SUPPLEMENTAL DATA

Genome expression analysis of non-proliferating intracellular *Salmonella* unravels an acid pH-dependent PhoP-PhoQ response essential for dormancy

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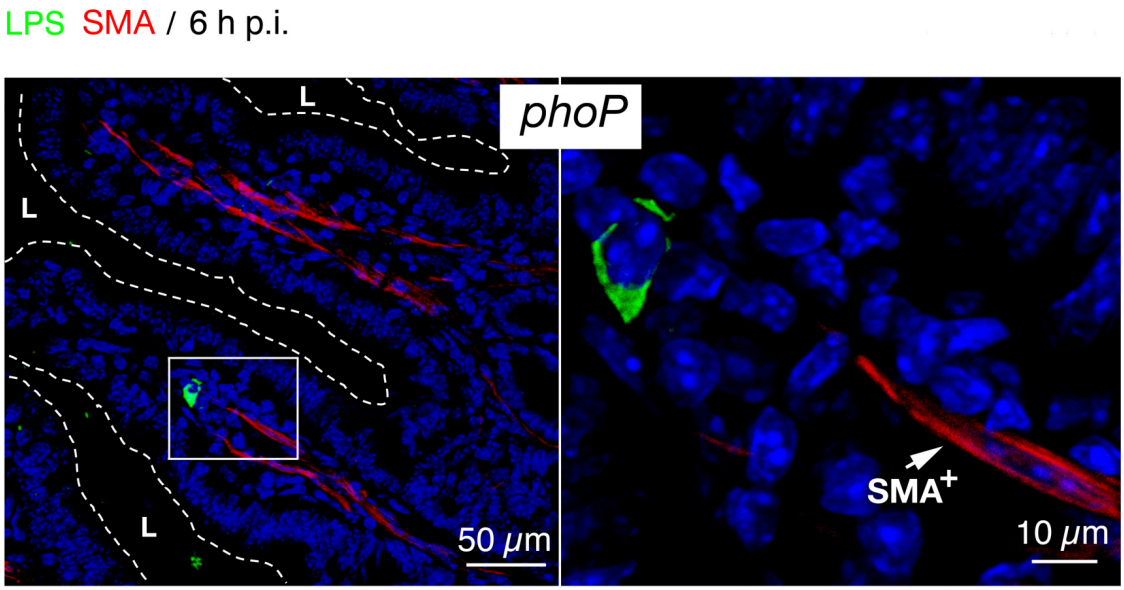

Figure S1. S. Typhimurium *phoP* bacteria overgrow in stromal cells positioned in the lamina propria of mouse intestinal villi negative for the smooth-muscle actin (SMA) marker. Samples were processed at 6 h after the oral administration of bacteria. SMA is shown in red and *S.* Typhimruium LPS in green. Nuclei were stained with To-Pro3. The image on the right is a higher magnification of the area outlined with a box in the left image. L: intestinal lumen.

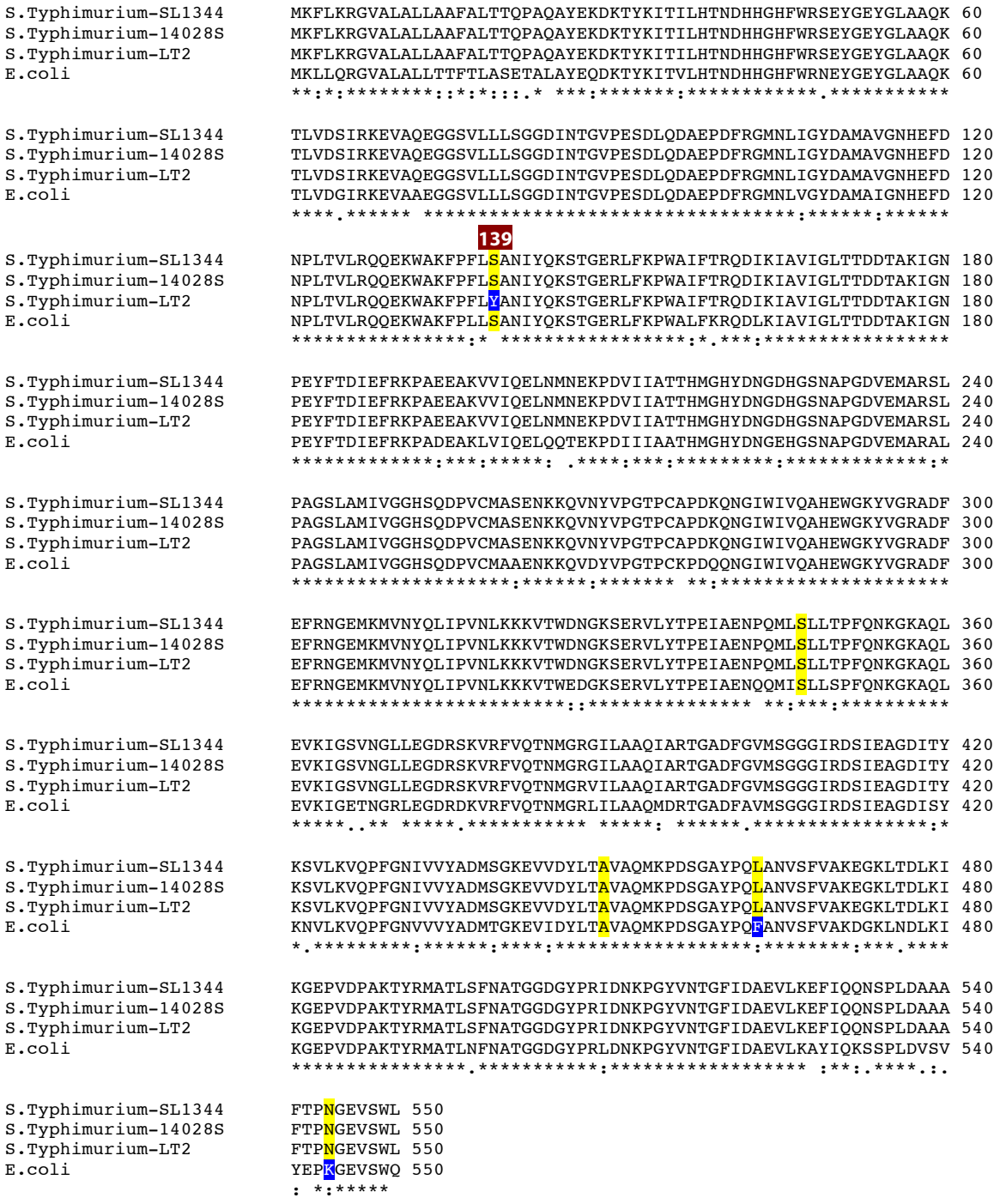

Figure S2. Multiple alignment of the UshA enzymes encoded by the genomes of *Escherichia coli* K-12 strain MG1655 and in *S.* Typhimurium strains LT2, SL1344 and 14028s. Highlighted is the residue 139, for which Innes et al. (1) reported that a S139Y missense mutation caused loss of enzymatic activity (5' nucleotidase) in some *S.* Typhimurium strains. This non-functional allele was named *ushA*^{c}. The figure shows in color other residues analyzed by Innes et al. (1) for which variations among some *S. enterica* serovars and *S.* Typhimruium strains were found.

1. **Innes, D., I. R. Beacham, C. A. Beven, M. Douglas, M. W. Laird, J. C. Joly, and D. M. Burns.** 2001. The cryptic *ushA* gene (ushA(c)) in natural isolates of *Salmonella enterica* (serotype Typhimurium) has been inactivated by a single missense mutation. Microbiology **147:**1887-1896.

Table S1. Gene expression comparison between *S. enterica* serovar Typhimurium wild-type strain SV5015 (SL1344, His$^+$) and the isogenic mutant MD1120 (*phoP*::Tn*10*,His$^+$) in active growth conditions (LB-exponential phase)

			Extracellular *phoP* LB-exponential ↓ relative to extracellular WT, LB-exponential	
Systematic name	**Name**	**Product**	**log2Ratio (M)**	*p* value
STM0002	thrA	bifunctional aspartokinase I/homeserine dehydrogenase I	**0.19**	0.76008
STM0002	thrA	bifunctional aspartokinase I/homeserine dehydrogenase I	**-0.27**	0.62199
STM0003	thrB	homoserine kinase	**-0.45**	0.31280
STM0003	thrB	homoserine kinase	**-0.02**	0.96687
STM0004	thrC	threonine synthase	**-0.35**	0.38919
STM0004	thrC	threonine synthase	**-0.50**	0.27312
STM0005	yaaA	hypothetical protein STM0005	**-0.36**	0.31280
STM0005	yaaA	hypothetical protein STM0005	**0.21**	0.55956
STM0006	yaaJ	putative alanine/glycine transport protein	**-0.22**	0.56759
STM0006	yaaJ	putative alanine/glycine transport protein	**0.08**	0.86296
STM0007	talB	transaldolase	**0.20**	0.62980
STM0007	talB	transaldolase	**0.35**	0.52101
STM0008	mogA	molybdenum cofactor biosynthesis protein	**-0.40**	0.39186
STM0008	mogA	molybdenum cofactor biosynthesis protein	**-0.29**	0.56569
STM0009	yaaH	putative regulatory protein	**-0.76**	0.30519
STM0009	yaaH	putative regulatory protein	**-0.20**	0.88198
STM0010	htgA	positive regulator	**-0.23**	0.69828
STM0010	htgA	positive regulator	**-0.64**	0.33452
STM0011	yaaI	putative periplasmic protein	**0.13**	0.78844
STM0011	yaaI	putative periplasmic protein	**0.16**	0.74436
STM0012	dnaK	molecular chaperone DnaK	**-0.92**	0.14154
STM0012	dnaK	molecular chaperone DnaK	**-0.36**	0.38320
STM0013	dnaJ	heat shock protein	**-0.77**	0.14285
STM0013	dnaJ	heat shock protein	**-0.12**	0.74361
STM0014	STM0014	putative transcriptional regulator	**-0.32**	0.45629
STM0014	STM0014	putative transcriptional regulator	**-0.65**	0.15799
STM0015	STM0015	putative bacteriophage protein	**-0.09**	0.83949
STM0015	STM0015	putative bacteriophage protein	**-0.05**	0.89675
STM0016	STM0016	hypothetical protein STM0016	**0.36**	0.56101
STM0016	STM0016	hypothetical protein STM0016	**0.26**	0.70137
STM0017	STM0017	hypothetical protein STM0017	**0.57**	0.38729
STM0017	STM0017	hypothetical protein STM0017	**0.91**	0.37342
STM0018	STM0018	putative exochitinase	**-0.38**	0.59237
STM0018	STM0018	putative exochitinase	**0.11**	0.86947
STM0019	STM0019	putative hydroxymethyltransferase	**-0.03**	0.96568
STM0019	STM0019	putative hydroxymethyltransferase	**0.55**	0.31139
STM0020	STM0020	putative cytoplasmic protein	**0.15**	0.80843
STM0020	STM0020	putative cytoplasmic protein	**0.69**	0.19927
STM0021	bcfA	fimbrial subunit	**-0.34**	0.51487
STM0021	bcfA	fimbrial subunit	**-0.05**	0.92884
STM0022	bcfB	fimbrial chaperone	**-0.45**	0.35955
STM0022	bcfB	fimbrial chaperone	**0.23**	0.64838
STM0023	bcfC	fimbrial usher	**-0.23**	0.66177
STM0023	bcfC	fimbrial usher	**0.32**	0.61833
STM0024	bcfD	fimbrial subunit	**-0.27**	0.53840
STM0024	bcfD	fimbrial subunit	**0.90**	0.29912
STM0025	bcfE	fimbrial subunit	**0.10**	0.84244
STM0025	bcfE	fimbrial subunit	**0.48**	0.30813
STM0026	bcfF	fimbrial subunit	**-0.05**	0.92161
STM0026	bcfF	fimbrial subunit	**-0.10**	0.87826
STM0027	bcfG	fimbrial chaperone	**-0.59**	0.34449
STM0027	bcfG	fimbrial chaperone	**-0.28**	0.51300
STM0028	bcfH	putative thiol-disulfide isomerase	**0.15**	0.77801
STM0028	bcfH	putative thiol-disulfide isomerase	**0.44**	0.45367

STM0028,1n	STM0028,1n	hypothetical protein STM0028,1n	**-0.50**	0.19843
STM0028,1n	STM0028,1n	hypothetical protein STM0028,1n	**-0.03**	0.97415
STM0029	STM0029	putative transcriptional regulator	**-0.48**	0.41285
STM0029	STM0029	putative transcriptional regulator	**0.59**	0.40227
STM0030	STM0030	putative transcriptional regulator	**-0.12**	0.81419
STM0030	STM0030	putative transcriptional regulator	**0.25**	0.69398
STM0031	STM0031	putative transcriptional regulator	**-0.22**	0.70913
STM0031	STM0031	putative transcriptional regulator	**0.62**	0.51486
STM0032	STM0032	putative arylsulfatase	**-0.63**	0.20285
STM0032	STM0032	putative arylsulfatase	**-0.11**	0.84486
STM0033	STM0033	putative 5'-nucleotidase	**-0.33**	0.65130
STM0033	STM0033	putative 5'-nucleotidase	**-0.20**	0.69882
STM0034	STM0034	putative outer membrane/exported protein	**0.30**	0.59096
STM0034	STM0034	putative outer membrane/exported protein	**1.09**	0.19994
STM0035	STM0035	putative arylsulfatase	**-0.65**	0.26261
STM0035	STM0035	putative arylsulfatase	**0.44**	0.36017
STM0036	STM0036	putative arylsulfatase regulator	**0.03**	0.95892
STM0036	STM0036	putative arylsulfatase regulator	**-0.97**	0.70229
STM0037	STM0037	putative cytoplasmic protein	**0.00**	0.99452
STM0037	STM0037	putative cytoplasmic protein	**0.42**	0.36636
STM0038	STM0038	putative arylsulfatase	**-0.08**	0.88575
STM0038	STM0038	putative arylsulfatase	**0.09**	0.82839
STM0039	nhaA	Na+/H antiporter	**-0.18**	0.66443
STM0039	nhaA	Na+/H antiporter	**0.04**	0.93582
STM0040	nhaR	transcriptional activator	**-0.45**	0.33531
STM0040	nhaR	transcriptional activator	**0.33**	0.43219
STM0041	STM0041	putative glycosyl hydrolase	**-0.36**	0.50190
STM0041	STM0041	putative glycosyl hydrolase	**0.07**	0.89542
STM0042	STM0042	putative sodium galactoside symporter	**-0.23**	0.76074
STM0042	STM0042	putative sodium galactoside symporter	**0.60**	0.30481
STM0043	rpsT	30S ribosomal protein S20	**-0.64**	0.38068
STM0043	rpsT	30S ribosomal protein S20	**-0.47**	0.62054
STM0044	yaaY	putative cytoplasmic protein	**-0.38**	0.29726
STM0044	yaaY	putative cytoplasmic protein	**-0.35**	0.44020
STM0045	ribF	hypothetical protein STM0045	**0.07**	0.86296
STM0045	ribF	hypothetical protein STM0045	**0.18**	0.65130
STM0046	ileS	isoleucyl-tRNA synthetase	**-0.14**	0.70726
STM0046	ileS	isoleucyl-tRNA synthetase	**0.11**	0.79185
STM0047	lspA	signal peptidase II	**-0.25**	0.52101
STM0047	lspA	signal peptidase II	**-0.10**	0.87154
STM0048	slpA	FKBP-type peptidyl-prolyl cis-trans isomerase	**-0.15**	0.75544
STM0048	slpA	FKBP-type peptidyl-prolyl cis-trans isomerase	**0.38**	0.36092
STM0049	lytB	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	**-0.25**	0.47159
STM0049	lytB	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	**-0.16**	0.67919
STM0050	STM0050	putative nitrite reductase	**-0.28**	0.62174
STM0050	STM0050	putative nitrite reductase	**0.13**	0.81667
STM0051	rihC	putative purine nucleoside hydrolase	**-0.41**	0.37241
STM0051	rihC	putative purine nucleoside hydrolase	**0.01**	0.99268
STM0052	STM0052	putative transcriptional regulator	**-0.38**	0.34051
STM0052	STM0052	putative transcriptional regulator	**0.22**	0.74243
STM0053	STM0053	putative transcriptional regulator	**-0.14**	0.75371
STM0053	STM0053	putative transcriptional regulator	**-0.32**	0.54735
STM0054	STM0054	putative oxalacetate decarboxylase subunit beta	**-0.38**	0.55145
STM0054	STM0054	putative oxalacetate decarboxylase subunit beta	**0.02**	0.96595
STM0054	STM0054	putative oxalacetate decarboxylase subunit beta	**0.22**	0.67943
STM0054	STM0054	putative oxalacetate decarboxylase subunit beta	**0.40**	0.40121
STM0056	STM0056	putative oxaloacetate decarboxylase subunit gamma	**0.12**	0.80840
STM0056	STM0056	putative oxaloacetate decarboxylase subunit gamma	**1.05**	0.19946
STM0057	STM0057	putative citrate-sodium symporter	**-0.02**	0.98620
STM0057	STM0057	putative citrate-sodium symporter	**0.71**	0.35824
STM0058	citC2	putative citrate lyase synthetase	**-0.63**	0.25759
STM0058	citC2	putative citrate lyase synthetase	**-0.15**	0.80976
STM0059	citD2	putative citrate lyase acyl carrier protein gamma chain	**0.09**	0.94102

STM0059	citD2	putative citrate lyase acyl carrier protein gamma chain	**-0.04**	0.97108
STM0060	citE2	putative citrate lyase beta chain	**0.01**	0.98800
STM0060	citE2	putative citrate lyase beta chain	**0.59**	0.46720
STM0061	citF2	putative citrate lyase alpha chain/citrate-ACP transferase	**0.23**	0.65795
STM0061	citF2	putative citrate lyase alpha chain/citrate-ACP transferase	**0.54**	0.56129
STM0062	citX2	putative cytoplasmic protein	**-0.57**	0.18265
STM0062	citX2	putative cytoplasmic protein	**0.31**	0.38668
STM0063	citG2	triphosphoribosyl-dephospho-CoA synthase	**-0.50**	0.34070
STM0063	citG2	triphosphoribosyl-dephospho-CoA synthase	**-0.16**	0.68830
STM0064	dapB	dihydrodipicolinate reductase	**-0.03**	0.95815
STM0064	dapB	dihydrodipicolinate reductase	**0.17**	0.73103
STM0066	carA	carbamoyl-phosphate synthase small subunit	**-0.13**	0.78755
STM0066	carA	carbamoyl-phosphate synthase small subunit	**0.24**	0.62216
STM0067	carB	carbamoyl-phosphate synthase large subunit	**-0.15**	0.79893
STM0067	carB	carbamoyl-phosphate synthase large subunit	**0.05**	0.93419
STM0068	caiF	of cai/fix operon transcriptional regulator	**0.12**	0.92074
STM0068	caiF	of cai/fix operon transcriptional regulator	**-0.73**	0.37466
STM0069	caiE	carnitine racemase stimulation factor	**-1.44**	0.04499
STM0069	caiE	carnitine racemase stimulation factor	**0.24**	0.62617
STM0070	caiD	carnitinyl-CoA dehydratase	**-0.73**	0.25357
STM0070	caiD	carnitinyl-CoA dehydratase	**-0.17**	0.78990
STM0071	caiC	crotonobetaine/carnitine-CoA ligase	**-0.23**	0.65181
STM0071	caiC	crotonobetaine/carnitine-CoA ligase	**0.67**	0.16696
STM0072	caiB	crotonobetainyl-CoA:carnitineCoA-transferase	**-0.60**	0.19398
STM0072	caiB	crotonobetainyl-CoA:carnitineCoA-transferase	**-0.10**	0.89487
STM0073	caiA	crotonobetainyl-CoA dehydrogenase	**-0.26**	0.66893
STM0073	caiA	crotonobetainyl-CoA dehydrogenase	**0.03**	0.95703
STM0074	caiT	L-carnitine/gamma-butyrobetaine antiporter	**-0.46**	0.45852
STM0074	caiT	L-carnitine/gamma-butyrobetaine antiporter	**-0.04**	0.94573
STM0075	fixA	putative electron transfer flavoprotein subunit beta	**-0.74**	0.24907
STM0075	fixA	putative electron transfer flavoprotein subunit beta	**0.92**	0.28406
STM0076	fixB	putative electron transfer flavoprotein subunit alpha	**-0.32**	0.65724
STM0076	fixB	putative electron transfer flavoprotein subunit alpha	**0.02**	0.96687
STM0077	fixC	flavoprotein	**0.06**	0.94765
STM0077	fixC	flavoprotein	**0.53**	0.31458
STM0078	fixX	putative ferredoxin	**-0.15**	0.85270
STM0078	fixX	putative ferredoxin	**1.03**	0.16658
STM0079	yaaU	putative transport protein	**0.01**	0.98332
STM0079	yaaU	putative transport protein	**1.18**	0.11416
STM0080	STM0080	putative outer membrane lipoprotein	**-0.17**	0.71298
STM0080	STM0080	putative outer membrane lipoprotein	**0.86**	0.13112
STM0081	STM0081	putative secreted protein	**-0.96**	0.12727
STM0081	STM0081	putative secreted protein	**-0.02**	0.97050
STM0082	STM0082	putative secreted protein	**0.12**	0.77474
STM0082	STM0082	putative secreted protein	**0.87**	0.17276
STM0084	STM0084	putative sulfatase	**-0.73**	0.19843
STM0084	STM0084	putative sulfatase	**-0.14**	0.80103
STM0085	yabF	glutathione-regulated potassium-efflux system ancillary protein	**-0.03**	0.96165
STM0085	yabF	glutathione-regulated potassium-efflux system ancillary protein	**0.31**	0.59497
STM0086	kefC	glutathione-regulated potassium-efflux system protein	**0.09**	0.89580
STM0086	kefC	glutathione-regulated potassium-efflux system protein	**0.41**	0.57686
STM0087	folA	dihydrofolate reductase type I	**-0.01**	0.98555
STM0087	folA	dihydrofolate reductase type I	**0.21**	0.62757
STM0088	apaH	diadenosinetetraphosphatase	**-0.11**	0.84910
STM0088	apaH	diadenosinetetraphosphatase	**0.23**	0.64525
STM0089	apaG	hypothetical protein STM0089	**-0.25**	0.53453
STM0089	apaG	hypothetical protein STM0089	**-0.08**	0.87740
STM0090	ksgA	dimethyladenosine transferase	**0.03**	0.95380
STM0090	ksgA	dimethyladenosine transferase	**-0.04**	0.92637

STM0091	pdxA	4-hydroxythreonine-4-phosphate dehydrogenase	**-0.16**	0.68240
STM0091	pdxA	4-hydroxythreonine-4-phosphate dehydrogenase	**-0.39**	0.29044
STM0092	surA	peptidyl-prolyl cis-trans isomerase	**-0.45**	0.26869
STM0092	surA	peptidyl-prolyl cis-trans isomerase	**0.26**	0.52101
STM0093	imp	organic solvent tolerance protein precursor	**0.04**	0.93039
STM0093	imp	organic solvent tolerance protein precursor	**0.01**	0.97994
STM0094	djlA	Dna-J like membrane chaperone protein	**-0.32**	0.62216
STM0094	djlA	Dna-J like membrane chaperone protein	**0.25**	0.69882
STM0095	rluA	23S rRNA pseudouridylate 746 synthase	**-0.44**	0.29912
STM0095	rluA	23S rRNA pseudouridylate 746 synthase	**-0.03**	0.95563
STM0096	hepA	ATP-dependent helicase HepA	**-0.13**	0.76622
STM0096	hepA	ATP-dependent helicase HepA	**0.32**	0.49035
STM0097	polB	DNA polymerase II	**-0.01**	0.98581
STM0097	polB	DNA polymerase II	**0.29**	0.47610
STM0098	STM0098	putative secreted protein	**-0.24**	0.70144
STM0098	STM0098	putative secreted protein	**-0.03**	0.97050
STM0100	STM0100	putative cytoplasmic protein	**-0.46**	0.38277
STM0100	STM0100	putative cytoplasmic protein	**-0.08**	0.89105
STM0101	araD	L-ribulose-5-phosphate 4-epimerase	**-0.67**	0.31989
STM0101	araD	L-ribulose-5-phosphate 4-epimerase	**0.18**	0.81960
STM0102	araA	L-arabinose isomerase	**-0.76**	0.20285
STM0102	araA	L-arabinose isomerase	**0.16**	0.73473
STM0103	araB	ribulokinase	**-0.38**	0.62216
STM0103	araB	ribulokinase	**-0.57**	0.46088
STM0104	araC	arabinose operon transcriptional regulator	**-0.49**	0.27591
STM0104	araC	arabinose operon transcriptional regulator	**0.82**	0.34148
STM0105	yabI	hypothetical protein STM0105	**-0.36**	0.50375
STM0105	yabI	hypothetical protein STM0105	**-0.22**	0.65974
STM0106	yabJ	putative ABC transporter protein	**-0.49**	0.46539
STM0106	yabJ	putative ABC transporter protein	**-0.30**	0.43439
STM0107	thiP	thiamin ABC transporter membrane component	**-0.18**	0.72213
STM0107	thiP	thiamin ABC transporter membrane component	**-0.04**	0.95608
STM0108	tbpA	thiamine-binding periplasmic protein	**-1.05**	0.11849
STM0108	tbpA	thiamine-binding periplasmic protein	**-0.24**	0.61597
STM0109	yabN	putative periplasmic binding protein	**-0.01**	0.99505
STM0109	yabN	putative periplasmic binding protein	**0.09**	0.83240
STM0110	leuD	isopropylmalate isomerase small subunit	**-0.11**	0.89039
STM0110	leuD	isopropylmalate isomerase small subunit	**0.29**	0.54510
STM0111	leuC	isopropylmalate isomerase large subunit	**-0.37**	0.55598
STM0111	leuC	isopropylmalate isomerase large subunit	**0.40**	0.47107
STM0112	leuB	3-isopropylmalate dehydrogenase	**-0.06**	0.93586
STM0112	leuB	3-isopropylmalate dehydrogenase	**0.12**	0.79285
STM0113	leuA	2-isopropylmalate synthase	**-0.79**	0.18265
STM0113	leuA	2-isopropylmalate synthase	**-0.13**	0.79662
STM0115	leuO	leucine transcriptional activator	**0.40**	0.48808
STM0115	leuO	leucine transcriptional activator	**0.91**	0.18634
STM0116	ilvI	acetolactate synthase III large subunit	**-0.07**	0.90671
STM0116	ilvI	acetolactate synthase III large subunit	**0.80**	0.24907
STM0117	ilvH	acetolactate synthase small subunit	**-0.16**	0.68032
STM0117	ilvH	acetolactate synthase small subunit	**0.15**	0.72476
STM0118	fruR	fru operon transcriptional repressor	**-0.22**	0.62477
STM0118	fruR	fru operon transcriptional repressor	**0.12**	0.81533
STM0119	yabB	hypothetical protein STM0119	**-0.24**	0.54162
STM0119	yabB	hypothetical protein STM0119	**-0.02**	0.98132
STM0120	mraW	S-adenosyl-methyltransferase	**0.10**	0.83109
STM0120	mraW	S-adenosyl-methyltransferase	**0.32**	0.41024
STM0121	ftsL	cell division protein	**-0.17**	0.71931
STM0121	ftsL	cell division protein	**0.77**	0.11671
STM0122	ftsI	division specific transpeptidase	**-0.69**	0.22087
STM0122	ftsI	division specific transpeptidase	**-0.16**	0.74231
STM0123	murE	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase	**-0.19**	0.65502

STM0123	murE	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase	**0.08**	0.88045
STM0124	murF	D-alanine-D-alanine ligase	**-0.13**	0.75721
STM0124	murF	D-alanine-D-alanine ligase	**0.01**	0.98140
STM0125	mraY	phospho-N-acetylmuramoyl-pentapeptide-transferase	**-0.31**	0.48062
STM0125	mraY	phospho-N-acetylmuramoyl-pentapeptide-transferase	**0.07**	0.88156
STM0126	murD	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase	**-0.41**	0.36311
STM0126	murD	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase	**-0.11**	0.81027
STM0127	ftsW	essential cell division gene	**0.09**	0.83100
STM0127	ftsW	essential cell division gene	**-0.02**	0.96027
STM0128	murG	N-acetylglucosaminyl transferase	**0.00**	0.99512
STM0128	murG	N-acetylglucosaminyl transferase	**-0.01**	0.98193
STM0129	murC	UDP-N-acetylmuramate--L-alanine ligase	**-0.10**	0.83443
STM0129	murC	UDP-N-acetylmuramate--L-alanine ligase	**0.08**	0.86895
STM0130	ddl	D-alanylalanine synthetase	**-0.02**	0.96785
STM0130	ddl	D-alanylalanine synthetase	**-0.19**	0.69398
STM0131	ftsQ	cell division protein	**-0.38**	0.56162
STM0131	ftsQ	cell division protein	**-0.11**	0.82585
STM0132	ftsA	cell division protein	**-0.05**	0.91144
STM0132	ftsA	cell division protein	**0.55**	0.18706
STM0133	ftsZ	cell division protein FtsZ	**-0.13**	0.74995
STM0133	ftsZ	cell division protein FtsZ	**0.15**	0.69398
STM0134	lpxC	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase	**-0.09**	0.82656
STM0134	lpxC	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase	**0.10**	0.77677
STM0135	yacA	SecA regulator SecM	**-0.07**	0.87368
STM0135	yacA	SecA regulator SecM	**0.20**	0.60936
STM0136	secA	translocase	**-0.52**	0.28030
STM0136	secA	translocase	**-0.30**	0.44020
STM0137	mutT	7,8-dihydro-8-oxoguanine-triphosphatase	**-0.16**	0.72247
STM0137	mutT	7,8-dihydro-8-oxoguanine-triphosphatase	**-0.01**	0.98640
STM0138	yacG	zinc-binding protein	**-0.40**	0.31989
STM0138	yacG	zinc-binding protein	**0.38**	0.43417
STM0139	yacF	hypothetical protein STM0139	**-0.20**	0.64595
STM0139	yacF	hypothetical protein STM0139	**-0.03**	0.95855
STM0140	coaE	dephospho-CoA kinase	**-0.20**	0.71973
STM0140	coaE	dephospho-CoA kinase	**0.15**	0.73106
STM0141	guaC	guanosine 5'-monophosphate oxidoreductase	**-0.24**	0.55008
STM0141	guaC	guanosine 5'-monophosphate oxidoreductase	**0.34**	0.38875
STM0142	hofC	putative type IV pilin assembly protein	**-0.04**	0.94223
STM0142	hofC	putative type IV pilin assembly protein	**-0.39**	0.34148
STM0143	hofB	putative type IV fimbrial biosynthetic protein	**-0.55**	0.20483
STM0143	hofB	putative type IV fimbrial biosynthetic protein	**0.00**	0.99733
STM0144	ppdD	putative type IV pilin major component	**-0.21**	0.72518
STM0144	ppdD	putative type IV pilin major component	**0.11**	0.83476
STM0145	nadC	nicotinate-nucleotide pyrophosphorylase	**-0.13**	0.83657
STM0145	nadC	nicotinate-nucleotide pyrophosphorylase	**0.10**	0.84930
STM0146	ampD	N-acetyl-anhydromuramyl-L-alanine amidase	**0.05**	0.91783
STM0146	ampD	N-acetyl-anhydromuramyl-L-alanine amidase	**0.31**	0.52897
STM0147	ampE	putative beta lactamase regulator	**-0.16**	0.86370
STM0147	ampE	putative beta lactamase regulator	**-0.34**	0.38389
STM0148	STM0148	putative cytoplasmic protein	**-0.08**	0.85893
STM0148	STM0148	putative cytoplasmic protein	**1.08**	0.15736
STM0149	STM0149	Na+/galactoside symporter	**-1.12**	0.06780
STM0149	STM0149	Na+/galactoside symporter	**0.11**	0.84687
STM0150	aroP	aromatic amino acid transporter	**-0.39**	0.37657
STM0150	aroP	aromatic amino acid transporter	**0.44**	0.42277
STM0151	pdhR	transcriptional regulator of pyruvate dehydrogenase complex	**-0.32**	0.40500

STM0151	pdhR	transcriptional regulator of pyruvate dehydrogenase complex	**0.11**	0.84456
STM0152	aceE	pyruvate dehydrogenase E1 component	**-0.12**	0.84187
STM0152	aceE	pyruvate dehydrogenase E1 component	**0.03**	0.97474
STM0153	aceF	dihydrolipoamide acetyltransferase	**-0.08**	0.85988
STM0153	aceF	dihydrolipoamide acetyltransferase	**-0.52**	0.24571
STM0154	lpdA	dihydrolipoamide dehydrogenase	**-0.39**	0.34070
STM0154	lpdA	dihydrolipoamide dehydrogenase	**0.05**	0.92183
STM0155	STM0155	putative outer membrane protein	**0.15**	0.77683
STM0155	STM0155	putative outer membrane protein	**0.71**	0.27269
STM0156	STM0156	putative periplasmic protein	**-0.25**	0.56095
STM0156	STM0156	putative periplasmic protein	**0.46**	0.30605
STM0157	yacH	putative outer membrane protein	**0.22**	0.74807
STM0157	yacH	putative outer membrane protein	**0.77**	0.13813
STM0158	acnB	aconitate hydratase	**-0.24**	0.55338
STM0158	acnB	aconitate hydratase	**-0.24**	0.55956
STM0159	STM0159	putative restriction endonuclease	**-0.19**	0.70458
STM0159	STM0159	putative restriction endonuclease	**0.26**	0.65413
STM0160	yacL	hypothetical protein STM0160	**0.01**	0.98032
STM0160	yacL	hypothetical protein STM0160	**0.31**	0.49336
STM0161	kdgT	2-keto-3-deoxygluconate permease	**0.09**	0.91428
STM0161	kdgT	2-keto-3-deoxygluconate permease	**0.38**	0.36243
STM0162	STM0162	putative inner membrane protein	**-0.15**	0.78973
STM0162	STM0162	putative inner membrane protein	**0.35**	0.57019
STM0163	STM0163	4-hydroxythreonine-4-phosphate dehydrogenase	**-0.55**	0.21979
STM0163	STM0163	4-hydroxythreonine-4-phosphate dehydrogenase	**0.38**	0.36311
STM0164	STM0164	putative transcriptional regulator	**-0.06**	0.87707
STM0164	STM0164	putative transcriptional regulator	**0.29**	0.40930
STM0165	speD	S-adenosylmethionine decarboxylase proenzyme	**-0.13**	0.82521
STM0165	speD	S-adenosylmethionine decarboxylase proenzyme	**0.17**	0.64180
STM0166	speE	spermidine synthase	**-0.04**	0.93023
STM0166	speE	spermidine synthase	**0.07**	0.86385
STM0167	yacC	putative periplasmic protein	**-0.04**	0.93385
STM0167	yacC	putative periplasmic protein	**0.08**	0.86190
STM0168	cueO	putative multicopper oxidase	**-0.50**	0.28240
STM0168	cueO	putative multicopper oxidase	**0.30**	0.43550
STM0169	gcd	glucose dehydrogenase	**-0.40**	0.39721
STM0169	gcd	glucose dehydrogenase	**0.40**	0.43577
STM0170	hpt	hypoxanthine-guanine phosphoribosyltransferase	**-0.17**	0.65795
STM0170	hpt	hypoxanthine-guanine phosphoribosyltransferase	**-0.04**	0.94087
STM0171	yadF	putative carbonic anhydrase	**0.05**	0.94990
STM0171	yadF	putative carbonic anhydrase	**0.04**	0.94050
STM0172	yadG	putative ABC-type multidrug transport system ATPase component	**-0.36**	0.37241
STM0172	yadG	putative ABC-type multidrug transport system ATPase component	**0.26**	0.63223
STM0173	yadH	putative transport protein	**0.04**	0.93949
STM0173	yadH	putative transport protein	**0.27**	0.64174
STM0174	stiH	putative fimbrial protein precurosr	**-0.88**	0.08679
STM0174	stiH	putative fimbrial protein precurosr	**0.14**	0.79936
STM0175	stiC	putativie fimbrial usher	**0.02**	0.97092
STM0175	stiC	putativie fimbrial usher	**0.75**	0.17754
STM0176	stiB	putative fimbrial chaperone	**-0.18**	0.89058
STM0176	stiB	putative fimbrial chaperone	**0.13**	0.87298
STM0177	stiA	putative fimbrial subunit	**0.20**	0.72143
STM0177	stiA	putative fimbrial subunit	**-0.12**	0.79213
STM0178	yadI	putative PTS enzyme	**-0.12**	0.76970
STM0178	yadI	putative PTS enzyme	**-0.13**	0.82521
STM0179	yadE	putative xylanase/chitin deacetylase	**-0.16**	0.70472
STM0179	yadE	putative xylanase/chitin deacetylase	**-0.36**	0.52861
STM0180	panD	aspartate 1-decarboxylase precursor	**-0.29**	0.51988
STM0180	panD	aspartate 1-decarboxylase precursor	**0.25**	0.73473
STM0181	panC	pantoate--beta-alanine ligase	**-0.02**	0.96568

