Table S11

GeneFamily	Coefficient	AIC	P-value	FDR	Annotation
TIGR01496	5.34	59.73	0	0	dihydropteroate synthase
TIGR01455	2.95	36.03	2.71E-93	3.88E-90	phosphoglucosamine mutase
TIGR01541	-21.52	40.76	4.24E-23	4.05E-20	phage tail tape measure protein, lambda family
TIGR02763	-0.79	429.60	4.96E-15	3.56E-12	scaffolding protein
TIGR01642	-1.19	42.75	2.70E-13	1.55E-10	U2 snRNP auxilliary factor, large subunit, splicing factor
TIGR01389	-1.34	51.80	1.68E-12	8.04E-10	ATP-dependent DNA helicase RecQ
TIGR02768	0.95	54.19	1.73E-11	7.09E-09	Ti-type conjugative transfer relaxase TraA
TIGR02168	1.29	29.60	4.77E-11	1.71E-08	chromosome segregation protein SMC
TIGR00048	1.29	42.98	1.16E-06	0.00037	radical SAM enzyme, Cfr family
TIGR02601	-1.97	24.57	1.81E-06	0.00052	autotransporter-associated beta strand repeat
TIGR01629	0.87	35.57	2.56E-06	0.000626	phage/plasmid replication protein, gene II/X family
TIGR03253	-1.60	31.83	2.62E-06	0.000626	formyl-CoA transferase
TIGR02419	-21.00	15.08	3.77E-06	0.000833	phage/conjugal plasmid C-4 type zinc finger protein, TraR family
TIGR00786	-1.40	27.81	6.15E-06	0.001261	TRAP transporter, DctM subunit
TIGR03194	-1.53	26.28	9.72E-06	0.00186	4-hydroxybenzoyl-CoA reductase, alpha subunit
TIGR02037	-0.98	27.61	1.05E-05	0.001882	protease Do
TIGR00601	-1.06	33.19	1.17E-05	0.001982	UV excision repair protein Rad23
TIGR02385	2.28	27.63	1.74E-05	0.00278	addiction module toxin, RelE/StbE family
TIGR01613	1.48	36.32	7.09E-05	0.01071	phage/plasmid primase, P4 family, C-terminal domain
TIGR02866	-1.87	26.61	8.57E-05	0.012292	cytochrome c oxidase, subunit II
TIGR03436	-2.04	18.04	0.000102	0.013951	VWFA-related Acidobacterial domain
TIGR01972	-0.91	29.89	0.000152	0.019126	proton-translocating NADH-quinone oxidoreductase, chain M
TIGR02416	-22.59	10.53	0.00016	0.019126	carbon-monoxide dehydrogenase, large subunit
TIGR02621	-20.59	12.43	0.00016	0.019126	CRISPR-associated helicase Cas3, Anaes-subtype
TIGR02099	-2.76	15.55	0.000207	0.023226	conserved hypothetical protein TIGR02099
TIGR01109	20.66	17.85	0.00021	0.023226	sodium ion-translocating decarboxylase, beta subunit
TIGR00680	-2.23	16.77	0.00024	0.025203	K+-transporting ATPase, A subunit

TIGR03453	1.01	27.85	0.000246	0.025203	plasmid partitioning protein RepA
TIGR01830	-0.54	35.07	0.000295	0.029205	3-oxoacyl-[acyl-carrier-protein] reductase
TIGR03365	-22.46	11.38	0.000414	0.039559	7-cyano-7-deazaguanosine (preQ0) biosynthesis protein QueE
TIGR03339	-1.41	22.45	0.000499	0.046174	aminoethylphosphonate catabolism associated LysR family transcriptional regulator
TIGR02169	0.92	29.30	0.000689	0.061764	chromosome segregation protein SMC
TIGR02668	-1.68	21.16	0.000739	0.064208	probable molybdenum cofactor biosynthesis protein A
TIGR01770	-0.88	31.64	0.00081	0.066386	proton-translocating NADH-quinone oxidoreductase, chain N
TIGR03207	-0.88	27.71	0.00081	0.066386	cyclohexanecarboxyl-CoA dehydrogenase
TIGR01127	2.41	17.26	0.000873	0.068709	threonine dehydratase
TIGR02013	-0.83	27.67	0.000886	0.068709	DNA-directed RNA polymerase, beta subunit
TIGR02224	0.66	45.52	0.00102	0.075942	tyrosine recombinase XerC
TIGR01571	-23.30	10.12	0.001078	0.075942	uncharacterized Cys-rich domain
TIGR02435	-23.30	10.12	0.001078	0.075942	precorrin-3B synthase
TIGR01085	1.28	24.51	0.001106	0.075942	UDP-N-acetylmuramyl-tripeptide synthetases
TIGR03329	-2.56	18.10	0.001139	0.075942	putative aminophosphonate oxidoreductase
TIGR01845	-1.10	27.16	0.001139	0.075942	efflux transporter, outer membrane factor (OMF) lipoprotein, NodT family
TIGR01929	-2.07	21.18	0.001165	0.075942	naphthoate synthase
TIGR01974	-0.74	32.89	0.001444	0.09204	proton-translocating NADH-quinone oxidoreductase, chain L