

**Table S1. Biological function of genes within transcriptional expression clusters.**

Category/ Gene No.	Gene Name	log <sub>2</sub> ratio			Gene description/function
		7 min	45 min	90 min	
<b>Cluster 1</b>					
<b>Regulators</b>					
RSP_0601	<i>rpoH2</i>	1.99	2.13	2.24	RNA polymerase sigma factor
RSP_0847	<i>ompR</i>	2.45	1.48	0.72	two component transcriptional regulator, winged helix family
RSP_1092	<i>rpoE</i>	2.23	1.95	2.05	RNA polymerase sigma-70 factor
RSP_1093	<i>chrR</i>	2.05	2.20	2.33	Anti-sigma factor ChrR
RSP_2410	<i>rpoH1</i>	1.55	1.85	1.43	RNA polymerase sigma factor
<b>Stress defense</b>					
RSP_0799	<i>gloB</i>	1.35	2.11	1.84	Putative hydroxyacylglutathione hydrolase: glyoxalase II
RSP_1591	<i>gst</i>	1.55	1.92	1.92	Predicted Glutathione S-transferase
RSP_2143	<i>phrA</i>	1.58	1.46	1.58	DNA photolyase, Cryptochrome 1 apoprotein (Blue light photoreceptor)
RSP_2389		0.99	1.69	1.43	putative glutathione peroxidase
RSP_2617	<i>msrB</i>	0.88	1.83	1.50	Peptide methionine sulfoxide reductase
RSP_3212	<i>qxtA</i>	1.20	2.02	1.60	Quinol oxidase subunit I QxtA
<b>Iron metabolism</b>					
RSP_0904	<i>sitA</i>	0.80	1.81	1.96	ABC Mn+2/Fe+2 transporter, periplasmic substrate-binding protein SitA
RSP_0905	<i>sitB</i>	0.80	1.72	1.98	ABC Mn+2/Fe+2 transporter, ATPase subunit SitB
RSP_1546	<i>bfr</i>	1.14	1.79	1.60	Bacterioferritin
<b>Others</b>					
RSP_0600		2.21	1.89	2.06	hypothetical protein
RSP_1089		1.91	1.85	1.91	sugar/cation symporter, GPH family
RSP_1090		2.40	1.94	2.21	Putative cyclopropane/cyclopropene fatty acid synthesis protein
RSP_1091		2.16	1.97	2.00	Putative cyclopropane/cyclopropene fatty acid synthesis protein, flavin amine oxidase
RSP_1409		2.81	4.47	4.58	Beta-Ig-H3/Fasciclin
RSP_1491		1.09	1.70	1.61	hypothetical protein
RSP_1760		1.06	1.81	1.56	hypothetical protein
RSP_1852	<i>folE2</i>	2.22	2.33	2.39	GTP cyclohydrolase
RSP_1853	<i>trkH2</i>	1.24	1.65	1.66	potassium uptake transporter, transmembrane component, TrkH
RSP_2314		0.68	1.75	1.66	oxidoreductase, Chromogranin/secretogranin
RSP_2718		1.69	2.82	2.72	possible outer membrane protein
RSP_3075		0.95	1.65	1.52	hypothetical protein
RSP_3076		1.06	1.85	1.79	hypothetical protein
RSP_3537		1.13	1.76	1.59	alcohol dehydrogenase, zinc-containing
RSP_3866		1.83	2.00	1.79	conserved hypothetical protein
RSP_4209		1.42	1.59	1.41	Acyltransferase 3 family
RSP_6229		1.15	1.56	1.44	hypothetical protein
<b>Cluster 2A</b>					
<b>Stress defense</b>					
RSP_0392	<i>gloA</i>	1.00	1.32	1.18	probable lactoylglutathione lyase
RSP_2268		0.98	1.39	1.26	metallo Beta lactamase superfamily
RSP_2973		0.69	1.37	1.24	Peroxiredoxin
RSP_3272	<i>ggt</i>	0.99	1.25	1.31	Gamma-glutamyltranspeptidase
<b>Chaperones</b>					
RSP_0152		0.81	1.18	1.10	P-loop ATPase
RSP_1016	<i>ibpA</i>	0.98	1.40	0.96	small heat shock protein; molecular chaperone IbpA
RSP_1024	<i>moxR</i>	0.44	1.34	1.17	Putative MoxR family protein
RSP_2293	<i>clpA</i>	0.66	1.41	1.18	Chaperonin clpA/B
<b>Redox reaction</b>					
RSP_0351		0.89	1.27	1.02	D-threo-aldose 1-dehydrogenase
RSP_0398	<i>gluD</i>	0.47	1.56	1.46	dehydrogenase
RSP_1410	<i>yedY</i>	0.82	1.59	1.30	Sulfite oxidase subunit YedY
RSP_2734	<i>zwf</i>	0.49	1.10	1.22	glucose-6-phosphate 1-dehydrogenase
RSP_2785	<i>cycF</i>	0.40	1.78	1.71	Cytochrome c-554
<b>Others</b>					
RSP_0370		0.92	1.43	1.27	hypothetical protein
RSP_0595		0.70	1.38	1.45	hypothetical protein
RSP_0906	<i>sitC</i>	0.66	1.25	1.41	ABC Mn+2/Fe+2 transporter, inner membrane subunit SitC
RSP_1258		1.10	1.52	1.34	putative hydrolase
RSP_1421		0.91	1.42	1.13	hypothetical protein
RSP_1490		1.11	1.48	1.18	Putative ATP-dependent protease La, LON
RSP_1542		0.90	1.40	1.23	ABC transporter, ATPase subunit
RSP_1759		0.91	1.51	1.37	hypothetical protein
RSP_1895		0.79	1.38	1.10	Small-conductance mechanosensitive ion channel
RSP_2163		0.66	1.35	1.20	lytic murein transglycosylase, putative
RSP_2225		0.64	1.33	1.08	hypothetical protein
RSP_2388		0.81	1.58	1.30	hypothetical protein