STM0181	panC	pantoate--beta-alanine ligase	**0.38**	0.40905
STM0182	panB	3-methyl-2-oxobutanoate hydroxymethyltransferase	**0.09**	0.84503
STM0182	panB	3-methyl-2-oxobutanoate hydroxymethyltransferase	**0.13**	0.82814
STM0183	folK	7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase	**-0.22**	0.59675
STM0183	folK	7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase	**0.01**	0.97849
STM0184	pcnB	polyA polymerase I	**-0.10**	0.83610
STM0184	pcnB	polyA polymerase I	**0.05**	0.92262
STM0185	yadB	glutamyl-tRNA synthetase	**0.15**	0.72146
STM0185	yadB	glutamyl-tRNA synthetase	**0.21**	0.66489
STM0186	dksA	dnaK suppressor protein	**0.00**	0.99512
STM0186	dksA	dnaK suppressor protein	**0.06**	0.91359
STM0187	sfsA	sugar fermentation stimulation protein	**0.01**	0.98398
STM0187	sfsA	sugar fermentation stimulation protein	**0.17**	0.65730
STM0188	ligT	2'-5' RNA ligase	**0.05**	0.92403
STM0188	ligT	2'-5' RNA ligase	**0.09**	0.83982
STM0189	hrpB	ATP-dependent helicase	**-0.49**	0.39428
STM0189	hrpB	ATP-dependent helicase	**0.24**	0.55978
STM0190	mrcB	penicillin-binding protein 1b	**-0.27**	0.53206
STM0190	mrcB	penicillin-binding protein 1b	**-0.04**	0.93280
STM0191	fhuA	outer membrane ferrichrome receptor protein precursor	**0.10**	0.81763
STM0191	fhuA	outer membrane ferrichrome receptor protein precursor	**0.18**	0.65301
STM0192	fhuC	hydroxymate-dependent iron transport protein	**-0.20**	0.67557
STM0192	fhuC	hydroxymate-dependent iron transport protein	**0.10**	0.88115
STM0193	fhuD	hydroxamate-dependent iron uptake protein	**-0.11**	0.78266
STM0193	fhuD	hydroxamate-dependent iron uptake protein	**0.11**	0.82384
STM0194	fhuB	hydroxamate-dependent iron uptake protein	**-0.10**	0.80987
STM0194	fhuB	hydroxamate-dependent iron uptake protein	**0.09**	0.86339
STM0195	stfA	putative fimbrial subunit	**-0.27**	0.70474
STM0195	stfA	putative fimbrial subunit	**0.30**	0.52208
STM0196	stfC	putative fimbrial outer membrane usher	**-0.11**	0.80081
STM0196	stfC	putative fimbrial outer membrane usher	**0.45**	0.45398
STM0197	stfD	putative periplasmic fimbrial chaperone	**-0.86**	0.13112
STM0197	stfD	putative periplasmic fimbrial chaperone	**0.19**	0.59544
STM0198	stfE	putative minor fimbrial subunit	**-0.32**	0.54625
STM0198	stfE	putative minor fimbrial subunit	**0.09**	0.83191
STM0199	stfF	putative minor fimbrial subunit	**-1.34**	0.19843
STM0199	stfF	putative minor fimbrial subunit	**0.41**	0.28030
STM0200	stfG	putative minor fimbrial subunit	**-0.05**	0.90585
STM0200	stfG	putative minor fimbrial subunit	**0.33**	0.55598
STM0201	STM0201	putative outer membrane protein	**-0.07**	0.85504
STM0201	STM0201	putative outer membrane protein	**-0.02**	0.96595
STM0202	hemL	glutamate-1-semialdehyde aminotransferase	**-0.25**	0.53676
STM0202	hemL	glutamate-1-semialdehyde aminotransferase	**0.26**	0.71693
STM0203	yadQ	chloride channel protein	**-0.79**	0.15859
STM0203	yadQ	chloride channel protein	**-0.35**	0.42084
STM0204,S	yadR	hypothetical protein STM0204,S	**-0.07**	0.86629
STM0204,S	yadR	hypothetical protein STM0204,S	**0.23**	0.56860
STM0205	yadS	putative inner membrane protein	**-0.21**	0.60042
STM0205	yadS	putative inner membrane protein	**0.08**	0.87290
STM0206	btuF	vitamin B12-transporter protein BtuF	**0.05**	0.89979
STM0206	btuF	vitamin B12-transporter protein BtuF	**0.21**	0.62629
STM0207	pfs	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase	**-0.38**	0.31305
STM0207	pfs	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase	**0.18**	0.72646
STM0208	dgt	deoxyguanosinetriphosphate triphosphohydrolase	**-0.39**	0.61809
STM0208	dgt	deoxyguanosinetriphosphate triphosphohydrolase	**0.11**	0.87512
STM0209	htrA	high temperature requirement A protein precursor	**-0.06**	0.90797
STM0209	htrA	high temperature requirement A protein precursor	**-0.13**	0.78633
STM0210	cdaR	putative inner membrane protein	**0.05**	0.92173
STM0210	cdaR	putative inner membrane protein	**0.74**	0.18961
STM0211	yaeH	putative cytoplasmic protein	**-0.10**	0.86017
STM0211	yaeH	putative cytoplasmic protein	**0.28**	0.44980

STM0212	STM0212	putative inner membrane protein	**-0.05**	0.91723
STM0212	STM0212	putative inner membrane protein	**0.10**	0.82443
STM0213	dapD	2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase	**-0.09**	0.88018
STM0213	dapD	2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase	**-0.16**	0.70966
STM0214	glnD	PII uridylyl-transferase	**-0.03**	0.94565
STM0214	glnD	PII uridylyl-transferase	**0.08**	0.84862
STM0215	map	methionine aminopeptidase	**-0.47**	0.23798
STM0215	map	methionine aminopeptidase	**-0.22**	0.61654
STM0216	rpsB	30S ribosomal protein S2	**-0.09**	0.80335
STM0216	rpsB	30S ribosomal protein S2	**0.53**	0.24005
STM0217	tsf	elongation factor Ts	**-0.28**	0.49499
STM0217	tsf	elongation factor Ts	**0.01**	0.98840
STM0218	pyrH	uridylate kinase	**-0.27**	0.70229
STM0218	pyrH	uridylate kinase	**0.24**	0.68642
STM0219	frr	ribosome releasing factor	**-0.73**	0.15799
STM0219	frr	ribosome releasing factor	**-0.24**	0.67351
STM0220	dxr	1-deoxy-D-xylulose 5-phosphate reductoisomerase	**-0.03**	0.94426
STM0220	dxr	1-deoxy-D-xylulose 5-phosphate reductoisomerase	**-0.21**	0.66506
STM0221	uppS	undecaprenyl pyrophosphate synthetase	**-0.08**	0.85718
STM0221	uppS	undecaprenyl pyrophosphate synthetase	**0.14**	0.73542
STM0222	cdsA	CDP-diglyceride synthase	**-0.04**	0.94174
STM0222	cdsA	CDP-diglyceride synthase	**-0.02**	0.97064
STM0223	yaeL	putative membrane-associated Zn-dependent protease	**0.17**	0.65983
STM0223	yaeL	putative membrane-associated Zn-dependent protease	**0.30**	0.41134
STM0224	yaeT	putative outer membrane protein precursor	**-0.23**	0.62166
STM0224	yaeT	putative outer membrane protein precursor	**0.03**	0.94417
STM0225	hlpA	outer membrane protein H precursor	**-0.12**	0.84456
STM0225	hlpA	outer membrane protein H precursor	**-0.23**	0.65181
STM0226	lpxD	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	**0.05**	0.90265
STM0226	lpxD	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	**0.08**	0.89410
STM0227	fabZ	(3R)-hydroxymyristoyl ACP dehydratase	**-0.08**	0.85592
STM0227	fabZ	(3R)-hydroxymyristoyl ACP dehydratase	**0.02**	0.96785
STM0228	lpxA	UDP-N-acetylglucosamine acyltransferase	**-0.02**	0.96595
STM0228	lpxA	UDP-N-acetylglucosamine acyltransferase	**0.10**	0.82667
STM0229	lpxB	lipid-A-disaccharide synthase	**-0.28**	0.45520
STM0229	lpxB	lipid-A-disaccharide synthase	**0.44**	0.30599
STM0230	rnhB	ribonuclease HII	**0.03**	0.94992
STM0230	rnhB	ribonuclease HII	**-0.41**	0.34156
STM0231	dnaE	DNA polymerase III subunit alpha	**0.00**	0.99938
STM0231	dnaE	DNA polymerase III subunit alpha	**0.05**	0.90671
STM0232	accA	acetyl-CoA carboxylase alpha subunit	**-0.35**	0.42169
STM0232	accA	acetyl-CoA carboxylase alpha subunit	**0.08**	0.87126
STM0233	STM0233	putative endochitinase	**0.07**	0.90733
STM0233	STM0233	putative endochitinase	**0.03**	0.95679
STM0234	ldcC	lysine decarboxylase 2	**-0.48**	0.29285
STM0234	ldcC	lysine decarboxylase 2	**0.05**	0.89979
STM0235	yaeR	putative lactoylglutathione lyase	**-0.01**	0.99072
STM0235	yaeR	putative lactoylglutathione lyase	**0.00**	0.99997
STM0236	mesJ	cell cycle protein	**-0.24**	0.62988
STM0236	mesJ	cell cycle protein	**-0.04**	0.95059
STM0237	rof	Rho-dependent transcription termination modulator	**-0.38**	0.36162
STM0237	rof	Rho-dependent transcription termination modulator	**0.08**	0.84956
STM0238	yaeP	hypothetical protein STM0238	**-0.06**	0.88967
STM0238	yaeP	hypothetical protein STM0238	**0.00**	0.99698
STM0239	yaeQ	putative cytoplasmic protein	**-0.12**	0.78877
STM0239	yaeQ	putative cytoplasmic protein	**0.07**	0.88466
STM0240	yaeJ	hypothetical protein STM0240	**-0.23**	0.58387
STM0240	yaeJ	hypothetical protein STM0240	**0.41**	0.34148
STM0242	proS	prolyl-tRNA synthetase	**0.83**	0.30087

STM0242	proS	prolyl-tRNA synthetase	**1.21**	0.30611
STM0243	yaeB	putative regulatory protein	**-0.24**	0.51385
STM0243	yaeB	putative regulatory protein	**0.06**	0.92308
STM0244	rcsF	colanic acid synthesis regulator	**0.00**	0.99938
STM0244	rcsF	colanic acid synthesis regulator	**0.08**	0.87512
STM0245	yaeC	putative outer membrane lipoprotein	**-0.34**	0.64975
STM0245	yaeC	putative outer membrane lipoprotein	**0.05**	0.90534
STM0246	yaeE	putative transport protein	**-0.02**	0.97348
STM0246	yaeE	putative transport protein	**0.03**	0.95505
STM0247	abc	putative transport protein	**0.05**	0.93485
STM0247	abc	putative transport protein	**0.23**	0.51267
STM0248	yaeD	hypothetical protein STM0248	**-0.72**	0.21747
STM0248	yaeD	hypothetical protein STM0248	**0.07**	0.91600
STM0249	rrsH	STM0249	**-0.49**	0.37178
STM0249	rrsH	STM0249	**-0.46**	0.49870
STM0252	rrlH	STM0252	**-0.37**	0.50736
STM0252	rrlH	STM0252	**-0.50**	0.31004
STM0255	yafB	2,5-diketo-D-gluconate reductase B	**-0.04**	0.96107
STM0255	yafB	2,5-diketo-D-gluconate reductase B	**0.27**	0.63742
STM0256	yafC	putative transcriptional regulator	**-0.10**	0.87356
STM0256	yafC	putative transcriptional regulator	**-0.09**	0.85534
STM0257	STM0257	putative drug efflux protein	**0.30**	0.40337
STM0257	STM0257	putative drug efflux protein	**0.79**	0.12784
STM0258	yafD	hypothetical protein STM0258	**-0.25**	0.57026
STM0258	yafD	hypothetical protein STM0258	**0.13**	0.76622
STM0259	yafE	putative methyltransferase	**-0.38**	0.34148
STM0259	yafE	putative methyltransferase	**0.13**	0.77346
STM0260	dniR	transcriptional regulator	**-0.09**	0.84436
STM0260	dniR	transcriptional regulator	**0.40**	0.37942
STM0261	gloB	hydroxyacylglutathione hydrolase	**-0.12**	0.85358
STM0261	gloB	hydroxyacylglutathione hydrolase	**0.40**	0.42940
STM0262	yafS	putative SAM-dependent methyltransferase	**-0.48**	0.35635
STM0262	yafS	putative SAM-dependent methyltransferase	**0.09**	0.86017
STM0263	rnhA	ribonuclease H	**-0.18**	0.76387
STM0263	rnhA	ribonuclease H	**0.06**	0.92994
STM0264	dnaQ	DNA polymerase III subunit epsilon	**0.10**	0.81896
STM0264	dnaQ	DNA polymerase III subunit epsilon	**0.07**	0.93554
STM0266	STM0266	putative cytoplasmic protein	**-0.42**	0.36818
STM0266	STM0266	putative cytoplasmic protein	**0.16**	0.80637
STM0267	STM0267	putative cytoplasmic protein	**0.03**	0.95532
STM0267	STM0267	putative cytoplasmic protein	**0.22**	0.54160
STM0268	STM0268	putative cytoplasmic protein	**0.49**	0.48447
STM0268	STM0268	putative cytoplasmic protein	**1.14**	0.18614
STM0269	STM0269	putative cytoplasmic protein	**-0.74**	0.18248
STM0269	STM0269	putative cytoplasmic protein	**-0.82**	0.52419
STM0270	STM0270	putative cytoplasmic protein	**-0.11**	0.83190
STM0270	STM0270	putative cytoplasmic protein	**0.16**	0.75075
STM0271	STM0271	putative cytoplasmic protein	**-1.26**	0.09304
STM0271	STM0271	putative cytoplasmic protein	**-0.34**	0.68070
STM0272	STM0272	putative chaperone ATPase	**0.09**	0.91674
STM0272	STM0272	putative chaperone ATPase	**0.06**	0.93846
STM0273	STM0273	putative cytoplasmic protein	**-0.20**	0.78211
STM0273	STM0273	putative cytoplasmic protein	**0.06**	0.93023
STM0274	STM0274	putative cytoplasmic protein	**-0.39**	0.65730
STM0274	STM0274	putative cytoplasmic protein	**0.91**	0.35350
STM0275,s	STM0275,s	putative cytoplasmic protein	**-0.07**	0.93778
STM0275,s	STM0275,s	putative cytoplasmic protein	**0.62**	0.37142
STM0276	STM0276	putative cytoplasmic protein	**-0.32**	0.46793
STM0276	STM0276	putative cytoplasmic protein	**0.79**	0.35564
STM0277	STM0277	putative cytoplasmic protein	**0.12**	0.83443
STM0277	STM0277	putative cytoplasmic protein	**0.59**	0.31280
STM0278	STM0278	putative periplasmic protein	**-0.15**	0.84911
STM0278	STM0278	putative periplasmic protein	**0.35**	0.61201

STM0279	STM0279	putative cytoplasmic protein	**0.83**	0.41676
STM0279	STM0279	putative cytoplasmic protein	**0.70**	0.35245
STM0280	STM0280	putative outer membrane lipoprotein	**-0.24**	0.70065
STM0280	STM0280	putative outer membrane lipoprotein	**0.33**	0.56563
STM0281	STM0281	putative cytoplasmic protein	**0.00**	0.99500
STM0281	STM0281	putative cytoplasmic protein	**0.57**	0.38947
STM0282	STM0282	hypothetical protein STM0282	**-0.06**	0.94223
STM0282	STM0282	hypothetical protein STM0282	**-0.20**	0.75376
STM0283	STM0283	putative inner membrane protein	**-0.50**	0.35824
STM0283	STM0283	putative inner membrane protein	**-0.02**	0.98558
STM0284	STM0284	putative Shiga-like toxin A subunit	**-0.23**	0.54882
STM0284	STM0284	putative Shiga-like toxin A subunit	**-0.20**	0.68528
STM0285	STM0285	putative inner membrane protein	**0.13**	0.78844
STM0285	STM0285	putative inner membrane protein	**0.94**	0.16783
STM0286	STM0286	putative cytoplasmic protein	**-0.55**	0.25195
STM0286	STM0286	putative cytoplasmic protein	**0.08**	0.92658
STM0287	STM0287	putative periplasmic protein	**-0.27**	0.54618
STM0287	STM0287	putative periplasmic protein	**0.37**	0.45797
STM0288	STM0288	putative cytoplasmic protein	**-0.15**	0.80415
STM0288	STM0288	putative cytoplasmic protein	**0.50**	0.32590
STM0289	STM0289	putative cytoplasmic protein	**-0.65**	0.31971
STM0289	STM0289	putative cytoplasmic protein	**0.14**	0.82494
STM0290	STM0290	putative cytoplasmic protein	**0.14**	0.87999
STM0290	STM0290	putative cytoplasmic protein	**0.68**	0.15799
STM0291	STM0291	putative RHS-like protein	**-0.37**	0.52511
STM0291	STM0291	putative RHS-like protein	**0.20**	0.65795
STM0292	STM0292	putative RHS-like protein	**-0.08**	0.87512
STM0292	STM0292	putative RHS-like protein	**-0.03**	0.95564
STM0293	STM0293	putative cytoplasmic protein	**-0.19**	0.72398
STM0293	STM0293	putative cytoplasmic protein	**-0.11**	0.83003
STM0294	STM0294	putative cytoplasmic protein	**-0.31**	0.42811
STM0294	STM0294	putative cytoplasmic protein	**-0.14**	0.80306
STM0294,1N	STM0294,1N	hypothetical protein STM0294,1N	**0.31**	0.63958
STM0294,1N	STM0294,1N	hypothetical protein STM0294,1N	**0.43**	0.84634
STM0295	STM0295	putative cytoplasmic protein	**-0.39**	0.55482
STM0295	STM0295	putative cytoplasmic protein	**-0.13**	0.86947
STM0300	safB	putative fimbrial assembly chaperone	**-0.47**	0.46772
STM0300	safB	putative fimbrial assembly chaperone	**0.82**	0.24125
STM0301	safC	putative fimbrial usher	**0.49**	0.32760
STM0301	safC	putative fimbrial usher	**-0.05**	0.92074
STM0302	safD	putative fimbrial subunit	**-0.56**	0.19967
STM0302	safD	putative fimbrial subunit	**-0.09**	0.85706
STM0303	ybeJ	putative xylanase/chitin deacetylase	**0.22**	0.59160
STM0303	ybeJ	putative xylanase/chitin deacetylase	**0.48**	0.35325
STM0304	sinR	transcriptional regulator	**0.03**	0.96344
STM0304	sinR	transcriptional regulator	**0.02**	0.96278
STM0306	STM0306	SapA-like protein	**-0.61**	0.17919
STM0306	STM0306	SapA-like protein	**0.01**	0.99447
STM0307	STM0307	VirG-like protein	**-0.95**	0.16425
STM0307	STM0307	VirG-like protein	**-0.13**	0.77923
STM0308	yafV	putative amidohydrolase	**0.03**	0.96850
STM0308	yafV	putative amidohydrolase	**0.21**	0.65383
STM0309	fadE	acyl-CoA dehydrogenase	**-0.37**	0.44969
STM0309	fadE	acyl-CoA dehydrogenase	**0.08**	0.92264
STM0310	ghmA	phosphoheptose isomerase	**-0.15**	0.70966
STM0310	ghmA	phosphoheptose isomerase	**-0.13**	0.81455
STM0311	yafJ	putative glutamine amidotransferase	**-0.21**	0.63003
STM0311	yafJ	putative glutamine amidotransferase	**0.12**	0.80355
STM0312	yafK	putative periplasmic protein	**-0.29**	0.40947
STM0312	yafK	putative periplasmic protein	**-0.02**	0.96850
STM0313	dinP	DNA polymerase IV	**-0.23**	0.56162
STM0313	dinP	DNA polymerase IV	**0.61**	0.55945
STM0315	prfH	peptide chain release factor 2	**0.17**	0.67551

STM0315	prfH	peptide chain release factor 2	**0.06**	0.89468
STM0316	pepD	aminoacyl-histidine dipeptidase	**-0.44**	0.24520
STM0316	pepD	aminoacyl-histidine dipeptidase	**-0.40**	0.36628
STM0317	gpt	xanthine phosphoribosyltransferase	**0.00**	0.99713
STM0317	gpt	xanthine phosphoribosyltransferase	**0.28**	0.44020
STM0318	yafA	hypothetical protein STM0318	**0.20**	0.66636
STM0318	yafA	hypothetical protein STM0318	**0.50**	0.32760
STM0319	crl	transcriptional regulator	**0.38**	0.37241
STM0319	crl	transcriptional regulator	**0.37**	0.41812
STM0320	phoE	outer membrane pore protein E precursor	**0.79**	0.31305
STM0320	phoE	outer membrane pore protein E precursor	**0.69**	0.19142
STM0321	proB	gamma-glutamyl kinase	**-0.16**	0.74779
STM0321	proB	gamma-glutamyl kinase	**0.31**	0.59820
STM0322	proA	gamma-glutamyl phosphate reductase	**-0.16**	0.72861
STM0322	proA	gamma-glutamyl phosphate reductase	**0.21**	0.58788
STM0323	thrW	STM0323	**0.38**	0.62814
STM0323	thrW	STM0323	**0.49**	0.28799
STM0325	STM0325	putative truncated IS3 transposase	**-0.70**	0.30607
STM0325	STM0325	putative truncated IS3 transposase	**0.14**	0.83223
STM0327	STM0327	putative cytoplasmic protein	**0.07**	0.90609
STM0327	STM0327	putative cytoplasmic protein	**0.55**	0.31458
STM0328,s	STM0328,s	putative permease	**-0.20**	0.76538
STM0328,s	STM0328,s	putative permease	**0.11**	0.81061
STM0329	STM0329	isopropylmalate isomerase large subunit	**-0.15**	0.75165
STM0329	STM0329	isopropylmalate isomerase large subunit	**0.27**	0.55598
STM0330	STM0330	putative 3-isopropylmalate isomerase	**0.39**	0.46629
STM0330	STM0330	putative 3-isopropylmalate isomerase	**0.63**	0.32760
STM0331	STM0331	putative fumarylacetoacetate hydrolase	**-0.71**	0.35824
STM0331	STM0331	putative fumarylacetoacetate hydrolase	**-0.15**	0.82624
STM0332	STM0332	putative hydrolase/acyltransferase	**-0.19**	0.68032
STM0332	STM0332	putative hydrolase/acyltransferase	**0.01**	0.99447
STM0333	STM0333	putative transcriptional regulator	**0.16**	0.78010
STM0333	STM0333	putative transcriptional regulator	**0.59**	0.23918
STM0335	STM0335	putative outer membrane protein	**-0.47**	0.37153
STM0335	STM0335	putative outer membrane protein	**0.09**	0.88770
STM0336	stbE	putative fimbrial chaperone	**-0.11**	0.86626
STM0336	stbE	putative fimbrial chaperone	**0.65**	0.20065
STM0337	stbD	putative fimbrial usher	**-0.56**	0.42580
STM0337	stbD	putative fimbrial usher	**0.24**	0.73968
STM0338	stbC	putative fimbrial usher	**-0.15**	0.76387
STM0338	stbC	putative fimbrial usher	**0.17**	0.81272
STM0339	stbB	putative fimbrial chaperone	**-0.62**	0.24515
STM0339	stbB	putative fimbrial chaperone	**-0.42**	0.74378
STM0340	stbA	putative fimbrial major subunit	**-0.53**	0.45487
STM0340	stbA	putative fimbrial major subunit	**0.35**	0.62861
STM0341	STM0341	putative inner membrane protein	**-0.06**	0.90277
STM0341	STM0341	putative inner membrane protein	**0.49**	0.45643
STM0342	STM0342	putative periplasmic protein	**0.30**	0.62975
STM0342	STM0342	putative periplasmic protein	**0.28**	0.42935
STM0343	STM0343	hypothetical protein STM0343	**-0.78**	0.16534
STM0343	STM0343	hypothetical protein STM0343	**-0.03**	0.96251
STM0344	STM0344	putative response regulator	**-0.02**	0.97267
STM0344	STM0344	putative response regulator	**0.61**	0.24163
STM0345	STM0345	putative inner membrane protein	**-0.27**	0.51039
STM0345	STM0345	putative inner membrane protein	**0.09**	0.87126
STM0346	STM0346	putative outer membrane protein	**-0.39**	0.47804
STM0346	STM0346	putative outer membrane protein	**0.45**	0.42266
STM0347	STM0347	putative response regulator	**-0.77**	0.23989
STM0347	STM0347	putative response regulator	**0.17**	0.79308
STM0348	STM0348	putative inner membrane protein	**-0.46**	0.63974
STM0348	STM0348	putative inner membrane protein	**-0.21**	0.81862
STM0349	STM0349	putative outer membrane lipoprotein	**-0.13**	0.83443
STM0349	STM0349	putative outer membrane lipoprotein	**0.62**	0.30481

STM0350,S	STM0350,S	outer membrane efflux-like protein	**-0.62**	0.27893
STM0350,S	STM0350,S	outer membrane efflux-like protein	**0.26**	0.66026
STM0351	STM0351	putative cation efflux system protein	**-0.50**	0.31823
STM0351	STM0351	putative cation efflux system protein	**0.34**	0.54094
STM0352,S	STM0352,S	putative cation efflux pump	**-0.41**	0.40412
STM0352,S	STM0352,S	putative cation efflux pump	**0.22**	0.58965
STM0353	STM0353	putative cation transport ATPase	**0.06**	0.92840
STM0353	STM0353	putative cation transport ATPase	**1.02**	0.26429
STM0354	STM0354	putative transcriptional regulator	**0.01**	0.98840
STM0354	STM0354	putative transcriptional regulator	**1.00**	0.21562
STM0355	STM0355	putative copper chaperone	**0.05**	0.91937
STM0355	STM0355	putative copper chaperone	**0.98**	0.11224
STM0356	STM0356	putative inner membrane protein	**0.07**	0.87909
STM0356	STM0356	putative inner membrane protein	**-0.24**	0.69192
STM0357	mod	DNA methylase	**0.41**	0.34051
STM0357	mod	DNA methylase	**0.28**	0.55338
STM0358,S	res	DNA restriction enzyme	**-0.32**	0.37821
STM0358,S	res	DNA restriction enzyme	**0.08**	0.89979
STM0359	STM0359	putative cytoplasmic protein	**0.34**	0.87368
STM0359	STM0359	putative cytoplasmic protein	**1.00**	0.44416
STM0360	STM0360	cytochrome BD2 subunit I	**-0.14**	0.83943
STM0360	STM0360	cytochrome BD2 subunit I	**0.30**	0.52571
STM0361	STM0361	cytochrome BD2 subunit II	**-0.46**	0.38875
STM0361	STM0361	cytochrome BD2 subunit II	**-0.04**	0.93960
STM0363	STM0363	putative transcriptional regulator	**0.01**	0.98140
STM0363	STM0363	putative transcriptional regulator	**-1.21**	0.64422
STM0364	foxA	ferrioxamine receptor	**-0.03**	0.95081
STM0364	foxA	ferrioxamine receptor	**0.05**	0.95219
STM0365	yahN	putative transport protein	**-0.18**	0.77567
STM0365	yahN	putative transport protein	**0.17**	0.81142
STM0366	yahO	putative periplasmic protein	**0.16**	0.82624
STM0366	yahO	putative periplasmic protein	**0.98**	0.37942
STM0367	prpR	prp operon regulator	**0.26**	0.62691
STM0367	prpR	prp operon regulator	**0.31**	0.52142
STM0368	prpB	putative carboxyphosphonoenolpyruvate mutase	**-1.18**	0.14043
STM0368	prpB	putative carboxyphosphonoenolpyruvate mutase	**-0.03**	0.96655
STM0369	prpC	citrate synthase	**0.15**	0.70545
STM0369	prpC	citrate synthase	**0.98**	0.17139
STM0370	prpD	2-methylcitrate dehydratase	**-0.20**	0.60891
STM0370	prpD	2-methylcitrate dehydratase	**0.20**	0.82637
STM0371	prpE	putative acetyl-CoA synthetase	**-0.39**	0.33356
STM0371	prpE	putative acetyl-CoA synthetase	**0.36**	0.42106
STM0372	hemB	delta-aminolevulinic acid dehydratase	**0.10**	0.82975
STM0372	hemB	delta-aminolevulinic acid dehydratase	**-0.07**	0.87844
STM0373	yaiU	flagellar protein	**-0.11**	0.82656
STM0373	yaiU	flagellar protein	**0.68**	0.37241
STM0374	yaiV	putative inner membrane protein	**-0.15**	0.85492
STM0374	yaiV	putative inner membrane protein	**0.36**	0.55338
STM0375	ampH	penicillin-binding protein	**-0.35**	0.59675
STM0375	ampH	penicillin-binding protein	**0.16**	0.77152
STM0376	sbmA	putative ABC transporter membrane protein	**-0.87**	0.11913
STM0376	sbmA	putative ABC transporter membrane protein	**-0.34**	0.44271
STM0377	yaiW	putative outer membrane lipoprotein	**-0.44**	0.45797
STM0377	yaiW	putative outer membrane lipoprotein	**0.30**	0.54288
STM0378	yaiY	putative inner membrane protein	**-0.23**	0.57686
STM0378	yaiY	putative inner membrane protein	**0.12**	0.83901
STM0379	yaiZ	putative inner membrane protein	**-0.27**	0.59974
STM0379	yaiZ	putative inner membrane protein	**0.02**	0.97200
STM0380	ddl	D-alanylalanine synthetase	**-0.32**	0.45462
STM0380	ddl	D-alanylalanine synthetase	**0.19**	0.69398
STM0381	STM0381	putative inner membrane protein	**-0.33**	0.56565
STM0381	STM0381	putative inner membrane protein	**1.16**	0.18417
STM0382	STM0382	putative permease	**-0.76**	0.13813

STM0382	STM0382	putative permease	**-0.17**	0.73473
STM0383	yaiB	putative cytoplasmic protein	**-0.48**	0.20129
STM0383	yaiB	putative cytoplasmic protein	**-0.25**	0.52364
STM0384	psiF	phosphate starvation-inducible protein	**-0.60**	0.30496
STM0384	psiF	phosphate starvation-inducible protein	**-0.48**	0.45800
STM0385	yaiC	hypothetical protein STM0385	**-0.51**	0.22393
STM0385	yaiC	hypothetical protein STM0385	**-0.12**	0.84162
STM0386	proC	pyrroline-5-carboxylate reductase	**-0.29**	0.53840
STM0386	proC	pyrroline-5-carboxylate reductase	**-0.25**	0.61367
STM0387	yaiI	hypothetical protein STM0387	**-0.63**	0.34110
STM0387	yaiI	hypothetical protein STM0387	**0.24**	0.69882
STM0388	aroL	shikimate kinase II	**0.07**	0.87187
STM0388	aroL	shikimate kinase II	**0.29**	0.59887
STM0389	yaiA	putative cytoplasmic protein	**0.00**	0.99929
STM0389	yaiA	putative cytoplasmic protein	**0.90**	0.22283
STM0390	aroM	aro operon protein	**-0.05**	0.94360
STM0390	aroM	aro operon protein	**-0.02**	0.96785
STM0391	yaiE	putative cytoplasmic protein	**0.15**	0.71367
STM0391	yaiE	putative cytoplasmic protein	**0.33**	0.47553
STM0392	rdgC	recombination associated protein	**-0.40**	0.34666
STM0392	rdgC	recombination associated protein	**-0.02**	0.98026
STM0393	yajF	putative sugar kinase/transcriptional regulator	**-0.09**	0.89730
STM0393	yajF	putative sugar kinase/transcriptional regulator	**0.34**	0.46207
STM0394	araJ	arabinose polymer transporter	**-0.36**	0.61229
STM0394	araJ	arabinose polymer transporter	**-0.09**	0.90534
STM0395	sbcC	ATP-dependent dsDNA exonuclease	**-0.20**	0.67390
STM0395	sbcC	ATP-dependent dsDNA exonuclease	**0.96**	0.13824
STM0396	sbcD	ATP-dependent dsDNA exonuclease	**0.22**	0.76989
STM0396	sbcD	ATP-dependent dsDNA exonuclease	**0.53**	0.31751
STM0397	phoB	response regulator	**0.30**	0.54194
STM0397	phoB	response regulator	**1.03**	0.25460
STM0398	phoR	sensor kinase	**-0.41**	0.32755
STM0398	phoR	sensor kinase	**-0.02**	0.97219
STM0399	brnQ	branched-chain amino acid transporter	**-0.10**	0.86190
STM0399	brnQ	branched-chain amino acid transporter	**0.48**	0.39385
STM0400	proY	putative proline transporter	**-0.01**	0.98551
STM0400	proY	putative proline transporter	**-0.10**	0.83190
STM0401	malZ	maltodextrin glucosidase	**0.07**	0.85492
STM0401	malZ	maltodextrin glucosidase	**0.39**	0.37250
STM0402	STM0402	putative thiol-alkyl hydroperoxide reductase	**0.17**	0.62691
STM0402	STM0402	putative thiol-alkyl hydroperoxide reductase	**0.64**	0.19843
STM0403	yajB	putative cytoplasmic protein	**0.04**	0.94318
STM0403	yajB	putative cytoplasmic protein	**0.03**	0.96251
STM0404	queA	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	**-0.02**	0.97333
STM0404	queA	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	**0.19**	0.67097
STM0405	tgt	queuine tRNA-ribosyltransferase	**0.04**	0.92371
STM0405	tgt	queuine tRNA-ribosyltransferase	**0.17**	0.62757
STM0406	yajC	preprotein translocase subunit YajC	**-0.06**	0.89668
STM0406	yajC	preprotein translocase subunit YajC	**0.02**	0.95932
STM0407	secD	protein export protein SecD	**-0.30**	0.38260
STM0407	secD	protein export protein SecD	**-0.16**	0.69668
STM0408	secF	protein export protein SecF	**-0.05**	0.93767
STM0408	secF	protein export protein SecF	**0.67**	0.21933
STM0409	STM0409	hypothetical protein STM0409	**-0.20**	0.56860
STM0409	STM0409	hypothetical protein STM0409	**-0.14**	0.76955
STM0410	STM0410	putative regulatory protein	**0.31**	0.39002
STM0410	STM0410	putative regulatory protein	**0.36**	0.36989
STM0411	yajD	putative cytoplasmic protein	**-0.03**	0.95747
STM0411	yajD	putative cytoplasmic protein	**0.38**	0.38722
STM0413	tsx	nucleoside channel	**0.47**	0.43799
STM0413	tsx	nucleoside channel	**1.28**	0.16281

