Supplemental Tables

Each of the tables below lists all genes that were upregulated or downregulated by a factor of 2^2 or greater in at least one of a set of replicate samples. Each table contains either upregulated or downregulated genes and contains all such genes for one set of samples. Other sample sets are included for comparison in some cases. All samples were normalized to the average of two samples of MG1655 grown to an OD of ~0.4, except for the pulldown samples, which were normalized to the pulldown control samples, and the UV treated samples, where were normalized to the membrane anchor expressing samples. Nomenclature: MA = cells expressing the eCPX-strep tag membrane anchor, SN = supernatant of the SOS pulldown cells, SNC = supernatant of the control pulldown cells, PDC = control pulldown cells, PD = SOS pulldown cells, UV = UV treated cells. Genes in boldface indicate that the gene was noted as regulated by LexA in Courcelle 2001 (see paper references). See the Materials and Methods for details of sample generation and harvesting.

Table S1: Upregulated membrane anchor genes

Name	Description	MA1	MA2
	Hypothetical and predicted genes		
ycgF	predicted FAD-binding phosphodiesterase (NCBI)	3.02	1.14
ydcI	putative transcriptional regulator LYSR-type (VIMSS)	2.25	2.02
yejG	hypothetical protein (NCBI)	2.77	2.14
	Metabolism		
sdhC	succinate dehydrogenase cytochrome b556 large membrane subunit (NCBI)	2.43	2.41
sdhD	succinate dehydrogenase cytochrome b556 small membrane subunit (NCBI)	1.96	2.10
	Other		
cusF	periplasmic copper-binding protein (NCBI)	3.43	-1.57
	Transport		
cusA	copper/silver efflux system, membrane component (NCBI)	2.78	0.08
cusB	copper/silver efflux system, membrane fusion protein (NCBI)	3.21	-0.03
oppB	oligopeptide permease ABC transporter membrane protein (NCBI)	2.50	-0.47
oppC	oligopeptide transporter subunit (NCBI)	2.95	-0.25
oppD	oligopeptide transporter ATP-binding component (NCBI)	2.75	-0.21
oppF	oligopeptide transporter subunit (NCBI)	2.62	-0.25

Table S2: Downregulated membrane anchor genes

Name	Description	MA1	MA2
	Hypothetical and predicted genes		
b1593	orf, hypothetical protein (VIMSS)	-2.36	-1.79
ybhC	predicted pectinesterase (NCBI)	-3.71	-3.43
ycgK	hypothetical protein (NCBI)	-4.58	-0.44
yebA	orf, hypothetical protein (VIMSS)	-2.78	0.40
yebL	putative adhesin (VIMSS)	-4.04	-0.05
yjgF	orf, hypothetical protein (VIMSS)	-2.13	0.32
yodA	conserved metal-binding protein (NCBI)	-6.46	-0.13
yodB	putative cytochrome (VIMSS)	-4.41	0.38

Iron chelation and transport			
feoA	ferrous iron transport protein A (NCBI)	-2.17	-1.98
Metabolism			
argA	N-acetylglutamate synthase (NCBI)	-2.76	0.97
argB	acetylglutamate kinase (RefSeq)	-2.50	0.83
argC	N-acetyl-gamma-glutamyl-phosphate reductase (NCBI)	-3.13	0.82
argD	bifunctional acetylornithine aminotransferase/ succinyldiaminopimelate aminotransferase (NCBI)	-2.32	0.78
argF	CP4-6 prophage; ornithine carbamoyltransferase 2, chain F (NCBI)	-2.64	0.98
argG	argininosuccinate synthase (NCBI)	-2.10	0.52
argI	ornithine carbamoyltransferase 1 (NCBI)	-3.81	0.87
carB	carbamoyl-phosphate synthase large subunit (NCBI)	-2.96	0.43
cysH	phosphoadenosine phosphosulfate reductase (NCBI)	-3.49	0.49
metE	5-methyltetrahydropteroyltriglutamate-- homocysteine methyltransferase (NCBI)	-2.19	0.32
nirB	nitrite reductase, large subunit, NAD(P)H-binding (NCBI)	-3.98	-3.70
nirD	nitrite reductase small subunit (NCBI)	-2.76	-3.23
pyrB	aspartate carbamoyltransferase catalytic subunit (NCBI)	-3.17	0.21
pyrI	aspartate carbamoyltransferase regulatory subunit (NCBI)	-3.21	0.28
Other			
cueO	multicopper oxidase (laccase) (NCBI)	-1.38	-2.11
GadE	acid-responsive regulator of gadA and gadBC (Katherine Huang)	-2.05	-1.41
ykgM	50S ribosomal protein L31 (NCBI)	-7.43	0.15
ykgO	rpmJ (L36) paralog (NCBI)	-6.87	0.08
Stress response			
yfiD	pyruvate formate lyase subunit (NCBI)	-1.87	-2.14
Transport			
artJ	arginine transporter subunit (NCBI)	-2.58	0.76
codB	cytosine transporter (NCBI)	-2.09	0.48
copA	copper transporter (NCBI)	-1.53	-2.00
cusC	copper/silver efflux system, outer membrane component (NCBI)	-2.22	-3.13
focA	formate transporter (NCBI)	-2.05	-2.02
fruB	fused fructose-specific PTS enzymes: IIA component/HPr component (NCBI)	-0.53	-2.24
narK	nitrate/nitrite transporter (NCBI)	-2.19	-1.99
nikA	nickel transporter subunit (NCBI)	-2.20	-0.64
uraA	uracil transporter (NCBI)	-2.03	0.33
znuB	high-affinity zinc transporter membrane component (NCBI)	-2.06	0.10
znuC	high-affinity zinc transporter ATPase (NCBI)	-2.42	0.07

Table S3: Upregulated control supernatant genes

Name	Description	SN1	SN2	SN3	SNC1	SNC2	SNC3
DNA synthesis							
nrdD	anaerobic ribonucleoside triphosphate reductase (NCBI)	2.07	1.99	1.53	1.72	2.05	1.44
nrdG	anaerobic ribonucleotide reductase activating protein (NCBI)	2.23	2.22	1.32	2.17	2.19	1.51
Hypothetical and predicted genes							
b1593	orf, hypothetical protein (VIMSS)	2.27	2.95	2.22	2.20	3.33	2.44
b1754	orf, hypothetical protein (VIMSS)	2.25	2.05	2.42	1.75	2.05	1.70
b1757	putative thiosulfate sulfur transferase (VIMSS)	3.72	3.70	3.54	3.04	3.71	2.90
b2343	orf, hypothetical protein (VIMSS)	3.61	3.67	2.38	3.35	3.80	3.28

b4140	orf, hypothetical protein (VIMSS)	1.52	2.00	1.52	1.99	2.19	1.83
ttcC	Pseudogene	0.88	1.67	1.35	0.96	2.45	1.64
yaaJ	predicted transporter (NCBI)	1.10	1.66	1.68	0.90	2.30	1.02
ybgE	conserved inner membrane protein (NCBI)	1.59	1.61	1.29	2.21	2.06	2.63
ybgT	hypothetical protein (NCBI)	1.24	1.44	1.34	1.59	2.03	2.36
ybjM	predicted inner membrane protein (NCBI)	2.11	2.67	2.38	1.57	2.55	2.25
ycbJ	hypothetical protein (NCBI)	2.53	2.85	2.93	2.32	3.05	1.82
yceP	orf, hypothetical protein (VIMSS)	3.38	3.68	2.83	3.09	3.89	3.33
ydeH	hypothetical protein (NCBI)	1.22	1.14	1.04	2.15	0.97	1.23
ydfZ	hypothetical protein (NCBI)	2.42	2.42	2.31	1.52	2.72	1.95
ydjX	orf, hypothetical protein (VIMSS)	2.50	3.72	3.83	2.77	4.29	2.59
ydjY	orf, hypothetical protein (VIMSS)	2.99	3.16	3.10	2.85	3.28	2.70
ydjZ	conserved inner membrane protein (NCBI)	3.04	3.10	2.69	2.69	3.06	2.69
yecH	hypothetical protein (NCBI)	3.01	3.25	3.17	2.70	3.92	2.70
yedL	predicted acyltransferase (NCBI)	0.46	1.61	0.29	0.47	2.74	2.36
yedX	hypothetical protein (NCBI)	-0.29	-0.26	0.11	2.01	0.19	-0.22
yfbS	predicted transporter (NCBI)	2.36	2.70	2.56	2.33	3.21	2.21
yfcC	putative S-transferase (VIMSS)	2.51	2.87	2.90	1.98	2.97	1.94
ygaW	predicted inner membrane protein (NCBI)	0.34	1.28	2.46	0.43	2.65	3.30
ygcN	orf, hypothetical protein (VIMSS)	1.85	2.23	2.40	1.42	2.83	2.10
ygcO	orf, hypothetical protein (VIMSS)	1.54	1.84	2.08	0.94	2.26	1.74
ygiP	predicted DNA-binding transcriptional regulator (NCBI)	1.61	2.86	3.48	1.67	3.82	2.00
yhbS	predicted acyltransferase with acyl-CoA N-acyltransferase domain (NCBI)	2.01	2.25	2.22	1.77	2.54	1.94
yhbT	predicted lipid carrier protein (NCBI)	1.50	1.80	1.20	1.42	2.18	1.52
yhbU	predicted peptidase (collagenase-like) (NCBI)	2.08	2.33	2.85	1.94	2.43	1.84
yhcC	predicted Fe-S oxidoreductase (NCBI)	0.96	1.48	2.30	0.95	2.31	0.91
yhgG	predicted DNA-binding transcriptional regulator (NCBI)	2.12	2.24	2.14	1.67	2.56	2.28
yiaI	predicted hydrogenase, 4Fe-4S ferredoxin-type component (NCBI)	2.60	3.06	2.94	1.98	3.59	2.16
yjaI	orf, hypothetical protein (VIMSS)	0.12	0.11	0.16	3.55	0.50	0.13
yjiD	orf, hypothetical protein (VIMSS)	1.42	1.85	2.02	0.89	2.08	0.82
yjiM	orf, hypothetical protein (VIMSS)	3.59	3.51	2.58	2.56	2.22	1.35
yjjB	conserved inner membrane protein (RefSeq)	1.59	2.14	2.18	1.36	2.33	1.66
yjjI	hypothetical protein (NCBI)	2.84	3.21	3.08	1.80	3.24	2.09
yjjP	putative structural protein (VIMSS)	1.62	2.24	2.65	1.36	2.61	1.44
yjjW	predicted pyruvate formate lyase activating enzyme (NCBI)	2.74	2.91	3.00	2.10	2.83	2.15
ynaF	putative filament protein (VIMSS)	2.43	2.62	2.06	1.94	2.90	2.16
yneM	hypothetical protein (RefSeq)	1.73	1.98	1.34	2.06	1.64	1.68
ynfG	oxidoreductase, Fe-S subunit (NCBI)	3.28	3.28	1.64	2.61	2.07	1.00
ynfM	predicted transporter (NCBI)	-0.55	0.71	1.16	-0.85	2.16	0.99
ynjA	hypothetical protein (NCBI)	1.81	2.04	1.78	1.59	2.11	1.73
yoeG	Pseudogene (MicrobesOnline)	1.90	2.51	2.45	2.09	2.60	1.97
yqfA	predicted oxidoreductase, inner membrane subunit (NCBI)	2.25	2.37	1.55	1.96	2.47	2.00
yqgA	predicted inner membrane protein (NCBI)	0.79	1.48	1.90	0.78	2.34	1.14
	Metabolism						
ansB	periplasmic L-asparaginase II (NCBI)	3.11	3.08	2.54	2.01	2.24	1.59
aspA	aspartate ammonia-lyase (aspartase) (VIMSS)	1.62	2.62	2.87	1.30	3.01	1.86
cysG	fused siroheme synthase 1,3-dimethyluroporphyriongen III dehydrogenase and siroheme ferrochelatase/uroporphyrinogen methyltransferase (NCBI)	0.21	1.28	1.88	-0.14	2.54	1.80

dmsA	anaerobic dimethyl sulfoxide reductase subunit A (VIMSS)	3.30	3.69	2.78	2.47	3.28	2.73
dmsB	dimethyl sulfoxide reductase, anaerobic, subunit B (NCBI)	3.93	4.23	3.27	3.16	3.98	3.15
dmsC	dimethyl sulfoxide reductase, anaerobic, subunit C (NCBI)	3.85	4.13	2.78	3.09	3.90	2.89
edd	phosphogluconate dehydratase (NCBI)	1.49	1.89	1.93	1.55	2.12	1.37
frdA	fumarate reductase (NCBI)	3.42	3.62	3.55	2.82	3.53	2.99
frdB	fumarate reductase (anaerobic), Fe-S subunit (NCBI)	4.18	4.21	3.28	3.62	4.12	3.71
frdC	fumarate reductase subunit C (NCBI)	4.45	4.46	4.43	3.86	4.55	4.04
frdD	fumarate reductase subunit D (NCBI)	5.00	5.04	4.30	4.41	4.85	4.38
fumB	anaerobic class I fumarate hydratase (fumarase B) (NCBI)	5.44	5.25	3.67	4.11	3.03	2.33
gldA	glycerol dehydrogenase, (NAD) (VIMSS)	4.36	4.22	3.81	3.62	4.29	3.46
glnK	nitrogen assimilation regulatory protein for GlnL, GlnE, and AmtB (NCBI)	2.45	3.12	0.90	-0.15	4.09	1.60
hcr	HCP oxidoreductase, NADH-dependent (NCBI)	1.30	1.63	1.78	0.93	2.01	1.09
hybA	hydrogenase 2 4Fe-4S ferredoxin-type component (NCBI)	3.78	3.86	3.29	2.90	3.13	2.67
hybB	predicted hydrogenase 2 cytochrome b type component (NCBI)	2.90	3.02	2.30	1.80	2.20	1.63
hybO	hydrogenase 2, small subunit (NCBI)	3.40	3.66	3.65	2.63	3.39	2.27
hypA	protein involved in nickel insertion into hydrogenases 3 (NCBI)	2.09	2.59	2.74	1.48	2.84	1.84
hypB	GTP hydrolase involved in nickel liganding into hydrogenases (NCBI)	2.77	3.21	2.85	1.84	3.42	2.37
hypC	protein required for maturation of hydrogenases 1 and 3 (NCBI)	2.79	3.14	2.83	1.97	3.15	2.50
hypD	protein required for maturation of hydrogenases (NCBI)	2.59	2.74	2.14	1.82	2.70	2.11
hypE	carbamoyl phosphate phosphatase, hydrogenase 3 maturation protein (RefSeq)	2.06	2.28	2.39	1.40	2.27	1.54
nac	DNA-binding transcriptional dual regulator of nitrogen assimilation (NCBI)	1.49	2.20	0.45	0.18	3.51	1.18
napA	nitrate reductase, periplasmic, large subunit (NCBI)	0.50	1.87	3.10	-0.24	2.94	2.44
napB	cytochrome c-type protein (VIMSS)	0.91	2.49	3.31	0.23	3.36	2.68
napC	nitrate reductase, cytochrome c-type, periplasmic (NCBI)	1.37	2.34	2.97	1.00	2.97	2.17
napD	assembly protein for periplasmic nitrate reductase (NCBI)	-0.29	1.17	2.23	-0.61	2.24	1.85
napF	ferredoxin-type protein, predicted role in electron transfer to periplasmic nitrate reductase (NapA) (NCBI)	0.02	1.56	2.25	-0.42	2.84	1.76
napG	quinol dehydrogenase periplasmic component (NCBI)	0.72	1.89	3.06	0.26	2.64	2.17
napH	quinol dehydrogenase membrane component (NCBI)	0.83	2.30	3.46	0.23	3.21	2.48
narG	nitrate reductase 1, alpha subunit (NCBI)	1.18	1.73	2.57	0.06	3.40	2.23
narH	nitrate reductase 1, beta (Fe-S) subunit (NCBI)	2.29	3.03	3.83	1.43	4.51	3.24
narI	nitrate reductase 1, gamma (cytochrome b(NR)) subunit (NCBI)	2.24	2.86	3.02	1.59	4.34	2.75
narJ	molybdenum-cofactor-assembly chaperone subunit (delta subunit) of nitrate reductase 1 (NCBI)	2.42	3.14	3.58	1.66	4.58	3.18
nirB	nitrite reductase, large subunit, NAD(P)H-binding (NCBI)	-1.48	0.91	1.93	-2.22	2.22	1.82
nirD	nitrite reductase small subunit (NCBI)	-0.66	1.92	2.87	-1.51	3.23	2.67
nrfA	nitrite reductase, formate-dependent, cytochrome (NCBI)	0.99	1.88	3.03	0.06	2.90	1.33
pflA	pyruvate formate lyase activating enzyme 1 (NCBI)	1.79	1.73	1.72	1.52	1.56	2.14
pta	phosphate acetyltransferase (NCBI)	2.43	2.32	2.61	2.11	2.35	2.13
pykA	pyruvate kinase (NCBI)	2.18	2.30	1.72	1.98	2.38	1.93
ynfE	oxidoreductase subunit (NCBI)	4.00	3.91	2.81	3.26	2.70	1.98
ynfF	oxidoreductase subunit (RefSeq)	3.70	3.70	2.11	2.84	2.24	1.08
Other							

