

Supplementary Table S1. The key enzymes for autotrophic growth in *C. metallidurans*

Name	Rmet-number	Spec.	Predicted Mass, (kDa)	Determined Mass, (kDa)
		Activity		
HOS	Rmet_1522 to Rmet_1525	28.7	65.2, 25.4, 23.4, 52.8 = 166.8	62.4±1.8, 26.4±1.3, 24.0±0.6, 54.1±2.5, =235±20 ^a
HOP	Rmet_1297, Rmet_1298,	67.0	69.0 + 38.6 = 108	148±24 ^a
CAX	Rmet_1500, Rmet_1501	2.82	8 * (13.6 + 52.5) = 529	475±36 ^a
PRK	Rmet_1512	0.994	8 * 32.4 = 259	256±11 ^a

^aMean value of masses determined by S300 size exclusion chromatography and sucrose gradient centrifugation. HOS, NAD-reducing soluble hydrogenase; HOP, membrane-bound hydrogenase; CAX, ribulose-bis-phosphate carboxylase/oxygenase; PRK, phosphoribulokinase. Specific activity in U/mg protein.

Supplementary Table S2. Genes expressed differently in AE104 compared to CH34 wild type^a

Operon Region	Name	Gene	Q	D	Description
UP					
Op1321r	Rmet_4594	<i>zntA</i>	1.72	2.88	Q1LEH0 Heavy metal translocating P-type ATPase
Op1322f	Rmet_4595	<i>czcI2</i>	2.03	2.92	Q1LEG9 Putative uncharacterized protein
Op1322f	Rmet_4596	<i>czcC2</i>	23.34	5.36	Q1LEG8 Outer membrane efflux protein
Op1322f	Rmet_4597	<i>czcB2'</i>	15.36	9.68	Q1LEG7 Secretion protein HlyD
Op0075f	Rmet_0260	-	2.31	2.48	Q1LRT0 Putative transmembrane protein
Op0075f	Rmet_0261	<i>coxB</i>	2.08	2.49	Q1LRS9 Cytochrome c oxidase subunit 2
Adjacent to CMGI-7					
Op0335f	Rmet_1171	<i>tnpA</i>	7.03	21.74	Q9F8S6 Transposase (Transposase, IS4 family)
CMGI-2					
Op0362r	Rmet_1251	<i>tnp</i>	4.08	0.61	Q1LNY9 Putative uncharacterized protein
CMGI-1					
Op0663f	Rmet_2349	-	2.44	1.15	Q8GQ59 Putative uncharacterized protein ORF C51
Op0671f	Rmet_2382	<i>tnpA</i>	4.49	23.38	Q1LB62 Integrase, catalytic region
CMGI-10					
Op0934r	Rmet_3353	<i>tnpA</i>	2.77	4.55	Q9F8S6 Transposase (Transposase, IS4 family)
DOWN					
aut region 1, Region 1, CMGI-3					
Op0421f	Rmet_1491	-	0.13	3.76	Q6SKD6 Transposase
Op0422r	Rmet_1492	<i>cbbA1</i>	0.49	2.07	Q1LNA1 Fructose-bisphosphate aldolase
Op0422r	Rmet_1493	<i>fbaA</i>	0.69	0.87	Q1LNA0 Putative uncharacterized protein
Op0422r	Rmet_1494	-	0.43	1.71	Q1LN99 Putative uncharacterized protein
Op0422r	Rmet_1495	-	0.59	1.51	Q1LN98 Putative uncharacterized protein
Op0422r	Rmet_1496	-	0.20	1.49	Q1LN97 Putative uncharacterized protein
Op0422r	Rmet_1497	-	0.63	2.71	Q1LN96 Putative uncharacterized protein
Op0422r	Rmet_1498	<i>cbbO</i>	0.12	4.01	Q1LN95 von Willebrand factor, type A
Op0422r	Rmet_1499	<i>cbbQ</i>	0.06	5.07	Q1LN94 ATPase associated with various cellular activities, AAA_5
Op0422r	Rmet_1500	<i>cbbS</i>	0.08	5.16	Q1LN93 Ribulose bisphosphate carboxylase small chain
Op0422r	Rmet_1501	<i>rbcl</i>	0.09	12.53	Q1LN92 Ribulose bisphosphate carboxylase large chain

Op0423f	Rmet_1502	-	0.04	5.13	Q1LN91 Transcriptional regulator, LysR family
Op0423f	Rmet_1503	-	0.64	4.64	Q9RBF5 Ralstonia eutropha insertion sequence IS1090
Op0424r	Rmet_1504	-	0.48	3.26	Q1LN89 Putative uncharacterized protein
Op0424r	Rmet_1505	-	0.12	6.40	Q1LN88 ISSod11, transposase
Op0424r	Rmet_1506	-	0.21	5.26	Q6SKD6 Transposase
Op0424r	Rmet_1507	<i>cbbF1</i>	0.59	1.57	Q1LN86 D-fructose 1,6-bisphosphatase
Op0424r	Rmet_1508	<i>cbbR</i>	0.41	3.08	Q1LN85 Transcriptional regulator, LysR family
Op0425f	Rmet_1509	-	0.09	5.62	Q1LN84 Putative uncharacterized protein
Op0425f	Rmet_1510	<i>cbbE1</i>	0.04	8.48	Q1LN83 Ribulose-5-phosphate 3-epimerase
Op0425f	Rmet_1511	<i>cbbF2</i>	0.08	8.54	Q1LN82 D-fructose 1,6-bisphosphatase
Op0425f	Rmet_1512	<i>cbbP</i>	0.09	5.82	Q1LN81 Phosphoribulokinase
Op0425f	Rmet_1513	<i>cbbT1</i>	0.54	2.53	Q1LN80 Transketolase
Op0425f	Rmet_1514	<i>cbbZ1</i>	0.12	4.77	Q1LN79 Phosphoglycolate phosphatase
Op0425f	Rmet_1515	<i>cbbG1</i>	0.16	5.40	Q1LN78 Glyceraldehyde-3-phosphate dehydrogenase
Op0425f	Rmet_1517	<i>cbbY</i>	0.10	9.03	Q1LN76 HAD-superfamily hydrolase subfamily IA, variant 3
Op0425f	Rmet_1518	<i>cbbA2</i>	0.07	5.00	Q1LN75 Fructose-bisphosphate aldolase
Op0425f	Rmet_1519	<i>pykA2</i>	0.17	9.60	Q1LN74 Pyruvate kinase
Op0425f	Rmet_1520	<i>cbbJ1</i>	0.34	6.95	Q1LN73 Triosephosphate isomerase
Op0425f	Rmet_1521	<i>cbbI1</i>	0.13	4.52	Q1LN72 Ribose-5-phosphate isomerase
Op0425f	Rmet_1522	<i>hoxF</i>	0.01	4.95	Q1LN71 Respiratory-chain NADH dehydrogenase domain, 51 kDa subunit
Op0425f	Rmet_1523	<i>hoxU</i>	0.01	5.14	Q1LN70 Ferredoxin
Op0425f	Rmet_1524	<i>hoxY</i>	0.00	6.62	Q1LN69 NADH ubiquinone oxidoreductase, 20 kDa subunit
Op0425f	Rmet_1525	<i>hoxH</i>	0.02	8.18	Q1LN68 Nickel-dependent hydrogenase, large subunit
Op0425f	Rmet_1526	<i>hoxW</i>	0.00	8.28	Q1LN67 HoxW protein
Op0425f	Rmet_1527	<i>hoxI</i>	0.00	13.64	Q1LN66 Cyclic nucleotide-binding domain (CNMP-BD) protein
Op0425f	Rmet_1528	-	0.39	7.34	Q1LN65 Alanine dehydrogenase/PNT-like protein
Op0426r	Rmet_1529	-	0.70	2.67	Q1LB62 Integrase, catalytic region
Op0427f	Rmet_1530	-	0.35	2.22	Q1LN63 Alanine dehydrogenase/PNT-like protein
Op0427f	Rmet_1531	<i>pntA</i>	0.26	5.08	Q1LN62 Pyridine nucleotide transhydrogenase subunit alpha
Op0427f	Rmet_1532	<i>pntB</i>	0.44	2.92	Q1LN61 NAD(P) transhydrogenase, beta subunit
Op0427f	Rmet_1533	<i>hoxN</i>	0.77	0.15	Q1LN60 High-affinity nickel-transporter
Op0427f	Rmet_1534	-	0.00	7.06	Q1LN59 Putative uncharacterized protein
Op0427f	Rmet_1535	<i>hypA</i>	0.00	7.12	Q1LN58 Hydrogenase nickel insertion protein HypA
Op0427f	Rmet_1536	<i>hypB</i>	0.01	14.80	Q1LN57 Hydrogenase accessory protein HypB

Op0427f	Rmet_1537	<i>hypF</i>	0.01	8.22	Q1LN56 (NiFe) hydrogenase maturation protein HypF
Op0427f	Rmet_1538	<i>hypC</i>	0.01	13.63	Q1LN55 Hydrogenase assembly chaperone hypC/hupF
Op0427f	Rmet_1539	<i>hypD</i>	0.00	14.76	Q1LN54 Hydrogenase expression/formation protein HypD
Op0427f	Rmet_1540	<i>hypE</i>	0.00	4.08	Q1LN53 Hydrogenase expression/formation protein HypE
Op0427f	Rmet_1541	<i>hoxX</i>	0.02	5.68	Q1LN52 Formyl transferase-like protein
Op0427f	Rmet_1542	<i>hoxA</i>	0.01	6.68	Q1LN51 Response regulator receiver domain protein (CheY-like)
Op0428r	Rmet_1543	-	0.29	2.39	Q1LN50 Stress responsive alpha-beta barrel
Op0430r	Rmet_1545	-	0.17	3.42	Q1LN48 Putative uncharacterized protein
Op0431f	Rmet_1546	-	0.25	2.48	Q1LN47 Transcriptional regulator, LysR family
Op0431f	Rmet_1547	-	0.31	2.99	Q1LN46 Putative lipoprotein

Region 2 = CMGI-4

Op0847f	Rmet_3013	<i>yodB</i>	0.06	5.94	Q1LIZ0 Cytochrome B561
Op0847f	Rmet_3014	-	0.16	4.62	A0HB61 Putative uncharacterized protein
Op0848r	Rmet_3015	<i>hmzS</i>	0.48	2.64	Q1LIY8 Sensor protein
Op0848r	Rmet_3016	<i>hmzR</i>	0.25	3.62	Q1LIY7 Two component transcriptional regulator, winged helix family
Op0848r	Rmet_3017	-	0.26	2.03	Q1LIY6 Ferric reductase-like transmembrane component-like
Op0848r	Rmet_3018	<i>virD2</i>	0.37	2.26	Q1LIY5 Putative uncharacterized protein
Op0848r	Rmet_3019	-	1.00	0.01	Q1LIY4 Putative uncharacterized protein
Op0848r	Rmet_3020	<i>traF</i>	0.68	0.96	Q1LIY3 TraF peptidase. Serine peptidase. MEROPS family S26C
Op0848r	Rmet_3021	-	0.41	1.39	A0HB67 Putative uncharacterized protein
Op0848r	Rmet_3022	<i>parG</i>	0.44	1.58	Q1LIY1 Putative uncharacterized protein
Op0848r	Rmet_3023	<i>parA</i>	0.61	1.89	A0HB69 Cobyrinic acid a,c-diamide synthase A9BTU5 Conserved hypothetical replication initiator and transcription repressor protein
Op0848r	Rmet_3024	<i>repA</i>	0.87	0.61	repressor protein
Op0848r	Rmet_3025	-	0.27	1.51	Q1LIX8 Putative uncharacterized protein
Op0848r	Rmet_3026	-	0.52	0.82	A9BTV1 Putative uncharacterized protein
Op0848r	Rmet_3027	-	0.23	3.86	A9BTV2 Putative lipoprotein
Op0849f	Rmet_3028	-	0.07	12.79	A9BTV3 Helix-turn-helix domain protein
Op0850r	Rmet_3029	-	0.43	3.32	Q1LIX4 Putative uncharacterized protein
Op0850r	Rmet_3030	-	0.15	7.09	Q1LIX3 Putative uncharacterized protein
Op0851f	Rmet_3031	-	0.17	3.16	A9BTV5 GCN5-related N-acetyltransferase
Op0852r	Rmet_3032	-	0.28	4.14	A9BTV6 Putative uncharacterized protein
Op0852r	Rmet_3033	<i>parB</i>	0.85	0.74	A9BTV7 ParB domain protein nuclease

Op0852r	Rmet_3034	<i>yupB</i>	0.61	1.39	A9BTV8 Putative uncharacterized protein
Op0853f	Rmet_3035		0.65	5.14	pseudo
Op0853f	Rmet_3036		0.61	0.72	B2UA43 Putative uncharacterized protein
Op0854r	Rmet_3037		0.32	2.74	Q1LIW7 Putative uncharacterized protein
Op0854r	Rmet_3038		0.62	3.27	B2UA41 Putative uncharacterized protein
Op0854r	Rmet_3039		0.06	12.37	B2UA40 Putative uncharacterized protein
Op0854r	Rmet_3040		0.14	3.09	Q1LIW4 UBA/THIF-type NAD/FAD binding fold
Op0854r	Rmet_3041		0.05	6.72	A9BTW5 Putative uncharacterized protein
Op0855f	Rmet_3042		0.00	15.97	Q1LIW2 Putative uncharacterized protein
Op0855f	Rmet_3043		0.10	8.00	B2UA36 Putative uncharacterized protein
Op0856r	Rmet_3044		0.01	7.42	A9BTW8 Putative uncharacterized protein
Op0856r	Rmet_3045	<i>int</i>	0.20	4.74	Q1LIV9 Phage integrase
Op0856r	Rmet_3046	<i>maeB1</i>	0.47	4.29	Q1LIV8 Malic enzyme, NAD-binding

Region 3 = CMGI-2

Op0366r	Rmet_1274		0.48	1.24	Q1LNW7 Transposase IS66
Op0366r	Rmet_1275		0.72	0.80	Q1LNW6 IS66 Orf2 like
Op0366r	Rmet_1276		0.60	0.77	Q1LNW5 Putative uncharacterized protein
Op0366r	Rmet_1277		0.31	1.93	Q1LNW4 ATPase component ABC-type multidrug transport system
Op0367f	Rmet_1278		0.22	1.13	Q1LNW3 Transposase
Op0368r	Rmet_1279		0.28	3.44	Q1LNW2 Putative transposase
Op0369f	Rmet_1280	<i>tnpA</i>	0.15	5.58	Q1LNW1 Integrase, catalytic region
Op0370r	Rmet_1281	<i>hypE1</i>	0.21	4.05	Q1LNW0 Hydrogenase expression/formation protein HypE
Op0370r	Rmet_1282	<i>hypD1</i>	0.55	4.07	Q1LNV9 Hydrogenase expression/formation protein HypD
Op0370r	Rmet_1283	<i>hypC1</i>	0.17	2.60	Q1LNV8 Hydrogenase assembly chaperone hypC/hupF
Op0370r	Rmet_1284	<i>hyoF1</i>	0.65	1.79	Q1LNV7 Hydrogenase maturation protein hypF
Op0370r	Rmet_1285	<i>hypB1</i>	0.12	2.06	Q1LNV6 Hydrogenase accessory protein HypB
Op0370r	Rmet_1286	<i>hypA1</i>	0.37	1.43	Q1LNV5 Hydrogenase nickel insertion protein HypA
Op0370r	Rmet_1287	<i>hoxV</i>	0.71	0.97	Q1LNV4 Putative uncharacterized protein
Op0370r	Rmet_1288		0.09	5.22	Q1LNV3 HupJ, contains rubredoxin domain
Op0370r	Rmet_1289		0.16	5.13	Q1LNV2 Rubredoxin
Op0370r	Rmet_1290	<i>hoxQ</i>	0.07	9.33	Q1LNV1 HupH hydrogenase expression protein
Op0370r	Rmet_1291		0.14	4.47	Q1LNV0 Hydrogenase-1 expression HyaE
Op0370r	Rmet_1292	<i>hypC2</i>	0.28	5.01	Q1LNU9 Hydrogenase assembly chaperone hypC/hupF

Op0370r	Rmet_1293	-	0.13	2.48	Q1LNU8 HyaD peptidase. Aspartic peptidase. MEROPS family A31
Op0370r	Rmet_1294	-	0.16	3.61	Q1LNU7 Putative plasmid maintenance system antidote protein, XRE family
Op0370r	Rmet_1295	-	0.03	4.15	Q1LNU6 Nickel-dependent hydrogenase b-type cytochrome subunit
Op0370r	Rmet_1296	<i>hupE</i>	0.06	7.77	Q1LNU5 HupE/UreJ protein
Op0370r	Rmet_1297	<i>hoxG</i>	0.05	4.48	Q1LNU4 Nickel-dependent hydrogenase, large subunit
Op0370r	Rmet_1298	<i>hoxK</i>	0.01	6.37	Q1LNU3 Hydrogenase (NiFe) small subunit (HydA)
Op0371f	Rmet_1299	-	0.83	1.23	Q1LNU2 Putative uncharacterized protein
Op0372r	Rmet_1300	-	0.38	1.71	Q1LNU1 GMC oxidoreductase
Op0373f	Rmet_1301	<i>tnpA</i>	1.10	0.58	Q1LNU1 Integrase, catalytic region
Op0374r	Rmet_1302	-	0.29	4.74	Q1LNT9 Putative transposase
Op0374r	Rmet_1303	-	0.28	2.81	Q1LNT8 Transposase IS3/IS911
Op0375f	Rmet_1304	-	0.37	2.06	Q1LNT7 Putative uncharacterized protein
Op0376r	Rmet_1305	<i>patR</i>	0.19	2.32	Q1LNT6 Sigma-54 factor, interaction region
Op0376r	Rmet_1306	-	0.34	4.95	A4JW31 Alpha/beta hydrolase fold
Op0376r	Rmet_1307	-	0.63	1.74	Q1LNT4 Membrane protein involved in aromatic hydrocarbon degradation
Op0376r	Rmet_1308	-	0.32	1.70	Q1LNT3 Alcohol dehydrogenase GroES-like protein
Op0376r	Rmet_1309	-	0.21	3.07	not annotated
Op0376r	Rmet_1310	-	0.42	1.51	not annotated
Op0376r	Rmet_1311	-	0.48	1.87	Q1LNT2 Oxidoreductase FAD-binding region
Op0376r	Rmet_1312	<i>tmoE</i>	0.59	1.30	Q1LNT1 Methane/phenol/toluene hydroxylase
Op0376r	Rmet_1313	<i>tmoD</i>	0.24	5.40	Q1LNT0 Monooxygenase component MmoB/DmpM
Op0376r	Rmet_1314	<i>tmoC</i>	0.20	7.77	Q1LNS9 Rieske (2Fe-2S) region
Op0376r	Rmet_1315	<i>tmoB</i>	0.13	3.30	Q1LNS8 Toluene-4-monooxygenase system B
Op0376r	Rmet_1316	<i>tmoA</i>	0.19	4.91	Q1LNS7 Methane/phenol/toluene hydroxylase
Op0376r	Rmet_1317	<i>nahJ</i>	0.42	1.37	Q1LNS6 4-oxalocrotonate tautomerase family enzyme
Op0376r	Rmet_1318	<i>dmpH</i>	0.15	3.27	Q1LNS5 Hydratase/decarboxylase
Op0376r	Rmet_1319	<i>mhpE</i>	0.54	2.02	Q1LNS4 Pyruvate carboxyltransferase
Op0376r	Rmet_1320	<i>mhpF</i>	0.61	1.24	Q1LNS3 Semialdehyde dehydrogenase, NAD-binding
Op0376r	Rmet_1321	-	0.50	1.71	Q1LNS2 Hydratase/decarboxylase
Op0376r	Rmet_1322	<i>dmpC</i>	0.46	2.42	Q1LNS1 Aldehyde dehydrogenase
Op0376r	Rmet_1323	-	0.62	1.68	Q1LNS0 Putative uncharacterized protein
Op0376r	Rmet_1324	<i>dmpB</i>	0.31	1.97	Q1LNR9 Catechol 2,3-dioxygenase
Op0376r	Rmet_1325	<i>hcaD</i>	0.31	2.28	Q1LNR8 Ferredoxin

Op0376r	Rmet_1326	-	0.58	1.26	Q1LNR7 Oxidoreductase FAD-binding region
Op0376r	Rmet_1327	-	0.09	3.26	Q9ANX1 TomA4
Op0376r	Rmet_1328	<i>tomA3</i>	0.07	5.40	Q1LNR5 Methane/phenol/toluene hydroxylase
Op0376r	Rmet_1329	-	0.31	3.54	Q1LNR4 Monooxygenase component MmoB/DmpM
Op0376r	Rmet_1330	-	0.37	1.62	Q1LNR3 Methane/phenol/toluene hydroxylase
Op0376r	Rmet_1331	-	0.26	2.51	Q1LNR2 Phenol hydroxylase subunit
Op0377f	Rmet_1332	-	0.24	5.61	Q1LNR1 Putative uncharacterized protein
Op0377f	Rmet_1333	<i>phaB2</i>	0.08	6.16	Q1LNR0 Acetoacetyl-CoA reductase
Op0377f	Rmet_1334	-	0.37	1.56	Q1LNQ9 UspA
Op0377f	Rmet_1335	<i>chnA</i>	0.12	7.40	Q1LNQ8 Short-chain dehydrogenase/reductase SDR
Op0377f	Rmet_1336	-	0.11	4.77	Q1LNQ7 Transcriptional regulator, LysR family
Op0377f	Rmet_1337	-	0.15	6.06	Q1LNQ6 Putative lipoprotein
Op0378r	Rmet_1338	-	0.28	3.05	Q1LNQ5 Putative uncharacterized protein

