Table S8

GeneFamily	Coefficient	AIC	P-value	FDR	Annotation
COG0294	4.83732	882.9636	0	0	Dihydropteroate synthase and related enzymes
COG3668	3.473867	179.9825	1.03E-90	1.98E-87	Plasmid stabilization system protein
COG1109	2.149108	224.3091	1.60E-52	2.05E-49	Phosphomannomutase
COG3570	20.37122	202.1669	6.47E-52	6.22E-49	Streptomycin 6-kinase
COG0553	-2.44114	86.51388	2.69E-41	2.07E-38	Superfamily II DNA/RNA helicases, SNF2 family
COG3231	20.073	127.2489	5.55E-39	3.56E-36	Aminoglycoside phosphotransferase
COG5281	-21.5854	36.21681	8.97E-28	4.93E-25	Phage-related minor tail protein
COG5527	1.076983	97.55947	3.66E-26	1.76E-23	Protein involved in initiation of plasmid replication
COG5655	2.053102	53.74112	4.73E-18	2.02E-15	Plasmid rolling circle replication initiator protein and truncated derivatives
COG0711	2.449213	55.00266	7.25E-16	2.79E-13	F0F1-type ATP synthase, subunit b
COG0513	-1.03611	66.25597	4.67E-14	1.63E-11	Superfamily II DNA and RNA helicases
COG4710	3.645639	33.3332	1.19E-13	3.82E-11	Predicted DNA-binding protein with an HTH domain
COG2026	1.828561	44.96162	2.82E-13	8.35E-11	Cytotoxic translational repressor of toxin-antitoxin stability system
COG3328	1.456498	46.78137	2.96E-10	8.12E-08	Transposase and inactivated derivatives
COG1804	-1.52485	40.40488	1.26E-09	3.24E-07	Predicted acyl-CoA transferases/carnitine dehydratase
COG2602	2.602289	48.50502	1.72E-08	4.14E-06	Beta-lactamase class D
COG0820	1.211376	47.18473	7.36E-07	0.000167	Predicted Fe-S-cluster redox enzyme
COG3598	2.387178	29.99889	9.86E-07	0.000201	RecA-family ATPase
COG0243	-1.06531	32.6891	9.91E-07	0.000201	Anaerobic dehydrogenases, typically selenocysteine-containing
COG2352	-2.50567	19.66826	1.08E-06	0.000209	Phosphoenolpyruvate carboxylase
COG1593	-1.39968	29.40679	2.26E-06	0.000414	TRAP-type C4-dicarboxylate transport system, large permease component
COG3041	2.857181	28.60766	2.88E-06	0.000504	Uncharacterized protein conserved in bacteria

COG3333	-1.79678	32.26377	3.14E-06	0.000525	Uncharacterized protein conserved in bacteria
COG1028	-0.5674	43.24647	4.89E-06	0.000784	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)
COG3181	-0.91174	56.93775	6.61E-06	0.001017	Uncharacterized protein conserved in bacteria
COG2060	-2.37214	18.95494	8.92E-06	0.001319	K+-transporting ATPase, A chain
COG0665	-1.35495	30.00449	1.16E-05	0.001655	Glycine/D-amino acid oxidases (deaminating)
COG3590	-1.99485	21.77857	1.50E-05	0.002059	Predicted metalloendopeptidase
COG4942	1.898331	30.48405	2.41E-05	0.003198	Membrane-bound metallopeptidase
COG0488	0.562759	63.00203	3.33E-05	0.004269	ATPase components of ABC transporters with duplicated ATPase domains
COG3378	1.45408	40.37061	3.86E-05	0.004788	Predicted ATPase
COG4642	19.74466	30.68517	4.56E-05	0.00548	Uncharacterized protein conserved in bacteria
COG1961	0.800554	45.58435	4.84E-05	0.005643	Site-specific recombinases, DNA invertase Pin homologs
COG1008	-1.01975	42.79718	5.36E-05	0.006066	NADH:ubiquinone oxidoreductase subunit 4 (chain M)
COG3696	-0.53416	42.04681	6.56E-05	0.007133	Putative silver efflux pump
COG1883	20.70021	22.26912	6.68E-05	0.007133	Na+-transporting methylmalonyl-CoA/oxaloacetate decarboxylase, beta subunit
COG0069	-1.35779	24.88907	7.38E-05	0.007528	Glutamate synthase domain 2
COG3164	-3.02892	14.44343	7.44E-05	0.007528	Predicted membrane protein
COG5276	-2.01035	21.69716	8.88E-05	0.008594	Uncharacterized conserved protein
COG1290	-1.42954	31.1688	8.94E-05	0.008594	Cytochrome b subunit of the bc complex
COG1845	-1.21736	34.319	9.42E-05	0.008636	Heme/copper-type cytochrome/quinol oxidase, subunit 3
COG1529	-0.77454	44.06892	9.43E-05	0.008636	Aerobic-type carbon monoxide dehydrogenase, large subunit CoxL/CutL homologs
COG1024	-0.85523	32.20973	1.00E-04	0.008752	Enoyl-CoA hydratase/carnithine racemase