cusF	periplasmic copper-binding protein (NCBI)	-1.78	-1.99	-1.79	5.92	-1.69	-2.05
hlyE	hemolysin E (VIMSS)	3.17	3.31	2.96	2.65	3.39	2.33
pepE	peptidase E (NCBI)	3.67	3.69	3.30	3.05	3.78	3.10
slp	outer membrane protein induced after carbon starvation (VIMSS)	1.83	2.00	2.01	2.13	1.53	1.70
ycgV	predicted adhesin (NCBI)	1.66	2.05	1.63	1.47	2.45	1.80
yehD	predicted fimbrial-like adhesin protein (NCBI)	1.77	1.79	1.85	2.40	1.86	1.33
yhfL	conserved secreted peptide (NCBI)	0.51	1.18	1.49	0.25	2.54	1.46
yliH	hypothetical protein (NCBI)	2.37	2.58	1.54	2.42	3.07	2.19
yqhD	alcohol dehydrogenase, NAD(P)-dependent (NCBI)	2.67	2.73	1.24	1.31	2.48	2.54
	Stress response						
cspH	stress protein, member of the CspA-family (NCBI)	1.46	1.56	0.89	1.94	1.06	2.07
cspI	Qin prophage; cold shock protein (NCBI)	2.04	2.29	1.59	3.20	2.20	2.51
uspG	universal stress protein UP12 (NCBI)	3.02	2.64	2.08	2.91	2.58	2.32
	Transport						
amtB	ammonium transporter (NCBI)	1.62	2.51	1.00	0.63	3.86	1.79
ccmA	ATP binding protein of heme exporter A (VIMSS)	1.40	2.10	2.44	1.09	2.53	1.74
copA	copper transporter (NCBI)	-1.26	-1.48	-1.51	2.04	-1.70	-1.60
cusA	copper/silver efflux system, membrane component (NCBI)	0.07	-0.05	-0.04	6.20	0.10	0.13
cusB	copper/silver efflux system, membrane fusion protein (NCBI)	-0.14	-0.25	-0.11	7.45	-0.36	0.05
cusC	copper/silver efflux system, outer membrane component (NCBI)	-3.06	-3.20	-3.00	4.62	-2.92	-3.04
cusR	DNA-binding response regulator in two-component regulatory system with CusS (NCBI)	-0.08	-0.29	-0.25	3.10	-0.75	-0.20
cusS	sensory histidine kinase in two-component regulatory system with CusR, senses copper ions (NCBI)	-0.49	-0.75	-0.69	2.74	-1.07	-0.82
dcuB	C4-dicarboxylate antiporter (NCBI)	5.57	5.84	4.29	5.05	3.99	3.02
dcuC	anaerobic C4-dicarboxylate transport (NCBI)	4.08	4.52	4.61	3.37	4.79	3.99
fruA	fused fructose-specific PTS enzymes: IIBcomponent/IIC components (NCBI)	1.95	2.28	1.12	1.80	2.63	2.19
narK	nitrate/nitrite transporter (NCBI)	0.93	1.35	2.40	0.70	2.81	1.67
nirC	nitrite transporter (NCBI)	0.23	3.18	4.07	-0.75	4.52	3.87
ompW	outer membrane protein W (NCBI)	1.79	1.67	1.56	2.27	1.33	1.59
oppB	oligopeptide permease ABC transporter membrane protein (NCBI)	2.60	2.86	2.85	2.77	2.88	2.91
oppC	oligopeptide transporter subunit (NCBI)	2.96	3.17	3.09	2.97	3.20	3.13
oppD	oligopeptide transporter ATP-binding component (NCBI)	3.03	3.21	3.13	2.96	3.32	3.18
oppF	oligopeptide transporter subunit (NCBI)	3.29	3.42	2.94	3.30	3.57	3.56
pheP	phenylalanine transporter (NCBI)	0.05	-0.23	-0.15	2.17	-0.50	-0.19
tppB	putative tripeptide transporter permease (NCBI)	0.50	1.57	1.38	0.89	2.03	2.75

Table S4: Downregulated control supernatant genes

Name	Description	SN1	SN2	SN3	SNC1	SNC2	SNC3
	Hypothetical and predicted genes						
efeU	Pseudogene	-1.64	-2.18	-1.93	-1.83	-2.44	-1.90
nmpC	DLP12 prophage; truncated outer membrane porin (pseudogene) (RefSeq)	-2.51	-2.53	-1.93	-2.86	-2.98	-3.04
pqqL	predicted peptidase (NCBI)	-2.52	-2.57	-2.09	-2.32	-2.51	-2.30
ybdB	hypothetical protein (NCBI)	-2.45	-2.66	-1.47	-2.16	-2.19	-1.59
ybiI	hypothetical protein (NCBI)	-2.21	-2.16	-2.62	-2.34	-1.69	-2.36
ybiX	putative enzyme (VIMSS)	-3.94	-4.03	-3.68	-3.71	-3.91	-3.97

ycdB	hypothetical protein (NCBI)	-2.95	-3.03	-2.77	-2.89	-3.22	-3.14
ycdO	hypothetical protein (NCBI)	-3.33	-3.61	-2.96	-3.23	-3.67	-3.55
yceA	hypothetical protein (NCBI)	-1.82	-1.99	-2.10	-1.55	-2.36	-1.77
yceI	hypothetical protein (NCBI)	-2.56	-2.29	-2.53	-2.00	-1.85	-1.88
yciF	hypothetical protein (NCBI)	-2.31	-2.27	-2.51	-2.40	-2.44	-2.49
yddA	fused predicted multidrug transporter subunits of ABC superfamily: membrane component/ATP-binding component (NCBI)	-2.00	-2.03	-1.17	-1.44	-2.29	-1.44
yddB	predicted porin protein (NCBI)	-2.89	-2.97	-2.74	-2.47	-2.83	-2.67
yicE	predicted transporter (NCBI)	0.49	-0.33	-0.01	0.53	-2.64	0.08
yieG	predicted inner membrane protein (NCBI)	-0.41	-1.03	-0.89	-0.12	-2.01	-0.75
yifK	predicted transporter (NCBI)	-2.26	-2.23	-2.13	-1.89	-2.43	-2.16
yjcD	predicted permease (NCBI)	-0.49	-0.98	-0.33	-0.04	-2.24	-1.10
ylaC	orf, hypothetical protein (VIMSS)	-1.66	-2.08	-1.70	-2.15	-2.56	-2.41
	Iron chelation and transport						
cirA	ferric iron-catecholate outer membrane transporter (NCBI)	-2.96	-3.12	-2.39	-2.37	-2.58	-2.38
entA	2,3-dihydroxybenzoate-2,3-dehydrogenase (NCBI)	-2.55	-2.78	-1.88	-2.45	-2.30	-1.83
entB	isochorismatase (NCBI)	-2.79	-2.82	-2.00	-2.42	-2.36	-1.97
entC	isochorismate synthase (NCBI)	-1.99	-2.38	-1.83	-2.13	-2.59	-1.84
entD	phosphopantetheinyltransferase component of enterobactin synthase multienzyme complex (NCBI)	-2.38	-2.55	-1.71	-1.82	-2.13	-1.78
entE	2,3-dihydroxybenzoate-AMP ligase component of enterobactin synthase multienzyme complex (NCBI)	-2.75	-3.01	-2.09	-2.67	-2.75	-2.68
fiu	predicted iron outer membrane transporter (NCBI)	-5.24	-5.30	-5.01	-5.11	-4.79	-5.46
	Metabolism						
aceA	isocitrate lyase (NCBI)	-2.82	-2.96	-3.21	-2.49	-2.83	-2.85
aceB	malate synthase (NCBI)	-2.28	-2.52	-2.73	-2.14	-2.72	-2.86
aceE	pyruvate dehydrogenase subunit E1 (NCBI)	-2.73	-2.60	-1.84	-1.65	-2.21	-2.02
aceF	dihydrolipoamide acetyltransferase (NCBI)	-2.47	-2.44	-1.23	-1.52	-2.03	-1.60
aceK	bifunctional isocitrate dehydrogenase kinase/phosphatase protein (NCBI)	-2.98	-3.13	-3.12	-2.53	-3.24	-3.60
acs	acetyl-coenzyme A synthetase (NCBI)	-2.94	-2.78	-2.98	-3.09	-2.80	-2.46
aldA	aldehyde dehydrogenase A, NAD-linked (NCBI)	-2.95	-2.84	-3.03	-3.05	-3.04	-3.05
argA	N-acetylglutamate synthase (NCBI)	-0.90	-0.37	0.04	-1.03	0.36	-2.11
argC	N-acetyl-gamma-glutamyl-phosphate reductase (NCBI)	-0.72	0.10	0.10	-0.94	0.99	-2.05
betA	choline dehydrogenase (NCBI)	-2.47	-2.33	-2.39	-2.09	-2.13	-2.30
betB	betaine aldehyde dehydrogenase, NAD-dependent (NCBI)	-2.70	-2.65	-2.49	-2.38	-2.61	-2.69
betI	probably transcriptional repressor of bet genes (VIMSS)	-2.56	-2.60	-2.63	-2.47	-2.68	-2.59
carA	carbamoyl-phosphate synthase small subunit (NCBI)	-3.25	-2.86	-1.62	-2.80	-2.13	-3.90
carB	carbamoyl-phosphate synthase large subunit (NCBI)	-3.17	-2.93	-2.17	-2.78	-2.34	-3.27
codA	cytosine deaminase (NCBI)	-1.88	-1.95	-1.42	-1.84	-2.08	-2.06
cyoA	cytochrome o ubiquinol oxidase subunit II (NCBI)	-2.86	-3.08	-3.01	-2.47	-2.90	-3.04
cyoB	cytochrome o ubiquinol oxidase subunit I (NCBI)	-3.49	-3.43	-3.41	-3.13	-3.29	-3.47
cyoC	cytochrome o ubiquinol oxidase subunit III (NCBI)	-3.69	-3.51	-3.14	-3.33	-3.28	-3.35
cyoD	cytochrome o ubiquinol oxidase subunit IV (NCBI)	-3.57	-3.47	-3.38	-3.14	-2.87	-2.95
cyoE	protoheme IX farnesyltransferase (NCBI)	-3.13	-2.94	-2.76	-2.79	-2.31	-2.33
cysM	cysteine synthase B (O-acetylserine sulfhydrolase B) (NCBI)	-0.07	-0.47	0.01	0.31	-2.03	-0.75
eutB	ethanolamine ammonia-lyase, heavy chain (VIMSS)	-1.78	-1.75	-1.73	-1.72	-1.61	-2.15
gcd	glucose dehydrogenase (NCBI)	-2.04	-2.07	-2.30	-1.91	-2.02	-2.45
gltA	citrate synthase (NCBI)	-2.10	-2.17	-2.09	-1.94	-2.16	-2.28

guaB	inositol-5-monophosphate dehydrogenase (NCBI)	-0.89	-1.49	-1.19	-0.44	-2.45	-1.41
icd	isocitrate dehydrogenase (NCBI)	-1.40	-1.15	-1.03	-2.11	-0.92	-1.05
ilvB	acetolactate synthase large subunit (NCBI)	-1.14	-1.02	-0.84	-2.27	-1.31	-1.18
ilvC	ketol-acid reductoisomerase (NCBI)	-1.31	-1.40	-0.85	-1.31	-2.24	-1.60
leuB	3-isopropylmalate dehydrogenase (VIMSS)	-1.30	-1.37	-1.29	-2.13	-1.91	-2.13
leuC	isopropylmalate isomerase large subunit (NCBI)	-1.65	-1.58	-1.82	-2.28	-2.11	-2.15
lldD	L-lactate dehydrogenase, FMN-linked (NCBI)	-2.01	-1.92	-1.79	-2.07	-1.83	-2.11
mdh	malate dehydrogenase (NCBI)	-2.02	-1.85	-2.09	-2.14	-1.56	-1.41
mqo	malate:quinone oxidoreductase (NCBI)	-1.93	-1.89	-1.64	-2.04	-1.95	-2.31
ndk	nucleoside diphosphate kinase (NCBI)	-1.77	-2.21	-1.87	-1.67	-2.68	-2.15
nirB	nitrite reductase, large subunit, NAD(P)H-binding (NCBI)	-1.48	0.91	1.93	-2.22	2.22	1.82
pdhR	transcriptional regulator of pyruvate dehydrogenase complex (NCBI)	-0.22	-1.72	-1.97	-0.37	-2.24	-0.94
purB	adenylosuccinate lyase (NCBI)	-0.72	-1.04	-0.60	-0.70	-2.31	-1.39
purC	phosphoribosylaminoimidazole-succinocarboxamidesynthase (NCBI)	0.57	-0.09	0.38	0.66	-2.25	-0.47
purD	phosphoribosylamine--glycine ligase (NCBI)	-0.94	-1.67	-0.94	-1.20	-2.82	-2.63
purH	bifunctionalphosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase (NCBI)	-0.44	-1.19	-0.60	-0.75	-2.79	-1.56
purL	phosphoribosylformylglycinamidine synthase (NCBI)	-0.48	-1.34	-1.16	-0.26	-2.70	-2.76
purM	phosphoribosylaminoimidazole synthetase (NCBI)	0.97	0.20	0.61	1.02	-2.03	0.12
purT	phosphoribosylglycinamide formyltransferase 2 (NCBI)	0.17	-0.63	-0.96	0.40	-2.63	-0.71
pyrB	aspartate carbamoyltransferase catalytic subunit (NCBI)	-1.96	-1.06	-1.26	-3.14	-0.42	-1.32
pyrC	dihydroorotase (NCBI)	-1.15	-1.45	-1.13	-1.21	-2.21	-1.59
pyrD	dihydroorotate dehydrogenase (NCBI)	-1.25	-1.20	-0.59	-0.90	-2.11	-1.32
pyrI	aspartate carbamoyltransferase regulatory subunit (NCBI)	-2.06	-1.17	-1.77	-3.16	-0.41	-1.18
sdhA	succinate dehydrogenase flavoprotein subunit (NCBI)	-2.69	-2.67	-2.86	-2.80	-3.27	-3.49
sdhB	succinate dehydrogenase, FeS subunit (NCBI)	-2.36	-2.41	-2.42	-2.36	-2.74	-2.58
sdhC	succinate dehydrogenase cytochrome b556 large membrane subunit (NCBI)	-1.58	-1.94	-1.88	-1.89	-2.40	-2.67
sdhD	succinate dehydrogenase cytochrome b556 small membrane subunit (NCBI)	-1.90	-2.11	-2.03	-2.30	-2.51	-2.85
sucA	alpha-ketoglutarate decarboxylase (NCBI)	-2.54	-2.58	-2.41	-2.35	-2.33	-2.54
sucB	dihydrolipoamide acetyltransferase (NCBI)	-2.34	-2.38	-2.31	-2.38	-2.18	-2.18
sucC	succinyl-CoA synthetase subunit beta (NCBI)	-2.66	-2.60	-2.38	-2.47	-2.47	-2.54
sucD	succinyl-CoA synthetase subunit alpha (NCBI)	-2.21	-2.14	-1.98	-2.26	-1.71	-1.83
sufC	cysteine desulfurase ATPase component (NCBI)	-2.35	-1.83	-1.91	-2.28	-1.45	-1.40
sufD	component of SufBCD complex (NCBI)	-2.20	-1.78	-2.21	-2.23	-1.36	-1.40
sufS	selenocysteine lyase (NCBI)	-2.18	-1.85	-1.77	-2.38	-1.27	-1.43
thrA	bifunctional aspartokinase I/homeserine dehydrogenase I (NCBI)	-2.47	-2.56	-1.19	-2.05	-2.89	-2.47
thrB	homoserine kinase (NCBI)	-2.20	-2.32	-1.07	-1.89	-2.62	-2.00
thrC	threonine synthase (NCBI)	-2.12	-2.18	-0.91	-1.86	-2.08	-1.29
ynhE	orf, hypothetical protein (VIMSS)	-2.26	-1.89	-2.30	-2.37	-1.40	-1.49
	Other						
cusF	periplasmic copper-binding protein (NCBI)	-1.78	-1.99	-1.79	5.92	-1.69	-2.05
ilvG	Disrupted gene (Ecocyc)	-2.16	-1.96	-0.98	-2.20	-2.02	-1.83
	Stress response						
ompT	DLP12 prophage; outer membrane protease VII (outer membrane protein 3b) (NCBI)	-2.64	-2.32	-2.57	-2.25	-1.95	-2.07
osmY	periplasmic protein (NCBI)	-2.10	-1.90	-2.26	-2.36	-1.88	-1.79
stpA	DNA binding protein, nucleoid-associated (NCBI)	-2.29	-2.65	-2.65	-2.67	-2.89	-2.50

sufA	iron-sulfur cluster assembly scaffold protein (NCBI)	-2.20	-1.79	-2.41	-2.49	-1.45	-1.46
tpx	thiol peroxidase (NCBI)	-2.10	-2.47	-2.14	-1.74	-2.36	-1.76
	Transport						
argT	lysine/arginine/ornithine transporter subunit (NCBI)	-1.42	-0.89	-2.09	-2.41	0.17	-2.42
codB	cytosine transporter (NCBI)	-2.30	-2.73	-1.78	-2.09	-2.97	-2.62
cusC	copper/silver efflux system, outer membrane component (NCBI)	-3.06	-3.20	-3.00	4.62	-2.92	-3.04
hisJ	histidine/lysine/arginine/ornithine transporter subunit (NCBI)	-1.81	-1.43	-1.88	-2.02	-0.79	-2.00
hisM	histidine/lysine/arginine/ornithine transporter subunit (NCBI)	-1.47	-1.17	-1.24	-1.41	-0.70	-2.17
hisQ	histidine/lysine/arginine/ornithine transporter subunit (NCBI)	-1.37	-1.08	-1.26	-1.40	-0.66	-2.18
mprA	DNA-binding transcriptional repressor of microcin B17 synthesis and multidrug efflux (NCBI)	-1.21	-1.40	-0.98	-0.98	-2.00	-1.64
nikA	nickel transporter subunit (NCBI)	-0.41	-0.43	1.68	-2.19	0.21	-0.51
potG	ATP-binding component of putrescine transport system (VIMSS)	-1.12	-1.06	-1.12	-1.37	-0.56	-2.04
uraA	uracil transporter (NCBI)	-2.72	-2.76	-1.99	-2.23	-2.51	-2.71

