6.81	Op0103f_5	NA	Q1LRG0 NUDIX hydrolase
3UTR_2028	406598 -	407433 Rmet_0382	<i>mobB</i>			Op0104r_1		
NPKM_2901	406662 +	407418 Rmet_0381		48.33	2.52	Op0103f_5	NA	Q1LRF9 Endonuclease/exonuclease/phosphatase
NPKM_2902	407434 -	407944 Rmet_0382	<i>mobB</i>	93.00	4.58	Op0104r_1	MET-COF-Folate	Q1LRF8 Molybdopterin-guanine dinucleotide biosynthesis protein B
NPKM_2903	408001 +	409387 Rmet_0383		45.00	2.00	Op0105f_1	MET-LIP-GlycLip	Q1LRF7 Phospholipase D/Transphosphatidylase
NPKM_2904	409721 +	410360 Rmet_0384		213.00	40.34	Op0105f_2	NA	Q1LRF6 Transcriptional regulator, TetR family
NPKM_2905	410450 +	412238 Rmet_0385		117.00	35.59	Op0105f_2	NA	Q1LRF5 Acyl-CoA dehydrogenase-like protein
NPKM_2906	412351 +	414778 Rmet_0386		32.67	2.52	Op0105f_2	MET-CAH-But	Q1LRF4 3-hydroxyacyl-CoA dehydrogenase
NPKM_2907	414802 +	415999 Rmet_0387	<i>fadA</i>	63.00	1.73	Op0105f_2	MET-LIP-FAMet	Q1LRF3 Thiolase
NPKM_2908	416112 +	417069 Rmet_0388		17.67	1.15	Op0105f_2	NA	Q1LRF2 DegV
3UTR_2027	417060 -	417960 Rmet_0390	<i>yciA</i>			Op0106r_1		
NPKM_2909	417103 +	417880 Rmet_0389		120.67	1.53	Op0105f_3	MET-CAH-Prop	Q1LRF1 Enoyl-CoA hydratase
NPKM_2910	417961 -	418435 Rmet_0390	<i>yciA</i>	82.67	0.58	Op0106r_1	NA	Q1LRF0 Thioesterase superfamily
NPKM_2911	418453 +	420346 Rmet_0391	<i>atmA</i>	25.00	1.73	Op0107f_1	EIP-TRA-ABC	Q1LRE9 ABC transporter-related protein
NPKM_2912	420528 +	421587 Rmet_0392		4.33	0.58	Op0107f_1	EIP-TRA-ABC	Q1LRE8 Twin-arginine translocation pathway signal
NPKM_2913	421583 +	422429 Rmet_0393	<i>tauB</i>	1.67	0.58	Op0107f_1	EIP-TRA-ABC	Q1LRE7 ABC transporter-related protein
3UTR_2026	421999 -	423271 Rmet_0395	<i>ybaO</i>			Op0108r_1		
NPKM_2914	422425 +	423205 Rmet_0394		2.00	1.00	Op0107f_1	EIP-TRA-ABC	Q1LRE6 Binding-protein-dependent transport systems inner membrane component
NPKM_2915	423272 -	423731 Rmet_0395	<i>ybaO</i>	44.33	3.21	Op0108r_1	NA	Q1LRE5 Transcriptional regulator, AsnC family
5UTR_921	423698 +	424372 Rmet_6413				Op0109f_1		
NPKM_2916	423794 -	424349 Rmet_0396		79.67	7.37	Op0108r_1	NA	Q1LRE4 Cysteine dioxygenase type I
5UTR_1708	424350 -	424386 Rmet_0396				Op0108r_1		
NPKM_2917	424372 +	424546 Rmet_6413		3.33	0.58	Op0109f_1	NA	NA
NPKM_2918	424481 +	425471 Rmet_0397		25.67	1.53	Op0109f_2	NA	Q1LRE3 Transcriptional regulator, LysR family
NPKM_2919	425605 +	426913 Rmet_0398	<i>gdhA</i>	212.00	32.08	Op0109f_3	MET-EN-Nitrog	Q1LRE2 Glu/Leu/Phe/Val dehydrogenase
NPKM_2920	427216 +	428116 Rmet_0399	<i>gltI</i>	3038.67	81.51	Op0109f_4	EIP-TRA-ABC	Q1LRE1 Extracellular solute-binding protein, family 3
NPKM_2921	428181 +	428910 Rmet_0400	<i>gltI</i>	494.33	26.86	Op0109f_4	NA	Q1LRE0 Amino acid ABC transporter, permease protein, 3-TM region, His/Glu/Gln/
NPKM_2922	428921 +	429605 Rmet_0401	<i>gltK</i>	482.67	14.01	Op0109f_4	NA	Q1LRD9 Amino acid ABC transporter, permease protein, 3-TM region, His/Glu/Gln/
NPKM_2923	429601 +	430336 Rmet_0402	<i>gltL</i>	775.33	22.37	Op0109f_4	NA	Q1LRD8 ABC transporter-related protein

3UTR_2025	429651 -	430455 Rmet_0403	yafJ			Op0110r_1		
NPKM_2924	430456 -	431287 Rmet_0403	yafJ	67.00	3.00	Op0110r_1	NA	Q1LRD7 Glutamine amidotransferase, class-II
5UTR_1707	431288 -	431330 Rmet_0403	yafJ			Op0110r_1		
NPKM_2925	431491 +	432490 Rmet_0404	ttuC	111.67	2.89	Op0111f_1	MET-CAH-But	Q1LRD6 Tartrate dehydrogenase
NPKM_2926	432486 +	433785 Rmet_0405	ttuD	107.00	2.00	Op0111f_1	MET-CAH-DiCarb	Q1LRD5 MOFRL
NPKM_2927	433817 +	434852 Rmet_0406	pyrC	180.33	6.66	Op0111f_1	MET-NUC-Pyr	Q1LRD4 Dihydroorotase
NPKM_2928	434857 +	435646 Rmet_0407		54.33	1.15	Op0111f_1	NA	Q1LRD3 Putative transmembrane protein
NPKM_2929	435725 +	436006 Rmet_R0004	rnpB	4913.67	285.31	Op0111f_2	NA	NA
3UTR_2024	435959 -	436103 Rmet_0408				Op0112r_2		
3UTR_1128	436007 +	436542 Rmet_R0004	rnpB			Op0111f_2		
NPKM_2930	436104 -	436527 Rmet_0408		224.00	19.31	Op0112r_2	NA	Q1LRD1 Putative uncharacterized protein
NPKM_2931	436609 +	436819 Rmet_6414		0.67	0.58	Op2001f_1	NA	NA
NPKM_2932	436755 -	437100 Rmet_0409		13.00	1.00	Op0112r_1	GIP-TL-Ribo	Q1LRD0 50S ribosomal protein L13
NPKM_2933	436842 +	437034 Rmet_6415		785.67	101.93	Op0113f_1	NA	NA
NPKM_2934	437286 +	437715 Rmet_0410	rplM	5175.00	23.52	Op0113f_2	GIP-TL-Ribo	Q1LRC9 30S ribosomal protein S9
NPKM_2935	437729 +	438122 Rmet_0411	rpsI	5739.33	110.00	Op0113f_2	NA	Q1LRC8 Putative uncharacterized protein
NPKM_2936	438340 +	439096 Rmet_0412		65.33	4.04	Op0113f_2	NA	Q1LRC7 Putative uncharacterized protein
NPKM_2937	439119 +	439614 Rmet_0413		115.33	1.15	Op0113f_2	NA	Q1LRC6 Putative iron-sulfur cluster insertion protein erpA
NPKM_2938	439722 +	440091 Rmet_0414	erpA	966.00	58.51	Op0113f_3	NA	Q1LRC5 Anhydro-N-acetylmuramic acid kinase
3UTR_2023	440068 -	440181 Rmet_0415	anmK			Op0114r_1		
3UTR_1129	440092 +	441378 Rmet_0414	erpA			Op0113f_3		
NPKM_2939	440182 -	441325 Rmet_0415	anmK	129.33	5.51	Op0114r_1	NA	NA
NPKM_2940	441327 -	442722 Rmet_0416		188.67	7.09	Op0114r_1	MET-AA-PheTyrTrp	Q1LRC3 Tyrosyl-tRNA synthetase
5UTR_922	442056 +	442940 Rmet_0417	tyrS			Op0115f_1		
5UTR_1706	442723 -	443431 Rmet_0416				Op0114r_1		
NPKM_2941	442940 +	444182 Rmet_0417	tyrS	309.00	8.19	Op0115f_1	GIP-TL-Ass	Q1LRC2 D-tyrosyl-tRNA(Tyr) deacylase
NPKM_2942	444195 +	444666 Rmet_0418	dtd	291.33	9.07	Op0115f_1	NA	Q1LRC1 Phospholipid-binding protein, PBP family
NPKM_2943	444699 +	445347 Rmet_0419	ybhB	494.67	8.96	Op0115f_1	MET-CAH-FbP	Q1LRC0 Phosphoglycerate mutase
3UTR_2022	445233 -	446211 Rmet_0421				Op0116r_4		
NPKM_2944	445408 +	446083 Rmet_0420	gpmB	334.33	10.26	Op0115f_1	NA	Q1LRB9 Putative lipoprotein
3UTR_1130	446084 +	447975 Rmet_0420	gpmB			Op0115f_1		
NPKM_2945	446212 -	446797 Rmet_0421		1927.33	186.53	Op0116r_4	NA	Q1LRB8 Putative uncharacterized protein
NPKM_2946	446843 -	447455 Rmet_0422		1040.67	116.36	Op0116r_4	GIP-REP-Recomb	Q1LRB7 Holliday junction ATP-dependent DNA helicase ruvB
NPKM_2947	447657 -	448725 Rmet_0423	ruvB	97.33	4.04	Op0116r_3	GIP-REP-Recomb	Q1LRB6 Holliday junction ATP-dependent DNA helicase ruvA
NPKM_2948	448794 -	449376 Rmet_0424	ruvA	103.33	4.04	Op0116r_3	MET-LIP-GlycPLip	Q1LRB5 Glycerophosphoryl diester phosphodiesterase
NPKM_2949	449430 -	450609 Rmet_0425	glpQ	95.00	2.00	Op0116r_3	GIP-REP-Recomb	Q1LRB4 Crossover junction endodeoxyribonuclease ruvC
NPKM_2950	450723 -	451269 Rmet_0426	ruvC	61.00	5.29	Op0116r_3	MET-NUC-Pur	Q1LRB3 Bifunctional purine biosynthesis protein purH
NPKM_2951	451395 -	452970 Rmet_0427	purH	291.00	6.08	Op0116r_3	NA	Q1LRB2 DNA-binding protein Fis
NPKM_2952	452992 -	453226 Rmet_0428		87.67	9.29	Op0116r_2	GIP-TL-Ass	Q1LRB1 Dihydrouridine synthase TIM-barrel protein nifR3
NPKM_2953	453222 -	454368 Rmet_0429	dusB	114.00	7.00	Op0116r_2	MET-COF-CoQ	Q1LRB0 Ubiquinone biosynthesis hydroxylase, UbiH/UbiF/VisC/COQ6 family
NPKM_2954	454490 -	455744 Rmet_0430	ubiH	239.33	10.79	Op0116r_2	NA	Q1LRA9 Putative uncharacterized protein
NPKM_2955	455721 -	456186 Rmet_0431		281.33	7.23	Op0116r_2	NA	Q1LRA8 Aminopeptidase P. Metallo peptidase. MEROPS family M24B
NPKM_2956	456182 -	457580 Rmet_0432	pepP	211.00	8.00	Op0116r_2	NA	Q1LRA7 Nucleotidyl transferase

NPKM_2957	457708 -	458407 Rmet_0433		93.00	3.00	Op0116r_1	NA	Q1LRA6 AzlC-like protein
NPKM_2958	458412 -	458736 Rmet_6416		83.33	2.31	Op0116r_1	NA	NA
NPKM_2959	458732 -	459530 Rmet_0434		65.67	5.69	Op0116r_1	NA	Q1LRA5 Aminoglycoside phosphotransferase
NPKM_2960	459541 -	460588 Rmet_0435		100.00	4.00	Op0116r_1	NA	Q1LRA4 LPS-assembly protein
5UTR_923	460475 +	460770 Rmet_0436	<i>ostA</i>			Op0117f_1		
NPKM_2961	460770 +	463245 Rmet_0436	<i>ostA</i>	160.67	6.81	Op0117f_1	GIP-PTL-Fold	Q1LRA3 Chaperone surA
NPKM_2962	463254 +	464736 Rmet_0437	<i>surA</i>	196.67	5.69	Op0117f_1	MET-COF-B6	Q1LRA2 4-hydroxythreonine-4-phosphate dehydrogenase
NPKM_2963	464752 +	465829 Rmet_0438	<i>pdxA</i>	132.33	6.51	Op0117f_1	NA	NA
NPKM_2964	465832 +	466669 Rmet_0439	<i>ksgA</i>	124.33	2.31	Op0117f_1	GIP-TL-Ass	Q1LRA1 Dimethyladenosine transferase
3UTR_2021	466601 -	467804 Rmet_0441				Op0118r_4		
NPKM_2965	466711 +	467740 Rmet_0440	<i>trpS</i>	261.00	8.66	Op0117f_2	MET-AA-Trp	Q1LRA0 Tryptophanyl-tRNA synthetase
3UTR_1131	467741 +	468943 Rmet_0440	<i>trpS</i>			Op0117f_2		
NPKM_2966	467805 -	468711 Rmet_0441		150.33	6.51	Op0118r_4	NA	Q1LR99 Putative uncharacterized protein
NPKM_2967	468717 -	469125 Rmet_0442	<i>gloA</i>	258.33	10.02	Op0118r_4	MET-CAH-Pyr	Q1LR98 Glyoxalase I
NPKM_2968	469175 +	469373 Rmet_6417		2.00	1.73	Op0117f_2	NA	NA
3UTR_1132	469374 +	469387 Rmet_6417				Op0117f_2		
NPKM_2969	469432 -	470311 Rmet_0443		112.67	5.03	Op0118r_3	NA	Q1LR97 Putative uncharacterized protein
NPKM_2970	470307 -	471069 Rmet_0444	<i>plsC</i>	98.00	2.00	Op0118r_3	MET-LIP-GlycLip	Q1LR96 Phospholipid/glycerol acyltransferase
NPKM_2971	471098 -	471680 Rmet_0445	<i>gmhB</i>	119.33	3.06	Op0118r_3	MET-GLYC-LPS	Q1LR95 D-alpha,beta-D-heptose 1,7-bisphosphate phosphatase
NPKM_2972	471715 -	473839 Rmet_0446	<i>glyS</i>	151.33	1.15	Op0118r_3	MET-AA-GlySerThr	Q1LR94 Glycyl-tRNA synthetase, beta subunit
NPKM_2973	473869 -	474490 Rmet_0447		103.33	1.15	Op0118r_3	NA	Q1LR93 Conserved hypothetical signal peptide protein
NPKM_2974	474486 -	475440 Rmet_0448	<i>glyQ</i>	154.00	8.00	Op0118r_3	MET-AA-GlySerThr	Q1LR92 Glycyl-tRNA synthetase alpha subunit
NPKM_2975	475923 -	477456 Rmet_0449	<i>Int</i>	28.33	2.08	Op0118r_2	NA	Q1LR91 Apolipoprotein N-acyltransferase
NPKM_2976	477548 -	478436 Rmet_0450	<i>corC</i>	107.33	10.02	Op0118r_2	EIP-TRA-Other	Q1LR90 CBS transporter-associated protein
NPKM_2977	478580 -	479318 Rmet_0451		92.33	9.45	Op0118r_2	NA	B2AHA2 Putative metal-dependent hydrolase, COG0319; putative diacylglycerol kina
NPKM_2978	479320 -	480316 Rmet_0452	<i>phoL</i>	88.00	5.57	Op0118r_2	NA	Q1LR88 PhoH-like protein
NPKM_2979	480336 -	481689 Rmet_0453	<i>miaB</i>	142.67	2.89	Op0118r_2	GIP-TL-Ass	Q1LR87 tRNA-i(6)A37 thiotransferase enzyme MiaB
NPKM_2980	481752 -	482130 Rmet_0454		196.33	23.18	Op0118r_2	NA	Q1LR86 Putative uncharacterized protein
NPKM_2981	482295 -	483978 Rmet_0455	<i>clcB</i>	28.00	1.00	Op0118r_1	EIP-TRA-Pores	Q1LR85 Cl-channel, voltage gated
5UTR_1705	483979 -	484029 Rmet_0455	<i>clcB</i>			Op0118r_1		
5UTR_924	484113 +	484217 Rmet_0456	<i>rhIE1</i>			Op0119f_1		
NPKM_2982	484217 +	485840 Rmet_0456	<i>rhIE1</i>	109.67	6.11	Op0119f_1	NA	Q1LR84 DEAD/DEAH box helicase-like protein
3UTR_2020	485365 -	486951 Rmet_0458	<i>uspA1</i>			Op0120r_1		
NPKM_2983	485851 +	486898 Rmet_0457	<i>yihE</i>	51.67	0.58	Op0119f_1	NA	Q1LR83 Aminoglycoside phosphotransferase
3UTR_1133	486899 +	487249 Rmet_0457	<i>yihE</i>			Op0119f_1		
NPKM_2984	486952 -	487387 Rmet_0458	<i>uspA1</i>	189.33	7.51	Op0120r_1	NA	Q1LR82 UspA
5UTR_925	487564 +	487716 Rmet_0459				Op0121f_1		
NPKM_2985	487716 +	488340 Rmet_0459		7.00	1.00	Op0121f_1	EIP-SIG-2Comp	Q1LR81 Two component transcriptional regulator, LuxR family
NPKM_2986	488467 +	490126 Rmet_0460		38.00	1.73	Op0121f_2	MET-CAH-But	Q1LR80 Pyridoxal-dependent decarboxylase
NPKM_2987	490135 -	490390 Rmet_0461		43.67	5.51	Op0122r_3	NA	Q1LR79 Putative uncharacterized protein
NPKM_2988	490316 +	490487 Rmet_6418		15.00	1.73	Op0121f_2	NA	NA
3UTR_1134	490488 +	490517 Rmet_6418				Op0121f_2		
NPKM_2989	490488 -	490565 Rmet_R0005		8.33	5.13	Op0122r_2	NA	NA

3UTR_2019	490573 -	490732 Rmet_0462				Op0122r_2		
NPKM_2990	490733 -	492431 Rmet_0462		81.67	16.26	Op0122r_2	NA	Q1LR78 Major facilitator superfamily MFS_1
NPKM_2991	492789 -	493110 Rmet_0463		24.67	2.31	Op0122r_1	NA	Q1LR77 Putative membrane protein
NPKM_2992	493106 -	494681 Rmet_0464		37.00	2.65	Op0122r_1	EIP-SIG-2Comp	Q1LR76 Sensor protein
NPKM_2993	494702 -	495392 Rmet_0465		101.67	4.93	Op0122r_1	EIP-SIG-2Comp	Q1LR75 Two component transcriptional regulator, winged helix family
5UTR_1704	495393 -	495582 Rmet_0465				Op0122r_1		
5UTR_926	495508 +	495631 Rmet_0466	recA			Op0123f_1		
NPKM_2994	495631 +	496693 Rmet_0466	recA	787.33	17.16	Op0123f_1	GIP-REP-Recomb	Q1LR74 Protein recA
NPKM_2995	496731 +	497280 Rmet_0467	recX	67.00	2.65	Op0123f_1	NA	Q1LR73 Regulatory protein RecX
NPKM_2996	497529 +	498291 Rmet_0468		335.33	18.77	Op0123f_2	NA	Q1LR72 Putative uncharacterized protein
NPKM_2997	498380 +	499547 Rmet_0469	sucC	1674.00	136.82	Op0123f_3	MET-CAH-TCA	Q1LR71 Succinyl-CoA synthetase (ADP-forming) beta subunit
NPKM_2998	499605 +	500487 Rmet_0470	sucD	1957.67	172.10	Op0123f_3	MET-CAH-TCA	Q1LR70 Succinyl-CoA ligase [ADP-forming] subunit alpha
NPKM_2999	500529 +	500724 Rmet_6419		461.00	33.15	Op0123f_3	NA	NA
NPKM_3000	500800 +	501496 Rmet_0471		462.00	10.39	Op0123f_3	NA	Q1LR69 Integral membrane protein TerC
3UTR_1135	501497 +	501583 Rmet_0471				Op0123f_3		
NPKM_3001	501864 +	502413 Rmet_0472	pilA	3.33	1.15	Op0123f_3	GIP-PTL-T2S	Q1LR68 Fimbrial protein pilin
3UTR_1136	502414 +	502720 Rmet_0472	pilA			Op0123f_3		
NPKM_3002	502737 +	503157 Rmet_0473	pilE	1.67	0.58	Op0123f_3	GIP-PTL-T2S	Q1LR67 Fimbrial protein pilin
3UTR_1137	503158 +	503247 Rmet_0473	pilE			Op0123f_3		
NPKM_3003	503387 +	505175 Rmet_0474		38.67	0.58	Op0123f_4	NA	Q1LR66 O-antigen polymerase
3UTR_2018	504740 -	505196 Rmet_0475				Op0124r_1		
3UTR_1138	505176 +	506235 Rmet_0474				Op0123f_4		
NPKM_3004	505197 -	505737 Rmet_0475		14.33	1.53	Op0124r_1	NA	Q1LR65 Proline-rich region
NPKM_3005	505733 -	506198 Rmet_0476		12.67	1.53	Op0124r_1	NA	Q1LR64 Putative uncharacterized protein
5UTR_1703	506199 -	506447 Rmet_0476				Op0124r_1		
3UTR_2017	506475 -	506517 Rmet_0477				Op0124r_1		
NPKM_3006	506518 -	506764 Rmet_0477		31.00	3.61	Op0124r_1	NA	Q1LR63 Putative uncharacterized protein
NPKM_3007	506942 -	507131 Rmet_0478		57.33	6.03	Op0124r_1	NA	Q1LR62 Molybdenum cofactor biosynthesis enzyme-like protein
5UTR_1702	507132 -	507710 Rmet_0478				Op0124r_1		
5UTR_927	507275 +	507315 Rmet_0479				Op0125f_1		
NPKM_3008	507315 +	508245 Rmet_0479		48.67	2.89	Op0125f_1	NA	Q1LR61 ABC transporter, ATP-binding protein-related protein
3UTR_2016	507713 -	508284 Rmet_0480	tnpA			Op0126r_1		
3UTR_1139	508246 +	508295 Rmet_0479				Op0125f_1		
NPKM_3009	508285 -	509536 Rmet_0480	tnpA	0.00	0.00	Op0126r_1	GIP-REP-Recomb	Q9RBF5 Ralstonia eutropha insertion sequence IS1090
3UTR_2015	509547 -	510373 Rmet_0482				Op0128r_1		
5UTR_928	509570 +	509587 Rmet_0481				Op0127f_1		
NPKM_3010	509587 +	510289 Rmet_0481		4.00	0.00	Op0127f_1	NA	Q1LR59 Putative uncharacterized protein
3UTR_1140	510290 +	510751 Rmet_0481				Op0127f_1		
NPKM_3011	510374 -	510857 Rmet_0482		13.33	3.51	Op0128r_1	NA	Q1LR58 Putative uncharacterized protein
5UTR_929	510818 +	510845 Rmet_6420				Op0129f_1		
NPKM_3012	510845 +	511022 Rmet_6420		4.33	1.15	Op0129f_1	NA	NA
3UTR_1141	511023 +	511110 Rmet_6420				Op0129f_1		
NPKM_3013	511184 +	512711 Rmet_0483	tnpA	0.00	0.00	Op0129f_1	NA	Q1LHY9 Integrase, catalytic region

NPKM_3014	512700 +	513486 Rmet_0484	<i>tnpB</i>	0.00	0.00	Op0129f_1	NA	Q1LHZ0 IstB-like ATP-binding protein
3UTR_2014	513501 -	513542 Rmet_0485				Op0129f_1		
NPKM_3015	513543 -	513915 Rmet_0485		42.00	4.58	Op0129f_1	NA	Q1LR55 Putative uncharacterized protein
NPKM_3016	514058 -	514538 Rmet_0486	<i>moaC</i>	97.00	1.00	Op0130r_1	MET-COF-Folate	Q1LR54 Molybdenum cofactor biosynthesis protein C
5UTR_930	514119 +	514575 Rmet_0487				Op0131f_1		
5UTR_1701	514539 -	514560 Rmet_0486	<i>moaC</i>			Op0130r_1		
NPKM_3017	514575 +	516393 Rmet_0487		42.33	2.08	Op0131f_1	NA	Q1LR53 Peptidase M48, Ste24p
3UTR_2013	515679 -	516436 Rmet_0488				Op0132r_1		
3UTR_1142	516394 +	517051 Rmet_0487				Op0131f_1		
NPKM_3018	516437 -	517010 Rmet_0488		74.33	1.15	Op0132r_1	NA	Q1LR52 Putative uncharacterized protein
NPKM_3019	517073 -	518111 Rmet_0489		84.33	4.16	Op0132r_1	NA	Q1LR51 Alpha/beta hydrolase fold
NPKM_3020	518128 -	518569 Rmet_0490		151.00	2.00	Op0132r_1	NA	Q1LR50 Putative uncharacterized protein
NPKM_3021	518579 -	519644 Rmet_0491	<i>rfaF</i>	107.33	4.04	Op0132r_1	MET-GLYC-LPS	Q1LR49 Lipopolysaccharide heptosyltransferase II
NPKM_3022	519717 -	519912 Rmet_0492		529.33	34.82	Op0132r_1	NA	Q1LR48 Putative uncharacterized protein
NPKM_3023	519971 -	520892 Rmet_0493	<i>ilvE</i>	361.67	2.08	Op0132r_1	MET-AA-ValLeulle	Q1LR47 Branched chain amino acid aminotransferase / branched chain amino acid:
5UTR_931	520850 +	520890 Rmet_0494				Op0133f_1		
NPKM_3024	520890 +	523968 Rmet_0494		22.33	1.53	Op0133f_1	NA	Q1LR46 SNF2-related
5UTR_1700	520893 -	520971 Rmet_0493	<i>ilvE</i>			Op0132r_1		
3UTR_1143	523969 +	524098 Rmet_0494				Op0133f_1		
NPKM_3025	524192 +	525710 Rmet_0495		4.00	0.00	Op0133f_1	MET-AA-Phe	Q1LR45 Amidase
NPKM_3026	525746 +	527072 Rmet_0496		5.67	0.58	Op0133f_1	NA	Q1LR44 Major facilitator superfamily MFS_1
3UTR_1144	527073 +	527167 Rmet_0496				Op0133f_1		
5UTR_932	527171 +	527259 Rmet_0497				Op0133f_2		
NPKM_3027	527259 +	528060 Rmet_0497		38.33	5.51	Op0133f_2	NA	Q1LR43 AzlC-like protein
NPKM_3028	528056 +	528380 Rmet_0498		49.00	6.56	Op0133f_2	NA	Q1LR42 Branched-chain amino acid transport
3UTR_1145	528381 +	529189 Rmet_0498				Op0133f_2		
NPKM_3029	528431 -	529565 Rmet_0499		10.00	2.65	Op0134r_1	NA	Q1LR41 Transcriptional regulator, LuxR family
NPKM_3030	529626 -	530679 Rmet_0500		99.67	18.58	Op0134r_1	NA	Q1LR40 Regulatory protein, LuxR
5UTR_1699	530680 -	530803 Rmet_0500				Op0134r_1		
5UTR_933	530874 +	530996 Rmet_0501	<i>pgk2</i>			Op0135f_1		
NPKM_3031	530996 +	532253 Rmet_0501	<i>pgk2</i>	384.67	5.03	Op0135f_1	MET-CAH-FbP	Q1LR39 Phosphoglycerate kinase
NPKM_3032	532336 +	533776 Rmet_0502	<i>pykA1</i>	351.67	4.04	Op0135f_1	MET-CAH-FbP	Q1LR38 Pyruvate kinase
NPKM_3033	533896 +	534961 Rmet_0503	<i>cbbA3</i>	662.00	25.00	Op0135f_1	MET-CAH-FbP	Q1LR37 Fructose-bisphosphate aldolase
NPKM_3034	535063 +	535972 Rmet_0504	<i>purC</i>	314.67	8.96	Op0135f_1	MET-NUC-Pur	Q1LR36 Phosphoribosylaminoimidazole-succinocarboxamide synthase
NPKM_3035	535993 +	536491 Rmet_0505	<i>purE</i>	249.33	5.13	Op0135f_1	MET-NUC-Pur	Q1LR35 Phosphoribosylaminoimidazole carboxylase, catalytic subunit
NPKM_3036	536520 +	537765 Rmet_0506	<i>purK</i>	248.33	5.03	Op0135f_1	MET-NUC-Pur	Q1LR34 Phosphoribosylaminoimidazole carboxylase
NPKM_3037	537780 +	538773 Rmet_0507		194.67	3.51	Op0135f_1	GIP-TL-Ass	Q1LR33 Translation factor SUA5
3UTR_2012	537839 -	538840 Rmet_0508	<i>dacB</i>			Op0136r_1		
3UTR_1146	538774 +	539835 Rmet_0507				Op0135f_1		
NPKM_3038	538841 -	540398 Rmet_0508	<i>dacB</i>	34.33	2.52	Op0136r_1	NA	Q1LR32 D-Ala-D-Ala carboxypeptidase PBP3. Serine peptidase. MEROPS family S13
NPKM_3039	540399 -	540591 Rmet_6421		78.00	8.89	Op0136r_1	NA	NA
NPKM_3040	540514 -	540976 Rmet_0509		55.33	5.03	Op0136r_1	NA	Q1LR31 Transmembrane pair
5UTR_1698	540977 -	541032 Rmet_0509				Op0136r_1		

5UTR_934	541033 +	541122 Rmet_0510				Op0137f_1		
NPKM_3041	541122 +	542058 Rmet_0510		17.67	0.58	Op0137f_1	NA	Q1LR30 Transcriptional regulator, LysR family
3UTR_2011	541621 -	542096 Rmet_0511				Op0138r_1		
3UTR_1147	542059 +	542809 Rmet_0510				Op0137f_1		
NPKM_3042	542097 -	543591 Rmet_0511		20.67	0.58	Op0138r_1	NA	Q1LR29 RND efflux system, outer membrane lipoprotein, NodT
NPKM_3043	543590 -	546893 Rmet_0512	<i>mdtC</i>	13.33	0.58	Op0138r_1	EIP-TRA-Ion	Q1LR28 Acriflavin resistance protein
NPKM_3044	546892 -	550048 Rmet_0513	<i>mdtB</i>	18.00	1.00	Op0138r_1	EIP-TRA-Ion	Q1LR27 Acriflavin resistance protein
NPKM_3045	550069 -	551641 Rmet_0514	<i>mdtA</i>	25.00	1.00	Op0138r_1	EIP-TRA-Other	Q1LR26 Secretion protein HlyD
5UTR_1697	551642 -	551764 Rmet_0514	<i>mdtA</i>			Op0138r_1		
5UTR_935	551716 +	551783 Rmet_0515	<i>ompR</i>			Op0139f_1		
NPKM_3046	551783 +	552518 Rmet_0515	<i>ompR</i>	36.67	3.06	Op0139f_1	EIP-SIG-2Comp	Q1LR25 Two component transcriptional regulator, winged helix family
NPKM_3047	552514 +	553798 Rmet_0516	<i>envZ</i>	24.33	1.53	Op0139f_1	EIP-SIG-2Comp	Q1LR24 Sensor protein
3UTR_2010	553509 -	553871 Rmet_0517				Op0140r_2		
3UTR_1148	553799 +	554189 Rmet_0516	<i>envZ</i>			Op0139f_1		
NPKM_3048	553872 -	554481 Rmet_0517		98.67	4.16	Op0140r_2	NA	Q1LR23 UPF0078 membrane protein Rmet_0517
NPKM_3049	554579 -	555071 Rmet_0518		77.67	3.51	Op0140r_2	NA	Q1LR22 Putative uncharacterized protein
NPKM_3050	555093 -	556002 Rmet_0519	<i>xerD</i>	73.00	2.00	Op0140r_2	GIP-REP-Recomb	Q1LR21 Tyrosine recombinase XerD subunit
NPKM_3051	555998 -	556478 Rmet_0520	<i>ogt1</i>	118.33	0.58	Op0140r_2	GIP-REP-Recomb	Q1LR20 Methylated-DNA--protein-cysteine methyltransferase
NPKM_3052	556663 -	557644 Rmet_0521	<i>bug</i>	12116.00	510.82	Op0140r_2	NA	Q1LR19 Uncharacterized protein UPF0065
NPKM_3053	557747 -	558365 Rmet_0522		509.33	39.00	Op0140r_1	NA	Q1LR18 Putative uncharacterized protein
5UTR_936	558332 +	558366 Rmet_0523				Op0141f_1		
NPKM_3054	558366 +	559419 Rmet_0523		73.67	2.08	Op0141f_1	NA	Q1LR17 Auxin Efflux Carrier
5UTR_1696	558366 -	558511 Rmet_0522				Op0140r_1		
3UTR_2009	558603 -	559430 Rmet_0524				Op0142r_1		
NPKM_3055	559431 -	560565 Rmet_0524		43.00	2.65	Op0142r_1	NA	Q1LR16 4Fe-4S cluster binding
5UTR_1695	560566 -	560983 Rmet_0524				Op0142r_1		
NPKM_3056	560632 +	561166 Rmet_0525		103.00	3.46	Op0143f_1	NA	Q1LR15 Putative uncharacterized protein
3UTR_2008	561075 -	562771 Rmet_0527				Op0144r_1		
NPKM_3057	561159 +	562653 Rmet_0526	<i>amiC</i>	288.00	8.72	Op0143f_2	MET-PepGlyc	Q1LR14 Cell wall hydrolase/autolysin
NPKM_3058	562772 -	563864 Rmet_0527		91.33	1.15	Op0144r_1	NA	Q1LR13 Putative lipoprotein transmembrane
NPKM_3059	563892 +	564798 Rmet_0528		40.67	1.15	Op0145f_1	NA	Q1LR12 Transcriptional regulator, LysR family
3UTR_2007	563903 -	564833 Rmet_0529				Op0146r_1		
NPKM_3060	564834 -	565605 Rmet_0529		24.33	1.53	Op0146r_1	NA	Q1LR11 Methyltransferase type 11
NPKM_3061	565729 +	566524 Rmet_0530		41.00	1.73	Op0147f_1	NA	Q1LR10 Transcriptional regulator, XRE family
3UTR_1149	566525 +	567392 Rmet_0530				Op0147f_1		
NPKM_3062	566572 -	567331 Rmet_0531		75.67	4.04	Op0148r_1	NA	Q1LR09 Short-chain dehydrogenase/reductase SDR
NPKM_3063	567474 -	568140 Rmet_0532	<i>adk</i>	561.33	19.50	Op0148r_1	MET-NUC-Pur	Q1LR08 Adenylate kinase
NPKM_3064	568474 -	569284 Rmet_0533	<i>kdsB</i>	296.00	1.73	Op0148r_1	MET-GLYC-LPS	Q1LR07 3-deoxy-D-manno-octulosonate cytidyltransferase
NPKM_3065	569301 -	569511 Rmet_0534		253.33	17.62	Op0148r_1	NA	Q1LR06 UPF0434 protein Rmet_0534
NPKM_3066	569491 -	570610 Rmet_0535	<i>lpxK</i>	163.33	6.51	Op0148r_1	MET-GLYC-LPS	Q1LR05 Tetraacyldisaccharide 4'-kinase
NPKM_3067	570741 -	571173 Rmet_0536	<i>exbD2</i>	149.33	3.06	Op0148r_1	NA	Q1LR04 Biopolymer transport protein ExbD/TolR
NPKM_3068	571190 -	571811 Rmet_0537	<i>exbB2</i>	256.00	14.73	Op0148r_1	NA	Q1LR03 MotA/TolQ/ExbB proton channel
5UTR_1694	571812 -	571964 Rmet_0537	<i>exbB2</i>			Op0148r_1		

NPKM_3069	571867 +	572077 Rmet_6422		1.67	0.58	Op0149f_1	NA	NA
5UTR_937	572670 +	572769 Rmet_0538	<i>xseA</i>			Op0149f_2		
NPKM_3070	572769 +	574215 Rmet_0538	<i>xseA</i>	113.00	6.08	Op0149f_2	GIP-REP-Recomb	Q1LR02 Exodeoxyribonuclease 7 large subunit
NPKM_3071	574249 +	574462 Rmet_6423		895.33	96.20	Op0149f_3	NA	NA
NPKM_3072	574344 +	574923 Rmet_0539	<i>sodB</i>	3713.33	438.07	Op0149f_4	NA	Q1LR01 Superoxide dismutase
NPKM_3073	575082 +	575826 Rmet_0540		115.00	5.57	Op0149f_4	NA	Q1LR00 Transcriptional regulator, TetR family
NPKM_3074	575998 +	577333 Rmet_0541		14.33	0.58	Op0149f_4	NA	Q1LQZ9 Major facilitator superfamily MFS_1
3UTR_1150	577334 +	577384 Rmet_0541				Op0149f_4		
3UTR_2006	577394 -	577416 Rmet_0542				Op0150r_1		
NPKM_3075	577417 -	578500 Rmet_0542		19.00	5.29	Op0150r_1	NA	Q1LQZ8 Putative uncharacterized protein
5UTR_1693	578501 -	578545 Rmet_0542				Op0150r_1		
5UTR_938	578643 +	578672 Rmet_0543				Op0151f_1		
NPKM_3076	578672 +	579692 Rmet_0543		12.33	3.06	Op0151f_1	NA	Q1LQZ7 Ferredoxin
NPKM_3077	579688 +	580357 Rmet_0544		11.67	2.08	Op0151f_1	NA	Q1LQZ6 Transcriptional regulator, TetR family
NPKM_3078	580389 +	581487 Rmet_0545		41.67	0.58	Op0151f_2	MET-EN-Methane	Q1LQZ5 Alcohol dehydrogenase, zinc-binding
3UTR_2005	580808 -	581552 Rmet_0546	<i>bdhA</i>			Op0152r_1		
3UTR_1151	581488 +	582325 Rmet_0545				Op0151f_2		
NPKM_3079	581553 -	582330 Rmet_0546	<i>bdhA</i>	28.00	2.00	Op0152r_1	MET-CAH-But	Q1LQZ4 3-hydroxybutyrate dehydrogenase
NPKM_3080	582339 -	583731 Rmet_0547		20.00	2.00	Op0152r_1	NA	Q1LQZ3 Citrate transporter
5UTR_1692	583732 -	583937 Rmet_0547				Op0152r_1		
5UTR_939	583932 +	583965 Rmet_0548				Op0153f_1		
NPKM_3081	583965 +	585510 Rmet_0548		18.00	1.00	Op0153f_1	NA	Q1LQZ2 Sigma54 specific transcriptional regulator, Fis family
NPKM_3082	585530 +	586619 Rmet_0549		14.33	0.58	Op0153f_1	EIP-TRA-Ion	Q1LQZ1 Mg2+ transporter protein, CorA-like protein
NPKM_3083	586713 +	587664 Rmet_0550		25.00	1.00	Op0153f_1	NA	Q1LQZ0 Putative uncharacterized protein
NPKM_3084	587872 +	589606 Rmet_0551		5.00	1.00	Op0153f_1	NA	Q1LQY9 Hycolysin. Metallo peptidase. MEROPS family M30
3UTR_2004	589087 -	589656 Rmet_0552	<i>fdsR</i>			Op0154r_1		
3UTR_1152	589607 +	589622 Rmet_0551				Op0153f_1		
NPKM_3085	589657 -	590779 Rmet_0552	<i>fdsR</i>	29.33	1.53	Op0154r_1	NA	Q1LQY8 Transcriptional regulator of molybdate metabolism, LysR family
5UTR_940	590768 +	590892 Rmet_0553	<i>fdsG</i>			Op0155f_1		
5UTR_1691	590780 -	590826 Rmet_0552	<i>fdsR</i>			Op0154r_1		
NPKM_3086	590892 +	591402 Rmet_0553	<i>fdsG</i>	49.00	3.61	Op0155f_1	MET-CAH-DiCarb	Q1LQY7 NADH dehydrogenase (Ubiquinone), 24 kDa subunit
NPKM_3087	591398 +	592955 Rmet_0554	<i>fdsB</i>	30.67	0.58	Op0155f_1	MET-CAH-DiCarb	Q1LQY6 Respiratory-chain NADH dehydrogenase domain, 51 kDa subunit
NPKM_3088	593043 +	595917 Rmet_0555	<i>fdsA</i>	34.33	1.53	Op0155f_1	MET-CAH-DiCarb	Q1LQY5 Formate dehydrogenase, alpha subunit
NPKM_3089	595933 +	596779 Rmet_0556	<i>fdhD</i>	38.00	1.00	Op0155f_1	NA	Q1LQY4 Formate dehydrogenase family accessory protein FdhD
3UTR_2003	596441 -	597038 Rmet_0558				Op0156r_1		
NPKM_3090	596787 +	597030 Rmet_0557	<i>fdsD</i>	36.33	1.53	Op0155f_1	MET-CAH-DiCarb	Q1LQY3 Formate dehydrogenase delta subunit
3UTR_1153	597031 +	598441 Rmet_0557	<i>fdsD</i>			Op0155f_1		
NPKM_3091	597039 -	597735 Rmet_0558		21.33	2.08	Op0156r_1	NA	Q1LQY2 Glycosyl transferase, family 51
NPKM_3092	597824 -	598877 Rmet_0559	<i>ldh</i>	17.67	2.08	Op0156r_1	MET-CAH-FbP	Q1LQY1 Malate/L-lactate dehydrogenase
NPKM_3093	598935 -	600459 Rmet_0560		19.00	2.65	Op0156r_1	NA	Q1LQY0 Anion transporter
5UTR_1690	600460 -	600481 Rmet_0560				Op0156r_1		
5UTR_941	600614 +	600719 Rmet_0561				Op0157f_1		
NPKM_3094	600719 +	601559 Rmet_0561		69.00	1.73	Op0157f_1	NA	Q1LQX9 Protein tyrosine/serine phosphatase

3UTR_2002	600852 -	601554 Rmet_0562	<i>ackA2</i>			Op0158r_1		
NPKM_3095	601555 -	602773 Rmet_0562	<i>ackA2</i>	40.67	0.58	Op0158r_1	MET-CAH-Pyr	Q1LQX8 Acetate kinase
3UTR_1154	601560 +	602612 Rmet_0561				Op0157f_1		
NPKM_3096	602796 -	603747 Rmet_0563	<i>ptb</i>	43.33	3.21	Op0158r_1	MET-CAH-Pyr	Q1LQX7 Phosphate acetyl/butaryl transferase
5UTR_1689	603748 -	603791 Rmet_0563	<i>ptb</i>			Op0158r_1		
5UTR_942	603950 +	604053 Rmet_0564				Op0159f_1		
NPKM_3097	604053 +	606318 Rmet_0564		155.67	1.53	Op0159f_1	NA	Q1LQX6 Putative uncharacterized protein
NPKM_3098	606408 +	607188 Rmet_0565	<i>fabI</i>	71.67	3.51	Op0159f_1	MET-LIP-FASyn	Q1LQX5 Enoyl-[acyl-carrier-protein] reductase (NADH)
NPKM_3099	607293 +	607536 Rmet_0566	<i>moaA1</i>	53.33	1.53	Op0159f_1	NA	Q1LQX4 Putative uncharacterized protein
3UTR_1155	607537 +	607568 Rmet_0566	<i>moaA1</i>			Op0159f_1		
5UTR_943	607593 +	607646 Rmet_0567	<i>modE</i>			Op0159f_1		
NPKM_3100	607646 +	608453 Rmet_0567	<i>modE</i>	66.33	4.16	Op0159f_1	EIP-TRA-ABC	Q1LQX3 Transcriptional regulator, ModE family
NPKM_3101	608459 +	608999 Rmet_0568		54.33	4.93	Op0159f_1	MET-NUC-Pur	Q1LQX2 Adenylate cyclase
3UTR_2001	608705 -	608967 Rmet_0569	<i>modC</i>			Op0160r_1		
NPKM_3102	608968 -	609703 Rmet_0569	<i>modC</i>	12.33	1.53	Op0160r_1	EIP-TRA-ABC	Q1LQX1 ABC transporter-related protein
3UTR_1156	609000 +	610430 Rmet_0568				Op0159f_1		
NPKM_3103	609699 -	610416 Rmet_0570	<i>modB</i>	12.33	1.53	Op0160r_1	EIP-TRA-ABC	Q1LQX0 Molybdate ABC transporter, permease protein
NPKM_3104	610434 -	611211 Rmet_0571	<i>modA</i>	19.33	1.53	Op0160r_1	EIP-TRA-ABC	Q1LQW9 Molybdenum ABC transporter, periplasmic molybdate-binding protein
NPKM_3105	611473 +	613582 Rmet_0572	<i>cpdB</i>	1.33	0.58	Op0161f_1	MET-NUC-Pur	Q1LQW8 5'-Nucleotidase-like protein
NPKM_3106	613596 +	614400 Rmet_0573		2.00	0.00	Op0161f_1	NA	Q1LQW7 Sel1
3UTR_1157	614401 +	614439 Rmet_0573				Op0161f_1		
3UTR_2000	614556 -	614602 Rmet_0574	<i>htrE</i>			Op0162r_1		
NPKM_3107	614603 -	617162 Rmet_0574	<i>htrE</i>	1.33	0.58	Op0162r_1	NA	Q1LQW6 Fimbrial biogenesis outer membrane usher protein
NPKM_3108	617164 -	617935 Rmet_0575	<i>fimC</i>	0.67	0.58	Op0162r_1	NA	Q1LQW5 Pili assembly chaperone
3UTR_1999	617992 -	618019 Rmet_0576	<i>fimA</i>			Op0162r_1		
NPKM_3109	618020 -	618569 Rmet_0576	<i>fimA</i>	1.67	0.58	Op0162r_1	NA	Q1LQW4 Fimbrial protein
5UTR_1688	618570 -	618640 Rmet_0576	<i>fimA</i>			Op0162r_1		
NPKM_3110	619010 +	619532 Rmet_0577		13.33	2.08	Op0163f_1	MET-NUC-Pyr	Q1LQW3 Nucleoside 2-deoxyribosyltransferase
3UTR_1998	619233 -	619535 Rmet_0578				Op0164r_1		
3UTR_1158	619533 +	620413 Rmet_0577				Op0163f_1		
NPKM_3111	619536 -	620124 Rmet_0578		53.67	1.53	Op0164r_1	NA	Q1LQW2 Putative uncharacterized protein
NPKM_3112	620120 -	621761 Rmet_0579	<i>pqiB</i>	34.33	3.51	Op0164r_1	NA	Q1LQW1 Mammalian cell entry related
NPKM_3113	621744 -	622494 Rmet_0580	<i>pqiA1</i>	23.67	2.52	Op0164r_1	NA	Q1LQW0 Paraquat-inducible protein A
NPKM_3114	622532 -	623222 Rmet_0581	<i>pqiA2</i>	36.33	3.06	Op0164r_1	NA	Q1LQV9 Paraquat-inducible protein A
NPKM_3115	623214 -	624318 Rmet_0582		61.67	9.29	Op0164r_1	NA	Q1LQV8 Putative uncharacterized protein
NPKM_3116	624404 -	625535 Rmet_0583		39.67	16.65	Op0164r_1	NA	Q1LQV7 CBS domain containing membrane protein
5UTR_1687	625536 -	625609 Rmet_0583				Op0164r_1		
NPKM_3117	625582 +	627496 Rmet_0584		26.67	11.15	Op0165f_1	NA	Q1LQV6 Cl-channel, voltage gated
NPKM_3118	627652 +	628531 Rmet_0585		27.33	3.51	Op0165f_1	NA	Q1LQV5 Amidinotransferase
3UTR_1997	627966 -	629745 Rmet_0587				Op0166r_3		
NPKM_3119	628543 +	629644 Rmet_0586	<i>arcB</i>	25.00	1.00	Op0165f_1	MET-AA-ArgPro	Q1LQV4 Ornithine cyclodeaminase
3UTR_1159	629645 +	630691 Rmet_0586	<i>arcB</i>			Op0165f_1		
NPKM_3120	629746 -	630346 Rmet_0587		241.33	19.40	Op0166r_3	NA	Q1LQV3 Excisionase/Xis, DNA-binding

NPKM_3121	630828 -	632205 Rmet_0588	<i>gltR2</i>	58.33	17.79	Op0166r_2	NA	Q1LQV2 Two component, sigma54 specific, transcriptional regulator, Fis family
NPKM_3122	632194 -	633967 Rmet_0589	<i>gltS2</i>	33.33	1.53	Op0166r_2	NA	Q1LQV1 Sensor protein
5UTR_1686	633968 -	634071 Rmet_0589	<i>gltS2</i>			Op0166r_2		
3UTR_1996	634187 -	634209 Rmet_0590	<i>gltP2</i>			Op0166r_1		
NPKM_3123	634210 -	635518 Rmet_0590	<i>gltP2</i>	1.00	0.00	Op0166r_1	NA	Q1LQV0 Sodium:dicarboxylate symporter
3UTR_1995	635752 -	635810 Rmet_0591				Op0166r_1		
NPKM_3124	635811 -	639177 Rmet_0591		8.67	0.58	Op0166r_1	NA	Q1LQU9 Diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS,
5UTR_1685	639178 -	639223 Rmet_0591				Op0166r_1		
5UTR_944	639386 +	639454 Rmet_0592				Op0167f_1		
NPKM_3125	639454 +	639856 Rmet_0592		10.00	1.00	Op0167f_1	NA	Q1LQU8 Putative uncharacterized protein
NPKM_3126	640022 +	640901 Rmet_0593		15.67	0.58	Op0167f_1	NA	Q1LQU7 Putative uncharacterized protein
NPKM_3127	641063 +	641522 Rmet_0594	<i>iorA</i>	96.33	2.08	Op0167f_2	NA	Q1LQU6 (2Fe-2S)-binding
NPKM_3128	641531 +	643784 Rmet_0595	<i>iorB</i>	94.33	3.06	Op0167f_2	NA	Q1LQU5 Twin-arginine translocation pathway signal
3UTR_1994	643211 -	643879 Rmet_0596				Op0168r_1		
3UTR_1160	643785 +	644510 Rmet_0595	<i>iorB</i>			Op0167f_2		
NPKM_3129	643880 -	644681 Rmet_0596		33.00	0.00	Op0168r_1	GIP-TK-RNAP	Q1LQU4 Putative transmembrane transcriptional regulator (Anti-sigma factor)
NPKM_3130	644667 -	645297 Rmet_0597	<i>rpoO</i>	39.67	2.31	Op0168r_1	GIP-TK-RNAP	Q1LQU3 RNA polymerase sigma factor
5UTR_1684	645298 -	645337 Rmet_0597	<i>rpoO</i>			Op0168r_1		
NPKM_3131	645539 +	646430 Rmet_0598		9.33	0.58	Op0169f_1	NA	Q1LQU2 Twin-arginine translocation pathway signal
NPKM_3132	646426 +	646801 Rmet_0599		9.67	0.58	Op0169f_1	MET-EN-OxPhos	Q1LQU1 Cytochrome c oxidase subunit 2
3UTR_1161	646802 +	647360 Rmet_0599				Op0169f_1		
NPKM_3133	646846 -	650047 Rmet_0600	<i>mdtB</i>	1.33	0.58	Op0170r_1	EIP-TRA-Ion	Q1LQU0 Acriflavin resistance protein
NPKM_3134	650066 -	651446 Rmet_0601	<i>mdtA</i>	5.67	0.58	Op0170r_1	EIP-TRA-Other	Q1LQT9 Secretion protein HlyD
5UTR_1683	651447 -	651450 Rmet_0601	<i>mdtA</i>			Op0170r_1		
5UTR_945	651491 +	651559 Rmet_0602				Op0171f_1		
NPKM_3135	651559 +	651844 Rmet_0602		88.67	5.51	Op0171f_1	NA	Q1LQT8 Putative uncharacterized protein
NPKM_3136	651977 +	653267 Rmet_0603		44.00	4.36	Op0171f_1	NA	Q1LQT7 Putative integral membrane sensor protein
NPKM_3137	653263 +	654487 Rmet_0604		46.00	4.36	Op0171f_1	NA	Q1LQT6 Esterase/lipase-like protein
3UTR_1993	653973 -	654482 Rmet_0605				Op0172r_2		
NPKM_3138	654483 -	656787 Rmet_0605		10.67	0.58	Op0172r_2	NA	Q1LQT5 Patatin
3UTR_1162	654488 +	656831 Rmet_0604				Op0171f_1		
5UTR_1682	656788 -	656848 Rmet_0605				Op0172r_2		
3UTR_1992	656877 -	656904 Rmet_0606				Op0172r_2		
NPKM_3139	656905 -	658705 Rmet_0606		9.00	0.00	Op0172r_2	NA	Q1LQT4 Sulphate transporter
NPKM_3140	658788 -	659721 Rmet_0607		44.67	3.21	Op0172r_2	MET-CAH-But	Q1LQT3 Hydroxymethylglutaryl-CoA lyase
NPKM_3141	659922 -	661962 Rmet_0608	<i>accC</i>	50.67	1.53	Op0172r_2	MET-AA-ValLeulle	Q1LQT2 3-methylcrotonoyl-CoA carboxylase, alpha subunit
NPKM_3142	661975 -	663583 Rmet_0609	<i>accB</i>	49.67	0.58	Op0172r_2	MET-AA-ValLeulle	Q1LQT1 Carboxyl transferase
NPKM_3143	663587 -	665300 Rmet_0610		11.67	0.58	Op0172r_1	MET-LIP-FASyn	Q1LQT0 AMP-dependent synthetase and ligase
5UTR_1681	665301 -	665334 Rmet_0610				Op0172r_1		
5UTR_946	665460 +	665545 Rmet_0611				Op0173f_1		
NPKM_3144	665545 +	666292 Rmet_0611		32.67	1.53	Op0173f_1	NA	Q1LQS9 Transcriptional regulator, TetR family
NPKM_3145	666463 +	667159 Rmet_0612		30.00	3.61	Op0173f_1	NA	Q1LQS8 Two component transcriptional regulator, LuxR family
NPKM_3146	667170 +	669108 Rmet_0613		14.67	1.53	Op0173f_1	NA	Q1LQS7 Periplasmic sensor signal transduction histidine kinase

3UTR_1991	668916 -	668981 Rmet_0614				Op0174r_1		
NPKM_3147	668982 -	674208 Rmet_0614		2.00	0.00	Op0174r_1	NA	Q1LQS6 Outer membrane autotransporter barrel
3UTR_1163	669109 +	669951 Rmet_0613				Op0173f_1		
5UTR_1680	674209 -	674240 Rmet_0614				Op0174r_1		
5UTR_947	674394 +	674568 Rmet_0615	groS			Op0175f_1		
NPKM_3148	674568 +	674859 Rmet_0615	groS	1597.33	92.57	Op0175f_1	GIP-PTL-Fold	Q1LQS5 10 kDa chaperonin
NPKM_3149	674943 +	676587 Rmet_0616	groL	2894.33	268.19	Op0175f_1	GIP-PTL-Fold	Q1LQS4 60 kDa chaperonin
3UTR_1164	676588 +	677445 Rmet_0616	groL			Op0175f_1		
NPKM_3150	676886 -	677321 Rmet_0617		1.33	0.58	Op0176r_2	NA	Q1LQS3 Putative uncharacterized protein
NPKM_3151	677317 -	679999 Rmet_0618	clpB	2.67	0.58	Op0176r_2	NA	Q1LQS2 ATPase AAA-2
NPKM_3152	680083 -	680569 Rmet_0619		4.67	1.53	Op0176r_2	NA	Q1LQS1 Putative uncharacterized protein
NPKM_3153	680583 -	682302 Rmet_0620		3.33	0.58	Op0176r_2	NA	Q1LQS0 OmpA/MotB
NPKM_3154	682312 -	682969 Rmet_0621		0.33	0.58	Op0176r_1	NA	Q1LQR9 Putative uncharacterized protein
NPKM_3155	682965 -	683796 Rmet_0622		1.00	0.00	Op0176r_1	NA	Q1LQR8 Putative uncharacterized protein
NPKM_3156	683644 -	684205 Rmet_0623		2.00	1.00	Op0177f_1	NA	Q1LQR7 Putative uncharacterized protein
5UTR_1679	684206 -	684298 Rmet_0623				Op0177f_1		
3UTR_1990	684351 -	684360 Rmet_0624				Op0178r_1		
NPKM_3157	684361 -	685939 Rmet_0624		1.00	0.00	Op0178r_1	NA	Q1LQR6 Putative uncharacterized protein
NPKM_3158	685964 -	686480 Rmet_0625		1.33	0.58	Op0178r_1	NA	Q1LQR5 Uncharacterised conserved protein UCP028301
5UTR_948	686722 +	686769 Rmet_0626				Op0179f_1		
NPKM_3159	686769 +	689439 Rmet_0626		0.33	0.58	Op0179f_1	NA	Q1LQR4 Rhs element Vgr protein
NPKM_3160	689435 +	691403 Rmet_0627		1.00	0.00	Op0179f_2	NA	Q1LQR3 Phospholipase D/Transphosphatidylase
NPKM_3161	691406 +	692714 Rmet_0628		2.33	0.58	Op0179f_3	NA	Q1LQR2 Sel1
NPKM_3162	692710 +	692911 Rmet_0629		1.67	0.58	Op0179f_3	NA	Q1LQR1 Putative phospholipase protein
NPKM_3163	692914 +	694213 Rmet_0630		2.33	0.58	Op0179f_3	NA	Q1LQR0 Sel1
3UTR_1165	694214 +	694264 Rmet_0630				Op0179f_3		
5UTR_949	694303 +	694309 Rmet_0631				Op0179f_3		
NPKM_3164	694309 +	694564 Rmet_0631		0.67	1.15	Op0179f_3	NA	Q1LQQ9 PaaR
NPKM_3165	694530 +	695808 Rmet_0632		1.33	0.58	Op0179f_3	NA	Q1LQQ8 Putative uncharacterized protein
3UTR_1166	695809 +	695841 Rmet_0632				Op0179f_3		
5UTR_950	695854 +	695873 Rmet_0633				Op0179f_3		
NPKM_3166	695873 +	699221 Rmet_0633		2.00	0.00	Op0179f_3	NA	Q1LQQ7 ImcF-related
3UTR_1167	699222 +	699293 Rmet_0633				Op0179f_3		
5UTR_951	699316 +	699368 Rmet_0634				Op0179f_3		
NPKM_3167	699368 +	700940 Rmet_0634		3.33	0.58	Op0179f_3	NA	Q1LQQ6 ImpA-like protein
NPKM_3168	700961 +	702782 Rmet_0635		3.33	0.58	Op0179f_3	NA	Q1LQQ5 Putative uncharacterized protein
NPKM_3169	702799 +	703888 Rmet_0636		2.33	0.58	Op0179f_3	NA	Q1LQQ4 Putative uncharacterized protein
NPKM_3170	703924 +	704494 Rmet_0637		6.33	0.58	Op0179f_4	NA	Q1LQQ3 Putative uncharacterized protein
3UTR_1989	704203 -	704626 Rmet_0638				Op0180r_4		
3UTR_1168	704495 +	704758 Rmet_0637				Op0179f_4		
NPKM_3171	704627 -	705416 Rmet_0638		71.00	2.65	Op0180r_4	NA	Q1LQQ2 Metallophosphoesterase
5UTR_1678	705417 -	705443 Rmet_0638				Op0180r_4		
3UTR_1988	705541 -	705622 Rmet_0639	tadC			Op0180r_3		

NPKM_3172	705623 -	706595 Rmet_0639	<i>tadC</i>	1.00	0.00	Op0180r_3	NA	Q1LQQ1 Type II secretion system protein
NPKM_3173	706646 -	707624 Rmet_0640	<i>tadB</i>	2.33	0.58	Op0180r_3	NA	Q1LQQ0 Type II secretion system protein
3UTR_1987	707636 -	707665 Rmet_0641	<i>cpaF1</i>			Op0180r_3		
NPKM_3174	707666 -	709037 Rmet_0641	<i>cpaF1</i>	2.00	0.00	Op0180r_3	GIP-PTL-T2S	Q1LQP9 Type II secretion system protein E
3UTR_1986	709041 -	709098 Rmet_0642	<i>cpaE1</i>			Op0180r_3		
NPKM_3175	709099 -	710293 Rmet_0642	<i>cpaE1</i>	1.00	0.00	Op0180r_3	GIP-PTL-T2S	Q1LQP8 Response regulator receiver domain protein (CheY-like)
3UTR_1985	710341 -	710352 Rmet_0643				Op0180r_2		
NPKM_3176	710353 -	710812 Rmet_0643		0.00	0.00	Op0180r_2	NA	Q1LQP7 TadE-like protein
NPKM_3177	710808 -	711339 Rmet_0644		0.67	0.58	Op0180r_2	NA	Q1LQP6 TadE-like protein
NPKM_3178	711348 -	712653 Rmet_0645		1.00	0.00	Op0180r_2	NA	Q1LQP5 Putative uncharacterized protein
NPKM_3179	712675 -	713023 Rmet_0646		0.67	0.58	Op0180r_2	NA	Q1LQP4 Putative lipoprotein
5UTR_1677	713024 -	713042 Rmet_0646				Op0180r_2		
NPKM_3180	713058 -	714921 Rmet_0647	<i>cpaC1</i>	0.67	0.58	Op0180r_2	GIP-PTL-T2S	Q1LQP3 Type II and III secretion system protein
NPKM_3181	715008 -	715854 Rmet_0648	<i>cpaB1</i>	0.00	0.00	Op0180r_1	GIP-PTL-T2S	Q1LQP2 Flp pilus assembly CpaB
NPKM_3182	715898 -	717311 Rmet_0649		0.00	0.00	Op0180r_1	NA	Q1LQP1 ATPase
5UTR_1676	717312 -	717329 Rmet_0649				Op0180r_1		
NPKM_3183	717354 -	717858 Rmet_0650	<i>cpaA1</i>	0.00	0.00	Op0180r_1	GIP-PTL-T2S	Q1LQP0 Peptidase A24A, prepilin type IV
5UTR_1675	717859 -	717890 Rmet_0650	<i>cpaA1</i>			Op0180r_1		
3UTR_1984	717893 -	717894 Rmet_0651	<i>pilA</i>			Op0180r_1		
NPKM_3184	717895 -	718069 Rmet_0651	<i>pilA</i>	0.33	0.58	Op0180r_1	NA	Q1LQN9 Flp/Fap pilin component
3UTR_1983	718078 -	718108 Rmet_0652	<i>pilA</i>			Op0180r_1		
NPKM_3185	718109 -	718283 Rmet_0652	<i>pilA</i>	0.67	1.15	Op0180r_1	GIP-PTL-T2S	Q1LQN8 Flp/Fap pilin component
3UTR_1982	718363 -	718371 Rmet_0653	<i>pilA</i>			Op0180r_1		
NPKM_3186	718372 -	718546 Rmet_0653	<i>pilA</i>	1.67	0.58	Op0180r_1	GIP-PTL-T2S	Q1LQN7 Flp/Fap pilin component
5UTR_952	719662 +	719665 Rmet_0654				Op0181f_1		
NPKM_3187	719665 +	720922 Rmet_0654		1.33	0.58	Op0181f_1	NA	Q1LQN6 Putative membrane protein
NPKM_3188	720923 +	722162 Rmet_0655		1.00	0.00	Op0181f_1	NA	Q1LQN5 Putative membrane protein
NPKM_3189	722203 +	723220 Rmet_0656	<i>gtrB</i>	1.33	0.58	Op0181f_1	NA	Q1LQN4 Glycosyl transferase, family 2
3UTR_1169	723221 +	723236 Rmet_0656	<i>gtrB</i>			Op0181f_1		
NPKM_3190	723244 -	724471 Rmet_0657		1.00	0.00	Op0182r_1	NA	Q1LQN3 Putative membrane protein
NPKM_3191	724546 -	724993 Rmet_0658	<i>gtrA</i>	2.67	0.58	Op0182r_1	NA	Q1LQN2 GtrA-like protein
NPKM_3192	725027 -	726404 Rmet_0659		6.67	0.58	Op0182r_1	NA	Q1LQN1 Sigma54 specific transcriptional regulator, Fis family
5UTR_953	727135 +	728453 Rmet_0661				Op0183f_1		
NPKM_3193	727434 -	728376 Rmet_0660		22.33	1.53	Op0182r_1	NA	Q1LQN0 Transcriptional regulator, LysR family
NPKM_3194	728453 +	729710 Rmet_0661		33.67	0.58	Op0183f_1	NA	Q1LQM9 Major facilitator superfamily MFS_1
NPKM_3195	730032 +	730821 Rmet_0662		3.00	1.00	Op0183f_1	NA	Q1LQM8 Putative integral membrane sensor protein
3UTR_1981	730421 -	730865 Rmet_0663				Op0184r_1		
3UTR_1170	730822 +	730838 Rmet_0662				Op0183f_1		
NPKM_3196	730866 -	731403 Rmet_0663		70.00	2.00	Op0184r_1	NA	Q1LQM7 Putative uncharacterized protein
NPKM_3197	731416 -	732241 Rmet_0664		79.00	2.65	Op0184r_1	NA	Q1LQM6 Putative uncharacterized protein
NPKM_3198	732254 -	732857 Rmet_0665	<i>lemA</i>	106.67	5.03	Op0184r_1	NA	Q1LQM5 LemA
5UTR_954	732449 +	733256 Rmet_0666	<i>dapA</i>			Op0185f_1		
5UTR_1674	732858 -	733139 Rmet_0665	<i>lemA</i>			Op0184r_1		

NPKM_3199	733256 +	734165 Rmet_0666	<i>dapA</i>	34.33	4.04	Op0185f_1	MET-AA-Lys_Syn	Q1LQM4 Dihydrodipicolinate synthase
3UTR_1980	733271 -	734150 Rmet_0667	<i>hemL</i>			Op0186r_1		
NPKM_3200	734151 -	735444 Rmet_0667	<i>hemL</i>	243.67	6.35	Op0186r_1	MET-COF-Porph	Q1LQM3 Glutamate-1-semialdehyde 2,1-aminomutase
3UTR_1171	734166 +	735124 Rmet_0666	<i>dapA</i>			Op0185f_1		
5UTR_955	735135 +	735665 Rmet_0668	<i>rubA</i>			Op0187f_1		
5UTR_1673	735445 -	735619 Rmet_0667	<i>hemL</i>			Op0186r_1		
NPKM_3201	735665 +	735860 Rmet_0668	<i>rubA</i>	197.67	12.01	Op0187f_1	NA	Q1LQM2 Rubredoxin
NPKM_3202	736237 +	736741 Rmet_0669	<i>pilG</i>	378.00	13.89	Op0187f_1	GIP-PTL-T2S	Q1LQM1 Response regulator receiver domain protein (CheY-like)
NPKM_3203	736775 +	737144 Rmet_0670	<i>pilH</i>	378.67	6.51	Op0187f_1	GIP-PTL-T2S	Q1LQM0 Response regulator receiver domain protein (CheY-like)
NPKM_3204	737221 +	737764 Rmet_0671	<i>pilI</i>	410.33	8.33	Op0187f_1	GIP-PTL-T2S	Q1LQL9 CheW protein
NPKM_3205	737921 +	740123 Rmet_0672	<i>pilJ</i>	359.67	9.61	Op0187f_1	GIP-PTL-T2S	Q1LQL8 Methyl-accepting chemotaxis sensory transducer
NPKM_3206	740155 +	746125 Rmet_0673	<i>pilL2</i>	276.33	9.61	Op0187f_1	GIP-PTL-T2S	Q1LQL7 CheA signal transduction histidine kinases
3UTR_1979	745462 -	746196 Rmet_0674				Op0188r_1		
3UTR_1172	746126 +	746925 Rmet_0673	<i>pilL2</i>			Op0187f_1		
NPKM_3207	746197 -	747511 Rmet_0674		57.00	2.65	Op0188r_1	NA	Q1LQL6 Major facilitator superfamily MFS_1
NPKM_3208	747620 -	748382 Rmet_0675	<i>tsaC</i>	66.33	2.89	Op0188r_1	MET-LIP-FASyn	Q1LQL5 Short-chain dehydrogenase/reductase SDR
NPKM_3209	748452 -	748692 Rmet_0676		66.33	6.81	Op0188r_1	NA	Q1LQL4 Putative uncharacterized protein
NPKM_3210	748684 -	750121 Rmet_0677	<i>puuC</i>	87.33	2.08	Op0188r_1	MET-CAH-FbP	Q1LQL3 Aldehyde dehydrogenase
5UTR_1672	750122 -	750205 Rmet_0677	<i>puuC</i>			Op0188r_1		
5UTR_956	750274 +	750285 Rmet_0678	<i>ppa</i>			Op0189f_1		
NPKM_3211	750285 +	750813 Rmet_0678	<i>ppa</i>	225.67	1.15	Op0189f_1	MET-EN-OxPhos	Q1LQL2 Inorganic pyrophosphatase
3UTR_1173	750814 +	750848 Rmet_0678	<i>ppa</i>			Op0189f_1		
3UTR_1978	750819 -	750891 Rmet_0679				Op0190r_1		
NPKM_3212	750892 -	752095 Rmet_0679		29.33	1.15	Op0190r_1	NA	Q1LQL1 Putative uncharacterized protein
5UTR_1671	752096 -	752131 Rmet_0679				Op0190r_1		
NPKM_3213	752163 +	754314 Rmet_0680	<i>nadE</i>	59.00	3.00	Op0191f_1	MET-AA-GluGSH	Q1LQL0 NAD+ synthetase
NPKM_3214	754427 +	754766 Rmet_0681	<i>glnB</i>	538.33	52.17	Op0191f_2	EIP-SIG-2Comp	Q1LQK9 Nitrogen regulatory protein P-II
3UTR_1977	754623 -	754834 Rmet_0682				Op0192r_1		
3UTR_1174	754767 +	754795 Rmet_0681	<i>glnB</i>			Op0191f_2		
NPKM_3215	754835 -	755483 Rmet_0682		60.67	3.79	Op0192r_1	NA	Q1LQK8 Putative uncharacterized protein
NPKM_3216	755490 -	756165 Rmet_0683		109.33	4.04	Op0192r_1	NA	Q1LQK7 Smr protein/MutS2
NPKM_3217	756283 -	757237 Rmet_0684	<i>trxB</i>	138.33	7.09	Op0192r_1	MET-NUC-Pyr	Q1LQK6 Thioredoxin reductase
5UTR_1670	757238 -	757279 Rmet_0684	<i>trxB</i>			Op0192r_1		
5UTR_957	757360 +	757418 Rmet_0685	<i>ftsK</i>			Op0193f_1		
NPKM_3218	757418 +	759746 Rmet_0685	<i>ftsK</i>	97.33	4.93	Op0193f_1	EIP-TRA-Other	Q1LQK5 DNA translocase FtsK
3UTR_1976	758893 -	761104 Rmet_0688				Op0194r_1		
NPKM_3219	760007 +	760652 Rmet_0686	<i>lolA</i>	130.00	1.73	Op0193f_1	NA	Q1LQK4 Outer-membrane lipoprotein carrier protein
NPKM_3220	760660 +	761077 Rmet_0687		169.67	5.13	Op0193f_1	NA	Q1LQK3 Putative lipoprotein transmembrane
NPKM_3221	761105 -	761333 Rmet_0688		65.33	13.01	Op0194r_1	NA	Q1LQK2 Putative uncharacterized protein
NPKM_3222	761435 -	762119 Rmet_0689		57.00	9.54	Op0194r_1	NA	Q1LQK1 Putative uncharacterized protein
5UTR_1669	762120 -	762474 Rmet_0689				Op0194r_1		
NPKM_3223	762385 +	763234 Rmet_0690		134.00	11.14	Op0195f_1	EIP-TRA-ABC	Q1LQK0 Extracellular solute-binding protein, family 3
NPKM_3224	763339 +	764035 Rmet_0691	<i>gltJ</i>	24.00	3.46	Op0195f_1	EIP-TRA-ABC	Q1LQJ9 Amino acid ABC transporter, permease protein, 3-TM region, His/Glu/Gln/A

NPKM_3225	764037 +	764730 Rmet_0692	<i>aapM</i>	13.33	0.58	Op0195f_1	EIP-TRA-ABC	Q1LQJ8 Amino acid ABC transporter, permease protein, 3-TM region, His/Glu/Gln/Asp
NPKM_3226	764732 +	765482 Rmet_0693	<i>aapP</i>	19.67	2.52	Op0195f_1	EIP-TRA-ABC	Q1LQJ7 ABC transporter-related protein
NPKM_3227	765596 +	766934 Rmet_0694	<i>ycal</i>	64.33	2.52	Op0195f_2	GIP-REP-Recomb	Q1LQJ6 Recombination protein MgsA
NPKM_3228	767101 +	768409 Rmet_0695	<i>serS</i>	308.33	9.29	Op0195f_3	MET-AA-GlySerThr	Q1LQJ5 Seryl-tRNA synthetase
NPKM_3229	768491 -	768749 Rmet_0696		26.33	1.53	Op0196r_2	NA	Q1LQJ4 Putative uncharacterized protein
NPKM_3230	768496 +	768586 Rmet_R0006		309.67	57.50	Op2002f_1	NA	NA
NPKM_3231	768774 +	769047 Rmet_6424		10.33	2.31	Op2002f_1	NA	NA
3UTR_1175	769048 +	769439 Rmet_6424				Op2002f_1		
NPKM_3232	769206 -	769671 Rmet_0697	<i>pilA</i>	3431.67	266.36	Op0196r_2	GIP-PTL-T2S	Q1LQJ3 Pilus assembly protein major pilin PilA
NPKM_3233	769930 -	771247 Rmet_0698		134.67	18.18	Op0196r_1	NA	Q1LQJ2 Putative uncharacterized protein
NPKM_3234	771329 -	772283 Rmet_0699		135.33	16.92	Op0196r_1	NA	Q1LQJ1 Transcriptional regulator, LysR family
5UTR_958	772166 +	772475 Rmet_0700	<i>dadA2</i>			Op0197f_1		
5UTR_1668	772284 -	772366 Rmet_0699				Op0196r_1		
NPKM_3235	772475 +	773753 Rmet_0700	<i>dadA2</i>	26.33	3.06	Op0197f_1	MET-EN-Nitrog	Q1LQJ0 FAD dependent oxidoreductase
3UTR_1975	772639 -	774927 Rmet_0702				Op0198r_1		
NPKM_3236	773841 +	774750 Rmet_0701	<i>gltI</i>	75.33	7.57	Op0197f_2	EIP-TRA-ABC	Q1LQJ9 Extracellular solute-binding protein, family 3
3UTR_1176	774751 +	776028 Rmet_0701	<i>gltI</i>			Op0197f_2		
NPKM_3237	774928 -	775405 Rmet_0702		75.67	7.51	Op0198r_1	NA	Q1LQI8 Putative uncharacterized protein
NPKM_3238	775642 -	778213 Rmet_0703	<i>cphA1</i>	131.33	1.53	Op0198r_1	NA	Q1LQI7 Cyanophycin synthetase
NPKM_3239	778249 -	780901 Rmet_0704	<i>cphA2</i>	174.00	14.00	Op0198r_1	NA	Q1LQI6 Cyanophycin synthetase
5UTR_1667	780902 -	782005 Rmet_0704	<i>cphA2</i>			Op0198r_1		
5UTR_959	781106 +	781144 Rmet_0705				Op0199f_1		
NPKM_3240	781144 +	783499 Rmet_0705		66.67	2.31	Op0199f_1	EIP-TRA-ABC	Q1LQI5 ABC transporter-related protein
3UTR_1974	783250 -	784101 Rmet_0707				Op0200r_2		
NPKM_3241	783488 +	784004 Rmet_0706		98.33	3.21	Op0199f_1	NA	Q1LQI4 Putative uncharacterized protein
3UTR_1177	784005 +	784265 Rmet_0706				Op0199f_1		
NPKM_3242	784102 -	784504 Rmet_0707		105.00	6.24	Op0200r_2	NA	Q1LQI3 Putative uncharacterized protein
5UTR_1666	784505 -	784527 Rmet_0707				Op0200r_2		
3UTR_1973	784643 -	784682 Rmet_0708				Op0200r_1		
NPKM_3243	784683 -	785016 Rmet_0708		2.00	1.00	Op0200r_1	NA	Q1LQI2 Putative uncharacterized protein
5UTR_960	784766 +	785081 Rmet_0709				Op0201f_1		
NPKM_3244	785081 +	785417 Rmet_0709		96.00	6.93	Op0201f_1	NA	Q1LQI1 Putative uncharacterized protein
3UTR_1972	785450 -	785495 Rmet_R0007	<i>ssrA</i>			Op0202r_2		
NPKM_3245	785482 +	785671 Rmet_6425		1.33	0.58	Op0201f_1	NA	NA
NPKM_3246	785496 -	785856 Rmet_R0007	<i>ssrA</i>	20.33	4.04	Op0202r_2	NA	NA
NPKM_3247	785929 -	786586 Rmet_0710	<i>gph</i>	143.33	1.53	Op0202r_2	MET-CAH-DiCarb	Q1LQI0 Phosphoglycolate phosphatase
NPKM_3248	786589 -	787333 Rmet_0711	<i>ubiG</i>	175.67	2.52	Op0202r_2	MET-COF-CoQ	Q1LQH9 3-demethylubiquinone-9 3-methyltransferase
NPKM_3249	787433 -	788087 Rmet_0712	<i>ompA</i>	14429.00	562.11	Op0202r_2	EIP-TRA-Pores	Q1LQH8 OmpA/MotB
5UTR_1665	788088 -	788264 Rmet_0712	<i>ompA</i>			Op0202r_2		
NPKM_3250	788269 -	788542 Rmet_6426		2.33	0.58	Op0202r_1	NA	NA
5UTR_961	788466 +	788533 Rmet_0713	<i>gyrA</i>			Op0203f_1		
NPKM_3251	788533 +	791227 Rmet_0713	<i>gyrA</i>	430.33	9.29	Op0203f_1	GIP-REP-Complex	Q1LQH7 DNA gyrase subunit A
5UTR_1664	788543 -	789316 Rmet_6426				Op0202r_1		

NPKM_3252	791309 +	791879 Rmet_0714		1441.33	67.90	Op0203f_2	NA	Q1LQH6 Putative signal peptide protein
NPKM_3253	792036 +	793200 Rmet_0715	<i>serC</i>	280.33	5.86	Op0203f_2	MET-AA-GlySerThr	Q1LQH5 Phosphoserine aminotransferase
NPKM_3254	793300 +	794464 Rmet_0716	<i>pheA</i>	270.00	7.00	Op0203f_2	NA	Q1LQH4 Prephenate dehydratase / chorismate mutase
NPKM_3255	794483 +	795608 Rmet_0717	<i>hisC1</i>	262.00	6.56	Op0203f_2	MET-AA-His	Q1LQH3 Aminotransferase
NPKM_3256	795617 +	796526 Rmet_0718	<i>tyrA</i>	215.00	10.54	Op0203f_2	MET-AA-PheTyrTrp	Q1LQH2 Prephenate dehydrogenase
NPKM_3257	796525 +	797884 Rmet_0719	<i>aroA</i>	206.00	8.00	Op0203f_2	MET-AA-PheTyrTrp	Q1LQH1 3-phosphoshikimate 1-carboxyvinyltransferase
3UTR_1971	797505 -	797910 Rmet_0720				Op0204r_1		
NPKM_3258	797911 -	798142 Rmet_0720		2.67	1.53	Op0204r_1	NA	Q1LQH0 Membrane protein-like protein
5UTR_1663	798143 -	798183 Rmet_0720				Op0204r_1		
NPKM_3259	798302 +	798962 Rmet_0721	<i>cmk</i>	394.67	8.50	Op0205f_1	MET-NUC-Pyr	Q1LQG9 Cytidylate kinase
NPKM_3260	799105 +	800800 Rmet_0722	<i>rpsA</i>	5905.33	68.65	Op0205f_2	GIP-TL-Ribo	Q1LQG8 SSU ribosomal protein S1P
NPKM_3261	800833 +	801241 Rmet_0723	<i>ihfB</i>	4654.67	106.64	Op0205f_2	GIP-REP-Recomb	Q1LQG7 Integration host factor, beta subunit
NPKM_3262	801469 +	801793 Rmet_0724		366.33	23.01	Op0205f_2	NA	Q1LQG6 Putative transmembrane protein
NPKM_3263	801796 +	803026 Rmet_0725		161.33	14.98	Op0205f_2	NA	Q1LQG5 Tetratricopeptide TPR_2
NPKM_3264	803083 +	804457 Rmet_0726	<i>ugd</i>	165.33	2.08	Op0205f_2	MET-CAH-Pent	Q1LQG4 UDP-glucose/GDP-mannose dehydrogenase
NPKM_3265	804536 +	805481 Rmet_0727	<i>rfaE</i>	199.33	4.51	Op0205f_2	NA	Q1LQG3 D-alpha,beta-D-heptose 7-phosphate 1-kinase
NPKM_3266	805507 +	806503 Rmet_0728	<i>rfaD</i>	162.33	4.93	Op0205f_2	MET-GLYC-LPS	Q1LQG2 ADP-L-glycero-D-manno-heptose-6-epimerase
NPKM_3267	806712 +	807093 Rmet_0729		37.00	2.65	Op0205f_2	GIP-PTL-T2S	Q1LQG1 Helix-hairpin-helix DNA-binding, class 1
NPKM_3268	807190 +	808639 Rmet_0730	<i>rutG</i>	76.00	7.00	Op0205f_3	EIP-TRA-Ion	Q1LQG0 Uracil-xanthine permease
NPKM_3269	808716 +	809652 Rmet_0731	<i>cysM</i>	295.67	12.74	Op0205f_4	NA	Q1LQF9 Cysteine synthase
3UTR_1178	809653 +	809689 Rmet_0731	<i>cysM</i>			Op0205f_4		
3UTR_1970	809657 -	809730 Rmet_0732	<i>mltB</i>			Op0206r_1		
NPKM_3270	809731 -	810958 Rmet_0732	<i>mltB</i>	112.67	5.69	Op0206r_1	NA	Q1LQF8 Lytic murein transglycosylase B
5UTR_962	810941 +	811002 Rmet_0733				Op0207f_1		
5UTR_1662	810959 -	810991 Rmet_0732	<i>mltB</i>			Op0206r_1		
NPKM_3271	811002 +	811926 Rmet_0733		120.33	5.51	Op0207f_1	NA	Q1LQF7 Histone deacetylase superfamily
NPKM_3272	812099 +	813134 Rmet_0734	<i>metN</i>	123.33	9.29	Op0207f_1	EIP-TRA-ABC	Q1LQF6 Methionine import ATP-binding protein metN
NPKM_3273	813123 +	813777 Rmet_0735	<i>metI</i>	99.33	10.21	Op0207f_1	EIP-TRA-ABC	Q1LQF5 Binding-protein-dependent transport systems inner membrane component
NPKM_3274	813843 +	814638 Rmet_0736	<i>metQ</i>	252.67	6.66	Op0207f_2	EIP-TRA-ABC	Q1LQF4 Lipoprotein YaeC
NPKM_3275	814796 +	815600 Rmet_0737	<i>etfB</i>	1500.67	146.03	Op0207f_3	NA	Q1LQF3 Electron transfer flavoprotein beta-subunit
NPKM_3276	815618 +	816554 Rmet_0738	<i>etfA</i>	1585.67	168.57	Op0207f_3	NA	Q1LQF2 Electron transfer flavoprotein, alpha subunit
NPKM_3277	816674 +	818459 Rmet_0739		223.00	17.06	Op0207f_3	NA	Q1LQF1 Acyl-CoA dehydrogenase-like protein
3UTR_1969	818355 -	818536 Rmet_0740	<i>dadA</i>			Op0208r_1		
3UTR_1179	818460 +	818498 Rmet_0739				Op0207f_3		
NPKM_3278	818537 -	819842 Rmet_0740	<i>dadA</i>	114.67	7.51	Op0208r_1	MET-EN-Nitrog	Q1LQF0 D-amino acid dehydrogenase small subunit
5UTR_963	819946 +	819950 Rmet_0741	<i>lrp</i>			Op0209f_1		
NPKM_3279	819950 +	820460 Rmet_0741	<i>lrp</i>	30.00	2.00	Op0209f_1	NA	Q1LQE9 Transcriptional regulator, AsnC family
3UTR_1180	820461 +	821592 Rmet_0741	<i>lrp</i>			Op0209f_1		
NPKM_3280	820479 -	821565 Rmet_0742	<i>splB</i>	82.00	14.80	Op0210r_1	NA	Q1LQE8 Radical SAM
5UTR_964	821595 +	823325 Rmet_0745				Op0211f_1		
NPKM_3281	821699 -	822632 Rmet_0743		140.67	22.14	Op0210r_1	NA	Q1LQE7 Transcriptional regulator, LysR family
NPKM_3282	822664 -	823156 Rmet_0744		417.67	42.03	Op0210r_1	NA	Q1LQE6 TM2
NPKM_3283	823240 -	823336 Rmet_6427		558.67	63.54	Op0210r_1	NA	NA

NPKM_3284	823325 +	823604 Rmet_0745		8.00	2.65	Op0211f_1	NA	Q1LQE5 Putative uncharacterized protein
3UTR_1181	823605 +	823908 Rmet_0745				Op0211f_1		
NPKM_3285	823620 -	824034 Rmet_0746		67.00	14.73	Op0212r_2	NA	Q1LQE4 Putative uncharacterized protein
NPKM_3286	824218 -	825352 Rmet_0747		17.33	0.58	Op0212r_1	NA	Q1LQE3 Putative membrane-bound dehydrogenase oxidoreductase protein
5UTR_965	824917 +	825449 Rmet_0748	<i>rpsP</i>			Op0213f_1		
5UTR_1661	825353 -	826214 Rmet_0747				Op0212r_1		
NPKM_3287	825449 +	825779 Rmet_0748	<i>rpsP</i>	1151.67	75.30	Op0213f_1	GIP-TL-Ribo	Q1LQE2 SSU ribosomal protein S16P
NPKM_3288	825837 +	826500 Rmet_0749	<i>rimM</i>	1846.33	38.28	Op0213f_1	GIP-TL-Ass	Q1LQE1 Ribosome maturation factor rimM
NPKM_3289	826519 +	827302 Rmet_0750	<i>trmD</i>	655.00	45.57	Op0213f_1	GIP-TL-Ass	Q1LQE0 tRNA (guanine-N(1)-)-methyltransferase
3UTR_1968	827355 -	828626 Rmet_0753				Op0214r_1		
NPKM_3290	827376 +	827769 Rmet_0751	<i>rplS</i>	4429.33	179.11	Op0213f_2	GIP-TL-Ribo	Q1LQD9 50S ribosomal protein L19
NPKM_3291	827861 +	828596 Rmet_0752		114.33	5.03	Op0213f_2	NA	Q1LQD8 NUDIX hydrolase
NPKM_3292	828627 -	829476 Rmet_0753		208.00	3.46	Op0214r_1	NA	Q1LQD7 UPF0176 protein Rmet_0753
5UTR_1660	829477 -	829504 Rmet_0753				Op0214r_1		
NPKM_3293	829626 +	833157 Rmet_0754	<i>dnaE</i>	155.67	5.03	Op0215f_1	GIP-REP-DNA_Pol	Q1LQD6 DNA polymerase III, alpha subunit
NPKM_3294	833149 +	834412 Rmet_0755		143.67	4.51	Op0215f_1	NA	Q1LQD5 Glycosyl transferase, group 1
3UTR_1967	833857 -	834343 Rmet_0756				Op0216r_1		
NPKM_3295	834344 -	835127 Rmet_0756		60.67	1.53	Op0216r_1	NA	Q1LQD4 Glycosyl transferase, family 2
NPKM_3296	835205 +	836990 Rmet_0757	<i>msbA</i>	85.67	2.08	Op0217f_1	NA	Q1LQD3 Lipid A export ATP-binding/permease protein msbA
NPKM_3297	837074 +	837659 Rmet_0758		169.00	8.89	Op0217f_1	NA	Q1LQD2 Uncharacterised peroxidase-related
3UTR_1182	837660 +	839949 Rmet_0758				Op0217f_1		
NPKM_3298	837681 -	838200 Rmet_0759		0.67	0.58	Op0218r_1	NA	Q1LQD1 Putative lipoprotein
3UTR_1966	838394 -	838434 Rmet_0760	<i>phnM</i>			Op0218r_1		
NPKM_3299	838435 -	839662 Rmet_0760	<i>phnM</i>	8.67	0.58	Op0218r_1	NA	Q1LQD0 Amidohydrolase 3
NPKM_3300	839654 -	840380 Rmet_0761	<i>phnL</i>	8.33	0.58	Op0218r_1	EIP-TRA-ABC	Q1LQC9 Phosphonate C-P lyase system, PhnL
NPKM_3301	840382 -	841159 Rmet_0762	<i>phnK</i>	8.00	1.00	Op0218r_1	EIP-TRA-ABC	Q1LQC8 Phosphonate C-P lyase system, PhnK
NPKM_3302	841155 -	842043 Rmet_0763	<i>phnJ</i>	8.33	0.58	Op0218r_1	NA	Q1LQC7 Phosphonate metabolism PhnJ
NPKM_3303	842039 -	843161 Rmet_0764	<i>phnI</i>	8.00	1.00	Op0218r_1	NA	Q1LQC6 Phosphonate metabolism
NPKM_3304	843162 -	843780 Rmet_0765	<i>phnH</i>	8.67	1.15	Op0218r_1	NA	Q1LQC5 Phosphonate metabolism
NPKM_3305	843781 -	844270 Rmet_0766	<i>phnG</i>	9.33	0.58	Op0218r_1	NA	Q1LQC4 Phosphonate metabolism PhnG
5UTR_966	844354 +	844432 Rmet_0767	<i>phnF</i>			Op0219f_1		
NPKM_3306	844432 +	845188 Rmet_0767	<i>phnF</i>	42.33	0.58	Op0219f_1	NA	Q1LQC3 Transcriptional regulator, GntR family
NPKM_3307	845280 +	846504 Rmet_0768	<i>phnM</i>	31.00	1.00	Op0219f_1	NA	Q1LQC2 Amidohydrolase 3
NPKM_3308	846500 +	847235 Rmet_0769		28.00	2.00	Op0219f_1	NA	Q1LQC1 Putative uncharacterized protein
NPKM_3309	847231 +	847819 Rmet_0770	<i>phnN</i>	23.33	1.15	Op0219f_1	MET-CAH-PP_KDPG	Q1LQC0 Phosphonate metabolism, 1,5-bisphosphokinase (PRPP-forming) PhnN
3UTR_1183	847820 +	848292 Rmet_0770	<i>phnN</i>			Op0219f_1		
3UTR_1965	847959 -	847970 Rmet_0771	<i>phnO</i>			Op0220r_1		
NPKM_3310	847971 -	848439 Rmet_0771	<i>phnO</i>	0.67	0.58	Op0220r_1	NA	Q1LQB9 GCN5-related N-acetyltransferase
NPKM_3311	848435 -	848975 Rmet_0772		1.33	0.58	Op0220r_1	NA	Q1LQB8 Putative uncharacterized protein
NPKM_3312	848971 -	849850 Rmet_0773	<i>phnE</i>	0.67	0.58	Op0220r_1	EIP-TRA-ABC	Q1LQB7 Phosphonate uptake transporter
NPKM_3313	849866 -	850847 Rmet_0774	<i>phnD</i>	1.00	0.00	Op0220r_1	EIP-TRA-ABC	Q1LQB6 Phosphonate-binding periplasmic protein
NPKM_3314	850967 -	851897 Rmet_0775	<i>phnC</i>	4.67	1.15	Op0220r_1	EIP-TRA-ABC	Q1LQB5 Phosphonates import ATP-binding protein phnC 1
5UTR_1659	851898 -	851955 Rmet_0775	<i>phnC</i>			Op0220r_1		

5UTR_967	852086 +	852102 Rmet_0776				Op0221f_1		
NPKM_3315	852102 +	853446 Rmet_0776		1.67	0.58	Op0221f_1	NA	Q1LQB4 Major facilitator superfamily MFS_1
NPKM_3316	853445 +	854702 Rmet_0777	<i>bcr</i>	0.67	0.58	Op0221f_1	NA	Q1LQB3 Drug resistance transporter Bcr/CfIA subfamily
3UTR_1964	853682 -	854687 Rmet_0778	<i>rng</i>			Op0222r_3		
NPKM_3317	854688 -	856221 Rmet_0778	<i>rng</i>	108.00	4.36	Op0222r_3	GIP-TL-Ass	Q1LQB2 RNase G
NPKM_3318	856279 -	856882 Rmet_0779	<i>maf</i>	40.33	0.58	Op0222r_2	DIV-Division	Q1LQB1 Maf-like protein Rmet_0779
NPKM_3319	856998 -	857478 Rmet_0780		100.67	2.08	Op0222r_2	NA	Q1LQB0 UPF0247 protein Rmet_0780
NPKM_3320	857512 -	858283 Rmet_0781		242.67	13.20	Op0222r_2	NA	Q1LQA9 lojap-related protein
NPKM_3321	858304 -	859012 Rmet_0782	<i>nadD</i>	104.00	9.54	Op0222r_1	MET-COF-NicAm	Q1LQA8 Nicotinate-nucleotide adenyllyltransferase
NPKM_3322	859016 -	859928 Rmet_0783	<i>hemF</i>	114.67	5.86	Op0222r_1	MET-COF-Porph	Q1LQA7 Coproporphyrinogen oxidase
NPKM_3323	860062 -	861331 Rmet_0784	<i>purD</i>	257.00	9.54	Op0222r_1	MET-NUC-Pur	Q1LQA6 Phosphoribosylamine--glycine ligase
NPKM_3324	861415 -	862141 Rmet_0785		309.00	8.72	Op0222r_1	NA	Q1LQA5 UPF0082 protein Rmet_0785
5UTR_1658	862142 -	862263 Rmet_0785				Op0222r_1		
5UTR_968	862334 +	862396 Rmet_0786	<i>yjgR</i>			Op0223f_1		
NPKM_3325	862396 +	863932 Rmet_0786	<i>yjgR</i>	63.67	3.79	Op0223f_1	NA	Q1LQA4 Putative uncharacterized protein
3UTR_1184	863933 +	864434 Rmet_0786	<i>yjgR</i>			Op0223f_1		
3UTR_1963	863942 -	864045 Rmet_0787				Op0224r_1		
NPKM_3326	864046 -	864199 Rmet_0787		18.00	2.00	Op0224r_1	NA	Q1LQA3 Putative uncharacterized protein
NPKM_3327	864346 -	864997 Rmet_0788	<i>upp</i>	95.33	5.51	Op0224r_1	MET-NUC-Pyr	Q1LQA2 Uracil phosphoribosyltransferase
NPKM_3328	865088 -	866078 Rmet_0789	<i>bug</i>	65.33	1.53	Op0224r_1	NA	Q1LQA1 Uncharacterized protein UPF0065
5UTR_1657	866079 -	866139 Rmet_0789	<i>bug</i>			Op0224r_1		
5UTR_969	866245 +	866321 Rmet_0790				Op0225f_1		
NPKM_3329	866321 +	867209 Rmet_0790		31.33	3.79	Op0225f_1	NA	Q1LQA0 Putative uncharacterized protein
3UTR_1962	867144 -	868482 Rmet_0793				Op0226r_2		
NPKM_3330	867318 +	868035 Rmet_0791		337.33	13.80	Op0225f_2	MET-LIP-FASyn	Q1LQ99 Short-chain dehydrogenase/reductase SDR
NPKM_3331	868036 +	868459 Rmet_0792	<i>mgsA</i>	192.33	13.32	Op0225f_2	MET-CAH-Pyr	Q1LQ98 Methylglyoxal synthase
3UTR_1185	868460 +	869075 Rmet_0792	<i>mgsA</i>			Op0225f_2		
NPKM_3332	868483 -	868777 Rmet_0793		247.00	17.35	Op0226r_2	NA	Q1LQ97 Putative uncharacterized protein
NPKM_3333	868909 -	870052 Rmet_0794		343.67	12.42	Op0226r_2	EIP-TRA-ABC	Q1LQ96 Basic membrane lipoprotein
NPKM_3334	870132 -	871053 Rmet_0795		49.33	3.21	Op0226r_1	EIP-TRA-ABC	Q1LQ95 Inner-membrane translocator
NPKM_3335	871071 -	872166 Rmet_0796		40.33	1.15	Op0226r_1	EIP-TRA-ABC	Q1LQ94 Inner-membrane translocator
NPKM_3336	872158 -	873772 Rmet_0797		60.00	1.73	Op0226r_1	EIP-TRA-ABC	Q1LQ93 ABC transporter-related protein
5UTR_1656	873773 -	873827 Rmet_0797				Op0226r_1		
3UTR_1961	874000 -	874048 Rmet_0798				Op0226r_1		
NPKM_3337	874049 -	874973 Rmet_0798		49.00	1.73	Op0226r_1	NA	Q1LQ92 Pirin-like protein
5UTR_1655	874974 -	875136 Rmet_0798				Op0226r_1		
5UTR_970	875235 +	875617 Rmet_0799				Op0227f_1		
NPKM_3338	875617 +	876334 Rmet_0799		1029.33	112.62	Op0227f_1	EIP-TRA-ABC	Q1LQ91 Binding-protein-dependent transport systems inner membrane component
NPKM_3339	876344 +	877295 Rmet_0800		734.33	32.32	Op0227f_1	EIP-TRA-ABC	Q1LQ90 Substrate-binding region of ABC-type glycine betaine transport system
NPKM_3340	877305 +	877956 Rmet_0801		726.33	28.31	Op0227f_1	EIP-TRA-ABC	Q1LQ89 Binding-protein-dependent transport systems inner membrane component
NPKM_3341	877952 +	879149 Rmet_0802		842.00	20.07	Op0227f_1	EIP-TRA-ABC	Q1LQ88 Glycine betaine/L-proline transport ATP binding subunit
3UTR_1960	878677 -	879369 Rmet_0803				Op0228r_2		
NPKM_3342	879370 -	879817 Rmet_0803		7.33	0.58	Op0228r_2	NA	Q1LQ87 Putative uncharacterized protein

5UTR_1654	879818 -	879888 Rmet_0803				Op0228r_2		
NPKM_3343	879971 -	880727 Rmet_0804	1.67	0.58	Op0228r_1	NA	Q1LQ86 SPFH domain, Band 7 family protein	
NPKM_3344	880763 -	882239 Rmet_0805	5.33	0.58	Op0228r_1	GIP-PTL-Fold	Q1LQ85 Putative uncharacterized protein	
NPKM_3345	882346 +	883618 Rmet_0806	71.00	12.77	Op0229f_1	NA	Q1LQ84 Putative uncharacterized protein	
NPKM_3346	883704 +	884478 Rmet_0807	89.67	9.29	Op0229f_1	NA	Q1LQ83 Class II aldolase/adducin-like protein	
NPKM_3347	884497 +	884686 Rmet_0808	311.00	26.51	Op0229f_2	NA	Q1LQ82 4-oxalocrotonate tautomerase family enzyme	
NPKM_3348	884705 +	885758 Rmet_0809	270.67	6.81	Op0229f_2	MET-AA-GlySerThr	Q1LQ81 L-threonine aldolase	
NPKM_3349	885825 +	886422 Rmet_0810	233.67	3.79	Op0229f_2	NA	Q1LQ80 NUDIX hydrolase	
NPKM_3350	886434 +	886662 Rmet_0811	218.67	17.24	Op0229f_2	GIP-PTL-Fold	Q1LQ79 SirA-like protein	
3UTR_1959	886521 -	886732 Rmet_0812			Op0230r_3			
3UTR_1186	886663 +	887223 Rmet_0811			Op0229f_2			
NPKM_3351	886733 -	887081 Rmet_0812	376.00	22.27	Op0230r_3	GIP-PTL-Fold	Q1LQ78 Peptidyl-prolyl cis-trans isomerase	
NPKM_3352	887111 -	887660 Rmet_0813	46.00	6.00	Op0230r_2	NA	Q1LQ77 YaeQ	
NPKM_3353	887792 -	888101 Rmet_0814	21.33	2.08	Op0230r_1	NA	Q1LQ76 Putative uncharacterized protein	
NPKM_3354	888228 -	888822 Rmet_0815	32.00	2.65	Op0230r_1	NA	Q1LQ75 YceI	
NPKM_3355	888861 -	889245 Rmet_0816	53.67	3.51	Op0230r_1	NA	Q1LQ74 Putative transmembrane protein	
NPKM_3356	889353 -	889584 Rmet_0817	125.33	10.02	Op0230r_1	NA	Q1LQ73 Putative uncharacterized protein	
NPKM_3357	889586 -	891335 Rmet_0818	142.00	3.00	Op0230r_1	MET-AA-GluGSH	Q1LQ72 GlutaminyI-tRNA synthetase	
5UTR_1653	891336 -	891548 Rmet_0818			Op0230r_1			
5UTR_971	891565 +	891614 Rmet_0819			Op0231f_1			
NPKM_3358	891614 +	893066 Rmet_0819	53.00	3.00	Op0231f_1	NA	Q1LQ71 L-carnitine dehydratase/bile acid-inducible protein F	
3UTR_1958	892324 -	893061 Rmet_0820			Op0232r_2			
NPKM_3359	893062 -	893680 Rmet_0820	46.00	2.65	Op0232r_2	NA	Q1LQ70 Pyridoxamine 5'-phosphate oxidase-related, FMN-binding	
3UTR_1187	893067 +	894153 Rmet_0819			Op0231f_1			
NPKM_3360	893693 -	894611 Rmet_0821	47.00	1.00	Op0232r_2	NA	Q1LQ69 Phenazine biosynthesis PhzC/PhzF protein	
NPKM_3361	894877 -	896503 Rmet_0822	119.00	18.36	Op0232r_2	MET-LIP-Others	Q1LQ68 Gamma-glutamyltransferase 2. Threonine peptidase. MEROPS family T03	
NPKM_3362	896581 -	897559 Rmet_0823	50.67	6.66	Op0232r_1	NA	Q1LQ67 Uncharacterized protein UPF0065	
5UTR_1652	897560 -	897561 Rmet_0823			Op0232r_1			
5UTR_972	897606 +	897728 Rmet_0824			Op0233f_1			
NPKM_3363	897728 +	898613 Rmet_0824	9.33	1.53	Op0233f_1	NA	Q1LQ66 Transcriptional regulator, LysR family	
3UTR_1957	898276 -	898719 Rmet_0825			Op0234r_1			
3UTR_1188	898614 +	898659 Rmet_0824			Op0233f_1			
NPKM_3364	898720 -	900223 Rmet_0825	570.00	7.81	Op0234r_1	NA	Q1LQ65 Putative uncharacterized protein	
NPKM_3365	900236 -	900698 Rmet_0826	483.67	29.57	Op0234r_1	NA	Q1LQ64 Putative uncharacterized protein	
5UTR_1651	900699 -	900799 Rmet_0826			Op0234r_1			
5UTR_973	900748 +	901072 Rmet_0827			Op0235f_1			
NPKM_3366	901072 +	902890 Rmet_0827	17.00	0.00	Op0235f_1	NA	Q1LQ63 Sodium/hydrogen exchanger	
3UTR_1956	902224 -	902860 Rmet_0828			Op0236r_2			
NPKM_3367	902861 -	903869 Rmet_0828	115.00	5.57	Op0236r_2	NA	Q1LQ62 Uncharacterized protein UPF0065	
3UTR_1189	902891 +	903791 Rmet_0827			Op0235f_1			
NPKM_3368	903966 -	904422 Rmet_0829	129.33	10.12	Op0236r_2	NA	Q1LQ61 Putative transmembrane protein	
NPKM_3369	904523 -	905744 Rmet_0830	34.33	0.58	Op0236r_1	NA	Q1LQ60 L-carnitine dehydratase/bile acid-inducible protein F	
5UTR_974	905106 +	905963 Rmet_0831			Op0237f_1			

5UTR_1650	905745 -	905908 Rmet_0830				Op0236r_1			
NPKM_3370	905963 +	908618 Rmet_0831	alaS	285.67	10.07	Op0237f_1	MET-AA-AlaAsp	Q1LQ59	Alanyl-tRNA synthetase
3UTR_1190	908619 +	908699 Rmet_0831	alaS			Op0237f_1			
3UTR_1955	908706 -	908721 Rmet_0832	aldH			Op0238r_1			
NPKM_3371	908722 -	910300 Rmet_0832	aldH	17.67	0.58	Op0238r_1	NA	Q1LQ58	Aldehyde dehydrogenase
NPKM_3372	910465 -	911284 Rmet_0833		141.33	3.21	Op0238r_1	NA	Q1LQ57	Transcriptional regulator, GntR family
5UTR_975	910610 +	911377 Rmet_0834	gudD			Op0239f_1			
5UTR_1649	911285 -	911459 Rmet_0833				Op0238r_1			
NPKM_3373	911377 +	912733 Rmet_0834	gudD	5.67	0.58	Op0239f_1	MET-CAH-Ascorb	Q1LQ56	D-glucarate dehydratase
NPKM_3374	912827 +	913883 Rmet_0835	bug	7.67	0.58	Op0239f_1	NA	Q1LQ55	Uncharacterized protein UPF0065
3UTR_1191	913884 +	913967 Rmet_0835	bug			Op0239f_1			
5UTR_976	914086 +	914094 Rmet_0836				Op0239f_1			
NPKM_3375	914094 +	914688 Rmet_0836		14.33	1.53	Op0239f_1	NA	Q1LQ54	Putative uncharacterized protein
3UTR_1192	914689 +	914912 Rmet_0836				Op0239f_1			
5UTR_977	914915 +	915138 Rmet_0837				Op0239f_1			
NPKM_3376	915138 +	917418 Rmet_0837		8.67	0.58	Op0239f_1	EIP-TRA-Pores	Q1LQ53	TonB-dependent siderophore receptor
NPKM_3377	917497 +	918184 Rmet_0838	piuC	22.67	0.58	Op0239f_2	NA	Q1LQ52	PKHD-type hydroxylase Rmet_0838
NPKM_3378	918189 +	919275 Rmet_0839		25.33	0.58	Op0239f_2	MET-CAH-DiCarb	Q1LQ51	FMN-dependent alpha-hydroxy acid dehydrogenase
3UTR_1954	918548 -	919276 Rmet_0840				Op0240r_1			
3UTR_1193	919276 +	919687 Rmet_0839				Op0239f_2			
NPKM_3379	919277 -	920093 Rmet_0840		14.67	1.15	Op0240r_1	NA	Q1LQ50	Transcriptional regulator, IclR family
NPKM_3380	920207 +	921026 Rmet_0841		1.33	0.58	Op0241f_1	MET-CAH-Prop	Q1LQ49	Enoyl-CoA hydratase/isomerase
NPKM_3381	921027 +	923130 Rmet_0842		1.00	0.00	Op0241f_1	NA	Q1LQ48	CoA-binding
NPKM_3382	923189 +	924161 Rmet_0843	bug	4.67	0.58	Op0241f_2	NA	Q1LQ47	Uncharacterized protein UPF0065
NPKM_3383	924164 +	925373 Rmet_0844		3.33	0.58	Op0241f_2	NA	Q1LQ46	Acyl-CoA dehydrogenase-like protein
NPKM_3384	925372 +	926569 Rmet_0845		5.33	0.58	Op0241f_2	MET-CAH-Prop	Q1LQ45	Acyl-CoA dehydrogenase-like protein
3UTR_1194	926570 +	926837 Rmet_0845				Op0241f_2			
5UTR_978	926847 +	926968 Rmet_0846				Op0241f_2			
3UTR_1953	926949 -	927471 Rmet_0847				Op0242r_1			
NPKM_3385	926968 +	927226 Rmet_0846		3.67	0.58	Op0241f_2	NA	Q1LQ44	Putative uncharacterized protein
3UTR_1195	927227 +	927329 Rmet_0846				Op0241f_2			
NPKM_3386	927472 -	928363 Rmet_0847		98.67	2.08	Op0242r_1	NA	Q1LQ43	Putative uncharacterized protein
NPKM_3387	928454 -	928652 Rmet_6428		153.00	1.73	Op0242r_1	NA	NA	
NPKM_3388	928871 -	929795 Rmet_0848		91.33	7.09	Op0242r_1	NA	Q1LQ42	Putative uncharacterized protein
5UTR_979	929738 +	930159 Rmet_0849				Op0243f_1			
NPKM_3389	929830 -	929920 Rmet_R0008		67.67	8.02	Op0242r_1	NA	NA	
5UTR_1648	929921 -	929975 Rmet_R0008				Op0242r_1			
NPKM_3390	930159 +	930678 Rmet_0849		856.00	30.20	Op0243f_1	NA	Q1LQ41	17 kDa surface antigen
3UTR_1196	930679 +	932349 Rmet_0849				Op0243f_1			
3UTR_1952	930729 -	930785 Rmet_0850	hemN			Op0244r_2			
NPKM_3391	930786 -	932046 Rmet_0850	hemN	64.33	3.51	Op0244r_2	MET-COF-Porph	Q1LQ40	Coproporphyrinogen III oxidase, anaerobic
NPKM_3392	932042 -	932657 Rmet_0851	ygjV	109.00	3.00	Op0244r_2	NA	Q1LQ39	Nucleoside-triphosphatase
NPKM_3393	932675 -	933392 Rmet_0852	rph	145.67	6.66	Op0244r_2	GIP-TL-Ass	Q1LQ38	Ribonuclease PH

5UTR_980	933456 +	935710 Rmet_0855				Op0245f_1		
NPKM_3394	933473 -	934388 Rmet_0853		129.67	7.37	Op0244r_2	NA	Q1LQ37 Protein serine/threonine phosphatases
NPKM_3395	934429 -	935491 Rmet_0854		184.67	12.01	Op0244r_2	NA	Q1LQ36 Serine/threonine protein kinase
NPKM_3396	935487 -	935724 Rmet_6429		4.33	1.53	Op0244r_1	NA	NA
NPKM_3397	935710 +	936646 Rmet_0855		183.33	7.02	Op0245f_1	NA	Q1LQ35 Putative uncharacterized protein
5UTR_1647	935725 -	936445 Rmet_6429				Op0244r_1		
NPKM_3398	936650 +	937301 Rmet_0856	<i>gmk</i>	247.00	6.24	Op0245f_1	MET-NUC-Pur	Q1LQ34 Guanylate kinase
3UTR_1951	937346 -	937363 Rmet_6430				Op2003r_1		
NPKM_3399	937364 -	937829 Rmet_6430		7.33	0.58	Op2003r_1	NA	NA
NPKM_3400	937385 +	937589 Rmet_0857	<i>rpoZ</i>	1067.00	57.17	Op0245f_2	GIP-TK-RNAP	B3R3N5 DNA-DIRECTED RNA POLYMERASE (OMEGA CHAIN) PROTEIN
NPKM_3401	937674 +	940299 Rmet_0858	<i>spoT</i>	223.00	14.18	Op0245f_2	MET-NUC-Pur	Q1LQ32 (P)ppGpp synthetase I (GTP pyrophosphokinase), SpoT/RelA
5UTR_1646	937830 -	938017 Rmet_6430				Op2003r_1		
3UTR_1950	939161 -	940294 Rmet_0859	<i>greB</i>			Op0246r_1		
NPKM_3402	940295 -	940856 Rmet_0859	<i>greB</i>	171.33	2.31	Op0246r_1	GIP-TK-Assoc	Q1LQ31 Transcription elongation factor
5UTR_1645	940857 -	940908 Rmet_0859	<i>greB</i>			Op0246r_1		
NPKM_3403	940980 +	941057 Rmet_R0009		17.33	2.31	Op0247f_1	NA	NA
NPKM_3404	941173 +	941521 Rmet_0860		70.67	6.81	Op0247f_2	NA	Q1LQ30 Putative uncharacterized protein
NPKM_3405	941684 +	941924 Rmet_0861		47.67	6.03	Op0247f_2	NA	Q1LQ29 Putative uncharacterized protein
NPKM_3406	942031 +	942108 Rmet_R0010		164.00	29.87	Op0247f_3	NA	NA
3UTR_1949	942080 -	942285 Rmet_0862				Op0248r_2		
NPKM_3407	942286 -	942547 Rmet_0862		331.00	16.70	Op0248r_2	NA	Q1LQ28 Putative uncharacterized protein
NPKM_3408	942597 -	942888 Rmet_0863		308.33	13.80	Op0248r_2	NA	Q1LQ27 Putative uncharacterized protein
5UTR_1644	942889 -	942889 Rmet_0863				Op0248r_2		
NPKM_3409	943015 -	943189 Rmet_6431		3.00	2.00	Op0248r_1	NA	NA
NPKM_3410	943048 +	944545 Rmet_0864		79.67	10.02	Op0249f_1	NA	Q1LQ26 Putative uncharacterized protein
5UTR_1643	943190 -	943246 Rmet_6431				Op0248r_1		
NPKM_3411	944571 +	944883 Rmet_0865		75.67	13.01	Op0249f_1	NA	Q1LQ25 Putative uncharacterized protein
NPKM_3412	945001 +	945904 Rmet_0866	<i>aspH</i>	393.00	4.36	Op0249f_2	NA	Q1LQ24 Aspartyl/Asparaginy beta-hydroxylase
3UTR_1197	945905 +	947131 Rmet_0866	<i>aspH</i>			Op0249f_2		
3UTR_1948	945947 -	945962 Rmet_0867				Op0250r_1		
NPKM_3413	945963 -	947442 Rmet_0867		68.00	1.00	Op0250r_1	NA	Q1LQ23 Diguanylate cyclase (GGDEF domain)
NPKM_3414	947556 -	949377 Rmet_0868	<i>gntR</i>	46.33	3.51	Op0250r_1	NA	Q1LQ22 Transcriptional regulator, GntR family
5UTR_981	949137 +	949637 Rmet_0869				Op0251f_1		
5UTR_1642	949378 -	949754 Rmet_0868	<i>gntR</i>			Op0250r_1		
NPKM_3415	949637 +	951257 Rmet_0869		117.67	5.03	Op0251f_1	NA	Q1LQ21 FAD dependent oxidoreductase
3UTR_1947	950585 -	951894 Rmet_0871				Op0252r_1		
NPKM_3416	951253 +	951847 Rmet_0870		75.33	6.81	Op0251f_1	NA	Q1LQ20 Putative uncharacterized protein
NPKM_3417	951895 -	952753 Rmet_0871		53.00	2.65	Op0252r_1	NA	Q1LQ19 Putative uncharacterized protein
5UTR_1641	952754 -	952769 Rmet_0871				Op0252r_1		
NPKM_3418	952942 +	954568 Rmet_0872		32.67	4.73	Op0253f_1	NA	Q1LQ18 Putative uncharacterized protein
3UTR_1946	954786 -	955685 Rmet_R0011				Op0254r_3		
NPKM_3419	954806 +	955220 Rmet_0873		10.33	2.52	Op0253f_1	NA	Q1LQ17 Response regulator receiver domain protein (CheY-like)
NPKM_3420	955666 +	956140 Rmet_0874		3.00	1.00	Op0253f_1	NA	Q1LQ16 Putative uncharacterized protein

NPKM_3421	955686 -	955762 Rmet_R0011		41.00	6.24	Op0254r_3	NA	NA
NPKM_3422	956112 -	957129 Rmet_0875	<i>cbbF3</i>	284.00	17.09	Op0254r_3	MET-CAH-FbP	Q1LQ15 D-fructose 1,6-bisphosphatase
3UTR_1198	956141 +	956680 Rmet_0874				Op0253f_1		
NPKM_3423	957195 -	959889 Rmet_0876	<i>pepN</i>	100.33	4.04	Op0254r_2	MET-OAA-GSH	Q1LQ14 Peptidase M1, alanyl aminopeptidase
5UTR_1640	959890 -	959920 Rmet_0876	<i>pepN</i>			Op0254r_2		
5UTR_982	959934 +	960098 Rmet_0877				Op0255f_1		
NPKM_3424	960015 -	960087 Rmet_6432		0.00	0.00	Op0254r_1	NA	NA
NPKM_3425	960098 +	960749 Rmet_0877		127.67	3.06	Op0255f_1	NA	Q1LQ13 Putative lipoprotein transmembrane
NPKM_3426	960936 +	963258 Rmet_0878	<i>maeB</i>	474.00	10.58	Op0255f_2	MET-CAH-Pyr	Q1LQ12 Malic enzyme, NAD-binding
3UTR_1199	963259 +	963306 Rmet_0878	<i>maeB</i>			Op0255f_2		
3UTR_1945	963318 -	963409 Rmet_0879				Op0256r_2		
NPKM_3427	963410 -	963656 Rmet_0879		51.67	4.04	Op0256r_2	NA	Q1LQ11 Putative uncharacterized protein
NPKM_3428	963897 -	964983 Rmet_0880		135.67	12.50	Op0256r_2	NA	Q1LQ10 Porin, gram-negative type
NPKM_3429	965179 -	965701 Rmet_0881		38.67	5.03	Op0256r_1	NA	Q1LQ09 Putative uncharacterized protein
NPKM_3430	965697 -	966642 Rmet_0882		28.33	2.08	Op0256r_1	NA	Q1LQ08 Polysaccharide deacetylase
NPKM_3431	966823 -	968230 Rmet_0883	<i>ygfU</i>	21.67	1.53	Op0256r_1	EIP-TRA-Ion	Q1LQ07 Uracil-xanthine permease
NPKM_3432	968441 -	969185 Rmet_0884		17.33	2.52	Op0256r_1	NA	Q1LQ06 Transcriptional regulator, GntR family
5UTR_1639	969186 -	969241 Rmet_0884				Op0256r_1		
3UTR_1944	969244 -	971287 Rmet_0887				Op0258r_3		
5UTR_983	969349 +	969528 Rmet_0885				Op0257f_1		
NPKM_3433	969528 +	969882 Rmet_0885		22.33	2.08	Op0257f_1	NA	Q1LQ05 Transthyretin
NPKM_3434	969913 +	971122 Rmet_0886		21.67	1.53	Op0257f_1	NA	Q1LQ04 Putative uncharacterized protein
3UTR_1200	971123 +	971211 Rmet_0886				Op0257f_1		
NPKM_3435	971288 -	972014 Rmet_0887		250.67	12.86	Op0258r_3	NA	Q1LQ03 Putative uncharacterized protein
NPKM_3437	972206 -	973388 Rmet_0888		23.67	3.21	Op0258r_2	NA	Q1LQ02 Fatty acid desaturase
NPKM_3438	973598 -	974939 Rmet_0889	<i>guaD</i>	43.67	2.52	Op0258r_2	MET-NUC-Pur	Q1LQ01 Guanine deaminase
NPKM_3439	975016 -	976081 Rmet_0890	<i>add</i>	59.67	2.08	Op0258r_2	MET-NUC-Pur	Q1LQ00 Adenosine deaminase
NPKM_3440	976125 -	977121 Rmet_0891	<i>xdhC</i>	10.67	0.58	Op0258r_1	GIP-PTL-Fold	Q1LPZ9 Molybdenum cofactor sulfurylase
NPKM_3441	977140 -	979492 Rmet_0892	<i>xdhB</i>	18.33	1.53	Op0258r_1	NA	Q1LPZ8 Xanthine oxidase
NPKM_3442	979503 -	981000 Rmet_0893	<i>xdhA</i>	21.67	2.08	Op0258r_1	NA	Q1LPZ7 Molybdopterin dehydrogenase, FAD-binding
5UTR_984	981147 +	981277 Rmet_0894				Op0259f_1		
NPKM_3443	981277 +	982228 Rmet_0894		88.67	1.53	Op0259f_1	NA	Q1LPZ6 Transcriptional regulator, LysR family
3UTR_1201	982229 +	982928 Rmet_0894				Op0259f_1		
NPKM_3444	982292 -	983147 Rmet_0895		135.33	5.69	Op0260r_1	EIP-TRA-ABC	Q1LPZ5 Putative signal peptide protein
5UTR_1638	983148 -	983207 Rmet_0895				Op0260r_1		
5UTR_985	983251 +	983289 Rmet_0896				Op0261f_1		
NPKM_3445	983289 +	984387 Rmet_0896		139.67	4.51	Op0261f_1	NA	Q1LPZ4 Transcriptional regulator of molybdate metabolism, LysR family
NPKM_3446	984483 +	985080 Rmet_0897		68.67	4.04	Op0261f_1	NA	Q1LPZ3 Putative transmembrane protein
NPKM_3447	985137 +	987693 Rmet_0898	<i>lolE</i>	32.00	1.00	Op0261f_1	EIP-TRA-ABC	Q1LPZ2 Putative uncharacterized protein
NPKM_3448	987708 +	988152 Rmet_0899		87.00	3.46	Op0261f_2	NA	Q1LPZ1 Globin
3UTR_1943	988016 -	990192 Rmet_0903	<i>dgkA</i>			Op0262r_2		
NPKM_3449	988138 +	988741 Rmet_0900		73.67	2.52	Op0261f_2	NA	Q1LPZ0 Putative uncharacterized protein
NPKM_3450	988842 +	989553 Rmet_0901		123.00	7.94	Op0261f_2	NA	Q1LPY9 Transcriptional regulator, TetR family

NPKM_3451	989549 +	990134 Rmet_0902		127.00	3.46	Op0261f_2	NA	Q1LPY8 Putative uncharacterized protein
3UTR_1202	990135 +	991207 Rmet_0902				Op0261f_2		
NPKM_3452	990193 -	990628 Rmet_0903	<i>dgkA</i>	36.00	1.00	Op0262r_2	MET-LIP-GlycLip	Q1LPY7 Diacylglycerol kinase
NPKM_3453	990617 -	991736 Rmet_0904		19.33	1.15	Op0262r_2	NA	Q1LPY6 Glycosyl transferase, group 1
NPKM_3454	991835 -	992765 Rmet_0905		12.67	2.89	Op0262r_2	NA	Q1LPY5 Metallophosphoesterase
NPKM_3455	992945 -	993980 Rmet_0906		58.33	4.51	Op0262r_2	NA	Q1LPY4 PGAP1-like protein
NPKM_3456	993976 -	994522 Rmet_0907		85.33	2.89	Op0262r_2	NA	Q1LPY3 RDD domain protein
NPKM_3457	994617 -	995424 Rmet_0908		235.33	24.79	Op0262r_2	NA	Q1LPY2 Putative transmembrane protein
NPKM_3458	995427 -	995865 Rmet_0909		503.00	42.93	Op0262r_2	NA	Q1LPY1 Putative transmembrane protein
NPKM_3459	995861 -	996428 Rmet_0910	<i>rpoR</i>	156.33	13.65	Op0262r_1	GIP-TK-RNAP	Q1LPY0 Sigma-24 (FecI-like)
5UTR_986	996283 +	996445 Rmet_6433				Op0263f_1		
5UTR_1637	996429 -	996510 Rmet_0910	<i>rpoR</i>			Op0262r_1		
NPKM_3460	996445 +	996625 Rmet_6433		3.67	1.53	Op0263f_1	NA	NA
NPKM_3461	996806 +	998570 Rmet_0911	<i>ilvI</i>	779.67	29.57	Op0263f_2	MET-CAH-But	Q1LPX9 Acetolactate synthase, large subunit
NPKM_3462	998569 +	999061 Rmet_0912	<i>ilvH</i>	693.33	20.13	Op0263f_2	MET-CAH-But	Q1LPX8 Acetolactate synthase, small subunit
NPKM_3463	999198 +	1000215 Rmet_0913	<i>ilvC</i>	1486.67	66.53	Op0263f_3	MET-AA-ValLeulle	Q1LPX7 Ketol-acid reductoisomerase
NPKM_3464	1000195 +	1000459 Rmet_0914		580.67	44.02	Op0263f_3	NA	Q1LPX6 Putative uncharacterized protein
NPKM_3465	1000496 +	1001081 Rmet_0915	<i>psd</i>	140.67	5.13	Op0263f_3	MET-LIP-GlycPLip	Q1LPX5 Phosphatidylserine decarboxylase proenzyme
NPKM_3466	1001106 +	1002000 Rmet_0916	<i>pssA</i>	120.00	4.58	Op0263f_3	MET-LIP-GlycPLip	Q1LPX4 CDP-diacylglycerol--serine O-phosphatidyltransferase
NPKM_3467	1002088 +	1002589 Rmet_0917		336.00	24.27	Op0263f_4	NA	Q1LPX3 Peptidoglycan-binding LysM
NPKM_3468	1002898 +	1004440 Rmet_0918	<i>leuA</i>	317.67	6.66	Op0263f_4	MET-CAH-Pyr	Q1LPX2 2-isopropylmalate synthase
3UTR_1942	1004411 -	1004535 Rmet_0919				Op0264r_1		
NPKM_3469	1004536 -	1005070 Rmet_0919		43.00	3.00	Op0264r_1	NA	Q1LPX1 Putative lipoprotein transmembrane
NPKM_3470	1005307 +	1006561 Rmet_0920		93.33	10.97	Op0265f_1	EIP-TRA-ABC	Q1LPX0 Putative transporter signal peptide protein
NPKM_3471	1006726 +	1006996 Rmet_0921	<i>rpsO</i>	3604.00	103.06	Op0265f_2	GIP-TL-Ribo	Q1LPW9 30S ribosomal protein S15
3UTR_1203	1006997 +	1007324 Rmet_0921	<i>rpsO</i>			Op0265f_2		
5UTR_987	1007326 +	1007461 Rmet_0923	<i>pnp</i>			Op0267f_1		
NPKM_3472	1007461 +	1009639 Rmet_0923	<i>pnp</i>	1058.00	45.92	Op0267f_1	MET-NUC-Pur	Q1LPW7 Polyribonucleotide nucleotidyltransferase
NPKM_3473	1009807 +	1010812 Rmet_0924		214.33	7.09	Op0267f_1	NA	Q1LPW6 Alcohol dehydrogenase, zinc-binding
NPKM_3474	1010939 +	1011677 Rmet_0925	<i>cbhJ2</i>	534.33	27.23	Op0267f_2	MET-CAH-FbP	Q1LPW5 Triosephosphate isomerase
NPKM_3475	1011727 +	1012096 Rmet_0926	<i>secG</i>	424.33	18.18	Op0267f_2	GIP-PTL-Exp	Q1LPW4 Protein translocase subunit secG
NPKM_3476	1012293 +	1012378 Rmet_R0013		926.00	74.00	Op0267f_3	NA	NA
NPKM_3477	1012546 +	1012906 Rmet_0927	<i>nuoA</i>	1236.67	109.02	Op0267f_3	MET-EN-OxPhos	Q1LPW3 NADH-quinone oxidoreductase subunit
NPKM_3478	1012912 +	1013395 Rmet_0928	<i>nuoB</i>	1236.33	82.37	Op0267f_3	MET-EN-OxPhos	Q1LPW2 NADH-quinone oxidoreductase subunit B
NPKM_3479	1013396 +	1013996 Rmet_0929	<i>nuoC</i>	1120.00	36.72	Op0267f_3	MET-EN-OxPhos	Q1LPW1 NADH-quinone oxidoreductase subunit C
NPKM_3480	1014005 +	1015259 Rmet_0930	<i>nuoD</i>	977.00	3.00	Op0267f_3	MET-EN-OxPhos	Q1LPW0 NADH dehydrogenase I, D subunit
NPKM_3481	1015464 +	1015971 Rmet_0931	<i>nuoE</i>	785.33	24.01	Op0267f_3	MET-EN-OxPhos	Q1LPV9 NADH-quinone oxidoreductase, E subunit
NPKM_3482	1015972 +	1017268 Rmet_0932	<i>nuoF</i>	804.00	29.51	Op0267f_3	MET-EN-OxPhos	Q1LPV8 NADH-quinone oxidoreductase, F subunit
NPKM_3483	1017281 +	1019654 Rmet_0933	<i>nuoG</i>	1015.00	23.58	Op0267f_3	MET-EN-OxPhos	Q1LPV7 NADH-quinone oxidoreductase
NPKM_3484	1019672 +	1020737 Rmet_0934	<i>nuoH</i>	787.67	18.01	Op0267f_3	MET-EN-OxPhos	Q1LPV6 NADH-quinone oxidoreductase subunit H
NPKM_3485	1020808 +	1021300 Rmet_0935	<i>nuoI</i>	668.67	7.57	Op0267f_3	MET-EN-OxPhos	Q1LPV5 NADH-quinone oxidoreductase subunit I
NPKM_3486	1021427 +	1022105 Rmet_0936	<i>nuoJ</i>	539.33	12.06	Op0267f_3	MET-EN-OxPhos	Q1LPV4 NADH-ubiquinone/plastoquinone oxidoreductase, chain 6
NPKM_3487	1022122 +	1022428 Rmet_0937	<i>nuoK</i>	438.67	10.07	Op0267f_3	MET-EN-OxPhos	Q1LPV3 NADH-ubiquinone oxidoreductase, chain 4L

NPKM_3488	1022489 +	1024568 Rmet_0938	<i>nuoL</i>	581.33	24.54	Op0267f_3	MET-EN-OxPhos	Q1LPV2 Proton-translocating NADH-quinone oxidoreductase, chain L
NPKM_3489	1024596 +	1026063 Rmet_0939	<i>nuoM</i>	545.33	9.81	Op0267f_3	MET-EN-OxPhos	Q1LPV1 Proton-translocating NADH-quinone oxidoreductase, chain M
NPKM_3490	1026082 +	1027558 Rmet_0940	<i>nuoN</i>	685.00	11.00	Op0267f_3	MET-EN-OxPhos	Q1LPV0 Proton-translocating NADH-quinone oxidoreductase, chain N
NPKM_3491	1027579 +	1027888 Rmet_0941		433.67	15.37	Op0267f_3	NA	Q1LPU9 Putative transmembrane protein
NPKM_3492	1027936 +	1028572 Rmet_0942		162.67	2.08	Op0267f_3	MET-NUC-Pur	Q1LPU8 NUDIX hydrolase
NPKM_3493	1028778 +	1029246 Rmet_0943		262.00	14.73	Op0267f_3	NA	Q1LPU7 Putative uncharacterized protein
NPKM_3494	1029337 +	1030540 Rmet_0944		374.33	38.76	Op0267f_3	NA	Q1LPU6 Acyl-CoA dehydrogenase-like protein
NPKM_3495	1030553 +	1031672 Rmet_0945		351.67	38.00	Op0267f_3	NA	Q1LPU5 Acyl-CoA dehydrogenase-like protein
NPKM_3496	1031737 +	1032187 Rmet_0946		58.33	3.51	Op0267f_3	NA	Q1LPU4 MaoC-like dehydratase
NPKM_3497	1032274 +	1032748 Rmet_0947		66.67	9.71	Op0267f_3	NA	Q1LPU3 MaoC-like dehydratase
3UTR_1204	1032749 +	1032891 Rmet_0947				Op0267f_3		
5UTR_988	1033001 +	1033350 Rmet_0948	<i>cyoA</i>			Op0267f_4		
NPKM_3498	1033350 +	1034319 Rmet_0948	<i>cyoA</i>	563.00	109.58	Op0267f_4	MET-EN-OxPhos	Q1LPU2 Ubiquinol oxidase, subunit II
NPKM_3499	1034327 +	1036301 Rmet_0949	<i>cyoB</i>	517.67	100.38	Op0267f_4	MET-EN-OxPhos	Q1LPU1 Cytochrome c oxidase, subunit I
NPKM_3500	1036306 +	1036951 Rmet_0950	<i>cyoC</i>	547.67	102.79	Op0267f_4	MET-EN-OxPhos	Q1LPU0 Cytochrome c oxidase, subunit III
NPKM_3501	1036951 +	1037302 Rmet_0951	<i>cyoD</i>	493.00	75.48	Op0267f_4	MET-EN-OxPhos	Q1LPT9 Cytochrome C oxidase subunit IV
NPKM_3502	1037318 +	1037594 Rmet_6434		4.00	1.00	Op0267f_4	NA	NA
NPKM_3503	1037620 +	1038880 Rmet_0952		1.67	0.58	Op0267f_4	EIP-TRA-ABC	Q1LPT8 Twin-arginine translocation pathway signal
5UTR_989	1038919 +	1038980 Rmet_0953				Op0267f_4		
NPKM_3504	1038980 +	1040618 Rmet_0953		0.67	0.58	Op0267f_4	EIP-TRA-ABC	Q1LPT7 Inner-membrane translocator
NPKM_3505	1040619 +	1041822 Rmet_0954		1.00	0.00	Op0267f_4	EIP-TRA-ABC	Q1LPT6 Inner-membrane translocator
NPKM_3506	1041818 +	1042667 Rmet_0955	<i>livG9</i>	1.33	0.58	Op0267f_4	EIP-TRA-ABC	Q1LPT5 ABC transporter-related protein
3UTR_1941	1041935 -	1049468 Rmet_0965				Op0268r_1		
NPKM_3507	1042669 +	1043362 Rmet_0956	<i>livF9</i>	2.33	0.58	Op0267f_4	EIP-TRA-ABC	Q1LPT4 ABC transporter-related protein
3UTR_1205	1043363 +	1043449 Rmet_0956	<i>livF9</i>			Op0267f_4		
5UTR_990	1043453 +	1043470 Rmet_0957	<i>ureD</i>			Op0267f_5		
NPKM_3508	1043470 +	1044352 Rmet_0957	<i>ureD</i>	24.00	1.00	Op0267f_5	GIP-PTL-Fold	Q1LPT3 Urease accessory protein ureD
NPKM_3509	1044386 +	1044689 Rmet_0958	<i>ureA</i>	23.00	1.00	Op0267f_5	MET-NUC-Pur	Q1LPT2 Urease subunit gamma
NPKM_3510	1044733 +	1045369 Rmet_0959	<i>ureJ</i>	37.33	1.53	Op0267f_5	GIP-PTL-Fold	Q1LPT1 HupE/UreJ protein
NPKM_3511	1045392 +	1045698 Rmet_0960	<i>ureB</i>	43.00	2.00	Op0267f_5	MET-NUC-Pur	Q1LPT0 Urease subunit beta
NPKM_3512	1045697 +	1047416 Rmet_0961	<i>ureC</i>	46.00	3.00	Op0267f_5	MET-NUC-Pur	Q1LPS9 Urease
NPKM_3513	1047419 +	1048040 Rmet_0962	<i>ureE</i>	52.00	3.61	Op0267f_5	GIP-PTL-Fold	Q1LPS8 UreE urease accessory-like protein
NPKM_3514	1048073 +	1048766 Rmet_0963	<i>ureF</i>	36.00	1.00	Op0267f_5	GIP-PTL-Fold	Q1LPS7 Urease accessory protein ureF
NPKM_3515	1048775 +	1049399 Rmet_0964	<i>ureG</i>	34.67	2.08	Op0267f_5	GIP-PTL-Fold	Q1LPS6 Urease accessory protein ureG
NPKM_3516	1049469 -	1049865 Rmet_0965		1510.67	146.49	Op0268r_1	NA	Q1LPS5 Transcriptional regulator, XRE family
NPKM_3517	1050135 +	1050825 Rmet_0966		10.33	3.21	Op0269f_1	NA	Q1LPS4 Putative uncharacterized protein
3UTR_1206	1050826 +	1051069 Rmet_0966				Op0269f_1		
NPKM_3518	1050833 -	1051526 Rmet_0967	<i>gstI</i>	247.33	34.65	Op0270r_1	MET-OAA-GSH	Q1LPS3 Glutathione S-transferase-like protein
5UTR_1636	1051527 -	1051555 Rmet_0967	<i>gstI</i>			Op0270r_1		
3UTR_1940	1051660 -	1051690 Rmet_0968				Op0270r_1		
NPKM_3519	1051691 -	1052954 Rmet_0968		126.33	10.69	Op0270r_1	MET-CAH-Prop	Q1LPS2 Acyl-CoA dehydrogenase-like protein
5UTR_1635	1052955 -	1053019 Rmet_0968				Op0270r_1		
5UTR_991	1053078 +	1053203 Rmet_0969				Op0271f_1		

NPKM_3520	1053203 +	1054145 Rmet_0969		61.00	2.00	Op0271f_1	NA	Q1LPS1 Transcriptional regulator, LysR family
NPKM_3521	1054234 +	1056196 Rmet_0970	<i>ggt</i>	392.00	21.66	Op0271f_2	MET-LIP-Others	Q1LPS0 Gamma-glutamyltransferase 1. Threonine peptidase. MEROPS family T03
3UTR_1207	1056197 +	1057515 Rmet_0970	<i>ggt</i>			Op0271f_2		
3UTR_1939	1056322 -	1056336 Rmet_0971	<i>bug</i>			Op0272r_1		
NPKM_3522	1056337 -	1057339 Rmet_0971	<i>bug</i>	4.00	0.00	Op0272r_1	NA	Q1LPR9 Twin-arginine translocation pathway signal
3UTR_1938	1057370 -	1057633 Rmet_0972				Op0272r_1		
NPKM_3523	1057634 -	1058711 Rmet_0972		110.67	12.34	Op0272r_1	NA	Q1LPR8 Aminoglycoside phosphotransferase
NPKM_3524	1058753 -	1059533 Rmet_0973	<i>paaG</i>	76.00	4.36	Op0272r_1	MET-CAH-Prop	Q1LPR7 Enoyl-CoA hydratase / short chain enoyl-CoA hydratase
NPKM_3525	1059599 -	1061123 Rmet_0974	<i>paaH</i>	150.33	12.66	Op0272r_1	MET-CAH-But	Q1LPR6 3-hydroxyacyl-CoA dehydrogenase
5UTR_992	1061003 +	1061299 Rmet_0975	<i>gst</i>			Op0273f_1		
NPKM_3526	1061299 +	1061941 Rmet_0975	<i>gst</i>	271.67	37.07	Op0273f_1	MET-OAA-GSH	Q1LPR5 Glutathione S-transferase-like protein
NPKM_3527	1062001 -	1063171 Rmet_0976	<i>ybdL</i>	117.00	5.20	Op0274r_2	NA	Q1LPR4 2-keto-4-methylthiobutyrate aminotransferase
NPKM_3528	1063219 -	1063759 Rmet_0977		40.33	2.08	Op0274r_1	NA	Q1LPR3 Putative uncharacterized protein
5UTR_1634	1063760 -	1064288 Rmet_0977				Op0274r_1		
NPKM_3529	1063799 +	1064585 Rmet_0978		65.67	1.15	Op0275f_1	NA	Q1LPR2 UPF0246 protein Rmet_0978
3UTR_1937	1064294 -	1065840 Rmet_0980				Op0276r_2		
NPKM_3530	1064603 +	1065746 Rmet_0979		121.00	3.61	Op0275f_1	NA	Q1LPR1 Peptidase M14, carboxypeptidase A
3UTR_1208	1065747 +	1067811 Rmet_0979				Op0275f_1		
NPKM_3531	1065841 -	1066594 Rmet_0980		214.00	4.00	Op0276r_2	NA	Q1LPR0 Putative lipoprotein transmembrane
NPKM_3532	1066887 -	1067760 Rmet_0981	<i>hutG</i>	31.00	1.00	Op0276r_1	MET-CAH-DiCarb	Q1LPQ9 N-formylglutamate amidohydrolase
NPKM_3533	1067780 -	1068767 Rmet_0982	<i>bug</i>	30.67	1.15	Op0276r_1	NA	Q1LPQ8 Uncharacterized protein UPF0065
5UTR_1633	1068768 -	1068780 Rmet_0982	<i>bug</i>			Op0276r_1		
5UTR_993	1068859 +	1068915 Rmet_0983				Op0277f_1		
NPKM_3534	1068915 +	1069818 Rmet_0983		68.00	2.00	Op0277f_1	NA	Q1LPQ7 Transcriptional regulator, LysR family
3UTR_1936	1068997 -	1069869 Rmet_0984				Op0278r_1		
3UTR_1209	1069819 +	1070845 Rmet_0983				Op0277f_1		
NPKM_3535	1069870 -	1071046 Rmet_0984		327.67	9.61	Op0278r_1	NA	Q1LPQ6 Putative uncharacterized protein
NPKM_3536	1071062 -	1071656 Rmet_0985		439.00	14.53	Op0278r_1	NA	Q1LPQ5 GCN5-related N-acetyltransferase
NPKM_3537	1071666 -	1072545 Rmet_0986		480.33	7.02	Op0278r_1	NA	Q1LPQ4 ATPase associated with various cellular activities, AAA_5
5UTR_1632	1072546 -	1072737 Rmet_0986				Op0278r_1		
5UTR_994	1072599 +	1072987 Rmet_0987				Op0279f_1		
NPKM_3538	1072987 +	1073332 Rmet_0987		255.33	35.92	Op0279f_1	NA	Q1LPQ3 Cytochrome c, class I
NPKM_3539	1073345 +	1073744 Rmet_0988		774.33	89.79	Op0279f_2	NA	Q1LPQ2 Cytochrome c, class I
3UTR_1935	1073641 -	1073840 Rmet_0989	<i>aroG</i>			Op0280r_1		
3UTR_1210	1073745 +	1073955 Rmet_0988				Op0279f_2		
NPKM_3540	1073841 -	1074921 Rmet_0989	<i>aroG</i>	301.00	6.56	Op0280r_1	MET-AA-PheTyrTrp	Q1LPQ1 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase
NPKM_3541	1075041 -	1075155 Rmet_6435		410.00	50.57	Op0280r_1	NA	NA
5UTR_1631	1075156 -	1075283 Rmet_6435				Op0280r_1		
NPKM_3542	1075376 +	1076432 Rmet_0990		6.00	0.00	Op0281f_1	NA	Q1LPQ0 Methyltransferase type 12
3UTR_1934	1075758 -	1076486 Rmet_0991	<i>tldD</i>			Op0282r_2		
3UTR_1211	1076433 +	1076443 Rmet_0990				Op0281f_1		
NPKM_3543	1076487 -	1077948 Rmet_0991	<i>tldD</i>	186.33	6.35	Op0282r_2	NA	Q1LPP9 Putative uncharacterized protein
NPKM_3544	1078014 -	1078836 Rmet_0992	<i>nit</i>	75.33	4.93	Op0282r_1	MET-EN-Nitrog	Q1LPP8 Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase

NPKM_3545	1078864 -	1083061 Rmet_0993		49.00	2.65	Op0282r_1	NA	Q1LPP7 Putative uncharacterized protein
5UTR_1630	1083062 -	1083417 Rmet_0993				Op0282r_1		
NPKM_3546	1083208 +	1086247 Rmet_0994	<i>glnE</i>	123.00	4.58	Op0283f_1	GIP-PTL-Fold	Q1LPP6 Glutamate-ammonia ligase adenyllyltransferase
NPKM_3547	1086233 +	1086848 Rmet_0995		70.33	5.03	Op0283f_1	NA	Q1LPP5 Putative transmembrane protein
3UTR_1933	1086614 -	1087004 Rmet_0996				Op0284r_1		
3UTR_1212	1086849 +	1087543 Rmet_0995				Op0283f_1		
NPKM_3548	1087005 -	1088628 Rmet_0996		33.00	2.65	Op0284r_1	NA	Q1LPP4 Peptidase MprA. Serine peptidase. MEROPS family S08A
NPKM_3549	1088727 -	1089153 Rmet_0997		174.00	14.53	Op0284r_1	NA	Q1LPP3 Putative lipoprotein
NPKM_3550	1089189 -	1090959 Rmet_0998	<i>recN</i>	114.33	7.77	Op0284r_1	GIP-REP-Recomb	Q1LPP2 DNA repair protein RecN
NPKM_3551	1091039 -	1091981 Rmet_0999	<i>nadK</i>	179.67	8.08	Op0284r_1	MET-COF-NicAm	Q1LPP1 ATP-NAD/AcoX kinase
5UTR_995	1091607 +	1092057 Rmet_1000				Op0285f_1		
5UTR_1629	1091982 -	1092138 Rmet_0999	<i>nadK</i>			Op0284r_1		
NPKM_3552	1092057 +	1093104 Rmet_1000		155.33	0.58	Op0285f_1	NA	Q1LPP0 Heat-inducible transcription repressor HrcA
NPKM_3553	1093214 +	1094330 Rmet_1001	<i>hemH</i>	107.00	4.58	Op0285f_1	MET-COF-Porph	Q1LPN9 Ferrochelatase
3UTR_1932	1093538 -	1094825 Rmet_1003				Op0286r_1		
NPKM_3554	1094379 +	1094775 Rmet_1002	<i>hslR</i>	129.33	9.07	Op0285f_1	GIP-TL-Ass	Q1LPN8 RNA-binding S4
NPKM_3555	1094826 -	1095018 Rmet_1003		81.33	17.93	Op0286r_1	NA	Q1LPN7 Putative uncharacterized protein
NPKM_3556	1095266 +	1095809 Rmet_1004	<i>grpE</i>	373.00	22.72	Op0287f_1	GIP-PTL-Fold	Q1LPN6 GrpE protein
3UTR_1931	1095574 -	1096279 Rmet_1006				Op0288r_1		
NPKM_3557	1095887 +	1096292 Rmet_1005		51.67	5.03	Op0287f_1	NA	Q1LPN5 Putative thioredoxin protein
NPKM_3558	1096280 -	1097690 Rmet_1006		59.67	5.69	Op0288r_1	MET-LIP-GlycPLip	Q1LPN4 Putative phospholipase
NPKM_3559	1097738 -	1098170 Rmet_1007		134.00	9.85	Op0288r_1	NA	Q1LPN3 Putative uncharacterized protein
5UTR_1628	1098171 -	1098209 Rmet_1007				Op0288r_1		
NPKM_3560	1098320 +	1099259 Rmet_1008		18.00	1.00	Op0289f_1	NA	Q1LPN2 Putative uncharacterized protein
NPKM_3561	1099346 +	1099934 Rmet_1009	<i>rutE</i>	183.67	9.29	Op0289f_2	NA	Q1LPN1 Nitroreductase
3UTR_1930	1099730 -	1100022 Rmet_1010				Op0290r_1		
3UTR_1213	1099935 +	1100039 Rmet_1009	<i>rutE</i>			Op0289f_2		
NPKM_3562	1100023 -	1100749 Rmet_1010		30.33	3.21	Op0290r_1	NA	Q1LPN0 Putative uncharacterized protein involved in ubiquinone biosynthesis
NPKM_3563	1100778 -	1101747 Rmet_1011		15.67	1.53	Op0290r_1	NA	Q1LPM9 Alpha/beta hydrolase fold
NPKM_3564	1101743 -	1103261 Rmet_1012		20.00	4.00	Op0290r_1	MET-XEN-Others	Q1LPM8 Cyclohexanone monooxygenase
5UTR_1627	1103262 -	1103300 Rmet_1012				Op0290r_1		
NPKM_3565	1103335 +	1103965 Rmet_1013		42.00	2.00	Op0291f_1	NA	Q1LPM7 Transcriptional regulator, TetR family
3UTR_1929	1103646 -	1103985 Rmet_1014	<i>nth</i>			Op0292r_1		
3UTR_1214	1103966 +	1104397 Rmet_1013				Op0291f_1		
NPKM_3566	1103986 -	1104631 Rmet_1014	<i>nth</i>	49.67	2.08	Op0292r_1	NA	Q1LPM6 DNA-(Apurinic or apyrimidinic site) lyase / endonuclease III
NPKM_3567	1104627 -	1105467 Rmet_1015	<i>rnfB</i>	56.67	0.58	Op0292r_1	NA	Q1LPM5 Electron transport complex, RnfABCDGE type, B subunit
5UTR_996	1105367 +	1105661 Rmet_1016				Op0293f_1		
5UTR_1626	1105468 -	1106061 Rmet_1015	<i>rnfB</i>			Op0292r_1		
NPKM_3568	1105661 +	1106294 Rmet_1016		113.33	6.43	Op0293f_1	NA	Q1LPM4 Transcriptional regulator, TetR family
3UTR_1215	1106295 +	1106562 Rmet_1016				Op0293f_1		
3UTR_1928	1106339 -	1106371 Rmet_1017	<i>phaZ1</i>			Op0294r_1		
NPKM_3569	1106372 -	1107617 Rmet_1017	<i>phaZ1</i>	138.33	6.03	Op0294r_1	NA	Q1LPM3 Polyhydroxyalkanoate depolymerase, intracellular
NPKM_3570	1107869 -	1109066 Rmet_1018	<i>tyrB</i>	1050.67	52.01	Op0294r_1	MET-AA-Met	Q1LPM2 Aminotransferase

5UTR_1625	1109067 -	1109517 Rmet_1018	<i>tyrB</i>			Op0294r_1		
5UTR_997	1109164 +	1109263 Rmet_1019	<i>uvrB</i>			Op0295f_1		
NPKM_3571	1109263 +	1111357 Rmet_1019	<i>uvrB</i>	38.00	2.00	Op0295f_1	GIP-REP-Recomb	Q1LPM1 UvrABC system protein B
NPKM_3572	1111451 +	1111673 Rmet_1020		100.33	4.62	Op0295f_2	NA	Q1LPM0 Putative uncharacterized protein
NPKM_3573	1111723 +	1111963 Rmet_1021		153.67	6.03	Op0295f_2	NA	Q1LPL9 Putative uncharacterized protein
NPKM_3574	1112012 +	1112492 Rmet_1022	<i>ptpA</i>	66.33	4.16	Op0295f_2	NA	Q1LPL8 Protein tyrosine phosphatase
NPKM_3575	1112491 +	1114603 Rmet_1023		32.67	2.08	Op0295f_2	NA	Q1LPL7 Putative site-specific recombinase transmembrane protein
NPKM_3576	1114700 +	1115255 Rmet_1024	<i>iscR</i>	1019.67	85.54	Op0295f_3	NA	Q1LPL6 Transcriptional regulator, BadM/Rrf2 family
NPKM_3577	1115330 +	1116551 Rmet_1025	<i>iscS</i>	825.00	50.24	Op0295f_3	NA	Q1LPL5 Cysteine desulfurase IscS
NPKM_3578	1116607 +	1117009 Rmet_1026	<i>iscU</i>	1093.33	22.72	Op0295f_3	MET-EN-Nitrog	Q1LPL4 FeS cluster assembly scaffold IscU
NPKM_3579	1117059 +	1117401 Rmet_1027	<i>iscA</i>	1142.00	27.06	Op0295f_3	NA	Q1LPL3 Iron-sulfur cluster assembly protein IscA
NPKM_3580	1117465 +	1117984 Rmet_1028	<i>hscB</i>	220.67	11.15	Op0295f_3	GIP-PTL-Fold	Q1LPL2 Co-chaperone Hsc20
NPKM_3581	1117993 +	1119859 Rmet_1029	<i>hscA</i>	198.67	9.87	Op0295f_3	GIP-PTL-Fold	Q1LPL1 Chaperone protein hscA homolog
NPKM_3582	1119900 +	1120239 Rmet_1030	<i>fdx</i>	193.00	7.00	Op0295f_3	NA	Q1LPL0 Ferredoxin, 2Fe-2S type
3UTR_1927	1120017 -	1120515 Rmet_1032				Op0296r_2		
NPKM_3583	1120261 +	1120456 Rmet_1031		196.67	5.86	Op0295f_3	NA	Q1LPK9 Putative uncharacterized protein
3UTR_1216	1120457 +	1121579 Rmet_1031				Op0295f_3		
NPKM_3584	1120516 -	1121563 Rmet_1032		56.67	1.15	Op0296r_2	NA	Q1LPK8 Putative uncharacterized protein
NPKM_3585	1121651 -	1122356 Rmet_1033		17.33	2.08	Op0296r_1	NA	Q1LPK7 17 kDa surface antigen
NPKM_3586	1122633 -	1124181 Rmet_1034	<i>lysS</i>	193.33	5.86	Op0296r_1	MET-AA-Lys_Syn	Q1LPK6 Lysyl-tRNA synthetase
NPKM_3587	1124240 -	1125011 Rmet_1035		217.67	3.51	Op0296r_1	NA	Q1LPK5 Short-chain dehydrogenase/reductase SDR
NPKM_3588	1125146 -	1126220 Rmet_1036	<i>prfB</i>	508.67	18.61	Op0296r_1	NA	Q1LPK4 Bacterial peptide chain release factor 2 (BRF-2)
5UTR_1624	1126221 -	1126366 Rmet_1036	<i>prfB</i>			Op0296r_1		
5UTR_998	1126327 +	1126455 Rmet_1037	<i>nlpD</i>			Op0297f_1		
3UTR_1926	1126374 -	1127251 Rmet_1038	<i>recJ</i>			Op0298r_1		
NPKM_3589	1126455 +	1127178 Rmet_1037	<i>nlpD</i>	103.00	1.73	Op0297f_1	NA	Q1LPK3 Peptidase M23B
3UTR_1217	1127179 +	1127953 Rmet_1037	<i>nlpD</i>			Op0297f_1		
NPKM_3590	1127252 -	1128953 Rmet_1038	<i>recJ</i>	53.33	2.52	Op0298r_1	GIP-REP-Recomb	Q1LPK2 Exonuclease RecJ
NPKM_3591	1128999 -	1130118 Rmet_1039		63.33	2.52	Op0298r_1	NA	Q1LPK1 Putative uncharacterized protein
5UTR_999	1129658 +	1130221 Rmet_1040	<i>lolE</i>			Op0299f_1		
NPKM_3592	1130221 +	1131472 Rmet_1040	<i>lolE</i>	84.33	5.69	Op0299f_1	NA	Q1LPK0 Lipoprotein releasing system, transmembrane protein, LolC/E family
NPKM_3593	1131464 +	1132214 Rmet_1041	<i>lolD</i>	118.00	6.24	Op0299f_1	NA	Q1LPJ9 Lipoprotein-releasing system ATP-binding protein lolD
NPKM_3594	1132265 +	1133093 Rmet_1042		66.00	2.00	Op0299f_1	GIP-PTL-Exp	Q1LPJ8 TatD-related deoxyribonuclease
NPKM_3595	1133223 +	1135779 Rmet_1043		11.67	1.15	Op0299f_1	GIP-PTL-T2S	Q1LPJ7 DNA internalization-related competence protein ComEC/Rec2
3UTR_1925	1134245 -	1135744 Rmet_1044	<i>yebK</i>			Op0300r_1		
NPKM_3596	1135745 -	1136762 Rmet_1044	<i>yebK</i>	258.00	11.53	Op0300r_1	NA	Q1LPJ6 Transcriptional regulator, RpiR family
3UTR_1218	1135780 +	1136114 Rmet_1043				Op0299f_1		
5UTR_1623	1136763 -	1137679 Rmet_1044	<i>yebK</i>			Op0300r_1		
5UTR_1000	1136984 +	1137060 Rmet_1045	<i>edd</i>			Op0301f_1		
NPKM_3597	1137060 +	1138950 Rmet_1045	<i>edd</i>	345.00	27.87	Op0301f_1	MET-CAH-PP_KDPG	Q1LPJ5 6-phosphogluconate dehydratase
NPKM_3598	1139121 +	1139637 Rmet_1046	<i>gntK</i>	397.00	17.44	Op0301f_1	MET-CAH-PP_KDPG	Q1LPJ4 Gluconate kinase
NPKM_3599	1139615 +	1139798 Rmet_6436		270.00	18.52	Op0301f_1	NA	NA
NPKM_3600	1139862 +	1141338 Rmet_1047		125.33	10.79	Op0301f_1	NA	Q1LPJ3 Putative uncharacterized protein

NPKM_3601	1141469 +	1142423 Rmet_1048		50.33	3.79	Op0301f_1	NA	Q1LPJ2 Putative uncharacterized protein
NPKM_3602	1142483 +	1143365 Rmet_1049		61.33	4.93	Op0301f_1	NA	Q1LPJ1 Transglutaminase-like protein
NPKM_3603	1143491 +	1144298 Rmet_1050		119.00	5.57	Op0301f_1	GIP-PTL-Fold	Q1LPJ0 Putative proteasome-type protease
NPKM_3604	1144345 +	1145167 Rmet_1051		115.00	7.94	Op0301f_1	NA	Q1LPJ9 Alpha/beta hydrolase fold
NPKM_3605	1145342 +	1146992 Rmet_1052	<i>pyrG</i>	613.33	18.18	Op0301f_2	MET-NUC-Pyr	Q1LPJ8 CTP synthase
NPKM_3606	1147017 +	1147887 Rmet_1053	<i>kdsA</i>	544.00	8.19	Op0301f_2	MET-GLYC-LPS	Q1LPJ7 2-dehydro-3-deoxyphosphooctonate aldolase
NPKM_3607	1148015 +	1148306 Rmet_1054		294.00	16.64	Op0301f_2	NA	Q1LPJ6 Putative uncharacterized protein
NPKM_3608	1148370 +	1149660 Rmet_1055	<i>eno</i>	874.33	49.32	Op0301f_3	MET-CAH-FbP	Q1LPJ5 Enolase 1
3UTR_1219	1149661 +	1149708 Rmet_1055	<i>eno</i>			Op0301f_3		
3UTR_1924	1149729 -	1150304 Rmet_1057				Op0302r_1		
5UTR_1001	1149812 +	1149865 Rmet_1056	<i>ftsB</i>			Op0301f_3		
NPKM_3609	1149865 +	1150207 Rmet_1056	<i>ftsB</i>	219.67	9.07	Op0301f_3	DIV-Division	Q1LPJ4 Cell division protein ftsB homolog
NPKM_3610	1150305 -	1150701 Rmet_1057		88.67	3.79	Op0302r_1	NA	Q1LPJ3 Putative uncharacterized protein
NPKM_3611	1150845 -	1151850 Rmet_1058	<i>hsIO</i>	271.67	8.39	Op0302r_1	GIP-PTL-Fold	Q1LPJ2 Hsp33 protein
NPKM_3612	1151899 -	1152424 Rmet_1059	<i>paaY</i>	421.33	16.74	Op0302r_1	NA	Q1LPJ1 Transferase hexapeptide repeat
NPKM_3613	1152549 +	1153401 Rmet_1060		47.67	1.53	Op0303f_1	NA	Q1LPJ0 Putative uncharacterized protein
NPKM_3614	1153397 -	1155185 Rmet_1061		93.33	5.51	Op0304r_1	MET-CAH-FbP	Q1LPH9 AMP-dependent synthetase and ligase
3UTR_1220	1153402 +	1154508 Rmet_1060				Op0303f_1		
5UTR_1002	1154511 +	1155270 Rmet_1062				Op0305f_1		
5UTR_1622	1155186 -	1155245 Rmet_1061				Op0304r_1		
NPKM_3615	1155270 +	1156164 Rmet_1062		58.67	3.21	Op0305f_1	NA	Q1LPH8 Alpha/beta hydrolase fold
3UTR_1923	1155585 -	1156219 Rmet_1063	<i>trxB1</i>			Op0306r_1		
3UTR_1221	1156165 +	1157052 Rmet_1062				Op0305f_1		
NPKM_3616	1156220 -	1157282 Rmet_1063	<i>trxB1</i>	69.00	3.46	Op0306r_1	MET-NUC-Pyr	Q1LPH7 FAD-dependent pyridine nucleotide-disulphide oxidoreductase
5UTR_1003	1157056 +	1157280 Rmet_1064				Op0307f_1		
NPKM_3617	1157280 +	1158249 Rmet_1064		118.00	6.24	Op0307f_1	NA	Q1LPH6 PHP-like protein
5UTR_1621	1157283 -	1157336 Rmet_1063	<i>trxB1</i>			Op0306r_1		
NPKM_3618	1158270 +	1158918 Rmet_1065		117.67	5.13	Op0307f_1	GIP-TL-Ass	Q1LPH5 Sua5/YciO/YrdC/YwIC
NPKM_3619	1158966 +	1159632 Rmet_1066		76.33	2.08	Op0307f_1	NA	Q1LPH4 Peptidase M50
NPKM_3620	1159672 +	1160248 Rmet_1067		113.00	8.72	Op0307f_1	NA	Q1LPH3 Methyltransferase type 12
NPKM_3621	1160385 +	1161270 Rmet_1068	<i>dapA</i>	525.67	19.50	Op0307f_2	MET-AA-Lys_Syn	Q1LPH2 Dihydrodipicolinate synthase
3UTR_1922	1160957 -	1163436 Rmet_1071				Op0308r_2		
NPKM_3622	1161327 +	1162569 Rmet_1069		818.00	20.07	Op0307f_2	NA	Q1LPH1 Putative transmembrane protein
NPKM_3623	1162639 +	1163428 Rmet_1070		107.00	7.94	Op0307f_2	NA	Q1LPH0 Beta-lactamase-like protein
3UTR_1222	1163429 +	1163565 Rmet_1070				Op0307f_2		
NPKM_3624	1163437 -	1163722 Rmet_1071		3532.00	80.67	Op0308r_2	NA	Q1LPG9 Putative uncharacterized protein
5UTR_1004	1163612 +	1165152 Rmet_1073	<i>slyD</i>			Op0309f_1		
NPKM_3625	1163816 -	1164044 Rmet_6437		124.67	11.72	Op0308r_1	NA	NA
NPKM_3626	1163959 -	1165087 Rmet_1072		102.67	1.53	Op0308r_1	NA	Q1LPG8 Cupin 4
5UTR_1620	1165088 -	1165218 Rmet_1072				Op0308r_1		
NPKM_3627	1165152 +	1165713 Rmet_1073	<i>slyD</i>	781.67	49.74	Op0309f_1	GIP-PTL-Fold	Q1LPG7 Putative fbp-type peptidyl-prolyl cis-trans isomerase (Rotamase) protein
3UTR_1223	1165714 +	1165822 Rmet_1073	<i>slyD</i>			Op0309f_1		
3UTR_1921	1165788 -	1165806 Rmet_1074				Op0310r_2		

NPKM_3628	1165807 -	1166860 Rmet_1074		46.67	0.58	Op0310r_2	NA	Q1LPG6 Putative transmembrane protein
NPKM_3629	1166856 -	1169607 Rmet_1075	<i>mutS</i>	104.00	3.00	Op0310r_2	GIP-REP-Recomb	Q1LPG5 DNA mismatch repair protein mutS
NPKM_3630	1169789 -	1170227 Rmet_1076		73.00	1.73	Op0310r_2	NA	Q1LPG4 Putative uncharacterized protein
NPKM_3631	1170223 -	1170403 Rmet_1077		18.33	4.04	Op0310r_1	NA	Q1LPG3 YcfA-like protein
5UTR_1619	1170404 -	1170411 Rmet_1077				Op0310r_1		
3UTR_1920	1170508 -	1170605 Rmet_1078	<i>suhB</i>			Op0310r_1		
NPKM_3632	1170606 -	1171428 Rmet_1078	<i>suhB</i>	248.33	8.39	Op0310r_1	MET-CAH-Inos	Q1LPG2 Inositol monophosphatase
5UTR_1005	1170970 +	1171655 Rmet_1079				Op0311f_1		
5UTR_1618	1171429 -	1171549 Rmet_1078	<i>suhB</i>			Op0310r_1		
NPKM_3633	1171655 +	1172525 Rmet_1079		95.33	6.51	Op0311f_1	GIP-TL-Ass	Q1LPG1 RNA methyltransferase TrmH, group 1
NPKM_3634	1172853 +	1173597 Rmet_1080	<i>cysE</i>	113.00	6.56	Op0311f_1	MET-EN-Sulf	Q1LPG0 Serine O-acetyltransferase
3UTR_1919	1173072 -	1173644 Rmet_1081	<i>lpxH</i>			Op0312r_3		
3UTR_1224	1173598 +	1174374 Rmet_1080	<i>cysE</i>			Op0311f_1		
NPKM_3635	1173645 -	1174437 Rmet_1081	<i>lpxH</i>	200.00	8.54	Op0312r_3	MET-GLYC-LPS	Q1LPF9 UDP-2,3-diacylglucosamine hydrolase
NPKM_3636	1174505 -	1175006 Rmet_1082	<i>ppiB</i>	1138.67	68.48	Op0312r_3	GIP-PTL-Fold	Q1LPF8 Peptidyl-prolyl cis-trans isomerase
NPKM_3637	1175060 -	1175669 Rmet_1083	<i>ppiA</i>	339.33	16.65	Op0312r_2	GIP-PTL-Fold	Q1LPF7 Peptidyl-prolyl cis-trans isomerase
NPKM_3638	1175750 -	1176506 Rmet_1084		164.67	1.15	Op0312r_1	NA	Q1LPF6 Tetratricopeptide TPR_2
5UTR_1617	1176507 -	1176587 Rmet_1084				Op0312r_1		
5UTR_1006	1176542 +	1176600 Rmet_1085	<i>cysS</i>			Op0313f_1		
NPKM_3639	1176600 +	1178076 Rmet_1085	<i>cysS</i>	163.33	9.02	Op0313f_1	MET-AA-Cys	Q1LPF5 CysteinyI-tRNA synthetase
NPKM_3640	1178072 +	1178858 Rmet_1086		175.67	12.22	Op0313f_1	GIP-REP-Recomb	Q1LPF4 HhH-GPD
NPKM_3641	1179005 +	1179977 Rmet_1087	<i>accA</i>	385.00	8.66	Op0313f_2	MET-CAH-Pyr	Q1LPF3 Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha
NPKM_3642	1179978 +	1181442 Rmet_1088	<i>tilS</i>	36.67	3.06	Op0313f_2	DIV-Division	Q1LPF2 tRNA(Ile)-lysine synthetase-like protein
NPKM_3643	1181323 +	1181491 Rmet_6438		14.33	1.53	Op0313f_2	NA	NA
NPKM_3644	1181620 +	1182871 Rmet_1089	<i>lysC</i>	581.00	53.73	Op0313f_3	MET-AA-GlySerThr	Q1LPF1 Aspartokinase
NPKM_3645	1183004 +	1183098 Rmet_R0014		388.00	43.55	Op0313f_3	NA	NA
3UTR_1225	1183099 +	1183923 Rmet_R0014				Op0313f_3		
3UTR_1918	1183433 -	1183531 Rmet_1090	<i>ylaB</i>			Op0314r_1		
NPKM_3646	1183532 -	1185125 Rmet_1090	<i>ylaB</i>	1.00	0.00	Op0314r_1	NA	Q1LPF0 EAL-containing signal transduction protein
5UTR_1616	1185126 -	1185322 Rmet_1090	<i>ylaB</i>			Op0314r_1		
NPKM_3647	1185360 -	1187322 Rmet_1091		2.33	0.58	Op0314r_1	NA	Q1LPE9 Diguanylate cyclase (GGDEF domain)
5UTR_1615	1187323 -	1187379 Rmet_1091				Op0314r_1		
NPKM_3648	1187733 +	1189239 Rmet_1092	<i>yfiS</i>	2.00	0.00	Op0315f_1	EIP-TRA-Ion	Q1LFA7 Anion transporter
5UTR_1007	1189245 +	1189386 Rmet_1093	<i>adh</i>			Op0315f_2		
NPKM_3649	1189386 +	1190415 Rmet_1093	<i>adh</i>	26.33	4.93	Op0315f_2	NA	Q1LPE7 Alcohol dehydrogenase GroES-like protein
NPKM_3650	1190642 +	1191692 Rmet_1094		6.67	2.08	Op0315f_2	NA	Q1LPE6 Putative uncharacterized protein
NPKM_3651	1191701 +	1192862 Rmet_1095		3.67	0.58	Op0315f_2	NA	Q1LPE5 Putative uncharacterized protein
3UTR_1226	1192863 +	1193023 Rmet_1095				Op0315f_2		
5UTR_1008	1193055 +	1193117 Rmet_1096				Op0315f_3		
NPKM_3652	1193117 +	1194269 Rmet_1096		28.00	2.00	Op0315f_3	NA	Q1LPE4 Glyceraldehyde 3-phosphate dehydrogenase
3UTR_1227	1194270 +	1194838 Rmet_1096				Op0315f_3		
NPKM_3653	1194299 -	1194596 Rmet_1097		0.00	0.00	Op0316r_1	NA	Q1LPE3 Putative uncharacterized protein
5UTR_1009	1194861 +	1194939 Rmet_1098	<i>cobW</i>			Op0317f_1		

NPKM_3654	1194939 +	1196133 Rmet_1098	<i>cobW</i>	4.00	0.00	Op0317f_1	NA	Q1LPE2 Cobalamin synthesis protein, P47K
NPKM_3655	1196148 +	1197123 Rmet_1099		1.67	0.58	Op0317f_1	NA	Q1LPE1 UPF0343 protein Rmet_1099
NPKM_3656	1197119 +	1198538 Rmet_1100	<i>cysS</i>	2.00	0.00	Op0317f_1	MET-AA-Cys	Q1LPE0 Cysteinyl-tRNA synthetase
NPKM_3657	1198547 +	1199129 Rmet_1101		1.67	0.58	Op0317f_1	MET-COF-Folate	Q1LPD9 6-pyruvoyl-tetrahydropterin synthase-like protein
5UTR_1010	1199132 +	1199148 Rmet_1102				Op0317f_1		
NPKM_3658	1199148 +	1199709 Rmet_1102		1.33	0.58	Op0317f_1	NA	Q1LPD8 Carbonic anhydrases/acetyltransferase isoleucine patch superfamily
5UTR_1011	1199731 +	1199766 Rmet_1103	<i>allB</i>			Op0317f_1		
NPKM_3659	1199766 +	1201164 Rmet_1103	<i>allB</i>	1.00	0.00	Op0317f_1	MET-NUC-Pyr	Q1LPD7 Dihydroorotase
3UTR_1228	1201165 +	1201224 Rmet_1103	<i>allB</i>			Op0317f_1		
3UTR_1917	1201210 -	1201228 Rmet_1104				Op0318r_1		
NPKM_3660	1201229 -	1203416 Rmet_1104		1.00	0.00	Op0318r_1	EIP-TRA-Pores	Q1LPD6 TonB-dependent siderophore receptor
5UTR_1614	1203417 -	1203457 Rmet_1104				Op0318r_1		
5UTR_1012	1203653 +	1203663 Rmet_1105				Op0319f_1		
NPKM_3661	1203663 +	1204074 Rmet_1105		1.00	0.00	Op0319f_1	NA	Q1LPD5 Putative uncharacterized protein
NPKM_3662	1204073 +	1205702 Rmet_1106		1.00	0.00	Op0319f_1	NA	Q1LPD4 PepSY-associated TM helix
NPKM_3663	1205698 +	1206061 Rmet_1107		0.33	0.58	Op0319f_1	NA	Q1LPD3 Putative uncharacterized protein
3UTR_1229	1206062 +	1206095 Rmet_1107				Op0319f_1		
NPKM_3664	1206097 +	1208383 Rmet_1108	<i>fcuA</i>	1.33	0.58	Op0319f_2	EIP-TRA-Pores	Q1LPD2 TonB-dependent siderophore receptor
3UTR_1916	1207719 -	1208440 Rmet_1109				Op0320r_3		
NPKM_3665	1208441 -	1208810 Rmet_1109		16.33	0.58	Op0320r_3	NA	Q1LPD1 Putative uncharacterized protein
5UTR_1613	1208811 -	1208890 Rmet_1109				Op0320r_3		
3UTR_1915	1208907 -	1208963 Rmet_1110	<i>lysA</i>			Op0320r_2		
NPKM_3666	1208964 -	1210158 Rmet_1110	<i>lysA</i>	6.33	1.15	Op0320r_2	MET-AA-Lys_Syn	Q1LPD0 Orn/DAP/Arg decarboxylase 2
NPKM_3667	1210196 -	1210952 Rmet_1111	<i>hpcH</i>	13.67	2.08	Op0320r_2	MET-AA-Tyr	Q1LPC9 HpcH/HpaI aldolase
NPKM_3668	1210948 -	1212802 Rmet_1112		16.33	2.08	Op0320r_2	NA	Q1LPC8 lucA/lucC
NPKM_3669	1212807 -	1214634 Rmet_1113		17.00	2.65	Op0320r_2	NA	Q1LPC7 lucA/lucC
NPKM_3670	1214620 -	1215808 Rmet_1114		14.00	2.65	Op0320r_2	NA	Q1LPC6 Major facilitator superfamily MFS_1
NPKM_3671	1215810 -	1217580 Rmet_1115		23.33	3.79	Op0320r_2	NA	Q1LPC5 lucA/lucC
NPKM_3672	1217576 -	1218644 Rmet_1116	<i>acd</i>	30.00	5.20	Op0320r_2	MET-AA-ArgPro	Q1LPC4 Ornithine cyclodeaminase
NPKM_3673	1218640 -	1219666 Rmet_1117	<i>cysK</i>	21.33	4.04	Op0320r_2	MET-EN-Sulf	Q44004 Cysteine synthase
NPKM_3674	1219765 -	1222285 Rmet_1118	<i>aleB</i>	191.33	38.48	Op0320r_2	EIP-TRA-Pores	Q1LPC2 TonB-dependent siderophore receptor
5UTR_1612	1222286 -	1222335 Rmet_1118	<i>aleB</i>			Op0320r_2		
3UTR_1914	1222338 -	1222376 Rmet_1119				Op0320r_1		
NPKM_3675	1222377 -	1223451 Rmet_1119		37.67	1.53	Op0320r_1	GIP-TK-RNAP	Q1LPC1 Putative FecR
NPKM_3676	1223514 -	1224015 Rmet_1120	<i>rpol</i>	31.00	2.00	Op0320r_1	GIP-TK-RNAP	Q1LPC0 Sigma-24 (FecI-like)
NPKM_3677	1224154 -	1227289 Rmet_1121	<i>acrD</i>	37.67	1.53	Op0320r_1	EIP-TRA-Ion	Q1LPB9 Hydrophobe/amphiphile efflux-1 HAE1
5UTR_1611	1227290 -	1227505 Rmet_1121	<i>acrD</i>			Op0320r_1		
5UTR_1013	1227629 +	1227738 Rmet_1122	<i>gltP2</i>			Op0321f_1		
NPKM_3678	1227738 +	1229031 Rmet_1122	<i>gltP2</i>	1.67	1.15	Op0321f_1	NA	Q1LPB8 Sodium:dicarboxylate symporter
NPKM_3679	1229035 +	1229947 Rmet_1123	<i>gltI</i>	2.67	0.58	Op0321f_1	NA	Q1LPB7 Extracellular solute-binding protein, family 3
5UTR_1014	1229958 +	1230082 Rmet_1124				Op0321f_2		
NPKM_3680	1230082 +	1232416 Rmet_1124		8.67	1.15	Op0321f_2	MET-CAH-DiCarb	Q1LPB6 Oxidoreductase alpha (Molybdopterin) subunit
NPKM_3681	1232430 +	1233303 Rmet_1125	<i>fdhD</i>	10.33	1.15	Op0321f_2	NA	Q1LPB5 Formate dehydrogenase family accessory protein FdhD

NPKM_3682	1233358 +	1234786 Rmet_1126		25.00	1.00	Op0321f_3	NA	Q1LPB4 Transcriptional regulator, GntR family
3UTR_1913	1234644 -	1235109 Rmet_1128	<i>glcD2</i>			Op0322r_2		
NPKM_3683	1234782 +	1235076 Rmet_1127		23.00	2.65	Op0321f_3	NA	Q1LPB3 Putative DNA-binding protein
3UTR_1230	1235077 +	1235788 Rmet_1127				Op0321f_3		
NPKM_3684	1235110 -	1236535 Rmet_1128	<i>glcD2</i>	138.33	8.02	Op0322r_2	NA	Q1LPB2 FAD linked oxidase-like protein
NPKM_3685	1236540 -	1236981 Rmet_1129		62.67	1.53	Op0322r_1	NA	Q1LPB1 Putative transmembrane protein
NPKM_3686	1236977 -	1237607 Rmet_1130	<i>wrbA</i>	63.67	1.53	Op0322r_1	NA	Q1LPB0 Flavodoxin/nitric oxide synthase
5UTR_1015	1237588 +	1237664 Rmet_1131	<i>rbn</i>			Op0323f_1		
NPKM_3687	1237664 +	1239008 Rmet_1131	<i>rbn</i>	79.00	2.65	Op0323f_1	NA	Q1LPA9 tRNA-processing RNase BN
3UTR_1231	1239009 +	1240324 Rmet_1131	<i>rbn</i>			Op0323f_1		
NPKM_3688	1239146 -	1239464 Rmet_1132		232.67	14.05	Op0324r_1	NA	Q1LPA8 Putative transmembrane protein
NPKM_3689	1239497 -	1240313 Rmet_1133		219.33	1.53	Op0324r_1	NA	Q1LPA7 Alpha/beta hydrolase fold
NPKM_3690	1240312 -	1241665 Rmet_1134	<i>metY</i>	168.67	1.15	Op0324r_1	MET-AA-Met	Q1LPA6 O-acetylhomoserine/O-acetylserine sulfhydrylase
5UTR_1016	1241586 +	1241844 Rmet_1135				Op0325f_1		
5UTR_1610	1241666 -	1241742 Rmet_1134	<i>metY</i>			Op0324r_1		
NPKM_3691	1241844 +	1242300 Rmet_1135		478.33	24.83	Op0325f_1	NA	Q1LPA5 Putative signal-transduction protein with CBS domains
NPKM_3692	1242391 +	1244296 Rmet_1136		91.33	2.52	Op0325f_1	NA	Q1LPA4 Phospholipid/glycerol acyltransferase
NPKM_3693	1244298 +	1245072 Rmet_1137		90.67	5.69	Op0325f_1	NA	Q1LPA3 Putative glutathione S-transferase
NPKM_3694	1245128 +	1246238 Rmet_1138	<i>aroC</i>	341.33	10.50	Op0325f_2	MET-AA-PheTyrTrp	Q1LPA2 Chorismate synthase
NPKM_3695	1246321 +	1247419 Rmet_1139		25.00	1.00	Op0325f_2	NA	Q1LPA1 Major facilitator superfamily MFS_1
3UTR_1912	1246832 -	1247500 Rmet_1140				Op0326r_2		
3UTR_1232	1247420 +	1248247 Rmet_1139				Op0325f_2		
NPKM_3696	1247501 -	1248608 Rmet_1140		56.00	1.00	Op0326r_2	NA	Q1LPA0 FAD dependent oxidoreductase
NPKM_3697	1248641 -	1249343 Rmet_1141		23.00	2.65	Op0326r_1	NA	Q1LP99 Transcriptional regulator, GntR family
5UTR_1609	1249344 -	1249356 Rmet_1141				Op0326r_1		
5UTR_1017	1249385 +	1249584 Rmet_1142				Op0327f_1		
NPKM_3698	1249584 +	1250550 Rmet_1142		16.67	2.89	Op0327f_1	NA	Q1LP98 Type IV pilus assembly PilZ
NPKM_3699	1250632 +	1250788 Rmet_6439		12.67	0.58	Op0327f_1	NA	NA
3UTR_1233	1250789 +	1251083 Rmet_6439				Op0327f_1		
5UTR_1018	1251087 +	1251128 Rmet_1143				Op0327f_1		
NPKM_3700	1251128 +	1252727 Rmet_1143		2.67	0.58	Op0327f_1	NA	Q1LP97 Putative uncharacterized protein
NPKM_3701	1252723 +	1253416 Rmet_1144		1.67	0.58	Op0327f_1	EIP-TRA-Electr	Q1LP96 DMSO-membrane protein
NPKM_3702	1253405 +	1255883 Rmet_1145	<i>torA</i>	5.33	0.58	Op0327f_2	EIP-TRA-Electr	Q1LP95 Molybdopterin guanine dinucleotide-containing S/N-oxide reductase
3UTR_1911	1255175 -	1255989 Rmet_1146	<i>etfD</i>			Op0328r_1		
3UTR_1234	1255884 +	1255914 Rmet_1145	<i>torA</i>			Op0327f_2		
NPKM_3703	1255990 -	1257676 Rmet_1146	<i>etfD</i>	459.33	33.71	Op0328r_1	NA	Q1LP94 Electron transfer flavoprotein-ubiquinone oxidoreductase
5UTR_1608	1257677 -	1257819 Rmet_1146	<i>etfD</i>			Op0328r_1		
5UTR_1019	1257845 +	1258007 Rmet_1147				Op0329f_1		
NPKM_3704	1258007 +	1258793 Rmet_1147		252.00	12.17	Op0329f_1	NA	Q1LP93 Short-chain dehydrogenase/reductase SDR
NPKM_3705	1258971 +	1259562 Rmet_1148		59.33	5.51	Op0329f_1	NA	Q1LP92 Tripartite ATP-independent periplasmic transporter, DctQ component
NPKM_3706	1259558 +	1260863 Rmet_1149		46.33	2.31	Op0329f_1	NA	Q1LP91 TRAP dicarboxylate transporter-DctM subunit
NPKM_3707	1260897 +	1261929 Rmet_1150		271.00	16.37	Op0329f_2	NA	Q1LP90 TRAP dicarboxylate transporter, DctP subunit
3UTR_1910	1261424 -	1262385 Rmet_1152				Op0330r_1		

NPKM_3708	1261925 +	1262327 Rmet_1151		276.67	8.08	Op0329f_2	NA	Q1LP89 Thioesterase superfamily
NPKM_3709	1262386 -	1262932 Rmet_1152		93.33	1.53	Op0330r_1	NA	Q1LP88 Transcriptional regulator, LuxR family
5UTR_1607	1262933 -	1263042 Rmet_1152				Op0330r_1		
NPKM_3710	1263127 +	1263826 Rmet_1153	<i>atoD</i>	252.33	18.93	Op0331f_1	MET-CAH-But	Q1LP87 3-oxoacid CoA-transferase, subunit A
3UTR_1909	1263804 -	1264608 Rmet_1155				Op0332r_1		
NPKM_3711	1263837 +	1264476 Rmet_1154	<i>atoA</i>	229.00	14.00	Op0331f_1	MET-CAH-But	Q1LP86 Butyryl-CoA:acetate CoA transferase
3UTR_1235	1264477 +	1264542 Rmet_1154	<i>atoA</i>			Op0331f_1		
NPKM_3712	1264609 -	1265083 Rmet_1155		589.33	28.57	Op0332r_1	NA	Q1LP85 Putative uncharacterized protein
NPKM_3713	1265103 -	1265880 Rmet_1156	<i>bdhA</i>	667.00	24.06	Op0332r_1	MET-CAH-But	Q1LP84 3-hydroxybutyrate dehydrogenase
5UTR_1606	1265881 -	1265910 Rmet_1156	<i>bdhA</i>			Op0332r_1		
5UTR_1020	1265913 +	1266067 Rmet_1157				Op0333f_1		
NPKM_3714	1266067 +	1266949 Rmet_1157		152.33	2.89	Op0333f_1	NA	Q1LP83 Alpha/beta hydrolase fold
NPKM_3715	1266974 +	1267337 Rmet_1158		119.67	7.37	Op0333f_1	NA	Q1LP82 Endoribonuclease L-PSP
NPKM_3716	1267353 +	1269582 Rmet_1159	<i>relA</i>	92.00	1.73	Op0333f_1	MET-NUC-Pur	Q1LP81 (P)ppGpp synthetase I (GTP pyrophosphokinase), SpoT/RelA
NPKM_3717	1269603 +	1269680 Rmet_R0015		72.33	14.84	Op0333f_1	NA	NA
NPKM_3718	1269992 +	1271984 Rmet_1160	<i>thrS</i>	400.33	32.75	Op0333f_2	MET-AA-GlySerThr	Q1LP80 Threonyl-tRNA synthetase / Ser-tRNA(Thr) hydrolase
NPKM_3719	1272088 +	1272553 Rmet_1161	<i>infC</i>	3619.00	267.78	Op0333f_3	NA	Q1LP79 Translation initiation factor IF-3
NPKM_3720	1272721 +	1272919 Rmet_1162	<i>rpmI</i>	5413.00	161.08	Op0333f_3	GIP-TL-Ribo	Q1LP78 50S ribosomal protein L35
NPKM_3721	1272947 +	1273304 Rmet_1163	<i>rplT</i>	4852.33	57.50	Op0333f_3	GIP-TL-Ribo	Q1LP77 50S ribosomal protein L20
NPKM_3722	1273512 +	1274544 Rmet_1164	<i>pheS</i>	323.67	15.04	Op0333f_3	MET-AA-PheTyrTrp	Q1LP76 Phenylalanyl-tRNA synthetase alpha chain
NPKM_3723	1274621 +	1277069 Rmet_1165	<i>pheT</i>	341.00	4.58	Op0333f_3	MET-AA-PheTyrTrp	Q1LP75 Phenylalanyl-tRNA synthetase beta subunit
NPKM_3724	1277153 +	1277564 Rmet_1166	<i>ihfA</i>	543.00	4.58	Op0333f_3	GIP-REP-Recomb	Q1LP74 Integration host factor, alpha subunit
NPKM_3725	1277743 +	1278178 Rmet_1167		298.00	19.92	Op0333f_3	NA	Q1LP73 Transcriptional regulator, MerR family
NPKM_3726	1278234 +	1278311 Rmet_R0016		46.33	7.51	Op0333f_3	NA	NA
NPKM_3727	1278472 +	1279126 Rmet_1168		446.33	13.58	Op0333f_4	NA	Q1LP72 Putative acetyl transferase protein
3UTR_1236	1279127 +	1279284 Rmet_1168				Op0333f_4		
3UTR_1908	1279300 -	1279573 Rmet_1169	<i>msrA</i>			Op0334r_1		
NPKM_3728	1279574 -	1280306 Rmet_1169	<i>msrA</i>	4.00	0.00	Op0334r_1	GIP-PTL-Fold	Q1LP71 Peptide methionine sulfoxide reductase
5UTR_1605	1280307 -	1280329 Rmet_1169	<i>msrA</i>			Op0334r_1		
NPKM_3729	1280333 -	1282124 Rmet_1170		2.00	0.00	Op0334r_1	NA	Q1LP70 Cytochrome c biogenesis protein, transmembrane region
NPKM_3730	1282323 +	1283424 Rmet_1171	<i>tnpA</i>	0.00	0.00	Op0335f_1	NA	Q9F8S6 Transposase (Transposase, IS4 family)
5UTR_1021	1283546 +	1284116 Rmet_1173				Op0337f_1		
3UTR_1907	1283547 -	1283571 Rmet_1172				Op0336r_1		
NPKM_3731	1283572 -	1284022 Rmet_1172		2.67	0.58	Op0336r_1	GIP-PTL-Fold	Q1LP68 Twin-arginine translocation pathway signal
5UTR_1604	1284023 -	1284039 Rmet_1172				Op0336r_1		
NPKM_3732	1284116 +	1284917 Rmet_1173		14.33	1.53	Op0337f_1	NA	Q1LP67 Two component transcriptional regulator, winged helix family
NPKM_3733	1284913 +	1286428 Rmet_1174		21.67	1.15	Op0337f_1	NA	Q1LP66 Sensor protein
3UTR_1906	1285430 -	1286347 Rmet_1175				Op0338r_1		
NPKM_3734	1286348 -	1287248 Rmet_1175		14.00	1.00	Op0338r_1	NA	Q1LP65 Transcriptional regulator, LysR family
NPKM_3735	1287367 +	1288645 Rmet_1176	<i>eno</i>	10.67	0.58	Op0339f_1	MET-CAH-FbP	Q1LP64 Enolase 2
NPKM_3736	1288649 -	1288910 Rmet_1177		78.33	14.74	Op0340r_1	NA	Q1LP63 Putative uncharacterized protein
5UTR_1603	1288911 -	1288922 Rmet_1177				Op0340r_1		
NPKM_3737	1288970 +	1289528 Rmet_1178		18.67	1.53	Op0341f_1	NA	Q1LP62 Putative uncharacterized protein

NPKM_3738	1289585 +	1289825 Rmet_1179		79.67	4.93	Op0341f_2	NA	Q1LP61 Putative uncharacterized protein
3UTR_1905	1289596 -	1290310 Rmet_1181	<i>gdhB</i>			Op0342r_2		
NPKM_3739	1289894 +	1290290 Rmet_1180		43.00	1.73	Op0341f_2	NA	Q1LP60 Putative uncharacterized protein
3UTR_1237	1290291 +	1291137 Rmet_1180				Op0341f_2		
NPKM_3740	1290311 -	1295183 Rmet_1181	<i>gdhB</i>	6.00	1.00	Op0342r_2	MET-EN-Nitrog	Q1LP59 Glutamate dehydrogenase (NAD)
NPKM_3741	1295303 -	1295825 Rmet_1182		57.33	7.64	Op0342r_2	NA	Q1LP58 Putative uncharacterized protein
NPKM_3742	1296026 +	1296173 Rmet_6440		2.00	0.00	Op2004f_1	NA	NA
NPKM_3743	1296131 -	1296194 Rmet_6441		186.00	9.54	Op0342r_2	NA	NA
3UTR_1238	1296174 +	1296180 Rmet_6440				Op2004f_1		
NPKM_3744	1296232 -	1296571 Rmet_1183		1754.00	135.64	Op0342r_2	NA	Q1LP57 Conserved hypothetical signal peptide protein
NPKM_3745	1296745 -	1297816 Rmet_1184	<i>bug</i>	257.00	18.52	Op0342r_1	NA	Q1LP56 Uncharacterized protein UPF0065
5UTR_1602	1297817 -	1297946 Rmet_1184	<i>bug</i>			Op0342r_1		
3UTR_1904	1297953 -	1297978 Rmet_R0017				Op2005r_1		
NPKM_3746	1297979 -	1298055 Rmet_R0017		2.67	0.58	Op2005r_1	NA	NA
5UTR_1022	1298046 +	1298143 Rmet_1185				Op0343f_1		
NPKM_3747	1298143 +	1299076 Rmet_1185		42.00	2.65	Op0343f_1	NA	Q1LP55 Transcriptional regulator, LysR family
NPKM_3748	1299191 +	1300595 Rmet_1186	<i>atzB</i>	34.00	4.36	Op0343f_1	MET-XEN-Others	Q1LP54 Amidohydrolase
3UTR_1239	1300596 +	1300759 Rmet_1186	<i>atzB</i>			Op0343f_1		
3UTR_1903	1300773 -	1300790 Rmet_R0018				Op2005r_1		
NPKM_3749	1300791 -	1300867 Rmet_R0018		2.33	0.58	Op2005r_1	NA	NA
5UTR_1601	1300868 -	1301028 Rmet_R0018				Op2005r_1		
3UTR_1902	1301039 -	1301498 Rmet_1188				Op0344r_1		
5UTR_1023	1301100 +	1301113 Rmet_1187				Op0343f_2		
NPKM_3750	1301113 +	1301380 Rmet_1187		568.33	28.11	Op0343f_2	NA	Q1LP53 Putative uncharacterized protein
3UTR_1240	1301381 +	1303950 Rmet_1187				Op0343f_2		
NPKM_3751	1301499 -	1303311 Rmet_1188		33.33	1.15	Op0344r_1	EIP-TRA-Ion	Q1LP52 Sulphate transporter
NPKM_3752	1303314 -	1304112 Rmet_1189	<i>xthA2</i>	106.00	3.46	Op0344r_1	GIP-REP-Recomb	Q1LP51 Exodeoxyribonuclease III
NPKM_3753	1304108 -	1304564 Rmet_1190		117.33	2.89	Op0344r_1	NA	Q1LP50 Putative uncharacterized protein
NPKM_3754	1304602 -	1306705 Rmet_1191	<i>prlC</i>	234.33	2.31	Op0344r_1	NA	Q1LP49 Oligopeptidase A. Metallo peptidase. MEROPS family M03A
5UTR_1024	1306388 +	1307865 Rmet_1193				Op0345f_1		
NPKM_3755	1306838 -	1307696 Rmet_1192	<i>folD</i>	185.00	5.57	Op0344r_1	MET-CAH-DiCarb	Q1LP48 Bifunctional protein folD
NPKM_3756	1307865 +	1308561 Rmet_1193		18.00	3.00	Op0345f_1	NA	Q1LP47 Putative membrane protein
3UTR_1241	1308562 +	1309295 Rmet_1193				Op0345f_1		
NPKM_3757	1308658 -	1309291 Rmet_1194		779.67	8.50	Op0346r_2	NA	Q1LP46 Two component transcriptional regulator, LuxR family
NPKM_3758	1309428 -	1312041 Rmet_1195		134.33	10.69	Op0346r_1	NA	Q1LP45 Sensor protein
5UTR_1600	1312042 -	1312192 Rmet_1195				Op0346r_1		
5UTR_1025	1312104 +	1312122 Rmet_6442				Op0347f_1		
NPKM_3759	1312122 +	1312200 Rmet_6442		7.00	1.73	Op0347f_1	NA	NA
NPKM_3760	1312478 +	1315166 Rmet_1196	<i>aceE</i>	646.33	30.09	Op0347f_2	MET-CAH-FbP	Q1LP44 2-oxo-acid dehydrogenase E1 component, homodimeric type
NPKM_3761	1315367 +	1317032 Rmet_1197	<i>aceF</i>	506.67	24.54	Op0347f_2	MET-CAH-FbP	Q1LP43 Dihydrolipoamide acetyltransferase
NPKM_3762	1317095 +	1317692 Rmet_1198		321.33	25.54	Op0347f_2	GIP-PTL-Fold	Q1LP42 20S proteasome, A and B subunits
NPKM_3763	1317731 +	1319510 Rmet_1199	<i>lpdA</i>	365.67	23.86	Op0347f_2	MET-CAH-FbP	Q1LP41 Dihydrolipoamide dehydrogenase
3UTR_1242	1319511 +	1319677 Rmet_1199	<i>lpdA</i>			Op0347f_2		

3UTR_1901	1319655 -	1319775 Rmet_1200	phaP				Op0348r_1		
NPKM_3764	1319776 -	1320355 Rmet_1200	phaP	3728.67	88.23	Op0348r_1	NA	Q1LP40 Phasin	
5UTR_1599	1320356 -	1320491 Rmet_1200	phaP			Op0348r_1			
5UTR_1026	1320649 +	1320741 Rmet_1201				Op0349f_1			
NPKM_3765	1320741 +	1321713 Rmet_1201		78.33	8.08	Op0349f_1	NA	Q1LP39 Histone deacetylase superfamily	
NPKM_3766	1321738 +	1322266 Rmet_1202		71.67	5.13	Op0349f_1	NA	Q1LP38 Thioesterase superfamily	
NPKM_3767	1322298 +	1322994 Rmet_1203		137.00	4.58	Op0349f_1	NA	Q1LP37 Nitroreductase	
NPKM_3768	1323301 +	1324483 Rmet_1204		359.67	10.50	Op0349f_2	NA	Q1LP36 Murein-DD-endopeptidase. Serine peptidase. MEROPS family S11	
3UTR_1243	1324484 +	1324534 Rmet_1204				Op0349f_2			
3UTR_1900	1324541 -	1324580 Rmet_1205				Op0350r_1			
NPKM_3769	1324581 -	1325367 Rmet_1205		118.00	3.00	Op0350r_1	NA	Q1LP35 Transcriptional regulator, IclR family	
5UTR_1027	1325082 +	1325607 Rmet_1206	ykgE			Op0351f_1			
NPKM_3770	1325607 +	1326333 Rmet_1206	ykgE	115.67	4.16	Op0351f_1	NA	Q1LP34 Putative uncharacterized protein	
NPKM_3771	1326355 +	1327768 Rmet_1207		148.00	6.93	Op0351f_1	NA	Q1LP33 Iron-sulfur cluster binding protein	
NPKM_3772	1327764 +	1328031 Rmet_1208		194.67	6.03	Op0351f_1	NA	Q1LP32 Putative uncharacterized protein	
3UTR_1244	1328032 +	1329396 Rmet_1208				Op0351f_1			
NPKM_3773	1328087 -	1328882 Rmet_1209		594.00	52.72	Op0352r_2	EIP-TRA-ABC	Q1LP31 ABC transporter-related protein	
NPKM_3774	1328883 -	1329780 Rmet_1210		499.00	33.41	Op0352r_2	EIP-TRA-ABC	Q1LP30 Inner-membrane translocator	
NPKM_3775	1329882 -	1330854 Rmet_1211		1602.00	161.90	Op0352r_2	EIP-TRA-ABC	Q1LP29 Putative uncharacterized protein	
NPKM_3776	1331146 -	1332205 Rmet_1212	tas	105.00	7.21	Op0352r_1	NA	Q1LP28 Aldo/keto reductase	
NPKM_3777	1332250 -	1333327 Rmet_1213	pyrD	174.00	10.15	Op0352r_1	MET-NUC-Pyr	Q1LP27 Dihydroorotate dehydrogenase	
NPKM_3778	1333358 -	1334147 Rmet_1214	ate	105.00	15.13	Op0352r_1	GIP-PTL-Fold	Q1LP26 Putative arginyl-tRNA--protein transferase	
NPKM_3779	1334639 -	1334822 Rmet_6443	yjgH	104.67	17.62	Op0352r_1	NA	NA	
NPKM_3780	1334904 -	1335654 Rmet_1216	aat	178.00	28.62	Op0354r_1	GIP-PTL-Fold	Q1LP24 Leucyl/phenylalanyl-tRNA--protein transferase	
NPKM_3781	1335713 -	1336298 Rmet_1217		318.67	39.37	Op0354r_1	NA	Q1LP23 NUDIX hydrolase	
NPKM_3782	1336449 -	1336525 Rmet_R0019		510.00	54.25	Op0352r_1	NA	NA	
NPKM_3783	1336647 -	1337310 Rmet_1218		35.00	2.00	Op0354r_2	NA	Q1LP22 Putative uncharacterized protein	
NPKM_3784	1337371 -	1337761 Rmet_1219		70.33	0.58	Op0354r_2	NA	Q1LP21 Putative uncharacterized protein	
NPKM_3785	1337866 -	1339114 Rmet_1220	boxA	23.67	1.53	Op0354r_1	NA	Q1LP20 Benzoyl-CoA oxygenase, component A	
NPKM_3786	1339140 -	1340565 Rmet_1221	boxB	25.67	2.52	Op0354r_1	NA	Q1LP19 Benzoyl-CoA oxygenase, component B	
NPKM_3787	1340606 -	1342283 Rmet_1222		25.33	3.51	Op0354r_1	MET-CAH-Prop	Q1LP18 2,3-dihydro-2,3-dihydroxybenzoyl-CoA ring cleavage enzyme	
5UTR_1598	1342284 -	1342316 Rmet_1222				Op0354r_1			
3UTR_1899	1342347 -	1342402 Rmet_1223	bzdR			Op0354r_1			
NPKM_3788	1342403 -	1343354 Rmet_1223	bzdR	29.00	1.73	Op0354r_1	MET-AA-PheTyrTrp	Q1LP17 Transcriptional regulator, XRE family with shikimate kinase activity	
5UTR_1597	1343355 -	1343413 Rmet_1223	bzdR			Op0354r_1			
5UTR_1028	1343457 +	1343602 Rmet_1224	bzdA			Op0355f_1			
NPKM_3789	1343602 +	1345252 Rmet_1224	bzdA	20.00	1.73	Op0355f_1	MET-XEN-Benz	Q1LP16 Benzoate-CoA ligase	
NPKM_3790	1345253 +	1346069 Rmet_1225		15.33	1.15	Op0355f_1	NA	Q1LP15 Alpha/beta hydrolase fold	
NPKM_3791	1346154 +	1347348 Rmet_1226		86.33	10.21	Op0355f_2	EIP-TRA-ABC	Q1LP14 Extracellular ligand-binding receptor	
NPKM_3792	1347373 +	1348240 Rmet_1227		55.67	5.69	Op0355f_2	EIP-TRA-ABC	Q1LP13 Inner-membrane translocator	
NPKM_3793	1348255 +	1349320 Rmet_1228		43.67	5.13	Op0355f_2	EIP-TRA-ABC	Q1LP12 Inner-membrane translocator	
NPKM_3794	1349316 +	1350084 Rmet_1229	livG6	58.00	2.00	Op0355f_2	EIP-TRA-ABC	Q1LP11 ABC transporter-related protein	
NPKM_3795	1350080 +	1350797 Rmet_1230	livF6	49.00	3.61	Op0355f_2	EIP-TRA-ABC	Q1LP10 ABC transporter-related protein	

3UTR_1898	1350951 -	1350977	Rmet_6444				Op2006r_1		
NPKM_3796	1350978 -	1351083	Rmet_6444		1.00	1.00	Op2006r_1	NA	NA
NPKM_3797	1351096 +	1353067	Rmet_1231	<i>trkD</i>	138.67	12.90	Op0355f_3	EIP-TRA-Ion	Q1LP09 Probable potassium transport system protein kup
3UTR_1897	1352941 -	1353158	Rmet_1232	<i>yhgF</i>			Op0356r_1		
3UTR_1245	1353068 +	1353099	Rmet_1231	<i>trkD</i>			Op0355f_3		
NPKM_3798	1353159 -	1355523	Rmet_1232	<i>yhgF</i>	133.33	3.51	Op0356r_1	NA	Q1LP08 RNA binding S1
5UTR_1029	1355458 +	1355700	Rmet_1233				Op0357f_1		
NPKM_3799	1355700 +	1356477	Rmet_1233		113.67	8.08	Op0357f_1	NA	Q1LP07 Putative uncharacterized protein
NPKM_3800	1356501 +	1356738	Rmet_1234		124.33	7.23	Op0357f_1	NA	Q1LP06 Putative uncharacterized protein
NPKM_3801	1356778 +	1359010	Rmet_1235	<i>yooA</i>	66.00	4.58	Op0357f_1	GIP-REP-Recomb	Q1LP05 Helicase c2
NPKM_3802	1359444 +	1360644	Rmet_1236	<i>int</i>	5.67	0.58	Op0357f_1	NA	Q1LP04 Phage integrase
NPKM_3803	1360640 +	1361717	Rmet_1237		3.33	0.58	Op0357f_1	NA	Q1LP03 Putative uncharacterized protein
NPKM_3804	1362068 +	1362485	Rmet_1238	<i>radC'</i>	0.00	0.00	Op0357f_1	GIP-REP-Recomb	Q1LP02 DNA repair protein RadC
NPKM_3805	1362582 +	1363842	Rmet_1239	<i>ritA2</i>	9.33	0.58	Op0357f_2	NA	Q1LP01 Phage integrase
NPKM_3806	1363838 +	1364831	Rmet_1240	<i>ritB2</i>	5.00	0.00	Op0357f_2	NA	Q1LP00 Phage integrase
NPKM_3807	1364827 +	1365838	Rmet_1241	<i>ritC2</i>	5.33	0.58	Op0357f_2	NA	Q1LNZ9 Phage integrase
NPKM_3808	1366075 +	1366186	Rmet_1242	<i>radC'</i>	17.00	1.00	Op0357f_3	NA	Q1LNZ8 RadC family protein
NPKM_3809	1366464 +	1366857	Rmet_1243		0.67	0.58	Op0357f_3	NA	Q1LNZ7 Putative uncharacterized protein
NPKM_3810	1367382 +	1368390	Rmet_1244	<i>yupB</i>	0.00	0.00	Op0357f_3	NA	Q1LNZ6 Putative uncharacterized protein
NPKM_3811	1368468 +	1370520	Rmet_1245	<i>parB</i>	2.67	0.58	Op0357f_4	NA	Q1LNZ5 ParB family protein
3UTR_1896	1370561 -	1370726	Rmet_1246				Op0358r_1		
NPKM_3812	1370727 -	1371246	Rmet_1246		17.00	1.00	Op0358r_1	NA	Q1LNZ4 GCN5-related N-acetyltransferase
5UTR_1596	1371247 -	1371480	Rmet_1246				Op0358r_1		
NPKM_3813	1371397 +	1371727	Rmet_1247		0.00	0.00	Op0359f_1	NA	Q1LNZ3 Putative uncharacterized protein
3UTR_1895	1371494 -	1371607	Rmet_6445				Op2007r_1		
NPKM_3814	1371608 -	1371872	Rmet_6445		41.67	3.21	Op2007r_1	NA	NA
NPKM_3815	1372034 +	1372388	Rmet_1248		1.00	0.00	Op0359f_2	NA	Q1LNZ2 Transcriptional regulator, XRE family
NPKM_3816	1372452 -	1372758	Rmet_1249		42.33	4.04	Op0360r_1	NA	Q1LNZ1 Putative lipoprotein
NPKM_3817	1372770 +	1373352	Rmet_1250		4.00	1.73	Op0361f_1	NA	Q1LNZ0 Integrase, catalytic region
NPKM_3818	1373578 -	1374580	Rmet_1251	<i>tnp</i>	5.67	0.58	Op0362r_1	NA	Q1LNY9 Putative uncharacterized protein
NPKM_3819	1374595 +	1375468	Rmet_1252		0.00	0.00	Op0363f_1	NA	Q1LNY8 Putative uncharacterized protein
NPKM_3820	1375515 +	1375833	Rmet_1253		0.33	0.58	Op0363f_2	NA	Q1LNY7 Conserved hypothetical replication initiator and transcription repressor prot
NPKM_3821	1375859 +	1376717	Rmet_1254	<i>repA</i>	0.00	0.00	Op0363f_2	DIV-Division	Q1LNY6 Cobyirnic acid a,c-diamide synthase
NPKM_3822	1376970 +	1377609	Rmet_1255	<i>parA</i>	0.00	0.00	Op0363f_2	NA	Q1LNY5 Putative uncharacterized protein
NPKM_3823	1377605 +	1377878	Rmet_1256	<i>parG</i>	0.00	0.00	Op0363f_2	NA	Q1LNY4 Putative uncharacterized protein
NPKM_3824	1377874 +	1378408	Rmet_1257		0.00	0.00	Op0363f_2	NA	Q1LNY3 TraF peptidase. Serine peptidase. MEROPS family S26C
NPKM_3825	1378404 +	1378992	Rmet_1258	<i>traF</i>	0.00	0.00	Op0363f_2	NA	Q1LNY2 Putative uncharacterized protein
NPKM_3826	1379308 +	1381414	Rmet_1259	<i>virD2</i>	0.00	0.00	Op0363f_2	NA	Q1LNY1 Putative uncharacterized protein
NPKM_3827	1381451 -	1381913	Rmet_1260		0.67	1.15	Op0364r_2	NA	Q1LNY0 Putative uncharacterized protein
NPKM_3828	1381973 -	1383101	Rmet_1261		0.67	0.58	Op0364r_2	GIP-REP-Recomb	Q1LL29 Transposase, mutator type
NPKM_3829	1383233 -	1384484	Rmet_1262	<i>tnpA</i>	0.00	0.00	Op0364r_1	NA	NA
3UTR_1894	1384563 -	1384632	Rmet_1263	<i>tnpB</i>			Op0364r_1		
NPKM_3830	1384633 -	1385440	Rmet_1263	<i>tnpB</i>	1.00	0.00	Op0364r_1	NA	Q1LNx8 IstB-like ATP-binding protein

NPKM_3831	1385439 -	1386450 Rmet_1264	<i>tnpA</i>	1.00	0.00	Op0364r_1	NA	Q1LNX7 Integrase, catalytic region
3UTR_1893	1386604 -	1386616 Rmet_1265				Op0364r_1		
NPKM_3832	1386617 -	1387484 Rmet_1265		1.33	0.58	Op0364r_1	NA	Q1LNX6 Putative uncharacterized protein
NPKM_3833	1387483 -	1388893 Rmet_1266		2.00	0.00	Op0364r_1	GIP-TL-Ass	Q1LNX5 Beta-lactamase-like protein
NPKM_3834	1388900 -	1389104 Rmet_6446		2.00	1.00	Op0364r_1	NA	NA
NPKM_3835	1389123 -	1390662 Rmet_1267	<i>oprN</i>	1.00	0.00	Op0364r_1	NA	Q1LNX4 RND efflux system, outer membrane lipoprotein, NodT
NPKM_3836	1390658 -	1391777 Rmet_1268	<i>ybhR</i>	0.67	0.58	Op0364r_1	NA	Q1LNX3 ABC-type multidrug transport system permease component
NPKM_3837	1391781 -	1392951 Rmet_1269	<i>ybhS</i>	3.00	0.00	Op0364r_1	NA	Q1LNX2 ABC-type multidrug transport system permease component
NPKM_3838	1393083 -	1393290 Rmet_1270		8.33	0.58	Op0364r_1	NA	Q1LNX1 ISPsy5, transposase
NPKM_3839	1393468 +	1394701 Rmet_1271	<i>ritA1</i>	1.00	0.00	Op0365f_1	NA	Q1LNX0 Phage integrase
NPKM_3840	1394697 +	1395645 Rmet_1272	<i>ritB1</i>	1.00	0.00	Op0365f_1	NA	Q1LNW9 Phage integrase
3UTR_1892	1395445 -	1396729 Rmet_1274	<i>tnpA</i>			Op0366r_2		
NPKM_3841	1395641 +	1396637 Rmet_1273	<i>ritC1</i>	1.00	0.00	Op0365f_1	NA	Q1LNW8 Phage integrase
NPKM_3842	1396730 -	1398221 Rmet_1274	<i>tnpA</i>	39.33	1.53	Op0366r_2	NA	Q1LNW7 Transposase IS66
NPKM_3843	1398243 -	1398603 Rmet_1275		2.00	1.00	Op0366r_1	NA	Q1LNW6 IS66 Orf2 like
NPKM_3844	1398602 -	1398938 Rmet_1276		3.67	0.58	Op0366r_1	NA	Q1LNW5 Putative uncharacterized protein
NPKM_3845	1398970 -	1399222 Rmet_1277		5.00	1.00	Op0366r_1	NA	Q1LNW4 ATPase component ABC-type multidrug transport system
NPKM_3846	1399237 +	1399627 Rmet_1278		0.33	0.58	Op0367f_1	NA	Q1LNW3 Transposase
NPKM_3847	1399618 -	1399882 Rmet_1279		11.00	1.00	Op0368r_1	NA	Q1LNW2 Putative transposase
5UTR_1595	1399883 -	1399965 Rmet_1279				Op0368r_1		
NPKM_3848	1400001 +	1401393 Rmet_1280	<i>tnpA</i>	3.00	0.00	Op0369f_1	NA	Q1LNW1 Integrase, catalytic region
3UTR_1891	1400915 -	1401175 Rmet_1281	<i>hypE1</i>			Op0370r_1		
NPKM_3849	1401176 -	1402289 Rmet_1281	<i>hypE1</i>	97.33	12.22	Op0370r_1	GIP-PTL-Fold	Q1LNV0 Hydrogenase expression/formation protein HypE
NPKM_3850	1402285 -	1403449 Rmet_1282	<i>hypD1</i>	80.33	10.02	Op0370r_1	GIP-PTL-Fold	Q1LNV9 Hydrogenase expression/formation protein HypD
NPKM_3851	1403457 -	1403685 Rmet_1283	<i>hypC1</i>	71.00	11.79	Op0370r_1	GIP-PTL-Fold	Q1LNV8 Hydrogenase assembly chaperone hypC/hupF
NPKM_3852	1403675 -	1404815 Rmet_1284	<i>hypF1</i>	61.00	8.54	Op0370r_1	GIP-PTL-Fold	Q1LNV7 Hydrogenase maturation protein hypF
NPKM_3853	1404828 -	1405866 Rmet_1285	<i>hypB1</i>	103.00	13.08	Op0370r_1	GIP-PTL-Fold	Q1LNV6 Hydrogenase accessory protein HypB
NPKM_3854	1405889 -	1406237 Rmet_1286	<i>hypA1</i>	59.00	7.00	Op0370r_1	GIP-PTL-Fold	Q1LNV5 Hydrogenase nickel insertion protein HypA
NPKM_3855	1406229 -	1407384 Rmet_1287	<i>hoxV</i>	109.67	10.02	Op0370r_1	NA	Q1LNV4 Putative uncharacterized protein
NPKM_3856	1407412 -	1407889 Rmet_1288	<i>hoxT</i>	164.33	17.04	Op0370r_1	NA	Q1LNV3 HupJ, contains rubredoxin domain
NPKM_3857	1407890 -	1408121 Rmet_1289	<i>hoxR</i>	136.67	17.79	Op0370r_1	NA	Q1LNV2 Rubredoxin
NPKM_3858	1408126 -	1408990 Rmet_1290	<i>hoxQ</i>	195.33	20.65	Op0370r_1	NA	Q1LNV1 HupH hydrogenase expression protein
NPKM_3859	1409021 -	1409471 Rmet_1291	<i>hoxO</i>	139.00	16.09	Op0370r_1	NA	Q1LNV0 Hydrogenase-1 expression HyaE
NPKM_3860	1409486 -	1409789 Rmet_1292	<i>hoxL</i>	104.00	9.54	Op0370r_1	GIP-PTL-Fold	Q1LNU9 Hydrogenase assembly chaperone hypC/hupF
NPKM_3861	1409790 -	1410456 Rmet_1293	<i>hoxM</i>	119.33	13.65	Op0370r_1	NA	Q1LNU8 HyaD peptidase. Aspartic peptidase. MEROPS family A31
NPKM_3862	1410477 -	1410861 Rmet_1294		130.33	16.92	Op0370r_1	NA	Q1LNU7 Putative plasmid maintenance system antidote protein, XRE family
NPKM_3863	1410944 -	1411676 Rmet_1295	<i>hoxZ</i>	335.67	38.79	Op0370r_1	NA	Q1LNU6 Nickel-dependent hydrogenase b-type cytochrome subunit
NPKM_3864	1411713 -	1412451 Rmet_1296	<i>hupE</i>	399.00	49.49	Op0370r_1	GIP-PTL-Fold	Q1LNU5 HupE/UreJ protein
NPKM_3865	1412447 -	1414307 Rmet_1297	<i>hoxG</i>	548.67	55.29	Op0370r_1	NA	Q1LNU4 Nickel-dependent hydrogenase, large subunit
NPKM_3866	1414327 -	1415422 Rmet_1298	<i>hoxK</i>	529.33	51.78	Op0370r_1	NA	Q1LNU3 Hydrogenase (NiFe) small subunit (HyaD)
5UTR_1594	1415423 -	1415465 Rmet_1298	<i>hoxK</i>			Op0370r_1		
NPKM_3867	1415554 +	1415956 Rmet_1299		1.00	1.00	Op0371f_1	NA	Q1LNU2 Putative uncharacterized protein
NPKM_3868	1415971 -	1416667 Rmet_1300		2.33	0.58	Op0372r_1	NA	Q1LNU1 GMC oxidoreductase