STM0415	ybaD	hypothetical protein STM0415	**0.07**	0.86626
STM0415	ybaD	hypothetical protein STM0415	**0.20**	0.57659
STM0416	ribD	pyrimidine deaminase/reductase	**-0.43**	0.43219
STM0416	ribD	pyrimidine deaminase/reductase	**-0.26**	0.55825
STM0417	ribH	riboflavin synthase subunit beta	**-0.03**	0.94402
STM0417	ribH	riboflavin synthase subunit beta	**0.18**	0.64070
STM0418	nusB	transcription antitermination protein NusB	**-0.24**	0.53679
STM0418	nusB	transcription antitermination protein NusB	**-0.19**	0.61833
STM0419	thiL	thiamine monophosphate kinase	**-0.08**	0.86587
STM0419	thiL	thiamine monophosphate kinase	**-0.10**	0.83240
STM0420	pgpA	phosphatidylglycerophosphatase A	**0.03**	0.95059
STM0420	pgpA	phosphatidylglycerophosphatase A	**0.28**	0.52101
STM0421	yajO	putative oxidoreductase	**-0.84**	0.18265
STM0421	yajO	putative oxidoreductase	**0.16**	0.69988
STM0422	dxs	1-deoxy-D-xylulose-5-phosphate synthase	**-0.41**	0.31637
STM0422	dxs	1-deoxy-D-xylulose-5-phosphate synthase	**0.33**	0.35853
STM0423	ispA	geranyltranstransferase	**-0.05**	0.93150
STM0423	ispA	geranyltranstransferase	**0.15**	0.82350
STM0424	xseB	exodeoxyribonuclease VII small subunit	**-0.20**	0.63432
STM0424	xseB	exodeoxyribonuclease VII small subunit	**0.12**	0.76553
STM0425	thiI	thiamine biosynthesis protein ThiI	**0.32**	0.43550
STM0425	thiI	thiamine biosynthesis protein ThiI	**0.53**	0.20540
STM0426	phnV	2-aminoethylphosphonate transporter	**-0.46**	0.38729
STM0426	phnV	2-aminoethylphosphonate transporter	**-0.36**	0.32093
STM0427	phnU	2-aminoethylphosphonate transporter	**0.02**	0.96687
STM0427	phnU	2-aminoethylphosphonate transporter	**0.08**	0.91937
STM0428	phnT	2-aminoethylphosphonate transporter	**0.02**	0.97835
STM0428	phnT	2-aminoethylphosphonate transporter	**-0.13**	0.81667
STM0429	phnS	2-aminoethylphosphonate transporter	**-0.19**	0.66101
STM0429	phnS	2-aminoethylphosphonate transporter	**0.06**	0.94470
STM0430	phnR	2-aminoethylphosphonate transport protein	**0.15**	0.78755
STM0430	phnR	2-aminoethylphosphonate transport protein	**0.50**	0.24049
STM0431	phnW	2-aminoethylphosphonate transport	**0.15**	0.79752
STM0431	phnW	2-aminoethylphosphonate transport	**-0.03**	0.98658
STM0432	phnX	2-aminoethylphosphonate transport	**-0.58**	0.28696
STM0432	phnX	2-aminoethylphosphonate transport	**0.12**	0.81667
STM0433	thiJ	4-methyl-5(beta-hydroxyethyl)-thiazole synthesis	**-0.06**	0.91597
STM0433	thiJ	4-methyl-5(beta-hydroxyethyl)-thiazole synthesis	**0.60**	0.19142
STM0434	apbA	2-dehydropantoate 2-reductase	**0.18**	0.77346
STM0434	apbA	2-dehydropantoate 2-reductase	**-0.48**	0.43817
STM0435	yajQ	hypothetical protein STM0435	**-0.03**	0.96785
STM0435	yajQ	hypothetical protein STM0435	**0.12**	0.84021
STM0436,S	yajR	putative transport protein	**-0.25**	0.55892
STM0436,S	yajR	putative transport protein	**0.58**	0.17359
STM0437	STM0437	putative periplasmic protein	**-0.01**	0.98226
STM0437	STM0437	putative periplasmic protein	**0.02**	0.98193
STM0438	STM0438	tetratricopeptide repeat protein	**0.06**	0.89130
STM0438	STM0438	tetratricopeptide repeat protein	**-0.02**	0.96785
STM0439	cyoE	protoheme IX farnesyltransferase	**0.21**	0.58164
STM0439	cyoE	protoheme IX farnesyltransferase	**0.08**	0.83949
STM0440	cyoD	cytochrome o ubiquinol oxidase subunit IV	**0.35**	0.38552
STM0440	cyoD	cytochrome o ubiquinol oxidase subunit IV	**0.12**	0.74997
STM0441	cyoC	cytochrome o ubiquinol oxidase subunit III	**0.86**	0.09135
STM0441	cyoC	cytochrome o ubiquinol oxidase subunit III	**0.70**	0.24313
STM0442	cyoB	cytochrome o ubiquinol oxidase subunit I	**-0.03**	0.95532
STM0442	cyoB	cytochrome o ubiquinol oxidase subunit I	**0.10**	0.80335
STM0443	cyoA	cytochrome o ubiquinol oxidase subunit II	**-0.24**	0.72027
STM0443	cyoA	cytochrome o ubiquinol oxidase subunit II	**0.43**	0.36233
STM0444	ampG	muropeptide transporter	**-0.03**	0.95608
STM0444	ampG	muropeptide transporter	**0.35**	0.37310
STM0445	yajG	putative lipoprotein	**0.11**	0.77474
STM0445	yajG	putative lipoprotein	**0.15**	0.70229
STM0446	bolA	putative regulatory protein	**0.04**	0.93830

STM0446	bolA	putative regulatory protein	**0.00**	0.99512
STM0447	tig	trigger factor	**-0.25**	0.50811
STM0447	tig	trigger factor	**0.29**	0.48214
STM0448	clpP	ATP-dependent Clp protease proteolytic subunit	**-0.04**	0.94045
STM0448	clpP	ATP-dependent Clp protease proteolytic subunit	**0.16**	0.69955
STM0449	clpX	ATP-dependent protease ATP-binding subunit	**-0.39**	0.31280
STM0449	clpX	ATP-dependent protease ATP-binding subunit	**-0.10**	0.83899
STM0450	lon	ATP-dependent protease Lon	**-0.63**	0.17330
STM0450	lon	ATP-dependent protease Lon	**-0.64**	0.17603
STM0451	hupB	DNA-binding protein HU-beta	**-0.40**	0.35770
STM0451	hupB	DNA-binding protein HU-beta	**0.24**	0.60051
STM0452	cypD	peptidyl-prolyl isomerase	**0.12**	0.93582
STM0452	cypD	peptidyl-prolyl isomerase	**0.21**	0.83190
STM0453	ybaV	putative DNA uptake protein	**-0.56**	0.18265
STM0453	ybaV	putative DNA uptake protein	**0.04**	0.94990
STM0454	ybaW	putative esterase	**-0.29**	0.64335
STM0454	ybaW	putative esterase	**0.46**	0.47610
STM0455	ybaX	putative aluminum resistance protein	**-0.29**	0.40721
STM0455	ybaX	putative aluminum resistance protein	**0.38**	0.46436
STM0456	ybaE	putative ABC transporter periplasmic binding protein	**-0.02**	0.97267
STM0456	ybaE	putative ABC transporter periplasmic binding protein	**0.59**	0.19925
STM0457	cof	putative hydrolase	**-0.37**	0.38884
STM0457	cof	putative hydrolase	**-0.38**	0.58461
STM0458	STM0458	putative cysteine synthase/cystathionine beta-synthase	**-0.04**	0.94341
STM0458	STM0458	putative cysteine synthase/cystathionine beta-synthase	**1.28**	0.11224
STM0459	ybaO	putative transcriptional regulator	**-0.08**	0.86102
STM0459	ybaO	putative transcriptional regulator	**-0.06**	0.92322
STM0460	mdlA	ATP-binding component	**0.01**	0.98539
STM0460	mdlA	ATP-binding component	**0.39**	0.46720
STM0461	mdlB	putative transporter	**-0.08**	0.85743
STM0461	mdlB	putative transporter	**0.19**	0.75326
STM0462	glnK	nitrogen regulatory protein P-II 2	**-0.09**	0.85053
STM0462	glnK	nitrogen regulatory protein P-II 2	**0.63**	0.24973
STM0463	amtB	putative ammonium transport protein	**-0.28**	0.67461
STM0463	amtB	putative ammonium transport protein	**0.05**	0.94716
STM0464	tesB	acyl-CoA thioesterase II	**-0.79**	0.14285
STM0464	tesB	acyl-CoA thioesterase II	**-0.35**	0.38729
STM0465	ybaY	hypothetical protein STM0465	**-0.08**	0.91170
STM0465	ybaY	hypothetical protein STM0465	**0.34**	0.40930
STM0466	ybaZ	putative methyltransferase	**-0.27**	0.80762
STM0466	ybaZ	putative methyltransferase	**0.75**	0.21007
STM0467	ffs	STM0467	**-0.20**	0.82145
STM0467	ffs	STM0467	**0.49**	0.35911
STM0468	ylaB	hypothetical protein STM0468	**-0.32**	0.70891
STM0468	ylaB	hypothetical protein STM0468	**0.22**	0.54624
STM0469	rpmE2	50S ribosomal protein L31	**-0.11**	0.79096
STM0469	rpmE2	50S ribosomal protein L31	**0.37**	0.36835
STM0470	rpmJ2	50S ribosomal protein L36	**-0.08**	0.89566
STM0470	rpmJ2	50S ribosomal protein L36	**-0.02**	0.96785
STM0471	ylaC	putative inner membrane protein	**-0.16**	0.79549
STM0471	ylaC	putative inner membrane protein	**-0.09**	0.86317
STM0472	maa	maltose O-acetyltransferase	**-0.30**	0.54595
STM0472	maa	maltose O-acetyltransferase	**-0.15**	0.71037
STM0473	hha	hemolysin expression-modulating protein	**0.27**	0.59675
STM0473	hha	hemolysin expression-modulating protein	**0.16**	0.64327
STM0474	ybaJ	putative cytoplasmic protein	**-0.09**	0.83655
STM0474	ybaJ	putative cytoplasmic protein	**-0.01**	0.98140
STM0475	acrB	acridine efflux pump	**0.18**	0.76720
STM0475	acrB	acridine efflux pump	**0.06**	0.93023
STM0476	acrA	acridine efflux pump	**-0.20**	0.69398
STM0476	acrA	acridine efflux pump	**0.35**	0.45797
STM0477	acrR	acrAB operon repressor	**-0.10**	0.78877
STM0477	acrR	acrAB operon repressor	**0.31**	0.46267

STM0478	aefA	putative small-conductance mechanosensitive channel	**-0.61**	0.24313
STM0478	aefA	putative small-conductance mechanosensitive channel	**0.61**	0.22602
STM0479	STM0479	putative transposase	**-0.33**	0.38991
STM0479	STM0479	putative transposase	**-0.21**	0.65145
STM0480	ybaM	putative inner membrane protein	**0.00**	0.99721
STM0480	ybaM	putative inner membrane protein	**0.79**	0.11913
STM0481	priC	primosomal replication protein N	**-0.51**	0.23371
STM0481	priC	primosomal replication protein N	**0.17**	0.64730
STM0482	ybaN	hypothetical protein STM0482	**-0.15**	0.71138
STM0482	ybaN	hypothetical protein STM0482	**0.09**	0.84783
STM0483	apt	adenine phosphoribosyltransferase	**-0.27**	0.48668
STM0483	apt	adenine phosphoribosyltransferase	**0.22**	0.64331
STM0484	dnaX	DNA polymerase III subunits gamma and tau	**-0.39**	0.35937
STM0484	dnaX	DNA polymerase III subunits gamma and tau	**-0.10**	0.81667
STM0485	ybaB	hypothetical protein STM0485	**-0.37**	0.41996
STM0485	ybaB	hypothetical protein STM0485	**0.27**	0.49708
STM0486	recR	recombination protein RecR	**-0.70**	0.20065
STM0486	recR	recombination protein RecR	**-0.44**	0.29453
STM0487,S	htpG	heat shock protein 90	**-0.59**	0.15529
STM0487,S	htpG	heat shock protein 90	**-0.50**	0.19909
STM0488	adk	adenylate kinase	**-0.04**	0.91900
STM0488	adk	adenylate kinase	**-0.06**	0.90736
STM0489	hemH	ferrochelatase	**0.02**	0.96896
STM0489	hemH	ferrochelatase	**0.08**	0.88977
STM0490	aes	acetyl esterase	**0.04**	0.94050
STM0490	aes	acetyl esterase	**0.14**	0.70726
STM0491	gsk	inosine-guanosine kinase	**-0.18**	0.67842
STM0491	gsk	inosine-guanosine kinase	**0.02**	0.97168
STM0492	ybaL	putative transport protein	**-0.60**	0.26833
STM0492	ybaL	putative transport protein	**0.23**	0.56294
STM0493	fsr	putative transport protein	**0.12**	0.76526
STM0493	fsr	putative transport protein	**0.13**	0.81312
STM0494	ushA	UDP-sugar hydrolase/5'-nucleotidase	**0.11**	0.79893
STM0494	ushA	UDP-sugar hydrolase/5'-nucleotidase	**0.04**	0.93023
STM0495	ybaK	putative cytoplasmic protein	**-0.17**	0.73157
STM0495	ybaK	putative cytoplasmic protein	**-0.19**	0.61634
STM0496	ybaP	putative cytoplasmic protein	**-0.52**	0.21812
STM0496	ybaP	putative cytoplasmic protein	**0.20**	0.70809
STM0497	STM0497	putative periplasmic protein	**-0.70**	0.13905
STM0497	STM0497	putative periplasmic protein	**0.32**	0.58108
STM0498	copA	putative copper-transporting ATPase	**0.00**	0.99938
STM0498	copA	putative copper-transporting ATPase	**0.13**	0.76538
STM0499	cueR	putative heavy metal transcriptional repressor	**-0.22**	0.62970
STM0499	cueR	putative heavy metal transcriptional repressor	**0.92**	0.08322
STM0500	ybbJ	hypothetical protein STM0500	**-0.15**	0.73469
STM0500	ybbJ	hypothetical protein STM0500	**-0.20**	0.64590
STM0501	ybbK	putative inner membrane protein	**-0.10**	0.85174
STM0501	ybbK	putative inner membrane protein	**0.50**	0.33452
STM0502	ybbL	putative ABC-type sugar/spermidine/putrescine transport system	**-0.23**	0.58164
STM0502	ybbL	putative ABC-type sugar/spermidine/putrescine transport system	**0.05**	0.91484
STM0503	ybbM	putative transport protein	**-0.49**	0.21393
STM0503	ybbM	putative transport protein	**-0.64**	0.14030
STM0504	ybbN	putative thioredoxin protein	**-0.32**	0.55112
STM0504	ybbN	putative thioredoxin protein	**-0.58**	0.19967
STM0505	ybbO	short chain dehydrogenase	**-0.59**	0.20129
STM0505	ybbO	short chain dehydrogenase	**-0.12**	0.75683
STM0506	tesA	multifunctional acyl-CoA thioesterase I	**-0.12**	0.75395
STM0506	tesA	multifunctional acyl-CoA thioesterase I	**0.32**	0.42511
STM0507	ybbA	putative transporter	**-0.09**	0.86017
STM0507	ybbA	putative transporter	**0.46**	0.54160
STM0508	ybbP	putative inner membrane protein	**-0.40**	0.35937

STM0508	ybbP	putative inner membrane protein	**0.45**	0.36311
STM0509	STM0509	putative outer membrane protein	**-0.37**	0.36253
STM0509	STM0509	putative outer membrane protein	**-0.12**	0.79954
STM0510	sfbA	putative ABC-type transport system ATPase component	**-0.32**	0.42737
STM0510	sfbA	putative ABC-type transport system ATPase component	**0.60**	0.19870
STM0511	sfbB	putative ABC-type transport system ATPase component	**0.13**	0.73895
STM0511	sfbB	putative ABC-type transport system ATPase component	**0.58**	0.37919
STM0512	sfbC	putative ABC transporter permease component	**-0.55**	0.54134
STM0512	sfbC	putative ABC transporter permease component	**-0.12**	0.80096
STM0513	ybbB	putative ATPase	**-0.07**	0.89445
STM0513	ybbB	putative ATPase	**0.08**	0.87649
STM0514	ybbS	putative transcriptional regulator	**-0.34**	0.46992
STM0514	ybbS	putative transcriptional regulator	**-0.01**	0.99447
STM0515	allA	ureidoglycolate hydrolase	**0.13**	0.85437
STM0515	allA	ureidoglycolate hydrolase	**0.29**	0.54094
STM0516	allR	putative regulatory protein	**-0.63**	0.16783
STM0516	allR	putative regulatory protein	**0.23**	0.60427
STM0517	gcl	glyoxylate carboligase	**-0.43**	0.35937
STM0517	gcl	glyoxylate carboligase	**-0.03**	0.95574
STM0518	gip	glyoxylate-induced protein	**0.27**	0.74099
STM0518	gip	glyoxylate-induced protein	**0.28**	0.49226
STM0519	glxR	tartronic semialdehyde reductase	**-0.34**	0.49487
STM0519	glxR	tartronic semialdehyde reductase	**0.97**	0.19843
STM0520	STM0520	putative permease	**-0.11**	0.91175
STM0520	STM0520	putative permease	**0.21**	0.65795
STM0522	allP	putative allantoin transport protein	**-0.38**	0.43209
STM0522	allP	putative allantoin transport protein	**-0.11**	0.83899
STM0523	allB	allantoinase	**0.08**	0.91455
STM0523	allB	allantoinase	**0.93**	0.22540
STM0524	ybbY	putative transport protein	**-0.13**	0.86528
STM0524	ybbY	putative transport protein	**0.15**	0.80574
STM0525	glxK	glycerate kinase II	**-0.22**	0.72999
STM0525	glxK	glycerate kinase II	**-0.06**	0.93367
STM0526	ylbA	putative glyoxylate utilization protein	**0.25**	0.61064
STM0526	ylbA	putative glyoxylate utilization protein	**0.33**	0.65451
STM0527	allC	N-carbamoyl-L-amino acid amidohydrolase	**-0.38**	0.42811
STM0527	allC	N-carbamoyl-L-amino acid amidohydrolase	**0.12**	0.88018
STM0528	allD	ureidoglycolate dehydrogenase	**-0.63**	0.42811
STM0528	allD	ureidoglycolate dehydrogenase	**0.07**	0.95497
STM0529	fdrA	succinyl-CoA synthetase alpha subunit	**-0.70**	0.22540
STM0529	fdrA	succinyl-CoA synthetase alpha subunit	**-0.03**	0.96568
STM0530	ylbE	putative cytoplasmic protein	**-0.33**	0.78016
STM0530	ylbE	putative cytoplasmic protein	**0.23**	0.73151
STM0531	ylbF	putative cytoplasmic protein	**0.11**	0.79137
STM0531	ylbF	putative cytoplasmic protein	**0.48**	0.32016
STM0532	arcC	carbamate kinase	**0.00**	0.99857
STM0532	arcC	carbamate kinase	**0.23**	0.69668
STM0533	purK	phosphoribosylaminoimidazole carboxylase	**-0.53**	0.23635
STM0533	purK	phosphoribosylaminoimidazole carboxylase	**0.60**	0.24520
STM0534	purE	phosphoribosylaminoimidazole carboxylase catalytic subunit	**-0.42**	0.26833
STM0534	purE	phosphoribosylaminoimidazole carboxylase catalytic subunit	**-0.01**	0.99372
STM0535	lpxH	UDP-2,3-diacylglucosamine hydrolase	**-0.29**	0.52208
STM0535	lpxH	UDP-2,3-diacylglucosamine hydrolase	**-0.09**	0.85548
STM0536	ppiB	peptidyl-prolyl cis-trans isomerase B	**-0.37**	0.42511
STM0536	ppiB	peptidyl-prolyl cis-trans isomerase B	**-0.19**	0.65925
STM0537	cysS	cysteinyl-tRNA synthetase	**-0.15**	0.70430
STM0537	cysS	cysteinyl-tRNA synthetase	**0.14**	0.74260
STM0538	STM0538	putative outer membrane protein	**0.19**	0.74562
STM0538	STM0538	putative outer membrane protein	**0.58**	0.38596
STM0539	STM0539	putative inner membrane protein	**-0.02**	0.97625
STM0539	STM0539	putative inner membrane protein	**0.18**	0.73811

STM0540	ybcI	putative membrane-bound metal-dependent hydrolase	**-0.14**	0.74779
STM0540	ybcI	putative membrane-bound metal-dependent hydrolase	**-0.09**	0.88902
STM0541	ybcJ	putative cytoplasmic protein	**-0.79**	0.11224
STM0541	ybcJ	putative cytoplasmic protein	**-0.25**	0.53399
STM0542	folD	5,10-methylene-tetrahydrofolate	**-0.06**	0.91378
STM0542	folD	5,10-methylene-tetrahydrofolate	**-0.06**	0.91937
STM0543	fimA	fimbrin	**-0.63**	0.20505
STM0543	fimA	fimbrin	**0.02**	0.98539
STM0544	fimI	fimbrial protein	**-0.09**	0.83982
STM0544	fimI	fimbrial protein	**0.35**	0.49362
STM0545	fimC	periplasmic chaperone	**-0.25**	0.74807
STM0545	fimC	periplasmic chaperone	**0.25**	0.72518
STM0546	fimD	outer membrane usher protein precursor	**-0.17**	0.70048
STM0546	fimD	outer membrane usher protein precursor	**0.50**	0.32481
STM0547	fimH	minor fimbrial subunit	**-0.51**	0.23892
STM0547	fimH	minor fimbrial subunit	**0.00**	0.99697
STM0548	fimF	putative fimbrial protein	**-0.25**	0.49871
STM0548	fimF	putative fimbrial protein	**0.76**	0.29285
STM0549	fimZ	fimbrial protein Z	**-0.43**	0.38641
STM0549	fimZ	fimbrial protein Z	**0.17**	0.79102
STM0550	fimY	putative regulatory protein	**-0.47**	0.28861
STM0550	fimY	putative regulatory protein	**-0.04**	0.97583
STM0551	STM0551	hypothetical protein STM0551	**-0.25**	0.76538
STM0551	STM0551	hypothetical protein STM0551	**0.29**	0.68136
STM0552	fimW	putative fimbrial protein	**-0.28**	0.71169
STM0552	fimW	putative fimbrial protein	**0.21**	0.72210
STM0553	argU	STM0553	**-0.31**	0.67085
STM0553	argU	STM0553	**0.34**	0.73568
STM05559.T1	-	STM05559.T1	**-0.11**	0.85718
STM05559.T1	-	STM05559.T1	**0.48**	0.38552
STM0557	STM0557	putative inner membrane protein	**-0.31**	0.51526
STM0557	STM0557	putative inner membrane protein	**0.36**	0.57278
STM0558	yfdH	putative glycosyltransferase	**-0.24**	0.72247
STM0558	yfdH	putative glycosyltransferase	**-0.33**	0.48994
STM0559	rfbI	putative glycosyl translocase	**0.02**	0.97513
STM0559	rfbI	putative glycosyl translocase	**0.03**	0.97431
STM0561	STM0561	sensor kinase	**-0.20**	0.67509
STM0561	STM0561	sensor kinase	**0.52**	0.35014
STM0563	STM0563	putative transcriptional regulator	**-0.40**	0.35538
STM0563	STM0563	putative transcriptional regulator	**0.18**	0.70474
STM0564	STM0564	pyridine nucleotide-disulfide oxidoreductase	**-0.43**	0.37718
STM0564	STM0564	pyridine nucleotide-disulfide oxidoreductase	**0.07**	0.92683
STM0565	STM0565	putative periplasmic protein	**-0.41**	0.57070
STM0565	STM0565	putative periplasmic protein	**0.05**	0.95498
STM0566	STM0566	putative inner membrane protein	**-0.24**	0.56162
STM0566	STM0566	putative inner membrane protein	**-0.12**	0.83034
STM0567	STM0567	putative DNA repair ATPase	**0.13**	0.76610
STM0567	STM0567	putative DNA repair ATPase	**-0.02**	0.98212
STM0568	pheP	phenylalanine transporter	**-0.05**	0.94179
STM0568	pheP	phenylalanine transporter	**-0.08**	0.83723
STM0569	ybdG	hypothetical protein STM0569	**-0.43**	0.41154
STM0569	ybdG	hypothetical protein STM0569	**-0.37**	0.38919
STM0570	apeE	outer membrane esterase	**-0.28**	0.40947
STM0570	apeE	outer membrane esterase	**0.29**	0.45800
STM0571	STM0571	putative inner membrane protein	**-0.17**	0.78332
STM0571	STM0571	putative inner membrane protein	**0.46**	0.38668
STM0572	STM0572	putative phosphosugar isomerase	**0.00**	0.99928
STM0572	STM0572	putative phosphosugar isomerase	**0.35**	0.48600
STM0573	STM0573	putative inner membrane protein	**-0.18**	0.89617
STM0573	STM0573	putative inner membrane protein	**0.88**	0.13027
STM0574	STM0574	putative PTS system mannose-specific enzyme IID	**-0.47**	0.36270
STM0574	STM0574	putative PTS system mannose-specific enzyme IID	**0.33**	0.38668
STM0575	STM0575	putative inner membrane protein	**0.13**	0.87244

STM0575	STM0575	putative inner membrane protein	**0.24**	0.53533
STM0576	STM0576	putative PTS system mannose-specific enzyme IIAB	**-0.08**	0.85312
STM0576	STM0576	putative PTS system mannose-specific enzyme IIAB	**0.68**	0.45550
STM0577	STM0577	putative PTS system mannose-specific enzyme IIAB	**-0.84**	0.11913
STM0577	STM0577	putative PTS system mannose-specific enzyme IIAB	**0.28**	0.76211
STM0578	nfnB	dihydropteridine reductase/oxygen-insensitive NAD(P)H	**-0.27**	0.54624
STM0578	nfnB	dihydropteridine reductase/oxygen-insensitive NAD(P)H	**0.33**	0.61201
STM0579	ybdF	putative cytoplasmic protein	**-0.03**	0.96775
STM0579	ybdF	putative cytoplasmic protein	**0.45**	0.39520
STM0580	STM0580	putative regulatory protein	**-0.13**	0.80915
STM0580	STM0580	putative regulatory protein	**0.21**	0.60240
STM0581	STM0581	putative regulatory protein	**-0.13**	0.78755
STM0581	STM0581	putative regulatory protein	**1.03**	0.12860
STM0582	ybdJ	putative inner membrane protein	**0.02**	0.98539
STM0582	ybdJ	putative inner membrane protein	**0.28**	0.51052
STM0583	ybdK	putative cytoplasmic protein	**0.04**	0.95532
STM0583	ybdK	putative cytoplasmic protein	**0.50**	0.52364
STM0584	entD	enterochelin synthetase component D	**-0.06**	0.91171
STM0584	entD	enterochelin synthetase component D	**0.17**	0.81342
STM0585	fepA	outer membrane ferric enterobactin receptor precursor	**0.49**	0.35419
STM0585	fepA	outer membrane ferric enterobactin receptor precursor	**1.11**	0.15078
STM0586	fes	enterochelin esterase	**0.57**	0.25382
STM0586	fes	enterochelin esterase	**0.75**	0.17074
STM0587	ybdZ	putative cytoplasmic protein	**0.20**	0.65040
STM0587	ybdZ	putative cytoplasmic protein	**0.82**	0.13128
STM0588	entF	enterobactin synthetase component F	**0.33**	0.34473
STM0588	entF	enterobactin synthetase component F	**0.55**	0.19425
STM0589	fepE	ferric enterobactin/enterochelin transporter	**0.18**	0.72213
STM0589	fepE	ferric enterobactin/enterochelin transporter	**0.54**	0.36311
STM0590	fepC	enterobactin transporter	**-0.17**	0.72781
STM0590	fepC	enterobactin transporter	**0.51**	0.21747
STM0591	fepG	ferric enterobactin transporter	**0.22**	0.62906
STM0591	fepG	ferric enterobactin transporter	**0.43**	0.37692
STM0592	fepD	ferric enterobactin/enterochelin transporter	**0.31**	0.69882
STM0592	fepD	ferric enterobactin/enterochelin transporter	**0.48**	0.32481
STM0593	ybdA	putative transport protein	**-0.08**	0.92513
STM0593	ybdA	putative transport protein	**0.51**	0.46720
STM0594	fepB	ferric enterobactin transporter	**0.16**	0.70157
STM0594	fepB	ferric enterobactin transporter	**0.21**	0.66474
STM0595	entC	isochorismate synthase	**0.63**	0.26621
STM0595	entC	isochorismate synthase	**0.84**	0.10586
STM0596	entE	2,3-dihydroxybenzoate-AMP ligase	**0.53**	0.20129
STM0596	entE	2,3-dihydroxybenzoate-AMP ligase	**0.80**	0.17139
STM0597	entB	2,3-dihydro-2,3-dihydroxybenzoate synthetase	**0.37**	0.34824
STM0597	entB	2,3-dihydro-2,3-dihydroxybenzoate synthetase	**0.85**	0.13831
STM0598	entA	2,3-dihydroxybenzoate-2,3-dehydrogenase	**0.66**	0.20160
STM0598	entA	2,3-dihydroxybenzoate-2,3-dehydrogenase	**0.65**	0.20432
STM0599	ybdB	hypothetical protein STM0599	**0.13**	0.83268
STM0599	ybdB	hypothetical protein STM0599	**0.83**	0.11913
STM0600	cstA	carbon starvation protein	**-0.39**	0.42909
STM0600	cstA	carbon starvation protein	**0.49**	0.35564
STM0601	ybdD	putative cytoplasmic protein	**0.17**	0.81667
STM0601	ybdD	putative cytoplasmic protein	**0.18**	0.69988
STM0602	ybdH	putative glycerol dehydrogenase	**0.14**	0.75424
STM0602	ybdH	putative glycerol dehydrogenase	**0.38**	0.36341
STM0603	ybdL	putative aminotransferase	**-0.32**	0.49362
STM0603	ybdL	putative aminotransferase	**0.11**	0.82624
STM0604	ybdM	putative transcriptional regulator	**-0.64**	0.17041
STM0604	ybdM	putative transcriptional regulator	**-0.12**	0.84998
STM0605	ybdN	putative 3'-phosphoadenosine 5'-phosphosulfate sulfotransferase	**-0.54**	0.34793
STM0605	ybdN	putative 3'-phosphoadenosine 5'-phosphosulfate sulfotransferase	**0.10**	0.92161

STM0606	ybdO	putative transcriptional regulator	**-0.22**	0.61654
STM0606	ybdO	putative transcriptional regulator	**0.59**	0.29044
STM0607	dsbG	periplasmic disulfide isomerase/thiol-disulphide oxidase	**-0.89**	0.18961
STM0607	dsbG	periplasmic disulfide isomerase/thiol-disulphide oxidase	**0.07**	0.91684
STM0608	ahpC	alkyl hydroperoxide reductase C22 subunit	**-0.36**	0.33587
STM0608	ahpC	alkyl hydroperoxide reductase C22 subunit	**0.23**	0.53513
STM0609	ahpF	alkyl hydroperoxide reductase F52a subunit	**-0.18**	0.72341
STM0609	ahpF	alkyl hydroperoxide reductase F52a subunit	**0.07**	0.90181
STM0610	STM0610	putative anaerobic dehydrogenase component	**0.37**	0.61960
STM0610	STM0610	putative anaerobic dehydrogenase component	**0.91**	0.45107
STM0611	STM0611	putative oxidoreductase protein	**0.50**	0.43434
STM0611	STM0611	putative oxidoreductase protein	**0.73**	0.24444
STM0612	STM0612	putative hydrogenase protein	**0.29**	0.50811
STM0612	STM0612	putative hydrogenase protein	**0.18**	0.73713
STM0613	STM0613	putative hydrogenase protein	**-0.26**	0.58965
STM0613	STM0613	putative hydrogenase protein	**-0.22**	0.72976
STM0614	ybdQ	putative universal stress protein	**-0.29**	0.49878
STM0614	ybdQ	putative universal stress protein	**0.43**	0.46862
STM0615	ybdR	putative dehydrogenase	**0.03**	0.96228
STM0615	ybdR	putative dehydrogenase	**0.32**	0.52810
STM0616	rnk	nucleoside diphosphate kinase regulator	**-0.26**	0.48987
STM0616	rnk	nucleoside diphosphate kinase regulator	**0.31**	0.40020
STM0617	rna	RNase I	**-0.09**	0.86190
STM0617	rna	RNase I	**0.16**	0.73568
STM0618	citT	citrate/succinate transport antiport protein	**-0.57**	0.22938
STM0618	citT	citrate/succinate transport antiport protein	**-0.03**	0.96107
STM0619	citG	triphosphoribosyl-dephospho-CoA synthase	**0.10**	0.85504
STM0619	citG	triphosphoribosyl-dephospho-CoA synthase	**0.19**	0.72219
STM0620	citX	2'-(5'-triphosphoribosyl)-3'-dephospho-CoA:apo-citrate lyase	**-0.11**	0.83100
STM0620	citX	2'-(5'-triphosphoribosyl)-3'-dephospho-CoA:apo-citrate lyase	**0.24**	0.75395
STM0621	citF	citrate lyase alpha chain/citrate-ACP transferase	**-0.02**	0.97168
STM0621	citF	citrate lyase alpha chain/citrate-ACP transferase	**0.58**	0.53515
STM0622	citE	citrate lyase beta chain	**-0.40**	0.49035
STM0622	citE	citrate lyase beta chain	**0.40**	0.40701
STM0623	citD	citrate lyase acyl carrier protein gamma chain	**0.46**	0.43914
STM0623	citD	citrate lyase acyl carrier protein gamma chain	**1.15**	0.07542
STM0624	citC	citrate lyase synthetase	**-0.98**	0.13645
STM0624	citC	citrate lyase synthetase	**-0.02**	0.96968
STM0625	dpiB	sensory histidine kinase	**-0.44**	0.25759
STM0625	dpiB	sensory histidine kinase	**0.43**	0.33833
STM0626	dpiA	response regulator	**-0.11**	0.84657
STM0626	dpiA	response regulator	**0.56**	0.39861
STM0627	dcuC	dicarboxylate transporter	**-0.32**	0.61811
STM0627	dcuC	dicarboxylate transporter	**0.47**	0.45450
STM0628	pagP	PhoPQ-activated gene	**-0.87**	0.13027
STM0628	pagP	PhoPQ-activated gene	**-0.84**	0.21015
STM0629	cspE	cold shock protein E	**-0.24**	0.80406
STM0629	cspE	cold shock protein E	**0.07**	0.94050
STM0630	ccrB	camphor resistance protein CrcB	**0.17**	0.77801
STM0630	ccrB	camphor resistance protein CrcB	**0.05**	0.94867
STM0631	ybeM	putative hydrolase	**-0.37**	0.29912
STM0631	ybeM	putative hydrolase	**0.38**	0.40020
STM0632	tatE	twin argininte translocase protein A	**-0.31**	0.53200
STM0632	tatE	twin argininte translocase protein A	**-0.51**	0.36444
STM0633	lipA	lipoyl synthase	**-0.32**	0.42111
STM0633	lipA	lipoyl synthase	**0.05**	0.91170
STM0634	ybeF	putative transcriptional regulator	**-0.09**	0.89796
STM0634	ybeF	putative transcriptional regulator	**0.64**	0.25473
STM0635,S	lipB	lipoyltransferase	**-0.12**	0.78929
STM0635,S	lipB	lipoyltransferase	**0.02**	0.97474
STM0636	ybeD	hypothetical protein STM0636	**-0.44**	0.31293