RSP_2390	<i>acuC1</i>	0.96	1.22	1.17	putative Acetoin utilization protein
RSP_3089		0.65	1.23	1.06	hypothetical protein
RSP_3265		0.41	1.52	1.04	hypothetical protein
RSP_3327		0.85	1.31	1.14	possible Rhomboid family membrane protein
RSP_3351		1.23	1.23	1.16	hypothetical protein
RSP_6016		0.84	1.50	1.16	hypothetical protein
RSP_6106		0.80	1.34	1.41	hypothetical protein
RSP_6107		0.89	1.57	1.30	hypothetical protein
<b>Cluster 2B</b>					
<b>Stress defense</b>					
RSP_2144	<i>cfaS</i>	1.37	1.04	1.07	Cyclopropane-fatty-acyl-phospholipid synthase CfaS
RSP_2413	<i>lig2</i>	0.82	0.97	0.96	DNA ligase
RSP_2966	<i>uvrA</i>	0.69	0.88	0.64	excinuclease ABC subunit A
RSP_3210	<i>qxtB</i>	1.12	1.13	1.10	Quinol oxidase subunit II QxtB
<b>Chaperones</b>					
RSP_1207	<i>hslO</i>	0.84	1.01	0.67	putative Hsp33 protein
RSP_2310	<i>groES</i>	1.37	1.30	0.51	Chaperonin Cpn10 (GroES)
<b>Redox reaction</b>					
RSP_1087		0.91	0.68	0.88	Short-chain dehydrogenase/reductase family member
RSP_1411	<i>yedZ</i>	0.69	1.23	0.94	sulfite oxidase subunit YedZ
RSP_3163		0.99	0.86	0.86	Probable oxidoreductase
RSP_3164		0.73	1.15	0.97	ferredoxin like protein
<b>Transport process</b>					
RSP_2803		0.85	1.05	0.88	multidrug/cation efflux pump, RND superfamily
RSP_3273		0.98	1.08	0.91	ABC multidrug/carbohydrate efflux transporter, inner membrane subunit
RSP_3274		0.98	0.86	0.78	ABC multidrug/carbohydrate efflux transporter, ATPase subunit
RSP_3603		0.94	1.18	0.91	Possible ABC efflux transporter, fused inner membrane domains
<b>Porphyrin metabolism</b>					
RSP_0602	<i>cobP</i>	1.24	1.19	1.01	Possible adenosyl cobinamide kinase/ cobinamide phosphate guanylyltransferase
RSP_1197	<i>hemH</i>	0.82	1.15	0.88	ferrochelatase
<b>Others</b>					
RSP_0011		0.73	0.93	0.82	Predicted hydrolase or acyltransferase (alpha/beta hydrolase)
RSP_0013		0.98	0.91	0.82	hypothetical protein
RSP_0472		0.67	1.03	1.01	hypothetical protein
RSP_0473		0.78	0.85	0.73	phospholipase-D family protein
RSP_0569		0.71	1.05	0.79	hypothetical protein