Region 4

Op1698f	Rmet_5689	<i>pilY1</i>	0.07	23.92	Q1LBC8 Putative type 4 fimbrial biogenesis pily1-related protein signal peptide
Op1698f	Rmet_5690	-	0.05	11.37	Q1LBC7 Putative lipoprotein
Op1700f	Rmet_5692	-	0.41	1.88	Q1LBC5 Putative uncharacterized protein
Op1700f	Rmet_5693	-	0.22	3.43	Q1LBC4 Putative uncharacterized protein
Op1701r	Rmet_5694	-	0.32	2.41	Q1LBC3 Putative uncharacterized protein
Op1702f	Rmet_5695	-	0.16	3.46	Q1LBC2 Beta-lactamase-like protein
Op1702f	Rmet_5696	-	0.16	3.10	Q1LBC1 Putative uncharacterized protein
Op1703r	Rmet_5697	-	0.39	1.73	Q1LBC0 Putative uncharacterized protein
Op1704f	Rmet_5698	-	0.37	3.61	Q1LBB9 Putative uncharacterized protein
Op1708f	Rmet_5710	<i>bvgS1</i>	0.48	2.06	Q1LBA7 Sensor protein
Op1709r	Rmet_5714	<i>bvgA</i>	0.22	7.17	Q1LBA3 Two component transcriptional regulator, LuxR family
Op1709r	Rmet_5715	-	0.12	4.25	Q1LBA2 Putative uncharacterized protein
Op1710f	Rmet_5716	-	0.12	2.33	Q1LBA1 Putative uncharacterized protein
Op1714f	Rmet_5724	-	0.26	4.85	Q1LB93 Sensor protein
Op1715r	Rmet_5728	-	0.16	2.33	Q1LB89 Glycosyl transferase, group 1
Op1715r	Rmet_5729	-	0.25	5.76	Q1LB88 Polysaccharide export protein
Op1715r	Rmet_5730	<i>kpsE</i>	0.23	2.73	Q1LB87 Chain length determinant protein
Op1715r	Rmet_5731	<i>kpsT</i>	0.30	6.70	Q1LB86 ABC transporter related

Op1716f	Rmet_5735	-	0.38	1.67	Q1LB82 KpsF/GutQ family protein
Op1716f	Rmet_5738	-	0.26	6.71	Q1LB79 Putative uncharacterized protein
Op1716f	Rmet_5739	-	0.32	4.91	Q1LB78 Putative uncharacterized protein
Op1717r	Rmet_5742	-	0.11	3.12	Q1LB75 Putative uncharacterized protein
Op1717r	Rmet_5743	-	0.38	3.47	Q1LB74 AMP-dependent synthetase and ligase
Op1718f	Rmet_5744	-	0.18	2.95	Q1LB73 Putative uncharacterized protein
Op1718f	Rmet_5745	-	0.10	3.46	Q1LB72 Putative uncharacterized protein
Op1720f	Rmet_5749	-	0.07	5.57	Q1LB68 Transcriptional regulator, PadR family
Op1721r	Rmet_5750	-	0.25	4.09	Q1LB67 Diguanylate cyclase/phosphodiesterase
Op1722f	Rmet_5751	-	0.25	2.12	Q1LB66 Diguanylate cyclase (GGDEF domain) with PAS/PAC sensor
Op1723r	Rmet_5752	-	0.14	5.80	Q1LB65 Putative uncharacterized protein
Op1724f	Rmet_5753	-	0.12	5.46	Q1LB64 Putative uncharacterized protein
Op1724f	Rmet_5754	-	0.48	10.58	Q1LB63 Fumarate hydratase, class II

Region 5

Op0034r	Rmet_0133	-	0.28	2.49	Q1LS57 Nuclear export factor GLE1
Op0037f	Rmet_0137	-	0.36	1.42	Q1LS53 Putative uncharacterized protein
Op0038r	Rmet_0138	-	0.37	2.11	Q1LS52 Transcriptional regulator, LysR family
Op0038r	Rmet_0139	-	0.46	2.87	Q1LS51 Putative uncharacterized protein
Op0107f	Rmet_0392	-	0.45	1.08	Q1LRE8 Twin-arginine translocation pathway signal

Region 6 = CMGI-2

Op0357f	Rmet_1238	<i>radC</i>	0.35	0.86	Q1LP02 DNA repair protein RadC
Op0357f	Rmet_1239	<i>int</i>	0.10	8.76	Q1LP01 Phage integrase
Op0357f	Rmet_1240	<i>int</i>	0.41	2.85	Q1LP00 Phage integrase
Op0357f	Rmet_1241	<i>ritC</i>	0.27	5.52	Q1LNZ9 Phage integrase
Op0357f	Rmet_1242	<i>radC</i>	0.06	16.41	Q1LNZ8 RadC family protein
Op0357f	Rmet_1245	<i>parB</i>	0.21	3.31	Q1LNZ5 ParB family protein
Op0358r	Rmet_1246	-	0.44	2.88	Q1LNZ4 GCN5-related N-acetyltransferase
Op035xx	Rmet_1247	-	0.29	3.32	Q1LNZ3 Putative uncharacterized protein
Op0359f	Rmet_1248	-	0.13	7.64	Q1LNZ2 Transcriptional regulator, XRE family
Op0363f	Rmet_1255	-	0.48	2.76	Q1LNY5 Putative uncharacterized protein
Op0363f	Rmet_1259	<i>virD</i>	0.45	1.57	Q1LNY1 Putative uncharacterized protein
Op0364r	Rmet_1264	-	0.14	3.57	Q1LNX7 Integrase, catalytic region

Op0364r	Rmet_1266	-	0.43	4.14	Q1LNX5 Beta-lactamase-like protein
Op0365f	Rmet_1271	<i>ritA</i>	0.48	0.90	Q1LNX0 Phage integrase
Op0365f	Rmet_1272	<i>int</i>	0.39	3.82	Q1LNW9 Phage integrase
Op0365f	Rmet_1273	<i>int</i>	0.38	2.27	Q1LNW8 Phage integrase
others					
Op0153f	Rmet_0550	-	0.19	0.50	Q1LQZ0 Putative uncharacterized protein
CMGI-2					
Op0379f	Rmet_1350	<i>virB10</i>	0.16	5.63	Q1LNP3 Conjugation TrbI-like protein
Op0379f	Rmet_1351	-	0.15	7.48	Q1LNP2 Putative uncharacterized protein
CMGI-3					
Op0413f	Rmet_1475	-	0.28	7.53	Q1LNB8 Putative uncharacterized protein
Op0415f	Rmet_1477	<i>yupB</i>	0.45	0.96	Q1LNB6 Putative uncharacterized protein
Op0417f	Rmet_1480	-	0.40	5.38	Q1LNB3 Putative uncharacterized protein
Op0431f	Rmet_1560	-	0.25	7.14	Q1LN33 Putative uncharacterized protein
Op0565f	Rmet_1934	-	0.41	1.38	Q1LM13 Binding-protein-dependent transport systems inner membrane component
CMGI-1					
Op0663f	Rmet_2354	-	0.47	1.55	Q8GQ64 Putative uncharacterized protein ORF C46
Op0698r	Rmet_2529	-	0.39	0.98	Q1LKC0 Thiolase
Op0716r	Rmet_2579	-	0.27	1.55	Q1LK70 Pirin-like protein
Op0802r	Rmet_2848	-	0.41	1.84	Q1LJF5 Putative uncharacterized protein
CMGI-4					
Op0842r	Rmet_2987	-	0.40	3.67	Q1LJ16 Putative uncharacterized protein
Op0842r	Rmet_2993	<i>ptxC</i>	0.37	4.26	A0HB23 Phosphonate ABC transporter, inner membrane subunit
Op0843f	Rmet_2996	-	0.25	2.66	A0HB26 Transcriptional regulator, LysR family
Op0843f	Rmet_2997	-	0.25	4.63	A9BTQ2 Putative uncharacterized protein
Op0878r	Rmet_3138	-	0.24	0.43	Q1LIL6 2-nonaprenyl-3-methyl-6-methoxy-1,4-benzoquinol hydroxylase
Op1148f	Rmet_4084	<i>phoA1</i>	0.47	0.68	Q1LFX5 Alkaline phosphatase
Op1219r	Rmet_4291	-	0.45	1.30	Q1LFB9 2,3-dimethylmalate lyase
Op1314f	Rmet_4565	-	0.14	1.63	Q1LEJ9 TonB-dependent receptor
Op1315r	Rmet_4566	-	0.17	1.68	Q1LEJ8 Putative uncharacterized protein
Op1327r	Rmet_4607	-	0.28	1.26	Q1LEF7 TonB-dependent copper receptor
Op1327r	Rmet_4608	-	0.46	1.07	Q1LEF6 Putative uncharacterized protein

Op1521r Rmet_5171 - **0.50** 1.60 Q1LCU6 Cold-shock DNA-binding protein family

^aCells of wild type strain CH34(pMOL28, pMOL30) and its plasmid-free derivative strain AE104 were cultivated in TMM minerals salts medium without further additions on gluconate to the exponential phase of growth. RNA was isolated, reversely transcribed, labeled and hybridized against a CH34-specific gene array. Provided are the Q-ratios AE104/CH34, red if at least 2-fold down-regulated, green up, bold-faced letters indicate significant differences, letters in italics not significant differences. The D-value for each comparison is also given. This is the distance of both mean values divided by the sum of both deviations. If $D > 1$ (the deviation bars do not touch or overlap) the data points are different with a probability in the t-test of $> 95\%$. Three biological repeats for both strains. Genes associated to catabolic metabolic genomic islands (CMGIs) are on a yellow ground with the CMGI number directly above the respective gene(s), operon regions are in a box.

Supplementary Table S3. Genes expressed differently in AE104 in the presence of 100 μ M Zn(II)^a

Operon	Region	Name	Gene	Q_AE104_Zn	D	Description
Up-regulated genes						
Op0027f	Rmet_0094	-		2.10	4.17	Q1LS96 Putative uncharacterized protein
Op0033f	Rmet_0131	-		2.22	4.11	Q1LS59 ATP-dependent protease hslV
Op0033f	Rmet_0132	<i>hslU</i>		2.29	4.53	Q1LS58 Heat shock protein HslVU, ATPase subunit HslU
Op0039f	Rmet_0144	-		2.03	2.02	Q1LS46 Methionine biosynthesis MetW
Op0043f	Rmet_0151	-		2.62	3.17	Q1LS39 Patatin
Op0052r	Rmet_0175	-		2.49	4.45	Q1LS15 5-formyltetrahydrofolate cyclo-ligase
Op0066r	Rmet_0227	-		2.09	5.04	Q1LRW3 Ferredoxin-like protein
Op0078r	Rmet_0272	-		2.64	9.15	Q1LRR8 RNA polymerase sigma factor
Op0080r	Rmet_0277	<i>nasF</i>		2.40	0.76	Q1LRR3 Putative nitrate transporter protein
Op0083f	Rmet_0282	-		2.16	3.97	Q1LRQ8 Peptidase M16-like protein
Op0083f	Rmet_0283	-		2.41	5.70	Q1LRQ7 Peptidase M16-like protein
Op0103f	Rmet_0369	-		2.01	3.30	Q1LRH1 ABC transporter-like protein
Op0103f	Rmet_0372	-		2.04	6.87	Q1LRG8 Import inner membrane translocase, subunit Tim44
Op0103f	Rmet_0379	-		2.03	6.25	Q1LRG1 Putative transmembrane protein
Op0151f	Rmet_0543	-		3.01	0.50	Q1LQZ7 Ferredoxin
Op0151f	Rmet_0545	-		3.26	0.57	Q1LQZ5 Alcohol dehydrogenase, zinc-binding
Op0153f	Rmet_0550	-		6.66	0.64	Q1LQZ0 Putative uncharacterized protein
Op0222r	Rmet_0778	-		3.08	4.58	Q1LQB2 RNase G
Op0243f	Rmet_0849	-		2.29	7.96	Q1LQ41 17 kDa surface antigen
Op0270r	Rmet_0967	<i>gstI</i>		2.08	3.17	Q1LPS3 Glutathione S-transferase-like protein
Op0287f	Rmet_1004	-		2.07	6.26	Q1LPN6 GrpE protein
Op0287f	Rmet_1005	-		2.14	6.22	Q1LPN5 Putative thioredoxin protein
Op0295f	Rmet_1024	-		3.26	7.83	Q1LPL6 Transcriptional regulator, BadM/Rrf2 family
Op0295f	Rmet_1025	<i>iscS</i>		4.22	10.12	Q1LPL5 Cysteine desulfurase IscS
Op0295f	Rmet_1026	-		4.14	16.89	Q1LPL4 FeS cluster assembly scaffold IscU
Op0295f	Rmet_1027	-		4.06	8.15	Q1LPL3 Iron-sulfur cluster assembly protein IscA
Op0295f	Rmet_1028	<i>hscB</i>		3.10	7.35	Q1LPL2 Co-chaperone Hsc20
Op0295f	Rmet_1029	<i>hscA</i>		2.97	3.68	Q1LPL1 Chaperone protein hscA homolog
Op0295f	Rmet_1030	-		2.84	7.59	Q1LPL0 Ferredoxin, 2Fe-2S type

Op0295f	Rmet_1031	-	2.61	5.89	Q1LPK9 Putative uncharacterized protein
Op0357f	Rmet_1242	-	2.62	2.25	Q1LNZ8 RadC family protein
Op0363f	Rmet_1255	-	2.18	2.76	Q1LNY5 Putative uncharacterized protein
Op0370r	Rmet_1298	<i>hoxK</i>	2.29	1.40	Q1LNU3 Hydrogenase (NiFe) small subunit (HydA)
Op0376r	Rmet_1315	<i>tmoB</i>	2.53	1.25	Q1LNS8 Toluene-4-monooxygenase system B
Op0376r	Rmet_1318	<i>dmpH</i>	3.95	1.19	Q1LNS5 Hydratase/decarboxylase
Op0376r	Rmet_1324	<i>dmpB</i>	2.10	0.59	Q1LNR9 Catechol 2,3-dioxygenase
Op0379f	Rmet_1350	<i>trbI</i>	2.71	1.75	Q1LNP3 Conjugation TrbI-like protein
Op0425f	Rmet_1510	<i>cbbE1</i>	2.31	1.72	Q1LN83 Ribulose-5-phosphate 3-epimerase
Op0425f	Rmet_1512	<i>cbbP</i>	2.43	0.83	Q1LN81 Phosphoribulokinase
Op0425f	Rmet_1518	<i>cbbA2</i>	2.26	0.56	Q1LN75 Fructose-bisphosphate aldolase
Op0539f	Rmet_1864	-	2.15	4.37	Q1LM83 UPF0061 protein Rmet_1864
Op0539f	Rmet_1865	-	2.33	5.50	Q1LM82 Methionine sulfoxide reductase B
Op0560r	Rmet_1920	-	2.17	1.50	Q1LM27 Isochorismatase hydrolase Q1LM13 Binding-protein-dependent transport systems inner membrane component
Op0565f	Rmet_1934	-	2.19	0.57	
Op0574r	Rmet_1959	-	2.04	4.13	Q1LLY8 ATPase AAA-2
Op0609f	Rmet_2111	-	2.37	6.64	Q1LLI6 Putative uncharacterized protein
Op0621f	Rmet_2149	-	2.21	0.53	Q1LLE8 Beta-lactamase-like protein
Op0626r	Rmet_2177	<i>ppx</i>	3.58	2.88	Q1LLC0 Ppx/GppA phosphatase
Op0627f	Rmet_2178	<i>ppk</i>	4.28	5.76	Q1LLB9 Polyphosphate kinase
Op0628r	Rmet_2181	-	6.00	7.60	Q1LLB6 Phosphate uptake regulator, PhoU
Op0628r	Rmet_2182	<i>pstB</i>	6.21	5.97	Q1LLB5 Phosphate import ATP-binding protein pstB
Op0628r	Rmet_2183	<i>pstA</i>	6.64	4.14	Q1LLB4 Phosphate transport system permease protein 2
Op0628r	Rmet_2184	<i>pstC</i>	5.88	3.12	Q1LLB3 Phosphate ABC transporter, permease protein PstC
Op0628r	Rmet_2185	<i>pstS</i>	10.26	5.66	Q1LLB2 Periplasmic phosphate binding protein
Op0651f	Rmet_2280	-	2.35	13.55	Q1LL17 Putative uncharacterized protein
Op0656r	Rmet_2299	-	12.67	8.21	Q8GQ11 Putative integral membrane protein / transporter
Op0659f	Rmet_2303	<i>cadA</i>	18.85	5.09	A7HYL0 Heavy metal translocating P-type ATPase
Op0659f	Rmet_2304	<i>pbrC2</i>	22.96	5.39	Q8GQ15 Lipoprotein signal peptidase
Op0659f	Rmet_2305	-	4.42	3.49	Q8GQ16 Putative uncharacterized protein ORF C95
Op0661f	Rmet_2317	-	2.42	3.27	Q1LKY2 Transposase Tn3
Op0663f	Rmet_2354	-	2.04	1.16	Q8GQ64 Putative uncharacterized protein ORF C46
Op0669f	Rmet_2372	-	2.69	4.34	Q8GQ82 Putative uncharacterized protein ORF C28

Op0669f	Rmet_2373	-	2.99	3.19	Q8GQ83 Putative uncharacterized protein ORF C27
Op0669f	Rmet_2374	-	2.51	6.62	Q1LKS5 Putative uncharacterized protein
Op0694r	Rmet_2505	-	2.12	1.19	Q1LKE4 Uracil-DNA glycosylase superfamily
Op0719f	Rmet_2583	<i>phoD</i>	2.65	1.86	Q1LK66 Alkaline phosphatase
Op0741f	Rmet_2636	-	2.09	8.53	Q1LK13 Thioredoxin
Op0742r	Rmet_2637	-	2.31	3.65	Q1LK12 Hemerythrin-like, metal-binding
Op0785f	Rmet_2793	-	2.87	12.22	Q1LJL0 Putative uncharacterized protein
Op0804r	Rmet_2853	-	2.25	1.16	Q1LJF0 Putative uncharacterized protein
Op0826r	Rmet_2922	<i>dnaK</i>	2.46	3.04	O33522 Chaperone protein dnaK
Op0843f	Rmet_2997	-	3.87	6.72	A9BTQ2 Putative uncharacterized protein
Op0845f	Rmet_2999	-	2.67	1.97	Q1LDD1 Propeptide, PepSY amd peptidase M4
Op0845f	Rmet_3000	-	2.82	1.99	Q1LDD2 Undecaprenyl-diphosphatase (Phosphoesterase, PA-phosphatase related)
Op0845f	Rmet_3001	-	3.27	4.91	Q1LDD3 Putative uncharacterized protein
Op0845f	Rmet_3002	-	2.73	3.14	Q1LDD4 Conserved hypothetical signal peptide protein
Op0855f	Rmet_3042	-	2.36	0.99	Q1LIW2 Putative uncharacterized protein
Op0878r	Rmet_3138	-	5.84	0.62	Q1LIL6 2-nonaprenyl-3-methyl-6-methoxy-1,4-benzoquinol hydroxylase
Op0947f	Rmet_3407	-	5.87	8.05	Q1LHU7 Glycosyl transferase, family 2
Op0947f	Rmet_3408	-	14.33	6.58	Q1LHU6 Radical SAM
Op0947f	Rmet_3409	-	12.20	4.92	Q1LHU5 YdjC-like protein
Op0947f	Rmet_3410	-	11.76	4.23	Q1LHU4 Putative uncharacterized protein
Op0948r	Rmet_3411	-	13.88	4.33	Q1LHU3 Uncharacterized protein UPF0065
Op0950r	Rmet_3430	-	2.00	10.45	Q1LHS4 UPF0102 protein Rmet_3430
Op0962r	Rmet_3456	-	2.91	5.45	Q1LHP8 Transcriptional regulator, MerR family
Op0970r	Rmet_3501	-	2.15	3.50	Q1LHK3 ATP synthase I chain
Op0975f	Rmet_3525	-	2.45	8.67	Q1LHH9 Heavy metal transport/detoxification protein
Op1008f	Rmet_3620	<i>degP</i>	118.07	8.38	Q1LH84 Peptidase degP, priplasmic protease
Op1008f	Rmet_3621	-	5.87	6.03	Q1LH83 Putative uncharacterized protein
Op1009r	Rmet_3622	-	2.10	2.44	Q1LH82 Major facilitator superfamily MFS_1
Op1025r	Rmet_3677	-	2.47	4.36	Q1LH27 Nucleoid protein H-NS
Op1040f	Rmet_3728	-	2.40	0.83	Q1LGX6 Acyl-CoA dehydrogenase-like protein
Op1064f	Rmet_3826	-	3.21	3.23	Q1LGN0 Putative uncharacterized protein
Op1091r	Rmet_3903	-	2.13	2.84	Q1LGF5 Putative uncharacterized protein

