Supplementary data

Comparative insights into the catabolic model of a formaldehyde degrading strain *Methylobacterium* sp. XJLW

Yunhai Shao†, Jun Li†, Yanxin Wang, Fengmei Yi, Yanan Zhang, Peiwu Cui, Weihong Zhong*

College of Biotechnology and Bioengineering, Zhejiang University of Technology, Hangzhou , PR China

†These authors have contributed equally to this work.

*Corresponding author:

WeihongZhong, College of Biotechnology and Bioengineering, Zhejiang University of Technology, hangzhou, Tel/Fax: 86-571-88320739, whzhong@zjut.edu.cn

Supplementary data

Table S1 Insertion sequence types, genome coordinates and sequences of target site duplication if applicable.

Table S2 The information of Genomic Islands

Table S3 601 specific genes of XJLW against four *Methylobacterium* strains identified by all-against-all BLASTn pipelines.

Table S4 The results of NCBI alignment on the upstream and downstream contexts of the XJLW Met cluster.

Table S5 623 significant up-regulated genes and 90 significant up-regulated strain-specific genes (orange) in the whole genome.

Table S6 The genes and enzymes of carbon metabolism.

Supplementary data

Table S1 Insertion sequence types, genome coordinates and sequences of target site duplication if applicable.

IS type	Genome coordinate (bp)		Orientation (+/-)	Locus tag of transposase gene(s)	Sequence of Target Site Duplication	
	Start	End			Flanking region left	Flanking region right
IS*Mdi7*	6356926	6359493	+	A3862_28940	ATGCTCGGCACTGTCGCGGTGGTGGTCGCTACTCACGACCTCGCCAAGGGTGTGC	GATCTCGTCGCGACGCTGATGGAAGGCGTCGTGACCGGCTCGGGCATGGCACCTC
	2419082	2416518	-	A3862_10925	GTGACGACGGAAGAAGCGCCCGGCCCGGCCTGAACCGGCGCCGTATCGAAGCCGA	CCTCGATCAGGTCGCTGGTGTCCTCGTCGTCCTCGTCGACCACGAGGGTGTCATC
	5903724	5906288	+	A3862_26690	CGATCAGGTTGGCCACGACGCGGCGCAGGGCGACCGCGTCGCCGGCCACCGTGGC	CCAGCCGTATATCCGGAACCGCGGCGGCTTCGCCCTGCTCAACAGTCAAAATGAA
	4918848	4916285	-	A3862_22360	GATCGTGACCTTGCGGTCCACTCTGAGAACGGCCCCGTTGATGAAGATGCGCTCC	CGCTCCTGGCCTCGCAGGCTGAGATTGATCGAGCGGCTCATTGGAGACCATCGCG
	3394077	3391518	-	A3862_15395	CGGGCGCTCGGGGCGACCAGGAAGGCGAGGCGAAGTCCGGCACCCAGGCACTTGG	CACTTGGCGAGACCCGCCACGTAGTAGGTGATCTCCGGAGCAAGCTCCGCAAAAC
IS*Mex11*	1560381	1561607	+	A3862_07060	TCTGATGAAAACGGCATCCGGCTTTAACGAACTTCGACCCTGAGATGGGTTGGAC	GGACCGTCCATCCGGAGACGGCGATTCATCCTAGGTCCGCTTTAGAACGTCTTGC
	5391425	5390534	-	A3862_24355	NA	NA
	5388876	5388539	-	A3862_24340	NA	NA
IS*Mex12*	1494230	1492813	–	A3862_06790	CTCGACGGCTCTGGGGCGGCGCGCGAAGCCATGCTGAGCGCAGCGCGCCGCCCTG	GACCACGGTGCCGCGTGCATCGGCTGGATCCTGTGTTCGCTATGGCCGAGAGTTC
	5388950	5390365	+	A3862_24350	CTCGACGGCTCTGGGGCGGCGCGCGAAGCCATGCTGAGCGCAGCGCGCCGCCCTG	GACCACGGTGCCGCGTGCATCGGCTGGATCCTGTGTTCGCTATGGCCGAGAGTTC
IS*Mex3*	1580196	1578799	-	A3862_07140	CATCTGATGACGGTCGAAGCTGGACAAATCGAGCGGACCGGGCTCACCCGCCGAC	CCCGCCGACTGCCCGGCGATCTGGAAGCTCCAGGTGAATGAGGCCCAGGCATGCG

[a] Orientation was defined in terms of the transposase gene.

[b] NA: not available.

Supplementary data

Table S2 The information of Genomic Islands

Gene islands that contain specific genes and are significantly up-regulated				**Significantly up-regulated genes**		
ID	**Start（bp）**	**End（bp）**	**Size（bp）**	**Locus_tag**	**Gene**	**Product**
1	6001717	6054842	53126	A3862_27225		hypothetical protein
				A3862_27235		hypothetical protein
				A3862_27240		hypothetical protein
				A3862_27245		hypothetical protein
				A3862_27270		hypothetical protein
				A3862_27335		hypothetical protein
				A3862_27395		hypothetical protein
				A3862_27410		hypothetical protein
				A3862_27420		hypothetical protein
				A3862_27445		hypothetical protein
				A3862_27455		hypothetical protein
				A3862_27470		hypothetical protein
				A3862_27480		hypothetical protein
				A3862_27490		hypothetical protein

Other gene islands			
ID	**Start（bp）/ Locus_tag**	**End（bp）/ Locus_tag**	**Size（bp）**
2	15715	25265	9551
3	25805	30437	4633
4	79518	91828	12311
5	180104	191014	10911
6	208506	212905	4400
7	254397	258612	4216
8	925471	929809	4339
9	935859	977211	41353
10	989185	999777	10593
11	992084	1015469	23386
12	1032850	1039284	6435

13	1040958	1073869	32912
14	1116794	1124077	7284
15	1147378	1164716	17339
16	1375124	1399752	24629
17	1405488	1423217	17729
18	1426205	1432392	6188
19	1445026	1452362	7337
20	1479890	1488788	8899
21	1500704	1510804	10101
22	1515250	1521007	5758
23	1718657	1723785	5129
24	1751581	1756415	4835
25	1875028	1879867	4840
26	1880622	1886408	5787
27	1898944	1904788	5845
28	2470301	2475115	4815
29	2794828	2802883	8056
30	3271699	3280795	9097
31	3302571	3330052	27482
32	3331081	3338452	7372
33	3350396	3358565	8170
34	3365268	3371437	6170
35	3390562	3394568	4007
36	3397683	3407668	9986
37	3428502	3432537	4036
38	3490642	3505370	14729
39	3549286	3559208	9923
40	4437803	4443333	5531
41	4444322	4450061	5740

42	4453071	4466910	13840
43	4576374	4580838	4465
44	4593975	4608607	14633
45	4852535	4861064	8530
46	4914742	4919236	4495
47	5360285	5397282	36998
48	5432788	5436892	4105
49	5452467	5457958	5492
50	5458489	5462617	4129
51	5464834	5479669	14836
52	5903831	5909610	5780
53	6305390	6313310	7921
54	6318025	6338329	20305
55	6369376	6381777	12402
56	6386018	6390088	4071
57	6399465	6406152	6688
58	6417151	6424578	7428
59	6446540	6450899	4360
60	6476467	6481056	4590

Table S3 601 specific genes of XJLW against four *Methylobacterium* strains identified by all-against-all BLASTn pipelines.

Gene ID	Coordinate*	XJLW_G_FPKM	XJLW_M_FPKM	log2(XJLW_M/XJLW_G)	up-or-down	Description
A3862_00280	c65246-63189	85.2601	157.543	0.885804	up	chromosome segregation protein SMC
A3862_00285	c65773-65243	89.404	104.112	0.21973	up	hypothetical protein
A3862_00290	c67056-65773	51.8847	137.104	1.40189	up	hypothetical protein
A3862_00295	c68037-67369	106.287	134.684	0.341615	up	uracil-DNA glycosylase
A3862_00300	c69185-68034	100.519	160.519	0.675283	up	pyrophosphatase
A3862_00305	69392-69919	730.685	911.208	0.318532	up	hypothetical protein
A3862_00310	69927-70520	136.061	270.216	0.98986	up	hypothetical protein
A3862_00320	c75650-74421	34.1896	122.893	1.84578	up	efflux transporter periplasmic adaptor subunit
A3862_00325	c76032-75721	13.1696	38.6518	1.55332	up	hypothetical protein
A3862_00330	76140-76412	10.6116	18.9658	0.83776	up	nickel resistance protein
A3862_00335	76421-77755	28.554	145.131	2.34559	up	MFS transporter
A3862_00355	c82418-80559	40.6766	154.24	1.9229	up	hypothetical protein
A3862_00360	c83556-82429	28.375	126.354	2.15478	up	hypothetical protein
A3862_00365	c85828-83567	30.1559	158.768	2.39641	up	integrase
A3862_00370	c86031-85810	17.4766	22.298	0.351492	up	hypothetical protein
A3862_00375	c86723-86028	20.4836	95.7198	2.22435	up	hypothetical protein
A3862_00380	c87922-86723	32.6193	154.097	2.24004	up	hypothetical protein
A3862_00385	c89158-88658	225.117	205.307	-0.132893	down	hypothetical protein
A3862_00390	c91048-89687	20.541	130.087	2.6629	up	hypothetical protein
A3862_00395	c92517-91597	26.4061	111.958	2.08402	up	3'-5' exonuclease
A3862_00400	c93521-92541	29.4601	136.373	2.21072	up	hypothetical protein
A3862_00405	c95461-93518	35.74	150.241	2.07167	up	AAA family ATPase
A3862_00410	c96337-95546	16.9098	106.207	2.65095	up	metallophosphoesterase
A3862_00415	c96823-96392	5.93535	42.9242	2.85439	up	hypothetical protein
A3862_00420	c97941-96913	67.4844	152.075	1.17216	up	hypothetical protein
A3862_00425	98700-99485	35.1817	122.199	1.79634	up	hypothetical protein

A3862_00430	99503-99835	8.65242	32.2198	1.89677	up	hypothetical protein
A3862_00435	100463-100777	16.3646	27.7923	0.764103	up	transcriptional regulator
A3862_00440	100966-102288	73.825	144.581	0.969694	up	type II restriction endonuclease
A3862_00445	102294-102677	30.0138	49.4685	0.720884	up	hypothetical protein
A3862_00450	c103871-102753	122.269	154.392	0.336541	up	hypothetical protein
A3862_00460	c107693-105252	46.2354	184.905	1.99971	up	haloacid dehalogenase
A3862_00465	c108275-107778	119.607	200.143	0.742732	up	DUF305 domain-containing protein
A3862_00470	c108664-108332	46.0074	101.274	1.13832	up	ferredoxin
A3862_00475	c109512-109036	962.698	317.674	-1.59954	down	hypothetical protein
A3862_00480	c109819-109607	15.1406	17.3332	0.19512	up	heavy metal transporter
A3862_00490	111089-111448	27.5911	37.0074	0.423608	up	transcriptional regulator
A3862_00495	111441-111968	44.4531	85.7562	0.947958	up	ArsR family transcriptional regulator
A3862_00515	c115611-115135	71.5381	107.508	0.587663	up	metal-binding protein
A3862_00520	c118784-115632	31.6924	155.082	2.29083	up	cation transporter
A3862_00525	c120304-118781	33.1965	174.973	2.39802	up	efflux transporter periplasmic adaptor subunit
A3862_00530	c120705-120301	12.1018	70.8834	2.55023	up	heavy metal RND transporter
A3862_00535	c121200-120787	304.734	188.803	-0.69067	down	hypothetical protein
A3862_00540	c122020-121778	9.17378	6.31353	-0.53907	down	hypothetical protein
A3862_00545	c123030-122380	38.8484	83.235	1.09933	up	hypothetical protein
A3862_00550	c123581-123027	33.6686	79.8236	1.24541	up	RNA polymerase subunit sigma
A3862_00555	124104-124715	48.8425	162.667	1.73572	up	hypothetical protein
A3862_00560	124952-125389	114.802	94.7664	-0.276703	down	hypothetical protein
A3862_00565	125558-125854	13.1255	26.3908	1.00766	up	hypothetical protein
A3862_00570	125902-127434	41.0655	170.239	2.05156	up	transporter
A3862_00575	127476-128894	104.534	231.511	1.14711	up	copper oxidase
A3862_00580	129058-129348	14.5726	47.4509	1.70317	up	RND transporter
A3862_00585	129424-130134	32.1554	125.401	1.96342	up	DUF305 domain-containing protein
A3862_00590	130134-130844	25.676	114.479	2.1566	up	lytic transglycosylase

A3862_00595	130966-131763	38.0806	132.731	1.80137	up	GCN5 family acetyltransferase
A3862_00600	131830-133134	24.1763	143.271	2.56708	up	multidrug ABC transporter ATPase
A3862_00605	133462-133737	1.49842	14.9368	3.31736	up	hypothetical protein
A3862_00610	c134444-134091	15.4003	21.5197	0.4827	up	hypothetical protein
A3862_00615	134583-135008	38.8224	58.3426	0.58766	up	MerR family transcriptional regulator
A3862_00625	135767-136522	23.6006	113.684	2.26813	up	cation transporter
A3862_00635	137563-138249	16.5974	73.0374	2.13768	up	transporter
A3862_00640	138262-139008	34.5079	105.93	1.61811	up	DNA-binding response regulator
A3862_00645	139005-140339	21.5037	141.911	2.72233	up	two-component sensor histidine kinase
A3862_00650	140439-140702	43.8541	18.5224	-1.24344	down	hypothetical protein
A3862_00655	c141155-140916	211.783	93.176	-1.18456	down	hypothetical protein
A3862_00660	c141564-141328	60.237	12.322	-2.28942	down	hypothetical protein
A3862_00665	141795-142166	54.8368	43.3966	-0.337564	down	hypothetical protein
A3862_00680	146905-147462	19.5679	77.7393	1.99015	up	threonyl-trna synthetase
A3862_00685	147503-148444	37.9575	122.219	1.68701	up	cation transporter
A3862_00690	148715-148948	2.90515	10.5035	1.85418	up	hypothetical protein
A3862_00695	149133-149741	50.5855	93.143	0.880724	up	hypothetical protein
A3862_00700	149873-150310	8.92839	31.6347	1.82504	up	transporter
A3862_00705	150378-151037	18.4438	100.412	2.44472	up	DNA-binding response regulator
A3862_00710	151034-152329	35.7628	147.904	2.04813	up	two-component sensor histidine kinase
A3862_00715	152422-153198	33.8345	109.157	1.68983	up	hypothetical protein
A3862_00720	153267-153674	10.1841	48.4198	2.24927	up	histidine kinase
A3862_00725	153704-154486	22.1558	109.424	2.30417	up	hypothetical protein
A3862_00730	154516-155295	39.988	106.911	1.41877	up	hypothetical protein
A3862_00735	c155607-155413	0	34.5924	1.79769e+308	up	hypothetical protein
A3862_00740	155619-156236	31.9252	89.8006	1.49203	up	hypothetical protein
A3862_00830	181031-181723	16.8576	77.0288	2.192	up	hypothetical protein
A3862_00835	181720-183921	35.5384	150.222	2.07964	up	hypothetical protein

A3862_00840	183918-185078	25.6766	134.763	2.3919	up	hypothetical protein
A3862_00845	185075-186967	46.1764	149.206	1.69208	up	hypothetical protein
A3862_00850	186998-187237	93.2709	88.9956	-0.067692	down	hypothetical protein
A3862_00855	187234-187647	172.637	96.7714	-0.835086	down	hypothetical protein
A3862_00860	187641-187913	57.6516	26.0892	-1.14391	down	hypothetical protein
A3862_04125	904133-904645	31.331	68.0997	1.12006	up	hypothetical protein
A3862_04130	904642-905790	41.2175	131.164	1.67004	up	hypothetical protein
A3862_04135	c907069-905777	26.1755	143.938	2.45916	up	hypothetical protein
A3862_04140	c907400-907062	11.0952	22.9488	1.04848	up	hypothetical protein
A3862_04145	907879-908307	50.6003	87.3558	0.787757	up	hypothetical protein
A3862_04150	908420-908842	24.1134	56.5838	1.23055	up	hypothetical protein
A3862_04155	908919-909476	39.4878	102.568	1.3771	up	hypothetical protein
A3862_04160	909549-911186	34.6544	163.534	2.23848	up	hypothetical protein
A3862_04165	911198-911395	6.82174	32.3779	2.2468	up	hypothetical protein
A3862_04170	911382-911603	0	47.7743	1.79769e+308	up	hypothetical protein
A3862_04175	911576-911932	6.44917	46.6706	2.85533	up	hypothetical protein
A3862_04180	911947-912372	21.1881	44.8441	1.08166	up	hypothetical protein
A3862_04185	c913008-912592	6.52837	45.6851	2.80693	up	hypothetical protein
A3862_04190	c913175-912993	0	22.8819	1.79769e+308	up	hypothetical protein
A3862_04195	c913405-913172	7.20846	29.3281	2.02452	up	hypothetical protein
A3862_04200	c913785-913402	24.5829	56.7926	1.20805	up	hypothetical protein
A3862_04205	c915062-913782	25.9452	126.356	2.28396	up	hypothetical protein
A3862_04210	c915624-915223	12.0083	40.9196	1.76876	up	hypothetical protein
A3862_04215	c916082-915594	17.4967	80.1424	2.19549	up	hypothetical protein
A3862_04220	c916369-916079	5.77351	42.6429	2.88479	up	hypothetical protein
A3862_04225	c916836-916369	17.6927	90.4136	2.35339	up	hypothetical protein
A3862_04230	c917045-916833	3.10984	18.5543	2.57684	up	hypothetical protein
A3862_04235	c917491-917048	16.5836	54.5314	1.71733	up	lysozyme

A3862_04240	c917907-917641	0	17.816	1.79769e+308	up	hypothetical protein
A3862_04245	c918185-917907	0	22.2983	1.79769e+308	up	hypothetical protein
A3862_04250	c918445-918185	0	17.0373	1.79769e+308	up	hypothetical protein
A3862_04255	c919029-918445	20.9113	74.4618	1.83222	up	hypothetical protein
A3862_04260	c919388-919029	2.66866	36.5802	3.77688	up	hypothetical protein
A3862_04265	919793-923947	31.1594	169.216	2.44113	up	hypothetical protein
A3862_04270	925241-925666	22.5625	46.3338	1.03814	up	hypothetical protein
A3862_04275	925817-926710	53.4969	128.895	1.26867	up	hypothetical protein
A3862_04280	926713-927006	22.1947	28.6028	0.365943	up	hypothetical protein
A3862_04285	c927585-927340	11.0471	7.52436	-0.554032	down	hypothetical protein
A3862_04295	c930328-929795	35.6135	67.3797	0.919888	up	TetR family transcriptional regulator
A3862_04300	931152-932870	44.226	155.687	1.81568	up	NADH-quinone oxidoreductase subunit F
A3862_04305	932926-935898	86.106	191.093	1.15009	up	formate dehydrogenase subunit alpha
A3862_04310	937811-938755	36.6946	132.659	1.85409	up	ferredoxin
A3862_04315	938766-939827	50.2755	134.207	1.41653	up	hypothetical protein
A3862_04320	940141-940524	5.82076	18.5969	1.67578	up	hypothetical protein
A3862_04325	940751-942466	104.118	144.171	0.469566	up	amino acid permease
A3862_04330	942776-943102	3.61402	8.19617	1.18134	up	hypothetical protein
A3862_04335	943222-944355	78.3843	120.538	0.620848	up	aminomethyltransferase
A3862_04340	947283-948533	46.9049	128.514	1.45411	up	sarcosine oxidase subunit beta
A3862_04345	948546-948833	17.4821	32.6819	0.902616	up	sarcosine oxidase subunit delta
A3862_04350	948830-951865	69.9556	154.46	1.14272	up	sarcosine oxidase subunit alpha
A3862_04355	951858-952481	54.5444	82.3575	0.594468	up	sarcosine oxidase subunit gamma
A3862_04365	956674-956910	2.43887	9.95467	2.02916	up	hypothetical protein
A3862_04370	c958771-957314	173.507	183.795	0.0831026	up	transporter
A3862_04375	c959708-959403	22.7246	31.1756	0.456163	up	hypothetical protein
A3862_04380	960598-961491	268.587	162.469	-0.725224	down	glutamine amidotransferase
A3862_04385	961491-962180	178.842	116.289	-0.620973	down	protein glxC

A3862_04390	962180-963526	358.879	200.137	-0.842507	down	glutamate synthase
A3862_04395	963611-964909	304.86	162.349	-0.909044	down	type III glutamate--ammonia ligase
A3862_04415	c969097-967814	211.601	140.91	-0.586573	down	hypothetical protein
A3862_04425	971977-972885	17.7368	117.891	2.73264	up	integrase
A3862_04430	972892-974088	25.7271	108.048	2.07031	up	transposase
A3862_04485	c992084-991266	20.4885	119.804	2.54779	up	transposase
A3862_04495	993818-994636	17.8158	108.724	2.60944	up	hypothetical protein
A3862_04505	c999777-999565	3.7564	14.6416	1.96265	up	dodecin flavoprotein
A3862_04520	1006051-1006365	12.1712	15.3079	0.330798	up	hypothetical protein
A3862_04525	c1008648-1006573	47.4099	140.273	1.56497	up	chemotaxis protein
A3862_04530	1009752-1010021	8.50976	11.3492	0.415404	up	hypothetical protein
A3862_04535	c1010822-1010253	33.0604	80.7824	1.28894	up	hypothetical protein
A3862_04540	c1011894-1010839	120.937	158.137	0.386917	up	hypothetical protein
A3862_04545	c1012287-1012090	0	8.13103	1.79769e+308	up	hypothetical protein
A3862_04550	1012489-1012683	6.3418	2.18812	-1.5352	down	hypothetical protein
A3862_04555	c1013012-1012761	14.2728	15.3771	0.10751	up	hypothetical protein
A3862_04560	c1013970-1013140	96.5256	125.57	0.379503	up	hypothetical protein
A3862_04565	1014154-1015020	87.2705	106.799	0.291327	up	hypothetical protein
A3862_04570	c1015278-1015090	0	13.7884	1.79769e+308	up	hypothetical protein
A3862_04575	c1015871-1015632	7.07535	9.85918	0.478666	up	hypothetical protein
A3862_04580	1016475-1016795	27.3688	69.2025	1.33829	up	hypothetical protein
A3862_04585	c1017595-1016948	97.3551	107.845	0.147627	up	hypothetical protein
A3862_04590	c1018090-1017641	28.0683	58.6331	1.06277	up	hypothetical protein
A3862_04595	1018477-1018680	0	31.1572	1.79769e+308	up	hypothetical protein
A3862_04600	1018667-1018852	0	19.6394	1.79769e+308	up	hypothetical protein
A3862_04605	1018852-1019238	14.741	53.0241	1.84681	up	hypothetical protein
A3862_04610	1019305-1021086	33.3055	158.803	2.25341	up	hypothetical protein
A3862_04615	c1021283-1021032	5.52755	9.22958	0.739625	up	hypothetical protein