NPKM_3869	1416783 +	1417749 Rmet_1301	<i>tnpA</i>	0.00	0.00	Op0373f_1	NA	Q1LNW1 Integrase, catalytic region	
3UTR_1890	1417698 -	1417719 Rmet_1302	<i>tnpB</i>			Op0374r_1			
NPKM_3870	1417720 -	1418242 Rmet_1302	<i>tnpB</i>	15.33	1.15	Op0374r_1	NA	Q1LNT9 Putative transposase	
NPKM_3871	1418274 -	1418538 Rmet_1303	<i>tnpA</i>	19.67	1.53	Op0374r_1	GIP-REP-Recomb	Q1LNT8 Transposase IS3/IS911	
NPKM_3872	1418612 +	1419044 Rmet_1304		0.33	0.58	Op0375f_1	NA	Q1LNT7 Putative uncharacterized protein	
NPKM_3873	1419137 -	1420982 Rmet_1305	<i>patR</i>	48.67	4.73	Op0376r_6	NA	Q1LNT6 Sigma-54 factor, interaction region	
NPKM_3874	1421154 -	1421985 Rmet_1306		36.00	0.00	Op0376r_6	NA	A4JW31 Alpha/beta hydrolase fold	
NPKM_3875	1422084 -	1422249 Rmet_6447		12.67	2.52	Op0376r_5	NA	NA	
NPKM_3876	1422720 -	1424115 Rmet_1307		14.33	1.15	Op0376r_5	EIP-TRA-Pores	Q1LNT4 Membrane protein involved in aromatic hydrocarbon degradation	
NPKM_3877	1424193 -	1425255 Rmet_1308		17.00	1.73	Op0376r_5	NA	Q1LNT3 Alcohol dehydrogenase GroES-like protein	
NPKM_3878	1425424 +	1425835 Rmet_1309	<i>tnpA</i>	10.33	1.15	Op0375f_1	NA		0
NPKM_3879	1425897 +	1426242 Rmet_6448		5.00	1.00	Op0375f_1	NA	NA	
NPKM_3880	1426312 -	1426765 Rmet_1310		23.00	3.61	Op0376r_5	NA		0
NPKM_3881	1426984 -	1428007 Rmet_1311		29.67	0.58	Op0376r_5	NA	Q1LNT2 Oxidoreductase FAD-binding region	
NPKM_3882	1428106 -	1429093 Rmet_1312	<i>tmoE</i>	59.67	1.15	Op0376r_5	NA	Q1LNT1 Methane/phenol/toluene hydroxylase	
NPKM_3883	1429147 -	1429462 Rmet_1313	<i>tmoD</i>	54.67	1.15	Op0376r_5	NA	Q1LNT0 Monooxygenase component MmoB/DmpM	
NPKM_3884	1429502 -	1429838 Rmet_1314	<i>tmoC</i>	60.67	4.51	Op0376r_5	NA	Q1LNS9 Rieske (2Fe-2S) region	
NPKM_3885	1429893 -	1430160 Rmet_1315	<i>tmoB</i>	58.33	3.51	Op0376r_5	NA	Q1LNS8 Toluene-4-monooxygenase system B	
NPKM_3886	1430228 -	1431731 Rmet_1316	<i>tmoA</i>	63.33	1.53	Op0376r_5	NA	Q1LNS7 Methane/phenol/toluene hydroxylase	
NPKM_3887	1431790 -	1431982 Rmet_1317	<i>nahJ</i>	21.33	3.79	Op0376r_4	NA	Q1LNS6 4-oxalocrotonate tautomerase family enzyme	
NPKM_3888	1431993 -	1432782 Rmet_1318	<i>dmpH</i>	17.67	0.58	Op0376r_4	MET-XEN-Toluene	Q1LNS5 Hydratase/decarboxylase	
NPKM_3889	1432778 -	1433825 Rmet_1319	<i>bphI</i>	16.33	0.58	Op0376r_4	MET-AA-Phe	Q1LNS4 Pyruvate carboxyltransferase	
NPKM_3890	1433844 -	1434756 Rmet_1320	<i>mhpF</i>	11.33	1.15	Op0376r_4	MET-CAH-Pyr	Q1LNS3 Semialdehyde dehydrogenase, NAD-binding	
NPKM_3891	1434834 -	1435623 Rmet_1321	<i>xyIJ</i>	9.00	1.00	Op0376r_4	MET-XEN-Toluene	Q1LNS2 Hydratase/decarboxylase	
NPKM_3892	1435619 -	1437131 Rmet_1322	<i>dmpC</i>	7.67	0.58	Op0376r_4	NA	Q1LNS1 Aldehyde dehydrogenase	
NPKM_3893	1437197 -	1437647 Rmet_1323		4.67	0.58	Op0376r_4	NA	Q1LNS0 Putative uncharacterized protein	
NPKM_3894	1437668 -	1438613 Rmet_1324	<i>dmpB</i>	5.67	0.58	Op0376r_4	MET-XEN-Toluene	Q1LNR9 Catechol 2,3-dioxygenase	
NPKM_3895	1438630 -	1438987 Rmet_1325		2.00	0.00	Op0376r_3	MET-LIP-FAMet	Q1LNR8 Ferredoxin	
NPKM_3896	1438989 -	1440054 Rmet_1326	<i>tomA5</i>	3.00	0.00	Op0376r_3	MET-XEN-Toluene	Q1LNR7 Oxidoreductase FAD-binding region	
5UTR_1593	1440055 -	1440100 Rmet_1326	<i>tomA5</i>			Op0376r_3			
3UTR_1889	1440116 -	1440131 Rmet_1327	<i>tomA4</i>			Op0376r_3			
NPKM_3897	1440132 -	1440489 Rmet_1327	<i>tomA4</i>	4.67	0.58	Op0376r_3	NA	Q9ANX1 TomA4	
NPKM_3898	1440485 -	1442045 Rmet_1328	<i>tomA3</i>	3.67	0.58	Op0376r_3	MET-EN-Methane	Q1LNR5 Methane/phenol/toluene hydroxylase	
NPKM_3899	1442067 -	1442337 Rmet_1329	<i>tomA2</i>	1.67	1.15	Op0376r_2	NA	Q1LNR4 Monooxygenase component MmoB/DmpM	
NPKM_3900	1442376 -	1443372 Rmet_1330	<i>tomA1</i>	1.33	0.58	Op0376r_2	NA	Q1LNR3 Methane/phenol/toluene hydroxylase	
5UTR_1592	1443373 -	1443417 Rmet_1330	<i>tomA1</i>			Op0376r_2			
NPKM_3901	1443459 -	1443684 Rmet_1331	<i>tomA0</i>	0.00	0.00	Op0376r_1	MET-XEN-Toluene	Q1LNR2 Phenol hydroxylase subunit	
NPKM_3902	1444218 +	1444560 Rmet_1332		14.67	2.08	Op0377f_1	NA	Q1LNR1 Putative uncharacterized protein	
NPKM_3903	1444570 +	1445317 Rmet_1333	<i>phaB2</i>	14.00	2.00	Op0377f_1	MET-CAH-But	Q1LNR0 Acetoacetyl-CoA reductase	
NPKM_3904	1445376 +	1445841 Rmet_1334	<i>uspA2</i>	9.67	1.15	Op0377f_1	NA	Q1LNQ9 UspA	
NPKM_3905	1446017 +	1446806 Rmet_1335	<i>chnA</i>	23.67	2.31	Op0377f_2	NA	Q1LNQ8 Short-chain dehydrogenase/reductase SDR	
NPKM_3906	1446802 +	1447765 Rmet_1336	<i>traR</i>	15.33	0.58	Op0377f_2	NA	Q1LNQ7 Transcriptional regulator, LysR family	
NPKM_3907	1447761 +	1448040 Rmet_1337		10.00	1.00	Op0377f_2	NA	Q1LNQ6 Putative lipoprotein	

NPKM_3908	1447985 -	1448282 Rmet_1338		0.00	0.00	Op0378r_1	NA	Q1LNQ5 Putative uncharacterized protein
NPKM_3909	1448291 +	1450286 Rmet_1339	<i>traG</i>	0.00	0.00	Op0379f_1	GIP-PTL-T4S	Q1LNQ4 TRAG protein
NPKM_3910	1450282 +	1450747 Rmet_1340		0.00	0.00	Op0379f_1	NA	Q1LN44 CopG-like DNA-binding
NPKM_3911	1450743 +	1451808 Rmet_1341	<i>trbB</i>	0.00	0.00	Op0379f_1	GIP-PTL-T4S	Q1LNQ2 Type II secretion system protein E
NPKM_3912	1451804 +	1452188 Rmet_1342	<i>trbC</i>	0.00	0.00	Op0379f_1	GIP-PTL-T4S	Q1LNQ1 Conjugal transfer protein TrbC
NPKM_3913	1452184 +	1452457 Rmet_1343	<i>trbD</i>	0.00	0.00	Op0379f_1	GIP-PTL-T4S	Q1LNQ0 Putative conjugal transfer trbD transmembrane protein
NPKM_3914	1452469 +	1454929 Rmet_1344	<i>trbE</i>	0.00	0.00	Op0379f_1	GIP-PTL-T4S	Q1LNP9 ATPase
NPKM_3915	1454925 +	1455663 Rmet_1345	<i>trbJ</i>	0.33	0.58	Op0379f_2	NA	Q1LNP8 Putative conjugal transfer TrbJ signal peptide protein
NPKM_3916	1455675 +	1455996 Rmet_1346		0.00	0.00	Op0379f_2	NA	Q1LNP7 Putative lipoprotein
NPKM_3917	1455992 +	1457372 Rmet_1347	<i>trbL</i>	0.67	0.58	Op0379f_3	GIP-PTL-T4S	Q1LNP6 TrbL/VirB6 plasmid conjugal transfer protein
NPKM_3918	1457396 +	1458101 Rmet_1348	<i>trbF</i>	0.00	0.00	Op0379f_3	GIP-PTL-T4S	Q1LNP5 Conjugal transfer protein
NPKM_3919	1458097 +	1459090 Rmet_1349	<i>trbG</i>	2.00	1.00	Op0379f_4	GIP-PTL-T4S	Q1LNP4 Conjugal transfer protein TrbG/VirB9/CagX
3UTR_1888	1458779 -	1460939 Rmet_1352	<i>comL</i>			Op0380r_1		
NPKM_3920	1459092 +	1460364 Rmet_1350	<i>trbI</i>	2.00	0.00	Op0379f_4	GIP-PTL-T4S	Q1LNP3 Conjugation TrbI-like protein
NPKM_3921	1460360 +	1460606 Rmet_1351		4.00	1.73	Op0379f_4	NA	Q1LNP2 Putative uncharacterized protein
NPKM_3922	1460940 -	1461777 Rmet_1352	<i>comL</i>	384.33	12.90	Op0380r_1	NA	Q1LNP1 Putative transmembrane protein
5UTR_1591	1461778 -	1462203 Rmet_1352	<i>comL</i>			Op0380r_1		
NPKM_3923	1461788 +	1463000 Rmet_1353	<i>rluD</i>	142.00	4.36	Op0381f_1	GIP-TL-Ass	Q1LNP0 Pseudouridine synthase
NPKM_3924	1462986 +	1463778 Rmet_1354		126.67	7.64	Op0381f_1	NA	Q1LNN9 Putative uncharacterized protein
3UTR_1887	1463002 -	1463802 Rmet_1355				Op0382r_1		
3UTR_1246	1463779 +	1464080 Rmet_1354				Op0381f_1		
NPKM_3925	1463803 -	1464031 Rmet_1355		48.00	3.61	Op0382r_1	NA	Q1LNN8 Putative transmembrane protein
5UTR_1590	1464032 -	1464212 Rmet_1355				Op0382r_1		
5UTR_1030	1464082 +	1464176 Rmet_1356	<i>phaC1</i>			Op0383f_1		
NPKM_3926	1464176 +	1466267 Rmet_1356	<i>phaC1</i>	364.67	20.43	Op0383f_1	MET-CAH-But	Q1LNN7 Poly(R)-hydroxyalkanoic acid synthase, class I
NPKM_3927	1466343 +	1467525 Rmet_1357	<i>phaA</i>	1130.00	69.07	Op0383f_2	MET-CAH-Pyr	Q1LNN6 Acetyl-CoA acetyltransferase
NPKM_3928	1467641 +	1468382 Rmet_1358	<i>phaB</i>	1787.00	100.16	Op0383f_2	MET-CAH-But	Q1LNN5 Acetoacetyl-CoA reductase
NPKM_3929	1468750 +	1469302 Rmet_1359	<i>phaR</i>	687.00	15.72	Op0383f_2	NA	Q1LNN4 Polyhydroxyalkanoate synthesis repressor PhaR
NPKM_3930	1469428 +	1469872 Rmet_1360		53.00	3.00	Op0383f_2	NA	Q1LNN3 Putative uncharacterized protein
NPKM_3931	1470058 +	1471429 Rmet_1361		131.67	3.21	Op0383f_3	NA	Q1LNN2 Putative uncharacterized protein
NPKM_3932	1471528 +	1472713 Rmet_1362	<i>bktB</i>	360.67	28.02	Op0383f_4	MET-CAH-Pyr	Q1LNN1 3-ketoacyl-CoA thiolase
NPKM_3933	1472788 +	1473370 Rmet_1363		164.67	8.62	Op0383f_4	NA	Q1LNN0 Putative signal peptide protein
NPKM_3934	1473496 +	1474699 Rmet_1364	<i>metC</i>	148.33	1.53	Op0383f_4	MET-EN-Nitrog	Q1LNM9 Cystathionine beta-lyase
3UTR_1886	1474575 -	1474722 Rmet_1365				Op0384r_1		
3UTR_1247	1474700 +	1475697 Rmet_1364	<i>metC</i>			Op0383f_4		
NPKM_3935	1474723 -	1476355 Rmet_1365		3.33	0.58	Op0384r_1	NA	Q1LNM8 PepSY-associated TM helix
NPKM_3936	1476374 -	1476665 Rmet_1366		4.00	1.73	Op0384r_1	NA	Q1LNM7 Putative transmembrane protein
NPKM_3937	1476661 -	1476934 Rmet_1367		7.00	1.00	Op0384r_1	NA	Q1LNM6 Putative lipoprotein transmembrane
5UTR_1589	1476935 -	1476953 Rmet_1367				Op0384r_1		
3UTR_1885	1477032 -	1477161 Rmet_1368	<i>serB</i>			Op0384r_1		
NPKM_3938	1477162 -	1478017 Rmet_1368	<i>serB</i>	75.00	3.46	Op0384r_1	MET-AA-GlySerThr	Q1LNM5 Phosphoserine phosphatase
5UTR_1588	1478018 -	1478048 Rmet_1368	<i>serB</i>			Op0384r_1		
5UTR_1031	1478259 +	1478330 Rmet_1369	<i>cysP</i>			Op0385f_1		

NPKM_3939	1478330 +	1479338 Rmet_1369	<i>cysP</i>	8.00	1.00	Op0385f_1	EIP-TRA-ABC	Q1LNM4 Thiosulphate-binding protein
3UTR_1248	1479339 +	1479476 Rmet_1369	<i>cysP</i>			Op0385f_1		
NPKM_3940	1479577 +	1480615 Rmet_1370	<i>ssuA</i>	0.67	0.58	Op0385f_1	EIP-TRA-ABC	Q1LNM3 ABC transporter, substrate-binding protein, aliphatic sulphonates
NPKM_3941	1480642 +	1481806 Rmet_1371	<i>ssuD</i>	1.00	0.00	Op0385f_1	NA	Q1LNM2 Alkanesulfonate monooxygenase
NPKM_3942	1481818 +	1482625 Rmet_1372	<i>ssuC</i>	1.00	0.00	Op0385f_1	EIP-TRA-ABC	Q1LNM1 Binding-protein-dependent transport systems inner membrane component
3UTR_1249	1482626 +	1482633 Rmet_1372	<i>ssuC</i>			Op0385f_1		
5UTR_1032	1482635 +	1482665 Rmet_1373	<i>ssuB</i>			Op0385f_1		
NPKM_3943	1482665 +	1483541 Rmet_1373	<i>ssuB</i>	1.33	0.58	Op0385f_1	EIP-TRA-ABC	Q1LNM0 Aliphatic sulfonates import ATP-binding protein ssuB
5UTR_1033	1483567 +	1483592 Rmet_1374	<i>eal</i>			Op0385f_2		
NPKM_3944	1483592 +	1484420 Rmet_1374	<i>eal</i>	5.33	0.58	Op0385f_2	NA	Q1LNL9 Putative diguanylate phosphodiesterase (EAL domain)
NPKM_3945	1484416 +	1485082 Rmet_1375		7.67	1.15	Op0385f_2	NA	Q1LNL8 Putative uncharacterized protein
3UTR_1250	1485083 +	1485089 Rmet_1375				Op0385f_2		
5UTR_1034	1485173 +	1485320 Rmet_1376	<i>cysU</i>			Op0385f_3		
NPKM_3946	1485320 +	1486169 Rmet_1376	<i>cysU</i>	67.00	1.73	Op0385f_3	EIP-TRA-ABC	Q1LNL7 Sulfate ABC transporter, permease protein CysT
NPKM_3947	1486170 +	1487088 Rmet_1377	<i>cysW</i>	56.00	2.65	Op0385f_3	EIP-TRA-ABC	Q1LNL6 Sulfate ABC transporter, permease protein CysW
NPKM_3948	1487084 +	1488188 Rmet_1378	<i>cysA</i>	65.00	4.58	Op0385f_3	EIP-TRA-ABC	Q1LNL5 Sulphate transport system permease protein 1
NPKM_3949	1488184 +	1489135 Rmet_1379	<i>cysB</i>	79.00	5.20	Op0385f_3	NA	Q1LNL4 Transcriptional regulator, LysR family
NPKM_3950	1489377 +	1490550 Rmet_1380		17.00	1.00	Op0385f_3	NA	Q1LNL3 Histidine kinase internal region
NPKM_3951	1490575 +	1491397 Rmet_1381	<i>lytT</i>	12.33	1.15	Op0385f_3	NA	Q1LNL2 Transcriptional regulator, LytR/AlgR family
3UTR_1251	1491398 +	1491423 Rmet_1381	<i>lytT</i>			Op0385f_3		
5UTR_1035	1491440 +	1491465 Rmet_1382	<i>rraA</i>			Op0385f_4		
NPKM_3952	1491465 +	1491978 Rmet_1382	<i>rraA</i>	130.67	10.26	Op0385f_4	NA	Q1LNL1 Putative uncharacterized protein
NPKM_3953	1491981 +	1492398 Rmet_1383	<i>ytfP</i>	126.00	9.64	Op0385f_4	NA	Q1LNL0 Putative uncharacterized protein
NPKM_3954	1492489 +	1493452 Rmet_1384		34.33	0.58	Op0385f_4	NA	Q1LNK9 Alpha/beta hydrolase fold
3UTR_1252	1493453 +	1493532 Rmet_1384				Op0385f_4		
5UTR_1036	1493534 +	1493755 Rmet_1385	<i>aceA</i>			Op0385f_4		
NPKM_3955	1493755 +	1495051 Rmet_1385	<i>aceA</i>	10.00	1.73	Op0385f_4	MET-CAH-DiCarb	Q1LNK8 Isocitrate lyase
3UTR_1884	1494996 -	1495149 Rmet_1386				Op0386r_1		
3UTR_1253	1495052 +	1495100 Rmet_1385	<i>aceA</i>			Op0385f_4		
NPKM_3956	1495150 -	1496740 Rmet_1386		6.67	0.58	Op0386r_1	NA	Q1LNK7 Putative uncharacterized protein
NPKM_3957	1496856 -	1497291 Rmet_1387	<i>uspA3</i>	94.67	4.04	Op0386r_1	NA	Q1LNK6 UspA
NPKM_3958	1497448 -	1498537 Rmet_1388	<i>lysR</i>	50.00	1.73	Op0386r_1	NA	Q1LNK5 Transcriptional regulator, LysR family
5UTR_1037	1497956 +	1498573 Rmet_1389	<i>dehII</i>			Op0387f_1		
NPKM_3959	1498573 +	1499287 Rmet_1389	<i>dehII</i>	27.00	3.61	Op0387f_1	MET-XEN-Hex	Q1LNK4 Haloacid dehalogenase, type II
NPKM_3960	1499336 +	1500920 Rmet_1390	<i>aceB</i>	153.33	5.13	Op0387f_2	MET-CAH-Pyr	Q1LNK3 Malate synthase
3UTR_1883	1500881 -	1501031 Rmet_1391				Op0388r_1		
3UTR_1254	1500921 +	1500954 Rmet_1390	<i>aceB</i>			Op0387f_2		
NPKM_3961	1501032 -	1501443 Rmet_1391		44.33	1.53	Op0388r_1	NA	Q1LNK2 Glyoxalase/bleomycin resistance protein/dioxygenase
5UTR_1587	1501444 -	1501603 Rmet_1391				Op0388r_1		
NPKM_3962	1501579 +	1502158 Rmet_1392		170.67	1.53	Op0389f_1	NA	Q1LNK1 Putative uncharacterized protein
NPKM_3963	1502154 +	1503681 Rmet_1393		65.67	3.51	Op0389f_1	NA	Q1LNK0 Drug resistance transporter EmrB/QacA subfamily
3UTR_1882	1502702 -	1503680 Rmet_1394				Op0390r_1		
NPKM_3964	1503681 -	1503951 Rmet_1394		118.67	15.63	Op0390r_1	NA	Q1LNJ9 Acyl-coA-binding protein, ACBP

3UTR_1255	1503682 +	1504042 Rmet_1393					Op0389f_1		
5UTR_1586	1503952 -	1504173 Rmet_1394					Op0390r_1		
5UTR_1038	1504048 +	1504061 Rmet_1395	yeaZ				Op0391f_1		
NPKM_3965	1504061 +	1504907 Rmet_1395	yeaZ	110.00	7.21	Op0391f_1	NA	Q1LNJ8	Peptidase M22, glycoprotease
NPKM_3966	1504903 +	1505470 Rmet_1396	rimI	146.00	11.36	Op0391f_1	GIP-TL-Ass	Q1LNJ7	SSU ribosomal protein S18P alanine acetyltransferase
NPKM_3967	1505466 +	1506420 Rmet_1397		142.33	8.50	Op0391f_1	GIP-REP-DNA_Pol	Q1LNJ6	Phage SPO1 DNA polymerase-related protein
3UTR_1881	1505799 -	1507559 Rmet_1399					Op0392r_1		
NPKM_3968	1506400 +	1507510 Rmet_1398		72.33	4.04	Op0391f_1	NA	Q1LNJ5	Putative uncharacterized protein
3UTR_1256	1507511 +	1508201 Rmet_1398					Op0391f_1		
NPKM_3969	1507560 -	1508880 Rmet_1399		72.67	11.59	Op0392r_1	NA	Q1LNJ4	Major facilitator superfamily MFS_1
5UTR_1585	1508881 -	1509213 Rmet_1399					Op0392r_1		
5UTR_1039	1509049 +	1509339 Rmet_1400	dadX				Op0393f_1		
NPKM_3970	1509339 +	1510446 Rmet_1400	dadX	116.33	13.43	Op0393f_1	MET-AA-AlaAsp	Q1LNJ3	Alanine racemase
NPKM_3971	1510446 +	1511814 Rmet_1401	radA	90.67	13.65	Op0393f_1	GIP-REP-Recomb	Q1LNJ2	DNA repair protein radA
3UTR_1257	1511815 +	1511958 Rmet_1401	radA				Op0393f_1		
3UTR_1880	1511856 -	1511887 Rmet_1402					Op0394r_1		
NPKM_3972	1511888 -	1513985 Rmet_1402		45.00	1.00	Op0394r_1	NA	Q1LNJ1	Putative uncharacterized protein
5UTR_1584	1513986 -	1514362 Rmet_1402					Op0394r_1		
5UTR_1040	1514277 +	1514287 Rmet_1403	dsbB				Op0395f_1		
NPKM_3973	1514287 +	1514773 Rmet_1403	dsbB	214.33	90.43	Op0395f_1	GIP-PTL-Fold	Q1LNJ0	Disulfide bond formation protein B
3UTR_1879	1514365 -	1514867 Rmet_1404	yheS				Op0396r_1		
3UTR_1258	1514774 +	1516054 Rmet_1403	dsbB				Op0395f_1		
NPKM_3974	1514868 -	1516791 Rmet_1404	yheS	76.67	2.52	Op0396r_1	GIP-TL-Ass	Q1LNI9	ABC transporter-related protein
5UTR_1583	1516792 -	1516809 Rmet_1404	yheS				Op0396r_1		
NPKM_3975	1516969 +	1517983 Rmet_1405		19.67	2.52	Op0397f_1	NA	Q1LNI8	Transcriptional regulator, RpiR family
NPKM_3976	1518008 +	1518977 Rmet_1406	ansB	27.67	2.89	Op0397f_1	NA	Q1LNI7	Asparaginase
NPKM_3977	1518978 +	1520871 Rmet_1407	dppD1	34.00	1.00	Op0397f_1	NA	Q1LNI6	Oligopeptide/dipeptide ABC transporter, ATP-binding protein-like protein
NPKM_3978	1520899 +	1522456 Rmet_1408	dppA1b	107.00	6.56	Op0397f_2	NA	Q1LNI5	Extracellular solute-binding protein, family 5
NPKM_3979	1522672 +	1523593 Rmet_1409	dppB1	31.67	2.08	Op0397f_2	NA	Q1LNI4	Binding-protein-dependent transport systems inner membrane component
NPKM_3980	1523603 +	1524506 Rmet_1410	yliD	28.33	2.08	Op0397f_2	NA	Q1LNI3	Binding-protein-dependent transport systems inner membrane component
NPKM_3981	1524505 +	1525564 Rmet_1411	dmpA	23.33	0.58	Op0397f_2	NA	Q1LNI2	Peptidase S58, DmpA
NPKM_3982	1525560 +	1526388 Rmet_1412	dppA	20.33	2.31	Op0397f_2	EIP-TRA-ABC	Q1LNI1	D-aminopeptidase DppA. Metallo peptidase. MEROPS family M55
NPKM_3983	1526475 +	1527213 Rmet_1413		24.00	1.00	Op0397f_2	NA	Q1LNI0	Putative uncharacterized protein
NPKM_3984	1527285 +	1528371 Rmet_1414		48.00	3.61	Op0397f_2	NA	Q1LNH9	Putative uncharacterized protein
NPKM_3985	1528703 +	1531529 Rmet_1415		6.67	0.58	Op0397f_2	NA	Q1LNH8	Twin-arginine translocation pathway signal
NPKM_3986	1531525 +	1532080 Rmet_1416		7.00	1.00	Op0397f_2	NA	Q1LNH7	(2Fe-2S)-binding
NPKM_3987	1532076 +	1533342 Rmet_1417		7.67	0.58	Op0397f_2	NA	Q1LNH6	Cytochrome c, class I
3UTR_1259	1533343 +	1533433 Rmet_1417					Op0397f_2		
5UTR_1041	1533527 +	1533569 Rmet_1418					Op0397f_3		
NPKM_3988	1533569 +	1533920 Rmet_1418		323.67	0.58	Op0397f_3	NA	Q1LNH5	Putative integral membrane protein
3UTR_1878	1533764 -	1534086 Rmet_1419	prmB				Op0398r_2		
3UTR_1260	1533921 +	1533974 Rmet_1418					Op0397f_3		
NPKM_3989	1534087 -	1534981 Rmet_1419	prmB	199.33	8.14	Op0398r_2	GIP-TL-Ass	Q1LNH4	Modification methylase, HemK family

NPKM_3990	1534986 -	1536138 Rmet_1420	<i>dapE</i>	238.00	7.00	Op0398r_2	MET-AA-Lys_Syn	Q1LNH3 Succinyl diamino pimelate desuccinylase
NPKM_3991	1536156 -	1536504 Rmet_1421	<i>arsC3</i>	161.33	6.81	Op0398r_2	NA	Q1LNH2 Putative uncharacterized protein
NPKM_3992	1536520 -	1536949 Rmet_1422		245.67	7.23	Op0398r_2	NA	Q1LNH1 Twin-arginine translocation pathway signal
NPKM_3993	1536966 -	1537791 Rmet_1423	<i>dapD</i>	443.67	21.13	Op0398r_2	MET-AA-Lys_Syn	Q1LNH0 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase
NPKM_3994	1537891 -	1539124 Rmet_1424	<i>dapC</i>	193.00	6.00	Op0398r_1	NA	Q1LNG9 Succinyl diamino pimelate aminotransferase
NPKM_3995	1539191 -	1540031 Rmet_1425		273.00	17.09	Op0398r_1	NA	Q1LNG8 Putative uncharacterized protein
5UTR_1582	1540032 -	1540135 Rmet_1425				Op0398r_1		
5UTR_1042	1540253 +	1540485 Rmet_1426	<i>smc</i>			Op0399f_1		
NPKM_3996	1540485 +	1544001 Rmet_1426	<i>smc</i>	175.33	5.13	Op0399f_1	DIV-Division	Q1LNG7 Condensin subunit Smc
NPKM_3997	1544002 +	1545322 Rmet_1427		184.33	5.51	Op0399f_1	NA	Q1LNG6 Conserved hypothetical transmembrane protein
NPKM_3998	1545333 +	1547499 Rmet_1428	<i>ligA</i>	155.00	7.81	Op0399f_1	GIP-REP-Recomb	Q1LNG5 DNA ligase
NPKM_3999	1547522 +	1548056 Rmet_1429	<i>dmf</i>	244.33	8.39	Op0399f_1	NA	Q1LNG4 Peptide deformylase
3UTR_1877	1547861 -	1548042 Rmet_1430				Op0400r_1		
NPKM_4000	1548043 -	1549486 Rmet_1430		2.00	0.00	Op0400r_1	NA	Q1LNG3 Major facilitator superfamily MFS_1
3UTR_1261	1548057 +	1549430 Rmet_1429	<i>dmf</i>			Op0399f_1		
5UTR_1581	1549487 -	1549519 Rmet_1430				Op0400r_1		
5UTR_1043	1549546 +	1549605 Rmet_1431				Op0401f_1		
3UTR_1876	1549583 -	1550579 Rmet_1432	<i>rsuA1</i>			Op0402r_1		
NPKM_4001	1549605 +	1550517 Rmet_1431		45.33	2.08	Op0401f_1	NA	Q1LNG2 Transcriptional regulator, XRE family
3UTR_1262	1550518 +	1552431 Rmet_1431				Op0401f_1		
NPKM_4002	1550580 -	1552413 Rmet_1432	<i>rsuA1</i>	123.33	2.52	Op0402r_1	GIP-TL-Ass	Q1LNG1 Pseudouridine synthase, Rsu
NPKM_4003	1552440 -	1555014 Rmet_1433	<i>glnD</i>	78.33	2.08	Op0402r_1	GIP-PTL-Fold	Q1LNG0 [Protein-PilI] uridylyltransferase
NPKM_4004	1555093 -	1555912 Rmet_1434	<i>map</i>	320.67	4.04	Op0402r_1	GIP-TL-Ass	Q1LNF9 Methionine aminopeptidase
5UTR_1044	1555752 +	1556259 Rmet_1435	<i>rpsB</i>			Op0403f_1		
5UTR_1580	1555913 -	1555959 Rmet_1434	<i>map</i>			Op0402r_1		
NPKM_4005	1556259 +	1557003 Rmet_1435	<i>rpsB</i>	3096.33	52.27	Op0403f_1	GIP-TL-Ribo	Q1LNF8 30S ribosomal protein S2
NPKM_4006	1557230 +	1558109 Rmet_1436	<i>tsf</i>	1329.67	30.55	Op0403f_1	NA	Q1LNF7 Elongation factor Ts
NPKM_4007	1558347 +	1559124 Rmet_1437	<i>pyrH</i>	297.33	13.20	Op0403f_1	NA	Q1LNF6 Uridylate kinase
NPKM_4008	1559232 +	1559793 Rmet_1438	<i>frr</i>	744.67	24.95	Op0403f_2	NA	Q1LNF5 Ribosome-recycling factor
NPKM_4009	1559845 +	1560616 Rmet_1439	<i>uppS</i>	485.67	8.14	Op0403f_2	Met-SecMetab	Q1LNF4 Undecaprenyl pyrophosphate synthetase
NPKM_4010	1560658 +	1561480 Rmet_1440	<i>cdsA</i>	300.67	16.20	Op0403f_2	MET-LIP-GlycPLip	Q1LNF3 Phosphatidate cytidyltransferase
NPKM_4011	1561511 +	1562690 Rmet_1441	<i>dxr</i>	256.67	12.90	Op0403f_2	MET-LIP-Ster	Q1LNF2 1-deoxy-D-xylulose 5-phosphate reductoisomerase
NPKM_4012	1562731 +	1564123 Rmet_1442	<i>yaeL</i>	135.67	8.50	Op0403f_2	NA	Q1LNF1 RseP peptidase. Metallo peptidase. MEROPS family M50B
NPKM_4013	1564199 +	1566575 Rmet_1443	<i>yaeT</i>	644.67	24.01	Op0403f_3	NA	Q1LNF0 Surface antigen (D15)
NPKM_4014	1566596 +	1567130 Rmet_1444	<i>hlpA</i>	923.33	29.74	Op0403f_3	NA	Q1LNE9 Outer membrane chaperone Skp (OmpH)
NPKM_4015	1567182 +	1568292 Rmet_1445	<i>lpxD</i>	316.67	7.57	Op0403f_3	MET-GLYC-LPS	Q1LNE8 UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase
NPKM_4016	1568288 +	1568741 Rmet_1446	<i>fabZ</i>	378.67	16.65	Op0403f_3	MET-LIP-FASyn	Q1LNE7 (3R)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase
NPKM_4017	1568780 +	1569584 Rmet_1447	<i>lpxA</i>	481.00	16.37	Op0403f_3	MET-GLYC-LPS	Q1LNE6 Acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O-acyltransferase
NPKM_4018	1569596 +	1570802 Rmet_1448	<i>lpxB</i>	291.33	21.50	Op0403f_3	MET-GLYC-LPS	Q1LNE5 Lipid-A-disaccharide synthase
NPKM_4019	1570801 +	1571482 Rmet_1449	<i>rnhB</i>	183.33	12.66	Op0403f_3	GIP-REP-Recomb	Q1LNE4 Ribonuclease HII
NPKM_4020	1571491 +	1572280 Rmet_1450	<i>rlmB</i>	134.00	6.56	Op0403f_3	GIP-TL-Ass	Q1LNE3 tRNA/rRNA methyltransferase (SpoU)
3UTR_1875	1572012 -	1572312 Rmet_1451				Op0404r_1		
NPKM_4021	1572313 -	1572853 Rmet_1451		50.33	0.58	Op0404r_1	NA	Q1LNE2 Putative uncharacterized protein

NPKM_4022	1572943 -	1573756 Rmet_1452		220.33	6.81	Op0404r_1	NA	Q1LNE1 Putative phosphotransferase Rmet_1452
5UTR_1579	1573757 -	1573917 Rmet_1452				Op0404r_1		
NPKM_4023	1574129 +	1576514 Rmet_1453	<i>pps</i>	433.00	19.08	Op0405f_1	MET-CAH-Pyr	Q1LNE0 Phosphoenolpyruvate synthase
NPKM_4024	1576694 +	1577129 Rmet_1454		97.00	4.00	Op0405f_1	NA	Q1LND9 Putative uncharacterized protein
NPKM_4025	1577178 +	1578117 Rmet_1455	<i>ybbK</i>	151.33	9.71	Op0405f_1	NA	Q1LND8 SPFH domain, Band 7 family protein
3UTR_1874	1578075 -	1578201 Rmet_1456	<i>smpB</i>			Op0406r_1		
3UTR_1263	1578118 +	1578165 Rmet_1455	<i>ybbK</i>			Op0405f_1		
NPKM_4026	1578202 -	1578655 Rmet_1456	<i>smpB</i>	102.00	1.73	Op0406r_1	GIP-PTL-Fold	Q1LND7 SsrA-binding protein
5UTR_1045	1578389 +	1578693 Rmet_6449				Op0407f_1		
NPKM_4027	1578693 +	1578822 Rmet_6449		7.00	3.00	Op0407f_1	NA	NA
NPKM_4028	1578831 +	1579281 Rmet_1457	<i>yfiG</i>	128.33	7.51	Op0407f_2	NA	Q1LND6 Cyclase/dehydrase
NPKM_4029	1579255 +	1579621 Rmet_1458	<i>yfiF</i>	196.00	4.00	Op0407f_2	NA	Q1LND5 Putative uncharacterized protein
NPKM_4030	1579786 -	1580326 Rmet_1459		1086.00	42.00	Op0408r_2	NA	Q1LND4 Putative transmembrane protein
NPKM_4031	1580420 -	1581380 Rmet_1460	<i>ytfF</i>	16.33	1.15	Op0408r_1	NA	Q1LND3 Putative transmembrane protein
5UTR_1578	1581381 -	1581921 Rmet_1460	<i>ytfF</i>			Op0408r_1		
NPKM_4032	1581505 +	1582969 Rmet_1461	<i>guaB</i>	1227.33	20.03	Op0409f_1	MET-NUC-Pur	Q1LND2 Inosine-5'-monophosphate dehydrogenase
3UTR_1873	1581926 -	1587869 Rmet_1468				Op0412r_1		
NPKM_4033	1583056 +	1583698 Rmet_1462		308.67	21.08	Op0409f_1	NA	Q1LND1 Putative transmembrane protein
NPKM_4034	1583672 +	1585292 Rmet_1463	<i>guaA</i>	365.33	17.62	Op0409f_1	MET-NUC-Pur	Q1LND0 GMP synthase (Glutamine-hydrolyzing)
NPKM_4035	1585593 +	1586850 Rmet_1465	<i>int</i>	83.33	11.06	Op0411f_1	NA	Q1LNC8 Phage integrase
NPKM_4036	1587050 +	1587326 Rmet_1466		103.00	14.00	Op0411f_1	NA	Q1LNC7 Putative uncharacterized protein
NPKM_4037	1587330 +	1587855 Rmet_1467		148.00	8.89	Op0411f_1	NA	Q1LNC6 Prophage CP4-57 regulatory
NPKM_4038	1587870 -	1588281 Rmet_1468		64.33	8.39	Op0412r_1	NA	Q1LNC5 Phage transcriptional regulator, AlpA
NPKM_4039	1588374 -	1589124 Rmet_1469		121.67	9.81	Op0412r_1	GIP-PTL-Exp	Q1LNC4 TatD-related deoxyribonuclease
NPKM_4040	1589137 -	1590505 Rmet_1470		191.33	13.32	Op0412r_1	NA	Q1LNC3 Putative uncharacterized protein
NPKM_4041	1590501 -	1591383 Rmet_1471		225.67	20.74	Op0412r_1	NA	Q1LNC2 Putative uncharacterized protein
NPKM_4042	1591382 -	1593317 Rmet_1472		296.00	28.79	Op0412r_1	NA	Q1LNC1 KAP P-loop
NPKM_4043	1593335 -	1594307 Rmet_1473		631.67	83.76	Op0412r_1	NA	Q1LNC0 Retron reverse transcriptase
NPKM_4044	1594272 -	1594578 Rmet_6450		1460.00	160.56	Op0412r_1	NA	NA
NPKM_4045	1594630 -	1594870 Rmet_1474		2594.00	131.10	Op0412r_1	NA	Q1LNB9 Putative uncharacterized protein
5UTR_1577	1594871 -	1595230 Rmet_1474				Op0412r_1		
NPKM_4046	1595651 +	1596002 Rmet_1475		2.33	0.58	Op0413f_1	NA	Q1LNB8 Putative uncharacterized protein
3UTR_1872	1595810 -	1596100 Rmet_1476				Op0414r_1		
NPKM_4047	1596101 -	1596440 Rmet_1476		3.33	0.58	Op0414r_1	NA	Q1LNB7 Putative uncharacterized protein
NPKM_4048	1596747 +	1597578 Rmet_1477	<i>yupB</i>	0.67	0.58	Op0415f_1	NA	Q1LNB6 Putative uncharacterized protein
NPKM_4049	1597642 +	1599685 Rmet_1478	<i>parB</i>	1.33	0.58	Op0415f_1	NA	Q1LNB5 ParB family protein
3UTR_1871	1599825 -	1599886 Rmet_1479				Op0416r_1		
NPKM_4050	1599887 -	1600910 Rmet_1479		34.67	2.52	Op0416r_1	NA	Q1LNB4 Putative uncharacterized protein
5UTR_1576	1600911 -	1601306 Rmet_1479				Op0416r_1		
NPKM_4051	1601775 +	1602090 Rmet_1480		7.67	0.58	Op0417f_1	NA	Q1LNB3 Putative uncharacterized protein
3UTR_1870	1601855 -	1602446 Rmet_1481	<i>ycdN</i>			Op0418r_1		
NPKM_4052	1602447 -	1602741 Rmet_1481	<i>ycdN</i>	59.00	3.00	Op0418r_1	NA	A9IL07 Predicted transcriptional regulator
5UTR_1575	1602742 -	1603494 Rmet_1481	<i>ycdN</i>			Op0418r_1		

NPKM_4053	1602956 +	1603304 Rmet_1482		3.67	1.15	Op0419f_1	NA	Q1LNB1 Putative lipoprotein
NPKM_4054	1603647 +	1604439 Rmet_1483		1.67	0.58	Op0419f_1	NA	Q1LNB0 Putative uncharacterized protein
NPKM_4055	1604477 +	1604804 Rmet_1484		0.00	0.00	Op0419f_1	NA	Q1LNA9 Putative uncharacterized protein
NPKM_4056	1604818 +	1605688 Rmet_1485	<i>repA</i>	0.67	0.58	Op0419f_2	NA	Q1LNA8 Conserved hypothetical replication initiator and transcription repressor prot
NPKM_4057	1605941 +	1606580 Rmet_1486	<i>parA</i>	2.33	0.58	Op0419f_3	DIV-Division	Q1LNA7 Cobyrinic acid a,c-diamide synthase
NPKM_4058	1606576 +	1606861 Rmet_6451	<i>parG</i>	1.33	0.58	Op0419f_3	NA	NA
NPKM_4059	1606857 +	1607400 Rmet_1487		0.33	0.58	Op0419f_3	NA	Q1LNA6 Putative uncharacterized protein
NPKM_4060	1607396 +	1607984 Rmet_1488	<i>traF</i>	0.67	0.58	Op0419f_3	NA	Q1LNA5 TraF peptidase. Serine peptidase. MEROPS family S26C
NPKM_4061	1608306 +	1610409 Rmet_1489	<i>virD2</i>	1.33	0.58	Op0419f_3	NA	Q1LNA4 Putative uncharacterized protein
3UTR_1869	1609977 -	1610416 Rmet_1490				Op0420r_1		
NPKM_4062	1610417 -	1611011 Rmet_1490		13.00	1.73	Op0420r_1	NA	Q1LNA3 Transcriptional regulator, AraC family
5UTR_1574	1611012 -	1611088 Rmet_1490				Op0420r_1		
NPKM_4063	1611194 +	1614110 Rmet_1491	<i>tnpA</i>	0.00	0.00	Op0421f_1	NA	Q6SKD6 Transposase
NPKM_4064	1614222 -	1615083 Rmet_1492	<i>cbbA1</i>	8.00	0.00	Op0422r_1	MET-CAH-FbP	Q1LNA1 Fructose-bisphosphate aldolase
NPKM_4065	1615176 -	1615350 Rmet_1493		19.00	2.65	Op0422r_1	NA	Q1LNA0 Putative uncharacterized protein
NPKM_4066	1615528 -	1615732 Rmet_1494	<i>cbbY (del</i>	16.00	2.65	Op0422r_1	NA	Q1LN99 Putative uncharacterized protein
NPKM_4067	1615744 -	1615948 Rmet_1495	<i>cbbY (del</i>	23.67	3.51	Op0422r_1	NA	Q1LN98 Putative uncharacterized protein
NPKM_4068	1615993 -	1616368 Rmet_1496		20.67	2.31	Op0422r_1	NA	Q1LN97 Putative uncharacterized protein
NPKM_4069	1616383 -	1616680 Rmet_1497		37.33	7.09	Op0422r_1	NA	Q1LN96 Putative uncharacterized protein
NPKM_4070	1616688 -	1619046 Rmet_1498	<i>cbbO</i>	44.67	3.79	Op0422r_1	NA	Q1LN95 von Willebrand factor, type A
NPKM_4071	1619058 -	1619862 Rmet_1499	<i>cbbQ</i>	83.67	6.35	Op0422r_1	MET-EN-Nitrog	Q1LN94 ATPase associated with various cellular activities, AAA_5
NPKM_4072	1620011 -	1620368 Rmet_1500	<i>cbbS</i>	330.33	16.26	Op0422r_1	MET-CAH-DiCarb	Q1LN93 Ribulose bisphosphate carboxylase small chain
NPKM_4073	1620445 -	1621867 Rmet_1501	<i>cbbL</i>	303.67	26.39	Op0422r_1	MET-CAH-DiCarb	Q1LN92 Ribulose bisphosphate carboxylase large chain
5UTR_1573	1621868 -	1621894 Rmet_1501	<i>cbbL</i>			Op0422r_1		
NPKM_4074	1621991 +	1622873 Rmet_1502	<i>cbbR1</i>	36.33	3.51	Op0423f_1	NA	Q1LN91 Transcriptional regulator, LysR family
NPKM_4075	1622911 +	1623031 Rmet_6452		22.67	4.93	Op0423f_1	NA	NA
NPKM_4076	1623051 +	1624302 Rmet_1503	<i>tnpA</i>	0.00	0.00	Op0423f_1	GIP-REP-Recomb	Q9RBF5 Ralstonia eutropha insertion sequence IS1090
3UTR_1868	1624300 -	1624304 Rmet_1504				Op0424r_3		
NPKM_4077	1624305 -	1624614 Rmet_1504		4.33	1.15	Op0424r_3	NA	Q1LN89 Putative uncharacterized protein
5UTR_1572	1624615 -	1624708 Rmet_1504				Op0424r_3		
3UTR_1867	1624710 -	1624711 Rmet_1505				Op0424r_3		
NPKM_4078	1624712 -	1625294 Rmet_1505		3.00	1.00	Op0424r_3	NA	Q1LN88 ISSod11, transposase
NPKM_4079	1625590 -	1628506 Rmet_1506	<i>tnpA</i>	0.00	0.00	Op0424r_2	NA	Q6SKD6 Transposase
NPKM_4080	1628604 -	1629444 Rmet_1507	<i>cbbF1</i>	8.67	1.53	Op0424r_2	MET-CAH-FbP	Q1LN86 D-fructose 1,6-bisphosphatase
NPKM_4081	1629649 -	1629802 Rmet_6453		192.33	36.91	Op0424r_2	NA	NA
NPKM_4082	1629951 -	1630875 Rmet_1508	<i>cbbR2</i>	30.67	1.53	Op0424r_1	NA	Q1LN85 Transcriptional regulator, LysR family
NPKM_4083	1630980 +	1631145 Rmet_1509	<i>cbbS(delta</i>	19.00	2.65	Op0425f_1	NA	Q1LN84 Putative uncharacterized protein
NPKM_4084	1631162 +	1631861 Rmet_1510	<i>cbbE1</i>	22.00	2.65	Op0425f_1	MET-CAH-PP_KDPG	Q1LN83 Ribulose-5-phosphate 3-epimerase
NPKM_4085	1632040 +	1633138 Rmet_1511	<i>cbbF2</i>	13.67	0.58	Op0425f_1	MET-CAH-FbP	Q1LN82 D-fructose 1,6-bisphosphatase
NPKM_4086	1633170 +	1634055 Rmet_1512	<i>cbbP</i>	19.00	1.00	Op0425f_1	MET-EN-CalCyc	Q1LN81 Phosphoribulokinase
NPKM_4087	1634054 +	1636109 Rmet_1513	<i>cbbT1</i>	19.33	1.53	Op0425f_1	MET-CAH-PP_KDPG	Q1LN80 Transketolase
NPKM_4088	1636110 +	1636842 Rmet_1514	<i>cbbZ1</i>	15.33	1.15	Op0425f_1	MET-CAH-DiCarb	Q1LN79 Phosphoglycolate phosphatase
NPKM_4089	1636838 +	1637846 Rmet_1515	<i>cbbG1</i>	27.00	2.00	Op0425f_1	MET-CAH-FbP	Q1LN78 Glyceraldehyde-3-phosphate dehydrogenase

NPKM_4090	1637842 +	1639033 Rmet_1516	<i>pgk1</i>	23.33	1.15	Op0425f_1	NA	NA
NPKM_4091	1639029 +	1639848 Rmet_1517	<i>cbbY</i>	17.00	1.00	Op0425f_1	NA	Q1LN76 HAD-superfamily hydrolase subfamily IA, variant 3
NPKM_4092	1639907 +	1640945 Rmet_1518	<i>cbbA2</i>	21.33	2.08	Op0425f_1	MET-CAH-FbP	Q1LN75 Fructose-bisphosphate aldolase
NPKM_4093	1640959 +	1642378 Rmet_1519	<i>pykA2</i>	19.00	1.00	Op0425f_1	MET-CAH-FbP	Q1LN74 Pyruvate kinase
NPKM_4094	1642413 +	1643232 Rmet_1520	<i>cbbJ1</i>	9.67	0.58	Op0425f_1	MET-CAH-FbP	Q1LN73 Triosephosphate isomerase
NPKM_4095	1643231 +	1643891 Rmet_1521	<i>cbbI1</i>	10.67	2.31	Op0425f_1	MET-CAH-PP_KDPG	Q1LN72 Ribose-5-phosphate isomerase
NPKM_4096	1644016 +	1645825 Rmet_1522	<i>hoxF</i>	203.67	8.74	Op0425f_2	MET-CAH-DiCarb	Q1LN71 Respiratory-chain NADH dehydrogenase domain, 51 kDa subunit
NPKM_4097	1645821 +	1646532 Rmet_1523	<i>hoxU</i>	246.67	3.79	Op0425f_2	MET-CAH-DiCarb	Q1LN70 Ferredoxin
NPKM_4098	1646528 +	1647158 Rmet_1524	<i>hoxY</i>	256.00	9.00	Op0425f_2	MET-CAH-DiCarb	Q1LN69 NADH ubiquinone oxidoreductase, 20 kDa subunit
NPKM_4099	1647175 +	1648642 Rmet_1525	<i>hoxH</i>	354.00	5.57	Op0425f_2	MET-CAH-DiCarb	Q1LN68 Nickel-dependent hydrogenase, large subunit
NPKM_4100	1648625 +	1649132 Rmet_1526	<i>hoxW</i>	348.00	6.08	Op0425f_2	NA	Q1LN67 HoxW protein
NPKM_4101	1649144 +	1649648 Rmet_1527	<i>hoxI</i>	812.00	11.79	Op0425f_3	NA	Q1LN66 Cyclic nucleotide-binding domain (CNMP-BD) protein
NPKM_4102	1649984 +	1650716 Rmet_1528	<i>pntAA'</i>	225.00	8.54	Op0425f_3	NA	Q1LN65 Alanine dehydrogenase/PNT-like protein
NPKM_4103	1650746 -	1651775 Rmet_1529	<i>tnpA</i>	0.00	0.00	Op0426r_1	NA	Q1LB62 Integrase, catalytic region
NPKM_4104	1651819 +	1652236 Rmet_1530	<i>pntAA'</i>	10.00	1.00	Op0427f_1	NA	Q1LN63 Alanine dehydrogenase/PNT-like protein
NPKM_4105	1652236 +	1652542 Rmet_1531	<i>pntAB</i>	3.67	1.15	Op0427f_1	MET-COF-NicAm	Q1LN62 Pyridine nucleotide transhydrogenase subunit alpha
NPKM_4106	1652538 +	1653912 Rmet_1532	<i>pntB</i>	2.33	0.58	Op0427f_1	MET-COF-NicAm	Q1LN61 NAD(P) transhydrogenase, beta subunit
NPKM_4107	1653973 +	1654810 Rmet_1533	<i>hoxN</i>	72.67	6.51	Op0427f_2	EIP-TRA-Ion	Q1LN60 High-affinity nickel-transporter
NPKM_4108	1655014 +	1655209 Rmet_6454		70.00	6.56	Op0427f_2	NA	NA
NPKM_4109	1655262 +	1655568 Rmet_1534		295.33	33.86	Op0427f_3	NA	Q1LN59 Putative uncharacterized protein
NPKM_4110	1655560 +	1655902 Rmet_1535	<i>hypA2</i>	963.67	120.62	Op0427f_4	GIP-PTL-Fold	Q1LN58 Hydrogenase nickel insertion protein HypA
NPKM_4111	1655935 +	1656916 Rmet_1536	<i>hypB2</i>	1215.00	78.54	Op0427f_4	GIP-PTL-Fold	Q1LN57 Hydrogenase accessory protein HypB
NPKM_4112	1656929 +	1659287 Rmet_1537	<i>hypF2</i>	560.33	35.02	Op0427f_4	GIP-PTL-Fold	Q1LN56 (NiFe) hydrogenase maturation protein HypF
NPKM_4113	1659339 +	1659528 Rmet_1538	<i>hypC2</i>	487.67	52.58	Op0427f_4	GIP-PTL-Fold	Q1LN55 Hydrogenase assembly chaperone hypC/hupF
NPKM_4114	1659524 +	1660667 Rmet_1539	<i>hypD2</i>	566.33	37.45	Op0427f_4	GIP-PTL-Fold	Q1LN54 Hydrogenase expression/formation protein HypD
NPKM_4115	1660740 +	1661790 Rmet_1540	<i>hypE2</i>	429.33	25.15	Op0427f_4	GIP-PTL-Fold	Q1LN53 Hydrogenase expression/formation protein HypE
NPKM_4116	1661888 +	1663628 Rmet_1541	<i>hoxX</i>	244.67	20.98	Op0427f_4	NA	Q1LN52 Formyl transferase-like protein
NPKM_4117	1663624 +	1664554 Rmet_1542	<i>hoxA</i>	236.67	14.57	Op0427f_4	NA	Q1LN51 Response regulator receiver domain protein (CheY-like)
NPKM_4118	1663966 -	1664401 Rmet_6455		0.00	0.00	Op0428r_1	NA	NA
NPKM_4119	1664543 -	1664927 Rmet_1543	<i>cbbA (del)</i>	0.00	0.00	Op0428r_1	NA	Q1LN50 Stress responsive alpha-beta barrel
NPKM_4120	1665102 +	1668018 Rmet_1544	<i>tnpA</i>	0.00	0.00	Op2008f_1	NA	NA
NPKM_4121	1668180 -	1668588 Rmet_1545		4.67	1.15	Op0430r_1	NA	Q1LN48 Putative uncharacterized protein
5UTR_1571	1668589 -	1668622 Rmet_1545				Op0430r_1		
NPKM_4122	1668623 +	1669604 Rmet_1546	<i>traR</i>	14.67	1.53	Op0431f_1	NA	Q1LN47 Transcriptional regulator, LysR family
NPKM_4123	1669600 +	1669879 Rmet_1547		24.67	2.08	Op0431f_1	NA	Q1LN46 Putative lipoprotein
NPKM_4124	1670130 +	1672125 Rmet_1548	<i>traG</i>	0.00	0.00	Op0431f_1	GIP-PTL-T4S	Q1LN45 TRAG protein
NPKM_4125	1672121 +	1672586 Rmet_1549		0.00	0.00	Op0431f_1	NA	NA
NPKM_4126	1672582 +	1673659 Rmet_1550	<i>trbB</i>	0.00	0.00	Op0431f_1	GIP-PTL-T4S	Q1LN43 Type II secretion system protein E
NPKM_4127	1673655 +	1674039 Rmet_1551	<i>trbC</i>	0.00	0.00	Op0431f_1	GIP-PTL-T4S	A6V7M4 Conjugal transfer protein TrbC
NPKM_4128	1674035 +	1674308 Rmet_1552	<i>trbD</i>	0.00	0.00	Op0431f_1	GIP-PTL-T4S	Q1LN41 Putative conjugal transfer trbD transmembrane protein
NPKM_4129	1674323 +	1676753 Rmet_1553	<i>trbE</i>	0.00	0.00	Op0431f_1	GIP-PTL-T4S	Q1LN40 ATPase
NPKM_4130	1676749 +	1677475 Rmet_1554	<i>trbI</i>	0.00	0.00	Op0431f_1	NA	Q1LN39 Putative conjugal transfer TrbI signal peptide protein
NPKM_4131	1677487 +	1677820 Rmet_1555		0.33	0.58	Op0431f_2	NA	Q1LN38 Putative lipoprotein

NPKM_4132	1677816 +	1679202 Rmet_1556	<i>trbL</i>	0.00	0.00	Op0431f_2	GIP-PTL-T4S	Q1LN37 TrbL/VirB6 plasmid conjugal transfer protein
NPKM_4133	1679214 +	1679919 Rmet_1557	<i>trbF</i>	0.00	0.00	Op0431f_2	GIP-PTL-T4S	Q1LN36 Conjugal transfer protein
NPKM_4134	1679915 +	1680917 Rmet_1558	<i>trbG</i>	0.00	0.00	Op0431f_2	GIP-PTL-T4S	Q1LN35 Conjugal transfer protein TrbG/VirB9/CagX
NPKM_4135	1680919 +	1682188 Rmet_1559	<i>trbI</i>	1.00	0.00	Op0431f_3	GIP-PTL-T4S	Q1LN34 Conjugation TrbI-like protein
NPKM_4136	1682184 +	1682445 Rmet_1560		1.33	0.58	Op0431f_3	NA	Q1LN33 Putative uncharacterized protein
NPKM_4137	1682539 +	1683277 Rmet_1561		45.33	1.53	Op0431f_4	NA	Q1LN32 Putative uncharacterized protein
NPKM_4138	1683273 +	1684194 Rmet_1562		44.67	5.03	Op0431f_4	NA	Q1LN31 Putative uncharacterized protein
3UTR_1264	1684195 +	1684461 Rmet_1562				Op0431f_4		
NPKM_4139	1684482 +	1685010 Rmet_1563	<i>tnpA</i>	9.67	0.58	Op0431f_4	GIP-REP-Recomb	Q1LN30 ISRSO11-transposase orfA protein
NPKM_4140	1685009 +	1685846 Rmet_1564	<i>tnpB</i>	15.33	1.15	Op0431f_4	NA	Q1LN29 Integrase, catalytic region
3UTR_1866	1685838 -	1685942 Rmet_1565				Op0432r_1		
3UTR_1265	1685847 +	1686108 Rmet_1564	<i>tnpB</i>			Op0431f_4		
NPKM_4141	1685943 -	1687476 Rmet_1565		10.33	0.58	Op0432r_1	NA	Q1LN28 FAD dependent oxidoreductase
NPKM_4142	1687538 -	1688372 Rmet_1566		11.67	2.08	Op0432r_1	NA	Q1LN27 Alpha/beta hydrolase fold
NPKM_4143	1688472 -	1689258 Rmet_1567		24.33	5.03	Op0432r_1	NA	Q1LN26 Transcriptional regulator, TetR family
NPKM_4144	1689493 -	1689913 Rmet_1568		53.67	3.21	Op0432r_1	NA	Q1LN25 Transcriptional regulator
NPKM_4145	1690033 -	1690630 Rmet_1569		41.33	1.53	Op0432r_1	NA	Q1LN24 Putative uncharacterized protein
5UTR_1046	1690940 +	1691001 Rmet_1570				Op0433f_1		
NPKM_4146	1691001 +	1691514 Rmet_1570		72.00	3.00	Op0433f_1	NA	Q1LN23 Putative uncharacterized protein
NPKM_4147	1691692 +	1692328 Rmet_1571		250.67	19.09	Op0433f_2	NA	Q1LN22 Putative uncharacterized protein
NPKM_4148	1692331 +	1692808 Rmet_1572	<i>ptpS</i>	154.67	11.59	Op0433f_2	MET-COF-Folate	Q1LN21 Putative uncharacterized protein
NPKM_4149	1692829 +	1693399 Rmet_1573	<i>tadA</i>	137.33	7.77	Op0433f_2	NA	Q1LN20 tRNA-adenosine deaminase
NPKM_4150	1693395 +	1694316 Rmet_1574	<i>ldcA</i>	187.00	7.55	Op0433f_2	NA	Q1LN19 Peptidase U61, LD-carboxypeptidase A
NPKM_4151	1694500 +	1696123 Rmet_1575		229.33	7.02	Op0433f_2	NA	Q1LN18 ABC transporter-related protein
3UTR_1865	1695516 -	1696196 Rmet_1576				Op0434r_1		
NPKM_4152	1696197 -	1696881 Rmet_1576		78.67	3.21	Op0434r_1	NA	Q1LN17 Putative proline-rich protein
5UTR_1570	1696882 -	1697035 Rmet_1576				Op0434r_1		
NPKM_4153	1697103 +	1698534 Rmet_1577	<i>betB</i>	298.33	23.25	Op0435f_1	MET-AA-GlySerThr	Q1LN16 Aldehyde dehydrogenase
NPKM_4154	1698625 +	1701091 Rmet_1578		34.67	1.53	Op0435f_1	Met-SecMetab	Q1LN15 Peptidase S45, penicillin amidase
NPKM_4155	1701212 +	1701941 Rmet_1579		74.33	3.21	Op0435f_2	MET-NUC-Pur	Q1LN14 Glutamine amidotransferase class-I
3UTR_1864	1701570 -	1702674 Rmet_1581				Op0436r_1		
NPKM_4156	1701940 +	1702648 Rmet_1580		70.33	3.51	Op0435f_2	NA	Q1LN13 MOSC domain protein
NPKM_4157	1702675 -	1702927 Rmet_1581		85.67	3.51	Op0436r_1	NA	Q1LN12 Putative uncharacterized protein
NPKM_4158	1703080 +	1703521 Rmet_1582		11.33	1.15	Op0437f_1	NA	Q1LN11 Phenylacetic acid degradation-related protein
3UTR_1266	1703522 +	1704366 Rmet_1582				Op0437f_1		
NPKM_4159	1703542 -	1704670 Rmet_1583	<i>ansB</i>	908.00	68.56	Op0438r_3	MET-EN-Nitrog	Q1LN10 Asparaginase
5UTR_1569	1704671 -	1704777 Rmet_1583	<i>ansB</i>			Op0438r_3		
3UTR_1863	1704798 -	1704943 Rmet_1584				Op0438r_2		
NPKM_4160	1704944 -	1706138 Rmet_1584		106.00	3.61	Op0438r_2	NA	Q1LN09 Methylitaconate delta2-delta3-isomerase
NPKM_4161	1706152 -	1708750 Rmet_1585	<i>acnA1</i>	88.00	3.61	Op0438r_2	MET-CAH-TCA	Q1LN08 Aconitase
NPKM_4162	1708846 -	1710004 Rmet_1586	<i>prpC</i>	122.67	4.04	Op0438r_2	MET-CAH-Prop	Q1LN07 2-methylcitrate synthase
NPKM_4163	1710062 -	1710971 Rmet_1587	<i>prpB</i>	33.67	3.06	Op0438r_1	MET-CAH-Prop	Q1LN06 2,3-dimethylmalate lyase
5UTR_1568	1710972 -	1711191 Rmet_1587	<i>prpB</i>			Op0438r_1		

5UTR_1047	1711254 +	1711363 Rmet_1588	<i>prpR</i>			Op0439f_1		
NPKM_4164	1711363 +	1713265 Rmet_1588	<i>prpR</i>	25.00	1.00	Op0439f_1	NA	Q1LN05 Putative PAS/PAC sensor protein
3UTR_1862	1712531 -	1713408 Rmet_1589				Op0440r_2		
3UTR_1267	1713266 +	1713923 Rmet_1588	<i>prpR</i>			Op0439f_1		
NPKM_4165	1713409 -	1714699 Rmet_1589		44.67	4.04	Op0440r_2	NA	Q1LN04 Putative uncharacterized protein
5UTR_1567	1714700 -	1714735 Rmet_1589				Op0440r_2		
5UTR_1048	1714838 +	1715607 Rmet_1591				Op0441f_1		
3UTR_1861	1714843 -	1714906 Rmet_1590	<i>azoR1</i>			Op0440r_1		
NPKM_4166	1714907 -	1715531 Rmet_1590	<i>azoR1</i>	9.33	0.58	Op0440r_1	NA	Q1LN03 NAD(P)H dehydrogenase (Quinone)
NPKM_4167	1715607 +	1716147 Rmet_1591		287.67	6.11	Op0441f_1	NA	Q1LN02 Transcriptional regulator, LysR family
3UTR_1268	1716148 +	1716191 Rmet_1591				Op0441f_1		
NPKM_4168	1716177 -	1717206 Rmet_1592	<i>tnpA</i>	0.00	0.00	Op2009r_1	NA	NA
5UTR_1049	1717210 +	1717250 Rmet_1593				Op0443f_1		
NPKM_4169	1717250 +	1717793 Rmet_1593		14.00	0.00	Op0443f_1	NA	Q1LN00 Transcriptional regulatory protein
NPKM_4170	1717949 +	1718363 Rmet_1594		42.33	3.51	Op0443f_2	NA	Q1LMZ9 DoxX
NPKM_4171	1718376 +	1718961 Rmet_1595		41.00	1.73	Op0443f_2	NA	Q1LMZ8 Putative lipoprotein
NPKM_4172	1719120 +	1722492 Rmet_1596	<i>ftsK</i>	41.67	1.53	Op0443f_2	EIP-TRA-Other	Q1LMZ7 DNA translocase FtsK
NPKM_4173	1722502 +	1722850 Rmet_1597		33.67	3.79	Op0443f_2	NA	Q1LMZ6 Cupin 2, conserved barrel
NPKM_4174	1722931 +	1724482 Rmet_1598		23.33	1.15	Op0443f_2	EIP-TRA-ABC	Q1LMZ5 Substrate-binding region of ABC-type glycine betaine transport system
NPKM_4175	1724500 +	1725817 Rmet_1599		82.33	6.43	Op0443f_3	NA	Q1LMZ4 Cytochrome c, class I
NPKM_4176	1725813 +	1727646 Rmet_1600		69.67	7.09	Op0443f_3	MET-AA-Urea	Q1LMZ3 Twin-arginine translocation pathway signal
3UTR_1860	1726467 -	1727753 Rmet_1601				Op0444r_2		
NPKM_4177	1727754 -	1728192 Rmet_1601		116.67	21.08	Op0444r_2	NA	Q1LMZ2 Transcriptional regulator, MarR family
5UTR_1566	1728193 -	1728224 Rmet_1601				Op0444r_2		
3UTR_1859	1728404 -	1728411 Rmet_6456				Op0444r_1		
NPKM_4178	1728412 -	1728478 Rmet_6456		0.33	0.58	Op0444r_1	NA	NA
NPKM_4179	1728557 +	1729835 Rmet_1602		13.67	3.79	Op0445f_1	NA	Q1LMZ1 Glyceraldehyde 3-phosphate dehydrogenase
3UTR_1269	1729836 +	1729991 Rmet_1602				Op0445f_1		
NPKM_4180	1729889 -	1730429 Rmet_1603		3.67	0.58	Op0446r_1	NA	Q1LMZ0 Alkylhydroperoxidase AhpD core
5UTR_1565	1730430 -	1730446 Rmet_1603				Op0446r_1		
NPKM_4181	1730581 +	1731532 Rmet_1604		22.67	1.15	Op0447f_1	NA	Q1LMY9 Transcriptional regulator, AraC family
NPKM_4182	1731572 +	1732490 Rmet_1605		14.67	0.58	Op0447f_1	NA	Q1LMY8 Transcriptional regulator, LysR family
NPKM_4183	1732494 -	1732659 Rmet_6457		0.33	0.58	Op2010r_1	NA	NA
NPKM_4184	1732537 +	1733098 Rmet_1606		9.33	0.58	Op0447f_1	EIP-TRA-Pores	Q1LMY7 LrgA
5UTR_1564	1732660 -	1732710 Rmet_6457				Op2010r_1		
NPKM_4185	1733099 +	1733825 Rmet_1607		5.33	0.58	Op0447f_1	NA	Q1LMY6 LrgB-like protein
3UTR_1858	1733224 -	1733871 Rmet_1608				Op0448r_1		
3UTR_1270	1733826 +	1734187 Rmet_1607				Op0447f_1		
NPKM_4186	1733872 -	1735279 Rmet_1608		39.00	3.61	Op0448r_1	NA	Q1LMY5 FAD linked oxidase-like protein
NPKM_4187	1735390 -	1737100 Rmet_1609		35.33	2.08	Op0448r_1	NA	Q1LMY4 Transcriptional regulator, GntR family
5UTR_1050	1737089 +	1737098 Rmet_1610	<i>dapE</i>			Op0449f_1		
NPKM_4188	1737098 +	1738442 Rmet_1610	<i>dapE</i>	9.33	1.53	Op0449f_1	MET-AA-Urea	Q1LMY3 Acetylornithine deacetylase or succinyl-diaminopimelate desuccinylase
5UTR_1563	1737101 -	1737134 Rmet_1609				Op0448r_1		

3UTR_1857	1738267 -	1738437 Rmet_6458				Op2011r_1		
NPKM_4189	1738438 -	1738621 Rmet_6458		4.00	1.00	Op2011r_1	NA	NA
3UTR_1271	1738443 +	1738542 Rmet_1610	dapE			Op0449f_1		
NPKM_4190	1738544 +	1739291 Rmet_1611		2.67	0.58	Op0449f_1	EIP-TRA-ABC	Q1LMY2 Extracellular solute-binding protein, family 5
5UTR_1562	1738622 -	1739331 Rmet_6458				Op2011r_1		
3UTR_1272	1739292 +	1739328 Rmet_1611				Op0449f_1		
NPKM_4191	1739333 -	1740227 Rmet_1612	tnpB	0.00	0.00	Op0450r_1	NA	B2UH78 Integrase catalytic region
NPKM_4192	1740223 -	1740520 Rmet_1613	tnpA	0.00	0.00	Op0450r_1	NA	Q58AB8 OrfA protein (Transposase IS3/IS911)
NPKM_4193	1740582 +	1741434 Rmet_1614		0.67	0.58	Op0451f_1	EIP-TRA-ABC	Q1LMX9 Putative solute-binding transport protein (Periplasmic)
3UTR_1273	1741435 +	1741441 Rmet_1614				Op0451f_1		
NPKM_4194	1741483 +	1742506 Rmet_1615	dppB	0.33	0.58	Op0451f_1	EIP-TRA-ABC	Q1LMX8 Binding-protein-dependent transport systems inner membrane component
NPKM_4195	1742502 +	1743342 Rmet_1616	dppC	0.33	0.58	Op0451f_1	EIP-TRA-ABC	Q1LMX7 Binding-protein-dependent transport systems inner membrane component
5UTR_1051	1743349 +	1743353 Rmet_1617				Op0451f_1		
NPKM_4196	1743353 +	1744997 Rmet_1617		0.33	0.58	Op0451f_1	EIP-TRA-ABC	Q1LMX6 ABC transporter-related protein
NPKM_4197	1745039 +	1746302 Rmet_1618	puuE	1.00	0.00	Op0451f_2	MET-CAH-Prop	Q1LMX5 4-aminobutyrate aminotransferase
NPKM_4198	1746324 +	1746624 Rmet_1619		1.33	1.15	Op0451f_2	NA	Q1LMX4 Putative uncharacterized protein
NPKM_4199	1746620 +	1748324 Rmet_1620	ilvG	1.67	0.58	Op0451f_2	MET-CAH-But	Q1LMX3 Thiamine pyrophosphate enzyme-like TPP binding region
NPKM_4200	1748371 +	1749445 Rmet_1621		1.00	0.00	Op0451f_2	NA	Q1LMX2 Histone deacetylase superfamily
3UTR_1274	1749446 +	1749450 Rmet_1621				Op0451f_2		
NPKM_4201	1749458 +	1750715 Rmet_1622	amaB-1	2.33	0.58	Op0451f_3	NA	Q1LMX1 Amidase, hydantoinase/carbamoylase
NPKM_4202	1750711 +	1752211 Rmet_1623	puuC	2.67	0.58	Op0451f_3	MET-AA-Urea	Q1LMX0 Aldehyde dehydrogenase (Acceptor)
3UTR_1856	1752001 -	1752243 Rmet_1624				Op0452r_1		
3UTR_1275	1752212 +	1752329 Rmet_1623	puuC			Op0451f_3		
NPKM_4203	1752244 -	1753843 Rmet_1624		5.33	0.58	Op0452r_1	NA	Q1LMW9 Drug resistance transporter EmrB/QacA subfamily
5UTR_1052	1753874 +	1753925 Rmet_1625				Op0453f_1		
NPKM_4204	1753925 +	1754396 Rmet_1625		51.00	3.46	Op0453f_1	NA	Q1LMW8 Transcriptional regulator, MarR family
3UTR_1855	1754044 -	1754312 Rmet_1626				Op0454r_1		
NPKM_4205	1754313 -	1755750 Rmet_1626		19.00	1.00	Op0454r_1	EIP-SIG-2Comp	Q1LMW7 Sensor protein
3UTR_1276	1754397 +	1754792 Rmet_1625				Op0453f_1		
NPKM_4206	1755746 -	1756439 Rmet_1627		68.67	6.43	Op0454r_1	EIP-SIG-2Comp	Q1LMW6 Two component transcriptional regulator, winged helix family
5UTR_1561	1756440 -	1756477 Rmet_1627				Op0454r_1		
5UTR_1053	1756617 +	1756657 Rmet_1628				Op0455f_1		
NPKM_4207	1756657 +	1757722 Rmet_1628		200.33	11.72	Op0455f_1	NA	Q1LMW5 Porin, Gram-negative type
3UTR_1854	1757802 -	1757840 Rmet_1629				Op0456r_1		
NPKM_4208	1757841 -	1758327 Rmet_1629		6.33	0.58	Op0456r_1	NA	Q1LMW4 Glutathione-dependent formaldehyde-activating, GFA
5UTR_1560	1758328 -	1758436 Rmet_1629				Op0456r_1		
NPKM_4209	1758599 +	1759814 Rmet_1630		31.00	1.73	Op0457f_1	NA	Q1LMW3 Sodium/hydrogen exchanger
3UTR_1853	1758803 -	1759870 Rmet_1631				Op0458r_1		
3UTR_1277	1759815 +	1760467 Rmet_1630				Op0457f_1		
NPKM_4210	1759871 -	1760807 Rmet_1631		68.33	3.21	Op0458r_1	NA	Q1LMW2 Transcriptional regulator, LysR family
NPKM_4211	1760806 -	1761718 Rmet_1632	garR	103.67	2.89	Op0458r_1	MET-CAH-DiCarb	Q1LMW1 2-hydroxy-3-oxopropionate reductase
NPKM_4212	1761741 -	1762527 Rmet_1633	garL	108.00	4.36	Op0458r_1	MET-CAH-Ascorb	Q1LMW0 5-dehydro-4-deoxy-D-glucarate aldolase
NPKM_4213	1762542 -	1763637 Rmet_1634	ybiC	83.67	3.06	Op0458r_1	NA	Q1LMV9 Malate/L-lactate dehydrogenase

NPKM_4214	1763639 -	1764641 Rmet_1635	<i>bug</i>	59.33	4.93	Op0458r_1	NA	Q1LMV8 Uncharacterized protein UPF0065
5UTR_1054	1764775 +	1764890 Rmet_1636				Op0459f_1		
NPKM_4215	1764890 +	1766570 Rmet_1636		47.33	5.86	Op0459f_1	MET-CAH-But	Q1LMV7 Thiamine pyrophosphate enzyme-like TPP-binding
3UTR_1278	1766571 +	1766762 Rmet_1636				Op0459f_1		
NPKM_4216	1766628 -	1766946 Rmet_1637		139.33	25.54	Op0460r_1	NA	Q1LMV6 Putative uncharacterized protein
5UTR_1559	1766947 -	1766958 Rmet_1637				Op0460r_1		
NPKM_4217	1767069 +	1767243 Rmet_6459		0.33	0.58	Op0461f_1	NA	NA
3UTR_1279	1767244 +	1767387 Rmet_6459				Op0461f_1		
5UTR_1055	1767479 +	1767488 Rmet_1638	<i>pyc</i>			Op0461f_2		
NPKM_4218	1767488 +	1770992 Rmet_1638	<i>pyc</i>	2.33	0.58	Op0461f_2	MET-CAH-TCA	Q1LMV5 Pyruvate carboxylase
3UTR_1280	1770993 +	1771042 Rmet_1638	<i>pyc</i>			Op0461f_2		
3UTR_1852	1771100 -	1771125 Rmet_1639				Op0462r_3		
NPKM_4219	1771126 -	1772230 Rmet_1639		3.67	0.58	Op0462r_3	NA	Q1LMV4 Porin, Gram-negative type
5UTR_1558	1772231 -	1772579 Rmet_1639				Op0462r_3		
3UTR_1851	1772582 -	1772605 Rmet_1640				Op0462r_3		
NPKM_4220	1772606 -	1773845 Rmet_1640		19.67	1.15	Op0462r_3	EIP-TRA-ABC	Q1LMV3 Putative UreA/short-chain amide ABC transporter
NPKM_4221	1773927 -	1774986 Rmet_1641		55.33	1.53	Op0462r_3	NA	Q1LMV2 Putative uncharacterized protein
NPKM_4222	1775216 -	1775531 Rmet_1642		686.00	73.00	Op0462r_3	NA	Q1LMV1 Putative uncharacterized protein
5UTR_1557	1775532 -	1775589 Rmet_1642				Op0462r_3		
3UTR_1850	1775591 -	1775616 Rmet_1643				Op0462r_2		
NPKM_4223	1775617 -	1776067 Rmet_1643		31.67	1.53	Op0462r_2	NA	Q1LMV0 Putative uncharacterized protein
NPKM_4224	1776203 -	1777904 Rmet_1644		123.33	5.13	Op0462r_2	NA	Q1LMU9 Beta-lactamase-like protein
NPKM_4225	1777995 -	1780365 Rmet_1645	<i>polB</i>	20.33	1.15	Op0462r_1	GIP-REP-DNA_Pol	Q1LMU8 DNA polymerase
5UTR_1556	1780366 -	1780380 Rmet_1645	<i>polB</i>			Op0462r_1		
5UTR_1056	1780410 +	1780503 Rmet_1646				Op0463f_1		
NPKM_4226	1780503 +	1782177 Rmet_1646		18.00	3.46	Op0463f_1	NA	Q1LMU7 MscS Mechanosensitive ion channel
3UTR_1849	1782069 -	1782194 Rmet_1647				Op0464r_1		
3UTR_1281	1782178 +	1782976 Rmet_1646				Op0463f_1		
NPKM_4227	1782195 -	1782924 Rmet_1647		3.00	0.00	Op0464r_1	NA	Q1LMU6 Putative transmembrane protein
NPKM_4228	1782920 -	1783520 Rmet_1648	<i>rpoP</i>	9.67	1.53	Op0464r_1	GIP-TK-RNAP	Q1LMU5 Sigma-24 (FecI-like)
5UTR_1555	1783521 -	1783631 Rmet_1648	<i>rpoP</i>			Op0464r_1		
NPKM_4229	1783671 +	1784292 Rmet_1649		0.67	0.58	Op0465f_1	NA	Q1LMU4 Putative uncharacterized protein
3UTR_1848	1784415 -	1784419 Rmet_1650	<i>creD</i>			Op0466r_3		
NPKM_4230	1784420 -	1785863 Rmet_1650	<i>creD</i>	1.67	0.58	Op0466r_3	NA	Q1LMU3 Inner membrane CreD
NPKM_4231	1785984 -	1787430 Rmet_1651	<i>creC</i>	12.00	0.00	Op0466r_3	EIP-SIG-2Comp	Q1LMU2 Sensor protein
NPKM_4232	1787448 -	1788147 Rmet_1652	<i>creB</i>	17.00	0.00	Op0466r_3	EIP-SIG-2Comp	Q1LMU1 Two component transcriptional regulator, winged helix family
NPKM_4233	1788169 -	1789384 Rmet_1653		5.00	0.00	Op0466r_2	NA	Q1LMU0 Monooxygenase, FAD-binding
5UTR_1554	1789385 -	1789420 Rmet_1653				Op0466r_2		
3UTR_1847	1789442 -	1789470 Rmet_1654				Op0466r_1		
NPKM_4234	1789471 -	1790029 Rmet_1654		0.67	0.58	Op0466r_1	GIP-TL-Ass	Q1LMT9 SmpA/OmlA
NPKM_4235	1789986 -	1790172 Rmet_6460		0.33	0.58	Op0466r_1	NA	NA
5UTR_1553	1790173 -	1790175 Rmet_6460				Op0466r_1		
NPKM_4236	1790272 -	1790455 Rmet_1655		0.67	1.15	Op0466r_1	NA	Q1LMT8 Putative uncharacterized protein

5UTR_1057	1790643 +	1790793 Rmet_1656	<i>yqjG</i>			Op0467f_1			
NPKM_4237	1790793 +	1791780 Rmet_1656	<i>yqjG</i>	21.00	1.00	Op0467f_1	GIP-PTL-Fold	Q1LMT7 Glutathione S-transferase-like protein	
3UTR_1282	1791781 +	1792627 Rmet_1656	<i>yqjG</i>			Op0467f_1			
3UTR_1846	1792147 -	1792156 Rmet_1657				Op0468r_4			
NPKM_4238	1792157 -	1793579 Rmet_1657		6.67	0.58	Op0468r_4	NA	Q1LMT6 Putative uncharacterized protein	
NPKM_4239	1793591 -	1794161 Rmet_1658		31.33	2.08	Op0468r_4	NA	Q1LMT5 Putative uncharacterized protein	
5UTR_1552	1794162 -	1794272 Rmet_1658				Op0468r_4			
3UTR_1845	1794579 -	1794649 Rmet_1659				Op0468r_3			
NPKM_4240	1794650 -	1794761 Rmet_1659		4.00	2.00	Op0468r_3	NA	Q1LMT4 Addiction module toxin, Txe/YoeB	
NPKM_4241	1794804 -	1795596 Rmet_1660	<i>tnp</i>	5.33	1.15	Op0468r_3	NA	Q1LMT3 Transposase and inactivated derivatives-like protein	
3UTR_1844	1795636 -	1795766 Rmet_6461				Op0468r_3			
NPKM_4242	1795767 -	1796001 Rmet_6461		12.67	1.53	Op0468r_3	NA	NA	
5UTR_1058	1795849 +	1795999 Rmet_1661				Op0469f_1			
NPKM_4243	1795999 +	1796209 Rmet_1661		6.33	1.15	Op0469f_1	NA		0
NPKM_4244	1796224 +	1796413 Rmet_6462		7.67	1.53	Op0469f_1	NA	NA	
NPKM_4245	1796395 -	1796566 Rmet_6463		26.33	6.51	Op0468r_3	NA	NA	
NPKM_4246	1796409 -	1796658 Rmet_6464		28.33	5.51	Op0468r_3	NA	NA	
3UTR_1283	1796414 +	1797026 Rmet_6462				Op0469f_1			
NPKM_4247	1796578 -	1797052 Rmet_1662		34.33	1.53	Op0468r_3	NA		0
NPKM_4248	1797400 +	1797484 Rmet_6465		1.67	1.53	Op2012f_1	NA	NA	
NPKM_4249	1797424 -	1798252 Rmet_1663	<i>papD</i>	7.67	0.58	Op0468r_2	NA	Q1LMT2 Pili assembly chaperone	
3UTR_1284	1797485 +	1797638 Rmet_6465				Op2012f_1			
NPKM_4250	1798316 -	1799744 Rmet_1664		12.67	0.58	Op0468r_2	NA	Q1LMT1 Putative uncharacterized protein	
NPKM_4251	1799750 -	1802540 Rmet_1665	<i>papC</i>	8.00	1.00	Op0468r_2	NA	Q1LMT0 Fimbrial biogenesis outer membrane usher protein	
NPKM_4252	1802541 -	1803300 Rmet_1666	<i>fimC</i>	2.00	1.00	Op0468r_1	NA	Q1LMS9 Pili assembly chaperone	
NPKM_4253	1803379 -	1803919 Rmet_1667	<i>fimA</i>	17.00	1.00	Op0468r_1	NA	Q1LMS8 Fimbrial protein	
5UTR_1551	1803920 -	1804151 Rmet_1667	<i>fimA</i>			Op0468r_1			
NPKM_4254	1804903 +	1805929 Rmet_1668	<i>tnp</i>	0.00	0.00	Op0469f_1	NA	Q1LMS7 Transposase and inactivated derivatives-like protein	
NPKM_4255	1805906 +	1806902 Rmet_1669		2.00	0.00	Op0469f_2	NA	Q1LMS6 Dipeptidyl aminopeptidase/acylaminoacyl-peptidase	
3UTR_1285	1806903 +	1806950 Rmet_1669				Op0469f_2			
NPKM_4256	1807125 +	1807230 Rmet_1670		0.67	0.58	Op0469f_2	NA	Q1LMS5 Putative uncharacterized protein	
3UTR_1286	1807231 +	1807322 Rmet_1670				Op0469f_2			
3UTR_1843	1807309 -	1807367 Rmet_1671	<i>phaC2</i>			Op0470r_2			
NPKM_4257	1807368 -	1809087 Rmet_1671	<i>phaC2</i>	2.00	0.00	Op0470r_2	MET-CAH-But	Q1LMS4 Poly(R)-hydroxyalkanoic acid synthase, class I	
NPKM_4258	1809083 -	1809524 Rmet_1672		0.33	0.58	Op0470r_1	NA	Q1LMS3 MaoC-like dehydratase	
5UTR_1550	1809525 -	1809571 Rmet_1672				Op0470r_1			
5UTR_1059	1809577 +	1809738 Rmet_1673				Op0471f_1			
NPKM_4259	1809738 +	1810062 Rmet_1673		3.00	1.00	Op0471f_1	NA	Q1LMS2 Putative uncharacterized protein	
NPKM_4260	1810133 +	1813415 Rmet_1674		14.33	1.53	Op0471f_2	NA	Q1LMS1 Membrane protein-like protein	
NPKM_4261	1813411 +	1814740 Rmet_1675		13.33	0.58	Op0471f_2	NA	Q1LMS0 Putative transmembrane protein	
NPKM_4262	1815061 +	1815493 Rmet_1676	<i>uspA4</i>	13.67	2.52	Op0471f_2	NA	Q1LMR9 UspA	
NPKM_4263	1815540 +	1815981 Rmet_1677	<i>uspA5</i>	24.33	2.52	Op0471f_2	NA	Q1LMR8 UspA	
NPKM_4264	1816224 +	1816452 Rmet_6466		8.67	2.89	Op0471f_2	NA	NA	

NPKM_4265	1816554 +	1817031 Rmet_1678		4.00	1.00	Op0471f_2	NA	Q1LMR7 Putative uncharacterized protein
3UTR_1287	1817032 +	1817039 Rmet_1678				Op0471f_2		
3UTR_1842	1817092 -	1817158 Rmet_1679				Op0472r_1		
NPKM_4266	1817159 -	1817324 Rmet_1679		7.33	0.58	Op0472r_1	NA	Q1LMR6 Phage integrase
5UTR_1060	1817341 +	1817366 Rmet_1680				Op0473f_1		
NPKM_4267	1817366 +	1817708 Rmet_1680		4.67	0.58	Op0473f_1	NA	Q1LMR5 Putative uncharacterized protein
3UTR_1288	1817709 +	1818095 Rmet_1680				Op0473f_1		
NPKM_4268	1817804 -	1818947 Rmet_1681	aroG	27.33	1.53	Op0474r_1	MET-AA-PheTyrTrp	Q1LMR4 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase
5UTR_1061	1818847 +	1819237 Rmet_1682				Op0475f_1		
5UTR_1549	1818948 -	1819030 Rmet_1681	aroG			Op0474r_1		
NPKM_4269	1819237 +	1820473 Rmet_1682		6.67	0.58	Op0475f_1	NA	Q1LMR3 Major facilitator superfamily MFS_1
3UTR_1841	1820300 -	1820558 Rmet_1683				Op0476r_2		
3UTR_1289	1820474 +	1820575 Rmet_1682				Op0475f_1		
NPKM_4270	1820559 -	1821753 Rmet_1683		18.00	2.65	Op0476r_2	NA	Q1LMR2 ABC-type multidrug transport system permease component
NPKM_4271	1821752 -	1824512 Rmet_1684	rbbA	34.33	2.31	Op0476r_2	NA	Q1LMR1 Response regulator receiver domain protein (CheY-like)
NPKM_4272	1824522 -	1825590 Rmet_1685		45.33	5.51	Op0476r_2	EIP-TRA-ABC	Q1LMR0 Secretion protein HlyD
NPKM_4273	1825602 -	1827153 Rmet_1686		40.67	4.73	Op0476r_2	NA	Q1LMQ9 RND efflux system, outer membrane lipoprotein, NodT
5UTR_1548	1827154 -	1827203 Rmet_1686				Op0476r_2		
3UTR_1840	1827234 -	1827362 Rmet_1687				Op0476r_1		
NPKM_4274	1827297 +	1827570 Rmet_6467		3.00	1.73	Op2013f_1	NA	NA
NPKM_4275	1827363 -	1827744 Rmet_1687		4.33	1.53	Op0476r_1	NA	Q1LMQ8 Putative uncharacterized protein
3UTR_1290	1827571 +	1827906 Rmet_6467				Op2013f_1		
5UTR_1547	1827745 -	1828182 Rmet_1687				Op0476r_1		
5UTR_1062	1827908 +	1828104 Rmet_1688				Op0477f_1		
NPKM_4276	1828104 +	1829745 Rmet_1688		6.67	0.58	Op0477f_1	NA	Q1LMQ7 Diguanylate cyclase (GGDEF domain) with PAS/PAC sensor
3UTR_1839	1828664 -	1829809 Rmet_1689				Op0478r_2		
3UTR_1291	1829746 +	1830466 Rmet_1688				Op0477f_1		
NPKM_4277	1829810 -	1830845 Rmet_1689		7.00	1.00	Op0478r_2	NA	Q1LMQ6 Diguanylate phosphodiesterase (EAL domain)
5UTR_1546	1830846 -	1830881 Rmet_1689				Op0478r_2		
NPKM_4278	1831139 -	1831229 Rmet_6468		0.33	0.58	Op0478r_1	NA	NA
5UTR_1545	1831230 -	1831313 Rmet_6468				Op0478r_1		
NPKM_4279	1831247 +	1831565 Rmet_1690	flhD1	1.00	1.00	Op0479f_1	EIP-SIG-2Comp	Q1LMQ5 Flagellar transcriptional activator
NPKM_4280	1831580 +	1832222 Rmet_1691	flhC1	44.33	5.13	Op0479f_2	EIP-SIG-2Comp	Q1LMQ4 Flagellar transcriptional activator FlhC
3UTR_1292	1832223 +	1832405 Rmet_1691	flhC1			Op0479f_2		
NPKM_4281	1832332 -	1832533 Rmet_6469		0.00	0.00	Op0480r_1	NA	NA
NPKM_4282	1832541 -	1833276 Rmet_1692	fnr	2.33	0.58	Op0480r_1	NA	Q1LMQ3 Transcriptional regulator, Crp/Fnr family
5UTR_1063	1833084 +	1833257 Rmet_6470				Op2014f_1		
NPKM_4283	1833257 +	1833449 Rmet_6470		3.67	0.58	Op2014f_1	NA	NA
5UTR_1544	1833277 -	1833279 Rmet_1692	fnr			Op0480r_1		
3UTR_1838	1833414 -	1833450 Rmet_1693				Op0480r_1		
3UTR_1293	1833450 +	1834191 Rmet_6470				Op2014f_1		
NPKM_4284	1833451 -	1834675 Rmet_1693		1.33	0.58	Op0480r_1	NA	Q1LMQ2 Methyl-accepting chemotaxis sensory transducer
5UTR_1543	1834676 -	1834681 Rmet_1693				Op0480r_1		

3UTR_1837	1835083 -	1835227	Rmet_1694				Op0480r_1		
NPKM_4285	1835228 -	1836302	Rmet_1694		14.67	3.79	Op0480r_1	NA	Q1LMQ1 Putative uncharacterized protein
5UTR_1542	1836303 -	1836360	Rmet_1694				Op0480r_1		
5UTR_1064	1836364 +	1836399	Rmet_1695				Op0481f_1		
NPKM_4286	1836399 +	1837869	Rmet_1695		19.67	6.43	Op0481f_1	NA	Q1LMQ0 Putative uncharacterized protein
NPKM_4287	1837327 +	1837918	Rmet_6471		16.67	6.35	Op0481f_1	NA	NA
NPKM_4288	1837905 +	1838820	Rmet_1696		22.33	8.50	Op0481f_1	NA	Q1LMP9 Putative uncharacterized protein
3UTR_1294	1838821 +	1838896	Rmet_1696				Op0481f_1		
3UTR_1836	1838844 -	1838876	Rmet_6472				Op2015r_1		
NPKM_4289	1838877 -	1838973	Rmet_6472		0.33	0.58	Op2015r_1	NA	NA
5UTR_1065	1838992 +	1839377	Rmet_1697				Op0481f_1		
NPKM_4290	1839377 +	1840331	Rmet_1697		33.67	8.08	Op0481f_1	NA	Q1LMP8 Sensor protein
NPKM_4291	1840341 +	1840917	Rmet_1698		60.33	17.10	Op0481f_1	NA	Q1LMP7 Two component transcriptional regulator, LuxR family
NPKM_4292	1841039 +	1841414	Rmet_1699		37.33	17.21	Op0481f_1	NA	Q1LMP6 Response regulator receiver domain protein (CheY-like)
NPKM_4293	1841543 +	1841798	Rmet_1700		90.00	25.12	Op0481f_2	NA	Q1LMP5 Putative uncharacterized protein
NPKM_4294	1841877 +	1843116	Rmet_1701	acrA	69.33	17.90	Op0481f_2	EIP-TRA-Other	Q1LMP4 Secretion protein HlyD
NPKM_4295	1843112 +	1846304	Rmet_1702	acrF	45.00	15.62	Op0481f_2	EIP-TRA-Ion	Q1LMP3 Hydrophobe/amphiphile efflux-1 HAE1
NPKM_4296	1846300 +	1847761	Rmet_1703	acrC	48.67	16.74	Op0481f_2	NA	Q1LMP2 RND efflux system, outer membrane lipoprotein, NodT
NPKM_4297	1847765 +	1848239	Rmet_1704		72.00	23.07	Op0481f_2	NA	Q1LMP1 Putative uncharacterized protein
NPKM_4298	1848279 +	1848867	Rmet_1705		120.00	40.45	Op0481f_2	NA	Q1LMP0 Putative uncharacterized protein
NPKM_4299	1848903 +	1849290	Rmet_1706		111.00	32.05	Op0481f_2	NA	Q1LMN9 Putative uncharacterized protein
3UTR_1295	1849291 +	1850113	Rmet_1706				Op0481f_2		
3UTR_1835	1849337 -	1849366	Rmet_1707				Op0482r_1		
NPKM_4300	1849367 -	1850186	Rmet_1707		7.33	3.21	Op0482r_1	NA	Q1LMN8 Putative uncharacterized protein
5UTR_1066	1850274 +	1850276	Rmet_1708				Op0483f_1		
NPKM_4301	1850276 +	1850648	Rmet_1708		57.67	7.37	Op0483f_1	NA	Q1LMN7 Putative uncharacterized protein
NPKM_4302	1850697 +	1851864	Rmet_1709		31.00	6.08	Op0483f_1	NA	Q1LMN6 Putative uncharacterized protein
NPKM_4303	1851866 +	1853426	Rmet_1710		11.33	2.31	Op0483f_1	NA	Q1LMN5 RND efflux system, outer membrane lipoprotein, NodT
NPKM_4304	1853422 +	1854559	Rmet_1711		5.67	0.58	Op0483f_1	NA	Q1LMN4 Secretion protein HlyD
NPKM_4305	1854548 +	1855613	Rmet_1712		3.33	0.58	Op0483f_1	NA	Q1LMN3 Membrane protein, putative
3UTR_1834	1854608 -	1856082	Rmet_1714				Op0484r_2		
NPKM_4306	1855629 +	1856079	Rmet_1713		2.67	0.58	Op0483f_1	NA	Q1LMN2 Ion transport 2
3UTR_1296	1856080 +	1856092	Rmet_1713				Op0483f_1		
NPKM_4307	1856083 -	1856506	Rmet_1714		159.00	19.47	Op0484r_2	NA	Q1LMN1 Putative uncharacterized protein
NPKM_4308	1856502 -	1857630	Rmet_1715		51.33	6.66	Op0484r_1	NA	Q1LMN0 Transcriptional regulator, AraC family
5UTR_1541	1857631 -	1857790	Rmet_1715				Op0484r_1		
NPKM_4309	1857710 +	1858691	Rmet_1716	qor	1.67	0.58	Op0485f_1	NA	Q1LMM9 Alcohol dehydrogenase, zinc-binding
NPKM_4310	1858701 +	1859550	Rmet_1717	tauD	1.33	0.58	Op0485f_1	MET-OAA-Taur	Q1LMM8 Taurine catabolism dioxygenase TauD/TfdA
3UTR_1297	1859551 +	1859561	Rmet_1717	tauD			Op0485f_1		
5UTR_1067	1859563 +	1859567	Rmet_1718				Op0485f_1		
NPKM_4311	1859567 +	1861214	Rmet_1718		2.33	0.58	Op0485f_1	MET-LIP-FASyn	Q1LMM7 AMP-dependent synthetase and ligase
NPKM_4312	1861210 +	1861396	Rmet_6473		0.67	0.58	Op0485f_1	NA	NA
3UTR_1298	1861397 +	1861406	Rmet_6473				Op0485f_1		

NPKM_4313	1861428 +	1862412 Rmet_1719	<i>bug</i>	6.67	1.15	Op0485f_2	NA	Q1LMM6 Uncharacterized protein UPF0065
3UTR_1833	1861846 -	1862436 Rmet_1720				Op0486r_1		
3UTR_1299	1862413 +	1862677 Rmet_1719	<i>bug</i>			Op0485f_2		
NPKM_4314	1862437 -	1863370 Rmet_1720		6.67	0.58	Op0486r_1	NA	Q1LMM5 Transcriptional regulator, IclR family
NPKM_4315	1863368 +	1864988 Rmet_1721	<i>pccB</i>	0.33	0.58	Op0487f_1	NA	Q1LMM4 Carboxyl transferase
NPKM_4316	1865057 +	1866224 Rmet_1722		1.33	0.58	Op0487f_2	NA	Q1LMM3 Acyl-CoA dehydrogenase-like protein
NPKM_4317	1866232 +	1867066 Rmet_1723		1.67	0.58	Op0487f_2	NA	Q1LMM2 Enoyl-CoA hydratase/isomerase
5UTR_1068	1867070 +	1867094 Rmet_1724	<i>accC</i>			Op0487f_2		
NPKM_4318	1867094 +	1869092 Rmet_1724	<i>accC</i>	2.00	0.00	Op0487f_2	NA	Q1LMM1 Carbamoyl-phosphate synthase L chain, ATP-binding
NPKM_4319	1869088 +	1870972 Rmet_1725		2.33	0.58	Op0487f_2	NA	Q1LMM0 Putative uncharacterized protein
NPKM_4320	1871005 +	1872019 Rmet_1726	<i>bug</i>	2.33	0.58	Op0487f_2	NA	Q1LML9 Uncharacterized protein UPF0065
NPKM_4321	1872128 -	1873346 Rmet_1727		2.33	0.58	Op0488r_1	NA	Q1LML8 L-carnitine dehydratase/bile acid-inducible protein F
5UTR_1540	1873347 -	1873387 Rmet_1727				Op0488r_1		
NPKM_4322	1873538 +	1874306 Rmet_1728		31.00	3.00	Op0489f_1	NA	Q46NG6 General substrate transporter:Major facilitator superfamily MFS_1
NPKM_4323	1874305 +	1874938 Rmet_6474		21.67	3.79	Op0489f_1	NA	NA
3UTR_1300	1874939 +	1876416 Rmet_6474				Op0489f_1		
3UTR_1832	1875077 -	1875121 Rmet_1730				Op0490r_1		
NPKM_4324	1875122 -	1875323 Rmet_1730		0.67	0.58	Op0490r_1	NA	Q1LML7 Putative uncharacterized protein
NPKM_4325	1875331 -	1876390 Rmet_1731		1.33	0.58	Op0490r_1	NA	Q1LML6 Putative uncharacterized protein
5UTR_1069	1876421 +	1876509 Rmet_1732				Op0491f_1		
NPKM_4326	1876509 +	1877532 Rmet_1732		71.67	5.69	Op0491f_1	NA	Q1LML5 Transcriptional regulator, AraC family
3UTR_1831	1877519 -	1877663 Rmet_1733				Op0492r_2		
3UTR_1301	1877533 +	1880065 Rmet_1732				Op0491f_1		
NPKM_4327	1877664 -	1878861 Rmet_1733		4.67	0.58	Op0492r_2	NA	Q1LML4 Porin, Gram-negative type
5UTR_1539	1878862 -	1878893 Rmet_1733				Op0492r_2		
NPKM_4328	1878972 -	1879542 Rmet_1734		0.67	0.58	Op0492r_1	NA	Q1LML3 Putative uncharacterized protein
3UTR_1830	1879556 -	1879568 Rmet_1735				Op0492r_1		
NPKM_4329	1879569 -	1880901 Rmet_1735		1.00	0.00	Op0492r_1	NA	Q1LML2 Major facilitator superfamily MFS_1
5UTR_1538	1880902 -	1880926 Rmet_1735				Op0492r_1		
5UTR_1070	1881072 +	1881188 Rmet_1736	<i>cybB</i>			Op0493f_1		
NPKM_4330	1881188 +	1881746 Rmet_1736	<i>cybB</i>	85.33	5.51	Op0493f_1	NA	Q1LML1 Cytochrome B561
3UTR_1829	1881550 -	1881724 Rmet_1737				Op0494r_1		
NPKM_4331	1881725 -	1883219 Rmet_1737		2.67	0.58	Op0494r_1	NA	Q1LML0 RND efflux system, outer membrane lipoprotein, NodT
3UTR_1302	1881747 +	1882592 Rmet_1736	<i>cybB</i>			Op0493f_1		
NPKM_4332	1883222 -	1885199 Rmet_1738		2.33	0.58	Op0494r_1	MET-CAH-Starch	Q1LMK9 Glycosyl transferase, family 2
NPKM_4333	1885213 -	1886569 Rmet_1739		2.67	1.15	Op0494r_1	NA	Q1LMK8 Putative uncharacterized protein
NPKM_4334	1886639 -	1887971 Rmet_1740		4.67	1.15	Op0494r_1	NA	Q1LMK7 Putative membrane protein
5UTR_1537	1887972 -	1888223 Rmet_1740				Op0494r_1		
5UTR_1071	1888292 +	1888431 Rmet_1741	<i>uspA6</i>			Op0495f_1		
NPKM_4335	1888431 +	1888863 Rmet_1741	<i>uspA6</i>	98.67	4.93	Op0495f_1	NA	Q1LMK6 UspA
NPKM_4336	1889075 +	1889915 Rmet_1742		46.00	1.73	Op0495f_1	NA	Q1LMK5 Putative uncharacterized protein
NPKM_4337	1889914 +	1890772 Rmet_1743		15.33	1.15	Op0495f_1	NA	Q1LMK4 Transcriptional regulator, AraC family
3UTR_1828	1890373 -	1890803 Rmet_1744				Op0496r_1		

3UTR_1303	1890773 +	1891183 Rmet_1743				Op0495f_1		
NPKM_4338	1890804 -	1892658 Rmet_1744		15.00	0.00	Op0496r_1	MET-LIP-FASyn	Q1LMK3 AMP-dependent synthetase and ligase
NPKM_4339	1893094 -	1893640 Rmet_1745		34.33	2.31	Op0496r_1	NA	Q1LMK2 Putative uncharacterized protein
5UTR_1072	1893797 +	1893800 Rmet_1746				Op0497f_1		
NPKM_4340	1893800 +	1894040 Rmet_1746		1.33	1.15	Op0497f_1	NA	Q1LMK1 Putative transposase protein
NPKM_4341	1894005 -	1894539 Rmet_1747		46.00	7.00	Op0498r_2	NA	Q1LMK0 Putative uncharacterized protein
3UTR_1304	1894041 +	1894070 Rmet_1746				Op0497f_1		
NPKM_4342	1894767 -	1896234 Rmet_1748	agrC	3.00	0.00	Op0498r_1	NA	Q1LMJ9 RND efflux system, outer membrane lipoprotein, NodT
NPKM_4343	1896233 -	1897430 Rmet_1749	agrB	3.00	0.00	Op0498r_1	NA	Q1LMJ8 Secretion protein HlyD
NPKM_4344	1897426 -	1900624 Rmet_1750	agrA	2.00	0.00	Op0498r_1	NA	Q1LMJ7 Acriflavin resistance protein
5UTR_1073	1900756 +	1900802 Rmet_1751	agrR			Op0499f_1		
NPKM_4345	1900802 +	1901477 Rmet_1751	agrR	15.67	1.53	Op0499f_1	EIP-SIG-2Comp	Q1LMJ6 Two component heavy metal response transcriptional regulator, winged he
NPKM_4346	1901476 +	1902886 Rmet_1752	agrS	7.33	0.58	Op0499f_1	EIP-SIG-2Comp	Q1LMJ5 Sensor protein
3UTR_1305	1902887 +	1902967 Rmet_1752	agrS			Op0499f_1		
5UTR_1074	1903171 +	1903172 Rmet_1753				Op0499f_1		
NPKM_4347	1903172 +	1903475 Rmet_1753		12.33	2.31	Op0499f_1	NA	Q1LMJ4 Putative uncharacterized protein
3UTR_1827	1903249 -	1903695 Rmet_1754				Op0500r_2		
3UTR_1306	1903476 +	1904088 Rmet_1753				Op0499f_1		
NPKM_4348	1903696 -	1904224 Rmet_1754		9.67	0.58	Op0500r_2	NA	Q1LMJ3 Putative uncharacterized protein
NPKM_4349	1904451 -	1905450 Rmet_1755	bug	7.67	0.58	Op0500r_2	NA	Q1LMJ2 Twin-arginine translocation pathway signal
NPKM_4350	1905484 -	1906696 Rmet_1756		3.67	0.58	Op0500r_1	NA	Q1LMJ1 L-carnitine dehydratase/bile acid-inducible protein F
NPKM_4351	1906832 +	1907726 Rmet_1757		9.67	1.53	Op0501f_1	NA	Q1LMJ0 Transcriptional regulator, LysR family
NPKM_4352	1907907 +	1907973 Rmet_6475		3.00	1.00	Op0501f_1	NA	NA
NPKM_4353	1908006 +	1908927 Rmet_1758		16.00	1.00	Op0501f_2	NA	Q1LMI9 Putative uncharacterized protein
3UTR_1307	1908928 +	1909096 Rmet_1758				Op0501f_2		
5UTR_1075	1909236 +	1909326 Rmet_1759	yheS			Op0501f_3		
NPKM_4354	1909326 +	1910991 Rmet_1759	yheS	39.33	2.52	Op0501f_3	GIP-TL-Ass	Q1LMI8 ABC transporter-related protein
3UTR_1826	1910977 -	1911298 Rmet_1760				Op0502r_1		
3UTR_1308	1910992 +	1911531 Rmet_1759	yheS			Op0501f_3		
NPKM_4355	1911299 -	1912208 Rmet_1760		5.33	0.58	Op0502r_1	NA	Q1LMI7 Alpha/beta hydrolase fold
5UTR_1536	1912209 -	1912340 Rmet_1760				Op0502r_1		
5UTR_1076	1912341 +	1912491 Rmet_1761				Op0503f_1		
NPKM_4356	1912491 +	1913148 Rmet_1761		18.33	1.15	Op0503f_1	NA	Q1LMI6 Putative uncharacterized protein
3UTR_1825	1912873 -	1913192 Rmet_1762	yoeE			Op0504r_1		
3UTR_1309	1913149 +	1913513 Rmet_1761				Op0503f_1		
NPKM_4357	1913193 -	1914786 Rmet_1762	yoeE	8.33	1.15	Op0504r_1	NA	Q1LMI5 Integral membrane protein TerC
5UTR_1077	1914775 +	1915002 Rmet_1763				Op0505f_1		
5UTR_1535	1914787 -	1914851 Rmet_1762	yoeE			Op0504r_1		
NPKM_4358	1915002 +	1915452 Rmet_1763		7.67	1.53	Op0505f_1	NA	Q1LMI4 Putative uncharacterized protein
3UTR_1824	1915266 -	1915412 Rmet_6476				Op2016r_1		
NPKM_4359	1915413 -	1915518 Rmet_6476		4.33	0.58	Op2016r_1	NA	NA
5UTR_1534	1915519 -	1915872 Rmet_6476				Op2016r_1		
NPKM_4360	1915576 +	1916599 Rmet_1764		14.00	2.00	Op0505f_1	NA	Q1LMI3 Putative uncharacterized protein

3UTR_1823	1915879 -	1916606 Rmet_1765				Op0506r_1			
3UTR_1310	1916600 +	1916770 Rmet_1764				Op0505f_1			
NPKM_4361	1916607 -	1917006 Rmet_1765	23.67	3.21	Op0506r_1	NA		Q1LMI2 Putative uncharacterized protein	
5UTR_1533	1917007 -	1917044 Rmet_1765			Op0506r_1				
5UTR_1078	1917234 +	1917381 Rmet_1766			Op0507f_1				
NPKM_4362	1917381 +	1918764 Rmet_1766	73.33	25.93	Op0507f_1	MET-CAH-But		Q1LMI1 Glutamate decarboxylase	
3UTR_1822	1918598 -	1918830 Rmet_1767			Op0508r_1				
3UTR_1311	1918765 +	1919373 Rmet_1766			Op0507f_1				
NPKM_4363	1918831 -	1919716 Rmet_1767	13.00	1.73	Op0508r_1	NA		Q1LMI0 Transcriptional regulator, LysR family	
5UTR_1532	1919717 -	1919768 Rmet_1767			Op0508r_1				
5UTR_1079	1919844 +	1919852 Rmet_1768			Op0509f_1				
NPKM_4364	1919852 +	1920782 Rmet_1768	6.67	0.58	Op0509f_1	MET-AA-Urea		Q1LMH9 N-acetyl-gamma-glutamyl-phosphate reductase	
3UTR_1821	1920097 -	1920922 Rmet_1769			Op0510r_2				
3UTR_1312	1920783 +	1920829 Rmet_1768			Op0509f_1				
NPKM_4365	1920923 -	1921916 Rmet_1769	138.00	4.36	Op0510r_2	NA		Q1LMH8 Uncharacterized protein UPF0065	
NPKM_4366	1922028 -	1923456 Rmet_1770	86.00	6.24	Op0510r_2	GIP-TL-Ass		Q1LSE1 Glutamyl-tRNA(Gln) amidotransferase subunit A	
NPKM_4367	1923551 -	1923995 Rmet_1771	9.00	1.73	Op0510r_1	NA		Q1LMH6 Putative lipoprotein	
5UTR_1531	1923996 -	1924062 Rmet_1771			Op0510r_1				
5UTR_1080	1924207 +	1924220 Rmet_1772			Op0511f_1				
NPKM_4368	1924220 +	1924787 Rmet_1772	12.00	0.00	Op0511f_1	NA		Q1LMH5 GCN5-related N-acetyltransferase	
3UTR_1820	1924568 -	1925232 Rmet_1774			Op0512r_1				
NPKM_4369	1924805 +	1925237 Rmet_1773	8.00	1.00	Op0511f_1	NA		Q1LMH4 Glyoxalase/bleomycin resistance protein/dioxygenase	
NPKM_4370	1925233 -	1926178 Rmet_1774	3.67	0.58	Op0512r_1	NA		Q1LMH3 Transcriptional regulator, LysR family	
3UTR_1313	1925238 +	1925646 Rmet_1773			Op0511f_1				
5UTR_1530	1926179 -	1926187 Rmet_1774			Op0512r_1				
NPKM_4371	1926290 +	1927682 Rmet_1775	1.67	0.58	Op0513f_1	NA		Q1LMH2 FAD linked oxidase-like protein	
3UTR_1819	1927296 -	1927743 Rmet_1776			Op0514r_1				
NPKM_4372	1927744 -	1928917 Rmet_1776	36.67	2.52	Op0514r_1	Met-SecMetab		Q1LMH1 Beta-lactamase	
5UTR_1529	1928918 -	1928953 Rmet_1776			Op0514r_1				
5UTR_1081	1928930 +	1928941 Rmet_1777			Op0515f_1				
NPKM_4373	1928941 +	1930744 Rmet_1777	31.33	3.21	Op0515f_1	EIP-TRA-Ion		Q1LMH0 Na/Pi cotransporter II-related	
3UTR_1818	1929375 -	1930799 Rmet_1778			Op0516r_1				
3UTR_1314	1930745 +	1931195 Rmet_1777			Op0515f_1				
NPKM_4374	1930800 -	1931166 Rmet_1778	47.00	1.00	Op0516r_1	NA		Q1LMG9 Glyoxalase/bleomycin resistance protein/dioxygenase	
5UTR_1528	1931167 -	1931184 Rmet_1778			Op0516r_1				
5UTR_1082	1931219 +	1931327 Rmet_1779			Op0517f_1				
NPKM_4375	1931327 +	1932491 Rmet_1779	24.33	0.58	Op0517f_1	NA		Q1LMG8 Putative uncharacterized protein	
NPKM_4376	1932493 +	1933090 Rmet_1780	36.00	3.61	Op0517f_1	NA		Q1LMG7 Methyltransferase type 11	
3UTR_1817	1932509 -	1933157 Rmet_1781			Op0518r_3				
3UTR_1315	1933091 +	1933719 Rmet_1780			Op0517f_1				
NPKM_4377	1933158 -	1934076 Rmet_1781	12.33	1.15	Op0518r_3	MET-XEN-Toluene		Q1LMG6 Catechol 1,2-dioxygenase	
NPKM_4378	1934103 -	1935174 Rmet_1782	2.00	0.00	Op0518r_2	MET-XEN-Toluene		Q1LMG5 Oxidoreductase FAD/NAD(P)-binding	
3UTR_1816	1935185 -	1935193 Rmet_1783			Op0518r_2				

NPKM_4379	1935194 -	1935557	Rmet_1783	<i>phyD</i>	1.67	0.58	Op0518r_2	NA	Q1LMG4 Phenol hydroxylase conserved region
5UTR_1527	1935558 -	1935565	Rmet_1783	<i>phyD</i>			Op0518r_2		
NPKM_4380	1935573 -	1937121	Rmet_1784	<i>phyC</i>	1.33	0.58	Op0518r_2	MET-EN-Methane	Q1LMG3 Methane/phenol/toluene hydroxylase
NPKM_4381	1937149 -	1937422	Rmet_1785	<i>phyB</i>	1.00	1.00	Op0518r_2	NA	Q1LMG2 Monooxygenase component MmoB/DmpM
3UTR_1815	1937431 -	1937432	Rmet_1786	<i>phyA</i>			Op0518r_2		
NPKM_4382	1937433 -	1938429	Rmet_1786	<i>phyA</i>	1.00	0.00	Op0518r_2	MET-XEN-Toluene	Q1LMG1 Methane/phenol/toluene hydroxylase
5UTR_1526	1938430 -	1938435	Rmet_1786	<i>phyA</i>			Op0518r_2		
NPKM_4383	1938472 -	1938670	Rmet_1787		0.00	0.00	Op0518r_1	NA	Q1LMG0 Phenol hydroxylase subunit
5UTR_1083	1938951 +	1938997	Rmet_1788	<i>poxR</i>			Op0519f_1		
NPKM_4384	1938997 +	1940626	Rmet_1788	<i>poxR</i>	32.00	1.73	Op0519f_1	NA	Q1LMF9 Sigma-54 factor, interaction region
NPKM_4385	1940720 +	1941419	Rmet_1789		16.00	0.00	Op0519f_1	NA	Q1LMF8 Transcriptional regulator, GntR family
NPKM_4386	1941479 +	1942892	Rmet_1790	<i>glcD</i>	33.00	0.00	Op0519f_2	NA	Q1LMF7 FAD linked oxidase-like protein
NPKM_4387	1943010 +	1944219	Rmet_1791		48.00	2.65	Op0519f_2	NA	Q1LMF6 Secretion protein HlyD
NPKM_4388	1944241 +	1944946	Rmet_1792	<i>ybbA</i>	51.67	2.89	Op0519f_2	EIP-TRA-ABC	Q1LMF5 ABC transporter-related protein
NPKM_4389	1944948 +	1946103	Rmet_1793		14.67	1.53	Op0519f_2	EIP-TRA-ABC	Q1LMF4 Putative uncharacterized protein
NPKM_4390	1946108 +	1947275	Rmet_1794		9.33	0.58	Op0519f_2	EIP-TRA-ABC	Q1LMF3 Putative uncharacterized protein
3UTR_1814	1946432 -	1947322	Rmet_1795				Op0520r_1		
3UTR_1316	1947276 +	1947387	Rmet_1794				Op0519f_2		
NPKM_4391	1947323 -	1948214	Rmet_1795		49.00	1.00	Op0520r_1	NA	Q1LMF2 Transcriptional regulator, LysR family
5UTR_1525	1948215 -	1948269	Rmet_1795				Op0520r_1		
NPKM_4392	1948342 +	1950220	Rmet_1796		0.33	0.58	Op0521f_1	NA	Q1LMF1 Fusaric acid resistance protein conserved region
3UTR_1813	1949430 -	1950374	Rmet_6477				Op2017r_1		
NPKM_4393	1950375 -	1950942	Rmet_6477		13.33	2.08	Op2017r_1	NA	NA
NPKM_4394	1950402 +	1950720	Rmet_1797		1.00	1.00	Op0521f_2	NA	Q1LMF0 Putative uncharacterized protein
3UTR_1317	1950721 +	1950820	Rmet_1797				Op0521f_2		
NPKM_4395	1950997 -	1951987	Rmet_1798		64.33	5.51	Op0522r_2	NA	Q1LME9 Putative uncharacterized protein
NPKM_4396	1951970 -	1952336	Rmet_1799		28.33	2.52	Op0522r_1	NA	Q1LME8 Transcriptional regulator, ArsR family
3UTR_1812	1952353 -	1952515	Rmet_1800				Op0522r_1		
NPKM_4397	1952516 -	1953068	Rmet_1800		21.00	2.65	Op0522r_1	NA	Q1LME7 Transcriptional regulator, MarR family
NPKM_4398	1953173 +	1954205	Rmet_1801	<i>bug</i>	6.00	0.00	Op0523f_1	NA	Q1LME6 Uncharacterized protein UPF0065
NPKM_4399	1954250 +	1955807	Rmet_1802	<i>ydjI</i>	7.00	0.00	Op0523f_1	NA	Q1LME5 Sulfatase
3UTR_1318	1955808 +	1955814	Rmet_1802	<i>ydjI</i>			Op0523f_1		
5UTR_1084	1955818 +	1955966	Rmet_1803	<i>ynjF</i>			Op0523f_2		
NPKM_4400	1955966 +	1956632	Rmet_1803	<i>ynjF</i>	137.33	9.61	Op0523f_2	NA	Q1LME4 CDP-alcohol phosphatidyltransferase
NPKM_4401	1956643 +	1957447	Rmet_1804		176.00	5.57	Op0523f_2	NA	Q1LME3 2OG-Fe(II) oxygenase
NPKM_4402	1957452 +	1958451	Rmet_1805		98.33	7.23	Op0523f_2	NA	Q1LME2 Putative uncharacterized protein
NPKM_4403	1958447 -	1958666	Rmet_1806		9.00	2.65	Op0524r_1	NA	Q1LME1 Putative uncharacterized protein
NPKM_4404	1958680 +	1959436	Rmet_1807		111.33	5.51	Op0525f_1	NA	Q1LME0 RfbF; ADP-glucose pyrophosphorylase
NPKM_4405	1959432 +	1961127	Rmet_1808	<i>pepM</i>	168.00	4.00	Op0525f_1	MET-OAA-Other	Q1LMD9 2,3-dimethylmalate lyase
NPKM_4406	1961123 +	1962323	Rmet_1809	<i>ppd</i>	164.00	3.00	Op0525f_1	NA	Q1LMD8 Thiamine pyrophosphate enzyme-like TPP-binding
NPKM_4407	1962309 +	1963377	Rmet_1810	<i>phnW</i>	195.00	1.73	Op0525f_1	MET-OAA-Other	Q1LMD7 Aminotransferase, class V
3UTR_1319	1963378 +	1964533	Rmet_1810	<i>phnW</i>			Op0525f_1		
NPKM_4408	1963447 -	1965046	Rmet_1811	<i>ymdC</i>	159.00	13.08	Op0526r_2	NA	Q1LMD6 Phospholipase D/Transphosphatidylase

NPKM_4409	1965116 -	1966268 Rmet_1812		745.00	72.92	Op0526r_2	NA	Q1LMD5 Rieske (2Fe-2S) region
5UTR_1524	1966269 -	1966313 Rmet_1812				Op0526r_2		
3UTR_1811	1966419 -	1966447 Rmet_1813				Op0526r_1		
NPKM_4410	1966448 -	1967669 Rmet_1813		2.67	0.58	Op0526r_1	NA	Q1LMD4 L-carnitine dehydratase/bile acid-inducible protein F
NPKM_4411	1967695 -	1968871 Rmet_1814		4.00	0.00	Op0526r_1	MET-CAH-Prop	Q1LMD3 Acyl-CoA dehydrogenase-like protein
NPKM_4412	1968867 -	1969845 Rmet_1815	bug	4.33	0.58	Op0526r_1	NA	Q1LMD2 Uncharacterized protein UPF0065
NPKM_4413	1969902 -	1971192 Rmet_1816		2.33	0.58	Op0526r_1	MET-XEN-Others	Q1LMD1 Acyl-CoA dehydrogenase-like protein
5UTR_1085	1971194 +	1971204 Rmet_1817				Op0527f_1		
NPKM_4414	1971204 +	1971987 Rmet_1817		22.00	1.73	Op0527f_1	NA	Q1LMD0 Transcriptional regulator, IclR family
NPKM_4415	1971989 +	1972784 Rmet_1818		16.00	2.00	Op0527f_1	NA	Q1LMC9 Transcriptional regulator, IclR family
3UTR_1320	1972785 +	1972948 Rmet_1818				Op0527f_1		
5UTR_1086	1972990 +	1973010 Rmet_1819				Op0527f_1		
NPKM_4416	1973010 +	1975239 Rmet_1819		1.00	0.00	Op0527f_1	EIP-TRA-Pores	Q1LMC8 TonB-dependent siderophore receptor
5UTR_1087	1975313 +	1975330 Rmet_1820	purT			Op0527f_2		
NPKM_4417	1975330 +	1976533 Rmet_1820	purT	149.67	5.51	Op0527f_2	MET-NUC-Pur	Q1LMC7 Phosphoribosylglycinamide formyltransferase 2
3UTR_1810	1975948 -	1976609 Rmet_1821	ybdG			Op0528r_1		
3UTR_1321	1976534 +	1977784 Rmet_1820	purT			Op0527f_2		
NPKM_4418	1976610 -	1977954 Rmet_1821	ybdG	36.00	1.73	Op0528r_1	NA	Q1LMC6 MscS Mechanosensitive ion channel
NPKM_4419	1978061 -	1979249 Rmet_1822		30.00	3.00	Op0528r_1	NA	Q1LMC5 Metal dependent phosphohydrolase
5UTR_1523	1979250 -	1979675 Rmet_1822				Op0528r_1		
5UTR_1088	1979439 +	1979558 Rmet_1823				Op0529f_1		
NPKM_4420	1979558 +	1980596 Rmet_1823		26.33	2.52	Op0529f_1	NA	Q1LMC4 Heat shock protein DnaJ-like protein
3UTR_1809	1979724 -	1980652 Rmet_1824	arp3			Op0530r_2		
3UTR_1322	1980597 +	1980796 Rmet_1823				Op0529f_1		
NPKM_4421	1980653 -	1981334 Rmet_1824	arp3	239.33	9.07	Op0530r_2	NA	Q1LMC3 Ankyrin
NPKM_4422	1981362 -	1982160 Rmet_1825		193.67	7.51	Op0530r_2	GIP-PTL-Exp	Q1LMC2 TatD-related deoxyribonuclease
NPKM_4423	1982325 -	1982736 Rmet_1826	pilZ	249.67	4.51	Op0530r_2	GIP-PTL-T2S	Q1LMC1 Type IV pilus assembly PilZ
NPKM_4424	1982841 -	1983855 Rmet_1827	holB	131.00	7.00	Op0530r_2	GIP-REP-DNA_Pol	Q1LMC0 DNA polymerase III, delta prime subunit
NPKM_4425	1983941 -	1984544 Rmet_1828	tmk	123.33	11.68	Op0530r_2	NA	NA
NPKM_4426	1984548 -	1985547 Rmet_1829	yceG	58.67	5.13	Op0530r_1	MET-NUC-Pyr	Q1LMB9 Thymidylate kinase
5UTR_1522	1985548 -	1986133 Rmet_1829	yceG			Op0530r_1		
5UTR_1089	1985655 +	1985733 Rmet_1830	gcvT			Op0531f_1		
NPKM_4427	1985733 +	1986744 Rmet_1830	gcvT	165.00	1.00	Op0531f_1	NA	Q1LMB7 Glycine cleavage T protein (Aminomethyl transferase)
NPKM_4428	1986763 +	1987054 Rmet_1831		134.33	3.51	Op0531f_1	NA	Q1LMB6 Putative uncharacterized protein
NPKM_4429	1987132 +	1987987 Rmet_1832		106.33	6.66	Op0531f_1	NA	Q1LMB5 Putative uncharacterized protein
3UTR_1808	1987217 -	1988009 Rmet_1833				Op0532r_1		
NPKM_4430	1988010 -	1988454 Rmet_1833		38.00	3.00	Op0532r_1	NA	Q1LMB4 GCN5-related N-acetyltransferase
5UTR_1521	1988455 -	1988581 Rmet_1833				Op0532r_1		
NPKM_4431	1988631 +	1989375 Rmet_1834		14.33	2.31	Op0533f_1	NA	Q1LMB3 Transcriptional regulator, GntR family
NPKM_4432	1989434 +	1990331 Rmet_1835	ygbJ	14.67	0.58	Op0533f_1	MET-AA-ValLeulle	Q1LMB2 6-phosphogluconate dehydrogenase, NAD-binding
NPKM_4433	1990353 +	1991622 Rmet_1836		16.33	1.53	Op0533f_1	NA	Q1LMB1 Type III effector Hrp-dependent outers
NPKM_4434	1991618 +	1992257 Rmet_1837	ygbL	13.67	0.58	Op0533f_1	NA	Q1LMB0 Class II aldolase/adducin-like protein
NPKM_4435	1992264 +	1992438 Rmet_6478		11.67	1.53	Op0533f_1	NA	NA

NPKM_4436	1992434 +	1993793 Rmet_1838		17.67	2.08	Op0533f_1	NA	Q1LMA9 Major facilitator superfamily MFS_1
NPKM_4437	1993823 +	1994606 Rmet_1839	<i>hyi1</i>	65.33	4.04	Op0533f_2	MET-CAH-DiCarb	Q1LMA8 Xylose isomerase-like TIM barrel
NPKM_4438	1994670 +	1995642 Rmet_1840		75.33	0.58	Op0533f_2	NA	Q1LMA7 NAD-dependent epimerase/dehydratase
3UTR_1807	1995261 -	1995727 Rmet_1841				Op0534r_2		
3UTR_1323	1995643 +	1996676 Rmet_1840				Op0533f_2		
NPKM_4439	1995728 -	1996166 Rmet_1841		26.33	3.06	Op0534r_2	NA	Q1LMA6 4-hydroxybenzoyl-CoA thioesterase
NPKM_4440	1996226 -	1997210 Rmet_1842	<i>bug</i>	84.33	6.51	Op0534r_2	NA	Q1LMA5 Twin-arginine translocation pathway signal
NPKM_4441	1997341 -	1998376 Rmet_1843		31.00	2.00	Op0534r_1	MET-CAH-But	Q1LMA4 Alpha/beta hydrolase fold-3
5UTR_1090	1998424 +	1998515 Rmet_1844				Op0535f_1		
NPKM_4442	1998515 +	1999037 Rmet_1844		59.00	2.65	Op0535f_1	NA	Q1LMA3 Appr-1-p processing
3UTR_1324	1999038 +	1999905 Rmet_1844				Op0535f_1		
NPKM_4443	1999067 -	1999988 Rmet_1845		43.00	2.00	Op0536r_1	NA	Q1LMA2 Alpha/beta hydrolase fold
NPKM_4444	2000069 -	2000972 Rmet_1846		42.00	1.00	Op0536r_1	NA	Q1LMA1 Short-chain dehydrogenase/reductase SDR
NPKM_4445	2001048 -	2001981 Rmet_1847		39.33	1.15	Op0536r_1	MET-OAA-GSH	Q1LMA0 Putative glutathione S-transferase-related protein
NPKM_4446	2001999 -	2002833 Rmet_1848		76.33	1.15	Op0536r_1	NA	Q1LM99 Class II aldolase/adducin-like protein
NPKM_4447	2002899 -	2003913 Rmet_1849		72.00	1.00	Op0536r_1	NA	Q1LM98 Alcohol dehydrogenase, zinc-binding
NPKM_4448	2003968 -	2004433 Rmet_1850		43.00	4.58	Op0536r_1	NA	Q1LM97 Phenylacetic acid degradation-related protein
NPKM_4449	2004492 -	2005275 Rmet_1851		48.33	2.89	Op0536r_1	NA	Q1LM96 Short-chain dehydrogenase/reductase SDR
NPKM_4450	2005366 -	2007226 Rmet_1852		46.33	1.53	Op0536r_1	MET-CAH-But	Q1LM95 Acyl-CoA dehydrogenase-like protein
NPKM_4451	2007268 -	2007478 Rmet_6479		127.00	4.58	Op0536r_1	NA	NA
NPKM_4452	2007440 -	2008619 Rmet_1853	<i>atoB</i>	165.67	12.58	Op0536r_1	MET-CAH-Pyr	Q1LM94 Thiolase
NPKM_4453	2008699 -	2009365 Rmet_1854	<i>pncA</i>	130.00	9.64	Op0536r_1	NA	Q1LM93 Isochorismatase hydrolase
NPKM_4454	2009401 -	2011483 Rmet_1855	<i>fadB</i>	188.00	13.89	Op0536r_1	MET-CAH-But	Q1LM92 3-hydroxyacyl-CoA dehydrogenase / short chain enoyl-CoA hydratase
5UTR_1520	2011484 -	2011693 Rmet_1855	<i>fadB</i>			Op0536r_1		
5UTR_1091	2011925 +	2011949 Rmet_1856	<i>lysP</i>			Op0537f_1		
NPKM_4455	2011949 +	2013431 Rmet_1856	<i>lysP</i>	3.00	1.00	Op0537f_1	EIP-TRA-Ion	Q1LM91 Amino acid permease-associated region
3UTR_1806	2012873 -	2013511 Rmet_6480				Op0538r_2		
3UTR_1325	2013432 +	2013469 Rmet_1856	<i>lysP</i>			Op0537f_1		
NPKM_4456	2013512 -	2013632 Rmet_6480		9.00	1.00	Op0538r_2	NA	NA
NPKM_4457	2013699 -	2014134 Rmet_1857		1.67	0.58	Op0538r_1	NA	Q1LM90 Putative uncharacterized protein
5UTR_1519	2014135 -	2014190 Rmet_1857				Op0538r_1		
3UTR_1805	2014203 -	2014479 Rmet_1858	<i>livF7</i>			Op0538r_1		
NPKM_4458	2014480 -	2015194 Rmet_1858	<i>livF7</i>	68.00	3.61	Op0538r_1	EIP-TRA-ABC	Q1LM89 ABC transporter-related protein
NPKM_4459	2015190 -	2015970 Rmet_1859	<i>livG7</i>	72.33	4.16	Op0538r_1	EIP-TRA-ABC	Q1LM88 ABC transporter-related protein
NPKM_4460	2015966 -	2017280 Rmet_1860		52.67	2.08	Op0538r_1	EIP-TRA-ABC	Q1LM87 Inner-membrane translocator
NPKM_4461	2017283 -	2018255 Rmet_1861		48.33	1.53	Op0538r_1	EIP-TRA-ABC	Q1LM86 Inner-membrane translocator
NPKM_4462	2018337 -	2019588 Rmet_1862		124.00	5.00	Op0538r_1	EIP-TRA-ABC	Q1LM85 Extracellular ligand-binding receptor
NPKM_4463	2019747 -	2021352 Rmet_1863		174.33	11.15	Op0538r_1	MET-LIP-FASyn	Q1LM84 AMP-dependent synthetase and ligase
5UTR_1518	2021353 -	2022442 Rmet_1863				Op0538r_1		
5UTR_1092	2021502 +	2021690 Rmet_1864				Op0539f_1		
NPKM_4464	2021690 +	2023325 Rmet_1864		80.00	5.57	Op0539f_1	NA	Q1LM83 UPF0061 protein Rmet_1864
NPKM_4465	2023373 +	2023781 Rmet_1865	<i>msrB</i>	145.33	4.04	Op0539f_1	GIP-PTL-Fold	Q1LM82 Methionine sulfoxide reductase B
NPKM_4466	2023876 +	2024416 Rmet_1866	<i>ispZ</i>	132.33	4.93	Op0539f_1	DIV-Division	Q1LM81 Probable intracellular septation protein

NPKM_4467	2024467 +	2024782 Rmet_1867	<i>bolA</i>	147.33	3.51	Op0539f_1	NA	Q1LM80 Transcriptional regulator BolA
NPKM_4468	2024786 +	2025581 Rmet_1868		612.33	28.29	Op0539f_2	GIP-PTL-Fold	Q1LM79 PpiC-type peptidyl-prolyl cis-trans isomerase
3UTR_1804	2025757 -	2026245 Rmet_1870	<i>purl</i>			Op0540r_2		
NPKM_4469	2025770 +	2026118 Rmet_1869		38.00	5.57	Op0539f_2	NA	Q1LM78 Putative uncharacterized protein
3UTR_1326	2026119 +	2026613 Rmet_1869				Op0539f_2		
NPKM_4470	2026246 -	2030293 Rmet_1870	<i>purl</i>	275.00	1.73	Op0540r_2	MET-NUC-Pur	Q1LM77 Phosphoribosylformylglycinamide synthase
5UTR_1093	2030294 +	2030344 Rmet_6481				Op2018f_1		
NPKM_4471	2030344 +	2030524 Rmet_6481		3.33	0.58	Op2018f_1	NA	NA
NPKM_4472	2030520 -	2031108 Rmet_1871		66.33	3.79	Op0540r_1	NA	Q1LM76 Putative transcriptional regulator
NPKM_4473	2031010 +	2031265 Rmet_6482		2.33	0.58	Op0541f_1	NA	NA
5UTR_1517	2031109 -	2031449 Rmet_1871				Op0540r_1		
3UTR_1327	2031266 +	2031305 Rmet_6482				Op0541f_1		
5UTR_1094	2031309 +	2031387 Rmet_1872				Op0541f_2		
NPKM_4474	2031387 +	2033148 Rmet_1872		15.00	1.73	Op0541f_2	NA	Q1LM75 Diguanylate cyclase (GGDEF domain)
NPKM_4475	2033360 +	2034713 Rmet_1873		83.67	12.50	Op0541f_3	GIP-TL-Ass	Q1LM74 Amidase
NPKM_4476	2034856 +	2035840 Rmet_1874		52.33	3.51	Op0541f_3	NA	Q1LM73 TRAP dicarboxylate transporter-DctP subunit
NPKM_4477	2035984 +	2036536 Rmet_1875		5.00	1.73	Op0541f_3	NA	Q1LM72 TRAP-type C4-dicarboxylate transport system, small permease component
NPKM_4478	2036535 +	2037846 Rmet_1876		10.67	0.58	Op0541f_4	NA	Q1LM71 TRAP dicarboxylate transporter-DctM subunit
NPKM_4479	2037880 +	2039170 Rmet_1877	<i>dadA</i>	20.00	1.73	Op0541f_4	MET-EN-Nitrog	Q1LM70 FAD dependent oxidoreductase
NPKM_4480	2039177 +	2040785 Rmet_1878		53.33	2.52	Op0541f_5	NA	Q1LM69 Putative uncharacterized protein
NPKM_4481	2040839 +	2040914 Rmet_6483		15.33	3.79	Op0541f_5	NA	NA
NPKM_4482	2041065 +	2042691 Rmet_1879	<i>pgi</i>	134.00	8.19	Op0541f_6	MET-CAH-FbP	Q1LM68 Glucose-6-phosphate isomerase
3UTR_1803	2041406 -	2042705 Rmet_1880	<i>ybbA</i>			Op0542r_1		
NPKM_4483	2042706 -	2043294 Rmet_1880	<i>ybbA</i>	107.33	4.51	Op0542r_1	EIP-TRA-ABC	Q1LM67 ABC transporter-related protein
NPKM_4484	2043391 +	2044072 Rmet_1881		57.00	1.00	Op0543f_1	NA	Q1LM66 Lipolytic enzyme, G-D-S-L
3UTR_1328	2044073 +	2044730 Rmet_1881				Op0543f_1		
NPKM_4485	2044207 -	2046151 Rmet_1882	<i>ppiD</i>	293.67	3.51	Op0544r_2	GIP-PTL-Fold	Q1LM65 PpiC-type peptidyl-prolyl cis-trans isomerase
NPKM_4486	2046394 -	2046471 Rmet_R0020		234.00	26.85	Op0544r_2	NA	NA
NPKM_4487	2046514 -	2046590 Rmet_R0021		178.00	29.00	Op0544r_2	NA	NA
NPKM_4488	2046843 -	2049255 Rmet_1883	<i>lon</i>	623.00	16.70	Op0544r_2	GIP-PTL-Fold	Q1LM64 ATP-dependent protease La
NPKM_4489	2049501 -	2050779 Rmet_1884	<i>clpX</i>	500.67	12.01	Op0544r_2	GIP-PTL-Fold	Q1LM63 ATP-dependent Clp protease ATP-binding subunit clpX
NPKM_4490	2051059 -	2051710 Rmet_1885	<i>clpP</i>	913.67	32.01	Op0544r_2	GIP-PTL-Fold	Q1LM62 ATP-dependent Clp protease proteolytic subunit
NPKM_4491	2051819 -	2053169 Rmet_1886	<i>tig</i>	1343.33	72.98	Op0544r_2	GIP-PTL-Fold	Q1LM61 Trigger factor
NPKM_4492	2053318 -	2055337 Rmet_1887	<i>trmC</i>	30.00	2.65	Op0544r_1	NA	Q1LM60 tRNA 5-methylaminomethyl-2-thiouridine biosynthesis bifunctional protein
5UTR_1516	2055338 -	2056396 Rmet_1887	<i>trmC</i>			Op0544r_1		
5UTR_1095	2055355 +	2055460 Rmet_1888	<i>yhiR</i>			Op0545f_1		
NPKM_4493	2055460 +	2056318 Rmet_1888	<i>yhiR</i>	41.67	1.15	Op0545f_1	NA	Q1LM59 Putative uncharacterized protein
3UTR_1329	2056319 +	2056538 Rmet_1888	<i>yhiR</i>			Op0545f_1		
3UTR_1802	2056402 -	2057085 Rmet_1889				Op0546r_1		
5UTR_1096	2056555 +	2056611 Rmet_6484				Op0545f_1		
NPKM_4494	2056611 +	2056830 Rmet_6484		19.00	0.00	Op0545f_1	NA	NA
3UTR_1330	2056831 +	2057411 Rmet_6484				Op0545f_1		
NPKM_4495	2057086 -	2057329 Rmet_1889		4.67	0.58	Op0546r_1	NA	Q1LM58 Putative uncharacterized protein

5UTR_1515	2057330 -	2057354 Rmet_1889				Op0546r_1		
3UTR_1801	2057376 -	2057593 Rmet_6485				Op0546r_1		
NPKM_4496	2057594 -	2057666 Rmet_6485	3.33	3.21		Op0546r_1	NA	NA
5UTR_1097	2057691 +	2057813 Rmet_1890				Op0547f_1		
NPKM_4497	2057701 -	2057944 Rmet_6486	2.67	1.15		Op0546r_1	NA	NA
NPKM_4498	2057813 +	2058395 Rmet_1890	14.00	1.00		Op0547f_1	NA	Q1LM57 Endonuclease
5UTR_1514	2057945 -	2057952 Rmet_6486				Op0546r_1		
NPKM_4499	2058459 +	2058639 Rmet_6487	6.67	2.08		Op0547f_1	NA	NA
NPKM_4500	2058653 +	2059556 Rmet_1891	1.67	0.58		Op0547f_1	NA	Q1LM56 Putative uncharacterized protein
3UTR_1331	2059557 +	2059566 Rmet_1891				Op0547f_1		
NPKM_4501	2059635 +	2059767 Rmet_6488	0.67	1.15		Op0547f_1	NA	NA
3UTR_1332	2059768 +	2059769 Rmet_6488				Op0547f_1		
NPKM_4502	2059890 -	2060691 Rmet_1892	6.67	0.58		Op0548r_1	NA	Q1LM55 Transcriptional regulator, LuxR family
3UTR_1800	2060942 -	2061035 Rmet_1893				Op0548r_1		
5UTR_1098	2060979 +	2061072 Rmet_6489				Op2019f_1		
NPKM_4503	2061036 -	2061537 Rmet_1893	6.33	2.31		Op0548r_1	NA	Q1LM54 Putative uncharacterized protein
NPKM_4504	2061072 +	2061522 Rmet_6489	6.00	1.73		Op2019f_1	NA	NA
3UTR_1333	2061523 +	2061610 Rmet_6489				Op2019f_1		
NPKM_4505	2061561 -	2062536 Rmet_1894	36.33	2.08		Op0548r_1	NA	Q1LM53 Transcriptional regulator, LysR family
5UTR_1513	2062537 -	2062541 Rmet_1894				Op0548r_1		
5UTR_1099	2062672 +	2062685 Rmet_1895				Op0549f_1		
NPKM_4506	2062685 +	2064230 Rmet_1895	3.33	0.58		Op0549f_1	MET-CAH-But	Q1LM52 Thiamine pyrophosphate enzyme-like TPP-binding
3UTR_1799	2063866 -	2064739 Rmet_1897				Op0550r_1		
NPKM_4507	2064370 +	2064781 Rmet_1896	2.67	0.58		Op0549f_1	NA	Q1LM51 4-oxalocrotonate tautomerase
NPKM_4508	2064740 -	2065646 Rmet_1897	16.33	0.58		Op0550r_1	NA	Q1LM50 Transcriptional regulator, LysR family
3UTR_1334	2064782 +	2064789 Rmet_1896				Op0549f_1		
NPKM_4509	2065749 +	2067165 Rmet_1898	4.33	0.58		Op0551f_1	MET-CAH-FbP	Q1LM49 Aldehyde dehydrogenase
3UTR_1335	2067166 +	2067397 Rmet_1898				Op0551f_1		
3UTR_1798	2067176 -	2067193 Rmet_1899				Op0552r_1		
NPKM_4510	2067194 -	2068907 Rmet_1899	3.67	0.58		Op0552r_1	MET-CAH-Pyr	Q1LM48 Pyruvate dehydrogenase (Cytochrome)
5UTR_1512	2068908 -	2069263 Rmet_1899				Op0552r_1		
NPKM_4511	2069027 +	2069426 Rmet_6490	0.33	0.58		Op0553f_1	NA	NA
3UTR_1336	2069427 +	2069429 Rmet_6490				Op0553f_1		
NPKM_4512	2069484 +	2070387 Rmet_1900	4.33	0.58		Op0553f_2	NA	Q1LM47 Transcriptional regulator, LysR family
3UTR_1797	2070182 -	2070329 Rmet_6491				Op0554r_1		
NPKM_4513	2070330 -	2070522 Rmet_6491	5.33	1.53		Op0554r_1	NA	NA
3UTR_1337	2070388 +	2070788 Rmet_1900				Op0553f_2		
NPKM_4514	2070610 -	2071351 Rmet_1901	12.33	0.58		Op0554r_1	NA	Q1LM46 Transcriptional regulator, XRE family
5UTR_1511	2071352 -	2071381 Rmet_1901				Op0554r_1		
NPKM_4515	2071505 +	2072135 Rmet_1902	3.00	0.00		Op0555f_1	NA	Q1LM45 Putative uncharacterized protein
NPKM_4516	2072131 +	2072869 Rmet_1903	1.00	1.00		Op0555f_1	NA	Q1LM44 Putative uncharacterized protein
3UTR_1338	2072870 +	2072998 Rmet_1903				Op0555f_1		
NPKM_4517	2073234 +	2073357 Rmet_6492	3.33	2.31		Op0555f_2	NA	NA

NPKM_4518	2073322 +	2074219 Rmet_1904		17.33	6.81	Op0555f_3	NA	Q1LM43 Putative uncharacterized protein
3UTR_1796	2074025 -	2074615 Rmet_1905				Op0556r_3		
3UTR_1339	2074220 +	2074743 Rmet_1904				Op0555f_3		
NPKM_4519	2074616 -	2075684 Rmet_1905		26.00	1.73	Op0556r_3	NA	Q1LM42 Transcriptional regulator, LacI family
5UTR_1510	2075685 -	2075685 Rmet_1905				Op0556r_3		
3UTR_1795	2075711 -	2075739 Rmet_1906	bug			Op0556r_2		
NPKM_4520	2075740 -	2076718 Rmet_1906	bug	1.67	0.58	Op0556r_2	NA	Q1LM41 Uncharacterized protein UPF0065
NPKM_4521	2076763 -	2077879 Rmet_1907		0.00	0.00	Op0556r_1	NA	Q1LM40 Porin, Gram-negative type
5UTR_1509	2077880 -	2077897 Rmet_1907				Op0556r_1		
3UTR_1794	2077963 -	2077990 Rmet_1908				Op0556r_1		
NPKM_4522	2077991 -	2078342 Rmet_1908		4.67	1.15	Op0556r_1	NA	Q1LM39 Cupin 2, conserved barrel
NPKM_4523	2078338 -	2079328 Rmet_1909		9.00	1.00	Op0556r_1	NA	Q1LM38 Alcohol dehydrogenase, zinc-binding
NPKM_4524	2079343 -	2080279 Rmet_1910		6.67	1.15	Op0556r_1	NA	Q1LM37 Putative uncharacterized protein
NPKM_4525	2080256 -	2081006 Rmet_1911		4.67	1.15	Op0556r_1	MET-LIP-FASyn	Q1LM36 Short-chain dehydrogenase/reductase SDR
NPKM_4526	2081073 -	2082012 Rmet_1912		2.67	0.58	Op0556r_1	MET-XEN-Toluene	Q1LM35 Intradiol ring-cleavage dioxygenase
3UTR_1793	2082068 -	2082209 Rmet_1913				Op0556r_1		
NPKM_4527	2082210 -	2082777 Rmet_1913		3.00	1.00	Op0556r_1	NA	Q1LM34 Antibiotic biosynthesis monooxygenase
5UTR_1508	2082778 -	2082816 Rmet_1913				Op0556r_1		
NPKM_4528	2083057 +	2083756 Rmet_1914		6.33	0.58	Op0557f_1	NA	Q1LM33 Isochorismatase hydrolase
3UTR_1340	2083757 +	2083887 Rmet_1914				Op0557f_1		
NPKM_4529	2083960 -	2084368 Rmet_1915		1.00	0.00	Op0558r_1	NA	Q1LM32 Two component transcriptional regulator, LuxR family
5UTR_1507	2084369 -	2084375 Rmet_1915				Op0558r_1		
NPKM_4530	2084419 +	2085034 Rmet_1916		0.00	0.00	Op0559f_1	NA	Q1LM31 Isochorismatase hydrolase
NPKM_4531	2085179 +	2085833 Rmet_1917		1.00	0.00	Op0559f_2	NA	Q1LM30 DSBA oxidoreductase
3UTR_1792	2085203 -	2085887 Rmet_1918				Op0560r_1		
NPKM_4532	2085888 -	2086488 Rmet_1918		5.33	0.58	Op0560r_1	NA	Q1LM29 Putative uncharacterized protein
NPKM_4533	2086496 -	2087210 Rmet_1919		8.67	0.58	Op0560r_1	NA	Q1LM28 Putative uncharacterized protein
NPKM_4534	2087257 -	2087884 Rmet_1920		11.00	1.00	Op0560r_1	NA	Q1LM27 Isochorismatase hydrolase
5UTR_1506	2087885 -	2087951 Rmet_1920				Op0560r_1		
3UTR_1791	2088101 -	2088154 Rmet_1921				Op0560r_1		
NPKM_4535	2088155 -	2088458 Rmet_1921		8.33	2.08	Op0560r_1	NA	Q1LM26 Putative uncharacterized protein
NPKM_4536	2088454 -	2090107 Rmet_1922		11.00	1.00	Op0560r_1	MET-NUC-Pyr	Q1LM25 Cyclic nucleotide-regulated FAD-dependent pyridine nucleotide-disulphide
NPKM_4537	2090200 -	2090584 Rmet_1923		13.33	1.53	Op0560r_1	GIP-PTL-Fold	Q1LM24 OsmC-like protein
NPKM_4538	2091300 +	2092017 Rmet_1924		23.67	3.21	Op0561f_1	NA	Q1LM23 Short-chain dehydrogenase/reductase SDR
3UTR_1341	2092018 +	2092762 Rmet_1924				Op0561f_1		
NPKM_4539	2092026 -	2092224 Rmet_6493		15.00	2.00	Op0562r_2	NA	NA
NPKM_4540	2092438 -	2093029 Rmet_1925		17.67	2.08	Op0562r_2	NA	Q1LM22 Putative uncharacterized protein
NPKM_4541	2093377 -	2093464 Rmet_R0022		106.33	23.35	Op0562r_2	NA	NA
NPKM_4542	2093664 -	2094990 Rmet_1926	yfaV	18.33	1.53	Op0562r_1	NA	Q1LM21 Major facilitator superfamily MFS_1
NPKM_4543	2095099 -	2096422 Rmet_1927	gata3	26.33	2.08	Op0562r_1	GIP-TL-Ass	Q1LM20 Amidase
NPKM_4544	2096418 -	2097096 Rmet_1928		31.67	0.58	Op0562r_1	NA	Q1LM19 Putative uncharacterized protein
NPKM_4545	2097131 -	2097881 Rmet_1929		17.00	1.00	Op0562r_1	NA	Q1LM18 Transcriptional regulator, GntR family
5UTR_1100	2097278 +	2098059 Rmet_1930				Op0563f_1		

NPKM_4546	2098059 +	2098845 Rmet_1930		42.33	4.04	Op0563f_1	NA	Q1LM17 Transcriptional regulator, lclR family
3UTR_1790	2098619 -	2098856 Rmet_1931	amaB-2			Op0564r_1		
NPKM_4547	2098857 -	2100105 Rmet_1931	amaB-2	7.33	0.58	Op0564r_1	MET-NUC-Pyr	Q1LM16 Amidase, hydantoinase/carbamoylase
5UTR_1505	2100106 -	2102734 Rmet_1931	amaB-2			Op0564r_1		
NPKM_4548	2100201 +	2101962 Rmet_1932	dppA	3.00	1.00	Op0565f_1	NA	Q1LM15 Extracellular solute-binding protein, family 5
NPKM_4549	2102048 +	2102999 Rmet_1933	dppB	2.33	0.58	Op0565f_1	EIP-TRA-ABC	Q1LM14 Binding-protein-dependent transport systems inner membrane component
NPKM_4550	2103009 +	2103897 Rmet_1934	dppC	2.00	1.00	Op0565f_1	EIP-TRA-ABC	Q1LM13 Binding-protein-dependent transport systems inner membrane component
NPKM_4551	2103899 +	2104979 Rmet_1935	dppF	2.33	0.58	Op0565f_1	EIP-TRA-ABC	Q1LM12 Oligopeptide/dipeptide ABC transporter, ATP-binding protein-like protein
NPKM_4552	2104995 +	2106009 Rmet_1936	ddpD	1.67	0.58	Op0565f_1	EIP-TRA-ABC	Q1LM11 Oligopeptide/dipeptide ABC transporter, ATP-binding protein-like protein
NPKM_4553	2106042 +	2107233 Rmet_1937		2.67	0.58	Op0565f_1	MET-AA-Phe	Q1LM10 Amidase
3UTR_1789	2106635 -	2107729 Rmet_1939				Op0566r_1		
3UTR_1342	2107234 +	2107260 Rmet_1937				Op0565f_1		
5UTR_1101	2107272 +	2107314 Rmet_1938				Op0565f_2		
NPKM_4554	2107314 +	2107725 Rmet_1938		22.33	0.58	Op0565f_2	NA	Q1LM09 Putative uncharacterized protein
3UTR_1343	2107726 +	2108552 Rmet_1938				Op0565f_2		
NPKM_4555	2107730 -	2108669 Rmet_1939		29.33	1.15	Op0566r_1	NA	Q1LM08 Transcriptional regulator, LysR family
NPKM_4556	2108667 +	2109522 Rmet_1940		1.67	0.58	Op0567f_1	NA	Q1LM07 Putative uncharacterized protein
5UTR_1504	2108670 -	2108883 Rmet_1939				Op0566r_1		
3UTR_1788	2108887 -	2109890 Rmet_1942	acrB3			Op0568r_1		
NPKM_4557	2109628 +	2109865 Rmet_1941		8.00	2.00	Op0567f_2	NA	Q1LM06 Putative uncharacterized protein
3UTR_1344	2109866 +	2110854 Rmet_1941				Op0567f_2		
NPKM_4558	2109891 -	2113002 Rmet_1942	acrB3	33.33	1.53	Op0568r_1	NA	Q1LM05 Acriflavin resistance protein
NPKM_4559	2113011 -	2114583 Rmet_1943		65.33	3.79	Op0568r_1	NA	Q1LM04 Secretion protein HlyD
5UTR_1102	2114512 +	2114597 Rmet_1944				Op0569f_1		
5UTR_1503	2114584 -	2114585 Rmet_1943				Op0568r_1		
NPKM_4560	2114597 +	2115428 Rmet_1944		40.67	4.16	Op0569f_1	MET-LIP-Ster	Q1LM03 Squalene/phytoene synthase
NPKM_4561	2115487 +	2116750 Rmet_1945		60.00	1.00	Op0569f_1	NA	Q1LM02 Amidase, hydantoinase/carbamoylase
3UTR_1787	2116614 -	2116842 Rmet_1946				Op0570r_1		
3UTR_1345	2116751 +	2116767 Rmet_1945				Op0569f_1		
NPKM_4562	2116843 -	2117269 Rmet_1946		28.67	6.51	Op0570r_1	NA	Q1LM01 Putative transmembrane protein
5UTR_1103	2116864 +	2117482 Rmet_1947	ompR			Op0571f_1		
5UTR_1502	2117270 -	2117365 Rmet_1946				Op0570r_1		
NPKM_4563	2117482 +	2118205 Rmet_1947	ompR	363.33	12.50	Op0571f_1	EIP-SIG-2Comp	Q1LM00 Two component transcriptional regulator, winged helix family
NPKM_4564	2118231 +	2119581 Rmet_1948	ompB	83.67	3.51	Op0571f_1	EIP-SIG-2Comp	Q1LLZ9 Sensor protein
NPKM_4565	2119555 -	2119729 Rmet_6494		1.00	1.00	Op2020r_1	NA	NA
NPKM_4566	2119835 +	2121125 Rmet_1949		7.67	0.58	Op0571f_1	NA	Q1LLZ8 General substrate transporter
3UTR_1346	2121126 +	2121182 Rmet_1949				Op0571f_1		
5UTR_1104	2121315 +	2121471 Rmet_1950	ahpC			Op0571f_2		
NPKM_4567	2121471 +	2122020 Rmet_1950	ahpC	3582.67	295.65	Op0571f_2	GIP-PTL-Fold	Q1LLZ7 Alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen
NPKM_4568	2122141 +	2122663 Rmet_1951	ahpD	247.00	12.77	Op0571f_2	NA	Q1LLZ6 Alkylhydroperoxidase AhpD core
3UTR_1786	2122395 -	2123483 Rmet_1953	ispF			Op0572r_2		
NPKM_4569	2122868 +	2123447 Rmet_1952		205.33	5.51	Op0571f_2	NA	Q1LLZ5 GCN5-related N-acetyltransferase
3UTR_1347	2123448 +	2124777 Rmet_1952				Op0571f_2		

NPKM_4570	2123484 -	2123991 Rmet_1953	<i>ispF</i>	207.00	4.00	Op0572r_2	MET-LIP-Ster	Q1LLZ4 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase
NPKM_4571	2124023 -	2124848 Rmet_1954	<i>ispD</i>	97.00	1.73	Op0572r_1	MET-LIP-Ster	Q1LLZ3 2-C-methyl-D-erythritol 4-phosphate cytidyltransferase
5UTR_1105	2124780 +	2124982 Rmet_1955	<i>mfd</i>			Op0573f_1		
5UTR_1501	2124849 -	2124863 Rmet_1954	<i>ispD</i>			Op0572r_1		
NPKM_4572	2124982 +	2128435 Rmet_1955	<i>mfd</i>	58.33	2.52	Op0573f_1	GIP-REP-Recomb	Q1LLZ2 Transcription-repair coupling factor
NPKM_4573	2128465 +	2129701 Rmet_1956	<i>argE1</i>	124.33	3.06	Op0573f_2	MET-AA-Urea	Q1LLZ1 Acetylornithine deacetylase / acetylornithine deacetylase ArgE. Metallo pep
3UTR_1348	2129702 +	2130398 Rmet_1956	<i>argE1</i>			Op0573f_2		
3UTR_1785	2129801 -	2129987 Rmet_1957				Op0574r_2		
NPKM_4574	2129988 -	2131839 Rmet_1957		42.67	2.08	Op0574r_2	MET-LIP-Others	Q1LLZ0 Gamma-glutamyltranspeptidase
NPKM_4575	2131940 -	2132411 Rmet_1958		120.33	8.08	Op0574r_2	NA	Q1LLY9 OsmC-like protein
NPKM_4576	2132546 -	2135135 Rmet_1959	<i>clpB</i>	150.33	1.15	Op0574r_2	GIP-PTL-Fold	Q1LLY8 ATPase AAA-2
5UTR_1500	2135136 -	2135183 Rmet_1959	<i>clpB</i>			Op0574r_2		
3UTR_1784	2135308 -	2135350 Rmet_1960	<i>phaY</i>			Op0574r_1		
NPKM_4577	2135351 -	2137520 Rmet_1960	<i>phaY</i>	20.33	1.53	Op0574r_1	MET-CAH-But	Q1LLY7 D(-)-3-hydroxybutyrate oligomer hydrolase
NPKM_4578	2137797 -	2138178 Rmet_1961	<i>moaF</i>	60.00	3.00	Op0574r_1	NA	Q1LLY6 Protein crcB homolog
NPKM_4579	2138177 -	2138669 Rmet_1962	<i>moaE</i>	71.00	3.61	Op0574r_1	MET-COF-Folate	Q1LLY5 Molybdopterin synthase subunit MoaE
NPKM_4580	2138670 -	2138928 Rmet_1963	<i>moaD</i>	81.67	5.51	Op0574r_1	MET-COF-Folate	Q1LLY4 Molybdopterin synthase subunit MoaD
NPKM_4581	2138930 -	2140166 Rmet_1964	<i>moeA</i>	130.67	5.77	Op0574r_1	MET-COF-Folate	Q1LLY3 MoeA-like, domain I and II
NPKM_4582	2140319 -	2141765 Rmet_1965	<i>thrC</i>	443.33	13.87	Op0574r_1	MET-AA-GlySerThr	Q1LLY2 L-threonine synthase
NPKM_4583	2141793 -	2143104 Rmet_1966	<i>thrA</i>	391.00	9.54	Op0574r_1	MET-AA-GlySerThr	Q1LLY1 Homoserine dehydrogenase
NPKM_4584	2143154 -	2144516 Rmet_1967	<i>aatA</i>	238.00	11.14	Op0574r_1	NA	Q1LLY0 Aminotransferase
5UTR_1499	2144517 -	2144581 Rmet_1967	<i>aatA</i>			Op0574r_1		
5UTR_1106	2144566 +	2144691 Rmet_1968				Op0575f_1		
NPKM_4585	2144691 +	2145072 Rmet_1968		104.33	2.08	Op0575f_1	NA	Q1LLX9 Putative uncharacterized protein
NPKM_4586	2145272 +	2145734 Rmet_1969	<i>bcp</i>	274.00	8.72	Op0575f_2	GIP-PTL-Fold	Q1LLX8 Alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen
NPKM_4587	2146080 +	2147775 Rmet_1970		169.67	5.69	Op0575f_2	NA	Q1LLX7 PhoH-like protein
NPKM_4588	2147936 +	2148413 Rmet_1971		103.33	1.53	Op0575f_2	NA	Q1LLX6 Putative signal peptide protein
NPKM_4589	2148461 +	2149100 Rmet_1972		136.33	5.13	Op0575f_2	NA	Q1LLX5 NLP/P60
3UTR_1783	2149058 -	2149159 Rmet_1973	<i>pitA</i>			Op0576r_2		
3UTR_1349	2149101 +	2149914 Rmet_1972				Op0575f_2		
NPKM_4590	2149160 -	2150171 Rmet_1973	<i>pitA</i>	221.67	7.09	Op0576r_2	EIP-TRA-Ion	Q1LLX4 Phosphate transporter
NPKM_4591	2150184 -	2150811 Rmet_1974		261.33	8.02	Op0576r_2	NA	Q1LLX3 Putative uncharacterized protein
NPKM_4592	2150961 -	2152353 Rmet_1975	<i>dnaB</i>	182.33	4.73	Op0576r_2	GIP-REP-Complex	Q1LLX2 Primary replicative DNA helicase
NPKM_4593	2152473 -	2152926 Rmet_1976	<i>rplI</i>	3402.00	169.05	Op0576r_2	GIP-TL-Ribo	Q1LLX1 50S ribosomal protein L9
NPKM_4594	2152956 -	2153235 Rmet_1977	<i>rpsR</i>	3062.33	88.69	Op0576r_2	GIP-TL-Ribo	Q1LLX0 30S ribosomal protein S18
NPKM_4595	2153238 -	2153538 Rmet_1978	<i>priB</i>	2449.00	104.10	Op0576r_2	GIP-REP-Complex	Q1LLW9 Restart primosome assembly protein PriB
NPKM_4596	2153558 -	2153933 Rmet_1979	<i>rpsF</i>	2824.00	39.96	Op0576r_2	GIP-TL-Ribo	Q1LLW8 30S ribosomal protein S6
NPKM_4597	2154050 -	2155052 Rmet_1980	<i>ansB</i>	62.33	2.08	Op0576r_1	MET-EN-Nitrog	Q1LLW7 Asparaginase
5UTR_1498	2155053 -	2155131 Rmet_1980	<i>ansB</i>			Op0576r_1		
5UTR_1107	2155111 +	2155257 Rmet_1981	<i>lexA</i>			Op0577f_1		
3UTR_1782	2155139 -	2156323 Rmet_1983				Op0578r_1		
NPKM_4598	2155257 +	2155914 Rmet_1981	<i>lexA</i>	626.67	62.32	Op0577f_1	GIP-TK-Assoc	Q1LLW6 LexA repressor
NPKM_4599	2156037 +	2156211 Rmet_1982		366.00	44.51	Op0577f_1	NA	Q1LLW5 Putative uncharacterized protein

NPKM_4600	2156324 -	2156597 Rmet_1983		11.33	1.15	Op0578r_1	NA	Q1LLW4 Putative uncharacterized protein
5UTR_1497	2156598 -	2157025 Rmet_1983				Op0578r_1		
NPKM_4601	2156865 +	2158482 Rmet_1984	<i>asdA</i>	115.33	40.53	Op0579f_1	NA	Q1LLW3 Aminotransferase
3UTR_1781	2158124 -	2160299 Rmet_1986				Op0580r_1		
NPKM_4602	2158537 +	2160223 Rmet_1985	<i>ybjL</i>	90.33	30.04	Op0579f_1	NA	Q1LLW2 YidE/YbjL duplication
NPKM_4603	2160189 +	2160363 Rmet_6495		42.67	11.24	Op0579f_1	NA	NA
NPKM_4604	2160300 -	2160510 Rmet_1986		80.00	16.09	Op0580r_1	NA	Q1LLW1 Putative uncharacterized protein
NPKM_4605	2160683 -	2160759 Rmet_R0023		62.33	7.77	Op0580r_1	NA	NA
NPKM_4606	2160687 +	2160921 Rmet_1987		1.00	1.00	Op0581f_1	NA	Q1LLW0 Putative uncharacterized protein
NPKM_4607	2160874 -	2161135 Rmet_1988		115.00	8.72	Op0582r_1	NA	Q1LLV9 Putative uncharacterized protein
5UTR_1496	2161136 -	2161844 Rmet_1988				Op0582r_1		
NPKM_4608	2161176 +	2161395 Rmet_6496		2.00	1.00	Op2021f_1	NA	NA
5UTR_1108	2161406 +	2161449 Rmet_6497				Op2021f_2		
NPKM_4609	2161449 +	2161728 Rmet_6497		24.67	4.04	Op2021f_2	NA	NA
3UTR_1780	2161849 -	2162057 Rmet_1989	<i>dus</i>			Op0582r_1		
NPKM_4610	2162058 -	2163114 Rmet_1989	<i>dus</i>	74.00	4.36	Op0582r_1	GIP-TL-Ass	Q1LLV8 TIM-barrel protein, yjbN family
5UTR_1495	2163115 -	2163654 Rmet_1989	<i>dus</i>			Op0582r_1		
NPKM_4611	2163199 +	2163421 Rmet_1990		13.00	3.61	Op0583f_1	NA	Q1LLV7 Putative uncharacterized protein
NPKM_4612	2163365 +	2163506 Rmet_6498		13.33	2.52	Op0583f_1	NA	NA
3UTR_1350	2163507 +	2163559 Rmet_6498				Op0583f_1		
5UTR_1109	2163647 +	2163668 Rmet_1991				Op0583f_1		
NPKM_4613	2163668 +	2164088 Rmet_1991		3.00	1.00	Op0583f_1	NA	Q1LLV6 Putative uncharacterized protein
NPKM_4614	2164214 +	2164418 Rmet_6499		3.33	1.53	Op0583f_1	NA	NA
NPKM_4615	2164422 +	2164824 Rmet_1992	<i>tnpA</i>	0.00	0.00	Op0583f_1	GIP-REP-Recomb	Q1LK92 Transposase IS3/IS911
NPKM_4616	2164820 +	2165657 Rmet_1993	<i>tnpB</i>	0.00	0.00	Op0583f_1	GIP-REP-Recomb	Q1LK93 Integrase, catalytic region
3UTR_1779	2165665 -	2166164 Rmet_6500				Op2022r_1		
NPKM_4617	2165711 +	2165960 Rmet_1994		23.33	0.58	Op0583f_2	NA	Q1LLV3 Putative uncharacterized protein
3UTR_1351	2165961 +	2166151 Rmet_1994				Op0583f_2		
NPKM_4618	2166165 -	2166276 Rmet_6500		9.67	1.15	Op2022r_1	NA	NA
5UTR_1494	2166277 -	2166317 Rmet_6500				Op2022r_1		
5UTR_1110	2166295 +	2166344 Rmet_6501				Op0583f_2		
NPKM_4619	2166344 +	2166458 Rmet_6501		2.00	0.00	Op0583f_2	NA	NA
NPKM_4620	2166476 +	2166923 Rmet_1995		7.00	0.00	Op0583f_3	NA	Q1LLV2 Putative uncharacterized protein
3UTR_1778	2166687 -	2166896 Rmet_1996				Op0584r_1		
NPKM_4621	2166897 -	2167281 Rmet_1996		1.00	1.00	Op0584r_1	NA	Q1LLV1 Putative uncharacterized protein
3UTR_1352	2166924 +	2167273 Rmet_1995				Op0583f_3		
NPKM_4622	2167505 +	2168345 Rmet_1997		19.00	0.00	Op0585f_1	NA	Q1LLV0 Site specific recombinase
NPKM_4623	2168523 -	2168739 Rmet_1998	<i>tnmC</i>	0.00	0.00	Op2023r_1	NA	NA
NPKM_4624	2168792 -	2169626 Rmet_1999	<i>gspA</i>	0.00	0.00	Op2023r_1	NA	NA
NPKM_4625	2169622 -	2171062 Rmet_2000	<i>tnmA</i>	0.00	0.00	Op2023r_1	NA	NA
NPKM_4626	2171173 -	2171743 Rmet_2001	<i>tnmB</i>	0.00	0.00	Op2023r_1	NA	NA
NPKM_4627	2171757 +	2172324 Rmet_2002		17.33	1.53	Op0587f_1	NA	Q1LLU5 Phage integrase
NPKM_4628	2172320 +	2172926 Rmet_2003		2.67	0.58	Op0587f_1	NA	Q1LLU4 Putative uncharacterized protein

NPKM_4629	2173033	+	2173426	Rmet_2004		4.00	1.00	Op0587f_1	NA	Q1LLU3	Putative uncharacterized protein
NPKM_4630	2173433	+	2173736	Rmet_2005		2.67	1.53	Op0587f_1	NA	Q1LLU2	Putative uncharacterized protein
NPKM_4631	2173738	+	2174605	Rmet_2006		2.00	0.00	Op0587f_1	NA	Q1LLU1	Putative uncharacterized protein
NPKM_4632	2174706	+	2175276	Rmet_2007	<i>tnmB</i>	0.00	0.00	Op0587f_1	NA	NA	
NPKM_4633	2175387	+	2176827	Rmet_2008	<i>tnmA</i>	0.00	0.00	Op0587f_1	NA	NA	
NPKM_4634	2176823	+	2177657	Rmet_2009	<i>gspA</i>	0.00	0.00	Op0587f_1	NA	NA	
NPKM_4635	2177710	+	2177926	Rmet_2010	<i>tnmC</i>	0.00	0.00	Op0587f_1	NA	NA	
NPKM_4636	2178198	+	2178678	Rmet_2011		0.33	0.58	Op0587f_2	NA	Q1LLT6	Putative uncharacterized protein
NPKM_4637	2178784	+	2179141	Rmet_2012		0.00	0.00	Op0587f_2	NA	Q1LLT5	Putative uncharacterized protein
NPKM_4638	2179133	+	2179424	Rmet_2013		1.00	1.00	Op0587f_3	NA	Q1LLT4	Putative uncharacterized protein
NPKM_4639	2179440	+	2179737	Rmet_2014		1.00	0.00	Op0587f_3	NA	Q1LLT3	Putative uncharacterized protein
NPKM_4640	2180114	+	2181455	Rmet_2015		4.00	0.00	Op0587f_4	NA	Q1LLT2	Putative phage-related protein
NPKM_4641	2181615	+	2182293	Rmet_2016		76.67	5.13	Op0587f_5	NA	Q1LLT1	Putative uncharacterized protein
3UTR_1777	2182095	-	2182357	Rmet_2017				Op0588r_1			
NPKM_4642	2182358	-	2183306	Rmet_2017		36.00	2.65	Op0588r_1	NA	Q1LLT0	Putative uncharacterized protein
NPKM_4643	2183223	+	2183829	Rmet_6502		30.00	3.61	Op2024f_1	NA	NA	
NPKM_4644	2183502	-	2183811	Rmet_2018		25.67	1.53	Op0588r_1	NA	Q1LLS9	Putative uncharacterized protein
NPKM_4645	2183866	-	2184271	Rmet_2019		14.00	1.00	Op0588r_1	NA	Q1LLS8	Putative uncharacterized protein
5UTR_1493	2184272	-	2184273	Rmet_2019				Op0588r_1			
NPKM_4646	2184279	+	2184756	Rmet_2020		18.67	0.58	Op0589f_1	NA	Q1LLS7	Putative uncharacterized protein
3UTR_1776	2184314	-	2184910	Rmet_R0024				Op0590r_2			
NPKM_4647	2184911	-	2184987	Rmet_R0024		18.33	2.52	Op0590r_2	NA	NA	
3UTR_1775	2185058	-	2185253	Rmet_2021				Op0590r_2			
NPKM_4648	2185254	-	2185815	Rmet_2021		320.00	9.54	Op0590r_2	NA	Q1LLS6	NADPH-dependent FMN reductase
NPKM_4649	2185908	-	2187060	Rmet_2022		118.33	1.15	Op0590r_1	MET-CAH-Prop	Q1LLS5	Enoyl-CoA hydratase/isomerase
5UTR_1492	2187061	-	2188021	Rmet_2022				Op0590r_1			
NPKM_4650	2187079	+	2188048	Rmet_2023		6.67	0.58	Op0591f_1	NA	Q1LLS4	Sterol desaturase-like protein
3UTR_1353	2188049	+	2188084	Rmet_2023				Op0591f_1			
3UTR_1774	2188100	-	2188133	Rmet_2024	<i>bipA</i>			Op0592r_1			
NPKM_4651	2188134	-	2189958	Rmet_2024	<i>bipA</i>	448.67	12.66	Op0592r_1	NA	Q1LLS3	GTP-binding protein TypA
5UTR_1491	2189959	-	2190089	Rmet_2024	<i>bipA</i>			Op0592r_1			
5UTR_1112	2190051	+	2190078	Rmet_2025				Op0593f_1			
NPKM_4652	2190078	+	2190660	Rmet_2025		33.33	3.21	Op0593f_1	NA	Q1LLS2	Transcriptional regulator, MarR family
3UTR_1773	2190459	-	2190722	Rmet_6503				Op2025r_1			
NPKM_4653	2190685	+	2192245	Rmet_2026		34.67	1.15	Op0593f_1	NA	Q1LLS1	RND efflux system, outer membrane lipoprotein, NodT
NPKM_4654	2190723	-	2190906	Rmet_6503		4.00	2.00	Op2025r_1	NA	NA	
5UTR_1490	2190907	-	2191363	Rmet_6503				Op2025r_1			
NPKM_4655	2192291	+	2193533	Rmet_2027	<i>emrA</i>	40.00	1.00	Op0593f_1	EIP-TRA-Other	Q1LLS0	Secretion protein HlyD
NPKM_4656	2193552	+	2195166	Rmet_2028	<i>emrB</i>	24.00	1.73	Op0593f_1	NA	Q1LLR9	Drug resistance transporter EmrB/QacA subfamily
3UTR_1772	2193614	-	2195239	Rmet_2029	<i>truB</i>			Op0594r_2			
3UTR_1354	2195167	+	2195196	Rmet_2028	<i>emrB</i>			Op0593f_1			
NPKM_4657	2195240	-	2196185	Rmet_2029	<i>truB</i>	144.67	7.77	Op0594r_2	GIP-TL-Ass	Q1LLR8	tRNA pseudouridine synthase B
NPKM_4658	2196244	-	2196616	Rmet_2030	<i>rbfA</i>	280.00	14.18	Op0594r_2	GIP-TL-Ass	Q1LLR7	Ribosome-binding factor A

NPKM_4659	2196680 -	2199620 Rmet_2031	<i>infB</i>	1373.67	20.55	Op0594r_2	NA	Q1LLR6 Translation initiation factor IF-2
NPKM_4660	2199703 -	2201179 Rmet_2032	<i>nusA</i>	1081.00	46.23	Op0594r_2	GIP-TK-Assoc	Q1LLR5 NusA antitermination factor
NPKM_4661	2201175 -	2201664 Rmet_2033		982.00	119.55	Op0594r_2	NA	Q1LLR4 UPF0090 protein Rmet_2033
NPKM_4662	2201992 -	2203888 Rmet_2034		504.67	5.77	Op0594r_2	GIP-TL-Ass	Q1LLR3 Pseudouridine synthase
NPKM_4663	2203916 -	2204825 Rmet_2035		418.00	23.58	Op0594r_2	DIV-Division	Q1LLR2 Condensin subunit ScpB
NPKM_4664	2205375 -	2206143 Rmet_2036		59.33	3.79	Op0594r_1	NA	Q1LLR1 Putative transmembrane protein
5UTR_1113	2206213 +	2206255 Rmet_2037	<i>fnrL</i>			Op0595f_1		
NPKM_4665	2206255 +	2206954 Rmet_2037	<i>fnrL</i>	276.00	7.21	Op0595f_1	NA	Q1LLR0 Transcriptional regulator, Crp/Fnr family
3UTR_1355	2206955 +	2209264 Rmet_2037	<i>fnrL</i>			Op0595f_1		
NPKM_4666	2207037 -	2207283 Rmet_2038		290.67	11.72	Op0596r_2	NA	Q1LLQ9 Putative uncharacterized protein
NPKM_4667	2207279 -	2207516 Rmet_2039		221.33	19.09	Op0596r_2	NA	Q1LLQ8 Putative uncharacterized protein
NPKM_4668	2207529 -	2209059 Rmet_2040	<i>rdxB</i>	162.67	15.14	Op0596r_2	NA	Q1LLQ7 4Fe-4S ferredoxin, iron-sulfur binding
NPKM_4669	2209114 -	2210029 Rmet_2041	<i>ccoP</i>	266.00	21.17	Op0596r_2	MET-EN-OxPhos	Q1LLQ6 Cytochrome c oxidase, cbb3-type, subunit III
NPKM_4670	2210025 -	2210193 Rmet_2042	<i>ccoQ</i>	295.00	19.16	Op0596r_2	MET-EN-OxPhos	Q1LLQ5 Cytochrome c oxidase subunit
NPKM_4671	2210197 -	2210863 Rmet_2043	<i>ccoO</i>	272.00	16.64	Op0596r_2	MET-EN-OxPhos	Q1LLQ4 Cytochrome c oxidase, cbb3-type, subunit II
NPKM_4672	2210880 -	2212329 Rmet_2044	<i>ccoN</i>	217.33	20.21	Op0596r_2	MET-EN-OxPhos	Q1LLQ3 Cytochrome c oxidase, cbb3-type, subunit I
NPKM_4673	2212500 -	2212647 Rmet_2045	<i>rdxS</i>	129.33	15.04	Op0596r_2	NA	Q1LLQ2 Cytochrome oxidase maturation protein, cbb3-type
NPKM_4674	2212649 -	2215235 Rmet_2046	<i>rdxI</i>	90.33	7.09	Op0596r_2	MET-EN-P_ATPase	Q1LLQ1 Heavy metal translocating P-type ATPase
NPKM_4675	2214922 -	2215255 Rmet_6504		91.33	1.53	Op0596r_2	NA	NA
NPKM_4676	2215381 -	2216479 Rmet_2047		129.33	5.13	Op0596r_2	NA	Q1LLQ0 AFG1-like ATPase
NPKM_4677	2216564 -	2217989 Rmet_2048	<i>odhL</i>	680.33	40.77	Op0596r_2	MET-CAH-FbP	Q1LLP9 Dihydrolipoyl dehydrogenase
NPKM_4678	2218114 -	2219374 Rmet_2049	<i>sucB</i>	902.00	18.03	Op0596r_2	MET-CAH-TCA	Q1LLP8 2-oxoglutarate dehydrogenase E2 component
NPKM_4679	2219467 -	2222320 Rmet_2050	<i>sucA</i>	1037.33	21.94	Op0596r_2	NA	
NPKM_4680	2222600 -	2223338 Rmet_2051	<i>ugpQ</i>	66.00	5.57	Op0596r_1	MET-LIP-GlycPLip	Q1LLP6 Glycerophosphoryl diester phosphodiesterase
NPKM_4681	2223334 -	2224438 Rmet_2052	<i>ugpC</i>	87.00	6.00	Op0596r_1	EIP-TRA-ABC	Q1LLP5 sn-glycerol-3-phosphate import ATP-binding protein ugpC
NPKM_4682	2224447 -	2225296 Rmet_2053	<i>ugpE</i>	44.67	4.04	Op0596r_1	EIP-TRA-ABC	Q1LLP4 Binding-protein-dependent transport systems inner membrane component
NPKM_4683	2225306 -	2226188 Rmet_2054	<i>ugpA</i>	37.00	5.29	Op0596r_1	EIP-TRA-ABC	Q1LLP3 Binding-protein-dependent transport systems inner membrane component
NPKM_4684	2226264 -	2227575 Rmet_2055	<i>ugpB</i>	236.33	9.71	Op0596r_1	EIP-TRA-ABC	Q1LLP2 Extracellular solute-binding protein, family 1
5UTR_1489	2227576 -	2228186 Rmet_2055	<i>ugpB</i>			Op0596r_1		
5UTR_1114	2227697 +	2227780 Rmet_2056				Op0597f_1		
NPKM_4685	2227780 +	2228587 Rmet_2056		50.33	22.14	Op0597f_1	NA	Q1LLP1 HAD-superfamily hydrolase subfamily IIB
NPKM_4686	2228705 +	2230391 Rmet_2057		5.00	1.00	Op0597f_1	NA	Q1LLP0 Hycolysin. Metallo peptidase. MEROPS family M30
3UTR_1771	2230286 -	2230822 Rmet_2059	<i>glnG</i>			Op0598r_3		
NPKM_4687	2230437 +	2230746 Rmet_2058		11.67	1.15	Op0597f_2	NA	Q1LLN9 Putative uncharacterized protein
3UTR_1356	2230747 +	2231033 Rmet_2058				Op0597f_2		
NPKM_4688	2230823 -	2232410 Rmet_2059	<i>glnG</i>	57.33	3.79	Op0598r_3	EIP-SIG-2Comp	Q1LLN8 Nitrogen metabolism transcriptional regulator, NtrC, Fis family
NPKM_4689	2232478 -	2233642 Rmet_2060	<i>glnL</i>	86.33	3.79	Op0598r_3	EIP-SIG-2Comp	Q1LLN7 Sensor protein
NPKM_4690	2233647 -	2234121 Rmet_2061		156.67	13.58	Op0598r_3	NA	Q1LLN6 Conserved hypothetical signal peptide protein
NPKM_4691	2234350 -	2235766 Rmet_2062	<i>glnA</i>	862.67	30.66	Op0598r_3	MET-EN-Nitrog	Q1LLN5 Glutamine synthetase
NPKM_4692	2235768 -	2235954 Rmet_6505		200.00	12.12	Op0598r_2	NA	NA
NPKM_4693	2236084 -	2236177 Rmet_6506		10.33	2.08	Op0598r_1	NA	NA
5UTR_1115	2236220 +	2236293 Rmet_2063				Op0599f_1		
NPKM_4694	2236293 +	2236758 Rmet_2063		178.67	8.74	Op0599f_1	NA	Q1LLN4 Rhodanese-like protein

3UTR_1357	2236759 +	2237677 Rmet_2063				Op0599f_1		
NPKM_4695	2236786 -	2237587 Rmet_2064	88.67	3.21	Op0600r_2	NA	Q1LLN3 Molybdopterin binding domain	
NPKM_4696	2237610 -	2238486 Rmet_2065	51.67	2.52	Op0600r_2	NA	Q1LLN2 Putative transmembrane protein	
NPKM_4697	2238597 -	2239593 Rmet_2066	24.67	2.52	Op0600r_1	NA	Q1LLN1 Putative transmembrane protein	
NPKM_4698	2239592 -	2240468 Rmet_2067	43.00	3.46	Op0600r_1	NA	Q1LLN0 Polysaccharide deacetylase	
NPKM_4699	2240481 -	2241468 Rmet_2068	62.33	2.89	Op0600r_1	NA	Q1LLM9 40-residue YVTN beta-propeller repeat	
NPKM_4700	2241600 -	2245551 Rmet_2069	41.67	3.21	Op0600r_1	GIP-REP-Recomb	Q1LLM8 ATP-dependent helicase HrpA	
5UTR_1116	2245369 +	2245574 Rmet_2070			Op0601f_1			
NPKM_4701	2245574 +	2247011 Rmet_2070	59.00	2.00	Op0601f_1	MET-AA-Urea	Q1LLM7 N-acetylglutamate synthase	
NPKM_4702	2247041 +	2247386 Rmet_2071	207.33	6.66	Op0601f_2	NA	Q1LLM6 Probable Fe(2+)-trafficking protein	
NPKM_4703	2247654 +	2248938 Rmet_2072	3.67	0.58	Op0601f_2	NA	Q1LLM5 Major facilitator superfamily MFS_1	
NPKM_4704	2248974 +	2250357 Rmet_2073	2.00	1.00	Op0601f_2	NA	Q1LLM4 Nitrate transporter	
3UTR_1358	2250358 +	2250366 Rmet_2073			Op0601f_2			
NPKM_4705	2250388 +	2254147 Rmet_2074	1.67	0.58	Op0601f_2	MET-EN-Nitrog	Q1LLM3 Respiratory nitrate reductase alpha subunit apoprotein	
NPKM_4706	2254146 +	2255700 Rmet_2075	1.33	0.58	Op0601f_2	MET-EN-Nitrog	Q1LLM2 Respiratory nitrate reductase beta subunit	
3UTR_1359	2255701 +	2255709 Rmet_2075			Op0601f_2			
5UTR_1117	2255711 +	2255717 Rmet_2076			Op0601f_2			
NPKM_4707	2255717 +	2256377 Rmet_2076	1.67	0.58	Op0601f_2	MET-EN-Nitrog	Q1LLM1 Respiratory nitrate reductase chaperone NarJ	
3UTR_1360	2256378 +	2256406 Rmet_2076			Op0601f_2			
5UTR_1118	2256413 +	2256414 Rmet_2077			Op0601f_2			
NPKM_4708	2256414 +	2257098 Rmet_2077	3.00	0.00	Op0601f_2	MET-EN-Nitrog	Q1LLM0 Respiratory nitrate reductase gamma subunit	
NPKM_4709	2257110 +	2257845 Rmet_2078	1.00	0.00	Op0601f_2	MET-EN-Nitrog	Q1LLL9 Carbonic anhydrase	
NPKM_4710	2257847 +	2258237 Rmet_2079	3.00	1.00	Op0601f_3	NA	Q1LLL8 Putative uncharacterized protein	
NPKM_4711	2258236 +	2259409 Rmet_2080	3.33	0.58	Op0601f_3	NA	Q1LLL7 Cytochrome d1, heme region	
NPKM_4712	2259411 +	2259861 Rmet_2081	1.33	0.58	Op0601f_3	NA	Q1LLL6 Transcriptional regulator, AsnC family	
NPKM_4713	2259857 +	2260349 Rmet_6507	1.00	1.00	Op0601f_3	NA	NA	
NPKM_4714	2260351 +	2261317 Rmet_2082	1.00	0.00	Op0601f_3	NA	Q1LLL5 Radical SAM	
NPKM_4715	2261435 +	2262617 Rmet_2083	5.33	0.58	Op0601f_4	MET-EN-Nitrog	Q1LLL4 2-nitropropane dioxygenase, NPD	
3UTR_1770	2262597 -	2262619 Rmet_2084			Op0602r_1			
3UTR_1361	2262618 +	2262717 Rmet_2083			Op0601f_4			
NPKM_4716	2262620 -	2263955 Rmet_2084	7.33	0.58	Op0602r_1	NA	Q1LLL3 Putative uncharacterized protein	
NPKM_4717	2263971 -	2264418 Rmet_2085	8.67	0.58	Op0602r_1	NA	Q1LLL2 Hemerythrin HHE cation binding region	
5UTR_1488	2264419 -	2264498 Rmet_2085			Op0602r_1			
5UTR_1119	2264657 +	2264668 Rmet_2086			Op0603f_1			
NPKM_4718	2264668 +	2266684 Rmet_2086	4.67	0.58	Op0603f_1	EIP-SIG-2Comp	Q1LLL1 Signal transduction histidine kinase, nitrate/nitrite-specific, NarQ	
3UTR_1769	2265998 -	2267394 Rmet_2088			Op0604r_1			
NPKM_4719	2266680 +	2267334 Rmet_2087	7.67	0.58	Op0603f_1	EIP-SIG-2Comp	Q1LLL0 Two component transcriptional regulator, LuxR family	
3UTR_1362	2267335 +	2267926 Rmet_2087			Op0603f_1			
NPKM_4720	2267395 -	2268082 Rmet_2088	211.67	16.92	Op0604r_1	MET-CAH-PP_KDPG	Q1LLK9 Ribose-5-phosphate isomerase	
5UTR_1487	2268083 -	2268171 Rmet_2088			Op0604r_1			
5UTR_1120	2268140 +	2268200 Rmet_2089			Op0605f_1			
NPKM_4721	2268200 +	2269157 Rmet_2089	213.00	12.77	Op0605f_1	MET-CAH-PP_KDPG	Q1LLK8 Transaldolase	
3UTR_1768	2268271 -	2269219 Rmet_2090			Op0606r_1			

3UTR_1363	2269158 +	2270183 Rmet_2089	<i>talB</i>			Op0605f_1		
NPKM_4722	2269220 -	2269955 Rmet_2090	<i>npdA</i>	94.33	3.06	Op0606r_1	NA	Q1LLK7 Silent information regulator protein Sir2
NPKM_4723	2269957 -	2270701 Rmet_2091	<i>rlmB</i>	138.00	1.00	Op0606r_1	GIP-TL-Ass	Q1LLK6 RNA methyltransferase TrmH, group 3
NPKM_4724	2270744 -	2273375 Rmet_2092	<i>rnrr</i>	257.67	10.02	Op0606r_1	NA	Q1LLK5 RNase R
5UTR_1486	2273376 -	2273422 Rmet_2092	<i>rnrr</i>			Op0606r_1		
NPKM_4725	2273444 +	2273531 Rmet_R0025		33.33	5.86	Op0607f_1	NA	NA
3UTR_1767	2273504 -	2275032 Rmet_2095				Op0608r_4		
3UTR_1364	2273532 +	2273633 Rmet_R0025				Op0607f_1		
5UTR_1121	2273636 +	2273794 Rmet_2093				Op0607f_2		
NPKM_4726	2273794 +	2274229 Rmet_2093		157.33	9.02	Op0607f_2	NA	Q1LLK4 Transcriptional regulator, BadM/Rrf2 family
NPKM_4727	2274292 +	2274904 Rmet_2094		95.00	7.21	Op0607f_2	NA	Q1LLK3 NAD-dependent epimerase/dehydratase
3UTR_1365	2274905 +	2275640 Rmet_2094				Op0607f_2		
NPKM_4728	2275033 -	2275642 Rmet_2095		177.00	5.29	Op0608r_4	NA	Q1LLK2 Phosphoribosyltransferase
NPKM_4729	2275729 -	2277073 Rmet_2096	<i>purA</i>	697.33	26.27	Op0608r_4	MET-NUC-Pur	Q1LLK1 Adenylosuccinate synthetase
NPKM_4730	2277252 -	2278404 Rmet_2097	<i>hisZ</i>	253.67	6.66	Op0608r_3	GIP-TL-Ass	Q1LLK0 ATP phosphoribosyltransferase regulatory subunit
NPKM_4731	2278525 -	2279428 Rmet_2098	<i>hflC</i>	519.33	23.46	Op0608r_3	GIP-PTL-Fold	Q1LLJ9 HflC protein
NPKM_4732	2279439 -	2280783 Rmet_2099	<i>hflK</i>	448.00	15.00	Op0608r_3	GIP-PTL-Fold	Q1LLJ8 HflK protein
NPKM_4733	2280888 -	2282124 Rmet_2100	<i>hflX</i>	178.67	10.69	Op0608r_2	NA	Q1LLJ7 Small GTP-binding protein domain
NPKM_4734	2282347 -	2282587 Rmet_2101	<i>hfq</i>	1405.67	41.05	Op0608r_2	NA	Q1LLJ6 Protein hfq
NPKM_4735	2282795 -	2284139 Rmet_2102	<i>der</i>	241.67	8.08	Op0608r_1	NA	Q1LLJ5 GTP-binding protein engA
NPKM_4736	2284370 -	2285522 Rmet_2103	<i>yfgL</i>	340.67	12.86	Op0608r_1	NA	Q1LLJ4 Pyrrolo-quinoline quinone
NPKM_4737	2285555 -	2286188 Rmet_2104		292.33	16.50	Op0608r_1	NA	Q1LLJ3 Conserved hypothetical transmembrane protein
NPKM_4738	2286271 -	2287615 Rmet_2105	<i>hisS</i>	273.67	6.35	Op0608r_1	MET-AA-His	Q1LLJ2 Histidyl-tRNA synthetase
NPKM_4739	2287669 -	2288962 Rmet_2106	<i>ispG</i>	288.00	7.00	Op0608r_1	MET-LIP-Ster	Q1LLJ1 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase
NPKM_4740	2289010 -	2290066 Rmet_2107		229.67	9.87	Op0608r_1	NA	Q1LLJ0 Transcriptional regulator, XRE family
NPKM_4741	2290058 -	2290835 Rmet_2108	<i>pilF</i>	204.33	4.73	Op0608r_1	GIP-PTL-T2S	Q1LLI9 TPR repeat
NPKM_4742	2290831 -	2291986 Rmet_2109	<i>yfgB</i>	486.00	23.26	Op0608r_1	NA	Q1LLI8 Ribosomal RNA large subunit methyltransferase N
NPKM_4743	2292035 -	2292461 Rmet_2110	<i>ndk</i>	1054.33	49.34	Op0608r_1	MET-NUC-Pur	Q1LLI7 Nucleoside diphosphate kinase
5UTR_1485	2292462 -	2292520 Rmet_2110	<i>ndk</i>			Op0608r_1		
5UTR_1122	2292496 +	2292801 Rmet_2111				Op0609f_1		
NPKM_4744	2292801 +	2293509 Rmet_2111		1121.33	36.46	Op0609f_1	NA	Q1LLI6 Putative uncharacterized protein
3UTR_1766	2292969 -	2293573 Rmet_2112	<i>rumA</i>			Op0610r_1		
3UTR_1366	2293510 +	2294761 Rmet_2111				Op0609f_1		
NPKM_4745	2293574 -	2295050 Rmet_2112	<i>rumA</i>	65.00	4.36	Op0610r_1	GIP-TL-Ass	Q1LLI5 23S rRNA (uracil-5-)-methyltransferase rumA
5UTR_1123	2294939 +	2295065 Rmet_2113				Op0611f_1		
NPKM_4746	2295065 +	2295920 Rmet_2113		17.67	1.53	Op0611f_1	NA	Q1LLI4 Endonuclease/exonuclease/phosphatase
3UTR_1367	2295921 +	2296085 Rmet_2113				Op0611f_1		
NPKM_4747	2295921 -	2296758 Rmet_2114		129.00	13.45	Op0612r_2	NA	Q1LLI3 Putative uncharacterized protein
NPKM_4748	2296754 -	2297915 Rmet_2115	<i>rpoS</i>	370.33	6.66	Op0612r_2	GIP-TK-RNAP	Q1LLI2 RNA polymerase sigma factor
NPKM_4749	2297921 -	2298809 Rmet_2116		401.00	9.54	Op0612r_2	NA	Q1LLI1 Peptidase M23B
NPKM_4750	2298817 -	2299726 Rmet_2117		123.33	5.13	Op0612r_1	GIP-PTL-Fold	Q1LLI0 Protein-L-isoaspartate O-methyltransferase
NPKM_4751	2299814 -	2300567 Rmet_2118	<i>surE</i>	156.00	9.17	Op0612r_1	MET-NUC-Pur	Q1LLH9 5'-nucleotidase / 3'-nucleotidase / exopolyphosphatase
5UTR_1124	2300341 +	2300634 Rmet_2119				Op0613f_1		

NPKM_4752	2300634 +	2301720 Rmet_2119		104.67	9.61	Op0613f_1	NA	Q1LLH8 Alcohol dehydrogenase, zinc-binding
3UTR_1368	2301721 +	2302478 Rmet_2119				Op0613f_1		
NPKM_4753	2301788 -	2302580 Rmet_2120		123.00	2.65	Op0614r_2	EIP-TRA-ABC	Q1LLH7 Binding-protein-dependent transport systems inner membrane component
NPKM_4754	2302607 -	2303420 Rmet_2121		154.67	5.03	Op0614r_2	EIP-TRA-ABC	Q1LLH6 ABC transporter-related protein
NPKM_4755	2303522 -	2304566 Rmet_2122		389.33	17.21	Op0614r_2	EIP-TRA-ABC	Q1LLH5 Extracellular solute-binding protein, family 3
NPKM_4756	2304737 -	2305718 Rmet_2123	bug	202.00	36.43	Op0614r_2	NA	Q1LLH4 Uncharacterized protein UPF0065
NPKM_4757	2305776 -	2306757 Rmet_2124		111.67	21.57	Op0614r_2	MET-CAH-But	Q1LLH3 Hydroxymethylglutaryl-CoA lyase
NPKM_4758	2306753 -	2307950 Rmet_2125		103.33	23.71	Op0614r_2	NA	Q1LLH2 L-carnitine dehydratase/bile acid-inducible protein F
NPKM_4759	2308115 -	2309021 Rmet_2126		115.00	9.00	Op0614r_2	NA	Q1LLH1 Transcriptional regulator, LysR family
NPKM_4760	2309027 -	2309642 Rmet_2127	recR	345.33	21.08	Op0614r_2	GIP-REP-Recomb	Q1LLH0 Recombination protein recR
NPKM_4761	2309670 -	2309997 Rmet_2128		404.67	30.02	Op0614r_2	NA	Q1LLG9 UPF0133 protein Rmet_2128
NPKM_4762	2310077 -	2312465 Rmet_2129	dnaX	274.67	8.14	Op0614r_2	GIP-REP-DNA_Pol	Q1LLG8 DNA polymerase III, gamma subunit / DNA polymerase III, tau subunit
NPKM_4763	2312561 -	2315060 Rmet_2130	nrkJ	46.33	2.08	Op0614r_1	MET-NUC-Pur	Q1LLG7 Ribonucleoside-diphosphate reductase
5UTR_1484	2315061 -	2315188 Rmet_2130	nrkJ			Op0614r_1		
5UTR_1125	2315179 +	2315224 Rmet_R0026	ffs			Op2026f_1		
NPKM_4764	2315224 +	2315328 Rmet_R0026	ffs	124.00	11.14	Op2026f_1	NA	NA
3UTR_1765	2315302 -	2315449 Rmet_2131	addA			Op0614r_1		
NPKM_4765	2315450 -	2319014 Rmet_2131	addA	70.33	4.51	Op0614r_1	GIP-REP-Recomb	Q1LLG6 DNA helicase/exodeoxyribonuclease V, subunit A
NPKM_4766	2319010 -	2321941 Rmet_2132	addB	139.33	3.51	Op0614r_1	GIP-REP-Recomb	Q1LLG5 DNA helicase/exodeoxyribonuclease V, subunit B
NPKM_4767	2322002 -	2322278 Rmet_2133		325.33	12.86	Op0614r_1	NA	Q1LLG4 Putative uncharacterized protein
5UTR_1483	2322279 -	2324413 Rmet_2133				Op0614r_1		
NPKM_4768	2322740 +	2323067 Rmet_2134	trxA	1176.00	63.51	Op0615f_1	GIP-PTL-Fold	Q1LLG3 Thioredoxin
NPKM_4769	2323248 +	2324511 Rmet_2135	rho	556.00	21.00	Op0615f_1	GIP-TK-Assoc	Q1LLG2 Transcription termination factor Rho
NPKM_4770	2324593 +	2325484 Rmet_2136		41.00	4.00	Op0615f_1	NA	Q1LLG1 Putative uncharacterized protein
3UTR_1764	2324825 -	2329477 Rmet_R0027				Op0616r_3		
NPKM_4771	2325651 +	2325912 Rmet_2137		1499.00	153.60	Op0615f_2	GIP-TL-Ribo	Q1LLG0 50S ribosomal protein L31 type B
NPKM_4772	2326048 +	2327851 Rmet_2138	arnT	76.00	7.21	Op0615f_2	NA	Q1LLF9 Putative inner membrane transmembrane protein
NPKM_4773	2327926 +	2329276 Rmet_2139	mdtK	22.33	2.52	Op0615f_2	EIP-TRA-Ion	Q1LLF8 MATE efflux family protein
3UTR_1369	2329277 +	2329452 Rmet_2139	mdtK			Op0615f_2		
NPKM_4774	2329478 -	2329555 Rmet_R0027		566.00	93.62	Op0616r_3	NA	NA
NPKM_4775	2329621 -	2329697 Rmet_R0028		106.00	22.07	Op0616r_2	NA	NA
NPKM_4776	2329806 -	2329882 Rmet_R0029		198.33	49.22	Op0616r_2	NA	NA
NPKM_4777	2330032 -	2330109 Rmet_R0030		725.67	101.36	Op0616r_2	NA	NA
NPKM_4778	2330175 -	2330251 Rmet_R0031		437.00	62.27	Op0616r_2	NA	NA
NPKM_4779	2330258 -	2330334 Rmet_R0032		728.33	99.08	Op0616r_2	NA	NA
NPKM_4780	2330542 -	2331940 Rmet_2140	gltX	173.67	1.53	Op0616r_1	MET-AA-GluGSH	Q1LLF7 Glutamyl-tRNA synthetase
5UTR_1126	2331796 +	2332135 Rmet_2141				Op0617f_1		
5UTR_1482	2331941 -	2331971 Rmet_2140	gltX			Op0616r_1		
NPKM_4781	2332135 +	2333086 Rmet_2141		82.33	3.21	Op0617f_1	NA	Q1LLF6 Patatin
3UTR_1763	2332336 -	2333218 Rmet_2142				Op0618r_2		
3UTR_1370	2333087 +	2333151 Rmet_2141				Op0617f_1		
NPKM_4782	2333219 -	2333900 Rmet_2142		607.67	33.17	Op0618r_2	NA	Q1LLF5 NLP/P60
NPKM_4783	2334257 -	2335907 Rmet_2143	yejF	129.00	9.85	Op0618r_1	NA	Q1LLF4 ABC transporter-related protein

NPKM_4784	2335903 -	2337034 Rmet_2144	<i>yejE</i>	83.33	8.74	Op0618r_1	NA	Q1LLF3 Binding-protein-dependent transport systems inner membrane component
NPKM_4785	2337030 -	2338080 Rmet_2145	<i>yejB</i>	71.00	4.00	Op0618r_1	NA	Q1LLF2 Binding-protein-dependent transport systems inner membrane component
NPKM_4786	2338098 -	2340084 Rmet_2146	<i>yejA</i>	82.33	6.43	Op0618r_1	NA	Q1LLF1 Extracellular solute-binding protein, family 5
5UTR_1127	2339771 +	2340194 Rmet_2147	<i>fabI</i>			Op0619f_1		
5UTR_1481	2340085 -	2340267 Rmet_2146	<i>yejA</i>			Op0618r_1		
NPKM_4787	2340194 +	2340977 Rmet_2147	<i>fabI</i>	768.67	23.09	Op0619f_1	MET-LIP-FASyn	Q1LLF0 Enoyl-[acyl-carrier-protein] reductase (NADH)
3UTR_1762	2340497 -	2341037 Rmet_2148				Op0620r_1		
3UTR_1371	2340978 +	2341433 Rmet_2147	<i>fabI</i>			Op0619f_1		
NPKM_4788	2341038 -	2341992 Rmet_2148		8.33	1.15	Op0620r_1	NA	Q1LLE9 Transcriptional regulator, LysR family
5UTR_1480	2341993 -	2342136 Rmet_2148				Op0620r_1		
NPKM_4789	2342033 +	2344007 Rmet_2149		23.00	7.55	Op0621f_1	NA	Q1LLE8 Beta-lactamase-like protein
NPKM_4790	2344146 +	2346036 Rmet_2150	<i>fliC1</i>	21.67	3.79	Op0621f_1	EIP-SIG-2Comp	Q1LLE7 Flagellin-like protein
3UTR_1372	2346037 +	2346262 Rmet_2150	<i>fliC1</i>			Op0621f_1		
5UTR_1128	2346584 +	2346607 Rmet_2151	<i>ftsI1</i>			Op0621f_1		
NPKM_4791	2346607 +	2348353 Rmet_2151	<i>ftsI1</i>	0.67	0.58	Op0621f_1	MET-PepGlyc	Q1LLE6 Penicillin-binding protein, transpeptidase
NPKM_4792	2348480 +	2350802 Rmet_2152	<i>mrcA1</i>	1.00	0.00	Op0621f_1	NA	Q1LLE5 Penicillin-binding protein 1A
3UTR_1373	2350803 +	2350858 Rmet_2152	<i>mrcA1</i>			Op0621f_1		
NPKM_4793	2350868 +	2351510 Rmet_2153		30.00	2.65	Op0621f_2	NA	Q1LLE4 Two component transcriptional regulator, LuxR family
NPKM_4794	2351525 +	2353973 Rmet_2154	<i>evgS</i>	6.67	0.58	Op0621f_2	EIP-SIG-2Comp	Q1LLE3 Sensor protein
NPKM_4795	2354039 +	2354144 Rmet_6508		2.67	1.15	Op2027f_1	NA	NA
3UTR_1374	2354145 +	2354154 Rmet_6508				Op2027f_1		
5UTR_1129	2354204 +	2354266 Rmet_2155				Op0621f_1		
NPKM_4796	2354266 +	2356453 Rmet_2155		6.67	1.15	Op0621f_1	NA	Q1LLE2 Cytochrome c, class I
3UTR_1761	2355949 -	2357160 Rmet_6509				Op2029r_1		
3UTR_1375	2356454 +	2356712 Rmet_2155				Op0621f_1		
5UTR_1130	2357082 +	2357122 Rmet_2156				Op0621f_1		
NPKM_4797	2357122 +	2357656 Rmet_2156		3.00	1.00	Op0621f_1	NA	Q1LLE1 Putative uncharacterized protein
NPKM_4798	2357161 -	2357422 Rmet_6509		91.67	7.51	Op2029r_1	NA	NA
5UTR_1479	2357423 -	2357477 Rmet_6509				Op2029r_1		
5UTR_1131	2357693 +	2357719 Rmet_2157				Op0621f_1		
NPKM_4799	2357719 +	2358049 Rmet_2157		4.33	0.58	Op0621f_1	NA	Q1LLE0 Putative uncharacterized protein
3UTR_1760	2357770 -	2360304 Rmet_2161				Op0622r_1		
NPKM_4800	2358093 +	2358663 Rmet_2158		3.00	0.00	Op0621f_1	NA	Q1LLD9 Putative uncharacterized protein
NPKM_4801	2358702 +	2359029 Rmet_6510		8.67	0.58	Op0621f_2	NA	NA
NPKM_4802	2358806 +	2359403 Rmet_2159		7.00	0.00	Op0621f_2	NA	Q1LLD8 Putative uncharacterized protein
NPKM_4803	2359622 +	2360255 Rmet_2160		24.33	1.15	Op0621f_3	NA	Q1LLD7 Putative uncharacterized protein
3UTR_1376	2360256 +	2361038 Rmet_2160				Op0621f_3		
NPKM_4804	2360305 -	2361757 Rmet_2161		110.33	4.16	Op0622r_1	NA	Q1LLD6 Putative uncharacterized protein
NPKM_4805	2361753 -	2363073 Rmet_2162		72.00	1.00	Op0622r_1	NA	Q1LLD5 Putative uncharacterized protein
5UTR_1478	2363074 -	2363182 Rmet_2162				Op0622r_1		
5UTR_1132	2363675 +	2363694 Rmet_2163				Op0623f_1		
NPKM_4806	2363694 +	2365827 Rmet_2163		88.67	3.06	Op0623f_1	NA	Q1LLD4 Transcriptional regulator, XRE family
NPKM_4807	2365943 +	2367812 Rmet_2164		79.33	3.51	Op0623f_1	NA	Q1LLD3 KAP P-loop

NPKM_4808	2367811 +	2368684 Rmet_2165	82.00	3.46	Op0623f_1	NA	Q1LLD2 Putative uncharacterized protein
NPKM_4809	2368680 +	2369940 Rmet_2166	78.33	3.21	Op0623f_1	NA	Q1LLD1 Putative uncharacterized protein
NPKM_4810	2369936 +	2370686 Rmet_2167	77.67	6.43	Op0623f_1	GIP-PTL-Exp	Q1LLD0 TatD-related deoxyribonuclease
NPKM_4811	2370834 +	2371083 Rmet_2168	57.00	3.00	Op0623f_1	NA	Q1LLC9 Putative uncharacterized protein
3UTR_1759	2370840 -	2371386 Rmet_2169			Op0624r_2		
3UTR_1377	2371084 +	2372173 Rmet_2168			Op0623f_1		
NPKM_4812	2371387 -	2372035 Rmet_2169	15.67	2.52	Op0624r_2	NA	Q1LLC8 Putative uncharacterized protein
NPKM_4813	2372324 -	2372993 Rmet_2170	32.00	2.65	Op0624r_2	NA	Q1LLC7 Putative uncharacterized protein
NPKM_4814	2372992 -	2375995 Rmet_2171	14.33	0.58	Op0624r_1	NA	Q1LLC6 Putative uncharacterized protein
NPKM_4815	2376376 -	2377771 Rmet_2172	40.67	2.31	Op0624r_1	NA	Q1LLC5 Phage integrase
NPKM_4816	2377925 -	2377999 Rmet_R0033	23.33	4.62	Op0624r_1	NA	NA
NPKM_4817	2378180 -	2379431 Rmet_2173	15.00	1.73	Op0624r_1	NA	Q1LLC4 Diguanylate cyclase (GGDEF domain)
NPKM_4818	2379456 -	2379666 Rmet_6511	29.00	5.29	Op0624r_1	NA	NA
5UTR_1477	2379667 -	2379752 Rmet_6511			Op0624r_1		
5UTR_1133	2379763 +	2379876 Rmet_R0034			Op0625f_1		
NPKM_4819	2379876 +	2379953 Rmet_R0034	21.00	6.56	Op0625f_1	NA	NA
3UTR_1378	2379954 +	2379988 Rmet_R0034			0		
5UTR_1134	2379994 +	2380155 Rmet_6512			Op0625f_2		
NPKM_4820	2380155 +	2380308 Rmet_6512	63.33	8.33	Op0625f_2	NA	NA
NPKM_4821	2380737 +	2380959 Rmet_2174	2524.33	184.80	Op0625f_3	NA	Q1LLC3 Translation initiation factor IF-1 1
NPKM_4822	2381121 +	2381598 Rmet_2175	66.67	8.96	Op0625f_3	NA	Q1LLC2 Putative phosphohistidine phosphatase, SixA
NPKM_4823	2381844 +	2382696 Rmet_2176	17.67	2.52	Op0625f_3	NA	Q1LLC1 Ornithine-acyl[acyl carrier protein] N-acyltransferase
3UTR_1758	2382139 -	2382817 Rmet_2177			Op0626r_1		
3UTR_1379	2382697 +	2383260 Rmet_2176			Op0625f_3		
NPKM_4824	2382818 -	2384351 Rmet_2177	109.33	2.31	Op0626r_1	MET-NUC-Pur	Q1LLC0 Ppx/GppA phosphatase
5UTR_1476	2384352 -	2384782 Rmet_2177			Op0626r_1		
5UTR_1135	2384424 +	2384500 Rmet_2178			Op0627f_1		
NPKM_4825	2384500 +	2386582 Rmet_2178	67.67	5.51	Op0627f_1	MET-EN-OxPhos	Q1LLB9 Polyphosphate kinase
3UTR_1380	2386583 +	2386620 Rmet_2178			Op0627f_1		
3UTR_1757	2386627 -	2386669 Rmet_2179			Op0628r_4		
NPKM_4826	2386670 -	2388023 Rmet_2179	21.00	3.61	Op0628r_4	EIP-SIG-2Comp	Q1LLB8 Sensor protein
NPKM_4827	2388146 -	2388854 Rmet_2180	82.33	5.13	Op0628r_4	EIP-SIG-2Comp	Q1LLB7 Two component transcriptional regulator, winged helix family
NPKM_4828	2388890 -	2389595 Rmet_2181	70.00	3.61	Op0628r_4	EIP-TRA-ABC	Q1LLB6 Phosphate uptake regulator, PhoU
NPKM_4829	2389665 -	2390454 Rmet_2182	50.33	2.52	Op0628r_4	EIP-TRA-ABC	Q1LLB5 Phosphate import ATP-binding protein pstB
NPKM_4830	2390475 -	2391378 Rmet_2183	55.33	6.43	Op0628r_4	EIP-TRA-ABC	Q1LLB4 Phosphate transport system permease protein 2
NPKM_4831	2391374 -	2392340 Rmet_2184	93.00	12.12	Op0628r_4	EIP-TRA-ABC	Q1LLB3 Phosphate ABC transporter, permease protein PstC
NPKM_4832	2392453 -	2393485 Rmet_2185	766.33	36.83	Op0628r_4	EIP-TRA-ABC	Q1LLB2 Periplasmic phosphate binding protein
5UTR_1475	2393486 -	2393652 Rmet_2185			Op0628r_4		
3UTR_1756	2393691 -	2393787 Rmet_2186			Op0628r_3		
NPKM_4833	2393788 -	2395132 Rmet_2186	260.67	7.09	Op0628r_3	MET-CAH-AminSug	Q1LLB1 Phosphoglucosamine mutase
NPKM_4834	2395137 -	2396007 Rmet_2187	76.33	4.62	Op0628r_2	MET-COF-Folate	Q1LLB0 Dihydropteroate synthase
NPKM_4835	2396119 -	2398069 Rmet_2188	986.33	29.02	Op0628r_2	GIP-PTL-Fold	Q1LLA9 ATP-dependent metalloprotease FtsH
NPKM_4836	2398222 -	2398888 Rmet_2189	89.33	1.53	Op0628r_1	DIV-Division	Q1LLA8 Ribosomal RNA large subunit methyltransferase J

NPKM_4837	2399044 +	2399554 Rmet_2190		284.67	3.21	Op0629f_1	NA	Q1LLA7 Putative uncharacterized protein
3UTR_1381	2399555 +	2400599 Rmet_2190				Op0629f_1		
NPKM_4838	2399619 -	2400111 Rmet_2191		303.67	3.79	Op0630r_3	NA	Q1LLA6 Putative transmembrane protein
NPKM_4839	2400126 -	2400648 Rmet_2192	<i>greA</i>	514.67	19.86	Op0630r_3	GIP-TK-Assoc	Q1LLA5 Transcription elongation factor
NPKM_4840	2400840 -	2404089 Rmet_2193	<i>carB</i>	517.00	21.00	Op0630r_3	MET-NUC-Pyr	Q1LLA4 Carbamoyl-phosphate synthase large subunit
NPKM_4841	2404159 -	2404831 Rmet_2194	<i>yeaS</i>	516.33	38.89	Op0630r_3	NA	Q1LLA3 Lysine exporter protein (LYSE/YGGA)
NPKM_4842	2404865 -	2406014 Rmet_2195	<i>carA</i>	1264.00	128.37	Op0630r_3	MET-NUC-Pyr	Q1LLA2 Carbamoyl-phosphate synthase small subunit
NPKM_4843	2406334 -	2406748 Rmet_2196	<i>abmE</i>	13.00	2.00	Op0630r_2	NA	Q1LLA1 Endoribonuclease L-PSP
NPKM_4844	2406783 -	2407203 Rmet_2197		8.00	1.00	Op0630r_2	MET-XEN-24D	Q1LLA0 Thioesterase superfamily
NPKM_4845	2407205 -	2408867 Rmet_2198		16.33	0.58	Op0630r_2	MET-XEN-Others	Q1LL99 AMP-dependent synthetase and ligase
NPKM_4846	2408888 -	2410055 Rmet_2199		11.67	0.58	Op0630r_2	MET-CAH-Prop	Q1LL98 Acyl-CoA dehydrogenase-like protein
NPKM_4847	2410064 -	2410916 Rmet_2200		11.33	1.53	Op0630r_2	MET-CAH-Prop	Q1LL97 Enoyl-CoA hydratase
NPKM_4848	2410946 -	2411741 Rmet_2201		9.33	0.58	Op0630r_2	NA	Q1LL96 Short-chain dehydrogenase/reductase SDR
NPKM_4849	2411743 -	2414119 Rmet_2202	<i>abmA</i>	10.00	0.00	Op0630r_2	MET-XEN-Others	Q1LL95 NADH:flavin oxidoreductase/NADH oxidase
NPKM_4850	2414267 -	2416157 Rmet_2203	<i>prpE</i>	52.33	3.06	Op0630r_2	MET-CAH-Prop	Q1LL94 Propionate--CoA ligase
NPKM_4851	2416239 -	2417289 Rmet_2204		12.33	3.21	Op0630r_1	MET-LIP-GlycPLip	Q1LL93 Glycerophosphoryl diester phosphodiesterase
NPKM_4852	2417369 -	2419082 Rmet_2205		87.33	3.79	Op0630r_1	NA	Q1LL92 Lytic transglycosylase, catalytic
NPKM_4853	2419218 -	2420019 Rmet_2206	<i>gloB</i>	65.33	6.43	Op0630r_1	MET-CAH-Pyr	Q1LL91 Beta-lactamase-like protein
5UTR_1136	2419863 +	2420031 Rmet_2207				Op0631f_1		
5UTR_1474	2420020 -	2420739 Rmet_2206	<i>gloB</i>			Op0630r_1		
NPKM_4854	2420031 +	2420826 Rmet_2207		88.33	4.51	Op0631f_1	NA	Q1LL90 Methyltransferase type 11
NPKM_4855	2420844 +	2421282 Rmet_2208	<i>rnhA</i>	48.33	2.08	Op0631f_1	GIP-REP-Recomb	Q1LL89 Ribonuclease H
NPKM_4856	2421304 +	2422030 Rmet_2209	<i>dnaQ</i>	116.33	3.79	Op0631f_2	GIP-REP-DNA_Pol	Q1LL88 DNA polymerase III, epsilon subunit
NPKM_4857	2422154 +	2422229 Rmet_R0035		404.00	83.14	Op0631f_3	NA	NA
3UTR_1755	2422238 -	2422411 Rmet_2210				Op0632r_1		
NPKM_4858	2422412 -	2422700 Rmet_2210		3.00	1.00	Op0632r_1	NA	Q1LL87 Putative uncharacterized protein
5UTR_1473	2422701 -	2422786 Rmet_2210				Op0632r_1		
NPKM_4859	2422848 +	2425587 Rmet_2211	<i>ctpF</i>	23.67	1.15	Op0633f_1	EIP-TRA-Ion	Q1LL86 ATPase, E1-E2 type
NPKM_4860	2425611 +	2426505 Rmet_2212	<i>uspA7</i>	47.33	4.51	Op0633f_1	NA	Q1LL85 UspA
3UTR_1754	2425744 -	2426627 Rmet_2213				Op0634r_3		
3UTR_1382	2426506 +	2427325 Rmet_2212	<i>uspA7</i>			Op0633f_1		
NPKM_4861	2426628 -	2427312 Rmet_2213		65.33	4.16	Op0634r_3	MET-COF-Porph	Q1LL84 Cob(II)yrinic acid a,c-diamide reductase
NPKM_4862	2427415 -	2428012 Rmet_2214		10.33	0.58	Op0634r_2	NA	Q1LL83 Putative uncharacterized protein
5UTR_1472	2428013 -	2428105 Rmet_2214				Op0634r_2		
3UTR_1753	2428125 -	2428175 Rmet_2215				Op0634r_2		
NPKM_4863	2428176 -	2429775 Rmet_2215		70.00	2.00	Op0634r_2	NA	Q1LL82 Rhodanese-like protein
NPKM_4864	2429771 -	2430392 Rmet_2216		37.67	0.58	Op0634r_2	NA	Q1LL81 Cysteine dioxygenase type I
5UTR_1471	2430393 -	2430478 Rmet_2216				Op0634r_2		
3UTR_1752	2430487 -	2430493 Rmet_2217				Op0634r_1		
NPKM_4865	2430494 -	2431703 Rmet_2217		4.00	0.00	Op0634r_1	NA	Q1LL80 Acyl-CoA dehydrogenase
5UTR_1137	2431673 +	2431897 Rmet_2218	<i>ssuD1</i>			Op0635f_1		
5UTR_1470	2431704 -	2431727 Rmet_2217				Op0634r_1		
NPKM_4866	2431897 +	2432989 Rmet_2218	<i>ssuD1</i>	1.67	0.58	Op0635f_1	NA	Q1LL79 Luciferase-like protein