STM0636	ybeD	hypothetical protein STM0636	**-0.14**	0.70077
STM0637	dacA	D-alanyl-D-alanine carboxypeptidase	**-0.43**	0.35937
STM0637	dacA	D-alanyl-D-alanine carboxypeptidase	**-0.25**	0.65974
STM0638	rlpA	minor lipoprotein	**-0.36**	0.40818
STM0638	rlpA	minor lipoprotein	**0.22**	0.71603
STM0639	mrdB	rod shape-determining membrane protein	**-0.18**	0.66743
STM0639	mrdB	rod shape-determining membrane protein	**0.15**	0.73473
STM0640	mrdA	cell elongation-specific transpeptidase	**-0.39**	0.41329
STM0640	mrdA	cell elongation-specific transpeptidase	**0.05**	0.93709
STM0641	ybeA	hypothetical protein STM0641	**-0.21**	0.56370
STM0641	ybeA	hypothetical protein STM0641	**0.29**	0.49336
STM0642	ybeB	hypothetical protein STM0642	**0.04**	0.94050
STM0642	ybeB	hypothetical protein STM0642	**0.18**	0.65810
STM0643	cobC	alpha ribazole-5'-P phosphatase	**0.17**	0.66406
STM0643	cobC	alpha ribazole-5'-P phosphatase	**0.13**	0.75831
STM0644	cobD	threonine-phosphate decarboxylase	**0.22**	0.61343
STM0644	cobD	threonine-phosphate decarboxylase	**0.20**	0.57310
STM0645	nadD	nicotinic acid mononucleotide adenyltransferase	**-0.01**	0.98790
STM0645	nadD	nicotinic acid mononucleotide adenyltransferase	**0.07**	0.92506
STM0646	holA	DNA polymerase III subunit delta	**0.16**	0.70140
STM0646	holA	DNA polymerase III subunit delta	**0.35**	0.39987
STM0647	rlpB	minor lipoprotein	**-0.17**	0.70545
STM0647	rlpB	minor lipoprotein	**-0.16**	0.67262
STM0648	leuS	leucyl-tRNA synthetase	**0.12**	0.73904
STM0648	leuS	leucyl-tRNA synthetase	**0.06**	0.89126
STM0649,S	STM0649,S	putative hydrolase	**-0.15**	0.84383
STM0649,S	STM0649,S	putative hydrolase	**0.12**	0.77217
STM0650	STM0650	putative hydrolas	**-0.30**	0.50190
STM0650	STM0650	putative hydrolas	**0.48**	0.59526
STM0651	STM0651	2-keto-3-deoxygluconate permease	**-1.11**	0.20065
STM0651	STM0651	2-keto-3-deoxygluconate permease	**0.00**	0.99887
STM0652	STM0652	putative sigma-54 dependent transcriptional regulator	**0.15**	0.87999
STM0652	STM0652	putative sigma-54 dependent transcriptional regulator	**0.85**	0.32373
STM0653	ybeL	putative cytoplasmic protein	**0.21**	0.80637
STM0653	ybeL	putative cytoplasmic protein	**0.45**	0.36444
STM0654	ybeQ	tetratricopeptide repeat protein	**-0.29**	0.60051
STM0654	ybeQ	tetratricopeptide repeat protein	**0.35**	0.67097
STM0655	ybeR	putative cytoplasmic protein	**-0.33**	0.58822
STM0655	ybeR	putative cytoplasmic protein	**0.20**	0.76622
STM0656	ybeS	putative molecular chaperone	**-0.41**	0.33167
STM0656	ybeS	putative molecular chaperone	**0.43**	0.35248
STM0657	ybeU	putative cytoplasmic protein	**-0.17**	0.74434
STM0657	ybeU	putative cytoplasmic protein	**-0.62**	0.21019
STM0657	ybeU	putative cytoplasmic protein	**0.21**	0.63075
STM0657	ybeU	putative cytoplasmic protein	**-0.12**	0.89004
STM0658	ybeV	putative molecular chaperone	**-0.17**	0.83718
STM0658	ybeV	putative molecular chaperone	**-1.02**	0.70229
STM0659	hscC	putative heatshock protein	**0.00**	0.99902
STM0659	hscC	putative heatshock protein	**0.32**	0.48600
STM0660	STM0660	putative cytoplasmic protein	**0.33**	0.68232
STM0660	STM0660	putative cytoplasmic protein	**0.85**	0.17139
STM0661	ybeK	putative purine nucleoside hydrolase	**0.69**	0.16534
STM0661	ybeK	putative purine nucleoside hydrolase	**0.93**	0.21880
STM0662	gltL	glutamate/aspartate transporter	**-0.24**	0.65305
STM0662	gltL	glutamate/aspartate transporter	**0.08**	0.87512
STM0663	gltK	glutamate/aspartate transporter	**0.13**	0.73473
STM0663	gltK	glutamate/aspartate transporter	**1.19**	0.11690
STM0664	gltJ	glutamate/aspartate transporter	**-0.68**	0.68232
STM0664	gltJ	glutamate/aspartate transporter	**0.79**	0.47479
STM0665	gltI	glutamate/aspartate transporter	**-0.16**	0.72677
STM0665	gltI	glutamate/aspartate transporter	**1.07**	0.32093
STM0666	lnt	apolipoprotein N-acyltransferase	**0.00**	0.99583
STM0666	lnt	apolipoprotein N-acyltransferase	**0.09**	0.82964

STM0667	ybeX	putative transport protein	**-0.15**	0.78667
STM0667	ybeX	putative transport protein	**0.29**	0.46927
STM0668	ybeY	hypothetical protein STM0668	**-0.04**	0.93699
STM0668	ybeY	hypothetical protein STM0668	**-0.38**	0.31280
STM0669	phoL	putative phosphate starvation-inducible protein	**-0.95**	0.15276
STM0669	phoL	putative phosphate starvation-inducible protein	**-0.43**	0.32170
STM0670	miaB	rRNA modification protein	**-0.68**	0.18763
STM0670	miaB	rRNA modification protein	**-0.43**	0.34201
STM0671	ubiF	2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinol hydroxylase	**0.16**	0.69398
STM0671	ubiF	2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinol hydroxylase	**0.08**	0.91874
STM0672	STM0672	putative inner membrane protein	**-0.14**	0.72821
STM0672	STM0672	putative inner membrane protein	**0.02**	0.97645
STM0674	glnV	STM0674	**-0.36**	0.54461
STM0674	glnV	STM0674	**-0.07**	0.91387
STM0674	glnV	STM0674	**0.00**	0.99512
STM0674	glnV	STM0674	**0.65**	0.20285
STM0677	glnU	STM0677	**-0.76**	0.22540
STM0677	glnU	STM0677	**-0.35**	0.50555
STM0677	glnU	STM0677	**-0.33**	0.50811
STM0677	glnU	STM0677	**0.19**	0.83084
STM0678	leuW	STM0678	**-0.03**	0.95177
STM0678	leuW	STM0678	**0.17**	0.67264
STM0679	metT	STM0679	**-0.22**	0.85636
STM0679	metT	STM0679	**-0.68**	0.34051
STM0679	metT	STM0679	**-0.08**	0.91170
STM0679	metT	STM0679	**-0.20**	0.72970
STM0680	asnB	asparagine synthetase B	**-0.41**	0.26910
STM0680	asnB	asparagine synthetase B	**-0.21**	0.69797
STM0681	nagD	putative phosphatase	**-0.24**	0.63222
STM0681	nagD	putative phosphatase	**0.13**	0.80754
STM0682	nagC	N-acetylglucosamine operon transcriptional repressor	**0.18**	0.68332
STM0682	nagC	N-acetylglucosamine operon transcriptional repressor	**0.51**	0.32055
STM0683	nagA	N-acetylglucosamine-6-phosphate deacetylase	**-0.01**	0.99213
STM0683	nagA	N-acetylglucosamine-6-phosphate deacetylase	**0.14**	0.74361
STM0684	nagB	glucosamine-6-phosphate deaminase	**0.04**	0.94134
STM0684	nagB	glucosamine-6-phosphate deaminase	**0.57**	0.22602
STM0685	nagE	N-acetylglucosamine-specific enzyme IIABC	**0.57**	0.17139
STM0685	nagE	N-acetylglucosamine-specific enzyme IIABC	**0.72**	0.13645
STM0686	glnS	glutaminyl-tRNA synthetase	**-0.26**	0.74243
STM0686	glnS	glutaminyl-tRNA synthetase	**0.12**	0.88339
STM0687	ybfM	putative outer membrane protein	**-0.14**	0.74556
STM0687	ybfM	putative outer membrane protein	**0.28**	0.69398
STM0688	ybfN	putative lipoprotein	**-0.31**	0.55338
STM0688	ybfN	putative lipoprotein	**0.63**	0.26378
STM0689	citA	citrate-proton symporter	**0.02**	0.97474
STM0689	citA	citrate-proton symporter	**-0.27**	0.58887
STM0690	citB	citrate utilization protein b	**-0.16**	0.79668
STM0690	citB	citrate utilization protein b	**0.57**	0.37836
STM0691	STM0691	hypothetical protein STM0691	**0.04**	0.96568
STM0691	STM0691	hypothetical protein STM0691	**0.49**	0.34148
STM0692	STM0692	putative transcriptional regulator	**-0.01**	0.99394
STM0692	STM0692	putative transcriptional regulator	**0.37**	0.53827
STM0693	fur	ferric uptake regulator	**0.08**	0.85534
STM0693	fur	ferric uptake regulator	**-0.11**	0.78641
STM0694	fldA	flavodoxin	**-0.23**	0.52101
STM0694	fldA	flavodoxin	**0.12**	0.78822
STM0695	ybfE	putative SOS response protein	**-0.12**	0.76313
STM0695	ybfE	putative SOS response protein	**-0.26**	0.56769
STM0696	ybfF	putative enzyme	**-0.21**	0.62757
STM0696	ybfF	putative enzyme	**0.03**	0.96278
STM0697	seqA	sequestration protein A	**-0.19**	0.60010

STM0697	seqA	sequestration protein A	**0.33**	0.37454
STM0698	pgm	phosphoglucomutase	**-0.17**	0.65549
STM0698	pgm	phosphoglucomutase	**0.35**	0.46148
STM0699	STM0699	putative cytoplasmic protein	**-0.31**	0.49035
STM0699	STM0699	putative cytoplasmic protein	**0.12**	0.81455
STM0700	potE	putrescine/ornithine antiporter	**-0.55**	0.25514
STM0700	potE	putrescine/ornithine antiporter	**0.10**	0.86385
STM0701	speF	ornithine decarboxylase isozyme	**-0.20**	0.64371
STM0701	speF	ornithine decarboxylase isozyme	**-0.16**	0.79093
STM0702	kdpE	response regulator	**-0.19**	0.76622
STM0702	kdpE	response regulator	**1.15**	0.13509
STM0703	kdpD	sensor kinase	**0.16**	0.66992
STM0703	kdpD	sensor kinase	**0.74**	0.15984
STM0704	kdpC	potassium-transporting ATPase subunit C	**0.12**	0.78572
STM0704	kdpC	potassium-transporting ATPase subunit C	**0.67**	0.38307
STM0705	kdpB	potassium-transporting ATPase subunit B	**-0.64**	0.30748
STM0705	kdpB	potassium-transporting ATPase subunit B	**-0.74**	0.34541
STM0706	kdpA	potassium-transporting ATPase subunit A	**0.65**	0.49336
STM0706	kdpA	potassium-transporting ATPase subunit A	**0.65**	0.29848
STM0708	ybfA	putative periplasmic protein	**-0.35**	0.46772
STM0708	ybfA	putative periplasmic protein	**0.31**	0.63357
STM0709	phrB	deoxyribodipyrimidine photolyase	**-0.23**	0.67885
STM0709	phrB	deoxyribodipyrimidine photolyase	**0.28**	0.51073
STM0710	ybgH	putative POT family transport protein	**-0.24**	0.65130
STM0710	ybgH	putative POT family transport protein	**0.21**	0.62617
STM0711	ybgI	putative cytoplasmic protein	**-0.36**	0.37025
STM0711	ybgI	putative cytoplasmic protein	**0.55**	0.22602
STM0712	ybgJ	putative carboxylase	**-0.34**	0.48360
STM0712	ybgJ	putative carboxylase	**0.23**	0.57189
STM0713	ybgK	putative carboxylase	**-0.04**	0.93804
STM0713	ybgK	putative carboxylase	**-0.02**	0.95655
STM0714	ybgL	hypothetical protein STM0714	**-0.09**	0.84355
STM0714	ybgL	hypothetical protein STM0714	**-0.08**	0.89730
STM0715	STM0715	putative cytoplasmic protein	**-0.51**	0.42277
STM0715	STM0715	putative cytoplasmic protein	**0.42**	0.43062
STM0716	NT_FimBE_C	putative phage integrase	**-0.77**	0.27696
STM0716	NT_FimBE_C	putative phage integrase	**0.17**	0.69297
STM0719	STM0719	putative UDP-galactopyranose mutase	**-0.87**	0.21747
STM0719	STM0719	putative UDP-galactopyranose mutase	**-0.20**	0.64727
STM0719	STM0719	putative UDP-galactopyranose mutase	**-0.10**	0.82667
STM0719	STM0719	putative UDP-galactopyranose mutase	**0.43**	0.39910
STM0719	STM0719	putative UDP-galactopyranose mutase	**0.93**	0.31305
STM0719	STM0719	putative UDP-galactopyranose mutase	**0.19**	0.79631
STM0720	STM0720	putative glycosyl transferase	**-0.01**	0.98066
STM0720	STM0720	putative glycosyl transferase	**-0.13**	0.88415
STM0721	STM0721	putative glycosyl transferase	**0.16**	0.71139
STM0721	STM0721	putative glycosyl transferase	**0.76**	0.16631
STM0722	STM0722	putative ABC transporter permease protein	**-0.11**	0.87330
STM0722	STM0722	putative ABC transporter permease protein	**0.00**	0.99742
STM0723	STM0723	putative ABC-type polysaccharide/polyol phosphate transport system	**-1.18**	0.11879
STM0723	STM0723	putative ABC-type polysaccharide/polyol phosphate transport system	**-0.15**	0.82350
STM0724	STM0724	putative glycosyltransferase	**-0.14**	0.87154
STM0724	STM0724	putative glycosyltransferase	**0.08**	0.92506
STM0725	STM0725	putative glycosyltransferase	**-0.21**	0.73473
STM0725	STM0725	putative glycosyltransferase	**0.16**	0.69988
STM0726	STM0726	putative glycosyl transferase	**-0.39**	0.36017
STM0726	STM0726	putative glycosyl transferase	**1.03**	0.19398
STM0728	nei	endonuclease VIII	**-0.20**	0.58903
STM0728	nei	endonuclease VIII	**0.74**	0.19843
STM0729	abrB	putative transport protein	**-0.04**	0.95876
STM0729	abrB	putative transport protein	**-0.08**	0.91937

STM0730	gltA	citrate synthase	**0.18**	0.70249
STM0730	gltA	citrate synthase	**0.40**	0.53062
STM0732	sdhC	succinate dehydrogenase cytochrome b556 large membrane subunit	**0.77**	0.23181
STM0732	sdhC	succinate dehydrogenase cytochrome b556 large membrane subunit	**0.88**	0.16281
STM0733	sdhD	succinate dehydrogenase cytochrome b556 small membrane subunit	**0.66**	0.21677
STM0733	sdhD	succinate dehydrogenase cytochrome b556 small membrane subunit	**0.43**	0.34913
STM0734	sdhA	succinate dehydrogenase catalytic subunit	**0.30**	0.68258
STM0734	sdhA	succinate dehydrogenase catalytic subunit	**0.45**	0.39635
STM0735	sdhB	succinate dehydrogenase catalytic subunit	**0.33**	0.50190
STM0735	sdhB	succinate dehydrogenase catalytic subunit	**0.51**	0.40947
STM0736	sucA	2-oxoglutarate dehydrogenase	**0.62**	0.38596
STM0736	sucA	2-oxoglutarate dehydrogenase	**0.66**	0.38044
STM0737	sucB	dihydrolipoamide acetyltransferase	**0.45**	0.55649
STM0737	sucB	dihydrolipoamide acetyltransferase	**0.44**	0.51116
STM0738	sucC	succinyl-CoA synthetase subunit beta	**0.30**	0.60423
STM0738	sucC	succinyl-CoA synthetase subunit beta	**0.33**	0.65130
STM0739	sucD	succinyl-CoA synthetase alpha subunit	**-0.50**	0.42008
STM0739	sucD	succinyl-CoA synthetase alpha subunit	**0.35**	0.53840
STM0740	cydA	cytochrome d terminal oxidase polypeptide subunit I	**0.05**	0.91915
STM0740	cydA	cytochrome d terminal oxidase polypeptide subunit I	**0.05**	0.93639
STM0741	cydB	cytochrome d terminal oxidase polypeptide subunit II	**-0.29**	0.45047
STM0741	cydB	cytochrome d terminal oxidase polypeptide subunit II	**-0.27**	0.50267
STM0742	ybgT	putative outer membrane lipoprotein	**-0.32**	0.41545
STM0742	ybgT	putative outer membrane lipoprotein	**-0.29**	0.58506
STM0743	ybgE	putative inner membrane lipoprotein	**-0.15**	0.69462
STM0743	ybgE	putative inner membrane lipoprotein	**-0.25**	0.58108
STM0744	ybgC	putative esterase	**-0.21**	0.55482
STM0744	ybgC	putative esterase	**-0.03**	0.95608
STM0745	tolQ	Tol import system inner membrane protein	**-0.05**	0.91456
STM0745	tolQ	Tol import system inner membrane protein	**0.35**	0.41329
STM0746	tolR	Tol import sytem inner membrane protein	**-0.16**	0.76651
STM0746	tolR	Tol import sytem inner membrane protein	**0.02**	0.97361
STM0747	tolA	cell envelope integrity inner membrane protein TolA	**-0.57**	0.19142
STM0747	tolA	cell envelope integrity inner membrane protein TolA	**-0.25**	0.55482
STM0748	tolB	translocation protein TolB precursor	**-0.08**	0.84611
STM0748	tolB	translocation protein TolB precursor	**0.17**	0.70726
STM0749	pal	peptidoglycan-associated lipoprotein precursor	**-0.05**	0.92014
STM0749	pal	peptidoglycan-associated lipoprotein precursor	**0.10**	0.80406
STM0750	ybgF	putative periplasmic protein	**-0.58**	0.17074
STM0750	ybgF	putative periplasmic protein	**0.15**	0.72976
STM0756	nadA	quinolinate synthetase	**-0.20**	0.56800
STM0756	nadA	quinolinate synthetase	**-0.15**	0.81862
STM0757	pnuC	nucleoside/purine/pyrimidine transporter	**-0.23**	0.52151
STM0757	pnuC	nucleoside/purine/pyrimidine transporter	**-0.08**	0.90462
STM0758	ybgR	zinc transporter ZitB	**-0.20**	0.59984
STM0758	ybgR	zinc transporter ZitB	**0.04**	0.94990
STM0759	ybgS	hypothetical protein STM0759	**-0.23**	0.69392
STM0759	ybgS	hypothetical protein STM0759	**0.67**	0.22602
STM0760	aroG	3-deoxy-7-phosphoheptulonate synthase	**0.19**	0.72247
STM0760	aroG	3-deoxy-7-phosphoheptulonate synthase	**0.30**	0.49336
STM0761	STM0761	fumarate hydratase	**-0.09**	0.85801
STM0761	STM0761	fumarate hydratase	**-0.04**	0.96164
STM0762	STM0762	fumarate hydratase	**0.25**	0.58570
STM0762	STM0762	fumarate hydratase	**0.19**	0.81121
STM0763,s	STM0763,s	transcriptional regulator	**-0.49**	0.34698
STM0763,s	STM0763,s	transcriptional regulator	**-0.14**	0.84673
STM0764	STM0764	transcriptional regulator	**-0.13**	0.89233
STM0764	STM0764	transcriptional regulator	**-0.30**	0.73541
STM0765	STM0765	putative cation transporter	**0.01**	0.98228

STM0765	STM0765	putative cation transporter	**0.23**	0.63849
STM0766	dcoC	putative oxaloacetate decarboxylase subunit gamma	**-0.21**	0.65730
STM0766	dcoC	putative oxaloacetate decarboxylase subunit gamma	**0.63**	0.20065
STM0769	STM0769	putative cytoplasmic protein	**-0.46**	0.52364
STM0769	STM0769	putative cytoplasmic protein	**0.13**	0.76483
STM0770	STM0770	putative ABC transport protein	**-0.58**	0.19843
STM0770	STM0770	putative ABC transport protein	**-0.05**	0.92871
STM0771	STM0771	putative ABC-type cobalamin/Fe3+-siderophore transport component	**-0.21**	0.65377
STM0771	STM0771	putative ABC-type cobalamin/Fe3+-siderophore transport component	**-0.14**	0.79308
STM0772	gpmA	phosphoglyceromutase	**-0.41**	0.29044
STM0772	gpmA	phosphoglyceromutase	**0.04**	0.93023
STM0773	galM	galactose-1-epimerase	**0.16**	0.65592
STM0773	galM	galactose-1-epimerase	**0.16**	0.69882
STM0774	galK	galactokinase	**-0.61**	0.23449
STM0774	galK	galactokinase	**-0.21**	0.62403
STM0775	galT	galactose-1-phosphate uridylyltransferase	**0.12**	0.77425
STM0775	galT	galactose-1-phosphate uridylyltransferase	**0.09**	0.85228
STM0776	galE	UDP-galactose 4-epimerase	**-0.45**	0.45041
STM0776	galE	UDP-galactose 4-epimerase	**-0.11**	0.78335
STM0777	STM0777	putative inner membrane protein	**0.20**	0.61809
STM0777	STM0777	putative inner membrane protein	**0.28**	0.65377
STM0778	modF	putative molybdenum transporter	**-0.04**	0.93720
STM0778	modF	putative molybdenum transporter	**0.43**	0.30607
STM0779	modE	molybdate uptake operon transcriptional repressor	**-0.11**	0.81419
STM0779	modE	molybdate uptake operon transcriptional repressor	**-0.04**	0.95537
STM0781	modA	molybdate transporter	**0.15**	0.69882
STM0781	modA	molybdate transporter	**0.25**	0.71356
STM0782	modB	molybdate transport permease protein	**-0.27**	0.48210
STM0782	modB	molybdate transport permease protein	**0.38**	0.44208
STM0783	modC	molybdate transporter	**-0.11**	0.79356
STM0783	modC	molybdate transporter	**0.31**	0.41687
STM0784	ybhA	putative hydrolase	**-0.07**	0.87655
STM0784	ybhA	putative hydrolase	**0.00**	0.99856
STM0785	ybhE	putative 3-carboxymuconate cyclase	**-0.36**	0.40289
STM0785	ybhE	putative 3-carboxymuconate cyclase	**0.12**	0.75510
STM0786	ybhC	putative pectinesterase	**-0.34**	0.35366
STM0786	ybhC	putative pectinesterase	**0.23**	0.49502
STM0787	hutI	imidazolonepropionase	**-0.91**	0.16658
STM0787	hutI	imidazolonepropionase	**-0.02**	0.97050
STM0788	hutG	formimidoylglutamase	**-0.20**	0.66229
STM0788	hutG	formimidoylglutamase	**0.10**	0.84687
STM0789	hutC	histidine utilization repressor	**0.05**	0.92513
STM0789	hutC	histidine utilization repressor	**-0.24**	0.72518
STM0791	hutH	histidine ammonia-lyase	**0.22**	0.74359
STM0791	hutH	histidine ammonia-lyase	**-0.25**	0.73356
STM0792	ybhB	putative phospholipid-binding protein	**-0.19**	0.61824
STM0792	ybhB	putative phospholipid-binding protein	**0.46**	0.27383
STM0793	bioA	adenosylmethionine--8-amino-7-oxononanoate transaminase	**-0.61**	0.18265
STM0793	bioA	adenosylmethionine--8-amino-7-oxononanoate transaminase	**0.08**	0.86190
STM0794	bioB	biotin synthetase	**0.06**	0.93841
STM0794	bioB	biotin synthetase	**0.98**	0.22602
STM0795	bioF	8-amino-7-oxononanoate synthase	**0.82**	0.53099
STM0795	bioF	8-amino-7-oxononanoate synthase	**1.58**	0.27453
STM0796	bioC	biotin biosynthetic protein	**-0.18**	0.63101
STM0796	bioC	biotin biosynthetic protein	**0.42**	0.31049
STM0797	bioD	dithiobiotin synthetase	**-0.32**	0.73653
STM0797	bioD	dithiobiotin synthetase	**0.50**	0.44552
STM0798	uvrB	excinuclease ABC subunit B	**-0.01**	0.98879
STM0798	uvrB	excinuclease ABC subunit B	**-0.20**	0.73698

STM0800	slrP	leucine-rich repeat protein	**-0.43**	0.44208
STM0800	slrP	leucine-rich repeat protein	**0.65**	0.24520
STM0801	ybhK	putative cytoplasmic protein	**-0.06**	0.94426
STM0801	ybhK	putative cytoplasmic protein	**0.51**	0.35853
STM0802	moaA	molybdenum cofactor biosynthesis protein A	**0.10**	0.82338
STM0802	moaA	molybdenum cofactor biosynthesis protein A	**0.18**	0.65612
STM0803	moaB	molybdopterin biosynthetic protein B	**-0.40**	0.38894
STM0803	moaB	molybdopterin biosynthetic protein B	**-0.06**	0.89546
STM0804	moaC	molybdenum cofactor biosynthesis protein C	**0.07**	0.89111
STM0804	moaC	molybdenum cofactor biosynthesis protein C	**-0.05**	0.94179
STM0805	moaD	molybdopterin biosynthetic protein	**0.05**	0.95081
STM0805	moaD	molybdopterin biosynthetic protein	**0.45**	0.33651
STM0806	moaE	molybdopterin converting factor subunit 2	**-0.09**	0.83497
STM0806	moaE	molybdopterin converting factor subunit 2	**-0.22**	0.52364
STM0807	ybhL	putative permease	**-0.18**	0.63153
STM0807	ybhL	putative permease	**-0.04**	0.93235
STM0808	ybhM	putative integral membrane protein	**0.15**	0.78332
STM0808	ybhM	putative integral membrane protein	**-0.24**	0.62988
STM0809	STM0809	putative inner membrane protein	**-0.50**	0.31242
STM0809	STM0809	putative inner membrane protein	**0.17**	0.85340
STM0810	STM0810	putative inner membrane protein	**-0.21**	0.59824
STM0810	STM0810	putative inner membrane protein	**0.32**	0.70726
STM0811	ybhN	hypothetical protein STM0811	**0.31**	0.67097
STM0811	ybhN	hypothetical protein STM0811	**1.26**	0.13645
STM0812	ybhO	cardiolipin synthase	**-0.39**	0.66677
STM0812	ybhO	cardiolipin synthase	**0.33**	0.75208
STM0813	ybhP	putative cytoplasmic protein	**-0.33**	0.62757
STM0813	ybhP	putative cytoplasmic protein	**-0.10**	0.89640
STM0814	ybhQ	putative inner membrane protein	**0.10**	0.86968
STM0814	ybhQ	putative inner membrane protein	**0.06**	0.92637
STM0815	ybhR	putative transport protein	**-0.07**	0.91937
STM0815	ybhR	putative transport protein	**-0.37**	0.44137
STM0816	ybhS	putative transport protein	**-0.46**	0.21840
STM0816	ybhS	putative transport protein	**0.20**	0.66594
STM0817	ybhF	putative ABC-type multidrug transport system ATPase component	**-0.10**	0.79271
STM0817	ybhF	putative ABC-type multidrug transport system ATPase component	**0.33**	0.35248
STM0818	STM0818	hypothetical protein STM0818	**-0.52**	0.20151
STM0818	STM0818	hypothetical protein STM0818	**0.20**	0.76313
STM0819	ybiH	putative transcriptional repressor	**-0.31**	0.56200
STM0819	ybiH	putative transcriptional repressor	**-0.07**	0.88018
STM0820	rhlE	putative ATP-dependent RNA helicase	**0.06**	0.91170
STM0820	rhlE	putative ATP-dependent RNA helicase	**0.17**	0.70199
STM0821	dinG	SOS repair enzyme	**-0.17**	0.70458
STM0821	dinG	SOS repair enzyme	**0.61**	0.18918
STM0822	ybiB	hypothetical protein STM0822	**0.07**	0.95836
STM0822	ybiB	hypothetical protein STM0822	**-0.36**	0.58071
STM0823	ybiJ	putative periplasmic protein	**-0.22**	0.65196
STM0823	ybiJ	putative periplasmic protein	**-0.13**	0.78973
STM0825	ybiI	hypothetical protein STM0825	**0.02**	0.98615
STM0825	ybiI	hypothetical protein STM0825	**0.16**	0.82350
STM0826	ybiN	putative SAM-dependent methyltransferase	**0.10**	0.86108
STM0826	ybiN	putative SAM-dependent methyltransferase	**0.16**	0.81449
STM0827	ybiO	putative transport protein	**-0.17**	0.67351
STM0827	ybiO	putative transport protein	**0.05**	0.91484
STM0828	glnQ	glutamine ABC transporter ATP-binding component	**0.04**	0.94368
STM0828	glnQ	glutamine ABC transporter ATP-binding component	**0.71**	0.12727
STM0829	glnP	glutamine ABC transporter permease component	**0.61**	0.34666
STM0829	glnP	glutamine ABC transporter permease component	**0.48**	0.36407
STM0830	glnH	glutamine ABC transporter periplasmic-binding protein	**0.11**	0.79924
STM0830	glnH	glutamine ABC transporter periplasmic-binding protein	**0.58**	0.17603
STM0831	dps	DNA protection during starvation conditions	**0.38**	0.35824

STM0831	dps	DNA protection during starvation conditions	**0.15**	0.74374
STM0832	ybiF	putative permease	**0.06**	0.91170
STM0832	ybiF	putative permease	**-0.05**	0.94421
STM0833	ompX	outer membrane protein X	**-0.32**	0.41443
STM0833	ompX	outer membrane protein X	**-0.21**	0.59455
STM0834	ybiP	putative Integral membrane protein	**-0.19**	0.63887
STM0834	ybiP	putative Integral membrane protein	**-0.08**	0.83897
STM0835	STM0835	putative Mn-dependent transcriptional regulator	**-0.44**	0.34793
STM0835	STM0835	putative Mn-dependent transcriptional regulator	**-0.01**	0.98539
STM0836	ybiR	putative transporter	**0.24**	0.59096
STM0836	ybiR	putative transporter	**0.06**	0.92197
STM0837	ybiS	putative periplasmic protein	**0.11**	0.80527
STM0837	ybiS	putative periplasmic protein	**0.31**	0.37610
STM0838	ybiT	putative ABC transporter ATPase component	**0.05**	0.94573
STM0838	ybiT	putative ABC transporter ATPase component	**0.12**	0.87512
STM0839	STM0839	putative inner membrane protein	**-0.06**	0.91387
STM0839	STM0839	putative inner membrane protein	**0.33**	0.45861
STM0840	ybiV(2)	putative hydrolase	**-0.56**	0.35824
STM0840	ybiV(2)	putative hydrolase	**-0.26**	0.72092
STM0841	ybiU	putative cytoplasmic protein	**-0.23**	0.60552
STM0841	ybiU	putative cytoplasmic protein	**0.18**	0.66743
STM0842	ybiV(1)	putative hydrolase	**0.17**	0.75017
STM0842	ybiV(1)	putative hydrolase	**0.56**	0.28991
STM0843	pflF	putative pyruvate formate lyase	**0.04**	0.95107
STM0843	pflF	putative pyruvate formate lyase	**0.93**	0.11690
STM0844	pflE	putative pyruvate formate lyase activating enzyme	**-1.05**	0.17074
STM0844	pflE	putative pyruvate formate lyase activating enzyme	**-0.02**	0.98332
STM0845	moeB	molybdopterin biosynthesis protein MoeB	**0.11**	0.84436
STM0845	moeB	molybdopterin biosynthesis protein MoeB	**0.53**	0.40891
STM0846	moeA	molybdopterin biosynthesis protein	**-0.16**	0.70229
STM0846	moeA	molybdopterin biosynthesis protein	**0.20**	0.68474
STM0847	ybiK	putative asparaginase	**-0.41**	0.54424
STM0847	ybiK	putative asparaginase	**-0.09**	0.87135
STM0848	yliA	putative ABC transporter ATPase components	**0.08**	0.85513
STM0848	yliA	putative ABC transporter ATPase components	**0.45**	0.31242
STM0849	yliB	putative ABC transporter periplasmic binding protein	**-0.24**	0.66677
STM0849	yliB	putative ABC transporter periplasmic binding protein	**-0.01**	0.99182
STM0850	yliC	putative ABC transporter periplasmic binding protein	**-0.12**	0.76970
STM0850	yliC	putative ABC transporter periplasmic binding protein	**0.11**	0.83443
STM0851	yliD	putative ABC transporter inner membrane component	**-0.35**	0.40562
STM0851	yliD	putative ABC transporter inner membrane component	**-0.18**	0.65012
STM0852	yliG	putative FeS oxidoreductase	**-0.88**	0.13206
STM0852	yliG	putative FeS oxidoreductase	**-0.18**	0.67908
STM0853	yliH	putative cytoplasmic protein	**-0.02**	0.98135
STM0853	yliH	putative cytoplasmic protein	**0.15**	0.76989
STM0854	STM0854	putative cytoplasmic protein	**-0.47**	0.44998
STM0854	STM0854	putative cytoplasmic protein	**0.24**	0.75706
STM0855	STM0855	putative electron transfer protein beta subunit	**-0.46**	0.36017
STM0855	STM0855	putative electron transfer protein beta subunit	**0.35**	0.49496
STM0856	STM0856	putative electron transfer protein alpha subunit	**-0.30**	0.54162
STM0856	STM0856	putative electron transfer protein alpha subunit	**0.16**	0.82986
STM0857	STM0857	putative acyl-CoA dehydrogenase	**-0.07**	0.89445
STM0857	STM0857	putative acyl-CoA dehydrogenase	**0.41**	0.42721
STM0858	STM0858	putative dehydrogenase	**-0.64**	0.15331
STM0858	STM0858	putative dehydrogenase	**0.34**	0.55338
STM0859	STM0859	putative transcriptional regulator	**-0.04**	0.95546
STM0859	STM0859	putative transcriptional regulator	**0.22**	0.58155
STM0860	STM0860	putative inner membrane protein	**-0.26**	0.58117
STM0860	STM0860	putative inner membrane protein	**-0.17**	0.79708
STM0862	yliJ	putative glutathione S-transferase	**-0.46**	0.29912
STM0862	yliJ	putative glutathione S-transferase	**-0.63**	0.33983
STM0863	dacC	D-alanyl-D-alanine carboxypeptidase	**-0.19**	0.58300
STM0863	dacC	D-alanyl-D-alanine carboxypeptidase	**-0.48**	0.24520