A3862_04620	1021574-1021813	4.90879	19.7918	2.01146	up	hypothetical protein
A3862_04625	1021810-1022328	31.9521	77.7231	1.28243	up	hypothetical protein
A3862_04630	1022321-1022815	33.3639	77.8342	1.22212	up	hypothetical protein
A3862_04635	1022902-1023330	68.9098	85.1383	0.305099	up	hypothetical protein
A3862_04640	1023327-1023593	27.1974	26.5689	-0.0337314	down	hypothetical protein
A3862_04645	c1024203-1023628	80.7468	96.2909	0.253995	up	metallophosphoesterase
A3862_04650	1024502-1024708	14.057	2.48422	-2.50042	down	hypothetical protein
A3862_04655	c1026230-1024665	497.88	247.293	-1.00958	down	hypothetical protein
A3862_04660	1026618-1027367	100.022	135.859	0.441796	up	hypothetical protein
A3862_04665	1027364-1028290	81.2229	122.084	0.587912	up	hypothetical protein
A3862_04670	c1029047-1028451	116.734	77.031	-0.599711	down	hypothetical protein
A3862_04675	c1030315-1030091	13.0016	21.9337	0.754462	up	hypothetical protein
A3862_04680	c1030518-1030312	15.4667	23.0754	0.577187	up	hypothetical protein
A3862_04690	1031577-1033265	30.4187	142.093	2.22381	up	hypothetical protein
A3862_04695	1033276-1033512	29.6532	19.6187	-0.595958	down	hypothetical protein
A3862_04700	1033839-1034261	17.8235	44.6864	1.32605	up	hypothetical protein
A3862_04705	c1034788-1034270	29.497	58.903	0.997774	up	hypothetical protein
A3862_04710	c1035672-1034785	91.5024	111.13	0.280368	up	hypothetical protein
A3862_04715	1036376-1038508	109.88	202.689	0.883345	up	hypothetical protein
A3862_04720	c1040041-1039166	20.7109	102.395	2.30569	up	hydroxyquinol 1,2-dioxygenase
A3862_04725	c1040504-1040118	7.24406	46.8711	2.69383	up	hypothetical protein
A3862_04730	c1040958-1040572	75.2636	54.4253	-0.467674	down	hypothetical protein
A3862_04750	1045985-1046530	175.756	123.251	-0.511971	down	hypothetical protein
A3862_04770	1049733-1050098	17.8466	30.8378	0.789049	up	transposase
A3862_04780	1050639-1050848	3.03014	14.9935	2.30689	up	hypothetical protein
A3862_04785	1050965-1052245	122.196	228.352	0.90206	up	amine oxidase
A3862_04790	c1054080-1052338	36.1711	167.39	2.21031	up	hypothetical protein
A3862_04795	c1055210-1054221	291.179	197.392	-0.560843	down	alcohol dehydrogenase

A3862_04800	c1055933-1055340	148.66	103.737	-0.519079	down	NADPH-dependent F420 reductase
A3862_04810	c1058140-1056983	119.052	147.498	0.309104	up	-
A3862_04815	1058311-1058961	44.565	113.115	1.34381	up	TetR family transcriptional regulator
A3862_04820	c1059885-1059058	28.1147	118.613	2.07687	up	transposase
A3862_04830	c1063090-1061522	2967.23	229.409	-3.69313	down	2-keto-gluconate dehydrogenase
A3862_04835	c1063742-1063206	1963.82	123.543	-3.99058	down	Twin-arginine translocation pathway signal
A3862_04840	c1064212-1063811	1447.48	70.454	-4.36072	down	lactoylglutathione lyase
A3862_04845	1064548-1064970	223.641	82.8107	-1.4333	down	hypothetical protein
A3862_04850	1065538-1065885	6.15306	25.2883	2.03909	up	isocitrate lyase
A3862_04855	1065963-1067519	32.5923	136.972	2.07128	up	transposase
A3862_04860	1067713-1068918	700.56	313.13	-1.16175	down	hypothetical protein
A3862_04865	1069938-1070822	58.6367	116.295	0.98791	up	NAD(P)-dependent oxidoreductase
A3862_04885	1073291-1073869	26.2343	82.7685	1.65763	up	polyisoprenoid-binding protein
A3862_04890	1073897-1074826	52.5506	137.524	1.3879	up	glyoxalase
A3862_04895	1075314-1075502	0	7.95381	1.79769e+308	up	hypothetical protein
A3862_04905	1076815-1077384	815.299	319.006	-1.35375	down	protease
A3862_04910	c1077908-1077495	192.31	79.6916	-1.27093	down	hypothetical protein
A3862_04915	c1079446-1078334	417.885	243.408	-0.779731	down	alkene reductase
A3862_04920	c1080314-1079493	371.183	193.094	-0.942829	down	arylesterase
A3862_04925	1081063-1082121	202.715	155.414	-0.383335	down	NAD-dependent dehydratase
A3862_04930	c1083346-1082324	288.677	243.33	-0.246547	down	Zn-dependent oxidoreductase
A3862_04935	c1085083-1083644	102.936	281.009	1.44887	up	transposase
A3862_04940	c1085678-1085295	12.1429	48.2353	1.98998	up	histidine kinase
A3862_04945	c1088254-1085675	31.9345	158.121	2.30784	up	hypothetical protein
A3862_04950	c1090458-1088569	34.0404	152.124	2.15993	up	hypothetical protein
A3862_05050	1117928-1118548	54.5421	121.928	1.16059	up	transcriptional regulator
A3862_05055	1118550-1119083	18.1118	80.144	2.14567	up	isochorismatase
A3862_05065	c1121528-1120263	63.1215	167.966	1.41196	up	isovaleryl-CoA dehydrogenase

A3862_05070	1121655-1122197	22.0798	74.6712	1.75783	up	cytidyltransferase
A3862_05075	1122194-1123546	47.8961	152.112	1.66715	up	phosphoglycerate mutase
A3862_05080	c1123907-1123614	22.4806	27.159	0.272753	up	hypothetical protein
A3862_05090	1125530-1127860	30.2952	169.05	2.48029	up	DNA topoisomerase
A3862_05100	1130164-1130715	52.9407	85.7442	0.695662	up	hypothetical protein
A3862_05105	c1131000-1130767	0	14.2359	1.79769e+308	up	hypothetical protein
A3862_05110	c1132086-1131376	42.5415	95.8097	1.1713	up	GntR family transcriptional regulator
A3862_05115	1132199-1133257	57.1161	143.189	1.32596	up	sorbitol dehydrogenase
A3862_05120	1133254-1134270	76.369	125.027	0.711181	up	NAD(P)H-quinone oxidoreductase
A3862_05125	1134270-1135997	88.0614	150.367	0.771909	up	acetolactate synthase catalytic subunit
A3862_05130	1136065-1137285	192.79	125.782	-0.616108	down	amino acid-binding protein
A3862_05135	1137342-1138229	78.2312	130.338	0.736437	up	branched-chain amino acid ABC transporter permease
A3862_05140	1138241-1140070	88.9057	148.752	0.742557	up	branched-chain amino acid ABC transporter ATP-binding protein
A3862_05145	1140057-1140761	57.2554	91.8839	0.6824	up	branched-chain amino acid ABC transporter ATP-binding protein
A3862_05150	1140763-1141569	72.3908	122.054	0.753638	up	3-oxoacyl-[acyl-carrier-protein] reductase
A3862_05155	1141610-1142419	77.8904	131.207	0.752329	up	shikimate dehydrogenase
A3862_05160	1142441-1144075	53.9535	139.048	1.36579	up	choline dehydrogenase
A3862_05165	1144625-1145098	21.4733	55.1883	1.36182	up	hypothetical protein
A3862_05170	1145446-1146354	26.5498	113.012	2.0897	up	integrase
A3862_05180	1147558-1147773	943.953	1063.49	0.172013	up	hypothetical protein
A3862_05185	1148432-1150006	38.3226	127.484	1.73405	up	hypothetical protein
A3862_05190	1150535-1150957	16.4853	41.9066	1.346	up	hypothetical protein
A3862_05195	1151038-1151367	4.47563	16.949	1.92104	up	hypothetical protein
A3862_05200	1151705-1151887	11.2602	22.9978	1.03026	up	hypothetical protein
A3862_05205	1151904-1153010	22.8191	116.989	2.35806	up	hypothetical protein
A3862_05210	1153012-1153665	13.5845	77.8157	2.51809	up	hypothetical protein
A3862_05215	1153665-1155068	32.9277	142.762	2.11624	up	hypothetical protein

A3862_05220	c1155671-1155075	11.974	68.1866	2.50959	up	hypothetical protein
A3862_05225	1155900-1156259	191.984	81.173	-1.24191	down	hypothetical protein
A3862_05230	c1157045-1156398	71.4721	109.505	0.615538	up	hypothetical protein
A3862_05235	c1158393-1157116	22.7694	141.538	2.63602	up	hypothetical protein
A3862_05240	1158611-1158880	21.8638	44.6677	1.03069	up	hypothetical protein
A3862_05245	1158877-1159200	17.9837	34.1021	0.923167	up	hypothetical protein
A3862_05250	1159197-1160021	19.9657	114.456	2.5192	up	hypothetical protein
A3862_05255	1160068-1160268	0	27.1786	1.79769e+308	up	hypothetical protein
A3862_05260	1160265-1160768	20.5452	77.2987	1.91164	up	hypothetical protein
A3862_05265	1160842-1161354	121.466	85.2749	-0.510357	down	hypothetical protein
A3862_05270	c1161720-1161412	50.5042	28.0256	-0.849657	down	hypothetical protein
A3862_05275	c1162261-1161683	29.5033	73.5213	1.31729	up	metallophosphoesterase
A3862_05280	c1164270-1162762	57.7102	158.213	1.45497	up	hypothetical protein
A3862_06300	c1375405-1375124	12.6577	14.0961	0.155282	up	hypothetical protein
A3862_06305	c1377708-1376584	32.8561	124.814	1.92555	up	mechanosensitive ion channel protein MscS
A3862_06310	1379043-1379771	26.2009	99.1306	1.91971	up	hypothetical protein
A3862_06315	c1380779-1379958	448.737	196.361	-1.19236	down	hypothetical protein
A3862_06320	c1385078-1382172	58.0194	192.479	1.73009	up	hypothetical protein
A3862_06325	c1385532-1385080	190.711	121.869	-0.646059	down	hypothetical protein
A3862_06330	c1386620-1386225	95.6592	57.032	-0.746131	down	hypothetical protein
A3862_06335	c1387991-1387407	67.0122	85.1292	0.345231	up	hypothetical protein
A3862_06340	c1391027-1389507	226.362	203	-0.15715	down	phospholipase
A3862_06345	1391192-1391803	116.762	123.377	0.0795121	up	alkaline phosphatase
A3862_06350	1391865-1393151	45.0999	169.199	1.90752	up	sodium:proton exchanger
A3862_06355	c1394309-1393638	24.4533	96.6793	1.98318	up	hypothetical protein
A3862_06360	c1395208-1394333	45.2902	141.613	1.64468	up	hypothetical protein
A3862_06365	c1397039-1395765	67.8523	172.357	1.34493	up	hypothetical protein
A3862_06370	c1398291-1397233	92.3284	160.078	0.793931	up	hypothetical protein

A3862_06375	1399054-1399266	3.5458	18.2235	2.36161	up	hypothetical protein
A3862_06380	c1400488-1399574	54.6611	139.85	1.35529	up	3'-5' exonuclease
A3862_06385	c1401925-1401035	61.1956	139.562	1.18941	up	hypothetical protein
A3862_06390	c1404485-1402392	35.0686	143.454	2.03234	up	hypothetical protein
A3862_06395	c1404835-1404431	18.6973	49.1975	1.39576	up	hypothetical protein
A3862_06400	c1405856-1404933	34.8256	141.635	2.02396	up	metallophosphoesterase
A3862_06405	c1406743-1405934	27.3827	136.751	2.32021	up	AAA family ATPase
A3862_06410	c1408506-1407724	29.2772	120.754	2.04422	up	metallophosphoesterase
A3862_06415	c1408923-1408606	2.0433	22.3158	3.44909	up	hypothetical protein
A3862_06420	c1410517-1410254	16.128	11.2881	-0.514762	down	hypothetical protein
A3862_06425	c1411125-1410895	2.265	11.6923	2.36797	up	hypothetical protein
A3862_06430	c1412282-1411374	88.7788	179.081	1.01233	up	hypothetical protein
A3862_06435	c1413557-1413144	270.189	136.05	-0.989833	down	MerR family transcriptional regulator
A3862_06445	c1416575-1414479	66.1194	168.219	1.3472	up	hypothetical protein
A3862_06450	1417163-1417465	27.5701	29.7729	0.110895	up	hypothetical protein
A3862_06455	c1418788-1417775	61.5689	138.997	1.17478	up	hypothetical protein
A3862_06460	1419363-1420787	64.1355	169.242	1.39989	up	hypothetical protein
A3862_06465	c1422539-1421019	52.0155	161.114	1.63106	up	hypothetical protein
A3862_06470	1422917-1425598	60.2224	176.508	1.55136	up	diguanylate cyclase
A3862_06480	1427024-1427659	141.602	122.756	-0.206054	down	hypothetical protein
A3862_06485	1427922-1428584	22.0091	95.3417	2.115	up	hypothetical protein
A3862_06490	c1430265-1428598	21.9803	150.159	2.77221	up	hypothetical protein
A3862_06495	c1430768-1430262	17.3321	67.5365	1.96222	up	hypothetical protein
A3862_06500	1431564-1432259	62.0567	100.977	0.702364	up	hypothetical protein
A3862_06505	c1432730-1432392	9.43284	40.4567	2.10061	up	hypothetical protein
A3862_06510	c1434124-1432730	25.4303	159.978	2.65325	up	thiamine biosynthesis protein ThiF
A3862_06515	c1434816-1434124	44.0812	109.02	1.30636	up	hypothetical protein
A3862_06520	c1438388-1434960	49.6267	170.028	1.77658	up	DNA helicase UvrD

A3862_06525	c1439007-1438375	120.828	121.211	0.00456048	up	hypothetical protein
A3862_06530	c1439777-1439004	116.395	124.982	0.102685	up	RNA polymerase subunit sigma-24
A3862_06535	c1440708-1439911	27.2702	130.729	2.26118	up	hypothetical protein
A3862_06540	c1441259-1440705	27.6034	83.87	1.60331	up	metallophosphoesterase
A3862_06545	1441960-1442208	3.65053	7.49293	1.03742	up	hypothetical protein
A3862_06550	c1442932-1442336	42.885	85.2122	0.990588	up	hypothetical protein
A3862_06555	1443330-1443539	84.1155	90.8735	0.111488	up	hypothetical protein
A3862_06560	c1443779-1443567	385.813	308.747	-0.321478	down	hypothetical protein
A3862_06565	1443877-1444233	46.7216	44.9747	-0.0549764	down	hypothetical protein
A3862_06570	c1444837-1444256	63.0065	70.703	0.166271	up	molecular chaperone Tir
A3862_06575	c1445809-1445057	33.0406	119.313	1.85244	up	hypothetical protein
A3862_06580	1446325-1446987	52.0046	103.6	0.994316	up	hypothetical protein
A3862_06585	1447221-1447517	5.97777	22.6289	1.92049	up	hypothetical protein
A3862_06590	1447963-1448949	24.3287	134.233	2.464	up	hypothetical protein
A3862_06595	1449100-1449885	20.3968	88.027	2.10961	up	hypothetical protein
A3862_06600	1449984-1452086	29.5571	161.571	2.45059	up	hypothetical protein
A3862_06605	1452110-1453210	44.845	140.044	1.64286	up	hypothetical protein
A3862_06610	1453200-1455119	38.8271	172.488	2.15136	up	hypothetical protein
A3862_06615	1455999-1456304	10.8598	23.2778	1.09995	up	hypothetical protein
A3862_06620	c1456920-1456369	20.8204	74.3895	1.8371	up	hypothetical protein
A3862_06625	c1460224-1458893	27.8031	154.627	2.47548	up	MFS transporter
A3862_06630	c1460507-1460235	11.828	41.0875	1.79649	up	nickel resistance protein
A3862_06635	1460616-1460915	5.65654	28.9296	2.35455	up	hypothetical protein
A3862_06640	c1461965-1461765	0	6.38459	1.79769e+308	up	hypothetical protein
A3862_06645	c1462500-1462210	21.1719	20.91	-0.017953	down	hypothetical protein
A3862_06650	c1463728-1462787	55.3409	134.168	1.27762	up	cation transporter
A3862_06655	c1464293-1463769	18.1246	70.1359	1.9522	up	threonyl-trna synthetase
A3862_06670	c1469464-1469084	165.01	82.4678	-1.00065	down	hypothetical protein

A3862_06675	c1470019-1469756	56.1331	36.8273	-0.608078	down	hypothetical protein
A3862_06690	c1473115-1472369	43.4564	121.153	1.47919	up	DNA-binding response regulator
A3862_06700	c1474357-1474040	1.15697	17.6424	3.93062	up	hypothetical protein
A3862_06705	1474695-1476890	44.3283	174.622	1.97794	up	ATPase
A3862_06710	c1477629-1477018	34.6638	87.9807	1.34376	up	hypothetical protein
A3862_06715	1478188-1479126	66.2637	169.996	1.35921	up	thioredoxin reductase
A3862_06720	c1480537-1480112	30.7993	51.2649	0.735071	up	magnesium transporter MgtC
A3862_06725	c1481095-1480772	21.3797	24.7659	0.212113	up	hypothetical protein
A3862_06730	c1481745-1481152	35.0201	67.6276	0.949427	up	hypothetical protein
A3862_06735	c1482485-1482135	7.34693	24.9744	1.76524	up	hypothetical protein
A3862_06740	1482733-1483608	28.1599	130.321	2.21036	up	hypothetical protein
A3862_06745	c1485251-1484565	42.3104	100.253	1.24456	up	transporter
A3862_06750	c1485552-1485259	90.4367	58.9853	-0.616552	down	hypothetical protein
A3862_06755	1485960-1486457	23.1012	73.2696	1.66525	up	hypothetical protein
A3862_06760	1487279-1489390	47.1691	165.959	1.81491	up	porin
A3862_06765	c1489789-1489490	20.5693	23.8192	0.211631	up	hypothetical protein
A3862_06770	1490024-1490650	31.8448	103.392	1.69899	up	hypothetical protein
A3862_06775	c1491704-1490700	23.7469	144.807	2.60832	up	hypothetical protein
A3862_06780	1491808-1492089	20.761	21.8146	0.0714177	up	transposase
A3862_06790	c1494159-1492882	38.695	172.697	2.15802	up	transposase
A3862_06800	c1496095-1494851	39.3772	152.028	1.9489	up	hypothetical protein
A3862_06815	1501468-1502553	211.042	257.651	0.287886	up	3-isopropylmalate dehydrogenase
A3862_06820	c1503818-1503438	22.9037	46.3455	1.01685	up	hypothetical protein
A3862_06825	1504126-1506267	75.1485	170.01	1.1778	up	hypothetical protein
A3862_06830	1506264-1507604	95.0025	176.865	0.896613	up	ATP-binding protein
A3862_06835	1507601-1509919	46.1084	176.399	1.93574	up	ATP-dependent helicase
A3862_06840	1510044-1512698	331.828	216.853	-0.61372	down	hypothetical protein
A3862_06845	1512698-1516111	240.95	211.307	-0.189394	down	ATP-dependent endonuclease

A3862_06850	c1516741-1516256	14.7839	51.5746	1.80263	up	hypothetical protein
A3862_06855	c1518444-1516738	119.351	288.461	1.27317	up	hypothetical protein
A3862_06860	c1518821-1518459	318.237	415.419	0.384465	up	hypothetical protein
A3862_06865	1518986-1519933	66.9306	152.729	1.19024	up	hypothetical protein
A3862_06870	1520131-1520364	0	6.77784	1.79769e+308	up	hypothetical protein
A3862_06875	c1521059-1520625	21.1241	48.3832	1.19562	up	hypothetical protein
A3862_06880	1521653-1524235	50.9023	187.862	1.88387	up	hypothetical protein
A3862_06885	1524232-1524615	53.443	48.267	-0.146964	down	histidine kinase
A3862_06890	c1527108-1524658	44.0144	166.406	1.91866	up	-
A3862_06895	c1528635-1527829	399.12	214.01	-0.899145	down	ketoacyl reductase
A3862_06905	c1529859-1529545	71.6245	31.0841	-1.20428	down	hypothetical protein
A3862_06945	c1536496-1536263	321.412	145.811	-1.14032	down	hypothetical protein
A3862_06950	1537057-1539612	83.509	196.424	1.23397	up	-
A3862_06955	c1541599-1539902	57.6216	161.098	1.48325	up	choline dehydrogenase
A3862_06960	c1542273-1541614	27.2211	93.6236	1.78215	up	gluconate 2-dehydrogenase
A3862_06965	c1543331-1542288	38.3611	117.1	1.61002	up	hypothetical protein
A3862_06970	c1544409-1543315	45.9281	136.216	1.56845	up	mandelate racemase
A3862_06975	c1546212-1544425	128.115	163.199	0.349198	up	thiamine pyrophosphate-requiring protein
A3862_06980	c1547337-1546393	55.2482	128.42	1.21687	up	gluconolactonase
A3862_06990	c1549874-1549422	11.1809	45.6607	2.02992	up	DUF305 domain-containing protein
A3862_06995	1550056-1550439	53.4042	89.8124	0.749961	up	hypothetical protein
A3862_07000	1550483-1550992	38.9748	91.7323	1.23489	up	RNA polymerase subunit sigma-24
A3862_07005	1550989-1551798	28.9865	116.94	2.01231	up	anti-sigma factor
A3862_07010	1551795-1552685	39.6321	128.322	1.69502	up	LysR family transcriptional regulator
A3862_07015	1552682-1553053	23.7869	38.849	0.707713	up	hypothetical protein
A3862_07020	c1554142-1553057	116.851	158.281	0.437819	up	molybdopterin oxidoreductase
A3862_07025	c1555204-1554221	238.559	123.173	-0.95366	down	phosphate ABC transporter substrate-binding protein
A3862_07030	c1555726-1555388	647.275	161.744	-2.00067	down	sulfite:cytochrome C oxidoreductase subunit b precursor