NPKM_4867	2433025 +	2434051 Rmet_2219		1.67	0.58	Op0635f_1	EIP-TRA-ABC	Q1LL78 ABC-type nitrate/sulfonate/bicarbonate transport systems periplasmic com
NPKM_4868	2434055 +	2435099 Rmet_2220		1.67	0.58	Op0635f_1	EIP-TRA-ABC	Q1LL77 Binding-protein-dependent transport systems inner membrane component
NPKM_4869	2435092 +	2435881 Rmet_2221	<i>ssuB1</i>	1.67	0.58	Op0635f_1	EIP-TRA-ABC	Q1LL76 ABC transporter-related protein
NPKM_4870	2435896 +	2437084 Rmet_2222		2.00	0.00	Op0635f_1	NA	Q1LL75 Cytochrome c, class I
3UTR_1383	2437085 +	2437094 Rmet_2222				Op0635f_1		
5UTR_1138	2437200 +	2437226 Rmet_2223				Op0635f_1		
NPKM_4871	2437226 +	2437916 Rmet_2223		1.33	0.58	Op0635f_1	NA	Q1LL74 Putative uncharacterized protein
3UTR_1751	2437346 -	2437869 Rmet_2224	<i>rfaC</i>			Op0636r_2		
NPKM_4872	2437870 -	2438893 Rmet_2224	<i>rfaC</i>	61.00	2.00	Op0636r_2	MET-GLYC-LPS	Q1LL73 Lipopolysaccharide heptosyltransferase I
3UTR_1384	2437917 +	2437956 Rmet_2223				Op0635f_1		
5UTR_1469	2438894 -	2439039 Rmet_2224	<i>rfaC</i>			Op0636r_2		
3UTR_1750	2439055 -	2439106 Rmet_2225				Op0636r_1		
NPKM_4873	2439107 -	2439716 Rmet_2225		2.00	0.00	Op0636r_1	NA	Q1LL72 Isochorismatase hydrolase
5UTR_1468	2439717 -	2439718 Rmet_2225				Op0636r_1		
NPKM_4874	2439801 +	2440662 Rmet_2226		27.67	1.53	Op0637f_1	NA	Q1LL71 Transcriptional regulator, LysR family
NPKM_4875	2440893 +	2442882 Rmet_2227		18.67	1.53	Op0637f_1	NA	Q1LL70 Diguanylate cyclase (GGDEF domain) with PAS/PAC sensor
3UTR_1749	2442657 -	2442908 Rmet_2228				Op0638r_2		
3UTR_1385	2442883 +	2443287 Rmet_2227				Op0637f_1		
NPKM_4876	2442909 -	2444121 Rmet_2228		6.67	0.58	Op0638r_2	NA	Q1LL69 Putative uncharacterized protein
5UTR_1139	2444100 +	2444101 Rmet_6513				Op2030f_1		
NPKM_4877	2444101 +	2444182 Rmet_6513		0.33	0.58	Op2030f_1	NA	NA
NPKM_4878	2444304 -	2446047 Rmet_2229		79.33	4.73	Op0638r_2	EIP-TRA-ABC	Q1LL68 Extracellular solute-binding protein, family 1
NPKM_4879	2446158 -	2446467 Rmet_2230		12.00	1.73	Op0638r_1	NA	Q1LL67 Putative integral membrane protein
NPKM_4880	2446478 -	2447309 Rmet_2231		12.33	1.15	Op0638r_1	EIP-TRA-ABC	Q1LL66 Binding-protein-dependent transport systems inner membrane component
NPKM_4881	2447301 -	2448186 Rmet_2232		13.67	1.53	Op0638r_1	EIP-TRA-ABC	Q1LL65 Binding-protein-dependent transport systems inner membrane component
NPKM_4882	2448182 -	2449283 Rmet_2233		21.33	1.15	Op0638r_1	EIP-TRA-ABC	Q1LL64 ABC transporter-related protein
NPKM_4883	2449284 -	2450409 Rmet_2234		26.67	0.58	Op0638r_1	EIP-TRA-ABC	Q1LL63 ABC transporter-related protein
5UTR_1467	2450410 -	2450455 Rmet_2234				Op0638r_1		
5UTR_1140	2450557 +	2450562 Rmet_2235	<i>glpR</i>			Op0639f_1		
NPKM_4884	2450562 +	2451342 Rmet_2235	<i>glpR</i>	40.33	2.08	Op0639f_1	NA	Q1LL62 Transcriptional regulator, DeoR family
3UTR_1748	2450914 -	2451522 Rmet_2236	<i>purU</i>			Op0640r_2		
NPKM_4885	2451523 -	2452390 Rmet_2236	<i>purU</i>	155.67	8.39	Op0640r_2	MET-CAH-DiCarb	Q1LL61 Formyltetrahydrofolate deformylase
NPKM_4886	2452437 -	2453289 Rmet_2237		37.00	1.00	Op0640r_1	NA	Q1LL60 NUDIX hydrolase
5UTR_1466	2453290 -	2453343 Rmet_2237				Op0640r_1		
NPKM_4887	2453322 +	2454855 Rmet_2238	<i>glpK</i>	21.00	1.00	Op0641f_1	MET-LIP-GlycLip	Q1LL59 Glycerol kinase
NPKM_4888	2454838 +	2456479 Rmet_2239	<i>glpD</i>	25.67	0.58	Op0641f_1	MET-LIP-GlycLip	Q1LL58 FAD dependent oxidoreductase
NPKM_4889	2456548 +	2456941 Rmet_2240		265.67	14.57	Op0641f_2	NA	Q1LL57 Putative uncharacterized protein
3UTR_1386	2456942 +	2456976 Rmet_2240				Op0641f_2		
3UTR_1747	2456976 -	2457049 Rmet_2241				Op0642r_1		
NPKM_4890	2457050 -	2457275 Rmet_2241		174.00	7.94	Op0642r_1	NA	Q1LL56 Putative uncharacterized protein
NPKM_4891	2457373 -	2457805 Rmet_2242		210.33	4.73	Op0642r_1	NA	Q1LL55 Putative signal peptide protein
NPKM_4892	2457930 -	2458134 Rmet_2243		127.67	4.51	Op0642r_1	NA	Q1LL54 Putative uncharacterized protein
5UTR_1465	2458135 -	2458148 Rmet_2243				Op0642r_1		

5UTR_1141	2458291 +	2458308 Rmet_2244				Op0643f_1		
NPKM_4893	2458308 +	2458959 Rmet_2244	3.67	1.15	Op0643f_1	NA		Q1LL53 Putative uncharacterized protein
NPKM_4894	2458955 +	2460236 Rmet_2245	2.67	1.15	Op0643f_1	NA		Q1LL52 Diguanylate cyclase (GGDEF domain)
NPKM_4895	2460245 +	2460749 Rmet_2246	1.67	0.58	Op0643f_1	NA		Q1LL51 OmpA/MotB
5UTR_1142	2460955 +	2460965 Rmet_2247				Op0643f_2		
NPKM_4896	2460965 +	2463587 Rmet_2247		20.33	1.53	Op0643f_2	NA	Q1LL50 Diguanylate cyclase/phosphodiesterase with PAS/PAC sensor(S)
3UTR_1746	2462856 -	2463601 Rmet_2248				Op0644r_1		
3UTR_1387	2463588 +	2463837 Rmet_2247				Op0643f_2		
NPKM_4897	2463602 -	2463878 Rmet_2248	107.67	0.58	Op0644r_1	NA		Q1LL49 Putative uncharacterized protein
NPKM_4898	2463947 -	2464796 Rmet_2249	89.00	4.00	Op0644r_1	MET-AA-Lys_Deg		Q1LL48 Branched chain amino acid: 2-keto-4-methylthiobutyrate aminotransferase
5UTR_1464	2464797 -	2464894 Rmet_2249				Op0644r_1		
5UTR_1143	2465024 +	2465105 Rmet_2250				Op0645f_1		
NPKM_4899	2465105 +	2467409 Rmet_2250	65.00	8.66	Op0645f_1	NA		Q1LL47 Cellulose synthase, subunit B
NPKM_4900	2467410 +	2468574 Rmet_2251	45.33	7.02	Op0645f_1	MET-CAH-Starch		Q1LL46 Glycoside hydrolase, family 8
NPKM_4901	2468555 +	2472359 Rmet_2252	39.67	4.51	Op0645f_1	NA		Q1LL45 Cellulose synthase operon C-like protein
NPKM_4902	2472387 +	2474136 Rmet_2253	50.67	5.69	Op0645f_1	NA		Q1LL44 Putative uncharacterized protein
NPKM_4903	2474139 +	2474340 Rmet_2254	58.00	5.57	Op0645f_1	NA		Q1LL43 Putative uncharacterized protein
NPKM_4904	2474336 +	2475092 Rmet_2255	56.00	5.57	Op0645f_1	NA		Q1LL42 Putative uncharacterized protein
NPKM_4905	2475088 +	2477662 Rmet_2256	27.00	2.65	Op0645f_1	MET-CAH-Starch		Q1LL41 Glycosyl transferase, family 2
NPKM_4906	2477689 +	2479252 Rmet_2257	22.67	4.04	Op0645f_1	NA		Q1LL40 Putative membrane protein
NPKM_4907	2479248 +	2479476 Rmet_2258	36.00	1.73	Op0645f_1	NA		Q1LL39 Putative uncharacterized protein
NPKM_4908	2479624 +	2480872 Rmet_2259	3.67	1.15	Op0645f_1	NA		Q1LL38 Serine phosphatase
NPKM_4909	2480907 +	2481480 Rmet_2260	0.67	0.58	Op0645f_1	NA		Q1LL37 Putative uncharacterized protein
NPKM_4910	2481501 +	2481891 Rmet_2261	0.00	0.00	Op0645f_1	NA		Q1LL36 Putative lipoprotein
NPKM_4911	2481917 +	2482631 Rmet_2262	0.33	0.58	Op0645f_2	NA		Q1LL35 Diguanylate cyclase
NPKM_4912	2482701 +	2482998 Rmet_2263	2.00	1.00	Op0645f_3	NA		Q1LL34 Putative uncharacterized protein
NPKM_4913	2483059 +	2483150 Rmet_R0036	15.00	2.65	Op0645f_4	NA		NA
3UTR_1745	2483121 -	2483295 Rmet_6514				Op2031r_1		
NPKM_4914	2483296 -	2483509 Rmet_6514	15.00	3.61	Op2031r_1	NA		NA
NPKM_4915	2483501 +	2484872 Rmet_2264	36.67	5.69	Op0645f_5	NA		Q1LL33 Putative uncharacterized protein
5UTR_1463	2483510 -	2483791 Rmet_6514				Op2031r_1		
NPKM_4916	2484864 +	2485029 Rmet_6515	72.33	10.07	Op0645f_5	NA		NA
3UTR_1744	2484920 -	2485053 Rmet_2265				Op0646r_1		
NPKM_4917	2485054 -	2485282 Rmet_2265	2.33	1.15	Op0646r_1	NA		Q1LL32 Putative uncharacterized protein
3UTR_1743	2485358 -	2485563 Rmet_6516				Op0648r_3		
NPKM_4918	2485374 +	2485581 Rmet_2266	27.33	4.04	Op0647f_1	NA		Q1LL31 Putative uncharacterized protein
NPKM_4919	2485564 -	2485750 Rmet_6516	8.00	0.00	Op0648r_3	NA		NA
3UTR_1388	2485582 +	2485762 Rmet_2266				Op0647f_1		
NPKM_4920	2485942 -	2487439 Rmet_2267	14.33	0.58	Op0648r_3	DIV-MOT-Flagel		Q1LL30 Flagellar hook-associated 2-like protein
NPKM_4921	2487743 -	2488994 Rmet_2268	0.00	0.00	Op0648r_2	NA		NA
3UTR_1742	2489020 -	2489371 Rmet_2269				Op0648r_2		
NPKM_4922	2489372 -	2491424 Rmet_2269	21.00	1.73	Op0648r_2	GIP-REP-Recomb		Q9RBF5 Ralstonia eutropha insertion sequence IS1090
NPKM_4923	2491532 -	2493515 Rmet_2270	290.33	5.03	Op0648r_2	MET-CAH-FbP		Q1LL27 Acetyl-coenzyme A synthetase

NPKM_4924	2493712 -	2493808	Rmet_6517		4.67	3.06	Op0648r_1	NA	NA
5UTR_1144	2493735 +	2493811	Rmet_2271				Op0649f_1		
5UTR_1462	2493809 -	2494276	Rmet_6517				Op0648r_1		
NPKM_4925	2493811 +	2494738	Rmet_2271		9.00	1.00	Op0649f_1	NA	Q1LL26 Putative uncharacterized protein
NPKM_4926	2494831 +	2495386	Rmet_2272		60.67	4.04	Op0649f_2	NA	Q1LL25 Uncharacterized protein UPF0114
NPKM_4927	2495496 +	2497062	Rmet_2273	<i>fumA</i>	730.33	39.07	Op0649f_3	MET-CAH-TCA	Q1LL24 Fumarase
3UTR_1741	2497202 -	2498039	Rmet_2275				Op0650r_1		
NPKM_4928	2497238 +	2498051	Rmet_2274	<i>murl</i>	105.00	4.36	Op0649f_3	MET-AA-GluGSH	Q1LL23 Glutamate racemase
NPKM_4929	2498040 -	2500356	Rmet_2275		19.00	0.00	Op0650r_1	NA	Q1LL22 AAA ATPase, central region
3UTR_1389	2498052 +	2498445	Rmet_2274	<i>murl</i>			Op0649f_3		
5UTR_1145	2500297 +	2500535	Rmet_2276				Op0651f_1		
5UTR_1461	2500357 -	2502766	Rmet_2275				Op0650r_1		
NPKM_4930	2500535 +	2500778	Rmet_2276		8.33	0.58	Op0651f_1	NA	Q1LL21 Putative uncharacterized protein
NPKM_4931	2500812 +	2501472	Rmet_2277	<i>tonB</i>	51.33	2.52	Op0651f_2	NA	Q1LL20 TonB-like protein
NPKM_4932	2501525 +	2502257	Rmet_2278	<i>exbB1</i>	170.00	4.36	Op0651f_3	NA	Q1LL19 MotA/TolQ/ExbB proton channel
NPKM_4933	2502289 +	2502703	Rmet_2279	<i>exbD1</i>	173.67	7.37	Op0651f_3	NA	Q1LL18 Biopolymer transport protein ExbD/TolR
3UTR_1390	2502704 +	2502742	Rmet_2279	<i>exbD1</i>			Op0651f_3		
3UTR_1740	2502768 -	2503447	Rmet_2281				Op0652r_3		
5UTR_1146	2502830 +	2502911	Rmet_2280	<i>hemP</i>			Op0651f_3		
NPKM_4934	2502911 +	2503238	Rmet_2280	<i>hemP</i>	89.33	7.23	Op0651f_3	NA	Q1LL17 Putative uncharacterized protein
3UTR_1391	2503239 +	2503413	Rmet_2280	<i>hemP</i>			Op0651f_3		
NPKM_4935	2503448 -	2503856	Rmet_2281		1529.33	126.23	Op0652r_3	NA	Q1LL16 Putative uncharacterized protein
NPKM_4936	2503878 -	2504091	Rmet_6518		38.67	7.02	Op0652r_2	NA	NA
NPKM_4937	2504103 -	2504430	Rmet_2282		303.00	46.81	Op0652r_2	NA	Q1LL15 Virulence protein
NPKM_4938	2504603 +	2504689	Rmet_R0037		4.67	2.31	Op2032f_1	NA	NA
3UTR_1392	2504690 +	2505710	Rmet_R0037				Op2032f_1		
NPKM_4939	2504697 -	2505786	Rmet_2283		33.00	8.00	Op0652r_1	NA	Q1LL14 Putative uncharacterized protein
5UTR_1460	2505787 -	2505827	Rmet_2283				Op0652r_1		
3UTR_1739	2505849 -	2506825	Rmet_2285				Op0654r_2		
NPKM_4940	2505888 +	2506806	Rmet_2284	<i>yeiE</i>	35.33	1.53	Op0653f_1	NA	Q1LL13 Transcriptional regulator, LysR family
3UTR_1393	2506807 +	2507497	Rmet_2284	<i>yeiE</i>			Op0653f_1		
NPKM_4941	2506826 -	2508053	Rmet_2285		145.00	12.53	Op0654r_2	EIP-TRA-Ion	Q1LL12 Sodium/hydrogen exchanger
5UTR_1459	2508054 -	2508387	Rmet_2285				Op0654r_2		
3UTR_1738	2508422 -	2508444	Rmet_R0038				Op0654r_2		
NPKM_4942	2508445 -	2508519	Rmet_R0038		692.00	86.88	Op0654r_2	NA	NA
NPKM_4943	2509037 -	2509493	Rmet_2287		47.67	4.73	Op0654r_1	NA	Q8GQ00 Putative uncharacterized protein ORF C111
5UTR_1458	2509494 -	2509863	Rmet_2287				Op0654r_1		
NPKM_4944	2509988 +	2510735	Rmet_2288		2.33	0.58	Op0655f_1	NA	Q8GQ01 Putative uncharacterized protein ORF C110
NPKM_4945	2510853 +	2511066	Rmet_2289	<i>alpA</i>	0.33	0.58	Op0655f_1	NA	Q8GQ02 Phage-related protein
NPKM_4946	2511108 +	2511984	Rmet_2290	<i>soj</i>	0.00	0.00	Op0655f_1	NA	Q8GQ03 Putative chromosome partitioning related protein
NPKM_4947	2511967 +	2512237	Rmet_2291		0.67	0.58	Op0655f_2	NA	A1W5L3 Putative uncharacterized protein
NPKM_4948	2512229 +	2513909	Rmet_2292		0.00	0.00	Op0655f_2	NA	Q1LL05 Putative uncharacterized protein
NPKM_4949	2513923 +	2514484	Rmet_2293		0.00	0.00	Op0655f_2	NA	Q8GQ05 Putative uncharacterized protein ORF C106

NPKM_4950	2514487 +	2515726 Rmet_2294		0.00	0.00	Op0655f_2	NA	Q8GQ06 Putative uncharacterized protein ORF C105
NPKM_4951	2516155 +	2516947 Rmet_2295		0.00	0.00	Op0655f_2	NA	Q8GQ07 Putative uncharacterized protein ORF C104
NPKM_4952	2516943 +	2517471 Rmet_2296	<i>inrR</i>	0.00	0.00	Op0655f_2	NA	Q8GQ08 Putative uncharacterized protein ORF C103
NPKM_4953	2517544 +	2517985 Rmet_2297	<i>ssb2</i>	2.33	0.58	Op0655f_3	GIP-REP-Complex	Q8GQ09 Putative single-stranded DNA binding protein
NPKM_4954	2518268 +	2520299 Rmet_2298	<i>topB2</i>	0.00	0.00	Op0655f_3	GIP-REP-Complex	Q8GQ10 DNA topoisomerase
3UTR_1737	2520533 -	2521021 Rmet_2299				Op0656r_1		
NPKM_4955	2521022 -	2521658 Rmet_2299		61.67	8.50	Op0656r_1	NA	Q8GQ11 Putative integral membrane protein / transporter
NPKM_4956	2521864 -	2522035 Rmet_6519		85.33	12.10	Op0656r_1	NA	NA
NPKM_4957	2521982 -	2522282 Rmet_2300		86.33	7.51	Op0656r_1	NA	Q1LKZ7 Putative uncharacterized protein
NPKM_4958	2522042 +	2522279 Rmet_6520		1.00	1.00	Op0657f_1	NA	NA
NPKM_4959	2522291 +	2522666 Rmet_2301		1.33	0.58	Op0657f_1	NA	Q1LKZ6 Putative uncharacterized protein
NPKM_4960	2522733 -	2523132 Rmet_2302	<i>pbrR2</i>	262.67	4.51	Op0658r_1	NA	A7HYK9 Putative transcriptional regulator, MerR family
5UTR_1457	2523133 -	2523184 Rmet_2302	<i>pbrR2</i>			Op0658r_1		
NPKM_4961	2523181 +	2526136 Rmet_2303	<i>cdaA</i>	15.33	1.53	Op0659f_1	MET-EN-P_ATPase	A7HYL0 Heavy metal translocating P-type ATPase
NPKM_4962	2526139 +	2526640 Rmet_2304	<i>pbrC2</i>	11.67	1.15	Op0659f_1	GIP-PTL-Exp	Q8GQ15 Lipoprotein signal peptidase
NPKM_4963	2526976 +	2527288 Rmet_2305		11.67	2.31	Op0659f_1	NA	Q8GQ16 Putative uncharacterized protein ORF C95
NPKM_4964	2527424 +	2527838 Rmet_2306		0.00	0.00	Op0659f_1	NA	Q8GQ17 Putative uncharacterized protein ORF C94
NPKM_4965	2527859 +	2528252 Rmet_2307		0.00	0.00	Op0659f_1	NA	Q8GQ18 Putative uncharacterized protein ORF C93
NPKM_4966	2528434 +	2529121 Rmet_2308		0.00	0.00	Op0659f_1	NA	Q8GQ19 Putative uncharacterized protein ORF C92
NPKM_4967	2529204 +	2529942 Rmet_2309		3.33	0.58	Op0659f_2	NA	Q8GQ20 Putative uncharacterized protein ORF C91
NPKM_4968	2530039 +	2530318 Rmet_2310		1.00	1.00	Op0659f_2	NA	Q8GQ21 Putative uncharacterized protein ORF C90
NPKM_4969	2530606 +	2531431 Rmet_2311		0.00	0.00	Op0659f_2	NA	Q8GQ22 Putative uncharacterized protein ORF C89
3UTR_1736	2530792 -	2531691 Rmet_2312	<i>merR</i>			Op0660r_1		
NPKM_4970	2531692 -	2532100 Rmet_2312	<i>merR</i>	11.33	2.52	Op0660r_1	NA	Q8GQ23 Organomercurial resistance regulatory protein MerR
5UTR_1456	2532101 -	2532354 Rmet_2312	<i>merR</i>			Op0660r_1		
NPKM_4971	2532171 +	2532522 Rmet_2313	<i>merT</i>	0.00	0.00	Op0661f_1	EIP-TRA-Other	Q8GQ24 Mercuric transport protein MerT
NPKM_4972	2532534 +	2532822 Rmet_2314	<i>merP</i>	1.33	0.58	Op0661f_2	EIP-TRA-Other	Q8GQ25 Periplasmic mercuric ion binding protein MerP
NPKM_4973	2532832 +	2533951 Rmet_6521	<i>merA'</i>	1.33	0.58	Op0661f_2	NA	NA
NPKM_4974	2533661 +	2534519 Rmet_2315	<i>merA''</i>	1.00	0.00	Op0661f_2	NA	Q8GQ26 Mercuric (Hg(II)) reductase
NPKM_4975	2534537 +	2535053 Rmet_6522	<i>tnpA</i>	0.00	0.00	Op0661f_2	NA	NA
NPKM_4976	2534893 +	2535535 Rmet_2317		0.00	0.00	Op0661f_2	NA	Q1LKY2 Transposase Tn3
NPKM_4977	2535604 +	2535865 Rmet_2318		1.00	0.00	Op0661f_3	NA	A1W5J4 Putative uncharacterized protein
NPKM_4978	2536172 +	2536457 Rmet_2319		0.00	0.00	Op0661f_3	NA	Q8GQ28 Putative uncharacterized protein ORF C82
NPKM_4979	2536674 +	2537673 Rmet_2320		0.00	0.00	Op0661f_3	NA	Q8GQ29 Putative uncharacterized protein ORF C81
NPKM_4980	2537818 +	2538646 Rmet_2321	<i>yubP</i>	0.33	0.58	Op0661f_4	NA	Q8GQ30 Putative uncharacterized protein ORF C80
NPKM_4981	2538740 +	2539430 Rmet_2322		1.33	0.58	Op0661f_5	NA	Q1LKX7 Putative uncharacterized protein
NPKM_4982	2539524 +	2539866 Rmet_2323	<i>cggAll</i>	0.00	0.00	Op0661f_5	NA	Q8GQ32 Conserved hypothetical plasmid protein
NPKM_4983	2539970 +	2540378 Rmet_2324		0.33	0.58	Op0661f_6	NA	Q8GQ33 Putative uncharacterized protein ORF C77
NPKM_4984	2540394 +	2540655 Rmet_2325		0.00	0.00	Op0661f_6	NA	Q1LKX4 Putative uncharacterized protein
NPKM_4985	2540731 +	2541379 Rmet_2326		0.00	0.00	Op0661f_6	NA	Q1LKX3 Putative uncharacterized protein
NPKM_4986	2541443 +	2542553 Rmet_2327		0.00	0.00	Op0661f_6	NA	Q8GQ36 Conserved hypothetical plasmid protein
NPKM_4987	2542603 +	2542924 Rmet_2328		0.33	0.58	Op0661f_7	NA	Q8GQ37 Putative uncharacterized protein ORF C73
3UTR_1735	2542896 -	2551960 Rmet_2338				Op0662r_1		

NPKM_4988	2543013 +	2543319 Rmet_2329		0.67	0.58	Op0661f_7	NA	Q1LKX0 Putative uncharacterized protein
NPKM_4989	2543455 +	2545735 Rmet_2330		1.67	0.58	Op0661f_8	NA	Q8GQ39 Conserved hypothetical plasmid protein
NPKM_4990	2545873 +	2546473 Rmet_2331	<i>pilL</i>	0.00	0.00	Op0661f_8	GIP-PTL-T2S	Q1LKW8 Putative secreted protein
NPKM_4991	2546469 +	2547114 Rmet_2332		0.00	0.00	Op0661f_8	NA	Q8GQ41 Putative uncharacterized protein ORF C69
NPKM_4992	2547126 +	2547864 Rmet_2333		0.00	0.00	Op0661f_8	NA	Q8GQ42 Putative uncharacterized protein ORF C68
NPKM_4993	2547845 +	2548436 Rmet_2334		0.00	0.00	Op0661f_8	NA	Q8GQ43 Putative uncharacterized protein ORF C67
NPKM_4994	2548432 +	2548981 Rmet_2335		0.00	0.00	Op0661f_8	NA	Q8GQ44 Putative uncharacterized protein ORF C66
NPKM_4995	2548985 +	2551175 Rmet_2336	<i>virD4</i>	0.00	0.00	Op0661f_8	NA	Q8GQ45 Putative uncharacterized protein ORF C65
NPKM_4996	2551171 +	2551921 Rmet_2337		0.00	0.00	Op0661f_8	NA	A3LCI0 Putative uncharacterized protein
NPKM_4997	2551961 -	2554586 Rmet_2338		96.67	8.08	Op0662r_1	NA	Q8GQ47 Putative uncharacterized protein ORF C63
NPKM_4998	2554595 -	2555321 Rmet_2339		140.33	12.86	Op0662r_1	NA	Q8GQ48 Putative uncharacterized protein ORF C62
NPKM_4999	2555359 -	2556262 Rmet_2340		185.33	13.32	Op0662r_1	NA	Q8GQ49 Putative uncharacterized protein ORF C61
NPKM_5000	2556261 -	2556915 Rmet_2341		205.33	23.63	Op0662r_1	NA	Q1LKV8 Putative uncharacterized protein
NPKM_5001	2556758 -	2557229 Rmet_6523		297.00	29.31	Op0662r_1	NA	NA
NPKM_5002	2557225 -	2558140 Rmet_2342		287.33	37.00	Op0662r_1	NA	A0H9A7 AAA ATPase, central region
NPKM_5003	2558157 -	2558733 Rmet_2343		474.33	55.19	Op0662r_1	NA	Q8GQ53 Putative uncharacterized protein ORF C57
NPKM_5004	2558729 -	2559200 Rmet_2344		597.00	71.90	Op0662r_1	NA	Q8GQ54 Putative excisionase
NPKM_5005	2559403 +	2559787 Rmet_2345		0.67	0.58	Op0663f_1	NA	Q8GQ55 Putative uncharacterized protein ORF C55
NPKM_5006	2559783 +	2560017 Rmet_2346		0.67	0.58	Op0663f_1	NA	Q8GQ56 Putative uncharacterized protein ORF C54
NPKM_5007	2560033 +	2560393 Rmet_2347		0.33	0.58	Op0663f_1	NA	Q8GQ57 Putative uncharacterized protein ORF C53
NPKM_5008	2560405 +	2560804 Rmet_2348		1.33	1.15	Op0663f_2	NA	Q8GQ58 Putative uncharacterized protein ORF C52
NPKM_5009	2560800 +	2561493 Rmet_2349		0.00	0.00	Op0663f_2	NA	Q8GQ59 Putative uncharacterized protein ORF C51
NPKM_5010	2561489 +	2562401 Rmet_2350		0.00	0.00	Op0663f_2	NA	Q8GQ60 Putative uncharacterized protein ORF C50
NPKM_5011	2562390 +	2563809 Rmet_2351		0.00	0.00	Op0663f_2	NA	Q1LKU8 Putative secreted protein
NPKM_5012	2563789 +	2564230 Rmet_2352		0.00	0.00	Op0663f_2	NA	Q8GQ62 Putative uncharacterized protein ORF C48
NPKM_5013	2564229 +	2567121 Rmet_2353		0.33	0.58	Op0663f_3	NA	Q1LKU6 Putative uncharacterized protein
NPKM_5014	2567145 +	2567910 Rmet_2354		0.67	0.58	Op0663f_3	NA	Q8GQ64 Putative uncharacterized protein ORF C46
NPKM_5015	2568085 +	2568580 Rmet_2355	<i>radC</i>	0.00	0.00	Op0663f_3	GIP-REP-Recomb	Q8GQ65 Putative DNA repair protein RadC
NPKM_5016	2568744 +	2569191 Rmet_2356		0.00	0.00	Op0663f_3	NA	Q8GQ66 Putative uncharacterized protein ORF C44
NPKM_5017	2569187 +	2570138 Rmet_2357		0.00	0.00	Op0663f_3	NA	Q8GQ67 Putative uncharacterized protein ORF C43
NPKM_5018	2570147 +	2571542 Rmet_2358		0.00	0.00	Op0663f_3	NA	Q8GQ68 Putative uncharacterized protein ORF C42
NPKM_5019	2571538 +	2571895 Rmet_2359		0.67	0.58	Op0663f_4	NA	Q8GQ69 Putative uncharacterized protein ORF C41
NPKM_5020	2571910 +	2573458 Rmet_2360		1.67	0.58	Op0663f_5	NA	Q8GQ70 Putative uncharacterized protein ORF C40
NPKM_5021	2573473 -	2573833 Rmet_2361		419.00	54.95	Op0664r_1	NA	Q8GQ71 Putative uncharacterized protein ORF C39
NPKM_5022	2573906 -	2574539 Rmet_2362		549.00	82.46	Op0664r_1	NA	Q8GQ72 Putative uncharacterized protein ORF C38
NPKM_5023	2574551 -	2575178 Rmet_2363		859.00	109.19	Op0664r_1	NA	Q8GQ73 Putative uncharacterized protein ORF C37
5UTR_1455	2575179 -	2575434 Rmet_2363				Op0664r_1		
NPKM_5024	2575343 +	2577386 Rmet_2364		2.67	0.58	Op0665f_1	NA	Q1LKT5 Relaxase
3UTR_1734	2576858 -	2577432 Rmet_2365				Op0666r_1		
NPKM_5025	2577433 -	2578429 Rmet_2365		10.33	0.58	Op0666r_1	NA	Q8GQ75 Putative transcriptional regulator
NPKM_5026	2578765 +	2579635 Rmet_2366		6.67	0.58	Op0667f_1	MET-CAH-Prop	Q1LKT3 Enoyl-CoA hydratase/isomerase
NPKM_5027	2579694 -	2580120 Rmet_2367		42.67	1.53	Op0668r_2	NA	Q1LKT2 Putative uncharacterized protein
NPKM_5028	2580176 -	2580554 Rmet_2368		33.67	3.51	Op0668r_2	NA	Q8GQ78 Putative uncharacterized protein ORF C32

NPKM_5029	2580630 -	2581857 Rmet_2369		12.67	0.58	Op0668r_1	EIP-TRA-Ion	Q8GQ79 Similar to metabolite transport protein
5UTR_1454	2581858 -	2581894 Rmet_2369				Op0668r_1		
NPKM_5030	2582006 +	2582318 Rmet_2370	ygaV	33.00	5.29	Op0669f_1	NA	Q8GQ80 Putative transcriptional activator
NPKM_5031	2582340 +	2582868 Rmet_2371		53.67	9.07	Op0669f_1	NA	Q8GQ81 Putative uncharacterized protein ORF C29
NPKM_5032	2582974 +	2583934 Rmet_2372		68.00	4.58	Op0669f_1	MET-CAH-Pyr	Q8GQ82 Putative uncharacterized protein ORF C28
NPKM_5033	2583982 +	2585653 Rmet_2373		40.33	2.52	Op0669f_1	NA	Q8GQ83 Putative uncharacterized protein ORF C27
NPKM_5034	2585699 +	2586179 Rmet_2374		14.33	1.15	Op0669f_1	NA	Q1LKS5 Putative uncharacterized protein
NPKM_5035	2586171 +	2587728 Rmet_2375	ccoN	54.33	6.11	Op0669f_2	MET-EN-OxPhos	Q8GQ84 Putative cytochrome-c oxidase
NPKM_5036	2587784 +	2588366 Rmet_2376	ccoO	60.00	4.58	Op0669f_2	MET-EN-OxPhos	Q8GQ85 Putative cytochrome-c oxidase
NPKM_5037	2588506 +	2589181 Rmet_2377		54.00	3.46	Op0669f_2	NA	Q8GQ86 Putative cytochrome c4
NPKM_5038	2589413 +	2590262 Rmet_2378		44.00	1.73	Op0669f_2	NA	Q8GQ87 Putative cytochrome c
NPKM_5039	2590242 +	2592501 Rmet_2379	ctpA1	31.33	1.53	Op0669f_2	MET-EN-P_ATPase	Q8GQ88 Putative metal transporter ATPase
NPKM_5040	2592525 +	2594124 Rmet_2380	cutE	6.67	1.15	Op0669f_2	NA	Q8GQ89 Putative apolipoprotein N-acyltransferase
3UTR_1733	2594008 -	2594276 Rmet_2381	armS (delta)			Op0670r_1		
NPKM_5041	2594277 -	2594646 Rmet_2381	armS (del	4.67	0.58	Op0670r_1	NA	Q1LKR8 Histidine kinase
5UTR_1453	2594647 -	2594660 Rmet_2381	armS (delta)			Op0670r_1		
NPKM_5042	2594663 +	2595692 Rmet_2382	tnpA	0.00	0.00	Op0671f_1	NA	Q1LB62 Integrase, catalytic region
3UTR_1732	2595674 -	2595679 Rmet_2383	armS (delta)			Op0672r_1		
NPKM_5043	2595680 -	2596769 Rmet_2383	armS (del	25.33	0.58	Op0672r_1	EIP-SIG-2Comp	Q1LKR6 Histidine kinase A-like protein
NPKM_5044	2596765 -	2597434 Rmet_2384	armR	46.33	3.79	Op0672r_1	NA	Q8GQ91 Putative response-regulator ArmR
5UTR_1452	2597435 -	2597656 Rmet_2384	armR			Op0672r_1		
NPKM_5045	2597602 +	2598226 Rmet_2385	ccmA	9.67	2.08	Op0673f_1	MET-EN-Nitrog	Q1LKR4 Cytochrome c biogenesis ATP-binding export protein ccmA 1
NPKM_5046	2598222 +	2598909 Rmet_2386	ccmB	11.00	1.73	Op0673f_1	MET-EN-Nitrog	Q8GQ93 Putative cytochrome c maturation protein B
NPKM_5047	2598921 +	2599659 Rmet_2387	ccmC	4.33	0.58	Op0673f_1	MET-EN-Nitrog	Q8GQ94 Putative heme exporter protein C
NPKM_5048	2599655 +	2599847 Rmet_2388	ccmD	6.67	1.15	Op0673f_1	MET-EN-Nitrog	Q8GQ95 Putative heme exporter protein D
NPKM_5049	2599830 +	2600277 Rmet_2389	ccmE	7.33	0.58	Op0673f_1	MET-EN-Nitrog	Q8GQ96 Cytochrome c-type biogenesis protein ccmE
NPKM_5050	2600280 +	2602242 Rmet_2390	ccmF	4.67	0.58	Op0673f_1	MET-EN-Nitrog	Q8GQ97 Putative cytochrome C-type biogenesis protein CcmF
NPKM_5051	2602238 +	2602763 Rmet_2391	ccmG	3.67	0.58	Op0673f_1	MET-EN-Nitrog	Q8GQ98 Putative cytochrome C biogenesis protein CcmG
NPKM_5052	2602759 +	2603215 Rmet_2392	cycl	4.33	2.08	Op0673f_1	MET-EN-Nitrog	Q8GB67 Putative cytochrome c-type biogenesis protein Cycl
NPKM_5053	2603211 +	2604093 Rmet_2393	cycH	3.67	1.15	Op0673f_1	MET-EN-Nitrog	Q8GQ99 Putative cytochrome c-type biogenesis protein CycH
NPKM_5054	2604190 +	2606029 Rmet_2394	dsbD	10.33	1.53	Op0673f_2	GIP-PTL-Fold	Q8GQA0 Putative thiol:disulfide interchange protein
NPKM_5055	2606028 +	2606865 Rmet_2395	dsbE	6.00	1.00	Op0673f_2	NA	Q8GQA1 Putative thiol:disulfide interchange protein
NPKM_5056	2606867 +	2607641 Rmet_2396	dsbG	10.00	1.00	Op0673f_2	GIP-PTL-Fold	Q8GQA2 Putative thiol:disulfide interchange protein
NPKM_5057	2607731 +	2608538 Rmet_2397		8.67	0.58	Op0673f_2	NA	Q8GQA3 Conserved hypothetical membrane protein
NPKM_5058	2608580 +	2609957 Rmet_2398		23.00	1.00	Op0673f_3	MET-CAH-Fbp	Q8GQA4 Putative pyridine nucleotide-disulfide oxidoreductase, class I
NPKM_5059	2609988 +	2610312 Rmet_2399		29.67	1.15	Op0673f_3	NA	Q8GQA5 Putative uncharacterized protein ORF C5
NPKM_5060	2610349 +	2611240 Rmet_2400	traR2	15.67	0.58	Op0673f_3	NA	Q8GQA6 Putative transcriptional regulator
3UTR_1731	2610476 -	2611260 Rmet_2401				Op0674r_1		
NPKM_5061	2611261 -	2611555 Rmet_2401		25.67	1.53	Op0674r_1	NA	Q8GQA7 Putative uncharacterized protein ORF C3
5UTR_1451	2611556 -	2611572 Rmet_2401				Op0674r_1		
3UTR_1730	2611575 -	2612529 Rmet_2403	int			Op0676r_1		
NPKM_5062	2611674 +	2612331 Rmet_2402	traR	5.67	0.58	Op0675f_1	NA	Q8GQA8 Putative uncharacterized protein ORF C2
NPKM_5063	2612530 -	2613865 Rmet_2403	int	22.00	1.73	Op0676r_1	NA	Q1LKP6 Phage integrase

5UTR_1450	2613866 -	2613903 Rmet_2403	<i>int</i>				Op0676r_1		
NPKM_5064	2613968 +	2614538 Rmet_2404	<i>tnmB</i>	0.00	0.00	Op2033f_1	NA	NA	
NPKM_5065	2614649 +	2616089 Rmet_2405	<i>tnmA</i>	0.00	0.00	Op2033f_1	NA	NA	
NPKM_5066	2616085 +	2616919 Rmet_2406	<i>gspA</i>	0.00	0.00	Op2033f_1	NA	NA	
NPKM_5067	2616972 +	2617188 Rmet_2407	<i>tnmC</i>	0.00	0.00	Op2033f_1	NA	NA	
3UTR_1729	2617329 -	2617365 Rmet_2408	<i>int</i>				Op0678r_2		
NPKM_5068	2617366 -	2617987 Rmet_2408	<i>int</i>	133.00	14.42	Op0678r_2	NA	Q1LKP1 Phage-related integrase	
NPKM_5069	2618212 -	2618288 Rmet_R0039		161.33	28.50	Op0678r_2	NA	NA	
NPKM_5070	2618371 -	2618447 Rmet_R0040		352.33	58.16	Op0678r_2	NA	NA	
NPKM_5071	2618627 -	2619227 Rmet_2409	<i>pgsA</i>	70.33	5.51	Op0678r_1	MET-LIP-GlycPLip	Q1LKP0 CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	
NPKM_5072	2619360 -	2621382 Rmet_2410	<i>uvrC</i>	49.67	3.79	Op0678r_1	GIP-REP-Recomb	Q1LKN9 UvrABC system protein C	
5UTR_1449	2621383 -	2621432 Rmet_2410	<i>uvrC</i>				Op0678r_1		
5UTR_1147	2621447 +	2621494 Rmet_2411					Op0679f_1		
NPKM_5073	2621494 +	2622646 Rmet_2411		33.67	0.58	Op0679f_1	NA	Q1LKN8 Putative uncharacterized protein	
NPKM_5074	2622775 +	2623336 Rmet_2412	<i>efp</i>	1168.67	43.68	Op0679f_2	NA	Q1LKN7 Elongation factor P	
3UTR_1728	2623190 -	2623454 Rmet_2413	<i>nagZ</i>				Op0680r_4		
3UTR_1394	2623337 +	2624352 Rmet_2412	<i>efp</i>				Op0679f_2		
NPKM_5075	2623455 -	2624505 Rmet_2413	<i>nagZ</i>	185.00	8.54	Op0680r_4	MET-CAH-AminSug	Q1LKN6 Glycoside hydrolase, family 3-like protein	
NPKM_5076	2624519 -	2624951 Rmet_2414	<i>acpS</i>	127.33	5.69	Op0680r_4	MET-COF-Pant	Q1LKN5 Holo-[acyl-carrier-protein] synthase	
NPKM_5077	2624947 -	2625730 Rmet_2415	<i>pdxI</i>	202.00	11.36	Op0680r_4	MET-COF-B6	Q1LKN4 Pyridoxal phosphate biosynthetic protein PdxI	
NPKM_5078	2625758 -	2626655 Rmet_2416	<i>recO</i>	184.33	6.81	Op0680r_4	GIP-REP-Recomb	Q1LKN3 DNA repair protein recO	
NPKM_5079	2626660 -	2627599 Rmet_2417	<i>era</i>	315.67	24.99	Op0680r_4	NA	Q1LKN2 GTP-binding protein Era	
NPKM_5080	2627595 -	2628366 Rmet_2418	<i>rnc</i>	367.67	12.50	Op0680r_4	GIP-TL-Ass	Q1LKN1 Ribonuclease 3	
NPKM_5081	2628370 -	2628763 Rmet_2419		431.33	28.04	Op0680r_4	NA	Q1LKN0 Putative transmembrane protein	
NPKM_5082	2628816 -	2629716 Rmet_2420	<i>lepB</i>	234.67	6.35	Op0680r_4	GIP-PTL-Exp	Q1LKM9 Signal peptidase I	
NPKM_5083	2629761 -	2631555 Rmet_2421	<i>lepA</i>	261.67	14.50	Op0680r_4	NA	Q1LKM8 GTP-binding protein lepA	
5UTR_1148	2631542 +	2631546 Rmet_6524					Op2034f_1		
NPKM_5084	2631546 +	2631723 Rmet_6524		8.67	1.53	Op2034f_1	NA	NA	
3UTR_1395	2631724 +	2632287 Rmet_6524					Op2034f_1		
NPKM_5085	2631802 -	2633308 Rmet_2422	<i>mucD</i>	645.00	10.54	Op0680r_4	NA	Q1LKM7 Peptidase S1C, Do	
NPKM_5086	2633327 -	2633528 Rmet_6525		453.33	28.04	Op0680r_4	NA	NA	
NPKM_5087	2633437 -	2634517 Rmet_2423	<i>rseB</i>	509.67	25.77	Op0680r_4	NA	Q1LKM6 Sigma E regulatory protein, MucB/RseB	
NPKM_5088	2634525 -	2635182 Rmet_2424	<i>rseA</i>	1424.00	50.11	Op0680r_4	NA	Q1LKM5 Anti sigma-E protein RseA	
NPKM_5089	2635318 -	2635918 Rmet_2425	<i>rpoE</i>	481.67	29.19	Op0680r_3	GIP-TK-RNAP	Q1LKM4 RNA polymerase sigma factor	
NPKM_5090	2636173 -	2637406 Rmet_2426	<i>fabF</i>	904.33	23.54	Op0680r_3	MET-LIP-FASyn	Q1LKM3 3-oxoacyl-[acyl-carrier-protein] synthase II	
NPKM_5091	2637617 -	2637857 Rmet_2427	<i>acpP</i>	2696.00	214.50	Op0680r_3	MET-LIP-FASyn	Q1LKM2 Acyl carrier protein	
NPKM_5092	2638026 -	2638776 Rmet_2428	<i>fabG</i>	430.67	6.35	Op0680r_2	MET-LIP-FASyn	Q1LKM1 3-oxoacyl-[acyl-carrier-protein] reductase	
NPKM_5093	2638796 -	2639732 Rmet_2429	<i>fabD</i>	363.33	4.04	Op0680r_2	MET-LIP-FASyn	Q1LKM0 [Acyl-carrier-protein] S-malonyltransferase	
NPKM_5094	2639805 -	2640858 Rmet_2430	<i>fabH</i>	272.33	10.07	Op0680r_2	MET-LIP-FASyn	Q1LKL9 3-oxoacyl-[acyl-carrier-protein] synthase III	
NPKM_5095	2640864 -	2641944 Rmet_2431	<i>plsX</i>	255.33	25.11	Op0680r_2	MET-LIP-FASyn	Q1LKL8 Fatty acid/phospholipid synthesis protein plsX	
NPKM_5096	2642136 -	2642316 Rmet_2432	<i>rpmF</i>	2845.00	175.27	Op0680r_2	GIP-TL-Ribo	Q1LKL7 50S ribosomal protein L32	
NPKM_5097	2642436 -	2643054 Rmet_2433		741.33	67.45	Op0680r_1	NA	Q1LKL6 Putative uncharacterized protein	
5UTR_1149	2642910 +	2643114 Rmet_6526					Op0681f_1		

5UTR_1448	2643055 -	2643133 Rmet_2433				Op0680r_1		
NPKM_5098	2643114 +	2643216 Rmet_6526	19.67	4.73	Op0681f_1	NA	NA	
NPKM_5099	2643220 +	2643820 Rmet_2434	41.33	1.53	Op0681f_2	DIV-Division	Q1LKL5 Maf-like protein Rmet_2434	
NPKM_5100	2643823 +	2644555 Rmet_2435	38.67	3.51	Op0681f_2	NA	Q1LKL4 Uroporphyrin-III C/tetrapyrrole (Corrin/Porphyrin) methyltransferase	
3UTR_1396	2644556 +	2644574 Rmet_2435			Op0681f_2			
3UTR_1727	2644566 -	2644610 Rmet_2436			Op0682r_1			
NPKM_5101	2644611 -	2645775 Rmet_2436	156.00	3.61	Op0682r_1	GIP-PTL-Fold	Q1LKL3 Peptidase S49	
NPKM_5102	2645816 -	2646200 Rmet_2437	102.33	12.01	Op0682r_1	NA	Q1LKL2 Rieske (2Fe-2S) region	
NPKM_5103	2646192 -	2646852 Rmet_2438	123.33	1.15	Op0682r_1	MET-CAH-DiCarb	Q1LKL1 HAD-superfamily hydrolase subfamily IA, variant 3	
NPKM_5104	2646910 -	2647927 Rmet_2439	79.33	6.03	Op0682r_1	GIP-TL-Ass	Q1LKL0 Pseudouridine synthase	
5UTR_1447	2647928 -	2648255 Rmet_2439			Op0682r_1			
5UTR_1150	2647948 +	2648902 Rmet_2440			Op0683f_1			
NPKM_5105	2648902 +	2652016 Rmet_2440	522.33	8.50	Op0683f_1	GIP-TL-Ass	Q1LKK9 RNase E	
3UTR_1397	2652017 +	2652140 Rmet_2440			Op0683f_1			
5UTR_1151	2652169 +	2652198 Rmet_2441			Op0683f_1			
NPKM_5106	2652198 +	2653386 Rmet_2441	73.00	4.00	Op0683f_1	MET-COF-Folate	Q1LKK8 GTP cyclohydrolase subunit MoaA	
NPKM_5107	2653423 +	2654035 Rmet_2442	67.67	2.08	Op0683f_1	MET-COF-Folate	Q1LKK7 Probable molybdopterin-guanine dinucleotide biosynthesis protein A	
NPKM_5108	2654129 +	2655416 Rmet_2443	65.00	1.00	Op0683f_1	MET-COF-Folate	Q1LKK6 Molybdopterin molybdochelatase	
3UTR_1726	2654485 -	2656029 Rmet_2445			Op0684r_1			
NPKM_5109	2655595 +	2655877 Rmet_2444	192.67	10.26	Op0683f_2	NA	Q1LKK5 Putative uncharacterized protein	
3UTR_1398	2655878 +	2656584 Rmet_2444			Op0683f_2			
NPKM_5110	2656030 -	2657377 Rmet_2445	60.00	2.65	Op0684r_1	NA	Q1LKK4 Putative uncharacterized protein	
NPKM_5111	2657396 -	2658401 Rmet_2446	145.67	7.57	Op0684r_1	NA	Q1LKK3 D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding	
NPKM_5112	2658397 -	2659828 Rmet_2447	110.67	6.51	Op0684r_1	NA	Q1LKK2 Putative transmembrane protein	
NPKM_5113	2659926 -	2660613 Rmet_2448	94.33	1.15	Op0684r_1	NA	Q1LKK1 Putative uncharacterized protein	
NPKM_5114	2660688 -	2661888 Rmet_2449	75.33	5.69	Op0684r_1	MET-COF-NicAm	Q1LKK0 Nicotinate phosphoribosyltransferase	
5UTR_1152	2661940 +	2662613 Rmet_6527			Op0685f_1			
NPKM_5115	2661954 -	2662485 Rmet_2450	69.67	2.89	Op0684r_1	NA	Q1LKK9 Putative uncharacterized protein	
5UTR_1446	2662486 -	2662608 Rmet_2450			Op0684r_1			
NPKM_5116	2662613 +	2662685 Rmet_6527	12.00	3.00	Op0685f_1	NA	NA	
NPKM_5117	2662903 +	2663227 Rmet_2451	1104.67	47.44	Op0685f_2	NA	Q1LKK8 4Fe-4S ferredoxin, iron-sulfur binding	
NPKM_5118	2663303 +	2664407 Rmet_2452	1169.67	41.63	Op0685f_2	MET-NUC-Pyr	Q1LKK7 FAD-dependent pyridine nucleotide-disulphide oxidoreductase	
NPKM_5119	2664645 +	2664721 Rmet_R0041	559.67	82.98	Op0685f_2	NA	NA	
NPKM_5120	2664866 +	2665706 Rmet_2453	24.00	2.65	Op0685f_2	NA	Q1LKK6 Transcriptional regulator, AraC family	
NPKM_5121	2665730 +	2666339 Rmet_2454	9.00	2.00	Op0685f_2	NA	Q1LKK5 Lysine exporter protein (LYSE/YGGA)	
3UTR_1725	2666442 -	2666965 Rmet_2456			Op0686r_1			
NPKM_5122	2666689 +	2666902 Rmet_2455	9202.67	345.57	Op0685f_3	GIP-TL-Ribo	Q46YX7 30S ribosomal protein S21	
NPKM_5123	2666966 -	2667584 Rmet_2456	64.67	1.53	Op0686r_1	NA	Q1LKK3 Lysine exporter protein (LYSE/YGGA)	
5UTR_1445	2667585 -	2667830 Rmet_2456			Op0686r_1			
NPKM_5124	2667750 +	2668662 Rmet_2457	38.67	1.53	Op0687f_1	NA	Q1LKK2 Nod factor export ATP-binding protein I	
3UTR_1724	2668412 -	2669565 Rmet_2459			Op0688r_6			
NPKM_5125	2668663 +	2669521 Rmet_2458	39.33	1.15	Op0687f_1	NA	Q1LKK1 ABC-2 type transporter, NodJ family	
3UTR_1399	2669522 +	2670350 Rmet_2458			Op0687f_1			

NPKM_5126	2669566 -	2670775 Rmet_2459	<i>metB</i>	304.67	9.45	Op0688r_6	NA	Q1LKJ0 O-succinylhomoserine sulfhydrylase
NPKM_5127	2670811 -	2672344 Rmet_2460	<i>purF</i>	348.33	16.50	Op0688r_6	MET-NUC-Pur	Q1LKI9 Amidophosphoribosyltransferase
NPKM_5128	2672459 -	2672957 Rmet_2461	<i>cvpA</i>	106.67	8.33	Op0688r_5	NA	Q1LKI8 Colicin V production protein
NPKM_5129	2673172 -	2673910 Rmet_2462		253.00	16.09	Op0688r_5	NA	Q1LKI7 Sporulation related
NPKM_5130	2673951 -	2675262 Rmet_2463	<i>folC</i>	113.67	6.81	Op0688r_4	NA	Q1LKI6 FolC bifunctional protein
NPKM_5131	2675340 -	2676213 Rmet_2464	<i>accD</i>	622.00	6.24	Op0688r_4	MET-CAH-Pyr	Q1LKI5 Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha
NPKM_5132	2676406 -	2677204 Rmet_2465	<i>trpA</i>	227.67	7.77	Op0688r_3	MET-AA-PheTyrTrp	Q1LKI4 Tryptophan synthase alpha chain
NPKM_5133	2677215 -	2678151 Rmet_2466		181.00	2.65	Op0688r_3	GIP-REP-Recomb	Q1LKI3 DNA methylase N-4/N-6
NPKM_5134	2678150 -	2679374 Rmet_2467	<i>trpB</i>	223.00	5.00	Op0688r_3	MET-AA-PheTyrTrp	Q1LKI2 Tryptophan synthase, beta chain
NPKM_5135	2679433 -	2680129 Rmet_2468	<i>trpF</i>	112.33	6.35	Op0688r_3	MET-AA-PheTyrTrp	Q1LKI1 N-(5'-phosphoribosyl)anthranilate isomerase
NPKM_5136	2680118 -	2680955 Rmet_2469	<i>truA</i>	69.00	3.00	Op0688r_3	GIP-TL-Ass	Q1LKI0 Pseudouridylate synthase
NPKM_5137	2681101 -	2683924 Rmet_2470		764.00	21.70	Op0688r_3	NA	Q1LKH9 Peptidoglycan-binding LysM
NPKM_5138	2684225 -	2685362 Rmet_2471	<i>asd</i>	1549.33	75.70	Op0688r_3	MET-AA-GlySerThr	Q1LKH8 Aspartate semialdehyde dehydrogenase
NPKM_5139	2685803 -	2686871 Rmet_2472	<i>leuB</i>	568.67	30.83	Op0688r_2	MET-AA-ValLeulle	Q1LKH7 3-isopropylmalate dehydrogenase
NPKM_5140	2686898 -	2687549 Rmet_2473	<i>leuD</i>	478.33	20.23	Op0688r_2	NA	NA
NPKM_5141	2687558 -	2687693 Rmet_2474		453.00	15.52	Op0688r_2	NA	Q1LKH5 Entericidin EcnAB
NPKM_5142	2687719 -	2689129 Rmet_2475	<i>leuC</i>	529.67	29.16	Op0688r_2	MET-AA-ValLeulle	Q1LKH4 3-isopropylmalate dehydratase, large subunit
NPKM_5143	2689443 -	2690145 Rmet_2476	<i>livF1</i>	405.00	8.89	Op0688r_2	EIP-TRA-ABC	Q1LKH3 ABC transporter-related protein
NPKM_5144	2690144 -	2690912 Rmet_2477	<i>livG1</i>	374.00	7.81	Op0688r_2	EIP-TRA-ABC	Q1LKH2 ABC transporter-related protein
NPKM_5145	2690908 -	2692183 Rmet_2478	<i>livM1</i>	323.00	8.89	Op0688r_2	EIP-TRA-ABC	Q1LKH1 Inner-membrane translocator
NPKM_5146	2692195 -	2693122 Rmet_2479	<i>livH1</i>	282.00	1.73	Op0688r_2	EIP-TRA-ABC	Q1LKH0 Inner-membrane translocator
NPKM_5147	2693262 -	2694390 Rmet_2480	<i>livK1</i>	4428.00	193.88	Op0688r_2	EIP-TRA-ABC	Q1LKG9 Extracellular ligand-binding receptor
NPKM_5148	2695055 -	2696357 Rmet_2481	<i>glfA</i>	2856.00	174.16	Op0688r_2	MET-CAH-TCA	Q1LKG8 Citrate synthase
NPKM_5149	2696399 -	2696726 Rmet_2482		1776.33	73.04	Op0688r_2	NA	Q1LKG7 Putative uncharacterized protein
NPKM_5150	2696815 -	2697517 Rmet_2483	<i>sdhB</i>	1664.67	116.98	Op0688r_2	MET-CAH-TCA	Q1LKG6 Succinate dehydrogenase subunit B
NPKM_5151	2697551 -	2699330 Rmet_2484	<i>sdhA</i>	2217.33	137.85	Op0688r_2	MET-CAH-TCA	Q1LKG5 Succinate dehydrogenase subunit A
NPKM_5152	2699333 -	2699699 Rmet_2485	<i>sdhD</i>	1725.67	67.42	Op0688r_2	MET-CAH-TCA	Q1LKG4 Succinate dehydrogenase subunit D
NPKM_5153	2699710 -	2700121 Rmet_2486	<i>sdhC</i>	1674.00	52.46	Op0688r_2	MET-CAH-TCA	Q1LKG3 Succinate dehydrogenase subunit C
NPKM_5154	2700494 -	2701349 Rmet_2488		86.67	6.03	Op0688r_1	NA	Q1LKG1 Transcriptional regulator, GntR family
5UTR_1153	2701200 +	2701740 Rmet_2489	<i>mdh</i>			Op0689f_1		
5UTR_1444	2701350 -	2701367 Rmet_2488				Op0688r_1		
NPKM_5155	2701740 +	2702724 Rmet_2489	<i>mdh</i>	2157.00	189.76	Op0689f_1	MET-CAH-TCA	Q1LKG0 Malate dehydrogenase
NPKM_5156	2702858 +	2703839 Rmet_2490		51.67	0.58	Op0689f_1	MET-CAH-TCA	Q1LKF9 HpcH/Hpal aldolase
NPKM_5157	2704064 +	2704616 Rmet_2491		491.00	11.14	Op0689f_2	NA	Q1LKF8 Putative signal peptide protein
NPKM_5158	2704804 +	2707510 Rmet_2492	<i>acnA2</i>	401.33	18.82	Op0689f_2	MET-CAH-TCA	Q1LKF7 Aconitase
NPKM_5159	2707686 +	2707821 Rmet_2493		48.00	12.00	Op0689f_2	NA	Q1LKF6 Putative uncharacterized protein
NPKM_5160	2707925 +	2709128 Rmet_2494		232.00	9.64	Op0689f_3	NA	Q1LKF5 Putative uncharacterized protein
3UTR_1400	2709129 +	2709166 Rmet_2494				Op0689f_3		
3UTR_1723	2709164 -	2709199 Rmet_2495				Op0690r_1		
NPKM_5161	2709200 -	2709911 Rmet_2495		23.00	2.00	Op0690r_1	NA	Q1LKF4 Putative methyltransferase
5UTR_1154	2709902 +	2709914 Rmet_2496				Op0691f_1		
NPKM_5162	2709914 +	2711531 Rmet_2496		101.33	4.16	Op0691f_1	EIP-TRA-ABC	Q1LKF3 Extracellular solute-binding protein, family 5
3UTR_1401	2711532 +	2712701 Rmet_2496				Op0691f_1		

NPKM_5163	2711584 -	2712517 Rmet_2497		61.33	5.13	Op0692r_2	MET-AA-Met	Q1LKF2 Putative uncharacterized protein
NPKM_5164	2712513 -	2713275 Rmet_2498		33.67	0.58	Op0692r_2	NA	Q1LKF1 Tetratricopeptide TPR_4
5UTR_1443	2713276 -	2713312 Rmet_2498				Op0692r_2		
NPKM_5165	2713393 -	2713549 Rmet_6528		0.33	0.58	Op0692r_1	NA	NA
5UTR_1155	2713421 +	2713430 Rmet_2499				Op0693f_1		
NPKM_5166	2713430 +	2713913 Rmet_2499		18.00	1.00	Op0693f_1	NA	Q1LKF0 Putative uncharacterized protein
5UTR_1442	2713550 -	2713551 Rmet_6528				Op0692r_1		
NPKM_5167	2714070 +	2714427 Rmet_2500		23.67	3.21	Op0693f_1	NA	Q1LKE9 Transcriptional regulator, ArsR family
NPKM_5168	2714423 +	2715506 Rmet_2501	<i>gstF</i>	29.33	1.53	Op0693f_1	MET-OAA-GSH	Q1LKE8 Glutathione S-transferase-like protein
3UTR_1722	2715275 -	2715560 Rmet_2502				Op0694r_2		
3UTR_1402	2715507 +	2715872 Rmet_2501	<i>gstF</i>			Op0693f_1		
NPKM_5169	2715561 -	2716914 Rmet_2502		7.33	0.58	Op0694r_2	NA	Q1LKE7 Cytochrome c, class I
NPKM_5170	2716924 -	2718700 Rmet_2503		8.67	0.58	Op0694r_2	MET-CAH-PP_KDPG	Q1LKE6 Glucose-methanol-choline oxidoreductase
NPKM_5171	2718702 -	2719524 Rmet_2504		7.33	1.15	Op0694r_2	MET-CAH-PP_KDPG	Q1LKE5 Putative uncharacterized protein
5UTR_1441	2719525 -	2719581 Rmet_2504				Op0694r_2		
3UTR_1721	2719585 -	2719743 Rmet_2505				Op0694r_2		
NPKM_5172	2719744 -	2720239 Rmet_2505		38.33	2.52	Op0694r_2	NA	Q1LKE4 Uracil-DNA glycosylase superfamily
NPKM_5173	2720364 -	2722266 Rmet_2506	<i>htpG</i>	156.33	6.11	Op0694r_2	GIP-PTL-Fold	Q1LKE3 Chaperone protein htpG
NPKM_5174	2722366 -	2723914 Rmet_2507		27.00	0.00	Op0694r_1	NA	Q1LKE2 Transcriptional regulator, GntR family
5UTR_1440	2723915 -	2723951 Rmet_2507				Op0694r_1		
5UTR_1156	2723996 +	2723998 Rmet_2508				Op0695f_1		
NPKM_5175	2723998 +	2724676 Rmet_2508		29.00	2.00	Op0695f_1	NA	Q1LKE1 Putative uncharacterized protein
NPKM_5176	2724703 +	2725420 Rmet_2509		31.67	2.52	Op0695f_1	NA	Q1LKE0 Ala-tRNA(Pro) hydrolase
NPKM_5177	2725442 +	2726072 Rmet_2510		20.00	0.00	Op0695f_1	NA	Q1LKD9 Lysine exporter protein (LYSE/YGGA)
NPKM_5178	2726068 +	2727052 Rmet_2511		89.33	3.21	Op0695f_2	NA	Q1LKD8 Putative uncharacterized protein
NPKM_5179	2727064 +	2727517 Rmet_2512		657.33	19.55	Op0695f_3	NA	Q1LKD7 Endoribonuclease L-PSP
NPKM_5180	2727577 +	2728792 Rmet_2513		474.33	12.74	Op0695f_3	NA	Q1LKD6 Aminotransferase, class I and II
NPKM_5181	2728829 +	2729474 Rmet_2514	<i>h</i>	432.33	16.20	Op0695f_3	MET-OAA-GSH	Q1LKD5 Glutathione S-transferase-like protein
NPKM_5182	2729410 +	2729638 Rmet_6529		266.33	11.15	Op0695f_3	NA	NA
3UTR_1403	2729639 +	2729695 Rmet_6529				Op0695f_3		
5UTR_1157	2729697 +	2729991 Rmet_2515	<i>lldP</i>			Op0695f_3		
NPKM_5183	2729991 +	2731668 Rmet_2515	<i>lldP</i>	135.33	20.53	Op0695f_3	EIP-TRA-Ion	Q1LKD4 L-lactate transport
3UTR_1404	2731669 +	2731707 Rmet_2515	<i>lldP</i>			Op0695f_3		
5UTR_1158	2731729 +	2731777 Rmet_2516				Op0695f_3		
NPKM_5184	2731777 +	2733610 Rmet_2516		24.33	1.53	Op0695f_3	EIP-TRA-ABC	Q1LKD3 ABC transporter-related protein
3UTR_1720	2733074 -	2733617 Rmet_2517				Op0696r_1		
3UTR_1405	2733611 +	2734281 Rmet_2516				Op0695f_3		
NPKM_5185	2733618 -	2734149 Rmet_2517		11.33	1.53	Op0696r_1	EIP-TRA-Ion	Q1LKD2 Chromate transporter
NPKM_5186	2734145 -	2734727 Rmet_2518		20.33	1.15	Op0696r_1	EIP-TRA-Ion	Q1LKD1 Chromate transporter
NPKM_5187	2735046 -	2737377 Rmet_2519	<i>parC</i>	91.67	3.06	Op0696r_1	GIP-REP-Complex	Q1LKD0 DNA topoisomerase IV subunit A
NPKM_5188	2737531 -	2738374 Rmet_2520		53.67	2.08	Op0696r_1	NA	Q1LKC9 Lytic transglycosylase, catalytic
NPKM_5189	2738386 -	2740459 Rmet_2521	<i>parE</i>	73.67	1.15	Op0696r_1	GIP-REP-Complex	Q1LKC8 DNA topoisomerase IV subunit B
5UTR_1159	2740545 +	2740582 Rmet_2522				Op0697f_1		

NPKM_5190	2740582	+	2741794	Rmet_2522		23.00	2.65	Op0697f_1	NA	Q1LKC7 Major facilitator superfamily MFS_1
3UTR_1719	2741569	-	2741989	Rmet_2523	<i>uup</i>			Op0698r_4		
NPKM_5191	2741795	+	2741921	Rmet_6530		17.67	4.04	Op0697f_1	NA	NA
3UTR_1406	2741922	+	2742483	Rmet_6530				Op0697f_1		
NPKM_5192	2741990	-	2743916	Rmet_2523	<i>uup</i>	35.67	1.15	Op0698r_4	NA	Q1LKC6 ABC transporter-related protein
3UTR_1718	2744088	-	2744169	Rmet_2524				Op0698r_3		
NPKM_5193	2744170	-	2746915	Rmet_2524		3.00	0.00	Op0698r_3	NA	Q1LKC5 ATP-dependent transcriptional regulator, MalT-like, LuxR family
NPKM_5194	2747025	-	2748576	Rmet_2525		8.67	0.58	Op0698r_3	MET-LIP-FAMet	Q1LKC4 AMP-dependent synthetase and ligase
NPKM_5195	2748693	-	2749563	Rmet_2526	<i>fabG</i>	7.00	1.00	Op0698r_3	MET-LIP-FASyn	Q1LKC3 Short-chain dehydrogenase/reductase SDR
NPKM_5196	2749606	-	2750026	Rmet_2527		4.33	0.58	Op0698r_3	NA	Q1LKC2 MaoC-like dehydratase
NPKM_5197	2750049	-	2750499	Rmet_2528		6.00	1.00	Op0698r_3	NA	Q1LKC1 Putative uncharacterized protein
NPKM_5198	2750565	-	2751759	Rmet_2529		2.67	0.58	Op0698r_2	NA	Q1LKC0 Thiolase
NPKM_5199	2751790	-	2752927	Rmet_2530	<i>ivd</i>	0.33	0.58	Op0698r_1	MET-CAH-Prop	Q1LKB9 Acyl-CoA dehydrogenase-like protein
NPKM_5200	2753205	+	2754345	Rmet_2531	<i>ivd1</i>	0.67	0.58	Op0699f_1	NA	Q1LKB8 Acyl-CoA dehydrogenase-like protein
NPKM_5201	2754412	+	2755600	Rmet_2532		2.33	0.58	Op0699f_2	NA	Q1LKB7 Thiolase
3UTR_1407	2755601	+	2755606	Rmet_2532				Op0699f_2		
5UTR_1160	2755620	+	2755688	Rmet_2533				Op0699f_2		
NPKM_5202	2755688	+	2756519	Rmet_2533		3.00	0.00	Op0699f_2	MET-LIP-FASyn	Q1LKB6 Short-chain dehydrogenase/reductase SDR
3UTR_1717	2756103	-	2756622	Rmet_2534				Op0700r_1		
3UTR_1408	2756520	+	2756824	Rmet_2533				Op0699f_2		
NPKM_5203	2756623	-	2759401	Rmet_2534		57.33	3.06	Op0700r_1	NA	Q1LKB5 ATP-dependent transcriptional regulator, MalT-like, LuxR family
5UTR_1439	2759402	-	2759431	Rmet_2534				Op0700r_1		
5UTR_1161	2759513	+	2759741	Rmet_2535	<i>bug</i>			Op0701f_1		
NPKM_5204	2759741	+	2760716	Rmet_2535	<i>bug</i>	3.00	0.00	Op0701f_1	NA	Q1LKB4 Uncharacterized protein UPF0065
5UTR_1162	2760924	+	2760929	Rmet_2536				Op0701f_1		
NPKM_5205	2760929	+	2762051	Rmet_2536		1.33	0.58	Op0701f_1	NA	Q1LKB3 L-carnitine dehydratase/bile acid-inducible protein F
NPKM_5206	2762064	+	2762814	Rmet_2537		0.33	0.58	Op0701f_1	NA	Q1LKB2 Putative uncharacterized protein
3UTR_1409	2762815	+	2762828	Rmet_2537				Op0701f_1		
NPKM_5207	2763064	+	2763424	Rmet_6531		0.33	0.58	Op0701f_1	NA	NA
NPKM_5208	2763332	+	2764481	Rmet_2538		3.00	0.00	Op0701f_2	NA	Q1LKB1 Porin, Gram-negative type
5UTR_1163	2764521	+	2764633	Rmet_2539				Op0701f_2		
NPKM_5209	2764633	+	2765206	Rmet_2539		1.67	0.58	Op0701f_2	NA	Q1LKB0 Putative uncharacterized protein
3UTR_1410	2765207	+	2765441	Rmet_2539				Op0701f_2		
5UTR_1164	2765655	+	2765850	Rmet_2540				Op0701f_3		
NPKM_5210	2765850	+	2766783	Rmet_2540		81.33	5.51	Op0701f_3	EIP-TRA-ABC	Q1LKA9 Extracellular solute-binding protein, family 3
NPKM_5211	2766915	+	2768103	Rmet_2541	<i>ydco</i>	30.33	3.21	Op0701f_3	EIP-TRA-Ion	Q1LKA8 Benzoate transporter
3UTR_1716	2767890	-	2768164	Rmet_2542				Op0702r_1		
3UTR_1411	2768104	+	2768569	Rmet_2541	<i>ydco</i>			Op0701f_3		
NPKM_5212	2768165	-	2768690	Rmet_2542		20.67	1.15	Op0702r_1	NA	Q1LKA7 Putative uncharacterized protein
5UTR_1165	2768989	+	2769028	Rmet_2543	<i>emrE</i>			Op0703f_1		
NPKM_5213	2769028	+	2769358	Rmet_2543	<i>emrE</i>	17.00	0.00	Op0703f_1	EIP-TRA-Ion	Q1LKA6 Small multidrug resistance protein
3UTR_1412	2769359	+	2769886	Rmet_2543	<i>emrE</i>			Op0703f_1		
NPKM_5214	2769385	-	2769712	Rmet_2544		39.00	3.61	Op0704r_1	NA	Q1LKA5 Putative uncharacterized protein

5UTR_1438	2769713 -	2769834 Rmet_2544				Op0704r_1			
5UTR_1166	2769904 +	2769980 Rmet_2545				Op0705f_1			
NPKM_5215	2769980 +	2771063 Rmet_2545	7.33	0.58		Op0705f_1	NA	Q1LKA4 Fimbrial protein	
3UTR_1715	2770270 -	2771151 Rmet_2546				Op0706r_1			
3UTR_1413	2771064 +	2771394 Rmet_2545				Op0705f_1			
NPKM_5216	2771152 -	2771401 Rmet_2546	9.33	3.21		Op0706r_1	NA	Q1LKA3 Putative uncharacterized protein	
5UTR_1437	2771402 -	2771438 Rmet_2546				Op0706r_1			
3UTR_1714	2771679 -	2773301 Rmet_6533				Op2035r_1			
5UTR_1167	2771711 +	2771715 Rmet_6532				Op0707f_1			
NPKM_5217	2771715 +	2771811 Rmet_6532	1.33	0.58		Op0707f_1	NA	NA	
3UTR_1414	2771812 +	2772091 Rmet_6532				Op0707f_1			
5UTR_1168	2772099 +	2772293 Rmet_2547				Op0707f_2			
NPKM_5218	2772293 +	2773127 Rmet_2547	355.00	20.52		Op0707f_2	NA	Q1LKA2 Proline hydroxylase-like protein	
NPKM_5219	2773302 -	2773566 Rmet_6533	15.00	1.73		Op2035r_1	NA	NA	
NPKM_5220	2773426 +	2773801 Rmet_2548	8.67	0.58		Op0707f_2	NA	Q1LKA1 Putative uncharacterized protein	
5UTR_1436	2773567 -	2773846 Rmet_6533				Op2035r_1			
NPKM_5221	2773949 -	2774921 Rmet_2549	0.00	0.00		Op0708r_4	NA	Q1LKA0 Putative uncharacterized protein	
NPKM_5222	2775039 -	2775255 Rmet_2550	0.00	0.00		Op0708r_4	NA	NA	
NPKM_5223	2775308 -	2776142 Rmet_2551	0.00	0.00		Op0708r_4	NA	NA	
NPKM_5224	2776138 -	2777578 Rmet_2552	0.00	0.00		Op0708r_4	NA	NA	
NPKM_5225	2777689 -	2778259 Rmet_2553	0.00	0.00		Op0708r_4	NA	NA	
3UTR_1713	2778467 -	2778516 Rmet_6534				Op0708r_4			
NPKM_5226	2778517 -	2778742 Rmet_6534	0.00	0.00		Op0708r_4	NA	NA	
NPKM_5227	2778738 -	2779044 Rmet_2554	0.67	0.58		Op0708r_4	NA	Q1LK95 Putative uncharacterized protein	
NPKM_5228	2779040 -	2779238 Rmet_6535	0.33	0.58		Op0708r_4	NA	NA	
3UTR_1712	2779530 -	2779660 Rmet_2555				Op0708r_4			
NPKM_5229	2779661 -	2779925 Rmet_2555	12.33	3.21		Op0708r_4	NA	Q1LK94 Putative uncharacterized protein	
NPKM_5230	2780000 -	2780837 Rmet_2556	0.00	0.00		Op0708r_3	GIP-REP-Recomb	Q1LK93 Integrase, catalytic region	
NPKM_5231	2780833 -	2781235 Rmet_2557	0.00	0.00		Op0708r_3	GIP-REP-Recomb	Q1LK92 Transposase IS3/IS911	
3UTR_1711	2781281 -	2781339 Rmet_6536				Op0708r_3			
NPKM_5232	2781340 -	2781550 Rmet_6536	1.00	1.00		Op0708r_3	NA	NA	
NPKM_5233	2781558 +	2781633 Rmet_6537	1.67	0.58		Op2036f_1	NA	NA	
NPKM_5234	2781573 -	2781834 Rmet_2558	0.33	0.58		Op0708r_2	NA	Q1LK91 Putative uncharacterized protein	
NPKM_5235	2781789 +	2781984 Rmet_6538	3.67	0.58		Op2037f_1	NA	NA	
5UTR_1435	2781835 -	2781932 Rmet_2558				Op0708r_2			
3UTR_1710	2781967 -	2782318 Rmet_2559				Op0708r_2			
NPKM_5236	2782207 +	2782306 Rmet_6539	7.33	1.15		Op2037f_1	NA	NA	
NPKM_5237	2782319 -	2782988 Rmet_2559	20.33	1.53		Op0708r_2	NA	Q1LK90 Resolvase-like protein	
NPKM_5238	2783110 -	2783302 Rmet_6540	7.00	1.00		Op0708r_1	NA	NA	
NPKM_5239	2783457 -	2784375 Rmet_2560	26.33	1.53		Op0708r_1	NA	Q1LK89 Putative uncharacterized protein	
NPKM_5240	2784561 -	2785938 Rmet_2561	40.33	1.53		Op0708r_1	NA	Q1LK88 Phage integrase	
NPKM_5241	2786047 -	2786122 Rmet_R0042	34.00	12.49		Op0708r_1	NA	NA	
5UTR_1169	2786109 +	2786231 Rmet_2562				Op0709f_1			

5UTR_1434	2786123 -	2786147 Rmet_R0042				Op0708r_1		
NPKM_5242	2786231 +	2787002 Rmet_2562		14.00	1.73	Op0709f_1	NA	Q1LK87 Protein serine/threonine phosphatases
NPKM_5243	2787139 +	2787463 Rmet_2563		4.67	1.53	Op0709f_1	NA	Q1LK86 Putative uncharacterized protein
5UTR_1170	2787467 +	2787818 Rmet_2564	<i>rhIE2</i>			Op0709f_2		
NPKM_5244	2787818 +	2789723 Rmet_2564	<i>rhIE2</i>	442.67	35.81	Op0709f_2	NA	Q1LK85 DEAD/DEAH box helicase-like protein
3UTR_1415	2789724 +	2789765 Rmet_2564	<i>rhIE2</i>			Op0709f_2		
3UTR_1709	2789745 -	2789798 Rmet_2565				Op0710r_2		
NPKM_5245	2789799 -	2791056 Rmet_2565		56.67	0.58	Op0710r_2	NA	Q1LK84 Putative uncharacterized protein
NPKM_5246	2791186 -	2792275 Rmet_2566		19.33	1.53	Op0710r_1	NA	Q1LK83 Putative uncharacterized conserved protein
5UTR_1433	2792276 -	2792401 Rmet_2566				Op0710r_1		
NPKM_5248	2792846 +	2793545 Rmet_2567		138.33	21.22	Op0711f_1	NA	Q1LK82 Integral membrane protein TerC
NPKM_5249	2793652 +	2794447 Rmet_2568	<i>thyA</i>	174.67	4.16	Op0711f_1	MET-NUC-Pyr	Q1LK81 Thymidylate synthase
NPKM_5250	2794443 +	2794944 Rmet_2569	<i>folA</i>	174.33	8.14	Op0711f_1	MET-COF-Folate	Q1LK80 Dihydrofolate reductase
3UTR_1416	2794945 +	2795377 Rmet_2569	<i>folA</i>			Op0711f_1		
3UTR_1708	2794967 -	2795041 Rmet_2570	<i>pmbA</i>			Op0712r_1		
NPKM_5251	2795042 -	2796410 Rmet_2570	<i>pmbA</i>	246.67	14.57	Op0712r_1	NA	Q1LK79 Putative uncharacterized protein
5UTR_1172	2795380 +	2796458 Rmet_2571				Op0713f_1		
5UTR_1432	2796411 -	2796926 Rmet_2570	<i>pmbA</i>			Op0712r_1		
NPKM_5252	2796458 +	2797067 Rmet_2571		176.00	6.56	Op0713f_1	NA	Q1LK78 UPF0307 protein Rmet_2571
3UTR_1707	2796940 -	2797791 Rmet_2573				Op0714r_1		
NPKM_5253	2797063 +	2797714 Rmet_2572	<i>mogA</i>	225.33	7.37	Op0713f_1	MET-COF-Folate	Q1LK77 Molybdopterin adenyltransferase
3UTR_1417	2797715 +	2798693 Rmet_2572	<i>mogA</i>			Op0713f_1		
NPKM_5254	2797792 -	2798674 Rmet_2573		75.00	2.65	Op0714r_1	NA	Q1LK76 Auxin Efflux Carrier
NPKM_5255	2798747 -	2799365 Rmet_2574	<i>orn</i>	185.00	6.08	Op0714r_1	NA	Q1LK75 Exonuclease
5UTR_1173	2798959 +	2799358 Rmet_2575				Op0715f_1		
NPKM_5256	2799358 +	2800768 Rmet_2575		69.00	2.65	Op0715f_1	NA	Q1LK74 Peptidase M48, Ste24p
5UTR_1431	2799366 -	2799756 Rmet_2574	<i>orn</i>			Op0714r_1		
NPKM_5257	2800764 +	2801736 Rmet_2576	<i>rsgA</i>	87.00	4.36	Op0715f_1	NA	Q1LK73 GTPase EngC
NPKM_5258	2801770 +	2802088 Rmet_2577		117.67	5.13	Op0715f_1	NA	Q1LK72 Putative uncharacterized protein
3UTR_1418	2802089 +	2802169 Rmet_2577				Op0715f_1		
3UTR_1706	2802131 -	2802183 Rmet_2578				Op0716r_2		
NPKM_5259	2802184 -	2803165 Rmet_2578		117.00	6.24	Op0716r_2	MET-COF-Porph	Q1LK71 Cobalamin biosynthesis protein CbiB
NPKM_5260	2803360 -	2804059 Rmet_2579		27.00	2.65	Op0716r_1	NA	Q1LK70 Pirin-like protein
5UTR_1174	2804105 +	2804110 Rmet_2580				Op0717f_1		
NPKM_5261	2804110 +	2805139 Rmet_2580		50.00	4.58	Op0717f_1	NA	Q1LK69 Transcriptional regulator, LysR family
NPKM_5262	2805180 +	2806113 Rmet_2581	<i>gluQ</i>	52.33	4.16	Op0717f_1	NA	Q1LK68 Glutamyl-Q tRNA(Asp) synthetase
NPKM_5263	2806055 -	2807726 Rmet_2582	<i>rhIE</i>	271.00	14.11	Op0718r_1	NA	Q1LK67 DEAD/DEAH box helicase-like protein
NPKM_5264	2807713 +	2809417 Rmet_2583	<i>phoD</i>	4.67	0.58	Op0719f_1	NA	Q1LK66 Alkaline phosphatase
5UTR_1430	2807727 -	2808270 Rmet_2582	<i>rhIE</i>			Op0718r_1		
3UTR_1705	2808611 -	2809484 Rmet_2584	<i>bug</i>			Op0720r_1		
3UTR_1419	2809418 +	2809555 Rmet_2583	<i>phoD</i>			Op0719f_1		
NPKM_5265	2809485 -	2810499 Rmet_2584	<i>bug</i>	32.00	2.00	Op0720r_1	NA	Q1LK65 Uncharacterized protein UPF0065
NPKM_5266	2810568 -	2812212 Rmet_2585		30.67	1.15	Op0720r_1	MET-CAH-Pyr	Q1LK64 Propionate CoA-transferase

5UTR_1175	2812191 +	2812198 Rmet_2586				Op0721f_1		
NPKM_5267	2812198 +	2813176 Rmet_2586		14.00	0.00	Op0721f_1	NA	Q1LK63 Transcriptional regulator, lclR family
5UTR_1429	2812213 -	2812271 Rmet_2585				Op0720r_1		
3UTR_1704	2812963 -	2813364 Rmet_2587	<i>gstN</i>			Op0722r_1		
3UTR_1420	2813177 +	2813884 Rmet_2586				Op0721f_1		
NPKM_5268	2813365 -	2813974 Rmet_2587	<i>gstN</i>	77.00	1.73	Op0722r_1	MET-OAA-GSH	Q1LK62 Putative uncharacterized protein
5UTR_1428	2813975 -	2813996 Rmet_2587	<i>gstN</i>			Op0722r_1		
NPKM_5269	2814244 +	2815228 Rmet_2588	<i>kdgT</i>	6.67	1.15	Op0723f_1	EIP-TRA-Ion	Q1LK61 2-keto-3-deoxygluconate permease
NPKM_5270	2815224 +	2816457 Rmet_2589		5.00	0.00	Op0723f_1	NA	Q1LK60 Type III effector Hrp-dependent outers
NPKM_5271	2816487 +	2817489 Rmet_2590	<i>pdxA</i>	7.67	0.58	Op0723f_1	NA	NA
NPKM_5272	2817589 +	2818366 Rmet_2591		23.33	2.31	Op0723f_2	NA	Q1LK58 Transcriptional regulator, DeoR family
3UTR_1703	2818327 -	2818404 Rmet_2592				Op0724r_1		
3UTR_1421	2818367 +	2819038 Rmet_2591				Op0723f_2		
NPKM_5273	2818405 -	2819203 Rmet_2592		2.33	0.58	Op0724r_1	NA	Q1LK57 Putative uncharacterized protein
5UTR_1176	2819133 +	2819242 Rmet_2593				Op0725f_1		
NPKM_5274	2819242 +	2820481 Rmet_2593		23.33	2.08	Op0725f_1	NA	Q1LK56 Glycosyl transferase, family 28
3UTR_1422	2820482 +	2821512 Rmet_2593				Op0725f_1		
3UTR_1702	2820581 -	2820597 Rmet_2594				Op0726r_1		
NPKM_5275	2820598 -	2821888 Rmet_2594		4.00	1.00	Op0726r_1	NA	Q1LK55 Putative uncharacterized protein
5UTR_1177	2821726 +	2821748 Rmet_6541				Op0727f_1		
NPKM_5276	2821748 +	2821943 Rmet_6541		1.67	0.58	Op0727f_1	NA	NA
3UTR_1423	2821944 +	2821989 Rmet_6541				Op0727f_1		
5UTR_1178	2822073 +	2822097 Rmet_2595				Op0727f_2		
NPKM_5277	2822097 +	2822355 Rmet_2595		42.67	6.43	Op0727f_2	NA	Q1LK54 Putative uncharacterized protein
3UTR_1424	2822356 +	2822493 Rmet_2595				Op0727f_2		
NPKM_5278	2822571 +	2823555 Rmet_2596	<i>bug</i>	8.33	1.15	Op0727f_2	NA	Q1LK53 Uncharacterized protein UPF0065
3UTR_1701	2823360 -	2823628 Rmet_2597	<i>mcr</i>			Op0728r_1		
3UTR_1425	2823556 +	2823578 Rmet_2596	<i>bug</i>			Op0727f_2		
NPKM_5279	2823629 -	2824733 Rmet_2597	<i>mcr</i>	20.00	0.00	Op0728r_1	NA	Q1LK52 L-carnitine dehydratase/bile acid-inducible protein F
NPKM_5280	2824729 -	2826856 Rmet_2598	<i>pauA</i>	19.00	0.00	Op0728r_1	NA	Q1LK51 CoA-binding
NPKM_5281	2826960 -	2828109 Rmet_2599	<i>acdA</i>	22.33	2.08	Op0728r_1	NA	Q1LK50 Acyl-CoA dehydrogenase-like protein
NPKM_5282	2828217 -	2828967 Rmet_2600		23.33	1.53	Op0728r_1	NA	Q1LK49 Transcriptional regulator, lclR family
5UTR_1427	2828968 -	2829012 Rmet_2600				Op0728r_1		
5UTR_1179	2829126 +	2829200 Rmet_2601				Op0729f_1		
NPKM_5283	2829200 +	2829605 Rmet_2601		11.33	1.53	Op0729f_1	NA	Q1LK48 Putative uncharacterized protein
NPKM_5284	2829601 +	2830750 Rmet_2602		11.67	1.53	Op0729f_1	NA	Q1LK47 Thiolase
NPKM_5285	2830823 +	2831615 Rmet_2603	<i>paaG1</i>	10.67	0.58	Op0729f_1	MET-CAH-Prop	Q1LK46 Short chain enoyl-CoA hydratase
NPKM_5286	2831669 +	2832482 Rmet_2604		16.67	0.58	Op0729f_1	MET-LIP-FASyn	Q1LK45 Short-chain dehydrogenase/reductase SDR
NPKM_5287	2832533 +	2833562 Rmet_2605		9.67	2.31	Op0729f_1	MET-EN-Nitrog	Q1LK44 2-nitropropane dioxxygenase, NPD
3UTR_1700	2832586 -	2833663 Rmet_R0044				Op0730r_3		
3UTR_1426	2833563 +	2833620 Rmet_2605				Op0729f_1		
NPKM_5288	2833664 -	2833743 Rmet_R0044		366.67	16.65	Op0730r_3	NA	NA
NPKM_5289	2833753 -	2836321 Rmet_2606	<i>rpoD1</i>	830.33	10.12	Op0730r_3	GIP-TK-RNAP	Q1LK43 RNA polymerase sigma factor

NPKM_5290	2836512 -	2838354 Rmet_2607	<i>dnaG</i>	163.00	9.54	Op0730r_2	GIP-REP-Complex	Q1LK42 DNA primase
5UTR_1180	2838231 +	2838426 Rmet_6542				Op2038f_1		
NPKM_5291	2838426 +	2838498 Rmet_6542		6.67	3.51	Op2038f_1	NA	NA
3UTR_1427	2838499 +	2839114 Rmet_6542				Op2038f_1		
NPKM_5292	2838581 -	2839031 Rmet_2608		195.67	6.66	Op0730r_2	NA	Q1LK41 GatB/Yqey
NPKM_5293	2839155 -	2839368 Rmet_2609	<i>rpsU2</i>	212.33	9.29	Op0730r_2	GIP-TL-Ribo	Q1LK40 30S ribosomal protein S21 2
NPKM_5294	2839529 -	2840666 Rmet_2610	<i>yhiN</i>	43.67	0.58	Op0730r_1	NA	Q1LK39 HI0933-like protein
5UTR_1426	2840667 -	2840799 Rmet_2610	<i>yhiN</i>			Op0730r_1		
5UTR_1181	2840870 +	2840948 Rmet_2611				Op0731f_1		
NPKM_5295	2840948 +	2841239 Rmet_2611		64.00	1.00	Op0731f_1	NA	Q1LK38 Putative uncharacterized protein
NPKM_5296	2841235 +	2841961 Rmet_2612	<i>gcp</i>	76.00	3.61	Op0731f_1	GIP-PTL-Fold	Q1LK37 Probable O-sialoglycoprotein endopeptidase
NPKM_5297	2842059 +	2844099 Rmet_2613		4.67	0.58	Op0731f_1	NA	Q1LK36 Alkaline phosphatase
3UTR_1699	2843161 -	2844164 Rmet_2614				Op0732r_2		
3UTR_1428	2844100 +	2844124 Rmet_2613				Op0731f_1		
NPKM_5298	2844165 -	2844969 Rmet_2614		330.67	11.02	Op0732r_2	NA	Q1LK35 UPF0343 protein Rmet_2614
NPKM_5299	2844940 +	2845171 Rmet_6543		0.33	0.58	Op2039f_1	NA	NA
3UTR_1429	2845172 +	2845226 Rmet_6543				Op2039f_1		
NPKM_5300	2845300 -	2847214 Rmet_2615	<i>dxs</i>	508.33	3.79	Op0732r_2	MET-LIP-Ster	Q1LK34 1-deoxy-D-xylulose-5-phosphate synthase
NPKM_5301	2847258 -	2848143 Rmet_2616	<i>ispA</i>	498.33	28.99	Op0732r_2	MET-LIP-Ster	Q1LK33 Farnesyl-diphosphate synthase
NPKM_5302	2848139 -	2848448 Rmet_2617	<i>xseB</i>	179.67	16.86	Op0732r_1	GIP-REP-Recomb	Q1LK32 Exodeoxyribonuclease VII small subunit
5UTR_1425	2848449 -	2848635 Rmet_2617	<i>xseB</i>			Op0732r_1		
5UTR_1182	2848621 +	2848906 Rmet_2618				Op0733f_1		
NPKM_5303	2848906 +	2850010 Rmet_2618		284.67	6.66	Op0733f_1	NA	Q1LK31 Rieske (2Fe-2S) region
NPKM_5304	2850209 +	2851130 Rmet_2619		10.67	0.58	Op0733f_1	NA	Q1LK30 Putative uncharacterized protein
3UTR_1698	2851063 -	2852061 Rmet_2621	<i>zupT</i>			Op0734r_2		
NPKM_5305	2851182 +	2852040 Rmet_2620	<i>sseA</i>	85.67	7.23	Op0733f_2	MET-AA-Cys	Q1LK29 Rhodanese-like protein
3UTR_1430	2852041 +	2853022 Rmet_2620	<i>sseA</i>			Op0733f_2		
NPKM_5306	2852062 -	2852938 Rmet_2621	<i>zupT</i>	74.67	3.51	Op0734r_2	EIP-TRA-Ion	Q1LK28 Zinc/iron permease
NPKM_5307	2853061 -	2853937 Rmet_2622		184.33	7.77	Op0734r_2	MET-XEN-Hex	Q1LK27 Twin-arginine translocation pathway signal
NPKM_5308	2854065 -	2855469 Rmet_2623	<i>ndh</i>	45.00	1.00	Op0734r_1	MET-EN-OxPhos	Q1LK26 FAD-dependent pyridine nucleotide-disulphide oxidoreductase
NPKM_5309	2855701 -	2858506 Rmet_2624	<i>polA</i>	70.33	3.06	Op0734r_1	MET-NUC-Pur	Q1LK25 DNA polymerase I
5UTR_1183	2858394 +	2858738 Rmet_2625				Op0735f_1		
5UTR_1424	2858507 -	2858847 Rmet_2624	<i>polA</i>			Op0734r_1		
NPKM_5310	2858738 +	2859458 Rmet_2625		189.00	8.89	Op0735f_1	NA	Q1LK24 Putative uncharacterized protein
NPKM_5311	2859632 +	2860052 Rmet_2626		320.67	11.59	Op0735f_1	NA	Q1LK23 Putative transmembrane protein
NPKM_5312	2860221 +	2861208 Rmet_2627	<i>thrB</i>	105.33	5.77	Op0735f_1	MET-AA-GlySerThr	Q1LK22 Homoserine kinase
3UTR_1697	2860807 -	2862068 Rmet_2629	<i>uvrD</i>			Op0736r_1		
NPKM_5313	2861214 +	2862018 Rmet_2628		106.00	3.00	Op0735f_1	NA	Q1LK21 Putative transmembrane protein
3UTR_1431	2862019 +	2862775 Rmet_2628				Op0735f_1		
NPKM_5314	2862069 -	2864433 Rmet_2629	<i>uvrD</i>	96.33	3.51	Op0736r_1	GIP-REP-Recomb	Q1LK20 ATP-dependent DNA helicase UvrD
5UTR_1184	2864434 +	2864651 Rmet_2630	<i>valS</i>			Op0737f_1		
5UTR_1423	2864434 -	2864440 Rmet_2629	<i>uvrD</i>			Op0736r_1		
NPKM_5315	2864651 +	2867519 Rmet_2630	<i>valS</i>	255.00	1.73	Op0737f_1	MET-AA-ValLeulle	Q1LK19 Valyl-tRNA synthetase

NPKM_5316	2867633	+	2868533	Rmet_2631	<i>galU</i>	691.33	16.65	Op0737f_2	MET-CAH-Pent	Q1LK18 UDP-glucose pyrophosphorylase
3UTR_1432	2868534	+	2868613	Rmet_2631	<i>galU</i>			Op0737f_2		
3UTR_1696	2868578	-	2868640	Rmet_2632				Op0738r_2		
NPKM_5317	2868641	-	2868962	Rmet_2632		157.67	11.24	Op0738r_2	NA	Q1LK17 Putative uncharacterized protein
5UTR_1185	2868743	+	2869137	Rmet_2633				Op0739f_1		
NPKM_5318	2868915	-	2869083	Rmet_6544		20.00	1.00	Op0738r_1	NA	NA
5UTR_1422	2869084	-	2869854	Rmet_6544				Op0738r_1		
NPKM_5319	2869137	+	2869917	Rmet_2633		133.00	12.49	Op0739f_1	NA	Q1LK16 ChaC-like protein
3UTR_1695	2869872	-	2870782	Rmet_2635	<i>fadD</i>			Op0740r_1		
NPKM_5320	2869938	+	2870748	Rmet_2634		70.33	7.57	Op0739f_1	NA	Q1LK15 Ankyrin
3UTR_1433	2870749	+	2871546	Rmet_2634				Op0739f_1		
NPKM_5321	2870783	-	2872484	Rmet_2635	<i>fadD</i>	114.33	8.74	Op0740r_1	MET-LIP-FASyn	Q1LK14 AMP-dependent synthetase and ligase
5UTR_1421	2872485	-	2872544	Rmet_2635	<i>fadD</i>			Op0740r_1		
5UTR_1186	2872668	+	2872718	Rmet_2636				Op0741f_1		
NPKM_5322	2872718	+	2873561	Rmet_2636		80.33	1.53	Op0741f_1	GIP-PTL-Fold	Q1LK13 Thioredoxin
3UTR_1694	2872931	-	2873591	Rmet_2637				Op0742r_1		
NPKM_5323	2873592	-	2874075	Rmet_2637		76.67	1.53	Op0742r_1	NA	Q1LK12 Hemerythrin-like, metal-binding
NPKM_5324	2874208	+	2874787	Rmet_2638		89.67	0.58	Op0743f_1	NA	Q1LK11 Putative ATP-ase
NPKM_5325	2874775	-	2875684	Rmet_2639		65.00	6.56	Op0744r_1	NA	Q1LK10 UBA/THIF-type NAD/FAD binding fold
3UTR_1434	2874788	+	2875566	Rmet_2638				Op0743f_1		
5UTR_1187	2875569	+	2875824	Rmet_2640				Op0745f_1		
5UTR_1420	2875685	-	2875750	Rmet_2639				Op0744r_1		
NPKM_5326	2875824	+	2878032	Rmet_2640		35.67	2.89	Op0745f_1	NA	Q1LK09 AsmA
NPKM_5327	2878341	+	2879532	Rmet_2641		17.00	2.00	Op0745f_1	NA	Q1LK08 Major facilitator superfamily MFS_1
NPKM_5328	2879665	+	2880304	Rmet_2642	<i>pdxH</i>	97.00	4.00	Op0745f_2	MET-COF-B6	Q1LK07 Pyridoxine/pyridoxamine 5'-phosphate oxidase
NPKM_5329	2880518	+	2881760	Rmet_2643	<i>cfa</i>	235.00	14.93	Op0745f_3	NA	Q1LK06 Cyclopropane-fatty-acyl-phospholipid synthase
NPKM_5330	2881763	+	2882834	Rmet_2644		72.67	7.09	Op0745f_3	NA	Q1LK05 Putative uncharacterized protein
3UTR_1693	2882073	-	2882829	Rmet_2645	<i>msrA</i>			Op0746r_1		
NPKM_5331	2882830	-	2883373	Rmet_2645	<i>msrA</i>	11.67	0.58	Op0746r_1	GIP-PTL-Fold	Q1LK04 Peptide methionine sulfoxide reductase
5UTR_1419	2883374	-	2883433	Rmet_2645	<i>msrA</i>			Op0746r_1		
3UTR_1692	2883436	-	2884220	Rmet_2647				Op0748r_1		
NPKM_5332	2883605	+	2884220	Rmet_2646		88.33	2.31	Op0747f_1	NA	Q1LK03 Flavin reductase-like, FMN-binding
3UTR_1435	2884221	+	2884662	Rmet_2646				Op0747f_1		
NPKM_5333	2884221	-	2884701	Rmet_2647		19.00	1.00	Op0748r_1	NA	Q1LK02 Transcriptional regulator, AsnC family
5UTR_1188	2884831	+	2884852	Rmet_2648				Op0749f_1		
NPKM_5334	2884852	+	2885101	Rmet_2648		8.00	1.73	Op0749f_1	NA	Q0K7X9 Predicted metal-dependent hydrolase/Putative cyclase
NPKM_5335	2885101	+	2885509	Rmet_6545		7.00	1.00	Op0749f_1	NA	NA
NPKM_5336	2885544	+	2886801	Rmet_2650	<i>kynU</i>	5.67	0.58	Op0749f_1	MET-AA-Trp	Q1LK01 Kynureninase
NPKM_5337	2886814	+	2887714	Rmet_2651	<i>tdo</i>	6.67	1.15	Op0749f_1	MET-AA-Trp	Q1LK00 Tryptophan 2,3-dioxygenase
3UTR_1691	2886872	-	2887775	Rmet_2652				Op0750r_1		
3UTR_1436	2887715	+	2887732	Rmet_2651	<i>tdo</i>			Op0749f_1		
NPKM_5338	2887776	-	2888601	Rmet_2652		32.33	1.53	Op0750r_1	NA	Q1LJZ9 Transcriptional regulator, lclR family
5UTR_1418	2888602	-	2888653	Rmet_2652				Op0750r_1		

5UTR_1189	2888719 +	2888823 Rmet_2653	<i>gcdH</i>			Op0751f_1		
NPKM_5339	2888823 +	2890017 Rmet_2653	<i>gcdH</i>	84.67	5.03	Op0751f_1	MET-LIP-FAMet	Q1LJZ8 Acyl-CoA dehydrogenase-like protein
3UTR_1690	2889356 -	2890171 Rmet_2654				Op0752r_2		
3UTR_1437	2890018 +	2890149 Rmet_2653	<i>gcdH</i>			Op0751f_1		
NPKM_5340	2890172 -	2890811 Rmet_2654		1068.00	45.31	Op0752r_2	NA	Q1LJZ7 1-Cys peroxiredoxin
5UTR_1190	2890387 +	2891158 Rmet_2655	<i>elaB</i>			Op0753f_1		
NPKM_5341	2890773 -	2890938 Rmet_6546		32.00	5.29	Op0752r_1	NA	NA
5UTR_1417	2890939 -	2891049 Rmet_6546				Op0752r_1		
NPKM_5342	2891158 +	2891434 Rmet_2655	<i>elaB</i>	3874.67	162.65	Op0753f_1	NA	B3R5S9 Putative uncharacterized protein
NPKM_5343	2891579 +	2891957 Rmet_2656		751.67	28.75	Op0753f_1	NA	Q1LJZ5 Putative transmembrane protein
NPKM_5344	2891953 +	2892490 Rmet_2657		556.67	10.79	Op0753f_1	NA	Q1LJZ4 Putative uncharacterized protein
3UTR_1689	2892484 -	2892489 Rmet_6547				Op0754r_4		
NPKM_5345	2892490 -	2893210 Rmet_6547		1.67	0.58	Op0754r_4	NA	NA
3UTR_1438	2892491 +	2895133 Rmet_2657				Op0753f_1		
NPKM_5346	2893131 -	2894508 Rmet_6548		1.67	0.58	Op0754r_4	NA	NA
5UTR_1416	2894509 -	2894557 Rmet_6548				Op0754r_4		
NPKM_5347	2894649 -	2895459 Rmet_2660		9.00	1.73	Op0754r_4	NA	Q1LJZ3 Putative uncharacterized protein
NPKM_5348	2895468 -	2895597 Rmet_6549		0.00	0.00	Op0754r_3	NA	NA
NPKM_5349	2895704 -	2895956 Rmet_2661		0.00	0.00	Op0754r_3	NA	Q1LJZ2 Putative uncharacterized protein
3UTR_1688	2896149 -	2896359 Rmet_2662				Op0754r_3		
NPKM_5350	2896360 -	2898259 Rmet_2662		9.00	1.00	Op0754r_3	NA	Q1LJZ1 Phage/plasmid primase P4-like protein
5UTR_1415	2898260 -	2898284 Rmet_2662				Op0754r_3		
3UTR_1687	2898292 -	2898377 Rmet_6550				Op0754r_2		
NPKM_5351	2898378 -	2898489 Rmet_6550		2.00	1.73	Op0754r_2	NA	NA
NPKM_5352	2898605 -	2899202 Rmet_2663		0.33	0.58	Op0754r_1	NA	Q1LJZ0 Putative uncharacterized protein
3UTR_1686	2899212 -	2899244 Rmet_2664				Op0754r_1		
NPKM_5353	2899245 -	2899635 Rmet_2664		6.00	1.00	Op0754r_1	NA	Q1LJY9 Putative uncharacterized protein
NPKM_5354	2899718 +	2900036 Rmet_2665		0.00	0.00	Op0755f_1	NA	Q1LJY8 Putative uncharacterized protein
3UTR_1439	2900037 +	2900041 Rmet_2665				Op0755f_1		
NPKM_5355	2900188 -	2900827 Rmet_2666		50.33	5.51	Op0756r_5	NA	Q1LJY7 Putative uncharacterized protein
NPKM_5356	2900851 -	2902126 Rmet_2667		104.33	10.97	Op0756r_5	NA	Q1LJY6 McrBC 5-methylcytosine restriction system component-like protein
NPKM_5357	2902128 -	2903040 Rmet_2668		233.00	13.08	Op0756r_5	NA	Q1LJY5 ATPase associated with various cellular activities, AAA_5
NPKM_5358	2903041 -	2903458 Rmet_2669		226.33	5.51	Op0756r_5	NA	Q1LJY4 Putative uncharacterized protein
NPKM_5359	2903603 -	2904770 Rmet_2670		157.33	1.53	Op0756r_5	NA	Q1LJY3 DNA methylase N-4/N-6
NPKM_5360	2904766 -	2904967 Rmet_6551		39.67	8.02	Op0756r_4	NA	NA
NPKM_5361	2904992 -	2905068 Rmet_R0045		23.33	5.03	Op0756r_4	NA	NA
NPKM_5362	2905137 -	2906253 Rmet_2671		67.00	1.73	Op0756r_4	NA	Q1LJY2 Putative uncharacterized protein
NPKM_5363	2906323 -	2907007 Rmet_2672	<i>queC</i>	96.00	3.46	Op0756r_4	NA	Q1LJY1 Queuosine biosynthesis protein queC
NPKM_5364	2907197 -	2907956 Rmet_2673		1361.67	98.57	Op0756r_4	NA	Q1LJY0 TPR repeat
NPKM_5365	2907973 -	2908483 Rmet_2674	<i>pal</i>	1301.00	72.63	Op0756r_4	NA	Q1LJX9 OmpA/MotB
NPKM_5366	2908502 -	2909843 Rmet_2675	<i>tolB</i>	323.00	2.00	Op0756r_3	NA	Q1LJX8 Protein tolB
NPKM_5367	2910057 -	2911140 Rmet_2676	<i>tolA</i>	83.33	3.21	Op0756r_2	EIP-TRA-Pores	Q1LJX7 TonB-like protein
NPKM_5368	2911163 -	2911601 Rmet_2677	<i>tolR</i>	134.00	2.00	Op0756r_2	NA	Q1LJX6 Biopolymer transport protein ExbD/TolR

NPKM_5369	2911625 -	2912309 Rmet_2678	<i>tolQ</i>	159.67	3.06	Op0756r_2	NA	Q1LJX5 MotA/TolQ/ExbB proton channel
NPKM_5370	2912305 -	2912710 Rmet_2679	<i>ybgC</i>	66.67	4.04	Op0756r_1	NA	Q1LJX4 4-hydroxybenzoyl-CoA thioesterase
5UTR_1191	2912765 +	2912882 Rmet_2680	<i>glyA</i>			Op0757f_1		
NPKM_5371	2912882 +	2914409 Rmet_2680	<i>glyA</i>	1110.00	29.46	Op0757f_1	MET-EN-Methane	Q1LJX3 Serine hydroxymethyltransferase
NPKM_5372	2914554 +	2915022 Rmet_2681	<i>nrdR</i>	97.67	3.06	Op0757f_1	NA	Q1LJX2 Transcriptional repressor nrdR
NPKM_5373	2915299 +	2915689 Rmet_2682		6.00	1.00	Op0757f_1	NA	Q1LJX1 Putative uncharacterized protein
NPKM_5374	2915685 +	2916546 Rmet_2683		7.33	1.53	Op0757f_1	GIP-PTL-T2S	Q1LJX0 Putative transmembrane protein
NPKM_5375	2916539 +	2917100 Rmet_2684		5.67	1.53	Op0757f_1	GIP-PTL-T2S	Q1LJW9 Putative signal peptide protein
NPKM_5376	2917099 +	2918914 Rmet_2685		4.33	1.53	Op0757f_1	GIP-PTL-T2S	Q1LJW8 Putative type 4 fimbrial biogenesis PilY1-related protein transmembrane
NPKM_5377	2918910 +	2919387 Rmet_2686		3.00	1.00	Op0757f_1	NA	Q1LJW7 Pilus assembly protein PilE
NPKM_5378	2919388 +	2919913 Rmet_2687		8.67	0.58	Op0757f_2	NA	Q1LJW6 Pilus assembly protein Fim
NPKM_5379	2919957 +	2921079 Rmet_2688	<i>ribD</i>	115.00	6.56	Op0757f_3	NA	Q1LJW5 5-amino-6-(5-phosphoribosylamino)uracil reductase / diaminohydroxyphos
NPKM_5380	2921106 +	2921739 Rmet_2689	<i>ribC</i>	137.33	8.62	Op0757f_3	MET-COF-Ribo	Q1LJW4 Riboflavin synthase, alpha subunit
3UTR_1685	2921638 -	2921867 Rmet_2690				Op0758r_2		
3UTR_1440	2921740 +	2922102 Rmet_2689	<i>ribC</i>			Op0757f_3		
NPKM_5381	2921868 -	2922060 Rmet_2690		196.33	10.41	Op0758r_2	NA	Q1LJW3 Putative uncharacterized protein
NPKM_5382	2922203 -	2923052 Rmet_2691		38.00	3.46	Op0758r_1	NA	Q1LJW2 Putative uncharacterized protein
NPKM_5383	2923108 -	2924143 Rmet_2692		53.00	1.00	Op0758r_1	NA	Q1LJW1 L-carnitine dehydratase/bile acid-inducible protein F
5UTR_1414	2924144 -	2924951 Rmet_2692				Op0758r_1		
5UTR_1192	2924322 +	2924378 Rmet_2693	<i>ribBA</i>			Op0759f_1		
NPKM_5384	2924378 +	2925494 Rmet_2693	<i>ribBA</i>	276.67	10.26	Op0759f_1	MET-COF-Ribo	Q1LJW0 3,4-dihydroxy-2-butanone 4-phosphate synthase / GTP cyclohydrolase II
3UTR_1684	2924953 -	2928064 Rmet_2697				Op0760r_1		
NPKM_5385	2925572 +	2926082 Rmet_2694	<i>ribE</i>	429.67	25.93	Op0759f_1	MET-COF-Ribo	Q1LJV9 6,7-dimethyl-8-ribityllumazine synthase
NPKM_5386	2926074 +	2926590 Rmet_2695	<i>nusB</i>	378.00	29.46	Op0759f_1	GIP-TK-Assoc	Q1LJV8 N utilization substance protein B homolog
NPKM_5387	2926771 +	2927953 Rmet_2696		59.67	10.26	Op0759f_1	NA	Q1LJV7 Aminotransferase
3UTR_1441	2927954 +	2928023 Rmet_2696				Op0759f_1		
NPKM_5388	2928065 -	2929133 Rmet_2697		1390.67	17.01	Op0760r_1	NA	Q1LJV6 Lytic transglycosylase, catalytic
5UTR_1413	2929134 -	2929529 Rmet_2697				Op0760r_1		
5UTR_1193	2929666 +	2929741 Rmet_2698	<i>ubiD</i>			Op0761f_1		
NPKM_5389	2929741 +	2931304 Rmet_2698	<i>ubiD</i>	129.67	3.21	Op0761f_1	MET-COF-CoQ	Q1LJV5 3-octaprenyl-4-hydroxybenzoate carboxy-lyase
NPKM_5390	2931390 +	2933400 Rmet_2699	<i>acsA</i>	135.33	6.11	Op0761f_1	MET-CAH-But	Q1LJV4 Acetoacetyl-CoA synthase
3UTR_1683	2933332 -	2933408 Rmet_2700	<i>gst1</i>			Op0762r_1		
3UTR_1442	2933401 +	2934075 Rmet_2699	<i>acsA</i>			Op0761f_1		
NPKM_5391	2933409 -	2934066 Rmet_2700	<i>gst1</i>	7.00	1.00	Op0762r_1	MET-OAA-GSH	Q1LJV3 Glutathione S-transferase-like protein
5UTR_1412	2934067 -	2934174 Rmet_2700	<i>gst1</i>			Op0762r_1		
NPKM_5392	2934350 +	2935583 Rmet_2701	<i>phaZ2</i>	3.67	0.58	Op0763f_1	NA	Q1LJV2 Polyhydroxyalkanoate depolymerase, intracellular
5UTR_1194	2935589 +	2935681 Rmet_2702	<i>galM</i>			Op0763f_2		
NPKM_5393	2935681 +	2936587 Rmet_2702	<i>galM</i>	12.33	1.53	Op0763f_2	MET-CAH-FbP	Q1LJV1 Aldose 1-epimerase
3UTR_1682	2935713 -	2936668 Rmet_2703				Op0764r_1		
3UTR_1443	2936588 +	2936974 Rmet_2702	<i>galM</i>			Op0763f_2		
NPKM_5394	2936669 -	2937059 Rmet_2703		16.67	1.53	Op0764r_1	NA	Q1LJV0 Putative uncharacterized protein
5UTR_1411	2937060 -	2937119 Rmet_2703				Op0764r_1		
5UTR_1195	2937183 +	2937777 Rmet_R0046				Op0765f_1		

NPKM_5395	2937777 +	2937852 Rmet_R0046		12.67	3.21	Op0765f_1	NA	NA
3UTR_1681	2937831 -	2938804 Rmet_2705	<i>bacA</i>			Op0766r_2		
NPKM_5396	2937927 +	2938716 Rmet_2704	<i>trmB</i>	127.00	1.00	Op0765f_2	NA	Q1LJU9 tRNA (guanine-N(7)-)-methyltransferase
NPKM_5397	2938805 -	2939687 Rmet_2705	<i>bacA</i>	112.33	5.86	Op0766r_2	MET-PepGlyc	Q1LJU8 Undecaprenyl-diphosphatase
NPKM_5398	2939600 +	2939765 Rmet_6552		3.67	1.53	Op2040f_1	NA	NA
3UTR_1444	2939766 +	2940305 Rmet_6552				Op2040f_1		
NPKM_5399	2939772 -	2940339 Rmet_2706		45.67	5.03	Op0766r_1	NA	Q1LJU7 Putative transmembrane protein
NPKM_5400	2940352 -	2940652 Rmet_2707		57.33	5.86	Op0766r_1	NA	Q1LJU6 Putative uncharacterized protein
5UTR_1410	2940653 -	2940759 Rmet_2707				Op0766r_1		
5UTR_1196	2940861 +	2940892 Rmet_2708				Op0767f_1		
NPKM_5401	2940892 +	2941693 Rmet_2708		49.00	1.00	Op0767f_1	NA	Q1LJU5 Transcriptional regulator, TetR family
NPKM_5402	2941953 +	2942607 Rmet_2709	<i>pcm</i>	458.67	19.66	Op0767f_2	GIP-PTL-Fold	Q1LJU4 Protein-L-isoaspartate(D-aspartate) O-methyltransferase
NPKM_5403	2942620 +	2942944 Rmet_2710	<i>pspE2</i>	430.67	21.22	Op0767f_2	NA	Q1LJU3 Rhodanese-like protein
NPKM_5404	2943080 +	2944562 Rmet_2711		95.67	2.89	Op0767f_2	NA	Q1LJU2 Type I secretion outer membrane protein, TolC
3UTR_1680	2943919 -	2944573 Rmet_2712				Op0768r_2		
3UTR_1445	2944563 +	2945872 Rmet_2711				Op0767f_2		
NPKM_5405	2944574 -	2945816 Rmet_2712		51.00	1.73	Op0768r_2	NA	Q1LJU1 O-antigen polymerase
NPKM_5406	2945939 -	2946749 Rmet_2713		77.33	4.16	Op0768r_2	NA	Q1LJU0 Putative uncharacterized protein
5UTR_1409	2946750 -	2946810 Rmet_2713				Op0768r_2		
3UTR_1679	2946812 -	2946888 Rmet_2714	<i>kdtA</i>			Op0768r_1		
NPKM_5407	2946889 -	2948164 Rmet_2714	<i>kdtA</i>	33.67	1.53	Op0768r_1	MET-GLYC-LPS	Q1LJT9 Three-deoxy-D-manno-octulosonic-acid transferase-like protein
NPKM_5408	2948163 -	2949255 Rmet_2715	<i>rfaC</i>	81.33	1.53	Op0768r_1	MET-GLYC-LPS	Q1LJT8 Lipopolysaccharide heptosyltransferase I
NPKM_5409	2949235 -	2950621 Rmet_2716	<i>cpsG</i>	145.00	5.20	Op0768r_1	MET-CAH-FbP	Q1LJT7 Phosphomannomutase
5UTR_1408	2950622 -	2950904 Rmet_2716	<i>cpsG</i>			Op0768r_1		
5UTR_1197	2950732 +	2950832 Rmet_2717				Op0769f_1		
NPKM_5410	2950832 +	2952002 Rmet_2717		68.33	6.43	Op0769f_1	NA	Q1LJT6 Glycosyl transferase, group 1
NPKM_5411	2952003 +	2953329 Rmet_2718		24.33	2.89	Op0769f_1	NA	Q1LJT5 Sugar transferase
NPKM_5412	2953328 +	2954492 Rmet_2719		39.67	2.31	Op0769f_1	NA	Q1LJT4 Glycosyl transferase, group 1
NPKM_5413	2954491 +	2955742 Rmet_2720		17.33	0.58	Op0769f_1	EIP-TRA-Ion	Q1LJT3 Polysaccharide biosynthesis protein
NPKM_5414	2955738 +	2956833 Rmet_2721		26.00	1.73	Op0769f_1	NA	Q1LJT2 Glycosyl transferase, group 1
NPKM_5415	2956887 -	2956989 Rmet_6553		5.67	3.79	Op2041r_1	NA	NA
NPKM_5416	2956930 +	2957788 Rmet_2722		169.67	6.35	Op0769f_2	NA	Q1LJT1 Lipopolysaccharide biosynthesis
3UTR_1446	2957789 +	2959061 Rmet_2722				Op0769f_2		
NPKM_5417	2957897 -	2959847 Rmet_2723		163.67	6.51	Op0770r_2	NA	Q1LJT0 Polysaccharide biosynthesis protein CapD
NPKM_5418	2959843 -	2961019 Rmet_2724		203.67	5.86	Op0770r_2	NA	Q1LJS9 DegT/DnrJ/EryC1/StrS aminotransferase
5UTR_1198	2961044 +	2961272 Rmet_6554				Op2042f_1		
NPKM_5419	2961080 -	2961626 Rmet_2725		64.67	3.51	Op0770r_1	NA	Q1LJS8 Putative acetyltransferase
NPKM_5420	2961272 +	2961392 Rmet_6554		16.00	6.93	Op2042f_1	NA	NA
3UTR_1447	2961393 +	2962322 Rmet_6554				Op2042f_1		
NPKM_5421	2961692 -	2962286 Rmet_2726		111.33	2.52	Op0770r_1	NA	Q1LJS7 Sugar transferase
NPKM_5422	2962462 -	2963674 Rmet_2727		94.33	5.86	Op0770r_1	NA	Q1LJS6 Glycosyl transferase, group 1
NPKM_5423	2963663 -	2964782 Rmet_2728		82.67	7.02	Op0770r_1	NA	Q1LJS5 Glycosyl transferase, group 1
NPKM_5424	2965017 -	2965914 Rmet_2729		95.33	2.31	Op0770r_1	NA	Q1LJS4 Glycosyl transferase, family 2

NPKM_5425	2965958 -	2966201 Rmet_6555		49.67	4.93	Op0770r_1	NA	NA
NPKM_5426	2966191 -	2966512 Rmet_2730		68.00	5.00	Op0770r_1	NA	Q1LJS3 Putative uncharacterized protein
NPKM_5427	2966584 -	2967844 Rmet_2731		84.00	3.00	Op0770r_1	NA	Q1LJS2 Polysaccharide biosynthesis protein
NPKM_5428	2968059 -	2968614 Rmet_2732	<i>rfbC</i>	294.67	7.51	Op0770r_1	MET-CAH-NucSug	Q1LJS1 dTDP-4-dehydrorhamnose 3,5-epimerase
NPKM_5429	2968610 -	2969489 Rmet_2733	<i>rfbA</i>	327.67	3.79	Op0770r_1	MET-CAH-NucSug	Q1LJS0 Glucose-1-phosphate thymidyltransferase
NPKM_5430	2969500 -	2970421 Rmet_2734	<i>rfbD</i>	333.33	12.10	Op0770r_1	MET-CAH-NucSug	Q1LJR9 dTDP-4-dehydrorhamnose reductase
NPKM_5431	2970410 -	2971475 Rmet_2735	<i>rfbB</i>	408.33	7.09	Op0770r_1	MET-CAH-NucSug	Q1LJR8 dTDP-glucose 4,6-dehydratase
5UTR_1199	2971644 +	2971677 Rmet_2736	<i>apaH</i>			Op0771f_1		
NPKM_5432	2971677 +	2972559 Rmet_2736	<i>apaH</i>	50.33	2.08	Op0771f_1	MET-NUC-Pur	Q1LJR7 Bis(5'nucleosyl)-tetrphosphatase, ApaH
3UTR_1448	2972560 +	2973188 Rmet_2736	<i>apaH</i>			Op0771f_1		
NPKM_5433	2972599 -	2973796 Rmet_2737		213.33	5.51	Op0772r_2	NA	Q1LJR6 Putative uncharacterized protein
NPKM_5434	2974017 -	2974854 Rmet_2738	<i>plsC</i>	129.67	4.51	Op0772r_2	MET-LIP-GlycLip	Q1LJR5 Lyso-ornithine lipid acyltransferase
NPKM_5435	2974890 -	2976210 Rmet_2739	<i>pyrX</i>	222.67	3.51	Op0772r_2	MET-NUC-Pyr	Q1LJR4 Dihydroorotase
NPKM_5436	2976206 -	2977178 Rmet_2740	<i>pyrB</i>	223.67	5.03	Op0772r_2	MET-NUC-Pyr	Q1LJR3 Aspartate carbamoyltransferase
NPKM_5437	2977228 -	2977753 Rmet_2741	<i>pyrR</i>	173.33	9.87	Op0772r_2	MET-NUC-Pyr	Q1LJR2 Phosphoribosyltransferase
NPKM_5438	2977749 -	2978199 Rmet_2742		188.00	12.00	Op0772r_2	GIP-REP-Recomb	Q1LJR1 Putative Holliday junction resolvase
NPKM_5439	2978179 -	2978761 Rmet_2743		302.67	21.57	Op0772r_2	NA	Q1LJR0 UPF0301 protein Rmet_2743
NPKM_5440	2978839 -	2979556 Rmet_2744	<i>rsuA</i>	64.67	3.21	Op0772r_1	GIP-TL-Ass	Q1LJQ9 Pseudouridine synthase
5UTR_1200	2979555 +	2979621 Rmet_2745	<i>phr</i>			Op0773f_1		
5UTR_1407	2979557 -	2979939 Rmet_2744	<i>rsuA</i>			Op0772r_1		
NPKM_5441	2979621 +	2981163 Rmet_2745	<i>phr</i>	17.33	1.53	Op0773f_1	GIP-REP-Recomb	Q1LJQ8 Deoxyribodipyrimidine photo-lyase type I
3UTR_1678	2980865 -	2982558 Rmet_2747	<i>hemY</i>			Op0774r_1		
NPKM_5442	2981247 +	2982474 Rmet_2746		31.00	2.65	Op0773f_1	NA	Q1LJQ7 Acyltransferase 3
3UTR_1449	2982475 +	2983145 Rmet_2746				Op0773f_1		
NPKM_5443	2982559 -	2983750 Rmet_2747	<i>hemY</i>	119.00	5.57	Op0774r_1	MET-COF-Porph	Q1LJQ6 HemY-like protein
NPKM_5444	2983755 -	2985837 Rmet_2748	<i>hemDX</i>	152.67	4.04	Op0774r_1	NA	Q1LJQ5 HemX family protein / uroporphyrinogen-III synthase
NPKM_5445	2985847 -	2986852 Rmet_2749	<i>hemC</i>	186.67	5.51	Op0774r_1	MET-COF-Porph	Q1LJQ4 Hydroxymethylbilane synthase
5UTR_1201	2986750 +	2986976 Rmet_2750	<i>ppc</i>			Op0775f_1		
5UTR_1406	2986853 -	2986869 Rmet_2749	<i>hemC</i>			Op0774r_1		
NPKM_5446	2986976 +	2990006 Rmet_2750	<i>ppc</i>	181.00	6.00	Op0775f_1	MET-CAH-Pyr	Q1LJQ3 Phosphoenolpyruvate carboxylase
NPKM_5447	2990234 +	2991644 Rmet_2751	<i>argH</i>	287.33	10.02	Op0775f_1	MET-AA-AlaAsp	Q1LJQ2 Argininosuccinate lyase
NPKM_5448	2991676 +	2991781 Rmet_6556		1.67	1.15	Op0775f_1	NA	NA
3UTR_1450	2991782 +	2991848 Rmet_6556				Op0775f_1		
NPKM_5449	2991851 +	2992394 Rmet_2752		150.00	19.52	Op0775f_2	NA	Q1LJQ1 Tripartite ATP-independent periplasmic transporter, DctQ component
NPKM_5450	2992393 +	2994118 Rmet_2753		195.67	25.38	Op0775f_2	NA	Q1LJQ0 TRAP C4-dicarboxylate transport system permease DctM subunit
3UTR_1451	2994119 +	2994449 Rmet_2753				Op0775f_2		
3UTR_1677	2994206 -	2994252 Rmet_2754	<i>ldcC</i>			Op0776r_2		
NPKM_5451	2994253 -	2996518 Rmet_2754	<i>ldcC</i>	99.67	2.52	Op0776r_2	MET-AA-GluGSH	Q1LJP9 Ornithine decarboxylase
NPKM_5452	2996677 -	2997244 Rmet_2755	<i>dcd</i>	117.33	2.52	Op0776r_2	MET-NUC-Pyr	Q1LJP8 Deoxycytidine triphosphate deaminase
NPKM_5453	2997367 -	2998204 Rmet_2756	<i>fdhD</i>	73.00	1.00	Op0776r_2	NA	Q1LJP7 Formate dehydrogenase, subunit FdhD
NPKM_5454	2998266 -	2998842 Rmet_2757	<i>sodC</i>	327.00	8.00	Op0776r_2	OTHERS	Q1LJP6 Superoxide dismutase [Cu-Zn]
5UTR_1202	2998385 +	2998687 Rmet_6557				Op2043f_1		
NPKM_5455	2998687 +	2998939 Rmet_6557		2.00	1.00	Op2043f_1	NA	NA

NPKM_5456	2998939 -	3000133 Rmet_2758	<i>fdhC</i>	30.67	2.08	Op0776r_1	MET-CAH-DiCarb	Q1LJP5 Formate dehydrogenase gamma subunit
NPKM_5457	3000152 -	3000386 Rmet_2759		44.67	2.52	Op0776r_1	NA	Q1LJP4 Putative lipoprotein
NPKM_5458	3000382 -	3001063 Rmet_2760	<i>fdhB</i>	45.67	1.53	Op0776r_1	MET-CAH-DiCarb	Q1LJP3 4Fe-4S ferredoxin, iron-sulfur binding
NPKM_5459	3001077 -	3004155 Rmet_2761	<i>fdhA</i>	51.67	0.58	Op0776r_1	MET-CAH-DiCarb	Q1LJP2 Twin-arginine translocation pathway signal
NPKM_5460	3004227 -	3004443 Rmet_2762		109.67	4.62	Op0776r_1	NA	Q1LJP1 Twin-arginine translocation pathway signal
NPKM_5461	3004583 -	3005237 Rmet_2763	<i>torD</i>	89.00	3.61	Op0776r_1	NA	Q1LJP0 Cytoplasmic chaperone TorD
NPKM_5462	3005282 -	3007463 Rmet_2764		99.33	4.04	Op0776r_1	NA	Q1LJN9 4Fe-4S ferredoxin, iron-sulfur binding
NPKM_5463	3007566 -	3008175 Rmet_2765		107.00	9.54	Op0776r_1	NA	Q1LJN8 Proline rich protein
NPKM_5464	3008184 -	3008721 Rmet_2766		218.67	5.13	Op0776r_1	NA	Q1LJN7 Putative uncharacterized protein
NPKM_5465	3008739 -	3009828 Rmet_2767	<i>mrp</i>	216.33	12.06	Op0776r_1	DIV-Division	Q1LJN6 Cobyirinic acid a,c-diamide synthase
5UTR_1405	3009829 -	3009960 Rmet_2767	<i>mrp</i>			Op0776r_1		
5UTR_1203	3009882 +	3009932 Rmet_2768	<i>ompA</i>			Op0777f_1		
NPKM_5466	3009932 +	3010817 Rmet_2768	<i>ompA</i>	568.33	27.43	Op0777f_1	NA	Q1LJN5 OmpA/MotB
NPKM_5467	3011162 +	3013235 Rmet_2769	<i>metG</i>	332.67	7.37	Op0777f_1	MET-AA-Met	Q1LJN4 Methionyl-tRNA synthetase
3UTR_1676	3012227 -	3013307 Rmet_2770				Op0778r_2		
3UTR_1452	3013236 +	3018836 Rmet_2769	<i>metG</i>			Op0777f_1		
NPKM_5468	3013308 -	3013911 Rmet_2770		81.67	3.21	Op0778r_2	NA	Q1LJN3 Putative lipoprotein
NPKM_5469	3013907 -	3018086 Rmet_2771		23.00	1.00	Op0778r_1	NA	Q1LJN2 Putative uncharacterized protein
NPKM_5470	3018085 -	3020176 Rmet_2772		40.33	2.08	Op0778r_1	NA	Q1LJN1 Surface antigen (D15)
5UTR_1204	3018862 +	3020168 Rmet_6558				Op0779f_1		
NPKM_5471	3020168 +	3020360 Rmet_6558		270.33	4.04	Op0779f_1	NA	NA
5UTR_1404	3020177 -	3020178 Rmet_2772				Op0778r_1		
NPKM_5472	3020382 +	3021288 Rmet_2773	<i>scpA</i>	272.00	10.82	Op0779f_1	DIV-Division	Q1LJN0 Condensin subunit ScpA
NPKM_5473	3021449 +	3022292 Rmet_2774	<i>panC</i>	153.00	2.00	Op0779f_1	MET-OAA-Other	Q1LJM9 Pantothenate synthetase
3UTR_1453	3022293 +	3022774 Rmet_2774	<i>panC</i>			Op0779f_1		
3UTR_1675	3022352 -	3022395 Rmet_2775				Op0780r_1		
NPKM_5474	3022396 -	3023578 Rmet_2775		15.33	2.52	Op0780r_1	NA	Q1LJM8 PepSY-associated TM helix
5UTR_1205	3023282 +	3023713 Rmet_2776				Op0781f_1		
5UTR_1403	3023579 -	3023646 Rmet_2775				Op0780r_1		
3UTR_1674	3023706 -	3024259 Rmet_2777	<i>cbiA</i>			Op0782r_2		
NPKM_5475	3023713 +	3024289 Rmet_2776		82.33	5.69	Op0781f_1	NA	Q1LJM7 GCN5-related N-acetyltransferase
NPKM_5476	3024260 -	3024923 Rmet_2777	<i>cbiA</i>	80.67	2.52	Op0782r_2	DIV-Division	Q1LJM6 Cobyirinic acid a,c-diamide synthase
3UTR_1454	3024290 +	3025097 Rmet_2776				Op0781f_1		
NPKM_5477	3025051 -	3026569 Rmet_2778	<i>cobQ</i>	34.00	2.00	Op0782r_1	MET-COF-Porph	Q1LJM5 Adenosylcobyric acid synthase (Glutamine-hydrolysing)
5UTR_1402	3026570 -	3026578 Rmet_2778	<i>cobQ</i>			Op0782r_1		
5UTR_1206	3026696 +	3026728 Rmet_2779	<i>cobU</i>			Op0783f_1		
NPKM_5478	3026728 +	3027373 Rmet_2779	<i>cobU</i>	99.00	6.08	Op0783f_1	MET-COF-Porph	Q1LJM4 Adenosylcobinamide kinase
NPKM_5479	3027369 +	3028350 Rmet_2780	<i>cobD</i>	31.00	1.00	Op0783f_1	MET-COF-Porph	Q1LJM3 Adenosylcobinamide-phosphate synthase
NPKM_5480	3028346 +	3029378 Rmet_2781	<i>cobC</i>	32.33	2.52	Op0783f_1	MET-COF-Porph	Q1LJM2 Aminotransferase
NPKM_5481	3029384 +	3030287 Rmet_2782	<i>btuF</i>	29.00	3.61	Op0783f_1	EIP-TRA-ABC	Q1LJM1 Periplasmic binding protein
3UTR_1673	3029676 -	3030296 Rmet_2783				Op0784r_1		
3UTR_1455	3030288 +	3031021 Rmet_2782	<i>btuF</i>			Op0783f_1		
NPKM_5482	3030297 -	3030885 Rmet_2783		51.33	2.08	Op0784r_1	NA	Q1LJM0 Phosphoglycerate mutase

NPKM_5483	3030869 -	3031649 Rmet_2784	<i>cobS</i>	75.00	2.65	Op0784r_1	MET-COF-Porph	Q1LJL9 Cobalamin-5'-phosphate synthase
NPKM_5484	3031665 -	3032736 Rmet_2785	<i>cobT</i>	102.00	7.55	Op0784r_1	MET-COF-Ribo	Q1LJL8 Nicotinate-nucleotide-dimethylbenzimidazole phosphoribosyltransferase
NPKM_5485	3032759 -	3033389 Rmet_2786	<i>btuR</i>	87.33	4.51	Op0784r_1	MET-COF-Porph	Q1LJL7 Cob(I)yrinic acid a,c-diamide adenosyltransferase
NPKM_5486	3033385 -	3034195 Rmet_2787	<i>btuD</i>	89.00	3.46	Op0784r_1	EIP-TRA-ABC	Q1LJL6 ABC transporter-related protein
NPKM_5487	3034191 -	3035199 Rmet_2788	<i>btuC</i>	148.33	7.77	Op0784r_1	EIP-TRA-ABC	Q1LJL5 Transport system permease protein
NPKM_5488	3035217 -	3037314 Rmet_2789	<i>btuB</i>	268.67	16.07	Op0784r_1	EIP-TRA-Pores	Q1LJL4 TonB-dependent receptor, plug
5UTR_1207	3037711 +	3037779 Rmet_2790				Op0785f_1		
NPKM_5490	3037779 +	3038100 Rmet_2790		267.67	8.62	Op0785f_1	NA	Q1LJL3 Putative uncharacterized protein
NPKM_5491	3038096 +	3038420 Rmet_2791	<i>zapA</i>	424.00	18.36	Op0785f_1	NA	Q1LJL2 Putative uncharacterized protein
NPKM_5492	3039049 +	3039529 Rmet_2792		99.33	3.06	Op0785f_1	NA	Q1LJL1 Putative uncharacterized protein
3UTR_1672	3039595 -	3040474 Rmet_2794	<i>matB</i>			Op0786r_3		
NPKM_5493	3039712 +	3040402 Rmet_2793		354.33	21.39	Op0785f_2	NA	Q1LJL0 Putative uncharacterized protein
3UTR_1456	3040403 +	3041628 Rmet_2793				Op0785f_2		
NPKM_5494	3040475 -	3042029 Rmet_2794	<i>matB</i>	102.00	2.00	Op0786r_3	NA	Q1LJK9 AMP-dependent synthetase and ligase
NPKM_5495	3042144 -	3042927 Rmet_2795		80.67	3.21	Op0786r_3	NA	Q1LJK8 Enoyl-CoA hydratase/isomerase
NPKM_5496	3042926 -	3043937 Rmet_2796	<i>bug</i>	115.67	6.51	Op0786r_3	NA	Q1LJK7 Uncharacterized protein UPF0065
NPKM_5497	3044056 -	3045478 Rmet_2797	<i>matA</i>	21.67	0.58	Op0786r_2	MET-CAH-Prop	Q1LJK6 Malonyl-CoA decarboxylase
NPKM_5498	3045519 -	3046221 Rmet_2798	<i>matR</i>	30.00	1.73	Op0786r_2	NA	Q1LJK5 Transcriptional regulator, GntR family
5UTR_1208	3046311 +	3046751 Rmet_6559				Op0787f_1		
NPKM_5499	3046326 -	3046638 Rmet_2799		8.33	0.58	Op0786r_1	NA	Q1LJK4 Putative uncharacterized protein
5UTR_1401	3046639 -	3046795 Rmet_2799				Op0786r_1		
NPKM_5500	3046751 +	3046958 Rmet_6559		2.00	0.00	Op0787f_1	NA	NA
NPKM_5501	3047012 +	3048083 Rmet_2800		52.33	4.73	Op0787f_2	NA	Q1LJK3 Putative uncharacterized protein
NPKM_5502	3048117 +	3049143 Rmet_2801		48.00	2.00	Op0787f_2	NA	Q1LJK2 Peptidase M48, Ste24p
3UTR_1671	3048251 -	3049210 Rmet_2802	<i>lgt</i>			Op0788r_2		
3UTR_1457	3049144 +	3049866 Rmet_2801				Op0787f_2		
NPKM_5503	3049211 -	3050024 Rmet_2802	<i>lgt</i>	107.67	2.08	Op0788r_2	NA	Q1LJK1 Prolipoprotein diacylglycerol transferase
NPKM_5504	3050076 -	3051027 Rmet_2803	<i>ilvR</i>	34.00	1.73	Op0788r_1	NA	Q1LJK0 Transcriptional regulator, LysR family
5UTR_1400	3051028 -	3051046 Rmet_2803	<i>ilvR</i>			Op0788r_1		
5UTR_1209	3051139 +	3051157 Rmet_2804	<i>ilvD</i>			Op0789f_1		
NPKM_5505	3051157 +	3052831 Rmet_2804	<i>ilvD</i>	63.33	4.93	Op0789f_1	MET-AA-ValLeulle	Q1LJJ9 Dihydroxyacid dehydratase
3UTR_1670	3052766 -	3052933 Rmet_2805				Op0790r_1		
3UTR_1458	3052832 +	3052890 Rmet_2804	<i>ilvD</i>			Op0789f_1		
NPKM_5506	3052934 -	3053447 Rmet_2805		285.00	10.39	Op0790r_1	NA	Q1LJJ8 Putative uncharacterized protein
NPKM_5507	3053443 -	3053878 Rmet_2806	<i>holC</i>	338.00	23.90	Op0790r_1	GIP-REP-DNA_Pol	Q1LJJ7 DNA polymerase III, chi subunit
NPKM_5508	3053923 -	3055456 Rmet_2807	<i>pepA</i>	429.00	22.07	Op0790r_1	NA	Q1LJJ6 Probable cytosol aminopeptidase
5UTR_1399	3055457 -	3055623 Rmet_2807	<i>pepA</i>			Op0790r_1		
5UTR_1210	3055494 +	3055620 Rmet_2808	<i>yjgP</i>			Op0791f_1		
NPKM_5509	3055620 +	3056739 Rmet_2808	<i>yjgP</i>	111.67	3.06	Op0791f_1	NA	Q1LJJ5 Permease YjgP/YjgQ
NPKM_5510	3056735 +	3057899 Rmet_2809	<i>yjgQ</i>	103.33	2.52	Op0791f_1	NA	Q1LJJ4 Permease YjgP/YjgQ
NPKM_5511	3057901 +	3058306 Rmet_2810	<i>cbiX</i>	115.67	5.51	Op0791f_1	MET-COF-Porph	Q1LJJ3 Cobalamin (Vitamin B12) biosynthesis CbiX protein
3UTR_1669	3058269 -	3058370 Rmet_2811	<i>cysG</i>			Op0792r_2		
3UTR_1459	3058307 +	3058880 Rmet_2810	<i>cbiX</i>			Op0791f_1		

NPKM_5512	3058371 -	3059136 Rmet_2811	<i>cysG</i>	517.00	23.52	Op0792r_2	MET-COF-Porph	Q1LJJ2 Uroporphyrinogen-III C-methyltransferase
NPKM_5513	3059175 -	3060480 Rmet_2812	<i>cysN</i>	744.33	33.56	Op0792r_2	MET-EN-Sulf	Q1LJJ1 Sulfate adenylyltransferase subunit 1
NPKM_5514	3060505 -	3061477 Rmet_2813	<i>cysD</i>	779.67	34.02	Op0792r_2	MET-EN-Sulf	Q1LJJ0 Sulfate adenylyltransferase subunit 2
NPKM_5515	3061503 -	3062304 Rmet_2814	<i>cysH</i>	599.33	28.22	Op0792r_2	MET-EN-Sulf	Q1LJI9 Phosphoadenylylsulfate reductase (Thioredoxin)
NPKM_5516	3062300 -	3062876 Rmet_2815		687.67	9.87	Op0792r_2	NA	Q1LJI8 Uncharacterised conserved protein UCP030820
NPKM_5517	3062894 -	3064577 Rmet_2816	<i>cysI</i>	601.67	32.19	Op0792r_2	MET-EN-Sulf	Q1LJI7 Sulfite reductase (NADPH) beta subunit
NPKM_5518	3064685 -	3065459 Rmet_2817		151.67	7.64	Op0792r_1	NA	Q1LJI6 Putative uncharacterized protein
5UTR_1398	3065460 -	3065708 Rmet_2817				Op0792r_1		
NPKM_5519	3065631 +	3066573 Rmet_2818	<i>cysB</i>	137.00	6.24	Op0793f_1	NA	Q1LJI5 Transcriptional regulator, LysR family
NPKM_5520	3066603 +	3067743 Rmet_2819	<i>hemK1</i>	145.67	2.89	Op0793f_1	NA	Q1LJI4 Methyltransferase small
NPKM_5521	3067828 +	3068998 Rmet_2820		83.67	5.51	Op0793f_1	EIP-TRA-ABC	Q1LJI3 Extracellular ligand-binding receptor
NPKM_5522	3069019 +	3069889 Rmet_2821	<i>garR</i>	109.00	6.24	Op0793f_1	MET-AA-ValLeulle	Q1LJI2 6-phosphogluconate dehydrogenase, NAD-binding
3UTR_1668	3069232 -	3069947 Rmet_2822				Op0794r_1		
3UTR_1460	3069890 +	3070837 Rmet_2821	<i>garR</i>			Op0793f_1		
NPKM_5523	3069948 -	3070890 Rmet_2822		76.67	2.89	Op0794r_1	NA	Q1LJI1 Putative uncharacterized protein
5UTR_1211	3070853 +	3070989 Rmet_2823				Op0795f_1		
5UTR_1397	3070891 -	3071487 Rmet_2822				Op0794r_1		
NPKM_5524	3070989 +	3071352 Rmet_2823		12.33	1.15	Op0795f_1	NA	Q1LJI0 Putative uncharacterized protein
NPKM_5525	3071450 +	3071535 Rmet_R0048		80.00	8.89	Op0795f_2	NA	NA
NPKM_5526	3071961 +	3072240 Rmet_2824		211.00	10.54	Op0795f_3	NA	Q1LJH9 Putative uncharacterized protein
NPKM_5527	3072236 +	3073226 Rmet_2825	<i>repA</i>	41.00	5.57	Op0795f_3	NA	Q1LJH8 Plasmid encoded RepA protein
NPKM_5528	3073222 +	3073552 Rmet_2826		29.33	6.11	Op0795f_3	NA	Q1LJH7 Putative uncharacterized protein
NPKM_5529	3073481 +	3073712 Rmet_6560		27.67	5.51	Op0795f_3	NA	NA
NPKM_5530	3073901 +	3076157 Rmet_2827	<i>traY</i>	15.33	2.31	Op0795f_3	NA	Q1LJH6 Putative TraY/DotA-like type IV secretion system protein
3UTR_1667	3074472 -	3076274 Rmet_2828				Op0796r_1		
NPKM_5531	3076275 -	3077700 Rmet_2828		232.67	6.81	Op0796r_1	NA	Q1LJH5 Putative uncharacterized protein
NPKM_5532	3077714 +	3078089 Rmet_2829		118.33	4.04	Op0797f_1	NA	Q1LJH4 Putative uncharacterized protein
NPKM_5533	3078309 +	3080340 Rmet_2830		356.33	9.07	Op0797f_2	NA	Q1LJH3 Putative uncharacterized protein
NPKM_5534	3080323 +	3080989 Rmet_2831		219.67	14.50	Op0797f_2	NA	Q1LJH2 Putative uncharacterized protein
3UTR_1666	3080856 -	3082828 Rmet_2834	<i>mobA''</i>			Op0798r_2		
NPKM_5535	3080978 +	3082142 Rmet_2832		189.33	11.68	Op0797f_2	NA	Q1LJH1 Putative uncharacterized protein
NPKM_5536	3082188 +	3082692 Rmet_2833		55.67	3.21	Op0797f_2	NA	Q1LJH0 Putative uncharacterized protein
NPKM_5537	3082829 -	3084155 Rmet_2834	<i>mobA''</i>	7.00	0.00	Op0798r_2	NA	Q1LJG9 Putative uncharacterized protein
NPKM_5538	3084280 -	3084496 Rmet_2835	<i>tnmC</i>	0.00	0.00	Op0798r_1	NA	NA
NPKM_5539	3084549 -	3085383 Rmet_2836	<i>gspA</i>	0.00	0.00	Op0798r_1	NA	NA
NPKM_5540	3085379 -	3086819 Rmet_2837	<i>tnmA</i>	0.00	0.00	Op0798r_1	NA	NA
NPKM_5541	3086930 -	3087500 Rmet_2838	<i>tnmB</i>	0.00	0.00	Op0798r_1	NA	NA
NPKM_5542	3087566 -	3088193 Rmet_2839	<i>mobA'</i>	9.00	1.73	Op0798r_1	NA	Q1LJG4 Putative uncharacterized protein
NPKM_5543	3088189 -	3088540 Rmet_2840	<i>mobC</i>	14.00	2.00	Op0798r_1	NA	Q1LJG3 Putative uncharacterized protein
5UTR_1396	3088541 -	3088832 Rmet_2840	<i>mobC</i>			Op0798r_1		
3UTR_1665	3088851 -	3089495 Rmet_2842	<i>tnpA</i>			Op2044r_1		
NPKM_5544	3088865 +	3089138 Rmet_2841		4.00	2.65	Op0799f_1	NA	Q1LJG2 Putative uncharacterized protein
NPKM_5545	3089496 -	3090516 Rmet_2842	<i>tnpA</i>	0.00	0.00	Op2044r_1	NA	NA

NPKM_5546	3090664 +	3091069 Rmet_6561		2.33	1.53	Op0801f_1	NA	NA
NPKM_5547	3092063 +	3092324 Rmet_6562		10.67	0.58	Op0801f_2	NA	NA
NPKM_5548	3092496 +	3092754 Rmet_2843		9.00	1.73	Op0801f_2	NA	Q1LJG0 Putative uncharacterized protein
3UTR_1664	3092499 -	3092880 Rmet_6563				Op2045r_1		
NPKM_5549	3092881 -	3093061 Rmet_6563		4.33	1.15	Op2045r_1	NA	NA
5UTR_1395	3093062 -	3093120 Rmet_6563				Op2045r_1		
3UTR_1663	3093718 -	3095086 Rmet_2846				Op0802r_2		
NPKM_5550	3093804 +	3094497 Rmet_2844		17.67	1.15	Op0801f_2	NA	Q1LJF9 Putative uncharacterized protein
NPKM_5551	3094614 +	3094773 Rmet_2845		29.33	3.51	Op0801f_2	NA	Q1LJF8 Putative uncharacterized protein
NPKM_5552	3095087 -	3095672 Rmet_2846		140.67	4.51	Op0802r_2	NA	Q1LJF7 Exonuclease
NPKM_5553	3095668 -	3096769 Rmet_2847	int	148.33	4.73	Op0802r_2	NA	Q1LJF6 Phage integrase
5UTR_1394	3096770 -	3096780 Rmet_2847	int			Op0802r_2		
NPKM_5554	3096819 -	3097218 Rmet_2848		3.33	0.58	Op0802r_1	NA	Q1LJF5 Putative uncharacterized protein
NPKM_5555	3097334 +	3098084 Rmet_2849	yggG	343.67	13.28	Op0803f_1	GIP-PTL-Fold	Q1LJF4 Peptidase M48, Ste24p
3UTR_1662	3097427 -	3098202 Rmet_2850	hutG1			Op0804r_2		
3UTR_1461	3098085 +	3099759 Rmet_2849	yggG			Op0803f_1		
NPKM_5556	3098203 -	3099019 Rmet_2850	hutG1	174.33	12.01	Op0804r_2	MET-CAH-DiCarb	Q1LJF3 N-formylglutamate amidohydrolase
NPKM_5557	3099068 -	3100478 Rmet_2851	hutF	10.00	0.00	Op0804r_1	MET-AA-His	Q1LJF2 Formimidoylglutamate deiminase
NPKM_5558	3100474 -	3101722 Rmet_2852	hutI	7.33	0.58	Op0804r_1	MET-AA-His	Q1LJF1 Imidazolonepropionase
NPKM_5559	3101718 -	3102294 Rmet_2853		6.33	0.58	Op0804r_1	NA	Q1LJF0 Putative uncharacterized protein
NPKM_5560	3102290 -	3103997 Rmet_2854	hutU1	4.67	0.58	Op0804r_1	MET-AA-His	Q1LJE9 Urocanate hydratase
NPKM_5561	3104065 -	3105634 Rmet_2855	hutH	4.67	0.58	Op0804r_1	MET-EN-Nitrog	Q1LJE8 Histidine ammonia-lyase
NPKM_5562	3105743 -	3106511 Rmet_2856	hutC	44.67	2.52	Op0804r_1	NA	Q1LJE7 Transcriptional regulator, histidine utilization repressor, GntR family
NPKM_5563	3106515 -	3107295 Rmet_2857	tauB	24.67	1.15	Op0804r_1	EIP-TRA-ABC	Q1LJE6 ABC transporter-related protein
NPKM_5564	3107291 -	3108167 Rmet_2858	tauC	25.33	1.53	Op0804r_1	EIP-TRA-ABC	Q1LJE5 Binding-protein-dependent transport systems inner membrane component
NPKM_5565	3108183 -	3109137 Rmet_2859	tauA	38.33	1.53	Op0804r_1	EIP-TRA-ABC	Q1LJE4 Substrate-binding region of ABC-type glycine betaine transport system
5UTR_1393	3109138 -	3109215 Rmet_2859	tauA			Op0804r_1		
3UTR_1661	3109234 -	3109465 Rmet_2860				Op0804r_1		
NPKM_5566	3109466 -	3110462 Rmet_2860		47.67	0.58	Op0804r_1	NA	Q1LJE3 NAD-dependent epimerase/dehydratase
5UTR_1212	3109991 +	3110502 Rmet_2861				Op0805f_1		
5UTR_1392	3110463 -	3110505 Rmet_2860				Op0804r_1		
NPKM_5567	3110502 +	3111558 Rmet_2861		190.67	5.13	Op0805f_1	NA	Q1LJE2 Oxidoreductase FAD/NAD(P)-binding
NPKM_5568	3111835 +	3113023 Rmet_2862	argD	285.00	13.23	Op0805f_1	MET-AA-Lys_Syn	Q1LJE1 Acetylornithine aminotransferase
3UTR_1462	3113024 +	3113486 Rmet_2862	argD			Op0805f_1		
3UTR_1660	3113048 -	3113134 Rmet_2863	livF2			Op0806r_1		
NPKM_5569	3113135 -	3113852 Rmet_2863	livF2	129.33	20.65	Op0806r_1	EIP-TRA-ABC	Q1LJE0 ABC transporter-related protein
NPKM_5570	3113868 -	3114645 Rmet_2864	livG2	122.00	26.85	Op0806r_1	EIP-TRA-ABC	Q1LJD9 ABC transporter-related protein
NPKM_5571	3114658 -	3115813 Rmet_2865	livM2	101.00	23.52	Op0806r_1	EIP-TRA-ABC	Q1LJD8 Inner-membrane translocator
NPKM_5572	3115826 -	3116762 Rmet_2866	livH2	114.67	27.21	Op0806r_1	EIP-TRA-ABC	Q1LJD7 Inner-membrane translocator
NPKM_5573	3116979 -	3118185 Rmet_2867	livK2	544.33	100.03	Op0806r_1	EIP-TRA-ABC	Q1LJD6 Extracellular ligand-binding receptor
5UTR_1391	3118186 -	3118514 Rmet_2867	livK2			Op0806r_1		
3UTR_1659	3118601 -	3118858 Rmet_2868	ispH			Op0806r_1		
NPKM_5574	3118859 -	3119852 Rmet_2868	ispH	351.33	10.79	Op0806r_1	NA	NA

NPKM_5575	3119851 -	3120370 Rmet_2869	<i>fkpB</i>	235.00	7.55	Op0806r_1	GIP-PTL-Fold	Q1LJD4 Peptidyl-prolyl cis-trans isomerase
5UTR_1390	3120371 -	3120816 Rmet_2869	<i>fkpB</i>			Op0806r_1		
5UTR_1213	3120464 +	3120725 Rmet_2870	<i>rpmB</i>			Op0807f_1		
NPKM_5576	3120725 +	3120959 Rmet_2870	<i>rpmB</i>	4715.00	211.54	Op0807f_1	GIP-TL-Ribo	Q1LJD3 50S ribosomal protein L28
NPKM_5577	3120972 +	3121143 Rmet_2871	<i>rpmG</i>	5500.00	136.72	Op0807f_1	GIP-TL-Ribo	Q1LJD2 50S ribosomal protein L33
3UTR_1658	3121181 -	3122958 Rmet_2873	<i>nadC</i>			Op0808r_2		
NPKM_5578	3121324 +	3122932 Rmet_2872	<i>nadB</i>	225.00	15.72	Op0807f_1	MET-AA-AlaAsp	Q1LJD1 L-aspartate oxidase
3UTR_1463	3122933 +	3130306 Rmet_2872	<i>nadB</i>			Op0807f_1		
NPKM_5579	3122959 -	3123823 Rmet_2873	<i>nadC</i>	214.00	6.00	Op0808r_2	MET-COF-NicAm	Q1LJD0 Nicotinate-nucleotide pyrophosphorylase (Carboxylating)
NPKM_5580	3123819 -	3124974 Rmet_2874	<i>nadA</i>	260.00	9.64	Op0808r_2	MET-COF-NicAm	Q1LJC9 Quinolinate synthetase A
NPKM_5581	3125115 -	3126354 Rmet_2875	<i>scd</i>	1237.00	21.28	Op0808r_2	DIV-Ass	Q1LJC8 Fatty acid desaturase
NPKM_5582	3126601 -	3127972 Rmet_2876	<i>mscS1</i>	104.67	5.86	Op0808r_1	NA	Q1LJC7 MscS Mechanosensitive ion channel
NPKM_5583	3127971 -	3129372 Rmet_2877	<i>sun1</i>	202.33	3.06	Op0808r_1	GIP-TL-Ass	Q1LJC6 Fmu (Sun)
NPKM_5584	3129368 -	3130031 Rmet_2878	<i>purN</i>	111.33	9.61	Op0808r_1	NA	Q1LJC5 Phosphoribosylglycinamide formyltransferase
5UTR_1389	3130032 -	3130078 Rmet_2878	<i>purN</i>			Op0808r_1		
NPKM_5585	3130317 +	3131526 Rmet_2879	<i>tnpA</i>	0.00	0.00	Op0809f_1	NA	A4JGL4 Transposase, IS4 family protein
NPKM_5586	3131530 +	3131704 Rmet_6564		5.33	0.58	Op0809f_2	NA	NA
NPKM_5587	3131732 +	3132392 Rmet_2880	<i>vsrC</i>	59.00	1.73	Op0809f_3	NA	Q1LJC3 Two component transcriptional regulator, LuxR family
3UTR_1464	3132393 +	3132429 Rmet_2880	<i>vsrC</i>			Op0809f_3		
3UTR_1657	3132439 -	3132456 Rmet_2881	<i>vsrB</i>			Op0810r_2		
NPKM_5588	3132457 -	3134356 Rmet_2881	<i>vsrB</i>	44.33	5.03	Op0810r_2	NA	Q1LJC2 Sensor protein
5UTR_1214	3133282 +	3135680 Rmet_2883				Op0811f_1		
5UTR_1388	3134357 -	3134532 Rmet_2881	<i>vsrB</i>			Op0810r_2		
3UTR_1656	3135069 -	3135079 Rmet_2882				Op0810r_1		
NPKM_5589	3135080 -	3135440 Rmet_2882		1.00	0.00	Op0810r_1	NA	Q1LJC1 Putative uncharacterized protein
5UTR_1387	3135441 -	3135444 Rmet_2882				Op0810r_1		
NPKM_5590	3135680 +	3137381 Rmet_2883		936.33	79.10	Op0811f_1	GIP-REP-Recomb	Q1LJC0 RNA-directed DNA polymerase
NPKM_5591	3137459 +	3138488 Rmet_2884	<i>ribF</i>	270.33	21.39	Op0811f_1	NA	Q1LJB9 Riboflavin kinase / FMN adenylyltransferase
NPKM_5592	3138607 +	3141487 Rmet_2885	<i>ileS</i>	214.67	7.23	Op0811f_1	MET-AA-ValLeulle	Q1LJB8 Isoleucyl-tRNA synthetase
NPKM_5593	3141486 +	3142023 Rmet_2886	<i>lspA</i>	158.33	7.51	Op0811f_1	GIP-PTL-Exp	Q1LJB7 Lipoprotein signal peptidase
NPKM_5594	3142144 +	3143344 Rmet_2887	<i>dfp</i>	134.33	3.21	Op0811f_1	NA	Q1LJB6 Phosphopantothenoylecysteine decarboxylase / Phosphopantothenate-cysteir
NPKM_5595	3143362 +	3144382 Rmet_2888		78.33	3.06	Op0811f_1	NA	Q1LJB5 Luciferase-like protein
3UTR_1655	3143373 -	3145031 Rmet_2890				Op0812r_2		
NPKM_5596	3144486 +	3144981 Rmet_2889	<i>dut</i>	149.00	6.24	Op0811f_1	MET-NUC-Pyr	Q1LJB4 Deoxyuridine 5'-triphosphate nucleotidohydrolase
3UTR_1465	3144982 +	3145933 Rmet_2889	<i>dut</i>			Op0811f_1		
NPKM_5597	3145032 -	3145878 Rmet_2890		194.67	3.79	Op0812r_2	NA	Q1LJB3 Putative uncharacterized protein
NPKM_5598	3145892 -	3146897 Rmet_2891	<i>bug</i>	203.00	3.46	Op0812r_2	NA	Q1LJB2 Uncharacterized protein UPF0065
NPKM_5599	3147103 -	3149401 Rmet_2892	<i>clpA</i>	350.00	5.20	Op0812r_2	GIP-PTL-Fold	Q1LJB1 ATP-dependent Clp protease ATP-binding subunit ClpA
NPKM_5600	3149397 -	3149724 Rmet_2893	<i>clpS</i>	143.67	10.41	Op0812r_1	GIP-PTL-Fold	Q1LJB0 ATP-dependent Clp protease adapter protein clpS
5UTR_1215	3149623 +	3150288 Rmet_2894	<i>cspE</i>			Op0813f_1		
5UTR_1386	3149725 -	3149904 Rmet_2893	<i>clpS</i>			Op0812r_1		
NPKM_5601	3150288 +	3150498 Rmet_2894	<i>cspE</i>	319.00	32.42	Op0813f_1	NA	Q1LJA9 Cold-shock DNA-binding protein family
3UTR_1466	3150499 +	3151464 Rmet_2894	<i>cspE</i>			Op0813f_1		

3UTR_1654	3150865 -	3150902 Rmet_2895	<i>icd</i>			Op0814r_1		
NPKM_5602	3150903 -	3152154 Rmet_2895	<i>icd</i>	294.67	17.39	Op0814r_1	MET-CAH-TCA	Q1LJA8 Isocitrate dehydrogenase [NADP]
NPKM_5603	3152392 +	3153037 Rmet_2896	<i>rluE</i>	9.00	0.00	Op0815f_1	GIP-TL-Ass	Q1LJA7 Pseudouridine synthase
NPKM_5604	3153143 +	3153344 Rmet_2897		874.33	86.33	Op0815f_2	NA	Q1LJA6 Putative uncharacterized protein
NPKM_5605	3153457 +	3153940 Rmet_2898		91.33	8.02	Op0815f_2	NA	Q1LJA5 Putative uncharacterized protein
NPKM_5606	3153996 -	3154482 Rmet_2899		216.33	9.29	Op0816r_1	NA	Q1LJA4 UPF0234 protein Rmet_2899
NPKM_5607	3154616 +	3155627 Rmet_2900	<i>murB</i>	74.67	3.79	Op0817f_1	MET-CAH-AminSug	Q1LJA3 UDP-N-acetylmuramate dehydrogenase
3UTR_1467	3155628 +	3157055 Rmet_2900	<i>murB</i>			Op0817f_1		
NPKM_5608	3155684 -	3155996 Rmet_2901		227.00	14.73	Op0818r_1	NA	Q1LJA2 UPF0345 protein Rmet_2901
NPKM_5609	3156090 -	3157014 Rmet_2902	<i>argF</i>	530.00	18.25	Op0818r_1	NA	Q1LJA1 Ornithine carbamoyltransferase
5UTR_1216	3157069 +	3157290 Rmet_2903				Op0819f_1		
NPKM_5610	3157290 +	3157755 Rmet_2903		142.33	11.93	Op0819f_1	NA	Q1LJA0 Putative uncharacterized protein
3UTR_1468	3157756 +	3157894 Rmet_2903				Op0819f_1		
5UTR_1217	3157896 +	3158213 Rmet_6565				Op0821f_1		
NPKM_5611	3157936 -	3158203 Rmet_2904	<i>rpsT</i>	3578.67	318.30	Op0820r_1	GIP-TL-Ribo	Q1LJ99 30S ribosomal protein S20
5UTR_1385	3158204 -	3159076 Rmet_2904	<i>rpsT</i>			Op0820r_1		
NPKM_5612	3158213 +	3158468 Rmet_6565		5.67	0.58	Op0821f_1	NA	NA
NPKM_5613	3158537 +	3160142 Rmet_2905	<i>mviN</i>	39.67	3.51	Op0821f_2	EIP-TRA-Ion	Q1LJ98 Integral membrane protein MviN
NPKM_5614	3160155 +	3161004 Rmet_2906		66.33	3.06	Op0821f_2	NA	Q1LJ97 Putative uncharacterized protein
3UTR_1653	3160515 -	3161033 Rmet_2907	<i>dedA</i>			Op0822r_1		
3UTR_1469	3161005 +	3161389 Rmet_2906				Op0821f_2		
NPKM_5615	3161034 -	3161694 Rmet_2907	<i>dedA</i>	198.00	7.21	Op0822r_1	NA	Q1LJ96 DedA
5UTR_1384	3161695 -	3162349 Rmet_2907	<i>dedA</i>			Op0822r_1		
5UTR_1218	3161792 +	3161818 Rmet_2908	<i>mutL</i>			Op0823f_1		
NPKM_5616	3161818 +	3163786 Rmet_2908	<i>mutL</i>	72.33	2.52	Op0823f_1	GIP-REP-Recomb	Q1LJ95 DNA mismatch repair protein MutL
NPKM_5617	3163802 +	3164750 Rmet_2909	<i>miaA</i>	50.00	4.58	Op0823f_1	GIP-TL-Ass	Q1LJ94 tRNA delta(2)-isopentenylpyrophosphate transferase
NPKM_5618	3164814 +	3165306 Rmet_2910		110.00	2.65	Op0823f_2	NA	Q1LJ93 GCN5-related N-acetyltransferase
3UTR_1652	3165297 -	3165376 Rmet_2911	<i>purM</i>			Op0824r_1		
3UTR_1470	3165307 +	3166360 Rmet_2910				Op0823f_2		
NPKM_5619	3165377 -	3166430 Rmet_2911	<i>purM</i>	571.33	23.07	Op0824r_1	MET-NUC-Pur	Q1LJ92 Phosphoribosylformylglycinamide cyclo-ligase
5UTR_1383	3166431 -	3166935 Rmet_2911	<i>purM</i>			Op0824r_1		
5UTR_1219	3166578 +	3166622 Rmet_2912	<i>hda</i>			Op0825f_1		
NPKM_5620	3166622 +	3167330 Rmet_2912	<i>hda</i>	83.67	6.43	Op0825f_1	NA	Q1LJ91 Regulatory inactivation of DnaA Hda protein
NPKM_5621	3167453 +	3168128 Rmet_2913	<i>serB2</i>	198.67	7.77	Op0825f_2	NA	Q1LJ90 HAD-superfamily subfamily IB, PSPase-like protein
NPKM_5622	3168129 +	3169719 Rmet_2914	<i>pcnB</i>	197.33	5.13	Op0825f_2	GIP-TL-Ass	Q1LJ89 Poly(A) polymerase
NPKM_5623	3169720 +	3170242 Rmet_2915	<i>folK</i>	358.33	13.80	Op0825f_2	MET-COF-Folate	Q1LJ88 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase
NPKM_5624	3170265 +	3170907 Rmet_2916		100.67	4.93	Op0825f_2	MET-NUC-Pur	Q1LJ87 Deoxynucleoside kinase
NPKM_5625	3171043 +	3171865 Rmet_2917	<i>panB</i>	320.33	23.46	Op0825f_3	MET-COF-Pant	Q1LJ86 3-methyl-2-oxobutanoate hydroxymethyltransferase
NPKM_5626	3171872 +	3172571 Rmet_2918	<i>tupB</i>	114.33	4.51	Op0825f_3	EIP-TRA-ABC	Q1LJ85 Binding-protein-dependent transport systems inner membrane component
NPKM_5627	3172567 +	3173257 Rmet_2919		48.67	3.79	Op0825f_3	EIP-TRA-ABC	Q1LJ84 ABC transporter-related protein
3UTR_1651	3172675 -	3173286 Rmet_2920	<i>pabB</i>			Op0826r_2		
3UTR_1471	3173258 +	3173847 Rmet_2919				Op0825f_3		
NPKM_5628	3173287 -	3175201 Rmet_2920	<i>pabB</i>	26.67	2.08	Op0826r_2	MET-COF-Folate	Q1LJ83 Para-aminobenzoate synthase, component I

3UTR_1650	3175218 -	3175265 Rmet_2921	<i>dnaJ</i>			Op0826r_2		
NPKM_5629	3175266 -	3176406 Rmet_2921	<i>dnaJ</i>	210.67	7.57	Op0826r_2	GIP-PTL-Fold	Q1LJ82 Chaperone protein dnaJ
NPKM_5630	3176580 -	3178527 Rmet_2922	<i>dnaK</i>	640.33	20.50	Op0826r_2	GIP-PTL-Fold	O33522 Chaperone protein dnaK
NPKM_5631	3178689 -	3179244 Rmet_2923	<i>cobO</i>	49.67	1.53	Op0826r_1	MET-COF-Porph	Q1LJ80 ATP:cob(I)alamin adenosyltransferase
5UTR_1220	3178817 +	3179333 Rmet_2924	<i>dld</i>			Op0827f_1		
5UTR_1382	3179245 -	3179261 Rmet_2923	<i>cobO</i>			Op0826r_1		
NPKM_5632	3179333 +	3180821 Rmet_2924	<i>dld</i>	71.00	1.73	Op0827f_1	MET-CAH-Pyr	Q1LJ79 FAD linked oxidase-like protein
NPKM_5633	3180831 +	3181722 Rmet_2925		55.67	2.08	Op0827f_1	NA	Q1LJ78 Transcriptional regulator, LysR family
NPKM_5634	3181935 +	3183438 Rmet_2926	<i>glcD</i>	79.67	6.81	Op0827f_1	MET-CAH-DiCarb	Q1LJ77 FAD linked oxidase-like protein
NPKM_5635	3183490 +	3184414 Rmet_2927	<i>kch</i>	26.00	1.73	Op0827f_1	NA	Q1LJ76 Ion transport protein
NPKM_5636	3184447 +	3185551 Rmet_2928	<i>glcE</i>	35.33	3.21	Op0827f_1	NA	Q1LJ75 FAD linked oxidase-like protein
NPKM_5637	3185601 +	3186873 Rmet_2929	<i>glcF</i>	48.00	1.73	Op0827f_1	NA	Q1LJ74 Putative uncharacterized protein
NPKM_5638	3187009 +	3187396 Rmet_2930	<i>lrgA</i>	41.67	4.73	Op0827f_1	EIP-TRA-Pores	Q1LJ73 LrgA
NPKM_5639	3187392 +	3188118 Rmet_2931	<i>lrgB</i>	40.67	0.58	Op0827f_1	NA	Q1LJ72 LrgB-like protein
3UTR_1649	3188152 -	3189321 Rmet_2934	<i>gpo</i>			Op0828r_1		
NPKM_5640	3188164 +	3188584 Rmet_2932		80.00	1.00	Op0827f_1	NA	Q1LJ71 Glyoxalase/bleomycin resistance protein/dioxygenase
NPKM_5641	3188603 +	3189296 Rmet_2933		51.67	3.21	Op0827f_1	NA	Q1LJ70 Helix-turn-helix, type 11
3UTR_1472	3189297 +	3189950 Rmet_2933				Op0827f_1		
NPKM_5642	3189322 -	3189817 Rmet_2934	<i>gpo</i>	223.67	7.77	Op0828r_1	MET-LIP-Others	Q1LJ69 Glutathione peroxidase
NPKM_5643	3189872 -	3191018 Rmet_2935	<i>pilU</i>	206.33	10.50	Op0828r_1	GIP-PTL-T2S	Q1LJ68 Twitching motility protein
NPKM_5644	3191029 -	3192073 Rmet_2936	<i>pilT</i>	229.00	11.36	Op0828r_1	GIP-PTL-T2S	Q1LJ67 Twitching motility protein
5UTR_1381	3192074 -	3192111 Rmet_2936	<i>pilT</i>			Op0828r_1		
5UTR_1221	3192105 +	3192136 Rmet_2937	<i>yggS</i>			Op0829f_1		
NPKM_5645	3192136 +	3192826 Rmet_2937	<i>yggS</i>	127.33	3.51	Op0829f_1	NA	Q1LJ66 Putative uncharacterized protein
NPKM_5646	3192911 +	3193733 Rmet_2938	<i>proC</i>	164.00	11.36	Op0829f_1	MET-AA-ArgPro	Q1LJ65 Pyrroline-5-carboxylate reductase
3UTR_1648	3193154 -	3193760 Rmet_2939	<i>ubiA</i>			Op0830r_3		
3UTR_1473	3193734 +	3194630 Rmet_2938	<i>proC</i>			Op0829f_1		
NPKM_5647	3193761 -	3194646 Rmet_2939	<i>ubiA</i>	127.33	4.16	Op0830r_3	MET-COF-CoQ	Q1LJ64 4-hydroxybenzoate octaprenyltransferase
NPKM_5648	3194760 -	3195246 Rmet_2940	<i>dpsA</i>	1475.33	108.56	Op0830r_3	GIP-REP-Recomb	Q1LJ63 Ferritin and Dps
NPKM_5649	3195331 -	3195523 Rmet_6566		64.67	9.81	Op0830r_2	NA	NA
NPKM_5650	3195690 -	3196647 Rmet_2941	<i>oxyR</i>	166.33	3.79	Op0830r_2	NA	Q1LJ62 Transcriptional regulator, LysR family
NPKM_5651	3196767 -	3198981 Rmet_2942	<i>recG</i>	40.67	1.15	Op0830r_1	GIP-REP-Recomb	Q1LJ61 ATP-dependent DNA helicase RecG
5UTR_1380	3198982 -	3199194 Rmet_2942	<i>recG</i>			Op0830r_1		
5UTR_1222	3199038 +	3199088 Rmet_2943	<i>queA</i>			Op0831f_1		
NPKM_5652	3199088 +	3200150 Rmet_2943	<i>queA</i>	61.00	4.00	Op0831f_1	GIP-TL-Ass	Q1LJ60 S-adenosylmethionine:tRNA ribosyltransferase-isomerase
NPKM_5653	3200169 +	3201300 Rmet_2944	<i>tgt</i>	88.67	6.35	Op0831f_1	GIP-TL-Ass	Q1LJ59 Queuine tRNA-ribosyltransferase
NPKM_5654	3201519 +	3201846 Rmet_2945	<i>yajC</i>	1140.33	66.79	Op0831f_2	GIP-PTL-Exp	Q1LJ58 Protein translocase subunit yajC
NPKM_5655	3201874 +	3202054 Rmet_6567		775.00	36.35	Op0831f_2	NA	NA
NPKM_5656	3202005 +	3203916 Rmet_2946	<i>secD</i>	349.67	12.58	Op0831f_2	GIP-PTL-Exp	Q1LJ57 Protein-export membrane protein SecD
NPKM_5657	3203940 +	3204915 Rmet_2947	<i>secF</i>	325.33	14.64	Op0831f_2	GIP-PTL-Exp	Q1LJ56 Protein translocase subunit secF
NPKM_5658	3205204 +	3206455 Rmet_2948		87.33	5.51	Op0831f_2	NA	Q1LJ55 L-carnitine dehydratase/bile acid-inducible protein F
3UTR_1647	3205530 -	3206690 Rmet_2949	<i>phcQ</i>			Op0832r_4		
3UTR_1474	3206456 +	3207028 Rmet_2948				Op0831f_2		

NPKM_5659	3206691 -	3207690 Rmet_2949	<i>phcQ</i>	485.00	59.03	Op0832r_4	NA	Q1LJ54 Response regulator receiver domain protein (CheY-like)
NPKM_5660	3207686 -	3208823 Rmet_2950	<i>phcR</i>	214.00	23.64	Op0832r_3	NA	Q1LJ53 Sensor protein
NPKM_5661	3208826 -	3210215 Rmet_2951	<i>phcS</i>	178.33	17.95	Op0832r_3	NA	Q1LJ52 Sensor protein
NPKM_5662	3210186 -	3211656 Rmet_2952	<i>phcB</i>	286.33	28.75	Op0832r_3	NA	Q1LJ51 MCP methyltransferase, CheR-type
NPKM_5663	3211944 -	3212535 Rmet_2953	<i>yceI</i>	791.67	373.12	Op0832r_3	NA	Q1LJ50 YceI
NPKM_5664	3212632 -	3213208 Rmet_2954		250.67	106.24	Op0832r_2	NA	Q1LJ49 YceI
NPKM_5665	3213242 -	3213809 Rmet_2955	<i>yceI</i>	108.33	42.71	Op0832r_1	NA	Q1LJ48 Cytochrome B561
NPKM_5666	3214133 -	3215510 Rmet_2956	<i>purB</i>	273.33	19.76	Op0832r_1	MET-NUC-Pur	Q1LJ47 Adenylosuccinate lyase
5UTR_1379	3215511 -	3215686 Rmet_2956	<i>purB</i>			Op0832r_1		
NPKM_5667	3215690 +	3215897 Rmet_6568	<i>cobT</i>	2.67	1.15	Op0833f_1	NA	NA
3UTR_1646	3215887 -	3216615 Rmet_2958	<i>trmU</i>			Op0834r_2		
NPKM_5668	3215893 +	3216508 Rmet_2957	<i>gst-1</i>	209.33	12.66	Op0833f_2	MET-OAA-GSH	Q1LJ46 Glutathione S-transferase-like protein
3UTR_1475	3216509 +	3216851 Rmet_2957	<i>gst-1</i>			Op0833f_2		
NPKM_5669	3216616 -	3217696 Rmet_2958	<i>trmU</i>	139.33	8.62	Op0834r_2	GIP-TL-Ass	Q1LJ45 tRNA-specific 2-thiouridylase mnmA
NPKM_5670	3217692 -	3218244 Rmet_2959		139.00	10.58	Op0834r_2	NA	Q1LJ44 NUDIX hydrolase
5UTR_1378	3218245 -	3218264 Rmet_2959				Op0834r_2		
3UTR_1645	3218285 -	3218361 Rmet_2960	<i>dapA3</i>			Op0834r_1		
NPKM_5671	3218362 -	3219271 Rmet_2960	<i>dapA3</i>	4.33	0.58	Op0834r_1	MET-AA-Lys_Syn	Q1LJ43 Dihydrodipicolinate synthase
NPKM_5672	3219257 -	3219578 Rmet_2961		3.33	1.53	Op0834r_1	NA	Q1LJ42 Putative uncharacterized protein
5UTR_1377	3219579 -	3219607 Rmet_2961				Op0834r_1		
3UTR_1644	3219645 -	3219700 Rmet_2962				Op0834r_1		
NPKM_5673	3219701 -	3220499 Rmet_2962		2.00	0.00	Op0834r_1	NA	Q1LJ41 Putative uncharacterized protein
5UTR_1223	3220510 +	3220749 Rmet_2963	<i>pntAa</i>			Op0835f_1		
NPKM_5674	3220749 +	3221955 Rmet_2963	<i>pntAa</i>	367.33	11.02	Op0835f_1	MET-COF-NicAm	Q1LJ40 Alanine dehydrogenase/PNT-like protein
NPKM_5675	3222135 +	3222459 Rmet_2964	<i>pntAb</i>	272.00	10.82	Op0835f_1	MET-COF-NicAm	Q1LJ39 NAD/NADP transhydrogenase alpha subunit-like protein
NPKM_5676	3222458 +	3223931 Rmet_2965	<i>pntB</i>	336.33	14.47	Op0835f_1	MET-COF-NicAm	Q1LJ38 NAD(P) transhydrogenase, beta subunit
3UTR_1643	3223865 -	3223926 Rmet_6569				Op2046r_1		
NPKM_5677	3223927 -	3224170 Rmet_6569		3.33	0.58	Op2046r_1	NA	NA
NPKM_5678	3224147 +	3225197 Rmet_2966		253.33	13.05	Op0835f_1	NA	Q1LJ37 Response regulator receiver domain protein (CheY-like)
5UTR_1376	3224171 -	3224291 Rmet_6569				Op2046r_1		
3UTR_1642	3224301 -	3225268 Rmet_2967	<i>ycbY</i>			Op0836r_2		
3UTR_1476	3225198 +	3225864 Rmet_2966				Op0835f_1		
NPKM_5679	3225269 -	3226529 Rmet_2967	<i>ycbY</i>	78.33	1.15	Op0836r_2	GIP-REP-Recomb	Q1LJ36 Putative RNA methylase
NPKM_5680	3226597 -	3227203 Rmet_2968		219.33	2.52	Op0836r_2	NA	Q1LJ35 DSBA oxidoreductase
NPKM_5681	3227238 -	3227661 Rmet_2969		104.33	2.52	Op0836r_1	NA	Q1LJ34 Putative uncharacterized protein
NPKM_5682	3227679 -	3228960 Rmet_2970	<i>proA</i>	115.67	0.58	Op0836r_1	MET-AA-Urea	Q1LJ33 Gamma-glutamyl phosphate reductase
NPKM_5683	3229086 -	3230157 Rmet_2971	<i>hoIA</i>	125.33	6.81	Op0836r_1	GIP-REP-DNA_Pol	Q1LJ32 DNA polymerase III, delta subunit
NPKM_5684	3230208 -	3230724 Rmet_2972	<i>rlpB</i>	219.33	7.51	Op0836r_1	NA	Q1LJ31 Rare lipoprotein B
NPKM_5685	3230760 -	3233382 Rmet_2973	<i>leuS</i>	239.67	8.02	Op0836r_1	MET-AA-ValLeulle	Q1LJ30 Leucyl-tRNA synthetase
NPKM_5686	3233551 -	3234349 Rmet_2974	<i>dapB</i>	146.67	6.66	Op0836r_1	MET-AA-Lys_Syn	Q1LJ29 Dihydrodipicolinate reductase
NPKM_5687	3234427 -	3235204 Rmet_2975	<i>omIA</i>	385.00	25.94	Op0836r_1	GIP-TL-Ass	Q1LJ28 SmpA/OmlA
5UTR_1224	3234906 +	3235280 Rmet_2976	<i>fur</i>			Op0837f_1		
5UTR_1375	3235205 -	3235213 Rmet_2975	<i>omIA</i>			Op0836r_1		

NPKM_5688	3235280 +	3235712 Rmet_2976	<i>fur</i>	600.00	8.72	Op0837f_1	NA	O30330 Ferric uptake regulation protein
3UTR_1477	3235713 +	3235769 Rmet_2976	<i>fur</i>			Op0837f_1		
3UTR_1641	3235764 -	3235791 Rmet_2977	<i>phcA</i>			Op0838r_2		
5UTR_1225	3235771 +	3237079 Rmet_2978				Op0839f_1		
NPKM_5689	3235792 -	3236794 Rmet_2977	<i>phcA</i>	322.67	12.06	Op0838r_2	NA	Q1LJ26 Transcriptional regulator, LysR family
NPKM_5690	3236810 -	3236918 Rmet_6570		5.33	1.15	Op0838r_1	NA	NA
5UTR_1374	3236919 -	3236952 Rmet_6570				Op0838r_1		
3UTR_1640	3236991 -	3237745 Rmet_2979	<i>cbbG2</i>			Op0840r_2		
NPKM_5691	3237079 +	3237697 Rmet_2978		42.33	1.53	Op0839f_1	NA	Q1LJ25 Flavin reductase-like, FMN-binding
3UTR_1478	3237698 +	3237854 Rmet_2978				Op0839f_1		
NPKM_5692	3237746 -	3238745 Rmet_2979	<i>cbbG2</i>	1153.00	86.75	Op0840r_2	MET-CAH-FbP	Q1LJ24 Glyceraldehyde-3-phosphate dehydrogenase
NPKM_5693	3238830 -	3240810 Rmet_2980	<i>cbbT2</i>	564.00	16.70	Op0840r_1	MET-CAH-PP_KDPG	Q1LJ23 Transketolase
5UTR_1226	3240303 +	3240865 Rmet_2981	<i>speE</i>			Op0841f_1		
5UTR_1373	3240811 -	3241684 Rmet_2980	<i>cbbT2</i>			Op0840r_1		
NPKM_5694	3240865 +	3241840 Rmet_2981	<i>speE</i>	34.00	1.00	Op0841f_1	MET-AA-Met	Q1LJ22 Spermidine synthase
NPKM_5695	3241905 +	3242340 Rmet_2982		110.33	1.15	Op0841f_2	NA	Q1LJ21 Glyoxalase/bleomycin resistance protein/dioxygenase
NPKM_5696	3242339 +	3243083 Rmet_2983		72.00	3.00	Op0841f_2	NA	Q1LJ20 Putative uncharacterized protein
3UTR_1639	3242758 -	3243826 Rmet_2985				Op0842r_4		
NPKM_5697	3243100 +	3243730 Rmet_2984		185.00	6.24	Op0841f_3	NA	Q1LJ19 Putative uncharacterized protein
3UTR_1479	3243731 +	3243758 Rmet_2984				Op0841f_3		
NPKM_5698	3243827 -	3244436 Rmet_2985		664.67	38.66	Op0842r_4	NA	Q1LJ18 Putative uncharacterized protein
NPKM_5699	3244432 -	3244876 Rmet_2986		994.33	88.86	Op0842r_4	NA	Q1LJ17 Guanine-specific ribonuclease N1 and T1
NPKM_5700	3245066 -	3245168 Rmet_6571		17.33	3.21	Op0842r_3	NA	NA
NPKM_5701	3245216 -	3245570 Rmet_2987		2.33	0.58	Op0842r_2	NA	Q1LJ16 Putative uncharacterized protein
3UTR_1638	3245604 -	3245624 Rmet_2988	<i>metF2</i>			Op0842r_2		
NPKM_5702	3245625 -	3246528 Rmet_2988	<i>metF2</i>	1.33	0.58	Op0842r_2	MET-EN-Methane	A0HB18 Methylenetetrahydrofolate reductase
5UTR_1372	3246529 -	3246582 Rmet_2988	<i>metF2</i>			Op0842r_2		
3UTR_1637	3246590 -	3246618 Rmet_2989				Op0842r_2		
NPKM_5703	3246619 -	3247288 Rmet_2989		1.00	0.00	Op0842r_2	NA	Q1LJ14 Putative uncharacterized protein
NPKM_5704	3247284 -	3247785 Rmet_2990	<i>metR</i>	4.00	1.00	Op0842r_2	NA	A9BTP5 Transcriptional regulator, LysR family
NPKM_5705	3247825 -	3249364 Rmet_2991	<i>tnpAB</i>	2.33	0.58	Op0842r_2	NA	A0HB21 Integrase, catalytic region
NPKM_5706	3249941 -	3250925 Rmet_2992	<i>ptxD</i>	7.00	1.00	Op0842r_2	NA	Q1LJ11 D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding
NPKM_5707	3250933 -	3251734 Rmet_2993	<i>ptxC</i>	3.00	0.00	Op0842r_1	EIP-TRA-ABC	A0HB23 Phosphonate ABC transporter, inner membrane subunit
NPKM_5708	3251730 -	3252609 Rmet_2994	<i>ptxB</i>	5.67	0.58	Op0842r_1	EIP-TRA-ABC	A9BTP9 Phosphonate ABC transporter, periplasmic phosphonate-binding protein
NPKM_5709	3252602 -	3253442 Rmet_2995	<i>ptxA</i>	5.33	0.58	Op0842r_1	EIP-TRA-ABC	Q1LJ08 Phosphonates import ATP-binding protein phnC 2
5UTR_1371	3253443 -	3253474 Rmet_2995	<i>ptxA</i>			Op0842r_1		
NPKM_5710	3253676 +	3254501 Rmet_2996	<i>ptxR</i>	1.67	0.58	Op0843f_1	NA	A0HB26 Transcriptional regulator, LysR family
NPKM_5711	3254608 +	3255076 Rmet_2997		5.33	1.53	Op0843f_2	NA	A9BTQ2 Putative uncharacterized protein
3UTR_1636	3255040 -	3255071 Rmet_2998				Op0844r_1		
NPKM_5712	3255072 -	3257340 Rmet_2998		3.67	0.58	Op0844r_1	NA	Q1LJ05 Transposase Tn3
5UTR_1370	3257341 -	3257353 Rmet_2998				Op0844r_1		
NPKM_5713	3257482 +	3257818 Rmet_2999	<i>mmfA</i>	0.00	0.00	Op0845f_1	NA	Q1LDD1 Propeptide, PepSY amd peptidase M4
NPKM_5714	3257874 +	3258471 Rmet_3000	<i>mmfB</i>	0.00	0.00	Op0845f_1	MET-PepGlyc	Q1LDD2 Undecaprenyl-diphosphatase (Phosphoesterase, PA-phosphatase related)

NPKM_5715	3258541 +	3259324 Rmet_3001	<i>mmfC1</i>	0.00	0.00	Op0845f_1	NA	Q1LDD3 Putative uncharacterized protein
NPKM_5716	3259353 +	3259803 Rmet_3002	<i>mmfD</i>	0.00	0.00	Op0845f_1	NA	Q1LDD4 Conserved hypothetical signal peptide protein
NPKM_5717	3259812 +	3260571 Rmet_3003	<i>mmfC2</i>	0.00	0.00	Op0845f_1	NA	Q1LDD5 Putative uncharacterized protein
NPKM_5718	3260593 +	3261259 Rmet_3004	<i>mmfR</i>	0.00	0.00	Op0845f_1	EIP-SIG-2Comp	Q1LDD6 Two component transcriptional regulator, winged helix family
NPKM_5719	3261255 +	3262587 Rmet_3005	<i>mmfS</i>	0.00	0.00	Op0845f_1	EIP-SIG-2Comp	Q1LDD7 Sensor protein
NPKM_5720	3262615 +	3263047 Rmet_3006		0.00	0.00	Op0845f_1	NA	Q1LDD8 Putative uncharacterized protein
NPKM_5721	3263113 -	3263728 Rmet_3007	<i>tniR</i>	0.00	0.00	Op0846r_1	NA	Q1LDD9 Resolvase-like protein
NPKM_5722	3263788 -	3265006 Rmet_3008	<i>tniQ</i>	0.00	0.00	Op0846r_1	NA	Q1LDE0 TniQ
NPKM_5723	3265002 -	3265911 Rmet_3009	<i>tniB</i>	0.00	0.00	Op0846r_1	NA	Q1LDE1 TniB
NPKM_5724	3265913 -	3267443 Rmet_3010	<i>tniA</i>	0.00	0.00	Op0846r_1	GIP-REP-Recomb	A4VG30 TniA transposase
NPKM_5725	3267468 -	3270498 Rmet_3011	<i>hmzA</i>	3.00	0.00	Op0846r_1	EIP-TRA-Ion	Q1LIZ2 Heavy metal efflux pump CzcA
3UTR_1635	3270506 -	3270510 Rmet_3012	<i>hmzB</i>			Op0846r_1		
NPKM_5726	3270511 -	3271735 Rmet_3012	<i>hmzB</i>	3.67	0.58	Op0846r_1	EIP-TRA-Ion	Q1LIZ1 Secretion protein HlyD
5UTR_1369	3271736 -	3271866 Rmet_3012	<i>hmzB</i>			Op0846r_1		
NPKM_5727	3272056 +	3272608 Rmet_3013	<i>yodB</i>	20.33	2.08	Op0847f_1	NA	Q1LIZ0 Cytochrome B561
NPKM_5728	3272649 +	3273357 Rmet_3014		25.67	2.89	Op0847f_1	NA	A0HB61 Putative uncharacterized protein
3UTR_1634	3272833 -	3273369 Rmet_3015	<i>hmzS</i>			Op0848r_4		
NPKM_5729	3273370 -	3274783 Rmet_3015	<i>hmzS</i>	16.67	1.53	Op0848r_4	NA	Q1LIY8 Sensor protein
NPKM_5730	3274786 -	3275452 Rmet_3016	<i>hmzR</i>	37.33	2.31	Op0848r_4	NA	Q1LIY7 Two component transcriptional regulator, winged helix family
NPKM_5731	3275466 -	3276810 Rmet_3017		25.00	1.73	Op0848r_4	NA	Q1LIY6 Ferric reductase-like transmembrane component-like
5UTR_1368	3276811 -	3276888 Rmet_3017				Op0848r_4		
NPKM_5732	3277025 -	3279002 Rmet_3018	<i>virD2</i>	1.00	0.00	Op0848r_3	NA	Q1LIY5 Putative uncharacterized protein
NPKM_5733	3278998 -	3279388 Rmet_3019		0.33	0.58	Op0848r_2	NA	Q1LIY4 Putative uncharacterized protein
NPKM_5734	3279449 -	3280037 Rmet_3020	<i>traF</i>	0.67	0.58	Op0848r_2	NA	Q1LIY3 TraF peptidase. Serine peptidase. MEROPS family S26C
NPKM_5735	3280033 -	3280558 Rmet_3021		1.00	0.00	Op0848r_2	NA	A0HB67 Putative uncharacterized protein
NPKM_5736	3280554 -	3280818 Rmet_3022	<i>parG</i>	0.67	0.58	Op0848r_2	NA	Q1LIY1 Putative uncharacterized protein
NPKM_5737	3280814 -	3281453 Rmet_3023	<i>paraA</i>	2.00	1.00	Op0848r_2	DIV-Division	A0HB69 Cobyric acid a,c-diamide synthase
5UTR_1367	3281454 -	3281470 Rmet_3023	<i>paraA</i>			Op0848r_2		
3UTR_1633	3281696 -	3281705 Rmet_3024	<i>repA</i>			Op0848r_2		
NPKM_5738	3281706 -	3282564 Rmet_3024	<i>repA</i>	1.00	0.00	Op0848r_2	NA	A9BTU5 Conserved hypothetical replication initiator and transcription repressor prot
NPKM_5739	3282590 -	3282917 Rmet_3025		1.33	0.58	Op0848r_2	NA	Q1LIX8 Putative uncharacterized protein
NPKM_5740	3282955 -	3283714 Rmet_3026		3.00	2.00	Op0848r_2	NA	A9BTV1 Putative uncharacterized protein
5UTR_1366	3283715 -	3283728 Rmet_3026				Op0848r_2		
3UTR_1632	3284025 -	3284054 Rmet_3027				Op0848r_2		
NPKM_5741	3284055 -	3284403 Rmet_3027		4.67	0.58	Op0848r_2	NA	A9BTV2 Putative lipoprotein
NPKM_5742	3284408 -	3284657 Rmet_6572		1.00	0.00	Op0848r_1	NA	NA
NPKM_5743	3284626 +	3284920 Rmet_3028		72.33	2.52	Op0849f_1	NA	A9BTV3 Helix-turn-helix domain protein
NPKM_5744	3285273 -	3285588 Rmet_3029		4.67	1.15	Op0850r_1	NA	Q1LIX4 Putative uncharacterized protein
5UTR_1365	3285589 -	3285615 Rmet_3029				Op0850r_1		
3UTR_1631	3285683 -	3285932 Rmet_3030				Op0850r_1		
NPKM_5745	3285933 -	3286326 Rmet_3030		6.00	3.00	Op0850r_1	NA	Q1LIX3 Putative uncharacterized protein
5UTR_1364	3286327 -	3286638 Rmet_3030				Op0850r_1		
NPKM_5746	3286409 +	3286928 Rmet_3031		12.00	1.00	Op0851f_1	NA	A9BTV5 GCN5-related N-acetyltransferase

3UTR_1630	3287050 -	3287057 Rmet_3032				Op0852r_1		
NPKM_5747	3287058 -	3287268 Rmet_3032		4.00	1.00	Op0852r_1	NA	A9BTV6 Putative uncharacterized protein
NPKM_5748	3287330 -	3289397 Rmet_3033	<i>parB</i>	5.00	1.00	Op0852r_1	NA	A9BTV7 ParB domain protein nuclease
NPKM_5749	3289472 -	3290300 Rmet_3034	<i>yupB</i>	5.33	1.53	Op0852r_1	NA	A9BTV8 Putative uncharacterized protein
NPKM_5750	3290253 +	3290583 Rmet_6573		1.67	1.53	Op0853f_1	NA	NA
5UTR_1363	3290301 -	3290317 Rmet_3034	<i>yupB</i>			Op0852r_1		
3UTR_1629	3290659 -	3291676 Rmet_3037				Op0854r_1		
NPKM_5751	3290824 +	3291088 Rmet_3035		1.33	0.58	Op0853f_1	NA	
NPKM_5752	3291235 +	3291535 Rmet_3036		0.33	0.58	Op0853f_1	NA	B2UA43 Putative uncharacterized protein
NPKM_5753	3291677 -	3291956 Rmet_3037		31.33	3.21	Op0854r_1	NA	Q1LIW7 Putative uncharacterized protein
NPKM_5754	3292019 -	3292370 Rmet_3038		42.33	2.89	Op0854r_1	NA	B2UA41 Putative uncharacterized protein
NPKM_5755	3293010 -	3293817 Rmet_3039		195.67	9.81	Op0854r_1	NA	B2UA40 Putative uncharacterized protein
NPKM_5756	3293862 -	3296118 Rmet_3040		186.67	12.01	Op0854r_1	NA	Q1LIW4 UBA/THIF-type NAD/FAD binding fold
NPKM_5757	3296114 -	3297308 Rmet_3041		358.67	22.81	Op0854r_1	NA	A9BTW5 Putative uncharacterized protein
5UTR_1362	3297309 -	3297380 Rmet_3041				Op0854r_1		
NPKM_5758	3297397 +	3298300 Rmet_3042		376.67	37.63	Op0855f_1	NA	Q1LIW2 Putative uncharacterized protein
NPKM_5759	3298306 +	3299095 Rmet_3043		231.33	17.24	Op0855f_1	NA	B2UA36 Putative uncharacterized protein
3UTR_1628	3299100 -	3299139 Rmet_3044				Op0856r_1		
NPKM_5760	3299140 -	3300277 Rmet_3044		4.67	0.58	Op0856r_1	NA	A9BTW8 Putative uncharacterized protein
NPKM_5761	3300273 -	3301521 Rmet_3045	<i>int</i>	10.33	0.58	Op0856r_1	NA	Q1LIV9 Phage integrase
NPKM_5762	3301715 -	3304301 Rmet_3046	<i>maeB1</i>	991.00	41.04	Op0856r_1	MET-CAH-Pyr	Q1LIV8 Malic enzyme, NAD-binding
NPKM_5763	3304299 +	3305277 Rmet_3047	<i>thiL</i>	177.00	4.58	Op0857f_1	MET-COF-Thia	Q1LIV7 Thiamine-monophosphate kinase
NPKM_5764	3305374 +	3305947 Rmet_3048	<i>pgpA</i>	146.67	4.73	Op0857f_1	MET-LIP-GlycLip	Q1LIV6 Phosphatidylglycerophosphatase
NPKM_5765	3305993 +	3306491 Rmet_3049		159.00	3.46	Op0857f_1	NA	Q1LIV5 CinA-like protein
NPKM_5766	3306540 -	3307359 Rmet_3050	<i>pyrF</i>	130.00	3.00	Op0858r_1	MET-NUC-Pyr	Q1LIV4 Orotidine 5'-phosphate decarboxylase
5UTR_1361	3307360 -	3307537 Rmet_3050	<i>pyrF</i>			Op0858r_1		
NPKM_5767	3307601 +	3308486 Rmet_3051		28.33	2.08	Op0859f_1	NA	Q1LIV3 Putative uncharacterized protein
NPKM_5768	3309012 +	3309975 Rmet_3052	<i>corA</i>	54.00	6.24	Op0859f_1	EIP-TRA-Ion	Q1LIV2 Magnesium and cobalt transport protein CorA
3UTR_1627	3309308 -	3310023 Rmet_3053	<i>mtgA</i>			Op0860r_2		
3UTR_1480	3309976 +	3311580 Rmet_3052	<i>corA</i>			Op0859f_1		
NPKM_5769	3310024 -	3310726 Rmet_3053	<i>mtgA</i>	31.67	3.06	Op0860r_2	NA	Q1LIV1 Monofunctional biosynthetic peptidoglycan transglycosylase
NPKM_5770	3310809 -	3311718 Rmet_3054	<i>aroE</i>	138.67	7.64	Op0860r_2	MET-AA-PheTyrTrp	Q1LIV0 Shikimate dehydrogenase
NPKM_5771	3311717 -	3312704 Rmet_3055		111.33	4.51	Op0860r_2	NA	Q1LIU9 TonB-like protein
NPKM_5772	3312780 -	3314919 Rmet_3056		128.00	7.21	Op0860r_2	GIP-TL-Ass	Q1LIU8 Ribonuclease II
NPKM_5773	3315064 -	3315805 Rmet_3057	<i>fabG</i>	245.67	27.47	Op0860r_2	MET-LIP-FASyn	Q1LIU7 3-oxoacyl-[acyl-carrier-protein] reductase
NPKM_5774	3315801 -	3316464 Rmet_3058	<i>ubiC</i>	103.67	4.51	Op0860r_1	MET-COF-CoQ	Q1LIU6 Probable chorismate--pyruvate lyase
NPKM_5775	3316460 -	3317060 Rmet_3059		147.67	4.93	Op0860r_1	NA	Q1LIU5 Putative uncharacterized protein
NPKM_5776	3317072 -	3318506 Rmet_3060	<i>mpl</i>	150.00	7.00	Op0860r_1	NA	Q1LIU4 UDP-N-acetylmuramate
5UTR_1227	3318415 +	3318576 Rmet_3061				Op0861f_1		
5UTR_1360	3318507 -	3318688 Rmet_3060	<i>mpl</i>			Op0860r_1		
NPKM_5777	3318576 +	3319260 Rmet_3061		40.67	1.15	Op0861f_1	NA	Q1LIU3 Putative uncharacterized protein
NPKM_5778	3319342 +	3319885 Rmet_3062		96.33	4.51	Op0861f_2	NA	Q1LIU2 Thioredoxin-like protein
NPKM_5779	3320114 +	3320603 Rmet_3063	<i>aroQ</i>	258.33	16.04	Op0861f_3	MET-AA-PheTyrTrp	Q1LIU1 3-dehydroquinone dehydratase

NPKM_5780	3320862	+	3321324	Rmet_3064	<i>accB</i>	543.00	7.55	Op0861f_4	MET-CAH-Pyr	Q1LIU0 Biotin carboxyl carrier protein
NPKM_5781	3321372	+	3322806	Rmet_3065	<i>accC</i>	825.67	10.02	Op0861f_4	MET-CAH-Pyr	Q1LIT9 Acetyl-CoA carboxylase, biotin carboxylase
NPKM_5782	3322848	+	3323763	Rmet_3066	<i>prmA</i>	334.67	6.11	Op0861f_4	GIP-TL-Ass	Q1LIT8 Ribosomal protein L11 methyltransferase
NPKM_5783	3323772	+	3325458	Rmet_3067		98.00	3.46	Op0861f_4	NA	Q1LIT7 Zinc finger/thioredoxin putative
NPKM_5784	3325536	+	3326037	Rmet_3068	<i>tpx</i>	704.67	42.45	Op0861f_5	NA	Q1LIT6 Thiol peroxidase (Atypical 2-Cys peroxiredoxin)
NPKM_5785	3326139	+	3327087	Rmet_3069		463.00	16.82	Op0861f_5	MET-NUC-Pur	Q1LIT5 PfkB
3UTR_1626	3326200	-	3327910	Rmet_3071				Op0862r_3		
NPKM_5786	3327152	+	3327620	Rmet_3070		847.67	46.88	Op0861f_5	NA	Q1LIT4 17 kDa surface antigen
3UTR_1481	3327621	+	3329165	Rmet_3070				Op0861f_5		
NPKM_5787	3327911	-	3328517	Rmet_3071		7291.33	273.13	Op0862r_3	NA	Q1LIT3 Histone H1-like protein
NPKM_5788	3328553	-	3328988	Rmet_3072		726.33	49.24	Op0862r_2	NA	Q1LIT2 Putative uncharacterized protein
5UTR_1359	3328989	-	3329191	Rmet_3072				Op0862r_2		
NPKM_5789	3329193	-	3329598	Rmet_3073		2.00	1.00	Op0862r_1	NA	Q1LIT1 Putative uncharacterized protein
5UTR_1228	3329204	+	3329640	Rmet_3074				Op0863f_1		
NPKM_5790	3329404	-	3329608	Rmet_6574		2.33	2.08	Op0862r_1	NA	NA
5UTR_1358	3329609	-	3329822	Rmet_6574				Op0862r_1		
NPKM_5791	3329640	+	3330198	Rmet_3074		9.33	2.08	Op0863f_1	NA	Q1LIT0 Putative uncharacterized protein
NPKM_5792	3330214	+	3330676	Rmet_3075		187.00	14.00	Op0863f_2	NA	Q1LIS9 Conserved hypothetical signal peptide protein
NPKM_5793	3330657	+	3330834	Rmet_6575		104.67	10.79	Op0863f_2	NA	NA
NPKM_5794	3330836	+	3331808	Rmet_3076	<i>bug</i>	146.00	7.55	Op0863f_2	NA	Q1LIS8 Uncharacterized protein UPF0065
3UTR_1482	3331809	+	3331944	Rmet_3076	<i>bug</i>			Op0863f_2		
5UTR_1229	3332065	+	3332073	Rmet_3077				Op0863f_2		
NPKM_5795	3332073	+	3334335	Rmet_3077		3.00	0.00	Op0863f_2	EIP-TRA-Pores	Q1LIS7 TonB-dependent siderophore receptor
3UTR_1625	3333242	-	3335103	Rmet_3079				Op0864r_1		
NPKM_5796	3334396	+	3335083	Rmet_3078	<i>ybiX</i>	20.00	2.65	Op0863f_3	NA	Q1LIS6 PKHD-type hydroxylase Rmet_3078
3UTR_1483	3335084	+	3335536	Rmet_3078	<i>ybiX</i>			Op0863f_3		
NPKM_5797	3335104	-	3336142	Rmet_3079		18.33	0.58	Op0864r_1	NA	Q1LIS5 Transcriptional regulator, LysR family
5UTR_1230	3336107	+	3336140	Rmet_3080				Op0865f_1		
NPKM_5798	3336140	+	3336539	Rmet_3080		8.33	0.58	Op0865f_1	NA	Q1LIS4 4-oxalocrotonate tautomerase
NPKM_5799	3336653	+	3337487	Rmet_3081		28.33	3.21	Op0865f_2	NA	Q1LIS3 Aldo/keto reductase
NPKM_5800	3337541	-	3338078	Rmet_3082		71.33	1.53	Op0866r_1	NA	Q1LIS2 Putative uncharacterized protein
5UTR_1357	3338079	-	3338104	Rmet_3082				Op0866r_1		
NPKM_5801	3338125	+	3338821	Rmet_3083		309.33	24.21	Op0867f_1	NA	Q1LIS1 Putative lipoprotein
NPKM_5802	3339081	+	3340020	Rmet_3084	<i>rdgC</i>	196.33	21.39	Op0867f_1	GIP-REP-Recomb	Q1LIS0 Putative exonuclease, RdgC
3UTR_1624	3339827	-	3340047	Rmet_3085				Op0868r_1		
NPKM_5803	3340048	-	3341011	Rmet_3085		4.00	0.00	Op0868r_1	NA	Q1LIR9 Alcohol dehydrogenase, zinc-binding
NPKM_5804	3341090	+	3342089	Rmet_3086	<i>bug</i>	124.67	10.69	Op0869f_1	NA	Q1LIR8 Uncharacterized protein UPF0065
3UTR_1484	3342090	+	3347893	Rmet_3086	<i>bug</i>			Op0869f_1		
NPKM_5805	3342182	-	3343370	Rmet_3087	<i>nrdB</i>	489.00	26.46	Op0870r_3	MET-NUC-Pur	Q1LIR7 Ribonucleotide reductase
NPKM_5806	3343510	-	3346450	Rmet_3088	<i>nrdA</i>	525.67	22.81	Op0870r_3	MET-NUC-Pur	Q1LIR6 Ribonucleoside-diphosphate reductase
NPKM_5807	3346968	-	3347571	Rmet_3089	<i>ampD</i>	69.00	2.00	Op0870r_2	NA	Q1LIR5 Negative regulator of AmpC, AmpD
NPKM_5808	3347563	-	3349246	Rmet_3090	<i>pehR</i>	87.00	3.00	Op0870r_2	GIP-PTL-T2S	Q1LIR4 Two component, sigma54 specific, transcriptional regulator, Fis family
NPKM_5809	3349251	-	3351288	Rmet_3091	<i>pehS</i>	41.00	2.65	Op0870r_1	GIP-PTL-T2S	Q1LIR3 Sensor protein

NPKM_5810	3351284 -	3351557 Rmet_3092		92.00	1.73	Op0870r_1	NA	Q1LIR2 Putative uncharacterized protein
NPKM_5811	3351572 -	3352511 Rmet_3093		74.33	0.58	Op0870r_1	NA	Q1LIR1 Cytochrome c assembly protein
5UTR_1356	3352512 -	3352516 Rmet_3093				Op0870r_1		
5UTR_1231	3352529 +	3352628 Rmet_3094	<i>ffh</i>			Op0871f_1		
NPKM_5812	3352628 +	3354020 Rmet_3094	<i>ffh</i>	203.33	6.51	Op0871f_1	GIP-PTL-Exp	Q1LIR0 Signal recognition particle subunit FFH/SRP54 (Srp54)
NPKM_5813	3354094 +	3354637 Rmet_3095	<i>hpt</i>	207.67	4.51	Op0871f_1	MET-NUC-Pur	Q1LIQ9 Phosphoribosyltransferase
3UTR_1485	3354638 +	3356059 Rmet_3095	<i>hpt</i>			Op0871f_1		
3UTR_1623	3354690 -	3354861 Rmet_3096				Op0872r_1		
NPKM_5814	3354862 -	3355501 Rmet_3096		9.33	1.15	Op0872r_1	NA	Q1LIQ8 Lysine exporter protein (LYSE/YGGA)
NPKM_5815	3355654 -	3357076 Rmet_3097		9.00	1.00	Op0872r_1	NA	Q1LIQ7 Putative uncharacterized protein
5UTR_1355	3357077 -	3357130 Rmet_3097				Op0872r_1		
3UTR_1622	3357184 -	3357348 Rmet_3098				Op0872r_1		
NPKM_5816	3357349 -	3358231 Rmet_3098		80.33	4.51	Op0872r_1	MET-AA-ArgPro	Q1LIQ6 2OG-Fe(II) oxygenase
NPKM_5817	3358235 -	3358991 Rmet_3099		175.00	7.00	Op0872r_1	NA	Q1LIQ5 Lytic transglycosylase, catalytic
NPKM_5818	3359006 -	3360851 Rmet_3100	<i>proS</i>	247.67	9.61	Op0872r_1	MET-AA-ArgPro	Q1LIQ4 Prolyl-tRNA synthetase
5UTR_1232	3360779 +	3360912 Rmet_3101	<i>nudH</i>			Op0873f_1		
5UTR_1354	3360852 -	3361242 Rmet_3100	<i>proS</i>			Op0872r_1		
NPKM_5819	3360912 +	3361638 Rmet_3101	<i>nudH</i>	392.33	14.74	Op0873f_1	NA	Q1LIQ3 NUDIX hydrolase
NPKM_5820	3361630 +	3362236 Rmet_3102		442.00	13.89	Op0873f_1	NA	Q1LIQ2 Putative lipoprotein
3UTR_1486	3362237 +	3362270 Rmet_3102				Op0873f_1		
3UTR_1621	3362274 -	3362317 Rmet_3103	<i>proB</i>			Op0874r_1		
NPKM_5821	3362318 -	3363437 Rmet_3103	<i>proB</i>	220.33	5.51	Op0874r_1	MET-AA-Urea	Q1LIQ1 Glutamate 5-kinase
NPKM_5822	3363474 -	3364572 Rmet_3104	<i>obgE</i>	370.67	10.21	Op0874r_1	NA	Q1LIQ0 GTP1/OBG subdomain
NPKM_5823	3364697 -	3364958 Rmet_3105	<i>rpmA</i>	8133.00	60.11	Op0874r_1	GIP-TL-Ribo	Q1LIP9 50S ribosomal protein L27
5UTR_1233	3364985 +	3365782 Rmet_3107	<i>ispB</i>			Op0875f_1		
NPKM_5824	3365009 -	3365321 Rmet_3106	<i>rplU</i>	4493.33	164.15	Op0874r_1	GIP-TL-Ribo	Q1LIP8 50S ribosomal protein L21
5UTR_1353	3365322 -	3366099 Rmet_3106	<i>rplU</i>			Op0874r_1		
NPKM_5825	3365782 +	3366760 Rmet_3107	<i>ispB</i>	303.67	9.61	Op0875f_1	NA	Q1LIP7 Polyprenyl synthetase
NPKM_5826	3366864 +	3366941 Rmet_R0049		63.00	9.54	Op0875f_1	NA	NA
NPKM_5827	3367232 +	3368954 Rmet_3108	<i>pilB</i>	251.00	23.39	Op0875f_2	GIP-PTL-T2S	Q1LIP6 Type II secretion system protein E
NPKM_5828	3368983 +	3370249 Rmet_3109	<i>pilC</i>	234.00	15.72	Op0875f_2	GIP-PTL-T2S	Q1LIP5 Type II secretion system protein
NPKM_5829	3370267 +	3371137 Rmet_3110	<i>pilD</i>	132.33	11.72	Op0875f_2	GIP-PTL-T2S	Q1LIP4 Type 4 prepilin peptidase 1. Aspartic peptidase. MEROPS family A24A
NPKM_5830	3371207 +	3371852 Rmet_3111	<i>coaE</i>	145.00	6.08	Op0875f_2	MET-COF-Pant	Q1LIP3 Dephospho-CoA kinase
NPKM_5831	3372074 +	3372833 Rmet_3112		345.00	15.10	Op0875f_3	NA	Q1LIP2 UPF0289 protein Rmet_3112
3UTR_1620	3372234 -	3373117 Rmet_3114				Op0876r_2		
NPKM_5832	3372841 +	3373033 Rmet_3113		163.33	1.53	Op0875f_3	NA	Q1LIP1 Putative uncharacterized protein
3UTR_1487	3373034 +	3373638 Rmet_3113				Op0875f_3		
NPKM_5833	3373118 -	3375149 Rmet_3114		32.00	2.65	Op0876r_2	NA	Q1LIP0 Oligopeptide transporter OPT
NPKM_5834	3375204 -	3375648 Rmet_3115	<i>mutT</i>	180.00	14.00	Op0876r_2	GIP-REP-Recomb	Q1LIN9 NUDIX hydrolase
NPKM_5835	3375644 -	3376556 Rmet_3116		223.00	11.53	Op0876r_2	NA	Q1LIN8 Putative uncharacterized protein
NPKM_5836	3376582 -	3377809 Rmet_3117	<i>argJ</i>	345.33	11.93	Op0876r_2	MET-AA-Urea	Q1LIN7 Glutamate N-acetyltransferase
5UTR_1234	3377401 +	3377782 Rmet_6576				Op2047f_1		
NPKM_5837	3377782 +	3377968 Rmet_6576		3.33	0.58	Op2047f_1	NA	NA

NPKM_5838	3377939 -	3380732 Rmet_3118	<i>secA</i>	393.33	14.74	Op0876r_2	GIP-PTL-Exp	Q1LIN6 Protein translocase subunit secA
3UTR_1488	3377969 +	3378719 Rmet_6576				Op2047f_1		
5UTR_1235	3380700 +	3382020 Rmet_3120				Op0877f_1		
NPKM_5839	3380979 -	3381912 Rmet_3119		68.00	0.00	Op0876r_1	NA	Q1LIN5 Peptidase M23B
NPKM_5840	3382020 +	3382524 Rmet_3120		63.00	2.65	Op0877f_1	NA	Q1LIN4 Putative uncharacterized protein
3UTR_1489	3382525 +	3383292 Rmet_3120				Op0877f_1		
NPKM_5841	3382671 -	3383589 Rmet_3121	<i>lpxC</i>	567.67	29.96	Op0878r_4	MET-GLYC-LPS	Q1LIN3 UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase
NPKM_5842	3383742 -	3384249 Rmet_3122		257.67	9.07	Op0878r_3	GIP-PTL-Fold	Q1LIN2 Peptidase S8 and S53, subtilisin, kexin, sedolisin
NPKM_5843	3384659 -	3385850 Rmet_3123	<i>ftsZ</i>	1348.33	67.72	Op0878r_3	DIV-Division	Q1LIN1 Cell division protein ftsZ
NPKM_5844	3386037 -	3387270 Rmet_3124	<i>ftsA</i>	252.33	3.21	Op0878r_2	DIV-Division	Q1LIN0 Cell division protein FtsA
NPKM_5845	3387266 -	3388169 Rmet_3125	<i>ftsQ</i>	135.33	8.08	Op0878r_2	DIV-Division	Q1LIM9 Cell division protein FtsQ
NPKM_5846	3388199 -	3389183 Rmet_3126	<i>ddlB</i>	196.33	1.15	Op0878r_2	MET-OAA-Other	Q1LIM8 D-alanine--D-alanine ligase
NPKM_5847	3389179 -	3390595 Rmet_3127	<i>murC</i>	206.00	9.54	Op0878r_2	MET-OAA-Other	Q1LIM7 UDP-N-acetylmuramate--L-alanine ligase
NPKM_5848	3390605 -	3391676 Rmet_3128	<i>murG</i>	103.67	13.61	Op0878r_2	MET-PepGlyc	Q1LIM6 UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphor
NPKM_5849	3391672 -	3392914 Rmet_3129	<i>ftsW</i>	138.33	12.58	Op0878r_2	DIV-Division	Q1LIM5 Cell cycle protein
NPKM_5850	3392910 -	3394425 Rmet_3130	<i>murD</i>	202.00	14.73	Op0878r_2	MET-OAA-Other	Q1LIM4 UDP-N-acetylmuramoylalanine--D-glutamate ligase
NPKM_5851	3394475 -	3395645 Rmet_3131	<i>mraY</i>	125.67	7.37	Op0878r_2	MET-PepGlyc	Q1LIM3 Phospho-N-acetylmuramoyl-pentapeptide-transferase
NPKM_5852	3395660 -	3397061 Rmet_3132	<i>murF</i>	172.67	9.71	Op0878r_2	MET-AA-Lys_Syn	Q1LIM2 UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase
NPKM_5853	3397057 -	3398605 Rmet_3133	<i>murE</i>	182.33	14.36	Op0878r_2	MET-AA-Lys_Syn	Q1LIM1 UDP-N-acetylmuramoylalanyl-D-glutamate--2, 6-diaminopimelate ligase
NPKM_5854	3398601 -	3400419 Rmet_3134	<i>ftsI</i>	136.67	6.11	Op0878r_2	MET-PepGlyc	Q1LIM0 Peptidoglycan synthetase FtsI
NPKM_5855	3400415 -	3400733 Rmet_3135	<i>ftsL</i>	202.00	7.21	Op0878r_2	DIV-Division	Q1LIL9 Cell division protein, FtsL-like protein
NPKM_5856	3400729 -	3401707 Rmet_3136	<i>mraW</i>	404.00	12.12	Op0878r_2	NA	Q1LIL8 Methyltransferase
NPKM_5857	3401714 -	3402170 Rmet_3137	<i>mraZ</i>	732.00	47.15	Op0878r_2	NA	Q1LIL7 Putative uncharacterized protein
NPKM_5858	3402641 -	3403265 Rmet_3138		128.00	1.00	Op0878r_1	MET-COF-CoQ	Q1LIL6 2-nonaprenyl-3-methyl-6-methoxy-1,4-benzoquinol hydroxylase
5UTR_1352	3403266 -	3403803 Rmet_3138				Op0878r_1		
5UTR_1236	3403529 +	3403549 Rmet_3139				Op0879f_1		
NPKM_5859	3403549 +	3403813 Rmet_3139		1034.33	32.93	Op0879f_1	NA	Q1LIL5 Putative uncharacterized protein
NPKM_5860	3403991 -	3404207 Rmet_3140	<i>tnmC</i>	0.00	0.00	Op0880r_1	NA	NA
NPKM_5861	3404260 -	3405094 Rmet_3141	<i>gspA</i>	0.00	0.00	Op0880r_1	NA	NA
NPKM_5862	3405090 -	3406530 Rmet_3142	<i>tnmA</i>	0.00	0.00	Op0880r_1	NA	NA
NPKM_5863	3406641 -	3407211 Rmet_3143	<i>tnmB</i>	0.00	0.00	Op0880r_1	NA	Q1LIL1 Putative uncharacterized protein
NPKM_5864	3407225 +	3408314 Rmet_3144		1815.00	103.18	Op0881f_1	NA	Q1LIL0 Porin, Gram-negative type
3UTR_1619	3407341 -	3410534 Rmet_3148	<i>fadD</i>			Op0882r_3		
NPKM_5865	3408485 +	3409487 Rmet_3145	<i>bug</i>	213.33	10.21	Op0881f_1	NA	Q1LIK9 Uncharacterized protein UPF0065
NPKM_5866	3409554 +	3410061 Rmet_3146		119.33	5.86	Op0881f_1	NA	Q1LIK8 Transcriptional regulator, MarR family
NPKM_5867	3410057 +	3410519 Rmet_3147		56.33	2.52	Op0881f_1	NA	Q1LIK7 Putative uncharacterized protein
3UTR_1490	3410520 +	3411174 Rmet_3147				Op0881f_1		
NPKM_5868	3410535 -	3412218 Rmet_3148	<i>fadD</i>	217.67	21.94	Op0882r_3	MET-LIP-FAMet	Q1LIK6 AMP-dependent synthetase and ligase
NPKM_5869	3412399 -	3413101 Rmet_3149		42.33	6.66	Op0882r_2	NA	Q1LIK5 Transcriptional regulator, TetR family
NPKM_5870	3413130 -	3414288 Rmet_3150		34.00	2.65	Op0882r_2	NA	Q1LIK4 Putative zinc protease protein
NPKM_5871	3414284 -	3416390 Rmet_3151		93.00	4.00	Op0882r_2	NA	Q1LIK3 Molybdopterin oxidoreductase
NPKM_5872	3416414 -	3416666 Rmet_3152		25.33	2.31	Op0882r_1	NA	Q1LIK2 Putative uncharacterized protein
5UTR_1237	3416490 +	3416491 Rmet_6577				Op0883f_1		