Op1092f	Rmet_3904	-	2.38	3.93	Q1LGF4 Putative serine protein kinase, PrkA
Op1092f	Rmet_3905	-	2.17	2.16	Q1LGF3 Putative uncharacterized protein
Op1092f	Rmet_3906	-	2.28	2.78	Q1LGF2 SpoVR
Op1132f	Rmet_4025	-	4.52	4.89	Q1LG33 Major facilitator superfamily MFS_1
Op1133r	Rmet_4026	-	25.48	6.52	Q1LG32 Putative periplasmic ligand-binding sensor protein
Op1134f	Rmet_4027	-	2.92	3.64	Q1LG31 Proline iminopeptidase
Op1134f	Rmet_4028	-	2.66	6.07	Q1LG30 Putative uncharacterized protein
Op1148f	Rmet_4084	<i>phoA1</i>	6.21	1.66	Q1LFX5 Alkaline phosphatase
Op1148f	Rmet_4085	<i>phoA2</i>	2.94	2.48	Q1LFX4 Alkaline phosphatase
Op1148f	Rmet_4086	-	2.66	2.98	Q1LFX3 Putative signal peptide protein
Op1199r	Rmet_4230	-	2.37	1.94	Q1LFI0 Two component transcriptional regulator, LuxR family
Op1202f	Rmet_4245	-	2.72	5.36	Q1LFG5 Transcriptional regulator, LysR family
#NV	Rmet_4246	#NV	2.51	4.85	Q1LFG4 Putative uncharacterized protein
Op1217r	Rmet_4284	-	2.10	5.27	Q1LFC6 Entericidin EcnAB
Op1219r	Rmet_4290	-	2.10	2.11	Q1LFC0 Transcriptional regulator, AraC family
Op1298f	Rmet_4537	<i>serA2</i>	2.74	3.57	Q1LEM4 D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding
Op1318f	Rmet_4583	-	2.24	3.76	Q1LEI1 Extracellular solute-binding protein, family 3
Op1320f	Rmet_4593	-	2.06	6.14	Q1LEH1 Polysaccharide deacetylase
Op1321r	Rmet_4594	<i>zntA</i>	15.61	7.79	Q1LEH0 Heavy metal translocating P-type ATPase
Op1322f	Rmet_4595	<i>czcI2</i>	4.28	6.74	Q1LEG9 Putative uncharacterized protein
Op1322f	Rmet_4596	<i>czcC2</i>	6.01	5.24	Q1LEG8 Outer membrane efflux protein
Op1322f	Rmet_4597	<i>czcB2'</i>	4.99	6.01	Q1LEG7 Secretion protein HlyD
Op1323r	Rmet_4598	-	3.66	3.14	B1LRU9 Tn3 family transposase
Op1398f	Rmet_4807	-	3.85	7.37	Q1LDV7 Putative uncharacterized protein
Op1409r	Rmet_4834	-	2.08	5.63	Q1LDT0 Porin, Gram-negative type
Op1412f	Rmet_4839	-	4.20	3.01	Q1LDS5 Transcriptional regulator, LacI family
Op1412f	Rmet_4840	-	2.52	4.30	Q1LDS4 Putative periplasmic solute-binding protein
Op1412f	Rmet_4841	-	2.40	3.49	Q1LDS3 Binding-protein-dependent transport systems inner membrane component
Op1412f	Rmet_4843	-	2.10	3.56	Q1LDS1 ABC transporter related
Op1452f	Rmet_4942	<i>gabD</i>	2.30	4.44	Q1LDH2 Succinate semialdehyde dehydrogenase
Op1469r	Rmet_5005	-	2.15	4.66	Q1LDA9 Isochorismatase hydrolase
Op1509r	Rmet_5122	<i>phaC3</i>	2.42	5.24	Q1LCZ5 Poly-beta-hydroxybutyrate polymerase-like protein

Op1509r	Rmet_5123	<i>phaB3</i>	2.23	8.42	Q1LCZ4 3-oxoacyl-[acyl-carrier-protein] reductase
Op1509r	Rmet_5124	-	2.49	7.74	Q1LCZ3 Putative uncharacterized protein
Op1540f	Rmet_5223	-	2.16	4.57	Q1LCP4 Putative uncharacterized protein
Op1571r	Rmet_5319	-	2.49	7.21	Q1LCE8 Heavy metal efflux pump CzcA
Op1571r	Rmet_5320	-	2.44	5.05	Q1LCE7 Secretion protein HlyD Q1LCE6 RND efflux system, outer membrane lipoprotein,
Op1572f	Rmet_5321	-	2.37	8.97	NodT
Op1573r	Rmet_5322	-	2.36	4.09	Q1LCE5 Sensor protein
Op1575r	Rmet_5324	-	2.45	1.32	Q1LCE3 Putative signal peptide protein
Op1576f	Rmet_5325	-	4.10	6.84	Q1LCE2 Putative uncharacterized protein Q1LCE1 Two component transcriptional regulator, winged
Op1576f	Rmet_5326	-	2.52	3.78	helix family
Op1576f	Rmet_5327	-	3.05	11.89	Q1LCE0 Sensor protein
Op1607r	Rmet_5395	-	2.22	2.09	Q1LC72 Putative uncharacterized protein
Op1620f	Rmet_5450	-	2.07	1.12	Q1LC17 Putative uncharacterized protein
Op1629r	Rmet_5485	-	2.84	6.55	Q1LBY2 Putative uncharacterized protein
Op1662f	Rmet_5582	-	2.16	12.21	Q1LBN5 Putative membrane protein
Op1695r	Rmet_5668	-	2.69	3.77	Q1LBE9 Copper resistance D
Op1695r	Rmet_5670	-	2.66	2.31	Q1LBE7 Copper resistance B Q1LBE5 Two component heavy metal response
Op1696f	Rmet_5672	<i>copR2</i>	2.18	2.52	transcriptional regulator, winged helix family
Op1696f	Rmet_5673	<i>copS2</i>	2.12	3.36	Q1LBE4 Sensor protein
Op1710f	Rmet_5716	-	2.65	7.02	Q1LBA1 Putative uncharacterized protein
Op1715r	Rmet_5728	-	2.39	0.49	Q1LB89 Glycosyl transferase, group 1
Op1718f	Rmet_5746	<i>furB</i>	2.05	1.15	Q1LB71 Ferric uptake regulator, Fur family
Op1747r	Rmet_5801	<i>zwf</i>	2.28	5.11	Q1LB16 Glucose-6-phosphate 1-dehydrogenase
Op1748f	Rmet_5802	<i>edd1</i>	2.61	3.82	Q1LB15 6-phosphogluconate dehydratase
Op1749r	Rmet_5803	-	2.90	7.40	Q1LB14 MscS Mechanosensitive ion channel
Op1755r	Rmet_5814	-	2.35	4.21	Q1LB03 Putative uncharacterized protein
Op1766f	Rmet_5846	-	2.11	3.74	Q1LAX1 Putative uncharacterized protein
Down-regulated genes					
Op0007f	Rmet_0025	-	-0.06	0.58	Q1LSG5 Putative uncharacterized protein
Op0019f	Rmet_0062	-	0.43	3.25	Q1LSC8 Putative uncharacterized protein

Op0019f	Rmet_0063	-	0.29	3.33	Q1LSC7 Allophanate hydrolase subunit 2
Op0019f	Rmet_0064	-	0.39	3.76	Q1LSC6 UPF0271 protein Rmet_0064
Op0019f	Rmet_0065	-	0.42	4.07	Q1LSC5 Putative uncharacterized protein
Op0019f	Rmet_0066	-	0.47	2.96	Q1LSC4 Putative uncharacterized protein
Op0019f	Rmet_0067	-	0.49	5.02	Q1LSC3 Pyroglutamyl-peptidase I. Cysteine peptidase. MEROPS family C15
Op0033f	Rmet_0130	-	0.27	11.54	Q1LS60 Uncharacterized protein UPF0065
Op0051f	Rmet_0170	<i>ahcY</i>	0.44	6.33	Q1LS20 Adenosylhomocysteinase
Op0051f	Rmet_0171	-	0.42	4.85	Q1LS19 Putative uncharacterized protein
Op0051f	Rmet_0173	-	0.48	2.82	Q1LS17 TfoX-like protein
Op0057f	Rmet_0188	-	0.38	2.47	Q1LS02 Pilus assembly protein
Op0057f	Rmet_0189	-	0.40	2.34	Q1LS01 Type-4 fimbrial biogenesis pilV transmembrane protein
Op0057f	Rmet_0190	-	0.39	2.17	Q1LS00 Type-4 fimbrial biogenesis transmembrane protein
Op0057f	Rmet_0191	-	0.36	3.49	Q1LRZ9 Putative type-4 fimbrial biogenesis transmembrane protein
Op0057f	Rmet_0192	-	0.45	3.40	Q1LRZ8 Putative type-4 fimbrial biogenesis pily1-related protein
Op0057f	Rmet_0193	-	0.45	3.66	Q1LRZ7 Pilus assembly protein PilE
Op0085f	Rmet_0294	-	0.36	3.29	Q1LRP6 Putative uncharacterized protein
Op0109f	Rmet_0400	<i>gltJ</i>	0.46	4.34	Q1LRE0 Amino acid ABC transporter, permease protein, 3-TM region, His/Glu/Gln/Arg/opine
Op0109f	Rmet_0402	<i>gltL</i>	0.48	4.44	Q1LRD8 ABC transporter-related protein
Op0140r	Rmet_0522	-	0.35	3.29	Q1LR18 Putative uncharacterized protein
Op0182r	Rmet_0657	-	-126.85	0.52	Q1LQN3 Putative membrane protein
Op0197f	Rmet_0700	<i>dadA2</i>	0.40	4.82	Q1LQJ0 FAD dependent oxidoreductase
Op0201f	Rmet_0709	-	0.42	3.94	Q1LQI1 Putative uncharacterized protein
Op0207f	Rmet_0733	-	-0.13	0.59	Q1LQF7 Histone deacetylase superfamily
Op0224r	Rmet_0789	-	0.00	0.58	Q1LQA1 Uncharacterized protein UPF0065
Op0256r	Rmet_0879	-	-0.29	0.53	Q1LQ11 Putative uncharacterized protein
Op0265f	Rmet_0920	-	0.47	3.03	Q1LPX0 Putative transporter signal peptide protein
Op0271f	Rmet_0970	<i>ggt</i>	0.41	4.88	Q1LPS0 Gamma-glutamyltransferase 1. Threonine peptidase. MEROPS family T03
Op0290r	Rmet_1011	-	0.05	0.58	Q1LPM9 Alpha/beta hydrolase fold

Op0321f	Rmet_1123	-	-0.56	0.59	Q1LPB7 Extracellular solute-binding protein, family 3
Op0340r	Rmet_1177	-	0.21	0.56	Q1LP63 Putative uncharacterized protein
Op0342r	Rmet_1184	-	0.49	3.80	Q1LP56 Uncharacterized protein UPF0065
Op0346r	Rmet_1195	-	0.49	2.91	Q1LP45 Sensor protein
Op0355f	Rmet_1225	-	0.35	17.27	Q1LP15 Alpha/beta hydrolase fold
Op0355f	Rmet_1226	-	0.41	6.03	Q1LP14 Extracellular ligand-binding receptor
Op0355f	Rmet_1227	-	0.34	10.81	Q1LP13 Inner-membrane translocator
Op0355f	Rmet_1228	-	0.45	4.52	Q1LP12 Inner-membrane translocator
Op0355f	Rmet_1229	<i>livG6</i>	0.48	4.22	Q1LP11 ABC transporter-related protein
Op0355f	Rmet_1231	-	0.46	6.90	Q1LP09 Probable potassium transport system protein kup
Op0370r	Rmet_1285	-	0.49	0.93	Q1LNV6 Hydrogenase accessory protein HypB
Op0427f	Rmet_1533	-	0.04	0.58	Q1LN60 High-affinity nickel-transporter
Op0450r	Rmet_1612	-	0.38	5.21	B2UH78 Integrase catalytic region
Op0455f	Rmet_1628	-	0.26	6.73	Q1LMW5 Porin, Gram-negative type
Op0456r	Rmet_1629	-	0.49	3.61	Q1LMW4 Glutathione-dependent formaldehyde-activating, GFA
Op0486r	Rmet_1720	-	0.15	0.54	Q1LMM5 Transcriptional regulator, lclR family
Op0538r	Rmet_1862	-	0.42	6.31	Q1LM85 Extracellular ligand-binding receptor
Op0568r	Rmet_1943	-	-2.10	0.64	Q1LM04 Secretion protein HlyD
Op0596r	Rmet_2052	<i>ugpC</i>	0.46	4.71	Q1LLP5 sn-glycerol-3-phosphate import ATP-binding protein ugpC
Op0596r	Rmet_2053	<i>ugpE</i>	0.47	2.10	Q1LLP4 Binding-protein-dependent transport systems inner membrane component
Op0596r	Rmet_2055	<i>ugpB</i>	0.49	9.43	Q1LLP2 Extracellular solute-binding protein, family 1
Op0630r	Rmet_2205	-	0.01	0.58	Q1LL92 Lytic transglycosylase, catalytic
Op0655f	Rmet_2294	-	0.01	0.58	Q8GQ06 Putative uncharacterized protein ORF C105
Op0680r	Rmet_2429	<i>fabD</i>	0.30	0.62	Q1LKM0 [Acyl-carrier-protein] S-malonyltransferase
Op0695f	Rmet_2515	-	0.49	2.93	Q1LKD4 L-lactate transport
Op0729f	Rmet_2605	-	0.01	0.58	Q1LK44 2-nitropropane dioxygenase, NPD
Op0775f	Rmet_2752	-	0.17	3.79	Q1LJQ1 Tripartite ATP-independent periplasmic transporter, DctQ component
Op0775f	Rmet_2753	-	0.22	4.79	Q1LJQ0 TRAP C4-dicarboxylate transport system permease DctM subunit
Op0806r	Rmet_2864	<i>livG2</i>	0.42	2.91	Q1LJD9 ABC transporter-related protein

Op0806r	Rmet_2865	<i>livM2</i>	0.36	3.94	Q1LJD8 Inner-membrane translocator
Op0806r	Rmet_2866	<i>livH2</i>	0.30	3.31	Q1LJD7 Inner-membrane translocator
Op0806r	Rmet_2867	<i>livK2</i>	0.34	6.86	Q1LJD6 Extracellular ligand-binding receptor
Op0813f	Rmet_2894	-	0.30	13.64	Q1LJA9 Cold-shock DNA-binding protein family
Op0879f	Rmet_3139	-	0.10	6.12	Q1LIL5 Putative uncharacterized protein
Op0881f	Rmet_3144	-	0.07	7.66	Q1LIL0 Porin, Gram-negative type
Op0900r	Rmet_3199	-	0.03	0.58	Q1LIF5 Conserved hypothetical transmembrane protein
Op0918r	Rmet_3234	-	0.33	10.96	Q1LIC0 Porin, Gram-negative type
Op0920r	Rmet_3262	<i>gltD</i>	0.39	8.85	Q1LI92 Glutamate synthase (NADH) small subunit
Op0920r	Rmet_3263	<i>gltB</i>	-1.98	0.36	Q1LI91 Glutamate synthase (NADH) large subunit
Op0920r	Rmet_3269	-	0.33	2.77	Q1LI85 Pilus assembly protein, PilQ
Op0920r	Rmet_3270	-	0.30	6.99	Q1LI84 Pilus assembly protein, PilO
Op0920r	Rmet_3271	-	0.32	2.26	Q1LI83 Fimbrial assembly
Op0920r	Rmet_3272	-	0.34	5.32	Q1LI82 Type IV pilus assembly protein PilM
Op0926r	Rmet_3309	<i>rpmC</i>	0.49	4.69	Q1LI45 50S ribosomal protein L29
Op0926r	Rmet_3313	<i>rpsS</i>	0.46	3.43	Q1LI41 30S ribosomal protein S19
Op0926r	Rmet_3318	-	-3.29	0.53	Q1LI36 Flavin reductase-like, FMN-binding
Op0941f	Rmet_3389	<i>gspL</i>	0.48	5.08	Q1LHW5 General secretion pathway L
Op0941f	Rmet_3390	<i>gspM</i>	0.44	6.68	Q1LHW4 General secretion pathway M protein
Op0941f	Rmet_3391	-	0.16	0.77	Q1LHW3 Type II secretion system protein N
Op0941f	Rmet_3392	<i>gspD</i>	0.50	4.62	Q1LHW2 Type II and III secretion system protein
Op0941f	Rmet_3393	<i>gspE</i>	0.44	5.87	Q1LHW1 Type II secretion system protein E (GspE)
Op0941f	Rmet_3394	<i>gspF</i>	0.39	5.46	Q1LHW0 General secretion pathway protein F
Op0974r	Rmet_3516	<i>livM5</i>	0.39	5.26	Q1LHI8 Inner-membrane translocator
Op0974r	Rmet_3517	<i>livH5</i>	0.26	7.25	Q1LHI7 Inner-membrane translocator
Op0974r	Rmet_3518	-	0.21	4.98	Q1LHI6 Extracellular ligand-binding receptor
Op0974r	Rmet_3519	<i>livF5</i>	0.40	6.93	Q1LHI5 ABC transporter-related protein
Op0974r	Rmet_3520	<i>livG5</i>	0.21	5.26	Q1LHI4 ABC transporter-related protein
Op0976r	Rmet_3526	-	0.29	5.52	Q1LHH8 OmpW
Op0983f	Rmet_3543	-	0.36	6.19	Q1LHG1 Twin-arginine translocation pathway signal
Op0985f	Rmet_3549	<i>tctC</i>	0.19	5.11	Q1LHF5 Uncharacterized protein UPF0065
Op0985f	Rmet_3550	<i>tctB</i>	0.26	5.34	Q1LHF4 Conserved hypothetical membrane protein
Op0985f	Rmet_3552	-	-0.06	0.58	Q1LHF2 Phenylacetic acid degradation-related protein
Op1026f	Rmet_3699	<i>flhA</i>	0.48	2.82	Q1LH05 Flagellar biosynthesis protein FlhA

Op1042f	Rmet_3734	<i>flgB</i>	0.42	4.19	Q1LGX0 Flagellar basal-body rod protein FlgB
Op1042f	Rmet_3735	<i>flgC</i>	0.44	3.30	Q1LGW9 Flagellar basal-body rod protein FlgC
Op1042f	Rmet_3736	<i>flgD</i>	0.44	3.80	Q1LGW8 Flagellar hook capping protein
Op1066f	Rmet_3836	-	0.41	6.85	Q1LGM0 Outer membrane efflux protein
Op1066f	Rmet_3837	-	0.36	5.76	Q1LGL9 Secretion protein HlyD
Op1066f	Rmet_3838	-	0.40	5.00	Q46VH3 Heavy metal efflux pump CzcA
Op1086f	Rmet_3894	-	0.35	4.68	Q1LGG4 Putative uncharacterized protein
Op1088f	Rmet_3900	-	0.38	1.90	Q1LGF8 Uncharacterized protein UPF0065
Op1095r	Rmet_3913	-	-0.08	0.58	Q1LGE5 Uncharacterized protein UPF0065
Op1115r	Rmet_3980	<i>livH4</i>	-0.02	0.57	Q1LG78 Inner-membrane translocator
Op1123r	Rmet_3998	-	-0.06	0.59	Q1LG60 Putative uncharacterized protein
Op1128f	Rmet_4019	<i>surE</i>	0.17	0.54	Q1LG39 Exopolyphosphatase / 3'-nucleotidase / 5'-nucleotidase
Op1184f	Rmet_4188	-	0.45	5.60	Q1LFM1 Transcriptional regulator, TetR family
Op1198f	Rmet_4222	-	0.47	12.52	Q1LFI7 Transcriptional regulator, lclR family
Op1219r	Rmet_4287	-	0.48	2.52	Q1LFC3 Rare lipoprotein A
Op1276f	Rmet_4477	<i>livM3</i>	0.37	4.54	Q1LET4 Inner-membrane translocator
Op1305r	Rmet_4549	<i>uvrA2</i>	0.19	0.56	Q1LEL2 UvrA family protein
Op1314f	Rmet_4564	<i>metE</i>	0.06	17.81	Q1LEK0 Methionine synthase (B12-independent)
Op1314f	Rmet_4565	-	0.25	1.22	Q1LEJ9 TonB-dependent receptor
Op1316f	Rmet_4575	-	0.38	1.19	Q1LEI9 Acyl-CoA dehydrogenase-like protein
Op1316f	Rmet_4576	-	0.02	0.58	Q1LEI8 Binding-protein-dependent transport systems inner membrane component
Op1325r	Rmet_4605	-	-0.11	0.59	Q1LEF9 Sensor protein
Op1362f	Rmet_4721	-	0.22	4.10	Q1LE43 Putative uncharacterized protein
Op1377r	Rmet_4749	-	0.32	4.21	Q46TY9 HU family DNA-binding protein
Op1396f	Rmet_4796	-	-2.33	0.68	Q1LDW8 Rhs element Vgr protein
Op1417r	Rmet_4857	-	0.00	0.58	Q1LDQ7 Putative uncharacterized protein
Op1431r	Rmet_4893	-	0.49	4.02	Q1LDM1 Putative uncharacterized protein
Op1446f	Rmet_4931	-	0.48	1.96	Q1LDI3 Uncharacterized protein UPF0065
Op1466f	Rmet_4994	-	0.16	5.62	Q1LDC0 Porin, Gram-negative type
Op1493r	Rmet_5073	<i>metE</i>	0.17	18.51	Q1LD41 Putative uncharacterized protein
Op1493r	Rmet_5074	-	0.15	10.79	Q1LD40 NADPH-dependent FMN reductase
Op1493r	Rmet_5075	<i>msuE1</i>	0.23	8.46	Q1LD39 Putative uncharacterized protein

Op1517r	Rmet_5152	-	<i>0.46</i>	0.77	Q1LCW5 Acyl-CoA dehydrogenase-like protein
Op1560f	Rmet_5288	-	0.24	7.17	Q1LCH9 Porin, Gram-negative type
Op1566f	Rmet_5297	-	0.44	1.73	Q1LCH0 Flagellar basal body-associated protein FliL
Op1566f	Rmet_5298	<i>fliM</i>	0.49	1.44	Q1LCG9 Flagellar motor switch protein FliM
Op1566f	Rmet_5299	<i>fliN</i>	0.48	1.96	Q1LCG8 Flagellar motor switch FliN
Op1709r	Rmet_5713	-	<i>0.49</i>	0.88	Q1LBA4 Hpt domain protein
Op1719r	Rmet_5748	-	<i>0.00</i>	0.58	Q1LB69 Putative uncharacterized protein
Op1740f	Rmet_5785	-	<i>-0.06</i>	0.57	Q1LB32 Putative uncharacterized protein
Op1750f	Rmet_5807	-	<i>-0.01</i>	0.58	Q1LB10 TonB-dependent siderophore receptor
Op1759r	Rmet_5821	-	<i>-0.04</i>	0.58	Q1LAZ6 Putative integrase/recombinase protein
Op1778f	Rmet_5877	-	0.25	4.22	Q1LAU0 Extracellular ligand-binding receptor
Op1792f	Rmet_5907	-	<i>-0.01</i>	0.58	Q1LAR0 Putative uncharacterized protein

^aCells of strain AE104 was confronted with 100 μ M zinc chloride for 10 min or not, RNA was isolated, reversely transcribed, labeled and hybridized against a CH34-specific gene array. Provided are the Q-ratios \pm Zn for, red if at least 2-fold down-regulated, green up, bold-faced letters indicate significant differences, letters in italics not significant differences. The D-value for each comparison is also given. This is the distance of both mean values divided by the sum of both deviations. If $D > 1$ (the deviation bars do not touch or overlap) the data points are different with a probability in the t-test of $> 95\%$. Three biological repeats. Genes in operon regions or adjacent operon regions are in a box. Regions with a gene up- or down-regulated at least four-fold are on a green ground. A yellow ground indicates genes of interest, e.g. hydrogenase genes.

