Table S7

GeneFamily	Coefficient	AIC	P-value	FDR	Annotation
COG0553	-2.34	77.17	1.11E-26	4.29E-23	Superfamily II DNA/RNA helicases, SNF2 family
COG2026	2.35	31.91	2.75E-22	5.28E-19	Cytotoxic translational repressor of toxin-antitoxin stability system
COG4710	4.12	22.08	7.28E-19	9.34E-16	Predicted DNA-binding protein with an HTH domain
COG5281	-20.58	36.22	1.07E-17	1.03E-14	Phage-related minor tail protein
COG1357	2.31	28.97	4.27E-17	3.29E-14	Uncharacterized low-complexity proteins
COG5527	0.97	64.27	1.50E-16	9.61E-14	Protein involved in initiation of plasmid replication
COG0513	-1.36	47.51	1.78E-14	9.78E-12	Superfamily II DNA and RNA helicases
COG3668	2.07	23.11	6.28E-14	3.02E-11	Plasmid stabilization system protein
COG1961	1.33	45.82	8.28E-12	3.54E-09	Site-specific recombinases, DNA invertase Pin homologs
COG5655	1.78	34.17	2.84E-10	1.09E-07	Plasmid rolling circle replication initiator protein and truncated derivatives
COG2946	1.03	49.51	1.55E-09	5.43E-07	Putative phage replication protein RstA
COG3108	3.35	32.18	8.67E-09	2.78E-06	Uncharacterized protein conserved in bacteria
COG3378	1.94	27.71	2.97E-08	8.80E-06	Predicted ATPase
COG5534	20.36	28.33	3.14E-07	8.63E-05	Plasmid replication initiator protein
COG1192	0.84	36.98	4.90E-07	0.000126	ATPases involved in chromosome partitioning
COG0294	1.42	21.82	3.53E-05	0.008489	Dihydropteroate synthase and related enzymes
COG4886	-2.79	15.75	6.89E-05	0.015582	Leucine-rich repeat (LRR) protein
COG0532	-1.35	21.58	7.90E-05	0.016877	Translation initiation factor 2 (IF-2; GTPase)
COG4983	2.17	31.49	0.000134	0.027193	Uncharacterized conserved protein
COG1486	21.76	13.28	0.000149	0.028596	Alpha-galactosidases/6-phospho-beta-glucosidases, family 4 of glycosyl hydrolases
COG3041	2.63	16.46	0.000225	0.041265	Uncharacterized protein conserved in bacteria
COG0817	24.66	10.93	0.000298	0.049897	Holliday junction resolvasome, endonuclease subunit
COG1951	23.66	11.30	0.000298	0.049897	Tartrate dehydratase alpha subunit/Fumarate hydratase class I, N-terminal domain

COG0069	-1.56	18.68	0.000319	0.050641	Glutamate synthase domain 2
COG3696	-0.57	31.02	0.000348	0.050641	Putative silver efflux pump
COG3505	1.82	23.84	0.000355	0.050641	Type IV secretory pathway, VirD4 components
COG4942	1.82	19.60	0.000355	0.050641	Membrane-bound metallopeptidase
COG3598	2.06	21.62	0.000433	0.058479	RecA-family ATPase
COG0474	-0.69	24.73	0.000441	0.058479	Cation transport ATPase
COG3905	1.77	22.52	0.000615	0.078811	Predicted transcriptional regulator
COG3692	2.49	13.98	0.000789	0.095571	Uncharacterized protein conserved in bacteria
COG1410	0.95	25.92	0.000795	0.095571	Methionine synthase I, cobalamin-binding domain