Table S5: Upregulated supernatant genes

Name	Description	SN1	SN2	SN3	SNC1	SNC2	SNC3
	DNA synthesis						
nrdD	anaerobic ribonucleoside triphosphate reductase (NCBI)	2.07	1.99	1.53	1.72	2.05	1.44
nrdG	anaerobic ribonucleotide reductase activating protein (NCBI)	2.23	2.22	1.32	2.17	2.19	1.51
	Hypothetical and predicted genes						
b1593	orf, hypothetical protein (VIMSS)	2.27	2.95	2.22	2.20	3.33	2.44
b1754	orf, hypothetical protein (VIMSS)	2.25	2.05	2.42	1.75	2.05	1.70
b1757	putative thiosulfate sulfur transferase (VIMSS)	3.72	3.70	3.54	3.04	3.71	2.90
b2343	orf, hypothetical protein (VIMSS)	3.61	3.67	2.38	3.35	3.80	3.28
b4140	orf, hypothetical protein (VIMSS)	1.52	2.00	1.52	1.99	2.19	1.83
yaiE	hypothetical protein (NCBI)	2.17	2.01	1.51	1.77	1.64	1.65
ybjM	predicted inner membrane protein (NCBI)	2.11	2.67	2.38	1.57	2.55	2.25
ycbJ	hypothetical protein (NCBI)	2.53	2.85	2.93	2.32	3.05	1.82
ycdF	orf, hypothetical protein (VIMSS)	2.18	1.61	0.96	1.42	0.92	0.41
yceP	orf, hypothetical protein (VIMSS)	3.38	3.68	2.83	3.09	3.89	3.33
ydfZ	hypothetical protein (NCBI)	2.42	2.42	2.31	1.52	2.72	1.95
ydjX	orf, hypothetical protein (VIMSS)	2.50	3.72	3.83	2.77	4.29	2.59
ydjY	orf, hypothetical protein (VIMSS)	2.99	3.16	3.10	2.85	3.28	2.70
ydjZ	conserved inner membrane protein (NCBI)	3.04	3.10	2.69	2.69	3.06	2.69
yecH	hypothetical protein (NCBI)	3.01	3.25	3.17	2.70	3.92	2.70
yfbS	predicted transporter (NCBI)	2.36	2.70	2.56	2.33	3.21	2.21
yfcC	putative S-transferase (VIMSS)	2.51	2.87	2.90	1.98	2.97	1.94
ygaW	predicted inner membrane protein (NCBI)	0.34	1.28	2.46	0.43	2.65	3.30
ygcN	orf, hypothetical protein (VIMSS)	1.85	2.23	2.40	1.42	2.83	2.10
ygcO	orf, hypothetical protein (VIMSS)	1.54	1.84	2.08	0.94	2.26	1.74
ygiP	predicted DNA-binding transcriptional regulator (NCBI)	1.61	2.86	3.48	1.67	3.82	2.00
yhbS	predicted acyltransferase with acyl-CoA N-acyltransferase domain (NCBI)	2.01	2.25	2.22	1.77	2.54	1.94
yhbU	predicted peptidase (collagenase-like) (NCBI)	2.08	2.33	2.85	1.94	2.43	1.84
yhbV	orf, hypothetical protein (VIMSS)	2.00	1.94	2.36	1.68	1.77	1.73
yhcC	predicted Fe-S oxidoreductase (NCBI)	0.96	1.48	2.30	0.95	2.31	0.91

yhgG	predicted DNA-binding transcriptional regulator (NCBI)	2.12	2.24	2.14	1.67	2.56	2.28
yiaI	predicted hydrogenase, 4Fe-4S ferredoxin-type component (NCBI)	2.60	3.06	2.94	1.98	3.59	2.16
yjiD	orf, hypothetical protein (VIMSS)	1.42	1.85	2.02	0.89	2.08	0.82
yjiL	putative enzyme (VIMSS)	2.92	2.63	1.93	1.84	1.22	0.91
yjiM	orf, hypothetical protein (VIMSS)	3.59	3.51	2.58	2.56	2.22	1.35
yjjB	conserved inner membrane protein (RefSeq)	1.59	2.14	2.18	1.36	2.33	1.66
yjjI	hypothetical protein (NCBI)	2.84	3.21	3.08	1.80	3.24	2.09
yjjP	putative structural protein (VIMSS)	1.62	2.24	2.65	1.36	2.61	1.44
yjjW	predicted pyruvate formate lyase activating enzyme (NCBI)	2.74	2.91	3.00	2.10	2.83	2.15
ynaF	putative filament protein (VIMSS)	2.43	2.62	2.06	1.94	2.90	2.16
ynfG	oxidoreductase, Fe-S subunit (NCBI)	3.28	3.28	1.64	2.61	2.07	1.00
ynhF	hypothetical protein (RefSeq)	2.11	1.94	1.40	1.90	1.72	1.28
ynjA	hypothetical protein (NCBI)	1.81	2.04	1.78	1.59	2.11	1.73
ynjC	fused transporter subunits of ABC superfamily: membrane components (RefSeq)	1.76	1.68	2.29	1.47	1.49	0.98
yoeG	Pseudogene (MicrobesOnline)	1.90	2.51	2.45	2.09	2.60	1.97
yqfA	predicted oxidoreductase, inner membrane subunit (NCBI)	2.25	2.37	1.55	1.96	2.47	2.00
	Metabolism						
ansB	periplasmic L-asparaginase II (NCBI)	3.11	3.08	2.54	2.01	2.24	1.59
aspA	aspartate ammonia-lyase (aspartase) (VIMSS)	1.62	2.62	2.87	1.30	3.01	1.86
caiF	transcriptional regulator of cai operon (VIMSS)	2.01	2.01	1.12	1.48	1.79	1.08
dmsA	anaerobic dimethyl sulfoxide reductase subunit A (VIMSS)	3.30	3.69	2.78	2.47	3.28	2.73
dmsB	dimethyl sulfoxide reductase, anaerobic, subunit B (NCBI)	3.93	4.23	3.27	3.16	3.98	3.15
dmsC	dimethyl sulfoxide reductase, anaerobic, subunit C (NCBI)	3.85	4.13	2.78	3.09	3.90	2.89
frdA	fumarate reductase (NCBI)	3.42	3.62	3.55	2.82	3.53	2.99
frdB	fumarate reductase (anaerobic), Fe-S subunit (NCBI)	4.18	4.21	3.28	3.62	4.12	3.71
frdC	fumarate reductase subunit C (NCBI)	4.45	4.46	4.43	3.86	4.55	4.04
frdD	fumarate reductase subunit D (NCBI)	5.00	5.04	4.30	4.41	4.85	4.38
fumB	anaerobic class I fumarate hydratase (fumarase B) (NCBI)	5.44	5.25	3.67	4.11	3.03	2.33
gldA	glycerol dehydrogenase, (NAD) (VIMSS)	4.36	4.22	3.81	3.62	4.29	3.46
glnK	nitrogen assimilation regulatory protein for GlnL, GlnE, and AmtB (NCBI)	2.45	3.12	0.90	-0.15	4.09	1.60
hyaA	hydrogenase 1, small subunit (NCBI)	3.19	2.58	2.17	1.99	0.80	0.21
hyaB	hydrogenase 1, large subunit (NCBI)	2.73	2.20	1.89	1.83	0.30	0.40
hybA	hydrogenase 2 4Fe-4S ferredoxin-type component (NCBI)	3.78	3.86	3.29	2.90	3.13	2.67
hybB	predicted hydrogenase 2 cytochrome b type component (NCBI)	2.90	3.02	2.30	1.80	2.20	1.63
hybC	hydrogenase 2, large subunit (NCBI)	2.50	2.39	1.99	1.67	2.00	1.10
hybO	hydrogenase 2, small subunit (NCBI)	3.40	3.66	3.65	2.63	3.39	2.27
hypA	protein involved in nickel insertion into hydrogenases 3 (NCBI)	2.09	2.59	2.74	1.48	2.84	1.84
hypB	GTP hydrolase involved in nickel liganding into hydrogenases (NCBI)	2.77	3.21	2.85	1.84	3.42	2.37
hypC	protein required for maturation of hydrogenases 1 and 3 (NCBI)	2.79	3.14	2.83	1.97	3.15	2.50
hypD	protein required for maturation of hydrogenases (NCBI)	2.59	2.74	2.14	1.82	2.70	2.11
hypE	carbamoyl phosphate phosphatase, hydrogenase 3 maturation protein (RefSeq)	2.06	2.28	2.39	1.40	2.27	1.54
nac	DNA-binding transcriptional dual regulator of nitrogen assimilation (NCBI)	1.49	2.20	0.45	0.18	3.51	1.18

napA	nitrate reductase, periplasmic, large subunit (NCBI)	0.50	1.87	3.10	-0.24	2.94	2.44
napB	cytochrome c-type protein (VIMSS)	0.91	2.49	3.31	0.23	3.36	2.68
napC	nitrate reductase, cytochrome c-type, periplasmic (NCBI)	1.37	2.34	2.97	1.00	2.97	2.17
napD	assembly protein for periplasmic nitrate reductase (NCBI)	-0.29	1.17	2.23	-0.61	2.24	1.85
napF	ferredoxin-type protein, predicted role in electron transfer to periplasmic nitrate reductase (NapA) (NCBI)	0.02	1.56	2.25	-0.42	2.84	1.76
napG	quinol dehydrogenase periplasmic component (NCBI)	0.72	1.89	3.06	0.26	2.64	2.17
napH	quinol dehydrogenase membrane component (NCBI)	0.83	2.30	3.46	0.23	3.21	2.48
narG	nitrate reductase 1, alpha subunit (NCBI)	1.18	1.73	2.57	0.06	3.40	2.23
narH	nitrate reductase 1, beta (Fe-S) subunit (NCBI)	2.29	3.03	3.83	1.43	4.51	3.24
narI	nitrate reductase 1, gamma (cytochrome b(NR)) subunit (NCBI)	2.24	2.86	3.02	1.59	4.34	2.75
narJ	molybdenum-cofactor-assembly chaperone subunit (delta subunit) of nitrate reductase 1 (NCBI)	2.42	3.14	3.58	1.66	4.58	3.18
nirD	nitrite reductase small subunit (NCBI)	-0.66	1.92	2.87	-1.51	3.23	2.67
nrfA	nitrite reductase, formate-dependent, cytochrome (NCBI)	0.99	1.88	3.03	0.06	2.90	1.33
nrfB	formate-dependent nitrite reductase; a penta-haeme cytochrome c (VIMSS)	1.04	1.42	2.08	0.17	1.83	1.30
pta	phosphate acetyltransferase (NCBI)	2.43	2.32	2.61	2.11	2.35	2.13
pykA	pyruvate kinase (NCBI)	2.18	2.30	1.72	1.98	2.38	1.93
ynfE	oxidoreductase subunit (NCBI)	4.00	3.91	2.81	3.26	2.70	1.98
ynfF	oxidoreductase subunit (RefSeq)	3.70	3.70	2.11	2.84	2.24	1.08
ynfH	oxidoreductase, membrane subunit (NCBI)	2.49	2.46	1.20	1.91	0.99	0.44
	Other						
hlyE	hemolysin E (VIMSS)	3.17	3.31	2.96	2.65	3.39	2.33
pepE	peptidase E (NCBI)	3.67	3.69	3.30	3.05	3.78	3.10
slp	outer membrane protein induced after carbon starvation (VIMSS)	1.83	2.00	2.01	2.13	1.53	1.70
ycgV	predicted adhesin (NCBI)	1.66	2.05	1.63	1.47	2.45	1.80
yliH	hypothetical protein (NCBI)	2.37	2.58	1.54	2.42	3.07	2.19
yqhD	alcohol dehydrogenase, NAD(P)-dependent (NCBI)	2.67	2.73	1.24	1.31	2.48	2.54
	Stress response						
cspI	Qin prophage; cold shock protein (NCBI)	2.04	2.29	1.59	3.20	2.20	2.51
sodB	superoxide dismutase, Fe (NCBI)	2.12	2.54	0.71	1.16	0.81	0.36
uspG	universal stress protein UP12 (NCBI)	3.02	2.64	2.08	2.91	2.58	2.32
	Transport						
amtB	ammonium transporter (NCBI)	1.62	2.51	1.00	0.63	3.86	1.79
ccmA	ATP binding protein of heme exporter A (VIMSS)	1.40	2.10	2.44	1.09	2.53	1.74
dcuB	C4-dicarboxylate antiporter (NCBI)	5.57	5.84	4.29	5.05	3.99	3.02
dcuC	anaerobic C4-dicarboxylate transport (NCBI)	4.08	4.52	4.61	3.37	4.79	3.99
fruA	fused fructose-specific PTS enzymes: IIBcomponent/IIC components (NCBI)	1.95	2.28	1.12	1.80	2.63	2.19
narK	nitrate/nitrite transporter (NCBI)	0.93	1.35	2.40	0.70	2.81	1.67
nikD	nickel transporter subunit (NCBI)	0.92	0.57	2.53	-0.74	1.06	0.39
nikE	nickel transporter subunit (NCBI)	0.66	0.41	2.34	-0.50	0.94	0.33
nirC	nitrite transporter (NCBI)	0.23	3.18	4.07	-0.75	4.52	3.87
oppB	oligopeptide permease ABC transporter membrane protein (NCBI)	2.60	2.86	2.85	2.77	2.88	2.91
oppC	oligopeptide transporter subunit (NCBI)	2.96	3.17	3.09	2.97	3.20	3.13
oppD	oligopeptide transporter ATP-binding component (NCBI)	3.03	3.21	3.13	2.96	3.32	3.18
oppF	oligopeptide transporter subunit (NCBI)	3.29	3.42	2.94	3.30	3.57	3.56