Supplementary Table S4. Genes specifically up- or down-regulated in the comparison $\Delta zupT/$ AE104 under EDTA and/or zinc stress^a.

Locus		Q($\Delta zupT/$ AE104)					Description
Rmet	Gene	Region ^b	Q(Zn)	D(Zn)	Q(EDTA)	D(EDTA)	
Q(EDTA)≥2							
Q(EDTA)≥2, Q(Zn)≤0.5.							
Rmet_1098		Op0317f	0.48	2.94	17.91	16.54	Q1LPE2 Cobalamin synthesis protein, P47K
Rmet_1099		Op0317f	0.35	3.02	22.52	52.14	Q1LPE1 UPF0343 protein Rmet_1099
Rmet_1100	<i>cysS</i>	Op0317f	0.46	2.29	21.00	6.82	Q1LPE0 Cysteinyl-tRNA synthetase
Rmet_1101		Op0317f	0.49	2.84	14.38	4.34	Q1LPD9 6-pyruvoyl-tetrahydropterin synthase-like protein Q1LPD8 Carbonic anhydrases/acetyltransferase isoleucine
Rmet_1102		Op0317f	0.40	1.69	15.38	3.83	patch superfamily
Rmet_1103	<i>allB</i>	Op0317f	0.49	3.91	13.61	6.60	Q1LPD7 Dihydroorotase
Rmet_1104		Op0318r	0.42	4.33	3.35	8.54	Q1LPD6 TonB-dependent siderophore receptor Q58AN1 Mercury regulatory protein (Transcriptional
Rmet_5990		Op1825r	0.50	1.67	2.83	0.37	regulator, MerR family)
Q(EDTA)≥2, Q(Zn)≥2.							
CMGI-3							
Rmet_1499	<i>cbbQ</i>	Op0422r	2.08	5.54	3.15	1.89	Q1LN94 ATPase associated with various cellular activities, AAA_5
Rmet_1502		Op0423f	4.28	6.65	3.05	2.66	Q1LN91 Transcriptional regulator, LysR family
Rmet_1511	<i>cbbF2</i>	Op0425f	4.16	11.31	2.61	1.65	Q1LN82 D-fructose 1,6-bisphosphatase
Rmet_1521	<i>cbbI1</i>	Op0425f	3.22	3.39	2.87	1.20	Q1LN72 Ribose-5-phosphate isomerase Q1LN71 Respiratory-chain NADH dehydrogenase domain,
Rmet_1522	<i>hoxF</i>	Op0425f	4.18	2.94	2.84	3.46	51 kDa subunit
Rmet_1523	<i>hoxU</i>	Op0425f	6.99	4.38	5.85	1.59	Q1LN70 Ferredoxin
Rmet_1524	<i>hoxY</i>	Op0425f	8.81	3.62	6.85	1.37	Q1LN69 NADH ubiquinone oxidoreductase, 20 kDa subunit
Rmet_1525	<i>hoxH</i>	Op0425f	7.85	2.73	6.77	1.57	Q1LN68 Nickel-dependent hydrogenase, large subunit
Rmet_1526		Op0425f	8.57	3.55	6.44	1.80	Q1LN67 HoxW protein Q1LN66 Cyclic nucleotide-binding domain (CNMP-BD)
Rmet_1527		Op0425f	8.67	2.67	5.70	1.55	protein
Rmet_1528		Op0425f	4.17	3.70	2.38	1.84	Q1LN65 Alanine dehydrogenase/PNT-like protein
Rmet_1533		Op0427f	7.24	3.20	4.85	1.55	Q1LN60 High-affinity nickel-transporter

Rmet_1534	Op0427f	11.16	3.60	4.92	2.68	Q1LN59 Putative uncharacterized protein
Rmet_1535	Op0427f	11.88	9.49	5.14	3.42	Q1LN58 Hydrogenase nickel insertion protein HypA
Rmet_1536	Op0427f	10.59	14.26	5.67	5.50	Q1LN57 Hydrogenase accessory protein HypB
Rmet_1537	Op0427f	9.31	7.74	4.98	1.85	Q1LN56 (NiFe) hydrogenase maturation protein HypF
Rmet_1538	Op0427f	8.36	7.75	4.24	4.77	Q1LN55 Hydrogenase assembly chaperone hypC/hupF
Rmet_1539	Op0427f	11.50	8.31	4.80	4.21	Q1LN54 Hydrogenase expression/formation protein HypD
Rmet_1540	Op0427f	11.83	11.02	5.08	7.40	Q1LN53 Hydrogenase expression/formation protein HypE
Rmet_1541	Op0427f	10.76	6.95	4.83	6.55	Q1LN52 Formyl transferase-like protein
Rmet_1542	Op0427f	10.37	7.28	4.64	3.71	Q1LN51 Response regulator receiver domain protein (CheY-like)

Rmet_6333	Op1926f	5.76	2.73	3.91	5.94	Q1L9I4 Transposase Tn3 Q5NUU5 Hypothetical general secretion pathway protein A
Rmet_6338	Op1926f	3.57	2.82	2.72	3.74	(ATPase) (

Q(EDTA)≥2, Q(Zn) unchanged.

CMGI-3						
Rmet_1498	Op0422r	1.69	1.34	2.27	3.81	Q1LN95 von Willebrand factor, type A
Rmet_1517	Op0425f	1.66	1.01	2.51	1.70	Q1LN76 HAD-superfamily hydrolase subfamily IA, variant 3
Rmet_3842	Op1067r	1.46	0.35	3.02	0.55	Q1LGL6 Putative uncharacterized protein

Q(EDTA)≤0.5

Q(EDTA)≤0.5, Q(Zn)≥2.

CMGI-1						
Rmet_2305	Op0659f	2.34	0.83	0.49	0.48	Q8GQ16 Putative uncharacterized protein ORF C95

Q(EDTA)≤0.5, Q(Zn)≤0.5.

Rmet_0005	Op0002r	0.45	2.21	0.42	4.29	Q1LSI5 Twin-arginine translocation pathway signal
Rmet_0007	Op0002r	0.43	2.79	0.46	5.65	Q1LSI3 Transcriptional regulator, AraC family
Rmet_0022	Op0004r	0.44	2.07	0.21	10.68	Q1LSG8 Transcriptional regulator, AraC family
Rmet_0086	Op0024r	0.50	3.60	0.48	4.36	Q1LSA4 Rhodanese-like protein
Rmet_0092	Op0026r	0.33	1.83	0.12	11.12	Q1LS98 Histidine kinase
Rmet_0093	Op0027f	0.48	1.40	0.26	1.94	Q1LS97 UPF0391 membrane protein Rmet_0093
Rmet_0094	Op0027f	0.44	1.64	0.29	2.26	Q1LS96 Putative uncharacterized protein
Rmet_0095	Op0028r	0.33	1.43	0.14	4.68	Q1LS95 Putative uncharacterized protein
Rmet_0097	Op0029f	0.47	4.00	0.47	2.56	Q1LS93 Sporulation related
Rmet_0123	Op0032r	0.44	1.64	0.48	2.39	Q1LS67 TonB-dependent receptor
Rmet_0156	metK Op0045f	0.48	4.19	0.49	2.57	Q1LS34 S-adenosylmethionine synthetase

Rmet_0157	Op0045f	0.44	2.69	0.44	2.47	Q1LS33 Putative uncharacterized protein
Rmet_0160	Op0048r	0.40	2.26	0.41	4.85	Q1LS30 Methyl-accepting chemotaxis sensory transducer
CMGI-7						
Rmet_0320	Op0092r	0.46	2.26	0.41	7.60	Q5NUU5 Hypothetical general secretion pathway protein A (ATPase)
Rmet_0361	Op0102r	0.45	1.65	0.48	1.24	Q1LRH9 VWA containing CoxE-like protein Q1LRH6 Xanthine dehydrogenase, molybdenum binding subunit apoprotein
Rmet_0364	Op0102r	0.39	1.42	0.19	10.43	
Rmet_0366	Op0103f	0.42	2.76	0.34	7.49	Q1LRH4 Putative membrane protein Q1LRG8 Import inner membrane translocase, subunit
Rmet_0372	Op0103f	0.48	4.02	0.37	4.49	Tim44
Rmet_0393	Op0107f	0.44	1.26	0.48	2.93	Q1LRE7 ABC transporter-related protein
Rmet_0409	Op0112r	0.38	2.03	0.26	8.26	Q1LRD0 50S ribosomal protein L13
Rmet_0410	<i>rplM</i> Op0113f	0.49	2.50	0.44	2.05	Q1LRC9 30S ribosomal protein S9
Rmet_0412	Op0113f	0.49	2.38	0.48	2.86	Q1LRC7 Putative uncharacterized protein
Rmet_0457	Op0119f	0.34	1.72	0.43	1.75	Q1LR83 Aminoglycoside phosphotransferase
Rmet_0483	Op0129f	0.42	1.93	0.42	5.41	Q1LHY9 Integrase, catalytic region
Rmet_0485	Op0129f	0.43	3.18	0.49	10.00	Q1LR55 Putative uncharacterized protein Q1LQY9 Hycolysin. Metallo peptidase. MEROPS family
Rmet_0551	Op0153f	0.48	3.37	0.50	3.67	M30
Rmet_0585	Op0165f	0.38	5.16	0.44	4.90	Q1LQV5 Amidinotransferase
Rmet_0586	<i>arcB</i> Op0165f	0.45	2.06	0.38	4.46	Q1LQV4 Ornithine cyclodeaminase
Rmet_0650	Op0180r	0.27	1.02	0.48	2.59	Q1LQP0 Peptidase A24A, prepilin type IV
Rmet_0651	Op0180r	0.38	4.44	0.50	5.38	Q1LQN9 Flp/Fap pilin component
Rmet_0652	Op0180r	0.32	2.96	0.43	5.86	Q1LQN8 Flp/Fap pilin component
Rmet_0671	<i>pill</i> Op0187f	0.40	6.26	0.48	2.39	Q1LQL9 CheW protein
Rmet_0744	Op0210r	0.46	1.06	0.39	8.88	Q1LQE6 TM2
Rmet_0745	Op0211f	0.34	0.96	0.30	8.89	Q1LQE5 Putative uncharacterized protein
Rmet_0751	<i>rplS</i> Op0213f	0.49	3.93	0.41	5.29	Q1LQD9 50S ribosomal protein L19
Rmet_0795	Op0226r	0.25	1.21	0.42	14.87	Q1LQ95 Inner-membrane translocator Q1LQ88 Glycine betaine/L-proline transport ATP binding subunit
Rmet_0802	Op0227f	0.38	2.41	0.38	4.39	
Rmet_0803	Op0228r	0.34	2.42	0.25	3.36	Q1LQ87 Putative uncharacterized protein
Rmet_0804	Op0228r	0.15	1.81	0.08	12.37	Q1LQ86 SPFH domain, Band 7 family protein

Rmet_0805	Op0228r	0.21	2.04	0.12	8.89	Q1LQ85 Putative uncharacterized protein
Rmet_0816	Op0230r	0.47	2.59	0.45	8.60	Q1LQ74 Putative transmembrane protein
Rmet_0817	Op0230r	0.46	1.56	0.34	10.80	Q1LQ73 Putative uncharacterized protein
Rmet_0821	Op0232r	0.35	3.56	0.47	4.74	Q1LQ69 Phenazine biosynthesis PhzC/PhzF protein
Rmet_0861	Op0247f	0.48	13.87	0.45	4.28	Q1LQ29 Putative uncharacterized protein
Rmet_0863	Op0248r	0.41	2.45	0.14	14.25	Q1LQ27 Putative uncharacterized protein
Rmet_0864	Op0249f	0.18	1.52	0.16	6.21	Q1LQ26 Putative uncharacterized protein
Rmet_0865	Op0249f	0.14	1.84	0.16	8.21	Q1LQ25 Putative uncharacterized protein
Rmet_0872	Op0253f	0.47	1.61	0.46	2.26	Q1LQ18 Putative uncharacterized protein
						Q1LQ17 Response regulator receiver domain protein
Rmet_0873	Op0253f	0.46	2.70	0.46	6.18	(CheY-like)
Rmet_0880	Op0256r	0.47	3.15	0.49	4.29	Q1LQ10 Porin, gram-negative type
Rmet_0930	<i>nuoD</i> Op0267f	0.37	7.21	0.36	5.74	Q1LPW0 NADH dehydrogenase I, D subunit
Rmet_0933	<i>nuoG</i> Op0267f	0.50	3.46	0.42	8.79	Q1LPV7 NADH-quinone oxidoreductase
Rmet_0934	<i>nuoH</i> Op0267f	0.37	2.34	0.37	1.90	Q1LPV6 NADH-quinone oxidoreductase subunit H
Rmet_1026	Op0295f	0.49	2.52	0.41	9.40	Q1LPL4 FeS cluster assembly scaffold IscU
Rmet_1141	Op0326r	0.34	2.35	0.29	6.69	Q1LP99 Transcriptional regulator, GntR family
Rmet_1142	Op0327f	0.36	2.67	0.44	2.59	Q1LP98 Type IV pilus assembly PilZ
Rmet_1161	Op0333f	0.35	2.02	0.48	6.04	Q1LP79 Translation initiation factor IF-3
Rmet_1215	Op0353f	0.48	3.49	0.34	4.32	Q1LP25 Putative uncharacterized protein

CMGI-2

Rmet_1251	Op0362r	0.44	2.23	0.30	3.88	Q1LNY9 Putative uncharacterized protein
Rmet_1301	Op0373f	0.32	2.93	0.19	4.85	Q1LNW1 Integrase, catalytic region
Rmet_1436	<i>tsf</i> Op0403f	0.34	11.22	0.43	3.43	Q1LNF7 Elongation factor Ts

CMGI-3

Rmet_1465	Op0411f	0.47	2.16	0.34	3.41	Q1LNC8 Phage integrase
Rmet_1469	Op0412r	0.44	1.96	0.30	12.12	Q1LNC4 TatD-related deoxyribonuclease
Rmet_1567	Op0432r	0.35	4.21	0.45	4.52	Q1LN26 Transcriptional regulator, TetR family
Rmet_1571	Op0433f	0.42	2.23	0.43	2.76	Q1LN22 Putative uncharacterized protein
Rmet_1573	Op0433f	0.39	2.17	0.32	5.39	Q1LN20 tRNA-adenosine deaminase
						Q46NG6 General substrate transporter:Major facilitator
Rmet_1728	Op0489f	0.40	2.25	0.31	3.54	superfamily MFS_1
Rmet_1932	Op0565f	0.42	2.70	0.39	4.55	Q1LM15 Extracellular solute-binding protein, family 5
Rmet_1936	Op0565f	0.38	2.05	0.34	7.08	Q1LM11 Oligopeptide/dipeptide ABC transporter, ATP-

Rmet_1954	<i>ispD</i>	Op0572r	0.37	1.02	0.49	2.61	binding protein Q1LLZ3 2-C-methyl-D-erythritol 4-phosphate cytidyltransferase
Rmet_2067		Op0600r	0.48	5.60	0.48	5.33	Q1LLN0 Polysaccharide deacetylase
Rmet_2081		Op0601f	0.42	4.26	0.48	3.09	Q1LLL6 Transcriptional regulator, AsnC family
Rmet_2131		Op0614r	0.48	2.69	0.36	5.04	Q1LLG6 DNA helicase/exodeoxyribonuclease V, subunit A
Rmet_2155		Op0621f	0.31	2.24	0.37	4.31	Q1LLE2 Cytochrome c, class I
Rmet_2214		Op0634r	0.42	4.28	0.41	3.24	Q1LL83 Putative uncharacterized protein
Rmet_2218		Op0635f	0.29	2.30	0.18	11.21	Q1LL79 Luciferase-like protein
Rmet_2230		Op0638r	0.41	2.26	0.42	4.71	Q1LL67 Putative integral membrane protein Q1LL66 ABC transport systems inner membrane
Rmet_2231		Op0638r	0.24	3.11	0.19	18.42	component Q1LL65 ABC transport systems inner membrane
Rmet_2232		Op0638r	0.37	1.97	0.46	2.60	component

CMGI-1

Rmet_2271		Op0649f	0.48	5.00	0.42	11.21	Q1LL26 Putative uncharacterized protein
Rmet_2325		Op0661f	0.36	1.52	0.49	1.45	Q1LKX4 Putative uncharacterized protein
Rmet_2331	<i>pilL</i>	Op0661f	0.42	3.09	0.50	1.67	Q1LKW8 Putative secreted protein
Rmet_2332		Op0661f	0.39	2.38	0.41	3.13	Q8GQ41 Putative uncharacterized protein ORF C69
Rmet_2337		Op0661f	0.48	2.04	0.44	5.43	A3LCI0 Putative uncharacterized protein
Rmet_2343		Op0662r	0.39	1.49	0.25	16.58	Q8GQ53 Putative uncharacterized protein ORF C57
Rmet_2344		Op0662r	0.47	1.91	0.27	6.66	Q8GQ54 Putative excisionase
Rmet_2346		Op0663f	0.46	1.41	0.49	2.88	Q8GQ56 Putative uncharacterized protein ORF C54
Rmet_2349		Op0663f	0.30	3.19	0.31	4.02	Q8GQ59 Putative uncharacterized protein ORF C51
Rmet_2350		Op0663f	0.34	1.12	0.39	5.92	Q8GQ60 Putative uncharacterized protein ORF C50
Rmet_2352		Op0663f	0.39	2.56	0.45	1.65	Q8GQ62 Putative uncharacterized protein ORF C48
Rmet_2354		Op0663f	0.31	1.06	0.41	1.97	Q8GQ64 Putative uncharacterized protein ORF C46
Rmet_2355		Op0663f	0.43	2.00	0.47	3.06	Q8GQ65 Putative DNA repair protein RadC
Rmet_2356		Op0663f	0.41	2.55	0.38	4.28	Q8GQ66 Putative uncharacterized protein ORF C44
Rmet_2357		Op0663f	0.30	1.18	0.50	2.85	Q8GQ67 Putative uncharacterized protein ORF C43
Rmet_2358		Op0663f	0.36	3.55	0.42	3.93	Q8GQ68 Putative uncharacterized protein ORF C42
Rmet_2359		Op0663f	0.43	2.06	0.39	5.88	Q8GQ69 Putative uncharacterized protein ORF C41
Rmet_2360		Op0663f	0.35	8.03	0.25	4.86	Q8GQ70 Putative uncharacterized protein ORF C40
Rmet_2361		Op0664r	0.30	1.22	0.26	6.05	Q8GQ71 Putative uncharacterized protein ORF C39