RSP_0570		0.70	0.95	0.74	hypothetical protein
RSP_1025		1.17	0.91	1.00	hypothetical protein
RSP_1088		1.11	0.81	0.88	hypothetical protein
RSP_1497		0.78	0.88	0.35	Putative outer membrane lipoprotein carrier protein
RSP_1540		0.66	1.16	1.00	Predicted secreted hydrolase
RSP_1692	<i>pduO</i>	0.66	1.18	1.03	hypothetical protein
RSP_1840		0.86	0.97	0.96	hypothetical protein
RSP_1985		0.86	0.96	0.97	hypothetical protein
RSP_2391	<i>ligT</i>	0.81	0.89	0.83	2'-5' RNA ligase
RSP_2414		0.64	1.05	1.04	putative mRNA 3-end processing factor
RSP_2421		0.67	1.13	1.00	hypothetical protein
RSP_2569	<i>sqdB</i>	0.68	0.85	0.78	sulfolipid (UDP-sulfoquinovose) biosynthesis protein
RSP_2735	<i>pgl</i>	0.59	0.99	1.18	6-phosphogluconolactonase
RSP_3162		1.16	0.96	0.94	hypothetical protein
RSP_6176		0.76	0.92	0.73	putative tail fiber assembly protein
<b>Cluster 2C</b>					
<b>Stress defense</b>					
RSP_0559	<i>msrA</i>	0.32	0.82	0.65	Peptide methionine sulfoxide reductase
RSP_0725		0.39	1.08	0.88	Thioredoxin, thioldisulfide interchange protein
RSP_0899		0.39	1.04	0.76	Thiol peroxidase
RSP_1397	<i>gst</i>	0.40	0.91	0.79	Glutathione S-transferase
RSP_2083	<i>uvrB</i>	0.60	0.97	0.78	excinuclease ABC subunit B
RSP_2294	<i>gloB</i>	0.46	0.86	0.75	putative hydroxyacylglutathione hydrolase (glyoxalase II) (GLX II) protein
RSP_2693	<i>sodB</i>	0.20	1.19	1.03	Superoxide dismutase, Fe-Mn family
RSP_3077	<i>cryB</i>	0.52	1.11	1.00	Cryptochrome (deoxyribodipyrimidine photolyase-related protein)
RSP_3423	<i>xthA1</i>	0.62	0.81	0.72	Probable exodeoxyribonuclease III
<b>Proteases</b>					
RSP_0355	<i>degP</i>	0.45	0.87	0.70	possible serine protease
RSP_0356	<i>hflC</i>	0.67	0.84	0.53	HflC protein; K04087 membrane protease subunit HflC
RSP_0665	<i>ftsH</i>	0.42	0.99	0.76	membrane protease FtsH catalytic subunit
RSP_0686	<i>clpS</i>	0.36	0.82	0.76	ATP-dependent Clp protease adaptor protein clpS
RSP_1076	<i>sohB</i>	0.55	1.18	0.80	Peptidase family S49
RSP_1096		0.56	1.27	0.93	putative zinc protease
RSP_1097		0.41	1.10	0.66	putative zinc protease