NPKM_5873	3416491 +	3416581 Rmet_6577		0.67	1.15	Op0883f_1	NA	NA
5UTR_1238	3416609 +	3416710 Rmet_3153				Op0883f_2		
5UTR_1351	3416667 -	3417327 Rmet_3152				Op0882r_1		
NPKM_5874	3416710 +	3417907 Rmet_3153		131.00	1.73	Op0883f_2	NA	Q1LIK1 Extracellular ligand-binding receptor
3UTR_1618	3417332 -	3417964 Rmet_3154	dppF			Op0884r_1		
3UTR_1491	3417908 +	3419579 Rmet_3153				Op0883f_2		
NPKM_5875	3417965 -	3419030 Rmet_3154	dppF	35.67	3.79	Op0884r_1	EIP-TRA-ABC	Q1LIK0 Oligopeptide/dipeptide ABC transporter, ATP-binding protein-like protein
NPKM_5876	3419026 -	3420025 Rmet_3155	dppD	41.00	6.24	Op0884r_1	EIP-TRA-ABC	Q1LIJ9 Oligopeptide/dipeptide ABC transporter, ATP-binding protein-like protein
NPKM_5877	3420041 -	3420971 Rmet_3156	dppC	41.67	8.96	Op0884r_1	EIP-TRA-ABC	Q1LIJ8 Binding-protein-dependent transport systems inner membrane component
NPKM_5878	3420974 -	3421952 Rmet_3157	dppB	46.67	7.23	Op0884r_1	EIP-TRA-ABC	Q1LIJ7 Binding-protein-dependent transport systems inner membrane component
NPKM_5879	3422106 -	3423714 Rmet_3158	dppA	65.67	9.87	Op0884r_1	EIP-TRA-ABC	Q1LIJ6 Extracellular solute-binding protein, family 5
5UTR_1239	3424094 +	3424123 Rmet_3159	hipO			Op0885f_1		
NPKM_5880	3424123 +	3425317 Rmet_3159	hipO	161.67	4.04	Op0885f_1	MET-AA-Phe	Q1LIJ5 Peptidase M20D, amidohydrolase
NPKM_5881	3425357 +	3426383 Rmet_3160		88.67	1.15	Op0885f_1	NA	Q1LIJ4 Putative uncharacterized protein
3UTR_1492	3426384 +	3427175 Rmet_3160				Op0885f_1		
NPKM_5882	3426389 -	3427310 Rmet_3161		384.67	52.27	Op0886r_2	NA	Q1LIJ3 Putative uncharacterized protein
5UTR_1350	3427311 -	3427559 Rmet_3161				Op0886r_2		
NPKM_5883	3427572 -	3427686 Rmet_R0050		0.00	0.00	Op0886r_1	NA	NA
NPKM_5884	3427865 -	3430683 Rmet_R0051		0.00	0.00	Op0886r_1	NA	NA
NPKM_5885	3430965 -	3431041 Rmet_R0052		0.00	0.00	Op0886r_1	NA	NA
NPKM_5886	3431052 -	3431129 Rmet_R0053		0.00	0.00	Op0886r_1	NA	NA
NPKM_5887	3431193 -	3432720 Rmet_R0054		0.00	0.00	Op0886r_1	NA	NA
NPKM_5888	3432504 +	3432849 Rmet_6578		0.00	0.00	Op2048f_1	NA	NA
NPKM_5889	3433029 -	3433245 Rmet_6579		1.67	1.15	Op0886r_1	NA	NA
NPKM_5890	3433324 -	3434101 Rmet_3162	paaF	250.33	14.57	Op0886r_1	MET-CAH-Prop	Q1LIJ2 Short chain enoyl-CoA hydratase
5UTR_1240	3433386 +	3434328 Rmet_3163	paaG			Op0887f_1		
5UTR_1349	3434102 -	3434500 Rmet_3162	paaF			Op0886r_1		
NPKM_5891	3434328 +	3435171 Rmet_3163	paaG	76.33	7.23	Op0887f_1	MET-CAH-Prop	Q1LIJ1 Enoyl-CoA hydratase / short chain enoyl-CoA hydratase
NPKM_5892	3435203 +	3435644 Rmet_3164	paal	59.67	3.21	Op0887f_1	NA	Q1LIJ0 Phenylacetic acid degradation protein PaaD
NPKM_5893	3435737 +	3437042 Rmet_3165	paaK	54.00	3.61	Op0887f_1	MET-AA-Tyr	Q1LIJ9 Phenylacetate-CoA ligase
3UTR_1617	3436559 -	3437066 Rmet_3166	norR			Op0888r_1		
3UTR_1493	3437043 +	3437910 Rmet_3165	paaK			Op0887f_1		
NPKM_5894	3437067 -	3438645 Rmet_3166	norR	37.33	0.58	Op0888r_1	NA	Q1LIJ8 Transcriptional regulator, NifA subfamily, Fis family
5UTR_1241	3438553 +	3438582 Rmet_6580				Op2049f_1		
NPKM_5895	3438582 +	3438666 Rmet_6580		0.67	1.15	Op2049f_1	NA	NA
3UTR_1494	3438667 +	3438674 Rmet_6580				Op2049f_1		
NPKM_5896	3438677 -	3438749 Rmet_6581		0.33	0.58	Op2050r_1	NA	NA
NPKM_5897	3438805 +	3441085 Rmet_3167	norB	1.67	0.58	Op0889f_1	MET-EN-Nitrog	Q1LIJ7 Nitric oxide reductase large subunit
3UTR_1616	3440810 -	3440949 Rmet_3168	nirE			Op0890r_1		
NPKM_5898	3440950 -	3441808 Rmet_3168	nirE	5.67	0.58	Op0890r_1	MET-COF-Porph	Q1LIJ6 Uroporphyrinogen-III C-methyltransferase
3UTR_1495	3441086 +	3441645 Rmet_3167	norB			Op0889f_1		
NPKM_5899	3441819 -	3443301 Rmet_3169	nirN	4.67	0.58	Op0890r_1	MET-EN-Nitrog	Q1LIJ5 Cytochrome d1, heme region
NPKM_5900	3443297 -	3444461 Rmet_3170	nirJ	6.33	0.58	Op0890r_1	NA	Q1LIJ4 Radical SAM

NPKM_5901	3444464 -	3444770 Rmet_3171	<i>nirM</i>	17.33	0.58	Op0890r_1	NA	Q1LI3 Cytochrome c, class I
NPKM_5902	3444790 -	3446440 Rmet_3172	<i>nirS</i>	13.67	1.15	Op0890r_1	MET-EN-Nitrog	Q1LI2 Cytochrome d1, heme region
NPKM_5903	3446651 -	3447800 Rmet_3173	<i>mltA</i>	114.33	5.03	Op0890r_1	NA	Q1LI1 MltA
NPKM_5904	3447889 +	3448087 Rmet_3174		44.67	5.69	Op0891f_1	NA	Q1LI0 Putative uncharacterized protein
NPKM_5905	3448105 -	3448480 Rmet_3175	<i>apaG</i>	205.33	15.01	Op0892r_1	NA	Q1LI9 ApaG
5UTR_1348	3448481 -	3448980 Rmet_3175	<i>apaG</i>			Op0892r_1		
NPKM_5906	3448549 +	3449350 Rmet_3176	<i>cbbE2</i>	146.33	11.68	Op0893f_1	MET-CAH-PP_KDPG	Q1LIH8 Ribulose-5-phosphate 3-epimerase
NPKM_5907	3449371 +	3450112 Rmet_3177	<i>cbbZ2</i>	116.67	6.66	Op0893f_1	MET-CAH-DiCarb	Q1LIH7 Phosphoglycolate phosphatase
NPKM_5908	3450571 +	3452098 Rmet_3178	<i>trpE</i>	128.00	1.73	Op0893f_1	MET-AA-PheTyrTrp	Q1LIH6 Anthranilate synthase, component I
NPKM_5909	3452121 +	3452691 Rmet_3179	<i>trpG</i>	106.33	4.16	Op0893f_1	MET-AA-PheTyrTrp	Q1LIH5 Anthranilate synthase, component II
NPKM_5910	3452687 +	3453770 Rmet_3180	<i>trpD</i>	135.67	5.03	Op0893f_1	MET-AA-PheTyrTrp	Q1LIH4 Anthranilate phosphoribosyltransferase
NPKM_5911	3453776 +	3454589 Rmet_3181	<i>trpC</i>	115.00	5.57	Op0893f_1	MET-AA-PheTyrTrp	Q1LIH3 Indole-3-glycerol phosphate synthase
NPKM_5912	3454596 +	3455220 Rmet_3182		99.00	3.61	Op0893f_1	NA	Q1LIH2 Adenylate cyclase
3UTR_1615	3454842 -	3456050 Rmet_3184	<i>acyP</i>			Op0894r_2		
NPKM_5913	3455219 +	3455990 Rmet_3183	<i>ung</i>	56.00	3.61	Op0893f_1	GIP-REP-Recomb	Q1LIH1 Uracil-DNA glycosylase
3UTR_1496	3455991 +	3456408 Rmet_3183	<i>ung</i>			Op0893f_1		
NPKM_5914	3456051 -	3456339 Rmet_3184	<i>acyP</i>	13.67	0.58	Op0894r_2	MET-CAH-FbP	Q1LIH0 Acylphosphatase
5UTR_1347	3456340 -	3456458 Rmet_3184	<i>acyP</i>			Op0894r_2		
5UTR_1242	3456425 +	3456669 Rmet_3185				Op0895f_1		
NPKM_5915	3456477 -	3456684 Rmet_6582		2.33	1.15	Op0894r_1	NA	NA
NPKM_5916	3456669 +	3458415 Rmet_3185		22.67	1.15	Op0895f_1	EIP-TRA-ABC	Q1LIG9 Binding-protein-dependent transport systems inner membrane component
5UTR_1346	3456685 -	3456707 Rmet_6582				Op0894r_1		
NPKM_5917	3458425 +	3459772 Rmet_3186		30.67	1.15	Op0895f_1	EIP-TRA-ABC	Q1LIG8 ABC transporter-related protein
3UTR_1614	3458924 -	3459850 Rmet_3187				Op0896r_1		
3UTR_1497	3459773 +	3460645 Rmet_3186				Op0895f_1		
NPKM_5918	3459851 -	3462224 Rmet_3187		37.00	2.00	Op0896r_1	NA	Q1LIG7 Putative uncharacterized protein
NPKM_5919	3462309 -	3464124 Rmet_3188		130.00	6.00	Op0896r_1	NA	Q1LIG6 Peptidase M61
NPKM_5920	3464188 -	3465190 Rmet_3189	<i>yhdH</i>	127.00	6.56	Op0896r_1	MET-CAH-FbP	Q1LIG5 Alcohol dehydrogenase, zinc-binding
NPKM_5921	3465300 -	3466059 Rmet_3190	<i>dsbC</i>	376.00	12.12	Op0896r_1	GIP-PTL-Fold	Q1LIG4 Putative thiol:disulfide interchange protein
NPKM_5922	3466171 -	3467596 Rmet_3191		207.33	9.29	Op0896r_1	NA	Q1LIG3 2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinol hydroxylase
5UTR_1243	3467365 +	3467381 Rmet_6583				Op0897f_1		
NPKM_5923	3467381 +	3467492 Rmet_6583		0.67	0.58	Op0897f_1	NA	NA
3UTR_1498	3467493 +	3467514 Rmet_6583				Op0897f_1		
5UTR_1345	3467597 -	3467598 Rmet_3191				Op0896r_1		
5UTR_1244	3467802 +	3467914 Rmet_3192				Op0897f_2		
NPKM_5924	3467914 +	3468733 Rmet_3192		4.00	1.00	Op0897f_2	NA	Q1LIG2 Putative uncharacterized protein
3UTR_1499	3468734 +	3468851 Rmet_3192				Op0897f_2		
5UTR_1245	3468869 +	3469047 Rmet_3193	<i>ychF</i>			Op0897f_3		
NPKM_5925	3469047 +	3470139 Rmet_3193	<i>ychF</i>	231.33	6.43	Op0897f_3	NA	Q1LIG1 Putative uncharacterized protein
3UTR_1500	3470140 +	3470230 Rmet_3193	<i>ychF</i>			Op0897f_3		
3UTR_1613	3470190 -	3470242 Rmet_3194				Op0898r_1		
NPKM_5926	3470243 -	3470429 Rmet_3194		34.67	1.53	Op0898r_1	NA	Q1LIG0 Putative uncharacterized protein
NPKM_5927	3470471 -	3470972 Rmet_3195		43.33	3.21	Op0898r_1	NA	Q1LIF9 Putative membrane protein

NPKM_5928	3470968 -	3472096 Rmet_3196		38.67	0.58	Op0898r_1	NA	Q1LIF8 Putative uncharacterized protein
NPKM_5929	3472092 -	3473106 Rmet_3197		39.33	1.15	Op0898r_1	NA	Q1LIF7 Putative membrane protein
NPKM_5930	3473198 +	3474053 Rmet_3198	<i>mtnN</i>	37.67	2.08	Op0899f_1	MET-AA-Met	Q1LIF6 Methylthioadenosine nucleosidase
3UTR_1501	3474054 +	3474360 Rmet_3198	<i>mtnN</i>			Op0899f_1		
NPKM_5931	3474103 -	3474346 Rmet_3199		43.67	3.51	Op0900r_1	NA	Q1LIF5 Conserved hypothetical transmembrane protein
5UTR_1344	3474347 -	3475160 Rmet_3199				Op0900r_1		
NPKM_5932	3474462 +	3475815 Rmet_3200	<i>hemA</i>	407.67	3.79	Op0901f_1	MET-COF-Porph	Q1LIF4 Glutamyl-tRNA reductase
3UTR_1612	3475181 -	3479647 Rmet_3206				Op0902r_2		
NPKM_5933	3475884 +	3477000 Rmet_3201	<i>prfA</i>	65.67	4.04	Op0901f_1	NA	Q1LIF3 Peptide chain release factor 1
NPKM_5934	3477162 +	3477486 Rmet_3202		431.33	50.34	Op0901f_2	NA	Q1LIF2 Outer membrane protein
NPKM_5935	3477573 +	3478506 Rmet_3203	<i>prmC</i>	111.00	10.58	Op0901f_2	MET-COF-Porph	Q1LIF1 Modification methylase, HemK family
NPKM_5936	3478582 +	3478936 Rmet_3204	<i>ydhD</i>	417.67	12.66	Op0901f_3	GIP-PTL-Fold	Q1LIF0 Glutaredoxin-related protein
NPKM_5937	3478967 +	3479582 Rmet_3205	<i>ubiX</i>	373.33	4.51	Op0901f_3	MET-COF-CoQ	Q1LIE9 3-octaprenyl-4-hydroxybenzoate carboxy-lyase
3UTR_1502	3479583 +	3481955 Rmet_3205	<i>ubiX</i>			Op0901f_3		
NPKM_5938	3479648 -	3479855 Rmet_3206		51.67	5.03	Op0902r_2	NA	Q1LIE8 Putative uncharacterized protein
NPKM_5939	3480011 -	3481535 Rmet_3207		13.33	1.15	Op0902r_1	MET-CAH-FbP	Q1LIE7 Aldehyde dehydrogenase
NPKM_5940	3481531 -	3482725 Rmet_3208		13.67	1.53	Op0902r_1	NA	Q1LIE6 Saccharopine dehydrogenase
5UTR_1343	3482726 -	3482779 Rmet_3208				Op0902r_1		
5UTR_1246	3482837 +	3482873 Rmet_3209				Op0903f_1		
NPKM_5941	3482873 +	3483323 Rmet_3209		21.67	0.58	Op0903f_1	NA	Q1LIE5 Transcriptional regulator, AsnC family
3UTR_1611	3483313 -	3484235 Rmet_3211				Op0904r_1		
NPKM_5942	3483403 +	3484213 Rmet_3210		70.33	3.51	Op0903f_2	MET-AA-Lys_Syn	Q1LIE4 Dihydrodipicolinate reductase
NPKM_5943	3484236 -	3484989 Rmet_3211		101.33	5.51	Op0904r_1	NA	Q1LIE3 Conserved hypothetical signal peptide protein
NPKM_5944	3485090 -	3485432 Rmet_6584		166.67	3.51	Op0904r_1	NA	NA
NPKM_5945	3485100 +	3485631 Rmet_3212		5.00	1.00	Op0905f_1	NA	Q1LIE2 Putative uncharacterized protein
NPKM_5946	3485616 -	3487185 Rmet_3213		58.67	0.58	Op0906r_2	NA	Q1LIE1 Cl-channel, voltage gated
3UTR_1503	3485632 +	3486328 Rmet_3212				Op0905f_1		
5UTR_1247	3486913 +	3487093 Rmet_6585				Op2051f_1		
NPKM_5947	3487093 +	3487294 Rmet_6585		9.00	1.00	Op2051f_1	NA	NA
3UTR_1610	3487357 -	3487446 Rmet_3214	<i>bug</i>			Op0906r_1		
NPKM_5948	3487447 -	3488419 Rmet_3214	<i>bug</i>	11.33	1.15	Op0906r_1	NA	Q1LIE0 Uncharacterized protein UPF0065
NPKM_5949	3488528 -	3490031 Rmet_3215		12.33	0.58	Op0906r_1	MET-LIP-FAMet	Q1LID9 AMP-dependent synthetase and ligase
5UTR_1342	3490032 -	3490072 Rmet_3215				Op0906r_1		
5UTR_1248	3490123 +	3490155 Rmet_3216				Op0907f_1		
NPKM_5950	3490155 +	3491076 Rmet_3216		14.33	0.58	Op0907f_1	NA	Q1LID8 Transcriptional regulator, LysR family
3UTR_1504	3491077 +	3491135 Rmet_3216				Op0907f_1		
5UTR_1249	3491140 +	3491189 Rmet_3217				Op0907f_1		
NPKM_5951	3491189 +	3491702 Rmet_3217		15.00	0.00	Op0907f_1	NA	Q1LID7 Putative transcriptional regulator
NPKM_5952	3491688 +	3493056 Rmet_3218		13.33	1.15	Op0907f_1	NA	Q1LID6 Multi antimicrobial extrusion protein MatE
3UTR_1609	3492243 -	3493101 Rmet_3219				Op0908r_2		
3UTR_1505	3493057 +	3493061 Rmet_3218				Op0907f_1		
NPKM_5953	3493102 -	3495538 Rmet_3219		62.33	8.74	Op0908r_2	NA	Q1LID5 Carbohydrate-binding family V/XII
NPKM_5954	3495510 -	3495708 Rmet_6586		5.67	1.53	Op0908r_1	NA	NA

5UTR_1341	3495709 -	3495751 Rmet_6586				Op0908r_1			
5UTR_1250	3495720 +	3495805 Rmet_3220				Op0909f_1			
NPKM_5955	3495805 +	3496948 Rmet_3220		18.00	1.00	Op0909f_1	NA	Q1LID4 Metallophosphoesterase	
3UTR_1608	3496508 -	3497030 Rmet_3221	yjjK			Op0910r_1			
3UTR_1506	3496949 +	3497622 Rmet_3220				Op0909f_1			
NPKM_5956	3497031 -	3498801 Rmet_3221	yjjK	161.33	9.81	Op0910r_1	NA	Q1LID3 ABC transporter-related protein	
5UTR_1251	3498742 +	3498840 Rmet_3222				Op0911f_1			
NPKM_5957	3498840 +	3499062 Rmet_3222		82.00	9.54	Op0911f_1	NA	Q1LID2 Putative uncharacterized protein	
NPKM_5958	3499103 +	3499601 Rmet_3223	ygjP	82.67	4.51	Op0911f_1	NA	Q1LID1 Putative uncharacterized protein	
3UTR_1507	3499602 +	3499964 Rmet_3223	ygjP			Op0911f_1			
NPKM_5959	3499614 -	3500514 Rmet_3224		30.67	1.53	Op0912r_1	NA	Q1LID0 TM1410 hypothetical-related protein	
5UTR_1252	3500491 +	3500874 Rmet_3225				Op0913f_1			
5UTR_1340	3500515 -	3500848 Rmet_3224				Op0912r_1			
NPKM_5960	3500874 +	3502674 Rmet_3225		21.00	3.46	Op0913f_1	NA	Q1LIC9 Diguanylate cyclase (GGDEF domain)	
3UTR_1508	3502675 +	3502818 Rmet_3225				Op0913f_1			
3UTR_1607	3502823 -	3502846 Rmet_R0055				Op0914r_1			
NPKM_5961	3502847 -	3502923 Rmet_R0055		59.67	7.51	Op0914r_1	NA	NA	
NPKM_5962	3502975 -	3503473 Rmet_3226	sspB	633.33	36.47	Op0914r_1	NA	Q1LIC8 Stringent starvation protein B	
NPKM_5963	3503504 -	3504116 Rmet_3227	sspA	780.67	15.18	Op0914r_1	GIP-PTL-Fold	Q1LIC7 Glutathione S-transferase-like protein	
NPKM_5964	3504394 -	3505138 Rmet_3228	petC	1122.00	30.64	Op0914r_1	MET-EN-OxPhos	Q1LIC6 Cytochrome c1	
NPKM_5965	3505175 -	3506579 Rmet_3229	petB	1115.67	34.56	Op0914r_1	MET-EN-OxPhos	Q1LIC5 Cytochrome b	
NPKM_5966	3506581 -	3507199 Rmet_3230	petA	1363.67	28.29	Op0914r_1	MET-EN-OxPhos	Q1LIC4 Ubiquinol-cytochrome c reductase, iron-sulfur subunit	
5UTR_1253	3507394 +	3507418 Rmet_3231	mscL			Op0915f_1			
NPKM_5967	3507418 +	3507853 Rmet_3231	mscL	458.00	13.00	Op0915f_1	EIP-TRA-Pores	Q1LIC3 Large-conductance mechanosensitive channel	
NPKM_5968	3507868 -	3508615 Rmet_3232		136.33	0.58	Op0916r_1	NA	Q1LIC2 Putative uncharacterized protein	
5UTR_1339	3508616 -	3509473 Rmet_3232				Op0916r_1			
NPKM_5969	3508635 +	3509832 Rmet_3233		156.00	3.61	Op0917f_1	NA	Q1LIC1 Peptidase S1 and S6, chymotrypsin/Hap	
3UTR_1606	3509483 -	3510307 Rmet_3234				Op0918r_4			
3UTR_1509	3509833 +	3509891 Rmet_3233				Op0917f_1			
NPKM_5970	3510308 -	3511514 Rmet_3234		37040.33	1243.13	Op0918r_4	NA	Q1LIC0 Porin, Gram-negative type	
NPKM_5971	3511705 -	3512488 Rmet_3235	tatC	143.67	5.13	Op0918r_3	GIP-PTL-Exp	Q1LIB9 Sec-independent protein translocase TatC	
NPKM_5972	3512490 -	3512997 Rmet_3236	tatB	397.33	16.62	Op0918r_3	GIP-PTL-Exp	Q1LIB8 Sec-independent protein translocase protein tatB homolog	
NPKM_5973	3513098 -	3513332 Rmet_3237	tatA	594.00	34.18	Op0918r_3	GIP-PTL-Exp	Q1LIB7 Sec-independent protein translocase protein tatA/E homolog	
NPKM_5974	3513485 -	3513842 Rmet_3238		311.33	11.15	Op0918r_3	EIP-TRA-ABC	Q1LIB6 Histidine triad (HIT) protein	
NPKM_5975	3513914 -	3514307 Rmet_3239		220.00	12.17	Op0918r_3	NA	Q1LIB5 Putative transmembrane protein	
NPKM_5976	3514363 -	3514732 Rmet_3240	hisE	261.33	3.79	Op0918r_3	MET-AA-His	Q1LIB4 Phosphoribosyl-ATP pyrophosphatase	
NPKM_5977	3514728 -	3515136 Rmet_3241	hisI	364.67	10.97	Op0918r_3	MET-AA-His	Q1LIB3 Phosphoribosyl-AMP cyclohydrolase	
NPKM_5978	3515138 -	3515909 Rmet_3242	hisF	392.33	10.26	Op0918r_3	MET-AA-His	Q1LIB2 Imidazole glycerol phosphate synthase subunit hisF	
NPKM_5979	3515970 -	3516714 Rmet_3243	hisA	422.00	9.54	Op0918r_3	MET-AA-His	Q1LIB1 1-(5-phosphoribosyl)-5-[(5- phosphoribosylamino)methylideneamino] imida	
NPKM_5980	3516893 -	3517547 Rmet_3244	hisH	212.00	13.08	Op0918r_3	MET-AA-His	Q1LIB0 Imidazole glycerol phosphate synthase subunit hisH	
NPKM_5981	3517543 -	3518167 Rmet_3245		253.00	9.54	Op0918r_3	EIP-TRA-Other	Q1LIA9 Multiple antibiotic resistance (MarC)-related proteins	
NPKM_5982	3518248 -	3518836 Rmet_3246	hisB	459.00	14.11	Op0918r_3	MET-AA-His	Q1LIA8 Imidazoleglycerol-phosphate dehydratase	
NPKM_5983	3518843 -	3519944 Rmet_3247	hisC	311.00	6.08	Op0918r_3	MET-AA-His	Q1LIA7 Histidinol phosphate aminotransferase	

NPKM_5984	3519980 -	3521315 Rmet_3248	<i>hisD</i>	285.00	7.00	Op0918r_3	MET-AA-His	Q1LIA6 Histidinol dehydrogenase
NPKM_5985	3521352 -	3522027 Rmet_3249	<i>hisG</i>	197.00	1.00	Op0918r_3	MET-AA-His	Q1LIA5 ATP phosphoribosyltransferase
NPKM_5986	3522095 -	3523346 Rmet_3250	<i>murA</i>	327.00	4.36	Op0918r_3	MET-CAH-AminSug	Q1LIA4 UDP-N-acetylglucosamine 1-carboxyvinyltransferase
NPKM_5987	3523414 -	3523660 Rmet_3251		236.67	6.35	Op0918r_3	NA	Q1LIA3 BoIA-like protein
NPKM_5988	3523694 -	3524516 Rmet_3252		132.33	5.86	Op0918r_3	NA	Q1LIA2 ABC-type multidrug transport system permease component
NPKM_5989	3524512 -	3525463 Rmet_3253	<i>yadG</i>	224.33	5.03	Op0918r_3	NA	Q1LIA1 ABC transporter-related protein
NPKM_5990	3525718 -	3526015 Rmet_3254		441.33	1.53	Op0918r_3	NA	Q1LIA0 Sulfate transporter/antisigma-factor antagonist STAS
NPKM_5991	3526135 -	3526762 Rmet_3255	<i>ttg2D</i>	455.33	22.85	Op0918r_3	EIP-TRA-ABC	Q1LI99 Toluene tolerance
NPKM_5992	3526947 -	3527748 Rmet_3256		193.33	7.02	Op0918r_2	NA	Q1LI98 VacJ-like lipoprotein
NPKM_5993	3527744 -	3528284 Rmet_3257	<i>yrbD</i>	164.00	6.93	Op0918r_2	EIP-TRA-ABC	Q1LI97 Mammalian cell entry related
NPKM_5994	3528319 -	3529096 Rmet_3258	<i>yrbE</i>	100.33	0.58	Op0918r_2	EIP-TRA-ABC	Q1LI96 Putative uncharacterized protein
NPKM_5995	3529092 -	3529944 Rmet_3259	<i>yrbF</i>	250.00	16.52	Op0918r_2	EIP-TRA-ABC	Q1LI95 ABC transporter-related protein
NPKM_5996	3530078 -	3531197 Rmet_3260	<i>bug</i>	62.33	7.77	Op0918r_1	NA	Q1LI94 Uncharacterized protein UPF0065
5UTR_1338	3531198 -	3531307 Rmet_3260	<i>bug</i>			Op0918r_1		
3UTR_1605	3531329 -	3531971 Rmet_3262	<i>gltD</i>			Op0920r_3		
5UTR_1254	3531336 +	3531369 Rmet_3261				Op0919f_1		
NPKM_5997	3531369 +	3531879 Rmet_3261		48.00	3.61	Op0919f_1	NA	Q1LI93 GCN5-related N-acetyltransferase
3UTR_1510	3531880 +	3531942 Rmet_3261				Op0919f_1		
NPKM_5998	3531972 -	3533436 Rmet_3262	<i>gltD</i>	1048.67	66.52	Op0920r_3	MET-EN-Nitrog	Q1LI92 Glutamate synthase (NADH) small subunit
NPKM_5999	3533547 -	3538443 Rmet_3263	<i>gltB</i>	838.00	54.84	Op0920r_3	MET-EN-Nitrog	Q1LI91 Glutamate synthase (NADH) large subunit
NPKM_6000	3538581 -	3539325 Rmet_3264		33.67	0.58	Op0920r_2	GIP-REP-Recomb	Q1LI90 Putative uncharacterized protein
NPKM_6001	3539411 -	3540560 Rmet_3265	<i>dgt</i>	154.67	7.37	Op0920r_2	MET-NUC-Pur	Q1LI89 Deoxyguanosinetriphosphate triphosphohydrolase
NPKM_6002	3540613 -	3541720 Rmet_3266	<i>aroB</i>	285.33	15.04	Op0920r_2	MET-AA-PheTyrTrp	Q1LI88 3-dehydroquininate synthase
NPKM_6003	3541716 -	3542406 Rmet_3267	<i>aroK</i>	166.00	9.54	Op0920r_2	MET-AA-PheTyrTrp	Q1LI87 Shikimate kinase
NPKM_6004	3542535 -	3544668 Rmet_3268	<i>pilQ</i>	240.67	15.95	Op0920r_2	GIP-PTL-T2S	Q1LI86 Type II and III secretion system protein
NPKM_6005	3544664 -	3545204 Rmet_3269	<i>pilP</i>	223.67	24.38	Op0920r_2	GIP-PTL-T2S	Q1LI85 Pilus assembly protein, PilQ
NPKM_6006	3545200 -	3545872 Rmet_3270	<i>pilO</i>	185.33	12.34	Op0920r_2	GIP-PTL-T2S	Q1LI84 Pilus assembly protein, PilO
NPKM_6007	3545874 -	3546519 Rmet_3271	<i>pilN</i>	201.00	12.49	Op0920r_2	GIP-PTL-T2S	Q1LI83 Fimbrial assembly
NPKM_6008	3546536 -	3547622 Rmet_3272	<i>pilM</i>	332.00	12.29	Op0920r_2	GIP-PTL-T2S	Q1LI82 Type IV pilus assembly protein PilM
NPKM_6009	3547690 +	3547762 Rmet_6587		11.67	8.33	Op2052f_1	NA	NA
NPKM_6010	3547708 -	3547975 Rmet_3273		3.33	0.58	Op0920r_1	NA	Q1LI81 Putative uncharacterized protein
5UTR_1337	3547976 -	3548046 Rmet_3273				Op0920r_1		
NPKM_6011	3548076 +	3550455 Rmet_3274	<i>mrcA</i>	92.33	5.51	Op0921f_1	NA	Q1LI80 Penicillin-binding protein 1A
3UTR_1604	3550237 -	3550526 Rmet_3275	<i>cyaY</i>			Op2053r_1		
3UTR_1511	3550456 +	3550483 Rmet_3274	<i>mrcA</i>			Op0921f_1		
5UTR_1255	3550492 +	3550995 Rmet_6588				Op0923f_1		
NPKM_6012	3550527 -	3550863 Rmet_3275	<i>cyaY</i>	100.33	10.69	Op2053r_1	NA	NA
5UTR_1336	3550864 -	3551499 Rmet_3275	<i>cyaY</i>			Op2053r_1		
NPKM_6013	3550995 +	3551253 Rmet_6588		207.00	22.54	Op0923f_1	NA	NA
NPKM_6014	3551266 +	3552526 Rmet_3276	<i>lysA2</i>	96.00	3.00	Op0923f_1	MET-AA-Lys_Syn	Q1LI78 Diaminopimelate decarboxylase
3UTR_1512	3552527 +	3553337 Rmet_3276	<i>lysA2</i>			Op0923f_1		
3UTR_1603	3552604 -	3552618 Rmet_3277	<i>yedZ</i>			Op0924r_2		
NPKM_6015	3552619 -	3553294 Rmet_3277	<i>yedZ</i>	46.33	1.53	Op0924r_2	NA	Q1LI77 Ferric reductase-like transmembrane component-like

NPKM_6016	3553293 -	3554304 Rmet_3278	<i>yedY</i>	126.00	1.00	Op0924r_2	NA	Q1LI76 Twin-arginine translocation pathway signal
NPKM_6017	3554374 -	3555208 Rmet_3279		159.67	8.50	Op0924r_2	GIP-TK-RNAP	Q1LI75 Putative transmembrane transcriptional regulator (Anti-sigma factor)
NPKM_6018	3555207 -	3555741 Rmet_3280	<i>rpoL</i>	398.33	35.47	Op0924r_2	GIP-TK-RNAP	Q1LI74 Sigma-24 (FecI-like)
NPKM_6019	3555770 -	3556196 Rmet_3281		823.00	53.11	Op0924r_2	NA	Q1LI73 Putative uncharacterized protein
5UTR_1335	3556197 -	3556357 Rmet_3281				Op0924r_2		
3UTR_1602	3556403 -	3556488 Rmet_3282				Op0924r_1		
NPKM_6020	3556489 -	3557713 Rmet_3282		114.67	4.04	Op0924r_1	NA	Q1LI72 Cytochrome c assembly protein
NPKM_6021	3557815 -	3560068 Rmet_3283		128.00	3.61	Op0924r_1	GIP-PTL-Fold	Q1LI71 ResB-like protein
NPKM_6022	3560237 -	3560897 Rmet_3284		1352.67	18.15	Op0924r_1	NA	Q1LI70 Cytochrome c, class I
5UTR_1256	3560761 +	3561159 Rmet_3285	<i>engB</i>			Op0925f_1		
5UTR_1334	3560898 -	3562766 Rmet_3284				Op0924r_1		
NPKM_6023	3561159 +	3561912 Rmet_3285	<i>engB</i>	226.67	10.02	Op0925f_1	NA	Q1LI69 Probable GTP-binding protein engB
NPKM_6024	3562182 +	3563175 Rmet_3286	<i>hemB</i>	354.00	15.87	Op0925f_1	MET-COF-Porph	Q1LI68 Delta-aminolevulinic acid dehydratase
3UTR_1601	3562780 -	3564381 Rmet_3288	<i>dsbD</i>			Op0926r_2		
NPKM_6025	3563182 +	3564364 Rmet_3287		145.67	9.07	Op0925f_1	EIP-TRA-Ion	Q1LI67 Mg2+ transporter protein, CorA-like protein
3UTR_1513	3564365 +	3565140 Rmet_3287				Op0925f_1		
NPKM_6026	3564382 -	3566257 Rmet_3288	<i>dsbD</i>	202.00	53.70	Op0926r_2	GIP-PTL-Fold	Q1LI66 Cytochrome c biogenesis protein, transmembrane region
NPKM_6027	3566348 -	3566729 Rmet_3289	<i>cutA</i>	187.67	32.72	Op0926r_2	NA	Q1LI65 CutA1 divalent ion tolerance protein
NPKM_6028	3566841 -	3567237 Rmet_3290	<i>rplQ</i>	2966.00	26.29	Op0926r_2	GIP-TL-Ribo	Q1LI64 50S ribosomal protein L17
NPKM_6029	3567388 -	3568369 Rmet_3291	<i>rpoA</i>	2136.00	61.02	Op0926r_2	GIP-TK-RNAP	Q1LI63 DNA-directed RNA polymerase subunit alpha
5UTR_1257	3568476 +	3569210 Rmet_6589				Op2054f_1		
NPKM_6030	3568544 -	3569168 Rmet_3292	<i>rpsD</i>	3681.67	76.11	Op0926r_2	GIP-TL-Ribo	Q1LI62 30S ribosomal protein S4
NPKM_6031	3569210 +	3569390 Rmet_6589		6.00	1.00	Op2054f_1	NA	NA
3UTR_1514	3569391 +	3571247 Rmet_6589				Op2054f_1		
NPKM_6032	3569461 -	3569863 Rmet_3293	<i>rpsK</i>	6460.67	112.30	Op0926r_2	GIP-TL-Ribo	Q1LI61 30S ribosomal protein S11
NPKM_6033	3569887 -	3570253 Rmet_3294	<i>rpsM</i>	5207.00	120.58	Op0926r_2	GIP-TL-Ribo	Q1LI60 30S ribosomal protein S13
NPKM_6034	3570272 -	3570389 Rmet_3295	<i>rpmJ</i>	3345.00	78.31	Op0926r_2	GIP-TL-Ribo	Q1LI59 50S ribosomal protein L36
NPKM_6035	3570420 -	3570639 Rmet_3296	<i>infA</i>	2940.67	186.56	Op0926r_2	NA	Q1LI58 Translation initiation factor IF-1 2
NPKM_6036	3570663 -	3572007 Rmet_3297	<i>secY</i>	3202.00	81.61	Op0926r_2	GIP-PTL-Exp	Q1LI57 Preprotein translocase secY subunit
NPKM_6037	3572056 -	3572491 Rmet_3298	<i>rplO</i>	4977.67	232.75	Op0926r_2	GIP-TL-Ribo	Q1LI56 50S ribosomal protein L15
NPKM_6038	3572510 -	3572693 Rmet_3299	<i>rpmD</i>	4631.67	270.59	Op0926r_2	GIP-TL-Ribo	Q1LI55 50S ribosomal protein L30
NPKM_6039	3572703 -	3573222 Rmet_3300	<i>rpsE</i>	5916.00	289.19	Op0926r_2	GIP-TL-Ribo	Q1LI54 30S ribosomal protein S5
NPKM_6040	3573243 -	3573603 Rmet_3301	<i>rplR</i>	5447.67	327.24	Op0926r_2	GIP-TL-Ribo	Q1LI53 50S ribosomal protein L18
NPKM_6041	3573611 -	3574145 Rmet_3302	<i>rplF</i>	5226.67	280.79	Op0926r_2	GIP-TL-Ribo	Q1LI52 50S ribosomal protein L6
NPKM_6042	3574154 -	3574550 Rmet_3303	<i>rpsH</i>	5370.33	317.31	Op0926r_2	GIP-TL-Ribo	Q1LI51 30S ribosomal protein S8
NPKM_6043	3574577 -	3574883 Rmet_3304	<i>rpsN</i>	5152.00	275.07	Op0926r_2	GIP-TL-Ribo	Q1LI50 SSU ribosomal protein S14P
NPKM_6044	3574892 -	3575435 Rmet_3305	<i>rplE</i>	5946.67	394.26	Op0926r_2	GIP-TL-Ribo	Q1LI49 50S ribosomal protein L5
NPKM_6045	3575460 -	3575769 Rmet_3306	<i>rplX</i>	7932.67	426.04	Op0926r_2	GIP-TL-Ribo	Q1LI48 50S ribosomal protein L24
NPKM_6046	3575778 -	3576147 Rmet_3307	<i>rplN</i>	8049.33	494.52	Op0926r_2	GIP-TL-Ribo	Q1LI47 50S ribosomal protein L14
NPKM_6047	3576424 -	3576703 Rmet_3308	<i>rpsQ</i>	5633.67	181.62	Op0926r_2	GIP-TL-Ribo	Q1LI46 30S ribosomal protein S17
NPKM_6048	3576699 -	3576894 Rmet_3309	<i>rpmC</i>	4681.33	118.56	Op0926r_2	GIP-TL-Ribo	Q1LI45 50S ribosomal protein L29
NPKM_6049	3576906 -	3577323 Rmet_3310	<i>rplP</i>	4391.67	132.58	Op0926r_2	GIP-TL-Ribo	Q1LI44 50S ribosomal protein L16
NPKM_6050	3577325 -	3578123 Rmet_3311	<i>rpsC</i>	4415.33	108.65	Op0926r_2	GIP-TL-Ribo	Q1LI43 30S ribosomal protein S3

NPKM_6051	3578132 -	3578462 Rmet_3312	<i>rplV</i>	5059.33	123.31	Op0926r_2	GIP-TL-Ribo	Q1LI42 50S ribosomal protein L22
NPKM_6052	3578471 -	3578747 Rmet_3313	<i>rpsS</i>	4433.33	135.43	Op0926r_2	GIP-TL-Ribo	Q1LI41 30S ribosomal protein S19
NPKM_6053	3578769 -	3579600 Rmet_3314	<i>rplB</i>	4487.33	90.67	Op0926r_2	GIP-TL-Ribo	Q1LI40 50S ribosomal protein L2
NPKM_6054	3579602 -	3579917 Rmet_3315	<i>rplW</i>	3568.00	144.73	Op0926r_2	GIP-TL-Ribo	B3R7S1 50S ribosomal subunit protein L23
NPKM_6055	3579913 -	3580534 Rmet_3316	<i>rplD</i>	5069.00	73.08	Op0926r_2	GIP-TL-Ribo	Q1LI38 50S ribosomal protein L4
NPKM_6056	3580546 -	3581191 Rmet_3317	<i>rplC</i>	6085.00	189.58	Op0926r_2	GIP-TL-Ribo	Q1LI37 50S ribosomal protein L3
5UTR_1333	3581192 -	3581304 Rmet_3317	<i>rplC</i>			Op0926r_2		
3UTR_1600	3581313 -	3581459 Rmet_3318				Op0926r_1		
NPKM_6057	3581460 -	3581973 Rmet_3318		22.00	0.00	Op0926r_1	NA	Q1LI36 Flavin reductase-like, FMN-binding
NPKM_6058	3581974 -	3583216 Rmet_3319		34.67	2.52	Op0926r_1	NA	Q1LI35 Putative oxygenase subunit protein
NPKM_6059	3583249 -	3584038 Rmet_3320		61.33	4.73	Op0926r_1	NA	Q1LI34 Short-chain dehydrogenase/reductase SDR
NPKM_6060	3584124 -	3585354 Rmet_3321		144.00	9.54	Op0926r_1	MET-XEN-Hex	Q1LI33 Dienelactone hydrolase
5UTR_1258	3585236 +	3585673 Rmet_3322				Op0927f_1		
NPKM_6061	3585673 +	3586687 Rmet_3322		27.00	1.00	Op0927f_1	NA	Q1LI32 Transcriptional regulator, AraC family
3UTR_1515	3586688 +	3586726 Rmet_3322				Op0927f_1		
NPKM_6062	3586781 -	3587090 Rmet_3323	<i>rpsJ</i>	4768.67	178.86	Op0928r_3	GIP-TL-Ribo	B3R7S9 30S ribosomal subunit protein S10
NPKM_6063	3587169 -	3588360 Rmet_3324	<i>tuf</i>	288.67	20.74	Op0928r_2	NA	Q1LI13 Elongation factor Tu
NPKM_6064	3588437 -	3590549 Rmet_3325	<i>fusA1</i>	2674.67	136.47	Op0928r_2	NA	Q1LI29 Elongation factor G 1
NPKM_6065	3590667 -	3591138 Rmet_3326	<i>rpsG</i>	4496.67	110.02	Op0928r_2	GIP-TL-Ribo	Q1LI28 30S ribosomal protein S7
NPKM_6066	3591345 -	3591723 Rmet_3327	<i>rpsL</i>	4610.67	32.72	Op0928r_2	GIP-TL-Ribo	Q1LI27 30S ribosomal protein S12
NPKM_6067	3592026 -	3593919 Rmet_3328	<i>recQ</i>	114.33	4.16	Op0928r_1	GIP-REP-Recomb	Q1LI26 ATP-dependent DNA helicase RecQ
5UTR_1259	3594070 +	3594113 Rmet_3329				Op0929f_1		
NPKM_6068	3594113 +	3595661 Rmet_3329		4.00	1.00	Op0929f_1	NA	Q1LI25 Transcriptional regulator, GntR family
3UTR_1599	3595410 -	3595634 Rmet_3330				Op0930r_4		
NPKM_6069	3595635 -	3595965 Rmet_3330		6.33	2.08	Op0930r_4	NA	Q1LI24 Cytochrome c553-like protein
3UTR_1516	3595662 +	3595687 Rmet_3329				Op0929f_1		
NPKM_6070	3595980 -	3597540 Rmet_3331		6.67	1.15	Op0930r_4	NA	Q1LI23 Cytochrome d1, heme region
5UTR_1332	3597541 -	3597579 Rmet_3331				Op0930r_4		
3UTR_1598	3597587 -	3597683 Rmet_3332				Op0930r_4		
NPKM_6071	3597684 -	3598140 Rmet_3332		10.33	0.58	Op0930r_4	NA	Q1LI22 Putative uncharacterized protein
NPKM_6072	3598218 -	3602460 Rmet_3333	<i>rpoC</i>	1347.33	43.04	Op0930r_4	GIP-TK-RNAP	Q1LI21 DNA-directed RNA polymerase subunit beta'
NPKM_6073	3602575 -	3606682 Rmet_3334	<i>rpoB</i>	1510.00	33.51	Op0930r_4	GIP-TK-RNAP	Q1LI20 DNA-directed RNA polymerase subunit beta
NPKM_6074	3607118 -	3607493 Rmet_3335	<i>rplL</i>	8619.00	235.62	Op0930r_4	GIP-TL-Ribo	Q1LI19 50S ribosomal protein L7/L12
NPKM_6075	3607553 -	3608075 Rmet_3336	<i>rplJ</i>	5592.67	56.52	Op0930r_4	GIP-TL-Ribo	Q1LI18 50S ribosomal protein L10
NPKM_6076	3608469 -	3609165 Rmet_3337	<i>rplA</i>	4613.33	202.79	Op0930r_4	GIP-TL-Ribo	Q1LI17 50S ribosomal protein L1
NPKM_6077	3609165 -	3609597 Rmet_3338	<i>rplK</i>	3976.00	198.65	Op0930r_4	GIP-TL-Ribo	Q1LI16 50S ribosomal protein L11
NPKM_6078	3609759 -	3610341 Rmet_3339	<i>nusG</i>	1995.67	106.03	Op0930r_4	GIP-TK-Assoc	Q1LI15 Transcription antitermination protein nusG
NPKM_6079	3610351 -	3610732 Rmet_3340	<i>secE</i>	1879.33	120.70	Op0930r_4	GIP-PTL-Exp	Q1LI14 Protein translocase subunit secE/sec61 gamma
NPKM_6080	3610791 -	3610867 Rmet_R0056		2264.00	93.05	Op0930r_4	NA	NA
NPKM_6081	3610951 -	3612142 Rmet_3341	<i>tuf</i>	590.67	7.23	Op0930r_3	NA	NA
NPKM_6082	3612185 -	3612260 Rmet_R0057		3348.67	553.45	Op0930r_3	NA	NA
NPKM_6083	3612297 -	3612371 Rmet_R0058		3312.33	465.76	Op0930r_3	NA	NA
NPKM_6084	3612421 -	3612507 Rmet_R0059		800.67	119.63	Op0930r_2	NA	NA

5UTR_1331	3612508 -	3612792 Rmet_R0059				Op0930r_2		
NPKM_6085	3612805 -	3612919 Rmet_R0060		0.00	0.00	Op0930r_1	NA	NA
NPKM_6086	3613098 -	3615916 Rmet_R0061		0.00	0.00	Op0930r_1	NA	NA
NPKM_6087	3616198 -	3616274 Rmet_R0062		0.00	0.00	Op0930r_1	NA	NA
NPKM_6088	3616285 -	3616362 Rmet_R0063		0.00	0.00	Op0930r_1	NA	NA
NPKM_6089	3616426 -	3617953 Rmet_R0064		0.00	0.00	Op0930r_1	NA	NA
NPKM_6090	3618016 +	3618082 Rmet_6590		0.00	0.00	Op0931f_1	NA	NA
NPKM_6091	3618054 -	3618255 Rmet_6591		0.00	0.00	Op0930r_1	NA	NA
5UTR_1260	3618440 +	3618456 Rmet_6592				Op0931f_2		
NPKM_6092	3618456 +	3618630 Rmet_6592		14.00	3.46	Op0931f_2	NA	NA
NPKM_6093	3618583 +	3618970 Rmet_3342		83.00	3.00	Op0931f_3	NA	Q1LI12 Putative uncharacterized protein
NPKM_6094	3619048 +	3620293 Rmet_3343		28.33	2.08	Op0931f_3	NA	Q1LI11 Nucleoside recognition
3UTR_1597	3620444 -	3623189 Rmet_3346	<i>uspA8</i>			Op0932r_3		
NPKM_6095	3620878 +	3622777 Rmet_3344		156.67	27.21	Op0931f_4	NA	Q1LI10 Putative membrane protein
NPKM_6096	3622891 +	3623170 Rmet_3345		75.00	7.94	Op0931f_4	NA	Q1LI09 Putative uncharacterized protein
3UTR_1517	3623171 +	3625442 Rmet_3345				Op0931f_4		
NPKM_6097	3623190 -	3623661 Rmet_3346	<i>uspA8</i>	339.00	16.37	Op0932r_3	NA	Q1LI08 UspA
NPKM_6098	3624124 -	3625423 Rmet_3347		105.33	8.08	Op0932r_2	NA	Q1LI07 Putative uncharacterized protein
5UTR_1330	3625424 -	3625432 Rmet_3347				Op0932r_2		
NPKM_6099	3625434 -	3626328 Rmet_3348	<i>tnpB</i>	0.00	0.00	Op0932r_1	NA	NA
NPKM_6100	3626324 -	3626621 Rmet_3349	<i>tnpA</i>	0.00	0.00	Op0932r_1	NA	NA
3UTR_1596	3626636 -	3626772 Rmet_3350				Op0932r_1		
NPKM_6101	3626773 -	3627178 Rmet_3350		49.00	4.58	Op0932r_1	NA	Q1LI04 Putative uncharacterized protein
NPKM_6102	3627433 -	3628195 Rmet_3351		70.00	5.20	Op0932r_1	NA	Q1LI03 Putative uncharacterized protein
5UTR_1329	3628196 -	3629016 Rmet_3351				Op0932r_1		
5UTR_1261	3628246 +	3628398 Rmet_3352				Op0933f_1		
NPKM_6103	3628398 +	3629298 Rmet_3352		109.00	5.00	Op0933f_1	NA	Q1LI02 Cytidine/deoxycytidylate deaminase family protein
3UTR_1518	3629299 +	3629330 Rmet_3352				Op0933f_1		
NPKM_6104	3629433 -	3630534 Rmet_3353	<i>tnpA</i>	0.00	0.00	Op0934r_1	NA	Q9F8S6 Transposase (Transposase, IS4 family)
5UTR_1262	3630583 +	3630720 Rmet_3354				Op0935f_1		
NPKM_6105	3630720 +	3631350 Rmet_3354		58.67	6.66	Op0935f_1	NA	Q1LI00 CMP/dCMP deaminase, zinc-binding
NPKM_6106	3631552 +	3631792 Rmet_3355		192.00	16.09	Op0935f_2	NA	Q1LHZ9 Putative uncharacterized protein
NPKM_6107	3631985 +	3633089 Rmet_3356		111.33	8.62	Op0935f_2	NA	Q1LHZ8 ATP-binding region, ATPase-like protein
NPKM_6108	3633098 +	3633656 Rmet_3357		135.33	9.02	Op0935f_2	NA	Q1LHZ7 Putative uncharacterized protein
NPKM_6109	3633851 +	3634499 Rmet_3358		1134.33	150.17	Op0935f_3	NA	Q1LHZ6 Putative uncharacterized protein
NPKM_6110	3634536 +	3635643 Rmet_3359		1028.33	123.96	Op0935f_3	NA	Q1LHZ5 UBA/THIF-type NAD/FAD binding fold
NPKM_6111	3635639 +	3636101 Rmet_3360		563.33	73.04	Op0935f_3	NA	Q1LHZ4 Putative uncharacterized protein
NPKM_6112	3636100 +	3637780 Rmet_3361		245.67	32.13	Op0935f_3	NA	Q1LHZ3 Putative uncharacterized protein
NPKM_6113	3637861 +	3638128 Rmet_3362		86.00	7.81	Op0935f_3	NA	Q1LHZ2 Putative uncharacterized protein
3UTR_1519	3638129 +	3639567 Rmet_3362				Op0935f_3		
3UTR_1595	3638264 -	3638459 Rmet_3363				Op0936r_2		
NPKM_6114	3638460 -	3639450 Rmet_3363		13.00	2.65	Op0936r_2	NA	Q1LHZ1 Putative uncharacterized protein
5UTR_1328	3639451 -	3639537 Rmet_3363				Op0936r_2		

NPKM_6115	3639582 -	3640368 Rmet_3364	<i>tnpB</i>	0.00	0.00	Op0936r_1	NA	Q1LHZ0 IstB-like ATP-binding protein
NPKM_6116	3640357 -	3641884 Rmet_3365	<i>tnpA</i>	0.00	0.00	Op0936r_1	NA	Q1LHY9 Integrase, catalytic region
3UTR_1594	3641943 -	3642032 Rmet_3366				Op0936r_1		
NPKM_6117	3642033 -	3642210 Rmet_3366		44.33	5.69	Op0936r_1	GIP-REP-Recomb	Q1LHY8 Putative uncharacterized protein
NPKM_6118	3642148 -	3642418 Rmet_6593		73.00	5.57	Op0936r_1	NA	NA
NPKM_6119	3642448 -	3642907 Rmet_3367		99.00	6.24	Op0936r_1	NA	Q1LHY7 Transcriptional regulator
NPKM_6120	3642903 -	3645072 Rmet_3368		77.00	5.57	Op0936r_1	NA	Q1LHY6 GCN5-related N-acetyltransferase
5UTR_1263	3644064 +	3645797 Rmet_3369	<i>paaA</i>			Op0937f_1		
5UTR_1327	3645073 -	3645248 Rmet_3368				Op0936r_1		
NPKM_6121	3645797 +	3646805 Rmet_3369	<i>paaA</i>	14.00	1.73	Op0937f_1	NA	Q1LHY5 Phenylacetate-CoA oxygenase, PaaG subunit
NPKM_6122	3646824 +	3647112 Rmet_3370	<i>paaB</i>	17.67	0.58	Op0937f_1	NA	Q1LHY4 Phenylacetic acid degradation B
NPKM_6123	3647122 +	3647980 Rmet_3371	<i>paaC</i>	16.33	0.58	Op0937f_1	NA	Q1LHY3 Phenylacetate-CoA oxygenase, PaaI subunit
NPKM_6124	3647996 +	3648605 Rmet_3372	<i>paaD</i>	13.67	2.31	Op0937f_1	NA	Q1LHY2 Phenylacetate-CoA oxygenase, PaaJ subunit
NPKM_6125	3648617 +	3649703 Rmet_3373	<i>paaI</i>	14.33	0.58	Op0937f_1	NA	Q1LHY1 Phenylacetate-CoA oxygenase/reductase, PaaK subunit
NPKM_6126	3649823 +	3650621 Rmet_3374		135.33	4.04	Op0937f_2	NA	Q1LHY0 Putative uncharacterized protein
3UTR_1593	3650372 -	3651341 Rmet_3376	<i>kefC</i>			Op0938r_1		
NPKM_6127	3650694 +	3651315 Rmet_3375		78.67	5.13	Op0937f_2	NA	Q1LHX9 Transcriptional regulator, TetR family
3UTR_1520	3651316 +	3652752 Rmet_3375				Op0937f_2		
NPKM_6128	3651342 -	3653157 Rmet_3376	<i>kefC</i>	36.33	1.53	Op0938r_1	NA	Q1LHX8 Potassium efflux system protein
NPKM_6129	3653153 -	3653813 Rmet_3377		46.00	1.73	Op0938r_1	NA	Q1LHX7 NAD(P)H dehydrogenase (Quinone)
5UTR_1264	3653608 +	3654026 Rmet_3378				Op0939f_1		
5UTR_1326	3653814 -	3654015 Rmet_3377				Op0938r_1		
NPKM_6130	3654026 +	3654764 Rmet_3378		913.33	70.12	Op0939f_1	NA	Q1LHX6 GCN5-related N-acetyltransferase
3UTR_1521	3654765 +	3658412 Rmet_3378				Op0939f_1		
3UTR_1592	3654823 -	3654862 Rmet_3379				Op0940r_3		
NPKM_6131	3654863 -	3655358 Rmet_3379		137.67	2.08	Op0940r_3	NA	Q1LHX5 Transcriptional regulator, AsnC family
5UTR_1325	3655359 -	3655433 Rmet_3379				Op0940r_3		
3UTR_1591	3655469 -	3655585 Rmet_3380				Op0940r_3		
NPKM_6132	3655586 -	3656216 Rmet_3380		199.33	13.87	Op0940r_3	NA	Q1LHX4 Putative signal transduction protein with EFhand domain
NPKM_6133	3656361 -	3656976 Rmet_3381	<i>gspC</i>	69.33	4.51	Op0940r_2	GIP-PTL-T2S	Q1LHX3 Putative uncharacterized protein
5UTR_1324	3656977 -	3657053 Rmet_3381	<i>gspC</i>			Op0940r_2		
3UTR_1590	3657078 -	3657145 Rmet_3382	<i>hmp</i>			Op0940r_1		
NPKM_6134	3657146 -	3658436 Rmet_3382	<i>hmp</i>	4.67	1.53	Op0940r_1	NA	Q1LHX2 Globin
3UTR_1589	3658439 -	3658459 Rmet_3383				Op0940r_1		
NPKM_6135	3658460 -	3658928 Rmet_3383		60.00	5.29	Op0940r_1	NA	Q1LHX1 Transcriptional regulator, BadM/Rrf2 family
5UTR_1265	3658944 +	3659106 Rmet_3384	<i>gspG</i>			Op0941f_1		
NPKM_6136	3659106 +	3659571 Rmet_3384	<i>gspG</i>	151.33	8.02	Op0941f_1	GIP-PTL-T2S	Q1LHX0 General secretion pathway protein G
NPKM_6137	3659587 +	3660112 Rmet_3385	<i>gspH</i>	144.00	4.36	Op0941f_1	GIP-PTL-T2S	Q1LHW9 General secretion pathway protein H
NPKM_6138	3660108 +	3660513 Rmet_3386	<i>gspI</i>	47.00	3.00	Op0941f_1	GIP-PTL-T2S	Q1LHW8 General secretion pathway protein I
NPKM_6139	3660502 +	3661195 Rmet_3387	<i>gspJ</i>	30.00	3.00	Op0941f_1	GIP-PTL-T2S	Q1LHW7 Type II secretory pathway component PulJ
NPKM_6140	3661197 +	3662208 Rmet_3388	<i>gspK</i>	23.33	2.52	Op0941f_1	GIP-PTL-T2S	Q1LHW6 General secretion pathway protein K
NPKM_6141	3662439 +	3663969 Rmet_3389	<i>gspL</i>	102.67	8.50	Op0941f_2	GIP-PTL-T2S	Q1LHW5 General secretion pathway L
NPKM_6142	3663965 +	3664532 Rmet_3390	<i>gspM</i>	78.00	6.56	Op0941f_2	GIP-PTL-T2S	Q1LHW4 General secretion pathway M protein

NPKM_6143	3664531 +	3665338 Rmet_3391	<i>gspN</i>	61.33	2.89	Op0941f_2	GIP-PTL-T2S	Q1LHW3 Type II secretion system protein N
NPKM_6144	3665369 +	3667721 Rmet_3392	<i>gspD</i>	94.00	4.58	Op0941f_2	GIP-PTL-T2S	Q1LHW2 Type II and III secretion system protein
NPKM_6145	3667735 +	3669277 Rmet_3393	<i>gspE</i>	88.33	6.43	Op0941f_2	GIP-PTL-T2S	Q1LHW1 Type II secretion system protein E (GspE)
NPKM_6146	3669297 +	3670515 Rmet_3394	<i>gspF</i>	52.67	4.93	Op0941f_2	GIP-PTL-T2S	Q1LHW0 General secretion pathway protein F
3UTR_1588	3669923 -	3670648 Rmet_3395				Op0942r_1		
3UTR_1522	3670516 +	3671210 Rmet_3394	<i>gspF</i>			Op0941f_2		
NPKM_6147	3670649 -	3671948 Rmet_3395		68.00	1.00	Op0942r_1	NA	Q1LHV9 Putative uncharacterized protein
5UTR_1323	3671949 -	3672051 Rmet_3395				Op0942r_1		
5UTR_1266	3672123 +	3672255 Rmet_3396	<i>porG</i>			Op0943f_1		
NPKM_6148	3672255 +	3675849 Rmet_3396	<i>porG</i>	80.00	2.65	Op0943f_1	MET-CAH-PyrOx	Q1LHV8 Pyruvate ferredoxin/flavodoxin oxidoreductase
3UTR_1523	3675850 +	3675879 Rmet_3396	<i>porG</i>			Op0943f_1		
5UTR_1267	3675882 +	3675973 Rmet_3397	<i>ypeA</i>			Op0943f_1		
NPKM_6149	3675973 +	3676393 Rmet_3397	<i>ypeA</i>	34.67	1.53	Op0943f_1	NA	Q1LHV7 GCN5-related N-acetyltransferase
NPKM_6150	3676426 +	3676837 Rmet_3398		22.67	2.31	Op0943f_1	NA	Q1LHV6 Glyoxalase/bleomycin resistance protein/dioxygenase
NPKM_6151	3676948 +	3678202 Rmet_3399		41.33	2.08	Op0943f_1	NA	Q1LHV5 Major facilitator superfamily MFS_1
NPKM_6152	3678278 +	3679481 Rmet_3400	<i>mosC</i>	33.00	1.00	Op0943f_1	NA	Q1LHV4 Major facilitator superfamily MFS_1
3UTR_1587	3679184 -	3679497 Rmet_3401				Op0944r_1		
3UTR_1524	3679482 +	3680260 Rmet_3400	<i>mosC</i>			Op0943f_1		
NPKM_6153	3679498 -	3680389 Rmet_3401		11.33	1.15	Op0944r_1	NA	Q1LHV3 Extradial ring-cleavage dioxygenase, class III enzyme, subunit B
5UTR_1322	3680390 -	3680729 Rmet_3401				Op0944r_1		
NPKM_6154	3680411 +	3680990 Rmet_3402		23.67	2.08	Op0945f_1	NA	Q1LHV2 Putative uncharacterized protein
NPKM_6155	3681020 +	3682406 Rmet_3403	<i>proP</i>	73.00	5.00	Op0945f_2	NA	Q1LHV1 Major facilitator superfamily MFS_1
NPKM_6156	3682341 +	3682539 Rmet_6594		50.33	6.43	Op0945f_2	NA	NA
5UTR_1268	3682567 +	3682595 Rmet_3404	<i>tag</i>			Op0945f_2		
NPKM_6157	3682595 +	3683222 Rmet_3404	<i>tag</i>	28.33	1.53	Op0945f_2	GIP-REP-Recomb	Q1LHV0 DNA-3-methyladenine glycosylase I
NPKM_6158	3683322 +	3683616 Rmet_6595		29.00	3.61	Op0945f_2	NA	NA
3UTR_1586	3683543 -	3684205 Rmet_3406	<i>fieF</i>			Op0946r_1		
NPKM_6159	3683576 +	3684215 Rmet_3405		56.67	2.08	Op0945f_2	NA	Q1LHU9 Lysine exporter protein (LYSE/YGGA)
NPKM_6160	3684206 -	3685220 Rmet_3406	<i>fieF</i>	44.33	1.53	Op0946r_1	EIP-TRA-Ion	Q1LHU8 Cation diffusion facilitator family transporter
3UTR_1525	3684216 +	3684861 Rmet_3405				Op0945f_2		
5UTR_1321	3685221 -	3685253 Rmet_3406	<i>fieF</i>			Op0946r_1		
5UTR_1269	3685348 +	3685509 Rmet_3407				Op0947f_1		
NPKM_6161	3685509 +	3686652 Rmet_3407		16.67	1.15	Op0947f_1	MET-LIP-Others	Q1LHU7 Glycosyl transferase, family 2
NPKM_6162	3686648 +	3688070 Rmet_3408		14.00	0.00	Op0947f_1	NA	Q1LHU6 Radical SAM
NPKM_6163	3688075 +	3688903 Rmet_3409		9.00	1.73	Op0947f_1	NA	Q1LHU5 YdjC-like protein
NPKM_6164	3688899 +	3689889 Rmet_3410		3.67	1.53	Op0947f_1	NA	Q1LHU4 Putative uncharacterized protein
3UTR_1585	3689818 -	3689916 Rmet_3411	<i>bug</i>			Op0948r_1		
3UTR_1526	3689890 +	3690337 Rmet_3410				Op0947f_1		
NPKM_6165	3689917 -	3690910 Rmet_3411	<i>bug</i>	3.33	0.58	Op0948r_1	NA	Q1LHU3 Uncharacterized protein UPF0065
NPKM_6166	3690963 -	3693366 Rmet_3412		4.33	0.58	Op0948r_1	MET-CAH-Prop	Q1LHU2 Acyl-CoA dehydrogenase-like protein
NPKM_6167	3693371 -	3694142 Rmet_3413		5.33	0.58	Op0948r_1	MET-CAH-Prop	Q1LHU1 Enoyl-CoA hydratase/isomerase
NPKM_6168	3694152 -	3695391 Rmet_3414		3.67	0.58	Op0948r_1	NA	Q1LHU0 L-carnitine dehydratase/bile acid-inducible protein F
NPKM_6169	3695468 -	3696443 Rmet_3415	<i>bug</i>	5.67	1.53	Op0948r_1	NA	Q1LHT9 Uncharacterized protein UPF0065

5UTR_1320	3696444 -	3696831 Rmet_3415	<i>bug</i>			Op0948r_1		
5UTR_1270	3696582 +	3696644 Rmet_3416				Op0949f_1		
NPKM_6170	3696644 +	3697607 Rmet_3416		16.67	1.15	Op0949f_1	NA	Q1LHT8 Transcriptional regulator, LysR family
3UTR_1584	3696834 -	3697699 Rmet_R0065				Op0950r_2		
3UTR_1527	3697608 +	3697670 Rmet_3416				Op0949f_1		
NPKM_6171	3697700 -	3697776 Rmet_R0065		36.00	4.00	Op0950r_2	NA	NA
NPKM_6172	3697843 -	3699568 Rmet_3417	<i>soxB</i>	158.33	4.16	Op0950r_2	NA	Q1LHT7 Sulfate thiol esterase SoxB
NPKM_6173	3699595 -	3700096 Rmet_3418	<i>dsbX</i>	256.00	11.53	Op0950r_2	NA	Q1LHT6 Thioredoxin-like protein
NPKM_6174	3700106 -	3700769 Rmet_3419	<i>soxX</i>	389.67	14.50	Op0950r_2	NA	Q1LHT5 Conserved hypothetical transmembrane protein
NPKM_6175	3700780 -	3701656 Rmet_3420	<i>soxA</i>	361.33	7.64	Op0950r_2	NA	Q1LHT4 Putative uncharacterized protein
NPKM_6176	3701798 -	3702257 Rmet_3421		519.33	25.32	Op0950r_2	NA	Q1LHT3 Conserved hypothetical signal peptide protein
NPKM_6177	3702280 -	3702592 Rmet_3422	<i>soxZ</i>	607.33	19.40	Op0950r_2	NA	Q1LHT2 Sulfur compound chelating protein SoxZ
NPKM_6178	3702655 -	3703111 Rmet_3423	<i>soxY</i>	649.67	35.30	Op0950r_2	NA	Q1LHT1 Twin-arginine translocation pathway signal
NPKM_6179	3703365 -	3703692 Rmet_3424		4490.67	354.47	Op0950r_2	NA	Q1LHT0 Cytochrome c, class I
NPKM_6180	3703969 -	3704863 Rmet_3425	<i>eamA</i>	85.33	3.79	Op0950r_1	EIP-TRA-Ion	Q1LHS9 Putative uncharacterized protein
NPKM_6181	3705013 -	3706294 Rmet_3426	<i>soxF</i>	122.33	7.09	Op0950r_1	NA	Q1LHS8 Sulfide dehydrogenase (Flavocytochrome), flavoprotein subunit
NPKM_6182	3706297 -	3706675 Rmet_3427		179.33	10.12	Op0950r_1	NA	Q1LHS7 Cytochrome c, class I
NPKM_6183	3706680 -	3707535 Rmet_3428		249.67	5.51	Op0950r_1	NA	Q1LHS6 Transport-associated
NPKM_6184	3707689 -	3708277 Rmet_3429	<i>yraO</i>	187.00	9.64	Op0950r_1	MET-GLYC-LPS	Q1LHS5 Phosphoheptose isomerase
NPKM_6185	3708307 -	3708712 Rmet_3430		108.67	9.61	Op0950r_1	GIP-REP-Recomb	Q1LHS4 UPF0102 protein Rmet_3430
5UTR_1271	3708340 +	3708764 Rmet_3431	<i>yraL</i>			Op0951f_1		
NPKM_6186	3708764 +	3709664 Rmet_3431	<i>yraL</i>	93.67	3.06	Op0951f_1	NA	Q1LHS3 Putative uncharacterized protein
3UTR_1528	3709665 +	3710534 Rmet_3431	<i>yraL</i>			Op0951f_1		
NPKM_6187	3709748 -	3710504 Rmet_3432		486.67	43.47	Op0952r_1	NA	Q1LHS2 Rare lipoprotein A
5UTR_1319	3710505 -	3710770 Rmet_3432				Op0952r_1		
5UTR_1272	3710680 +	3710782 Rmet_3433	<i>ycbL</i>			Op0953f_1		
NPKM_6188	3710782 +	3711451 Rmet_3433	<i>ycbL</i>	89.00	7.55	Op0953f_1	MET-CAH-Pyr	Q1LHS1 Beta-lactamase-like protein
3UTR_1583	3711021 -	3712630 Rmet_3436	<i>yfgD</i>			Op0954r_1		
NPKM_6189	3711454 +	3712102 Rmet_3434		58.00	3.61	Op0953f_1	NA	Q1LHS0 Conserved hypothetical transmembrane protein
NPKM_6190	3712309 +	3712540 Rmet_3435		35.00	3.46	Op0953f_1	NA	Q1LHR9 Putative uncharacterized protein
NPKM_6191	3712631 -	3712991 Rmet_3436	<i>yfgD</i>	103.33	2.52	Op0954r_1	NA	Q1LHR8 Arsenate reductase
5UTR_1318	3712992 -	3713106 Rmet_3436	<i>yfgD</i>			Op0954r_1		
3UTR_1582	3713109 -	3713789 Rmet_3438	<i>azoR2</i>			Op0956r_1		
NPKM_6192	3713133 +	3713754 Rmet_3437	<i>pat</i>	11.67	1.15	Op0955f_1	NA	Q1LHR7 GCN5-related N-acetyltransferase
3UTR_1529	3713755 +	3714342 Rmet_3437	<i>pat</i>			Op0955f_1		
NPKM_6193	3713790 -	3714411 Rmet_3438	<i>azoR2</i>	25.67	0.58	Op0956r_1	NA	Q1LHR6 NAD(P)H dehydrogenase (Quinone)
NPKM_6194	3714487 -	3714937 Rmet_3439		33.00	1.00	Op0956r_1	NA	Q1LHR5 GCN5-related N-acetyltransferase
NPKM_6195	3714933 -	3715392 Rmet_3440		45.67	9.02	Op0956r_1	NA	Q1LHR4 Alkylhydroperoxidase AhpD core
NPKM_6196	3715451 +	3715976 Rmet_3441		11.00	1.00	Op0957f_1	NA	Q1LHR3 Transcriptional regulator, MarR family
3UTR_1530	3715977 +	3716852 Rmet_3441				Op0957f_1		
3UTR_1581	3715996 -	3716053 Rmet_3442				Op0958r_1		
NPKM_6197	3716054 -	3717323 Rmet_3442		60.00	2.65	Op0958r_1	NA	Q1LHR2 Acetylornithine deacetylase or succinyl-diaminopimelate desuccinylase
NPKM_6198	3717367 -	3718624 Rmet_3443		42.67	1.53	Op0958r_1	MET-NUC-Pur	Q1LHR1 Amidase, hydantoinase/carbamoylase

5UTR_1317	3718625 -	3718724 Rmet_3443				Op0958r_1		
5UTR_1273	3718822 +	3719030 Rmet_3444	dctA2			Op0959f_1		
NPKM_6199	3719030 +	3720434 Rmet_3444	dctA2	15.67	2.08	Op0959f_1	NA	Q1LHR0 Sodium:dicarboxylate symporter
3UTR_1580	3720175 -	3721410 Rmet_3446				Op0960r_1		
NPKM_6200	3720486 +	3721179 Rmet_3445		52.33	2.08	Op0959f_2	NA	Q1LHQ9 Transcriptional regulator, GntR family
3UTR_1531	3721180 +	3721782 Rmet_3445				Op0959f_2		
NPKM_6201	3721411 -	3722407 Rmet_3446		79.67	5.51	Op0960r_1	NA	Q1LHQ8 Transcriptional regulator, LysR family
NPKM_6202	3722454 -	3723138 Rmet_3447		43.00	1.73	Op0960r_1	NA	Q1LHQ7 Putative uncharacterized protein
5UTR_1316	3723139 -	3723231 Rmet_3447				Op0960r_1		
NPKM_6203	3723422 +	3725213 Rmet_3448	gcl	1.33	0.58	Op0961f_1	MET-CAH-DiCarb	Q1LHQ6 Glyoxylate carboligase
3UTR_1532	3725214 +	3725234 Rmet_3448	gcl			Op0961f_1		
5UTR_1274	3725261 +	3725270 Rmet_3449	hyi			Op0961f_1		
NPKM_6204	3725270 +	3726086 Rmet_3449	hyi	1.33	0.58	Op0961f_1	MET-CAH-DiCarb	Q1LHQ5 Xylose isomerase-like TIM barrel
3UTR_1533	3726087 +	3726134 Rmet_3449	hyi			Op0961f_1		
NPKM_6205	3726140 +	3727064 Rmet_3450	glxR	4.33	0.58	Op0961f_2	MET-CAH-DiCarb	Q1LHQ4 2-hydroxy-3-oxopropionate reductase
3UTR_1534	3727065 +	3727067 Rmet_3450	glxR			Op0961f_2		
5UTR_1275	3727085 +	3727152 Rmet_3451	ttuD2			Op0961f_2		
NPKM_6206	3727152 +	3728484 Rmet_3451	ttuD2	3.00	1.00	Op0961f_2	MET-CAH-DiCarb	Q1LHQ3 Glycerate 2-kinase
NPKM_6207	3728522 +	3729989 Rmet_3452	pyk	5.00	0.00	Op0961f_2	MET-CAH-FbP	Q1LHQ2 Pyruvate kinase
3UTR_1579	3729131 -	3731331 Rmet_3454				Op0962r_3		
3UTR_1535	3729990 +	3730016 Rmet_3452	pyk			Op0961f_2		
5UTR_1276	3730232 +	3730286 Rmet_3453				Op0961f_3		
NPKM_6208	3730286 +	3731180 Rmet_3453		33.33	4.04	Op0961f_3	NA	Q1LHQ1 Putative uncharacterized protein
NPKM_6209	3731332 -	3731680 Rmet_3454		31.33	0.58	Op0962r_3	NA	Q1LHQ0 Putative uncharacterized protein
NPKM_6210	3731730 +	3731952 Rmet_6596		19.00	3.61	Op2055f_1	NA	NA
3UTR_1536	3731953 +	3733332 Rmet_6596				Op2055f_1		
NPKM_6211	3731968 -	3732406 Rmet_3455	rnk	129.67	3.79	Op0962r_3	NA	Q1LHP9 Transcription elongation factor
NPKM_6212	3732628 -	3732766 Rmet_6597		174.67	12.50	Op0962r_3	NA	NA
NPKM_6213	3732945 -	3733395 Rmet_3456	pbrR3	149.00	9.17	Op0962r_3	NA	Q1LHP8 Transcriptional regulator, MerR family
NPKM_6214	3733446 -	3733833 Rmet_3457	speH	56.67	5.03	Op0962r_2	MET-AA-Met	Q1LHP7 S-adenosylmethionine decarboxylase related
NPKM_6215	3734028 -	3735573 Rmet_3458		69.00	1.73	Op0962r_2	NA	Q1LHP6 Putative transmembrane protein
NPKM_6216	3735582 -	3736605 Rmet_3459		143.33	4.04	Op0962r_2	NA	Q1LHP5 Putative transmembrane protein
5UTR_1277	3736374 +	3737235 Rmet_3461				Op0963f_1		
NPKM_6217	3736645 -	3737032 Rmet_3460		68.00	9.54	Op0962r_1	NA	Q1LHP4 Putative uncharacterized protein
5UTR_1315	3737033 -	3737120 Rmet_3460				Op0962r_1		
NPKM_6218	3737235 +	3738747 Rmet_3461		9.67	1.53	Op0963f_1	MET-AA-Met	Q1LHP3 Spermidine synthase
NPKM_6219	3738828 +	3740499 Rmet_3462		14.00	1.00	Op0963f_1	NA	Q1LHP2 Conserved hypothetical transmembrane protein
NPKM_6220	3740509 +	3741007 Rmet_3463		88.00	5.29	Op0963f_2	NA	Q1LHP1 Putative uncharacterized protein
NPKM_6221	3741118 +	3741997 Rmet_3464	htpX	103.00	1.73	Op0963f_2	GIP-PTL-Fold	Q1LHP0 HtpX peptidase. Metallo peptidase. MEROPS family M48B
3UTR_1578	3741589 +	3742016 Rmet_3465				Op0964r_3		
3UTR_1537	3741998 +	3743389 Rmet_3464	htpX			Op0963f_2		
NPKM_6222	3742017 -	3743043 Rmet_3465		15.67	0.58	Op0964r_3	NA	Q1LHN9 Transcriptional regulator, AraC family with amidase-like domain
NPKM_6223	3743076 -	3744285 Rmet_3466		4.67	0.58	Op0964r_2	EIP-TRA-Ion	Q1LHN8 Major facilitator superfamily MFS_1

NPKM_6224	3744389 -	3747584 Rmet_3467		18.67	0.58	Op0964r_2	NA	Q1LHN7 Cytochrome P450
NPKM_6225	3747790 -	3748207 Rmet_3468		51.67	4.93	Op0964r_2	NA	Q1LHN6 Class I peptide chain release factor
NPKM_6226	3748243 -	3749635 Rmet_3469		14.67	1.15	Op0964r_1	NA	Q1LHN5 FAD linked oxidase-like protein
NPKM_6227	3749854 -	3750655 Rmet_3470		79.33	3.51	Op0964r_1	MET-CAH-Prop	Q1LHN4 Enoyl-CoA hydratase
5UTR_1278	3750898 +	3750919 Rmet_3471				Op0965f_1		
NPKM_6228	3750919 +	3751300 Rmet_3471		145.33	7.09	Op0965f_1	NA	Q1LHN3 Putative uncharacterized protein
NPKM_6229	3751309 +	3751543 Rmet_3472	<i>osmB</i>	118.00	12.49	Op0965f_1	NA	Q1LHN2 Putative uncharacterized protein
NPKM_6230	3751720 -	3751796 Rmet_R0066		69.67	13.32	Op2056r_1	NA	NA
5UTR_1314	3751797 -	3751879 Rmet_R0066				Op2056r_1		
NPKM_6231	3752222 +	3753107 Rmet_3473		579.33	24.21	Op0965f_2	NA	Q1LHN1 Cytochrome c, class I
3UTR_1538	3753108 +	3753175 Rmet_3473				Op0965f_2		
3UTR_1577	3753187 -	3753225 Rmet_3474	<i>hemN</i>			Op0966r_1		
NPKM_6232	3753226 -	3754729 Rmet_3474	<i>hemN</i>	22.67	2.52	Op0966r_1	MET-COF-Porph	Q1LHN0 Coproporphyrinogen III oxidase, anaerobic
5UTR_1279	3754781 +	3754964 Rmet_3475				Op0967f_1		
NPKM_6233	3754964 +	3756143 Rmet_3475		1.00	0.00	Op0967f_1	NA	Q1LHM9 Putative ABC-type branched-chain amino acid transport systems periplasm
3UTR_1576	3755718 -	3756165 Rmet_3476	<i>envZ</i>			Op0968r_1		
3UTR_1539	3756144 +	3756367 Rmet_3475				Op0967f_1		
NPKM_6234	3756166 -	3757480 Rmet_3476	<i>envZ</i>	9.33	0.58	Op0968r_1	NA	Q1LHM8 Sensor protein
NPKM_6235	3757484 -	3758270 Rmet_3477	<i>ompR</i>	15.67	1.53	Op0968r_1	EIP-SIG-2Comp	Q1LHM7 Two component transcriptional regulator, winged helix family
NPKM_6236	3758540 -	3760628 Rmet_3478	<i>rep</i>	24.00	1.00	Op0968r_1	GIP-REP-Recomb	Q1LHM6 ATP-dependent DNA helicase Rep
5UTR_1313	3760629 -	3760817 Rmet_3478	<i>rep</i>			Op0968r_1		
5UTR_1280	3760897 +	3760921 Rmet_3479	<i>osmB</i>			Op0969f_1		
NPKM_6237	3760921 +	3761143 Rmet_3479	<i>osmB</i>	60.00	5.29	Op0969f_1	NA	Q1LHM5 Osmotically inducible lipoprotein
3UTR_1540	3761527 +	3761550 misc_feature				0		
5UTR_1281	3761578 +	3761633 Rmet_3480	<i>gcvT</i>			Op0969f_1		
NPKM_6240	3761633 +	3762761 Rmet_3480	<i>gcvT</i>	77.00	3.00	Op0969f_1	MET-EN-Nitrog	Q1LHM4 Aminomethyltransferase
NPKM_6241	3762864 +	3763245 Rmet_3481	<i>gcvH</i>	644.33	42.25	Op0969f_2	NA	Q1LHM3 Glycine cleavage system H protein
NPKM_6242	3763330 +	3766255 Rmet_3482	<i>gcvP</i>	85.33	3.06	Op0969f_2	MET-AA-GlySerThr	Q1LHM2 Glycine dehydrogenase [decarboxylating]
3UTR_1575	3763727 -	3768614 Rmet_3485	<i>ybdK</i>			Op0970r_4		
NPKM_6243	3766363 +	3767740 Rmet_3483	<i>sdaA</i>	28.67	1.15	Op0969f_2	MET-AA-GlySerThr	Q1LHM1 L-serine ammonia-lyase
NPKM_6244	3767832 +	3768579 Rmet_3484		47.67	2.31	Op0969f_2	MET-CAH-Pyr	Q1LHM0 Beta-lactamase-like protein
3UTR_1541	3768580 +	3770710 Rmet_3484				Op0969f_2		
NPKM_6245	3768615 -	3769734 Rmet_3485	<i>ybdK</i>	210.67	5.13	Op0970r_4	NA	Q1LHL9 Carboxylate-amine ligase Rmet_3485
NPKM_6246	3769733 -	3770954 Rmet_3486		187.67	4.16	Op0970r_4	NA	Q1LHL8 Sodium/hydrogen exchanger
NPKM_6247	3771094 -	3773050 Rmet_3487		100.00	3.61	Op0970r_4	NA	Q1LHL7 Tetratricopeptide TPR_4
NPKM_6248	3773251 -	3774403 Rmet_3488		230.00	4.36	Op0970r_4	EIP-TRA-ABC	Q1LHL6 Extracellular ligand-binding receptor
NPKM_6249	3774557 -	3778520 Rmet_3489	<i>putA</i>	49.00	0.00	Op0970r_3	NA	Q1LHL5 L-proline dehydrogenase / delta-1-pyrroline-5-carboxylate dehydrogenase
NPKM_6250	3778717 -	3781012 Rmet_3490	<i>priA</i>	55.67	7.09	Op0970r_3	GIP-REP-Complex	Q1LHL4 Replication restart DNA helicase PriA
NPKM_6251	3781008 -	3781224 Rmet_6598		116.00	22.61	Op0970r_3	NA	NA
NPKM_6252	3781513 -	3782617 Rmet_3491	<i>hemE</i>	280.33	15.95	Op0970r_3	MET-COF-Porph	Q1LHL3 Uroporphyrinogen decarboxylase
NPKM_6253	3782732 -	3783689 Rmet_3492		69.33	4.51	Op0970r_2	MET-CAH-But	Q1LHL2 Alpha/beta hydrolase fold-3
5UTR_1282	3784000 +	3792171 Rmet_3502				Op0971f_1		
NPKM_6254	3784412 -	3784829 Rmet_3493	<i>atpC</i>	1428.67	50.96	Op0970r_2	MET-EN-OxPhos	Q1LHL1 ATP synthase epsilon chain

NPKM_6255	3784967 -	3786371 Rmet_3494	<i>atpD</i>	2046.33	95.82	Op0970r_2	MET-EN-OxPhos	Q1LHL0 ATP synthase subunit beta
NPKM_6256	3786404 -	3787280 Rmet_3495	<i>atpG</i>	1594.00	78.10	Op0970r_2	MET-EN-OxPhos	Q1LHK9 ATP synthase gamma chain
NPKM_6257	3787350 -	3788892 Rmet_3496	<i>atpA</i>	2179.00	105.53	Op0970r_2	MET-EN-OxPhos	Q1LHK8 ATP synthase subunit alpha
NPKM_6258	3788931 -	3789474 Rmet_3497	<i>atpH</i>	2239.67	150.16	Op0970r_2	MET-EN-OxPhos	Q1LHK7 ATP synthase F1, delta subunit
NPKM_6259	3789476 -	3789947 Rmet_3498	<i>atpF</i>	1984.33	157.02	Op0970r_2	MET-EN-OxPhos	Q1LHK6 ATP synthase B chain
NPKM_6260	3789971 -	3790037 Rmet_6599		1016.00	55.24	Op0970r_2	NA	NA
NPKM_6261	3790052 -	3790319 Rmet_3499	<i>atpE</i>	2894.33	55.77	Op0970r_2	MET-EN-OxPhos	Q1LHK5 ATP synthase F0, C subunit
NPKM_6262	3790380 -	3791250 Rmet_3500	<i>atpB</i>	620.33	23.50	Op0970r_1	MET-EN-OxPhos	Q1LHK4 ATP synthase A chain
NPKM_6263	3791484 -	3792024 Rmet_3501	<i>atpI</i>	1138.33	48.79	Op0970r_1	MET-EN-OxPhos	Q1LHK3 ATP synthase I chain
NPKM_6264	3792171 +	3792429 Rmet_3502		9.67	1.53	Op0971f_1	NA	Q1LHK2 Putative uncharacterized protein
NPKM_6265	3792394 -	3793297 Rmet_3503	<i>parB</i>	155.33	6.66	Op0972r_2	NA	Q1LHK1 Chromosome segregation DNA-binding protein
3UTR_1542	3792430 +	3793206 Rmet_3502				Op0971f_1		
NPKM_6266	3793333 -	3794107 Rmet_3504	<i>parA</i>	109.67	10.02	Op0972r_2	DIV-Division	Q1LHK0 Chromosome segregation ATPase
NPKM_6267	3794178 -	3794886 Rmet_3505	<i>gidB</i>	99.33	9.29	Op0972r_2	DIV-Division	Q1LHJ9 Ribosomal RNA small subunit methyltransferase G
NPKM_6268	3794886 -	3796851 Rmet_3506	<i>gidA</i>	166.33	6.03	Op0972r_2	DIV-Division	Q1LHJ8 tRNA uridine 5-carboxymethylaminomethyl modification enzyme mnmG
5UTR_1312	3796852 -	3796860 Rmet_3506	<i>gidA</i>			Op0972r_2		
3UTR_1574	3797048 -	3797087 Rmet_3507	<i>hutG4</i>			Op0972r_1		
NPKM_6269	3797088 -	3797967 Rmet_3507	<i>hutG4</i>	10.33	0.58	Op0972r_1	MET-CAH-DiCarb	Q1LHJ7 N-formylglutamate amidohydrolase
NPKM_6270	3797970 -	3798933 Rmet_3508	<i>bug</i>	15.00	2.65	Op0972r_1	NA	Q1LHJ6 Uncharacterized protein UPF0065
5UTR_1311	3798934 -	3800062 Rmet_3508	<i>bug</i>			Op0972r_1		
5UTR_1283	3799067 +	3799120 Rmet_3509				Op0973f_1		
NPKM_6271	3799120 +	3800023 Rmet_3509		36.67	2.52	Op0973f_1	NA	Q1LHJ5 Transcriptional regulator, LysR family
3UTR_1543	3800024 +	3800573 Rmet_3509				Op0973f_1		
3UTR_1573	3800067 -	3800132 Rmet_3510	<i>livF11</i>			Op0974r_6		
NPKM_6272	3800133 -	3800877 Rmet_3510	<i>livF11</i>	46.67	1.15	Op0974r_6	EIP-TRA-ABC	Q1LHJ4 ABC transporter-related protein
NPKM_6273	3800886 -	3802740 Rmet_3511		29.00	1.00	Op0974r_6	EIP-TRA-ABC	Q1LHJ3 ABC transporter-related protein
NPKM_6274	3802743 -	3803796 Rmet_3512		25.67	0.58	Op0974r_6	EIP-TRA-ABC	Q1LHJ2 Inner-membrane translocator
NPKM_6275	3803967 -	3805116 Rmet_3513		205.00	1.73	Op0974r_6	EIP-TRA-ABC	Q1LHJ1 Extracellular ligand-binding receptor
NPKM_6276	3805452 -	3806211 Rmet_3514		20.00	1.73	Op0974r_5	NA	Q1LHJ0 Putative uncharacterized protein
NPKM_6277	3806245 -	3806761 Rmet_3515		53.33	4.51	Op0974r_5	NA	Q1LHI9 Conserved hypothetical transmembrane protein
NPKM_6278	3807084 -	3808119 Rmet_3516	<i>livM5</i>	364.33	29.37	Op0974r_5	EIP-TRA-ABC	Q1LHI8 Inner-membrane translocator
NPKM_6279	3808118 -	3809003 Rmet_3517	<i>livH5</i>	383.33	36.25	Op0974r_5	EIP-TRA-ABC	Q1LHI7 Inner-membrane translocator
NPKM_6280	3809176 -	3810385 Rmet_3518		1160.67	54.78	Op0974r_5	EIP-TRA-ABC	Q1LHI6 Extracellular ligand-binding receptor
NPKM_6281	3810484 -	3811210 Rmet_3519	<i>livF5</i>	323.67	23.71	Op0974r_4	EIP-TRA-ABC	Q1LHI5 ABC transporter-related protein
NPKM_6282	3811222 -	3811996 Rmet_3520	<i>livG5</i>	321.67	31.64	Op0974r_4	EIP-TRA-ABC	Q1LHI4 ABC transporter-related protein
5UTR_1284	3812083 +	3812119 Rmet_6600				Op2057f_1		
NPKM_6283	3812119 +	3812314 Rmet_6600		2.33	1.53	Op2057f_1	NA	NA
3UTR_1544	3812315 +	3812319 Rmet_6600				Op2057f_1		
NPKM_6284	3812355 -	3814023 Rmet_3521	<i>betA2</i>	137.67	2.89	Op0974r_3	MET-AA-GlySerThr	Q1LHI3 Glucose-methanol-choline oxidoreductase
NPKM_6285	3814103 -	3815012 Rmet_3522	<i>pldB</i>	62.00	5.57	Op0974r_2	MET-LIP-GlycLIp	Q1LHI2 Alpha/beta hydrolase fold
NPKM_6286	3815130 -	3815550 Rmet_3523	<i>cupR</i>	84.00	2.65	Op0974r_2	NA	Q1LHI1 Transcriptional regulator, MerR family
NPKM_6287	3815546 -	3817988 Rmet_3524	<i>cupA</i>	26.33	1.53	Op0974r_1	MET-EN-P_ATPase	Q1LHI0 Heavy metal translocating P-type ATPase
5UTR_1285	3817809 +	3817969 Rmet_3525	<i>cupC</i>			Op0975f_1		

NPKM_6288	3817969 +	3818371 Rmet_3525	<i>cupC</i>	76.33	1.53	Op0975f_1	NA	Q1LHH9 Heavy metal transport/detoxification protein
3UTR_1545	3818372 +	3818928 Rmet_3525	<i>cupC</i>			Op0975f_1		
NPKM_6289	3818435 -	3819161 Rmet_3526	<i>ompW1</i>	602.67	58.59	Op0976r_3	NA	Q1LHH8 OmpW
NPKM_6290	3819449 -	3820418 Rmet_3527		42.33	1.15	Op0976r_2	MET-AA-ArgPro	Q1LHH7 Ornithine cyclodeaminase
NPKM_6291	3820512 -	3821511 Rmet_3528		52.67	0.58	Op0976r_2	NA	Q1LHH6 Aldo/keto reductase
NPKM_6292	3821571 -	3823752 Rmet_3529	<i>pbpC</i>	41.67	2.08	Op0976r_2	NA	Q1LHH5 Penicillin-binding protein 1C
NPKM_6293	3823795 -	3824482 Rmet_3530		56.33	3.51	Op0976r_2	NA	Q1LHH4 YhhN-like protein
NPKM_6294	3824493 -	3830475 Rmet_3531		70.67	1.15	Op0976r_2	NA	Q1LHH3 Alpha-2-macroglobulin-like protein
NPKM_6295	3830568 -	3831048 Rmet_3532		21.33	0.58	Op0976r_1	NA	Q1LHH2 Transcriptional regulator, AsnC family
5UTR_1310	3831049 -	3831052 Rmet_3532				Op0976r_1		
NPKM_6296	3831186 +	3832119 Rmet_3533	<i>phhA</i>	26.67	3.06	Op0977f_1	MET-AA-PheTyrTrp	Q1LHH1 Phenylalanine 4-hydroxylase
NPKM_6297	3832153 +	3832531 Rmet_3534	<i>phhB</i>	54.33	1.15	Op0977f_2	NA	NA
3UTR_1572	3832199 -	3835085 Rmet_3537				Op0978r_1		
NPKM_6298	3832631 +	3833336 Rmet_3535	<i>phhR</i>	143.00	2.00	Op0977f_3	NA	Q1LHG9 Two component transcriptional regulator, winged helix family
NPKM_6299	3833370 +	3835053 Rmet_3536	<i>phhS</i>	27.67	0.58	Op0977f_3	NA	Q1LHG8 Sensor protein
3UTR_1546	3835054 +	3835639 Rmet_3536	<i>phhS</i>			Op0977f_3		
NPKM_6300	3835086 -	3835599 Rmet_3537		143.67	5.13	Op0978r_1	NA	Q1LHG7 Nuclear protein SET
5UTR_1309	3835600 -	3836160 Rmet_3537				Op0978r_1		
5UTR_1286	3835664 +	3836079 Rmet_6601				Op0979f_1		
NPKM_6301	3836079 +	3836295 Rmet_6601		7.33	2.08	Op0979f_1	NA	NA
NPKM_6302	3836432 +	3836711 Rmet_3538	<i>hup</i>	1528.33	161.85	Op0979f_2	GIP-REP-Recomb	Q1LHG6 HU family DNA-binding protein
3UTR_1571	3836576 -	3836699 Rmet_3539				Op0980r_1		
NPKM_6303	3836700 -	3836940 Rmet_3539		5.00	1.00	Op0980r_1	NA	Q1LHG5 Putative uncharacterized protein
5UTR_1308	3836941 -	3837007 Rmet_3539				Op0980r_1		
NPKM_6304	3836949 +	3837930 Rmet_3540		99.33	3.21	Op0981f_1	NA	Q1LHG4 Conserved hypothetical transmembrane protein
3UTR_1570	3837286 -	3838972 Rmet_3542				Op0982r_1		
NPKM_6305	3838105 +	3838990 Rmet_3541		16.33	1.15	Op0981f_1	NA	Q1LHG3 Major intrinsic protein
NPKM_6306	3838973 -	3840821 Rmet_3542		107.33	6.66	Op0982r_1	NA	Q1LHG2 Putative uncharacterized protein
3UTR_1547	3838991 +	3839372 Rmet_3541				Op0981f_1		
5UTR_1287	3840770 +	3840853 Rmet_6602				Op0983f_1		
5UTR_1307	3840822 -	3842065 Rmet_3542				Op0982r_1		
NPKM_6307	3840853 +	3841027 Rmet_6602		4.33	2.52	Op0983f_1	NA	NA
NPKM_6308	3841040 +	3842180 Rmet_3543		546.33	8.33	Op0983f_2	NA	Q1LHG1 Twin-arginine translocation pathway signal
NPKM_6309	3842330 +	3843245 Rmet_3544		30.33	2.89	Op0983f_2	EIP-TRA-Ion	Q1LHG0 RarD protein
NPKM_6310	3843360 +	3844542 Rmet_3545	<i>dinB</i>	69.67	9.61	Op0983f_3	GIP-REP-DNA_Pol	Q1LHF9 UMUC-like DNA-repair protein
NPKM_6311	3844602 +	3845799 Rmet_3546		31.67	3.79	Op0983f_3	NA	Q1LHF8 Major facilitator superfamily MFS_1
NPKM_6312	3845943 +	3847707 Rmet_3547		11.00	1.73	Op0983f_3	NA	Q1LHF7 Diguanylate cyclase (GGDEF domain)
3UTR_1569	3846004 -	3847767 Rmet_3548				Op0984r_1		
3UTR_1548	3847708 +	3847897 Rmet_3547				Op0983f_3		
NPKM_6313	3847768 -	3848263 Rmet_3548		273.00	40.11	Op0984r_1	NA	Q1LHF6 Putative uncharacterized protein
5UTR_1306	3848264 -	3848512 Rmet_3548				Op0984r_1		
5UTR_1288	3848608 +	3848674 Rmet_3549	<i>tctC</i>			Op0985f_1		
NPKM_6314	3848674 +	3849643 Rmet_3549	<i>tctC</i>	206.00	3.61	Op0985f_1	EIP-TRA-Ion	Q1LHF5 Uncharacterized protein UPF0065

NPKM_6315	3849795 +	3850344 Rmet_3550	<i>tctB</i>	102.00	3.61	Op0985f_1	EIP-TRA-Ion	Q1LHF4 Conserved hypothetical membrane protein
NPKM_6316	3850372 +	3851887 Rmet_3551	<i>tctA</i>	68.00	3.61	Op0985f_1	EIP-TRA-Ion	Q1LHF3 Putative uncharacterized protein
NPKM_6317	3851992 +	3852409 Rmet_3552		71.33	2.52	Op0985f_1	NA	Q1LHF2 Phenylacetic acid degradation-related protein
NPKM_6318	3852417 +	3853329 Rmet_3553		63.00	6.24	Op0985f_1	NA	Q1LHF1 Patatin
NPKM_6319	3853410 +	3854892 Rmet_3554		57.67	4.51	Op0985f_1	MET-AA-GluGSH	Q1LHF0 FAD-dependent pyridine nucleotide-disulphide oxidoreductase
3UTR_1568	3854444 -	3854900 Rmet_3555				Op0986r_1		
3UTR_1549	3854893 +	3855767 Rmet_3554				Op0985f_1		
NPKM_6320	3854901 -	3855810 Rmet_3555		18.00	2.00	Op0986r_1	NA	Q1LHE9 Transcriptional regulator, LysR family
5UTR_1305	3855811 -	3859038 Rmet_3555				Op0986r_1		
5UTR_1289	3855970 +	3855994 Rmet_3556				Op0987f_1		
NPKM_6321	3855994 +	3857416 Rmet_3556		3.67	0.58	Op0987f_1	MET-AA-Phe	Q1LHE8 Amidase
NPKM_6322	3857429 +	3857639 Rmet_3557		2.00	1.00	Op0987f_1	NA	Q1LHE7 Putative uncharacterized protein
NPKM_6323	3857657 +	3859043 Rmet_3558		2.00	0.00	Op0987f_1	EIP-TRA-Ion	Q1LHE6 Na+/solute symporter
3UTR_1550	3859044 +	3859134 Rmet_3558				Op0987f_1		
3UTR_1567	3859140 -	3859159 Rmet_R0069				Op0988r_3		
NPKM_6324	3859160 -	3859236 Rmet_R0069		60.33	9.29	Op0988r_3	NA	NA
NPKM_6325	3859293 -	3860010 Rmet_3559		454.33	5.69	Op0988r_3	NA	Q1LHE5 Response regulator receiver domain protein (CheY-like)
NPKM_6326	3860066 -	3862550 Rmet_3560		91.67	7.77	Op0988r_2	NA	Q1LHE4 Sensor protein
NPKM_6327	3862546 -	3863377 Rmet_3561		167.00	2.00	Op0988r_2	NA	Q1LHE3 Putative periplasmic ligand-binding sensor protein
NPKM_6328	3863386 -	3864760 Rmet_3562	<i>sun</i>	112.33	1.15	Op0988r_2	GIP-TL-Ass	Q1LHE2 Sun protein
NPKM_6329	3864905 -	3865766 Rmet_3563		236.67	13.87	Op0988r_2	GIP-PTL-Fold	Q1LHE1 HtpX-2 peptidase. Metallo peptidase. MEROPS family M48B
NPKM_6330	3865930 -	3866965 Rmet_3564	<i>fmt</i>	98.33	1.53	Op0988r_1	MET-AA-Met	Q1LHE0 Methionyl-tRNA formyltransferase
NPKM_6331	3867044 -	3867551 Rmet_3565		165.33	4.62	Op0988r_1	NA	Q1LHD9 Peptide deformylase
5UTR_1290	3867155 +	3867814 Rmet_3566				Op0989f_1		
5UTR_1304	3867552 -	3868324 Rmet_3565				Op0988r_1		
NPKM_6332	3867814 +	3868891 Rmet_3566		416.00	6.08	Op0989f_1	NA	Q1LHD8 Peptidoglycan-binding LysM
NPKM_6333	3868929 +	3870045 Rmet_3567		134.00	7.55	Op0989f_1	GIP-REP-Recomb	Q1LHD7 DNA processing protein DprA, putative
NPKM_6334	3870081 +	3870471 Rmet_3568		72.67	5.77	Op0989f_1	NA	Q1LHD6 Putative uncharacterized protein
NPKM_6335	3870646 +	3873322 Rmet_3569	<i>topB</i>	260.33	7.51	Op0989f_2	GIP-REP-Complex	Q1LHD5 DNA topoisomerase
3UTR_1566	3872573 -	3873379 Rmet_3570				Op0990r_1		
NPKM_6336	3873380 -	3874313 Rmet_3570		428.67	19.76	Op0990r_1	NA	Q1LHD4 Transcriptional regulator, LysR family
NPKM_6337	3874481 +	3874754 Rmet_3571	<i>copQ1</i>	46.67	3.21	Op0991f_1	NA	Q1LHD3 Putative uncharacterized protein
3UTR_1551	3874755 +	3874839 Rmet_3571	<i>copQ1</i>			Op0991f_1		
NPKM_6338	3874883 -	3875327 Rmet_3572		434.00	49.33	Op0992r_2	NA	Q1LHD2 17 kDa surface antigen
NPKM_6339	3875562 -	3875757 Rmet_3573		142.67	51.98	Op0992r_1	NA	Q1LHD1 Putative uncharacterized protein
NPKM_6340	3875773 -	3877849 Rmet_3574	<i>cstA</i>	140.00	52.92	Op0992r_1	NA	Q1LHD0 Carbon starvation protein CstA
5UTR_1303	3877850 -	3878073 Rmet_3574	<i>cstA</i>			Op0992r_1		
NPKM_6341	3877871 +	3878117 Rmet_6603		1.33	0.58	Op0993f_1	NA	NA
3UTR_1552	3878118 +	3878139 Rmet_6603				Op0993f_1		
5UTR_1291	3878160 +	3878195 Rmet_3575				Op0993f_2		
NPKM_6342	3878195 +	3879623 Rmet_3575		17.67	0.58	Op0993f_2	EIP-SIG-2Comp	Q1LHC9 Periplasmic sensor signal transduction histidine kinase
NPKM_6343	3879619 +	3880306 Rmet_3576		19.67	3.51	Op0993f_2	NA	Q1LHC8 Two component transcriptional regulator, LuxR family
3UTR_1553	3880307 +	3881452 Rmet_3576				Op0993f_2		

3UTR_1565	3880362 -	3880393 Rmet_3577	<i>pckG</i>			Op0994r_1		
NPKM_6344	3880394 -	3882251 Rmet_3577	<i>pckG</i>	464.67	18.77	Op0994r_1	MET-CAH-TCA	Q1LHC7 Phosphoenolpyruvate carboxykinase (GTP)
5UTR_1292	3882207 +	3882689 Rmet_3578	<i>gyaR</i>			Op0995f_1		
5UTR_1302	3882252 -	3882698 Rmet_3577	<i>pckG</i>			Op0994r_1		
NPKM_6345	3882689 +	3883790 Rmet_3578	<i>gyaR</i>	103.33	1.53	Op0995f_1	MET-AA-GlySerThr	Q1LHC6 D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding
NPKM_6346	3883957 +	3884326 Rmet_3579		261.00	10.00	Op0995f_2	NA	Q1LHC5 Calcium-binding EF-hand
NPKM_6347	3884546 +	3885203 Rmet_3580		44.00	2.00	Op0995f_2	NA	Q1LHC4 MOSC domain protein
NPKM_6348	3885467 +	3886691 Rmet_3581		46.67	2.52	Op0995f_2	NA	Q1LHC3 Secretion protein HlyD
NPKM_6349	3886695 +	3889905 Rmet_3582	<i>acr</i>	36.67	0.58	Op0995f_2	EIP-TRA-Ion	Q1LHC2 Acriflavin resistance protein
NPKM_6350	3889989 +	3890826 Rmet_3583		29.33	1.53	Op0995f_2	NA	Q1LHC1 Putative uncharacterized protein
3UTR_1564	3890405 -	3890849 Rmet_3584				Op0996r_1		
3UTR_1554	3890827 +	3891771 Rmet_3583				Op0995f_2		
NPKM_6351	3890850 -	3892338 Rmet_3584		20.00	1.00	Op0996r_1	EIP-SIG-2Comp	Q1LHC0 Sensor protein
NPKM_6352	3892337 -	3893012 Rmet_3585		84.00	1.00	Op0996r_1	EIP-SIG-2Comp	Q1LHB9 Two component transcriptional regulator, winged helix family
5UTR_1293	3893186 +	3893209 Rmet_3586				Op0997f_1		
NPKM_6353	3893209 +	3894325 Rmet_3586		78.33	1.53	Op0997f_1	EIP-TRA-ABC	Q1LHB8 Putative uncharacterized protein
NPKM_6354	3894392 -	3895121 Rmet_3587	<i>acrR</i>	101.67	5.86	Op0998r_1	NA	Q1LHB7 Transcriptional regulator, TetR family
5UTR_1301	3895122 -	3895274 Rmet_3587	<i>acrR</i>			Op0998r_1		
NPKM_6355	3895167 +	3895356 Rmet_6604		2.00	1.00	Op0999f_1	NA	NA
5UTR_1294	3895387 +	3895612 Rmet_3588	<i>acrA</i>			Op0999f_2		
NPKM_6356	3895612 +	3896860 Rmet_3588	<i>acrA</i>	285.00	10.39	Op0999f_2	EIP-TRA-Other	Q1LHB6 Secretion protein HlyD
NPKM_6357	3896886 +	3900039 Rmet_3589	<i>acrB</i>	158.67	4.16	Op0999f_2	EIP-TRA-Ion	Q1LHB5 Hydrophobe/amphiphile efflux-1 HAE1
NPKM_6358	3900041 +	3901517 Rmet_3590		206.67	5.03	Op0999f_2	NA	Q1LHB4 RND efflux system, outer membrane lipoprotein, NodT
3UTR_1555	3901518 +	3901623 Rmet_3590				Op0999f_2		
3UTR_1563	3901578 -	3901590 Rmet_3591	<i>ompW2</i>			Op1000r_2		
NPKM_6359	3901591 -	3902452 Rmet_3591	<i>ompW2</i>	2.00	1.00	Op1000r_2	NA	Q1LHB3 OmpW
NPKM_6360	3902469 -	3903756 Rmet_3592		1.67	0.58	Op1000r_2	NA	Q1LHB2 Putative lipoprotein
NPKM_6361	3903808 -	3905119 Rmet_3593		1.67	0.58	Op1000r_2	NA	Q1LHB1 Putative lipoprotein
5UTR_1300	3905120 -	3905182 Rmet_3593				Op1000r_2		
3UTR_1562	3905370 -	3905403 Rmet_3594				Op1000r_2		
NPKM_6362	3905404 -	3906304 Rmet_3594		1.67	1.15	Op1000r_2	NA	Q1LHB0 Putative lipoprotein transmembrane
3UTR_1561	3906311 -	3906510 Rmet_3595				Op1000r_2		
NPKM_6363	3906511 -	3907453 Rmet_3595		86.33	10.02	Op1000r_2	NA	Q1LHA9 Transcriptional regulator, TetR family
NPKM_6364	3907655 -	3909251 Rmet_3596		18.67	0.58	Op1000r_1	MET-AA-GlySerThr	Q1LHA8 Glucose-methanol-choline oxidoreductase
NPKM_6365	3909259 -	3909841 Rmet_3597		15.67	2.08	Op1000r_1	NA	Q1LHA7 Putative uncharacterized protein
5UTR_1299	3909842 -	3910329 Rmet_3597				Op1000r_1		
5UTR_1295	3910135 +	3910185 Rmet_3598				Op1001f_1		
NPKM_6366	3910185 +	3911760 Rmet_3598		4.33	1.15	Op1001f_1	NA	Q1LHA6 Flavin-containing monooxygenase FMO
NPKM_6367	3911837 +	3912728 Rmet_3599		3.33	0.58	Op1001f_1	NA	Q1LHA5 Short-chain dehydrogenase/reductase SDR
NPKM_6368	3912724 +	3913726 Rmet_3600		3.33	0.58	Op1001f_1	NA	Q1LHA4 Alpha/beta hydrolase fold
NPKM_6369	3913722 +	3914595 Rmet_3601		3.33	0.58	Op1001f_1	NA	Q1LHA3 FF domain protein
3UTR_1560	3914070 -	3914640 Rmet_3602				Op1002r_1		
3UTR_1556	3914596 +	3914805 Rmet_3601				Op1001f_1		

NPKM_6370	3914641 -	3915523 Rmet_3602		51.00	4.36	Op1002r_1	NA	Q1LHA2 Transcriptional regulator, MerR family
5UTR_1298	3915524 -	3916125 Rmet_3602				Op1002r_1		
NPKM_6371	3915540 +	3916479 Rmet_3603		34.67	1.15	Op1003f_1	NA	Q1LHA1 Transcriptional regulator, LysR family
NPKM_6372	3916543 +	3917614 Rmet_3604	bug	13.67	1.15	Op1003f_1	NA	Q1LHA0 Uncharacterized protein UPF0065
3UTR_1559	3917598 -	3918727 Rmet_3606				Op1004r_2		
NPKM_6373	3917631 +	3918606 Rmet_3605		15.67	0.58	Op1003f_1	NA	Q1LH99 Succinylglutamate desuccinylase/aspartoacylase
3UTR_1557	3918607 +	3919161 Rmet_3605				Op1003f_1		
NPKM_6374	3918728 -	3919328 Rmet_3606		30.00	1.00	Op1004r_2	NA	Q1LH98 Putative uncharacterized protein
NPKM_6375	3919508 -	3920075 Rmet_3607		50.33	2.52	Op1004r_2	NA	Q1LH97 Putative uncharacterized protein
NPKM_6376	3920134 -	3920731 Rmet_3608		73.00	6.00	Op1004r_2	NA	Q1LH96 Transcriptional regulator, TetR family
NPKM_6377	3920743 -	3921334 Rmet_3609		36.67	2.08	Op1004r_2	NA	Q1LH95 Putative uncharacterized protein
NPKM_6378	3921380 -	3922808 Rmet_3610	trmE	94.33	3.21	Op1004r_2	NA	Q1LH94 tRNA modification GTPase mnME
NPKM_6379	3922860 -	3923622 Rmet_3611		16.67	1.15	Op1004r_1	NA	Q1LH93 Putative uncharacterized protein
NPKM_6380	3923728 -	3924499 Rmet_3612	tam	24.33	1.15	Op1004r_1	NA	Q1LH92 Methyltransferase type 11
5UTR_1297	3924500 -	3924513 Rmet_3612	tam			Op1004r_1		
3UTR_1558	3924557 -	3924631 Rmet_3613	yidC			Op1004r_1		
NPKM_6381	3924632 -	3926300 Rmet_3613	yidC	438.67	10.41	Op1004r_1	GIP-PTL-Exp	Q1LH91 Inner membrane protein oxaA
NPKM_6382	3926322 -	3926613 Rmet_3614		460.00	15.52	Op1004r_1	NA	Q1LH90 UPF0161 protein Rmet_3614
NPKM_6383	3926621 -	3927779 Rmet_3615		1194.67	53.72	Op1004r_1	GIP-TL-Ass	Q1LH89 Ribonuclease P protein component
5UTR_1296	3927780 -	3928031 Rmet_3615				Op1004r_1		
Chromid (replicon CP000353)								
5UTR_127	204 +	833 Rmet_6605				Op1756f_1		
NPKM_1	833 +	929 Rmet_6605		8.00	2.65	Op1756f_1	NA	NA
NPKM_2	945 +	2040 Rmet_5817	repA	388.00	13.53	Op1756f_2	NA	Q1LB00 Plasmid encoded RepA protein
3UTR_1082	1041 -	2141 Rmet_5818	csp			Op1757r_1		
NPKM_3	2142 -	2346 Rmet_5818	csp	5961.00	437.68	Op1757r_1	NA	Q46Q97 Cold-shock DNA-binding protein family
5UTR_881	2347 -	3170 Rmet_5818	csp			Op1757r_1		
NPKM_4	2767 +	3424 Rmet_5819	para	100.00	1.73	Op1758f_1	DIV-Division	Q1LAZ8 Cobyrinic acid a,c-diamide synthase
3UTR_1081	3175 -	4512 Rmet_5821	xerD			Op1759r_1		
NPKM_5	3429 +	4446 Rmet_5820	parB	137.67	2.52	Op1758f_1	NA	Q1LAZ7 ParB family protein
3UTR_148	4447 +	6599 Rmet_5820	parB			Op1758f_1		
NPKM_6	4513 -	6094 Rmet_5821	xerD	48.00	2.65	Op1759r_1	NA	Q1LAZ6 Putative integrase/recombinase protein
5UTR_880	6095 -	6723 Rmet_5821	xerD			Op1759r_1		
5UTR_128	6916 +	7264 Rmet_5822				Op1760f_1		
NPKM_7	7264 +	10009 Rmet_5822		27.67	1.53	Op1760f_1	NA	Q1LAZ5 ATP-dependent transcriptional regulator, MalT-like, LuxR family
3UTR_1080	9618 -	10070 Rmet_5823	tauD			Op1761r_3		
3UTR_149	10010 +	10920 Rmet_5822				Op1760f_1		
NPKM_8	10071 -	10959 Rmet_5823	tauD	9.33	0.58	Op1761r_3	MET-OAA-Taur	Q1LAZ4 Taurine catabolism dioxygenase TauD/TfdA
NPKM_9	11004 -	11997 Rmet_5824	bug	3.00	0.00	Op1761r_2	NA	Q1LAZ3 Uncharacterized protein UPF0065
NPKM_10	12013 -	12910 Rmet_5825		3.00	1.00	Op1761r_2	MET-LIP-FASyn	Q1LAZ2 Short-chain dehydrogenase/reductase SDR
NPKM_11	12906 -	14091 Rmet_5826		1.33	0.58	Op1761r_1	NA	Q1LAZ1 Thiolase
NPKM_12	14158 -	15715 Rmet_5827		1.00	0.00	Op1761r_1	MET-LIP-FAMet	Q1LAZ0 AMP-dependent synthetase and ligase
5UTR_879	15716 -	15750 Rmet_5827				Op1761r_1		

5UTR_129	16077 +	16128 Rmet_5828	ycaC			Op1762f_1		
NPKM_13	16128 +	16806 Rmet_5828	ycaC	5.00	1.00	Op1762f_1	NA	Q1LAY9 Isochorismatase hydrolase
3UTR_1079	16650 -	16990 Rmet_5829	pstS1			Op1763r_1		
3UTR_150	16807 +	17161 Rmet_5828	ycaC			Op1762f_1		
NPKM_14	16991 -	17993 Rmet_5829	pstS1	8.33	0.58	Op1763r_1	EIP-TRA-ABC	Q1LAY8 Periplasmic phosphate binding protein
NPKM_15	18169 -	19339 Rmet_5830		13.67	0.58	Op1763r_1	NA	Q1LAY7 Putative uncharacterized protein
5UTR_878	19340 -	19376 Rmet_5830				Op1763r_1		
5UTR_130	19585 +	19627 Rmet_5831				Op1764f_1		
NPKM_16	19627 +	20458 Rmet_5831		4.00	1.00	Op1764f_1	NA	Q1LAY6 Transcriptional regulator, LuxR family
3UTR_151	20459 +	20514 Rmet_5831				Op1764f_1		
NPKM_17	20612 +	21206 Rmet_5832		2.33	0.58	Op1764f_1	NA	Q1LAY5 Response regulator receiver domain protein (CheY-like)
NPKM_18	21301 +	21580 Rmet_5833		11.33	0.58	Op1764f_2	NA	Q1LAY4 Putative uncharacterized protein
3UTR_152	21581 +	21810 Rmet_5833				Op1764f_2		
5UTR_131	21822 +	21862 Rmet_6606				Op1764f_2		
NPKM_19	21862 +	21937 Rmet_6606		2.00	1.00	Op1764f_2	NA	NA
NPKM_20	21933 +	22614 Rmet_5834		0.33	0.58	Op1764f_2	NA	Q1LAY3 Phosphoesterase, PA-phosphatase related
NPKM_21	22529 +	22805 Rmet_6607		0.67	0.58	Op1764f_2	NA	NA
NPKM_22	22726 +	24133 Rmet_5835		0.67	0.58	Op1764f_2	NA	Q1LAY2 Sugar transferase
NPKM_23	24258 +	24510 Rmet_5836		1.33	0.58	Op1764f_2	NA	Q1LAY1 Phosphopantetheine-binding
NPKM_24	24506 +	25709 Rmet_5837		1.00	0.00	Op1764f_2	MET-CAH-Prop	Q1LAY0 Acyl-CoA dehydrogenase-like protein
NPKM_25	25720 +	26686 Rmet_5838		2.00	0.00	Op1764f_2	NA	Q1LAX9 Putative uncharacterized protein
NPKM_26	26686 +	27670 Rmet_5839		2.33	0.58	Op1764f_2	NA	Q1LAX8 Putative uncharacterized protein
NPKM_27	27666 +	30237 Rmet_5840		3.33	0.58	Op1764f_2	MET-Nglyc	Q1LAX7 Glycoside hydrolase family 2, immunoglobulin-like beta-sandwich
3UTR_153	30238 +	30256 Rmet_5840				Op1764f_2		
5UTR_132	30621 +	30635 Rmet_5841				Op1764f_3		
NPKM_28	30635 +	31364 Rmet_5841		7.00	1.00	Op1764f_3	NA	Q1LAX6 Transcriptional regulator, Crp/Fnr family
3UTR_154	31365 +	31460 Rmet_5841				Op1764f_3		
NPKM_29	31444 -	32497 Rmet_5842		0.67	0.58	Op1765r_1	NA	Q1LAX5 Putative uncharacterized protein
5UTR_877	32498 -	32499 Rmet_5842				Op1765r_1		
5UTR_133	32788 +	32871 Rmet_5843	manC			Op1766f_1		
NPKM_30	32871 +	34368 Rmet_5843	manC	2.00	0.00	Op1766f_1	MET-CAH-FruMan	Q1LAX4 Mannose-1-phosphate guanylyltransferase (GDP)
NPKM_31	34429 +	36772 Rmet_5844	epsB1	2.00	0.00	Op1766f_1	NA	Q1LAX3 Lipopolysaccharide biosynthesis
NPKM_32	36879 +	38727 Rmet_5845		1.33	0.58	Op1766f_1	NA	Q1LAX2 Putative uncharacterized protein
5UTR_134	38754 +	38778 Rmet_5846				Op1766f_1		
NPKM_33	38778 +	40389 Rmet_5846		0.67	0.58	Op1766f_1	NA	Q1LAX1 Putative uncharacterized protein
3UTR_1078	39951 -	40408 Rmet_5847				Op1767r_1		
3UTR_155	40390 +	40392 Rmet_5846				Op1766f_1		
NPKM_34	40409 -	41255 Rmet_5847		16.00	1.00	Op1767r_1	NA	Q1LAX0 Short-chain dehydrogenase/reductase SDR
5UTR_876	41256 -	41257 Rmet_5847				Op1767r_1		
5UTR_135	41369 +	41435 Rmet_5848				Op1768f_1		
NPKM_35	41435 +	42629 Rmet_5848		7.00	0.00	Op1768f_1	NA	Q1LAW9 Putative uncharacterized protein
3UTR_156	42630 +	42661 Rmet_5848				Op1768f_1		
3UTR_1077	42696 -	42709 Rmet_5849	epsB			Op1769r_2		

NPKM_36	42710 -	44957 Rmet_5849	<i>epsB</i>	2.00	0.00	Op1769r_2	NA	Q1LAW8 Exopolysaccharide transport protein
NPKM_37	44956 -	45451 Rmet_5850	<i>epsP</i>	0.00	0.00	Op1769r_1	NA	Q1LAW7 Protein tyrosine phosphatase
NPKM_38	45454 -	46543 Rmet_5851	<i>epsA</i>	0.00	0.00	Op1769r_1	EIP-TRA-Pores	Q1LAW6 Polysaccharide export protein
5UTR_136	46853 +	46880 Rmet_5852				Op1770f_1		
NPKM_39	46880 +	47642 Rmet_5852		1.00	0.00	Op1770f_1	NA	Q1LAW5 Putative uncharacterized protein
3UTR_1076	47594 -	47675 Rmet_5853				Op1771r_3		
3UTR_157	47643 +	47768 Rmet_5852				Op1770f_1		
NPKM_40	47676 -	48909 Rmet_5853		1.67	0.58	Op1771r_3	NA	Q1LAW4 Glycosyl transferase, group 1
NPKM_41	48905 -	50051 Rmet_5854		1.67	0.58	Op1771r_3	NA	Q1LAW3 Glycosyl transferase, group 1
NPKM_42	50094 -	50715 Rmet_5855	<i>wcaF</i>	0.67	0.58	Op1771r_2	NA	Q1LAW2 Transferase hexapeptide repeat
3UTR_1075	50853 -	50856 Rmet_5856	<i>wcaI</i>			Op1771r_2		
NPKM_43	50857 -	52120 Rmet_5856	<i>wcaI</i>	2.33	0.58	Op1771r_2	NA	Q1LAW1 Glycosyl transferase, group 1
NPKM_44	52210 -	52381 Rmet_6608		0.00	0.00	Op1771r_1	NA	NA
NPKM_45	52442 +	53846 Rmet_5857		1.67	0.58	Op1772f_1	NA	Q1LAW0 Putative uncharacterized protein
3UTR_158	53847 +	53907 Rmet_5857				Op1772f_1		
3UTR_1074	53931 -	53977 Rmet_5858				Op1773r_3		
NPKM_46	53978 -	55418 Rmet_5858		0.00	0.00	Op1773r_3	NA	Q1LAV9 Putative uncharacterized protein
NPKM_47	55456 -	56458 Rmet_5859	<i>wcaG</i>	1.67	0.58	Op1773r_3	MET-CAH-FruMan	Q1LAV8 NAD-dependent epimerase/dehydratase
NPKM_48	56441 -	57647 Rmet_5860	<i>gmd</i>	2.00	0.00	Op1773r_3	MET-CAH-FruMan	Q1LAV7 GDP-mannose 4,6-dehydratase
5UTR_875	57648 -	57714 Rmet_5860	<i>gmd</i>			Op1773r_3		
3UTR_1073	57733 -	57825 Rmet_5861				Op1773r_3		
NPKM_49	57826 -	58756 Rmet_5861		46.33	2.08	Op1773r_3	NA	Q1LAV6 Transcriptional regulator, LuxR family
5UTR_137	59231 +	60865 Rmet_5864	<i>cynS</i>			Op1774f_1		
NPKM_50	59295 -	59502 Rmet_6609		9.67	1.53	Op1773r_2	NA	NA
NPKM_51	59564 -	59873 Rmet_5862		16.00	3.61	Op1773r_2	NA	Q1LAV5 Putative signal peptide protein
NPKM_52	59935 -	60067 Rmet_6610		6.67	2.89	Op1773r_1	NA	NA
5UTR_874	60068 -	60097 Rmet_6610				Op1773r_1		
3UTR_1072	60230 -	60290 Rmet_5863				Op1773r_1		
NPKM_53	60291 -	60825 Rmet_5863		9.67	0.58	Op1773r_1	NA	Q1LAV4 Putative uncharacterized protein
NPKM_54	60865 +	61267 Rmet_5864	<i>cynS</i>	41.67	5.03	Op1774f_1	MET-EN-Nitrog	Q1LAV3 Cyanate lyase
NPKM_55	61345 -	61510 Rmet_5865		87.67	5.86	Op1775r_1	NA	Q1LAV2 Putative uncharacterized protein
5UTR_873	61511 -	61749 Rmet_5865				Op1775r_1		
NPKM_56	61849 +	62632 Rmet_5866		16.67	2.31	Op1776f_1	NA	Q1LAV1 Phosphoribosyltransferase
3UTR_1071	62235 -	62641 Rmet_5867	<i>leuD</i>			Op1777r_1		
3UTR_159	62633 +	63713 Rmet_5866				Op1776f_1		
NPKM_57	62642 -	63155 Rmet_5867	<i>leuD</i>	21.33	0.58	Op1777r_1	MET-AA-ValLeulle	Q1LAV0 3-isopropylmalate dehydratase, small subunit
NPKM_58	63151 -	64474 Rmet_5868	<i>leuC</i>	38.33	1.53	Op1777r_1	MET-AA-ValLeulle	Q1LAU9 3-isopropylmalate dehydratase, large subunit
NPKM_59	64470 -	65511 Rmet_5869	<i>bug</i>	66.33	2.31	Op1777r_1	NA	Q1LAU8 Uncharacterized protein UPF0065
NPKM_60	65611 -	66394 Rmet_5870		135.67	6.66	Op1777r_1	NA	Q1LAU7 Transcriptional regulator, GntR family
5UTR_872	66395 -	66513 Rmet_5870				Op1777r_1		
5UTR_138	66685 +	67093 Rmet_5871				Op1778f_1		
NPKM_61	67093 +	68575 Rmet_5871		5.33	0.58	Op1778f_1	NA	Q1LAU6 Putative glycin-rich signal peptide protein
NPKM_62	68767 +	69229 Rmet_5872		3.33	0.58	Op1778f_1	NA	Q1LAU5 Conserved hypothetical signal peptide protein

NPKM_63	69225 +	69924 Rmet_5873		1.67	0.58	Op1778f_1	NA	Q1LAU4 Peptidase C39, bacteriocin processing
NPKM_64	69937 +	71077 Rmet_5874		1.33	0.58	Op1778f_1	NA	Q1LAU3 Putative uncharacterized protein
3UTR_160	71078 +	71109 Rmet_5874				Op1778f_1		
NPKM_65	71185 +	72658 Rmet_5875		2.33	0.58	Op1778f_1	NA	Q1LAU2 Putative uncharacterized protein
3UTR_161	72659 +	72765 Rmet_5875				Op1778f_1		
5UTR_139	72804 +	72826 Rmet_5876				Op1778f_2		
NPKM_66	72826 +	73339 Rmet_5876		32.33	1.53	Op1778f_2	NA	Q1LAU1 Putative transmembrane protein
NPKM_67	73622 +	74762 Rmet_5877		236.33	7.23	Op1778f_3	NA	Q1LAU0 Extracellular ligand-binding receptor
NPKM_68	74792 +	75572 Rmet_5878		127.33	3.21	Op1778f_3	NA	Q1LAT9 Short-chain dehydrogenase/reductase SDR
3UTR_1070	75008 -	75593 Rmet_5879				Op1779r_1		
3UTR_162	75573 +	76282 Rmet_5878				Op1778f_3		
NPKM_69	75594 -	76494 Rmet_5879		13.67	0.58	Op1779r_1	NA	Q1LAT8 Transcriptional regulator, LysR family
5UTR_140	76534 +	76578 Rmet_5880				Op1780f_1		
NPKM_70	76578 +	77979 Rmet_5880		8.33	0.58	Op1780f_1	NA	Q1LAT7 Putative uncharacterized protein
NPKM_71	77991 +	78336 Rmet_5881		4.33	0.58	Op1780f_1	NA	Q1LAT6 Putative uncharacterized protein
NPKM_72	78378 +	79365 Rmet_5882	bug	14.33	1.15	Op1780f_2	NA	Q1LAT5 Uncharacterized protein UPF0065
3UTR_1069	78915 -	80293 Rmet_5884				Op1781r_1		
NPKM_73	79484 +	80234 Rmet_5883		19.67	1.15	Op1780f_2	NA	Q1LAT4 Twin-arginine translocation pathway signal
3UTR_163	80235 +	80466 Rmet_5883				Op1780f_2		
NPKM_74	80294 -	80684 Rmet_5884		179.67	4.04	Op1781r_1	NA	Q1LAT3 GCN5-related N-acetyltransferase
5UTR_871	80685 -	80795 Rmet_5884				Op1781r_1		
5UTR_141	80844 +	80910 Rmet_5885	amn			Op1782f_1		
NPKM_75	80910 +	82401 Rmet_5885	amn	69.33	0.58	Op1782f_1	MET-NUC-Pur	Q1LAT2 AMP nucleosidase
3UTR_164	82402 +	83308 Rmet_5885	amn			Op1782f_1		
3UTR_1068	82463 -	82526 Rmet_5886				Op1783r_1		
NPKM_76	82527 -	83265 Rmet_5886		25.00	2.65	Op1783r_1	NA	Q1LAT1 OmpW
NPKM_77	83540 -	85244 Rmet_5887	leuA1	51.33	4.16	Op1783r_1	MET-CAH-Pyr	Q1LAT0 2-isopropylmalate synthase
NPKM_78	85346 -	85496 Rmet_6611		256.00	9.54	Op1783r_1	NA	NA
5UTR_870	85497 -	85518 Rmet_6611				Op1783r_1		
5UTR_142	85614 +	85768 Rmet_5888				Op1784f_1		
NPKM_79	85768 +	87154 Rmet_5888		3.00	0.00	Op1784f_1	NA	Q1LAS9 Putative uncharacterized protein
3UTR_1067	87124 -	87127 Rmet_6612				Op1785r_2		
NPKM_80	87128 -	87431 Rmet_6612		4.00	1.00	Op1785r_2	NA	NA
3UTR_165	87155 +	87159 Rmet_5888				Op1784f_1		
NPKM_81	87446 -	87767 Rmet_5889		54.67	1.53	Op1785r_2	NA	Q1LAS8 Putative transmembrane protein
NPKM_82	87782 -	89645 Rmet_5890	feoB	58.00	1.00	Op1785r_2	EIP-TRA-Ion	Q1LAS7 Ferrous iron transport protein B
NPKM_83	89668 -	89971 Rmet_5891	feoA	65.67	3.06	Op1785r_2	EIP-TRA-Ion	Q1LAS6 FeoA
NPKM_84	90309 -	91203 Rmet_5892		11.67	1.15	Op1785r_1	NA	Q1LAS5 Transcriptional regulator, LysR family
5UTR_869	91204 -	91243 Rmet_5892				Op1785r_1		
5UTR_143	91329 +	91346 Rmet_5893				Op1786f_1		
NPKM_85	91346 +	93143 Rmet_5893		4.67	0.58	Op1786f_1	NA	Q1LAS4 Acyl-CoA dehydrogenase-like protein
NPKM_86	93174 +	94251 Rmet_5894	bug	10.67	1.15	Op1786f_2	NA	Q1LAS3 Uncharacterized protein UPF0065
NPKM_87	94274 +	95414 Rmet_5895		91.33	6.35	Op1786f_3	NA	Q1LAS2 L-carnitine dehydratase/bile acid-inducible protein F

3UTR_1066	95376 -	95487 Rmet_5896				Op1787r_1		
3UTR_166	95415 +	96452 Rmet_5895				Op1786f_3		
NPKM_88	95488 -	97189 Rmet_5896		1.33	0.58	Op1787r_1	EIP-TRA-Ion	Q1LAS1 L-lactate transport
5UTR_868	97190 -	97209 Rmet_5896				Op1787r_1		
NPKM_89	97247 -	98693 Rmet_5897		1.33	0.58	Op1787r_1	NA	Q1LAS0 Iron-sulfur cluster binding protein
NPKM_90	98689 -	99400 Rmet_5898		2.67	0.58	Op1787r_1	NA	Q1LAR9 Putative uncharacterized protein
NPKM_91	99396 -	100182 Rmet_5899		2.33	0.58	Op1787r_1	NA	Q1LAR8 Putative uncharacterized protein
3UTR_1065	100191 -	101088 Rmet_5901				Op1789r_1		
5UTR_144	100193 +	100319 Rmet_5900				Op1788f_1		
NPKM_92	100319 +	101018 Rmet_5900		20.33	0.58	Op1788f_1	NA	Q1LAR7 Transcriptional regulator, GntR family
3UTR_167	101019 +	101148 Rmet_5900				Op1788f_1		
NPKM_93	101089 -	102184 Rmet_5901		34.67	1.15	Op1789r_1	NA	Q1LAR6 Membrane protein, putative
5UTR_145	102224 +	102386 Rmet_5902	<i>eutB</i>			Op1790f_1		
NPKM_94	102386 +	103769 Rmet_5902	<i>eutB</i>	5.00	0.00	Op1790f_1	MET-LIP-GlycPLip	Q1LAR5 Ethanolamine ammonia-lyase heavy chain
NPKM_95	103786 +	104557 Rmet_5903	<i>eutC</i>	4.67	0.58	Op1790f_1	MET-LIP-GlycPLip	Q1LAR4 Ethanolamine ammonia-lyase light chain
3UTR_1064	104547 -	104574 Rmet_5904				Op1791r_1		
3UTR_168	104558 +	104727 Rmet_5903	<i>eutC</i>			Op1790f_1		
NPKM_96	104575 -	105049 Rmet_5904		21.00	1.73	Op1791r_1	NA	Q1LAR3 YbaK/prolyl-tRNA synthetase associated region
NPKM_97	105083 -	106037 Rmet_5905		21.33	2.52	Op1791r_1	NA	Q1LAR2 Transcriptional regulator, LysR family
NPKM_98	106121 -	107435 Rmet_5906	<i>kgtP</i>	63.00	2.00	Op1791r_1	NA	Q1LAR1 Metabolite
5UTR_146	107831 +	107832 Rmet_5907				Op1792f_1		
NPKM_99	107832 +	108156 Rmet_5907		22.67	1.53	Op1792f_1	NA	Q1LAR0 Putative uncharacterized protein
NPKM_100	108282 +	109440 Rmet_5908		83.00	6.24	Op1792f_2	MET-XEN-Others	Q1LAQ9 Acyl-CoA dehydrogenase-like protein
NPKM_101	109500 +	110076 Rmet_5909		201.00	19.97	Op1792f_3	NA	Q1LAQ8 Putative uncharacterized protein
NPKM_102	109955 +	110264 Rmet_6613		86.33	6.66	Op1792f_3	NA	NA
NPKM_103	110234 -	110606 Rmet_5910		394.00	39.66	Op1793r_2	NA	Q1LAQ7 Putative uncharacterized protein
NPKM_104	110565 +	110649 Rmet_6614		0.67	0.58	Op2058f_1	NA	NA
3UTR_169	110650 +	110690 Rmet_6614				Op2058f_1		
NPKM_105	110711 -	113585 Rmet_5911		14.00	1.00	Op1793r_1	NA	Q1LAQ6 Peptidase M16-like protein
5UTR_867	113586 -	113609 Rmet_5911				Op1793r_1		
5UTR_147	113723 +	113773 Rmet_5912				Op1794f_1		
NPKM_106	113773 +	115276 Rmet_5912		18.00	1.73	Op1794f_1	NA	Q1LAQ5 Transcriptional regulator Ada / DNA-3-methyladenine glycosylase II / DNA-
NPKM_107	115272 +	115821 Rmet_5913	<i>ogt3</i>	19.33	1.53	Op1794f_1	GIP-REP-Recomb	Q1LAQ4 Methylated-DNA--protein-cysteine methyltransferase
NPKM_108	115838 +	116405 Rmet_5914	<i>ligT</i>	16.00	1.00	Op1794f_1	GIP-TL-Ass	Q1LAQ3 2',5' RNA ligase
3UTR_1063	115869 -	116536 Rmet_5915				Op1795r_1		
3UTR_170	116406 +	116476 Rmet_5914	<i>ligT</i>			Op1794f_1		
NPKM_109	116537 -	117152 Rmet_5915		3.33	1.15	Op1795r_1	NA	Q1LAQ2 Lysine exporter protein (LYSE/YGGA)
5UTR_866	117153 -	117187 Rmet_5915				Op1795r_1		
5UTR_148	117273 +	117299 Rmet_5916				Op1796f_1		
NPKM_110	117299 +	118160 Rmet_5916		23.00	1.00	Op1796f_1	NA	Q1LAQ1 Transcriptional regulator, LysR family
3UTR_171	118161 +	118282 Rmet_5916				Op1796f_1		
5UTR_149	118288 +	118406 Rmet_5917				Op1796f_2		
NPKM_111	118406 +	119201 Rmet_5917		103.67	4.73	Op1796f_2	NA	Q1LAQ0 YcgR

3UTR_1062	118406 -	119258 Rmet_5918				Op1797r_2			
3UTR_172	119202 +	120176 Rmet_5917				Op1796f_2			
NPKM_112	119259 -	120156 Rmet_5918	70.00	1.00		Op1797r_2	NA	Q1LAP9	Transcriptional regulator, IclR family
5UTR_150	120325 +	122736 Rmet_5920				Op1798f_1			
NPKM_113	120409 -	122662 Rmet_5919	8.33	1.53		Op1797r_1	NA	Q1LAP8	Patatin
5UTR_865	122663 -	122788 Rmet_5919				Op1797r_1			
NPKM_114	122736 +	123123 Rmet_5920	28.00	1.73		Op1798f_1	NA	Q1LAP7	Putative uncharacterized protein
NPKM_115	123119 +	123953 Rmet_5921	58.00	2.65		Op1798f_2	NA	Q1LAP6	Silent information regulator protein Sir2
NPKM_116	124196 +	125093 Rmet_5922	6.00	1.00		Op1798f_2	NA	Q1LAP5	Putative uncharacterized protein
3UTR_1061	124254 -	125088 Rmet_5923				Op1799r_1			
NPKM_117	125089 -	125671 Rmet_5923	53.33	5.51		Op1799r_1	NA	Q1LAP4	Putative transmembrane protein
3UTR_173	125094 +	125549 Rmet_5922				Op1798f_2			
NPKM_118	125762 -	125966 Rmet_5924	34.67	5.86		Op1799r_1	NA	Q1LAP3	SlyX
NPKM_119	126057 -	126486 Rmet_5925	149.67	8.74		Op1799r_1	NA	Q1LAP2	3-demethylubiquinone-9 3-methyltransferase
5UTR_864	126487 -	126545 Rmet_5925				Op1799r_1			
5UTR_151	126613 +	126775 Rmet_5926				Op1800f_1			
NPKM_120	126775 +	128101 Rmet_5926	556.67	10.41		Op1800f_1	MET-AA-AlaAsp	Q1LAP1	Argininosuccinate synthase
3UTR_174	128102 +	128139 Rmet_5926				Op1800f_1			
5UTR_152	128179 +	128253 Rmet_5927				Op1800f_1			
NPKM_121	128253 +	129279 Rmet_5927	98.00	2.65		Op1800f_1	NA	Q1LAP0	Aldo/keto reductase
NPKM_122	129505 +	132574 Rmet_5928	16.00	1.00		Op1800f_1	NA	Q1LAN9	Putative transmembrane protein
3UTR_1060	131802 -	132626 Rmet_5929				Op1801r_2			
3UTR_175	132575 +	132825 Rmet_5928				Op1800f_1			
NPKM_123	132627 -	132879 Rmet_5929	84.00	5.29		Op1801r_2	NA	Q1LAN8	Transglycosylase-associated protein
NPKM_124	132980 -	135089 Rmet_5930	74.67	0.58		Op1801r_2	NA	Q1LAN7	Elongation factor G 2
NPKM_125	135192 -	136092 Rmet_5931	8.67	0.58		Op1801r_1	NA	Q1LAN6	Polysaccharide deacetylase
NPKM_126	136294 -	136612 Rmet_5932	12.33	1.15		Op1801r_1	NA	Q1LAN5	Putative uncharacterized protein
5UTR_153	136603 +	136636 Rmet_5933				Op1802f_1			
5UTR_863	136613 -	137199 Rmet_5932				Op1801r_1			
NPKM_127	136636 +	137380 Rmet_5933	22.33	1.53		Op1802f_1	NA	Q1LAN4	Putative uncharacterized protein
3UTR_1059	137222 -	137385 Rmet_5934				Op1803r_1			
3UTR_176	137381 +	138144 Rmet_5933				Op1802f_1			
NPKM_128	137386 -	138127 Rmet_5934	25.00	1.00		Op1803r_1	NA	Q1LAN3	Putative uncharacterized protein
5UTR_862	138128 -	138206 Rmet_5934				Op1803r_1			
5UTR_154	138171 +	138283 Rmet_5935				Op1804f_1			
NPKM_129	138283 +	139846 Rmet_5935	10.33	0.58		Op1804f_1	DIV-MOT-Chemotax	Q1LAN2	Methyl-accepting chemotaxis sensory transducer
3UTR_1058	139137 -	139882 Rmet_5936				Op1805r_3			
3UTR_177	139847 +	141543 Rmet_5935				Op1804f_1			
NPKM_130	139883 -	140915 Rmet_5936	30.00	2.65		Op1805r_3	NA	Q1LAN1	Luciferase-like protein
NPKM_131	141044 -	143852 Rmet_5937	8.00	0.00		Op1805r_2	NA	Q1LAN0	Putative uncharacterized protein
NPKM_132	143939 -	144914 Rmet_5938	54.00	1.00		Op1805r_2	NA	Q1LAM9	Rhodanese-like protein
5UTR_861	144915 -	144940 Rmet_5938				Op1805r_2			
3UTR_1057	144971 -	145040 Rmet_5939				Op1805r_1			

NPKM_133	145041 -	145458 Rmet_5939		3.33	1.15	Op1805r_1	NA	Q1LAM8 Hpt domain protein
NPKM_134	145454 -	146117 Rmet_5940		4.00	0.00	Op1805r_1	EIP-SIG-2Comp	Q1LAM7 Two component transcriptional regulator, LuxR family
5UTR_860	146118 -	146230 Rmet_5940				Op1805r_1		
3UTR_1056	146288 -	146401 Rmet_5941				Op1805r_1		
NPKM_135	146402 -	147080 Rmet_5941		10.00	1.73	Op1805r_1	NA	Q1LAM6 Putative uncharacterized protein
NPKM_136	147613 -	148003 Rmet_3616		106.00	4.58	Op1005r_1	GIP-PTL-Fold	Q1LH88 OsmC-like protein
5UTR_859	148004 -	148063 Rmet_3616				Op1005r_1		
NPKM_137	148292 +	148493 Rmet_6615		0.00	0.00	Op1006f_1	NA	NA
3UTR_178	148494 +	148546 Rmet_6615				Op1006f_1		
NPKM_138	148594 +	150121 Rmet_R0070		0.00	0.00	Op1006f_1	NA	NA
NPKM_139	150185 +	150262 Rmet_R0071	<i>tRNA-I</i>	0.00	0.00	Op1006f_1	NA	NA
NPKM_140	150273 +	150349 Rmet_R0072	<i>tRNA-A</i>	0.00	0.00	Op1006f_1	NA	NA
NPKM_141	150631 +	153449 Rmet_R0073		0.00	0.00	Op1006f_1	NA	NA
NPKM_142	153628 +	153742 Rmet_R0074		0.00	0.00	Op1006f_1	NA	NA
5UTR_155	153770 +	153881 Rmet_3617				Op1006f_2		
NPKM_143	153881 +	154178 Rmet_3617		212.33	46.31	Op1006f_2	GIP-REP-Recomb	Q1LH87 Excinuclease ABC, C subunit-like protein
3UTR_1055	154198 -	154230 Rmet_3618	<i>ohrB</i>			Op1007r_3		
NPKM_144	154231 -	154654 Rmet_3618	<i>ohrB</i>	249.33	10.07	Op1007r_3	NA	Q1LH86 OsmC-like protein
NPKM_145	154715 -	155204 Rmet_3619	<i>ohrR</i>	21.00	1.73	Op1007r_2	NA	Q1LH85 Transcriptional regulator, MarR family
NPKM_146	155207 -	155309 Rmet_6616		5.33	1.53	Op1007r_1	NA	NA
NPKM_147	155449 +	156913 Rmet_3620	<i>degP</i>	55.33	6.81	Op1008f_1	NA	Q1LH84 Peptidase S1C, Do
NPKM_148	157138 +	157462 Rmet_3621		284.67	8.74	Op1008f_2	NA	Q1LH83 Putative uncharacterized protein
3UTR_179	157463 +	159661 Rmet_3621				Op1008f_2		
NPKM_149	157586 -	159164 Rmet_3622		29.33	4.93	Op1009r_1	NA	Q1LH82 Major facilitator superfamily MFS_1
NPKM_150	159160 -	159658 Rmet_3623		40.33	6.11	Op1009r_1	NA	Q1LH81 Transcriptional regulator, MarR family
NPKM_151	159744 -	161760 Rmet_3624		78.67	12.66	Op1009r_1	NA	Q1LH80 Transglutaminase-like protein
NPKM_152	161756 -	162707 Rmet_3625		120.33	21.46	Op1009r_1	NA	Q1LH79 Putative uncharacterized protein
5UTR_156	162145 +	163974 Rmet_3627				Op1010f_1		
NPKM_153	162794 -	163721 Rmet_3626	<i>moxR</i>	191.67	25.89	Op1009r_1	NA	Q1LH78 ATPase associated with various cellular activities, AAA_3
NPKM_154	163974 +	164820 Rmet_3627		122.00	3.61	Op1010f_1	NA	Q1LH77 Phytanoyl-CoA dioxygenase
3UTR_180	164821 +	164924 Rmet_3627				Op1010f_1		
NPKM_155	164923 -	165106 Rmet_3628		848.33	133.29	Op1011r_3	NA	Q1LH76 Putative uncharacterized protein
NPKM_156	165315 -	166056 Rmet_3629		111.67	0.58	Op1011r_2	NA	Q1LH75 Transcriptional regulator, GntR family
NPKM_157	166188 -	167193 Rmet_3630		4.33	0.58	Op1011r_1	NA	Q1LH74 Oxidoreductase FAD/NAD(P)-binding
NPKM_158	167210 -	167690 Rmet_3631		3.33	1.15	Op1011r_1	NA	Q1LH73 Putative uncharacterized protein
NPKM_159	167714 -	169163 Rmet_3632		3.33	0.58	Op1011r_1	MET-CAH-FbP	Q1LH72 Aldehyde dehydrogenase
NPKM_160	169238 -	169955 Rmet_3633		5.00	1.00	Op1011r_1	NA	Q1LH71 TENA/THI-4 protein
5UTR_157	169382 +	171132 Rmet_6617				Op1012f_1		
5UTR_858	169956 -	169973 Rmet_3633				Op1011r_1		
3UTR_1054	170089 -	170103 Rmet_3634				Op1011r_1		
NPKM_161	170104 -	171082 Rmet_3634		3.67	0.58	Op1011r_1	MET-AA-ArgPro	Q1LH70 Ornithine cyclodeaminase
NPKM_162	171132 +	171318 Rmet_6617		2.67	1.53	Op1012f_1	NA	NA
NPKM_163	171302 +	172841 Rmet_3635		9.33	1.53	Op1012f_2	NA	Q1LH69 Putative membrane protein

NPKM_164	172893 +	173196 Rmet_3636	<i>fdx</i>	10.33	0.58	Op1012f_2	NA	Q1LH68 Ferredoxin
NPKM_165	173235 +	173556 Rmet_3637		11.67	0.58	Op1012f_2	NA	Q1LH67 Putative uncharacterized protein
3UTR_1053	173429 -	173939 Rmet_3639				Op1013r_1		
NPKM_166	173552 +	173912 Rmet_3638		13.00	1.00	Op1012f_2	NA	Q1LH66 Ferredoxin
3UTR_181	173913 +	174206 Rmet_3638				Op1012f_2		
NPKM_167	173940 -	174852 Rmet_3639		73.33	3.21	Op1013r_1	NA	Q1LH65 Transcriptional regulator, IclR family
5UTR_857	174853 -	174868 Rmet_3639				Op1013r_1		
5UTR_158	174905 +	175022 Rmet_3640				Op1014f_1		
NPKM_168	175022 +	175889 Rmet_3640		98.33	3.79	Op1014f_1	NA	Q1LH64 Transcriptional regulator, LysR family
3UTR_1052	175375 -	175959 Rmet_3641				Op1015r_1		
NPKM_169	175960 -	176233 Rmet_3641		46.00	1.73	Op1015r_1	NA	Q1LH63 Putative uncharacterized protein
NPKM_170	176445 -	177054 Rmet_3642		80.67	3.06	Op1015r_1	NA	Q1LH62 Putative uncharacterized protein
5UTR_856	177055 -	177145 Rmet_3642				Op1015r_1		
NPKM_171	177146 +	177656 Rmet_3643		55.33	6.11	Op1016f_1	NA	Q1LH61 Transcriptional regulator, MarR family
3UTR_1051	177170 -	178630 Rmet_3645				Op1017r_2		
NPKM_172	177815 +	178556 Rmet_3644		21.33	2.52	Op1016f_1	NA	Q1LH60 17 kDa surface antigen
3UTR_182	178557 +	179171 Rmet_3644				Op1016f_1		
NPKM_173	178631 -	179342 Rmet_3645		231.33	12.86	Op1017r_2	MET-XEN-Hex	Q1LH59 Dienelactone hydrolase
NPKM_174	179529 -	179949 Rmet_3646		19.33	1.53	Op1017r_1	NA	Q1LH58 Putative signal peptide protein
5UTR_855	179950 -	180010 Rmet_3646				Op1017r_1		
5UTR_159	180164 +	180254 Rmet_3647				Op1018f_1		
NPKM_175	180254 +	180461 Rmet_3647		23.33	0.58	Op1018f_1	NA	Q1LH57 Putative uncharacterized protein
3UTR_183	180462 +	181942 Rmet_3647				Op1018f_1		
NPKM_176	180512 -	182189 Rmet_3648		0.00	0.00	Op1019r_1	NA	Q1LH56 Putative activation/secretion signal peptide protein
NPKM_177	182340 -	183924 Rmet_3649		0.33	0.58	Op1019r_1	NA	Q1LH55 Putative uncharacterized protein
5UTR_160	184331 +	184429 Rmet_3650				Op1020f_1		
NPKM_178	184429 +	185659 Rmet_3650		2.67	1.53	Op1020f_1	NA	Q1LH54 Putative hemagglutinin-related transmembrane protein
3UTR_184	185660 +	185739 Rmet_3650				Op1020f_1		
5UTR_161	185795 +	185810 Rmet_6618				Op1020f_1		
NPKM_179	185810 +	185984 Rmet_6618		1.00	0.00	Op1020f_1	NA	NA
NPKM_180	186103 +	186295 Rmet_3651	<i>pilA</i>	101.33	14.57	Op1020f_2	GIP-PTL-T2S	Q1LH53 FliP/Fap pilin component
NPKM_181	186632 +	187094 Rmet_3652		6.33	1.53	Op1020f_2	NA	Q1LH52 TadE-like protein
3UTR_185	187095 +	187097 Rmet_3652				Op1020f_2		
5UTR_162	187116 +	187168 Rmet_3653	<i>cpaB</i>			Op1020f_2		
NPKM_182	187168 +	188128 Rmet_3653	<i>cpaB</i>	3.67	0.58	Op1020f_2	GIP-PTL-T2S	Q1LH51 FliP pilus assembly CpaB
NPKM_183	188141 +	189563 Rmet_3654	<i>cpaC</i>	4.00	1.00	Op1020f_2	GIP-PTL-T2S	Q1LH50 Type II and III secretion system protein
NPKM_184	189574 +	190813 Rmet_3655	<i>cpaE2</i>	3.33	0.58	Op1020f_2	GIP-PTL-T2S	Q1LH49 Response regulator receiver domain protein (CheY-like)
NPKM_185	190814 +	192131 Rmet_3656	<i>tadA</i>	5.33	0.58	Op1020f_2	GIP-PTL-T2S	Q1LH48 Type II secretion system protein E
NPKM_186	192120 +	193050 Rmet_3657	<i>tadB</i>	3.00	0.00	Op1020f_2	NA	Q1LH47 Type II secretion system protein
NPKM_187	193059 +	194169 Rmet_3658	<i>tadC</i>	3.33	0.58	Op1020f_2	NA	Q1LH46 Type II secretion system protein
NPKM_188	194169 +	194991 Rmet_3659	<i>tadD</i>	5.67	1.15	Op1020f_2	NA	Q1LH45 TPR repeat
NPKM_189	194987 +	195356 Rmet_3660		6.33	1.15	Op1020f_2	NA	Q1LH44 Putative lipoprotein
NPKM_190	195364 +	197092 Rmet_3661		6.00	0.00	Op1020f_2	NA	Q1LH43 Putative transmembrane protein

NPKM_191	197103 +	198468 Rmet_3662		5.33	0.58	Op1020f_2	NA	Q1LH42 Sigma54 specific transcriptional regulator, Fis family
3UTR_186	198469 +	198480 Rmet_3662				Op1020f_2		
5UTR_163	198494 +	198564 Rmet_3663	<i>sbcD</i>			Op1020f_3		
NPKM_192	198564 +	199710 Rmet_3663	<i>sbcD</i>	22.00	1.00	Op1020f_3	GIP-REP-Recomb	Q1LH41 Exodeoxyribonuclease I subunit D
NPKM_193	199706 +	202760 Rmet_3664	<i>sbcC</i>	17.33	0.58	Op1020f_3	GIP-REP-Recomb	Q1LH40 Exonuclease SbcC, putative
NPKM_194	203004 +	204441 Rmet_3665		151.33	6.81	Op1020f_4	NA	Q1LH39 Peptidase M20
NPKM_195	204660 +	204945 Rmet_3666		40.67	6.51	Op1020f_4	NA	Q1LH38 Putative uncharacterized protein
NPKM_196	204965 +	205631 Rmet_3667		65.33	2.08	Op1020f_4	MET-XEN-Benz	Q1LH37 3-oxoacid CoA-transferase, subunit A
NPKM_197	205659 +	206307 Rmet_3668		72.67	1.53	Op1020f_4	MET-XEN-Benz	Q1LH36 Butyryl-CoA:acetate CoA transferase
NPKM_198	206335 +	207538 Rmet_3669		240.67	9.71	Op1020f_5	MET-LIP-FAMet	Q1LH35 Beta-ketoadipyl CoA thiolase
NPKM_199	207797 +	208529 Rmet_3670		159.67	6.43	Op1020f_5	NA	Q1LH34 Short-chain dehydrogenase/reductase SDR
3UTR_1050	207925 -	209832 Rmet_3672				Op1021r_1		
NPKM_200	208632 +	209637 Rmet_3671	<i>bug</i>	459.67	21.22	Op1020f_6	NA	Q1LH33 Uncharacterized protein UPF0065
3UTR_187	209638 +	209719 Rmet_3671	<i>bug</i>			Op1020f_6		
NPKM_201	209833 -	210043 Rmet_3672		724.00	321.86	Op1021r_1	NA	Q1LH32 Putative uncharacterized protein
5UTR_854	210044 -	210141 Rmet_3672				Op1021r_1		
5UTR_164	210251 +	210369 Rmet_3673				Op1022f_1		
NPKM_202	210369 +	210939 Rmet_3673		184.67	18.18	Op1022f_1	NA	Q1LH31 Transcriptional regulator, PadR family
3UTR_1049	210818 -	210971 Rmet_3674				Op1023r_1		
NPKM_203	210972 -	211962 Rmet_3674		9.33	1.15	Op1023r_1	MET-EN-Nitrog	Q1LH30 2-nitropropane dioxygenase, NPD
5UTR_853	211963 -	212033 Rmet_3674				Op1023r_1		
NPKM_204	212142 +	213219 Rmet_3675	<i>int</i>	53.00	2.65	Op1024f_1	NA	Q1LH29 Phage integrase
NPKM_205	213311 +	214331 Rmet_3676		114.00	3.61	Op1024f_2	MET-CAH-Gal	Q1LH28 UDP-galactose 4-epimerase
3UTR_188	214332 +	214488 Rmet_3676				Op1024f_2		
3UTR_1048	214437 -	214531 Rmet_3677	<i>stpA</i>			Op1025r_1		
NPKM_206	214532 -	214841 Rmet_3677	<i>stpA</i>	1052.67	103.75	Op1025r_1	NA	Q1LH27 Nucleoid protein H-NS
5UTR_852	214842 -	214899 Rmet_3677	<i>stpA</i>			Op1025r_1		
5UTR_165	215303 +	215392 Rmet_3678				Op1026f_1		
NPKM_207	215392 +	217210 Rmet_3678		19.67	2.89	Op1026f_1	DIV-MOT-Chemotax	Q1LH26 Methyl-accepting chemotaxis sensory transducer
NPKM_208	217346 +	219329 Rmet_3679		13.00	2.00	Op1026f_1	NA	Q1LH25 Diguanylate cyclase/phosphodiesterase
NPKM_209	219488 +	219872 Rmet_3680		61.67	12.50	Op1026f_2	EIP-SIG-2Comp	Q1LH24 Response regulator receiver domain protein (CheY-like)
NPKM_210	219959 +	220511 Rmet_3681	<i>cheW</i>	113.67	20.43	Op1026f_2	DIV-MOT-Chemotax	Q1LH23 CheW protein
NPKM_211	220628 +	222287 Rmet_3682	<i>aer</i>	37.67	3.79	Op1026f_2	DIV-MOT-Chemotax	Q1LH22 Methyl-accepting chemotaxis sensory transducer with Pas/Pac sensor
NPKM_212	222325 +	224167 Rmet_3683		72.33	7.51	Op1026f_2	DIV-MOT-Chemotax	Q1LH21 Methyl-accepting chemotaxis sensory transducer
NPKM_213	224275 +	225028 Rmet_3684		30.67	1.15	Op1026f_2	NA	Q1LH20 Putative uncharacterized protein
NPKM_214	225426 +	225744 Rmet_3685	<i>flhD2</i>	622.33	14.36	Op1026f_3	EIP-SIG-2Comp	Q1LH19 Flagellar transcriptional activator
NPKM_215	225740 +	226346 Rmet_3686	<i>flhC2</i>	267.00	6.56	Op1026f_3	EIP-SIG-2Comp	Q1LH18 Flagellar transcriptional activator FlhC
NPKM_216	226432 +	227332 Rmet_3687	<i>motA</i>	140.00	20.42	Op1026f_3	EIP-TRA-Pores	Q1LH17 Chemotaxis MotA protein
NPKM_217	227345 +	228323 Rmet_3688	<i>motB</i>	52.67	7.02	Op1026f_3	EIP-TRA-Pores	Q1LH16 OmpA/MotB
NPKM_218	228383 +	230399 Rmet_3689	<i>cheA</i>	70.33	7.51	Op1026f_3	EIP-SIG-2Comp	Q1LH15 CheA signal transduction histidine kinases
NPKM_219	230423 +	230918 Rmet_3690	<i>cheW</i>	74.00	5.29	Op1026f_3	DIV-MOT-Chemotax	Q1LH14 CheW protein
NPKM_220	230981 +	231893 Rmet_3691	<i>cheR</i>	45.33	2.31	Op1026f_3	DIV-MOT-Chemotax	Q1LH13 MCP methyltransferase, CheR-type
NPKM_221	231889 +	232552 Rmet_3692	<i>cheD</i>	22.00	0.00	Op1026f_3	DIV-MOT-Chemotax	Q1LH12 Probable chemoreceptor glutamine deamidase cheD

NPKM_222	232619 +	233693 Rmet_3693	<i>cheB1</i>	32.33	1.15	Op1026f_3	EIP-SIG-2Comp	Q1LH11 Chemotaxis response regulator protein-glutamate methylesterase 1
NPKM_223	233732 +	234152 Rmet_3694	<i>cheY</i>	57.67	7.51	Op1026f_3	EIP-SIG-2Comp	Q1LH10 Response regulator receiver domain protein (CheY-like)
NPKM_224	234164 +	234800 Rmet_3695	<i>cheZ</i>	66.67	3.06	Op1026f_3	DIV-MOT-Chemotax	Q1LH09 Chemotaxis phosphatase, CheZ
NPKM_225	234928 +	236287 Rmet_3696		50.67	1.53	Op1026f_3	NA	Q1LH08 Peptidase M20
NPKM_226	236402 +	237134 Rmet_3697		83.67	2.08	Op1026f_3	NA	Q1LH07 UPF0502 protein Rmet_3697
NPKM_227	237412 +	238555 Rmet_3698	<i>flhB</i>	14.33	2.08	Op1026f_3	GIP-PTL-T3S	Q1LH06 Flagellar biosynthetic protein FlhB
NPKM_228	238551 +	240639 Rmet_3699	<i>flhA</i>	18.00	2.00	Op1026f_3	GIP-PTL-T3S	Q1LH05 Flagellar biosynthesis protein FlhA
NPKM_229	240648 +	243126 Rmet_3700	<i>flhF</i>	29.33	4.16	Op1026f_3	DIV-MOT-Flagel	Q1LH04 GTP-binding signal recognition particle SRP54, G-domain
NPKM_230	243129 +	243954 Rmet_3701	<i>flhG</i>	22.67	4.62	Op1026f_3	DIV-MOT-Flagel	Q1LH03 Flagellar biosynthesis protein FlhG
NPKM_231	244061 +	244778 Rmet_3702	<i>fliA</i>	13.00	2.65	Op1026f_3	GIP-TK-RNAP	Q1LH02 RNA polymerase sigma factor
NPKM_232	244777 +	245224 Rmet_3703	<i>flhE</i>	15.67	2.08	Op1026f_3	DIV-MOT-Flagel	Q1LH01 Flagellar FlhE
3UTR_189	245225 +	245560 Rmet_3703	<i>flhE</i>			Op1026f_3		
3UTR_1047	245379 -	245408 Rmet_3704				Op1027r_1		
NPKM_233	245409 -	246501 Rmet_3704		0.00	0.00	Op1027r_1	NA	Q1LH00 Porin, Gram-negative type
5UTR_851	246502 -	246523 Rmet_3704				Op1027r_1		
NPKM_234	246579 -	247605 Rmet_3705	<i>ligJ</i>	0.00	0.00	Op1027r_1	NA	Q1LGZ9 Amidohydrolase 2
NPKM_235	247601 -	248750 Rmet_3706		0.33	0.58	Op1027r_1	NA	Q1LGZ8 Methylitaconate delta2-delta3-isomerase
5UTR_850	248751 -	248778 Rmet_3706				Op1027r_1		
5UTR_166	248917 +	248921 Rmet_3707				Op1028f_1		
NPKM_236	248921 +	250142 Rmet_3707		16.67	0.58	Op1028f_1	NA	Q1LGZ7 Transcriptional regulator, LysR family
NPKM_237	250311 +	251637 Rmet_3708	<i>pcaK2</i>	6.00	0.00	Op1028f_1	NA	Q1LGZ6 Major facilitator superfamily MFS_1
NPKM_238	251646 +	252939 Rmet_3709		14.33	0.58	Op1028f_2	MET-XEN-24D	Q1LGZ5 Extradial ring-cleavage dioxygenase, class III enzyme, subunit B
NPKM_239	252920 +	253460 Rmet_3710		24.33	1.53	Op1028f_2	NA	Q1LGZ4 Rubredoxin
3UTR_1046	253742 -	254370 Rmet_3712	<i>nagH</i>			Op1029r_1		
NPKM_240	253749 +	254337 Rmet_3711		25.33	1.15	Op1028f_2	NA	Q1LGZ3 GCN5-related N-acetyltransferase
3UTR_190	254338 +	254667 Rmet_3711				Op1028f_2		
NPKM_241	254371 -	254848 Rmet_3712	<i>nagH</i>	6.67	1.53	Op1029r_1	MET-AA-Phe	Q1LGZ2 Putative salicylate-5-hydroxylase small oxygenase component oxidoreducta
5UTR_849	254849 -	255012 Rmet_3712	<i>nagH</i>			Op1029r_1		
NPKM_242	255170 +	256133 Rmet_3713		11.00	1.00	Op1030f_1	NA	Q1LGZ1 Transcriptional regulator, LysR family
3UTR_1045	255589 -	256112 Rmet_3714				Op1031r_1		
NPKM_243	256113 -	256314 Rmet_3714		7.67	1.15	Op1031r_1	NA	Q1LGZ0 Putative uncharacterized protein
NPKM_244	256368 -	256686 Rmet_3715		5.67	1.15	Op1031r_1	NA	Q1LGY9 Conserved hypothetical signal peptide protein
5UTR_848	256687 -	256699 Rmet_3715				Op1031r_1		
3UTR_1044	256780 -	257470 Rmet_3717				Op1033r_2		
NPKM_245	256840 +	257371 Rmet_3716		9.33	2.31	Op1032f_1	NA	Q1LGY8 Putative uncharacterized protein
3UTR_191	257372 +	257610 Rmet_3716				Op1032f_1		
NPKM_246	257471 -	258134 Rmet_3717		24.33	4.51	Op1033r_2	NA	Q1LGY7 Dihydropteridine reductase
NPKM_247	258206 -	258671 Rmet_3718		8.33	1.53	Op1033r_1	NA	Q1LGY6 Putative uncharacterized protein
5UTR_847	258672 -	258710 Rmet_3718				Op1033r_1		
5UTR_167	258774 +	258804 Rmet_3719				Op1034f_1		
NPKM_248	258804 +	259713 Rmet_3719		15.33	0.58	Op1034f_1	NA	Q1LGY5 Transcriptional regulator, LysR family
NPKM_249	259796 +	261557 Rmet_3720		12.00	0.00	Op1034f_1	NA	Q1LGY4 Sulfate permease
3UTR_1043	261416 -	261658 Rmet_3721	<i>bug</i>			Op1035r_1		

3UTR_192	261558 +	262261 Rmet_3720				Op1034f_1		
NPKM_250	261659 -	262697 Rmet_3721	<i>bug</i>	57.00	3.00	Op1035r_1	NA	Q1LGY3 Uncharacterized protein UPF0065
NPKM_251	262571 +	262802 Rmet_6619		1.00	0.00	Op1036f_1	NA	NA
5UTR_846	262698 -	262704 Rmet_3721	<i>bug</i>			Op1035r_1		
NPKM_252	262883 +	263354 Rmet_3722		48.67	1.53	Op1036f_2	MET-NUC-Pur	Q1LGY2 CMP/dCMP deaminase, zinc-binding
3UTR_1042	263305 -	263353 Rmet_3723				Op1037r_1		
NPKM_253	263354 -	265241 Rmet_3723		2.67	0.58	Op1037r_1	DIV-MOT-Chemotax	Q1LGY1 Methyl-accepting chemotaxis sensory transducer
3UTR_193	263355 +	263947 Rmet_3722				Op1036f_2		
5UTR_168	265482 +	265503 Rmet_3724				Op1038f_1		
NPKM_254	265503 +	267114 Rmet_3724		3.33	0.58	Op1038f_1	NA	Q1LGY0 EAL-containing signal transduction protein
5UTR_169	267117 +	267170 Rmet_3725	<i>pbuX</i>			Op1038f_2		
NPKM_255	267170 +	268508 Rmet_3725	<i>pbuX</i>	11.00	0.00	Op1038f_2	EIP-TRA-Ion	Q1LGX9 Uracil-xanthine permease
3UTR_1041	267829 -	268589 Rmet_3726				Op1039r_1		
3UTR_194	268509 +	268534 Rmet_3725	<i>pbuX</i>			Op1038f_2		
NPKM_256	268590 -	269181 Rmet_3726		20.33	1.15	Op1039r_1	NA	Q1LGX8 Putative uncharacterized protein
5UTR_170	269233 +	269269 Rmet_3727				Op1040f_1		
NPKM_257	269269 +	270469 Rmet_3727		2.00	0.00	Op1040f_1	MET-CAH-Prop	Q1LGX7 Acyl-CoA dehydrogenase-like protein
NPKM_258	270492 +	271638 Rmet_3728		2.00	0.00	Op1040f_1	NA	Q1LGX6 Acyl-CoA dehydrogenase-like protein
3UTR_195	271639 +	271684 Rmet_3728				Op1040f_1		
3UTR_1040	271714 -	271789 Rmet_3729	<i>icdA</i>			Op1041r_3		
NPKM_259	271790 -	274034 Rmet_3729	<i>icdA</i>	1307.67	58.50	Op1041r_3	MET-CAH-TCA	Q1LGX5 Isocitrate dehydrogenase, NADP-dependent
NPKM_260	274401 -	275490 Rmet_3730		58.33	6.51	Op1041r_2	NA	Q1LGX4 Putative transmembrane protein
NPKM_261	275554 -	276019 Rmet_3731	<i>flgN</i>	155.33	25.54	Op1041r_2	DIV-MOT-Flagel	Q1LGX3 FlgN
NPKM_262	276026 -	276407 Rmet_3732	<i>flgM</i>	145.00	18.00	Op1041r_2	DIV-MOT-Flagel	Q1LGX2 Anti-sigma-28 factor, FlgM
NPKM_263	276585 -	277323 Rmet_3733	<i>flgA</i>	28.67	1.15	Op1041r_1	DIV-MOT-Flagel	Q1LGX1 Flageller protein FlgA
5UTR_171	277305 +	277379 Rmet_6620				Op1042f_1		
5UTR_845	277324 -	277356 Rmet_3733	<i>flgA</i>			Op1041r_1		
NPKM_264	277379 +	277577 Rmet_6620		0.67	0.58	Op1042f_1	NA	NA
NPKM_265	277601 +	278006 Rmet_3734	<i>flgB</i>	58.00	8.19	Op1042f_2	DIV-MOT-Flagel	Q1LGX0 Flagellar basal-body rod protein FlgB
NPKM_266	278017 +	278425 Rmet_3735	<i>flgC</i>	59.00	4.36	Op1042f_2	DIV-MOT-Flagel	Q1LGW9 Flagellar basal-body rod protein FlgC
NPKM_267	278466 +	279135 Rmet_3736	<i>flgD</i>	74.00	9.64	Op1042f_2	DIV-MOT-Flagel	Q1LGW8 Flagellar hook capping protein
NPKM_268	279208 +	280456 Rmet_3737	<i>flgE</i>	155.00	17.58	Op1042f_3	DIV-MOT-Flagel	Q1LGW7 Putative uncharacterized protein
NPKM_269	280482 +	281226 Rmet_3738	<i>flgF</i>	122.00	12.17	Op1042f_3	DIV-MOT-Flagel	Q1LGW6 Flagellar basal-body rod FlgF
NPKM_270	281274 +	282060 Rmet_3739	<i>flgG</i>	90.67	14.19	Op1042f_3	DIV-MOT-Flagel	Q1LGW5 Flagellar basal-body rod FlgG
NPKM_271	282066 +	282780 Rmet_3740	<i>flgH</i>	55.00	5.29	Op1042f_3	DIV-MOT-Flagel	Q1LGW4 Flagellar L-ring protein
NPKM_272	282787 +	283972 Rmet_3741	<i>flgI</i>	32.00	3.46	Op1042f_3	DIV-MOT-Flagel	Q1LGW3 Flagellar P-ring protein
NPKM_273	283971 +	284994 Rmet_3742	<i>flgJ</i>	27.67	2.08	Op1042f_3	DIV-MOT-Flagel	Q1LGW2 Mannosyl-glycoprotein endo-beta-N-acetylglucosamidase
NPKM_274	285259 +	287155 Rmet_3743	<i>flgK</i>	41.67	8.96	Op1042f_3	DIV-MOT-Flagel	Q1LGW1 Flagellar hook-associated protein
NPKM_275	287210 +	288449 Rmet_3744	<i>flgL</i>	48.33	4.16	Op1042f_3	DIV-MOT-Flagel	Q1LGW0 Flagellin-like protein
3UTR_1039	287875 -	288810 Rmet_3745				Op1043r_1		
3UTR_196	288450 +	288706 Rmet_3744	<i>flgL</i>			Op1042f_3		
NPKM_276	288811 -	289990 Rmet_3745		13.00	1.73	Op1043r_1	NA	Q1LGV9 Diguanylate cyclase (GGDEF domain)
5UTR_844	289991 -	290070 Rmet_3745				Op1043r_1		

3UTR_1038	290077 -	290269 Rmet_3746				Op1043r_1		
NPKM_277	290270 -	290633 Rmet_3746	12.00	1.00	Op1043r_1	NA	Q1LGV8 Putative uncharacterized protein	
NPKM_278	290644 -	290851 Rmet_6621	16.67	0.58	Op1043r_1	NA	NA	
NPKM_279	290889 -	291969 Rmet_3747	22.33	0.58	Op1043r_1	NA	Q1LGV7 Putative uncharacterized protein	
5UTR_843	291970 -	291971 Rmet_3747			Op1043r_1			
5UTR_172	292051 +	292059 Rmet_6622			Op1044f_1			
NPKM_280	292059 +	292257 Rmet_6622	2.67	0.58	Op1044f_1	NA	NA	
NPKM_281	292290 +	292650 Rmet_3748	5.00	1.00	Op1044f_1	NA	Q1LGV6 Putative uncharacterized protein	
NPKM_282	292669 +	293776 Rmet_3749	9.33	0.58	Op1044f_1	NA	Q1LGV5 Putative uncharacterized protein	
NPKM_283	293834 +	295460 Rmet_3750	8.00	1.00	Op1044f_1	NA	Q1LGV4 Putative uncharacterized protein	
NPKM_284	295456 +	295738 Rmet_3751	6.67	1.53	Op1044f_1	NA	Q1LGV3 Putative uncharacterized protein	
NPKM_285	296327 +	296630 Rmet_3752	20.00	4.36	Op1044f_2	NA	Q1LGV2 Putative uncharacterized protein	
NPKM_286	296687 +	296855 Rmet_3753	24.67	4.51	Op1044f_2	NA	Q1LGV1 Putative uncharacterized protein	
NPKM_287	296965 +	297283 Rmet_3754	18.67	1.15	Op1044f_2	NA	Q1LGV0 Putative uncharacterized protein	
3UTR_1037	297071 -	297686 Rmet_3756			Op1045r_2			
NPKM_288	297352 +	297604 Rmet_3755	13.00	0.00	Op1044f_2	NA	Q1LGU9 Endoribonuclease L-PSP	
3UTR_197	297605 +	298157 Rmet_3755			Op1044f_2			
NPKM_289	297687 -	298311 Rmet_3756	4.33	0.58	Op1045r_2	NA	Q1LGU8 Acyl-CoA dehydrogenase-like protein	
5UTR_842	298312 -	298341 Rmet_3756			Op1045r_2			
3UTR_1036	298558 -	298664 Rmet_3757			Op1045r_1			
NPKM_290	298665 -	298821 Rmet_3757	1.33	0.58	Op1045r_1	NA	Q1LGU7 Putative uncharacterized protein	
NPKM_291	298817 -	299003 Rmet_6623	0.67	1.15	Op1045r_1	NA	NA	
5UTR_173	298896 +	298910 Rmet_3758			Op1046f_1			
NPKM_292	298910 +	299258 Rmet_3758	3.00	1.00	Op1046f_1	NA	Q1LGU6 Putative uncharacterized protein	
5UTR_174	299267 +	299271 Rmet_3759			Op1046f_1			
NPKM_293	299271 +	299661 Rmet_3759	3.33	0.58	Op1046f_1	MET-EN-Nitrog	Q1LGU5 L-glutaminase	
NPKM_294	299749 +	300748 Rmet_3760	12.33	0.58	Op1046f_2	NA	Q1LGU4 Putative uncharacterized protein	
3UTR_1035	300707 -	300845 Rmet_3761			Op1047r_1			
3UTR_198	300749 +	301433 Rmet_3760			Op1046f_2			
NPKM_295	300846 -	301074 Rmet_3761	6.67	1.53	Op1047r_1	NA	Q1LGU3 Putative uncharacterized protein	
5UTR_841	301075 -	301130 Rmet_3761			Op1047r_1			
3UTR_1034	301161 -	301197 Rmet_3762			Op1047r_1			
NPKM_296	301198 -	301582 Rmet_3762	6.00	1.00	Op1047r_1	NA	Q1LGU2 Putative uncharacterized protein	
3UTR_1033	302069 -	302181 Rmet_3763			Op1047r_1			
NPKM_297	302182 -	302521 Rmet_3763	4.67	0.58	Op1047r_1	NA	Q1LGU1 Transcriptional regulator, AraC family / DNA-O6-methylguanine--protein-c	
NPKM_298	302510 -	303215 Rmet_3764	5.00	1.00	Op1047r_1	GIP-REP-Recomb	Q1LGU0 HhH-GPD	
NPKM_299	303229 -	304294 Rmet_3765	7.33	1.15	Op1047r_1	GIP-REP-Recomb	Q1LGT9 Methylated-DNA--protein-cysteine methyltransferase	
NPKM_300	304377 -	305034 Rmet_3766	4.67	1.15	Op1047r_1	NA	Q1LGT8 Putative uncharacterized protein	
NPKM_301	305036 -	305588 Rmet_3767	3.67	0.58	Op1047r_1	GIP-REP-Recomb	Q1LGT7 DNA-N1-methyladenine dioxygenase	
NPKM_302	305636 -	305828 Rmet_3768	3.00	1.00	Op1047r_1	NA	Q1LGT6 Transposase IS3/IS911	
NPKM_303	305912 -	306497 Rmet_3769	5.33	1.15	Op1047r_1	NA	B2UH78 Integrase catalytic region	
5UTR_840	306498 -	306581 Rmet_3769			Op1047r_1			
NPKM_304	306671 +	306968 Rmet_3770	0.00	0.00	Op1048f_1	NA	NA	

NPKM_305	306964 +	307858 Rmet_3771	<i>tnpB</i>	0.00	0.00	Op1048f_1	NA	NA
NPKM_306	307931 +	308213 Rmet_3772		19.67	2.31	Op1048f_2	NA	Q1LGT4 Putative uncharacterized protein
NPKM_307	308209 +	309517 Rmet_3773	<i>tnsD</i>	10.33	1.53	Op1048f_2	NA	Q1LGT3 Putative uncharacterized protein
NPKM_308	309513 +	311229 Rmet_3774		15.33	0.58	Op1048f_2	NA	Q1LGT2 Putative uncharacterized protein
3UTR_199	311230 +	311785 Rmet_3774				Op1048f_2		
NPKM_309	311251 -	311470 Rmet_6624		0.33	0.58	Op1049r_1	NA	NA
NPKM_310	311510 -	311786 Rmet_3775		0.33	0.58	Op1049r_1	NA	Q1LGT1 Putative uncharacterized protein
5UTR_175	311839 +	311903 Rmet_3776				Op1050f_1		
NPKM_311	311903 +	313091 Rmet_3776		17.67	2.08	Op1050f_1	NA	Q1LGT0 Putative uncharacterized protein
NPKM_312	313134 +	314838 Rmet_3777	<i>entE</i>	12.33	1.15	Op1050f_1	NA	Q1LGS9 AMP-dependent synthetase and ligase
NPKM_313	314851 +	315730 Rmet_3778		14.33	1.15	Op1050f_1	NA	Q1LGS8 Glyoxalase/bleomycin resistance protein/dioxygenase
NPKM_314	315726 +	316887 Rmet_3779		14.67	0.58	Op1050f_1	NA	Q1LGS7 Monooxygenase, FAD-binding
NPKM_315	316883 +	317333 Rmet_3780		11.67	1.15	Op1050f_1	NA	Q1LGS6 Thioesterase-like protein
NPKM_316	317353 +	318112 Rmet_3781		8.33	0.58	Op1050f_1	MET-CAH-But	Q1LGS5 Asp/Glu racemase
NPKM_317	318177 +	319425 Rmet_3782		6.67	0.58	Op1050f_1	NA	Q1LGS4 Major facilitator superfamily MFS_1
NPKM_318	319438 +	320317 Rmet_3783		52.67	0.58	Op1050f_2	NA	Q1LGS3 Putative transcriptional regulator, TetR family
3UTR_200	320318 +	320400 Rmet_3783				Op1050f_2		
5UTR_176	320432 +	320472 Rmet_3784	<i>bugT</i>			Op1050f_2		
NPKM_319	320472 +	321429 Rmet_3784	<i>bugT</i>	2.33	0.58	Op1050f_2	NA	Q1LGS2 Uncharacterized protein UPF0065
NPKM_320	321464 +	322646 Rmet_3785	<i>rnz</i>	1.33	0.58	Op1050f_2	NA	Q1LGS1 Beta-lactamase-like protein
3UTR_201	322647 +	322700 Rmet_3785	<i>rnz</i>			Op1050f_2		
NPKM_321	322786 +	323962 Rmet_3786		1.33	0.58	Op1050f_2	NA	Q1LGS0 Porin, Gram-negative type
3UTR_202	323963 +	323988 Rmet_3786				Op1050f_2		
5UTR_177	323994 +	324071 Rmet_6625				Op1050f_2		
NPKM_322	324071 +	324281 Rmet_6625		1.00	1.00	Op1050f_2	NA	NA
3UTR_203	324282 +	324292 Rmet_6625				Op1050f_2		
5UTR_178	324302 +	324334 Rmet_3787				Op1050f_3		
NPKM_323	324334 +	324766 Rmet_3787		29.00	3.46	Op1050f_3	NA	Q1LGR9 Putative uncharacterized protein
NPKM_324	324897 +	325086 Rmet_6626		10.33	1.53	Op1050f_3	NA	NA
NPKM_325	325106 +	326678 Rmet_3788	<i>fadD</i>	6.00	0.00	Op1050f_3	MET-LIP-FASyn	Q1LGR8 AMP-dependent synthetase and ligase
NPKM_326	326743 +	327724 Rmet_3789	<i>bugT</i>	5.67	1.15	Op1050f_3	NA	Q1LGR7 Uncharacterized protein UPF0065
3UTR_204	327725 +	327755 Rmet_3789	<i>bugT</i>			Op1050f_3		
3UTR_1032	327796 -	327886 Rmet_3790				Op1051r_2		
NPKM_327	327887 -	329678 Rmet_3790		5.67	0.58	Op1051r_2	NA	Q1LGR6 Acyl-CoA dehydrogenase-like protein
5UTR_839	329679 -	329694 Rmet_3790				Op1051r_2		
NPKM_328	329738 -	330962 Rmet_3791		2.00	0.00	Op1051r_1	NA	Q1LGR5 L-carnitine dehydratase/bile acid-inducible protein F
NPKM_329	330977 -	331958 Rmet_3792	<i>bug</i>	2.33	0.58	Op1051r_1	NA	Q1LGR4 Uncharacterized protein UPF0065
5UTR_838	331959 -	331965 Rmet_3792	<i>bug</i>			Op1051r_1		
NPKM_330	332105 +	333020 Rmet_3793		9.00	1.00	Op1052f_1	NA	Q1LGR3 Transcriptional regulator, LysR family
3UTR_1031	332274 -	333030 Rmet_3794				Op1053r_2		
3UTR_205	333021 +	333428 Rmet_3793				Op1052f_1		
NPKM_331	333031 -	333634 Rmet_3794		18.67	2.08	Op1053r_2	NA	Q1LGR2 Putative transcriptional regulator, TetR family
5UTR_837	333635 -	333663 Rmet_3794				Op1053r_2		

3UTR_1030	333776 -	333823 Rmet_3795	<i>lipB</i>			Op1053r_1			
NPKM_332	333824 -	334880 Rmet_3795	<i>lipB</i>	4.67	0.58	Op1053r_1	NA	Q1LGR1 Lipase chaperone	
NPKM_333	334866 -	336000 Rmet_3796	<i>lipA</i>	8.33	1.15	Op1053r_1	MET-LIP-GlycLip	Q1LGR0 Alpha/beta hydrolase fold	
5UTR_836	336001 -	336017 Rmet_3796	<i>lipA</i>			Op1053r_1			
NPKM_334	336028 +	336268 Rmet_6627		1.00	1.00	Op1054f_1	NA	NA	
3UTR_206	336269 +	336313 Rmet_6627				Op1054f_1			
NPKM_335	336314 +	337277 Rmet_3797	<i>bugT</i>	2.00	1.00	Op1054f_1	NA	Q1LGQ9 Uncharacterized protein UPF0065	
3UTR_207	337278 +	337330 Rmet_3797	<i>bugT</i>			Op1054f_1			
5UTR_179	337333 +	337481 Rmet_3798				Op1054f_2			
NPKM_336	337481 +	339014 Rmet_3798		17.67	0.58	Op1054f_2	NA	Q1LGQ8 AMP-dependent synthetase and ligase	
3UTR_1029	338277 -	339047 Rmet_3799				Op1055r_1			
3UTR_208	339015 +	339353 Rmet_3798				Op1054f_2			
NPKM_337	339048 -	339951 Rmet_3799		38.00	1.73	Op1055r_1	NA	Q1LGQ7 Transcriptional regulator, LysR family	
NPKM_338	340059 +	340923 Rmet_3800		4.67	0.58	Op1056f_1	MET-CAH-Prop	Q1LGQ6 Enoyl-CoA hydratase / short chain enoyl-CoA hydratase	
3UTR_209	340924 +	340985 Rmet_3800				Op1056f_1			
3UTR_1028	340955 -	340985 Rmet_3801	<i>bug</i>			Op1057r_1			
NPKM_339	340986 -	341979 Rmet_3801	<i>bug</i>	1.00	0.00	Op1057r_1	NA	Q1LGQ5 Uncharacterized protein UPF0065	
3UTR_1027	341982 -	341988 Rmet_3802				Op1057r_1			
NPKM_340	341989 -	343627 Rmet_3802		1.00	0.00	Op1057r_1	NA	Q1LGQ4 AMP-dependent synthetase and ligase	
5UTR_180	343584 +	343716 Rmet_3803				Op1058f_1			
NPKM_341	343716 +	344910 Rmet_3803		11.33	0.58	Op1058f_1	NA	Q1LGQ3 Acyl-CoA dehydrogenase-like protein	
NPKM_342	344927 +	346037 Rmet_3804		10.00	1.00	Op1058f_1	NA	Q1LGQ2 Acyl-CoA dehydrogenase-like protein	
NPKM_343	346063 +	347230 Rmet_3805		16.67	0.58	Op1058f_1	MET-CAH-Pyr	Q1LGQ1 Acetyl-CoA acetyltransferase (Thiolase)	
NPKM_344	347244 +	347643 Rmet_3806		17.33	1.53	Op1058f_1	NA	Q1LGQ0 Putative uncharacterized protein	
NPKM_345	347656 +	348550 Rmet_3807		12.33	0.58	Op1058f_1	NA	Q1LGP9 MaoC-like dehydratase	
NPKM_346	348567 +	349860 Rmet_3808		9.00	1.00	Op1058f_1	NA	Q1LGP8 L-carnitine dehydratase/bile acid-inducible protein F	
3UTR_210	349861 +	350219 Rmet_3808				Op1058f_1			
3UTR_1026	349896 -	349914 Rmet_3809				Op1059r_1			
NPKM_347	349915 -	351106 Rmet_3809		7.33	1.53	Op1059r_1	NA	Q1LGP7 L-carnitine dehydratase/bile acid-inducible protein F	
NPKM_348	351212 -	352331 Rmet_3810		30.33	1.15	Op1059r_1	NA	Q1LGP6 Transcriptional regulator, LysR family	
NPKM_349	352329 +	353313 Rmet_3811	<i>bugT</i>	2.00	0.00	Op1060f_1	NA	Q1LGP5 Uncharacterized protein UPF0065	
5UTR_835	352332 -	353242 Rmet_3810				Op1059r_1			
3UTR_1025	353252 -	354795 Rmet_6628				Op1061r_1			
NPKM_350	353344 +	353815 Rmet_3812		5.33	0.58	Op1060f_2	NA	Q1LGP4 MaoC-like dehydratase	
NPKM_351	353804 +	354782 Rmet_3813	<i>bugT</i>	5.67	0.58	Op1060f_2	NA	Q1LGP3 Uncharacterized protein UPF0065	
3UTR_211	354783 +	355015 Rmet_3813	<i>bugT</i>			Op1060f_2			
NPKM_352	354796 -	354976 Rmet_6628		100.67	13.58	Op1061r_1	NA	NA	
NPKM_353	355192 -	355804 Rmet_3814		80.33	3.51	Op1061r_1	NA	Q1LGP2 Putative uncharacterized protein	
NPKM_354	355800 -	357423 Rmet_3815		51.33	1.53	Op1061r_1	NA	Q1LGP1 Peptidoglycan-binding domain 1	
NPKM_355	357537 -	358233 Rmet_3816		34.67	2.52	Op1061r_1	NA	Q1LGP0 Transcriptional regulator, TetR family	
5UTR_834	358234 -	358332 Rmet_3816				Op1061r_1			
NPKM_356	358330 +	359977 Rmet_3817	<i>acd</i>	8.33	0.58	Op1062f_1	NA	Q1LGN9 Acyl-CoA dehydrogenase-like protein	
3UTR_212	359978 +	360003 Rmet_3817	<i>acd</i>			Op1062f_1			

5UTR_181	360005 +	360115 Rmet_3818				Op1062f_1		
NPKM_357	360115 +	361621 Rmet_3818		6.67	0.58	Op1062f_1	NA	Q1LGN8 AMP-dependent synthetase and ligase
NPKM_358	361744 +	362719 Rmet_3819	<i>cysK</i>	2.33	0.58	Op1062f_1	MET-EN-Sulf	Q1LGN7 Cysteine synthase
5UTR_182	362745 +	362838 Rmet_3820				Op1062f_1		
NPKM_359	362838 +	363990 Rmet_3820		3.33	0.58	Op1062f_1	NA	Q1LGN6 Putative cytochrome p450 oxidoreductase
NPKM_360	364005 +	364362 Rmet_3821		7.00	2.00	Op1062f_2	NA	Q1LGN5 Antibiotic biosynthesis monooxygenase
NPKM_361	364380 +	365136 Rmet_3822		6.00	1.00	Op1062f_2	NA	Q1LGN4 Putative uncharacterized protein
NPKM_362	365239 +	366364 Rmet_3823	<i>phaZ</i>	10.00	0.00	Op1062f_2	NA	Q1LGN3 Esterase, PHB depolymerase
3UTR_1024	366144 -	366432 Rmet_3824				Op1063r_1		
3UTR_213	366365 +	366916 Rmet_3823	<i>phaZ</i>			Op1062f_2		
NPKM_363	366433 -	366742 Rmet_3824		12.00	1.00	Op1063r_1	NA	Q1LGN2 Ferredoxin
NPKM_364	366738 -	367476 Rmet_3825		18.67	0.58	Op1063r_1	NA	Q1LGN1 Putative uncharacterized protein
5UTR_183	367530 +	367548 Rmet_3826				Op1064f_1		
NPKM_365	367548 +	369537 Rmet_3826		8.00	1.00	Op1064f_1	NA	Q1LGN0 Putative uncharacterized protein
3UTR_214	369538 +	369567 Rmet_3826				Op1064f_1		
5UTR_184	369569 +	369617 Rmet_3827				Op1064f_2		
NPKM_366	369617 +	370232 Rmet_3827		37.67	2.52	Op1064f_2	NA	Q1LGM9 Putative uncharacterized protein
NPKM_367	370228 +	370903 Rmet_3828		51.00	5.00	Op1064f_2	NA	Q1LGM8 Hydrolases of HD superfamily-like protein
NPKM_368	371074 +	371632 Rmet_3829		24.33	2.52	Op1064f_2	NA	Q1LGM7 Putative uncharacterized protein
NPKM_369	371628 +	372339 Rmet_3830		10.67	1.15	Op1064f_2	NA	Q1LGM6 Putative uncharacterized protein
3UTR_1023	372311 -	372461 Rmet_3831				Op1065r_1		
3UTR_215	372340 +	372399 Rmet_3830				Op1064f_2		
NPKM_370	372462 -	373296 Rmet_3831		3.33	0.58	Op1065r_1	NA	Q1LGM5 Putative uncharacterized protein
NPKM_371	373376 -	374345 Rmet_3832	<i>bugT</i>	11.00	1.00	Op1065r_1	NA	Q1LGM4 Uncharacterized protein UPF0065
NPKM_372	374529 -	375468 Rmet_3833		12.67	1.53	Op1065r_1	NA	Q1LGM3 Transcriptional regulator, LysR family
5UTR_185	375592 +	375610 Rmet_3834				Op1066f_1		
NPKM_373	375610 +	376783 Rmet_3834		9.00	1.00	Op1066f_1	NA	Q1LGM2 L-carnitine dehydratase/bile acid-inducible protein F
NPKM_374	376795 +	377626 Rmet_3835		8.33	0.58	Op1066f_1	MET-CAH-TCA	Q1LGM1 HpCh/HpaI aldolase
NPKM_375	377956 +	379294 Rmet_3836	<i>hmvC</i>	63.67	10.02	Op1066f_2	EIP-TRA-Ion	Q1LGM0 Outer membrane efflux protein
NPKM_376	379277 +	380495 Rmet_3837	<i>hmvB</i>	46.00	4.36	Op1066f_2	EIP-TRA-Ion	Q1LGL9 Secretion protein HlyD
NPKM_377	380508 +	383031 Rmet_3838	<i>hmvA</i>	41.67	4.04	Op1066f_2	EIP-TRA-Ion	Q46VH3 Heavy metal efflux pump CzcA
NPKM_378	383079 +	383634 Rmet_6629	<i>hmvA</i>	39.67	6.43	Op1066f_2	NA	NA
3UTR_216	383635 +	383661 Rmet_6629	<i>hmvA</i>			Op1066f_2		
5UTR_186	383675 +	383851 Rmet_3840				Op1066f_2		
NPKM_379	383851 +	384868 Rmet_3840		14.67	2.31	Op1066f_2	NA	Q1LGL8 Diguanylate cyclase
3UTR_1022	385145 -	385201 Rmet_6630				Op1067r_1		
NPKM_380	385164 +	386979 Rmet_3841	<i>tanA</i>	1.33	0.58	Op1066f_2	MET-AA-Urea	Q1LGL7 Tannase and feruloyl esterase
NPKM_381	385202 -	385382 Rmet_6630		3.33	2.08	Op1067r_1	NA	NA
5UTR_833	385383 -	385624 Rmet_6630				Op1067r_1		
3UTR_1021	385905 -	386998 Rmet_3842				Op1067r_1		
NPKM_382	386999 -	387530 Rmet_3842		38.00	1.00	Op1067r_1	NA	Q1LGL6 Putative uncharacterized protein
5UTR_832	387531 -	387536 Rmet_3842				Op1067r_1		
NPKM_383	387645 +	388149 Rmet_3843		26.00	4.36	Op1068f_1	NA	Q1LGL5 Alkylhydroperoxidase AhpD core

NPKM_384	388148 +	389009 Rmet_3844	<i>rpoT</i>	27.33	2.52	Op1068f_1	GIP-TK-RNAP	Q1LGL4 RNA polymerase, sigma-24 subunit, ECF subfamily
3UTR_1020	388639 -	389040 Rmet_6631				Op2059r_1		
NPKM_385	389041 -	389272 Rmet_6631		3.67	1.53	Op2059r_1	NA	NA
NPKM_386	389095 +	389434 Rmet_3845		12.00	2.65	Op1068f_1	NA	Q1LGL3 Putative uncharacterized protein
NPKM_387	389403 -	390222 Rmet_3846		14.00	1.00	Op1069r_1	NA	Q1LGL2 Methyltransferase type 11
3UTR_217	389435 +	389441 Rmet_3845				Op1068f_1		
NPKM_388	390291 -	390531 Rmet_3847		24.67	3.06	Op1069r_1	NA	Q1LGL1 Putative uncharacterized protein
5UTR_187	390474 +	390736 Rmet_3848				Op1070f_1		
5UTR_831	390532 -	390543 Rmet_3847				Op1069r_1		
NPKM_389	390736 +	391222 Rmet_3848		33.33	2.89	Op1070f_1	MET-COF-CoQ	Q1LGL0 3-demethylubiquinone-9 3-methyltransferase
3UTR_1019	390993 -	391229 Rmet_3849				Op1071r_1		
3UTR_218	391223 +	392124 Rmet_3848				Op1070f_1		
NPKM_390	391230 -	392700 Rmet_3849		3.67	0.58	Op1071r_1	NA	Q1LGK9 Putative uncharacterized protein
NPKM_391	392696 -	393578 Rmet_3850		6.00	1.00	Op1071r_1	NA	Q1LGK8 Putative thiol-disulphide oxidoreductase DCC
NPKM_392	393626 -	394070 Rmet_3851		4.67	0.58	Op1071r_1	NA	Q1LGK7 Integral membrane protein-like protein
NPKM_393	394066 -	395359 Rmet_3852		5.00	0.00	Op1071r_1	NA	Q1LGK6 NAD-dependent epimerase/dehydratase
NPKM_394	395462 -	396008 Rmet_3853		51.67	2.08	Op1071r_1	NA	Q1LGK5 Transcriptional regulators-like protein
NPKM_395	396065 +	397544 Rmet_3854		0.67	0.58	Op1072f_1	NA	Q1LGK4 Putative nitrilotriacetate monooxygenase component A
3UTR_219	397545 +	397592 Rmet_3854				Op1072f_1		
NPKM_396	397663 +	398485 Rmet_3855	<i>metQ</i>	1.00	0.00	Op1072f_1	EIP-TRA-ABC	Q1LGK3 NLPA lipoprotein
NPKM_397	398500 +	399325 Rmet_3856	<i>metN</i>	1.00	0.00	Op1072f_1	EIP-TRA-ABC	Q1LGK2 ABC transporter related
NPKM_398	399308 +	399962 Rmet_3857	<i>metI</i>	1.67	0.58	Op1072f_1	EIP-TRA-ABC	Q1LGK1 Binding-protein-dependent transport systems inner membrane component
3UTR_1018	399995 -	400020 Rmet_3858				Op1073r_2		
NPKM_399	400021 -	401377 Rmet_3858		6.00	0.00	Op1073r_2	NA	Q1LGK0 Acyl-CoA dehydrogenase
NPKM_400	401418 -	402480 Rmet_3859		20.00	1.00	Op1073r_2	NA	Q1LGJ9 Rhodanese-like protein
NPKM_401	402476 -	403550 Rmet_3860	<i>selD</i>	30.67	3.21	Op1073r_2	MET-OAA-Other	Q1LGJ8 Selenophosphate synthase
NPKM_402	403658 -	405323 Rmet_3861		25.33	3.21	Op1073r_2	NA	Q1LGJ7 Rhomboid-like protein
NPKM_403	405506 -	406157 Rmet_3862		4.00	1.00	Op1073r_1	NA	Q1LGJ6 Lysine exporter protein (LYSE/YGGA)
NPKM_404	406231 +	407128 Rmet_3863		6.67	1.53	Op1074f_1	NA	Q1LGJ5 Transcriptional regulator, LysR family
3UTR_220	407129 +	407625 Rmet_3863				Op1074f_1		
NPKM_405	407281 -	407740 Rmet_3864	<i>chrF2</i>	2.00	0.00	Op1075r_2	NA	Q1LGJ4 Putative uncharacterized protein
NPKM_406	407753 -	408926 Rmet_3865	<i>chrA2</i>	2.33	0.58	Op1075r_2	EIP-TRA-Ion	Q1LGJ3 Chromate transporter
NPKM_407	408945 -	409953 Rmet_3866	<i>chrB2</i>	1.00	0.00	Op1075r_1	NA	Q1LGJ2 Putative chromate resistance signal peptide protein
NPKM_408	410052 -	410991 Rmet_3867		14.00	1.00	Op1075r_1	NA	Q1LGJ1 Transcriptional regulator, AraC family
5UTR_830	410992 -	411002 Rmet_3867				Op1075r_1		
NPKM_409	411077 +	412499 Rmet_3868		4.00	1.00	Op1076f_1	MET-LIP-FAMet	Q1LGJ0 Cytochrome P450
3UTR_221	412500 +	412526 Rmet_3868				Op1076f_1		
3UTR_1017	412574 -	412575 Rmet_3869				Op1077r_1		
NPKM_410	412576 -	413656 Rmet_3869		2.00	0.00	Op1077r_1	NA	Q1LGI9 NADH:flavin oxidoreductase/NADH oxidase
5UTR_829	413657 -	413714 Rmet_3869				Op1077r_1		
NPKM_411	413829 +	414699 Rmet_3870		8.00	1.00	Op1078f_1	NA	Q1LGI8 Transcriptional regulator, LysR family
3UTR_222	414700 +	415183 Rmet_3870				Op1078f_1		
3UTR_1016	414749 -	414849 Rmet_3871				Op1079r_2		

NPKM_412	414850 -	415282 Rmet_3871	3.00	1.00	Op1079r_2	NA	Q1LGI7 Conserved hypothetical signal peptide protein
3UTR_1015	415373 -	415420 Rmet_3872			Op1079r_2		
NPKM_413	415421 -	416408 Rmet_3872	2.00	0.00	Op1079r_2	NA	Q1LGI6 Putative uncharacterized protein
5UTR_828	416409 -	416417 Rmet_3872			Op1079r_2		
3UTR_1014	416576 -	416685 Rmet_3873			Op1079r_2		
NPKM_414	416686 -	417205 Rmet_3873	43.33	1.15	Op1079r_2	NA	Q1LGI5 Transcriptional regulator, MarR family
5UTR_827	417206 -	417228 Rmet_3873			Op1079r_2		
3UTR_1013	417385 -	417437 Rmet_3874			Op1079r_1		
NPKM_415	417438 -	418209 Rmet_3874	3.67	0.58	Op1079r_1	MET-LIP-FASyn	Q1LGI4 Short-chain dehydrogenase/reductase SDR
NPKM_416	418321 +	419245 Rmet_3875	17.33	1.15	Op1080f_1	NA	Q1LGI3 Transcriptional regulator, LysR family
NPKM_417	419283 +	422205 Rmet_3876	6.67	0.58	Op1080f_1	NA	Q1LGI2 Metal dependent phosphohydrolase
3UTR_1012	421290 -	422228 Rmet_3877			Op1081r_2		
3UTR_223	422206 +	422701 Rmet_3876			Op1080f_1		
NPKM_418	422229 -	423036 Rmet_3877	19.00	1.73	Op1081r_2	NA	Q1LGI1 Putative uncharacterized protein
NPKM_419	423141 -	424065 Rmet_3878	6.33	1.15	Op1081r_1	NA	Q1LGI0 Putative uncharacterized protein
5UTR_188	424308 +	424316 Rmet_3879			Op1082f_1		
NPKM_420	424316 +	425180 Rmet_3879	2.00	0.00	Op1082f_1	NA	Q1LGH9 Putative uncharacterized protein
NPKM_421	425260 +	425590 Rmet_3880	12.67	2.52	Op1082f_2	NA	Q1LGH8 Putative uncharacterized protein
NPKM_422	425608 +	426322 Rmet_3881	15.00	2.65	Op1082f_2	NA	Q1LGH7 Two component transcriptional regulator, winged helix family
NPKM_423	426321 +	427635 Rmet_3882	5.33	0.58	Op1082f_2	EIP-SIG-2Comp	Q1LGH6 Sensor protein
NPKM_424	427758 +	428514 Rmet_3883	5.33	0.58	Op1082f_2	NA	Q1LGH5 Putative uncharacterized protein
NPKM_425	428645 +	429179 Rmet_3884	57.67	0.58	Op1082f_3	NA	Q1LGH4 Transcriptional regulator, MarR family
3UTR_224	429180 +	429902 Rmet_3884			Op1082f_3		
3UTR_1011	429223 -	429242 Rmet_3885			Op1083r_1		
NPKM_426	429243 -	429981 Rmet_3885	3.33	0.58	Op1083r_1	NA	Q1LGH3 Asp/Glu racemase
NPKM_427	429987 -	431406 Rmet_3886	3.00	1.00	Op1083r_1	MET-NUC-Pyr	Q1LGH2 Dihydropyrimidinase
NPKM_428	431431 -	432160 Rmet_3887	1.67	0.58	Op1083r_1	MET-CAH-But	Q1LGH1 Asp/Glu racemase
NPKM_429	432255 -	433557 Rmet_3888	3.67	0.58	Op1083r_1	NA	Q1LGH0 Major facilitator superfamily MFS_1
NPKM_430	433744 +	434467 Rmet_3889	42.00	1.73	Op1084f_1	NA	Q1LGG9 Transcriptional regulator, GntR family
NPKM_431	434647 +	435418 Rmet_3890	15.00	1.73	Op1084f_1	EIP-TRA-ABC	Q1LGG8 Extracellular solute-binding protein, family 1
3UTR_225	435419 +	435451 Rmet_3890			Op1084f_1		
NPKM_432	435470 -	435929 Rmet_3891	1.33	0.58	Op1085r_1	NA	Q1LGG7 Endoribonuclease L-PSP
5UTR_826	435930 -	435941 Rmet_3891			Op1085r_1		
NPKM_433	436052 -	436787 Rmet_3892	1.33	0.58	Op1085r_1	NA	Q1LGG6 Short-chain dehydrogenase/reductase SDR
5UTR_825	436788 -	436831 Rmet_3892			Op1085r_1		
5UTR_189	436909 +	436924 Rmet_3893			Op1086f_1		
NPKM_434	436924 +	437878 Rmet_3893	8.33	0.58	Op1086f_1	NA	Q1LGG5 Transcriptional regulator, LysR family
NPKM_435	438178 +	439204 Rmet_3894	103.33	7.77	Op1086f_2	NA	Q1LGG4 Putative uncharacterized protein
NPKM_436	439314 +	440064 Rmet_3895	13.00	2.00	Op1086f_2	NA	Q1LGG3 Transcriptional regulator, GntR family
NPKM_437	440109 +	441651 Rmet_3896	60.67	1.53	Op1086f_3	MET-CAH-But	Q1LGG2 Thiamine pyrophosphate enzyme-like TPP-binding
3UTR_1010	441115 -	441716 Rmet_3897			Op1087r_1		
3UTR_226	441652 +	442348 Rmet_3896			Op1086f_3		
NPKM_438	441717 -	442578 Rmet_3897	9.67	1.15	Op1087r_1	NA	Q1LGG1 Putative uncharacterized protein

NPKM_439	442604 -	443984 Rmet_3898		9.67	2.08	Op1087r_1	NA	Q1LGG0 MmgE/PrpD
NPKM_440	443992 -	445162 Rmet_3899		8.00	1.00	Op1087r_1	MET-CAH-Prop	Q1LGF9 Acyl-CoA dehydrogenase-like protein
5UTR_824	445163 -	445345 Rmet_3899				Op1087r_1		
5UTR_190	445225 +	445273 Rmet_3900	bug			Op1088f_1		
NPKM_441	445273 +	446470 Rmet_3900	bug	19.33	2.08	Op1088f_1	NA	Q1LGF8 Uncharacterized protein UPF0065
3UTR_1009	446154 -	446491 Rmet_3901				Op1089r_1		
3UTR_227	446471 +	447107 Rmet_3900	bug			Op1088f_1		
NPKM_442	446492 -	447395 Rmet_3901		34.00	4.36	Op1089r_1	NA	Q1LGF7 Transcriptional regulator, LysR family
NPKM_443	447393 +	448446 Rmet_3902		40.33	9.07	Op1090f_1	NA	Q1LGF6 Short-chain dehydrogenase/reductase SDR
5UTR_823	447396 -	447425 Rmet_3901				Op1089r_1		
3UTR_228	448447 +	448722 Rmet_3902				Op1090f_1		
3UTR_1008	448715 -	448725 Rmet_3903				Op1091r_1		
NPKM_444	448726 -	449173 Rmet_3903		1.33	0.58	Op1091r_1	NA	Q1LGF5 Putative uncharacterized protein
5UTR_191	448792 +	449323 Rmet_3904	yeaG			Op1092f_1		
NPKM_445	449323 +	451246 Rmet_3904	yeaG	134.33	25.38	Op1092f_1	NA	Q1LGF4 Putative serine protein kinase, PrkA
NPKM_446	451342 +	452614 Rmet_3905		46.00	9.17	Op1092f_1	NA	Q1LGF3 Putative uncharacterized protein
NPKM_447	452651 +	454190 Rmet_3906		26.00	3.61	Op1092f_1	NA	Q1LGF2 SpoVR
3UTR_1007	453847 -	454210 Rmet_3907				Op1093r_1		
3UTR_229	454191 +	455043 Rmet_3906				Op1092f_1		
NPKM_448	454211 -	455390 Rmet_3907		40.00	3.46	Op1093r_1	NA	Q1LGF1 Transcriptional regulator, LuxR family
NPKM_449	455764 -	458080 Rmet_3908		22.33	2.08	Op1093r_1	NA	Q1LGF0 MscS Mechanosensitive ion channel
5UTR_822	458081 -	458091 Rmet_3908				Op1093r_1		
NPKM_450	458362 +	458683 Rmet_3909		3.00	0.00	Op1094f_1	NA	Q1LGE9 Putative uncharacterized protein
3UTR_1006	458560 -	458709 Rmet_6632				Op2060r_1		
3UTR_230	458684 +	458714 Rmet_3909				Op1094f_1		
NPKM_451	458710 -	458929 Rmet_6632		3.00	2.00	Op2060r_1	NA	NA
5UTR_192	458885 +	458889 Rmet_3910				Op1094f_1		
NPKM_452	458889 +	459240 Rmet_3910		1.67	0.58	Op1094f_1	NA	Q1LGE8 Putative uncharacterized protein
5UTR_821	458930 -	459644 Rmet_6632				Op2060r_1		
3UTR_231	459241 +	459273 Rmet_3910				Op1094f_1		
NPKM_453	459279 +	459906 Rmet_3911		76.33	2.89	Op1094f_2	NA	Q1LGE7 Lysine exporter protein (LYSE/YGGA)
3UTR_1005	459655 -	459932 Rmet_3912				Op1095r_1		
3UTR_232	459907 +	460676 Rmet_3911				Op1094f_2		
NPKM_454	459933 -	460608 Rmet_3912		18.67	0.58	Op1095r_1	MET-CAH-FruMan	Q1LGE6 Phosphoglycerate mutase
NPKM_455	460794 -	461793 Rmet_3913	bug	25.67	2.89	Op1095r_1	NA	Q1LGE5 Uncharacterized protein UPF0065
NPKM_456	461907 -	462612 Rmet_3914		21.33	0.58	Op1095r_1	NA	Q1LGE4 Transcriptional regulator, TetR family
5UTR_193	462710 +	462743 Rmet_3915				Op1096f_1		
NPKM_457	462743 +	463556 Rmet_3915		12.67	0.58	Op1096f_1	NA	Q1LGE3 Transcriptional regulator, IclR family
NPKM_458	463638 +	465750 Rmet_3916		13.00	1.00	Op1096f_1	MET-COF-Biotine	Q1LGE2 CoA-binding
NPKM_459	465792 +	466779 Rmet_3917	bug	4.67	0.58	Op1096f_1	NA	Q1LGE1 Uncharacterized protein UPF0065
NPKM_460	466806 +	468120 Rmet_3918		6.33	0.58	Op1096f_1	NA	Q1LGE0 Putative uncharacterized protein
NPKM_461	468159 +	469476 Rmet_3919		7.00	1.00	Op1096f_1	NA	Q1LGD9 Putative uncharacterized protein
NPKM_462	469472 +	470450 Rmet_3920	bug	8.67	0.58	Op1096f_1	NA	Q1LGD8 Uncharacterized protein UPF0065

3UTR_1004	470388 -	470502 Rmet_3921				Op1097r_2		
3UTR_233	470451 +	471148 Rmet_3920	bug			Op1096f_1		
NPKM_463	470503 -	470932 Rmet_3921		10.00	1.00	Op1097r_2	NA	Q1LGD7 Putative uncharacterized protein
NPKM_464	471044 -	472637 Rmet_3922	ydjQ	29.67	1.53	Op1097r_2	GIP-REP-DNA_Pol	Q1LGD6 DNA polymerase III, epsilon subunit
5UTR_820	472638 -	472643 Rmet_3922	ydjQ			Op1097r_2		
NPKM_465	473015 -	473081 Rmet_6633		0.00	0.00	Op1097r_1	NA	NA
NPKM_466	473144 +	474671 Rmet_R0075		0.00	0.00	Op1098f_1	NA	NA
NPKM_467	474735 +	474812 Rmet_R0076		0.00	0.00	Op1098f_1	NA	NA
NPKM_468	474823 +	474899 Rmet_R0077		0.00	0.00	Op1098f_1	NA	NA
NPKM_469	475181 +	477999 Rmet_R0078		0.00	0.00	Op1098f_1	NA	NA
NPKM_470	478178 +	478292 Rmet_R0079		0.00	0.00	Op1098f_1	NA	NA
NPKM_471	478646 +	479051 Rmet_6634		82.33	8.14	Op1098f_2	NA	NA
NPKM_472	479174 +	480338 Rmet_3923	acrA	99.00	2.65	Op1098f_2	EIP-TRA-Other	Q1LGD5 Secretion protein HlyD
NPKM_473	480364 +	483511 Rmet_3924	acrB	100.00	2.00	Op1098f_2	EIP-TRA-Ion	Q1LGD4 Hydrophobe/amphiphile efflux-1 HAE1
NPKM_474	483507 +	485007 Rmet_3925		121.67	1.53	Op1098f_2	NA	Q1LGD3 RND efflux system, outer membrane lipoprotein, NodT
3UTR_1003	484816 -	485099 Rmet_3926				Op1099r_3		
3UTR_234	485008 +	485083 Rmet_3925				Op1098f_2		
NPKM_475	485100 -	486009 Rmet_3926		16.67	1.15	Op1099r_3	MET-AA-ArgPro	Q1LGD2 Arginase
NPKM_476	486106 -	487096 Rmet_3927	bug	3.33	0.58	Op1099r_2	NA	Q1LGD1 Twin-arginine translocation pathway signal
NPKM_477	487177 -	487414 Rmet_3928		0.00	0.00	Op1099r_1	NA	Q1LGD0 Putative uncharacterized protein
NPKM_478	487453 -	487669 Rmet_3929	tnmC	0.00	0.00	Op1099r_1	NA	NA
NPKM_479	487722 -	488556 Rmet_3930	gspA	0.00	0.00	Op1099r_1	NA	NA
NPKM_480	488552 -	489992 Rmet_3931	tnmA	0.00	0.00	Op1099r_1	NA	NA
NPKM_481	490103 -	490673 Rmet_3932	tnmB	0.00	0.00	Op1099r_1	NA	NA
NPKM_482	490739 -	491675 Rmet_3933	tctC	4.67	0.58	Op1099r_1	EIP-TRA-Ion	Q1LGC5 Uncharacterized protein UPF0065
3UTR_235	490784 +	491702 mobile_element				0		
5UTR_819	491676 -	491726 Rmet_3933	tctC			Op1099r_1		
5UTR_195	491779 +	491818 Rmet_3934				Op1100f_1		
NPKM_483	491818 +	492490 Rmet_3934		22.33	2.89	Op1100f_1	EIP-SIG-2Comp	Q1LGC4 Two component transcriptional regulator, winged helix family
NPKM_484	492482 +	493910 Rmet_3935		11.00	1.00	Op1100f_1	EIP-SIG-2Comp	Q1LGC3 Sensor protein
NPKM_485	494023 +	495670 Rmet_3936		6.00	1.00	Op1100f_1	NA	Q1LGC2 Drug resistance transporter EmrB/QacA subfamily
NPKM_486	495717 +	496179 Rmet_3937		164.00	6.56	Op1100f_2	NA	Q1LGC1 Transcriptional regulator, MarR family
3UTR_1002	495789 -	496203 Rmet_3938	cobB			Op1101r_3		
3UTR_236	496180 +	496993 Rmet_3937				Op1100f_2		
NPKM_487	496204 -	497626 Rmet_3938	cobB	32.33	1.53	Op1101r_3	MET-COF-Porph	Q1LGC0 Cobyrinate a,c-diamide synthase / hydrogenobyrinic acid a,c-diamide synthase
NPKM_488	497634 -	498537 Rmet_3939		4.33	1.53	Op1101r_2	EIP-SIG-2Comp	Q1LGB9 Two component transcriptional regulator, LuxR family
NPKM_489	498602 -	499556 Rmet_3940		202.00	22.11	Op1101r_2	NA	Q1LGB8 Transcriptional regulator, LysR family
NPKM_490	500135 -	500309 Rmet_6635		5.00	2.00	Op1101r_1	NA	NA
5UTR_196	500186 +	500241 Rmet_3941				Op1102f_1		
NPKM_491	500241 +	500538 Rmet_3941		70.00	17.09	Op1102f_1	NA	Q1LGB7 Putative uncharacterized protein
NPKM_492	500534 -	501428 Rmet_3942	tnpB	0.00	0.00	Op2061r_1	NA	NA
3UTR_237	500539 +	500541 Rmet_3941				Op1102f_1		
NPKM_493	501424 -	501721 Rmet_3943	tnpA	0.00	0.00	Op2061r_1	NA	NA