Table S6: Downregulated supernatant genes

Name	Description	SN1	SN2	SN3	SNC1	SNC2	SNC3
	Hypothetical and predicted genes						
b2001	orf, hypothetical protein (VIMSS)	-3.07	-3.03	-3.08	-1.46	-1.32	-1.28
efeU	Pseudogene	-1.64	-2.18	-1.93	-1.83	-2.44	-1.90
nmpC	DLP12 prophage; truncated outer membrane porin (pseudogene) (RefSeq)	-2.51	-2.53	-1.93	-2.86	-2.98	-3.04
pqqL	predicted peptidase (NCBI)	-2.52	-2.57	-2.09	-2.32	-2.51	-2.30
ybdB	hypothetical protein (NCBI)	-2.45	-2.66	-1.47	-2.16	-2.19	-1.59
ybdZ	hypothetical protein (NCBI)	-1.87	-2.10	-1.28	-1.88	-1.73	-1.57
ybhC	predicted pectinesterase (NCBI)	-3.64	-3.67	-3.72	-0.85	-1.46	-1.01
ybiI	hypothetical protein (NCBI)	-2.21	-2.16	-2.62	-2.34	-1.69	-2.36
ybiX	putative enzyme (VIMSS)	-3.94	-4.03	-3.68	-3.71	-3.91	-3.97
ycdB	hypothetical protein (NCBI)	-2.95	-3.03	-2.77	-2.89	-3.22	-3.14
ycdO	hypothetical protein (NCBI)	-3.33	-3.61	-2.96	-3.23	-3.67	-3.55
yceA	hypothetical protein (NCBI)	-1.82	-1.99	-2.10	-1.55	-2.36	-1.77
yceI	hypothetical protein (NCBI)	-2.56	-2.29	-2.53	-2.00	-1.85	-1.88
yciF	hypothetical protein (NCBI)	-2.31	-2.27	-2.51	-2.40	-2.44	-2.49
yddA	fused predicted multidrug transporter subunits of ABC superfamily: membrane component/ATP-binding component (NCBI)	-2.00	-2.03	-1.17	-1.44	-2.29	-1.44
yddB	predicted porin protein (NCBI)	-2.89	-2.97	-2.74	-2.47	-2.83	-2.67
yhjE	predicted transporter (NCBI)	-1.79	-1.93	-2.16	-1.60	-1.95	-1.69
yifK	predicted transporter (NCBI)	-2.26	-2.23	-2.13	-1.89	-2.43	-2.16
ylaC	orf, hypothetical protein (VIMSS)	-1.66	-2.08	-1.70	-2.15	-2.56	-2.41
	Iron chelation and transport						
cirA	ferric iron-catecholate outer membrane transporter (NCBI)	-2.96	-3.12	-2.39	-2.37	-2.58	-2.38
entA	2,3-dihydroxybenzoate-2,3-dehydrogenase (NCBI)	-2.55	-2.78	-1.88	-2.45	-2.30	-1.83
entB	isochorismatase (NCBI)	-2.79	-2.82	-2.00	-2.42	-2.36	-1.97
entC	isochorismate synthase (NCBI)	-1.99	-2.38	-1.83	-2.13	-2.59	-1.84
entD	phosphopantetheinyltransferase component of enterobactin synthase multienzyme complex (NCBI)	-2.38	-2.55	-1.71	-1.82	-2.13	-1.78
entE	2,3-dihydroxybenzoate-AMP ligase component of enterobactin synthase multienzyme complex (NCBI)	-2.75	-3.01	-2.09	-2.67	-2.75	-2.68
entF	enterobactin synthase multienzyme complex component, ATP-dependent (NCBI)	-2.07	-2.13	-1.31	-1.88	-1.75	-1.49
fepA	iron-enterobactin outer membrane transporter (NCBI)	-2.14	-2.33	-1.21	-1.61	-1.86	-1.78
fiu	predicted iron outer membrane transporter (NCBI)	-5.24	-5.30	-5.01	-5.11	-4.79	-5.46
	Metabolism						
aceA	isocitrate lyase (NCBI)	-2.82	-2.96	-3.21	-2.49	-2.83	-2.85
aceB	malate synthase (NCBI)	-2.28	-2.52	-2.73	-2.14	-2.72	-2.86
aceE	pyruvate dehydrogenase subunit E1 (NCBI)	-2.73	-2.60	-1.84	-1.65	-2.21	-2.02
aceF	dihydrolipoamide acetyltransferase (NCBI)	-2.47	-2.44	-1.23	-1.52	-2.03	-1.60
aceK	bifunctional isocitrate dehydrogenase kinase/phosphatase protein (NCBI)	-2.98	-3.13	-3.12	-2.53	-3.24	-3.60
acs	acetyl-coenzyme A synthetase (NCBI)	-2.94	-2.78	-2.98	-3.09	-2.80	-2.46
aldA	aldehyde dehydrogenase A, NAD-linked (NCBI)	-2.95	-2.84	-3.03	-3.05	-3.04	-3.05
betA	choline dehydrogenase (NCBI)	-2.47	-2.33	-2.39	-2.09	-2.13	-2.30
betB	betaine aldehyde dehydrogenase, NAD-dependent (NCBI)	-2.70	-2.65	-2.49	-2.38	-2.61	-2.69

betI	probably transcriptional repressor of bet genes (VIMSS)	-2.56	-2.60	-2.63	-2.47	-2.68	-2.59
can	carbonic anhydrase (NCBI)	-1.55	-1.70	-2.29	-1.63	-1.95	-1.37
carA	carbamoyl-phosphate synthase small subunit (NCBI)	-3.25	-2.86	-1.62	-2.80	-2.13	-3.90
carB	carbamoyl-phosphate synthase large subunit (NCBI)	-3.17	-2.93	-2.17	-2.78	-2.34	-3.27
cyoA	cytochrome o ubiquinol oxidase subunit II (NCBI)	-2.86	-3.08	-3.01	-2.47	-2.90	-3.04
cyoB	cytochrome o ubiquinol oxidase subunit I (NCBI)	-3.49	-3.43	-3.41	-3.13	-3.29	-3.47
cyoC	cytochrome o ubiquinol oxidase subunit III (NCBI)	-3.69	-3.51	-3.14	-3.33	-3.28	-3.35
cyoD	cytochrome o ubiquinol oxidase subunit IV (NCBI)	-3.57	-3.47	-3.38	-3.14	-2.87	-2.95
cyoE	protoheme IX farnesyltransferase (NCBI)	-3.13	-2.94	-2.76	-2.79	-2.31	-2.33
folE	GTP cyclohydrolase I (NCBI)	-1.63	-1.48	-2.10	-1.48	-1.48	-1.16
gcd	glucose dehydrogenase (NCBI)	-2.04	-2.07	-2.30	-1.91	-2.02	-2.45
gltA	citrate synthase (NCBI)	-2.10	-2.17	-2.09	-1.94	-2.16	-2.28
lldD	L-lactate dehydrogenase, FMN-linked (NCBI)	-2.01	-1.92	-1.79	-2.07	-1.83	-2.11
lpd	dihydrolipoamide dehydrogenase (NCBI)	-1.95	-2.04	-1.17	-1.31	-1.98	-1.39
mdh	malate dehydrogenase (NCBI)	-2.02	-1.85	-2.09	-2.14	-1.56	-1.41
ndk	nucleoside diphosphate kinase (NCBI)	-1.77	-2.21	-1.87	-1.67	-2.68	-2.15
pyrI	aspartate carbamoyltransferase regulatory subunit (NCBI)	-2.06	-1.17	-1.77	-3.16	-0.41	-1.18
sdhA	succinate dehydrogenase flavoprotein subunit (NCBI)	-2.69	-2.67	-2.86	-2.80	-3.27	-3.49
sdhB	succinate dehydrogenase, FeS subunit (NCBI)	-2.36	-2.41	-2.42	-2.36	-2.74	-2.58
sdhD	succinate dehydrogenase cytochrome b556 small membrane subunit (NCBI)	-1.90	-2.11	-2.03	-2.30	-2.51	-2.85
sucA	alpha-ketoglutarate decarboxylase (NCBI)	-2.54	-2.58	-2.41	-2.35	-2.33	-2.54
sucB	dihydrolipoamide acetyltransferase (NCBI)	-2.34	-2.38	-2.31	-2.38	-2.18	-2.18
sucC	succinyl-CoA synthetase subunit beta (NCBI)	-2.66	-2.60	-2.38	-2.47	-2.47	-2.54
sucD	succinyl-CoA synthetase subunit alpha (NCBI)	-2.21	-2.14	-1.98	-2.26	-1.71	-1.83
sufC	cysteine desulfurase ATPase component (NCBI)	-2.35	-1.83	-1.91	-2.28	-1.45	-1.40
sufD	component of SufBCD complex (NCBI)	-2.20	-1.78	-2.21	-2.23	-1.36	-1.40
sufS	selenocysteine lyase (NCBI)	-2.18	-1.85	-1.77	-2.38	-1.27	-1.43
thrA	bifunctional aspartokinase I/homeserine dehydrogenase I (NCBI)	-2.47	-2.56	-1.19	-2.05	-2.89	-2.47
thrB	homoserine kinase (NCBI)	-2.20	-2.32	-1.07	-1.89	-2.62	-2.00
thrC	threonine synthase (NCBI)	-2.12	-2.18	-0.91	-1.86	-2.08	-1.29
trpB	tryptophan synthase subunit beta (NCBI)	-2.16	-0.78	-2.04	-1.02	-0.57	-1.56
trpC	N-(5-phosphoribosyl)anthranilate isomerase and indole-3-glycerolphosphate synthetase (VIMSS)	-2.47	-1.09	-1.61	-1.39	-0.60	-1.57
trpD	bifunctional indole-3-glycerol-phosphate synthase/anthranilate phosphoribosyltransferase (NCBI)	-2.88	-1.12	-0.90	-1.86	-0.36	-0.94
trpE	anthranilate synthase component I (NCBI)	-3.10	-0.92	-1.34	-1.81	0.01	0.06
ynhE	orf, hypothetical protein (VIMSS)	-2.26	-1.89	-2.30	-2.37	-1.40	-1.49
	Other						
cueO	multicopper oxidase (laccase) (NCBI)	-1.87	-1.89	-2.18	1.25	-1.92	-1.91
ilvG	Disrupted gene (Ecocyc)	-2.16	-1.96	-0.98	-2.20	-2.02	-1.83
	Prophage						
flu	CP4-44 prophage; antigen 43 (Ag43) phase-variable biofilm formation autotransporter (NCBI)	-5.79	-5.32	-5.39	-1.90	-1.59	-1.60
	Stress response						
cspA	major cold shock protein (NCBI)	-0.92	-0.91	-2.21	-0.13	-0.79	-0.15
ompT	DLP12 prophage; outer membrane protease VII (outer membrane protein 3b) (NCBI)	-2.64	-2.32	-2.57	-2.25	-1.95	-2.07
osmY	periplasmic protein (NCBI)	-2.10	-1.90	-2.26	-2.36	-1.88	-1.79

stpA	DNA binding protein, nucleoid-associated (NCBI)	-2.29	-2.65	-2.65	-2.67	-2.89	-2.50
sufA	iron-sulfur cluster assembly scaffold protein (NCBI)	-2.20	-1.79	-2.41	-2.49	-1.45	-1.46
tpx	thiol peroxidase (NCBI)	-2.10	-2.47	-2.14	-1.74	-2.36	-1.76
	Transcription						
rpoA	DNA-directed RNA polymerase subunit alpha (NCBI)	-0.14	-0.25	-2.55	-0.03	-0.14	0.04
	Transport						
argT	lysine/arginine/ornithine transporter subunit (NCBI)	-1.42	-0.89	-2.09	-2.41	0.17	-2.42
codB	cytosine transporter (NCBI)	-2.30	-2.73	-1.78	-2.09	-2.97	-2.62
cusC	copper/silver efflux system, outer membrane component (NCBI)	-3.06	-3.20	-3.00	4.62	-2.92	-3.04
kgtP	alpha-ketoglutarate transporter (NCBI)	-1.58	-1.77	-2.14	-1.06	-1.79	-1.72
uraA	uracil transporter (NCBI)	-2.72	-2.76	-1.99	-2.23	-2.51	-2.71

Table S7: Upregulated pulldown control genes

Name	Description	PDC1	PDC2	PDC3	SNC1	SNC2	SNC3
	Hypothetical and predicted genes						
b1297	putative glutamine synthetase (EC 6.3.1.2) (VIMSS)	2.03	2.98	2.21	-1.19	-1.26	-1.59
b1445	orf, hypothetical protein (VIMSS)	3.52	2.82	3.20	0.20	-0.63	0.83
b1551	orf, hypothetical protein (VIMSS)	2.14	1.02	1.28	1.73	0.93	1.47
b1757	putative thiosulfate sulfur transferase (VIMSS)	2.44	1.20	0.82	3.04	3.71	2.90
b2343	orf, hypothetical protein (VIMSS)	2.41	0.85	0.68	3.35	3.80	3.28
tsgA	hypothetical protein (NCBI)	2.40	2.25	2.73	0.95	0.31	1.21
yaaH	conserved inner membrane protein associated with acetate transport (NCBI)	2.74	0.95	1.55	0.91	0.39	0.42
yagI	CP4-6 prophage; predicted DNA-binding transcriptional regulator (NCBI)	2.11	1.45	2.08	-0.09	1.11	-0.24
ybdH	predicted oxidoreductase (NCBI)	3.15	2.02	2.28	0.21	0.14	-0.03
ybdL	putative aminotransferase (NCBI)	3.59	2.40	2.95	0.67	0.37	0.45
ybgE	conserved inner membrane protein (NCBI)	2.91	1.45	1.73	2.21	2.06	2.63
ybgT	hypothetical protein (NCBI)	2.27	0.68	1.27	1.59	2.03	2.36
ycbO	orf, hypothetical protein (VIMSS)	0.29	2.12	0.92	-0.26	-0.22	-0.09
ycfJ	hypothetical protein (NCBI)	2.23	2.25	2.44	-0.18	0.79	0.28
ycgF	predicted FAD-binding phosphodiesterase (NCBI)	2.66	2.53	2.77	0.34	-0.04	-0.03
yciH	orf, hypothetical protein (VIMSS)	2.30	2.09	2.29	-0.45	-0.45	-0.52
ycjJ	putative amino acid/amine transport protein (VIMSS)	1.83	2.15	1.71	-0.26	-0.25	-0.25
ycjL	probable amidotransferase subunit (VIMSS)	2.36	2.91	2.43	-0.87	-0.79	-1.02
ydcI	putative transcriptional regulator LYSR-type (VIMSS)	2.48	2.35	2.54	-1.36	-1.58	-1.77
ydeH	hypothetical protein (NCBI)	2.01	1.52	1.71	2.15	0.97	1.23
ydiY	hypothetical protein (NCBI)	2.09	0.68	1.55	-0.32	-0.80	-0.55
yecF	hypothetical protein (NCBI)	2.51	1.85	2.14	1.32	1.47	1.56
yedL	predicted acyltransferase (NCBI)	2.80	3.05	3.00	0.47	2.74	2.36
yeeD	hypothetical protein (NCBI)	0.44	2.05	1.58	1.04	-0.10	1.04
yeeE	predicted inner membrane protein (NCBI)	0.34	2.02	1.48	0.85	0.16	0.99
yejG	hypothetical protein (NCBI)	4.05	3.42	3.80	0.22	-0.56	-1.03
yfhL	predicted 4Fe-4S cluster-containing protein (NCBI)	2.64	2.13	2.25	1.25	0.44	1.29
ygiQ	hypothetical protein (NCBI)	2.77	2.58	2.74	0.48	0.08	0.44
ygjO	putative enzyme (VIMSS)	2.66	2.39	2.49	0.81	0.16	1.02
yhdW	predicted amino-acid transporter subunit (RefSeq)	2.61	1.47	1.84	-0.04	1.09	0.19