Rmet_2362	Op0664r	0.18	1.48	0.08	17.80	Q8GQ72 Putative uncharacterized protein ORF C38
Rmet_2363	Op0664r	0.47	1.46	0.27	5.37	Q8GQ73 Putative uncharacterized protein ORF C37
Rmet_2369	Op0668r	0.39	2.99	0.33	4.38	Q8GQ79 Similar to metabolite transport protein
Rmet_2370	Op0669f	0.45	4.94	0.42	3.99	Q8GQ80 Putative transcriptional activator
Rmet_2371	Op0669f	0.44	1.76	0.47	3.60	Q8GQ81 Putative uncharacterized protein ORF C29
Rmet_2503	Op0694r	0.49	1.97	0.47	1.67	Q1LKE6 Glucose-methanol-choline oxidoreductase
Rmet_2525	Op0698r	0.46	1.98	0.49	3.55	Q1LKC4 AMP-dependent synthetase and ligase
Rmet_2548	Op0707f	0.44	2.10	0.46	1.86	Q1LKA1 Putative uncharacterized protein
Rmet_2619	Op0733f	0.36	3.54	0.48	5.41	Q1LK30 Putative uncharacterized protein
Rmet_2621 <i>zupT</i>	Op0734r	0.20	5.50	0.23	4.42	Q1LK28 Zinc/iron permease
Rmet_2647	Op0748r	0.27	1.65	0.20	5.04	Q1LK02 Transcriptional regulator, AsnC family Q0K7X0 Signal transduction protein containing PAS, GGDEF and EAL domains
Rmet_2658	Op0754r	0.36	2.53	0.22	23.80	
Rmet_2683	Op0757f	0.45	1.44	0.28	6.31	Q1LJX0 Putative transmembrane protein
Rmet_2686	Op0757f	0.40	2.81	0.35	3.41	Q1LJW7 Pilus assembly protein PilE
Rmet_2687	Op0757f	0.27	3.91	0.26	5.16	Q1LJW6 Pilus assembly protein Fim
Rmet_2758 <i>fdhC</i>	Op0776r	0.47	2.76	0.48	3.61	Q1LJP5 Formate dehydrogenase gamma subunit Q1LJM5 Adenosylcobyrinic acid synthase (Glutamine- hydrolysing)
Rmet_2778 <i>cobQ</i>	Op0782r	0.43	3.43	0.49	6.67	
Rmet_2780 <i>cobD</i>	Op0783f	0.48	2.14	0.48	4.80	Q1LJM3 Adenosylcobinamide-phosphate synthase
Rmet_2798	Op0786r	0.40	2.01	0.37	6.69	Q1LJK5 Transcriptional regulator, GntR family
Rmet_2802	Op0788r	0.23	0.68	0.48	3.85	Q1LJK1 Prolipoprotein diacylglyceryl transferase
CMGI-5						
Rmet_2825	Op0795f	0.42	3.69	0.45	8.97	Q1LJH8 Plasmid encoded RepA protein
Rmet_2826	Op0795f	0.48	1.70	0.46	7.64	Q1LJH7 Putative uncharacterized protein Q1LJH6 Putative TraY/DotA-like type IV secretion system protein
Rmet_2827	Op0795f	0.37	3.22	0.35	19.84	
Rmet_2858	Op0804r	0.45	3.36	0.47	2.97	Q1LJE5 ABC transport systems inner membrane component
Rmet_2859	Op0804r	0.49	1.21	0.49	3.76	Q1LJE4 Substrate-binding region of ABC-type glycine betaine transporter s
Rmet_2876	Op0808r	0.20	1.56	0.09	30.50	Q1LJC7 MscS Mechanosensitive ion channel
Rmet_2883	Op0811f	0.49	4.31	0.45	2.37	Q1LJC0 RNA-directed DNA polymerase
Rmet_2898	Op0815f	0.44	3.45	0.50	2.01	Q1LJA5 Putative uncharacterized protein

Rmet_2921	Op0826r	0.49	3.29	0.50	3.59	Q1LJ82 Chaperone protein dnaJ
Rmet_3086	Op0869f	0.33	4.07	0.09	2.82	Q1LIR8 Uncharacterized protein UPF0065
Rmet_3087	<i>nrdB</i> Op0870r	0.40	2.00	0.15	27.29	Q1LIR7 Ribonucleotide reductase
Rmet_3092	Op0870r	0.50	2.08	0.40	11.96	Q1LIR2 Putative uncharacterized protein
Rmet_3093	Op0870r	0.48	2.88	0.35	4.61	Q1LIR1 Cytochrome c assembly protein
Rmet_3097	Op0872r	0.46	1.19	0.35	11.52	Q1LIQ7 Putative uncharacterized protein
Rmet_3158	Op0884r	0.36	1.33	0.46	3.46	Q1LIJ6 Extracellular solute-binding protein, family 5
Rmet_3169	Op0890r	0.48	2.43	0.48	8.29	Q1LI5 Cytochrome d1, heme region
Rmet_3187	Op0896r	0.41	1.52	0.49	3.40	Q1LIG7 Putative uncharacterized protein
Rmet_3188	Op0896r	0.43	2.78	0.34	4.17	Q1LIG6 Peptidase M61
Rmet_3206	Op0902r	0.41	1.44	0.39	3.20	Q1LIE8 Putative uncharacterized protein
Rmet_3213	Op0906r	0.43	2.41	0.40	3.85	Q1LIE1 Cl-channel, voltage gated
Rmet_3344	Op0931f	0.46	2.59	0.43	5.17	Q1LI10 Putative membrane protein
Rmet_3345	Op0931f	0.45	3.10	0.29	5.63	Q1LI09 Putative uncharacterized protein
CMGI-10						
Rmet_3358	Op0935f	0.24	1.61	0.13	10.22	Q1LHZ6 Putative uncharacterized protein
Rmet_3359	Op0935f	0.14	1.77	0.11	5.64	Q1LHZ5 UBA/THIF-type NAD/FAD binding fold
Rmet_3360	Op0935f	0.36	1.98	0.17	7.63	Q1LHZ4 Putative uncharacterized protein
Rmet_3361	Op0935f	0.26	1.91	0.19	7.91	Q1LHZ3 Putative uncharacterized protein
Rmet_3362	Op0935f	0.27	1.43	0.19	6.47	Q1LHZ2 Putative uncharacterized protein
Rmet_3363	Op0936r	0.48	1.69	0.48	3.96	Q1LHZ1 Putative uncharacterized protein
Rmet_3365	Op0936r	0.14	1.46	0.12	12.82	Q1LHY9 Integrase, catalytic region
Rmet_3366	Op0936r	0.49	1.40	0.43	3.74	Q1LHY8 Putative uncharacterized protein
Rmet_3369	Op0937f	0.43	2.08	0.43	7.71	Q1LHY5 Phenylacetate-CoA oxygenase, PaaG subunit
Rmet_3370	Op0937f	0.42	2.79	0.44	6.31	Q1LHY4 Phenylacetic acid degradation B
Rmet_3372	Op0937f	0.32	3.40	0.34	2.72	Q1LHY2 Phenylacetate-CoA oxygenase, PaaJ subunit
Rmet_3382	Op0940r	0.41	1.75	0.38	4.14	Q1LHX2 Globin
Rmet_3594	Op1000r	0.33	2.33	0.30	3.95	Q1LHB0 Putative lipoprotein transmembrane
Rmet_3619	Op1007r	0.38	2.49	0.18	4.63	Q1LH85 Transcriptional regulator, MarR family
Rmet_3623	Op1009r	0.42	2.38	0.28	6.46	Q1LH81 Transcriptional regulator, MarR family
Rmet_3625	Op1009r	0.16	1.89	0.12	20.09	Q1LH79 Putative uncharacterized protein
Rmet_3628	Op1011r	0.48	1.30	0.27	7.98	Q1LH76 Putative uncharacterized protein
Rmet_3681	<i>cheW</i> Op1026f	0.45	2.74	0.35	5.09	Q1LH23 CheW protein
Rmet_3682	<i>aer</i> Op1026f	0.42	2.20	0.43	1.64	Q1LH22 Methyl-accepting chemotaxis sensory transducer,

						Pas/Pac sensor
Rmet_3684		Op1026f	0.42	3.74	0.37	1.62 Q1LH20 Putative uncharacterized protein
Rmet_3691	<i>cheR</i>	Op1026f	0.46	1.69	0.46	5.78 Q1LH13 MCP methyltransferase, CheR-type Q1LH11 Chemotaxis response regulator protein-glutamate
Rmet_3693	<i>cheB1</i>	Op1026f	0.46	3.08	0.48	3.73 methylesterase 1
Rmet_3698	<i>flhB</i>	Op1026f	0.42	2.75	0.49	3.16 Q1LH06 Flagellar biosynthetic protein FlhB
Rmet_3701	<i>flhG</i>	Op1026f	0.35	4.08	0.39	4.03 Q1LH03 Flagellar biosynthesis protein FlhG
Rmet_3702	<i>fliA</i>	Op1026f	0.24	0.89	0.45	3.48 Q1LH02 RNA polymerase sigma factor
Rmet_3735	<i>flgC</i>	Op1042f	0.48	0.96	0.33	4.10 Q1LGW9 Flagellar basal-body rod protein FlgC
Rmet_3736	<i>flgD</i>	Op1042f	0.47	3.08	0.40	3.34 Q1LGW8 Flagellar hook capping protein
Rmet_3737	<i>flgE</i>	Op1042f	0.49	2.10	0.46	2.93 Q1LGW7 Putative uncharacterized protein
Rmet_3738	<i>flgF</i>	Op1042f	0.44	2.01	0.35	3.15 Q1LGW6 Flagellar basal-body rod FlgF
Rmet_3741	<i>flgI</i>	Op1042f	0.49	2.33	0.44	4.47 Q1LGW3 Flagellar P-ring protein
Rmet_3744	<i>flgL</i>	Op1042f	0.44	1.39	0.38	5.63 Q1LGW0 Flagellin-like protein
Rmet_3820		Op1062f	0.42	1.86	0.39	2.31 Q1LGN6 Putative cytochrome p450 oxidoreductase
Rmet_3826		Op1064f	0.38	1.52	0.46	1.85 Q1LGN0 Putative uncharacterized protein
Rmet_3832		Op1065r	0.45	2.61	0.34	7.83 Q1LGM4 Uncharacterized protein UPF0065
Rmet_3979	<i>livM4</i>	Op1115r	0.24	1.16	0.47	5.92 Q1LG79 Inner-membrane translocator
Rmet_4009		Op1125r	0.38	4.28	0.50	2.32 Q1LG49 Putative uncharacterized protein
Rmet_4010	<i>aroK</i>	Op1125r	0.47	2.58	0.49	9.25 Q1LG48 Shikimate kinase
Rmet_4029		Op1135r	0.45	2.38	0.49	3.48 Q1LG29 MscS Mechanosensitive ion channel
Rmet_4033		Op1137r	0.44	1.36	0.48	4.65 Q1LG25 Transcriptional regulator, LysR family
Rmet_4054		Op1141r	0.43	3.61	0.50	4.40 Q1LG04 Cytochrome C biogenesis protein
Rmet_4084	<i>phoA1</i>	Op1148f	0.34	2.25	0.46	2.38 Q1LFX5 Alkaline phosphatase
Rmet_4121		Op1160f	0.35	1.55	0.45	2.11 Q1LFT8 Secretion protein HlyD
Rmet_4123		Op1162f	0.34	2.17	0.35	18.41 Q1LFT6 Heavy metal efflux pump CzcA
Rmet_4128		Op1164f	0.33	2.29	0.19	3.70 Q1LFT1 Putative uncharacterized protein
Rmet_4134	<i>pdhA</i>	Op1165r	0.09	0.62	0.46	4.56 Q1LFS5 Dehydrogenase, E1 component
Rmet_4135		Op1165r	0.39	3.34	0.39	4.61 Q1LFS4 Putative uncharacterized protein
Rmet_4136	<i>tauD</i>	Op1166f	0.47	4.50	0.42	7.90 Q1LFS3 Taurine catabolism dioxygenase TauD/TfdA
Rmet_4157		Op1170f	0.29	0.98	0.49	5.12 Q1LFQ2 Putative lipoprotein
Rmet_4159		Op1170f	0.37	6.65	0.48	2.85 Q1LFQ0 Putative transmembrane protein
Rmet_4173		Op1175r	0.22	0.98	0.45	6.32 Q1LFN6 Putative uncharacterized protein
Rmet_4198		Op1190f	0.44	2.35	0.26	3.45 Q1LFL1 Transcriptional regulator, PadR family

Rmet_4203		Op1192f	0.45	1.49	0.47	3.80	Q1LFK6 Uncharacterized protein UPF0065
Rmet_4204		Op1192f	0.44	3.27	0.39	15.12	Q1LFK5 LmbE-like protein
Rmet_4218		Op1197r	0.36	3.01	0.33	26.42	Q1LFJ1 Lysine exporter protein (LYSE/YGGA)
Rmet_4279		Op1215r	0.47	1.97	0.49	1.67	Q1LFD1 Fusaric acid resistance protein conserved region
Rmet_4283		Op1217r	0.31	0.77	0.50	5.24	Q1LFC7 Putative uncharacterized protein
Rmet_4350		Op1239r	0.39	1.63	0.47	2.91	Q1LF61 UvrD/REP helicase family protein
Rmet_4351		Op1240f	0.46	8.25	0.35	4.00	Q1LF60 Putative uncharacterized protein Q1LF50 L-carnitine dehydratase/bile acid-inducible protein
Rmet_4361		Op1244f	0.43	2.69	0.48	3.89	F
Rmet_4369		Op1246f	0.33	2.23	0.34	3.98	Q1LF42 Major facilitator superfamily MFS_1
Rmet_4414		Op1257r	0.42	1.08	0.50	11.45	Q1LEZ7 Short-chain dehydrogenase/reductase SDR
Rmet_4440		Op1263r	0.34	3.77	0.41	9.67	Q1LEX1 Endoribonuclease L-PSP
Rmet_4461		Op1271r	0.16	0.62	0.47	3.87	Q1LEV0 Putative uncharacterized protein Q1LEU6 Two component heavy metal response
Rmet_4465	<i>czcR2</i>	Op1274f	0.38	2.78	0.33	5.89	transcriptional regulator
Rmet_4472		Op1275r	0.32	1.54	0.24	7.49	Q1LEG4 Sulphate transporter
Rmet_4489		Op1279r	0.37	3.44	0.40	5.63	Q1LES2 Zonular occludens toxin
Rmet_4490		Op1279r	0.31	1.99	0.22	6.48	Q1LES1 Putative uncharacterized protein
Rmet_4492		Op1279r	0.46	2.18	0.38	5.45	Q1LER9 Putative uncharacterized protein
Rmet_4493		Op1279r	0.38	1.83	0.17	4.37	Q1LER8 Putative uncharacterized protein
Rmet_4494		Op1279r	0.26	1.37	0.15	6.40	Q1LER7 Putative uncharacterized protein Q1LEN9 Transcriptional regulator, AraC family with
Rmet_4522		Op1295r	0.48	1.65	0.39	3.09	amidase-like domain
Rmet_4587		Op1320f	0.30	3.56	0.31	4.88	Q1LEH7 Glycosyl transferase, family 39 Q1LEH6 Putative small multidrug resistance
Rmet_4588		Op1320f	0.37	4.50	0.39	6.14	transmembrane protein
Rmet_4590	<i>arnC</i>	Op1320f	0.28	3.32	0.40	3.38	Q1LEH4 Glycosyl transferase, family 2
Rmet_4591		Op1320f	0.35	12.67	0.46	3.12	Q1LEH3 Formyl transferase-like protein
Rmet_4593		Op1320f	0.47	10.58	0.46	3.06	Q1LEH1 Polysaccharide deacetylase
Rmet_4600		Op1324f	0.27	2.31	0.18	19.44	Q1LEG4 Sulphate transporter
Rmet_4601		Op1324f	0.45	3.30	0.45	2.62	Q1LEG3 UspA
Rmet_4603		Op1324f	0.19	3.25	0.21	6.70	Q1LEG1 Transcriptional regulator, GntR family
Rmet_4604		Op1324f	0.17	2.56	0.13	9.07	Q1LEG0 Putative uncharacterized protein
Rmet_4606	<i>metY</i>	Op1326f	0.38	2.16	0.37	1.96	Q1LEF8 O-acetylhomoserine/O-acetylserine sulfhydrylase

Rmet_4609	Op1328f	0.36	2.65	0.39	7.82	Q1LEF5 Uncharacterized protein UPF0065
Rmet_4611	Op1328f	0.35	3.23	0.39	4.49	Q1LEF3 Putative uncharacterized protein
Rmet_4613	Op1329r	0.38	1.67	0.33	10.54	Q1LEF1 Acyl-CoA dehydrogenase-like protein
Rmet_4615	Op1330f	0.36	3.40	0.33	9.84	Q1LEE9 Transcriptional regulator, GntR family
Rmet_4616	Op1330f	0.29	3.32	0.32	6.09	Q1LEE8 Putative uncharacterized protein
Rmet_4617	Op1330f	0.31	1.92	0.23	5.10	Q1LEE7 TonB-dependent siderophore receptor
Rmet_4618	Op1331r	0.31	2.56	0.22	4.65	Q1LEE6 Putative uncharacterized protein Q1LEE5 RND efflux system, outer membrane lipoprotein,
Rmet_4619	Op1331r	0.33	1.98	0.26	5.07	NodT
Rmet_4623	Op1332f	0.42	2.50	0.49	1.66	Q1LEE1 Putative uncharacterized protein
Rmet_4629	Op1334f	0.44	3.41	0.49	1.43	Q1LED5 Transcriptional regulator, AraC family
Rmet_4633	<i>tauD</i> Op1337r	0.38	2.94	0.47	4.78	Q1LED1 Taurine catabolism dioxygenase TauD/TfdA
Rmet_4635	Op1339r	0.29	1.72	0.47	3.10	Q1LEC9 Sulphate transporter
Rmet_4640	Op1341r	0.37	4.35	0.47	4.05	Q1LEC4 Putative uncharacterized protein Q1LEC3 ATP-dependent endonuclease of the OLD family-
Rmet_4641	Op1341r	0.45	4.33	0.49	16.93	like protein
Rmet_4642	Op1341r	0.43	2.24	0.49	1.83	Q1LEC2 Putative uncharacterized protein
Rmet_4643	Op1341r	0.37	2.20	0.32	12.30	Q1LEC1 Putative uncharacterized protein
Rmet_4644	Op1341r	0.36	1.73	0.22	9.14	Q1LEC0 Carboxymuconolactone decarboxylase
Rmet_4645	Op1341r	0.17	2.96	0.08	3.60	Q1LEB9 Uncharacterized protein UPF0065
Rmet_4646	Op1341r	0.40	4.50	0.43	4.53	Q1LEB8 Short-chain dehydrogenase/reductase SDR
Rmet_4647	Op1342f	0.44	4.12	0.36	6.95	Q1LEB7 Transcriptional regulator, LacI family
Rmet_4648	Op1343r	0.40	3.80	0.35	5.55	Q1LEB6 Filamentation induced by cAMP protein Fic Q1LEB5 RND efflux system, outer membrane lipoprotein,
Rmet_4649	Op1343r	0.34	5.15	0.33	3.79	NodT
Rmet_4650	Op1344f	0.46	3.50	0.48	5.22	Q1LEB4 Putative transcriptional regulator
Rmet_4662	Op1349r	0.42	2.24	0.47	2.69	Q1LEA2 Putative uncharacterized protein
Rmet_4668	Op1351r	0.39	2.88	0.39	5.81	Q1LE96 NADH/Ubiquinone/plastoquinone (Complex I)
Rmet_4685	Op1355r	0.39	2.63	0.50	3.38	Q1LE79 Putative uncharacterized protein
Rmet_4700	Op1359r	0.39	3.89	0.47	3.51	Q1LE64 Conserved hypothetical signal peptide protein
Rmet_4730	Op1367r	0.35	6.39	0.39	6.57	Q1LE34 Uncharacterised peroxidase-related
Rmet_4735	Op1369r	0.36	3.86	0.48	3.75	Q1LE29 D-galactonate transporter
Rmet_4754	Op1381r	0.47	3.05	0.42	11.28	Q1LE10 Glycosyl transferase, family 2
Rmet_4805	<i>kbl</i> Op1397r	0.42	2.86	0.39	2.10	Q1LDV9 2-amino-3-ketobutyrate coenzyme A ligase