A3862_07035	c1556961-1555738	502.493	233.322	-1.10678	down	oxidase
A3862_07040	c1558297-1557158	27.725	146.553	2.40217	up	guanylate cyclase
A3862_07050	c1560282-1559644	38.5227	91.7578	1.25212	up	phosphoglycerate mutase
A3862_07065	1561876-1563111	36.2402	151.275	2.06151	up	MFS transporter
A3862_07070	1563131-1563859	51.1181	116.727	1.19123	up	PA-phosphatase
A3862_07140	c1579988-1578831	27.4723	139.862	2.34796	up	transposase
A3862_15410	3395841-3397379	187.184	249.692	0.415693	up	hypothetical protein
A3862_15415	c3397552-3397352	13.9085	14.0325	0.0128129	up	hypothetical protein
A3862_15420	3398049-3398606	86.0075	93.2787	0.117085	up	metallophosphoesterase
A3862_15425	c3399216-3398638	216.191	190.123	-0.185368	down	hypothetical protein
A3862_15430	c3400059-3399385	29.0725	87.6853	1.59268	up	hypothetical protein
A3862_15435	c3400567-3400136	12.7133	44.3877	1.80382	up	hypothetical protein
A3862_15440	c3401063-3400632	12.94	48.3821	1.90264	up	hypothetical protein
A3862_15445	c3401374-3401060	9.31562	28.4524	1.61082	up	hypothetical protein
A3862_15450	c3401709-3401371	13.6336	49.31	1.85472	up	hypothetical protein
A3862_15455	c3401924-3401709	0	21.3029	1.79769e+308	up	hypothetical protein
A3862_15460	c3402334-3401921	16.808	48.1046	1.51703	up	hypothetical protein
A3862_15465	c3403254-3402334	33.1875	103.24	1.63729	up	hypothetical protein
A3862_15470	3403711-3404172	13.6122	77.1592	2.50294	up	hypothetical protein
A3862_15475	3404222-3404800	47.4487	79.0193	0.735836	up	hypothetical protein
A3862_15480	c3405236-3404940	56.5817	46.2692	-0.290283	down	hypothetical protein
A3862_15485	c3405949-3405524	28.5521	55.0329	0.946695	up	hypothetical protein
A3862_15490	3406189-3406410	0	13.5145	1.79769e+308	up	hypothetical protein
A3862_15510	c3414118-3411665	47.7726	166.474	1.80104	up	-
A3862_15515	c3414747-3414535	0	11.5349	1.79769e+308	up	hypothetical protein
A3862_15520	c3415718-3414744	37.0616	149.815	2.01518	up	LysR family transcriptional regulator
A3862_15525	3415825-3416547	27.7586	86.6351	1.64202	up	short-chain dehydrogenase
A3862_15555	c3423232-3421943	124.415	198.413	0.673339	up	amine oxidase

A3862_15625	3435787-3436593	57.6989	128.517	1.15535	up	cyclic nucleotide-binding protein
A3862_15640	3440270-3440470	3.59317	16.2435	2.17653	up	hypothetical protein
A3862_15650	3443278-3443652	29.3123	44.1058	0.589465	up	NADH dehydrogenase
A3862_15655	3443649-3445394	118.926	163.647	0.460527	up	chemotaxis protein
A3862_15660	c3446536-3445460	193.469	163.074	-0.246577	down	patatin
A3862_15670	c3448847-3447846	121.772	158.229	0.377838	up	short-chain dehydrogenase
A3862_15675	c3449562-3448891	276.323	137.363	-1.00836	down	urea carboxylase-associated protein
A3862_15680	c3450256-3449552	655.871	186.865	-1.81142	down	hypothetical protein
A3862_15685	c3450726-3450472	24.9015	13.8584	-0.845477	down	hypothetical protein
A3862_15690	c3452487-3451204	35.4395	148.049	2.06264	up	porin
A3862_15695	3452911-3453393	4468.87	425.59	-3.39237	down	heat-shock protein
A3862_15705	3454128-3454532	361.682	86.5266	-2.06351	down	hypothetical protein
A3862_15710	3454549-3454893	199.052	58.0543	-1.77767	down	hypothetical protein
A3862_15715	3454925-3455674	153.939	105.458	-0.545693	down	hypothetical protein
A3862_15720	3455735-3456178	65.9431	39.9947	-0.721414	down	hypothetical protein
A3862_15725	3456532-3457074	33.4929	78.0718	1.22095	up	diguanylate cyclase
A3862_15745	3461902-3462105	3.98236	31.447	2.98123	up	hypothetical protein
A3862_15750	3462110-3464923	36.2374	153.668	2.08427	up	hypothetical protein
A3862_15755	c3467627-3465252	55.9517	153.774	1.45856	up	-
A3862_15760	c3468340-3467699	35.2916	75.0562	1.08865	up	chemotaxis protein CheX
A3862_15765	c3468720-3468337	45.3517	54.1035	0.254567	up	response regulator receiver protein
A3862_15770	c3469082-3468831	4.11135	17.3339	2.07592	up	hypothetical protein
A3862_15775	c3471355-3469082	48.8575	168.471	1.78585	up	chemotaxis protein CheA
A3862_15780	c3471756-3471352	40.523	51.9057	0.35715	up	two-component system response regulator
A3862_15785	c3472612-3471749	24.1155	113.91	2.23986	up	chemotaxis protein CheR
A3862_15790	c3473189-3472617	41.5108	105.82	1.35005	up	PBS lyase
A3862_15795	c3474295-3473189	41.9104	162.665	1.95653	up	chemotaxis response regulator protein-glutamate methylesterase
A3862_15800	c3475773-3474292	62.0053	172.815	1.47876	up	hypothetical protein

A3862_15805	c3477697-3475766	82.7332	166.887	1.01233	up	chemotaxis protein
A3862_15815	c3479159-3478899	3.71823	5.10248	0.456583	up	hypothetical protein
A3862_15820	c3481533-3479518	46.5563	149.088	1.67912	up	-
A3862_15825	c3485299-3481886	48.0529	180.277	1.90752	up	hypothetical protein
A3862_15830	c3485480-3485286	0	6.04564	1.79769e+308	up	CopG family transcriptional regulator
A3862_15840	c3488706-3488509	0	6.46808	1.79769e+308	up	hypothetical protein
A3862_15845	c3489059-3488847	0	13.1161	1.79769e+308	up	hypothetical protein
A3862_15855	c3490928-3490269	62.8724	104.176	0.728529	up	hypothetical protein
A3862_15860	c3493933-3490928	116.34	182.203	0.647199	up	hypothetical protein
A3862_15865	3494625-3495032	16.8438	52.9716	1.653	up	hypothetical protein
A3862_15870	c3495657-3495145	26.6036	74.7446	1.49035	up	hypothetical protein
A3862_15875	c3497861-3495699	432.935	426.929	-0.0201567	down	hypothetical protein
A3862_15880	3498392-3498712	86.4927	47.6664	-0.859605	down	hypothetical protein
A3862_15885	c3499383-3499033	10.9689	37.6627	1.77971	up	hypothetical protein
A3862_15890	c3499865-3499422	13.8226	63.8979	2.20874	up	hypothetical protein
A3862_15895	c3500106-3499888	8.29571	34.0489	2.03717	up	hypothetical protein
A3862_15900	c3500300-3500073	14.2152	20.1047	0.500096	up	hypothetical protein
A3862_15905	c3500545-3500297	39.9011	30.6231	-0.38181	down	hypothetical protein
A3862_15910	c3500913-3500542	39.5121	52.5142	0.410411	up	hypothetical protein
A3862_15915	c3501573-3501055	31.6766	85.4401	1.43149	up	hypothetical protein
A3862_15920	c3501836-3501600	11.0022	21.7602	0.983902	up	hypothetical protein
A3862_15925	c3504425-3501846	57.2124	184.846	1.69192	up	hypothetical protein
A3862_15930	c3505034-3504510	70.2142	86.1251	0.294671	up	hypothetical protein
A3862_15935	c3505333-3505040	10.4067	19.2223	0.885268	up	hypothetical protein
A3862_16170	3549286-3551019	121.448	181.522	0.579812	up	hypothetical protein
A3862_16175	3551284-3551466	0	14.0115	1.79769e+308	up	hypothetical protein
A3862_16180	c3551723-3551442	7.23998	23.1332	1.6759	up	hypothetical protein
A3862_16185	c3552421-3551906	11.8831	57.8022	2.28222	up	hypothetical protein

A3862_16190	c3552663-3552424	3.59542	9.10759	1.34091	up	hypothetical protein
A3862_16195	c3553162-3552971	0	8.64585	1.79769e+308	up	hypothetical protein
A3862_16200	c3553876-3553379	28.7153	61.1176	1.08977	up	hypothetical protein
A3862_16205	c3554464-3554192	23.6667	17.5765	-0.429206	down	hypothetical protein
A3862_16210	3554606-3554881	107.189	49.5304	-1.11377	down	hypothetical protein
A3862_16215	c3556068-3554920	15.4918	93.3801	2.59161	up	hypothetical protein
A3862_16220	3556269-3556511	24.5619	28.131	0.19574	up	hypothetical protein
A3862_16225	c3556705-3556508	8.7636	27.9741	1.67449	up	hypothetical protein
A3862_16230	c3557133-3556933	0	10.7675	1.79769e+308	up	hypothetical protein
A3862_16235	3557392-3557955	207.36	163.2	-0.345497	down	integrase
A3862_16240	c3559208-3558891	12.281	26.9969	1.13637	up	hypothetical protein
A3862_20260	4434337-4435608	51.757	124.309	1.2641	up	hypothetical protein
A3862_20335	4453071-4453610	19.359	62.3969	1.68847	up	hypothetical protein
A3862_20340	c4455456-4453687	36.2035	154.687	2.09515	up	hypothetical protein
A3862_20345	c4455965-4455651	1.28826	12.6927	3.3005	up	hypothetical protein
A3862_20350	c4456805-4456497	19.4955	20.8749	0.0986317	up	hypothetical protein
A3862_20355	c4457768-4457496	8.16419	6.78308	-0.267368	down	hypothetical protein
A3862_20365	4458929-4459387	30.105	58.1771	0.950448	up	hypothetical protein
A3862_20370	4459735-4459980	8.43536	10.5074	0.316883	up	hypothetical protein
A3862_20375	4460228-4464019	43.3119	161.462	1.89836	up	hypothetical protein
A3862_20380	4464162-4464782	8.22921	69.1418	3.07073	up	integrase
A3862_20820	4576420-4578072	54.4374	175.045	1.68506	up	hypothetical protein
A3862_20825	c4580301-4578280	169.741	282.197	0.733367	up	hypothetical protein
A3862_20830	c4581376-4580753	54.8381	103.203	0.912234	up	DNA resolvase
A3862_20835	c4584603-4583836	85.5775	122.893	0.522094	up	hypothetical protein
A3862_20840	c4585620-4585120	14.4431	45.0712	1.64182	up	hypothetical protein
A3862_20845	c4586414-4585635	11.2319	94.8511	3.07806	up	hypothetical protein
A3862_20855	4588068-4589060	25.1863	117.352	2.22013	up	hypothetical protein

A3862_20860	4589069-4590073	38.7267	129.907	1.74608	up	hypothetical protein
A3862_20865	4590173-4590385	52.8497	28.6721	-0.882247	down	DUF3892 domain-containing protein
A3862_20870	c4590894-4590673	5.58936	7.94851	0.508001	up	hypothetical protein
A3862_20875	4591004-4591744	26.3928	125.692	2.25168	up	hypothetical protein
A3862_20880	c4592154-4591747	19.1334	57.6165	1.59039	up	hypothetical protein
A3862_20885	c4592796-4592197	28.4184	94.5582	1.73438	up	hypothetical protein
A3862_20890	4593975-4594358	104.595	68.711	-0.606202	down	hypothetical protein
A3862_20895	4594476-4596011	36.0767	158.816	2.13822	up	hypothetical protein
A3862_20900	c4597859-4596045	142.17	169.659	0.255014	up	hypothetical protein
A3862_20905	c4600852-4597856	112.371	192.453	0.776232	up	hypothetical protein
A3862_20910	c4601238-4600849	32.4338	49.2213	0.601781	up	very short patch repair endonuclease
A3862_20915	c4602329-4601289	94.6689	144.561	0.610717	up	hypothetical protein
A3862_20920	4603661-4604437	126.787	120.047	-0.0788045	down	hypothetical protein
A3862_20925	4604628-4604948	53.172	44.349	-0.261764	down	DUF2845 domain-containing protein
A3862_20930	c4606878-4604956	66.2716	169.871	1.35798	up	hypothetical protein
A3862_20935	c4607695-4606889	110.01	162.635	0.564001	up	hypothetical protein
A3862_20940	c4608345-4607680	307.352	232.477	-0.402805	down	hypothetical protein
A3862_24280	5360533-5363160	125.358	192.856	0.621466	up	hypothetical protein
A3862_24285	c5366031-5365108	54.9735	98.1185	0.835788	up	restriction endonuclease
A3862_24290	c5368891-5367407	202.499	135.835	-0.576052	down	SAM-dependent methyltransferase
A3862_24295	c5372289-5368891	86.8414	143.411	0.7237	up	type I restriction-modification system endonuclease
A3862_24300	5372518-5374716	359.573	219.576	-0.711564	down	XRE family transcriptional regulator
A3862_24305	5375255-5375644	13.7017	36.5851	1.4169	up	hypothetical protein
A3862_24310	5378905-5379276	6.3881	32.7215	2.35678	up	hypothetical protein
A3862_24315	5379721-5380209	10.3211	59.5678	2.52893	up	hypothetical protein
A3862_24320	5380810-5382318	32.5202	138.008	2.08535	up	hypothetical protein
A3862_24325	c5382708-5382322	15.3962	49.8882	1.69613	up	hypothetical protein
A3862_24330	5384200-5386857	87.5652	166.392	0.92616	up	hypothetical protein

A3862_24335	5386877-5388109	146.893	147.362	0.00459519	up	hypothetical protein
A3862_24340	c5388447-5388247	0	7.00859	1.79769e+308	up	hypothetical protein
A3862_24350	5389021-5390313	31.7993	163.252	2.36003	up	transposase
A3862_27175	c6003601-6003185	30.5424	82.4829	1.43328	up	hypothetical protein
A3862_27180	c6003824-6003594	12.5304	29.0034	1.21078	up	hypothetical protein
A3862_27185	c6004539-6003814	52.2259	139.94	1.42197	up	hypothetical protein
A3862_27190	c6005401-6004532	43.5071	144.333	1.73008	up	hypothetical protein
A3862_27195	c6005882-6005646	15.332	19.9004	0.37625	up	hypothetical protein
A3862_27200	c6006162-6005887	12.4188	21.1615	0.768919	up	hypothetical protein
A3862_27205	c6006499-6006167	16.8833	48.6863	1.52792	up	hypothetical protein
A3862_27210	c6006854-6006492	16.3411	33.8779	1.05184	up	hypothetical protein
A3862_27215	c6007406-6006858	53.4044	111.562	1.06282	up	hypothetical protein
A3862_27220	c6008085-6007873	2.69418	9.27527	1.78354	up	hypothetical protein
A3862_27225	c6008989-6008147	21.1856	156.626	2.88616	up	Methyltransferase
A3862_27230	c6009218-6008982	27.6397	44.6219	0.691011	up	hypothetical protein
A3862_27235	c6009480-6009211	6.64189	41.6976	2.6503	up	hypothetical protein
A3862_27240	c6010030-6009641	6.6041	48.9575	2.8901	up	hypothetical protein
A3862_27245	c6010502-6010179	9.42598	50.9064	2.43313	up	hypothetical protein
A3862_27250	c6010888-6010499	13.1629	56.569	2.10354	up	hypothetical protein
A3862_27255	c6011536-6010901	40.4338	116.105	1.5218	up	exonuclease
A3862_27260	c6012210-6011539	38.9205	114.666	1.55883	up	ERF family protein
A3862_27265	c6012629-6012291	18.9605	34.9419	0.88196	up	hypothetical protein
A3862_27270	c6013027-6012626	13.6107	83.5632	2.61813	up	hypothetical protein
A3862_27275	c6013272-6013024	0	46.2729	1.79769e+308	up	hypothetical protein
A3862_27280	c6013535-6013269	7.55976	28.8471	1.93202	up	hypothetical protein
A3862_27285	c6013956-6013594	26.2675	49.9063	0.925944	up	hypothetical protein
A3862_27290	c6014171-6013956	27.0865	30.5611	0.174121	up	hypothetical protein
A3862_27295	6014516-6014773	22.6299	19.9705	-0.18036	down	hypothetical protein

A3862_27300	c6015117-6014770	49.1197	50.9012	0.051398	up	hypothetical protein
A3862_27305	c6015455-6015120	148.843	94.5565	-0.654547	down	hypothetical protein
A3862_27310	6015548-6015778	2.71699	30.0568	3.46761	up	hypothetical protein
A3862_27315	6016668-6016886	126.553	56.3778	-1.16654	down	hypothetical protein
A3862_27320	6016946-6017296	12.8945	40.3466	1.6457	up	hypothetical protein
A3862_27325	6017293-6017880	36.0947	118.045	1.70948	up	hypothetical protein
A3862_27330	6017885-6018142	5.58503	18.5782	1.73398	up	hypothetical protein
A3862_27335	6018139-6019599	32.0725	172.566	2.42774	up	hypothetical protein
A3862_27340	6020294-6020503	3.2743	16.1975	2.30651	up	hypothetical protein
A3862_27345	6020503-6020778	15.6818	43.1561	1.46047	up	hypothetical protein
A3862_27350	c6021256-6020948	12.0851	30.5877	1.33973	up	hypothetical protein
A3862_27355	6021239-6021874	40.7786	129.597	1.66815	up	hypothetical protein
A3862_27360	6022293-6022607	46.3685	81.2835	0.809817	up	hypothetical protein
A3862_27365	6022607-6023989	106.636	262.379	1.29896	up	hypothetical protein
A3862_27370	6024012-6024272	25.7311	20.0894	-0.35708	down	hypothetical protein
A3862_27375	6024858-6025139	22.9196	20.4325	-0.165714	down	hypothetical protein
A3862_27380	6025145-6025948	32.0189	135.712	2.08355	up	hypothetical protein
A3862_27385	6025948-6026436	21.9789	91.5522	2.05848	up	hypothetical protein
A3862_27390	6026472-6026717	27.7268	33.9603	0.29257	up	hypothetical protein
A3862_27395	6026732-6028309	38.607	204.036	2.40189	up	hypothetical protein
A3862_27400	6028306-6028491	5.60977	12.4171	1.14632	up	hypothetical protein
A3862_27405	6028676-6028954	10.4803	25.464	1.28079	up	hypothetical protein
A3862_27410	6029413-6031125	48.2929	215.338	2.15672	up	hypothetical protein
A3862_27415	6031122-6031412	10.0887	27.7663	1.4606	up	hypothetical protein
A3862_27420	6031409-6031711	2.6469	29.3786	3.47239	up	hypothetical protein
A3862_27425	6031701-6032714	40.176	172.924	2.10573	up	hypothetical protein
A3862_27430	6032906-6033763	79.5062	141.247	0.829077	up	hypothetical protein
A3862_27435	6033829-6034116	8.54431	26.0292	1.60709	up	hypothetical protein

A3862_27440	6034187-6034654	31.496	75.7876	1.26679	up	hypothetical protein
A3862_27445	6034663-6037083	46.687	227.637	2.28564	up	hypothetical protein
A3862_27450	6037088-6038773	48.0364	204.754	2.09169	up	hypothetical protein
A3862_27455	6038777-6041689	40.6088	222.91	2.4566	up	hypothetical protein
A3862_27460	6041686-6042042	25.1444	72.136	1.52048	up	hypothetical protein
A3862_27465	6042050-6042544	28.6787	111.356	1.95713	up	hypothetical protein
A3862_27470	6042544-6044880	45.252	232.935	2.36387	up	hypothetical protein
A3862_27475	6044895-6050888	44.969	235.612	2.38941	up	hypothetical protein
A3862_27480	6051083-6051988	25.4765	131.073	2.36313	up	hypothetical protein
A3862_27485	6051991-6052575	37.3461	123.283	1.72295	up	hypothetical protein
A3862_27490	6052602-6053036	17.3841	79.9089	2.20059	up	hypothetical protein
A3862_27495	6053033-6053515	32.887	95.8769	1.54367	up	hypothetical protein
A3862_27500	c6054254-6053508	120.714	134.443	0.155403	up	hypothetical protein
A3862_27505	c6055068-6054787	12.1438	33.0253	1.44335	up	hypothetical protein
A3862_28940	6357033-6358532	229.151	1287.29	2.48997	up	transposase
A3862_28945	6358529-6359371	161.361	607.597	1.91282	up	AAA family ATPase

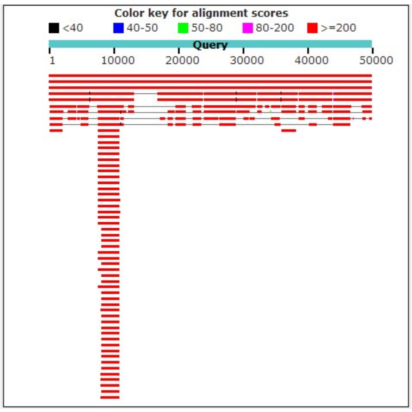
*^{c}: complementary strand

Table S4 The results of NCBI alignment on the upstream and downstream contexts of the XJLW

Supplementary data

Met cluster.