5UTR_197	501766 +	501782 Rmet_3944				Op1104f_1		
NPKM_494	501782 +	502013 Rmet_3944		4.00	1.73	Op1104f_1	GIP-REP-Recomb	Q1LGB4 Transposase IS3/IS911
NPKM_495	502135 +	502453 Rmet_3945		180.33	10.21	Op1104f_2	NA	Q1LGB3 Putative uncharacterized protein
NPKM_496	502544 +	503957 Rmet_3946		33.33	1.53	Op1104f_2	NA	Q1LGB2 Putative uncharacterized protein
3UTR_1001	503682 -	504834 Rmet_3948				Op1105r_1		
NPKM_497	503959 +	504805 Rmet_3947		22.00	2.00	Op1104f_2	NA	Q1LGB1 Putative uncharacterized protein
3UTR_238	504806 +	505139 Rmet_3947				Op1104f_2		
NPKM_498	504835 -	505495 Rmet_3948		101.33	13.58	Op1105r_1	NA	Q1LGB0 Transcriptional regulator, Crp/Fnr family
5UTR_818	505496 -	505614 Rmet_3948				Op1105r_1		
5UTR_198	505823 +	505862 Rmet_3949	phaZ3			Op1106f_1		
NPKM_499	505862 +	506936 Rmet_3949	phaZ3	143.00	9.00	Op1106f_1	NA	Q1LGA9 Esterase, PHB depolymerase
3UTR_239	506937 +	506985 Rmet_3949	phaZ3			Op1106f_1		
3UTR_1000	506995 -	507038 Rmet_3950				Op1107r_2		
NPKM_500	507039 -	508350 Rmet_3950		81.67	1.53	Op1107r_2	NA	Q1LGA8 Major facilitator superfamily MFS_1
5UTR_199	508369 +	508631 Rmet_3951				Op1108f_1		
NPKM_501	508372 -	508600 Rmet_6636		4.33	1.15	Op1107r_1	NA	NA
NPKM_502	508631 +	512645 Rmet_3951		37.00	1.00	Op1108f_1	NA	Q1LGA7 Putative uncharacterized protein
NPKM_503	512755 +	512941 Rmet_3952		71.67	3.06	Op1108f_1	NA	Q1LGA6 Rubredoxin
3UTR_999	512857 -	512947 Rmet_6637				Op1109r_1		
3UTR_240	512942 +	513610 Rmet_3952				Op1108f_1		
NPKM_504	512948 -	513104 Rmet_6637		4.67	2.31	Op1109r_1	NA	NA
3UTR_998	513122 -	513202 Rmet_3953				Op1109r_1		
NPKM_505	513203 -	513392 Rmet_3953		8.33	2.08	Op1109r_1	NA	Q1LGA5 Putative membrane protein
5UTR_817	513393 -	513400 Rmet_3953				Op1109r_1		
5UTR_200	513613 +	513668 Rmet_3954				Op1110f_1		
NPKM_506	513668 +	514172 Rmet_3954		4.00	1.73	Op1110f_1	NA	Q1LGA4 Conserved hypothetical transmembrane protein
3UTR_241	514173 +	514264 Rmet_3954				Op1110f_1		
NPKM_507	514447 +	515623 Rmet_3955		0.33	0.58	Op1110f_1	MET-EN-OxPhos	Q1LGA3 Cytochrome c oxidase subunit 2
NPKM_508	515660 +	517418 Rmet_3956		1.00	0.00	Op1110f_2	MET-EN-OxPhos	Q1LGA2 Cytochrome c oxidase, subunit I
NPKM_509	517414 +	518083 Rmet_3957		1.00	0.00	Op1110f_2	MET-EN-OxPhos	Q1LGA1 Cytochrome c oxidase subunit III
NPKM_510	518095 +	518800 Rmet_3958		0.67	0.58	Op1110f_2	MET-EN-OxPhos	Q1LGA0 Cytochrome c oxidase, subunit III
NPKM_511	518808 +	519162 Rmet_3959		0.00	0.00	Op1110f_2	NA	Q1LG99 Conserved hypothetical transmembrane protein
5UTR_201	519197 +	519221 Rmet_3960				Op1110f_3		
NPKM_512	519221 +	520421 Rmet_3960		23.67	0.58	Op1110f_3	NA	Q1LG98 Putative uncharacterized protein
3UTR_997	519907 -	520508 Rmet_3961	gabD			Op1111r_1		
3UTR_242	520422 +	520691 Rmet_3960				Op1110f_3		
NPKM_513	520509 -	521937 Rmet_3961	gabD	276.00	13.11	Op1111r_1	MET-CAH-But	Q1LG97 Succinate semialdehyde dehydrogenase
5UTR_816	521938 -	522045 Rmet_3961	gabD			Op1111r_1		
5UTR_202	522149 +	522169 Rmet_3962				Op1112f_1		
NPKM_514	522169 +	523648 Rmet_3962		14.00	1.00	Op1112f_1	NA	Q1LG96 MATE efflux family protein
3UTR_243	523649 +	523827 Rmet_3962				Op1112f_1		
5UTR_203	523958 +	524028 Rmet_3963				Op1112f_2		
NPKM_515	524028 +	524523 Rmet_3963		62.00	3.46	Op1112f_2	NA	Q1LG95 Putative uncharacterized protein

NPKM_516	524536 +	526039 Rmet_3964		72.33	5.13	Op1112f_2	NA	Q1LG94 Putative uncharacterized protein
NPKM_517	526168 +	526510 Rmet_3965		17.67	5.03	Op1112f_2	NA	Q1LG93 Transcriptional regulator, PadR family
3UTR_244	526511 +	526654 Rmet_3965				Op1112f_2		
3UTR_996	526699 -	526731 Rmet_3966				Op1113r_2		
NPKM_518	526732 -	529198 Rmet_3966		5.00	1.00	Op1113r_2	NA	Q1LG92 Putative uncharacterized protein
3UTR_995	529419 -	529675 Rmet_3967				Op1113r_2		
NPKM_519	529676 -	530684 Rmet_3967		81.67	4.04	Op1113r_2	NA	Q1LG91 Response regulator receiver modulated diguanylate cyclase
NPKM_520	530707 -	531724 Rmet_3968		60.00	3.46	Op1113r_2	NA	Q1LG90 Chemotaxis response regulator protein-glutamate methylesterase 2
NPKM_521	531720 -	534027 Rmet_3969		56.33	5.03	Op1113r_2	NA	Q1LG89 CheA signal transduction histidine kinases
NPKM_522	534023 -	534776 Rmet_3970		36.67	4.04	Op1113r_2	NA	Q1LG88 CheW protein
NPKM_523	534768 -	536058 Rmet_3971		53.67	4.73	Op1113r_2	NA	Q1LG87 MCP methyltransferase, CheR-type
NPKM_524	536054 -	536528 Rmet_3972		68.33	2.08	Op1113r_2	NA	Q1LG86 CheW protein
NPKM_525	536555 -	538376 Rmet_3973		91.33	8.39	Op1113r_2	NA	Q1LG85 Methyl-accepting chemotaxis sensory transducer
NPKM_526	538246 -	538417 Rmet_6638		1.67	1.15	Op1113r_1	NA	NA
5UTR_204	538298 +	538449 Rmet_3974				Op1114f_1		
NPKM_527	538449 +	539775 Rmet_3974		130.33	5.51	Op1114f_1	NA	Q1LG84 Diguanylate cyclase/phosphodiesterase
NPKM_528	539963 +	542471 Rmet_3975		68.00	8.19	Op1114f_1	NA	Q1LG83 Putative chromosome segregation ATPases
3UTR_245	542472 +	542571 Rmet_3975				Op1114f_1		
3UTR_994	542566 -	542663 Rmet_3976				Op1115r_2		
NPKM_529	542664 -	543837 Rmet_3976		28.67	3.06	Op1115r_2	EIP-TRA-ABC	Q1LG82 Extracellular ligand-binding receptor
NPKM_530	543939 -	544647 Rmet_3977	<i>livF4</i>	9.33	1.15	Op1115r_1	EIP-TRA-ABC	Q1LG81 ABC transporter related
NPKM_531	544633 -	545398 Rmet_3978	<i>livG4</i>	10.00	0.00	Op1115r_1	EIP-TRA-ABC	Q1LG80 ABC transporter related
NPKM_532	545390 -	546419 Rmet_3979	<i>livM4</i>	7.67	1.15	Op1115r_1	EIP-TRA-ABC	Q1LG79 Inner-membrane translocator
NPKM_533	546438 -	547302 Rmet_3980	<i>livH4</i>	7.00	1.00	Op1115r_1	EIP-TRA-ABC	Q1LG78 Inner-membrane translocator
5UTR_815	547303 -	547388 Rmet_3980	<i>livH4</i>			Op1115r_1		
5UTR_205	547472 +	547610 Rmet_3981				Op1116f_1		
NPKM_534	547610 +	548453 Rmet_3981		16.67	2.08	Op1116f_1	NA	Q1LG77 Transcriptional regulator, IclR family
3UTR_993	548114 -	550413 Rmet_3984	<i>yebQ</i>			Op1117r_2		
NPKM_535	548490 +	549303 Rmet_3982		26.67	2.31	Op1116f_1	NA	Q1LG76 Short-chain dehydrogenase/reductase SDR
NPKM_536	549372 +	550359 Rmet_3983	<i>bug</i>	29.67	1.53	Op1116f_1	NA	Q1LG75 Uncharacterized protein UPF0065
3UTR_246	550360 +	551342 Rmet_3983	<i>bug</i>			Op1116f_1		
NPKM_537	550414 -	551836 Rmet_3984	<i>yebQ</i>	66.00	5.20	Op1117r_2	NA	Q1LG74 Major facilitator superfamily MFS_1
NPKM_538	551993 -	555464 Rmet_3985		3.33	0.58	Op1117r_1	EIP-SIG-2Comp	Q1LG73 Sensor protein
NPKM_539	555472 -	556126 Rmet_3986		5.67	0.58	Op1117r_1	EIP-SIG-2Comp	Q1LG72 Two component transcriptional regulator, LuxR family
5UTR_814	556127 -	556258 Rmet_3986				Op1117r_1		
NPKM_540	556504 -	557440 Rmet_3987		6.00	0.00	Op1117r_1	NA	Q1LG71 Putative uncharacterized protein
5UTR_206	556634 +	557518 Rmet_3988				Op1118f_1		
NPKM_541	557518 +	557953 Rmet_3988		10.67	1.53	Op1118f_1	NA	Q1LG70 Putative uncharacterized protein
3UTR_247	557954 +	558374 Rmet_3988				Op1118f_1		
NPKM_542	558010 -	558454 Rmet_3989		66.00	3.00	Op1119r_2	NA	Q1LG69 Putative uncharacterized protein
NPKM_543	558477 -	559203 Rmet_3990	<i>folE</i>	61.33	1.53	Op1119r_2	MET-COF-Folate	Q1LG68 GTP cyclohydrolase
NPKM_544	559310 -	560570 Rmet_3991	<i>arsB1</i>	14.00	1.73	Op1119r_1	EIP-TRA-Ion	Q1LG67 Arsenical pump membrane protein
NPKM_545	560581 -	562645 Rmet_3992	<i>mrcB</i>	27.33	1.53	Op1119r_1	NA	Q1LG66 Penicillin-binding protein 1A

NPKM_546	562646 -	563537 Rmet_3993		27.67	2.52	Op1119r_1	NA	Q1LG65 Putative uncharacterized protein	
5UTR_207	563642 +	563681 Rmet_3994				Op1120f_1			
NPKM_547	563681 +	563915 Rmet_3994		51.33	5.69	Op1120f_1	NA	Q1LG64 Putative uncharacterized protein	
3UTR_248	563916 +	564964 Rmet_3994				Op1120f_1			
NPKM_548	563921 -	566246 Rmet_3995	<i>bglX</i>	50.00	2.00	Op1121r_1	MET-CAH-Starch	Q1LG63 Glycoside hydrolase, family 3-like protein	
5UTR_813	566247 -	566351 Rmet_3995	<i>bglX</i>			Op1121r_1			
5UTR_208	566340 +	566453 Rmet_3996	<i>mdoG</i>			Op1122f_1			
3UTR_992	566357 -	568075 Rmet_3997				Op1123r_3			
NPKM_549	566453 +	568064 Rmet_3996	<i>mdoG</i>	82.67	3.06	Op1122f_1		0	0
3UTR_249	568065 +	569877 Rmet_3996	<i>mdoG</i>			Op1122f_1			
NPKM_550	568076 -	568307 Rmet_3997		27.00	2.65	Op1123r_3	NA	Q1LG61 Putative uncharacterized protein	
5UTR_812	568308 -	568357 Rmet_3997				Op1123r_3			
3UTR_991	568378 -	568379 Rmet_3998				Op1123r_2			
NPKM_551	568380 -	569091 Rmet_3998		3.00	1.00	Op1123r_2	NA	Q1LG60 Putative uncharacterized protein	
NPKM_552	569100 -	571566 Rmet_3999		1.00	0.00	Op1123r_1	EIP-TRA-Pores	Q1LG59 TonB-dependent siderophore receptor	
3UTR_990	571618 -	571661 Rmet_4000	<i>fecR</i>			Op1123r_1			
NPKM_553	571662 -	572607 Rmet_4000	<i>fecR</i>	7.33	0.58	Op1123r_1	GIP-TK-RNAP	Q1LG58 FecR family protein	
NPKM_554	572636 -	573146 Rmet_4001	<i>rpoK</i>	15.00	1.00	Op1123r_1	GIP-TK-RNAP	Q1LG57 Sigma-24 (FecI-like)	
NPKM_555	573156 +	573357 Rmet_6639		1.33	1.15	Op2062f_1	NA	NA	
3UTR_250	573358 +	573390 Rmet_6639				Op2062f_1			
NPKM_556	573383 -	574598 Rmet_4002		11.67	1.53	Op1123r_1	NA	Q1LG56 Response regulator receiver (CheY-like) modulated diguanylate phosphodie	
5UTR_209	574221 +	574793 Rmet_4003				Op1124f_1			
5UTR_811	574599 -	574629 Rmet_4002				Op1123r_1			
NPKM_557	574793 +	575522 Rmet_4003		43.00	1.00	Op1124f_1	MET-AA-AlaAsp	Q1LG55 Aspartate racemase	
3UTR_251	575523 +	575730 Rmet_4003				Op1124f_1			
NPKM_558	576112 +	577132 Rmet_4004	<i>tnpA</i>	0.00	0.00	Op1124f_1	NA	P37248 Transposase for insertion sequence element IS1086	
5UTR_210	577139 +	577168 Rmet_4005				Op1124f_2			
NPKM_559	577168 +	578071 Rmet_4005		22.00	1.73	Op1124f_2	NA	Q1LG53 Fimbrial protein	
3UTR_989	577223 -	578197 Rmet_4006				Op1125r_3			
3UTR_252	578072 +	578989 Rmet_4005				Op1124f_2			
NPKM_560	578198 -	578834 Rmet_4006		24.33	2.52	Op1125r_3	NA	Q1LG52 Putative uncharacterized protein	
NPKM_561	578857 -	579244 Rmet_4007		23.67	1.15	Op1125r_3	NA	Q1LG51 Putative uncharacterized protein	
5UTR_810	579245 -	579264 Rmet_4007				Op1125r_3			
3UTR_988	579286 -	579308 Rmet_4008				Op1125r_2			
NPKM_562	579309 -	579801 Rmet_4008		2.33	0.58	Op1125r_2	NA	Q1LG50 PiIT protein-like protein	
NPKM_563	579816 -	580194 Rmet_4009		1.33	0.58	Op1125r_2	NA	Q1LG49 Putative uncharacterized protein	
5UTR_211	580254 +	582248 Rmet_6640				Op2063f_1			
NPKM_564	580293 -	580884 Rmet_4010	<i>aroK</i>	36.67	2.31	Op1125r_2	MET-AA-PheTyrTrp	Q1LG48 Shikimate kinase	
NPKM_565	580927 -	582307 Rmet_4011	<i>pcaK</i>	6.00	0.00	Op1125r_1	NA	Q1LG47 Major facilitator superfamily MFS_1	
NPKM_566	582248 +	582416 Rmet_6640		3.67	1.53	Op2063f_1	NA	NA	
5UTR_809	582308 -	582365 Rmet_4011	<i>pcaK</i>			Op1125r_1			
3UTR_987	582395 -	582584 Rmet_4012				Op1125r_1			
3UTR_253	582417 +	582491 Rmet_6640				Op2063f_1			

NPKM_567	582585 -	583539 Rmet_4012		8.33	1.15	Op1125r_1	NA	Q1LG46 Transcriptional regulator, LysR family
5UTR_808	583540 -	583560 Rmet_4012				Op1125r_1		
NPKM_568	583644 +	584358 Rmet_4013	<i>pcaH</i>	26.67	1.53	Op1126f_1	MET-XEN-24D	Q1LG45 Protocatechuate 3,4-dioxygenase, beta subunit
NPKM_569	584362 +	584932 Rmet_4014	<i>pcaG</i>	34.00	4.00	Op1126f_1	MET-XEN-24D	Q1LG44 Protocatechuate 3,4-dioxygenase, alpha subunit
NPKM_570	584936 +	586409 Rmet_4015	<i>pcaB</i>	26.00	2.00	Op1126f_1	MET-XEN-Benz	Q1LG43 3-carboxy-cis,cis-muconate cycloisomerase
NPKM_571	586442 +	587621 Rmet_4016	<i>pcaD</i>	46.00	2.65	Op1126f_1	MET-XEN-Benz	Q1LG42 3-oxoadipate enol-lactonase / 4-carboxymuconolactone decarboxylase
3UTR_986	587492 -	587623 Rmet_4017	<i>pobR</i>			Op1127r_1		
3UTR_254	587622 +	588167 Rmet_4016	<i>pcaD</i>			Op1126f_1		
NPKM_572	587624 -	588554 Rmet_4017	<i>pobR</i>	9.67	0.58	Op1127r_1	NA	Q1LG41 Transcriptional regulator, AraC family
5UTR_807	588555 -	588614 Rmet_4017	<i>pobR</i>			Op1127r_1		
NPKM_573	588681 +	589878 Rmet_4018	<i>pobA</i>	3.00	0.00	Op1128f_1	MET-XEN-24D	Q1LG40 4-hydroxybenzoate 3-monooxygenase
3UTR_255	589879 +	589886 Rmet_4018	<i>pobA</i>			Op1128f_1		
5UTR_212	589890 +	590044 Rmet_4019	<i>surE</i>			Op1128f_2		
NPKM_574	590044 +	590824 Rmet_4019	<i>surE</i>	72.33	2.52	Op1128f_2	MET-NUC-Pur	Q1LG39 Exopolyphosphatase / 3'-nucleotidase / 5'-nucleotidase
3UTR_985	590871 -	591240 Rmet_4021				Op1129r_1		
NPKM_575	590948 +	591245 Rmet_4020		109.33	11.15	Op1128f_2	NA	Q1LG38 Putative uncharacterized protein
NPKM_576	591241 -	592027 Rmet_4021		13.00	1.73	Op1129r_1	MET-LIP-Ster	Q1LG37 NAD(P)H dehydrogenase (Quinone)
3UTR_256	591246 +	592075 Rmet_4020				Op1128f_2		
5UTR_806	592028 -	592033 Rmet_4021				Op1129r_1		
5UTR_213	592086 +	592120 Rmet_4022				Op1130f_1		
NPKM_577	592120 +	593017 Rmet_4022		10.67	1.53	Op1130f_1	NA	Q1LG36 Transcriptional regulator, LysR family
3UTR_984	592490 -	593138 Rmet_4023				Op1131r_1		
NPKM_578	593139 -	593547 Rmet_4023		4.00	0.00	Op1131r_1	NA	Q1LG35 Putative uncharacterized protein
NPKM_579	593587 -	593923 Rmet_4024		3.67	0.58	Op1131r_1	NA	Q1LG34 Putative uncharacterized protein
NPKM_580	594025 +	595174 Rmet_4025		13.33	2.08	Op1132f_1	NA	Q1LG33 Major facilitator superfamily MFS_1
3UTR_257	595175 +	595862 Rmet_4025				Op1132f_1		
NPKM_581	595238 -	595958 Rmet_4026		8.00	1.73	Op1133r_1	NA	Q1LG32 Putative periplasmic ligand-binding sensor protein
5UTR_805	595959 -	596828 Rmet_4026				Op1133r_1		
5UTR_214	596070 +	596090 Rmet_4027				Op1134f_1		
NPKM_582	596090 +	597047 Rmet_4027		32.33	1.53	Op1134f_1	MET-AA-ArgPro	Q1LG31 Proline iminopeptidase
3UTR_983	596832 -	597442 Rmet_4029				Op1135r_1		
NPKM_583	597080 +	597380 Rmet_4028		25.33	1.53	Op1134f_1	NA	Q1LG30 Putative uncharacterized protein
3UTR_258	597381 +	597896 Rmet_4028				Op1134f_1		
NPKM_584	597443 -	599942 Rmet_4029		25.33	3.21	Op1135r_1	NA	Q1LG29 MscS Mechanosensitive ion channel
5UTR_804	599943 -	600143 Rmet_4029				Op1135r_1		
5UTR_215	600086 +	600207 Rmet_4030				Op1136f_1		
3UTR_982	600155 -	601084 Rmet_4032				Op1137r_1		
NPKM_585	600207 +	600615 Rmet_4030		68.33	2.52	Op1136f_1	NA	Q1LG28 Glyoxalase/bleomycin resistance protein/dioxygenase
NPKM_586	600611 +	601001 Rmet_4031		62.00	2.65	Op1136f_1	DIV-Apoptosis	Q1LG27 Cytochrome c, class I
3UTR_259	601002 +	602274 Rmet_4031				Op1136f_1		
NPKM_587	601085 -	601403 Rmet_4032		44.67	2.52	Op1137r_1	NA	Q1LG26 UPF0060 membrane protein Rmet_4032
NPKM_588	601440 -	602421 Rmet_4033		42.33	1.15	Op1137r_1	NA	Q1LG25 Transcriptional regulator, LysR family
5UTR_803	602422 -	602533 Rmet_4033				Op1137r_1		

NPKM_589	602638 +	602974 Rmet_4034	<i>mmfA</i>	0.00	0.00	Op2064f_1	NA	NA
NPKM_590	603030 +	603627 Rmet_4035	<i>mmfB</i>	0.00	0.00	Op2064f_1	NA	NA
NPKM_591	603697 +	604480 Rmet_4036	<i>mmfC1</i>	0.00	0.00	Op2064f_1	NA	NA
NPKM_592	604509 +	604959 Rmet_4037	<i>mmfD</i>	0.00	0.00	Op2064f_1	NA	NA
NPKM_593	604968 +	605727 Rmet_4038	<i>mmfC2</i>	0.00	0.00	Op2064f_1	NA	NA
NPKM_594	605749 +	606415 Rmet_4039	<i>mmfR</i>	0.00	0.00	Op2064f_1	NA	NA
NPKM_595	606411 +	607743 Rmet_4040	<i>mmfS</i>	0.00	0.00	Op2064f_1	NA	NA
NPKM_596	607771 +	608203 Rmet_4041		0.00	0.00	Op2064f_1	NA	NA
NPKM_597	608269 -	608884 Rmet_4042	<i>tniR</i>	0.00	0.00	Op1139r_1	NA	NA
NPKM_598	608944 -	610162 Rmet_4043	<i>tniQ</i>	0.00	0.00	Op1139r_1	NA	NA
NPKM_599	610158 -	611067 Rmet_4044	<i>tniB</i>	0.00	0.00	Op1139r_1	NA	NA
NPKM_600	611069 -	612788 Rmet_4045	<i>tniA</i>	0.00	0.00	Op1139r_1	GIP-REP-Recomb	Q1LG13 Integrase, catalytic region
NPKM_601	612865 +	614740 Rmet_4046	<i>ggt</i>	4.33	0.58	Op1140f_1	MET-LIP-Others	Q1LG12 Gamma-glutamyltransferase 2. Threonine peptidase. MEROPS family T03
NPKM_602	614797 +	615787 Rmet_4047	<i>bug</i>	2.00	0.00	Op1140f_1	NA	Q1LG11 Uncharacterized protein UPF0065
NPKM_603	615786 +	616305 Rmet_4048		1.67	0.58	Op1140f_1	NA	Q1LG10 Putative uncharacterized protein
3UTR_981	615962 -	616320 Rmet_4049				Op1141r_3		
3UTR_260	616306 +	616375 Rmet_4048				Op1140f_1		
NPKM_604	616321 -	616531 Rmet_4049		11.00	0.00	Op1141r_3	NA	Q1LG09 Putative uncharacterized protein
NPKM_605	616538 -	617531 Rmet_4050		10.33	0.58	Op1141r_3	NA	Q1LG08 Pyridoxamine 5'-phosphate oxidase-related, FMN-binding
NPKM_606	617586 -	618258 Rmet_4051		13.33	1.53	Op1141r_3	MET-OAA-GSH	Q1LG07 Glutathione S-transferase-like protein
NPKM_607	618354 -	619257 Rmet_4052		31.67	3.21	Op1141r_3	NA	Q1LG06 Transcriptional regulator, LysR family
NPKM_608	619269 -	620355 Rmet_4053		25.67	2.08	Op1141r_3	NA	Q1LG05 Putative uncharacterized protein
5UTR_802	620356 -	620395 Rmet_4053				Op1141r_3		
3UTR_980	620406 -	620452 Rmet_4054	<i>cycl</i>			Op1141r_2		
NPKM_609	620453 -	621488 Rmet_4054	<i>cycl</i>	4.67	0.58	Op1141r_2	MET-EN-Nitrog	Q1LG04 Cytochrome C biogenesis protein
NPKM_610	621480 -	622032 Rmet_4055	<i>ccmG</i>	4.33	1.53	Op1141r_2	MET-EN-Nitrog	Q1LG03 Periplasmic protein thiol
NPKM_611	622028 -	624071 Rmet_4056	<i>ccmF</i>	2.67	0.58	Op1141r_2	MET-EN-Nitrog	Q1LG02 Cytochrome c-type biogenesis protein CcmF
NPKM_612	624067 -	624517 Rmet_4057	<i>ccmE</i>	1.67	0.58	Op1141r_2	MET-EN-Nitrog	Q1LG01 CcmE/CycJ protein
NPKM_613	624513 -	624660 Rmet_6641		4.67	2.52	Op1141r_2	NA	NA
NPKM_614	624656 -	625436 Rmet_4058	<i>ccmC</i>	2.00	0.00	Op1141r_1	MET-EN-Nitrog	Q1LG00 Heme exporter protein CcmC
NPKM_615	625440 -	626109 Rmet_4059	<i>ccmB</i>	2.00	0.00	Op1141r_1	MET-EN-Nitrog	Q1LFZ9 Heme exporter protein CcmB
NPKM_616	626105 -	626741 Rmet_4060	<i>ccmA</i>	9.00	1.00	Op1141r_1	MET-EN-Nitrog	Q1LFZ8 Cytochrome c biogenesis ATP-binding export protein ccmA 2
NPKM_617	626744 -	627332 Rmet_4061	<i>napC</i>	9.67	1.15	Op1141r_1	MET-EN-Nitrog	Q1LFZ7 Periplasmic nitrate reductase subunit NapC
NPKM_618	627352 -	627844 Rmet_4062	<i>napB</i>	9.00	1.00	Op1141r_1	MET-EN-Nitrog	Q1LFZ6 Periplasmic nitrate reductase subunit NapB
NPKM_619	627861 -	630357 Rmet_4063	<i>napA</i>	16.33	0.58	Op1141r_1	MET-EN-Nitrog	Q1LFZ5 Periplasmic nitrate reductase subunit NapA apoprotein
NPKM_620	630337 -	630667 Rmet_4064	<i>napD</i>	28.33	2.89	Op1141r_1	MET-EN-Nitrog	Q1LFZ4 Periplasmic nitrate reductase chaperone NapD
NPKM_621	630762 -	630927 Rmet_4065	<i>napE</i>	27.33	3.51	Op1141r_1	MET-EN-Nitrog	Q1LFZ3 Periplasmic nitrate reductase NapE
5UTR_801	630928 -	630935 Rmet_4065	<i>napE</i>			Op1141r_1		
NPKM_622	630941 +	631826 Rmet_4066		4.33	0.58	Op1142f_1	NA	Q1LFZ2 Methyltransferase type 11
3UTR_979	631728 -	631797 Rmet_4067	<i>bug</i>			Op1143r_1		
NPKM_623	631798 -	632776 Rmet_4067	<i>bug</i>	1.67	0.58	Op1143r_1	NA	Q1LFZ1 Twin-arginine translocation pathway signal
3UTR_261	631827 +	631852 Rmet_4066				Op1142f_1		
3UTR_978	632811 -	632824 Rmet_4068				Op1143r_1		

NPKM_624	632825 -	634565 Rmet_4068		1.00	1.00	Op1143r_1	MET-LIP-FAMet	Q1LFZ0 AMP-dependent synthetase and ligase
3UTR_977	634571 -	634642 Rmet_4069				Op1143r_1		
NPKM_625	634643 -	638024 Rmet_4069		1.00	0.00	Op1143r_1	NA	Q1LFY9 Carbamoyl-phosphate synthase L chain, ATP-binding
5UTR_800	638025 -	638061 Rmet_4069				Op1143r_1		
3UTR_976	638065 -	638130 Rmet_4070				Op1143r_1		
NPKM_626	638131 -	639025 Rmet_4070		9.67	0.58	Op1143r_1	NA	Q1LFY8 Transcriptional regulator, LysR family
5UTR_799	639026 -	639060 Rmet_4070				Op1143r_1		
NPKM_627	639137 +	640313 Rmet_4071		4.33	0.58	Op1144f_1	NA	Q1LFY7 L-carnitine dehydratase/bile acid-inducible protein F
NPKM_628	640348 +	640810 Rmet_4072		4.33	1.15	Op1144f_1	NA	Q1LFY6 Putative uncharacterized protein
NPKM_629	640868 +	641867 Rmet_4073	bug	6.00	0.00	Op1144f_1	NA	Q1LFY5 Uncharacterized protein UPF0065
NPKM_630	641909 +	643070 Rmet_4074		6.33	1.15	Op1144f_1	NA	Q1LFY4 Acyl-CoA dehydrogenase-like protein
3UTR_262	643071 +	643096 Rmet_4074				Op1144f_1		
NPKM_631	643249 +	644245 Rmet_4075		2.67	0.58	Op1144f_1	MET-CAH-Prop	Q1LFY3 Acyl-CoA dehydrogenase-like protein
3UTR_975	643680 -	644306 Rmet_4076				Op1145r_1		
3UTR_263	644246 +	644258 Rmet_4075				Op1144f_1		
NPKM_632	644307 -	645102 Rmet_4076		29.00	2.00	Op1145r_1	NA	Q1LFY2 Short-chain dehydrogenase/reductase SDR
NPKM_633	645291 -	646635 Rmet_4077		28.00	2.65	Op1145r_1	NA	Q1LFY1 TRAP transporter solute receptor, TAXI family
NPKM_634	646835 -	646967 Rmet_6642		352.00	32.19	Op1145r_1	NA	NA
NPKM_635	646988 -	648416 Rmet_4078	oxlT	232.00	25.51	Op1145r_1	NA	Q1LFY0 Major facilitator superfamily MFS_1
5UTR_216	648358 +	648484 Rmet_6643				Op2064f_1		
5UTR_798	648417 -	648882 Rmet_4078	oxlT			Op1145r_1		
NPKM_636	648484 +	648757 Rmet_6643		0.67	0.58	Op2064f_1	NA	NA
3UTR_974	648884 -	649175 Rmet_4079				Op2065r_1		
NPKM_637	649176 -	649314 Rmet_4079		23.00	2.65	Op2065r_1	NA	
NPKM_638	649394 -	649583 Rmet_6644		13.67	6.66	Op2065r_1	NA	NA
NPKM_639	649492 -	649771 Rmet_6645		25.67	4.04	Op2065r_1	NA	NA
5UTR_217	649660 +	649750 Rmet_4080				Op1146f_1		
NPKM_640	649750 +	650134 Rmet_4080		1.33	0.58	Op1146f_1	NA	Q1LFX9 Putative uncharacterized protein
NPKM_641	649803 -	650019 Rmet_6646		31.67	7.51	Op1147r_3	NA	NA
5UTR_797	650020 -	650029 Rmet_6646				Op1147r_3		
3UTR_264	650135 +	650278 Rmet_4080				Op1146f_1		
3UTR_973	650287 -	650325 Rmet_4081				Op1147r_2		
NPKM_642	650326 -	650776 Rmet_4081		1.33	0.58	Op1147r_2	NA	Q1LFX8 Putative uncharacterized protein
5UTR_796	650777 -	650781 Rmet_4081				Op1147r_2		
3UTR_972	650950 -	650952 Rmet_4082				Op1147r_1		
NPKM_643	650953 -	651247 Rmet_4082		0.33	0.58	Op1147r_1	NA	Q1LFX7 Putative uncharacterized protein
NPKM_644	651342 -	651627 Rmet_4083		1.00	0.00	Op1147r_1	NA	Q1LFX6 Putative uncharacterized protein
5UTR_218	651703 +	651729 Rmet_4084	phoA1			Op1148f_1		
NPKM_645	651729 +	653190 Rmet_4084	phoA1	8.67	1.15	Op1148f_1	MET-COF-Folate	Q1LFX5 Alkaline phosphatase
NPKM_646	653225 +	654629 Rmet_4085	phoA2	3.67	1.15	Op1148f_1	MET-COF-Folate	Q1LFX4 Alkaline phosphatase
3UTR_265	654630 +	654651 Rmet_4085	phoA2			Op1148f_1		
5UTR_219	654663 +	654719 Rmet_4086				Op1148f_1		
NPKM_647	654719 +	655469 Rmet_4086		5.33	1.15	Op1148f_1	NA	Q1LFX3 Putative signal peptide protein

3UTR_971	655440 -	655528 Rmet_4087				Op1149r_1			
3UTR_266	655470 +	656208 Rmet_4086				Op1148f_1			
NPKM_648	655529 -	656096 Rmet_4087		1.33	0.58	Op1149r_1	NA	Q1LFX2	Putative uncharacterized protein
NPKM_649	656128 -	657655 Rmet_4088	pqiB	3.00	1.00	Op1149r_1	NA	Q1LFX1	Mammalian cell entry related
5UTR_795	657656 -	657690 Rmet_4088	pqiB			Op1149r_1			
3UTR_970	657711 -	657757 Rmet_4089	pqiA3			Op1149r_1			
NPKM_650	657758 -	659030 Rmet_4089	pqiA3	6.67	2.08	Op1149r_1	NA	Q1LFX0	Putative uncharacterized protein
NPKM_651	659289 -	659703 Rmet_4090		19.67	2.31	Op1149r_1	NA	Q1LFW9	Transcriptional regulator, MerR family
NPKM_652	659771 +	661034 Rmet_4091		4.00	0.00	Op1150f_1	NA	Q1LFW8	NADH:flavin oxidoreductase/NADH oxidase
3UTR_969	661004 -	661061 Rmet_4092				Op1151r_1			
3UTR_267	661035 +	661311 Rmet_4091				Op1150f_1			
NPKM_653	661062 -	661980 Rmet_4092		8.00	0.00	Op1151r_1	NA	Q1LFW7	Transcriptional regulator, LysR family
5UTR_794	661981 -	661981 Rmet_4092				Op1151r_1			
NPKM_654	662160 +	662859 Rmet_4093		1.00	0.00	Op1152f_1	NA	Q1LFW6	Pirin-like protein
NPKM_655	662911 +	663334 Rmet_4094		2.33	1.15	Op1152f_2	NA	Q1LFW5	DoxX
NPKM_656	663384 +	663750 Rmet_4095		4.33	0.58	Op1152f_2	NA	Q1LFW4	Putative uncharacterized protein
NPKM_657	663838 +	664438 Rmet_4096	wrbA	18.33	0.58	Op1152f_3	NA	Q1LFW3	Flavoprotein wrbA
3UTR_268	664439 +	664589 Rmet_4096	wrbA			Op1152f_3			
3UTR_968	664546 -	664562 Rmet_4097				Op1153r_1			
NPKM_658	664563 -	665688 Rmet_4097		3.00	0.00	Op1153r_1	NA	Q1LFW2	Porin, Gram-negative type
5UTR_793	665689 -	665718 Rmet_4097				Op1153r_1			
NPKM_659	665783 +	666494 Rmet_4098		2.33	0.58	Op1154f_1	NA	Q1LFW1	Putative uncharacterized protein
3UTR_269	666495 +	666502 Rmet_4098				Op1154f_1			
5UTR_220	666567 +	666580 Rmet_4099	caiB			Op1154f_2			
NPKM_660	666580 +	667816 Rmet_4099	caiB	11.33	0.58	Op1154f_2	NA	Q1LFW0	L-carnitine dehydratase/bile acid-inducible protein F
3UTR_967	667394 -	667829 Rmet_6647				Op2066r_1			
3UTR_270	667817 +	668415 Rmet_4099	caiB			Op1154f_2			
NPKM_661	667830 -	668514 Rmet_6647		38.00	4.58	Op2066r_1	NA	NA	
5UTR_221	668684 +	668703 Rmet_4100				Op1154f_2			
NPKM_662	668703 +	669462 Rmet_4100		2.67	0.58	Op1154f_2	MET-CAH-Prop	Q1LFV9	Enoyl-CoA hydratase/isomerase
NPKM_663	669509 +	670496 Rmet_4101	bugT	12.00	1.00	Op1154f_3	NA	Q1LFV8	Uncharacterized protein UPF0065
3UTR_271	670497 +	670558 Rmet_4101	bugT			Op1154f_3			
5UTR_222	670567 +	670595 Rmet_4102				Op1154f_4			
NPKM_664	670595 +	671231 Rmet_4102		24.33	0.58	Op1154f_4	NA	Q1LFV7	Transcriptional regulator, TetR family
NPKM_665	671238 +	672348 Rmet_4103	nemA	109.67	6.03	Op1154f_5	NA	Q1LFV6	NADH:flavin oxidoreductase/NADH oxidase
3UTR_272	672349 +	672476 Rmet_4103	nemA			Op1154f_5			
3UTR_966	672592 -	672615 Rmet_4104	acxR			Op1155r_1			
NPKM_666	672616 -	674602 Rmet_4104	acxR	9.33	0.58	Op1155r_1	NA	Q1LFV5	Sigma54 specific transcriptional regulator with GAF sensor, Fis family
NPKM_667	674903 +	677072 Rmet_4105	acxA	1.00	0.00	Op1156f_1	NA	Q1LFV4	Acetone carboxylase, beta subunit
3UTR_273	677073 +	677078 Rmet_4105	acxA			Op1156f_1			
NPKM_668	677083 +	679408 Rmet_4106	acxB	2.00	0.00	Op1156f_1	NA	Q1LFV3	Acetone carboxylase, alpha subunit
NPKM_669	679431 +	679941 Rmet_4107	acxC	3.00	1.00	Op1156f_1	NA	Q1LFV2	Acetone carboxylase, gamma subunit
3UTR_965	679836 -	680119 Rmet_4108				Op1157r_2			

3UTR_274	679942 +	679954 Rmet_4107	<i>acxC</i>			Op1156f_1		
NPKM_670	680120 -	680897 Rmet_4108		3.67	1.15	Op1157r_2	MET-CAH-FruMan	Q1LFV1 Class II aldolase/adducin-like protein
NPKM_671	680942 -	681947 Rmet_4109	<i>bug</i>	1.67	0.58	Op1157r_1	NA	Q1LFV0 Uncharacterized protein UPF0065
5UTR_792	681948 -	681955 Rmet_4109	<i>bug</i>			Op1157r_1		
NPKM_672	682056 +	682695 Rmet_4110		35.33	0.58	Op1158f_1	NA	Q1LFU9 Transcriptional regulator, XRE family with cupin sensor domain
NPKM_673	682834 +	683359 Rmet_4111		15.33	0.58	Op1158f_1	NA	Q1LFU8 MOSC domain protein
NPKM_674	683358 +	684312 Rmet_4112		11.33	0.58	Op1158f_1	MET-XEN-24D	Q1LFU7 Oxidoreductase FAD-binding region
NPKM_675	684481 +	685342 Rmet_4113		7.33	0.58	Op1158f_1	NA	Q1LFU6 Putative uncharacterized protein
NPKM_676	685378 +	686245 Rmet_4114	<i>pdxK</i>	6.67	0.58	Op1158f_1	MET-COF-B6	Q1LFU5 Pyridoxine kinase
3UTR_964	685683 -	686557 Rmet_4116	<i>psd</i>			Op1159r_3		
NPKM_677	686249 +	686501 Rmet_4115		4.67	1.53	Op1158f_1	NA	Q1LFU4 Putative uncharacterized protein
3UTR_275	686502 +	686552 Rmet_4115				Op1158f_1		
NPKM_678	686558 -	687413 Rmet_4116	<i>psd</i>	64.33	3.21	Op1159r_3	MET-LIP-GlycPLip	Q1LFU3 Phosphatidylserine decarboxylase
5UTR_223	687337 +	687389 Rmet_6648				Op2068f_1		
NPKM_679	687389 +	687602 Rmet_6648		1.67	1.15	Op2068f_1	NA	NA
NPKM_680	687582 -	688878 Rmet_4117	<i>pdxR</i>	22.33	2.08	Op1159r_2	NA	Q1LFU2 Transcriptional regulator, GntR family
3UTR_276	687603 +	688387 Rmet_6648				Op2068f_1		
5UTR_224	688857 +	689289 Rmet_4119	<i>hmyF</i>			Op1160f_1		
NPKM_681	688956 -	689208 Rmet_4118		6.67	2.08	Op1159r_1	NA	Q1LFU1 Putative uncharacterized protein
5UTR_791	689209 -	689212 Rmet_4118				Op1159r_1		
NPKM_682	689289 +	689727 Rmet_4119	<i>hmyF</i>	623.00	58.97	Op1160f_1	NA	Q1LFU0 Putative uncharacterized protein
NPKM_683	689925 +	691308 Rmet_4120	<i>hmyC</i>	62.67	8.96	Op1160f_1	EIP-TRA-Ion	Q1LFT9 Outer membrane efflux protein
NPKM_684	691310 +	692465 Rmet_4121	<i>hmyB</i>	31.67	6.35	Op1160f_1	EIP-TRA-Ion	Q1LFT8 Secretion protein HlyD
3UTR_277	692466 +	692559 Rmet_4121	<i>hmyB</i>			Op1160f_1		
NPKM_685	692549 -	693578 Rmet_4122	<i>tnpA</i>	0.00	0.00	Op2067r_1	NA	NA
5UTR_225	693582 +	693622 Rmet_4123	<i>hmyA</i>			Op1162f_1		
NPKM_686	693622 +	696694 Rmet_4123	<i>hmyA</i>	18.67	2.89	Op1162f_1	EIP-TRA-Ion	Q1LFT6 Heavy metal efflux pump CzcA
NPKM_687	696795 +	697170 Rmet_4124		104.00	3.46	Op1162f_2	NA	Q1LFT5 Putative uncharacterized protein
NPKM_688	697318 +	697816 Rmet_4125		38.33	3.79	Op1162f_2	NA	Q1LFT4 Putative uncharacterized protein
3UTR_963	697888 -	698600 Rmet_4127				Op1163r_1		
NPKM_689	697910 +	698543 Rmet_4126		26.67	3.79	Op1162f_2	NA	Q1LFT3 Nitrogen fixation protein NifQ, putative
3UTR_278	698544 +	699089 Rmet_4126				Op1162f_2		
NPKM_690	698601 -	698946 Rmet_4127		55.67	6.03	Op1163r_1	NA	Q1LFT2 Putative uncharacterized protein
5UTR_790	698947 -	699038 Rmet_4127				Op1163r_1		
5UTR_226	699095 +	699160 Rmet_4128	<i>imuA</i>			Op1164f_1		
NPKM_691	699160 +	700090 Rmet_4128	<i>imuA</i>	64.00	6.24	Op1164f_1	NA	Q1LFT1 Putative uncharacterized protein
NPKM_692	700106 +	701690 Rmet_4129	<i>imuB</i>	49.33	6.11	Op1164f_1	NA	Q1LFT0 Putative uncharacterized protein
NPKM_693	701716 +	705178 Rmet_4130	<i>dnaE2</i>	20.00	2.00	Op1164f_1	NA	NA
3UTR_962	704911 -	705455 Rmet_4131				Op1165r_2		
3UTR_279	705179 +	705769 Rmet_4130	<i>dnaE2</i>			Op1164f_1		
NPKM_694	705456 -	706110 Rmet_4131		39.00	3.46	Op1165r_2	NA	Q1LFS8 Alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen
NPKM_695	706283 -	707417 Rmet_4132		3.00	1.00	Op1165r_1	MET-CAH-FbP	Q1LFS7 Catalytic domain of components of various dehydrogenase complexes
NPKM_696	707433 -	708414 Rmet_4133	<i>pdhB</i>	2.00	0.00	Op1165r_1	MET-CAH-FbP	Q1LFS6 Transketolase, central region

NPKM_697	708406 -	709510 Rmet_4134	<i>pdhA</i>	3.00	0.00	Op1165r_1	MET-CAH-FbP	Q1LFS5 Dehydrogenase, E1 component
NPKM_698	709697 -	710168 Rmet_4135		11.67	0.58	Op1165r_1	NA	Q1LFS4 Putative uncharacterized protein
5UTR_227	709946 +	710004 Rmet_6649				Op1166f_1		
NPKM_699	710004 +	710352 Rmet_6649		2.33	1.15	Op1166f_1	NA	NA
5UTR_789	710169 -	710235 Rmet_4135				Op1165r_1		
NPKM_700	710348 +	711275 Rmet_4136	<i>tauD</i>	4.33	0.58	Op1166f_1	MET-OAA-Taur	Q1LFS3 Taurine catabolism dioxygenase TauD/TfdA
NPKM_701	711324 +	712350 Rmet_4137		5.67	0.58	Op1166f_1	EIP-TRA-ABC	Q1LFS2 Putative periplasmic protein
NPKM_702	712351 +	713191 Rmet_4138	<i>tauB</i>	6.67	0.58	Op1166f_1	EIP-TRA-ABC	Q1LFS1 ABC transporter related
NPKM_703	713229 +	714108 Rmet_4139		4.00	0.00	Op1166f_1	EIP-TRA-ABC	Q1LFS0 Binding-protein-dependent transport systems inner membrane component
3UTR_280	714109 +	714139 Rmet_4139				Op1166f_1		
5UTR_228	714154 +	714192 Rmet_4140				Op1166f_2		
NPKM_704	714192 +	714960 Rmet_4140		125.33	1.15	Op1166f_2	NA	Q1LFR9 Methyltransferase type 11
3UTR_961	714409 -	714992 Rmet_4141				Op1167r_1		
NPKM_705	714993 -	716220 Rmet_4141		10.67	1.53	Op1167r_1	NA	Q1LFR8 Major facilitator superfamily MFS_1
5UTR_788	716221 -	716280 Rmet_4141				Op1167r_1		
NPKM_706	716422 +	717199 Rmet_4142		58.00	5.00	Op1168f_1	NA	Q1LFR7 Transcriptional regulator, IclR family
NPKM_707	717350 +	718580 Rmet_4143		38.33	3.06	Op1168f_1	NA	Q1LFR6 Diguanylate cyclase (GGDEF domain)
3UTR_960	718438 -	718621 Rmet_4144	<i>gltA2</i>			Op1169r_3		
3UTR_281	718581 +	719454 Rmet_4143				Op1168f_1		
NPKM_708	718622 -	719477 Rmet_4144	<i>gltA2</i>	14.00	1.00	Op1169r_3	MET-CAH-TCA	Q1LFR5 Citrate synthase
NPKM_709	719473 -	720718 Rmet_4145	<i>caiB1</i>	9.67	1.53	Op1169r_3	NA	Q1LFR4 L-carnitine dehydratase/bile acid-inducible protein F
NPKM_710	720710 -	721730 Rmet_4146	<i>bugT</i>	7.67	0.58	Op1169r_3	NA	Q1LFR3 Uncharacterized protein UPF0065
5UTR_787	721731 -	721738 Rmet_4146	<i>bugT</i>			Op1169r_3		
3UTR_959	721938 -	722045 Rmet_4147				Op1169r_3		
NPKM_711	722046 -	722694 Rmet_4147		82.33	2.08	Op1169r_3	NA	Q1LFR2 Putative uncharacterized protein
NPKM_712	722722 -	724732 Rmet_4148	<i>sqhC</i>	102.67	0.58	Op1169r_3	NA	Q1LFR1 Squalene cyclase
NPKM_713	724807 -	725656 Rmet_4149	<i>crtB</i>	151.33	10.69	Op1169r_3	MET-LIP-Ster	Q1LFR0 Squalene/phytoene synthase
5UTR_786	725657 -	725720 Rmet_4149	<i>crtB</i>			Op1169r_3		
3UTR_958	725735 -	725765 Rmet_4150				Op1169r_2		
NPKM_714	725766 -	726336 Rmet_4150		19.00	3.46	Op1169r_2	NA	Q1LFQ9 Conserved hypothetical signal peptide protein
NPKM_715	726420 -	726624 Rmet_4151		439.00	24.98	Op1169r_2	NA	Q1LFQ8 Cold-shock DNA-binding protein family
NPKM_716	726628 -	727594 Rmet_4152	<i>tnp</i>	0.00	0.00	Op1169r_1	NA	NA
NPKM_717	727969 -	729070 Rmet_4153	<i>tnpA</i>	0.00	0.00	Op1169r_1	NA	NA
NPKM_718	729825 +	731034 Rmet_4154	<i>tnpA</i>	0.00	0.00	Op1170f_1	NA	NA
5UTR_229	731180 +	731322 Rmet_4155	<i>peIA</i>			Op1170f_2		
NPKM_719	731322 +	734184 Rmet_4155	<i>peIA</i>	10.00	0.00	Op1170f_2	NA	Q1LFQ4 Putative signal peptide protein
NPKM_720	734197 +	738304 Rmet_4156	<i>peIB</i>	7.00	0.00	Op1170f_2	NA	Q1LFQ3 Tetratricopeptide TPR_4
NPKM_721	738355 +	738904 Rmet_4157	<i>peIC</i>	21.33	3.06	Op1170f_3	NA	Q1LFQ2 Putative lipoprotein
NPKM_722	738927 +	740391 Rmet_4158	<i>peID</i>	22.33	1.15	Op1170f_3	NA	Q1LFQ1 Putative transmembrane protein
NPKM_723	740394 +	741381 Rmet_4159	<i>peIE</i>	14.33	1.53	Op1170f_3	NA	Q1LFQ0 Putative transmembrane protein
NPKM_724	741377 +	742967 Rmet_4160	<i>peIF</i>	11.00	0.00	Op1170f_3	NA	Q1LFP9 Glycosyl transferase, group 1
NPKM_725	742968 +	744339 Rmet_4161	<i>peIG</i>	10.00	1.00	Op1170f_3	NA	Q1LFP8 Putative transmembrane protein
NPKM_726	744547 +	745246 Rmet_4162		114.00	7.81	Op1170f_4	NA	Q1LFP7 Two component transcriptional regulator, winged helix family

NPKM_727	745238 +	746909 Rmet_4163		77.67	5.69	Op1170f_4	NA	Q1LFP6 Peptidoglycan-binding LysM
NPKM_728	746895 +	749355 Rmet_4164		36.67	2.08	Op1170f_4	NA	Q1LFP5 Sensor protein
3UTR_957	748901 -	749598 Rmet_4165				Op1171r_1		
3UTR_282	749356 +	750269 Rmet_4164				Op1170f_4		
NPKM_729	749599 -	750475 Rmet_4165		96.67	2.08	Op1171r_1	NA	Q1LFP4 VacJ-like lipoprotein
NPKM_730	750519 -	753246 Rmet_4166	<i>hpnN</i>	61.00	1.00	Op1171r_1	NA	Q1LFP3 Membrane protein, putative
5UTR_785	753247 -	754100 Rmet_4166	<i>hpnN</i>			Op1171r_1		
5UTR_230	753384 +	753427 Rmet_4167	<i>ttg2</i>			Op1172f_1		
NPKM_731	753427 +	754057 Rmet_4167	<i>ttg2</i>	133.67	11.15	Op1172f_1	NA	Q1LFP2 Toluene tolerance
3UTR_283	754058 +	754118 Rmet_4167	<i>ttg2</i>			Op1172f_1		
3UTR_956	754117 -	754159 Rmet_4168	<i>hpnH</i>			Op1173r_1		
NPKM_732	754160 -	755327 Rmet_4168	<i>hpnH</i>	586.67	25.42	Op1173r_1	NA	Q1LFP1 Radical SAM
NPKM_733	755355 -	756354 Rmet_4169	<i>ispH</i>	441.67	16.65	Op1173r_1	NA	NA
5UTR_784	756355 -	756970 Rmet_4169	<i>ispH</i>			Op1173r_1		
5UTR_231	756478 +	756508 Rmet_4170				Op1174f_1		
NPKM_734	756508 +	757585 Rmet_4170		150.00	3.61	Op1174f_1	Met-SecMetab	Q1LFN9 NAD-dependent epimerase/dehydratase
3UTR_955	756972 -	757621 Rmet_4171				Op1175r_2		
3UTR_284	757586 +	758676 Rmet_4170				Op1174f_1		
NPKM_735	757622 -	758765 Rmet_4171		69.67	2.89	Op1175r_2	NA	Q1LFN8 Glycosyl transferase, family 2
NPKM_736	758771 -	759788 Rmet_4172		103.00	2.65	Op1175r_2	NA	Q1LFN7 Putative uncharacterized protein
5UTR_783	759789 -	759795 Rmet_4172				Op1175r_2		
3UTR_954	759904 -	759919 Rmet_4173				Op1175r_1		
NPKM_737	759920 -	760196 Rmet_4173		5.00	1.00	Op1175r_1	NA	Q1LFN6 Putative uncharacterized protein
NPKM_738	760258 -	760504 Rmet_4174		6.00	1.00	Op1175r_1	NA	Q1LFN5 Putative uncharacterized protein
5UTR_782	760505 -	760544 Rmet_4174				Op1175r_1		
5UTR_232	760609 +	760613 Rmet_4175	<i>pmi</i>			Op1176f_1		
NPKM_739	760613 +	761840 Rmet_4175	<i>pmi</i>	42.00	4.36	Op1176f_1	MET-CAH-FruMan	Q1LFN4 N-acylglucosamine 2-epimerase
3UTR_953	761347 -	761846 Rmet_4176				Op1177r_1		
3UTR_285	761841 +	762723 Rmet_4175	<i>pmi</i>			Op1176f_1		
NPKM_740	761847 -	762744 Rmet_4176		33.67	3.21	Op1177r_1	NA	Q1LFN3 Transcriptional regulator, LysR family
5UTR_233	762735 +	762832 Rmet_4177				Op1178f_1		
5UTR_781	762745 -	762823 Rmet_4176				Op1177r_1		
NPKM_741	762832 +	764242 Rmet_4177		6.67	1.15	Op1178f_1	NA	Q1LFN2 Drug resistance transporter EmrB/QacA subfamily
3UTR_952	762837 -	764441 Rmet_4179				Op1179r_1		
3UTR_286	764243 +	764600 Rmet_4177				Op1178f_1		
NPKM_742	764442 -	764817 Rmet_4179		35.33	1.53	Op1179r_1	NA	Q1LFN0 Putative uncharacterized protein
NPKM_743	765093 -	765960 Rmet_4180		36.00	0.00	Op1179r_1	NA	Q1LFM9 Transcriptional regulator, LysR family
5UTR_234	765618 +	765657 Rmet_6650				Op1180f_1		
NPKM_744	765657 +	766008 Rmet_6650		0.67	0.58	Op1180f_1	NA	NA
5UTR_235	766049 +	766056 Rmet_4181	<i>xylH</i>			Op1180f_2		
NPKM_745	766056 +	766437 Rmet_4181	<i>xylH</i>	11.67	0.58	Op1180f_2	NA	Q1LFM8 4-oxalocrotonate tautomerase
3UTR_287	766438 +	767723 Rmet_4181	<i>xylH</i>			Op1180f_2		
NPKM_746	766702 -	767374 Rmet_4182	<i>estB</i>	65.33	3.21	Op1181r_2	NA	Q1LFM7 Phospholipase/Carboxylesterase

NPKM_747	767500 -	767797 Rmet_4183		91.33	8.08	Op1181r_2	NA	Q1LFM6 Putative uncharacterized protein
5UTR_780	767798 -	767800 Rmet_4183				Op1181r_2		
3UTR_951	767809 -	767859 Rmet_4184				Op1181r_1		
5UTR_236	767837 +	767971 Rmet_6651				Op1182f_1		
NPKM_748	767860 -	768169 Rmet_4184		1.00	0.00	Op1181r_1	NA	Q1LFM5 Putative uncharacterized protein
NPKM_749	767971 +	768193 Rmet_6651		10.67	3.06	Op1182f_1	NA	NA
NPKM_750	768369 +	769443 Rmet_4185	cheD	58.33	6.11	Op1182f_2	DIV-MOT-Chemotax	Q1LFM4 Methyl-accepting chemotaxis sensory transducer
3UTR_950	769171 -	769459 Rmet_4186				Op1183r_1		
3UTR_288	769444 +	770413 Rmet_4185	cheD			Op1182f_2		
NPKM_751	769460 -	770330 Rmet_4186		55.00	6.56	Op1183r_1	NA	Q1LFM3 Putative uncharacterized protein
5UTR_779	770331 -	770353 Rmet_4186				Op1183r_1		
5UTR_237	770658 +	770786 Rmet_4187	mmtQ			Op1184f_1		
NPKM_752	770786 +	771284 Rmet_4187	mmtQ	13.33	4.16	Op1184f_1	NA	Q1LFM2 Putative uncharacterized protein
3UTR_289	771285 +	771320 Rmet_4187	mmtQ			Op1184f_1		
5UTR_238	771323 +	771504 Rmet_4188				Op1184f_2		
NPKM_753	771504 +	772140 Rmet_4188		86.67	3.51	Op1184f_2	NA	Q1LFM1 Transcriptional regulator, TetR family
3UTR_949	772130 -	772185 Rmet_4189				Op1185r_1		
3UTR_290	772141 +	772470 Rmet_4188				Op1184f_2		
NPKM_754	772186 -	772963 Rmet_4189		7.67	0.58	Op1185r_1	NA	Q1LFM0 Hydrolase, alpha/beta fold family
NPKM_755	772959 -	773991 Rmet_4190		5.67	0.58	Op1185r_1	NA	Q1LFL9 Putative uncharacterized protein
NPKM_756	774036 -	774951 Rmet_4191		9.33	0.58	Op1185r_1	NA	Q1LFL8 Transcriptional regulator, LysR family
3UTR_948	775091 -	775232 Rmet_4192	plcN			Op1185r_1		
NPKM_757	775233 -	777378 Rmet_4192	plcN	6.00	0.00	Op1185r_1	MET-CAH-Inos	Q1LFL7 Twin-arginine translocation pathway signal
NPKM_758	777429 -	777648 Rmet_6652		10.67	0.58	Op1185r_1	NA	NA
5UTR_778	777649 -	777728 Rmet_6652				Op1185r_1		
5UTR_239	777906 +	778104 Rmet_4193				Op1186f_1		
3UTR_947	778062 -	778614 Rmet_4194				Op1187r_1		
NPKM_759	778104 +	778590 Rmet_4193		143.00	2.65	Op1186f_1	NA	Q1LFL6 Putative uncharacterized protein
3UTR_291	778591 +	779432 Rmet_4193				Op1186f_1		
NPKM_760	778615 -	779764 Rmet_4194		38.67	1.53	Op1187r_1	NA	Q1LFL5 Alanine racemase-like protein
5UTR_240	779452 +	779981 Rmet_4195	cheD			Op1188f_1		
5UTR_777	779765 -	779787 Rmet_4194				Op1187r_1		
NPKM_761	779981 +	781529 Rmet_4195	cheD	10.67	1.15	Op1188f_1	DIV-MOT-Chemotax	Q1LFL4 Methyl-accepting chemotaxis sensory transducer
3UTR_946	780539 -	781577 Rmet_4196				Op1189r_2		
3UTR_292	781530 +	782536 Rmet_4195	cheD			Op1188f_1		
NPKM_762	781578 -	782172 Rmet_4196		71.67	1.53	Op1189r_2	NA	Q1LFL3 DSBA oxidoreductase
NPKM_763	782241 -	783138 Rmet_4197		25.33	1.53	Op1189r_1	NA	Q1LFL2 Short-chain dehydrogenase/reductase SDR
5UTR_241	783142 +	783162 Rmet_4198				Op1190f_1		
NPKM_764	783162 +	783906 Rmet_4198		134.00	12.49	Op1190f_1	NA	Q1LFL1 Transcriptional regulator, PadR family
NPKM_765	783902 +	784715 Rmet_4199	viuB	153.67	9.07	Op1190f_1	NA	Q1LFL0 FAD-binding 9, siderophore-interacting
NPKM_766	784814 +	785216 Rmet_4200		146.00	16.46	Op1190f_1	NA	Q1LFL9 Putative uncharacterized protein
NPKM_767	785359 +	786577 Rmet_4201		111.33	6.51	Op1190f_1	NA	Q1LFL8 Transcriptional regulator, LysR family
3UTR_945	786420 -	786644 Rmet_4202				Op1191r_1		

3UTR_293	786578 +	787610 Rmet_4201				Op1190f_1		
NPKM_768	786645 -	787533 Rmet_4202		22.67	0.58	Op1191r_1	NA	Q1LFK7 Transcriptional regulator, LysR family
5UTR_242	787612 +	787633 Rmet_4203	bug			Op1192f_1		
NPKM_769	787633 +	788641 Rmet_4203	bug	16.67	2.08	Op1192f_1	NA	Q1LFK6 Uncharacterized protein UPF0065
NPKM_770	788734 +	789472 Rmet_4204		15.33	1.53	Op1192f_1	NA	Q1LFK5 LmbE-like protein
NPKM_771	789468 +	790182 Rmet_4205		15.67	0.58	Op1192f_1	NA	Q1LFK4 Dimethylmenaquinone methyltransferase
NPKM_772	790293 +	791244 Rmet_4206		20.00	1.73	Op1192f_1	NA	Q1LFK3 Transcriptional regulator, LysR family
3UTR_294	791245 +	791326 Rmet_4206				Op1192f_1		
NPKM_773	791417 -	791576 Rmet_6653		0.67	0.58	Op1193r_2	NA	NA
NPKM_774	791653 +	792682 Rmet_4207	tnpA	0.00	0.00	Op1192f_1	NA	NA
NPKM_775	792670 -	792940 Rmet_4208		3.67	1.15	Op1193r_2	NA	Q1LFK1 Putative uncharacterized protein
3UTR_295	792683 +	792731 Rmet_4207	tnpA			Op1192f_1		
NPKM_776	792936 -	793314 Rmet_4209		1.33	0.58	Op1193r_1	NA	Q1LFK0 Putative uncharacterized protein
5UTR_243	793301 +	793632 Rmet_4210	tcuA			Op1194f_1		
NPKM_777	793632 +	795066 Rmet_4210	tcuA	5.00	1.00	Op1194f_1	NA	Q1LFJ9 Precorrin 3B synthase CobZ
NPKM_778	795052 +	796225 Rmet_4211	citB	3.00	1.00	Op1194f_1	NA	Q1LFJ8 Citrate utilization protein B
NPKM_779	796267 +	797056 Rmet_4212		7.33	0.58	Op1194f_2	NA	Q1LFJ7 Class II aldolase/adducin-like protein
NPKM_780	797256 +	798237 Rmet_4213	bug	3.67	0.58	Op1194f_2	NA	Q1LFJ6 Uncharacterized protein UPF0065
NPKM_781	798246 +	799272 Rmet_4214		4.33	0.58	Op1194f_2	NA	Q1LFJ5 D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding
3UTR_944	799369 -	799843 Rmet_4216	lpdA2			Op1195r_1		
NPKM_782	799385 +	799838 Rmet_4215		7.00	1.73	Op1194f_2	NA	Q1LFJ4 Response regulator receiver domain protein (CheY-like)
3UTR_296	799839 +	800217 Rmet_4215				Op1194f_2		
NPKM_783	799844 -	801641 Rmet_4216	lpdA2	13.33	0.58	Op1195r_1	MET-CAH-FbP	Q1LFJ3 Dihydrolipoamide dehydrogenase
NPKM_784	801842 +	802490 Rmet_4217		2.00	1.00	Op1196f_1	NA	Q1LFJ2 Putative uncharacterized protein
3UTR_943	802127 -	802502 Rmet_4218				Op1197r_1		
3UTR_297	802491 +	802576 Rmet_4217				Op1196f_1		
NPKM_785	802503 -	803142 Rmet_4218		8.67	0.58	Op1197r_1	NA	Q1LFJ1 Lysine exporter protein (LYSE/YGGA)
NPKM_786	803255 +	804107 Rmet_4219		11.00	1.73	Op1198f_1	NA	Q1LFJ0 Transcriptional regulator, LysR family
NPKM_787	804284 +	805181 Rmet_4220		41.33	3.21	Op1198f_2	NA	Q1LFI9 Alpha/beta hydrolase fold
3UTR_298	805182 +	805800 Rmet_4220				Op1198f_2		
5UTR_244	805809 +	805895 Rmet_4221	omp			Op1198f_2		
NPKM_788	805895 +	806984 Rmet_4221	omp	4.33	0.58	Op1198f_2	NA	Q1LFI8 Porin, Gram-negative type
3UTR_299	806985 +	807036 Rmet_4221	omp			Op1198f_2		
5UTR_245	807233 +	807289 Rmet_4222				Op1198f_3		
NPKM_789	807289 +	808090 Rmet_4222		32.00	3.61	Op1198f_3	NA	Q1LFI7 Transcriptional regulator, IclR family
3UTR_300	808091 +	808440 Rmet_4222				Op1198f_3		
5UTR_246	808458 +	808507 Rmet_4223	bug			Op1198f_3		
NPKM_790	808507 +	809461 Rmet_4223	bug	8.00	1.73	Op1198f_3	NA	Q1LFI6 Uncharacterized protein UPF0065
NPKM_791	809457 +	810612 Rmet_4224		7.67	0.58	Op1198f_3	NA	Q1LFI5 L-carnitine dehydratase/bile acid-inducible protein F
NPKM_792	810608 +	811412 Rmet_4225		15.00	1.00	Op1198f_3	MET-CAH-Prop	Q1LFI4 Enoyl-CoA hydratase/isomerase
NPKM_793	811440 +	812376 Rmet_4226		18.33	2.08	Op1198f_3	NA	Q1LFI3 Transcriptional regulator, LysR family
3UTR_301	812377 +	812714 Rmet_4226				Op1198f_3		
3UTR_942	812397 -	812575 Rmet_4227				Op1199r_4		

NPKM_794	812576 -	812900 Rmet_4227		4.33	1.15	Op1199r_4	NA	Q1LFI2 Putative uncharacterized protein
5UTR_776	812901 -	812949 Rmet_4227				Op1199r_4		
3UTR_941	813074 -	813085 Rmet_6654				Op1199r_3		
NPKM_795	813086 -	813266 Rmet_6654		1.67	0.58	Op1199r_3	NA	NA
NPKM_796	813318 -	814419 Rmet_4228	<i>tnpA</i>	0.00	0.00	Op1199r_2	NA	NA
NPKM_797	814676 -	815324 Rmet_4229		0.00	0.00	Op1199r_2	NA	Q9F8S6 Transposase (Transposase, IS4 family)
NPKM_798	815688 -	816828 Rmet_4230	<i>omp</i>	1.00	0.00	Op1199r_2	EIP-SIG-2Comp	Q1LFI0 Two component transcriptional regulator, LuxR family
5UTR_775	816829 -	816866 Rmet_4230	<i>omp</i>			Op1199r_2		
NPKM_799	816980 -	817295 Rmet_4231		0.33	0.58	Op1199r_1	NA	Q1LFH9 Porin, Gram-negative type
NPKM_800	817353 +	818298 Rmet_4232	<i>bug</i>	1.00	0.00	Op1200f_1	NA	Q1LFH8 Putative uncharacterized protein
3UTR_302	818299 +	818334 Rmet_4232	<i>bug</i>			Op1200f_1		
5UTR_247	818420 +	818452 Rmet_4233				Op1200f_2		
NPKM_801	818452 +	819151 Rmet_4233		2.33	0.58	Op1200f_2	NA	Q1LFH7 Uncharacterized protein UPF0065
NPKM_802	819153 +	820092 Rmet_4234		1.00	0.00	Op1200f_2	NA	Q1LFH6 Dimethylmenaquinone methyltransferase
3UTR_303	820093 +	820098 Rmet_4234				Op1200f_2		
NPKM_803	820349 +	820997 Rmet_4235		0.00	0.00	Op1200f_2	MET-AA-GlySerThr	Q1LFH5 D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding
NPKM_804	821323 +	821698 Rmet_4236		0.33	0.58	Op1200f_3	EIP-SIG-2Comp	Q1LFH4 Two component transcriptional regulator, LuxR family
3UTR_304	821699 +	821741 Rmet_4236				Op1200f_3		
NPKM_805	822360 -	823422 Rmet_4237		1.00	0.00	Op1201r_2	NA	Q1LFH3 Putative uncharacterized protein
NPKM_806	823418 -	823898 Rmet_4238		0.33	0.58	Op1201r_1	NA	Q1LFH2 Diguanylate phosphodiesterase (EAL domain)
3UTR_940	824660 -	824698 Rmet_4239	<i>omp</i>			Op1201r_1		
NPKM_807	824699 -	825833 Rmet_4239	<i>omp</i>	3.33	0.58	Op1201r_1	NA	Q1LFH1 Putative uncharacterized protein
3UTR_939	825972 -	825983 Rmet_4240	<i>acnA3</i>			Op1201r_1		
NPKM_808	825984 -	828639 Rmet_4240	<i>acnA3</i>	2.33	0.58	Op1201r_1	NA	Q1LFH0 Porin, Gram-negative type
5UTR_774	828640 -	828767 Rmet_4240	<i>acnA3</i>			Op1201r_1		
5UTR_248	828796 +	828822 Rmet_4241				Op1202f_1		
NPKM_809	828822 +	829695 Rmet_4241		2.33	0.58	Op1202f_1	MET-CAH-TCA	Q1LFG9 Aconitase
NPKM_810	829728 +	830721 Rmet_4242	<i>bug</i>	5.67	0.58	Op1202f_2	NA	Q1LFG8 Alpha/beta hydrolase fold
NPKM_811	830687 +	831605 Rmet_4243		3.67	0.58	Op1202f_2	NA	Q1LFG7 Uncharacterized protein UPF0065
5UTR_249	831683 +	831684 Rmet_4244				Op1202f_3		
NPKM_812	831684 +	832581 Rmet_4244		14.33	0.58	Op1202f_3	NA	Q1LFG6 Transcriptional regulator, Crp/Fnr family
NPKM_813	832712 +	832901 Rmet_6655		2.67	1.15	Op1202f_3	NA	NA
NPKM_814	832912 +	833347 Rmet_4245		73.33	4.51	Op1202f_4	NA	Q1LFG5 Transcriptional regulator, LysR family
NPKM_815	833346 +	833556 Rmet_4246		61.00	6.24	Op1202f_4	NA	Q1LFG4 Putative uncharacterized protein
NPKM_816	833844 +	835005 Rmet_4247		17.33	1.15	Op1202f_4	NA	Q1LFG3 Putative uncharacterized protein
NPKM_817	835097 +	835505 Rmet_4248		13.00	0.00	Op1202f_4	NA	Q1LFG2 Putative uncharacterized protein
3UTR_305	835506 +	835904 Rmet_4248				Op1202f_4		
3UTR_938	835841 -	835944 Rmet_4249				Op1203r_1		
NPKM_818	835945 -	836203 Rmet_4249		3.00	1.00	Op1203r_1	NA	Q1LFG1 Putative uncharacterized protein
5UTR_773	836204 -	836276 Rmet_4249				Op1203r_1		
5UTR_250	836421 +	836446 Rmet_6656				Op1204f_1		
NPKM_819	836446 +	836626 Rmet_6656		0.67	0.58	Op1204f_1	NA	NA
NPKM_820	836641 +	837169 Rmet_4250	<i>fimA</i>	4.67	1.15	Op1204f_2	NA	Q1LFG0 Fimbrial protein

3UTR_306	837170 +	837175 Rmet_4250	<i>fimA</i>							
5UTR_251	837180 +	837240 Rmet_4251	<i>ecpD</i>							
NPKM_821	837240 +	837993 Rmet_4251	<i>ecpD</i>	2.33	0.58	Op1204f_2	NA		Q1LFF9 Pili assembly chaperone	
3UTR_307	837994 +	838035 Rmet_4251	<i>ecpD</i>			Op1204f_2				
5UTR_252	838065 +	838106 Rmet_4252	<i>htrE</i>			Op1204f_2				
NPKM_822	838106 +	840659 Rmet_4252	<i>htrE</i>	1.33	0.58	Op1204f_2	NA		Q1LFF8 Fimbrial biogenesis outer membrane usher protein	
3UTR_308	840660 +	840702 Rmet_4252	<i>htrE</i>			Op1204f_2				
NPKM_823	840723 +	841734 Rmet_4253		1.67	0.58	Op1204f_2	NA		Q1LFF7 Fimbrial protein	
3UTR_309	841735 +	841807 Rmet_4253				Op1204f_2				
5UTR_253	841824 +	841981 Rmet_4254				Op1204f_2				
NPKM_824	841981 +	844027 Rmet_4254		3.00	0.00	Op1204f_2	NA		Q1LFF6 Sensor protein	
NPKM_825	844244 +	848501 Rmet_4255		4.67	0.58	Op1204f_2	NA		Q1LFF5 Sensor protein	
3UTR_937	848651 -	848656 Rmet_4256				Op1205r_1				
NPKM_826	848657 -	848879 Rmet_4256		0.67	0.58	Op1205r_1	NA		Q1LFF4 Putative transcriptional regulator	
NPKM_827	848981 +	849674 Rmet_4257		2.33	0.58	Op1206f_1	NA		Q1LFF3 General substrate transporter	
3UTR_936	849600 -	849850 Rmet_4259	<i>ycaC</i>			Op1207r_1				
3UTR_310	849675 +	849710 Rmet_4257				Op1206f_1				
NPKM_828	849726 +	849915 Rmet_4258		1.00	0.00	Op1206f_1	NA		Q1LFF2 Putative uncharacterized protein	
NPKM_829	849851 -	850226 Rmet_4259	<i>ycaC</i>	2.33	0.58	Op1207r_1	NA		Q1LFF1 Isochorismatase hydrolase	
NPKM_830	850228 -	851110 Rmet_4260		5.67	1.15	Op1207r_1	NA		Q1LFF0 Pirin-like protein	
NPKM_831	851294 -	852206 Rmet_4261		31.00	3.61	Op1207r_1	NA		Q1LFE9 Transcriptional regulator, LysR family	
5UTR_772	852207 -	852237 Rmet_4261				Op1207r_1				
NPKM_832	852291 +	853344 Rmet_4262		2.33	0.58	Op1208f_1	NA		Q1LFE8 Transcriptional regulator, LysR family	
3UTR_935	852851 -	853351 Rmet_4263	<i>aceE</i>			Op1209r_1				
3UTR_311	853345 +	853443 Rmet_4262				Op1208f_1				
NPKM_833	853352 -	856031 Rmet_4263	<i>aceE</i>	18.00	1.00	Op1209r_1	MET-CAH-FbP		Q1LFE7 2-oxo-acid dehydrogenase E1 component, homodimeric type	
NPKM_834	856218 -	856464 Rmet_4264		29.00	1.00	Op1211r_1	NA		Q1LFE6 Putative uncharacterized protein	
5UTR_771	856465 -	856485 Rmet_4264				Op1211r_1				
5UTR_254	856582 +	856644 Rmet_4265				Op1210f_1				
NPKM_835	856644 +	857331 Rmet_4265		29.67	3.21	Op1210f_1	NA		Q1LFE5 Transcriptional regulator, TetR family	
3UTR_934	857208 -	857335 Rmet_4266				Op1211r_1				
NPKM_836	857336 -	857636 Rmet_4266		6.67	0.58	Op1211r_1	NA		Q1LFE4 Antibiotic biosynthesis monooxygenase	
5UTR_770	857637 -	857821 Rmet_4266				Op1211r_1				
NPKM_837	857869 +	858511 Rmet_4267	<i>ycaC</i>	36.67	2.08	Op1212f_1	NA		Q1LFE3 Isochorismatase hydrolase	
3UTR_312	858512 +	858636 Rmet_4267	<i>ycaC</i>			Op1212f_1				
NPKM_838	858750 +	859548 Rmet_4268	<i>citA</i>	22.33	0.58	Op1212f_1	MET-CAH-TCA		Q1LFE2 Citrate synthase	
NPKM_839	859544 +	861164 Rmet_4269		24.00	1.00	Op1212f_1	NA		Q1LFE1 AMP-dependent synthetase and ligase	
3UTR_933	860824 -	862050 Rmet_4271				Op1213r_1				
NPKM_840	861221 +	862055 Rmet_4270	<i>pcA</i>	33.67	0.58	Op1212f_1	NA		Q1LFE0 Intradiol ring-cleavage dioxygenase	
NPKM_841	862051 -	862906 Rmet_4271		56.67	1.53	Op1213r_1	NA		Q1LFD9 Transcriptional regulator, IclR family	
5UTR_769	862907 -	862916 Rmet_4271				Op1213r_1				
NPKM_842	863024 +	863735 Rmet_4272		10.00	1.00	Op1214f_1	NA		Q1LFD8 L-carnitine dehydratase/bile acid-inducible protein F	
NPKM_843	863773 +	865207 Rmet_4273	<i>leuC</i>	12.67	1.53	Op1214f_1	MET-AA-ValLeulle		Q1LFD7 3-isopropylmalate dehydratase, large subunit	

NPKM_844	865203 +	865842 Rmet_4274	<i>leuD</i>	8.67	1.53	Op1214f_1	MET-AA-ValLeulle	Q1LFD6 3-isopropylmalate dehydratase, small subunit
NPKM_845	865900 +	866926 Rmet_4275	<i>bug</i>	13.67	0.58	Op1214f_1	NA	Q1LFD5 Uncharacterized protein UPF0065
3UTR_932	866511 -	866976 Rmet_4276				Op1215r_2		
3UTR_313	866927 +	867396 Rmet_4275	<i>bug</i>			Op1214f_1		
NPKM_846	866977 -	867871 Rmet_4276		5.00	0.00	Op1215r_2	NA	Q1LFD4 Secretion protein HlyD
NPKM_847	867870 -	868095 Rmet_4277		2.00	0.00	Op1215r_1	NA	Q1LFD3 Putative uncharacterized protein
NPKM_848	868091 -	869543 Rmet_4278		3.33	0.58	Op1215r_1	NA	Q1LFD2 RND efflux system, outer membrane lipoprotein, NodT
NPKM_849	869550 -	871737 Rmet_4279		5.00	1.00	Op1215r_1	NA	Q1LFD1 Fusaric acid resistance protein conserved region
NPKM_850	871745 -	872132 Rmet_4280		6.00	1.73	Op1215r_1	NA	Q1LFD0 DoxX
NPKM_851	872784 -	873819 Rmet_4281		8.67	1.15	Op1215r_1	NA	Q1LFC9 Alcohol dehydrogenase, zinc-binding
5UTR_255	873945 +	873974 Rmet_4282				Op1216f_1		
NPKM_852	873974 +	874841 Rmet_4282		4.33	1.15	Op1216f_1	NA	Q1LFC8 Transcriptional regulator, LysR family
3UTR_314	874842 +	874972 Rmet_4282				Op1216f_1		
NPKM_853	875525 -	876002 Rmet_4283		52.00	2.00	Op1217r_2	NA	Q1LFC7 Putative uncharacterized protein
NPKM_854	876174 -	876318 Rmet_4284	<i>encAB</i>	43.00	9.00	Op1217r_2	NA	Q1LFC6 Entericidin EcnAB
NPKM_855	876854 -	877268 Rmet_4285		14.33	1.53	Op1217r_1	MET-CAH-Pyr	Q1LFC5 Glyoxalase/bleomycin resistance protein/dioxygenase
5UTR_768	877269 -	877372 Rmet_4285				Op1217r_1		
NPKM_856	877332 +	878394 Rmet_4286	<i>bug</i>	272.00	1.73	Op1218f_1	NA	Q1LFC4 Uncharacterized protein UPF0065
3UTR_931	878006 -	878511 Rmet_4287	<i>rlpA</i>			Op1219r_2		
3UTR_315	878395 +	879803 Rmet_4286	<i>bug</i>			Op1218f_1		
NPKM_857	878512 -	878797 Rmet_4287	<i>rlpA</i>	7.67	2.52	Op1219r_2	NA	Q1LFC3 Rare lipoprotein A
NPKM_858	879345 -	880209 Rmet_4288		3.33	0.58	Op1219r_1	NA	Q1LFC2 Short-chain dehydrogenase/reductase SDR
5UTR_767	880210 -	880268 Rmet_4288				Op1219r_1		
3UTR_930	880279 -	880380 Rmet_4289	<i>yraR</i>			Op1219r_1		
NPKM_859	880381 -	881053 Rmet_4289	<i>yraR</i>	5.00	0.00	Op1219r_1	NA	Q1LFC1 Nucleoside-diphosphate-sugar epimerase
NPKM_860	881066 -	882077 Rmet_4290		7.67	0.58	Op1219r_1	NA	Q1LFC0 Transcriptional regulator, AraC family
NPKM_861	882414 -	883302 Rmet_4291	<i>prpB</i>	6.33	0.58	Op1219r_1	NA	Q1LFB9 2,3-dimethylmalate lyase
5UTR_766	883303 -	883350 Rmet_4291	<i>prpB</i>			Op1219r_1		
NPKM_862	883484 +	885422 Rmet_4292	<i>prpR</i>	19.33	1.53	Op1220f_1	NA	Q1LFB8 Propionate catabolism, transcriptional regulator PrpR
NPKM_863	886097 +	886220 Rmet_6657		5.33	1.15	Op1220f_1	NA	NA
3UTR_316	886221 +	886239 Rmet_6657				Op1220f_1		
3UTR_929	886830 -	886936 Rmet_4293				Op1221r_1		
NPKM_864	886937 -	887864 Rmet_4293		1.67	0.58	Op1221r_1	NA	Q1LFB7 Alcohol dehydrogenase, zinc-binding
NPKM_865	887860 -	888292 Rmet_4294		1.00	1.00	Op1221r_1	NA	Q1LFB6 Putative uncharacterized protein
NPKM_866	888318 -	888741 Rmet_4295		0.67	0.58	Op1221r_1	NA	Q1LFB5 DoxX
5UTR_765	888742 -	888758 Rmet_4295				Op1221r_1		
NPKM_867	888892 +	889807 Rmet_4296		10.67	0.58	Op1222f_1	NA	Q1LFB4 Transcriptional regulator, LysR family
NPKM_868	889996 -	891172 Rmet_4297		3.33	0.58	Op1223r_1	NA	Q1LFB3 Putative uncharacterized protein
NPKM_869	891134 +	891314 Rmet_6658		2.33	1.15	Op1224f_1	NA	NA
5UTR_764	891173 -	891281 Rmet_4297				Op1223r_1		
5UTR_256	891503 +	891835 Rmet_4298				Op1224f_1		
NPKM_870	891835 +	892132 Rmet_4298		3.67	0.58	Op1224f_1	NA	Q1LFB2 Putative uncharacterized protein
3UTR_317	892133 +	892231 Rmet_4298				Op1224f_1		

3UTR_928	892290 -	892357 Rmet_4299	<i>dctA</i>			Op1225r_1			
NPKM_871	892358 -	893717 Rmet_4299	<i>dctA</i>	1.33	0.58	Op1225r_1	NA	Q1LFB1 C4-dicarboxylate transport protein 2	
5UTR_763	893718 -	893730 Rmet_4299	<i>dctA</i>			Op1225r_1			
3UTR_927	893735 -	893831 Rmet_4300	<i>nuoF</i>			Op1225r_1			
NPKM_872	893832 -	895077 Rmet_4300	<i>nuoF</i>	3.00	0.00	Op1225r_1	MET-EN-OxPhos	Q1LFB0 Respiratory-chain NADH dehydrogenase domain, 51 kDa subunit	
NPKM_873	895096 -	896746 Rmet_4301		4.00	0.00	Op1225r_1	MET-AA-AlaAsp	Q1LFA9 Fumarate reductase/succinate dehydrogenase flavoprotein-like protein	
NPKM_874	896760 -	897399 Rmet_4302		8.00	1.00	Op1225r_1	NA	Q1LFA8 Ferredoxin	
5UTR_762	897400 -	897410 Rmet_4302				Op1225r_1			
NPKM_875	897789 +	899295 Rmet_4303		0.67	0.58	Op1226f_1	EIP-TRA-Ion	Q1LFA7 Anion transporter	
3UTR_318	899296 +	899324 Rmet_4303				Op1226f_1			
NPKM_876	899390 -	899675 Rmet_4304		1.00	0.00	Op1227r_1	NA	Q1LFA6 Putative uncharacterized protein	
NPKM_877	899947 -	900292 Rmet_4305		1.33	0.58	Op1227r_1	NA	Q1LFA5 Putative uncharacterized protein	
3UTR_926	900300 -	900599 Rmet_4306				Op1227r_1			
NPKM_878	900600 -	901842 Rmet_4306		3.67	0.58	Op1227r_1	NA	Q1LFA4 Major facilitator superfamily MFS_1	
NPKM_879	901920 -	902523 Rmet_4307		11.00	1.00	Op1227r_1	NA	Q1LFA3 Transcriptional regulator, TetR family	
5UTR_761	902524 -	902579 Rmet_4307				Op1227r_1			
3UTR_925	902587 -	902672 Rmet_4308				Op1227r_1			
NPKM_880	902673 -	903639 Rmet_4308		7.67	0.58	Op1227r_1	NA	Q1LFA2 Transcriptional regulator, AraC family	
5UTR_760	903640 -	903907 Rmet_4308				Op1227r_1			
5UTR_257	903870 +	903880 Rmet_4309				Op1228f_1			
NPKM_881	903880 +	904132 Rmet_4309		4.00	0.00	Op1228f_1	NA	Q1LFA1 Putative uncharacterized protein	
3UTR_319	904133 +	904347 Rmet_4309				Op1228f_1			
NPKM_882	904459 +	905668 Rmet_4310		11.33	1.15	Op1228f_2	MET-EN-OxPhos	Q1LFA0 FAD-dependent pyridine nucleotide-disulphide oxidoreductase	
NPKM_883	905736 +	905967 Rmet_4311		5.33	1.53	Op1228f_2	NA		
3UTR_924	905827 -	906011 Rmet_4312				Op1229r_2			
3UTR_320	905968 +	905981 Rmet_4311				Op1228f_2			
NPKM_884	906012 -	906588 Rmet_4312		16.33	1.53	Op1229r_2	NA	Q1LF99 Transcriptional regulator, BadM/Rrf2 family	
5UTR_759	906589 -	906711 Rmet_4312				Op1229r_2			
NPKM_885	906713 -	908273 Rmet_4313	<i>emrB</i>	1.00	0.00	Op1229r_1	NA	Q1LF98 Drug resistance transporter EmrB/QacA subfamily	
NPKM_886	908305 -	909577 Rmet_4314	<i>emrA</i>	2.00	0.00	Op1229r_1	EIP-TRA-Other	Q1LF97 Secretion protein HlyD	
NPKM_887	909606 -	911121 Rmet_4315		1.00	0.00	Op1229r_1	NA	Q1LF96 RND efflux system, outer membrane lipoprotein, NodT	
3UTR_923	911229 -	911389 Rmet_4316				Op1229r_1			
NPKM_888	911390 -	911831 Rmet_4316		3.00	1.00	Op1229r_1	NA	Q1LF95 Cupin 2, conserved barrel	
NPKM_889	911839 -	912277 Rmet_4317		3.67	0.58	Op1229r_1	NA	Q1LF94 Alkylhydroperoxidase AhpD core	
NPKM_890	912408 -	913923 Rmet_4318		6.00	0.00	Op1229r_1	NA	Q1LF93 Transcriptional regulator, GntR family	
5UTR_258	913979 +	914045 Rmet_4319				Op1230f_1			
NPKM_891	914045 +	914765 Rmet_4319		6.33	0.58	Op1230f_1	NA	Q1LF92 Short-chain dehydrogenase/reductase SDR	
NPKM_892	915046 +	916048 Rmet_4320		2.00	0.00	Op1230f_1	NA	Q1LF91 Transcriptional regulator, AraC family	
NPKM_893	916051 +	917023 Rmet_4321		0.33	0.58	Op1230f_1	NA	Q1LF90 Putative uncharacterized protein	
3UTR_321	917024 +	917045 Rmet_4321				Op1230f_1			
NPKM_894	917179 +	918769 Rmet_4322	<i>ccoN</i>	0.00	0.00	Op1230f_1	MET-EN-OxPhos	Q1LF89 Cytochrome c oxidase, subunit I	
NPKM_895	918765 +	919365 Rmet_4323	<i>ccoO</i>	0.67	0.58	Op1230f_2	MET-EN-OxPhos	Q1LF88 Cytochrome C oxidase, mono-heme subunit/FixO	
NPKM_896	919380 +	919989 Rmet_4324	<i>ccoP</i>	0.67	0.58	Op1230f_2	NA	Q1LF87 Cytochrome c, class I	

5UTR_259	920025 +	920056 Rmet_4325				Op1230f_2		
NPKM_897	920056 +	920605 Rmet_4325		0.00	0.00	Op1230f_2	NA	Q1LF86 Putative transmembrane protein
NPKM_898	920601 +	921177 Rmet_4326		0.67	0.58	Op1230f_3	NA	Q1LF85 Putative transmembrane protein
3UTR_922	920986 -	921182 Rmet_4327				Op1231r_1		
3UTR_322	921178 +	921202 Rmet_4326				Op1230f_3		
NPKM_899	921183 -	921606 Rmet_4327		10.67	0.58	Op1231r_1	NA	Q1LF84 Putative uncharacterized protein
NPKM_900	921649 -	922624 Rmet_4328		14.33	2.08	Op1231r_1	NA	Q1LF83 Alpha/beta hydrolase fold
5UTR_260	922674 +	922708 Rmet_4329				Op1232f_1		
NPKM_901	922708 +	923152 Rmet_4329		7.67	1.15	Op1232f_1	NA	Q1LF82 Transcriptional regulator, BadM/Rrf2 family
NPKM_902	923400 +	924447 Rmet_4330		6.00	0.00	Op1232f_1	NA	Q1LF81 Twin-arginine translocation pathway signal
NPKM_903	924453 +	925224 Rmet_4331	<i>tauB</i>	2.67	0.58	Op1232f_1	EIP-TRA-ABC	Q1LF80 ABC transporter related
NPKM_904	925220 +	926117 Rmet_4332	<i>tauC</i>	2.33	0.58	Op1232f_1	EIP-TRA-ABC	Q1LF79 Binding-protein-dependent transport systems inner membrane component
NPKM_905	926120 +	927794 Rmet_4333		5.00	0.00	Op1232f_2	NA	Q1LF78 Amidohydrolase 3
3UTR_323	927795 +	928780 Rmet_4333				Op1232f_2		
NPKM_906	927880 -	928216 Rmet_4334	<i>asfB</i>	2.67	1.15	Op1233r_2	NA	Q1LF77 4Fe-4S ferredoxin, iron-sulfur binding
NPKM_907	928212 -	929862 Rmet_4335	<i>asfA</i>	3.00	0.00	Op1233r_2	NA	Q1LF76 Fumarate reductase/succinate dehydrogenase flavoprotein-like protein
5UTR_758	929863 -	929866 Rmet_4335	<i>asfA</i>			Op1233r_2		
NPKM_908	929982 -	931014 Rmet_4336		0.00	0.00	Op1233r_1	NA	Q1LF75 Fatty acid desaturase
5UTR_261	931203 +	931228 Rmet_4337	<i>bug</i>			Op1234f_1		
NPKM_909	931228 +	932236 Rmet_4337	<i>bug</i>	1.00	0.00	Op1234f_1	NA	Q1LF74 Uncharacterized protein UPF0065
NPKM_910	932299 +	933949 Rmet_4338		2.00	0.00	Op1234f_1	NA	Q1LF73 Rhodanese-like protein
3UTR_324	933950 +	934016 Rmet_4338				Op1234f_1		
5UTR_262	934051 +	934061 Rmet_4339				Op1234f_1		
NPKM_911	934061 +	934307 Rmet_4339		2.33	0.58	Op1234f_1	EIP-SIG-2Comp	Q1LF72 Histidine kinase
3UTR_325	934308 +	934311 Rmet_4339				Op1234f_1		
5UTR_263	934435 +	934577 Rmet_4340	<i>mgo</i>			Op1234f_2		
NPKM_912	934577 +	936293 Rmet_4340	<i>mgo</i>	11.67	1.53	Op1234f_2	MET-CAH-Pyr	Q1LF71 Twin-arginine translocation pathway signal
3UTR_326	936294 +	936643 Rmet_4340	<i>mgo</i>			Op1234f_2		
3UTR_921	936672 -	936723 Rmet_4341	<i>bug</i>			Op1235r_1		
NPKM_913	936724 -	937687 Rmet_4341	<i>bug</i>	3.67	1.15	Op1235r_1	NA	Q1LF70 Uncharacterized protein UPF0065
3UTR_920	937727 -	937732 Rmet_4342				Op1235r_1		
NPKM_914	937733 -	939236 Rmet_4342		2.00	0.00	Op1235r_1	MET-AA-AlaAsp	Q1LF69 Argininosuccinate lyase
5UTR_757	939237 -	939272 Rmet_4342				Op1235r_1		
3UTR_919	939495 -	939519 Rmet_4343				Op1235r_1		
NPKM_915	939520 -	940426 Rmet_4343		6.67	0.58	Op1235r_1	NA	Q1LF68 Transcriptional regulator, LysR family
5UTR_756	940427 -	940506 Rmet_4343				Op1235r_1		
NPKM_916	940675 +	941791 Rmet_4344		2.67	0.58	Op1236f_1	NA	Q1LF67 Porin, Gram-negative type
3UTR_327	941792 +	941825 Rmet_4344				Op1236f_1		
5UTR_264	941852 +	941881 Rmet_4345				Op1236f_2		
NPKM_917	941881 +	942253 Rmet_4345		33.00	2.65	Op1236f_2	NA	Q1LF66 Putative uncharacterized protein
3UTR_918	942196 -	943350 Rmet_4346				Op1237r_2		
3UTR_328	942254 +	944439 Rmet_4345				Op1236f_2		
NPKM_918	943351 -	943882 Rmet_4346		37.00	1.00	Op1237r_2	NA	Q1LF65 Putative uncharacterized protein

NPKM_919	944168 -	944678 Rmet_4347		39.00	2.65	Op1237r_2	NA	Q1LF64 Alkylhydroperoxidase AhpD core
5UTR_265	944456 +	945192 Rmet_4349				Op1238f_1		
NPKM_920	944699 -	945089 Rmet_4348		3.67	1.15	Op1237r_1	NA	Q1LF63 Putative uncharacterized protein
NPKM_921	945108 -	945354 Rmet_6659		2.67	1.15	Op1237r_1	NA	NA
NPKM_922	945192 +	945543 Rmet_4349		44.00	3.61	Op1238f_1	NA	Q1LF62 Putative uncharacterized protein
5UTR_755	945355 -	945435 Rmet_6659				Op1237r_1		
NPKM_923	945924 +	946140 Rmet_6660		123.00	3.61	Op1238f_2	NA	NA
3UTR_917	946605 -	946881 Rmet_4350				Op1239r_1		
NPKM_924	946882 -	947128 Rmet_4350		2.33	1.53	Op1239r_1	NA	Q1LF61 UvrD/REP helicase family protein
NPKM_925	946897 +	947176 Rmet_6661		13.33	1.15	Op1240f_1	NA	NA
NPKM_926	947250 +	947436 Rmet_4351		476.67	36.12	Op1240f_2	NA	Q1LF60 Putative uncharacterized protein
3UTR_329	947437 +	947543 Rmet_4351				Op1240f_2		
3UTR_916	947553 -	947577 Rmet_4352				Op1241r_2		
NPKM_927	947578 -	947956 Rmet_4352		14.00	0.00	Op1241r_2	NA	Q1LF59 Putative uncharacterized protein
5UTR_754	947957 -	948151 Rmet_4352				Op1241r_2		
3UTR_915	948222 -	948270 Rmet_4353				Op1241r_2		
NPKM_928	948271 -	949144 Rmet_4353		79.33	7.64	Op1241r_2	NA	Q1LF58 Transcriptional regulator, GntR family
NPKM_929	949211 -	950063 Rmet_4354		22.00	1.00	Op1241r_1	NA	Q1LF57 Transcriptional regulator, LuxR family
NPKM_930	950199 -	950961 Rmet_4355		21.33	2.52	Op1241r_1	NA	Q1LF56 Integral membrane protein TerC
5UTR_753	950962 -	950976 Rmet_4355				Op1241r_1		
5UTR_266	951132 +	951156 Rmet_4356	<i>panE</i>			Op1242f_1		
NPKM_931	951156 +	952164 Rmet_4356	<i>panE</i>	8.33	1.15	Op1242f_1	MET-COF-Pant	Q1LF55 2-dehydropantoate 2-reductase
NPKM_932	952412 +	953135 Rmet_4357		79.67	1.53	Op1242f_2	NA	Q1LF54 Transcriptional regulator, GntR family
3UTR_914	953019 -	953246 Rmet_4358	<i>sucD1</i>			Op1243r_2		
3UTR_330	953136 +	954527 Rmet_4357				Op1242f_2		
NPKM_933	953247 -	954120 Rmet_4358	<i>sucD1</i>	3.33	0.58	Op1243r_2	MET-CAH-TCA	Q1LF53 Succinyl-CoA ligase [ADP-forming] subunit alpha
NPKM_934	954121 -	955333 Rmet_4359	<i>sucC1</i>	1.00	0.00	Op1243r_1	MET-CAH-TCA	Q1LF52 Succinyl-CoA synthetase (ADP-forming) beta subunit
5UTR_752	955334 -	955361 Rmet_4359	<i>sucC1</i>			Op1243r_1		
5UTR_267	955490 +	955560 Rmet_4360	<i>oxc</i>			Op1244f_1		
NPKM_935	955560 +	957483 Rmet_4360	<i>oxc</i>	5.33	0.58	Op1244f_1	MET-CAH-But	Q1LF51 Thiamine pyrophosphate enzyme-like TPP binding region
NPKM_936	957537 +	958770 Rmet_4361	<i>frc</i>	5.33	1.15	Op1244f_1	NA	Q1LF50 L-carnitine dehydratase/bile acid-inducible protein F
3UTR_331	958771 +	958878 Rmet_4361	<i>frc</i>			Op1244f_1		
5UTR_268	958907 +	958936 Rmet_4362				Op1244f_1		
NPKM_937	958936 +	961066 Rmet_4362		1.67	0.58	Op1244f_1	NA	Q1LF49 CoA-binding
3UTR_332	961067 +	961070 Rmet_4362				Op1244f_1		
5UTR_269	961130 +	961213 Rmet_4363				Op1244f_1		
NPKM_938	961213 +	961990 Rmet_4363		2.33	0.58	Op1244f_1	NA	Q1LF48 Fumarylacetoacetate (FAA) hydrolase
3UTR_913	961845 -	962055 Rmet_4364				Op1245r_1		
3UTR_333	961991 +	962009 Rmet_4363				Op1244f_1		
NPKM_939	962056 -	962365 Rmet_4364		19.00	2.65	Op1245r_1	NA	Q1LF47 Putative uncharacterized protein
NPKM_940	962477 -	963428 Rmet_4365	<i>cbbR3</i>	27.67	1.15	Op1245r_1	NA	Q1LF46 Transcriptional regulator, LysR family
5UTR_270	963085 +	963644 Rmet_4366				Op1246f_1		
5UTR_751	963429 -	963434 Rmet_4365	<i>cbbR3</i>			Op1245r_1		

NPKM_941	963644 +	964988 Rmet_4366		8.00	1.00	Op1246f_1	NA	Q1LF45 Major facilitator superfamily MFS_1
NPKM_942	965020 +	965950 Rmet_4367		9.67	0.58	Op1246f_1	NA	Q1LF44 Transcriptional regulator, LysR family
3UTR_334	965951 +	966116 Rmet_4367				Op1246f_1		
5UTR_271	966141 +	966168 Rmet_4368				Op1246f_2		
NPKM_943	966168 +	966387 Rmet_4368		150.00	9.00	Op1246f_2	NA	Q1LF43 Putative uncharacterized protein
NPKM_944	966997 +	968323 Rmet_4369		17.00	1.00	Op1246f_2	NA	Q1LF42 Major facilitator superfamily MFS_1
3UTR_335	968324 +	968352 Rmet_4369				Op1246f_2		
5UTR_272	968358 +	968478 Rmet_4370				Op1246f_3		
NPKM_945	968478 +	969495 Rmet_4370		56.33	4.16	Op1246f_3	MET-CAH-FbP	Q1LF41 Alcohol dehydrogenase GroES-like protein
3UTR_336	969496 +	969554 Rmet_4370				Op1246f_3		
3UTR_912	969577 -	969601 Rmet_4371				Op1247r_1		
NPKM_946	969602 -	970634 Rmet_4371		36.33	3.21	Op1247r_1	NA	Q1LF40 Putative uncharacterized protein
NPKM_947	970831 -	971506 Rmet_4372		66.00	4.58	Op1247r_1	NA	Q1LF39 Transcriptional regulator, TetR family
5UTR_750	971507 -	971595 Rmet_4372				Op1247r_1		
5UTR_273	971585 +	971734 Rmet_4373				Op1248f_1		
NPKM_948	971734 +	972106 Rmet_4373		1039.67	35.13	Op1248f_1	NA	Q1LF38 Transcriptional regulator, XRE family
NPKM_949	972202 +	972421 Rmet_6662		158.00	18.00	Op1248f_1	NA	NA
NPKM_950	972561 +	973890 Rmet_4374	hmgA	48.33	4.16	Op1248f_1	MET-AA-Tyr	Q1LF37 Homogentisate 1,2-dioxygenase
NPKM_951	973928 +	975191 Rmet_4375	fahA	37.33	2.08	Op1248f_1	MET-AA-Tyr	Q1LF36 Fumarylacetoacetate hydrolase
NPKM_952	975327 +	976188 Rmet_4376		105.33	5.69	Op1248f_2	NA	Q1LF35 Putative uncharacterized protein
NPKM_953	976180 +	976960 Rmet_4377	plsC	51.00	3.46	Op1248f_2	NA	Q1LF34 Phospholipid/glycerol acyltransferase
NPKM_954	976946 +	977216 Rmet_4378	acpP	35.67	5.69	Op1248f_2	MET-LIP-FASyn	Q1LF33 Putative acyl carrier protein
NPKM_955	977268 +	977526 Rmet_4379	acpP2	61.67	3.79	Op1248f_2	MET-LIP-FASyn	Q1LF32 Putative acyl-carrier-protein
NPKM_956	977533 +	978091 Rmet_4380		52.33	2.08	Op1248f_2	NA	Q1LF31 Membrane protein, putative
NPKM_957	978083 +	979757 Rmet_4381		42.00	2.00	Op1248f_2	NA	Q1LF30 AMP-dependent synthetase and ligase
NPKM_958	979753 +	980506 Rmet_4382		35.33	2.52	Op1248f_2	NA	Q1LF29 Glycosyl transferase, family 2
NPKM_959	980502 +	981534 Rmet_4383		24.00	2.00	Op1248f_2	NA	Q1LF28 Lipid A biosynthesis acyltransferase
NPKM_960	981511 +	981928 Rmet_4384		32.00	4.58	Op1248f_2	NA	Q1LF27 Thioesterase superfamily
NPKM_961	981924 +	982554 Rmet_4385	lolA	41.33	3.21	Op1248f_2	NA	Q1LF26 Outer membrane lipoprotein carrier protein LolA
NPKM_962	982573 +	984934 Rmet_4386		24.33	0.58	Op1248f_2	NA	Q1LF25 Putative lipoprotein transmembrane
NPKM_963	984930 +	986160 Rmet_4387		48.00	2.00	Op1248f_2	NA	Q1LF24 Tryptophan halogenase
NPKM_964	986156 +	986729 Rmet_4388		41.00	2.00	Op1248f_2	NA	Q1LF23 Putative uncharacterized protein
NPKM_965	986725 +	987916 Rmet_4389		39.67	1.53	Op1248f_2	MET-LIP-FASyn	Q1LF22 Beta-ketoacyl synthase
NPKM_966	987918 +	988392 Rmet_4390		35.00	4.36	Op1248f_2	NA	Q1LF21 Putative uncharacterized protein
NPKM_967	988388 +	989120 Rmet_4391	fabG	31.33	0.58	Op1248f_2	NA	NA
NPKM_968	989116 +	990346 Rmet_4392	fabB	38.00	2.00	Op1248f_2	MET-LIP-FASyn	Q1LF19 Beta-ketoacyl synthase
3UTR_911	990428 -	991120 Rmet_4394				Op1249r_1		
NPKM_969	990488 +	991115 Rmet_4393	acpT	33.67	4.04	Op1248f_2	NA	Q1LF18 4'-phosphopantetheinyl transferase
3UTR_337	991116 +	991799 Rmet_4393	acpT			Op1248f_2		
NPKM_970	991121 -	992132 Rmet_4394		35.67	1.53	Op1249r_1	NA	Q1LF17 Transcriptional regulator, IclR family
5UTR_274	992060 +	992149 Rmet_4395	uspA9			Op1250f_1		
5UTR_749	992133 -	992333 Rmet_4394				Op1249r_1		
NPKM_971	992149 +	992644 Rmet_4395	uspA9	110.00	6.08	Op1250f_1	NA	Q1LF16 UspA

3UTR_338	992645 +	993184 Rmet_4395	<i>uspA9</i>			Op1250f_1			
3UTR_910	992665 -	992675 Rmet_4396	<i>potF</i>			Op1251r_1			
NPKM_972	992676 -	993765 Rmet_4396	<i>potF</i>	1.00	0.00	Op1251r_1	NA	Q1LF15	Extracellular solute-binding protein, family 1
NPKM_973	993761 -	994544 Rmet_4397	<i>potI</i>	1.00	0.00	Op1251r_1	NA	Q1LF14	Binding-protein-dependent transport systems inner membrane component
NPKM_974	994540 -	995557 Rmet_4398	<i>potH</i>	1.00	0.00	Op1251r_1	NA	Q1LF13	Binding-protein-dependent transport systems inner membrane component
NPKM_975	995572 -	996667 Rmet_4399	<i>potG</i>	6.00	1.00	Op1251r_1	NA	Q1LF12	Spermidine/putrescine ABC transporter ATP-binding subunit
NPKM_976	996915 -	997176 Rmet_4400		296.33	98.08	Op1251r_1	NA	Q1LF11	Putative uncharacterized protein
5UTR_748	997177 -	997287 Rmet_4400				Op1251r_1			
5UTR_275	997251 +	997260 Rmet_4401				Op1252f_1			
NPKM_977	997260 +	997704 Rmet_4401		4.33	0.58	Op1252f_1	NA	Q1LF10	Putative uncharacterized protein
3UTR_909	997299 -	997721 Rmet_4402				Op1253r_1			
3UTR_339	997705 +	997957 Rmet_4401				Op1252f_1			
NPKM_978	997722 -	998643 Rmet_4402		26.33	5.03	Op1253r_1	NA	Q1LF09	Putative uncharacterized protein
NPKM_979	998717 -	1000703 Rmet_4403	<i>shc</i>	64.67	16.56	Op1253r_1	NA	Q1LF08	Squalene cyclase
NPKM_980	1000699 -	1001299 Rmet_4404	<i>shcR</i>	61.67	13.05	Op1253r_1	NA	Q1LF07	Transcriptional regulator, TetR family
5UTR_747	1001300 -	1001307 Rmet_4404	<i>shcR</i>			Op1253r_1			
3UTR_908	1001341 -	1001838 Rmet_4406				Op1255r_1			
NPKM_981	1001414 +	1001771 Rmet_4405		9.00	0.00	Op1254f_1	NA	Q1LF06	Putative uncharacterized protein
3UTR_340	1001772 +	1002152 Rmet_4405				Op1254f_1			
NPKM_982	1001839 -	1002064 Rmet_4406		14.67	2.08	Op1255r_1	NA	Q1LF05	Zinc finger, CDGSH-type
5UTR_746	1002065 -	1002074 Rmet_4406				Op1255r_1			
5UTR_276	1002201 +	1002258 Rmet_4407				Op1256f_1			
NPKM_983	1002258 +	1002648 Rmet_4407		3.33	1.53	Op1256f_1	NA	Q1LF04	Putative uncharacterized protein
NPKM_984	1002806 +	1002883 Rmet_R0080		4.00	1.73	Op1256f_1	NA	NA	
3UTR_341	1002884 +	1003246 Rmet_R0080				Op1256f_1			
3UTR_907	1002938 -	1002990 Rmet_4408	<i>bug</i>			Op1257r_3			
NPKM_985	1002991 -	1003960 Rmet_4408	<i>bug</i>	2.33	0.58	Op1257r_3	NA	Q1LF03	Uncharacterized protein UPF0065
5UTR_745	1003961 -	1003964 Rmet_4408	<i>bug</i>			Op1257r_3			
3UTR_906	1004073 -	1004109 Rmet_4409	<i>tauD</i>			Op1257r_3			
NPKM_986	1004110 -	1005016 Rmet_4409	<i>tauD</i>	1.33	1.15	Op1257r_3	MET-OAA-Taur	Q1LF02	Taurine catabolism dioxygenase TauD/TfdA
NPKM_987	1005071 -	1006304 Rmet_4410		1.67	0.58	Op1257r_3	MET-CAH-Prop	Q1LF01	Acyl-CoA dehydrogenase-like protein
NPKM_988	1006300 -	1008439 Rmet_4411	<i>pauA</i>	1.00	0.00	Op1257r_3	NA	Q1LF00	CoA-binding
5UTR_744	1008440 -	1008448 Rmet_4411	<i>pauA</i>			Op1257r_3			
NPKM_989	1008465 -	1008864 Rmet_4412		0.33	0.58	Op1257r_2	NA	Q1LEZ9	Putative uncharacterized protein
NPKM_990	1008865 -	1010035 Rmet_4413		1.00	0.00	Op1257r_2	MET-CAH-Pyr	Q1LEZ8	Acetyl-CoA acetyltransferase (Thiolase)
NPKM_991	1010045 -	1010960 Rmet_4414	<i>fabG</i>	1.67	0.58	Op1257r_2	NA	Q1LEZ7	Short-chain dehydrogenase/reductase SDR
3UTR_905	1010972 -	1011006 Rmet_4415	<i>bug</i>			Op1257r_1			
NPKM_992	1011007 -	1011970 Rmet_4415	<i>bug</i>	0.67	0.58	Op1257r_1	NA	Q1LEZ6	Uncharacterized protein UPF0065
5UTR_277	1011908 +	1011953 Rmet_6663				Op1258f_1			
NPKM_993	1011953 +	1012016 Rmet_6663		0.33	0.58	Op1258f_1	NA	NA	
5UTR_278	1012270 +	1012361 Rmet_4416				Op1258f_2			
NPKM_994	1012361 +	1013138 Rmet_4416		35.00	1.73	Op1258f_2	NA	Q1LEZ5	Transcriptional regulator, GntR family
3UTR_342	1013139 +	1013407 Rmet_4416				Op1258f_2			

3UTR_904	1013153 -	1013177 Rmet_4417	<i>bug</i>			Op1259r_2		
NPKM_995	1013178 -	1013400 Rmet_4417	<i>bug</i>	0.67	0.58	Op1259r_2	NA	Q1LEZ4 Uncharacterized protein UPF0065
NPKM_996	1013404 -	1014433 Rmet_4418	<i>tnpA</i>	0.00	0.00	Op1259r_1	NA	NA
NPKM_997	1014440 -	1015256 Rmet_4419	<i>bug</i>	0.00	0.00	Op1259r_1	NA	Q1LEZ2 Uncharacterized protein UPF0065
NPKM_998	1015299 -	1016541 Rmet_4420	<i>caiB</i>	0.00	0.00	Op1259r_1	NA	Q1LEZ1 L-carnitine dehydratase/bile acid-inducible protein F
NPKM_999	1016566 -	1017760 Rmet_4421		0.00	0.00	Op1259r_1	NA	Q1LEZ0 MmgE/PrpD family protein
NPKM_1000	1017799 -	1018015 Rmet_4422	<i>tnmC</i>	0.00	0.00	Op1259r_1	NA	NA
NPKM_1001	1018068 -	1018902 Rmet_4423	<i>gspA</i>	0.00	0.00	Op1259r_1	NA	NA
NPKM_1002	1018898 -	1020338 Rmet_4424	<i>tnmA</i>	0.00	0.00	Op1259r_1	NA	NA
NPKM_1003	1020449 -	1021019 Rmet_4425	<i>tnmB</i>	0.00	0.00	Op1259r_1	NA	NA
3UTR_903	1021104 -	1021119 Rmet_4426				Op1259r_1		
NPKM_1004	1021120 -	1021450 Rmet_4426		14.33	3.06	Op1259r_1	NA	Q1LEY5 MmgE/PrpD family protein
3UTR_343	1021130 +	1022571 mobile_element				0		
NPKM_1005	1021465 -	1022632 Rmet_4427		15.67	2.08	Op1259r_1	MET-CAH-But	Q1LEY4 Acyl-CoA dehydrogenase-like protein
5UTR_280	1022794 +	1022842 Rmet_4428				Op1260f_1		
NPKM_1006	1022842 +	1023904 Rmet_4428		10.33	1.53	Op1260f_1	NA	Q1LEY3 MaoC-like dehydratase
NPKM_1007	1023903 +	1025025 Rmet_4429	<i>citE</i>	15.33	0.58	Op1260f_1	MET-CAH-TCA	Q1LEY2 Citrate lyase beta subunit-like protein
3UTR_344	1025026 +	1025204 Rmet_4429	<i>citE</i>			Op1260f_1		
NPKM_1008	1025225 -	1025411 Rmet_6664		0.33	0.58	Op2069r_1	NA	NA
5UTR_281	1025274 +	1025399 Rmet_4430	<i>betB</i>			Op1260f_2		
NPKM_1009	1025399 +	1026890 Rmet_4430	<i>betB</i>	40.33	1.15	Op1260f_2	NA	Q1LEY1 Aldehyde dehydrogenase
5UTR_743	1025412 -	1025437 Rmet_6664				Op2069r_1		
NPKM_1010	1026926 +	1027808 Rmet_4431		36.00	1.73	Op1260f_2	NA	Q1LEY0 6-phosphogluconate dehydrogenase, NAD-binding
3UTR_902	1027225 -	1027884 Rmet_4432				Op1261r_1		
NPKM_1011	1027885 -	1028890 Rmet_4432		52.67	0.58	Op1261r_1	NA	Q1LEX9 Transcriptional regulator, lclR family
5UTR_742	1028891 -	1028920 Rmet_4432				Op1261r_1		
NPKM_1012	1028966 +	1029950 Rmet_4433	<i>bug</i>	36.67	1.53	Op1262f_1	NA	Q1LEX8 Uncharacterized protein UPF0065
NPKM_1013	1030156 +	1030636 Rmet_4434		27.67	3.21	Op1262f_1	NA	Q1LEX7 Putative uncharacterized protein
3UTR_901	1030203 -	1030743 Rmet_4435	<i>nit</i>			Op1263r_2		
3UTR_345	1030637 +	1031289 Rmet_4434				Op1262f_1		
NPKM_1014	1030744 -	1031581 Rmet_4435	<i>nit</i>	16.67	0.58	Op1263r_2	NA	Q1LEX6 Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase
NPKM_1015	1031577 -	1032459 Rmet_4436	<i>bla</i>	16.33	1.53	Op1263r_2	Met-SecMetab	Q1LEX5 Beta-lactamase class A-like protein
NPKM_1016	1032468 -	1033782 Rmet_4437		11.00	0.00	Op1263r_2	NA	Q1LEX4 Putative uncharacterized protein
NPKM_1017	1034013 -	1035003 Rmet_4438	<i>bug</i>	18.00	1.00	Op1263r_2	NA	Q1LEX3 Uncharacterized protein UPF0065
NPKM_1018	1035061 -	1036495 Rmet_4439		11.67	0.58	Op1263r_2	NA	Q1LEX2 Dihydroorotase
NPKM_1019	1036536 -	1036959 Rmet_4440		6.00	1.00	Op1263r_2	NA	Q1LEX1 Endoribonuclease L-PSP
NPKM_1020	1036974 -	1038228 Rmet_4441	<i>dadA3</i>	7.67	0.58	Op1263r_2	MET-EN-Nitrog	Q1LEX0 FAD dependent oxidoreductase
5UTR_741	1038229 -	1038273 Rmet_4441	<i>dadA3</i>			Op1263r_2		
3UTR_900	1038276 -	1038344 Rmet_4442				Op1263r_2		
NPKM_1021	1038345 -	1039350 Rmet_4442		17.33	0.58	Op1263r_2	NA	Q1LEW9 Transcriptional regulator, LysR family
NPKM_1022	1039366 -	1040662 Rmet_4443		3.00	0.00	Op1263r_1	NA	Q1LEW8 Putative uncharacterized protein
NPKM_1023	1040726 -	1041698 Rmet_4444	<i>bug</i>	3.67	1.53	Op1263r_1	NA	Q1LEW7 Uncharacterized protein UPF0065
5UTR_740	1041699 -	1041772 Rmet_4444	<i>bug</i>			Op1263r_1		

NPKM_1024	1041838 +	1042729 Rmet_4445		16.33	3.06	Op1264f_1	NA	Q1LEW6 Transcriptional regulator, LysR family
3UTR_346	1042730 +	1042834 Rmet_4445				Op1264f_1		
5UTR_282	1042900 +	1042919 Rmet_4446	<i>caiB</i>			Op1264f_1		
NPKM_1025	1042919 +	1044101 Rmet_4446	<i>caiB</i>	7.67	0.58	Op1264f_1	NA	Q1LEW5 L-carnitine dehydratase/bile acid-inducible protein F
NPKM_1026	1044152 +	1044911 Rmet_4447		20.00	0.00	Op1264f_2	NA	Q1LEW4 Transcriptional regulator, GntR family
NPKM_1027	1044907 +	1045732 Rmet_4448		13.00	1.00	Op1264f_2	MET-CAH-Prop	Q1LEW3 Enoyl-CoA hydratase/isomerase
NPKM_1028	1045812 +	1046796 Rmet_4449	<i>bug</i>	15.00	1.00	Op1264f_2	NA	Q1LEW2 Uncharacterized protein UPF0065
NPKM_1029	1046821 -	1046992 Rmet_6665		3.67	0.58	Op2070r_1	NA	NA
NPKM_1030	1046891 +	1047503 Rmet_4450		9.67	0.58	Op1264f_2	NA	Q1LEW1 Putative transcription regulator protein
5UTR_739	1046993 -	1047068 Rmet_6665				Op2070r_1		
3UTR_347	1047504 +	1047803 Rmet_4450				Op1264f_2		
NPKM_1031	1047528 -	1048014 Rmet_4451	<i>uspA10</i>	5.33	1.53	Op1265r_1	NA	Q1LEW0 UspA
NPKM_1032	1048050 -	1048461 Rmet_4452		4.00	1.00	Op1265r_1	NA	Q1LEV9 Response regulator receiver domain protein (CheY-like)
5UTR_738	1048462 -	1048640 Rmet_4452				Op1265r_1		
3UTR_899	1048652 -	1049217 Rmet_6666				Op1267r_1		
5UTR_283	1048718 +	1048769 Rmet_4453				Op1266f_1		
NPKM_1033	1048769 +	1049141 Rmet_4453		10.33	1.53	Op1266f_1	NA	Q1LEV8 Transcriptional regulators, TraR/DksA family
3UTR_348	1049142 +	1049706 Rmet_4453				Op1266f_1		
NPKM_1034	1049218 -	1049494 Rmet_6666		13.00	2.00	Op1267r_1	NA	NA
NPKM_1035	1049673 -	1051341 Rmet_4454	<i>fadD</i>	11.00	1.00	Op1267r_1	MET-LIP-FAMet	Q1LEV7 AMP-dependent synthetase and ligase
NPKM_1036	1051454 -	1052417 Rmet_4455		18.67	0.58	Op1267r_1	NA	Q1LEV6 Putative uncharacterized protein
5UTR_284	1052765 +	1052768 Rmet_4456				Op1268f_1		
NPKM_1037	1052768 +	1053158 Rmet_4456		7.67	0.58	Op1268f_1	NA	Q1LEV5 Cupin 2, conserved barrel
NPKM_1038	1053220 +	1054204 Rmet_4457	<i>bug</i>	11.33	0.58	Op1268f_1	NA	Q1LEV4 Uncharacterized protein UPF0065
NPKM_1039	1054216 +	1055389 Rmet_4458	<i>acdA</i>	19.00	0.00	Op1268f_1	MET-CAH-Prop	Q1LEV3 Acyl-CoA dehydrogenase-like protein
3UTR_349	1055390 +	1055838 Rmet_4458	<i>acdA</i>			Op1268f_1		
NPKM_1040	1055829 -	1056705 Rmet_4459		49.33	0.58	Op1269r_1	MET-AA-ValLeulle	Q1LEV2 6-phosphogluconate dehydrogenase, NAD-binding
5UTR_737	1056706 -	1057455 Rmet_4459				Op1269r_1		
5UTR_285	1056751 +	1056768 Rmet_4460				Op1270f_1		
NPKM_1041	1056768 +	1058898 Rmet_4460		11.33	0.58	Op1270f_1	NA	Q1LEV1 Diguanylate cyclase/phosphodiesterase
3UTR_898	1058071 -	1058936 Rmet_4461	<i>mmmQ</i>			Op1271r_1		
NPKM_1042	1058937 -	1059204 Rmet_4461	<i>mmmQ</i>	20.67	1.53	Op1271r_1	NA	Q1LEV0 Putative uncharacterized protein
5UTR_736	1059205 -	1059964 Rmet_4461	<i>mmmQ</i>			Op1271r_1		
NPKM_1043	1059537 +	1059837 Rmet_4462	<i>hns</i>	128.67	13.61	Op1272f_1	NA	Q1LEU9 Putative uncharacterized protein
3UTR_350	1059838 +	1059961 Rmet_4462	<i>hns</i>			Op1272f_1		
NPKM_1044	1059967 +	1060996 Rmet_4463	<i>tnpA</i>	0.00	0.00	Op1272f_1	NA	NA
NPKM_1045	1060984 -	1061449 Rmet_4464		64.67	4.51	Op1273r_1	NA	Q1LEU7 Putative uncharacterized protein
3UTR_351	1060997 +	1061464 Rmet_4463	<i>tnpA</i>			Op1272f_1		
5UTR_735	1061450 -	1062076 Rmet_4464				Op1273r_1		
5UTR_286	1061603 +	1061658 Rmet_4465	<i>czcR2</i>			Op1274f_1		
NPKM_1046	1061658 +	1062279 Rmet_4465	<i>czcR2</i>	15.67	1.15	Op1274f_1	EIP-SIG-2Comp	Q1LEU6 Two component heavy metal response transcriptional regulator, winged he
NPKM_1047	1062335 +	1063778 Rmet_4466	<i>czcS2</i>	7.67	1.15	Op1274f_1	EIP-SIG-2Comp	Q1LEU5 Sensor protein
3UTR_897	1063757 -	1064350 Rmet_4468	<i>czcA2</i>			Op1275r_2		

NPKM_1048	1063795 +	1064230 Rmet_4467	<i>ubiG</i>	66.00	4.00	Op1274f_2	NA	Q1LEU4 3-demethylubiquinone-9 3-methyltransferase
3UTR_352	1064231 +	1065245 Rmet_4467	<i>ubiG</i>			Op1274f_2		
NPKM_1049	1064351 -	1067483 Rmet_4468	<i>czcA2</i>	14.00	2.65	Op1275r_2	EIP-TRA-Ion	Q1LEU3 Heavy metal efflux pump CzcA
NPKM_1050	1067497 -	1068391 Rmet_4469	<i>czcB2''</i>	34.33	5.51	Op1275r_2	NA	Q1LEU2 Secretion protein HlyD
5UTR_734	1068392 -	1068465 Rmet_4469	<i>czcB2''</i>			Op1275r_2		
NPKM_1051	1068494 -	1068830 Rmet_4470		0.00	0.00	Op1275r_1	NA	Q1LEG2 Transcriptional regulators, TraR/DksA family
NPKM_1052	1068846 -	1069710 Rmet_4471	<i>uspA11</i>	0.00	0.00	Op1275r_1	NA	Q1LEG3 UspA
NPKM_1053	1069724 -	1071203 Rmet_4472	<i>sulP</i>	0.00	0.00	Op1275r_1	NA	Q1LEG4 Sulphate transporter
NPKM_1054	1071616 +	1072177 Rmet_4473	<i>tnpR</i>	0.00	0.00	Op1276f_1	NA	Q7X3A9 Putative resolvase
NPKM_1055	1072179 +	1075146 Rmet_4474	<i>tnpA</i>	0.00	0.00	Op1276f_1	NA	NA
NPKM_1056	1075182 +	1076361 Rmet_4475		4.67	0.58	Op1276f_2	EIP-TRA-ABC	Q1LET6 Branched-chain amino acid ABC transporter, periplasmic amino acid-binding
3UTR_353	1076362 +	1076450 Rmet_4475				Op1276f_2		
NPKM_1057	1076465 +	1077323 Rmet_4476	<i>livH3</i>	0.00	0.00	Op1276f_2	EIP-TRA-ABC	Q1LET5 Inner-membrane translocator
NPKM_1058	1077322 +	1078321 Rmet_4477	<i>livM3</i>	1.00	0.00	Op1276f_3	EIP-TRA-ABC	Q1LET4 Inner-membrane translocator
NPKM_1059	1078317 +	1079085 Rmet_4478	<i>livG3</i>	0.67	0.58	Op1276f_3	EIP-TRA-ABC	Q1LET3 ABC transporter related
NPKM_1060	1079081 +	1079786 Rmet_4479	<i>livF3</i>	1.00	0.00	Op1276f_3	EIP-TRA-ABC	Q1LET2 ABC transporter related
NPKM_1061	1079809 +	1081072 Rmet_4480	<i>amaB-3</i>	2.00	0.00	Op1276f_3	NA	Q1LET1 Amidase, hydantoinase/carbamoylase
3UTR_896	1080100 -	1082637 Rmet_4482				Op1277r_1		
NPKM_1062	1081105 +	1082599 Rmet_4481		5.00	1.00	Op1276f_4	NA	Q1LET0 MlrC-like protein
3UTR_354	1082600 +	1082788 Rmet_4481				Op1276f_4		
NPKM_1063	1082638 -	1083232 Rmet_4482		14.00	2.00	Op1277r_1	NA	Q1LES9 Transcriptional regulator, TetR family
NPKM_1064	1083307 +	1083733 Rmet_4483		10.33	0.58	Op1278f_1	NA	Q1LES8 Phenylacetic acid degradation-related protein
NPKM_1065	1083838 +	1084483 Rmet_4484		38.67	4.04	Op1278f_2	NA	Q1LES7 Bifunctional deaminase-reductase-like protein
3UTR_355	1084484 +	1085098 Rmet_4484				Op1278f_2		
NPKM_1066	1084522 -	1085386 Rmet_4485		29.00	4.36	Op1279r_2	NA	Q1LES6 Putative uncharacterized protein
5UTR_288	1085534 +	1085653 Rmet_6667				Op2071f_1		
NPKM_1067	1085653 +	1085869 Rmet_6667		2.33	1.15	Op2071f_1	NA	NA
NPKM_1068	1085949 -	1086870 Rmet_4486		44.00	3.61	Op1279r_2	NA	Q1LES5 Putative uncharacterized protein
NPKM_1069	1086976 -	1087336 Rmet_4487		115.33	8.39	Op1279r_2	NA	Q1LES4 Putative uncharacterized protein
NPKM_1070	1087386 +	1087461 Rmet_6668		0.00	0.00	Op2072f_1	NA	NA
NPKM_1071	1087992 -	1088859 Rmet_4488		23.33	3.21	Op1279r_1	NA	Q1LES3 Putative uncharacterized protein
NPKM_1072	1089029 -	1090106 Rmet_4489	<i>zot</i>	48.67	10.97	Op1279r_1	NA	Q1LES2 Zonular occludens toxin
NPKM_1073	1090105 -	1090369 Rmet_4490		56.67	8.96	Op1279r_1	NA	Q1LES1 Putative uncharacterized protein
NPKM_1074	1090372 -	1090711 Rmet_4491		42.33	6.66	Op1279r_1	NA	Q1LES0 Putative uncharacterized protein
NPKM_1075	1090713 -	1092249 Rmet_4492		144.33	24.21	Op1279r_1	NA	Q1LER9 Putative uncharacterized protein
NPKM_1076	1092468 +	1092723 Rmet_6669		0.00	0.00	Op2073f_1	NA	NA
NPKM_1077	1092769 -	1092937 Rmet_6670		1117.00	111.95	Op1279r_1	NA	NA
NPKM_1078	1092940 -	1093195 Rmet_4493		1702.33	219.14	Op1279r_1	NA	Q1LER8 Putative uncharacterized protein
NPKM_1079	1093650 -	1093821 Rmet_6671		1036.00	129.72	Op1279r_1	NA	NA
NPKM_1080	1093906 -	1094218 Rmet_4494		5184.67	700.92	Op1279r_1	NA	Q1LER7 Putative uncharacterized protein
5UTR_733	1094219 -	1094314 Rmet_4494				Op1279r_1		
NPKM_1081	1094304 +	1094655 Rmet_4495		493.00	25.24	Op1280f_1	NA	Q1LER6 Putative uncharacterized protein
3UTR_356	1094656 +	1095979 Rmet_4495				Op1280f_1		

3UTR_895	1094762 -	1094836 Rmet_4496	<i>ffcA2</i>			Op1281r_2		
NPKM_1082	1094837 -	1097252 Rmet_4496	<i>ffcA2</i>	5.00	0.00	Op1281r_2	EIP-TRA-Pores	Q1LER5 TonB-dependent siderophore receptor
NPKM_1083	1097262 -	1099497 Rmet_4497	<i>ffcA1</i>	2.00	0.00	Op1281r_1	EIP-TRA-Pores	Q1LER4 TonB-dependent siderophore receptor
5UTR_732	1099498 -	1099514 Rmet_4497	<i>ffcA1</i>			Op1281r_1		
3UTR_894	1099569 -	1099599 Rmet_4498	<i>fecR</i>			Op1281r_1		
NPKM_1084	1099600 -	1100587 Rmet_4498	<i>fecR</i>	5.00	1.00	Op1281r_1	GIP-TK-RNAP	Q1LER3 Putative FecR
NPKM_1085	1100614 -	1101115 Rmet_4499	<i>rpoJ</i>	7.00	1.00	Op1281r_1	GIP-TK-RNAP	Q1LER2 Sigma-24 (FecI-like)
5UTR_731	1101116 -	1101262 Rmet_4499	<i>rpoJ</i>			Op1281r_1		
3UTR_893	1101377 -	1101796 Rmet_4501	<i>bug</i>			Op1283r_2		
NPKM_1086	1101420 +	1101786 Rmet_4500		1.33	0.58	Op1282f_1	NA	Q1LER1 Putative uncharacterized protein
3UTR_357	1101787 +	1101816 Rmet_4500				Op1282f_1		
NPKM_1087	1101797 -	1102781 Rmet_4501	<i>bug</i>	5.67	0.58	Op1283r_2	NA	Q1LER0 Twin-arginine translocation pathway signal
NPKM_1088	1102856 -	1104551 Rmet_4502	<i>fabD</i>	2.67	0.58	Op1283r_1	MET-LIP-FAMet	Q1LEQ9 AMP-dependent synthetase and ligase
NPKM_1089	1104564 -	1105665 Rmet_4503	<i>bug</i>	2.00	1.00	Op1283r_1	NA	Q1LEQ8 Uncharacterized protein UPF0065
5UTR_730	1105666 -	1105702 Rmet_4503	<i>bug</i>			Op1283r_1		
5UTR_289	1105808 +	1105868 Rmet_4504				Op1284f_1		
NPKM_1090	1105868 +	1107071 Rmet_4504		8.67	1.15	Op1284f_1	NA	Q1LEQ7 Transcriptional regulator, AraC family
3UTR_892	1105924 -	1107026 Rmet_4505				Op1285r_1		
NPKM_1091	1107027 -	1107954 Rmet_4505		18.67	0.58	Op1285r_1	NA	Q1LEQ6 Transcriptional regulator, LysR family
3UTR_358	1107072 +	1107852 Rmet_4504				Op1284f_1		
5UTR_729	1107955 -	1108165 Rmet_4505				Op1285r_1		
NPKM_1092	1108246 +	1109551 Rmet_4506		0.67	0.58	Op1286f_1	NA	Q1LEQ5 Major facilitator superfamily MFS_1
NPKM_1093	1109605 +	1110817 Rmet_4507	<i>hipO</i>	4.00	0.00	Op1286f_2	MET-AA-Phe	Q1LEQ4 Peptidase M20D, amidohydrolase
3UTR_891	1109898 -	1110868 Rmet_4508				Op1287r_1		
3UTR_359	1110818 +	1111078 Rmet_4507	<i>hipO</i>			Op1286f_2		
NPKM_1094	1110869 -	1111742 Rmet_4508		49.67	3.06	Op1287r_1	NA	Q1LEQ3 Type IV pilus assembly PilZ
5UTR_728	1111743 -	1112200 Rmet_4508				Op1287r_1		
5UTR_290	1111935 +	1112042 Rmet_4509				Op1288f_1		
NPKM_1095	1112042 +	1112351 Rmet_4509		41.00	6.24	Op1288f_1	NA	Q1LEQ2 Putative uncharacterized protein
NPKM_1096	1112347 +	1113397 Rmet_4510		46.00	3.61	Op1288f_1	NA	Q1LEQ1 Secretion protein HlyD
NPKM_1097	1113377 +	1115369 Rmet_4511		24.33	3.21	Op1288f_1	NA	Q1LEQ0 Fusaric acid resistance protein conserved region
NPKM_1098	1115361 +	1116924 Rmet_4512		36.67	4.51	Op1288f_1	NA	Q1LEP9 Outer membrane efflux protein
3UTR_890	1116511 -	1116930 Rmet_4513	<i>fabA</i>			Op1289r_1		
3UTR_360	1116925 +	1118076 Rmet_4512				Op1288f_1		
NPKM_1099	1116931 -	1117783 Rmet_4513	<i>fabA</i>	9.67	1.15	Op1289r_1	NA	Q1LEP8 Beta-hydroxyacyl-(Acyl-carrier-protein) dehydratase, FabA/FabZ
NPKM_1100	1117958 -	1119638 Rmet_4514	<i>int</i>	41.00	2.00	Op1289r_1	NA	Q1LEP7 Phage integrase
5UTR_291	1120129 +	1120202 Rmet_4515				Op1290f_1		
NPKM_1101	1120202 +	1121354 Rmet_4515		68.33	3.21	Op1290f_1	NA	Q1LEP6 Putative PAS/PAC sensor protein
NPKM_1102	1121350 +	1121995 Rmet_4516		50.00	3.00	Op1290f_1	NA	Q1LEP5 Two component transcriptional regulator, LuxR family
3UTR_889	1121876 -	1122024 Rmet_4517	<i>uspA12</i>			Op1291r_1		
NPKM_1103	1122025 -	1122478 Rmet_4517	<i>uspA12</i>	4.33	1.15	Op1291r_1	NA	Q1LEP4 UspA
NPKM_1104	1122676 +	1123525 Rmet_4518	<i>uspA13</i>	5.33	1.53	Op1292f_1	NA	Q1LEP3 UspA
3UTR_888	1123118 -	1123599 Rmet_4519				Op1293r_1		

3UTR_361	1123526 +	1123551 Rmet_4518	<i>uspA13</i>				Op1292f_1		
NPKM_1105	1123600 -	1124959 Rmet_4519		7.00	0.00	Op1293r_1	GIP-TL-Ass	Q1LEP2 Beta-lactamase-like protein	
NPKM_1106	1125063 -	1125888 Rmet_4520	<i>uspA14</i>	12.67	0.58	Op1293r_1	NA	Q1LEP1 UspA	
5UTR_292	1125619 +	1126288 Rmet_4521				Op1294f_1			
5UTR_727	1125889 -	1125914 Rmet_4520	<i>uspA14</i>			Op1293r_1			
3UTR_887	1126273 -	1127081 Rmet_4522				Op1295r_1			
NPKM_1107	1126288 +	1127062 Rmet_4521		31.33	2.89	Op1294f_1	NA	Q1LEP0 Transcriptional regulator, Crp/Fnr family	
NPKM_1108	1127082 -	1128024 Rmet_4522		22.00	0.00	Op1295r_1	NA	Q1LEN9 Transcriptional regulator, AraC family with amidase-like domain	
5UTR_726	1128025 -	1128246 Rmet_4522				Op1295r_1			
NPKM_1109	1128167 +	1128968 Rmet_4523		10.67	2.08	Op1296f_1	NA	Q1LEN8 Short-chain dehydrogenase/reductase SDR	
3UTR_886	1128252 -	1129000 Rmet_4524				Op1297r_3			
3UTR_362	1128969 +	1129245 Rmet_4523				Op1296f_1			
NPKM_1110	1129001 -	1129652 Rmet_4524		56.33	4.04	Op1297r_3	NA	Q1LEN7 Negative transcriptional regulator	
NPKM_1111	1129912 -	1130920 Rmet_4525		44.67	6.35	Op1297r_3	NA	Q1LEN6 Putative uncharacterized protein	
NPKM_1112	1130937 -	1131918 Rmet_4526	<i>moxR</i>	75.00	7.21	Op1297r_3	NA	Q1LEN5 ATPase associated with various cellular activities, AAA_3	
NPKM_1113	1131914 -	1134449 Rmet_4527		73.67	10.26	Op1297r_3	MET-AA-Met	Q1LEN4 Spermine synthase	
NPKM_1114	1134644 -	1135721 Rmet_4528		154.33	18.82	Op1297r_3	NA	Q1LEN3 Putative nonspecific acid phosphatase	
NPKM_1115	1135784 -	1137011 Rmet_4529	<i>sumF1</i>	230.67	18.18	Op1297r_3	NA	Q1LEN2 Putative uncharacterized protein	
NPKM_1116	1137139 -	1138231 Rmet_4530		17.00	3.00	Op1297r_2	NA	Q1LEN1 Putative uncharacterized protein	
NPKM_1117	1138227 -	1139823 Rmet_4531		18.00	4.36	Op1297r_2	NA	Q1LEN0 Tetratricopeptide TPR_2	
NPKM_1118	1139819 -	1140824 Rmet_4532		42.33	7.57	Op1297r_2	NA	Q1LEM9 von Willebrand factor, type A	
NPKM_1119	1140810 -	1141308 Rmet_4533		75.00	11.79	Op1297r_2	NA	Q1LEM8 Putative uncharacterized protein	
NPKM_1120	1141451 -	1142291 Rmet_4534	<i>int</i>	2.33	1.15	Op1297r_1	NA	Q1LEM7 Phage integrase	
NPKM_1121	1142384 -	1143092 Rmet_4535	<i>int</i>	18.33	3.21	Op1297r_1	NA	Q1LEM6 Putative uncharacterized protein	
NPKM_1122	1143202 -	1144159 Rmet_4536		54.67	12.42	Op1297r_1	NA	Q1LEM5 Putative uncharacterized protein	
5UTR_725	1144160 -	1144200 Rmet_4536				Op1297r_1			
NPKM_1123	1144357 +	1145656 Rmet_4537	<i>serA2</i>	95.00	7.21	Op1298f_1	MET-AA-GlySerThr	Q1LEM4 D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding	
3UTR_885	1144853 -	1145679 Rmet_4538	<i>soxR</i>			Op1299r_1			
3UTR_363	1145657 +	1146230 Rmet_4537	<i>serA2</i>			Op1298f_1			
NPKM_1124	1145680 -	1146190 Rmet_4538	<i>soxR</i>	20.33	1.53	Op1299r_1	NA	Q1LEM3 Transcriptional regulator, MerR family	
5UTR_724	1146191 -	1146258 Rmet_4538	<i>soxR</i>			Op1299r_1			
5UTR_293	1146277 +	1146312 Rmet_4539				Op1300f_1			
NPKM_1125	1146312 +	1146741 Rmet_4539		24.33	2.08	Op1300f_1	NA	Q1LEM2 Endoribonuclease L-PSP	
NPKM_1126	1146843 +	1147311 Rmet_4540		17.67	1.53	Op1300f_1	NA	Q1LEM1 Putative uncharacterized protein	
3UTR_884	1147178 -	1147298 Rmet_4541				Op1301r_1			
NPKM_1127	1147299 -	1147857 Rmet_4541		10.00	1.00	Op1301r_1	NA	Q1LEM0 Putative uncharacterized protein	
3UTR_364	1147312 +	1147801 Rmet_4540				Op1300f_1			
NPKM_1128	1148048 -	1149521 Rmet_4542		17.33	1.53	Op1301r_1	NA	Q1LEL9 Major facilitator superfamily MFS_1	
NPKM_1129	1149614 -	1150529 Rmet_4543		17.33	0.58	Op1301r_1	NA	Q1LEL8 Transcriptional regulator, LysR family	
NPKM_1130	1150632 +	1151397 Rmet_4544		3.00	0.00	Op1302f_1	MET-LIP-FASyn	Q1LEL7 Short-chain dehydrogenase/reductase SDR	
3UTR_365	1151398 +	1151414 Rmet_4544				Op1302f_1			
NPKM_1131	1151431 -	1151845 Rmet_4545		204.67	6.03	Op1303r_2	NA	Q1LEL6 Putative uncharacterized protein	
NPKM_1132	1151949 -	1152531 Rmet_4546		102.00	9.17	Op1303r_1	NA	Q1LEL5 Putative transcriptional regulator	

NPKM_1133	1152683 -	1153841 Rmet_4547		63.67	5.51	Op1303r_1	NA	Q1LEL4 Putative outer membrane porin signal peptide protein	
5UTR_294	1154115 +	1154133 Rmet_4548				Op1304f_1			
NPKM_1134	1154133 +	1154877 Rmet_4548		25.67	1.53	Op1304f_1	NA	Q1LEL3 Transcriptional regulator, TetR family	
3UTR_366	1154878 +	1155065 Rmet_4548				Op1304f_1			
NPKM_1135	1154917 -	1160797 Rmet_4549	uvrA2	163.00	5.20	Op1305r_1	GIP-REP-Recomb	Q1LEL2 UvrA family protein	
5UTR_723	1160798 -	1161100 Rmet_4549	uvrA2			Op1305r_1			
5UTR_295	1161013 +	1161057 Rmet_6672				Op1306f_1			
NPKM_1136	1161057 +	1161444 Rmet_6672		15.67	4.04	Op1306f_1	NA	NA	
NPKM_1137	1161483 +	1161792 Rmet_4550		61.33	3.79	Op1306f_2	NA	Q1LEL1 Putative uncharacterized protein	
NPKM_1138	1161788 +	1162010 Rmet_6673		33.67	8.50	Op1306f_2	NA	NA	
NPKM_1139	1162166 +	1162454 Rmet_4551		8.33	1.53	Op1306f_2	NA	Q1LEL0 Putative uncharacterized protein	
3UTR_367	1162455 +	1162524 Rmet_4551				Op1306f_2			
5UTR_296	1162551 +	1162589 Rmet_6674				Op1306f_2			
NPKM_1140	1162589 +	1162790 Rmet_6674		3.00	0.00	Op1306f_2	NA	NA	
3UTR_368	1162791 +	1162877 Rmet_6674				Op1306f_2			
5UTR_297	1162946 +	1163033 Rmet_4552				Op1306f_3			
NPKM_1141	1163033 +	1165592 Rmet_4552		7.33	0.58	Op1306f_3	NA	Q1LEK9 Curculin-like (Mannose-binding) lectin	
3UTR_883	1163979 -	1165891 Rmet_6675				Op2074r_1			
NPKM_1142	1165721 +	1166387 Rmet_4553		11.00	0.00	Op1306f_3	NA		0
NPKM_1143	1165892 -	1166096 Rmet_6675		11.33	1.53	Op2074r_1	NA	NA	
NPKM_1144	1166404 +	1166884 Rmet_4554		6.33	2.52	Op1306f_3	NA		0
NPKM_1145	1166897 +	1167134 Rmet_4555		5.67	1.53	Op1306f_3	NA		0
NPKM_1146	1167301 +	1167757 Rmet_4556	int	17.00	1.00	Op1306f_4	NA	Q1LEK8 Phage integrase	
3UTR_369	1167758 +	1167766 Rmet_4556	int			Op1306f_4			
5UTR_298	1168014 +	1168621 Rmet_4558				Op1308f_1			
NPKM_1147	1168048 -	1168555 Rmet_4557	msrA	72.33	6.03	Op1307r_1	GIP-PTL-Fold	Q1LEK7 Peptide methionine sulfoxide reductase	
NPKM_1148	1168621 +	1169227 Rmet_4558		23.00	2.00	Op1308f_1	NA	Q1LEK6 Uracil-DNA glycosylase superfamily	
3UTR_370	1169228 +	1169735 Rmet_4558				Op1308f_1			
NPKM_1149	1169243 -	1169714 Rmet_4559		15.67	0.58	Op1309r_1	NA	Q1LEK5 Transcriptional regulator, AsnC family	
5UTR_722	1169715 -	1170090 Rmet_4559				Op1309r_1			
5UTR_299	1169802 +	1169840 Rmet_4560				Op1310f_1			
NPKM_1150	1169840 +	1170779 Rmet_4560		6.00	2.00	Op1310f_1	NA	Q1LEK4 Putative uncharacterized protein	
3UTR_882	1170096 -	1170791 Rmet_4561				Op1311r_1			
3UTR_371	1170780 +	1170809 Rmet_4560				Op1310f_1			
NPKM_1151	1170792 -	1171263 Rmet_4561		34.00	1.00	Op1311r_1	NA	Q1LEK3 Transcriptional regulator, AsnC family	
5UTR_300	1171373 +	1171431 Rmet_4562				Op1312f_1			
NPKM_1152	1171431 +	1171737 Rmet_4562		18.33	3.06	Op1312f_1	NA	Q1LEK2 Putative uncharacterized protein	
NPKM_1153	1171753 -	1172677 Rmet_4563		167.00	1.00	Op1313r_1	NA	Q1LEK1 Transcriptional regulator, LysR family	
5UTR_721	1172678 -	1172704 Rmet_4563				Op1313r_1			
NPKM_1154	1172798 +	1175210 Rmet_4564	metE	1017.67	92.29	Op1314f_1	MET-AA-Met	Q1LEK0 Methionine synthase (B12-independent)	
3UTR_881	1173750 -	1177512 Rmet_4566				Op1315r_4			
NPKM_1155	1175241 +	1177443 Rmet_4565		772.00	575.35	Op1314f_1	EIP-TRA-Pores	Q1LEJ9 TonB-dependent receptor	
3UTR_372	1177444 +	1178644 Rmet_4565				Op1314f_1			

NPKM_1156	1177513 -	1178926 Rmet_4566		281.33	20.01	Op1315r_4	NA	Q1LEJ8 Putative uncharacterized protein
5UTR_720	1178927 -	1179506 Rmet_4566				Op1315r_4		
3UTR_880	1179508 -	1179521 Rmet_R0081				Op1315r_3		
NPKM_1157	1179522 -	1179599 Rmet_R0081		5.33	3.06	Op1315r_3	NA	NA
NPKM_1158	1179717 -	1180608 Rmet_4567		22.00	2.65	Op1315r_3	NA	Q1LEJ7 Putative uncharacterized protein
5UTR_719	1180609 -	1180752 Rmet_4567				Op1315r_3		
3UTR_879	1180930 -	1180979 Rmet_R0082				Op1315r_2		
NPKM_1159	1180980 -	1181067 Rmet_R0082		8.33	4.73	Op1315r_2	NA	NA
NPKM_1160	1181174 -	1182455 Rmet_4568	<i>codA</i>	22.00	1.73	Op1315r_2	MET-NUC-Pyr	Q1LEJ6 Amidohydrolase 3
5UTR_718	1182456 -	1182485 Rmet_4568	<i>codA</i>			Op1315r_2		
NPKM_1161	1182538 -	1183204 Rmet_4569		3.67	1.15	Op1315r_1	NA	Q1LEJ5 Transcriptional regulator, TetR family
NPKM_1162	1183200 -	1183818 Rmet_4570	<i>upp</i>	7.33	1.15	Op1315r_1	MET-NUC-Pyr	Q1LEJ4 Uracil phosphoribosyltransferase
NPKM_1163	1184042 -	1185350 Rmet_4571		11.67	1.15	Op1315r_1	NA	Q1LEJ3 Putative uncharacterized protein
NPKM_1164	1185346 -	1186585 Rmet_4572		7.00	1.00	Op1315r_1	NA	Q1LEJ2 GTP cyclohydrolase II
NPKM_1165	1186791 -	1187892 Rmet_4573		21.67	2.31	Op1315r_1	NA	Q1LEJ1 Acyltransferase 3
5UTR_717	1187893 -	1187995 Rmet_4573				Op1315r_1		
5UTR_301	1188552 +	1188655 Rmet_4574				Op1316f_1		
NPKM_1166	1188655 +	1189840 Rmet_4574		77.67	0.58	Op1316f_1	MET-CAH-Prop	Q1LEJ0 Acyl-CoA dehydrogenase-like protein
NPKM_1167	1189923 +	1191063 Rmet_4575		61.33	1.15	Op1316f_1	MET-CAH-Prop	Q1LEI9 Acyl-CoA dehydrogenase-like protein
NPKM_1168	1191273 +	1192230 Rmet_4576	<i>dppB</i>	14.33	0.58	Op1316f_1	EIP-TRA-ABC	Q1LEI8 Binding-protein-dependent transport systems inner membrane component
NPKM_1169	1192229 +	1193156 Rmet_4577	<i>dppC</i>	18.67	0.58	Op1316f_1	EIP-TRA-ABC	Q1LEI7 Binding-protein-dependent transport systems inner membrane component
NPKM_1170	1193230 +	1194958 Rmet_4578	<i>dppA</i>	25.33	0.58	Op1316f_1	NA	Q1LEI6 Extracellular solute-binding protein, family 5
NPKM_1171	1194998 +	1195976 Rmet_4579	<i>dppD</i>	23.00	2.00	Op1316f_1	EIP-TRA-ABC	Q1LEI5 Oligopeptide/dipeptide ABC transporter, ATP-binding protein-like protein
NPKM_1172	1196088 +	1197066 Rmet_4580	<i>dppF</i>	22.67	1.15	Op1316f_1	EIP-TRA-ABC	Q1LEI4 Oligopeptide/dipeptide ABC transporter, ATP-binding protein-like protein
3UTR_878	1196287 -	1197112 Rmet_4581				Op1317r_1		
3UTR_373	1197067 +	1197618 Rmet_4580	<i>dppF</i>			Op1316f_1		
NPKM_1173	1197113 -	1198475 Rmet_4581		13.00	1.00	Op1317r_1	NA	Q1LEI3 Transcriptional regulator, TetR family
5UTR_716	1198476 -	1198596 Rmet_4581				Op1317r_1		
5UTR_302	1198533 +	1198670 Rmet_4582	<i>fadB</i>			Op1318f_1		
NPKM_1174	1198670 +	1200761 Rmet_4582	<i>fadB</i>	40.00	2.00	Op1318f_1	MET-CAH-But	Q1LEI2 3-hydroxyacyl-CoA dehydrogenase / short chain enoyl-CoA hydratase
NPKM_1175	1200954 +	1201869 Rmet_4583	<i>gltI</i>	283.67	10.97	Op1318f_2	NA	Q1LEI1 Extracellular solute-binding protein, family 3
NPKM_1176	1202024 +	1202324 Rmet_4584		994.00	38.97	Op1318f_3	NA	Q1LEI0 Putative uncharacterized protein
3UTR_877	1202135 -	1202463 Rmet_4585	<i>ilvD</i>			Op1319r_2		
3UTR_374	1202325 +	1202416 Rmet_4584				Op1318f_3		
NPKM_1177	1202464 -	1204327 Rmet_4585	<i>ilvD</i>	213.67	10.60	Op1319r_2	MET-AA-ValLeulle	Q1LEH9 Dihydroxyacid dehydratase
5UTR_715	1204328 -	1204434 Rmet_4585	<i>ilvD</i>			Op1319r_2		
3UTR_876	1204439 -	1204657 Rmet_4586				Op1319r_1		
NPKM_1178	1204658 -	1205519 Rmet_4586		45.67	2.08	Op1319r_1	NA	Q1LEH8 Conserved hypothetical transmembrane protein
5UTR_714	1205520 -	1205534 Rmet_4586				Op1319r_1		
5UTR_303	1205672 +	1205866 Rmet_4587				Op1320f_1		
NPKM_1179	1205866 +	1207609 Rmet_4587		49.00	2.65	Op1320f_1	NA	Q1LEH7 Glycosyl transferase, family 39
NPKM_1180	1207605 +	1207977 Rmet_4588		46.00	2.00	Op1320f_1	NA	Q1LEH6 Putative small multidrug resistance transmembrane protein
NPKM_1181	1207982 +	1209158 Rmet_4589	<i>arnB</i>	125.67	1.15	Op1320f_2	NA	Q1LEH5 DegT/DnrJ/EryC1/StrS aminotransferase

NPKM_1182	1209136 +	1210138 Rmet_4590	<i>arnC</i>	128.00	2.00	Op1320f_2	NA	Q1LEH4 Glycosyl transferase, family 2
NPKM_1183	1210125 +	1211052 Rmet_4591		139.33	2.08	Op1320f_2	MET-AA-Met	Q1LEH3 Formyl transferase-like protein
NPKM_1184	1211063 +	1212116 Rmet_4592		103.67	3.79	Op1320f_2	NA	Q1LEH2 NAD-dependent epimerase/dehydratase
3UTR_875	1212009 -	1213066 Rmet_4594	<i>zntA</i>			Op1321r_1		
NPKM_1185	1212123 +	1213014 Rmet_4593		174.67	4.93	Op1320f_2	NA	Q1LEH1 Polysaccharide deacetylase
3UTR_375	1213015 +	1213671 Rmet_4593				Op1320f_2		
NPKM_1186	1213067 -	1215452 Rmet_4594	<i>zntA</i>	48.33	2.31	Op1321r_1	MET-EN-P_ATPase	Q1LEH0 Heavy metal translocating P-type ATPase
5UTR_713	1215453 -	1215462 Rmet_4594	<i>zntA</i>			Op1321r_1		
5UTR_304	1215579 +	1215586 Rmet_4595	<i>czcI2</i>			Op1322f_1		
NPKM_1187	1215586 +	1215964 Rmet_4595	<i>czcI2</i>	26.00	1.00	Op1322f_1	NA	Q1LEG9 Putative uncharacterized protein
NPKM_1188	1216061 +	1217357 Rmet_4596	<i>czcC2</i>	2.00	0.00	Op1322f_1	NA	Q1LEG8 Outer membrane efflux protein
3UTR_874	1217139 -	1217705 Rmet_4598	<i>tnpA</i>			Op1323r_1		
NPKM_1189	1217368 +	1217710 Rmet_4597	<i>czcB2'</i>	0.67	0.58	Op1322f_1	NA	Q1LEG7 Secretion protein HlyD
NPKM_1190	1217706 -	1220673 Rmet_4598	<i>tnpA</i>	0.00	0.00	Op1323r_1	NA	B1LRU9 Tn3 family transposase
NPKM_1191	1220675 -	1221236 Rmet_4599	<i>tnpR</i>	0.00	0.00	Op1323r_1	NA	Q7X3A9 Putative resolvase
NPKM_1192	1221649 +	1223128 Rmet_4600	<i>sulP</i>	0.00	0.00	Op1324f_1	NA	Q1LEG4 Sulphate transporter
NPKM_1193	1223142 +	1224006 Rmet_4601	<i>uspA11</i>	0.00	0.00	Op1324f_1	NA	Q1LEG3 UspA
NPKM_1194	1224022 +	1224358 Rmet_4602		0.00	0.00	Op1324f_1	NA	Q1LEG2 Transcriptional regulators, TraR/DksA family
NPKM_1195	1224822 +	1225659 Rmet_4603		51.67	3.79	Op1324f_2	NA	Q1LEG1 Transcriptional regulator, GntR family
NPKM_1196	1225743 +	1226088 Rmet_4604		34.00	1.73	Op1324f_2	NA	Q1LEG0 Putative uncharacterized protein
3UTR_873	1226400 -	1226502 Rmet_4605				Op1325r_1		
NPKM_1197	1226503 -	1230433 Rmet_4605		1.00	0.00	Op1325r_1	NA	Q1LEF9 Sensor protein
NPKM_1198	1230922 +	1232218 Rmet_4606	<i>metY</i>	545.33	62.17	Op1326f_1	MET-AA-Met	Q1LEF8 O-acetylhomoserine/O-acetylserine sulfhydrylase
3UTR_872	1231297 -	1232295 Rmet_4607	<i>oprC</i>			Op1327r_1		
3UTR_376	1232219 +	1235099 Rmet_4606	<i>metY</i>			Op1326f_1		
NPKM_1199	1232296 -	1234471 Rmet_4607	<i>oprC</i>	360.67	312.29	Op1327r_1	EIP-TRA-Pores	Q1LEF7 TonB-dependent copper receptor
NPKM_1200	1234517 -	1234886 Rmet_4608		281.33	242.96	Op1327r_1	NA	Q1LEF6 Putative uncharacterized protein
5UTR_712	1234887 -	1235123 Rmet_4608				Op1327r_1		
5UTR_305	1235113 +	1235334 Rmet_4609	<i>bug</i>			Op1328f_1		
NPKM_1201	1235334 +	1236321 Rmet_4609	<i>bug</i>	17.67	5.77	Op1328f_1	NA	Q1LEF5 Uncharacterized protein UPF0065
NPKM_1202	1236366 +	1237722 Rmet_4610		17.67	7.51	Op1328f_1	NA	Q1LEF4 Putative uncharacterized protein
NPKM_1203	1237751 +	1238102 Rmet_4611		21.67	8.39	Op1328f_1	NA	Q1LEF3 Putative uncharacterized protein
3UTR_871	1237898 -	1238010 Rmet_4612				Op1329r_1		
NPKM_1204	1238011 -	1238869 Rmet_4612		24.67	0.58	Op1329r_1	NA	Q1LEF2 Transcriptional regulator, IclR family
3UTR_377	1238103 +	1238610 Rmet_4611				Op1328f_1		
NPKM_1205	1238912 -	1240106 Rmet_4613		34.00	2.65	Op1329r_1	MET-CAH-Prop	Q1LEF1 Acyl-CoA dehydrogenase-like protein
NPKM_1206	1240120 -	1240873 Rmet_4614		17.00	2.65	Op1329r_1	NA	Q1LEF0 Short-chain dehydrogenase/reductase SDR
5UTR_711	1240874 -	1240932 Rmet_4614				Op1329r_1		
5UTR_306	1240910 +	1240915 Rmet_4615				Op1330f_1		
NPKM_1207	1240915 +	1241680 Rmet_4615		31.67	2.52	Op1330f_1	NA	Q1LEE9 Transcriptional regulator, GntR family
NPKM_1208	1241856 +	1242702 Rmet_4616		25.00	1.73	Op1330f_1	NA	Q1LEE8 Putative uncharacterized protein
3UTR_378	1242703 +	1242949 Rmet_4616				Op1330f_1		
5UTR_307	1242974 +	1243029 Rmet_4617	<i>piuA</i>			Op1330f_1		

NPKM_1209	1243029 +	1245255 Rmet_4617	<i>piuA</i>	20.00	1.00	Op1330f_1	EIP-TRA-Pores	Q1LEE7 TonB-dependent siderophore receptor
3UTR_870	1244539 -	1245307 Rmet_4618				Op1331r_3		
3UTR_379	1245256 +	1245293 Rmet_4617	<i>piuA</i>			Op1330f_1		
NPKM_1210	1245308 -	1245704 Rmet_4618		13.00	1.73	Op1331r_3	NA	Q1LEE6 Putative uncharacterized protein
5UTR_710	1245705 -	1245749 Rmet_4618				Op1331r_3		
NPKM_1211	1245793 -	1247224 Rmet_4619	<i>nodT</i>	1.33	0.58	Op1331r_2	NA	Q1LEE5 RND efflux system, outer membrane lipoprotein, NodT
NPKM_1212	1247242 -	1248421 Rmet_4620		1.00	0.00	Op1331r_2	NA	Q1LEE4 Secretion protein HlyD
NPKM_1213	1248421 -	1248814 Rmet_4621		0.33	0.58	Op1331r_1	NA	Q1LEE3 Putative uncharacterized protein
5UTR_709	1248815 -	1248857 Rmet_4621				Op1331r_1		
NPKM_1214	1248867 -	1249203 Rmet_6676		0.33	0.58	Op1331r_1	NA	NA
5UTR_708	1249204 -	1249209 Rmet_6676				Op1331r_1		
NPKM_1215	1249413 +	1249872 Rmet_4622		1.67	0.58	Op1332f_1	NA	Q1LEE2 Putative uncharacterized protein
3UTR_380	1249873 +	1249906 Rmet_4622				Op1332f_1		
5UTR_308	1249974 +	1249981 Rmet_4623				Op1332f_1		
NPKM_1216	1249981 +	1250230 Rmet_4623		0.67	0.58	Op1332f_1	NA	Q1LEE1 Putative uncharacterized protein
NPKM_1217	1250262 +	1252500 Rmet_4624	<i>plcN2</i>	1.00	0.00	Op1332f_1	MET-CAH-Inos	Q1LEE0 Twin-arginine translocation pathway signal
3UTR_869	1252522 -	1252557 Rmet_4625				Op1333r_1		
NPKM_1218	1252558 -	1253056 Rmet_4625		2.33	0.58	Op1333r_1	NA	Q1LED9 Putative uncharacterized protein
5UTR_707	1253057 -	1253182 Rmet_4625				Op1333r_1		
3UTR_868	1253215 -	1253383 Rmet_4626				Op1333r_1		
NPKM_1219	1253384 -	1256336 Rmet_4626		9.67	0.58	Op1333r_1	EIP-SIG-2Comp	Q1LED8 Sensor protein
NPKM_1220	1256332 -	1256983 Rmet_4627		20.33	0.58	Op1333r_1	EIP-SIG-2Comp	Q1LED7 Two component transcriptional regulator, LuxR family
5UTR_309	1256843 +	1257041 Rmet_4628	<i>qor</i>			Op1334f_1		
5UTR_706	1256984 -	1257081 Rmet_4627				Op1333r_1		
NPKM_1221	1257041 +	1258280 Rmet_4628	<i>qor</i>	6.33	1.15	Op1334f_1	NA	Q1LED6 Alcohol dehydrogenase, zinc-binding
NPKM_1222	1258397 +	1259489 Rmet_4629		13.00	1.00	Op1334f_2	NA	Q1LED5 Transcriptional regulator, AraC family
3UTR_867	1259101 -	1259548 Rmet_4630	<i>bug</i>			Op1335r_1		
3UTR_381	1259490 +	1259707 Rmet_4629				Op1334f_2		
NPKM_1223	1259549 -	1260611 Rmet_4630	<i>bug</i>	2.00	0.00	Op1335r_1	NA	Q1LED4 Uncharacterized protein UPF0065
5UTR_310	1260940 +	1260965 Rmet_4631				Op1336f_1		
NPKM_1224	1260965 +	1262024 Rmet_4631		2.00	0.00	Op1336f_1	NA	Q1LED3 Putative uncharacterized protein
3UTR_382	1262025 +	1262108 Rmet_4631				Op1336f_1		
5UTR_311	1262112 +	1262166 Rmet_4632				Op1336f_2		
NPKM_1225	1262166 +	1263174 Rmet_4632		17.33	4.16	Op1336f_2	NA	Q1LED2 Transcriptional regulator, AraC family
3UTR_866	1262983 -	1263217 Rmet_4633	<i>tauD</i>			Op1337r_1		
3UTR_383	1263175 +	1263756 Rmet_4632				Op1336f_2		
NPKM_1226	1263218 -	1264061 Rmet_4633	<i>tauD</i>	2.00	1.00	Op1337r_1	MET-OAA-Taur	Q1LED1 Taurine catabolism dioxygenase TauD/TfdA
5UTR_312	1263759 +	1264380 Rmet_4634				Op1338f_1		
5UTR_705	1264062 -	1264125 Rmet_4633	<i>tauD</i>			Op1337r_1		
NPKM_1227	1264380 +	1265274 Rmet_4634		45.33	1.53	Op1338f_1	DIV-Apoptosis	Q1LED0 DNA/RNA non-specific endonuclease
3UTR_865	1264433 -	1265293 Rmet_4635				Op1339r_1		
3UTR_384	1265275 +	1267099 Rmet_4634				Op1338f_1		
NPKM_1228	1265294 -	1267031 Rmet_4635		25.33	0.58	Op1339r_1	NA	Q1LEC9 Sulphate transporter

NPKM_1229	1267066 -	1267939 Rmet_4636	33.33	1.15	Op1339r_1	NA	Q1LEC8 Putative uncharacterized protein
5UTR_313	1268114 +	1268206 Rmet_4637			Op1340f_1		
NPKM_1230	1268206 +	1268476 Rmet_4637	14.33	1.15	Op1340f_1	NA	Q1LEC7 ThiamineS
NPKM_1231	1268510 +	1269644 Rmet_4638	12.00	2.00	Op1340f_1	NA	Q1LEC6 Putative uncharacterized protein
3UTR_864	1269707 -	1270062 Rmet_4640			Op1341r_2		
NPKM_1232	1269728 +	1270127 Rmet_4639	20.33	1.53	Op1340f_1	NA	Q1LEC5 Glyoxalase/bleomycin resistance protein/dioxygenase
NPKM_1233	1270063 -	1270654 Rmet_4640	13.67	0.58	Op1341r_2	NA	Q1LEC4 Putative uncharacterized protein
NPKM_1234	1270492 +	1270660 Rmet_6677	6.67	1.53	Op2075f_1	NA	NA
3UTR_385	1270661 +	1270850 Rmet_6677			Op2075f_1		
NPKM_1235	1270791 -	1272672 Rmet_4641	25.33	1.53	Op1341r_2	NA	Q1LEC3 ATP-dependent endonuclease of the OLD family-like protein
NPKM_1236	1272885 -	1273416 Rmet_4642	19.67	1.15	Op1341r_2	NA	Q1LEC2 Putative uncharacterized protein
NPKM_1237	1274015 -	1274540 Rmet_4643	85.00	2.00	Op1341r_2	NA	Q1LEC1 Putative uncharacterized protein
NPKM_1238	1274590 -	1275124 Rmet_4644	17.67	0.58	Op1341r_1	NA	Q1LEC0 Carboxymuconolactone decarboxylase
NPKM_1239	1275142 -	1276189 Rmet_4645	13.00	1.00	Op1341r_1	NA	Q1LEB9 Uncharacterized protein UPF0065
NPKM_1240	1276199 -	1277153 Rmet_4646	10.00	1.00	Op1341r_1	NA	Q1LEB8 Short-chain dehydrogenase/reductase SDR
5UTR_314	1277127 +	1277164 Rmet_4647			Op1342f_1		
NPKM_1241	1277164 +	1278184 Rmet_4647	34.00	4.36	Op1342f_1	NA	Q1LEB7 Transcriptional regulator, LacI family
3UTR_863	1277716 -	1278218 Rmet_4648			Op1343r_2		
3UTR_386	1278185 +	1279254 Rmet_4647			Op1342f_1		
NPKM_1242	1278219 -	1279374 Rmet_4648	20.33	0.58	Op1343r_2	NA	Q1LEB6 Filamentation induced by cAMP protein Fic
5UTR_704	1279375 -	1279523 Rmet_4648			Op1343r_2		
NPKM_1243	1279529 -	1281017 Rmet_4649	0.67	0.58	Op1343r_1	NA	Q1LEB5 RND efflux system, outer membrane lipoprotein, NodT
5UTR_315	1281120 +	1281139 Rmet_4650			Op1344f_1		
NPKM_1244	1281139 +	1281673 Rmet_4650	3.67	0.58	Op1344f_1	NA	Q1LEB4 Putative transcriptional regulator
NPKM_1245	1281696 +	1282839 Rmet_4651	4.00	1.00	Op1344f_1	EIP-TRA-Other	Q1LEB3 Secretion protein HlyD
NPKM_1246	1282946 +	1284473 Rmet_4652	2.33	0.58	Op1344f_1	NA	Q1LEB2 Drug resistance transporter EmrB/QacA subfamily
3UTR_387	1284474 +	1284480 Rmet_4652			Op1344f_1		
5UTR_316	1284656 +	1284791 Rmet_4653			Op1344f_2		
NPKM_1247	1284791 +	1286474 Rmet_4653	18.67	3.79	Op1344f_2	NA	Q1LEB1 Amidohydrolase 3
3UTR_388	1286475 +	1286527 Rmet_4653			Op1344f_2		
NPKM_1248	1286536 -	1286809 Rmet_4654	1.33	0.58	Op1345r_1	NA	Q1LEB0 Putative uncharacterized protein
5UTR_703	1286810 -	1286867 Rmet_4654			Op1345r_1		
NPKM_1249	1286826 +	1288353 Rmet_4655	45.00	1.00	Op1346f_1	MET-AA-AlaAsp	Q1LEA9 Argininosuccinate lyase
NPKM_1250	1288409 +	1288790 Rmet_4656	40.67	2.08	Op1346f_1	NA	Q1LEA8 Antibiotic biosynthesis monooxygenase
3UTR_862	1288637 -	1289104 Rmet_4657			Op1347r_1		
3UTR_389	1288791 +	1289698 Rmet_4656			Op1346f_1		
NPKM_1251	1289105 -	1291151 Rmet_4657	11.67	0.58	Op1347r_1	NA	Q1LEA7 Diguanylate cyclase/phosphodiesterase
5UTR_702	1291152 -	1291173 Rmet_4657			Op1347r_1		
NPKM_1252	1291224 +	1291521 Rmet_4658	0.00	0.00	Op2076f_1	NA	NA
NPKM_1253	1291517 +	1292411 Rmet_4659	0.00	0.00	Op2076f_1	NA	NA
3UTR_861	1292415 -	1292447 Rmet_4660			Op1349r_1		
NPKM_1254	1292448 -	1292958 Rmet_4660	5.67	2.08	Op1349r_1	NA	Q1LEA4 Putative uncharacterized protein
5UTR_701	1292959 -	1293115 Rmet_4660			Op1349r_1		

3UTR_860	1293138 -	1293474 Rmet_4661	rpoD2				Op1349r_1		
NPKM_1255	1293475 -	1295329 Rmet_4661	rpoD2	19.00	1.73	Op1349r_1	GIP-TK-RNAP	Q1LEA3 RNA polymerase sigma factor	
NPKM_1256	1295325 -	1296486 Rmet_4662		27.00	4.58	Op1349r_1	NA	Q1LEA2 Putative uncharacterized protein	
NPKM_1257	1296545 -	1297361 Rmet_4663		54.00	3.00	Op1349r_1	MET-AA-Met	Q1LEA1 Putative spermidine synthase protein	
NPKM_1258	1297390 -	1297642 Rmet_4664		76.33	11.68	Op1349r_1	NA	Q1LEA0 HPrNtr	
5UTR_700	1297643 -	1297715 Rmet_4664				Op1349r_1			
NPKM_1259	1297760 +	1297982 Rmet_4665		60.33	2.08	Op1350f_1	NA	Q1LE99 Helix-turn-helix protein, CopG	
3UTR_859	1297814 -	1298004 Rmet_4666	hyfI			Op1351r_1			
3UTR_390	1297983 +	1300489 Rmet_4665				Op1350f_1			
NPKM_1260	1298005 -	1298521 Rmet_4666	hyfI	2.67	0.58	Op1351r_1	NA	Q1LE98 NADH ubiquinone oxidoreductase, 20 kDa subunit	
NPKM_1261	1298520 -	1300065 Rmet_4667	hyfG	2.33	0.58	Op1351r_1	NA	Q1LE97 NADH-ubiquinone oxidoreductase, chain 49kDa	
NPKM_1262	1300069 -	1301524 Rmet_4668	hyfF	1.33	0.58	Op1351r_1	NA	Q1LE96 NADH/Ubiquinone/plastoquinone (Complex I)	
NPKM_1263	1301525 -	1302185 Rmet_4669	hyfE	1.00	0.00	Op1351r_1	NA	Q1LE95 Hydrogenase 4 membrane component	
NPKM_1264	1302186 -	1303134 Rmet_4670	hyfC	2.00	1.00	Op1351r_1	NA	Q1LE94 Respiratory-chain NADH dehydrogenase, subunit 1	
NPKM_1265	1303144 -	1305169 Rmet_4671	hyfB	7.33	1.15	Op1351r_1	MET-EN-OxPhos	Q1LE93 NADH/Ubiquinone/plastoquinone (Complex I)	
NPKM_1266	1305172 -	1305457 Rmet_4672		23.67	4.04	Op1351r_1	NA	Q1LE92 CopG-like DNA-binding	
5UTR_699	1305458 -	1305488 Rmet_4672				Op1351r_1			
5UTR_317	1305555 +	1305954 Rmet_4673				Op1352f_1			
NPKM_1267	1305954 +	1306383 Rmet_4673		10.00	1.00	Op1352f_1	NA	Q1LE91 Putative uncharacterized protein	
NPKM_1268	1306379 -	1306640 Rmet_6678		0.00	0.00	Op2077r_1	NA	NA	
5UTR_698	1306641 -	1306767 Rmet_6678				Op2077r_1			
NPKM_1269	1306715 +	1307213 Rmet_4674		13.67	2.52	Op1352f_1	NA	Q1LE90 Putative uncharacterized protein	
NPKM_1270	1307166 +	1307337 Rmet_6679		12.00	1.00	Op1352f_1	NA	NA	
3UTR_858	1307319 -	1307484 Rmet_4675				Op1353r_2			
3UTR_391	1307338 +	1308092 Rmet_6679				Op1352f_1			
NPKM_1271	1307485 -	1308298 Rmet_4675		33.33	1.15	Op1353r_2	NA	Q1LE89 Putative uncharacterized protein	
NPKM_1272	1308373 -	1309153 Rmet_4676	catD2	52.67	0.58	Op1353r_2	MET-XEN-Benz	Q1LE88 3-oxoadipate enol-lactonase	
NPKM_1273	1309168 -	1309453 Rmet_4677	catC2	49.33	3.79	Op1353r_2	MET-XEN-Benz	Q1LE87 Muconolactone delta-isomerase	
NPKM_1274	1309481 -	1310540 Rmet_4678		50.00	3.61	Op1353r_2	NA	Q1LE86 Putative uncharacterized protein	
NPKM_1275	1310562 -	1310859 Rmet_4679		51.67	4.62	Op1353r_2	NA	Q1LE85 YCII-related	
NPKM_1276	1310881 -	1312219 Rmet_4680	atoE	9.33	0.58	Op1353r_1	EIP-SIG-2Comp	Q1LE84 Short chain fatty acid transporter	
5UTR_318	1312293 +	1312347 Rmet_4681				Op1354f_1			
NPKM_1277	1312347 +	1312611 Rmet_4681		2.67	0.58	Op1354f_1	NA	Q1LE83 Putative uncharacterized protein	
3UTR_857	1312501 -	1312602 Rmet_4682	doxX			Op1355r_1			
NPKM_1278	1312603 -	1313074 Rmet_4682	doxX	2.67	0.58	Op1355r_1	NA	Q1LE82 DoxX	
3UTR_392	1312612 +	1312851 Rmet_4681				Op1354f_1			
NPKM_1279	1313099 -	1313876 Rmet_4683		6.00	0.00	Op1355r_1	NA	Q1LE81 Putative uncharacterized protein	
NPKM_1280	1313872 -	1314709 Rmet_4684		11.00	1.00	Op1355r_1	NA	Q1LE80 Putative uncharacterized protein	
NPKM_1281	1314740 -	1315025 Rmet_4685		19.00	4.36	Op1355r_1	NA	Q1LE79 Putative uncharacterized protein	
5UTR_697	1315026 -	1315055 Rmet_4685				Op1355r_1			
5UTR_319	1315114 +	1315261 Rmet_4686	rpoQ			Op1356f_1			
NPKM_1282	1315261 +	1315936 Rmet_4686	rpoQ	41.33	4.16	Op1356f_1	GIP-TK-RNAP	Q1LE78 Sigma-24 (FecI-like)	
NPKM_1283	1315932 +	1316574 Rmet_4687		20.67	2.08	Op1356f_1	NA	Q1LE77 Putative uncharacterized protein	

NPKM_1284	1316742	+	1320900	Rmet_4688		3.00	0.00	Op1356f_1	NA	Q1LE76 Putative uncharacterized protein
NPKM_1285	1320929	+	1325612	Rmet_4689		3.33	0.58	Op1356f_1	NA	Q1LE75 Putative uncharacterized protein
NPKM_1286	1325677	+	1326730	Rmet_4690		63.33	4.93	Op1356f_2	NA	Q1LE74 Patatin
NPKM_1287	1326733	+	1328191	Rmet_4691		33.67	2.08	Op1356f_2	NA	Q1LE73 Citrate transporter
3UTR_856	1327508	-	1328224	Rmet_4692				Op1357r_1		
3UTR_393	1328192	+	1328856	Rmet_4691				Op1356f_2		
NPKM_1288	1328225	-	1328804	Rmet_4692		9.33	1.53	Op1357r_1	NA	Q1LE72 Putative uncharacterized protein
5UTR_696	1328805	-	1328887	Rmet_4692				Op1357r_1		
5UTR_320	1329062	+	1329071	Rmet_4693				Op1358f_1		
NPKM_1289	1329071	+	1329719	Rmet_4693		2.00	1.00	Op1358f_1	NA	Q1LE71 Lytic transglycosylase, catalytic
3UTR_394	1329720	+	1329766	Rmet_4693				Op1358f_1		
NPKM_1290	1329803	-	1330679	Rmet_4694		1.00	0.00	Op1359r_4	NA	Q1LE70 PpiC-type peptidyl-prolyl cis-trans isomerase
NPKM_1291	1330731	-	1331439	Rmet_4695		1.00	0.00	Op1359r_4	NA	Q1LE69 Electron transport protein SCO1/SenC
5UTR_695	1331440	-	1331445	Rmet_4695				Op1359r_4		
3UTR_855	1331472	-	1331485	Rmet_4696				Op1359r_4		
NPKM_1292	1331486	-	1333112	Rmet_4696		1.33	0.58	Op1359r_4	NA	Q1LE68 Putative uncharacterized protein
NPKM_1293	1333108	-	1333957	Rmet_4697		1.67	0.58	Op1359r_4	NA	Q1LE67 Putative uncharacterized protein
NPKM_1294	1333972	-	1334752	Rmet_4698		2.67	0.58	Op1359r_4	NA	Q1LE66 Conserved hypothetical signal peptide protein
5UTR_694	1334753	-	1334780	Rmet_4698				Op1359r_4		
NPKM_1295	1334800	-	1335289	Rmet_4699		1.33	0.58	Op1359r_4	NA	Q1LE65 Putative transmembrane protein
NPKM_1296	1335301	-	1343398	Rmet_4700		1.00	0.00	Op1359r_4	NA	Q1LE64 Conserved hypothetical signal peptide protein
NPKM_1297	1343415	-	1345011	Rmet_4701		1.00	0.00	Op1359r_4	NA	Q1LE63 Multicopper oxidase, type 3
3UTR_854	1345024	-	1345056	Rmet_4702				Op1359r_3		
NPKM_1298	1345057	-	1346572	Rmet_4702		0.33	0.58	Op1359r_3	NA	Q1LE62 Multicopper oxidase, type 3
NPKM_1299	1346783	-	1347395	Rmet_4703		1.00	0.00	Op1359r_3	NA	Q1LE61 Putative uncharacterized protein
NPKM_1300	1347391	-	1347829	Rmet_4704		2.33	0.58	Op1359r_3	GIP-PTL-T2S	Q1LE60 Secretory pathway pseudopilin PulG
NPKM_1301	1347834	-	1348365	Rmet_4705		1.00	0.00	Op1359r_2	GIP-PTL-T2S	Q1LE59 Secretory pathway pseudopilin PulG
NPKM_1302	1348368	-	1350573	Rmet_4706		1.33	0.58	Op1359r_2	GIP-PTL-T2S	Q1LE58 Type II and III secretion system protein
NPKM_1303	1350573	-	1351182	Rmet_4707		2.00	0.00	Op1359r_2	NA	Q1LE57 Putative uncharacterized protein
NPKM_1304	1351178	-	1351745	Rmet_4708		1.67	0.58	Op1359r_2	NA	Q1LE56 Putative transmembrane protein
NPKM_1305	1351741	-	1352272	Rmet_4709		2.33	0.58	Op1359r_2	NA	Q1LE55 Putative transmembrane protein
NPKM_1306	1352268	-	1353183	Rmet_4710		3.33	0.58	Op1359r_2	NA	Q1LE54 Putative signal peptide protein
NPKM_1307	1353163	-	1354870	Rmet_4711	<i>gspE</i>	1.33	0.58	Op1359r_1	GIP-PTL-T2S	Q1LE53 Type II secretion system protein E
NPKM_1308	1354876	-	1356118	Rmet_4712	<i>gspF</i>	2.00	0.00	Op1359r_1	GIP-PTL-T2S	Q1LE52 Type II secretion system protein
NPKM_1309	1356122	-	1356623	Rmet_4713	<i>gspG</i>	3.00	2.00	Op1359r_1	GIP-PTL-T2S	Q1LE51 General secretion pathway protein G
5UTR_321	1356624	+	1356729	Rmet_4714				Op1360f_1		
5UTR_693	1356624	-	1356646	Rmet_4713	<i>gspG</i>			Op1359r_1		
NPKM_1310	1356729	+	1358073	Rmet_4714		6.00	0.00	Op1360f_1	NA	Q1LE50 Putative PAS/PAC sensor protein
3UTR_853	1357736	-	1358112	Rmet_4715				Op1361r_1		
3UTR_395	1358074	+	1358292	Rmet_4714				Op1360f_1		
NPKM_1311	1358113	-	1358908	Rmet_4715		4.67	0.58	Op1361r_1	NA	Q1LE49 Two component transcriptional regulator, LuxR family
NPKM_1312	1359168	-	1359348	Rmet_6680		4.33	2.08	Op1361r_1	NA	NA
NPKM_1313	1359517	-	1359964	Rmet_4716		21.67	2.52	Op1361r_1	NA	Q1LE48 Putative uncharacterized protein

NPKM_1314	1360024 -	1360606 Rmet_4717		25.33	2.89	Op1361r_1	NA	Q1LE47 Putative uncharacterized protein
5UTR_322	1360610 +	1360794 Rmet_4718				Op1362f_1		
NPKM_1315	1360794 +	1361703 Rmet_4718		17.67	2.31	Op1362f_1	NA	Q1LE46 Putative uncharacterized protein
NPKM_1316	1361686 +	1362454 Rmet_4719		24.67	3.06	Op1362f_1	NA	Q1LE45 Transcriptional regulator, AraC family
NPKM_1317	1362534 +	1363635 Rmet_4720		38.00	2.65	Op1362f_1	MET-EN-Sulf	Q1LE44 Alpha/beta hydrolase fold
NPKM_1318	1363933 +	1364359 Rmet_4721		186.00	33.06	Op1362f_2	NA	Q1LE43 Putative uncharacterized protein
3UTR_396	1364360 +	1364868 Rmet_4721				Op1362f_2		
NPKM_1319	1364419 -	1364605 Rmet_6681		49.67	2.89	Op1363r_2	NA	NA
NPKM_1320	1364640 -	1365156 Rmet_4722		75.67	3.21	Op1363r_2	NA	Q1LE42 Lipoprotein, putative
NPKM_1321	1365388 -	1366081 Rmet_4723		28.00	1.00	Op1363r_1	NA	Q1LE41 Transcriptional regulator, TetR family
NPKM_1322	1366190 -	1367708 Rmet_4724	<i>cls</i>	36.00	1.73	Op1363r_1	MET-LIP-GlycPLip	Q1LE40 Phospholipase D/Transphosphatidylase
5UTR_692	1367709 -	1367786 Rmet_4724	<i>cls</i>			Op1363r_1		
5UTR_323	1367930 +	1367947 Rmet_4725				Op1364f_1		
NPKM_1323	1367947 +	1368733 Rmet_4725		6.33	0.58	Op1364f_1	NA	Q1LE39 Two component transcriptional regulator, winged helix family
3UTR_397	1368734 +	1368842 Rmet_4725				Op1364f_1		
NPKM_1324	1368753 -	1370784 Rmet_4726		4.33	0.58	Op1365r_1	NA	Q1LE38 Diguanylate cyclase/phosphodiesterase
5UTR_324	1370748 +	1370886 Rmet_4727				Op1366f_1		
NPKM_1325	1370886 +	1372491 Rmet_4727		2.00	1.00	Op1366f_1	DIV-MOT-Chemotax	Q1LE37 Methyl-accepting chemotaxis sensory transducer
3UTR_852	1371914 -	1372680 Rmet_6682				Op2078r_1		
3UTR_398	1372492 +	1372499 Rmet_4727				Op1366f_1		
NPKM_1326	1372615 +	1372879 Rmet_4728		10.33	2.08	Op1366f_2	NA	Q1LE36 Putative uncharacterized protein
NPKM_1327	1372681 -	1372930 Rmet_6682		5.67	2.08	Op2078r_1	NA	NA
5UTR_691	1372931 -	1373073 Rmet_6682				Op2078r_1		
NPKM_1328	1373213 +	1373864 Rmet_4729		235.33	41.49	Op1366f_3	NA	Q1LE35 Putative uncharacterized protein
3UTR_851	1373999 -	1374008 Rmet_4730				Op1367r_1		
NPKM_1329	1374009 -	1374687 Rmet_4730		4.00	1.00	Op1367r_1	NA	Q1LE34 Uncharacterised peroxidase-related
NPKM_1330	1374695 +	1375565 Rmet_4731		9.67	1.53	Op1368f_1	NA	Q1LE33 Transcriptional regulator, AraC family
NPKM_1331	1375838 +	1376663 Rmet_4732		41.67	3.79	Op1368f_2	NA	Q1LE32 Transcriptional regulator, IclR family
3UTR_850	1376427 -	1377194 Rmet_4734	<i>garD</i>			Op1369r_2		
NPKM_1332	1376694 +	1377129 Rmet_4733	<i>hpcD</i>	104.33	4.73	Op1368f_3	MET-AA-Tyr	Q1LE31 5-carboxymethyl-2-hydroxymuconate isomerase
3UTR_399	1377130 +	1377845 Rmet_4733	<i>hpcD</i>			Op1368f_3		
NPKM_1333	1377195 -	1378788 Rmet_4734	<i>garD</i>	24.67	0.58	Op1369r_2	MET-CAH-Ascorb	Q1LE30 Galactarate dehydratase
NPKM_1334	1378804 -	1380166 Rmet_4735	<i>garP</i>	8.67	0.58	Op1369r_1	NA	Q1LE29 D-galactonate transporter
5UTR_690	1380167 -	1380202 Rmet_4735	<i>garP</i>			Op1369r_1		
5UTR_325	1380582 +	1380585 Rmet_4736	<i>kdgD</i>			Op1370f_1		
NPKM_1335	1380585 +	1381500 Rmet_4736	<i>kdgD</i>	11.00	0.00	Op1370f_1	MET-CAH-Ascorb	Q1LE28 Dihydrodipicolinate synthetase
3UTR_400	1381501 +	1381568 Rmet_4736	<i>kdgD</i>			Op1370f_1		
3UTR_849	1381603 -	1381641 Rmet_4737	<i>aceA</i>			Op1371r_1		
NPKM_1336	1381642 -	1383223 Rmet_4737	<i>aceA</i>	47.67	0.58	Op1371r_1	MET-CAH-DiCarb	Q1LE27 Isocitrate lyase
5UTR_326	1383404 +	1383790 Rmet_4738				Op1372f_1		
3UTR_848	1383548 -	1384266 Rmet_4739	<i>nnrU</i>			Op1373r_1		
NPKM_1337	1383790 +	1384216 Rmet_4738		23.33	2.08	Op1372f_1	NA	Q1LE26 Cupin 2, conserved barrel
3UTR_401	1384217 +	1384794 Rmet_4738				Op1372f_1		

NPKM_1338	1384267 -	1384960 Rmet_4739	<i>nnrU</i>	14.33	1.53	Op1373r_1	NA	Q1LE25 NnrU
5UTR_689	1384961 -	1385043 Rmet_4739	<i>nnrU</i>			Op1373r_1		
NPKM_1339	1385047 +	1385554 Rmet_4740		41.67	2.08	Op1374f_1	NA	Q1LE24 GCN5-related N-acetyltransferase
3UTR_847	1385270 -	1386909 Rmet_4742				Op1375r_3		
NPKM_1340	1385793 +	1386786 Rmet_4741		4.00	0.00	Op1374f_1	NA	Q1LE23 ZOG-Fe(II) oxygenase
3UTR_402	1386787 +	1386818 Rmet_4741				Op1374f_1		
NPKM_1341	1386910 -	1387603 Rmet_4742		3849.33	219.22	Op1375r_3	NA	Q1LE22 Histone-like DNA-binding protein
NPKM_1342	1387640 -	1388138 Rmet_4743		41.00	2.00	Op1375r_2	NA	Q1LE21 Putative uncharacterized protein
NPKM_1343	1388088 -	1388322 Rmet_6683		3.67	1.15	Op1375r_1	NA	NA
5UTR_327	1388241 +	1388280 Rmet_4744	<i>nhoA</i>			Op1376f_1		
NPKM_1344	1388280 +	1389159 Rmet_4744	<i>nhoA</i>	17.00	1.00	Op1376f_1	NA	Q1LE20 N-acetyltransferase
5UTR_688	1388323 -	1388329 Rmet_6683				Op1375r_1		
NPKM_1345	1389348 +	1390113 Rmet_4745		59.33	3.51	Op1376f_2	NA	Q1LE19 Short-chain dehydrogenase/reductase SDR
NPKM_1346	1390138 +	1391944 Rmet_4746		44.67	3.51	Op1376f_2	MET-LIP-FAMet	Q1LE18 AMP-dependent synthetase and ligase
3UTR_846	1391171 -	1392008 Rmet_4747				Op1377r_2		
3UTR_403	1391945 +	1392379 Rmet_4746				Op1376f_2		
NPKM_1347	1392009 -	1392486 Rmet_4747		110.33	2.08	Op1377r_2	NA	Q1LE17 CreA
NPKM_1348	1392493 -	1393003 Rmet_4748		149.00	8.00	Op1377r_2	NA	Q1LE16 Thioesterase superfamily
NPKM_1349	1393133 -	1393415 Rmet_4749	<i>hupB</i>	3394.33	87.67	Op1377r_2	GIP-REP-Recomb	Q46TY9 HU family DNA-binding protein
NPKM_1350	1393411 -	1393774 Rmet_6684		15.33	3.21	Op1377r_1	NA	NA
5UTR_687	1393775 -	1393886 Rmet_6684				Op1377r_1		
5UTR_328	1393936 +	1393966 Rmet_4750				Op1378f_1		
NPKM_1351	1393966 +	1395169 Rmet_4750		4.67	0.58	Op1378f_1	EIP-TRA-Ion	Q1LE14 Rh-like protein/ammonium transporter
3UTR_404	1395170 +	1395199 Rmet_4750				Op1378f_1		
3UTR_845	1395241 -	1396306 Rmet_4752	<i>bcr</i>			Op1379r_1		
5UTR_329	1395311 +	1395410 Rmet_4751	<i>mscS</i>			Op1378f_2		
NPKM_1352	1395410 +	1396277 Rmet_4751	<i>mscS</i>	112.67	8.08	Op1378f_2	EIP-TRA-Pores	Q1LE13 MscS Mechanosensitive ion channel
NPKM_1353	1396307 -	1397588 Rmet_4752	<i>bcr</i>	41.33	2.52	Op1379r_1	NA	Q1LE12 Drug resistance transporter Bcr/CflA subfamily
NPKM_1354	1397698 +	1398373 Rmet_4753		164.33	6.35	Op1380f_1	NA	Q1LE11 Putative uncharacterized protein
3UTR_405	1398374 +	1399003 Rmet_4753				Op1380f_1		
NPKM_1355	1398622 -	1401094 Rmet_4754	<i>mdoH</i>	195.67	20.82	Op1381r_1	NA	Q1LE10 Glycosyl transferase, family 2
NPKM_1356	1401201 -	1402968 Rmet_4755	<i>mdoG</i>	306.67	39.32	Op1381r_1	NA	NA
5UTR_330	1403137 +	1403237 Rmet_4756				Op1382f_1		
NPKM_1357	1403237 +	1403639 Rmet_4756		256.67	23.18	Op1382f_1	NA	Q1LE08 Putative uncharacterized protein
NPKM_1358	1403721 -	1404312 Rmet_4757		121.67	1.15	Op1383r_2	NA	Q1LE07 Putative transmembrane protein
NPKM_1359	1404434 -	1405121 Rmet_4758	<i>ribB</i>	47.33	4.16	Op1383r_1	MET-COF-Ribo	Q1LE06 3,4-dihydroxy-2-butanone 4-phosphate synthase
NPKM_1360	1405166 +	1405469 Rmet_4759		4.00	1.00	Op1384f_1	NA	Q1LE05 Putative uncharacterized protein
3UTR_406	1405470 +	1405577 Rmet_4759				Op1384f_1		
NPKM_1362	1405473 -	1406364 Rmet_4760		36.00	1.73	Op1385r_1	NA	Q1LE04 Transcriptional regulator, XRE family
5UTR_686	1406365 -	1406783 Rmet_4760				Op1385r_1		
5UTR_331	1406652 +	1406673 Rmet_4761				Op1386f_1		
NPKM_1363	1406673 +	1406892 Rmet_4761		9.00	2.00	Op1386f_1	NA	Q1LE03 Putative uncharacterized protein
NPKM_1364	1406893 +	1408045 Rmet_4762		11.33	1.15	Op1386f_1	NA	Q1LE02 Putative uncharacterized protein

3UTR_407	1408046 +	1408080 Rmet_4762				Op1386f_1		
5UTR_332	1408154 +	1408221 Rmet_4763				Op1386f_1		
NPKM_1365	1408221 +	1408506 Rmet_4763		1.33	0.58	Op1386f_1	NA	Q1LE01 Plasmid maintenance system killer
NPKM_1366	1408515 +	1408863 Rmet_4764		0.33	0.58	Op1386f_1	NA	Q1LE00 Plasmid maintenance system antidote protein, XRE family
3UTR_408	1408864 +	1408957 Rmet_4764				Op1386f_1		
5UTR_333	1408971 +	1408977 Rmet_4765				Op1386f_2		
NPKM_1367	1408977 +	1410291 Rmet_4765		88.67	8.08	Op1386f_2	NA	Q1LDZ9 Putative uncharacterized protein
3UTR_409	1410292 +	1410459 Rmet_4765				Op1386f_2		
5UTR_334	1410489 +	1410690 Rmet_4766				Op1386f_2		
NPKM_1368	1410690 +	1412028 Rmet_4766		39.67	4.04	Op1386f_2	NA	Q1LDZ8 Diguanylate cyclase/phosphodiesterase
3UTR_844	1411705 -	1412418 Rmet_4768	eda			Op1387r_1		
NPKM_1369	1412172 +	1412301 Rmet_4767	ecnAB	80.67	3.79	Op1386f_3	NA	Q1LDZ7 Entericidin EcnAB
3UTR_410	1412302 +	1414048 Rmet_4767	ecnAB			Op1386f_3		
NPKM_1370	1412419 -	1413061 Rmet_4768	eda	415.67	32.15	Op1387r_1	MET-CAH-PP_KDPG	Q1LDZ6 2-keto-3-deoxy-phosphogluconate aldolase
NPKM_1371	1413164 -	1414100 Rmet_4769	kdgK	325.33	15.95	Op1387r_1	MET-CAH-PP_KDPG	Q1LDZ5 PfkB
NPKM_1372	1414157 -	1415429 Rmet_4770		334.33	25.89	Op1387r_1	MET-AA-GlySerThr	Q1LDZ4 D-serine deaminase (D-serine dehydratase)
5UTR_685	1415430 -	1415430 Rmet_4770				Op1387r_1		
5UTR_335	1415516 +	1415561 Rmet_4771				Op1388f_1		
NPKM_1373	1415561 +	1416467 Rmet_4771		319.33	33.02	Op1388f_1	NA	Q1LDZ3 Transcriptional regulator, RpiR family
NPKM_1374	1416469 +	1417933 Rmet_4772		322.00	20.52	Op1388f_1	NA	Q1LDZ2 Amidohydrolase 3
NPKM_1375	1417947 +	1418340 Rmet_4773		817.33	65.58	Op1388f_2	NA	Q1LDZ1 Endoribonuclease L-PSP
NPKM_1376	1418513 +	1419875 Rmet_4774	gntT	654.00	21.66	Op1388f_2	EIP-TRA-Ion	Q1LDZ0 Gluconate transporter
NPKM_1377	1420009 +	1421191 Rmet_4775		115.33	1.15	Op1388f_2	EIP-TRA-ABC	Q1LDY9 Extracellular ligand-binding receptor
3UTR_843	1420667 -	1421227 Rmet_4776				Op1389r_1		
3UTR_411	1421192 +	1421720 Rmet_4775				Op1388f_2		
NPKM_1378	1421228 -	1421696 Rmet_4776		14.00	1.00	Op1389r_1	NA	Q1LDY8 GCN5-related N-acetyltransferase
5UTR_684	1421697 -	1421750 Rmet_4776				Op1389r_1		
3UTR_842	1421764 -	1421928 Rmet_6685				Op1391r_2		
NPKM_1379	1421884 +	1422409 Rmet_4777		1.33	0.58	Op1390f_1	NA	Q1LDY7 Putative uncharacterized protein
NPKM_1380	1421929 -	1422196 Rmet_6685		26.67	2.52	Op1391r_2	NA	NA
3UTR_412	1422410 +	1422668 Rmet_4777				Op1390f_1		
NPKM_1381	1422429 -	1423131 Rmet_4778	livF10	19.33	1.53	Op1391r_2	EIP-TRA-ABC	Q1LDY6 ABC transporter related
NPKM_1382	1423123 -	1423876 Rmet_4779	livG10	14.67	0.58	Op1391r_2	EIP-TRA-ABC	Q1LDY5 ABC transporter related
NPKM_1383	1423872 -	1424868 Rmet_4780		6.33	0.58	Op1391r_1	EIP-TRA-ABC	Q1LDY4 Inner-membrane translocator
NPKM_1384	1424864 -	1425731 Rmet_4781		18.00	1.73	Op1391r_1	EIP-TRA-ABC	Q1LDY3 Inner-membrane translocator
5UTR_683	1425732 -	1425734 Rmet_4781				Op1391r_1		
NPKM_1385	1425899 +	1426823 Rmet_4782		18.33	1.53	Op1392f_1	NA	Q1LDY2 Twin-arginine translocation pathway signal
NPKM_1386	1426862 +	1428224 Rmet_4783		3.00	0.00	Op1392f_1	EIP-TRA-Ion	Q1LDY1 Major facilitator superfamily MFS_1
NPKM_1387	1428334 +	1429441 Rmet_4784	frmA	197.33	2.52	Op1392f_2	MET-EN-Methane	Q1LDY0 Alcohol dehydrogenase, zinc-binding
NPKM_1388	1429452 +	1430301 Rmet_4785	frmC	135.67	4.93	Op1392f_2	MET-EN-Methane	Q1LDX9 Putative esterase
3UTR_841	1429455 -	1430352 Rmet_4786				Op1393r_1		
3UTR_413	1430302 +	1430600 Rmet_4785	frmC			Op1392f_2		
NPKM_1389	1430353 -	1430668 Rmet_4786		41.00	6.56	Op1393r_1	NA	Q1LDX8 Cold-shock protein, DNA-binding

5UTR_682	1430669 -	1430696 Rmet_4786				Op1393r_1		
5UTR_336	1430743 +	1430777 Rmet_4787				Op1394f_1		
NPKM_1390	1430777 +	1432295 Rmet_4787		34.67	2.52	Op1394f_1	MET-AA-Phe	Q1LDX7 Amidase
3UTR_840	1431728 -	1432348 Rmet_4788	<i>msuE</i>			Op1395r_3		
3UTR_414	1432296 +	1433112 Rmet_4787				Op1394f_1		
NPKM_1391	1432349 -	1433015 Rmet_4788	<i>msuE</i>	32.00	1.00	Op1395r_3	NA	Q1LDX6 NADPH-dependent FMN reductase
NPKM_1392	1433252 -	1434065 Rmet_4789	<i>metQ</i>	163.67	14.05	Op1395r_3	EIP-TRA-ABC	Q1LDX5 Lipoprotein YaeC
NPKM_1393	1434296 -	1435787 Rmet_4790		30.00	4.58	Op1395r_2	NA	Q1LDX4 RND efflux system, outer membrane lipoprotein, NodT
NPKM_1394	1435783 -	1436770 Rmet_4791		29.33	4.04	Op1395r_2	NA	Q1LDX3 Secretion protein HlyD
NPKM_1395	1436766 -	1436979 Rmet_4792		10.33	2.52	Op1395r_1	NA	Q1LDX2 Putative uncharacterized protein
NPKM_1396	1436975 -	1438955 Rmet_4793		21.00	1.73	Op1395r_1	NA	Q1LDX1 Fusaric acid resistance protein conserved region
NPKM_1397	1438960 -	1439419 Rmet_4794	<i>slyA</i>	39.00	4.00	Op1395r_1	NA	Q1LDX0 Transcriptional regulator, MarR family
5UTR_681	1439420 -	1439454 Rmet_4794	<i>slyA</i>			Op1395r_1		
NPKM_1398	1439449 +	1440121 Rmet_4795		0.00	0.00	Op1396f_1	NA	Q1LDW9 Putative uncharacterized protein
NPKM_1399	1440416 +	1443152 Rmet_4796		0.33	0.58	Op1396f_2	NA	Q1LDW8 Rhs element Vgr protein
NPKM_1400	1443202 +	1448083 Rmet_4797	<i>rhsC</i>	2.00	0.00	Op1396f_3	NA	Q1LDW7 YD repeat
NPKM_1401	1448094 +	1448343 Rmet_4798		7.00	0.00	Op1396f_4	NA	Q1LDW6 Putative uncharacterized protein
NPKM_1402	1448488 +	1448716 Rmet_6686		13.67	2.08	Op1396f_4	NA	NA
NPKM_1403	1448885 +	1449419 Rmet_4799		42.00	5.20	Op1396f_5	NA	Q1LDW5 Putative uncharacterized protein
NPKM_1404	1449415 +	1449865 Rmet_4800		51.00	3.00	Op1396f_5	NA	Q1LDW4 Putative uncharacterized protein
NPKM_1405	1449896 +	1450163 Rmet_4801		36.33	4.04	Op1396f_5	NA	Q1LDW3 PAAR
NPKM_1406	1450423 +	1450687 Rmet_4802		172.00	13.45	Op1396f_6	NA	Q1LDW2 Putative uncharacterized protein
3UTR_839	1450695 -	1451342 Rmet_4804				Op1397r_1		
NPKM_1407	1450702 +	1451326 Rmet_4803		79.33	4.16	Op1396f_6	NA	Q1LDW1 Putative uncharacterized protein
NPKM_1408	1451343 -	1452345 Rmet_4804		25.67	1.53	Op1397r_1	NA	Q1LDW0 L-threonine 3-dehydrogenase
NPKM_1409	1452341 -	1453544 Rmet_4805	<i>kbl</i>	25.00	1.00	Op1397r_1	MET-AA-GlySerThr	Q1LDV9 2-amino-3-ketobutyrate coenzyme A ligase
5UTR_680	1453545 -	1454749 Rmet_4805	<i>kbl</i>			Op1397r_1		
NPKM_1410	1453637 +	1454249 Rmet_4806		28.67	3.21	Op1398f_1	NA	Q1LDV8 Transcriptional regulator, XRE family
NPKM_1411	1454534 +	1454819 Rmet_4807		188.67	12.22	Op1398f_2	NA	Q1LDV7 Putative uncharacterized protein
3UTR_838	1454781 -	1454854 Rmet_4808				Op1399r_1		
NPKM_1412	1454855 -	1456223 Rmet_4808		1.33	0.58	Op1399r_1	NA	Q1LDV6 Di-haem cytochrome c peroxidase
5UTR_679	1456224 -	1456261 Rmet_4808				Op1399r_1		
NPKM_1413	1456462 +	1458592 Rmet_4809	<i>acpA</i>	7.00	1.00	Op1400f_1	MET-COF-Ribo	Q1LDV5 Phosphoesterase
3UTR_415	1458593 +	1458614 Rmet_4809	<i>acpA</i>			Op1400f_1		
NPKM_1414	1458665 +	1460210 Rmet_4810		11.67	1.53	Op1400f_1	NA	Q1LDV4 Major facilitator superfamily MFS_1
NPKM_1415	1460225 +	1460522 Rmet_4811		11.67	1.15	Op1400f_1	NA	Q1LDV3 Putative uncharacterized protein
3UTR_837	1460467 -	1461125 Rmet_4813				Op1401r_1		
NPKM_1416	1460518 +	1460821 Rmet_4812		9.67	1.53	Op1400f_1	NA	Q1LDV2 Putative uncharacterized protein
NPKM_1417	1460866 +	1461040 Rmet_6687		5.67	0.58	Op1400f_1	NA	NA
NPKM_1418	1461126 -	1461846 Rmet_4813		34.00	1.00	Op1401r_1	NA	Q1LDV1 Short-chain dehydrogenase/reductase SDR
5UTR_678	1461847 -	1462011 Rmet_4813				Op1401r_1		
NPKM_1419	1462025 +	1462892 Rmet_4814	<i>rhtA</i>	11.67	0.58	Op1402f_1	NA	Q1LDV0 Putative uncharacterized protein
3UTR_836	1462196 -	1462887 Rmet_4815				Op1403r_1		

NPKM_1420	1462888 -	1463494 Rmet_4815		1.67	0.58	Op1403r_1	NA	Q1LDU9 GCN5-related N-acetyltransferase
3UTR_416	1462893 +	1463242 Rmet_4814	<i>rhtA</i>			Op1402f_1		
NPKM_1421	1463555 +	1464053 Rmet_4816		13.00	1.73	Op1404f_1	NA	Q1LDU8 Putative transcriptional regulator
3UTR_417	1464054 +	1464316 Rmet_4816				Op1404f_1		
5UTR_337	1464347 +	1464365 Rmet_4817	<i>nark</i>			Op1404f_1		
NPKM_1422	1464365 +	1465679 Rmet_4817	<i>nark</i>	1.00	0.00	Op1404f_1	NA	Q1LDU7 Major facilitator superfamily MFS_1
3UTR_418	1465680 +	1465701 Rmet_4817	<i>nark</i>			Op1404f_1		
5UTR_338	1465703 +	1465716 Rmet_4818	<i>nirB</i>			Op1404f_1		
NPKM_1423	1465716 +	1468278 Rmet_4818	<i>nirB</i>	0.00	0.00	Op1404f_1	MET-EN-Nitrog	Q1LDU6 Assimilatory nitrite reductase (NAD(P)H) large subunit
5UTR_339	1468284 +	1468303 Rmet_4819	<i>nirD</i>			Op1404f_2		
NPKM_1424	1468303 +	1468705 Rmet_4819	<i>nirD</i>	1.33	0.58	Op1404f_2	MET-EN-Nitrog	Q1LDU5 Assimilatory nitrite reductase (NAD(P)H) small subunit
NPKM_1425	1468758 +	1470000 Rmet_4820	<i>nasB</i>	1.00	0.00	Op1404f_2	MET-EN-Nitrog	Q1LDU4 Assimilatory nitrate reductase (NADH) beta subunit
NPKM_1426	1470018 +	1472766 Rmet_4821	<i>nasA</i>	2.00	0.00	Op1404f_2	MET-EN-Nitrog	Q1LDU3 Assimilatory nitrate reductase (NADH) alpha subunit apoprotein
3UTR_835	1472125 -	1472965 Rmet_4822				Op1405r_1		
NPKM_1427	1472966 -	1475171 Rmet_4822		30.33	1.53	Op1405r_1	NA	Q1LDU2 Putative uncharacterized protein
5UTR_677	1475172 -	1475204 Rmet_4822				Op1405r_1		
5UTR_340	1475683 +	1475714 Rmet_4823				Op1406f_1		
NPKM_1428	1475714 +	1476341 Rmet_4823		32.00	3.61	Op1406f_1	NA	Q1LDU1 Putative uncharacterized protein
NPKM_1429	1476330 +	1477311 Rmet_4824		25.67	1.53	Op1406f_1	MET-AA-ArgPro	Q1LDU0 Ornithine cyclodeaminase
3UTR_834	1476635 -	1478364 Rmet_4826	<i>mdtD</i>			Op1407r_1		
NPKM_1430	1477334 +	1478303 Rmet_4825	<i>tdcB</i>	46.33	1.15	Op1406f_1	MET-AA-GlySerThr	Q1LDT9 Pyridoxal-5'-phosphate-dependent enzyme, beta subunit
3UTR_419	1478304 +	1479024 Rmet_4825	<i>tdcB</i>			Op1406f_1		
NPKM_1431	1478365 -	1479820 Rmet_4826	<i>mdtD</i>	39.33	2.31	Op1407r_1	NA	Q1LDT8 Drug resistance transporter EmrB/QacA subfamily
NPKM_1432	1479988 -	1481047 Rmet_4827		20.33	0.58	Op1407r_1	NA	Q1LDT7 NAD-dependent epimerase/dehydratase
NPKM_1433	1481115 -	1482843 Rmet_4828		27.00	1.73	Op1407r_1	NA	Q1LDT6 Glycosyl transferase, family 39
5UTR_676	1482844 -	1483157 Rmet_4828				Op1407r_1		
5UTR_341	1483056 +	1483081 Rmet_4829	<i>qseB</i>			Op1408f_1		
NPKM_1434	1483081 +	1483789 Rmet_4829	<i>qseB</i>	111.33	4.73	Op1408f_1	EIP-SIG-2Comp	Q1LDT5 Two component transcriptional regulator, winged helix family
NPKM_1435	1483785 +	1485159 Rmet_4830	<i>qseC</i>	45.00	3.61	Op1408f_1	EIP-SIG-2Comp	Q1LDT4 Sensor protein
NPKM_1436	1485207 +	1486434 Rmet_4831		30.67	2.31	Op1408f_1	EIP-TRA-Ion	Q1LDT3 Chromate transporter
NPKM_1437	1486414 +	1487092 Rmet_4832		14.33	2.08	Op1408f_1	NA	Q1LDT2 Putative uncharacterized protein
NPKM_1438	1487112 +	1487313 Rmet_6688		4.67	1.53	Op1408f_1	NA	NA
3UTR_420	1487314 +	1487369 Rmet_6688				Op1408f_1		
5UTR_342	1487383 +	1487479 Rmet_6689				Op1408f_1		
NPKM_1439	1487479 +	1487737 Rmet_6689		1.67	0.58	Op1408f_1	NA	NA
NPKM_1440	1487768 +	1488083 Rmet_4833		150.00	4.00	Op1408f_2	NA	Q1LDT1 Putative uncharacterized protein
3UTR_833	1487816 -	1488208 Rmet_4834	<i>ompP</i>			Op1409r_1		
3UTR_421	1488084 +	1488122 Rmet_4833				Op1408f_2		
NPKM_1441	1488209 -	1489271 Rmet_4834	<i>ompP</i>	52.00	2.65	Op1409r_1	NA	Q1LDT0 Porin, Gram-negative type
5UTR_675	1489272 -	1489331 Rmet_4834	<i>ompP</i>			Op1409r_1		
5UTR_343	1489344 +	1489587 Rmet_4835				Op1410f_1		
NPKM_1442	1489587 +	1492068 Rmet_4835		37.33	2.31	Op1410f_1	NA	Q1LDS9 Glycosyl transferase, family 51
3UTR_832	1491179 -	1492094 Rmet_4836				Op1411r_2		

3UTR_422	1492069 +	1492405 Rmet_4835				Op1410f_1		
NPKM_1443	1492095 -	1492860 Rmet_4836	18.33	4.04	Op1411r_2	NA	Q1LDS8 Diguanylate phosphodiesterase (EAL domain)	
5UTR_674	1492861 -	1492914 Rmet_4836			Op1411r_2			
3UTR_831	1492922 -	1493058 Rmet_4837			Op1411r_1			
NPKM_1444	1493059 -	1494352 Rmet_4837	7.00	0.00	Op1411r_1	NA	Q1LDS7 Twin-arginine translocation pathway signal	
NPKM_1445	1494370 -	1495951 Rmet_4838	6.33	0.58	Op1411r_1	NA	Q1LDS6 Putative uncharacterized protein	
5UTR_344	1496206 +	1496246 Rmet_4839			Op1412f_1			
NPKM_1446	1496246 +	1497323 Rmet_4839	6.67	1.53	Op1412f_1	NA	Q1LDS5 Transcriptional regulator, LacI family	
NPKM_1447	1497385 +	1498408 Rmet_4840	8.67	0.58	Op1412f_1	EIP-TRA-ABC	Q1LDS4 Putative periplasmic solute-binding protein	
NPKM_1448	1498431 +	1499250 Rmet_4841	4.00	1.00	Op1412f_1	EIP-TRA-ABC	Q1LDS3 Binding-protein-dependent transport systems inner membrane component	
NPKM_1449	1499383 +	1500259 Rmet_4842	2.00	0.00	Op1412f_1	EIP-TRA-ABC	Q1LDS2 Binding-protein-dependent transport systems inner membrane component	
NPKM_1450	1500251 +	1501310 Rmet_4843	3.67	1.15	Op1412f_1	EIP-TRA-ABC	Q1LDS1 ABC transporter related	
NPKM_1451	1501306 +	1502179 Rmet_4844	3.67	0.58	Op1412f_1	NA	Q1LDS0 Metallophosphoesterase	
5UTR_345	1502278 +	1502300 Rmet_4845			Op1412f_1			
NPKM_1452	1502300 +	1503086 Rmet_4845	7.00	1.00	Op1412f_1	NA	Q1LDR9 Putative uncharacterized protein	
NPKM_1453	1503093 +	1503285 Rmet_6690	6.67	1.53	Op1412f_1	NA	NA	
NPKM_1454	1503245 +	1504301 Rmet_4846	34.00	0.00	Op1412f_2	NA	Q1LDR8 TRAP dicarboxylate transporter-DctP subunit	
NPKM_1455	1504534 +	1506238 Rmet_4847	17.33	4.16	Op1412f_2	NA	Q1LDR7 YidE/YbjL duplication	
3UTR_830	1505112 -	1506332 Rmet_4848	phnA		Op1413r_1			
3UTR_423	1506239 +	1506774 Rmet_4847			Op1412f_2			
NPKM_1456	1506333 -	1506726 Rmet_4848	phnA	65.33	3.21	Op1413r_1	NA	Q1LDR6 Alkylphosphonate utilization operon protein PhnA
5UTR_673	1506727 -	1507058 Rmet_4848	phnA		Op1413r_1			
5UTR_346	1506812 +	1506879 Rmet_4849			Op1414f_1			
NPKM_1457	1506879 +	1507773 Rmet_4849		15.67	1.53	Op1414f_1	NA	Q1LDR5 Putative uncharacterized protein
3UTR_829	1507094 -	1507818 Rmet_4850			Op1415r_1			
3UTR_424	1507774 +	1508343 Rmet_4849			Op1414f_1			
NPKM_1458	1507819 -	1508770 Rmet_4850		23.33	0.58	Op1415r_1	NA	Q1LDR4 Transcriptional regulator, LysR family
NPKM_1459	1508860 +	1510099 Rmet_4851	caiB	5.67	0.58	Op1416f_1	NA	Q1LDR3 L-carnitine dehydratase/bile acid-inducible protein F
NPKM_1460	1510098 +	1511109 Rmet_4852		7.33	0.58	Op1416f_1	NA	Q1LDR2 Alcohol dehydrogenase, zinc-binding
3UTR_425	1511110 +	1511132 Rmet_4852			Op1416f_1			
5UTR_347	1511138 +	1511165 Rmet_4853	bugT		Op1416f_1			
NPKM_1461	1511165 +	1512110 Rmet_4853	bugT	6.33	0.58	Op1416f_1	NA	Q1LDR1 Uncharacterized protein UPF0065
NPKM_1462	1512365 +	1513001 Rmet_4854		30.67	1.53	Op1416f_2	NA	Q1LDR0 Two component transcriptional regulator, LuxR family
NPKM_1463	1513013 +	1514789 Rmet_4855		13.33	2.08	Op1416f_2	NA	Q1LDQ9 Sensor protein
NPKM_1464	1514945 +	1516397 Rmet_4856	puuC	5.67	0.58	Op1416f_2	MET-CAH-FbP	Q1LDQ8 Aldehyde dehydrogenase (Acceptor)
3UTR_828	1516175 -	1516508 Rmet_4857			Op1417r_1			
3UTR_426	1516398 +	1516459 Rmet_4856	puuC		Op1416f_2			
NPKM_1465	1516509 -	1516677 Rmet_4857		68.33	12.10	Op1417r_1	NA	Q1LDQ7 Putative uncharacterized protein
5UTR_672	1516678 -	1516844 Rmet_4857			Op1417r_1			
5UTR_348	1516850 +	1517035 Rmet_4858			Op1418f_1			
NPKM_1466	1517035 +	1517251 Rmet_4858		38.33	2.89	Op1418f_1	NA	Q1LDQ6 Putative uncharacterized protein
3UTR_427	1517252 +	1517344 Rmet_4858			Op1418f_1			
3UTR_827	1517259 -	1517385 Rmet_4859			Op1419r_5			