yhhQ	conserved inner membrane protein (NCBI)	2.79	2.27	2.74	0.75	0.54	0.60
yjbO	orf, hypothetical protein (VIMSS)	2.15	1.66	1.83	0.84	0.53	0.59
yjiY	putative carbon starvation protein (VIMSS)	2.63	1.89	1.76	0.81	0.22	0.05
ynjC	fused transporter subunits of ABC superfamily: membrane components (RefSeq)	2.20	0.78	0.75	1.47	1.49	0.98
ynjD	predicted transporter subunit: ATP-binding component of ABC superfamily (NCBI)	2.02	0.67	0.62	1.03	1.08	0.59
yoeG	Pseudogene (MicrobesOnline)	2.03	1.89	1.98	2.09	2.60	1.97
yraQ	predicted permease (NCBI)	2.29	1.76	1.92	0.75	0.30	0.28
	Metabolism						
argF	CP4-6 prophage; ornithine carbamoyltransferase 2, chain F (NCBI)	2.07	1.95	2.17	-0.35	1.24	-1.09
argH	argininosuccinate lyase (NCBI)	2.50	1.80	2.07	-0.33	0.73	-1.11
argI	ornithine carbamoyltransferase 1 (NCBI)	2.50	1.99	2.37	-0.52	1.27	-1.88
caiF	transcriptional regulator of cai operon (VIMSS)	2.52	2.21	2.43	1.48	1.79	1.08
codA	cytosine deaminase (NCBI)	1.98	2.08	2.11	-1.84	-2.08	-2.06
cysG	fused siroheme synthase 1,3-dimethyluroporphyriongen III dehydrogenase and siroheme ferrochelatase/uroporphyrinogen methyltransferase (NCBI)	2.44	0.89	0.92	-0.14	2.54	1.80
dmsC	dimethyl sulfoxide reductase, anaerobic, subunit C (NCBI)	2.40	0.97	0.53	3.09	3.90	2.89
fdnG	formate dehydrogenase-N, alpha subunit, nitrate-inducible (NCBI)	3.83	1.81	1.58	0.64	1.19	1.60
fdnH	formate dehydrogenase-N, Fe-S (beta) subunit, nitrate-inducible (NCBI)	3.57	1.32	1.42	0.45	0.97	1.27
fdnI	formate dehydrogenase-N, cytochrome B556 (gamma) subunit, nitrate-inducible (NCBI)	3.31	1.13	1.15	0.53	0.94	0.94
fdoG	formate dehydrogenase-O, large subunit (NCBI)	3.10	3.02	3.09	-1.31	-1.64	-1.05
fdoH	formate dehydrogenase-O, Fe-S subunit (NCBI)	2.53	2.91	2.78	-0.92	-1.11	-0.81
frdC	fumarate reductase subunit C (NCBI)	2.67	1.48	0.49	3.86	4.55	4.04
frdD	fumarate reductase subunit D (NCBI)	3.31	1.77	1.24	4.41	4.85	4.38
glcC	DNA-binding transcriptional dual regulator, glycolate-binding (NCBI)	2.50	2.23	2.35	-0.58	-0.57	-0.75
gldA	glycerol dehydrogenase, (NAD) (VIMSS)	2.12	1.26	1.34	3.62	4.29	3.46
glnG	fused DNA-binding response regulator in two-component regulatory system with GlnL: response regulator/sigma54 interaction protein (NCBI)	2.95	1.69	1.96	0.33	1.84	-0.57
glnK	nitrogen assimilation regulatory protein for GlnL, GlnE, and AmtB (NCBI)	3.62	3.27	3.46	-0.15	4.09	1.60
glnL	sensory histidine kinase in two-component regulatory system with GlnG (NCBI)	2.49	1.57	1.70	-0.10	1.44	-0.49
gpt	xanthine phosphoribosyltransferase (NCBI)	1.95	2.11	2.26	0.68	-0.59	0.82
grxA	glutaredoxin 1, redox coenzyme for ribonucleotide reductase (RNR1a) (NCBI)	2.16	-0.42	0.33	-0.51	-0.72	-0.77
hybB	predicted hydrogenase 2 cytochrome b type component (NCBI)	2.19	0.98	0.56	1.80	2.20	1.63
hybC	hydrogenase 2, large subunit (NCBI)	2.28	0.49	0.64	1.67	2.00	1.10
metB	cystathionine gamma-synthase (NCBI)	2.75	1.75	2.16	-0.33	-0.35	-0.38
metF	5,10-methylenetetrahydrofolate reductase (NCBI)	3.89	2.94	3.28	1.08	0.62	0.59
metL	bifunctional aspartate kinase II/homoserine dehydrogenase II (NCBI)	2.11	1.05	1.53	-0.53	-0.67	-0.65
metR	DNA-binding transcriptional activator, homocysteine-binding (NCBI)	2.92	1.67	2.16	0.01	-0.26	-0.13
nac	DNA-binding transcriptional dual regulator of nitrogen assimilation (NCBI)	2.88	2.55	2.78	0.18	3.51	1.18
napA	nitrate reductase, periplasmic, large subunit (NCBI)	3.05	2.12	1.02	-0.24	2.94	2.44

napB	cytochrome c-type protein (VIMSS)	4.45	2.89	2.55	0.23	3.36	2.68
napC	nitrate reductase, cytochrome c-type, periplasmic (NCBI)	3.77	1.78	1.64	1.00	2.97	2.17
napG	quinol dehydrogenase periplasmic component (NCBI)	3.79	2.12	1.47	0.26	2.64	2.17
napH	quinol dehydrogenase membrane component (NCBI)	4.26	2.14	1.97	0.23	3.21	2.48
narG	nitrate reductase 1, alpha subunit (NCBI)	2.20	0.88	-0.21	0.06	3.40	2.23
narH	nitrate reductase 1, beta (Fe-S) subunit (NCBI)	4.35	2.20	2.05	1.43	4.51	3.24
narI	nitrate reductase 1, gamma (cytochrome b(NR)) subunit (NCBI)	4.72	1.57	2.47	1.59	4.34	2.75
narJ	molybdenum-cofactor-assembly chaperone subunit (delta subunit) of nitrate reductase 1 (NCBI)	4.75	2.36	2.57	1.66	4.58	3.18
ndk	nucleoside diphosphate kinase (NCBI)	2.11	2.17	2.18	-1.67	-2.68	-2.15
nrfD	formate-dependent nitrite reductase, membrane subunit (NCBI)	2.21	0.67	0.52	0.07	1.09	0.93
pdhR	transcriptional regulator of pyruvate dehydrogenase complex (NCBI)	2.07	1.37	1.87	-0.37	-2.24	-0.94
pflA	pyruvate formate lyase activating enzyme 1 (NCBI)	2.27	1.31	0.94	1.52	1.56	2.14
pta	phosphate acetyltransferase (NCBI)	2.27	1.08	1.13	2.11	2.35	2.13
purT	phosphoribosylglycinamide formyltransferase 2 (NCBI)	2.09	1.72	1.81	0.40	-2.63	-0.71
puuB	gamma-Glu-putrescine oxidase, FAD/NAD(P)-binding (NCBI)	0.71	2.14	1.07	-1.39	-0.97	-0.93
puuC	gamma-Glu-gamma-aminobutyraldehyde dehydrogenase, NAD(P)H-dependent (NCBI)	0.74	2.27	1.20	-1.42	-1.22	-1.68
puuR	DNA-binding transcriptional repressor (NCBI)	1.37	2.20	1.70	-0.36	-0.33	-0.47
pyrD	dihydroorotate dehydrogenase (NCBI)	2.44	2.23	2.34	-0.90	-2.11	-1.32
pyrF	orotidine 5'-phosphate decarboxylase (NCBI)	2.35	2.21	2.35	-0.29	-0.76	-0.23
sdhC	succinate dehydrogenase cytochrome b556 large membrane subunit (NCBI)	3.43	3.02	2.96	-1.89	-2.40	-2.67
sdhD	succinate dehydrogenase cytochrome b556 small membrane subunit (NCBI)	2.91	2.66	2.41	-2.30	-2.51	-2.85
ygcM	6-pyruvoyl tetrahydrobiopterin synthase (PTPS) (NCBI)	2.10	1.98	2.12	0.37	-0.40	0.21
	Other						
fis	DNA-binding protein Fis (NCBI)	2.21	2.04	2.17	1.28	1.15	1.25
ftn	ferritin iron storage protein (cytoplasmic) (NCBI)	3.34	3.61	3.59	-0.84	-1.21	-0.85
pepE	peptidase E (NCBI)	3.01	1.55	1.13	3.05	3.78	3.10
suhB	inositol monophosphatase (NCBI)	3.16	2.46	2.80	0.24	-0.59	0.15
yhdJ	putative methyltransferase (VIMSS)	2.46	1.82	2.25	0.45	0.22	0.43
yhfL	conserved secreted peptide (NCBI)	2.55	0.67	0.87	0.25	2.54	1.46
	Peptidoglycan						
ddpX	D-ala-D-ala dipeptidase, Zn-dependent (NCBI)	1.44	1.82	2.07	-0.48	-0.03	0.07
	Phantom Genes						
b1903	orf, hypothetical protein (VIMSS)	2.13	1.99	2.33	-0.26	-0.51	-0.26
tisA	lexA-regulated predicted protein (phantom gene)	2.33	1.29	1.61	1.71	1.33	1.28
	Stress response						
cspF	Qin prophage; cold shock protein (NCBI)	2.93	2.75	3.14	1.10	0.68	1.66
cspH	stress protein, member of the CspA-family (NCBI)	3.45	2.63	3.22	1.94	1.06	2.07
cspI	Qin prophage; cold shock protein (NCBI)	3.03	1.48	2.10	3.20	2.20	2.51
mutM	formamidopyrimidine-DNA glycosylase (NCBI)	2.49	2.19	2.41	0.39	0.38	0.44
sodB	superoxide dismutase, Fe (NCBI)	2.29	0.92	0.88	1.16	0.81	0.36
tisB	lexA-regulated toxic peptide (RefSeq)	2.26	1.12	1.50	1.60	1.16	1.29
	Translation						

dusB	tRNA-dihydrouridine synthase B (NCBI)	2.10	2.10	2.14	1.15	0.95	1.28
rhlE	RNA helicase (NCBI)	2.64	2.58	2.84	1.14	0.34	0.90
rluB	23S rRNA pseudouridylate synthase (NCBI)	2.56	1.93	2.28	1.06	0.52	1.07
rph	ribonuclease PH (NCBI)	2.58	2.09	2.17	0.64	-0.05	0.61
rplI	50S ribosomal protein L9 (NCBI)	2.10	1.30	1.51	0.66	-0.66	0.05
yibK	predicted rRNA methylase (NCBI)	2.19	2.00	2.22	0.04	-0.16	0.27
	Transport						
amtB	ammonium transporter (NCBI)	4.06	3.20	3.47	0.63	3.86	1.79
ccmA	ATP binding protein of heme exporter A (VIMSS)	2.66	0.90	0.87	1.09	2.53	1.74
ccmB	heme exporter subunit (NCBI)	2.05	0.63	0.67	0.53	1.85	1.41
ccmD	cytochrome c biogenesis protein (NCBI)	2.01	0.30	0.44	1.23	1.95	1.80
codB	cytosine transporter (NCBI)	2.54	2.48	2.53	-2.09	-2.97	-2.62
fadL	long-chain fatty acid outer membrane transporter (RefSeq)	2.44	2.00	1.97	0.38	0.03	0.27
glnQ	glutamine ABC transporter ATP-binding protein (NCBI)	2.40	1.13	1.26	-0.27	1.51	-0.11
metN	DL-methionine transporter subunit (NCBI)	2.10	1.76	2.05	-0.18	-0.81	-0.65
mgtA	magnesium transporter (NCBI)	2.39	1.58	1.77	0.60	0.55	0.19
nirC	nitrite transporter (NCBI)	3.85	2.29	2.02	-0.75	4.52	3.87
ompW	outer membrane protein W (NCBI)	2.61	0.68	0.26	2.27	1.33	1.59
oppB	oligopeptide permease ABC transporter membrane protein (NCBI)	2.86	1.98	2.34	2.77	2.88	2.91
oppC	oligopeptide transporter subunit (NCBI)	2.84	2.39	2.75	2.97	3.20	3.13
oppD	oligopeptide transporter ATP-binding component (NCBI)	3.15	2.22	2.72	2.96	3.32	3.18
oppF	oligopeptide transporter subunit (NCBI)	3.63	2.21	2.81	3.30	3.57	3.56
sbp	sulfate transporter subunit (NCBI)	2.21	3.94	2.90	1.76	0.70	1.63
tauA	taurine transport system periplasmic protein (VIMSS)	0.35	2.56	1.42	0.15	0.73	0.74
tauB	taurine transporter subunit (NCBI)	0.23	2.22	1.25	0.17	0.45	0.67
tppB	putative tripeptide transporter permease (NCBI)	2.05	0.55	0.65	0.89	2.03	2.75
uraA	uracil transporter (NCBI)	3.14	2.79	2.90	-2.23	-2.51	-2.71
yeeF	putative amino acid/amine transport protein (VIMSS)	2.71	1.95	2.15	-0.76	-1.57	-1.00
ykfD	putative amino acid/amine transport protein (VIMSS)	2.97	1.87	2.47	0.11	0.06	0.00
zntA	zinc, cobalt and lead efflux system (NCBI)	3.40	3.77	3.60	-0.18	0.01	-0.01

Table S8: Downregulated pulldown control genes

Name	Description	PDC1	PDC2	PDC3	SNC1	SNC2	SNC3
	DNA Synthesis						
nrdE	ribonucleotide-diphosphate reductase alpha subunit (NCBI)	-5.39	-5.29	-5.37	-0.02	0.17	-0.08
nrdF	ribonucleotide-diphosphate reductase beta subunit (NCBI)	-5.48	-5.60	-4.83	0.16	0.13	-0.23
nrdH	glutaredoxin-like protein (NCBI)	-6.68	-6.70	-6.24	-0.01	0.23	0.29
nrdI	hypothetical protein (NCBI)	-5.98	-5.94	-5.80	0.00	0.29	0.34
	Hypothetical and predicted genes						
b1200	putative dihydroxyacetone kinase (EC 2.7.1.2) (VIMSS)	-2.11	-2.23	-2.50	0.10	1.09	0.38
b1593	orf, hypothetical protein (VIMSS)	-1.04	-1.18	-2.16	2.20	3.33	2.44
b2001	orf, hypothetical protein (VIMSS)	-1.07	-3.08	-1.58	-1.46	-1.32	-1.28
b2080	orf, hypothetical protein (VIMSS)	-4.10	-3.02	-3.52	-1.65	-1.10	-1.44
efeU	Pseudogene	-3.18	-3.55	-3.60	-1.83	-2.44	-1.90

nmpC	DLP12 prophage; truncated outer membrane porin (pseudogene) (RefSeq)	-3.20	-3.25	-3.54	-2.86	-2.98	-3.04
pqqL	predicted peptidase (NCBI)	-2.86	-2.51	-2.07	-2.32	-2.51	-2.30
rspB	predicted oxidoreductase, Zn-dependent and NAD(P)-binding (NCBI)	-2.19	-2.10	-1.82	-1.81	-1.79	-1.87
yahK	predicted oxidoreductase, Zn-dependent and NAD(P)-binding (NCBI)	-2.25	-1.46	-1.81	-0.52	-0.88	-1.05
yahO	hypothetical protein (NCBI)	-2.46	-1.48	-1.76	-0.58	-0.68	-0.84
ybaN	conserved inner membrane protein (NCBI)	-2.52	-2.65	-2.67	-0.22	-1.16	-0.52
ybdA	predicted transporter (NCBI)	-3.40	-3.10	-3.47	-0.52	-1.40	-0.71
ybdB	hypothetical protein (NCBI)	-5.61	-5.83	-5.20	-2.16	-2.19	-1.59
ybdZ	hypothetical protein (NCBI)	-6.78	-6.39	-6.59	-1.88	-1.73	-1.57
ybeL	hypothetical protein (NCBI)	-2.16	-1.61	-1.97	-0.12	0.04	-0.12
ybhC	predicted pectinesterase (NCBI)	-1.70	-3.17	-2.67	-0.85	-1.46	-1.01
ybiI	hypothetical protein (NCBI)	-3.73	-3.63	-3.43	-2.34	-1.69	-2.36
ybiJ	hypothetical protein (NCBI)	-2.10	-1.39	-1.37	-1.98	-1.54	-1.81
ybiM	orf, hypothetical protein (VIMSS)	-2.29	-1.56	-1.64	-0.74	-0.22	-0.61
ybiX	putative enzyme (VIMSS)	-4.62	-4.65	-4.47	-3.71	-3.91	-3.97
ybjP	predicted lipoprotein (NCBI)	-2.66	-1.97	-2.28	-0.58	0.01	-0.19
ycdB	hypothetical protein (NCBI)	-3.58	-3.46	-3.39	-2.89	-3.22	-3.14
ycdO	hypothetical protein (NCBI)	-4.12	-4.22	-3.79	-3.23	-3.67	-3.55
ycgB	hypothetical protein (NCBI)	-2.31	-1.39	-1.68	-0.31	0.61	-0.04
ycgK	hypothetical protein (NCBI)	-6.90	-5.88	-5.85	-1.50	-0.80	-0.97
yciE	hypothetical protein (NCBI)	-3.01	-2.31	-2.29	-1.86	-1.73	-1.75
yciF	hypothetical protein (NCBI)	-3.70	-2.97	-2.99	-2.40	-2.44	-2.49
yciG	orf, hypothetical protein (VIMSS)	-2.98	-2.16	-2.39	-1.38	-1.50	-1.64
ydcK	predicted enzyme (NCBI)	-2.10	-1.51	-1.79	-0.69	-0.59	-0.71
yddA	fused predicted multidrug transporter subunits of ABC superfamily: membrane component/ATP-binding component (NCBI)	-2.67	-2.48	-2.82	-1.44	-2.29	-1.44
yddB	predicted porin protein (NCBI)	-3.67	-3.21	-3.27	-2.47	-2.83	-2.67
yddV	predicted diguanylate cyclase (RefSeq)	-2.21	-0.79	-1.26	-0.18	0.53	0.38
ydhS	conserved protein with FAD/NAD(P)-binding domain (NCBI)	-2.17	-1.80	-1.89	-0.72	-0.38	-0.51
ydiE	hypothetical protein (NCBI)	-3.96	-4.02	-4.22	0.24	-0.22	0.07
yebA	orf, hypothetical protein (VIMSS)	-2.22	-2.39	-2.24	0.71	0.47	0.61
yebL	putative adhesin (VIMSS)	-3.51	-1.83	-2.01	-0.10	-0.13	-0.15
yfiL	orf, hypothetical protein (VIMSS)	-2.17	-1.74	-1.59	-0.80	1.14	0.56
ygaU	hypothetical protein (NCBI)	-2.24	-1.79	-1.84	-0.02	0.25	0.07
yhgG	predicted DNA-binding transcriptional regulator (NCBI)	-2.74	-2.62	-2.90	1.67	2.56	2.28
yhhJ	predicted transporter subunit: membrane component of ABC superfamily (RefSeq)	-1.64	-2.02	-1.83	-0.93	-0.90	-0.99
yhiM	conserved inner membrane protein (RefSeq)	-2.24	-2.15	-2.31	-0.41	-0.75	-1.22
yhjD	conserved inner membrane protein (NCBI)	-2.22	-1.20	-1.57	-0.46	-0.07	-0.34
yiaG	predicted transcriptional regulator (NCBI)	-3.00	-1.82	-2.24	-0.30	0.16	-0.27
yibT	hypothetical protein (NCBI)	-3.24	-1.94	-2.31	-1.15	0.17	-0.37
yiiS	hypothetical protein (NCBI)	-1.95	-2.10	-2.18	0.35	1.15	0.38
yjdI	hypothetical protein (NCBI)	-2.06	-1.05	-1.42	-0.14	0.68	0.42
yjjZ	hypothetical protein (NCBI)	-6.53	-5.43	-5.03	-0.16	-0.17	-0.10
yncE	hypothetical protein (NCBI)	-2.89	-2.47	-2.04	-0.62	-1.33	-0.96
ynhG	hypothetical protein (NCBI)	-2.14	-1.30	-1.52	0.21	1.09	0.91
yodA	conserved metal-binding protein (NCBI)	-2.58	-1.36	-1.41	-0.14	-0.25	-0.19
yodB	putative cytochrome (VIMSS)	-4.32	-4.13	-4.45	0.50	-0.55	0.21