Upstream

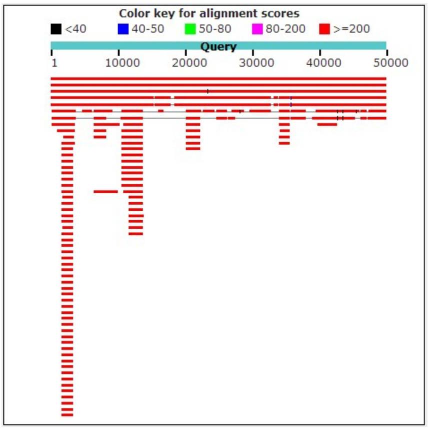


Description	Max score	Total score	Query cover	E value	Ident	Accession
Methylobacterium oryzae CBMB20, complete genome	92078	93046	100%	0.0	99%	CP003811.1
Methylobacterium phyllosphaerae strain CBMB27, complete genome	90204	91168	100%	0.0	99%	CP015367.1
Methylobacterium sp. C1, complete genome	9629	64136	90%	0.0	92%	CP017640.1
Methylobacterium radiotolerans JCM 2831, complete genome	9585	64408	91%	0.0	91%	CP001001.1
Methylobacterium sp. 17Sr1-43 chromosome, complete genome	5877	29717	69%	0.0	80%	CP029551.1
Methylobacterium sp. 17SD2-17 chromosome, complete genome	4311	28325	65%	0.0	89%	CP029550.1
Methylobacterium sp. 17Sr1-1 chromosome, complete genome	4167	21082	52%	0.0	88%	CP029552.1
Methylobacterium sp. PR1016A chromosome 1	4098	17573	46%	0.0	88%	CP028843.1
Methylobacterium sp. AMS5, complete genome	4084	26077	61%	0.0	88%	CP006992.1
Methylobacterium sp. DM1 chromosome, complete genome	4039	23455	57%	0.0	88%	CP029173.1
Methylobacterium aquaticum plasmid pMaq22A_1p DNA, complete genome, strain: MA-22A	4039	6234	12%	0.0	88%	AP014705.1
Methylobacterium sp. 17Sr1-28 chromosome, complete genome	4017	19120	47%	0.0	88%	CP029553.1
Methylobacterium extorquens str. DM4 chromosome, complete genome	4017	25423	61%	0.0	88%	FP103042.2
Methylorubrum zatmanii strain PSBB041 chromosome, complete genome	4012	25236	59%	0.0	88%	CP021054.1
Methylobacterium extorquens strain TK 0001, genome assembly, chromosome: TK0001	4006	25607	61%	0.0	87%	LT962688.1
Methylobacterium populi BJ001, complete genome	4000	24872	58%	0.0	87%	CP001029.1
Methylorubrum extorquens strain PSBB040 chromosome, complete genome	3995	25851	63%	0.0	87%	CP019322.1
Methylobacterium extorquens AM1, complete genome	3995	25942	62%	0.0	87%	CP001510.1
Methylobacterium extorquens PA1, complete genome	3973	26326	62%	0.0	87%	CP000908.1
Methylobacterium populi DNA, complete genome	3967	26105	62%	0.0	87%	AP014809.1
Methylobacterium sp. 4-46, complete genome	3947	19694	50%	0.0	87%	CP000943.1
Methylobacterium extorquens CM4, complete genome	3940	25858	62%	0.0	87%	CP001298.1
Methylobacterium nodulans ORS 2060, complete genome	3919	17306	43%	0.0	87%	CP001349.1
Microvirga sp. 17 mud 1-3 chromosome, complete genome	3507	9444	25%	0.0	85%	CP029481.1
Microvirga ossetica strain V5/3M, complete genome	3419	11154	30%	0.0	85%	CP016616.1
Chelatococcus sp. CO-6, complete genome	2881	9535	29%	0.0	85%	CP012398.1
Bosea sp. RAC05, complete genome	2702	8349	27%	0.0	84%	CP016464.1
Chelatococcus daeguensis strain TAD1, complete genome	2699	7465	23%	0.0	84%	CP018095.1

Bosea vaviloviae strain Vaf18, complete genome	2579	6245	18%	0.0	83%	CP017147.1
Pleomorphomonas sp. SM30 DNA, complete genome	2555	6661	19%	0.0	81%	AP017626.1
Bradyrhizobium sp. ORS 285 strain ORS285 genome assembly, chromosome: BRAD285	2532	5974	18%	0.0	80%	LT859959.1
Bosea sp. AS-1, complete genome	2525	5967	15%	0.0	83%	CP022372.1
Bradyrhizobium sp. BF49 genome assembly, chromosome: I	2516	5448	16%	0.0	80%	LN901633.1
Bosea sp. PAMC 26642, complete genome	2508	6598	18%	0.0	83%	CP014301.1
Azorhizobium caulinodans ORS 571 DNA, complete genome	2475	6840	19%	0.0	83%	AP009384.1
Rhodopseudomonas palustris BisB18, complete genome	2398	5275	13%	0.0	80%	CP000301.1
Bradyrhizobium sp. 2 39S1MB chromosome, complete genome	2372	6149	18%	0.0	82%	CP029426.1
Xanthobacter autotrophicus Py2, complete genome	2362	4947	14%	0.0	82%	CP000781.1
Starkeya novella DSM 506, complete genome	2357	6126	19%	0.0	82%	CP002026.1
Bradyrhizobium ottawaense strain OO99 chromosome, complete genome	2350	5724	18%	0.0	82%	CP029425.1
Bradyrhizobium sp. ORS 3257 isolate ORS3257 genome assembly, chromosome: BRAD3257	2344	5279	15%	0.0	82%	LS398110.1
Bradyrhizobium sp. G22 genome assembly, chromosome: I	2342	4844	14%	0.0	82%	LN907826.1
Bradyrhizobium japonicum strain E109, complete genome	2342	6145	17%	0.0	82%	CP010313.1
Bradyrhizobium japonicum SEMIA 5079 genome	2342	6345	18%	0.0	82%	CP007569.1
Bradyrhizobium japonicum USDA 6 DNA, complete genome	2342	6145	17%	0.0	82%	AP012206.1
Phreatobacter cathodiphilus strain S-12 chromosome, complete genome	2337	7717	25%	0.0	82%	CP027668.1
Bradyrhizobium oligotrophicum S58 DNA, complete genome	2331	5989	17%	0.0	82%	AP012603.1
Bradyrhizobium japonicum strain J5, complete genome	2326	5075	12%	0.0	82%	CP017637.1
Bradyrhizobium sp. SK17 chromosome, complete genome	2322	5128	15%	0.0	81%	CP025113.1
Bradyrhizobium sp. 3 85S1MB chromosome, complete genome	2309	5215	15%	0.0	82%	CP029427.1
Bradyrhizobium diazoefficiens strain XF7 chromosome, complete genome	2300	7085	23%	0.0	81%	CP029603.1
Bradyrhizobium diazoefficiens USDA 110, complete genome	2300	7079	23%	0.0	81%	CP011360.1
Bradyrhizobium diazoefficiens USDA 110 DNA, complete genome	2300	7079	23%	0.0	81%	BA000040.2
Bradyrhizobium sp. CCGE-LA001, complete genome	2283	6258	20%	0.0	81%	CP013949.1
Bradyrhizobium diazoefficiens strain USDA 122, complete genome	2278	6562	22%	0.0	81%	CP013127.1
Bradyrhizobium sp. ORS278,complete sequence	2261	5361	15%	0.0	81%	CU234118.1
Bradyrhizobium diazoefficiens DNA, complete genome, strain: NK6	2255	5984	18%	0.0	81%	AP014685.1
Bradyrhizobium sp. S23321 DNA, complete genome	2239	5246	14%	0.0	81%	AP012279.1
Rhodopseudomonas palustris strain PS3 chromosome, complete genome	2198	5410	15%	0.0	81%	CP019966.1
Bradyrhizobium lablabi strain MT34 genome assembly, chromosome: I	2194	3972	10%	0.0	81%	LT670845.1
Bradyrhizobium ottawaense strain GAS524 genome assembly, chromosome: I	2194	3851	10%	0.0	81%	LT629693.1
Bradyrhizobium icense strain LMTR 13, complete genome	2191	4665	14%	0.0	81%	CP016428.1
Afipia sp. GAS231 genome assembly, chromosome: I	2189	4948	17%	0.0	81%	LT629703.1
Bradyrhizobium sp. BTAi1, complete genome	2180	5351	13%	0.0	81%	CP000494.1
Rhodopseudomonas palustris strain YSC3 chromosome, complete genome	2176	5401	15%	0.0	81%	CP019967.1
Methylosinus trichosporium OB3b chromosome, complete genome	2176	4173	14%	0.0	78%	CP023737.1
Rhodopseudomonas palustris TIE-1, complete genome	2148	5934	18%	0.0	81%	CP001096.1
Rhodopseudomonas palustris BisA53, complete genome	2141	3990	11%	0.0	81%	CP000463.1
Nitrobacter hamburgensis X14, complete genome	2139	3882	12%	0.0	80%	CP000319.1
Methylobacterium aquaticum DNA, complete genome, strain: MA-22A	2135	13422	37%	0.0	86%	AP014704.1
Rhodopseudomonas palustris CGA009 complete genome; segment 14/16	2126	2714	7%	0.0	81%	BX572606.1

Nitrobacter winogradskyi Nb-255, complete genome	2117	4725	13%	0.0	80%	CP000115.1
Rhodopseudomonas palustris HaA2, complete genome	2109	4884	14%	0.0	81%	CP000250.1
Rhodopseudomonas palustris DX-1, complete genome	2098	6172	19%	0.0	80%	CP002418.1
Shinella sp. HZN7, complete genome	2084	5055	15%	0.0	78%	CP015736.1
Aminobacter aminovorans strain KCTC 2477, complete genome	2065	4968	19%	0.0	78%	CP015005.1
Bradyrhizobium erythrophlei strain GAS401 genome assembly, chromosome: I	2039	4708	13%	0.0	80%	LT670849.1
Rhodopseudomonas palustris BisB5, complete genome	2037	4570	13%	0.0	80%	CP000283.1
Mesorhizobium oceanicum strain B7, complete genome	2010	5440	19%	0.0	78%	CP018171.1
Oligotropha carboxidovorans OM5, complete genome	2002	4465	13%	0.0	80%	CP002826.1
Oligotropha carboxidovorans OM4, complete genome	2002	4465	13%	0.0	80%	CP002821.1
Oligotropha carboxidovorans OM5 strain OM5, complete genome	2002	4465	13%	0.0	80%	CP001196.1
Methylobacterium extorquens strain AM1 Fdh4A (fdh4A) and Fdh4B (fdh4B) genes, complete cds	1982	1982	4%	0.0	83%	EU073598.1
Bradyrhizobium erythrophlei strain GAS138 genome assembly, chromosome: I	1962	3384	10%	0.0	80%	LT670817.1
Bradyrhizobium erythrophlei strain GAS242 genome assembly, chromosome: I	1921	5456	16%	0.0	79%	LT670818.1
Sinorhizobium sp. RAC02, complete genome	1917	3802	12%	0.0	77%	CP016450.1
Bradyrhizobium lablabi strain GAS499 genome assembly, chromosome: I	1916	3131	10%	0.0	79%	LT670844.1
Rhizobium sp. ACO-34A chromosome, complete genome	1897	4112	14%	0.0	77%	CP021371.1
Neorhizobium galegae, complete genome	1882	3658	11%	0.0	77%	HG938355.1
Agrobacterium sp. RAC06, complete genome	1873	4100	14%	0.0	77%	CP016499.1
Bradyrhizobium canariense strain GAS369 genome assembly, chromosome: I	1857	2855	9%	0.0	79%	LT629750.1
Methylocella silvestris BL2, complete genome	1849	3048	8%	0.0	79%	CP001280.1
Rhizobium sp. NXC24 chromosome, complete genome	1799	2084	8%	0.0	77%	CP024311.1
Sinorhizobium medicae WSM419, complete genome	1777	3497	11%	0.0	77%	CP000738.1
Methylocystis bryophila strain S285 chromosome, complete genome	1661	2963	9%	0.0	78%	CP019948.1
Ensifer sojae CCBAU 05684, complete genome	1626	3874	11%	0.0	78%	CP023067.1
Neorhizobium galegae, complete genome	1615	4015	12%	0.0	79%	HG938353.1
Sinorhizobium sp. CCBAU 05631, complete genome	1496	4070	13%	0.0	77%	CP023063.1
Rhizobium sp. 11515TR chromosome, complete genome	1480	2941	11%	0.0	77%	CP022998.1

Downstream



Description	**Max score**	**Total score**	**Query cover**	**E value**	**Ident**	**Accession**

Methylobacterium sp. XJLM chromosome, complete genome	92333	94165	100%	0.0	100%	CP016429.1
Methylobacterium oryzae CBMB20, complete genome	91929	94498	100%	0.0	99%	CP003811.1
Methylobacterium phyllosphaerae strain CBMB27, complete genome	47781	91603	100%	0.0	99%	CP015367.1
Methylobacterium radiotolerans JCM 2831, complete genome	20389	65311	96%	0.0	91%	CP001001.1
Methylobacterium sp. C1, complete genome	20351	65210	96%	0.0	91%	CP017640.1
Methylobacterium sp. 17Sr1-43 chromosome, complete genome	3687	32849	72%	0.0	85%	CP029551.1
Methylobacterium sp. 17SD2-17 chromosome, complete genome	3155	28094	58%	0.0	83%	CP029550.1
Methylobacterium sp. DM1 chromosome, complete genome	3048	27045	58%	0.0	81%	CP029173.1
Methylobacterium populi BJ001, complete genome	2929	29186	69%	0.0	83%	CP001029.1
Methylobacterium extorquens str. DM4 chromosome, complete genome	2835	28347	66%	0.0	83%	FP103042.2
Methylobacterium populi DNA, complete genome	2809	26586	60%	0.0	82%	AP014809.1
Methylobacterium sp. AMS5, complete genome	2789	30368	67%	0.0	82%	CP006992.1
Methylorubrum extorquens strain PSBB040 chromosome, complete genome	2763	28900	65%	0.0	82%	CP019322.1
Methylobacterium extorquens CM4, complete genome	2756	29651	68%	0.0	82%	CP001298.1
Methylorubrum zatmanii strain PSBB041 chromosome, complete genome	2745	29962	68%	0.0	82%	CP021054.1
Methylobacterium extorquens AM1, complete genome	2741	30253	65%	0.0	82%	CP001510.1
Methylobacterium extorquens strain TK 0001, genome assembly, chromosome: TK0001	2739	29798	67%	0.0	82%	LT962688.1
Methylobacterium extorquens PA1, complete genome	2734	29041	66%	0.0	82%	CP000908.1
Methylobacterium sp. 17Sr1-1 chromosome, complete genome	2649	26921	62%	0.0	81%	CP029552.1
Methylobacterium sp. 4-46, complete genome	2614	23741	50%	0.0	85%	CP000943.1
Methylobacterium sp. PR1016A chromosome 1	2495	25123	58%	0.0	79%	CP028843.1
Methylobacterium sp. MAFF 211642 MDH gene for methanol dehydrogenase, complete cds	2459	2459	3%	0.0	93%	AB550662.1
Methylobacterium extorquens methylotrophy region containing methylotrophic phosphoenolpyruvate carboxylase (ppcA), malyl-CoA lyase (mclA), orf1, orf2, putative ABC transporter subunit A (abcA), putative ABC transporter subunit B (abcB), putative ABC transporter ATP-binding subunit (abcC), methanol dehydrogenase large subunit homolog (mxaF'), cytochrome c (maxG'), mxaJ homolog (mxaJ'), 6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase (folA), dihydroneopterin aldolase (folB), dihydroxypteroate synthase (folC), orf3, orf4, and PqqE (pqqE) genes, complete cds; and PqqC/D (pqqC/D) gene, partial cds	2405	3167	6%	0.0	91%	U72662.2
Methylobacterium sp. 17Sr1-28 chromosome, complete genome	2324	26677	58%	0.0	81%	CP029553.1
Methylobacterium aquaticum DNA, complete genome, strain: MA-22A	2318	17860	41%	0.0	81%	AP014704.1
Methylobacterium nodulans ORS 2060, complete genome	2102	21266	48%	0.0	85%	CP001349.1
Methylobacterium extorquens CM4 plasmid pCMU01, complete sequence	1953	1953	3%	0.0	87%	CP001299.1
Methylobacterium aquaticum plasmid pMaq22A_1p DNA, complete genome, strain: MA-22A	1727	8303	22%	0.0	78%	AP014705.1
Starkeya novella DSM 506, complete genome	1703	10057	33%	0.0	85%	CP002026.1
Pleomorphomonas sp. SM30 DNA, complete genome	1578	10134	28%	0.0	84%	AP017626.1
Chelatococcus daeguensis strain TAD1, complete genome	1576	9872	30%	0.0	82%	CP018095.1
Microvirga sp. 17 mud 1-3 chromosome, complete genome	1563	9367	28%	0.0	79%	CP029481.1
Chelatococcus sp. CO-6, complete genome	1543	10828	31%	0.0	82%	CP012398.1
Xanthobacter autotrophicus Py2, complete genome	1502	7621	23%	0.0	83%	CP000781.1
Bosea sp. RAC05, complete genome	1491	6898	21%	0.0	79%	CP016464.1
Bosea vaviloviae strain Vaf18, complete genome	1485	5811	18%	0.0	79%	CP017147.1
Microvirga ossetica strain V5/3M, complete genome	1426	6716	18%	0.0	84%	CP016616.1

Bosea sp. PAMC 26642, complete genome	1408	7387	24%	0.0	78%	CP014301.1
Polymorphum gilvum SL003B-26A1, complete genome	1406	8339	26%	0.0	82%	CP002568.1
Rhodobacter sp. CZR27 chromosome, complete genome	1397	5627	19%	0.0	82%	CP023548.1
Bosea sp. AS-1, complete genome	1367	7611	22%	0.0	78%	CP022372.1
Bradyrhizobium diazoefficiens strain USDA 122, complete genome	1354	3983	13%	0.0	81%	CP013127.1
Bradyrhizobium japonicum strain J5, complete genome	1352	5993	20%	0.0	81%	CP017637.1
Bradyrhizobium diazoefficiens DNA, complete genome, strain: NK6	1352	2293	6%	0.0	82%	AP014685.1
Yangia pacifica strain YSBP01 plasmid unnamed2, complete sequence	1349	1349	3%	0.0	81%	CP022192.1
Bradyrhizobium diazoefficiens USDA 110, complete genome	1349	2295	6%	0.0	81%	CP011360.1
Bradyrhizobium diazoefficiens USDA 110 DNA, complete genome	1349	2295	6%	0.0	81%	BA000040.2
Bradyrhizobium diazoefficiens strain XF7 chromosome, complete genome	1338	2289	6%	0.0	81%	CP029603.1
Bradyrhizobium japonicum SEMIA 5079 genome	1336	6525	20%	0.0	82%	CP007569.1
Hartmannibacter diazotrophicus strain E19T genome assembly, chromosome: 1	1334	6179	19%	0.0	81%	LT960614.1
Bradyrhizobium japonicum strain E109, complete genome	1330	6542	21%	0.0	81%	CP010313.1
Bradyrhizobium japonicum USDA 6 DNA, complete genome	1330	6542	21%	0.0	81%	AP012206.1
Rhizobium sp. ACO-34A chromosome, complete genome	1314	3661	12%	0.0	81%	CP021371.1
Salipiger profundus strain JLT2016 chromosome, complete genome	1312	3777	13%	0.0	81%	CP014796.1
Sagittula sp. P11 plasmid unnamed1, complete sequence	1308	1308	3%	0.0	81%	CP021914.1
Bradyrhizobium sp. CCGE-LA001, complete genome	1303	7337	27%	0.0	81%	CP013949.1
Rhodopseudomonas palustris BisA53, complete genome	1301	4533	14%	0.0	81%	CP000463.1
Bradyrhizobium sp. 3 85S1MB chromosome, complete genome	1291	6899	26%	0.0	81%	CP029427.1
Yangia sp. CCB-MM3 plasmid unnamed3, complete sequence	1290	1290	3%	0.0	81%	CP014599.1
Bradyrhizobium sp. ORS 3257 isolate ORS3257 genome assembly, chromosome: BRAD3257	1288	6473	22%	0.0	81%	LS398110.1
Bradyrhizobium ottawaense strain OO99 chromosome, complete genome	1256	5591	18%	0.0	80%	CP029425.1
Rhodobacter sphaeroides ATCC 17029 chromosome 1, complete sequence	1254	4493	16%	0.0	80%	CP000577.1
Rhodobacter sphaeroides 2.4.1 chromosome 1, complete sequence	1249	4428	16%	0.0	80%	CP030271.1
Phreatobacter cathodiphilus strain S-12 chromosome, complete genome	1249	7744	23%	0.0	78%	CP027668.1
Rhodobacter sphaeroides strain MBTLJ-20 chromosome 1, complete sequence	1249	4428	16%	0.0	80%	CP015287.1
Rhodobacter sphaeroides strain MBTLJ-13 chromosome 1, complete sequence	1249	4428	16%	0.0	80%	CP015210.1
Rhodobacter sphaeroides strain MBTLJ-8 chromosome 1, complete sequence	1249	4428	16%	0.0	80%	CP012960.1
Rhodobacter sphaeroides 2.4.1 chromosome 1, complete sequence	1249	4428	16%	0.0	80%	CP000143.2
Rhodobacter sphaeroides ATCC 17025, complete genome	1249	5056	19%	0.0	80%	CP000661.1
Bradyrhizobium sp. MAFF 211645 mxaF' gene for methanol dehydrogenase alpha subunit, complete cds	1247	1247	3%	0.0	80%	AB548312.1
Rhodobacter sphaeroides KD131 chromosome 1, complete sequence	1232	4411	16%	0.0	80%	CP001150.1
Bradyrhizobium sp. BF49 genome assembly, chromosome: I	1216	9510	26%	0.0	80%	LN901633.1
Bradyrhizobium sp. ORS 285 strain ORS285 genome assembly, chromosome: BRAD285	1214	6972	22%	0.0	80%	LT859959.1
Paracoccus aminovorans isolate JCM7685 genome assembly, chromosome: I	1206	3044	9%	0.0	80%	LN832559.1
Bradyrhizobium sp. S23321 DNA, complete genome	1205	7797	29%	0.0	80%	AP012279.1
Bradyrhizobium sp. 2 39S1MB chromosome, complete genome	1194	5255	17%	0.0	80%	CP029426.1
Bradyrhizobium sp. ORS278,complete sequence	1192	6396	21%	0.0	77%	CU234118.1
Pelagibaca abyssi strain JLT2014 plasmid pPABY2, complete sequence	1190	1190	3%	0.0	80%	CP015090.1
Bradyrhizobium sp. BTAi1, complete genome	1190	6079	19%	0.0	77%	CP000494.1
Blastochloris viridis DNA, complete genome, strain: DSM 133	1188	5184	18%	0.0	77%	AP014854.2

Blastochloris viridis genome assembly Blastochloris viridis genome, chromosome : I	1188	5184	18%	0.0	77%	LN907867.1
Blastochloris viridis strain ATCC 19567, complete genome	1188	5184	18%	0.0	77%	CP012946.1
Bradyrhizobium lablabi strain MT34 genome assembly, chromosome: I	1186	5755	19%	0.0	80%	LT670845.1
Bradyrhizobium sp. G22 genome assembly, chromosome: I	1186	7364	24%	0.0	80%	LN907826.1
Bradyrhizobium sp. SK17 chromosome, complete genome	1175	6163	21%	0.0	80%	CP025113.1
Methylosinus trichosporium OB3b chromosome, complete genome	1173	3601	11%	0.0	82%	CP023737.1
Bradyrhizobium ottawaense strain GAS524 genome assembly, chromosome: I	1170	5753	19%	0.0	79%	LT629693.1
Methylocella silvestris BL2, complete genome	1170	3138	13%	0.0	80%	CP001280.1
Rhodovulum sp. P5, complete genome	1160	2053	8%	0.0	79%	CP015039.1
Methylocystis bryophila strain S285 chromosome, complete genome	1138	2591	10%	0.0	80%	CP019948.1
Rhodopseudomonas palustris strain PS3 chromosome, complete genome	1136	3407	14%	0.0	81%	CP019966.1
Bradyrhizobium oligotrophicum S58 DNA, complete genome	1134	8126	27%	0.0	79%	AP012603.1
Afipia sp. GAS231 genome assembly, chromosome: I	1133	5808	20%	0.0	79%	LT629703.1
Rubrivivax gelatinosus IL144 DNA, complete genome	1123	2854	10%	0.0	80%	AP012320.1
Bradyrhizobium icense strain LMTR 13, complete genome	1120	6882	24%	0.0	79%	CP016428.1
Rhodopseudomonas palustris HaA2, complete genome	1118	4911	19%	0.0	81%	CP000250.1
Sinorhizobium meliloti strain T073 plasmid psymB, complete sequence	1105	1105	3%	0.0	79%	CP021806.1
Sinorhizobium meliloti strain USDA1021 plasmid psymB, complete sequence	1105	1105	3%	0.0	79%	CP021802.1
Sinorhizobium meliloti BL225C plasmid pSINMEB02, complete sequence	1105	1105	3%	0.0	79%	CP002742.1
Bradyrhizobium sp. SM-2017B XoxF gene for methanol dehydrogenase, partial cds, isolate: SM32	1101	1101	2%	0.0	81%	LC218415.1

Table S5 623 significant up-regulated genes and 90 significant up-regulated strain-specific genes(orange) in the whole genome.