STM0864	deoR	deoxyribose operon transcriptional repressor	**-0.32**	0.46199
STM0864	deoR	deoxyribose operon transcriptional repressor	**0.39**	0.43674
STM0865	ybjG	putative permease	**-0.71**	0.15859
STM0865	ybjG	putative permease	**-0.57**	0.20285
STM0866	mdfA	multidrug translocase	**-0.12**	0.86947
STM0866	mdfA	multidrug translocase	**0.63**	0.26856
STM0867	STM0867	putative hydrolase	**-0.25**	0.64727
STM0867	STM0867	putative hydrolase	**-0.35**	0.46927
STM0868	STM0868	putative transport protein/regulator	**0.33**	0.55355
STM0868	STM0868	putative transport protein/regulator	**0.77**	0.19425
STM0869	STM0869	putative regulatory protein	**-0.72**	0.13206
STM0869	STM0869	putative regulatory protein	**0.09**	0.85149
STM0870	STM0870	hypothetical protein STM0870	**-0.25**	0.52208
STM0870	STM0870	hypothetical protein STM0870	**0.32**	0.49336
STM0871	ybjM	putative inner membrane protein	**0.18**	0.64730
STM0871	ybjM	putative inner membrane protein	**0.22**	0.61643
STM0872	grxA	glutaredoxin 1	**-0.08**	0.86718
STM0872	grxA	glutaredoxin 1	**0.28**	0.51863
STM0873	ybjC	putative inner membrane protein	**-0.33**	0.40096
STM0873	ybjC	putative inner membrane protein	**0.11**	0.77346
STM0874	mdaA	oxygen-insensitive NADPH nitroreductase	**-0.35**	0.41153
STM0874	mdaA	oxygen-insensitive NADPH nitroreductase	**-0.05**	0.94087
STM0875	rimK	ribosomal protein S6 modification protein	**-0.05**	0.92262
STM0875	rimK	ribosomal protein S6 modification protein	**-0.19**	0.71783
STM0876	ybjN	putative cytoplasmic protein	**-0.72**	0.22521
STM0876	ybjN	putative cytoplasmic protein	**-0.26**	0.48563
STM0877	potF	putrescine transporter	**0.34**	0.37836
STM0877	potF	putrescine transporter	**0.36**	0.49009
STM0878	potG	putrescine transporter	**-0.34**	0.82637
STM0878	potG	putrescine transporter	**1.27**	0.17595
STM0879	potH	putrescine transporter	**0.06**	0.96775
STM0879	potH	putrescine transporter	**0.50**	0.76622
STM0880	potI	putrescine transporter	**-0.50**	0.34449
STM0880	potI	putrescine transporter	**0.06**	0.89004
STM0881	ybjO	putative inner membrane protein	**-0.14**	0.81946
STM0881	ybjO	putative inner membrane protein	**0.21**	0.65730
STM0882	ybjF	23S rRNA (uracil-5-)-methyltransferase	**0.01**	0.99295
STM0882	ybjF	23S rRNA (uracil-5-)-methyltransferase	**0.31**	0.48600
STM0884	ulaA	ascorbate-specific PTS system enzyme IIC	**-0.31**	0.43219
STM0884	ulaA	ascorbate-specific PTS system enzyme IIC	**0.50**	0.61285
STM0885	STM0885	putative inner membrane protein	**-0.26**	0.72700
STM0885	STM0885	putative inner membrane protein	**0.03**	0.96896
STM0886	STM0886	putative sulfatase	**0.10**	0.85513
STM0886	STM0886	putative sulfatase	**-0.17**	0.74626
STM0887	artJ	arginine transport system component	**-0.15**	0.83045
STM0887	artJ	arginine transport system component	**0.21**	0.69797
STM0888	artM	arginine transport system component	**-0.08**	0.86208
STM0888	artM	arginine transport system component	**0.05**	0.91919
STM0889	artQ	arginine transport system component	**0.17**	0.68094
STM0889	artQ	arginine transport system component	**0.21**	0.60174
STM0890	artI	arginine transport system	**0.11**	0.78992
STM0890	artI	arginine transport system	**0.07**	0.87304
STM0891	artP	arginine transport system	**-0.26**	0.53497
STM0891	artP	arginine transport system	**0.45**	0.26910
STM0892	ybjP	putative lipoprotein	**-0.14**	0.81437
STM0892	ybjP	putative lipoprotein	**0.28**	0.53399
STM0893	STM0893	putative integrase	**0.02**	0.97720
STM0893	STM0893	putative integrase	**0.05**	0.90071
STM0898	STM0898	putative transcriptional regulator	**-0.32**	0.45973
STM0898	STM0898	putative transcriptional regulator	**0.17**	0.66175
STM0906	STM0906	hypothetical protein STM0906 [Phage Fels-1]	**-0.38**	0.51003
STM0906	STM0906	hypothetical protein STM0906 [Phage Fels-1]	**-0.32**	0.46629
STM0907	STM0907	putative chitinase [Phage Fels-1]	**-0.77**	0.31146

STM0907	STM0907	putative chitinase [Phage Fels-1]	**0.00**	0.99540
STM0908	STM0908	hypothetical protein STM0908 [Phage Fels-1]	**-0.17**	0.89742
STM0908	STM0908	hypothetical protein STM0908 [Phage Fels-1]	**-0.06**	0.87999
STM0930	orfB	hypothetical protein STM0930	**-0.43**	0.32481
STM0930	orfB	hypothetical protein STM0930	**0.24**	0.55397
STM0931	ybjR	putative aminidase	**-0.26**	0.73542
STM0931	ybjR	putative aminidase	**0.11**	0.79592
STM0932	STM0932	putative nucleoside-diphosphate-sugar epimerase	**-0.29**	0.49336
STM0932	STM0932	putative nucleoside-diphosphate-sugar epimerase	**0.08**	0.87456
STM0933	ybjT	putative nucleoside-diphosphate-sugar epimerase	**-0.11**	0.82367
STM0933	ybjT	putative nucleoside-diphosphate-sugar epimerase	**0.97**	0.21062
STM0934	ltaA	L-allo-threonine aldolase	**-0.03**	0.96001
STM0934	ltaA	L-allo-threonine aldolase	**0.39**	0.41715
STM0935	poxB	pyruvate dehydrogenase	**-0.20**	0.78844
STM0935	poxB	pyruvate dehydrogenase	**0.07**	0.87512
STM0936	hcr	NADH oxidoreductase	**-0.13**	0.75376
STM0936	hcr	NADH oxidoreductase	**0.48**	0.43672
STM0937	hcp	hydroxylamine reductase	**-0.23**	0.65025
STM0937	hcp	hydroxylamine reductase	**0.09**	0.87790
STM0938	ybjE	putative inner membrane protein	**-0.53**	0.37241
STM0938	ybjE	putative inner membrane protein	**-0.40**	0.51300
STM0939	ybjD	hypothetical protein STM0939	**-2.36**	0.00231
STM0939	ybjD	hypothetical protein STM0939	**-2.34**	0.00220
STM0940	ybjX	VirK-like protein	**-3.86**	0.00220
STM0940	ybjX	VirK-like protein	**-3.50**	0.00184
STM0941	ybjY	hypothetical protein STM0941	**-0.89**	0.08384
STM0941	ybjY	hypothetical protein STM0941	**-0.43**	0.32295
STM0942	ybjZ	putative transport protein	**-0.32**	0.51182
STM0942	ybjZ	putative transport protein	**0.21**	0.63493
STM0943	cspD	stress response protein	**-0.57**	0.27004
STM0943	cspD	stress response protein	**0.44**	0.46469
STM0944	clpS	ATP-dependent Clp protease adaptor protein ClpS	**-0.13**	0.74779
STM0944	clpS	ATP-dependent Clp protease adaptor protein ClpS	**0.67**	0.26820
STM0945	clpA	ATP-binding subunit of serine protease	**-0.46**	0.30956
STM0945	clpA	ATP-binding subunit of serine protease	**0.13**	0.78657
STM0947	STM0947	putative integrase	**-0.19**	0.80335
STM0947	STM0947	putative integrase	**0.00**	0.99540
STM0948	STM0948	putative cytoplasmic protein	**-0.81**	0.19909
STM0948	STM0948	putative cytoplasmic protein	**0.85**	0.19874
STM0950	STM0950	SlsA	**0.05**	0.94617
STM0950	STM0950	SlsA	**0.36**	0.36243
STM0951	STM0951	putative cytoplasmic protein	**-0.36**	0.54341
STM0951	STM0951	putative cytoplasmic protein	**-0.17**	0.72554
STM0952	STM0952	putative transcriptional regulator	**-0.19**	0.69805
STM0952	STM0952	putative transcriptional regulator	**0.00**	0.99449
STM0953	infA	translation initiation factor IF-1	**-0.06**	0.91170
STM0953	infA	translation initiation factor IF-1	**0.20**	0.67788
STM0955	aat	leucyl/phenylalanyl-tRNA--protein transferase	**-0.14**	0.71937
STM0955	aat	leucyl/phenylalanyl-tRNA--protein transferase	**0.01**	0.99184
STM0956	cydC	cytochrome-related transporter	**-0.08**	0.86947
STM0956	cydC	cytochrome-related transporter	**0.14**	0.70629
STM0957	cydD	cytochrome-related transporter	**0.06**	0.87126
STM0957	cydD	cytochrome-related transporter	**-0.03**	0.96568
STM0958	trxB	thioredoxin reductase	**-0.88**	0.17139
STM0958	trxB	thioredoxin reductase	**-0.58**	0.30605
STM0959	lrp	leucine-responsive regulatory protein	**-0.12**	0.79185
STM0959	lrp	leucine-responsive regulatory protein	**0.79**	0.15859
STM0960	ftsK	cell division protein	**0.52**	0.19909
STM0960	ftsK	cell division protein	**0.50**	0.37154
STM0961	lolA	outer-membrane lipoprotein carrier protein precursor	**-0.11**	0.79761
STM0961	lolA	outer-membrane lipoprotein carrier protein precursor	**0.18**	0.62552
STM0962	ycaJ	hypothetical protein STM0962	**-0.08**	0.84120
STM0962	ycaJ	hypothetical protein STM0962	**0.39**	0.32481

STM0963	serS	seryl-tRNA synthetase	**-0.08**	0.82637
STM0963	serS	seryl-tRNA synthetase	**0.00**	0.99856
STM0964	dmsA	anaerobic dimethyl sulfoxide reductase subunit A	**0.01**	0.99726
STM0964	dmsA	anaerobic dimethyl sulfoxide reductase subunit A	**0.28**	0.72143
STM0965	dmsB	anaerobic dimethyl sulfoxide reductase subunit B	**-0.09**	0.95574
STM0965	dmsB	anaerobic dimethyl sulfoxide reductase subunit B	**0.06**	0.91378
STM0966	dmsC	anaerobic dimethyl sulfoxide reductase subunit C	**0.13**	0.78176
STM0966	dmsC	anaerobic dimethyl sulfoxide reductase subunit C	**0.55**	0.39025
STM0968	ycaD	putative MFS family transporter protein	**0.05**	0.94004
STM0968	ycaD	putative MFS family transporter protein	**0.36**	0.36311
STM0969	ycaM	putative amino-acid transporter	**-0.58**	0.23398
STM0969	ycaM	putative amino-acid transporter	**-0.37**	0.63482
STM0970	pflA	pyruvate formate lyase-activating enzyme 1	**-1.06**	0.08580
STM0970	pflA	pyruvate formate lyase-activating enzyme 1	**-0.42**	0.27005
STM0972	STM0972	SopD-like protein	**-0.13**	0.75739
STM0972	STM0972	SopD-like protein	**-0.17**	0.63006
STM0973	pflB	pyruvate formate lyase I	**-0.02**	0.96595
STM0973	pflB	pyruvate formate lyase I	**-0.17**	0.77639
STM0974	focA	putative formate transporter	**-0.13**	0.74455
STM0974	focA	putative formate transporter	**0.06**	0.89388
STM0975	ycaO	putative cytoplasmic protein	**-0.31**	0.36414
STM0975	ycaO	putative cytoplasmic protein	**0.15**	0.69634
STM0976	ycaP	putative inner membrane protein	**-0.23**	0.56618
STM0976	ycaP	putative inner membrane protein	**-2.00**	0.53263
STM0977	serC	phosphoserine aminotransferase	**0.13**	0.77637
STM0977	serC	phosphoserine aminotransferase	**0.23**	0.62209
STM0978	aroA	3-phosphoshikimate 1-carboxyvinyltransferase	**0.10**	0.81744
STM0978	aroA	3-phosphoshikimate 1-carboxyvinyltransferase	**0.21**	0.59423
STM0979	ycaL	putative Zn-dependent protease	**-0.03**	0.96595
STM0979	ycaL	putative Zn-dependent protease	**0.24**	0.58254
STM0980	cmk	cytidylate kinase	**-0.04**	0.93381
STM0980	cmk	cytidylate kinase	**0.13**	0.77186
STM0981	rpsA	30S ribosomal protein S1	**-0.06**	0.87917
STM0981	rpsA	30S ribosomal protein S1	**-0.01**	0.99512
STM0982	himD	integration host factor beta subunit	**-0.11**	0.76674
STM0982	himD	integration host factor beta subunit	**-0.24**	0.53722
STM0983	ycaI	putative recombination protein	**-0.01**	0.98546
STM0983	ycaI	putative recombination protein	**-0.02**	0.96785
STM0984	msbA	transport protein	**-0.17**	0.65474
STM0984	msbA	transport protein	**0.42**	0.30019
STM0985	lpxK	tetraacyldisaccharide 4'-kinase	**-0.31**	0.52804
STM0985	lpxK	tetraacyldisaccharide 4'-kinase	**0.02**	0.97273
STM0986	ycaQ	putative cytoplasmic protein	**-0.09**	0.88937
STM0986	ycaQ	putative cytoplasmic protein	**-0.15**	0.71417
STM0987	ycaR	putative inner membrane protein	**0.04**	0.92506
STM0987	ycaR	putative inner membrane protein	**0.16**	0.70077
STM0988	kdsB	3-deoxy-manno-octulosonate cytidylyltransferase	**-0.04**	0.94990
STM0988	kdsB	3-deoxy-manno-octulosonate cytidylyltransferase	**-0.09**	0.83223
STM0989	STM0989	hypothetical protein STM0989	**0.01**	0.98640
STM0989	STM0989	hypothetical protein STM0989	**-0.68**	0.65814
STM0990	ycbC	putative KicA-like protein	**-0.42**	0.34574
STM0990	ycbC	putative KicA-like protein	**0.51**	0.46026
STM0991	smtA	S-adenosylmethionine-dependent methyltransferase	**-0.23**	0.55892
STM0991	smtA	S-adenosylmethionine-dependent methyltransferase	**0.55**	0.22421
STM0992	mukF	condesin subunit F	**-0.10**	0.80754
STM0992	mukF	condesin subunit F	**0.24**	0.56860
STM0993	mukE	condesin subunit E	**-0.28**	0.46629
STM0993	mukE	condesin subunit E	**0.22**	0.53840
STM0994	mukB	condesin subunit B	**-0.07**	0.85592
STM0994	mukB	condesin subunit B	**0.05**	0.93506
STM0995	ycbB	putative periplasmic protein	**-0.03**	0.94050
STM0995	ycbB	putative periplasmic protein	**0.38**	0.36017
STM0996	ycbK	putative outer membrane protein	**-0.24**	0.49035

STM0996	ycbK	putative outer membrane protein	**-0.05**	0.91047
STM0997	ycbL	putative metallo-beta-lactamase	**-0.41**	0.32549
STM0997	ycbL	putative metallo-beta-lactamase	**-0.14**	0.72330
STM0998	aspC	aspartate aminotransferase	**-0.19**	0.63514
STM0998	aspC	aspartate aminotransferase	**-0.03**	0.96739
STM0999	ompF	outer membrane protein F precursor	**0.07**	0.88548
STM0999	ompF	outer membrane protein F precursor	**0.47**	0.32187
STM1000	asnS	asparaginyl-tRNA synthetase	**-0.18**	0.62860
STM1000	asnS	asparaginyl-tRNA synthetase	**-0.04**	0.94060
STM1001	STM1001	putative leucine response regulator	**-0.16**	0.68240
STM1001	STM1001	putative leucine response regulator	**-0.15**	0.72040
STM1002	STM1002	diaminopropionate ammonia-lyase	**-0.29**	0.43848
STM1002	STM1002	diaminopropionate ammonia-lyase	**-0.42**	0.51973
STM1003	STM1003	putative transcriptional regulator	**-0.34**	0.42761
STM1003	STM1003	putative transcriptional regulator	**-0.02**	0.97837
STM1004	pncB	nicotinate phosphoribosyltransferase	**-0.13**	0.81667
STM1004	pncB	nicotinate phosphoribosyltransferase	**-0.02**	0.96851
STM1005	STM1005	integrase	**-0.35**	0.52364
STM1005	STM1005	integrase	**-0.05**	0.92418
STM1006	STM1006	excisionase	**-0.59**	0.32984
STM1006	STM1006	excisionase	**0.24**	0.48126
STM1008,S	STM1008,S	hypothetical protein STM1008,S	**-0.42**	0.36311
STM1008,S	STM1008,S	hypothetical protein STM1008,S	**-0.51**	0.80335
STM1008,S	STM1008,S	hypothetical protein STM1008,S	**0.28**	0.45425
STM1008,S	STM1008,S	hypothetical protein STM1008,S	**0.65**	0.42243
STM1010,1n	STM1010,1n	hypothetical protein STM1010,1n	**-0.64**	0.31059
STM1010,1n	STM1010,1n	hypothetical protein STM1010,1n	**0.45**	0.33167
STM1020	STM1020	hypothetical protein STM1020 [Phage Gifsy-2]	**-0.23**	0.79081
STM1020	STM1020	hypothetical protein STM1020 [Phage Gifsy-2]	**0.46**	0.40227
STM1020	STM1020	hypothetical protein STM1020 [Phage Gifsy-2]	**-0.15**	0.69398
STM1020	STM1020	hypothetical protein STM1020 [Phage Gifsy-2]	**0.76**	0.39571
STM1021	STM1021	hypothetical protein STM1021 [Phage Gifsy-2]	**-0.15**	0.80395
STM1021	STM1021	hypothetical protein STM1021 [Phage Gifsy-2]	**0.43**	0.32016
STM1022	STM1022	putative molecular chaperone [Phage Gifsy-2]	**-0.66**	0.18622
STM1022	STM1022	putative molecular chaperone [Phage Gifsy-2]	**0.14**	0.89336
STM1028	STM1028	lysozyme [Phage Gifsy-2]	**-0.59**	0.17211
STM1028	STM1028	lysozyme [Phage Gifsy-2]	**0.31**	0.62917
STM1029	STM1029	hypothetical protein STM1029 [Phage Gifsy-2]	**0.20**	0.65451
STM1029	STM1029	hypothetical protein STM1029 [Phage Gifsy-2]	**1.20**	0.11913
STM1030	STM1030	hypothetical protein STM1030 [Phage Gifsy-2]	**-0.31**	0.54925
STM1030	STM1030	hypothetical protein STM1030 [Phage Gifsy-2]	**0.37**	0.41391
STM1031	STM1031	hypothetical protein STM1031 [Phage Gifsy-2]	**-0.47**	0.39721
STM1031	STM1031	hypothetical protein STM1031 [Phage Gifsy-2]	**1.09**	0.47270
STM1032	STM1032	hypothetical protein STM1032 [Phage Gifsy-2]	**-0.13**	0.94474
STM1032	STM1032	hypothetical protein STM1032 [Phage Gifsy-2]	**1.52**	0.38641
STM1033	STM1033	Clp protease-like protein [Phage Gifsy-2]	**-0.65**	0.39552
STM1033	STM1033	Clp protease-like protein [Phage Gifsy-2]	**-0.24**	0.63118
STM1034	STM1034	putative RecA/RadA recombinase [Phage Gifsy-2]	**-0.72**	0.27621
STM1034	STM1034	putative RecA/RadA recombinase [Phage Gifsy-2]	**0.21**	0.60499
STM1035	STM1035	ATP-binding sugar transporter-like protein [Phage Gifsy-2]	**-0.54**	0.23114
STM1035	STM1035	ATP-binding sugar transporter-like protein [Phage Gifsy-2]	**-0.27**	0.65383
STM1036	STM1036	probable minor tail protein [Phage Gifsy-2]	**-0.06**	0.89979
STM1036	STM1036	probable minor tail protein [Phage Gifsy-2]	**-0.33**	0.63148
STM1037	STM1037	probable minor tail protein [Phage Gifsy-2]	**0.00**	0.99822
STM1037	STM1037	probable minor tail protein [Phage Gifsy-2]	**1.02**	0.21855
STM1038	STM1038	probable major tail protein [Phage Gifsy-2]	**0.60**	0.65526
STM1038	STM1038	probable major tail protein [Phage Gifsy-2]	**1.13**	0.30019
STM1039	STM1039	probable minor tail protein [Phage Gifsy-2]	**-0.86**	0.25785
STM1039	STM1039	probable minor tail protein [Phage Gifsy-2]	**-0.40**	0.65196
STM1040	STM1040	probable minor tail protein [Phage Gifsy-2]	**-0.35**	0.55482
STM1040	STM1040	probable minor tail protein [Phage Gifsy-2]	**0.35**	0.47838

STM1041	STM1041	probable minor tail protein [Phage Gifsy-2]	**0.21**	0.88541
STM1041	STM1041	probable minor tail protein [Phage Gifsy-2]	**0.34**	0.61183
STM1042	STM1042	probable minor tail protein [Phage Gifsy-2]	**-0.41**	0.46629
STM1042	STM1042	probable minor tail protein [Phage Gifsy-2]	**-0.20**	0.74087
STM1043	STM1043	attachment/invasion protein [Phage Gifsy-2]	**-0.47**	0.38200
STM1043	STM1043	attachment/invasion protein [Phage Gifsy-2]	**0.30**	0.46199
STM1044	sodC	superoxide dismutase precursor	**-0.65**	0.20432
STM1044	sodC	superoxide dismutase precursor	**0.06**	0.91484
STM1045	STM1045	probable minor tail protein [Phage Gifsy-2]	**0.45**	0.60240
STM1045	STM1045	probable minor tail protein [Phage Gifsy-2]	**1.37**	0.19967
STM1046	STM1046	probable tail assembly protein [Phage Gifsy-2]	**-0.63**	0.21360
STM1046	STM1046	probable tail assembly protein [Phage Gifsy-2]	**-0.03**	0.96785
STM1047	STM1047	probable tail assembly protein [Phage Gifsy-2]	**0.33**	0.52334
STM1047	STM1047	probable tail assembly protein [Phage Gifsy-2]	**1.54**	0.17144
STM1048	STM1048	host specificity protein J [Phage Gifsy-2]	**0.21**	0.69776
STM1048	STM1048	host specificity protein J [Phage Gifsy-2]	**0.83**	0.48814
STM1049	STM1049	probable tail fiber protein [Phage Gifsy-2]	**-0.29**	0.59052
STM1049	STM1049	probable tail fiber protein [Phage Gifsy-2]	**0.54**	0.20916
STM1050	STM1050	tail fiber assembly like-protein [Phage Gifsy-2]	**-0.42**	0.38103
STM1050	STM1050	tail fiber assembly like-protein [Phage Gifsy-2]	**-0.09**	0.93362
STM1051	sseI	secreted effector protein [Phage Gifsy-2]	**0.09**	0.94421
STM1051	sseI	secreted effector protein [Phage Gifsy-2]	**0.55**	0.32016
STM1053	STM1053	hypothetical protein STM1053	**-0.06**	0.89529
STM1053	STM1053	hypothetical protein STM1053	**1.06**	0.23879
STM1055	STM1055	hypothetical protein STM1055	**0.22**	0.61833
STM1055	STM1055	hypothetical protein STM1055	**0.50**	0.23958
STM1056	STM1056	MsgA-like protein	**-0.83**	0.21318
STM1056	STM1056	MsgA-like protein	**-0.26**	0.68978
STM1057	pepN	aminopeptidase N	**0.09**	0.86385
STM1057	pepN	aminopeptidase N	**0.33**	0.60844
STM1058	pyrD	dihydroorotate dehydrogenase	**-0.06**	0.90277
STM1058	pyrD	dihydroorotate dehydrogenase	**0.20**	0.61732
STM1059	ycbW	putative cytoplasmic protein	**-0.43**	0.32812
STM1059	ycbW	putative cytoplasmic protein	**0.04**	0.96968
STM1060	STM1060	putative iron-sulfur protein	**-0.44**	0.35245
STM1060	STM1060	putative iron-sulfur protein	**0.31**	0.54747
STM1061	ycbY	putative N6-adenine-specific DNA methylase	**0.02**	0.97580
STM1061	ycbY	putative N6-adenine-specific DNA methylase	**0.19**	0.71104
STM1062	uup	putative ABC transporter ATPase component	**-0.28**	0.46266
STM1062	uup	putative ABC transporter ATPase component	**0.34**	0.42591
STM1063	pqiA	paraquat-inducible protein A	**-0.18**	0.68545
STM1063	pqiA	paraquat-inducible protein A	**0.13**	0.76571
STM1064	pqiB	paraquat-inducible protein B	**-0.36**	0.35816
STM1064	pqiB	paraquat-inducible protein B	**0.17**	0.75338
STM1065	ymbA	putative outer membrane protein	**-0.49**	0.25125
STM1065	ymbA	putative outer membrane protein	**-0.19**	0.72951
STM1067	fabA	3-hydroxydecanoyl-ACP dehydratase	**-0.03**	0.95497
STM1067	fabA	3-hydroxydecanoyl-ACP dehydratase	**0.27**	0.47366
STM1068	lonH	putative protease	**-0.07**	0.89004
STM1068	lonH	putative protease	**0.08**	0.87999
STM1069	ycbG	hypothetical protein STM1069	**-0.62**	0.17611
STM1069	ycbG	hypothetical protein STM1069	**-0.17**	0.71931
STM1070	ompA	putative hydrogenase membrane component precurosr	**-0.19**	0.68830
STM1070	ompA	putative hydrogenase membrane component precurosr	**-0.13**	0.73129
STM1070	ompA	putative hydrogenase membrane component precurosr	**0.07**	0.86580
STM1070	ompA	putative hydrogenase membrane component precurosr	**-0.13**	0.72805
STM1070	ompA	putative hydrogenase membrane component precurosr	**-0.15**	0.68599
STM1070	ompA	putative hydrogenase membrane component precurosr	**0.03**	0.94472
STM1070	ompA	putative hydrogenase membrane component precurosr	**-0.05**	0.91047
STM1070	ompA	putative hydrogenase membrane component precurosr	**-0.10**	0.81667
STM1070	ompA	putative hydrogenase membrane component precurosr	**-0.13**	0.74820
STM1070	ompA	putative hydrogenase membrane component precurosr	**0.02**	0.96797
STM1070	ompA	putative hydrogenase membrane component precurosr	**0.03**	0.94360

STM1070	ompA	putative hydrogenase membrane component precurosr	**0.70**	0.61843
STM1070	ompA	putative hydrogenase membrane component precurosr	**-0.07**	0.84956
STM1070	ompA	putative hydrogenase membrane component precurosr	**0.03**	0.94143
STM1070	ompA	putative hydrogenase membrane component precurosr	**-0.16**	0.68444
STM1070	ompA	putative hydrogenase membrane component precurosr	**-0.16**	0.65383
STM1070	ompA	putative hydrogenase membrane component precurosr	**-0.15**	0.72120
STM1070	ompA	putative hydrogenase membrane component precurosr	**0.10**	0.85887
STM1070	ompA	putative hydrogenase membrane component precurosr	**0.05**	0.93767
STM1070	ompA	putative hydrogenase membrane component precurosr	**0.12**	0.82117
STM1070	ompA	putative hydrogenase membrane component precurosr	**-0.08**	0.85626
STM1070	ompA	putative hydrogenase membrane component precurosr	**-0.06**	0.88934
STM1070	ompA	putative hydrogenase membrane component precurosr	**0.26**	0.57827
STM1070	ompA	putative hydrogenase membrane component precurosr	**0.09**	0.85053
STM1070	ompA	putative hydrogenase membrane component precurosr	**0.00**	0.99800
STM1070	ompA	putative hydrogenase membrane component precurosr	**0.15**	0.67264
STM1070	ompA	putative hydrogenase membrane component precurosr	**0.40**	0.38260
STM1070	ompA	putative hydrogenase membrane component precurosr	**0.06**	0.89624
STM1070	ompA	putative hydrogenase membrane component precurosr	**0.07**	0.86861
STM1070	ompA	putative hydrogenase membrane component precurosr	**0.08**	0.84456
STM1070	ompA	putative hydrogenase membrane component precurosr	**0.20**	0.71661
STM1070	ompA	putative hydrogenase membrane component precurosr	**0.03**	0.95747
STM1070	ompA	putative hydrogenase membrane component precurosr	**-0.12**	0.77427
STM1070	ompA	putative hydrogenase membrane component precurosr	**0.22**	0.54624
STM1071	sulA	cell division inhibitor	**-0.05**	0.91170
STM1071	sulA	cell division inhibitor	**0.18**	0.67662
STM1074	yccF	putative inner membrane protein	**-0.24**	0.54996
STM1074	yccF	putative inner membrane protein	**0.22**	0.67137
STM1075	helD	DNA helicase IV	**-0.23**	0.82571
STM1075	helD	DNA helicase IV	**0.23**	0.65301
STM1076	mgsA	methylglyoxal synthase	**-0.07**	0.90534
STM1076	mgsA	methylglyoxal synthase	**0.25**	0.62134
STM1077	yccT	hypothetical protein STM1077	**-0.59**	0.17611
STM1077	yccT	hypothetical protein STM1077	**0.26**	0.67892
STM1078	STM1078	putative cytoplasmic protein	**-0.87**	0.12854
STM1078	STM1078	putative cytoplasmic protein	**-0.33**	0.38236
STM1079	yccV	putative inner membrane protein	**-0.42**	0.30233
STM1079	yccV	putative inner membrane protein	**-0.02**	0.98094
STM1080	yccW	putative SAM-dependent methyltransferase	**-0.05**	0.89625
STM1080	yccW	putative SAM-dependent methyltransferase	**0.01**	0.98094
STM1081	STM1081	putative outer membrane protein	**-0.10**	0.86828
STM1081	STM1081	putative outer membrane protein	**0.49**	0.34241
STM1082	STM1082	bacterial regulatory protein	**-0.20**	0.71978
STM1082	STM1082	bacterial regulatory protein	**0.48**	0.42497
STM1083	yccX	putative phosphohydrolase	**-0.78**	0.13813
STM1083	yccX	putative phosphohydrolase	**-0.44**	0.51973
STM1084	yccK	putative sulfite reductase gamma subunit	**-0.44**	0.34812
STM1084	yccK	putative sulfite reductase gamma subunit	**0.62**	0.37154
STM1085	yccA	putative transport protein	**0.11**	0.78257
STM1085	yccA	putative transport protein	**0.18**	0.65916
STM1086	serT	STM1086	**-0.33**	0.68642
STM1086	serT	STM1086	**-0.05**	0.96386
STM1087	pipA	pathogenicity island-encoded protein A	**-0.39**	0.32760
STM1087	pipA	pathogenicity island-encoded protein A	**0.14**	0.71917
STM1088	pipB	secreted effector protein	**-0.64**	0.31482
STM1088	pipB	secreted effector protein	**0.52**	0.46892
STM1090	pipC	pathogenicity island-encoded protein C	**0.73**	0.17041
STM1090	pipC	pathogenicity island-encoded protein C	**1.33**	0.04872
STM1091	sopB	secreted effector protein	**0.27**	0.76172
STM1091	sopB	secreted effector protein	**1.27**	0.18157
STM1094	pipD	pathogenicity island-encoded protein D	**-0.23**	0.63901
STM1094	pipD	pathogenicity island-encoded protein D	**0.28**	0.65271
STM1095	copS	copper resistance protein	**0.08**	0.90423
STM1095	copS	copper resistance protein	**0.40**	0.42277

STM1096	copR	copper resistance protein	**-0.60**	0.15984
STM1096	copR	copper resistance protein	**0.48**	0.43219
STM1097	STM1097	hypothetical protein STM1097	**0.02**	0.98123
STM1097	STM1097	hypothetical protein STM1097	**0.19**	0.65113
STM1098	hpaC	4-hydroxyphenylacetate catabolism	**0.09**	0.88502
STM1098	hpaC	4-hydroxyphenylacetate catabolism	**0.23**	0.68439
STM1099	hpaB	4-hydroxyphenylacetate catabolism	**-0.24**	0.65012
STM1099	hpaB	4-hydroxyphenylacetate catabolism	**0.64**	0.38260
STM1100	hpaR	4-hydroxyphenylacetate catabolism	**-0.28**	0.48343
STM1100	hpaR	4-hydroxyphenylacetate catabolism	**0.86**	0.34449
STM1101	hpaG	4-hydroxyphenylacetate catabolism	**-0.45**	0.34184
STM1101	hpaG	4-hydroxyphenylacetate catabolism	**0.59**	0.34193
STM1102	hpaE	4-hydroxyphenylacetate catabolism	**-0.26**	0.76387
STM1102	hpaE	4-hydroxyphenylacetate catabolism	**-1.05**	0.45374
STM1103	hpaD	4-hydroxyphenylacetate catabolism	**-0.19**	0.85766
STM1103	hpaD	4-hydroxyphenylacetate catabolism	**0.58**	0.23613
STM1104	hpaF	4-hydroxyphenylacetate catabolism	**-0.33**	0.65849
STM1104	hpaF	4-hydroxyphenylacetate catabolism	**0.37**	0.63498
STM1105	hpaH	4-hydroxyphenylacetate catabolism	**0.11**	0.80652
STM1105	hpaH	4-hydroxyphenylacetate catabolism	**0.71**	0.40020
STM1106	hpaI	4-hydroxyphenylacetate catabolism	**0.03**	0.98124
STM1106	hpaI	4-hydroxyphenylacetate catabolism	**-0.02**	0.98140
STM1107	hpaX	4-hydroxyphenylacetate catabolism	**0.02**	0.97314
STM1107	hpaX	4-hydroxyphenylacetate catabolism	**0.42**	0.34449
STM1108	hpaA	4-hydroxyphenylacetate catabolism	**-0.05**	0.94174
STM1108	hpaA	4-hydroxyphenylacetate catabolism	**0.42**	0.55482
STM1109	STM1109	putative periplasmic protein	**-0.49**	0.26213
STM1109	STM1109	putative periplasmic protein	**1.37**	0.13645
STM1111	yccD	putative cytoplasmic protein	**-0.63**	0.19967
STM1111	yccD	putative cytoplasmic protein	**-0.09**	0.88862
STM1112	cbpA	DNA-binding protein	**-0.45**	0.22621
STM1112	cbpA	DNA-binding protein	**-0.26**	0.54566
STM1113	scsA	suppression of copper sensitivity protein A	**-0.23**	0.58927
STM1113	scsA	suppression of copper sensitivity protein A	**0.22**	0.75418
STM1114	scsB	suppression of copper sensitivity protein	**-0.17**	0.80012
STM1114	scsB	suppression of copper sensitivity protein	**0.11**	0.90193
STM1115	scsC	suppression of copper sensitivity protein	**-0.28**	0.64525
STM1115	scsC	suppression of copper sensitivity protein	**0.17**	0.75424
STM1116	scsD	suppression of copper sensitivity protein	**-0.31**	0.59325
STM1116	scsD	suppression of copper sensitivity protein	**-0.32**	0.53679
STM1117	agp	glucose-1-phosphatase	**-0.33**	0.58387
STM1117	agp	glucose-1-phosphatase	**0.06**	0.91270
STM1118	yccJ	putative cytoplasmic protein	**-0.40**	0.53006
STM1118	yccJ	putative cytoplasmic protein	**0.50**	0.38552
STM1119	wraB	TrpR binding protein WrbA	**0.23**	0.60034
STM1119	wraB	TrpR binding protein WrbA	**0.44**	0.60249
STM1121	ymdF	putative cytoplasmic protein	**-1.09**	0.11913
STM1121	ymdF	putative cytoplasmic protein	**-0.13**	0.79635
STM1122	ycdC	putative transcriptional repressor	**-0.24**	0.49865
STM1122	ycdC	putative transcriptional repressor	**-0.13**	0.77139
STM1123	STM1123	putative periplasmic protein	**0.87**	0.36942
STM1123	STM1123	putative periplasmic protein	**0.55**	0.70740
STM1125	putP	major sodium/proline symporter	**0.15**	0.76502
STM1125	putP	major sodium/proline symporter	**0.22**	0.57132
STM1127	STM1127	putative transcriptional regulator	**-0.56**	0.20256
STM1127	STM1127	putative transcriptional regulator	**0.27**	0.62433
STM1128	STM1128	putative sodium/glucose cotransporter	**-0.28**	0.58694
STM1128	STM1128	putative sodium/glucose cotransporter	**-0.18**	0.65145
STM1129	STM1129	putative inner membrane protein	**-0.05**	0.95476
STM1129	STM1129	putative inner membrane protein	**0.18**	0.79897
STM1130	STM1130	putative inner membrane protein	**-0.26**	0.79308
STM1130	STM1130	putative inner membrane protein	**0.37**	0.76562
STM1131	STM1131	putative outer membrane protein	**-0.38**	0.45082