NPKM_1467	1517386 -	1518502 Rmet_4859		80.67	2.89	Op1419r_5	NA	Q1LDQ5 NADH:flavin oxidoreductase/NADH oxidase
NPKM_1468	1518637 -	1521052 Rmet_4860		29.33	0.58	Op1419r_4	NA	Q1LDQ4 Peptidase S45, penicillin amidase
NPKM_1469	1521265 -	1521898 Rmet_4861		138.00	2.65	Op1419r_4	MET-LIP-GlycPLip	Q1LDQ3 CDP-diacylglycerol--serine O-phosphatidyltransferase
NPKM_1470	1521923 -	1522214 Rmet_4862		209.67	9.81	Op1419r_4	NA	Q1LDQ2 Antibiotic biosynthesis monooxygenase
NPKM_1471	1522316 -	1522781 Rmet_4863		27.33	0.58	Op1419r_3	NA	Q1LDQ1 Putative uncharacterized protein
NPKM_1472	1522837 -	1523275 Rmet_4864		7.00	1.73	Op1419r_2	NA	Q1LDQ0 Putative uncharacterized protein
NPKM_1473	1523380 -	1524862 Rmet_4865	<i>nodT</i>	15.67	1.15	Op1419r_2	NA	Q1LDP9 RND efflux system, outer membrane lipoprotein, NodT
NPKM_1474	1524873 -	1528119 Rmet_4866	<i>acrB</i>	13.33	0.58	Op1419r_2	EIP-TRA-Ion	Q1LDP8 Hydrophobe/amphiphile efflux-1 HAE1
NPKM_1475	1528169 -	1529405 Rmet_4867	<i>acrA</i>	55.00	1.73	Op1419r_2	NA	Q1LDP7 Secretion protein HlyD
NPKM_1476	1529617 -	1530493 Rmet_4868	<i>llpE</i>	94.33	3.51	Op1419r_2	MET-CAH-But	Q1LDP6 Alpha/beta hydrolase fold-3
5UTR_349	1530458 +	1530865 Rmet_4869				Op1420f_1		
5UTR_671	1530494 -	1530547 Rmet_4868	<i>llpE</i>			Op1419r_2		
NPKM_1477	1530659 -	1530863 Rmet_6691		2.67	0.58	Op1419r_1	NA	NA
NPKM_1478	1530865 +	1531792 Rmet_4869		77.33	4.93	Op1420f_1	NA	Q1LDP5 Transcriptional regulator, LysR family
3UTR_428	1531793 +	1532519 Rmet_4869				Op1420f_1		
NPKM_1479	1531862 -	1533116 Rmet_4870		68.00	4.58	Op1421r_1	NA	Q1LDP4 Peptidase M20
5UTR_670	1533117 -	1533179 Rmet_4870				Op1421r_1		
5UTR_350	1533245 +	1533289 Rmet_4871				Op1422f_1		
NPKM_1480	1533289 +	1534375 Rmet_4871		17.33	0.58	Op1422f_1	NA	Q1LDP3 Transcriptional regulator, AraC family
3UTR_826	1534231 -	1534402 Rmet_4872				Op1423r_1		
3UTR_429	1534376 +	1534898 Rmet_4871				Op1422f_1		
NPKM_1481	1534403 -	1535219 Rmet_4872		9.00	1.00	Op1423r_1	NA	Q1LDP2 Transport-associated
5UTR_669	1535220 -	1535463 Rmet_4872				Op1423r_1		
5UTR_351	1535326 +	1535366 Rmet_4873				Op1424f_1		
NPKM_1482	1535366 +	1536080 Rmet_4873		18.67	1.53	Op1424f_1	NA	Q1LDP1 Putative uncharacterized protein
NPKM_1483	1536207 +	1536405 Rmet_6692		21.67	2.89	Op1424f_1	NA	NA
NPKM_1484	1536426 +	1537605 Rmet_4874		79.67	6.03	Op1424f_2	EIP-TRA-Ion	Q1LDP0 Sodium/calcium exchanger membrane region
3UTR_825	1537032 -	1537672 Rmet_4875	<i>catD</i>			Op1425r_2		
3UTR_430	1537606 +	1539515 Rmet_4874				Op1424f_2		
NPKM_1485	1537673 -	1538450 Rmet_4875	<i>catD</i>	14.33	1.53	Op1425r_2	MET-XEN-Benz	Q1LDN9 3-oxoadipate enol-lactonase
NPKM_1486	1538439 -	1539426 Rmet_4876	<i>bugT</i>	20.67	1.53	Op1425r_2	NA	Q1LDN8 Uncharacterized protein UPF0065
NPKM_1487	1539456 -	1539735 Rmet_4877	<i>catC</i>	13.67	1.15	Op1425r_2	MET-XEN-Benz	Q1LDN7 Muconolactone delta-isomerase
NPKM_1488	1539788 -	1540913 Rmet_4878	<i>catB</i>	6.67	0.58	Op1425r_1	MET-XEN-Toluene	Q1LDN6 Muconate cycloisomerase
5UTR_668	1540914 -	1540952 Rmet_4878	<i>catB</i>			Op1425r_1		
5UTR_352	1541049 +	1541085 Rmet_4879	<i>catM</i>			Op1426f_1		
3UTR_824	1541075 -	1541960 Rmet_4880	<i>catM</i>			Op1427r_1		
NPKM_1489	1541085 +	1541961 Rmet_4879	<i>catM</i>	15.33	1.53	Op1426f_1	NA	Q1LDN5 Transcriptional regulator, LysR family
NPKM_1490	1541961 -	1542879 Rmet_4880	<i>catM</i>	14.67	1.53	Op1427r_1	NA	Q1LDN4 Transcriptional regulator, LysR family
3UTR_431	1541962 +	1542532 Rmet_4879	<i>catM</i>			Op1426f_1		
NPKM_1491	1543052 +	1543976 Rmet_4881	<i>catA</i>	4.00	0.00	Op1428f_1	MET-XEN-Toluene	Q1LDN3 Catechol 1,2-dioxygenase
3UTR_432	1543977 +	1544037 Rmet_4881	<i>catA</i>			Op1428f_1		
5UTR_353	1544057 +	1544107 Rmet_4882	<i>benA</i>			Op1428f_1		
NPKM_1492	1544107 +	1545502 Rmet_4882	<i>benA</i>	2.33	0.58	Op1428f_1	MET-XEN-Benz	Q1LDN2 Benzoate 1,2-dioxygenase, alpha subunit

NPKM_1493	1545498 +	1545993 Rmet_4883	<i>benB</i>	3.67	1.53	Op1428f_1	MET-XEN-Benz	Q1LDN1 Benzoate 1,2-dioxygenase, beta subunit
NPKM_1494	1546034 +	1547054 Rmet_4884	<i>benC</i>	3.33	0.58	Op1428f_1	MET-XEN-Benz	Q1LDN0 Oxidoreductase FAD-binding region
NPKM_1495	1547053 +	1547848 Rmet_4885	<i>benD</i>	2.67	0.58	Op1428f_1	MET-XEN-Benz	Q1LDM9 Short-chain dehydrogenase/reductase SDR
3UTR_823	1547521 -	1547931 Rmet_4886				Op1429r_2		
3UTR_433	1547849 +	1547881 Rmet_4885	<i>benD</i>			Op1428f_1		
NPKM_1496	1547932 -	1549084 Rmet_4886		19.67	0.58	Op1429r_2	NA	Q1LDM8 Putative uncharacterized protein
NPKM_1497	1549193 -	1549769 Rmet_4887		16.67	1.53	Op1429r_2	NA	Q1LDM7 Transcriptional regulator, TetR family
3UTR_822	1549919 -	1549936 Rmet_4888	<i>lpdA</i>			Op1429r_1		
NPKM_1498	1549937 -	1551380 Rmet_4888	<i>lpdA</i>	2.33	0.58	Op1429r_1	MET-CAH-FbP	Q1LDM6 FAD-dependent pyridine nucleotide-disulphide oxidoreductase
3UTR_821	1551450 -	1551518 Rmet_4889	<i>prx5</i>			Op1429r_1		
NPKM_1499	1551519 -	1552251 Rmet_4889	<i>prx5</i>	8.00	1.00	Op1429r_1	GIP-PTL-Fold	Q1LDM5 Glutaredoxin-like region
5UTR_354	1552360 +	1552499 Rmet_4890				Op1430f_1		
NPKM_1500	1552499 +	1554239 Rmet_4890		62.67	1.53	Op1430f_1	NA	Q1LDM4 Peptidase M20A, peptidase V
3UTR_434	1554240 +	1554297 Rmet_4890				Op1430f_1		
NPKM_1501	1554301 +	1554484 Rmet_6693		24.33	1.53	Op1430f_1	NA	NA
NPKM_1502	1554680 +	1555913 Rmet_4891	<i>sorA</i>	28.33	4.04	Op1430f_1	NA	Q1LDM3 Sulfite dehydrogenase (Cytochrome) subunit SorA apoprotein
3UTR_820	1555918 -	1556589 Rmet_4893				Op1431r_1		
NPKM_1503	1555923 +	1556580 Rmet_4892	<i>sorB</i>	20.67	1.53	Op1430f_1	MET-EN-Sulf	Q1LDM2 Sulfite dehydrogenase (Cytochrome) subunit SorB
3UTR_435	1556581 +	1557107 Rmet_4892	<i>sorB</i>			Op1430f_1		
NPKM_1504	1556590 -	1557070 Rmet_4893		17.67	2.08	Op1431r_1	NA	Q1LDM1 Putative uncharacterized protein
NPKM_1505	1557193 -	1558960 Rmet_4894		17.00	1.00	Op1431r_1	MET-NUC-Pyr	Q1LDM0 Cyclic nucleotide-regulated FAD-dependent pyridine nucleotide-disulphide
5UTR_667	1558961 -	1559024 Rmet_4894				Op1431r_1		
5UTR_355	1559264 +	1559287 Rmet_4895	<i>ygfH</i>			Op1432f_1		
NPKM_1506	1559287 +	1560820 Rmet_4895	<i>ygfH</i>	20.00	3.46	Op1432f_1	MET-CAH-Pyr	Q1LDL9 Acetyl-CoA hydrolase/transferase
3UTR_819	1560488 -	1560843 Rmet_4896				Op1433r_1		
3UTR_436	1560821 +	1561159 Rmet_4895	<i>ygfH</i>			Op1432f_1		
NPKM_1507	1560844 -	1561639 Rmet_4896		9.67	1.53	Op1433r_1	NA	Q1LDL8 SMC protein-like protein
NPKM_1508	1561798 +	1561906 Rmet_4897		0.67	0.58	Op1434f_1	NA	Q1LDL7 Putative uncharacterized protein
5UTR_356	1561977 +	1562015 Rmet_4898				Op1434f_2		
NPKM_1509	1562015 +	1562957 Rmet_4898		35.33	1.53	Op1434f_2	NA	Q1LDL6 Patatin
NPKM_1510	1563030 +	1563567 Rmet_4899		52.67	2.52	Op1434f_2	NA	Q1LDL5 Putative uncharacterized protein
NPKM_1511	1563695 +	1564013 Rmet_4900		56.00	1.73	Op1434f_2	NA	Q1LDL4 Transcriptional regulator, XRE family
NPKM_1512	1564009 +	1565311 Rmet_4901		39.33	1.53	Op1434f_2	NA	Q1LDL3 HipA-like protein
3UTR_818	1565138 -	1565361 Rmet_4902				Op1435r_1		
3UTR_437	1565312 +	1566026 Rmet_4901				Op1434f_2		
NPKM_1513	1565362 -	1566127 Rmet_4902		2.67	0.58	Op1435r_1	NA	Q1LDL2 Short-chain dehydrogenase/reductase SDR
NPKM_1514	1566272 +	1566875 Rmet_4903		1.67	0.58	Op1436f_1	NA	Q1LDL1 Transcriptional regulator, TetR family
3UTR_438	1566876 +	1566888 Rmet_4903				Op1436f_1		
NPKM_1515	1566916 +	1568224 Rmet_4904		1.33	0.58	Op1436f_1	NA	Q1LDL0 Major facilitator superfamily MFS_1
3UTR_817	1567092 -	1568251 Rmet_4905				Op1437r_1		
3UTR_439	1568225 +	1568242 Rmet_4904				Op1436f_1		
NPKM_1516	1568252 -	1569158 Rmet_4905		15.00	1.73	Op1437r_1	NA	Q1LDK9 Transcriptional regulator, LysR family
5UTR_666	1569159 -	1569172 Rmet_4905				Op1437r_1		

NPKM_1517	1569239 +	1569662 Rmet_4906		28.67	1.53	Op1438f_1	NA	Q1LDK8 Glyoxalase/bleomycin resistance protein/dioxygenase
NPKM_1518	1569704 +	1570400 Rmet_4907		43.33	2.08	Op1438f_1	NA	Q1LDK7 Fumarylacetoacetate (FAA) hydrolase
3UTR_440	1570401 +	1570444 Rmet_4907				Op1438f_1		
NPKM_1519	1570797 +	1571295 Rmet_4908	mmsQ	4.00	1.00	Op1438f_1	NA	Q1LDK6 Putative uncharacterized protein
NPKM_1520	1571364 +	1571466 Rmet_6694		3.33	1.53	Op1438f_1	NA	NA
NPKM_1521	1571519 +	1572125 Rmet_4909		5.33	1.53	Op1438f_1	NA	Q1LDK5 Transcriptional regulator, TetR family
3UTR_816	1572016 -	1572149 Rmet_4910	xthA3			Op1439r_2		
3UTR_441	1572126 +	1572170 Rmet_4909				Op1438f_1		
NPKM_1522	1572150 -	1573002 Rmet_4910	xthA3	3.00	0.00	Op1439r_2	GIP-REP-Recomb	Q1LDK4 Exodeoxyribonuclease III
NPKM_1523	1573125 -	1573671 Rmet_4911		3.67	0.58	Op1439r_2	NA	Q1LDK3 Putative uncharacterized protein
NPKM_1524	1573721 -	1574252 Rmet_4912	nosL	3.67	0.58	Op1439r_2	NA	Q1LDK2 NosL
NPKM_1525	1574248 -	1575070 Rmet_4913	nosY	0.33	0.58	Op1439r_1	EIP-TRA-ABC	Q1LDK1 ABC-type transport system protein
NPKM_1526	1575069 -	1576020 Rmet_4914	nosF	1.00	1.00	Op1439r_1	EIP-TRA-ABC	Q1LDK0 ABC transporter related
NPKM_1527	1575997 -	1577275 Rmet_4915	nosD	1.67	0.58	Op1439r_1	NA	Q1LDJ9 Periplasmic copper-binding
NPKM_1528	1577271 -	1579890 Rmet_4916	nosR	1.00	0.00	Op1439r_1	NA	Q1LDJ8 FMN-binding
NPKM_1529	1579945 -	1581886 Rmet_4917	nosZ	1.00	0.00	Op1439r_1	MET-EN-Nitrog	Q1LDJ7 Cytochrome c oxidase, subunit II
NPKM_1530	1582049 +	1582310 Rmet_6695		0.00	0.00	Op1440f_1	NA	NA
NPKM_1531	1582158 +	1582572 Rmet_4918	nosC	1.00	0.00	Op1440f_2	NA	Q1LDJ6 Cytochrome c, class I
NPKM_1532	1582576 +	1583599 Rmet_4919	nosX	2.00	0.00	Op1440f_2	MET-COF-Thia	Q1LDJ5 ApbE-like lipoprotein
3UTR_815	1583450 -	1583600 Rmet_6696				Op2079r_1		
3UTR_442	1583600 +	1583714 Rmet_4919	nosX			Op1440f_2		
NPKM_1533	1583601 -	1583724 Rmet_6696		1.00	1.73	Op2079r_1	NA	NA
5UTR_357	1583721 +	1583833 Rmet_4920				Op1440f_3		
5UTR_665	1583725 -	1583729 Rmet_6696				Op2079r_1		
NPKM_1534	1583833 +	1584736 Rmet_4920		28.33	0.58	Op1440f_3	NA	Q1LDJ4 Phospholipid/glycerol acyltransferase
3UTR_443	1584737 +	1585388 Rmet_4920				Op1440f_3		
NPKM_1535	1584809 -	1585214 Rmet_4921		0.33	0.58	Op1441r_1	NA	Q1LDJ3 Putative lipoprotein
3UTR_814	1585283 -	1585291 Rmet_4922				Op1441r_1		
NPKM_1536	1585292 -	1585580 Rmet_4922		1.33	0.58	Op1441r_1	NA	Q1LDJ2 Putative uncharacterized protein
5UTR_664	1585581 -	1585581 Rmet_4922				Op1441r_1		
3UTR_813	1585602 -	1586233 Rmet_4924				Op1443r_1		
5UTR_358	1585804 +	1585855 Rmet_4923				Op1442f_1		
NPKM_1537	1585855 +	1586182 Rmet_4923		86.33	3.06	Op1442f_1	GIP-PTL-Fold	Q1LDJ1 Thioredoxin-related
3UTR_444	1586183 +	1586606 Rmet_4923				Op1442f_1		
NPKM_1538	1586234 -	1586708 Rmet_4924		23.00	1.00	Op1443r_1	NA	Q1LDJ0 Transcriptional regulator, AsnC family
5UTR_663	1586709 -	1586722 Rmet_4924				Op1443r_1		
5UTR_359	1586882 +	1586911 Rmet_4925				Op1444f_1		
NPKM_1539	1586911 +	1587985 Rmet_4925		16.67	0.58	Op1444f_1	MET-AA-Tyr	Q1LDI9 4-hydroxyphenylpyruvate dioxygenase
3UTR_445	1587986 +	1588048 Rmet_4925				Op1444f_1		
5UTR_360	1588060 +	1588164 Rmet_4926	aroP			Op1444f_1		
NPKM_1540	1588164 +	1589553 Rmet_4926	aroP	2.00	0.00	Op1444f_1	EIP-TRA-Ion	Q1LDI8 Amino acid permease-associated region
NPKM_1541	1589610 +	1590807 Rmet_4927	tyrB	194.67	8.14	Op1444f_2	MET-AA-Met	Q1LDI7 Aminotransferase
3UTR_446	1590808 +	1590845 Rmet_4927	tyrB			Op1444f_2		

5UTR_361	1590850 +	1590918 Rmet_4928	<i>lysP2</i>			Op1444f_2		
NPKM_1542	1590918 +	1592451 Rmet_4928	<i>lysP2</i>	19.67	1.53	Op1444f_2	EIP-TRA-Ion	Q1LDI6 Amino acid permease-associated region
3UTR_812	1592525 -	1593293 Rmet_4930				Op1445r_1		
NPKM_1543	1592548 +	1593256 Rmet_4929	<i>gst</i>	211.67	9.02	Op1444f_3	MET-OAA-GSH	Q1LDI5 Glutathione S-transferase-like protein
3UTR_447	1593257 +	1593964 Rmet_4929	<i>gst</i>			Op1444f_3		
NPKM_1544	1593294 -	1594110 Rmet_4930		9.67	1.15	Op1445r_1	NA	Q1LDI4 Transcriptional regulator, IclR family
5UTR_362	1594194 +	1594229 Rmet_4931	<i>bug</i>			Op1446f_1		
NPKM_1545	1594229 +	1595222 Rmet_4931	<i>bug</i>	19.67	0.58	Op1446f_1	NA	Q1LDI3 Uncharacterized protein UPF0065
NPKM_1546	1595253 +	1597596 Rmet_4932	<i>thcB</i>	19.33	0.58	Op1446f_1	NA	Q1LDI2 Ferredoxin
3UTR_811	1595961 -	1597663 Rmet_4933				Op1447r_1		
3UTR_448	1597597 +	1598108 Rmet_4932	<i>thcB</i>			Op1446f_1		
NPKM_1547	1597664 -	1598627 Rmet_4933		26.00	3.46	Op1447r_1	EIP-SIG-2Comp	Q1LDI1 Response regulator receiver (CheY-like) modulated CheW protein
5UTR_662	1598628 -	1598706 Rmet_4933				Op1447r_1		
5UTR_363	1598962 +	1599119 Rmet_4934				Op1448f_1		
NPKM_1548	1599119 +	1600502 Rmet_4934		2.00	1.00	Op1448f_1	NA	Q1LDI0 Xanthine/uracil/vitamin C permease
3UTR_449	1600503 +	1600526 Rmet_4934				Op1448f_1		
3UTR_810	1600605 -	1600614 Rmet_6697				Op2080r_1		
NPKM_1549	1600615 -	1600792 Rmet_6697		3.00	1.73	Op2080r_1	NA	NA
5UTR_661	1600793 -	1600866 Rmet_6697				Op2080r_1		
5UTR_364	1600878 +	1601063 Rmet_4935				Op1448f_2		
3UTR_809	1600965 -	1601431 Rmet_4936				Op1449r_1		
NPKM_1550	1601063 +	1601378 Rmet_4935		378.00	10.44	Op1448f_2	NA	Q1LDH9 H-NS family DNA-binding protein
3UTR_450	1601379 +	1602456 Rmet_4935				Op1448f_2		
NPKM_1551	1601432 -	1602191 Rmet_4936		13.67	2.08	Op1449r_1	NA	Q1LDH8 Putative uncharacterized protein
5UTR_660	1602192 -	1602453 Rmet_4936				Op1449r_1		
5UTR_365	1602460 +	1602472 Rmet_4937				Op1450f_1		
NPKM_1552	1602472 +	1603465 Rmet_4937		2.67	0.58	Op1450f_1	NA	Q1LDH7 Transcriptional regulator, AsnC family
3UTR_808	1603505 -	1603515 Rmet_4938				Op1451r_1		
NPKM_1553	1603516 -	1603972 Rmet_4938		1.00	0.00	Op1451r_1	NA	Q1LDH6 Putative uncharacterized protein
NPKM_1554	1603968 -	1604889 Rmet_4939		1.00	0.00	Op1451r_1	NA	Q1LDH5 Peptidase U32
NPKM_1555	1604922 -	1605951 Rmet_4940		2.33	0.58	Op1451r_1	OTHERS	Q1LDH4 Peptidase U32
NPKM_1556	1606068 -	1606974 Rmet_4941		10.00	1.73	Op1451r_1	NA	Q1LDH3 Transcriptional regulator, IclR family
5UTR_366	1606998 +	1607057 Rmet_4942	<i>gabD</i>			Op1452f_1		
NPKM_1557	1607057 +	1608506 Rmet_4942	<i>gabD</i>	79.00	1.00	Op1452f_1	MET-CAH-But	Q1LDH2 Succinate semialdehyde dehydrogenase
NPKM_1558	1608578 +	1609736 Rmet_4943		70.67	1.53	Op1452f_1	MET-CAH-FbP	Q1LDH1 Iron-containing alcohol dehydrogenase
3UTR_451	1609737 +	1609858 Rmet_4943				Op1452f_1		
3UTR_807	1609915 -	1610294 Rmet_4945				Op1453r_2		
5UTR_367	1609948 +	1610032 Rmet_4944				Op1452f_1		
NPKM_1559	1610032 +	1610314 Rmet_4944		31.67	3.06	Op1452f_1	NA	Q1LDH0 Putative uncharacterized protein
NPKM_1560	1610295 -	1610760 Rmet_4945		64.67	4.04	Op1453r_2	NA	Q1LDG9 PRC-barrel
3UTR_452	1610315 +	1610936 Rmet_4944				Op1452f_1		
NPKM_1561	1611013 -	1611772 Rmet_4946		28.33	2.08	Op1453r_1	MET-CAH-TCA	Q1LDG8 Putative uncharacterized protein
NPKM_1562	1611785 -	1612769 Rmet_4947	<i>bug</i>	35.33	1.15	Op1453r_1	NA	Q1LDG7 Uncharacterized protein UPF0065

NPKM_1563	1612780 -	1613593 Rmet_4948		27.00	1.00	Op1453r_1	NA	Q1LDG6 Short-chain dehydrogenase/reductase SDR
NPKM_1564	1613608 -	1615174 Rmet_4949		27.67	0.58	Op1453r_1	MET-LIP-FASyn	Q1LDG5 AMP-dependent synthetase and ligase
5UTR_659	1615175 -	1615195 Rmet_4949				Op1453r_1		
5UTR_368	1615285 +	1615312 Rmet_4950				Op1454f_1		
NPKM_1565	1615312 +	1616338 Rmet_4950		43.00	3.00	Op1454f_1	NA	Q1LDG4 Transcriptional regulator, LacI family
3UTR_806	1615946 -	1616364 Rmet_4951	bugT			Op1455r_1		
3UTR_453	1616339 +	1617086 Rmet_4950				Op1454f_1		
NPKM_1566	1616365 -	1617355 Rmet_4951	bugT	6.00	0.00	Op1455r_1	NA	Q1LDG3 Uncharacterized protein UPF0065
NPKM_1567	1617382 -	1618192 Rmet_4952		5.33	0.58	Op1455r_1	NA	Q1LDG2 Short-chain dehydrogenase/reductase SDR
NPKM_1568	1618214 -	1619237 Rmet_4953		8.33	0.58	Op1455r_1	NA	Q1LDG1 Putative uncharacterized protein
NPKM_1569	1619636 -	1621037 Rmet_4954		20.00	1.00	Op1455r_1	NA	Q1LDG0 Transcriptional regulator, GntR family
5UTR_658	1621038 -	1621108 Rmet_4954				Op1455r_1		
5UTR_369	1621153 +	1621216 Rmet_4955	appC			Op1456f_1		
NPKM_1570	1621216 +	1622650 Rmet_4955	appC	10.67	1.15	Op1456f_1	MET-EN-OxPhos	Q1LDF9 Cytochrome bd ubiquinol oxidase, subunit I
NPKM_1571	1622654 +	1623662 Rmet_4956	appB	9.67	1.53	Op1456f_1	MET-EN-OxPhos	Q1LDF8 Cytochrome d ubiquinol oxidase, subunit II
NPKM_1572	1623941 +	1624640 Rmet_4957		24.33	1.15	Op1456f_2	NA	Q1LDF7 Putative uncharacterized protein
3UTR_805	1624540 -	1624876 Rmet_4958				Op1457r_3		
NPKM_1573	1624649 +	1624865 Rmet_6698		16.00	2.65	Op1456f_2	NA	NA
3UTR_454	1624866 +	1625291 Rmet_6698				Op1456f_2		
NPKM_1574	1624877 -	1625969 Rmet_4958		9.67	0.58	Op1457r_3	NA	Q1LDF6 Fimbrial protein
3UTR_804	1626128 -	1626154 Rmet_4959	fimD			Op1457r_2		
NPKM_1575	1626155 -	1628759 Rmet_4959	fimD	0.33	0.58	Op1457r_2	NA	Q1LDF5 Fimbrial biogenesis outer membrane usher protein
3UTR_803	1628785 -	1628872 Rmet_4960	fimC			Op1457r_2		
NPKM_1576	1628873 -	1629578 Rmet_4960	fimC	3.67	1.15	Op1457r_2	NA	Q1LDF4 Pili assembly chaperone
5UTR_657	1629579 -	1629623 Rmet_4960	fimC			Op1457r_2		
3UTR_802	1629646 -	1629705 Rmet_4961	fimA			Op1457r_2		
NPKM_1577	1629706 -	1630261 Rmet_4961	fimA	8.67	0.58	Op1457r_2	NA	Q1LDF3 Fimbrial protein
5UTR_656	1630262 -	1630287 Rmet_4961	fimA			Op1457r_2		
3UTR_801	1630522 -	1630561 Rmet_4962				Op1457r_1		
NPKM_1578	1630562 -	1631459 Rmet_4962		3.67	1.15	Op1457r_1	NA	Q1LDF2 Diguanylate phosphodiesterase (EAL domain)
5UTR_655	1631460 -	1631510 Rmet_4962				Op1457r_1		
NPKM_1579	1631671 -	1635040 Rmet_4963		2.33	0.58	Op1457r_1	EIP-SIG-2Comp	Q1LDF1 Sensor protein
NPKM_1580	1635293 -	1635965 Rmet_4964		1.67	0.58	Op1457r_1	NA	Q1LDF0 Two component transcriptional regulator, LuxR family
5UTR_370	1635760 +	1635770 Rmet_6699				Op2081f_1		
NPKM_1581	1635770 +	1635950 Rmet_6699		1.00	1.00	Op2081f_1	NA	NA
5UTR_654	1635966 -	1635979 Rmet_4964				Op1457r_1		
3UTR_800	1635991 -	1636241 Rmet_4965				Op1457r_1		
NPKM_1582	1636242 -	1636887 Rmet_4965		14.67	0.58	Op1457r_1	EIP-SIG-2Comp	Q1LDE9 Two component transcriptional regulator, LuxR family
NPKM_1583	1637061 -	1639917 Rmet_4966		7.33	1.15	Op1457r_1	NA	Q1LDE8 Sensor protein
5UTR_653	1639918 -	1639947 Rmet_4966				Op1457r_1		
5UTR_371	1640119 +	1640197 Rmet_4967				Op1458f_1		
NPKM_1584	1640197 +	1640461 Rmet_4967		112.00	7.21	Op1458f_1	NA	Q1LDE7 Putative uncharacterized protein
3UTR_799	1640423 -	1640541 Rmet_4968				Op1459r_2		

3UTR_455	1640462 +	1641872 Rmet_4967				Op1458f_1		
NPKM_1585	1640542 -	1641571 Rmet_4968	1.33	0.58	Op1459r_2	NA	Q1LDE6 Di-haem cytochrome c peroxidase	
5UTR_652	1641572 -	1641610 Rmet_4968			Op1459r_2			
3UTR_798	1641790 -	1641823 Rmet_4969	bug		Op1459r_2			
NPKM_1586	1641824 -	1642919 Rmet_4969	bug	2.33	0.58	Op1459r_2	NA	Q1LDE5 Uncharacterized protein UPF0065
NPKM_1587	1642915 -	1645387 Rmet_4970		1.00	0.00	Op1459r_1	NA	Q1LDE4 L-carnitine dehydratase/bile acid-inducible protein F
5UTR_651	1645388 -	1645419 Rmet_4970			Op1459r_1			
3UTR_797	1645445 -	1645468 Rmet_4971			Op1459r_1			
NPKM_1588	1645469 -	1648928 Rmet_4971		1.00	0.00	Op1459r_1	NA	Q1LDE3 Carbamoyl-phosphate synthase L chain, ATP-binding
NPKM_1589	1648937 +	1650626 Rmet_4972	tniA	0.00	0.00	Op1460f_1	GIP-REP-Recomb	Q1LG13 Integrase, catalytic region
NPKM_1590	1650628 +	1651537 Rmet_4973	tniB	0.00	0.00	Op1460f_1	NA	Q1LDE1 TniB
NPKM_1591	1651533 +	1652751 Rmet_4974	tniQ	0.00	0.00	Op1460f_1	NA	Q1LDE0 TniQ
NPKM_1592	1652811 +	1653426 Rmet_4975	tniR	0.00	0.00	Op1460f_1	NA	Q1LDD9 Resolvase-like protein
NPKM_1593	1653492 -	1653924 Rmet_4976		0.00	0.00	Op1461r_1	NA	Q1LDD8 Putative uncharacterized protein
NPKM_1594	1653952 -	1655284 Rmet_4977	mmfS	0.00	0.00	Op1461r_1	EIP-SIG-2Comp	Q1LDD7 Sensor protein
NPKM_1595	1655280 -	1655946 Rmet_4978	mmfR	0.00	0.00	Op1461r_1	EIP-SIG-2Comp	Q1LDD6 Two component transcriptional regulator, winged helix family
NPKM_1596	1655968 -	1656727 Rmet_4979	mmfC2	0.00	0.00	Op1461r_1	NA	Q1LDD5 Putative uncharacterized protein
NPKM_1597	1656736 -	1657186 Rmet_4980	mmfD	0.00	0.00	Op1461r_1	NA	Q1LDD4 Conserved hypothetical signal peptide protein
NPKM_1598	1657215 -	1657998 Rmet_4981	mmfC1	0.00	0.00	Op1461r_1	NA	Q1LDD3 Putative uncharacterized protein
NPKM_1599	1658068 -	1658665 Rmet_4982	mmfB	0.00	0.00	Op1461r_1	MET-PepGlyc	Q1LDD2 Undecaprenyl-diphosphatase (Phosphoesterase, PA-phosphatase related)
NPKM_1600	1658721 -	1659057 Rmet_4983	mmfA	0.00	0.00	Op1461r_1	NA	Q1LDD1 Propeptide, PepSY amd peptidase M4
NPKM_1601	1659180 +	1659948 Rmet_4984		4.00	0.00	Op1462f_1	NA	Q1LDD0 Putative uncharacterized protein
3UTR_456	1659949 +	1660096 Rmet_4984			Op1462f_1			
NPKM_1602	1659954 -	1661262 Rmet_4985		2.00	0.00	Op1463r_1	EIP-TRA-Ion	Q1LDC9 Sodium/hydrogen exchanger
5UTR_372	1661153 +	1661621 Rmet_4986			Op1464f_1			
NPKM_1603	1661621 +	1662335 Rmet_4986		72.33	10.97	Op1464f_1	NA	Q1LDC8 Two component transcriptional regulator, LuxR family
NPKM_1604	1662343 +	1664329 Rmet_4987		13.00	1.00	Op1464f_1	NA	Q1LDC7 Periplasmic sensor signal transduction histidine kinase
NPKM_1605	1664504 +	1665317 Rmet_4988		191.33	4.73	Op1464f_2	EIP-TRA-ABC	Q1LDC6 NLPA lipoprotein
NPKM_1606	1665845 +	1668392 Rmet_4989		4.67	0.58	Op1464f_2	NA	Q1LDC5 Endonuclease/exonuclease/phosphatase
NPKM_1607	1668379 +	1669042 Rmet_4990		4.33	0.58	Op1464f_2	NA	Q1LDC4 Rhomboid-like protein
3UTR_796	1668458 -	1668999 Rmet_4991			Op1465r_1			
NPKM_1608	1669000 -	1670182 Rmet_4991		4.00	1.00	Op1465r_1	NA	Q1LDC3 Porin, Gram-negative type
3UTR_457	1669043 +	1669048 Rmet_4990			Op1464f_2			
5UTR_650	1670183 -	1670285 Rmet_4991			Op1465r_1			
3UTR_795	1670308 -	1670368 Rmet_4992			Op1465r_1			
NPKM_1609	1670369 -	1671884 Rmet_4992		7.00	0.00	Op1465r_1	NA	Q1LDC2 Major facilitator superfamily MFS_1
NPKM_1610	1671882 +	1673463 Rmet_4993		14.00	1.73	Op1466f_1	NA	Q1LDC1 Major facilitator superfamily MFS_1
5UTR_649	1671885 -	1672006 Rmet_4992			Op1465r_1			
3UTR_458	1673464 +	1673730 Rmet_4993			Op1466f_1			
NPKM_1611	1673539 -	1673611 Rmet_6700		1.00	1.00	Op2082r_1	NA	NA
5UTR_648	1673612 -	1673686 Rmet_6700			Op2082r_1			
5UTR_373	1673740 +	1673785 Rmet_4994			Op1466f_1			
NPKM_1612	1673785 +	1674931 Rmet_4994		3.00	0.00	Op1466f_1	NA	Q1LDC0 Porin, Gram-negative type

NPKM_1613	1674946 +	1675591 Rmet_4995	29.00	2.00	Op1466f_2	NA	Q1LDB9 Putative uncharacterized protein
3UTR_794	1675236 -	1675268 Rmet_6701			Op1467r_2		
NPKM_1614	1675269 -	1675449 Rmet_6701	3.67	1.53	Op1467r_2	NA	NA
3UTR_459	1675592 +	1676476 Rmet_4995			Op1466f_2		
NPKM_1615	1675839 -	1676394 Rmet_4996	23.67	1.53	Op1467r_2	NA	Q1LDB8 Putative uncharacterized protein
NPKM_1616	1676621 -	1676933 Rmet_4997	8.33	1.53	Op1467r_1	NA	Q1LDB7 Putative uncharacterized protein
NPKM_1617	1677113 -	1678460 Rmet_4998	8.00	1.73	Op1467r_1	NA	Q1LDB6 Citrate carrier protein
NPKM_1618	1678703 -	1678799 Rmet_6702	18.00	4.36	Op1467r_1	NA	NA
NPKM_1619	1678987 -	1680508 Rmet_4999	34.67	6.35	Op1467r_1	NA	Q1LDB5 Putative uncharacterized protein
NPKM_1620	1680551 -	1682090 Rmet_5000	40.67	9.87	Op1467r_1	NA	Q1LDB4 Putative uncharacterized protein
NPKM_1621	1682430 -	1682526 Rmet_5001	26.33	7.57	Op1467r_1	NA	Q1LDB3 Putative uncharacterized protein
NPKM_1622	1682627 -	1683953 Rmet_5002	39.33	3.21	Op1467r_1	NA	Q1LDB2 Major facilitator superfamily MFS_1
NPKM_1623	1683986 -	1684439 Rmet_5003	100.00	13.86	Op1467r_1	NA	Q1LDB1 Transcriptional regulator, MarR family
5UTR_647	1684440 -	1684441 Rmet_5003			Op1467r_1		
NPKM_1624	1684678 +	1684960 Rmet_5004	117.00	9.54	Op1468f_1	NA	Q1LDB0 Antibiotic biosynthesis monooxygenase
3UTR_793	1685266 -	1685286 Rmet_5005			Op1469r_2		
NPKM_1625	1685287 -	1685857 Rmet_5005	16.67	0.58	Op1469r_2	NA	Q1LDA9 Isochorismatase hydrolase
NPKM_1626	1685859 -	1686297 Rmet_5006	4.33	0.58	Op1469r_1	NA	Q1LDA8 Putative uncharacterized protein
NPKM_1627	1686378 +	1686954 Rmet_5007	64.00	11.36	Op1470f_1	NA	Q1LDA7 Putative uncharacterized protein
3UTR_792	1686945 -	1687509 Rmet_5009			Op1471r_1		
NPKM_1628	1687048 +	1687252 Rmet_5008	56.33	8.39	Op1470f_1	NA	Q1LDA6 CsbD-like protein
NPKM_1629	1687312 +	1687459 Rmet_6703	39.33	8.50	Op1470f_1	NA	NA
NPKM_1630	1687510 -	1688776 Rmet_5009	31.00	2.00	Op1471r_1	NA	Q1LDA5 HI0933-like protein
5UTR_646	1688777 -	1689133 Rmet_5009			Op1471r_1		
NPKM_1631	1688850 +	1689483 Rmet_5010	20.67	4.16	Op1472f_1	NA	Q1LDA4 Putative uncharacterized protein
3UTR_791	1689426 -	1689507 Rmet_5011			Op1473r_1		
3UTR_460	1689484 +	1690185 Rmet_5010			Op1472f_1		
NPKM_1632	1689508 -	1690888 Rmet_5011	7.67	0.58	Op1473r_1	NA	Q1LDA3 Pyridine nucleotide-disulphide oxidoreductase dimerisation region
5UTR_645	1690889 -	1691476 Rmet_5011			Op1473r_1		
5UTR_374	1691060 +	1691189 Rmet_5012			Op1474f_1		
NPKM_1633	1691189 +	1691657 Rmet_5012	24.33	2.89	Op1474f_1	NA	Q1LDA2 Cupin 2, conserved barrel
3UTR_461	1691658 +	1691797 Rmet_5012			Op1474f_1		
5UTR_375	1691805 +	1691818 Rmet_5013			Op1474f_1		
NPKM_1634	1691818 +	1693393 Rmet_5013	4.33	0.58	Op1474f_1	NA	Q1LDA1 FAD dependent oxidoreductase
3UTR_462	1693394 +	1693400 Rmet_5013			Op1474f_1		
5UTR_376	1693404 +	1693451 Rmet_5014			Op1474f_1		
NPKM_1635	1693451 +	1694459 Rmet_5014	3.00	1.00	Op1474f_1	NA	Q1LDA0 Aldo/keto reductase
3UTR_463	1694460 +	1694503 Rmet_5014			Op1474f_1		
NPKM_1636	1694587 -	1694800 Rmet_6704	0.00	0.00	Op2083r_1	NA	NA
NPKM_1637	1694791 +	1696465 Rmet_5015	2.00	0.00	Op1474f_1	NA	Q1LD99 Glucose-methanol-choline oxidoreductase
NPKM_1638	1696497 +	1698264 Rmet_5016	2.33	0.58	Op1474f_1	NA	Q1LD98 Putative uncharacterized protein
NPKM_1639	1698295 +	1699717 Rmet_5017	2.33	0.58	Op1474f_1	MET-CAH-FbP	Q1LD97 Aldehyde dehydrogenase
3UTR_790	1699548 -	1699795 Rmet_5018			Op1475r_1		

3UTR_464	1699718 +	1699757 Rmet_5017	<i>betB</i>			Op1474f_1			
NPKM_1640	1699796 -	1700435 Rmet_5018		5.00	0.00	Op1475r_1	NA	Q1LD96	Putative uncharacterized protein
5UTR_644	1700436 -	1700449 Rmet_5018				Op1475r_1			
5UTR_377	1700578 +	1700585 Rmet_5019				Op1476f_1			
NPKM_1641	1700585 +	1701752 Rmet_5019		3.00	0.00	Op1476f_1	NA	Q1LD95	L-carnitine dehydratase/bile acid-inducible protein F
NPKM_1642	1701748 +	1702180 Rmet_5020		2.33	0.58	Op1476f_1	NA	Q1LD94	Thioesterase superfamily
3UTR_465	1702181 +	1702234 Rmet_5020				Op1476f_1			
NPKM_1643	1702231 -	1704799 Rmet_5021		1.33	0.58	Op1477r_1	NA	Q1LD93	ATP-dependent transcriptional regulator, MalT-like, LuxR family
5UTR_378	1705009 +	1705049 Rmet_5022				Op1478f_1			
NPKM_1644	1705049 +	1707893 Rmet_5022		25.33	1.53	Op1478f_1	NA	Q1LD92	ATP-dependent transcriptional regulator, MalT-like, LuxR family
NPKM_1645	1708066 +	1709962 Rmet_5023		1.33	0.58	Op1478f_1	NA	Q1LD91	AMP-dependent synthetase and ligase
NPKM_1646	1709999 +	1711139 Rmet_5024		1.67	0.58	Op1478f_1	MET-CAH-Prop	Q1LD90	Acyl-CoA dehydrogenase-like protein
3UTR_466	1711140 +	1711158 Rmet_5024				Op1478f_1			
NPKM_1647	1711191 +	1712379 Rmet_5025		5.33	0.58	Op1478f_2	MET-LIP-FAMet	Q1LD89	Thiolase
NPKM_1648	1712390 +	1712831 Rmet_5026		5.67	1.15	Op1478f_2	NA	Q1LD88	Putative uncharacterized protein
NPKM_1649	1712844 +	1713261 Rmet_5027		7.00	1.00	Op1478f_2	NA	Q1LD87	MaoC-like dehydratase
NPKM_1650	1713303 +	1714128 Rmet_5028	<i>fabG</i>	13.67	0.58	Op1478f_2	MET-LIP-FASyn	Q1LD86	Short-chain dehydrogenase/reductase SDR
3UTR_467	1714129 +	1714210 Rmet_5028	<i>fabG</i>			Op1478f_2			
3UTR_789	1714252 -	1714258 Rmet_5029				Op1479r_1			
NPKM_1651	1714259 -	1715594 Rmet_5029		5.33	0.58	Op1479r_1	NA	Q1LD85	Lipolytic enzyme, G-D-S-L
5UTR_379	1715107 +	1715262 Rmet_6705				Op1480f_1			
NPKM_1652	1715262 +	1715664 Rmet_6705		3.00	1.00	Op1480f_1	NA	NA	
5UTR_643	1715595 -	1715628 Rmet_5029				Op1479r_1			
5UTR_380	1715670 +	1715690 Rmet_6706				Op1480f_1			
NPKM_1653	1715690 +	1715900 Rmet_6706		1.67	0.58	Op1480f_1	NA	NA	
3UTR_468	1715901 +	1715952 Rmet_6706				Op1480f_1			
5UTR_381	1715964 +	1716010 Rmet_5030	<i>cusD</i>			Op1480f_2			
NPKM_1654	1716010 +	1716412 Rmet_5030	<i>cusD</i>	42.00	6.08	Op1480f_2	NA	Q1LD84	Putative uncharacterized protein
NPKM_1655	1716484 +	1717786 Rmet_5031	<i>cusC</i>	3.33	0.58	Op1480f_2	NA	Q1LD83	Putative outer membrane cation efflux protein
3UTR_788	1717140 -	1722952 Rmet_5035				Op1481r_4			
NPKM_1656	1717782 +	1719300 Rmet_5032	<i>cusB</i>	1.33	0.58	Op1480f_2	EIP-TRA-Ion	Q1LD82	Secretion protein HlyD
NPKM_1657	1719296 +	1722464 Rmet_5033	<i>cusA</i>	1.00	0.00	Op1480f_2	EIP-TRA-Ion	Q1LD81	Heavy metal efflux pump CzcA
NPKM_1658	1722460 +	1722832 Rmet_5034	<i>cusF</i>	4.67	0.58	Op1480f_3	EIP-TRA-Ion	Q1LD80	Conserved hypothetical signal peptide protein
3UTR_469	1722833 +	1722963 Rmet_5034	<i>cusF</i>			Op1480f_3			
NPKM_1659	1722953 -	1723172 Rmet_5035		243.00	5.20	Op1481r_4	NA	Q1LD79	Putative uncharacterized protein
NPKM_1660	1722965 +	1723169 Rmet_6707		2.00	1.00	Op2084f_1	NA	NA	
NPKM_1661	1723199 -	1723433 Rmet_5036		102.33	5.03	Op1481r_3	NA	Q1LD78	Putative uncharacterized protein
NPKM_1662	1723646 -	1724087 Rmet_5037		27.67	4.51	Op1481r_2	NA	Q1LD77	Phenylacetic acid degradation-related protein
NPKM_1663	1724188 -	1725235 Rmet_5038	<i>bug</i>	8.00	1.00	Op1481r_1	NA	Q1LD76	Uncharacterized protein UPF0065
NPKM_1664	1725277 -	1727113 Rmet_5039		12.00	1.00	Op1481r_1	MET-CAH-But	Q1LD75	Acetolactate synthase, large subunit
5UTR_642	1727114 -	1727188 Rmet_5039				Op1481r_1			
NPKM_1665	1727130 +	1727862 Rmet_5040		27.00	1.73	Op1482f_1	NA	Q1LD74	Transcriptional regulator, GntR family
3UTR_787	1727356 -	1727939 Rmet_5041				Op1483r_1			

3UTR_470	1727863 +	1729187 Rmet_5040				Op1482f_1		
NPKM_1666	1727940 -	1729143 Rmet_5041		48.00	4.36	Op1483r_1	NA	Q1LD73 Diguanylate cyclase (GGDEF domain)
NPKM_1667	1729264 -	1729522 Rmet_5042		69.67	2.08	Op1483r_1	NA	Q1LD72 Putative uncharacterized protein
NPKM_1668	1729566 +	1730223 Rmet_5043		73.67	5.69	Op1484f_1	NA	Q1LD71 Phasin
3UTR_471	1730224 +	1731029 Rmet_5043				Op1484f_1		
NPKM_1669	1730336 -	1731410 Rmet_5044		138.00	10.15	Op1485r_4	NA	Q1LD70 MscS Mechanosensitive ion channel
NPKM_1670	1731571 -	1732561 Rmet_5045	hutG	15.00	1.00	Op1485r_3	MET-AA-His	Q1LD69 Formiminoglutamase
NPKM_1671	1732550 -	1733975 Rmet_5046	hutT	19.00	1.73	Op1485r_3	EIP-TRA-Ion	Q1LD68 Amino acid permease-associated region
NPKM_1672	1734018 -	1735575 Rmet_5047	hutH	22.00	1.73	Op1485r_3	MET-EN-Nitrog	Q1LD67 Histidine ammonia-lyase
NPKM_1673	1735590 -	1737270 Rmet_5048	hutU	8.67	0.58	Op1485r_2	MET-AA-His	Q1LD66 Urocanate hydratase
NPKM_1674	1737488 -	1738244 Rmet_5049	hutC	39.67	0.58	Op1485r_2	NA	Q1LD65 Transcriptional regulator, histidine utilization repressor, GntR family
5UTR_641	1738245 -	1738278 Rmet_5049	hutC			Op1485r_2		
3UTR_786	1738443 -	1738516 Rmet_5050				Op1485r_1		
NPKM_1675	1738517 -	1740620 Rmet_5050		7.67	0.58	Op1485r_1	NA	Q1LD64 Putative uncharacterized protein
NPKM_1676	1740668 -	1741529 Rmet_5051		5.00	1.00	Op1485r_1	NA	Q1LD63 Putative uncharacterized protein
5UTR_640	1741530 -	1741674 Rmet_5051				Op1485r_1		
NPKM_1677	1741824 +	1742883 Rmet_5052		3.00	1.00	Op1486f_1	NA	Q1LD62 Twin-arginine translocation pathway signal
3UTR_785	1742733 -	1742950 Rmet_5053				Op1487r_1		
3UTR_472	1742884 +	1743028 Rmet_5052				Op1486f_1		
NPKM_1678	1742951 -	1744562 Rmet_5053		8.67	1.15	Op1487r_1	NA	Q1LD61 ABC transporter related
NPKM_1679	1744755 -	1745949 Rmet_5054		16.33	2.52	Op1487r_1	NA	Q1LD60 Peptidase M24
NPKM_1680	1745977 -	1746946 Rmet_5055	bug	8.33	0.58	Op1487r_1	NA	Q1LD59 Uncharacterized protein UPF0065
NPKM_1681	1747071 +	1747506 Rmet_5056		0.00	0.00	Op1488f_1	NA	Q1LD58 Putative uncharacterized protein
3UTR_784	1747092 -	1747573 Rmet_5057				Op1489r_1		
NPKM_1682	1747574 -	1748219 Rmet_5057		21.00	1.73	Op1489r_1	NA	Q1LD57 Transcriptional regulator, TetR family
5UTR_382	1748421 +	1748466 Rmet_5058	bugT			Op1490f_1		
NPKM_1683	1748466 +	1749453 Rmet_5058	bugT	2.33	0.58	Op1490f_1	NA	Q1LD56 Uncharacterized protein UPF0065
NPKM_1684	1749494 +	1750175 Rmet_5059	atoD	2.00	1.00	Op1490f_1	MET-XEN-Benz	Q1LD55 3-oxoacid CoA-transferase, subunit A
NPKM_1685	1750167 +	1750869 Rmet_5060	atoA1	3.00	0.00	Op1490f_1	MET-XEN-Benz	Q1LD54 Butyryl-CoA:acetate CoA transferase
NPKM_1686	1750921 +	1751929 Rmet_5061	bugT	2.00	0.00	Op1490f_1	NA	Q1LD53 Uncharacterized protein UPF0065
3UTR_783	1751062 -	1751946 Rmet_5062				Op1491r_2		
3UTR_473	1751930 +	1752192 Rmet_5061	bugT			Op1490f_1		
NPKM_1687	1751947 -	1752838 Rmet_5062		16.67	0.58	Op1491r_2	MET-XEN-Toluene	Q1LD52 Intradiol ring-cleavage dioxygenase
NPKM_1688	1752879 -	1753947 Rmet_5063	macA	18.00	1.00	Op1491r_2	MET-XEN-Hex	Q1LD51 Iron-containing alcohol dehydrogenase
NPKM_1689	1754055 -	1754514 Rmet_5064		18.00	2.65	Op1491r_2	NA	Q1LD50 Putative uncharacterized protein
NPKM_1690	1754625 -	1755030 Rmet_5065		341.00	10.15	Op1491r_2	NA	Q1LD49 Putative uncharacterized protein
NPKM_1691	1755026 -	1756331 Rmet_5066		21.33	0.58	Op1491r_1	NA	Q1LD48 Major facilitator superfamily MFS_1
NPKM_1692	1756522 -	1757710 Rmet_5067		40.33	4.04	Op1491r_1	NA	Q1LD47 Major facilitator superfamily MFS_1
NPKM_1693	1757737 -	1758232 Rmet_5068		80.33	4.73	Op1491r_1	NA	Q1LD46 GCN5-related N-acetyltransferase
5UTR_383	1758147 +	1758230 Rmet_5069				Op1492f_1		
NPKM_1694	1758230 +	1758503 Rmet_5069		0.33	0.58	Op1492f_1	NA	Q1LD45 Hydroxyneurosporene-O-methyltransferase
5UTR_639	1758233 -	1758327 Rmet_5068				Op1491r_1		
3UTR_474	1758504 +	1758522 Rmet_5069				Op1492f_1		

5UTR_384	1758613 +	1758700 Rmet_5070				Op1492f_2		
NPKM_1695	1758700 +	1759810 Rmet_5070		10.67	2.08	Op1492f_2	NA	Q1LD44 Putative uncharacterized protein
3UTR_782	1759058 -	1760790 Rmet_5072				Op1493r_1		
NPKM_1696	1760050 +	1760551 Rmet_5071		206.33	10.21	Op1492f_3	NA	Q1LD43 Putative uncharacterized protein
3UTR_475	1760552 +	1761494 Rmet_5071				Op1492f_3		
NPKM_1697	1760791 -	1760923 Rmet_5072		499.67	51.59	Op1493r_1	MET-AA-Met	Q1LD42 Methionine synthase (B12-independent)
NPKM_1698	1761215 -	1762244 Rmet_5073	metE	918.67	88.33	Op1493r_1	NA	Q1LD41 Putative uncharacterized protein
NPKM_1699	1762273 -	1763263 Rmet_5074		653.00	67.10	Op1493r_1	NA	Q1LD40 NADPH-dependent FMN reductase
5UTR_385	1762784 +	1764878 Rmet_5076				Op1494f_1		
NPKM_1700	1763323 -	1763917 Rmet_5075	msuE1	652.00	89.44	Op1493r_1	NA	Q1LD39 Putative uncharacterized protein
5UTR_638	1763918 -	1764231 Rmet_5075	msuE1			Op1493r_1		
NPKM_1701	1764878 +	1765307 Rmet_5076		344.33	18.61	Op1494f_1	NA	A5FF57 Sulfatase
3UTR_781	1765269 -	1765381 Rmet_6708				Op1495r_1		
NPKM_1702	1765382 -	1765703 Rmet_6708		5.67	2.08	Op1495r_1	NA	NA
NPKM_1703	1765715 -	1766051 Rmet_5077		5.67	1.15	Op1495r_1	NA	A5FF57 Sulfatase
5UTR_637	1766052 -	1766072 Rmet_5077				Op1495r_1		
NPKM_1704	1766379 +	1767438 Rmet_5079		68.67	6.66	Op1496f_1	NA	Q1LD38 Putative uncharacterized protein
NPKM_1705	1768075 +	1768768 Rmet_5080		42.67	3.06	Op1496f_1	NA	Q1LD37 Putative uncharacterized protein
NPKM_1706	1768777 +	1771873 Rmet_5081		21.67	2.08	Op1496f_1	NA	Q1LD36 Putative uncharacterized protein
NPKM_1707	1771869 +	1772523 Rmet_5082		26.33	1.53	Op1496f_1	NA	Q1LD35 OmpA/MotB
NPKM_1708	1772515 +	1773214 Rmet_5083		25.67	4.04	Op1496f_1	NA	Q1LD34 Putative uncharacterized protein
3UTR_780	1772959 -	1773848 Rmet_5085				Op1497r_1		
NPKM_1709	1773363 +	1773807 Rmet_5084		7.00	1.00	Op1496f_1	NA	Q1LD33 Cupin 2, conserved barrel
3UTR_476	1773808 +	1774017 Rmet_5084				Op1496f_1		
NPKM_1710	1773849 -	1774605 Rmet_5085		24.00	3.46	Op1497r_1	NA	Q1LD32 Transcriptional regulator, XRE family with cupin sensor domain
5UTR_636	1774606 -	1774648 Rmet_5085				Op1497r_1		
5UTR_386	1774730 +	1774805 Rmet_5086				Op1498f_1		
NPKM_1711	1774805 +	1775963 Rmet_5086		37.67	3.21	Op1498f_1	NA	Q1LD31 FAD dependent oxidoreductase
NPKM_1712	1776045 +	1777494 Rmet_5087		32.33	0.58	Op1498f_1	NA	Q1LD30 Uncharacterised conserved protein UCP012702
NPKM_1713	1777571 +	1779155 Rmet_5088	dppA	24.33	1.15	Op1498f_1	EIP-TRA-ABC	Q1LD29 Extracellular solute-binding protein, family 5
NPKM_1714	1779166 +	1780102 Rmet_5089	dppB	15.33	1.15	Op1498f_1	EIP-TRA-ABC	Q1LD28 Binding-protein-dependent transport systems inner membrane component
NPKM_1715	1780108 +	1781008 Rmet_5090	dppC	14.67	0.58	Op1498f_1	EIP-TRA-ABC	Q1LD27 Binding-protein-dependent transport systems inner membrane component
NPKM_1716	1781021 +	1782068 Rmet_5091	dppD	16.33	0.58	Op1498f_1	EIP-TRA-ABC	Q1LD26 Oligopeptide/dipeptide ABC transporter, ATP-binding protein-like protein
NPKM_1717	1782064 +	1783078 Rmet_5092	dppE	16.67	0.58	Op1498f_1	EIP-TRA-ABC	Q1LD25 Oligopeptide/dipeptide ABC transporter, ATP-binding protein-like protein
NPKM_1718	1783090 +	1784575 Rmet_5093		19.67	0.58	Op1498f_1	NA	Q1LD24 D-aminoacylase-like protein
NPKM_1719	1784552 -	1784732 Rmet_6709		0.00	0.00	Op2085r_1	NA	NA
NPKM_1720	1784888 +	1785758 Rmet_5094		32.67	2.52	Op1498f_1	MET-CAH-Prop	Q1LD23 Enoyl-CoA hydratase
3UTR_779	1785305 -	1785822 Rmet_5095				Op1499r_2		
3UTR_477	1785759 +	1786497 Rmet_5094				Op1498f_1		
NPKM_1721	1785823 -	1786834 Rmet_5095		23.67	0.58	Op1499r_2	NA	Q1LD22 Malate/L-lactate dehydrogenase
NPKM_1722	1786871 -	1788359 Rmet_5096	aldH	9.67	1.15	Op1499r_1	NA	Q1LD21 Aldehyde dehydrogenase
NPKM_1723	1788446 -	1789391 Rmet_5097		37.00	2.00	Op1499r_1	MET-AA-Lys_Syn	Q1LD20 Dihydrodipicolinate synthetase
5UTR_635	1789392 -	1789444 Rmet_5097				Op1499r_1		

5UTR_387	1789500 +	1789792 Rmet_5098				Op1500f_1		
NPKM_1724	1789792 +	1791172 Rmet_5098		18.33	1.53	Op1500f_1	NA	Q1LD19 Major facilitator superfamily MFS_1
3UTR_778	1791159 -	1791254 Rmet_5099				Op1501r_2		
3UTR_478	1791173 +	1791205 Rmet_5098				Op1500f_1		
NPKM_1725	1791255 -	1791978 Rmet_5099		33.33	1.53	Op1501r_2	NA	Q1LD18 Transcriptional regulator, GntR family
NPKM_1726	1792011 -	1792692 Rmet_5100		58.67	2.52	Op1501r_2	NA	Q1LD17 Transcriptional regulator, GntR family
NPKM_1727	1792802 -	1793750 Rmet_5101		9.00	1.00	Op1501r_1	NA	Q1LD16 Transcriptional regulator, LysR family
NPKM_1728	1793827 +	1794904 Rmet_5102		1.67	0.58	Op1502f_1	MET-CAH-FbP	Q1LD15 Alcohol dehydrogenase, zinc-binding
3UTR_479	1794905 +	1794918 Rmet_5102				Op1502f_1		
NPKM_1729	1794980 -	1795514 Rmet_5103		62.00	2.65	Op1503r_1	NA	Q1LD14 Bifunctional deaminase-reductase-like protein
5UTR_388	1795490 +	1795501 Rmet_6710				Op1504f_1		
NPKM_1730	1795501 +	1795687 Rmet_6710		1.67	1.15	Op1504f_1	NA	NA
5UTR_634	1795515 -	1795526 Rmet_5103				Op1503r_1		
NPKM_1731	1795683 +	1796721 Rmet_5104		127.67	1.53	Op1504f_2	NA	Q1LD13 Cytidyltransferase-related
NPKM_1732	1796806 +	1798240 Rmet_5105		14.00	0.00	Op1504f_2	MET-COF-NicAm	Q1LD12 Nicotinate phosphoribosyltransferase and related
NPKM_1733	1798411 +	1799359 Rmet_5106		30.00	1.00	Op1504f_3	NA	Q1LD11 Transcriptional regulator, LysR family
3UTR_777	1798664 -	1799364 Rmet_5107				Op1505r_3		
3UTR_480	1799360 +	1799855 Rmet_5106				Op1504f_3		
NPKM_1734	1799365 -	1800142 Rmet_5107		12.33	1.53	Op1505r_3	MET-CAH-Prop	Q1LD10 Short chain enoyl-CoA hydratase
NPKM_1735	1800155 -	1801136 Rmet_5108	bug	4.67	0.58	Op1505r_2	NA	Q1LD09 Uncharacterized protein UPF0065
NPKM_1736	1801186 -	1802371 Rmet_5109		2.00	0.00	Op1505r_1	NA	Q1LD08 L-carnitine dehydratase/bile acid-inducible protein F
3UTR_776	1802378 -	1802419 Rmet_5110	fadB1			Op1505r_1		
NPKM_1737	1802420 -	1804568 Rmet_5110	fadB1	1.33	0.58	Op1505r_1	MET-CAH-But	Q1LD07 Short chain enoyl-CoA hydratase / 3-hydroxyacyl-CoA dehydrogenase
NPKM_1738	1804612 -	1805785 Rmet_5111		2.00	0.00	Op1505r_1	NA	Q1LD06 Thiolase
NPKM_1739	1805781 -	1806180 Rmet_5112		2.33	1.53	Op1505r_1	NA	Q1LD05 Putative uncharacterized protein
NPKM_1740	1806188 -	1807181 Rmet_5113	bug	1.67	0.58	Op1505r_1	NA	Q1LD04 Uncharacterized protein UPF0065
5UTR_389	1807634 +	1807731 Rmet_5114	gdhA			Op1506f_1		
NPKM_1741	1807731 +	1809120 Rmet_5114	gdhA	100.67	1.15	Op1506f_1	MET-EN-Nitrog	Q1LD03 Glutamate dehydrogenase (NADP)
NPKM_1742	1809309 +	1809921 Rmet_5115		14.00	1.00	Op1506f_1	EIP-TRA-Ion	Q1LD02 Lysine exporter protein (LYSE/YGGA)
3UTR_481	1809922 +	1810440 Rmet_5115				Op1506f_1		
3UTR_775	1809959 -	1809993 Rmet_5116				Op1507r_1		
NPKM_1743	1809994 -	1811014 Rmet_5116		3.00	0.00	Op1507r_1	NA	Q1LD01 Fimbrial protein
5UTR_633	1811015 -	1811018 Rmet_5116				Op1507r_1		
NPKM_1744	1811185 +	1811671 Rmet_5117		18.00	2.65	Op1508f_1	NA	Q1LD00 Putative uncharacterized protein
3UTR_482	1811672 +	1811876 Rmet_5117				Op1508f_1		
5UTR_390	1811896 +	1811908 Rmet_5118				Op1508f_1		
NPKM_1745	1811908 +	1812976 Rmet_5118		2.67	0.58	Op1508f_1	NA	Q1LCZ9 Porin, Gram-negative type
3UTR_483	1812977 +	1813003 Rmet_5118				Op1508f_1		
NPKM_1746	1813372 +	1814272 Rmet_5119		0.33	0.58	Op1508f_1	MET-OAA-Taur	Q1LCZ8 Taurine catabolism dioxygenase TauD/TfdA
3UTR_774	1814129 -	1816140 Rmet_5122	phaC3			Op1509r_1		
NPKM_1747	1814296 +	1815358 Rmet_5120		1.33	0.58	Op1508f_2	NA	Q1LCZ7 Putative uncharacterized protein
3UTR_484	1815359 +	1815368 Rmet_5120				Op1508f_2		
NPKM_1748	1815598 +	1816027 Rmet_5121	mopl	20.67	1.15	Op1508f_3	NA	Q1LCZ6 Molybdenum-pterin binding domain

3UTR_485	1816028 +	1816407 Rmet_5121	<i>mopI</i>			Op1508f_3		
NPKM_1749	1816141 -	1818052 Rmet_5122	<i>phaC3</i>	68.00	7.00	Op1509r_1	MET-CAH-But	Q1LCZ5 Poly-beta-hydroxybutyrate polymerase-like protein
NPKM_1750	1818055 -	1818802 Rmet_5123	<i>phaB3</i>	96.00	8.72	Op1509r_1	MET-CAH-But	Q1LCZ4 3-oxoacyl-[acyl-carrier-protein] reductase
NPKM_1751	1818798 -	1819347 Rmet_5124		136.33	9.45	Op1509r_1	NA	Q1LCZ3 Putative uncharacterized protein
5UTR_632	1819348 -	1819451 Rmet_5124				Op1509r_1		
5UTR_391	1819521 +	1819809 Rmet_5125				Op1510f_1		
NPKM_1752	1819809 +	1821303 Rmet_5125		4.33	0.58	Op1510f_1	NA	Q1LCZ2 Putative uncharacterized protein
3UTR_773	1820926 -	1821340 Rmet_5126				Op1511r_1		
3UTR_486	1821304 +	1821351 Rmet_5125				Op1510f_1		
NPKM_1753	1821341 -	1822265 Rmet_5126		7.00	1.00	Op1511r_1	NA	Q1LCZ1 Putative uncharacterized protein
5UTR_631	1822266 -	1822291 Rmet_5126				Op1511r_1		
5UTR_392	1822439 +	1822504 Rmet_5127				Op1512f_1		
NPKM_1754	1822504 +	1824469 Rmet_5127		32.67	0.58	Op1512f_1	NA	Q1LCZ0 Sigma54 specific transcriptional regulator with GAF sensor, Fis family
3UTR_487	1824470 +	1825059 Rmet_5127				Op1512f_1		
3UTR_772	1824503 -	1824526 Rmet_5128	<i>aldB</i>			Op1513r_3		
NPKM_1755	1824527 -	1826048 Rmet_5128	<i>aldB</i>	23.00	1.00	Op1513r_3	MET-CAH-FbP	Q1LCY9 Aldehyde dehydrogenase
NPKM_1756	1826279 -	1827626 Rmet_5129		23.67	2.31	Op1513r_3	NA	Q1LCY8 Sensor protein
NPKM_1757	1827622 -	1828294 Rmet_5130		49.33	3.51	Op1513r_3	EIP-SIG-2Comp	Q1LCY7 Two component transcriptional regulator, winged helix family
NPKM_1758	1828299 -	1828662 Rmet_5131		30.00	3.00	Op1513r_3	NA	Q1LCY6 Putative uncharacterized protein
NPKM_1759	1828965 -	1829964 Rmet_5132	<i>bugT</i>	6.33	0.58	Op1513r_2	NA	Q1LCY5 Uncharacterized protein UPF0065
5UTR_630	1829965 -	1830022 Rmet_5132	<i>bugT</i>			Op1513r_2		
3UTR_771	1830059 -	1830063 Rmet_5133				Op1513r_1		
NPKM_1760	1830064 -	1831240 Rmet_5133		1.33	0.58	Op1513r_1	MET-CAH-Prop	Q1LCY4 Acyl-CoA dehydrogenase-like protein
NPKM_1761	1831250 -	1832804 Rmet_5134		1.33	0.58	Op1513r_1	NA	Q1LCY3 AMP-dependent synthetase and ligase
5UTR_393	1832893 +	1832912 Rmet_5135				Op1514f_1		
NPKM_1762	1832912 +	1833803 Rmet_5135		9.67	0.58	Op1514f_1	NA	Q1LCY2 Transcriptional regulator, LysR family
NPKM_1763	1833799 +	1834585 Rmet_5136		10.67	2.08	Op1514f_1	NA	Q1LCY1 Putative uncharacterized protein
3UTR_770	1834538 -	1834585 Rmet_5137	<i>nrdG</i>			Op1515r_2		
3UTR_488	1834586 +	1835019 Rmet_5136				Op1514f_1		
NPKM_1764	1834586 -	1835258 Rmet_5137	<i>nrdG</i>	0.33	0.58	Op1515r_2	GIP-PTL-Fold	Q1LCY0 Ribonucleoside-triphosphate reductase, anaerobic-like protein
NPKM_1765	1835265 -	1835457 Rmet_5138		0.67	0.58	Op1515r_2	NA	Q1LCX9 Putative uncharacterized protein
NPKM_1766	1835504 -	1837229 Rmet_5139	<i>nrdD</i>	0.33	0.58	Op1515r_2	MET-NUC-Pur	Q1LCX8 Ribonucleoside-triphosphate reductase, anaerobic
5UTR_629	1837230 -	1837261 Rmet_5139	<i>nrdD</i>			Op1515r_2		
3UTR_769	1837268 -	1837438 Rmet_5140				Op1515r_2		
NPKM_1767	1837439 -	1839017 Rmet_5140		4.00	0.00	Op1515r_2	MET-LIP-FAMet	Q1LCX7 AMP-dependent synthetase and ligase
5UTR_628	1839018 -	1839039 Rmet_5140				Op1515r_2		
3UTR_768	1839051 -	1839091 Rmet_5141				Op1515r_2		
NPKM_1768	1839092 -	1840331 Rmet_5141		3.00	0.00	Op1515r_2	NA	Q1LCX6 Acyl-CoA dehydrogenase-like protein
NPKM_1769	1840339 -	1841518 Rmet_5142		4.00	1.00	Op1515r_2	NA	Q1LCX5 Acyl-CoA dehydrogenase-like protein
5UTR_627	1841519 -	1841532 Rmet_5142				Op1515r_2		
3UTR_767	1841534 -	1841571 Rmet_5143				Op1515r_2		
NPKM_1770	1841572 -	1842556 Rmet_5143		8.00	1.00	Op1515r_2	NA	Q1LCX4 Acyl-CoA dehydrogenase-like protein
NPKM_1771	1842574 -	1843732 Rmet_5144		4.67	0.58	Op1515r_2	MET-AA-ValLeulle	Q1LCX3 Acyl-CoA dehydrogenase-like protein

NPKM_1772	1843851 -	1844634 Rmet_5145		4.00	1.00	Op1515r_2	MET-CAH-Prop	Q1LCX2 Enoyl-CoA hydratase
NPKM_1773	1844652 -	1845111 Rmet_5146		1.67	0.58	Op1515r_1	NA	Q1LCX1 MaoC-like dehydratase
NPKM_1774	1845114 -	1846077 Rmet_5147	<i>bugT</i>	3.00	0.00	Op1515r_1	NA	Q1LCX0 Uncharacterized protein UPF0065
NPKM_1775	1846111 -	1847335 Rmet_5148	<i>caiB</i>	1.67	0.58	Op1515r_1	NA	Q1LCW9 L-carnitine dehydratase/bile acid-inducible protein F
5UTR_394	1847548 +	1847568 Rmet_5149	<i>bugT</i>			Op1516f_1		
NPKM_1776	1847568 +	1848555 Rmet_5149	<i>bugT</i>	3.00	0.00	Op1516f_1	NA	Q1LCW8 Uncharacterized protein UPF0065
NPKM_1777	1848600 +	1849395 Rmet_5150		6.67	1.15	Op1516f_2	MET-CAH-Prop	Q1LCW7 Enoyl-CoA hydratase / short chain enoyl-CoA hydratase
3UTR_489	1849396 +	1849476 Rmet_5150				Op1516f_2		
5UTR_395	1849568 +	1849604 Rmet_5151				Op1516f_2		
NPKM_1778	1849604 +	1850513 Rmet_5151		13.00	1.00	Op1516f_2	NA	Q1LCW6 Transcriptional regulator, LysR family
3UTR_766	1850243 -	1850578 Rmet_5152				Op1517r_1		
3UTR_490	1850514 +	1850867 Rmet_5151				Op1516f_2		
NPKM_1779	1850579 -	1851725 Rmet_5152		7.00	1.00	Op1517r_1	MET-CAH-Prop	Q1LCW5 Acyl-CoA dehydrogenase-like protein
NPKM_1780	1851780 -	1852770 Rmet_5153	<i>bugT</i>	3.67	0.58	Op1517r_1	NA	Q1LCW4 Uncharacterized protein UPF0065
NPKM_1781	1852941 -	1853706 Rmet_5154		10.67	0.58	Op1517r_1	MET-CAH-Prop	Q1LCW3 Short chain enoyl-CoA hydratase
NPKM_1782	1853716 -	1854484 Rmet_5155	<i>hadH</i>	11.67	1.15	Op1517r_1	NA	Q1LCW2 Short-chain dehydrogenase/reductase SDR
NPKM_1783	1854521 -	1855700 Rmet_5156	<i>paaE</i>	12.67	2.08	Op1517r_1	MET-CAH-Pyr	Q1LCW1 Thiolase
5UTR_396	1855792 +	1855911 Rmet_5157				Op1518f_1		
NPKM_1784	1855911 +	1856724 Rmet_5157		62.33	0.58	Op1518f_1	NA	Q1LCW0 Transcriptional regulator, lclR family
NPKM_1785	1856767 +	1858351 Rmet_5158		48.67	1.53	Op1518f_1	NA	Q1LCV9 AMP-dependent synthetase and ligase
NPKM_1786	1858483 +	1859440 Rmet_5159		29.00	1.00	Op1518f_1	NA	Q1LCV8 Transcriptional regulator, LysR family
NPKM_1787	1859640 +	1860894 Rmet_5160		5.67	1.15	Op1518f_1	NA	Q1LCV7 Beta-lactamase-like protein
NPKM_1788	1860903 +	1861929 Rmet_5161	<i>bug</i>	1.67	0.58	Op1518f_1	NA	Q1LCV6 Uncharacterized protein UPF0065
NPKM_1789	1861950 +	1863249 Rmet_5162		4.00	0.00	Op1518f_2	NA	Q1LCV5 Putative uncharacterized protein
5UTR_397	1863466 +	1863664 Rmet_5164				Op1520f_1		
NPKM_1790	1863477 -	1863636 Rmet_5163		0.33	0.58	Op1519r_1	NA	Q1LCV4 Autotransporter
NPKM_1791	1863664 +	1863994 Rmet_5164		1.67	0.58	Op1520f_1	NA	Q1LCV3 Putative uncharacterized protein
NPKM_1792	1863693 -	1863900 Rmet_6711		0.67	0.58	Op2086r_1	NA	NA
5UTR_398	1864196 +	1864219 Rmet_5165				Op1520f_2		
NPKM_1793	1864219 +	1864915 Rmet_5165		14.33	1.53	Op1520f_2	NA	Q1LCV2 Two component transcriptional regulator, LuxR family
NPKM_1794	1864911 +	1866834 Rmet_5166		3.33	0.58	Op1520f_2	NA	Q1LCV1 Putative signal transduction histidine kinase
3UTR_491	1866835 +	1866901 Rmet_5166				Op1520f_2		
NPKM_1795	1866923 +	1867331 Rmet_5167	<i>hip</i>	3.33	0.58	Op1520f_2	NA	Q1LCV0 Twin-arginine translocation pathway signal
NPKM_1796	1867436 +	1867676 Rmet_5168		2.33	0.58	Op1520f_2	NA	Q1LCU9 Putative uncharacterized protein
3UTR_492	1867677 +	1867694 Rmet_5168				Op1520f_2		
NPKM_1797	1867715 +	1868138 Rmet_5169		11.67	0.58	Op1520f_3	NA	Q1LCU8 Transcriptional regulator, LysR family
NPKM_1798	1868210 +	1868585 Rmet_5170		17.00	2.00	Op1520f_3	NA	Q1LCU7 NUDIX hydrolase
3UTR_493	1868586 +	1869009 Rmet_5170				Op1520f_3		
3UTR_765	1868889 -	1868925 Rmet_5171	<i>cspA</i>			Op1521r_1		
NPKM_1799	1868926 -	1869307 Rmet_5171	<i>cspA</i>	154.00	18.36	Op1521r_1	NA	Q1LCU6 Cold-shock DNA-binding protein family
5UTR_626	1869308 -	1869560 Rmet_5171	<i>cspA</i>			Op1521r_1		
5UTR_399	1869323 +	1870027 Rmet_6712				Op1522f_1		
NPKM_1800	1870027 +	1870204 Rmet_6712		15.67	3.51	Op1522f_1	NA	NA

NPKM_1801	1870232 +	1870505 Rmet_5172	22.67	6.66	Op1522f_1	NA	Q1LCU5 Putative uncharacterized protein
NPKM_1802	1870718 +	1871003 Rmet_5173	12.33	1.53	Op1522f_1	NA	Q1LCU4 Putative uncharacterized protein
NPKM_1803	1871131 +	1871563 Rmet_5174	10.00	1.73	Op1522f_1	NA	Q1LCU3 Putative uncharacterized protein
NPKM_1804	1871992 +	1872256 Rmet_5175	28.00	4.36	Op1522f_2	NA	Q1LCU2 Putative uncharacterized protein
NPKM_1805	1872283 +	1872505 Rmet_5176	22.67	5.51	Op1522f_2	NA	Q1LCU1 Translation initiation factor IF-1 3
3UTR_764	1872456 -	1872625 Rmet_5177			Op1523r_1		
NPKM_1806	1872626 -	1872998 Rmet_5177	3.67	0.58	Op1523r_1	NA	Q1LCU0 Putative uncharacterized protein
NPKM_1807	1873042 +	1873777 Rmet_5178	12.67	3.06	Op1524f_1	NA	Q1LCT9 Putative uncharacterized protein
3UTR_763	1873055 -	1873905 Rmet_5179			Op1525r_2		
3UTR_494	1873778 +	1875460 Rmet_5178			Op1524f_1		
NPKM_1808	1873906 -	1874362 Rmet_5179	26.67	1.15	Op1525r_2	NA	Q1LCT8 Putative uncharacterized protein
NPKM_1809	1874549 -	1874774 Rmet_6713	20.67	0.58	Op1525r_2	NA	NA
NPKM_1810	1875067 -	1875316 Rmet_5180	3.33	1.15	Op1525r_1	NA	Q1LCT7 Putative uncharacterized protein
5UTR_625	1875317 -	1875323 Rmet_5180			Op1525r_1		
3UTR_762	1875347 -	1875388 Rmet_5181			Op1525r_1		
NPKM_1811	1875389 -	1875908 Rmet_5181	2.67	0.58	Op1525r_1	NA	Q1LCT6 Putative uncharacterized protein
5UTR_400	1875493 +	1876052 Rmet_5182			Op1526f_1		
NPKM_1812	1876052 +	1876694 Rmet_5182	3.00	0.00	Op1526f_1	NA	Q1LCT5 Putative uncharacterized protein
3UTR_761	1876612 -	1877724 Rmet_5184			Op1527r_1		
3UTR_495	1876695 +	1876735 Rmet_5182			Op1526f_1		
NPKM_1813	1876975 +	1877425 Rmet_5183	3.67	0.58	Op1526f_1	NA	Q1LCT4 Putative uncharacterized protein
3UTR_496	1877426 +	1877644 Rmet_5183			Op1526f_1		
NPKM_1814	1877725 -	1878154 Rmet_5184	61.33	6.11	Op1527r_1	NA	Q1LCT3 Phenylacetic acid degradation-related protein
NPKM_1815	1877992 +	1878157 Rmet_6714	1.67	0.58	Op1528f_1	NA	NA
5UTR_624	1878155 -	1878231 Rmet_5184			Op1527r_1		
5UTR_401	1878406 +	1878858 Rmet_5185			Op1528f_1		
NPKM_1816	1878858 +	1879536 Rmet_5185	2.67	1.15	Op1528f_1	MET-EN-Nitrog	Q1LCT2 Carbonic anhydrase
NPKM_1817	1879555 +	1880245 Rmet_5186	1.67	1.15	Op1528f_1	NA	Q1LCT1 Ion transport 2
3UTR_497	1880246 +	1880307 Rmet_5186			Op1528f_1		
3UTR_760	1880248 -	1880254 Rmet_5187			Op1529r_1		
NPKM_1818	1880255 -	1882196 Rmet_5187	6.00	0.00	Op1529r_1	NA	Q1LCT0 Putative Ig
5UTR_623	1882197 -	1882393 Rmet_5187			Op1529r_1		
5UTR_402	1882831 +	1882858 Rmet_5188			Op1530f_1		
NPKM_1819	1882858 +	1883140 Rmet_5188	1.33	1.15	Op1530f_1	NA	Q1LCS9 Galactose-binding protein regulator
3UTR_498	1883141 +	1883257 Rmet_5188			Op1530f_1		
5UTR_403	1883460 +	1883491 Rmet_5189			Op1530f_2		
NPKM_1820	1883491 +	1883878 Rmet_5189	66.00	2.65	Op1530f_2	NA	Q1LCS8 Glyoxalase/bleomycin resistance protein/dioxygenase
3UTR_499	1883879 +	1884845 Rmet_5189			Op1530f_2		
NPKM_1821	1883911 -	1885027 Rmet_5190	5.33	0.58	Op1531r_1	NA	Q1LCS7 Porin, Gram-negative type
NPKM_1822	1885144 -	1886572 Rmet_5191	3.33	0.58	Op1531r_1	NA	Q1LCS6 Amino acid permease-associated region
NPKM_1823	1886606 -	1887836 Rmet_5192	4.00	1.00	Op1531r_1	MET-AA-Trp	Q1LCS5 Kynureninase
5UTR_622	1887837 -	1887898 Rmet_5192			Op1531r_1		
3UTR_759	1887901 -	1887905 Rmet_5193			Op1531r_1		

NPKM_1824	1887906 -	1888431 Rmet_5193	4.33	0.58	Op1531r_1	MET-AA-Trp	Q1LCS4 3-hydroxyanthranilate 3,4-dioxygenase
5UTR_621	1888432 -	1888485 Rmet_5193			Op1531r_1		
3UTR_758	1888487 -	1888598 Rmet_5194			Op1531r_1		
NPKM_1825	1888599 -	1889664 Rmet_5194	8.00	1.00	Op1531r_1	NA	Q1LCS3 Transcriptional regulator, LysR family
5UTR_620	1889665 -	1889670 Rmet_5194			Op1531r_1		
NPKM_1826	1889821 +	1890970 Rmet_5195	1.67	0.58	Op1532f_1	NA	Q1LCS2 Porin, Gram-negative type
NPKM_1827	1890947 +	1892885 Rmet_5196	3.00	0.00	Op1532f_1	NA	Q1LCS1 Putative uncharacterized protein
NPKM_1828	1892887 +	1893304 Rmet_5197	3.33	1.53	Op1532f_1	NA	Q1LCS0 Cytochrome c, class I
3UTR_500	1893305 +	1893308 Rmet_5197			Op1532f_1		
3UTR_757	1893338 -	1893350 Rmet_5198			Op1533r_1		
NPKM_1829	1893351 -	1894305 Rmet_5198	5.67	0.58	Op1533r_1	MET-AA-GlySerThr	Q1LCR9 D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding
5UTR_619	1894306 -	1894344 Rmet_5198			Op1533r_1		
5UTR_404	1894466 +	1894501 Rmet_5199			Op1534f_1		
NPKM_1830	1894501 +	1895440 Rmet_5199	18.33	1.15	Op1534f_1	NA	Q1LCR8 Fumarylacetoacetate (FAA) hydrolase
NPKM_1831	1895494 +	1896100 Rmet_5200	31.67	0.58	Op1534f_1	MET-XEN-Toluene	Q1LCR7 Glyoxalase/bleomycin resistance protein/dioxygenase
NPKM_1832	1896111 +	1897044 Rmet_5201	23.67	1.53	Op1534f_1	NA	Q1LCR6 Lipase, active site
NPKM_1833	1897111 +	1898014 Rmet_5202	12.00	1.00	Op1534f_1	MET-AA-Lys_Syn	Q1LCR5 Dihydrodipicolinate synthetase
NPKM_1834	1898010 +	1898454 Rmet_5203	6.67	1.15	Op1534f_1	NA	Q1LCR4 Endoribonuclease L-PSP
NPKM_1835	1898450 +	1899044 Rmet_5204	5.00	1.00	Op1534f_1	NA	Q1LCR3 Nitroreductase
NPKM_1836	1899122 +	1900115 Rmet_5205	17.33	0.58	Op1534f_2	NA	Q1LCR2 Uncharacterized protein UPF0065
NPKM_1837	1900225 +	1901689 Rmet_5206	2.33	0.58	Op1534f_2	NA	Q1LCR1 Aldehyde dehydrogenase
NPKM_1838	1901708 +	1902530 Rmet_5207	1.00	0.00	Op1534f_2	MET-AA-Phe	Q1LCR0 Hydratase/decarboxylase
NPKM_1839	1902531 +	1903476 Rmet_5208	3.00	1.00	Op1534f_3	MET-CAH-Pyr	Q1LCQ9 Semialdehyde dehydrogenase, NAD-binding
NPKM_1840	1903486 +	1904524 Rmet_5209	2.33	0.58	Op1534f_3	MET-AA-Phe	Q1LCQ8 Pyruvate carboxyltransferase
NPKM_1841	1904520 +	1905285 Rmet_5210	2.67	0.58	Op1534f_3	MET-XEN-Toluene	Q1LCQ7 Hydratase/decarboxylase
3UTR_756	1904708 -	1906843 Rmet_5213			Op1535r_1		
NPKM_1842	1905336 +	1905774 Rmet_5211	3.67	0.58	Op1534f_3	NA	Q1LCQ6 Endoribonuclease L-PSP
NPKM_1843	1905770 +	1906772 Rmet_5212	3.00	1.00	Op1534f_3	MET-AA-Trp	Q1LCQ5 Amidohydrolase 2
3UTR_501	1906773 +	1906875 Rmet_5212			Op1534f_3		
NPKM_1844	1906844 -	1907510 Rmet_5213	149.67	4.93	Op1535r_1	NA	Q1LCQ4 Transcriptional regulator, GntR family
5UTR_618	1907511 -	1907555 Rmet_5213			Op1535r_1		
5UTR_405	1907683 +	1907714 Rmet_5214			Op1536f_1		
NPKM_1845	1907714 +	1908188 Rmet_5214	8.00	2.00	Op1536f_1	MET-CAH-Pyr	Q1LCQ3 Glyoxalase/bleomycin resistance protein/dioxygenase
3UTR_502	1908189 +	1908260 Rmet_5214			Op1536f_1		
3UTR_755	1908461 -	1908821 Rmet_5215			Op1537r_1		
NPKM_1846	1908822 -	1910013 Rmet_5215	2.67	0.58	Op1537r_1	NA	Q1LCQ2 Putative uncharacterized protein
NPKM_1847	1909987 -	1911256 Rmet_5216	4.67	0.58	Op1537r_1	NA	Q1LCQ1 Putative uncharacterized protein
NPKM_1848	1911252 -	1912566 Rmet_5217	19.00	2.00	Op1537r_1	NA	Q1LCQ0 Putative uncharacterized protein
5UTR_617	1912567 -	1913288 Rmet_5217			Op1537r_1		
NPKM_1849	1912710 +	1912959 Rmet_5218	2.00	1.00	Op1538f_1	NA	Q1LCP9 Putative uncharacterized protein
3UTR_503	1912960 +	1913062 Rmet_5218			Op1538f_1		
5UTR_406	1913087 +	1913120 Rmet_5219			Op1538f_2		
NPKM_1850	1913120 +	1913687 Rmet_5219	14.00	1.73	Op1538f_2	NA	Q1LCP8 Putative uncharacterized protein

3UTR_754	1913545 -	1914110 Rmet_5220				Op1539r_1			
3UTR_504	1913688 +	1914500 Rmet_5219				Op1538f_2			
NPKM_1851	1914111 -	1915038 Rmet_5220	23.67	2.52	Op1539r_1	NA		Q1LCP7 Transcriptional regulator, LysR family	
5UTR_407	1914941 +	1915079 Rmet_5221			Op1540f_1				
5UTR_616	1915039 -	1915458 Rmet_5220			Op1539r_1				
NPKM_1852	1915079 +	1916123 Rmet_5221	5.00	1.00	Op1540f_1	NA		Q1LCP6 Twin-arginine translocation pathway signal	
3UTR_753	1916010 -	1916079 Rmet_6715			Op2087r_1				
NPKM_1853	1916080 -	1916443 Rmet_6715	1.67	1.15	Op2087r_1	NA		NA	
NPKM_1854	1916119 +	1917316 Rmet_5222	3.67	0.58	Op1540f_1	MET-AA-Phe		Q1LCP5 Peptidase M20D, amidohydrolase	
5UTR_615	1916444 -	1916466 Rmet_6715			Op2087r_1				
3UTR_752	1916490 -	1918638 Rmet_5224			Op1541r_3				
3UTR_505	1917317 +	1917393 Rmet_5222			Op1540f_1				
5UTR_408	1917636 +	1917757 Rmet_5223			Op1540f_2				
NPKM_1855	1917757 +	1918225 Rmet_5223	26.00	1.73	Op1540f_2	NA		Q1LCP4 Putative uncharacterized protein	
3UTR_506	1918226 +	1918420 Rmet_5223			Op1540f_2				
NPKM_1856	1918639 -	1919608 Rmet_5224	12.33	1.15	Op1541r_3	NA		Q1LCP3 Putative uncharacterized protein	
NPKM_1857	1919789 -	1920836 Rmet_5225	25.67	0.58	Op1541r_3	NA		Q1LCP2 Putative uncharacterized protein	
NPKM_1858	1920900 -	1922343 Rmet_5226	7.67	0.58	Op1541r_2	NA		Q1LCP1 Putative uncharacterized protein	
NPKM_1859	1922426 -	1923374 Rmet_5227	3.00	0.00	Op1541r_1	NA		Q1LCP0 Alpha/beta hydrolase fold	
NPKM_1860	1923405 -	1924935 Rmet_5228	4.67	0.58	Op1541r_1	NA		Q1LCN9 FAD dependent oxidoreductase	
5UTR_409	1925017 +	1925034 Rmet_5229			Op1542f_1				
NPKM_1861	1925034 +	1926054 Rmet_5229	65.00	2.00	Op1542f_1	NA		Q1LCN8 Transcriptional regulator, AraC family	
3UTR_507	1926055 +	1928268 Rmet_5229			Op1542f_1				
3UTR_751	1926098 -	1926590 Rmet_5230			Op1543r_1				
NPKM_1862	1926591 -	1928097 Rmet_5230	16.67	2.08	Op1543r_1	NA		Q1LCN7 Aminotransferase, class V	
5UTR_614	1928098 -	1928130 Rmet_5230			Op1543r_1				
5UTR_410	1928301 +	1928525 Rmet_5231			Op1544f_1				
NPKM_1863	1928525 +	1929170 Rmet_5231	65.67	20.50	Op1544f_1	NA		Q1LCN6 Transcriptional regulator, ArsR family	
NPKM_1864	1929173 +	1930535 Rmet_5232	88.00	33.15	Op1544f_1	MET-EN-OxPhos		Q1LCN5 Cytochrome bd ubiquinol oxidase, subunit I	
NPKM_1865	1930531 +	1931569 Rmet_5233	83.33	29.94	Op1544f_1	MET-EN-OxPhos		Q1LCN4 Cytochrome d ubiquinol oxidase, subunit II	
NPKM_1866	1931618 +	1932551 Rmet_5234	67.00	13.75	Op1544f_1	NA		Q1LCN3 Putative uncharacterized protein	
NPKM_1867	1932691 +	1935085 Rmet_5235	17.00	3.00	Op1544f_1	NA		Q1LCN2 Tetratricopeptide TPR_2	
NPKM_1868	1935097 +	1936243 Rmet_5236	13.33	2.31	Op1544f_1	NA		Q1LCN1 DegT/DnrJ/EryC1/StrS aminotransferase	
NPKM_1869	1936245 +	1936947 Rmet_5237	9.33	2.31	Op1544f_1	NA		Q1LCN0 WbnG	
NPKM_1870	1936943 +	1937918 Rmet_5238	6.33	1.53	Op1544f_1	NA		Q1LCM9 Putative uncharacterized protein	
NPKM_1871	1937943 +	1938723 Rmet_5239	7.67	1.53	Op1544f_1	NA		Q1LCM8 Phytanoyl-CoA dioxygenase	
NPKM_1872	1938727 +	1939465 Rmet_5240	13.33	2.31	Op1544f_1	NA		Q1LCM7 Methyltransferase type 12	
3UTR_750	1939038 -	1942309 Rmet_5244			Op1545r_2				
NPKM_1873	1939476 +	1940766 Rmet_5241	12.67	2.08	Op1544f_1	NA		Q1LCM6 Putative uncharacterized protein	
NPKM_1874	1940775 +	1941540 Rmet_5242	14.00	1.73	Op1544f_1	NA		Q1LCM5 Putative uncharacterized protein	
NPKM_1875	1941586 +	1942282 Rmet_5243	9.67	1.15	Op1544f_1	NA		Q1LCM4 Methyltransferase type 11	
3UTR_508	1942283 +	1942637 Rmet_5243			Op1544f_1				
NPKM_1876	1942310 -	1943852 Rmet_5244	88.00	3.61	Op1545r_2	NA		Q1LCM3 Major facilitator superfamily MFS_1	

NPKM_1877	1944016 -	1944928 Rmet_5245		25.33	3.79	Op1545r_1	NA	Q1LCM2 Transcriptional regulator, LysR family
NPKM_1878	1945037 +	1945592 Rmet_5246		2.67	0.58	Op1546f_1	NA	Q1LCM1 Putative uncharacterized protein
NPKM_1879	1945548 -	1946520 Rmet_5247		21.33	0.58	Op1547r_1	NA	Q1LCM0 Transcriptional regulator, LysR family
3UTR_509	1945593 +	1945809 Rmet_5246				Op1546f_1		
NPKM_1880	1946631 +	1947633 Rmet_5248	bug	5.00	1.00	Op1548f_1	NA	Q1LCL9 Uncharacterized protein UPF0065
NPKM_1881	1947641 +	1948754 Rmet_5249		4.67	0.58	Op1548f_1	NA	Q1LCL8 L-carnitine dehydratase/bile acid-inducible protein F
3UTR_749	1948121 -	1948820 Rmet_5250				Op1549r_1		
3UTR_510	1948755 +	1948956 Rmet_5249				Op1548f_1		
NPKM_1882	1948821 -	1950855 Rmet_5250		21.33	3.21	Op1549r_1	DIV-MOT-Chemotax	Q1LCL7 Methyl-accepting chemotaxis sensory transducer
5UTR_613	1950856 -	1951028 Rmet_5250				Op1549r_1		
5UTR_411	1951070 +	1951766 Rmet_5251				Op1550f_1		
NPKM_1883	1951766 +	1952087 Rmet_5251		101.00	11.53	Op1550f_1	NA	Q1LCL6 Host factor-I protein
NPKM_1884	1952309 +	1953506 Rmet_5252	fliC2	1317.00	98.65	Op1550f_2	EIP-SIG-2Comp	Q1LCL5 Flagellin-like protein
NPKM_1885	1953621 +	1954002 Rmet_5253	flaG	29.67	2.89	Op1550f_2	DIV-MOT-Flagel	Q1LCL4 Flagellar protein FlaG protein
NPKM_1886	1954044 +	1955517 Rmet_5254	fliD2	30.33	2.31	Op1550f_2	DIV-MOT-Flagel	Q1LCL3 Flagellar hook-associated 2-like protein
NPKM_1887	1955541 +	1955976 Rmet_5255	fliS	39.33	3.21	Op1550f_2	DIV-MOT-Flagel	Q1LCL2 Flagellar protein FliS
NPKM_1888	1955997 +	1956342 Rmet_5256		35.33	4.16	Op1550f_2	DIV-MOT-Flagel	Q1LCL1 Flagellar protein FliT
NPKM_1889	1956441 +	1957785 Rmet_5257		14.33	1.53	Op1550f_2	NA	Q1LCL0 Putative uncharacterized protein
3UTR_748	1957546 -	1958126 Rmet_5259	fliE			Op1551r_1		
NPKM_1890	1957781 +	1958057 Rmet_5258		11.33	2.31	Op1550f_2	GIP-PTL-T3S	Q1LCK9 Putative flagellar protein
3UTR_511	1958058 +	1958199 Rmet_5258				Op1550f_2		
NPKM_1891	1958127 -	1958448 Rmet_5259	fliE	28.00	4.00	Op1551r_1	DIV-MOT-Flagel	Q1LCK8 Flagellar hook-basal body complex protein (FliE)
5UTR_612	1958449 -	1958687 Rmet_5259	fliE			Op1551r_1		
NPKM_1892	1958551 +	1958821 Rmet_5260		9.67	0.58	Op1552f_1	NA	Q1LCK7 Putative uncharacterized protein
NPKM_1893	1958817 +	1960509 Rmet_5261	fliF	21.00	2.65	Op1552f_2	GIP-PTL-T3S	Q1LCK6 Flagellar M-ring protein FliF
NPKM_1894	1960495 +	1961509 Rmet_5262	fliG	28.33	3.21	Op1552f_2	DIV-MOT-Chemotax	Q1LCK5 Flagellar motor switch protein FliG
NPKM_1895	1961495 +	1962332 Rmet_5263	fliH	26.33	4.93	Op1552f_2	GIP-PTL-T3S	Q1LCK4 Flagellar assembly protein FliH
NPKM_1896	1962324 +	1963785 Rmet_5264	fliI	19.00	3.46	Op1552f_2	GIP-PTL-T3S	Q1LCK3 ATPase FliI/YscN
NPKM_1897	1963777 +	1964230 Rmet_5265	fliJ	23.00	3.46	Op1552f_2	DIV-MOT-Flagel	Q1LCK2 Flagellar export FliJ
NPKM_1898	1964245 +	1965733 Rmet_5266	fliK	25.00	3.61	Op1552f_2	DIV-MOT-Flagel	Q1LCK1 Flagellar hook-length control protein
NPKM_1899	1965915 +	1966950 Rmet_5267		38.33	1.15	Op1552f_2	NA	Q1LCK0 Alpha/beta hydrolase fold
NPKM_1900	1967007 +	1967679 Rmet_5268	alkB2	51.33	2.08	Op1552f_2	GIP-REP-Recomb	Q1LCJ9 DNA-N1-methyladenine dioxxygenase
3UTR_747	1967010 -	1969355 Rmet_5270				Op1553r_1		
NPKM_1901	1967712 +	1969305 Rmet_5269		44.67	2.52	Op1552f_2	NA	Q1LCJ8 Sodium/sulphate symporter
3UTR_512	1969306 +	1969674 Rmet_5269				Op1552f_2		
NPKM_1902	1969356 -	1969662 Rmet_5270		44.00	7.21	Op1553r_1	NA	Q1LCJ7 Transcriptional regulator, XRE family
5UTR_611	1969663 -	1969667 Rmet_5270				Op1553r_1		
NPKM_1903	1969850 +	1971635 Rmet_5271		12.00	1.00	Op1554f_1	MET-AA-ValLeulle	Q1LCJ6 Dihydroxyacid dehydratase
NPKM_1904	1971642 +	1972362 Rmet_5272		9.67	1.15	Op1554f_1	NA	Q1LCJ5 Dimethylmenaquinone methyltransferase
NPKM_1905	1972441 +	1973410 Rmet_5273	bug	6.00	0.00	Op1554f_1	NA	Q1LCJ4 Uncharacterized protein UPF0065
NPKM_1906	1973453 +	1974392 Rmet_5274	gyaR	27.33	1.15	Op1554f_2	NA	Q1LCJ3 D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding
NPKM_1907	1974499 +	1975333 Rmet_5275		11.33	1.15	Op1554f_2	NA	Q1LCJ2 Intradiol ring-cleavage dioxxygenase
3UTR_513	1975334 +	1975401 Rmet_5275				Op1554f_2		

5UTR_412	1975548 +	1975618 Rmet_5276				Op1554f_2		
NPKM_1908	1975618 +	1977208 Rmet_5276		8.67	1.15	Op1554f_2	NA	Q1LCJ1 EAL-containing signal transduction protein
3UTR_746	1977266 -	1977953 Rmet_5278	bug			Op1555r_1		
NPKM_1909	1977282 +	1977900 Rmet_5277		10.67	1.53	Op1554f_2	NA	Q1LCJ0 Lysine exporter protein (LYSE/YGGA)
3UTR_514	1977901 +	1977998 Rmet_5277				Op1554f_2		
NPKM_1910	1977954 -	1978950 Rmet_5278	bug	17.33	1.53	Op1555r_1	NA	Q1LCI9 Uncharacterized protein UPF0065
NPKM_1911	1979050 -	1979977 Rmet_5279		36.33	2.52	Op1555r_1	NA	Q1LCI8 Transcriptional regulator, LysR family
5UTR_610	1979978 -	1980056 Rmet_5279				Op1555r_1		
NPKM_1912	1980039 +	1980675 Rmet_5280		14.33	1.53	Op1556f_1	NA	Q1LCI7 Putative uncharacterized protein
NPKM_1913	1980839 +	1981181 Rmet_5281		12.33	0.58	Op1556f_1	NA	Q1LCI6 Conserved hypothetical signal peptide protein
3UTR_745	1980894 -	1981343 Rmet_5282				Op1557r_1		
3UTR_515	1981182 +	1981275 Rmet_5281				Op1556f_1		
NPKM_1914	1981344 -	1982349 Rmet_5282		2.67	0.58	Op1557r_1	NA	Q1LCI5 Dienelactone hydrolase
5UTR_609	1982350 -	1982355 Rmet_5282				Op1557r_1		
NPKM_1915	1982615 +	1983968 Rmet_5283	nylB	4.67	0.58	Op1558f_1	NA	Q1LCI4 Beta-lactamase
3UTR_744	1983446 -	1984129 Rmet_5284	dbpA			Op1559r_1		
3UTR_516	1983969 +	1984059 Rmet_5283	nylB			Op1558f_1		
NPKM_1916	1984130 -	1985534 Rmet_5284	dbpA	23.00	1.00	Op1559r_1	GIP-REP-Recomb	Q1LCI3 DEAD/DEAH box helicase-like protein
5UTR_608	1985535 -	1985568 Rmet_5284	dbpA			Op1559r_1		
NPKM_1917	1985865 +	1986846 Rmet_5285	qor	0.67	0.58	Op1560f_1	NA	Q1LCI2 Alcohol dehydrogenase, zinc-binding
NPKM_1918	1986916 +	1987984 Rmet_5286		0.67	0.58	Op1560f_1	NA	Q1LCI1 Putative uncharacterized protein
3UTR_517	1987985 +	1988003 Rmet_5286				Op1560f_1		
5UTR_413	1988064 +	1988101 Rmet_5287	bug			Op1560f_1		
NPKM_1919	1988101 +	1989094 Rmet_5287	bug	0.00	0.00	Op1560f_1	NA	Q1LCI0 Uncharacterized protein UPF0065
NPKM_1920	1989403 +	1990564 Rmet_5288		0.33	0.58	Op1560f_2	NA	Q1LCH9 Porin, Gram-negative type
3UTR_518	1990565 +	1990575 Rmet_5288				Op1560f_2		
5UTR_414	1990612 +	1990658 Rmet_5289				Op1560f_3		
NPKM_1921	1990658 +	1991417 Rmet_5289		7.67	1.15	Op1560f_3	NA	Q1LCH8 Short-chain dehydrogenase/reductase SDR
3UTR_519	1991418 +	1991586 Rmet_5289				Op1560f_3		
NPKM_1922	1991496 -	1992321 Rmet_5290		1.67	0.58	Op1561r_1	NA	Q1LCH7 Short-chain dehydrogenase/reductase SDR
5UTR_415	1991993 +	1992024 Rmet_6716				Op2088f_1		
NPKM_1923	1992024 +	1992261 Rmet_6716		1.00	0.00	Op2088f_1	NA	NA
3UTR_520	1992262 +	1992272 Rmet_6716				Op2088f_1		
NPKM_1924	1992304 -	1993240 Rmet_5291		1.00	0.00	Op1561r_1	NA	Q1LCH6 Putative uncharacterized protein
5UTR_416	1993400 +	1993440 Rmet_5292	tauD			Op1562f_1		
NPKM_1925	1993440 +	1994286 Rmet_5292	tauD	3.00	0.00	Op1562f_1	MET-OAA-Taur	Q1LCH5 Taurine catabolism dioxygenase TauD/TfdA
NPKM_1926	1994313 +	1994883 Rmet_5293		2.33	0.58	Op1562f_1	NA	Q1LCH4 Putative uncharacterized protein
3UTR_521	1994884 +	1994890 Rmet_5293				Op1562f_1		
NPKM_1927	1994937 -	1995930 Rmet_5294	bug	0.33	0.58	Op1563r_1	NA	Q1LCH3 Uncharacterized protein UPF0065
NPKM_1928	1995923 +	1996142 Rmet_6717		0.33	0.58	Op1564f_1	NA	NA
NPKM_1929	1996216 +	1997260 Rmet_5295		11.00	1.00	Op1564f_2	NA	Q1LCH2 Transcriptional regulator, AraC family
3UTR_522	1997261 +	1997416 Rmet_5295				Op1564f_2		
3UTR_743	1997437 -	1997503 Rmet_5296	acnB			Op1565r_1		

NPKM_1930	1997504 -	2000096 Rmet_5296	<i>acnB</i>	299.00	10.15	Op1565r_1	MET-CAH-TCA	Q1LCH1 Aconitase
5UTR_607	2000097 -	2000126 Rmet_5296	<i>acnB</i>			Op1565r_1		
5UTR_417	2000452 +	2000517 Rmet_5297	<i>fliL</i>			Op1566f_1		
NPKM_1931	2000517 +	2001033 Rmet_5297	<i>fliL</i>	48.00	10.15	Op1566f_1	DIV-MOT-Flagel	Q1LCH0 Flagellar basal body-associated protein FliL
NPKM_1932	2001179 +	2002190 Rmet_5298	<i>fliM</i>	32.33	5.86	Op1566f_1	DIV-MOT-Chemotax	Q1LCG9 Flagellar motor switch protein FliM
NPKM_1933	2002182 +	2002653 Rmet_5299	<i>fliN</i>	50.33	7.09	Op1566f_1	GIP-PTL-T3S	Q1LCG8 Flagellar motor switch FliN
NPKM_1934	2002649 +	2003210 Rmet_5300	<i>fliO</i>	43.67	6.51	Op1566f_1	DIV-MOT-Flagel	Q1LCG7 Flagellar biosynthesis protein, FliO
NPKM_1935	2003206 +	2004001 Rmet_5301	<i>fliP</i>	11.00	1.73	Op1566f_1	GIP-PTL-T3S	Q1LCG6 Flagellar biosynthetic protein FliP
NPKM_1936	2004014 +	2004284 Rmet_5302	<i>fliQ</i>	10.67	0.58	Op1566f_1	GIP-PTL-T3S	Q1LCG5 Flagellar biosynthetic protein FliQ
NPKM_1937	2004329 +	2005115 Rmet_5303	<i>fliR</i>	3.33	0.58	Op1566f_1	GIP-PTL-T3S	Q1LCG4 Flagellar biosynthetic protein fliR
3UTR_523	2005116 +	2005258 Rmet_5303	<i>fliR</i>			Op1566f_1		
NPKM_1938	2005350 +	2006880 Rmet_5304		1.33	0.58	Op1566f_1	NA	Q1LCG3 Metallophosphoesterase
NPKM_1939	2006890 +	2008192 Rmet_5305		0.00	0.00	Op1566f_1	NA	Q1LCG2 Di-haem cytochrome c peroxidase
3UTR_742	2008092 -	2008160 Rmet_5306	<i>tar</i>			Op1567r_1		
NPKM_1940	2008161 -	2009859 Rmet_5306	<i>tar</i>	3.00	0.00	Op1567r_1	DIV-MOT-Chemotax	Q1LCG1 Methyl-accepting chemotaxis sensory transducer
NPKM_1941	2010105 +	2011311 Rmet_5307		6.00	0.00	Op1568f_1	NA	Q1LCG0 NnrS
3UTR_524	2011312 +	2011470 Rmet_5307				Op1568f_1		
3UTR_741	2011487 -	2011546 Rmet_5308				Op1569r_1		
NPKM_1942	2011547 -	2011847 Rmet_5308		10.33	2.52	Op1569r_1	NA	Q1LCF9 Putative uncharacterized protein
NPKM_1943	2012007 -	2017242 Rmet_5309		21.33	2.08	Op1569r_1	NA	Q1LCF8 Sensor protein
NPKM_1944	2017291 -	2017978 Rmet_5310		34.33	3.51	Op1569r_1	NA	Q1LCF7 Two component transcriptional regulator, LuxR family
5UTR_606	2017979 -	2017989 Rmet_5310				Op1569r_1		
5UTR_418	2018225 +	2018292 Rmet_5311				Op1570f_1		
NPKM_1945	2018292 +	2018979 Rmet_5311		64.33	11.93	Op1570f_1	NA	Q1LCF6 Isochorismatase hydrolase
NPKM_1946	2019036 +	2019858 Rmet_5312	<i>cpo</i>	51.33	11.02	Op1570f_1	NA	Q1LCF5 Alpha/beta hydrolase fold
NPKM_1947	2019944 +	2021810 Rmet_5313		24.00	7.00	Op1570f_1	NA	Q1LCF4 Amidohydrolase 3
NPKM_1948	2021840 +	2022263 Rmet_5314		15.67	5.51	Op1570f_1	NA	Q1LCF3 DoxX
NPKM_1949	2022281 +	2023901 Rmet_5315		8.33	1.53	Op1570f_1	NA	Q1LCF2 Putative uncharacterized protein
NPKM_1950	2023966 +	2024242 Rmet_5316		8.67	1.53	Op1570f_1	NA	Q1LCF1 Putative uncharacterized protein
NPKM_1951	2024332 +	2024665 Rmet_5317		12.33	3.51	Op1570f_1	NA	Q1LCF0 Response regulator receiver domain protein (CheY-like)
3UTR_740	2024342 -	2024672 Rmet_5318				Op1571r_1		
3UTR_525	2024666 +	2025212 Rmet_5317				Op1570f_1		
NPKM_1952	2024673 -	2025417 Rmet_5318		22.00	3.00	Op1571r_1	NA	Q1LCE9 Two component transcriptional regulator, LuxR family
NPKM_1953	2025491 -	2028629 Rmet_5319	<i>zniA</i>	18.67	0.58	Op1571r_1	EIP-TRA-Ion	Q1LCE8 Heavy metal efflux pump CzcA
NPKM_1954	2028680 -	2029895 Rmet_5320	<i>zniB</i>	29.67	3.21	Op1571r_1	EIP-TRA-Ion	Q1LCE7 Secretion protein HlyD
5UTR_419	2030016 +	2030064 Rmet_5321	<i>zniC</i>			Op1572f_1		
NPKM_1955	2030064 +	2031621 Rmet_5321	<i>zniC</i>	31.33	2.08	Op1572f_1	NA	Q1LCE6 RND efflux system, outer membrane lipoprotein, NodT
3UTR_739	2030737 -	2031609 Rmet_5322	<i>zniS</i>			Op1573r_1		
NPKM_1956	2031610 -	2033200 Rmet_5322	<i>zniS</i>	13.67	0.58	Op1573r_1	NA	Q1LCE5 Sensor protein
3UTR_526	2031622 +	2032219 Rmet_5321	<i>zniC</i>			Op1572f_1		
NPKM_1957	2033309 +	2033930 Rmet_5323	<i>zniR</i>	45.33	2.31	Op1574f_1	NA	Q1LCE4 Two component transcriptional regulator, LuxR family
3UTR_527	2033931 +	2034419 Rmet_5323	<i>zniR</i>			Op1574f_1		
NPKM_1958	2033937 -	2034249 Rmet_5324		11.33	2.08	Op1575r_1	NA	Q1LCE3 Putative signal peptide protein

5UTR_605	2034250 -	2034429 Rmet_5324							
5UTR_420	2034442 +	2034553 Rmet_5325	<i>zneP</i>						
NPKM_1959	2034553 +	2035318 Rmet_5325	<i>zneP</i>	5.33	0.58	Op1575r_1	NA	Q1LCE2	Putative uncharacterized protein
NPKM_1960	2035366 +	2036032 Rmet_5326	<i>zneR</i>	19.33	0.58	Op1576f_1	EIP-SIG-2Comp	Q1LCE1	Two component transcriptional regulator, winged helix family
NPKM_1961	2036007 +	2037450 Rmet_5327	<i>zneS</i>	7.00	1.00	Op1576f_2	EIP-SIG-2Comp	Q1LCE0	Sensor protein
3UTR_738	2036484 -	2037433 Rmet_5328	<i>zneC</i>			Op1577r_1			
NPKM_1962	2037434 -	2038970 Rmet_5328	<i>zneC</i>	10.33	1.15	Op1577r_1	EIP-TRA-Ion	Q1LCD9	RND efflux system, outer membrane lipoprotein, NodT
3UTR_528	2037451 +	2037587 Rmet_5327	<i>zneS</i>			Op1576f_2			
NPKM_1963	2038969 -	2042089 Rmet_5329	<i>zneA</i>	6.67	0.58	Op1577r_1	EIP-TRA-Ion	Q1LCD8	Heavy metal efflux pump CzcA
NPKM_1964	2042081 -	2043239 Rmet_5330	<i>zneB</i>	14.67	1.15	Op1577r_1	EIP-TRA-Ion	Q1LCD7	Secretion protein HlyD
5UTR_604	2043240 -	2043277 Rmet_5330	<i>zneB</i>			Op1577r_1			
NPKM_1965	2043416 +	2044094 Rmet_5331		31.67	1.53	Op1578f_1	EIP-SIG-2Comp	Q1LCD6	Two component transcriptional regulator, winged helix family
NPKM_1966	2044095 +	2045511 Rmet_5332		23.00	0.00	Op1578f_1	EIP-SIG-2Comp	Q1LCD5	Sensor protein
3UTR_737	2045663 -	2045692 Rmet_5333				Op1579r_1			
NPKM_1967	2045693 -	2046101 Rmet_5333		5.00	0.00	Op1579r_1	NA	Q1LCD4	Putative uncharacterized protein
NPKM_1968	2046112 +	2046835 Rmet_5334		4.67	0.58	Op1580f_1	EIP-TRA-Other	Q1LCD3	MgtC/SapB transporter
3UTR_529	2046836 +	2047031 Rmet_5334				Op1580f_1			
NPKM_1969	2046874 -	2047930 Rmet_5335		46.67	0.58	Op1581r_1	NA	Q1LCD2	Beta-lactamase-like protein
5UTR_603	2047931 -	2047987 Rmet_5335				Op1581r_1			
3UTR_736	2048008 -	2048725 Rmet_5337				Op1583r_3			
5UTR_421	2048093 +	2048121 Rmet_5336				Op1582f_1			
NPKM_1970	2048121 +	2048607 Rmet_5336		10.33	2.31	Op1582f_1	NA	Q1LCD1	Putative uncharacterized protein
3UTR_530	2048608 +	2049285 Rmet_5336				Op1582f_1			
NPKM_1971	2048726 -	2049386 Rmet_5337		72.33	5.51	Op1583r_3	NA	Q1LCD0	Putative uncharacterized protein
NPKM_1972	2049382 -	2049820 Rmet_5338		71.33	6.11	Op1583r_3	NA	Q1LCC9	Putative uncharacterized protein
NPKM_1973	2049866 -	2050541 Rmet_5339		83.00	5.20	Op1583r_3	NA	Q1LCC8	Curli production assembly/transport component CsgG
NPKM_1974	2050599 -	2052366 Rmet_5340	<i>hlyB</i>	6.00	0.00	Op1583r_2	NA	Q1LCC7	TonB box-like protein
NPKM_1975	2052369 -	2052561 Rmet_6718		11.33	2.52	Op1583r_2	NA	NA	
NPKM_1976	2052772 -	2052964 Rmet_6719		15.00	2.65	Op1583r_2	NA	NA	
5UTR_602	2052965 -	2053128 Rmet_6719				Op1583r_2			
3UTR_735	2053141 -	2053614 Rmet_5341				Op1583r_1			
NPKM_1977	2053615 -	2062630 Rmet_5341		4.33	0.58	Op1583r_1	NA	Q1LCC6	Adhesin HecA 20-residue repeat x2
5UTR_601	2062631 -	2062806 Rmet_5341				Op1583r_1			
5UTR_422	2062698 +	2062765 Rmet_5342				Op1584f_1			
NPKM_1978	2062765 +	2063074 Rmet_5342		4.33	0.58	Op1584f_1	NA	Q1LCC5	Putative uncharacterized protein
3UTR_734	2062815 -	2063050 Rmet_5343				Op1585r_1			
NPKM_1979	2063051 -	2063399 Rmet_5343		47.33	2.52	Op1585r_1	NA	Q1LCC4	Putative uncharacterized protein
3UTR_531	2063075 +	2063330 Rmet_5342				Op1584f_1			
5UTR_423	2063450 +	2063494 Rmet_5344				Op1586f_1			
NPKM_1980	2063494 +	2064088 Rmet_5344		22.67	3.21	Op1586f_1	NA	Q1LCC3	Putative uncharacterized protein
NPKM_1981	2064017 -	2064845 Rmet_5345	<i>xpsR</i>	29.67	2.08	Op1587r_1	NA	Q1LCC2	Transcription regulator XpsR transcription regulator protein
3UTR_532	2064089 +	2064221 Rmet_5344				Op1586f_1			
5UTR_600	2064846 -	2064904 Rmet_5345	<i>xpsR</i>			Op1587r_1			

5UTR_424	2065002 +	2065053 Rmet_5346				Op1588f_1		
NPKM_1982	2065053 +	2065965 Rmet_5346	54.00	2.65	Op1588f_1	NA	Q1LCC1 Putative uncharacterized protein	
3UTR_733	2065148 -	2065983 Rmet_5347			Op1589r_2			
3UTR_533	2065966 +	2066468 Rmet_5346			Op1588f_1			
NPKM_1983	2065984 -	2066803 Rmet_5347	48.67	0.58	Op1589r_2	NA	Q1LCC0 Cytochrome c, class I	
NPKM_1984	2066851 -	2067847 Rmet_5348	13.33	0.58	Op1589r_1	NA	Q1LCB9 Putative uncharacterized protein	
NPKM_1985	2067929 -	2069255 Rmet_5349	40.33	1.53	Op1589r_1	NA	Q1LCB8 Sigma-54 factor, interaction region	
5UTR_599	2069256 -	2069389 Rmet_5349			Op1589r_1			
5UTR_425	2069427 +	2069468 Rmet_6720			Op1590f_1			
NPKM_1986	2069468 +	2070347 Rmet_6720	6.00	1.00	Op1590f_1	NA	NA	
NPKM_1987	2070480 +	2071671 Rmet_5350	4.00	1.00	Op1590f_1	NA	Q1LCB7 FAD-dependent pyridine nucleotide-disulphide oxidoreductase	
NPKM_1988	2071740 +	2072955 Rmet_5351	4.67	0.58	Op1590f_1	NA	Q1LCB6 Major facilitator superfamily MFS_1	
3UTR_534	2072956 +	2073020 Rmet_5351			Op1590f_1			
5UTR_426	2073070 +	2073130 Rmet_5352			Op1590f_2			
NPKM_1989	2073130 +	2073424 Rmet_5352	271.33	46.44	Op1590f_2	NA	Q1LCB5 Putative uncharacterized protein	
NPKM_1990	2073739 +	2074393 Rmet_5353	46.33	3.21	Op1590f_2	NA	Q1LCB4 Pyridoxamine 5'-phosphate oxidase-related, FMN-binding	
NPKM_1991	2074479 +	2074659 Rmet_6721	29.67	2.52	Op1590f_2	NA	NA	
NPKM_1992	2074655 +	2075990 Rmet_5354	25.33	3.21	Op1590f_2	NA	Q1LCB3 Putative uncharacterized protein	
NPKM_1993	2076002 +	2076908 Rmet_5355	13.67	0.58	Op1590f_2	NA	Q1LCB2 Putative uncharacterized protein	
3UTR_732	2076463 -	2076955 Rmet_5356	bug		Op1591r_1			
NPKM_1994	2076956 -	2077922 Rmet_5356	bug	16.00	1.73	Op1591r_1	NA	Q1LCB1 Uncharacterized protein UPF0065
NPKM_1995	2078172 +	2079324 Rmet_5357		16.00	1.73	Op1592f_1	MET-CAH-Prop	Q1LCB0 Acyl-CoA dehydrogenase-like protein
NPKM_1996	2079320 +	2080361 Rmet_5358		16.67	1.15	Op1592f_1	MET-CAH-Prop	Q1LCA9 Acyl-CoA dehydrogenase-like protein
NPKM_1997	2080357 +	2081329 Rmet_5359	bug	14.33	2.08	Op1592f_1	NA	Q1LCA8 Uncharacterized protein UPF0065
3UTR_731	2080441 -	2081382 Rmet_5360			Op1593r_1			
NPKM_1998	2081383 -	2082379 Rmet_5360		48.33	2.08	Op1593r_1	NA	Q1LCA7 Transcriptional regulator, LysR family
NPKM_1999	2082482 +	2083304 Rmet_5361		9.00	1.00	Op1594f_1	MET-CAH-Prop	Q1LCA6 Enoyl-CoA hydratase/isomerase
NPKM_2000	2083310 +	2084522 Rmet_5362		12.00	1.00	Op1594f_1	NA	Q1LCA5 L-carnitine dehydratase/bile acid-inducible protein F
3UTR_730	2083885 -	2084627 Rmet_5363	nema		Op1595r_1			
3UTR_535	2084523 +	2085153 Rmet_5362			Op1594f_1			
NPKM_2001	2084628 -	2085750 Rmet_5363	nema	12.67	1.53	Op1595r_1	NA	Q1LCA4 NADH:flavin oxidoreductase/NADH oxidase
NPKM_2002	2085757 -	2086561 Rmet_5364	dkgB	9.33	1.53	Op1595r_1	NA	Q1LCA3 Aldo/keto reductase
NPKM_2003	2086670 +	2087573 Rmet_5365		12.00	0.00	Op1596f_1	NA	Q1LCA2 Transcriptional regulator, LysR family
NPKM_2004	2087706 +	2087901 Rmet_6722		11.67	2.08	Op1596f_1	NA	NA
NPKM_2005	2087897 +	2089064 Rmet_5366		9.67	1.15	Op1596f_1	NA	Q1LCA1 Major facilitator superfamily MFS_1
3UTR_536	2089065 +	2089518 Rmet_5366			Op1596f_1			
3UTR_729	2089088 -	2089113 Rmet_5367			Op1597r_1			
NPKM_2006	2089114 -	2091262 Rmet_5367		1.00	0.00	Op1597r_1	NA	Q1LCA0 CoA-binding
NPKM_2007	2091298 -	2092654 Rmet_5368		1.00	0.00	Op1597r_1	NA	Q1LC99 MmgE/PrpD
NPKM_2008	2092657 +	2093740 Rmet_5369		11.67	1.53	Op1598f_1	NA	Q1LC98 Transcriptional regulator, LysR family
NPKM_2009	2093851 +	2094820 Rmet_5370		2.67	0.58	Op1598f_1	NA	Q1LC97 Uncharacterized protein UPF0065
3UTR_537	2094821 +	2094849 Rmet_5370	bug		Op1598f_1			
3UTR_728	2094875 -	2094934 Rmet_5371	katG		Op1599r_1			

NPKM_2010	2094935 -	2097116 Rmet_5371	<i>katG</i>	19.00	1.73	Op1599r_1	MET-EN-Methane	Q1LC96 Catalase-peroxidase
5UTR_598	2097117 -	2097176 Rmet_5371	<i>katG</i>			Op1599r_1		
5UTR_427	2097251 +	2097338 Rmet_5372				Op1600f_1		
NPKM_2011	2097338 +	2097827 Rmet_5372		12.33	2.31	Op1600f_1	NA	Q1LC95 YbaK/prolyl-tRNA synthetase associated region
3UTR_538	2097828 +	2097870 Rmet_5372				Op1600f_1		
NPKM_2012	2098196 +	2100182 Rmet_5373		0.00	0.00	Op1600f_1	EIP-TRA-Pores	Q1LC94 TonB-dependent receptor
5UTR_428	2100187 +	2100218 Rmet_5374				Op1600f_2		
NPKM_2013	2100218 +	2101559 Rmet_5374		0.67	0.58	Op1600f_2	NA	Q1LC93 Putative uncharacterized protein
NPKM_2014	2101576 +	2102617 Rmet_5375	<i>hmuS</i>	1.00	0.00	Op1600f_2	NA	Q1LC92 Haemin-degrading
NPKM_2015	2102635 +	2103487 Rmet_5376	<i>hmuT</i>	2.33	0.58	Op1600f_3	EIP-TRA-ABC	Q1LC91 Periplasmic binding protein
NPKM_2016	2103483 +	2104485 Rmet_5377	<i>hmuU</i>	1.67	0.58	Op1600f_3	EIP-TRA-ABC	Q1LC90 Transport system permease protein
NPKM_2017	2104504 +	2105290 Rmet_5378	<i>hmuV</i>	1.00	0.00	Op1600f_3	EIP-TRA-ABC	Q1LC89 Hemin import ATP-binding protein hmuV
3UTR_727	2105082 -	2105336 Rmet_5379				Op1601r_1		
3UTR_539	2105291 +	2105437 Rmet_5378	<i>hmuV</i>			Op1600f_3		
NPKM_2018	2105337 -	2106147 Rmet_5379		2.33	0.58	Op1601r_1	NA	Q1LC88 Short-chain dehydrogenase/reductase SDR
NPKM_2019	2106143 -	2106929 Rmet_5380		2.33	0.58	Op1601r_1	MET-CAH-TCA	Q1LC87 Putative uncharacterized protein
NPKM_2020	2106925 -	2108458 Rmet_5381		1.67	0.58	Op1601r_1	NA	Q1LC86 AMP-dependent synthetase and ligase
NPKM_2021	2108477 -	2109473 Rmet_5382	<i>bug</i>	2.00	0.00	Op1601r_1	NA	Q1LC85 Uncharacterized protein UPF0065
NPKM_2022	2109597 +	2110404 Rmet_5383		20.67	0.58	Op1602f_1	NA	Q1LC84 Transcriptional regulator, IclR family
3UTR_726	2110277 -	2111437 Rmet_5386				Op1603r_1		
NPKM_2023	2110604 +	2110805 Rmet_5384		54.67	1.15	Op1602f_2	NA	Q1LC83 Putative uncharacterized protein
NPKM_2024	2110801 +	2111380 Rmet_5385		68.67	6.35	Op1602f_2	NA	Q1LC82 Putative uncharacterized protein
NPKM_2025	2111438 -	2111993 Rmet_5386		90.67	8.33	Op1603r_1	NA	Q1LC81 Putative uncharacterized protein
5UTR_597	2111994 -	2112036 Rmet_5386				Op1603r_1		
NPKM_2026	2112185 +	2113508 Rmet_5387		46.00	3.61	Op1604f_1	NA	Q1LC80 Putative uncharacterized protein
3UTR_725	2112585 -	2113514 Rmet_5388	<i>apbE</i>			Op1605r_1		
3UTR_540	2113509 +	2114097 Rmet_5387				Op1604f_1		
NPKM_2027	2113515 -	2114505 Rmet_5388	<i>apbE</i>	18.33	0.58	Op1605r_1	MET-COF-Thia	Q1LC79 ApbE-like lipoprotein
NPKM_2028	2114485 -	2116684 Rmet_5389		18.33	1.15	Op1605r_1	MET-EN-Sulf	Q1LC78 Oxidoreductase FAD/NAD(P)-binding
NPKM_2029	2116732 -	2117200 Rmet_5390		27.00	2.00	Op1605r_1	NA	Q1LC77 Putative uncharacterized protein
NPKM_2030	2117313 -	2117739 Rmet_5391		37.33	3.21	Op1605r_1	NA	Q1LC76 Putative uncharacterized protein
5UTR_596	2117740 -	2117750 Rmet_5391				Op1605r_1		
5UTR_429	2117803 +	2117888 Rmet_5392				Op1606f_1		
NPKM_2031	2117888 +	2118548 Rmet_5392		40.67	4.62	Op1606f_1	EIP-SIG-2Comp	Q1LC75 Two component transcriptional regulator, winged helix family
NPKM_2032	2118550 +	2119903 Rmet_5393		21.00	3.00	Op1606f_1	EIP-SIG-2Comp	Q1LC74 Sensor protein
NPKM_2033	2120131 +	2120707 Rmet_5394		6.67	0.58	Op1606f_1	NA	Q1LC73 Putative uncharacterized protein
3UTR_724	2120275 -	2120726 Rmet_5395				Op1607r_1		
3UTR_541	2120708 +	2121511 Rmet_5394				Op1606f_1		
NPKM_2034	2120727 -	2122353 Rmet_5395		6.00	1.00	Op1607r_1	NA	Q1LC72 Putative uncharacterized protein
NPKM_2035	2122371 -	2125134 Rmet_5396		11.33	0.58	Op1607r_1	EIP-TRA-Ion	Q1LC71 ATPase, E1-E2 type
NPKM_2036	2125237 -	2126152 Rmet_5397		16.00	1.00	Op1607r_1	NA	Q1LC70 Polyphosphate:AMP phosphotransferase
NPKM_2037	2126320 +	2126464 Rmet_6723		1.33	1.15	Op2089f_1	NA	NA
3UTR_542	2126465 +	2126487 Rmet_6723				Op2089f_1		

NPKM_2038	2126524 -	2126725 Rmet_6724		31.33	4.04	Op2090r_1	NA	NA
5UTR_595	2126726 -	2126734 Rmet_6724				Op2090r_1		
5UTR_430	2126869 +	2126914 Rmet_5398				Op1608f_1		
NPKM_2039	2126914 +	2127373 Rmet_5398		7.67	2.08	Op1608f_1	NA	Q1LC69 Putative uncharacterized protein
NPKM_2040	2127372 +	2128875 Rmet_5399		8.33	0.58	Op1608f_1	NA	Q1LC68 40-residue YVTN beta-propeller repeat
NPKM_2041	2128950 +	2129448 Rmet_5400	rpoM	11.00	1.00	Op1608f_1	GIP-TK-RNAP	Q1LC67 Sigma-24 (FecI-like)
NPKM_2042	2129444 +	2130260 Rmet_5401		6.67	0.58	Op1608f_1	GIP-TK-RNAP	Q1LC66 Putative transmembrane transcriptional regulator (Anti-sigma factor)
3UTR_543	2130261 +	2130483 Rmet_5401				Op1608f_1		
5UTR_431	2130689 +	2130726 Rmet_5402				Op1608f_1		
NPKM_2043	2130726 +	2132709 Rmet_5402		12.33	3.21	Op1608f_1	NA	Q1LC65 Beta-lactamase-like protein
3UTR_723	2132747 -	2132779 Rmet_5403				Op1609r_1		
NPKM_2044	2132780 -	2134193 Rmet_5403		8.33	0.58	Op1609r_1	NA	Q1LC64 Putative uncharacterized protein
5UTR_594	2134194 -	2134264 Rmet_5403				Op1609r_1		
5UTR_432	2134685 +	2134742 Rmet_5404				Op1610f_1		
NPKM_2045	2134742 +	2135276 Rmet_5404		4.67	2.08	Op1610f_1	NA	Q1LC63 Putative uncharacterized protein
NPKM_2046	2135436 +	2136405 Rmet_5405		9.00	1.73	Op1610f_1	NA	Q1LC62 Putative periplasmic protein
NPKM_2047	2136416 +	2136944 Rmet_5406		9.33	3.21	Op1610f_1	NA	Q1LC61 Putative uncharacterized protein
3UTR_544	2136945 +	2137195 Rmet_5406				Op1610f_1		
5UTR_433	2137497 +	2137531 Rmet_5407				Op1610f_1		
NPKM_2048	2137531 +	2148676 Rmet_5407		4.67	1.15	Op1610f_1	NA	Q1LC60 Putative uncharacterized protein
NPKM_2049	2148662 +	2150183 Rmet_5408		7.33	1.53	Op1610f_1	NA	Q1LC59 Outer membrane efflux protein
NPKM_2050	2150179 +	2151001 Rmet_5409		5.67	1.15	Op1610f_1	NA	Q1LC58 Putative uncharacterized protein
NPKM_2051	2151006 +	2152356 Rmet_5410		6.00	1.73	Op1610f_1	NA	Q1LC57 Putative uncharacterized protein
NPKM_2052	2152357 +	2154457 Rmet_5411		3.33	0.58	Op1610f_1	NA	Q1LC56 Peptidase M50
3UTR_722	2153189 -	2154518 Rmet_5412				Op1611r_1		
3UTR_545	2154458 +	2154892 Rmet_5411				Op1610f_1		
NPKM_2053	2154519 -	2155158 Rmet_5412		81.00	4.36	Op1611r_1	NA	Q1LC55 Transcriptional regulator, TetR family
5UTR_593	2155159 -	2155164 Rmet_5412				Op1611r_1		
NPKM_2054	2155362 +	2156796 Rmet_5413	calB	2.33	0.58	Op1612f_1	NA	Q1LC54 Aldehyde dehydrogenase
3UTR_546	2156797 +	2156808 Rmet_5413	calB			Op1612f_1		
NPKM_2055	2156821 +	2158426 Rmet_5414	betA4	0.67	0.58	Op1612f_1	NA	Q1LC53 Glucose-methanol-choline oxidoreductase
NPKM_2056	2158499 +	2160488 Rmet_5415		1.00	0.00	Op1612f_1	NA	Q1LC52 Beta-lactamase-like protein
3UTR_547	2160489 +	2160512 Rmet_5415				Op1612f_1		
5UTR_434	2160921 +	2160935 Rmet_5416	asIA			Op1612f_2		
NPKM_2057	2160935 +	2162675 Rmet_5416	asIA	112.00	38.16	Op1612f_2	MET-LIP-Others	Q1LC51 Sulfatase
3UTR_548	2162676 +	2162774 Rmet_5416	asIA			Op1612f_2		
5UTR_435	2162792 +	2162830 Rmet_5417				Op1612f_2		
NPKM_2058	2162830 +	2163739 Rmet_5417		11.67	2.08	Op1612f_2	NA	Q1LC50 Transcriptional regulator, LysR family
NPKM_2059	2163892 +	2165197 Rmet_5418		0.33	0.58	Op1612f_2	NA	Q1LC49 Major facilitator superfamily MFS_1
5UTR_436	2165239 +	2165249 Rmet_5419				Op1612f_3		
NPKM_2060	2165249 +	2166431 Rmet_5419		1.67	0.58	Op1612f_3	MET-AA-Phe	Q1LC48 Peptidase M20D, amidohydrolase
NPKM_2061	2166420 -	2167293 Rmet_5420		1.00	0.00	Op1613r_1	NA	Q1LC47 Putative uncharacterized protein
3UTR_549	2166432 +	2166537 Rmet_5419				Op1612f_3		

NPKM_2062	2167289 -	2168105 Rmet_5421		1.67	0.58	Op1613r_1	NA	Q1LC46 NLPA lipoprotein
NPKM_2063	2168097 -	2169156 Rmet_5422	sumF	4.33	0.58	Op1613r_1	NA	Q1LC45 Putative uncharacterized protein
NPKM_2064	2169175 -	2171158 Rmet_5423	atsA	4.33	0.58	Op1613r_1	MET-LIP-Others	Q1LC44 Sulfatase
5UTR_592	2171159 -	2171181 Rmet_5423	atsA			Op1613r_1		
5UTR_437	2171376 +	2171530 Rmet_5424				Op1614f_1		
NPKM_2065	2171530 +	2172445 Rmet_5424		33.00	2.00	Op1614f_1	NA	Q1LC43 Transcriptional regulator, LysR family
3UTR_721	2172529 -	2172554 Rmet_6725				Op2091r_1		
NPKM_2066	2172555 -	2172618 Rmet_6725		0.33	0.58	Op2091r_1	NA	NA
5UTR_591	2172619 -	2172662 Rmet_6725				Op2091r_1		
NPKM_2067	2172793 +	2173948 Rmet_5425		6.00	0.00	Op1614f_1	NA	Q1LC42 Acyl-CoA dehydrogenase-like protein
3UTR_720	2174410 -	2175133 Rmet_5428				Op1615r_2		
NPKM_2068	2174455 +	2174707 Rmet_5426		18.33	4.04	Op1614f_2	NA	Q1LC41 Putative uncharacterized protein
NPKM_2069	2174810 +	2175065 Rmet_5427		13.00	1.73	Op1614f_2	NA	Q1LC40 Putative uncharacterized protein
NPKM_2070	2175134 -	2175509 Rmet_5428		110.33	3.79	Op1615r_2	NA	Q1LC39 Putative uncharacterized protein
NPKM_2071	2175610 -	2175898 Rmet_5429		51.00	4.36	Op1615r_1	NA	Q1LC38 Putative uncharacterized protein
NPKM_2072	2176192 +	2177122 Rmet_5430		39.00	4.58	Op1616f_1	MET-GLYC-LPS	Q1LC37 Lipid A biosynthesis acyltransferase
3UTR_550	2177123 +	2177720 Rmet_5430				Op1616f_1		
NPKM_2073	2177191 -	2178034 Rmet_5431		28.67	2.52	Op1617r_2	MET-CAH-Prop	Q1LC36 Enoyl-CoA hydratase/isomerase
NPKM_2074	2178172 -	2179351 Rmet_5432		56.00	1.73	Op1617r_2	MET-CAH-Pyr	Q1LC35 Thiolase
NPKM_2075	2179427 -	2180210 Rmet_5433		61.33	1.53	Op1617r_2	NA	Q1LC34 Short-chain dehydrogenase/reductase SDR
NPKM_2076	2180292 -	2181264 Rmet_5434		50.00	3.00	Op1617r_2	MET-EN-Nitrog	Q1LC33 2-nitropropane dioxygenase, NPD
NPKM_2077	2181341 -	2182454 Rmet_5435		42.00	2.65	Op1617r_2	NA	Q1LC32 L-carnitine dehydratase/bile acid-inducible protein F
NPKM_2078	2182600 -	2185315 Rmet_5436		28.33	1.15	Op1617r_2	NA	Q1LC31 ATP-dependent transcriptional regulator, Malt-like, LuxR family
NPKM_2079	2185409 -	2186573 Rmet_5437		5.67	0.58	Op1617r_1	MET-CAH-Prop	Q1LC30 Acyl-CoA dehydrogenase-like protein
5UTR_590	2186574 -	2186677 Rmet_5437				Op1617r_1		
5UTR_438	2186756 +	2186770 Rmet_5438				Op1618f_1		
NPKM_2080	2186770 +	2188318 Rmet_5438		11.33	1.53	Op1618f_1	MET-LIP-FAMet	Q1LC29 AMP-dependent synthetase and ligase
3UTR_719	2187976 -	2188365 Rmet_5439	alkK			Op1619r_3		
3UTR_551	2188319 +	2188639 Rmet_5438				Op1618f_1		
NPKM_2081	2188366 -	2190004 Rmet_5439	alkK	15.67	1.15	Op1619r_3	MET-LIP-FASyn	Q1LC28 AMP-dependent synthetase and ligase
NPKM_2082	2190174 -	2190690 Rmet_5440		20.67	0.58	Op1619r_3	NA	Q1LC27 Putative uncharacterized protein
NPKM_2083	2190942 -	2191287 Rmet_5441		20.67	0.58	Op1619r_3	NA	Q1LC26 Antibiotic biosynthesis monooxygenase
NPKM_2084	2191255 -	2191846 Rmet_5442		26.33	0.58	Op1619r_3	NA	Q1LC25 Glycerol-3-phosphate responsive antiterminator (MRNA-binding)-like protei
NPKM_2085	2191849 -	2193403 Rmet_5443		9.67	1.15	Op1619r_2	MET-LIP-Others	Q1LC24 FAD linked oxidase-like protein
NPKM_2086	2193399 -	2195079 Rmet_5444		5.67	0.58	Op1619r_2	MET-LIP-GlycPLip	Q1LC23 FAD dependent oxidoreductase
NPKM_2087	2195101 -	2196622 Rmet_5445		7.67	1.53	Op1619r_2	MET-LIP-GlycLip	Q1LC22 Carbohydrate kinase, FGGY
NPKM_2088	2196626 -	2198081 Rmet_5446		19.67	2.08	Op1619r_2	NA	Q1LC21 Major facilitator superfamily MFS_1
5UTR_589	2198082 -	2198139 Rmet_5446				Op1619r_2		
NPKM_2089	2198144 -	2198534 Rmet_5447		1.00	0.00	Op1619r_1	NA	Q1LC20 Putative uncharacterized protein
NPKM_2090	2198540 -	2198831 Rmet_5448		2.33	0.58	Op1619r_1	NA	Q1LC19 Putative uncharacterized protein
5UTR_588	2198832 -	2198897 Rmet_5448				Op1619r_1		
NPKM_2091	2199205 +	2199673 Rmet_5449		2.33	0.58	Op1620f_1	NA	Q1LC18 Putative uncharacterized protein
3UTR_552	2199674 +	2199739 Rmet_5449				Op1620f_1		

NPKM_2092	2199922 +	2200213 Rmet_5450		0.33	0.58	Op1620f_1	NA	Q1LC17 Putative uncharacterized protein
NPKM_2093	2200209 +	2200857 Rmet_5451		1.00	0.00	Op1620f_2	NA	Q1LC16 Putative uncharacterized protein
3UTR_718	2200398 -	2200893 Rmet_5452	<i>tnpB</i>			Op1621r_2		
3UTR_553	2200858 +	2200888 Rmet_5451				Op1620f_2		
NPKM_2094	2200894 -	2201788 Rmet_5452	<i>tnpB</i>	0.00	0.00	Op1621r_2	NA	NA
NPKM_2095	2201784 -	2202081 Rmet_5453	<i>tnpA</i>	0.00	0.00	Op1621r_2	NA	NA
3UTR_717	2202118 -	2202138 Rmet_5454				Op1621r_2		
NPKM_2096	2202139 -	2202655 Rmet_5454		7.00	1.00	Op1621r_2	NA	Q1LC13 Transposon Tn7 transposition protein TnsC
NPKM_2097	2202651 -	2203503 Rmet_5455	<i>tnpB</i>	0.00	0.00	Op1621r_1	GIP-REP-Recomb	Q1LBX0 Integrase, catalytic region
NPKM_2098	2203520 -	2203793 Rmet_5456	<i>tnpA</i>	0.00	0.00	Op1621r_1	GIP-REP-Recomb	Q1LBX1 Transposase IS3/IS911
NPKM_2099	2203817 -	2204621 Rmet_5457	<i>tnsC</i>	1.00	1.00	Op1621r_1	NA	Q1LC10 Tn7-like transposition protein C
NPKM_2100	2204604 -	2206782 Rmet_5458	<i>tnsB</i>	0.67	0.58	Op1621r_1	NA	Q1LC09 Putative uncharacterized protein
NPKM_2101	2206781 -	2207735 Rmet_5459	<i>tnsA</i>	0.33	0.58	Op1621r_1	NA	Q1LC08 Putative uncharacterized protein
5UTR_587	2207736 -	2207777 Rmet_5459	<i>tnsA</i>			Op1621r_1		
5UTR_439	2207784 +	2207787 Rmet_6726				Op2092f_1		
NPKM_2102	2207787 +	2207850 Rmet_6726		1.33	0.58	Op2092f_1	NA	NA
3UTR_554	2207851 +	2207872 Rmet_6726				Op2092f_1		
NPKM_2103	2208083 -	2208821 Rmet_5460		0.67	0.58	Op1621r_1	NA	Q1LC07 Putative uncharacterized protein
5UTR_440	2208669 +	2208842 Rmet_5461				Op1622f_1		
5UTR_586	2208822 -	2208886 Rmet_5460				Op1621r_1		
NPKM_2104	2208842 +	2209337 Rmet_5461		26.00	1.00	Op1622f_1	NA	Q1LC06 Putative uncharacterized protein
3UTR_716	2209138 -	2209150 Rmet_6727				Op1623r_1		
NPKM_2105	2209151 -	2209229 Rmet_6727		2.00	1.73	Op1623r_1	NA	NA
5UTR_585	2209230 -	2209433 Rmet_6727				Op1623r_1		
3UTR_555	2209338 +	2209837 Rmet_5461				Op1622f_1		
3UTR_715	2209531 -	2209571 Rmet_5462				Op1623r_1		
NPKM_2106	2209572 -	2209923 Rmet_5462		3.33	0.58	Op1623r_1	NA	Q1LC05 Putative uncharacterized protein
5UTR_584	2209924 -	2209952 Rmet_5462				Op1623r_1		
NPKM_2107	2209992 +	2210229 Rmet_6728		0.67	0.58	Op2093f_1	NA	NA
3UTR_714	2210195 -	2210220 Rmet_5463				Op1623r_1		
NPKM_2108	2210221 -	2210443 Rmet_5463		4.00	1.00	Op1623r_1	NA	Q1LC04 Putative uncharacterized protein
5UTR_583	2210444 -	2210620 Rmet_5463				Op1623r_1		
NPKM_2109	2210458 +	2210770 Rmet_5464		1.67	0.58	Op1624f_1	NA	Q1LC03 Putative uncharacterized protein
3UTR_713	2210673 -	2210918 Rmet_5465				Op1625r_2		
3UTR_556	2210771 +	2210837 Rmet_5464				Op1624f_1		
NPKM_2110	2210919 -	2211411 Rmet_5465		8.67	1.53	Op1625r_2	NA	Q1LC02 Putative uncharacterized protein
NPKM_2111	2211550 -	2211868 Rmet_5466		11.00	2.65	Op1625r_2	NA	Q1LC01 Putative uncharacterized protein
NPKM_2112	2211961 -	2213122 Rmet_5467		11.67	1.53	Op1625r_2	NA	Q1LC00 Putative uncharacterized protein
NPKM_2113	2213106 -	2213553 Rmet_5468		7.33	1.15	Op1625r_2	NA	Q1LBZ9 Putative uncharacterized protein
NPKM_2114	2213661 -	2214351 Rmet_5469		6.33	1.15	Op1625r_2	NA	Q1LBZ8 Putative uncharacterized protein
5UTR_582	2214352 -	2214384 Rmet_5469				Op1625r_2		
3UTR_712	2214807 -	2215439 Rmet_5470				Op1625r_2		
5UTR_441	2215111 +	2215215 Rmet_6729				Op2094f_1		

NPKM_2115	2215215 +	2215386 Rmet_6729		3.67	1.15	Op2094f_1	NA	NA
3UTR_557	2215387 +	2215572 Rmet_6729				Op2094f_1		
NPKM_2116	2215440 -	2216169 Rmet_5470		33.67	3.21	Op1625r_2	NA	Q1LBZ7 Transcriptional regulator, GntR family
NPKM_2117	2216281 -	2216845 Rmet_5471	<i>fumB</i>	45.00	4.58	Op1625r_2	MET-CAH-TCA	Q1LBZ6 Hydro-lyases, Fe-S type, tartrate/fumarate subfamily, beta region
NPKM_2118	2216858 -	2217701 Rmet_5472	<i>fumA</i>	47.67	5.51	Op1625r_2	MET-CAH-TCA	Q1LBZ5 Fumarase alpha subunit
NPKM_2119	2217706 -	2218876 Rmet_5473		31.67	4.04	Op1625r_2	NA	Q1LBZ4 Mandelate racemase/muconate lactonizing enzyme
NPKM_2120	2218886 -	2219870 Rmet_5474	<i>bug</i>	39.33	3.06	Op1625r_2	NA	Q1LBZ3 Uncharacterized protein UPF0065
5UTR_581	2219871 -	2219874 Rmet_5474	<i>bug</i>			Op1625r_2		
3UTR_711	2219896 -	2219950 Rmet_6730				Op1625r_1		
NPKM_2121	2219951 -	2220275 Rmet_6730		0.67	0.58	Op1625r_1	NA	NA
5UTR_442	2220226 +	2220464 Rmet_5475				Op1626f_1		
5UTR_580	2220276 -	2220344 Rmet_6730				Op1625r_1		
NPKM_2122	2220464 +	2220788 Rmet_5475		72.00	14.73	Op1626f_1	NA	Q1LBZ2 Putative uncharacterized protein
NPKM_2123	2220929 +	2221175 Rmet_5476		24.00	5.00	Op1626f_1	NA	Q1LBZ1 Putative uncharacterized protein
NPKM_2124	2221358 +	2221856 Rmet_5477		139.00	5.29	Op1626f_2	NA	Q1LBZ0 Putative uncharacterized protein
NPKM_2125	2221997 -	2222213 Rmet_5478	<i>tnmC</i>	0.00	0.00	Op2095r_1	NA	NA
NPKM_2126	2222266 -	2223100 Rmet_5479	<i>gspA</i>	0.00	0.00	Op2095r_1	NA	NA
NPKM_2127	2223096 -	2224536 Rmet_5480	<i>tnmA</i>	0.00	0.00	Op2095r_1	NA	NA
NPKM_2128	2224647 -	2225217 Rmet_5481	<i>tnmB</i>	0.00	0.00	Op2095r_1	NA	NA
NPKM_2129	2225279 +	2225702 Rmet_5482		10.33	2.08	Op1628f_1	NA	Q1LBY5 Putative uncharacterized protein
3UTR_710	2225282 -	2227304 Rmet_5485				Op1629r_2		
3UTR_558	2225703 +	2225712 Rmet_5482				Op1628f_1		
5UTR_443	2225715 +	2225953 Rmet_5483	<i>dam</i>			Op1628f_1		
NPKM_2130	2225953 +	2226751 Rmet_5483	<i>dam</i>	3.33	0.58	Op1628f_1	GIP-REP-Recomb	Q1LBY4 DNA adenine methylase Dam
3UTR_559	2226752 +	2226795 Rmet_5483	<i>dam</i>			Op1628f_1		
5UTR_444	2226798 +	2226837 Rmet_5484				Op1628f_2		
NPKM_2131	2226837 +	2227245 Rmet_5484		189.33	9.29	Op1628f_2	NA	Q1LBY3 Putative uncharacterized protein
3UTR_560	2227246 +	2228053 Rmet_5484				Op1628f_2		
NPKM_2132	2227305 -	2227602 Rmet_5485		30.00	1.00	Op1629r_2	NA	Q1LBY2 Putative uncharacterized protein
NPKM_2133	2227609 -	2227888 Rmet_6731		7.67	1.15	Op1629r_1	NA	NA
NPKM_2134	2227884 -	2228790 Rmet_5486		23.67	0.58	Op1629r_1	NA	Q1LBY1 Putative uncharacterized protein
NPKM_2135	2228956 -	2230732 Rmet_5487		35.00	2.65	Op1629r_1	GIP-REP-Recomb	Q1LBY0 Superfamily I DNA and RNA helicases-like protein
5UTR_445	2229921 +	2229937 Rmet_6732				Op2096f_1		
NPKM_2136	2229937 +	2230237 Rmet_6732		1.67	1.53	Op2096f_1	NA	NA
3UTR_561	2230238 +	2230250 Rmet_6732				Op2096f_1		
NPKM_2137	2230724 -	2232521 Rmet_5488		42.33	1.53	Op1629r_1	GIP-REP-Recomb	Q1LBX9 Putative exonuclease
5UTR_446	2232819 +	2233003 Rmet_6733				Op2097f_1		
NPKM_2138	2233003 +	2233201 Rmet_6733		18.00	2.65	Op2097f_1	NA	NA
NPKM_2139	2233325 +	2233559 Rmet_5489		43.00	6.08	Op1630f_1	NA	Q1LBX8 Putative uncharacterized protein
NPKM_2140	2233635 +	2233719 Rmet_6734		18.33	5.77	Op1630f_1	NA	NA
NPKM_2141	2233957 +	2234128 Rmet_6735		79.33	0.58	Op1630f_2	NA	NA
NPKM_2142	2234616 -	2235795 Rmet_5490	<i>pobA</i>	57.33	4.93	Op1631r_1	MET-XEN-24D	Q1LBX7 Monooxygenase, FAD-binding
NPKM_2143	2235543 +	2235858 Rmet_6736		7.00	3.00	Op1632f_1	NA	NA

SUTR_579	2235796 -	2235897 Rmet_5490	pobA				Op1631r_1		
NPKM_2144	2236163 +	2237129 Rmet_5491	bug	33.67	2.08	Op1632f_2	NA	Q1LBX6	Uncharacterized protein UPF0065
NPKM_2145	2237143 +	2238847 Rmet_5492		24.67	1.15	Op1632f_2	NA	Q1LBX5	Fumarate reductase/succinate dehydrogenase flavoprotein-like protein
NPKM_2146	2238843 +	2239191 Rmet_5493		19.67	2.08	Op1632f_2	NA	Q1LBX4	NIPSNAP domain protein
NPKM_2147	2239286 +	2240276 Rmet_5494	bug	21.33	0.58	Op1632f_2	NA	Q1LBX3	Uncharacterized protein UPF0065
3UTR_562	2240277 +	2241010 Rmet_5494	bug			Op1632f_2			
3UTR_709	2240415 -	2240426 Rmet_5495				Op1633r_1			
NPKM_2148	2240427 -	2241225 Rmet_5495		2.33	0.58	Op1633r_1	NA	Q1LBX2	Alcohol dehydrogenase, zinc-binding
NPKM_2149	2241262 +	2241535 Rmet_5496		0.00	0.00	Op1634f_1	GIP-REP-Recomb	Q1LBX1	Transposase IS3/IS911
NPKM_2150	2241552 +	2242404 Rmet_5497	tnpB	0.00	0.00	Op1634f_1	GIP-REP-Recomb	Q1LBX0	Integrase, catalytic region
3UTR_708	2242389 -	2242407 Rmet_5498				Op1635r_1			
NPKM_2151	2242408 -	2242654 Rmet_5498		6.33	0.58	Op1635r_1	NA	Q1LBW9	Oxidoreductase, zinc-binding
5UTR_578	2242655 -	2242739 Rmet_5498				Op1635r_1			
NPKM_2152	2242828 +	2244004 Rmet_5499		14.00	1.00	Op1636f_1	MET-CAH-Pyr	Q1LBW8	Acetyl-CoA acetyltransferase (Thiolase)
NPKM_2153	2244007 +	2244406 Rmet_5500		13.00	3.00	Op1636f_1	NA	Q1LBW7	Putative uncharacterized protein
3UTR_563	2244407 +	2244414 Rmet_5500				Op1636f_1			
5UTR_447	2244416 +	2244417 Rmet_5501				Op1636f_1			
NPKM_2154	2244417 +	2245212 Rmet_5501		6.33	0.58	Op1636f_1	NA	Q1LBW6	Enoyl-CoA hydratase
NPKM_2155	2245214 +	2246030 Rmet_5502		10.33	1.53	Op1636f_1	NA	Q1LBW5	Short-chain dehydrogenase/reductase SDR
NPKM_2156	2246239 +	2247208 Rmet_5503	bug	11.33	1.15	Op1636f_1	NA	Q1LBW4	Uncharacterized protein UPF0065
3UTR_564	2247209 +	2247477 Rmet_5503	bug			Op1636f_1			
3UTR_707	2247326 -	2247345 Rmet_5504				Op1637r_1			
NPKM_2157	2247346 -	2248486 Rmet_5504		4.67	0.58	Op1637r_1	NA	Q1LBW3	Porin, Gram-negative type
5UTR_448	2248682 +	2248960 Rmet_6737				Op1638f_1			
NPKM_2158	2248960 +	2249149 Rmet_6737		8.33	3.06	Op1638f_1	NA	NA	
NPKM_2159	2249196 +	2250078 Rmet_5505		20.67	1.53	Op1638f_2	MET-CAH-Prop	Q1LBW2	Enoyl-CoA hydratase/isomerase
3UTR_706	2249967 -	2250195 Rmet_5506				Op1639r_1			
3UTR_565	2250079 +	2250372 Rmet_5505				Op1638f_2			
NPKM_2160	2250196 -	2250751 Rmet_5506		9.67	1.15	Op1639r_1	NA	Q1LBW1	Putative uncharacterized protein
NPKM_2161	2250812 -	2251970 Rmet_5507		5.33	0.58	Op1639r_1	MET-CAH-Prop	Q1LBW0	Acyl-CoA dehydrogenase-like protein
NPKM_2162	2251987 -	2254015 Rmet_5508		3.67	1.15	Op1639r_1	NA	Q1LBV9	AMP-dependent synthetase and ligase
5UTR_449	2253838 +	2254103 Rmet_5509				Op1640f_1			
5UTR_577	2254016 -	2254143 Rmet_5508				Op1639r_1			
NPKM_2163	2254103 +	2254679 Rmet_5509		5.00	1.00	Op1640f_1	NA	Q1LBV8	Short-chain dehydrogenase/reductase SDR
NPKM_2164	2254710 +	2255919 Rmet_5510		7.00	0.00	Op1640f_1	MET-CAH-Pyr	Q1LBV7	Thiolase
NPKM_2165	2255927 +	2258072 Rmet_5511		8.67	0.58	Op1640f_1	MET-CAH-But	Q1LBV6	Short chain enoyl-CoA hydratase / 3-hydroxyacyl-CoA dehydrogenase
NPKM_2166	2258085 +	2258946 Rmet_5512		4.67	1.53	Op1640f_1	MET-CAH-Prop	Q1LBV5	Enoyl-CoA hydratase/isomerase
NPKM_2167	2258984 +	2260031 Rmet_5513		5.33	1.15	Op1640f_1	NA	Q1LBV4	Transcriptional regulator, AraC family
NPKM_2168	2259707 -	2259896 Rmet_6738		2.33	2.52	Op1641r_2	NA	NA	
NPKM_2169	2259903 -	2260125 Rmet_6739		5.33	1.15	Op1641r_2	NA	NA	
NPKM_2170	2260027 -	2260822 Rmet_5514	cpnA	6.33	0.58	Op1641r_2	NA	Q1LBV3	Short-chain dehydrogenase/reductase SDR
3UTR_566	2260032 +	2260912 Rmet_5513				Op1640f_1			
NPKM_2171	2260858 -	2262298 Rmet_5515		2.67	0.58	Op1641r_1	NA	Q1LBV2	Aldehyde dehydrogenase

NPKM_2172	2262294 -	2263584 Rmet_5516	<i>cyp</i>	1.33	0.58	Op1641r_1	NA	Q1LBV1 Cytochrome P450
NPKM_2173	2263613 -	2264609 Rmet_5517	<i>vanB</i>	1.33	0.58	Op1641r_1	MET-XEN-24D	Q1LBV0 Ferredoxin
5UTR_576	2264610 -	2264620 Rmet_5517	<i>vanB</i>			Op1641r_1		
3UTR_705	2264942 -	2265042 Rmet_5518	<i>etfA</i>			Op1641r_1		
NPKM_2174	2265043 -	2265976 Rmet_5518	<i>etfA</i>	14.00	2.00	Op1641r_1	NA	Q1LBU9 Electron transfer flavoprotein, alpha subunit
NPKM_2175	2265994 -	2266744 Rmet_5519	<i>etfB</i>	13.00	1.73	Op1641r_1	NA	Q1LBU8 Electron transfer flavoprotein beta-subunit
NPKM_2176	2266816 -	2267692 Rmet_5520		9.00	1.00	Op1641r_1	NA	Q1LBU7 MaoC-like dehydratase
NPKM_2177	2267684 -	2268506 Rmet_5521		9.00	1.00	Op1641r_1	MET-CAH-Prop	Q1LBU6 Enoyl-CoA hydratase/isomerase
NPKM_2178	2268502 -	2269540 Rmet_5522		6.33	0.58	Op1641r_1	NA	Q1LBU5 Putative uncharacterized protein
NPKM_2179	2269580 -	2270645 Rmet_5523		8.33	0.58	Op1641r_1	NA	Q1LBU4 Aminoglycoside phosphotransferase
NPKM_2180	2270647 -	2271421 Rmet_5524		17.00	3.61	Op1641r_1	MET-LIP-FASyn	Q1LBU3 Short-chain dehydrogenase/reductase SDR
5UTR_575	2271422 -	2271531 Rmet_5524				Op1641r_1		
5UTR_450	2271530 +	2271578 Rmet_5525				Op1642f_1		
NPKM_2181	2271578 +	2272715 Rmet_5525		3.33	1.53	Op1642f_1	NA	Q1LBU2 L-carnitine dehydratase/bile acid-inducible protein F
3UTR_704	2271928 -	2272770 Rmet_5526				Op1643r_2		
3UTR_567	2272716 +	2273343 Rmet_5525				Op1642f_1		
NPKM_2182	2272771 -	2273137 Rmet_5526		13.33	2.08	Op1643r_2	NA	Q1LBU1 Putative uncharacterized protein
NPKM_2183	2273153 -	2274089 Rmet_5527		10.00	1.00	Op1643r_2	NA	Q1LBU0 Aminoglycoside phosphotransferase
NPKM_2184	2274160 -	2275690 Rmet_5528		14.67	2.08	Op1643r_2	MET-LIP-FAMet	Q1LBT9 AMP-dependent synthetase and ligase
NPKM_2185	2275725 -	2276865 Rmet_5529		16.33	1.53	Op1643r_2	MET-XEN-Benz	Q1LBT8 Acyl-CoA dehydrogenase-like protein
NPKM_2186	2276874 -	2278035 Rmet_5530		18.67	1.15	Op1643r_2	MET-XEN-Benz	Q1LBT7 Acyl-CoA dehydrogenase-like protein
NPKM_2187	2277902 -	2278094 Rmet_6740		9.00	1.00	Op1643r_1	NA	NA
5UTR_451	2278111 +	2278124 Rmet_5531				Op1644f_1		
NPKM_2188	2278124 +	2279036 Rmet_5531		135.33	5.51	Op1644f_1	NA	Q1LBT6 Transcriptional regulator, GntR family
NPKM_2189	2279056 +	2279860 Rmet_5532		137.33	7.09	Op1644f_1	NA	Q1LBT5 Transcriptional regulator, GntR family
3UTR_703	2279687 -	2279859 Rmet_5533				Op1645r_2		
NPKM_2190	2279860 -	2280553 Rmet_5533		12.33	0.58	Op1645r_2	NA	Q1LBT4 Nitroreductase
3UTR_568	2279861 +	2280954 Rmet_5532				Op1644f_1		
NPKM_2191	2280604 -	2281576 Rmet_5534		8.00	2.00	Op1645r_2	MET-EN-Nitrog	Q1LBT3 2-nitropropane dioxygenase, NPD
NPKM_2192	2281670 -	2282792 Rmet_5535		10.00	0.00	Op1645r_2	NA	Q1LBT2 L-carnitine dehydratase/bile acid-inducible protein F
NPKM_2193	2282737 -	2282956 Rmet_6741		4.67	0.58	Op1645r_1	NA	NA
5UTR_452	2282860 +	2282998 Rmet_5536				Op1646f_1		
NPKM_2194	2282998 +	2283577 Rmet_5536		6.00	1.73	Op1646f_1	NA	Q1LBT1 Putative uncharacterized protein
NPKM_2195	2283582 +	2284056 Rmet_5537		8.00	0.00	Op1646f_1	NA	Q1LBT0 MaoC-like dehydratase
3UTR_569	2284057 +	2284442 Rmet_5537				Op1646f_1		
3UTR_702	2284207 -	2284231 Rmet_5538				Op1647r_5		
NPKM_2196	2284232 -	2285387 Rmet_5538		12.67	0.58	Op1647r_5	NA	Q1LBS9 Acyl-CoA dehydrogenase-like protein
5UTR_574	2285388 -	2285417 Rmet_5538				Op1647r_5		
3UTR_701	2285433 -	2285484 Rmet_5539				Op1647r_4		
NPKM_2197	2285485 -	2285911 Rmet_5539		2.67	0.58	Op1647r_4	NA	Q1LBS8 Putative uncharacterized protein
NPKM_2198	2285907 -	2287002 Rmet_5540		3.33	0.58	Op1647r_4	NA	Q1LBS7 Thiolase family protein
5UTR_573	2287003 -	2287100 Rmet_5540				Op1647r_4		
NPKM_2199	2287114 -	2287972 Rmet_5541	<i>tnpB</i>	0.00	0.00	Op1647r_3	NA	NA

NPKM_2200	2288025 -	2288364 Rmet_5542	<i>tnpA</i>	0.00	0.00	Op1647r_3	NA	NA
NPKM_2201	2288448 -	2289714 Rmet_5543	<i>caiB</i>	3.33	0.58	Op1647r_3	NA	Q1LBS4 L-carnitine dehydratase/bile acid-inducible protein F
3UTR_700	2290135 -	2290149 Rmet_5544				Op1647r_2		
NPKM_2202	2290150 -	2291611 Rmet_5544		0.67	0.58	Op1647r_2	NA	Q1LBS3 Aldehyde dehydrogenase
5UTR_572	2291612 -	2291616 Rmet_5544				Op1647r_2		
3UTR_699	2291618 -	2291626 Rmet_5545				Op1647r_2		
NPKM_2203	2291627 -	2292686 Rmet_5545		5.33	1.53	Op1647r_2	NA	Q1LBS2 Alcohol dehydrogenase GroES-like protein
NPKM_2204	2292699 -	2293743 Rmet_5546	<i>vanA</i>	8.67	0.58	Op1647r_2	MET-XEN-24D	Q1LBS1 Rieske (2Fe-2S) region
5UTR_453	2292939 +	2293732 Rmet_6742				Op2098f_1		
NPKM_2205	2293732 +	2293933 Rmet_6742		4.00	1.00	Op2098f_1	NA	NA
NPKM_2206	2293863 -	2294694 Rmet_5547		24.33	2.08	Op1647r_2	NA	Q1LBS0 Transcriptional regulator, LuxR family
3UTR_570	2293934 +	2294258 Rmet_6742				Op2098f_1		
5UTR_454	2294287 +	2294784 Rmet_6744				Op1648f_1		
NPKM_2207	2294644 -	2294824 Rmet_6743		5.67	1.15	Op1647r_1	NA	NA
NPKM_2208	2294784 +	2295045 Rmet_6744		2.00	1.00	Op1648f_1	NA	NA
5UTR_571	2294825 -	2294834 Rmet_6743				Op1647r_1		
5UTR_455	2295146 +	2295180 Rmet_5548				Op1648f_2		
NPKM_2209	2295180 +	2296500 Rmet_5548		8.33	0.58	Op1648f_2	NA	Q1LBR9 Rieske (2Fe-2S) region
NPKM_2210	2296515 +	2297481 Rmet_5549	<i>pobB</i>	8.67	1.15	Op1648f_2	MET-XEN-24D	Q1LBR8 Ferredoxin
NPKM_2211	2297522 +	2298245 Rmet_5550		34.67	1.53	Op1648f_3	NA	Q1LBR7 Transcriptional regulator, GntR family
NPKM_2212	2298290 +	2299259 Rmet_5551	<i>bug</i>	8.33	0.58	Op1648f_3	NA	Q1LBR6 Uncharacterized protein UPF0065
NPKM_2213	2299273 +	2300563 Rmet_5552		8.00	0.00	Op1648f_3	NA	Q1LBR5 L-carnitine dehydratase/bile acid-inducible protein F
NPKM_2214	2300589 +	2301741 Rmet_5553		8.67	0.58	Op1648f_3	NA	Q1LBR4 Putative uncharacterized protein
NPKM_2215	2301737 +	2302211 Rmet_5554		9.33	1.15	Op1648f_3	NA	Q1LBR3 Putative uncharacterized protein
NPKM_2216	2302270 +	2303938 Rmet_5555		5.67	0.58	Op1648f_3	NA	Q1LBR2 Fumarate reductase/succinate dehydrogenase flavoprotein-like protein
NPKM_2217	2303942 +	2305052 Rmet_5556		6.33	0.58	Op1648f_3	NA	Q1LBR1 L-carnitine dehydratase/bile acid-inducible protein F
3UTR_698	2304455 -	2306150 Rmet_5558				Op1649r_1		
NPKM_2218	2305090 +	2305885 Rmet_5557		9.33	0.58	Op1648f_3	MET-CAH-Prop	Q1LBR0 Short chain enoyl-CoA hydratase
3UTR_571	2305886 +	2306403 Rmet_5557				Op1648f_3		
NPKM_2219	2306151 -	2306574 Rmet_5558		344.67	11.72	Op1649r_1	NA	Q1LBQ9 Histone-like DNA-binding protein
5UTR_570	2306575 -	2307363 Rmet_5558				Op1649r_1		
5UTR_456	2307209 +	2307297 Rmet_5559				Op1650f_1		
NPKM_2220	2307297 +	2309700 Rmet_5559		25.67	1.15	Op1650f_1	NA	Q1LBQ8 Putative uncharacterized protein
3UTR_697	2307832 -	2308106 Rmet_6745				Op2099r_1		
NPKM_2221	2308107 -	2308293 Rmet_6745		1.33	1.15	Op2099r_1	NA	NA
5UTR_569	2308294 -	2308307 Rmet_6745				Op2099r_1		
NPKM_2222	2308653 -	2308725 Rmet_6746		4.00	2.00	Op2099r_1	NA	NA
5UTR_568	2308726 -	2308904 Rmet_6746				Op2099r_1		
3UTR_696	2308907 -	2311010 Rmet_5561				Op1651r_1		
NPKM_2223	2309804 +	2310776 Rmet_5560		40.33	0.58	Op1650f_1	NA	Q1LBQ7 Putative uncharacterized protein
3UTR_572	2310777 +	2311694 Rmet_5560				Op1650f_1		
NPKM_2224	2311011 -	2315052 Rmet_5561		47.00	3.61	Op1651r_1	NA	Q1LBQ6 Transcriptional regulator, XRE family
NPKM_2225	2315044 -	2315251 Rmet_6747		317.33	11.24	Op1651r_1	NA	NA

5UTR_457	2315122 +	2315700 Rmet_5563				Op1652f_1		
NPKM_2226	2315251 -	2315566 Rmet_5562	350.00	21.28	Op1651r_1	NA		Q1LBQ5 H-NS family DNA-binding protein
5UTR_567	2315567 -	2315781 Rmet_5562			Op1651r_1			
NPKM_2227	2315700 +	2318079 Rmet_5563	46.67	2.31	Op1652f_1	NA		Q1LBQ4 Putative uncharacterized protein
3UTR_695	2318235 -	2318252 Rmet_5564			Op1653r_2			
NPKM_2228	2318253 -	2318790 Rmet_5564	31.33	2.31	Op1653r_2	NA		Q1LBQ3 Putative uncharacterized protein
5UTR_566	2318791 -	2318812 Rmet_5564			Op1653r_2			
NPKM_2229	2319079 -	2319181 Rmet_6748	1.33	1.53	Op1653r_1	NA		NA
NPKM_2230	2319124 +	2319424 Rmet_5565	13.00	2.65	Op1654f_1	NA		Q1LBQ2 Putative uncharacterized protein
5UTR_565	2319182 -	2319315 Rmet_6748			Op1653r_1			
3UTR_573	2319425 +	2320596 Rmet_5565			Op1654f_1			
3UTR_694	2319627 -	2319687 Rmet_6749			Op1655r_1			
NPKM_2231	2319688 -	2319889 Rmet_6749	6.00	3.46	Op1655r_1	NA		NA
5UTR_564	2319890 -	2320042 Rmet_6749			Op1655r_1			
3UTR_693	2320048 -	2320074 Rmet_5566			Op1655r_1			
NPKM_2232	2320075 -	2320750 Rmet_5566	8.67	1.15	Op1655r_1	NA		Q1LBQ1 Putative uncharacterized protein
NPKM_2233	2320756 -	2321356 Rmet_5567	6.00	1.00	Op1655r_1	NA		Q1LBQ0 Putative uncharacterized protein
5UTR_458	2321136 +	2323220 Rmet_5569			Op1656f_1			
3UTR_692	2321613 -	2321641 Rmet_5568			Op1655r_1			
NPKM_2234	2321642 -	2322293 Rmet_5568	3.00	1.00	Op1655r_1	NA		Q1LBP9 Putative uncharacterized protein
5UTR_563	2322294 -	2322315 Rmet_5568			Op1655r_1			
NPKM_2235	2323220 +	2323928 Rmet_5569	120.67	3.21	Op1656f_1	NA		Q1LBP8 Transcriptional regulator, ArsR family
3UTR_691	2323806 -	2324427 Rmet_5571			Op1657r_2			
NPKM_2236	2323918 +	2324425 Rmet_5570	169.00	12.53	Op1656f_1	NA		Q1LBP7 Putative uncharacterized protein
3UTR_574	2324426 +	2325625 Rmet_5570			Op1656f_1			
NPKM_2237	2324428 -	2325427 Rmet_5571	96.00	3.46	Op1657r_2	NA		Q1LBP6 Transcriptional regulator, LysR family
NPKM_2238	2325780 -	2326728 Rmet_5572	81.33	6.66	Op1657r_2	NA		Q1LBP5 Dyp-type peroxidase
NPKM_2239	2326938 -	2327844 Rmet_5573	15.00	3.00	Op1657r_1	NA		Q1LBP4 Transcriptional regulator, LysR family
5UTR_562	2327845 -	2327875 Rmet_5573			Op1657r_1			
5UTR_459	2327888 +	2328004 Rmet_5574			Op1658f_1			
NPKM_2240	2328004 +	2328997 Rmet_5574	13.67	0.58	Op1658f_1	NA		Q1LBP3 Uncharacterized protein UPF0065
NPKM_2241	2329054 +	2330074 Rmet_5575	12.00	1.00	Op1658f_1	NA		Q1LBP2 Putative uncharacterized protein
NPKM_2242	2330103 +	2331327 Rmet_5576	11.33	1.15	Op1658f_1	NA		Q1LBP1 Aminotransferase, class I and II
3UTR_690	2330979 -	2331335 Rmet_5577			Op1659r_1			
3UTR_575	2331328 +	2331470 Rmet_5576			Op1658f_1			
NPKM_2243	2331336 -	2331660 Rmet_5577	7.67	1.53	Op1659r_1	NA		Q1LBP0 DUF190
5UTR_561	2331661 -	2331760 Rmet_5577			Op1659r_1			
5UTR_460	2331863 +	2331868 Rmet_5578			Op1660f_1			
NPKM_2244	2331868 +	2332135 Rmet_5578	239.00	20.00	Op1660f_1	NA		Q1LBN9 Putative uncharacterized protein
NPKM_2245	2332137 +	2332692 Rmet_5579	208.67	6.81	Op1660f_1	NA		Q1LBN8 Cytochrome B561
NPKM_2248	2332999 +	2334268 Rmet_5580	27.00	2.65	Op1660f_1	MET-EN-Nitrog		Q1LBN7 D-amino acid dehydrogenase small subunit
3UTR_576	2334269 +	2334291 Rmet_5580			Op1660f_1			
3UTR_689	2334316 -	2334330 Rmet_R0086			Op1661r_1			

NPKM_2249	2334331 -	2334418 Rmet_R0086	5.00	2.65	Op1661r_1	NA	NA
NPKM_2250	2334494 -	2336141 Rmet_5581	19.67	2.31	Op1661r_1	NA	Q1LBN6 Diguanylate cyclase (GGDEF domain)
5UTR_461	2335482 +	2336178 Rmet_5582			Op1662f_1		
5UTR_560	2336142 -	2336200 Rmet_5581			Op1661r_1		
NPKM_2251	2336178 +	2336685 Rmet_5582	106.33	6.66	Op1662f_1	NA	Q1LBN5 Putative membrane protein
3UTR_688	2336219 -	2337122 Rmet_5584			Op1663r_2		
NPKM_2252	2336717 +	2337059 Rmet_5583	336.00	19.00	Op1662f_2	NA	Q1LBN4 Putative uncharacterized protein
3UTR_577	2337060 +	2338354 Rmet_5583			Op1662f_2		
NPKM_2253	2337123 -	2337636 Rmet_5584	86.67	1.15	Op1663r_2	NA	Q1LBN3 Putative transmembrane protein
5UTR_559	2337637 -	2337687 Rmet_5584			Op1663r_2		
3UTR_687	2337756 -	2337768 Rmet_5585			Op1663r_1		
NPKM_2254	2337769 -	2339212 Rmet_5585	1.33	0.58	Op1663r_1	NA	Q1LBN2 Major facilitator superfamily MFS_1
5UTR_462	2338368 +	2339210 Rmet_5586			Op1664f_1		
NPKM_2255	2339210 +	2340212 Rmet_5586	14.67	1.15	Op1664f_1	NA	Q1LBN1 Transcriptional regulator, LysR family
5UTR_558	2339213 -	2339293 Rmet_5585			Op1663r_1		
3UTR_686	2340197 -	2340668 Rmet_5588			Op1665r_1		
NPKM_2256	2340262 +	2340649 Rmet_5587	63.67	4.51	Op1664f_2	NA	Q1LBN0 Putative uncharacterized protein
3UTR_578	2340650 +	2341333 Rmet_5587			Op1664f_2		
NPKM_2257	2340669 -	2342274 Rmet_5588	4.00	1.00	Op1665r_1	NA	Q1LBM9 Phospholipase D/Transphosphatidylase
NPKM_2258	2342295 -	2343123 Rmet_5589	10.67	0.58	Op1665r_1	NA	Q1LBM8 MscS Mechanosensitive ion channel
5UTR_557	2343124 -	2343174 Rmet_5589			Op1665r_1		
3UTR_685	2343314 -	2343425 Rmet_5590			Op1665r_1		
NPKM_2259	2343426 -	2344884 Rmet_5590	5.33	0.58	Op1665r_1	NA	Q1LBM7 RND efflux system, outer membrane lipoprotein, NodT
NPKM_2260	2344886 -	2346461 Rmet_5591	4.67	0.58	Op1665r_1	NA	Q1LBM6 Drug resistance transporter EmrB/QacA subfamily
NPKM_2261	2346453 -	2347599 Rmet_5592	11.33	1.15	Op1665r_1	EIP-TRA-Other	Q1LBM5 Secretion protein HlyD
5UTR_556	2347600 -	2347632 Rmet_5592			Op1665r_1		
NPKM_2262	2347706 +	2348408 Rmet_5593	50.00	3.46	Op1666f_1	NA	Q1LBM4 Transcriptional regulator, TetR family
3UTR_579	2348409 +	2348545 Rmet_5593			Op1666f_1		
NPKM_2263	2348831 +	2349329 Rmet_5594	14.67	0.58	Op1666f_1	NA	Q1LBM3 Putative uncharacterized protein
3UTR_580	2349330 +	2349618 Rmet_5594			Op1666f_1		
5UTR_463	2349625 +	2349714 Rmet_5595			Op1666f_1		
NPKM_2264	2349714 +	2350179 Rmet_5595	13.00	2.00	Op1666f_1	NA	Q1LBM2 Kef-type K+ transport system NAD-binding component-related membrane
3UTR_684	2350349 -	2351282 Rmet_5597			Op1667r_3		
NPKM_2265	2350360 +	2351260 Rmet_5596	67.33	2.31	Op1666f_2	NA	Q1LBM1 MltA-interacting MipA
3UTR_581	2351261 +	2351838 Rmet_5596			Op1666f_2		
NPKM_2266	2351283 -	2351997 Rmet_5597	107.33	3.51	Op1667r_3	NA	Q1LBM0 Putative hydrolase of the alpha/beta superfamily
NPKM_2267	2352075 -	2352387 Rmet_5598	14.00	2.00	Op1667r_2	NA	Q1LBL9 Putative uncharacterized protein
NPKM_2268	2352518 -	2352677 Rmet_6750	5.67	1.53	Op1667r_1	NA	NA
5UTR_555	2352678 -	2352729 Rmet_6750			Op1667r_1		
3UTR_683	2352765 -	2352947 Rmet_6751			Op1667r_1		
5UTR_464	2352919 +	2353056 Rmet_5599			Op1668f_1		
NPKM_2269	2352948 -	2353146 Rmet_6751	3.00	1.00	Op1667r_1	NA	NA
NPKM_2270	2353056 +	2354502 Rmet_5599	71.00	9.64	Op1668f_1	MET-EN-Methane	Q1LBL8 Catalase-like protein

NPKM_2271	2354594 +	2355107 Rmet_5600	43.67	5.69	Op1668f_1	NA	Q1LBL7 Ankyrin
3UTR_582	2355108 +	2355964 Rmet_5600			Op1668f_1		
NPKM_2272	2355164 -	2355923 Rmet_5601	142.67	4.62	Op1669r_1	NA	Q1LBL6 Short-chain dehydrogenase/reductase SDR
NPKM_2273	2356032 -	2357124 Rmet_5602	101.00	3.46	Op1669r_1	NA	Q1LBL5 L-threonine ammonia-lyase
5UTR_554	2357125 -	2357531 Rmet_5602			Op1669r_1		
5UTR_465	2357470 +	2357594 Rmet_5603			Op1670f_1		
NPKM_2274	2357594 +	2359364 Rmet_5603	40.00	6.56	Op1670f_1	NA	Q1LBL4 Diguanylate cyclase/phosphodiesterase with PAS/PAC sensor(S)
NPKM_2275	2359363 +	2360806 Rmet_5604	30.67	3.51	Op1670f_1	NA	Q1LBL3 Putative signal transduction protein
3UTR_682	2360792 -	2360824 Rmet_5605			Op1671r_1		
3UTR_583	2360807 +	2361423 Rmet_5604			Op1670f_1		
NPKM_2276	2360825 -	2361476 Rmet_5605	9.33	1.53	Op1671r_1	MET-EN-Nitrog	Q1LBL2 Carbonic anhydrase
5UTR_553	2361477 -	2361513 Rmet_5605			Op1671r_1		
NPKM_2277	2361499 +	2362486 Rmet_5606	7.33	0.58	Op1672f_1	NA	Q1LBL1 Transcriptional regulator, LysR family
3UTR_681	2361797 -	2362453 Rmet_5607			Op1673r_1		
NPKM_2278	2362454 -	2363774 Rmet_5607	8.67	1.15	Op1673r_1	NA	Q1LBL0 Major facilitator superfamily MFS_1
3UTR_584	2362487 +	2362798 Rmet_5606			Op1672f_1		
5UTR_552	2363775 -	2364273 Rmet_5607			Op1673r_1		
5UTR_466	2363916 +	2363923 Rmet_5608			Op1674f_1		
NPKM_2279	2363923 +	2364973 Rmet_5608	9.33	0.58	Op1674f_1	MET-EN-OxPhos	Q1LBK9 Ubiquinol oxidase, subunit II
NPKM_2280	2365054 +	2367058 Rmet_5609	5.00	0.00	Op1674f_1	MET-EN-OxPhos	Q1LBK8 Cytochrome c oxidase, subunit I
3UTR_680	2366428 -	2368149 Rmet_5612			Op1675r_3		
NPKM_2281	2367050 +	2367707 Rmet_5610	6.67	0.58	Op1674f_1	MET-EN-OxPhos	Q1LBK7 Cytochrome c oxidase, subunit III
NPKM_2282	2367703 +	2368132 Rmet_5611	6.33	0.58	Op1674f_1	MET-EN-OxPhos	Q1LBK6 Cytochrome C oxidase subunit IV
3UTR_585	2368133 +	2368354 Rmet_5611			Op1674f_1		
NPKM_2283	2368150 -	2369692 Rmet_5612	46.00	7.81	Op1675r_3	DIV-MOT-Chemotax	Q1LBK5 Methyl-accepting chemotaxis sensory transducer
NPKM_2284	2369904 -	2371203 Rmet_5613	13.33	1.53	Op1675r_2	NA	Q1LBK4 Major facilitator superfamily MFS_1
NPKM_2285	2371309 -	2372080 Rmet_5614	48.00	3.61	Op1675r_2	MET-LIP-GlycPLip	Q1LBK3 Putative CDP-diacylglycerol pyrophosphatase
NPKM_2286	2372101 -	2372335 Rmet_6752	153.67	18.90	Op1675r_2	NA	NA
NPKM_2287	2372291 -	2372681 Rmet_5615	55.33	5.51	Op1675r_1	NA	Q1LBK2 Putative uncharacterized protein
NPKM_2288	2372717 -	2373707 Rmet_5616	80.67	2.31	Op1675r_1	NA	Q1LBK1 Uncharacterized protein UPF0065
5UTR_551	2373708 -	2373720 Rmet_5616			Op1675r_1		
5UTR_467	2373754 +	2373889 Rmet_5617			Op1676f_1		
NPKM_2289	2373889 +	2374951 Rmet_5617	29.00	2.00	Op1676f_1	MET-LIP-Ster	Q1LBK0 Farnesyl-diphosphate farnesyltransferase
3UTR_679	2374815 -	2374970 Rmet_5618			Op1677r_1		
3UTR_586	2374952 +	2375418 Rmet_5617			Op1676f_1		
NPKM_2290	2374971 -	2376042 Rmet_5618	3.67	0.58	Op1677r_1	NA	Q1LBK9 Glycosyl transferase, family 2
NPKM_2291	2376195 -	2377398 Rmet_5619	3.00	0.00	Op1677r_1	NA	Q1LBK8 Collagen triple helix repeat
5UTR_550	2377399 -	2377421 Rmet_5619			Op1677r_1		
5UTR_468	2377400 +	2377609 Rmet_6753			Op2100f_1		
NPKM_2292	2377609 +	2377789 Rmet_6753	6.33	1.15	Op2100f_1	NA	NA
3UTR_587	2377790 +	2377837 Rmet_6753			Op2100f_1		
3UTR_678	2378011 -	2378107 Rmet_5620			Op1677r_1		
NPKM_2293	2378108 -	2378432 Rmet_5620	41.67	4.93	Op1677r_1	NA	Q1LBK7 Putative uncharacterized protein

NPKM_2294	2378560 -	2378698 Rmet_5621		36.33	4.16	Op1677r_1	NA	Q1LBJ6 Putative uncharacterized protein
NPKM_2295	2378789 -	2379536 Rmet_5622		66.33	1.53	Op1677r_1	NA	Q1LBJ5 Putative uncharacterized protein
NPKM_2296	2379634 -	2380030 Rmet_5623		408.67	28.45	Op1677r_1	GIP-PTL-Fold	Q1LBJ4 Peptidyl-prolyl cis-trans isomerase
5UTR_549	2380031 -	2380341 Rmet_5623				Op1677r_1		
5UTR_469	2380176 +	2380201 Rmet_5624				Op1678f_1		
NPKM_2297	2380201 +	2380819 Rmet_5624		41.67	2.08	Op1678f_1	NA	Q1LBJ3 Channel protein, hemolysin III family
3UTR_677	2380356 -	2380833 Rmet_5625				Op1679r_1		
3UTR_588	2380820 +	2381228 Rmet_5624				Op1678f_1		
NPKM_2298	2380834 -	2382082 Rmet_5625		4.33	0.58	Op1679r_1	NA	Q1LBJ2 L-carnitine dehydratase/bile acid-inducible protein F
NPKM_2299	2382097 -	2382895 Rmet_5626		5.00	0.00	Op1679r_1	MET-CAH-Prop	Q1LBJ1 Enoyl-CoA hydratase/isomerase
NPKM_2300	2382891 -	2384418 Rmet_5627	tctA	5.67	0.58	Op1679r_1	NA	Q1LBJ0 Putative uncharacterized protein
NPKM_2301	2384429 -	2384969 Rmet_5628	tctB	7.33	0.58	Op1679r_1	NA	Q1LBI9 Putative uncharacterized protein
NPKM_2302	2385011 -	2386013 Rmet_5629	tctC	10.33	0.58	Op1679r_1	NA	Q1LBI8 Uncharacterized protein UPF0065
NPKM_2303	2386115 -	2387321 Rmet_5630	sgaA	26.67	3.06	Op1679r_1	MET-AA-GlySerThr	Q1LBI7 Aminotransferase, class V
5UTR_548	2387322 -	2387466 Rmet_5630	sgaA			Op1679r_1		
5UTR_470	2387477 +	2387571 Rmet_5631				Op1680f_1		
NPKM_2304	2387571 +	2388261 Rmet_5631		34.33	1.53	Op1680f_1	NA	Q1LBI6 Transcriptional regulator, GntR family
NPKM_2305	2388347 +	2391371 Rmet_5632		17.00	1.00	Op1680f_1	NA	Q1LBI5 FAD linked oxidase-like protein
NPKM_2306	2391457 +	2392393 Rmet_5633	yddG	13.00	1.00	Op1680f_1	NA	Q1LBI4 Putative transmembrane protein
3UTR_676	2392634 -	2392643 Rmet_6754				Op1681r_3		
NPKM_2307	2392641 +	2392977 Rmet_5634		9.33	0.58	Op1680f_1	NA	Q1LBI3 Putative uncharacterized protein
NPKM_2308	2392644 -	2392974 Rmet_6754		3.67	1.53	Op1681r_3	NA	NA
3UTR_589	2392978 +	2393291 Rmet_5634				Op1680f_1		
NPKM_2309	2393096 -	2395535 Rmet_5635		99.00	3.61	Op1681r_3	Met-SecMetab	Q1LBI2 Peptidase S45, penicillin amidase
NPKM_2310	2395662 -	2397264 Rmet_5636		11.33	1.15	Op1681r_2	MET-EN-Sulf	Q1LBI1 Flavodoxin/nitric oxide synthase
NPKM_2311	2397260 -	2398274 Rmet_5637	apbE	28.00	1.73	Op1681r_2	MET-COF-Thia	Q1LBI0 ApbE-like lipoprotein
NPKM_2312	2398296 -	2399130 Rmet_5638		33.00	1.00	Op1681r_2	NA	Q1LBH9 Putative uncharacterized protein
NPKM_2313	2399181 -	2399703 Rmet_5639		21.33	0.58	Op1681r_2	NA	Q1LBH8 Putative uncharacterized protein
NPKM_2314	2399730 -	2400402 Rmet_5640		7.67	1.15	Op1681r_1	NA	Q1LBH7 PepSY-associated TM helix
5UTR_547	2400403 -	2400473 Rmet_5640				Op1681r_1		
NPKM_2315	2400458 +	2400764 Rmet_6755		0.00	0.00	Op1682f_1	NA	NA
5UTR_471	2400772 +	2400777 Rmet_5641				Op1682f_2		
NPKM_2316	2400777 +	2402337 Rmet_5641		4.00	0.00	Op1682f_2	DIV-MOT-Chemotax	Q1LBH6 Methyl-accepting chemotaxis sensory transducer
3UTR_675	2401936 -	2402524 Rmet_5642	fliD3			Op1683r_3		
3UTR_590	2402338 +	2402344 Rmet_5641				Op1682f_2		
NPKM_2317	2402525 -	2403989 Rmet_5642	fliD3	168.33	20.65	Op1683r_3	DIV-MOT-Flagel	Q1LBH5 Flagellar hook-associated 2-like protein
5UTR_546	2403990 -	2404047 Rmet_5642	fliD3			Op1683r_3		
3UTR_674	2404051 -	2404199 Rmet_5643				Op1683r_2		
NPKM_2318	2404200 -	2404899 Rmet_5643		35.00	2.00	Op1683r_2	NA	Q1LBH4 Transcriptional regulator, TetR family
NPKM_2319	2404915 -	2406352 Rmet_5644	carX	4.33	0.58	Op1683r_1	NA	Q1LBH3 Carotenoid oxygenase
5UTR_472	2406520 +	2406564 Rmet_5645	adh			Op1684f_1		
NPKM_2320	2406564 +	2407638 Rmet_5645	adh	21.33	1.53	Op1684f_1	NA	Q1LBH2 Alcohol dehydrogenase, zinc-binding
3UTR_591	2407639 +	2407705 Rmet_5645	adh			Op1684f_1		

NPKM_2321	2407830 +	2408526 Rmet_5646		0.33	0.58	Op1684f_1	NA	Q1LBH1 Transcriptional regulator, LuxR family
3UTR_673	2407931 -	2408570 Rmet_5647	<i>uspA15</i>			Op1685r_1		
3UTR_592	2408527 +	2408533 Rmet_5646				Op1684f_1		
NPKM_2322	2408571 -	2409093 Rmet_5647	<i>uspA15</i>	7.00	1.00	Op1685r_1	NA	Q1LBH0 UspA
5UTR_545	2409094 -	2409123 Rmet_5647	<i>uspA15</i>			Op1685r_1		
5UTR_473	2409290 +	2409329 Rmet_5648				Op1686f_1		
NPKM_2323	2409329 +	2409752 Rmet_5648		10.67	1.53	Op1686f_1	NA	Q1LBG9 Transcriptional regulator, AsnC family
3UTR_672	2409634 -	2409770 Rmet_5649				Op1687r_1		
3UTR_593	2409753 +	2410428 Rmet_5648				Op1686f_1		
NPKM_2324	2409771 -	2410209 Rmet_5649		8.67	0.58	Op1687r_1	NA	Q1LBG8 Putative uncharacterized protein
5UTR_544	2410210 -	2410365 Rmet_5649				Op1687r_1		
5UTR_474	2410463 +	2410601 Rmet_5650				Op1688f_1		
NPKM_2325	2410601 +	2410907 Rmet_5650		2.00	1.00	Op1688f_1	NA	Q1LBG7 Putative uncharacterized protein
NPKM_2326	2411083 +	2411290 Rmet_5651		1.00	1.00	Op1688f_1	NA	Q1LBG6 Putative uncharacterized protein
NPKM_2327	2411313 +	2411535 Rmet_6756		0.00	0.00	Op1688f_1	NA	NA
3UTR_594	2411536 +	2411573 Rmet_6756				Op1688f_1		
5UTR_475	2411600 +	2411734 Rmet_5652				Op1688f_2		
NPKM_2328	2411734 +	2412217 Rmet_5652		4.00	1.00	Op1688f_2	NA	Q1LBG5 Putative uncharacterized protein
NPKM_2329	2412222 +	2413764 Rmet_5653		4.33	0.58	Op1688f_2	NA	Q1LBG4 Putative uncharacterized protein
3UTR_595	2413765 +	2413784 Rmet_5653				Op1688f_2		
5UTR_476	2413926 +	2413941 Rmet_5654				Op1688f_3		
NPKM_2330	2413941 +	2414331 Rmet_5654		17.00	1.00	Op1688f_3	NA	Q1LBG3 Putative dehydrogenase
3UTR_671	2414422 -	2414776 Rmet_5656				Op1689r_1		
NPKM_2331	2414432 +	2414765 Rmet_5655		36.67	2.89	Op1688f_4	NA	Q1LBG2 Putative uncharacterized protein
3UTR_596	2414766 +	2415345 Rmet_5655				Op1688f_4		
NPKM_2332	2414777 -	2415254 Rmet_5656		3.33	0.58	Op1689r_1	NA	Q1LBG1 Putative uncharacterized protein
NPKM_2333	2415373 -	2415598 Rmet_6757		2.00	1.00	Op1689r_1	NA	NA
5UTR_477	2415555 +	2415563 Rmet_5657				Op1690f_1		
NPKM_2334	2415563 +	2416817 Rmet_5657		18.00	1.73	Op1690f_1	GIP-PTL-Fold	Q1LBG0 Putative heat shock protein
5UTR_543	2415599 -	2415840 Rmet_6757				Op1689r_1		
3UTR_670	2416206 -	2416840 Rmet_5658				Op1691r_2		
3UTR_597	2416818 +	2417184 Rmet_5657				Op1690f_1		
NPKM_2335	2416841 -	2418029 Rmet_5658		8.00	1.00	Op1691r_2	NA	Q1LBF9 Diguanylate cyclase
NPKM_2336	2418077 -	2418611 Rmet_5659		22.00	2.00	Op1691r_2	NA	Q1LBF8 Isochorismatase hydrolase
NPKM_2337	2418766 -	2421286 Rmet_5660		5.33	0.58	Op1691r_1	NA	Q1LBF7 Diguanylate cyclase/phosphodiesterase with PAS/PAC sensor(S)
NPKM_2338	2421460 -	2421826 Rmet_5661		10.00	2.65	Op1691r_1	NA	Q1LBF6 Putative uncharacterized protein
5UTR_478	2421785 +	2421898 Rmet_5662				Op1692f_1		
NPKM_2339	2421898 +	2422240 Rmet_5662		34.00	5.57	Op1692f_1	NA	Q1LBF5 Putative uncharacterized protein
3UTR_598	2422241 +	2422720 Rmet_5662				Op1692f_1		
NPKM_2340	2422289 -	2423357 Rmet_5663	<i>pstS</i>	25.33	1.53	Op1693r_3	EIP-TRA-ABC	Q1LBF4 Periplasmic phosphate binding protein
NPKM_2341	2423289 -	2423472 Rmet_6758		6.67	1.53	Op1693r_2	NA	NA
NPKM_2342	2423547 -	2424045 Rmet_5664		24.67	4.73	Op1693r_2	NA	Q1LBF3 Putative uncharacterized protein
NPKM_2343	2424213 -	2425188 Rmet_5665		8.00	1.00	Op1693r_1	NA	Q1LBF2 NmrA-like protein

NPKM_2344	2425086 +	2425281 Rmet_6759		0.67	0.58	Op1694f_1	NA	NA
NPKM_2345	2425304 +	2426225 Rmet_5666		8.33	0.58	Op1694f_2	NA	Q1LBF1 Transcriptional regulator, LysR family
3UTR_599	2426226 +	2426419 Rmet_5666				Op1694f_2		
5UTR_479	2426430 +	2426486 Rmet_5667				Op1694f_3		
NPKM_2346	2426486 +	2426867 Rmet_5667		29.00	5.00	Op1694f_3	NA	Q1LBF0 Putative uncharacterized protein
3UTR_669	2426784 -	2426896 Rmet_5668	<i>copD2</i>			Op1695r_2		
3UTR_600	2426868 +	2427644 Rmet_5667				Op1694f_3		
NPKM_2347	2426897 -	2427797 Rmet_5668	<i>copD2</i>	2.67	0.58	Op1695r_2	EIP-TRA-Ion	Q1LBE9 Copper resistance D
NPKM_2348	2427815 -	2428202 Rmet_5669	<i>copC2</i>	4.67	1.15	Op1695r_2	NA	Q1LBE8 Copper resistance protein CopC
NPKM_2349	2428240 -	2429323 Rmet_5670	<i>copB2</i>	1.67	0.58	Op1695r_1	NA	Q1LBE7 Copper resistance B
NPKM_2350	2429319 -	2431137 Rmet_5671	<i>copA2</i>	3.33	0.58	Op1695r_1	NA	Q1LBE6 Copper-resistance protein CopA
5UTR_542	2431138 -	2431170 Rmet_5671	<i>copA2</i>			Op1695r_1		
5UTR_480	2431232 +	2431332 Rmet_5672	<i>copR2</i>			Op1696f_1		
NPKM_2351	2431332 +	2432019 Rmet_5672	<i>copR2</i>	8.00	1.00	Op1696f_1	EIP-SIG-2Comp	Q1LBE5 Two component heavy metal response transcriptional regulator, winged he
NPKM_2352	2432018 +	2433407 Rmet_5673	<i>copS2</i>	6.33	0.58	Op1696f_1	EIP-SIG-2Comp	Q1LBE4 Sensor protein
3UTR_668	2432366 -	2433406 Rmet_5674				Op1697r_2		
NPKM_2353	2433407 -	2433839 Rmet_5674		24.00	0.00	Op1697r_2	NA	Q1LBE3 Putative uncharacterized protein
3UTR_601	2433408 +	2433616 Rmet_5673	<i>copS2</i>			Op1696f_1		
NPKM_2354	2433840 -	2434278 Rmet_5675		24.33	2.52	Op1697r_2	NA	Q1LBE2 Putative uncharacterized protein
NPKM_2355	2434287 -	2434608 Rmet_5676		23.67	3.21	Op1697r_2	NA	Q1LBE1 Transcriptional regulator, ArsR family
5UTR_541	2434609 -	2434637 Rmet_5676				Op1697r_2		
3UTR_667	2434730 -	2434740 Rmet_5677	<i>nimC</i>			Op1697r_2		
NPKM_2356	2434741 -	2436001 Rmet_5677	<i>nimC</i>	22.67	1.53	Op1697r_2	NA	Q1LBE0 Putative uncharacterized protein
NPKM_2357	2435997 -	2437095 Rmet_5678	<i>nimA1</i>	44.67	0.58	Op1697r_2	EIP-TRA-Ion	Q1LBD9 Heavy metal efflux pump CzcA
NPKM_2358	2437106 -	2438000 Rmet_5679	<i>tnpB</i>	0.00	0.00	Op1697r_1	NA	NA
NPKM_2359	2437996 -	2438293 Rmet_5680	<i>tnpA</i>	0.00	0.00	Op1697r_1	NA	NA
NPKM_2360	2438320 -	2440396 Rmet_5681	<i>nimA2</i>	22.00	1.00	Op1697r_1	EIP-TRA-Ion	Q1LBD6 Acriflavin resistance protein
NPKM_2361	2440395 -	2441496 Rmet_5682	<i>nimB</i>	33.33	2.31	Op1697r_1	EIP-TRA-Ion	Q1LBD5 Secretion protein HlyD
NPKM_2362	2441583 -	2442033 Rmet_5683		79.67	8.08	Op1697r_1	NA	Q1LBD4 Putative uncharacterized protein
5UTR_540	2442034 -	2442164 Rmet_5683				Op1697r_1		
5UTR_481	2442254 +	2442330 Rmet_5684	<i>pilE</i>			Op1698f_1		
NPKM_2363	2442330 +	2442834 Rmet_5684	<i>pilE</i>	106.33	8.50	Op1698f_1	GIP-PTL-T2S	Q1LBD3 Pilus assembly protein PilE
NPKM_2364	2442837 +	2443332 Rmet_5685	<i>fimT</i>	52.67	1.53	Op1698f_1	NA	Q1LBD2 Pilus assembly protein FimT
NPKM_2365	2443331 +	2443940 Rmet_5686	<i>pilV</i>	58.00	4.58	Op1698f_1	GIP-PTL-T2S	Q1LBD1 Tfp pilus assembly protein PilV-like protein
NPKM_2366	2443936 +	2444980 Rmet_5687	<i>pilW</i>	44.33	4.51	Op1698f_1	GIP-PTL-T2S	Q1LBD0 Type 4 fimbrial biogenesis pilw-related protein transmembrane
NPKM_2367	2444976 +	2445522 Rmet_5688		54.33	7.51	Op1698f_1	NA	Q1LBC9 Putative transmembrane protein
NPKM_2368	2445567 +	2448876 Rmet_5689	<i>pilY1</i>	75.00	8.00	Op1698f_1	GIP-PTL-T2S	Q1LBC8 Putative type 4 fimbrial biogenesis pily1-related protein signal peptide
NPKM_2369	2448981 +	2450175 Rmet_5690		47.33	7.23	Op1698f_1	NA	Q1LBC7 Putative lipoprotein
3UTR_602	2450176 +	2450533 Rmet_5690				Op1698f_1		
3UTR_666	2450259 -	2450326 Rmet_5691				Op1699r_1		
NPKM_2370	2450327 -	2451101 Rmet_5691		2.00	0.00	Op1699r_1	NA	Q1LBC6 Putative uncharacterized protein
5UTR_539	2451102 -	2451112 Rmet_5691				Op1699r_1		
5UTR_482	2451151 +	2451190 Rmet_5692				Op1700f_1		

NPKM_2371	2451190 +	2452411 Rmet_5692		17.00	1.00	Op1700f_1	NA	Q1LBC5 Putative uncharacterized protein
NPKM_2372	2452440 +	2453079 Rmet_5693		26.33	1.53	Op1700f_1	NA	Q1LBC4 Putative uncharacterized protein
3UTR_665	2452721 -	2453138 Rmet_5694				Op1701r_1		
3UTR_603	2453080 +	2453588 Rmet_5693				Op1700f_1		
NPKM_2373	2453139 -	2453781 Rmet_5694		7.00	0.00	Op1701r_1	NA	Q1LBC3 Putative uncharacterized protein
5UTR_483	2453628 +	2453823 Rmet_5695				Op1702f_1		
5UTR_538	2453782 -	2453800 Rmet_5694				Op1701r_1		
NPKM_2374	2453823 +	2454699 Rmet_5695		30.67	3.51	Op1702f_1	NA	Q1LBC2 Beta-lactamase-like protein
NPKM_2375	2454748 +	2455168 Rmet_5696	bug	25.00	1.00	Op1702f_1	NA	Q1LBC1 Putative uncharacterized protein
3UTR_604	2455169 +	2455463 Rmet_5696	bug			Op1702f_1		
3UTR_664	2455203 -	2455297 Rmet_5697				Op1703r_1		
NPKM_2376	2455298 -	2455607 Rmet_5697		2.67	0.58	Op1703r_1	NA	Q1LBC0 Putative uncharacterized protein
5UTR_537	2455608 -	2455646 Rmet_5697				Op1703r_1		
NPKM_2377	2455723 +	2456119 Rmet_6760		2.00	1.00	Op2101f_1	NA	NA
3UTR_663	2456031 -	2456077 Rmet_6761				Op2102r_1		
NPKM_2378	2456078 -	2456336 Rmet_6761		2.33	0.58	Op2102r_1	NA	NA
3UTR_605	2456120 +	2456419 Rmet_6760				Op2101f_1		
5UTR_536	2456337 -	2456420 Rmet_6761				Op2102r_1		
5UTR_484	2456679 +	2456726 Rmet_5698				Op1704f_1		
NPKM_2379	2456726 +	2456969 Rmet_5698		1.67	0.58	Op1704f_1	NA	Q1LBB9 Putative uncharacterized protein
3UTR_662	2457047 -	2457091 Rmet_5699				Op1705r_2		
NPKM_2380	2457092 -	2458436 Rmet_5699		1.67	0.58	Op1705r_2	NA	Q1LBB8 Putative uncharacterized protein
5UTR_535	2458437 -	2458439 Rmet_5699				Op1705r_2		
3UTR_661	2458441 -	2458456 Rmet_5700				Op1705r_2		
NPKM_2381	2458457 -	2459138 Rmet_5700		1.00	0.00	Op1705r_2	NA	Q1LBB7 Putative uncharacterized protein
NPKM_2382	2459211 -	2460285 Rmet_5701		1.00	0.00	Op1705r_2	NA	Q1LBB6 Putative uncharacterized protein
NPKM_2383	2460275 -	2461430 Rmet_5702		0.00	0.00	Op1705r_1	NA	Q1LBB5 Putative uncharacterized protein
3UTR_660	2461565 -	2461570 Rmet_5703				Op1705r_1		
NPKM_2384	2461571 -	2462486 Rmet_5703		1.00	0.00	Op1705r_1	NA	Q1LBB4 Two component transcriptional regulator, winged helix family
5UTR_534	2462487 -	2462564 Rmet_5703				Op1705r_1		
NPKM_2385	2462526 +	2462847 Rmet_5704		0.67	0.58	Op1706f_1	NA	Q1LBB3 Putative uncharacterized protein
3UTR_606	2462848 +	2462894 Rmet_5704				Op1706f_1		
5UTR_485	2463032 +	2463180 Rmet_5705	aqpZ			Op1706f_2		
NPKM_2386	2463180 +	2463885 Rmet_5705	aqpZ	2.00	0.00	Op1706f_2	EIP-TRA-Pores	Q1LBB2 MIP family channel proteins
NPKM_2387	2463901 +	2464282 Rmet_5706		0.67	0.58	Op1706f_2	NA	Q1LBB1 Putative uncharacterized protein
5UTR_486	2464297 +	2464303 Rmet_6762				Op1706f_2		
NPKM_2388	2464303 +	2464486 Rmet_6762		0.00	0.00	Op1706f_2	NA	NA
NPKM_2389	2464562 +	2465396 Rmet_5707		1.00	1.00	Op1706f_3	NA	Q1LBB0 Two component transcriptional regulator, winged helix family
3UTR_659	2465587 -	2465589 Rmet_6763				Op1707r_1		
NPKM_2390	2465590 -	2465665 Rmet_6763		2.67	3.06	Op1707r_1	NA	NA
NPKM_2391	2465646 -	2466336 Rmet_5708		2.00	1.00	Op1707r_1	NA	Q1LBA9 SmpA/OmlA
5UTR_533	2466337 -	2466476 Rmet_5708				Op1707r_1		
NPKM_2392	2466519 -	2466780 Rmet_5709		1.67	0.58	Op1707r_1	NA	Q1LBA8 Putative uncharacterized protein

5UTR_532	2466781 -	2467627 Rmet_5709				Op1707r_1		
5UTR_487	2467148 +	2467213 Rmet_5710	bvgS1			Op1708f_1		
NPKM_2393	2467213 +	2470336 Rmet_5710	bvgS1	1.00	0.00	Op1708f_1	EIP-SIG-2Comp	Q1LBA7 Sensor protein
3UTR_607	2470337 +	2470393 Rmet_5710	bvgS1			Op1708f_1		
NPKM_2394	2470519 +	2471986 Rmet_5711		0.33	0.58	Op1708f_1	NA	Q1LBA6 Tetratricopeptide TPR_2
3UTR_658	2471206 -	2472277 Rmet_5713				Op1709r_2		
NPKM_2395	2472012 +	2472243 Rmet_5712		0.33	0.58	Op1708f_1	NA	Q1LBA5 TPR repeat protein
NPKM_2396	2472278 -	2472953 Rmet_5713		34.33	2.31	Op1709r_2	NA	Q1LBA4 Hpt domain protein
NPKM_2397	2472967 -	2473600 Rmet_5714	bvgA	44.33	3.79	Op1709r_2	EIP-SIG-2Comp	Q1LBA3 Two component transcriptional regulator, LuxR family
5UTR_488	2473465 +	2474397 Rmet_5716				Op1710f_1		
5UTR_531	2473601 -	2473677 Rmet_5714	bvgA			Op1709r_2		
3UTR_657	2473892 -	2473894 Rmet_5715				Op1709r_1		
NPKM_2398	2473895 -	2474213 Rmet_5715		2.33	0.58	Op1709r_1	NA	Q1LBA2 Putative uncharacterized protein
5UTR_530	2474214 -	2474510 Rmet_5715				Op1709r_1		
NPKM_2399	2474397 +	2475189 Rmet_5716		9.33	0.58	Op1710f_1	NA	Q1LBA1 Putative uncharacterized protein
3UTR_608	2475190 +	2475244 Rmet_5716				Op1710f_1		
3UTR_656	2475192 -	2475243 Rmet_5717				Op1711r_1		
NPKM_2400	2475244 -	2475805 Rmet_5717		1.00	1.00	Op1711r_1	NA	Q1LBA0 Putative serine protease protein
NPKM_2401	2475822 +	2476851 Rmet_5718	tnpA	0.00	0.00	Op2103f_1	NA	NA
NPKM_2402	2476839 -	2477874 Rmet_5719		2.00	0.00	Op1713r_1	NA	Q1LB98 Peptidase S8 and S53, subtilisin, kexin, sedolisin
3UTR_655	2477913 -	2477936 Rmet_5720				Op1713r_1		
NPKM_2403	2477937 -	2478408 Rmet_5720		2.67	0.58	Op1713r_1	NA	Q1LB97 Putative uncharacterized protein
3UTR_654	2478551 -	2478610 Rmet_5721				Op1713r_1		
NPKM_2404	2478611 -	2479670 Rmet_5721		3.67	1.15	Op1713r_1	NA	Q1LB96 Porin, Gram-negative type
NPKM_2405	2480241 +	2480667 Rmet_5722		1.33	0.58	Op1714f_1	NA	Q1LB95 Transcriptional regulator, XRE family
5UTR_489	2480715 +	2480728 Rmet_5723				Op1714f_1		
NPKM_2406	2480728 +	2481094 Rmet_5723		0.33	0.58	Op1714f_1	NA	Q1LB94 Putative uncharacterized protein
3UTR_609	2481095 +	2481143 Rmet_5723				Op1714f_1		
5UTR_490	2481247 +	2481278 Rmet_5724	bvgS2			Op1714f_2		
NPKM_2407	2481278 +	2483633 Rmet_5724	bvgS2	8.33	1.15	Op1714f_2	NA	Q1LB93 Sensor protein
3UTR_653	2483414 -	2483906 Rmet_5725				Op1715r_3		
3UTR_610	2483634 +	2484134 Rmet_5724	bvgS2			Op1714f_2		
NPKM_2408	2483907 -	2484897 Rmet_5725		3.33	0.58	Op1715r_3	NA	Q1LB92 Putative uncharacterized protein
5UTR_529	2484898 -	2484934 Rmet_5725				Op1715r_3		
3UTR_652	2485002 -	2485036 Rmet_5726	cat			Op1715r_3		
NPKM_2409	2485037 -	2485763 Rmet_5726	cat	2.33	0.58	Op1715r_3	NA	Q1LB91 Transferase hexapeptide repeat
NPKM_2410	2485776 -	2487321 Rmet_5727		2.00	0.00	Op1715r_3	NA	Q1LB90 Putative uncharacterized protein
NPKM_2411	2487302 -	2488301 Rmet_5728		1.33	0.58	Op1715r_3	NA	Q1LB89 Glycosyl transferase, group 1
NPKM_2412	2488302 -	2490123 Rmet_5729	kpsD	0.33	0.58	Op1715r_2	NA	Q1LB88 Polysaccharide export protein
NPKM_2413	2490133 -	2491240 Rmet_5730	kpsE	0.33	0.58	Op1715r_2	NA	Q1LB87 Chain length determinant protein
NPKM_2414	2491236 -	2491902 Rmet_5731	kpsT	0.00	0.00	Op1715r_1	NA	Q1LB86 ABC transporter related
NPKM_2415	2491898 -	2492807 Rmet_5732	kpsM	0.00	0.00	Op1715r_1	NA	Q1LB85 ABC-type polysaccharide/polyol phosphate export systems permease comp
5UTR_491	2492620 +	2493001 Rmet_6764				Op1716f_1		