Rmet_4808		Op1399r	0.47	3.56	0.33	5.24	Q1LDV6 Di-haem cytochrome c peroxidase
Rmet_4836		Op1411r	0.37	1.62	0.41	0.83	Q1LDS8 Diguanylate phosphodiesterase (EAL domain)
Rmet_4875	<i>catD</i>	Op1425r	0.49	12.74	0.46	4.48	Q1LDN9 3-oxoadipate enol-lactonase
Rmet_4876		Op1425r	0.41	4.15	0.33	2.34	Q1LDN8 Uncharacterized protein UPF0065
Rmet_4881	<i>catA</i>	Op1428f	0.50	1.73	0.45	4.43	Q1LDN3 Catechol 1,2-dioxygenase Q1LDM3 Sulfite dehydrogenase (Cytochrome) subunit SorA
Rmet_4891		Op1430f	0.44	1.68	0.47	6.77	apoprotein
Rmet_4960		Op1457r	0.33	1.18	0.50	4.41	Q1LDF4 Pili assembly chaperone
Rmet_4962		Op1457r	0.38	1.57	0.42	3.37	Q1LDF2 Diguanylate phosphodiesterase (EAL domain) Q1LDF0 Two component transcriptional regulator, LuxR
Rmet_4964		Op1457r	0.42	1.36	0.47	3.34	family
Rmet_4977		Op1461r	0.45	1.81	0.42	4.54	Q1LDD7 Sensor protein Q1LDD6 Two component transcriptional regulator, winged
Rmet_4978		Op1461r	0.27	1.17	0.12	39.35	helix family
Rmet_4979		Op1461r	0.38	2.57	0.24	4.86	Q1LDD5 Putative uncharacterized protein
Rmet_4981		Op1461r	0.43	2.07	0.36	4.96	Q1LDD3 Putative uncharacterized protein
Rmet_4982		Op1461r	0.35	4.46	0.34	10.49	Q1LDD2 Undecaprenyl-diphosphatase
Rmet_5007		Op1470f	0.36	2.49	0.36	4.44	Q1LDA7 Putative uncharacterized protein
Rmet_5008		Op1470f	0.42	2.31	0.42	2.47	Q1LDA6 CsbD-like protein Q1LDA3 Pyridine nucleotide-disulphide oxidoreductase
Rmet_5011		Op1473r	0.43	2.88	0.44	6.62	dimerisation region
Rmet_5033	<i>cusA</i>	Op1480f	0.38	3.68	0.32	6.53	Q1LD81 Heavy metal efflux pump CzcA
Rmet_5040		Op1482f	0.48	2.36	0.47	1.65	Q1LD74 Transcriptional regulator, GntR family
Rmet_5079		Op1496f	0.41	2.41	0.37	5.40	Q1LD38 Putative uncharacterized protein
Rmet_5082		Op1496f	0.44	2.57	0.47	11.07	Q1LD35 OmpA/MotB
Rmet_5111		Op1505r	0.38	2.51	0.46	1.66	Q1LD06 Thiolase
Rmet_5112		Op1505r	0.21	2.44	0.17	8.94	Q1LD05 Putative uncharacterized protein
Rmet_5128	<i>aldB</i>	Op1513r	0.46	5.39	0.46	7.48	Q1LCY9 Aldehyde dehydrogenase
Rmet_5133		Op1513r	0.42	1.81	0.29	4.25	Q1LCY4 Acyl-CoA dehydrogenase-like protein
Rmet_5172		Op1522f	0.36	2.49	0.43	2.88	Q1LCU5 Putative uncharacterized protein
Rmet_5175		Op1522f	0.37	1.81	0.44	4.14	Q1LCU2 Putative uncharacterized protein
Rmet_5176		Op1522f	0.33	1.05	0.44	2.42	Q1LCU1 Translation initiation factor IF-1 3
Rmet_5177		Op1523r	0.33	0.98	0.36	3.76	Q1LCU0 Putative uncharacterized protein
Rmet_5178		Op1524f	0.49	1.97	0.43	3.86	Q1LCT9 Putative uncharacterized protein

Rmet_5179	Op1525r	0.48	3.22	0.48	8.34	Q1LCT8 Putative uncharacterized protein
Rmet_5185	Op1528f	0.40	3.36	0.47	2.07	Q1LCT2 Carbonic anhydrase
Rmet_5195	Op1532f	0.45	2.56	0.50	1.82	Q1LCS2 Porin, Gram-negative type
Rmet_5225	Op1541r	0.36	2.60	0.40	7.06	Q1LCP2 Putative uncharacterized protein
Rmet_5230	<i>iscS2</i> Op1543r	0.47	2.88	0.47	3.39	Q1LCN7 Aminotransferase, class V
Rmet_5236	Op1544f	0.50	1.79	0.37	3.06	Q1LCN1 DegT/DnrJ/EryC1/StrS aminotransferase
Rmet_5237	Op1544f	0.44	2.66	0.46	2.19	Q1LCN0 WbnG
Rmet_5238	Op1544f	0.45	2.83	0.39	3.41	Q1LCM9 Putative uncharacterized protein
Rmet_5239	Op1544f	0.48	1.48	0.40	3.46	Q1LCM8 Phytanoyl-CoA dioxygenase
Rmet_5252	<i>fliC2</i> Op1550f	0.49	3.76	0.27	3.48	Q1LCL5 Flagellin-like protein
Rmet_5253	Op1550f	0.33	4.61	0.36	2.13	Q1LCL4 Flagellar protein FlaG protein
Rmet_5255	<i>fliS</i> Op1550f	0.46	6.70	0.40	4.03	Q1LCL2 Flagellar protein FliS
Rmet_5256	Op1550f	0.46	3.51	0.46	6.43	Q1LCL1 Flagellar protein FliT
Rmet_5263	<i>fliH</i> Op1552f	0.43	1.47	0.46	3.31	Q1LCK4 Flagellar assembly protein FliH
Rmet_5265	<i>fliJ</i> Op1552f	0.49	1.60	0.47	3.14	Q1LCK2 Flagellar export FliJ
Rmet_5266	<i>fliK</i> Op1552f	0.32	0.68	0.50	1.87	Q1LCK1 Flagellar hook-length control protein
Rmet_5300	<i>fliO</i> Op1566f	0.44	1.05	0.47	2.50	Q1LCG7 Flagellar biosynthesis protein, FliO
Rmet_5332	Op1578f	0.39	3.65	0.50	3.11	Q1LCD5 Sensor protein
Rmet_5333	Op1579r	0.25	1.17	0.24	1.31	Q1LCD4 Putative uncharacterized protein
Rmet_5352	Op1590f	0.48	3.24	0.41	2.29	Q1LCB5 Putative uncharacterized protein
Rmet_5353	Op1590f	0.42	1.64	0.50	5.66	Q1LCB4 Pyridoxamine 5'-phosphate oxidase-related, FMN-binding
Rmet_5365	Op1596f	0.34	1.51	0.39	0.83	Q1LCA2 Transcriptional regulator, LysR family
Rmet_5376	<i>hmuT</i> Op1600f	0.48	1.93	0.47	2.64	Q1LC91 Periplasmic binding protein
Rmet_5378	<i>hmuV</i> Op1600f	0.48	1.65	0.49	1.77	Q1LC89 Hemin import ATP-binding protein hmuV
Rmet_5379	Op1601r	0.44	4.32	0.47	2.48	Q1LC88 Short-chain dehydrogenase/reductase SDR
Rmet_5380	Op1601r	0.47	2.63	0.47	3.00	Q1LC87 Putative uncharacterized protein
Rmet_5386	Op1603r	0.42	3.17	0.38	7.06	Q1LC81 Putative uncharacterized protein
Rmet_5394	Op1606f	0.38	1.86	0.40	5.16	Q1LC73 Putative uncharacterized protein
Rmet_5426	Op1614f	0.26	1.77	0.40	3.69	Q1LC41 Putative uncharacterized protein
Rmet_5428	Op1615r	0.49	1.51	0.48	4.90	Q1LC39 Putative uncharacterized protein
Rmet_5437	Op1617r	0.43	2.88	0.48	2.55	Q1LC30 Acyl-CoA dehydrogenase-like protein
Rmet_5467	Op1625r	0.45	2.58	0.35	4.61	Q1LC00 Putative uncharacterized protein
Rmet_5490	<i>pobA</i> Op1631r	0.50	1.95	0.42	6.50	Q1LBX7 Monooxygenase, FAD-binding

Rmet_5497	Op1634f	0.38	3.41	0.45	5.35 Q1LBX0 Integrase, catalytic region
Rmet_5500	Op1636f	0.44	1.69	0.48	5.01 Q1LBW7 Putative uncharacterized protein
Rmet_5503	Op1636f	0.35	3.36	0.50	5.63 Q1LBW4 Uncharacterized protein UPF0065
Rmet_5515	Op1641r	0.40	2.38	0.46	3.87 Q1LBV2 Aldehyde dehydrogenase
Rmet_5516	<i>cyp</i> Op1641r	0.45	2.03	<i>0.50</i>	3.19 Q1LBV1 Cytochrome P450
Rmet_5517	<i>vanB</i> Op1641r	0.31	2.17	0.37	10.73 Q1LBV0 Ferredoxin
Rmet_5521	Op1641r	0.44	2.71	<i>0.46</i>	2.08 Q1LBU6 Enoyl-CoA hydratase/isomerase
Rmet_5522	Op1641r	<i>0.45</i>	2.23	0.50	11.07 Q1LBU5 Putative uncharacterized protein Q1LBU2 L-carnitine dehydratase/bile acid-inducible protein
Rmet_5525	Op1642f	0.44	2.89	0.47	3.50 F
Rmet_5526	Op1643r	0.38	1.73	0.29	6.70 Q1LBU1 Putative uncharacterized protein
Rmet_5528	Op1643r	<i>0.45</i>	1.88	0.42	4.15 Q1LBT9 AMP-dependent synthetase and ligase
Rmet_5533	Op1645r	0.24	1.86	0.21	22.47 Q1LBT4 Nitroreductase
Rmet_5539	Op1647r	0.34	2.95	0.44	3.71 Q1LBS8 Putative uncharacterized protein
Rmet_5627	Op1679r	0.44	1.64	0.49	3.84 Q1LBJ0 Putative uncharacterized protein
Rmet_5682	Op1697r	0.43	2.42	0.39	3.44 Q1LBD5 Secretion protein HlyD
Rmet_5685	Op1698f	0.38	3.58	0.35	28.05 Q1LBD2 Pilus assembly protein FimT
Rmet_5688	Op1698f	0.44	2.87	0.49	4.81 Q1LBC9 Putative transmembrane protein
Rmet_5728	Op1715r	0.37	2.56	0.42	6.37 Q1LB89 Glycosyl transferase, group 1
Rmet_5762	Op1728f	0.50	3.69	0.44	4.24 Q1LB55 Putative uncharacterized protein
Rmet_5764	Op1729r	<i>0.44</i>	1.82	0.47	4.49 Q1LB53 Putative uncharacterized protein
Rmet_5818	Op1757r	<i>0.44</i>	1.58	0.39	2.77 Q46Q97 Cold-shock DNA-binding protein family
Rmet_5821	Op1759r	0.36	7.99	0.32	10.91 Q1LAZ6 Putative integrase/recombinase protein Q1LAY5 Response regulator receiver domain protein (CheY- like)
Rmet_5832	Op1764f	0.34	2.16	0.43	3.17
Rmet_5835	Op1764f	<i>0.43</i>	1.82	0.49	4.98 Q1LAY2 Sugar transferase
Rmet_5850	Op1769r	0.43	1.72	<i>0.48</i>	3.87 Q1LAW7 Protein tyrosine phosphatase
Rmet_5899	Op1787r	0.37	1.89	0.44	2.78 Q1LAR8 Putative uncharacterized protein
Rmet_5918	Op1797r	0.45	6.37	0.46	3.25 Q1LAP9 Transcriptional regulator, IclR family
Rmet_5937	Op1805r	0.47	2.58	0.46	4.09 Q1LAN0 Putative uncharacterized protein
Rmet_5970	Op1817r	0.24	2.11	<i>0.49</i>	1.02 Q1LAJ7 Heavy metal translocating P-type ATPase P37248 Transposase for insertion sequence element
Rmet_6282	Op1915r	<i>0.45</i>	2.74	<i>0.47</i>	2.59 IS1086

Q(EDTA)≤0.5, Q(Zn) unchanged.

Rmet_0090		Op0025f	0.86	0.21	0.48	2.69	Q1LSA0 Two component transcriptional regulator, LuxR family
Rmet_0091		Op0025f	0.65	0.75	0.42	3.39	Q1LS99 Response regulator receiver domain protein (CheY-like)
Rmet_0096	<i>argS</i>	Op0029f	0.64	2.58	0.43	4.56	Q1LS94 Arginyl-tRNA synthetase
Rmet_0133		Op0034r	0.84	0.73	0.41	1.49	Q1LS57 Nuclear export factor GLE1
Rmet_0137		Op0037f	0.70	0.85	0.30	1.13	Q1LS53 Putative uncharacterized protein
Rmet_0138		Op0038r	0.80	0.70	0.29	1.22	Q1LS52 Transcriptional regulator, LysR family
Rmet_0139		Op0038r	0.64	3.42	0.39	1.86	Q1LS51 Putative uncharacterized protein
Rmet_0158		Op0046r	0.51	2.58	0.34	4.94	Q1LS32 Aldehyde dehydrogenase
Rmet_0170	<i>ahcY</i>	Op0051f	0.63	3.47	0.49	3.11	Q1LS20 Adenosylhomocysteinase
Rmet_0175		Op0052r	0.59	1.36	0.48	2.53	Q1LS15 5-formyltetrahydrofolate cyclo-ligase
Rmet_0191		Op0057f	0.57	2.02	0.47	2.15	Q1LRZ9 Putative type-4 fimbrial biogenesis transmembrane protein
Rmet_0192		Op0057f	0.51	1.56	0.41	4.20	Q1LRZ8 Putative type-4 fimbrial biogenesis pily1-related protein
Rmet_0193		Op0057f	0.63	1.51	0.45	4.85	Q1LRZ7 Pilus assembly protein PilE
Rmet_0208		Op0062r	0.56	2.47	0.48	3.21	Q1LRY2 Transcriptional regulator, GntR family
Rmet_0227		Op0066r	0.90	0.35	0.49	5.98	Q1LRW3 Ferredoxin-like protein
Rmet_0271		Op0077f	0.74	0.40	0.37	1.26	Q1LRR9 Electron transport protein SCO1/SenC
Rmet_0289	<i>prs</i>	Op0084r	0.81	1.66	0.40	15.86	Q1LRQ1 Ribose-phosphate pyrophosphokinase
Rmet_0310		Op0088r	0.52	5.32	0.46	1.78	Q1LRN0 Peptidase C56, PfpI
Rmet_0355	<i>otsB</i>	Op0101f	0.94	0.25	0.39	4.04	Q1LRI5 HAD-superfamily hydrolase subfamily IIB
Rmet_0356		Op0101f	0.59	1.96	0.42	2.88	Q1LRI4 Glycoside hydrolase 15-related
Rmet_0359		Op0102r	0.67	7.20	0.39	5.59	Q1LRI1 Predicted sulfurylase large subunit, molybdopterin cytosine dinucleotide biosynthesis / predicted sulfurylase small subunit, molybdopterin cytosine dinucleotide biosynthesis
Rmet_0360		Op0102r	0.52	0.84	0.17	7.23	Q1LRI0 Carbon monoxide dehydrogenase subunit G
Rmet_0363	<i>coxM</i>	Op0102r	0.54	2.36	0.44	8.01	Q1LRH7 Molybdopterin dehydrogenase, FAD-binding
Rmet_0365	<i>coxS</i>	Op0102r	0.54	3.81	0.44	3.38	Q1LRH5 (2Fe-2S)-binding
Rmet_0367		Op0103f	0.53	2.71	0.45	5.67	Q1LRH3 FAD linked oxidase-like protein
Rmet_0368		Op0103f	0.80	0.58	0.42	2.99	Q1LRH2 Histidine triad (HIT) protein
Rmet_0369		Op0103f	0.62	1.38	0.43	3.69	Q1LRH1 ABC transporter-like protein

Rmet_0411	<i>rpsI</i>	Op0113f	0.67	3.01	0.47	3.15	Q1LRC8 Putative uncharacterized protein
Rmet_0452		Op0118r	0.56	1.90	0.43	9.44	Q1LR88 PhoH-like protein
Rmet_0456	<i>rhIE1</i>	Op0119f	0.58	2.17	0.42	3.90	Q1LR84 DEAD/DEAH box helicase-like protein
Rmet_0466	<i>recA</i>	Op0123f	0.67	1.25	0.43	3.18	Q1LR74 Protein recA
Rmet_0673	<i>pilL2</i>	Op0187f	0.65	1.60	0.45	3.07	Q1LQL7 CheA signal transduction histidine kinases
Rmet_0674		Op0188r	0.68	1.01	0.49	3.22	Q1LQL6 Major facilitator superfamily MFS_1
Rmet_0696		Op0196r	0.79	0.29	0.43	2.02	Q1LQJ4 Putative uncharacterized protein
Rmet_0697	<i>pilA</i>	Op0196r	0.62	1.18	0.41	7.21	Q1LQJ3 Pilus assembly protein major pilin PilA
Rmet_0730		Op0205f	0.69	1.15	0.49	3.45	Q1LQG0 Uracil-xanthine permease
Rmet_0742		Op0210r	0.55	2.51	0.50	14.63	Q1LQE8 Radical SAM
Rmet_0748	<i>rpsP</i>	Op0213f	0.96	0.31	0.42	8.79	Q1LQE2 SSU ribosomal protein S16P
Rmet_0749	<i>rimM</i>	Op0213f	0.59	1.08	0.35	4.64	Q1LQE1 Ribosome maturation factor rimM
Rmet_0750	<i>trmD</i>	Op0213f	0.77	0.79	0.36	5.53	Q1LQE0 tRNA (guanine-N(1)-)-methyltransferase
Rmet_0752		Op0213f	0.53	3.22	0.44	4.87	Q1LQD8 NUDIX hydrolase
Rmet_0790		Op0225f	0.61	1.14	0.45	3.97	Q1LQA0 Putative uncharacterized protein
Rmet_0799		Op0227f	0.63	0.89	0.23	6.98	Q1LQ91 ABC transport systems inner membrane component
Rmet_0800		Op0227f	0.67	1.47	0.31	11.81	Q1LQ90 Substrate-binding region of ABC-type glycine betaine transporter
Rmet_0801		Op0227f	0.52	2.65	0.33	15.86	Q1LQ89 ABC transport systems inner membrane component
Rmet_0806		Op0229f	0.51	2.56	0.43	2.77	Q1LQ84 Putative uncharacterized protein
Rmet_0807		Op0229f	0.52	2.51	0.42	4.74	Q1LQ83 Class II aldolase/adducin-like protein
Rmet_0808		Op0229f	0.56	1.61	0.47	3.42	Q1LQ82 4-oxalocrotonate tautomerase family enzyme
Rmet_0814		Op0230r	0.52	3.33	0.48	3.73	Q1LQ76 Putative uncharacterized protein
Rmet_0818	<i>glnS</i>	Op0230r	0.60	1.58	0.49	4.54	Q1LQ72 Glutaminyl-tRNA synthetase
Rmet_0822	<i>ggt</i>	Op0232r	0.54	1.79	-0.37	0.60	Q1LQ68 Gamma-glutamyltransferase 2. Threonine peptidase.
Rmet_0825		Op0234r	0.67	6.36	0.49	18.72	Q1LQ65 Putative uncharacterized protein
Rmet_0828		Op0236r	0.55	2.02	0.50	3.92	Q1LQ62 Uncharacterized protein UPF0065
Rmet_0829		Op0236r	0.52	2.00	0.42	9.06	Q1LQ61 Putative transmembrane protein
Rmet_0830		Op0236r	0.67	2.55	0.44	1.54	Q1LQ60 L-carnitine dehydratase/bile acid-inducible protein
Rmet_0833		Op0238r	0.59	1.70	0.46	4.69	F
							Q1LQ57 Transcriptional regulator, GntR family