yqhE	orf, hypothetical protein (VIMSS)	-2.13	-0.99	-1.16	0.49	1.15	1.09
yqjG	predicted S-transferase (NCBI)	-2.21	-1.16	-1.52	-0.29	0.38	0.07
ysgA	predicted hydrolase (NCBI)	-2.17	-0.97	-1.38	-1.13	-0.88	-0.76
	Iron chelation and transport						
bfd	bacterioferritin-associated ferredoxin (NCBI)	-4.73	-5.51	-5.15	-0.30	-0.23	-0.12
cirA	ferric iron-catecholate outer membrane transporter (NCBI)	-5.80	-4.77	-3.66	-2.37	-2.58	-2.38
entA	2,3-dihydroxybenzoate-2,3-dehydrogenase (NCBI)	-5.84	-6.09	-5.28	-2.45	-2.30	-1.83
entB	isochorismatase (NCBI)	-6.53	-6.23	-5.91	-2.42	-2.36	-1.97
entC	isochorismate synthase (NCBI)	-6.51	-6.27	-6.24	-2.13	-2.59	-1.84
entD	phosphopantetheinyltransferase component of enterobactin synthase multienzyme complex (NCBI)	-5.08	-4.73	-4.84	-1.82	-2.13	-1.78
entE	2,3-dihydroxybenzoate-AMP ligase component of enterobactin synthase multienzyme complex (NCBI)	-6.59	-6.48	-6.45	-2.67	-2.75	-2.68
entF	enterobactin synthase multienzyme complex component, ATP-dependent (NCBI)	-5.97	-6.01	-5.64	-1.88	-1.75	-1.49
exbB	membrane spanning protein in TonB-ExbB-ExbD complex (NCBI)	-3.87	-4.18	-4.11	0.02	0.14	0.10
exbD	membrane spanning protein in TonB-ExbB-ExbD complex (NCBI)	-3.61	-3.71	-3.72	0.31	0.35	0.37
fecA	KpLE2 phage-like element; ferric citrate outer membrane transporter (NCBI)	-3.28	-3.26	-3.28	-0.89	-0.91	-0.75
fecB	citrate-dependent iron transport, periplasmic protein (VIMSS)	-2.24	-2.11	-2.33	-0.93	-0.58	-0.83
fecI	KpLE2 phage-like element; RNA polymerase, sigma 19 factor (NCBI)	-5.34	-5.89	-5.32	-0.48	-0.55	-0.27
fecR	KpLE2 phage-like element; transmembrane signal transducer for ferric citrate transport (NCBI)	-4.83	-4.86	-4.85	-0.47	-0.77	-0.40
feoA	ferrous iron transport protein A (NCBI)	-4.56	-5.04	-5.36	0.43	1.16	0.60
feoB	ferrous iron transport protein B (NCBI)	-3.79	-3.87	-4.22	1.31	1.77	1.58
fepA	iron-enterobactin outer membrane transporter (NCBI)	-6.15	-5.57	-5.02	-1.61	-1.86	-1.78
fepB	iron-enterobactin transporter subunit (NCBI)	-3.89	-4.23	-3.61	-0.79	-1.18	-0.66
fepC	iron-enterobactin transporter subunit (NCBI)	-3.75	-3.79	-3.74	-0.52	-0.63	-0.34
fepD	iron-enterobactin transporter subunit (NCBI)	-3.11	-3.12	-2.74	-0.14	-0.37	0.05
fepG	iron-enterobactin transporter subunit (NCBI)	-3.34	-3.32	-3.04	-0.56	-0.49	-0.42
fes	enterobactin/ferric enterobactin esterase (NCBI)	-6.24	-6.23	-6.29	-1.63	-1.62	-1.34
fhuA	ferrichrome outer membrane transporter (NCBI)	-3.22	-3.84	-3.38	0.27	0.30	0.32
fhuB	fused iron-hydroxamate transporter subunits of ABC superfamily: membrane components (NCBI)	-2.03	-1.93	-1.93	0.05	0.05	-0.06
fhuC	iron-hydroxamate transporter subunit (NCBI)	-2.73	-3.22	-3.08	0.26	0.22	0.44
fhuD	iron-hydroxamate transporter subunit (NCBI)	-2.20	-2.28	-2.31	0.15	0.33	0.37
fhuE	ferric-rhodotorulic acid outer membrane transporter (NCBI)	-4.87	-4.05	-4.03	-0.20	-0.54	-0.52
fhuF	ferric iron reductase involved in ferric hydroximate transport (NCBI)	-5.65	-6.63	-6.05	0.03	0.15	0.16
fiu	predicted iron outer membrane transporter (NCBI)	-6.17	-5.87	-5.74	-5.11	-4.79	-5.46
mntH	manganese transport protein MntH (NCBI)	-4.00	-4.11	-4.12	0.13	-0.04	0.09
tonB	membrane spanning protein in TonB-ExbB-ExbD complex (NCBI)	-4.10	-4.36	-4.10	-0.50	0.22	-0.27
yqjH	predicted siderophore interacting protein (NCBI)	-3.81	-3.56	-3.84	-0.31	-0.19	-0.05
	Metabolism						
aceA	isocitrate lyase (NCBI)	-2.25	-0.96	-1.12	-2.49	-2.83	-2.85

aceB	malate synthase (NCBI)	-2.33	-1.20	-1.37	-2.14	-2.72	-2.86
aceK	bifunctional isocitrate dehydrogenase kinase/phosphatase protein (NCBI)	-2.34	-1.19	-1.33	-2.53	-3.24	-3.60
aroF	3-deoxy-D-arabino-heptulosonate-7-phosphate synthase, tyrosine-repressible (NCBI)	-3.99	-4.05	-4.31	-0.37	0.53	0.61
bioB	biotin synthase (NCBI)	-2.32	-0.88	-1.05	-1.76	-0.57	-0.68
dhaL	dihydroxyacetone kinase, C-terminal domain (NCBI)	-1.69	-1.71	-2.04	0.38	1.20	0.61
dhaM	fused predicted dihydroxyacetone-specific PTS enzymes: HPr component/EI component (RefSeq)	-1.65	-1.64	-2.15	0.41	1.03	0.60
eutB	ethanolamine ammonia-lyase, heavy chain (VIMSS)	-2.16	-2.09	-1.78	-1.72	-1.61	-2.15
gatD	galactitol-1-phosphate dehydrogenase, Zn-dependent and NAD(P)-binding (NCBI)	-0.13	-1.91	-2.28	0.86	1.04	0.52
gatY	tagatose-bisphosphate aldolase 1 (VIMSS)	-1.71	-1.70	-2.23	-0.55	-0.14	-0.52
gpmA	phosphoglyceromutase (NCBI)	-2.03	-1.66	-1.57	0.00	0.08	0.09
poxB	pyruvate dehydrogenase (NCBI)	-2.59	-1.19	-1.55	-0.43	-0.04	-0.37
qor	quinone oxidoreductase, NADPH-dependent (NCBI)	-2.01	-1.41	-1.83	0.86	0.98	0.76
sufC	cysteine desulfurase ATPase component (NCBI)	-4.69	-3.82	-4.26	-2.28	-1.45	-1.40
sufD	component of SufBCD complex (NCBI)	-4.69	-3.86	-4.01	-2.23	-1.36	-1.40
sufE	cysteine desufuration protein SufE (NCBI)	-3.99	-3.66	-3.69	-1.96	-0.99	-1.01
sufS	selenocysteine lyase (NCBI)	-4.65	-3.69	-3.87	-2.38	-1.27	-1.43
talA	transaldolase A (NCBI)	-3.02	-1.37	-1.82	-0.40	-0.13	-0.28
tktB	transketolase 2, thiamin-binding (NCBI)	-2.45	-0.93	-1.22	0.15	0.36	0.17
trpA	tryptophan synthase subunit alpha (NCBI)	-2.34	-1.91	-1.86	-0.61	-0.29	-1.08
trpB	tryptophan synthase subunit beta (NCBI)	-2.71	-2.10	-2.16	-1.02	-0.57	-1.56
trpC	N-(5-phosphoribosyl)anthranilate isomerase and indole-3-glycerolphosphate synthetase (VIMSS)	-2.78	-2.22	-2.39	-1.39	-0.60	-1.57
trpD	bifunctional indole-3-glycerol-phosphate synthase/anthranilate phosphoribosyltransferase (NCBI)	-3.91	-2.85	-3.37	-1.86	-0.36	-0.94
trpE	anthranilate synthase component I (NCBI)	-4.09	-2.89	-3.76	-1.81	0.01	0.06
tyrA	fused chorismate mutase T/prephenate dehydrogenase (NCBI)	-3.58	-3.86	-4.02	-0.37	0.53	0.56
uxaC	glucuronate isomerase (NCBI)	-2.64	-2.63	-2.74	-0.88	0.26	-0.42
ybhE	6-phosphogluconolactonase (NCBI)	-2.22	-1.40	-1.69	-0.47	-0.46	-0.54
ynhE	orf, hypothetical protein (VIMSS)	-4.84	-4.17	-4.50	-2.37	-1.40	-1.49
	Other						
csgD	DNA-binding transcriptional activator in two-component regulatory system (NCBI)	-2.34	-2.07	-2.57	-0.02	-0.48	-0.48
csgE	predicted transport protein (NCBI)	-1.94	-1.85	-2.21	0.05	-0.87	-0.70
csgF	predicted transport protein (NCBI)	-2.01	-1.79	-2.26	-0.05	-0.56	-0.74
GadE	acid-responsive regulator of gadA and gadBC (Katherine Huang)	-1.14	-1.75	-2.21	1.41	1.19	0.85
msyB	acidic protein suppresses mutants lacking function of protein export (VIMSS)	-2.45	-1.49	-1.74	-1.41	-1.13	-1.16
yiiT	stress-induced protein (NCBI)	-1.60	-2.02	-1.85	0.52	1.36	0.73
ykgM	50S ribosomal protein L31 (NCBI)	-3.44	-1.49	-1.46	0.34	0.38	0.40
ykgO	rpmJ (L36) paralog (NCBI)	-4.04	-2.57	-2.47	0.44	0.36	0.34
	Prophage						
flu	CP4-44 prophage; antigen 43 (Ag43) phase-variable biofilm formation autotransporter (NCBI)	-1.90	-5.47	-2.18	-1.90	-1.59	-1.60
	Stress response						

aidB	putative acyl coenzyme A dehydrogenase (VIMSS)	-2.39	-2.23	-2.31	-0.04	-0.05	-0.43
appY	DLP12 prophage; DNA-binding transcriptional activator (NCBI)	-1.84	-1.27	-2.10	-0.65	-0.62	-0.34
gadA	glutamate decarboxylase A, PLP-dependent (NCBI)	-2.17	-2.27	-2.86	0.30	-0.47	-0.64
gadB	glutamate decarboxylase B, PLP-dependent (NCBI)	-1.73	-2.00	-2.46	0.36	-0.44	-0.53
gadC	predicted glutamate:gamma-aminobutyric acid antiporter (NCBI)	-1.21	-1.65	-2.02	1.10	0.06	0.00
hchA	chaperone protein HchA (NCBI)	-3.93	-3.52	-3.50	-1.87	-1.71	-1.86
hdeB	acid stress chaperone (Ecocyc)	-1.42	-1.62	-2.04	0.08	-0.23	-0.33
hdeD	acid-resistance membrane protein (NCBI)	-1.32	-1.76	-2.25	0.94	0.53	0.38
hdhA	7-alpha-hydroxysteroid dehydrogenase (NCBI)	-2.54	-2.13	-2.20	-0.69	-0.64	-0.74
ompT	DLP12 prophage; outer membrane protease VII (outer membrane protein 3b) (NCBI)	-2.44	-2.29	-2.38	-2.25	-1.95	-2.07
otsB	trehalose-6-phosphate phosphatase, biosynthetic (NCBI)	-2.23	-1.26	-1.66	-0.54	-0.16	-0.53
sodA	superoxide dismutase, manganese (VIMSS)	-2.31	-1.52	-1.03	-1.88	-1.14	-1.23
stpA	DNA binding protein, nucleoid-associated (NCBI)	-2.93	-2.95	-2.74	-2.67	-2.89	-2.50
sufA	iron-sulfur cluster assembly scaffold protein (NCBI)	-5.51	-4.49	-4.93	-2.49	-1.45	-1.46
yhiO	universal stress protein UspB (NCBI)	-2.13	-1.49	-1.87	0.05	0.74	0.41
	Translation						
rbbA	fused ribosome-associated ATPase: ATP-binding protein/ATP-binding protein/predicted membrane protein (NCBI)	-1.41	-1.75	-2.02	-1.10	-1.00	-1.27
yfiA	cold shock protein associated with 30S ribosomal subunit (NCBI)	-1.85	-1.48	-2.06	0.50	0.73	0.32
	Transport						
copA	copper transporter (NCBI)	0.22	-2.25	-2.23	2.04	-1.70	-1.60
cusC	copper/silver efflux system, outer membrane component (NCBI)	-2.72	-2.65	-2.92	4.62	-2.92	-3.04
focA	formate transporter (NCBI)	-1.73	-1.44	-2.26	0.75	1.19	1.13
lamB	maltoporin precursor (NCBI)	-1.21	-2.33	-1.85	-0.30	-0.27	-0.46
malE	maltose ABC transporter periplasmic protein (NCBI)	-1.25	-2.46	-2.06	-0.48	-0.43	-0.64
malK	fused maltose transport subunit, ATP-binding component of ABC superfamily/regulatory protein (NCBI)	-1.54	-1.73	-2.03	-0.75	-0.72	-1.07
nikA	nickel transporter subunit (NCBI)	-2.04	-0.91	-1.49	-2.19	0.21	-0.51
znuB	high-affinity zinc transporter membrane component (NCBI)	-1.83	-2.41	-2.11	0.90	0.55	0.81
znuC	high-affinity zinc transporter ATPase (NCBI)	-1.96	-2.43	-2.14	0.85	0.65	0.75
	Type 1 pilius						
fimI	fimbrial protein (VIMSS)	-1.48	-2.07	-1.81	0.32	0.06	0.04