STM1131	STM1131	putative outer membrane protein	**-0.15**	0.85893
STM1132	STM1132	putative sialic acid transporter	**-0.19**	0.63669
STM1132	STM1132	putative sialic acid transporter	**0.15**	0.79018
STM1133	STM1133	putative dehydrogenase	**-0.02**	0.97355
STM1133	STM1133	putative dehydrogenase	**-0.46**	0.37121
STM1134	serX	STM1134	**-0.37**	0.39896
STM1134	serX	STM1134	**-0.15**	0.78010
STM1134	serX	STM1134	**0.04**	0.94223
STM1134	serX	STM1134	**0.39**	0.48014
STM1135	ycdW	putative oxidoreductase	**-0.17**	0.70932
STM1135	ycdW	putative oxidoreductase	**-0.13**	0.80915
STM1136	ycdX	hypothetical protein STM1136	**-0.03**	0.95532
STM1136	ycdX	hypothetical protein STM1136	**0.08**	0.84187
STM1137	ycdY	putative oxidoreductase component	**-0.29**	0.48814
STM1137	ycdY	putative oxidoreductase component	**0.26**	0.47857
STM1138	ycdZ	putative inner membrane protein	**-0.15**	0.75002
STM1138	ycdZ	putative inner membrane protein	**0.35**	0.42277
STM1139	csgG	putative curli operon transcriptional regulator	**0.22**	0.57021
STM1139	csgG	putative curli operon transcriptional regulator	**0.80**	0.14168
STM1140	csgF	curli production assembly/transport component	**-0.27**	0.70686
STM1140	csgF	curli production assembly/transport component	**0.76**	0.14354
STM1141	csgE	curli production assembly/transport component	**-0.09**	0.87223
STM1141	csgE	curli production assembly/transport component	**0.10**	0.89611
STM1142	csgD	putative transcriptional regulator	**-0.41**	0.57021
STM1142	csgD	putative transcriptional regulator	**0.77**	0.23534
STM1143	csgB	minor curlin subunit precursor	**-0.52**	0.36635
STM1143	csgB	minor curlin subunit precursor	**0.22**	0.87512
STM1144	csgA	major curlin subunit precursor	**-0.80**	0.19398
STM1144	csgA	major curlin subunit precursor	**0.06**	0.91974
STM1145	csgC	putative curli production protein precursor	**0.05**	0.91170
STM1145	csgC	putative curli production protein precursor	**0.32**	0.56421
STM1146	ymdA	putative periplasmic protein	**0.35**	0.46112
STM1146	ymdA	putative periplasmic protein	**0.40**	0.47844
STM1147	STM1147	hypothetical protein STM1147	**0.18**	0.86639
STM1147	STM1147	hypothetical protein STM1147	**0.80**	0.43914
STM1148,S	ymdC	putative phospholipase	**0.27**	0.51952
STM1148,S	ymdC	putative phospholipase	**0.39**	0.39186
STM1149	mdoC	glucans biosynthesis protein	**0.00**	0.99394
STM1149	mdoC	glucans biosynthesis protein	**0.50**	0.22621
STM1150	mdoG	periplasmic glucans biosynthesis protein	**0.16**	0.79096
STM1150	mdoG	periplasmic glucans biosynthesis protein	**-0.06**	0.94426
STM1151	mdoH	glucosyltransferase MdoH	**-0.12**	0.76970
STM1151	mdoH	glucosyltransferase MdoH	**-0.20**	0.68444
STM1152	yceK	putative outer membrane lipoprotein	**-0.10**	0.83525
STM1152	yceK	putative outer membrane lipoprotein	**0.23**	0.56535
STM1153	msyB	acidic protein	**-1.19**	0.07353
STM1153	msyB	acidic protein	**-0.23**	0.76720
STM1154	yceE	putative transport protein	**-0.15**	0.72518
STM1154	yceE	putative transport protein	**0.48**	0.42591
STM1155	htrB	lipid A biosynthesis lauroyl acyltransferase	**0.03**	0.95932
STM1155	htrB	lipid A biosynthesis lauroyl acyltransferase	**-0.11**	0.81339
STM1156	yceA	hypothetical protein STM1156	**-0.02**	0.96774
STM1156	yceA	hypothetical protein STM1156	**0.35**	0.45739
STM1157	yceI	hypothetical protein STM1157	**-0.42**	0.31367
STM1157	yceI	hypothetical protein STM1157	**0.21**	0.61341
STM1158	STM1158	putative inner membrane protein	**-0.28**	0.47610
STM1158	STM1158	putative inner membrane protein	**0.63**	0.29796
STM1159	yceO	putative inner membrane protein	**-0.20**	0.60249
STM1159	yceO	putative inner membrane protein	**-0.26**	0.65526
STM1160	solA	putative sarcosine oxidase	**-0.08**	0.89468
STM1160	solA	putative sarcosine oxidase	**0.56**	0.35937
STM1161,S	yceP	putative cytoplasmic protein	**0.18**	0.82348
STM1161,S	yceP	putative cytoplasmic protein	**0.89**	0.26261

STM1162	dinI	DNA damage-inducible protein I	**-0.19**	0.70933
STM1162	dinI	DNA damage-inducible protein I	**0.31**	0.47656
STM1163	pyrC	dihydroorotase	**0.14**	0.76970
STM1163	pyrC	dihydroorotase	**0.26**	0.52101
STM1164	yceB	putative outer membrane lipoprotein	**-0.26**	0.70848
STM1164	yceB	putative outer membrane lipoprotein	**0.59**	0.38075
STM1165	grxB	glutaredoxin 2	**0.07**	0.90534
STM1165	grxB	glutaredoxin 2	**0.07**	0.88784
STM1166	yceL	putative transport protein	**0.45**	0.34812
STM1166	yceL	putative transport protein	**0.56**	0.30422
STM1167	rimJ	acetylatase	**0.40**	0.34201
STM1167	rimJ	acetylatase	**0.55**	0.19425
STM1168	yceH	putative cytoplasmic protein	**-0.39**	0.36636
STM1168	yceH	putative cytoplasmic protein	**0.17**	0.70691
STM1169	mviM	putative virulence protein	**0.33**	0.62403
STM1169	mviM	putative virulence protein	**0.92**	0.27696
STM1170	mviN	putative virulence protein	**0.09**	0.83305
STM1170	mviN	putative virulence protein	**0.08**	0.85893
STM1171	flgN	putative FlgK/FlgL export chaperone	**0.17**	0.66888
STM1171	flgN	putative FlgK/FlgL export chaperone	**0.09**	0.83304
STM1172	flgM	anti-FliA factor	**0.02**	0.97054
STM1172	flgM	anti-FliA factor	**0.13**	0.85152
STM1173	flgA	flagellar basal body P-ring biosynthesis protein	**0.20**	0.61234
STM1173	flgA	flagellar basal body P-ring biosynthesis protein	**0.18**	0.60750
STM1174	flgB	flagellar basal body rod protein	**0.01**	0.98124
STM1174	flgB	flagellar basal body rod protein	**0.34**	0.54235
STM1175	flgC	flagellar basal body rod protein	**-0.32**	0.52101
STM1175	flgC	flagellar basal body rod protein	**0.42**	0.35424
STM1176	flgD	flagellar basal body rod modification protein	**0.01**	0.98539
STM1176	flgD	flagellar basal body rod modification protein	**0.32**	0.58430
STM1177	flgE	flagellar hook protein	**0.00**	0.99484
STM1177	flgE	flagellar hook protein	**0.23**	0.56565
STM1178	flgF	cell-proximal portion of basal-body rod	**-0.26**	0.70933
STM1178	flgF	cell-proximal portion of basal-body rod	**0.14**	0.72819
STM1179	flgG	flagellar basal-body rod protein	**-0.29**	0.45943
STM1179	flgG	flagellar basal-body rod protein	**0.39**	0.42344
STM1180	flgH	flagellar L-ring protein precursor	**0.16**	0.79241
STM1180	flgH	flagellar L-ring protein precursor	**0.95**	0.13813
STM1181	flgI	flagellar P-ring protein precursor	**0.20**	0.60891
STM1181	flgI	flagellar P-ring protein precursor	**0.35**	0.42455
STM1182	flgJ	flagellar biosynthesis protein	**-0.10**	0.80574
STM1182	flgJ	flagellar biosynthesis protein	**0.55**	0.17603
STM1183	flgK	flagellar hook-associated protein	**0.15**	0.74995
STM1183	flgK	flagellar hook-associated protein	**0.32**	0.35325
STM1184	flgL	flagellar hook-associated protein	**-0.09**	0.85340
STM1184	flgL	flagellar hook-associated protein	**0.26**	0.54654
STM1185	rne	RNase E	**-0.41**	0.34051
STM1185	rne	RNase E	**0.35**	0.39577
STM1187	rluC	23S rRNA pseudouridylate synthase	**-0.02**	0.97168
STM1187	rluC	23S rRNA pseudouridylate synthase	**-0.14**	0.72286
STM1188	STM1188	putative inner membrane lipoprotein	**-0.09**	0.82696
STM1188	STM1188	putative inner membrane lipoprotein	**-0.13**	0.74979
STM1189	maf	Maf-like protein	**-0.30**	0.46266
STM1189	maf	Maf-like protein	**-0.04**	0.94045
STM1190	yceD	putative metal-binding protein	**-0.15**	0.69882
STM1190	yceD	putative metal-binding protein	**0.35**	0.43235
STM1192	plsX	fatty acid/phospholipid synthesis protein	**-0.09**	0.87223
STM1192	plsX	fatty acid/phospholipid synthesis protein	**0.05**	0.92584
STM1193	fabH	3-oxoacyl-(acyl carrier protein) synthase	**0.14**	0.76811
STM1193	fabH	3-oxoacyl-(acyl carrier protein) synthase	**0.15**	0.72247
STM1194	fabD	acyl carrier protein S-malonyltransferase	**-0.19**	0.74374
STM1194	fabD	acyl carrier protein S-malonyltransferase	**-0.18**	0.64525
STM1194	fabD	acyl carrier protein S-malonyltransferase	**-0.18**	0.79890

STM1194	fabD	acyl carrier protein S-malonyltransferase	**-0.05**	0.92120
STM1195	fabG	3-ketoacyl-(acyl-carrier-protein) reductase	**-0.04**	0.96001
STM1195	fabG	3-ketoacyl-(acyl-carrier-protein) reductase	**0.19**	0.61335
STM1196	acpP	acyl carrier protein	**0.13**	0.74127
STM1196	acpP	acyl carrier protein	**0.53**	0.24707
STM1197	fabF	3-oxoacyl-(acyl carrier protein) synthase	**-0.32**	0.53679
STM1197	fabF	3-oxoacyl-(acyl carrier protein) synthase	**-0.23**	0.72647
STM1198	pabC	4-amino-4-deoxychorismate lyase	**-0.21**	0.59088
STM1198	pabC	4-amino-4-deoxychorismate lyase	**0.08**	0.84854
STM1199	yceG	putative periplasmic solute-binding protein	**-0.28**	0.40749
STM1199	yceG	putative periplasmic solute-binding protein	**0.59**	0.22602
STM1200	tmk	thymidylate kinase	**-0.32**	0.43439
STM1200	tmk	thymidylate kinase	**-0.33**	0.37880
STM1201	holB	DNA polymerase III subunit delta	**-0.13**	0.75706
STM1201	holB	DNA polymerase III subunit delta	**-0.08**	0.83191
STM1202	ycfH	putative metal-dependent hydrolase	**-0.20**	0.64401
STM1202	ycfH	putative metal-dependent hydrolase	**0.16**	0.72143
STM1203	ptsG	glucose-specific IIBC component	**-0.06**	0.89566
STM1203	ptsG	glucose-specific IIBC component	**0.11**	0.80539
STM1204	fhuE	outer membrane receptor protein precursor	**0.14**	0.75403
STM1204	fhuE	outer membrane receptor protein precursor	**0.14**	0.74436
STM1205	ycfF	putative protein kinase C inhibitor	**0.41**	0.25845
STM1205	ycfF	putative protein kinase C inhibitor	**0.50**	0.23114
STM1206	ycfL	putative outer membrane lipoprotein	**-0.21**	0.63840
STM1206	ycfL	putative outer membrane lipoprotein	**0.05**	0.93420
STM1207	ycfM	putative outer membrane lipoprotein	**-0.47**	0.26971
STM1207	ycfM	putative outer membrane lipoprotein	**0.07**	0.87016
STM1208	ycfN	putative cytoplasmic protein	**-0.12**	0.79256
STM1208	ycfN	putative cytoplasmic protein	**0.04**	0.91937
STM1209	nagZ	beta-hexosaminidase	**-0.05**	0.93748
STM1209	nagZ	beta-hexosaminidase	**0.05**	0.92188
STM1210	ycfP	hypothetical protein STM1210	**-0.10**	0.82350
STM1210	ycfP	hypothetical protein STM1210	**-0.08**	0.85887
STM1211	ndh	respiratory NADH dehydrogenase 2	**0.01**	0.98958
STM1211	ndh	respiratory NADH dehydrogenase 2	**0.32**	0.38641
STM1212	ycfJ	putative outer membrane lipoprotein	**-0.17**	0.80672
STM1212	ycfJ	putative outer membrane lipoprotein	**0.01**	0.98640
STM1213	ycfQ	putative transcriptional repressor	**-0.40**	0.56790
STM1213	ycfQ	putative transcriptional repressor	**0.28**	0.62082
STM1214	ycfR	putative outer membrane protein	**-0.74**	0.19967
STM1214	ycfR	putative outer membrane protein	**-0.38**	0.49712
STM1215	ycfS	putative periplasmic protein	**-0.48**	0.28396
STM1215	ycfS	putative periplasmic protein	**0.01**	0.98958
STM1216	mfd	transcription-repair coupling factor	**-0.61**	0.27312
STM1216	mfd	transcription-repair coupling factor	**-0.10**	0.85174
STM1217,S	ycfU	integral membrane protein	**0.02**	0.97660
STM1217,S	ycfU	integral membrane protein	**0.09**	0.80406
STM1218	ycfV	ATP-binding protein	**-0.41**	0.34824
STM1218	ycfV	ATP-binding protein	**-0.03**	0.96018
STM1219	ycfW	integral membrane protein	**0.20**	0.60112
STM1219	ycfW	integral membrane protein	**-0.09**	0.88018
STM1220	ycfX	putative regulatory protein	**-0.32**	0.37011
STM1220	ycfX	putative regulatory protein	**0.16**	0.75739
STM1221	cobB	NAD-dependent deacetylase	**-0.01**	0.97720
STM1221	cobB	NAD-dependent deacetylase	**-0.02**	0.98266
STM1222	potD	spermidine/putrescine ABC transporter periplasmic substrate-binding	**-0.40**	0.38668
STM1222	potD	spermidine/putrescine ABC transporter periplasmic substrate-binding	**0.16**	0.84021
STM1223	potC	spermidine/putrescine ABC transporter membrane component	**-0.03**	0.95491
STM1223	potC	spermidine/putrescine ABC transporter membrane component	**0.18**	0.74374

STM1224	sifA	secreted effector protein	**-0.23**	0.67005
STM1224	sifA	secreted effector protein	**0.14**	0.74312
STM1225	potB	spermidine/putrescine ABC transporter membrane component	**0.02**	0.97168
STM1225	potB	spermidine/putrescine ABC transporter membrane component	**0.04**	0.93767
STM1226	potA	putrescine/spermidine ABC transporter ATPase	**0.01**	0.98280
STM1226	potA	putrescine/spermidine ABC transporter ATPase	**0.65**	0.15859
STM1227	pepT	peptidase T	**-0.14**	0.72518
STM1227	pepT	peptidase T	**0.58**	0.30525
STM1228	STM1228	putative periplasmic protein	**-0.50**	0.22540
STM1228	STM1228	putative periplasmic protein	**0.05**	0.93767
STM1229	ycfD	putative cytoplasmic protein	**-0.95**	0.14285
STM1229	ycfD	putative cytoplasmic protein	**-0.24**	0.49708
STM1230	phoQ	sensor kinase protein	**-1.56**	0.02425
STM1230	phoQ	sensor kinase protein	**-1.48**	0.02425
STM1231	phoP	response regulator	**-2.91**	0.00655
STM1231	phoP	response regulator	**-2.09**	0.01765
STM1232	purB	adenylosuccinate lyase	**-0.47**	0.34193
STM1232	purB	adenylosuccinate lyase	**-0.10**	0.86017
STM1233	ycfC	hypothetical protein STM1233	**0.05**	0.90990
STM1233	ycfC	hypothetical protein STM1233	**0.12**	0.76074
STM1234,S	trmU	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	**-0.17**	0.74481
STM1234,S	trmU	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	**-0.15**	0.70229
STM1235	ymfB	putative MutT-like protein	**-0.07**	0.86339
STM1235	ymfB	putative MutT-like protein	**-0.17**	0.72521
STM1236	STM1236	putative periplasmic protein	**-0.10**	0.82624
STM1236	STM1236	putative periplasmic protein	**0.09**	0.87727
STM1237	ymfC	putative ribosomal large subunit pseudouridine synthase	**0.08**	0.89621
STM1237	ymfC	putative ribosomal large subunit pseudouridine synthase	**0.79**	0.26261
STM1238	icdA	isocitrate dehydrogenase	**0.24**	0.66155
STM1238	icdA	isocitrate dehydrogenase	**0.53**	0.25565
STM1239	STM1239	putative cytoplasmic protein	**0.09**	0.88240
STM1239	STM1239	putative cytoplasmic protein	**0.26**	0.53827
STM1240	envF	putative envelope lipoprotein	**-0.99**	0.13645
STM1240	envF	putative envelope lipoprotein	**0.40**	0.61837
STM1241	msgA	macrophage survival protein	**-0.14**	0.72247
STM1241	msgA	macrophage survival protein	**0.16**	0.79676
STM1242	envE	putative envelope protein	**-0.41**	0.31249
STM1242	envE	putative envelope protein	**0.92**	0.08322
STM1246	pagC	virulence membrane protein PAGC precursor	**-0.09**	0.90057
STM1246	pagC	virulence membrane protein PAGC precursor	**0.27**	0.68915
STM1247	-	STM1247	**0.79**	0.58802
STM1247	-	STM1247	**0.44**	0.30422
STM1249	STM1249	putative periplasmic protein	**0.21**	0.76538
STM1249	STM1249	putative periplasmic protein	**0.31**	0.62503
STM1250	STM1250	putative cytoplasmic protein	**-0.14**	0.71139
STM1250	STM1250	putative cytoplasmic protein	**0.28**	0.66715
STM1251	STM1251	putative molecular chaperone	**0.07**	0.94985
STM1251	STM1251	putative molecular chaperone	**0.22**	0.69921
STM1252	STM1252	putative cytoplasmic protein	**-0.35**	0.67685
STM1252	STM1252	putative cytoplasmic protein	**0.49**	0.42735
STM1253	STM1253	putative inner membrane protein	**-0.41**	0.54624
STM1253	STM1253	putative inner membrane protein	**0.09**	0.89130
STM1254	STM1254	putative outer membrane lipoprotein	**-0.73**	0.18248
STM1254	STM1254	putative outer membrane lipoprotein	**-0.87**	0.15466
STM1255	STM1255	putative ABC transporter periplasmic binding protein	**-0.18**	0.72247
STM1255	STM1255	putative ABC transporter periplasmic binding protein	**0.10**	0.83040
STM1256	STM1256	putative ABC transporter protein	**-0.07**	0.90400
STM1256	STM1256	putative ABC transporter protein	**0.24**	0.72821
STM1257	STM1257	putative ABC transporter protein	**-0.23**	0.65612

STM1257	STM1257	putative ABC transporter protein	**-0.02**	0.97348
STM1258	STM1258	putative ABC-type transport system ATPase component	**-0.39**	0.31236
STM1258	STM1258	putative ABC-type transport system ATPase component	**0.62**	0.24319
STM1259	STM1259	putative ABC-type transport system ATPase component	**-0.06**	0.93974
STM1259	STM1259	putative ABC-type transport system ATPase component	**0.14**	0.85504
STM1260	STM1260	putative inner membrane protein	**0.08**	0.89546
STM1260	STM1260	putative inner membrane protein	**0.52**	0.30748
STM1261	STM1261	putative cytoplasmic protein	**-0.02**	0.97415
STM1261	STM1261	putative cytoplasmic protein	**0.44**	0.27004
STM1262	-	STM1262	**-0.47**	0.63562
STM1262	-	STM1262	**-0.11**	0.85718
STM1263	STM1263	putative periplasmic protein	**-0.54**	0.18883
STM1263	STM1263	putative periplasmic protein	**-0.10**	0.88897
STM1264	aadA	aminoglycoside adenyltransferase	**0.07**	0.89126
STM1264	aadA	aminoglycoside adenyltransferase	**0.42**	0.27378
STM1265	STM1265	putative response regulator	**-0.78**	0.38277
STM1265	STM1265	putative response regulator	**0.11**	0.84783
STM1266	STM1266	putative transcriptional regulator	**-0.01**	0.99213
STM1266	STM1266	putative transcriptional regulator	**0.56**	0.42486
STM1267	STM1267	putative cytoplasmic protein	**-0.02**	0.98332
STM1267	STM1267	putative cytoplasmic protein	**0.52**	0.31456
STM1268	STM1268	putative cytoplasmic protein	**-0.11**	0.85718
STM1268	STM1268	putative cytoplasmic protein	**-0.14**	0.76387
STM1269	STM1269	chorismate mutase	**-0.79**	0.11913
STM1269	STM1269	chorismate mutase	**-0.20**	0.65181
STM1270	yeaS	putative transport protein	**0.15**	0.72821
STM1270	yeaS	putative transport protein	**-0.08**	0.88213
STM1271	yeaR	putative cytoplasmic protein	**-0.38**	0.38425
STM1271	yeaR	putative cytoplasmic protein	**0.10**	0.86947
STM1273	STM1273	putative nitric oxide reductase	**0.16**	0.79898
STM1273	STM1273	putative nitric oxide reductase	**1.06**	0.14030
STM1273,1n	STM1273,1n	hypothetical protein STM1273,1n	**0.14**	0.69882
STM1273,1n	STM1273,1n	hypothetical protein STM1273,1n	**0.35**	0.42580
STM1274	yeaQ	putative inner membrane protein	**-0.05**	0.93023
STM1274	yeaQ	putative inner membrane protein	**0.17**	0.78973
STM1275	yaoF	putative hemolysin	**-0.09**	0.88306
STM1275	yaoF	putative hemolysin	**0.46**	0.34070
STM1276	STM1276	putative periplasmic protein	**-0.36**	0.48567
STM1276	STM1276	putative periplasmic protein	**0.24**	0.59757
STM1277	yeaO	putative cytoplasmic protein	**-0.68**	0.25845
STM1277	yeaO	putative cytoplasmic protein	**0.25**	0.55618
STM1278	yeaN	putative amino acid/amine transport protein	**-0.19**	0.67486
STM1278	yeaN	putative amino acid/amine transport protein	**0.27**	0.60620
STM1279	yeaM	putative regulatory protein	**-0.56**	0.23772
STM1279	yeaM	putative regulatory protein	**0.22**	0.67184
STM1280	yeaL	putative inner membrane protein	**0.44**	0.61656
STM1280	yeaL	putative inner membrane protein	**0.53**	0.33452
STM1282	yeaK	putative cytoplasmic protein	**0.54**	0.35373
STM1282	yeaK	putative cytoplasmic protein	**1.11**	0.24444
STM1283	yeaJ	putative methyl-accepting chemotaxis protein	**-0.49**	0.32172
STM1283	yeaJ	putative methyl-accepting chemotaxis protein	**0.32**	0.62290
STM1284	yeaH	hypothetical protein STM1284	**-0.32**	0.68418
STM1284	yeaH	hypothetical protein STM1284	**0.43**	0.55927
STM1285	yeaG	putative serine protein kinase	**-0.15**	0.85548
STM1285	yeaG	putative serine protein kinase	**0.25**	0.62988
STM1286	mipA	MltA-interacting protein A	**-0.04**	0.93804
STM1286	mipA	MltA-interacting protein A	**-0.11**	0.81556
STM1287	STM1287	arylsulfatase regulator	**-0.04**	0.95608
STM1287	STM1287	arylsulfatase regulator	**0.16**	0.81518
STM1288	STM1288	putative aldehyde reductase	**-0.37**	0.42811
STM1288	STM1288	putative aldehyde reductase	**0.02**	0.98001
STM1289	yeaD	aldose 1-epimerase	**-0.12**	0.80406
STM1289	yeaD	aldose 1-epimerase	**-0.22**	0.66743

STM1290	gapA	glyceraldehyde-3-phosphate dehydrogenase	**-0.22**	0.78879
STM1290	gapA	glyceraldehyde-3-phosphate dehydrogenase	**0.26**	0.72958
STM1291	yeaA	methionine sulfoxide reductase B	**-0.23**	0.54162
STM1291	yeaA	methionine sulfoxide reductase B	**0.04**	0.94727
STM1292	yeaC	putative cytoplasmic protein	**-0.81**	0.13112
STM1292	yeaC	putative cytoplasmic protein	**-0.40**	0.32016
STM1293	pncA	nicotinamidase/pyrazinamidase	**-0.26**	0.53336
STM1293	pncA	nicotinamidase/pyrazinamidase	**0.19**	0.61843
STM1294	ansA	cytoplasmic asparaginase I	**-0.10**	0.80198
STM1294	ansA	cytoplasmic asparaginase I	**0.49**	0.24721
STM1295	sppA	protease IV	**-0.23**	0.54347
STM1295	sppA	protease IV	**0.03**	0.95059
STM1296	ydjA	putative oxidoreductase	**-0.12**	0.74585
STM1296	ydjA	putative oxidoreductase	**0.07**	0.88004
STM1297	selD	selenophosphate synthetase	**0.07**	0.85718
STM1297	selD	selenophosphate synthetase	**0.59**	0.15859
STM1298	topB	DNA topoisomerase III	**0.12**	0.86017
STM1298	topB	DNA topoisomerase III	**-0.25**	0.52208
STM1299	gdhA	glutamate dehydrogenase	**-0.45**	0.35373
STM1299	gdhA	glutamate dehydrogenase	**0.05**	0.93568
STM1300	STM1300	putative periplasmic protein	**-0.49**	0.35955
STM1300	STM1300	putative periplasmic protein	**0.31**	0.37881
STM1301	STM1301	putative mutator protein	**-0.11**	0.76319
STM1301	STM1301	putative mutator protein	**-0.09**	0.87727
STM1302	xthA	exonuclease III	**-0.34**	0.46629
STM1302	xthA	exonuclease III	**-0.17**	0.69198
STM1303	argD	bifunctional	**-0.17**	0.72254
STM1303	argD	bifunctional	**0.00**	0.99800
STM1304	astA	arginine succinyltransferase	**-0.29**	0.44998
STM1304	astA	arginine succinyltransferase	**0.46**	0.24444
STM1305	astD	aldehyde dehyrogenase	**0.16**	0.87733
STM1305	astD	aldehyde dehyrogenase	**-0.19**	0.75002
STM1306	astB	succinylarginine dihydrolase	**0.11**	0.86654
STM1306	astB	succinylarginine dihydrolase	**0.62**	0.29543
STM1307	astE	succinylglutamate desuccinylase	**-0.49**	0.26378
STM1307	astE	succinylglutamate desuccinylase	**0.17**	0.73904
STM1308	spy	putative stress response protein	**-0.08**	0.93492
STM1308	spy	putative stress response protein	**0.12**	0.84099
STM1309	STM1309	putative excinuclease subunit	**-0.12**	0.76811
STM1309	STM1309	putative excinuclease subunit	**0.37**	0.36701
STM1310	nadE	NAD(+) synthetase	**-0.81**	0.13978
STM1310	nadE	NAD(+) synthetase	**-0.02**	0.96785
STM1311	osmE	transcriptional activator	**-0.55**	0.20783
STM1311	osmE	transcriptional activator	**0.46**	0.48814
STM1312	celA	sugar-specific enzyme IIB	**0.27**	0.47804
STM1312	celA	sugar-specific enzyme IIB	**0.34**	0.49740
STM1313	celB	sugar-specific enzyme II	**-0.78**	0.14030
STM1313	celB	sugar-specific enzyme II	**0.46**	0.44127
STM1314	celC	sugar-specific enzyme III	**-0.26**	0.58851
STM1314	celC	sugar-specific enzyme III	**0.05**	0.93023
STM1315	celD	transcriptional repressor of cel operon	**-0.17**	0.74087
STM1315	celD	transcriptional repressor of cel operon	**-0.15**	0.77895
STM1316	celF	phospho-beta-glucosidase/cellobiose-6-phosphate hydrolase	**-0.88**	0.13112
STM1316	celF	phospho-beta-glucosidase/cellobiose-6-phosphate hydrolase	**-0.22**	0.59824
STM1317	celG	hypothetical protein STM1317	**-0.61**	0.22283
STM1317	celG	hypothetical protein STM1317	**0.17**	0.74807
STM1318	katE	hydroperoxidase HPII	**-0.31**	0.66112
STM1318	katE	hydroperoxidase HPII	**0.72**	0.43219
STM1319	cedA	cell division modulator protein	**0.15**	0.74243
STM1319	cedA	cell division modulator protein	**0.33**	0.46927
STM1320	ydjN	kinase/transporter-like protein	**-0.28**	0.57021

STM1320	ydjN	kinase/transporter-like protein	**-0.32**	0.48600
STM1321	ydjM	putative SOS response protein	**-0.07**	0.88959
STM1321	ydjM	putative SOS response protein	**0.22**	0.66677
STM1322	yniC	putative enzyme	**-0.50**	0.19843
STM1322	yniC	putative enzyme	**0.06**	0.91301
STM1323	yniB	putative regulatory protein	**-0.13**	0.74374
STM1323	yniB	putative regulatory protein	**0.02**	0.96568
STM1324	STM1324	putative cytoplasmic protein	**-0.05**	0.92937
STM1324	STM1324	putative cytoplasmic protein	**0.09**	0.87110
STM1325	ydiZ	putative cytoplasmic protein	**-0.74**	0.14030
STM1325	ydiZ	putative cytoplasmic protein	**-0.10**	0.85431
STM1326	pfkB	6-phosphofructokinase II	**-0.06**	0.92351
STM1326	pfkB	6-phosphofructokinase II	**-0.32**	0.50474
STM1327	ydiY	putative outer membrane protein	**0.00**	0.99447
STM1327	ydiY	putative outer membrane protein	**0.17**	0.68240
STM1328	STM1328	putative outer membrane protein	**0.16**	0.67363
STM1328	STM1328	putative outer membrane protein	**0.63**	0.19967
STM1329	STM1329	putative inner membrane protein	**0.17**	0.69633
STM1329	STM1329	putative inner membrane protein	**0.03**	0.95721
STM1330	STM1330	putative DNA/RNA non-specific endonuclease	**-0.17**	0.70545
STM1330	STM1330	putative DNA/RNA non-specific endonuclease	**0.42**	0.26910
STM1332	rfc	O-antigen polymerase	**-0.24**	0.61720
STM1332	rfc	O-antigen polymerase	**0.11**	0.78992
STM1333	thrS	threonyl-tRNA synthetase	**-0.07**	0.91456
STM1333	thrS	threonyl-tRNA synthetase	**0.23**	0.65355
STM1334,c	infC	translation initiation factor IF-3	**0.08**	0.85758
STM1334,c	infC	translation initiation factor IF-3	**0.34**	0.58410
STM1335	rpmI	50S ribosomal protein L35	**-0.13**	0.75512
STM1335	rpmI	50S ribosomal protein L35	**0.24**	0.57506
STM1336	rplT	50S ribosomal protein L20	**-0.09**	0.84994
STM1336	rplT	50S ribosomal protein L20	**0.00**	0.99452
STM1337	pheS	phenylalanyl-tRNA synthetase alpha subunit	**-0.18**	0.61809
STM1337	pheS	phenylalanyl-tRNA synthetase alpha subunit	**0.12**	0.78255
STM1338	pheT	phenylalanyl-tRNA synthetase beta subunit	**-0.07**	0.87733
STM1338	pheT	phenylalanyl-tRNA synthetase beta subunit	**0.12**	0.79473
STM1339	himA	integration host factor alpha subunit	**-0.62**	0.25197
STM1339	himA	integration host factor alpha subunit	**-0.35**	0.35694
STM1340	btuC	vtamin B12-transporter permease	**-0.20**	0.72341
STM1340	btuC	vtamin B12-transporter permease	**0.11**	0.77324
STM1341	btuE	vitamin B12 transport protein	**-0.39**	0.31422
STM1341	btuE	vitamin B12 transport protein	**0.38**	0.40562
STM1342	btuD	vitamin B12-transporter ATPase	**0.04**	0.93841
STM1342	btuD	vitamin B12-transporter ATPase	**0.55**	0.42735
STM1343	nlpC	lipoprotein	**-0.37**	0.52897
STM1343	nlpC	lipoprotein	**0.03**	0.94880
STM1344	ydiV	hypothetical protein STM1344	**0.10**	0.83107
STM1344	ydiV	hypothetical protein STM1344	**0.58**	0.21360
STM1345	ydiU	hypothetical protein STM1345	**-0.16**	0.72375
STM1345	ydiU	hypothetical protein STM1345	**0.80**	0.14030
STM1346	ydiE	putative cytoplasmic protein	**0.22**	0.54560
STM1346	ydiE	putative cytoplasmic protein	**0.64**	0.23114
STM1347	aroH	3-deoxy-7-phosphoheptulonate synthase	**-0.40**	0.49336
STM1347	aroH	3-deoxy-7-phosphoheptulonate synthase	**0.10**	0.86895
STM1348	ydiA	hypothetical protein STM1348	**-0.18**	0.68021
STM1348	ydiA	hypothetical protein STM1348	**0.42**	0.31280
STM1349	pps	phosphoenolpyruvate synthase	**-0.05**	0.93554
STM1349	pps	phosphoenolpyruvate synthase	**0.63**	0.17793
STM1350	ydiD	hypothetical protein STM1350	**0.50**	0.33452
STM1350	ydiD	hypothetical protein STM1350	**0.39**	0.58345
STM1351	ydiT	putative ferredoxin	**-0.18**	0.69372
STM1351	ydiT	putative ferredoxin	**0.86**	0.16534
STM1352	ydiS	flavoprotein	**-0.28**	0.70846
STM1352	ydiS	flavoprotein	**0.17**	0.64416