GeneName	Locus	XJLW_G_FPKM	XJLW_M_FPKM	log2(XJLW_M/XJLW_G)	up-or-down	p_value	q_value	Descriptiion
A3862_00335	CP016429:76420-77755	28.554	145.131	2.34559	up	0.000537666	0.0112224	MFS transporter
A3862_00360	CP016429:82428-83556	28.375	126.354	2.15478	up	0.00146884	0.015278	hypothetical protein
A3862_00365	CP016429:83566-87922	30.1559	158.768	2.39641	up	0.000760976	0.0120972	integrase
A3862_00375	CP016429:83566-87922	20.4836	95.7198	2.22435	up	0.00394453	0.023993	hypothetical protein
A3862_00380	CP016429:83566-87922	32.6193	154.097	2.24004	up	0.000862865	0.0125618	hypothetical protein
A3862_00390	CP016429:89686-91048	20.541	130.087	2.6629	up	0.000126887	0.008338	hypothetical protein
A3862_00400	CP016429:92540-95461	29.4601	136.373	2.21072	up	0.00140341	0.0149154	hypothetical protein
A3862_00410	CP016429:95545-96337	16.9098	106.207	2.65095	up	0.000502777	0.0109047	metallophosphoesterase
A3862_00415	CP016429:96391-96823	5.93535	42.9242	2.85439	up	0.000172832	0.00852131	hypothetical protein
A3862_00520	CP016429:115631-120705	31.6924	155.082	2.29083	up	0.00265463	0.019327	cation transporter
A3862_00525	CP016429:115631-120705	33.1965	174.973	2.39802	up	0.000438337	0.0104416	efflux transporter periplasmic adaptor subunit
A3862_00530	CP016429:115631-120705	12.1018	70.8834	2.55023	up	6.34E-05	0.00629678	heavy metal RND transporter
A3862_00590	CP016429:129423-130844	25.676	114.479	2.1566	up	0.0032544	0.021349	lytic transglycosylase
A3862_00600	CP016429:131829-133134	24.1763	143.271	2.56708	up	0.000193028	0.00872802	multidrug ABC transporter ATPase
A3862_00625	CP016429:135766-136522	23.6006	113.684	2.26813	up	0.00230996	0.0182773	cation transporter
A3862_00645	CP016429:138261-140339	21.5037	141.911	2.72233	up	9.03E-05	0.00753901	two-component sensor histidine kinase
A3862_00705	CP016429:150377-152329	18.4438	100.412	2.44472	up	0.00141322	0.0149637	DNA-binding response regulator
A3862_00720	CP016429:153266-153674	10.1841	48.4198	2.24927	up	0.000774616	0.0120972	histidine kinase
A3862_00725	CP016429:153703-154486	22.1558	109.424	2.30417	up	0.00189151	0.0168713	hypothetical protein
A3862_00830	CP016429:181030-186967	16.8576	77.0288	2.192	up	0.0045265	0.0257102	hypothetical protein
A3862_00840	CP016429:181030-186967	25.6766	134.763	2.3919	up	0.000428266	0.0103633	hypothetical protein
A3862_04135	CP016429:904132-907400	26.1755	143.938	2.45916	up	0.00028046	0.00895725	hypothetical protein
A3862_04160	CP016429:909548-911186	34.6544	163.534	2.23848	up	0.000897945	0.0126736	hypothetical protein
A3862_04175	CP016429:911197-911932	6.44917	46.6706	2.85533	up	0.000687213	0.0120023	hypothetical protein
A3862_04185	CP016429:912591-915062	6.52837	45.6851	2.80693	up	0.000132417	0.008338	hypothetical protein
A3862_04205	CP016429:912591-915062	25.9452	126.356	2.28396	up	0.000724059	0.0120023	hypothetical protein
A3862_04215	CP016429:915222-917045	17.4967	80.1424	2.19549	up	0.0014201	0.014984	hypothetical protein
A3862_04220	CP016429:915222-917045	5.77351	42.6429	2.88479	up	0.00246083	0.0186615	hypothetical protein
A3862_04225	CP016429:915222-917045	17.6927	90.4136	2.35339	up	0.000223072	0.0088602	hypothetical protein
A3862_04260	CP016429:917640-919388	2.66866	36.5802	3.77688	up	0.000249918	0.00890144	hypothetical protein
A3862_04265	CP016429:919792-923947	31.1594	169.216	2.44113	up	0.00381548	0.0235442	hypothetical protein
A3862_04425	CP016429:971976-972885	17.7368	117.891	2.73264	up	0.00027097	0.00890144	integrase
A3862_04485	CP016429:991265-992084	20.4885	119.804	2.54779	up	0.000711832	0.0120023	transposase

Supplementary data

A3862_04495	CP016429:993817-994636	17.8158	108.724	2.60944	up	0.00061176	0.0115653	hypothetical protein
A3862_04610	CP016429:1019304-1021283	33.3055	158.803	2.25341	up	0.00109144	0.013794	hypothetical protein
A3862_04690	CP016429:1031576-1033265	30.4187	142.093	2.22381	up	0.000934096	0.0129316	hypothetical protein
A3862_04720	CP016429:1039165-1040041	20.7109	102.395	2.30569	up	0.00193889	0.0168713	hydroxyquinol 1,2-dioxygenase
A3862_04725	CP016429:1040117-1040504	7.24406	46.8711	2.69383	up	0.000281444	0.00895725	hypothetical protein
A3862_04790	CP016429:1052337-1054080	36.1711	167.39	2.21031	up	0.00143113	0.0150158	hypothetical protein
A3862_04945	CP016429:1085294-1088254	31.9345	158.121	2.30784	up	0.00163914	0.015998	hypothetical protein
A3862_04950	CP016429:1088568-1090458	34.0404	152.124	2.15993	up	0.0017009	0.0162223	hypothetical protein
A3862_05055	CP016429:1118549-1119083	18.1118	80.144	2.14567	up	0.00413217	0.0243196	isochorismatase
A3862_05090	CP016429:1125529-1127860	30.2952	169.05	2.48029	up	0.000819399	0.0122758	DNA topoisomerase
A3862_05205	CP016429:1151903-1153010	22.8191	116.989	2.35806	up	0.000682403	0.0120023	hypothetical protein
A3862_05210	CP016429:1153011-1155068	13.5845	77.8157	2.51809	up	0.000723176	0.0120023	hypothetical protein
A3862_05220	CP016429:1155074-1155671	11.974	68.1866	2.50959	up	0.000141487	0.00850278	hypothetical protein
A3862_05235	CP016429:1157115-1158393	22.7694	141.538	2.63602	up	0.000131403	0.008338	hypothetical protein
A3862_05250	CP016429:1158610-1160021	19.9657	114.456	2.5192	up	0.00078694	0.0120972	hypothetical protein
A3862_06405	CP016429:1405933-1406743	27.3827	136.751	2.32021	up	0.00126718	0.0146528	AAA family ATPase
A3862_06415	CP016429:1408605-1408923	2.0433	22.3158	3.44909	up	0.00294539	0.0204344	hypothetical protein
A3862_06490	CP016429:1428597-1430768	21.9803	150.159	2.77221	up	7.24E-05	0.00652307	hypothetical protein
A3862_06510	CP016429:1432391-1434816	25.4303	159.978	2.65325	up	0.00012284	0.008338	thiamine biosynthesis protein ThiF
A3862_06535	CP016429:1439910-1441259	27.2702	130.729	2.26118	up	0.00171078	0.0162371	hypothetical protein
A3862_06590	CP016429:1447962-1448949	24.3287	134.233	2.464	up	0.000401495	0.010054	hypothetical protein
A3862_06600	CP016429:1449983-1452086	29.5571	161.571	2.45059	up	0.000622837	0.0115828	hypothetical protein
A3862_06610	CP016429:1452109-1455119	38.8271	172.488	2.15136	up	0.00235659	0.0184002	hypothetical protein
A3862_06625	CP016429:1458892-1460224	27.8031	154.627	2.47548	up	0.000286174	0.00902539	MFS transporter
A3862_06635	CP016429:1460615-1460915	5.65654	28.9296	2.35455	up	0.00693107	0.0326144	hypothetical protein
A3862_06700	CP016429:1474039-1474357	1.15697	17.6424	3.93062	up	0.0077078	0.0346253	hypothetical protein
A3862_06740	CP016429:1482732-1483608	28.1599	130.321	2.21036	up	0.0018206	0.0165294	hypothetical protein
A3862_06775	CP016429:1490699-1491704	23.7469	144.807	2.60832	up	0.000195551	0.00872802	hypothetical protein
A3862_06790	CP016429:1492881-1494159	38.695	172.697	2.15802	up	0.00122817	0.0144668	transposase
A3862_07040	CP016429:1557157-1558297	27.725	146.553	2.40217	up	0.000448008	0.0104416	guanylate cyclase
A3862_07140	CP016429:1578830-1579988	27.4723	139.862	2.34796	up	0.000560443	0.0113804	transposase
A3862_15470	CP016429:3403710-3404172	13.6122	77.1592	2.50294	up	1.86E-05	0.00303159	hypothetical protein
A3862_15785	CP016429:3468830-3472612	24.1155	113.91	2.23986	up	0.00212191	0.0174683	chemotaxis protein CheR
A3862_15890	CP016429:3499421-3499865	13.8226	63.8979	2.20874	up	0.000315341	0.00919753	hypothetical protein
A3862_16185	CP016429:3551905-3552421	11.8831	57.8022	2.28222	up	0.000157557	0.00850278	hypothetical protein
A3862_16215	CP016429:3554919-3556068	15.4918	93.3801	2.59161	up	0.000314522	0.00919753	hypothetical protein
A3862_20380	CP016429:4464161-4464782	8.22921	69.1418	3.07073	up	6.63E-08	6.47E-05	integrase
A3862_20845	CP016429:4585634-4586414	11.2319	94.8511	3.07806	up	1.79E-05	0.00300026	hypothetical protein
A3862_20855	CP016429:4588067-4589060	25.1863	117.352	2.22013	up	0.00133027	0.0148311	hypothetical protein

Supplementary data

A3862_20875	CP016429:4591003-4591744	26.3928	125.692	2.25168	up	0.0021143	0.0174683	hypothetical protein
A3862_24310	CP016429:5378904-5379276	6.3881	32.7215	2.35678	up	0.00433791	0.0250448	hypothetical protein
A3862_24315	CP016429:5379720-5380209	10.3211	59.5678	2.52893	up	2.40E-05	0.00359773	hypothetical protein
A3862_24350	CP016429:5389020-5391029	31.7993	163.252	2.36003	up	0.000470192	0.0105593	transposase
A3862_27225	CP016429:6008146-6009480	21.1856	156.626	2.88616	up	6.94E-05	0.0064468	hypothetical protein
A3862_27235	CP016429:6008146-6009480	6.64189	41.6976	2.6503	up	0.00461343	0.0258528	hypothetical protein
A3862_27240	CP016429:6009640-6010030	6.6041	48.9575	2.8901	up	0.000134294	0.00836621	hypothetical protein
A3862_27245	CP016429:6010178-6010888	9.42598	50.9064	2.43313	up	0.00133777	0.0148311	hypothetical protein
A3862_27270	CP016429:6012290-6013535	13.6107	83.5632	2.61813	up	1.35E-05	0.00254515	hypothetical protein
A3862_27335	CP016429:6017884-6019599	32.0725	172.566	2.42774	up	0.000401749	0.010054	hypothetical protein
A3862_27395	CP016429:6026731-6028491	38.607	204.036	2.40189	up	0.000715418	0.0120023	hypothetical protein
A3862_27410	CP016429:6029412-6032714	48.2929	215.338	2.15672	up	0.00256889	0.0190188	hypothetical protein
A3862_27420	CP016429:6029412-6032714	2.6469	29.3786	3.47239	up	0.00292409	0.0204337	hypothetical protein
A3862_27445	CP016429:6034662-6037083	46.687	227.637	2.28564	up	0.00385615	0.0237702	hypothetical protein
A3862_27455	CP016429:6038776-6042042	40.6088	222.91	2.4566	up	0.00298415	0.0204868	hypothetical protein
A3862_27470	CP016429:6042049-6044880	45.252	232.935	2.36387	up	0.00308087	0.0208618	hypothetical protein
A3862_27480	CP016429:6051082-6051988	25.4765	131.073	2.36313	up	0.000761691	0.0120972	hypothetical protein
A3862_27490	CP016429:6052601-6054254	17.3841	79.9089	2.20059	up	0.000647261	0.0116986	hypothetical protein
A3862_00045	CP016429:10081-11782	24.3517	136.996	2.49204	up	0.000276132	0.00890144	ABC transporter ATP-binding protein
A3862_00055	CP016429:13100-14545	24.7256	124.662	2.33394	up	0.000782969	0.0120972	hypothetical protein
A3862_00120	CP016429:26880-27774	19.4733	97.1639	2.31892	up	0.00159148	0.0158044	hypothetical protein
A3862_00270	CP016429:58990-60682	23.1564	146.728	2.66366	up	0.000128778	0.008338	glutamate-1-semialdehyde 2,1-aminomutase
A3862_00275	CP016429:60714-61617	20.4319	117.201	2.5201	up	0.000613462	0.0115653	phosphatidylserine decarboxylase
A3862_00510	CP016429:113731-114892	22.468	124.051	2.46499	up	0.000410711	0.0102346	MFS transporter
A3862_00880	CP016429:195111-195495	3.43174	38.5661	3.49032	up	0.000195742	0.00872802	hypothetical protein
A3862_00915	CP016429:205999-208654	31.1353	147.111	2.24028	up	0.00230527	0.018268	-
A3862_00935	CP016429:213441-214662	29.8654	139.381	2.22249	up	0.000906174	0.0126736	monooxygenase
A3862_00955	CP016429:218684-219434	19.894	87.8082	2.14203	up	0.00504773	0.0272656	metal ABC transporter substrate-binding protein
A3862_00970	CP016429:220924-222966	32.5898	148.215	2.18519	up	0.00115366	0.014104	sulfate transporter
A3862_00980	CP016429:224842-230575	25.7244	133.143	2.37177	up	0.000446615	0.0104416	hypothetical protein
A3862_01040	CP016429:239182-241021	43.3848	195.704	2.17341	up	0.00242195	0.0185387	AMP-dependent synthetase
A3862_01100	CP016429:252088-252976	28.0154	131.282	2.22837	up	0.0018528	0.0167438	transporter
A3862_01135	CP016429:259261-262531	25.0596	148.844	2.57037	up	0.000741771	0.0120972	RND transporter
A3862_01140	CP016429:262638-263916	25.689	125.312	2.2863	up	0.000684156	0.0120023	efflux transporter periplasmic adaptor subunit
A3862_01155	CP016429:266211-266505	2.83112	21.3395	2.91408	up	0.00623912	0.0308844	hypothetical protein
A3862_01160	CP016429:267225-268824	16.8508	130.978	2.95843	up	2.67E-05	0.00382483	porin

A3862_01225	CP016429:285058-287149	27.6904	143.787	2.37647	up	0.000726496	0.0120023	K+-transporting ATPase subunit B
A3862_01275	CP016429:301054-302686	27.3409	142.936	2.38624	up	0.000449332	0.0104416	hypothetical protein
A3862_01280	CP016429:302722-303676	22.0578	132.518	2.58682	up	0.000315694	0.00919753	sugar ABC transporter substrate-binding protein
A3862_01305	CP016429:308337-313854	28.2916	137.063	2.27639	up	0.000697561	0.0120023	hypothetical protein
A3862_01340	CP016429:317595-318684	24.5939	133.047	2.43556	up	0.000485387	0.0107054	acyltransferase
A3862_01375	CP016429:326125-328857	30.1784	155.545	2.36574	up	0.000521425	0.0110729	lipopolysaccharide biosynthesis protein
A3862_01395	CP016429:332971-336179	23.2047	120.908	2.38142	up	0.000864481	0.0125618	acyl transferase
A3862_01430	CP016429:338879-339644	16.9039	94.222	2.47871	up	0.00118107	0.0142626	malonate transporter subunit MadM
A3862_01675	CP016429:383943-384597	15.6725	90.1519	2.52412	up	0.000891538	0.0126736	alkylated DNA repair dioxygenase
A3862_01885	CP016429:429727-430219	11.8023	62.4557	2.40377	up	6.76E-05	0.00638739	tRNA-specific adenosine deaminase
A3862_02180	CP016429:486861-488154	31.9618	141.796	2.1494	up	0.00132839	0.0148311	MFS transporter
A3862_02195	CP016429:491644-492706	23.4289	115.199	2.29777	up	0.000967653	0.0131781	threonine aldolase
A3862_02240	CP016429:502526-503830	17.2877	89.3806	2.37022	up	0.0019556	0.0168713	heme exporter protein CcmB
A3862_02440	CP016429:548589-549264	15.4447	83.7871	2.43962	up	0.00125845	0.0146266	RNA polymerase subunit sigma-24
A3862_02545	CP016429:567847-570180	15.2594	103.892	2.76731	up	0.000276637	0.00890144	cellulose biosynthesis protein BcsS
A3862_02550	CP016429:567847-570180	34.4812	166.839	2.27457	up	0.000891959	0.0126736	deoxyribodipyrimidine photolyase
A3862_02640	CP016429:584530-586240	34.4206	217.728	2.66119	up	0.000311344	0.00919753	dihydrolipoyl dehydrogenase
A3862_02910	CP016429:652536-653910	30.3851	135.456	2.15639	up	0.00120645	0.0144295	acyltransferase
A3862_03025	CP016429:676977-678453	28.7743	139.201	2.27432	up	0.000714857	0.0120023	histidine kinase
A3862_03080	CP016429:689029-692305	20.9709	106.315	2.34188	up	0.00181627	0.0165156	ABC transporter
A3862_03110	CP016429:695535-699820	19.6695	102.629	2.38341	up	0.00137037	0.0148609	DNA-binding response regulator
A3862_03115	CP016429:695535-699820	25.9186	162.051	2.64439	up	0.00108744	0.0137924	-
A3862_03120	CP016429:700105-701374	20.6931	118.49	2.51755	up	0.000252345	0.00890144	urea ABC transporter substrate-binding protein
A3862_03130	CP016429:702548-703721	21.422	112.211	2.38905	up	0.000627009	0.0115828	urea ABC transporter permease subunit UrtC
A3862_03135	CP016429:703728-704514	17.3072	86.6933	2.32455	up	0.00253274	0.0189581	urea ABC transporter ATP-binding protein UrtD
A3862_03140	CP016429:704516-705281	14.758	83.4592	2.49957	up	0.00106578	0.0137479	urea ABC transporter ATP-binding subunit UrtE
A3862_03145	CP016429:705291-706311	15.2992	97.84	2.67697	up	0.000354418	0.00939126	hypothetical protein
amiE	CP016429:708347-709403	26.9082	123.964	2.20381	up	0.00112234	0.0139624	acylamide amidohydrolase
A3862_03180	CP016429:713050-713944	31.7183	141.273	2.1551	up	0.00174939	0.0163047	LysR family transcriptional regulator
A3862_03405	CP016429:762466-763714	28.3527	135.856	2.26052	up	0.000839646	0.0123503	nucleoside permease
A3862_03455	CP016429:774623-774968	9.59879	44.6685	2.21833	up	0.0040009	0.0242221	hypothetical protein
A3862_03460	CP016429:775184-777173	38.7876	178.126	2.19923	up	0.00198568	0.0168984	hypothetical protein
A3862_03745	CP016429:831455-831713	5.02934	41.0115	3.02758	up	0.00283504	0.0201578	response regulator SirA
A3862_03835	CP016429:845830-847969	24.2818	142.185	2.54983	up	0.000351711	0.00939126	TonB-dependent receptor
A3862_03900	CP016429:858089-861496	26.492	143.441	2.43683	up	0.00035758	0.00941148	hypothetical protein

A3862_03925	CP016429:866644-867910	25.7209	142.766	2.47264	up	0.000310863	0.00919753	hypothetical protein
A3862_03935	CP016429:869402-870653	31.8783	152.304	2.2563	up	0.000798349	0.0121117	molybdopterin molybdenumtransferase MoeA
A3862_04030	CP016429:886077-886773	24.6376	116.31	2.23904	up	0.00258196	0.0190188	Fe-S cluster assembly protein HesB
A3862_04050	CP016429:889456-891532	29.6786	146.196	2.30041	up	0.00102749	0.0135518	chemotaxis protein
A3862_04290	CP016429:927796-929734	31.1537	150.931	2.27641	up	0.000906873	0.0126736	squalene-hopene cyclase
A3862_05030	CP016429:1111565-1113272	26.3968	148.42	2.49125	up	0.000299755	0.00914254	glucose-methanol-choline oxidoreductase
A3862_05325	CP016429:1171709-1174489	33.0969	158.964	2.26393	up	0.00175687	0.0163047	marine proteobacterial sortase target protein
A3862_05350	CP016429:1178402-1179455	12.0679	119.197	3.3041	up	1.11E-05	0.00216296	ABC transporter substrate-binding protein
A3862_05355	CP016429:1179459-1181182	22.605	120.045	2.40886	up	0.000740439	0.0120972	ABC transporter permease
A3862_05360	CP016429:1179459-1181182	23.1894	128.315	2.46815	up	0.000823393	0.0122758	ABC transporter ATP-binding protein
A3862_05365	CP016429:1181208-1182750	24.2357	126.178	2.38025	up	0.000419366	0.0102471	amidohydrolase
A3862_05370	CP016429:1182772-1184122	28.6141	143.909	2.33036	up	0.000538892	0.0112224	glucarate dehydratase
A3862_05375	CP016429:1184201-1185557	21.5683	147.927	2.7779	up	7.23E-05	0.00652307	glucarate transporter
A3862_05385	CP016429:1186678-1187581	24.776	128.155	2.37088	up	0.000692843	0.0120023	LysR family transcriptional regulator
A3862_05690	CP016429:1254630-1256277	21.4173	129.198	2.59274	up	0.000158871	0.00850278	porin
A3862_05945	CP016429:1312838-1313318	12.7359	61.9764	2.28282	up	0.000196738	0.00872802	sodium:calcium antiporter
A3862_05950	CP016429:1313369-1313885	10.3878	71.5245	2.78355	up	9.58E-07	0.00043176	hypothetical protein
A3862_06185	CP016429:1354339-1354699	7.5821	42.3829	2.48281	up	0.001626	0.015946	hypothetical protein
A3862_06195	CP016429:1355327-1355837	12.3337	58.6046	2.24841	up	0.000109347	0.00790538	hypothetical protein
A3862_06205	CP016429:1356523-1357774	25.1392	134.159	2.41593	up	0.000389938	0.00988519	hypothetical protein
A3862_06210	CP016429:1357792-1363136	34.6201	172.981	2.32093	up	0.00671272	0.032274	hypothetical protein
A3862_06215	CP016429:1357792-1363136	14.3029	79.0362	2.46621	up	0.000625396	0.0115828	peptidase P60
A3862_06225	CP016429:1363150-1363792	20.8244	108.974	2.38763	up	0.00186576	0.016809	glycoside hydrolase family 24
A3862_06235	CP016429:1364635-1364968	6.92798	31.1704	2.16967	up	0.0088739	0.0377931	hypothetical protein
A3862_06245	CP016429:1365395-1366174	12.2737	54.3466	2.14662	up	0.000612378	0.0115653	hypothetical protein
A3862_06250	CP016429:1365395-1366174	8.85371	52.1016	2.55698	up	0.000638795	0.0116727	head-tail adaptor protein
A3862_06280	CP016429:1370851-1371364	14.9267	78.6395	2.39736	up	0.000165525	0.00850278	peptidase U35
A3862_06680	CP016429:1470285-1471017	18.9074	107.726	2.51035	up	0.00100168	0.0133618	hypothetical protein
A3862_07045	CP016429:1558398-1559460	28.4379	163.202	2.52078	up	0.000294298	0.00907058	hypothetical protein
A3862_07060	CP016429:1560459-1561559	26.3485	155.611	2.56216	up	0.000416927	0.0102471	transposase
A3862_07120	CP016429:1573087-1574779	28.4565	164.007	2.52693	up	0.000331376	0.00929878	hypothetical protein
A3862_07205	CP016429:1596849-1598847	35.8463	169.523	2.24158	up	0.00165251	0.0160217	chemotaxis protein
A3862_07240	CP016429:1604496-1604907	11.9707	68.0293	2.50665	up	8.59E-05	0.0073959	LysR family transcriptional regulator
A3862_07275	CP016429:1609273-1610403	46.1987	320.311	2.79355	up	0.000112278	0.00796897	cytochrome d ubiquinol oxidase subunit II
A3862_07280	CP016429:1610410-1611829	147.469	826.279	2.48622	up	0.00725401	0.0333958	cytochrome D ubiquinol oxidase subunit I
A3862_07370	CP016429:1623562-1623943	9.30664	43.4389	2.22266	up	0.00214425	0.0174683	hypothetical protein
A3862_07460	CP016429:1636662-1638075	31.3643	151.064	2.26796	up	0.000808296	0.0122182	MFS transporter

