SUPPLEMENTARY MATERIALS

Table S 1. Promoter analysis and mRNA stability of the pseudogenes and their functional parents

Sr. No	**Sequence ID**	**Protein sequence identity with parent proteins**	**LDF**		**MFE (kcal/mol)**	
		I: Identity (%) **Q: Query Coverage (%)**	**Pseudo**	**Parent**	**Pseudo**	**Parent**
1	dcoA (1252287)	Oxaloacetate decarboxylase [*S. typhimurium*] I:99;Q:100	4.25	0.31	-202	-204.6
2	STM4431 (2673766)	Putative thiamine pyrophosphate-requiring enzyme [*S. typhimurium*] I:100;Q:100	5.06	5.06	-451	-459
3	hutU (1252310)	Urocanate hydratase [*S. Enteritidis*] I:83;Q:100	2.66	2.34	-518	-515.5
4	STM3191 (1254714)	Putative aryl sulfate sulfotransferase [*S. typhimurium]* I:100;Q:100	8.94	8.94	-347.3	-347.3
5	treB (1255980)	Trehalose-specific PTS system IIBC protein [*S. typhimurium*] I:100;Q:100	1.92	1.54	-225.8	-225.8
6	fucP (1254498)	L-fucose transporter [*S. Enterica*] I:100;Q:90	3.22	3.22	-328.2	-506.6
7	STM1860 (2673760)	Transposase [*S. Enterica*] I:100;Q:99	3.91	1.79	-289.5	-288.4
8	yhbE (1254825)	Transporter [*S. Enterica*] I:97;Q:100	1.06	3.15	-251.1	-240.7
9	STM2006 (2673718)	Penicillin-binding protein AmpH, partial [*S. Rubislaw*] I:100;Q:83	0.44	ND*	-3	-78.6
10	STM0326 (1251845)	Glycerol dehyrdratase activator [*S. Newport*] I:100;Q:100	0.47	0.47	-149.7	-149.7
11	STM1553 (1253071)	Putative transposase [*S. heidelberg*] I:100;Q:100	0.43	1.96	-143.8	-166.3
12	STM3828.1N (2673742)	2-Dehydro-3-deoxy-6-phosphogalactonate aldolase [*S. enterica*] I:100;Q:98	0.37	0.37	-217.6	-287.3
13	STM2764 (2673748)	Putative integrase core domain protein [*S. typhimurium*] I:99;Q:100	1.8	1.09	-173.8	-173.8
14	STM0555 (2673757)	Transposase [*S. heidelberg*] I:100;Q:100	2.25	1.18	-66.2	-66.2
15	STM1052 (1252570)	Putative prophage protein [*S. typhimurium*] I:100;Q:100	5.04	2.36	-143	-145.8
16	STM3945 (1255471)	Putative exported protein [*S. typhimurium*] I:100;Q:100	1.94	2.08	-91.4	-91.4
17	STM3654 (1255178)	Transposase [*S. wandsworth*] I:100;Q:91	2.53	3	-28.3	-50
18	ycdF (1252638)	Acetolactate synthase large subunit [*Vibrio variabilis*] I:100;Q:100	0.48	1.09	-0.7	-23.7

***Not determined**

Table S 2. Tertiary structure prediction of the pseudogenes and functional parents.

Sr. No	Sequence ID	Protein sequence identity with parent proteins	Predicted 3D Structures		Instability Index
	Pseudogene	(%)	Pseudogene	Parent	Pseudogene
1	dcoA (1252287)	Oxaloacetate decarboxylase [*S. typhimurium*] I:99;Q:100	Oxaloacetate decarboxylase 2, subunit alpha SI: 75.17 %	Oxaloacetate decarboxylase 2, subunit alpha SI: 85.37%	50.13
2	STM4431 (2673766)	Putative thiamine pyrophosphate-requiring enzyme [*S. typhimurium*] I:100;Q:100	Acetohydroxy-acid synthase SI:25.31%	Acetohydroxy-acid synthase SI: 25.31%	36.34
3	hutU (1252310)	Urocanate hydratase [*S. Enteritidis*] I:83;Q:100	Urocanate hydratase SI: 66.67 %	Urocanate hydratase SI: 75.75%	42.55
4	STM3191 (1254714)	Putative aryl sulfate sulfotransferase [*S. typhimurium]* I:100;Q:100	Aryl sulfate sulfotransferase AssT SI:87.31%	Aryl sulfate sulfotransferase AssT SI: 87.31%	31.75
5	treB (1255980)	Trehalose-specific PTS system IIBC protein [*S. typhimurium*] I:100;Q:100	PTS system, IIabc component SI: 37.04%	PTS system, IIabc component SI: 37.04%	45.96
6	fucP (1254498)	L-fucose transporter [*S. Enterica*] I:100;Q:90	L-fucose-proton symporter SI:91.15%	L-fucose-proton symporter SI:92.24%	38.85
7	STM1860 (2673760)	Transposase [*S. Enterica*] I:100;Q:99	Bacteriophage mu transposase SI:16.47%	Bacteriophage mu transposase SI:16.47%	33.44
8	yhbE (1254825)	Transporter [*S. Enterica*] I:97;Q:100	NADH-quinone oxidoreductase subunit J SI: 5.04%	Ammonia channel SI: 15.67%	45.62
9	STM2006 (2673718)	Penicillin-binding protein AmpH, partial [*S. Rubislaw*] I:100;Q:83	No structure could be predicted	Beta-lactamase/D-alanine Carboxypeptidase SI: 74.58%	56.52
10	STM0326 (1251845)	Glycerol dehyrdratase activator [*S. Newport*] I:100;Q:100	Glycerol dehydratase reactivase alpha subunit SI:80.43%	Glycerol dehydratase reactivase alpha subunit SI:80.43%	39.63
11	STM1553 (1253071)	Putative transposase [*S. Enterica*] I:100;Q:100	Protein (Prd paired) SI:18.27%	Paired box protein PAX-5 SI:14.68%	30.04
12	STM3828.1N (2673742)	2-Dehydro-3-deoxy-6-phosphogalactonate aldolase [*S. Enterica*] I:100;Q:98	2-Dehydro-3-deoxy-6-phosphogalactonate aldolase SI: 83.77%	2-Dehydro-3-deoxy-6-phosphogalactonate aldolase SI: 86.27%	29.96
13	STM2764 (2673748)	Putative integrase core domain protein [*S. typhimurium*] I:99;Q:100	Integrase SI: 15.28%	Integrase SI: 15.28%	52.66
14	STM0555 (2673757)	Transposase [*S. heidelberg*] I:100;Q:100	Protein Cgl2762 SI: 33.33%	Protein Cgl2762 SI: 33.33%	56.47
15	STM1052 (1252570)	Putative prophage protein [*S. typhimurium*] I:100;Q:100	Dihydrolipoyl-transacetylase SI:20.45%	Dihydrolipoyl-transacetylase SI:20.45%	53.15
16	STM3945 (1255471)	Putative exported protein [*S. typhimurium*] I:100;Q:100	Fusion protein SI: 27.03%	Fusion protein SI: 27.03%	72.86
17	STM3654 (1255178)	Transposase [*S. wandsworth*] I:100;Q:91	C-Score:-1.74	Bacteriophage mu transposase SI:11.29%	ND*
18	ycdF (1252638)	Acetolactate synthase large subunit [*Vibrio variabilis*] I:100;Q:100	No structure could be predicted	Acetolactate synthase, chloroplastic SI:47.37%	ND

*Not determined