Table S9

GeneFamily	Coefficient	AIC	P-value	FDR	Annotation
TIGR01496	-3.80	64.47	0	0	dihydropteroate synthase
TIGR01455	-2.85	37.16	4.10E-94	5.89E-91	phosphoglucosamine mutase
TIGR01629	1.20	140.64	6.87E-30	6.57E-27	phage/plasmid replication protein, gene II/X family
TIGR03434	1.04	64.56	1.15E-11	8.26E-09	Acidobacterial duplicated orphan permease
TIGR01642	1.04	35.96	4.88E-10	2.80E-07	U2 snRNP auxilliary factor, large subunit, splicing factor
TIGR02794	0.80	48.41	1.31E-07	6.28E-05	protein TolA
TIGR02763	-0.74	80.93	7.20E-07	0.000295	scaffolding protein
TIGR02416	21.86	13.50	1.29E-05	0.004627	carbon-monoxide dehydrogenase, large subunit
TIGR02082	0.99	28.69	2.99E-05	0.009437	methionine synthase
TIGR00048	-1.01	42.28	3.29E-05	0.009437	radical SAM enzyme, Cfr family
TIGR03436	2.05	28.49	7.14E-05	0.018616	VWFA-related Acidobacterial domain
TIGR01652	-19.92	21.58	9.13E-05	0.021837	phospholipid-translocating P-type ATPase, flippase
TIGR01622	1.01	25.02	0.000414	0.091362	splicing factor, CC1-like family
TIGR02294	1.23	29.57	0.000454	0.093133	nickel ABC transporter, periplasmic nickel-binding protein
TIGR03619	21.41	12.18	0.000502	0.093861	probable F420-dependent oxidoreductase, Rv2161c family
TIGR02866	1.70	24.37	0.000523	0.093861	cytochrome c oxidase, subunit II
TIGR00348	-1.03	27.08	0.000557	0.09407	type I site-specific deoxyribonuclease, HsdR family