A3862_07470	CP016429:1638199-1642624	30.1762	168.747	2.48338	up	0.00059644	0.0114725	ABC transporter
A3862_07540	CP016429:1657946-1658933	28.7913	145.074	2.33309	up	0.000832654	0.0122822	cytochrome d ubiquinol oxidase subunit II
A3862_07545	CP016429:1658980-1661049	30.1113	165.605	2.45937	up	0.000476347	0.0106461	fusaric acid resistance protein
A3862_07555	CP016429:1661050-1662046	26.4966	133.679	2.33489	up	0.000581019	0.011465	RND transporter
A3862_07625	CP016429:1672722-1673637	28.1689	129.458	2.20031	up	0.00159943	0.0158482	hypothetical protein
A3862_07655	CP016429:1680112-1681483	29.5297	147.28	2.31832	up	0.000593219	0.011465	branched-chain amino acid ABC transporter permease
A3862_07665	CP016429:1681580-1684003	18.7375	106.73	2.50997	up	0.000795323	0.0120972	3-hydroxyisobutyrate dehydrogenase
A3862_07690	CP016429:1688032-1689292	41.3291	193.538	2.22739	up	0.0010164	0.0134689	D-amino acid dehydrogenase small subunit
A3862_07750	CP016429:1701395-1702352	19.4176	125.774	2.6954	up	0.000217404	0.0088602	antibiotic biosynthesis monooxygenase
A3862_07760	CP016429:1703968-1705381	30.4074	140.2	2.20499	up	0.000952864	0.0130373	FAD-linked oxidase
A3862_07780	CP016429:1709100-1710582	20.4831	124.243	2.60065	up	0.000155373	0.00850278	porin
A3862_07790	CP016429:1712882-1713308	47.8779	748.897	3.96734	up	5.45E-07	0.000395283	hypothetical protein
A3862_07795	CP016429:1713422-1713854	41.4028	503.336	3.60372	up	2.04E-06	0.000745817	hypothetical protein
A3862_07800	CP016429:1714325-1714859	217.524	2166.08	3.31584	up	0.000562604	0.0113804	hypothetical protein
A3862_07805	CP016429:1714987-1715602	17.3389	177.478	3.35555	up	5.73E-06	0.00139915	hypothetical protein
A3862_07810	CP016429:1715677-1717084	32.8749	193.392	2.55647	up	0.000220103	0.0088602	C4-dicarboxylate ABC transporter substrate-binding protein
A3862_07815	CP016429:1717147-1717450	11.9936	82.3842	2.78011	up	8.58E-05	0.0073959	hypothetical protein
A3862_07820	CP016429:1718656-1720303	24.9321	136.448	2.45227	up	0.000304583	0.009194	diguanylate cyclase
A3862_07855	CP016429:1729663-1730908	20.4536	122.64	2.58401	up	0.000169389	0.00851943	urea ABC transporter
A3862_07860	CP016429:1730913-1733593	17.3652	109.578	2.65769	up	0.000457829	0.0104612	urea ABC transporter
A3862_07865	CP016429:1730913-1733593	21.2766	136.196	2.67834	up	0.000144751	0.00850278	urea ABC transporter
A3862_07905	CP016429:1739909-1742930	24.7273	113.977	2.20457	up	0.0019191	0.0168713	aminoglycoside phosphotransferase
A3862_07920	CP016429:1743035-1744880	37.7164	171.793	2.18741	up	0.00179979	0.0165011	glutathione ABC transporter ATP-binding protein
A3862_07925	CP016429:1744885-1746786	24.555	155.154	2.65962	up	0.000203414	0.0088602	peptide ABC transporter permease
A3862_07930	CP016429:1744885-1746786	24.8804	114.47	2.20189	up	0.00195035	0.0168713	peptide ABC transporter permease
A3862_07935	CP016429:1746842-1748402	21.5541	150.164	2.8005	up	5.50E-05	0.00608914	diguanylate cyclase
A3862_07945	CP016429:1751135-1753202	15.061	108.323	2.84646	up	0.000170214	0.00851943	glutamate ABC transporter ATP-binding protein
A3862_07950	CP016429:1751135-1753202	17.6088	98.9472	2.49036	up	0.00109532	0.013794	polar amino acid ABC transporter permease
A3862_07955	CP016429:1751135-1753202	18.3744	83.7232	2.18793	up	0.0045417	0.0257359	ABC transporter permease
A3862_07970	CP016429:1754714-1756121	24.5525	139.976	2.51124	up	0.000227731	0.00890144	GntR family transcriptional regulator
A3862_07980	CP016429:1757607-1759263	19.0702	119.401	2.64643	up	0.000109281	0.00790538	porin
A3862_07990	CP016429:1759819-1761617	28.386	148.714	2.38929	up	0.000515185	0.011051	hypothetical protein
A3862_07995	CP016429:1761618-1764176	20.2653	129.888	2.68018	up	0.000105581	0.00782634	-
A3862_08120	CP016429:1784941-1787041	30.5232	155.218	2.34631	up	0.00107879	0.0137924	chemotaxis protein
A3862_08230	CP016429:1808997-1810346	28.7635	141.606	2.29957	up	0.000741508	0.0120972	hypothetical protein

A3862_08235	CP016429:1810352-1811285	27.1091	120.074	2.14708	up	0.00230473	0.018268	curli production assembly protein CsgG
A3862_08250	CP016429:1812674-1812995	7.05683	35.6478	2.33672	up	0.00645722	0.0314588	hypothetical protein
A3862_08330	CP016429:1829503-1831367	20.3383	132.497	2.70369	up	0.000151615	0.00850278	iron ABC transporter
A3862_08335	CP016429:1829503-1831367	21.9113	133.712	2.60938	up	0.000358395	0.00941148	heme ABC transporter ATP-binding protein
A3862_08340	CP016429:1831548-1833684	26.0083	159.545	2.61692	up	0.000321447	0.00922743	TonB-dependent receptor
A3862_08350	CP016429:1834637-1835672	29.3392	141.637	2.27129	up	0.000782824	0.0120972	glycosyl transferase
A3862_08360	CP016429:1836495-1837572	23.2559	136.222	2.55029	up	0.000287052	0.00902539	acyltransferase
A3862_08375	CP016429:1839379-1840213	18.9522	125.216	2.72399	up	0.000244658	0.00890144	glycoside hydrolase
A3862_08380	CP016429:1840415-1841441	27.3909	125.694	2.19815	up	0.00138186	0.0149044	glycosyl transferase family A
A3862_08410	CP016429:1845610-1849200	31.5567	174.811	2.46978	up	0.000304335	0.009194	glucosyl transferase
A3862_08415	CP016429:1845610-1849200	29.3006	160.641	2.45483	up	0.000811626	0.0122182	lipopolysaccharide biosynthesis protein
A3862_08420	CP016429:1849292-1850582	23.7914	146.445	2.62185	up	0.000131817	0.008338	sugar transporter
A3862_08485	CP016429:1863216-1864296	24.5769	115.559	2.23326	up	0.00113702	0.0140472	glycosyltransferase
A3862_08515	CP016429:1869509-1870511	27.1155	127.42	2.2324	up	0.00112401	0.0139624	AraC family transcriptional regulator
A3862_08530	CP016429:1875854-1882751	28.665	154.289	2.42827	up	0.0114334	0.0443993	hypothetical protein
A3862_08535	CP016429:1883536-1884481	22.3179	122.813	2.46019	up	0.000664058	0.01194	AraC family transcriptional regulator
A3862_08545	CP016429:1885188-1885899	18.1426	111.918	2.62499	up	0.000574709	0.0114473	metallophosphoesterase
A3862_08555	CP016429:1886392-1888405	25.0194	164.356	2.71571	up	0.000174082	0.00852131	hypothetical protein
A3862_08575	CP016429:1892156-1894684	24.0008	139.862	2.54285	up	0.000238873	0.00890144	acyl-CoA dehydrogenase
A3862_08580	CP016429:1892156-1894684	23.654	136.461	2.52834	up	0.000222031	0.0088602	rubredoxin
A3862_08590	CP016429:1895473-1896829	27.3368	121.086	2.14712	up	0.00118125	0.0142626	nitrate ABC transporter substrate-binding protein
A3862_08595	CP016429:1896832-1897672	21.784	123.391	2.50189	up	0.000794067	0.0120972	nitrate ABC transporter, permease protein
A3862_08600	CP016429:1897680-1898661	32.2911	151.318	2.22838	up	0.00108485	0.0137924	-
A3862_08615	CP016429:1900303-1901458	17.3163	149.13	3.10637	up	1.79E-05	0.00300026	NADH:flavin oxidoreductase
actP	CP016429:1901777-1903364	32.414	159.192	2.29608	up	0.000709706	0.0120023	cation acetate symporter
A3862_08635	CP016429:1905035-1906442	20.9393	132.807	2.66505	up	0.000105451	0.00782634	5,10-methylene tetrahydromethanopterin reductase
A3862_08640	CP016429:1906450-1907221	16.7346	83.7857	2.32387	up	0.00251808	0.018936	ABC transporter ATP-binding protein
A3862_08645	CP016429:1907231-1908113	18.0266	118.474	2.71637	up	0.000291994	0.00904717	ABC transporter permease
A3862_08650	CP016429:1908117-1911325	27.588	137.562	2.31796	up	0.000760477	0.0120972	ABC transporter permease
A3862_08655	CP016429:1908117-1911325	28.8645	140.952	2.28783	up	0.000601818	0.0115046	ABC transporter permease
A3862_08660	CP016429:1908117-1911325	25.6474	128.832	2.32861	up	0.00126861	0.0146528	ABC transporter ATP-binding protein
A3862_08675	CP016429:1914114-1915526	22.6281	123.675	2.45036	up	0.00102606	0.0135518	GlcNAc-PI de-N-acetylase
A3862_08680	CP016429:1914114-1915526	16.3561	87.6254	2.42152	up	0.00157833	0.0157725	-
A3862_08720	CP016429:1923359-1925225	37.2505	175.362	2.235	up	0.0016077	0.0158516	histidine kinase
A3862_08730	CP016429:1926554-1926827	11.4833	301.196	4.71309	up	4.52E-12	2.65E-08	hypothetical protein
A3862_08800	CP016429:1942716-1943571	30.1104	138.369	2.20019	up	0.00175424	0.0163047	abortive infection protein

A3862_08970	CP016429:1975101-1975539	11.7852	52.7774	2.16294	up	0.000442102	0.0104416	transporter
A3862_09095	CP016429:2004239-2004611	9.58757	54.1963	2.49896	up	0.000589185	0.011465	hypothetical protein
A3862_09140	CP016429:2013041-2013713	17.407	89.232	2.35789	up	0.00214313	0.0174683	transcriptional regulator
A3862_09205	CP016429:2029492-2031830	31.7614	163.11	2.36049	up	0.000556992	0.011365	amidase
A3862_09210	CP016429:2029492-2031830	27.3945	148.465	2.43816	up	0.000432111	0.0104133	hypothetical protein
A3862_09215	CP016429:2031833-2035213	20.1505	114.638	2.5082	up	0.000908969	0.0126736	ABC transporter ATP-binding protein
A3862_09220	CP016429:2031833-2035213	28.1176	151.38	2.42863	up	0.000451224	0.0104441	branched-chain amino acid ABC transporter substrate-binding protein
A3862_09225	CP016429:2031833-2035213	25.8467	125.285	2.27716	up	0.00167057	0.0160638	amino acid ABC transporter
A3862_09260	CP016429:2042280-2043510	33.0105	153.322	2.21557	up	0.000997331	0.0133342	hypothetical protein
A3862_09330	CP016429:2058742-2060872	32.694	162.179	2.31049	up	0.00125971	0.0146266	energy transducer TonB
A3862_09365	CP016429:2067611-2068568	30.9488	153.806	2.31315	up	0.000586339	0.011465	LysR family transcriptional regulator
A3862_09615	CP016429:2125361-2127085	22.2041	131.699	2.56835	up	0.000495144	0.0107995	hypothetical protein
A3862_09800	CP016429:2172191-2172677	8.39282	43.428	2.3714	up	0.00035311	0.00939126	ribonuclease HI
A3862_09880	CP016429:2190914-2194041	29.7647	136.146	2.19348	up	0.00129849	0.0148059	VWA domain-containing protein
A3862_09960	CP016429:2206381-2206993	28.7381	130.551	2.18358	up	0.00338289	0.0218928	septum formation protein Maf
A3862_09975	CP016429:2207005-2209487	20.1142	98.0947	2.28596	up	0.00291603	0.0204262	dephospho-CoA kinase
A3862_10010	CP016429:2213644-2215506	27.2342	155.577	2.51414	up	0.000247155	0.00890144	hypothetical protein
A3862_10035	CP016429:2219717-2220647	32.6056	144.363	2.14651	up	0.00160336	0.0158516	transporter
A3862_10065	CP016429:2227618-2230225	30.2927	173.944	2.52158	up	0.00117187	0.0142253	TonB-dependent receptor
A3862_10175	CP016429:2251474-2253327	37.9213	169.61	2.16114	up	0.00134446	0.0148311	histidine kinase
A3862_10235	CP016429:2268385-2269609	24.7276	146.964	2.57127	up	0.000177145	0.00852131	metallophosphoesterase
A3862_10240	CP016429:2269676-2270945	31.8221	157.888	2.3108	up	0.000624682	0.0115828	arsenic transporter
A3862_10245	CP016429:2270975-2271923	31.2337	144.55	2.21039	up	0.00127597	0.0146799	hypothetical protein
A3862_10250	CP016429:2271935-2273333	29.7127	155.455	2.38735	up	0.000437898	0.0104416	C4-dicarboxylate ABC transporter substrate-binding protein
A3862_10255	CP016429:2273457-2274744	32.9403	148.557	2.17309	up	0.00112539	0.0139624	guanylate cyclase
A3862_10390	CP016429:2303948-2304560	24.4424	121.217	2.31014	up	0.00242172	0.0185387	glutathione S-transferase
A3862_10630	CP016429:2354286-2355612	32.7339	179.824	2.45772	up	0.000348336	0.00939126	tRNA uridine(34) 5-carboxymethylaminomethyl synthesis GTPase MnmE
A3862_10740	CP016429:2379678-2380425	24.9046	122.493	2.29821	up	0.00180621	0.0165011	arsenical resistance protein ArsH
A3862_10760	CP016429:2382602-2383772	26.5511	141.669	2.41568	up	0.00044279	0.0104416	MFS transporter
A3862_10780	CP016429:2389343-2390162	25.1996	124.488	2.30453	up	0.00161962	0.0159136	hypothetical protein
A3862_10840	CP016429:2400052-2403281	45.1445	211.699	2.22939	up	0.00375626	0.0233262	kojibiose phosphorylase
A3862_10860	CP016429:2404459-2405680	26.3999	149.551	2.50203	up	0.000247151	0.00890144	ATP-grasp domain-containing protein
A3862_10865	CP016429:2405976-2407850	25.6426	145.101	2.50045	up	0.000551534	0.0113454	ABC transporter ATP-binding protein
A3862_10870	CP016429:2405976-2407850	62.4806	318.515	2.34988	up	0.00103716	0.0136485	multidrug ABC transporter substrate-binding protein
A3862_10875	CP016429:2408019-2408346	16.4166	97.8028	2.57472	up	3.81E-05	0.00495617	hypothetical protein

A3862_10900	CP016429:2411917-2413366	77.2073	418.082	2.43698	up	0.00268888	0.0194877	hypothetical protein
A3862_10950	CP016429:2423840-2424857	34.8257	156.993	2.17248	up	0.00121041	0.0144362	epimerase
A3862_10955	CP016429:2425294-2426064	19.7498	97.1498	2.29838	up	0.00202746	0.0170832	hypothetical protein
A3862_10960	CP016429:2425294-2426064	1.5428	20.8667	3.75758	up	0.0110289	0.0432795	hypothetical protein
A3862_10970	CP016429:2427787-2431986	30.1746	157.708	2.38585	up	0.00189429	0.0168713	multidrug transporter
A3862_10980	CP016429:2432571-2435040	36.7497	167.856	2.19142	up	0.00252545	0.018936	hypothetical protein
A3862_10985	CP016429:2436701-2438741	35.34	156.095	2.14305	up	0.00249649	0.0188152	TonB-dependent receptor
A3862_11110	CP016429:2463063-2465808	40.7134	193.66	2.24995	up	0.00454861	0.0257359	multidrug ABC transporter ATP-binding protein
A3862_11115	CP016429:2465827-2466949	26.3613	153.299	2.53985	up	0.000252203	0.00890144	ABC transporter permease
A3862_11235	CP016429:2485564-2486467	31.1827	159.13	2.35139	up	0.000668372	0.0119416	multidrug ABC transporter ATPase
A3862_11290	CP016429:2497200-2498562	42.7806	202.501	2.2429	up	0.00106332	0.0137479	carboxyl-terminal protease
A3862_11345	CP016429:2507754-2509912	24.5835	133.361	2.43957	up	0.00138952	0.0149077	DNA-binding response regulator
A3862_11350	CP016429:2507754-2509912	44.5335	200.03	2.16725	up	0.00180486	0.0165011	PAS domain-containing sensor histidine kinase
A3862_11435	CP016429:2522127-2523936	38.0741	180.65	2.24631	up	0.00136108	0.0148426	chloride channel protein
A3862_11545	CP016429:2541911-2545604	37.6235	184.598	2.29468	up	0.00241069	0.0185387	hypothetical protein
A3862_11715	CP016429:2577129-2578020	29.7382	135.233	2.18506	up	0.00174541	0.0163016	ABC transporter permease
A3862_11740	CP016429:2583368-2584930	29.2875	134.357	2.19772	up	0.00127141	0.0146563	AraC family transcriptional regulator
A3862_12105	CP016429:2659366-2659714	4.52221	32.9543	2.86537	up	0.00138551	0.0149077	hypothetical protein
A3862_12125	CP016429:2661214-2662843	24.8827	145.67	2.54949	up	0.000217117	0.0088602	nuclease PIN
A3862_12135	CP016429:2666562-2667711	24.3762	146.801	2.59032	up	0.000187739	0.00865667	ceramide glucosyltransferase
A3862_12140	CP016429:2667738-2669038	24.5489	118.696	2.27355	up	0.0024734	0.0187135	phosphonate metabolism protein
A3862_12150	CP016429:2669150-2669999	21.4027	107.833	2.33293	up	0.00137396	0.0148723	phosphonate ABC transporter ATP-binding protein
A3862_12160	CP016429:2671042-2672787	20.5301	111.14	2.43656	up	0.000975432	0.0132219	phosphonate ABC transporter, permease protein PhnE
A3862_12345	CP016429:2712864-2713869	26.1767	137.041	2.38825	up	0.000567464	0.0113804	magnesium transporter
A3862_12385	CP016429:2719058-2720957	32.5367	165.487	2.34658	up	0.000871068	0.0126262	hypothetical protein
A3862_12875	CP016429:2828177-2829071	20.4678	124.194	2.60117	up	0.000374063	0.00969254	LysR family transcriptional regulator
A3862_13015	CP016429:2855559-2856507	27.3332	127.633	2.22328	up	0.00138202	0.0149044	methyltransferase type 12
A3862_13105	CP016429:2879109-2880225	25.5528	132.132	2.37043	up	0.000521879	0.0110729	DNA repair photolyase
A3862_13110	CP016429:2880534-2882637	28.2021	153.01	2.43975	up	0.000597528	0.0114725	chemotaxis protein
A3862_13115	CP016429:2882653-2883253	17.665	85.4791	2.27468	up	0.00295953	0.0204344	ribonuclease HII
A3862_13120	CP016429:2883396-2884443	25.0917	137.234	2.45136	up	0.000378449	0.00976298	alpha-mannosyltransferase
A3862_13125	CP016429:2884453-2885269	21.4709	118.507	2.46451	up	0.000828863	0.0122758	UDP-2,3-diacylglucosamine hydrolase
A3862_13235	CP016429:2906719-2907835	28.9372	136.939	2.24253	up	0.000986678	0.0132219	-
A3862_13250	CP016429:2909749-2910559	29.908	140.974	2.23682	up	0.001715	0.0162509	AraC family transcriptional regulator
A3862_13255	CP016429:2910572-2912036	32.7966	157.828	2.26674	up	0.00079463	0.0120972	pyridine nucleotide-disulfide oxidoreductase

