

Table A5. RNA-sequencing analysis of the triple-phase process. The RNA-sequencing yielded a total of 28,720,937 reads as assignable and unique mapping events. Differential gene expression calculations were performed applying RPKM (reads per kilobase) and TPM (transcripts per million) normalization (compare sheet *Complete data*). The strict aerobic state of sample ① served as reference for all following analysis. We defined a significance level at an empirical log₂-fold change (m-value) of > 1.50 and < -1.50 (corresponding to a fold-change of 2.80 and 0.40, respectively) and an average value (a-value) > 1.00 to exclude results that are derived from very few reads. Differentially expressed genes are given within the aerobic (②), microaerobic (③, ④, ⑤) and anaerobic (⑥) phase. Values within the significance constraints were highlighted as significantly up- (black) or downregulated (grey) genes. The locus, feature, product and major COG class is given.

Locus	Feature	Product	COG	m-values				
				②	③	④	⑤	⑥
				vs. ①	vs. ①	vs. ①	vs. ①	vs. ①
cg0001	<i>dnaA</i>	Chromosomal replication initiator protein DnaA	L	-0.07	-0.32	-0.33	-0.16	-1.56
cg0005	<i>recF</i>	DNA replication and repair protein RecF	L	0.11	0.01	-0.47	-0.69	-1.83
cg0007	<i>gyrB</i>	DNA gyrase subunit B	L	0.06	-0.19	-0.64	-0.53	-1.80
cg0009	-	Putative membrane protein	-	-0.44	-0.78	-1.04	-1.11	-2.99
cg0010	-	Conserved hypothetical protein	-	-0.08	-0.07	-0.34	-0.78	-1.65
cg0012	<i>ssuR</i>	Transcriptional activator of sulfonate(ester) utilization, RO K	K	0.26	0.41	0.30	0.65	-2.92
cg0027	-	Putative transcriptional regulator, MarR-family	K	0.48	0.58	-0.08	-0.71	-1.96
cg0029	-	Conserved putative membrane protein	O	0.21	-1.26	-0.21	-0.35	-1.78
cg0038	<i>ohr</i>	putative organic hydroperoxide detoxification protein	O	-0.93	-1.36	-1.28	-1.18	-1.67
cg0044	-	ABC-type putative sugar transporter, substrate-binding lip G	G	-0.26	-0.47	-1.05	-1.44	-3.51
cg0045	-	ABC-type putative sugar transporter, permease subunit	G	-0.09	-0.36	-1.00	-1.38	-3.93
cg0046	-	ABC-type putative sugar transporter, ATPase subunit	P	-0.15	-0.27	-1.20	-1.37	-3.74
cg0057	<i>pknB</i>	Serine/threonine protein kinase	R	-0.11	-0.16	-0.70	-0.92	-1.94
cg0059	<i>pknA</i>	Serine/threonine protein kinase	R	-0.14	-0.44	-0.89	-1.19	-2.68
cg0060	<i>pbpA</i>	D-alanyl-D-alanine carboxypeptidase	M	0.12	-0.30	-0.68	-1.14	-2.14
cg0061	<i>rodA</i>	Putative FtsW/RodA/SpoE-family cell cycle protein	D	0.15	-0.24	-0.51	-0.95	-1.89
cg0062	<i>ppp</i>	Protein phosphatase	T	-0.06	-0.08	-0.45	-0.86	-1.91
cg0063	-	Putative secreted protein, FHA domain	T	0.14	-0.16	-0.39	-0.75	-1.72
cg0064	-	Conserved hypothetical protein, FHA dpmain	T	0.15	-0.22	-0.51	-0.80	-1.61
cg0065	-	Hypothetical protein	-	-0.91	-0.94	-0.94	-1.46	-2.46
cg0071	-	Metallo-beta-lactamase superfamily, RHOD domain	R	0.22	-0.40	-1.78	-1.48	-1.79
cg0072	-	Conserved putative membrane protein	R	-0.26	-0.35	-0.86	-0.64	-2.16
cg0073	-	RHOD domain-containing protein	P	-0.32	-1.16	-2.62	-2.97	-4.22
cg0074	-	RHOD-domain-containing protein	P	0.28	-1.41	-1.43	-1.87	-2.58
cg0076	-	Hypothetical protein	-	-0.26	-0.18	-1.02	-1.20	-3.01
cg0077	-	Conserved hypothetical protein, VTC domain	P	0.59	-0.06	-0.51	-1.28	-1.77
cg0082	-	Chloride ion channel, ClC-family	P	0.05	-2.08	-2.19	-2.45	-5.65
cg0085	<i>phoH1</i>	NYN ribonuclease and ATPase of PhoH family	T	1.64	2.87	3.04	2.70	3.32
cg0088	<i>citP</i>	Putative secondary Mg2+/H+:citrate transporter, CitMHS-C	C	-0.02	-4.78	-2.76	-3.48	-5.09
cg0095	<i>bioB</i>	Biotin synthase	H	-0.08	-0.96	-1.41	3.37	3.30
cg0096	-	Conserved hypothetical protein	-	-0.16	-1.23	-1.95	4.81	4.54
cg0097	-	Conserved hypothetical protein, putative zinc finger	S	0.22	-0.32	0.14	5.34	4.89
cg0105	-	Hypothetical protein	-	-0.91	-1.78	-1.88	-2.07	-2.74
cg0107	-	Putative secreted protein	-	-0.47	-0.57	-1.20	-1.51	-2.05
cg0108	-	Putative acetyltransferase/hydrolase, SIR2 superfamily	K	-0.24	0.33	0.00	-0.59	-1.93
cg0110	<i>lip2</i>	Triacylglycerol lipase	R	-0.48	-0.60	-0.97	-1.39	-2.33
cg0111	-	Hypothetical protein	-	-0.43	-0.06	-0.15	-0.82	2.54
cg0114	<i>ureB</i>	Urease beta subunit	E	0.11	-0.01	-0.16	0.46	-1.85
cg0115	<i>ureC</i>	Urease alpha subunit	E	-0.04	-0.11	-0.50	0.36	-1.76
cg0116	<i>ureE</i>	Urease accessory protein UreE	-	0.15	-0.23	-0.33	0.11	-2.06
cg0117	<i>ureF</i>	Urease accessory protein UreF	O	0.30	-0.03	-0.04	0.29	-2.12
cg0119	<i>ureD</i>	Urease accessory protein UreD	O	-0.37	-0.06	-0.55	0.38	-1.73
cg0120	-	Putative hydrolase	R	0.09	0.80	0.66	0.56	2.89
cg0121	-	Putative multidrug efflux permease, MFS-type	G	0.80	-0.68	-1.26	-2.06	-3.63
cg0122	-	Hypothetical protein	-	0.03	0.17	-0.44	-0.79	-1.50
cg0127	-	Thiamine pyrophosphate-dependent enzyme	E	-0.69	-0.28	-1.08	-0.61	-1.84
cg0133	-	Putative p-aminobenzoyl-glutamate transporter, anion per H	H	1.76	-1.22	-1.70	-2.23	-2.76
cg0134	-	Metal-dependent amidase/aminoacylase/carboxypeptidas R	R	1.70	0.16	-0.49	-0.41	-0.65
cg0144	<i>rbtT</i>	Putative sugar/metabolite permease, MFS-type	G	0.05	-0.82	-0.95	-0.58	-3.54

Locus	Feature	Product	COG	m-values				
				②	③	④	⑤	⑥
				vs. ①	vs. ①	vs. ①	vs. ①	vs. ①
cg0146	<i>sucR</i>	Transcriptional repressor, DeoR-family	K	-0.29	-0.76	-0.84	-1.58	-2.32
cg0147	<i>xyfB</i>	Xylulose kinase	C	0.02	-0.64	-0.80	-1.76	-2.20
cg0148	<i>panC</i>	Pantoate--beta-alanine ligase	H	0.20	-0.93	-1.46	-1.54	-4.08
cg0149	<i>panB</i>	3-Methyl-2-oxobutanoate hydroxymethyltransferase	H	0.24	-0.85	-1.10	-1.30	-3.42
cg0150	-	Putative transcriptional regulatory protein, Fic/Doc family	S	-1.20	-1.24	-1.30	-1.71	-2.21
cg0153	<i>hde</i>	Putative esterase/lipase	I	0.23	0.37	-0.14	-1.00	-1.68
cg0156	<i>cysR</i>	Transcriptional activator of assimilatory sulfate reduction,	K	-0.31	0.00	-0.59	-0.37	-3.85
cg0158	-	Putative drug efflux permease, MFS-type	G	-0.06	-0.85	-1.59	-2.17	-3.54
cg0161	-	Putative membrane protein	-	0.10	0.23	-0.39	-0.87	-3.01
cg0162	-	Putative membrane protein	-	0.22	0.24	-0.28	-0.79	-3.58
cg0163	-	Putative membrane protein	M	0.21	0.43	-0.25	-0.79	-3.19
cg0165	-	Putative membrane protein	-	0.05	0.34	-0.21	-0.75	-3.22
cg0167	-	Putative membrane protein, DUF81-family	R	0.03	-0.44	-0.81	-1.41	-3.09
cg0172	<i>panD</i>	Aspartate 1-decarboxylase	H	-0.19	-0.36	-0.67	-1.05	-2.49
cg0173	-	Conserved hypothetical protein	S	-0.07	-0.69	-1.22	-2.01	-4.00
cg0175	-	Putative secreted protein	-	1.38	2.89	2.78	3.04	4.11
cg0181	<i>alkB</i>	Alkylated DNA repair protein AlkB	-	0.08	0.20	-0.43	-0.47	-2.52
cg0182	<i>tagA2</i>	DNA-3-methyladenine glycosylase I	L	0.23	-1.11	-0.41	-0.78	-2.74
cg0183	-	Putative threonine efflux transporter, resistance to homos	E	-0.01	-0.10	-0.54	-1.32	-2.05
cg0187	-	Conserved hypothetical protein	-	-0.78	-1.56	-1.62	-1.75	-3.43
cg0195	-	Putative membrane protein	S	0.06	1.60	0.95	1.01	0.85
cg0197	<i>iolC</i>	Putative 5-dehydro-2-deoxygluconokinase	G	-0.36	-3.20	-3.87	-4.86	-4.38
cg0198	-	Conserved hypothetical protein, probably involved in myo-	-	0.15	-3.35	-3.36	-2.81	-4.78
cg0199	<i>iolA</i>	Methylmalonate-semialdehyde dehydrogenase	C	-0.04	-2.89	-3.51	-3.91	-4.33
cg0201	<i>iolB</i>	Uncharacterized enzyme involved in inositol metabolism	G	-0.17	-2.57	-2.60	-3.41	-3.70
cg0202	<i>iolD</i>	Putative acetolactate synthase, large subunit	E	-0.06	-2.29	-2.65	-3.32	-3.48
cg0203	<i>iolE</i>	Putative myo-inosose-2 dehydratase	G	-0.34	-2.74	-3.82	-3.34	-4.76
cg0204	<i>iolG</i>	Myo-inositol 2-dehydrogenase	R	-0.45	-2.45	-2.93	-3.37	-4.01
cg0205	<i>iolH</i>	Myo-inositol catabolism protein	G	-0.32	-1.56	-2.49	-2.35	-2.92
cg0206	<i>iolP</i>	Putative myo-inositol permease, MFS-type	E	-0.05	-0.77	-1.44	-1.92	-2.89
cg0207	-	Hypothetical oxidoreductase	R	-0.01	-1.71	-2.01	-2.00	-4.93
cg0210	-	Putative transcriptional regulator, Lacl-family	K	-0.38	-1.60	-2.91	-4.48	-1.92
cg0211	-	Putative oxidoreductase	R	-0.40	-4.44	-4.53	-4.07	-4.76
cg0212	-	Conserved hypothetical protein	G	0.01	-3.55	-3.66	-3.32	-4.50
cg0215	<i>cspA</i>	Cold-shock protein A	K	-0.52	-1.33	-1.79	-1.95	-2.97
cg0216	-	Putative membrane protein	-	-0.83	-0.94	-0.63	-0.88	-1.74
cg0223	-	Putative sugar/metabolite permease, MFS-type	G	-0.37	-3.19	-4.16	-3.67	-4.62
cg0226	<i>tnp2f(ISCg2f)</i>	Transposase	L	-0.78	-0.53	-0.64	-0.57	-1.66
cg0228	-	Two-component system, sensory histidine kinase, putativ	T	0.04	-2.69	-3.37	-3.06	-3.54
cg0229	<i>glfB</i>	Glutamate synthase (NADPH), large chain	E	-0.20	1.03	1.67	2.27	-3.73
cg0230	<i>glfD</i>	Glutamate synthase (NADPH), small chain	E	0.13	1.13	1.62	2.17	-3.34
cg0231	-	Putative membrane protein	-	-0.25	-0.40	-0.48	-0.75	-2.02
cg0235	<i>emb</i>	arabinofuranosyltransferase	-	-0.08	-0.34	-1.14	-1.57	-3.02
cg0236	-	Putative membrane protein	-	-0.11	-0.04	-0.68	-1.01	-2.16
cg0237	-	Putative oxidoreductase	I	0.09	2.15	1.72	1.68	1.38
cg0238	-	FAD/FMN-containing dehydrogenase	G	0.18	2.09	1.59	1.72	1.35
cg0248	-	ABC-type putative polysaccharide transporter, ATPase su	G	0.01	0.67	-0.02	-0.55	-2.11
cg0249	-	ABC-type putative polysaccharide transporter, permease :G	G	-0.16	0.04	-0.74	-1.16	-2.30
cg0252	-	Putative membrane protein	-	0.66	-1.00	-0.76	-1.27	-1.62
cg0254	-	Putative secondary Na+/alanine symporter, alanine or gly	E	0.17	-1.82	-2.55	-3.29	-5.12
cg0262	<i>modB</i>	ABC-type putative molybdenum transporter, permease su	P	0.04	-0.26	-0.41	-0.75	-1.91
cg0263	<i>modA</i>	ABC-type putative molybdenum transporter, substrate-bin	P	0.51	0.40	-0.10	-0.66	-1.74
cg0266	-	Putative membrane protein	S	0.08	0.07	-0.13	-0.55	-1.61
cg0273	-	Putative alcohol dehydrogenase, type III	R	-0.27	-0.94	-1.16	-1.59	-2.83
cg0274	-	Putative oxidoreductase	E	-0.24	-1.02	-1.24	-0.81	-2.42
cg0275	<i>mgtE2</i>	Putative Mg2+/Co2+/Ni2+ transporter, Mg2+ transporter-E	P	0.23	-0.37	-0.22	-0.40	-1.54
cg0277	<i>dccT</i>	Secondary Na+:succinate/malate/fumarate symporter, div	P	0.36	-0.51	-1.17	-1.50	-5.26
cg0281	-	tRNA-specific adenosine deaminase	H	0.10	-0.22	-0.37	-0.60	-2.03
cg0282	-	CsbD family protein probably involved in stress response	-	1.75	2.68	2.24	1.95	2.40
cg0285	<i>tgt</i>	Queuine tRNA-ribosyltransferase	J	-0.02	-0.35	-0.97	-1.33	-2.78
cg0286	-	Conserved putative membrane protein	S	-0.03	-1.42	-1.86	-2.64	-6.05
cg0293	-	Hypothetical protein	-	-1.03	-0.50	-0.91	-1.01	-3.30
cg0298	<i>recR</i>	DNA repair protein (RecF pathway)	L	-0.22	-1.22	-1.12	-1.43	-2.99
cg0302	-	Putative DNA polymerase III, epsilon subunit or related 3'	L	-0.18	0.08	-0.20	-0.58	-1.95
cg0303	<i>leuA</i>	2-Isopropylmalate synthase	E	0.29	-0.70	-1.41	-1.90	-3.32

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				vs. ①	vs. ①	vs. ①	vs. ①	vs. ①
cg0304	-	Putative membrane protein	G	-0.48	-0.50	-1.15	-1.73	-4.43
cg0306	<i>lysC</i>	Aspartate kinase	E	0.06	0.27	-0.26	-0.62	-2.49
cg0307	<i>asd</i>	Aspartate-semialdehyde dehydrogenase	E	0.10	0.44	-0.14	-0.43	-2.10
cg0308	-	Putative membrane protein	-	-0.35	-0.80	-1.27	-1.44	-2.72
cg0310	<i>katA</i>	Catalase	P	-0.33	-0.58	-1.05	-0.83	-1.83
cg0314	<i>brnF</i>	Secondary branched-chain amino acid efflux transporter, I	E	-1.52	-1.06	-1.00	-1.25	-1.60
cg0315	<i>brnE</i>	Secondary branched-chain amino acid efflux transporter, I	E	-0.68	-1.73	-1.69	-1.48	-1.60
cg0316	-	Putative secreted protein	-	1.06	4.15	4.51	3.83	4.21
cg0321	<i>mnhG</i>	Putative Na ⁺ /H ⁺ antiporter, membrane subunit	P	0.19	-0.47	-0.81	-1.42	-2.75
cg0322	<i>mnhF</i>	Putative Na ⁺ /H ⁺ antiporter, permease subunit	-	-0.15	-0.54	-0.82	-1.62	-3.65
cg0323	<i>mnhE</i>	Putative Na ⁺ /H ⁺ antiporter, MnhE subunit	P	-0.13	-0.05	-1.39	-1.43	-3.32
cg0324	<i>mnhD</i>	Putative secondary Na ⁺ /H ⁺ antiporter, monovalent cation C	C	-0.01	-0.29	-0.82	-0.86	-2.34
cg0325	<i>mnhC</i>	Putative secondary Na ⁺ /H ⁺ antiporter, monovalent cation P	P	-0.12	-0.53	-0.88	-1.16	-2.58
cg0326	<i>mnhAB</i>	Putative secondary Na ⁺ /H ⁺ antiporter, monovalent cation C	C	0.13	-0.28	-0.68	-0.80	-2.55
cg0327	-	Putative membrane protein	S	0.21	0.14	-0.47	-1.32	-2.11
cg0328	-	Hypothetical protein	S	-0.26	-0.48	-0.52	-0.97	-2.11
cg0330	<i>cgtR1</i>	Two-component system, transcriptional response regulat	T	-0.07	-0.06	-0.27	-1.03	-1.54
cg0331	<i>cgtS1</i>	Two-component system, sensory histidine kinase	T	-0.02	-0.47	-0.91	-0.63	-1.96
cg0334	-	Putative secreted protein, probable acting as esterase	R	-0.21	-0.40	-0.83	-1.23	-2.79
cg0336	<i>ponA</i>	Putative penicillin-binding protein 1B	M	-0.22	-1.10	-1.68	-2.11	-3.76
cg0340	-	Putative sugar/metabolite permease, MFS-type	G	0.74	-2.80	-1.88	-1.50	-1.89
cg0344	<i>fabG1</i>	3-Oxoacyl-(acyl-carrier protein) reductase	I	0.45	-2.16	-1.40	-0.97	-0.89
cg0345	-	Putative metal-dependent amidohydrolase of the TIM-bar	R	0.03	-1.14	-1.76	-1.38	-1.39
cg0346	<i>fadE</i>	Glutaryl-CoA dehydrogenase	I	-0.48	-2.07	-1.69	-2.46	-2.76
cg0347	-	Putative dehydratase, MaoC-family	I	0.33	-1.78	-0.89	-1.29	-1.31
cg0356	-	Putative membrane-associated serine protease, membr	O	-0.51	-0.71	-1.07	-1.32	-2.78
cg0369	-	Conserved putative secreted protein	-	-1.43	-0.38	-1.19	-2.45	-0.76
cg0370	-	Putative ATP-dependent RNA helicase, DEAD/DEAH-box	R	-0.15	-0.44	-0.83	-1.23	-2.31
cg0371	<i>cspB</i>	Cold-shock protein B	K	-0.08	-0.42	-0.68	-0.85	-2.30
cg0373	<i>topA</i>	DNA topoisomerase I	L	-0.03	-0.32	-0.57	-0.74	-1.58
cg0374	-	Conserved hypothetical protein	-	-0.54	-0.28	-0.49	-0.72	-1.51
cg0384	<i>rluC1</i>	Pseudouridylate synthase	J	0.06	-1.25	-0.89	-1.95	-3.03
cg0390	-	Putative multidrug efflux permease, MFS-type	G	0.23	-0.17	-0.42	-0.67	-2.82
cg0394	-	Putative glycosyl transferase	M	-0.04	-0.08	-0.53	-0.90	-1.67
cg0395	-	putative ribonuclease H	L	-0.11	-0.18	-0.48	-0.93	-1.71
cg0397	-	Putative 5'-nucleotidase	F	-0.49	-0.61	-0.57	-0.60	-1.53
cg0398	-	Hypothetical protein	-	-0.25	-0.29	-0.28	-0.10	-2.05
cg0399	-	Hypothetical protein	-	-0.33	-0.17	-0.50	-0.42	-1.81
cg0401	<i>rmlA1</i>	Glucose-1-phosphate thymidyltransferase	M	-0.02	0.11	-0.39	-0.42	-1.59
cg0403	<i>rmlB1</i>	dTDP-glucose 4,6-dehydratase	M	-0.30	-0.34	-1.02	-1.04	-2.24
cg0404	-	Conserved hypothetical protein, nitroreductase-family	C	-0.02	-0.77	-1.40	-1.88	-5.18
cg0405	-	ABC-type putative iron(III) dicitrate transporter, substrate-	P	-0.03	-2.80	-4.40	-5.80	-6.67
cg0407	-	Putative secreted protein	-	-0.08	-0.89	-0.91	-1.60	-3.57
cg0408	-	Putative membrane protein	-	0.04	0.29	-0.14	-0.49	-1.62
cg0411	-	Putative membrane protein	-	0.70	0.98	0.68	0.26	-3.21
cg0412	-	Putative membrane protein	S	-0.28	0.07	-0.19	-0.44	-1.65
cg0413	<i>cmt1</i>	Trehalose corynomycolyl transferase	R	-0.38	-0.57	-0.94	-1.15	-2.77
cg0414	<i>wzz</i>	Cell surface polysaccharide biosynthesis/chain length det	M	0.40	0.38	-0.08	-0.63	-3.12
cg0415	<i>ptpA2</i>	Putative protein-tyrosine-phosphatase	T	0.28	0.31	-0.14	-0.68	-3.27
cg0416	-	Putative secreted protein, carrying a eukaryotic domain	-	0.03	0.23	-0.27	-0.86	-3.66
cg0417	<i>capD</i>	Putative dTDP-glucose 4,6-dehydratase, transmembrane	M	0.12	0.35	-0.06	-0.58	-3.52
cg0418	-	Putative aminotransferase, involved in cell wall biosynthe	-	0.09	0.45	-0.01	-0.49	-3.37
cg0419	-	Putative glycosyltransferase	M	0.13	0.49	-0.04	-0.56	-3.57
cg0420	-	Putative glycosyltransferase	M	-0.15	-0.34	-0.77	-1.02	-2.17
cg0421	<i>wzx</i>	Putative PST O-antigen protein, multidrug/oligosaccharid	R	-0.30	-0.45	-0.74	-1.02	-2.86
cg0422	<i>murA</i>	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	M	0.16	-0.09	-0.35	-0.46	-1.63
cg0423	<i>murB</i>	UDP-N-acetylenolpyruvoylglucosamine reductase	M	-0.06	-0.23	-0.56	-0.76	-2.12
cg0424	-	Putative glycosyltransferase	M	-0.05	-0.20	-0.49	-0.63	-2.09
cg0426	<i>tnp17a(ISCg17)</i>	Transposase, putative pseudogene	L	-0.78	-3.06	-2.37	-1.35	-2.37
cg0427	<i>tnp17b(ISCg17)</i>	Transposase, putative pseudogene	-	-0.75	-2.06	-2.99	-2.97	-2.89
cg0428	<i>tnp17c(ISCg17)</i>	Transposase, putative pseudogene	L	-0.39	-1.70	-2.31	-1.91	-4.02
cg0431	-	Putative membrane protein, involved in polysaccharide ac	I	-0.59	-1.34	-1.31	-1.76	-2.81
cg0435	<i>udgA1</i>	UDP-glucose 6-dehydrogenase	M	0.24	0.79	0.48	0.22	-2.90
cg0436	-	Hypothetical protein	-	0.29	-0.07	-0.13	-0.62	-2.16
cg0437	<i>wzy</i>	Putative membrane protein, involved in polysaccharide pc	-	-0.13	-0.20	-0.65	-1.01	-2.30

Locus	Feature	Product	COG	m-values				
				②	③	④	⑤	⑥
				vs. ①	vs. ①	vs. ①	vs. ①	vs. ①
cg0438	-	Putative glycosyltransferase	M	-0.04	-0.24	-0.64	-1.09	-1.96
cg0444	<i>ramB</i>	Transcriptional regulator, MerR-family	R	-0.20	-3.29	-3.50	-3.43	-3.55
cg0445	<i>sdhCD</i>	Succinate dehydrogenase, subunit CD	-	0.38	0.95	0.83	1.19	-2.45
cg0446	<i>sdhA</i>	Succinate dehydrogenase, subunit A	C	0.24	0.94	0.77	1.23	-2.37
cg0447	<i>sdhB</i>	Succinate dehydrogenase, subunit B	C	0.36	0.99	0.96	1.27	-2.13
cg0450	-	Conserved hypothetical protein	-	0.58	1.84	1.48	1.54	1.29
cg0454	-	Putative transcriptional regulator, TetR-family	K	-0.01	-0.86	-0.48	-0.96	-2.03
cg0455	-	Putative multidrug efflux permease, MFS-type	G	-0.05	-0.17	-0.69	-1.08	-2.43
cg0456	-	Putative multidrug efflux permease, MFS-type	G	0.37	-0.17	-0.43	-0.73	-2.22
cg0457	<i>purU</i>	Putative formyltetrahydrofolate deformylase	F	0.09	-0.36	-0.95	-1.54	-3.35
cg0461	-	Hypothetical protein	-	0.22	0.11	0.54	-1.03	-3.37
cg0462	-	Conserved hypothetical protein	L	-0.40	-0.12	-0.66	-0.43	-2.32
cg0465	-	Conserved putative membrane protein	-	0.20	-1.56	-3.45	-1.63	-4.46
cg0466	-	Conserved putative secreted protein	N	0.20	-1.38	-3.27	-3.72	-5.74
cg0469	-	ABC-type putative hemin transporter, ATPase subunit	G	-0.50	-0.48	-1.56	-1.24	-1.12
cg0470	-	Conserved secreted protein	-	0.25	-0.36	-1.56	-2.54	-2.20
cg0471	-	Conserved secreted protein	-	-0.34	-1.21	-1.88	-0.86	-1.53
cg0472	-	Conserved hypothetical protein	-	-0.30	-0.70	-1.14	-1.54	-3.14
cg0474	-	Conserved hypothetical protein	-	-0.04	-0.01	-0.76	-0.92	-1.74
cg0476	<i>murB2</i>	Putative UDP-N-acetylmuramate dehydrogenase	M	0.10	-0.27	-1.20	-1.11	-2.44
cg0477	-	Hypothetical protein	-	0.17	0.24	-0.39	-0.64	-1.76
cg0478	-	Hypothetical protein	-	-0.52	-0.36	-2.37	-2.35	-2.05
cg0485	-	Hypothetical protein	S	-0.50	-0.37	-0.59	-1.28	-1.77
cg0486	-	ABC-type transporter, ATPase and permease subunit	V	-0.99	-0.75	-1.52	-2.08	-2.83
cg0487	-	Conserved hypothetical protein	-	-0.40	0.02	-0.15	-0.51	-1.66
cg0492	-	Putative DNA-binding (excisionase) protein	-	0.13	-0.12	-0.30	-0.50	-1.52
cg0493	-	Hypothetical protein	-	0.14	-0.33	-0.65	-1.02	-3.71
cg0494	-	Conserved hypothetical protein	-	0.11	-0.34	-0.71	-1.07	-4.08
cg0499	-	Hypothetical protein	-	-0.38	-1.37	-1.78	-1.62	-2.97
cg0501	<i>qsuA</i>	Putative shikimate permease, MFS-type	G	0.06	-0.25	-0.62	-0.58	-1.86
cg0502	<i>qsuB</i>	putative dehydroshikimate dehydratase, 2 domain protein	G	-0.02	-0.24	-0.72	-0.74	-2.12
cg0504	<i>aroE</i>	Putative shikimate 5-dehydrogenase	E	-0.04	-0.26	-0.74	-0.49	-2.01
cg0506	-	ABC-type putative spermidine/putrescine/iron(III) transpor	G	0.96	-1.26	-1.63	-1.25	-3.22
cg0507	-	ABC-type putative spermidine/putrescine/iron(III) transpor	P	0.43	-2.04	-2.58	-3.11	-4.41
cg0508	-	ABC-type putative spermidine/putrescine/iron(III) transpor	P	0.77	-1.60	-2.04	-2.87	-3.90
cg0510	<i>hemD</i>	Uroporphyrinogen-III synthase	H	-0.09	-0.88	-1.11	-1.05	-3.21
cg0520	-	Secreted thiol-disulfide isomerase	O	-0.53	-0.13	-0.55	-0.70	-1.52
cg0522	<i>ccsA</i>	Cytochrome c biogenesis membrane protein, DsbD-family	O	-0.61	0.20	-0.44	-0.64	-1.55
cg0523	-	Cytochrome c biogenesis membrane protein, ResB-family	-	-0.42	0.20	-0.61	-0.62	-1.80
cg0524	<i>ccsB</i>	Cytochrome c biogenesis membrane protein, CcsA-family	O	-0.55	0.17	-0.34	-0.36	-1.55
cg0531	<i>menA</i>	1,4-Dihydroxy-2-naphthoate octaprenyltransferase	H	0.23	0.06	-0.47	-0.50	-1.55
cg0533	<i>menE</i>	O-Succinylbenzoic acid--CoA ligase	I	-0.05	0.01	-0.38	-0.86	-2.02
cg0534	-	Putative integral membrane protein	S	-1.10	-2.00	-2.57	-2.70	-3.90
cg0535	-	Putative ketoglutarate semialdehyde dehydrogenase	C	-0.23	0.34	-0.63	-0.97	-1.88
cg0540	-	Putative metal-dependent amidohydrolase, TIM-barrel fold	R	0.16	-0.35	-0.94	-1.24	-1.69
cg0542	-	Hypothetical protein	R	0.32	-0.79	-0.75	-1.56	-2.21
cg0543	-	Hypothetical protein	-	-0.07	-1.05	-0.91	-0.96	-2.28
cg0544	-	Putative membrane protein	-	-0.04	-0.51	-1.31	-3.08	-5.11
cg0545	<i>pitA</i>	Putative phosphate/sulfate transporter, inorganic phosphate	P	0.22	-0.31	-1.13	-2.16	-5.32
cg0552	<i>menD</i>	2-Oxoglutarate decarboxylase	H	0.09	0.02	-0.45	-0.67	-1.72
cg0555	-	Putative secondary gamma-aminobutyrate transporter, an	E	-0.24	-0.65	-1.53	-1.62	-2.71
cg0556	<i>ubiE</i>	Ubiquinone/menaquinone biosynthesis methyltransferase	H	-0.14	0.06	-0.34	-0.51	-1.87
cg0559	<i>ispB</i>	Putative octaprenyl-diphosphate synthase	H	-0.17	0.13	-0.49	-0.66	-1.59
cg0563	<i>rplK</i>	50S ribosomal protein L11	J	0.18	-1.12	-1.39	-1.38	-4.59
cg0564	<i>rplA</i>	50S ribosomal protein L1	J	0.34	-0.92	-1.18	-1.22	-4.07
cg0569	-	Putative Cd ²⁺ transporting P-type ATPase	P	0.46	3.01	5.43	6.87	7.59
cg0570	-	Putative dehydrogenase	Q	-0.10	0.18	1.08	2.37	2.59
cg0572	<i>rplJ</i>	50S ribosomal protein L10	J	0.23	-1.00	-1.45	-1.46	-4.40
cg0573	<i>rplL</i>	Putative 50S ribosomal protein L7/L12	J	0.30	-0.84	-1.24	-1.21	-3.94
cg0578	-	Putative membrane protein	-	0.01	-1.06	-0.14	0.15	-1.64
cg0581	<i>rpsL</i>	30S ribosomal protein S12	J	0.17	-0.78	-0.97	-0.81	-3.25
cg0582	<i>rpsG</i>	30S ribosomal protein S7	J	0.21	-0.75	-0.95	-0.77	-3.22
cg0583	<i>fusA</i>	Elongation factor G	J	0.12	-0.08	-0.61	-0.59	-1.83
cg0587	<i>tuf</i>	Elongation factor Tu	J	0.35	0.20	-0.33	-0.36	-2.26
cg0589	-	ABC-type putative iron-siderophore transporter, ATPase subunit	G	-0.45	-1.89	-5.84	-5.24	-6.85

Locus	Feature	Product	COG	m-values				
				②	③	④	⑤	⑥
				vs. ①	vs. ①	vs. ①	vs. ①	vs. ①
cg0590	-	ABC-type putative iron-siderophore transporter, permease P	P	0.56	-1.26	-1.89	-2.69	-3.90
cg0591	-	ABC-type putative iron-siderophore transporter, permease P	P	0.02	-1.52	-3.19	-4.27	-6.42
cg0592	-	Putative acetate CoA-transferase	C	-0.95	-0.82	-1.42	-0.65	-2.81
cg0593	<i>rpsJ</i>	30S ribosomal protein S10	J	0.12	-0.96	-1.11	-1.23	-2.71
cg0594	<i>rplC</i>	50S ribosomal protein L3	J	0.02	-1.07	-1.24	-1.27	-2.88
cg0596	<i>rplD</i>	50S ribosomal protein L4	J	0.15	-0.88	-1.14	-1.08	-2.71
cg0597	<i>rplW</i>	50S ribosomal protein L23	J	0.09	-1.00	-1.30	-1.16	-2.86
cg0598	<i>rplB</i>	50S ribosomal protein L2	J	0.01	-0.85	-1.24	-1.06	-2.72
cg0599	<i>rpsS</i>	30S ribosomal protein S19	J	0.02	-0.87	-1.19	-1.00	-2.74
cg0600	<i>rplV</i>	50S ribosomal protein L22	J	0.04	-0.78	-1.12	-1.02	-2.76
cg0601	<i>rpsC</i>	30S ribosomal protein S3	J	0.04	-0.67	-1.07	-0.97	-2.81
cg0602	<i>rplP</i>	50S ribosomal protein L16	J	0.10	-0.70	-1.09	-0.94	-2.76
cg0603	<i>rpmC</i>	50S ribosomal protein L29	-	0.22	-0.71	-0.92	-0.81	-2.43
cg0604	<i>rpsQ</i>	30S ribosomal protein S17	J	0.05	-0.80	-0.82	-0.70	-2.02
cg0607	-	Putative secreted protein	-	-1.07	-2.27	-3.25	-3.55	-4.59
cg0608	<i>rplN</i>	50S ribosomal protein L14	J	0.20	-0.83	-1.11	-1.19	-3.92
cg0609	<i>rplX</i>	50S ribosomal protein L24	J	0.19	-0.75	-1.11	-1.23	-3.77
cg0610	<i>rplE</i>	50S ribosomal protein L5	J	0.26	-0.68	-1.03	-1.05	-3.79
cg0611	-	Putative secreted protein	-	0.18	-0.15	-0.89	-1.25	-3.63
cg0614	-	Hypothetical protein	-	-0.24	-0.08	-0.85	-1.61	-1.43
cg0621	-	Putative integral membrane protein	-	0.27	0.08	-0.72	-1.01	-3.67
cg0622	-	ABC-type putative cobalt transporter, ATPase subunit	R	0.12	-0.07	-0.71	-0.93	-3.88
cg0623	-	ABC-type putative cobalt transporter, permease subunit	P	0.18	-0.24	-0.54	-0.85	-4.11
cg0624	-	Putative secreted oxidoreductase	-	0.27	-0.05	-0.53	-0.56	-3.55
cg0625	-	Putative secreted protein	I	0.25	-0.26	-0.63	-0.64	-3.91
cg0627	-	Putative acetyltransferase, GNAT-family	R	-0.57	-0.87	-2.01	-2.43	-4.96
cg0628	<i>rpsH</i>	30S ribosomal protein S8	J	0.16	-0.89	-1.29	-1.30	-4.03
cg0629	<i>rplF</i>	50S ribosomal protein L6	J	0.15	-0.99	-1.34	-1.26	-3.97
cg0630	<i>rplR</i>	50S ribosomal protein L18	J	0.27	-0.83	-1.12	-1.17	-3.91
cg0631	<i>rpsE</i>	30S ribosomal protein S5	J	0.25	-0.84	-1.10	-1.10	-3.88
cg0632	<i>rpmD</i>	50S ribosomal protein L30	-	0.25	-0.84	-1.16	-1.22	-4.07
cg0634	<i>rplO</i>	50S ribosomal protein L15	J	0.17	-0.89	-1.16	-1.14	-3.71
cg0636	-	Putative membrane protein	-	0.55	1.23	1.51	1.24	1.20
cg0637	<i>betB</i>	Putative betaine aldehyde dehydrogenase (BADH)	C	-0.60	-1.05	-1.82	-1.82	-3.01
cg0638	-	Hypothetical protein	-	-0.69	-1.65	-1.95	-1.41	-2.35
cg0639	-	Putative ferredoxin reductase	C	0.07	-0.58	-1.17	-1.50	-1.61
cg0640	<i>fdxB</i>	2Fe-2S ferredoxin	-	0.20	-1.76	-0.61	-1.73	-2.49
cg0641	<i>fabG2</i>	Putative secreted short-chain dehydrogenase	I	-0.29	-1.96	-1.40	-1.71	-3.15
cg0642	-	Conserved hypothetical protein, probably DNA-binding	G	-0.26	-1.95	-1.94	-1.66	-2.33
cg0644	-	Pyruvate phosphate dikinase, PEP/pyruvate-binding	G	0.02	-1.40	-1.71	-1.59	-2.42
cg0645	<i>cytP</i>	Putative cytochrome P450	Q	-0.28	-1.93	-1.68	-1.91	-2.01
cg0647	<i>secY</i>	Preprotein translocase, SecY subunit	U	0.12	0.14	-0.09	-0.40	-1.66
cg0650	-	Putative secreted protein	S	0.03	-0.30	-0.70	-1.12	-1.71
cg0651	<i>infA</i>	Translation initiation factor IF-1	J	0.10	-0.59	-0.75	-0.72	-2.69
cg0652	<i>rpsM</i>	30S ribosomal protein S13	J	0.07	-0.77	-1.05	-0.89	-3.17
cg0653	<i>rpsK</i>	30S ribosomal protein S11	J	0.18	-0.62	-0.85	-0.73	-3.13
cg0654	<i>rpsD</i>	30S ribosomal protein S4	J	0.18	-0.61	-0.86	-0.74	-3.05
cg0655	<i>rpoA</i>	DNA-directed RNA polymerase, alpha subunit	K	0.20	-0.59	-0.92	-0.83	-3.28
cg0656	<i>rplQ</i>	50S ribosomal protein L17	J	0.14	-0.75	-1.04	-0.96	-3.44
cg0657	<i>truA</i>	tRNA pseudouridine synthase A	J	0.06	-0.55	-1.20	-1.15	-3.55
cg0658	-	Putative membrane protein	-	-0.10	-0.29	-0.78	-1.23	-2.91
cg0660	-	Hypothetical protein	-	0.84	0.25	-0.31	0.05	-1.85
cg0661	-	Conserved hypothetical protein	-	0.74	0.46	0.01	-1.93	-1.58
cg0671	-	Conserved hypothetical protein	S	-0.56	-0.71	-1.02	-1.22	-2.83
cg0672	-	Conserved hypothetical protein	-	-1.69	-1.06	-1.73	-1.71	-2.96
cg0673	<i>rplM</i>	50S ribosomal protein L13	J	0.17	-0.94	-1.25	-1.32	-3.89
cg0674	<i>rpsI</i>	30S ribosomal protein S9	J	0.20	-0.86	-1.26	-1.34	-3.96
cg0675	<i>mrsA</i>	Putative phosphoglucosamine mutase/phosphomannomu	G	0.19	0.13	-0.34	-0.87	-1.77
cg0676	-	Conserved hypothetical protein	-	0.15	-1.29	-1.34	-2.30	-5.13
cg0678	-	Conserved hypothetical protein	C	0.27	-0.48	-0.75	-0.96	-2.20
cg0681	<i>alr</i>	Alanine racemase	M	-0.08	-0.11	-0.66	-1.26	-2.61
cg0683	-	Putative permease	R	0.24	2.50	2.17	1.94	2.48
cg0684	<i>papA</i>	Prolyl aminopeptidase A	R	0.23	1.63	1.21	1.54	1.54
cg0689	-	Hypothetical protein	-	-0.16	-0.26	-0.98	-0.93	-1.68
cg0690	<i>groES</i>	10kDa chaperonin	O	0.14	-0.33	-1.03	-1.11	-3.06

Locus	Feature	Product	COG	m-values				
				②	③	④	⑤	⑥
				vs. ①	vs. ①	vs. ①	vs. ①	vs. ①
cg0691	<i>groEL'</i>	60kDa chaperonin, putative pseudogene (N-terminal fragr	O	0.06	-0.37	-1.03	-1.29	-3.19
cg0693	<i>'groEL</i>	60kDa chaperonin, putative pseudogene (C-terminal fragr	O	0.15	-0.26	-1.02	-1.13	-2.94
cg0695	<i>whiB3</i>	Transcriptional regulator protein, WhiB-family	-	-0.63	-0.95	-0.48	-2.05	-3.08
cg0696	<i>sigD</i>	RNA polymerase sigma factor, ECF-family	K	-0.66	-1.11	-1.35	-1.54	-2.55
cg0697	-	Conserved hypothetical protein	-	-0.79	-1.15	-1.51	-1.55	-2.61
cg0699	<i>guaB2</i>	IMP dehydrogenase	F	0.02	0.47	0.02	-0.42	-1.75
cg0700	<i>guaB3</i>	IMP dehydrogenase/GMP reductase	F	0.28	0.17	-0.32	-0.68	-1.59
cg0706	-	Conserved putative membrane protein	-	1.00	1.83	1.13	1.00	0.81
cg0712	-	Putative secreted protein	-	0.46	-0.64	-0.99	-1.58	-1.81
cg0717	<i>crtEb</i>	Lycopene elongase	O	-0.28	-0.43	-0.59	-0.59	-2.53
cg0718	<i>crtYf</i>	C50 carotenoid epsilon cyclase	-	0.47	-0.04	-0.07	-0.46	-1.60
cg0719	<i>crtYe</i>	C50 carotenoid epsilon cyclase	-	0.40	-0.19	0.28	-0.53	-2.64
cg0720	<i>crtI2</i>	Phytoene dehydrogenase (desaturase)	Q	0.01	-0.33	-0.97	-1.08	-2.26
cg0721	<i>crtB2</i>	Phytoene synthetase	I	0.12	-0.86	-1.16	-1.28	-3.41
cg0722	-	Putative multidrug efflux protein, resistance-nodulation-ce	R	0.19	-0.45	-0.77	-0.91	-3.15
cg0723	<i>crtE</i>	Geranylgeranyl pyrophosphate synthase	H	-0.12	-0.90	-1.12	-1.34	-3.15
cg0727	-	Putative nucleoside-diphosphate-sugar epimerase	M	-0.45	-1.04	-0.95	-1.21	-2.06
cg0728	<i>phr</i>	Deoxyribodipyrimidine photo-lyase	L	-0.01	-0.49	-1.20	-1.79	-2.85
cg0730	<i>crtX</i>	Carotenoid glycosyl transferase	M	-0.13	-0.76	-0.94	-1.45	-2.28
cg0732	-	ABC-type transporter, permease subunit	V	-0.09	-0.75	-1.51	-2.37	-4.98
cg0733	-	ABC-type transporter, ATPase subunit	V	0.04	-1.07	-1.47	-2.34	-4.98
cg0735	<i>metI</i>	ABC-type methionine transporter, permease subunit (TC :P	P	-0.13	-0.91	-1.57	-1.81	-5.14
cg0736	<i>metN</i>	ABC-type methionine transporter, ATPase subunit (TC 3./P	P	0.00	-0.61	-1.29	-1.98	-5.11
cg0737	<i>metQ</i>	ABC-type methionine transporter, substrate-binding lipopr	P	0.17	0.14	-0.62	-0.43	-4.48
cg0738	<i>dnaE2</i>	Putative DNA polymerase III, alpha chain	L	-0.24	-0.07	-0.30	-0.69	-1.67
cg0742	-	Putative integral membrane protein	-	-0.22	-0.60	-1.60	-1.69	-2.13
cg0748	-	ABC-type putative iron-siderophore transporter, substrate	P	-0.20	-0.89	-1.32	-2.30	-3.14
cg0749	<i>spoU</i>	Putative tRNA/rRNA methyltransferase	J	0.43	0.41	0.14	-0.15	-2.00
cg0750	<i>folD</i>	Methylenetetrahydrofolate dehydrogenase (NADP(+))/met	H	0.13	0.46	0.03	-0.26	-1.54
cg0751	-	Putative membrane protein	-	-0.25	-0.20	-0.63	-0.96	-2.40
cg0753	-	Putative secreted protein	-	-0.98	-1.51	-1.72	-1.62	-1.49
cg0754	<i>metX</i>	Homoserine O-acetyltransferase	E	-0.20	0.00	-0.62	-0.43	-3.41
cg0755	<i>metY</i>	O-Acetylhomoserine sulfhydrylase	E	-0.18	-0.29	-1.08	-0.53	-4.86
cg0756	<i>cstA</i>	Putative carbon starvation protein A	T	0.28	-0.65	-1.55	-3.34	-3.75
cg0757	-	Conserved hypothetical protein	-	0.48	-0.86	-1.28	-2.10	-3.61
cg0758	-	Hypothetical protein	-	-2.69	-1.65	-2.95	-2.93	-2.96
cg0759	<i>prpD2</i>	2-Methylcitrate dehydratase, involved in propionate catab	R	2.04	-3.78	-4.09	-4.28	-3.49
cg0760	<i>prpB2</i>	Methylisocitrate lyase, involved in propionate catabolism	G	2.32	-3.15	-3.45	-3.95	-5.20
cg0762	<i>prpC2</i>	2-Methylcitrate synthase, involved in propionate catabolis	C	2.00	-2.68	-2.98	-4.84	-4.45
cg0763	<i>mdh2</i>	Putative malate/L-lactate dehydrogenase	C	-0.55	-1.97	-1.78	-0.86	-1.98
cg0767	-	Siderophore-interacting protein	-	-0.51	-1.15	-2.28	-4.70	-4.73
cg0768	-	ABC-type putative iron-siderophore transporter, ATPase s	E	-0.75	-1.33	-4.04	-4.83	-5.27
cg0769	-	ABC-type putative iron-siderophore transporter, permease	P	0.03	-1.01	-2.50	-4.04	-6.06
cg0770	-	ABC-type putative iron-siderophore transporter, permease	P	0.03	-1.02	-2.76	-3.96	-6.40
cg0771	<i>irp1</i>	ABC-type putative iron-siderophore transporter, substrate	P	-0.13	-1.17	-3.14	-4.62	-6.13
cg0772	-	Putative sugar/drug permease, MFS-type	G	0.07	0.34	-0.45	-1.05	-2.80
cg0774	-	Putative membrane protein	-	0.15	0.62	0.34	0.32	-2.04
cg0776	-	ABC-type putative iron-siderophore transporter, substrate	P	-0.04	1.56	1.00	1.54	-0.20
cg0777	-	ABC-type putative iron-siderophore transporter, ATPase s	E	0.69	1.51	0.73	1.31	0.08
cg0781	-	Putative membrane protein	-	0.77	1.59	1.16	1.01	0.88
cg0782	<i>dac</i>	D-alanyl-D-alanine carboxypeptidase	M	0.07	-1.21	-2.11	-2.69	-4.57
cg0783	-	Conserved hypothetical protein	-	-0.28	-0.44	-0.97	-1.14	-2.19
cg0786	<i>upp</i>	Putative uracil phosphoribosyltransferase	F	0.16	0.13	-0.37	-0.58	-1.92
cg0787	-	Putative transcriptional regulator, HTH_3-family	K	-0.15	-0.44	-0.65	-1.04	-2.59
cg0791	<i>pyc</i>	Pyruvate carboxylase	C	0.18	-0.65	-0.98	-1.31	-3.91
cg0792	-	Hypothetical protein	O	0.16	4.26	3.95	3.81	3.57
cg0793	-	Putative secreted protein	S	0.80	2.99	2.74	2.76	2.61
cg0795	-	Putative oxidoreductase	O	-0.15	6.00	6.02	5.81	4.64
cg0796	<i>prpD1</i>	Putative (2-methyl) citrate dehydratase	R	0.33	3.06	2.91	2.76	1.80
cg0799	-	Conserved hypothetical protein	-	-0.04	-0.82	-1.42	-1.19	-2.85
cg0800	-	Transcriptional activator of propionate catabolism, HTH_3	K	0.06	-0.97	-1.31	-0.99	-2.04
cg0801	-	Hypothetical protein	-	0.26	0.30	0.73	-1.57	-1.18
cg0806	-	Conserved hypothetical protein	-	0.19	0.63	-0.22	-0.71	-2.81
cg0808	<i>wbpC</i>	Conserved putative membrane protein	I	-0.25	-0.31	-0.66	-1.07	-2.87
cg0809	<i>maf</i>	Septum formation protein Maf	D	0.13	-0.15	-0.63	-0.70	-2.05

Locus	Feature	Product	COG	m-values				
				②	③	④	⑤	⑥
				vs. ①	vs. ①	vs. ①	vs. ①	vs. ①
cg0811	<i>dtbR2</i>	Acetyl/propionyl-CoA carboxylase, beta chain	I	0.37	0.16	-0.23	-0.22	-1.52
cg0816	<i>purK</i>	Phosphoribosylaminoimidazole carboxylase, ATPase subunit	F	0.07	0.46	-0.38	-0.42	-1.86
cg0817	<i>kup</i>	Putative secondary K+ uptake permease, K+ uptake permease	P	-0.46	-0.30	-0.63	-1.23	-2.94
cg0819	-	Hypothetical protein	-	-0.01	-0.49	-0.57	-0.68	-1.68
cg0822	-	Conserved hypothetical protein	-	0.33	0.00	-0.45	-0.55	-1.87
cg0823	<i>ntaA</i>	Putative nitrilotriacetate monooxygenase, subunit A	C	-0.56	-1.00	-1.02	-2.22	-2.37
cg0828	-	Putative dihydrofolate reductase	H	-0.69	-0.59	-0.83	-1.23	-1.52
cg0831	<i>tusG</i>	ABC-type trehalose transporter, permease subunit	G	0.22	-1.00	-1.84	-1.55	-1.80
cg0832	<i>tusF</i>	ABC-type trehalose transporter, permease subunit	G	0.16	-1.03	-1.59	-1.54	-1.70
cg0834	<i>tusE</i>	ABC-type trehalose transporter, substrate-binding lipoprotein	G	0.59	-1.91	-2.08	-1.38	-1.23
cg0835	<i>tusK</i>	ABC-type trehalose transporter, substrate-binding lipoprotein	G	0.05	-1.46	-1.89	-2.43	-3.20
cg0838	-	Putative helicase	R	0.25	1.78	1.31	0.88	-0.13
cg0839	-	Hypothetical protein	-	0.32	1.64	1.01	0.66	-0.23
cg0847	-	Conserved hypothetical protein	K	-0.06	-0.13	-0.85	-1.28	-2.80
cg0848	<i>wbbL</i>	Putative glycosyltransferase	M	0.12	-0.73	-1.44	-1.94	-4.08
cg0849	<i>rmlA2</i>	Mannose-1-phosphate guanylyltransferase (GDP)	M	0.20	-0.42	-1.19	-1.74	-2.63
cg0851	-	Hypothetical protein	-	-0.82	-1.58	-2.89	-2.07	-3.31
cg0853	-	Conserved hypothetical protein	-	0.06	0.26	0.04	-0.27	-2.23
cg0854	<i>pmmA</i>	Phosphomannomutase	G	-0.11	0.15	-0.13	-0.49	-1.53
cg0858	-	Putative secreted protein	R	-1.61	-1.35	-1.33	-1.12	-1.66
cg0864	<i>mtrB</i>	Two-component system, sensory histidine kinase involved in	T	-0.06	0.22	-0.19	-0.54	-1.85
cg0865	-	Putative secreted lipoprotein	-	0.08	0.30	0.12	-0.32	-1.67
cg0868	<i>secA</i>	Preprotein translocase, SecA subunit	U	0.13	0.20	-0.42	-0.59	-1.53
cg0869	-	conserved hypothetical protein	-	0.35	-1.49	-0.99	-0.25	-1.63
cg0875	-	Conserved hypothetical protein	V	0.35	-1.31	-0.71	-1.79	-1.82
cg0878	<i>whcE</i>	Transcriptional regulator, WhiB-family	-	0.02	0.56	0.59	0.37	-1.88
cg0880	-	Putative secreted protein	-	-0.48	0.32	-0.38	-0.59	-1.62
cg0891	-	Putative metal-dependent hydrolase	R	-0.34	-0.86	-0.89	-0.93	-2.61
cg0893	-	Putative secreted protein, containing a PDZ-domain	T	-0.17	-0.86	-1.63	-1.79	-3.62
cg0894	-	Conserved hypothetical protein, possibly secreted	-	-0.03	-0.31	-0.63	-0.66	-1.63
cg0898	<i>pdxS</i>	pyridoxal 5'-phosphate (PLP) synthase subunit	H	-0.67	-1.06	-2.47	-3.46	-1.85
cg0899	<i>pdxT</i>	pyridoxal 5'-phosphate (PLP) synthase subunit, glutamine-dependent	H	-0.76	-1.30	-2.60	-3.62	-2.39
cg0901	-	Putative secreted protein	-	0.03	1.10	0.97	0.21	-2.13
cg0904	-	Hypothetical protein	-	0.19	-0.52	-1.50	-1.00	-1.25
cg0905	<i>psp2</i>	Putative secreted protein	M	0.46	2.04	2.09	2.07	0.78
cg0909	-	Hypothetical protein	-	-0.15	-0.73	-1.48	-1.67	-2.00
cg0913	<i>prfB</i>	Peptide chain release factor 2 (RF-2)	J	-0.08	-0.04	-0.37	-0.84	-2.05
cg0914	<i>ftsE</i>	Cell division ATP-binding protein FtsE-family	E	-0.58	-1.16	-1.92	-2.42	-3.84
cg0915	<i>ftsX</i>	Putative cell division protein, FtsX-family	D	-0.31	-1.33	-1.81	-2.23	-3.42
cg0919	<i>tnp18a(ISCg18)</i>	Transposase	-	0.40	-0.61	-0.91	-0.79	-1.82
cg0921	-	Siderophore-interacting protein	P	-0.21	-3.45	-4.61	-6.91	-4.61
cg0922	-	ABC-type putative iron-siderophore transporter, substrate-binding	P	0.09	-2.27	-7.03	-7.02	-7.04
cg0923	-	Putative membrane protein	S	0.15	1.54	0.90	0.64	-0.24
cg0924	-	ABC-type putative iron-siderophore transporter, substrate-binding	P	0.00	-2.01	-4.80	-6.34	-7.69
cg0926	-	ABC-type putative iron-siderophore transporter, permease	P	-0.18	-1.34	-3.09	-3.84	-5.99
cg0927	-	ABC-type putative iron-siderophore transporter, permease	P	-0.14	-1.28	-2.92	-3.52	-5.64
cg0928	-	ABC-type putative iron-siderophore transporter, ATPase subunit	E	0.08	-1.27	-2.83	-3.40	-4.44
cg0931	-	Putative aminotransferase, AT class I	E	0.11	0.03	-0.51	-0.98	-1.68
cg0936	<i>rpf1</i>	RPF-protein precursor	-	-0.78	-2.54	-2.93	-3.59	-5.49
cg0938	-	Cold shock protein	K	0.03	-0.78	-0.74	-0.92	-2.79
cg0940	-	Glutamine cyclotransferase	O	-0.13	-0.26	-0.52	-0.74	-1.93
cg0944	-	Putative xanthine/uracil symporter, nucleobase:cation symporter	R	0.00	0.48	-0.07	-0.64	-2.15
cg0945	-	Putative 23S ribosomal rRNA methyltransferase	J	0.36	0.86	0.04	-0.35	-1.87
cg0949	<i>gltA</i>	Citrate synthase	C	0.20	0.27	-0.14	-0.04	-1.77
cg0952	-	Putative integral membrane protein	S	0.34	-3.51	-3.42	-2.98	-3.29
cg0953	<i>mctC</i>	secondary acetate/propionate/pyruvate transporter	R	0.36	-3.26	-3.32	-2.89	-3.29
cg0954	-	Putative secreted protein	-	-0.19	-0.24	-0.62	-0.76	-2.03
cg0958	-	Putative secreted protein	-	-0.36	-0.26	-1.13	-2.01	-2.95
cg0960	-	Hypothetical protein	-	-0.17	-0.28	-0.70	-1.88	-3.74
cg0961	-	Putative hydrolase, alpha/beta-fold	E	-0.15	-3.47	-3.37	-3.65	-5.05
cg0962	-	Putative secreted protein	-	-0.56	-0.31	-0.32	-0.84	-1.59
cg0963	-	Hypothetical protein	-	0.90	1.80	1.93	2.53	2.47
cg0978	-	ABC-type transporter, ATPase subunit	E	-0.43	-0.46	-1.48	-2.40	-3.81
cg0979	-	Putative transcriptional regulator, PadR-family	-	0.07	-0.31	-1.10	-1.08	-2.26
cg0980	-	Putative secreted protein, related to metalloendopeptidase	M	-0.51	-0.41	-0.39	-0.53	-2.56