**Redox reaction**

RSP_0423		0.44	0.80	0.58	Aldo/keto reductase
RSP_1545		0.64	0.95	0.73	Probable thiol oxidoreductase with 2 cytochrome c heme-binding sites
RSP_2199		0.59	0.90	0.48	putative acyl-CoA dehydrogenase
RSP_2784	<i>cycG</i>	0.40	1.11	1.07	Diheme class I cytochrome c
RSP_3183		0.50	0.90	0.97	3-hydroxyacyl-CoA dehydrogenase type II

**Transport process**

RSP_0908	<i>sitD</i>	0.45	0.92	1.06	ABC Mn+2/Fe+2 transporter, inner membrane subunit SitD
RSP_1204		0.62	0.94	0.66	ABC multidrug efflux pump, fused ATPase and inner membrane subunits
RSP_2373		0.24	0.87	0.76	Putative Transporter, Major facilitator superfamily (MFS)
RSP_2608	<i>corA</i>	0.60	0.88	0.62	magnesium/cobalt transport protein, MIT family
RSP_2802		0.54	1.21	0.95	multidrug/cation efflux pump, membrane fusion protein subunit
RSP_2854		0.64	0.94	0.77	Cation/multidrug efflux pump, Membrane fusion protein (MFP) family

**Carbohydrate metabolism**

RSP_1415		0.16	1.07	0.98	putative polysaccharide deacetylase
RSP_2115	<i>envA</i>	0.34	1.07	1.18	putative UDP-3-O-acyl N-acetylglucosamine deacetylase
RSP_2550	<i>exoK</i>	0.34	1.02	0.74	endo-beta-1,3-1,4-glycanase protein
RSP_2645	<i>eda</i>	0.07	0.53	0.88	KDPG/KHG bifunctional aldolase
RSP_4045	<i>fbaB</i>	0.16	0.84	0.50	fructose-bisphosphate aldolase

**Regulators**

RSP_1083		0.10	0.71	0.88	two component transcriptional regulator, winged helix family
RSP_2719	<i>lrp</i>	0.24	0.86	0.73	transcriptional regulator, AsnC/Lrp family
RSP_2853		0.45	1.04	0.74	Transcriptional regulator, TetR family

**Others**

RSP_0119		0.46	1.15	0.88	PA-phosphatase related phosphoesterase
RSP_0730		0.45	0.88	0.77	hypothetical protein
RSP_0850		0.48	0.83	1.08	hypothetical protein
RSP_0870		0.55	1.12	0.92	hypothetical protein
RSP_1000		0.27	0.91	0.80	hypothetical protein
RSP_1022		0.47	0.95	0.86	conserved hypothetical protein (possibly transmembrane)
RSP_1023		0.44	1.03	0.88	hypothetical protein
RSP_1026		0.56	0.87	0.78	hypothetical protein
RSP_1199		0.19	1.07	1.01	secreted conserved hypothetical protein
RSP_1399		0.52	0.86	0.73	N-formylglutamate amidohydrolase
RSP_1825	<i>tldD</i>	0.52	0.99	0.79	probable modulator of DNA gyrase
RSP_2202		-0.04	0.68	0.81	hypothetical protein
RSP_2218		0.40	1.09	0.89	hypothetical protein
RSP_2235		0.62	0.84	0.64	hypothetical protein
RSP_2480		0.49	1.00	0.89	hypothetical protein
RSP_2481	<i>cysE</i>	0.49	0.88	0.77	serine acetyltransferase
RSP_2625	<i>nifU</i>	0.47	0.75	0.83	NifU-related protein involved in Fe-S cluster formation
RSP_2646	<i>edd</i>	0.29	0.91	1.16	Pseudogene
RSP_2763		0.36	0.93	0.76	hypothetical protein
RSP_3138		0.57	0.93	0.79	Smp-30/Cgr1 family protein
RSP_3305	<i>abc1</i>	0.41	0.95	0.77	putative ubiquinol-cytochrome-c reductase assembly protein
RSP_3310		0.30	1.01	0.92	Pseudogene
RSP_3331		-0.07	0.69	0.86	Cupin domain containing protein
RSP_3601		0.45	1.02	0.82	Lipolytic enzyme, G-D-S-L family
RSP_3653		0.34	0.95	0.51	hypothetical protein
RSP_6022		0.07	0.93	0.63	hypothetical protein
RSP_6156		0.37	0.82	0.67	hypothetical protein

**Cluster 3****Chaperones**

RSP_1173	<i>dnaK</i>	0.93	0.81	0.23	Heat shock protein (Hsp70, DnaK)
RSP_1408	<i>clpB</i>	0.84	0.45	0.27	Chaperone ClpB
RSP_1532	<i>hslU</i>	0.82	0.14	-0.11	ATP-dependent protease ATP-binding subunit
RSP_2311	<i>groEL</i>	1.58	1.09	0.41	chaperonin GroEL

**Amino acid & sulfur metabolism**

RSP_1352	<i>serA</i>	1.15	-0.56	-0.63	D-3-phosphoglycerate dehydrogenase
RSP_1941	<i>cysH</i>	1.08	-0.36	-0.25	phosphoadenosine phosphosulfate reductase
RSP_1942	<i>cysI</i>	1.13	-0.14	0.02	Sulfite/nitrite reductase hemoprotein subunit
RSP_1944	<i>cysG</i>	1.22	0.02	0.17	Uroporphyrin-III C-methyltransferase/siroheme synthase

**Others**

RSP_0846	<i>ribA</i>	0.97	0.55	0.71	GTP cyclohydrolase II
RSP_2661		0.90	0.29	0.43	Iron-containing alcohol dehydrogenase
RSP_1854	<i>trkH3</i>	1.07	0.57	0.74	potassium uptake transporter, transmembrane component, TrkH

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