NPKM_2416	2493001 +	2493193 Rmet_6764		3.33	1.53	Op1716f_1	NA	NA
NPKM_2417	2493268 +	2494108 Rmet_5733	<i>kdsA</i>	3.33	0.58	Op1716f_1	MET-GLYC-LPS	Q1LB84 2-dehydro-3-deoxyphosphooctonate aldolase
NPKM_2418	2494107 +	2494851 Rmet_5734	<i>kdsB</i>	2.00	0.00	Op1716f_1	MET-GLYC-LPS	Q1LB83 3-deoxy-D-manno-octulosonate cytidyltransferase
NPKM_2419	2494890 +	2495853 Rmet_5735	<i>kpsF</i>	5.00	1.00	Op1716f_2	NA	Q1LB82 KpsF/GutQ family protein
NPKM_2420	2495903 +	2497952 Rmet_5736	<i>kpsC</i>	3.00	1.00	Op1716f_2	NA	Q1LB81 Capsule polysaccharide biosynthesis
NPKM_2421	2497957 +	2499343 Rmet_5737	<i>kpsS</i>	2.00	0.00	Op1716f_2	NA	Q1LB80 Capsule polysaccharide biosynthesis
3UTR_611	2499344 +	2499437 Rmet_5737	<i>kpsS</i>			Op1716f_2		
5UTR_492	2500270 +	2500427 Rmet_5738				Op1716f_2		
NPKM_2422	2500427 +	2501039 Rmet_5738		1.33	0.58	Op1716f_2	NA	Q1LB79 Putative uncharacterized protein
5UTR_493	2501159 +	2501170 Rmet_5739				Op1716f_2		
NPKM_2423	2501170 +	2501518 Rmet_5739		2.33	0.58	Op1716f_2	NA	Q1LB78 Putative uncharacterized protein
NPKM_2424	2501523 +	2501781 Rmet_5740		2.33	0.58	Op1716f_2	NA	Q1LB77 Putative uncharacterized protein
3UTR_651	2501573 -	2501757 Rmet_5741				Op1717r_1		
NPKM_2425	2501758 -	2503453 Rmet_5741		2.67	0.58	Op1717r_1	NA	Q1LB76 Peptidase MprA. Serine peptidase. MEROPS family S08A
3UTR_612	2501782 +	2501887 Rmet_5740				Op1716f_2		
NPKM_2426	2503778 -	2504045 Rmet_5742		31.67	2.31	Op1717r_1	NA	Q1LB75 Putative uncharacterized protein
NPKM_2427	2504147 -	2505851 Rmet_5743		33.33	1.53	Op1717r_1	MET-CAH-FbP	Q1LB74 AMP-dependent synthetase and ligase
5UTR_528	2505852 -	2506285 Rmet_5743				Op1717r_1		
5UTR_494	2505967 +	2506047 Rmet_5744				Op1718f_1		
NPKM_2428	2506047 +	2506476 Rmet_5744		2.33	0.58	Op1718f_1	NA	Q1LB73 Putative uncharacterized protein
NPKM_2429	2506516 +	2507059 Rmet_5745		17.00	1.73	Op1718f_2	NA	Q1LB72 Putative uncharacterized protein
3UTR_650	2506561 -	2508018 Rmet_5748				Op1719r_1		
NPKM_2430	2507055 -	2507529 Rmet_5746	<i>fur</i>	9.33	2.08	Op1718f_2	NA	Q1LB71 Ferric uptake regulator, Fur family
NPKM_2431	2507649 +	2508006 Rmet_5747		11.00	1.00	Op1718f_2	NA	Q1LB70 Putative membrane protein
3UTR_613	2508007 +	2508621 Rmet_5747				Op1718f_2		
NPKM_2432	2508019 -	2508931 Rmet_5748		48.67	0.58	Op1719r_1	NA	Q1LB69 Putative uncharacterized protein
NPKM_2433	2508966 -	2509212 Rmet_6765		39.67	4.16	Op1719r_1	NA	NA
5UTR_495	2509416 +	2509419 Rmet_5749				Op1720f_1		
NPKM_2434	2509419 +	2509803 Rmet_5749		68.33	6.51	Op1720f_1	NA	Q1LB68 Transcriptional regulator, PadR family
3UTR_614	2509804 +	2510014 Rmet_5749				Op1720f_1		
NPKM_2435	2509983 -	2511729 Rmet_5750		36.33	1.15	Op1721r_1	NA	Q1LB67 Diguanylate cyclase/phosphodiesterase
5UTR_496	2511652 +	2511747 Rmet_5751				Op1722f_1		
5UTR_527	2511730 -	2511936 Rmet_5750				Op1721r_1		
NPKM_2436	2511747 +	2513736 Rmet_5751		15.67	1.53	Op1722f_1	NA	Q1LB66 Diguanylate cyclase (GGDEF domain) with PAS/PAC sensor
3UTR_649	2513000 -	2513816 Rmet_5752				Op1723r_1		
3UTR_615	2513737 +	2514030 Rmet_5751				Op1722f_1		
NPKM_2437	2513817 -	2514273 Rmet_5752		238.67	6.11	Op1723r_1	NA	Q1LB65 Putative uncharacterized protein
5UTR_526	2514274 -	2514549 Rmet_5752				Op1723r_1		
NPKM_2438	2514399 +	2514750 Rmet_5753		35.00	2.00	Op1724f_1	NA	Q1LB64 Putative uncharacterized protein
NPKM_2439	2514915 +	2515212 Rmet_5754	<i>fumCa</i>	64.33	3.51	Op1724f_1	NA	Q1LB63 Fumarate hydratase, class II
NPKM_2440	2515200 -	2516229 Rmet_5755	<i>tnpA</i>	0.00	0.00	Op2104r_1	NA	NA
3UTR_616	2515213 +	2515219 Rmet_5754	<i>fumCa</i>			Op1724f_1		
5UTR_497	2516232 +	2516246 Rmet_5756	<i>fumC</i>			Op1726f_1		

NPKM_2441	2516246 +	2517425 Rmet_5756	<i>fumC</i>	2.33	0.58	Op1726f_1	MET-CAH-TCA	Q1LB61 Fumarase
3UTR_617	2517426 +	2517476 Rmet_5756	<i>fumC</i>			Op1726f_1		
3UTR_648	2517519 -	2517539 Rmet_5757				Op1727r_1		
NPKM_2442	2517540 -	2518704 Rmet_5757		4.00	1.00	Op1727r_1	NA	Q1LB60 Porin, gram-negative type
3UTR_647	2518840 -	2518929 Rmet_5758				Op1727r_1		
NPKM_2443	2518930 -	2520262 Rmet_5758		2.33	0.58	Op1727r_1	NA	Q1LB59 Major facilitator superfamily MFS_1
5UTR_525	2520263 -	2520305 Rmet_5758				Op1727r_1		
NPKM_2444	2520311 -	2521421 Rmet_5759		2.00	0.00	Op1727r_1	NA	Q1LB58 Putative uncharacterized protein
5UTR_524	2521422 -	2521431 Rmet_5759				Op1727r_1		
NPKM_2445	2521433 -	2522237 Rmet_5760		1.00	1.00	Op1727r_1	NA	Q1LB57 Peptidase C26
NPKM_2446	2522353 +	2523301 Rmet_5761		11.00	1.00	Op1728f_1	NA	Q1LB56 Transcriptional regulator, LysR family
NPKM_2447	2523454 +	2523991 Rmet_5762		27.67	0.58	Op1728f_2	NA	Q1LB55 Putative uncharacterized protein
3UTR_646	2523896 -	2524524 Rmet_5764				Op1729r_1		
NPKM_2448	2523987 +	2524494 Rmet_5763		14.33	1.53	Op1728f_2	NA	Q1LB54 Putative uncharacterized protein
3UTR_618	2524495 +	2524859 Rmet_5763				Op1728f_2		
NPKM_2449	2524525 -	2524969 Rmet_5764		20.00	1.73	Op1729r_1	NA	Q1LB53 Putative uncharacterized protein
5UTR_498	2525054 +	2525087 Rmet_5765				Op1730f_1		
NPKM_2450	2525087 +	2525516 Rmet_5765		4.67	0.58	Op1730f_1	NA	Q1LB52 Putative uncharacterized protein
3UTR_619	2525517 +	2525528 Rmet_5765				Op1730f_1		
NPKM_2451	2525566 -	2525785 Rmet_6766		33.00	5.57	Op2105r_1	NA	NA
5UTR_499	2525572 +	2525606 Rmet_5766				Op1730f_1		
NPKM_2452	2525606 +	2525864 Rmet_5766		0.67	1.15	Op1730f_1	NA	Q1LB51 Putative uncharacterized protein
5UTR_523	2525786 -	2525829 Rmet_6766				Op2105r_1		
3UTR_645	2525833 -	2525990 Rmet_5767				Op1731r_1		
3UTR_620	2525865 +	2525904 Rmet_5766				Op1730f_1		
NPKM_2453	2525991 -	2526753 Rmet_5767		18.00	0.00	Op1731r_1	NA	Q1LB50 Transcriptional regulator, Crp/Fnr family
5UTR_500	2526780 +	2526842 Rmet_5768				Op1732f_1		
NPKM_2454	2526842 +	2528477 Rmet_5768		11.67	0.58	Op1732f_1	MET-LIP-FASyn	Q1LB49 AMP-dependent synthetase and ligase
3UTR_621	2528478 +	2528513 Rmet_5768				Op1732f_1		
3UTR_644	2528551 -	2528563 Rmet_5769				Op1733r_2		
NPKM_2455	2528564 -	2530148 Rmet_5769		18.33	1.53	Op1733r_2	NA	Q1LB48 Putative uncharacterized protein
NPKM_2456	2530317 -	2531241 Rmet_5770	<i>panE</i>	116.67	4.51	Op1733r_2	MET-COF-Pant	Q1LB47 2-dehydropantoate 2-reductase
NPKM_2457	2531405 -	2531519 Rmet_6767		33.67	5.03	Op1733r_1	NA	NA
5UTR_522	2531520 -	2531556 Rmet_6767				Op1733r_1		
5UTR_501	2531776 +	2531807 Rmet_5771				Op1734f_1		
3UTR_643	2531777 -	2532640 Rmet_5772				Op1735r_2		
NPKM_2458	2531807 +	2532584 Rmet_5771		14.33	0.58	Op1734f_1	MET-CAH-Prop	Q1LB46 Enoyl-CoA hydratase
3UTR_622	2532585 +	2532991 Rmet_5771				Op1734f_1		
NPKM_2459	2532641 -	2533070 Rmet_5772		39.33	3.06	Op1735r_2	NA	Q1LB45 Transcriptional regulator, MarR family
NPKM_2460	2533227 -	2533557 Rmet_5773		80.00	15.62	Op1735r_2	NA	Q1LB44 Calcium-binding EF-hand
5UTR_521	2533558 -	2533616 Rmet_5773				Op1735r_2		
NPKM_2461	2533711 -	2533939 Rmet_6768		0.67	1.15	Op1735r_1	NA	NA
NPKM_2462	2534097 +	2534967 Rmet_5774		0.67	0.58	Op1736f_1	NA	Q1LB43 Putative uncharacterized protein

NPKM_2463	2535060 +	2535768 Rmet_5775	19.33	1.15	Op1736f_2	NA	Q1LB42 Haloacid dehalogenase-like hydrolase
3UTR_623	2535769 +	2536212 Rmet_5775			Op1736f_2		
NPKM_2464	2535807 -	2536833 Rmet_5776	11.00	0.00	Op1737r_1	NA	Q1LB41 Putative uncharacterized protein
NPKM_2465	2536856 -	2537192 Rmet_5777	8.00	0.00	Op1737r_1	NA	Q1LB40 Cupin 2, conserved barrel
5UTR_520	2537193 -	2537230 Rmet_5777			Op1737r_1		
5UTR_502	2537355 +	2537701 Rmet_5778			Op1738f_1		
NPKM_2466	2537701 +	2538778 Rmet_5778	71.00	3.00	Op1738f_1	NA	Q1LB39 Porin, Gram-negative type
NPKM_2467	2538823 +	2539279 Rmet_5779	36.00	3.61	Op1738f_1	NA	Q1LB38 Putative uncharacterized protein
NPKM_2468	2539354 +	2540062 Rmet_5780	18.67	2.08	Op1738f_1	NA	Q1LB37 Putative uncharacterized protein
NPKM_2469	2540063 +	2540711 Rmet_5781	8.33	2.31	Op1738f_1	NA	Q1LB36 Putative uncharacterized protein
NPKM_2470	2540939 +	2541245 Rmet_5782	15.33	4.62	Op1738f_1	NA	Q1LB35 Putative uncharacterized protein
NPKM_2471	2541241 +	2542903 Rmet_5783	16.00	3.00	Op1738f_1	NA	NA
3UTR_642	2542377 -	2542930 Rmet_5784			Op1739r_1		
3UTR_624	2542904 -	2543263 Rmet_5783			Op1738f_1		
NPKM_2472	2542931 -	2543210 Rmet_5784	9.67	3.79	Op1739r_1	NA	Q1LB33 Putative uncharacterized protein
5UTR_519	2543211 -	2543226 Rmet_5784			Op1739r_1		
5UTR_503	2543290 +	2543379 Rmet_5785			Op1740f_1		
NPKM_2473	2543379 +	2543559 Rmet_5785	25.33	4.16	Op1740f_1	NA	Q1LB32 Putative uncharacterized protein
NPKM_2474	2543641 +	2544904 Rmet_5786	197.00	5.20	Op1740f_2	NA	Q1LB31 Beta-lactamase
3UTR_641	2544227 -	2545296 Rmet_5788			Op1741r_1		
NPKM_2475	2544966 +	2545215 Rmet_5787	178.00	6.08	Op1740f_2	NA	Q1LB30 Putative uncharacterized protein
3UTR_625	2545216 +	2545743 Rmet_5787			Op1740f_2		
NPKM_2476	2545297 -	2545945 Rmet_5788	89.67	3.79	Op1741r_1	NA	Q1LB29 DSBA oxidoreductase
5UTR_504	2546107 +	2546183 Rmet_5789			Op1742f_1		
NPKM_2477	2546183 +	2546378 Rmet_5789	4.67	1.15	Op1742f_1	NA	Q1LB28 Putative uncharacterized protein
3UTR_626	2546379 +	2546385 Rmet_5789			Op1742f_1		
NPKM_2478	2546459 -	2546825 Rmet_5790	10.33	1.15	Op1743r_1	MET-EN-OxPhos	Q1LB27 Cytochrome C oxidase subunit IV
NPKM_2479	2546821 -	2547502 Rmet_5791	9.33	1.53	Op1743r_1	MET-EN-OxPhos	Q1LB26 Cytochrome c oxidase, subunit III
NPKM_2480	2547504 -	2549481 Rmet_5792	12.00	1.73	Op1743r_1	MET-EN-OxPhos	Q1LB25 Cytochrome c oxidase, subunit I
NPKM_2481	2549484 -	2550444 Rmet_5793	11.67	0.58	Op1743r_1	MET-EN-OxPhos	Q1LB24 Ubiquinol oxidase, subunit II
5UTR_518	2550445 -	2550809 Rmet_5793			Op1743r_1		
5UTR_505	2550509 +	2550555 Rmet_5794			Op1744f_1		
NPKM_2482	2550555 +	2551953 Rmet_5794	15.33	1.53	Op1744f_1	NA	Q1LB23 Transcriptional regulator, GntR family
3UTR_640	2550825 -	2551961 Rmet_5795			Op1745r_1		
3UTR_627	2551954 +	2553032 Rmet_5794			Op1744f_1		
NPKM_2483	2551962 -	2553867 Rmet_5795	12.67	0.58	Op1745r_1	NA	Q1LB22 Oligopeptide transporter OPT superfamily
5UTR_517	2553868 -	2554229 Rmet_5795			Op1745r_1		
NPKM_2484	2553877 +	2554885 Rmet_5796	116.67	4.93	Op1746f_1	NA	Q1LB21 D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding
3UTR_639	2554237 -	2554896 Rmet_5797			Op1747r_1		
3UTR_628	2554886 +	2555808 Rmet_5796			Op1746f_1		
NPKM_2485	2554897 -	2556229 Rmet_5797	44.00	2.65	Op1747r_1	EIP-SIG-2Comp	Q1LB20 Sensor protein
NPKM_2486	2556228 -	2556957 Rmet_5798	81.00	3.46	Op1747r_1	EIP-SIG-2Comp	Q1LB19 Two component transcriptional regulator, winged helix family
NPKM_2487	2556963 -	2557974 Rmet_5799	99.67	6.11	Op1747r_1	MET-CAH-FbP	Q1LB18 Glucokinase

NPKM_2488	2557978 -	2558659 Rmet_5800		120.33	7.23	Op1747r_1	MET-CAH-PP_KDPG	Q1LB17 6-phosphogluconolactonase
NPKM_2489	2558740 -	2560231 Rmet_5801	<i>zwf</i>	148.67	5.03	Op1747r_1	MET-CAH-PP_KDPG	Q1LB16 Glucose-6-phosphate 1-dehydrogenase
NPKM_2490	2560234 +	2562337 Rmet_5802	<i>edd1</i>	67.33	4.16	Op1748f_1	MET-CAH-PP_KDPG	Q1LB15 6-phosphogluconate dehydratase
3UTR_629	2562338 +	2563548 Rmet_5802	<i>edd1</i>			Op1748f_1		
NPKM_2491	2562450 -	2563305 Rmet_5803	<i>mscS</i>	102.67	7.02	Op1749r_2	NA	Q1LB14 MscS Mechanosensitive ion channel
NPKM_2492	2563435 -	2564353 Rmet_5804		37.00	1.00	Op1749r_1	NA	Q1LB13 Transcriptional regulator, AraC family
NPKM_2493	2564424 -	2565684 Rmet_5805		42.67	1.53	Op1749r_1	NA	Q1LB12 Major facilitator superfamily MFS_1
5UTR_516	2565685 -	2565855 Rmet_5805				Op1749r_1		
5UTR_506	2565893 +	2565958 Rmet_5806	<i>fecA1</i>			Op1750f_1		
NPKM_2494	2565958 +	2568154 Rmet_5806	<i>fecA1</i>	1.00	0.00	Op1750f_1	EIP-TRA-Pores	Q1LB11 TonB-dependent siderophore receptor
3UTR_638	2568296 -	2568325 Rmet_6769				Op2106r_1		
NPKM_2495	2568326 -	2568392 Rmet_6769		2.00	1.73	Op2106r_1	NA	NA
5UTR_507	2568386 +	2568415 Rmet_5807	<i>fecA2</i>			Op1750f_1		
5UTR_515	2568393 -	2568631 Rmet_6769				Op2106r_1		
NPKM_2496	2568415 +	2570569 Rmet_5807	<i>fecA2</i>	1.00	0.00	Op1750f_1	EIP-TRA-Pores	Q1LB10 TonB-dependent siderophore receptor
3UTR_637	2570331 -	2570642 Rmet_5808	<i>prfC</i>			Op1751r_2		
3UTR_630	2570570 +	2570584 Rmet_5807	<i>fecA2</i>			Op1750f_1		
NPKM_2497	2570643 -	2572236 Rmet_5808	<i>prfC</i>	118.33	3.21	Op1751r_2	NA	Q1LB09 Bacterial peptide chain release factor 3 (BRF-3)
NPKM_2498	2572332 -	2573298 Rmet_5809		38.67	1.15	Op1751r_1	NA	Q1LB08 Ribonuclease BN, putative
5UTR_514	2573299 -	2573664 Rmet_5809				Op1751r_1		
NPKM_2499	2573420 +	2573714 Rmet_5810		28.67	3.06	Op1752f_1	NA	Q1LB07 Putative uncharacterized protein
3UTR_631	2573715 +	2574167 Rmet_5810				Op1752f_1		
3UTR_636	2573794 -	2573799 Rmet_5811				Op1753r_1		
NPKM_2500	2573800 -	2574253 Rmet_5811		3.33	0.58	Op1753r_1	NA	Q1LB06 Putative uncharacterized protein
5UTR_513	2574254 -	2574284 Rmet_5811				Op1753r_1		
5UTR_508	2574381 +	2574388 Rmet_6770				Op1754f_1		
NPKM_2501	2574388 +	2574685 Rmet_6770		5.00	0.00	Op1754f_1	NA	NA
NPKM_2502	2574579 +	2574900 Rmet_5812		13.00	1.73	Op1754f_2	NA	Q1LB05 Putative uncharacterized protein
3UTR_632	2574901 +	2575184 Rmet_5812				Op1754f_2		
3UTR_635	2574992 -	2575063 Rmet_5813				Op1755r_1		
NPKM_2503	2575064 -	2576567 Rmet_5813		20.00	2.00	Op1755r_1	NA	Q1LB04 Sigma54 specific transcriptional regulator, Fis family
NPKM_2504	2576563 -	2577049 Rmet_5814		91.33	6.43	Op1755r_1	NA	Q1LB03 Putative uncharacterized protein
5UTR_512	2577050 -	2577283 Rmet_5814				Op1755r_1		
3UTR_634	2577465 -	2577638 Rmet_5815				Op1755r_1		
NPKM_2505	2577639 -	2579001 Rmet_5815		70.33	1.15	Op1755r_1	NA	Q1LB02 Xanthine/uracil/vitamin C permease
5UTR_509	2578389 +	2579326 Rmet_5816	<i>cspA</i>			Op1756f_1		
5UTR_511	2579002 -	2579301 Rmet_5815				Op1755r_1		
NPKM_2506	2579326 +	2579530 Rmet_5816	<i>cspA</i>	2917.00	190.83	Op1756f_1	NA	Q1LB01 Cold-shock DNA-binding protein family
3UTR_633	2579531 +	2580081 Rmet_5816	<i>cspA</i>			Op1756f_1		
NPKM_2507	2579664 -	2579874 Rmet_6771		6.33	1.53	Op2107r_1	NA	NA
5UTR_510	2579875 -	2580083 Rmet_6771				Op2107r_1		
Plasmid pMOL30 (Replicon CP000354)								
NPKM_6385	1121 +	2231 Rmet_6062	<i>parB</i>	250.33	8.08	Op1847f_1	NA	Q1LAA5 ParB family protein

3UTR_1	2232 +	2341 Rmet_6062	<i>parB</i>			Op1847f_1			
5UTR_1	2345 +	2816 Rmet_6061				Op1847f_1			
NPKM_6386	2816 +	3419 Rmet_6061		2.33	0.58	Op1847f_1	NA	Q1LAA6	Putative uncharacterized protein
3UTR_102	3149 -	3484 Rmet_6060	<i>repA</i>			Op1846r_1			
NPKM_6387	3485 -	4823 Rmet_6060	<i>repA</i>	97.00	3.00	Op1846r_1	NA	Q1LAA7	Putative uncharacterized protein
5UTR_95	4824 -	5634 Rmet_6060	<i>repA</i>			Op1846r_1			
5UTR_2	5281 +	5742 Rmet_6347				Op1845f_1			
NPKM_6388	5742 +	5922 Rmet_6347		20.00	2.65	Op1845f_1	NA	NA	
3UTR_2	5923 +	6661 Rmet_6347				Op1845f_1			
5UTR_3	6712 +	6750 Rmet_6059				Op1845f_1			
NPKM_6389	6750 +	7236 Rmet_6059		2.67	1.15	Op1845f_1	NA	Q58AT1	Putative uncharacterized protein RMe0218 (Putative uncharacterized protei
3UTR_3	7237 +	7241 Rmet_6059				Op1845f_1			
5UTR_4	7421 +	7610 Rmet_6058				Op1845f_1			
NPKM_6390	7610 +	9965 Rmet_6058		5.33	1.15	Op1845f_1	NA	Q1LAA9	Diguanylate cyclase/phosphodiesterase
NPKM_6391	10018 +	10939 Rmet_6057		7.67	0.58	Op1845f_1	NA	Q1LAB0	Putative uncharacterized protein
NPKM_6392	10941 +	11175 Rmet_6348		15.67	1.53	Op1845f_2	NA	NA	
NPKM_6393	11324 +	11564 Rmet_6056		5.00	1.00	Op1845f_2	NA	Q58AS9	Putative uncharacterized protein RMe0220 (Putative uncharacterized protei
NPKM_6394	11599 +	11803 Rmet_6349		9.67	1.53	Op1845f_2	NA	NA	
3UTR_4	11804 +	11817 Rmet_6349				Op1845f_2			
3UTR_101	12305 -	12361 Rmet_6055				Op1844r_4			
NPKM_6395	12362 -	13508 Rmet_6055		293.67	13.61	Op1844r_4	NA	Q1LAB2	Putative uncharacterized protein
NPKM_6396	13534 -	13819 Rmet_6054		230.67	10.02	Op1844r_4	NA	Q1LAB3	Putative uncharacterized protein
NPKM_6397	14003 -	14288 Rmet_6053		42.33	6.66	Op1844r_3	NA	Q1LAB4	Putative uncharacterized protein
5UTR_94	14289 -	14320 Rmet_6053				Op1844r_3			
3UTR_100	14602 -	14605 Rmet_6052				Op1844r_2			
NPKM_6398	14606 -	15404 Rmet_6052		6.00	1.00	Op1844r_2	NA	Q1LAB5	Putative uncharacterized protein
NPKM_6399	15534 -	15870 Rmet_6051		2.67	0.58	Op1844r_1	NA	Q1LAB6	Putative uncharacterized protein
NPKM_6400	15866 -	16205 Rmet_6050		2.67	0.58	Op1844r_1	NA	Q1LAB7	Putative uncharacterized protein
5UTR_93	16206 -	16247 Rmet_6050				Op1844r_1			
5UTR_5	16353 +	16420 Rmet_6049				Op1843f_1			
NPKM_6401	16420 +	16690 Rmet_6049		49.67	4.04	Op1843f_1	NA	Q1LAB8	Putative uncharacterized protein
NPKM_6402	16725 +	18663 Rmet_6048	<i>uvrD</i>	40.67	1.15	Op1843f_1	NA	Q58AS5	Putative DNA helicase
NPKM_6403	18716 +	19085 Rmet_6047		16.00	1.73	Op1843f_1	NA	Q58AS4	Putative uncharacterized protein RMe0225 (Putative uncharacterized protei
NPKM_6404	19165 +	19393 Rmet_6350		29.67	4.51	Op1843f_1	NA	NA	
NPKM_6405	19683 +	19947 Rmet_6046		37.33	1.53	Op1843f_1	NA	Q58AS3	Putative uncharacterized protein RMe0226 (Putative uncharacterized protei
NPKM_6406	20221 +	20419 Rmet_6351		23.33	3.79	Op1843f_1	NA	NA	
NPKM_6407	20415 +	20724 Rmet_6045		16.33	3.51	Op1843f_1	NA	Q1LAC2	Putative uncharacterized protein
NPKM_6408	20758 +	21493 Rmet_6044		15.67	2.08	Op1843f_1	NA	Q1LAC3	Putative uncharacterized protein
3UTR_99	21373 -	22795 Rmet_6352				Op1842r_2			
NPKM_6409	21505 +	22732 Rmet_6043		14.67	1.15	Op1843f_1	NA	Q1LAC4	Putative uncharacterized protein
NPKM_6410	22796 -	22976 Rmet_6352		439.33	7.02	Op1842r_2	NA	NA	
NPKM_6411	22972 -	23329 Rmet_6042		4.67	1.15	Op1842r_1	NA	Q1LAC5	Putative uncharacterized protein
5UTR_92	23330 -	23401 Rmet_6042				Op1842r_1			

NPKM_6412	23406 +	23538 Rmet_6353	8.67	0.58	Op1841f_1	NA	NA
NPKM_6413	23675 +	24482 Rmet_6041	77.67	8.50	Op1841f_2	NA	Q1LAC6 Putative uncharacterized protein
NPKM_6414	24499 +	24715 Rmet_6354	53.67	6.43	Op1841f_2	NA	NA
NPKM_6415	24945 +	25209 Rmet_6355	65.67	7.57	Op1841f_2	NA	NA
NPKM_6416	25238 +	25460 Rmet_6356	31.33	2.52	Op1841f_2	NA	NA
NPKM_6417	25250 -	25631 Rmet_6040	2.00	1.00	Op1840r_1	NA	Q1LAC7 Putative uncharacterized protein
3UTR_98	25633 -	26371 Rmet_6038			Op1838r_1		
NPKM_6418	25711 +	25936 Rmet_6357	52.00	4.36	Op1839f_1	NA	NA
NPKM_6419	25942 +	26341 Rmet_6039	49.67	4.73	Op1839f_1	NA	Q1LAC8 Putative uncharacterized protein
3UTR_5	26342 +	29025 Rmet_6039			Op1839f_1		
NPKM_6420	26372 -	26819 Rmet_6038	62.00	5.20	Op1838r_1	NA	Q1LAC9 Putative uncharacterized protein
NPKM_6421	26820 -	27261 Rmet_6358	69.00	5.20	Op1838r_1	NA	NA
NPKM_6422	27257 -	27626 Rmet_6037	58.33	7.77	Op1838r_1	NA	Q1LAD0 Putative uncharacterized protein
NPKM_6423	27854 -	28124 Rmet_6036	84.33	1.53	Op1838r_1	NA	Q58AR6 Putative uncharacterized protein RMe0233
NPKM_6424	28157 -	29108 Rmet_6035	77.00	4.58	Op1838r_1	NA	Q58AR5 Putative uncharacterized protein RMe0234 (Putative uncharacterized prote
5UTR_6	29029 +	29995 Rmet_6033			Op1837f_1		
NPKM_6425	29104 -	29830 Rmet_6034	70.00	1.00	Op1838r_1	NA	Q1LAD3 Putative uncharacterized protein
5UTR_91	29831 -	29850 Rmet_6034			Op1838r_1		
NPKM_6426	29995 +	30193 Rmet_6033	186.33	19.30	Op1837f_1	NA	Q58AR4 Putative uncharacterized protein RMe0235 (Putative uncharacterized prote
NPKM_6427	30189 +	30561 Rmet_6032	269.67	13.61	Op1837f_1	NA	Q58AR3 Putative uncharacterized protein RMe0236 (PiIT protein-like protein)
NPKM_6428	30617 +	31286 Rmet_6031	156.33	8.39	Op1837f_1	NA	Q1LAD6 Putative uncharacterized protein
NPKM_6429	31306 +	32302 Rmet_6030	67.00	7.00	Op1837f_1	NA	Q1LAD7 Putative uncharacterized protein
3UTR_97	32139 -	32252 Rmet_6029			Op1836r_1		
NPKM_6430	32253 -	32514 Rmet_6029	1.67	0.58	Op1836r_1	NA	Q1LAD8 Putative uncharacterized protein
NPKM_6431	32539 -	32908 Rmet_6028	4.00	0.00	Op1836r_1	NA	Q1LAD9 Putative uncharacterized protein
NPKM_6432	32897 -	33176 Rmet_6027	3.33	1.53	Op1836r_1	NA	Q1LAE0 Putative uncharacterized protein
3UTR_96	33193 -	33436 Rmet_6026			Op1836r_1		
NPKM_6433	33437 -	33938 Rmet_6026	6.33	0.58	Op1836r_1	NA	Q1LAE1 Putative uncharacterized protein
5UTR_90	33939 -	35162 Rmet_6026			Op1836r_1		
NPKM_6434	34218 +	34668 Rmet_6025	29.00	2.65	Op1835f_1	NA	Q1LAE2 Putative uncharacterized protein
NPKM_6435	34862 +	35834 Rmet_6024	23.00	3.61	Op1835f_1	NA	Q1LAE3 Putative lipoprotein transmembrane
3UTR_6	35835 +	35858 Rmet_6024			Op1835f_1		
5UTR_7	36178 +	36488 Rmet_6023			Op1835f_1		
NPKM_6436	36488 +	37487 Rmet_6023	45.67	4.73	Op1835f_1	NA	Q1LAE4 Putative uncharacterized protein
NPKM_6437	37534 +	37894 Rmet_6022	39.00	1.00	Op1835f_1	NA	Q58AQ9 Putative uncharacterized protein RMe0240 (Putative uncharacterized prote
NPKM_6438	37906 +	38428 Rmet_6021	29.00	2.00	Op1835f_1	NA	Q1LAE6 Putative uncharacterized protein
3UTR_95	38393 -	38449 Rmet_6359			Op2108r_1		
3UTR_7	38429 +	38537 Rmet_6021			Op1835f_1		
NPKM_6439	38450 -	38615 Rmet_6359	0.67	0.58	Op2108r_1	NA	NA
5UTR_8	38565 +	38604 Rmet_6020			Op1835f_1		
NPKM_6440	38604 +	38865 Rmet_6020	15.67	1.53	Op1835f_1	NA	Q1LAE7 Putative uncharacterized protein
5UTR_89	38616 -	38710 Rmet_6359			Op2108r_1		
NPKM_6441	38981 +	39806 Rmet_6019	8.00	0.00	Op1835f_1	NA	Q1LAE8 Putative uncharacterized protein

NPKM_6442	39805 +	40660 Rmet_6018		15.33	1.15	Op1835f_1	NA	Q58AQ5 Putative uncharacterized protein RMe0244
NPKM_6443	40771 +	41287 Rmet_6017		14.33	3.21	Op1835f_1	NA	Q1LAF0 Putative uncharacterized protein
NPKM_6444	41443 +	41809 Rmet_6016		16.67	2.08	Op1835f_1	NA	Q58AQ4 Putative uncharacterized protein RMe0245 (Putative uncharacterized prote
3UTR_8	41810 +	41840 Rmet_6016				Op1835f_1		
5UTR_9	42121 +	42164 Rmet_6015				Op1835f_1		
NPKM_6445	42164 +	42818 Rmet_6015		1.00	0.00	Op1835f_1	NA	Q58AQ3 Putative uncharacterized protein RMe0246 (Putative uncharacterized prote
NPKM_6446	43215 +	45009 Rmet_6014		7.67	0.58	Op1835f_2	NA	Q58AQ2 Putative uncharacterized protein RMe0247 (Putative uncharacterized prote
3UTR_9	45010 +	45021 Rmet_6014				Op1835f_2		
5UTR_10	45131 +	45233 Rmet_6013				Op1835f_2		
NPKM_6447	45233 +	45662 Rmet_6013		10.33	0.58	Op1835f_2	NA	Q58AQ1 Putative uncharacterized protein RMe0248 (Putative uncharacterized prote
3UTR_10	45663 +	45725 Rmet_6013				Op1835f_2		
NPKM_6448	45854 +	46310 Rmet_6012		4.33	0.58	Op1834f_1	NA	Q1LAF5 Putative uncharacterized protein
NPKM_6449	46348 +	46963 Rmet_6011		3.00	0.00	Op1833f_1	NA	Q1LAF6 Putative uncharacterized protein
NPKM_6450	47025 +	47418 Rmet_6010		10.33	0.58	Op1833f_2	NA	Q1LAF7 Putative uncharacterized protein
NPKM_6451	47434 +	47554 Rmet_6360	traB	27.00	3.61	Op1833f_3	NA	NA
3UTR_11	47555 +	47588 Rmet_6360	traB			Op1833f_3		
NPKM_6452	47690 +	48530 Rmet_6009		2.00	0.00	Op1833f_3	NA	Q58AP7 Putative uncharacterized protein RMe0252 (Putative uncharacterized protei
3UTR_12	48531 +	48543 Rmet_6009				Op1833f_3		
3UTR_94	48655 -	49485 Rmet_6007				Op1832r_1		
NPKM_6453	48728 +	48935 Rmet_6361		0.00	0.00	Op1833f_3	NA	NA
5UTR_11	49006 +	49040 Rmet_6008				Op1833f_4		
NPKM_6454	49040 +	49415 Rmet_6008		16.00	3.61	Op1833f_4	NA	Q58AP5 Putative uncharacterized protein RMe0254 (Putative uncharacterized protei
3UTR_13	49416 +	49443 Rmet_6008				Op1833f_4		
NPKM_6455	49486 -	50491 Rmet_6007		41.67	1.53	Op1832r_1	NA	Q1LAG0 Putative uncharacterized protein
5UTR_88	50492 -	51136 Rmet_6007				Op1832r_1		
5UTR_12	50902 +	50916 Rmet_6006	int			Op1831f_1		
NPKM_6456	50916 +	52092 Rmet_6006	int	75.67	5.69	Op1831f_1	NA	Q58AP4 Putative uncharacterized protein RMe0255 (Phage integrase)
3UTR_93	51663 -	52228 Rmet_6005	dnaJ			Op1830r_1		
3UTR_14	52093 +	54097 Rmet_6006	int			Op1831f_1		
NPKM_6457	52229 -	54167 Rmet_6005	dnaJ	16.33	1.15	Op1830r_1	NA	Q1LAG2 Heat shock protein DnaJ-like protein
NPKM_6458	54328 -	54541 Rmet_6004		1.33	1.15	Op1829r_1	NA	Q1LAG3 Putative uncharacterized protein
NPKM_6459	54555 -	54810 Rmet_6362		0.67	0.58	Op1829r_1	NA	NA
5UTR_13	54580 +	54663 Rmet_6003				Op1829f_1		
NPKM_6460	54663 +	55194 Rmet_6003		8.00	1.00	Op1829f_1	NA	Q58AP2 Putative uncharacterized protein RMe0257 (Putative uncharacterized protei
5UTR_87	54811 -	54851 Rmet_6362				Op1829r_1		
3UTR_15	55195 +	55208 Rmet_6003				Op1829f_1		
NPKM_6461	55265 +	55475 Rmet_6363		1.33	0.58	Op1829f_1	NA	NA
3UTR_16	55476 +	55517 Rmet_6363				Op1829f_1		
5UTR_14	55979 +	56002 Rmet_6002	tnpA			Op1829f_1		
NPKM_6462	56002 +	56677 Rmet_6002	tnpA	0.00	0.00	Op1829f_1	NA	Q58AP1 Putative uncharacterized protein RMe0258 (Transposase Tn3)
3UTR_92	56669 -	57533 Rmet_6000				Op1828r_3		
NPKM_6463	56710 +	57547 Rmet_6001		0.00	0.00	Op1829f_1	NA	Q58AP0 Putative uncharacterized protein RMe0259 (Cointegrate resolution protein
NPKM_6464	57534 -	57810 Rmet_6000		57.00	2.65	Op1828r_3	NA	Q1LAG7 Putative uncharacterized protein

NPKM_6465	57921 -	58980 Rmet_5999	<i>ompP3</i>	7.33	0.58	Op1828r_2	NA	Q1LAG8 Porin, Gram-negative type
NPKM_6466	59114 -	60359 Rmet_5998	<i>atsH</i>	20.67	1.53	Op1828r_2	NA	Q1LAG9 Putative uncharacterized protein
NPKM_6467	60630 -	61962 Rmet_5997		20.67	1.53	Op1828r_2	NA	Q58AN8 Aryldialkylphosphatase-related protein (Amidohydrolase)
NPKM_6468	61983 -	62766 Rmet_5996		9.67	1.53	Op1828r_1	NA	Q1LAH1 Alpha/beta hydrolase fold
NPKM_6469	62765 -	63644 Rmet_5995	<i>mhpD</i>	16.67	2.89	Op1828r_1	NA	Q1LAH2 Fumarylacetoacetate (FAA) hydrolase
5UTR_86	63645 -	63701 Rmet_5995	<i>mhpD</i>			Op1828r_1		
5UTR_15	63755 +	63810 Rmet_5994	<i>gntR</i>			Op1827f_1		
NPKM_6470	63810 +	64506 Rmet_5994	<i>gntR</i>	59.67	4.04	Op1827f_1	NA	Q58AN5 Transcriptional regulator (Transcriptional regulator, GntR family)
3UTR_91	63815 -	64953 Rmet_5993	<i>ahpD</i>			Op1826r_2		
NPKM_6471	64688 +	64889 Rmet_6364		17.00	2.65	Op1827f_1	NA	NA
NPKM_6472	64954 -	65329 Rmet_5993	<i>ahpD</i>	52.33	0.58	Op1826r_2	NA	Q58AN4 Putative uncharacterized protein RMe0265 (Alkylhydroperoxidase AhpD cor
NPKM_6473	65333 -	65600 Rmet_5992	<i>merP</i>	36.33	3.21	Op1826r_2	EIP-TRA-Other	Q58AN3 Periplasmic transport protein (Heavy metal transport/detoxification protei
NPKM_6474	65625 -	65973 Rmet_5991	<i>merT</i>	8.00	2.00	Op1826r_1	EIP-TRA-Other	Q58AN2 Mercuric transport protein (Mercuric transport protein MerT)
NPKM_6475	66050 +	66449 Rmet_5990	<i>merR</i>	46.00	4.36	Op1825f_1	NA	Q58AN1 Mercury regulatory protein (Transcriptional regulator, MerR family)
3UTR_17	66450 +	69214 Rmet_5990	<i>merR</i>			Op1825f_1		
NPKM_6476	66877 -	69199 Rmet_5989		119.33	3.51	Op1824r_2	NA	Q1LAH8 Cytochrome c, class I
5UTR_85	69200 -	69217 Rmet_5989				Op1824r_2		
3UTR_90	69382 -	69697 Rmet_5988	<i>bimA2</i>			Op1824r_1		
NPKM_6477	69698 -	71186 Rmet_5988	<i>bimA2</i>	28.67	1.15	Op1824r_1	NA	Q58AM9 Putative integrase/recombinase (Phage integrase-like SAM-like)
NPKM_6478	71182 -	72121 Rmet_5987	<i>bimB2</i>	35.33	0.58	Op1824r_1	NA	Q58AM8 Putative uncharacterized protein RMe0271
5UTR_84	72122 -	72170 Rmet_5987	<i>bimB2</i>			Op1824r_1		
5UTR_16	72334 +	72428 Rmet_6365				Op2109f_1		
3UTR_89	72377 -	72548 Rmet_6366				Op2110r_1		
NPKM_6479	72428 +	72521 Rmet_6365		5.33	1.15	Op2109f_1	NA	NA
NPKM_6480	72549 -	72654 Rmet_6366		4.00	0.00	Op2110r_1	NA	NA
NPKM_6481	72607 +	72898 Rmet_5986		6.00	1.00	Op1823f_1	NA	Q1LAI1 Putative uncharacterized protein
NPKM_6482	72985 -	73165 Rmet_6367		5.67	0.58	Op1822r_1	NA	NA
5UTR_83	73166 -	73330 Rmet_6367				Op1822r_1		
3UTR_88	73336 -	73500 Rmet_5985	<i>czcM</i>			Op1822r_1		
NPKM_6483	73501 -	73960 Rmet_5985	<i>czcM</i>	3.00	0.00	Op1822r_1	EIP-TRA-Other	Q58AM5 MgtC protein (MgtC/SapB transporter)
5UTR_82	73961 -	74084 Rmet_5985	<i>czcM</i>			Op1822r_1		
NPKM_6484	74039 +	74861 Rmet_5984	<i>czcN</i>	8.00	1.73	Op1821f_1	NA	B2UED1 Isoprenylcysteine carboxyl methyltransferase
NPKM_6485	74890 +	75070 Rmet_6368		8.67	2.08	Op1821f_1	NA	NA
NPKM_6486	75175 +	75523 Rmet_5983	<i>czcI</i>	357.33	45.18	Op1820f_1	NA	Q1LAI4 Putative uncharacterized protein
NPKM_6487	75598 +	76855 Rmet_5982	<i>czcC</i>	57.00	4.00	Op1819f_1	EIP-TRA-Ion	P13509 Cobalt-zinc-cadmium resistance protein czcC
NPKM_6488	76872 +	78435 Rmet_5981	<i>czcB</i>	39.00	1.00	Op1819f_1	EIP-TRA-Ion	P13510 Cobalt-zinc-cadmium resistance protein czcB
NPKM_6489	78451 +	81643 Rmet_5980	<i>czcA</i>	42.33	0.58	Op1819f_1	EIP-TRA-Ion	P13511 Cobalt-zinc-cadmium resistance protein czcA
NPKM_6490	81693 +	82644 Rmet_5979	<i>czcD</i>	26.33	0.58	Op1819f_1	EIP-TRA-Ion	P13512 Cobalt-zinc-cadmium resistance protein czcD
NPKM_6491	82645 +	83323 Rmet_5978	<i>czcR</i>	38.67	0.58	Op1819f_1	EIP-SIG-2Comp	Q44006 Transcriptional activator protein czcR
NPKM_6492	83327 +	84758 Rmet_5977	<i>czcS</i>	22.33	1.53	Op1819f_1	EIP-SIG-2Comp	Q44007 Sensor protein czcS
NPKM_6493	84866 +	85268 Rmet_5976	<i>czcE</i>	26.33	3.06	Op1819f_1	NA	Q1LAJ1 Putative uncharacterized protein
3UTR_18	85269 +	85286 Rmet_5976	<i>czcE</i>			Op1819f_1		
3UTR_87	85460 -	85565 Rmet_5975	<i>czcI</i>			Op1818r_2		

NPKM_6494	85566 -	85845 Rmet_5975	<i>czcI</i>	9.33	1.15	Op1818r_2	NA	B2UEC1 Putative uncharacterized protein
5UTR_81	85846 -	85846 Rmet_5975	<i>czcI</i>			Op1818r_2		
3UTR_86	85973 -	86026 Rmet_5974	<i>ompP</i>			Op1818r_2		
NPKM_6495	86027 -	87095 Rmet_5974	<i>ompP</i>	31.00	1.00	Op1818r_2	NA	B2UEC0 Porin Gram-negative type
5UTR_80	87096 -	87210 Rmet_5974	<i>ompP</i>			Op1818r_2		
NPKM_6496	87211 -	88105 Rmet_5973	<i>tnpB</i>	0.00	0.00	Op1818r_1	NA	B2UH78 Integrase catalytic region
NPKM_6497	88101 -	88398 Rmet_5972	<i>tnpA</i>	0.00	0.00	Op1818r_1	NA	A7C8W8 Transposase IS3/IS911 family protein
5UTR_17	88533 +	88682 Rmet_5971	<i>flgB</i>			Op1817f_1		
NPKM_6498	88682 +	89105 Rmet_5971	<i>flgB</i>	4.67	1.53	Op1817f_1	DIV-MOT-Flagel	Q58AL6 Putative flagellar basal-body rod protein (Flagellar basal-body rod protein F
3UTR_19	89106 +	89159 Rmet_5971	<i>flgB</i>			Op1817f_1		
NPKM_6499	89119 -	89401 Rmet_6369		3.00	0.00	Op2111r_1	NA	NA
5UTR_18	89572 +	89604 Rmet_5970	<i>czcP</i>			Op1817f_1		
NPKM_6500	89604 +	92094 Rmet_5970	<i>czcP</i>	7.67	0.58	Op1817f_1	MET-EN-P_ATPase	Q1LAJ7 Heavy metal translocating P-type ATPase
3UTR_85	91183 -	92150 Rmet_5969				Op1816r_3		
3UTR_20	92095 +	92461 Rmet_5970	<i>czcP</i>			Op1817f_1		
NPKM_6501	92151 -	92454 Rmet_5969		20.33	2.08	Op1816r_3	NA	B2UEB6 Putative uncharacterized protein
NPKM_6502	92686 -	93808 Rmet_5968	<i>gtrB1</i>	3.67	0.58	Op1816r_2	NA	B2UEB5 Glycosyl transferase family 2
NPKM_6503	93804 -	94188 Rmet_5967	<i>gtrA1</i>	1.67	0.58	Op1816r_1	NA	B2UEB4 GtrA family protein
NPKM_6504	94184 -	95792 Rmet_5966	<i>gtrM1</i>	2.00	0.00	Op1816r_1	NA	Q58AL3 Putative transmembrane protein
5UTR_19	96219 +	96293 Rmet_5965	<i>tnpA</i>			Op1815f_1		
NPKM_6505	96293 +	96572 Rmet_5965	<i>tnpA</i>	17.00	2.00	Op1815f_1	NA	Q58AL2 Insertion element protein (Putative uncharacterized protein)
3UTR_21	96573 +	97138 Rmet_5965	<i>tnpA</i>			Op1815f_1		
NPKM_6506	96758 -	96812 Rmet_6370		29.67	4.16	Op1814r_1	NA	NA
NPKM_6507	96789 -	97116 Rmet_5964	<i>tnpA</i>	21.67	2.08	Op1814r_1	NA	Q1LAK3 Transposase IS3/IS911
5UTR_79	97117 -	97145 Rmet_5964	<i>tnpA</i>			Op1814r_1		
5UTR_20	97141 +	97226 Rmet_5963				Op1813f_1		
NPKM_6508	97226 +	97472 Rmet_5963		26.67	2.31	Op1813f_1	NA	Q1LAK4 Putative uncharacterized protein
3UTR_22	97473 +	97802 Rmet_5963				Op1813f_1		
5UTR_21	97987 +	98191 Rmet_5962	<i>gtrM3</i>			Op1813f_1		
NPKM_6509	98191 +	99877 Rmet_5962	<i>gtrM3</i>	2.67	0.58	Op1813f_1	NA	Q58AL0 Putative transmembrane protein (Glycosyl transferase, family 39)
3UTR_23	99878 +	100127 Rmet_5962	<i>gtrM3</i>			Op1813f_1		
3UTR_84	100144 -	100165 Rmet_5961				Op2112r_1		
NPKM_6510	100166 -	100400 Rmet_5961		12.67	2.52	Op2112r_1	NA	Q1LAK6 Putative uncharacterized protein
5UTR_22	100535 +	101353 Rmet_5960	<i>int</i>			Op1813f_2		
NPKM_6511	100698 -	100866 Rmet_6371		14.67	2.08	Op2112r_1	NA	NA
5UTR_78	100867 -	101716 Rmet_6371				Op2112r_1		
NPKM_6512	101353 +	101728 Rmet_5960	<i>int</i>	10.33	1.15	Op1813f_2	NA	Q58AK9 Putative uncharacterized protein RMe0295
NPKM_6513	101870 +	102392 Rmet_5959	<i>int</i>	1.67	1.15	Op1813f_2	NA	Q58AK7 Putative uncharacterized protein RMe0297 (Phage integrase)
3UTR_24	102393 +	102415 Rmet_5959	<i>int</i>			Op1813f_2		
5UTR_23	102418 +	102445 Rmet_6372				Op1813f_2		
NPKM_6514	102445 +	102823 Rmet_6372		2.33	1.15	Op1813f_2	NA	NA
NPKM_6515	102798 +	103014 Rmet_5958		1.33	0.58	Op1813f_2	NA	Q1LAK9 Putative uncharacterized protein
5UTR_24	103027 +	103063 Rmet_6373				Op1813f_3		

NPKM_6516	103063 +	103291 Rmet_6373		5.00	1.00	Op1813f_3	NA	NA
NPKM_6517	103179 +	104361 Rmet_5957	<i>tnpA</i>	5.00	1.00	Op1813f_3	NA	Q1LAL0 Transposase IS66
3UTR_25	104362 +	104371 Rmet_5957	<i>tnpA</i>			Op1813f_3		
5UTR_25	104408 +	104415 Rmet_5956	<i>tnp</i>			Op1813f_3		
NPKM_6518	104415 +	104562 Rmet_5956	<i>tnp</i>	1.00	0.00	Op1813f_3	NA	Q1LAL1 ISPPu14, transposase Orf3
3UTR_26	104563 +	104567 Rmet_5956	<i>tnp</i>			Op1813f_3		
NPKM_6519	104609 +	104714 Rmet_5955	<i>int</i>	1.33	0.58	Op1813f_3	NA	Q1LAL2 Phage integrase
3UTR_83	104624 -	104783 Rmet_5954	<i>tnpA</i>			Op1812r_1		
NPKM_6520	104784 -	105795 Rmet_5954	<i>tnpA</i>	9.00	1.73	Op1812r_1	NA	Q58AK3 Insertion element protein (Integrase, catalytic region)
5UTR_26	105794 +	105879 Rmet_5953	<i>cusF</i>			Op1811f_1		
5UTR_77	105796 -	106207 Rmet_5954	<i>tnpA</i>			Op1812r_1		
NPKM_6521	105879 +	106143 Rmet_5953	<i>cusF</i>	2.33	1.15	Op1811f_1	NA	Q58AK2 Putative uncharacterized protein RMe0302 (Conserved hypothetical signal p
3UTR_27	106144 +	106158 Rmet_5953	<i>cusF</i>			Op1811f_1		
3UTR_82	106223 -	106298 Rmet_5952	<i>tnpA</i>			Op1810r_2		
NPKM_6522	106299 -	107298 Rmet_5952	<i>tnpA</i>	17.00	3.00	Op1810r_2	NA	Q58AK1 Insertion element IRSme11 protein
5UTR_76	107299 -	107316 Rmet_5952	<i>tnpA</i>			Op1810r_2		
NPKM_6523	107323 -	109240 Rmet_5951	<i>tnpA</i>	3.33	0.58	Op1810r_1	NA	Q58AK0 Insertion element IRSme11 protein (Transposase Tn3)
3UTR_81	109364 -	109985 Rmet_5949	<i>pbrD</i>			Op1808r_2		
NPKM_6524	109467 +	109881 Rmet_5950	<i>int</i>	1.33	0.58	Op1809f_1	NA	Q58AJ9 Putative integrase/recombinase (Phage integrase)
3UTR_28	109882 +	109895 Rmet_5950	<i>int</i>			Op1809f_1		
NPKM_6525	109986 -	110856 Rmet_5949	<i>pbrD</i>	15.67	1.53	Op1808r_2	NA	Q1LAL8 Putative uncharacterized protein
NPKM_6526	111023 -	112100 Rmet_5948	<i>pbrB/C</i>	5.67	0.58	Op1808r_1	GIP-PTL-Exp	Q58AJ7 PbrB/pbrC lead resistance fusion protein (Signal peptidase II. Aspartic pepti
NPKM_6527	112096 -	114496 Rmet_5947	<i>pbrA</i>	7.67	0.58	Op1808r_1	MET-EN-P_ATPase	Q58AJ6 Pb-efflux ATPase (Heavy metal translocating P-type ATPase)
5UTR_75	114497 -	115282 Rmet_5947	<i>pbrA</i>			Op1808r_1		
5UTR_27	114579 +	114582 Rmet_5946	<i>pbrR</i>			Op1807f_1		
NPKM_6528	114582 +	115020 Rmet_5946	<i>pbrR</i>	15.67	1.53	Op1807f_1	NA	Q58AJ5 PbrR protein (Transcriptional regulator, MerR family)
NPKM_6529	115141 +	117070 Rmet_5945	<i>pbrT</i>	53.33	4.73	Op1807f_2	EIP-TRA-Ion	Q58AJ4 PbrT protein (Iron permease FTR1)
NPKM_6530	117257 +	118196 Rmet_5944	<i>pbrUa</i>	12.67	0.58	Op1807f_2	NA	Q58AJ3 Putative uncharacterized protein RMe0312 (Major facilitator superfamily M
NPKM_6531	118337 -	118553 Rmet_5943	<i>tnmC</i>	0.00	0.00	Op1806r_1	NA	Q58AJ2 Putative uncharacterized protein RMe0313 (Putative uncharacterized protei
NPKM_6532	118606 -	119440 Rmet_5942	<i>gspA</i>	0.00	0.00	Op1806r_1	NA	Q5NUU5 Hypothetical general secretion pathway protein A (ATPase) (General secre
NPKM_6533	119436 -	120876 Rmet_6374	<i>tnmA</i>	0.00	0.00	Op1806r_1	NA	NA
NPKM_6534	120987 -	121557 Rmet_6181	<i>tnmB</i>	0.00	0.00	Op1892r_1	NA	Q1L9I3 Putative uncharacterized protein
NPKM_6535	121692 +	122070 Rmet_6180	<i>pbrUb</i>	6.67	2.08	Op1891f_1	NA	Q1L9Y7 General substrate transporter
3UTR_29	122071 +	122346 Rmet_6180	<i>pbrUb</i>			Op1891f_1		
3UTR_80	122238 -	122242 Rmet_6375				Op1890r_3		
NPKM_6536	122243 -	122411 Rmet_6375		1.33	0.58	Op1890r_3	NA	NA
5UTR_74	122412 -	122443 Rmet_6375				Op1890r_3		
NPKM_6537	122480 -	125447 Rmet_6179	<i>tnpA</i>	0.00	0.00	Op1890r_2	NA	Q58AI7 Transposase (Transposase Tn3)
NPKM_6538	125449 -	125932 Rmet_6178	<i>tnpR</i>	0.00	0.00	Op1890r_2	NA	Q1LEG5 Resolvase-like protein
NPKM_6539	125924 -	126926 Rmet_6177	<i>urf-2</i>	0.00	0.00	Op1890r_2	NA	Q58AI5 Putative uncharacterized protein (Diguanylate phosphodiesterase) (EAL dom
NPKM_6540	126922 -	127159 Rmet_6176	<i>merE</i>	0.00	0.00	Op1890r_2	NA	P06690 Uncharacterized mercuric resistance protein merE
NPKM_6541	127155 -	127521 Rmet_6175	<i>merD</i>	0.00	0.00	Op1890r_2	NA	Q5NUV1 Putative secondary regulatory protein MerD (Transcriptional regulator, Me
NPKM_6542	127538 -	129224 Rmet_6174	<i>merA</i>	1.00	0.00	Op1890r_2	NA	Q1L9Z3 Mercuric reductase MerA

NPKM_6543	129295 -	129571 Rmet_6173	<i>merP</i>	0.00	0.00	Op1890r_1	EIP-TRA-Other	Q58AI1 Periplasmic mercuric-ion binding protein (Mercuric transport protein peripla
NPKM_6544	129583 -	129934 Rmet_6172	<i>merT</i>	0.00	0.00	Op1890r_1	EIP-TRA-Other	Q5NUU8 Hypothetical mercuric ion transport protein (Mercuric transport protein M
NPKM_6545	130005 +	130440 Rmet_6171	<i>merR</i>	0.00	0.00	Op1888f_1	NA	P69413 Mercuric resistance operon regulatory protein
NPKM_6546	130436 -	131219 Rmet_6170		12.00	1.73	Op1888r_1	NA	Q1L9Z7 Putative uncharacterized protein
3UTR_30	130475 +	130965 mobile_element					0	
5UTR_73	131220 -	131251 Rmet_6170				Op1888r_1		
5UTR_29	131438 +	131448 Rmet_6169	<i>dsbC</i>			Op1887f_1		
NPKM_6547	131448 +	132165 Rmet_6169	<i>dsbC</i>	5.67	1.15	Op1887f_1	GIP-PTL-Fold	Q58AH8 Putative thiol:disulfide interchange protein (Protein-disulfide isomerase)
3UTR_31	132166 +	132177 Rmet_6169	<i>dsbC</i>			Op1887f_1		
NPKM_6548	132266 +	132899 Rmet_6168	<i>traW</i>	3.67	0.58	Op1887f_1	NA	Q58AH7 Sex pilus assembly and synthesis protein (Sex pilus assembly and synthesis
NPKM_6549	132895 +	133930 Rmet_6167	<i>traU</i>	3.33	0.58	Op1887f_1	NA	Q58AH6 Sex pilus assembly and synthesis protein (TraU)
5UTR_30	133936 +	133997 Rmet_6166	<i>trbC</i>			Op1887f_1		
NPKM_6550	133997 +	134615 Rmet_6166	<i>trbC</i>	6.00	0.00	Op1887f_1	NA	Q58AH5 Sex pilus assembly and mating pair formation protein
NPKM_6551	134718 +	135492 Rmet_6165		8.67	0.58	Op1887f_1	NA	Q58AH4 Putative uncharacterized protein RMe0331 (Putative uncharacterized prote
3UTR_32	135493 +	135603 Rmet_6165				Op1887f_1		
NPKM_6552	135569 -	135818 Rmet_6376	<i>trbK</i>	4.67	1.15	Op1886r_1	NA	NA
NPKM_6553	135786 -	136233 Rmet_6164		4.67	0.58	Op1886r_1	NA	Q1LA03 Putative uncharacterized protein
5UTR_72	136234 -	136332 Rmet_6164				Op1886r_1		
NPKM_6554	136461 +	137529 Rmet_6163		2.67	0.58	Op1885f_1	NA	Q58AH3 Putative uncharacterized protein RMe0332 (Putative uncharacterized prote
3UTR_79	136529 -	137585 Rmet_6162				Op1884r_1		
3UTR_33	137530 +	137538 Rmet_6163				Op1885f_1		
NPKM_6555	137586 -	138210 Rmet_6162		530.33	14.57	Op1884r_1	NA	Q1LA05 Putative transcriptional regulator, XRE family
5UTR_71	138211 -	138303 Rmet_6162				Op1884r_1		
5UTR_31	138365 +	138399 Rmet_6161				Op1883f_1		
NPKM_6556	138399 +	138900 Rmet_6161		10.33	1.53	Op1883f_1	NA	Q1LA06 Putative uncharacterized protein
3UTR_78	138440 -	139084 Rmet_6160	<i>stbD</i>			Op1882r_2		
3UTR_34	138901 +	138946 Rmet_6161				Op1883f_1		
NPKM_6557	139085 -	139361 Rmet_6160	<i>stbD</i>	16.33	3.06	Op1882r_2	NA	Q1LA07 Prevent-host-death protein
NPKM_6558	139747 -	139945 Rmet_6159		23.33	0.58	Op1882r_2	NA	Q58AH0 Putative uncharacterized protein RMe0335 (Putative uncharacterized prote
5UTR_70	139946 -	140450 Rmet_6159				Op1882r_2		
5UTR_32	139971 +	140052 Rmet_6377				Op2113f_1		
NPKM_6559	140052 +	140268 Rmet_6377		9.33	2.08	Op2113f_1	NA	NA
3UTR_35	140269 +	140423 Rmet_6377				Op2113f_1		
3UTR_77	140477 -	141070 Rmet_6158				Op1882r_1		
NPKM_6560	141071 -	141317 Rmet_6158		7.00	1.00	Op1882r_1	NA	Q1LA09 Putative uncharacterized protein
NPKM_6561	141447 -	141939 Rmet_6157		4.67	1.53	Op1882r_1	NA	Q1LA10 Putative uncharacterized protein
NPKM_6562	141951 +	142284 Rmet_6378		2.33	1.15	Op2114f_1	NA	NA
3UTR_76	142207 -	142419 Rmet_6156				Op1882r_1		
3UTR_36	142285 +	142383 Rmet_6378				Op2114f_1		
NPKM_6563	142420 -	142648 Rmet_6156		11.67	4.04	Op1882r_1	NA	Q1LA11 Putative uncharacterized protein
NPKM_6564	142707 -	143115 Rmet_6155		20.00	1.00	Op1882r_1	NA	Q1LA12 Putative uncharacterized protein
NPKM_6565	143139 -	143721 Rmet_6154		17.67	0.58	Op1882r_1	NA	Q1LA13 Putative uncharacterized protein
5UTR_33	143833 +	143855 Rmet_6153	<i>tnpA</i>			Op1881f_1		

NPKM_6566	143855 +	144182 Rmet_6153	<i>tnpA</i>	8.00	0.00	Op1881f_1	NA	Q58AG9 Putative uncharacterized protein ISRme8aa1 (Putative uncharacterized pro
NPKM_6567	144202 +	144451 Rmet_6152	<i>tnpB</i>	8.67	2.52	Op1881f_1	NA	Q58AG8 Putative uncharacterized protein ISRme8aa2
3UTR_37	144452 +	144989 Rmet_6152	<i>tnpB</i>			Op1881f_1		
NPKM_6568	144600 -	145917 Rmet_6151		57.67	1.53	Op1880r_2	NA	Q58AG7 Putative uncharacterized protein RMe0338 (ATPase involved in DNA repair
5UTR_69	145918 -	146478 Rmet_6151				Op1880r_2		
3UTR_75	146505 -	146924 Rmet_6150				Op1880r_1		
NPKM_6569	146925 -	147867 Rmet_6150		15.00	2.00	Op1880r_1	NA	Q1LA17 Alpha/beta hydrolase fold
NPKM_6570	147847 -	147952 Rmet_6379		1.00	1.00	Op1879r_1	NA	NA
5UTR_34	148117 +	148145 Rmet_6149	<i>bug</i>			Op1879f_1		
NPKM_6571	148145 +	149165 Rmet_6149	<i>bug</i>	4.67	0.58	Op1879f_1	NA	Q1LA18 Twin-arginine translocation pathway signal
3UTR_38	149166 +	149169 Rmet_6149	<i>bug</i>			Op1879f_1		
5UTR_35	149172 +	149195 Rmet_6148	<i>nccC</i>			Op1879f_1		
NPKM_6572	149195 +	150542 Rmet_6148	<i>nccC</i>	4.33	0.58	Op1879f_1	NA	Q1LA19 Outer membrane efflux protein
NPKM_6573	150538 +	150820 Rmet_6147	<i>nccBa</i>	4.00	0.00	Op1879f_1	NA	Q1LA20 Putative uncharacterized protein
NPKM_6574	150847 +	151732 Rmet_6146	<i>nccBb</i>	2.33	0.58	Op1879f_1	EIP-TRA-Ion	Q58AG3 Putative nickel and cobalt resistance protein (Secretion protein HlyD)
NPKM_6575	151728 +	154959 Rmet_6145	<i>nccA</i>	1.33	0.58	Op1879f_1	EIP-TRA-Ion	Q58AG2 Putative nickel and cobalt resistance protein (Heavy metal efflux pump Czc
NPKM_6576	154967 +	156194 Rmet_6144	<i>nreB</i>	1.00	0.00	Op1879f_1	EIP-SIG-2Comp	Q58AG1 NreB protein (Drug antiporter protein)
3UTR_74	156637 -	156845 Rmet_6143	<i>mmrQ</i>			Op1878r_1		
NPKM_6577	156846 -	157092 Rmet_6143	<i>mmrQ</i>	21.00	1.00	Op1878r_1	NA	Q58AG0 Putative uncharacterized protein RMe0345 (Conserved hypothetical signal
5UTR_68	157093 -	157141 Rmet_6143	<i>mmrQ</i>			Op1878r_1		
NPKM_6578	157364 +	157787 Rmet_6142	<i>flgB</i>	13.33	1.53	Op1877f_1	DIV-MOT-Flagel	Q58AF9 Putative flagellar basal-body ROD protein (Flagellar basal-body rod protein
NPKM_6579	157981 +	158317 Rmet_6141		75.00	5.57	Op1877f_2	NA	Q1LA26 Putative uncharacterized protein
NPKM_6580	158326 +	160444 Rmet_6140		42.33	1.15	Op1877f_2	NA	Q58AF7 Putative uncharacterized protein RMe0348 (Diguanylate cyclase/phosphodi
3UTR_73	160442 -	160539 Rmet_6139				Op1876r_1		
3UTR_39	160445 +	161468 Rmet_6140				Op1877f_2		
NPKM_6581	160540 -	161821 Rmet_6139		9.67	0.58	Op1876r_1	NA	Q58AF6 MFS transporter family protein (Major facilitator superfamily MFS_1)
NPKM_6582	161783 -	162065 Rmet_6138		13.00	3.00	Op1876r_1	NA	Q1LA29 Putative uncharacterized protein
5UTR_36	161956 +	162304 Rmet_6137	<i>ubiE</i>			Op1875f_1		
5UTR_67	162066 -	162083 Rmet_6138				Op1876r_1		
3UTR_72	162147 -	163912 Rmet_6136	<i>silA</i>			Op1874r_1		
NPKM_6583	162304 +	163177 Rmet_6137	<i>ubiE</i>	3.33	0.58	Op1875f_1	NA	Q58AF5 Methyltransferase (Methyltransferase type 11)
NPKM_6584	163235 +	163424 Rmet_6380		1.67	0.58	Op1875f_1	NA	NA
3UTR_40	163425 +	163724 Rmet_6380				Op1875f_1		
NPKM_6585	163913 -	167084 Rmet_6136	<i>silA</i>	12.67	0.58	Op1874r_1	EIP-TRA-Ion	Q58AF4 Silver efflux protein (Heavy metal efflux pump CzcA)
NPKM_6586	167080 -	168646 Rmet_6135	<i>silB</i>	6.33	0.58	Op1874r_1	EIP-TRA-Ion	Q58AF3 Silver efflux protein (Secretion protein HlyD)
NPKM_6587	168642 -	169950 Rmet_6134	<i>silC</i>	8.00	0.00	Op1874r_1	EIP-TRA-Ion	Q58AF2 Outer membrane silver efflux protein (Outer membrane efflux protein)
NPKM_6588	170022 -	170418 Rmet_6133	<i>silD</i>	25.00	4.00	Op1874r_1	NA	Q1LA34 Putative uncharacterized protein
5UTR_66	170419 -	170892 Rmet_6133	<i>silD</i>			Op1874r_1		
5UTR_37	170697 +	170699 Rmet_6132				Op1873f_1		
NPKM_6589	170699 +	171095 Rmet_6132		2.67	0.58	Op1873f_1	NA	Q1LA35 Putative uncharacterized protein
3UTR_41	171096 +	171171 Rmet_6132				Op1873f_1		
5UTR_38	171233 +	171274 Rmet_6131	<i>ubiE2</i>			Op1873f_1		
NPKM_6590	171274 +	172144 Rmet_6131	<i>ubiE2</i>	1.00	0.00	Op1873f_1	NA	Q58AF1 Methyltransferase (Methyltransferase type 11)

NPKM_6591	172140 +	173766 Rmet_6130	<i>gtrM2</i>	0.33	0.58	Op1873f_1	NA	Q58AF0 Putative transmembrane protein (Glycosyl transferase, family 39)
NPKM_6592	173762 +	174146 Rmet_6129	<i>gtrA2</i>	0.33	0.58	Op1873f_1	NA	Q58AE9 Putative uncharacterized protein RMe0356 (GtrA-like protein)
NPKM_6593	174142 +	175246 Rmet_6128	<i>gtrB2</i>	0.67	0.58	Op1873f_1	NA	Q58AE8 Putative polymixin resistance glycosyltransferase transmembrane protein (
NPKM_6594	175450 +	176518 Rmet_6127	<i>ompP2</i>	19.33	1.53	Op1873f_2	NA	Q58AE7 Putative porin signal peptide protein (Porin, Gram-negative type)
3UTR_42	176519 +	176605 Rmet_6127	<i>ompP2</i>			Op1873f_2		
5UTR_39	176632 +	176891 Rmet_6381				Op1873f_2		
NPKM_6595	176891 +	177215 Rmet_6381		4.67	0.58	Op1873f_2	NA	NA
NPKM_6596	177051 +	177348 Rmet_6126		3.33	1.53	Op1873f_2	NA	Q1LA41 Putative uncharacterized protein
3UTR_71	177345 -	177572 Rmet_6125	<i>resU</i>			Op1872r_1		
3UTR_43	177349 +	177419 Rmet_6126				Op1873f_2		
NPKM_6597	177573 -	178152 Rmet_6125	<i>resU</i>	5.33	0.58	Op1872r_1	NA	Q58AE6 Putative integrase/recombinase
5UTR_65	178153 -	178193 Rmet_6125	<i>resU</i>			Op1872r_1		
3UTR_70	178280 -	178555 Rmet_6124	<i>copW</i>			Op1871r_1		
NPKM_6598	178556 -	178766 Rmet_6124	<i>copW</i>	22.33	1.15	Op1871r_1	NA	Q1LA43 Putative uncharacterized protein
NPKM_6599	178965 -	179601 Rmet_6123	<i>copE</i>	5.67	0.58	Op1870r_1	NA	Q1LA44 Putative uncharacterized protein
5UTR_64	179602 -	179684 Rmet_6123	<i>copE</i>			Op1870r_1		
NPKM_6600	179773 +	180235 Rmet_6122	<i>copH</i>	3.33	1.15	Op1869f_1	NA	Q58AE5 CopH protein (Putative uncharacterized protein)
3UTR_69	180348 -	180702 Rmet_6120	<i>copL</i>			Op1868r_1		
NPKM_6601	180357 +	180594 Rmet_6121	<i>copQ</i>	6.67	1.53	Op1869f_1	NA	Q1LA46 Putative uncharacterized protein
3UTR_44	180595 +	181413 Rmet_6121	<i>copQ</i>			Op1869f_1		
NPKM_6602	180703 -	181969 Rmet_6120	<i>copL</i>	27.67	1.15	Op1868r_1	NA	Q58AE4 Putative type II restriction enzyme (Putative uncharacterized protein)
5UTR_40	181512 +	182211 Rmet_6382	<i>copO</i>			Op1867f_1		
5UTR_63	181970 -	182058 Rmet_6120	<i>copL</i>			Op1868r_1		
NPKM_6603	182211 +	182403 Rmet_6382	<i>copO</i>	27.00	1.00	Op1867f_1	NA	NA
NPKM_6604	182395 +	184813 Rmet_6119	<i>copF</i>	49.00	2.00	Op1867f_1	MET-EN-P_ATPase	Q58AE3 Cation-transporting p-atpase (Heavy metal translocating P-type ATPase)
NPKM_6605	184857 +	185271 Rmet_6118	<i>copG</i>	65.33	3.79	Op1867f_1	NA	Q9F3R7 CopG protein
3UTR_68	185310 -	185932 Rmet_6116	<i>copI</i>			Op1866r_2		
NPKM_6606	185314 +	185839 Rmet_6117	<i>copI</i>	54.00	2.00	Op1867f_1	NA	Q58AE1 CopI protein (Cytochrome c, class I)
3UTR_45	185840 +	187137 Rmet_6117	<i>copI</i>			Op1867f_1		
NPKM_6607	185933 -	186410 Rmet_6116	<i>copI</i>	11.00	2.65	Op1866r_2	NA	Q58AE0 Putative oxydoreductase (Blue (Type 1) copper domain)
NPKM_6608	186481 -	187399 Rmet_6115	<i>copD1</i>	30.33	1.15	Op1866r_2	EIP-TRA-Other	Q58AD9 Copper resistance D transmembrane protein (Copper resistance D)
NPKM_6609	187405 -	187804 Rmet_6114	<i>copC1</i>	50.33	3.06	Op1866r_2	NA	Q1LA53 Copper resistance protein CopC
NPKM_6610	187835 -	189323 Rmet_6113	<i>copB1</i>	8.00	1.00	Op1866r_1	NA	Q58AD7 CopB protein (Copper resistance B)
NPKM_6611	189354 -	191199 Rmet_6112	<i>copA1</i>	10.33	0.58	Op1866r_1	NA	Q58AD6 Copper resistance transmembrane protein (Copper-resistance protein CopA)
5UTR_41	191031 +	191402 Rmet_6111	<i>copR1</i>			Op1865f_1		
5UTR_62	191200 -	191249 Rmet_6112	<i>copA1</i>			Op1866r_1		
NPKM_6612	191402 +	192089 Rmet_6111	<i>copR1</i>	17.67	1.53	Op1865f_1	EIP-SIG-2Comp	Q58AD5 Two component response transcription regulator (Two component heavy m
NPKM_6613	192085 +	193477 Rmet_6110	<i>copS1</i>	14.33	2.08	Op1865f_1	EIP-SIG-2Comp	Q58AD4 Sensor protein
NPKM_6614	193527 +	194022 Rmet_6109	<i>copN</i>	26.00	1.00	Op1865f_1	NA	Q1LA58 Putative uncharacterized protein
3UTR_67	193598 -	194045 Rmet_6108	<i>copK</i>			Op1864r_2		
3UTR_46	194023 +	194380 Rmet_6109	<i>copN</i>			Op1865f_1		
NPKM_6615	194046 -	194331 Rmet_6108	<i>copK</i>	18.67	2.08	Op1864r_2	NA	Q58AD3 Copper resistance protein K
NPKM_6616	194360 -	194771 Rmet_6107	<i>copM</i>	3.67	0.58	Op1864r_1	NA	Q1LA60 Putative uncharacterized protein

5UTR_61	194772 -	194796 Rmet_6107	<i>copM</i>				Op1864r_1		
5UTR_42	195250 +	195637 Rmet_6106	<i>copT</i>				Op1863f_1		
NPKM_6617	195637 +	196402 Rmet_6106	<i>copT</i>	22.33	2.08	Op1863f_1	NA	Q58AD2 Putative uncharacterized protein copT	
NPKM_6618	196469 +	196823 Rmet_6105	<i>copV</i>	18.67	0.58	Op1863f_1	NA	Q1LA62 Putative uncharacterized protein	
NPKM_6619	197453 +	198098 Rmet_6103		6.33	0.58	Op1863f_1	NA	Q58AD1 Acyl-CoA dehydrogenase	
3UTR_47	198099 +	198290 Rmet_6103					Op1863f_1		
3UTR_66	198411 -	198528 Rmet_6102	<i>int</i>				Op1862r_1		
NPKM_6620	198529 -	199156 Rmet_6102	<i>int</i>	6.67	0.58	Op1862r_1	NA	Q1LA65 Phage integrase	
5UTR_43	199153 +	199286 Rmet_6383					Op1861f_1		
5UTR_60	199157 -	199720 Rmet_6102	<i>int</i>				Op1862r_1		
NPKM_6621	199286 +	199652 Rmet_6383		2.00	1.00	Op1861f_1	NA	NA	
NPKM_6622	199593 +	200025 Rmet_6101		16.67	0.58	Op1861f_2	NA	Q1LA66 Putative uncharacterized protein	
3UTR_48	200026 +	200896 Rmet_6101					Op1861f_2		
3UTR_65	200146 -	200341 Rmet_6384					Op1860r_1		
NPKM_6623	200342 -	200558 Rmet_6384		14.00	2.00	Op1860r_1	NA	NA	
NPKM_6624	200568 -	200814 Rmet_6385		29.33	2.08	Op1860r_1	NA	NA	
NPKM_6625	200767 -	201004 Rmet_6100		22.00	3.00	Op1860r_1	NA	Q58AC9 Putative uncharacterized protein RMe0376 (Putative uncharacterized protei	
NPKM_6626	201326 -	201680 Rmet_6099		30.00	1.73	Op1860r_1	NA	Q58AC8 Putative uncharacterized protein RMe0377 (Putative uncharacterized protei	
5UTR_59	201681 -	202048 Rmet_6099					Op1860r_1		
5UTR_44	201860 +	201994 Rmet_6386					Op1859f_1		
NPKM_6627	201994 +	202111 Rmet_6386		1.33	1.53	Op1859f_1	NA	NA	
3UTR_49	202112 +	202150 Rmet_6386					Op1859f_1		
5UTR_45	202154 +	202202 Rmet_6098	<i>npd-a</i>				Op1859f_2		
NPKM_6628	202202 +	202799 Rmet_6098	<i>npd-a</i>	25.67	2.52	Op1859f_2	NA	Q1LA69 2-nitropropane dioxygenase, NPD	
NPKM_6629	202853 +	203360 Rmet_6097	<i>npd-b</i>	12.00	1.00	Op1859f_2	NA	Q1LA70 2-nitropropane dioxygenase, NPD	
3UTR_64	203319 -	203371 Rmet_6096					Op1858r_1		
3UTR_50	203361 +	204158 Rmet_6097	<i>npd-b</i>				Op1859f_2		
NPKM_6630	203372 -	203918 Rmet_6096		4.67	0.58	Op1858r_1	NA	Q1LA71 Putative uncharacterized protein	
5UTR_58	203919 -	204094 Rmet_6096					Op1858r_1		
5UTR_46	204309 +	204724 Rmet_6095					Op1857f_1		
NPKM_6631	204724 +	207289 Rmet_6095		23.00	3.46	Op1857f_1	NA	Q1LA72 Putative uncharacterized protein	
NPKM_6632	207292 +	207589 Rmet_6094		14.00	2.65	Op1857f_1	NA	Q58AC7 Putative uncharacterized protein RMe0378 (Putative uncharacterized protei	
NPKM_6633	207696 +	209484 Rmet_6093		30.00	3.46	Op1857f_2	NA	Q58AC6 Putative hemagglutinin-related transmembrane protein (Hycolysin. Metall	
3UTR_63	209022 -	209624 Rmet_6092					Op1856r_1		
3UTR_51	209485 +	209537 Rmet_6093					Op1857f_2		
NPKM_6634	209625 -	210378 Rmet_6092		13.67	2.08	Op1856r_1	NA	Q1LA75 Putative uncharacterized protein	
5UTR_47	210326 +	210403 Rmet_6091					Op1855f_1		
5UTR_57	210379 -	210446 Rmet_6092					Op1856r_1		
NPKM_6635	210403 +	210712 Rmet_6091		2.33	0.58	Op1855f_1	NA	Q1LA76 Putative uncharacterized protein	
3UTR_62	210457 -	211270 Rmet_6089					Op1854r_1		
NPKM_6636	2110735 +	211179 Rmet_6090		787.67	26.27	Op1855f_2	NA	Q1LA77 Histone-like DNA-binding protein	
3UTR_52	211180 +	212031 Rmet_6090					Op1855f_2		
NPKM_6637	211271 -	212489 Rmet_6089		16.33	1.53	Op1854r_1	NA	Q1LA78 Putative uncharacterized protein	

5UTR_56	212490 -	213624 Rmet_6089				Op1854r_1		
5UTR_48	212669 +	212710 Rmet_6387				Op1853f_1		
NPKM_6638	212710 +	212911 Rmet_6387		3.67	0.58	Op1853f_1	NA	NA
NPKM_6639	213076 +	213475 Rmet_6088		174.67	6.66	Op1853f_2	NA	Q1LA79 Putative uncharacterized protein
3UTR_53	213476 +	213508 Rmet_6088				Op1853f_2		
5UTR_49	213812 +	213852 Rmet_6087				Op1853f_2		
NPKM_6640	213852 +	215121 Rmet_6087		62.67	2.52	Op1853f_2	NA	Q58AC3 Putative uncharacterized protein RMe0202 (Putative uncharacterized protei
NPKM_6641	215117 +	217268 Rmet_6086	int	57.33	3.06	Op1853f_2	NA	Q58AC2 Putative integrase/recombinase protein (Phage integrase)
NPKM_6642	217281 +	217623 Rmet_6085		32.67	2.08	Op1853f_2	NA	Q1LA82 Putative uncharacterized protein
NPKM_6643	217695 +	218316 Rmet_6084		50.33	3.06	Op1853f_2	NA	Q1LA83 Putative uncharacterized protein
NPKM_6644	218430 +	219240 Rmet_6083		43.67	4.04	Op1853f_2	NA	Q1LA84 Putative uncharacterized protein
NPKM_6645	219345 +	220488 Rmet_6082		36.67	1.53	Op1853f_2	NA	Q1LA85 Putative uncharacterized protein
NPKM_6646	220595 +	221288 Rmet_6081		56.67	2.08	Op1853f_2	NA	Q1LA86 Putative uncharacterized protein
NPKM_6647	221502 +	223089 Rmet_6080		406.67	15.95	Op1853f_3	NA	Q1LA87 Putative uncharacterized protein
3UTR_61	223082 -	223095 Rmet_6388				Op2115r_1		
NPKM_6648	223096 -	223294 Rmet_6388		1.00	0.00	Op2115r_1	NA	NA
NPKM_6649	223201 +	223534 Rmet_6079		188.67	4.04	Op1853f_3	NA	Q1LA88 Putative uncharacterized protein
5UTR_55	223295 -	223371 Rmet_6388				Op2115r_1		
3UTR_60	223387 -	223595 Rmet_6078				Op1852r_1		
NPKM_6650	223596 -	224046 Rmet_6078		101.00	14.00	Op1852r_1	NA	Q1LA89 Putative uncharacterized protein
NPKM_6651	223776 +	223944 Rmet_6389		8.00	2.65	Op2116f_1	NA	NA
5UTR_54	224047 -	224388 Rmet_6078				Op1852r_1		
NPKM_6652	224590 +	225229 Rmet_6077		135.67	12.58	Op1851f_1	NA	Q1LA90 Putative uncharacterized protein
3UTR_59	225264 -	226473 Rmet_6075				Op1850r_2		
NPKM_6653	225694 +	226093 Rmet_6076		128.00	3.61	Op1851f_1	NA	Q1LA91 Putative uncharacterized protein
3UTR_54	226094 +	226798 Rmet_6076				Op1851f_1		
NPKM_6654	226474 -	226747 Rmet_6075		37.00	1.00	Op1850r_2	NA	Q1LA92 Putative uncharacterized protein
NPKM_6655	226790 -	227684 Rmet_6074	tnpB	0.00	0.00	Op1850r_1	NA	NA
NPKM_6656	227680 -	227977 Rmet_6073	tnpA	0.00	0.00	Op1850r_1	NA	NA
3UTR_58	228002 -	228034 Rmet_6072				Op1850r_1		
NPKM_6657	228035 -	228737 Rmet_6072		31.67	2.08	Op1850r_1	NA	Q1LA95 Transcriptional regulator, XRE family
5UTR_53	228738 -	229156 Rmet_6072				Op1850r_1		
5UTR_50	228863 +	228966 Rmet_6071				Op1849f_1		
NPKM_6658	228966 +	229338 Rmet_6071		30.67	4.04	Op1849f_1	NA	Q1LA96 Putative uncharacterized protein
NPKM_6659	229495 +	229972 Rmet_6070		13.33	2.08	Op1849f_1	GIP-REP-Recomb	Q58AB6 Putative uncharacterized protein RMe0209 (ATP dependent DNA ligase)
3UTR_55	229973 +	230014 Rmet_6070				Op1849f_1		
5UTR_51	230246 +	230269 Rmet_6069				Op1849f_1		
NPKM_6660	230269 +	230587 Rmet_6069		23.67	3.06	Op1849f_1	NA	Q1LA98 Putative uncharacterized protein
NPKM_6661	230591 +	230930 Rmet_6068	tnpA	0.00	0.00	Op1849f_1	NA	Q58AB4 Putative uncharacterized protein ISRme8aa1 (Transposase IS3/IS911)
NPKM_6662	230983 +	231841 Rmet_6067	tnpB	0.00	0.00	Op1849f_1	NA	A7CEH6 Integrase, catalytic region
3UTR_57	231863 -	232656 Rmet_6065				Op1848r_1		
NPKM_6663	231974 +	232661 Rmet_6066		82.00	3.61	Op1849f_2	NA	Q58AB2 Putative uncharacterized protein RMe0213 (Putative uncharacterized prote
NPKM_6664	232657 -	233119 Rmet_6065		8.00	1.73	Op1848r_1	NA	Q58AB1 Putative uncharacterized protein RMe0214 (Putative uncharacterized prote

3UTR_56	232662 +	233389 Rmet_6066				Op1849f_2		
NPKM_6665	233115 -	233424 Rmet_6064		5.33	0.58	Op1848r_1	NA	Q1LAA3 Putative uncharacterized protein
NPKM_6666	233317 -	233515 Rmet_6390		3.00	1.00	Op1848r_1	NA	NA
5UTR_52	233516 -	233696 Rmet_6390				Op1848r_1		
Plasmid pMOL28 (Replicon CP000355)								
NPKM_6667	0 +	1191 Rmet_6315	<i>parA</i>	149.00	7.55	Op1918f_4	NA	Q5NUY7 Hypothetical plasmid replication protein (Cobyrinic acid a,c-diamide syntha
NPKM_6668	1187 +	2186 Rmet_6316	<i>parB</i>	173.67	1.15	Op1918f_4	NA	Q5NUY5 Hypothetical ParB-like partition protein (ParB family protein)
NPKM_6669	2424 +	3603 Rmet_6317	<i>repA</i>	32.67	0.58	Op1918f_4	NA	Q5NUY6 Hypothetical replication protein (Putative uncharacterized protein)
NPKM_6670	4150 +	4324 Rmet_6391		13.33	1.53	Op1918f_4	NA	NA
NPKM_6671	4665 +	5484 Rmet_6318		440.67	55.43	Op1918f_5	NA	Q1L9J9 Putative uncharacterized protein
3UTR_147	4761 -	6169 Rmet_6320	<i>int</i>			Op1919r_1		
NPKM_6672	5483 +	6140 Rmet_6319		435.00	48.75	Op1918f_5	NA	Q1L9J8 Putative uncharacterized protein
NPKM_6673	6170 -	7367 Rmet_6320	<i>int</i>	87.00	7.00	Op1919r_1	NA	Q1L9J7 Phage integrase
5UTR_126	7368 -	7432 Rmet_6320	<i>int</i>			Op1919r_1		
NPKM_6674	7592 +	8423 Rmet_6321	<i>tolA</i>	157.67	15.57	Op1920f_1	NA	Q5NUU3 Hypothetical TolA Transport Protein (Putative uncharacterized protein)
NPKM_6675	8373 +	8592 Rmet_6392		69.33	2.31	Op1920f_1	NA	NA
NPKM_6676	8778 +	9168 Rmet_6322		80.67	10.97	Op1920f_1	NA	Q1L9J5 Putative uncharacterized protein
NPKM_6677	9242 +	9872 Rmet_6323		81.33	6.03	Op1920f_1	NA	Q1L9J4 Putative uncharacterized protein
NPKM_6678	9879 +	10077 Rmet_6393		713.00	24.98	Op1920f_2	NA	NA
NPKM_6679	10168 +	10978 Rmet_6324	<i>ymh</i>	56.67	4.04	Op1920f_2	NA	Q1L9J3 Putative uncharacterized protein
NPKM_6680	11026 +	12466 Rmet_6325		49.00	2.65	Op1920f_2	NA	Q1L9J2 Putative uncharacterized protein
3UTR_146	11356 -	12529 Rmet_6326				Op1921r_1		
3UTR_103	12467 +	14530 Rmet_6325				Op1920f_2		
NPKM_6681	12530 -	16334 Rmet_6326		24.33	0.58	Op1921r_1	NA	Q1L9J1 Putative uncharacterized protein
5UTR_96	14550 +	16530 Rmet_6327				Op1922f_1		
5UTR_125	16335 -	16738 Rmet_6326				Op1921r_1		
NPKM_6682	16530 +	17799 Rmet_6327		137.67	4.16	Op1922f_1	NA	Q1L9J0 Putative uncharacterized protein
3UTR_145	17560 -	18155 Rmet_6329				Op1923r_1		
NPKM_6683	17873 +	18146 Rmet_6328		72.33	4.93	Op1922f_1	NA	Q1L9I9 Putative uncharacterized protein
NPKM_6684	18156 -	19203 Rmet_6329		32.67	1.53	Op1923r_1	NA	Q1L9I8 HNH nuclease
NPKM_6685	19398 +	19764 Rmet_6330		132.00	8.19	Op1924f_1	NA	Q1L9I7 Putative uncharacterized protein
NPKM_6686	19777 +	20917 Rmet_6331		36.00	1.00	Op1924f_1	NA	Q1L9I6 Putative uncharacterized protein
3UTR_144	20400 -	20973 Rmet_6332				Op1925r_1		
3UTR_104	20918 +	21515 Rmet_6331				Op1924f_1		
NPKM_6687	20974 -	21325 Rmet_6332		7.33	1.15	Op1925r_1	NA	Q1L9I5 Putative uncharacterized protein
5UTR_124	21326 -	21507 Rmet_6332				Op1925r_1		
NPKM_6688	21612 +	22260 Rmet_6333	<i>tnpA</i>	0.00	0.00	Op1926f_1	NA	Q1L9I4 Transposase Tn3
NPKM_6689	22361 +	22931 Rmet_6334	<i>tnmB</i>	0.00	0.00	Op1926f_1	NA	NA
NPKM_6690	23042 +	24482 Rmet_6335	<i>tnmA</i>	0.00	0.00	Op1926f_1	NA	Q5NUU4 ISRme2 transposase protein (Integrase, catalytic region) (Insertion eleme
NPKM_6691	24478 +	25312 Rmet_6336	<i>gspA</i>	0.00	0.00	Op1926f_1	NA	NA
NPKM_6692	25365 +	25581 Rmet_6337	<i>tnmC</i>	0.00	0.00	Op1926f_1	NA	NA
NPKM_6693	25620 +	28050 Rmet_6338	<i>tnpA</i>	0.00	0.00	Op1926f_1	NA	Q5NUU5 Hypothetical general secretion pathway protein A (ATPase) (General secre
3UTR_143	28123 -	28607 Rmet_6339				Op1927r_2		

NPKM_6694	28608 -	29091 Rmet_6339		598.00	37.04	Op1927r_2	NA	A6N8V6 Cupin 2
NPKM_6695	29098 -	29659 Rmet_6340		595.33	29.02	Op1927r_2	NA	B2UC46 Putative uncharacterized protein
NPKM_6696	30065 -	30350 Rmet_6341	<i>stbE</i>	286.67	8.96	Op1927r_1	NA	Q4LCG4 Plasmid stabilization protein ParE
NPKM_6697	30346 -	30625 Rmet_6342	<i>stbD</i>	155.33	5.03	Op1927r_1	NA	Q4LCG5 Putative uncharacterized protein
5UTR_97	30850 +	30863 Rmet_6343	<i>tnpR</i>			Op1928f_1		
NPKM_6698	30863 +	31229 Rmet_6343	<i>tnpR</i>	124.00	6.08	Op1928f_1	NA	Q1L9H4 Resolvase-like protein
NPKM_6699	31225 -	31714 Rmet_6344	<i>merR</i>	0.00	0.00	Op1929r_1	NA	Q9AFK4 Tn501 repressor
NPKM_6700	31731 +	32082 Rmet_6345	<i>merT</i>	0.00	0.00	Op1894f_1	NA	NA
NPKM_6701	32094 +	32370 Rmet_6346	<i>merP</i>	0.00	0.00	Op1894f_1	NA	NA
NPKM_6702	32441 +	34127 Rmet_6183	<i>merA</i>	5.00	1.00	Op1894f_2	NA	A6UXG5 Mercuric reductase
NPKM_6703	34144 +	34510 Rmet_6184	<i>merD</i>	0.00	0.00	Op1894f_2	NA	NA
NPKM_6704	34506 +	34743 Rmet_6185	<i>merE</i>	0.00	0.00	Op1894f_2	NA	NA
NPKM_6705	34739 +	35729 Rmet_6186	<i>urf-2</i>	1.00	0.00	Op1894f_3	NA	NA
NPKM_6706	35858 +	36419 Rmet_6187	<i>tnpR</i>	49.33	2.52	Op1894f_4	NA	Q5NUY9 Resolvase of Tn4378 (Resolvase-like protein)
NPKM_6707	36421 +	39391 Rmet_6188	<i>tnpA</i>	18.67	1.15	Op1894f_4	NA	Q5NUZ0 Hypothetical transposase for transposon Tn4378 (Transposase Tn3)
NPKM_6708	39447 +	39882 Rmet_6189		8.67	1.53	Op1894f_4	NA	Q1L9X8 Putative uncharacterized protein
NPKM_6709	39921 +	40980 Rmet_6190		36.33	2.08	Op1894f_5	NA	Q1L9X7 Putative uncharacterized protein
NPKM_6710	41063 +	41486 Rmet_6191	<i>bph2</i>	1498.33	96.23	Op1894f_6	NA	Q5NUZ1 Putative uncharacterized protein bph2 (Histone-like DNA-binding protein)
3UTR_105	41487 +	41743 Rmet_6191	<i>bph2</i>			Op1894f_6		
5UTR_98	41848 +	41850 Rmet_6192	<i>bimB1</i>			Op1894f_6		
NPKM_6711	41850 +	42804 Rmet_6192	<i>bimB1</i>	47.33	3.51	Op1894f_6	NA	Q1L9X5 Putative uncharacterized protein
NPKM_6712	42800 +	44288 Rmet_6193	<i>bimA1</i>	38.67	2.08	Op1894f_6	NA	Q5NUZ3 Hypothetical Integrase/recombinase xerD (Phage integrase-like SAM-like)
3UTR_142	44235 -	44474 Rmet_6194	<i>chrZ</i>			Op1895r_2		
3UTR_106	44289 +	45238 Rmet_6193	<i>bimA1</i>			Op1894f_6		
NPKM_6713	44475 -	45522 Rmet_6194	<i>chrZ</i>	5.67	0.58	Op1895r_2	NA	Q1L9X3 Putative uncharacterized protein
NPKM_6714	45538 -	46465 Rmet_6195	<i>chrY</i>	4.33	0.58	Op1895r_2	NA	Q1L9X2 Putative uncharacterized protein
NPKM_6715	46522 -	47764 Rmet_6196	<i>chrP</i>	3.33	0.58	Op1895r_2	NA	Q5NUZ6 Hypothetical 42.6 kDa protein (Major facilitator superfamily MFS_1)
NPKM_6716	47786 -	48095 Rmet_6197	<i>chrN</i>	11.00	1.73	Op1895r_2	NA	Q1L9X0 Putative uncharacterized protein
NPKM_6717	48114 -	48474 Rmet_6198	<i>chrO</i>	11.67	0.58	Op1895r_2	NA	Q1L9W9 Putative uncharacterized protein
NPKM_6718	48532 -	48955 Rmet_6199	<i>chrF1</i>	11.33	0.58	Op1895r_2	NA	Q5NUZ7 Putative uncharacterized protein chrF (Putative uncharacterized protein)
NPKM_6719	48951 -	49293 Rmet_6200	<i>chrE</i>	11.00	0.00	Op1895r_2	NA	Q5NUZ8 Superoxide dismutase SodM-like protein (Rhodanese-like protein)
NPKM_6720	49310 -	49904 Rmet_6201	<i>chrC</i>	10.67	2.08	Op1895r_2	NA	P17550 Superoxide dismutase [Fe]
NPKM_6721	49923 -	51129 Rmet_6202	<i>chrA1</i>	12.33	1.53	Op1895r_2	EIP-TRA-Ion	P17551 Chromate transport protein
NPKM_6722	51171 -	52146 Rmet_6203	<i>chrB1</i>	6.00	1.00	Op1895r_1	NA	P17552 Protein chrB
NPKM_6723	52300 +	52795 Rmet_6204	<i>chrI</i>	11.33	0.58	Op1896f_1	NA	Q1L9W3 Putative uncharacterized protein
3UTR_107	52796 +	52867 Rmet_6204	<i>chrI</i>			Op1896f_1		
5UTR_99	52869 +	53309 Rmet_6205	<i>cnrY</i>			Op1896f_2		
NPKM_6724	53309 +	53597 Rmet_6205	<i>cnrY</i>	50.33	3.51	Op1896f_2	NA	P56621 Nickel and cobalt resistance protein cnrY
NPKM_6725	53593 +	54040 Rmet_6206	<i>cnrX</i>	43.67	2.52	Op1896f_2	NA	P37975 Nickel and cobalt resistance protein cnrR
NPKM_6726	54036 +	54612 Rmet_6207	<i>cnrH</i>	35.33	3.21	Op1896f_2	GIP-TK-RNAP	P37978 RNA polymerase sigma factor cnrH
NPKM_6727	54684 +	55941 Rmet_6208	<i>cnrC</i>	32.00	2.65	Op1896f_2	EIP-TRA-Ion	P37974 Nickel and cobalt resistance protein cnrC
NPKM_6728	55937 +	57125 Rmet_6209	<i>cnrB</i>	25.00	1.00	Op1896f_2	EIP-TRA-Ion	P37973 Nickel and cobalt resistance protein cnrB
NPKM_6729	57121 +	60352 Rmet_6210	<i>cnrA</i>	17.33	0.58	Op1896f_2	EIP-TRA-Ion	P37972 Nickel and cobalt resistance protein cnrA

NPKM_6730	60397 +	61453 Rmet_6211	<i>cnrT</i>	17.33	1.15	Op1896f_2	NA	Q9L3G0 CnrT protein
3UTR_108	61454 +	62261 Rmet_6211	<i>cnrT</i>			Op1896f_2		
3UTR_141	61465 -	61542 Rmet_6212	<i>tnpA</i>			Op1897r_1		
NPKM_6731	61543 -	64483 Rmet_6212	<i>tnpA</i>	6.00	0.00	Op1897r_1	NA	Q5NUX7 Hypothetical Tn21 related transposase (Transposase Tn3)
NPKM_6732	64694 -	65126 Rmet_6213		18.00	1.00	Op1897r_1	NA	Q1L9V4 Putative uncharacterized protein
NPKM_6733	65204 -	65447 Rmet_6214		25.67	2.08	Op1897r_1	NA	Q1L9V3 Putative uncharacterized protein
NPKM_6734	65516 -	65864 Rmet_6215		27.00	1.00	Op1899r_4	NA	Q1L9V2 Putative uncharacterized protein
3UTR_140	66009 -	66023 Rmet_6216				Op1899r_4		
NPKM_6735	66024 -	67515 Rmet_6216		3.00	1.00	Op1899r_4	NA	Q1L9V1 Putative uncharacterized protein
NPKM_6736	67901 -	68186 Rmet_6217		0.00	0.00	Op1899r_3	NA	Q5NUX9 Putative uncharacterized protein
3UTR_139	68454 -	68476 Rmet_6218	<i>sbcC</i>			Op1899r_3		
NPKM_6737	68477 -	70751 Rmet_6218	<i>sbcC</i>	2.33	0.58	Op1899r_3	GIP-REP-Recomb	Q5NUY0 Hypothetical nuclease sbcCD subunit C
5UTR_123	70752 -	70752 Rmet_6218	<i>sbcC</i>			Op1899r_3		
3UTR_138	70783 -	70788 Rmet_6219				Op1899r_2		
NPKM_6738	70789 -	71305 Rmet_6219		0.00	0.00	Op1899r_2	NA	Q1L9U8 Putative uncharacterized protein
3UTR_137	71471 -	71482 Rmet_6220	<i>sbcD</i>			Op1899r_2		
NPKM_6739	71483 -	72932 Rmet_6220	<i>sbcD</i>	0.33	0.58	Op1899r_2	GIP-REP-Recomb	Q5NUY1 Putative uncharacterized protein yhaO (DNA repair exonuclease-like protei
3UTR_136	73007 -	73027 Rmet_6221				Op1899r_1		
NPKM_6740	73028 -	74282 Rmet_6221		0.00	0.00	Op1899r_1	NA	Q5NUY2 Putative uncharacterized protein
NPKM_6741	74293 -	74803 Rmet_6222		0.00	0.00	Op1899r_1	NA	Q1L9U5 Putative uncharacterized protein
5UTR_122	74804 -	74904 Rmet_6222				Op1899r_1		
NPKM_6742	75251 +	75818 Rmet_6223		2.67	0.58	Op1900f_1	NA	Q5NUY3 Putative uncharacterized protein
NPKM_6743	75804 +	76443 Rmet_6224		7.67	0.58	Op1900f_2	NA	Q5NUY4 Putative uncharacterized protein zipA (Putative uncharacterized protein)
NPKM_6744	76454 +	76874 Rmet_6225		5.67	0.58	Op1900f_2	NA	Q5NUV4 Putative uncharacterized protein ybcA (Putative uncharacterized protein)
3UTR_109	76875 +	76939 Rmet_6225				Op1900f_2		
NPKM_6745	76974 -	77496 Rmet_6226		4.00	1.00	Op1901r_3	NA	Q1L9U1 Putative uncharacterized protein
3UTR_135	77570 -	77612 Rmet_6227				Op1901r_3		
NPKM_6746	77613 -	78588 Rmet_6227		3.33	0.58	Op1901r_3	NA	Q5NUV5 Putative uncharacterized protein
3UTR_134	78923 -	79036 Rmet_6228				Op1901r_3		
NPKM_6747	79037 -	80588 Rmet_6228		7.00	1.00	Op1901r_3	NA	Q5NUV6 Putative uncharacterized protein
NPKM_6748	80653 -	81007 Rmet_6229		9.33	2.52	Op1901r_3	NA	Q5NUV7 Putative uncharacterized protein
NPKM_6749	81064 -	81457 Rmet_6230		13.67	2.08	Op1901r_3	NA	Q5NUV8 Putative uncharacterized protein
NPKM_6750	81700 -	82171 Rmet_6231		35.00	4.58	Op1901r_3	NA	Q5NUV9 Putative uncharacterized protein
NPKM_6751	82183 -	82708 Rmet_6232		36.33	4.51	Op1901r_3	NA	Q1L9T5 Putative uncharacterized protein
NPKM_6752	82789 -	83263 Rmet_6233	<i>slyB</i>	167.33	11.15	Op1901r_3	NA	Q5NUW1 Hypothetical outer membrane lipoprotein SlyB (Putative outer membrane
NPKM_6753	83413 -	83671 Rmet_6394		6.00	1.73	Op1901r_2	NA	NA
NPKM_6754	83744 -	84449 Rmet_6234		18.33	2.08	Op1901r_2	NA	Q1L9T3 Putative uncharacterized protein
5UTR_121	84450 -	84485 Rmet_6234				Op1901r_2		
NPKM_6755	84643 -	85447 Rmet_6235	<i>thiF</i>	4.33	1.53	Op1901r_1	NA	Q5NUW3 Putative uncharacterized protein (UBA/THIF-type NAD/FAD binding fold)
NPKM_6756	85443 -	86085 Rmet_6236		4.00	1.00	Op1901r_1	NA	Q1L9T1 Putative uncharacterized protein
NPKM_6757	86087 -	86807 Rmet_6237		2.00	0.00	Op1901r_1	NA	Q5NUW6 Putative uncharacterized protein
NPKM_6758	86816 -	87956 Rmet_6238		1.00	0.00	Op1901r_1	NA	Q5NUW7 Putative uncharacterized protein
3UTR_133	88008 -	88045 Rmet_6239				Op1901r_1		

NPKM_6759	88046 -	88271 Rmet_6239		16.33	2.52	Op1901r_1	NA	Q1L9S8 Putative uncharacterized protein
NPKM_6760	88281 -	88800 Rmet_6240		15.00	1.00	Op1901r_1	NA	Q1L9S7 Putative uncharacterized protein
NPKM_6761	88825 -	90550 Rmet_6241	<i>parB2</i>	67.00	6.24	Op1901r_1	NA	Q5NUW9 Putative chromosome partitioning protein ParB
5UTR_120	90551 -	91314 Rmet_6241	<i>parB2</i>			Op1901r_1		
5UTR_100	91069 +	91158 Rmet_6242				Op1902f_1		
NPKM_6762	91158 +	91578 Rmet_6242		4.33	0.58	Op1902f_1	NA	Q1L9S5 Putative uncharacterized protein
3UTR_110	91579 +	91629 Rmet_6242				Op1902f_1		
3UTR_132	91692 -	91801 Rmet_6243				Op1903r_2		
NPKM_6763	91802 -	92696 Rmet_6243		14.00	1.73	Op1903r_2	NA	Q5NUW5 Putative uncharacterized protein
NPKM_6764	92837 -	93317 Rmet_6244		39.00	3.61	Op1903r_2	NA	Q5NV11 Putative uncharacterized protein
NPKM_6765	93420 -	93657 Rmet_6245		65.67	7.37	Op1903r_2	NA	Q1L9S2 Putative uncharacterized protein
NPKM_6766	93786 -	94470 Rmet_6246		29.67	1.53	Op1903r_1	NA	Q1L9S1 Putative uncharacterized protein
NPKM_6767	94468 +	94918 Rmet_6247		0.00	0.00	Op1904f_1	NA	Q5NV13 Putative uncharacterized protein
5UTR_119	94471 -	94669 Rmet_6246				Op1903r_1		
NPKM_6768	94914 +	96375 Rmet_6248	<i>uvrD2</i>	1.00	0.00	Op1904f_2	NA	Q5NV14 Putative DNA helicase
3UTR_111	96376 +	96383 Rmet_6248	<i>uvrD2</i>			Op1904f_2		
NPKM_6769	96386 +	97613 Rmet_6249		2.33	0.58	Op1904f_3	NA	Q5NV15 Putative uncharacterized protein
NPKM_6770	97599 +	97968 Rmet_6250		1.67	0.58	Op1904f_3	NA	Q5NV16 Putative uncharacterized protein
5UTR_101	97976 +	98031 Rmet_6251				Op1904f_3		
NPKM_6771	98031 +	98349 Rmet_6251		1.67	1.53	Op1904f_3	NA	Q1L9R6 Putative uncharacterized protein
3UTR_112	98350 +	98433 Rmet_6251				Op1904f_3		
5UTR_102	98442 +	98747 Rmet_6252	<i>int</i>			Op1904f_4		
NPKM_6772	98747 +	99893 Rmet_6252	<i>int</i>	49.67	2.31	Op1904f_4	NA	Q5NV17 Hypothetical transposase A from transposon TN554 (Phage integrase-like 5
NPKM_6773	99867 +	101526 Rmet_6253		27.00	2.65	Op1904f_4	NA	Q1L9R4 Phage integrase
NPKM_6774	101585 +	103436 Rmet_6254		34.67	0.58	Op1904f_4	NA	Q1L9R3 Phage integrase
NPKM_6775	103432 +	103933 Rmet_6255		44.00	1.73	Op1904f_4	NA	Q1L9R2 Putative uncharacterized protein
3UTR_131	103724 -	104233 Rmet_6256				Op1905r_1		
3UTR_113	103934 +	104670 Rmet_6255				Op1904f_4		
NPKM_6776	104234 -	105680 Rmet_6256		32.67	1.53	Op1905r_1	NA	Q1L9R1 Putative uncharacterized protein
NPKM_6777	105676 -	110101 Rmet_6257		50.67	2.52	Op1905r_1	NA	Q1L9R0 Putative uncharacterized protein
5UTR_118	110102 -	111015 Rmet_6257				Op1905r_1		
5UTR_103	110559 +	110769 Rmet_6258	<i>rhsC</i>			Op1906f_1		
NPKM_6778	110769 +	112299 Rmet_6258	<i>rhsC</i>	70.33	4.51	Op1906f_1	NA	Q1L9Q9 YD repeat
3UTR_130	111107 -	112302 Rmet_6259	<i>tnpB</i>			Op1907r_1		
3UTR_114	112300 +	113561 Rmet_6258	<i>rhsC</i>			Op1906f_1		
NPKM_6779	112303 -	113059 Rmet_6259	<i>tnpB</i>	2.33	0.58	Op1907r_1	NA	Q5NV20 ISRme9-transposase ORFB protein (IstB-like ATP-binding protein)
NPKM_6780	113066 -	114620 Rmet_6260	<i>tnpA</i>	2.00	0.00	Op1907r_1	NA	Q5NV21 ISRme9 transposase ORFA protein (Integrase, catalytic region)
NPKM_6781	115049 +	116249 Rmet_6261	<i>rhsB</i>	8.67	1.15	Op1908f_1	NA	Q1L9Q6 YD repeat
3UTR_129	116016 -	116586 Rmet_6262				Op1909r_1		
NPKM_6782	116258 +	116474 Rmet_6395		51.67	4.16	Op1908f_2	NA	NA
3UTR_115	116475 +	117258 Rmet_6395				Op1908f_2		
NPKM_6783	116587 -	117280 Rmet_6262		65.33	5.69	Op1909r_1	NA	Q1L9Q5 Alpha/beta hydrolase
5UTR_117	117281 -	117867 Rmet_6262				Op1909r_1		

5UTR_104	117556 +	117593 Rmet_6263	rhsA			Op1910f_1		
NPKM_6784	117593 +	120413 Rmet_6263	rhsA	244.33	14.05	Op1910f_1	NA	Q1L9Q4 YD repeat
NPKM_6785	120425 +	120641 Rmet_6396		487.33	11.15	Op1910f_1	NA	NA
NPKM_6786	121056 +	122067 Rmet_6264		98.67	6.81	Op1910f_1	NA	Q1L9Q3 Phage Gp37Gp68
NPKM_6787	122112 +	122355 Rmet_6265	mtp2	47.00	6.56	Op1910f_1	NA	Q5NV24 Putative DNA methyltransferase
NPKM_6788	122351 +	122597 Rmet_6266		81.33	11.68	Op1910f_1	NA	Q1L9Q1 Putative uncharacterized protein
NPKM_6789	122691 +	123282 Rmet_6267		29.33	3.21	Op1910f_1	NA	Q5LK38 Putative uncharacterized protein
NPKM_6790	123311 +	124226 Rmet_6268		6.00	1.00	Op1910f_1	DIV-Apoptosis	Q1L9P9 DNA/RNA non-specific endonuclease
3UTR_128	123976 -	124315 Rmet_6269				Op1911r_1		
3UTR_116	124227 +	124274 Rmet_6268				Op1910f_1		
NPKM_6791	124316 -	125111 Rmet_6269		11.67	1.53	Op1911r_1	NA	Q1L9P8 Putative uncharacterized protein
NPKM_6792	125095 -	125530 Rmet_6397	hupB	18.33	0.58	Op1911r_1	NA	NA
NPKM_6793	125615 -	125924 Rmet_6398		18.33	3.21	Op1911r_1	NA	NA
5UTR_105	125947 +	126003 Rmet_6271				Op1912f_1		
NPKM_6794	126003 +	126750 Rmet_6271		80.67	1.53	Op1912f_1	NA	Q1L9P6 Putative uncharacterized protein
3UTR_117	126751 +	127248 Rmet_6271				Op1912f_1		
NPKM_6795	127142 -	128279 Rmet_6272		21.00	1.00	Op1913r_2	NA	Q5NV28 Putative uncharacterized protein
5UTR_116	128280 -	128528 Rmet_6272				Op1913r_2		
3UTR_127	128671 -	128891 Rmet_6273				Op1913r_1		
NPKM_6796	128892 -	130047 Rmet_6273		5.00	1.00	Op1913r_1	NA	Q5NV29 Putative uncharacterized protein (Helix-turn-helix, Fis-type)
NPKM_6797	130514 -	130712 Rmet_6399		5.00	1.00	Op1913r_1	NA	NA
NPKM_6798	130613 +	130856 Rmet_6274		0.33	0.58	Op1914f_1	NA	Q1L9P3 Putative uncharacterized protein
5UTR_115	130713 -	130911 Rmet_6399				Op1913r_1		
5UTR_106	131050 +	131175 Rmet_6275	parM			Op1914f_2		
NPKM_6799	131175 +	132201 Rmet_6275	parM	6.33	1.53	Op1914f_2	NA	Q5NV30 Putative uncharacterized protein
3UTR_126	132291 -	132297 Rmet_6400				Op2117r_1		
NPKM_6800	132298 -	132535 Rmet_6400		3.00	0.00	Op2117r_1	NA	NA
5UTR_114	132536 -	132609 Rmet_6400				Op2117r_1		
NPKM_6801	132692 +	132824 Rmet_6401		16.00	1.00	Op2118f_1	NA	NA
3UTR_118	132825 +	133317 Rmet_6401				Op2118f_1		
3UTR_125	132872 -	132898 Rmet_6276				Op1915r_2		
NPKM_6802	132899 -	133166 Rmet_6276		8.33	0.58	Op1915r_2	NA	Q1L9P1 Putative uncharacterized protein
NPKM_6803	133208 -	134276 Rmet_6277	pri	9.67	1.15	Op1915r_2	NA	Q1L9P0 Phage P4 alpha, zinc-binding
3UTR_124	134373 -	134540 Rmet_6278	traC2			Op1915r_2		
NPKM_6804	134541 -	135114 Rmet_6278	traC2	19.67	2.08	Op1915r_2	GIP-REP-Complex	Q5NV32 Single-stranded DNA-binding protein
NPKM_6805	135125 -	135908 Rmet_6279		15.67	4.04	Op1915r_2	NA	Q1L9N8 Putative uncharacterized protein
NPKM_6806	135915 -	136347 Rmet_6280		20.33	3.51	Op1915r_2	NA	Q1L9N7 Putative uncharacterized protein
NPKM_6807	136445 -	136754 Rmet_6281		54.00	2.65	Op1915r_2	NA	Q1L9N6 Putative uncharacterized protein
5UTR_113	136755 -	136814 Rmet_6281				Op1915r_2		
5UTR_107	136768 +	136786 Rmet_6402	cbnB			Op2119f_1		
NPKM_6808	136786 +	137011 Rmet_6402	cbnB	1.33	1.53	Op2119f_1	NA	NA
NPKM_6809	137455 -	138475 Rmet_6282	tnpA	0.00	0.00	Op1915r_1	NA	P37248 Transposase for insertion sequence element IS1086
5UTR_108	138493 +	138549 Rmet_6283				Op1916f_1		

NPKM_6810	138549 +	139728 Rmet_6283		3.33	0.58	Op1916f_1	NA	Q5NV34 Putative myosin heavy chain protein (Putative uncharacterized protein)
NPKM_6811	139729 +	140908 Rmet_6284		1.33	0.58	Op1916f_1	NA	Q5NV35 Putative uncharacterized protein
5UTR_109	140939 +	140949 Rmet_6285				Op1916f_2		
NPKM_6812	140949 +	141282 Rmet_6285		12.33	1.15	Op1916f_2	NA	Q1L9N2 Putative uncharacterized protein
3UTR_123	141298 -	142556 Rmet_6288	<i>pilV</i>			Op1917r_5		
NPKM_6813	141383 +	141581 Rmet_6286		45.67	5.03	Op1916f_3	NA	Q5NV36 Putative uncharacterized protein
NPKM_6814	141678 +	142500 Rmet_6287		112.67	4.04	Op1916f_4	NA	Q5NV37 Putative transmembrane lipoprotein (Putative lipoprotein transmembrane)
3UTR_119	142501 +	142803 Rmet_6287				Op1916f_4		
NPKM_6815	142557 -	143778 Rmet_6288	<i>pilV</i>	12.33	1.53	Op1917r_5	NA	Q5NV38 Putative uncharacterized protein pilV (Putative uncharacterized protein)
NPKM_6816	143843 -	144476 Rmet_6289	<i>pilS</i>	3.00	0.00	Op1917r_4	NA	Q5NV39 Hypothetical type IV prepilin protein PilS (Putative uncharacterized protein)
NPKM_6817	144492 -	145728 Rmet_6290	<i>pilR</i>	1.00	0.00	Op1917r_3	NA	Q5NV02 Hypothetical Toxin coregulated pilus biosynthesis protein E (Type II secret
NPKM_6818	145724 -	147542 Rmet_6291	<i>pilB</i>	1.33	0.58	Op1917r_3	NA	Q5NV03 Hypothetical Toxin coregulated pilus biosynthesis protein T (Type II secreti
5UTR_112	147543 -	147543 Rmet_6291	<i>pilB</i>			Op1917r_3		
3UTR_122	147549 -	147551 Rmet_6292				Op1917r_3		
NPKM_6819	147552 -	148188 Rmet_6292		2.33	0.58	Op1917r_3	NA	Q5NV04 Putative uncharacterized protein (Putative uncharacterized protein)
NPKM_6820	148184 -	149549 Rmet_6293	<i>pilO</i>	2.33	0.58	Op1917r_3	NA	Q5NV05 ATPase (Putative uncharacterized protein)
3UTR_121	149569 -	149615 Rmet_6294	<i>pilN</i>			Op1917r_2		
NPKM_6821	149616 -	151419 Rmet_6294	<i>pilN</i>	1.00	0.00	Op1917r_2	NA	Q5NV06 Putative uncharacterized protein pilN (Putative uncharacterized protein)
NPKM_6822	151430 -	152018 Rmet_6295		0.33	0.58	Op1917r_1	NA	Q1L9M2 Putative uncharacterized protein
NPKM_6823	152046 -	152469 Rmet_6296	<i>pilT</i>	0.67	0.58	Op1917r_1	NA	Q5NV10 Hypothetical 17.0 kDa protein (Lytic transglycosylase, catalytic)
NPKM_6824	152465 -	153692 Rmet_6297	<i>pilL</i>	1.00	0.00	Op1917r_1	NA	Q5NV07 Hypothetical lipoprotein PilL (Putative uncharacterized protein)
NPKM_6825	153688 -	154486 Rmet_6298	<i>trbN</i>	1.00	0.00	Op1917r_1	NA	Q5NV08 Putative uncharacterized protein (Putative uncharacterized protein)
NPKM_6826	154478 -	155723 Rmet_6299	<i>trbI</i>	1.00	0.00	Op1917r_1	GIP-PTL-T4S	Q5NV40 Putative uncharacterized protein trbI (Conjugation TrbI-like protein)
NPKM_6827	155722 -	156634 Rmet_6300	<i>trbG</i>	1.00	0.00	Op1917r_1	GIP-PTL-T4S	Q5NV41 Putative uncharacterized protein trbG (Conjugal transfer protein TrbG/VirB
NPKM_6828	156651 -	157359 Rmet_6301	<i>trbF</i>	1.67	0.58	Op1917r_1	NA	Q5NV42 Putative uncharacterized protein
5UTR_111	157360 -	157370 Rmet_6301	<i>trbF</i>			Op1917r_1		
5UTR_110	157756 +	157757 Rmet_6302	<i>trbB</i>			Op1918f_1		
NPKM_6829	157757 +	158807 Rmet_6302	<i>trbB</i>	0.67	0.58	Op1918f_1	NA	Q5NV43 Putative uncharacterized protein traJ (Type II secretion system protein E)
NPKM_6830	158826 +	159174 Rmet_6303	<i>trbC</i>	1.00	1.00	Op1918f_1	NA	Q5NV44 Putative uncharacterized protein (Putative uncharacterized protein)
NPKM_6831	159175 +	159505 Rmet_6304	<i>trbD</i>	0.33	0.58	Op1918f_1	GIP-PTL-T4S	Q1L9L3 Putative uncharacterized protein
NPKM_6832	159498 +	161955 Rmet_6305	<i>trbE</i>	1.00	0.00	Op1918f_2	GIP-PTL-T4S	Q5NV45 Putative uncharacterized protein trbE (Type IV secretory pathway VirB4 cor
NPKM_6833	161971 +	162730 Rmet_6306	<i>trbI</i>	1.33	0.58	Op1918f_2	NA	Q5NV46 Hypothetical entry exclusion protein A TrbJ (Putative uncharacterized prote
NPKM_6834	162742 +	163795 Rmet_6307	<i>trbL</i>	0.67	0.58	Op1918f_2	NA	Q5NV47 Conjugal transfer protein trbL (Putative uncharacterized protein)
NPKM_6835	163794 +	165036 Rmet_6308	<i>tral</i>	2.33	0.58	Op1918f_3	NA	Q1L9K9 Putative uncharacterized protein
NPKM_6836	165032 +	166901 Rmet_6309	<i>traG</i>	2.67	0.58	Op1918f_3	NA	Q5NV49 Hypothetical conjugative coupling factor protein (Putative uncharacterized
NPKM_6837	166907 +	167414 Rmet_6310		3.00	1.73	Op1918f_3	NA	Q5NV50 Putative uncharacterized protein
NPKM_6838	167403 +	167685 Rmet_6311		4.00	1.00	Op1918f_3	NA	Q1L9K6 Putative uncharacterized protein
NPKM_6839	167688 +	168306 Rmet_6312		3.00	1.00	Op1918f_3	NA	Q1L9K5 Putative uncharacterized protein
NPKM_6840	168292 +	169195 Rmet_6313		16.33	1.15	Op1918f_4	NA	Q1L9K4 Putative uncharacterized protein
NPKM_6841	169473 +	171213 Rmet_6314	<i>uvrD</i>	6.67	0.58	Op1918f_4	NA	Q5NV53 Helicase
3UTR_120	171214 +	171369 Rmet_6314	<i>uvrD</i>			Op1918f_4		

1125204.67 total

Supplementary Table S2. DNA regions up-regulated in wild type and mutant cells upon multiple metal shock^a

Rmet	Gene	NPKM	OperonReg	Q(WT)	Q2(WT)	Q(DN546)	QQ546	Q(DN553)	QQ553	Q(DN554)	QQ554	Q(DN555)	QQ555	Description
Environmental Information Processing (49 operons)														
<i>Membrane Transport (48 operons)</i>														
Other transporters (9 operons)														
Rmet_2313	<i>merT</i>	0.00	Op0661f_1	407.43	32.40	20.20	0.62	43.41	1.34	17.26	0.53	18.35	0.57	Mercuric transport protein MerT
Rmet_2314	<i>merP</i>	1.33	Op0661f_2	15.21	3.48	3.62	1.03	6.18	1.77	3.16	0.90	2.80	0.80	Periplasmic mercuric ion binding protein MerP
Rmet_2315	<i>merA</i>	1.00	Op0661f_2	18.06	27.76	29.69	1.07	64.87	2.34	28.57	1.03	24.95	0.90	Mercuric (Hg(II)) reductase
Rmet_2317		0.00	Op0661f_2	11.39	24.81	19.86	0.80	27.01	1.09	18.44	0.74	15.24	0.62	Transposase Tn3
Rmet_6172	<i>merT</i>	0.00	Op1890r_1	91.98	18.14	12.95	0.71	23.40	1.29	11.18	0.62	11.32	0.62	Mercuric transport protein MerT
Rmet_6173	<i>merP</i>	0.00	Op1890r_1	309.53	49.19	23.57	0.48	43.59	0.89	20.12	0.41	21.46	0.44	Periplasmic mercuric ion binding protein MerP
Rmet_6174	<i>merA</i>	1.00	Op1890r_2	67.25	90.31	56.77	0.63	75.28	0.83	40.74	0.45	42.08	0.47	Mercuric (Hg(II)) reductase
Rmet_6175	<i>merD</i>	0.00	Op1890r_2	41.92	104.93	73.77	0.70	92.93	0.89	50.24	0.48	55.23	0.53	Putative secondary regulatory protein MerD
Rmet_6176	<i>merE</i>	0.00	Op1890r_2	36.74	67.54	41.41	0.61	62.42	0.92	33.71	0.50	35.24	0.52	Mercuric resistance protein merE
Rmet_6177		0.00	Op1890r_2	68.73	78.53	37.74	0.48	56.55	0.72	35.15	0.45	32.94	0.42	Diguanylate phosphodiesterase (EAL domain)
Rmet_6178		0.00	Op1890r_2	29.31	50.46	25.72	0.51	28.99	0.57	18.67	0.37	18.63	0.37	Resolvase-like protein
Rmet_6179		0.00	Op1890r_2	9.85	18.48	12.37	0.67	13.01	0.70	10.20	0.55	8.81	0.48	Transposase (Transposase Tn3)
Rmet_6180		6.67	Op1891f_1	7.21	11.69	17.16	1.46	20.86	1.79	16.37	1.40	11.23	0.96	General substrate transporter
Rmet_6183	<i>merA</i>	5.00	Op1894f_2	40.39	79.53	50.92	0.64	68.16	0.86	34.44	0.43	37.06	0.47	Mercuric reductase
Rmet_6187		49.33	Op1894f_4	13.83	13.71	9.17	0.67	12.16	0.89	11.93	0.87	7.95	0.58	Resolvase of Tn4378 (Resolvase-like protein)
Rmet_6188		18.67	Op1894f_4	6.32	7.65	7.23	0.95	8.57	1.12	6.91	0.91	5.09	0.67	Hypothetical transposase for transposon Tn4378
Rmet_6189		8.67	Op1894f_4	2.50	5.52	5.57	1.01	6.36	1.15	6.44	1.16	4.10	0.74	Putative uncharacterized protein
Rmet_2299		61.67	Op0656r_1	6.65	31.17	32.73	1.05	25.80	0.83	45.75	1.47	21.06	0.68	Putative integral membrane protein / transporter
Other ion-coupled transporters (28 operons)														
Rmet_5973	<i>tnpB</i>	0.00	Op1818r_1	2.42	1.71	1.77	1.04	1.53	0.90	2.30	1.35	1.85	1.09	Integrase catalytic region
Rmet_5974	<i>ompP</i>	31.00	Op1818r_2	2.76	1.96	2.09	1.06	2.26	1.15	2.36	1.20	1.98	1.01	Porin Gram-negative type
Rmet_5975	<i>czcJ</i>	9.33	Op1818r_2	330.95	32.38	49.39	1.52	29.97	0.93	49.28	1.52	39.42	1.22	Putative uncharacterized protein
Rmet_5976	<i>czcE</i>	26.33	Op1819f_1	6.32	3.24	4.80	1.53	4.40	1.36	4.94	1.57	4.35	1.38	Putative uncharacterized protein
Rmet_5977	<i>czcS</i>	22.33	Op1819f_1	8.30	10.57	14.62	1.39	7.90	0.75	9.74	0.92	10.11	0.96	Sensor protein CzcS
Rmet_5978	<i>czcR</i>	38.67	Op1819f_1	40.54	1.07	1.05	0.98	0.79	0.74	0.88	0.83	0.85	0.80	Transcriptional activator protein CzcR
Rmet_5979	<i>czcD</i>	26.33	Op1819f_1	17.36	10.41	12.59	1.21	8.01	0.77	9.39	0.90	9.69	0.93	Cobalt-zinc-cadmium resistance protein CzcD
Rmet_5980	<i>czcA</i>	42.33	Op1819f_1	15.12	13.54	20.01	1.48	9.99	0.74	12.11	0.89	14.17	1.04	Cobalt-zinc-cadmium resistance protein CzcA
Rmet_5981	<i>czcB</i>	39.00	Op1819f_1	21.46	22.35	34.53	1.55	14.68	0.66	20.14	0.90	21.56	0.97	Cobalt-zinc-cadmium resistance protein CzcB
Rmet_5982	<i>czcC</i>	57.00	Op1819f_1	19.09	32.80	42.76	1.30	24.20	0.74	25.32	0.77	30.74	0.94	Cobalt-zinc-cadmium resistance protein CzcC
Rmet_5983	<i>czcI</i>	357.33	Op1820f_1	8.18	18.33	26.30	1.43	14.28	0.78	13.67	0.75	18.26	0.99	Putative uncharacterized protein
Rmet_5031	<i>cusC</i>	3.33	Op1480f_2	23.34	15.22	20.46	1.34	17.18	1.13	21.08	1.38	22.81	1.50	Putative outer membrane cation efflux protein
Rmet_5032	<i>cucB</i>	1.33	Op1480f_2	16.96	7.44	10.74	1.43	8.60	1.16	12.55	1.67	11.49	1.53	Secretion protein HlyD
Rmet_5033	<i>cusA</i>	1.00	Op1480f_2	254.92	76.37	118.10	1.55	94.31	1.23	152.76	2.00	149.90	1.96	Heavy metal efflux pump CzcA, HME1
Rmet_5034	<i>cusF</i>	4.67	Op1480f_3	21.19	1.84	2.18	1.19	1.63	0.89	1.99	1.09	2.37	1.29	Conserved hypothetical signal peptide protein
Rmet_5035		243.00	Op1481r_4	8.91	10.20	17.49	1.71	13.23	1.30	17.84	1.75	19.16	1.87	Putative uncharacterized protein
Rmet_5036		102.33	Op1481r_3	2.51	4.77	7.88	1.67	6.78	1.42	8.71	1.84	9.14	1.93	Putative uncharacterized protein
Rmet_5037		27.67	Op1481r_2	4.34	3.38	4.44	1.33	3.27	0.97	4.98	1.49	4.83	1.44	Phenylacetic acid degradation-related protein
Rmet_6106	<i>copT</i>	22.33	Op1863f_1	1.69	1.86	2.50	1.30	2.27	1.22	3.01	1.57	2.77	1.45	Putative uncharacterized protein CopT
Rmet_6107		3.67	Op1864r_1	21.79	7.51	10.91	1.44	8.67	1.15	13.84	1.83	11.48	1.52	Putative uncharacterized protein
Rmet_6108	<i>copK</i>	18.67	Op1864r_2	92.04	27.81	44.56	1.60	36.16	1.30	72.21	2.60	49.65	1.79	Copper resistance protein K
Rmet_6109		26.00	Op1865f_1	5.06	9.62	23.02	2.38	17.37	1.80	27.65	2.86	26.37	2.73	Putative uncharacterized protein

Rmet_6110	<i>copS</i>	14.33	Op1865f_1	4.90	2.70	3.01	1.13	2.82	1.05	3.97	1.48	3.56	1.33	Sensor protein
Rmet_6111	<i>copR</i>	17.67	Op1865f_1	5.64	7.01	9.66	1.39	7.34	1.05	9.19	1.32	9.63	1.38	Two component response transcription regulator
Rmet_6112	<i>copA</i>	10.33	Op1866r_1	207.66	67.05	99.15	1.48	51.11	0.76	99.35	1.48	86.69	1.29	Copper resistance transmembrane protein
Rmet_6113	<i>copB</i>	8.00	Op1866r_1	36.72	19.00	33.00	1.74	16.52	0.87	35.95	1.89	25.25	1.33	CopB protein (Copper resistance B)
Rmet_6114	<i>copC</i>	50.33	Op1866r_2	24.51	17.98	31.46	1.75	15.69	0.87	36.40	2.03	24.40	1.36	Copper resistance protein CopC
Rmet_6115	<i>copD</i>	30.33	Op1866r_2	15.36	20.90	40.79	1.95	20.76	0.99	50.77	2.43	31.98	1.53	Copper resistance D transmembrane protein
Rmet_6116		11.00	Op1866r_2	24.42	20.42	34.90	1.71	17.33	0.85	38.82	1.90	27.26	1.34	Putative oxydoreductase (Blue copper domain)
Rmet_5668	<i>copD</i>	2.67	Op1695r_2	3.59	1.86	2.39	1.27	1.74	0.94	2.02	1.07	2.75	1.45	Copper resistance D
Rmet_5669	<i>copC</i>	4.67	Op1695r_2	4.17	2.67	3.57	1.34	2.25	0.84	2.90	1.09	3.96	1.48	Copper resistance protein CopC
Rmet_5670	<i>copB</i>	1.67	Op1695r_1	12.95	4.64	3.94	0.84	2.71	0.58	3.40	0.73	4.36	0.94	Copper resistance B
Rmet_5671	<i>copA</i>	3.33	Op1695r_1	138.74	2.76	2.96	1.07	1.99	0.72	2.96	1.07	2.65	0.96	Copper-resistance protein CopA
Rmet_5672	<i>copR</i>	8.00	Op1696f_1	3.80	7.84	11.50	1.47	10.13	1.29	13.00	1.66	11.21	1.43	Two component transcriptional regulator
Rmet_5673	<i>copS</i>	6.33	Op1696f_1	4.23	5.21	4.45	0.86	3.54	0.68	4.95	0.96	4.18	0.81	Sensor protein
Rmet_5674		24.00	Op1697r_2	1.77	1.97	2.22	1.11	2.30	1.17	2.07	1.03	2.69	1.35	Putative uncharacterized protein
Rmet_5675		24.33	Op1697r_2	1.61	1.79	1.90	1.07	2.13	1.19	1.90	1.07	2.02	1.14	Putative uncharacterized protein
Rmet_5681	<i>nimA2</i>	22.00	Op1697r_1	1.91	2.70	3.31	1.22	2.82	1.04	3.24	1.19	3.54	1.30	Acriflavin resistance protein
Rmet_5682	<i>nimB</i>	33.33	Op1697r_1	7.77	3.81	6.36	1.67	5.17	1.36	6.21	1.63	6.75	1.77	Secretion protein HlyD
Rmet_4465	<i>hmuR</i>	15.67	Op1274f_1	7.51	3.96	6.27	1.59	5.68	1.43	4.94	1.25	5.28	1.33	Two component transcriptional regulator
Rmet_4466	<i>hmuS</i>	7.67	Op1274f_1	5.65	5.87	9.86	1.68	8.33	1.42	10.99	1.88	7.81	1.33	Sensor protein
Rmet_4467		66.00	Op1274f_2	1.87	2.12	3.27	1.52	3.24	1.53	3.37	1.57	3.21	1.49	3-demethylubiquinone-9 3-methyltransferase
Rmet_4468	<i>hmuA</i>	14.00	Op1275r_2	3.83	2.36	3.48	1.52	2.41	1.02	2.05	0.90	2.83	1.24	Heavy metal efflux pump HmuA, HME1
Rmet_6143	<i>mmrQ</i>	21.00	Op1878r_1	6.19	3.21	6.21	1.90	5.64	1.76	11.15	3.42	5.63	1.73	Putative uncharacterized protein RMe0345
Rmet_6144	<i>nreB</i>	1.00	Op1879f_1	2.47	1.75	3.10	1.83	3.56	2.03	2.87	1.70	2.87	1.70	NreB protein (nickel resistance)
Rmet_6136	<i>silA</i>	12.67	Op1874r_1	4.22	9.35	18.01	1.92	15.90	1.70	23.35	2.49	21.35	2.28	Silver efflux protein
Rmet_6134	<i>silC</i>	8.00	Op1874r_1	3.83	2.72	4.26	1.59	3.83	1.41	6.97	2.60	4.15	1.55	Outer membrane silver efflux protein
Rmet_6135	<i>silB</i>	6.33	Op1874r_1	1.77	1.71	2.54	1.44	2.42	1.42	3.47	1.96	2.58	1.46	Silver efflux protein
Rmet_0333		8.00	Op0094r_2	8.89	5.50	5.48	0.99	14.64	2.66	4.43	0.80	4.91	0.89	Transcriptional regulator, ArsR family
Rmet_0327		5.00	Op0094r_3	1.53	1.95	1.39	0.74	3.30	1.69	1.67	0.89	1.63	0.86	Major facilitator superfamily MFS_1
Rmet_0328		13.00	Op0094r_3	3.65	3.62	2.14	0.59	6.87	1.90	2.52	0.69	2.16	0.59	NADPH-dependent FMN reductase
Rmet_0329	<i>arsC</i>	13.67	Op0094r_3	2.47	3.63	2.09	0.58	8.33	2.29	2.88	0.80	2.18	0.61	Arsenate reductase
Rmet_0330		8.67	Op0094r_3	1.71	1.30	1.16	0.92	2.51	1.94	1.18	0.94	1.08	0.86	Bile acid:sodium symporter
ATPases (11 operons)														
Rmet_4594	<i>zntA</i>	48.33	Op1321r_1	6.97	7.26	8.20	1.13	5.90	0.81	6.75	0.93	6.84	0.94	Heavy metal translocating P-type ATPase
Rmet_4595	<i>czcI2</i>	26.00	Op1322f_1	4.16	16.76	27.43	1.64	19.93	1.19	28.08	1.68	23.60	1.41	Putative uncharacterized protein
Rmet_4596	<i>czcC2</i>	2.00	Op1322f_1	164.80	227.36	349.28	1.54	186.86	0.82	237.56	1.05	213.20	0.94	Outer membrane efflux protein
Rmet_4597	<i>czcB2'</i>	0.67	Op1322f_1	16.02	41.89	79.85	1.91	38.31	0.91	44.69	1.07	52.41	1.25	Secretion protein HlyD
Rmet_4598		0.00	Op1323r_1	8.92	18.23	25.00	1.37	18.30	1.00	21.94	1.20	18.75	1.03	Tn3 family transposase
Rmet_4599		0.00	Op1323r_1	6.32	11.25	5.29	0.47	5.85	0.52	3.53	0.31	4.51	0.40	Putative resolvase
Rmet_5947	<i>pbrA</i>	7.67	Op1808r_1	64.27	70.90	70.87	1.00	70.83	1.00	55.32	0.78	51.41	0.73	Pb-efflux ATPase
Rmet_5948	<i>pbrB</i>	5.67	Op1808r_1	14.65	35.25	42.47	1.20	36.27	1.03	33.39	0.95	31.22	0.89	PbrB/pbrC lead resistance fusion protein
Rmet_5949		15.67	Op1808r_2	37.84	60.51	57.71	0.95	53.69	0.89	47.19	0.78	45.19	0.75	Putative uncharacterized protein
Rmet_5950		1.33	Op1809f_1	4.67	16.87	24.61	1.46	21.61	1.28	17.85	1.06	20.84	1.23	Putative integrase/recombinase (Phages)
Rmet_5969		20.33	Op1816r_3	56.49	87.18	142.38	1.63	108.52	1.24	109.11	1.25	104.69	1.20	Putative uncharacterized protein
Rmet_5970	<i>czcP</i>	7.67	Op1817f_1	40.01	59.10	102.02	1.73	71.36	1.21	73.77	1.25	77.38	1.31	Heavy metal translocating P-type ATPase
Rmet_2303	<i>cadA</i>	15.33	Op0659f_1	54.48	78.76	89.86	1.14	69.59	0.88	79.79	1.01	61.53	0.78	Heavy metal translocating P-type ATPase
Rmet_2304		11.67	Op0659f_1	33.28	76.58	96.15	1.26	61.69	0.81	87.32	1.14	61.90	0.81	Lipoprotein signal peptidase
Rmet_3522		62.00	Op0974r_2	3.84	12.62	8.60	0.68	13.36	1.06	7.02	0.56	8.15	0.65	Alpha/beta hydrolase fold
Rmet_3523	<i>cupR</i>	84.00	Op0974r_2	20.23	32.54	21.61	0.67	42.06	1.29	17.96	0.55	19.56	0.60	Transcriptional regulator, MerR family
Rmet_3524	<i>cupA</i>	26.33	Op0974r_1	15.20	23.82	16.66	0.70	45.85	1.92	18.91	0.79	18.93	0.80	Heavy metal translocating P-type ATPase
Rmet_3525	<i>cupC</i>	76.33	Op0975f_1	9.52	19.05	14.33	0.75	18.88	0.99	13.77	0.72	12.13	0.64	Heavy metal transport/detoxification protein

Rmet_6117	<i>copJ</i>	54.00	Op1867f_1	1.99	5.36	<u>6.61</u>	1.23	<u>5.45</u>	1.02	<u>6.17</u>	1.15	<u>6.28</u>	1.17	CopJ protein (Cytochrome c, class I)
Rmet_6118	<i>copG</i>	65.33	Op1867f_1	<u>5.92</u>	5.23	<u>3.21</u>	0.62	<u>5.11</u>	0.98	<u>2.68</u>	0.52	<u>3.18</u>	0.61	CopG protein
Rmet_6119	<i>copF</i>	49.00	Op1867f_1	<u>3.25</u>	4.01	<u>2.81</u>	0.71	<u>5.53</u>	1.38	<u>2.49</u>	0.63	<u>3.13</u>	0.79	Cation-transporting P-type ATPase
Signal Transduction (1 operon)				-	-	-	-	-	-	-	-	-	-	-
Two-component system [PATH:ko02020]				-	-	-	-	-	-	-	-	-	-	-
Rmet_4026	<i>Rmet_4026</i>	8.00	Op1133r_1	<u>9.00</u>	17.31	<u>20.60</u>	1.19	<u>10.44</u>	0.60	<u>9.17</u>	0.53	<u>13.54</u>	0.78	Putative periplasmic ligand-binding sensor protein
Genetic Information Processing (9 operons)				-	-	-	-	-	-	-	-	-	-	-
Folding, Sorting and Degradation (5 operons)				-	-	-	-	-	-	-	-	-	-	-
Protein folding and associated processing (4 operons)				-	-	-	-	-	-	-	-	-	-	-
Rmet_3620		55.33	Op1008f_1	<u>186.44</u>	119.01	<u>129.33</u>	1.09	<u>76.48</u>	0.64	<u>49.23</u>	0.41	<u>78.31</u>	0.66	Peptidase S1C, Do
Rmet_3621		284.67	Op1008f_2	1.94	5.15	<u>7.72</u>	1.50	<u>5.20</u>	1.01	<u>2.90</u>	0.56	<u>5.94</u>	1.15	Putative uncharacterized protein
Rmet_1864		80.00	Op0539f_1	<u>5.83</u>	2.14	1.49	0.69	1.34	0.63	1.68	0.79	1.56	0.73	UPF0061 protein Rmet_1864
Rmet_1865	<i>msrB</i>	145.33	Op0539f_1	<u>4.37</u>	2.13	1.95	0.91	1.20	0.56	1.89	0.88	1.53	0.72	Methionine sulfoxide reductase B
Type II secretion system [PATH:ko03090] (1 operon)				-	-	-	-	-	-	-	-	-	-	-
Rmet_2331		0.00	Op0661f_8	<u>7.62</u>	2.98	<u>3.58</u>	1.20	<u>2.92</u>	0.98	<u>2.92</u>	0.98	<u>3.59</u>	1.20	Putative secreted protein
Rmet_2332		0.00	Op0661f_8	<u>3.76</u>	0.82	<u>2.50</u>	3.02	1.89	<u>2.30</u>	0.53	0.64	1.96	<u>2.37</u>	Putative uncharacterized protein ORF C69
Replication and Repair (3 operons)				-	-	-	-	-	-	-	-	-	-	-
Other replication, recombination and repair proteins (3 operons)				-	-	-	-	-	-	-	-	-	-	-
Rmet_4473		0.00	Op1276f_1	<u>55.90</u>	64.02	<u>29.59</u>	0.46	<u>32.53</u>	0.51	<u>22.11</u>	0.35	<u>22.19</u>	0.35	Putative resolvase
Rmet_6002		0.00	Op1829f_1	<u>37.96</u>	54.12	<u>89.61</u>	1.66	<u>52.46</u>	0.97	<u>63.49</u>	1.17	<u>67.69</u>	1.25	Putative Transposase Tn3
Rmet_2998		3.67	Op0844r_1	2.40	1.89	<u>2.97</u>	1.55	<u>2.47</u>	1.31	<u>2.27</u>	1.18	<u>2.30</u>	1.20	Transposase Tn3
Transcription (1 operon)				-	-	-	-	-	-	-	-	-	-	-
Other transcription related proteins (1 operon)				-	-	-	-	-	-	-	-	-	-	-
Rmet_3456		149.00	Op0962r_3	<u>2.06</u>	3.25	<u>3.18</u>	0.99	<u>2.98</u>	0.92	<u>2.20</u>	0.68	<u>2.47</u>	0.77	Transcriptional regulator, MerR family
Metabolism (1 operon)				-	-	-	-	-	-	-	-	-	-	-
Metabolism of Cofactors and Vitamins (1 operon)				-	-	-	-	-	-	-	-	-	-	-
Iron-sulfur-cluster biosynthesis (1 operon)				-	-	-	-	-	-	-	-	-	-	-
Rmet_1024		1019	Op0295f_3	<u>2.14</u>	2.33	<u>5.40</u>	2.32	<u>3.83</u>	1.64	<u>2.73</u>	1.17	<u>3.27</u>	1.40	Transcriptional regulator, BadM/Rrf2 family
Rmet_1025		825	Op0295f_3	1.59	2.66	<u>6.60</u>	2.48	<u>3.57</u>	1.34	<u>3.70</u>	1.39	<u>3.53</u>	1.33	Cysteine desulfurase IscS
Rmet_1026		1093	Op0295f_3	<u>2.91</u>	2.20	<u>2.90</u>	1.32	<u>2.17</u>	0.98	<u>2.43</u>	1.10	<u>2.14</u>	0.97	FeS cluster assembly scaffold IscU
Not assigned (7 operons)				-	-	-	-	-	-	-	-	-	-	-
Rmet_4128		64.00	Op1164f_1	<u>40.82</u>	0.92	1.61	1.75	<u>2.17</u>	2.36	0.60	0.66	1.41	1.54	Putative uncharacterized protein
Rmet_5307		6.00	Op1568f_1	<u>5.82</u>	1.68	<u>2.09</u>	1.23	1.71	1.02	1.81	1.06	<u>2.07</u>	1.22	NnrS
Rmet_5308		10.33	Op1569r_1	<u>25.45</u>	22.02	<u>34.48</u>	1.57	<u>20.95</u>	0.95	<u>27.82</u>	1.27	<u>29.73</u>	1.35	Putative uncharacterized protein
Rmet_3408		14.00	Op0947f_1	<u>10.69</u>	4.15	<u>4.44</u>	1.07	<u>2.36</u>	0.57	1.85	0.44	<u>3.05</u>	0.73	Radical SAM
Rmet_3409		9.00	Op0947f_1	1.55	3.30	<u>5.61</u>	1.70	<u>2.50</u>	0.76	<u>2.22</u>	0.67	<u>3.71</u>	1.12	YdjC-like protein
Rmet_3410		3.67	Op0947f_1	<u>2.07</u>	2.97	<u>4.34</u>	1.47	<u>2.16</u>	0.73	1.96	0.66	<u>3.03</u>	1.02	Putative uncharacterized protein
Rmet_5051		5.00	Op1485r_1	<u>7.76</u>	3.36	<u>2.25</u>	0.68	<u>4.51</u>	1.34	<u>2.08</u>	0.63	<u>2.09</u>	0.63	Putative uncharacterized protein
Rmet_4807		188.67	Op1398f_2	<u>2.02</u>	4.14	<u>4.89</u>	1.18	<u>4.38</u>	1.06	<u>2.04</u>	0.49	<u>3.28</u>	0.79	Putative uncharacterized protein
Rmet_4808		1.33	Op1399r_1	2.34	0.97	<u>2.57</u>	2.73	<u>2.54</u>	2.63	0.75	0.80	1.73	1.84	Di-haem cytochrome c peroxidase

^aThe table gives the regulation (Q values) of genes in metal-mix-treated *C. metallidurans* cells compared to the untreated control cells. “Op” gives the operon, Q(WT) and Q2(WT) the comparison of metal-treated CH34 cells to untreated cells. The Q(DN..) values compare metal-treated mutant cells to untreated CH34 cells, the QQ(DN..) values metal-treated mutant cells to metal-treated CH34 cells. Values Q > 2 in green, Q < 0.5 in red, significant values (D > 1) bold-faced and underlined. The genes were sorted into the KEGG orthology system according to the gene that was most strongly up-regulated.

Supplementary Table S3. Regulation of genes for transport and regulatory proteins upon multiple metal shock^a

Gene	Name	NPKM	Q(WT)	Q2WT	Q(DN546)	Q546	Q(DN553)	Q553	Q(DN554)	Q554	Q(DN555)	Q555	Description
Import Systems													
<i>corA1</i>	Rmet_3052	54.00	0.45	0.34	0.97	1.40	1.42	1.98	0.74	1.06	1.23	1.77	Magnesium and cobalt transport protein CorA
<i>corA2</i>	Rmet_0036	68.00	1.03	1.02	0.96	1.14	0.78	0.93	1.03	1.22	0.83	0.99	Mg2+ transporter protein, CorA-like protein
<i>corA3</i>	Rmet_3287	145.7	0.37	1.09	1.40	1.16	0.92	0.77	1.34	1.12	1.24	1.03	Mg2+ transporter protein, CorA-like protein
<i>zntB</i>	Rmet_0549	14.33	0.34	0.95	0.88	0.96	0.94	0.99	1.04	1.14	0.93	1.02	Mg2+ transporter protein, CorA-like protein
<i>mgtB</i>	Rmet_2211	23.67	1.41	0.94	1.12	1.22	1.16	1.23	0.80	0.87	1.17	1.27	Mg2+/Ca2+-importing P-type ATPase
<i>mgtA</i>	Rmet_5396	11.33	1.27	0.83	0.90	1.08	0.85	1.03	0.90	1.08	1.04	1.24	Mg2+/Ca2+-importing P-type ATPase
<i>zupT</i>	Rmet_2621	74.67	0.37	1.04	1.09	1.04	1.47	1.42	1.02	0.98	1.19	1.15	Zinc/iron permease
<i>hoxN</i>	Rmet_1533	72.67	0.03	1.36	0.51	0.37	0.54	0.40	0.52	0.39	56.82	42.09	High-affinity nickel-transporter
<i>pitA</i>	Rmet_1973	221.7	0.50	0.84	1.76	2.12	1.96	2.33	0.26	0.32	1.36	1.64	Phosphate transporter
HME-RND efflux systems													
<i>czcA</i>	Rmet_5980	42.33	15.12	13.54	20.01	1.48	9.99	0.74	12.11	0.89	14.17	1.04	Cobalt-zinc-cadmium resistance protein CzcA
<i>hmuA</i>	Rmet_4468	14.00	3.83	2.36	3.48	1.52	2.41	1.02	2.05	0.90	2.83	1.24	Cobalt-zinc-cadmium resistance protein
<i>cnrA</i>	Rmet_6210	17.33	2.59	4.28	3.82	0.89	3.22	0.75	6.80	1.58	1.86	0.43	Cobalt-nickel resistance protein
<i>nccA</i>	Rmet_6145	1.33	1.45	0.92	0.91	0.93	1.13	1.23	0.93	0.95	0.97	1.00	Cobalt-nickel resistance protein
<i>zniA</i>	Rmet_5319	18.67	0.99	0.98	0.89	0.92	1.02	1.04	0.95	0.99	0.96	0.99	HME3a-RND protein
<i>hmvA</i>	Rmet_3838	41.67	0.40	0.48	0.47	1.00	0.60	1.27	0.77	1.62	0.62	1.31	HME3a-RND protein
<i>zneA</i>	Rmet_5329	6.67	1.12	0.85	0.83	0.89	1.14	1.35	0.95	1.03	0.86	0.93	HME3a-RND protein
<i>hmyA</i>	Rmet_4123	18.67	0.94	1.04	1.69	1.61	1.97	1.89	1.10	1.05	1.11	1.06	HME3c-RND protein
<i>nimA1</i>	Rmet_5678	44.67	1.05	1.23	1.70	1.22	1.55	1.16	1.88	1.35	1.74	1.25	HME3b-RND protein
<i>nimA2</i>	Rmet_5681	22.00	1.91	2.70	3.31	1.22	2.82	1.04	3.24	1.19	3.54	1.30	HME3b-RND protein
<i>hmzA</i>	Rmet_3011	3.00	1.67	1.09	1.26	1.09	1.08	0.99	0.97	0.83	1.07	0.92	HME3b-RND protein, second part
<i>cusA</i>	Rmet_5033	1.00	254.92	76.37	118.10	1.55	94.31	1.23	152.76	2.00	149.90	1.96	Copper-silver resistance protein
<i>silA</i>	Rmet_6136	12.67	4.22	9.35	18.01	1.92	15.90	1.70	23.35	2.49	21.35	2.28	Copper-silver resistance protein
P-type efflux ATPases													
<i>czcP</i>	Rmet_5970	7.67	40.01	87.18	102.02	1.73	71.36	1.21	73.77	1.25	77.38	1.31	Zn-translocating P-type ATPase
<i>zntA</i>	Rmet_4594	48.33	6.97	7.26	8.20	1.13	5.90	0.81	6.75	0.93	6.84	0.94	Zn/Cd-translocating P-type ATPase
<i>cadA</i>	Rmet_2303	15.33	54.48	78.76	89.86	1.14	69.59	0.88	79.79	1.01	61.53	0.78	Cd/Zn-translocating P-type ATPase
<i>pbrA</i>	Rmet_5947	7.67	64.27	70.90	70.87	1.00	70.83	1.00	55.32	0.78	51.41	0.73	Pb-efflux ATPase (Heavy metal translocating P-type ATPase)
<i>cupA</i>	Rmet_3524	26.33	15.20	23.82	16.66	0.70	45.85	1.92	18.91	0.79	18.93	0.80	Cu-translocating P-type ATPase
<i>copF</i>	Rmet_6119	49.00	3.25	4.01	2.81	0.71	5.53	1.38	2.49	0.63	3.13	0.79	Cu-translocating P-type ATPase
<i>ctpA1</i>	Rmet_2379	31.33	0.42	1.21	1.09	0.91	1.08	0.90	1.16	0.96	1.36	1.13	Cu-translocating P-type ATPase
<i>rdxI</i>	Rmet_2046	90.33	0.78	1.00	1.01	1.04	0.99	0.99	0.94	0.97	1.42	1.47	Cu-translocating P-type ATPase
CDF proteins													
<i>czcD</i>	Rmet_5979	26.33	17.36	10.41	12.59	1.21	8.01	0.77	9.39	0.90	9.69	0.93	Cobalt-zinc-cadmium resistance protein CzcD
<i>dmeF</i>	Rmet_0198	38.00	0.37	0.83	2.70	1.17	1.73	0.74	1.43	0.62	2.45	1.06	Cation diffusion facilitator family transporter
<i>fieF</i>	Rmet_3406	44.33	3.27	0.96	1.37	1.15	1.38	1.16	1.29	1.08	1.40	1.17	Cation diffusion facilitator family transporter
Other transport proteins													
<i>atmA</i>	Rmet_0391	25.00	1.30	1.08	1.40	1.12	0.80	1.18	0.84	1.16	0.83	1.11	Q1LRE9 ABC transporter-related protein
Other Zur regulon components													
<i>cobW1</i>	Rmet_1098	4.00	1.16	0.84	0.98	1.03	0.97	1.20	1.23	0.98	0.92	1.17	Cobalamin synthesis CobW-like protein
<i>cobW2</i>	Rmet_0127	222.67	0.92	0.48	0.44	0.49	1.13	0.41	0.93	0.47	1.10	0.50	Cobalamin synthesis CobW-like protein
<i>cobW3</i>	Rmet_0125	127.67	0.25	3.44	0.85	1.00	1.20	0.99	1.17	0.95	1.13	1.03	Cobalamin synthesis CobW-like protein
<i>dksA1</i>	Rmet_0126	1312	0.48	1.60	0.77	0.70	0.91	0.71	0.92	0.83	1.07	0.66	Transcriptional regulators, TraR/DksA family
MerR-type regulators													
	Rmet_2302	262.67	1.35	0.85	1.71	1.46	1.25	1.08	1.03	0.88	1.24	1.06	Putative transcriptional regulator, MerR family
<i>cupR</i>	Rmet_3523	84.00	20.23	32.54	21.61	0.67	42.06	1.29	17.96	0.55	19.56	0.60	Transcriptional regulator, MerR family

<i>merD</i>	Rmet_3456	149.00	<u>2.06</u>	<u>3.25</u>	<u>3.18</u>	0.99	<u>2.98</u>	0.92	<u>2.20</u>	0.68	<u>2.47</u>	0.77	Transcriptional regulator, MerR family
	Rmet_1167	298.00	0.11	1.52	1.63	1.58	1.28	1.25	1.73	1.68	1.88	1.83	Transcriptional regulator, MerR family
	Rmet_3602	51.00	0.70	1.36	0.86	0.94	0.93	1.05	0.82	0.90	0.83	0.91	Transcriptional regulator, MerR family
ArsR-type regulators													
	Rmet_5676	23.67	0.44	1.21	0.86	0.98	1.00	1.17	0.78	0.88	0.83	0.94	Transcriptional regulator, ArsR family
	Rmet_2370	33.00	0.77	0.81	0.99	1.46	0.77	1.12	0.55	0.81	0.49	0.73	Putative transcriptional activator
	Rmet_2500	23.67	0.62	0.99	0.77	0.88	0.77	0.89	1.01	1.14	0.64	0.73	Transcriptional regulator, ArsR family
	Rmet_1799	28.33	1.63	1.30	0.83	1.02	0.81	1.05	0.65	0.80	0.76	0.94	Transcriptional regulator, ArsR family
	Rmet_5569	120.7	0.32	1.04	1.74	1.74	1.25	1.24	1.33	1.33	1.44	1.44	Transcriptional regulator, ArsR family
Fur-type regulators													
<i>furB</i>	Rmet_5746	9.33	0.32	0.44	0.55	1.28	0.79	1.80	0.56	1.30	0.53	1.23	Ferric uptake regulator, Fur family@(8E-85)-
<i>furC = zur</i>	Rmet_0128	52.67	0.42	0.92	0.93	1.09	0.97	1.17	0.98	1.16	0.96	1.13	Putative ferric uptake regulator, FUR family@(1E-94)-
<i>furA</i>	Rmet_2976	600	0.26	1.05	1.72	1.63	1.15	1.10	1.16	1.10	1.37	1.30	Ferric uptake regulation protein@(2E-78)-
MntR-type regulators													
	Rmet_1141	23.00	1.22	0.68	<u>2.20</u>	<u>2.18</u>	<u>2.59</u>	<u>2.61</u>	0.65	0.64	<u>2.09</u>	<u>2.08</u>	Transcriptional regulator, GntR family
	Rmet_2798	30.00	2.37	1.01	1.41	1.86	<u>3.38</u>	<u>4.51</u>	0.68	0.90	1.19	1.57	Transcriptional regulator, GntR family
	Rmet_0884	17.33	0.58	1.05	1.32	1.29	1.11	1.08	1.07	1.05	1.29	1.27	Transcriptional regulator, GntR family
Two-component regulatory systems (only those that were regulated)													
<i>creC</i>	Rmet_1651	12.00	0.59	1.07	1.31	1.19	1.28	1.20	1.12	1.01	<u>5.15</u>	<u>4.68</u>	Sensor protein
<i>creB</i>	Rmet_1652	17.00	0.99	1.12	1.27	1.12	1.20	1.07	1.01	0.89	<u>2.81</u>	<u>2.48</u>	Two component transcriptional regulator
<i>cusR</i>	Rmet_1751	15.67	0.92	1.57	<u>2.35</u>	1.51	1.69	1.08	<u>2.41</u>	1.55	<u>2.31</u>	1.49	Two component response transcriptional regulator
<i>cusS</i>	Rmet_1752	7.33	0.69	1.37	1.53	1.07	1.39	1.02	1.46	1.02	1.66	1.17	Sensor protein
<i>cheB</i>	Rmet_3693	32.33	<u>2.02</u>	0.86	0.39	0.45	0.62	0.73	1.09	1.27	0.37	0.42	Chemotaxis response regulator
<i>cheY</i>	Rmet_3694	57.67	1.85	0.80	0.42	0.52	0.53	0.66	0.96	1.20	0.34	0.42	Response regulator receiver domain protein
<i>hmuR</i>	Rmet_4465	15.67	<u>7.51</u>	<u>3.96</u>	<u>6.27</u>	1.59	<u>5.68</u>	1.43	<u>4.94</u>	1.25	<u>5.28</u>	1.33	Two component response transcriptional regulator
<i>hmuS</i>	Rmet_4466	7.67	<u>5.65</u>	<u>5.87</u>	<u>9.86</u>	1.68	<u>8.33</u>	1.42	<u>10.99</u>	1.88	<u>7.81</u>	1.33	Sensor protein
	Rmet_4977	0.00	0.78	1.01	<u>2.15</u>	<u>2.19</u>	1.70	1.66	0.68	0.69	<u>2.24</u>	<u>2.28</u>	Sensor protein
	Rmet_4978	0.00	<u>2.63</u>	1.05	<u>4.06</u>	<u>4.31</u>	<u>3.16</u>	<u>3.38</u>	0.34	0.36	<u>2.48</u>	<u>2.64</u>	Two component transcriptional regulator
	Rmet_5392	40.67	0.78	0.95	<u>3.07</u>	1.62	<u>2.28</u>	1.18	<u>2.69</u>	1.42	<u>3.05</u>	1.61	Two component transcriptional regulator
	Rmet_5393	21.00	0.77	0.99	<u>4.59</u>	<u>2.57</u>	<u>2.92</u>	1.63	<u>3.40</u>	1.90	<u>5.30</u>	<u>2.97</u>	Sensor protein
<i>copR</i>	Rmet_5672	8.00	<u>3.80</u>	<u>7.84</u>	<u>11.50</u>	1.47	<u>10.13</u>	1.29	<u>13.00</u>	1.66	<u>11.21</u>	1.43	Two component response transcriptional regulator
<i>copS</i>	Rmet_5673	6.33	<u>4.23</u>	<u>5.21</u>	<u>4.45</u>	0.86	<u>3.54</u>	0.68	<u>4.95</u>	0.96	<u>4.18</u>	0.81	Sensor protein
<i>czcS</i>	Rmet_5977	22.33	<u>8.30</u>	<u>10.57</u>	<u>14.62</u>	1.39	<u>7.90</u>	0.75	<u>9.74</u>	0.92	<u>10.11</u>	0.96	Sensor protein CzcS
<i>czcR</i>	Rmet_5978	38.67	40.54	1.07	1.05	0.98	0.79	0.74	0.88	0.83	0.85	0.80	Transcriptional activator protein
<i>silS</i>	Rmet_6110	14.33	<u>4.90</u>	<u>2.70</u>	<u>3.01</u>	1.13	<u>2.82</u>	1.05	<u>3.97</u>	1.48	<u>3.56</u>	1.33	Sensor protein
<i>silR</i>	Rmet_6111	17.67	<u>5.64</u>	<u>7.01</u>	<u>9.66</u>	1.39	<u>7.34</u>	1.05	<u>9.19</u>	1.32	<u>9.63</u>	1.38	Two component response transcription regulator

^aThe table gives the regulation (Q values) of genes involved in metal homeostasis in metal-mix-treated *C. metallidurans* cells compared to the untreated control cells. Q(WT) and Q2(WT) give the comparison of metal-treated CH34 cells to untreated cells. The Q(DN..) values compare metal-treated mutant cells to untreated CH34 cells, the QQ(DN...) values metal-treated mutant cells to metal-treated CH34 cells. Values Q > 2 in green, Q < 0.5 in red, significant values (D > 1) bold-faced and underlined.

Supplementary Table S4. Genes up-regulated in wild type but not all mutants

Rmet	Gene	NPKM	OpReg	Q(WT)	Q2(WT)	Q(DN546)	QQ546	Q(DN553)	QQ553	Q(DN554)	QQ554	Q(DN555)	QQ555	Description
DN546 not														
Rmet_3862	<i>lysE</i>	4.00	Op1073r_1	<u>9.91</u>	<u>3.68</u>	0.82	0.22	<u>2.80</u>	0.76	<u>5.71</u>	1.55	<u>3.76</u>	1.02	Lysine exporter protein (LYSE/YGGA)
DN555 not														
Rmet_5936		30.00	Op1805r_3	<u>4.47</u>	<u>3.18</u>	<u>2.19</u>	0.69	<u>2.16</u>	0.68	<u>2.00</u>	0.63	1.94	0.61	Luciferase-like protein
Rmet_6123		5.67	Op1870r_1	<u>2.81</u>	1.23	1.13	0.92	0.99	0.81	1.20	0.98	0.89	0.73	Putative uncharacterized protein
Rmet_6124		22.33	Op1871r_1	<u>2.47</u>	2.04	<u>2.15</u>	1.04	<u>2.03</u>	0.99	<u>2.91</u>	1.41	1.92	0.93	Putative uncharacterized protein
Rmet_6205	<i>cnrY</i>	50.33	Op1896f_2	<u>9.64</u>	<u>6.80</u>	<u>6.45</u>	0.95	<u>7.20</u>	1.06	<u>12.52</u>	1.84	<u>2.42</u>	0.36	Nickel and cobalt resistance protein CnrY
Rmet_6206	<i>cnrX</i>	43.67	Op1896f_2	<u>2.28</u>	<u>4.26</u>	<u>6.71</u>	1.57	<u>5.57</u>	1.31	<u>9.47</u>	<u>2.22</u>	<u>6.17</u>	1.45	Nickel and cobalt resistance protein CnrX
Rmet_6207	<i>cnrH</i>	35.33	Op1896f_2	<u>2.24</u>	<u>4.04</u>	<u>5.69</u>	1.39	<u>4.99</u>	1.24	<u>8.89</u>	<u>2.17</u>	<u>4.67</u>	1.14	RNA polymerase sigma factor CnrH
Rmet_6208	<i>cnrC</i>	32.00	Op1896f_2	<u>4.61</u>	<u>6.29</u>	<u>5.93</u>	0.94	<u>5.81</u>	0.92	<u>9.56</u>	1.52	<u>2.61</u>	0.41	Nickel and cobalt resistance proteinCnrC
Rmet_6209	<i>cnrB</i>	25.00	Op1896f_2	<u>2.53</u>	<u>3.23</u>	<u>3.53</u>	1.11	<u>3.20</u>	0.99	<u>5.17</u>	1.62	1.57	0.49	Nickel and cobalt resistance protein CnrB
Rmet_6210	<i>cnrA</i>	17.33	Op1896f_2	<u>2.59</u>	<u>4.28</u>	<u>3.82</u>	0.89	<u>3.22</u>	0.75	<u>6.80</u>	1.58	1.86	0.43	Nickel and cobalt resistance protein CnrA
Rmet_6211	<i>cnrT</i>	17.33	Op1896f_2	<u>3.43</u>	<u>2.60</u>	<u>2.50</u>	0.96	<u>2.23</u>	0.86	<u>4.25</u>	1.64	1.42	0.55	CnrT protein
DN554 not														
Rmet_4684	<i>gigA</i>	11.00	Op1355r_1	<u>2.04</u>	1.09	<u>8.65</u>	<u>8.06</u>	1.02	0.93	0.75	0.70	1.15	1.07	Putative uncharacterized protein
Rmet_4685	<i>gigP</i>	19.00	Op1355r_1	<u>3.83</u>	<u>2.48</u>	<u>8.66</u>	<u>3.42</u>	<u>3.59</u>	1.45	1.63	0.64	<u>2.21</u>	0.87	Putative uncharacterized protein
Rmet_4686	<i>rpoQ</i>	41.33	Op1356f_1	<u>3.91</u>	1.11	0.02	0.01	1.19	1.07	0.97	0.87	1.15	1.04	Sigma-24 (FecI-like)
Rmet_5133	<i>acd</i>	1.33	Op1513r_1	<u>3.44</u>	1.00	<u>3.91</u>	<u>4.05</u>	<u>3.30</u>	<u>3.29</u>	0.56	0.58	<u>7.98</u>	<u>8.27</u>	Acyl-CoA dehydrogenase-like protein
Rmet_4351		476.7	Op1240f_2	<u>2.16</u>	<u>2.44</u>	<u>4.27</u>	1.74	<u>4.32</u>	1.77	1.97	0.81	<u>2.90</u>	1.18	Putative uncharacterized protein
Not DN553/555														
Rmet_0830		34.33	Op0236r_1	<u>8.22</u>	<u>2.16</u>	<u>2.18</u>	1.00	1.44	0.67	<u>2.10</u>	0.96	1.53	0.70	L-carnitine dehydratase/
Rmet_3612		24.33	Op1004r_1	<u>3.43</u>	<u>2.62</u>	<u>2.39</u>	0.91	1.91	0.73	<u>2.44</u>	0.93	1.73	0.66	Methyltransferase type 11
Nearly all Mutants down														
Rmet_2636		80.33	Op0741f_1	<u>2.28</u>	<u>2.96</u>	1.57	0.53	<u>2.65</u>	0.89	1.52	0.51	1.51	0.51	Thioredoxin
All Mutants down														
Rmet_5446		19.67	Op1619r_2	<u>156.14</u>	<u>63.60</u>	0.79	0.01	1.01	0.02	0.77	0.01	0.86	0.01	Major facilitator superfamily MFS_1
Only 555 down														
Rmet_0175		24.33	Op0052r_1	<u>3.40</u>	<u>2.36</u>	1.40	0.59	1.65	0.70	1.94	0.82	0.27	0.11	5-formyltetrahydrofolate cyclo-ligase
WT_up_Mut_unchanged														
Rmet_0131	<i>hslV</i>	157.0	Op0033f_2	<u>9.91</u>	<u>2.31</u>	0.97	0.42	1.42	0.61	1.07	0.46	0.82	0.35	ATP-dependent protease hslV
Rmet_3501	<i>atpI</i>	1138	Op0970r_1	<u>4.02</u>	<u>2.98</u>	1.55	0.52	1.98	0.67	1.63	0.55	1.25	0.42	ATP synthase I chain
Rmet_4024		3.67	Op1131r_1	<u>4.03</u>	<u>2.09</u>	1.30	0.62	1.72	0.82	1.24	0.59	1.26	0.60	Putative uncharacterized protein
Rmet_5927		98.00	Op1800f_1	<u>2.30</u>	<u>2.25</u>	1.35	0.67	0.82	0.41	0.86	0.43	0.93	0.46	Aldo/keto reductase
Rmet_5952		17.00	Op1810r_2	<u>2.13</u>	<u>2.39</u>	1.63	0.80	1.88	0.91	1.84	0.90	1.12	0.55	Insertion element IRSme11 protein

^aThe table gives the regulation (Q values) of genes in metal-mix-treated *C. metallidurans* cells compared to the untreated control cells. “Op” gives the operon Q(WT) and Q2(WT) the comparison of metal-treated CH34 cells to untreated cells. The Q(DN..) values compare metal-treated mutant cells to untreated CH34 cells, the QQ(DN...) values metal-treated mutant cells to metal-treated CH34 cells. Values Q > 2 in green, Q < 0.5 in red, significant values (D > 1) bold-faced and underlined.

Supplementary Table S5. Changes in expression of the genes in the vicinity of those for ECF sigma factors

Name	Gene	NPKM	OperonReg	Q(WT)	Q2WT	Q(DN546)	Q546	Q(DN553)	Q553	Q(DN554)	Q554	Q(DN555)	Q555	Description
RpoI				<i>ΔrpoQR</i>				<i>ΔrpoIJK</i>		<i>ΔrpoLMO</i>		<i>ΔrpoPE-cnrH</i>		
Rmet_1117	<i>cysK</i>	21.33	Op0320r_2	1.02	0.87	0.93	1.14	0.91	1.05	0.81	0.99	1.03	1.26	Cysteine synthase
Rmet_1118	<i>aleB</i>	191.33	Op0320r_2	0.60	0.72	0.67	0.91	0.36	0.50	0.85	1.15	0.73	0.99	TonB-dependent siderophore receptor
Rmet_1119	<i>rsiA</i>	37.67	Op0320r_1	0.24	0.80	0.93	1.19	0.91	1.14	0.89	1.13	1.07	1.36	Putative FecR
Rmet_1120	<i>rpoI</i>	31.00	Op0320r_1	0.43	0.78	0.79	1.03	0.31	0.40	0.73	0.96	0.83	1.09	Sigma-24 (FecI-like)
Rmet_1121		37.67	Op0320r_1	0.35	1.08	1.01	0.96	2.67	2.47	1.60	1.52	1.22	1.15	Hydrophobe/amphiphile efflux-1 HAE1
Rmet_1122		1.67	Op0321f_1	2.08	0.90	1.00	1.10	9.10	10.09	0.83	0.90	1.05	1.14	Sodium:dicarboxylate symporter
Rmet_1123		2.67	Op0321f_1	1.46	1.04	1.17	1.17	8.53	8.22	0.94	0.94	1.15	1.15	Extracellular solute-binding protein, family 3
Rmet_1124		8.67	Op0321f_2	1.91	0.96	0.88	0.94	1.81	1.89	0.74	0.79	1.07	1.15	Formate dehydrogenase, alpha subunit
RpoJ														
Rmet_4498	<i>rsjA</i>	5.00	Op1281r_1	1.29	1.04	1.30	1.18	1.72	1.67	0.94	0.85	1.21	1.10	Putative FecR
Rmet_4499	<i>rpoJ</i>	7.00	Op1281r_1	1.74	1.16	1.18	1.00	0.95	0.81	0.98	0.83	1.19	1.01	Sigma-24 (FecI-like)
Rmet_4500		1.33	Op1282f_1	1.77	0.90	0.92	1.05	17.25	19.14	0.81	0.92	1.00	1.15	Putative uncharacterized protein
Rmet_4501		5.67	Op1283r_2	1.28	0.83	1.42	1.65	27.58	33.30	0.79	0.92	1.20	1.40	Twin-arginine translocation pathway signal
Rmet_4502	<i>fadB</i>	2.67	Op1283r_1	1.14	0.96	1.09	1.05	3.98	4.13	0.98	0.95	1.14	1.10	Long-chain fatty-acid-CoA ligase
Rmet_4503		2.00	Op1283r_1	0.82	1.05	1.13	1.05	2.43	2.32	0.87	0.81	1.03	0.96	Uncharacterized protein UPF0065
Rmet_4504		8.67	Op1284f_1	1.45	0.45	0.58	1.32	3.01	6.76	0.45	1.03	0.59	1.34	Transcriptional regulator, AraC family
RpoK														
Rmet_4000	<i>rskA</i>	7.33	Op1123r_1	0.73	1.13	1.27	1.15	1.74	1.54	1.12	1.02	1.32	1.20	FecR family protein
Rmet_4001	<i>rpoK</i>	15.00	Op1123r_1	0.77	0.97	0.94	0.90	0.80	0.82	0.84	0.81	1.14	1.10	Sigma-24 (FecI-like)
Rmet_4002		11.67	Op1123r_1	0.74	1.08	1.37	1.32	99.71	92.02	1.11	1.07	1.41	1.36	Response regulator, diguanylate phosphodiesterase
Rmet_4003		43.00	Op1124f_1	2.32	1.12	1.23	1.09	17.84	15.91	1.28	1.14	0.97	0.87	Aspartate racemase
Rmet_4004		0.00	Op1124f_1	0.32	0.96	1.29	1.35	0.75	0.78	0.76	0.80	0.94	0.98	Transposase for insertion sequence element IS1086
RpoL														
Rmet_3277	<i>rsIC</i>	46.33	Op0924r_2	0.48	0.97	0.82	0.87	1.17	1.21	1.24	1.32	0.93	0.99	Ferric reductase-like transmembrane component-like
Rmet_3278	<i>rsIB</i>	126.00	Op0924r_2	0.80	1.07	0.98	0.95	0.94	0.88	0.88	0.85	0.73	0.70	Twin-arginine translocation pathway signal
Rmet_3279	<i>rsIA</i>	159.67	Op0924r_2	0.54	0.96	1.02	1.03	0.95	1.00	0.83	0.84	1.06	1.07	Putative transmembrane anti-sigma factor
Rmet_3280	<i>rpoL</i>	398.33	Op0924r_2	0.73	0.86	0.92	1.04	0.79	0.92	0.25	0.28	0.91	1.03	Sigma-24 (FecI-like)
Rmet_3281		823.00	Op0924r_2	1.72	1.03	0.96	0.93	0.73	0.71	8.63	8.34	0.95	0.92	Putative uncharacterized protein
Rmet_3282		114.67	Op0924r_1	0.64	0.97	1.06	1.06	1.15	1.19	8.35	8.35	1.07	1.07	Cytochrome c assembly protein
Rmet_3283	<i>ccs1</i>	128.00	Op0924r_1	0.40	1.09	0.92	0.86	0.96	0.88	1.08	1.01	0.99	0.92	Cytochrome c biogenesis protein
RpoM														
Rmet_5398	<i>rsmA</i>	7.67	Op1608f_1	1.06	0.87	0.87	1.02	0.97	1.11	1.03	1.20	1.01	1.18	Putative uncharacterized protein
Rmet_5399	<i>rsmB</i>	8.33	Op1608f_1	3.55	0.73	0.60	0.83	0.44	0.61	0.69	0.94	0.63	0.86	40-residue YVTN beta-propeller repeat
Rmet_5400	<i>rpoM</i>	11.00	Op1608f_1	0.58	0.93	1.01	1.07	0.94	1.01	1.74	1.84	1.10	1.16	Sigma-24 (FecI-like)
Rmet_5401	<i>rsmC</i>	6.67	Op1608f_1	0.78	0.94	0.94	0.99	0.96	1.03	1.69	1.78	1.12	1.18	Putative transmembrane anti-sigma factor
Rmet_5402		12.33	Op1608f_1	1.91	0.85	1.53	1.78	0.96	1.12	1.61	1.87	7.29	8.44	Beta-lactamase-like protein
RpoO														
Rmet_0596	<i>rsoA</i>	33.00	Op0168r_1	0.34	1.46	1.64	1.11	1.19	0.81	1.39	0.95	1.45	0.98	Putative transmembrane anti-sigma factor
Rmet_0597	<i>rpoO</i>	39.67	Op0168r_1	0.84	0.90	0.92	1.02	0.91	1.01	0.55	0.61	0.92	1.02	RNA polymerase sigma factor
Rmet_0598		9.33	Op0169f_1	1.45	0.83	0.91	1.07	0.87	1.05	12.59	14.74	1.02	1.19	Twin-arginine translocation pathway signal
Rmet_0599	<i>coxB</i>	9.67	Op0169f_1	1.14	0.80	1.01	1.22	0.97	1.21	18.70	22.59	1.17	1.42	Cytochrome c oxidase subunit 2

RpoP														
Rmet_1647	<i>rspA</i>	3.00	Op0464r_1	0.52	1.05	1.51	1.45	1.68	1.61	1.23	1.18	<u>5.95</u>	<u>5.71</u>	Putative transmembrane protein
Rmet_1648	<i>rpoP</i>	9.67	Op0464r_1	1.31	1.10	1.30	1.18	1.48	1.34	1.35	1.23	<u>1.13</u>	<u>1.03</u>	Sigma-24 (FecI-like)
Rmet_1649		0.67	Op0465f_1	1.99	1.05	1.06	0.97	1.27	1.22	0.87	0.80	<u>49.57</u>	<u>45.36</u>	Putative uncharacterized protein
Rmet_1650		1.67	Op0466r_3	0.61	1.02	1.50	1.56	1.30	1.27	1.29	1.34	<u>14.51</u>	<u>15.01</u>	Inner membrane CreD
Rmet_1651	<i>creC</i>	12.00	Op0466r_3	0.59	1.07	1.31	1.19	1.28	1.20	1.12	1.01	<u>5.15</u>	<u>4.68</u>	Sensor histidine kinase
Rmet_1652	<i>creB</i>	17.00	Op0466r_3	0.99	1.12	1.27	1.12	1.20	1.07	1.01	0.89	<u>2.81</u>	<u>2.48</u>	Two component transcriptional regulator
Rmet_1653		5.00	Op0466r_2	0.62	1.07	1.65	1.46	1.32	1.24	1.58	1.40	<u>3.09</u>	<u>2.73</u>	Monooxygenase, FAD-binding
Rmet_1654	<i>smpA</i>	0.67	Op0466r_1	1.24	0.95	1.08	1.16	1.37	1.44	1.29	1.39	<u>2.82</u>	<u>3.05</u>	SmpA/OmlA
Rmet_1655		0.67	Op0466r_1	0.81	0.93	1.16	1.17	1.10	1.18	1.21	1.23	<u>2.51</u>	<u>2.54</u>	Putative uncharacterized protein
RpoE														
Rmet_2421	<i>lepA</i>	261.7	Op0680r_4	<u>0.38</u>	0.96	0.84	0.88	0.79	0.82	0.96	1.01	0.73	0.77	GTP-binding protein lepA
Rmet_2422		645.0	Op0680r_4	0.72	1.14	1.15	0.99	0.92	0.81	1.20	1.03	0.54	<u>0.46</u>	Peptidase S1C, Do
Rmet_2423	<i>rseB</i>	509.7	Op0680r_4	0.65	1.36	1.16	0.85	1.01	0.74	1.08	0.79	<u>0.40</u>	<u>0.29</u>	Sigma E regulatory protein, MucB/RseB
Rmet_2424	<i>rseA</i>	1424	Op0680r_4	0.61	1.58	1.52	0.96	1.38	0.87	1.17	0.74	0.53	<u>0.33</u>	Anti sigma-E protein RseA
Rmet_2425	<i>rpoE</i>	481.7	Op0680r_3	<u>0.39</u>	1.11	1.04	0.93	1.17	1.05	0.86	0.77	<u>0.13</u>	<u>0.11</u>	RNA polymerase sigma factor
Rmet_2426	<i>fabF</i>	904.3	Op0680r_3	0.59	0.78	0.91	1.18	0.67	0.85	1.11	1.43	<u>2.17</u>	<u>2.80</u>	3-oxoacyl-[acyl-carrier-protein] synthase II
Rmet_2428	<i>fabG</i>	430.7	Op0680r_2	<u>0.36</u>	0.82	0.77	0.94	0.59	0.73	0.79	0.97	1.32	1.63	3-oxoacyl-[acyl-carrier-protein] reductase
CnrH														
Rmet_6204		11.33	Op1896f_1	1.61	1.11	1.10	1.01	1.22	1.10	1.14	1.05	1.11	1.03	Putative uncharacterized protein
Rmet_6205	<i>cnrY</i>	50.33	Op1896f_2	<u>9.64</u>	<u>6.80</u>	<u>6.45</u>	0.95	<u>7.20</u>	1.06	<u>12.52</u>	1.84	<u>2.42</u>	<u>0.36</u>	Nickel and cobalt resistance protein cnrY
Rmet_6206	<i>cnrX</i>	43.67	Op1896f_2	<u>2.28</u>	<u>4.26</u>	<u>6.71</u>	1.57	<u>5.57</u>	1.31	<u>9.47</u>	2.22	<u>6.17</u>	1.45	Nickel and cobalt resistance protein cnrR
Rmet_6207	<i>cnrH</i>	35.33	Op1896f_2	<u>2.24</u>	<u>4.04</u>	<u>5.69</u>	1.39	<u>4.99</u>	1.24	<u>8.89</u>	2.17	<u>4.67</u>	<u>1.14</u>	RNA polymerase sigma factor cnrH
Rmet_6208	<i>cnrC</i>	32.00	Op1896f_2	<u>4.61</u>	<u>6.29</u>	<u>5.93</u>	0.94	<u>5.81</u>	0.92	<u>9.56</u>	1.52	<u>2.61</u>	<u>0.41</u>	Nickel and cobalt resistance protein cnrC
Rmet_6209	<i>cnrB</i>	25.00	Op1896f_2	<u>2.53</u>	<u>3.23</u>	<u>3.53</u>	1.11	<u>3.20</u>	0.99	<u>5.17</u>	1.62	1.57	<u>0.49</u>	Nickel and cobalt resistance protein cnrB
Rmet_6210	<i>cnrA</i>	17.33	Op1896f_2	<u>2.59</u>	<u>4.28</u>	<u>3.82</u>	0.89	<u>3.22</u>	0.75	<u>6.80</u>	1.58	1.86	<u>0.43</u>	Nickel and cobalt resistance protein cnrA
Rmet_6211	<i>cnrT</i>	17.33	Op1896f_2	<u>3.43</u>	<u>2.60</u>	<u>2.50</u>	0.96	<u>2.23</u>	0.86	<u>4.25</u>	1.64	1.42	0.55	CnrT protein
RpoQ														
Rmet_4682	<i>gigT</i>	2.67	Op1355r_1	1.33	0.93	<u>5.56</u>	<u>5.51</u>	1.00	1.08	0.90	0.89	1.06	1.05	Gold-induced gene
Rmet_4683	<i>gigB</i>	6.00	Op1355r_1	1.89	0.64	1.36	<u>2.13</u>	<u>0.48</u>	0.74	0.62	0.98	0.71	1.12	Gold-induced gene
Rmet_4684	<i>gigA</i>	11.00	Op1355r_1	<u>2.04</u>	1.09	<u>8.65</u>	<u>8.06</u>	1.02	0.93	0.75	0.70	1.15	1.07	Gold-induced gene
Rmet_4685	<i>gigP</i>	19.00	Op1355r_1	<u>3.83</u>	<u>2.48</u>	<u>8.66</u>	<u>3.42</u>	<u>3.59</u>	1.45	1.63	0.64	<u>2.21</u>	0.87	Gold-induced gene
Rmet_4686	<i>rpoQ</i>	41.33	Op1356f_1	<u>3.91</u>	1.11	<u>0.02</u>	<u>0.01</u>	1.19	1.07	0.97	0.87	1.15	1.04	Sigma-24 (FecI-like)
Rmet_4687	<i>rsqA</i>	20.67	Op1356f_1	0.77	1.13	1.36	1.18	0.98	0.87	1.16	1.00	1.18	1.03	Putative uncharacterized protein
Rmet_4688		3.00	Op1356f_1	1.14	0.99	1.05	1.01	0.99	1.00	0.95	0.91	1.08	1.04	Putative uncharacterized protein
RpoR														
Rmet_0908	<i>rsrB</i>	235.3	Op0262r_2	<u>0.47</u>	0.86	0.72	0.81	1.32	1.54	0.68	0.77	1.34	1.51	Putative transmembrane protein
Rmet_0909	<i>rsrA</i>	503.0	Op0262r_2	<u>0.41</u>	0.89	1.07	1.20	1.39	1.55	0.79	0.88	1.41	1.59	Putative transmembrane protein
Rmet_0910	<i>rpoR</i>	156.3	Op0262r_1	<u>0.35</u>	0.71	<u>0.17</u>	<u>0.24</u>	0.65	0.92	0.88	1.24	0.68	0.96	Sigma-24 (FecI-like)
Rmet_0911	<i>ilvB</i>	779.7	Op0263f_2	<u>0.09</u>	0.95	1.17	1.23	0.99	1.04	1.48	1.56	0.92	0.97	Acetolactate synthase, large subunit

^aThe table gives the regulation (Q values) of genes in metal-mix-treated *C. metallidurans* cells compared to the untreated control cells. “Op” gives the operon, Q(WT) and Q2(WT) the comparison of metal-treated CH34 cells to untreated cells. The Q(DN..) values compare metal-treated mutant cells to untreated CH34 cells, the QQ(DN...) values metal-treated mutant cells to metal-treated CH34 cells. Values Q > 2 in green, Q < 0.5 in red, significant values (D > 1) bold-faced and underlined. Sigma factor genes in the mutants are on a yellow field.

Supplementary Table S5 continued. Control values

Replicon	gene	Rmet	Region	Q-value	NPKM	Deviation	Description
zur				0:AE104±zur			
Rep1	-	Rmet_0124	Op0032r	2.01	85.33	3.79	Q1LS66 Putative uncharacterized protein
Rep1	cobW3	Rmet_0125	Op0032r	3.53	172.67	1.15	Q1LS65 Cobalamin synthesis CobW-like protein
Rep1	dksA	Rmet_0126	Op0032r	1.42	1311.67	78.49	Q1LS64 Transcriptional regulators, TraR/DksA family
Rep1	cobW2	Rmet_0127	Op0032r	7.10	222.67	17.04	Q1LS63 Cobalamin synthesis protein, P47K
Rep1	zur	Rmet_0128	Op0032r	1.09	52.67	1.53	Q1LS62 Putative ferric uptake regulator, FUR family
Rep1	dehH2	Rmet_0129	Op0033f	42.13	18.33	1.53	Q1LS61 Alpha/beta hydrolase fold
zupT				EDTA:ΔzupT/AE104			
Rep1	-	Rmet_2619	Op0733f	0.72	10.67	0.58	Q1LK30 Putative uncharacterized protein
Rep1	sseA	Rmet_2620	Op0733f	1.08	85.67	7.23	Q1LK29 Rhodanese-like protein
Rep1	zupT	Rmet_2621	Op0734r	0.35	74.67	3.51	Q1LK28 Zinc/iron permease
Rep1	-	Rmet_2622	Op0734r	2.70	184.33	7.77	Q1LK27 Twin-arginine translocation pathway signal
Rep1	ndh	Rmet_2623	Op0734r	1.33	45.00	1.00	Q1LK26 FAD-dependent pyridine nucleotide-disulphide oxidoreductase
Rep1	polA	Rmet_2624	Op0734r	1.03	70.33	3.06	Q1LK25 DNA polymerase I
zupT				0:Δe4ΔzupT/Δe4			
Rep1	-	Rmet_2619	Op0733f	1.07	10.67	0.58	Q1LK30 Putative uncharacterized protein
Rep1	sseA	Rmet_2620	Op0733f	1.18	85.67	7.23	Q1LK29 Rhodanese-like protein
Rep1	zupT	Rmet_2621	Op0734r	0.06	74.67	3.51	Q1LK28 Zinc/iron permease
Rep1	-	Rmet_2622	Op0734r	7.25	184.33	7.77	Q1LK27 Twin-arginine translocation pathway signal
Rep1	ndh	Rmet_2623	Op0734r	4.90	45.00	1.00	Q1LK26 FAD-dependent pyridine nucleotide-disulphide oxidoreductase
Rep1	polA	Rmet_2624	Op0734r	1.17	70.33	3.06	Q1LK25 DNA polymerase I
pitA				EDTA:Δ7/ΔzupT			
Rep1	-	Rmet_1970	Op0575f	1.06	169.67	5.69	Q1LLX7 PhoH-like protein
Rep1	-	Rmet_1971	Op0575f	1.04	103.33	1.53	Rmet_1971
Rep1	-	Rmet_1972	Op0575f	0.99	136.33	5.13	Rmet_1972
Rep1	pitA	Rmet_1973	Op0576r	0.87	221.67	7.09	Q1LLX4 Phosphate transporter
Rep1	-	Rmet_1974	Op0576r	1.85	261.33	8.02	Q1LLX3 Putative uncharacterized protein
Rep1	dnaB	Rmet_1975	Op0576r	1.01	182.33	4.73	Q1LLX2 Primary replicative DNA helicase
Rep1	rplI	Rmet_1976	Op0576r	1.12	3402.00	169.05	Q1LLX1 50S ribosomal protein L9
Rep1	rpsR	Rmet_1977	Op0576r	1.06	3062.33	88.69	Q1LLX0 30S ribosomal protein S18
Rep1	priB	Rmet_1978	Op0576r	1.12	2449.00	104.10	Q1LLW9 Restart primosome assembly protein PriB
Rep1	rpsF	Rmet_1979	Op0576r	0.79	2824.00	39.96	Q1LLW8 30S ribosomal protein S6
Rep1	ansB	Rmet_1980	Op0576r	1.02	62.33	2.08	Q1LLW7 Asparaginase
corA1				EDTA:Δ7/ΔzupT			
Rep1	-	Rmet_3049	Op0857f	1.03	159.00	3.46	Q1LIV5 CinA-like protein
Rep1	pyrF	Rmet_3050	Op0858r	1.17	130.00	3.00	Q1LIV4 Orotidine 5'-phosphate decarboxylase
Rep1	-	Rmet_3051	Op0859f	1.02	28.33	2.08	Q1LIV3 Putative uncharacterized protein
Rep1	corA1	Rmet_3052	Op0859f	0.97	54.00	6.24	Q1LIV2 Magnesium and cobalt transport protein CorA
Rep1	mtgA	Rmet_3053	Op0860r	3.10	31.67	3.06	Q1LIV1 Monofunctional biosynthetic peptidoglycan transglycosylase
Rep1	aroE	Rmet_3054	Op0860r	1.33	138.67	7.64	Q1LIV0 Shikimate dehydrogenase
Rep1	-	Rmet_3055	Op0860r	1.43	111.33	4.51	Q1LIU9 TonB-like protein
corA2				EDTA:Δ7/ΔzupT			
Rep1	minE	Rmet_0033	Op0012r	0.96	361.33	21.55	Q1LSF7 Cell division topological specificity factor
Rep1	minD	Rmet_0034	Op0012r	0.80	225.33	12.50	Q1LSF6 Septum site-determining protein MinD
Rep1	minC	Rmet_0035	Op0012r	1.13	106.00	8.00	Q1LSF5 Probable septum site-determining protein minC
Rep1	corA2	Rmet_0036	Op0013f	0.75	68.00	2.00	Q1LSF4 Mg2+ transporter protein, CorA-like protein
Rep1	-	Rmet_0037	Op0014r	1.05	3.00	1.00	Q1LSF3 Putative uncharacterized protein
Rep1	kdpA	Rmet_0038	Op0015f	1.00	1.00	0.00	Q1LSF2 Potassium-transporting ATPase, A subunit
Rep1	kdpB	Rmet_0039	Op0015f	1.50	2.67	0.58	Q1LSF1 Potassium-translocating P-type ATPase, B subunit
Rep1	kdpC	Rmet_0040	Op0015f	2.67	0.58		Q1LSF0 Potassium-transporting ATPase, C subunit

Rep1	<i>kdpD</i>	Rmet_0041	Op0015f	31.00	1.00		Q1LSE9 Sensor protein
Rep1	<i>kdpE</i>	Rmet_0042	Op0015f	29.67	2.08		Q1LSE8 Two component transcriptional regulator, winged helix family
Rep1	-	Rmet_0043	Op0015f	18.67	2.52		Q1LSE7 Sel1
corA3 EDTA:Δ7/ΔzupT							
Rep1	-	Rmet_3284	Op0924r	0.72	1352.67	18.15	Q1LI70 Cytochrome c, class I
Rep1	-	Rmet_3285	Op0925f	0.87	226.67	10.02	Q1LI69 Probable GTP-binding protein engB
Rep1	<i>hemB</i>	Rmet_3286	Op0925f	0.94	354.00	15.87	Q1LI68 Delta-aminolevulinic acid dehydratase
Rep1	<i>corA3</i>	Rmet_3287	Op0925f	0.92	145.67	9.07	Q1LI67 Mg2+ transporter protein, CorA-like protein
Rep1	-	Rmet_3288	Op0926r	0.79	202.00	53.70	Q1LI66 Cytochrome c biogenesis protein, transmembrane region
Rep1	-	Rmet_3289	Op0926r	0.75	187.67	32.72	Q1LI65 CutA1 divalent ion tolerance protein
Rep1	<i>rplQ</i>	Rmet_3290	Op0926r	0.89	2966.00	26.29	Q1LI64 50S ribosomal protein L17
zntB EDTA:Δ7/ΔzupT							
Rep1	<i>bdhA</i>	Rmet_0546	Op0152r	1.02	28.00	2.00	Q1LQZ4 3-hydroxybutyrate dehydrogenase
Rep1	-	Rmet_0547	Op0152r	1.14	20.00	2.00	Q1LQZ3 Citrate transporter
Rep1	-	Rmet_0548	Op0153f	1.19	18.00	1.00	Q1LQZ2 Sigma54 specific transcriptional regulator, Fis family
Rep1	<i>zntB</i>	Rmet_0549	Op0153f	1.05	14.33	0.58	Q1LQZ1 Mg2+ transporter protein, CorA-like protein
Rep1	-	Rmet_0550	Op0153f	1.40	25.00	1.00	Q1LQZ0 Putative uncharacterized protein
Rep1	-	Rmet_0551	Op0153f	1.23	5.00	1.00	Q1LQY9 Hycolysin. Metallo peptidase. MEROPS family M30
Rep1	-	Rmet_0552	Op0154r	1.00	29.33	1.53	Q1LQY8 Transcriptional regulator of molybdate metabolism, LysR family
hoxN EDTA:Δ7/ΔzupT							
Rep1	-	Rmet_1530	Op0427f	1.28	10.00	1.00	Q1LN63 Alanine dehydrogenase/PNT-like protein
Rep1	-	Rmet_1531	Op0427f	1.19	3.67	1.15	Q1LN62 Pyridine nucleotide transhydrogenase subunit alpha
Rep1	<i>pntB</i>	Rmet_1532	Op0427f	1.54	2.33	0.58	Q1LN61 NAD(P) transhydrogenase, beta subunit
Rep1	<i>hoxN</i>	Rmet_1533	Op0427f	0.02	72.67	6.51	Q1LN60 High-affinity nickel-transporter
Rep1	-	Rmet_1534	Op0427f	0.89	295.33	33.86	Q1LN59 Putative uncharacterized protein
Rep1	-	Rmet_1535	Op0427f	0.95	963.67	120.62	Q1LN58 Hydrogenase nickel insertion protein HypA
Rep1	-	Rmet_1536	Op0427f	0.81	1215.00	78.54	Q1LN57 Hydrogenase accessory protein HypB
fieF 0:Δe4/AE104							
Rep1	-	Rmet_3403	Op0945f	0.65	73.00	5.00	Q1LHV1 Major facilitator superfamily MFS_1
Rep1	<i>tag</i>	Rmet_3404	Op0945f	1.00	28.33	1.53	Q1LHV0 DNA-3-methyladenine glycosylase I
Rep1	-	Rmet_3405	Op0945f	1.04	56.67	2.08	Q1LHU9 Lysine exporter protein (LYSE/YGGA)
Rep1	<i>fieF</i>	Rmet_3406	Op0946r	0.08	44.33	1.53	Q1LHU8 Cation diffusion facilitator family transporter
Rep1	-	Rmet_3407	Op0947f	1.24	16.67	1.15	Q1LHU7 Glycosyl transferase, family 2
Rep1	-	Rmet_3408	Op0947f	1.78	14.00	0.00	Q1LHU6 Radical SAM
Rep1	-	Rmet_3409	Op0947f	1.59	9.00	1.73	Q1LHU5 YdjC-like protein
dmeF 0:Δe4/AE104							
Rep1	<i>dmeF</i>	Rmet_0198	Op0058r	0.02	38.00	2.65	Q1LRZ2 Cation diffusion facilitator family transporter
Rep1	-	Rmet_0199	Op0058r	5.45	11.33	0.58	Q1LRZ1 Transcriptional regulator, LysR family
Rep1	<i>leuC</i>	Rmet_0200	Op0059f	2.91	4.67	0.58	Q1LRZ0 3-isopropylmalate dehydratase, large subunit
Rep1	<i>leuD</i>	Rmet_0201	Op0059f	2.44	4.00	1.00	Q1LRY9 3-isopropylmalate dehydratase, small subunit
Rep1	<i>dehH1</i>	Rmet_0202	Op0059f	1.01	51.00	2.65	Q1LRY8 Alpha/beta hydrolase fold
cadA 0:Δe4/AE104							
Rep1	-	Rmet_2300	Op0656r	1.30	86.33	7.51	Q1LKZ7 Putative uncharacterized protein
Rep1	-	Rmet_2301	Op0657f	1.00	1.33	0.58	Q1LKZ6 Putative uncharacterized protein
Rep1	-	Rmet_2302	Op0658r	0.14	262.67	4.51	A7HYK9 Putative transcriptional regulator, MerR family
Rep1	<i>cadA</i>	Rmet_2303	Op0659f	0.08	15.33	1.53	A7HYL0 Heavy metal translocating P-type ATPase
Rep1	<i>pbrC2</i>	Rmet_2304	Op0659f	0.08	11.67	1.15	Q8GQ15 Lipoprotein signal peptidase
Rep1	-	Rmet_2305	Op0659f	0.93	11.67	2.31	Q8GQ16 Putative uncharacterized protein ORF C95
Rep1	-	Rmet_2306	Op0659f	1.57	0.00	0.00	Q8GQ17 Putative uncharacterized protein ORF C94
zntA 0:Δe4/AE104							
Rep2	-	Rmet_4591	Op1320f	1.07	139.33	2.08	Q1LEH3 Formyl transferase-like protein
Rep2	-	Rmet_4592	Op1320f	1.04	103.67	3.79	Q1LEH2 NAD-dependent epimerase/dehydratase

Rep2	-	Rmet_4593	Op1320f	1.15	174.67	4.93	Q1LEH1 Polysaccharide deacetylase
Rep2	<i>zntA</i>	Rmet_4594	Op1321r	0.36	48.33	2.31	Q1LEH0 Heavy metal translocating P-type ATPase
Rep2	<i>czcI2</i>	Rmet_4595	Op1322f	1.77	26.00	1.00	Q1LEG9 Putative uncharacterized protein
Rep2	<i>czcC2</i>	Rmet_4596	Op1322f	1.79	2.00	0.00	Q1LEG8 Outer membrane efflux protein
Rep2	<i>czcB2''</i>	Rmet_4597	Op1322f	2.15	0.67	0.58	Q1LEG7 Secretion protein HlyD

As a control, the effect of the deletion of other genes is given.

Supplementary Table S6. Genes down-regulated in wild type and mutant cells

Rmet	Gene	NPKM	Operon	Q(WT)	Q2(WT)	Q(DN546)	QQ546	Q(DN553)	QQ553	Q(DN554)	QQ554	Q(DN555)	QQ555	Description	
Environmental Information Processing															
Membrane Transport															
Pores ion channels															
Rmet_4564	metE	1017.7	Op1314f_1	0.34	0.87	0.91	1.05	0.83	0.95	1.11	1.27	0.95	1.09	Methionine synthase (B12-independent)	
Rmet_4565		772.00	Op1314f_1	0.02	0.05	0.07	1.43	0.06	1.25	0.08	1.50	0.09	1.75	TonB-dependent receptor	
Rmet_4566		281.33	Op1315r_4	0.05	0.25	0.30	1.19	0.22	0.89	0.28	1.11	0.31	1.26	Putative uncharacterized protein	
Rmet_4607		360.67	Op1327r_1	0.27	0.30	0.33	1.17	0.43	1.42	0.28	1.00	0.48	1.69	TonB-dependent copper receptor	
Rmet_4608		281.33	Op1327r_1	0.35	0.42	0.52	1.21	0.46	1.10	0.42	0.97	0.53	1.24	Putative uncharacterized protein	
Rmet_3139		1034.3	Op0879f_1	0.22	0.39	0.50	1.26	0.53	1.35	0.72	1.82	0.59	1.49	Putative uncharacterized protein	
Rmet_3143		0.00	Op0880r_1	0.44	1.12	1.20	1.06	1.25	1.12	0.92	0.82	1.92	1.70	Putative uncharacterized protein	
Rmet_3144		1815.0	Op0881f_1	0.07	0.21	0.32	1.53	0.35	1.66	0.41	1.91	0.29	1.37	Porin, Gram-negative type	
ABC transporters [PATH:ko02010]															
Rmet_0690	mgsA	134.00	Op0195f_1	0.34	0.35	0.37	1.06	0.25	0.72	0.34	0.97	0.37	1.06	Extracellular solute-binding protein, family 3	
Rmet_0691		24.00	Op0195f_1	0.10	0.40	0.53	1.30	0.37	0.91	0.50	1.23	0.49	1.19	Amino acid ABC transporter, permease protein	
Rmet_0692		13.33	Op0195f_1	0.61	0.56	0.56	1.00	0.54	0.97	0.59	1.06	0.58	1.03	Amino acid ABC transporter, permease proteine	
Rmet_0693		19.67	Op0195f_1	0.27	0.53	0.52	1.00	0.47	0.88	0.63	1.21	0.59	1.13	ABC transporter-related protein	
Rmet_0694		64.33	Op0195f_2	0.39	1.42	1.69	1.19	1.30	0.92	1.68	1.18	1.47	1.03	Recombination protein MgsA	
Rmet_0695		serS	308.33	Op0195f_3	0.23	0.96	0.99	1.04	0.84	0.87	1.10	1.15	0.88	0.92	Seryl-tRNA synthetase
Rmet_0696		26.33	Op0196r_2	0.17	1.11	1.22	1.10	1.48	1.34	1.77	1.59	1.20	1.08	Putative uncharacterized protein	
Rmet_R0006				0.24	1.01	1.32	1.31	1.27	1.26	3.72	3.69	1.02	1.01	tRNA	
Rmet_0697	pilA	3431.67	Op0196r_2	0.43	0.89	1.20	1.34	1.19	1.34	0.68	0.77	1.18	1.32	Pilus assembly protein major pilin PilA	
Rmet_3517	livH	383.33	Op0974r_5	0.36	0.37	0.39	1.09	0.35	0.95	0.49	1.35	0.37	1.02	branched-chain amino acid transport system permease protein	
Rmet_3518	livK	1160.67	Op0974r_5	0.19	0.26	0.28	1.08	0.18	0.69	0.27	1.05	0.23	0.88	branched-chain amino acid transport system substrate-binding protein	
Rmet_3520	livG	321.67	Op0974r_4	0.16	0.34	0.29	0.84	0.30	0.86	0.36	1.03	0.31	0.89	branched-chain amino acid transport system ATP-binding protein	
Rmet_2752	adj	150.00	Op0775f_2	0.08	0.19	0.21	1.09	0.30	1.56	0.53	2.75	0.27	1.39	Tripartite ATP-independent periplasmic transporter, DctQ component	
Rmet_2753		195.67	Op0775f_2	0.05	0.26	0.33	1.20	0.36	1.35	0.51	1.88	0.37	1.35	TRAP C4-dicarboxylate transport system permease DctM subunit	
Rmet_2754		99.67	Op0776r_2	0.50	0.93	0.76	0.81	1.04	1.12	0.79	0.84	0.77	0.81	Ornithine decarboxylase	
Rmet_2755		dcd	117.33	Op0776r_2	0.36	0.81	0.84	1.09	1.02	1.25	0.79	1.02	0.93	1.21	Deoxycytidine triphosphate deaminase
Rmet_2756		73.00	Op0776r_2	0.48	0.94	0.98	1.03	1.22	1.29	0.84	0.88	0.71	0.75	Formate dehydrogenase, subunit FdhD	
Metabolism															
Carbohydrate Metabolism															
Butanoate metabolism [PATH:ko00650]															
Rmet_3894	ilvB	103.33	Op1086f_2	0.04	0.25	0.31	1.25	0.42	1.69	0.44	1.78	0.36	1.47	Putative uncharacterized protein	
Rmet_3895		13.00	Op1086f_2	0.36	0.62	0.58	0.87	0.64	1.02	0.56	0.85	0.71	1.08	Transcriptional regulator, GntR family	
Rmet_3896		60.67	Op1086f_3	0.22	0.39	0.46	1.17	0.32	0.81	0.40	1.03	0.44	1.12	acetolactate synthase large subunit	
Lipid Metabolism															
Arachidonic acid metabolism [PATH:ko00590]															
Rmet_0970	ggt	392.00	Op0271f_2	0.16	0.26	0.31	1.19	0.20	0.77	0.41	1.55	0.25	0.95	gamma-glutamyltranspeptidase	
Energy Metabolism															
Oxidative phosphorylation [PATH:ko00190]															
Rmet_5231	cydA	65.67	Op1544f_1	0.23	0.23	0.33	1.47	0.30	1.33	0.20	0.89	0.48	2.12	Transcriptional regulator, ArsR family	
Rmet_5232		88.00	Op1544f_1	0.55	0.19	0.26	1.41	0.21	1.12	0.17	0.92	0.27	1.49	Cytochrome bd ubiquinol oxidase, subunit I	
Rmet_5233		cydB	83.33	Op1544f_1	0.19	0.23	0.35	1.54	0.29	1.27	0.22	0.97	0.37	1.63	Cytochrome d ubiquinol oxidase, subunit II
Rmet_5234		67.00	Op1544f_1	0.20	0.63	0.79	1.25	0.68	1.08	0.54	0.86	0.70	1.12	Putative uncharacterized protein	
Rmet_5235		17.00	Op1544f_1	0.53	0.45	0.40	0.86	0.42	0.93	0.49	1.07	0.56	1.23	Tetratricopeptide TPR_2	
Rmet_4891	sorA	28.33	Op1430f_1	0.45	0.38	0.44	1.15	0.40	1.05	0.32	0.84	0.30	0.78	Sulfite dehydrogenase (Cytochrome) subunit SorA apoprotein	

Rmet_4892	<i>sorB</i>	20.67	Op1430f_1	0.54	0.35	0.36	1.00	0.35	0.98	0.27	0.76	0.26	0.74	Sulfite dehydrogenase (Cytochrome) subunit SorB
Rmet_4893		17.67	Op1431r_1	0.32	0.47	0.62	1.29	0.63	1.33	0.38	0.79	0.42	0.87	Putative uncharacterized protein

Genetic Information Processing

Folding, Sorting and Degradation

Protein folding and associated processing

Rmet_1288	<i>hupJ</i>	164.33	Op0370r_1	0.29	0.33	0.05	0.15	0.06	0.19	0.05	0.17	0.28	0.86	HupJ, contains rubredoxin domain
Rmet_1289		136.67	Op0370r_1	0.40	0.28	0.05	0.19	0.07	0.25	0.06	0.21	0.22	0.77	Rubredoxin
Rmet_1290	<i>hupH</i>	195.33	Op0370r_1	0.17	0.30	0.06	0.19	0.06	0.21	0.06	0.20	0.27	0.90	HupH hydrogenase expression protein
Rmet_1291	<i>hyaE</i>	139.00	Op0370r_1	0.23	0.22	0.04	0.19	0.06	0.25	0.05	0.23	0.19	0.85	Hydrogenase-1 expression HyaE
Rmet_1292	<i>hypC</i>	104.00	Op0370r_1	0.32	0.21	0.06	0.27	0.07	0.35	0.07	0.32	0.19	0.87	Hydrogenase assembly chaperone hypC/hupF
Rmet_1293	<i>hyaD</i>	119.33	Op0370r_1	0.13	0.30	0.14	0.45	0.16	0.54	0.14	0.46	0.31	1.00	HyaD peptidase. Aspartic peptidase. MEROPS family A31
Rmet_1294		130.33	Op0370r_1	0.14	0.27	0.12	0.45	0.14	0.51	0.13	0.48	0.31	1.16	Putative plasmid maintenance system antidote protein, XRE family
Rmet_1295		335.67	Op0370r_1	0.29	0.14	0.01	0.04	0.01	0.04	0.01	0.04	0.16	1.15	Nickel-dependent hydrogenase b-type cytochrome subunit
Rmet_1296	<i>hupE</i>	399.00	Op0370r_1	0.06	0.14	0.04	0.29	0.05	0.32	0.08	0.56	0.16	1.09	HupE/UreJ protein
Rmet_1297		548.67	Op0370r_1	0.08	0.16	0.04	0.21	0.03	0.20	0.03	0.19	0.15	0.92	Nickel-dependent hydrogenase, large subunit
Rmet_1298		529.33	Op0370r_1	0.07	0.14	0.02	0.18	0.03	0.18	0.03	0.21	0.15	1.07	Hydrogenase (NiFe) small subunit (HydA)

Type II secretion system [PATH:ko03090]

Rmet_3391	<i>gspN</i>	61.33	Op0941f_2	0.61	0.49	0.48	0.98	0.55	1.13	0.62	1.27	0.57	1.16	general secretion pathway protein N
Rmet_3392	<i>gspD</i>	94.00	Op0941f_2	0.27	0.55	0.68	1.20	0.55	1.00	0.75	1.33	0.69	1.23	general secretion pathway protein D
Rmet_3393	<i>gspE</i>	88.33	Op0941f_2	0.49	0.42	0.40	0.94	0.34	0.80	0.47	1.11	0.45	1.07	GSPE; general secretion pathway protein E

Transcription

Transcriptional regulators

Rmet_0133		1378.67	Op0034r_1	0.15	0.18	0.12	0.68	0.17	0.92	0.16	0.88	0.12	0.66	Nuclear export factor GLE1
Rmet_0134		31.00	Op0035f_1	0.50	1.34	1.01	0.74	1.47	1.10	1.27	0.93	1.10	0.80	Putative uncharacterized protein
Rmet_0135		424.33	Op0036r_1	0.35	0.64	0.67	1.07	0.68	1.05	0.41	0.66	0.60	0.96	Response regulator receiver domain protein (CheY-like)
Rmet_0136		245.00	Op0036r_1	0.38	0.27	0.36	1.35	0.32	1.20	0.27	1.02	0.42	1.60	Sensor protein
Rmet_0137		1262.67	Op0037f_1	0.11	0.17	0.20	1.16	0.12	0.69	0.14	0.81	0.15	0.85	Putative uncharacterized protein
Rmet_0138		152.00	Op0038r_2	0.05	0.22	0.33	1.50	0.24	1.13	0.24	1.10	0.28	1.31	Transcriptional regulator, LysR family
Rmet_0139		68.67	Op0038r_1	0.12	0.45	0.57	1.25	0.57	1.27	0.52	1.14	0.62	1.37	Putative uncharacterized protein
Rmet_3145		213.33	Op0881f_1	0.42	0.39	0.48	1.23	0.32	0.82	0.37	0.94	0.41	1.04	Uncharacterized protein UPF0065
Rmet_3146		119.33	Op0881f_1	0.63	0.64	0.62	0.97	0.46	0.71	0.67	1.04	0.52	0.82	Transcriptional regulator, MarR family
Rmet_5578		239.00	Op1660f_1	0.08	0.27	0.39	1.47	0.33	1.22	0.34	1.27	0.33	1.23	Putative uncharacterized protein
Rmet_5579		208.67	Op1660f_1	0.07	0.27	0.38	1.38	0.37	1.36	0.31	1.15	0.35	1.28	Cytochrome B561
Rmet_0271		562.33	Op0077f_2	0.16	0.19	0.18	0.96	0.15	0.81	0.19	1.01	0.17	0.89	Electron transport protein SCO1/SenC

Cellular Processes

Cell Motility

Flagellar assembly [PATH:ko02040]

Rmet_3737	<i>flgE</i>	155.00	Op1042f_3	0.20	0.33	0.23	0.71	0.16	0.48	0.31	0.94	0.16	0.48	flagellar hook protein FlgE
Rmet_3738	<i>flgF</i>	122.00	Op1042f_3	0.46	0.26	0.16	0.60	0.10	0.37	0.19	0.73	0.09	0.35	flagellar basal-body rod protein FlgF
Rmet_3739	<i>flgG</i>	90.67	Op1042f_3	0.17	0.32	0.19	0.60	0.14	0.42	0.21	0.67	0.12	0.39	FLGG; flagellar basal-body rod protein FlgG
Rmet_3740	<i>flgH</i>	55.00	Op1042f_3	0.27	0.43	0.26	0.61	0.25	0.58	0.35	0.81	0.23	0.52	flagellar L-ring protein precursor FlgH
Rmet_3741	<i>flgI</i>	32.00	Op1042f_3	0.22	0.42	0.26	0.62	0.22	0.54	0.38	0.92	0.21	0.50	flagellar P-ring protein precursor FlgI
Rmet_3742	<i>flgJ</i>	27.67	Op1042f_3	0.19	0.52	0.37	0.74	0.26	0.50	0.45	0.88	0.31	0.61	flagellar protein FlgJ
Rmet_3743	<i>flgK</i>	41.67	Op1042f_3	0.46	0.96	0.69	0.73	0.88	0.91	1.08	1.14	0.70	0.75	flagellar hook-associated protein 1 FlgK
Rmet_3744	<i>flgL</i>	48.33	Op1042f_3	0.23	0.81	0.60	0.73	0.75	0.92	0.93	1.14	0.47	0.57	flagellar hook-associated protein 3 FlgL
Rmet_3698	<i>flhB</i>	14.33	Op1026f_3	0.50	0.41	0.37	0.86	0.45	1.08	0.34	0.79	0.48	1.10	flagellar biosynthetic protein FlhB
Rmet_3699	<i>flhA</i>	18.00	Op1026f_3	0.22	0.67	0.55	0.80	0.72	1.08	0.70	1.03	0.65	0.95	flagellar biosynthesis protein FlhA
Rmet_3700	<i>flhF</i>	29.33	Op1026f_3	0.20	0.53	0.42	0.79	0.48	0.90	0.42	0.80	0.44	0.83	flagellar biosynthesis protein FlhF
Rmet_5262	<i>fliG</i>	28.33	Op1552f_2	0.18	0.43	0.30	0.68	0.31	0.72	0.50	1.14	0.29	0.67	flagellar motor switch protein FliG

Rmet_5265	<i>fliJ</i>	23.00	Op1552f_2	<u>0.22</u>	<u>0.46</u>	<u>0.46</u>	1.02	<u>0.37</u>	0.82	<u>0.39</u>	0.86	<u>0.34</u>	0.76	flagellar FliJ protein
Rmet_5264	<i>fliI</i>	19.00	Op1552f_2	<u>0.25</u>	<u>0.43</u>	<u>0.33</u>	0.75	<u>0.33</u>	0.76	<u>0.40</u>	0.92	<u>0.33</u>	0.76	flagellum-specific ATP synthase
Rmet_5263	<i>fliH</i>	26.33	Op1552f_2	<u>0.26</u>	<u>0.35</u>	<u>0.26</u>	0.73	<u>0.28</u>	0.80	<u>0.32</u>	0.92	<u>0.23</u>	0.64	flagellar assembly protein FliH
Not assigned														
Rmet_4721		186.00	Op1362f_2	<u>0.04</u>	<u>0.24</u>	<u>0.27</u>	1.13	<u>0.38</u>	1.58	<u>0.33</u>	1.37	<u>0.29</u>	1.21	Putative uncharacterized protein
Rmet_3543		546.33	Op0983f_2	<u>0.12</u>	<u>0.44</u>	0.70	1.65	<u>0.47</u>	1.08	0.71	1.67	0.64	1.51	Twin-arginine translocation pathway signal
Rmet_0521		12,116	Op0140r_2	<u>0.20</u>	<u>0.49</u>	0.68	1.40	<u>0.38</u>	0.79	0.75	1.55	<u>0.42</u>	0.86	Uncharacterized protein UPF0065
Rmet_0522		509.33	Op0140r_1	<u>0.05</u>	<u>0.35</u>	<u>0.42</u>	1.18	<u>0.42</u>	1.20	0.73	2.07	<u>0.43</u>	1.22	Putative uncharacterized protein
Rmet_2056		50.33	Op0597f_1	<u>0.26</u>	<u>0.22</u>	<u>0.28</u>	1.29	<u>0.26</u>	1.20	<u>0.40</u>	1.90	<u>0.28</u>	1.31	HAD-superfamily hydrolase subfamily IIB
Rmet_0063		27.33	Op0019f_2	<u>0.40</u>	<u>0.42</u>	<u>0.44</u>	1.08	<u>0.35</u>	0.83	<u>0.41</u>	1.02	<u>0.46</u>	1.12	Allophanate hydrolase subunit 2
Rmet_5241		12.67	Op1544f_1	<u>0.45</u>	<u>0.49</u>	<u>0.34</u>	0.72	<u>0.32</u>	0.67	<u>0.36</u>	0.76	<u>0.40</u>	0.84	Putative uncharacterized protein

^aThe table gives the regulation (Q values) of genes in metal-mix-treated *C. metallidurans* cells compared to the untreated control cells. “Op” gives the operon, Q(WT) and Q2(WT) the comparison of metal-treated CH34 cells to untreated cells. The Q(DN..) values compare metal-treated mutant cells to untreated CH34 cells, the QQ(DN...) values metal-treated mutant cells to metal-treated CH34 cells. Values Q > 2 in green, Q < 0.5 in red, significant values (D > 1) bold-faced and underlined. The down-regulated gene cluster for the membrane-bound hydrogenase is on a yellow field. The KEGG orthology system was also used for sorting.

Supplementary Table S7. Genes down-regulated in wild type but not in all mutant cells

Rmet	Gene	NMPG	Operon	Q(WT)	Q2(WT)	Q(DN546)	QQ546	Q(DN553)	QQ553	Q(DN554)	QQ554	Q(DN555)	QQ555	Description
DH553 Not														
Rmet_2579		27.00	Op0716r_1	0.17	0.22	0.36	1.64	0.55	2.39	0.20	0.92	0.32	1.43	Pirin-like protein
DN554 Not														
Cellular Processes				Cell Motility				Flagellar assembly [PATH:ko02040]						
Rmet_5297	fliL	48.00	Op1566f_1	0.23	0.44	0.28	0.64	0.45	1.03	0.54	1.23	0.25	0.58	Flagellar basal body-associated protein FliL
Rmet_5298	fliM	32.33	Op1566f_1	0.28	0.57	0.35	0.64	0.49	0.85	0.54	0.98	0.43	0.77	Flagellar motor switch protein FliM
Rmet_5299	fliN	50.33	Op1566f_1	0.27	0.50	0.33	0.65	0.46	0.93	0.52	1.02	0.28	0.55	Flagellar motor switch FliN
Rmet_5300	fliO	43.67	Op1566f_1	0.19	0.54	0.41	0.78	0.50	0.93	0.63	1.20	0.37	0.70	Flagellar biosynthesis protein, FliO
Rmet_5301	fliP	11.00	Op1566f_1	0.14	0.52	0.39	0.74	0.52	1.00	0.59	1.12	0.37	0.71	Flagellar biosynthetic protein FliP
Metabolism				Carbohydrate Metabolism				Propanoate metabolism [PATH:ko00640]						
Rmet_4574	acd	77.67	Op1316f_1	0.18	0.44	0.59	1.34	0.52	1.20	0.64	1.44	0.57	1.29	Acyl-CoA dehydrogenase-like protein
Rmet_4575	acd	61.33	Op1316f_1	0.24	0.38	0.46	1.19	0.35	0.92	0.55	1.41	0.42	1.07	Acyl-CoA dehydrogenase-like protein
Environmental Information														
Processing				Membrane Transport				Other ion-coupled transporters						
Rmet_3549	tctC	206.00	Op0985f_1	0.45	0.23	0.38	1.69	0.29	1.27	1.49	6.55	0.33	1.47	putative tricarboxylic transport membrane protein
Rmet_3550	tctB	102.00	Op0985f_1	0.26	0.26	0.44	1.72	0.35	1.36	1.66	6.48	0.41	1.61	putative tricarboxylic transport membrane protein
Rmet_3551	tctA	68.00	Op0985f_1	0.57	0.42	0.54	1.29	0.46	1.09	1.45	3.46	0.51	1.21	putative tricarboxylic transport membrane protein
Pores ion channels														
Rmet_3234		37040	Op0918r_4	0.16	0.39	0.50	1.29	0.42	1.07	0.77	1.98	0.48	1.25	Porin, Gram-negative type
ABC transporters [PATH:ko02010]														
Rmet_0400		494.33	Op0109f_4	0.32	0.33	0.40	1.21	0.23	0.71	0.61	1.88	0.29	0.89	Amino acid ABC transporter, permease protein
Rmet_0401		482.67	Op0109f_4	0.29	0.34	0.46	1.36	0.29	0.87	0.74	2.18	0.34	1.00	Amino acid ABC transporter, permease protein
Rmet_0402		775.33	Op0109f_4	0.18	0.41	0.53	1.32	0.34	0.84	0.86	2.17	0.43	1.07	ABC transporter-related protein
Rmet_1862	livK	124.00	Op0538r_1	0.29	0.46	0.49	1.06	0.40	0.86	0.50	1.10	0.49	1.07	periplasmic substrate-binding protein
Genetic Information Processing				Transkription				Transcription regulators						
Rmet_5151		13.00	Op1516f_2	0.29	0.37	0.47	1.28	0.47	1.28	0.73	2.00	0.50	1.37	Transcriptional regulator, LysR family
				Translation				Ribosome [PATH:ko03010]						
Rmet_3309	rpmC	4681.33	Op0926r_2	0.37	0.55	0.52	0.95	0.46	0.83	0.65	1.17	0.51	0.93	50S ribosomal protein L29
Rmet_3310	rplP	4391.67	Op0926r_2	0.40	0.53	0.51	0.97	0.41	0.78	0.62	1.18	0.50	0.94	50S ribosomal protein L16
Rmet_3311	rpsC	4415.33	Op0926r_2	0.49	0.57	0.51	0.89	0.39	0.70	0.73	1.28	0.46	0.82	30S ribosomal protein S3
Rmet_3312	rplV	5059.33	Op0926r_2	0.49	0.48	0.46	0.97	0.33	0.70	0.74	1.55	0.40	0.83	50S ribosomal protein L22
Folding, Sorting and														
DN555 Not				Genetic Information Processing				Degradation				Type II secretion system [PATH:ko03090]		
Rmet_5688		54.33	Op1698f_1	0.38	0.48	0.42	0.87	0.48	1.00	0.50	1.04	0.57	1.17	Putative transmembrane protein
Rmet_5689		75.00	Op1698f_1	0.53	0.45	0.39	0.86	0.36	0.79	0.40	0.88	0.57	1.24	type IV pilus assembly protein PilY1
Rmet_5690		47.33	Op1698f_1	0.13	0.53	0.65	1.18	0.67	1.26	0.44	0.80	0.95	1.73	Putative lipoprotein
Not 546/554 Environmental Information														
Processing				Membrane Transport				ABC transporters [PATH:ko02010]						
Rmet_2122		389.33	Op0614r_2	0.12	0.40	0.51	1.25	0.40	1.02	0.50	1.23	0.45	1.11	periplasmic substrate-binding protein
Rmet_2123		202.00	Op0614r_2	0.37	0.52	0.63	1.18	0.45	0.86	0.56	1.04	0.44	0.82	Uncharacterized protein UPF0065
Rmet_0130		3698.33	Op0033f_2	0.16	0.47	0.59	1.26	0.43	0.93	0.69	1.49	0.39	0.83	Uncharacterized protein UPF0065
Not 546/555 Genetic Information														
Processing				Folding, Sorting and				Degradation				Type II secretion system [PATH:ko03090]		
Rmet_0192		189.67	Op0057f_1	0.48	0.45	0.56	1.23	0.43	0.94	0.41	0.90	0.71	1.57	type IV pilus assembly protein PilY1
Rmet_3963		62.00	Op1112f_2	0.39	0.52	0.44	0.86	0.54	1.03	0.63	1.21	0.41	0.79	Putative uncharacterized protein

Rmet_3964		72.33	Op1112f_2	0.40	0.44	0.46	1.05	0.67	1.50	0.82	1.88	0.41	0.94	Putative uncharacterized protein	
Not 553/555	Metabolism				Amino Acid Metabolism			Tyrosine metabolism [PATH:ko00350]				Phenylalanine metabolism [PATH:ko00360]			
Rmet_0019		35.67	Op0003f_3	0.36	0.47	0.45	0.95	0.56	1.19	0.49	1.05	0.52	1.10	Beta-lactamase-like protein	
Rmet_0020	hpaF	249.00	Op0003f_4	0.43	1.27	1.58	1.25	1.48	1.16	1.26	1.00	1.22	0.97	Fumarylacetoacetate (FAA) hydrolase	
Rmet_0021	hipO	114.67	Op0003f_4	0.45	1.30	1.74	1.33	1.41	1.09	1.29	0.99	1.35	1.03	hippurate hydrolase	
Not 554/555	Genetic	Information			Folding, Sorting and										
	Processing				Degradation			Type II secretion system [PATH:ko03090]							
Rmet_3271	pilN	201.00	Op0920r_2	0.24	0.42	0.46	1.13	0.49	1.15	0.52	1.27	0.51	1.24	type IV pilus assembly protein PilN	
Only 546	Environmental	Information													
	Processing				Membrane Transport			ABC transporters [PATH:ko02010]							
Rmet_1226	livK	86.33	Op0355f_2	0.12	0.45	0.69	1.50	0.65	1.45	0.87	1.88	0.73	1.58	periplasmic substrate-binding protein	
Rmet_1227	livH	55.67	Op0355f_2	0.14	0.42	0.64	1.53	0.51	1.23	0.90	2.16	0.69	1.64		
Rmet_1228	livM	43.67	Op0355f_2	0.17	0.70	0.97	1.38	0.91	1.30	1.35	1.92	1.04	1.48		
Rmet_1229	livG	58.00	Op0355f_2	0.25	0.49	0.80	1.64	0.64	1.31	0.97	1.99	0.82	1.68		
Rmet_1230	livF	49.00	Op0355f_2	0.11	0.65	0.00	0.00	0.88	1.35	1.21	1.81	1.00	1.51		
								Other ion-coupled transporters							
Rmet_3837	hmvB	46.00	Op1066f_2	0.24	0.56	0.44	0.75	0.60	1.07	0.71	1.21	0.79	1.35	Membrane fusion protein	
Rmet_3838	hmvA	41.67	Op1066f_2	0.40	0.48	0.47	1.00	0.60	1.27	0.77	1.62	0.62	1.31	Heavy metal efflux pump HmvA, HME3a	
Only 553	Metabolism				Energy Metabolism			Nitrogen metabolism [PATH:ko00910]							
Rmet_3262	gltD	1048.7	Op0920r_3	0.16	0.50	0.74	1.48	0.44	0.87	0.82	1.63	0.61	1.20	Glutamate synthase (NADH) small subunit	
Rmet_3263	gltB	838.00	Op0920r	0.20	0.49	0.61	1.26	0.48	0.99	0.93	1.92	0.62	1.28		Glutamate synthase (NADH) large subunit
	Genetic	Information													
	Processing				-	Replication and Repair			Other replication, recombination and repair proteins						
Rmet_4742		3849.3	Op1375r_3	0.22	0.50	0.52	1.04	0.49	0.98	0.57	1.15	0.55	1.11	Histone-like DNA-binding protein	
Rmet_4749	hupB	3394.3	Op1377r_2	0.33	0.43	0.51	1.19	0.35	0.81	0.78	1.79	0.61	1.41	HUPB; DNA-binding protein HU-beta	
				-	Folding, Sorting and										
					Degradation			Protein folding and associated processing							
Rmet_0065		64.00	Op0019f_2	0.28	0.48	0.70	1.43	0.51	1.08	0.52	1.07	0.60	1.23	Putative uncharacterized protein	
Rmet_0066		63.33	Op0019f_2	0.34	0.56	0.73	1.39	0.55	0.98	0.64	1.22	0.65	1.23	Putative uncharacterized protein	
Rmet_0067	pcp	57.00	Op0019f_2	0.25	0.51	0.71	1.40	0.49	0.96	0.57	1.11	0.65	1.28	Pyroglutamyl-peptidase I. Cysteine peptidase.	
Only 554															
Rmet_0064		42.00	Op0019f_2	0.35	0.50	0.56	1.06	0.52	1.05	0.44	0.83	0.50	0.95	UPF0271 protein Rmet_0064	
only 546 up				-						-					
Rmet_5230		16.67	Op1543r_1	0.53	1.01	2.11	2.06	1.86	1.84	0.90	0.88	1.62	1.58	Aminotransferase, class V	
only 554 up															
Rmet_1628		200.33	Op0455f_1	0.17	0.45	0.60	1.34	0.59	1.31	1.54	3.44	0.62	1.38	Porin, Gram-negative type	
Rmet_1629		6.33	Op0456r_1	0.34	0.86	1.43	1.69	1.67	1.94	3.08	3.65	1.42	1.68	Glutathione-dependent formaldehyde-activating	
only 555 up															
Rmet_6336		0.00	Op1926f_1	0.07	1.12	1.68	1.49	1.62	1.44	1.13	1.00	15.24	13.51	General secretion pathway protein	
Rest															
Rmet_0700	dadA	26.33	Op0197f_1	0.14	0.47	0.56	1.20	0.79	1.69	0.82	1.75	0.60	1.27	D-amino-acid dehydrogenase	
Rmet_1404		76.67	Op0396r_1	0.16	0.49	0.58	1.21	0.58	1.19	0.51	1.06	0.57	1.18	ABC transporter-related, ATP-binding protein	
Rmet_5288		0.33	Op1560f_2	0.16	0.49	0.66	1.35	0.69	1.40	1.45	2.97	0.67	1.37	Porin, Gram-negative type	
Rmet_4477	livM	1.00	Op1276f_3	0.17	0.43	0.57	1.34	0.52	1.22	0.63	1.49	0.50	1.19	ABC transporter-related, permease	
Rmet_4222		32.00	Op1198f_3	0.19	0.45	0.54	1.26	0.61	1.34	0.83	1.91	0.63	1.45	Transcriptional regulator, lclR family	
Rmet_5746	furB	9.33	Op1718f_2	0.32	0.44	0.55	1.28	0.79	1.80	0.56	1.30	0.53	1.23	Ferric uptake regulator, Fur family	

Rmet_1612	0.00	Op0450r_1	<u>0.35</u>	0.43	1.07	2.21	1.24	2.57	0.95	1.95	1.25	2.58	Integrase catalytic region
-----------	------	-----------	-------------	------	------	------	------	------	------	------	------	------	----------------------------

^aThe table gives the regulation (Q values) of genes in metal-mix-treated *C. metallidurans* cells compared to the untreated control cells. “Op” gives the operon, Q(WT) and Q2(WT) the comparison of metal-treated CH34 cells to untreated cells. The Q(DN..) values compare metal-treated mutant cells to untreated CH34 cells, the QQ(DN...) values metal-treated mutant cells to metal-treated CH34 cells. Values Q > 2 in green, Q < 0.5 in red, significant values (D > 1) bold-faced and underlined. The genes were also sorted into the KEGG orthology system.

Supplementary Table S8. Genes not regulated in wild type but up-regulated on most mutant cells

Gene	NPKM	Operon	Q(WT)	Q2(WT)	Q(DN546)	QQ546	Q(DN553)	QQ553	Q(DN554)	QQ554	Q(DN555)	QQ555	Description
All mutants up-regulated													
Rmet_5391	37.33	Op1605r_1	1.89	1.77	2.93	1.72	2.00	1.13	2.25	1.32	3.06	1.79	Putative uncharacterized protein
Rmet_5594	14.67	Op1666f_1	1.73	1.81	2.09	1.15	2.70	1.49	2.18	1.20	3.25	1.79	Putative uncharacterized protein
Rmet_5389	18.33	Op1605r_1	3.22	1.47	2.12	1.39	1.41	0.96	1.92	1.26	2.12	1.39	Oxidoreductase FAD/NAD(P)-binding
Rmet_5390	27.00	Op1605r_1	1.69	2.24	3.88	1.75	2.48	1.11	2.99	1.35	3.93	1.78	Putative uncharacterized protein
Rmet_6122	3.33	Op1869f_1	1.64	2.54	2.63	1.04	2.76	1.09	3.02	1.19	2.55	1.01	CopH protein (Putative uncharacterized protein)
Rmet_0032	2280.00	Op0012r_3	1.59	2.59	2.81	1.09	2.44	0.94	3.87	1.49	3.23	1.25	Porin, gram-negative type
Rmet_1704	72.00	Op0481f_2	2.94	1.24	6.06	4.87	2.00	1.61	1.97	1.58	19.82	15.95	Putative uncharacterized protein
Rmet_1705	120.00	Op0481f_2	15.21	1.16	7.62	6.53	2.23	1.91	2.01	1.72	21.60	18.52	Putative uncharacterized protein
Rmet_3359	1028.33	Op0935f_3	10.08	0.86	5.92	6.88	8.15	9.45	2.27	2.64	6.72	7.81	UBA/THIF-type NAD/FAD binding fold
Rmet_5754	64.33	Op1724f_1	0.15	1.70	2.88	1.69	2.10	1.23	2.33	1.37	4.68	2.75	Fumarate hydratase, class II
Rmet_3940	202.00	Op1101r_2	0.49	0.82	0.99	1.21	0.91	1.12	0.82	1.00	1.59	1.94	Transcriptional regulator, LysR family
Rmet_3941	70.00	Op1102f_1	0.15	1.21	4.37	3.61	3.01	2.48	2.43	2.01	16.37	13.54	Putative uncharacterized protein
Rmet_1929	17.00	Op0562r_1	0.16	1.19	2.62	2.21	2.38	1.99	2.86	2.42	2.59	2.19	Transcriptional regulator, GntR family
Rmet_1930	42.33	Op0563f_1	0.33	0.88	1.87	2.11	1.66	1.88	1.41	1.59	1.79	2.02	Transcriptional regulator, lclR family
Rmet_0263	322.33	Op0075f_2	0.22	1.59	2.65	1.67	1.83	1.15	3.07	1.94	2.45	1.54	Cytochrome c oxidase assembly protein CtaG/Cox11
Rmet_0264	234.33	Op0075f_2	0.19	1.80	2.95	1.64	2.23	1.24	3.01	1.67	2.68	1.49	Putative transmembrane protein
Rmet_1706	111.00	Op0481f_2	0.22	1.24	9.73	7.68	2.70	2.18	2.09	1.65	26.75	21.13	Putative uncharacterized protein
Rmet_1668	0.00	Op0469f_1	0.23	1.40	2.17	1.55	2.29	1.63	2.00	1.43	2.48	1.77	Transposase and inactivated derivatives-like protein
Rmet_1699	37.33	Op0481f_1	0.25	1.13	6.56	6.02	2.81	2.48	2.12	1.94	28.43	26.09	Response regulator receiver domain protein (CheY-like)
Rmet_1700	90.00	Op0481f_2	0.45	1.13	5.30	4.59	2.19	1.93	2.11	1.83	19.06	16.53	Putative uncharacterized protein
Rmet_0357	213.33	Op0101f_1	0.32	1.42	2.26	1.59	1.75	1.23	2.15	1.52	1.99	1.41	Alpha,alpha-trehalose-phosphate synthase
Rmet_0358	51.67	Op0102r_2	0.26	1.57	2.90	1.84	2.09	1.33	2.85	1.81	2.44	1.55	Putative uncharacterized protein
Rmet_0359	59.00	Op0102r_2	0.42	1.17	2.37	2.01	2.20	1.88	1.65	1.40	2.01	1.70	Predicted sulfurylase large subunit, molybdopterin cytosine dinucleotide biosynthesis / predicted sulfurylase dinucleotide biosynthesis
Rmet_4193	143.00	Op1186f_1	0.29	1.76	2.56	1.45	3.14	1.78	2.42	1.37	2.49	1.41	Putative uncharacterized protein
Rmet_4194	38.67	Op1187r_1	0.47	1.83	2.29	1.25	2.82	1.54	2.04	1.11	2.23	1.22	Alanine racemase-like protein
Rmet_0260	731.33	Op0075f_2	0.32	2.31	3.39	1.49	2.67	1.17	5.07	2.23	3.29	1.45	Putative transmembrane protein
Rmet_3949	143.00	Op1106f_1	0.39	1.39	2.64	1.92	3.38	2.43	2.56	1.86	3.04	2.21	Esterase, PHB depolymerase
Rmet_0896	139.67	Op0261f_1	0.40	1.77	3.24	1.83	2.43	1.38	2.57	1.45	2.13	1.21	Transcriptional regulator of molybdate metabolism, LysR family
Rmet_0051	514.00	Op0017f_1	0.51	1.13	4.23	3.73	3.28	2.90	3.78	3.33	3.35	2.95	Rod shape-determining protein MreB
Rmet_6120	27.67	Op1868r_1	0.55	2.81	2.58	0.93	2.83	1.01	2.44	0.88	2.80	1.01	Putative type II restriction enzyme (Putative uncharacterized protein)
Rmet_1029	198.67	Op0295f_3	0.61	2.27	3.58	1.57	2.75	1.20	3.74	1.64	3.13	1.37	Chaperone protein hscA homolog
Rmet_1766	73.33	Op0507f_1	0.62	1.21	7.40	6.16	2.15	1.77	2.33	1.94	23.70	19.73	Glutamate decarboxylase
Rmet_4537	95.00	Op1298f_1	0.64	2.63	4.31	1.66	3.08	1.17	2.61	1.00	4.51	1.74	D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding
Rmet_3583	29.33	Op0995f_2	0.65	2.31	2.50	1.08	2.26	0.98	3.07	1.32	2.56	1.10	Putative uncharacterized protein
Rmet_5964	21.67	Op1814r_1	0.68	2.65	3.78	1.42	3.54	1.34	2.97	1.12	3.93	1.48	Transposase IS3/IS911
Rmet_3581	46.67	Op0995f_2	0.88	1.62	1.63	1.01	1.65	1.01	1.78	1.10	1.70	1.05	Secretion protein HlyD
Rmet_3582	36.67	Op0995f_2	0.75	1.98	2.19	1.10	2.11	1.06	2.94	1.47	2.17	1.09	Acriflavin resistance protein
Rmet_4461	20.67	Op1271r_1	0.75	3.09	5.43	1.75	4.49	1.45	4.80	1.55	4.95	1.60	Putative uncharacterized protein
Rmet_5392	40.67	Op1606f_1	0.78	1.94	3.07	1.62	2.28	1.18	2.69	1.42	3.05	1.61	Two component transcriptional regulator, winged helix family
Rmet_5393	21.00	Op1606f_1	0.77	1.79	4.59	2.57	2.92	1.63	3.40	1.90	5.30	2.97	Sensor protein
Rmet_2305	11.67	Op0659f_1	0.84	11.14	13.82	1.24	10.21	0.92	13.69	1.23	9.30	0.83	Putative uncharacterized protein ORF C95
Rmet_1984	115.33	Op0579f_1	1.42	1.04	7.25	6.99	3.05	2.95	1.35	1.30	20.93	20.18	Aminotransferase
Rmet_1985	90.33	Op0579f_1	0.88	1.51	7.17	4.66	2.68	1.78	2.05	1.34	19.38	12.61	YidE/YbjL duplication
Rmet_4025	13.33	Op1132f_1	0.89	3.80	2.69	0.70	2.45	0.64	2.14	0.56	2.33	0.61	Major facilitator superfamily MFS_1
Rmet_0052	75.00	Op0017f_1	0.90	1.15	2.98	2.62	2.86	2.48	2.89	2.54	2.71	2.39	Rod shape-determining protein MreC

Rmet_0053	55.33	Op0017f_1	1.03	1.20	<u>2.58</u>	2.14	<u>2.38</u>	1.97	<u>2.72</u>	2.26	<u>2.32</u>	1.92	Rod shape-determining protein MreD
Rmet_0054	41.67	Op0017f_1	0.71	0.96	1.30	1.33	1.28	1.34	1.29	1.33	1.31	1.35	Peptidoglycan glycosyltransferase
Rmet_0055	39.00	Op0017f_1	0.81	1.10	1.89	1.74	<u>2.03</u>	1.85	<u>2.06</u>	1.89	<u>2.11</u>	1.94	Rod shape-determining protein RodA
Rmet_5991	8.00	Op1826r_1	1.04	2.64	<u>3.59</u>	1.38	<u>3.72</u>	1.41	<u>2.26</u>	0.87	<u>2.87</u>	1.11	Mercuric transport protein (Mercuric transport protein MerT)
Rmet_5030	42.00	Op1480f_2	1.10	1.90	<u>2.35</u>	1.24	<u>2.18</u>	1.15	<u>2.11</u>	1.11	<u>2.97</u>	1.56	Putative uncharacterized protein
Rmet_1027	114	Op0295f_3	1.11	2.26	<u>3.37</u>	1.49	<u>2.15</u>	0.95	<u>2.54</u>	1.12	<u>2.43</u>	1.07	Iron-sulfur cluster assembly protein IscA
Rmet_5965	17.00	Op1815f_1	1.14	2.23	<u>3.28</u>	1.48	<u>3.62</u>	1.62	<u>2.76</u>	1.24	<u>3.33</u>	1.50	Insertion element protein (Putative uncharacterized protein)
Rmet_6121	6.67	Op1869f_1	1.25	4.83	<u>5.81</u>	1.22	<u>5.72</u>	1.18	<u>6.96</u>	1.46	<u>5.95</u>	1.25	Putative uncharacterized protein
Rmet_3411	3.33	Op0948r_1	1.26	3.02	<u>5.29</u>	1.73	<u>2.64</u>	0.87	<u>2.30</u>	0.75	<u>3.90</u>	1.28	Uncharacterized protein UPF0065
Rmet_4462	128.67	Op1272f_1	<u>0.29</u>	1.63	<u>2.49</u>	1.53	1.96	1.21	<u>2.61</u>	1.61	<u>2.03</u>	1.25	Putative uncharacterized protein
Rmet_4464	64.67	Op1273r_1	<u>0.49</u>	1.46	<u>2.38</u>	1.62	<u>2.11</u>	1.44	1.63	1.11	<u>2.41</u>	1.64	Putative uncharacterized protein
Rmet_R0071			<u>0.08</u>	1.49	<u>2.33</u>	1.56	<u>2.82</u>	1.89	<u>2.57</u>	1.73	<u>2.21</u>	1.48	GCN5-related N-acetyltransferase
Rmet_R0002			<u>0.25</u>	1.35	1.92	1.42	<u>2.03</u>	1.50	1.34	1.00	<u>2.05</u>	1.52	
Rmet_0196	92.00	Op0057f_2	<u>0.22</u>	1.29	<u>2.34</u>	1.81	1.74	1.35	1.43	1.11	<u>2.36</u>	1.83	

AllUpNot546:NONE

DN553 not

Rmet_0195	21.00	Op0057f_1	<u>0.36</u>	1.66	<u>2.57</u>	1.57	1.75	1.06	<u>2.01</u>	1.22	<u>2.44</u>	1.48	Bacterioferritin
Rmet_4694	1.00	Op1359r_4	<u>9.19</u>	1.83	<u>2.15</u>	1.17	1.97	1.08	<u>2.91</u>	1.59	<u>2.04</u>	1.11	PpiC-type peptidyl-prolyl cis-trans isomerase
Rmet_4125	38.33	Op1162f_2	<u>0.33</u>	1.54	<u>2.23</u>	1.42	1.83	1.19	<u>2.39</u>	1.52	<u>2.48</u>	1.57	Putative uncharacterized protein
Rmet_1594	42.33	Op0443f_2	<u>0.34</u>	1.19	<u>2.04</u>	1.69	1.72	1.44	<u>2.24</u>	1.85	<u>2.77</u>	<u>2.29</u>	DoxX
Rmet_1595	41.00	Op0443f_2	<u>0.47</u>	1.03	1.72	1.66	1.32	1.28	1.88	1.81	<u>2.36</u>	<u>2.27</u>	Putative lipoprotein
Rmet_1831	134.33	Op0531f_1	<u>0.46</u>	2.01	<u>2.64</u>	1.31	1.92	0.95	<u>2.05</u>	1.01	<u>2.26</u>	1.12	Putative uncharacterized protein
Rmet_1832	106.33	Op0531f_1	<u>0.29</u>	1.73	<u>2.05</u>	1.19	1.46	0.85	1.42	0.82	1.94	1.12	Putative uncharacterized protein
Rmet_5972	0.00	Op1818r_1	0.92	1.88	<u>2.14</u>	1.14	1.99	1.06	<u>2.79</u>	1.48	<u>2.31</u>	1.23	Transposase IS3/IS911 family protein
Rmet_1751	15.67	Op0499f_1	0.92	1.57	<u>2.35</u>	1.51	1.69	1.08	<u>2.41</u>	1.55	<u>2.31</u>	1.49	Two component heavy metal response transcriptional regulator, winged helix family
Rmet_5667	29.00	Op1694f_3	0.93	1.84	<u>2.60</u>	1.41	1.65	0.90	<u>2.10</u>	1.14	<u>5.11</u>	<u>2.76</u>	Putative uncharacterized protein
Rmet_5388	18.33	Op1605r_1	1.07	1.42	<u>2.58</u>	1.84	1.73	1.21	<u>2.27</u>	1.62	<u>2.47</u>	1.76	ApbE-like lipoprotein
Rmet_3574	140.00	Op0992r_1	1.28	1.77	<u>2.02</u>	1.14	1.39	0.78	<u>2.00</u>	1.13	<u>2.34</u>	1.32	Carbon starvation protein CstA

DN554 not

Rmet_0005	49.67	Op0002r_3	<u>0.43</u>		1.44	2.16	1.65	2.56	0.63	0.94	1.75	2.63	Twin-arginine translocation pathway signal
Rmet_2567	138.33	Op0711f_1	<u>0.08</u>	1.36	<u>3.15</u>	2.33	<u>5.52</u>	4.07	1.52	1.12	<u>3.95</u>	<u>2.92</u>	Integral membrane protein TerC
Rmet_2824	211.00	Op0795f_3	<u>0.06</u>	1.39	<u>2.35</u>	1.66	<u>4.25</u>	3.06	1.88	1.33	<u>2.68</u>	1.89	Putative uncharacterized protein
Rmet_2825	41.00	Op0795f_3	0.57	1.12	<u>2.62</u>	2.29	<u>4.21</u>	3.76	0.93	0.81	<u>3.36</u>	<u>2.93</u>	Plasmid encoded RepA protein
Rmet_2218	1.67	Op0635f_1	<u>6.11</u>	0.89	<u>3.26</u>	3.70	<u>3.11</u>	3.51	<u>0.40</u>	<u>0.45</u>	<u>2.92</u>	3.31	Luciferase-like protein
Rmet_3085	4.00	Op0868r_1	<u>9.03</u>	0.75	1.94	2.58	<u>2.52</u>	3.36	0.68	0.90	0.68	0.91	Alcohol dehydrogenase, zinc-binding
Rmet_3086	124.67	Op0869f_1	<u>11.05</u>	1.36	<u>8.38</u>	6.11	<u>11.79</u>	8.68	<u>0.34</u>	<u>0.25</u>	<u>2.39</u>	1.74	Uncharacterized protein UPF0065
Rmet_0864	79.67	Op0249f_1	<u>2.01</u>	0.93	<u>3.03</u>	3.27	<u>3.53</u>	3.80	<u>0.46</u>	<u>0.50</u>	<u>3.47</u>	3.74	Putative uncharacterized protein
Rmet_0865	75.67	Op0249f_1	<u>10.10</u>	0.95	<u>3.03</u>	3.18	<u>3.76</u>	3.95	<u>0.46</u>	<u>0.48</u>	<u>3.09</u>	3.24	Putative uncharacterized protein
Rmet_5111	2.00	Op1505r_1	<u>2.60</u>	1.25	<u>2.12</u>	1.61	1.98	1.58	1.09	0.83	<u>2.15</u>	1.63	Thiolase
Rmet_5112	2.33	Op1505r_1	<u>9.81</u>	0.96	<u>4.20</u>	4.33	<u>4.62</u>	4.79	<u>0.48</u>	<u>0.50</u>	<u>3.74</u>	3.86	Putative uncharacterized protein
Rmet_2349	0.00	Op0663f_2	<u>7.00</u>	0.89	<u>4.05</u>	4.69	<u>2.90</u>	3.26	<u>0.40</u>	<u>0.47</u>	<u>2.13</u>	2.47	Putative uncharacterized protein ORF C51
Rmet_3365	0.00	Op0936r_1	<u>5.91</u>	1.04	<u>4.93</u>	4.73	<u>4.54</u>	4.36	0.63	0.61	<u>3.85</u>	3.70	Integrase, catalytic region
Rmet_2876	104.67	Op0808r_1	<u>4.59</u>	1.07	<u>3.65</u>	3.39	<u>4.70</u>	4.37	<u>0.34</u>	<u>0.32</u>	<u>3.89</u>	3.61	MscS Mechanosensitive ion channel
Rmet_1476	3.33	Op0414r_1	<u>2.22</u>	0.78	1.16	1.49	1.08	1.38	0.63	0.81	1.53	1.98	Putative uncharacterized protein
Rmet_1477	0.67	Op0415f_1	<u>4.48</u>	1.13	<u>3.10</u>	2.80	<u>2.46</u>	2.17	<u>0.47</u>	0.42	<u>3.22</u>	2.90	Putative uncharacterized protein
Rmet_2231	12.33	Op0638r_1	<u>4.42</u>	1.08	<u>3.76</u>	3.45	<u>3.54</u>	3.28	<u>0.48</u>	0.44	<u>2.83</u>	2.60	Binding-protein-dependent transport systems inner membrane component
Rmet_2658	0	Op0754r_4	<u>3.36</u>	1.01	<u>3.16</u>	3.15	<u>4.39</u>	4.34	0.50	0.50	<u>2.27</u>	2.27	Predicted signal transduction protein containingPAS, GGDEF and EAL domains
Rmet_2647	19.00	Op0748r_1	<u>3.29</u>	0.83	<u>3.83</u>	4.56	<u>7.33</u>	8.83	<u>0.31</u>	<u>0.37</u>	<u>3.33</u>	3.97	Transcriptional regulator, AsnC family
Rmet_4490	56.67	Op1279r_1	<u>3.06</u>	0.75	<u>2.70</u>	3.68	<u>2.65</u>	3.52	<u>0.45</u>	0.62	<u>2.08</u>	2.83	Putative uncharacterized protein

Rmet_4491	42.33	Op1279r_1	<u>2.20</u>	0.95	1.35	1.45	1.43	1.51	0.72	0.78	1.53	1.65	Putative uncharacterized protein
Rmet_2683	7.33	Op0757f_1	<u>2.90</u>	1.03	<u>3.16</u>	3.06	<u>5.50</u>	5.36	0.49	0.48	<u>3.68</u>	3.56	Putative transmembrane protein
Rmet_2687	8.67	Op0757f_2	<u>2.87</u>	1.14	<u>2.74</u>	2.40	<u>5.28</u>	4.63	0.71	0.62	<u>3.11</u>	2.73	Pilus assembly protein Fim
Rmet_1701	69.33	Op0481f_2	<u>2.46</u>	0.94	<u>2.21</u>	2.32	1.04	1.10	1.14	1.20	<u>6.51</u>	6.86	Secretion protein HlyD
Rmet_1702	45.00	Op0481f_2	<u>2.85</u>	1.24	<u>5.61</u>	4.57	<u>2.18</u>	1.76	1.96	1.60	<u>20.11</u>	16.38	Hydrophobe/amphiphile efflux-1 HAE1
Rmet_3361	245.67	Op0935f_3	1.67	0.95	<u>4.26</u>	4.51	<u>3.63</u>	3.80	0.89	0.94	<u>5.80</u>	6.15	Putative uncharacterized protein
Rmet_3362	86.00	Op0935f_3	<u>2.84</u>	0.93	<u>4.13</u>	4.44	<u>3.30</u>	3.53	0.74	0.79	<u>4.15</u>	4.46	Putative uncharacterized protein
Rmet_1254	0.00	Op0363f_2	<u>2.74</u>	1.43	<u>2.37</u>	1.73	<u>2.10</u>	1.47	1.30	0.95	<u>2.97</u>	2.17	Cobyrinic acid a,c-diamide synthase
Rmet_4978	0.00	Op1461r_1	<u>2.63</u>	0.94	<u>4.06</u>	4.31	<u>3.16</u>	3.38	0.34	0.36	<u>2.48</u>	2.64	Two component transcriptional regulator, winged helix family
Rmet_4979	0.00	Op1461r_1	1.90	0.91	<u>3.39</u>	3.75	<u>2.89</u>	3.19	0.41	0.46	<u>2.10</u>	2.32	Putative uncharacterized protein
Rmet_4493	1702.33	Op1279r_1	<u>2.03</u>	1.08	<u>3.03</u>	2.77	<u>3.49</u>	3.23	0.62	0.57	<u>3.52</u>	3.22	Putative uncharacterized protein
Rmet_4494	5184.67	Op1279r_1	1.74	1.16	<u>2.87</u>	2.50	<u>3.04</u>	2.62	0.64	0.56	<u>2.15</u>	1.88	Putative uncharacterized protein
Rmet_4495	493.00	Op1280f_1	<u>5.38</u>	0.93	1.04	1.12	0.75	0.81	0.79	0.85	0.81	0.87	Putative uncharacterized protein
Rmet_0804	1.67	Op0228r_1	1.93	0.99	<u>3.56</u>	3.60	<u>4.82</u>	4.89	0.65	0.65	<u>3.48</u>	3.53	SPFH domain, Band 7 family protein
Rmet_0805	5.33	Op0228r_1	1.97	0.96	<u>3.38</u>	3.52	<u>3.65</u>	3.81	0.52	0.54	<u>3.79</u>	3.95	Putative uncharacterized protein
Rmet_2495	23.00	Op0690r_1	1.91	1.90	<u>2.02</u>	1.11	<u>2.59</u>	1.36	1.85	1.01	<u>2.13</u>	1.17	Putative methyltransferase
Rmet_2496	101.33	Op0691f_1	<u>3.24</u>	1.19	0.97	0.82	0.55	0.46	0.90	0.76	0.75	0.63	Extracellular solute-binding protein, family 5
Rmet_2685	4.33	Op0757f_1	1.66	1.04	<u>2.50</u>	2.51	<u>4.22</u>	4.06	0.67	0.68	<u>3.17</u>	3.18	Putative type 4 fimbrial biogenesis PilY1-related protein transmembrane
Rmet_0483	0.00	Op0129f_1	1.63	1.00	<u>2.57</u>	2.57	<u>2.25</u>	2.24	0.74	0.74	<u>2.08</u>	2.08	Integrase, catalytic region
Rmet_2827	15.33	Op0795f_3	1.63	1.16	<u>2.94</u>	2.48	<u>6.61</u>	5.68	0.90	0.76	<u>3.37</u>	2.84	Putative TraY/DotA-like type IV secretion system protein
Rmet_0092	31.00	Op0026r_1	1.59	1.01	<u>4.21</u>	4.18	<u>3.94</u>	3.89	0.44	0.44	<u>2.44</u>	2.42	Histidine kinase
Rmet_3625	120.33	Op1009r_1	1.57	0.97	<u>2.59</u>	2.67	<u>3.21</u>	3.31	0.40	0.41	<u>2.73</u>	2.81	Putative uncharacterized protein
Rmet_0860	70.67	Op0247f_2	0.31	1.03	<u>2.58</u>	2.54	<u>2.10</u>	2.04	0.92	0.91	<u>4.77</u>	4.70	Putative uncharacterized protein
Rmet_0861	47.67	Op0247f_2	0.28	0.95	<u>2.08</u>	2.23	<u>2.05</u>	2.16	0.88	0.94	<u>4.41</u>	4.73	Putative uncharacterized protein
Rmet_R0010			0.15	1.19	1.90	1.59	<u>2.22</u>	1.86	1.94	1.63	1.60	1.35	
Rmet_0862	331.00	Op0248r_2	0.15	1.01	<u>2.93</u>	2.89	<u>3.52</u>	3.49	0.70	0.69	<u>4.10</u>	4.05	Putative uncharacterized protein
Rmet_1013	42.00	Op0291f_1	0.27	1.32	<u>2.29</u>	1.75	<u>2.02</u>	1.52	1.96	1.49	<u>2.30</u>	1.75	Transcriptional regulator, TetR family
Rmet_1014	49.67	Op0292r_1	0.27	1.17	<u>2.11</u>	1.78	1.66	1.42	1.71	1.45	<u>2.06</u>	1.74	DNA-(Apurinic or apyrimidinic site) lyase / endonuclease III
Rmet_1981,lexA	626.67	Op0577f_1	0.29	1.12	<u>2.46</u>	2.19	<u>2.17</u>	1.94	1.25	1.11	<u>2.15</u>	1.91	LexA repressor
Rmet_0730	76.00	Op0205f_3	0.29	1.28	<u>2.29</u>	1.81	<u>2.17</u>	1.69	1.24	0.98	<u>2.75</u>	2.17	Uracil-xanthine permease
Rmet_3205	373.33	Op0901f_3	0.33	1.69	<u>2.55</u>	1.51	<u>2.19</u>	1.30	1.83	1.08	<u>2.48</u>	1.47	3-octaprenyl-4-hydroxybenzoate carboxy-lyase
Rmet_1465	83.33	Op0411f_1	0.52	1.09	1.83	1.69	<u>2.06</u>	1.89	0.87	0.80	1.89	1.74	Phage integrase
Rmet_1466	103.00	Op0411f_1	0.49	0.97	1.83	1.90	1.65	1.69	0.81	0.84	1.77	1.84	Putative uncharacterized protein
Rmet_1467	148.00	Op0411f_1	0.24	1.11	1.94	1.73	1.62	1.46	1.62	1.44	<u>2.03</u>	1.81	Prophage CP4-57 regulatory
Rmet_1468	64.33	Op0412r_1	0.33	0.86	<u>2.22</u>	2.51	<u>2.08</u>	2.42	0.74	0.84	<u>2.10</u>	2.38	Phage transcriptional regulator, AlpA
Rmet_6105	18.67	Op1863f_1	0.43	1.56	<u>2.11</u>	1.30	<u>2.19</u>	1.40	1.92	1.19	<u>2.23</u>	1.37	Putative uncharacterized protein
Rmet_0093	180.33	Op0027f_1	0.46	1.37	<u>3.26</u>	2.39	<u>3.02</u>	2.20	1.47	1.08	<u>2.24</u>	1.64	UPF0391 membrane protein Rmet_0093
Rmet_6323	81.33	Op1920f_1	0.57	1.11	<u>3.87</u>	3.59	<u>2.89</u>	2.61	0.89	0.83	<u>3.95</u>	3.67	Putative uncharacterized protein
Rmet_6324	56.67	Op1920f_2	0.49	1.16	1.41	1.24	1.48	1.28	1.13	0.99	<u>2.20</u>	1.93	Putative uncharacterized protein
Rmet_6325	49.00	Op1920f_2	0.29	1.21	<u>2.27</u>	1.87	1.87	1.55	1.35	1.12	<u>3.22</u>	2.66	Putative uncharacterized protein
Rmet_6326	24.33	Op1921r_1	0.50	1.09	1.72	1.60	1.55	1.43	1.10	1.02	<u>2.10</u>	1.96	Putative uncharacterized protein
Rmet_6327	137.67	Op1922f_1	0.42	1.19	1.72	1.43	1.41	1.18	1.80	1.50	1.97	1.64	Putative uncharacterized protein
Rmet_6328	72.33	Op1922f_1	0.50	1.19	<u>2.34</u>	1.95	<u>2.19</u>	1.84	1.97	1.64	<u>2.59</u>	2.16	Putative uncharacterized protein
Rmet_4975	0.00	Op1460f_1	0.55	1.29	<u>2.44</u>	1.89	<u>2.52</u>	1.95	1.27	0.98	<u>2.08</u>	1.61	Resolvase-like protein
Rmet_4976	0.00	Op1461r_1	0.63	1.02	<u>2.48</u>	2.43	<u>2.19</u>	2.15	0.93	0.91	1.75	1.72	Putative uncharacterized protein
Rmet_1695	19.67	Op0481f_1	0.56	1.19	<u>4.87</u>	4.12	<u>2.08</u>	1.75	1.74	1.47	<u>14.02</u>	11.87	Putative uncharacterized protein
Rmet_5326	19.33	Op1576f_2	0.56	1.84	<u>2.40</u>	1.30	<u>2.19</u>	1.19	1.79	0.97	<u>2.08</u>	1.13	Two component transcriptional regulator, winged helix family
Rmet_0363	23.67	Op0102r_1	0.57	1.00	<u>2.46</u>	2.57	<u>2.27</u>	2.27	0.88	0.91	<u>2.23</u>	2.32	Molybdopterin dehydrogenase, FAD-binding

Rmet_3546	31.67	Op0983f_3	0.57	1.50	2.19	1.46	2.26	1.51	1.44	0.96	2.07	1.39	Major facilitator superfamily MFS_1
Rmet_5992	36.33	Op1826r_2	0.58	1.93	2.56	1.33	2.48	1.29	1.77	0.92	2.23	1.16	Periplasmic transport protein (Heavy metal transport/detoxification protein)
Rmet_5993	52.33	Op1826r_2	0.58	1.91	2.55	1.35	2.26	1.19	1.92	1.01	2.12	1.12	Putative uncharacterized protein RMe0265 (Alkylhydroperoxidase AhpD core)
Rmet_3344	156.67	Op0931f_4	0.58	1.00	2.31	2.35	2.04	2.05	0.85	0.87	4.15	4.23	Putative membrane protein
Rmet_3345	75.00	Op0931f_4	0.52	1.26	2.33	1.82	1.93	1.53	0.95	0.75	3.22	2.52	Putative uncharacterized protein
Rmet_3622	29.33	Op1009r_1	0.58	1.23	2.47	2.00	2.57	2.08	0.93	0.75	2.26	1.83	Major facilitator superfamily MFS_1
Rmet_4983	0.00	Op1461r_1	0.59	1.32	2.38	1.80	2.02	1.53	1.06	0.81	2.00	1.52	Propeptide, PepSY amd peptidase M4
Rmet_3363	13.00	Op0936r_2	0.61	1.13	3.11	2.72	2.21	1.95	0.85	0.74	3.90	3.41	Putative uncharacterized protein
Rmet_3364	0.00	Op0936r_1	0.19	0.99	1.82	1.84	1.45	1.47	1.15	1.16	1.98	2.00	IstB-like ATP-binding protein
Rmet_1904	17.33	Op0555f_3	0.62	1.10	4.15	3.87	2.07	1.89	1.57	1.46	13.32	12.41	Putative uncharacterized protein
Rmet_0800	734.33	Op0227f_1	0.63	0.92	2.41	2.65	2.36	2.56	1.78	1.95	2.17	2.39	Substrate-binding region of ABC-type glycine betaine transport system
Rmet_6170	12.00	Op1888r_1	0.67	1.66	2.89	1.74	2.32	1.40	1.71	1.03	2.12	1.28	Putative uncharacterized protein
Rmet_0806	71.00	Op0229f_1	0.67	1.51	2.25	1.48	2.25	1.49	1.51	0.99	2.50	1.63	Putative uncharacterized protein
Rmet_3624	78.67	Op1009r_1	0.68	1.05	2.05	1.87	2.05	1.94	0.75	0.69	2.13	1.95	Transglutaminase-like protein
Rmet_2877	202.33	Op0808r_1	0.69	1.12	2.85	2.54	2.28	2.04	0.85	0.75	2.32	2.07	Fmu (Sun)
Rmet_5946	15.67	Op1807f_1	0.75	1.97	2.22	1.16	2.23	1.13	1.51	0.79	2.17	1.14	PbrR protein (Transcriptional regulator, MerR family)
Rmet_2826	29.33	Op0795f_3	0.75	1.02	2.10	1.95	3.25	3.19	0.76	0.70	2.66	2.47	Putative uncharacterized protein
Rmet_3381	69.33	Op0940r_2	0.75	1.10	2.27	2.12	2.26	2.06	0.82	0.77	3.60	3.36	Putative uncharacterized protein
Rmet_5177	3.67	Op1523r_1	0.77	0.95	2.12	2.34	2.32	2.45	1.41	1.56	2.16	2.39	Putative uncharacterized protein
Rmet_1215	0	Op0353f_1	0.79	1.11	2.62	2.44	2.49	2.24	0.88	0.82	2.01	1.87	Putative uncharacterized protein
Rmet_4538	20.33	Op1299r_1	0.82	1.85	2.43	1.32	2.04	1.10	1.98	1.07	2.53	1.37	Transcriptional regulator, MerR family
Rmet_1245	2.67	Op0357f_4	0.85	1.31	2.75	2.08	2.15	1.64	1.13	0.86	2.83	2.14	ParB family protein
Rmet_3051	28.33	Op0859f_1	0.86	0.97	2.63	2.70	2.37	2.44	1.09	1.12	3.19	3.27	Putative uncharacterized protein
Rmet_0160	2.33	Op0048r_2	0.94	1.14	2.14	1.85	2.45	2.16	0.63	0.55	2.84	2.46	Methyl-accepting chemotaxis sensory transducer
Rmet_2131	70.33	Op0614r_1	0.95	1.07	2.37	2.27	2.17	2.03	0.66	0.63	2.28	2.18	DNA helicase/exodeoxyribonuclease V, subunit A
Rmet_2301	1.33	Op0657f_1	0.97	1.32	2.45	1.96	2.33	1.77	1.21	0.96	2.08	1.66	Putative uncharacterized protein
Rmet_3618	249.33	Op1007r_3	0.98	1.08	2.44	2.24	2.76	2.55	0.66	0.61	2.28	2.10	OsmC-like protein
Rmet_3832	11.00	Op1065r_1	1.01	1.00	2.33	2.33	2.56	2.56	0.90	0.90	2.87	2.86	Uncharacterized protein UPF0065
Rmet_0095	197.67	Op0028r_1	1.02	1.14	4.41	3.87	4.47	3.92	0.85	0.74	2.31	2.03	Putative uncharacterized protein
Rmet_3623	40.33	Op1009r_1	1.06	1.13	2.43	2.12	2.49	2.20	0.59	0.52	2.63	2.30	Transcriptional regulator, MarR family
Rmet_3206	51.67	Op0902r_2	1.09	1.31	2.55	1.94	2.75	2.10	1.44	1.10	2.58	1.96	Putative uncharacterized protein
Rmet_3114	32.00	Op0876r_2	1.09	1.20	2.50	2.08	2.27	1.90	0.95	0.79	3.42	2.85	Oligopeptide transporter OPT
Rmet_3115	180.00	Op0876r_2	0.99	0.94	1.72	1.80	1.34	1.42	0.76	0.80	1.46	1.53	NUDIX hydrolase
Rmet_3360	563.33	Op0935f_3	1.10	0.97	5.51	5.64	4.95	5.08	1.10	1.13	7.35	7.53	Putative uncharacterized protein
Rmet_4489	48.67	Op1279r_1	1.11	1.00	2.20	2.14	2.22	2.21	0.78	0.75	2.58	2.51	Zonular occludens toxin
Rmet_4805	25.00	Op1397r_1	1.15	1.01	2.27	2.18	2.21	2.19	0.65	0.63	2.09	2.01	2-amino-3-ketobutyrate coenzyme A ligase
Rmet_1141	23.00	Op0326r_1	1.22	0.99	2.20	2.18	2.59	2.61	0.65	0.64	2.09	2.08	Transcriptional regulator, GntR family
Rmet_2643	235.00	Op0745f_3	1.23	2.06	2.43	1.18	2.12	1.03	1.46	0.71	2.01	0.98	Cyclopropane-fatty-acyl-phospholipid synthase
Rmet_0331	8.67	Op0094r_3	1.24	2.33	2.08	0.86	4.73	2.03	1.90	0.79	2.02	0.83	Protein tyrosine phosphatase
Rmet_3382	4.67	Op0940r_1	1.34	0.98	2.21	2.22	2.05	2.08	0.74	0.74	3.61	3.63	Globin
Rmet_0364	30.00	Op0102r_1	1.35	1.12	4.06	3.57	3.74	3.33	0.54	0.47	2.40	2.11	Xanthine dehydrogenase, molybdenum binding subunit apoprotein
Rmet_3619	21.00	Op1007r_2	1.36	1.00	2.92	2.90	3.59	3.59	0.51	0.50	3.38	3.36	Transcriptional regulator, MarR family
Rmet_2214	10.33	Op0634r_2	1.43	1.00	2.17	2.23	2.22	2.23	0.70	0.72	2.10	2.15	Putative uncharacterized protein
Rmet_3213	58.67	Op0906r_2	1.44	1.20	2.71	2.30	2.54	2.13	0.91	0.77	3.00	2.54	Cl-channel, voltage gated
Rmet_4604	34.00	Op1324f_2	1.49	0.87	3.08	3.53	3.01	3.46	0.60	0.69	2.32	2.66	Putative uncharacterized protein
Rmet_2686	3.00	Op0757f_1	1.50	1.31	3.16	2.40	5.52	4.21	0.96	0.73	3.78	2.87	Pilus assembly protein PilE
DN555 not													
Rmet_4245	73.33	Op1202f_4	0.60	2.02	2.23	1.10	2.04	1.01	2.81	1.39	0.64	0.32	Transcriptional regulator, LysR family
Rmet_4246	61.00	Op1202f_4	0.61	1.88	2.19	1.15	2.39	1.27	2.71	1.43	0.56	0.29	Putative uncharacterized protein

546/553 up														
Rmet_5629	10.33	Op1679r_1	2.95		1.63	2.17	1.78	2.34	0.81	1.08	0.98	1.31	Uncharacterized protein UPF0065	
Rmet_0022	26.33	Op0004r_1	0.63	0.72	2.73	3.75	2.20	3.07	0.50	0.69	1.05	1.44	Transcriptional regulator, AraC family	
Rmet_4644	17.67	Op1341r_1	2.05	0.85	2.38	2.81	2.74	3.22	0.40	0.47	0.42	0.50	Carboxymuconolactone decarboxylase	
Rmet_4645	13.00	Op1341r_1	11.46	1.00	3.33	3.30	4.38	4.37	0.27	0.27	0.31	0.31	Uncharacterized protein UPF0065	
Rmet_4646	10.00	Op1341r_1	3.43	0.71	0.96	1.35	1.00	1.42	0.52	0.73	0.61	0.85	Short-chain dehydrogenase/reductase SDR	
Rmet_1932	3.00	Op0565f_1	3.00	0.99	2.02	2.14	1.88	1.90	0.71	0.75	1.59	1.68	Extracellular solute-binding protein, family 5	
Rmet_1933	2.33	Op0565f_1	1.65	1.13	1.27	1.07	1.29	1.14	0.97	0.82	1.34	1.13	Binding-protein-dependent transport systems inner membrane component	
Rmet_1934	2.00	Op0565f_1	1.62	1.19	1.19	1.01	1.22	1.02	1.15	0.98	1.07	0.91	Binding-protein-dependent transport systems inner membrane component	
Rmet_1935	2.33	Op0565f_1	1.59	0.74	0.83	1.07	0.87	1.18	0.84	1.09	1.00	1.29	Oligopeptide/dipeptide ABC transporter, ATP-binding protein-like protein	
Rmet_1936	1.67	Op0565f_1	8.40	0.92	2.22	2.44	2.12	2.29	0.90	0.99	1.52	1.67	Oligopeptide/dipeptide ABC transporter, ATP-binding protein-like protein	
Rmet_2359	0.67	Op0663f_4	1.82	0.71	2.00	2.72	2.00	2.80	0.40	0.55	1.35	1.83	Putative uncharacterized protein ORF C41	
Rmet_2360	1.67	Op0663f_5	2.27	0.96	3.24	3.31	2.93	3.04	0.29	0.30	1.67	1.71	Putative uncharacterized protein ORF C40	
Rmet_2361	419.00	Op0664r_1	1.74	0.90	2.37	2.62	2.27	2.53	0.40	0.44	1.35	1.49	Putative uncharacterized protein ORF C39	
Rmet_2362	549.00	Op0664r_1	4.48	0.75	2.02	2.67	2.35	3.11	0.20	0.27	1.25	1.66	Putative uncharacterized protein ORF C38	
Rmet_4218	8.67	Op1197r_1	3.74	0.92	2.04	2.23	2.02	2.18	0.74	0.81	1.83	2.00	Lysine exporter protein (LYSE/YGGA)	
Rmet_5515	2.67	Op1641r_1	1.65	0.97	2.18	2.31	1.82	1.89	0.81	0.86	1.43	1.51	Aldehyde dehydrogenase	
Rmet_5516	1.33	Op1641r_1	2.11	1.02	2.58	2.42	1.34	1.31	0.79	0.74	1.31	1.23	Cytochrome P450	
Rmet_5517	1.33	Op1641r_1	3.60	0.95	2.63	2.85	2.57	2.70	0.80	0.87	1.70	1.84	Ferredoxin	
Rmet_1104	1.00	Op0318r_1	3.28	1.55	2.26	1.40	2.35	1.52	1.75	1.09	1.86	1.16	TonB-dependent siderophore receptor	
Rmet_4600	0.00	Op1324f_1	3.18	0.91	2.54	2.78	2.79	3.07	0.82	0.90	1.92	2.10	Sulphate transporter	
Rmet_4472	0.00	Op1275r_1	3.09	1.06	2.77	2.64	2.91	2.75	0.79	0.75	1.85	1.77	Sulphate transporter	
Rmet_5533	12.33	Op1645r_2	2.81	0.88	3.11	3.46	2.98	3.37	0.44	0.49	1.83	2.03	Nitroreductase	
Rmet_4668	1.33	Op1351r_1	2.74	1.02	2.43	2.46	2.45	2.41	0.62	0.63	1.76	1.78	NADH/Ubiquinone/plastoquinone (Complex I)	
Rmet_2354	0.67	Op0663f_3	2.49	0.93	2.67	3.00	2.07	2.22	0.55	0.61	1.45	1.62	Putative uncharacterized protein ORF C46	
Rmet_4962	3.67	Op1457r_1	2.07	1.02	2.17	2.01	2.06	2.01	0.78	0.72	1.43	1.32	Diguanylate phosphodiesterase (EAL domain)	
Rmet_4963	2.33	Op1457r_1	1.56	0.92	1.25	1.32	1.62	1.76	0.81	0.86	1.12	1.19	Sensor protein	
Rmet_4964	1.67	Op1457r_1	2.43	1.04	1.82	1.68	2.16	2.07	0.97	0.90	1.35	1.25	Two component transcriptional regulator, LuxR family	
Rmet_6020	15.67	Op1835f_1	1.97	0.94	2.11	2.11	2.06	2.19	0.88	0.88	1.13	1.13	Putative uncharacterized protein	
Rmet_5467	11.67	Op1625r_2	1.88	0.90	2.38	2.67	2.68	2.98	0.70	0.79	1.69	1.90	Putative uncharacterized protein	
Rmet_0803	7.33	Op0228r_2	1.87	0.79	2.19	2.76	2.57	3.24	1.62	2.04	1.48	1.87	Putative uncharacterized protein	
Rmet_2230	12.00	Op0638r_1	1.85	1.12	2.77	2.35	2.32	2.07	0.96	0.82	1.99	1.69	Putative integral membrane protein	
Rmet_2232	13.67	Op0638r_1	1.52	1.07	2.01	1.79	2.00	1.87	0.85	0.76	1.71	1.52	Binding-protein-dependent transport systems inner membrane component	
Rmet_5526	13.33	Op1643r_2	1.71	1.12	2.59	2.33	2.65	2.37	0.94	0.84	1.41	1.27	Putative uncharacterized protein	
Rmet_5728	1.33	Op1715r_3	1.68	1.11	2.24	2.03	2.82	2.55	1.14	1.03	1.82	1.65	Glycosyl transferase, group 1	
Rmet_2356	0.00	Op0663f_3	2.25	0.93	2.63	2.74	1.99	2.15	0.52	0.55	1.50	1.56	Putative uncharacterized protein ORF C44	
Rmet_2357	0.00	Op0663f_3	1.66	1.14	2.42	2.02	2.19	1.92	0.76	0.64	1.58	1.32	Putative uncharacterized protein ORF C43	
Rmet_4981	0.00	Op1461r_1	1.51	0.93	2.50	2.70	1.98	2.14	0.47	0.50	1.60	1.72	Putative uncharacterized protein	
Rmet_4982	0.00	Op1461r_1	1.60	1.08	2.82	2.64	2.23	2.06	0.71	0.67	1.73	1.61	Undecaprenyl-diphosphatase (Phosphoesterase, PA-phosphatase related)	
Rmet_0090	960.67	Op0025f_2	0.35	1.35	2.31	1.71	2.42	1.79	1.77	1.31	1.70	1.26	Two component transcriptional regulator, LuxR family	
Rmet_0091	347.33	Op0025f_2	0.24	1.26	2.62	2.08	2.62	2.08	1.47	1.17	1.90	1.51	Response regulator receiver domain protein (CheY-like)	
Rmet_1812	745.00	Op0526r_2	0.38	1.26	2.20	1.75	2.67	2.12	1.18	0.94	1.48	1.18	Rieske (2Fe-2S) region	
Rmet_5489	43.00	Op1630f_1	0.39	1.02	2.90	2.94	2.03	1.99	1.08	1.09	1.68	1.70	Putative uncharacterized protein	
Rmet_3092	92.00	Op0870r_1	0.55	1.08	2.92	2.83	2.68	2.49	1.06	1.02	1.62	1.57	Putative uncharacterized protein	
Rmet_4350	2.33	Op1239r_1	0.64	1.20	2.11	1.75	2.50	2.09	1.39	1.15	1.44	1.19	UvrD/REP helicase family protein	
Rmet_0094	486.00	Op0027f_2	0.68	1.39	2.46	1.77	2.34	1.69	1.24	0.89	1.91	1.37	Putative uncharacterized protein	
Rmet_6068	0.00	Op1849f_1	0.79	1.04	3.46	3.43	2.91	2.79	1.16	1.15	1.95	1.94	Putative uncharacterized protein ISRme8aa1 (Transposase IS3/IS911)	
Rmet_4523	10.67	Op1296f_1	1.37	0.93	1.26	1.42	1.62	1.73	0.79	0.89	0.90	1.01	Short-chain dehydrogenase/reductase SDR	
Rmet_4524	56.33	Op1297r_3	0.86	1.07	2.28	2.17	2.45	2.29	0.73	0.70	1.19	1.13	Negative transcriptional regulator	

Rmet_2341	205.33	Op0662r_1	1.04	0.88	1.78	1.99	1.44	1.64	0.54	0.60	1.37	1.53	Putative uncharacterized protein
Rmet_2342	287.33	Op0662r_1	0.87	1.02	2.14	2.13	1.86	1.83	0.54	0.54	1.52	1.51	AAA ATPase, central region
Rmet_2343	474.33	Op0662r_1	0.98	1.06	2.46	2.29	2.34	2.20	0.54	0.50	1.68	1.56	Putative uncharacterized protein ORF C57
Rmet_2344	597.00	Op0662r_1	0.87	1.08	2.53	2.33	2.45	2.27	0.50	0.46	1.72	1.58	Putative excisionase
Rmet_6169	5.67	Op1887f_1	0.87	1.35	2.06	1.48	2.17	1.61	1.25	0.90	1.60	1.15	Putative thiol:disulfide interchange protein (Protein-disulfide isomerase)
Rmet_3087	489.00	Op0870r_3	0.97	1.00	4.23	4.25	5.56	5.55	0.64	0.64	1.45	1.45	Ribonucleotide reductase
Rmet_3628	848.33	Op1011r_3	1.03	1.32	2.65	2.02	3.23	2.44	1.33	1.01	1.55	1.18	Putative uncharacterized protein
Rmet_0366	51.67	Op0103f_1	1.04	1.31	2.16	1.64	2.08	1.59	1.38	1.05	1.21	0.92	Putative membrane protein
Rmet_3093	74.33	Op0870r_1	1.23	0.98	2.47	2.65	2.43	2.49	0.76	0.81	1.36	1.45	Cytochrome c assembly protein
Rmet_0799	1029.33	Op0227f_1	1.30	0.88	2.52	2.85	2.92	3.30	1.78	2.01	1.76	1.98	Binding-protein-dependent transport systems inner membrane component
Rmet_3097	9.00	Op0872r_1	1.31	0.93	3.11	3.27	2.57	2.77	0.71	0.75	1.81	1.90	Putative uncharacterized protein
Rmet_4198	134.00	Op1190f_1	1.31	0.86	2.34	2.71	2.10	2.44	0.59	0.68	1.95	2.25	Transcriptional regulator, PadR family
Rmet_2363	859.00	Op0664r_1	1.32	0.92	2.34	2.55	2.68	2.92	0.55	0.60	1.39	1.51	Putative uncharacterized protein ORF C37
Rmet_2358	0.00	Op0663f_3	1.42	0.97	2.38	2.50	2.18	2.25	0.53	0.55	1.43	1.50	Putative uncharacterized protein ORF C42
546/554 up													
Rmet_4896	9.67	Op1433r_1	6.73	1.73	2.05	1.19	1.45	0.84	2.49	1.44	1.52	0.88	SMC protein-like protein
Rmet_4897	0.67	Op1434f_1	4.21	1.05	0.87	0.85	0.91	0.87	0.73	0.71	0.50	0.49	Putative uncharacterized protein
Rmet_5324	11.33	Op1575r_1	0.32	1.29	2.15	1.65	1.59	1.23	2.05	1.58	1.73	1.33	Putative signal peptide protein
Rmet_2821	109.00	Op0793f_1	0.33	1.39	2.18	1.56	1.77	1.27	2.39	1.70	1.80	1.28	6-phosphogluconate dehydrogenase, NAD-binding
Rmet_1187	568.33	Op0343f_2	0.48	1.59	2.23	1.40	1.67	1.05	2.31	1.45	1.85	1.16	Putative uncharacterized protein
546/555 up													
Rmet_5753	35.00	Op1724f_1	9.86	1.58	2.11	1.33	1.17	0.74	1.69	1.07	2.01	1.27	Putative uncharacterized protein
Rmet_1708	57.67	Op0483f_1	3.13	1.26	2.40	1.90	1.35	1.07	1.95	1.55	4.34	3.44	Putative uncharacterized protein
Rmet_R0023			2.62	1.49	4.44	2.98	1.94	1.30	1.96	1.32	2.02	1.36	
Rmet_1244	0	Op0357f_3	2.59	0.99	2.25	2.15	1.89	1.91	0.73	0.70	2.74	2.62	Putative uncharacterized protein
Rmet_1684	34.33	Op0476r_2	2.30	1.28	2.42	1.94	1.68	1.31	1.55	1.24	3.71	2.97	Response regulator receiver domain protein (CheY-like)
Rmet_4203	16.67	Op1192f_1	1.95	0.86	2.13	2.48	1.67	1.94	0.48	0.56	2.02	2.35	Uncharacterized protein UPF0065
Rmet_4613	34.00	Op1329r_1	1.65	0.93	2.17	2.31	1.96	2.11	0.68	0.72	2.11	2.24	Acyl-CoA dehydrogenase-like protein
Rmet_1986	80.00	Op0580r_1	1.61	1.07	2.16	2.01	1.10	1.02	1.08	1.01	4.33	4.02	Putative uncharacterized protein
Rmet_4935	378.00	Op1448f_2	0.14	1.17	2.03	1.70	1.54	1.32	1.64	1.37	2.27	1.90	H-NS family DNA-binding protein
Rmet_3673	184.67	Op1022f_1	0.19	1.19	2.41	2.02	1.67	1.40	1.62	1.36	2.40	2.01	Transcriptional regulator, PadR family
Rmet_3579	261.00	Op0995f_2	0.20	1.12	2.04	1.83	1.51	1.35	1.63	1.46	2.97	2.66	Calcium-binding EF-hand
Rmet_3580	44.00	Op0995f_2	0.20	1.12	2.15	1.92	1.52	1.35	1.55	1.38	4.03	3.59	MOSC domain protein
Rmet_1178	18.67	Op0341f_1	0.25	1.41	2.10	1.49	1.96	1.39	1.80	1.28	2.20	1.56	Putative uncharacterized protein
Rmet_0421	1927.33	Op0116r_4	0.26	0.96	2.43	2.53	1.36	1.42	1.27	1.33	3.99	4.15	Putative uncharacterized protein
Rmet_0422	1040.67	Op0116r_4	0.39	1.01	2.56	2.53	1.48	1.46	1.30	1.29	4.74	4.69	Holliday junction ATP-dependent DNA helicase ruvB
Rmet_5071	206.33	Op1492f_3	0.23	1.05	1.87	1.79	1.58	1.51	1.19	1.14	2.00	1.91	Putative uncharacterized protein
Rmet_5072	499.67	Op1493r_1	0.23	0.89	1.55	1.74	1.42	1.59	0.96	1.08	1.75	1.96	Methionine synthase (B12-independent)
Rmet_5073	918.67	Op1493r_1	0.31	0.70	1.20	1.71	0.87	1.23	0.68	0.97	1.28	1.81	Putative uncharacterized protein
Rmet_5074	653.00	Op1493r_1	0.35	0.80	0.90	1.14	0.58	0.73	1.10	1.38	0.96	1.21	NADPH-dependent FMN reductase
Rmet_5075	652.00	Op1493r_1	0.26	0.77	1.07	1.40	0.82	1.06	0.92	1.22	0.98	1.29	Putative uncharacterized protein
Rmet_5076	344.33	Op1494f_1	0.45	1.17	1.99	1.68	1.58	1.35	1.32	1.11	1.80	1.52	Sulfatase
Rmet_5077	5.67	Op1495r_1	0.27	0.96	2.08	2.17	1.92	1.99	1.06	1.10	2.25	2.33	Sulfatase
Rmet_1818	16.00	Op0527f_1	0.27	1.43	2.22	1.54	1.67	1.17	1.99	1.39	2.19	1.52	Transcriptional regulator, IclR family
Rmet_1983	11.33	Op0578r_1	0.27	1.05	2.25	2.16	1.84	1.75	0.96	0.92	2.42	2.33	Putative uncharacterized protein
Rmet_3043	231.33	Op0855f_1	0.27	1.14	1.82	1.60	1.29	1.13	1.18	1.03	2.44	2.14	Putative uncharacterized protein
Rmet_3044	4.67	Op0856r_1	0.28	1.24	2.09	1.68	1.55	1.25	1.11	0.89	2.37	1.91	Putative uncharacterized protein
Rmet_1952	205.33	Op0571f_2	0.29	1.45	2.33	1.60	1.69	1.17	1.52	1.05	2.05	1.41	GCN5-related N-acetyltransferase
Rmet_4692	9.33	Op1357r_1	0.30	1.13	2.19	1.96	1.50	1.32	1.36	1.22	2.18	1.95	Putative uncharacterized protein

Rmet_3119	68.00	Op0876r_1	0.32	1.30	2.21	1.67	1.82	1.40	1.68	1.27	2.29	1.72	Peptidase M23B
Rmet_3617	212.33	Op1006f_2	0.32	0.95	2.10	2.30	1.97	2.07	0.67	0.73	2.33	2.55	Excinuclease ABC, C subunit-like protein
Rmet_0198	38.00	Op0058r_2	0.37	2.33	2.70	1.17	1.73	0.74	1.43	0.62	2.45	1.06	Cation diffusion facilitator family transporter
Rmet_3472	118.00	Op0965f_1	0.42	1.34	2.05	1.51	1.45	1.08	1.63	1.20	2.05	1.51	Putative uncharacterized protein
Rmet_1697	33.67	Op0481f_1	0.58	1.01	1.96	1.99	1.54	1.52	1.14	1.16	6.81	6.92	Sensor protein
Rmet_1698	60.33	Op0481f_1	0.43	1.05	2.96	2.68	1.51	1.43	1.60	1.45	9.72	8.82	Two component transcriptional regulator, LuxR family
Rmet_6054	230.67	Op1844r_4	0.44	1.10	2.15	1.95	1.85	1.68	1.02	0.92	2.23	2.03	Putative uncharacterized protein
Rmet_4929	211.67	Op1444f_3	0.55	1.97	2.43	1.24	1.54	0.79	1.44	0.73	1.74	0.89	Glutathione S-transferase-like protein
Rmet_4930	9.67	Op1445r_1	0.47	2.11	2.85	1.36	1.97	0.93	1.65	0.79	2.17	1.03	Transcriptional regulator, IclR family
Rmet_4847	17.33	Op1412f_2	0.47	1.02	2.52	2.45	1.29	1.27	1.24	1.21	8.06	7.85	YidE/YbjL duplication
Rmet_4602	0.00	Op1324f_1	0.47	1.05	2.15	2.09	1.96	1.87	1.25	1.21	2.10	2.03	Transcriptional regulators, TraR/DksA family
Rmet_6322	80.67	Op1920f_1	0.52	0.97	2.05	2.10	1.85	1.90	0.95	0.97	2.59	2.66	Putative uncharacterized protein
Rmet_3050	130.00	Op0858r_1	0.55	1.07	2.15	1.98	1.82	1.70	0.82	0.76	3.18	2.92	Orotidine 5'-phosphate decarboxylase
Rmet_3366	44.33	Op0936r_1	0.58	0.99	2.64	2.58	1.80	1.82	0.68	0.66	3.13	3.06	Putative uncharacterized protein
Rmet_1709	31.00	Op0483f_1	0.59	1.08	2.52	2.29	1.71	1.58	1.81	1.64	6.29	5.70	Putative uncharacterized protein
Rmet_1707	7.33	Op0482r_1	0.62	1.39	3.14	2.28	1.77	1.27	1.91	1.39	8.62	6.27	Putative uncharacterized protein
Rmet_5781	8.33	Op1738f_1	0.63	0.94	2.15	2.28	1.60	1.70	1.18	1.25	5.02	5.31	Putative uncharacterized protein
Rmet_3346	339.00	Op0932r_3	0.68	1.13	2.12	1.88	1.65	1.47	0.76	0.67	2.66	2.36	UspA
Rmet_3368	77.00	Op0936r_1	0.70	1.18	2.27	1.97	1.82	1.54	1.03	0.89	2.07	1.79	GCN5-related N-acetyltransferase
Rmet_5985	3.00	Op1822r_1	0.71	1.69	2.14	1.25	1.91	1.13	1.67	0.98	2.03	1.19	MgtC protein (MgtC/SapB transporter)
Rmet_5986	6.00	Op1823f_1	0.73	1.65	2.01	1.25	1.66	1.01	1.25	0.77	1.66	1.03	Putative uncharacterized protein
Rmet_1696	22.33	Op0481f_1	0.75	1.27	2.80	2.32	1.61	1.27	1.48	1.22	8.51	7.04	Putative uncharacterized protein
Rmet_3045	10.33	Op0856r_1	0.76	0.86	2.04	2.48	1.51	1.75	0.73	0.89	3.18	3.87	Phage integrase
Rmet_1703	48.67	Op0481f_2	0.78	0.97	3.45	3.56	1.58	1.63	1.33	1.37	11.09	11.41	RND efflux system, outer membrane lipoprotein, NodT
Rmet_4977	0.00	Op1461r_1	0.78	1.02	2.15	2.19	1.70	1.66	0.68	0.69	2.24	2.28	Sensor protein
Rmet_4400	296.33	Op1251r_1	0.80	1.19	2.60	2.26	1.75	1.48	1.17	1.01	6.44	5.59	Putative uncharacterized protein
Rmet_1093	26.33	Op0315f_2	0.85	1.02	2.12	2.11	1.26	1.24	1.62	1.61	6.15	6.10	Alcohol dehydrogenase GroES-like protein
Rmet_1646	18.00	Op0463f_1	0.88	1.11	2.17	1.88	1.51	1.36	1.67	1.45	5.20	4.51	MscS Mechanosensitive ion channel
Rmet_1030	193.00	Op0295f_3	0.89	1.85	2.35	1.27	1.64	0.89	1.83	0.99	2.06	1.11	Ferredoxin, 2Fe-2S type
Rmet_5778	71.00	Op1738f_1	1.18	0.94	1.55	1.63	1.43	1.52	2.01	2.12	1.38	1.45	Porin, Gram-negative type
Rmet_5779	36.00	Op1738f_1	0.90	0.89	2.70	3.01	1.71	1.93	1.74	1.94	6.36	7.09	Putative uncharacterized protein
Rmet_5780	18.67	Op1738f_1	1.01	1.04	2.16	2.08	1.55	1.49	1.15	1.11	2.81	2.71	Putative uncharacterized protein
Rmet_1028	220.67	Op0295f_3	0.92	1.88	2.52	1.34	1.96	1.04	1.98	1.05	2.21	1.17	Co-chaperone Hsc20
Rmet_5416	112.00	Op1612f_2	1.00	0.88	3.83	4.19	1.62	1.84	1.96	2.15	17.12	18.72	Sulfatase
Rmet_5963	26.67	Op1813f_1	1.19	1.73	2.31	1.38	1.95	1.13	1.47	0.88	2.22	1.33	Putative uncharacterized protein
553/554 up													
Rmet_4470	0.00	Op1275r_1	0.13	0.66	1.24	1.88	1.36	2.06	0.86	1.31	1.46	2.22	Transcriptional regulators, TraR/DksA family
Rmet_4836	18.33	Op1411r_2	3.50	0.66	0.76	1.15	1.93	2.93	1.87	2.85	0.60	0.92	Diguanylate phosphodiesterase (EAL domain)
Rmet_5365	12.00	Op1596f_1	6.78		0.74	1.14	1.93	2.97	1.90	2.93	0.58	0.89	Transcriptional regulator, LysR family
Rmet_2286	0	Op0654r_2	0.16	0.65	0.91	1.41	0.86	1.33	2.32	3.61	0.89	1.38	Putative uncharacterized protein
Rmet_R0038			0.41	1.10	2.00	1.81	2.09	1.90	2.01	1.82	1.53	1.38	
Rmet_5484	189.33	Op1628f_2	0.52	1.88	1.55	0.83	2.25	1.20	2.19	1.16	1.51	0.80	Putative uncharacterized protein
Rmet_4340	11.67	Op1234f_2	0.96	1.73	1.72	1.02	2.13	1.23	2.03	1.21	1.87	1.11	Twin-arginine translocation pathway signal
Rmet_2185	766.33	Op0628r_4	1.02	1.90	1.66	0.88	2.41	1.27	3.20	1.70	1.44	0.77	Periplasmic phosphate binding protein
553/555 up													
Rmet_R0043			0.14	1.43	1.98	1.39	4.19	2.94	1.55	1.09	2.36	1.66	
Rmet_2645	11.67	Op0746r_1	0.27	1.25	1.82	1.49	2.46	1.97	1.27	1.03	2.12	1.73	Peptide methionine sulfoxide reductase
Rmet_5684	106.33	Op1698f_1	0.37	1.26	1.79	1.42	2.35	1.86	1.11	0.88	2.00	1.58	Pilus assembly protein PilE
Rmet_0516	24.33	Op0139f_1	0.43	1.87	1.82	0.99	2.03	1.08	1.98	1.07	2.03	1.10	Sensor protein

Rmet_3209	21.67	Op0903f_1	0.60	1.39	1.78	1.29	<u>2.56</u>	1.84	0.83	0.60	<u>2.12</u>	1.53	Transcriptional regulator, AsnC family
Rmet_0623	2.00	Op0177f_1	0.88	1.96	1.96	0.95	<u>2.85</u>	1.46	1.90	0.92	<u>2.72</u>	1.31	Putative uncharacterized protein
Rmet_2778	34.00	Op0782r_1	0.90	1.34	1.96	1.39	<u>3.81</u>	<u>2.83</u>	1.05	0.75	<u>2.20</u>	1.57	Adenosylcobyrlic acid synthase (Glutamine-hydrolysing)
Rmet_5937	8.00	Op1805r_2	1.00	0.93	1.46	1.61	<u>2.32</u>	<u>2.50</u>	0.88	0.97	<u>2.06</u>	<u>2.27</u>	Putative uncharacterized protein
Rmet_0161	10.33	Op0048r_2	1.06	1.08	1.93	1.70	<u>2.07</u>	1.92	0.99	0.87	<u>2.45</u>	<u>2.15</u>	Acyl-CoA dehydrogenase-like protein
Rmet_6164	4.67	Op1886r_1	1.17	1.32	1.73	1.31	<u>2.24</u>	1.70	1.08	0.82	<u>2.08</u>	1.57	Putative uncharacterized protein
Rmet_5824	3.00	Op1761r_2	1.19	1.00	1.80	1.81	<u>2.50</u>	<u>2.49</u>	0.94	0.95	<u>2.31</u>	<u>2.32</u>	Uncharacterized protein UPF0065
Rmet_5355	13.67	Op1590f_2	1.11	0.92	1.08	1.15	<u>1.99</u>	<u>2.16</u>	0.69	0.74	<u>3.98</u>	<u>4.23</u>	Putative uncharacterized protein
Rmet_5356	16.00	Op1591r_1	1.25	0.87	0.76	0.88	<u>2.54</u>	<u>2.91</u>	0.59	0.67	<u>3.48</u>	<u>3.99</u>	Uncharacterized protein UPF0065
Rmet_5821	48.00	Op1759r_1	1.28	0.92	1.78	1.87	<u>2.27</u>	<u>2.47</u>	0.69	0.72	<u>2.21</u>	<u>2.33</u>	Putative integrase/recombinase protein
554/555 up													
Rmet_1418	323.67	Op0397f_3	<u>0.40</u>	1.12	1.97	1.74	1.23	1.10	<u>2.16</u>	1.91	<u>2.11</u>	1.87	Putative integral membrane protein
Rmet_4032	44.67	Op1137r_1	0.82	2.13	1.96	0.92	1.79	0.84	<u>2.92</u>	1.37	<u>2.39</u>	1.12	UPF0060 membrane protein Rmet_4032
Only DN546 up													
Rmet_5495	2.33	Op1633r_1	<u>0.48</u>		1.65	<u>2.08</u>	1.48	1.86	0.85	1.07	1.24	1.56	Alcohol dehydrogenase, zinc-binding
Rmet_6192	47.33	Op1894f_6	0.53		1.87	<u>2.01</u>	1.31	1.41	1.28	1.38	1.47	1.58	Putative uncharacterized protein
Rmet_0151	79.33	Op0043f_1	<u>0.43</u>	1.98	<u>2.01</u>	1.02	1.33	0.67	1.74	0.88	0.67	<u>0.34</u>	Patatin
Rmet_2032	1081	Op0594r_2	<u>0.28</u>	0.99	<u>2.05</u>	<u>2.06</u>	1.03	1.03	1.13	1.13	1.03	1.04	NusA antitermination factor
Rmet_2033	982.00	Op0594r_2	<u>0.06</u>	1.05	<u>2.24</u>	<u>2.13</u>	1.42	1.35	1.12	1.07	1.28	1.22	UPF0090 protein Rmet_2033
Rmet_4404	61.67	Op1253r_1	<u>7.32</u>	1.93	<u>2.07</u>	1.07	1.33	0.69	1.97	1.02	1.26	0.65	Transcriptional regulator, TetR family
Rmet_5534	8.00	Op1645r_2	<u>3.62</u>	0.97	<u>2.25</u>	<u>2.34</u>	1.86	1.93	0.72	0.75	1.36	1.42	2-nitropropane dioxygenase, NPD
Rmet_5677	22.67	Op1697r_2	<u>2.71</u>	0.98	<u>186</u>	<u>184</u>	0.91	0.92	1.05	1.04	1.02	1.01	Putative uncharacterized protein
Rmet_4681	2.67	Op1354f_1	<u>2.39</u>	1.17	<u>2.06</u>	1.71	1.32	1.12	1.01	0.84	1.05	0.87	Putative uncharacterized protein
Rmet_2351	0.00	Op0663f_2	<u>2.05</u>	1.35	<u>2.06</u>	1.56	1.73	1.28	1.11	0.84	1.51	1.14	Putative secreted protein
Rmet_6046	37.33	Op1843f_1	<u>2.01</u>	0.91	<u>2.22</u>	<u>2.47</u>	1.74	1.90	0.54	0.60	0.97	1.08	Putative uncharacterized protein RMe0226 (Putative uncharacterized protein)
Rmet_5539	2.67	Op1647r_4	1.95	0.84	<u>2.03</u>	<u>2.40</u>	1.80	<u>2.14</u>	0.73	0.86	1.46	1.72	Putative uncharacterized protein
Rmet_R0065			1.80	1.29	<u>3.13</u>	<u>2.41</u>	1.58	1.22	1.77	1.36	1.58	1.22	
Rmet_5967	1.67	Op1816r_1	<u>3.06</u>	1.72	1.94	1.12	1.84	1.07	<u>2.14</u>	1.23	1.82	1.05	GtrA family protein
Rmet_5968	3.67	Op1816r_2	1.61	1.70	<u>2.08</u>	1.23	1.69	1.00	1.77	1.05	1.89	1.12	Glycosyl transferase family 2
Rmet_1759	39.33	Op0501f_3	<u>0.30</u>	0.80	<u>638</u>	<u>811</u>	0.73	0.91	1.23	1.57	0.86	1.10	ABC transporter-related protein
Rmet_6320	87.00	Op1919r_1	<u>0.38</u>	0.94	<u>2.16</u>	<u>2.30</u>	1.84	1.96	1.05	1.11	1.81	1.93	Phage integrase
Rmet_1217	318.67	Op0354r_1	<u>0.41</u>	0.90	<u>2.01</u>	<u>2.27</u>	<u>1.97</u>	<u>2.19</u>	0.78	0.88	1.61	1.82	NUDIX hydrolase
Rmet_0365	73.67	Op0102r_1	<u>0.47</u>	1.03	<u>2.13</u>	<u>2.11</u>	1.81	1.75	0.74	0.74	1.67	1.65	(2Fe-2S)-binding
Rmet_2037	276.00	Op0595f_1	0.51	1.03	<u>43.9</u>	<u>42.6</u>	0.75	0.73	1.10	1.07	1.00	0.97	Transcriptional regulator, Crp/Fnr family
Rmet_6067	0.00	Op1849f_1	0.64	1.07	<u>2.83</u>	<u>2.71</u>	1.58	1.48	1.42	1.36	1.30	1.25	Integrase, catalytic region
Rmet_2845	29.33	Op0801f_2	<u>0.24</u>	1.54	<u>2.07</u>	1.32	1.72	1.11	1.70	1.09	1.97	1.26	Putative uncharacterized protein
Rmet_3375	78.67	Op0937f_2	<u>0.25</u>	1.29	<u>2.01</u>	1.56	1.48	1.15	1.61	1.25	1.91	1.49	Transcriptional regulator, TetR family
Rmet_0204	23.67	Op0060r_1	<u>0.25</u>	1.30	<u>2.25</u>	1.72	1.50	1.15	1.45	1.11	1.92	1.47	Transcriptional regulator, GntR family
Rmet_6000	57.00	Op1828r_3	<u>0.28</u>	1.42	<u>2.27</u>	1.62	1.49	1.04	1.85	1.32	1.96	1.40	Putative uncharacterized protein
Rmet_1214	105.00	Op0352r_1	<u>0.30</u>	1.26	<u>2.08</u>	1.62	1.86	1.48	1.03	0.80	1.73	1.35	Putative arginyl-tRNA--protein transferase
Rmet_3027	4.67	Op0848r_2	<u>0.30</u>	1.51	<u>2.30</u>	1.53	1.75	1.16	1.52	1.01	1.95	1.29	Putative lipoprotein
Rmet_1844	59.00	Op0535f_1	<u>0.30</u>	1.23	<u>2.01</u>	1.63	1.43	1.16	1.31	1.07	1.51	1.23	Appr-1-p processing
Rmet_2071	207.33	Op0601f_2	<u>0.30</u>	1.52	<u>2.42</u>	1.57	1.68	1.11	1.67	1.09	2.00	1.30	Probable Fe(2+)-trafficking protein
Rmet_4674	13.67	Op1352f_1	<u>0.35</u>	1.48	<u>2.20</u>	1.46	1.72	1.17	1.90	1.26	1.96	1.30	Putative uncharacterized protein
Rmet_3996	82.67	Op1122f_1	<u>0.36</u>	1.64	<u>2.10</u>	1.18	1.66	0.93	2.00	1.12	1.40	0.79	Periplasmic glucan biosynthesis protein, MdoG
Rmet_0082	62.00	Op0023f_1	<u>0.39</u>	1.88	<u>2.33</u>	1.24	1.90	1.01	1.80	0.96	1.51	0.81	Transcriptional regulator, IclR family
Rmet_1972	136.33	Op0575f_2	<u>0.41</u>	1.25	<u>2.00</u>	1.59	1.32	1.06	1.35	1.07	1.54	1.22	NLP/P60
Rmet_0508	34.33	Op0136r_1	<u>0.42</u>	1.41	<u>2.32</u>	1.59	1.54	1.09	1.36	0.93	1.56	1.07	D-Ala-D-Ala carboxypeptidase PBP3. Serine peptidase. MEROPS family S13
Rmet_2382	0.00	Op0671f_1	<u>0.43</u>	1.45	<u>2.06</u>	1.41	1.65	1.14	1.99	1.37	1.73	1.19	Integrase, catalytic region

Rmet_0355	533.33	Op0101f_1	0.45	1.22	2.17	1.79	1.87	1.54	1.59	1.31	1.64	1.34	HAD-superfamily hydrolase subfamily IIB
Rmet_6152	8.67	Op1881f_1	0.48	1.58	2.14	1.36	1.63	1.03	1.95	1.24	1.95	1.24	Putative uncharacterized protein ISRme8aa2
Rmet_5921	58.00	Op1798f_2	0.52	1.72	2.08	1.20	1.64	0.95	1.77	1.02	1.93	1.11	Silent information regulator protein Sir2
Rmet_4205	15.67	Op1192f_1	0.60	1.13	2.05	1.84	1.63	1.44	0.89	0.80	1.86	1.67	Dimethylmenaquinone methyltransferase
Rmet_6181	0.00	Op1892r_1	0.64	1.40	2.04	1.46	1.50	1.08	1.45	1.04	1.93	1.38	Putative uncharacterized protein
Rmet_5079	68.67	Op1496f_1	0.80	0.90	2.22	2.43	1.75	1.95	0.79	0.87	1.84	2.02	Putative uncharacterized protein
Rmet_6048	40.67	Op1843f_1	0.81	1.05	2.12	2.03	1.76	1.67	0.52	0.50	1.41	1.35	Putative DNA helicase
Rmet_R0081			0.88	0.97	2.14	2.20	1.25	1.28	1.91	1.96	1.15	1.19	
Rmet_6032	269.67	Op1837f_1	0.98	1.14	3.01	2.59	1.94	1.70	1.12	0.97	1.55	1.33	Putative uncharacterized protein RMe0236 (PilT protein-like protein)
Rmet_2337	0.00	Op0661f_8	1.02	0.90	2.02	2.15	1.63	1.81	0.64	0.69	1.55	1.65	Putative uncharacterized protein
Rmet_4682	2.67	Op1355r_1	1.33	0.93	5.56	5.51	1.00	1.08	0.90	0.89	1.06	1.05	DoxX
Rmet_3465	15.67	Op0964r_3	0.85	1.56	2.55	1.65	1.54	0.99	1.63	1.06	1.84	1.20	Transcriptional regulator, AraC family with amidase-like domain
Rmet_4028	25.33	Op1134f_1	0.76	1.76	2.49	1.40	1.43	0.81	1.46	0.82	1.67	0.94	Putative uncharacterized protein
Rmet_1620	1.67	Op0451f_2	1.25	1.68	2.39	1.38	1.50	0.90	1.34	0.77	1.40	0.81	Thiamine pyrophosphate enzyme-like TPP binding region
Rmet_2997	5.33	Op0843f_2	0.73	1.59	2.38	1.50	1.84	1.15	1.72	1.08	1.95	1.23	Putative uncharacterized protein
Rmet_1425	273.00	Op0398r_1	1.18	2.03	2.28	1.10	1.81	0.89	1.58	0.76	1.52	0.73	Putative uncharacterized protein
Rmet_4027	32.33	Op1134f_1	0.91	1.91	2.22	1.16	1.94	1.02	1.37	0.72	1.77	0.92	Proline iminopeptidase
Rmet_5497	0.00	Op1634f_1	1.15	1.60	2.14	1.34	1.88	1.17	1.81	1.13	1.71	1.07	Integrase, catalytic region
Rmet_3813	5.67	Op1060f_2	0.81	1.82	2.11	1.12	1.83	1.00	1.68	0.90	1.96	1.04	Uncharacterized protein UPF0065
Rmet_5722	1.33	Op1714f_1	1.28	1.27	2.07	1.57	1.33	1.05	0.91	0.69	1.16	0.88	Transcriptional regulator, XRE family
Rmet_6044	15.67	Op1843f_1	1.37	1.06	2.03	1.91	1.83	1.73	0.68	0.64	1.98	1.87	Putative uncharacterized protein
Rmet_0485	42.00	Op0129f_1	0.92	1.04	2.03	1.93	1.58	1.52	0.72	0.68	1.53	1.45	Putative uncharacterized protein
Rmet_1062	58.67	Op0305f_1	0.67	1.43	2.02	1.41	1.55	1.08	1.48	1.03	1.40	0.98	Alpha/beta hydrolase fold
Rmet_0029	22.00	Op0010r_1	0.86	0.90	1.99	2.11	1.90	2.13	0.78	0.83	1.56	1.65	Porin, Gram-negative type
Rmet_5490	57.33	Op1631r_1	0.87	0.89	1.98	2.26	1.75	1.97	0.70	0.79	1.49	1.70	Monooxygenase, FAD-binding
Rmet_5503	11.33	Op1636f_1	1.47	0.76	1.54	2.05	1.32	1.74	0.87	1.15	0.91	1.21	Uncharacterized protein UPF0065

Only DN553 up

Rmet_2708	49.00	Op0767f_1	0.55		1.06	1.21	1.78	2.00	1.18	1.35	1.16	1.32	Transcriptional regulator, TetR family
Rmet_4618	13.00	Op1331r_3	0.14	0.72	1.07	1.47	1.74	2.41	0.79	1.09	1.10	1.52	Putative uncharacterized protein
Rmet_R0067			0.16	0.72	1.17	1.63	1.62	2.25	0.80	1.11	1.22	1.70	
Rmet_0602	88.67	Op0171f_1	0.17	0.88	1.10	1.26	1.83	2.09	1.05	1.20	1.20	1.37	Putative uncharacterized protein
Rmet_R0068			0.21	0.68	1.00	1.47	1.37	2.01	0.69	1.02	1.01	1.49	
Rmet_5627	5.67	Op1679r_1	2.01		1.67	1.83	1.99	2.20	0.71	0.77	1.48	1.63	Putative uncharacterized protein
Rmet_6213	18.00	Op1897r_1	1.54		1.66	1.67	1.98	2.09	0.88	0.89	1.89	1.90	Putative uncharacterized protein
Rmet_0338	9.00	Op0095f_1	1.84	0.71	0.82	1.17	1.58	2.21	0.83	1.19	0.74	1.05	Beta-lactamase-like protein
Rmet_2681	97.67	Op0757f_1	0.10	0.86	1.39	1.59	1.73	2.01	1.14	1.30	1.62	1.85	Transcriptional repressor nrdR
Rmet_5962	2.67	Op1813f_1	5.89	1.52	1.89	1.24	2.58	1.70	1.77	1.16	1.89	1.24	Putative transmembrane protein (Glycosyl transferase, family 39)
Rmet_5765	4.67	Op1730f_1	5.35	0.96	1.54	1.59	2.22	2.31	0.48	0.50	1.74	1.80	Putative uncharacterized protein
Rmet_4876	20.67	Op1425r_2	4.65	1.03	1.65	1.61	2.46	2.38	1.21	1.18	0.89	0.87	Uncharacterized protein UPF0065
Rmet_2589	5.00	Op0723f_1	3.94	0.78	0.89	1.13	2.86	3.67	0.61	0.78	0.91	1.16	Type III effector Hrp-dependent outers
Rmet_6165	8.67	Op1887f_1	3.89	1.26	1.86	1.44	2.22	1.76	0.90	0.70	1.70	1.32	Putative uncharacterized protein RMe0331 (Putative uncharacterized protein)
Rmet_4619	1.33	Op1331r_2	2.95	0.83	1.50	1.76	2.36	2.83	0.63	0.74	1.34	1.57	RND efflux system, outer membrane lipoprotein, NodT
Rmet_0651	0.33	Op0180r_1	2.19	0.93	1.70	1.81	2.30	2.47	1.12	1.19	1.57	1.67	Flp/Fap pilin component
Rmet_0652	0.67	Op0180r_1	2.95	0.94	1.61	1.75	2.34	2.49	1.21	1.32	1.58	1.71	Flp/Fap pilin component
Rmet_5899	2.33	Op1787r_1	2.80	0.95	1.72	1.77	2.40	2.53	0.96	0.99	1.84	1.89	Putative uncharacterized protein
Rmet_2798	30.00	Op0786r_2	2.37	0.75	1.41	1.86	3.38	4.51	0.68	0.90	1.19	1.57	Transcriptional regulator, GntR family
Rmet_4003	43.00	Op1124f_1	2.32	1.12	1.23	1.09	17.84	15.91	1.28	1.14	0.97	0.87	Aspartate racemase
Rmet_1738	2.33	Op0494r_1	2.29	1.22	1.93	1.53	2.11	1.74	0.99	0.78	1.47	1.16	Glycosyl transferase, family 2
Rmet_2619	10.67	Op0733f_1	2.19	0.92	1.04	1.11	3.23	3.53	1.31	1.40	1.29	1.38	Putative uncharacterized protein

Rmet_1122	1.67	Op0321f_1	2.08	0.90	1.00	1.10	9.10	10.09	0.83	0.90	1.05	1.14	Sodium:dicarboxylate symporter
Rmet_2663	0.33	Op0754r_1	2.04	1.13	1.68	1.48	3.51	3.11	1.00	0.88	1.41	1.24	Putative uncharacterized protein
Rmet_4102	24.33	Op1154f_4	1.96	1.80	1.67	0.93	2.76	1.53	1.74	0.97	1.35	0.75	Transcriptional regulator, TetR family
Rmet_5225	25.67	Op1541r_3	1.90	0.96	1.79	1.85	2.31	2.41	0.89	0.92	1.46	1.50	Putative uncharacterized protein
Rmet_4440	6.00	Op1263r_2	1.85	1.13	1.77	1.55	2.31	2.05	1.41	1.24	1.90	1.67	Endoribonuclease L-PSP
Rmet_4904	1.33	Op1436f_1	1.78	1.35	1.13	0.80	2.15	1.59	1.23	0.88	1.20	0.85	Major facilitator superfamily MFS_1
Rmet_4905	15.00	Op1437r_1	1.51	1.74	1.70	0.96	1.83	1.05	1.58	0.89	1.79	1.01	Transcriptional regulator, LysR family
Rmet_4906	28.67	Op1438f_1	2.01	0.42	0.52	1.26	0.37	0.88	0.38	0.92	0.42	1.01	Glyoxalase/bleomycin resistance protein/dioxygenase
Rmet_4500	1.33	Op1282f_1	1.77	0.90	0.92	1.05	17.25	19.14	0.81	0.92	1.00	1.15	Putative uncharacterized protein
Rmet_6132	2.67	Op1873f_1	1.57	1.34	1.47	1.09	2.33	1.74	1.56	1.16	1.51	1.12	Putative uncharacterized protein
Rmet_2994	5.67	Op0842r_1	1.56	1.37	1.69	1.26	2.26	1.65	1.72	1.29	1.46	1.09	Phosphonate ABC transporter, periplasmic phosphonate-binding protein
Rmet_4369	17.00	Op1246f_2	1.55	0.87	1.40	1.63	2.37	2.71	0.61	0.70	1.45	1.68	Major facilitator superfamily MFS_1
Rmet_5353	46.33	Op1590f_2	1.53	0.98	0.86	0.87	2.03	2.07	0.94	0.96	1.67	1.71	Pyridoxamine 5'-phosphate oxidase-related, FMN-binding
Rmet_1121	37.67	Op0320r_1	0.35	1.08	1.01	0.96	2.67	2.47	1.60	1.52	1.22	1.15	Hydrophobe/amphiphile efflux-1 HAE1
Rmet_2570	246.67	Op0712r_1	0.40	0.97	1.43	1.49	2.79	2.87	0.77	0.81	1.95	2.03	Putative uncharacterized protein
Rmet_5223	26.00	Op1540f_2	0.41	1.06	1.66	1.55	4.01	3.77	0.61	0.57	1.63	1.52	Putative uncharacterized protein
Rmet_4104	9.33	Op1155r_1	0.45	1.94	1.90	0.97	4.01	2.06	1.90	0.97	2.00	1.02	Sigma54 specific transcriptional regulator with GAF sensor, Fis family
Rmet_4505	18.67	Op1285r_1	0.52	0.98	1.30	1.38	2.82	2.89	1.10	1.18	1.23	1.31	Transcriptional regulator, LysR family
Rmet_2588	6.67	Op0723f_1	0.53	1.23	1.50	1.25	2.69	2.19	1.03	0.86	1.59	1.32	2-keto-3-deoxygluconate permease
Rmet_6061	2.33	Op1847f_1	0.55	0.79	1.70	2.13	2.01	2.53	0.72	0.90	1.77	2.22	Putative uncharacterized protein
Rmet_2706	45.67	Op0766r_1	0.57	1.25	1.40	1.14	3.50	2.80	0.98	0.79	1.44	1.17	Putative transmembrane protein
Rmet_0452	88.00	Op0118r_2	0.58	1.01	1.39	1.41	2.10	2.09	1.15	1.17	1.62	1.65	PhoH-like protein
Rmet_2775	15.33	Op0780r_1	0.63	1.01	1.08	1.10	2.52	2.49	0.76	0.77	1.43	1.45	PepSY-associated TM helix
Rmet_2632	157.67	Op0738r_2	0.63	0.93	1.81	1.93	2.77	2.99	0.96	1.03	1.31	1.40	Putative uncharacterized protein
Rmet_0132	237.67	Op0033f_2	0.26	2.14	1.68	0.78	2.36	1.10	1.38	0.64	1.48	0.69	Heat shock protein HslVU, ATPase subunit HslU
Rmet_2633	133.00	Op0739f_1	0.32	1.15	1.30	1.13	2.20	1.91	1.23	1.07	1.26	1.10	ChaC-like protein
Rmet_2556	0.00	Op0708r_3	0.35	1.07	1.46	1.35	2.01	1.87	1.17	1.08	1.67	1.54	Integrase, catalytic region
Rmet_5762	27.67	Op1728f_2	0.36	1.30	1.63	1.28	2.04	1.57	1.27	1.00	1.82	1.43	Putative uncharacterized protein
Rmet_2903	142.33	Op0819f_1	0.43	1.58	1.65	1.04	2.29	1.45	1.93	1.22	1.23	0.78	Putative uncharacterized protein
Rmet_2592	2.33	Op0724r_1	0.45	1.14	1.26	1.15	2.25	1.98	0.97	0.89	1.26	1.15	Putative uncharacterized protein
Rmet_2559	20.33	Op0708r_2	0.47	1.57	1.68	1.09	2.40	1.54	1.16	0.75	1.59	1.04	Resolvase-like protein
Rmet_2797	21.67	Op0786r_2	0.49	1.10	1.44	1.29	2.08	1.89	0.97	0.87	1.56	1.39	Malonyl-CoA decarboxylase
Rmet_1380	17.00	Op0385f_3	0.50	1.30	1.52	1.17	2.24	1.73	1.06	0.81	1.81	1.40	Histidine kinase internal region
Rmet_5834	0.33	Op1764f_2	0.53	1.62	1.41	0.83	2.08	1.28	1.72	1.01	1.78	1.05	Phosphoesterase, PA-phosphatase related
Rmet_2637	76.67	Op0742r_1	0.61	2.46	1.97	0.80	2.71	1.10	1.61	0.65	1.89	0.76	Hemerythrin-like, metal-binding
Rmet_2660	9.00	Op0754r_4	0.61	1.17	1.58	1.42	2.04	1.75	1.00	0.90	1.75	1.57	Putative uncharacterized protein
Rmet_5764	20.00	Op1729r_1	0.62	1.13	1.56	1.37	2.11	1.87	1.12	0.99	1.71	1.50	Putative uncharacterized protein
Rmet_0086	114.67	Op0024r_1	0.63	1.64	1.46	0.88	2.29	1.39	1.55	0.94	1.19	0.72	Rhodanese-like protein
Rmet_6016	16.67	Op1835f_1	0.63	1.07	1.72	1.56	2.01	1.88	1.15	1.05	1.74	1.58	Putative uncharacterized protein RMe0245 (Putative uncharacterized protein)
Rmet_1004	373.00	Op0287f_1	0.65	2.46	1.73	0.71	2.09	0.85	1.65	0.67	1.42	0.58	GrpE protein
Rmet_1691	44.33	Op0479f_2	0.66	1.47	1.75	1.16	2.14	1.46	1.23	0.82	0.84	0.56	Flagellar transcriptional activator FlhC
Rmet_4002	11.67	Op1123r_1	0.74	1.08	1.37	1.32	99.71	92.02	1.11	1.07	1.41	1.36	Response regulator receiver (CheY-like) modulated diguanylate phosphodiesterase (EAL domain)
Rmet_1123	2.67	Op0321f_1	1.46	1.04	1.17	1.17	8.53	8.22	0.94	0.94	1.15	1.15	Extracellular solute-binding protein, family 3
Rmet_2554	0.67	Op0708r_4	1.22	1.03	1.48	1.41	4.81	4.66	1.15	1.09	1.22	1.16	Putative uncharacterized protein
Rmet_4008	2.33	Op1125r_2	1.05	0.80	0.86	1.01	1.70	2.13	0.85	1.01	0.92	1.09	PilT protein-like protein
Rmet_4009	1.33	Op1125r_2	0.96	1.11	1.63	1.44	4.49	4.05	1.08	0.95	1.52	1.34	Putative uncharacterized protein
Rmet_4010	36.67	Op1125r_2	1.40	1.75	1.82	1.04	3.72	2.12	1.54	0.88	1.33	0.76	Shikimate kinase
Rmet_5334	4.67	Op1580f_1	0.93	1.18	1.03	0.88	4.11	3.47	0.93	0.80	1.29	1.11	MgtC/SapB transporter
Rmet_2707	57.33	Op0766r_1	1.10	1.22	1.27	1.03	3.95	3.25	0.93	0.75	1.28	1.03	Putative uncharacterized protein

Rmet_0332	25.00	Op0094r_3	1.03	1.81	1.97	1.11	<u>3.78</u>	<u>2.09</u>	1.39	0.79	1.64	0.93	Glyoxalase/bleomycin resistance protein/dioxygenase
Rmet_2802	107.67	Op0788r_2	1.20	1.11	1.71	1.55	<u>3.60</u>	<u>3.25</u>	1.00	0.92	1.49	1.36	Prolipoprotein diacylglyceryl transferase
Rmet_2646	88.33	Op0747f_1	1.36	1.32	1.83	1.37	<u>2.80</u>	<u>2.12</u>	0.93	0.70	1.88	1.41	Flavin reductase-like, FMN-binding
Rmet_2613	4.67	Op0731f_1	0.90	1.12	1.20	1.04	<u>2.67</u>	<u>2.39</u>	0.97	0.84	1.57	1.37	Alkaline phosphatase
Rmet_6237	2.00	Op1901r_1	0.98	1.05	1.92	1.80	<u>2.46</u>	<u>2.34</u>	1.26	1.18	1.86	1.74	Putative uncharacterized protein
Rmet_2771	23.00	Op0778r_1	0.78	0.99	1.87	1.80	<u>2.45</u>	<u>2.47</u>	0.67	0.65	1.59	1.54	Putative uncharacterized protein
Rmet_0795	49.33	Op0226r_1	1.18	1.03	1.81	1.73	<u>2.32</u>	<u>2.26</u>	0.91	0.86	1.89	1.81	Inner-membrane translocator
Rmet_4134	3.00	Op1165r_1	0.86	0.96	1.48	1.60	<u>2.19</u>	<u>2.29</u>	0.86	0.93	1.55	1.68	Dehydrogenase, E1 component
Rmet_4135	11.67	Op1165r_1	1.35	0.86	1.67	1.90	<u>1.89</u>	<u>2.18</u>	0.74	0.83	1.59	1.81	Putative uncharacterized protein
Rmet_0801	726.33	Op0227f_1	0.96	0.85	<u>1.96</u>	<u>2.30</u>	<u>2.17</u>	<u>2.55</u>	<u>1.96</u>	<u>2.30</u>	1.62	1.90	Binding-protein-dependent transport systems inner membrane component
Rmet_4880	14.67	Op1427r_1	0.86	0.86	1.62	1.87	<u>2.09</u>	<u>2.44</u>	0.82	0.95	1.20	1.39	Transcriptional regulator, LysR family
Rmet_4103	109.67	Op1154f_5	1.20	2.02	1.74	0.85	<u>2.73</u>	1.35	1.67	0.81	1.36	0.66	NADH:flavin oxidoreductase/NADH oxidase
Rmet_2641	17.00	Op0745f_1	0.75	1.33	1.63	1.23	<u>2.42</u>	1.82	1.66	1.25	1.81	1.36	Major facilitator superfamily MFS_1
Rmet_0745	8.00	Op0211f_1	1.36	1.35	1.53	1.11	<u>2.36</u>	1.74	1.11	0.81	0.74	0.54	Putative uncharacterized protein
Rmet_3521	137.67	Op0974r_3	1.36	2.61	1.91	0.74	<u>2.35</u>	0.90	1.68	0.65	1.99	0.77	Glucose-methanol-choline oxidoreductase
Rmet_6004	1.33	Op1829r_1	1.40	1.20	1.51	1.26	<u>2.22</u>	1.84	0.96	0.80	1.69	1.41	Putative uncharacterized protein
Rmet_0744	417.67	Op0210r_1	0.71	1.20	1.90	1.55	<u>2.20</u>	1.84	0.96	0.78	1.46	1.19	TM2
Rmet_0085	391.00	Op0023f_2	0.78	2.13	1.78	0.83	<u>2.19</u>	1.03	1.80	0.84	0.98	<u>0.46</u>	Putative uncharacterized protein
Rmet_5727	2.00	Op1715r_3	1.19	1.11	1.83	1.71	<u>2.18</u>	1.96	1.19	1.11	1.61	1.50	Putative uncharacterized protein
Rmet_2560	26.33	Op0708r_1	0.74	1.09	1.25	1.15	<u>2.15</u>	1.97	1.16	1.06	1.21	1.10	Putative uncharacterized protein
Rmet_5954	9.00	Op1812r_1	0.74	1.42	1.82	1.28	<u>2.09</u>	1.47	1.52	1.08	1.65	1.17	Insertion element protein (Integrase, catalytic region)
Rmet_2677	134.00	Op0756r_2	0.92	1.06	1.48	1.36	<u>2.09</u>	1.96	0.76	0.70	1.11	1.02	Biopolymer transport protein ExbD/TolR
Rmet_2184	93.00	Op0628r_4	0.87	1.46	1.53	1.04	<u>2.08</u>	1.42	1.52	1.03	1.54	1.05	Phosphate ABC transporter, permease protein PstC
Rmet_2780	31.00	Op0783f_1	0.94	1.28	1.24	0.98	<u>2.07</u>	1.61	1.15	0.90	1.48	1.16	Adenosylcobinamide-phosphate synthase
Rmet_3766	4.67	Op1047r_1	0.80	1.14	1.49	1.25	<u>2.05</u>	1.80	0.94	0.79	1.39	1.17	Putative uncharacterized protein
Rmet_2350	0.00	Op0663f_2	1.32	1.31	1.88	1.42	<u>2.03</u>	1.54	1.47	1.10	0.76	0.57	Putative uncharacterized protein ORF C50
Rmet_4160	11.00	Op1170f_3	0.86	1.56	1.52	0.98	<u>2.02</u>	1.29	1.58	1.02	1.41	0.91	Glycosyl transferase, group 1
Rmet_1188	33.33	Op0344r_1	<u>0.47</u>	1.24	1.57	1.27	<u>2.07</u>	1.67	1.78	1.45	1.71	1.39	Sulphate transporter
Rmet_4508	49.67	Op1287r_1	1.13	1.08	1.14	1.05	<u>2.01</u>	1.85	0.97	0.89	1.09	0.99	Type IV pilus assembly PilZ
Rmet_2796	115.67	Op0786r_3	0.95	0.71	1.03	1.47	1.95	<u>2.76</u>	0.61	0.87	1.09	1.55	Uncharacterized protein UPF0065
Rmet_5588	4.00	Op1665r_1	1.43	0.78	1.40	1.82	1.89	<u>2.42</u>	0.81	1.04	1.53	1.99	Phospholipase D/Transphosphatidylase
Rmet_3975	68.00	Op1114f_1	1.11	0.82	0.71	0.83	1.97	<u>2.39</u>	0.78	0.91	1.76	<u>2.08</u>	Putative chromosome segregation ATPases
Rmet_4227	4.33	Op1199r_4	1.35	0.80	1.50	1.98	1.87	<u>2.35</u>	0.75	0.98	1.39	1.83	Putative uncharacterized protein
Rmet_5956	1.00	Op1813f_3	1.30	0.86	1.44	1.70	1.86	<u>2.17</u>	0.90	1.06	1.03	1.22	ISPPu14, transposase Orf3
Rmet_5918	70.00	Op1797r_2	1.33	0.87	1.18	1.35	1.88	<u>2.17</u>	0.96	1.10	1.81	<u>2.06</u>	Transcriptional regulator, IclR family
Rmet_4662	27.00	Op1349r_1	1.42	0.88	1.56	1.76	1.89	<u>2.16</u>	0.87	0.98	1.12	1.26	Putative uncharacterized protein
Rmet_1366	4.00	Op0384r_1	1.26	0.90	1.68	1.91	1.88	<u>2.09</u>	0.80	0.91	1.55	1.76	Putative transmembrane protein
Rmet_3307	8049.33	Op0926r_2	0.71	0.67	1.27	1.90	1.37	<u>2.05</u>	0.69	1.03	0.79	1.18	50S ribosomal protein L14
Only 554 up													
Rmet_6287	112.67	Op1916f_4	0.55		0.88	1.03	0.87	1.02	1.77	<u>2.07</u>	0.74	0.87	Putative transmembrane lipoprotein (Putative lipoprotein transmembrane)
Rmet_R0036			<u>0.37</u>	0.70	1.29	1.84	0.93	1.32	<u>2.01</u>	<u>2.85</u>	0.88	1.25	
Rmet_1168	446.33	Op0333f_4	<u>0.16</u>	0.75	1.04	1.39	1.13	1.51	1.60	<u>2.12</u>	0.95	1.26	Putative acetyl transferase protein
Rmet_R0055			0.56	0.69	0.97	1.37	0.65	0.95	<u>3.39</u>	<u>4.81</u>	0.72	1.02	
Rmet_R0017			<u>0.08</u>	0.86	1.06	1.21	1.04	1.21	<u>2.05</u>	<u>2.33</u>	1.07	1.22	
Rmet_R0048			<u>0.32</u>	1.00	1.36	1.36	1.81	1.81	<u>3.08</u>	<u>3.09</u>	1.32	1.32	
Rmet_4084	8.67	Op1148f_1	<u>5.08</u>	0.88	0.86	0.98	1.63	1.84	<u>2.51</u>	<u>2.86</u>	1.05	1.20	Alkaline phosphatase
Rmet_4085	3.67	Op1148f_1	1.83	0.97	1.03	1.00	1.31	1.34	<u>2.18</u>	<u>2.11</u>	1.23	1.19	Alkaline phosphatase
Rmet_0010	1.67	Op0002r_1	1.91	1.53	1.47	1.03	1.64	1.07	<u>3.35</u>	<u>2.34</u>	1.84	1.29	ABC transporter-related protein
Rmet_1307	14.33	Op0376r_5	1.78	1.36	0.98	0.72	0.82	0.61	<u>5.98</u>	<u>4.39</u>	1.23	0.90	Membrane protein involved in aromatic hydrocarbon degradation

Rmet_1308	17.00	Op0376r_5	3.55	0.95	0.19	0.19	0.20	0.21	0.20	0.20	1.54	1.58	Alcohol dehydrogenase GroES-like protein
Rmet_4583	283.67	Op1318f_2	1.73	1.86	1.67	0.90	1.22	0.66	2.24	1.21	1.26	0.68	Extracellular solute-binding protein, family 3
Rmet_3281	823.00	Op0924r_2	1.72	1.03	0.96	0.93	0.73	0.71	8.63	8.34	0.95	0.92	Putative uncharacterized protein
Rmet_0261	746.33	Op0075f_2	1.58	1.13	1.42	1.26	0.87	0.77	2.08	1.84	1.24	1.10	Cytochrome c oxidase subunit 2
Rmet_2183	55.33	Op0628r_4	1.53	1.44	1.60	1.11	1.82	1.26	2.25	1.56	1.61	1.12	Phosphate transport system permease protein 2
Rmet_R0034			0.11	0.99	1.36	1.36	1.14	1.15	2.72	2.71	1.26	1.26	
Rmet_R0045			0.13	0.93	1.13	1.22	1.25	1.33	2.19	2.37	1.20	1.29	
Rmet_R0014			0.18	0.65	1.30	2.00	0.88	1.34	2.21	3.38	0.99	1.52	
Rmet_R0025			0.19	0.98	1.17	1.18	0.94	0.96	3.96	4.02	1.10	1.12	
Rmet_R0039			0.21	0.91	0.90	0.99	1.32	1.45	2.04	2.26	0.90	0.99	
Rmet_2882	1.00	Op0810r_1	0.40	1.19	1.75	1.46	1.07	0.90	3.22	2.70	1.35	1.13	Putative uncharacterized protein
Rmet_2883	936.33	Op0811f_1	0.39	1.22	1.57	1.29	1.25	1.03	2.11	1.73	1.23	1.01	RNA-directed DNA polymerase
Rmet_0872	32.67	Op0253f_1	0.44	1.02	0.88	0.86	1.43	1.40	2.08	2.02	0.83	0.81	Putative uncharacterized protein
Rmet_0873	10.33	Op0253f_1	0.30	0.94	1.26	1.33	2.00	2.12	1.60	1.68	1.91	2.01	Response regulator receiver domain protein (CheY-like)
Rmet_2177	109.33	Op0626r_1	0.53	1.24	1.37	1.12	1.70	1.37	2.60	2.13	1.47	1.20	Ppx/GppA phosphatase
Rmet_3282	114.67	Op0924r_1	0.64	0.97	1.06	1.06	1.15	1.19	8.35	8.35	1.07	1.07	Cytochrome c assembly protein
Rmet_1458	196.00	Op0407f_2	0.16	1.36	1.95	1.44	1.56	1.15	2.02	1.49	1.78	1.31	Putative uncharacterized protein
Rmet_6156	11.67	Op1882r_1	0.20	1.43	1.79	1.28	1.77	1.23	2.28	1.63	1.81	1.29	Putative uncharacterized protein
Rmet_5787	178.00	Op1740f_2	0.22	1.31	1.96	1.49	1.54	1.18	2.06	1.57	1.86	1.42	Putative uncharacterized protein
Rmet_4297	3.33	Op1223r_1	0.30	1.00	1.55	1.51	1.67	1.66	2.00	1.95	1.66	1.62	Putative uncharacterized protein
Rmet_0266	37.00	Op0076r_1	0.53	1.73	1.76	1.02	1.69	0.98	2.04	1.18	1.20	0.69	Putative transmembrane protein
Rmet_0267	119.00	Op0077f_1	0.66	1.57	1.71	1.09	1.62	1.03	2.29	1.46	1.47	0.94	Putative uncharacterized protein
Rmet_0597,													
rpoO	39.67	Op0168r_1	0.84	0.90	0.92	1.02	0.91	1.01	0.55	0.61	0.92	1.02	RNA polymerase sigma factor
Rmet_0598	9.33	Op0169f_1	1.45	0.83	0.91	1.07	0.87	1.05	12.59	14.74	1.02	1.19	Twin-arginine translocation pathway signal
Rmet_0599	9.67	Op0169f_1	1.14	0.80	1.01	1.22	0.97	1.21	18.70	22.59	1.17	1.42	Cytochrome c oxidase subunit 2
Rmet_0600	1.33	Op0170r_1	0.96	1.11	1.04	0.90	1.05	0.95	2.28	1.96	1.16	0.99	Acriflavin resistance protein
Rmet_0546	28.00	Op0152r_1	0.84	1.36	1.40	1.04	1.41	1.04	2.13	1.58	1.54	1.15	3-hydroxybutyrate dehydrogenase
Rmet_4345	33.00	Op1236f_2	0.88	1.21	1.35	1.10	0.97	0.80	2.25	1.85	0.94	0.77	Putative uncharacterized protein
Rmet_5996	9.67	Op1828r_1	1.05	1.12	1.14	1.04	1.30	1.15	2.12	1.93	1.16	1.05	Alpha/beta hydrolase fold
Rmet_4834	52.00	Op1409r_1	1.15	1.30	1.20	0.91	1.24	0.95	2.14	1.63	1.20	0.92	Porin, Gram-negative type
Rmet_1186	34.00	Op0343f_1	0.85	0.87	0.93	1.10	0.85	0.98	1.83	2.16	0.98	1.15	Amidohydrolase
Only 555 up													
pgk__2	NotAss		0.08	0.97	0.69	0.69	0.84	0.87	0.77	0.77	5.53	5.56	
Rmet_1502	36.33	Op0423f_1	0.01	0.87	0.58	0.65	0.78	0.89	0.65	0.73	25.33	28.48	Transcriptional regulator, LysR family
Rmet_1503	0.00	Op0423f_1	0.20	1.11	0.95	0.86	0.71	0.64	0.99	0.89	2.62	2.36	Ralstonia eutropha insertion sequence IS1090
Rmet_1504	4.33	Op0424r_3	0.24	1.05	0.82	0.79	0.64	0.61	0.79	0.76	2.77	2.68	Putative uncharacterized protein
Rmet_1505	3.00	Op0424r_3	0.06	0.96	0.80	0.81	0.87	0.91	0.87	0.88	10.46	10.64	ISSod11, transposase
Rmet_1506	0.00	Op0424r_2	0.26	1.09	1.50	1.36	1.40	1.28	1.09	0.99	3.06	2.77	Transposase
Rmet_1507	8.67	Op0424r_2	0.52	0.66	0.56	0.83	0.70	1.06	0.57	0.84	1.76	2.58	D-fructose 1,6-bisphosphatase
Rmet_1508	30.67	Op0424r_1	0.15	0.90	0.73	0.76	0.86	0.95	0.86	0.90	3.87	4.02	Transcriptional regulator, LysR family
Rmet_1500	330.33	Op0422r_1	0.08	1.12	0.77	0.66	1.22	1.09	1.08	0.93	9.14	7.83	Ribulose biphosphate carboxylase small chain
Rmet_1501	303.67	Op0422r_1	0.04	0.80	0.69	0.79	0.71	0.89	0.82	0.92	9.47	10.71	Ribulose biphosphate carboxylase large chain
Rmet_6333	0.00	Op1926f_1	0.04	1.01	1.49	1.50	1.47	1.46	1.21	1.23	11.61	11.72	Transposase Tn3
Rmet_1493	19.00	Op0422r_1	0.27	1.05	1.12	1.06	1.19	1.13	1.14	1.08	2.35	2.22	Putative uncharacterized protein
Rmet_1494	16.00	Op0422r_1	0.31	1.09	1.03	0.94	1.16	1.06	1.97	1.80	2.22	2.02	Putative uncharacterized protein
Rmet_1495	23.67	Op0422r_1	0.47	0.79	0.75	0.94	0.84	1.06	0.67	0.84	1.28	1.61	Putative uncharacterized protein
Rmet_1496	20.67	Op0422r_1	0.28	0.91	0.84	0.90	0.97	1.07	0.69	0.74	2.08	2.23	Putative uncharacterized protein
Rmet_1497	37.33	Op0422r_1	0.53	0.82	0.73	0.90	0.68	0.83	0.82	1.01	2.57	3.18	Putative uncharacterized protein

Rmet_1498	44.67	Op0422r_1	0.07	1.31	0.94	0.70	1.00	0.76	1.04	0.78	11.84	8.89	von Willebrand factor, type A
Rmet_1499	83.67	Op0422r_1	0.06	1.11	0.78	0.77	1.06	0.96	0.68	0.67	13.95	13.77	ATPase associated with various cellular activities, AAA_5
Rmet_5140	4.00	Op1515r_2	5.22	0.99	1.86	1.83	1.57	1.59	0.92	0.91	2.72	2.68	AMP-dependent synthetase and ligase
Rmet_1557	0.00	Op0431f_2	3.77	0.83	1.11	1.37	1.19	1.43	1.04	1.27	2.53	3.11	Conjugal transfer protein
Rmet_0560	19.00	Op0156r_1	3.54	1.00	1.93	1.95	1.66	1.66	1.17	1.18	3.04	3.06	Anion transporter
Rmet_5394	6.67	Op1606f_1	2.23	0.81	1.77	2.20	1.69	2.08	0.69	0.86	2.35	2.93	Putative uncharacterized protein
Rmet_4536	54.67	Op1297r_1	2.09	1.05	1.39	1.37	1.30	1.24	1.23	1.22	2.50	2.48	Putative uncharacterized protein
Rmet_3214	11.33	Op0906r_1	1.99	0.90	1.68	1.85	1.78	1.99	0.75	0.82	2.09	2.30	Uncharacterized protein UPF0065
Rmet_1649	0.67	Op0465f_1	1.99	1.05	1.06	0.97	1.27	1.22	0.87	0.80	49.57	45.36	Putative uncharacterized protein
Rmet_5132	6.33	Op1513r_2	1.95	0.87	1.39	1.55	1.33	1.52	0.73	0.81	2.44	2.72	Uncharacterized protein UPF0065
Rmet_5408	7.33	Op1610f_1	1.63	1.06	1.41	1.32	1.12	1.06	1.15	1.08	8.06	7.59	Outer membrane efflux protein
Rmet_5409	5.67	Op1610f_1	1.95	1.26	1.75	1.33	1.34	1.07	1.37	1.05	8.76	6.67	Putative uncharacterized protein
Rmet_5402	12.33	Op1608f_1	1.91	0.85	1.53	1.78	0.96	1.12	1.61	1.87	7.29	8.44	Beta-lactamase-like protein
Rmet_4183	91.33	Op1181r_2	1.89	1.25	1.69	1.36	1.58	1.27	1.26	1.02	2.14	1.72	Putative uncharacterized protein
Rmet_6102	6.67	Op1862r_1	1.81	0.98	1.04	1.02	0.95	0.97	0.82	0.80	3.28	3.20	Phage integrase
Rmet_5354	25.33	Op1590f_2	1.71	1.22	1.21	1.00	1.46	1.20	0.97	0.81	2.73	2.27	Putative uncharacterized protein
Rmet_6258	70.33	Op1906f_1	0.18	0.94	1.74	1.85	1.48	1.58	1.63	1.73	1.94	2.06	YD repeat
Rmet_6259	2.33	Op1907r_1	0.12	0.96	1.92	2.03	1.54	1.60	1.57	1.66	2.39	2.53	ISRme9-transposase ORFB protein (IstB-like ATP-binding protein)
Rmet_4417	0.67	Op1259r_2	0.12	1.22	1.86	1.49	1.65	1.35	1.82	1.45	3.23	2.59	Uncharacterized protein UPF0065
Rmet_3357	135.33	Op0935f_2	0.14	0.93	1.70	1.81	1.64	1.76	1.24	1.32	2.11	2.24	Putative uncharacterized protein
Rmet_1491	0.00	Op0421f_1	0.21	0.78	1.07	1.42	1.26	1.62	0.80	1.07	6.97	9.30	Transposase
Rmet_1492	8.00	Op0422r_1	0.26	0.60	0.68	1.22	0.67	1.11	0.65	1.18	1.75	3.16	Fructose-bisphosphate aldolase
Rmet_1475	2.33	Op0413f_1	0.25	0.96	1.85	1.88	1.56	1.62	1.19	1.21	2.85	2.91	Putative uncharacterized protein
Rmet_5601	142.67	Op1669r_1	0.25	0.98	1.74	1.80	1.01	1.03	1.10	1.14	4.09	4.24	Short-chain dehydrogenase/reductase SDR
Rmet_3053	31.67	Op0860r_2	0.26	0.91	1.47	1.60	1.55	1.71	0.79	0.86	2.09	2.26	Monofunctional biosynthetic peptidoglycan transglycosylase
Rmet_2175	66.67	Op0625f_3	0.26	0.97	1.74	1.81	1.76	1.81	1.26	1.31	2.09	2.18	Putative phosphohistidine phosphatase, SixA
Rmet_0545	41.67	Op0151f_2	0.28	0.96	1.43	1.50	1.28	1.33	1.78	1.86	2.22	2.32	Alcohol dehydrogenase, zinc-binding
Rmet_4199	153.67	Op1190f_1	0.31	1.00	1.83	1.84	1.61	1.61	0.95	0.95	2.42	2.42	FAD-binding 9, siderophore-interacting
Rmet_4200	146.00	Op1190f_1	0.45	0.88	1.88	2.20	1.47	1.68	0.90	1.05	2.68	3.13	Putative uncharacterized protein
Rmet_1092	2.00	Op0315f_1	0.34	0.84	1.54	1.76	1.37	1.63	1.46	1.68	4.54	5.22	Anion transporter
Rmet_3379	137.67	Op0940r_3	0.34	0.95	1.62	1.72	1.36	1.43	0.72	0.77	2.36	2.51	Transcriptional regulator, AsnC family
Rmet_5417	11.67	Op1612f_2	0.39	0.83	1.32	1.63	1.27	1.53	1.37	1.69	2.33	2.88	Transcriptional regulator, LysR family
Rmet_5412	81.00	Op1611r_1	0.44	1.16	1.60	1.38	1.29	1.11	1.49	1.28	3.15	2.72	Transcriptional regulator, TetR family
Rmet_1657	6.67	Op0468r_4	0.44	1.04	1.35	1.25	1.27	1.22	1.48	1.37	2.71	2.50	Putative uncharacterized protein
Rmet_3948	101.33	Op1105r_1	0.49	1.10	1.59	1.42	1.64	1.48	1.39	1.24	2.57	2.30	Transcriptional regulator, Crp/Fnr family
Rmet_5782	15.33	Op1738f_1	0.50	0.94	1.01	1.11	1.04	1.11	1.08	1.18	2.90	3.18	Putative uncharacterized protein
actP	16.00	Op1738f_1	0.55	1.10	1.22	1.14	1.31	1.19	1.37	1.28	2.69	2.51	SSS sodium solute transporter superfamily
Rmet_1647	3.00	Op0464r_1	0.52	1.05	1.51	1.45	1.68	1.61	1.23	1.18	5.95	5.71	Putative transmembrane protein
Rmet_5406	9.33	Op1610f_1	0.58	0.93	1.70	1.92	1.18	1.27	1.44	1.62	8.36	9.42	Putative uncharacterized protein
Rmet_5773	80.00	Op1735r_2	0.58	1.06	1.33	1.18	1.16	1.09	1.04	0.92	2.91	2.58	Calcium-binding EF-hand
Rmet_1651	12.00	Op0466r_3	0.59	1.07	1.31	1.19	1.28	1.20	1.12	1.01	5.15	4.68	Sensor protein
Rmet_4999	34.67	Op1467r_1	0.60	1.20	1.54	1.34	1.68	1.40	1.65	1.43	2.50	2.16	Putative uncharacterized protein
Rmet_1650	1.67	Op0466r_3	0.61	1.02	1.50	1.56	1.30	1.27	1.29	1.34	14.51	15.01	Inner membrane CreD
Rmet_1653	5.00	Op0466r_2	0.62	1.07	1.65	1.46	1.32	1.24	1.58	1.40	3.09	2.73	Monooxygenase, FAD-binding
Rmet_5404	4.67	Op1610f_1	0.63	0.86	1.22	1.37	1.12	1.30	1.09	1.22	3.31	3.72	Putative uncharacterized protein
Rmet_1601	116.67	Op0444r_2	0.19	1.15	1.99	1.71	1.35	1.17	1.34	1.15	2.32	2.00	Transcriptional regulator, MarR family
Rmet_0322	0.00	Op0092r_1	0.31	1.28	1.58	1.24	1.69	1.32	1.25	0.98	2.29	1.79	Putative uncharacterized protein
Rmet_6103	6.33	Op1863f_1	0.33	1.28	1.66	1.30	1.85	1.45	1.62	1.26	2.33	1.82	Acyl-CoA dehydrogenase
Rmet_3184	13.67	Op0894r_2	0.41	0.99	1.67	1.62	1.59	1.61	1.03	1.00	2.02	1.97	Acylphosphatase

Rmet_2258	36.00	Op0645f_1	0.46	1.36	1.92	1.41	1.31	0.97	1.51	1.10	2.01	1.48	Putative uncharacterized protein
Rmet_3347	105.33	Op0932r_2	0.48	1.08	1.60	1.45	1.45	1.35	1.03	0.94	2.05	1.87	Putative uncharacterized protein
Rmet_3672	724.00	Op1021r_1	0.48	1.10	1.86	1.64	1.41	1.29	1.10	0.98	2.23	1.98	Putative uncharacterized protein
Rmet_2878	111.33	Op0808r_1	0.51	1.10	1.62	1.46	1.68	1.53	1.18	1.06	2.03	1.84	Phosphoribosylglycinamide formyltransferase
Rmet_1095	3.67	Op0315f_2	0.56	1.17	1.33	1.10	1.35	1.15	1.25	1.03	2.27	1.87	Putative uncharacterized protein
Rmet_4066	4.33	Op1142f_1	0.60	1.30	1.51	1.14	1.45	1.12	1.56	1.17	2.01	1.51	Methyltransferase type 11
Rmet_4098	2.33	Op1154f_1	0.63	1.40	1.85	1.43	1.79	1.28	1.49	1.15	2.07	1.59	Putative uncharacterized protein
Rmet_5405	9.00	Op1610f_1	1.43	0.91	1.57	1.75	1.10	1.21	1.53	1.70	10.00	11.12	Putative periplasmic protein
Rmet_5410	6.00	Op1610f_1	1.33	0.99	1.17	1.10	1.01	1.02	1.06	1.00	4.31	4.06	Putative uncharacterized protein
Rmet_5411	3.33	Op1610f_1	1.24	0.86	1.08	1.33	1.06	1.23	0.98	1.21	3.24	3.98	Peptidase M50
Rmet_4303	0.67	Op1226f_1	0.77	1.06	1.61	1.57	1.63	1.54	1.39	1.35	4.30	4.19	Anion transporter
Rmet_5599	71.00	Op1668f_1	0.90	0.91	1.25	1.41	0.81	0.89	0.89	1.00	2.58	2.89	Catalase-like protein
Rmet_5600	43.67	Op1668f_1	1.05	0.96	1.71	1.80	0.91	0.95	1.14	1.19	4.20	4.41	Ankyrin
Rmet_1710	11.33	Op0483f_1	1.01	1.08	1.56	1.43	1.31	1.21	1.23	1.12	3.91	3.59	RND efflux system, outer membrane lipoprotein, NodT
Rmet_1711	5.67	Op0483f_1	1.15	0.99	1.16	1.19	1.23	1.24	0.97	1.00	2.20	2.27	Secretion protein HlyD
Rmet_1654	0.67	Op0466r_1	1.24	0.95	1.08	1.16	1.37	1.44	1.29	1.39	2.82	3.05	SmpA/OmlA
Rmet_1652	17.00	Op0466r_3	0.99	1.12	1.27	1.12	1.20	1.07	1.01	0.89	2.81	2.48	Two component transcriptional regulator, winged helix family
Rmet_1685	45.33	Op0476r_2	1.05	1.12	1.62	1.47	1.36	1.22	1.28	1.16	2.77	2.51	Secretion protein HlyD
Rmet_3380	199.33	Op0940r_3	0.82	1.21	1.67	1.39	1.63	1.35	0.68	0.57	2.77	2.29	Putative signal transduction protein with EFhand domain
Rmet_1602	13.67	Op0445f_1	0.76	1.19	1.39	1.11	1.33	1.12	1.18	0.95	2.77	2.21	Glyceraldehyde 3-phosphate dehydrogenase
Rmet_5407	4.67	Op1610f_1	1.22	0.85	0.94	1.12	0.89	1.05	0.87	1.03	2.62	3.10	Putative uncharacterized protein
Rmet_1655	0.67	Op0466r_1	0.81	0.93	1.16	1.17	1.10	1.18	1.21	1.23	2.51	2.54	Putative uncharacterized protein
Rmet_1872	15.00	Op0541f_2	0.96	1.15	1.41	1.21	1.08	0.94	1.10	0.95	2.48	2.13	Diguanylate cyclase (GGDEF domain)
Rmet_0208	23.00	Op0062r_1	0.79	0.87	1.68	1.92	1.78	2.05	0.82	0.94	2.39	2.72	Transcriptional regulator, GntR family
Rmet_6329	32.67	Op1923r_1	0.75	1.00	1.84	1.85	1.63	1.63	1.00	1.01	2.33	2.35	HNH nuclease
Rmet_3042	376.67	Op0855f_1	0.71	1.06	2.00	1.88	1.54	1.45	0.84	0.79	2.33	2.19	Putative uncharacterized protein
Rmet_4533	75.00	Op1297r_2	1.08	1.18	1.35	1.20	1.31	1.12	1.30	1.16	2.30	2.05	Putative uncharacterized protein
Rmet_1255	0.00	Op0363f_2	0.73	1.14	1.83	1.70	1.60	1.41	0.96	0.89	2.30	2.13	Putative uncharacterized protein
Rmet_3024	1.00	Op0848r_2	1.28	1.03	1.51	1.53	1.75	1.70	0.91	0.92	2.26	2.29	Conserved hypothetical replication initiator and transcription repressor protein
Rmet_3025	1.33	Op0848r_2	1.05	1.12	1.53	1.40	1.69	1.52	0.86	0.79	2.21	2.03	Putative uncharacterized protein
Rmet_0543	12.33	Op0151f_1	0.83	0.76	0.89	1.19	1.38	1.81	1.18	1.58	2.25	3.01	<i>Ferredoxin</i>
Rmet_4492	144.33	Op1279r_1	1.19	0.84	1.81	2.15	1.74	2.06	0.53	0.64	2.20	2.63	Putative uncharacterized protein
Rmet_5134	1.33	Op1513r_1	0.75	0.84	1.46	1.79	1.20	1.43	0.66	0.81	2.18	2.66	AMP-dependent synthetase and ligase
Rmet_3350	49.00	Op0932r_1	0.82	0.97	1.88	1.99	1.54	1.59	0.64	0.68	2.15	2.27	Putative uncharacterized protein
Rmet_1222	25.33	Op0354r_1	0.78	1.03	1.33	1.38	1.29	1.26	1.36	1.41	2.15	2.23	<i>2,3-dihydro-2,3-dihydroxybenzoyl-CoA ring cleavage enzyme</i>
Rmet_6321	157.67	Op1920f_1	1.25	1.07	1.68	1.65	1.49	1.39	1.01	0.99	2.13	2.09	Hypothetical TolA Transport Protein (Putative uncharacterized protein)
Rmet_5000	40.67	Op1467r_1	0.95	0.88	1.47	1.73	1.46	1.65	0.94	1.10	2.11	2.48	Putative uncharacterized protein
Rmet_0607	44.67	Op0172r_2	1.25	1.00	0.94	0.92	1.20	1.21	0.92	0.90	2.11	2.07	Hydroxymethylglutaryl-CoA lyase
Rmet_1094	6.67	Op0315f_2	1.12	0.91	1.38	1.52	1.12	1.24	1.12	1.23	2.02	2.22	Putative uncharacterized protein
Rmet_4078	232.00	Op1145r_1	1.03	0.70	1.07	1.56	1.09	1.56	0.97	1.42	2.01	2.94	Major facilitator superfamily MFS_1
Rmet_3219	62.33	Op0908r_2	0.68	0.97	1.19	1.29	1.16	1.20	1.06	1.15	2.00	2.17	Carbohydrate-binding family V/XII
Rmet_1566	11.67	Op0432r_1	0.88	1.25	1.68	1.36	1.67	1.33	1.71	1.38	2.34	1.89	Alpha/beta hydrolase fold
Rmet_1767	13.00	Op0508r_1	1.06	1.18	1.28	1.05	1.15	0.97	1.00	0.82	2.23	1.83	Transcriptional regulator, LysR family
Rmet_4908	4.00	Op1438f_1	1.22	1.44	1.54	1.11	1.88	1.31	1.71	1.23	2.19	1.58	Putative uncharacterized protein
Rmet_0500	99.67	Op0134r_1	1.09	0.95	1.60	1.75	1.83	1.93	0.99	1.08	1.96	2.14	Regulatory protein, LuxR
Rmet_1834	14.33	Op0533f_1	0.93	0.54	0.90	1.68	0.74	1.37	0.62	1.17	1.12	2.10	<i>Transcriptional regulator, GntR family</i>
Rmet_0007	36.67	Op0002r_2	1.69	0.95	1.75	1.88	1.55	1.62	0.86	0.92	1.96	2.10	Transcriptional regulator, AraC family
Rmet_4287	7.67	Op1219r_2	0.12	0.59	1.03	1.73	0.82	1.38	0.66	1.11	1.38	2.32	Rare lipoprotein A
Rmet_0604	46.00	Op0171f_1	0.13	0.76	0.95	1.26	1.12	1.46	1.49	1.98	1.51	2.02	Esterase/lipase-like protein

Rmet_1576	78.67	Op0434r_1	0.14	0.83	1.24	1.53	1.30	1.57	1.39	1.72	1.82	2.27	Putative proline-rich protein
Rmet_4471	0.00	Op1275r_1	0.17	0.82	1.42	1.80	1.56	1.91	0.84	1.06	1.82	2.32	UspA
Rmet_1874	52.33	Op0541f_3	0.17	0.55	0.90	1.65	0.66	1.20	0.72	1.32	1.73	3.17	TRAP dicarboxylate transporter-DctP subunit
Rmet_3652	6.33	Op1020f_2	0.44		1.16	1.32	1.25	1.40	1.07	1.22	1.90	2.16	TadE-like protein
Rmet_1389	27.00	Op0387f_1	0.46		1.21	1.43	1.34	1.57	1.24	1.46	1.74	2.05	<i>Haloacid dehalogenase, type II</i>

^aThe table gives the regulation (Q values) of genes in metal-mix-treated *C. metallidurans* cells compared to the untreated control cells. “Op” gives the operon, Q(WT) and Q2(WT) the comparison of metal-treated CH34 cells to untreated cells. The Q(DN..) values compare metal-treated mutant cells to untreated CH34 cells, the QQ(DN...) values metal-treated mutant cells to metal-treated CH34 cells. Values Q > 2 in green, Q < 0.5 in red, significant values (D > 1) bold-faced and underlined. Interesting results were highlighted on a yellow or green field.

Supplementary Table S9. Genes not regulated in wild type but down-regulated on most mutant cells

Gene	NPKM	Operon	Q(WT)	Q2(WT)	Q(DN546)	QQ546	Q(DN553)	QQ553	Q(DN554)	QQ554	Q(DN555)	QQ555	Description
All Mut down													
Rmet_3668	72.67	Op1020f_4	5.33	0.49	0.49	1.01	0.28	0.57	0.48	1.00	0.40	0.82	Butyryl-CoA:acetate CoA transferase
Rmet_5204	5.00	Op1534f_1	4.10	0.48	0.38	0.78	0.35	0.73	0.42	0.86	0.29	0.59	Nitroreductase
Rmet_0114	388.00	Op0031f_5	3.63	0.54	0.44	0.82	0.30	0.56	0.41	0.76	0.26	0.49	Adenosylmethionine-8-amino-7-oxononanoate aminotransferase
Rmet_0115	395.00	Op0031f_5	1.78	0.57	0.60	1.04	0.38	0.67	0.41	0.72	0.34	0.60	8-amino-7-oxononanoate synthase
Rmet_0116	336.67	Op0031f_5	1.98	0.62	0.64	1.03	0.38	0.62	0.51	0.83	0.32	0.52	Dethiobiotin synthase
Rmet_5239	7.67	Op1544f_1	2.71	0.49	0.34	0.70	0.28	0.58	0.30	0.61	0.30	0.62	Phytanoyl-CoA dioxygenase
Rmet_5238	6.33	Op1544f_1	2.53	0.39	0.36	0.91	0.32	0.81	0.24	0.61	0.41	1.02	Putative uncharacterized protein
Rmet_5273	6.00	Op1554f_1	2.08	0.63	0.47	0.74	0.42	0.66	0.47	0.73	0.44	0.68	Uncharacterized protein UPF0065
Rmet_4105	1.00	Op1156f_1	1.89	0.34	0.33	1.02	0.35	1.03	0.32	0.99	0.35	1.08	Acetone carboxylase, beta subunit
Rmet_3701	22.67	Op1026f_3	1.81	0.38	0.21	0.55	0.27	0.71	0.30	0.79	0.23	0.60	Flagellar biosynthesis protein FlhG
Rmet_3519	323.67	Op0974r_4	1.76	0.26	0.26	1.00	0.20	0.78	0.36	1.37	0.25	0.96	ABC transporter-related protein
Rmet_5236	13.33	Op1544f_1	1.69	0.30	0.32	1.04	0.27	0.90	0.23	0.75	0.35	1.16	DegT/DnrJ/EryC1/StrS aminotransferase
Rmet_1281	97.33	Op0370r_1	0.27	0.89	0.23	0.26	0.28	0.32	0.22	0.25	0.84	0.95	Hydrogenase expression/formation protein HypE
Rmet_1282	80.33	Op0370r_1	0.43	0.74	0.29	0.39	0.26	0.35	0.30	0.41	1.07	1.45	Hydrogenase expression/formation protein HypD
Rmet_1283	71.00	Op0370r_1	0.25	0.65	0.22	0.33	0.26	0.41	0.20	0.31	0.91	1.38	Hydrogenase assembly chaperone hypC/hupF
Rmet_1284	61.00	Op0370r_1	0.42	0.60	0.14	0.22	0.17	0.28	0.14	0.23	0.49	0.81	Hydrogenase maturation protein hypF
Rmet_1285	103.00	Op0370r_1	0.33	0.58	0.06	0.11	0.10	0.17	0.08	0.13	0.32	0.56	Hydrogenase accessory protein HypB
Rmet_3667	65.33	Op1020f_4	0.47	0.54	0.46	0.84	0.33	0.62	0.49	0.90	0.41	0.76	3-oxoacid CoA-transferase, subunit A
Rmet_4787	34.67	Op1394f_1	0.65	0.47	0.44	0.95	0.42	0.90	0.50	1.06	0.46	0.99	Amidase
Rmet_3734	58.00	Op1042f_2	0.66	0.18	0.10	0.57	0.08	0.47	0.17	0.96	0.07	0.42	Flagellar basal-body rod protein FlgB
Rmet_2953	791.67	Op0832r_3	0.75	0.64	0.48	0.75	0.38	0.59	0.46	0.72	0.42	0.66	Ycel
Rmet_4931	19.67	Op1446f_1	0.78	0.37	0.35	0.95	0.35	0.94	0.32	0.89	0.31	0.86	Uncharacterized protein UPF0065
Rmet_3516	364.33	Op0974r_5	0.81	0.37	0.49	1.32	0.34	0.91	0.47	1.26	0.44	1.19	Inner-membrane translocator
Rmet_4609	17.67	Op1328f_1	0.91	0.37	0.49	1.29	0.49	1.32	0.25	0.67	0.48	1.27	Uncharacterized protein UPF0065
Rmet_1286	59.00	Op0370r_1	1.10	0.63	0.29	0.46	0.34	0.54	0.21	0.34	0.35	0.55	Hydrogenase nickel insertion protein HypA
Rmet_4817	1.00	Op1404f_1	1.14	0.36	0.38	1.07	0.43	1.17	0.36	1.02	0.39	1.11	Major facilitator superfamily MFS_1
Rmet_3735	59.00	Op1042f_2	1.19	0.18	0.10	0.58	0.08	0.44	0.16	0.91	0.07	0.38	Flagellar basal-body rod protein FlgC
Rmet_3736	74.00	Op1042f_2	1.29	0.21	0.12	0.57	0.09	0.42	0.16	0.75	0.08	0.39	Flagellar hook capping protein
546 not down													
Rmet_4270	33.67	Op1212f_1	2.17	0.61	0.60	0.99	0.48	0.79	0.38	0.63	0.44	0.73	Intradiol ring-cleavage dioxygenase
Rmet_0233	267.33	Op0068r_2	0.24	0.52	0.50	0.98	0.43	0.82	0.40	0.79	0.45	0.89	Thioredoxin-like protein
Rmet_0117	501.00	Op0031f_5	0.96	0.66	0.64	0.98	0.31	0.47	0.48	0.73	0.34	0.52	Biotin synthase
553 not down													
Rmet_2155	6.67	Op0621f_1	11.71	0.46	0.37	0.81	0.50	1.10	0.36	0.79	0.30	0.65	Cytochrome c, class I
Rmet_5053	8.67	Op1487r_1	2.39	0.44	0.45	1.08	0.51	1.15	0.37	0.89	0.41	1.00	ABC transporter related
554 not down													
Rmet_1407	34.00	Op0397f_1	3.06	0.45	0.49	1.10	0.43	0.95	0.65	1.44	0.46	1.03	Oligopeptide/dipeptide ABC transporter, ATP-binding protein-like protein
Rmet_1154	229.00	Op0331f_1	2.76	0.53	0.48	0.90	0.42	0.78	0.71	1.33	0.33	0.62	Butyryl-CoA:acetate CoA transferase
Rmet_3666	40.67	Op1020f_4	2.47	0.27	0.36	1.33	0.34	1.28	0.51	1.88	0.38	1.39	Putative uncharacterized protein
Rmet_3702	13.00	Op1026f_3	0.48	0.64	0.42	0.66	0.56	0.88	0.51	0.81	0.38	0.60	RNA polymerase sigma factor
Rmet_3703	15.67	Op1026f_3	0.21	0.67	0.48	0.72	0.46	0.69	0.54	0.81	0.48	0.71	Flagellar FlhE
Rmet_2501	29.33	Op0693f_1	0.54	0.54	0.48	0.85	0.44	0.81	0.56	0.99	0.34	0.61	Glutathione S-transferase-like protein
Rmet_3313	4433.33	Op0926r_2	0.77	0.49	0.42	0.86	0.28	0.58	0.86	1.76	0.27	0.56	30S ribosomal protein S19
Rmet_5240	13.33	Op1544f_1	0.88	0.69	0.43	0.62	0.48	0.70	0.52	0.75	0.47	0.67	Methyltransferase type 12
Rmet_5261	21.00	Op1552f_2	0.91	0.42	0.39	0.93	0.34	0.82	0.65	1.56	0.38	0.90	Flagellar M-ring protein FlhF
Rmet_4518	5.33	Op1292f_1	1.01	0.42	0.49	1.16	0.25	0.60	0.54	1.29	0.28	0.68	UspA

Rmet_4521	31.33	Op1294f_1	0.69	1.42	1.37	0.96	2.05	1.45	1.44	1.01	1.13	0.79	Transcriptional regulator, Crp/Fnr family
Rmet_4522	22.00	Op1295r_1	1.36	1.06	<u>2.57</u>	<u>2.43</u>	<u>4.68</u>	<u>4.41</u>	0.79	0.74	1.03	0.97	Transcriptional regulator, AraC family with amidase-like domain
Rmet_4890	62.67	Op1430f_1	1.24	0.45	<u>0.44</u>	0.96	<u>0.35</u>	0.78	0.51	1.13	<u>0.35</u>	0.78	Peptidase M20A, peptidase V
Rmet_5203	6.67	Op1534f_1	1.26	0.58	<u>0.47</u>	0.84	<u>0.42</u>	0.71	0.53	0.94	<u>0.34</u>	0.60	Endoribonuclease L-PSP
555 not down													
Rmet_1334	9.67	Op0377f_1	<u>4.81</u>	1.00	<u>0.07</u>	<u>0.07</u>	<u>0.09</u>	<u>0.09</u>	<u>0.06</u>	0.06	1.00	1.01	UspA
Rmet_5315	8.33	Op1570f_1	<u>3.97</u>	0.59	<u>0.45</u>	0.77	<u>0.37</u>	0.64	<u>0.45</u>	0.76	0.64	1.08	Putative uncharacterized protein
Rmet_1319	16.33	Op0376r_4	<u>3.60</u>	0.96	<u>0.10</u>	<u>0.11</u>	<u>0.13</u>	<u>0.14</u>	<u>0.14</u>	0.15	1.08	1.12	Pyruvate carboxyltransferase
Rmet_1329	1.67	Op0376r_2	<u>2.53</u>	1.19	<u>0.28</u>	<u>0.23</u>	<u>0.33</u>	<u>0.28</u>	<u>0.32</u>	0.26	0.85	0.69	Monooxygenase component MmoB/DmpM
Rmet_1306	36.00	Op0376r_6	<u>2.16</u>	1.05	<u>0.12</u>	<u>0.11</u>	<u>0.13</u>	<u>0.12</u>	<u>0.11</u>	0.10	0.90	0.86	Alpha/beta hydrolase fold
Rmet_1533	72.67	Op0427f_2	<u>0.03</u>	1.36	0.51	<u>0.37</u>	0.54	<u>0.40</u>	0.52	<u>0.39</u>	<u>56.82</u>	42.09	High-affinity nickel-transporter
Rmet_1534	295.33	Op0427f_3	<u>0.01</u>	1.10	<u>0.29</u>	<u>0.27</u>	<u>0.32</u>	<u>0.29</u>	<u>0.25</u>	<u>0.23</u>	<u>97.79</u>	90.19	Putative uncharacterized protein
Rmet_1535	963.67	Op0427f_4	<u>0.01</u>	1.45	<u>0.09</u>	<u>0.06</u>	<u>0.12</u>	<u>0.09</u>	<u>0.10</u>	<u>0.07</u>	<u>133.36</u>	91.41	Hydrogenase nickel insertion protein HypA
Rmet_1536	1215.00	Op0427f_4	<u>0.02</u>	1.06	<u>0.24</u>	<u>0.23</u>	<u>0.26</u>	<u>0.24</u>	<u>0.22</u>	<u>0.21</u>	<u>66.51</u>	63.25	Hydrogenase accessory protein HypB
Rmet_1537	560.33	Op0427f_4	<u>0.01</u>	1.21	<u>0.23</u>	<u>0.19</u>	<u>0.28</u>	<u>0.23</u>	<u>0.23</u>	<u>0.19</u>	<u>108.03</u>	88.44	(NiFe) hydrogenase maturation protein HypF
Rmet_1538	487.67	Op0427f_4	<u>0.02</u>	0.68	<u>0.12</u>	<u>0.17</u>	<u>0.11</u>	<u>0.17</u>	<u>0.12</u>	<u>0.17</u>	<u>19.42</u>	28.36	Hydrogenase assembly chaperone hypC/hupF
Rmet_1539	566.33	Op0427f_4	<u>0.01</u>	1.14	<u>0.36</u>	<u>0.32</u>	<u>0.35</u>	<u>0.31</u>	<u>0.39</u>	<u>0.35</u>	<u>79.71</u>	72.31	Hydrogenase expression/formation protein HypD
Rmet_1540	429.33	Op0427f_4	<u>0.01</u>	1.31	<u>0.28</u>	<u>0.22</u>	<u>0.40</u>	<u>0.31</u>	<u>0.31</u>	<u>0.24</u>	<u>101.74</u>	79.02	Hydrogenase expression/formation protein HypE
Rmet_1541	244.67	Op0427f_4	<u>0.02</u>	0.86	<u>0.34</u>	<u>0.40</u>	<u>0.33</u>	<u>0.38</u>	<u>0.31</u>	<u>0.36</u>	<u>39.35</u>	45.99	Formyl transferase-like protein
Rmet_1542	236.67	Op0427f_4	<u>0.01</u>	1.17	<u>0.45</u>	<u>0.39</u>	0.53	<u>0.45</u>	<u>0.47</u>	<u>0.40</u>	<u>86.02</u>	73.28	Response regulator receiver domain protein (CheY-like)
Rmet_1543	0.00	Op0428r_1	<u>0.10</u>	0.77	0.72	0.93	1.06	1.38	0.90	1.18	<u>2.90</u>	3.79	Stress responsive alpha-beta barrel
Rmet_1545	4.67	Op0430r_1	<u>0.12</u>	1.05	1.45	1.42	1.27	1.21	1.58	1.55	<u>6.01</u>	5.89	Putative uncharacterized protein
Rmet_1546	14.67	Op0431f_1	<u>0.43</u>	0.91	1.26	1.35	1.30	1.43	1.44	1.54	<u>4.24</u>	4.53	Transcriptional regulator, LysR family
Rmet_1547	24.67	Op0431f_1	<u>0.21</u>	1.27	1.43	1.09	1.72	1.35	1.57	1.20	<u>3.32</u>	2.53	Putative lipoprotein
Rmet_1509	19.00	Op0425f_1	0.57	0.96	0.84	0.92	0.89	0.93	1.02	1.12	<u>2.45</u>	2.69	Putative uncharacterized protein
Rmet_1510	22.00	Op0425f_1	<u>0.11</u>	1.04	0.86	0.80	0.94	0.90	1.14	1.07	<u>6.03</u>	5.64	Ribulose-5-phosphate 3-epimerase
Rmet_1511	13.67	Op0425f_1	<u>0.07</u>	1.07	0.59	0.56	0.67	0.63	0.74	0.70	<u>22.86</u>	21.56	D-fructose 1,6-bisphosphatase
Rmet_1512	19.00	Op0425f_1	<u>0.12</u>	0.82	0.72	0.84	0.91	1.10	0.62	0.73	<u>4.93</u>	5.74	Phosphoribulokinase
Rmet_1513	19.33	Op0425f_1	<u>0.45</u>	0.88	0.76	0.86	0.57	0.65	0.91	1.04	<u>2.95</u>	3.35	Transketolase
Rmet_1514	15.33	Op0425f_1	<u>0.07</u>	1.16	0.80	0.64	1.02	0.88	1.01	0.80	<u>8.16</u>	6.47	Phosphoglycolate phosphatase
Rmet_1515	27.00	Op0425f_1	<u>0.06</u>	0.90	0.72	0.76	0.79	0.88	0.70	0.74	<u>4.65</u>	4.90	Glyceraldehyde-3-phosphate dehydrogenase
Rmet_1517	17.00	Op0425f_1	<u>0.06</u>	1.14	0.62	0.55	1.08	0.95	0.75	0.67	<u>16.07</u>	14.34	HAD-superfamily hydrolase subfamily IA, variant 3
Rmet_1518	21.33	Op0425f_1	<u>0.13</u>	0.98	0.65	0.63	0.74	0.76	0.63	0.60	<u>9.68</u>	9.33	Fructose-bisphosphate aldolase
Rmet_1519	19.00	Op0425f_1	<u>0.06</u>	0.94	0.71	0.82	0.76	0.81	1.02	1.18	<u>6.83</u>	7.90	Pyruvate kinase
Rmet_1520	9.67	Op0425f_1	<u>0.11</u>	1.30	0.99	0.77	1.06	0.82	1.09	0.84	<u>5.07</u>	3.90	Triosephosphate isomerase
Rmet_1521	10.67	Op0425f_1	<u>0.08</u>	0.88	0.56	0.62	0.64	0.73	0.54	0.60	<u>16.43</u>	18.08	Ribose-5-phosphate isomerase
Rmet_1522	203.67	Op0425f_2	<u>0.01</u>	1.40	1.03	0.67	1.17	0.84	1.14	0.74	<u>25.82</u>	16.86	Respiratory-chain NADH dehydrogenase domain, 51 kDa subunit
Rmet_1523	246.67	Op0425f_2	<u>0.01</u>	0.95	<u>0.27</u>	<u>0.27</u>	<u>0.37</u>	<u>0.39</u>	<u>0.28</u>	<u>0.29</u>	<u>47.21</u>	48.19	Ferredoxin
Rmet_1524	256.00	Op0425f_2	<u>0.05</u>	0.98	<u>0.07</u>	<u>0.07</u>	<u>0.07</u>	<u>0.07</u>	<u>0.07</u>	0.07	<u>57.32</u>	58.60	NADH ubiquinone oxidoreductase, 20 kDa subunit
Rmet_1525	354.00	Op0425f_2	<u>0.04</u>	1.02	<u>0.21</u>	<u>0.21</u>	<u>0.23</u>	<u>0.23</u>	<u>0.26</u>	0.26	<u>55.42</u>	54.83	Nickel-dependent hydrogenase, large subunit
Rmet_1526	348.00	Op0425f_2	<u>0.11</u>	1.16	<u>0.02</u>	<u>0.01</u>	<u>0.02</u>	<u>0.01</u>	<u>0.02</u>	0.01	<u>70.37</u>	60.63	HoxW protein
Rmet_1527	812.00	Op0425f_3	<u>0.01</u>	1.22	<u>0.23</u>	<u>0.18</u>	<u>0.26</u>	<u>0.21</u>	<u>0.26</u>	0.21	<u>69.85</u>	56.15	Cyclic nucleotide-binding domain (CNMP-BD) protein
Rmet_1528	225.00	Op0425f_3	<u>0.06</u>	1.47	<u>2.51</u>	1.70	1.82	1.24	<u>2.03</u>	1.38	<u>7.57</u>	5.14	Alanine dehydrogenase/PNT-like protein
Rmet_1529	0.00	Op0426r_1	<u>0.19</u>	1.98	<u>3.28</u>	1.65	<u>2.94</u>	1.48	<u>3.90</u>	1.97	<u>3.44</u>	1.73	Integrase, catalytic region
Rmet_1530	10.00	Op0427f_1	<u>0.19</u>	0.65	0.62	0.98	0.58	0.89	0.73	1.16	1.73	2.73	Alanine dehydrogenase/PNT-like protein
Rmet_1531	3.67	Op0427f_1	<u>0.12</u>	0.71	0.68	1.01	0.81	1.14	0.75	1.12	<u>2.65</u>	3.96	Pyridine nucleotide transhydrogenase subunit alpha
Rmet_1532	2.33	Op0427f_1	0.52	0.81	0.83	1.04	0.83	1.02	0.77	0.97	1.72	2.15	NAD(P) transhydrogenase, beta subunit
Rmet_1251	5.67	Op0362r_1	<u>0.16</u>	0.86	<u>0.42</u>	<u>0.49</u>	<u>0.30</u>	<u>0.35</u>	<u>0.31</u>	0.36	1.05	1.21	Putative uncharacterized protein
Rmet_1327	4.67	Op0376r_3	<u>0.21</u>	1.37	<u>0.47</u>	<u>0.35</u>	0.61	<u>0.45</u>	0.66	0.48	1.95	1.43	TomA4
Rmet_1328	3.67	Op0376r_3	<u>0.25</u>	1.18	<u>0.17</u>	<u>0.15</u>	<u>0.19</u>	<u>0.16</u>	<u>0.14</u>	0.12	1.49	1.27	Methane/phenol/toluene hydroxylase

Rmet_5551	8.33	Op1648f_3	5.63	0.75	0.63	0.84	0.45	0.60	0.70	0.93	0.40	0.53	Uncharacterized protein UPF0065
Rmet_5201	23.67	Op1534f_1	3.22	0.65	0.51	0.79	0.36	0.55	0.53	0.82	0.38	0.59	Lipase, active site
Rmet_0226	159.00	Op0066r_1	3.06	1.14	0.56	0.49	0.42	0.37	0.69	0.60	0.26	0.23	Putative transmembrane protein
Rmet_0877	127.67	Op0255f_1	2.87	1.67	1.20	0.72	1.05	0.63	1.11	0.67	0.39	0.23	Putative lipoprotein transmembrane
Rmet_0878	474.00	Op0255f_2	2.72	0.89	0.63	0.71	0.41	0.46	0.85	0.95	0.41	0.46	Malic enzyme, NAD-binding
Rmet_4578	25.33	Op1316f_1	1.52	0.40	0.55	1.38	0.33	0.82	0.56	1.41	0.45	1.13	Extracellular solute-binding protein, family 5
Rmet_4585	213.67	Op1319r_2	0.33	0.52	0.57	1.10	0.44	0.85	0.62	1.19	0.48	0.92	Dihydroxyacid dehydratase
Rmet_2477	374.00	Op0688r_2	0.54	0.49	0.48	0.98	0.38	0.78	0.50	1.02	0.51	1.03	ABC transporter-related protein
Rmet_2478	323.00	Op0688r_2	0.34	0.61	0.80	1.26	0.59	0.97	0.87	1.37	0.75	1.19	Inner-membrane translocator
Rmet_2479	282.00	Op0688r_2	0.45	0.89	0.93	1.05	0.78	0.88	0.88	0.99	0.65	0.73	Inner-membrane translocator
Rmet_2480	4428.00	Op0688r_2	0.37	0.52	0.54	1.05	0.34	0.66	0.58	1.12	0.49	0.94	Extracellular ligand-binding receptor
Rmet_2481	2856.00	Op0688r_2	0.28	0.86	0.95	1.10	0.50	0.58	0.91	1.05	0.74	0.86	Citrate synthase
Rmet_2482	1776.33	Op0688r_2	0.42	0.75	0.78	1.03	0.45	0.60	0.70	0.92	0.63	0.83	Putative uncharacterized protein
Rmet_3685	622.33	Op1026f_3	0.18	0.84	1.30	1.56	1.13	1.35	2.46	2.94	0.90	1.08	Flagellar transcriptional activator
Rmet_3686	267.00	Op1026f_3	0.42	0.61	0.53	0.87	0.47	0.77	1.51	2.47	0.36	0.58	Flagellar transcriptional activator FlhC
Rmet_3687	140.00	Op1026f_3	0.19	0.75	0.62	0.82	0.99	1.31	1.86	2.47	0.51	0.68	Chemotaxis MotA protein
Rmet_1046	397.00	Op0301f_1	0.55	0.40	0.51	1.26	0.32	0.78	0.70	1.72	0.38	0.93	Gluconate kinase
Rmet_R0049			0.64	0.60	0.61	1.03	0.50	0.83	1.81	3.03	0.44	0.75	
Rmet_0812	376.00	Op0230r_3	0.69	0.79	0.69	0.88	0.45	0.57	0.78	0.98	0.48	0.60	Peptidyl-prolyl cis-trans isomerase
Rmet_3983	29.67	Op1116f_1	0.81	0.62	0.58	0.92	0.50	0.80	0.66	1.05	0.49	0.77	Uncharacterized protein UPF0065
Rmet_4275	13.67	Op1214f_1	0.87	0.58	0.68	1.22	0.50	0.86	0.62	1.11	0.49	0.88	Uncharacterized protein UPF0065
Rmet_2979	1153.00	Op0840r_2	0.93	0.80	0.67	0.84	0.33	0.41	0.79	0.98	0.34	0.43	Glyceraldehyde-3-phosphate dehydrogenase
Rmet_3669	240.67	Op1020f_5	1.02	0.50	0.59	1.18	0.31	0.62	0.60	1.19	0.41	0.82	Beta-ketoadipyl CoA thiolase
Rmet_0399	3038.67	Op0109f_4	1.16	0.48	0.57	1.19	0.27	0.56	0.65	1.36	0.37	0.77	Extracellular solute-binding protein, family 3
Rmet_0179	164.33	Op0053f_2	1.24	0.79	0.67	0.86	0.44	0.55	0.69	0.87	0.46	0.59	Multifunctional CCA protein
Rmet_0701	75.33	Op0197f_2	1.37	0.36	0.54	1.49	0.31	0.86	0.54	1.47	0.40	1.11	Extracellular solute-binding protein, family 3
Rmet_1045	345.00	Op0301f_1	1.39	0.46	0.51	1.12	0.31	0.68	0.70	1.52	0.36	0.78	6-phosphogluconate dehydratase
Rmet_1719	6.67	Op0485f_2	1.46	0.45	0.50	1.14	0.44	0.96	0.63	1.41	0.45	1.01	Uncharacterized protein UPF0065
Rmet_3902	40.33	Op1090f_1	1.47	0.63	0.65	1.05	0.45	0.72	0.86	1.38	0.48	0.76	Short-chain dehydrogenase/reductase SDR
554 and 555 down													
Rmet_4452	4.00	Op1265r_1	0.58	0.86	0.50	1.33	0.51	1.24	0.49	1.30	0.43	1.15	Response regulator receiver domain protein (CheY-like)
Rmet_5528	14.67	Op1643r_2	1.11		1.68	2.09	1.64	1.91	0.83	1.03	1.29	1.61	AMP-dependent synthetase and ligase
Rmet_5529	16.33	Op1643r_2	0.72		1.10	0.95	1.15	1.03	1.18	1.02	1.01	0.87	Acyl-CoA dehydrogenase-like protein
Rmet_5530	18.67	Op1643r_2	0.90		0.52	1.26	0.54	1.26	0.43	1.06	0.47	1.14	Acyl-CoA dehydrogenase-like protein
Rmet_5100	58.67	Op1501r_2	1.13	0.48	0.60	1.19	0.52	1.07	0.44	0.87	0.44	0.88	Transcriptional regulator, GntR family
Rmet_5350	4.00	Op1590f_1	1.14	0.45	0.51	1.06	0.59	1.32	0.42	0.86	0.49	1.02	FAD-dependent pyridine nucleotide-disulphide oxidoreductase
Rmet_5351	4.67	Op1590f_1	1.27	2.95	1.67	0.56	2.04	0.69	1.61	0.54	1.76	0.58	Major facilitator superfamily MFS_1
Rmet_5352	271.33	Op1590f_2	1.09	1.08	0.69	0.67	3.01	2.79	0.97	0.95	1.92	1.86	Putative uncharacterized protein
Only 546 down													
Rmet_1330	1.33	Op0376r_2	0.48		0.56	0.44	0.72	0.56	0.56	0.44	1.01	0.79	Methane/phenol/toluene hydroxylase
Rmet_1269	3.00	Op0364r_1	2.23	0.81	0.46	0.58	0.69	0.84	0.55	0.69	1.33	1.67	ABC-type multidrug transport system permease component
Rmet_0956	2.33	Op0267f_4	2.04	0.49	0.47	0.95	0.52	1.06	0.82	1.66	0.51	1.04	ABC transporter-related protein
Rmet_2147	768.67	Op0619f_1	0.16	0.99	0.00	0.00	0.87	0.88	1.45	1.45	1.24	1.24	Enoyl-[acyl-carrier-protein] reductase (NADH)
Rmet_4803	79.33	Op1396f_6	0.24	0.82	1.43	1.77	1.28	1.55	1.24	1.53	2.76	3.42	Putative uncharacterized protein
Rmet_4804	25.67	Op1397r_1	0.32	0.95	0.00	0.00	1.50	1.58	1.45	1.48	1.81	1.85	L-threonine 3-dehydrogenase
Rmet_2873	214.00	Op0808r_2	0.36	1.12	1.79	1.59	1.57	1.40	0.95	0.84	2.46	2.19	Nicotinate-nucleotide pyrophosphorylase (Carboxylating)
Rmet_2874	260.00	Op0808r_2	0.53	1.02	2.10	2.05	2.06	2.02	0.89	0.87	2.12	2.07	Quinolate synthetase A
Rmet_2875	1237.00	Op0808r_2	0.33	0.93	0.00	0.00	1.17	1.26	0.88	0.94	1.14	1.22	Fatty acid desaturase
Rmet_0910, rpoR	156.33	Op0262r_1	0.35	0.71	0.17	0.24	0.65	0.92	0.88	1.24	0.68	0.96	Sigma-24 (Fecl-like)

Rmet_1272	1.00	Op0365f_1	0.39	1.30	0.43	0.34	0.54	0.42	0.54	0.43	1.53	1.21	Phage integrase
Rmet_0306	143.33	Op0086r_1	0.41	1.11	0.00	0.00	1.00	0.90	1.06	0.98	1.05	0.96	Putative uncharacterized protein
Rmet_1302	15.33	Op0374r_1	0.45	1.03	0.44	0.44	0.56	0.54	0.51	0.50	1.12	1.11	Putative transposase
Rmet_1174	21.67	Op0337f_1	0.51	1.00	0.00	0.00	1.07	1.07	1.09	1.11	1.04	1.07	Sensor protein
Rmet_1310	23.00	Op0376_r5	0.56	1.05	0.50	0.47	0.53	0.51	0.60	0.56	1.12	1.04	
Rmet_5638	33.00	Op1681r_2	0.65	0.95	0.00	0.00	0.86	0.90	0.80	0.84	1.01	1.06	Putative uncharacterized protein
Rmet_4587	49.00	Op1320f_1	0.70	0.67	0.48	0.73	0.58	0.86	1.02	1.54	0.59	0.89	Glycosyl transferase, family 39
Rmet_2897	874.33	Op0815f_2	0.81	1.11	0.20	0.18	1.55	1.40	0.95	0.86	1.41	1.26	Putative uncharacterized protein
Rmet_3782	6.67	Op1050f_1	1.04	0.86	0.00	0.00	0.89	1.04	0.86	1.03	0.69	0.84	Major facilitator superfamily MFS_1
Rmet_5563	46.67	Op1652f_1	1.19	1.26	0.18	0.15	0.60	0.48	0.79	0.63	0.77	0.62	Putative uncharacterized protein
Rmet_4839	6.67	Op1412f_1	1.22	0.76	0.47	0.60	0.69	0.91	0.51	0.65	0.53	0.67	Transcriptional regulator, LacI family
Rmet_1271	1.00	Op0365f_1	1.42	0.78	0.40	0.55	0.53	0.68	0.59	0.80	1.21	1.63	Phage integrase
Rmet_1331	0.00	Op0376r_1	0.73	1.24	0.56	0.44	0.58	0.47	0.61	0.48	1.66	1.31	Phenol hydroxylase subunit
Rmet_1323	4.67	Op0376r_4	0.84	1.19	0.60	0.49	0.76	0.64	0.57	0.47	1.12	0.93	Putative uncharacterized protein
Rmet_2506	156.33	Op0694r_2	0.93	2.05	1.02	0.50	1.23	0.60	1.15	0.56	1.03	0.50	Chaperone protein htpG
Only 553 down													
Rmet_4606	545.33	Op1326f_1	0.60	0.72	0.83	1.16	0.43	0.60	0.83	1.16	0.67	0.94	O-acetylhomoserine/O-acetylserine sulfhydrylase
Rmet_0197	187.00	Op0057f_3	3.58	1.99	1.60	0.81	0.99	0.50	1.10	0.55	1.21	0.61	Alcohol dehydrogenase, zinc-binding
Rmet_3229	1115.67	Op0914r_1	0.50	0.62	0.66	1.07	0.45	0.73	0.61	0.98	0.62	1.00	Cytochrome b
Rmet_2149	23.00	Op0621f_1	16.48	0.65	0.69	1.07	0.35	0.53	0.52	0.81	0.60	0.93	Beta-lactamase-like protein
Rmet_0913	1486.67	Op0263f_3	6.70	0.76	0.69	0.90	0.40	0.52	0.98	1.28	0.50	0.66	Ketol-acid reductoisomerase
Rmet_0855	183.33	Op0245f_1	6.49	0.84	0.67	0.80	0.48	0.58	0.74	0.88	0.61	0.73	Putative uncharacterized protein
Rmet_3842	38.00	Op1067r_1	5.99	1.07	0.96	0.91	0.36	0.34	0.66	0.62	1.07	1.00	Putative uncharacterized protein
Rmet_1955	58.33	Op0573f_1	3.91	0.93	0.69	0.74	0.46	0.49	0.85	0.91	0.58	0.62	Transcription-repair coupling factor
Rmet_5399	8.33	Op1608f_1	3.55	0.73	0.60	0.83	0.44	0.61	0.69	0.94	0.63	0.86	40-residue YVTN beta-propeller repeat
Rmet_0469	1674.00	Op0123f_3	2.47	0.90	0.78	0.87	0.45	0.50	0.79	0.88	0.58	0.65	Succinyl-CoA synthetase (ADP-forming) beta subunit
Rmet_0470	1957.67	Op0123f_3	3.45	0.82	0.67	0.81	0.39	0.47	0.67	0.82	0.52	0.64	Succinyl-CoA ligase [ADP-forming] subunit alpha
Rmet_1807	111.33	Op0525f_1	3.20	0.91	0.63	0.69	0.42	0.46	0.88	0.96	0.58	0.64	RfbF; ADP-glucose pyrophosphorylase
Rmet_0440	261.00	Op0117f_2	3.19	0.82	0.58	0.71	0.45	0.55	0.77	0.94	0.59	0.72	Tryptophanyl-tRNA synthetase
Rmet_3918	6.33	Op1096f_1	2.51	0.65	0.61	0.92	0.49	0.75	0.57	0.86	0.51	0.77	Putative uncharacterized protein
Rmet_0987	255.33	Op0279f_1	2.49	0.65	0.85	1.29	0.45	0.69	0.91	1.39	0.58	0.88	Cytochrome c, class I
Rmet_1979	2824.00	Op0576r_2	2.35	0.59	0.67	1.13	0.47	0.79	1.13	1.91	0.57	0.98	30S ribosomal protein S6
Rmet_0107	164.67	Op0031f_3	2.20	0.92	0.80	0.87	0.48	0.52	0.88	0.96	0.61	0.67	Short-chain dehydrogenase/reductase SDR
Rmet_0251	248.33	Op0072r_1	2.12	0.81	0.68	0.84	0.46	0.57	0.78	0.97	0.52	0.64	Phosphoglycerate mutase
Rmet_3243	422.00	Op0918r_3	2.03	0.85	0.70	0.83	0.45	0.53	0.71	0.84	0.61	0.72	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] isomerase
Rmet_4683	6.00	Op1355r_1	1.89	0.64	1.36	2.13	0.48	0.74	0.62	0.98	0.71	1.12	Putative uncharacterized protein
Rmet_2106	288.00	Op0608r_1	1.65	0.80	0.63	0.80	0.45	0.57	0.77	0.97	0.54	0.69	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase
Rmet_1031	196.67	Op0295f_3	0.44	1.63	2.15	1.32	1.68	1.03	1.70	1.04	2.02	1.24	Putative uncharacterized protein
Rmet_1032	56.67	Op0296r_2	0.25	0.70	0.50	0.72	0.41	0.59	0.89	1.26	0.53	0.76	Putative uncharacterized protein
Rmet_1886	1343.33	Op0544r_2	0.26	0.71	0.67	0.96	0.46	0.66	0.82	1.16	0.56	0.80	Trigger factor
Rmet_0284	123.00	Op0083f_2	0.30	1.51	2.07	1.37	1.62	1.08	1.79	1.18	1.69	1.11	Putative uncharacterized protein
Rmet_0285	854.00	Op0083f_3	0.22	0.96	1.33	1.39	1.17	1.22	1.14	1.19	1.27	1.32	Phosphopantetheine adenylyltransferase
Rmet_0286	811.00	Op0083f_3	0.59	0.98	1.24	1.26	0.93	0.95	1.00	1.03	1.05	1.08	4Fe-4S ferredoxin, iron-sulfur binding
Rmet_0287	120.67	Op0084r_4	0.22	0.88	0.88	1.00	1.06	1.21	0.84	0.96	1.03	1.18	Peptidyl-tRNA hydrolase
Rmet_0288	2856.33	Op0084r_4	0.29	0.61	0.55	0.89	0.50	0.81	0.70	1.13	0.58	0.95	50S ribosomal protein L25
Rmet_3424	4490.67	Op0950r_2	0.29	0.84	0.80	0.95	0.42	0.50	1.09	1.30	0.62	0.74	Cytochrome c, class I
Rmet_4745	59.33	Op1376f_2	0.32	0.73	0.57	0.77	0.44	0.60	0.64	0.87	0.52	0.70	Short-chain dehydrogenase/reductase SDR
Rmet_4746	44.67	Op1376f_2	0.30	0.61	0.61	0.97	0.45	0.72	0.65	1.05	0.59	0.94	AMP-dependent synthetase and ligase

Rmet_3325	2674.67	Op0928r_2	0.32	0.64	0.69	1.08	0.50	0.78	0.76	1.19	0.61	0.95	Elongation factor G 1
Rmet_1976	3402.00	Op0576r_2	0.36	0.55	0.56	1.03	0.42	0.77	0.85	1.55	0.51	0.94	50S ribosomal protein L9
Rmet_1977	3062.33	Op0576r_2	0.53	0.56	0.62	1.11	0.40	0.70	1.01	1.79	0.51	0.91	30S ribosomal protein S18
Rmet_2160	24.33	Op0621f_3	0.36	0.94	1.16	1.23	0.46	0.49	1.39	1.47	1.13	1.19	Putative uncharacterized protein
Rmet_0118	387.00	Op0031f_5	0.37	0.73	0.83	1.13	0.47	0.64	0.69	0.94	0.53	0.72	D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding
Rmet_2110	1054.33	Op0608r_1	0.39	0.87	0.76	0.87	0.49	0.56	1.02	1.17	0.58	0.67	Nucleoside diphosphate kinase
Rmet_3729	1307.67	Op1041r_3	0.39	0.95	0.88	0.94	0.50	0.53	0.75	0.80	0.68	0.72	Isocitrate dehydrogenase, NADP-dependent
Rmet_2452	1169.67	Op0685f_2	0.40	0.93	0.82	0.89	0.44	0.48	0.83	0.89	0.50	0.54	FAD-dependent pyridine nucleotide-disulphide oxidoreductase
Rmet_R0001			0.34	0.68	0.98	1.44	0.97	1.43	1.45	2.14	0.95	1.39	Thiamine biosynthesis protein thiC FAD dependent oxidoreductase Thiamine biosynthesis protein ThiS Thiazole biosynthesis protein thiG
Rmet_0162	413.00	Op0049f_1	0.38	0.60	0.79	1.33	0.57	0.96	0.84	1.40	0.73	1.22	
Rmet_0163	157.67	Op0049f_1	0.41	0.60	0.72	1.20	0.41	0.68	0.74	1.24	0.63	1.06	
Rmet_0164	137.33	Op0049f_1	0.38	0.70	0.77	1.11	0.51	0.73	0.87	1.26	0.69	0.99	
Rmet_0165	188.33	Op0049f_1	0.43	0.57	0.64	1.11	0.47	0.82	0.65	1.14	0.55	0.96	
Rmet_1120	31.00	Op0320r_1	0.43	0.78	0.79	1.03	0.31	0.40	0.73	0.96	0.83	1.09	Sigma-24 (Fecl-like)
Rmet_1211	1602.00	Op0352r_2	0.45	0.67	0.82	1.23	0.48	0.73	0.74	1.10	0.65	0.97	Putative uncharacterized protein
Rmet_2956	273.33	Op0832r_1	0.45	0.71	0.67	0.94	0.47	0.66	0.69	0.96	0.51	0.72	Adenylosuccinate lyase
Rmet_4591	139.33	Op1320f_2	0.49	0.78	0.54	0.69	0.44	0.56	0.75	0.96	0.56	0.72	Formyl transferase-like protein
Rmet_0109	214.67	Op0031f_3	0.52	0.99	1.05	1.06	0.50	0.50	0.85	0.86	0.75	0.76	DSBA oxidoreductase
Rmet_5926	556.67	Op1800f_1	0.53	0.67	0.66	0.98	0.48	0.71	0.95	1.40	0.53	0.78	Argininosuccinate synthase
Rmet_0985	439.00	Op0278r_1	0.54	0.87	0.65	0.74	0.47	0.54	0.61	0.70	0.57	0.65	GCN5-related N-acetyltransferase
Rmet_4774	654.00	Op1388f_2	0.57	0.65	0.73	1.12	0.42	0.64	0.94	1.45	0.63	0.96	Gluconate transporter
Rmet_1118	191.33	Op0320r_2	0.60	0.72	0.67	0.91	0.36	0.50	0.85	1.15	0.73	0.99	TonB-dependent siderophore receptor
Rmet_0503	662.00	Op0135f_1	0.61	0.79	0.74	0.94	0.49	0.61	0.82	1.04	0.62	0.78	Fructose-bisphosphate aldolase
Rmet_4773	817.33	Op1388f_2	0.63	0.67	0.65	0.98	0.45	0.68	0.85	1.27	0.57	0.86	Endoribonuclease L-PSP
Rmet_3488	230.00	Op0970r_4	0.66	0.85	0.54	0.62	0.49	0.57	0.53	0.61	0.90	1.03	Extracellular ligand-binding receptor
Rmet_1809	164.00	Op0525f_1	1.33	0.96	0.71	0.75	0.41	0.43	0.85	0.89	0.57	0.59	Thiamine pyrophosphate enzyme-like TPP-binding
Rmet_0141	139.67	Op0039f_1	0.67	0.74	0.69	0.92	0.48	0.64	0.83	1.11	0.61	0.82	Pyrimidine 5-nucleotidase
Rmet_0340	9.33	Op0095f_1	0.98	0.59	0.59	0.94	0.48	0.81	0.66	1.06	0.50	0.80	Putative uncharacterized protein
Rmet_0501	384.67	Op0135f_1	1.42	0.76	0.68	0.90	0.45	0.60	0.86	1.14	0.59	0.77	Phosphoglycerate kinase
Rmet_0504	314.67	Op0135f_1	0.73	0.78	0.76	0.98	0.44	0.57	0.80	1.03	0.59	0.76	Phosphoribosylaminoimidazole-succinocarboxamide synthase
Rmet_0505	249.33	Op0135f_1	1.24	0.75	0.73	0.98	0.44	0.59	0.77	1.03	0.56	0.75	Phosphoribosylaminoimidazole carboxylase, catalytic subunit
Rmet_0670	378.67	Op0187f_1	1.42	0.71	0.68	0.95	0.48	0.68	0.63	0.88	0.65	0.90	Response regulator receiver domain protein (CheY-like)
Rmet_0716	270.00	Op0203f_2	1.48	0.90	0.66	0.73	0.50	0.55	0.81	0.90	0.63	0.70	Prephenate dehydratase / chorismate mutase
Rmet_0912	693.33	Op0263f_2	1.32	0.75	0.65	0.87	0.45	0.60	0.94	1.26	0.51	0.68	Acetolactate synthase, small subunit
Rmet_1055	874.33	Op0301f_3	0.82	0.88	0.70	0.80	0.50	0.57	0.90	1.02	0.61	0.70	Enolase 1
Rmet_1089	581.00	Op0313f_3	1.29	0.65	0.62	0.96	0.44	0.68	1.11	1.71	0.53	0.82	Aspartokinase
Rmet_1146	459.33	Op0328r_1	1.23	0.62	0.81	1.32	0.48	0.78	0.68	1.11	0.69	1.13	Electron transfer flavoprotein-ubiquinone oxidoreductase
Rmet_1408	107.00	Op0397f_2	0.71	0.53	0.66	1.23	0.40	0.74	0.76	1.42	0.54	1.00	Extracellular solute-binding protein, family 5
Rmet_1421	161.33	Op0398r_2	0.68	0.87	0.64	0.73	0.47	0.54	0.66	0.75	0.60	0.69	Putative uncharacterized protein
Rmet_1422	245.67	Op0398r_2	0.71	0.89	0.63	0.72	0.46	0.52	0.72	0.82	0.62	0.71	Twin-arginine translocation pathway signal
Rmet_1978	2449.00	Op0576r_2	0.95	0.57	0.64	1.13	0.41	0.72	1.07	1.88	0.52	0.92	Restart primosome assembly protein PriB
Rmet_2089	213.00	Op0605f_1	1.37	0.83	0.76	0.91	0.45	0.54	1.07	1.28	0.62	0.74	Transaldolase
Rmet_2273	730.33	Op0649f_3	1.38	0.82	0.73	0.89	0.43	0.53	0.84	1.03	0.55	0.68	Fumarase
Rmet_2472	568.67	Op0688r_2	0.77	0.78	0.72	0.92	0.47	0.60	0.75	0.96	0.57	0.72	3-isopropylmalate dehydrogenase
Rmet_2484	2217.33	Op0688r_2	0.79	0.72	0.79	1.10	0.45	0.63	0.84	1.18	0.65	0.91	Succinate dehydrogenase subunit A
Rmet_3163	76.33	Op0887f_1	0.79	0.69	0.79	1.14	0.49	0.71	0.63	0.91	0.57	0.82	Enoyl-CoA hydratase / short chain enoyl-CoA hydratase
Rmet_4590	128.00	Op1320f_2	0.72	0.68	0.51	0.75	0.38	0.57	0.69	1.02	0.54	0.80	Glycosyl transferase, family 2
Rmet_1155	589.33	Op0332r_1	0.74	1.53	1.29	0.84	0.69	0.45	0.93	0.61	0.69	0.45	Putative uncharacterized protein
Rmet_0414	966.00	Op0113f_3	0.79	1.90	1.67	0.88	0.94	0.49	1.30	0.68	1.21	0.64	Anhydro-N-acetylmuramic acid kinase

Only 554 down

Rmet_5091	16.33	Op1498f_1	12.53	0.46	0.64	1.38	0.50	1.08	0.46	0.99	0.52	1.13	Oligopeptide/dipeptide ABC transporter, ATP-binding protein-like protein
Rmet_4268	22.33	Op1212f_1	2.24	0.85	0.87	1.03	0.70	0.83	0.46	0.54	0.65	0.76	Citrate synthase
Rmet_5161	1.67	Op1518f_1	3.63	0.43	0.79	1.81	0.91	2.14	0.40	0.91	0.89	2.03	Uncharacterized protein UPF0065
Rmet_0398	212.00	Op0109f_3	3.19	1.13	1.14	1.02	0.81	0.72	0.45	0.40	1.20	1.06	Glu/Leu/Phe/Val dehydrogenase
Rmet_1419	199.33	Op0398r_2	2.27	0.53	0.53	1.01	0.65	1.22	0.49	0.93	0.59	1.12	Modification methylase, HemK family
Rmet_0835	7.67	Op0239f_1	1.96	0.58	0.63	1.09	0.75	1.30	0.47	0.82	0.62	1.08	Uncharacterized protein UPF0065
Rmet_2537	0.33	Op0701f_1	1.58	0.50	0.60	1.21	0.63	1.27	0.48	0.97	0.61	1.23	Putative uncharacterized protein
Rmet_4649	0.67	Op1343r_1	1.52	0.82	1.88	2.30	1.99	2.43	0.46	0.56	0.66	0.81	RND efflux system, outer membrane lipoprotein, NodT
Rmet_0247	143.33	Op0071f_3	0.12	0.61	0.73	1.19	0.83	1.36	0.49	0.79	0.75	1.22	BFD-like (2Fe-2S)-binding region
Rmet_3890	15.00	Op1084f_1	0.26	0.53	0.71	1.35	0.88	1.67	0.50	0.94	1.00	1.89	Extracellular solute-binding protein, family 1
Rmet_1973, pitA	221.67	Op0576r_2	0.50	0.84	1.76	2.12	1.96	2.33	0.26	0.32	1.36	1.64	Phosphate transporter
Rmet_2023	6.67	Op0591f_1	0.65	0.50	0.59	1.26	0.55	1.09	0.49	1.05	0.60	1.27	Sterol desaturase-like protein
Rmet_4126	26.67	Op1162f_2	0.62	1.26	1.95	1.55	2.15	1.71	1.64	1.30	2.16	1.72	Nitrogen fixation protein NifQ, putative
Rmet_4127	55.67	Op1163r_1	0.66	0.89	1.07	1.20	1.67	1.89	0.45	0.51	1.32	1.48	Putative uncharacterized protein
Rmet_3280, rpoL	398.33	Op0924r_2	0.73	0.86	0.92	1.04	0.79	0.92	0.25	0.28	0.91	1.03	Sigma-24 (FecI-like)
Rmet_0228	11.33	Op0067f_1	0.74	1.07	0.81	0.75	1.34	1.25	0.47	0.43	0.65	0.60	C4-dicarboxylate transport protein 1
Rmet_0320	0.00	Op0092r_1	0.99	0.95	0.55	0.57	1.05	1.10	0.37	0.39	1.55	1.62	Hypothetical general secretion pathway protein A (ATPase) (General secretion pa
Rmet_1469	121.67	Op0412r_1	0.99	0.87	1.87	2.22	1.62	1.87	0.56	0.66	1.40	1.66	TatD-related deoxyribonuclease
Rmet_1470	191.33	Op0412r_1	1.14	1.09	1.85	1.68	1.61	1.47	0.69	0.62	1.39	1.26	Putative uncharacterized protein
Rmet_1471	225.67	Op0412r_1	0.74	0.93	2.22	2.38	1.77	1.90	0.54	0.57	1.65	1.77	Putative uncharacterized protein
Rmet_1472	296.00	Op0412r_1	0.74	0.91	2.21	2.38	1.77	1.95	0.47	0.51	1.54	1.66	KAP P-loop
Rmet_1473	631.67	Op0412r_1	1.04	1.02	2.46	2.46	2.44	2.38	0.44	0.44	1.52	1.52	Retron reverse transcriptase
Rmet_1474	2594.00	Op0412r_1	0.90	1.06	2.05	1.93	2.32	2.19	0.64	0.60	1.33	1.25	Putative uncharacterized protein
Rmet_0360	32.67	Op0102r_2	1.32	1.21	4.47	3.74	4.07	3.36	0.47	0.39	2.71	2.27	Carbon monoxide dehydrogenase subunit G
Rmet_0361	9.67	Op0102r_1	1.37	0.95	3.64	3.66	3.41	3.59	0.54	0.54	2.48	2.49	VWA containing CoxE-like protein
Rmet_0825	570.00	Op0234r_1	0.71	0.35	0.56	1.58	0.51	1.46	0.46	1.32	0.57	1.62	Putative uncharacterized protein
Rmet_0863	308.33	Op0248r_2	1.07	0.94	2.83	3.02	3.12	3.31	0.49	0.53	3.43	3.66	Putative uncharacterized protein
Rmet_1785	1.00	Op0518r_2	0.88	0.49	0.68	1.26	0.67	1.38	0.48	0.89	0.59	1.10	Monooxygenase component MmoB/DmpM
Rmet_3358	1134.33	Op0935f_3	1.28	0.86	2.10	2.45	2.02	2.35	0.47	0.55	2.50	2.92	Putative uncharacterized protein
Rmet_3508	15.00	Op0972r_1	1.39	0.48	0.77	1.58	0.69	1.44	0.49	1.01	0.81	1.67	Uncharacterized protein UPF0065
Rmet_4501	5.67	Op1283r_2	1.28	0.83	1.42	1.65	27.58	33.30	0.79	0.92	1.20	1.40	Twin-arginine translocation pathway signal
Rmet_4502	2.67	Op1283r_1	1.14	0.96	1.09	1.05	3.98	4.13	0.98	0.95	1.14	1.10	AMP-dependent synthetase and ligase
Rmet_4503	2.00	Op1283r_1	0.82	1.05	1.13	1.05	2.43	2.32	0.87	0.81	1.03	0.96	Uncharacterized protein UPF0065
Rmet_4504	8.67	Op1284f_1	1.45	0.45	0.58	1.32	3.01	6.76	0.45	1.03	0.59	1.34	Transcriptional regulator, AraC family
Rmet_6335	0.00	Op1926f_1	1.04	0.84	0.79	0.95	0.78	0.93	0.47	0.57	0.94	1.13	ISRme2 transposase protein (Integrase, catalytic region) (Insertion element ISRme
Rmet_3533	26.67	Op0977f_1	0.97	1.18	0.85	0.71	1.80	1.53	0.57	0.47	0.88	0.73	Phenylalanine 4-hydroxylase

Only 555 down

Rmet_4942	79.00	Op1452f_1	9.34	1.38	1.25	0.90	0.66	0.48	1.07	0.78	0.35	0.25	Succinate semialdehyde dehydrogenase
Rmet_4943	70.67	Op1452f_1	6.07	1.06	0.91	0.86	0.67	0.63	0.86	0.81	0.36	0.34	Iron-containing alcohol dehydrogenase
tolB	Rep1	Op0756r	3.62	1.13	0.91	0.80	0.64	0.57	0.87	0.77	0.44	0.39	Protein tolB
Rmet_0176	213.33	Op0053f_1	1.99	1.42	0.87	0.61	0.68	0.48	0.92	0.65	0.37	0.26	Lytic transglycosylase, catalytic
Rmet_2630	255.00	Op0737f_1	3.07	1.13	0.78	0.68	0.96	0.85	1.03	0.91	0.37	0.33	Valyl-tRNA synthetase
Rmet_0272, rpoH	Rep1	Op0078r	3.00	2.00	1.44	0.72	1.17	0.58	1.31	0.65	0.19	0.10	RNA polymerase sigma factor
Rmet_3671	563.00	Op0078r_1	2.74	0.74	0.91	1.24	0.51	0.69	1.09	1.48	0.48	0.65	Uncharacterized protein UPF0065
Rmet_1361	459.67	Op1020f_6	2.65	1.01	0.72	0.71	0.50	0.50	0.99	0.98	0.43	0.43	Putative uncharacterized protein
Rmet_2790	131.67	Op0383f_3	2.31	1.18	0.81	0.68	0.88	0.75	0.83	0.70	0.42	0.36	Putative uncharacterized protein
Rmet_5385	267.67	Op0785f_1	1.89	1.27	1.69	1.34	1.91	1.51	1.22	0.96	0.45	0.36	Putative uncharacterized protein
Rmet_5802	68.67	Op1602f_2	1.64	1.97	1.40	0.71	1.17	0.59	1.22	0.62	0.43	0.22	6-phosphogluconate dehydratase

Rmet_R0035			0.31	0.80	0.77	0.96	0.61	0.76	1.18	1.47	0.46	0.57	
Rmet_2210	3.00	Op0632r_1	0.45	1.08	1.51	1.45	1.58	1.46	0.73	0.70	2.08	1.99	Putative uncharacterized protein
Rmet_3695	66.67	Op1026f_3	0.35	0.92	0.59	0.64	0.81	0.89	1.39	1.51	0.48	0.52	Chemotaxis phosphatase, CheZ
Rmet_2425, rpoE	481.67	Op0680r_3	0.39	1.11	1.04	0.93	1.17	1.05	0.86	0.77	0.13	0.11	RNA polymerase sigma factor
Rmet_2426	904.33	Op0680r_3	0.59	0.78	0.91	1.18	0.67	0.85	1.11	1.43	2.17	2.80	3-oxoacyl-[acyl-carrier-protein] synthase II
Rmet_2926	79.67	Op0827f_1	0.39	0.69	0.78	1.14	0.82	1.19	0.66	0.96	0.50	0.72	FAD linked oxidase-like protein
Rmet_5814	91.33	Op1755r_1	0.40	2.68	2.53	0.94	2.21	0.82	2.28	0.85	0.23	0.09	Putative uncharacterized protein
Rmet_5005	16.67	Op1469r_2	0.56	2.04	2.50	1.22	2.63	1.29	2.56	1.25	0.31	0.15	Isochorismatase hydrolase
Rmet_5006	4.33	Op1469r_1	0.44	1.74	2.18	1.25	2.49	1.43	2.40	1.38	0.39	0.23	Putative uncharacterized protein
Rmet_3070	847.67	Op0861f_5	0.44	1.85	2.57	1.39	1.99	1.07	1.61	0.87	0.45	0.24	17 kDa surface antigen
Rmet_1153	252.33	Op0331f_1	0.45	0.67	0.68	1.01	0.67	1.01	0.79	1.18	0.48	0.71	3-oxoacid CoA-transferase, subunit A
Rmet_1202	71.67	Op0349f_1	0.50	1.35	0.93	0.69	0.82	0.61	1.23	0.92	0.54	0.40	Thioesterase superfamily
Rmet_1203	137.00	Op0349f_1	0.50	1.16	0.80	0.69	0.61	0.53	0.96	0.83	0.35	0.30	Nitroreductase
Rmet_0372	2986.33	Op0103f_4	0.55	1.70	2.03	1.19	1.89	1.11	1.87	1.10	0.30	0.17	Import inner membrane translocase, subunit Tim44
Rmet_3681	113.67	Op1026f_2	0.60	0.96	0.64	0.67	1.02	1.06	1.79	1.85	0.48	0.49	CheW protein
Rmet_2793	354.33	Op0785f_2	0.62	2.12	2.33	1.10	2.38	1.12	1.74	0.82	0.24	0.11	Putative uncharacterized protein
Rmet_2794	102.00	Op0786r_3	0.38	1.09	1.12	1.00	1.29	1.18	1.29	1.14	1.03	0.92	AMP-dependent synthetase and ligase
Rmet_2795	80.67	Op0786r_3	0.53	0.88	1.17	1.37	2.27	2.56	0.92	1.08	1.15	1.34	Enoyl-CoA hydratase/isomerase
Rmet_4634	45.33	Op1338f_1	0.62	1.22	0.67	0.55	0.64	0.52	0.96	0.79	0.41	0.34	DNA/RNA non-specific endonuclease
Rmet_2423	509.67	Op0680r_4	0.65	1.36	1.16	0.85	1.01	0.74	1.08	0.79	0.40	0.29	Sigma E regulatory protein, MucB/RseB
Rmet_2424	1424.00	Op0680r_4	0.61	1.58	1.52	0.96	1.38	0.87	1.17	0.74	0.53	0.33	Anti sigma-E protein RseA
Rmet_0224	261.33	Op0066r_1	0.75	1.18	0.84	0.72	0.62	0.53	0.77	0.65	0.46	0.40	Putative uncharacterized protein
Rmet_0225	188.00	Op0066r_1	0.70	1.24	0.75	0.61	0.64	0.51	0.73	0.59	0.42	0.34	Penicillin-binding protein 6. Serine peptidase. MEROPS family S11
Rmet_5794	15.33	Op1744f_1	0.70	0.61	0.63	1.03	0.57	0.93	0.56	0.91	0.46	0.75	Transcriptional regulator, GntR family
Rmet_5256	35.33	Op1550f_2	0.76	0.81	0.54	0.67	0.62	0.76	0.84	1.05	0.33	0.41	Flagellar protein FliT
Rmet_2370	33.00	Op0669f_1	0.77	0.69	0.99	1.46	0.77	1.12	0.55	0.81	0.49	0.73	Putative transcriptional activator
Rmet_3273	3.33	Op0920r_1	0.81	1.27	1.19	0.96	1.36	1.07	0.94	0.76	0.45	0.36	Putative uncharacterized protein
Rmet_5582	106.33	Op1662f_1	0.88	1.53	0.94	0.61	0.79	0.52	1.07	0.70	0.27	0.18	Putative membrane protein
Rmet_5200	31.67	Op1534f_1	0.90	0.74	0.64	0.86	0.51	0.70	0.64	0.87	0.49	0.66	Glyoxalase/bleomycin resistance protein/dioxygenase
Rmet_5061	2.00	Op1490f_1	1.04	0.59	0.53	0.86	0.57	0.96	0.51	0.83	0.49	0.79	Uncharacterized protein UPF0065
Rmet_2141	82.33	Op0617f_1	1.06	1.64	1.28	0.79	1.19	0.73	1.06	0.65	0.36	0.22	Patatin
Rmet_5252	1317.00	Op1550f_2	1.15	0.85	0.52	0.61	0.66	0.78	1.06	1.25	0.26	0.31	Flagellin-like protein
Rmet_5642	168.33	Op1683r_3	1.17	0.77	0.59	0.77	0.72	0.94	1.07	1.40	0.41	0.53	Flagellar hook-associated 2-like protein
Rmet_5798	81.00	Op1747r_1	1.27	1.11	0.69	0.62	0.56	0.50	0.79	0.71	0.44	0.40	Two component transcriptional regulator, winged helix family
Rmet_5124	136.33	Op1509r_1	1.28	1.14	1.04	0.92	0.89	0.78	1.05	0.92	0.44	0.39	Putative uncharacterized protein
Rmet_1728	31.00	Op0489f_1	1.34	1.10	2.06	1.92	2.04	1.85	1.00	0.93	0.48	0.44	General substrate transporter:Major facilitator superfamily MFS_1
Rmet_1730	0.67	Op0490r_1	0.81	1.52	1.93	1.24	2.18	1.43	1.60	1.03	1.23	0.79	Putative uncharacterized protein
Rmet_0227	191.33	Op0066r_1	1.35	1.53	0.92	0.60	0.99	0.65	0.96	0.63	0.15	0.10	Ferredoxin-like protein
Rmet_5846	0.67	Op1766f_1	1.42	2.00	1.25	0.62	1.68	0.84	1.56	0.77	0.32	0.16	Putative uncharacterized protein
Rmet_4119	623.00	Op1160f_1	1.45	1.58	1.52	0.96	2.01	1.27	1.21	0.76	0.28	0.18	Putative uncharacterized protein
Rmet_5803	102.67	Op1749r_2	0.70	2.09	1.87	0.89	1.29	0.62	1.67	0.80	0.53	0.25	MscS Mechanosensitive ion channel
Rmet_2099	448.00	Op0608r_3	1.09	1.61	1.24	0.76	1.12	0.70	1.16	0.72	0.58	0.36	HflK protein
Rmet_0369	81.00	Op0103f_2	0.97	1.88	1.60	0.85	1.39	0.74	1.80	0.96	0.69	0.37	ABC transporter-like protein
Rmet_2422	645.00	Op0680r_4	0.72	1.14	1.15	0.99	0.92	0.81	1.20	1.03	0.54	0.46	Peptidase S1C, Do
Rmet_1156	667.00	Op0332r_1	0.80	1.55	1.38	0.90	0.80	0.52	1.05	0.68	0.73	0.47	3-hydroxybutyrate dehydrogenase
Rmet_1400	116.33	Op0393f_1	0.87	1.04	0.77	0.74	0.65	0.63	0.76	0.73	0.50	0.48	Alanine racemase
Rmet_2974	146.67	Op0836r_1	0.83	1.13	0.74	0.65	0.66	0.58	0.92	0.81	0.55	0.48	Dihydrodipicolinate reductase
Rmet_3923	99.00	Op1098f_2	17.53	1.27	0.75	0.59	0.68	0.54	0.71	0.56	0.55	0.43	Secretion protein HlyD
Rmet_2280	89.33	Op0651f_3	3.58	1.61	0.81	0.50	1.06	0.66	1.11	0.69	0.64	0.39	Putative uncharacterized protein

Rmet_2922	640.33	Op0826r_2	1.63	2.68	1.37	0.51	1.76	0.65	1.13	0.42	1.22	0.45	Chaperone protein dnaK
Rmet_1001	107.00	Op0285f_1	0.36		1.30	0.76	1.15	0.67	1.65	0.96	0.83	0.49	Ferrochelatase
Rmet_0282	254.33	Op0083f_2	0.42		1.79	1.03	1.30	0.75	1.55	0.89	0.63	0.36	Peptidase M16-like protein
Rmet_0849	856.00	Op0243f_1	0.44		1.54	0.96	1.20	0.75	1.79	1.12	0.58	0.36	17 kDa surface antigen
Rmet_5583	336.00	Op1662f_2	0.46		1.50	1.12	0.94	0.70	1.09	0.81	0.64	0.47	Putative uncharacterized protein
Rmet_0098	602.33	Op0029f_1	0.46		1.23	0.95	1.02	0.79	0.86	0.67	0.55	0.42	DSBA oxidoreductase
Rmet_0283	163.33	Op0083f_2	0.46		1.31	0.83	0.80	0.51	0.96	0.61	0.51	0.32	Peptidase M16-like protein

^aThe table gives the regulation (Q values) of genes in metal-mix-treated *C. metallidurans* cells compared to the untreated control cells. “Op” gives the operon, Q(WT) and Q2(WT) the comparison of metal-treated CH34 cells to untreated cells. The Q(DN..) values compare metal-treated mutant cells to untreated CH34 cells, the QQ(DN...) values metal-treated mutant cells to metal-treated CH34 cells. Values Q > 2 in green, Q < 0.5 in red, significant values (D > 1) bold-faced and underlined. The genes were sorted into the KEGG orthology system. Interesting results were highlighted on a yellow or green field.

Supplementary Table S10. Primers used.

Name	orientation $\leftarrow/\rightarrow$	5' $\rightarrow$ 3'-sequenz ^a
<u>primers for deletion</u>		
SF crelox 611 <i>MunI</i> up	$\rightarrow$	ATA <u>CAA TTG</u> AGT GCT GTT TCG CCT TGG
SF crelox 611 <i>NcoI</i> down	$\leftarrow$	ATA <u>CCA TGG</u> CAC GAC TAC CTC ATC TCA CCG
SF crelox 611 <i>Apal</i> up	$\rightarrow$	ATA <u>GGG CCC</u> CAA CCG GCA CAA GCA CAG
SF crelox 611 <i>AgeI</i> down	$\leftarrow$	ATA <u>ACC GGT</u> GAC AAC CCA AAC GCC GAT
SF crelox 562 <i>MunI</i> up	$\rightarrow$	ATA <u>CAA TTG</u> CGA ACC CCC AGT GCG AAT
SF crelox 562 <i>NotI</i> down	$\leftarrow$	ATA <u>GCG GCC GC</u> CAG GTC GTC GAA GCG GCG
SF crelox 562 <i>Apal</i> up	$\rightarrow$	ATA <u>GGG CCC</u> CGC CCG CAA CCT GCT GCA
SF crelox 562 <i>AgeI</i> down	$\leftarrow$	ATA <u>ACC GGT</u> CGA CGG CTG CTG ATT GAA CTG
SF crelox 605 <i>MunI</i> up	$\rightarrow$	ATA <u>CAA TTG</u> CCT GGG TTT TTG CTC GGT
SF crelox 605 <i>NotI</i> down	$\leftarrow$	ATA <u>GCG GCC GC</u> GCA GGC AAA TAC AGC AGT TGG
SF crelox 605 <i>Apal</i> up	$\rightarrow$	ATA <u>GGG CCC</u> TGA GCA GAA ACG AAC GAG ATA
SF crelox 605 <i>AgeI</i> down	$\leftarrow$	ATA <u>ACC GGT</u> GAG CAG CAT CGC CGT ATC
SF crelox 680 <i>MunI</i> up	$\rightarrow$	ATA <u>CAA TTG</u> GTT CAT CCT TGG CGT GGT
SF crelox 680 <i>NotI</i> down	$\leftarrow$	ATA <u>GCG GCC GC</u> ATG GAT GGA GTG TCA GCT AAG A
SF crelox 680 <i>Apal</i> up	$\rightarrow$	ATA <u>GGG CCC</u> AAC AAT CTT GTC GAT GCC TG
SF crelox 680 <i>AgeI</i> down	$\leftarrow$	ATA <u>ACC GGT</u> GGC GAT AGT GGG GGT GTC
SF crelox 588 <i>MunI</i> up	$\rightarrow$	ATA <u>CAA TTG</u> TCG TGC TGG TGG AAT GCG
SF crelox 588 <i>NotI</i> down	$\leftarrow$	ATA <u>GCG GCC GC</u> GCG GCA CTC CAG GCT GAT
SF crelox 588 <i>Apal</i> up	$\rightarrow$	ATA <u>GGG CCC</u> ATC TTG TGC GCC ACC CTG A
SF crelox 588 <i>AgeI</i> down	$\leftarrow$	ATA <u>ACC GGT</u> TGG TGG CAA TAA CGG CGA T
SF crelox 681 <i>MunI</i> up	$\rightarrow$	ATA <u>CAA TTG</u> CAC AGA CAA CGC ACC TAC CAG C
SF crelox 681 <i>NotI</i> down	$\leftarrow$	ATA <u>GCG GCC GC</u> GGC AGC GGT GTC TCC GTC A
SF crelox 681 <i>Apal</i> up	$\rightarrow$	ATA <u>GGG CCC</u> ACG AGC ATC GAC CGA TAC A

SF crelox 681 <i>MluI</i> down	←	ATA <u>ACG CGT</u> CGG CAA ATA CCT GGA AGC
SF crelox 679 <i>MunI</i> up	→	ATA <u>CAA TTG</u> TGC CGC CTA CCG TGA AAG T
SF crelox 679 <i>NotI</i> down	←	ATA <u>GCG GCC GC</u> GGA TTG CCT AGC GAC GAT CAG
SF crelox 679 <i>Apal</i> up	→	ATA <u>GGG CCC</u> TGG TGA CCC CGA CTC CAG T
SF crelox 679 <i>AgeI</i> down	←	ATA <u>ACC GGT</u> CCA GGT CGG CGT CAA AAC
SF crelox 538 <i>MunI</i> up	→	ATA <u>CAA TTG</u> ATG GCG GGC TTG TCC TTG
SF crelox 538 <i>NotI</i> down	←	ATA <u>GCG GCC GC</u> GGC GAC AAT CCG CGT GCA
SF crelox 538 <i>Apal</i> up	→	ATA <u>GGG CCC</u> AGA CAG ACG ATC TCA TCT CCC T
SF crelox 538 <i>MluI</i> down	←	ATA <u>ACG CGT</u> GCA AGG ACA GGA ACA CGA TA
SF crelox <i>cnrH</i> <i>MunI</i> up	→	ATA <u>CAA TTG</u> ACT ACT TGG CGT GTC CGT CG
SF crelox <i>cnrH</i> <i>NotI</i> down	←	ATA <u>GCG GCC GC</u> TGC GAG CCG CGG CGT AGT
SF crelox <i>cnrH</i> <i>Apal</i> up	→	ATA <u>GGG CCC</u> TTT GGA TTC ACC GAG GGG A
SF crelox <i>cnrH</i> <i>AgeI</i> down	←	ATA <u>ACC GGT</u> CGC CAA GGT TTT CAA GCA C
SF crelox <i>rpoE</i> <i>MunI</i> up	→	ATA <u>CAA TTG</u> TGA AGA TTG ATG TCG CCG T
SF crelox <i>rpoE</i> <i>NotI</i> down	←	ATA <u>GCG GCC GC</u> GAA TAG TTC ACC TGC TGC AGT G
SF crelox <i>rpoE</i> <i>Apal</i> up	→	ATA <u>GGG CCC</u> GGG GAT GTC AGC AGG ATG
SF crelox <i>rpoE</i> <i>AgeI</i> down	←	ATA <u>ACC GGT</u> CCT GCG TGC GTC AAC TCT
SF crelox 697 <i>MunI</i> up	→	ATA <u>CAA TTG</u> CGC TTC ACG CAC TCG GGT
SF crelox 697 <i>NotI</i> down	←	ATA <u>GCG GCC GC</u> CGT CCA TTC CTT GTC GCC
SF crelox 697 <i>Apal</i> up	→	ATA <u>GGG CCC</u> GCG CGC AAG ATC TGG GGA
SF crelox 697 <i>AgeI</i> down	←	ATA <u>ACC GGT</u> AGG ACA ACA CGC CGC TCG

primers for disruption

dis 681 <i>PstI</i> 508 up	→	AAA <u>CTG CAG</u> CTG CCA CCC CTG ACG GAG AC
dis 681 <i>XbaI</i> 836 down	←	AAA <u>TCT AGA</u> TCA GCA GGT CCC GAT AAC GC
dis <i>cnrH</i> <i>PstI</i> 396 up	→	AAA <u>CTG CAG</u> AGC AAC CCA GGA AGT AGA GCG G
dis <i>cnrH</i> <i>XbaI</i> 774 down	←	AAA <u>TCT AGA</u> AGT CCC GCA TCT TGT TCA GCC C
Rmet2178dis2175 <i>SphI</i> up	→	AAA <u>GCA TGC</u> CCC GCA ATG GCA AGG AAG TGA
Rmet_2178dis2731 <i>XbaI</i> down	←	AAA <u>TCT AGA</u> CCT GGC ACT CCT GGG CGA AGC

primers for lacZ fusion

pitARm 3' Xba	AAA <u>TCT AGA</u> CCT GGC TTG TCA TTG GGA TTC
pitARm 5' Pst	AAA <u>CTG CAG</u> GTT CGG TTG GCG GAT TGT
JS RmcorA-Xba	AAA <u>TCT AGA</u> GGG GAC CAG GAA GGC TAT CAG
JS RmcorA-Pst	AAA <u>CTG CAG</u> CGA ACA GCA GGA CGA GGA CGA AGCG

primers for RT-PCR

Rmet1112 qPCR <i>up</i> 1019	→	GCG AGG TGG CGG GCG TCA G
Rmet1112 qPCR <i>down</i> 1134	←	GAG GGC GGT CAT CGG CAG C
Rmet1113 qPCR <i>up</i> 1346	→	AAG TCA CCC TGC TGC CGC TG
Rmet1113 qPCR <i>down</i> 1469	←	GCT GAT GCT GAC GCC CTC CA
Rmet1114 qPCR <i>up</i> 819	→	CGG GCG GCA TTT TCT CCT TG
Rmet1114 qPCR <i>down</i> 947	←	GCA ATG GGC GAG CAC GGA CA
Rmet1115 qPCR <i>up</i> 1045	→	GCT TGC CTG TTA CGC CGC TA
Rmet1115 qPCR <i>down</i> 1127	←	GAG TTC GCC GTC GCT GGT GA
Rmet1118 qPCR <i>up</i> 2322	→	GCG TTC AGC CAG GGT TTC AA
Rmet1118 qPCR <i>down</i> 2454	←	GAG CCG AGC GTG TTG CCG AA
Rmet5806 qPCR 2269 <i>up</i>	→	TGA CCG CCT ATG CCA CCT ACA
Rmet5806 qPCR 2393 <i>down</i>	←	CCG TCC ACA TTG AAA GCC CAG
Rmet5807 qPCR 4704 <i>up</i>	→	TTC ACG GAC GCC ACC TAC CA
Rmet5807 qPCR 4812 <i>down</i>	←	GCG AAG CCG TCC ACA TTG AA
Rmet2621 qPCR 612 <i>up</i>	→	CGG CGG GCT GGT CGG ATA
Rmet2621 qPCR 746 <i>down</i>	←	GCA CCG CCG ACT CCT TGA
rpoZ Ralme 28 <i>up</i> qPCR	→	CTG AAA CAC ATC CCG AAC C
rpoZ Ralme 120 <i>down</i> qPCR	←	ACG GTG GGC TTG TCC TTT G

^a underlined: sites for restriction enzymes