Locus	Feature	Product	COG	m-values				
				②	③	④	⑤	⑥
				vs. ①	vs. ①	vs. ①	vs. ①	vs. ①
cg0983	<i>purN</i>	Phosphoribosylglycinamide formyltransferase	F	0.24	0.04	-0.63	-0.94	-2.15
cg0986	<i>amtR</i>	Transcriptional repressor of nitrogen metabolism, TetR-fai-	-	0.03	0.01	-0.29	-0.59	-1.90
cg0988	<i>rpsR</i>	30S ribosomal protein S18	J	0.12	-0.79	-0.96	-1.07	-3.54
cg0989	<i>rpsN</i>	30S ribosomal protein S14	J	0.22	-0.72	-0.98	-1.14	-3.84
cg0990	<i>rpmG</i>	50S ribosomal protein L33	-	0.14	-0.78	-1.12	-1.26	-4.12
cg0991	<i>rpmB</i>	50S ribosomal protein L28	J	0.14	-0.85	-1.09	-1.20	-4.09
cg0992	-	Putative permease, sulfate permease (SulP) family	P	1.76	2.39	2.10	2.45	-0.01
cg0993	-	Putative transcriptional regulator, ArsR-family	-	2.32	2.70	2.66	2.90	0.36
cg0994	<i>rpmE</i>	Putative 50S ribosomal protein L31	J	0.28	-0.65	-0.82	-1.00	-4.12
cg0995	<i>rpmF</i>	50S ribosomal protein L32	-	0.35	-0.53	-0.61	-0.81	-3.74
cg1001	<i>mscL</i>	Large-conductance mechanosensitive ion channel, MscL-	-	0.17	0.04	-0.66	-1.66	-3.73
cg1002	-	Conserved putative secreted protein	-	-0.07	-1.37	-1.71	-1.88	-2.29
cg1003	<i>fthC</i>	5-Formyltetrahydrofolate cyclo-ligase	H	0.33	0.95	0.66	0.93	1.87
cg1006	-	Putative acetyltransferase	J	0.00	0.01	-0.63	-0.85	-1.88
cg1009	-	Putative cyanate permease, MFS-type	G	0.07	-0.35	-0.73	-0.90	-2.26
cg1010	-	Putative membrane protein	S	0.24	-0.05	-0.66	-1.15	-2.19
cg1011	-	Putative membrane protein	S	0.13	0.27	-0.24	-0.92	-1.95
cg1014	<i>pmt</i>	Protein O-mannosyltransferase	O	-0.27	-0.99	-1.50	-1.97	-3.93
cg1016	<i>betP</i>	Na+/glutamate symporter	M	1.35	1.62	1.27	1.01	0.09
cg1022	<i>tnp6a(ISCg6a)</i>	Transposase	L	-0.62	-0.52	-0.40	-0.37	-1.92
cg1023	<i>tnp6b(ISCg6a)</i>	Transposase	L	-1.17	-1.51	-1.17	-0.87	-3.35
cg1024	<i>tnp7a(ISCg7a)</i>	Transposase	L	-0.84	-1.06	-2.10	-2.09	-2.11
cg1030	<i>tnp6c(ISCg6c)</i>	Transposase	-	-0.44	-0.35	-0.29	-0.50	-1.71
cg1031	<i>tnp6d(ISCg6c)</i>	Transposase	L	-0.88	-0.69	-0.59	-0.93	-3.15
cg1035	-	DNase, TatD-related	L	-0.40	-1.04	-1.16	-1.21	-2.12
cg1037	<i>rpf2</i>	RPF2 precursor, secreted protein	-	-0.95	-0.91	-0.80	-1.32	-2.82
cg1038	<i>ksgA</i>	Putative dimethyladenosine transferase	J	-0.62	-0.43	-0.61	-0.83	-1.82
cg1045	-	Conserved hypothetical protein	S	0.40	1.21	1.20	1.44	2.34
cg1052	<i>cmt3</i>	Corynomycolyl transferase	R	-0.61	-1.19	-2.03	-2.49	-4.00
cg1053	-	Putative transcriptional regulator, TetR-family	K	-0.15	-0.65	-1.16	-1.57	-3.16
cg1054	<i>mmpL2</i>	Putative multidrug efflux protein, resistance-nodulation-ce	R	-0.12	-0.88	-1.19	-1.18	-3.08
cg1055	<i>menG</i>	S-Adenosylmethionine:2-demethylmenaquinone methyltra	H	0.53	-1.17	-1.29	-1.84	-2.06
cg1056	-	Putative membrane protein	-	-0.33	-1.55	-2.07	-2.46	-4.18
cg1060	<i>prfC</i>	Putative peptide chain release factor 3 (EF-G)	J	-0.19	0.31	-0.27	-0.63	-1.65
cg1066	<i>urtE</i>	ABC-type putative branched-chain amino acid transporter	E	0.77	0.52	0.51	1.35	-1.64
cg1067	<i>pth2</i>	Peptidyl-tRNA hydrolase	J	-0.12	-0.51	-0.98	-1.42	-3.40
cg1072	<i>rplY</i>	Ribosomal protein L25 (general stress protein Ctc)	J	0.15	-0.90	-1.31	-1.41	-3.80
cg1074	-	Conserved hypothetical protein	L	0.22	-0.08	-1.05	-1.67	-3.57
cg1075	<i>prsA</i>	Ribose-phosphate diphosphokinase	F	0.45	0.28	-0.57	-0.81	-2.60
cg1076	<i>glmU</i>	Putative UDP-N-acetylglucosamine diphosphorylase	M	0.48	-0.09	-0.84	-1.34	-2.83
cg1077	-	Putative permease, MFS-type	-	-0.18	-0.53	-1.17	-1.19	-2.70
cg1080	-	Putative multicopper oxidase	Q	0.27	2.22	2.07	2.46	2.70
cg1081	-	ABC-type putative daunorubicin transporter, ATPase sub	G	3.20	4.13	2.48	2.79	2.58
cg1082	-	Putative membrane protein	-	2.71	3.69	2.14	2.40	2.12
cg1083	<i>cgtS10</i>	Two-component system, sensory histidine kinase	T	1.16	2.03	0.61	0.95	0.42
cg1084	<i>cgtR10</i>	Two-component system, transcriptional response regulat	T	0.84	1.78	0.76	0.76	0.27
cg1086	-	Putative membrane protein	S	0.35	0.30	-0.18	-0.56	-1.68
cg1087	-	Putative membrane protein	-	0.19	-1.77	-1.64	-1.64	-0.98
cg1088	-	ABC-type putative multidrug transporter, ATPase and pen	V	0.17	-1.99	-1.80	-1.95	-1.75
cg1089	-	ABC-type putative multidrug transporter, ATPase and pen	V	-0.24	-1.08	-2.04	-2.59	-3.54
cg1090	<i>ggtB</i>	Putative gamma-glutamyltranspeptidase	E	0.40	-2.24	-2.78	-2.71	-2.75
cg1091	-	Hypothetical protein	-	-0.42	-1.21	-1.62	-1.26	-0.59
cg1092	-	Putative secreted protein	L	0.26	2.16	2.32	2.17	0.97
cg1095	-	Hypothetical protein	-	-0.68	-0.31	-0.18	-0.41	-1.60
cg1096	-	Hypothetical protein	-	-0.50	-0.21	-0.19	-0.28	-1.97
cg1100	-	ABC-type putative multidrug transporter, ATPase and pen	V	0.67	1.96	1.65	1.57	1.04
cg1104	-	Putative membrane protein, predicted esterase	R	0.23	0.03	-0.25	-0.72	-1.58
cg1105	<i>lysI</i>	Low capacity L-Lysine antiporter	E	-0.08	-1.12	-1.05	-1.46	-2.95
cg1108	-	Putative secreted protein	-	-0.18	-0.63	-1.13	-0.91	-3.07
cg1109	-	Hypothetical protein	-	-0.69	-4.65	-5.72	-6.56	-6.54
cg1110	-	Conserved hypothetical protein	M	-0.64	-1.58	-2.13	-2.04	-3.56
cg1120	<i>ripA</i>	Putative transcriptional regulator, AraC-family	K	-0.22	-1.78	-3.04	-4.19	-5.48
cg1122	-	Putative secreted protein	-	0.07	-0.25	-0.75	-0.63	-2.47
cg1123	<i>greA</i>	Transcription elongation factor	K	0.13	-0.27	-0.80	-0.70	-2.61
cg1125	-	Conserved hypothetical protein	-	0.34	1.51	1.22	1.18	0.88

					m-values				
Locus	Feature	Product	COG	②	③	④	⑤	⑥	
				vs. ①	vs. ①	vs. ①	vs. ①	vs. ①	
cg1129	<i>aroF</i>	Putative phospho-2-dehydro-3-deoxyheptonate aldolase	E	0.25	-0.81	-1.17	-1.06	-3.14	
cg1132	<i>coaA</i>	Pantothenate kinase	H	-0.15	-0.39	-0.69	-1.29	-1.91	
cg1133	<i>glyA</i>	Serine hydroxymethyltransferase	E	0.26	0.99	0.73	0.36	-2.20	
cg1134	<i>pab</i>	Para-aminobenzoate synthase	E	-0.03	0.95	0.37	-0.25	-2.84	
cg1135	-	Conserved hypothetical protein	E	-0.36	0.96	0.35	0.00	-1.80	
cg1138	-	Putative acetyltransferase, GNAT-family	M	-0.10	-0.78	-1.49	-2.05	-2.87	
cg1140	-	Allophanate hydrolase subunit 1	E	0.03	-1.70	-0.90	-0.78	-1.40	
cg1141	-	Conserved hypothetical protein, UPF0271-family	R	-0.02	-1.64	-1.13	-0.73	-1.27	
cg1142	-	Putative Mn2+ transporter, metal ion (Mn2+-iron) transpor	P	-0.01	-2.45	-1.14	-0.62	-1.16	
cg1144	-	Hypothetical protein	-	-0.15	-0.17	-0.24	-0.78	-1.86	
cg1145	<i>fum</i>	Fumarate hydratase	C	0.29	1.56	1.48	1.93	1.57	
cg1149	-	Hypothetical protein	-	-0.69	-1.65	-0.47	-1.09	-1.47	
cg1150	-	Putative NADPH-dependent FMN reductase	R	0.18	-0.33	-0.88	-1.16	-2.50	
cg1151	<i>seuA</i>	FMNH2-dependent monooxygenase, involved in sulfonate C	C	-0.44	-1.06	-0.75	-1.27	-3.14	
cg1156	<i>ssuD2</i>	FMNH2-dependent aliphatic sulfonate monooxygenase	C	-0.35	-0.40	-0.44	0.18	-2.16	
cg1157	<i>fbp</i>	Fructose-1,6-bisphosphatase	G	0.50	1.39	1.27	1.80	1.29	
cg1158	-	Putative secreted protein	-	-0.09	0.02	0.10	0.18	-1.62	
cg1160	-	Hypothetical protein, similar to arabinose efflux permease	-	0.27	-0.29	-0.23	-0.27	-1.51	
cg1164	<i>ispH</i>	4-Hydroxy-3-methylbut-2-enyl diphosphate reductase	I	0.12	1.37	1.38	1.56	1.18	
cg1165	-	Conserved putative membrane protein	-	-0.17	-0.30	-0.87	-0.85	-2.14	
cg1167	-	Putative acetyltransferase, GNAT-family	-	0.54	0.07	-1.11	-2.40	-1.86	
cg1171	-	Putative GTPase	J	-0.04	-0.16	-0.75	-1.11	-3.33	
cg1172	-	Conserved hypothetical protein, putative plasmid mainten	R	0.12	-0.04	-0.26	-0.77	-1.94	
cg1173	-	Conserved hypothetical protein, putative plasmid mainten	-	0.18	-0.23	-0.33	-0.94	-1.83	
cg1175	-	Putative acetyltransferase, GNAT-family	J	-0.24	-0.72	-1.50	-2.38	-6.21	
cg1178	<i>tnp9a(ISCg9a)</i>	Transposase	L	-0.40	-0.91	-0.95	-1.71	-1.54	
cg1194	-	Predicted nucleoside-diphosphate-sugar epimerase	M	-1.64	-0.81	-1.67	-1.65	-1.37	
cg1198	-	Hypothetical protein	-	-0.88	-0.25	-1.31	-0.76	-2.15	
cg1199	-	Hypothetical protein	-	-0.82	-0.78	-0.62	-0.84	-2.37	
cg1201	-	Hypothetical protein	-	0.31	0.35	-0.14	-0.61	-1.96	
cg1206	-	Conserved hypothetical protein	G	0.11	1.11	1.17	1.23	1.56	
cg1209	-	Putative Zn-ribbon-containing protein, involved in phospho	P	0.32	-0.52	-0.51	-0.93	-2.19	
cg1210	-	Putative membrane protein	-	0.24	0.22	-0.01	-0.02	-1.75	
cg1214	-	Putative cysteine desulfurase, AT class IV	E	-0.34	1.58	1.62	1.49	0.85	
cg1215	<i>nadC</i>	Putative nicotinate-nucleotide pyrophosphorylase	H	-0.37	1.62	1.66	1.57	1.05	
cg1216	<i>nadA</i>	Quinolinate synthetase, subunit A	H	-0.41	1.68	1.63	1.51	0.89	
cg1219	-	Putative membrane protein	S	0.33	-0.78	-1.22	-1.70	-3.08	
cg1224	-	Conserved hypothetical protein	S	-0.19	-1.66	-1.68	-1.60	-1.59	
cg1225	<i>pcaK</i>	MFS-type 4-hydroxybenzoate and protocatechuate perme	G	0.53	-2.45	-1.20	-0.79	-1.81	
cg1226	<i>pobA</i>	Putative 4-hydroxybenzoate 3-monooxygenase	H	-0.27	-2.05	-1.27	-0.91	-2.06	
cg1227	-	Putative membrane protein	S	-0.44	-0.13	-0.88	-1.11	-2.82	
cg1228	-	ABC-type putative cobalt transporter, ATPase subunit	R	-0.27	0.04	-0.86	-1.11	-2.81	
cg1229	-	ABC-type putative cobalt transporter, permease subunit	P	-0.20	-0.01	-0.76	-1.00	-2.84	
cg1230	-	Conserved hypothetical protein	F	-0.52	-0.81	-1.52	-1.93	-4.29	
cg1231	<i>chaA</i>	Putative secondary Na+/Ca2+ antiporter, Ca2+:cation ant	P	-0.81	-1.31	-2.10	-2.62	-5.17	
cg1234	-	Putative excinuclease, UvrA-like ATPase	L	0.09	-0.12	-0.61	-1.12	-1.93	
cg1245	-	Putative membrane protein	E	0.99	-0.39	-0.70	-1.21	-2.78	
cg1246	-	Conserved hypothetical protein	S	-0.64	-0.50	-1.25	-1.06	-2.27	
cg1247	-	Putative secreted protein	-	-0.78	-0.86	-1.49	-1.52	-2.68	
cg1248	-	Putative GTPase, probably involved in stress response	T	-0.07	-1.36	-1.82	-2.42	-3.71	
cg1249	-	ABC-type putative dipeptide/oligopeptide transporter, sub	E	0.20	0.29	-0.24	-0.86	-2.46	
cg1250	<i>mshB</i>	Putative N-acetyl-1-D-myo-inositol-2-amino-2-deoxy-alpha	S	0.08	0.53	-0.09	-0.55	-1.61	
cg1253	<i>dapC</i>	Succinyldiaminopimelate aminotransferase, AT class I	E	-0.21	0.27	-0.14	-0.49	-2.04	
cg1254	-	Putative membrane protein	-	-0.58	-0.84	-1.11	-1.54	-3.01	
cg1255	-	Conserved hypothetical protein, putative HNH endonuclea	V	-0.76	-1.97	-0.69	-1.67	-2.11	
cg1256	<i>dapD</i>	2,3,4,5-Tetrahydropyridine-2,6-dicarboxylate N-succinyltr	E	-0.13	-0.01	0.16	-0.08	-1.82	
cg1257	<i>aroP</i>	aromatic amino acids uptake system	E	-0.01	0.17	-0.26	-0.21	-1.70	
cg1279	-	Putative secreted protein	-	0.41	3.63	3.91	4.22	4.17	
cg1287	-	Conserved hypothetical protein	-	-0.92	-0.27	-1.19	-1.56	-2.47	
cg1290	<i>metE</i>	5-Methyltetrahydropteroyltriglutamate-- homocysteine met	E	-0.27	-0.29	-0.17	-2.41	-8.59	
cg1291	-	Putative membrane protein	-	1.06	5.09	5.53	5.54	5.22	
cg1292	-	Flavin-containing monooxygenase 3	P	0.62	0.32	1.74	2.48	1.52	
cg1296	-	Conserved hypothetical protein, putative non-ribosomal pr	Q	-0.36	-0.16	-0.44	-0.20	-1.63	
cg1298	<i>cydC</i>	ABC-type putative multidrug/protein/lipid transporter, ATP	V	0.04	0.71	2.98	3.65	2.98	
cg1299	<i>cydD</i>	ABC-type putative multidrug/protein/lipid transporter, ATP	V	0.76	1.18	3.36	3.82	3.39	

					m-values				
Locus	Feature	Product	COG	②	③	④	⑤	⑥	
				vs. ①	vs. ①	vs. ①	vs. ①	vs. ①	
cg1300	<i>cydB</i>	Cytochrome d ubiquinol oxidase subunit II	C	0.45	1.13	3.52	3.95	3.62	
cg1301	<i>cydA</i>	Cytochrome d ubiquinol oxidase subunit I	C	0.31	0.57	3.11	3.60	3.03	
cg1302	-	Putative nuclease, HKD-family	K	-0.32	0.01	-0.59	-1.01	-2.34	
cg1304	-	Putative secreted protein	-	0.21	-0.29	-0.88	-1.79	-2.87	
cg1305	-	Putative secondary proline transporter, amino acid-polyan	E	0.36	0.47	-0.70	-1.57	-3.26	
cg1307	-	DNA/RNA helicase, superfamily II	J	0.00	1.82	1.74	1.35	0.28	
cg1308	-	Putative transcriptional regulator, TetR-family	K	0.17	0.33	-0.20	-0.77	-2.15	
cg1309	-	Putative FAD-dependent oxidoreductase	H	-0.57	-2.31	-2.66	-2.43	-2.34	
cg1313	-	Putative secreted lipoprotein	S	-0.45	-2.16	-2.86	-2.38	-4.54	
cg1314	<i>putP</i>	Putative Na ⁺ /proline symporter, solute:sodium symporter	E	0.18	-1.82	-2.07	-1.90	-2.84	
cg1316	-	DNA/RNA helicase, SNF2 family	K	-0.14	-0.59	-0.73	-0.84	-1.96	
cg1325	-	Conserved hypothetical protein	-	1.77	2.73	1.89	1.01	-0.62	
cg1327	-	Putative transcriptional regulator, Crp-family	T	0.02	1.94	2.17	2.65	2.38	
cg1328	-	Putative heavy-metal ion transporting P-type ATPase	-	0.14	1.44	1.66	2.16	1.87	
cg1329	<i>ctpC</i>	Putative Cd ²⁺ transporting P-type ATPase	P	0.34	1.42	1.38	2.04	1.76	
cg1332	-	Putative secreted hydrolase	R	0.18	-0.20	-1.05	-1.73	-4.18	
cg1333	<i>argS</i>	Arginyl-tRNA synthetase	J	0.19	-0.34	-1.19	-1.67	-3.71	
cg1334	<i>lysA</i>	Diaminopimelate decarboxylase	E	0.11	-0.23	-1.08	-1.54	-3.13	
cg1335	-	Hypothetical protein	-	-0.18	-0.68	-1.32	-1.95	-3.16	
cg1336	-	Putative secreted protein	-	0.30	-0.55	-0.64	-1.87	-2.90	
cg1337	<i>hom</i>	Homoserine dehydrogenase	E	0.07	0.22	-0.02	0.01	-1.60	
cg1338	<i>thrB</i>	Homoserine kinase	E	0.03	0.12	-0.05	0.01	-1.63	
cg1341	<i>narI</i>	Respiratory nitrate reductase 2, gamma chain	C	1.02	0.99	0.98	1.35	1.60	
cg1342	<i>narJ</i>	Respiratory nitrate reductase 2, delta chain	C	1.05	1.16	0.96	1.46	1.72	
cg1343	<i>narH</i>	Respiratory nitrate reductase 2, beta chain	C	1.25	0.96	1.01	1.43	1.56	
cg1347	-	Putative secreted or membrane protein	I	-0.98	-0.80	-1.04	-1.01	-1.77	
cg1349	-	Putative membrane protein, containing a CBS domain	R	-0.34	-0.27	-0.93	-1.64	-1.78	
cg1354	<i>rho</i>	Transcription termination factor Rho	K	0.12	-0.42	-0.84	-1.05	-3.20	
cg1355	<i>prfA</i>	Peptide chain release factor 1 (RF-1)	J	0.21	-0.28	-0.65	-0.93	-3.28	
cg1356	-	Putative rRNA or tRNA methylase	J	0.15	-0.81	-1.17	-1.65	-3.83	
cg1358	-	Putative translation factor, Sua5/YciO/YrdC/YwIc-family	J	0.15	0.33	-0.29	-0.68	-2.17	
cg1359	-	Putative membrane protein	M	0.00	0.15	-0.36	-0.41	-2.16	
cg1360	-	Putative membrane protein	-	-0.18	-0.43	-1.01	-1.07	-4.59	
cg1361	<i>atpI</i>	Hypothetical protein	-	-1.16	-1.25	-4.01	-2.19	-5.02	
cg1362	<i>atpB</i>	ATP synthase F0, A chain	C	0.26	1.09	0.79	0.68	-2.64	
cg1363	<i>atpE</i>	ATP synthase F0, C chain	-	0.35	1.23	0.78	0.57	-3.17	
cg1364	<i>atpF</i>	ATP synthase F0, B chain	C	0.26	1.06	0.61	0.49	-3.15	
cg1365	<i>atpH</i>	ATP synthase F1, delta subunit	C	0.38	1.19	0.69	0.55	-3.37	
cg1366	<i>atpA</i>	ATP synthase F1, alpha chain	C	0.25	1.17	0.63	0.53	-3.27	
cg1367	<i>atpG</i>	ATP synthase F1, gamma chain	C	0.26	1.16	0.59	0.54	-3.15	
cg1368	<i>atpD</i>	ATP synthase F1, beta chain	C	0.36	1.33	0.80	0.76	-3.11	
cg1369	<i>atpC</i>	ATP synthase F1, epsilon chain	C	0.44	1.32	0.82	0.84	-2.04	
cg1373	-	Putative glyoxalase	E	1.05	1.80	1.67	2.09	0.99	
cg1376	<i>ssuD1</i>	FMNH ₂ -dependent aliphatic sulfonate monooxygenase	C	-0.62	-0.24	-1.79	-1.13	-3.48	
cg1377	<i>ssuC</i>	ABC-type aliphatic sulfonate transporter, permease subur	P	-0.63	-1.78	-1.31	-1.70	-4.90	
cg1380	<i>ssuA</i>	ABC-type aliphatic sulfonate transporter, substrate-binding	P	0.47	-0.58	-1.41	-0.87	-3.10	
cg1386	<i>fixA</i>	Putative electron transfer flavoprotein, beta subunit	C	0.11	0.23	-0.22	0.21	-1.61	
cg1393	-	Putative acetyltransferase, GNAT family	-	1.10	1.86	1.45	1.68	2.02	
cg1408	-	Putative membrane protein	-	0.37	1.69	1.92	1.74	1.25	
cg1409	<i>pfk</i>	6-Phosphofructokinase	G	0.43	1.48	1.52	1.35	1.23	
cg1410	<i>rbsR</i>	Transcriptional repressor of the ribose importer RbsACBDK	K	-0.11	-2.96	-1.97	-0.75	-1.16	
cg1411	<i>rbsA</i>	ABC-type ribose transporter, ATPase subunit (TC 3.A.1.2 G	G	-0.09	-2.38	-1.64	-0.75	-1.49	
cg1412	<i>rbsC</i>	ABC-type ribose transporter, permease subunit (TC 3.A.1 G	G	-0.20	-2.18	-1.98	-0.79	-1.41	
cg1413	<i>rbsB</i>	ABC-type ribose transporter, substrate-binding lipoprotein	G	-0.08	-2.19	-1.80	-0.84	-1.20	
cg1414	<i>rbsD</i>	ABC-type ribose transporter, uncharacterized component	G	0.05	-1.77	-1.56	-1.06	-1.34	
cg1417	-	Putative acetyltransferase	J	-0.27	-2.52	-4.17	-4.15	-5.08	
cg1418	-	ABC-type putative iron-siderophore transporter, substrate	P	0.35	-0.82	-1.87	-2.72	-2.37	
cg1419	-	Putative secondary Na ⁺ /bile acid symporter, bile acid:Na ⁺	R	0.03	0.39	-1.01	-2.68	-6.15	
cg1421	-	Conserved hypothetical protein, putative dinucleotide-binc	R	0.26	-0.83	-0.54	-0.61	-2.17	
cg1424	<i>lysE</i>	L-Lysine efflux permease, L-lysine exporter (LysE) family	E	0.14	1.39	2.55	2.67	0.75	
cg1427	-	Conserved putative secreted protein	S	0.30	-0.33	-0.97	-1.33	-3.35	
cg1435	<i>ilvB</i>	Acetohydroxy acid synthase (AHAS), large subunit	E	0.01	-0.27	-1.04	-1.45	-2.89	
cg1436	<i>ilvN</i>	Acetohydroxy acid synthase (AHAS), small subunit	E	-0.11	-0.58	-1.94	-2.89	-3.31	
cg1437	<i>ilvC</i>	Ketopantoate reductase	E	0.17	-0.08	-0.54	-0.81	-1.88	
cg1442	-	Acyl-CoA dehydrogenase family protein, putative pseudoç	I	-0.72	-1.32	-0.88	-0.63	-2.70	

Locus	Feature	Product	COG	m-values				
				②	③	④	⑤	⑥
				vs. ①	vs. ①	vs. ①	vs. ①	vs. ①
cg1443	-	Acyl-CoA dehydrogenase family protein, putative pseudogluc	I	-0.94	-1.61	-2.26	-1.62	-4.73
cg1444	-	Putative flavin:NADH reductase	R	-0.22	-0.42	-0.87	-1.38	-2.59
cg1447	-	Putative secondary Co2+/Zn2+/Cd2+ efflux transporter, c	P	-0.74	-1.86	-1.51	-1.37	-1.04
cg1451	<i>serA</i>	Phosphoglycerate dehydrogenase	H	0.49	1.23	0.99	0.53	-2.53
cg1453	<i>leuB</i>	3-Isopropylmalate dehydrogenase	C	-0.03	0.65	-0.28	-1.19	-2.14
cg1458	-	Putative hydrolase, FAA-family	Q	-0.01	-0.30	-0.91	-1.04	-2.51
cg1459	-	Putative SAM-dependent methyltransferase	Q	-0.22	-0.36	-0.93	-1.13	-2.51
cg1462	<i>entC</i>	Isochorismate synthase	H	-0.06	-0.33	-1.18	-1.73	-2.13
cg1471	-	Hypothetical protein	-	0.72	0.88	1.25	1.62	1.99
cg1473	-	Conserved hypothetical protein	-	-1.30	-2.06	-4.37	-3.35	-4.37
cg1475	-	Conserved hypothetical protein	-	0.12	-0.07	-0.26	-0.49	-1.54
cg1479	<i>glgP1</i>	Putative glycogen phosphorylase	G	0.26	0.45	0.10	0.04	-1.59
cg1481	-	Conserved hypothetical protein	-	-0.43	-0.71	-1.50	-1.72	-2.83
cg1482	-	Putative Zn-dependent hydrolase	R	-0.08	-0.75	-2.18	-2.49	-2.84
cg1486	<i>LtbR</i>	Transcriptional regulator, lclR-family	K	-0.23	0.74	-0.07	-0.47	-1.74
cg1487	<i>leuC</i>	3-Isopropylmalate dehydratase, large subunit	E	-0.01	0.89	-0.24	-1.10	-4.44
cg1488	<i>leuD</i>	3-Isopropylmalate dehydratase, small subunit	E	-0.07	0.82	-0.12	-0.92	-3.90
cg1492	<i>gpsA</i>	Glycerol-3-phosphate dehydrogenase (NAD(P)(+))	C	0.40	-0.86	-1.35	-2.01	-3.40
cg1493	<i>ddlA</i>	D-alanine--D-alanine ligase A	M	0.11	-0.07	-0.40	-0.64	-2.00
cg1502	-	ABC-type putative amino acid transporter, ATPase subun	E	0.16	-0.11	-0.79	-1.30	-2.68
cg1503	-	ABC-type putative amino acid transporter, permease sub	E	-0.05	-0.18	-0.99	-1.57	-3.34
cg1504	-	ABC-type putative amino acid transporter, substrate-bind	E	-0.11	-0.33	-1.08	-1.73	-3.43
cg1505	-	Putative secreted protein	-	0.19	-0.37	-0.80	-1.17	-2.71
cg1506	-	Putative membrane protein	S	-0.17	-0.82	-1.06	-1.64	-3.76
cg1508	-	similar to Psp1 - putative pseudogene	-	-0.40	-1.04	-0.97	-1.06	-2.68
cg1514	-	Secreted protein	-	0.31	1.24	1.43	1.62	1.07
cg1518	-	Hypothetical protein	-	-0.18	-1.31	-1.22	-1.79	-2.30
cg1520	-	Putative secreted protein	O	-0.17	-0.83	-0.95	-0.93	-1.86
cg1521	-	Putative membrane protein	-	1.03	-0.25	-0.97	-0.96	-1.79
cg1522	-	Putative membrane protein	-	0.29	-0.64	-1.38	-1.70	-3.90
cg1523	-	Conserved hypothetical protein	-	-0.45	-0.56	-0.97	-0.95	-2.26
cg1551	<i>uspA1</i>	Universal stress protein UspA	T	0.71	1.71	1.57	1.46	1.16
cg1560	<i>uvrA</i>	Excinuclease ABC, ATPase subunit A	L	-0.12	-0.44	-0.74	-0.86	-2.00
cg1562	-	Putative membrane protein	-	1.13	1.25	1.09	1.31	1.65
cg1563	<i>infC</i>	Translation initiation factor IF-3	J	0.11	-0.89	-1.15	-1.12	-3.01
cg1564	<i>rpml</i>	50S ribosomal protein L35	-	0.17	-0.85	-0.98	-1.03	-3.01
cg1565	<i>rplT</i>	50S ribosomal protein L20	J	0.11	-0.80	-1.06	-1.04	-2.98
cg1566	-	Hypothetical protein	-	-0.32	-0.34	-0.84	-0.90	-2.21
cg1571	<i>ugpC</i>	ABC-type sn-glycerol-3-phosphate transporter, ATPase s	G	-0.30	-0.35	0.18	0.12	-1.96
cg1578	-	Putative acyltransferase, membrane protein	I	0.28	-0.22	-0.50	-0.67	-1.70
cg1579	-	Putative secreted protein	-	0.38	-0.26	-1.00	-1.11	-1.83
cg1580	<i>argC</i>	N-acetyl-gamma-glutamyl-phosphate reductase	E	0.22	-0.51	-0.07	0.58	-1.54
cg1581	<i>argJ</i>	Glutamate N-acetyltransferase	E	0.13	-0.48	-0.07	0.54	-1.61
cg1582	<i>argB</i>	Acetylglutamate kinase	E	0.07	-0.41	-0.12	0.47	-2.04
cg1584	<i>argF</i>	Ornithine carbamoyltransferase	E	0.12	-0.30	-0.08	0.53	-1.82
cg1585	<i>argR</i>	Transcriptional repressor of arginine biosynthesis, ArgR-f	K	0.46	-0.25	0.11	0.67	-1.92
cg1586	<i>argG</i>	Argininosuccinate synthase	E	0.23	0.28	-0.26	0.17	-1.60
cg1588	<i>argH</i>	Argininosuccinate lyase	E	0.11	0.15	-0.19	0.23	-1.59
cg1595	<i>uspA2</i>	Universal stress protein UspA	T	0.17	-2.69	-3.80	-4.25	-5.12
cg1602	<i>recN</i>	DNA repair protein RecN	L	-0.25	-1.12	-1.90	-2.23	-2.80
cg1606	<i>pyrG</i>	CTP synthetase	F	-0.06	0.19	-0.09	0.05	-2.15
cg1608	<i>xerD</i>	Integrase/recombinase	L	-0.20	-0.06	-0.20	-0.32	-1.54
cg1609	-	ABC-type putative antibiotics transporter, ATPase subunit	R	-0.73	-1.20	-1.51	-1.72	-3.36
cg1611	<i>scpA</i>	Putative segregation and condensation protein A	S	-0.55	-0.63	-0.84	-0.92	-2.28
cg1612	-	Putative acetyltransferase	J	1.69	-2.79	-3.10	-3.83	-3.67
cg1613	<i>sseA2</i>	Rhodanese-related sulfurtransferase	P	0.38	-1.09	-0.93	-0.61	-1.86
cg1614	<i>scpB</i>	Putative segregation and condensation protein B	K	0.18	-1.30	-1.21	-1.08	-2.97
cg1621	-	ABC-type putative multidrug transporter, ATPase and per	V	0.16	-0.62	-1.81	-2.03	-4.56
cg1622	-	ABC-type putative multidrug transporter, ATPase and per	V	0.47	-0.42	-1.07	-1.65	-2.57
cg1623	-	Putative divalent heavy-metal cation transporter	P	-0.29	-0.33	-1.14	-1.90	-4.15
cg1624	-	Putative secondary Na+/H+ antiporter, monovalent cation	P	0.07	1.70	0.83	0.43	-0.52
cg1626	-	Conserved hypothetical protein	S	0.09	3.88	3.53	2.83	0.91
cg1628	-	Putative hydrolase, alpha/beta superfamily	R	-0.36	4.04	3.67	3.01	0.98
cg1638	-	Conserved hypothetical protein	-	-0.56	-1.38	-1.72	-2.56	-4.88
cg1639	-	Putative membrane protein, containing a CBS domain	R	0.02	-0.17	-0.63	-0.85	-1.77

Locus	Feature	Product	COG	m-values				
				②	③	④	⑤	⑥
				vs. ①	vs. ①	vs. ①	vs. ①	vs. ①
cg1640	-	Putative membrane protein, containing a CBS domain	R	-0.28	-0.46	-0.92	-1.29	-2.01
cg1641	-	DNA/RNA helicase, superfamily II	L	-0.30	-0.32	-0.84	-0.85	-1.62
cg1647	-	ABC-type multidrug transport system, permease subunit	V	0.01	1.36	1.40	1.43	1.51
cg1650	<i>pctC</i>	ABC-type phosphate/phosphonate transporter, permease	E	0.54	-1.06	-1.04	-0.59	-2.05
cg1651	<i>pctB</i>	ABC-type phosphate/phosphonate transporter, ATPase subunit	P	-0.58	-0.12	-1.69	-1.47	-2.21
cg1656	<i>ndh</i>	NADH dehydrogenase	C	0.16	-0.34	-0.83	-1.13	-2.83
cg1658	-	Putative metabolite permease, MFS-type	G	-0.02	0.62	0.14	-0.48	-2.43
cg1660	-	Putative membrane protein	S	0.06	-2.01	-1.96	-1.97	-3.00
cg1661	-	Putative secondary arsenite transporter, arsenical resistance protein	P	-0.54	-1.41	-1.45	-1.53	-4.06
cg1665	-	Putative secreted protein	M	2.27	0.76	0.78	0.45	1.43
cg1669	-	Putative secreted protein	S	0.00	0.36	-0.01	0.09	-1.96
cg1670	-	Conserved hypothetical protein	-	-0.23	-0.07	-0.14	-0.27	-1.80
cg1677	-	Conserved hypothetical protein	-	-0.34	-0.66	-0.71	-0.86	-2.12
cg1679	-	Hypothetical protein	P	-0.43	0.79	-0.52	-1.67	-1.11
cg1682	-	Trypsin-like serine protease	O	-0.20	-0.65	-0.75	-0.81	-1.85
cg1694	-	putative CRISPR-associated ATP-dependent nuclease	L	-0.01	-0.23	-0.40	-0.61	-1.86
cg1695	-	putative antidote protein, HTH-motif XRE family	-	-0.08	1.01	1.98	2.57	-0.38
cg1698	<i>hisG</i>	ATP phosphoribosyltransferase	E	-0.05	-0.19	-0.64	-0.76	-2.66
cg1699	<i>hisE</i>	Phosphoribosyl-ATP pyrophosphatase	E	0.04	-0.11	-0.53	-0.53	-1.88
cg1701	<i>metH</i>	Methionine synthase	E	-0.11	-0.09	-0.24	-0.10	-1.95
cg1709	<i>mshC</i>	Putative 1-D-myo-inositol-2-amino-2-deoxy-alpha-D-glucopyranose 1-phosphatase	J	-0.31	0.04	-0.23	-0.06	-1.83
cg1710	<i>bacA</i>	Putative undecaprenol kinase	V	0.01	-1.17	-1.49	-2.12	-4.55
cg1712	<i>lppL</i>	Putative secreted lipoprotein	-	-0.07	0.61	0.48	0.16	-1.86
cg1713	<i>pyrD</i>	Dihydroorotate oxidase	F	-0.20	0.64	0.34	0.27	-1.71
cg1718	-	Phospholipid-binding protein	R	0.74	1.36	1.63	1.93	1.93
cg1719	<i>tetB</i>	ABC-type multidrug transport system, ATPase and permease	V	-0.35	-1.04	-1.03	-1.54	-2.42
cg1720	<i>tetA</i>	ABC-type multidrug transport system, ATPase and permease	V	-0.10	-0.76	-1.27	-1.31	-2.29
cg1727	-	Putative membrane protein	S	0.64	-0.49	-0.24	-1.38	-1.99
cg1733	-	Conserved hypothetical protein	-	0.07	-0.52	-0.63	-1.36	-1.74
cg1735	-	Secreted cell wall-associated hydrolase (invasion-associated)	M	-0.11	-0.19	-0.28	-0.50	-1.57
cg1736	-	Putative membrane protein	-	0.41	0.07	-0.45	-0.45	-1.79
cg1739	-	Conserved hypothetical protein, containing a glutamine amidase domain	F	-0.09	0.32	0.17	0.05	-1.92
cg1740	-	Putative nucleoside-diphosphate-sugar epimerase	I	0.14	1.06	1.06	1.43	1.90
cg1744	<i>pacL</i>	Putative cation transporting P-type ATPase	P	-0.32	2.18	2.29	2.67	3.18
cg1748	-	Putative secreted protein	-	-0.10	0.62	1.77	1.85	1.30
cg1753	-	ABC-type transporter, ATPase subunit with duplicated ATPase domains	R	-0.23	-0.51	-0.76	-0.54	-2.17
cg1759	-	Putative metal-sulfur cluster biosynthetic enzyme	R	-1.15	0.21	-0.08	0.27	-1.74
cg1760	<i>sufU</i>	Protein involved in Fe-S cluster formation, NifU-family	C	-0.99	0.09	-0.05	0.17	-1.68
cg1761	<i>sufS</i>	cysteine desulfurase	E	-1.32	-0.05	-0.20	-0.05	-2.73
cg1762	<i>sufC</i>	FeS cluster assembly ATPase, SufC-family	G	-1.37	-0.08	-0.28	-0.10	-2.83
cg1763	<i>sufD</i>	FeS cluster assembly protein, SufD-family	O	-1.47	-0.14	-0.32	0.02	-2.44
cg1764	<i>sufB</i>	FeS cluster assembly protein, SufB-family	O	-1.50	-0.20	-0.34	-0.03	-2.60
cg1765	<i>sufR</i>	Transcriptional repressor of suf operon	K	-1.49	-0.15	-0.33	-0.06	-2.57
cg1766	-	Putative membrane protein	-	-0.45	0.06	-0.29	-0.45	-2.26
cg1769	<i>ctaA</i>	Cytochrome oxidase assembly protein	O	0.41	1.64	3.19	3.35	1.42
cg1771	<i>qor2</i>	Putative NADPH:quinone reductase, zeta-crystallin	C	0.83	1.72	1.80	2.30	2.46
cg1773	<i>ctaB</i>	Polyprenyltransferase, cytochrome oxidase assembly factor	O	0.31	-0.15	2.13	2.28	0.14
cg1778	<i>zwf</i>	Glucose-6-phosphate 1-dehydrogenase	G	-0.12	-0.85	-0.99	-1.07	-1.60
cg1781	<i>'soxA</i>	Putative oxidase, pseudogene (C-terminal fragment)	E	-0.10	-1.83	-1.28	-0.85	-4.46
cg1782	<i>tnp13b(ISCg13)</i>	Transposase	-	-0.19	-0.87	-0.96	-1.11	-1.87
cg1783	<i>soxA'</i>	Putative oxidase, pseudogene (N-terminal fragment)	E	-0.04	1.00	1.93	2.95	-1.03
cg1787	<i>ppc</i>	Phosphoenolpyruvate carboxylase	C	0.25	1.09	1.09	1.32	2.44
cg1789	<i>tpi</i>	Triosephosphate isomerase	G	0.37	1.29	1.40	1.52	2.42
cg1790	<i>pgk</i>	3-Phosphoglycerate kinase	G	0.31	1.23	1.19	1.38	2.25
cg1791	<i>gap</i>	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)	G	0.27	1.09	0.97	1.27	2.59
cg1805	<i>priA</i>	Primosomal protein N' (replication factor Y), helicase superfamily I	L	0.15	0.68	0.18	-0.11	-2.29
cg1806	<i>metK</i>	Methionine adenosyltransferase	H	-0.10	-0.09	-0.27	-0.51	-2.98
cg1809	-	DNA-directed RNA polymerase subunit K/omega	K	0.07	-0.22	-0.37	-0.54	-1.58
cg1810	<i>gmk</i>	Guanylate kinase	F	0.36	0.22	-0.16	-0.63	-1.56
cg1824	<i>nusB</i>	Transcription termination factor	K	0.19	-0.32	-0.44	-0.77	-2.57
cg1825	<i>efp</i>	Elongation factor P (EF-P)	J	0.17	-0.25	-0.56	-0.79	-2.49
cg1826	<i>pepQ</i>	Putative Xaa-Pro aminopeptidase	E	0.50	0.25	-0.26	-0.38	-1.65
cg1827	<i>aroB</i>	3-Dehydroquinate synthase	E	-0.12	0.61	-0.11	-0.41	-2.92
cg1828	<i>aroK</i>	Shikimate kinase	E	0.14	0.20	-0.39	-0.91	-3.40
cg1829	<i>aroC</i>	Chorismate synthase	E	0.08	0.01	-0.55	-0.83	-3.20

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cg1832	-	ABC-type putative iron-siderophore transporter, substrate P		0.37	2.14	4.16	3.96	1.65
cg1833	-	ABC-type putative iron-siderophore transporter, ATPase s P		-0.15	1.36	3.21	3.19	0.70
cg1835	<i>aroE3</i>	Shikimate 5-dehydrogenase	E	-0.22	-1.06	-2.01	-2.75	-4.15
cg1836	-	Conserved hypothetical protein, secreted solute-binding p R		0.05	-0.91	-1.94	-2.06	-4.10
cg1837	-	Putative endonuclease involved in recombination	L	-0.14	-1.18	-1.97	-2.58	-4.04
cg1838	<i>alaS</i>	Alanyl-tRNA synthetase	J	0.06	0.09	-0.45	-0.55	-2.02
cg1841	<i>aspS</i>	Aspartyl-tRNA synthetase	J	0.18	0.08	-0.60	-0.73	-2.71
cg1842	-	Putative secreted metalloprotease	R	0.45	0.24	-0.29	-0.85	-2.40
cg1843	-	Superfamily II DNA/RNA helicase, SNF2 family	K	-0.21	-0.81	-0.69	-1.53	-2.17
cg1844	-	Putative membrane protein membrane protein	S	0.09	-0.49	-1.20	-1.65	-3.38
cg1845	-	Conserved hypothetical protein	E	0.46	-0.23	-0.80	-1.07	-2.50
cg1846	-	Putative transcriptional regulator, TetR-family	K	0.20	0.07	-0.23	-0.69	-2.37
cg1849	-	Conserved hypothetical protein	-	2.22	2.88	1.96	2.15	1.74
cg1855	<i>hisS</i>	Histidyl-tRNA synthetase	J	0.05	0.17	-0.26	-0.31	-2.15
cg1856	-	Putative Zn-dependent hydrolase	R	-0.16	0.01	-0.58	-0.30	-1.83
cg1857	<i>ppiB</i>	Peptidyl-prolyl cis-trans isomerase	O	0.10	-0.06	-0.70	-0.99	-2.72
cg1860	-	Putative membrane protein	-	-0.33	0.42	0.36	0.04	-1.54
cg1862	<i>apt</i>	Adenine phosphoribosyltransferase	F	-0.04	-0.60	-1.01	-1.24	-2.11
cg1864	<i>dciAE</i>	ABC-type putative dipeptide transporter, substrate-binding	E	-0.08	-0.25	-0.50	-1.01	-2.07
cg1865	<i>secF</i>	Preprotein translocase, SecF subunit	U	0.30	-0.57	-1.40	-2.06	-2.75
cg1867	<i>secD</i>	Preprotein translocase, SecD subunit	U	0.18	-0.81	-1.57	-2.36	-3.76
cg1873	<i>tesB2</i>	Acyl-CoA thioesterase II	I	0.32	-0.39	-0.61	-0.90	-1.85
cg1874	-	Putative membrane protein	-	0.26	2.22	2.37	2.06	1.75
cg1875	-	Putative membrane protein	-	-0.24	-0.47	-0.61	-0.98	-4.81
cg1876	-	Glycosyltransferase	M	-0.23	0.39	-0.20	-0.50	-2.57
cg1877	-	Lauroyl/myristoyl acyltransferase, lipid A biosynthesis	M	0.00	0.49	-0.05	-0.40	-2.27
cg1878	<i>pgsA1</i>	Putative CDP-diacylglycerol-glycerol-3-phosphate 3-phos	I	0.01	0.76	0.09	-0.05	-1.88
cg1879	-	Putative HIT family hydrolase	F	0.19	0.71	0.14	-0.04	-1.80
cg1881	-	Conserved putative secreted protein, iron-dependent perc	P	0.98	2.07	4.76	5.09	3.51
cg1883	-	Putative secreted protein	S	1.08	2.00	4.63	4.92	3.36
cg1884	-	Putative membrane protein	-	0.98	1.92	4.60	4.83	3.32
cg1891	-	Hypothetical protein	-	1.41	0.41	0.02	-0.59	-2.08
cg1893	-	Putative N-acetyltransferase	K	-0.02	-0.75	-0.92	-1.38	-3.05
cg1905	-	Hypothetical protein	-	0.75	1.18	1.42	2.03	2.10
cg1906	-	Hypothetical protein	-	0.52	1.15	1.47	1.98	1.83
cg1907	-	Putative phosphopantothencycysteine synthetase/decarb	H	0.17	1.09	1.39	2.02	1.64
cg1908	-	Hypothetical protein	-	0.19	0.89	1.19	1.70	1.18
cg1910	-	Putative secreted or membrane protein	-	0.31	0.10	-0.04	-0.58	-1.95
cg1911	-	Putative secreted protein	-	0.44	0.07	-0.10	-0.64	-1.86
cg1916	-	Hypothetical protein	-	0.08	0.02	-1.24	-1.22	-1.58
cg1920	-	Hypothetical protein	-	0.16	-1.16	-2.27	-1.09	-1.47
cg1921	-	Hypothetical protein	-	0.48	-2.06	-1.37	-2.35	-1.37
cg1924	-	Hypothetical protein	-	-0.43	-1.38	-1.69	-1.09	-1.11
cg1927	-	Putative molecular chaperon	-	-0.40	-0.15	-1.20	-1.54	-2.05
cg1939	-	Hypothetical protein	-	-0.88	-1.65	-1.95	-1.13	-3.96
cg1942	-	Putative secreted protein	-	1.53	0.66	0.69	1.15	1.62
cg1943	-	Hypothetical protein	-	1.34	0.71	0.72	1.21	1.58
cg1948	-	Hypothetical protein	-	-1.10	-2.06	-0.78	-0.03	-1.05
cg1956	<i>recJ</i>	Putative exonuclease, single-stranded-DNA-specific	L	0.41	0.83	0.53	1.57	1.73
cg1960	-	Hypothetical protein	-	0.09	0.12	-0.31	-0.68	-1.84
cg1961	-	Hypothetical protein	-	1.26	0.30	1.07	1.70	1.40
cg1962	-	Putative membrane protein	-	0.19	-0.21	-1.23	-0.83	-1.84
cg1963	-	Putative DNA/RNA helicase, superfamily II	K	-0.28	-1.09	-1.09	-1.69	-1.40
cg1975	-	Conserved hypothetical protein	-	0.00	1.31	1.67	0.93	1.05
cg1977	-	Putative secreted protein	-	0.70	0.02	-0.02	-0.59	-1.68
cg1982	-	Putative ATPase with chaperone activity, ATP-binding sut	O	0.22	-1.56	-0.40	-1.07	-0.76
cg1985	-	Putative DNA helicase, superfamily I	L	-0.08	-0.62	-0.51	-1.27	-1.73
cg1986	-	Hypothetical protein	-	-0.80	-2.18	-1.48	-1.47	-3.08
cg1996	<i>cgIIIM</i>	DNA (cytosine-5-)-methyltransferase	L	-0.05	-0.52	-1.05	-1.67	-4.11
cg1997	<i>cgIIIR</i>	Putative type II restriction endonuclease	-	-0.12	-0.66	-1.36	-1.92	-4.28
cg1998	<i>cgIIIR</i>	ATP-dependent helicase probaly involved in restriction an	-	-0.16	-0.56	-1.15	-1.56	-3.78
cg2001	-	Conserved hypothetical protein	-	0.28	2.56	2.55	2.11	2.49
cg2002	-	Hypothetical protein	-	-0.10	1.14	1.50	1.35	1.06
cg2023	-	Putative membrane protein	-	0.79	1.41	0.93	0.07	-1.54
cg2025	-	Hypothetical protein	-	0.28	-1.32	-1.32	-1.41	-2.63