Table S9: Upregulated pulldown genes

Name	Description	PD1	PD2	PD3	UV1	UV2
	DNA synthesis					
nrdH	glutaredoxin-like protein (NCBI)	2.40	3.28	3.05	0.89	1.04
nrdI	hypothetical protein (NCBI)	1.67	2.45	2.37	0.05	0.29
	e14 prophage					
b1146	orf, hypothetical protein (VIMSS)	5.24	5.08	5.08	5.63	5.64
intE	e14 prophage; predicted integrase (NCBI)	4.14	4.18	4.23	4.00	4.39
ycfK	e14 prophage; predicted protein (NCBI)	2.05	2.23	2.00	2.16	1.60
ymfG	e14 prophage; predicted excisionase (NCBI)	4.78	4.91	3.79	4.74	4.82

ymfJ	orf, hypothetical protein (VIMSS)	5.87	5.96	5.80	5.06	5.09
ymfL	e14 prophage; predicted DNA-binding transcriptional regulator (RefSeq)	5.08	5.20	4.60	4.26	4.59
ymfM	e14 prophage; predicted protein (NCBI)	5.23	5.11	5.11	5.50	5.79
ymfN	e14 prophage; predicted DNA-binding transcriptional regulator	4.45	4.45	4.06	3.80	4.22
ymfO	e14 prophage; conserved protein (RefSeq)	4.20	4.32	4.06	3.84	3.89
ymfP	orf, hypothetical protein (VIMSS)	3.30	3.28	3.09	2.39	2.52
ymfQ	e14 prophage; conserved protein (NCBI)	2.25	2.49	2.02	1.73	1.49
ymfR	e14 prophage; predicted protein (NCBI)	4.25	4.38	4.03	3.90	4.22
	Heat shock					
ibpA	heat shock chaperone (NCBI)	2.10	2.49	2.31	0.67	0.91
ibpB	heat shock protein (VIMSS)	2.35	2.70	2.35	0.47	0.92
	Hypothetical and predicted genes					
b3022	predicted cyanide hydratase (NCBI)	1.92	1.92	2.11	1.81	1.58
b4140	orf, hypothetical protein (VIMSS)	2.04	2.21	2.29	1.13	1.08
ybhU	hypothetical protein (RefSeq)	1.74	2.05	1.93	3.11	2.45
ycbO	orf, hypothetical protein (VIMSS)	4.86	4.72	4.58	0.11	0.20
ycjX	conserved protein with nucleoside triphosphate hydrolase domain (NCBI)	1.76	2.05	1.59	0.88	1.74
ydjM	predicted inner membrane protein regulated by LexA (RefSeq)	2.08	2.24	2.00	1.87	2.07
yebF	predicted protein (RefSeq)	2.74	2.73	2.59	1.24	1.16
yebG	conserved protein regulated by LexA (NCBI)	3.74	3.74	3.20	2.64	2.30
yjjZ	hypothetical protein (NCBI)	1.03	2.10	1.38	-0.42	-0.91
yqfA	predicted oxidoreductase, inner membrane subunit (NCBI)	2.04	2.02	1.70	-0.25	0.16
	Iron chelation and transport					
bfd	bacterioferritin-associated ferredoxin (NCBI)	1.98	2.36	1.61	0.35	-0.01
cirA	ferric iron-catecholate outer membrane transporter (NCBI)	1.42	2.03	1.57	-1.63	-1.08
exbB	membrane spanning protein in TonB-ExbB-ExbD complex (NCBI)	1.97	2.43	1.65	-0.74	-0.92
fecI	KpLE2 phage-like element; RNA polymerase, sigma 19 factor (NCBI)	2.10	2.62	2.38	-0.72	-0.96
fhuF	ferric iron reductase involved in ferric hydroximate transport (NCBI)	2.97	3.78	3.46	-0.34	-0.29
	Other					
csgA	cryptic curlin major subunit (NCBI)	2.84	2.60	2.68	0.39	0.68
csgB	curlin nucleator protein, minor subunit in curli complex (NCBI)	3.47	3.30	3.01	0.65	0.50
	Phantom gene (Ecocyc)					
tisA	lexA-regulated predicted protein (phantom gene)	4.34	4.30	3.95	1.38	0.35
	Polymerases and repair genes					
dinB	DNA polymerase IV (NCBI)	2.44	2.47	1.91	2.21	2.25
dinD	DNA-damage-inducible protein (VIMSS)	3.32	3.41	2.98	2.71	2.46
dinF	DNA-damage-inducible SOS response protein (NCBI)	2.37	2.49	2.40	1.58	1.41
dinI	DNA damage-inducible protein I (NCBI)	2.55	2.52	2.61	2.54	2.04
lexA	LexA repressor (NCBI)	2.89	2.76	2.90	0.94	1.45
recA	recombinase A (NCBI)	2.88	2.83	2.24	0.41	0.55
recN	recombination and repair protein (NCBI)	4.72	4.75	4.59	4.66	4.87
recX	RecA regulator RecX (NCBI)	3.66	3.90	3.00	1.84	1.32
rmuC	predicted recombination limiting protein (NCBI)	2.07	2.17	1.53	1.62	1.72
sbmC	DNA gyrase inhibitor (NCBI)	2.17	1.90	1.46	2.32	2.38
sulA	SOS cell division inhibitor (NCBI)	4.68	4.69	4.21	3.93	4.03
umuC	DNA polymerase V subunit UmuC (NCBI)	3.67	3.75	2.98	3.18	3.20

umuD	DNA polymerase V, subunit D (NCBI)	4.48	4.57	3.74	3.63	3.62
uvrA	excinuclease ABC subunit A (NCBI)	2.50	2.53	2.60	0.81	0.65
uvrB	excinuclease ABC subunit B (NCBI)	2.01	2.08	2.20	0.88	0.97
ydjQ	endonuclease of nucleotide excision repair (NCBI)	2.57	2.73	2.68	1.98	1.60
	Stress response					
clpB	protein disaggregation chaperone (NCBI)	2.21	2.29	2.25	-0.11	0.43
cpxP	periplasmic protein combats stress (NCBI)	2.05	2.23	1.31	0.36	0.33
cspG	DNA-binding transcriptional regulator (NCBI)	2.31	2.63	1.98	-1.01	-1.63
dinQ	Damage inducible, function unknown (RefSeq)	2.77	2.85	2.43	0.24	0.10
tisB	lexA-regulated toxic peptide (RefSeq)	5.26	5.18	5.26	-0.07	-0.83
	Sulfur utilization					
ssuD	alkanesulfonate monooxygenase (NCBI)	4.77	4.41	4.52	0.31	0.31
ssuE	NAD(P)H-dependent FMN reductase (NCBI)	5.03	5.13	3.67	0.02	0.11
tauD	taurine dioxygenase (NCBI)	4.29	4.16	3.83	0.02	0.80
	Translation					
yheL	predicted intracellular sulfur oxidation protein (NCBI)	1.67	2.01	1.43	0.47	0.29
	Transport					
mtr	tryptophan transporter of high affinity (NCBI)	1.83	2.04	1.73	0.05	-0.79
ssuB	alkanesulfonate transporter subunit (NCBI)	3.72	3.19	3.40	0.59	0.45
tauA	taurine transport system periplasmic protein (VIMSS)	4.53	4.59	4.21	0.42	0.31
tauB	taurine transporter subunit (NCBI)	4.51	4.56	4.09	0.17	0.91
tauC	taurine transporter subunit (NCBI)	4.21	4.13	3.84	0.47	0.11
ycbM	putative transport system permease protein (VIMSS)	4.46	3.88	4.01	0.02	0.18

Table S10: Downregulated pulldown genes

Name	Description	PD1	PD2	PD3	UV1	UV2
	Hypothetical and predicted genes					
ydjN	predicted transporter (NCBI)	-0.47	-0.33	-2.32	-1.79	-1.51
ymfI	orf, hypothetical protein (VIMSS)	-2.13	-2.20	-1.87	0.47	0.67
	Metabolism					
cysC	adenylylsulfate kinase (NCBI)	-0.21	-0.55	-2.04	-0.49	-0.82
cysD	sulfate adenylyltransferase subunit 2 (NCBI)	-0.79	-0.55	-2.39	-0.20	0.24
cysH	phosphoadenosine phosphosulfate reductase (NCBI)	-0.04	-0.48	-2.18	-0.07	-0.31
cysI	sulfite reductase, beta subunit, NAD(P)-binding, heme-binding (NCBI)	-0.04	-0.32	-2.38	-0.71	-0.80
cysJ	sulfite reductase, alpha subunit, flavoprotein (NCBI)	-0.28	-0.22	-2.94	-1.11	-0.80
cysM	cysteine synthase B (O-acetylserine sulfhydrolase B) (NCBI)	-0.75	-0.77	-2.88	0.42	0.36
cysN	sulfate adenylyltransferase subunit 1 (NCBI)	-0.22	-0.34	-2.39	-1.11	-0.78
fdnG	formate dehydrogenase-N, alpha subunit, nitrate-inducible (NCBI)	-1.79	-1.89	-2.02	0.36	0.34
glnK	nitrogen assimilation regulatory protein for GlnL, GlnE, and AmtB (NCBI)	-2.52	-1.38	-2.02	-0.32	-0.64
nac	DNA-binding transcriptional dual regulator of nitrogen assimilation (NCBI)	-2.62	-1.46	-1.90	-0.18	-0.26
napB	cytochrome c-type protein (VIMSS)	-2.18	-2.20	-2.63	-1.00	-0.92
napC	nitrate reductase, cytochrome c-type, periplasmic (NCBI)	-1.72	-1.64	-2.01	-0.89	-0.51
napH	quinol dehydrogenase membrane component (NCBI)	-1.91	-1.86	-2.17	-0.70	-0.52
narG	nitrate reductase 1, alpha subunit (NCBI)	-3.02	-2.87	-2.95	-0.31	-0.26
narH	nitrate reductase 1, beta (Fe-S) subunit (NCBI)	-3.49	-3.45	-3.39	-1.13	-1.22
narI	nitrate reductase 1, gamma (cytochrome b(NR)) subunit (NCBI)	-2.77	-2.82	-2.62	-0.64	-0.69
narJ	molybdenum-cofactor-assembly chaperone subunit (delta	-3.15	-3.12	-2.95	-1.07	-1.20

	subunit) of nitrate reductase 1 (NCBI)					
nirB	nitrite reductase, large subunit, NAD(P)H-binding (NCBI)	-2.61	-2.36	-2.47	-0.90	-0.63
nirD	nitrite reductase small subunit (NCBI)	-2.86	-2.69	-2.60	-0.76	-0.20
	Prophage					
flu	CP4-44 prophage; antigen 43 (Ag43) phase-variable biofilm formation autotransporter (NCBI)	-3.49	-3.15	-3.33	-4.85	-5.06
	Stress response					
yfiD	pyruvate formate lyase subunit (NCBI)	-1.96	-2.09	-2.68	-2.38	-2.68
	Transport					
amtB	ammonium transporter (NCBI)	-2.17	-1.37	-1.65	-0.60	-0.25
cysA	sulfate/thiosulfate transporter subunit (NCBI)	-0.20	-0.29	-2.64	-0.26	-0.13
cysP	thiosulfate transporter subunit (NCBI)	-0.85	-0.65	-2.15	-1.67	-1.17
narK	nitrate/nitrite transporter (NCBI)	-2.49	-2.53	-2.50	-0.52	-0.53
nirC	nitrite transporter (NCBI)	-3.35	-3.11	-3.23	-2.30	-2.04
ompW	outer membrane protein W (NCBI)	-2.38	-2.84	-2.93	-0.90	-1.13
oppD	oligopeptide transporter ATP-binding component (NCBI)	-1.12	-0.61	-2.19	-2.52	-2.72

Table S11: Upregulated UV treated genes

Name	Description	PD1	PD2	PD3	UV1	UV2
	e14 prophage					
b1146	orf, hypothetical protein (VIMSS)	5.24	5.08	5.08	5.63	5.64
intE	e14 prophage; predicted integrase (NCBI)	4.14	4.18	4.23	4.00	4.39
ycfK	e14 prophage; predicted protein (NCBI)	2.05	2.23	2.00	2.16	1.60
ymfG	e14 prophage; predicted excisionase (NCBI)	4.78	4.91	3.79	4.74	4.82
ymfJ	orf, hypothetical protein (VIMSS)	5.87	5.96	5.80	5.06	5.09
ymfL	e14 prophage; predicted DNA-binding transcriptional regulator (RefSeq)	5.08	5.20	4.60	4.26	4.59
ymfM	e14 prophage; predicted protein (NCBI)	5.23	5.11	5.11	5.50	5.79
ymfN	e14 prophage; predicted DNA-binding transcriptional regulator	4.45	4.45	4.06	3.80	4.22
ymfO	e14 prophage; conserved protein (RefSeq)	4.20	4.32	4.06	3.84	3.89
ymfP	orf, hypothetical protein (VIMSS)	3.30	3.28	3.09	2.39	2.52
ymfR	e14 prophage; predicted protein (NCBI)	4.25	4.38	4.03	3.90	4.22
	Hypothetical and predicted genes					
b1085	orf, hypothetical protein (VIMSS)	-0.50	-0.73	-0.48	2.08	2.78
b1450	orf, hypothetical protein (VIMSS)	0.50	0.43	0.33	1.84	2.12
b1481	orf, hypothetical protein (VIMSS)	-0.68	-0.60	-0.45	3.77	3.56
b1586	orf, hypothetical protein (VIMSS)	0.30	0.33	-0.25	2.65	2.18
b2080	orf, hypothetical protein (VIMSS)	0.35	0.09	0.10	2.19	2.26
yaiB	hypothetical protein (NCBI)	0.16	0.12	-0.65	2.40	2.73
yaiY	predicted inner membrane protein (NCBI)	-0.19	-0.17	-0.17	2.03	1.65
ybaS	predicted glutaminase (NCBI)	0.55	0.19	-0.40	2.15	2.50
ybdR	predicted oxidoreductase, Zn-dependent and NAD(P)-binding (NCBI)	-0.26	-0.28	-0.48	2.29	2.29
ybgS	hypothetical protein (NCBI)	0.42	0.26	0.42	2.47	2.28
ybhU	hypothetical protein (RefSeq)	1.74	2.05	1.93	3.11	2.45
ybiM	orf, hypothetical protein (VIMSS)	-0.06	-0.03	-0.09	2.70	2.12
ycaP	conserved inner membrane protein (NCBI)	-0.15	-0.17	-0.43	1.89	2.24
ycdF	orf, hypothetical protein (VIMSS)	1.46	1.08	1.30	3.61	3.54
yceK	predicted lipoprotein (NCBI)	-0.67	-0.53	-0.37	1.72	4.24
ycgZ	hypothetical protein (NCBI)	0.58	0.59	0.25	2.85	3.30

yciE	hypothetical protein (NCBI)	0.29	0.36	0.22	2.05	2.21
yciF	hypothetical protein (NCBI)	0.28	0.32	0.36	3.14	3.56
yciG	orf, hypothetical protein (VIMSS)	0.68	0.72	0.84	2.77	2.89
ydcK	predicted enzyme (NCBI)	0.37	0.11	0.25	2.07	2.25
yddV	predicted diguanylate cyclase (RefSeq)	0.18	0.36	-0.21	1.70	2.07
ydeI	hypothetical protein (NCBI)	1.61	1.42	1.50	2.38	2.11
ydgT	predicted regulator (NCBI)	0.33	0.36	0.26	2.32	1.79
ydjM	predicted inner membrane protein regulated by LexA (RefSeq)	2.08	2.24	2.00	1.87	2.07
yebG	conserved protein regulated by LexA (NCBI)	3.74	3.74	3.20	2.64	2.30
yebW	orf, hypothetical protein (VIMSS)	0.12	0.23	0.17	2.99	2.79
yegS	hypothetical protein (NCBI)	0.07	0.06	-0.25	1.99	2.27
yfiL	orf, hypothetical protein (VIMSS)	0.27	0.23	0.10	3.02	1.58
yghA	oxidoreductase (NCBI)	-0.02	-0.08	-0.08	1.58	2.13
yghW	hypothetical protein (NCBI)	0.19	0.21	0.25	6.44	6.11
yhbO	orf, hypothetical protein (VIMSS)	-0.01	-0.18	-0.08	2.02	2.01
yhcO	predicted barnase inhibitor (NCBI)	0.27	-0.04	-0.16	2.04	1.89
yhdL	hypothetical protein (NCBI)	0.37	0.44	0.46	2.13	2.05
yhhA	hypothetical protein (NCBI)	0.22	0.20	0.23	2.02	1.87
yhiM	conserved inner membrane protein (RefSeq)	1.09	0.97	0.91	3.78	3.70
yiaG	predicted transcriptional regulator (NCBI)	1.16	0.99	0.61	2.33	2.06
yibT	hypothetical protein (NCBI)	0.14	0.33	0.18	2.15	2.25
yidB	orf, hypothetical protein (VIMSS)	-0.21	-0.26	-0.45	2.14	2.37
yjbJ	predicted stress response protein (NCBI)	1.11	1.11	1.12	2.05	1.56
yjdI	hypothetical protein (NCBI)	0.07	0.05	-0.92	2.25	2.16
yjfY	hypothetical protein (NCBI)	0.36	0.25	-0.04	2.69	2.65
yjhT	orf, hypothetical protein (VIMSS)	0.43	0.25	0.17	1.41	2.01
yjjY	hypothetical protein (NCBI)	-0.99	-0.81	-0.70	5.01	6.13
yliL	hypothetical protein (NCBI)	-0.48	-0.62	-0.58	1.36	2.04
ymgA	hypothetical protein (NCBI)	0.72	0.87	0.71	3.62	4.34
ymgB	hypothetical protein (NCBI)	0.61	0.55	0.57	2.17	2.85
yncG	predicted enzyme (NCBI)	0.58	0.43	0.31	2.10	1.59
yoaC	predicted protein (RefSeq)	0.53	0.40	0.18	2.12	2.37
ypeC	hypothetical protein (NCBI)	-0.06	-0.08	-0.01	2.22	2.10
yqgD	predicted inner membrane protein	-0.65	-0.63	-0.56	1.72	3.65
	Metabolism					
bglJ	DNA-binding transcriptional activator (RefSeq)	-0.14	-0.22	-0.13	1.76	2.23
hybA	hydrogenase 2 4Fe-4S ferredoxin-type component (NCBI)	-0.02	-0.04	-0.22	2.62	2.30
hybO	hydrogenase 2, small subunit (NCBI)	-0.09	-0.18	0.03	2.95	2.91
psiF	induced by phosphate starvation (VIMSS)	0.15	-0.02	-0.67	1.88	2.08
	Other					
GadE	acid-responsive regulator of gadA and gadBC (Katherine Huang)	0.70	0.52	0.35	3.56	3.34
slp	outer membrane protein induced after carbon starvation (VIMSS)	0.52	0.19	0.34	2.09	1.61
wza	lipoprotein required for capsular polysaccharide translocation through the outer membrane (NCBI)	0.83	1.01	1.01	2.07	1.16
	Polymerases and repair genes					
dinB	DNA polymerase IV (NCBI)	2.44	2.47	1.91	2.21	2.25
dinD	DNA-damage-inducible protein (VIMSS)	3.32	3.41	2.98	2.71	2.46
dinI	DNA damage-inducible protein I (NCBI)	2.55	2.52	2.61	2.54	2.04
recN	recombination and repair protein (NCBI)	4.72	4.75	4.59	4.66	4.87

sbmC	DNA gyrase inhibitor (NCBI)	2.17	1.90	1.46	2.32	2.38
sulA	SOS cell division inhibitor (NCBI)	4.68	4.69	4.21	3.93	4.03
umuC	DNA polymerase V subunit UmuC (NCBI)	3.67	3.75	2.98	3.18	3.20
umuD	DNA polymerase V, subunit D (NCBI)	4.48	4.57	3.74	3.63	3.62
	Stress response					
gadX	DNA-binding transcriptional dual regulator (NCBI)	0.49	0.55	0.15	2.04	2.06
hdhA	7-alpha-hydroxysteroid dehydrogenase (NCBI)	0.66	0.43	0.36	1.82	2.08
hslJ	heat-inducible protein (NCBI)	-0.07	-0.06	0.06	2.21	1.95
osmB	lipoprotein (NCBI)	0.30	0.08	0.14	2.58	2.18
otsB	trehalose-6-phosphate phosphatase, biosynthetic (NCBI)	0.42	0.29	0.17	1.96	2.08
yibA	lyase containing HEAT-repeat (NCBI)	0.37	0.23	0.21	2.20	1.95
	Transport					
mdtE	multidrug resistance efflux transporter (NCBI)	-0.12	-0.03	-0.40	1.86	2.46
modA	molybdate transporter subunit (NCBI)	-0.34	-0.26	-0.12	3.75	3.60
modB	molybdate ABC transporter permease protein (NCBI)	-0.17	0.07	-0.03	2.45	2.54

Table S12: Downregulated UV treated genes:

Name	Description	PD1	PD2	PD3	UV1	UV2
	Hypothetical and predicted genes					
b2001	orf, hypothetical protein (VIMSS)	-1.48	-1.43	-1.52	-2.44	-2.61
icdC	Pseudogene	1.77	1.46	1.68	-2.00	-2.50
ybgT	hypothetical protein (NCBI)	-1.05	-0.89	-1.49	-2.16	-2.06
ycgF	predicted FAD-binding phosphodiesterase (NCBI)	-0.42	-0.20	-0.43	-0.95	-2.10
yebA	orf, hypothetical protein (VIMSS)	0.69	0.96	0.23	-2.08	-2.11
yebL	putative adhesin (VIMSS)	-0.56	0.05	-0.82	-2.63	-2.63
yidD	hypothetical protein (NCBI)	-0.01	0.32	0.09	-1.71	-2.05
yobF	hypothetical protein (NCBI)	0.07	-0.02	-0.64	-3.83	-3.90
yodA	conserved metal-binding protein (NCBI)	-0.60	-0.05	-0.70	-3.79	-3.62
yodB	putative cytochrome (VIMSS)	0.25	0.20	0.15	-3.42	-3.34
	Membrane					
lpp	murein lipoprotein (NCBI)	-0.21	-0.39	-0.07	-6.28	-6.20
	Metabolism					
acpP	acyl carrier protein (NCBI)	-0.01	-0.12	-0.11	-3.37	-3.35
argA	N-acetylglutamate synthase (NCBI)	-0.03	-0.31	-0.18	-2.19	-1.74
argF	CP4-6 prophage; ornithine carbamoyltransferase 2, chain F (NCBI)	-0.51	-0.64	-0.56	-2.51	-2.38
argI	ornithine carbamoyltransferase 1 (NCBI)	-0.10	-0.36	-0.64	-2.78	-2.89
atpD	F0F1 ATP synthase subunit beta (NCBI)	0.45	0.32	0.48	-2.21	-2.03
atpE	F0F1 ATP synthase subunit C (NCBI)	0.08	0.08	0.13	-2.03	-1.97
ddg	putative heat shock protein (VIMSS)	0.20	0.67	-0.33	-1.51	-3.04
eno	phosphopyruvate hydratase (NCBI)	-0.27	-0.28	-1.38	-2.54	-2.32
fruK	1-phosphofructokinase (NCBI)	-0.91	-0.30	-0.43	-2.09	-1.66
gapA	glyceraldehyde-3-phosphate dehydrogenase (NCBI)	-0.20	-0.26	-0.34	-3.53	-3.97
gatD	galactitol-1-phosphate dehydrogenase, Zn-dependent and NAD(P)-binding (NCBI)	0.16	0.39	-0.51	-2.38	-2.29
gpmA	phosphoglyceromutase (NCBI)	0.13	0.03	-0.30	-2.08	-2.33
ivbL	ilvB operon leader peptide (NCBI)	0.89	0.76	0.68	-1.79	-2.13
leuL	leu operon leader peptide (NCBI)	-0.09	-0.34	-0.56	-3.54	-4.33
thrL	thr operon leader peptide (NCBI)	0.34	0.13	0.10	-5.13	-5.70
	Other					

bipA	GTP-binding protein (NCBI)	-0.16	-0.18	-0.87	-2.10	-2.19
cusF	periplasmic copper-binding protein (NCBI)	-0.83	-0.93	-0.81	-4.07	-3.53
deaD	inducible ATP-independent RNA helicase (VIMSS)	0.49	0.60	0.54	-1.75	-2.61
ompX	outer membrane protein X (NCBI)	0.79	0.77	0.30	-2.78	-2.99
ykgM	50S ribosomal protein L31 (NCBI)	-0.20	0.41	-0.51	-5.73	-5.73
ykgO	rpmJ (L36) paralog (NCBI)	-0.43	0.18	-0.78	-5.86	-5.73
	Polymerases and repair genes					
ruvC	Holliday junction resolvase (NCBI)	-0.12	-0.16	-0.37	-1.41	-2.12
	Prophage					
flu	CP4-44 prophage; antigen 43 (Ag43) phase-variable biofilm formation autotransporter (NCBI)	-3.49	-3.15	-3.33	-4.85	-5.06
	Stress response					
cspA	major cold shock protein (NCBI)	0.78	0.87	0.13	-2.93	-3.51
cspB	Qin prophage; cold shock protein (NCBI)	1.52	1.91	0.90	-1.07	-2.58
cspC	stress protein, member of the CspA-family (NCBI)	0.00	-0.12	-0.04	-4.26	-4.14
cspE	cold shock protein E (NCBI)	0.16	0.10	0.23	-3.13	-3.87
dps	DNA protection during starvation conditions (NCBI)	0.98	0.43	0.01	-1.86	-2.47
ecnB	entericidin B membrane lipoprotein (NCBI)	0.55	0.09	-0.13	-1.49	-2.69
evgS	hybrid sensory histidine kinase in two-component regulatory system with EvgA (NCBI)	-0.72	-0.64	-0.73	-1.32	-2.46
hdeA	acid-resistance protein, possible chaperone , subunit of HdeA dimer, inactive form of acid-resistance protein (Katherine Huang)	0.25	0.06	0.15	-2.09	-2.21
hns	global DNA-binding transcriptional dual regulator H-NS (NCBI)	0.04	0.01	-0.59	-1.80	-2.30
hupB	HU, DNA-binding transcriptional regulator, beta subunit (NCBI)	0.00	-0.29	-0.11	-2.26	-2.52
rsxG	electron transport complex protein RnfG (NCBI)	-0.14	-0.01	0.06	-0.98	-2.25
tpx	thiol peroxidase (NCBI)	0.49	0.25	0.51	-1.52	-2.01
yfiD	pyruvate formate lyase subunit (NCBI)	-1.96	-2.09	-2.68	-2.38	-2.68
	Transcription					
rpoA	DNA-directed RNA polymerase subunit alpha (NCBI)	0.11	0.12	0.13	-3.09	-2.59
rpoS	RNA polymerase sigma factor (NCBI)	0.55	0.52	0.02	-2.64	-2.28
	Translation					
infB	translation initiation factor IF-2 (NCBI)	0.29	0.53	-0.03	-1.78	-2.14
infC	translation initiation factor IF-3 (NCBI)	0.06	0.07	-0.42	-2.33	-2.39
rhlE	RNA helicase (NCBI)	-0.70	-0.37	-0.87	-1.52	-2.05
rmf	ribosome modulation factor (NCBI)	0.84	0.63	0.58	-3.77	-4.28
rplA	50S ribosomal protein L1 (NCBI)	0.18	0.18	0.11	-3.10	-2.83
rplB	50S ribosomal protein L2 (NCBI)	-0.06	0.04	-0.09	-2.42	-2.15
rplC	50S ribosomal protein L3 (NCBI)	-0.08	0.01	-0.69	-2.85	-2.66
rplD	50S ribosomal protein L4 (NCBI)	-0.03	0.02	-0.08	-3.01	-2.50
rplE	50S ribosomal protein L5 (NCBI)	-0.14	-0.10	-0.59	-3.82	-3.57
rplF	50S ribosomal protein L6 (NCBI)	-0.04	0.11	-0.59	-2.45	-1.93
rplI	50S ribosomal protein L9 (NCBI)	-0.03	-0.14	0.10	-2.33	-2.45
rplJ	50S ribosomal protein L10 (NCBI)	0.01	-0.05	-0.04	-2.76	-1.99
rplL	50S ribosomal protein L7/L12 (NCBI)	0.12	0.04	-0.97	-3.17	-3.03
rplN	50S ribosomal protein L14 (NCBI)	-0.03	0.02	-0.06	-2.78	-3.12
rplO	50S ribosomal protein L15 (NCBI)	0.18	0.19	0.07	-3.57	-3.33
rplP	50S ribosomal protein L16 (NCBI)	0.12	0.14	0.11	-2.76	-2.61
rplQ	50S ribosomal protein L17 (NCBI)	0.47	0.33	0.30	-3.98	-3.61
rplR	50S ribosomal protein L18 (NCBI)	0.14	0.10	0.07	-2.92	-2.94
rplS	50S ribosomal protein L19 (NCBI)	0.12	-0.01	0.17	-2.40	-2.84

rplT	50S ribosomal protein L20 (NCBI)	-0.20	-0.39	0.08	-3.95	-4.06
rplV	50S ribosomal protein L22 (NCBI)	0.17	0.12	0.07	-3.92	-3.89
rplW	50S ribosomal protein L23 (NCBI)	-0.10	0.00	-0.08	-3.67	-3.74
rplX	50S ribosomal protein L24 (NCBI)	-0.10	-0.02	-0.68	-3.00	-2.97
rpmA	50S ribosomal protein L27 (NCBI)	0.10	-0.12	0.11	-3.37	-3.31
rpmB	50S ribosomal protein L28 (NCBI)	0.05	-0.03	-0.54	-2.64	-2.89
rpmC	50S ribosomal protein L29 (NCBI)	0.28	0.32	-0.30	-3.00	-3.62
rpmD	50S ribosomal protein L30 (NCBI)	0.14	0.17	0.06	-3.91	-3.37
rpmF	50S ribosomal protein L32 (NCBI)	-0.03	-0.07	0.05	-2.35	-2.70
rpmG	50S ribosomal protein L33 (NCBI)	-0.23	-0.29	0.05	-4.65	-4.58
rpmH	50S ribosomal protein L34 (NCBI)	-0.05	0.13	-0.47	-2.50	-3.03
rpmI	50S ribosomal subunit protein A (VIMSS)	-0.03	-0.12	-0.44	-4.45	-4.85
rpmJ	50S ribosomal protein L36 (NCBI)	0.03	0.00	-1.13	-2.20	-1.97
rpsA	30S ribosomal protein S1 (NCBI)	0.00	0.06	-0.42	-2.43	-2.12
rpsC	30S ribosomal protein S3 (NCBI)	0.10	0.14	-0.85	-3.06	-2.76
rpsD	30S ribosomal protein S4 (NCBI)	0.11	0.10	0.03	-2.60	-2.53
rpsE	30S ribosomal protein S5 (NCBI)	0.10	0.15	-0.36	-3.05	-2.78
rpsG	30S ribosomal protein S7 (NCBI)	-0.05	-0.01	-0.58	-2.50	-2.50
rpsH	30S ribosomal protein S8 (NCBI)	0.02	0.05	-0.01	-2.55	-1.98
rpsI	30S ribosomal protein S9 (NCBI)	0.28	0.10	-0.05	-3.80	-3.57
rpsK	30S ribosomal protein S11 (NCBI)	0.01	0.04	-1.24	-3.03	-2.32
rpsM	30S ribosomal protein S13 (NCBI)	0.04	0.05	0.02	-2.55	-2.49
rpsN	30S ribosomal protein S14 (NCBI)	0.05	0.09	-0.59	-2.72	-2.49
rpsO	30S ribosomal protein S15 (NCBI)	0.01	-0.07	-0.24	-1.71	-2.47
rpsQ	30S ribosomal protein S17 (NCBI)	-0.10	-0.17	0.12	-4.32	-4.68
rpsR	30S ribosomal protein S18 (NCBI)	-0.10	-0.05	0.00	-3.06	-2.68
rpsS	30S ribosomal protein S19 (NCBI)	0.07	0.07	0.05	-3.29	-3.19
rpsT	30S ribosomal protein S20 (NCBI)	-0.01	-0.16	-1.28	-2.18	-2.58
tsf	elongation factor Ts (NCBI)	-0.17	-0.16	-0.10	-2.92	-2.73
tufA	protein chain elongation factor EF-Tu (duplicate of tufB) (NCBI)	0.00	0.01	-0.06	-3.43	-3.24
	Transport					
crr	glucose-specific PTS system enzyme IIA component (NCBI)	-0.11	-0.25	-0.01	-2.70	-2.86
cusB	copper/silver efflux system, membrane fusion protein (NCBI)	-0.02	-0.01	-0.08	-2.25	-2.44
fruA	fused fructose-specific PTS enzymes: IIBcomponent/IIC components (NCBI)	-0.35	0.01	-0.23	-2.35	-2.04
fruB	fused fructose-specific PTS enzymes: IIA component/HPr component (NCBI)	-1.25	-0.47	-1.05	-2.82	-2.32
gatB	galactitol-specific enzyme IIB component of PTS (NCBI)	-0.21	0.01	-0.69	-2.01	-2.14
gatC	galactitol-specific enzyme IIC component of PTS (NCBI)	0.06	0.22	-0.62	-2.56	-2.35
lysP	lysine transporter (NCBI)	-0.60	-1.10	-0.67	-1.75	-2.09
nirC	nitrite transporter (NCBI)	-3.35	-3.11	-3.23	-2.30	-2.04
ompA	outer membrane protein A (3a;II*;G;d) (NCBI)	-0.38	-0.41	-0.37	-3.02	-2.47
ompC	outer membrane porin protein C (NCBI)	0.03	-0.30	-0.17	-3.98	-3.78
oppB	oligopeptide permease ABC transporter membrane protein (NCBI)	-1.61	-1.02	-1.79	-2.09	-2.02
oppC	oligopeptide transporter subunit (NCBI)	-1.57	-0.94	-1.72	-2.22	-2.77
oppD	oligopeptide transporter ATP-binding component (NCBI)	-1.12	-0.61	-2.19	-2.52	-2.72
oppF	oligopeptide transporter subunit (NCBI)	-1.02	-0.58	-1.61	-2.51	-2.75
ptsG	fused glucose-specific PTS enzymes: IIB component/IIC component (NCBI)	-0.52	-0.35	-1.07	-2.09	-1.96
ptsI	PEP-protein phosphotransferase of PTS system (enzyme I) (NCBI)	-0.43	-0.31	-0.28	-1.94	-2.10
secY	protein translocase subunit SecY (NCBI)	0.03	0.10	0.02	-2.26	-2.00

znuB	high-affinity zinc transporter membrane component (NCBI)	0.39	0.52	0.31	-2.21	-1.83
znuC	high-affinity zinc transporter ATPase (NCBI)	0.15	0.31	-0.01	-2.12	-2.18