COG1009	-0.8317	35.79486	0.0001	0.008752	NADH:ubiquinone oxidoreductase subunit 5 (chain L)/Multisubunit Na+/H+ antiporter, MnhA subunit
COG0861	-1.25914	33.95779	0.000123	0.010545	Membrane protein TerC, possibly involved in tellurium resistance
COG0483	1.010072	187.6465	0.000145	0.012098	Archaeal fructose-1,6-bisphosphatase and related enzymes of inositol monophosphatase family
COG4941	-22.4651	12.00655	0.000154	0.012643	Predicted RNA polymerase sigma factor containing a TPR repeat domain
COG2946	0.621086	83.26417	0.000172	0.013793	Putative phage replication protein RstA
COG0085	-0.85837	32.44095	0.000244	0.01916	DNA-directed RNA polymerase, beta subunit/140 kD subunit
COG1192	0.570769	43.12763	0.000251	0.019306	ATPases involved in chromosome partitioning
COG4625	-1.59384	27.53733	0.000261	0.019323	Uncharacterized protein with a C-terminal OMP (outer membrane protein) domain
COG1734	-1.59384	27.21696	0.000261	0.019323	DnaK suppressor protein
COG0265	-0.76716	33.48066	0.000274	0.01988	Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain
COG1149	21.49954	18.23877	0.00031	0.021288	MinD superfamily P-loop ATPase containing an inserted ferredoxin domain
COG2855	21.49954	18.92465	0.00031	0.021288	Predicted membrane protein
COG5059	18.49954	39.42822	0.00031	0.021288	Kinesin-like protein
COG0043	-1.26248	24.52076	0.000334	0.022565	3-polyprenyl-4-hydroxybenzoate decarboxylase and related decarboxylases
COG0304	-0.7306	36.47608	0.000357	0.023709	3-oxoacyl-(acyl-carrier-protein) synthase
COG4983	1.94089	30.97676	0.000368	0.023998	Uncharacterized conserved protein
COG1419	-2.33578	18.22497	0.000409	0.026234	Flagellar GTP-binding protein
COG0863	1.055371	30.7231	0.000434	0.02739	DNA modification methylase
COG5534	20.44238	24.16563	0.000456	0.028118	Plasmid replication initiator protein

COG4948	-0.93706	31.06455	0.000468	0.028118	L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily
COG0583	-0.67207	38.26443	0.000469	0.028118	Transcriptional regulator
COG4974	0.482378	62.81666	0.000475	0.028118	Site-specific recombinase XerD
COG1122	2.387178	28.50933	0.000538	0.031236	ABC-type cobalt transport system, ATPase component
COG1231	-21.2828	10.12696	0.000552	0.031236	Monoamine oxidase
COG1462	-20.2828	16.46142	0.000552	0.031236	Uncharacterized protein involved in formation of curli polymers
COG1005	-0.86247	38.60624	0.000599	0.03342	NADH:ubiquinone oxidoreductase subunit 1 (chain H)
COG5616	-1.52485	24.80144	0.000614	0.033764	Predicted integral membrane protein
COG4805	-1.60489	22.72097	0.000639	0.034293	Uncharacterized protein conserved in bacteria
COG4972	-1.70717	27.08625	0.000642	0.034293	Tfp pilus assembly protein, ATPase PilM
COG0460	-1.21119	27.61382	0.000695	0.036614	Homoserine dehydrogenase
COG1007	-0.8317	34.30341	0.000721	0.037464	NADH:ubiquinone oxidoreductase subunit 2 (chain N)
COG1639	2.346356	21.16203	0.000761	0.039009	Predicted signal transduction protein
COG0365	-0.68712	35.41986	0.000913	0.046227	Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases
COG0035	21.31722	18.6919	0.000993	0.048333	Uracil phosphoribosyltransferase
COG0817	21.31722	17.28319	0.000993	0.048333	Holliday junction resolvasome, endonuclease subunit
COG1951	20.31722	21.02497	0.000993	0.048333	Tartrate dehydratase alpha subunit/Fumarate hydratase class I, N-terminal domain
COG0859	-1.11938	27.52567	0.001037	0.049848	ADP-heptose:LPS heptosyltransferase
COG1574	-0.95953	28.87123	0.001137	0.053886	Predicted metal-dependent hydrolase with the TIM-barrel fold
COG1032	-0.75374	30.27511	0.001149	0.053886	Fe-S oxidoreductase
COG0183	-0.69817	35.13863	0.001165	0.053886	Acetyl-CoA acetyltransferase

COG3320	-2.21799	17.23922	0.001177	0.053886	Putative dehydrogenase domain of multifunctional non-ribosomal peptide synthetases and related enzymes
COG2337	1.296533	30.78524	0.001239	0.056069	Growth inhibitor
COG0602	-1.93031	20.16251	0.001445	0.064632	Organic radical activating enzymes
COG4969	2.259344	38.46698	0.001515	0.067	Tfp pilus assembly protein, major pilin PilA
COG1999	-1.62016	20.44168	0.001577	0.068152	Uncharacterized protein SCO1/SenC/PrrC, involved in biogenesis of respiratory and photosynthetic systems
COG2079	-1.62016	21.47354	0.001577	0.068152	Uncharacterized protein involved in propionate catabolism
COG1138	-1.18	25.17271	0.001651	0.070584	Cytochrome c biogenesis factor
COG1960	-0.49523	35.77116	0.001891	0.077146	Acyl-CoA dehydrogenases
COG0412	-1.20639	27.11187	0.001914	0.077146	Dienelactone hydrolase and related enzymes
COG1858	-0.9783	32.05088	0.001936	0.077146	Cytochrome c peroxidase
COG2156	-25.0597	8.998584	0.002005	0.077146	K+-transporting ATPase, c chain
COG3910	-25.0597	8.998584	0.002005	0.077146	Predicted ATPase
COG2047	-22.0597	9.382839	0.002005	0.077146	Uncharacterized protein (ATP-grasp superfamily)
COG3603	-22.0597	9.382839	0.002005	0.077146	Uncharacterized conserved protein
COG4648	-22.0597	9.382839	0.002005	0.077146	Predicted membrane protein
COG5257	-22.0597	9.382839	0.002005	0.077146	Translation initiation factor 2, gamma subunit (eIF-2gamma; GTPase)
COG1848	-21.0597	13.77525	0.002005	0.077146	Predicted nucleic acid-binding protein, contains PIN domain
COG3712	2.212824	23.40338	0.002137	0.081386	Fe2+-dicitrate sensor, membrane component
COG2814	-0.64165	39.83976	0.002237	0.084027	Arabinose efflux permease
COG3889	-0.72348	29.75045	0.00225	0.084027	Predicted solute binding protein
COG2761	-2.62346	15.23113	0.002294	0.084519	Predicted dithiol-disulfide isomerase involved in polyketide biosynthesis
COG0535	-0.98585	28.19528	0.002311	0.084519	Predicted Fe-S

					oxidoreductases
COG0834	1.503677	24.35363	0.002329	0.084519	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain
COG0372	-1.08301	28.51916	0.002408	0.086568	Citrate synthase