Table S10

GeneFamily	Coefficient	AIC	P-value	FDR	Annotation
TIGR01629	2.07	134.70	2.26E-46	6.50E-43	phage/plasmid replication protein. gene II/X family
TIGR02763	-1.53	439.16	2.51E-31	3.60E-28	scaffolding protein
TIGR01541	-20.65	40.76	7.19E-19	6.87E-16	phage tail tape measure protein. lambda family
TIGR02794	1.40	46.08	5.11E-13	3.66E-10	protein TolA
TIGR01389	-1.48	41.54	6.10E-12	3.50E-09	ATP-dependent DNA helicase RecQ
TIGR01613	2.01	27.02	4.86E-09	2.32E-06	phage/plasmid primase. P4 family. C-terminal domain
TIGR02768	0.77	87.62	9.43E-07	0.000386699	Ti-type conjugative transfer relaxase TraA
TIGR03453	1.27	23.12	3.30E-06	0.001184891	plasmid partitioning protein RepA
TIGR02385	2.44	26.75	4.64E-06	0.001374351	addiction module toxin. RelE/StbE family
TIGR01496	1.54	21.28	4.79E-06	0.001374351	dihydropteroate synthase
TIGR02419	-21.13	15.08	3.41E-05	0.008897982	phage/conjugal plasmid C-4 type zinc finger protein. TraR family
TIGR03434	0.59	57.66	8.63E-05	0.019943037	Acidobacterial duplicated orphan permease
TIGR02668	-2.75	17.56	9.04E-05	0.019943037	probable molybdenum cofactor biosynthesis protein A
TIGR02680	0.93	23.33	0.000178465	0.034786634	conserved hypothetical protein TIGR02680
TIGR00487	-1.24	22.28	0.000181875	0.034786634	translation initiation factor IF-2
TIGR02601	-1.47	21.75	0.000255605	0.045833256	autotransporter-associated beta strand repeat
TIGR02168	0.84	23.06	0.000300892	0.05077996	chromosome segregation protein SMC
TIGR02745	-2.61	16.39	0.0003575	0.056981548	cytochrome c oxidase accessory protein CcoG
TIGR02188	-1.00	21.13	0.000493602	0.073031938	acetate--CoA ligase
TIGR00228	24.61	10.77	0.000509111	0.073031938	crossover junction endodeoxyribonuclease RuvC