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				②	③	④	⑤	⑥
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cg2035	-	Putative methyltransferase	-	-2.13	-1.03	-0.89	-1.38	-1.47
cg2036	-	Putative secreted protein	-	-0.50	-1.33	-1.11	-1.32	-2.42
cg2041	-	Hypothetical protein	-	0.61	0.01	0.15	-0.44	-1.65
cg2044	-	Putative secreted protein	-	-0.32	-0.13	-0.48	-0.44	-1.59
cg2045	-	Hypothetical protein	-	-0.78	-0.31	-0.32	-0.44	-2.20
cg2047	-	Putative secreted protein	-	-0.38	2.02	1.54	1.20	-1.18
cg2052	-	Putative secreted protein	-	1.02	1.24	1.63	1.81	1.35
cg2054	-	Putative membrane protein	-	-0.66	-0.43	0.11	-0.01	-1.97
cg2055	-	Putative membrane protein	-	-1.20	-0.51	-0.19	0.11	-2.28
cg2057	-	Putative secreted protein	-	0.72	1.79	1.87	2.12	1.44
cg2058	-	Hypothetical protein	-	0.21	1.73	1.71	2.12	0.88
cg2061	<i>psp3</i>	Putative secreted protein	M	1.01	3.09	2.99	2.93	1.01
cg2064	-	DNA topoisomerase	L	1.04	1.63	1.17	0.58	-0.34
cg2066	-	Hypothetical protein, low-complexity protein	S	-0.08	-0.21	-0.29	-0.50	-1.86
cg2070	<i>'int2</i>	Putative phage integrase (C-terminal fragment)	-	0.27	1.24	1.50	1.48	0.98
cg2071	<i>int2'</i>	Putative phage Integrase (N-terminal fragment)	L	0.44	1.21	1.39	1.52	1.06
cg2074	-	Hypothetical protein	-	2.31	2.35	1.86	1.52	1.63
cg2076	<i>ribD</i>	Putative riboflavin specific deaminase	H	0.55	1.60	1.71	1.81	1.91
cg2079	-	Conserved hypothetical protein, chlorite dismutase family	-	0.40	1.52	1.39	1.74	1.59
cg2087	-	Putative membrane protein	-	-0.03	0.51	0.10	0.23	-1.77
cg2089	-	Conserved hypothetical protein	-	0.30	-0.18	-0.52	-1.11	-3.02
cg2094	-	Hypothetical protein	-	0.25	0.85	1.28	1.60	2.44
cg2095	-	Putative membrane protein, yrkO-like	S	1.04	1.33	0.49	-0.16	-1.60
cg2096	-	Putative membrane protein	-	1.39	0.89	0.16	-0.52	-1.58
cg2102	<i>sigB</i>	RNA polymerase sigma factor rpoD (Sigma-A)	K	0.11	0.69	0.94	1.30	2.10
cg2111	<i>hrpA</i>	Putative ATP-dependent helicase	L	-0.15	-0.01	-0.59	-0.67	-1.58
cg2113	<i>divS</i>	cell wall hydrolase	D	0.28	-0.05	-0.46	-0.96	-1.83
cg2117	<i>ptsI</i>	Phosphotransferase system (PTS), Enzyme I	G	0.15	-1.28	-1.49	-1.55	-0.51
cg2124	-	Putative transcriptional regulator, AraC family	K	0.30	-0.03	-0.25	-0.53	-1.77
cg2125	<i>uraA</i>	Putative xanthine/uracil symporter, nucleobase:cation syn	F	-0.20	-0.60	-1.11	-1.36	-3.37
cg2128	-	Putative membrane protein	-	0.38	1.39	1.46	1.53	1.08
cg2129	<i>dapF</i>	Diaminopimelate epimerase	E	0.05	0.11	-0.48	-0.75	-2.69
cg2132	-	Conserved hypothetical protein	-	0.29	-0.10	-0.66	-0.77	-1.96
cg2133	-	Acetyltransferase, GNAT-family	K	0.00	0.39	-0.37	-0.28	-1.70
cg2135	<i>miaB</i>	tRNA methylthiotransferase	J	-0.06	-0.31	-0.71	-1.15	-3.91
cg2136	<i>gluA</i>	ABC-type glutamate transporter, ATPase subunit (TC 3.A	E	0.74	-1.64	-1.56	-1.44	-2.56
cg2137	<i>gluB</i>	ABC-type glutamate transporter, substrate-binding lipopro	E	0.60	-1.98	-1.97	-1.86	-3.47
cg2138	<i>gluC</i>	ABC-type glutamate transporter, permease subunit (TC 3.E	E	0.62	-2.01	-2.23	-2.40	-4.30
cg2139	<i>gluD</i>	ABC-type glutamate transporter, permease subunit (TC 3.E	E	1.04	-1.44	-1.37	-1.32	-3.44
cg2140	<i>recX</i>	Putative regulatory protein RecX	R	0.66	-0.51	-0.70	-1.56	-2.74
cg2141	<i>recA</i>	Recombinase A	L	0.05	-0.50	-0.82	-1.15	-2.36
cg2145	-	Conserved hypothetical protein	-	-0.01	-0.70	-0.79	-0.81	-1.98
cg2147	-	Membrane protein, BioY-family	R	0.05	-0.31	-0.33	3.85	2.23
cg2148	-	ABC-type putative cobalt transporter, ATPase subunit	G	0.27	0.41	0.26	2.87	1.26
cg2149	-	ABC-type putative cobalt transporter, permease subunit	P	0.21	0.62	0.56	2.99	1.72
cg2155	-	Conserved hypothetical protein	S	0.41	0.31	0.06	-0.41	-2.75
cg2156	-	Hypothetical protein	-	0.07	-0.30	-0.16	-0.93	-2.85
cg2157	<i>terC</i>	Putative integral membrane export protein, tellurium resis	P	-0.14	-0.44	-0.57	-0.85	-2.79
cg2166	<i>gpsI</i>	Polyribonucleotide nucleotidyltransferase	J	0.07	-0.23	-0.47	-0.61	-1.87
cg2167	<i>rpsO</i>	30S ribosomal protein S15	J	-0.04	-0.93	-1.15	-1.19	-4.45
cg2168	<i>iunH2</i>	Nucleoside hydrolase,inosine-uridine preferring	F	0.20	0.03	-0.78	-1.12	-2.38
cg2169	<i>ribF</i>	Riboflavin kinase / FMN adenyllyltransferase	H	-0.02	0.06	-0.43	-0.81	-2.76
cg2170	<i>truB</i>	Pseudouridylylate synthase	J	-0.33	0.03	-0.51	-0.70	-1.89
cg2173	<i>dinF</i>	Putative MATE multidrug efflux protein, multidrug/oligosac	V	0.09	-0.18	-0.42	-0.75	-1.83
cg2174	-	Exopolyphosphatase-related protein	R	0.18	0.23	-0.17	-0.51	-1.66
cg2178	<i>nusA</i>	Putative transcriptional termination/antitermination factor	K	-0.11	-0.96	-1.14	-1.38	-3.27
cg2179	-	Conserved hypothetical protein	S	-0.09	-0.22	-0.43	-0.63	-1.81
cg2180	-	Putative secreted protein	-	0.12	-0.16	-0.45	-0.27	-1.99
cg2181	-	ABC-type putative dipeptide/oligopeptide transporter, sub	E	0.28	-2.32	-2.36	-1.66	-5.48
cg2182	-	ABC-type putative dipeptide/oligopeptide transporter, perr	E	0.17	-2.07	-2.20	-1.85	-6.34
cg2183	-	ABC-type putative dipeptide/oligopeptide transporter, perr	E	0.26	-2.17	-1.98	-1.50	-5.49
cg2184	-	ABC-type putative dipeptide/oligopeptide transporter, ATFR	R	0.38	-2.12	-1.93	-1.69	-5.71
cg2185	<i>proS</i>	Prolyl-tRNA synthetase	J	0.62	0.47	-0.38	-1.01	-2.00
cg2186	-	Conserved hypothetical protein	S	0.08	-0.78	-1.15	-1.78	-3.09
cg2188	-	Mg-chelatase, subunit I	H	0.19	-0.27	-0.30	-0.36	-1.52

m-values

Locus	Feature	Product	COG	m-values				
				② vs. ①	③ vs. ①	④ vs. ①	⑤ vs. ①	⑥ vs. ①
cg2189	<i>cysG</i>	Putative uroporphyrinogen III synthase/methyltransferase	H	-0.11	0.04	-0.27	-0.73	-1.82
cg2191	-	Conserved hypothetical protein	S	-0.32	-1.78	-2.00	-2.50	-2.56
cg2198	<i>map2</i>	Methionine aminopeptidase	J	0.05	0.59	0.20	-0.18	-1.58
cg2200	-	Two-component system, transcriptional response regulatc	T	-0.22	-0.24	-0.61	-1.06	-2.69
cg2201	-	Two-component system, sensory histidine kinase	T	-0.24	-0.46	-1.00	-1.15	-2.51
cg2211	-	Putative membrane protein	-	0.41	1.46	1.40	1.57	-0.12
cg2214	-	Putative Fe-S-cluster redox enzyme	R	0.00	0.26	-0.09	-0.57	-1.66
cg2221	<i>tsf</i>	Translation elongation factor, EF-Ts	J	0.18	-0.15	-0.47	-0.71	-1.86
cg2222	<i>rpsB</i>	30S ribosomal protein S2	J	0.16	-0.70	-0.92	-1.05	-2.71
cg2223	-	Putative Secreted or membrane protein related to metallo M	M	-0.26	-2.38	-1.69	-2.09	-2.70
cg2226	-	Conserved hypothetical protein, Rossmann-fold nucleotid	L	-0.72	-1.50	-2.19	-0.79	-2.14
cg2230	<i>rmhB</i>	Ribonuclease HII	L	-0.27	-0.62	-0.88	-0.87	-2.09
cg2232	<i>lepB</i>	Signal peptidase I	U	0.02	-0.25	-0.71	-1.02	-2.87
cg2234	-	ABC-type putative iron(III) dicitrate transporter, substrate-	P	-0.12	-1.63	-4.90	-7.21	-7.23
cg2235	<i>rplS</i>	50S ribosomal protein L19	J	0.36	-0.62	-0.96	-1.16	-3.31
cg2238	<i>thiS</i>	Sulfur transfer protein involved in thiamine biosynthesis, T-	T	-0.46	0.22	-0.30	-0.37	-1.92
cg2240	<i>thiF</i>	Putative Dinucleotide-utilizing enzyme involved in thiamin	H	-0.30	0.36	-0.31	-0.49	-2.11
cg2241	<i>tex</i>	transcriptional accessory protein Tex	K	0.06	-0.82	-1.30	-1.76	-2.87
cg2242	-	Putative transcriptional regulator, Lacl-family	K	0.26	-0.61	-0.87	-0.94	-3.73
cg2249	<i>trmD</i>	tRNA (guanine-N1)-methyltransferase	J	0.11	0.00	-0.58	-0.70	-2.01
cg2250	-	Putative secreted protein	-	0.11	1.32	1.47	1.68	2.37
cg2251	<i>rimM</i>	Putative 16S rRNA processing protein, RimM-like	J	0.17	-0.01	-0.37	-0.88	-2.45
cg2253	<i>rpsP</i>	30S ribosomal protein S16	J	0.19	-0.99	-1.19	-1.38	-4.39
cg2257	<i>srp</i>	Putative signal recognition particle GTPase	U	0.02	-0.05	-0.49	-0.82	-1.87
cg2258	<i>glnD</i>	Putative protein PII uridylyltransferase	O	0.07	0.33	-0.29	-0.39	-2.28
cg2260	<i>glnK</i>	Nitrogen regulatory protein PII	E	0.13	0.22	0.10	0.05	-1.59
cg2261	<i>amtB</i>	Putative secondary ammonium transporter, Amt-family	P	-0.08	0.10	0.38	0.80	-3.00
cg2263	-	Hypothetical protein	-	-0.07	0.07	-0.36	-0.86	-1.84
cg2265	<i>smc</i>	Chromosome segregation ATPase	D	-0.24	-0.25	-0.78	-1.17	-2.68
cg2270	-	Conserved hypothetical protein	-	-0.17	0.18	-0.13	-0.17	-2.03
cg2271	-	Putative secondary Co2+/Zn2+/Cd2+ efflux transporter, c	P	-0.54	-0.04	-0.62	-0.74	-2.08
cg2272	<i>mutM1</i>	Formamidopyrimidine-DNA glycosylase	L	-0.19	-0.13	-0.68	-0.82	-1.86
cg2280	<i>gdh</i>	Glutamate dehydrogenase (NADP(+))	E	0.14	-0.21	-0.37	-0.29	-1.99
cg2290	-	Predicted ring-cleavage extradiol dioxygenase	R	-0.54	-1.18	-1.11	-0.76	-1.84
cg2293	-	protein similar to indole-3-glycerol phosphate synthases	E	-0.23	-0.46	-0.74	-0.86	-2.32
cg2294	-	Putative membrane protein	-	-0.28	0.16	-0.25	-0.48	-1.80
cg2298	<i>impA</i>	Putative inositol-phosphate phosphatase	G	-0.15	0.03	-0.34	-0.58	-1.99
cg2299	<i>hisA</i>	1-(5-phosphoribosyl)-5-[(5- phosphoribosylamino)methyl]c	E	0.08	0.35	-0.13	-0.34	-1.54
cg2300	<i>hisH</i>	Imidazole glycerol phosphate synthase subunit HisH	E	0.03	-0.01	-0.35	-0.68	-2.02
cg2301	-	Putative antibiotic efflux permease, MFS-type	G	-0.12	-0.31	-0.72	-0.79	-2.23
cg2307	-	Putative membrane protein	-	-0.22	-0.98	-1.71	-1.99	-2.67
cg2308	-	Putative secreted protein	-	0.16	-0.46	-1.09	-1.28	-2.11
cg2310	<i>glgX</i>	Glycogen debranching protein	G	0.14	-0.56	-1.03	-1.57	-3.09
cg2311	-	Putative SAM-dependent methyltransferase	H	-0.04	-0.88	-1.19	-1.92	-3.41
cg2315	-	ABC-type putative iron(III) dicitrate transporter, ATPase s	E	0.14	0.12	-0.70	-1.10	-2.09
cg2317	-	ABC-type putative iron(III) dicitrate transporter, permease P	P	-0.34	-0.45	-0.85	-1.16	-2.21
cg2318	-	ABC-type putative iron(III) dicitrate transporter, substrate-	P	-0.87	-0.96	-1.44	-1.48	-2.13
cg2320	-	Putative transcriptional regulator, ArsR-family	K	-0.99	-1.86	-2.68	-2.61	-3.60
cg2325	-	Hypothetical protein	-	-0.04	-0.26	-0.46	-0.83	-1.68
cg2334	<i>ilvA</i>	Threonine ammonia-lyase	E	0.01	-0.04	-0.52	-0.90	-2.51
cg2336	-	Putative secreted protein	-	-0.07	-1.44	-2.62	-3.67	-5.53
cg2338	<i>dnaE1</i>	DNA-directed DNA polymerase, polymerase III, alpha cha	L	-0.16	0.18	-0.16	-0.66	-1.87
cg2339	-	Putative secondary chloramphenicol transporter, drug/me	R	-0.83	-0.59	-1.13	-1.19	-2.53
cg2343	-	Putative decarboxylase	S	-0.30	-0.19	-0.49	-0.88	-1.59
cg2344	-	Cystathionine beta-synthase-like protein	E	-0.38	-0.76	-0.87	-1.63	-2.26
cg2345	-	Putative secreted protein	-	0.06	0.13	-0.24	-0.39	-1.97
cg2346	<i>rluD</i>	Pseudouridylate synthase	J	0.16	0.15	-0.05	-0.24	-1.89
cg2347	<i>lspA</i>	Signal peptidase II	M	-0.07	-0.11	-0.43	-0.48	-2.62
cg2348	-	Putative secreted protein	-	-0.50	-0.50	-1.32	-1.58	-3.58
cg2349	-	ABC-type putative antibiotic transporter, ATPase subunit	R	-0.85	-0.97	-1.28	-1.41	-2.48
cg2350	-	Conserved hypothetical protein	-	0.06	0.47	0.09	-0.41	-1.84
cg2352	<i>ansA</i>	Asparaginase	E	0.07	0.04	-0.38	-0.77	-2.03
cg2353	-	Hypothetical protein disrupted by insertion of ISCg2e	-	-0.65	-0.47	-0.99	-1.74	-2.13
cg2354	<i>tnp2e(ISCg2e)</i>	Transposase	L	-0.50	-0.37	-0.37	-0.88	-1.78
cg2356	-	Putative secondary drug/metabolite transporter, drug/met	R	0.02	0.05	-0.04	-1.02	-2.20

					m-values				
Locus	Feature	Product	COG	②	③	④	⑤	⑥	
				vs. ①	vs. ①	vs. ①	vs. ①	vs. ①	
cg2359	<i>ileS</i>	Isoleucine--tRNA ligase	J	-0.01	0.13	-0.61	-0.28	-2.18	
cg2360	-	Putative membrane protein	-	0.01	0.31	-0.34	-0.93	-1.53	
cg2367	<i>ftsQ</i>	Cell division septal protein	M	-0.09	-0.01	-0.31	-0.41	-1.91	
cg2370	<i>ftsW</i>	Bacterial cell division membrane protein	D	-0.15	0.02	-0.24	-0.53	-1.58	
cg2371	<i>murD</i>	UDP-N-acetylmuramoylalanine--D-glutamate ligase	M	0.07	-0.19	-0.61	-0.77	-2.46	
cg2372	<i>mraY</i>	Phospho-N-acetylmuramoyl-pentapeptide-transferase	M	0.04	-0.06	-0.45	-0.54	-1.75	
cg2373	<i>murF</i>	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase	M	-0.18	-0.36	-0.61	-0.94	-2.61	
cg2374	<i>murE</i>	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminop	M	-0.18	-0.40	-0.59	-0.83	-2.54	
cg2377	<i>mraW</i>	S-adenosylmethionine-dependent methyltransferase invol	M	-0.51	-0.25	-0.53	-0.51	-1.77	
cg2383	<i>metF</i>	5,10-Methylenetetrahydrofolate reductase (NAD(P)H)	E	-0.10	-0.78	-1.12	-1.64	-4.01	
cg2386	-	Conserved hypothetical protein	-	0.12	-0.01	-0.73	-0.99	-2.43	
cg2388	<i>pknL</i>	Putative serine/threonine protein kinase	R	-0.05	-0.18	-0.56	-1.00	-2.14	
cg2389	-	Putative membrane protein	-	-0.48	-0.42	-0.83	-1.47	-3.16	
cg2390	-	Putative membrane protein	-	-0.61	-1.71	-1.88	-2.82	-3.86	
cg2391	<i>aroG</i>	3-Deoxy-7-phosphoheptulonate synthase	-	0.31	-0.07	-0.64	-1.12	-3.63	
cg2394	<i>cmt4</i>	Corynomycolyl transferase	R	-0.28	0.00	-0.50	-1.11	-2.94	
cg2395	-	Putative secreted or membrane protein	-	-0.15	-0.34	-0.26	-0.03	-2.13	
cg2397	-	Putative membrane protein	I	-0.29	-0.63	-0.89	-1.51	-3.41	
cg2399	<i>glk</i>	Glucokinase	K	0.11	-0.16	-0.63	-1.24	-2.99	
cg2400	-	Putative glycosyltransferase	M	-0.12	0.10	-0.18	-0.50	-1.59	
cg2401	-	Secreted protein NLP/P60 family, putative peptidoglycan	IM	-0.28	-0.43	-0.73	-1.36	-3.14	
cg2402	-	Secreted protein NLP/P60 family	M	-0.81	-1.43	-1.49	-2.04	-3.67	
cg2403	<i>qcrB</i>	Cytochrome b	C	0.31	1.55	0.51	0.55	-2.13	
cg2404	<i>qcrA1</i>	Rieske iron-sulfur protein	C	0.22	1.48	0.29	0.41	-2.33	
cg2405	<i>qcrC</i>	Cytochrome c1	C	0.33	1.54	0.46	0.49	-2.17	
cg2406	<i>ctaE</i>	Cytochrome c oxidase subunit 3	C	0.35	1.48	0.43	0.42	-2.23	
cg2408	<i>ctaF</i>	Conserved putative membrane protein	-	0.41	1.59	1.59	1.45	-2.01	
cg2409	<i>ctaC</i>	Cytochrome c oxidase subunit II	C	0.48	1.57	1.51	1.45	-2.00	
cg2410	<i>ltsA</i>	Asparagine synthase (glutamine-hydrolyzing)	E	0.19	0.07	-0.50	-0.66	-2.81	
cg2412	-	Conserved putative membrane protein	-	0.07	0.09	-0.03	-0.15	-1.68	
cg2413	<i>cobU</i>	Putative Adenosylcobinamide kinase/cobinamide phospho	H	0.27	0.06	-0.17	-0.39	-2.65	
cg2414	<i>cobT</i>	Nicotinate-nucleotide--dimethylbenzimidazole phosphorib	H	0.18	0.35	-0.13	-0.06	-1.53	
cg2415	<i>cobS</i>	Adenosylcobinamide-GDP ribazoletransferase	H	0.19	0.27	-0.44	-0.54	-2.24	
cg2419	<i>pepB</i>	Leucyl aminopeptidase	E	0.51	1.56	1.50	1.87	1.05	
cg2425	-	Putative permease	R	0.78	2.89	2.83	3.14	3.05	
cg2426	<i>tnp2d(ISCg2d)</i>	Transposase	L	-0.73	-0.32	-0.36	-0.62	-1.56	
cg2429	<i>glnA</i>	Glutamate--ammonia ligase	E	-0.13	0.47	0.05	0.64	-1.97	
cg2430	-	Hypothetical protein	-	0.31	-0.52	-0.92	-1.01	-2.81	
cg2432	-	Conserved hypothetical protein, MUTT/NUDIX-family	L	0.21	1.31	1.27	1.27	1.51	
cg2437	<i>thrC</i>	Threonine synthase	E	-0.03	0.28	-0.38	-0.45	-2.06	
cg2438	-	Hypothetical protein	-	-0.32	-3.69	-3.78	-3.27	-4.81	
cg2440	-	Putative sugar/metabolite permease, MFS-type	G	-0.03	-0.19	-0.85	-1.75	-3.81	
cg2441	-	Permease of the major facilitator superfamily, N-terminal	IG	-0.34	0.21	-0.83	-1.10	-3.10	
cg2445	<i>hmuO</i>	Heme oxygenase (decyclizing)	-	-0.42	-1.62	-1.75	-1.94	-2.90	
cg2451	-	Conserved hypothetical protein	-	0.78	1.91	1.87	1.85	2.22	
cg2452	<i>galK</i>	Galactokinase	G	0.02	0.75	0.45	-0.06	-1.54	
cg2461	<i>tnp4a(ISCg4a)</i>	Transposase	L	-1.19	-0.45	-2.13	-1.85	-1.88	
cg2464	-	Conserved hypothetical protein	-	0.37	-0.01	-0.28	-0.33	-1.98	
cg2467	-	ABC-type transporter, ATPase subunit	E	0.23	-1.86	-2.62	-2.33	-3.99	
cg2468	-	ABC-type transporter, permease subunit	G	0.31	-2.14	-2.55	-2.30	-4.08	
cg2470	-	ABC-type transporter, substrate-binding lipoprotein	G	0.32	-1.93	-2.48	-2.23	-3.56	
cg2478	-	Putative penicillin binding protein	M	0.22	0.36	0.24	-0.12	-1.64	
cg2482	-	Hypothetical protein	-	-0.55	-0.29	-0.64	-1.12	-1.56	
cg2483	-	Hypothetical protein	-	-1.53	-1.32	-1.33	-2.78	-4.22	
cg2492	<i>glmS</i>	Glutamine--fructose-6-phosphate transaminase (isomerizi	M	0.05	-0.29	-0.67	-1.16	-2.80	
cg2500	-	Putative transcriptional regulator, ArsR-family	K	0.23	1.18	1.14	1.55	2.88	
cg2502	<i>fur</i>	Putative transcriptional regulator, FUR-family	P	0.02	0.83	0.89	0.97	1.64	
cg2507	-	Putative membrane protein	S	0.23	0.48	-0.57	-0.35	-1.69	
cg2508	<i>uppS2</i>	Di-trans,poly-cis-decaprenylcistransferase	I	0.10	0.04	-0.56	-0.83	-1.88	
cg2511	-	Putative membrane protein containing CBS domain	R	-0.18	-0.03	-0.62	-0.99	-1.76	
cg2524	-	ABC-type putative multidrug transporter, ATPase and me	V	0.04	0.08	-0.25	-0.33	-1.72	
cg2528	-	Putative carboxylesterase, lipase-family	I	0.09	-0.39	-0.82	-1.10	-2.51	
cg2533	-	Conserved hypothetical protein	-	0.48	-0.58	-1.02	-1.69	-2.83	
cg2534	-	Putative secreted protein	-	-0.33	-0.68	-1.60	-1.84	-3.67	
cg2539	<i>ectP</i>	Putative secondary glycine betaine/choline transporter, be	M	0.07	-0.88	-1.24	-1.71	-3.16	

Locus	Feature	Product	COG	m-values				
				②	③	④	⑤	⑥
				vs. ①	vs. ①	vs. ①	vs. ①	vs. ①
cg2542	-	Putative secondary malonate transporter, auxin efflux carrier	R	0.24	0.13	-0.49	-0.70	-1.55
cg2543	<i>gldD</i>	Putative (S)-2-hydroxy-acid oxidase	C	0.83	1.06	0.42	1.10	1.52
cg2545	-	Putative secreted or membrane protein	-	-0.26	-0.40	-1.14	-2.04	-3.65
cg2546	-	Putative secondary C4-dicarboxylate transporter, tripartite	G	0.09	-0.54	-1.80	-1.15	-3.83
cg2549	-	ABC-type putative dipeptide/oligopeptide transporter, subunit	E	-0.09	-0.81	-1.44	-1.61	-3.81
cg2550	-	ABC-type putative dipeptide/oligopeptide transporter, periplasmic	E	-0.10	-0.79	-1.33	-1.49	-3.08
cg2551	-	ABC-type putative dipeptide/oligopeptide transporter, periplasmic	E	-0.18	-0.33	-0.87	-1.81	-4.34
cg2552	-	ABC-type putative dipeptide/oligopeptide transporter, ATP-binding	R	-0.43	-0.53	-1.56	-1.82	-3.94
cg2554	<i>rbsK2</i>	Ribokinase	G	0.44	1.51	1.82	2.13	2.18
cg2556	-	Putative integral membrane protein	S	-0.03	0.23	1.77	1.27	-0.13
cg2557	-	Putative secondary Na ⁺ /bile acid symporter, bile acid:Na ⁺	R	0.28	-1.64	-2.78	-4.23	-4.63
cg2559	<i>aceB</i>	Malate synthase	C	0.06	-2.96	-2.16	-1.94	-5.48
cg2560	<i>aceA</i>	Isocitrate lyase	C	0.21	-1.87	-0.60	-0.15	-5.25
cg2561	<i>thiX</i>	Secreted protein, involved into thiamine biosynthesis	-	0.30	2.13	1.63	1.30	-0.05
cg2571	<i>lepA</i>	Membrane GTPase, LepA-like	M	-0.02	-0.29	-0.70	-0.94	-2.27
cg2573	<i>rpsT</i>	30S ribosomal protein S20	-	0.22	-0.85	-1.11	-1.31	-4.24
cg2574	-	Putative threonine efflux transporter, resistance to homoserine	E	-0.11	-0.12	-0.44	-0.78	-1.91
cg2576	-	DNA-directed DNA polymerase, polymerase III delta subunit	L	-0.22	0.18	-0.23	-0.36	-1.65
cg2577	-	Putative membrane protein Com family	R	1.02	-0.06	-0.05	-1.89	-1.77
cg2578	-	Secreted protein, DNA-binding	L	-0.48	-1.42	-1.44	-1.97	-2.62
cg2579	-	Conserved hypothetical protein, DegV-family	S	-0.21	-0.68	-1.07	-1.44	-2.55
cg2581	-	Putative fructose-2,6-bisphosphatase	G	0.04	-0.63	-1.27	-1.54	-3.23
cg2582	-	Conserved hypothetical protein	S	0.03	-0.85	-1.39	-1.66	-3.88
cg2583	-	Hypothetical protein	-	0.20	-0.80	-1.25	-1.47	-3.44
cg2584	<i>nadD</i>	Nicotinate-nucleotide adenyltransferase	H	-0.06	-0.86	-1.42	-2.03	-4.12
cg2590	-	Putative xanthine/uracil symporter, nucleobase:cation symporter	F	0.06	-0.12	-0.39	-0.60	-2.42
cg2592	-	Hypothetical protein	-	-0.17	0.21	0.02	-0.23	-1.79
cg2594	<i>rpmA</i>	50S ribosomal protein L27	J	0.27	-0.47	-0.78	-1.09	-3.67
cg2595	<i>rplU</i>	50S ribosomal protein L21	J	0.30	-0.63	-0.97	-1.25	-4.11
cg2603	<i>ndk</i>	Nucleoside-diphosphate kinase	F	0.31	0.25	-0.24	-0.69	-2.24
cg2606	-	Conserved hypothetical protein	-	0.13	0.06	-0.52	-1.31	-3.17
cg2607	-	Putative membrane protein	-	-0.19	-0.21	-0.32	-0.86	-2.44
cg2608	<i>folC</i>	Tetrahydrofolylpolyglutamate synthase	H	0.07	0.01	-0.63	-0.91	-2.69
cg2609	<i>valS</i>	Valyl-tRNA synthetase	J	0.12	0.15	-0.42	-0.59	-2.17
cg2610	-	ABC-type putative dipeptide/oligopeptide transporter, subunit	E	0.32	-6.47	-6.07	-5.41	-6.44
cg2612	-	Conserved hypothetical protein, lysine decarboxylase family	R	0.46	2.32	2.11	2.33	2.30
cg2613	<i>mdh</i>	Malate dehydrogenase	C	0.65	3.20	3.18	3.44	3.55
cg2616	<i>vanA</i>	Vanillate monoxygenase	P	0.50	-1.65	-5.12	-2.78	-5.13
cg2617	<i>vanB</i>	Vanillate O-demethylase oxidoreductase	C	-0.06	-0.61	-1.32	-1.43	-5.83
cg2618	<i>vanK</i>	MFS-type vanillate permease	G	-0.05	-0.42	-0.95	-1.40	-4.58
cg2628	<i>pcaC</i>	Putative 4-carboxymuconolactone decarboxylase	S	0.01	-1.13	-0.48	-0.17	-1.57
cg2630	<i>pcaG</i>	Protocatechuate 3,4-dioxygenase, alpha subunit	Q	-0.14	-1.65	-0.61	-0.32	-0.95
cg2631	<i>pcaH</i>	Protocatechuate 3,4-dioxygenase, beta subunit	Q	0.24	-2.01	-0.35	0.28	-0.74
cg2636	<i>catA</i>	Catechol 1,2-dioxygenase	Q	-0.19	-4.78	-4.42	-3.27	-2.60
cg2640	<i>benD</i>	Putative 1,6-dihydroxycyclohexa-2,4-diene-1-carboxylate	I	0.14	-1.15	-0.84	-0.96	-2.20
cg2643	<i>benE</i>	Putative secondary benzoate symporter, benzoate:H ⁺ symporter	F	-0.90	-1.03	-1.75	-1.38	-1.17
cg2647	<i>tig</i>	Putative Trigger factor, involved in cell division	O	-0.01	-0.49	-1.30	-1.69	-5.61
cg2648	-	Putative transcriptional regulator, ArsR-family	K	-0.23	-2.85	-1.83	-2.27	-2.94
cg2649	-	Beta-lactamase precursor	V	-0.93	-2.00	-1.92	-1.83	-4.31
cg2650	-	Putative membrane protein	-	1.26	-1.28	0.41	-0.07	-3.18
cg2651	-	Conserved hypothetical protein, putative pseudogen	-	-0.34	-1.50	-1.62	-2.03	-3.66
cg2664	-	Putative type IV restriction endonuclease	V	-0.60	-1.03	-1.33	-1.08	-3.10
cg2672	<i>crtB</i>	Geranylgeranyl-diphosphate geranylgeranyltransferase	I	-0.05	-0.17	-0.35	-0.40	-2.18
cg2673	-	Putative multidrug efflux permease, MFS-type	G	0.10	0.02	-0.06	-0.54	-1.65
cg2675	-	ABC-type putative dipeptide/oligopeptide transporter, ATP-binding	R	-0.07	0.61	0.10	0.49	-2.27
cg2676	-	ABC-type putative dipeptide/oligopeptide transporter, periplasmic	E	0.02	0.27	-0.17	0.38	-3.55
cg2677	-	ABC-type putative dipeptide/oligopeptide transporter, periplasmic	E	0.08	0.24	0.06	0.40	-3.74
cg2678	-	ABC-type putative dipeptide/oligopeptide transporter, subunit	E	0.22	0.67	0.05	0.64	-2.82
cg2684	-	Conserved hypothetical membrane protein, DedA-family	S	0.51	-0.11	-1.41	-2.97	-5.39
cg2685	-	Putative short-chain dehydrogenase/reductase	I	0.37	0.92	0.46	1.08	1.93
cg2687	<i>metB</i>	Cystathionine gamma-synthase	E	0.15	0.38	0.02	0.48	-2.19
cg2688	-	ABC-type putative molybdenum transporter, substrate-binding	E	0.33	-0.45	-1.33	-1.88	-3.99
cg2691	-	Conserved hypothetical protein	-	0.07	0.35	-0.14	-0.49	-2.54
cg2692	-	Putative thioesterase	R	0.20	0.38	-0.10	-0.45	-1.74
cg2693	-	Conserved hypothetical protein	R	-0.79	-0.70	-1.62	-2.53	-2.85

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				②	③	④	⑤	⑥
				vs. ①	vs. ①	vs. ①	vs. ①	vs. ①
cg2694	-	Hypothetical protein	-	-1.69	1.00	-0.78	-1.13	-2.37
cg2699	-	Conserved putative membrane protein	S	0.22	1.74	3.03	2.86	1.29
cg2703	-	ABC-type putative sugar transporter, permease subunit	G	0.09	-1.65	-2.04	-1.65	-2.16
cg2704	-	ABC-type putative sugar transporter, permease subunit	G	0.04	-1.81	-2.29	-1.94	-2.44
cg2705	amyE	ABC-type putative sugar transporter, substrate-binding lip	G	0.08	-2.00	-2.25	-1.91	-2.61
cg2707	-	Conserved hypothetical protein	-	-0.01	-1.74	-1.71	-1.19	-1.39
cg2708	msiK1	ABC-type putative sugar transporter, ATPase subunit	E	0.14	-1.45	-1.58	-0.99	-1.08
cg2709	-	Putative polyprenol phosphate mannosyl transferase, put	M	-1.15	-1.33	-2.90	-2.04	-3.65
cg2712	-	Putative transcriptional regulator, AraC-family - putative p	K	-0.20	-1.13	-1.44	-1.37	-1.98
cg2713	dhaS	Aldehyde dehydrogenase (NAD(+)) -putative pseudogene	C	-0.62	-1.52	-1.16	-1.07	-2.10
cg2719	-	Putative enterochelin esterase	R	-0.33	-2.60	-3.67	-4.46	-5.87
cg2722	-	Hypothetical protein, contains ankyrin-repeat	-	-0.25	-1.29	-1.14	-2.03	-3.57
cg2726	-	Putative membrane protein	-	-1.69	-1.48	-3.37	-1.48	-2.64
cg2730	-	Putative transcriptional regulator, LacI-family, putative ps	K	-0.23	-1.32	-2.95	-1.93	-1.37
cg2739	-	Putative multidrug efflux permease, MFS-type	G	0.23	0.06	-0.57	-1.34	-3.46
cg2740	-	Putative membrane protein	-	-1.14	-0.39	-0.89	-1.12	-2.37
cg2743	fas-IA	Fatty acid synthase, type I	O	0.21	-1.00	-1.06	-0.94	-1.90
cg2746	-	Putative transcriptional regulator	T	-0.11	-2.44	-2.58	-2.68	-3.46
cg2747	-	Putative secreted peptidase, M23/M37-family	M	-2.03	-2.46	-2.74	-3.87	-5.04
cg2748	-	Conserved putative membrane protein	K	-0.17	1.71	1.64	1.58	1.08
cg2750	-	Conserved putative membrane protein	-	0.17	1.61	3.08	3.15	2.47
cg2751	-	Xanthosine triphosphate pyrophosphatase	F	-0.09	-0.07	-0.59	-1.34	-3.29
cg2753	rph	tRNA nucleotidyltransferase	J	0.03	-0.29	-0.80	-1.54	-2.79
cg2755	-	Conserved hypothetical protein	-	-0.59	-1.28	-0.59	-0.16	-2.60
cg2756	-	Conserved hypothetical protein	-	-0.72	-0.90	-0.75	-1.19	-1.83
cg2761	-	Metal-dependent hydrolase of the beta-lactamase superfa	R	0.77	1.16	0.62	-0.26	-1.70
cg2773	-	Hypothetical protein, with SCP/PR1 domain	S	-0.16	-0.36	-0.74	-1.03	-2.86
cg2774	-	Nicotinic acid phosphoribosyltransferase	H	-0.26	-0.73	-1.19	-1.51	-2.15
cg2775	-	Hypothetical protein	-	-0.68	-1.24	-1.39	-2.08	-2.74
cg2776	dinG	Putative ATP-dependent DNA helicase protein	L	0.15	0.28	-0.10	-0.43	-1.67
cg2777	-	Conserved putative membrane protein	-	0.62	-0.12	-0.66	-1.46	-2.64
cg2778	-	Conserved hypothetical protein	-	0.06	-0.32	-0.80	-1.13	-2.95
cg2779	serB	Phosphoserine phosphatase	P	0.25	0.07	-0.31	-0.55	-1.99
cg2780	ctaD	Cytochrome C oxidase	C	0.40	1.52	1.38	1.63	-0.75
cg2782	ftn	Ferritin-like protein	P	0.23	1.84	2.69	3.59	3.65
cg2784	-	Putative transcriptional regulator, DtxR-family	K	-0.20	-1.74	-2.78	-2.76	-1.20
cg2786	nrpE	Ribonucleoside-diphosphate reductase, alpha chain	F	-0.19	-0.35	-1.14	-1.59	-2.63
cg2787	nrpI	Conserved hypothetical protein, flavodoxin-like protein Nr	F	-0.51	-0.79	-1.39	-1.83	-2.17
cg2789	mxr2	mycoredoxin 2	O	-0.08	-0.34	-1.17	-1.62	-1.46
cg2791	rpmJ	50S ribosomal protein L36	-	-0.01	-0.78	-1.03	-1.30	-3.72
cg2793	-	Conserved hypothetical protein	G	0.41	1.89	1.96	2.13	1.90
cg2794	-	Conserved hypothetical protein	R	0.27	1.77	1.69	1.98	1.84
cg2796	-	Conserved hypothetical protein, MMGE/PRPD-family, put	R	-1.20	0.47	-1.86	-2.95	-2.03
cg2797	-	Conserved hypothetical protein	S	-0.55	-0.19	-0.87	-1.91	-2.20
cg2801	crcB'	Putative membrane protein, CrcB-like protein, putative ps	-	0.15	0.12	-0.27	-0.21	-1.58
cg2802	'crcB	Putative membrane protein, CrcB-like protein, putative ps	-	-1.06	-0.41	-1.45	-1.66	-3.27
cg2806	-	Putative membrane protein	-	0.45	-0.46	-0.63	-0.95	-2.36
cg2807	tnp11a(ISCg11	Transposase, putative pseudogene	L	-1.16	-1.01	-3.12	-1.52	-2.13
cg2810	-	Putative secondary H+/Na+:glutamate/dicarboxylate sym	C	0.35	1.69	1.22	1.20	-0.44
cg2811	-	ABC-type lipoprotein release transporter, permease subun	V	0.79	1.15	0.59	-0.07	-1.75
cg2831	ramA	Putative transcriptional regulator, LuxR-family, Nif-specific	K	0.15	0.83	0.57	0.52	-1.91
cg2833	cysK	Cysteine synthase	E	0.22	0.91	0.12	1.04	-2.65
cg2834	cysE	Serine O-acetyltransferase	E	0.11	0.01	-0.42	-0.97	-2.54
cg2835	-	Putative acetyltransferase	-	0.07	1.21	1.40	1.20	1.80
cg2836	sucD	Succinate--CoA ligase (ADP-forming), alpha subunit	C	0.04	-5.49	-4.84	-4.80	-4.32
cg2837	sucC	Succinate--CoA ligase (ADP-forming), beta subunit	C	0.01	-5.14	-5.38	-5.36	-4.37
cg2838	-	Putative dithiol-disulfide isomerase	Q	-0.26	1.38	1.38	0.59	1.71
cg2841	-	Dihydrouridine synthase-like protein, contains TIM-barrel	J	-0.02	0.45	-0.03	-0.17	-2.03
cg2843	pstB	ABC-type putative phosphate transporter, ATPase subuni	P	0.70	1.76	1.14	0.98	-0.77
cg2844	pstA	ABC-type putative phosphate transporter, permease subu	P	0.43	1.91	1.25	1.10	-0.54
cg2845	pstC	ABC-type putative phosphate transporter, permease subu	P	0.67	2.15	1.69	1.10	-0.32
cg2846	pstS	ABC-type putative phosphate transporter, substrate-bindin	P	0.16	1.99	1.55	1.25	0.25
cg2847	mshD	Putative 1-D-myo-inositol-2-(L-cysteinyl)amido-2-deoxy-al	R	0.19	1.26	1.23	1.24	1.60
cg2857	purF	Amidophosphoribosyltransferase	F	-0.33	0.09	-0.40	-0.73	-3.39
cg2859	-	Conserved hypothetical protein	-	-0.01	-0.54	-0.63	-1.44	-2.40

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				②	③	④	⑤	⑥
				vs. ①	vs. ①	vs. ①	vs. ①	vs. ①
cg2860	-	Putative acyl-CoA thioester hydrolase-related protein	I	0.23	0.07	-0.27	-0.60	-2.17
cg2862	<i>purL</i>	Phosphoribosylformylglycinamide synthase subunit	F	0.10	0.35	-0.51	-0.72	-2.39
cg2863	<i>purQ</i>	Phosphoribosylformylglycinamide synthase subunit	F	0.07	0.33	-0.38	-0.62	-1.98
cg2870	<i>dctA</i>	Putative secondary H+/Na+:C4-dicarboxylate symporter, (C	C	-0.31	-2.05	-3.02	-4.18	-5.58
cg2873	<i>ptrB</i>	Oligopeptidase B	E	0.37	0.05	-0.36	-1.12	-2.83
cg2874	<i>purC</i>	Phosphoribosylaminoimidazolesuccinocarboxamide synth	F	-0.10	-0.61	-1.15	-2.11	-4.89
cg2875	-	Hypothetical protein	-	-1.21	-2.39	-3.09	-3.85	-3.75
cg2878	<i>purD</i>	Phosphoribosylamine--glycine ligase	F	0.12	-0.35	-1.00	-1.59	-3.81
cg2886	<i>bioD</i>	Dethiobiotin synthase	H	0.07	-0.15	-0.04	3.26	3.76
cg2889	-	Putative transcriptional regulator, MerR family	K	0.28	1.66	1.18	0.90	0.54
cg2893	-	Putative multidrug efflux permease, MFS-type	G	0.31	-0.17	-0.28	-0.75	-2.03
cg2895	-	Putative multidrug efflux permease, MFS-type	R	0.47	0.15	-0.26	-0.60	-1.57
cg2896	-	Putative secreted protein, hypothetical endoglucanase	-	0.88	1.68	1.37	1.38	0.03
cg2901	-	Putative poly(3-hydroxyalkanoate) depolymerase	R	0.54	0.34	0.09	-0.79	-1.90
cg2907	<i>otsA</i>	Trehalose-6-phosphate synthase	G	-0.34	-0.07	-0.27	-0.41	-1.65
cg2908	-	Putative membrane protein	-	-0.33	-0.15	-0.14	-0.79	-1.97
cg2911	-	ABC-type putative Mn/Zn transporter, substrate-binding lip	P	0.77	7.82	7.48	7.21	5.93
cg2912	-	ABC-type putative Mn/Zn transporter, ATPase subunit	G	0.49	5.50	5.24	4.90	3.44
cg2913	-	ABC-type putative Mn/Zn transporter, permease subunit	P	0.47	5.63	5.28	4.93	3.57
cg2914	<i>tnp5b(ISCg5b)</i>	Transposase	-	-0.45	0.21	-0.43	-0.79	-1.68
cg2915	-	Hypothetical protein	L	-1.10	-1.06	0.37	-0.93	-2.96
cg2921	-	Putative metabolite permease, MFS-type	G	1.34	-1.87	-1.17	-0.57	-3.18
cg2922	-	Putative transcriptional regulator, lclR-family	K	-0.21	-0.69	-1.07	-1.08	-1.98
cg2925	<i>ptsS</i>	Phosphotransferase system (PTS), sucrose-specific enzym	G	0.26	-0.51	-0.89	-1.62	-0.57
cg2927	<i>scrB</i>	Beta-fructofuranosidase	G	-0.04	-0.43	-1.08	-1.81	-3.11
cg2928	<i>nagB</i>	Glucosamine-6-phosphate deaminase	G	0.29	0.69	-0.36	-1.07	-2.30
cg2937	-	ABC-type putative dipeptide/oligopeptide transporter, sub	E	0.07	-5.49	-5.61	-4.78	-5.61
cg2938	-	ABC-type putative dipeptide/oligopeptide transporter, per	E	-0.14	-4.23	-4.12	-3.78	-4.13
cg2939	-	ABC-type putative dipeptide/oligopeptide transporter, ATF	E	0.01	-4.92	-4.94	-4.68	-5.41
cg2940	-	ABC-type putative dipeptide/oligopeptide transporter, ATF	E	-0.20	-3.09	-4.03	-3.86	-3.40
cg2954	<i>cynT</i>	Carbonate dehydratase	P	-0.18	-0.56	-1.16	-1.49	-2.98
cg2955	<i>mutY</i>	A/G-specific adenine glycosylase	L	0.08	-0.33	-1.23	-1.40	-2.67
cg2956	-	Putative secreted protein	-	-0.39	-0.25	-0.73	-0.94	-1.90
cg2958	<i>butA</i>	L-2,3-Butanediol dehydrogenase/acetoin reductase	I	0.08	2.36	2.01	1.84	2.38
cg2962	-	Hypothetical protein, uncharacterized enzyme involved in	-	0.37	3.93	3.53	2.95	3.38
cg2964	<i>guaB1</i>	IMP dehydrogenase	F	0.13	0.03	-0.79	-1.44	-2.95
cg2965	-	Putative transcriptional regulator, AraC-family	K	-0.52	-2.78	-3.24	-3.68	-4.31
cg2966	-	Putative phenol 2-monooxygenase	H	-0.43	-2.94	-2.39	-3.38	-2.87
cg2971	<i>lmrB</i>	Putative multidrug efflux permease, MFS-type	G	0.03	-2.51	-2.61	-3.26	-5.06
cg2974	<i>lysS</i>	Lysine--tRNA ligase	J	-0.06	0.16	-0.36	-0.54	-2.17
cg2975	-	conserved hypothetical protein, similar to pantothenate sy	H	-0.06	0.11	-0.20	-0.38	-1.50
cg2978	-	Putative membrane protein	-	-0.19	0.12	-0.58	-0.51	-1.97
cg2979	<i>folK</i>	2-Amino-4-hydroxy-6- hydroxymethylidihydropteridine diph	H	-0.02	-0.05	-0.42	-0.62	-1.66
cg2981	<i>folX</i>	Dihydroneopterin aldolase	H	-0.03	-0.03	-0.71	-0.70	-1.62
cg2982	<i>folP1</i>	Dihydropteroate synthase	H	0.04	-0.01	-0.57	-0.79	-1.88
cg2983	<i>folE</i>	GTP cyclohydrolase I	H	0.18	0.12	-0.39	-0.58	-1.77
cg2986	<i>mesJ</i>	Conserved hypothetical protein, contains ATPase of the F	D	-0.43	-0.50	-1.43	-1.60	-2.75
cg2987	<i>dacB</i>	Serine-type D-Ala-D-Ala carboxypeptidase	M	0.08	-0.38	-0.92	-1.36	-2.44
cg2990	<i>speE</i>	Putative spermidine synthase with a transmembrane dom	R	0.07	0.07	-0.82	-1.15	-3.19
cg2991	-	Putative membrane protein	-	0.39	0.39	-0.28	-1.02	-2.26
cg2992	-	Putative secreted protein	-	0.36	0.51	-0.36	-0.70	-2.03
cg2993	-	Conserved hypothetical protein	-	0.15	0.37	-0.56	-1.09	-2.13
cg2994	-	Putative secreted or membrane protein	-	0.23	0.32	-0.41	-0.90	-2.19
cg2995	' <i>ptsX</i> '	Phosphotransferase system (PTS), disfunctional enzyme	-	-0.46	-1.58	-1.08	-1.55	-1.90
cg2996	' <i>ptsX</i> '	Phosphotransferase system (PTS), disfunctional enzyme	-	-0.93	-2.02	-2.33	-3.05	-4.66
cg2999	-	Putative ferredoxin reductase	C	-0.01	1.37	1.68	2.21	2.48
cg3007	-	P-loop containing Nucleoside Triphosphate Hydrolase	S	0.36	-0.05	-0.53	-0.88	-1.68
cg3008	<i>porA</i>	Porin	-	0.08	-0.37	-0.70	-1.05	-2.47
cg3009	<i>porH</i>	Porin, cation-specific	-	-0.15	-0.71	-0.99	-1.24	-2.58
cg3011	<i>groEL</i>	Chaperonin Cpn60 (60Kd subunit)	O	0.29	-0.04	-0.69	-0.82	-2.48
cg3012	-	Putative membrane protein	-	0.06	0.13	-0.42	-0.56	-2.19
cg3013	-	Hypothetical protein	-	0.02	0.16	-0.39	-0.76	-1.88
cg3014	-	Hypothetical protein	-	-0.06	0.06	-0.45	-0.71	-1.98
cg3015	-	Hypothetical protein	-	0.06	0.28	-0.33	-0.68	-1.97
cg3016	-	Hypothetical protein	-	0.15	0.37	-0.35	-0.57	-1.62

m-values

Locus	Feature	Product	COG	m-values				
				② vs. ①	③ vs. ①	④ vs. ①	⑤ vs. ①	⑥ vs. ①
cg3017	-	Putative membrane protein	-	0.07	0.27	-0.38	-0.76	-1.55
cg3020	-	Putative membrane protein	-	0.21	0.30	-0.16	-0.54	-1.78
cg3022	-	Conserved hypothetical protein	-	-1.22	-4.34	-4.10	-3.79	-6.23
cg3024	<i>mrpA</i>	Putative secondary Na ⁺ /H ⁺ antiporter, monovalent cation C	C	-0.22	-0.10	-0.14	-0.40	-2.36
cg3025	<i>mrpC</i>	Putative secondary Na ⁺ /H ⁺ antiporter, monovalent cation P	P	-0.37	-0.28	-0.44	-0.53	-3.08
cg3026	<i>mrpD</i>	Putative secondary Na ⁺ /H ⁺ antiporter, monovalent cation C	C	-0.05	-0.02	-0.12	-0.25	-2.68
cg3027	<i>mrpE</i>	Putative secondary Na ⁺ /H ⁺ antiporter, monovalent cation P	P	0.17	0.06	-0.35	-0.31	-2.86
cg3028	<i>mrpF</i>	Putative secondary Na ⁺ /H ⁺ antiporter, monovalent cation -	-	-0.29	-0.41	-0.60	-0.69	-2.87
cg3029	<i>mrpG</i>	Putative secondary Na ⁺ /H ⁺ antiporter, monovalent cation -	-	0.29	0.47	0.20	0.05	-2.08
cg3030	-	Putative hydrolase or acyltransferase (alpha/beta hydrolase)	R	-0.19	-0.01	-0.47	-0.80	-2.11
cg3031	-	Conserved hypothetical protein, glutamate-cysteine ligase	H	-0.09	-0.13	-0.49	-0.92	-1.98
cg3032	-	Putative secreted protein	-	-0.08	-0.06	-0.45	-0.80	-1.61
cg3033	-	Conserved hypothetical protein	-	-0.12	-0.24	-1.25	-1.04	-1.67
cg3035	-	Putative GCN5-related N-acetyltransferase	K	0.05	0.30	-0.50	-0.74	-2.07
cg3038	-	Putative multidrug efflux permease, MFS-type	G	0.13	-0.77	-0.76	-1.07	-3.83
cg3040	-	Putative epimerase	R	-0.33	0.29	-0.37	-0.76	-2.03
cg3041	-	ABC-type putative multidrug transporter, permease subunit	-	-0.48	-0.13	-0.23	-0.70	-2.31
cg3043	-	Putative NTP pyrophosphohydrolase/oxidative damage repressor	L	0.47	1.74	1.46	1.14	0.88
cg3044	-	Putative membrane protein	-	-0.19	0.46	0.16	-0.04	-1.60
cg3053	-	Permease, MFS-type	-	-0.08	-0.21	-0.88	-2.22	-2.71
cg3054	<i>purT</i>	Phosphoribosylglycinamide formyltransferase	F	0.46	-0.02	-0.85	-1.42	-1.98
cg3058	<i>tnp8b(ISCg8a)</i>	Transposase	L	-0.17	-0.62	-0.47	-0.61	-2.52
cg3063	<i>purA</i>	Adenylosuccinate synthase	F	0.28	0.55	0.22	-0.08	-1.60
cg3065	-	Conserved hypothetical protein	-	0.30	0.29	-0.32	-0.66	-2.26
cg3066	-	Putative membrane protein	-	-0.03	0.46	-0.03	-0.03	-1.53
cg3068	<i>fdx</i>	Fructose-bisphosphate aldolase	G	0.39	1.24	1.02	1.29	1.55
cg3070	-	Putative RNA methyltransferase, SpoU tRNA/rRNA methylase	J	-0.10	-0.04	-0.60	-0.72	-1.70
cg3073	<i>sseA1</i>	Thiosulfate sulfurtransferase	P	-0.05	0.98	1.13	0.85	1.53
cg3074	-	Conserved hypothetical protein	-	-0.37	-0.13	-1.28	-1.47	-3.07
cg3075	<i>cmr</i>	Putative multidrug efflux permease, MFS-type	G	-0.21	0.22	-0.28	-0.89	-2.82
cg3080	-	secondary Na ⁺ /glutamate symporter	E	-0.05	-0.91	-1.14	-1.42	-2.92
cg3085	-	Putative monooxygenase	C	0.00	-0.40	-1.18	-1.68	-1.75
cg3089	<i>'arr</i>	Putative rifampin ADP-ribosyl transferase, putative pseudogene	-	-0.78	-0.69	-0.59	-1.61	-2.96
cg3096	<i>ald</i>	acetaldehyde dehydrogenase (acetylating)	C	0.06	-5.97	-5.63	-5.57	-4.20
cg3101	-	Putative permease	R	0.21	-0.14	-0.62	-0.87	-1.60
cg3102	-	Secreted nucleoside phosphorylase	F	0.01	-0.61	-1.23	-2.02	-2.67
cg3105	-	conserved hypothetical protein	-	-0.50	0.15	-0.34	-0.71	-1.75
cg3106	-	Conserved hypothetical protein	-	0.15	0.08	-0.19	-0.82	-2.13
cg3107	<i>adhA</i>	Alcohol dehydrogenase	R	-0.02	-9.13	-8.63	-8.10	-8.54
cg3110	<i>'mrr</i>	putative restriction endonuclease, Mrr family, putative pseudogene	-	-0.78	-1.12	-1.46	-2.03	-2.50
cg3112	<i>cysZ</i>	Sulfate transporter	R	-0.56	0.18	-0.06	0.83	-4.69
cg3113	<i>cysY</i>	Sirohydrochlorin ferredoxinase	S	-0.49	0.28	-0.23	0.87	-3.13
cg3114	<i>cysN</i>	Sulfate adenylyltransferase subunit 1	P	-0.03	0.69	0.00	1.16	-4.97
cg3115	<i>cysD</i>	Sulfate adenylyltransferase subunit 2	E	-0.08	0.63	0.05	0.96	-5.53
cg3116	<i>cysH</i>	Adenosine phosphosulfate reductase	E	-0.28	0.27	-0.16	0.74	-5.55
cg3117	<i>cysX</i>	Ferredoxin-like protein, involved in electron-transfer	-	-0.20	0.34	-0.15	0.91	-5.66
cg3118	<i>cysI</i>	Ferredoxin-sulfite reductase	P	-0.14	0.47	0.04	1.02	-4.97
cg3119	<i>fpr2</i>	Ferredoxin--NADP(+) reductase	E	-0.27	-0.18	-1.01	0.09	-5.67
cg3121	-	Putative membrane protein	-	0.05	-1.39	-1.31	-1.72	-1.63
cg3122	<i>phnB1</i>	Hypothetical protein, PhnB-like	S	0.08	-2.39	-2.11	-2.39	-1.70
cg3124	-	Conserved hypothetical protein	-	-0.23	-3.65	-2.95	-3.93	-2.37
cg3125	<i>tctA</i>	citrate uptake transporter, membrane subunit	S	0.05	-1.67	-2.51	-2.44	-2.81
cg3126	<i>tctB</i>	citrate uptake transporter, membrane subunit	-	-0.08	-1.78	-2.23	-2.21	-4.16
cg3127	<i>tctC</i>	citrate uptake transporter, substrate binding protein	S	0.39	-1.55	-1.24	-1.75	-2.83
cg3132	-	Putative membrane protein	C	0.04	0.59	0.12	0.35	-2.14
cg3133	-	ABC-type putative cobalt/sugar transporter, ATPase subunit	R	-0.21	-1.21	-1.93	-2.54	-4.69
cg3134	-	ABC-type putative cobalt/sugar transporter, permease subunit	P	-0.03	-1.40	-1.72	-2.28	-4.05
cg3135	-	Putative membrane protein	-	0.07	-1.48	-1.46	-2.23	-4.44
cg3137	<i>iunH1</i>	Purine nucleosidase	F	-0.32	-0.65	-1.49	-2.41	-3.32
cg3141	<i>hmp</i>	Globin-like flavohaemoprotein, putative nitric oxide dioxygenase	C	0.29	1.70	0.54	-0.58	-1.73
cg3144	<i>'bglG</i>	Putative transcriptional antiterminator, putative pseudogene	K	0.07	-0.31	-0.41	-0.40	-3.05
cg3146	<i>'bglY'</i>	6-Phospho-beta-glucosidase, putative pseudogene (C-terminal)	G	-0.29	-0.83	-0.77	-1.89	-2.77
cg3147	<i>'bglY'</i>	6-Phospho-beta-glucosidase, putative pseudogene (N-terminal)	G	-0.58	-0.70	-0.74	-0.95	-1.96
cg3148	<i>'fepC'</i>	ABC transporter, ATP-binding protein - pseudogene	-	-0.17	-0.65	-0.63	-0.69	-2.37
cg3149	<i>alaT</i>	Putative aspartate aminotransferase, AT class I	E	0.15	-0.22	-0.72	-1.05	-3.73