Rmet_0834	<i>gudD</i>	Op0239f	0.52	2.53	0.49	1.72	Q1LQ56 D-glucarate dehydratase
Rmet_0860		Op0247f	0.55	5.41	0.43	5.79	Q1LQ30 Putative uncharacterized protein
Rmet_0862		Op0248r	0.69	0.31	0.40	4.29	Q1LQ28 Putative uncharacterized protein
Rmet_0894		Op0259f	0.71	3.19	0.46	3.68	Q1LPZ6 Transcriptional regulator, LysR family
Rmet_0918	<i>leuA</i>	Op0263f	0.63	3.51	0.45	3.70	Q1LPX2 2-isopropylmalate synthase
Rmet_0921	<i>rpsO</i>	Op0265f	0.53	1.67	0.45	4.65	Q1LPW9 30S ribosomal protein S15
Rmet_0922		Op0266r	0.71	1.56	0.42	4.05	Q1LPW8 Putative uncharacterized protein
Rmet_0925	<i>tpiA</i>	Op0267f	0.85	0.56	0.46	7.77	Q1LPW5 Triosephosphate isomerase
Rmet_0926	<i>secG</i>	Op0267f	0.87	0.43	0.44	5.68	Q1LPW4 Protein translocase subunit secG
Rmet_0928	<i>nuoB</i>	Op0267f	0.74	1.89	0.35	3.39	Q1LPW2 NADH-quinone oxidoreductase subunit B
Rmet_0929	<i>nuoC</i>	Op0267f	0.71	2.05	0.37	4.12	Q1LPW1 NADH-quinone oxidoreductase subunit C
Rmet_0931	<i>nuoE</i>	Op0267f	0.54	2.22	0.38	8.82	Q1LPV9 NADH-quinone oxidoreductase, E subunit
Rmet_0932	<i>nuoF</i>	Op0267f	0.64	0.80	0.50	1.69	Q1LPV8 NADH-quinone oxidoreductase, F subunit
Rmet_0935	<i>nuoI</i>	Op0267f	0.59	2.97	0.48	3.81	Q1LPV5 NADH-quinone oxidoreductase subunit I
Rmet_0936	<i>nuoJ</i>	Op0267f	0.66	0.79	0.49	5.27	Q1LPV4 NADH-ubiquinone/plastoquinone oxidoreductase, chain 6
Rmet_0938	<i>nuoL</i>	Op0267f	0.67	1.24	0.47	2.93	Q1LPV2 Proton-translocating NADH-quinone oxidoreductase, chain L
Rmet_0939	<i>nuoM</i>	Op0267f	0.57	1.40	0.47	5.87	Q1LPV1 Proton-translocating NADH-quinone oxidoreductase, chain M
Rmet_1024		Op0295f	0.60	0.94	0.40	4.95	Q1LPL6 Transcriptional regulator, BadM/Rrf2 family
Rmet_1025	<i>iscS</i>	Op0295f	0.57	1.54	0.45	3.50	Q1LPL5 Cysteine desulfurase IscS
Rmet_1027		Op0295f	0.64	1.04	0.47	3.28	Q1LPL3 Iron-sulfur cluster assembly protein IscA
Rmet_1028	<i>hscB</i>	Op0295f	0.69	0.76	0.47	6.70	Q1LPL2 Co-chaperone Hsc20
Rmet_1029	<i>hscA</i>	Op0295f	0.71	1.69	0.45	3.28	Q1LPL1 Chaperone protein hscA homolog
Rmet_1030		Op0295f	0.66	0.95	0.43	10.86	Q1LPL0 Ferredoxin, 2Fe-2S type
Rmet_1031		Op0295f	0.86	0.15	0.49	5.18	Q1LPK9 Putative uncharacterized protein
Rmet_1053	<i>kdsA</i>	Op0301f	0.60	4.87	0.49	3.80	Q1LPI7 2-dehydro-3-deoxyphosphooctonate aldolase
Rmet_1054		Op0301f	0.77	1.46	0.49	4.32	Q1LPI6 Putative uncharacterized protein
Rmet_1140		Op0326r	0.62	2.33	0.49	3.32	Q1LPA0 FAD dependent oxidoreductase
Rmet_1160	<i>thrS</i>	Op0333f	0.53	1.98	0.30	1.99	Q1LP80 Threonyl-tRNA synthetase / Ser-tRNA(Thr) hydrolase
Rmet_1162	<i>rpml</i>	Op0333f	0.63	2.97	0.48	13.82	Q1LP78 50S ribosomal protein L35
Rmet_1163	<i>rplT</i>	Op0333f	0.62	4.10	0.42	14.25	Q1LP77 50S ribosomal protein L20

Rmet_1212		Op0352r	0.51	1.06	0.46	5.31	Q1LP28 Aldo/keto reductase
Rmet_1213	<i>pyrD</i>	Op0352r	0.83	0.65	0.48	3.37	Q1LP27 Dihydroorotate dehydrogenase
Rmet_1216	<i>aat</i>	Op0354r	0.53	4.26	0.47	14.56	Q1LP24 Leucyl/phenylalanyl-tRNA--protein transferase
Rmet_1217		Op0354r	0.79	0.85	0.42	4.14	Q1LP23 NUDIX hydrolase
Rmet_1363		Op0383f	0.67	1.53	0.42	1.17	Q1LNN0 Putative signal peptide protein
Rmet_1419		Op0398r	0.63	1.43	0.47	2.29	Q1LNH4 Modification methylase, HemK family
Rmet_1435	<i>rpsB</i>	Op0403f	0.77	0.55	0.37	10.15	Q1LNF8 30S ribosomal protein S2
Rmet_1437	<i>pyrH</i>	Op0403f	0.51	2.21	0.49	8.39	Q1LNF6 Uridylate kinase

CMGI-3							
Rmet_1463	<i>guaA</i>	Op0409f	0.70	1.98	0.45	6.62	Q1LND0 GMP synthase (Glutamine-hydrolyzing)
Rmet_1466		Op0411f	0.56	1.59	0.42	4.13	Q1LNC7 Putative uncharacterized protein
Rmet_1468		Op0412r	0.55	2.01	0.36	9.30	Q1LNC5 Phage transcriptional regulator, AlpA
Rmet_1470		Op0412r	0.71	0.62	0.39	5.62	Q1LNC3 Putative uncharacterized protein
Rmet_1471		Op0412r	0.60	1.22	0.36	7.37	Q1LNC2 Putative uncharacterized protein
Rmet_1472		Op0412r	0.63	0.80	0.35	33.59	Q1LNC1 KAP P-loop
Rmet_1473		Op0412r	0.58	1.25	0.27	6.24	Q1LNC0 Retron reverse transcriptase
Rmet_1474		Op0412r	0.56	3.18	0.26	13.76	Q1LNB9 Putative uncharacterized protein
Rmet_1572	<i>ptpS</i>	Op0433f	0.53	2.20	0.40	5.03	Q1LN21 Putative uncharacterized protein
Rmet_1576		Op0434r	0.73	0.69	0.45	8.07	Q1LN17 Putative proline-rich protein
Rmet_1732		Op0491f	0.52	2.34	0.43	8.92	Q1LML5 Transcriptional regulator, AraC family
Rmet_1812		Op0526r	0.66	1.22	0.48	6.21	Q1LMD5 Rieske (2Fe-2S) region
Rmet_1834		Op0533f	0.62	1.37	0.49	3.48	Q1LMB3 Transcriptional regulator, GntR family
Rmet_1931	<i>amaB-2</i>	Op0564r	0.55	5.23	0.49	11.59	Q1LM16 Amidase, hydantoinase/carbamoylase
Rmet_1946		Op0570r	0.51	4.55	0.43	10.12	Q1LM01 Putative transmembrane protein
Rmet_1973	<i>pitA</i>	Op0576r	0.64	1.76	0.43	89.36	Q1LLX4 Phosphate transporter
Rmet_1981		Op0577f	0.59	2.77	0.39	3.64	Q1LLW6 LexA repressor
Rmet_1982		Op0577f	0.59	4.39	0.37	4.28	Q1LLW5 Putative uncharacterized protein
Rmet_1983		Op0578r	0.78	1.20	0.41	11.84	Q1LLW4 Putative uncharacterized protein
Rmet_2024		Op0592r	0.88	0.23	0.49	2.46	Q1LLS3 GTP-binding protein TypA
Rmet_2033		Op0594r	1.06	0.55	0.43	8.01	Q1LLR4 UPF0090 protein Rmet_2033
Rmet_2039		Op0596r	0.73	0.74	0.50	3.31	Q1LLQ8 Putative uncharacterized protein
Rmet_2044	<i>ccoN</i>	Op0596r	0.72	1.66	0.48	11.06	Q1LLQ3 Cytochrome c oxidase, cbb3-type, subunit I
Rmet_2133		Op0614r	0.82	0.48	0.45	6.20	Q1LLG4 Putative uncharacterized protein
Rmet_2136		Op0615f	0.54	2.28	0.48	4.09	Q1LLG1 Putative uncharacterized protein

Rmet_2137	Op0615f	0.90	0.53	0.47	6.93	Q1LLG0 50S ribosomal protein L31 type B
Rmet_2138	Op0615f	0.83	1.82	0.46	4.61	Q1LLF9 Putative inner membrane transmembrane protein
Rmet_2139	Op0615f	0.52	4.50	0.40	4.60	Q1LLF8 MATE efflux family protein
Rmet_2141	Op0617f	0.64	4.32	0.43	15.96	Q1LLF6 Patatin
Rmet_2174	Op0625f	0.56	1.13	0.44	4.00	Q1LLC3 Translation initiation factor IF-1 1
Rmet_2177	<i>ppx</i> Op0626r	0.54	1.16	0.37	5.00	Q1LLC0 Ppx/GppA phosphatase
Rmet_2193	<i>carB</i> Op0630r	0.71	0.85	0.43	3.54	Q1LLA4 Carbamoyl-phosphate synthase large subunit
Rmet_2194	Op0630r	0.72	0.89	0.47	12.73	Q1LLA3 Lysine exporter protein (LYSE/YGGA)
Rmet_2195	<i>carA</i> Op0630r	0.61	1.58	0.32	8.25	Q1LLA2 Carbamoyl-phosphate synthase small subunit
Rmet_2210	Op0632r	0.65	1.06	0.47	1.73	Q1LL87 Putative uncharacterized protein
Rmet_2212	Op0633f	0.59	2.44	0.46	5.20	Q1LL85 UspA
Rmet_2264	Op0645f	0.90	0.45	0.50	1.69	Q1LL33 Putative uncharacterized protein
Rmet_2265	Op0646r	0.73	1.27	0.48	3.85	Q1LL32 Putative uncharacterized protein
Rmet_2266	Op0647f	0.61	1.79	0.50	2.56	Q1LL31 Putative uncharacterized protein
Rmet_2273	<i>fumA</i> Op0649f	0.65	2.66	0.50	12.19	Q1LL24 Fumarase
Rmet_2274	<i>murl</i> Op0649f	1.08	0.66	0.47	3.21	Q1LL23 Glutamate racemase
Rmet_2286	Op0654r	0.90	0.23	0.44	2.42	Q1LL11 Putative uncharacterized protein
Rmet_2300	Op0656r	0.50	2.18	0.48	3.83	Q1LKZ7 Putative uncharacterized protein
Rmet_2339	Op0662r	0.54	1.38	0.44	12.29	Q8GQ48 Putative uncharacterized protein ORF C62
Rmet_2340	Op0662r	0.64	1.18	0.45	5.40	Q8GQ49 Putative uncharacterized protein ORF C61
Rmet_2341	Op0662r	0.62	1.29	0.38	10.01	Q1LKV8 Putative uncharacterized protein
Rmet_2342	Op0662r	0.64	0.92	0.38	4.14	A0H9A7 AAA ATPase, central region
Rmet_2424	Op0680r	0.87	0.41	0.47	5.34	Q1LKM5 Anti sigma-E protein RseA
Rmet_2432	<i>rpmF</i> Op0680r	1.08	0.17	0.46	3.97	Q1LKL7 50S ribosomal protein L32
Rmet_2433	Op0680r	0.67	0.77	0.29	6.15	Q1LKL6 Putative uncharacterized protein
Rmet_2441	<i>moaA</i> Op0683f	0.73	2.47	0.50	3.46	Q1LKK8 GTP cyclohydrolase subunit MoaA
Rmet_2454	Op0685f	0.60	0.92	0.47	2.02	Q1LKJ5 Lysine exporter protein (LYSE/YGGA)
Rmet_2461	Op0688r	0.55	0.84	0.44	1.40	Q1LKI8 Colicin V production protein
Rmet_2484	<i>sdhA</i> Op0688r	0.90	0.16	0.45	3.01	Q1LKG5 Succinate dehydrogenase subunit A
Rmet_2485	<i>sdhD</i> Op0688r	0.84	0.26	0.36	6.78	Q1LKG4 Succinate dehydrogenase subunit D
Rmet_2486	<i>sdhC</i> Op0688r	0.69	1.00	0.28	6.73	Q1LKG3 Succinate dehydrogenase subunit C
Rmet_2487	Op0688r	0.71	1.58	0.38	5.48	Q1LKG2 Putative uncharacterized protein
Rmet_2547	Op0707f	0.72	1.31	0.50	2.79	Q1LKA2 Proline hydroxylase-like protein
Rmet_2564	Op0709f	0.57	0.86	0.37	5.09	Q1LK85 DEAD/DEAH box helicase-like protein

Rmet_2567	Op0711f	0.61	0.64	0.45	3.40	Q1LK82 Integral membrane protein TerC
Rmet_2579	Op0716r	0.53	6.69	0.35	3.34	Q1LK70 Pirin-like protein
Rmet_2618	Op0733f	0.65	0.81	0.50	4.31	Q1LK31 Rieske (2Fe-2S) region Q1LJW8 Putative type 4 fimbrial biogenesis PilY1-related protein
Rmet_2685	Op0757f	0.60	1.89	0.43	3.13	protein
Rmet_2694	<i>ribH</i> Op0759f	0.57	3.78	0.49	3.67	Q1LJV9 6,7-dimethyl-8-ribityllumazine synthase
Rmet_2704	<i>trmB</i> Op0765f	0.63	1.24	0.47	2.97	Q1LJU9 tRNA (guanine-N(7)-)-methyltransferase
Rmet_2723	Op0770r	0.64	1.42	0.45	5.13	Q1LJT0 Polysaccharide biosynthesis protein CapD
Rmet_2740	<i>pyrB</i> Op0772r	0.66	1.03	0.48	2.46	Q1LJR3 Aspartate carbamoyltransferase
Rmet_2771	Op0778r	0.52	2.46	0.48	2.83	Q1LJN2 Putative uncharacterized protein
Rmet_2796	Op0786r	0.65	0.89	0.43	2.34	Q1LJK7 Uncharacterized protein UPF0065
Rmet_2860	Op0804r	0.76	0.62	0.48	11.11	Q1LJE3 NAD-dependent epimerase/dehydratase
Rmet_2870	<i>rpmB</i> Op0807f	1.17	0.14	0.46	2.41	Q1LJD3 50S ribosomal protein L28
Rmet_2871	<i>rpmG</i> Op0807f	0.89	0.21	0.45	2.37	Q1LJD2 50S ribosomal protein L33
Rmet_2872	<i>nadB</i> Op0807f	0.71	1.31	0.45	4.39	Q1LJD1 L-aspartate oxidase Q1LJD0 Nicotinate-nucleotide pyrophosphorylase (Carboxylating)
Rmet_2873	<i>nadC</i> Op0808r	0.72	1.05	0.44	5.36	(Carboxylating)
Rmet_2874	<i>nadA</i> Op0808r	0.57	1.24	0.33	7.74	Q1LJC9 Quinolinate synthetase A
Rmet_2877	Op0808r	0.69	1.14	0.41	3.26	Q1LJC6 Fmu (Sun)
Rmet_2882	Op0810r	0.57	3.36	0.49	2.81	Q1LJC1 Putative uncharacterized protein
Rmet_2897	Op0815f	0.61	0.69	0.28	2.51	Q1LJA6 Putative uncharacterized protein
Rmet_2903	Op0819f	0.71	0.83	0.44	5.78	Q1LJA0 Putative uncharacterized protein
Rmet_3050	<i>pyrF</i> Op0858r	0.53	2.52	0.49	6.45	Q1LIV4 Orotidine 5'-phosphate decarboxylase
Rmet_3070	Op0861f	0.89	0.16	0.48	3.13	Q1LIT4 17 kDa surface antigen
Rmet_3084	<i>rdgC</i> Op0867f	0.65	1.16	0.22	5.47	Q1LIS0 Putative exonuclease, RdgC
Rmet_3085	Op0868r	0.50	2.25	0.16	9.60	Q1LIR9 Alcohol dehydrogenase, zinc-binding
Rmet_3105	<i>rpmA</i> Op0874r	1.14	0.27	0.39	6.65	Q1LIP9 50S ribosomal protein L27
Rmet_3106	<i>rplU</i> Op0874r	1.16	0.72	0.46	5.57	Q1LIP8 50S ribosomal protein L21
Rmet_3108	Op0875f	0.54	3.66	0.47	2.86	Q1LIP6 Type II secretion system protein E
Rmet_3109	Op0875f	0.66	1.83	0.48	4.04	Q1LIP5 Type II secretion system protein Q1LIP4 Type 4 prepilin peptidase 1. Aspartic peptidase.
Rmet_3110	Op0875f	0.73	1.74	0.46	7.65	MEROPS family A24A
Rmet_3114	Op0876r	0.53	2.60	0.47	2.25	Q1LIP0 Oligopeptide transporter OPT
Rmet_3115	Op0876r	0.63	1.15	0.47	4.33	Q1LIN9 NUDIX hydrolase

Rmet_3151	Op0882r	0.55	1.92	0.38	12.48	Q1LIK3 Molybdopterin oxidoreductase
Rmet_3153	Op0883f	0.70	1.06	0.49	2.33	Q1LIK1 Extracellular ligand-binding receptor Q1LIK0 Oligopeptide/dipeptide ABC transporter, ATP-binding protein
Rmet_3154	Op0884r	0.66	2.07	0.49	2.94	
Rmet_3178	<i>trpE</i> Op0893f	0.66	0.76	0.34	2.79	Q1LIH6 Anthranilate synthase, component I
Rmet_3179	<i>trpG</i> Op0893f	0.55	7.54	0.43	37.90	Q1LIH5 Anthranilate synthase, component II
Rmet_3200	<i>hemA</i> Op0901f	0.84	0.39	0.48	3.10	Q1LIF4 Glutamyl-tRNA reductase
Rmet_3201	<i>prfA</i> Op0901f	0.64	3.19	0.47	6.55	Q1LIF3 Peptide chain release factor 1
Rmet_3205	<i>ubiX</i> Op0901f	0.59	1.49	0.46	1.72	Q1LIE9 3-octaprenyl-4-hydroxybenzoate carboxy-lyase
Rmet_3209	Op0903f	0.52	1.47	0.47	3.36	Q1LIE5 Transcriptional regulator, AsnC family Q1LIA2 ABC-type multidrug transport system permease component
Rmet_3252	Op0918r	0.70	1.44	0.49	3.38	
Rmet_3274	<i>mrcA</i> Op0921f	0.63	2.40	0.46	2.87	Q1LI80 Penicillin-binding protein 1A
Rmet_3284	Op0924r	0.88	0.37	0.48	6.82	Q1LI70 Cytochrome c, class I
Rmet_3297	<i>secY</i> Op0926r	0.85	0.21	0.48	4.13	Q1LI57 Preprotein translocase secY subunit
Rmet_3298	<i>rplO</i> Op0926r	0.91	0.11	0.49	5.47	Q1LI56 50S ribosomal protein L15
Rmet_3301	<i>rplR</i> Op0926r	0.95	0.05	0.48	4.50	Q1LI53 50S ribosomal protein L18
Rmet_3302	<i>rplF</i> Op0926r	0.61	0.51	0.37	6.95	Q1LI52 50S ribosomal protein L6
Rmet_3303	<i>rpsH</i> Op0926r	0.89	0.12	0.44	7.95	Q1LI51 30S ribosomal protein S8
Rmet_3304	<i>rpsN</i> Op0926r	1.32	0.28	0.46	4.68	Q1LI50 SSU ribosomal protein S14P
Rmet_3305	<i>rplE</i> Op0926r	1.51	0.44	0.44	5.27	Q1LI49 50S ribosomal protein L5
Rmet_3306	<i>rplX</i> Op0926r	0.96	0.04	0.28	6.66	Q1LI48 50S ribosomal protein L24
Rmet_3307	<i>rplN</i> Op0926r	0.82	0.29	0.26	8.11	Q1LI47 50S ribosomal protein L14
Rmet_3314	<i>rplB</i> Op0926r	1.25	0.23	0.50	4.25	Q1LI40 50S ribosomal protein L2
Rmet_3317	<i>rplC</i> Op0926r	1.07	0.08	0.46	2.90	Q1LI37 50S ribosomal protein L3
Rmet_3324	Op0928r	1.30	0.29	0.43	10.18	Q1LI13 Elongation factor Tu
Rmet_3336	<i>rplJ</i> Op0930r	0.99	0.02	0.48	4.10	Q1LI18 50S ribosomal protein L10
Rmet_3337	<i>rplA</i> Op0930r	0.92	0.16	0.43	7.16	Q1LI17 50S ribosomal protein L1
Rmet_3338	<i>rplK</i> Op0930r	1.17	0.19	0.39	5.33	Q1LI16 50S ribosomal protein L11
Rmet_3339	<i>nusG</i> Op0930r	1.02	0.04	0.37	7.51	Q1LI15 Transcription antitermination protein nusG
Rmet_3340	<i>secE</i> Op0930r	0.90	0.63	0.45	8.54	Q1LI14 Protein translocase subunit secE/sec61 gamma
Rmet_3346	Op0932r	0.71	0.75	0.43	8.28	Q1LI08 UspA

CMGI-10

Rmet_3350	Op0932r	0.63	1.28	0.43	3.69	Q1LI04 Putative uncharacterized protein
-----------	---------	------	------	-------------	------	---