A3862_13595	CP016429:2993989-2994328	8.81081	39.6397	2.1696	up	0.00692405	0.0326144	hypothetical protein
A3862_13755	CP016429:3029125-3029762	7.46006	45.9026	2.62132	up	0.000711115	0.0120023	hypothetical protein
A3862_13890	CP016429:3060466-3061224	8.92363	41.1637	2.20567	up	0.00237151	0.0184447	hypothetical protein
A3862_13895	CP016429:3060466-3061224	4.71849	39.3271	3.05913	up	0.000233099	0.00890144	hypothetical protein
A3862_14120	CP016429:3101107-3103172	35.6788	157.705	2.14409	up	0.00132348	0.0148311	molybdopterin-binding protein
A3862_14125	CP016429:3103192-3103792	19.321	101.008	2.38623	up	0.00184391	0.0166892	4-diphosphocytidyl-2C-methyl-D-erythritol kinase
A3862_14135	CP016429:3104091-3105285	33.3252	151.027	2.18012	up	0.00115031	0.014104	hypothetical protein
A3862_14335	CP016429:3147470-3150319	31.5442	164.858	2.38578	up	0.000507828	0.0109736	two-component sensor histidine kinase
A3862_14355	CP016429:3152313-3153611	4.43081	30.1428	2.76617	up	0.00352735	0.0223552	phosphotyrosine protein phosphatase
A3862_14360	CP016429:3152313-3153611	32.1747	142.556	2.14753	up	0.00152345	0.0156514	hypothetical protein
A3862_14485	CP016429:3181170-3181980	21.0044	123.664	2.55766	up	0.000614207	0.0115653	thiamine biosynthesis protein ThiJ
A3862_14615	CP016429:3210114-3210612	11.7941	87.4765	2.89083	up	7.00E-07	0.000395283	hypothetical protein
A3862_14685	CP016429:3223828-3224644	28.4472	131.037	2.20361	up	0.00196198	0.0168713	hypothetical protein
A3862_14705	CP016429:3228611-3229313	25.39	112.601	2.14888	up	0.00392593	0.0239482	GntR family transcriptional regulator
A3862_14710	CP016429:3229323-3229740	11.8288	59.6128	2.33332	up	0.000262506	0.00890144	hypothetical protein
A3862_14720	CP016429:3231127-3231997	23.8757	128.076	2.42339	up	0.000784282	0.0120972	ABC transporter permease
A3862_14725	CP016429:3232001-3234470	29.2402	165.046	2.49685	up	0.000830111	0.0122758	ABC transporter
A3862_14760	CP016429:3240100-3241057	21.5319	122.758	2.51128	up	0.000483088	0.0107054	transcriptional regulator
A3862_14890	CP016429:3267232-3271487	25.5765	147.931	2.53203	up	0.00104993	0.0137479	acriflavin resistance protein
A3862_14895	CP016429:3267232-3271487	21.3862	136.5	2.67415	up	0.000142666	0.00850278	multidrug transporter
A3862_14925	CP016429:3278877-3279162	6.99985	49.7874	2.83039	up	0.0015904	0.0158044	hypothetical protein
A3862_14940	CP016429:3281239-3282652	27.7253	150.285	2.43842	up	0.000364949	0.0095408	sodium:proton antiporter
A3862_14960	CP016429:3284967-3285810	36.8752	276.824	2.90824	up	3.80E-05	0.00495617	polyphosphate kinase 2
A3862_14965	CP016429:3285853-3289036	26.059	203.249	2.96339	up	0.000369771	0.0096239	RND transporter
A3862_14970	CP016429:3289040-3290159	19.3126	266.17	3.78474	up	6.76E-07	0.000395283	efflux transporter periplasmic adaptor subunit
A3862_15130	CP016429:3336796-3337699	14.8903	74.1844	2.31674	up	0.00263291	0.0192009	hypothetical protein
A3862_15140	CP016429:3338471-3341884	16.7282	82.2227	2.29726	up	0.00284106	0.0201578	ABC transporter ATP-binding protein
A3862_15145	CP016429:3338471-3341884	16.9365	85.2674	2.33186	up	0.00240135	0.0185387	ABC transporter ATP-binding protein
A3862_15160	CP016429:3342281-3343430	21.8217	123.037	2.49526	up	0.000336636	0.00929878	ABC transporter substrate-binding protein
A3862_15165	CP016429:3343464-3348747	23.829	128.963	2.43617	up	0.000386602	0.00987952	carbon monoxide dehydrogenase
A3862_15170	CP016429:3343464-3348747	27.1647	122.51	2.17309	up	0.00197082	0.0168939	carbon monoxide dehydrogenase
A3862_15175	CP016429:3343464-3348747	22.2752	152.738	2.77754	up	0.000153633	0.00850278	carbon monoxide dehydrogenase
A3862_15180	CP016429:3343464-3348747	25.9228	123.012	2.2465	up	0.00142783	0.0150114	esterase
A3862_15185	CP016429:3348757-3350041	16.1595	102.919	2.67105	up	0.000180621	0.00852131	dihydroorotase
A3862_15195	CP016429:3351024-3353374	16.5241	99.6868	2.59283	up	0.000699356	0.0120023	GntR family transcriptional regulator
A3862_15200	CP016429:3351024-3353374	16.9739	107.293	2.66016	up	0.000486277	0.0107054	-
A3862_15205	CP016429:3351024-3353374	17.1578	98.0179	2.51418	up	0.000975267	0.0132219	nitrate ABC transporter permease

A3862_15215	CP016429:3354450-3355467	27.8389	123.762	2.15239	up	0.00160955	0.0158516	zinc-binding dehydrogenase
A3862_15230	CP016429:3355532-3358281	30.102	134.534	2.16004	up	0.00119893	0.0144295	acetyl-CoA synthetase
A3862_15235	CP016429:3358412-3360008	26.9142	151.391	2.49183	up	0.00027665	0.00890144	ABC transporter substrate-binding protein
A3862_15245	CP016429:3360531-3363059	25.0942	125.117	2.31785	up	0.00089449	0.0126736	urea amidolyase
A3862_15255	CP016429:3360531-3363059	16.0383	99.0507	2.62665	up	0.000573994	0.0114473	hypothetical protein
A3862_15260	CP016429:3363086-3364567	28.9056	137.164	2.24648	up	0.000841489	0.0123503	Zn-dependent hydrolase
A3862_15270	CP016429:3364771-3365578	20.9014	126.218	2.59425	up	0.00054234	0.0112224	-
A3862_15275	CP016429:3365612-3366296	14.9015	86.9803	2.54523	up	0.000684135	0.0120023	amino acid ABC transporter
A3862_15280	CP016429:3366362-3367160	20.5892	101.933	2.30766	up	0.00210667	0.0174493	amino acid ABC transporter
A3862_15315	CP016429:3374298-3375729	30.4202	137.068	2.17179	up	0.00105271	0.0137479	carotenoid oxygenase
A3862_15330	CP016429:3377799-3378807	25.6184	271.484	3.40561	up	4.45E-06	0.0013266	gliding motility-associated lipoprotein GldK
A3862_15335	CP016429:3378848-3381335	29.0078	388.445	3.7432	up	5.68E-05	0.00608914	arylsulfatase
A3862_15345	CP016429:3383217-3384486	25.0644	114.009	2.18544	up	0.00107548	0.0137813	FAD-dependent oxidoreductase
A3862_15355	CP016429:3384523-3385973	23.9217	129.115	2.43227	up	0.000419244	0.0102471	glycosyl transferase family 1
A3862_15360	CP016429:3386029-3389640	24.3614	136.659	2.48791	up	0.000478127	0.0106461	hypothetical protein
A3862_15370	CP016429:3386029-3389640	22.3626	130.83	2.54854	up	0.000246881	0.00890144	radical SAM protein
A3862_15375	CP016429:3386029-3389640	23.2727	122.447	2.39544	up	0.000567455	0.0113804	aliphatic nitrilase
A3862_15560	CP016429:3423613-3424288	20.3091	103.113	2.34402	up	0.00226756	0.018091	-
A3862_15570	CP016429:3425552-3426635	29.4592	147.213	2.32112	up	0.000709175	0.0120023	hypothetical protein
A3862_15605	CP016429:3432189-3432519	8.11325	40.3264	2.31337	up	0.0036128	0.0227265	sulfite:cytochrome C oxidoreductase subunit B
A3862_16250	CP016429:3562199-3563957	26.4243	145.708	2.46315	up	0.000319846	0.0092267	protein kinase
A3862_16570	CP016429:3631586-3633524	35.1033	159.188	2.18105	up	0.00197663	0.016898	selenocysteine-specific translation elongation factor
A3862_16660	CP016429:3652431-3654342	33.1449	167.589	2.33806	up	0.000781303	0.0120972	hypothetical protein
A3862_16670	CP016429:3658458-3660051	25.9694	124.012	2.25559	up	0.000766561	0.0120972	ABC transporter substrate-binding protein
A3862_16690	CP016429:3663060-3663525	9.53344	50.5606	2.40695	up	0.000148674	0.00850278	DNA mismatch repair protein MutT
A3862_16780	CP016429:3684631-3685513	21.0075	104.734	2.31776	up	0.00149949	0.0154868	LysR family transcriptional regulator
A3862_16785	CP016429:3685686-3686997	30.5556	148.73	2.28318	up	0.000668862	0.0119416	C4-dicarboxylate transporter DctA
A3862_16960	CP016429:3724956-3726648	34.1853	155.341	2.18399	up	0.00139875	0.01491	chemotaxis protein
A3862_17190	CP016429:3772742-3773429	17.1177	90.4795	2.40211	up	0.00173415	0.0162693	hypothetical protein
A3862_17355	CP016429:3812757-3816364	27.9445	136.118	2.28422	up	0.000904024	0.0126736	peptide ABC transporter permease
A3862_17360	CP016429:3812757-3816364	31.2182	144.51	2.21071	up	0.0013925	0.0149077	ABC transporter
A3862_17670	CP016429:3882213-3885900	22.8681	108.355	2.24436	up	0.00220272	0.0177813	hydroxyneurosporene synthase
A3862_17675	CP016429:3882213-3885900	28.445	142.646	2.32619	up	0.000619428	0.0115828	CrtD protein
A3862_17685	CP016429:3886899-3888036	24.9144	147.287	2.56358	up	0.000218846	0.0088602	methyltransferase
A3862_17695	CP016429:3888130-3890070	21.9928	132.439	2.59022	up	0.000272947	0.00890144	chlorophyllide reductase iron protein subunit X

A3862_17700	CP016429:3890073-3893069	31.9249	150.812	2.24	up	0.000899101	0.0126736	chlorophyllide reductase subunit Y
A3862_17705	CP016429:3890073-3893069	26.3288	130.227	2.30631	up	0.000587329	0.011465	chlorophyllide reductase subunit Z
A3862_17955	CP016429:3949313-3949997	20.228	104.874	2.37423	up	0.00194049	0.0168713	DNA-binding response regulator
A3862_18010	CP016429:3961217-3961649	11.0049	49.7237	2.17578	up	0.00122056	0.0144395	gamma-glutamylcyclotransferase
A3862_18640	CP016429:4085093-4085813	16.7207	92.1702	2.46266	up	0.00130209	0.0148059	CarD family transcriptional regulator
A3862_18670	CP016429:4094030-4097125	23.1401	134.11	2.53494	up	0.000341818	0.00935367	thiamine biosynthesis protein ApbE
A3862_18675	CP016429:4094030-4097125	26.5147	146.794	2.46893	up	0.000537712	0.0112224	4Fe-4S binding protein
A3862_18680	CP016429:4097498-4099684	19.952	104.516	2.38913	up	0.000986581	0.0132219	hypothetical protein
A3862_18870	CP016429:4147362-4148721	28.2732	138.881	2.29634	up	0.000641839	0.0116727	hypothetical protein
A3862_18875	CP016429:4149017-4149446	10.5779	53.6154	2.34159	up	0.000318632	0.0092267	hypothetical protein
A3862_19275	CP016429:4239175-4240444	24.8184	140.015	2.4961	up	0.000270287	0.00890144	hypothetical protein
A3862_19290	CP016429:4244082-4246779	28.1134	167.447	2.57438	up	0.000848718	0.0124252	nitrate reductase
A3862_19325	CP016429:4252013-4253207	27.8413	142.007	2.35066	up	0.000603125	0.0115046	acyltransferase
A3862_19730	CP016429:4325551-4326367	25.04	110.668	2.14393	up	0.00278482	0.0199784	amino acid ABC transporter substrate-binding protein
A3862_19735	CP016429:4326386-4327816	22.03	107.17	2.28236	up	0.00246334	0.0186615	amino acid ABC transporter permease
A3862_19740	CP016429:4326386-4327816	18.311	102.176	2.48028	up	0.00120045	0.0144295	ABC transporter permease
A3862_19995	CP016429:4371247-4374670	19.692	90.517	2.20058	up	0.00433931	0.0250448	pyridoxamine 5'-phosphate oxidase
A3862_20000	CP016429:4374914-4376606	24.3961	150.924	2.6291	up	0.000169489	0.00851943	chemotaxis protein
A3862_20020	CP016429:4381200-4383561	37.8301	171.755	2.18275	up	0.0026568	0.019327	hypothetical protein
A3862_20230	CP016429:4426410-4427769	22.6331	131.408	2.53755	up	0.000221975	0.0088602	hypothetical protein
A3862_20280	CP016429:4438530-4438851	10.416	48.1457	2.2086	up	0.00306867	0.0208229	sulfite:cytochrome C oxidoreductase subunit B
A3862_20315	CP016429:4444410-4445493	19.6128	135.419	2.78756	up	0.000126436	0.008338	hypothetical protein
A3862_20325	CP016429:4450245-4451670	26.8179	146.3	2.44766	up	0.000334964	0.00929878	exonuclease VII large subunit
A3862_20330	CP016429:4451748-4452618	19.0178	99.2503	2.38372	up	0.0015351	0.0156886	hypothetical protein
A3862_20360	CP016429:4458102-4459387	20.2357	89.8579	2.15075	up	0.0038917	0.0238251	hypothetical protein
A3862_20410	CP016429:4475676-4478838	28.6634	174.158	2.60311	up	0.0012185	0.0144395	multidrug efflux RND transporter permease subunit
A3862_20420	CP016429:4480051-4481860	34.98	163.625	2.22579	up	0.00126135	0.0146266	multidrug ABC transporter ATP-binding protein
A3862_20430	CP016429:4483248-4484940	21.7337	122.109	2.49017	up	0.000276548	0.00890144	chemotaxis protein
A3862_20450	CP016429:4491902-4493546	39.0577	180.445	2.20788	up	0.00147506	0.0152884	hypothetical protein
A3862_20620	CP016429:4529932-4530619	23.0312	106.744	2.2125	up	0.00348539	0.0222336	DNA-binding protein
A3862_20635	CP016429:4532970-4534362	33.5057	150.112	2.16356	up	0.00125152	0.0145994	GntR family transcriptional regulator
A3862_20850	CP016429:4586535-4587828	16.4968	120.747	2.87173	up	4.09E-05	0.00520768	flagellin
A3862_20980	CP016429:4614166-4619965	32.9661	167.215	2.34265	up	0.00350072	0.0222943	error-prone DNA polymerase
A3862_21050	CP016429:4630868-4632542	21.9023	126.949	2.53509	up	0.000229328	0.00890144	hypothetical protein
A3862_21175	CP016429:4653782-4654958	18.0851	91.5298	2.33944	up	0.00131496	0.0148311	MFS transporter

Supplementary data

A3862_21270	CP016429:4679866-4683986	38.1875	249.856	2.70993	up	0.00243447	0.0185387	autotransporter outer membrane beta-barrel domain-containing protein
A3862_21615	CP016429:4747218-4748139	23.9583	113.185	2.24008	up	0.00141562	0.0149637	LysR family transcriptional regulator
A3862_21620	CP016429:4748413-4749577	34.4132	156.165	2.18203	up	0.00121337	0.0144395	MFS transporter
A3862_21660	CP016429:4756658-4757543	26.9079	125.511	2.22171	up	0.00184157	0.0166892	-
A3862_21690	CP016429:4762314-4768482	34.4216	182.977	2.41027	up	0.00447912	0.0255502	magnesium chelatase subunit H
A3862_21700	CP016429:4768498-4770678	28.2626	132.478	2.22879	up	0.00199768	0.0169297	magnesium protoporphyrin IX methyltransferase
A3862_21705	CP016429:4768498-4770678	35.1333	159.225	2.18016	up	0.00125068	0.0145994	protein pucC
A3862_21990	CP016429:4838777-4840955	31.2457	144.221	2.20655	up	0.00164589	0.0160052	TonB-dependent receptor
A3862_22100	CP016429:4862235-4862853	22.2225	113.367	2.35091	up	0.00216268	0.0175898	uracil-DNA glycosylase
A3862_22295	CP016429:4905052-4906081	21.577	124.228	2.52542	up	0.000328251	0.00929878	flagellar motor switch protein FliG
A3862_22315	CP016429:4907833-4908721	20.683	111.303	2.42798	up	0.00107032	0.0137754	flagellar motor stator protein MotA
A3862_22320	CP016429:4908973-4909753	18.6944	92.7789	2.31119	up	0.00241576	0.0185387	hypothetical protein
flgF	CP016429:4909754-4910495	24.1616	110.047	2.18733	up	0.00321589	0.0212314	flagellar biosynthesis protein FlgF
A3862_22330	CP016429:4910543-4911863	31.5458	160.727	2.3491	up	0.000512418	0.0110321	flagellum-specific ATP synthase FliI
A3862_22335	CP016429:4912048-4913257	24.4903	122.564	2.32326	up	0.000535128	0.0112224	flagellar hook protein FlgE
A3862_22340	CP016429:4913279-4914737	22.9169	143.742	2.649	up	0.000114433	0.00797762	flagellar hook-associated protein FlgK
flbT	CP016429:4918855-4919236	11.5968	120.026	3.37155	up	3.75E-08	4.39E-05	flagellar biosynthesis repressor FlbT
flgD	CP016429:4919281-4919692	10.6798	49.7024	2.21843	up	0.000759076	0.0120972	flagellar basal body rod modification protein
A3862_22380	CP016429:4920501-4922592	30.0093	146.353	2.28597	up	0.000956287	0.0130537	flagellar biosynthesis protein FlhA
A3862_22390	CP016429:4923346-4924335	14.3494	90.7947	2.66162	up	8.79E-06	0.00177495	hypothetical protein
A3862_22395	CP016429:4923346-4924335	11.4981	65.6068	2.51244	up	2.74E-05	0.00382483	flagellar biosynthesis protein FlgJ
A3862_22405	CP016429:4924716-4925166	9.58631	43.3583	2.17726	up	0.00129962	0.0148059	hypothetical protein
A3862_22410	CP016429:4925728-4928458	33.4981	162.231	2.2759	up	0.00238736	0.0185108	hypothetical protein
A3862_22440	CP016429:4931868-4932354	10.0995	59.7045	2.56355	up	3.01E-05	0.00410225	flagella basal body P-ring formation protein FlgA
A3862_22455	CP016429:4933450-4934769	18.5042	98.6084	2.41386	up	0.00164808	0.0160052	flagellar biosynthesis protein FlgH
A3862_22460	CP016429:4934789-4935272	10.086	75.7824	2.90951	up	1.25E-06	0.000489772	flagellar basal body protein FliL
A3862_22465	CP016429:4935330-4936068	14.9788	71.7039	2.25913	up	0.00325094	0.021349	flagellar biosynthetic protein FliP
A3862_22470	CP016429:4936335-4937502	24.3233	123.488	2.34396	up	0.000552158	0.0113454	hypothetical protein
A3862_22475	CP016429:4937671-4939938	27.2054	148.148	2.44507	up	0.000332608	0.00929878	flagellar M-ring protein FliF
A3862_22480	CP016429:4937671-4939938	14.4349	95.8678	2.73149	up	0.000163531	0.00850278	hypothetical protein
A3862_22485	CP016429:4939940-4942480	23.3509	136.752	2.55002	up	0.000181893	0.00852131	hypothetical protein
A3862_22490	CP016429:4939940-4942480	33.2128	148.113	2.15689	up	0.00122711	0.0144668	chemotaxis protein
A3862_22495	CP016429:4942530-4944508	24.9235	150.606	2.5952	up	0.000161718	0.00850278	hypothetical protein
A3862_22500	CP016429:4942530-4944508	10.2935	64.162	2.63998	up	4.76E-06	0.00132827	lytic transglycosylase
A3862_22540	CP016429:4950805-4951234	6.96393	45.5614	2.70984	up	0.000162296	0.00850278	MucR family transcriptional regulator

A3862_22900	CP016429:5046117-5047815	37.2314	170.631	2.19629	up	0.00157374	0.0157725	chemotaxis protein
A3862_22905	CP016429:5048118-5049183	31.9759	149.28	2.22296	up	0.000933878	0.0129316	hypothetical protein
A3862_22955	CP016429:5058690-5060546	20.5926	108.194	2.39342	up	0.00139802	0.01491	pyrimidine utilization protein B
A3862_22960	CP016429:5060660-5061847	7.43917	56.4325	2.92331	up	5.72E-05	0.00608914	pyrimidine utilization protein C
A3862_22965	CP016429:5060660-5061847	20.9626	144.918	2.78935	up	0.000175336	0.00852131	pyrimidine utilization protein D
A3862_22970	CP016429:5061856-5062792	26.9651	134.894	2.32266	up	0.000881708	0.0126736	hypothetical protein
A3862_22975	CP016429:5062929-5064773	29.2227	140.374	2.26411	up	0.000985727	0.0132219	glycosyl transferase
A3862_23110	CP016429:5098511-5098865	5.96926	28.6852	2.26468	up	0.00625664	0.0309282	hypothetical protein
A3862_23160	CP016429:5107107-5108814	33.5836	169.777	2.33781	up	0.000826904	0.0122758	helicase
A3862_23215	CP016429:5119179-5121606	29.9271	174.869	2.54675	up	0.000689805	0.0120023	dehydrogenase
A3862_23375	CP016429:5157933-5160155	28.7498	152.917	2.41113	up	0.00044273	0.0104416	ABC transporter permease
A3862_23415	CP016429:5168857-5169919	21.8479	148.599	2.76586	up	0.000100864	0.00777183	oxidoreductase
A3862_23495	CP016429:5183950-5185957	32.3988	155.389	2.26188	up	0.000810075	0.0122182	threonine-phosphate decarboxylase
A3862_23500	CP016429:5183950-5185957	26.4958	144.548	2.44771	up	0.000418172	0.0102471	cobalamin biosynthesis protein CobD
A3862_23520	CP016429:5188660-5190103	27.4701	150.341	2.4523	up	0.000336595	0.00929878	cobyric acid synthase CobQ
A3862_23550	CP016429:5193092-5196242	33.7304	176.893	2.39076	up	0.00284689	0.0201589	multidrug transporter AcrB
A3862_23555	CP016429:5196253-5197987	38.4115	212.055	2.46483	up	0.000724938	0.0120023	RND transporter
A3862_23570	CP016429:5199310-5200474	30.8744	145.076	2.23233	up	0.00100805	0.0134162	chromate transporter
A3862_23590	CP016429:5202543-5202870	3.3852	18.4029	2.44262	up	0.00579467	0.0294562	hypothetical protein
A3862_23675	CP016429:5218929-5221724	31.4768	147.242	2.22583	up	0.000906768	0.0126736	hypothetical protein
A3862_23720	CP016429:5230410-5231106	11.5807	97.0449	3.06693	up	6.83E-06	0.00148035	urea ABC transporter ATP-binding subunit UrtE
A3862_23725	CP016429:5231108-5233057	18.0012	128.24	2.83268	up	0.000178849	0.00852131	urea ABC transporter ATP-binding protein UrtD
A3862_23730	CP016429:5231108-5233057	28.9	138.649	2.2623	up	0.00088215	0.0126736	urea ABC transporter permease subunit UrtC
A3862_23735	CP016429:5233062-5234637	34.1493	155.975	2.19138	up	0.0011733	0.0142253	urea ABC transporter permease subunit UrtB
A3862_23770	CP016429:5239826-5241646	25.3922	123.686	2.28423	up	0.00133113	0.0148311	ABC transporter permease
A3862_23785	CP016429:5244096-5244894	26.3032	121.936	2.21281	up	0.00246277	0.0186615	ABC transporter ATP-binding protein
A3862_23795	CP016429:5245235-5246459	18.4398	94.3903	2.35582	up	0.000853341	0.0124618	hypothetical protein
A3862_23890	CP016429:5263698-5264998	12.9147	57.7855	2.16169	up	0.000701169	0.0120023	hypothetical protein
A3862_23960	CP016429:5287956-5290924	23.0854	112.592	2.28605	up	0.00191435	0.0168713	hypothetical protein
A3862_24055	CP016429:5307309-5308086	18.0663	118.463	2.71307	up	0.000310924	0.00919753	GDSL family lipase
A3862_24165	CP016429:5332971-5334309	26.4828	139.266	2.39472	up	0.000383375	0.00984668	porin
A3862_24170	CP016429:5334582-5335524	27.023	128.74	2.2522	up	0.00120739	0.0144295	galactose 1-dehydrogenase
A3862_24175	CP016429:5335525-5336506	21.013	130.287	2.63234	up	0.000229979	0.00890144	FAH family protein
A3862_24180	CP016429:5336578-5338186	26.9428	136.893	2.34508	up	0.000591526	0.011465	2,5-dioxovalerate dehydrogenase
A3862_24205	CP016429:5343592-5344456	25.6865	118.791	2.20935	up	0.00194262	0.0168713	gluconolaconase