Locus	Feature	Product	COG	m-values				
				②	③	④	⑤	⑥
				vs. ①	vs. ①	vs. ①	vs. ①	vs. ①
cg3153	-	Putative membrane protein	S	0.14	-0.69	-1.25	-1.84	-3.51
cg3156	-	Putative secreted protein	-	0.62	-0.37	-1.48	-2.24	-5.08
cg3158	<i>nagA2</i>	Putative beta-glucosidase	G	-0.22	-0.67	-1.00	-1.19	-3.67
cg3161	-	Putative membrane protein	-	-0.36	-0.14	-0.62	-1.00	-2.08
cg3163	-	Putative acyltransferase	I	-0.63	-1.02	-0.90	-1.18	-2.19
cg3166	-	Putative glycosyltransferase	M	-0.20	-1.02	-1.29	-1.70	-1.87
cg3169	<i>pck</i>	Phosphoenolpyruvate carboxykinase (GTP)	-	0.73	2.32	2.11	2.74	2.34
cg3177	<i>pccB</i>	Propionyl-CoA carboxylase	I	-0.19	-0.48	-0.94	-0.94	-1.83
cg3178	<i>pks</i>	Putative polyketide synthase, PksM-like	Q	-0.30	-1.11	-1.68	-1.82	-3.34
cg3179	<i>fadD2</i>	Putative long-chain-fatty-acid--CoA ligase	I	-0.60	-1.08	-1.72	-1.63	-1.99
cg3180	-	Putative secreted protein	-	-0.28	-0.53	-1.13	-1.52	-2.62
cg3181	-	Putative secreted protein	-	-0.29	-0.58	-1.19	-1.37	-2.33
cg3182	<i>cop1</i>	Trehalose corynomycolyl transferase	R	-0.23	-0.39	-1.11	-1.32	-2.16
cg3186	<i>cmt2</i>	Trehalose corynomycolyl transferase	R	-0.48	-1.16	-1.60	-2.14	-3.41
cg3187	-	Putative membrane protein	-	0.00	-0.08	-0.71	-1.47	-3.03
cg3189	<i>ubiA</i>	Polyprenyltransferase, involved in decaprenol phosphoar	H	-0.04	-0.32	-1.10	-1.46	-2.93
cg3190	-	Membrane-associated decaprenylphosphoryl-5-phosphori	I	-0.09	-0.54	-1.30	-1.89	-3.32
cg3191	<i>glfT</i>	Putative glycosyltransferase	R	0.07	-0.40	-1.24	-1.70	-3.02
cg3193	-	Putative membrane-associated phospholipid phosphatase	-	-0.60	-1.20	-1.50	-2.28	-3.83
cg3194	-	Putative membrane-associated PA-phosphatase related p	-	0.06	-0.89	-1.25	-2.04	-3.99
cg3195	-	Putative flavin-containing monooxygenase	P	0.36	-6.29	-6.20	-6.20	-5.80
cg3196	<i>glf</i>	UDP-galactopyranose mutase	C	-0.19	-0.14	-0.80	-0.90	-1.82
cg3197	<i>psp5</i>	Putative secreted protein	M	0.07	-0.43	-1.29	-1.71	-3.08
cg3202	<i>farR</i>	Transcriptional regulator, GntR-family	K	0.48	1.61	1.08	0.80	0.26
cg3206	-	Putative phosphoglycerate mutase	G	0.24	-0.14	-0.76	-0.90	-2.06
cg3207	<i>pheA</i>	Prephenate dehydratase	E	0.15	0.15	-0.42	-0.80	-1.91
cg3208	-	Putative amidase	J	-0.26	-0.65	-0.82	-1.20	-2.04
cg3209	-	Putative metal-dependent membrane protease	R	-0.01	-0.61	-0.91	-1.74	-3.35
cg3210	-	Conserved hypothetical protein	K	-0.06	-0.39	-0.85	-1.43	-2.52
cg3213	-	Putative secreted protein	-	-0.50	-1.33	-2.19	-2.04	-4.61
cg3214	-	Conserved hypothetical protein	-	-0.05	-1.23	-1.70	-2.31	-3.77
cg3216	<i>gntP</i>	Putative secondary gluconate symporter, gluconate:H+ sy	G	-0.12	-3.73	-4.38	-4.50	-6.77
cg3218	-	Pyruvate kinase-like protein	G	0.12	1.92	1.27	1.04	1.35
cg3219	<i>ldh</i>	L-Lactate dehydrogenase	C	0.88	4.34	3.43	3.25	4.50
cg3226	-	Putative MFS-type L-lactate permease	G	1.55	2.33	1.81	1.58	-0.15
cg3227	<i>lldD</i>	Quinone dependent L-lactate dehydrogenase	C	0.55	1.63	1.07	1.13	0.24
cg3232	-	Putative secreted phosphohydrolases, ICC-family	R	-1.45	-1.10	-1.38	-2.34	-2.72
cg3233	-	Hypothetical protein	-	-0.61	-0.36	-0.84	-1.13	-1.95
cg3236	<i>msrA</i>	Protein-methionine-S-oxide reductase	O	-0.24	1.38	1.45	0.96	2.05
cg3240	-	Putative multidrug efflux permease, MFS-type	G	0.57	1.75	1.52	0.57	-0.78
cg3243	-	Conserved hypothetical protei, RecB-family nuclease	-	-0.50	-0.20	-0.65	-0.95	-3.17
cg3248	<i>cgtS11</i>	Two-component system, sensory histidine kinase	T	0.08	-0.16	-0.56	-1.04	-2.20
cg3249	-	Putative secreted protein	-	-0.06	0.24	-0.06	-1.45	-1.82
cg3250	-	Putative membrane protein	-	0.20	0.60	-0.10	-0.12	-1.63
cg3251	-	Putative sortase (surface protein transpeptidase)	M	-0.13	0.15	-0.19	-0.55	-1.71
cg3252	-	Putative 60 KD inner membrane protein, SpoIIJ homolog	U	-0.40	-0.51	-1.16	-1.40	-2.92
cg3253	<i>mcbR</i>	Global transcriptional repressor of sulfur metabolism, TefK	K	0.55	0.38	0.32	0.54	-1.88
cg3254	-	Putative membrane protein	-	1.25	1.95	1.73	1.50	2.03
cg3271	-	SAM-dependent methyltransferase	Q	-0.36	-0.63	-0.99	-1.44	-1.63
cg3272	-	Putative membrane protein	S	0.29	2.24	3.42	4.67	4.89
cg3275	<i>fdxA</i>	Putative ferredoxin	C	-0.48	-1.09	-1.43	-1.74	-2.25
cg3277	-	Hypothetical protein, containing double-stranded beta-heli	S	-0.31	-2.10	-2.18	-3.20	-5.21
cg3285	<i>cgtR9</i>	Two-component system, transcriptional response regulatc	T	0.25	0.29	-0.29	-1.93	0.04
cg3287	-	Putative secreted multicopper oxidase	Q	0.22	0.05	-0.51	-1.04	-2.26
cg3288	-	Hypothetical protein	-	-0.78	-0.06	-0.37	-0.54	-3.37
cg3289	-	Putative Thiol-disulfide isomerase or thioredoxin	O	-0.56	0.10	-0.60	-0.54	-1.83
cg3293	-	Hypothetical protein	-	0.70	0.52	0.03	-0.54	-1.57
cg3301	-	Putative sugar/metabolite permease, MFS-type	G	-0.03	-1.15	-1.85	-2.75	-4.07
cg3303	-	Putative transcriptional regulator, PadR-family	K	0.67	2.81	3.79	4.32	4.62
cg3306	<i>rplI</i>	50S ribosomal protein L9	J	0.35	-0.61	-0.98	-0.96	-2.31
cg3307	<i>ssb</i>	Single-strand binding protein	L	0.27	-0.72	-1.13	-1.18	-2.42
cg3308	<i>rpsF</i>	30S ribosomal protein S6	-	0.31	-0.62	-0.99	-1.15	-2.26
cg3313	<i>mrcB</i>	Putative membrane carboxypeptidase	M	-0.01	-0.31	-0.74	-0.88	-1.91
cg3314	-	Conserved hypothetical protein	-	-0.24	-0.34	-0.71	-1.08	-1.82
cg3319	-	Conserved hypothetical protein	R	0.15	0.29	-0.11	-0.18	-1.74

m-values

Locus	Feature	Product	COG	m-values				
				② vs. ①	③ vs. ①	④ vs. ①	⑤ vs. ①	⑥ vs. ①
cg3320	-	ABC-type transporter, ATPase and permease subunit	V	1.09	0.92	0.09	-0.29	-2.65
cg3321	-	ABC-type transporter, ATPase and permease subunit	G	0.85	0.93	0.12	-0.46	-3.19
cg3322	-	Putative secreted membrane-fusion protein	V	1.04	0.96	-0.25	-0.42	-2.85
cg3323	<i>ino1</i>	Inositol-3-phosphate synthase	I	0.14	0.43	0.09	-0.11	-3.09
cg3324	-	Putative secreted protein	-	0.30	0.25	-0.02	-0.48	-1.66
cg3325	-	Conserved hypothetical protein	S	0.06	-0.46	-1.29	-2.06	-4.18
cg3327	<i>dps</i>	Putative starvation-induced DNA protecting protein	P	-0.11	0.92	2.11	3.16	4.53
cg3330	-	Putative secreted protein	S	-0.27	-1.35	-1.64	-2.00	-3.03
cg3332	<i>qor</i>	NADPH:quinone reductase	C	0.32	0.91	1.03	1.40	1.60
cg3334	-	Putative sugar permease, MFS-type	G	0.31	-0.15	-0.40	-0.62	-4.03
cg3335	<i>mez</i>	Malate dehydrogenase (oxaloacetate-decarboxylating) (N.C	C	-0.11	-4.19	-4.65	-4.63	-5.99
cg3338	-	Putative membrane protein	V	-0.97	-1.38	-2.17	-1.40	-0.33
cg3343	-	Putative secreted membrane protein	-	0.78	1.62	1.48	1.93	0.91
cg3345	-	Hypothetical protein	-	-0.31	-0.21	-0.71	-0.72	-1.62
cg3346	<i>leuS</i>	Leucine--tRNA ligase	J	0.16	0.21	-0.46	-0.55	-1.61
cg3352	<i>nagR</i>	Transcriptional activator of gentisate catabolism, IclR-fam	K	-0.27	-2.60	-1.57	-1.25	-1.48
cg3356	-	Putative secondary H+/Na+:glutamate/dicarboxylate symport	C	-0.05	-0.32	-1.52	-1.65	-3.65
cg3359	<i>trpE</i>	Anthranilate synthase subunit I	E	0.10	0.23	-0.21	0.07	-3.07
cg3360	<i>trpG</i>	Anthranilate synthase subunit II	E	0.40	0.68	0.07	0.21	-2.20
cg3361	<i>trpD</i>	Anthranilate phosphoribosyltransferase	E	0.27	0.32	0.01	0.20	-2.58
cg3362	<i>trpCF</i>	Phosphoribosylantranilate isomerase	E	0.41	0.76	0.18	0.36	-2.40
cg3363	<i>trpB</i>	Tryptophan synthase beta chain	E	0.50	0.87	0.18	0.36	-1.90
cg3366	<i>rmpA</i>	Phosphotransferase system (PTS), putative ribitol/mannit	G	-0.07	0.07	-0.71	-1.36	-1.75
cg3367	-	ABC-type putative multidrug transporter, ATPase subunit	E	0.14	1.46	1.77	2.37	2.70
cg3368	-	ABC-type putative multidrug transporter, permease subun-	-	-0.03	1.67	1.93	2.33	2.87
cg3371	-	Putative secondary Na+/bile acid symporter, bile acid:Na+	P	0.30	-0.54	-0.67	-1.13	-2.62
cg3372	-	Conserved hypothetical protein	S	-0.37	-0.40	-0.81	-1.06	-3.11
cg3374	-	Putative NADH-dependent flavin oxidoreductase	C	-1.04	-2.85	-3.59	-3.48	-6.15
cg3375	-	Predicted nucleoside-diphosphate-sugar epimerase	M	-0.46	-0.94	-1.51	-1.67	-2.43
cg3376	-	Conserved hypothetical protein	-	0.01	-0.38	-1.10	-1.82	-5.02
cg3377	-	Conserved hypothetical protein	-	-0.94	-1.25	-1.72	-2.39	-2.73
cg3380	-	Putative oxidoreductase protein	I	0.47	0.10	-0.41	-0.82	-1.66
cg3382	-	Putative dipeptide/tripeptide:H+ transporter, proton-depen	E	-0.19	0.62	-0.09	-0.34	-2.49
cg3384	-	Putative transcriptional regulator, TetR-family	K	0.31	-0.30	-0.79	-0.33	-1.87
cg3385	<i>catA3</i>	Hydroxyquinol 1,2-dioxygenase	Q	-0.12	-1.38	-1.48	-2.67	-2.97
cg3386	<i>tcbF</i>	Maleylacetate reductase	C	0.24	-1.18	-2.12	-1.75	-3.26
cg3387	-	Putative sugar/metabolite permease, MFS-type	G	0.12	-1.32	-1.49	-1.76	-2.37
cg3388	-	Putative transcriptional regulator, IclR-family	K	0.15	-1.14	-2.45	-2.39	-2.58
cg3389	-	Predicted oxidoreductase	R	0.00	-2.53	-2.73	-1.74	-1.76
cg3390	-	Putative sugar phosphate isomerase/epimerase	G	0.64	-2.56	-2.28	-2.12	-0.60
cg3391	<i>idhA1</i>	Inositol 2-dehydrogenase	R	0.06	-2.70	-1.76	-2.41	-2.11
cg3392	<i>idhA2</i>	Inositol 2-dehydrogenase	R	-0.34	-1.52	-3.99	-1.47	-2.00
cg3393	-	Putative secreted protein, phosphoesterase	R	0.02	-1.07	-1.40	-1.76	-3.52
cg3395	<i>proP</i>	Putative proline/betaine permease, MFS-type	G	1.64	-0.02	-0.61	-1.49	-2.97
cg3399	-	Permease, MFS-type	-	0.39	0.59	-0.01	0.72	-3.61
cg3403	-	Putative proline/betaine permease, MFS-type	G	-0.76	-2.06	-2.13	-3.00	-4.25
cg3404	-	ABC-type putative iron(III) dicitrate transporter, substrate-P	C	0.19	-2.07	-3.86	-7.01	-7.72
cg3405	-	NADPH:quinone reductase Zn-dependent oxidoreductase C	C	-0.59	-0.14	-0.60	-1.44	-1.74
cg3407	-	Putative membrane protein	-	-0.21	0.21	0.12	-0.57	-2.00
cg3409	<i>thiD2</i>	Phosphomethylpyrimidine kinase	H	0.07	-0.15	-0.54	-0.86	-3.19
cg3412	<i>azlD</i>	Putative permease, branched-chain amino acid permease	E	-0.64	-0.45	-0.97	-0.87	-2.23
cg3413	<i>azlC</i>	Putative secondary branched-chain amino acid efflux tran	E	-0.22	-0.52	-0.72	-0.81	-2.60
cg3414	-	Conserved hypothetical protein	K	-0.02	0.01	-0.69	-0.70	-2.39
cg3415	<i>pcnA</i>	Polynucleotide adenyltransferase	J	-0.05	-0.57	-0.96	-1.09	-2.85
cg3417	-	Putative (Di)nucleoside polyphosphate hydrolase	F	-0.60	-0.47	-0.77	-0.86	-1.93
cg3418	-	Putative secreted protein	-	-0.27	0.05	-0.40	-0.62	-2.24
cg3419	-	Putative MVF virulence factor MviN-homolog protein, mult	R	0.18	-0.26	-1.01	-1.17	-2.46
cg3429	-	Putative 60 KD inner membrane protein, SpoIIJ homolog U	U	-0.02	-0.46	-0.82	-0.97	-2.87
cg3430	-	Conserved hypothetical protein	S	-0.22	-0.85	-1.02	-1.32	-2.63
cg3431	<i>rnpA</i>	Ribonuclease P	J	0.07	-0.88	-1.26	-1.31	-5.22
cg3432	<i>rpmH</i>	50S ribosomal protein L34	-	0.03	-1.10	-1.28	-1.42	-5.28
cg4009	-	-	-	-0.49	-0.75	-1.17	-0.94	-3.07
cg4011	-	Transposon Tn501 resolvase	-	0.28	-0.22	-2.19	-1.24	-2.85
cg4012	<i>trpL</i>	Trp operon leader peptide	-	-0.52	-0.57	-0.74	-0.53	-2.57
cg4013	-	-	-	-0.57	-1.20	-1.48	-1.17	-1.71

Locus	Feature	Product	COG	m-values				
				②	③	④	⑤	⑥
				vs. ①	vs. ①	vs. ①	vs. ①	vs. ①
cg4014	-	conserved hypothetical protein, possibly involved in stress	-	0.16	0.79	0.85	0.60	-2.02
cg4015	<i>leuL</i>	leucine-containing leader peptide	-	-0.01	-1.08	-1.42	-1.95	-2.87
cg4016	<i>ilvL</i>	valine-containing leader peptide	-	-0.52	-0.42	-0.59	-0.74	-2.13
cg4019	-	-	-	0.73	4.12	5.12	5.61	6.76
cg4020	-	-	-	0.15	0.20	-0.30	-1.12	-2.15
cg4021	-	-	-	-0.18	-0.26	-0.53	-0.97	-1.78
cg4027	-	-	-	-0.55	-0.90	-1.30	-1.17	-2.33

This supplementary table provides the full data for the calculation and development of Table A5.

Gene Information			Read Mapping			Raw Read Count			log ₂ TPM			m-values			m-values < ±1.5 (not significant)			m-values > ±1.5 (significant)															
Locus	Feature	Product	Major COG Cat.	Strand	Start	Stop	Length (bp)	Effective Length	1	2	3	4	5	6	1	2	3	4	5	6	1	2	3	4	5	6							
cs0001	dnaA	Chromosomal replication initiator protein DnaA	L	Fwd	1	1575	1575	1502	1017	1041	847	1041	1164	447	6.100	6.030	5.776	5.767	5.945	5.451	-0.070	-0.324	-0.333	-0.155	-1.556	6.065	-0.070	-0.324	-0.333	-0.155	-1.556		
cs0002	dnaA	Hypothetical protein	L	Rev	1920	1594	327	254	10	6	10	10	12	10	1.836	1.080	1.486	1.469	1.727	1.461	-0.756	-0.350	-0.367	-0.109	-0.375	1.458	-0.756	-0.350	-0.367	-0.109	-0.375		
cs0004	dnaN	DNA polymerase III, beta chain	L	Fwd	2292	3476	1185	1112	1700	1834	2245	1948	1702	894	7.251	7.467	7.591	7.081	6.903	5.950	0.006	0.340	-0.170	-0.348	-1.301	7.284	0.006	0.340	-0.170	-0.348	-1.301		
cs0005	refF	DNA replication and repair protein RefF	L	Fwd	3585	4769	1185	1112	469	544	492	438	372	171	5.395	5.505	5.402	4.930	4.710	3.566	0.110	0.007	-0.465	-0.685	-1.828	5.450	0.110	0.007	-0.465	-0.685	-1.828		
cs0006	ovrB	Conserved hypothetical protein	R	Fwd	4766	5302	537	464	75	78	135	107	112	51	3.909	3.861	4.682	4.049	4.125	2.973	-0.048	0.774	0.140	0.216	-0.936	3.885	-0.048	0.774	0.140	0.216	-0.936		
cs0007	ovrB	DNA gyrase subunit B	L	Fwd	5435	7489	2055	1982	8038	9028	7354	6663	7112	2989	8.697	8.761	8.508	8.060	8.171	6.896	0.064	-0.189	-0.637	-0.526	-1.991	8.759	0.064	-0.189	-0.637	-0.526	-1.991		
cs0008	ovrB	Putative esterase/lipase	R	Fwd	7923	8788	876	803	265	408	317	370	370	160	5.010	5.527	5.207	5.123	5.110	3.911	-0.517	0.197	0.113	0.130	-1.032	6.268	-0.517	0.197	0.113	0.130	-1.032		
cs0009	ovrB	Putative membrane protein	L	Rev	9466	8795	672	599	256	203	155	160	151	41	5.343	4.906	4.562	3.041	4.235	2.355	-0.437	-0.781	-1.041	-1.107	-2.988	5.124	-0.437	-0.781	-1.041	-1.107	-2.988		
cs0010	ovrB	Conserved hypothetical protein	L	Rev	9914	9471	444	370	1437	1464	1423	1468	1064	595	8.425	8.348	8.350	8.089	7.642	6.780	-0.077	-0.075	-0.336	-0.783	-1.645	6.386	-0.077	-0.075	-0.336	-0.783	-1.645		
cs0012	ovrB	Transcriptional activator of sulfonameter/sulfonamide utilization, ROK-family	K	Fwd	11171	10104	1068	994	151	195	209	240	303	25	3.917	4.160	4.322	4.215	4.657	3.995	0.263	0.406	0.298	0.650	-0.928	4.068	0.263	0.406	0.298	0.650	-0.928		
cs0013	ovrB	Putative transcriptional regulator, TetR-family	L	Fwd	11523	11260	264	185	15	20	10	13	11	12	2.685	2.939	2.084	2.073	1.920	2.011	0.254	-0.601	-0.612	-0.765	-0.674	2.812	0.254	-0.601	-0.612	-0.765	-0.674		
cs0014	ovrB	Helix-turn-helix protein, CopG-family	L	Rev	11729	11520	210	141	12	28	12	14	11	13	2.716	3.744	2.655	2.506	2.250	2.448	1.029	-0.061	-0.209	-0.465	-0.268	3.230	1.029	-0.061	-0.209	-0.465	-0.268		
cs0015	ovrA	DNA gyrase subunit A	L	Fwd	11831	14401	2571	2497	2875	3261	3006	2271	2900	1870	6.891	6.969	6.895	6.184	6.554	5.896	0.078	0.004	-0.707	-0.337	-0.995	6.930	0.078	0.004	-0.707	-0.337	-0.995		
cs0016	ovrA	Putative integral membrane protein	L	Fwd	14405	14749	345	271	490	630	459	430	386	249	7.116	7.450	7.084	6.684	6.545	6.091	0.334	-0.032	-0.432	-0.370	-1.115	7.263	0.334	-0.032	-0.432	-0.370	-1.115		
cs0018	ovrA	Conserved hypothetical membrane protein	S	Fwd	16243	15206	1038	964	66	56	51	77	88	80	2.776	4.239	2.350	2.629	2.836	2.675	-0.337	-0.426	-0.147	0.060	-0.101	2.607	-0.337	-0.426	-0.147	0.060	-0.101		
cs0019	ovrA	Putative transcriptional regulator, LysK-family	K	Fwd	16314	17210	897	824	143	147	153	199	140	94	4.090	4.026	4.127	4.198	3.710	3.116	-0.064	0.036	0.107	-0.380	-0.975	4.058	-0.064	0.036	0.107	-0.380	-0.975		
cs0021	ovrA	Hypothetical protein	L	Fwd	17251	17673	423	350	65	71	59	78	78	4	4.049	4.071	4.423	4.282	3.959	2.808	0.022	0.480	-0.233	-0.090	-1.249	4.000	0.022	0.480	-0.233	-0.090	-1.249		
cs0025	ovrA	Putative integral membrane protein	O	Rev	18729	18757	873	799	94	105	74	119	132	75	3.529	3.584	3.128	3.500	3.665	2.833	0.054	-0.402	-0.030	0.136	-0.696	3.587	0.054	-0.402	-0.030	0.136	-0.696		
cs0026	ovrA	Putative protein disulfide isomerase, secreted protein	O	Rev	19479	18733	747	674	132	129	106	167	210	106	4.240	4.103	3.865	4.210	4.556	3.551	-0.137	-0.374	-0.030	0.316	-0.688	4.171	-0.137	-0.374	-0.030	0.316	-0.688		
cs0027	ovrA	Putative transcriptional regulator, MarR-family	O	Fwd	19705	20076	372	299	17	26	27	21	13	5	2.360	2.841	2.937	2.283	1.648	0.401	0.481	0.577	-0.077	-0.712	-1.960	2.601	0.481	0.577	-0.077	-0.712	-1.960		
cs0029	ovrA	Conserved putative membrane protein	O	Fwd	20073	21068	996	923	52	45	22	58	52	19	2.497	2.710	2.232	2.285	2.148	0.717	-0.609	-0.280	-0.212	-0.350	-1.781	2.602	-0.609	-0.280	-0.212	-0.350	-1.781		
cs0031	ovrA	Hypothetical protein	L	Rev	21247	21071	177	103	2	0	2	3	0	0	0.847	-0.842	0.786	0.895	-1.688	-1.113	-1.689	-0.041	0.048	0.133	-1.960	0.002	-1.689	-0.041	0.048	0.133	-1.960		
cs0033	ovrA	Putative secreted protein	L	Fwd	21426	21257	102	28	2	0	0	0	1	1	1.642	-0.040	-0.004	-0.310	0.707	0.682	-1.689	-1.646	-1.956	-0.935	-0.960	0.798	-1.689	-1.646	-1.956	-0.935	-0.960		
cs0034	ovrA	S-Nucleotidase, putative pseudogene	F	Fwd	21597	21270	531	457	23	11	31	28	20	15	2.622	1.158	2.616	2.168	1.719	1.302	-1.104	0.354	-0.094	-0.542	-0.960	0.798	-1.104	0.354	-0.094	-0.542	-0.960		
cs0035	ovrA	S-Nucleotidase, putative pseudogene	F	Fwd	21646	21402	1239	1160	9	14	21	3	6	9	1.116	1.450	1.084	1.084	0.603	0.091	-0.934	-1.360	-1.279	-1.180	-1.674	0.488	-0.934	-1.360	-1.279	-1.180	-1.674		
cs0038	ovrA	putative organic hydroperoxide detoxification protein	O	Fwd	24295	24732	438	364	31	17	12	16	17	12	2.955	2.021	1.594	1.675	1.775	1.280	-0.129	0.448	-0.003	0.108	-0.036	2.627	-0.129	0.448	-0.003	0.108	-0.036		
cs0039	ovrA	Putative transcriptional regulator	K	Rev	26573	24882	1692	1619	411	404	585	529	565	520	4.691	4.563	5.139	4.688	4.800	4.655	0.728	1.209	9.168	8.483	7.386	3.407	0.969	0.728	1.209	9.168	8.483	7.386	3.407
cs0040	ovrA	Putative secreted protein	L	Rev	28099	26919	1281	1207	19	29	724	5569	2573	165	6.728	6.109	9.168	8.483	7.386	3.407	0.728	1.209	9.168	8.483	7.386	3.407	0.969	0.728	1.209	9.168	8.483	7.386	3.407
cs0041	ovrA	ABC-type putative manganese/zinc transporter, substrate-binding II	P	Fwd	31677	32703	1026	952	899	977	1007	808	643	489	6.489	6.599	6.625	5.951	6.124	5.761	-0.089	-0.364	-0.938	-1.377	-3.227	6.644	-0.089	-0.364	-0.938	-1.377	-3.227		
cs0042	ovrA	ABC-type putative manganese/zinc transporter, permease subunit	P	Rev	29965	24814	852	778	4	7	1024	712	462	124	-0.683	-0.109	6.935	6.106	5.998	3.586	0.574	-0.719	6.828	4.269	-0.396	5.574	0.574	-0.719	6.828	4.269			
cs0043	ovrA	ABC-type putative manganese/zinc transporter, ATPase subunit	G	Fwd	29995	30364	660	586	6	8	569	601	566	344	0.170	0.429	6.257	6.290	6.161	5.419	0.251	-0.627	6.060	5.930	5.249	0.300	0.251	-0.627	6.060	5.930	5.249		
cs0044	ovrA	ABC-type putative sugar transporter, substrate-binding lipoprotein	G	Fwd	30697	31080	984	911	1988	1788	1498	1234	935	226	7.745	7.488	4.276	6.690	6.307	4.239	-0.257	-0.469	-1.054	-1.438	-3.500	7.674	-0.257	-0.469	-1.054	-1.438	-3.500		
cs0045	ovrA	ABC-type putative sugar transporter, permease subunit	G	Fwd	31677	32703	1026	952	899	977	1007	808	643	489	6.489	6.599	6.625	5.951	6.124	5.761	-0.089	-0.364	-0.938	-1.377	-3.227	6.644	-0.089	-0.364	-0.938	-1.377	-3.227		
cs0046	ovrA	ABC-type putative sugar transporter, ATPase subunit	P	Fwd	32699	33462	762	688	473	459	408	264	233	45	6.043	5.897	5.769	4.839	4.676	2.305	-0.146	-0.274	-1.204	-1.367	-3.738	5.970	-0.146	-0.274	-1.204	-1.367	-3.738		
cs0047	ovrA	Conserved hypothetical protein	M	Rev	34274	34362	813	740	3219	4386	5260	4768	4906	5224	8.715	9.057	9.363	8.915	8.973	9.039	0.342	0.648	2.000	0.258	0.324	8.886	0.342	0.648	2.000	0.258	0.324		
cs0048	ovrA	Putative transmembrane protein	M	Fwd	34274	34362	813	740	3219	4386	5260	4768	4906	5224	10.127	10.716	-0.026	-0.111	-0.859	0.177	0.416	-0.026	-0.111	-0.859	10.716	0.177	0.416						

This supplementary table provides the full data for the calculation and development of Table 4A5.

Gene Information			Read Mapping			Raw Read Count			log ₂ TPM			m-values			m-values < ±1.5 (not significant)			m-values > ±1.5 (significant)													
Locus	Feature	Product	Major COG Cat.	Strand	Start	End	Effective Length	①	②	③	④	⑤	⑥	①	②	③	④	⑤	⑥	a-value	①	②	③	④	⑤	⑥					
cg0124	amm	AMP nucleosidase	F	Fwd	103504	104913	1410	1337	633	654	714	618	581	396	5,576	5,519	5,689	5,175	5,103	4,526	-0.057	0.113	-0.401	-0.473	-1.050	-0.233	-0.057	0.113	-0.401	-0.473	-1.050
cg0126	-	Putative TPP-requiring enzyme	F	Rev	157552	155511	582	509	0	1	1	4	0	0	-2,456	-2,516	-1,822	-0.483	-2,830	0.896	-0.061	0.633	-0.375	-0.375	-0.007	-0.061	0.633	-0.375	-0.375		
cg0127	-	Thiamine pyrophosphate-dependent enzyme	E	Rev	106393	105839	555	483	35	23	30	21	29	12	2,783	2,094	2,507	1,706	2,170	0,939	-0.689	-0.276	-1.077	-0.613	-1.844	-0.439	-0.276	-1.077	-0.613	-1.844	
cg0128	-	Putative secreted protein	-	Rev	107179	106628	552	478	17	25	39	29	50	52	1,791	2,217	2,882	2,161	2,944	2,974	0.427	1.091	0.370	1.153	1.183	2.004	0.427	1.091	0.370	1.153	1.183
cg0129	putA	Proline dehydrogenase/delta-1-pyrroline-5-carboxylate dehydrogenase	C	Fwd	107436	110894	3459	3386	983	1390	670	927	1559	1589	4,916	5,087	4,303	4,465	5,231	5,233	0.172	-0.613	-0.451	0.315	0.318	5.002	0.172	-0.613	-0.451	0.315	0.318
cg0131	-	Putative isoA-reductase	C	Fwd	111387	112322	936	862	583	826	1181	1121	1033	641	6,049	6,136	7,005	6,624	6,503	5,811	0.398	0.957	0.575	0.474	-0.238	-0.248	0.398	0.957	0.575	0.474	-0.238
cg0133	-	Putative p-aminobenzoate translocase, arn permease A	H	Fwd	112471	114087	1617	1544	691	2510	309	274	187	131	5,505	7,261	4,286	3,807	3,275	2,740	1.756	-1.219	-1.658	-1.230	-0.765	-0.765	3.383	-1.219	-1.658	-1.230	-0.765
cg0134	-	Metal-dependent amidase/aminoacylase/carboxypeptidase, AbgB1	R	Fwd	114094	115482	1389	1315	420	1464	491	385	403	346	5,007	6,702	5,171	4,515	4,598	4,354	1.693	0.164	-0.492	-0.409	-0.653	5.855	0.164	-0.492	-0.409	-0.653	
cg0135	-	Putative membrane protein	S	Rev	115579	115947	369	295	194	461	251	288	253	182	1,141	1,309	1,011	0,032	-0.466	0.736	-0.271	-0.183	-0.224	-0.472	-1.407	-0.271	-0.183	-0.224	-0.472	-1.407	
cg0136	-	Putative membrane protein	C	Fwd	119550	116467	1188	244	134	174	123	148	123	65	5,493	7,644	6,100	5,968	5,501	4,085	-0.265	0.360	0.094	-0.055	-0.477	5.466	-0.265	0.360	0.094	-0.055	-0.477
cg0138	-	ATP/GTP-binding protein	-	Rev	118558	116546	2013	1940	918	821	1229	264	1126	855	6,987	6,920	5,759	5,623	5,455	5,121	-0.067	0.288	0.034	-0.532	-0.863	6.953	-0.067	0.288	0.034	-0.532	-0.863
cg0139	-	Putative transcriptional regulator, DeorF-family	K	Rev	119590	118808	783	710	935	959	1191	1235	824	666	7,658	7,139	7,904	7,455	7,065	6,866	0.081	0.246	-0.203	-0.593	-0.752	6.668	0.081	0.246	-0.203	-0.593	-0.752
cg0141	-	Putative glyoxalase	E	Rev	120022	120414	393	220	747	849	924	837	631	559	6,489	6,136	7,005	6,624	6,503	5,811	-0.314	0.549	0.572	0.543	0.775	6.625	-0.314	0.549	0.572	0.543	0.775
cg0142	isoA	Putative arabinot-1-phosphatase	G	Rev	120923	120411	513	439	132	114	202	254	246	294	4,782	4,468	5,331	5,354	5,325	5,557	-0.640	0.234	-1.524	-1.888	-1.233	6.705	-0.640	0.234	-1.524	-1.888	-1.233
cg0143	mtiD	Mannitol-1-phosphate 5-dehydrogenase	G	Rev	122460	120949	1512	1439	28	119	25	12	9	3	1,025	0,385	-1,309	-0.499	-0.861	-2.207	0.048	-0.816	-0.952	-0.581	-1.544	6.712	0.048	-0.816	-0.952	-0.581	-1.544
cg0144	rftF	Putative sugar/metabolite permease, MFS-type	G	Rev	123842	122505	1338	1264	26	29	15	17	22	2	1,098	1,147	0,283	0,147	0,517	-1.446	-0.048	-0.816	-0.952	-0.581	-1.544	6.712	-0.048	-0.816	-0.952	-0.581	-1.544
cg0146	accZ	Transcriptional activator, DeoK-family	K	Fwd	124122	124970	849	775	245	215	155	176	104	63	4,942	4,461	4,178	4,301	3,864	2,625	0.020	-0.639	-0.800	-1.761	-2.199	5.339	0.020	-0.639	-0.800	-1.761	-2.199
cg0147	xyfB	Xylose kinase	C	Fwd	124972	126354	1383	1310	523	570	300	387	196	147	5,329	5,349	4,690	4,529	5,368	5,311	0.200	-0.933	-1.456	-1.937	-4.079	5.588	0.200	-0.933	-1.456	-1.937	-4.079
cg0148	panC	Pantoate-beta-alanine lyase	H	Rev	127190	126351	840	767	710	876	387	333	311	54	6,488	6,688	5,554	5,032	4,951	2,409	0.244	-0.849	-1.101	-1.296	-1.426	6.301	0.244	-0.849	-1.101	-1.296	-1.426
cg0149	panB	3-Methylcrotonyl-CoA hydratase/hydroxymethyltransferase	H	Rev	127999	127150	810	737	610	1177	1498	681	707	610	4,456	4,978	4,145	3,447	3,447	3,447	-1.203	-1.236	-1.300	-1.906	-2.206	5.944	-1.203	-1.236	-1.300	-1.906	-2.206
cg0150	panB	3-Methylcrotonyl-CoA hydratase/hydroxymethyltransferase	S	Rev	129050	126397	954	881	209	97	102	109	81	58	4,546	3,342	3,310	3,246	2,839	2,340	0.391	1.114	0.676	0.361	0.210	3.844	0.391	1.114	0.676	0.361	0.210
cg0151	mag	Putative 3-methylpurine DNA glycosylase	L	Rev	130056	129487	570	496	65	92	148	135	107	98	3,619	4,010	4,733	4,295	3,980	3,829	0.126	0.367	1.014	0.600	-0.004	2.290	0.126	0.367	1.014	0.600	-0.004
cg0152	-	Hypothetical protein	-	Fwd	130146	130802	657	584	57	67	77	150	111	74	3,228	3,353	3,594	4,241	3,827	3,224	-0.245	0.367	0.138	-1.002	-0.002	6.658	-0.245	0.367	0.138	-1.002	-0.002
cg0153	-	Putative esterase/lipase	L	Fwd	131712	130813	900	826	98	124	132	115	62	39	3,565	3,025	3,910	2,839	2,515	2,863	0.330	0.828	0.764	0.911	1.443	6.301	0.330	0.828	0.764	0.911	1.443
cg0154	-	Putative hydrolase	R	Fwd	131823	132428	606	533	401	542	743	825	961	1415	6,135	6,466	6,964	6,810	7,046	7,579	0.177	1.172	0.726	0.973	1.226	5.190	0.177	1.172	0.726	0.973	1.226
cg0155	-	Conserved hypothetical protein, carbonic anhydrases/acetyltransferase	R	Fwd	132425	132985	561	487	181	220	426	386	453	550	5,101	5,278	6,273	5,827	6,074	6,328	0.330	0.828	0.764	0.911	1.443	5.190	0.330	0.828	0.764	0.911	1.443
cg0156	cyuR	Transcriptional activator of assimilatory sulfate reduction, ROK-fam	K	Rev	134114	132969	1146	1073	1099	950	1143	938	1082	98	6,670	6,356	6,666	6,075	6,298	2,822	-0.314	-0.004	-0.505	-0.372	-1.848	6.658	-0.314	-0.004	-0.505	-0.372	-1.848
cg0158	-	Putative drug efflux permease, MFS-type	-	Rev	134479	134205	1275	1202	394	406	227	168	111	40	1,032	-0.194	-2.31	-2.657	-2.640	-2.665	-1.426	-0.383	-1.689	-1.672	-1.544	6.319	-1.426	-0.383	-1.689	-1.672	-1.544
cg0160	-	Hypothetical protein	-	Rev	136542	136120	423	349	47	7	5	2	1	0	1,005	0,486	-0.471	-2.362	-1.345	-2.370	-0.519	-1.476	-1.287	-2.350	-1.375	6.715	-0.519	-1.476	-1.287	-2.350	-1.375
cg0161	-	Putative membrane protein	-	Fwd	136601	137443	1184	1113	1219	281	287	214	187	140	6,078	6,136	5,178	4,814	5,178	4,814	0.218	0.236	-0.264	-0.788	-1.575	6.687	0.218	0.236	-0.264	-0.788	-1.575
cg0162	-	Putative membrane protein	-	Fwd	138792	140333	1542	1468	1388	1735	1075	1469	1024	102	6,088	6,296	6,515	5,837	5,298	2,894	0.208	0.427	-0.251	-0.790	-1.193	6.192	0.208	0.427	-0.251	-0.790	-1.193
cg0163	-	Putative membrane protein	M	Fwd	140330	141793	1464	1391	938	1164	1315	1016	691	132	6,088	6,296	6,515	5,837	5,298	2,894	0.048	0.343	-0.210	-0.752	-0.848	6.813	0.048	0.343	-0.210	-0.752	-0.848
cg0165	-	Putative membrane protein	-	Fwd	141797	143530	1734	1660	451	501	597	503	341	62	4,790	4,837	5,133	4,580	4,038	1,572	0.121	0.367	0.138	-1.002	-0.002	6.658	0.121	0.367	0.138	-1.002	-0.002
cg0166	-	Conserved hypothetical protein, Ankyrin repeat	-	Fwd	144729	144734	316	259	647	567	613	1068	994	657	4,821	4,709	5,909	5,555	5,127	4,833	-0.112	1.089	0.734	0.306	0.012	6.192	-0.112	1.089	0.734	0.306	0.012
cg0167	-	Putative membrane protein, DUF81-family	R	Fwd	144732	145484	753	680	229	252	176	168	109	34	5,018	5,052	4,580	4,207	3,665	1,928	0.034	-0.439	-0.811	-1.414	-1.091	5.035	0.034	-0.439	-0.811	-1.414	-1.091
cg0168	-	Putative secondary chromophore transporter, drug/metabolite t	R	Rev	146397	145516	882	808	47	84	63	88	83	56	2,530	3,250	2,884	3,054	2,987	2,403	0.721	0.354	0.524	0.458	-0.127	2.8					

This supplementary table provides the full data for the calculation and development of Table A5.

Gene Information				Read Mapping				Raw Read Count						log ₂ TPM						m-values						m-values						m-values > ±1.5 (significant)						
Locus	Feature	Product	Major COG Cat.	Strand	Start	End	Effective Length	1	2	3	4	5	6	1	2	3	4	5	6	1	2	3	4	5	6	1	2	3	4	5	6	1	2	3	4	5	6	
								VS.	VS.	VS.	VS.	VS.	VS.	VS.	VS.	VS.	VS.	VS.	VS.	VS.	VS.	VS.	VS.	VS.	VS.	VS.	VS.	VS.	VS.	VS.	VS.	VS.	VS.	VS.	VS.	VS.	VS.	
cg0239	-	Hypothetical protein	-	Rev	211760	211533	228	155	177	193	219	207	198	179	6.372	6.393	6.617	6.230	6.183	6.014	0.020	0.245	-0.142	-0.189	-0.358	6.382	0.020	0.245	-0.142	-0.189	-0.358	6.382	0.020	0.245	-0.142	-0.189	-0.358	
cg0240	-	Conserved hypothetical protein	-	Fwd	211786	212287	492	418	222	286	539	518	541	542	5.651	5.152	6.803	6.438	6.518	6.497	0.194	1.152	0.787	0.867	0.846	5.788	0.194	1.152	0.787	0.867	0.846	5.788	0.194	1.152	0.787	0.867	0.846	
cg0241	-	Conserved hypothetical protein	-	Fwd	212284	212739	456	382	130	135	346	340	340	265	4.930	4.875	6.275	5.941	5.797	5.577	-0.055	1.345	1.011	0.867	0.647	4.902	-0.055	1.345	1.011	0.867	0.647	4.902	-0.055	1.345	1.011	0.867	0.647	
cg0242	-	Hypothetical protein	-	Fwd	212765	213661	897	824	426	400	949	907	1061	1417	5.658	5.464	6.752	6.380	6.623	7.015	-0.194	1.093	0.722	0.965	1.357	5.561	-0.194	1.093	0.722	0.965	1.357	5.561	-0.194	1.093	0.722	0.965	1.357	
cg0243	-	Putative membrane protein	-	Fwd	213677	214111	435	362	369	305	319	266	258	260	6.496	6.118	6.226	5.659	5.632	5.618	-0.378	-0.270	-0.837	-0.884	-0.878	6.407	-0.378	-0.270	-0.837	-0.884	-0.878	6.407	-0.378	-0.270	-0.837	-0.884	-0.878	
cg0244	-	Putative membrane protein	-	Fwd	214122	214526	405	332	269	200	237	163	173	124	6.144	5.045	5.902	5.058	5.163	4.659	-0.530	-0.243	-1.086	-0.984	-1.486	6.080	-0.530	-0.243	-1.086	-0.984	-1.486	6.080	-0.530	-0.243	-1.086	-0.984	-1.486	
cg0245	-	Conserved hypothetical protein	S	Fwd	214528	215163	636	563	188	182	213	167	155	160	4.979	4.828	5.097	4.442	4.562	3.823	-0.150	0.319	-0.537	-0.627	-1.155	4.904	-0.150	0.319	-0.537	-0.627	-1.155	4.904	-0.150	0.319	-0.537	-0.627	-1.155	
cg0246	-	Glycosyl transferase	R	Rev	216092	216160	933	859	746	914	961	938	762	481	6.409	6.597	6.713	6.372	6.039	5.402	0.189	0.304	-0.037	-0.319	-1.007	6.503	0.189	0.304	-0.037	-0.319	-1.007	6.503	0.189	0.304	-0.037	-0.319	-1.007	
cg0247	-	Conserved hypothetical protein	-	Rev	216713	215144	600	526	220	266	353	355	257	178	5.288	5.457	5.968	5.610	5.162	4.610	0.169	0.619	0.321	-0.126	-0.679	5.275	0.169	0.619	0.321	-0.126	-0.679	5.275	0.169	0.619	0.321	-0.126	-0.679	
cg0248	-	ABC-type putative polysaccharide transporter, ATPase subunit	G	Rev	219823	212339	799	719	155	168	258	197	135	46	4.385	3.997	4.956	4.363	3.838	2.980	0.012	0.671	-0.023	-0.548	-0.937	4.391	0.012	0.671	-0.023	-0.548	-0.937	4.391	0.012	0.671	-0.023	-0.548	-0.937	
cg0249	-	ABC-type putative polysaccharide transporter, permease subunit	G	Rev	218837	217941	897	823	639	613	684	494	363	167	6.242	6.079	6.280	5.505	5.709	3.938	-0.164	0.037	-0.737	-1.164	-3.304	6.161	-0.164	0.037	-0.737	-1.164	-3.304	6.161	-0.164	0.037	-0.737	-1.164	-3.304	
cg0250	-	aminotransferase class V	R	Fwd	218980	220155	1176	1102	866	976	1294	1319	1258	806	6.290	6.358	6.808	6.529	6.478	5.812	0.069	0.518	0.240	0.188	-0.478	6.324	0.069	0.518	0.240	0.188	-0.478	6.324	0.069	0.518	0.240	0.188	-0.478	
cg0251	-	Quinone oxidoreductase	C	Rev	221132	220152	981	907	410	466	648	749	695	477	5.472	6.024	6.072	5.975	5.885	5.216	0.551	0.599	0.503	0.412	-0.156	5.788	0.551	0.599	0.503	0.412	-0.156	5.788	0.551	0.599	0.503	0.412	-0.156	
cg0252	-	Putative membrane protein	-	Rev	221656	221129	528	454	60	102	31	45	31	25	3.604	4.261	2.602	2.842	2.335	1.983	0.657	-1.002	-0.762	-1.269	-1.621	3.932	0.657	-1.002	-0.762	-1.269	-1.621	3.932	0.657	-1.002	-0.762	-1.269	-1.621	
cg0253	-	Putative 2Fe-2S ferredoxin	C	Fwd	221930	222211	282	208	70	75	159	135	134	125	4.740	4.734	5.851	5.311	5.357	5.193	0.640	0.466	0.422	0.380	0.277	4.737	-0.006	1.112	0.571	0.577	0.777	4.453	-0.006	1.112	0.571	0.577	0.777	4.453
cg0254	-	Conserved hypothetical protein	-	Fwd	222695	222708	1488	1415	1398	1692	413	308	181	51	6.640	6.812	6.823	6.095	5.348	5.156	0.171	0.524	-0.367	0.235	-0.638	6.724	0.171	0.524	-0.367	0.235	-0.638	6.724	0.171	0.524	-0.367	0.235	-0.638	
cg0255	-	Conserved hypothetical protein	-	Fwd	224355	225248	894	820	5	3	8	8	4	-0.490	-1.378	0.035	-0.856	-0.255	-1.327	-0.689	0.524	-0.367	0.235	-0.638	-0.724	6.724	-0.689	0.524	-0.367	0.235	-0.638	-0.724	6.724	-0.689	0.524	-0.367	0.235	-0.638
cg0256	mo08	Molybdopter cofactor synthase, subunit 3	H	Rev	226313	225240	1074	1000	173	238	372	462	564	478	4.104	4.455	5.143	5.149	5.452	5.188	0.351	1.039	1.045	1.348	1.085	4.279	0.351	1.039	1.045	1.348	1.085	4.279	0.351	1.039	1.045	1.348	1.085	
cg0258	mo0f	Molybdopter cofactor synthase, subunit 2	H	Rev	226768	226310	459	379	24	47	62	42	68	58	2.531	3.353	3.792	2.947	3.646	3.383	0.822	1.261	0.416	1.115	0.852	2.942	0.822	1.261	0.416	1.115	0.852	2.942	0.822	1.261	0.416	1.115	0.852	
cg0259	mo0h	Molybdopter cofactor biosynthesis protein, Moq-family	H	Rev	227231	227678	452	397	125	158	223	319	289	47	4.818	5.045	5.587	5.419	5.813	5.695	0.227	0.769	0.801	0.995	0.877	4.936	0.227	0.769	0.801	0.995	0.877	4.936	0.227	0.769	0.801	0.995	0.877	
cg0260	mo0C	Molybdopter cofactor synthase protein, Moa-family	H	Rev	227686	227216	471	397	321	383	637	808	846	813	6.181	6.329	7.105	7.143	7.225	7.144	0.148	0.925	0.962	1.045	0.963	6.255	0.148	0.925	0.962	1.045	0.963	6.255	0.148	0.925	0.962	1.045	0.963	
cg0261	mo0A1	Molybdopter cofactor synthase protein, Moa-family	H	Rev	228888	227701	1188	1115	293	363	350	320	263	149	4.715	4.919	4.910	4.475	4.210	3.369	0.204	0.195	-0.240	-0.505	-1.345	4.847	0.204	0.195	-0.240	-0.505	-1.345	4.847	0.204	0.195	-0.240	-0.505	-1.345	
cg0262	mo0B	ABC-type putative molybdenum transporter, permease subunit	P	Rev	229728	228889	840	765	195	215	170	190	148	67	6.430	4.666	4.372	4.222	3.880	2.717	0.036	-0.257	-0.408	-0.750	-1.917	6.448	0.036	-0.257	-0.408	-0.750	-1.917	6.448	0.036	-0.257	-0.408	-0.750	-1.917	
cg0263	mo0A	ABC-type putative molybdenum transporter, substrate-binding too	H	Rev	230515	229709	807	733	607	668	497	599	613	67	6.608	6.428	6.107	5.425	6.250	6.263	0.169	0.398	0.066	0.569	-0.459	6.466	0.169	0.398	0.066	0.569	-0.459	6.466	0.169	0.398	0.066	0.569	-0.459	
cg0264	-	Putative molybdopter converting factor, small subunit	-	Fwd	230675	230932	258	184	124	147	189	123	113	89	5.684	5.824	6.227	5.306	5.201	4.835	0.140	0.543	-0.378	-0.483	-0.848	5.754	0.140	0.543	-0.378	-0.483	-0.848	5.754	0.140	0.543	-0.378	-0.483	-0.848	
cg0265	-	ABC-type putative molybdenum transporter, ATPase subunit	G	Rev	231843	230929	915	842	498	538	661	555	463	245	5.855	5.862	6.202	5.644	5.400	4.460	0.007	0.347	-0.211	-0.455	-1.395	5.858	0.007	0.347	-0.211	-0.455	-1.395	5.858	0.007	0.347	-0.211	-0.455	-1.395	
cg0266	-	Putative membrane protein	S	Rev	232248	231846	423	349	319	363	351	376	278	135	6.327	6.409	6.402	6.197	5.777	4.712	0.082	0.075	-0.130	-0.550	-0.938	6.348	0.082	0.075	-0.130	-0.550	-0.938	6.348	0.082	0.075	-0.130	-0.550	-0.938	
cg0267	pot	Phenylalanine transferase, AT class 1	S	Rev	232823	232588	1026	952	876	917	847	688	401	67	6.622	6.399	6.007	6.008	6.804	6.001	0.167	0.275	-0.145	-0.428	-1.231	6.448	0.167	0.275	-0.145	-0.428	-1.231	6.448	0.167	0.275	-0.145	-0.428	-1.231	
cg0269	-	Conserved hypothetical protein	-	Fwd	233914	234822	909	836	184	224	237	323	317	167	4.337	4.611	4.735	4.874	4.864	3.919	0.179	0.303	0.442	0.432	-0.514	4.522	0.179	0.303	0.442	0.432	-0.514	4.522	0.179	0.303	0.442	0.432	-0.514	
cg0270	-	Hypothetical protein	-	Rev	235192	234908	2																															

This supplementary table provides the full data for the calculation and development of Table S3.

Gene Information			Read Mapping			Raw Read Count			log ₂ TPM			m-values			a-value			m-values < ±1.5 (not significant)			m-values ≥ ±1.5 (significant)											
Locus	Feature	Product	Major COG Cat.	Strand	Start	End	Length (bp)	Effective Length	1	2	3	4	5	6	1	2	3	4	5	6	1	2	3	4	5	6	1	2	3	4	5	6
cg0350	ghrR	Transcriptional regulator, Crp-family	T	Rev	307462	306779	684	610	7192	8492	3216	3984	4658	3588	10.239	10.260	8.902	8.905	9.148	8.746	0.020	-1.337	-1.334	-1.092	-1.493	10.230	0.020	-1.337	-1.334	-1.092	-1.493	
cg0352	Putative secreted protein	-	-	Rev	337909	337214	186	111	518	550	587	671	626	353	8.210	8.192	8.289	8.216	8.133	7.283	-0.027	-0.119	0.006	-0.077	-0.927	-0.201	-0.017	-0.119	0.006	-0.077	-0.927	
cg0353	nth	Putative endonuclease III	-	L	307955	308737	783	710	343	336	371	379	285	284	5.543	5.409	5.595	5.320	4.427	4.897	-0.133	0.052	-0.223	-0.616	-0.646	5.476	-0.133	0.052	-0.223	-0.616	-0.646	
cg0354	-	Putative secreted thiadiazole isomerase	-	O	Fwd	308745	309305	561	487	240	274	232	302	257	220	5.510	5.975	5.398	5.472	5.256	5.008	0.087	-0.112	-0.039	-0.254	-0.503	5.554	0.087	-0.112	-0.039	-0.254	-0.503
cg0355	-	Putative NTP pyrophosphohydrolase	-	L	Fwd	309298	310041	744	670	190	201	223	208	241	148	4.768	4.745	4.997	4.527	4.756	4.030	-0.023	0.229	-0.240	-0.011	-0.728	4.756	-0.023	0.229	-0.240	-0.011	-0.728
cg0356	-	Putative membrane-associated serine protease, membrane protein	-	O	Fwd	310132	311328	1197	1123	633	476	403	398	303	119	5.813	5.299	5.102	4.741	4.494	3.036	-0.514	-0.711	-1.071	-1.318	-0.978	5.855	-0.514	-0.711	-1.071	-1.318	-0.978
cg0358	-	Putative hydrolase/acyltransferase	-	R	Rev	312891	311896	996	923	569	612	662	770	889	493	5.924	5.925	6.462	5.993	6.217	5.343	0.001	0.538	0.069	0.293	-0.581	5.925	0.001	0.538	0.069	0.293	-0.581
cg0359	-	Putative membrane protein	-	Rev	313511	312906	606	532	1846	2060	2858	2616	3004	1953	8.337	8.392	8.907	8.473	8.690	8.044	0.054	0.570	0.136	0.352	-0.293	8.364	0.054	0.570	0.136	0.352	-0.293	
cg0360	-	Conserved hypothetical protein	-	E	Fwd	314444	313622	843	769	766	623	778	787	706	351	6.593	6.192	6.555	6.265	6.126	5.095	-0.401	-0.038	-0.328	-0.467	-1.498	6.593	-0.401	-0.038	-0.328	-0.467	-1.498
cg0362	-	Conserved hypothetical protein	-	D	Fwd	314908	316085	1098	1024	45	67	53	98	89	61	1.021	0.882	0.475	0.550	0.779	-0.045	-0.135	-0.546	-0.742	-1.066	1.021	-0.135	-0.546	-0.742	-1.066		
cg0363	-	Putative secreted ATPase	-	N	Fwd	316002	317135	1134	1060	9	19	10	15	4	0.096	0.764	-0.019	-0.325	0.232	-1.470	0.860	0.077	-0.229	0.328	-1.375	0.334	0.860	0.077	-0.229	0.328	-1.375	
cg0364	-	Putative membrane protein	-	U	Fwd	317120	317896	777	703	5	5	4	9	5	7	-0.287	-0.391	-0.611	0.083	-0.637	-0.247	-0.104	-0.324	0.370	-0.350	0.040	-0.334	-0.104	-0.324	0.370	-0.350	0.040
cg0365	-	Conserved hypothetical protein	-	U	Fwd	317893	318468	576	503	45	67	53	98	89	61	0.460	0.171	0.586	0.619	0.056	0.460	0.171	0.586	0.619	0.056	0.460	0.171	0.586	0.619	0.056		
cg0366	-	Conserved putative membrane protein	-	Fwd	318492	318692	201	127	7	5	8	7	4	4	2.078	1.559	2.188	1.712	1.051	1.026	-0.519	0.109	-0.367	-1.028	-1.053	1.819	-0.519	0.109	-0.367	-1.028	-1.053	
cg0368	-	Conserved putative secreted protein	-	Fwd	318696	319016	321	247	7	8	19	16	14	7	1.403	1.469	2.664	2.081	1.911	0.935	0.066	1.261	0.678	0.508	-0.468	1.436	0.066	1.261	0.678	0.508	-0.468	
cg0369	-	Conserved putative secreted protein	-	Fwd	318991	319338	348	274	14	14	5	11	8	3	2.193	0.768	1.811	1.007	-0.256	1.435	-1.426	-0.383	-1.181	-0.988	-1.758	1.440	-1.426	-0.383	-1.181	-0.988	-1.758	
cg0370	-	Conserved hypothetical protein	-	Fwd	321690	319333	2458	2284	662	639	511	478	359	172	4.899	4.764	4.463	4.066	3.668	2.986	0.489	4.764	4.463	4.066	3.668	2.986	0.489	4.764	4.463	4.066	3.668	2.986
cg0371	cpoB	Cold-shock protein B	R	K	Fwd	322007	322210	204	131	10323	10507	8024	8283	7307	2720	12.391	12.312	11.967	11.760	11.544	10.092	-0.078	-0.424	-0.684	-0.848	-2.298	12.352	-0.078	-0.424	-0.684	-0.848	-2.298
cg0373	topA	DNA topoisomerase I	L	Fwd	322911	325901	2991	2918	3851	3760	2999	3117	2736	1550	6.990	6.956	6.673	6.423	6.252	5.407	-0.033	-0.316	-0.567	-0.738	-1.582	6.973	-0.033	-0.316	-0.567	-0.738		
cg0374	-	Conserved hypothetical protein	-	Fwd	325905	324618	714	641	328	243	282	271	254	149	5.612	5.077	5.334	5.121	4.894	4.104	-0.535	-0.278	-0.490	-0.717	-1.582	5.644	-0.535	-0.278	-0.490	-0.717		
cg0375	cyoB	Adenylate cyclase	T	Rev	328219	326693	1527	1453	3825	1115	1104	1109	1012	625	5.843	6.176	6.202	5.903	5.788	5.068	0.330	3.359	0.060	-0.055	-0.775	6.008	0.330	3.359	0.060	-0.055	-0.775	
cg0376	dnaxX	Putative DNA polymerase III, delta' subunit	L	Fwd	328284	329543	1260	1187	278	260	399	384	382	260	4.554	4.354	5.013	4.652	4.662	4.084	-0.200	0.459	0.998	0.107	-0.471	4.454	-0.200	0.459	0.998	0.107	-0.471	
cg0378	-	Putative phase-associated protein	-	S	Fwd	329934	333080	447	374	380	507	645	940	814	915	6.499	6.810	7.200	7.437	7.246	7.390	0.311	0.701	0.938	0.747	0.891	6.655	0.311	0.701	0.938	0.747	0.891
cg0380	-	Conserved hypothetical protein	-	Fwd	329574	329013	240	167	456	426	414	295	414	187	5.556	5.908	6.481	6.268	6.576	6.258	-0.457	0.075	0.149	0.060	-0.560	5.652	-0.457	0.075	0.149	0.060	-0.560	
cg0382	-	Conserved hypothetical protein	-	Fwd	330974	331537	564	490	121	122	92	109	101	60	4.521	4.429	4.068	4.005	3.913	3.466	-0.092	-0.452	-0.516	-0.608	-1.375	4.475	-0.092	-0.452	-0.516	-0.608	-1.375	
cg0384	rbcC1	Pseudouridylyl synthase	J	Fwd	331553	332437	885	812	81	91	35	56	26	12	3.297	3.360	2.049	2.006	1.315	0.226	0.062	-1.248	-0.891	-0.932	-0.938	3.328	0.062	-1.248	-0.891	-0.932	-0.938	
cg0385	hsp27	Beta-glucosidase, putative pseudogene (N-terminal fragment)	-	Fwd	332920	334656	1647	1571	37	43	23	46	50	34	1.292	1.399	0.568	1.216	1.366	0.798	0.108	-0.724	-0.075	0.075	-0.493	1.244	0.108	-0.724	-0.075	0.075	-0.493	
cg0387	hsp25	Beta-glucosidase, putative pseudogene (C-terminal fragment)	-	Fwd	334550	334917	408	322	6	8	4	11	11	7	0.864	1.123	0.818	1.214	0.877	1.011	0.259	-0.446	0.350	1.013	0.519	0.781	0.259	-0.446	0.350	1.013	0.519	
cg0388	-	Putative NAD/methylol-dependent formaldehyde dehydrogenase	-	C	Fwd	335010	334616	1107	1034	2230	2534	2124	2971	3299	3791	7.740	7.821	7.610	7.787	7.955	8.131	0.080	-0.131	0.047	0.215	0.391	7.981	0.080	-0.131	0.047	0.215	0.391
cg0388	-	Putative Zn-dependent hydrolase	-	R	Fwd	336117	336752	636	565	1316	1475	1313	1756	2040	2184	7.780	7.840	7.716	7.829	8.062	8.135	0.061	-0.064	0.049	0.282	0.356	7.645	0.061	-0.064	0.049	0.282	0.356
cg0390	-	Putative Zn-dependent hydrolase	-	Fwd	336783	337451	672	599	1033	1162	1023	1166	1303	1461	1506	6.129	6.173	6.512	6.466	6.912	6.707	-0.019	0.053	-0.041	-0.339	-1.492	6.129	-0.019	0.053	-0.041	-0.339	-1.492
cg0390	-	Putative multidrug efflux permease, MFS-type	-	G	Fwd	337570	338772	1203	1129	523	659	486	504	419	95	5.330	5.759	5.354	5.110	4.861	2.707	0.229	-0.166	-0.420	-0.669	-0.823	5.615	0.229	-0.166	-0.420	-0.669	-0.823
cg0391	rmb2B	Conserved putative ATP-ase, 6,6-dehydratase	-	M	Fwd	338794	339729	936	863	1642	2138	1826	1929	1640	864	7.541	7.818	7.634	7.407	7.158	6.241	0.277	0.093	-0.134	-0.383	-1.300	7.680	0.277	0.093	-0.134	-0.383	-1.300
cg0393	-	Conserved putative membrane protein	-	R	Fwd	340570	340193	378	303	243	311	298	225	222	114	6.098	6.346	6.328	5.617	5.168	4.638	0.249	0.230	-0.480	-0.480	-1.460	6.222	0.249	0.230	-0.480	-0.480	-1.460
cg0393	-	Putative glycosyl transferase	-	M	Fwd	341288	341563	287	214	708	743	656	634	619	473	4.649	4.648	4.977	4.626	4.914	4.859	-0.047	0.083	-0.197	0.135	-0.271	4.649	-0.047	0.083	-0.197	0.135	-0.271
cg0395	-	putative ribonuclease H	-	L	Fwd	341357	342379	1023	950	297	295	273	274	199	117	4.950	4.836															

This supplementary table provides the full data for the calculation and development of Table 2.

Gene Information				Read Mapping				Raw Read Count						log ₂ TPM						m-values						m-values < ±1.5 (not significant)						m-values > ±1.5 (significant)													
Locus	Feature	Product	Major COG Cat.	Strand	Start	End	Effective Length	① ② ③ ④ ⑤ ⑥						① ② ③ ④ ⑤ ⑥						① ② ③ ④ ⑤ ⑥						① ② ③ ④ ⑤ ⑥						① ② ③ ④ ⑤ ⑥													
								1	2	3	4	5	6	1	2	3	4	5	6	1	2	3	4	5	6	1	2	3	4	5	6	1	2	3	4	5	6								
cg468	-	ABC-type putative hemin transporter, permease subunit	P	Fwd	413636	414712	1077	1003	86	107	128	136	124	110	3,100	3,308	3,607	3,388	3,273	3,076	0.208	0.508	0.288	0.173	-0.023	7,204	0.208	0.508	0.288	0.173	-0.023	7,204	0.208	0.508	0.288	0.173	-0.023	7,204	0.208	0.508	0.288	0.173	-0.023		
cg469	-	ABC-type putative hemin transporter, ATPase subunit	G	Fwd	41713	415528	816	742	86	65	64	37	46	51	3,500	3,702	4,019	3,938	2,262	2,383	-0.502	-0.481	-0.968	-1.238	-1.117	7,204	-0.502	-0.481	-0.968	-1.238	-1.117	7,204	-0.502	-0.481	-0.968	-1.238	-1.117	7,204	-0.502	-0.481	-0.968	-1.238	-1.117		
cg470	-	Conserved secreted protein	-	Fwd	415642	416601	960	887	31	40	25	13	6	8	1,822	2,076	1,462	0.263	-0.720	-0.382	0.254	-0.360	-1.559	-2.542	-2.025	1,949	0.254	-0.360	-1.559	-2.542	-2.025	1,949	0.254	-0.360	-1.559	-2.542	-2.025	1,949	0.254	-0.360	-1.559	-2.542	-2.025		
cg471	-	Conserved secreted protein	-	Fwd	416602	417441	840	767	19	16	8	6	13	8	1,337	0.999	0.124	-0.544	0.473	-0.190	-0.338	-1.213	-0.864	-1.527	-1.144	1,168	-0.338	-1.213	-0.864	-1.527	-1.144	1,168	-0.338	-1.213	-0.864	-1.527	-1.144	1,168	-0.338	-1.213	-0.864	-1.527	-1.144		
cg472	-	Conserved hypothetical protein	-	Rev	418347	417541	807	734	897	784	575	523	392	131	6,884	6,586	6,182	5,740	5,342	3,743	-0.298	-0.701	-1.144	-0.939	-1.144	6,775	-0.298	-0.701	-1.144	-0.939	-1.144	6,775	-0.298	-0.701	-1.144	-0.939	-1.144	6,775	-0.298	-0.701	-1.144	-0.939	-1.144		
cg474	-	Conserved hypothetical protein	-	Rev	419252	419437	816	742	781	816	807	596	506	202	6,668	6,421	6,455	5,912	5,749	4,926	-0.041	-0.013	-0.756	-0.913	-1.742	6,668	-0.041	-0.013	-0.756	-0.913	-1.742	6,668	-0.041	-0.013	-0.756	-0.913	-1.742	6,668	-0.041	-0.013	-0.756	-0.913	-1.742		
cg475	-	Conserved hypothetical protein	-	Rev	419756	419253	504	431	3389	3879	5356	4448	3974	2262	9,479	9,570	10,079	9,705	9,509	8,522	0.091	0.600	0.026	-0.120	-0.958	9,525	0.091	0.600	0.026	-0.120	-0.958	9,525	0.091	0.600	0.026	-0.120	-0.958	9,525	0.091	0.600	0.026	-0.120	-0.958		
cg476	murB2	Putative UDP-N-acetylmuramate dehydrogenase	M	Fwd	419781	420887	1107	1033	405	466	350	227	239	96	5,282	5,379	5,010	4,083	4,174	2,842	0.097	-0.273	-1.199	-1.108	-2.440	5,331	0.097	-0.273	-1.199	-1.108	-2.440	5,331	0.097	-0.273	-1.199	-1.108	-2.440	5,331	0.097	-0.273	-1.199	-1.108	-2.440		
cg477	-	Hypothetical protein	-	Fwd	420880	421518	639	565	164	159	203	161	134	62	4,776	4,946	5,018	4,383	4,137	3,012	0.303	0.242	-0.042	-0.093	-0.883	4,861	0.303	0.242	-0.042	-0.093	-0.883	4,861	0.303	0.242	-0.042	-0.093	-0.883	4,861	0.303	0.242	-0.042	-0.093	-0.883		
cg478	-	Hypothetical protein	-	Fwd	421568	421666	159	85	15	11	12	3	3	4	4,416	898	1,056	0.050	1.067	3.964	-0.519	-0.360	-0.960	-0.000	-0.000	4,586	-0.519	-0.360	-0.960	-0.000	-0.000	4,586	-0.519	-0.360	-0.960	-0.000	-0.000	4,586	-0.519	-0.360	-0.960	-0.000	-0.000		
cg480	fatD5	Long-chain fatty-acyl-CoA ligase	I	Fwd	423792	422086	1707	1634	2242	2415	3757	3340	3888	4824	7,123	7,127	7,807	7,322	7,568	7,854	0.003	0.684	0.208	0.444	0.731	7,125	0.003	0.684	0.208	0.444	0.731	7,125	0.003	0.684	0.208	0.444	0.731	7,125	0.003	0.684	0.208	0.444	0.731		
cg481	msmA	Phosphoglycerate mutase I	G	Fwd	423877	425133	1257	1184	628	735	921	974	870	807	5,731	5,853	6,222	5,996	5,850	5,717	0.123	0.491	0.266	0.120	-0.013	5,792	0.123	0.491	0.266	0.120	-0.013	5,792	0.123	0.491	0.266	0.120	-0.013	5,792	0.123	0.491	0.266	0.120	-0.013		
cg482	osmA	Phosphoglycerate mutase I	G	Fwd	425136	425292	747	673	5825	7138	14403	13973	15828	12667	9,695	9,999	10,938	10,588	10,785	10,439	0.303	0.242	0.893	1.090	0.744	9,887	0.303	0.242	0.893	1.090	0.744	9,887	0.303	0.242	0.893	1.090	0.744	9,887	0.303	0.242	0.893	1.090	0.744		
cg483	cut54	Two-component system, sensory histidine kinase	T	Fwd	425933	427174	1242	1169	1978	1819	2765	2715	3208	2245	7,401	7,177	7,824	7,492	7,439	7,210	-0.225	0.422	0.090	0.348	-0.192	7,289	-0.225	0.422	0.090	0.348	-0.192	7,289	-0.225	0.422	0.090	0.348	-0.192	7,289	-0.225	0.422	0.090	0.348	-0.192		
cg484	cutM4	Two-component system, transcriptional response regulator	T	Fwd	427171	427869	699	625	766	871	1405	1410	1452	834	6,863	6,945	7,676	7,376	7,435	6,611	0.081	0.813	0.513	0.572	-0.252	6,904	0.081	0.813	0.513	0.572	-0.252	6,904	0.081	0.813	0.513	0.572	-0.252	6,904	0.081	0.813	0.513	0.572	-0.252		
cg485	-	Hypothetical protein	-	S	Fwd	428560	429441	882	809	20	15	16	17	10	7	1,337	0.841	0.972	0.748	0.054	-0.430	-0.496	-0.365	-0.589	-1.767	1,089	-0.496	-0.365	-0.589	-1.767	1,089	-0.496	-0.365	-0.589	-1.767	1,089	-0.496	-0.365	-0.589	-1.767	1,089	-0.496	-0.365	-0.589	-1.767
cg486	-	ABC-type transporter, ATPase and permease subunit	V	Rev	432022	429434	239	231	718	388	822	922	215	130	4,881	4,891	4,135	3,360	2,796	2,050	-0.990	-0.746	-0.960	-0.000	-0.831	4,586	-0.990	-0.746	-0.960	-0.000	-0.831	4,586	-0.990	-0.746	-0.960	-0.000	-0.831	4,586	-0.990	-0.746	-0.960	-0.000	-0.831		
cg487	-	Conserved hypothetical protein	-	Rev	433027	432122	906	833	392	318	415	455	351	160	5,527	5,120	5,546	5,372	5,106	3,862	-0.405	0.021	-0.152	-0.509	-1.662	5,322	-0.405	0.021	-0.152	-0.509	-1.662	5,322	-0.405	0.021	-0.152	-0.509	-1.662	5,322	-0.405	0.021	-0.152	-0.509	-1.662		
cg488	pxp1	Polyphosphatase, Ppx/GpsA-family	F	Fwd	433061	433990	930	857	1829	2133	2277	2195	2169	1103	7,706	7,824	7,961	7,602	7,602	6,602	0.118	0.255	-0.104	-0.104	-1.104	7,765	0.118	0.255	-0.104	-0.104	-1.104	7,765	0.118	0.255	-0.104	-0.104	-1.104	7,765	0.118	0.255	-0.104	-0.104	-1.104		
cg489	-	Putative membrane protein	M	Fwd	434018	434824	816	734	1658	2021	2028	2076	1961	1165	7,769	7,951	7,999	7,727	7,676	6,886	0.182	0.230	-0.042	-0.093	-0.883	7,860	0.182	0.230	-0.042	-0.093	-0.883	7,860	0.182	0.230	-0.042	-0.093	-0.883	7,860	0.182	0.230	-0.042	-0.093	-0.883		
cg490	proc	Glutamate-5-carboxylase repressor	E	Fwd	434885	435697	813	740	1215	1321	1401	1315	1288	991	7,310	7,327	7,455	7,058	7,045	6,642	0.017	0.145	-0.253	-0.266	-0.668	7,319	0.017	0.145	-0.253	-0.266	-0.668	7,319	0.017	0.145	-0.253	-0.266	-0.668	7,319	0.017	0.145	-0.253	-0.266	-0.668		
cg491	-	Hypothetical protein	-	Fwd	435887	435955	69	1	731	900	717	787	681	348	10,136	10,032	10,047	9,875	9,868	8,693	0.197	-0.089	-0.260	-0.452	-1.442	10,234	0.197	-0.089	-0.260	-0.452	-1.442	10,234	0.197	-0.089	-0.260	-0.452	-1.442	10,234	0.197	-0.089	-0.260	-0.452	-1.442		
cg492	-	Putative DNA-binding (excisionase) protein	-	Fwd	435948	436139	192	117	1799	2114	1722	1883	1619	811	9,958	10,037	9,834	9,657	9,456	8,435	0.129	-0.124	-0.301	-0.502	-1.523	10,022	0.129	-0.124	-0.301	-0.502	-1.523	10,022	0.129	-0.124	-0.301	-0.502	-1.523	10,022	0.129	-0.124	-0.301	-0.502	-1.523		
cg493	-	Hypothetical protein	-	Fwd	436206	436446	141	88	1326	1028	1014	606	1279	869	12,172	12,284	12,094	11,606	11,079	9,829	0.129	-0.124	-0.301	-0.502	-1.523	12,260	0.129	-0.124	-0.301	-0.502	-1.523	12,260	0.129	-0.124	-0.301	-0.502	-1.523	12,260	0.129	-0.124	-0.301	-0.502	-1.523		
cg494	-	Conserved hypothetical protein	-	Fwd	436462	436563	102	28	2040	2374	1678	1606	1237	546	11,052	11,167	10,710	10,340	9,981	6,977	0.115	-0.342	-0.712	-1.071	-1.078	11,109	0.115	-0.342	-0.712	-1.071	-1.078	11,109	0.115	-0.342	-0.712	-1.071	-1.078	11,109	0.115	-0.342	-0.712	-1.071	-1.078		
cg495	-	Putative phosphatase	E	Rev	438043	436976	1																																						

This supplementary table provides the full data for the calculation and development of Table A5.

Gene Information				Read Mapping				Raw Read Count				log ₂ TPM				m-values				m-values < ±1.5 (not significant)				m-values ≥ ±1.5 (significant)								
Locus	Feature	Product	Major COG Cat.	Strand	Start	End	Effective Length	①	②	③	④	⑤	⑥	①	②	③	④	⑤	⑥	①	②	③	④	⑤	⑥	①	②	③	④	⑤	⑥	
cg0578	-	Putative membrane protein	-	Fwd	520670	520852	183	109	111	12	5	13	16	4	2,799	2,810	1,738	2,654	2,997	1,161	0.012	-1.061	-0.144	0.153	-0.688	7.874	0.012	-1.061	-0.144	0.153	-0.688	-1.628
cg0579	-	Transcriptional regulatory protein, HTH-3 family	-	Fwd	520864	521466	783	709	101	122	124	149	108	6	3,789	3,953	4,022	3,979	3,535	2,742	0.166	0.233	0.190	-0.254	-1.047	8.892	0.166	0.233	0.190	-0.254	-1.047	-0.892
cg0580	-	Conserved hypothetical protein	-	Fwd	522370	521675	696	623	447	454	542	538	521	962	6,094	6,012	6,311	5,994	5,965	6,823	-0.081	0.217	-0.100	-0.129	0.729	6.053	-0.081	0.217	-0.100	-0.129	0.729	-0.823
cg0581	rnsL	30S ribosomal protein S12	J	Fwd	522693	520361	369	296	6573	7964	3979	4333	4768	895	10,884	11,058	10,100	9,917	10,672	7,635	0.173	-0.785	-0.968	-0.813	-3.250	10.971	0.173	-0.785	-0.968	-0.813	-3.250	-3.250
cg0582	rpsG	50S ribosomal protein S7	J	Fwd	523068	525355	468	395	6881	8579	4276	4579	5138	955	10,608	10,822	9,861	9,653	9,987	7,385	0.214	-0.747	-0.954	-0.771	-3.222	10.715	0.214	-0.747	-0.954	-0.771	-3.222	-3.222
cg0583	lucA	Elongation factor G	J	Fwd	523983	520012	2130	2057	29358	33191	29041	23912	23993	10350	10,464	10,134	10,387	9,852	8,973	8,636	0.123	-0.077	-0.613	-0.591	-1.828	10.556	0.123	-0.077	-0.613	-0.591	-1.828	-1.828
cg0587	luf	Elongation factor T	J	Fwd	526375	527565	1911	1118	79137	108746	94780	80954	78416	21369	12,783	13,138	12,983	12,450	12,421	10,520	0.355	0.200	-0.334	-0.363	-2.263	12.961	0.355	0.200	-0.334	-0.363	-2.263	-2.263
cg0588	-	Hypothetical protein	-	Fwd	528039	528970	732	658	254	313	368	406	338	249	5,208	5,404	5,681	5,516	5,269	4,805	0.196	0.472	0.308	0.061	-0.403	5.306	0.196	0.472	0.308	0.061	-0.403	-0.403
cg0589	-	ABC-type putative iron-siderophore transporter, ATPase subunit	G	Fwd	528656	529775	795	722	88	69	24	1	2	0	3,750	3,120	1,678	-2,272	-1,470	-2,280	-0.450	-0.844	-0.848	-0.848	-0.848	6.315	-0.450	-0.844	-0.848	-0.848	-0.848	-0.848
cg0590	-	ABC-type putative iron-siderophore transporter, permease subunit	P	Fwd	530754	529588	1167	1093	126	200	54	43	24	10	3,524	3,084	2,282	1,634	3,835	-0.374	0.561	-1.262	-1.890	-1.890	-1.890	6.804	0.561	-1.262	-1.890	-1.890	-1.890	-1.890
cg0591	-	ABC-type putative iron-siderophore transporter, permease subunit	P	Fwd	531990	530704	1047	973	197	215	71	27	12	2	4,323	4,345	2,807	1,138	0,048	-2,092	0.022	-0.816	-1.385	-0.475	-6.415	4.334	0.022	-0.816	-1.385	-0.475	-6.415	-6.415
cg0592	-	Putative acetate CoA-transferase	C	Fwd	532007	532255	191	143	26	14	15	12	21	4	2,465	1,513	1,649	1,104	1,820	3,343	-0.952	-0.816	-1.421	-0.645	-2.808	4.989	-0.952	-0.816	-1.421	-0.645	-2.808	-2.808
cg0593	rnsI	30S ribosomal protein S10	J	Fwd	533071	532403	333	259	12603	14763	6769	7531	6855	2495	11,972	12,096	11,014	10,862	10,743	9,261	0.124	-0.957	-1.109	-1.228	-1.713	12.004	0.124	-0.957	-1.109	-1.228	-1.713	-1.713
cg0594	rpsC	50S ribosomal protein L3	J	Fwd	533436	534092	657	584	10597	16304	7419	8142	7911	2642	11,238	11,259	10,166	9,964	9,970	8,363	0.021	-1.072	-1.244	-1.269	-2.876	11.249	0.021	-1.072	-1.244	-1.269	-2.876	-2.876
cg0596	rpsD	50S ribosomal protein L4	J	Fwd	534089	534745	657	583	10331	12313	5845	6026	6226	2051	10,704	10,854	9,822	9,560	9,624	7,998	0.149	-0.882	-1.144	-1.080	-2.707	10.779	0.149	-0.882	-1.144	-1.080	-2.707	-2.707
cg0597	rpsW	50S ribosomal protein L23	J	Fwd	534745	535020	306	232	4293	4895	2235	2252	2441	768	10,540	10,624	9,538	9,243	9,376	7,684	0.085	-1.002	-1.297	-1.164	-2.856	10.583	0.085	-1.002	-1.297	-1.164	-2.856	-2.856
cg0598	rpsB	50S ribosomal protein L2	J	Fwd	535075	535917	843	769	11314	12349	6841	6921	6901	2233	10,476	10,487	9,631	9,240	8,413	7,761	0.031	-0.845	-1.236	-1.063	-2.715	10.481	0.031	-0.845	-1.236	-1.063	-2.715	-2.715
cg0599	rpsS	50S ribosomal protein S19	J	Fwd	535934	536023	279	206	4498	4914	2563	2549	2858	871	10,741	10,764	9,869	9,555	9,377	7,999	0.024	-0.872	-1.186	-1.004	-2.742	10.793	0.024	-0.872	-1.186	-1.004	-2.742	-2.742
cg0600	rpsV	50S ribosomal protein L22	J	Fwd	536216	536778	363	289	6384	7064	3890	3774	4025	1223	10,866	10,908	10,091	9,741	9,851	8,108	0.042	-0.775	-1.125	-1.015	-2.758	10.887	0.042	-0.775	-1.125	-1.015	-2.758	-2.758
cg0601	rpsC	50S ribosomal protein S3	J	Fwd	536578	537324	747	673	8865	9761	5819	5748	5784	1634	10,298	10,334	9,630	9,230	9,333	7,484	0.036	-0.668	-1.069	-0.966	-2.814	10.366	0.036	-0.668	-1.069	-0.966	-2.814	-2.814
cg0602	rpsP	50S ribosomal protein L16	J	Fwd	537327	537743	417	344	7617	8708	4885	4599	5054	1459	10,122	11,023	10,219	9,826	9,759	8,102	0.103	-0.701	-1.094	-0.941	-2.758	10.972	0.103	-0.701	-1.094	-0.941	-2.758	-2.758
cg0603	rpsM	50S ribosomal protein S29	-	Fwd	537743	537973	231	158	5198	6498	3318	3534	3767	1252	11,222	11,440	10,513	10,298	10,408	8,794	0.218	-0.708	-0.923	-0.814	-2.428	11.331	0.218	-0.708	-0.923	-0.814	-2.428	-2.428
cg0604	rpsQ	30S ribosomal protein S14	J	Fwd	537976	538254	279	206	3876	4320	2338	2833	3048	1239	10,526	10,579	9,725	9,707	9,430	8,507	0.051	-0.801	-0.819	-0.696	-2.808	10.552	0.051	-0.801	-0.819	-0.696	-2.808	-2.808
cg0605	-	Putative membrane protein	-	Fwd	538666	539377	270	197	316	386	186	147	133	4	6,867	6,120	6,190	7,482	6,817	6,316	0.127	-0.787	-1.018	-1.355	-3.812	6.133	0.127	-0.787	-1.018	-1.355	-3.812	-3.812
cg0607	-	Putative secreted protein	-	Rev	539412	538714	699	625	669	342	144	90	72	35	6,668	5,998	4,400	3,421	3,120	2,076	-1.070	-0.249	-0.247	-0.348	-4.593	6.133	-1.070	-0.249	-0.247	-0.348	-4.593	-4.593
cg0608	rpsM	50S ribosomal protein L4	J	Fwd	539740	540108	369	296	14491	17896	8484	8632	8088	1242	12,025	12,226	11,192	10,911	10,334	8,107	0.201	-0.833	-1.114	-1.191	-3.918	12.125	0.201	-0.833	-1.114	-1.191	-3.918	-3.918
cg0609	rpsP	50S ribosomal protein L24	J	Fwd	540111	540425	315	242	9353	11448	5789	5576	5089	889	11,621	11,809	10,869	10,509	10,394	7,853	0.188	-0.753	-1.113	-1.228	-3.746	11.775	0.188	-0.753	-1.113	-1.228	-3.746	-3.746
cg0610	rpsK	50S ribosomal protein L1	J	Fwd	540425	541000	576	502	12397	15908	8042	7835	7632	1160	11,497	11,423	10,472	10,128	9,716	8,463	0.256	-0.684	-1.028	-1.049	-3.781	11.794	0.256	-0.684	-1.028	-1.049	-3.781	-3.781
cg0611	-	Putative secreted protein	-	Fwd	541107	542081	975	902	180	219	169	125	96	18	6,200	4,418	4,149	3,441	3,050	6,73	0.178	-0.151	-0.889	-1.250	-3.626	6.389	0.178	-0.151	-0.889	-1.250	-3.626	-3.626
cg0612	dkz	Putative aldo/keto reductase, related to diketolactone reductase	R	Rev	542895	542086	810	737	489	486	801	1043	1000	1414	6,004	5,892	6,654	6,279	6,685	7,160	-0.113	0.650	0.725	0.681	1.155	5.948	-0.113	0.650	0.725	0.681	1.155	1.155
cg0614	rpsL	50S ribosomal protein L5	J	Fwd	542411	542973	562	492	614	624	475	421	421	604	11,421	11,421	10,472	10,128	9,716	8,463	0.256	-0.684	-1.028	-1.049	-3.781	11.794	0.256	-0.684	-1.028	-1.049	-3.781	-3.781
cg0616	fdhD	Putative formate dehydrogenase, FdhA-family	C	Rev	544238	544310	918	844	265	261	220	253	150	45	4,942	4,817	4,614	4,509	3,776	3,702	-0.126	-0.328	-0.433	-1.167	-1.240	4.879	-0.126	-0.328	-0.433	-1.167	-1.240	-1.240
cg0618	fdhF	Putative formate dehydrogenase, FdhA-family alpha chain	C	Rev	544669	544331	339	265	134	118	119	154	92	128	5,401	5,115	4,170	5,234	4,514	4,961	-0.286	-0.231	-0.167	-0.887	-0.440	6.258	-0.286	-0.231	-0.167	-0.887	-0.440	-0.440
cg0619	ftsZ	Putative secreted protein	-	Fwd	547041	544753	2289	2215	2136	3026	3017	3839	4363	2929	6,630	7,029	7,068	7,109	7,311	7,135	0.399	0.437	0.479	0.680	0.504	5.829						

This supplementary table provides the full data for the calculation and development of Table A5.

Gene Information			Read Mapping		Raw Read Count		log ₂ TPM		m-values		m-values < ±1.5 (not significant)		m-values > ±1.5 (significant)	
Locus	Feature	Product	Major COG Cat.	Strand	Start	End	Length (bp)	Effective Length	①	②	③	④	⑤	⑥
cg0690	groES	10kDa chaperonin	O	Fwd	610349	610648	300	226	5288	6245	4402	3328	3127	824
cg0691	groEL	60kDa chaperonin, putative pseudogenes (N-terminal fragment)	O	Fwd	610660	611034	375	301	3251	3551	2618	2047	1604	461
cg0692	hsp101(cy2c)	Thermoplasma	O	L	611123	612433	1311	1238	75	73	84	80	98	79
cg0693	groEL	60kDa chaperonin, putative pseudogenes (C-terminal fragment)	O	Fwd	612457	613737	1281	1208	14952	17792	12985	9501	8727	2531
cg0695	whiB3	Transcriptional regulator protein, WhiB-family	R	Rev	614175	612876	300	226	12	8	6	11	3	1
cg0696	sigP	RNA polymerase sigma factor, ECF-family	K	Fwd	614637	615183	567	494	5106	3477	2463	2578	2240	1129
cg0697	-	Conserved hypothetical protein	-	Rev	615183	612211	1029	956	9794	6072	4602	4439	4269	2079
cg0698	-	Conserved hypothetical protein	-	Rev	616641	616261	381	309	284	222	415	471	373	185
cg0699	impD	IMP dehydrogenase	F	Fwd	616797	618317	1521	1448	4927	5376	7124	6437	4704	1900
cg0700	quoB3	IMP dehydrogenase/GMP reductase	F	Fwd	618434	619588	1125	1052	2657	3473	3124	2121	2112	1140
cg0701	-	Putative secondary drug/metabolite transporter, drug/metabolite	R	Rev	620456	619551	906	832	5	12	12	8	12	
cg0702	-	Putative transcriptional regulator, LysK-family	K	Fwd	620547	621458	912	839	30	38	20	26	25	21
cg0703	quaA	Putative GMP synthase	F	Fwd	621465	622036	1572	1459	6190	6913	7877	7453	6887	3342
cg0704	-	Conserved hypothetical protein	-	Fwd	623178	623621	444	371	301	488	687	773	721	724
cg0705	-	Conserved putative membrane protein	-	Rev	625096	623918	1179	1106	422	905	1568	1195	1080	961
cg0707	cds57	Two-component system, sensory histidine kinase	T	Fwd	625213	626403	1191	1117	123	253	316	213	166	104
cg0712	capB7	Two-component system, transcriptional response regulator	T	Fwd	626446	627138	693	620	649	767	910	751		
cg0710	-	Putative membrane protein	-	Fwd	627138	626443	327	253	201	196	292	306	270	217
cg0711	-	Putative membrane protein	-	Rev	627971	627528	444	371	194	249	196	182	164	136
cg0712	-	Putative membrane protein	-	Rev	629000	628635	965	892	427	631	595	277	181	157
cg0713	-	Conserved hypothetical protein	-	Fwd	629224	630015	792	719	171	224	226	269	190	164
cg0714	-	Hypothetical protein	L	Fwd	630012	631604	1593	1520	135	233	260	323	250	162
cg0715	-	Putative secreted protein	-	Fwd	632247	631609	639	565	426	1025	642	639	418	261
cg0716	-	Putative secreted protein	-	Fwd	632410	632273	864	791	492	198	226	165	123	98
cg0717	crfB6	Lysozyme elongase	O	Rev	634145	633282	864	791	200	177	155	171	169	44
cg0718	crfY1	C50 carotenoid epsilon cyclase	-	Rev	634540	634148	393	319	60	90	90	61	74	56
cg0719	crfE	C50 carotenoid epsilon cyclase	-	Rev	634986	634537	450	377	47	67	63	74	22	9
cg0720	crfZ	Phytoene desaturase (desaturase)	I	Rev	636967	636843	965	892	366	397	304	241	242	99
cg0721	crf2	Phytoene synthase	Q	Rev	637550	636636	915	841	278	325	160	160	145	33
cg0722	-	Putative multidrug efflux protein, resistance-nodulation-cell division	R	Rev	639739	637547	2193	2120	590	722	451	446	399	85
cg0723	crf1	Phytoene synthase	H	Rev	640167	639715	454	381	402	477	409	323	244	129
cg0724	-	Putative transcriptional regulator, MarR-family	-	Rev	641094	641672	579	506	299	413	442	447	334	143
cg0725	-	Putative secreted lipoprotein	M	Rev	642340	641690	651	578	768	965	621	649	708	647
cg0727	-	Putative nucleoside-diphosphate-sugar epimerase	M	Fwd	642498	644021	1524	1451	1342	1055	662	893	740	416
cg0728	-	Dehydrodolichyl pyrophosphate synthase	F	Fwd	642498	644021	1524	1451	1342	1055	662	893	740	416
cg0730	crxX	Carotenoid glycosyl transferase	M	Fwd	645487	646424	756	683	490	482	301	328	228	130
cg0732	-	ABC-type transporter, permease subunit	V	Rev	649051	646634	2418	2345	584	590	361	264	143	23
cg0733	-	ABC-type transporter, ATPase subunit	V	Rev	649719	649051	669	596	340	375	168	158	85	13
cg0734	metI	ABC-type methionine transporter, permease subunit (TC 3.A.1.24.1)	P	Rev	650575	649888	678	604	650	640	368	288	233	20
cg0735	metN	ABC-type methionine transporter, ATPase subunit (TC 3.A.1.24.1)	P	Rev	651654	650572	1083	1010	1117	1199	719	591	361	41
cg0737	metQ	ABC-type methionine transporter, substrate-binding lipoprotein (TC 3.A.1.24.1)	P	Rev	652749	651850	900	827	5893	7131	6760	4960	5574	342
cg0738	dnaZ2	Putative DNA polymerase III subunit	S	Rev	652922	652605	317	244	251	267	215	207	182	129
cg0739	-	Putative integral membrane protein	-	Rev	656095	656586	492	419	262	268	443	559	539	515
cg0740	-	Putative membrane protein	-	Fwd	656583	657998	1146	1342	410	480	679	845	897	751
cg0741	srpK	Transcriptional repressor, DnaK-family	K	Fwd	658008	658679	672	599	268	318	448	452	442	262
cg0742	-	Putative integral membrane protein	-	Rev	658457	658663	795	722	519	425	392	345	307	215
cg0745	-	Putative NAD-dependent protein deacetylase, SIR2-family	K	Fwd	659816	660392	777	704	769	1070	1049	959	879	593
cg0747	-	Conserved hypothetical protein	-	Fwd	660394	660888	495	422	344	399	349	418	274	230
cg0748	-	ABC-type putative iron-siderophore transporter, substrate-binding	P	Fwd	661004	662002	999	926	359	353	201	185	92	56
cg0749	ispU	Putative RNA/RNA methyltransferase	F	Fwd	662381	662108	414	340	162	165	104	102	162	55
cg0751	-	Putative membrane protein	-	Fwd	662627	663481	855	782	2471	2915	3554	2642	2631	1100
cg0752	-	Putative membrane protein	-	Fwd	663488	663838	351	277	610	551	553	507	399	149
cg0753	-	Putative secreted protein	-	Rev	665222	663840	1383	1310	1341	1700	1891	2174	1467	931
cg0754	metX	Homoserine O-acetyltransferase	E	Rev	667774	666641	1364	1061	1241	1164	1298	1040	1171	151
cg0755	metY	O-Acetylhomoserine sulphydrilase	E	Rev	669231	667198	1314	1241	1369	1389	2075	2060	2969	149
cg0756	csdA	Putative carbon starvation protein A	F	Fwd	669663	671942	2280	2207	2491	3165	1606	1063	304	232
cg0757	-	Conserved hypothetical protein	-	Fwd	671946	672149	204	131	93	140	53	49	27	9
cg0758	-	Hypothetical protein	-	Fwd	672355	672474	120	47	5	0	1	0	0	0
cg0759	prpD2	2-Methylcitrate dehydratase, involved in propionate catabolism	R	Fwd	672615	674129	1515	1442	303	1340	22	22	19	34
cg0760	prpC2	2-Methylcitrate dehydratase, involved in propionate catabolism	R	Fwd	674129	675052	924	851	84	456	94	9	6	2
cg0761	prpC1	2-Methylcitrate dehydratase, involved in propionate catabolism	R	Fwd	675081	676232	1152	1078	134	581	21	21	5	7
cg0763	mdr2	Putative malate/L-lactate dehydrogenase	C	Rev	677595	676552	1044	971	63	46	16	23	44	20
cg0764	-	Putative transcriptional regulator, GntR-family	K	Rev	678410	677688	723	650	220	274	196	251	193	131
cg0765	-	Putative secreted protein	-	Rev	679221	678517	705	632	184	168	194	197	191	127
cg0766	icd	Isocitrate dehydrogenase (ICD)	C	Rev	681517	679301	2217	2144	5828	6503	12846	11108	13691	9087
cg0767	-	Siderophore-interacting protein	P	Rev	682500	681601	900	827	101	76	47	26	4	4
cg0768	-	ABC-type putative iron-siderophore transporter, ATPase subunit	P	Rev	683319	682510	810	736	89	56	166	6	3	2
cg0769	-	ABC-type putative iron-siderophore transporter, permease subunit	P	Rev	683434	683316	1029	955	205	225	106	46	15	3
cg0770	-	ABC-type putative iron-siderophore transporter, permease subunit	P	Rev	685336	684341	996	922	389	426	200	73	31	5
cg0771	hsp1	ABC-type putative iron-siderophore transporter, substrate-binding	P	Rev	685336	685343	1053	981	615	527	1113	1113	1169	1136
cg0772	-	Putative sugar/drug permease, MFS-type	-	Fwd	685682	687856	1275	1202	192	217	254	181	118	35
cg0773	-	Putative deoxyribosyltransferase	L	Fwd	687908	688822	915	841	655	827	1119	1155	1246	383
cg0774	-	Putative membrane protein	-	Fwd	688824	689483	660	587	326	390	522	531	519	102
cg0775	-	Hypothetical protein	-	Fwd	689811	689112	303	230	363	348	381	385	376	341
cg0776	-	ABC-type putative iron-siderophore transporter, substrate-binding	P	Rev	691363	690386	978	904	145	152	449	376	540	164
cg0777	-	ABC-type putative iron-siderophore transporter, ATPase subunit	P	Rev	692169	691387	783	710	37	65	112	80	119	51
cg0778	-	ABC-type putative iron-siderophore transporter, permease subunit	P	Rev	692195	692176	1020	946	978	655	815	1002	990	549
cg0779	hsp2	Heat shock protein 2	F	Rev	692325	692492	1038	965	904	825	232	202	163	90
cg0780	-	Membrane protein, ribonuclease BII-like family	S	Fwd	694501	695586	1086	1013	801	1403	2024	2011	1970	2320
cg0781	-	Putative membrane protein	-	Fwd	695645	695650	906	833	1125	2067	3414	3253	2894	2681
cg0782	cdc	D-2-aminocyclohexanecarboxylate	M	Rev	695647									

This supplementary table provides the full data for the calculation and development of Table A5.

Gene Information				Read Mapping				Raw Read Count				log ₂ TPM				m-values				m-values < ±1.5 (not significant)				m-values > ±1.5 (significant)									
Locus	Feature	Product	Major COG Cat.	Strand	Start	End	Length (bp)	Effective Length	①	②	③	④	⑤	⑥	①	②	③	④	⑤	⑥	Vs. ①	Vs. ②	Vs. ③	Vs. ④	Vs. ⑤	Vs. ⑥	a-value	Vs. ①	Vs. ②	Vs. ③	Vs. ④	Vs. ⑤	Vs. ⑥
cg0800	-	Transcriptional activator of propionate catabolism, HTH-3 family	K	Rev	719482	718157	1216	1253	492	553	261	255	315	154	5.302	5.229	3.990	4.311	3.258	0.064	-0.973	-1.212	-0.991	-0.064	5.334	-0.064	-0.973	-1.212	-0.991	-0.064	5.334		
cg0801	-	Hypothetical protein	-	Fwd	719644	719826	183	109	6	8	8	14	2	1	2.021	2.280	2.323	2.754	4.449	0.839	0.259	0.302	0.733	-1.072	-1.182	2.150	0.259	0.302	0.733	-1.182	-1.072	2.150	
cg0802	cccBC	Biotin carboxylase/biotin carboxyl carrier protein	I	Rev	721825	720050	1776	1703	13123	18852	14761	15507	21985	11411	9.165	10.034	9.724	9.489	10.100	9.039	0.419	0.109	-0.126	0.395	-0.576	9.824	0.419	0.109	-0.126	0.395	-0.576	9.824	
cg0803	thrK	Thiolase sulfurtransferase	P	Rev	722922	722017	906	833	1091	1268	1752	1644	2070	1839	6.999	7.112	7.621	7.223	7.572	7.377	0.113	0.622	0.224	0.574	0.378	7.055	0.113	0.622	0.224	0.574	0.378	7.055	
cg0806	-	Conserved hypothetical protein	-	Fwd	722020	724317	1068	934	366	450	590	404	284	67	5.188	5.192	5.815	4.964	4.474	2.382	0.194	0.627	-0.225	-0.715	-0.888	5.285	0.194	0.627	-0.225	-0.715	-0.888	5.285	
cg0807	-	Conserved hypothetical protein	-	Rev	724811	724395	417	343	731	894	1793	1892	2199	2116	7.541	7.727	8.774	8.545	8.779	8.699	0.186	1.233	1.004	1.238	1.158	7.634	0.186	1.233	1.004	1.238	1.158	7.634	
cg0808	wbfC	Conserved putative membrane protein	I	Fwd	724885	727035	2151	2078	850	768	715	693	517	150	5.392	5.142	5.082	4.731	4.326	2.522	-0.250	-0.310	-0.661	-1.066	-0.869	5.267	-0.250	-0.310	-0.661	-1.066	-0.869	5.267	
cg0809	mef	Septum formation protein Mef	D	Rev	727935	727342	594	520	1978	2322	1864	1652	1554	619	8.466	8.593	8.319	7.839	7.768	6.417	0.127	-0.146	-0.626	-0.698	-0.668	8.558	0.127	-0.146	-0.626	-0.698	-0.668	8.558	
cg0810	-	Conserved hypothetical protein	-	Fwd	728188	728140	249	176	1480	1895	1696	1545	1650	846	9.302	9.554	9.438	9.997	9.109	8.121	0.253	0.136	-0.305	-0.193	-1.181	9.295	0.253	0.136	-0.305	-0.193	-1.181	9.295	
cg0811	dtbR1	Acetyl/propionyl-CoA carboxylase, beta chain	I	Rev	729825	728212	1614	1541	11339	15784	12317	12463	12363	5110	9.542	9.915	9.703	9.312	9.317	8.018	0.373	0.160	-0.230	-0.225	-0.524	9.729	0.373	0.160	-0.230	-0.225	-0.524	9.729	
cg0812	dtbR2	Acetyl/propionyl-CoA carboxylase, beta chain	I	Rev	731797	730166	1632	1559	10473	11666	16613	1730	12902	15202	9.411	9.463	8.698	8.939	9.363	9.574	0.052	-0.724	-0.473	-0.049	0.163	9.437	0.052	-0.724	-0.473	-0.049	0.163	9.437	
cg0814	dtbA	Bifunctional biotin-tetrao-Cys-carboxylase synthetase/biotin coe	F	Rev	731966	732775	810	737	566	627	634	670	536	275	6.215	6.258	6.318	6.699	5.787	4.802	0.044	0.103	-0.124	-0.428	-1.413	6.237	0.044	0.103	-0.124	-0.428	-1.413	6.237	
cg0815	dtbB	Putative membrane protein	H	Fwd	732785	733273	489	415	281	340	574	572	470	385	5.935	6.106	6.902	5.951	6.326	6.014	0.170	0.967	0.656	0.390	0.078	6.020	0.170	0.967	0.656	0.390	0.078	6.020	
cg0816	purK	Phosphoribosylaminoimidazole carboxylase, ATPase subunit	S	Fwd	733294	734493	1200	1127	673	761	964	668	643	239	5.897	5.970	6.354	5.520	5.428	4.033	0.073	0.457	-0.377	-0.415	-1.864	5.934	0.073	0.457	-0.377	-0.415	-1.864	5.934	
cg0817	kup	Putative secondary K ⁺ uptake permease, K ⁺ catalytic subunit (KUP)	F	Fwd	734545	734431	1875	1801	294	230	249	244	159	49	4.061	3.605	3.762	3.227	2.829	1.126	-0.457	-0.299	-0.635	-1.232	-0.935	4.833	-0.457	-0.299	-0.635	-1.232	-0.935	4.833	
cg0818	purE	Phosphoribosylaminoimidazole carboxylase, catalytic subunit	P	Fwd	736457	736816	360	286	192	205	167	153	77	5.830	5.820	6.337	5.263	5.155	4.488	-0.010	-0.493	-0.567	-0.475	-0.682	6.056	-0.010	-0.493	-0.567	-0.475	-0.682	6.056		
cg0821	-	Conserved hypothetical protein	-	S	Fwd	737372	737827	456	383	420	457	471	458	339	203	6.614	6.632	6.717	6.372	5.956	5.194	0.018	0.103	-0.242	-0.658	-1.420	6.623	0.018	0.103	-0.242	-0.658	-1.420	6.623
cg0822	-	Conserved hypothetical protein	-	Fwd	737886	738680	795	722	452	609	470	394	160	160	5.918	6.243	6.914	5.473	5.371	4.051	0.325	-0.004	-0.445	-0.547	-0.988	6.096	0.325	-0.004	-0.445	-0.547	-0.988	6.096	
cg0823	ntaA	Putative nitrolicetate monoxygenase, subunit A	C	Fwd	740002	738686	1317	1243	43	31	22	27	11	10	1.826	1.263	0.829	0.807	-0.398	-0.549	-0.563	-0.996	-1.019	-0.224	-2.375	1.544	-0.563	-0.996	-1.019	-0.224	-2.375	1.544	
cg0824	trpS05/cg50	TrpS05	L	Rev	741645	740143	1503	1430	552	422	621	530	403	255	5.287	4.796	5.396	4.862	4.484	3.801	-0.490	-0.109	-0.425	-0.803	-1.486	5.042	-0.490	-0.109	-0.425	-0.803	-1.486	5.042	
cg0825	-	Putative short chain dehydrogenase related to 3-oxoacyl-acyl-carri	I	Rev	742489	741698	792	719	2005	1912	1650	1156	982	1222	8.070	7.898	7.648	8.910	6.691	6.859	-0.172	-0.422	-1.161	-1.379	-1.212	7.994	-0.172	-0.422	-1.161	-1.379	-1.212	7.994	
cg0826	-	Putative membrane protein	-	Fwd	742870	743261	312	298	598	627	432	114	274	96	6.717	6.780	6.826	7.386	6.710	6.222	0.125	0.909	0.569	0.353	0.315	6.237	0.125	0.909	0.569	0.353	0.315	6.237	
cg0828	-	Putative dihydrololate reductase	-	H	Rev	743854	743288	567	494	214	142	148	155	116	96	5.330	4.638	4.741	4.501	4.103	3.808	-0.692	-0.590	-0.829	-1.228	-0.524	4.984	-0.692	-0.590	-0.829	-1.228	-0.524	4.984
cg0829	-	Conserved hypothetical protein, α -glucosylase family	-	E	Fwd	743882	744304	423	349	134	116	147	145	100	94	5.082	4.771	5.154	4.288	4.303	4.200	-0.310	0.072	-0.254	-0.768	-0.882	4.927	-0.310	0.072	-0.254	-0.768	-0.882	4.927
cg0830	-	Conserved hypothetical protein	-	R	Fwd	744525	744301	225	152	82	64	83	84	60	52	5.291	4.834	5.247	4.958	4.906	4.269	-0.456	-0.043	-0.332	-0.385	-1.022	5.062	-0.456	-0.043	-0.332	-0.385	-1.022	5.062
cg0831	tusG	ABC-type trehalose transporter, permease subunit	G	Rev	745373	744537	837	763	462	676	884	351	242	293	252	6.422	6.398	6.419	4.978	4.768	4.023	0.217	-0.003	-0.262	-0.844	-0.844	6.230	0.217	-0.003	-0.262	-0.844	-0.844	6.230
cg0832	tusF	ABC-type trehalose transporter, permease subunit	G	Rev	746404	745370	1035	961	835	1001	1025	356	365	332	6.200	6.579	5.388	4.827	4.878	4.719	0.158	-1.032	-1.593	-1.342	-1.702	6.500	0.158	-1.032	-1.593	-1.342	-1.702	6.500	
cg0833	-	Conserved hypothetical protein	-	S	Rev	746971	746516	456	382	232	240	194	231	249	377	5.761	6.206	5.443	5.388	5.513	6.084	0.446	-0.317	-0.373	-0.248	0.323	5.983	0.446	-0.317	-0.373	-0.248	0.323	5.983
cg0834	tusE	ABC-type trehalose transporter, substrate-binding lipoprotein	G	Rev	748365	747612	1215	1203	1387	1180	1260	1537	1764	1478	8.026	8.166	6.659	6.450	6.073	6.076	6.718	0.050	-1.456	-1.889	-0.426	-2.020	7.908	0.050	-1.456	-1.889	-0.426	-2.020	7.908
cg0838	-	Putative helicase	-	R	Rev	755158	750356	4803	4730	4311	3427	3431	3050	2244	2111	4.399	4.646	5.184	5.708	5.282	4.270	0.247	1.785	1.309	0.883	-0.129	4.523	0.247	1.785	1.309	0.883	-0.129	4.523
cg0839	-	Hypothetical protein	-	-	Rev	758868	755167	3702	3629	1025	1372	327	2660	2069	1131	4.878	5.195	6.515	5.886	5.541	4.645	0.317	0.639	1.008	0.663	-0.233	5.036	0.317	0.639	1.008	0.663	-0.233	5.036
cg0840	-	Conserved hypothetical protein	-	Rev	759193	759103	654	581	752	723	654	581	752	723	6.026	6.059	6.450	6.073	6.076	6.718	0.433	0.634	0.447	0.449	-0.308	6.177	0.433	0.634	0.447	0.449	-0.308	6.177	
cg0841	-	Conserved hypothetical protein	-	S	Rev	762																											

This supplementary table provides the full data for the calculation and development of Table A5.

Gene Information				Read Mapping						Raw Read Count						log ₂ TPM						m-values						a-value						m-values < ±1.5 (not significant)						m-values > ±1.5 (significant)					
Locus	Feature	Product	Major COG Cat.	Strand	Start	End	Length (bp)	Effective Length	Reads						log ₂ TPM						m-values						a-value	m-values < ±1.5 (not significant)						m-values > ±1.5 (significant)											
									1	2	3	4	5	6	1	2	3	4	5	6	1	2	3	4	5	6		1	2	3	4	5	6	1	2	3	4	5	6						
cg007	-	Hypothetical protein	-	Fwd	840792	841106	315	233	235	125	238	334	370	276	6.313	5.298	6.267	6.449	6.616	6.167	-1.015	-0.045	0.137	0.303	-0.146	5.805	-1.015	-0.045	0.137	0.303	-0.146	5.805	-1.015	-0.045	0.137	0.303	-0.146	5.805							
cg008	-	Putative secreted protein	-	Fwd	841103	841615	513	440	243	219	323	407	448	236	5.657	5.206	6.031	6.187	5.241	-0.256	0.348	0.373	0.530	-0.417	5.559	-0.256	0.348	0.373	0.530	-0.417	5.559	-0.256	0.348	0.373	0.530	-0.417	5.559								
cg009	-	Hypothetical protein	-	Rev	842077	841907	171	98	64	62	40	29	25	20	5.334	5.185	4.608	3.852	3.662	3.329	-0.149	-0.725	-1.482	-1.572	-2.005	5.259	-0.149	-0.725	-1.482	-1.572	-2.005	5.259	-0.149	-0.725	-1.482	-1.572	-2.005	5.259							
cg010	hisM	L-histidinol-phosphate phosphatase	E	Rev	843769	842987	783	709	181	221	343	223	192	156	4.624	4.807	5.482	5.557	4.359	4.037	0.183	0.858	-0.067	-0.265	-0.588	4.716	0.183	0.858	-0.067	-0.265	-0.588	4.716	0.183	0.858	-0.067	-0.265	-0.588	4.716							
cg011	ftsX	Putative inositol monophosphatase	G	Rev	844642	843776	867	794	218	277	369	285	255	228	4.744	4.985	5.440	4.763	4.620	4.434	0.240	0.696	0.018	-0.124	-0.310	4.864	0.240	0.696	0.018	-0.124	-0.310	4.864	0.240	0.696	0.018	-0.124	-0.310	4.864							
cg012	prfB	Peptide chain release factor 2 (RF-2)	J	Fwd	844730	845386	1107	1034	1168	1190	1186	1167	804	366	6.808	6.076	6.769	6.440	5.973	4.762	-0.077	-0.039	-0.368	-0.835	-0.748	6.070	-0.077	-0.039	-0.368	-0.835	-0.748	6.070	-0.077	-0.039	-0.368	-0.835	-0.748	6.070							
cg014	ftsE	Cell division ATP-binding protein FtsE-family	E	Fwd	845968	846579	690	616	883	636	413	301	210	79	7.087	6.510	5.932	5.171	4.620	3.246	-0.577	-1.155	-1.816	-2.417	-3.841	6.799	-0.577	-1.155	-1.816	-2.417	-3.841	6.799	-0.577	-1.155	-1.816	-2.417	-3.841	6.799							
cg015	ftsX	Putative cell division protein, FtsX-family	D	Fwd	846671	847573	903	830	552	479	229	202	149	66	6.022	5.174	4.696	4.209	3.700	2.602	-0.308	-0.326	-0.816	-0.839	-1.420	5.868	-0.308	-0.326	-0.816	-0.839	-1.420	5.868	-0.308	-0.326	-0.816	-0.839	-1.420	5.868							
cg016	smgB	SmG-binding protein	O	Fwd	847610	848104	495	422	560	624	614	507	527	443	6.910	6.962	6.982	6.600	4.673	6.198	0.052	0.072	-0.510	-0.437	-0.712	6.936	0.052	0.072	-0.510	-0.437	-0.712	6.936	0.052	0.072	-0.510	-0.437	-0.712	6.936							
cg018	ftsH	Putative uracil-thymine-DNA C-methyltransferase	S	Fwd	848100	848458	534	280	145	124	121	143	158	75	5.452	5.124	4.132	3.545	3.235	4.135	-0.328	-0.320	-0.387	-0.227	-1.216	5.236	-0.328	-0.320	-0.387	-0.227	-1.216	5.236	-0.328	-0.320	-0.387	-0.227	-1.216	5.236							
cg019	trp28b/SC2	Trpase	-	Fwd	849198	849500	303	229	18	26	12	13	6	0	2.734	3.137	2.126	1.820	1.944	0.919	0.403	-0.608	-0.904	-0.620	-1.815	2.936	0.403	-0.608	-0.904	-0.620	-1.815	2.936	0.403	-0.608	-0.904	-0.620	-1.815	2.936							
cg021	-	Siderophore-interacting protein	P	Rev	850794	849967	828	754	94	87	8	4	0	4	3.598	3.392	0.145	-1.009	-1.314	-1.017	-0.207	-1.453	-0.617	-0.912	-4.615	4.495	-0.207	-1.453	-0.617	-0.912	-4.615	4.495	-0.207	-1.453	-0.617	-0.912	-4.615	4.495							
cg022	-	ABC-type putative iron-siderophore transporter, substrate-binding	P	Rev	851714	850794	921	847	101	115	21	0	0	0	3.548	3.636	1.281	-3.484	-3.467	-3.492	0.089	-0.267	-0.042	-0.035	-0.048	4.592	0.089	-0.267	-0.042	-0.035	-0.048	4.592	0.089	-0.267	-0.042	-0.035	-0.048	4.592							
cg023	-	Putative membrane protein	S	Rev	852469	851879	591	517	249	297	757	601	496	273	5.488	5.638	7.028	6.389	6.130	5.246	0.150	-1.540	0.901	0.642	-0.242	5.563	0.150	-1.540	0.901	0.642	-0.242	5.563	0.150	-1.540	0.901	0.642	-0.242	5.563							
cg024	-	ABC-type putative iron-siderophore transporter, substrate-binding	P	Fwd	852821	853837	1017	944	2550	2746	188	117	39	15	8.056	8.059	6.043	3.255	2.171	1.015	0.003	-0.203	-0.801	-0.345	-7.691	6.058	0.003	-0.203	-0.801	-0.345	-7.691	6.058	0.003	-0.203	-0.801	-0.345	-7.691	6.058							
cg026	-	ABC-type putative iron-siderophore transporter, permease subunit	P	Fwd	854088	855089	1002	928	684	650	282	103	60	13	6.181	6.003	4.842	3.094	2.342	0.193	-0.177	-1.338	-0.086	-0.839	-0.987	6.092	-0.177	-1.338	-0.086	-0.839	-0.987	6.092	-0.177	-1.338	-0.086	-0.839	-0.987	6.092							
cg028	-	ABC-type putative iron-siderophore transporter, permease subunit	P	Fwd	855076	856187	1122	1047	671	656	314	174	17	17	5.989	5.853	4.709	3.070	2.407	0.352	-0.135	-1.279	-0.919	-0.622	-0.637	6.061	-0.135	-1.279	-0.919	-0.622	-0.637	6.061	-0.135	-1.279	-0.919	-0.622	-0.637	6.061							
cg028	-	ABC-type putative iron-siderophore transporter, ATPase subunit	E	Fwd	856194	856499	756	682	443	504	191	80	53	26	5.960	6.043	4.691	3.131	2.559	1.520	0.084	-1.268	-0.829	-0.401	-0.439	6.002	0.084	-1.268	-0.829	-0.401	-0.439	6.002	0.084	-1.268	-0.829	-0.401	-0.439	6.002							
cg031	-	Putative aminotransferase, AT class I	E	Fwd	863063	864226	1164	1091	160	186	170	145	103	64	3.875	3.988	3.902	3.368	2.895	2.192	0.112	0.026	-0.508	-0.980	-1.881	4.932	0.112	0.026	-0.508	-0.980	-1.881	4.932	0.112	0.026	-0.508	-0.980	-1.881	4.932							
cg032	-	Putative membrane protein	D	Rev	864862	864221	612	569	291	360	724	74	529	224	5.593	5.795	6.462	6.577	6.103	4.842	0.202	1.251	0.985	0.510	-0.751	6.096	0.202	1.251	0.985	0.510	-0.751	6.096	0.202	1.251	0.985	0.510	-0.751	6.096							
cg033	-	DNA/RNA helicase, superfamily II	K	Rev	866537	864864	1674	1601	803	703	1506	1058	1065	638	6.071	5.376	6.157	6.213	5.239	4.965	-0.295	0.846	0.542	0.057	-0.706	5.524	-0.295	0.846	0.542	0.057	-0.706	5.524	-0.295	0.846	0.542	0.057	-0.706	5.524							
cg034	-	Conserved hypothetical protein	-	Rev	868788	868687	2202	2129	305	454	606	685	604	627	3.882	4.351	4.810	4.678	4.514	4.545	0.469	0.928	0.798	0.634	0.663	4.116	0.469	0.928	0.798	0.634	0.663	4.116	0.469	0.928	0.798	0.634	0.663	4.116							
cg035	-	Conserved hypothetical protein	-	Fwd	868854	869045	192	119	884	1130	2112	3104	3166	999	8.934	9.259	10.129	10.378	10.426	9.735	0.325	1.195	1.444	1.490	0.801	7.096	0.325	1.195	1.444	1.490	0.801	7.096	0.325	1.195	1.444	1.490	0.801	7.096							
cg036	ftsH	Putative secreted protein	-	Rev	869852	869271	582	509	1154	9464	273	2619	2618	244	11.459	10.491	9.822	8.428	6.733	6.968	-0.781	-0.840	-0.900	-0.900	-0.900	10.066	-0.781	-0.840	-0.900	-0.900	-0.900	10.066	-0.781	-0.840	-0.900	-0.900	-0.900	10.066							
cg038	-	Cold shock protein	K	Fwd	870409	870792	384	311	619	679	376	477	418	115	7.421	7.450	6.642	6.679	5.606	4.628	0.029	-0.778	-0.742	-0.915	-0.743	6.435	0.029	-0.778	-0.742	-0.915	-0.743	6.435	0.029	-0.778	-0.742	-0.915	-0.743	6.435							
cg039	-	Putative secreted protein	-	Rev	871374	870847	528	454	574	566	1059	977	826	389	6.852	6.728	7.674	7.252	7.027	5.918	-0.124	0.822	0.400	0.175	-0.935	6.790	-0.124	0.822	0.400	0.175	-0.935	6.790	-0.124	0.822	0.400	0.175	-0.935	6.790							
cg040	-	Glutamine oxidase/transferase	O	Rev	872162	871386	777	704	571	559	498	415	436	193	6.287	6.153	6.030	5.772	5.549	4.353	-0.134	-0.258	-0.515	-0.738	-0.749	6.220	-0.134	-0.258	-0.515	-0.738	-0.749	6.220	-0.134	-0.258	-0.515	-0.738	-0.749	6.220							
cg041	-	Hypothetical protein	-	Rev	872890	872189	702	628	627	603	390	255	499	266	6.209	6.025	6.512	5.962	5.388	3.881	-0.004	-0.484	-0.067	-0.641	-0.641	6.027	-0.004	-0.484	-0.067	-0.641	-0.641	6.027	-0.004	-0.484	-0.067	-0.641	-0.641	6.027							
cg045	-	Putative 23S ribosomal rRNA methyltransferase	J	Fwd	874684	875514	831	757	222	206	420	295	223	78	4.932	5.187	5.688	4.871	4.485	2.960	0.355	0.856	0.039	-0.346	-1.878																				

This supplementary table provides the full data for the calculation and development of Table A5.

Gene Information				Read Mapping							log ₂ TPM						m-values						a-value	m-values < 1.5 (not significant)						m-values ≥ 1.5 (significant)										
Locus	Feature	Product	Major COG Cat.	Strand	Start	End	Length (bp)	Effective Length	Raw Read Count							log ₂ TPM						m-values						a-value	m-values < 1.5 (not significant)						m-values ≥ 1.5 (significant)					
									①	②	③	④	⑤	⑥	①	②	③	④	⑤	⑥	①	②	③	④	⑤	⑥	①		②	③	④	⑤	⑥	①	②	③	④	⑤	⑥	
cg1019	-	Conserved hypothetical protein, probably metal-dependent hydrolase	S	Rev	952929	952929	636	563	55	76	45	47	25	25	3.224	3.979	2.879	2.635	1.767	1.742	0.356	-0.344	-0.589	-1.457	-1.481	0.002	-1.168	-0.414	-0.720	0.297	-0.040	-2.488	-1.168	-0.414	-0.720	0.297	-0.040			
cg1020	-	Conserved hypothetical protein, cupin domain	S	Rev	954460	953300	1161	1088	22	10	17	17	35	28	1.072	1.658	0.351	1.368	1.022	-1.168	-0.414	-0.720	0.297	-0.040	0.002	-1.168	-0.414	-0.720	0.297	-0.040	-2.488	-1.168	-0.414	-0.720	0.297	-0.040				
cg1021	-	putative esterase/lipase	S	Rev	955042	954509	534	463	1	2	0	0	0	0	-1.331	-0.850	-2.392	-1.113	-0.681	-1.121	0.481	-1.061	0.218	-1.350	0.210	-1.091	0.481	-1.061	0.218	-1.350	0.210	-2.488	-1.091	0.481	-1.061	0.218	-1.350	0.210		
cg1022	Imp60/5C60a	Transposase	L	Fwd	955442	955738	297	224	145	101	105	142	143	49	5.705	5.084	5.182	5.308	5.385	3.784	-0.621	-0.523	-0.397	-0.370	-1.921	0.002	-1.174	-1.174	-0.868	-0.868	-1.921	-1.921	-1.921	-1.921	-1.921	-1.921				
cg1023	Imp60/5C60b	Transposase	L	Fwd	955746	956225	480	407	62	29	22	35	43	7	3.870	2.626	2.285	2.626	2.932	0.448	-1.174	-1.174	-0.868	-0.868	-1.921	0.002	-1.174	-1.174	-0.868	-0.868	-1.921	-1.921	-1.921	-1.921	-1.921	-1.921				
cg1024	Imp60/5C60c	Transposase	L	Fwd	956443	956926	384	310	9	5	4	2	2	2	1.466	0.426	0.406	-0.637	-0.600	-0.645	-0.841	-1.051	-0.841	-0.841	-1.128	0.002	-1.051	-0.841	-0.841	-1.128	-1.128	-1.128	-1.128	-1.128	-1.128	-1.128				
cg1025	-	Hypothetical protein	-	Fwd	956823	956969	147	74	0	0	1	0	0	0	-0.470	-0.574	0.469	-0.837	-0.820	-0.845	-1.04	0.939	-0.367	-0.350	-0.375	-0.537	-1.04	0.939	-0.367	-0.350	-0.375	-0.537	-0.537	-0.537	-0.537	-0.537	-0.537			
cg1027	dlf	D-lactate dehydrogenase	C	Rev	958867	957152	1716	1643	1520	1780	2743	2703	2656	2049	6.555	6.679	7.346	7.019	7.100	6.611	0.124	0.791	0.463	0.455	0.056	0.637	0.124	0.791	0.463	0.455	0.056	0.637	0.637	0.637	0.637	0.637	0.637			
cg1028	-	Putative restriction-modification system methylase	L	Fwd	960667	959310	1158	1085	464	452	653	654	601	470	5.413	5.272	5.844	5.541	5.436	5.057	-0.142	0.431	0.128	0.023	-0.356	0.637	-0.142	0.431	0.128	0.023	-0.356	0.637	0.637	0.637	0.637	0.637	0.637			
cg1030	Imp60/5C60c	Transposase	L	Fwd	961551	961847	297	223	138	109	113	146	124	54	6.634	5.193	5.287	5.348	5.311	3.922	-0.441	-0.347	-0.286	-0.503	-0.503	0.002	-0.441	-0.347	-0.286	-0.503	-0.503	-0.503	-0.503	-0.503	-0.503	-0.503	-0.503			
cg1031	Imp60/5C60c	Transposase	L	Fwd	961855	962334	480	406	47	27	30	40	31	6	3.407	2.526	2.716	2.813	2.473	0.255	-0.881	-0.691	-0.594	-0.935	-1.152	0.002	-0.881	-0.691	-0.594	-0.935	-1.152	-1.152	-1.152	-1.152	-1.152	-1.152	-1.152			
cg1032	-	Putative transcriptional regulator, ArxR-family	L	Fwd	962767	963126	360	286	45	61	75	70	60	29	3.761	4.088	4.425	4.021	3.819	2.770	0.327	0.664	0.260	0.057	-0.991	0.002	0.327	0.664	0.260	0.057	-0.991	0.002	0.002	0.002	0.002	0.002	0.002	0.002		
cg1033	-	Putative secondary G2+ transporter, cadmium resistance (CafD) fad	F	Fwd	963226	963722	597	524	38	74	68	58	67	35	2.793	3.633	3.556	3.024	3.246	2.303	0.840	0.762	0.231	0.452	-0.450	0.002	0.840	0.762	0.231	0.452	-0.450	0.002	0.002	0.002	0.002	0.002	0.002	0.002		
cg1035	-	DNase, TatD-related	L	Fwd	964279	965182	834	760	523	425	265	302	287	155	6.059	5.656	5.020	4.902	4.846	3.936	-0.403	-0.109	-1.157	-1.213	-1.213	0.002	-0.403	-0.109	-1.157	-1.213	-1.213	-1.213	-1.213	-1.213	-1.213	-1.213	-1.213	-1.213		
cg1037	rfp2	RF2 precursor, secreted protein	L	Fwd	965283	964607	1125	1052	7522	4198	4173	5560	3844	1383	9.471	8.526	8.560	8.668	8.153	6.654	-0.945	-0.911	-0.803	-1.318	-1.817	0.002	-0.945	-0.911	-0.803	-1.318	-1.817	-1.817	-1.817	-1.817	-1.817	-1.817	-1.817			
cg1038	Isu4	Putative dimethyladenosine transferase	J	Fwd	964444	967325	882	808	2191	1528	1697	1850	1566	806	8.043	7.419	7.614	7.432	7.208	6.226	-0.623	-0.429	-0.611	-0.834	-0.834	0.002	-0.623	-0.429	-0.611	-0.834	-0.834	-0.834	-0.834	-0.834	-0.834	-0.834	-0.834			
cg1040	Imp60/5C60c	Transposase	L	Fwd	967322	968257	936	862	468	526	576	601	744	376	5.732	5.897	6.156	6.139	6.048	5.041	0.064	0.423	0.406	0.317	-0.691	0.002	0.064	0.423	0.406	0.317	-0.691	0.002	0.002	0.002	0.002	0.002	0.002	0.002		
cg1041	Imp60/5C60c	Transposase	L	Fwd	967856	969207	1452	1378	1076	1220	1572	1597	1441	663	5.960	6.037	6.446	6.162	6.103	4.887	0.077	0.486	0.203	0.071	-1.072	0.002	0.077	0.486	0.203	0.071	-1.072	-1.072	-1.072	-1.072	-1.072	-1.072	-1.072	-1.072		
cg1044	pdxK	Pyridoxal/pyridoxone/pyridoxamine kinase	H	Fwd	970137	970931	795	722	249	229	333	356	297	121	5.060	4.836	5.418	5.208	4.964	3.651	-0.224	0.357	0.147	-0.096	-1.410	0.002	-0.224	0.357	0.147	-0.096	-1.410	-1.410	-1.410	-1.410	-1.410	-1.410	-1.410	-1.410		
cg1043	-	Conserved hypothetical protein	O	Rev	971410	970288	403	409	296	387	124	168	177	244	6.028	6.310	4.719	4.848	4.940	5.376	-0.282	-1.309	-1.180	-1.088	-0.652	0.002	-0.282	-1.309	-1.180	-1.088	-0.652	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	
cg1045	-	Conserved hypothetical protein	S	Fwd	971499	971822	324	250	954	1262	2499	2577	2662	1764	8.289	8.588	9.617	9.355	9.419	8.800	0.399	1.328	1.066	1.130	0.512	0.002	0.399	1.328	1.066	1.130	0.512	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	
cg1046	ppk2	Putative inorganic polyphosphatase	S	Fwd	971888	972211	324	251	1254	1777	3035	3726	3513	8245	8.683	9.082	8.997	8.987	10.127	11.024	0.399	1.214	1.204	1.444	0.444	0.002	0.399	1.214	1.204	1.444	0.444	0.002	0.002	0.002	0.002	0.002	0.002	0.002		
cg1046	ppk2	Putative inorganic polyphosphatase	S	Fwd	972334	973296	963	890	2999	3694	3632	3432	2987	2538	8.364	8.586	8.584	8.197	8.013	7.753	0.202	0.220	-0.167	-0.351	-0.610	0.002	0.202	0.220	-0.167	-0.351	-0.610	0.002	0.002	0.002	0.002	0.002	0.002	0.002		
cg1048	-	Putative hydrolase, MAD superfamily	R	Rev	974550	973711	785	721	617	714	764	759	613	470	5.456	6.536	6.872	6.264	6.125	6.235	-0.536	-0.422	-0.395	-0.267	-0.242	0.002	-0.536	-0.422	-0.395	-0.267	-0.242	0.002	0.002	0.002	0.002	0.002	0.002	0.002		
cg1049	-	Putative enoyl-CoA hydratase/isomerase	L	Fwd	974609	975628	1020	947	666	1208	356	359	419	424	6.117	6.679	6.104	5.860	5.100	5.092	0.754	-0.962	-1.256	-1.017	-1.025	0.002	0.754	-0.962	-1.256	-1.017	-1.025	0.002	0.002	0.002	0.002	0.002	0.002	0.002		
cg1050	-	Putative membrane protein	R	Fwd	975713	976435	723	649	647	744	456	427	435	316	6.571	6.669	6.007	5.506	5.650	5.165	0.097	-0.564	-0.965	-0.921	-1.406	0.002	0.097	-0.564	-0.965	-0.921	-1.406	0.002	0.002	0.002	0.002	0.002	0.002	0.002		
cg1051	-	Hypothetical protein	L	Rev	977628	976432	1197	1124	327	399	556	567	534	44	4.831	5.044	5.573	5.259	5.354	5.193	0.214	0.742	0.428	0.524	0.362	0.002	0.214	0.742	0.428	0.524	0.362	0.002	0.002	0.002	0.002	0.002	0.002	0.002		
cg1052	cmr3	Conserved hypothetical protein	L	Fwd	977756	979207	1452	1378	1076	1220	1572	1597	1441	663	5.960	6.037	6.446	6.162	6.103	4.887	-0.607	-1.186	-0.834	-0.834	-0.834	0.002	-0.607	-1.186	-0.834	-0.834	-0.834	-0.834	-0.834	-0.834	-0.834	-0.834	-0.834	-0.834		
cg1053	-	Putative transcriptional regulator, TetR-family	K	Fwd	979848	979267	852	508	511	494	340	294	219	74	4.644	6.392	5.976	5.800	4.96	3.989	-0.153	-0.647	-1.165	-1.088	-1.165	0.002	-0.153	-0.647	-1.165	-1.088	-1.165	0.002	0.							

This supplementary table provides the full data for the calculation and development of Table A5.

Gene Information			Read Mapping			Raw Read Count			log ₂ TPM			m-values < 1.5 (not significant)			m-values ≥ 1.5 (significant)			a-value														
Locus	Feature	Product	Major COG Cat.	Strand	Start	End	Length (bp)	Effective Length	①	②	③	④	⑤	⑥	①	②	③		④	⑤	⑥											
cg1243	-	Secreted trypsin-like serine protease, containing a C-terminal P02-D	O	Rev	1142329	1141493	837	764	1064	1154	1235	1448	1351	962	7.077	7.090	7.231	7.154	7.177	6.557	0.013	0.154	0.078	-0.005	-0.520	-0.004	0.013	0.154	0.078	-0.005	-0.520	
cg1244	-	Arsenite oxidase or related protein, glutaredoxin family	P	Rev	1142713	1142366	348	274	226	365	323	269	388	228	6.113	6.566	5.997	6.540	5.751	6.557	0.585	0.453	0.116	0.427	-0.362	-0.468	0.585	0.453	0.116	0.427	-0.362	
cg1245	-	Putative membrane protein	E	Fwd	1142744	1143943	1203	1130	461	983	367	366	253	86	5.349	6.336	4.960	4.650	4.138	2.565	0.987	-0.389	-0.699	-1.213	-2.783	-0.842	0.987	-0.389	-0.699	-1.213	-2.783	
cg1246	-	Conserved hypothetical protein	S	Fwd	1144483	1143944	540	467	1042	720	770	565	635	279	7.679	7.043	7.183	6.413	6.616	5.407	-0.636	-0.497	-1.249	-1.063	-2.272	-0.781	-0.636	-0.497	-1.249	-1.063	-2.272	
cg1247	-	Putative secreted protein	E	Fwd	1145207	1144491	717	644	3693	234	2121	1697	1643	745	9.095	8.317	8.234	7.407	7.577	6.412	-0.778	-0.860	-1.488	-1.538	-2.682	-0.606	-0.778	-0.860	-1.488	-1.538	-2.682	
cg1248	-	Putative GTPase, probably involved in stress response	T	Fwd	1145577	1147459	1823	1849	9297	9495	3769	3392	2211	920	9.003	8.169	7.640	7.182	6.582	5.293	-0.073	-1.363	-0.928	-0.424	-1.718	-0.966	-0.073	-1.363	-0.928	-0.424	-1.718	
cg1249	-	ABC-type putative dipeptidyl/oligopeptide transporter, substrate-1	E	Fwd	1147571	1149073	1503	1429	663	816	845	723	465	155	5.550	5.746	5.839	5.309	4.689	3.087	0.196	0.289	-0.241	-0.861	-2.463	-0.648	0.196	0.289	-0.241	-0.861	-2.463	
cg1250	-	Putative membrane protein	S	Fwd	1149060	1149932	873	799	422	480	634	510	368	178	5.652	5.766	6.208	5.599	5.135	4.069	0.083	0.526	-0.092	-0.547	-1.634	-0.574	0.083	0.526	-0.092	-0.547	-1.634	
cg1251	-	Conserved hypothetical protein, putative HmR endonuclease	V	Fwd	1149940	1150353	414	341	224	255	290	245	238	112	5.850	5.832	6.160	5.612	5.847	4.882	0.082	0.310	-0.238	-0.263	-1.368	-0.591	0.082	0.310	-0.238	-0.263	-1.368	
cg1252	-	fnrC	C	Fwd	1150422	1150738	318	245	2563	2583	3022	3140	3636	176	8.741	9.648	9.558	8.967	8.985	8.243	-0.093	0.177	-0.074	0.155	-1.458	-0.606	-0.093	0.177	-0.074	0.155	-1.458	
cg1253	-	Succinylaminoimidazole aminotransferase, AT class I	E	Fwd	1150747	1151850	1104	1031	1491	1389	1880	1749	1353	470	7.164	6.958	7.438	7.027	6.674	5.126	-0.206	0.274	-0.137	-0.480	-2.038	-0.701	-0.206	0.274	-0.137	-0.480	-2.038	
cg1254	-	Putative membrane protein	E	Fwd	1151309	1152499	591	517	973	701	567	579	426	156	7.450	6.874	6.611	6.336	5.911	4.442	-0.576	-0.839	-1.115	-1.339	-3.008	-1.162	-0.576	-0.839	-1.115	-1.339	-3.008	
cg1255	-	Conserved hypothetical protein, putative HmR endonuclease	V	Fwd	1152654	1153941	1188	1114	29	18	7	23	11	8	1.422	0.659	-0.546	0.733	-0.250	-0.690	-0.765	-0.689	-0.689	-0.689	-1.112	-0.041	-0.765	-0.689	-0.689	-1.112		
cg1256	-	dapD	E	Rev	1154731	1155388	894	820	198	194	205	285	239	72	4.562	4.429	4.551	4.718	4.482	2.741	-0.133	-0.011	0.157	-0.079	-1.821	-0.495	-0.133	-0.011	0.157	-0.079	-1.821	
cg1257	-	2,3,4,5-Tetrahydrodipyrrole-2,6-dicarboxylate-N-succinyltransferase	E	Rev	1156151	1154760	1392	1319	550	593	648	598	608	220	5.400	5.392	5.568	5.411	5.187	3.700	-0.008	0.168	-0.259	-0.213	-1.700	-0.536	-0.008	0.168	-0.259	-0.213	-1.700	
cg1259	-	Putative 2,3,4,5-tetrahydrodipyrrole-2,6-dicarboxylate-N-succinyltransferase	E	Rev	1157093	1156194	900	827	367	456	655	673	852	851	4.539	5.648	6.213	5.946	6.268	6.276	0.209	0.773	0.506	0.829	0.837	0.543	0.209	0.773	0.506	0.829	0.837	
cg1260	-	dapC	E	Fwd	1157139	1158308	1110	1037	697	714	846	808	725	584	6.060	6.991	6.261	5.906	6.767	5.355	-0.069	0.201	-0.154	-0.293	-0.705	-0.656	-0.069	0.201	-0.154	-0.293	-0.705	
cg1261	-	Lysine decarboxylase family protein	R	Fwd	1158370	1159140	771	698	532	578	511	526	380	293	6.197	6.212	6.078	5.814	5.363	4.964	0.016	-0.119	-0.383	-0.834	-1.233	-0.626	0.016	-0.119	-0.383	-0.834	-1.233	
cg1262	-	Dihydrodipicolinate synthase	H	Fwd	11593162	1159995	834	761	216	324	354	367	414	313	4.787	5.266	5.437	5.182	5.373	4.946	0.479	0.649	0.395	0.586	0.159	0.526	0.479	0.649	0.395	0.586	0.159	
cg1263	-	Glycosyltransferase, involved in cell wall biogenesis	M	Fwd	1160007	1160723	717	643	93	128	114	197	147	7	3.798	4.151	4.434	4.134	4.523	4.078	0.353	0.836	0.336	0.725	0.280	0.606	0.353	0.836	0.336	0.725	0.280	
cg1264	-	Conserved hypothetical protein	C	Fwd	1160735	1161043	309	236	378	401	460	465	477	372	7.024	7.005	7.246	6.955	7.009	6.626	-0.019	0.222	-0.069	-0.015	-0.398	-0.606	-0.019	0.222	-0.069	-0.015	-0.398	
cg1265	-	Conserved hypothetical protein	E	Fwd	1161103	1161270	168	95	653	882	1144	1351	1217	1700	8.712	9.020	9.438	9.371	9.238	9.695	0.307	0.725	0.659	0.526	0.983	0.866	0.307	0.725	0.659	0.526	0.983	
cg1266	-	rmaA	Q	Fwd	1161333	1162190	867	794	1459	1787	2466	2538	2667	3125	7.481	7.170	8.177	7.913	8.001	8.205	0.189	0.696	0.432	0.520	0.724	0.576	0.189	0.696	0.432	0.520	0.724	
cg1267	-	28S ribosomal protein (L24)	G	Fwd	1162699	1162203	1497	1424	2668	1854	2465	2746	2807	2091	6.151	6.748	6.561	6.228	6.387	6.921	0.150	0.944	0.670	0.730	0.280	0.606	0.150	0.944	0.670	0.730	0.280	
cg1268	-	olpA	G	Fwd	1165016	1163844	1173	1100	1058	1658	2298	2605	3420	2569	6.582	7.124	7.640	7.514	7.924	7.486	0.542	1.058	0.932	1.342	0.905	0.883	0.542	1.058	0.932	1.342	0.905	
cg1269	-	olpC	G	Fwd	1165170	1166387	1218	1144	490	478	459	513	5520	3809	7.762	8.600	8.557	8.441	8.560	8.000	0.839	0.796	0.680	0.799	0.239	0.818	0.839	0.796	0.680	0.799	0.239	
cg1270	-	Putative O-methyltransferase	R	Fwd	1167080	1166439	642	569	132	175	185	189	233	211	4.458	4.759	4.881	4.606	4.924	4.756	0.300	0.423	0.148	0.465	0.298	0.608	0.300	0.423	0.148	0.465	0.298	
cg1271	-	siat	R	Fwd	1167214	1167855	642	569	2005	2457	2488	2988	2454	6.491	7.458	6.912	6.461	6.422	6.200	4.422	0.300	0.178	0.321	0.007	-0.606	-0.606	0.300	0.178	0.321	0.007	-0.606	
cg1272	-	csfE	E	Fwd	1168044	1168538	495	422	1912	1812	1941	2489	2385	2351	8.680	8.498	8.641	8.689	8.649	8.603	-0.181	-0.039	0.100	-0.031	-0.077	-0.589	-0.589	-0.181	-0.039	0.100	-0.031	-0.077
cg1273	-	Putative twin arginine targeting (Tat) Preprotein translocase subunit D	U	Rev	1168578	1169048	471	398	776	669	880	1072	980	673	7.452	7.134	7.572	7.551	7.438	6.872	-0.318	0.121	0.099	-0.013	-0.580	-0.733	-0.318	0.121	0.099	-0.013	-0.580	
cg1274	-	mrp	D	Fwd	1170171	1169512	1125	1053	2942	1570	2466	2466	2466	2466	11.025	11.025	11.025	11.025	11.025	11.025	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	
cg1275	-	Putative membrane protein	O	Rev	1170793	1170212	582	509	180	250	344	292	201	121	5.044	5.124	5.914	5.373	4.489	4.101	0.368	0.870	0.328	0.195	-0.944	-0.528	0.368	0.870	0.328	0.195	-0.944	
cg1276	-	Putative M2+ transporter, M2+ transporter-E (M2E) family	P	Rev	1172078	1170786	1293	1220	448	588	752	655	516	287	5.203	5.481	5.889	5.384	5.056	4.188	0.278	0.685	0.180	-0.148	-1.015	-0.606	0.278	0.685	0.180	-0.148	-1.015	
cg1277	-	Putative membrane protein	E	Fwd	1172161	1172658	498	425	616	598	657	746	913	1120	7.038	6.892	7.071	6.948	7.256	7.525	-0.147	0.032	-0.091	0.217	0.487	0.965	-0.147	0.032	-0.091	0.217	0.487	
cg1278	-	Putative secreted protein	E	Fwd	1172671	1173342	669	596	448	529	649	646	467	289	6.848	6.711	6.948	6.596	6.447	6.205	0.416	-0.025	0.300	0.425	0.471	0.402	0.416	-0.025	0.300	0.425	0.471	
cg1279	-	Putative secreted protein	E	Rev	1173867	1173334	534	461	106	152	137	20																				

This supplementary table provides the full data for the calculation and development of Table A5.

Gene Information			Read Mapping			Raw Read Count			log ₂ TPM			m-values			m-values < ±1.5 (not significant)			m-values > ±1.5 (significant)			a-value												
Locus	Feature	Product	Major COG Cat.	Strand	Start	End	Length (bp)	①	②	③	④	⑤	⑥	①	②	③	④	⑤	⑥	①	②	③	④	⑤	⑥	①	②	③	④	⑤	⑥		
cg1348	-	Putative membrane protein, containing a CDS domain	R	Rev	1259326	1259816	1011	937	1255	301	384	287	168	134	4.803	4.882	5.276	4.551	3.789	3.450	0.079	0.473	-0.252	-1.004	-1.353	4.843	4.843	0.079	0.473	-0.252	-1.004	-1.353	4.843
cg1349	-	Putative membrane protein, containing a CDS domain	R	Rev	1260773	1259330	1404	1331	1256	1151	1172	916	555	512	6.680	6.246	6.409	5.748	5.043	4.902	-0.340	-0.271	-0.932	-0.932	-0.932	6.580	6.580	-0.340	-0.271	-0.932	-0.932	-0.932	6.580
cg1350	mob	Putative molybdopterin-guanine dinucleotide biosynthesis protein	H	Rev	1261457	1260894	564	490	119	156	159	193	232	162	4.497	4.781	4.851	4.823	5.104	4.564	0.284	0.354	0.326	0.608	0.067	4.639	4.639	0.284	0.354	0.326	0.608	0.067	4.639
cg1351	moaA3	Molybdopterin biosynthesis protein MoaA	H	Rev	1262669	1261458	1212	1139	377	568	500	532	583	496	5.048	5.535	5.394	5.122	5.326	5.069	0.486	0.346	0.074	0.278	0.020	5.292	5.292	0.486	0.346	0.074	0.278	0.020	5.292
cg1352	moaA	Molybdopterin biosynthesis protein A	H	Rev	1264361	1263153	1209	1135	417	381	561	600	539	449	5.197	4.962	5.562	5.354	5.217	4.929	-0.236	0.365	0.157	0.020	-0.268	5.079	5.079	-0.236	0.365	0.157	0.020	-0.268	5.079
cg1353	fatD4	Putative acyl-CoA synthetase	F	Rev	1266078	1264631	1728	1654	585	719	1100	1027	916	507	5.169	5.162	6.038	5.613	5.466	4.989	0.150	0.849	0.444	0.296	-0.581	5.265	5.265	0.150	0.849	0.444	0.296	-0.581	5.265
cg1354	rho	Transcription termination factor Rho	K	Fwd	1266610	1268898	2289	2216	4500	5244	3498	3238	2777	632	7.705	7.822	7.281	6.864	6.559	4.500	0.117	-0.424	-0.841	-1.046	-1.205	7.763	7.763	0.117	-0.424	-0.841	-1.046	-1.205	7.763
cg1355	prfA	Peptide chain release factor 3 (RF-1)	J	Fwd	1266898	1266974	1077	1004	2284	2830	1965	1878	1550	307	7.815	8.020	7.537	7.166	6.887	4.539	0.205	-0.278	-0.649	-0.927	-1.275	7.937	7.937	0.205	-0.278	-0.649	-0.927	-1.275	7.937
cg1356	-	Putative RNA or rRNA methylase	J	Fwd	1266975	1270814	840	767	417	496	248	238	169	37	7.722	5.868	4.914	4.549	4.165	1.888	0.146	0.808	-1.173	-1.173	-1.834	7.795	7.795	0.146	0.808	-1.173	-1.173	-1.834	7.795
cg1358	-	Putative translation factor, SaeB/Yco/YrcD/YwcC-family	J	Fwd	1270864	1271514	651	578	758	903	992	799	600	215	6.951	7.099	7.278	6.788	6.289	5.786	0.141	0.327	-0.291	-0.682	-1.074	6.682	6.682	0.141	0.327	-0.291	-0.682	-1.074	6.682
cg1359	-	Putative membrane protein	M	Fwd	1271515	1272663	1149	1076	789	846	914	790	755	228	6.189	6.186	6.340	5.824	5.776	4.028	-0.003	0.151	-0.365	-0.413	-1.161	6.187	6.187	-0.003	0.151	-0.365	-0.413	-1.161	6.187
cg1361	atpB	ATP synthase F1, beta chain	F	Fwd	1272720	1273169	450	376	836	793	647	534	507	44	7.625	7.445	7.195	6.612	6.555	3.033	-0.180	-0.430	-1.012	-1.070	-1.592	7.535	7.535	-0.180	-0.430	-1.012	-1.070	-1.592	7.535
cg1362	atpB	ATP synthase F0, A chain	C	Fwd	1273348	1273590	243	169	24	11	10	19	6	0	3.448	2.286	2.203	-0.562	1.262	-1.970	-1.163	-1.245	-0.600	-0.600	-0.600	3.465	3.465	-1.163	-1.245	-0.600	-0.600	-0.600	3.465
cg1363	atpF	ATP synthase F0, C chain	F	Fwd	1274754	1274996	243	169	4399	6032	10743	9699	8308	631	10.905	10.259	12.135	11.682	11.475	7.834	0.259	1.089	0.791	0.678	-0.636	11.250	11.250	0.259	1.089	0.791	0.678	-0.636	11.250
cg1364	atpF	ATP synthase F0, B chain	C	Fwd	1275027	1275593	567	494	6697	8621	14559	13198	11968	978	10.292	10.552	11.351	10.904	10.779	7.143	0.260	1.060	0.612	0.488	-0.149	10.422	10.422	0.260	1.060	0.612	0.488	-0.149	10.422
cg1365	atpB	ATP synthase F1, beta subunit	C	Fwd	1275599	1276414	816	743	7488	10465	17865	15916	13942	1037	9.928	10.307	10.151	10.617	10.474	6.566	0.379	1.194	0.689	0.547	-0.372	10.557	10.557	0.379	1.194	0.689	0.547	-0.372	10.557
cg1366	atpB	ATP synthase F1, alpha chain	C	Fwd	1276476	1278119	1644	1571	12101	15496	28467	24166	22195	1628	9.069	9.862	10.783	10.240	10.135	6.342	0.253	1.173	0.631	0.525	-0.268	9.167	9.167	0.253	1.173	0.631	0.525	-0.268	9.167
cg1367	atpB	ATP synthase F1, gamma chain	C	Fwd	1278176	1279153	978	905	4846	6219	11257	9400	8949	709	9.039	9.295	10.194	9.628	9.574	5.893	0.256	1.155	0.589	0.535	-0.146	9.167	9.167	0.256	1.155	0.589	0.535	-0.146	9.167
cg1368	atpD	ATP synthase F1, beta chain	F	Fwd	1279156	1280667	1462	1379	9226	12767	20171	20512	18997	1384	9.397	9.762	10.722	10.197	10.156	6.287	0.365	1.300	0.800	0.759	-0.118	9.586	9.586	0.365	1.300	0.800	0.759	-0.118	9.586
cg1369	atpC	ATP synthase F1, epsilon chain	C	Fwd	1280619	1280993	375	302	1988	2899	5156	4519	4544	625	9.136	9.577	10.459	9.954	9.979	7.094	0.440	1.322	0.818	0.843	-0.202	9.357	9.357	0.440	1.322	0.818	0.843	-0.202	9.357
cg1370	-	Putative nucleoside	-	Fwd	1281238	1281711	474	400	1049	936	116	122	100	1059	7.877	7.609	7.621	7.737	7.322	7.516	-0.268	-0.256	-0.140	-0.555	-0.361	7.743	7.743	-0.268	-0.256	-0.140	-0.555	-0.361	7.743
cg1371	-	Putative nucleoside, RecB-family	-	Fwd	1281738	1282420	693	620	1031	794	808	1090	749	920	7.304	6.824	6.892	7.017	6.494	6.765	-0.480	-0.412	-0.286	-0.810	-0.539	7.004	7.004	-0.480	-0.412	-0.286	-0.810	-0.539	7.004
cg1372	-	Putative nucleoside	-	Fwd	1282425	1282722	288	219	322	175	139	239	187	103	6.019	5.800	5.580	5.267	5.370	6.269	0.106	0.458	0.230	0.356	-0.639	6.266	6.266	0.106	0.458	0.230	0.356	-0.639	6.266
cg1373	-	Putative glyoxalase	E	Rev	1283182	1282727	456	383	463	1031	1687	1904	2509	1393	6.754	7.804	8.557	8.425	8.840	7.744	1.049	1.802	1.671	2.086	0.989	6.279	6.279	1.049	1.802	1.671	2.086	0.989	6.279
cg1374	-	Conserved hypothetical protein	S	Fwd	1283271	1283576	306	233	130	188	243	287	346	352	5.505	5.930	6.342	6.275	6.761	6.256	0.425	0.837	0.770	1.056	1.056	5.738	5.738	0.425	0.837	0.770	1.056	1.056	5.738
cg1375	-	Putative thioesterase	P	Fwd	1283662	1284855	924	851	607	919	1187	1273	1255	1262	6.126	6.619	7.031	6.826	6.823	6.806	0.494	0.906	0.701	0.697	0.680	6.372	6.372	0.494	0.906	0.701	0.697	0.680	6.372
cg1376	suo1	Hydroxymethyl aliphatic sulfonate permease subunit	P	Fwd	1284787	1285987	1146	1073	764	884	1028	1156	1073	924	6.921	7.370	7.954	7.200	6.861	4.486	-0.627	-0.377	-1.305	-1.030	-1.498	6.865	6.865	-0.627	-0.377	-1.305	-1.030	-1.498	6.865
cg1377	sucC	ABC-type aliphatic sulfonate permease subunit	P	Fwd	1285985	1286755	771	697	22	15	6	11	8	0	1.662	1.635	-0.114	-0.357	-0.401	-3.236	0.534	-0.423	-0.367	-0.712	-1.544	6.650	6.650	0.534	-0.423	-0.367	-0.712	-1.544	6.650
cg1379	sucB	ABC-type aliphatic sulfonate permease subunit	P	Fwd	1286770	1287501	732	658	8	13	6	2	6	0	0.384	0.917	-0.040	0.017	-0.339	-3.161	0.534	-0.423	-0.367	-0.712	-1.544	6.650	6.650	0.534	-0.423	-0.367	-0.712	-1.544	6.650
cg1380	sucA	ABC-type aliphatic sulfonate permease subunit	P	Fwd	1287501	1288476	976	902	175	129	139	239	187	103	6.019	5.800	5.580	5.267	5.370	6.269	0.106	0.458	0.230	0.356	-0.639	6.266	6.266	0.106	0.458	0.230	0.356	-0.639	6.266
cg1381	alob	Allo-1,2-alpha-alkan branching enzyme	G	Rev	1290941	1289874	2196	2123	2466	3342	4359	3377	5451	3299	6.087	7.232	7.658	7.345	7.692	6.942	0.335	0.761	0.448	0.794	0.045	6.905	6.905	0.335	0.761	0.448	0.794	0.045	6.905
cg1382	alof	Putative alpha-amyrase	G	Rev	1293006	1290979	2028	1955	2479	3376	4066	4129	5179	3074	7.020	7.361	7.673	7.389	7.733	6.955	0.342	0.653	0.369	0.713	-0.064	6.910	6.910	0.342	0.653	0.369	0.713	-0.064	6.910
cg1383	-	Putative nucleoside molybdenum transporter, ATPase subunit	G	Rev	1293176	1294048	873	799	481	564	859	851	938	879	5.872	5.951	6.647	6.328	6.485	3.666	0.07												

This supplementary table provides the full data for the calculation and development of Table A5.

Gene Information				Read Mapping						log ₂ TPM						m-values						m-values < ±1.5 (not significant)						m-values ≥ ±1.5 (significant)										
Locus	Feature	Product	Major COG Cat.	Strand	Start	End	Length (bp)	Effective Length	Raw Read Count						log ₂ TPM						m-values						m-values < ±1.5 (not significant)						m-values ≥ ±1.5 (significant)					
									①	②	③	④	⑤	⑥	①	②	③	④	⑤	⑥	①	②	③	④	⑤	⑥	①	②	③	④	⑤	⑥	①	②	③	④	⑤	⑥
cg5465	-	Putative membrane protein	-	Rev	1365079	1364606	474	400	34	50	50	47	70	34	2.970	3.409	3.452	3.059	3.641	2.995	0.439	0.483	0.089	0.671	-0.375	-0.190	0.439	0.483	0.089	0.671	-0.375	-0.790	0.439	0.483	0.089	0.671	-0.375	
cg5466	-	Putative secreted protein	-	Rev	1365720	1365196	525	451	212	326	311	373	414	310	5.428	5.428	5.918	5.873	6.000	5.999	0.559	0.490	0.446	0.613	0.171	-0.558	0.490	0.446	0.613	0.171	-1.465	0.490	0.446	0.613	0.171			
cg5467	-	Putative transcriptional regulator, TerF-family	-	Rev	1366373	1365804	570	481	13	17	18	15	16	14	1.329	1.600	1.762	1.162	1.312	1.058	0.271	0.432	-0.167	-0.017	-0.271	0.271	0.432	-0.167	-0.017	-0.271	-0.921	0.271	0.432	-0.167	-0.017			
cg5468	-	Conserved hypothetical protein	S	Rev	1366647	1366342	306	217	13	9	10	8	9	6	2.227	2.166	1.817	1.193	1.444	0.798	-0.611	-0.356	-1.034	-0.783	-1.429	-0.611	-0.356	-1.034	-0.783	-1.429	-0.611	-0.356	-1.034	-0.783	-1.429			
cg5469	-	Putative secreted protein	-	Rev	1366863	1366681	183	109	2	2	5	8	5	6	0.799	0.695	1.738	2.017	1.449	1.646	-0.104	0.939	1.218	0.650	0.848	0.717	-0.104	0.939	1.218	0.650	0.848	-0.668	0.939	1.218	0.650	0.848		
cg5471	-	Hypothetical protein	-	Fwd	1366934	1366756	123	49	11	22	24	38	50	66	3.487	4.410	6.370	4.742	5.110	4.978	0.719	0.883	1.255	0.622	0.884	0.847	-0.719	0.883	1.255	0.622	0.884	-2.542	0.883	1.255	0.622	0.884		
cg5473	-	Conserved hypothetical protein	-	Rev	1369537	1369552	186	113	15	6	3	0	1	0	3.190	1.894	1.130	-1.176	-1.459	-1.184	-1.296	-0.061	-0.367	-0.350	-0.375	-0.439	-0.061	-0.367	-0.350	-0.375	-0.985	-0.061	-0.367	-0.350	-0.375			
cg5474	-	Hypothetical protein	-	Fwd	1369876	1371021	1146	1073	328	443	430	464	382	230	4.929	5.256	5.256	5.061	4.798	4.044	0.327	0.327	0.132	-0.130	-0.885	0.327	0.327	0.132	-0.130	-0.885	0.327	0.327	0.132	-0.130	-0.885			
cg5475	-	Conserved hypothetical protein	-	Fwd	1371018	1371344	327	253	75	88	75	81	68	33	4.624	4.740	4.554	4.367	4.135	3.089	0.116	-0.070	-0.257	-0.489	-0.688	0.116	-0.070	-0.257	-0.489	-0.688	-0.400	0.116	-0.070	-0.257	-0.489			
cg5476	hnc	Thyrosine kinase, related to dihydroxyacetone kinase	H	Fwd	1373104	1371461	1764	1691	6864	3845	7973	7346	7491	19640	89.200	7.750	8.827	4.421	4.466	9.832	-0.940	0.137	-0.269	-0.224	-1.142	-0.940	0.137	-0.269	-0.224	-1.142	-0.940	0.137	-0.269	-0.224	-1.142			
cg5478	-	Hypothetical protein	-	Fwd	1374140	1374601	462	388	195	115	206	210	208	190	5.492	4.632	5.510	5.232	5.235	5.080	-0.861	0.018	-0.260	-0.257	-0.412	-0.861	0.018	-0.260	-0.257	-0.412	-0.861	0.018	-0.260	-0.257	-0.412			
cg5479	olp1	Putative glycogen phosphorylase	G	Rev	1377201	1374814	2388	215	18951	24368	26965	26235	24771	8183	9.718	9.977	10.167	9.820	9.755	8.132	0.259	0.449	0.103	0.037	-1.598	0.259	0.449	0.103	0.037	-1.598	0.259	0.449	0.103	0.037				
cg5481	-	Conserved hypothetical protein	-	Rev	1377555	1377397	159	86	43	34	27	19	16	7	4.876	4.442	4.163	3.372	3.154	2.042	-0.434	-0.713	-0.989	-1.192	-1.834	-0.434	-0.713	-0.989	-1.192	-1.834	-0.434	-0.713	-0.989	-1.192	-1.834			
cg5482	-	Putative Zn-dependent hydrolase	R	Rev	1379022	1377613	1410	1337	308	313	391	87	69	55	4.539	4.459	3.792	2.361	2.407	1.701	-0.081	-0.747	-2.179	-2.492	-2.838	-0.081	-0.747	-2.179	-2.492	-2.838	-0.081	-0.747	-2.179	-2.492	-2.838			
cg5483	-	Putative membrane protein	R	Rev	1379882	1379130	753	679	65	60	63	40	71	48	3.217	3.000	3.112	2.164	2.993	2.413	-0.217	-0.105	-1.054	-0.224	-0.804	-0.217	-0.105	-1.054	-0.224	-0.804	-0.217	-0.105	-1.054	-0.224	-0.804			
cg5484	-	Putative secreted protein	-	Rev	1380409	1379930	480	406	92	124	143	119	159	242	4.362	4.684	4.932	4.363	4.795	5.373	0.323	0.570	0.001	0.433	1.011	0.323	0.570	0.001	0.433	1.011	0.323	0.570	0.001	0.433	1.011			
cg5485	-	Putative metal dependent phosphohydrolase, RelA/SpoI-like	T	Fwd	1380470	1381036	567	493	77	110	167	138	106	66	3.868	4.273	4.499	4.616	4.628	4.327	0.405	0.633	0.749	0.757	0.458	0.405	0.633	0.749	0.757	0.458	0.405	0.633	0.749	0.757	0.458			
cg5486	LtBR	Transcriptional regulator, iCR-family	K	Rev	1381726	1381019	708	634	169	155	295	208	155	65	4.671	4.443	5.111	4.402	4.197	2.932	-0.228	0.739	-0.069	-0.474	-1.740	-0.228	0.739	-0.069	-0.474	-1.740	-0.228	0.739	-0.069	-0.474				
cg5487	levC	3-hydroxyacyl dehydratase, large subunit	E	Fwd	1381907	1383352	1446	1372	2660	2839	5158	2907	1580	158	7.609	7.599	8.504	7.371	6.508	3.170	-0.010	0.894	-0.239	-1.101	-4.439	-0.010	0.894	-0.239	-1.101	-4.439	-0.010	0.894	-0.239	-1.101				
cg5488	levD	3-hydroxyacyl dehydratase, small subunit	E	Fwd	1383369	1383362	567	521	1572	1611	2892	1861	1058	136	6.134	8.066	6.953	8.021	7.214	4.239	-0.068	0.818	-0.123	-0.921	-2.886	-0.068	0.818	-0.123	-0.921	-2.886	-0.068	0.818	-0.123	-0.921				
cg5489	L	Putative NTP glycohydrolase	L	Fwd	1385319	1384309	1011	938	667	602	828	658	544	307	6.132	5.880	6.382	5.745	5.458	4.640	-0.251	0.251	-0.386	-0.643	-1.491	-0.251	0.251	-0.386	-0.643	-1.491	-0.251	0.251	-0.386	-0.643	-1.491			
cg5491	-	Hypothetical protein	-	Fwd	1385397	1385555	159	85	7	0	0	0	0	0	2.416	-0.687	-0.644	-0.950	-0.933	-0.958	-1.104	-3.361	-1.367	-3.350	-3.375	-1.104	-3.361	-1.367	-3.350	-3.375	-1.104	-3.361	-1.367	-3.350	-3.375			
cg5492	apsA	Glyceral-3-phosphate dehydrogenase (NAD(P)+)	C	Rev	1385597	1386595	999	925	602	852	345	303	190	73	6.001	6.998	5.139	4.646	3.993	2.600	0.397	-0.862	-1.355	-2.008	-3.401	0.397	-0.862	-1.355	-2.008	-3.401	0.397	-0.862	-1.355	-2.008	-3.401			
cg5493	apsB	D-ribulose biphosphate carboxylase	M	Fwd	1386620	1387702	1083	1030	1188	1281	1100	1086	908	388	7.754	7.860	6.693	6.268	6.627	6.000	0.195	0.071	-0.396	-0.637	-1.068	0.195	0.071	-0.396	-0.637	-1.068	0.195	0.071	-0.396	-0.637	-1.068			
cg5494	-	Putative secreted protein	-	Rev	1388737	1387757	981	908	355	313	408	509	483	170	5.267	4.982	5.407	5.419	5.360	3.835	-0.285	0.140	0.152	0.093	-1.432	-0.285	0.140	0.152	0.093	-1.432	-0.285	0.140	0.152	0.093	-1.432			
cg5495	zhl	Thiamine-phosphate kinase	H	Fwd	1388877	1389794	918	844	304	414	393	447	381	390	5.140	5.480	5.447	5.328	5.115	5.123	0.341	0.307	0.188	-0.025	-0.016	0.341	0.307	0.188	-0.025	-0.016	0.341	0.307	0.188	-0.025	-0.016			
cg5496	unp	Putative uracil-DNA glycosylase	L	Fwd	1389794	1390543	750	677	226	227	274	239	249	186	5.005	4.908	5.219	4.719	4.795	4.351	-0.097	0.213	-0.286	-0.210	-0.654	-0.097	0.213	-0.286	-0.210	-0.654	-0.097	0.213	-0.286	-0.210	-0.654			
cg5497	-	ATP-dependent DNA helicase, RecJ-like	L	Fwd	1390555	1392258	1704	1639	625	699	834	574	297	175	5.285	5.942	5.929	5.820	4.845	4.895	0.052	0.855	-0.464	-0.472	-1.445	0.052	0.855	-0.464	-0.472	-1.445	0.052	0.855	-0.464	-0.472	-1.445			
cg5498	L	ATP-dependent DNA helicase, RecJ-like	L	Fwd	1392263	1394386	2124	2051	541	603	668	860	703	398	4.759	4.811	5.379	6.000	4.787	3.942	0.052	0.620	0.301	0.028	-0.816	0.052	0.620	0.301	0.028	-0.816	0.052	0.620	0.301	0.028	-0.816			
cg5499	-	Conserved hypothetical protein	C	Fwd	1394406	1394621	216	141	197	205	214	281	298	189	6.600	6.557	6.662	6.745	6.846	6.170	-0.043	0.062	0.145	0.246	0.430	-0.043	0.062	0.145	0.246	0.430	-0.043	0.062	0.145	0.246	0.430			
cg5500	-	Helicase, putative	H	Fwd	1394621	1395255	634	513	342	493	483	435	29	9	6.151	6.422	6.440	6.420	6.423	6.839	0.052	0.355	-0.464	-0.472	-1.445	0.052	0.355	-0.464	-0.472	-1.445	0.052	0.355	-0.464	-0.472	-1.445			
cg5501	cooD</																																					

This supplementary table provides the full data for the calculation and development of Table A15.

Gene Information				Read Mapping						Raw Read Count						log ₂ TPM						a-value						m-values ± 1.5 (not significant)						m-values ± 1.5 (significant)					
Locus	Feature	Product	Major COG Cat.	Strand	Start	End	Length (bp)	Effective Length	①	②	③	④	⑤	⑥	①	②	③	④	⑤	⑥	①	②	③	④	⑤	⑥	①	②	③	④	⑤	⑥	①	②	③	④	⑤	⑥	
cg1689	psp	prokaryotic ubiquitin-like protein	-	Rev	1576603	1576409	195	121	531	548	360	418	427	387	8,177	8,119	7,557	7,466	7,514	7,347	-0.058	-0.620	-0.711	-0.664	-0.830	6,148	-0.058	-0.620	-0.711	-0.664	-0.830	6,148	-0.058	-0.620	-0.711	-0.664	-0.830		
cg1690	dop	Put decarboxinase	-	Rev	1578414	1578070	344	273	715	985	1244	1484	1604	1109	5,620	5,788	5,357	5,206	5,461	5,878	0.359	0.737	0.686	0.842	0.258	6,708	0.359	0.737	0.686	0.842	0.258	6,708	0.359	0.737	0.686	0.842	0.258		
cg1691	mpo	ATPase, AAA-class, putative proteasome subunit	O	Rev	1579989	1578415	1575	1025	1193	1501	1720	2055	2045	1473	6,330	6,557	6,797	6,747	6,763	6,259	0.227	0.467	0.417	0.434	-0.071	6,443	0.227	0.467	0.417	0.434	-0.071	6,443	0.227	0.467	0.417	0.434	-0.071		
cg1692	psmT	Putative SAM-dependent methyltransferase, involved in tRNA-Met	J	Rev	1580687	1580031	657	374	1133	1348	1216	1195	1140	988	7,167	7,314	7,209	6,878	6,767	6,596	0.147	0.041	-0.290	-0.341	-0.572	7,241	0.147	0.041	-0.290	-0.341	-0.572	7,241	0.147	0.041	-0.290	-0.341	-0.572		
cg1693	pepC	Putative aspartyl aminopeptidase	E	Rev	1582175	1580913	1263	1190	834	913	1377	1709	1705	1505	6,132	6,159	6,794	6,800	6,784	6,789	0.107	0.662	0.667	0.651	0.656	6,146	0.107	0.662	0.667	0.651	0.656	6,146	0.107	0.662	0.667	0.651	0.656		
cg1694	-	putative CRSP-associated ATP-dependent nuclease	L	Rev	1582274	1581110	837	764	431	461	384	422	359	153	5,775	5,768	5,548	5,378	5,162	3,913	-0.007	-0.227	-0.387	-0.613	-0.868	5,792	-0.007	-0.227	-0.387	-0.613	-0.868	5,792	-0.007	-0.227	-0.387	-0.613	-0.868		
cg1695	-	putative amino-terminus, HTP-mid XRE family	-	Fwd	1583324	1583584	261	187	360	367	756	1835	2737	358	7,197	7,121	8,205	9,177	9,711	6,815	-0.076	-1.008	-1.980	-2.573	-0.983	7,159	-0.076	1.008	-1.980	-2.573	-0.983	7,159	-0.076	1.008	-1.980	-2.573	-0.983		
cg1696	-	Putative antiporter efflux permease, MFS-type	G	Rev	1584948	1583737	1212	1139	19	17	143	244	408	278	0,808	0,552	3,395	4,056	4,812	4,236	-0.252	-0.287	-0.248	-0.404	-0.428	0,880	-0.252	-0.287	-0.248	-0.404	-0.428	0,880	-0.252	-0.287	-0.248	-0.404	-0.428		
cg1697	isoAA	Aspartate ammonia-lyase	C	Rev	1585957	1585777	1581	1507	1206	1384	1384	1478	1788	616	6,340	6,425	6,478	6,266	6,585	4,997	0.046	-0.185	-0.427	-0.757	-0.659	6,389	0.046	-0.185	-0.427	-0.757	-0.659	6,389	0.046	-0.185	-0.427	-0.757	-0.659		
cg1698	hsgG	ATP phosphoribosyltransferase	R	Rev	1587912	1587807	846	772	1181	1229	1083	979	890	242	7,212	7,166	7,026	6,575	6,454	4,555	0.041	-0.106	-0.528	-0.530	-1.880	6,687	0.041	-0.106	-0.528	-0.530	-1.880	6,687	0.041	-0.106	-0.528	-0.530	-1.880		
cg1699	hslE	Phosphoribosyl-ATP pyrophosphatase	R	Rev	1588192	1587929	264	191	1010	1117	979	903	891	355	8,667	8,708	8,561	8,138	8,136	6,786	0.079	-0.152	-0.110	-0.148	-0.931	6,267	0.079	-0.152	-0.110	-0.148	-0.931	6,267	0.079	-0.152	-0.110	-0.148	-0.931		
cg1700	-	Conserved hypothetical protein	-	Rev	1592627	1590937	3591	3518	1157	5132	5055	5629	6132	1733	7,252	7,141	7,162	7,011	7,152	5,305	0.006	-0.269	-0.322	-0.104	-0.457	6,267	0.006	-0.269	-0.322	-0.104	-0.457	6,267	0.006	-0.269	-0.322	-0.104	-0.457		
cg1701	metH	Methionine synthase	E	Fwd	1592810	1593382	573	499	109	100	107	147	120	59	4,348	4,121	4,261	4,410	4,136	3,099	-0.227	-0.087	0.061	-0.212	-1.249	4,235	-0.227	-0.087	0.061	-0.212	-1.249	4,235	-0.227	-0.087	0.061	-0.212	-1.249		
cg1702	-	Hypothetical protein	-	Fwd	1592810	1593382	573	499	109	100	107	147	120	59	4,348	4,121	4,261	4,410	4,136	3,099	-0.227	-0.087	0.061	-0.212	-1.249	4,235	-0.227	-0.087	0.061	-0.212	-1.249	4,235	-0.227	-0.087	0.061	-0.212	-1.249		
cg1703	-	Putative FAD-dependent pyridine nucleotide-disulphide oxidoreductase	O	Rev	1594433	1593405	1029	955	285	248	324	412	502	459	4,482	4,579	5,004	5,044	5,347	5,193	0.304	0.122	0.162	0.465	0.317	4,730	0.304	0.122	0.162	0.465	0.317	4,730	0.304	0.122	0.162	0.465	0.317		
cg1704	-	Putative transcriptional regulator, Arsf-family	-	Rev	1594789	1594430	360	285	67	70	88	185	173	209	4,325	4,283	4,644	4,506	5,331	5,577	-0.042	0.320	0.181	1.006	1.252	4,904	-0.042	0.320	0.181	1.006	1.252	4,904	-0.042	0.320	0.181	1.006	1.252		
cg1705	arcCZ	Putative secondary amine transporter, essential resistance-3 (ACF)	P	Rev	1594870	1595982	1113	1040	252	272	272	299	238	4	4,582	4,598	4,353	4,270	4,488	4,328	0.006	-0.269	-0.322	-0.104	-0.457	6,267	0.006	-0.269	-0.322	-0.104	-0.457	6,267	0.006	-0.269	-0.322	-0.104	-0.457		
cg1706	-	Putative arsenate reductase (arsenical pump modifier)	T	Fwd	1595999	1596421	423	350	108	78	114	92	121	86	4,773	4,205	4,790	4,177	4,586	4,073	-0.568	0.017	-0.596	-0.187	-0.700	4,489	-0.568	0.017	-0.596	-0.187	-0.700	4,489	-0.568	0.017	-0.596	-0.187	-0.700		
cg1707	-	Putative arsenate reductase (arsenical pump modifier)	T	Fwd	1596497	1597138	642	569	143	146	139	183	186	102	4,573	4,499	4,472	4,560	4,400	3,715	-0.074	-0.101	-0.013	0.027	-0.858	4,536	-0.074	-0.101	-0.013	0.027	-0.858	4,536	-0.074	-0.101	-0.013	0.027	-0.858		
cg1708	-	Conserved hypothetical protein	-	Rev	1597688	1597308	381	308	730	808	892	1125	945	463	7,469	7,712	8,084	8,084	7,692	6,639	0.042	0.367	0.414	0.022	-1.030	6,267	0.042	0.367	0.414	0.022	-1.030	6,267	0.042	0.367	0.414	0.022	-1.030		
cg1709	msnA	Putative 1-D-myo-inositol-2-amino-2-deoxy-alpha-D-glucopyranosidase	J	Rev	1598775	1597713	1263	1189	543	471	583	599	662	197	5,514	5,206	5,556	5,289	4,550	3,682	-0.309	0.042	-0.225	-0.064	-1.931	6,360	-0.309	0.042	-0.225	-0.064	-1.931	6,360	-0.309	0.042	-0.225	-0.064	-1.931		
cg1710	bacA	Putative ureidopropionyl kinase	V	Rev	1600090	1599209	882	808	975	1058	552	446	285	53	6,875	6,889	5,707	5,382	4,575	2,325	0.014	-1.168	-1.493	-0.231	-1.550	6,882	0.014	-1.168	-1.493	-0.231	-1.550	6,882	0.014	-1.168	-1.493	-0.231	-1.550		
cg1711	-	Putative ureidopropionyl kinase	C	Fwd	1600134	1601084	951	878	126	115	169	141	155	96	3,825	3,990	4,185	3,619	3,772	3,061	-0.235	0.360	-0.206	-0.053	-0.763	6,389	-0.235	0.360	-0.206	-0.053	-0.763	6,389	-0.235	0.360	-0.206	-0.053	-0.763		
cg1712	hsc70	Putative secreted lipoprotein	-	Rev	1601122	1602147	1026	953	446	416	416	426	316	238	6,051	6,443	6,981	6,981	6,967	6,206	-0.027	-0.609	-0.484	-0.366	-0.829	6,267	-0.027	-0.609	-0.484	-0.366	-0.829	6,267	-0.027	-0.609	-0.484	-0.366	-0.829		
cg1713	pyrD	Dihydroorotate oxidase	F	Fwd	1602159	1603274	1116	1042	594	555	969	973	911	235	5,822	5,620	6,466	6,166	6,088	4,113	-0.202	0.644	0.344	0.266	-1.709	6,267	-0.202	0.644	0.344	0.266	-1.709	6,267	-0.202	0.644	0.344	0.266	-1.709		
cg1714	-	Putative ABC-type ABC transporter system, ATPase and permease subunit	R	Rev	1603748	1603395	354	280	68	57	52	68	71	34	4,370	4,016	3,929	4,004	4,082	3,016	-0.354	-0.441	-0.367	-0.288	-1.354	4,193	-0.354	-0.441	-0.367	-0.288	-1.354	4,193	-0.354	-0.441	-0.367	-0.288	-1.354		
cg1715	-	Hypothetical protein	-	Rev	1604631	1604636	306	232	33	20	15	25	24	16	3,059	2,761	2,411	2,806	2,766	2,185	-0.799	-1.148	-0.754	-0.793	-1.375	4,140	-0.799	-1.148	-0.754	-0.793	-1.375	4,140	-0.799	-1.148	-0.754	-0.793	-1.375		
cg1716	Transposase	-	-	Rev	1604931	1606098	1167	1087	169	141	158	205	141	8	6,482	6,422	6,282	6,446	6,381	4,666	-0.246	0.289	-0.300	-0.509	-0.589	6,267	-0.246	0.289	-0.300	-0.509	-0.589	6,267	-0.246	0.289	-0.300	-0.509	-0.589		
cg1717	-	Putative membrane protein	-	Rev	1606728	1606294	435	362	1281	1500	1258	1900	2053	1915	8,289	8,142	8,202	8,490	8,169	8,494	0.124	-0.087	0.020	0.330	0.205	6,351	0.124	-0.087	0.020	0.330	0.205	6,351	0.124	-0.087	0.020	0.330	0.205		
cg1718	-	Phospholipid-binding protein	-	Rev	1607278	1606																																	

This supplementary table provides the full data for the calculation and development of Table A5.

Gene Information			Read Mapping		Raw Read Count						log ₂ TPM						m-values						a-value		m-values < ±1.5 (not significant)						m-values > ±1.5 (significant)																		
Locus	Feature	Product	Major COG Cat.	Strand	Start	End	Length (bp)	Effective Length	①	②	③	④	⑤	⑥	①	②	③	④	⑤	⑥	①	②	③	④	⑤	⑥	①	②	③	④	⑤	⑥	①	②	③	④	⑤	⑥	①	②	③	④	⑤	⑥					
cg1796	rbcK	Conserved putative membrane protein, RbcX-like	-	Rev	1691247	1691666	582	507	890	1013	1381	1634	1980	1289	7,344	7,427	7,916	7,853	8,147	7,503	0.083	0.573	0.509	0.803	0.159	7,183	0.083	0.573	0.509	0.803	0.159	7,183	0.083	0.573	0.509	0.803	0.159	7,183	0.083	0.573	0.509	0.803	0.159	7,183	0.083	0.573	0.509	0.803	0.159
cg1797	H	Riboflavin synthase, beta chain	-	Rev	1691813	1691234	480	407	300	369	373	355	371	173	6,056	6,200	6,309	5,932	6,012	4,991	0.194	0.253	-0.125	-0.044	-1.165	6,185	0.194	0.253	-0.125	-0.044	-1.165	6,185	0.194	0.253	-0.125	-0.044	-1.165	6,185	0.194	0.253	-0.125	-0.044	-1.165	6,185	0.194	0.253	-0.125	-0.044	-1.165
cg1798	rbaA	Putative GTP cyclohydrolase II/3,4-dihydroxy-2-butanoate-4-phosph	H	Rev	1693093	1691825	1269	1196	741	850	905	911	814	524	5,955	6,049	6,183	5,886	5,741	5,082	0.094	0.227	-0.069	-0.214	-0.874	6,002	0.094	0.227	-0.069	-0.214	-0.874	6,002	0.094	0.227	-0.069	-0.214	-0.874	6,002	0.094	0.227	-0.069	-0.214	-0.874	6,002	0.094	0.227	-0.069	-0.214	-0.874
cg1799	rbcC	Riboflavin synthase, alpha chain	H	Rev	1693739	1693104	636	563	311	371	395	501	561	402	5,702	5,852	5,985	6,021	6,201	5,697	0.150	0.283	0.319	0.499	-0.005	5,777	0.150	0.283	0.319	0.499	-0.005	5,777	0.150	0.283	0.319	0.499	-0.005	5,777	0.150	0.283	0.319	0.499	-0.005	5,777	0.150	0.283	0.319	0.499	-0.005
cg1800	rbcG	Riboflavin-specific deaminase/reductase	H	Rev	1694726	1693740	987	914	544	593	599	840	927	724	5,873	5,893	5,951	6,132	6,291	5,910	0.020	0.078	0.259	0.418	0.037	5,888	0.020	0.078	0.259	0.418	0.037	5,888	0.020	0.078	0.259	0.418	0.037	5,888	0.020	0.078	0.259	0.418	0.037	5,888	0.020	0.078	0.259	0.418	0.037
cg1801	rpe	Ribulose 5-phosphate 3-epimerase	G	Rev	1695386	1694277	660	586	1282	1524	1578	2004	2430	2496	7,688	7,707	7,927	7,966	8,261	8,274	0.145	0.239	0.277	0.572	0.586	7,763	0.145	0.239	0.277	0.572	0.586	7,763	0.145	0.239	0.277	0.572	0.586	7,763	0.145	0.239	0.277	0.572	0.586	7,763	0.145	0.239	0.277	0.572	0.586
cg1802	rfm	Ribosomal RNA small subunit methyltransferase B	J	Rev	1696967	1695432	1536	1462	823	1048	1263	1222	1273	890	5,830	6,075	6,387	6,252	6,199	5,569	0.245	0.557	0.422	0.279	-0.261	5,953	0.245	0.557	0.422	0.279	-0.261	5,953	0.245	0.557	0.422	0.279	-0.261	5,953	0.245	0.557	0.422	0.279	-0.261	5,953	0.245	0.557	0.422	0.279	-0.261
cg1803	fmt	Methionyl-tRNA formyltransferase	J	Rev	1697911	1696964	948	874	684	797	948	816	893	610	6,260	6,377	6,670	6,148	6,294	5,721	0.118	0.410	-0.111	0.035	-0.538	6,338	0.118	0.410	-0.111	0.035	-0.538	6,338	0.118	0.410	-0.111	0.035	-0.538	6,338	0.118	0.410	-0.111	0.035	-0.538	6,338	0.118	0.410	-0.111	0.035	-0.538
cg1804	dfp2	Polypeptide deformylase	J	Rev	1698440	1701973	510	436	587	554	620	620	693	530	6,935	6,748	6,953	6,647	6,804	6,413	-0.187	0.018	-0.288	-0.111	-0.522	6,941	-0.187	0.018	-0.288	-0.111	-0.522	6,941	-0.187	0.018	-0.288	-0.111	-0.522	6,941	-0.187	0.018	-0.288	-0.111	-0.522	6,941	-0.187	0.018	-0.288	-0.111	-0.522
cg1805	ork4	Primosomal protein IV (replication factor IV), helicase superfamily II-	L	Rev	1700615	1699429	2067	1993	493	587	822	723	881	130	4,664	4,812	4,340	4,428	4,551	3,975	0.148	0.676	-0.185	-0.113	-0.522	4,687	0.148	0.676	-0.185	-0.113	-0.522	4,687	0.148	0.676	-0.185	-0.113	-0.522	4,687	0.148	0.676	-0.185	-0.113	-0.522	4,687	0.148	0.676	-0.185	-0.113	-0.522
cg1806	metK	Methionine adenosyltransferase	H	Rev	1701865	1700642	1224	1151	3112	3115	3040	3327	2781	511	8,076	7,974	7,982	7,806	7,564	5,097	-0.102	-0.094	-0.270	-0.512	-0.978	8,025	-0.102	-0.094	-0.270	-0.512	-0.978	8,025	-0.102	-0.094	-0.270	-0.512	-0.978	8,025	-0.102	-0.094	-0.270	-0.512	-0.978	8,025	-0.102	-0.094	-0.270	-0.512	-0.978
cg1807	dfp	Putative flavoprotein, involved CoA metabolism	H	Rev	1703241	1701973	1269	1196	496	516	668	641	577	393	5,377	5,330	5,745	5,380	5,245	4,667	-0.047	0.368	0.000	-0.132	-0.710	5,354	-0.047	0.368	0.000	-0.132	-0.710	5,354	-0.047	0.368	0.000	-0.132	-0.710	5,354	-0.047	0.368	0.000	-0.132	-0.710	5,354	-0.047	0.368	0.000	-0.132	-0.710
cg1809	K	DNA-directed RNA polymerase subunit K/omeg	K	Rev	1703784	1703497	289	215	2593	2022	2327	2591	2275	1122	9,900	9,969	9,684	9,533	9,362	8,218	0.068	-0.217	-0.368	-0.338	-0.588	9,935	0.068	-0.217	-0.368	-0.338	-0.588	9,935	0.068	-0.217	-0.368	-0.338	-0.588	9,935	0.068	-0.217	-0.368	-0.338	-0.588	9,935	0.068	-0.217	-0.368	-0.338	-0.588
cg1810	omk	Guanlylase kinase	F	Rev	1704448	1703876	573	500	5271	7246	6390	6091	4355	2318	9,931	10,286	10,148	9,773	9,306	8,732	0.355	0.217	-0.158	-0.625	-1.559	10,109	0.355	0.217	-0.158	-0.625	-1.559	10,109	0.355	0.217	-0.158	-0.625	-1.559	10,109	0.355	0.217	-0.158	-0.625	-1.559	10,109	0.355	0.217	-0.158	-0.625	-1.559
cg1811	ihf	Conserved hypothetical protein, probable interactor host factor c1	-	Rev	1704776	1704456	321	248	5700	8011	7359	6971	5419	2851	10,880	11,267	11,188	10,804	10,357	9,506	0.387	0.308	-0.076	-0.423	-1.374	11,074	0.387	0.308	-0.076	-0.423	-1.374	11,074	0.387	0.308	-0.076	-0.423	-1.374	11,074	0.387	0.308	-0.076	-0.423	-1.374	11,074	0.387	0.308	-0.076	-0.423	-1.374
cg1812	pyrF	Ornithine-5-phosphate decarboxylase	J	Rev	1705818	1704982	837	763	459	656	643	732	1005	254	5,866	6,276	6,291	6,171	6,445	4,640	0.410	0.425	0.306	0.779	-1.226	6,071	0.410	0.425	0.306	0.779	-1.226	6,071	0.410	0.425	0.306	0.779	-1.226	6,071	0.410	0.425	0.306	0.779	-1.226	6,071	0.410	0.425	0.306	0.779	-1.226
cg1813	carB	Carbamoyl-phosphate synthase, large chain	E	Rev	1709165	1705824	3342	3269	2371	2741	2751	3144	4224	1277	6,235	6,340	6,409	6,275	6,718	4,968	0.105	0.175	0.040	0.483	-1.267	6,287	0.105	0.175	0.040	0.483	-1.267	6,287	0.105	0.175	0.040	0.483	-1.267	6,287	0.105	0.175	0.040	0.483	-1.267	6,287	0.105	0.175	0.040	0.483	-1.267
cg1814	carA	Carbamoyl-phosphate synthase, small chain	E	Rev	1710352	1709871	1182	1109	1376	1597	1542	1752	2426	719	5,866	6,071	6,053	6,931	7,148	5,640	0.111	0.104	-0.018	0.468	-1.310	7,005	0.111	0.104	-0.018	0.468	-1.310	7,005	0.111	0.104	-0.018	0.468	-1.310	7,005	0.111	0.104	-0.018	0.468	-1.310	7,005	0.111	0.104	-0.018	0.468	-1.310
cg1815	pyrC	Dihydroorotate	F	Rev	1711825	1710482	1344	1271	1101	1196	1186	1386	1477	574	6,443	6,458	6,490	6,408	6,517	5,130	0.016	0.047	-0.035	0.074	-1.313	6,451	0.016	0.047	-0.035	0.074	-1.313	6,451	0.016	0.047	-0.035	0.074	-1.313	6,451	0.016	0.047	-0.035	0.074	-1.313	6,451	0.016	0.047	-0.035	0.074	-1.313
cg1816	pyrB	Aspartate carboxyltransferase catalytic chain	F	Rev	1712816	1711878	939	865	760	876	762	915	995	526	6,426	6,527	6,358	6,327	6,465	5,521	0.101	-0.057	-0.099	0.039	-0.905	6,479	0.101	-0.057	-0.099	0.039	-0.905	6,479	0.101	-0.057	-0.099	0.039	-0.905	6,479	0.101	-0.057	-0.099	0.039	-0.905	6,479	0.101	-0.057	-0.099	0.039	-0.905
cg1817	pyrE	Putative RNA-binding regulatory protein, phosphoribosyltransferas	F	Rev	1713395	1712817	579	506	1477	1514	1512	1622	2025	1571	8,081	8,013	8,055	7,841	8,187	7,959	-0.068	-0.027	-0.241	0.105	-0.323	8,047	-0.068	-0.027	-0.241	0.105	-0.323	8,047	-0.068	-0.027	-0.241	0.105	-0.323	8,047	-0.068	-0.027	-0.241	0.105	-0.323	8,047	-0.068	-0.027	-0.241	0.105	-0.323
cg1819	-	Conserved hypothetical protein, nucleoside-diphosphate sugar epitr	S	Fwd	1713704	1715230	1527	1454	354	417	473	514	505	499	4,625	4,756	4,981	4,795	4,786	4,773	0.132	0.356	0.170	0.162	0.148	4,691	0.132	0.356	0.170	0.162	0.148	4,691	0.132	0.356	0.170	0.1													

This supplementary table provides the full data for the calculation and development of Table A15.

Gene Information			Read Mapping			Raw Read Count			log ₂ TPM			m-values			a-value			m-values < ±1.5 (not significant)			m-values > ±1.5 (significant)													
Locus	Feature	Product	Major COG Cat.	Strand	Start	End	Length (bp)	Effective Length	①	②	③	④	⑤	⑥	①	②	③	④	⑤	⑥	①	②	③	④	⑤	⑥	①	②	③	④	⑤	⑥		
cg507	-	Putative phosphotransferase/kinase synthetase/decarboxylase	H	Fwd	1797096	1797656	561	487	441	534	983	1493	2289	1785	6.385	6.256	7.479	7.776	8.409	8.025	0.170	1.094	1.390	2.023	1.600	6.471	0.170	1.094	1.390	2.023	1.600	6.471		
cg508	-	Hypothetical protein	-	Fwd	1797658	1798524	867	794	517	636	997	1525	2150	1517	5.986	6.181	6.872	7.176	7.691	7.163	0.195	0.885	1.190	1.826	1.177	6.084	0.195	0.885	1.190	1.826	1.177	6.084		
cg509	-	Hypothetical protein	-	Fwd	1798822	1799244	423	350	60	62	77	133	200	57	3.936	3.878	4.230	4.704	5.306	3.488	-0.057	0.294	0.769	1.371	-0.447	3.907	-0.057	0.294	0.769	1.371	-0.447	3.907		
cg510	-	Putative secreted or membrane protein	-	Rev	1799441	1799319	123	50	827	1103	926	1038	707	276	9.430	9.792	9.583	9.441	8.905	7.526	0.311	1.012	-0.039	-0.576	-1.954	6.936	0.311	1.012	-0.039	-0.576	-1.954	6.936		
cg511	-	Putative secreted protein	-	Rev	1800229	1800492	738	665	4227	6165	4632	5084	3455	1510	9.248	9.688	9.319	9.147	8.607	7.389	0.441	0.071	-0.100	-0.641	-1.889	6.448	0.441	0.071	-0.100	-0.641	-1.889	6.448		
cg512	-	Hypothetical protein	-	Fwd	1800654	1800881	228	154	5	2	1	0	2	1	-0.078	1.555	1.446	0.970	-1.013	0.284	-1.100	0.006	-0.950	-0.936	-1.375	-0.930	-1.100	0.006	-0.950	-0.936	-1.375	-0.930		
cg513	-	Hypothetical protein	-	Rev	1800945	1801841	897	823	4	7	4	2	3	0	-0.758	-0.183	-0.818	-1.861	-1.429	-0.647	0.574	-0.061	-1.104	-0.672	0.111	-0.471	0.574	-0.061	-1.104	-0.672	0.111	-0.471		
cg514	-	Hypothetical protein	-	Fwd	1802102	1802233	132	59	0	2	1	1	0	0	-0.315	1.166	0.624	0.318	-0.665	-0.690	1.481	0.939	0.633	-0.350	-0.375	0.426	1.481	0.939	0.633	-0.350	-0.375	0.426		
cg515	-	Hypothetical protein	-	Fwd	1802345	1802778	438	364	4	9	1	3	1	3	0.277	1.173	-1.106	-0.412	-1.395	-0.420	0.896	-1.383	-0.689	-0.789	-0.694	0.725	0.896	-1.383	-0.689	-0.789	-0.694	0.725		
cg516	-	Hypothetical protein	-	Fwd	1802964	1803021	606	533	52	59	55	28	28	22	1.214	3.089	3.233	1.978	1.934	1.635	0.075	0.019	-1.237	-1.220	-0.829	1.635	0.075	0.019	-1.237	-1.220	-0.829	1.635		
cg517	-	Hypothetical protein	-	Rev	1804049	1803624	426	353	275	296	428	449	467	207	6.103	6.105	6.679	6.442	6.515	6.868	0.002	0.576	0.390	0.412	0.765	6.104	0.002	0.576	0.390	0.412	0.765	6.104		
cg518	-	Putative secreted protein	-	Fwd	1804361	1804894	534	461	207	351	324	471	470	250	5.369	6.024	5.952	6.185	6.199	5.266	0.655	0.583	0.816	0.829	-0.103	5.607	0.655	0.583	0.816	0.829	-0.103	5.607		
cg519	-	Putative membrane protein	-	Fwd	1805033	1805688	336	263	2	9	8	7	1	4	-0.078	1.555	1.446	0.970	-1.013	0.284	0.441	0.071	-0.100	-0.641	-1.889	6.448	0.441	0.071	-0.100	-0.641	-1.889	6.448		
cg520	-	Hypothetical protein	-	Fwd	1805606	1806073	468	395	14	17	6	3	8	6	1.766	1.925	0.606	-0.508	0.679	0.292	0.159	-1.160	-2.274	-1.087	-1.474	1.846	0.159	-1.160	-2.274	-1.087	-1.474	1.846		
cg521	-	Hypothetical protein	-	Fwd	1806101	1806340	240	166	3	5	0	1	0	1	0.822	1.304	-1.238	-0.544	-1.327	-0.552	0.481	-2.061	-1.367	-0.230	-1.063	1.063	0.481	-2.061	-1.367	-0.230	-1.063	1.063		
cg522	-	Hypothetical protein	-	Fwd	1806440	1807074	615	541	2	2	3	2	0	0	-0.950	-1.054	-0.596	-1.317	-0.885	-2.910	-0.410	0.354	-0.367	-0.936	-0.940	-1.002	-0.410	0.354	-0.367	-0.936	-0.940	-1.002		
cg523	-	Hypothetical protein	-	Fwd	1807247	1808416	915	841	6	24	17	13	8	8	4.465	4.432	0.153	0.695	0.349	-0.313	0.304	0.076	1.218	0.870	0.210	0.454	0.304	0.076	1.218	0.870	0.210	0.454		
cg524	-	Hypothetical protein	-	Fwd	1808219	1808374	156	83	4	3	1	1	2	2	1.766	1.340	0.383	0.077	0.679	0.654	-0.426	-1.383	-1.689	-1.087	-1.112	1.553	-0.426	-1.383	-1.689	-1.087	-1.112	1.553		
cg525	-	Hypothetical protein	-	Fwd	1808662	1808871	210	137	44	56	73	91	84	47	4.507	4.744	5.164	5.172	5.075	4.226	0.237	0.657	0.665	0.568	-0.281	4.626	0.237	0.657	0.665	0.568	-0.281	4.626		
cg526	-	Hypothetical protein	-	Fwd	1808995	1809588	418	410	79	98	75	99	39	9	3.633	3.837	3.555	3.193	3.606	2.259	0.384	-0.843	-0.589	0.119	0.021	3.758	0.384	-0.843	-0.589	0.119	0.021	3.758		
cg527	-	Putative molecular chaperon	-	Fwd	1809609	1809898	288	215	15	12	14	8	6	4	2.559	2.746	2.506	1.363	1.017	0.507	-0.403	-0.154	-1.197	-1.542	-1.051	2.358	-0.403	-0.154	-1.197	-1.542	-1.051	2.358		
cg528	-	Hypothetical protein	-	Fwd	1809972	1810307	336	262	15	17	19	11	15	7	2.327	2.403	2.598	1.555	1.987	0.962	0.066	0.261	-0.782	-0.350	-1.375	3.370	0.066	0.261	-0.782	-0.350	-1.375	3.370		
cg529	res	Putative resolvase, family recombinase	L	Fwd	1811233	1811847	615	541	32	54	67	72	116	45	2.509	3.142	3.492	3.288	3.986	2.614	0.633	0.982	0.779	1.476	1.005	2.826	0.633	0.982	0.779	1.476	1.005	2.826		
cg530	-	Putative secreted hydrolase	-	Fwd	1812025	1812020	996	922	286	418	421	415	314	65	4.934	5.278	5.430	4.783	4.689	3.759	0.458	0.771	0.663	0.610	0.173	4.576	0.458	0.771	0.663	0.610	0.173	4.576		
cg531	-	Putative secreted protein	-	Fwd	1813036	1813413	378	305	144	213	257	295	281	211	5.347	5.805	6.118	6.110	5.957	5.520	-0.174	-0.453	-0.367	-0.494	-0.960	5.128	-0.174	-0.453	-0.367	-0.494	-0.960	5.128		
cg532	ppp2	Putative protein phosphatase	-	Fwd	1813687	1814166	480	406	20	19	15	20	18	13	2.215	2.041	1.762	1.848	1.721	1.255	-0.207	0.754	0.168	0.347	0.522	4.974	-0.207	0.754	0.168	0.347	0.522	4.974		
cg533	-	Hypothetical protein	-	Fwd	1814353	1815081	729	655	28	26	50	41	46	53	4.129	3.978	4.482	4.218	3.981	3.117	0.337	-0.168	-0.136	-0.402	-0.324	6.242	0.337	-0.168	-0.136	-0.402	-0.324	6.242		
cg534	gntB2	Transcriptional regulator, GntR-family	-	Fwd	1815252	1815998	741	668	496	666	688	425	687	555	2.952	2.289	1.784	1.636	1.550	1.628	4.559	4.243	4.016	3.963	3.444	3.294	6.242	4.559	4.243	4.016	3.963	3.444	3.294	6.242
cg535	-	Putative secreted protein	-	Fwd	1817145	1817603	459	386	101	87	72	86	59	54	1.817	1.921	1.811	1.111	1.111	1.111	-0.317	-0.543	-0.596	-1.115	-1.266	4.701	-0.317	-0.543	-0.596	-1.115	-1.266	4.701		
cg536	-	Putative secreted protein	-	Fwd	1817921	1818117	296	223	1	1	0	1	0	0	-0.295	1.554	0.104	0.544	-1.013	0.284	1.481	0.939	-0.367	-0.350	-0.375	3.907	1.481	0.939	-0.367	-0.350	-0.375	3.907		
cg537	-	Putative secreted protein	-	Rev	1819206	1819081	126	52	11	6	3	3	6	0	3.327	2.456	1.691	1.285	1.210	-0.622	-0.881	-1.646	-1.952	-1.127	-0.260	3.969	-0.881	-1.646	-1.952	-1.127	-0.260	3.969		
cg538	-	Putative secreted protein	-	Fwd	1818604	1819278	675	601	113	93	84	119	144	70	4.157	3.781	3.679	3.871	4.161	3.106	-0.376	-0.478	-0.286	0.044	-1.051	3.969	-0.376	-0.478	-0.286	0.044	-1.051	3.969		
cg539	-	Putative secreted protein	-	Fwd	1819275	1819694	420	345	33	12	29	19	40	31	3.081	1.612	2.861	1.970	3.232	2.641	-1.460	-0.220	-1.111	-0.058	-0.441	3.146	-1.460	-0.220	-1.111	-0.058	-0.441	3.146		
cg540	-	Putative secreted protein	-	Fwd	1819494	1819789	295	222	576	1745	95	119	1624	2306	2345	7.454	7.304	6.928	6.465	6.690	1.533	0.665	0.690	1.533	0.665	0.690	1.533	0.665	0.690	1.533	0.665	0.690	1.533	
cg541	-	Hypothetical protein	-	Fwd	1820270	1820641	372	299	515	1402	880	1093	1519	2005	7.201	8.541	7.913	7.919	8.410	8.786	0.606	0.593	0.687	0.957	0.978	7.871	0.606	0.593	0.687	0.957	0.978	7.871		
cg542	-	Hypothetical protein	-																															

This supplementary table provides the full data for the calculation and development of Table A5.

Gene Information				Read Mapping				Raw Read Count				log ₂ TPM				m-values				a-value	m-values < ±1.5 (not significant)				m-values > ±1.5 (significant)																
Locus	Feature	Product	Major COG Cat.	Strand	Start	End	Effective Length	①	②	③	④	⑤	⑥	①	②	③	④	⑤	⑥	①	②	③	④	⑤	⑥	①	②	③	④	⑤	⑥	①	②	③	④	⑤	⑥				
cg2011	-	Putative membrane protein	-	Rev	1902388	1901273	1116	1043	39	52	38	82	70	39	1.927	2.229	1.830	2.605	2.405	1.553	0.302	-0.097	0.678	0.478	-0.375	2.078	0.113	-0.226	-0.426	-0.887	-0.912	2.266	0.302	-0.097	0.678	0.478	-0.375	2.078			
cg2012	-	Putative secreted protein	-	Rev	1903383	1902535	849	775	73	85	65	70	50	39	2.209	2.322	1.984	2.783	2.322	2.298	0.113	-0.226	-0.426	-0.887	-0.912	2.266	0.113	-0.226	-0.426	-0.887	-0.912	2.266	0.113	-0.226	-0.426	-0.887	-0.912	2.266			
cg2014	-	Hypothetical protein	P	Rev	1904355	1903474	882	809	224	346	351	353	300	237	4.759	5.280	5.344	5.046	4.829	4.465	0.521	0.585	0.287	0.070	-0.294	5.019	0.521	0.585	0.287	0.070	-0.294	5.019	0.521	0.585	0.287	0.070	-0.294	5.019			
cg2015	-	Hypothetical protein	-	Rev	1907350	1904582	2769	2695	87	107	120	140	109	69	1.754	1.945	2.152	2.067	1.726	1.049	0.192	0.399	0.313	-0.028	-0.705	1.849	0.192	0.399	0.313	-0.028	-0.705	1.849	0.192	0.399	0.313	-0.028	-0.705	1.849			
cg2016	-	Hypothetical protein	-	Rev	1908044	1907442	603	531	32	26	46	52	62	41	2.538	2.144	2.987	2.855	3.121	2.511	-0.393	0.450	0.317	0.583	-0.027	2.341	-0.393	0.450	0.317	0.583	-0.027	2.341	-0.393	0.450	0.317	0.583	-0.027	2.341	-0.393		
cg2017	-	Hypothetical protein	-	Rev	1909386	1909133	1254	1180	43	85	117	127	88	60	1.896	2.160	3.259	2.989	3.087	2.538	0.863	1.363	1.093	1.191	0.642	2.538	0.863	1.363	1.093	1.191	0.642	2.538	0.863	1.363	1.093	1.191	0.642	2.538			
cg2018	-	Putative membrane protein	-	Rev	1910132	1909434	699	626	30	50	52	111	91	66	2.234	2.849	2.948	3.721	3.454	2.972	0.614	0.713	1.486	1.220	0.737	2.542	0.614	0.713	1.486	1.220	0.737	2.542	0.614	0.713	1.486	1.220	0.737	2.542			
cg2019	-	Putative membrane protein	-	Rev	1910970	1910254	717	643	78	73	113	105	104	65	3.538	3.349	4.016	3.605	3.608	2.913	-0.189	0.478	0.067	0.070	-0.625	3.444	-0.189	0.478	0.067	0.070	-0.625	3.444	-0.189	0.478	0.067	0.070	-0.625	3.444			
cg2020	-	Putative membrane protein	-	Rev	1911980	1910970	1011	936	29	44	68	62	67	50	1.630	2.156	2.796	2.758	2.486	2.046	0.505	1.165	0.728	0.855	0.415	3.483	0.505	1.165	0.728	0.855	0.415	3.483	0.505	1.165	0.728	0.855	0.415	3.483			
cg2021	-	Hypothetical membrane protein, similar to P18, bacteriophage CP-1	-	Rev	1913772	1912111	1662	1588	96	163	107	178	118	56	4.714	4.685	4.729	4.575	4.500	3.741	-0.029	0.015	-0.139	-0.214	-0.973	4.700	-0.029	0.015	-0.139	-0.214	-0.973	4.700	-0.029	0.015	-0.139	-0.214	-0.973	4.700			
cg2022	-	Putative secreted protein	-	Rev	1915265	1913802	1464	1390	33	80	87	86	61	21	1.301	2.450	2.612	2.290	1.818	0.299	1.149	1.311	0.989	0.517	-1.003	1.875	1.149	1.311	0.989	0.517	-1.003	1.875	1.149	1.311	0.989	0.517	-1.003	1.875			
cg2023	-	Putative membrane protein	-	Rev	1915801	1915442	360	286	53	99	149	132	71	23	3.992	4.778	5.006	4.926	4.058	2.448	0.785	1.413	0.934	0.065	-0.544	4.187	0.785	1.413	0.934	0.065	-0.544	4.187	0.785	1.413	0.934	0.065	-0.544	4.187			
cg2024	-	Putative membrane protein, putative nucleic acid subunit of the exocysteine	-	Rev	1917705	1916294	1512	1439	373	393	393	437	410	246	4.714	4.685	4.729	4.575	4.500	3.741	-0.029	0.015	-0.139	-0.214	-0.973	4.700	-0.029	0.015	-0.139	-0.214	-0.973	4.700	-0.029	0.015	-0.139	-0.214	-0.973	4.700			
cg2025	-	Hypothetical protein	-	Fwd	1917900	1918208	309	236	1208	1572	503	625	580	252	8.698	8.973	7.375	7.381	7.291	6.066	0.276	-1.323	-1.316	-1.407	-0.631	8.435	0.276	-1.323	-1.316	-1.407	-0.631	8.435	0.276	-1.323	-1.316	-1.407	-0.631	8.435			
cg2026	-	Hypothetical protein	-	Fwd	1918416	1918640	225	151	1623	2096	2235	1884	1554	283	9.581	9.846	9.982	9.429	9.169	10.020	0.265	0.401	-0.152	-0.412	0.439	9.733	0.265	0.401	-0.152	-0.412	0.439	9.733	0.265	0.401	-0.152	-0.412	0.439	9.733			
cg2027	-	Hypothetical protein	-	Rev	1918986	1918798	189	116	38	42	38	51	70	68	4.853	4.490	4.392	4.501	4.967	4.901	0.037	-0.061	0.048	0.515	0.449	4.471	0.037	-0.061	0.048	0.515	0.449	4.471	0.037	-0.061	0.048	0.515	0.449	4.471			
cg2028	-	Hypothetical protein	-	Rev	1919680	1919033	648	575	175	224	244	371	391	313	4.849	5.100	5.438	5.562	5.415	5.310	0.251	0.770	0.713	0.866	0.461	4.654	0.251	0.770	0.713	0.866	0.461	4.654	0.251	0.770	0.713	0.866	0.461	4.654			
cg2029	-	Hypothetical protein	-	Rev	1920933	1920172	762	689	249	219	360	508	460	272	5.122	4.833	5.591	5.781	5.585	4.874	-0.288	0.469	0.659	0.533	-0.248	4.977	-0.288	0.469	0.659	0.533	-0.248	4.977	-0.288	0.469	0.659	0.533	-0.248	4.977			
cg2030	-	Hypothetical protein	-	Rev	1921666	1921115	552	479	272	255	411	583	656	493	5.714	5.517	6.247	6.444	6.631	6.195	-0.197	0.533	0.730	0.917	0.481	5.635	-0.197	0.533	0.730	0.917	0.481	5.635	-0.197	0.533	0.730	0.917	0.481	5.635			
cg2031	-	Conserved hypothetical protein	-	Rev	1922748	1922184	931	860	655	648	677	860	608	408	6.221	6.102	6.715	6.303	6.264	5.739	-0.119	-0.056	0.082	0.043	-0.482	6.062	-0.119	-0.056	0.082	0.043	-0.482	6.062	-0.119	-0.056	0.082	0.043	-0.482	6.062			
cg2032	-	Putative membrane protein	U	Rev	1927482	1923016	4467	4393	302	450	514	508	412	212	2.847	3.317	3.552	3.229	2.845	1.964	0.470	0.705	0.382	0.097	-0.883	3.082	0.470	0.705	0.382	0.097	-0.883	3.082	0.470	0.705	0.382	0.097	-0.883	3.082			
cg2033	-	Putative secreted protein	-	Rev	1928309	1927728	582	509	782	899	663	893	913	413	7.157	7.254	6.859	6.520	6.301	5.863	0.097	-0.298	0.175	-0.127	-1.294	7.206	0.097	-0.298	0.175	-0.127	-1.294	7.206	0.097	-0.298	0.175	-0.127	-1.294	7.206			
cg2034	-	Hypothetical protein	-	Rev	1929649	1928714	936	863	1189	1349	1579	1841	1896	1419	7.076	7.154	7.424	7.339	7.399	6.956	0.078	0.348	0.264	0.323	-0.120	7.115	0.078	0.348	0.264	0.323	-0.120	7.115	0.078	0.348	0.264	0.323	-0.120	7.115			
cg2035	-	Putative methyltransferase	-	Fwd	1929682	1929256	74	33	23	28	11	24	23	22	4.291	2.468	4.810	4.231	3.522	3.820	0.406	0.406	0.406	0.406	0.406	4.066	0.406	0.406	0.406	0.406	0.406	0.406	0.406	0.406	0.406	0.406	0.406	0.406	0.406	0.406	0.406
cg2036	-	Putative secreted protein	-	Fwd	1930006	1930383	378	304	374	283	155	223	190	90	6.718	6.213	5.392	5.608	5.395	4.300	-0.505	-1.326	-1.110	-1.323	-0.411	6.465	-0.505	-1.326	-1.110	-1.323	-0.411	6.465	-0.505	-1.326	-1.110	-1.323	-0.411	6.465			
cg2037	-	Conserved hypothetical protein	-	Rev	1932351	1930528	1824	1751	1026	1125	1633	1978	1975	1064	5.901	5.930	6.510	6.480	6.495	5.979	0.029	0.609	0.580	0.594	-0.322	5.945	0.029	0.609	0.580	0.594	-0.322	5.945	0.029	0.609	0.580	0.594	-0.322	5.945			
cg2038	-	Hypothetical protein	-	Rev	1932662	1932459	204	131	162	180	224	286	300	150	6.006	6.453	6.810	6.855	6.941	5.921	0.047	0.404	0.500	0.535	-0.485	6.429	0.047	0.404	0.500	0.535	-0.485	6.429	0.047	0.404	0.500	0.535	-0.485	6.429			
cg2039	-	Hypothetical protein	-	Rev	1933351	1933048	462	389	485	609	722	747	848	462	6.805	6.726	7.333	7.133	7.288	6.388	0.442	0.313	0.284	0.324	-0.356	6.347	0.442	0.313	0.284	0.324	-0.356	6.347	0.442	0.313	0.284	0.324	-0.356	6.347			
cg2040	-	Putative transcriptional regulator, HTH 3-family	-	Rev	1933763	1933404	360	287	473	691	613	743	755	479	7.126	7.568	7.439	7.410	7.450	6.770	0.614	0.007	0.152	-0.435	-0.644	7.742	0.614	0.007	0.152	-0.435	-0.644	7.742	0.614</								

This supplementary table provides the full data for the calculation and development of Table A5.

Gene Information				Read Mapping				Raw Read Count				log ₂ TPM				m-values				m-values < ±1.5 (not significant)				m-values ≥ ±1.5 (significant)				a-value			
Locus	Feature	Product	Major COG Cat.	Strand	Start	Stop	Effective Length	1	2	3	4	5	6	1	2	3	4	5	6	1	2	3	4	5	6	1	2		3	4	5
cg2113	div5	cell wall hydrolase	D	Rev	2006458	2006036	423 349	106	139	107	99	69	38	4,746	5,030	4,699	4,282	3,784	2,916	0.284	-0.047	-0.464	-0.962	-1.888	4.488	0.284	-0.047	-0.464	-0.962	-1.888	-1.888
cg2114	lexA	Putative transcriptional regulator, LexA-family	K	Fwd	2000798	2007559	762 689	1262	1435	1951	1815	1927	1742	4,458	7,120	6,026	7,416	7,119	7,549	0.061	0.567	0.157	0.261	0.090	4.488	0.061	0.567	0.157	0.261	0.090	0.090
cg2115	sugR	Transcriptional regulator, DecR-family	K	Fwd	2007864	2008643	780 706	483	561	655	679	689	338	6,039	6,151	6,419	6,165	6,202	5,150	0.112	0.380	0.125	0.162	-0.889	6.085	0.112	0.380	0.125	0.162	-0.889	-0.889
cg2116	-	Putative phosphofruktokinase	G	Fwd	2008640	2009602	653 889	481	600	718	910	850	375	5,729	5,944	6,247	6,283	6,200	4,996	0.215	0.518	0.553	0.471	-0.733	5.837	0.215	0.518	0.553	0.471	-0.733	-0.733
cg2117	ptfI	Phosphotransferase system (PTS), Enzyme I	G	Rev	2011370	2009664	1707 1634	7576	9023	3259	3478	3288	6889	8,880	9,028	7,602	7,390	5,326	8,368	0.148	-1.277	-1.499	-1.758	-0.512	6.954	0.148	-1.277	-1.499	-1.758	-0.512	-0.512
cg2118	-	Transcriptional regulator, DecR-family	K	Fwd	2011777	2012571	795 721	1393	1269	916	844	859	1310	7,540	7,101	6,874	6,450	6,493	7,076	-0.238	-0.666	-1.090	-1.047	-0.463	4.500	-0.238	-0.666	-1.090	-1.047	-0.463	-0.463
cg2119	fruK	1-Phosphofruktokinase	G	Fwd	2012568	2013560	993 919	994	1099	769	575	588	900	6,732	6,773	6,302	5,576	5,168	6,322	0.042	-0.430	-1.156	-1.114	-0.410	6.752	0.042	-0.430	-1.156	-1.114	-0.410	-0.410
cg2120	ptfF	Phosphotransferase system (PTS), fructose-specific enzyme IIAB c	G	Fwd	2013557	2012023	2067 1993	2022	2554	1696	1494	1414	2335	6,698	6,931	6,384	5,895	5,832	6,531	0.233	-0.314	-0.803	-0.866	-0.167	6.835	0.233	-0.314	-0.803	-0.866	-0.167	-0.167
cg2121	ptfH	Phosphotransferase system (PTS), phosphocarrier protein HPr	G	Fwd	2015811	2016020	270 196	3721	4604	6809	6818	6834	6645	10,514	10,718	11,355	11,021	11,042	10,976	0.203	0.811	0.507	0.527	0.462	10.616	0.203	0.811	0.507	0.527	0.462	0.462
cg2122	-	Putative transcriptional regulator, ATfase subunit	K	Fwd	2017287	2017420	526 455	616	616	630	670	545	234	6,954	7,059	6,926	6,708	6,438	5,187	0.301	-0.028	-0.246	-0.266	-0.368	6.585	0.301	-0.028	-0.246	-0.266	-0.368	-0.368
cg2125	uraA	Putative xanthine/uracil symporter, nucleobase/symporter-2	R	Rev	2018649	2017366	1284 1211	639	597	438	382	316	79	5,725	5,523	5,120	4,617	4,362	2,350	-0.202	-0.604	-1.107	-1.363	-0.375	5.624	-0.202	-0.604	-1.107	-1.363	-0.375	-0.375
cg2126	-	GTP-binding protein	F	Rev	2020156	2018696	1461 1389	1338	1324	1181	1179	955	771	6,604	6,485	6,363	6,055	5,768	5,435	0.213	-0.247	-0.549	-0.836	-1.169	6.544	0.213	-0.247	-0.549	-0.836	-1.169	-1.169
cg2127	-	Hypothetical protein	F	Fwd	2020400	2021558	759 685	736	917	1954	1867	1150	473	6,687	6,900	6,034	7,662	6,980	5,676	0.213	1.247	0.975	0.293	-1.011	6.783	0.213	1.247	0.975	0.293	-1.011	-1.011
cg2128	-	Putative membrane protein	F	Fwd	2021355	2021894	540 467	318	444	869	1127	1176	874	5,970	6,346	7,357	7,425	7,504	7,051	0.376	1.387	1.455	1.534	1.081	6.158	0.376	1.387	1.455	1.534	1.081	1.081
cg2129	dapF	Daminopiminate epimerase	E	Rev	2022724	2021891	834 761	548	609	615	505	414	109	6,126	6,174	6,232	5,642	5,753	3,432	0.048	0.105	-0.484	-0.753	-0.694	6.150	0.048	0.105	-0.484	-0.753	-0.694	-0.694
cg2130	msiA	RNA superfamily protein	F	Fwd	2022625	2022730	906 833	267	314	355	304	342	213	4,972	5,101	5,321	4,792	4,978	4,273	0.129	0.349	-0.180	0.006	-0.699	5.037	0.129	0.349	-0.180	0.006	-0.699	-0.699
cg2131	-	Hypothetical protein	F	Rev	2024266	2023655	612 538	226	333	333	272	227	5,289	5,752	5,804	5,519	5,215	4,930	0.453	0.505	0.220	-0.083	-0.368	6.754	0.453	0.505	0.220	-0.083	-0.368	-0.368	
cg2132	-	Conserved hypothetical protein	F	Rev	2024452	2025813	1362 1289	2502	3294	2434	2039	1865	813	7,607	7,900	7,507	6,946	6,934	5,644	0.293	-0.100	-0.662	-0.773	-1.964	6.754	0.293	-0.100	-0.662	-0.773	-1.964	-1.964
cg2133	-	AcrNyl transferase, GNAT-family	K	Fwd	2025814	2026839	1026 953	175	188	239	174	184	69	4,186	4,185	4,573	3,811	3,908	2,481	-0.001	0.387	-0.375	-0.278	-1.708	4.185	-0.001	0.387	-0.375	-0.278	-1.708	-1.708
cg2134	-	Putative membrane protein	R	Rev	2027937	2027146	612 599	799	839	1876	2139	2301	2027	4,981	6,913	8,151	8,034	6,156	7,948	-0.068	1.170	1.053	1.175	0.967	6.945	-0.068	1.170	1.053	1.175	0.967	0.967
cg2135	msiB	RNA methylesterase	J	Rev	2029481	2027901	1581 1508	1370	1415	1149	1077	785	117	6,524	6,467	6,210	5,810	5,311	2,611	-0.057	-0.314	-0.714	-1.152	-1.913	6.495	-0.057	-0.314	-0.714	-1.152	-1.913	-1.913
cg2136	glaA	ABC-type glutamate transporter, ATPase subunit (TC.3.A.1.3.9)	E	Fwd	2029799	2030551	753 680	3128	5610	4043	1367	1466	686	8,784	9,525	7,140	7,224	7,342	6,222	0.741	-1.644	-1.560	-1.443	-2.562	9.155	0.741	-1.644	-1.560	-1.443	-2.562	-2.562
cg2137	gluB	ABC-type glutamate transporter, substrate-binding (isoportin) (TC.3.A.1.3.9)	E	Fwd	2030469	2031556	888 814	1843	2998	487	606	648	214	7,784	8,381	8,505	8,514	9,247	4,309	0.598	-1.979	-1.970	-1.936	-3.475	6.002	0.598	-1.979	-1.970	-1.936	-3.475	-3.475
cg2138	gluC	ABC-type glutamate transporter, substrate-binding (isoportin) (TC.3.A.1.3.9)	E	Fwd	2031678	2032364	1077 1003	5783	6699	677	815	836	316	9,886	8,859	8,292	8,274	8,385	6,838	0.265	-0.420	-0.820	-0.820	-2.005	6.585	0.265	-0.420	-0.820	-0.820	-2.005	-2.005
cg2139	gluO	ABC-type glutamate transporter, permease subunit (TC.3.A.1.3.9)	E	Fwd	2032364	2033311	948 875	334	738	128	166	170	39	5,226	6,266	6,791	3,858	3,909	1,788	1.040	-1.435	-1.369	-1.318	-1.438	5.746	1.040	-1.435	-1.369	-1.318	-1.438	-1.438
cg2140	recX	Putative recombination protein RecX	R	Rev	2033991	2033344	648 574	66	113	48	52	28	12	3,456	4,119	2,944	2,275	1,898	0,715	0.663	-0.512	-0.705	-0.538	-2.740	3.787	0.663	-0.512	-0.705	-0.538	-2.740	-2.740
cg2141	recA	Recombinase A	L	Rev	2035165	2034035	1131 1058	744	830	547	544	427	187	6,127	6,181	6,623	5,309	4,978	3,766	0.054	-0.504	-0.818	-1.149	-1.364	6.154	0.054	-0.504	-0.818	-1.149	-1.364	-1.364
cg2142	-	Conserved hypothetical protein	R	Rev	2035655	2035440	216 149	449	449	449	449	449	449	4,492	4,836	4,949	4,589	4,404	4,259	-0.020	0.663	-0.420	-0.420	-0.888	6.154	-0.020	0.663	-0.420	-0.420	-0.888	-0.888
cg2146	-	Hypothetical protein	R	Rev	2036393	2035713	681 607	95	153	133	127	300	143	3,907	4,481	4,323	3,951	5,202	4,113	0.578	0.420	0.408	1.298	0.210	6.154	0.578	0.420	0.408	1.298	0.210	0.210
cg2147	-	Membrane protein, bioM-family	R	Fwd	2036588	2037193	606 533	80	89	67	62	1485	492	3,326	3,874	3,513	3,495	1,774	6,057	0.048	-0.313	-0.331	3.848	2.231	1.850	0.048	-0.313	-0.331	3.848	2.231	2.231
cg2148	-	Putative glutamate transporter, ATPase subunit	K	Fwd	2037197	2037917	702 629	117	137	149	149	149	149	4,587	4,836	4,949	4,589	4,404	4,259	0.206	0.616	0.564	2.968	1.718	1.445	0.206	0.616	0.564	2.968	1.718	1.718
cg2149	-	ABC-type putative cation transporter, permease subunit	P	Fwd	2037915	2038526	612 538	58	72	93	111	590	249	3,842	3,548	3,958	3,906	3,628	5,060	0.263	0.402	0.120	-0.238	-1.026	4.486	0.263	0.402	0.120	-0.238	-1.026	-1.026
cg2151	-	Conserved hypothetical protein, similar to chapek shock protein A	K	Rev	2039432	2038862	681 757	5126	6068	7065	7185	5539	3262	9,355	9,617	9,757	9,475	9,117	8,329	0.263	0.402	0.120	-0.238	-1.026	4.486	0.263	0.402	0.120	-0.238	-1.026	-1.026
cg2152	cIcrP	Transcriptional activator of Cfo protease genes	K	Rev	2039985	2039662	324 251	1507	1241	1174	1600	1246	1442	8,948	8,864	8,527	8,668	8,324	8,510	-0.384	-0.421	-0.280	-0.428	-0.438	6.756	-0.384	-0.421	-0.280	-0.428	-0.438	-0.438
cg2153	-	Conserved hypothetical protein, Cink-like family	K	Rev	2040566	2040566	612 538	449	449	449	449																				

This supplementary table provides the full data for the calculation and development of Table A5.

Gene Information				Read Mapping				Raw Read Count				log ₂ TPM				m-values				a-value				m-values < 1.5 (not significant)				m-values > 1.5 (significant)										
Locus	Feature	Product	Major COG Cat.	Strand	Start	End	Effective Length	①	②	③	④	⑤	⑥	①	②	③	④	⑤	⑥	①	②	③	④	⑤	⑥	①	②	③	④	⑤	⑥	①	②	③	④	⑤	⑥	
cg2224	xerC	Putative site-specific recombinase	L	Rev	2112757	2111810	948	875	373	342	275	287	273	185	5.388	5.159	4.889	4.444	4.589	4.005	-0.229	-0.499	-0.744	-0.799	-1.382	5.273	-0.229	-0.499	-0.744	-0.799	-1.382	5.273	-0.229	-0.499	-0.744	-0.799	-1.382	5.273
cg2226	-	Conserved hypothetical protein, Rossmann-fold nucleotide-binding	L	Rev	2111416	2112932	1185	1111	45	29	16	12	33	13	2.042	1.546	1.248	1.236	-0.101	-0.720	-1.497	-0.786	-0.786	-0.786	-0.786	5.666	-0.720	-1.497	-0.786	-0.786	-0.786	5.666	-0.720	-1.497	-0.786	-0.786	-0.786	5.666
cg2227	-	Putative ATPase with chaperone activity	L	Rev	2115636	2114113	1524	1450	17	29	28	23	28	10	0.326	0.959	0.953	0.374	0.664	-0.827	0.633	0.627	0.048	0.338	-1.152	0.642	0.633	0.627	0.048	0.338	-1.152	0.642	0.633	0.627	0.048	0.338	-1.152	0.642
cg2228	-	Putative endonuclease	L	Rev	2115991	2115623	369	296	3	4	5	10	9	0	0.202	0.420	0.726	1.295	1.174	-2.713	0.218	0.524	1.093	0.972	-0.378	0.311	0.218	0.524	1.093	0.972	-0.378	0.311	0.218	0.524	1.093	0.972	-0.378	0.311
cg2229	-	Putative exonuclease ATPase subunit	L	Rev	2116616	2116311	306	232	382	457	476	650	586	358	7.089	7.207	7.308	7.451	7.319	6.985	0.119	0.219	0.362	0.231	-0.503	6.717	0.119	0.219	0.362	0.231	-0.503	6.717	0.119	0.219	0.362	0.231	-0.503	6.717
cg2230	rnhB	Ribonuclease H1	L	Rev	2117281	2116613	669	595	363	324	247	255	252	110	5.849	5.284	4.974	4.977	3.763	-0.265	-0.615	-0.875	-0.873	-0.088	5.937	-0.265	-0.615	-0.875	-0.873	-0.088	5.937	-0.265	-0.615	-0.875	-0.873	-0.088	5.937	
cg2232	lepB	Signal peptidase I	U	Rev	2118096	2117308	789	716	959	1033	833	746	598	168	6.999	7.016	6.749	6.284	5.982	4.132	0.017	-0.250	-0.715	-0.017	-2.867	7.007	0.017	-0.250	-0.715	-0.017	-2.867	7.007	0.017	-0.250	-0.715	-0.017	-2.867	7.007
cg2234	-	ABC-type putative iron(III) dicitrate transporter, substrate-binding II	P	Fwd	2118275	2119219	945	871	115	114	38	4	0	0	3.703	3.587	2.070	-1.200	-3.505	-3.529	-0.116	-0.633	-4.903	-7.208	-7.233	3.645	-0.116	-0.633	-4.903	-7.208	-7.233	3.645	-0.116	-0.633	-4.903	-7.208	-7.233	3.645
cg2235	rps5	SOS Ribosomal protein L13	J	Rev	2120022	2119681	342	269	787	1059	5346	5223	4496	1028	11.257	11.614	10.625	10.296	10.097	7.944	0.357	0.622	-0.961	-1.160	-0.888	11.436	0.357	0.622	-0.961	-1.160	-0.888	11.436	0.357	0.622	-0.961	-1.160	-0.888	11.436
cg2236	-	Thiamine pyrophosphate dehydrogenase	H	Rev	2120385	2120550	666	592	1632	1432	1983	2249	1188	990	8.023	7.731	7.244	8.128	8.049	6.928	-0.293	0.220	0.955	0.262	-1.095	8.465	-0.293	0.220	0.955	0.262	-1.095	8.465	-0.293	0.220	0.955	0.262	-1.095	8.465
cg2237	ihdO	Putative D-amino acid dehydrogenase, small subunit	E	Fwd	2121047	2122171	1125	1052	1815	1647	2570	2915	2469	1100	7.420	7.176	7.861	7.737	7.514	6.324	-0.244	0.441	0.316	0.094	-1.097	7.298	-0.244	0.441	0.316	0.094	-1.097	7.298	-0.244	0.441	0.316	0.094	-1.097	7.298
cg2238	ihmS	Sulfur transfer protein involved in thiamine biosynthesis, ThiS-like	H	Fwd	2122185	2122382	198	125	262	204	318	274	258	89	7.139	6.676	7.357	6.837	6.767	5.217	-0.463	0.218	-0.302	-0.372	-0.828	6.907	-0.463	0.218	-0.302	-0.372	-0.828	6.907	-0.463	0.218	-0.302	-0.372	-0.828	6.907
cg2239	ihgH	Thiamine biosynthesis protein, ThiG-like	H	Fwd	2122384	2122316	783	710	787	662	1011	922	846	365	6.739	6.366	7.039	6.600	6.493	5.258	-0.353	0.300	-0.139	-0.246	-1.451	6.565	-0.353	0.300	-0.139	-0.246	-1.451	6.565	-0.353	0.300	-0.139	-0.246	-1.451	6.565
cg2240	ihfF	Putative Dinucleotide-utilizing enzyme involved in thiamine biosynt	H	Fwd	2123168	2124244	1077	1004	687	600	917	713	622	206	6.083	5.784	6.438	5.770	5.590	3.975	-0.299	0.355	-0.313	-0.493	-1.017	5.933	-0.299	0.355	-0.313	-0.493	-1.017	5.933	-0.299	0.355	-0.313	-0.493	-1.017	5.933
cg2241	tex	Transcriptional accessory protein Tex	K	Rev	2126783	2124507	2277	2204	1129	1269	668	592	424	200	5.719	5.783	4.902	4.422	3.958	2.853	0.065	-0.817	-1.297	-0.133	-2.866	5.751	0.065	-0.817	-1.297	-0.133	-2.866	5.751	0.065	-0.817	-1.297	-0.133	-2.866	5.751
cg2242	-	Putative transcriptional regulator, LacI-family	K	Rev	2127771	2126794	978	905	91	117	62	64	60	8	3.319	3.575	2.712	2.451	2.377	-0.409	0.255	-0.607	-0.868	-0.943	-0.628	4.447	0.255	-0.607	-0.868	-0.943	-0.628	4.447	0.255	-0.607	-0.868	-0.943	-0.628	4.447
cg2243	-	Putative secondary Na ⁺ -coupled sulfate/malate/diL-tricarboxylate sy	F	Rev	2129832	2127801	1332	1258	66	76	76	76	65	53	2.416	2.513	2.017	2.202	2.045	1.730	0.097	-0.389	-0.166	-0.371	-0.684	4.465	0.097	-0.389	-0.166	-0.371	-0.684	4.465	0.097	-0.389	-0.166	-0.371	-0.684	4.465
cg2244	-	Lysine class I family	K	Rev	2130587	2129334	1254	1180	34	27	43	30	35	29	1.566	1.141	1.836	1.025	1.257	0.969	-0.426	0.270	-0.542	-0.309	-0.597	4.353	-0.426	0.270	-0.542	-0.309	-0.597	4.353	-0.426	0.270	-0.542	-0.309	-0.597	4.353
cg2247	-	Hypothetical protein	-	Rev	2131529	2131158	372	299	355	402	584	530	429	492	6.666	6.741	7.322	6.876	6.589	6.761	0.075	0.656	0.210	-0.077	0.095	6.703	0.075	0.656	0.210	-0.077	0.095	6.703	0.075	0.656	0.210	-0.077	0.095	6.703
cg2248	-	Putative membrane protein, DedA-family	-	Rev	2132246	2131554	674	619	275	248	355	268	171	5.401	5.149	5.536	4.762	4.650	4.344	-0.252	0.135	-0.639	-0.751	-1.057	6.256	-0.252	0.135	-0.639	-0.751	-1.057	6.256	-0.252	0.135	-0.639	-0.751	-1.057	6.256	
cg2249	trmD	RNA (guanine-N1)-methyltransferase	J	Rev	2133112	2132243	870	796	431	499	451	371	337	138	5.719	5.826	5.234	5.135	5.016	3.709	0.107	0.005	-0.584	-0.704	-2.011	5.773	0.107	0.005	-0.584	-0.704	-2.011	5.773	0.107	0.005	-0.584	-0.704	-2.011	5.773
cg2250	-	Putative secreted protein	-	Fwd	2133318	2133798	561	578	216	250	363	775	884	1454	5.114	5.251	6.462	6.162	6.823	7.515	0.106	1.317	1.477	-1.678	-2.311	5.198	0.106	1.317	1.477	-1.678	-2.311	5.198	0.106	1.317	1.477	-1.678	-2.311	5.198
cg2251	rimM	Putative 16S rRNA processing protein, RimM-like	J	Rev	2134310	2133795	516	443	370	446	383	369	256	87	6.253	6.418	6.262	5.883	5.734	3.803	0.165	-0.011	-0.371	-0.478	-0.498	6.336	0.165	-0.011	-0.371	-0.478	-0.498	6.336	0.165	-0.011	-0.371	-0.478	-0.498	6.336
cg2252	-	30S ribosomal protein S16	J	Fwd	2134400	2134790	351	287	38	44	39	44	72	38	6.559	6.828	6.905	6.206	6.114	4.782	-0.190	-0.989	-1.193	-1.382	-0.311	10.429	-0.190	-0.989	-1.193	-1.382	-0.311	10.429	-0.190	-0.989	-1.193	-1.382	-0.311	10.429
cg2254	-	Putative ankyrin repeat containing protein	R	Fwd	2135675	2136151	477	404	261	253	311	414	430	214	5.865	5.716	6.056	6.162	6.233	5.205	-0.149	0.191	0.297	0.368	-0.660	5.791	-0.149	0.191	0.297	0.368	-0.660	5.791	-0.149	0.191	0.297	0.368	-0.660	5.791
cg2255	-	ABC-type putative diazonium transporter, permease subunit	U	Rev	2137040	2136171	870	797	54	35	64	73	48	27	2.746	2.031	2.915	2.807	2.230	1.397	-0.715	0.169	0.041	-0.516	-1.349	4.388	-0.715	0.169	0.041	-0.516	-1.349	4.388	-0.715	0.169	0.041	-0.516	-1.349	4.388
cg2256	-	Putative putative diazonium transporter, ATPase subunit	U	Rev	2137914	2137037	879	800	379	417	389	482	515	247	3.491	3.322	3.983	3.283	3.283	2.485	-0.370	0.314	-0.408	-1.114	-1.309	4.465	-0.370	0.314	-0.408	-1.114	-1.309	4.465	-0.370	0.314	-0.408	-1.114	-1.309	4.465
cg2257	srp	Putative signal recognition particle GTPase	K	Rev	2139634	2137991	1644	1570	3770	4117	3792	3641	2720	1338	7.927	7.950	7.875	7.437	7.107	6.059	0.023	-0.052	-0.490	-0.821	-1.868	7.939	0.023	-0.052	-0.490	-0.821	-1.868	7.939	0.023	-0.052	-0.490	-0.821	-1.868	7.939
cg2258	ghdD	Putative protein PII uridylyltransferase	O	Rev	2141791	2139713	2079	2006	294	331	385	311	286	78	3.912	3.979	4.240	3.626	3.523	1.637	0.067	0.																

This supplementary table provides the full data for the calculation and development of Table A5.

Gene Information			Read Mapping			Raw Read			log ₂ TPM			m-values			m-values ± 1.5 (not significant)			m-values ± 1.5 (significant)			a-value					
Locus	Feature	Product	Major COG Cat.	Strand	Start	End	Effective Length	1	2	3	4	5	6	1	2	3	4	5	6	1		2	3	4	5	6
cg2445	hmoO	Heme oxygenase (cycling)		Rev	2331089	2330442	648	575	478	385	161	183	158	82	6.293	5.878	4.669	4.546	4.353	3.390	-0.411	-0.425	-0.747	-1.041	-2.093	6.076
cg2446	ohf	Glutamate-ammonia-lyase adenylyltransferase	O	Rev	2331421	2331284	1318	1065	1400	1973	2860	3527	3666	2720	5.566	5.931	5.535	5.522	6.004	6.149	0.391	0.969	0.966	1.038	0.583	-0.761
cg2447	ghaZ	Glutamate-ammonia-lyase	E	Rev	2335828	2334488	1341	1268	605	886	1291	1552	1583	1185	5.583	6.029	6.615	6.574	6.620	6.178	0.446	1.032	0.991	1.036	0.594	5.896
cg2449	-	Conserved hypothetical protein	-	Fwd	2336026	2337132	1107	1033	25	44	27	52	27	14	1.317	2.005	1.364	1.978	1.075	0.149	0.688	0.046	0.661	-0.243	-1.168	1.661
cg2450	-	Putative pyridoxal biosynthesis enzyme	S	Fwd	2337273	2339090	1818	1744	1088	1482	1929	1637	1342	716	5.990	6.532	6.755	6.212	5.943	5.013	0.342	0.765	0.222	-0.047	-0.978	6.161
cg2451	-	Conserved hypothetical protein	-	Rev	2339326	2339144	183	110	267	492	1047	1264	1619	1017	7.280	8.196	9.186	9.149	9.134	9.501	0.771	1.507	1.869	1.858	2.228	6.468
cg2452	oatK	Galactokinase	G	Fwd	2339464	2340759	1296	1222	277	301	488	487	338	123	4.508	4.524	5.263	4.954	4.445	2.969	0.016	0.754	0.445	-0.064	-0.533	4.516
cg2453	-	Putative exoribonuclease	L	Rev	2342195	2340786	1410	1336	755	630	918	959	774	704	5.830	5.466	6.051	5.588	5.156	5.355	-0.365	0.221	-0.022	-0.314	-0.475	5.648
cg2455	-	Ribonuclease III	K	Rev	2344230	2343082	1149	1076	724	709	1290	1237	1680	1320	6.065	5.931	6.837	6.470	6.309	6.556	-0.134	0.772	0.405	0.864	0.491	5.998
cg2456	-	Conserved hypothetical protein, Zn-ribbon protein possibly nucleic	-	Rev	2344962	2344483	720	646	392	412	745	629	999	729	4.806	4.498	5.321	5.235	5.188	4.989	-0.032	0.864	0.314	0.998	0.519	6.650
cg2457	-	Conserved hypothetical protein	-	Rev	2346135	2344993	1143	1069	536	574	857	969	1268	1320	5.640	5.634	6.406	6.126	6.531	6.564	-0.005	0.767	0.486	0.891	0.924	5.637
cg2458	nap2	Putative phosphatase, HAD-family	R	Fwd	2346217	2346873	657	583	433	559	857	925	959	1158	6.131	6.395	7.054	6.657	6.927	7.173	0.264	0.923	0.726	0.796	1.042	6.263
cg2459	gpaA	Protein tyrosine phosphatase	T	Fwd	2355288	2354497	789	718	1557	1960	2598	226	395	126	7.705	7.924	9.375	9.087	8.380	7.714	0.222	0.956	0.429	0.382	0.998	6.786
cg2460	-	Putative membrane protein	S	Fwd	2347395	2348396	1002	929	650	754	1441	1708	2001	1495	6.107	6.217	7.194	7.133	7.378	6.933	0.110	1.087	1.026	1.271	0.826	6.162
cg2461	trpA01Coa	Transposase	L	Rev	2349063	2348668	396	322	16	7	12	4	5	5	2.187	0.996	1.740	0.055	0.335	0.310	-1.191	-0.448	-1.026	-1.852	-1.877	1.592
cg2462	-	Putative transcriptional regulator, TetR-family	K	Rev	2349572	2349552	381	308	175	207	377	477	390	349	5.615	5.752	6.657	6.690	6.417	6.232	0.137	1.042	1.075	0.802	0.617	5.694
cg2463	-	Hypothetical protein	-	Rev	2349865	2350165	201	127	52	45	78	97	77	4	4.806	4.498	5.321	5.235	5.188	4.989	-0.308	0.815	0.429	0.382	0.183	6.650
cg2464	-	Conserved hypothetical protein	-	Rev	2350985	2350554	432	359	5879	8184	6106	6235	5953	3496	10.496	10.869	10.490	10.214	10.164	8.520	0.373	-0.006	-0.282	-0.332	-0.977	10.683
cg2465	ocfE	Pyruvate dehydrogenase (acetyl-forming)	C	Fwd	2351652	2354420	2769	2636	16703	19788	31318	34430	42675	31964	9.267	9.463	10.168	9.999	10.326	9.884	0.196	0.902	0.732	1.059	0.617	9.365
cg2466	-	ABC-type transporter, ATPase subunit	E	Rev	2355288	2354497	789	718	1557	1960	2598	226	395	126	7.705	7.924	9.375	9.087	8.380	7.714	0.222	0.956	0.429	0.382	0.998	6.786
cg2468	-	ABC-type transporter, permease subunit	G	Rev	2356182	2355292	891	817	1674	2377	423	392	461	316	7.732	8.042	8.596	8.180	8.341	8.654	0.310	0.924	0.552	0.201	-0.478	7.887
cg2470	-	ABC-type transporter, substrate-binding lipoprotein	G	Rev	2357171	2356179	993	919	3229	4335	886	744	879	354	8.431	8.752	6.505	5.947	6.205	4.871	0.321	0.924	0.552	0.201	-0.478	6.591
cg2471	-	Conserved hypothetical protein	-	Fwd	2357456	2358256	801	728	840	853	955	896	834	902	6.800	7.178	6.924	6.526	6.440	6.528	-0.082	0.124	-0.274	-0.360	-0.272	6.759
cg2472	-	Putative hydrolase or acyltransferase	-	Rev	2359300	2359284	187	94	67	45	38	82	33	26	4.897	4.255	5.393	5.248	6.086	5.943	0.182	0.616	0.760	1.468	1.355	6.759
cg2473	acqM	Acyl carrier protein	-	Fwd	2359340	2359363	294	221	408	498	567	621	529	407	7.206	7.389	7.619	7.444	7.230	6.828	0.183	0.413	0.238	0.024	-0.378	7.297
cg2474	naoD	Putative phosphatase involved in N-acetylglucosamine metabolism	G	Fwd	2359670	2360497	828	755	1335	2165	2250	2184	2448	1604	7.420	8.013	8.112	7.763	7.944	7.310	0.593	0.692	0.343	0.525	-0.110	7.716
cg2475	-	ABC-type transporter, ATPase subunit with duplicated ATPase doms	S	Fwd	2360511	2361545	1035	961	524	655	810	646	595	386	5.799	5.968	6.317	5.685	5.583	4.936	0.169	0.518	-0.114	-0.215	-0.863	6.047
cg2477	-	Conserved hypothetical protein	-	Rev	2362324	2362180	429	356	682	746	866	1944	1937	1884	10.478	10.791	11.097	11.093	11.859	11.562	0.113	0.419	0.215	1.181	0.884	10.478
cg2478	-	Putative penicillin binding protein	M	Rev	2362665	2362856	801	737	739	923	990	1129	864	307	6.599	6.816	6.960	6.843	6.474	4.960	0.217	0.361	0.244	-0.125	-0.643	6.707
cg2479	-	Hypothetical protein	-	Rev	2364205	2364747	459	385	64	54	68	65	50	42	3.909	3.565	3.935	3.565	3.210	2.939	-0.345	0.026	-0.345	-0.700	-0.971	4.737
cg2480	-	Hypothetical protein	-	Rev	2364814	2364251	564	498	62	64	82	82	64	42	3.909	3.565	3.935	3.565	3.210	2.939	-0.345	0.026	-0.345	-0.700	-0.971	4.737
cg2481	-	Conserved hypothetical protein	-	Fwd	2364839	2365081	243	169	158	127	136	131	145	92	6.117	5.701	5.842	5.842	6.645	4.969	-0.417	-0.275	-0.635	-0.473	-1.148	6.939
cg2482	-	Hypothetical protein	-	Fwd	2365103	2366468	546	472	122	89	104	101	71	53	4.579	4.025	4.290	3.942	3.637	3.017	-0.554	-0.289	-0.637	-1.122	-1.562	4.302
cg2483	-	Hypothetical protein	-	Fwd	2366073	2366545	429	355	42	15	17	21	7	2	3.411	1.881	2.094	2.077	0.655	-0.805	-0.538	-1.317	-1.333	-2.038	-2.044	2.646
cg2484	-	Hypothetical protein	-	Fwd	2366628	2366613	345	271	105	95	93	93	93	102	4.078	4.780	5.072	5.072	5.072	5.072	0.109	0.578	0.578	0.578	0.578	6.042
cg2485	phoD	Alkaline phosphatase, secreted precursor	P	Fwd	2366891	2368441	1551	1477	55	112	42	43	28	26	1.938	2.847	1.496	1.223	0.639	0.511	0.909	-0.442	-0.715	-1.299	-1.427	2.392
cg2487	-	Conserved hypothetical protein	G	Fwd	2368939	2370777	1839	1766	749	94	1025	1066	832	840	5.435	5.660	5.827	5.577	5.237	5.226	0.225	0.391	0.142	-0.198	-0.209	5.548
cg2488	-	Conserved hypothetical protein	-	Rev	2370823	2371075	243	170	434	408	496	504	537	498	7.569	7.577	7.701	7.418	7.536	7.393	-0.193	0.132	-0.151	-0.043	-0.177	7.479
cg2489	dnoc	DNA primase	-	Rev	2372972	2371077	1896	1824	611	646	966	943	960	772	5.098	5.074	5.605	5.387	5.070	4.981	-0.024	0.507	0.259	0.301	-0.038	6.246
cg2490	-	Guanine-specific ribonuclease, secreted precursor	F	Fwd	2373018	2373512	495	422	372	360	518	558	421	305	6.321	6.170	6.737	6.538	6.149	5.661	-0.151	0.416	0.217	-0.172	-0.660	6.134
cg2491	-	Conserved hypothetical protein	-	Fwd	2373513	2373758	246	173	184	153	191	228	212	117	6.318	5.950	6.311	6.259	6.172	5.295	-0.368	-0.007	-0.059	-0.146	-1.023	6.097
cg2492	ohf5	Glutamate-fructose-6-phosphate transaminase (isomerizing)	M	Fwd	2373687	2374618	1027	953	570	603	854	864	874	884	6.485	6.234	6.993	6.827	6.499	5.983	0.256	0.456	0.456	0.456	0.456	6.097
cg2494	odt	idGPase	F	Fwd	2377933	2376659	1275	1202	537	676	647															

This supplementary table provides the full data for the calculation and development of Table A5.

Gene Information				Read Mapping							log ₂ TPM							m-values						m-values < ±1.5 (not significant)						m-values > ±1.5 (significant)					
Locus	Feature	Product	Major COG Cat.	Strand	Start	End	Length (bp)	Effective Length	Raw Read Count							log ₂ TPM							m-values						a-value						
									1	2	3	4	5	6	1	2	3	4	5	6	1	2	3	4	5	6	1	2	3	4	5	6	1	2	3
cg3022	-	Conserved hypothetical protein	-	Fwd	2882539	2883099	561	487	1293	642	11	104	127	23	8,043	8,822	3,707	3,945	4,248	1,808	-1.220	-0.096	-0.144	-0.298	-0.235	-0.432	-1.220	-0.096	-0.144	-0.298	-0.235	-0.432			
cg3024	<i>mrsA</i>	Putative secondary Na ⁺ /H ⁺ antiporter, monovalent cation:proton a	-	Fwd	2883480	2883539	3060	2986	1425	1312	1390	1663	1378	360	5,628	5,531	5,484	5,230	3,271	-0.223	-0.096	-0.144	-0.298	-0.235	-0.432	-0.223	-0.096	-0.144	-0.298	-0.235	-0.432				
cg3025	<i>mrsC</i>	Putative secondary Na ⁺ /H ⁺ antiporter, monovalent cation:proton a	C	Fwd	2886543	2887034	492	417	149	124	128	142	132	22	5,016	4,643	4,737	5,800	4,487	1,936	-0.373	-0.278	-0.436	-0.529	-1.080	-0.373	-0.278	-0.436	-0.529	-1.080					
cg3026	<i>mrsD</i>	Putative secondary Na ⁺ /H ⁺ antiporter, monovalent cation:proton a	C	Fwd	2887027	2888277	1701	1627	521	541	534	618	559	105	5,024	4,974	5,000	4,904	4,775	2,344	-0.050	-0.024	-0.119	-0.248	-2.680	-0.050	-0.024	-0.119	-0.248	-2.680					
cg3027	<i>mrsE</i>	Putative secondary Na ⁺ /H ⁺ antiporter, monovalent cation:proton a	P	Fwd	2888724	2889233	510	486	181	219	197	183	186	32	5,239	5,413	5,304	4,892	4,932	2,383	0.174	0.065	-0.347	-0.307	-2.854	0.174	0.065	-0.347	-0.307	-2.854					
cg3028	<i>mrsF</i>	Putative secondary Na ⁺ /H ⁺ antiporter, monovalent cation:proton a	-	Fwd	2889237	2889512	276	202	112	98	98	95	88	19	5,441	5,161	5,036	4,838	4,747	2,568	-0.295	-0.405	-0.602	-0.694	-2.873	-0.295	-0.405	-0.602	-0.694	-2.873					
cg3029	<i>mrsG</i>	Putative secondary Na ⁺ /H ⁺ antiporter, monovalent cation:proton a	-	Fwd	2889513	2889893	381	308	116	153	168	172	153	35	5,026	5,319	5,496	5,224	5,073	2,951	0.293	0.470	0.198	0.047	-2.075	0.293	0.470	0.198	0.047	-2.075					
cg3030	-	Putative hydrolase or acyltransferase (alpha/beta hydrolase superfamily)	R	Rev	2890228	2890329	600	527	484	457	501	451	353	145	6,422	6,236	6,111	5,954	5,818	4,316	-0.186	-0.011	-0.468	-0.804	-2.107	-0.186	-0.011	-0.468	-0.804	-2.107					
cg3031	-	Conserved hypothetical protein, glutamate-cysteine ligase family	H	Rev	2890267	2890365	1131	1058	1439	1450	1371	1317	967	473	7,078	6,985	6,947	6,583	6,155	5,100	-0.093	-0.130	-0.494	-0.923	-1.978	-0.093	-0.130	-0.494	-0.923	-1.978					
cg3032	-	Putative secreted protein	-	Fwd	2891212	2891224	594	521	112	98	98	95	88	19	5,441	5,161	5,036	4,838	4,747	2,568	-0.295	-0.405	-0.602	-0.694	-2.873	-0.295	-0.405	-0.602	-0.694	-2.873					
cg3033	-	Conserved hypothetical protein	-	Rev	2893007	2892975	213	140	102	101	90	55	63	41	5,681	5,563	5,442	4,435	4,645	4,012	-0.118	-0.239	-1.246	-1.036	-1.668	-0.118	-0.239	-1.246	-1.036	-1.668					
cg3034	<i>def1</i>	Putative peptidase deformylase	J	Rev	2893023	2893604	582	508	705	959	1047	764	818	372	7,007	7,347	7,517	6,757	6,872	5,711	0.340	0.510	-0.250	-0.135	-1.296	0.340	0.510	-0.250	-0.135	-1.296					
cg3035	-	Putative CGAS-related N-acetyltransferase	K	Fwd	2893594	2894601	1008	934	560	623	720	511	427	172	5,883	5,933	6,185	5,385	5,142	3,808	0.050	0.303	-0.497	-0.740	-2.075	0.050	0.303	-0.497	-0.740	-2.075					
cg3036	<i>xthA</i>	Exodeoxyribonuclease III	L	Fwd	2894628	2895419	792	719	690	610	992	896	812	633	6,533	6,251	6,995	6,542	6,417	6,034	-0.281	0.462	0.100	-0.115	-0.499	-0.281	0.462	0.100	-0.115	-0.499					
cg3037	<i>cts</i>	Cardiolipin synthase	I	Fwd	2895426	2896928	1503	1430	313	200	362	276	226	167	4,470	3,723	4,619	3,923	3,653	3,193	-0.747	0.149	-0.548	-0.818	-1.277	-0.747	0.149	-0.548	-0.818	-1.277					
cg3038	-	Putative multidrug efflux permease, MFS-type	R	Rev	2898455	2897259	1197	1124	229	270	440	174	159	20	4,350	4,483	3,583	3,589	3,284	2,522	0.133	-0.767	-0.761	-1.066	-2.828	0.133	-0.767	-0.761	-1.066	-2.828					
cg3039	-	ABC-type putative multidrug transporter, ATPase subunit	P	Fwd	2898705	2900015	3311	3238	712	474	474	691	407	7	8,851	8,161	8,495	8,488	8,458	4,974	-0.690	-0.356	-0.363	-0.393	-1.180	-0.690	-0.356	-0.363	-0.393	-1.180					
cg3040	-	Putative epimerase	R	Rev	2900854	2900012	843	770	351	300	448	350	263	111	5,469	5,140	5,500	5,099	4,705	3,443	-0.330	0.291	-0.371	-0.765	-2.027	-0.330	0.291	-0.371	-0.765	-2.027					
cg3041	-	ABC-type putative multidrug transporter, permease subunit	R	Rev	2901614	2900556	759	685	353	271	335	388	276	92	5,267	5,142	5,493	5,398	4,925	3,318	-0.485	-0.134	-0.229	-0.702	-2.308	-0.485	-0.134	-0.229	-0.702	-2.308					
cg3042	-	ABC-type putative multidrug transporter, ATPase subunit	E	Rev	2902539	2901467	931	859	585	637	685	666	393	127	6,057	6,076	6,217	6,283	5,895	5,109	0.019	0.170	0.226	-0.162	-0.948	0.019	0.170	0.226	-0.162	-0.948					
cg3043	-	Putative NTP gamma-glutamylhydrolase/oxidative damage repair enzym	L	Rev	2903055	2902561	495	422	181	270	365	444	509	433	5,286	5,756	7,030	6,745	6,423	6,165	0.471	1.744	1.459	1.137	0.879	0.471	1.744	1.459	1.137	0.879					
cg3044	-	Putative membrane protein	-	Fwd	2903142	2904647	1506	1433	1082	1020	1549	1560	1344	463	6,254	6,065	6,710	6,414	6,217	4,656	-0.189	0.457	0.161	-0.037	-1.597	-0.189	0.457	0.161	-0.037	-1.597					
cg3045	-	ABC-type putative glutamine transporter, substrate-binding lipoprotein	E	Fwd	2904448	2905682	1035	961	545	453	783	723	694	351	5,805	5,435	6,267	5,846	5,805	4,799	-0.370	0.462	0.041	0.000	-1.007	-0.370	0.462	0.041	0.000	-1.007					
cg3046	<i>phnG</i>	Conserved hypothetical protein kinase	-	Fwd	2905672	2906140	2469	2395	1466	1404	2469	2395	1466	907	4,880	4,425	5,017	4,809	4,307	4,203	0.080	0.246	-0.073	-0.361	-0.748	0.080	0.246	-0.073	-0.361	-0.748					
cg3047	<i>ackA</i>	Acetate kinase	C	Rev	2908913	2908620	1194	1120	1303	292	570	769	1331	1495	6,856	5,757	5,603	5,730	6,537	6,680	0.711	-1.253	-1.126	-0.319	-0.176	0.711	-1.253	-1.126	-0.319	-0.176					
cg3048	<i>pto</i>	Phosphate acetyltransferase	C	Rev	2911938	2909813	1386	1313	743	270	551	810	1497	1263	8,006	7,589	5,339	5,590	6,491	6,751	0.781	-1.469	-1.218	-0.317	-0.057	0.781	-1.469	-1.218	-0.317	-0.057					
cg3049	<i>far1</i>	Ferredoxin-NAD(P)+ reductase	E	Rev	2911711	2913078	1368	1295	1586	1920	2340	2071	2143	1515	6,944	7,115	7,444	6,962	7,028	6,503	0.172	0.500	0.118	0.084	-0.441	0.172	0.500	0.118	0.084	-0.441					
cg3050	-	Putative CGAS-related N-acetyltransferase	R	Fwd	2912023	2913761	549	476	1360	1460	1440	1166	907	7	8,851	8,161	8,495	8,488	8,458	4,974	-0.690	-0.356	-0.363	-0.393	-1.180	-0.690	-0.356	-0.363	-0.393	-1.180					
cg3051	-	Putative secreted protein	-	Rev	2914760	2913750	1011	937	35	60	51	41	33	28	1,918	2,575	2,388	1,773	1,448	1,231	0.657	0.470	-0.144	-0.432	-0.687	0.657	0.470	-0.144	-0.432	-0.687					
cg3052	-	Putative secreted protein	-	Rev	2915806	2914775	1032	958	100	135	108	86	49	35	3,376	3,702	3,426	2,794	2,012	2,098	0.325	0.049	-0.582	-1.364	-1.278	0.325	0.049	-0.582	-1.364	-1.278					
cg3053	-	Putative secreted protein	-	Rev	2916310	2915162	420	346	232	210	222	210	186	29	4,556	4,214	4,022	3,212	3,212	2,098	-0.002	-0.214	-0.481	-0.804	-2.075	-0.002	-0.214	-0.481	-0.804	-2.075					
cg3054	<i>purT</i>	Putative gamma-glutamylcyclanamide formyltransferase	F	Rev	2917541	2916315	1227	1154	1118	1469	1152	798	533	368	6,596	7,053	6,579	5,774	5,179	4,621	0.456	-0.017	-0.853	-1.417	-1.973	0.456	-0.017	-0.853	-1.417	-1.973					
cg3055	-	Putative secreted protein	-	S	Rev	2919709	2918942	768	695	1547	1581	1082	1363	1419	825	7,741	7,668	7,165	7,911	7,266	6,460	-0.072	-0.576	-0.549	-0.474	-1.281	-0.072	-0.576	-0.549	-0.474	-1.281				
cg3058	<i>trpB5(Co)</i>	Transposase	L	Rev	2920897	2920001	897	823	83	79	56	77	69	18	3,313	3,139	2,693	2,839	2,700	0,794	-0.174	-0.620	-0.474	-0.613	-2.318	-0.174	-0.620	-0.474	-0.613	-2.318					
cg3059	<i>trpB5(Co)</i>	Transposase	L	Rev	2921192	2920243	270	195	325	267	132	137	125	26	4,789	5,086	5,079	4,467	4,129	2,507	0.297	0.248	-0.318	-0.468	-1.723	0.297	0.248	-0.318	-0.468	-1.723					
cg3060	<i>ctf56</i>	Two-component system, sensory histidine kinase	T	Rev	2922494	2921352	1143	1070	1022	916	1269	1756	1531	961																					

This supplementary table provides the full data for the calculation and development of Table S5.

Gene Information				Read Mapping				Raw Read Count						log ₂ TPM						m-values						a-value							
Locus	Feature	Product	Major COG Cat.	Strand	Start	End	Length (bp)	Effective Length	Read Count						log ₂ TPM						m-values						a-value						
									①	②	③	④	⑤	⑥	①	②	③	④	⑤	⑥	①	②	③	④	⑤	⑥	①	②	③	④	⑤	⑥	
cg3130	-	Putative multidrug efflux permease, MFS-type	G	Fwd	2987922	2989133	1212	1138	88	154	100	103	98	50	2.962	3.659	3.084	2.820	2.266	1.784	0.697	0.122	-0.142	-0.196	-1.178	0.330	0.697	0.122	-0.142	-0.196	-1.178	0.330	
cg3131	-	Activin/midline deacylase or related deacylase	E	Fwd	2990455	2998130	1216	1252	365	493	634	591	803	446	4.872	5.406	5.199	5.658	4.786	0.329	0.734	0.327	0.786	-0.086	0.307	0.329	0.734	0.327	0.786	-0.086	0.307		
cg3132	-	Putative membrane protein	R	Fwd	2990790	2992529	1740	1667	1141	1259	1797	1995	1848	335	6.122	6.160	6.716	6.238	6.467	0.038	0.594	0.116	0.345	-2.140	6.141	0.038	0.594	0.116	0.345	-2.140	6.141		
cg3133	-	ABC-type putative cobalamin/sugar transporter, ATPase subunit	C	R	2993873	2992845	1029	955	438	408	197	148	95	21	5.500	5.295	4.291	3.575	2.958	0.206	-1.209	-1.926	-2.543	-4.693	5.397	0.206	-1.209	-1.926	-2.543	-4.693	5.397		
cg3134	-	ABC-type putative cobalamin/sugar transporter, permease subunit	C	R	2994508	2993864	645	571	496	523	195	193	129	38	6.353	6.326	4.950	4.029	4.069	0.207	-1.403	-1.403	-2.284	-4.046	6.340	0.207	-1.403	-1.403	-2.284	-4.046	6.340		
cg3135	-	Putative membrane protein	P	Rev	2995299	2994511	789	715	767	866	287	360	207	45	6.690	6.162	5.215	5.235	4.456	0.071	-1.476	-1.455	-2.234	-4.438	6.576	0.071	-1.476	-1.455	-2.234	-4.438	6.576		
cg3136	-	Putative nitroreductase	C	Rev	2996234	2995416	819	745	366	301	472	589	575	327	5.571	5.186	3.477	5.890	5.872	0.385	0.305	0.318	0.301	-0.537	5.379	0.385	0.305	0.318	0.301	-0.537	5.379		
cg3137	iumH1	Purine nucleosidase	F	Rev	2997206	2996301	906	833	369	317	245	169	88	47	4.537	5.115	4.788	3.949	3.032	0.322	-0.649	-1.489	-2.405	-3.731	5.276	0.322	-0.649	-1.489	-2.405	-3.731	5.276		
cg3138	-	Band 7 domain-containing protein, stomatin/prohibitin homolog	O	Fwd	2997685	2998662	978	905	1169	1259	1440	1988	968	717	6.988	7.002	7.233	6.752	6.386	0.015	0.245	-0.236	-0.622	-1.079	6.995	0.015	0.245	-0.236	-0.622	-1.079	6.995		
cg3139	-	Conserved hypothetical protein	S	Fwd	2998667	2998866	195	121	143	193	170	156	153	105	6.292	6.614	6.475	6.054	6.034	0.322	0.183	-0.247	-0.258	-0.823	6.046	0.322	0.183	-0.247	-0.258	-0.823	6.046		
cg3140	topA1	DNA-3-methyladenine glycosylase I	L	Fwd	2998858	2999448	591	518	352	412	397	395	320	186	5.986	6.107	6.097	5.783	5.497	0.291	0.311	-0.203	-0.489	-1.295	6.053	0.291	0.311	-0.203	-0.489	-1.295	6.053		
cg3141	hmp	Globin-like Havahaemoprotein, putative nitric oxide dioxygenase	-	Fwd	3000605	2999445	1161	1087	40	53	138	76	34	15	1.906	2.199	3.607	2.448	1.328	0.124	0.124	0.543	-0.578	-0.778	2.053	0.124	0.124	0.543	-0.578	-0.778	2.053		
cg3142	-	Putative membrane protein	-	Fwd	3000667	3001712	1025	1442	217	142	158	224	188	122	6.033	5.456	5.329	5.296	5.084	0.474	-0.578	-0.704	-0.737	-0.949	6.046	0.474	-0.578	-0.704	-0.737	-0.949	6.046		
cg3143	-	Conserved putative secreted protein	R	Fwd	3001574	3002020	627	554	220	170	330	399	239	211	5.225	4.751	5.477	5.714	4.994	0.474	0.522	0.489	-0.231	-0.435	4.988	0.474	0.522	0.489	-0.231	-0.435	4.988		
cg3144	logG	Putative transcriptional antiterminal/putative pseudogene	K	R	3002777	3002187	591	517	31	35	26	30	30	4	2.522	2.988	2.217	2.110	2.127	0.066	-0.306	-0.412	-0.396	-3.053	2.555	0.066	-0.306	-0.412	-0.396	-3.053	2.555		
cg3146	logF	6-Phospho-beta-glucosidase, putative pseudogene (C-terminal frag	G	R	3003367	3003005	363	289	97	50	33	43	19	10	4.084	3.794	3.252	3.318	2.198	0.289	-0.831	-0.745	-0.698	-2.779	4.949	0.289	-0.831	-0.745	-0.698	-2.779	4.949		
cg3148	logP	6-Phospho-beta-glucosidase, putative pseudogene (N-terminal frag	G	Fwd	3003646	3003404	243	170	149	107	116	98	49	20	6.353	6.326	4.950	4.029	4.069	0.207	-1.403	-1.403	-2.284	-4.046	6.340	0.207	-1.403	-1.403	-2.284	-4.046	6.340		
cg3149	YecP	ABC transporter, ATP-binding protein - pseudogene	-	Fwd	3003626	3003844	219	146	23	22	15	19	18	5	3.540	3.374	2.894	2.910	2.853	0.165	-0.165	-0.646	-0.630	-0.687	-2.375	4.457	0.165	-0.646	-0.630	-0.687	-2.375	4.457	
cg3149	aloP	Putative aspartate aminotransferase, AT class I	E	Fwd	3003975	3005288	1314	1240	406	448	3634	3183	2501	396	8.360	8.509	8.137	7.640	7.309	0.149	-0.224	-0.721	-1.052	-1.728	8.435	0.149	-0.224	-0.721	-1.052	-1.728	8.435		
cg3151	InspH/Scp2C	Transposase	L	Fwd	3005658	3007172	1625	1442	217	142	158	224	188	122	6.033	5.456	5.329	5.296	5.084	0.474	-0.578	-0.704	-0.737	-0.949	6.046	0.474	-0.578	-0.704	-0.737	-0.949	6.046		
cg3153	-	Putative membrane protein	S	Fwd	3007487	3008746	1260	1187	683	811	441	370	247	77	5.848	5.992	5.557	4.599	4.005	0.241	0.144	-0.491	-1.249	-1.843	-3.207	5.920	0.241	0.144	-0.491	-1.249	-1.843	5.920	
cg3154	udgA2	UDP-glucose 4-epimerase	M	Fwd	3010062	3008743	1320	1247	1576	1843	2211	2293	1951	889	6.986	7.108	7.414	7.160	6.944	0.122	0.428	0.174	-0.042	-1.200	7.047	0.122	0.428	0.174	-0.042	-1.200	7.047		
cg3155	idP	ICP deaminase	F	Rev	3010717	3010148	570	497	1638	1846	2491	2574	2072	1225	8.253	8.322	8.797	8.538	8.242	0.069	0.544	0.285	-0.011	-0.793	8.287	0.069	0.544	0.285	-0.011	-0.793	8.287		
cg3157	-	Putative secreted protein	V	Fwd	3011478	3012251	714	630	612	622	158	224	188	122	6.033	5.456	5.329	5.296	5.084	0.474	-0.578	-0.704	-0.737	-0.949	6.046	0.474	-0.578	-0.704	-0.737	-0.949	6.046		
cg3157	-	Putative secreted protein	V	Rev	3011987	3012296	1692	1619	669	635	1484	1272	993	456	5.393	5.214	4.480	5.958	6.122	0.179	1.088	0.565	0.219	-0.927	5.303	0.179	1.088	0.565	0.219	-0.927	5.303		
cg3158	naqa2	Putative beta-glucosidase	G	Rev	3015208	3014051	1158	1084	668	523	372	367	317	57	5.704	5.482	5.034	4.709	4.515	0.223	-0.670	-0.995	-1.189	-3.668	5.593	0.223	-0.670	-0.995	-1.189	-3.668	5.593		
cg3159	-	Putative universal stress protein UspA or related nucleotide-binding	T	Fwd	3015300	3015746	447	374	440	569	1020	962	1066	1303	6.710	6.976	7.860	7.470	7.635	0.266	1.151	0.760	0.925	1.190	6.843	0.266	1.151	0.760	0.925	1.190	6.843		
cg3160	-	Putative membrane protein	-	Fwd	3015809	3016012	204	131	602	688	602	608	494	484	6.741	6.418	6.169	6.874	6.767	0.077	0.428	0.133	-0.009	-0.676	6.643	0.077	0.428	0.133	-0.009	-0.676	6.643		
cg3161	-	Putative universal stress protein UspA or related nucleotide-binding	T	Fwd	3016074	3019097	3024	2950	520	434	493	435	332	159	4.192	3.828	4.055	3.569	3.197	0.164	-0.364	-0.137	-0.624	-0.995	-2.078	4.010	0.164	-0.364	-0.137	-0.624	-0.995	-2.078	4.010
cg3163	-	Putative acyltransferase	I	Rev	3021345	3019425	1071	997	292	202	150	201	164	82	4.859	4.226	3.842	3.956	3.681	0.633	-0.107	-0.903	-1.178	-2.124	5.583	0.633	-0.107	-0.903	-1.178	-2.124	5.583		
cg3163	-	Putative secreted or membrane protein	-	Fwd	3022166	3022179	13	13	742	819	602	519	742	819	602	7.420	7.116	6.909	6.519	6.519	0.283	0.185	-0.332	-0.432	-1.144	7.484	0.283	0.185	-0.332	-0.432	-1.144	7.484	
cg3165	-	Putative membrane protein	-	Rev	3022194	3022788	1425	1352	368	42	497	483	326	171	4.780	4.907	5.152	4.805	4.256	0.127	0.372	0.205	-0.524	-1.476	4.844	0.127	0.372	0.205	-0.524	-1.476	4.844		
cg3166	-	Putative glycosyltransferase	M	Rev	3023862	3022759	1104	1031	279	261	143	147	109	98	4.750	4.550	3.730	3.464	3.053	0.200	-1.020	-1.286	-1.698	-1.874	4.650	0.200	-1.020	-1.286	-1.698	-1.874	4.650		
cg3167	-	Hypothetical protein	-	Fwd	3023909	3024499	591	517	214	236	340	322	301	317	5.251	5.307	5.875	5.941	5.411	0.037	0.605	0.221	0.141	0.190	5.289	0.037	0.605	0.221	0.141	0.190	5.289		
cg3167	-	UDP-SAM-dependent methyltransferase	A	Fwd	3024052	3025273	718	701	426	232	150	142	109	98	4.262	3.920	3.419	3.089	2.820	0.173	-0.527	-0.232	-0.310	-0.360	4.300	0.173	-0						

This supplementary table provides the full data for the calculation and development of Table A5.

Gene Information			Read Mapping			Raw Read Count						log ₂ TPM						m-values						a-value																		
Locus	Feature	Product	Major COG Cat.	Strand	Start	End	Length (bp)	Effective Length	①	②	③	④	⑤	⑥	①	②	③	④	⑤	⑥	①	②	③	④	⑤	⑥	①	②	③	④	⑤	⑥	①	②	③	④	⑤	⑥				
cg3243	-	Conserved hypothetical protein, RecB-family nuclease	-	Rev	3106335	3104812	1524	1451	359	258	308	279	223	48	4.565	4.069	4.367	3.918	3.213	1.396	-0.496	-0.199	-0.647	-0.952	-0.988	-0.988	4.137	-0.496	-0.199	-0.647	-0.952	-0.988	-0.988	-0.988	-0.988	-0.988	-0.988	-0.988	-0.988			
cg3244	-	Conserved hypothetical protein	-	Fwd	3105422	3107057	636	563	1545	1886	2668	2318	2286	1713	6.011	4.158	6.705	8.229	6.226	7.785	0.184	0.694	0.218	0.118	0.215	-0.226	4.137	0.184	0.694	0.218	0.118	0.215	-0.226	-0.226	-0.226	-0.226	-0.226	-0.226	-0.226	-0.226		
cg3245	-	Putative multidrug efflux permease, MFS-type	G	K	3108548	3107082	1467	1394	90	109	97	128	111	73	2.719	2.888	2.765	2.855	2.668	2.046	0.170	0.046	0.137	-0.050	-0.673	-0.673	2.803	0.170	0.046	0.137	-0.050	-0.673	-0.673	-0.673	-0.673	-0.673	-0.673	-0.673	-0.673			
cg3246	-	Putative transcriptional regulator, MarR-family	G	Fwd	3108604	3109062	459	386	41	44	55	71	85	58	3.279	3.275	3.634	3.630	3.964	3.395	-0.004	0.354	0.411	0.684	0.116	0.116	3.277	-0.004	0.354	0.411	0.684	0.116	0.116	0.116	0.116	0.116	0.116	0.116	0.116			
cg3247	cgf11	Two-component system, transcriptional response regulator, probal	T	Rev	3109798	3109160	639	565	411	553	533	392	320	248	6.096	6.420	6.410	5.661	5.386	4.995	0.323	0.314	-0.435	-0.710	-1.101	-1.101	6.258	0.323	0.314	-0.435	-0.710	-1.101	-1.101	-1.101	-1.101	-1.101	-1.101	-1.101	-1.101			
cg3248	cgf21	Two-component system, sensory histidine kinase	T	Rev	3111231	3109897	1335	1261	347	395	324	303	215	97	4.790	4.472	6.430	4.228	3.752	2.587	0.083	-0.159	-0.562	-1.038	-0.988	-0.988	4.681	0.083	-0.159	-0.562	-1.038	-0.988	-0.988	-0.988	-0.988	-0.988	-0.988	-0.988	-0.988	-0.988		
cg3249	-	Putative secreted protein	-	Fwd	3111230	3111781	552	479	29	30	36	36	13	10	2.528	2.471	2.770	2.464	1.079	0.706	-0.056	0.242	-0.064	-1.449	-1.822	-1.822	2.499	-0.056	0.242	-0.064	-1.449	-1.822	-1.822	-1.822	-1.822	-1.822	-1.822	-1.822	-1.822			
cg3250	-	Putative membrane protein	-	Rev	3111937	3111785	153	80	68	84	108	82	80	28	5.581	5.778	6.180	5.480	5.462	3.955	0.197	0.599	-0.100	-0.118	-1.625	-1.625	5.799	0.197	0.599	-0.100	-0.118	-1.625	-1.625	-1.625	-1.625	-1.625	-1.625	-1.625	-1.625			
cg3251	-	Putative surface protein, surface protein (translocase)	M	Rev	3112762	3111938	925	751	880	867	1018	994	766	347	6.824	6.699	6.973	6.633	6.275	5.110	-0.125	0.149	-0.191	-0.550	-1.715	-1.715	6.761	-0.125	0.149	-0.191	-0.550	-1.715	-1.715	-1.715	-1.715	-1.715	-1.715	-1.715	-1.715			
cg3252	-	Putative 60 KD inner membrane protein, SpoIII homolog, cytochrome	U	Fwd	3112994	3104262	1269	1195	924	750	677	531	447	157	4.843	4.838	6.692	4.762	4.439	4.658	-0.404	-0.509	-1.165	-1.396	-1.924	-1.924	4.671	-0.404	-0.509	-1.165	-1.396	-1.924	-1.924	-1.924	-1.924	-1.924	-1.924	-1.924	-1.924	-1.924		
cg3253	mcfR	Global transcriptional repressor of sulfur metabolism, TetR-family	K	Rev	3114830	3114189	642	568	721	1134	981	1162	1337	253	6.899	7.448	7.282	7.220	7.439	5.017	0.549	0.383	0.321	0.540	-1.882	-1.882	7.193	0.549	0.383	0.321	0.540	-1.882	-1.882	-1.882	-1.882	-1.882	-1.882	-1.882	-1.882	-1.882		
cg3254	-	Putative membrane protein	-	Rev	3115276	3115013	264	191	1528	3911	6157	6536	5493	2109	9.263	10.515	11.213	10.993	10.759	11.296	1.252	1.252	1.252	1.252	1.252	1.252	9.889	1.252	1.252	1.252	1.252	1.252	1.252	1.252	1.252	1.252	1.252	1.252	1.252	1.252	1.252	
cg3255	usgA2	Universal stress protein E	T	Rev	3114663	3115758	906	833	4282	6844	11234	11500	12951	13382	8.970	9.543	10.301	10.040	10.217	10.240	0.573	1.321	1.070	1.247	1.269	1.269	9.257	0.573	1.321	1.070	1.247	1.269	1.269	1.269	1.269	1.269	1.269	1.269	1.269			
cg3256	-	Putative monooxygenase	C	Rev	3117789	3116800	990	917	1007	1138	1989	1820	1868	1818	6.755	6.828	6.776	6.242	2.996	7.232	0.072	0.921	0.487	0.541	0.477	0.477	6.792	0.072	0.921	0.487	0.541	0.477	0.477	0.477	0.477	0.477	0.477	0.477	0.477	0.477		
cg3257	-	Conserved hypothetical protein	-	Rev	3117939	3117799	141	68	250	323	553	599	637	648	7.561	7.826	8.643	8.452	8.558	8.557	0.265	1.082	0.891	0.996	0.996	0.996	7.694	0.265	1.082	0.891	0.996	0.996	0.996	0.996	0.996	0.996	0.996	0.996	0.996			
cg3258	rfaC2	Pseudouridylyl synthase	J	Fwd	3117920	3118936	1017	944	63	58	89	63	76	32	2.739	2.518	3.170	2.373	2.656	1.409	-0.221	0.431	-0.367	-0.083	-1.330	-1.330	2.669	-0.221	0.431	-0.367	-0.083	-1.330	-1.330	-1.330	-1.330	-1.330	-1.330	-1.330	-1.330	-1.330		
cg3259	-	Putative transcriptional regulator, GntR-family	S	Rev	3125511	3125446	366	292	98	105	93	112	112	62	4.843	4.838	6.692	4.762	4.439	4.658	-0.005	-0.151	-0.101	-0.424	-0.184	-0.184	4.640	-0.005	-0.151	-0.101	-0.424	-0.184	-0.184	-0.184	-0.184	-0.184	-0.184	-0.184	-0.184			
cg3263	-	Conserved hypothetical protein	-	Fwd	3125720	3127138	1419	1346	1040	1141	1320	1411	1069	667	6.282	6.312	6.665	6.049	5.972	5.268	0.030	0.283	-0.233	-0.310	-1.015	-1.015	6.297	0.030	0.283	-0.233	-0.310	-1.015	-1.015	-1.015	-1.015	-1.015	-1.015	-1.015	-1.015			
cg3264	-	Conserved hypothetical protein	-	K	Rev	3128073	3127198	876	803	1675	2629	3975	4105	4026	3869	7.665	8.212	8.951	8.951	8.950	8.498	0.546	1.186	0.926	0.915	0.833	0.833	7.939	0.546	1.186	0.926	0.915	0.833	0.833	0.833	0.833	0.833	0.833	0.833	0.833	0.833	0.833
cg3266	ImpL1/cg5C6	Transposase	L	Rev	3122978	3122850	123	1161	48	57	57	58	10	40	2.069	2.209	2.481	1.958	1.805	1.420	0.139	0.412	-0.111	-0.264	-0.649	-0.649	2.268	0.139	0.412	-0.111	-0.264	-0.649	-0.649	-0.649	-0.649	-0.649	-0.649	-0.649	-0.649			
cg3267	-	Putative membrane protein, putative pseudogene (C-terminal frag)	R	Rev	3130530	3129610	921	833	15	12	10	12	10	13	0.882	0.479	0.281	0.160	-0.008	0.263	-0.403	-0.401	-0.723	-0.890	-0.620	-0.620	0.681	-0.403	-0.401	-0.723	-0.890	-0.620	-0.620	-0.620	-0.620	-0.620	-0.620	-0.620	-0.620			
cg3268	-	Putative membrane protein, putative pseudogene	-	Rev	3130778	3130527	252	179	9	10	18	15	21	7	2.074	2.108	2.939	2.385	2.862	1.378	0.034	0.865	0.311	0.788	-0.696	-0.696	2.091	0.034	0.865	0.311	0.788	-0.696	-0.696	-0.696	-0.696	-0.696	-0.696	-0.696	-0.696			
cg3269	-	Putative membrane protein, putative pseudogene	-	Rev	3131037	3130783	255	178	13	22	31	38	32	22	2.490	3.123	3.674	3.635	3.420	2.884	0.633	1.184	1.145	0.940	0.394	0.394	2.870	0.633	1.184	1.145	0.940	0.394	0.394	0.394	0.394	0.394	0.394	0.394	0.394			
cg3270	-	Putative membrane protein, putative pseudogene (N-terminal frag)	-	Rev	3131243	3131073	207	133	23	33	30	58	60	29	2.857	3.061	3.263	2.440	2.417	2.325	0.635	0.939	1.146	1.233	1.315	1.315	2.870	0.635	0.939	1.146	1.233	1.315	1.315	1.315	1.315	1.315	1.315	1.315	1.315	1.315		
cg3271	-	SAM-dependent methyltransferase	Q	Fwd	3131371	3132144	774	700	445	373	299	289	209	186	5.934	5.576	5.301	4.946	4.998	4.306	-0.358	-0.633	-0.988	-1.436	-1.436	-1.436	5.755	-0.358	-0.633	-0.988	-1.436	-1.436	-1.436	-1.436	-1.436	-1.436	-1.436	-1.436				
cg3272	-	Putative membrane protein	-	S	Rev	3133107	3132385	723	649	66	87	330	292	2171	3.298	3.587	5.542	6.715	7.967	8.190	0.299	2.244	3.417	4.669	4.893	4.893	3.442	0.299	2.244	3.417	4.669	4.893	4.893	4.893	4.893	4.893	4.893	4.893	4.893			
cg3273	-	Hypothetical protein	-	Rev	3133837	3133541	297	224	97	106	120	123	128	99	5.130	5.153	5.373	5.103	5.177	4.784	0.023	0.244	-0.027	0.047	-0.345	-0.345	5.141	0.023	0.244	-0.027	0.047	-0.345	-0.345	-0.345	-0.345	-0.345	-0.345	-0.345				
cg3274	-	Putative DNA invertase, putative pseudogene	-	Fwd	3142425	3143027	219	139	54	40	30	31	25	25	3.728	3.989	4.402	2.719	3.330	3.252	-0.481	-1.087	-1.420	-1.739	-2.249	-2.249	3.555	-0.481	-1.087	-1.420	-1.739</											

This supplementary table provides the full data for the calculation and development of Table A5.

Gene Information			Read Mapping			Raw Read Count			log ₂ TPM			m-values			m-values < 1.5 (not significant)			m-values > 1.5 (significant)									
Locus	Feature	Product	Major COG Cat.	Strand	Start	Stop	Effective Length	①	②	③	④	⑤	⑥	①	②	③	④	⑤	⑥	①	②	③	④	⑤	⑥		
cg3551	ngp	Genitase 1.2/divinase	Q	Rev	3199995	3198868	1128	1055	116	114	91	87	122	128	3.460	3.332	3.053	2.683	3.183	3.226	-0.129	-0.407	-0.778	-0.278	-0.234	-0.396	
cg3552	ngpr	Transcriptional activator of genitase catabolism, IcdR-family	Q	Rev	3200991	3200215	777	703	98	87	16	42	52	45	3.757	3.578	3.154	2.187	3.506	2.277	-0.274	-0.546	-0.916	-0.411	-1.251	-1.480	
cg3553	ngpT	MFS-type genitase permease	K	Fwd	3201032	3202390	1359	1285	13	8	1	8	10	10	0.128	-0.613	-2.740	-1.076	-0.569	-0.594	-0.741	-2.868	-1.004	-0.698	-0.722	-0.242	
cg3554	-	3-hydroxybutyrate 6-ironooxigenase	H	G	3202427	3203755	1329	1256	15	16	16	6	5	4	0.353	0.337	0.380	-1.206	-1.411	-1.699	-0.016	0.027	-1.559	-1.765	-2.053	-0.285	
cg3556	-	Putative secondary H ₂ N-glutamate/dicarboxylate symporter, dlc	C	E	3205612	3204359	1254	1181	640	665	534	289	259	65	5.761	5.713	5.440	4.245	4.110	2.107	-0.049	-0.321	-0.846	-0.659	-0.681	-0.577	
cg3557	trpF	Permease, tryptophan-specific	S	Rev	3205904	3204616	513	440	381	367	609	685	591	310	6.304	6.314	6.939	6.782	6.582	6.633	-0.158	0.615	0.478	0.259	-0.671	-0.242	
cg3559	trpE	Anthrillalate synthase subunit I	E	Fwd	3206711	3208267	1557	1483	527	608	647	587	703	81	5.169	5.271	5.404	4.958	3.255	2.099	0.102	0.235	-0.211	0.065	-3.070	-0.220	
cg3560	trpG	Anthrillalate synthase subunit II	E	Fwd	3208264	3208890	627	553	248	351	416	335	366	70	5.397	5.793	6.080	5.463	5.607	3.202	0.396	0.683	0.066	0.210	-2.195	-0.220	
cg3561	trpD	Anthrillalate phosphotransferase	E	Fwd	3208910	3209556	1047	973	439	569	573	642	94	5	4.477	5.748	5.800	5.492	5.676	2.993	0.271	0.323	0.015	0.199	-0.584	-0.615	
cg3562	trpCF	Phosphoribosyltransferase isoenzyme	E	Fwd	3209949	3211373	1425	1351	438	625	762	642	114	107	7.048	6.664	6.463	6.846	6.367	6.633	0.410	0.756	-0.184	0.356	-2.386	-0.244	
cg3563	trpB	Tryptophan synthase beta chain	E	Fwd	3211390	3212643	1254	1180	286	435	545	420	469	99	4.602	5.100	5.468	4.786	4.562	2.706	0.498	0.866	0.184	0.360	-1.896	-0.244	
cg3564	trpA	Tryptophan synthase alpha chain	E	Fwd	3212640	3213482	843	769	200	299	456	317	470	106	4.661	5.133	5.784	4.954	5.388	3.377	0.472	1.123	0.293	0.877	-1.284	-0.497	
cg3565	trpSC	Phosphotransferase system (PTS), putative ribitol/mannitol-specific	S	Rev	3215159	3213618	1542	1469	979	1177	1252	1023	643	452	6.075	6.237	6.369	5.772	5.120	4.588	0.162	0.294	-0.303	-0.955	-1.458	-0.156	
cg3566	trpPA	Phosphotransferase system (PTS), putative ribitol/mannitol-specific	G	Rev	3215996	3215184	813	739	827	849	903	650	410	318	6.756	6.690	6.822	6.404	5.396	5.005	-0.066	0.066	-0.714	-0.360	-1.765	-0.223	
cg3567	-	ABC-type putative multidrug transporter, ATPase subunit	E	Fwd	3216162	3217070	909	836	101	120	291	448	670	861	3.574	3.716	5.030	3.544	3.942	6.277	0.143	1.457	-1.710	-2.368	2.704	-0.592	
cg3568	-	ABC-type putative multidrug transporter, permease subunit	E	Fwd	3217067	3218653	1587	1514	100	95	301	446	583	864	2.605	2.578	4.275	4.533	4.937	5.478	-0.027	0.670	0.920	0.732	0.714	-0.681	
cg3569	acra2	Putative tRNA-sulfur protein	R	Fwd	3218694	3219077	384	311	478	468	890	1238	870	7	7.048	6.814	6.320	5.068	6.117	7.536	0.466	0.641	-0.463	0.840	0.204	-0.244	-0.244
cg3570	-	Putative NADH-dependent flavin oxidoreductase	C	R	3220212	3219127	1086	1012	301	287	507	743	707	402	4.883	4.711	5.573	5.817	5.762	5.087	-0.172	0.690	0.934	0.880	0.204	-0.244	
cg3571	-	Putative secondary Na ⁺ /bile acid symporter, bile acid-N ⁺ symporter	P	Fwd	3220542	3221516	975	901	629	830	452	510	365	332	6.099	6.295	5.563	5.431	4.966	3.481	0.296	-0.536	-0.669	-1.133	-0.618	-0.244	
cg3572	-	Conserved hypothetical protein	-	Fwd	3221700	3222476	717	704	1334	1106	1055	985	200	7	7.510	7.136	7.611	6.699	6.450	4.404	-0.374	-0.399	-0.911	-1.060	-0.244	-0.244	
cg3573	cyoR	Redox-sensory transcriptional repressor, ArsK-family	K	R	3222830	3222492	339	265	224	255	289	394	410	431	6.138	6.220	6.444	6.583	6.658	6.705	0.082	0.305	0.445	0.520	0.567	-0.244	
cg3574	-	Putative NADH-dependent flavin oxidoreductase	C	Fwd	3222971	3224053	1083	1010	730	371	102	75	80	12	6.120	5.084	3.274	2.530	2.639	-0.026	-1.036	-2.848	-3.590	-3.482	-6.148	-0.244	
cg3575	-	Predicted nucleoside-diphosphate-sugar epimerase	M	Fwd	3224066	3224716	651	578	549	429	297	248	219	131	6.486	6.027	5.541	4.976	4.815	4.053	-0.459	-0.945	-0.944	-1.472	-1.433	-0.244	
cg3576	-	Conserved hypothetical protein	-	Fwd	3224926	3224771	156	142	86	24	26	14	8	6	0.058	0.298	0.205	0.248	0.264	0.263	-0.007	-0.389	-1.104	-0.244	-0.244		
cg3577	-	Conserved hypothetical protein	-	Rev	3225206	3225048	159	86	40	22	17	15	9	7	4.774	3.836	3.526	3.050	2.389	2.042	-0.938	-1.248	-1.724	-2.385	-2.732	-0.244	
cg3578	-	Conserved hypothetical protein	-	Rev	3225608	3225438	171	98	14	20	26	21	7	2	3.218	3.600	4.006	3.404	1.962	1.744	0.382	0.787	1.086	-1.257	-1.474	-0.244	
cg3579	-	Putative oxidoreductase protein	I	Fwd	3226036	3226791	756	683	60	90	67	58	43	24	3.098	3.571	3.194	2.683	2.277	1.436	0.473	0.096	-0.415	-0.821	-0.821	-0.244	
cg3580	-	Putative beta-arginine taurine (TA) Peptidase transcription subunit	R	Fwd	3226468	3227050	183	110	768	899	760	349	244	162	6.099	6.476	6.800	6.861	6.436	3.767	0.189	0.228	0.468	-0.244	-0.244		
cg3581	-	Putative dipeptidyl/peptidase-H transceptor, proton-dependent	E	Rev	3228655	3227129	1527	1454	817	770	1306	990	825	188	5.829	5.640	6.444	5.739	5.493	3.341	-0.189	0.615	-0.090	-0.336	-2.448	-0.244	
cg3582	-	Putative transcriptional regulator, TetR-family	K	R	3229606	3229049	558	485	374	99	316	278	379	132	6.156	6.467	5.853	5.363	5.285	4.286	0.311	-0.303	-0.793	-0.331	-1.870	-0.244	
cg3583	trpD	Genitase 1.2/divinase	K	Rev	3230313	3229554	717	704	1334	1106	1055	985	200	7	7.510	7.136	7.611	6.699	6.450	4.404	-0.374	-0.399	-0.911	-1.060	-0.244	-0.244	
cg3584	trpC	Malesylacetate reductase	C	Rev	3231799	3230708	1092	1019	73	93	33	21	27	9	2.846	3.087	3.663	3.729	1.924	1.045	0.416	0.241	-1.183	-1.752	-1.202	-0.244	
cg3585	-	Putative sugar/metalloprotein permease, MFS-type	K	Rev	3233392	3231866	1527	1454	95	111	39	43	35	23	2.738	2.856	1.414	1.246	0.973	0.363	0.119	-1.324	-1.492	-1.765	-2.375	-0.244	
cg3586	-	Putative oxidoreductase protein	K	Fwd	3233816	3233500	1485	1411	452	539	213	106	109	97	5.016	5.166	3.874	2.568	2.625	2.433	0.150	-1.143	-2.449	-2.392	-2.583	-0.244	
cg3587	-	Putative oxidoreductase protein	K	Fwd	3233816	3233500	1485	1411	452	539	213	106	109	97	5.016	5.166	3.874	2.568	2.625	2.433	0.150	-1.143	-2.449	-2.392	-2.583	-0.244	
cg3588	-	Putative sugar/metalloprotein permease, MFS-type	K	Rev	3233816	3233500	1485	1411	452	539	213	106	109	97	5.016	5.166	3.874	2.568	2.625	2.433	0.150	-1.143	-2.449	-2.392	-2.583	-0.244	
cg3589	-	Putative sugar/metalloprotein permease, MFS-type	K	Rev	3233816	3233500	1485	1411	452	539	213	106	109	97	5.016	5.166	3.874	2.568	2.625	2.433	0.150	-1.143	-2.449	-2.392	-2.583	-0.244	
cg3590	-	Putative sugar/metalloprotein permease, MFS-type	K	Rev	3233816	3233500	1485	1411	452	539	213	106	109	97	5.016	5.166	3.874	2.568	2.625	2.433	0.150	-1.143	-2.449	-2.392	-2.583	-0.244	
cg3591	idhA1	Inositol 2-dehydrogenase	R	Fwd	3237450	3238457	1008	934	49	55	7	18	11	2	2.396	2.456	-0.309	0.633	-0.013	0.284	0.660	0.210	-1.763	-2.009	-2.112	-0.244	
cg3592	idhA2	Inositol 2-dehydrogenase	R	Fwd	3238492	3239577	1086	1012	73	62	26	5	33	23	2.854	2.518	1.339	-1.137	-1.382	0.855	-0.336	-0.826	-0.826	-1.472	-1.999	-0.244	
cg3593	-	Putative secreted protein, phosphotase	R	Fwd	3240019	3244404	4386	4313	132	144	65	64	48	14	1.686	1.707	0.614	0.286	-0.718	-1.937	-1.426	-1.446	-1.104	-0.797	-2.960	-0.244	
cg3594	-	Putative secreted protein	-	Fwd	3244700	3245788	1089	1016	29	11	9	17	21	4	2.187	2.022	-0.098	0.444	-0.150	-1.412	0.133	-0.021	-0.611	-1.493	-0.971	-0.244	
cg3595	prop	Putative proline/betaine permease, MFS-type	G	Rev	3247																						