Rmet_3353	Op0934r	0.67	1.21	0.49	20.36	Q9F8S6 Transposase (Transposase, IS4 family)
						Q1LHX4 Putative signal transduction protein with EFhand domain
Rmet_3380	Op0940r	0.67	0.88	0.48	3.47	
Rmet_3381	<i>gspC</i> Op0940r	0.59	1.09	0.38	4.27	Q1LHX3 Putative uncharacterized protein
Rmet_3396	Op0943f	0.81	1.13	0.49	12.24	Q1LHV8 Pyruvate ferredoxin/ferredoxin oxidoreductase
						Q1LHS8 Sulfide dehydrogenase (Flavocytochrome), flavoprotein subunit
Rmet_3426	Op0950r	0.62	2.95	0.49	10.10	
Rmet_3427	Op0950r	0.62	1.76	0.48	4.69	Q1LHS7 Cytochrome c, class I
Rmet_3428	Op0950r	0.60	3.33	0.48	2.79	Q1LHS6 Transport-associated
Rmet_3480	<i>gcvT</i> Op0969f	0.56	1.52	0.43	3.74	Q1LHM4 Aminomethyltransferase
Rmet_3545	Op0983f	0.58	4.20	0.46	3.69	Q1LHF9 UMUC-like DNA-repair protein
Rmet_3612	Op1004r	0.66	0.82	0.49	0.95	Q1LH92 Methyltransferase type 11
Rmet_3614	Op1004r	0.80	0.72	0.49	4.64	Q1LH90 UPF0161 protein Rmet_3614
Rmet_3617	Op1006f	0.56	4.10	0.34	5.76	Q1LH87 Excinuclease ABC, C subunit-like protein
Rmet_3618	Op1007r	0.52	1.44	0.27	4.44	Q1LH86 OsmC-like protein
Rmet_3620	Op1008f	0.62	2.14	0.39	36.02	Q1LH84 Peptidase S1C, Do
Rmet_3621	Op1008f	0.77	0.97	0.49	3.85	Q1LH83 Putative uncharacterized protein
Rmet_3622	Op1009r	0.74	0.50	0.35	5.41	Q1LH82 Major facilitator superfamily MFS_1
Rmet_3624	Op1009r	0.54	4.25	0.43	4.38	Q1LH80 Transglutaminase-like protein
						Q1LH78 ATPase associated with various cellular activities, AAA_3
Rmet_3626	Op1009r	0.56	2.68	0.41	4.35	
Rmet_3678	Op1026f	0.51	1.67	0.46	3.47	Q1LH26 Methyl-accepting chemotaxis sensory transducer
						Q1LH24 Response regulator receiver domain protein (CheY-like)
Rmet_3680	Op1026f	0.54	2.80	0.44	8.51	
Rmet_3683	Op1026f	0.50	1.72	0.42	2.95	Q1LH21 Methyl-accepting chemotaxis sensory transducer
Rmet_3689	<i>cheA</i> Op1026f	0.61	2.19	0.49	3.26	Q1LH15 CheA signal transduction histidine kinases
Rmet_3690	<i>cheW</i> Op1026f	0.52	2.24	0.49	7.65	Q1LH14 CheW protein
						Q1LH12 Probable chemoreceptor glutamine deamidase
Rmet_3692	<i>cheD</i> Op1026f	0.62	1.72	0.50	4.13	<i>cheD</i>
Rmet_3695	<i>cheZ</i> Op1026f	0.57	2.38	0.50	2.96	Q1LH09 Chemotaxis phosphatase, CheZ
Rmet_3703	Op1026f	0.51	1.93	0.47	1.86	Q1LH01 Flagellar FlhE
Rmet_3721	Op1035r	0.56	1.60	0.49	3.11	Q1LGY3 Uncharacterized protein UPF0065
Rmet_3734	<i>flgB</i> Op1042f	0.51	1.03	0.33	4.84	Q1LGX0 Flagellar basal-body rod protein FlgB
Rmet_3739	<i>flgG</i> Op1042f	0.51	1.25	0.41	3.53	Q1LGW5 Flagellar basal-body rod FlgG

Rmet_3740	<i>flgH</i>	Op1042f	0.51	1.72	0.45	2.77	Q1LGW4 Flagellar L-ring protein
							Q1LGW2 Mannosyl-glycoprotein endo-beta-N-
Rmet_3742	<i>flgJ</i>	Op1042f	0.51	2.12	0.46	7.29	acetylglucosamidase
Rmet_3894		Op1086f	0.72	0.82	0.48	1.49	Q1LGG4 Putative uncharacterized protein
Rmet_3904		Op1092f	0.54	1.58	0.44	1.68	Q1LGF4 Putative serine protein kinase, PrkA
Rmet_4119		Op1160f	0.60	1.37	0.21	8.14	Q1LFU0 Putative uncharacterized protein
Rmet_4127		Op1163r	0.66	0.70	0.42	8.42	Q1LFT2 Putative uncharacterized protein
Rmet_4199		Op1190f	0.59	16.36	0.48	5.57	Q1LFL0 FAD-binding 9, siderophore-interacting
Rmet_4206		Op1192f	0.61	2.70	0.48	4.82	Q1LFK3 Transcriptional regulator, LysR family
Rmet_4245		Op1202f	0.56	5.31	0.41	6.34	Q1LFG5 Transcriptional regulator, LysR family
Rmet_4246		#NV	0.71	2.28	0.44	4.58	Q1LFG4 Putative uncharacterized protein
Rmet_4426		Op1259r	0.65	2.13	0.50	3.24	Q1LEY5 MmgE/PrpD family protein
Rmet_4433		Op1262f	0.55	2.83	0.49	2.65	Q1LEX8 Uncharacterized protein UPF0065
Rmet_4464		Op1273r	0.62	1.60	0.48	2.68	Q1LEU7 Putative uncharacterized protein
Rmet_4466	<i>czcS2</i>	Op1274f	0.50	3.33	0.49	11.93	Q1LEU5 Sensor protein
Rmet_4524		Op1297r	0.54	1.55	0.38	6.02	Q1LEN7 Negative transcriptional regulator
Rmet_4561		Op1311r	0.55	2.55	0.42	1.82	Q1LEK3 Transcriptional regulator, AsnC family
Rmet_4565		Op1314f	0.58	2.13	0.25	1.34	Q1LEJ9 TonB-dependent receptor
Rmet_4566		Op1315r	0.62	2.06	0.30	1.35	Q1LEJ8 Putative uncharacterized protein
Rmet_4592		Op1320f	0.52	6.40	0.42	3.91	Q1LEH2 NAD-dependent epimerase/dehydratase
Rmet_4594	<i>zntA</i>	Op1321r	0.58	2.41	0.48	3.72	Q1LEH0 Heavy metal translocating P-type ATPase
Rmet_4602		Op1324f	0.51	3.64	0.46	6.10	Q1LEG2 Transcriptional regulators, TraR/DksA family
							Q1LED7 Two component transcriptional regulator, LuxR
Rmet_4627		Op1333r	0.51	3.99	0.50	2.43	family
Rmet_4761		Op1386f	0.53	1.16	0.45	5.60	Q1LE03 Putative uncharacterized protein
Rmet_4775		Op1388f	0.63	3.62	0.39	8.91	Q1LDY9 Extracellular ligand-binding receptor
Rmet_4802		Op1396f	0.64	1.64	0.50	3.11	Q1LDW2 Putative uncharacterized protein
Rmet_4806		Op1398f	0.61	2.18	0.50	8.75	Q1LDV8 Transcriptional regulator, XRE family
Rmet_4809	<i>acpA</i>	Op1400f	0.55	1.48	0.49	2.12	Q1LDV5 Phosphoesterase
Rmet_4864		Op1419r	1.90	2.95	0.49	1.08	Q1LDQ0 Putative uncharacterized protein
Rmet_4880		Op1427r	0.54	1.69	0.49	21.77	Q1LDN4 Transcriptional regulator, LysR family
Rmet_4893		Op1431r	0.63	3.12	0.47	2.94	Q1LDM1 Putative uncharacterized protein
Rmet_4954		Op1455r	0.52	1.47	0.48	2.65	Q1LDG0 Transcriptional regulator, GntR family
Rmet_4975		Op1460f	0.61	1.15	0.45	4.34	Q1LDD9 Resolvase-like protein

Rmet_4976	Op1461r	0.60	1.60	0.47	9.15	Q1LDD8 Putative uncharacterized protein
Rmet_5005	Op1469r	0.66	1.66	0.46	5.36	Q1LDA9 Isochorismatase hydrolase
Rmet_5006	Op1469r	0.66	1.94	0.43	7.67	Q1LDA8 Putative uncharacterized protein
Rmet_5076	Op1494f	0.56	7.04	0.42	4.24	A5FF57 Sulfatase
Rmet_5077	Op1495r	0.57	2.56	0.32	6.70	A5FF57 Sulfatase
Rmet_5080	Op1496f	0.71	2.01	0.49	2.76	Q1LD37 Putative uncharacterized protein
Rmet_5081	Op1496f	0.53	4.06	0.49	5.25	Q1LD36 Putative uncharacterized protein
Rmet_5140	Op1515r	0.52	1.89	0.43	4.10	Q1LCX7 AMP-dependent synthetase and ligase
Rmet_5213	Op1535r	0.64	1.92	0.44	4.04	Q1LCQ4 Transcriptional regulator, GntR family
Rmet_5297	Op1566f	0.58	1.77	0.37	3.64	Q1LCH0 Flagellar basal body-associated protein FliL
Rmet_5301	<i>fliP</i> Op1566f	0.51	3.99	0.47	2.44	Q1LCG6 Flagellar biosynthetic protein FliP
Rmet_5344	Op1586f	0.79	1.25	0.49	1.75	Q1LCC3 Putative uncharacterized protein
Rmet_5385	Op1602f	0.59	4.51	0.34	6.40	Q1LC82 Putative uncharacterized protein
Rmet_5427	Op1614f	0.50	1.52	0.47	2.21	Q1LC40 Putative uncharacterized protein
Rmet_5475	Op1626f	0.55	2.25	0.46	2.86	Q1LBZ2 Putative uncharacterized protein
Rmet_5507	Op1639r	0.52	2.25	0.44	6.69	Q1LBW0 Acyl-CoA dehydrogenase-like protein
Rmet_5534	Op1645r	0.51	3.68	0.41	2.13	Q1LBT3 2-nitropropane dioxygenase, NPD
Rmet_5547	Op1647r	0.51	2.26	0.50	3.19	Q1LBS0 Transcriptional regulator, LuxR family
Rmet_5549	Op1648f	0.51	2.69	0.50	2.44	Q1LBR8 Ferredoxin
Rmet_5572	Op1657r	0.53	1.26	0.44	3.56	Q1LBP5 Dyp-type peroxidase
Rmet_5594	Op1666f	0.54	1.97	0.45	3.06	Q1LBM3 Putative uncharacterized protein
Rmet_5642	<i>fliD3</i> Op1683r	0.50	2.45	0.44	3.92	Q1LBH5 Flagellar hook-associated 2-like protein
Rmet_5686	Op1698f	0.60	1.33	0.44	6.80	Q1LBD1 Tfp pilus assembly protein PilV-like protein
Rmet_5763	Op1728f	0.51	3.31	0.48	5.31	Q1LB54 Putative uncharacterized protein
Rmet_5785	Op1740f	0.53	1.93	0.48	2.54	Q1LB32 Putative uncharacterized protein
Rmet_5816	Op1756f	0.68	0.70	0.33	6.38	Q1LB01 Cold-shock DNA-binding protein family
Rmet_5846	Op1766f	0.52	4.86	0.44	3.70	Q1LAX1 Putative uncharacterized protein
Rmet_5862	Op1773r	0.52	8.19	0.47	6.21	Q1LAV5 Putative signal peptide protein
Rmet_5868	<i>leuC</i> Op1777r	0.59	1.52	0.45	6.10	Q1LAU9 3-isopropylmalate dehydratase, large subunit
Rmet_5935	Op1804f	0.53	10.26	0.42	4.74	Q1LAN2 Methyl-accepting chemotaxis sensory transducer
Rmet_6068	Op1849r	0.51	1.50	0.48	4.87	Q58AB4 ISRme8aa1 (Transposase IS3/IS911)
Rmet_6335	Op1926f	0.54	1.79	0.48	11.39	Q5NUU4 ISRme2 transposase protein (Integrase, catalytic region)

^aCells of strain $\Delta zupT$ and its parent AE104 were confronted with 50 μM EDTA or 10 μM zinc chloride until the turbidity reached 100 Klett units, RNA was isolated, reversely transcribed, labeled and hybridized against a CH34-specific gene array. Provided are the Q-ratios $\Delta zupT$ /AE104 for both treatments, red if at least 2-fold down-regulated, green up, bold-faced letters indicate significant differences, letters in italics not significant differences. The D-value for each comparison is also given. This is the distance of both mean values divided by the sum of both deviations. If $D > 1$ (the deviation bars do not touch or overlap) the data points are different with a probability in the t-test of $> 95\%$. Three biological repeats for AE104, two for the mutant strain. Genes associated to catabolic metabolic genomic islands (CMGIs) are on a yellow ground and in a box.

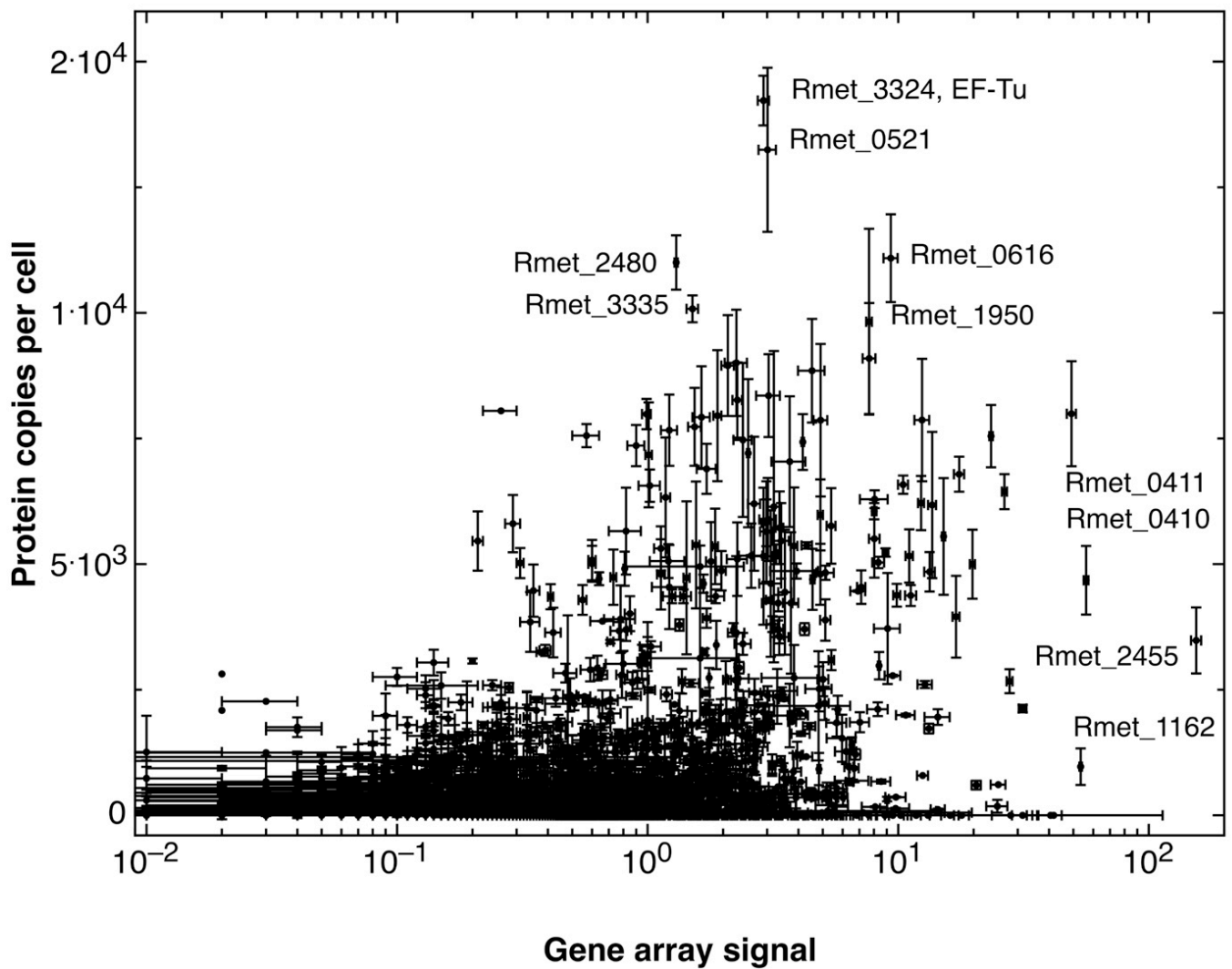
^bAn operon region was defined as adjacent genes in the same direction of transcription without interruption and all genes of the *C. metallidurans* genome were assigned to operon regions Op0001f on chromosome 1 to Op1929r on pMOL28 with “f” or “r” giving the direction of transcription.

Supplementary Table S5. Activity of *zupTp* and *cobW1p* promoters as determined with a *gfp* fusion *in trans* in various *C. metallidurans* strains^a.

	<i>zupTp-gfp</i>						<i>cobW1p-gfp</i>					
	AE104	$\Delta zupT$	$\Delta e4$	$\Delta e4 \Delta zupT$	Δzur	CH34	AE104	$\Delta zupT$	$\Delta e4$	$\Delta e4 \Delta zupT$	Δzur	CH34
Basal [EDTA], (μ M)	2.07	10.15	1.72	3.73	7.21	1.89	0.81	1.11	0.74	1.48	5.90	0.87
0	1	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
1	0.98	0.99	1.00	0.98	0.95	0.97	0.94	1.02	0.88	1.08	0.95	0.98
10	1.12	1.08	1.01	1.18	1.03	0.94	0.92	1.14	0.83	1.85	0.95	0.97
25	1.14	1.09	1.07	1.24	1.03	0.98	0.95	1.19	0.85	1.98	0.97	1.00
50	1.62	1.14	1.55	1.26	1.02	1.46	1.06	1.30	1.01	1.97	0.98	0.99
100	2.01	1.17	2.44	1.44	1.02	1.81	1.20	1.49	1.19	2.21	0.97	1.20
250	2.63	1.23	3.50	1.64	1.02	2.51	1.82	1.91	1.91	2.21	0.98	1.97
500	2.92	1.23	3.75	1.73	1.01	2.72	2.76	2.61	2.89	2.18	0.96	3.04
1000	2.78	1.37	4.12	1.84	0.96	2.63	2.67	2.53	3.27	2.01	0.93	3.16
Basal [Zn(II)], (μ M)	2.33	9.66	2.10	3.51	6.51	1.40	0.80	1.15	0.75	1.83	4.97	0.62
0	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
5	0.95	0.57	0.73	0.49	0.94	0.87	0.89	0.59	0.86	0.35	0.93	0.96
10	0.93	0.48	0.84	0.53	0.90	0.80	0.84	0.60	0.86	0.39	0.94	1.02
25	0.89	0.40	0.98	0.65	0.90	0.76	0.83	0.57	0.95	0.58	1.00	0.91
50	0.88	0.40	1.00	0.68	0.92	0.79	0.83	0.58	1.08	0.53	1.08	0.84
75	0.84	0.41	0.92	0.68	0.88	0.82	0.85	0.70	1.22	0.43	1.07	0.79
100	0.82	0.42	0.82	0.63	0.86	0.81	0.92	0.71	0.98	0.35	0.95	0.61
150	0.80	0.40	0.76	0.66	0.85	0.81	0.91	0.71	0.83	0.32	0.95	0.77
250	0.78	0.42	0.71	0.65	0.85	0.87	0.97	0.72	0.78	0.33	0.99	0.83
500	0.83	0.46	0.71	0.68	0.90	0.90	1.09	0.77	0.66	0.35	0.97	0.87
750	1.01	0.45	0.69	0.64	1.03	0.87	1.27	0.78	0.78	0.35	0.96	0.99
1000	0.97	0.46	0.72	0.64	1.05	0.93	1.05	0.70	0.82	0.33	0.90	1.20

A *gfp* fusion plasmid was constructed on the basis of plasmid pBBR_MCS2 and designated pBBR-GFP13. Fragments containing the promoter regions of *zupT* and *cobW1* were cloned upstream of the promoterless *gfp* gene). The resulting plasmids were transferred by conjugation into the *C. metallidurans* strains CH34 wild type, its plasmid-free derivative AE104, and the AE104 mutants $\Delta zupT$, $\Delta e4$ ($\Delta zntA \Delta cadA \Delta fieF \Delta dmeF$), $\Delta e4 \Delta zupT$, and Δzur (= $\Delta furC$). The negative control contained just plasmid pBBR-GFP13. The cells were

incubated in TMM containing various concentrations of EDTA or zinc chloride and the specific activity of the GFP fluorescence was calculated in nmol per μg dry weight. There was no difference of the specific activities from the negative controls, which always gave 11.27 ± 3.97 nmol/ μg . To obtain the basal expression levels, the specific fluorescence activity coming from the promoter fusions were divided by this background value coming from the negative controls and the D-value was calculated as a measure of significance ($D = \text{absolute distance of the mean values divided by the sum of the deviations}$, if $D > 1$, the differences are significant if $n \geq 3$). Bold basal values indicate $D > 1$, green and bold values additionally a ratio > 2 . Since the values resulting from cultures incubated without added zinc should be similar to those coming from cultures without added EDTA, another control for the integrity of the data was obtained. Secondly, all values coming from cultures with added zinc or EDTA were compared to the respective basal levels, indicating up- or down-regulation. Again, $D > 1$ is indicated by bold-faced numbers, green means more than 2-fold up-regulation and red more than 2-fold down-regulation with respect to the associated basal level value obtained for TMM without additions. Repeats (n) between 3 and 14.



Supplementary Figure S1. Comparison of transcriptome and proteome data. The spot densities from a gene array experiment with strain AE104 cells ($n = 3$, overall density of the array normalized to 10,000 arbitrary gene-specific and intergenic RNAs per cell) cultivated in TMM without additions were compared to the number of proteins per cell obtained from the same strain cultivated under the same conditions. Deviation bars for both axis are given. The position of a few proteins versus their gene array signals are labeled.