A3862_24225	CP016429:5347097-5348846	36.5811	169.665	2.21352	up	0.00135615	0.0148426	multidrug ABC transporter ATP-binding protein
A3862_24345	CP016429:5388586-5388883	6.46316	61.9196	3.26009	up	0.000201431	0.0088602	transposase
A3862_24355	CP016429:5389020-5391029	37.6054	198.555	2.40053	up	0.000521515	0.0110729	hypothetical protein
A3862_24380	CP016429:5396337-5397282	25.3583	120.149	2.2443	up	0.00130208	0.0148059	AraC family transcriptional regulator
A3862_24420	CP016429:5401750-5403921	23.1489	127.019	2.45603	up	0.000312342	0.00919753	amidase
A3862_24445	CP016429:5406736-5408565	28.3985	136.798	2.26816	up	0.000780189	0.0120972	-
A3862_24470	CP016429:5411684-5413797	30.0577	147.215	2.29212	up	0.000702129	0.0120023	histidine kinase
A3862_24475	CP016429:5411684-5413797	22.3117	110.131	2.30335	up	0.00242657	0.0185387	DNA-binding response regulator
A3862_24485	CP016429:5414344-5415715	30.294	144.062	2.24958	up	0.000795062	0.0120972	efflux transporter periplasmic adaptor subunit
A3862_24490	CP016429:5415723-5418888	26.1401	155.158	2.5694	up	0.00101661	0.0134689	cation transporter
A3862_24495	CP016429:5419049-5420460	25.5203	126.18	2.30576	up	0.000951216	0.0130373	glycosyl transferase
A3862_24505	CP016429:5420835-5422449	23.1265	135.308	2.54863	up	0.000211723	0.0088602	hypothetical protein
A3862_24795	CP016429:5499386-5500685	27.7108	138.297	2.31924	up	0.000554737	0.0113585	GDP-mannose dehydrogenase
A3862_25160	CP016429:5576839-5577823	26.2106	122.068	2.21947	up	0.00143337	0.0150158	oxidoreductase
A3862_25390	CP016429:5627716-5630049	19.807	90.0614	2.1849	up	0.00467997	0.0261009	cytochrome oxidase subunit III
A3862_25495	CP016429:5644620-5645100	13.1053	67.52	2.36516	up	5.51E-05	0.00608914	hypothetical protein
A3862_25785	CP016429:5703284-5704934	22.6888	130.487	2.52385	up	0.000223926	0.0088602	chemotaxis protein
A3862_25860	CP016429:5728392-5731060	22.2422	102.878	2.20956	up	0.0038772	0.0238251	hypothetical protein
A3862_25865	CP016429:5728392-5731060	39.7157	175.271	2.14181	up	0.00259898	0.0190961	hypothetical protein
A3862_25915	CP016429:5739124-5740930	31.7678	151.222	2.25103	up	0.00104065	0.0136638	restriction endonuclease subunit R
A3862_26005	CP016429:5758946-5760220	12.6503	57.2226	2.17741	up	0.000421714	0.0102471	hypothetical protein
A3862_26150	CP016429:5792241-5792985	22.2516	99.6455	2.1629	up	0.0040302	0.0242252	hypothetical protein
A3862_26255	CP016429:5813393-5815499	29.0984	151.357	2.37894	up	0.000792005	0.0120972	TonB-dependent receptor
A3862_26345	CP016429:5834671-5835838	28.0239	140.155	2.32229	up	0.000696147	0.0120023	MFS transporter
A3862_26550	CP016429:5874554-5876654	31.6556	158.249	2.32166	up	0.00121971	0.0144395	chemotaxis protein
A3862_26675	CP016429:5902522-5902858	3.96033	32.0128	3.01496	up	0.00156677	0.0157706	hypothetical protein
A3862_26685	CP016429:5903375-5903717	6.53024	97.6413	3.90228	up	6.67E-07	0.000395283	hypothetical protein
A3862_27030	CP016429:5977747-5978059	6.03739	29.8301	2.30477	up	0.00898052	0.0379995	hypothetical protein
A3862_27605	CP016429:6072347-6074133	23.7844	158.009	2.73191	up	9.67E-05	0.00764927	transcriptional regulator
A3862_27610	CP016429:6072347-6074133	2.53765	16.3108	2.68426	up	0.0125338	0.0470834	hypothetical protein
A3862_27615	CP016429:6074420-6075680	27.8775	123.407	2.14625	up	0.00131232	0.0148311	hypothetical protein
dppD	CP016429:6075768-6076806	25.2826	124.998	2.30569	up	0.000830126	0.0122758	dipeptide ABC transporter ATP-binding protein DppD
A3862_27625	CP016429:6076814-6078802	28.8119	140.911	2.29005	up	0.00076532	0.0120972	-
A3862_27640	CP016429:6080028-6081651	28.9999	130.537	2.17034	up	0.00108762	0.0137924	ABC transporter substrate-binding protein
A3862_27650	CP016429:6081760-6083732	29.9617	153.806	2.35993	up	0.000494154	0.0107995	amidase
A3862_27750	CP016429:6098065-6101390	39.4274	175.072	2.15067	up	0.00134285	0.0148311	MFS transporter

A3862_27765	CP016429:6103198-6104134	29.4019	134.823	2.19708	up	0.00127921	0.0146883	LysR family transcriptional regulator
A3862_27850	CP016429:6122051-6123113	19.9795	103.54	2.3736	up	0.000883869	0.0126736	sugar ABC transporter substrate-binding protein
A3862_27855	CP016429:6123214-6125973	25.5039	125.722	2.30145	up	0.000589498	0.011465	ABC transporter ATP-binding protein
A3862_28050	CP016429:6160297-6161452	25.5989	114.503	2.16124	up	0.00139102	0.0149077	glycosyl transferase
A3862_28230	CP016429:6202877-6204239	29.0209	153.063	2.39897	up	0.00044609	0.0104416	MATE family efflux transporter
A3862_28245	CP016429:6206086-6208684	27.9064	150.474	2.43085	up	0.000943254	0.0129969	DNA ligase-associated DEXH box helicase
A3862_28465	CP016429:6251687-6254204	28.4731	155.752	2.45158	up	0.000939151	0.0129709	chemotaxis protein
A3862_28750	CP016429:6308624-6310277	29.0236	132.515	2.19085	up	0.00110539	0.0138582	MFS transporter
A3862_28765	CP016429:6313240-6315214	29.7899	137.002	2.2013	up	0.00123779	0.0145261	aconitate hydratase
A3862_28815	CP016429:6329503-6330007	13.4651	63.7457	2.2431	up	0.000103837	0.00782634	cytochrome C oxidase subunit III
A3862_28825	CP016429:6331209-6332778	30.8177	137.626	2.15892	up	0.00120625	0.0144295	transcriptional regulator
A3862_28830	CP016429:6333229-6334237	22.6714	113.876	2.32852	up	0.00105684	0.0137479	hypothetical protein
A3862_28855	CP016429:6339666-6340391	15.0441	67.0787	2.15666	up	0.00277408	0.0199492	hypothetical protein
A3862_28895	CP016429:6345579-6347804	27.4879	129.398	2.23495	up	0.00106174	0.0137479	glycosyl transferase family 1
A3862_28960	CP016429:6361788-6362718	28.8958	128.14	2.14879	up	0.00237173	0.0184447	AraC family transcriptional regulator
A3862_28970	CP016429:6363909-6365151	12.9895	117.945	3.18269	up	1.56E-05	0.00285776	cytochrome
A3862_28985	CP016429:6367146-6367890	20.8156	104.045	2.32147	up	0.00214476	0.0174683	hypothetical protein
A3862_28995	CP016429:6368436-6369210	19.1076	99.5427	2.38117	up	0.00155447	0.0157706	molybdopterin-binding protein
A3862_29005	CP016429:6370039-6371026	25.0423	113.332	2.17812	up	0.00206842	0.0172776	AraC family transcriptional regulator
A3862_29010	CP016429:6371618-6372503	24.7567	114.037	2.20361	up	0.00222927	0.017883	-
A3862_29015	CP016429:6372563-6373334	20.941	95.2174	2.18489	up	0.00390884	0.0238688	short-chain dehydrogenase
A3862_29035	CP016429:6376052-6376727	24.4237	109.945	2.17042	up	0.00407245	0.0242252	alkyl hydroperoxide reductase
A3862_29040	CP016429:6376823-6377459	19.0136	98.394	2.37154	up	0.00197988	0.0168984	glutathione S-transferase
A3862_29050	CP016429:6378583-6379354	16.9526	98.8809	2.54419	up	0.000899321	0.0126736	crotonase
A3862_29060	CP016429:6380687-6381605	25.8446	121.09	2.22814	up	0.00155631	0.0157706	LysR family transcriptional regulator
A3862_29080	CP016429:6383502-6383922	6.83094	51.8707	2.92476	up	5.91E-05	0.0061783	hypothetical protein
A3862_29090	CP016429:6384626-6385037	8.52117	43.0488	2.33685	up	0.00110752	0.0138582	hypothetical protein
A3862_29095	CP016429:6385131-6385470	4.56325	27.1087	2.57062	up	0.00544115	0.0285258	hypothetical protein
A3862_29135	CP016429:6390093-6391871	8.03305	63.8285	2.99018	up	5.59E-06	0.00139915	peptidase S24
A3862_29140	CP016429:6390093-6391871	29.4909	133.584	2.17941	up	0.00107446	0.0137813	DNA polymerase V subunit UmuC
A3862_29175	CP016429:6406154-6407261	25.5435	125.728	2.29928	up	0.000768397	0.0120972	cyanuric acid amidohydrolase
A3862_29180	CP016429:6407751-6408708	20.4604	127.387	2.63831	up	0.000255191	0.00890144	AraC family transcriptional regulator
A3862_29190	CP016429:6410606-6411479	17.4955	95.8323	2.45352	up	0.0011401	0.0140557	methyltransferase type 11
A3862_29210	CP016429:6415140-6416952	29.8617	151.092	2.33906	up	0.000634739	0.0116727	guanylate cyclase
A3862_29235	CP016429:6422911-6423592	16.0941	84.51	2.39259	up	0.00175637	0.0163047	-
A3862_29240	CP016429:6423605-6424925	24.3425	131.882	2.4377	up	0.000331865	0.00929878	dihydroorotase
A3862_29245	CP016429:6424937-6426224	28.4888	134.657	2.24083	up	0.000824244	0.0122758	allantoate amidohydrolase
A3862_29255	CP016429:6426641-6429495	23.7666	150.578	2.6635	up	0.000136854	0.00843595	urea ABC transporter permease subunit

								UrtB
A3862_29260	CP016429:6429548-6432015	19.1376	121.989	2.67227	up	0.000232807	0.00890144	urea ABC transporter permease subunit UrtC
A3862_29265	CP016429:6429548-6432015	15.7909	103.128	2.70726	up	0.000339292	0.00932815	ABC transporter ATP-binding protein
A3862_29270	CP016429:6429548-6432015	18.6841	93.6742	2.32584	up	0.00241979	0.0185387	urea ABC transporter ATP-binding subunit UrtE
A3862_29285	CP016429:6433757-6435563	25.2443	147.527	2.54695	up	0.000267409	0.00890144	allophanate hydrolase
A3862_29295	CP016429:6435584-6438110	20.2816	109.052	2.42677	up	0.0013169	0.0148311	sulfonate ABC transporter ATP-binding protein
A3862_29300	CP016429:6435584-6438110	24.0257	121.006	2.33243	up	0.00159074	0.0158044	ABC transporter permease
A3862_29325	CP016429:6441642-6443244	23.4397	134.329	2.51874	up	0.000219161	0.0088602	hypothetical protein
A3862_29330	CP016429:6443248-6444220	18.6164	111.341	2.58033	up	0.000541949	0.0112224	ABC transporter permease
A3862_29335	CP016429:6444222-6447841	15.4204	111.449	2.85347	up	0.000161832	0.00850278	ABC transporter permease
A3862_29340	CP016429:6444222-6447841	25.1137	146.58	2.54514	up	0.000215955	0.0088602	microcin ABC transporter ATP-binding protein
A3862_29345	CP016429:6444222-6447841	23.8012	114.811	2.27015	up	0.000914117	0.0127151	glutamyl-tRNA amidotransferase
A3862_29350	CP016429:6447847-6448240	7.68082	34.5357	2.16876	up	0.0038717	0.0238251	DUF4440 domain-containing protein
A3862_29360	CP016429:6451274-6452285	29.1983	147.913	2.34079	up	0.000664691	0.01194	hypothetical protein
A3862_29425	CP016429:6471473-6473417	31.0565	160.753	2.37188	up	0.000753274	0.0120972	selenocysteine-specific translation elongation factor
A3862_29440	CP016429:6476751-6477666	19.1837	109.22	2.50929	up	0.000789983	0.0120972	esterase
A3862_29465	CP016429:6482735-6485066	29.0514	130.029	2.16216	up	0.00195032	0.0168713	formate dehydrogenase
A3862_29480	CP016429:6486176-6487148	23.0185	122.282	2.40935	up	0.000785293	0.0120972	-
A3862_29500	CP016429:6489171-6490184	14.3014	89.4508	2.64494	up	0.000496082	0.0107995	hypothetical protein
A3862_29505	CP016429:6490188-6490554	6.4573	36.8214	2.51154	up	0.00221109	0.0177859	hypothetical protein
A3862_29525	CP016429:6492939-6493926	23.9432	110.739	2.20947	up	0.00179203	0.0165011	PhnA-like protein
A3862_29535	CP016429:6495499-6496264	20.4316	108.779	2.41253	up	0.00157723	0.0157725	cyclic nucleotide-binding protein
A3862_29550	CP017427:167944-168543	70.116	381.086	2.4423	up	0.000348655	0.00939126	AAA family ATPase
A3862_29560	CP017427:1179-1539	4.54533	50.4826	3.47333	up	5.55E-05	0.00608914	hypothetical protein
A3862_29575	CP017427:2992-3505	11.9973	60.8106	2.34162	up	6.62E-05	0.00635223	hypothetical protein
A3862_29625	CP017427:9637-10906	30.2359	173.075	2.51706	up	0.000246804	0.00890144	IS256 family transposase
A3862_29640	CP017427:11926-13411	29.0335	140.299	2.27271	up	0.000724179	0.0120023	chemotaxis protein
A3862_29755	CP017427:46243-47169	11.2742	77.7644	2.78609	up	1.05E-06	0.000437108	hypothetical protein
A3862_29795	CP017427:52085-53099	13.6772	128.144	3.22793	up	1.74E-05	0.00300026	antirepressor
A3862_29835	CP017427:60021-62768	28.0051	163.619	2.54658	up	0.000470498	0.0105593	DNA-binding protein
A3862_29845	CP017427:63044-67403	33.4159	165.07	2.30447	up	0.00722018	0.0333415	methylase
A3862_29895	CP017427:75418-79156	27.9799	163.752	2.54905	up	0.00207839	0.0172884	Ti-type conjugative transfer relaxase TraA
A3862_29945	CP017427:84669-88537	34.9566	176.087	2.33265	up	0.00305021	0.0207682	hypothetical protein
A3862_29950	CP017427:84669-88537	11.5368	57.5249	2.31795	up	0.000184574	0.00857827	hypothetical protein
A3862_29960	CP017427:88548-90083	29.0142	142.039	2.29146	up	0.000640323	0.0116727	hypothetical protein

A3862_29990	CP017427:94149-94671	15.75	76.0002	2.27065	up	0.00153227	0.0156886	hypothetical protein
A3862_29995	CP017427:94914-96048	29.1539	130.142	2.15833	up	0.00116117	0.0141663	hypothetical protein
A3862_30000	CP017427:96051-98756	28.1865	134.642	2.25605	up	0.000748641	0.0120972	secretion system protein E
A3862_30025	CP017427:99564-102879	22.4116	111.286	2.31195	up	0.00202638	0.0170832	hypothetical protein
A3862_30030	CP017427:99564-102879	24.0901	114.593	2.25	up	0.00110267	0.0138567	hypothetical protein
A3862_30035	CP017427:99564-102879	15.2325	113.609	2.89885	up	0.000100849	0.00777183	hypothetical protein
A3862_30040	CP017427:102887-105143	32.056	144.51	2.17251	up	0.00194174	0.0168713	hypothetical protein
A3862_30045	CP017427:105146-106469	21.2917	133.718	2.65083	up	0.000129699	0.008338	hypothetical protein
A3862_30060	CP017427:109644-110856	24.9552	115.213	2.2069	up	0.00113254	0.0140214	replication initiation protein RepC
A3862_30075	CP017427:114063-115744	32.9165	186.142	2.49952	up	0.000291617	0.00904717	AAA family ATPase
A3862_30080	CP017427:114063-115744	17.4522	104.001	2.57511	up	0.000736142	0.0120972	hypothetical protein
A3862_30235	CP017427:147770-148954	22.0374	116.033	2.39651	up	0.00114861	0.014104	transposase
A3862_30265	CP017427:154375-155035	13.4302	80.9507	2.59157	up	0.000245069	0.00890144	dimethylallyltransferase
A3862_30270	CP017427:155101-155854	13.3967	114.647	3.09725	up	2.74E-05	0.00382483	IS6 family transposase
A3862_30275	CP017427:156030-156843	25.6813	157.636	2.61781	up	0.000241229	0.00890144	cytochrome C
A3862_30295	CP017427:160465-161065	13.9658	96.8361	2.79365	up	4.76E-05	0.00581271	cytochrome C
A3862_30325	CP017427:162959-164312	23.4649	138.181	2.55798	up	0.000565265	0.0113804	transposase

Supplementary data

Table S6 The genes and enzymes of carbon metabolism.

Number	Gene	Locus_tag	enzyme
(1)	mxaF	A3862_10295	methanol dehydrogenase (cytochrome c) subunit 1
(2)	mxaI	A3862_10310	methanol dehydrogenase (cytochrome c) subunit 2
(3)	fae	A3862_28280	5,6,7,8-tetrahydromethanopterin hydro-lyase
(4)	mtdB	A3862_28305	methylene-tetrahydromethanopterin dehydrogenase
(5)	mch	A3862_28295	methenyltetrahydromethanopterin cyclohydrolase
(6)	ftr	A3862_28325	formylmethanofuran--tetrahydromethanopterin N-formyltransferase
(7)	gfa	A3862_21035	S-(hydroxymethyl)glutathione synthase
(8)	folD	A3862_13140	methylenetetrahydrofolate dehydrogenase (NADP+) / methenyltetrahydrofolate cyclohydrolase
(9)		A3862_13145	
(10)	glyA	A3862_11650	glycine hydroxymethyltransferase
(11)	fhs	A3862_10675	formate--tetrahydrofolate ligase
(12)	glk	A3862_03200	glucokinase
(13)	gdh	A3862_22080	glucose 1-dehydrogenase
(14)	G6PD	A3862_09795	glucose-6-phosphate 1-dehydrogenase
(15)		A3862_11915	
(16)	pgl	A3862_19235	6-phosphogluconolactonase
(17)	gntK	A3862_22550	gluconokinase
(18)	gnd	A3862_19240	6-phosphogluconate dehydrogenase
(19)	prkB	A3862_13655	phosphoribulokinase
(20)	rpe	A3862_13660	ribulose-phosphate 3-epimerase
(21)	rpiA	A3862_18255	ribose 5-phosphate isomerase A
(22)	prsA	A3862_23440	ribose-phosphate pyrophosphokinase
(23)	fbaA	A3862_01470	fructose-bisphosphate aldolase, class II
(24)	glpX-SEBP	A3862_17200	fructose-1,6-bisphosphatase II / sedoheptulose-1,7-bisphosphatase
(25)	DAK	A3862_17345	triose/dihydroxyacetone kinase / FAD-AMP lyase (cyclizing)
(26)	E2.2.1.2	A3862_19245	transaldolase
(27)	ccr	A3862_25065	crotonyl-CoA carboxylase/reductase
(28)	epi	A3862_20735	methylmalonyl-CoA/ethylmalonyl-CoA epimerase
(29)	ecm	A3862_22180	ethylmalonyl-CoA mutase
(30)	mcd	A3862_09595	2S)-methylsuccinyl-CoA dehydrogenase
(31)	fbp	A3862_13650	fructose-1,6-bisphosphatase I
(32)	fbaA	A3862_17200	fructose-bisphosphate aldolase, class II
(33)	gapA	A3862_01450	glyceraldehyde 3-phosphate dehydrogenase
(34)	pgk	A3862_01460	phosphoglycerate kinase
(35)	gpmA	A3862_01680	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase
(36)		A3862_07050	
(37)	gckA	A3862_01620	glycerate 2-kinase
(38)	hprA	A3862_13135	glycerate dehydrogenase
(39)	AGXT	A3862_13130	alanine-glyoxylate transaminase / serine-glyoxylate transaminase / serine-pyruvate transaminase
(40)	aceB	A3862_22285	malate synthase

(41)	mcl	A3862_13165	malyl-CoA/(S)-citramalyl-CoA lyase
(42)	ppc	A3862_13160	phosphoenolpyruvate carboxylase
(43)		A3862_05580	
(44)	pckA	A3862_16140	phosphoenolpyruvate carboxykinase (ATP)
(45)	mcl	A3862_22620	malyl-CoA/(S)-citramalyl-CoA lyase
(46)	ppdK	A3862_17740	pyruvate, orthophosphate dikinase
(47)	pyk	A3862_01610	pyruvate kinase
(48)		A3862_14645	
(49)	aceE	A3862_25625	pyruvate dehydrogenase E1 component
(50)	maeB	A3862_16635	malate dehydrogenase (oxaloacetate-decarboxylating)(NADP+)
(51)	mtkB	A3862_28455	malate-CoA ligase subunit alpha
(52)	mdh	A3862_25975	malate dehydrogenase
(53)	mqo	A3862_00245	malate dehydrogenase (quinone)
		A3862_07530	
(54)	fumC	A3862_08820	fumarate hydratase, class II
(55)	sdhA, frdA	A3862_28655	succinate dehydrogenase / fumarate reductase, flavoprotein subunit
(56)	sdhB, frdB	A3862_28650	succinate dehydrogenase / fumarate reductase, iron-sulfur subunit
(57)	sdhC, frdC	A3862_28665	succinate dehydrogenase / fumarate reductase, cytochrome b subunit
(58)	sdhD, frdD	A3862_28660	succinate dehydrogenase / fumarate reductase, membrane anchor subunit
(59)	sucD	A3862_25965	succinyl-CoA synthetase alpha subunit
(60)	sucC	A3862_25970	succinyl-CoA synthetase beta subunit
(61)	sucA	A3862_25960	2-oxoglutarate dehydrogenase E1 component
(62)	icd	A3862_02260	isocitrate dehydrogenase
(63)	ACO	A3862_13550	aconitate hydratase
(64)		A3862_28765	
(65)	CS	A3862_20805	citrate synthase
(66)	MUT	A3862_22180	methylmalonyl-CoA mutase
(67)	epi	A3862_20735	methylmalonyl-CoA/ethylmalonyl-CoA epimerase
(68)	pccA	A3862_18005	propionyl-CoA carboxylase alpha chain
(69)	pccB	A3862_17605	propionyl-CoA carboxylase beta chain
(70)	mcd	A3862_09075	2-methylfumaryl-CoA hydratase
(71)	crt	A3862_11125	enoyl-CoA hydratase
(72)	fadJ	A3862_15055	3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase