Table S1. Description of microarray GEO #GSE53138.

COG Function Categories Distribution	Total	Up (by 2 fold)	Down (by 2 fold)	% differencially expressed
Amino acid transport and metabolism	360	36	93	35.83
Carbohydrate transport and metabolism	367	30	63	25.34
Cell cycle control, cell division, chromosome partitioning	33	3	5	24.24
Cell motility	109	15	2	15.60
Cell wall/membrane/envelope biogenesis	222	22	52	33.33
Coenzyme transport and metabolism	151	36	20	37.09
Defense mechanisms	45	7	6	28.89
Energy production and conversion	286	34	58	32.17
Function unknown	314	45	20	20.70
General function prediction only	400	48	36	21.00
Inorganic ion transport and metabolism	215	24	23	21.86
Intracellular trafficking, secretion, and vesicular transport	122	15	6	17.21
Lipid transport and metabolism	100	6	17	23.00
Nucleotide transport and metabolism	96	12	25	38.54
Posttranslational modification, protein turnover, chaperones	135	31	12	31.85
RNA processing and modification	2	0	0	0.00
Replication, recombination and repair	200	27	16	21.50
Secondary metabolites biosynthesis, transport and catabolism	64	7	11	28.13
Signal transduction mechanisms	175	16	23	22.29
Transcription	292	46	29	25.68
Translation, ribosomal structure and biogenesis	181	9	16	13.81

Top 100 up-regulated genes from microarray GEO #GSE53138.

Rank	Locus Tag	Gene name	Gene description	Mean Log Ratio	z score	GI#	COG	COGFun	COG Description
1	b3686	*ibpB*	heat shock protein (VIMSS)	6.52	2.77	90111637	COG71	O	Molecular chaperone (small heat shock protein)
2	b3010	*yqhC*	putative ARAC-type regulatory protein (VIMSS)	6.10	2.79	90111526	COG2207	K	AraC-type DNA-binding domain-containing proteins
3	b3687	*ibpA*	heat shock chaperone (NCBI)	5.32	2.64	16131555	COG71	O	Molecular chaperone (small heat shock protein)
4	b0355	*frmB*	predicted esterase (NCBI)	5.04	2.52	16128340	COG627	R	Predicted esterase
5	b1112	*ycfR*	hypothetical protein (NCBI)	5.01	2.80	16129075			
6	b3011	*yqhD*	alcohol dehydrogenase, NAD(P)-dependent (NCBI)	4.80	2.82	16130909	COG1979	C	Uncharacterized oxidoreductases, Fe-dependent alcohol dehydrogenase family
7	b3238	*yhcN*	orf, hypothetical protein (VIMSS)	4.54	2.63	90111561			
8	b4326	*yjiD*	orf, hypothetical protein (VIMSS)	4.39	2.47	90111730			
9	b1532	*marB*	hypothetical protein (NCBI)	4.22	2.45	16129491			
10	b1531	*marA*	multiple antibiotic resistance; transcriptional activator of defense systems (VIMSS)	3.94	2.53	90111290	COG2207	K	AraC-type DNA-binding domain-containing proteins
11	b2674	*nrdI*	hypothetical protein (NCBI)	3.76	2.32	16130588	COG1780	F	Protein involved in ribonucleotide reduction
12	b2673	*nrdH*	glutaredoxin-like protein (NCBI)	3.75	2.31	16130587	COG695	O	Glutaredoxin and related proteins
13	b3014	*yqhH*	predicted outer membrane lipoprotein (NCBI)	3.70	2.63	16130912	COG4238	M	Murein lipoprotein
14	b3013	*yqhG*	hypothetical protein (NCBI)	3.65	2.86	49176301			
15	b1530	*marR*	multiple antibiotic resistance protein; repressor of mar operon (VIMSS)	3.61	2.64	90111289	COG1846	K	Transcriptional regulators
16	b0356	*frmA*	alcohol dehydrogenase class III/glutathione-dependent formaldehyde dehydrogenase (NCBI)	3.58	2.44	16128341	COG1062	C	Zn-dependent alcohol dehydrogenases, class III
17	b0849	*grxA*	glutaredoxin 1, redox coenzyme for ribonucleotide reductase (RNR1a) (NCBI)	3.58	2.82	16128817	COG695	O	Glutaredoxin and related proteins
18	b4062	*soxS*	DNA-binding transcriptional dual regulator (NCBI)	3.51	2.81	16131888	COG2207	K	AraC-type DNA-binding domain-containing proteins
19	b1352	*ydaD*	orf, hypothetical protein (VIMSS)	3.50	2.69	90111255			
20	b1649	*ydhM*	predicted DNA-binding transcriptional regulator (RefSeq)	3.47	2.18	1.46E+08	COG1309	K	Transcriptional regulator
21	b3012	*yqhE*	orf, hypothetical protein (VIMSS)	3.46	2.55	90111527	COG656	R	Aldo/keto reductases, related to diketogulonate reductase
22	b1611	*fumC*	fumarate hydratase (NCBI)	3.35	2.85	16129569	COG114	C	Fumarase
23	b0447	*ybaO*	putative LRP-like transcriptional regulator (VIMSS)	3.27	2.83	90111137	COG1522	K	Transcriptional regulators
24	b4642	*yoeD*		3.23	2.42				
25	b1355	*b1355*	orf, hypothetical protein (VIMSS)	3.06	2.56	90111257			
26	b4554	*yibT*	hypothetical protein (NCBI)	2.99	2.52	94541127			
27	b0365	*tauA*	taurine transport system periplasmic protein (VIMSS)	2.95	1.81	90111122	COG4521	P	ABC-type taurine transport system, periplasmic component
28	b1351	*racC*	Rac prophage; predicted protein (NCBI)	2.93	2.64	16129312			
29	b0629	*ybeF*	putative transcriptional regulator LYSR-type (VIMSS)	2.93	2.56	90111155	COG583	K	Transcriptional regulator
30	b0357	*yaiN*	putative alpha helix chain (VIMSS)	2.93	2.90	1.62E+08	COG1937	S	Uncharacterized protein conserved in bacteria
31	b0366	*tauB*	taurine transporter subunit (NCBI)	2.92	1.69	16128351	COG4525	P	ABC-type taurine transport system, ATPase component
32	b1111	*ycfQ*	orf, hypothetical protein (VIMSS)	2.85	2.79	90111214	COG1309	K	Transcriptional regulator
33	b2675	*nrdE*	ribonucleotide-diphosphate reductase alpha subunit (NCBI)	2.80	2.37	16130589	COG209	F	Ribonucleotide reductase, alpha subunit
34	b1650	*nemA*	N-ethylmaleimide reductase, FMN-linked (NCBI)	2.77	1.99	16129608	COG1902	C	NADH:flavin oxidoreductases, Old Yellow Enzyme family

Top 100 up-regulated genes from microarray GEO #GSE53138.

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35	b0367	*tauC*	taurine transporter subunit (NCBI)	2.77	1.62	16128352	COG600	P	ABC-type nitrate/sulfonate/bicarbonate transport system, permease component
36	b1838	*pphA*	protein phosphatase 1 modulates phosphoproteins, signals protein misfolding (VIMSS)	2.74	2.60	90111344			
37	b4060	*yjcB*	orf, hypothetical protein (VIMSS)	2.74	2.40	90111681			
38	b0448	*mdlA*	fused predicted multidrug transporter subunits of ABC superfamily: ATP-binding components (NCBI)	2.72	2.52	16128433	COG1132	V	ABC-type multidrug transport system, ATPase and permease components
39	b2732	*ygbA*	hypothetical protein (NCBI)	2.70	2.80	16130639			
40	b3160	*yhbW*	predicted enzyme (NCBI)	2.68	2.23	16131052	COG2141	C	Coenzyme F420-dependent N5,N10-methylene tetrahydromethanopterin reductase and related flavin-dependent oxidoreductases
41	b1378	*ydbK*	fused predicted pyruvate-flavodoxin oxidoreductase: conserved protein/conserved protein/FeS binding protein (NCBI)	2.68	2.57	16129339	COG674	C	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit
42	b1463	*nhoA*	N-hydroxyarylamine O-acetyltransferase (NCBI)	2.63	2.56	16129422	COG2162	Q	Arylamine N-acetyltransferase
43	b3917	*sbp*	sulfate transporter subunit (NCBI)	2.62	1.92	16131755	COG1613	P	ABC-type sulfate transport system, periplasmic component
44	b0449	*mdlB*	fused predicted multidrug transporter subunits of ABC superfamily: ATP-binding components (NCBI)	2.57	2.55	16128434	COG1132	V	ABC-type multidrug transport system, ATPase and permease components
45	b1167	*ymgC*	hypothetical protein (NCBI)	2.55	2.17	16129130			
46	b3101	*yqjF*	orf, hypothetical protein (VIMSS)	2.52	2.43	90111539	COG2259	S	Predicted membrane protein
47	b0851	*nfsA*	nitroreductase A, NADPH-dependent, FMN-dependent (NCBI)	2.50	2.66	16128819	COG778	C	Nitroreductase
48	b0628	*lipA*	lipoyl synthase (NCBI)	2.49	2.78	16128611	COG320	H	Lipoate synthase
49	b2104	*thiM*	hydroxyethylthiazole kinase (NCBI)	2.49	2.44	16130042	COG2145	H	Hydroxyethylthiazole kinase, sugar kinase family
50	b2237	*inaA*	hypothetical protein (NCBI)	2.49	2.42	16130172			
51	b1322	*ycjF*	hypothetical protein (NCBI)	2.48	2.79	16129283	COG3768	S	Predicted membrane protein
52	b2531	*iscR*	DNA-binding transcriptional repressor (NCBI)	2.46	2.60	16130456	COG1959	K	Predicted transcriptional regulator
53	b1164	*ycgZ*	hypothetical protein (NCBI)	2.43	2.21	16129127			
54	b1380	*ldhA*	D-lactate dehydrogenase (NCBI)	2.43	2.50	16129341	COG1052	CHR	Lactate dehydrogenase and related dehydrogenases
55	b2681	*ygaY*	predicted transporter (pseudogene) (RefSeq)	2.42	2.26				
56	b4527	*b1354*	orf, hypothetical protein (VIMSS)	2.41	1.97	94541091			
57	b3924	*fpr*	ferredoxin-NADP reductase (NCBI)	2.40	2.39	16131762	COG1018	C	Flavodoxin reductases (ferredoxin-NADPH reductases) family 1
58	b1797	*yeaR*	hypothetical protein (NCBI)	2.38	2.37	16129751	COG3615	P	Uncharacterized protein/domain, possibly involved in tellurite resistance
59	b1974	*yodB*	putative cytochrome (VIMSS)	2.37	1.70	90111363	COG3038	C	Cytochrome B561
60	b0850	*ybjC*	predicted inner membrane protein (NCBI)	2.37	2.55	16128818			
61	b1652	*rnt*	ribonuclease T (NCBI)	2.36	2.50	16129610	COG847	L	DNA polymerase III, epsilon subunit and related 3'-5' exonucleases
62	b2173	*yeiR*	predicted enzyme (NCBI)	2.36	2.64	16130111	COG523	R	Putative GTPases (G3E family)
63	b3685	*yidE*	putative transport protein (VIMSS)	2.34	2.76	90111636	COG2985	R	Predicted permease
64	b3242	*yhcR*	orf, hypothetical protein (VIMSS)	2.33	2.82	90111562			
65	b2749	*ygbE*	conserved inner membrane protein (NCBI)	2.32	2.13	16130656			
66	b1321	*ycjX*	conserved protein with nucleoside triphosphate hydrolase domain (NCBI)	2.32	2.64	16129282	COG3106	R	Predicted ATPase
67	b3828	*metR*	DNA-binding transcriptional activator, homocysteine-binding (NCBI)	2.30	2.07	16131677	COG583	K	Transcriptional regulator
68	b0368	*tauD*	taurine dioxygenase (NCBI)	2.28	1.68	16128353	COG2175	Q	Probable taurine catabolism dioxygenase
69	b1053	*mdtG*	predicted drug efflux system (NCBI)	2.22	2.79	16129016	COG2814	G	Arabinose efflux permease
70	b2676	*nrdF*	ribonucleotide-diphosphate reductase beta subunit (NCBI)	2.22	2.59	16130590	COG208	F	Ribonucleotide reductase, beta subunit
71	b4011	*yjaA*	hypothetical protein (NCBI)	2.22	2.10	16131837			
72	b2582	*trxC*	thioredoxin 2 (NCBI)	2.21	2.33	16130507			
73	b0987	*ymcD*	orf, hypothetical protein (VIMSS)	2.20	2.53	90111199			
74	b2106	*yohM*	membrane protein conferring nickel and cobalt resistance (NCBI)	2.19	2.28	16130044	COG2215	R	ABC-type uncharacterized transport system, permease component
75	b0473	*htpG*	heat shock protein 90 (NCBI)	2.19	2.79	16128457	COG326	O	Molecular chaperone, HSP90 family
76	b1551	*b1551*	orf, hypothetical protein (VIMSS)	2.18	2.56	90111294			
77	b3662	*nepI*	predicted transporter (RefSeq)	2.18	2.16	1.46E+08	COG2814	G	Arabinose efflux permease
78	b2667	*ygaV*	predicted DNA-binding transcriptional regulator (NCBI)	2.17	2.58	16130581	COG640	K	Predicted transcriptional regulators
79	b3740	*gidB*	glucose-inhibited division protein B (NCBI)	2.17	2.08	16131608	COG357	M	Predicted S-adenosylmethionine-dependent methyltransferase involved in bacterial cell division
80	b4325	*yjiC*	orf, hypothetical protein (VIMSS)	2.17	1.60	49176489			
81	b3661	*nlpA*	cytoplasmic membrane lipoprotein-28 (NCBI)	2.16	2.09	16131531	COG1464	P	ABC-type metal ion transport system, periplasmic component/surface antigen
82	b0852	*rimK*	ribosomal protein S6 modification protein (NCBI)	2.14	2.37	16128820	COG189	HJ	Glutathione synthase/Ribosomal protein S6 modification enzyme (glutaminyl transferase)
83	b0476	*aes*	acetyl esterase (NCBI)	2.14	2.59	16128460	COG657	I	Esterase/lipase
84	b1165	*ymgA*	hypothetical protein (NCBI)	2.13	2.69	16129128			

Top 100 up-regulated genes from microarray GEO #GSE53138.

Rank	**Locus Tag**	**Gene name**	**Gene description**	**Mean Log Ratio**	**z score**	**GI#**	**COG**	**COGFun**	**COG Description**
85	b1667	*ydhR*	hypothetical protein (NCBI)	2.13	2.64	16129623			
86	b2592	*clpB*	protein disaggregation chaperone (NCBI)	2.12	2.20	16130513	COG542	O	ATPases with chaperone activity, ATP-binding subunit
87	b0156	*yadR*	hypothetical protein (NCBI)	2.10	2.44	16128149	COG316	S	Uncharacterized conserved protein
88	b1231	*tyrT*	tRNA-Tyr (NCBI)	2.06	2.52	1.46E+08			
89	b2236	*yfaE*	predicted 2Fe-2S cluster-containing protein (NCBI)	2.06	2.05	16130171	COG633	C	Ferredoxin
90	b0871	*poxB*	pyruvate dehydrogenase (NCBI)	2.04	2.43	16128839	COG28	EH	Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carboligase, phosphonopyruvate decarboxylase]
91	b1379	*hslJ*	heat-inducible protein (NCBI)	2.03	2.14	16129340	COG3187	O	Heat shock protein
92	b4063	*soxR*	DNA-binding transcriptional dual regulator, Fe-S center for redox-sensing (NCBI)	2.01	2.80	16131889	COG789	K	Predicted transcriptional regulators
93	b2167	*fruA*	fused fructose-specific PTS enzymes: IIBcomponent/IIC components (NCBI)	2.00	2.05	16130105	COG1299	G	Phosphotransferase system, fructose-specific IIC component
94	b1623	*add*	adenosine deaminase (NCBI)	2.00	2.51	16129581	COG1816	F	Adenosine deaminase
95	b2103	*thiD*	phosphomethylpyrimidine kinase (NCBI)	1.96	2.50	16130041	COG351	H	Hydroxymethylpyrimidine/phosphomethylpyrimidine
96	b4340	*yjiR*	fused predicted DNA-binding transcriptional regulator/predicted aminotransferase (NCBI)	1.94	2.43	16132161	COG1167	KE	Transcriptional regulators containing a DNA-binding HTH domain and an aminotransferase domain (MocR family) and their eukaryotic orthologs
97	b4526	*ydaE*	Rac prophage; conserved protein (NCBI)	1.94	2.21	94541109			
98	b3461	*rpoH*	RNA polymerase sigma factor (NCBI)	1.94	2.35	16131333	COG568	K	DNA-directed RNA polymerase, sigma subunit (sigma70/sigma32)
99	b1110	*ycfJ*	hypothetical protein (NCBI)	1.93	2.23	16129073	COG3134	S	Predicted outer membrane lipoprotein
100	b0439	*lon*	DNA-binding ATP-dependent protease La (NCBI)	1.91	2.56	16128424	COG466	O	ATP-dependent Lon protease, bacterial type

Top 100 down-regulated genes from microarray GEO #GSE53138.

Rank	**Locus Tag**	**Gene name**	**Gene description**	**Mean Log Ratio**	**z score**	**GI#**	**COG**	**COGFun**	**COG Description**
1	b3512	*gadE*	acid-responsive regulator of gadA and gadBC (Katherine Huang)	-5.26	-2.45	16131384			
2	b0342	*lacA*	galactoside O-acetyltransferase (NCBI)	-5.25	-2.45	16128327	COG110	R	Acetyltransferase (isoleucine patch superfamily)
3	b3506	*slp*	outer membrane protein induced after carbon starvation (VIMSS)	-4.95	-2.36	90111603	COG3065	M	Starvation-inducible outer membrane lipoprotein
4	b3509	*hdeB*	orf, hypothetical protein (VIMSS)	-4.89	-2.39	1.62E+08			
5	b3510	*hdeA*	acid-resistance protein, possible chaperone , subunit of HdeA dimer, inactive form of acid-resistance protein (Katherine Huang)	-4.78	-2.60	16131382			
6	b1494	*pqqL*	predicted peptidase (NCBI)	-4.40	-2.12	16129452	COG612	R	Predicted Zn-dependent peptidases
7	b0336	*codB*	cytosine transporter (NCBI)	-4.28	-2.63	16128321	COG1457	F	Purine-cytosine permease and related proteins
8	b0344	*lacZ*	beta-D-galactosidase (NCBI)	-4.26	-2.57	16128329	COG3250	G	Beta-galactosidase/beta-glucuronidase
9	b3517	*gadA*	glutamate decarboxylase A, PLP-dependent (NCBI)	-4.23	-1.92	16131389	COG76	E	Glutamate decarboxylase and related PLP-dependent proteins
10	b3511	*hdeD*	acid-resistance membrane protein (NCBI)	-4.17	-2.23	16131383	COG3247	S	Uncharacterized conserved protein
11	b0343	*lacY*	galactoside permease (NCBI)	-4.15	-2.50	16128328			
12	b0033	*carB*	carbamoyl-phosphate synthase large subunit (NCBI)	-4.14	-2.80	16128027	COG458	EF	Carbamoylphosphate synthase large subunit (split gene in MJ)
13	b2000	*flu*	CP4-44 prophage; antigen 43 (Ag43) phase-variable biofilm formation autotransporter (NCBI)	-4.08	-2.64	49176177	COG3468	MU	Type V secretory pathway, adhesin AidA
14	b0485	*ybaS*	predicted glutaminase (NCBI)	-4.04	-2.43	16128469	COG2066	E	Glutaminase
15	b2035	*wbbH*	O-antigen polymerase (NCBI)	-3.83	-2.84	16129975			
16	b0728	*sucC*	succinyl-CoA synthetase subunit beta (NCBI)	-3.76	-2.80	16128703	COG45	C	Succinyl-CoA synthetase, beta subunit
17	b1493	*gadB*	glutamate decarboxylase B, PLP-dependent (NCBI)	-3.73	-2.11	16129451	COG76	E	Glutamate decarboxylase and related PLP-dependent proteins
18	b3508	*yhiD*	predicted Mg(2+) transport ATPase inner membrane protein (NCBI)	-3.65	-2.52	16131380	COG1285	S	Uncharacterized membrane protein
19	b4354	*yjiY*	putative carbon starvation protein (VIMSS)	-3.61	-2.63	90111739	COG1966	T	Carbon starvation protein, predicted membrane protein
20	b0032	*carA*	carbamoyl-phosphate synthase small subunit (NCBI)	-3.60	-2.54	16128026	COG505	EF	Carbamoylphosphate synthase small subunit
21	b4034	*malE*	maltose ABC transporter periplasmic protein (NCBI)	-3.55	-2.13	16131860	COG2182	G	Maltose-binding periplasmic proteins/domains
22	b3460	*livJ*	leucine/isoleucine/valine transporter subunit (NCBI)	-3.54	-2.47	49176358	COG683	E	ABC-type branched-chain amino acid transport systems, periplasmic component
23	b3749	*rbsA*	fused D-ribose transporter subunits of ABC superfamily: ATP-binding components (NCBI)	-3.53	-2.45	16131617	COG1129	G	ABC-type sugar transport system, ATPase component
24	b0726	*sucA*	alpha-ketoglutarate decarboxylase (NCBI)	-3.53	-2.88	16128701	COG567	C	2-oxoglutarate dehydrogenase complex, dehydrogenase (E1) component, and related enzymes
25	b2032	*wbbK*	lipopolysaccharide biosynthesis protein (NCBI)	-3.49	-2.77	16129972	COG438	M	Glycosyltransferase
26	b0722	*sdhD*	succinate dehydrogenase cytochrome b556 small membrane subunit (NCBI)	-3.47	-2.70	16128697	COG2142	C	Succinate dehydrogenase, hydrophobic anchor subunit
27	b0729	*sucD*	succinyl-CoA synthetase subunit alpha (NCBI)	-3.46	-2.80	16128704	COG74	C	Succinyl-CoA synthetase, alpha subunit
28	b0287	*yagU*	conserved inner membrane protein (NCBI)	-3.46	-2.34	16128272	COG3477	S	Predicted periplasmic/secreted protein
29	b0723	*sdhA*	succinate dehydrogenase flavoprotein subunit (NCBI)	-3.45	-2.65	16128698	COG1053	C	Succinate dehydrogenase/fumarate reductase, flavoprotein subunit

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30	b0595	*entB*	isochorismatase (NCBI)	-3.40	-2.68	16128578	COG1535	Q	Isochorismate hydrolase
31	b4245	*pyrB*	aspartate carbamoyltransferase catalytic subunit (NCBI)	-3.39	-2.43	16132067	COG540	F	Aspartate carbamoyltransferase, catalytic chain
32	b3623	*rfaK*	lipopolysaccharide core biosynthesis (NCBI)	-3.38	-2.16	16131494	COG859	M	ADP-heptose:LPS heptosyltransferase
33	b0727	*sucB*	dihydrolipoamide acetyltransferase (NCBI)	-3.35	-2.81	16128702	COG508	C	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide acyltransferase (E2) component, and related enzymes
34	b0721	*sdhC*	succinate dehydrogenase cytochrome b556 large membrane subunit (NCBI)	-3.34	-2.55	16128696	COG2009	C	Succinate dehydrogenase/fumarate reductase, cytochrome b subunit
35	b0004	*thrC*	threonine synthase (NCBI)	-3.29	-2.41	16127998	COG498	E	Threonine synthase
36	b4571	*wbbL*		-3.28	-2.56				
37	b3750	*rbsC*	ribose ABC transporter permease protein (NCBI)	-3.27	-2.29	16131618	COG1172	G	Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components
38	b2034	*wbbI*	hypothetical protein (NCBI)	-3.27	-2.86	16129974			
39	b4069	*acs*	acetyl-coenzyme A synthetase (NCBI)	-3.17	-2.53	16131895	COG365	I	Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases
40	b0003	*thrB*	homoserine kinase (NCBI)	-3.15	-2.48	16127997	COG83	E	Homoserine kinase
41	b0565	*ompT*	DLP12 prophage; outer membrane protease VII (outer membrane protein 3b) (NCBI)	-3.14	-2.47	16128548	COG4571	M	Outer membrane protease
42	b0724	*sdhB*	succinate dehydrogenase, FeS subunit (NCBI)	-3.10	-2.35	16128699	COG479	C	Succinate dehydrogenase/fumarate reductase, Fe-S protein subunit
43	b0002	*thrA*	bifunctional aspartokinase I/homeserine dehydrogenase I (NCBI)	-3.03	-2.50	16127996	COG527	E	Aspartokinases
44	b3626	*rfaJ*	UDP-D-glucose:(galactosyl)lipopolysaccharide glucosyltransferase (NCBI)	-2.99	-2.58	16131497	COG1442	M	Lipopolysaccharide biosynthesis proteins, LPS:glycosyltransferases
45	b3748	*rbsD*	D-ribose high-affinity transport system; membrane-associated protein (VIMSS)	-2.97	-2.34	90111647	COG1869	G	ABC-type ribose transport system, auxiliary component
46	b0354	*yaiL*	nucleoprotein/polynucleotide-associated enzyme (VIMSS)	-2.95	-2.33	90111118	COG3122	S	Uncharacterized protein conserved in bacteria
47	b4244	*pyrI*	aspartate carbamoyltransferase regulatory subunit (NCBI)	-2.95	-2.42	16132066	COG1781	F	Aspartate carbamoyltransferase, regulatory subunit
48	b3469	*zntA*	zinc, cobalt and lead efflux system (NCBI)	-2.93	-1.48	16131341	COG2217	P	Cation transport ATPase
49	b3513	*mdtE*	multidrug resistance efflux transporter (NCBI)	-2.92	-1.94	16131385	COG845	M	Membrane-fusion protein
50	b2240	*glpT*	sn-glycerol-3-phosphate transporter (NCBI)	-2.88	-2.30	16130175	COG2271	G	Sugar phosphate permease
51	b2579	*yfiD*	pyruvate formate lyase subunit (NCBI)	-2.88	-2.12	16130504	COG3445	R	Acid-induced glycyl radical enzyme
52	b4035	*malK*	fused maltose transport subunit, ATP-binding component of ABC superfamily/regulatory protein (NCBI)	-2.87	-1.95	16131861	COG3839	G	ABC-type sugar transport systems, ATPase components
53	b2370	*evgS*	hybrid sensory histidine kinase in two-component regulatory system with EvgA (NCBI)	-2.86	-2.56	16130302	COG3290	T	Signal transduction histidine kinase regulating citrate/malate metabolism
54	b4036	*lamB*	maltoporin precursor (NCBI)	-2.83	-1.80	16131862	COG4580	G	Maltoporin (phage lambda and maltose receptor)
55	b1817	*manX*	fused mannose-specific PTS enzymes: IIA component/IIB component (NCBI)	-2.81	-2.64	16129771	COG3444	G	Phosphotransferase system, mannose/fructose/N-acetylgalactosamine-specific component IIB
56	b2276	*nuoN*	NADH:ubiquinone oxidoreductase, membrane subunit N (RefSeq)	-2.78	-2.56	1.46E+08	COG1007	C	NADH:ubiquinone oxidoreductase subunit 2 (chain N)
57	b3531	*bcsZ*	endo-1,4-D-glucanase (NCBI)	-2.76	-2.69	16131403	COG3405	G	Endoglucanase Y
58	b4068	*yjcH*	conserved inner membrane protein involved in acetate transport (NCBI)	-2.76	-2.06	16131894	COG3162	S	Predicted membrane protein
59	b4254	*argI*	ornithine carbamoyltransferase 1 (NCBI)	-2.73	-2.44	16132076	COG78	E	Ornithine carbamoyltransferase
60	b2277	*nuoM*	NADH dehydrogenase subunit M (NCBI)	-2.73	-2.74	16130212	COG1008	C	NADH:ubiquinone oxidoreductase subunit 4 (chain M)
61	b2037	*rfbX*	predicted polisoprenol-linked O-antigen transporter (NCBI)	-2.73	-2.79	16129977	COG2244	R	Membrane protein involved in the export of O-antigen and teichoic acid
62	b1818	*manY*	mannose-specific enzyme IIC component of PTS (NCBI)	-2.72	-2.81	16129772	COG3715	G	Phosphotransferase system, mannose/fructose/N-acetylgalactosamine-specific component IIC
63	b2028	*ugd*	UDP-glucose 6-dehydrogenase (NCBI)	-2.71	-2.41	16129969	COG1004	M	Predicted UDP-glucose 6-dehydrogenase
64	b2033	*wbbJ*	predicted acyl transferase (NCBI)	-2.70	-2.40	16129973	COG110	R	Acetyltransferase (isoleucine patch superfamily)
65	b0486	*ybaT*	predicted transporter (NCBI)	-2.66	-2.68	16128470	COG1113	E	Gamma-aminobutyrate permease and related permeases
66	b2278	*nuoL*	NADH dehydrogenase subunit L (NCBI)	-2.65	-2.76	16130213	COG1009	CP	NADH:ubiquinone oxidoreductase subunit 5 (chain L)/Multisubunit Na+/H+ antiporter, MnhA subunit
67	b2601	*aroF*	3-deoxy-D-arabino-heptulosonate-7-phosphate synthase, tyrosine-repressible (NCBI)	-2.63	-2.56	16130522	COG722	E	3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase
68	b3627	*rfaI*	UDP-D-galactose:(glucosyl)lipopolysaccharide-alpha-1,3-D-galactosyltransferase (NCBI)	-2.61	-2.43	16131498	COG1442	M	Lipopolysaccharide biosynthesis proteins, LPS:glycosyltransferases
69	b2036	*glf*	UDP-galactopyranose mutase, FAD/NAD(P)-binding (NCBI)	-2.61	-2.18	16129976	COG562	M	UDP-galactopyranose mutase
70	b4108	*phnA*	hypothetical protein (NCBI)	-2.61	-2.45	16131934	COG2824	P	Uncharacterized Zn-ribbon-containing protein involved in phosphonate metabolism
71	b3744	*asnA*	asparagine synthetase AsnA (NCBI)	-2.60	-2.39	16131612	COG2502	E	Asparagine synthetase A
72	b2001	*b2001*	orf, hypothetical protein (VIMSS)	-2.60	-2.58	90111368			
73	b2838	*lysA*	diaminopimelate decarboxylase, PLP-binding (NCBI)	-2.56	-2.25	16130742	COG19	E	Diaminopimelate decarboxylase
74	b3629	*rfaS*	lipopolysaccharide core biosynthesis protein (NCBI)	-2.54	-2.38	16131500			
75	b3418	*malT*	transcriptional regulator MalT (NCBI)	-2.53	-2.34	16131294	COG2909	K	ATP-dependent transcriptional regulator
76	b1415	*aldA*	aldehyde dehydrogenase A, NAD-linked (NCBI)	-2.51	-2.25	16129376	COG1012	C	NAD-dependent aldehyde dehydrogenases

Top 100 down-regulated genes from microarray GEO #GSE53138.

Rank	Locus Tag	Gene name	Gene description	Mean Log Ratio	z score	GI#	COG	COGFun	COG Description
77	b2497	*uraA*	uracil transporter (NCBI)	-2.49	-2.43	16130422	COG2233	F	Xanthine/uracil permeases
78	b3751	*rbsB*	D-ribose transporter subunit (NCBI)	-2.49	-2.45	16131619	COG1879	G	ABC-type sugar transport system, periplasmic component
79	b2094	*gatA*	galactitol-specific enzyme IIA component of PTS (NCBI)	-2.47	-2.30	16130032	COG1762	GT	Phosphotransferase system mannitol/fructose-specific IIA domain (Ntr-type)
80	b3507	*dctR*	protein involved in metabolism of C4-dicarboxylates (Katherine Huang)	-2.47	-2.29	16131379	COG2197	TK	Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain
81	b2600	*tyrA*	fused chorismate mutase T/prephenate dehydrogenase (NCBI)	-2.46	-2.39	16130521	COG287	E	Prephenate dehydrogenase
82	b1656	*sodB*	superoxide dismutase, Fe (NCBI)	-2.46	-2.77	16129614	COG605	P	Superoxide dismutase
83	b4015	*aceA*	isocitrate lyase (NCBI)	-2.45	-2.41	16131841	COG2224	C	Isocitrate lyase
84	b0594	*entE*	2,3-dihydroxybenzoate-AMP ligase component of enterobactin synthase multienzyme complex (NCBI)	-2.44	-1.88	16128577	COG1021	Q	Peptide arylation enzymes
85	b0596	*entA*	2,3-dihydroxybenzoate-2,3-dehydrogenase (NCBI)	-2.44	-2.62	16128579	COG1028	IQR	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)
86	b4348	*hsdS*	specificity determinant for hsdM and hsdR (NCBI)	-2.41	-2.60	16132169	COG732	V	Restriction endonuclease S subunits
87	b3625	*rfaY*	lipopolysaccharide core biosynthesis protein (NCBI)	-2.38	-2.09	16131496			
88	b2095	*gatZ*	D-tagatose 1,6-bisphosphate aldolase 2, subunit (NCBI)	-2.37	-2.35	16130033	COG4573	G	Predicted tagatose 6-phosphate kinase
89	b2279	*nuoK*	NADH dehydrogenase subunit K (NCBI)	-2.37	-2.79	16130214	COG713	C	NADH:ubiquinone oxidoreductase subunit 11 or 4L (chain K)
90	b2029	*gnd*	6-phosphogluconate dehydrogenase (NCBI)	-2.33	-2.79	16129970	COG362	G	6-phosphogluconate dehydrogenase
91	b3540	*dppF*	dipeptide transporter (NCBI)	-2.32	-2.45	16131412	COG4608	E	ABC-type oligopeptide transport system, ATPase component
92	b2024	*hisA*	N-(5'-phospho-L-ribosyl-formimino)-5-amino-1-(5'- phosphoribosyl)-4-imidazolecarboxamide isomerase (VIMSS)	-2.31	-2.32	90111374	COG106	E	Phosphoribosylformimino-5-aminoimidazole carboxamide ribonucleotide (ProFAR) isomerase
93	b4519	*icdC*		-2.30	-2.44				
94	b0929	*ompF*	outer membrane porin 1a (Ia;b;F) (NCBI)	-2.28	-2.62	16128896	COG3203	M	Outer membrane protein (porin)
95	b0273	*argF*	CP4-6 prophage; ornithine carbamoyltransferase 2, chain F (NCBI)	-2.28	-2.29	16128258	COG78	E	Ornithine carbamoyltransferase
96	b2025	*hisF*	imidazole glycerol phosphate synthase subunit HisF (NCBI)	-2.28	-2.33	16129966	COG107	E	Imidazoleglycerol-phosphate synthase
97	b3624	*rfaZ*	lipopolysaccharide core biosynthesis protein (NCBI)	-2.27	-2.45	16131495			
98	b2096	*gatY*	tagatose-bisphosphate aldolase 1 (VIMSS)	-2.26	-2.32	90111384	COG191	G	Fructose/tagatose bisphosphate aldolase
99	b3870	*glnA*	glutamine synthetase (NCBI)	-2.26	-2.79	16131710	COG174	E	Glutamine synthetase
100	b3416	*malQ*	4-alpha-glucanotransferase (amylomaltase) (NCBI)	-2.25	-2.59	16131292	COG1640	G	4-alpha-glucanotransferase