STM1353	ydiR	putative electron transfer flavoprotein subunit alpha	**-0.22**	0.76538
STM1353	ydiR	putative electron transfer flavoprotein subunit alpha	**0.51**	0.22283
STM1354	ydiQ	putative electron transfer flavoprotein subunit beta	**-0.32**	0.64422
STM1354	ydiQ	putative electron transfer flavoprotein subunit beta	**0.39**	0.37161
STM1355	ydiP	putative transcriptional regulator	**-0.67**	0.16534
STM1355	ydiP	putative transcriptional regulator	**-0.04**	0.95463
STM1356	ydiO	crotonobetainyl-CoA dehydrogenase	**-0.78**	0.70077
STM1356	ydiO	crotonobetainyl-CoA dehydrogenase	**0.83**	0.58912
STM1357,S	ydiF	putative acetyl-CoA/acetoacetyl-CoA transferase beta subunit	**-0.38**	0.34070
STM1357,S	ydiF	putative acetyl-CoA/acetoacetyl-CoA transferase beta subunit	**0.36**	0.36833
STM1358	aroD	3-dehydroquinate dehydratase	**-0.35**	0.46629
STM1358	aroD	3-dehydroquinate dehydratase	**0.40**	0.46199
STM1359	aroE	shikimate 5-dehydrogenase	**-0.28**	0.62873
STM1359	aroE	shikimate 5-dehydrogenase	**0.48**	0.34574
STM1360	ydiN	putative transport protein	**-0.49**	0.46266
STM1360	ydiN	putative transport protein	**-0.39**	0.68140
STM1361	ydiM	putative transport protein	**-0.89**	0.13645
STM1361	ydiM	putative transport protein	**0.67**	0.15842
STM1362	ydiL	putative cytoplasmic protein	**-0.18**	0.83902
STM1362	ydiL	putative cytoplasmic protein	**0.30**	0.72247
STM1363	rprA	STM1363	**-0.20**	0.75831
STM1363	rprA	STM1363	**-0.18**	0.70185
STM1364	ydiK	putative permease	**-0.48**	0.30496
STM1364	ydiK	putative permease	**0.11**	0.82637
STM1365	ydiJ	putative oxidase	**-0.08**	0.84963
STM1365	ydiJ	putative oxidase	**0.25**	0.56637
STM1366	STM1366	hypothetical protein STM1366	**-0.10**	0.85893
STM1366	STM1366	hypothetical protein STM1366	**-0.04**	0.91789
STM1367	ydiH	putative cytoplasmic protein	**-0.16**	0.82153
STM1367	ydiH	putative cytoplasmic protein	**-0.13**	0.88868
STM1368	STM1368	putative Na+-dicarboxylate symporter	**-0.21**	0.63148
STM1368	STM1368	putative Na+-dicarboxylate symporter	**0.50**	0.29796
STM1369	sufA	iron-sulfur cluster assembly scaffold protein	**0.13**	0.82964
STM1369	sufA	iron-sulfur cluster assembly scaffold protein	**0.65**	0.16281
STM1370	sufB	putative ABC transporter protein	**0.36**	0.39560
STM1370	sufB	putative ABC transporter protein	**-0.40**	0.78909
STM1371	sufC	putative transport protein	**0.01**	0.99452
STM1371	sufC	putative transport protein	**0.35**	0.55439
STM1372	sufD	cysteine desulfurase modulator	**-0.05**	0.93205
STM1372	sufD	cysteine desulfurase modulator	**-0.04**	0.92884
STM1373	sufS	selenocysteine lyase	**-0.05**	0.91378
STM1373	sufS	selenocysteine lyase	**0.72**	0.18876
STM1374	ynhA	cysteine desufuration protein SufE	**-0.17**	0.68439
STM1374	ynhA	cysteine desufuration protein SufE	**0.40**	0.34106
STM1375	ynhG	hypothetical protein STM1375	**-0.38**	0.43148
STM1375	ynhG	hypothetical protein STM1375	**-0.30**	0.57278
STM1376	lppB	putative methyl-accepting chemotaxis protein	**0.58**	0.55976
STM1376	lppB	putative methyl-accepting chemotaxis protein	**0.51**	0.47515
STM1377	lpp	murein lipoprotein	**-0.61**	0.40562
STM1377	lpp	murein lipoprotein	**-0.42**	0.44808
STM1378	pykF	pyruvate kinase	**-0.39**	0.38363
STM1378	pykF	pyruvate kinase	**-0.39**	0.35955
STM1379	orf48	putative amino acid permease	**-0.12**	0.78016
STM1379	orf48	putative amino acid permease	**0.06**	0.91111
STM1380	orf32	putative proline iminopeptidase	**0.37**	0.35010
STM1380	orf32	putative proline iminopeptidase	**0.16**	0.73213
STM1381	orf245	putative cytoplasmic protein	**-0.02**	0.97583
STM1381	orf245	putative cytoplasmic protein	**-0.12**	0.80406
STM1382	orf408	putative regulatory protein	**-0.02**	0.97168
STM1382	orf408	putative regulatory protein	**0.33**	0.37967
STM1383	ttrA	tetrathionate reductase complex subunit A	**0.30**	0.73473

STM1383	ttrA	tetrathionate reductase complex subunit A	**0.85**	0.29871
STM1384	ttrC	tetrathionate reductase complex subunit C	**-0.45**	0.23879
STM1384	ttrC	tetrathionate reductase complex subunit C	**0.32**	0.69447
STM1385	ttrB	tetrathionate reductase complex subunit B	**-0.03**	0.97837
STM1385	ttrB	tetrathionate reductase complex subunit B	**-0.07**	0.91170
STM1386	ttrS	sensory histidine kinase	**-0.09**	0.94357
STM1386	ttrS	sensory histidine kinase	**0.27**	0.73653
STM1387	ttrR	response regulator	**-0.30**	0.48166
STM1387	ttrR	response regulator	**-0.14**	0.76981
STM1388	orf70	putative cytoplasmic protein	**-0.39**	0.42277
STM1388	orf70	putative cytoplasmic protein	**-0.08**	0.87182
STM1389	orf319	putative inner membrane protein	**0.26**	0.49302
STM1389	orf319	putative inner membrane protein	**0.39**	0.56786
STM1390	orf242	putative regulatory protein	**-0.34**	0.61375
STM1390	orf242	putative regulatory protein	**0.61**	0.33452
STM1391	ssrB	transcriptional activator	**0.43**	0.52994
STM1391	ssrB	transcriptional activator	**0.26**	0.65474
STM1392	ssrA	sensor kinase	**-0.23**	0.86769
STM1392	ssrA	sensor kinase	**1.51**	0.24515
STM1394	ssaC	outer membrane secretin precursor	**-0.38**	0.41328
STM1394	ssaC	outer membrane secretin precursor	**0.21**	0.65916
STM1395	ssaD	virulence protein	**-0.39**	0.47610
STM1395	ssaD	virulence protein	**-0.45**	0.40190
STM1396	ssaE	secretion system effector	**-1.43**	0.06967
STM1396	ssaE	secretion system effector	**-0.03**	0.95608
STM1398	sseB	translocation machinery component	**0.01**	0.99252
STM1398	sseB	translocation machinery component	**0.44**	0.44556
STM1399	sscA	secretion system chaperone	**0.00**	0.99938
STM1399	sscA	secretion system chaperone	**0.67**	0.22063
STM1400	sseC	translocation machinery component	**-0.01**	0.98640
STM1400	sseC	translocation machinery component	**0.49**	0.25719
STM1401	sseD	translocation machinery component	**-0.46**	0.39642
STM1401	sseD	translocation machinery component	**0.09**	0.87126
STM1402	sseE	secreted effector protein	**-0.57**	0.25740
STM1402	sseE	secreted effector protein	**1.20**	0.14030
STM1403	sscB	secretion system chaperone	**-0.07**	0.93688
STM1403	sscB	secretion system chaperone	**1.01**	0.13831
STM1404	sseF	secreted effector protein	**-0.45**	0.40562
STM1404	sseF	secreted effector protein	**0.24**	0.63101
STM1405	sseG	secreted effector protein	**-0.29**	0.46629
STM1405	sseG	secreted effector protein	**0.17**	0.79096
STM1406	ssaG	type III secretion system apparatus protein	**-0.24**	0.61809
STM1406	ssaG	type III secretion system apparatus protein	**0.49**	0.59422
STM1407	ssaH	type III secretion system apparatus protein	**-0.47**	0.48814
STM1407	ssaH	type III secretion system apparatus protein	**-0.02**	0.98140
STM1408	ssaI	type III secretion system apparatus protein	**-0.23**	0.61960
STM1408	ssaI	type III secretion system apparatus protein	**0.89**	0.18464
STM1409	ssaJ	needle complex inner membrane lipoprotein	**-0.42**	0.34936
STM1409	ssaJ	needle complex inner membrane lipoprotein	**0.27**	0.52840
STM1410	STM1410	putative cytoplasmic protein	**-0.69**	0.41400
STM1410	STM1410	putative cytoplasmic protein	**-0.78**	0.76538
STM1411	ssaK	type III secretion system apparatus protein	**-0.31**	0.65730
STM1411	ssaK	type III secretion system apparatus protein	**-0.38**	0.44039
STM1412	ssaL	type III secretion system apparatus protein	**-0.18**	0.69189
STM1412	ssaL	type III secretion system apparatus protein	**1.09**	0.13824
STM1413	ssaM	type III secretion system apparatus protein	**-0.56**	0.17139
STM1413	ssaM	type III secretion system apparatus protein	**-0.10**	0.85391
STM1414	ssaV	type III secretion system apparatus protein	**-0.14**	0.91917
STM1414	ssaV	type III secretion system apparatus protein	**0.11**	0.83899
STM1415	ssaN	type III secretion system ATPase	**-0.25**	0.66636
STM1415	ssaN	type III secretion system ATPase	**0.02**	0.96968
STM1416	ssaO	type III secretion system apparatus protein	**-0.75**	0.17754
STM1416	ssaO	type III secretion system apparatus protein	**-0.45**	0.48129

STM1417	ssaP	type III secretion system apparatus protein	**0.02**	0.98210
STM1417	ssaP	type III secretion system apparatus protein	**0.21**	0.64524
STM1418	ssaQ	type III secretion protein	**-0.23**	0.62757
STM1418	ssaQ	type III secretion protein	**0.62**	0.26856
STM1419	ssaR	needle complex export protein	**-0.09**	0.91724
STM1419	ssaR	needle complex export protein	**0.12**	0.83386
STM1421	ssaT	type III secretion system apparatus protein	**-0.04**	0.95532
STM1421	ssaT	type III secretion system apparatus protein	**0.38**	0.41751
STM1422	ssaU	type III secretion system apparatus protein	**-0.09**	0.87208
STM1422	ssaU	type III secretion system apparatus protein	**0.52**	0.23114
STM1423	valW	STM1423	**0.43**	0.47824
STM1423	valW	STM1423	**0.72**	0.34449
STM1424	valV	STM1424	**0.45**	0.69802
STM1424	valV	STM1424	**0.93**	0.19967
STM1425	ydhE	multidrug efflux protein NorA	**-0.05**	0.92513
STM1425	ydhE	multidrug efflux protein NorA	**-0.15**	0.77217
STM1426	ribE	riboflavin synthase subunit alpha	**0.00**	0.99822
STM1426	ribE	riboflavin synthase subunit alpha	**0.48**	0.38722
STM1427	cfa	cyclopropane fatty acyl phospholipid synthase	**-0.06**	0.88811
STM1427	cfa	cyclopropane fatty acyl phospholipid synthase	**-0.18**	0.64742
STM1428	ydhC	putative transport protein	**-0.04**	0.95127
STM1428	ydhC	putative transport protein	**0.13**	0.77923
STM1429	ydhB	putative transcriptional regulator	**-0.32**	0.53678
STM1429	ydhB	putative transcriptional regulator	**0.12**	0.82384
STM1430	purR	pur regulon transcriptional repressor	**-0.10**	0.81449
STM1430	purR	pur regulon transcriptional repressor	**-0.11**	0.80070
STM1431	sodB	superoxide dismutase	**-0.52**	0.26975
STM1431	sodB	superoxide dismutase	**0.06**	0.93731
STM1432	ydhO	putative cell wall-associated hydrolase	**-0.61**	0.31367
STM1432	ydhO	putative cell wall-associated hydrolase	**-0.19**	0.61720
STM1433	ydhD	putative glutaredoxin protein	**-0.02**	0.96687
STM1433	ydhD	putative glutaredoxin protein	**0.19**	0.62069
STM1434	rnt	ribonuclease T	**0.08**	0.84058
STM1434	rnt	ribonuclease T	**-0.11**	0.79635
STM1435	gloA	glyoxalase I	**-0.31**	0.37942
STM1435	gloA	glyoxalase I	**0.14**	0.80915
STM1436	nemA	N-ethylmaleimide reductase	**-0.05**	0.92111
STM1436	nemA	N-ethylmaleimide reductase	**0.39**	0.48810
STM1437	ydhM	putative transcriptional repressor	**0.01**	0.98790
STM1437	ydhM	putative transcriptional repressor	**-0.13**	0.77923
STM1438	ydhL	putative oxidoreductase	**-0.29**	0.48479
STM1438	ydhL	putative oxidoreductase	**-0.29**	0.57026
STM1439	ydhF	putative aldo/keto reductase	**0.02**	0.96757
STM1439	ydhF	putative aldo/keto reductase	**-0.09**	0.83443
STM1440	sodC	copper/zinc superoxide dismutase	**0.20**	0.68319
STM1440	sodC	copper/zinc superoxide dismutase	**0.73**	0.27522
STM1441	STM1441	putative inner membrane protein	**-0.29**	0.59719
STM1441	STM1441	putative inner membrane protein	**-0.13**	0.77639
STM1442	ydhJ	putative multidrug resistance efflux pump	**-0.27**	0.58355
STM1442	ydhJ	putative multidrug resistance efflux pump	**0.45**	0.28799
STM1444	slyA	transcriptional regulator SlyA	**0.03**	0.94798
STM1444	slyA	transcriptional regulator SlyA	**-0.08**	0.89405
STM1445	slyB	putative outer membrane lipoprotein	**-1.47**	0.01937
STM1445	slyB	putative outer membrane lipoprotein	**-0.79**	0.11690
STM1446	ydhH	putative cytoplasmic protein	**-0.65**	0.44402
STM1446	ydhH	putative cytoplasmic protein	**0.21**	0.74374
STM1447	ydhA	putative outer membrane lipoprotein	**-0.20**	0.58117
STM1447	ydhA	putative outer membrane lipoprotein	**0.26**	0.56095
STM1448	pdxH	pyridoxamine 5'-phosphate oxidase	**-0.22**	0.55656
STM1448	pdxH	pyridoxamine 5'-phosphate oxidase	**-0.26**	0.49422
STM1449	tyrS	tyrosyl-tRNA synthetase	**-0.14**	0.70229
STM1449	tyrS	tyrosyl-tRNA synthetase	**0.16**	0.70249
STM1450	pdxY	pyridoxine kinase	**-0.69**	0.21069

STM1450	pdxY	pyridoxine kinase	**0.13**	0.78335
STM1451	gst	glutathionine S-transferase	**-0.23**	0.56120
STM1451	gst	glutathionine S-transferase	**0.14**	0.76475
STM1452	ydgR	putative peptide transport protein	**-0.62**	0.21078
STM1452	ydgR	putative peptide transport protein	**0.06**	0.90400
STM1453	nth	endonuclease III	**0.03**	0.98398
STM1453	nth	endonuclease III	**0.18**	0.77883
STM1454	ydgQ	NADH-ubiquinone oxidoreductase	**-0.40**	0.40121
STM1454	ydgQ	NADH-ubiquinone oxidoreductase	**0.25**	0.59820
STM1455	ydgP	electron transport complex protein RnfG	**-0.22**	0.61837
STM1455	ydgP	electron transport complex protein RnfG	**0.22**	0.67363
STM1456	rnfD	electron transport complex protein RnfD	**-0.21**	0.53263
STM1456	rnfD	electron transport complex protein RnfD	**0.06**	0.91032
STM1457	STM1457	electron transport complex protein RnfC	**-0.13**	0.78173
STM1457	STM1457	electron transport complex protein RnfC	**0.57**	0.23114
STM1458	ydgM	electron transport complex protein RnfB	**-0.02**	0.96568
STM1458	ydgM	electron transport complex protein RnfB	**0.29**	0.49336
STM1459	STM1459	Na(+)-translocating NADH-quinone reductase subunit E	**-0.10**	0.82956
STM1459	STM1459	Na(+)-translocating NADH-quinone reductase subunit E	**-0.07**	0.89863
STM1460	ydgK	putative inner membrane protein	**-0.05**	0.93076
STM1460	ydgK	putative inner membrane protein	**-0.19**	0.65312
STM1461,S	ydgT	putative cytoplasmic protein	**-0.29**	0.52258
STM1461,S	ydgT	putative cytoplasmic protein	**-0.04**	0.91900
STM1462,S	ydgJ	putative oxidoreductase	**-0.07**	0.86876
STM1462,S	ydgJ	putative oxidoreductase	**0.55**	0.17139
STM1463	add	adenosine deaminase	**-0.11**	0.79354
STM1463	add	adenosine deaminase	**0.06**	0.89979
STM1466	ydgA	putative periplasmic protein	**-0.04**	0.91571
STM1466	ydgA	putative periplasmic protein	**0.09**	0.83625
STM1467	manA	mannose-6-phosphate isomerase	**0.18**	0.64786
STM1467	manA	mannose-6-phosphate isomerase	**0.20**	0.61833
STM1468	fumA	fumarase A	**0.19**	0.67979
STM1468	fumA	fumarase A	**0.33**	0.56421
STM1469	fumC	fumarate hydratase	**0.31**	0.80045
STM1469	fumC	fumarate hydratase	**0.38**	0.62199
STM1470	tus	DNA replication terminus site-binding protein	**0.29**	0.61190
STM1470	tus	DNA replication terminus site-binding protein	**0.50**	0.24515
STM1471	rstB	sensory histidine kinase	**-0.13**	0.91170
STM1471	rstB	sensory histidine kinase	**0.76**	0.41836
STM1472	STM1472	putative periplasmic protein	**-0.39**	0.46376
STM1472	STM1472	putative periplasmic protein	**0.01**	0.99213
STM1473	ompN	outer membrane protein N precursor	**1.40**	0.38389
STM1473	ompN	outer membrane protein N precursor	**0.73**	0.54624
STM1475	rstA	response regulator	**-1.10**	0.04499
STM1475	rstA	response regulator	**-0.86**	0.11224
STM1476	ydgC	putative inner membrane protein	**-0.05**	0.90534
STM1476	ydgC	putative inner membrane protein	**-0.14**	0.79356
STM1477	ydgI	putative amino acid transporter	**-0.50**	0.29866
STM1477	ydgI	putative amino acid transporter	**-0.35**	0.41715
STM1478	ydgH	putative periplasmic protein	**-0.51**	0.23853
STM1478	ydgH	putative periplasmic protein	**-0.36**	0.45852
STM1479	pntA	NAD(P) transhydrogenase subunit alpha	**-0.28**	0.46101
STM1479	pntA	NAD(P) transhydrogenase subunit alpha	**-0.06**	0.89624
STM1480	pntB	pyridine nucleotide transhydrogenase	**-0.27**	0.53840
STM1480	pntB	pyridine nucleotide transhydrogenase	**0.30**	0.49009
STM1481	STM1481	putative transport protein	**-0.46**	0.23114
STM1481	STM1481	putative transport protein	**-0.12**	0.84187
STM1482	ydgF	putative cationic transporter	**-0.37**	0.51979
STM1482	ydgF	putative cationic transporter	**0.31**	0.36270
STM1483	ydgE	putative cationic transporter	**-0.68**	0.28582
STM1483	ydgE	putative cationic transporter	**0.00**	0.99698
STM1484	STM1484	putative protease	**-0.11**	0.80652
STM1484	STM1484	putative protease	**-0.07**	0.89405

STM1486	ynfM	putative transport protein	**0.27**	0.55956
STM1486	ynfM	putative transport protein	**0.19**	0.66155
STM1487	ynfL	putative transcriptional regulator	**-0.34**	0.49035
STM1487	ynfL	putative transcriptional regulator	**0.12**	0.78728
STM1488	mlc	pts operon transcriptional repressor	**-0.18**	0.69519
STM1488	mlc	pts operon transcriptional repressor	**0.06**	0.94990
STM1489	bioD	dithiobiotin synthetase	**0.08**	0.90292
STM1489	bioD	dithiobiotin synthetase	**0.16**	0.65305
STM1490	STM1490	putative voltage-gated ClC-type chloride channel ClcB	**-0.27**	0.54624
STM1490	STM1490	putative voltage-gated ClC-type chloride channel ClcB	**0.42**	0.45800
STM1491	STM1491	proline/glycine betaine transport systems	**-0.08**	0.91900
STM1491	STM1491	proline/glycine betaine transport systems	**0.76**	0.27477
STM1492	STM1492	putative ABC transporter permease component	**-0.03**	0.98156
STM1492	STM1492	putative ABC transporter permease component	**0.36**	0.49077
STM1493	STM1493	putative ABC transporter periplasmic component	**0.26**	0.64730
STM1493	STM1493	putative ABC transporter periplasmic component	**1.59**	0.08996
STM1494	STM1494	putative transport system permease component	**-0.13**	0.78410
STM1494	STM1494	putative transport system permease component	**0.93**	0.21015
STM1495	ynfI	putative anaerobic dehydrogenase component	**-0.16**	0.74779
STM1495	ynfI	putative anaerobic dehydrogenase component	**-0.40**	0.41715
STM1496	STM1496	putative dimethylsulfoxide reductase	**-0.39**	0.48814
STM1496	STM1496	putative dimethylsulfoxide reductase	**-0.32**	0.44935
STM1497	STM1497	putative dimethyl sulphoxide reductase	**-0.40**	0.65383
STM1497	STM1497	putative dimethyl sulphoxide reductase	**0.22**	0.76387
STM1498	STM1498	putative dimethyl sulphoxide reductase	**-0.33**	0.36341
STM1498	STM1498	putative dimethyl sulphoxide reductase	**-0.07**	0.85909
STM1499	STM1499	putative dimethyl sulphoxide reductase chain A1	**-1.32**	0.24313
STM1499	STM1499	putative dimethyl sulphoxide reductase chain A1	**-0.43**	0.66743
STM1500	ynfD	putative outer membrane protein	**-0.57**	0.25759
STM1500	ynfD	putative outer membrane protein	**0.44**	0.49983
STM1501	ynfC	hypothetical protein STM1501	**0.13**	0.78665
STM1501	ynfC	hypothetical protein STM1501	**0.00**	0.99713
STM1502	speG	spermidine N1-acetyltransferase	**-0.12**	0.81075
STM1502	speG	spermidine N1-acetyltransferase	**0.32**	0.60174
STM1503	ynfB	putative periplasmic protein	**-0.25**	0.57506
STM1503	ynfB	putative periplasmic protein	**0.08**	0.89405
STM1504	ynfA	hypothetical protein STM1504	**0.18**	0.72135
STM1504	ynfA	hypothetical protein STM1504	**0.47**	0.32481
STM1505	rspA	putative dehydratase	**-0.13**	0.84187
STM1505	rspA	putative dehydratase	**0.52**	0.43219
STM1506	rspB	putative dehydrogenase	**-0.23**	0.63793
STM1506	rspB	putative dehydrogenase	**0.47**	0.42756
STM1508	ydfI	putative mannitol dehydrogenase	**-0.29**	0.53840
STM1508	ydfI	putative mannitol dehydrogenase	**1.20**	0.11913
STM1510	ydfH	putative regulatory protein	**0.21**	0.81667
STM1510	ydfH	putative regulatory protein	**0.19**	0.83525
STM1511	ydfG	putative oxidoreductase	**-0.21**	0.63328
STM1511	ydfG	putative oxidoreductase	**-0.38**	0.44224
STM1512	dcp	dipeptidyl carboxypeptidase II	**-0.71**	0.13813
STM1512	dcp	dipeptidyl carboxypeptidase II	**-0.44**	0.22602
STM1514	ydeJ	competence damage-inducible protein A	**0.12**	0.84863
STM1514	ydeJ	competence damage-inducible protein A	**0.40**	0.36989
STM1515	ydeI	putative periplasmic protein	**-0.62**	0.21015
STM1515	ydeI	putative periplasmic protein	**-0.32**	0.79121
STM1516	ydeE	putative transport protein	**-0.14**	0.78929
STM1516	ydeE	putative transport protein	**0.06**	0.92716
STM1517	ydeD	putative permease	**-0.13**	0.76622
STM1517	ydeD	putative permease	**0.35**	0.38358
STM1518	marB	multiple antibiotic resistance protein	**-0.86**	0.16534
STM1518	marB	multiple antibiotic resistance protein	**-0.39**	0.55009
STM1519,S	marA	transcriptional activator	**-0.39**	0.55956
STM1519,S	marA	transcriptional activator	**0.28**	0.62975
STM1520	marR	marRAB operon repressor	**-0.04**	0.94417

STM1520	marR	marRAB operon repressor	**0.03**	0.95608
STM1521	marC	multiple antibiotic resistance transporter	**-0.73**	0.17139
STM1521	marC	multiple antibiotic resistance transporter	**-0.22**	0.66888
STM1522	ydeA	sugar efflux transporter	**-0.02**	0.98080
STM1522	ydeA	sugar efflux transporter	**0.04**	0.96595
STM1523	yneJ	putative transcriptional regulator	**-0.57**	0.20065
STM1523	yneJ	putative transcriptional regulator	**0.50**	0.57111
STM1524	yneI	putative succinate-semialdehyde dehydrogenase	**-0.34**	0.53731
STM1524	yneI	putative succinate-semialdehyde dehydrogenase	**-0.01**	0.98879
STM1525	yneH	glutaminase	**0.18**	0.70726
STM1525	yneH	glutaminase	**0.38**	0.47159
STM1526	yneG	putative cytoplasmic protein	**0.06**	0.93849
STM1526	yneG	putative cytoplasmic protein	**-0.24**	0.55374
STM1527	STM1527	putative inner membrane protein	**-0.20**	0.67137
STM1527	STM1527	putative inner membrane protein	**0.00**	0.99698
STM1528	STM1528	putative outer membrane protein	**0.18**	0.66636
STM1528	STM1528	putative outer membrane protein	**0.19**	0.70686
STM1530	STM1530	putative outer membrane protein	**-0.12**	0.77908
STM1530	STM1530	putative outer membrane protein	**0.87**	0.14030
STM1531	STM1531	putative hydrogenase	**-1.09**	0.07318
STM1531	STM1531	putative hydrogenase	**0.29**	0.59811
STM1532	STM1532	putative dehydrogenase protein	**-0.26**	0.62199
STM1532	STM1532	putative dehydrogenase protein	**-0.23**	0.70061
STM1533	STM1533	putative hydrogenase	**-0.09**	0.83400
STM1533	STM1533	putative hydrogenase	**-0.18**	0.75893
STM1534	STM1534	putative hydrogenase	**-0.16**	0.75739
STM1534	STM1534	putative hydrogenase	**0.62**	0.22602
STM1535	STM1535	putative hydrogenase protein	**-0.66**	0.27783
STM1535	STM1535	putative hydrogenase protein	**-0.53**	0.38317
STM1536	STM1536	putative hydrogenase maturation protease	**-0.40**	0.35536
STM1536	STM1536	putative hydrogenase maturation protease	**0.09**	0.85356
STM1537	STM1537	putative Ni/Fe hydrogenase 1 b-type cytochrome subunit	**-0.68**	0.20285
STM1537	STM1537	putative Ni/Fe hydrogenase 1 b-type cytochrome subunit	**0.41**	0.49870
STM1538	STM1538	putative hydrogenase-1 large subunit	**0.96**	0.19425
STM1538	STM1538	putative hydrogenase-1 large subunit	**1.19**	0.18961
STM1539	STM1539	putative hydrogenase-1 small subunit	**-0.49**	0.33839
STM1539	STM1539	putative hydrogenase-1 small subunit	**0.91**	0.17754
STM1540	STM1540	putative hydrolase	**-0.55**	0.24520
STM1540	STM1540	putative hydrolase	**0.20**	0.62199
STM1541	STM1541	putative regulatory protein	**-0.13**	0.84611
STM1541	STM1541	putative regulatory protein	**0.24**	0.68143
STM1542	STM1542	putative zinc-binding dehydrogenase	**-0.60**	0.22131
STM1542	STM1542	putative zinc-binding dehydrogenase	**0.01**	0.99200
STM1543	STM1543	putative transport protein	**-0.13**	0.86396
STM1543	STM1543	putative transport protein	**0.26**	0.67509
STM1544	pqaA	PhoPQ-regulated protein	**-0.22**	0.76970
STM1544	pqaA	PhoPQ-regulated protein	**0.74**	0.22063
STM1545	STM1545	putative multidrug efflux protein	**-0.92**	0.21812
STM1545	STM1545	putative multidrug efflux protein	**-0.35**	0.58300
STM1546	STM1546	hypothetical protein STM1546	**0.04**	0.95809
STM1546	STM1546	hypothetical protein STM1546	**-0.51**	0.38260
STM1547	STM1547	putative transcriptional regulator	**-0.20**	0.73757
STM1547	STM1547	putative transcriptional regulator	**-0.01**	0.98445
STM1548,s	STM1548,s	putative S-adenosylmethionine/tRNA-ribosyltransferase-isomerase	**-0.53**	0.29889
STM1548,s	STM1548,s	putative S-adenosylmethionine/tRNA-ribosyltransferase-isomerase	**-0.17**	0.74178
STM1549	STM1549	putative translation initiation inhibitor	**-0.07**	0.89542
STM1549	STM1549	putative translation initiation inhibitor	**0.26**	0.54916
STM1551	STM1551	putative cytoplasmic protein	**-0.27**	0.59306
STM1551	STM1551	putative cytoplasmic protein	**0.17**	0.68307
STM1551,1n	STM1551,1n	hypothetical protein STM1551,1n	**-0.24**	0.55956
STM1551,1n	STM1551,1n	hypothetical protein STM1551,1n	**-0.04**	0.96687

STM1552	STM1552	putative cytoplasmic protein	**0.07**	0.92876
STM1552	STM1552	putative cytoplasmic protein	**-0.03**	0.96426
STM1554	STM1554	putative coiled-coil protein	**-0.46**	0.40499
STM1554	STM1554	putative coiled-coil protein	**0.37**	0.40819
STM1555	STM1555	putative transcriptional regulator	**-0.32**	0.56200
STM1555	STM1555	putative transcriptional regulator	**-0.23**	0.72629
STM1556	STM1556	putative Na+/H+ antiporter	**-0.75**	0.17431
STM1556	STM1556	putative Na+/H+ antiporter	**-0.02**	0.98385
STM1557	STM1557	putative aminotransferase	**-0.57**	0.35824
STM1557	STM1557	putative aminotransferase	**0.43**	0.60249
STM1558	STM1558	putative glycosyl hydrolase	**0.03**	0.96774
STM1558	STM1558	putative glycosyl hydrolase	**1.09**	0.11913
STM1559	STM1559	putative glycosyl hydrolase	**0.55**	0.41137
STM1559	STM1559	putative glycosyl hydrolase	**1.11**	0.22540
STM1560	STM1560	putative alpha amylase	**-0.21**	0.76648
STM1560	STM1560	putative alpha amylase	**0.14**	0.76553
STM1561	STM1561	putative lipoprotein	**-0.29**	0.77963
STM1561	STM1561	putative lipoprotein	**0.60**	0.55008
STM1562	STM1562	putative periplasmic transport protein	**-0.40**	0.40595
STM1562	STM1562	putative periplasmic transport protein	**0.77**	0.13645
STM1563	osmC	putative envelope protein	**-0.36**	0.49986
STM1563	osmC	putative envelope protein	**-0.03**	0.96630
STM1564	yddX	putative cytoplasmic protein	**-0.76**	0.13645
STM1564	yddX	putative cytoplasmic protein	**0.35**	0.52101
STM1565	rpsV	30S ribosomal subunit protein S22	**0.06**	0.92478
STM1565	rpsV	30S ribosomal subunit protein S22	**0.72**	0.34070
STM1566	sfcA	NAD-linked malate dehydrogenase	**0.11**	0.80047
STM1566	sfcA	NAD-linked malate dehydrogenase	**0.96**	0.24568
STM1567	adhP	alcohol dehydrogenase	**-0.33**	0.36162
STM1567	adhP	alcohol dehydrogenase	**0.85**	0.13813
STM1568	fdnI	formate dehydrogenase-N gamma subunit	**-0.15**	0.68032
STM1568	fdnI	formate dehydrogenase-N gamma subunit	**0.91**	0.16281
STM1569	fdnH	formate dehydrogenase-N beta subunit	**-0.18**	0.80275
STM1569	fdnH	formate dehydrogenase-N beta subunit	**0.34**	0.36444
STM1570	fdnG	formate dehydorgenase-N alpha subunit	**0.33**	0.39315
STM1570	fdnG	formate dehydorgenase-N alpha subunit	**0.65**	0.31305
STM1571	yddG	putative permease	**0.25**	0.50801
STM1571	yddG	putative permease	**0.19**	0.68583
STM1572	nmpC	putative outer membrane porin precursor	**0.25**	0.58445
STM1572	nmpC	putative outer membrane porin precursor	**0.18**	0.67220
STM1573,Sc	STM1573,Sc	putative cytoplasmic protein	**-0.09**	0.91170
STM1573,Sc	STM1573,Sc	putative cytoplasmic protein	**0.31**	0.52777
STM1574	smvA	methyl viologen resistance	**-0.21**	0.58108
STM1574	smvA	methyl viologen resistance	**0.03**	0.96785
STM1575	STM1575	putative transcriptional regulator	**-0.19**	0.68450
STM1575	STM1575	putative transcriptional regulator	**0.00**	0.99698
STM1576	narU	nitrate extrusion protein	**-0.21**	0.65916
STM1576	narU	nitrate extrusion protein	**0.13**	0.79988
STM1577	narZ	nitrate reductase 2 alpha subunit	**-0.42**	0.34051
STM1577	narZ	nitrate reductase 2 alpha subunit	**0.93**	0.17431
STM1578	narY	nitrate reductase 2 beta subunit	**-0.35**	0.87655
STM1578	narY	nitrate reductase 2 beta subunit	**0.87**	0.62199
STM1579	narW	nitrate reductase 2 delta subunit	**0.10**	0.92529
STM1579	narW	nitrate reductase 2 delta subunit	**-0.02**	0.98090
STM1580	narV	nitrate reductase 2 gamma subunit	**0.05**	0.93083
STM1580	narV	nitrate reductase 2 gamma subunit	**1.19**	0.18763
STM1581	yddE	putative phenazine biosynthetic protein	**0.33**	0.46629
STM1581	yddE	putative phenazine biosynthetic protein	**0.57**	0.26535
STM1582	nhoA	putative arylamine N-acetyltransferase	**0.04**	0.93174
STM1582	nhoA	putative arylamine N-acetyltransferase	**0.42**	0.44768
STM1583	STM1583	putative cytoplasmic protein	**-0.04**	0.96785
STM1583	STM1583	putative cytoplasmic protein	**0.76**	0.51446
STM1584	ansP	L-asparagine transport protein	**-0.15**	0.81325

STM1584	ansP	L-asparagine transport protein	**-0.27**	0.47610
STM1585	STM1585	putative outer membrane lipoprotein	**-0.70**	0.16534
STM1585	STM1585	putative outer membrane lipoprotein	**0.37**	0.54332
STM1586	STM1586	putative periplasmic protein	**-0.12**	0.88568
STM1586	STM1586	putative periplasmic protein	**0.79**	0.11421
STM1587	yncD	putative outer membrane receptor	**-0.19**	0.66677
STM1587	yncD	putative outer membrane receptor	**-0.14**	0.77745
STM1588	yncC	putative regulatory protein	**-0.24**	0.48126
STM1588	yncC	putative regulatory protein	**0.32**	0.40819
STM1589	yncB	putative NADP-dependent oxidoreductase	**-0.35**	0.69914
STM1589	yncB	putative NADP-dependent oxidoreductase	**0.34**	0.54461
STM1590	yncA	putative acyltransferase	**-0.39**	0.41996
STM1590	yncA	putative acyltransferase	**0.03**	0.96251
STM1591	ydcZ	putative inner membrane protein	**-0.11**	0.80406
STM1591	ydcZ	putative inner membrane protein	**-0.21**	0.67551
STM1592	ydcY	putative cytoplasmic protein	**0.58**	0.58182
STM1592	ydcY	putative cytoplasmic protein	**1.39**	0.36243
STM1593	srfA	putative virulence protein	**-0.09**	0.86654
STM1593	srfA	putative virulence protein	**0.34**	0.40940
STM1594	srfB	putative virulence protein	**0.08**	0.84844
STM1594	srfB	putative virulence protein	**0.55**	0.24005
STM1595	srfC	putative virulence protein	**-0.29**	0.61201
STM1595	srfC	putative virulence protein	**0.28**	0.60548
STM1596	ydcX	putative inner membrane protein	**-0.15**	0.80038
STM1596	ydcX	putative inner membrane protein	**-0.14**	0.80093
STM1597	ydcW	putative aldehyde dehydrogenase	**-0.61**	0.19142
STM1597	ydcW	putative aldehyde dehydrogenase	**0.38**	0.40947
STM1598	ydcR	putative regulatory protein	**-0.56**	0.35955
STM1598	ydcR	putative regulatory protein	**0.01**	0.98718
STM1599	pdgL	periplasmic dipeptidase precursor	**-0.38**	0.53827
STM1599	pdgL	periplasmic dipeptidase precursor	**-0.12**	0.83918
STM1601	ugtL	hypothetical protein STM1601	**-0.14**	0.79180
STM1601	ugtL	hypothetical protein STM1601	**0.20**	0.83443
STM1602	sifB	secreted effector protein	**-0.98**	0.17041
STM1602	sifB	secreted effector protein	**-0.17**	0.79319
STM1603	yncJ	putative periplasmic protein	**-0.59**	0.26910
STM1603	yncJ	putative periplasmic protein	**-0.18**	0.63196
STM1604	ydcP	putative collagenase	**0.00**	0.99432
STM1604	ydcP	putative collagenase	**0.21**	0.72092
STM1605	ydcN	putative repressor	**-0.06**	0.89611
STM1605	ydcN	putative repressor	**0.32**	0.44402
STM1606	STM1606	putative benzoate membrane transport protein	**0.07**	0.87924
STM1606	STM1606	putative benzoate membrane transport protein	**0.08**	0.83718
STM1607	STM1607	putative outer membrane lipoprotein	**-0.77**	0.28406
STM1607	STM1607	putative outer membrane lipoprotein	**-0.08**	0.86385
STM1608	tehB	putative methyltransferase	**-0.15**	0.70417
STM1608	tehB	putative methyltransferase	**0.22**	0.64456
STM1609	tehA	K+-tellurite ethidium and proflavin transport protein	**-0.05**	0.91571
STM1609	tehA	K+-tellurite ethidium and proflavin transport protein	**0.40**	0.48429
STM1610	ydcK	putative nucleoside-diphosphate-sugar pyrophosphorylase	**-1.40**	0.11913
STM1610	ydcK	putative nucleoside-diphosphate-sugar pyrophosphorylase	**-0.28**	0.72001
STM1611	rimL	acetyl transferase	**0.10**	0.82159
STM1611	rimL	acetyl transferase	**0.31**	0.65974
STM1612	STM1612	putative cellulase protein	**-0.22**	0.74585
STM1612	STM1612	putative cellulase protein	**-0.32**	0.62757
STM1613	STM1613	putative PTS system enzymeIIB component	**-0.75**	0.18634
STM1613	STM1613	putative PTS system enzymeIIB component	**-0.60**	0.25360
STM1614	STM1614	putative PTS system enzyme IIC component	**-0.31**	0.48814
STM1614	STM1614	putative PTS system enzyme IIC component	**0.06**	0.93228
STM1615	STM1615	putative nucleoside triphosphatase	**-0.20**	0.64365
STM1615	STM1615	putative nucleoside triphosphatase	**-0.07**	0.93881

STM1616	STM1616	putative sugar-specific PTS enzyme II	**-0.08**	0.83718
STM1616	STM1616	putative sugar-specific PTS enzyme II	**0.48**	0.23631
STM1617	STM1617	ribulose-phosphate 3-epimerase	**0.75**	0.60453
STM1617	STM1617	ribulose-phosphate 3-epimerase	**0.95**	0.32481
STM1618	STM1618	putative transcriptional repressor of sgc operon	**-0.35**	0.57442
STM1618	STM1618	putative transcriptional repressor of sgc operon	**0.10**	0.90054
STM1619	STM1619	cryptic aminoglycoside resistance gene	**0.13**	0.88647
STM1619	STM1619	cryptic aminoglycoside resistance gene	**0.52**	0.31242
STM1620	STM1620	putative oxidase	**-1.02**	0.15859
STM1620	STM1620	putative oxidase	**-0.20**	0.83899
STM1621	STM1621	putative periplasmic protein	**-0.46**	0.45188
STM1621	STM1621	putative periplasmic protein	**0.20**	0.81806
STM1622	ydcG	putative MDO biosynthetic protein	**-0.18**	0.62312
STM1622	ydcG	putative MDO biosynthetic protein	**-0.18**	0.68240
STM1623	STM1623	putative carboxylesterase	**0.18**	0.61597
STM1623	STM1623	putative carboxylesterase	**0.27**	0.57233
STM1624	STM1624	putative cytoplasmic protein	**-0.37**	0.37161
STM1624	STM1624	putative cytoplasmic protein	**0.24**	0.65305
STM1625	ydcI	putative transcriptional regulator	**0.26**	0.52208
STM1625	ydcI	putative transcriptional regulator	**1.01**	0.09135
STM1626	trg	methyl-accepting chemotaxis protein III	**0.47**	0.38080
STM1626	trg	methyl-accepting chemotaxis protein III	**0.46**	0.28655
STM1627	STM1627	alcohol dehydrogenase class III	**0.10**	0.83832
STM1627	STM1627	alcohol dehydrogenase class III	**0.09**	0.90399
STM1628	STM1628	putative cytoplasmic protein	**0.11**	0.81667
STM1628	STM1628	putative cytoplasmic protein	**0.20**	0.66636
STM1630	STM1630	putative inner membrane protein	**0.01**	0.99452
STM1630	STM1630	putative inner membrane protein	**0.50**	0.61892
STM1631	sseJ	secreted effector protein	**0.32**	0.70474
STM1631	sseJ	secreted effector protein	**1.30**	0.31344
STM1632	STM1632	putative inner membrane protein	**-0.67**	0.20791
STM1632	STM1632	putative inner membrane protein	**0.14**	0.82644
STM1633	STM1633	putative periplasmic binding protein	**-0.50**	0.26261
STM1633	STM1633	putative periplasmic binding protein	**-0.07**	0.89730
STM1634	STM1634	putative ABC transporter permease component	**-0.18**	0.75552
STM1634	STM1634	putative ABC transporter permease component	**0.09**	0.86370
STM1635	STM1635	putative ABC-type polar amino acid transport system ATPase	**-0.01**	0.99381
STM1635	STM1635	putative ABC-type polar amino acid transport system ATPase	**0.58**	0.29871
STM1636	STM1636	putative ABC-type transport system membrane component	**-0.21**	0.68444
STM1636	STM1636	putative ABC-type transport system membrane component	**0.08**	0.91193
STM1637	STM1637	putative inner membrane protein	**-0.52**	0.33452
STM1637	STM1637	putative inner membrane protein	**0.19**	0.76610
STM1638	STM1638	putative SAM-dependent methyltransferase	**-0.08**	0.86199
STM1638	STM1638	putative SAM-dependent methyltransferase	**0.35**	0.45800
STM1639	cybB	cytochrome b561	**0.04**	0.93688
STM1639	cybB	cytochrome b561	**0.14**	0.72040
STM1640	ydcF	putative inner membrane protein	**0.00**	0.99822
STM1640	ydcF	putative inner membrane protein	**0.27**	0.46629
STM1641	hrpA	ATP-dependent helicase	**-0.26**	0.54625
STM1641	hrpA	ATP-dependent helicase	**0.14**	0.78929
STM1642	acpD	acyl carrier protein phosphodiesterase	**-0.03**	0.96559
STM1642	acpD	acyl carrier protein phosphodiesterase	**0.05**	0.92311
STM1643	STM1643	putative inner membrane protein	**-0.57**	0.17754
STM1643	STM1643	putative inner membrane protein	**-0.28**	0.57723
STM1644	ydbL	putative periplasmic protein	**-0.35**	0.39069
STM1644	ydbL	putative periplasmic protein	**0.89**	0.15078
STM1645	ynbE	putative outer membrane lipoprotein	**-0.28**	0.48814
STM1645	ynbE	putative outer membrane lipoprotein	**0.41**	0.34051
STM1646	ydbH	putative periplasmic protein	**0.23**	0.65945

STM1646	ydbH	putative periplasmic protein	**-0.19**	0.65305
STM1647	ldhA	D-lactate dehydrogenase	**0.27**	0.48300
STM1647	ldhA	D-lactate dehydrogenase	**0.54**	0.20881
STM1648	hslJ	heat shock protein hslJ	**-0.55**	0.41671
STM1648	hslJ	heat shock protein hslJ	**-0.09**	0.86172
STM1649	STM1649	putative cytoplasmic protein	**-0.13**	0.72781
STM1649	STM1649	putative cytoplasmic protein	**0.04**	0.94417
STM1651	nifJ	putative pyruvate-flavodoxin oxidoreductase	**-0.53**	0.26910
STM1651	nifJ	putative pyruvate-flavodoxin oxidoreductase	**0.21**	0.61895
STM1652	ynaF	putative universal stress protein	**0.26**	0.48062
STM1652	ynaF	putative universal stress protein	**0.37**	0.41626
STM1654	ydaO	putative ATPase	**-0.19**	0.66677
STM1654	ydaO	putative ATPase	**-0.28**	0.58117
STM1655	dbpA	ATP-dependent RNA helicase	**-0.60**	0.17109
STM1655	dbpA	ATP-dependent RNA helicase	**0.31**	0.51549
STM1656	STM1656	putative Zn transport protein	**-0.27**	0.60751
STM1656	STM1656	putative Zn transport protein	**0.25**	0.71690
STM1657	STM1657	putative methyl-accepting chemotaxis protein	**0.23**	0.62174
STM1657	STM1657	putative methyl-accepting chemotaxis protein	**0.28**	0.56337
STM1658	ydaL	hypothetical protein STM1658	**-0.41**	0.34021
STM1658	ydaL	hypothetical protein STM1658	**0.37**	0.45214
STM1659	ogt	O-6-alkylguanine-DNA/cysteine-protein methyltransferase	**-0.18**	0.78016
STM1659	ogt	O-6-alkylguanine-DNA/cysteine-protein methyltransferase	**0.24**	0.69816
STM1660,S	fnr	transcriptional regulator	**0.15**	0.70122
STM1660,S	fnr	transcriptional regulator	**0.52**	0.22421
STM1661	ydaA	putative universal stress protein	**0.42**	0.26261
STM1661	ydaA	putative universal stress protein	**0.08**	0.91387
STM1662	ynaJ	putative inner membrane protein	**0.09**	0.84187
STM1662	ynaJ	putative inner membrane protein	**0.22**	0.60014
STM1663	ynaI	putative integral membrane protein	**-0.18**	0.76502
STM1663	ynaI	putative integral membrane protein	**0.24**	0.59172
STM1664	STM1664	putative transcriptional regulator	**-1.10**	0.19398
STM1664	STM1664	putative transcriptional regulator	**-0.14**	0.87512
STM1665	STM1665	putative cytoplasmic protein	**-0.15**	0.76553
STM1665	STM1665	putative cytoplasmic protein	**0.35**	0.49871
STM1667	STM1667	putative thiol peroxidase	**-0.49**	0.44832
STM1667	STM1667	putative thiol peroxidase	**-0.20**	0.76008
STM1668	STM1668	hypothetical protein STM1668	**-0.32**	0.52897
STM1668	STM1668	hypothetical protein STM1668	**-0.01**	0.99080
STM1669	STM1669	invasin-like protein	**-0.35**	0.37619
STM1669	STM1669	invasin-like protein	**0.82**	0.29453
STM1670	STM1670	putative lipoprotein	**-0.54**	0.36465
STM1670	STM1670	putative lipoprotein	**0.17**	0.76378
STM1671	STM1671	putative regulatory protein	**-0.22**	0.68450
STM1671	STM1671	putative regulatory protein	**0.29**	0.54735
STM1673	STM1673	putative outer membrane lipoprotein	**-0.01**	0.98445
STM1673	STM1673	putative outer membrane lipoprotein	**0.14**	0.74721
STM1674	STM1674	putative regulatory protein	**-0.09**	0.86861
STM1674	STM1674	putative regulatory protein	**0.86**	0.36942
STM1675	STM1675	oxidoreductase	**-0.12**	0.76312
STM1675	STM1675	oxidoreductase	**0.81**	0.21855
STM1676	STM1676	putative aldo/keto reductase	**0.06**	0.93638
STM1676	STM1676	putative aldo/keto reductase	**0.51**	0.42935
STM1677	STM1677	putative transcriptional regulator	**-0.14**	0.83279
STM1677	STM1677	putative transcriptional regulator	**0.42**	0.39770
STM1678	STM1678	putative 2'-hydroxyisoflavone reductase	**-0.78**	0.15053
STM1678	STM1678	putative 2'-hydroxyisoflavone reductase	**0.01**	0.97646
STM1679	mppA	periplasmic murein tripeptide transport protein	**-0.07**	0.87512
STM1679	mppA	periplasmic murein tripeptide transport protein	**-0.17**	0.76810
STM1680	ycjI	putative carboxypeptidase	**-0.50**	0.21747
STM1680	ycjI	putative carboxypeptidase	**-0.19**	0.70082

STM1681	ycjG	putative chloromuconate cycloisomerase	**-0.20**	0.69094
STM1681	ycjG	putative chloromuconate cycloisomerase	**-0.02**	0.97348
STM1682	tpx	thiol peroxidase	**0.05**	0.92387
STM1682	tpx	thiol peroxidase	**-0.11**	0.82443
STM1683	tyrR	transcriptional regulator	**-0.30**	0.46859
STM1683	tyrR	transcriptional regulator	**-0.18**	0.69398
STM1684	ycjF	hypothetical protein STM1684	**-0.24**	0.48818
STM1684	ycjF	hypothetical protein STM1684	**-0.26**	0.70137
STM1685	ycjX	putative ATPase	**-0.27**	0.53812
STM1685	ycjX	putative ATPase	**-0.21**	0.58095
STM1686	pspE	phage shock protein	**-0.22**	0.72521
STM1686	pspE	phage shock protein	**-0.10**	0.82313
STM1687	pspD	phage shock protein	**-0.47**	0.32181
STM1687	pspD	phage shock protein	**0.04**	0.96164
STM1688	pspC	phage shock protein	**-0.11**	0.79356
STM1688	pspC	phage shock protein	**-0.04**	0.93772
STM1689	pspB	phage shock protein B	**-0.59**	0.18918
STM1689	pspB	phage shock protein B	**0.44**	0.33093
STM1690	pspA	phage shock protein	**-0.13**	0.78641
STM1690	pspA	phage shock protein	**0.24**	0.65025
STM1691	pspF	transcription activator	**-0.24**	0.66677
STM1691	pspF	transcription activator	**0.32**	0.41134
STM1692	sapA	peptide transport protein	**-0.64**	0.24005
STM1692	sapA	peptide transport protein	**0.04**	0.96205
STM1693	sapB	peptide transport protein	**-0.29**	0.56860
STM1693	sapB	peptide transport protein	**-0.09**	0.87126
STM1694	sapC	peptide transport protein	**0.24**	0.55397
STM1694	sapC	peptide transport protein	**0.14**	0.72083
STM1695	sapD	peptide transport protein	**-0.02**	0.98226
STM1695	sapD	peptide transport protein	**0.17**	0.68450
STM1696	sapF	peptide transport protein	**-0.47**	0.22285
STM1696	sapF	peptide transport protein	**-0.11**	0.85745
STM1697	STM1697	hypothetical protein STM1697	**-0.34**	0.39520
STM1697	STM1697	hypothetical protein STM1697	**0.00**	0.99938
STM1698	STM1698	putative inner membrane protein	**-0.72**	0.15859
STM1698	STM1698	putative inner membrane protein	**-0.19**	0.77025
STM1700	fabI	enoyl-(acyl carrier protein) reductase	**-0.42**	0.27681
STM1700	fabI	enoyl-(acyl carrier protein) reductase	**-0.07**	0.88902
STM1701	yciW	putative cytoplasmic protein	**0.01**	0.99274
STM1701	yciW	putative cytoplasmic protein	**-0.09**	0.86017
STM1702	rnb	exoribonuclease II	**-0.26**	0.46674
STM1702	rnb	exoribonuclease II	**0.19**	0.63688
STM1703	yciR	putative diguanylate cyclase/phosphodiesterase	**-0.72**	0.13112
STM1703	yciR	putative diguanylate cyclase/phosphodiesterase	**-0.01**	0.98519
STM1704	yciT	putative regulatory protein	**-0.53**	0.26820
STM1704	yciT	putative regulatory protein	**0.18**	0.65355
STM1705	osmB	lipoprotein B	**-0.32**	0.48808
STM1705	osmB	lipoprotein B	**0.32**	0.41286
STM1706	yciH	hypothetical protein STM1706	**-0.60**	0.20916
STM1706	yciH	hypothetical protein STM1706	**0.09**	0.91047
STM1707	pyrF	orotidine 5'-phosphate decarboxylase	**-0.43**	0.35937
STM1707	pyrF	orotidine 5'-phosphate decarboxylase	**-0.12**	0.84673
STM1708	yciM	putative N-acetylglucosaminyl transferase	**-0.12**	0.83443
STM1708	yciM	putative N-acetylglucosaminyl transferase	**-0.34**	0.34193
STM1709	yciS	putative inner membrane protein	**0.04**	0.93174
STM1709	yciS	putative inner membrane protein	**-0.04**	0.93023
STM1710	pgpB	phosphatidylglycerophosphate phosphatase B	**-0.44**	0.30106
STM1710	pgpB	phosphatidylglycerophosphate phosphatase B	**0.06**	0.89004
STM1711	ribA	GTP cyclohydrolase II protein	**-0.05**	0.91790
STM1711	ribA	GTP cyclohydrolase II protein	**-0.18**	0.62988
STM1712	acnA	aconitate hydratase	**-0.30**	0.55338
STM1712	acnA	aconitate hydratase	**0.41**	0.30560
STM1713	cysB	transcriptional regulator for cysteine regulon	**0.06**	0.95781

STM1713	cysB	transcriptional regulator for cysteine regulon	**0.16**	0.70417
STM1714	topA	DNA topoisomerase I	**-0.33**	0.61809
STM1714	topA	DNA topoisomerase I	**0.37**	0.42591
STM1715	yciN	putative cytoplasmic protein	**0.12**	0.89108
STM1715	yciN	putative cytoplasmic protein	**0.35**	0.41676
STM1716	sohB	putative peptidase	**-0.24**	0.59441
STM1716	sohB	putative peptidase	**-0.13**	0.80614
STM1717	yciK	short chain dehydrogenase	**-0.04**	0.94417
STM1717	yciK	short chain dehydrogenase	**0.20**	0.66743
STM1718	btuR	cob(I)yrinic acid a,c-diamide adenosyltransferase	**0.07**	0.85718
STM1718	btuR	cob(I)yrinic acid a,c-diamide adenosyltransferase	**0.21**	0.61614
STM1719	yciL	putative ribosomal large subunit pseudouridine synthase	**-0.12**	0.81284
STM1719	yciL	putative ribosomal large subunit pseudouridine synthase	**0.47**	0.22391
STM1720	yciO	putative dsRNA-binding protein	**-0.08**	0.89468
STM1720	yciO	putative dsRNA-binding protein	**-0.10**	0.86947
STM1721	trpH	hypothetical protein STM1721	**0.09**	0.84456
STM1721	trpH	hypothetical protein STM1721	**0.27**	0.60453
STM1723	trpE	anthranilate synthase component I	**0.09**	0.88561
STM1723	trpE	anthranilate synthase component I	**0.20**	0.67456
STM1724	trpD	anthranilate phosphoribosyltransferase	**-0.61**	0.38552
STM1724	trpD	anthranilate phosphoribosyltransferase	**-0.05**	0.93563
STM1725	trpC	bifunctional indole-3-glycerol phosphate	**-0.24**	0.63475
STM1725	trpC	bifunctional indole-3-glycerol phosphate	**0.09**	0.82464
STM1726	trpB	tryptophan synthase subunit beta	**-0.14**	0.83443
STM1726	trpB	tryptophan synthase subunit beta	**0.33**	0.48814
STM1727	trpA	tryptophan synthase subunit alpha	**-0.37**	0.46629
STM1727	trpA	tryptophan synthase subunit alpha	**0.53**	0.34051
STM1728	yciG	putative cytoplasmic protein	**-0.36**	0.51127
STM1728	yciG	putative cytoplasmic protein	**-0.04**	0.96568
STM1729	yciF	putative cytoplasmic protein	**-0.04**	0.97117
STM1729	yciF	putative cytoplasmic protein	**0.75**	0.34201
STM1730	yciE	putative cytoplasmic protein	**-0.31**	0.68649
STM1730	yciE	putative cytoplasmic protein	**-0.28**	0.74528
STM1731	STM1731	putative catalase	**0.04**	0.94617
STM1731	STM1731	putative catalase	**1.03**	0.22421
STM1732	ompW	outer membrane protein W precursor	**-0.34**	0.39260
STM1732	ompW	outer membrane protein W precursor	**0.30**	0.59543
STM1733	STM1733	putative ferredoxin	**-0.02**	0.96785
STM1733	STM1733	putative ferredoxin	**-0.05**	0.92809
STM1734	yciC	hypothetical protein STM1734	**-0.23**	0.54618
STM1734	yciC	hypothetical protein STM1734	**-0.12**	0.76240
STM1735	yciB	putative intracellular septation protein	**0.08**	0.84522
STM1735	yciB	putative intracellular septation protein	**0.41**	0.39151
STM1736	yciA	putative Acyl-CoA hydrolase	**0.05**	0.93767
STM1736	yciA	putative Acyl-CoA hydrolase	**0.31**	0.45438
STM1737	tonB	periplasmic protein	**-0.10**	0.83042
STM1737	tonB	periplasmic protein	**0.56**	0.24515
STM1738	yciI	putative cytoplasmic protein	**-0.20**	0.62617
STM1738	yciI	putative cytoplasmic protein	**0.10**	0.83443
STM1739	cls	cardiolipin synthetase	**-0.15**	0.70229
STM1739	cls	cardiolipin synthetase	**0.16**	0.69234
STM1741	STM1741	putative voltage-gated potassium channel	**0.03**	0.95980
STM1741	STM1741	putative voltage-gated potassium channel	**0.69**	0.22421
STM1742	oppF	oligopeptide transport protein	**-0.10**	0.83855
STM1742	oppF	oligopeptide transport protein	**0.16**	0.73473
STM1743	oppD	oligopeptide transporter ATP-binding component	**0.06**	0.89675
STM1743	oppD	oligopeptide transporter ATP-binding component	**0.36**	0.45797
STM1744	oppC	oligopeptide transport protein	**0.43**	0.43816
STM1744	oppC	oligopeptide transport protein	**0.01**	0.99310
STM1745	oppB	oligopeptide permease ABC transporter membrane component	**-0.87**	0.19843
STM1745	oppB	oligopeptide permease ABC transporter membrane component	**-0.12**	0.88337

STM1746,S	oppA	oligopeptide transport protein	**0.09**	0.84179
STM1746,S	oppA	oligopeptide transport protein	**0.19**	0.63859
STM1748	ychE	putative integral membrane protein	**0.06**	0.92418
STM1748	ychE	putative integral membrane protein	**0.27**	0.61285
STM1749	adhE	iron-dependent alcohol dehydrogenase	**-0.12**	0.81667
STM1749	adhE	iron-dependent alcohol dehydrogenase	**0.22**	0.53459
STM1750	tdk	thymidine kinase	**0.15**	0.70144
STM1750	tdk	thymidine kinase	**0.10**	0.89534
STM1751	hns	DNA-binding protein HLP-II	**-0.09**	0.86190
STM1751	hns	DNA-binding protein HLP-II	**0.07**	0.93506
STM1752	galU	glucose-1-phosphate uridylyltransferase	**-0.17**	0.69787
STM1752	galU	glucose-1-phosphate uridylyltransferase	**0.23**	0.52208
STM1753	hnr	response regulator	**0.29**	0.64645
STM1753	hnr	response regulator	**1.08**	0.22283
STM1754	ychK	putative phosphoesterase	**-0.03**	0.95497
STM1754	ychK	putative phosphoesterase	**-0.07**	0.87208
STM1755	ychJ	hypothetical protein STM1755	**-0.06**	0.91193
STM1755	ychJ	hypothetical protein STM1755	**0.38**	0.29943
STM1756	purU	formyltetrahydrofolate deformylase	**-0.17**	0.68474
STM1756	purU	formyltetrahydrofolate deformylase	**0.25**	0.60424
STM1758	rtT	STM1758	**-0.40**	0.26975
STM1758	rtT	STM1758	**-0.19**	0.65983
STM1759	tyrV	STM1759	**0.17**	0.84182
STM1759	tyrV	STM1759	**-0.35**	0.54917
STM1759	tyrV	STM1759	**0.18**	0.71978
STM1759	tyrV	STM1759	**0.50**	0.28970
STM1760	STM1760	tetratricopeptide repeat protein	**-0.37**	0.40096
STM1760	STM1760	tetratricopeptide repeat protein	**-0.23**	0.54029
STM1761	narI	nitrate reductase 1 gamma subunit	**-0.17**	0.64432
STM1761	narI	nitrate reductase 1 gamma subunit	**0.23**	0.63592
STM1762	narJ	nitrate reductase 1 delta subunit	**0.41**	0.48300
STM1762	narJ	nitrate reductase 1 delta subunit	**0.96**	0.11224
STM1763	narH	nitrate reductase 1 beta subunit	**-1.03**	0.17754
STM1763	narH	nitrate reductase 1 beta subunit	**-0.14**	0.75424
STM1764	narG	nitrate reductase 1 alpha subunit	**-0.84**	0.37336
STM1764	narG	nitrate reductase 1 alpha subunit	**-0.64**	0.21026
STM1765	narK	nitrite extrusion protein	**-0.33**	0.65810
STM1765	narK	nitrite extrusion protein	**0.17**	0.82443
STM1766	narX	sensory histidine kinase	**-0.62**	0.22283
STM1766	narX	sensory histidine kinase	**-0.35**	0.46088
STM1767	narL	response regulator	**-0.81**	0.35779
STM1767	narL	response regulator	**-0.18**	0.79018
STM1768	ychP	putative invasin	**-0.33**	0.61248
STM1768	ychP	putative invasin	**-0.06**	0.89336
STM1769	ychN	putative sulfur reduction protein	**-0.49**	0.44442
STM1769	ychN	putative sulfur reduction protein	**0.10**	0.82506
STM1770	chaB	cation transport regulator	**-0.17**	0.73713
STM1770	chaB	cation transport regulator	**0.07**	0.92021
STM1771	chaA	sodium-calcium/proton antiporter	**-0.16**	0.72781
STM1771	chaA	sodium-calcium/proton antiporter	**0.04**	0.93916
STM1772	kdsA	2-dehydro-3-deoxyphosphooctonate aldolase	**-0.43**	0.39315
STM1772	kdsA	2-dehydro-3-deoxyphosphooctonate aldolase	**-0.21**	0.65730
STM1773	ychA	putative transcriptional regulator	**-0.06**	0.89529
STM1773	ychA	putative transcriptional regulator	**-0.17**	0.65451
STM1774	sirC	transcriptional regulator	**0.00**	0.99316
STM1774	sirC	transcriptional regulator	**-0.08**	0.89878
STM1775	hemK	N5-glutamine S-adenosyl-L-methionine-dependent methyltransferase	**-0.22**	0.52351
STM1775	hemK	N5-glutamine S-adenosyl-L-methionine-dependent methyltransferase	**-0.05**	0.92685
STM1776	prfA	peptide chain release factor 1	**-0.04**	0.93011
STM1776	prfA	peptide chain release factor 1	**-0.02**	0.98348
STM1777	hemA	glutamyl-tRNA reductase	**-0.34**	0.37610

STM1777	hemA	glutamyl-tRNA reductase	**-0.25**	0.65502
STM1778	lolB	outer membrane lipoprotein LolB precursor	**0.10**	0.82664
STM1778	lolB	outer membrane lipoprotein LolB precursor	**0.27**	0.54094
STM1779	ipk	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase	**0.28**	0.45188
STM1779	ipk	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase	**0.28**	0.47610
STM1780	prsA	ribose-phosphate pyrophosphokinase	**-0.06**	0.90671
STM1780	prsA	ribose-phosphate pyrophosphokinase	**0.09**	0.84187
STM1781	ychM	putative transport protein	**-0.33**	0.47804
STM1781	ychM	putative transport protein	**0.24**	0.61960
STM1782	ychH	putative inner membrane protein	**-0.63**	0.17139
STM1782	ychH	putative inner membrane protein	**0.37**	0.54227
STM1783,S	pth	peptidyl-tRNA hydrolase	**-0.48**	0.21318
STM1783,S	pth	peptidyl-tRNA hydrolase	**0.06**	0.89979
STM1784	ychF	putative GTP-binding protein	**-0.25**	0.49870
STM1784	ychF	putative GTP-binding protein	**0.47**	0.27067
STM1785	STM1785	putative cytoplasmic protein	**-0.16**	0.71822
STM1785	STM1785	putative cytoplasmic protein	**0.10**	0.81667
STM1786	STM1786	hydrogenase-1 small subunit	**-0.06**	0.89979
STM1786	STM1786	hydrogenase-1 small subunit	**0.97**	0.12727
STM1787	STM1787	hydrogenase-1 large subunit	**0.89**	0.23495
STM1787	STM1787	hydrogenase-1 large subunit	**1.36**	0.18140
STM1788	STM1788	putative Ni/Fe hydrogenase 1 b-type cytochrome subunit	**-0.24**	0.56759
STM1788	STM1788	putative Ni/Fe hydrogenase 1 b-type cytochrome subunit	**0.49**	0.54347
STM1789	STM1789	putative hydrogenase maturation protease	**-0.51**	0.30652
STM1789	STM1789	putative hydrogenase maturation protease	**0.25**	0.82613
STM1790	STM1790	putative chaperone	**0.02**	0.98539
STM1790	STM1790	putative chaperone	**0.34**	0.50190
STM1791	STM1791	putative hydrogenase-1 protein	**-0.08**	0.85157
STM1791	STM1791	putative hydrogenase-1 protein	**0.58**	0.26856
STM1792	STM1792	putative cytochrome oxidase subunit I	**0.13**	0.78286
STM1792	STM1792	putative cytochrome oxidase subunit I	**0.10**	0.87016
STM1793	STM1793	putative cytochrome oxidase subunit II	**0.89**	0.12468
STM1793	STM1793	putative cytochrome oxidase subunit II	**0.88**	0.41969
STM1795	STM1795	putative glutamic dehyrogenase-like protein	**0.14**	0.76043
STM1795	STM1795	putative glutamic dehyrogenase-like protein	**0.73**	0.17481
STM1796	treA	trehalase	**-0.50**	0.40020
STM1796	treA	trehalase	**0.19**	0.63101
STM1797	ymgE	putative transglycosylase-associated protein	**-0.20**	0.69398
STM1797	ymgE	putative transglycosylase-associated protein	**0.07**	0.91359
STM1798	ycgR	putative inner membrane protein	**-0.36**	0.37331
STM1798	ycgR	putative inner membrane protein	**-0.01**	0.98615
STM1799	emtA	membrane-bound lytic murein transglycosylase E	**-0.06**	0.89979
STM1799	emtA	membrane-bound lytic murein transglycosylase E	**-0.08**	0.87131
STM1800	ycgQ	putative microcin C7 resistance protein	**-0.17**	0.76492
STM1800	ycgQ	putative microcin C7 resistance protein	**-0.01**	0.98855
STM1801	ycgO	cell volume regulation protein CvrA	**-0.73**	0.19870
STM1801	ycgO	cell volume regulation protein CvrA	**0.19**	0.75503
STM1802	alr	alanine racemase	**0.12**	0.76483
STM1802	alr	alanine racemase	**0.35**	0.63148
STM1803	dadA	D-amino acid dehydrogenase small subunit	**-0.16**	0.73546
STM1803	dadA	D-amino acid dehydrogenase small subunit	**0.66**	0.33840
STM1804,S	ycgB	putative cytoplasmic protein	**-0.44**	0.26213
STM1804,S	ycgB	putative cytoplasmic protein	**0.15**	0.73157
STM1805	fadR	fatty acid metabolism regulator	**-0.91**	0.16281
STM1805	fadR	fatty acid metabolism regulator	**0.03**	0.96630
STM1806	nhaB	Na+/H+ antiporter	**-0.40**	0.46970
STM1806	nhaB	Na+/H+ antiporter	**-0.08**	0.87837
STM1807	dsbB	disulfide bond formation protein B	**-0.45**	0.31344
STM1807	dsbB	disulfide bond formation protein B	**-0.06**	0.89542
STM1808	STM1808	putative cytoplasmic protein	**-0.18**	0.63493
STM1808	STM1808	putative cytoplasmic protein	**0.37**	0.51274
STM1810	STM1810	putative cytoplasmic protein	**-0.43**	0.35395
STM1810	STM1810	putative cytoplasmic protein	**-0.02**	0.97090

STM1811	ycgN	hypothetical protein STM1811	**-0.22**	0.61690
STM1811	ycgN	hypothetical protein STM1811	**0.14**	0.76538
STM1812	ycgM	putative fumarylacetoacetate hydrolase	**-0.52**	0.35564
STM1812	ycgM	putative fumarylacetoacetate hydrolase	**-0.16**	0.72518
STM1813	ycgL	putative cytoplasmic protein	**0.00**	0.99770
STM1813	ycgL	putative cytoplasmic protein	**0.25**	0.51033
STM1814	minC	septum formation inhibitor	**0.04**	0.93485
STM1814	minC	septum formation inhibitor	**0.05**	0.91047
STM1815	minD	cell division inhibitor protein	**-0.35**	0.34070
STM1815	minD	cell division inhibitor protein	**0.04**	0.92021
STM1816	minE	cell division topological specificity factor MinE	**0.01**	0.97742
STM1816	minE	cell division topological specificity factor MinE	**0.49**	0.25845
STM1817	rnd	RNase D	**0.17**	0.78822
STM1817	rnd	RNase D	**0.56**	0.27681
STM1818	fadD	acyl-CoA synthase	**-0.35**	0.42591
STM1818	fadD	acyl-CoA synthase	**0.08**	0.86654
STM1819	slp	putative outer membrane protein	**-0.11**	0.82518
STM1819	slp	putative outer membrane protein	**-0.10**	0.81994
STM1820	yeaZ	putative molecular chaperone	**-0.08**	0.86133
STM1820	yeaZ	putative molecular chaperone	**0.41**	0.32181
STM1821	yoaA	putative DNA helicase	**-0.12**	0.80406
STM1821	yoaA	putative DNA helicase	**-0.22**	0.67473
STM1822	yoaB	putative translation initiation inhibitor	**-0.17**	0.76883
STM1822	yoaB	putative translation initiation inhibitor	**-0.18**	0.69738
STM1823	yoaH	hypothetical protein STM1823	**-0.29**	0.52021
STM1823	yoaH	hypothetical protein STM1823	**0.26**	0.58164
STM1824	pabB	para-aminobenzoate synthase component I	**-0.35**	0.51545
STM1824	pabB	para-aminobenzoate synthase component I	**-0.28**	0.53173
STM1825	yeaB	putative NTP pyrophosphohydrolase	**0.25**	0.52799
STM1825	yeaB	putative NTP pyrophosphohydrolase	**0.47**	0.27996
STM1826	sdaA	L-serine deaminase I/L-threonine deaminase I	**-0.28**	0.57345
STM1826	sdaA	L-serine deaminase I/L-threonine deaminase I	**-0.04**	0.95747
STM1827,S	STM1827,S	putative diguanylate cyclase/phosphodiesterase	**0.11**	0.87359
STM1827,S	STM1827,S	putative diguanylate cyclase/phosphodiesterase	**0.66**	0.20285
STM1828	yoaE	putative inner membrane protein	**0.27**	0.67351
STM1828	yoaE	putative inner membrane protein	**0.62**	0.26365
STM1830	manX	mannose-specific enzyme IIAB	**0.12**	0.90797
STM1830	manX	mannose-specific enzyme IIAB	**0.87**	0.17139
STM1831	manY	mannose-specific enzyme IIC	**0.39**	0.59544
STM1831	manY	mannose-specific enzyme IIC	**0.54**	0.30715
STM1832	manZ	mannose-specific enzyme IID	**0.19**	0.65974
STM1832	manZ	mannose-specific enzyme IID	**0.30**	0.44344
STM1833	STM1833	hypothetical protein STM1833	**-0.12**	0.82350
STM1833	STM1833	hypothetical protein STM1833	**0.82**	0.13027
STM1834	yebN	putative transport protein	**-0.46**	0.25460
STM1834	yebN	putative transport protein	**-0.25**	0.55787
STM1835	rrmA	23S rRNA m1G745 methyltransferase	**-0.03**	0.96423
STM1835	rrmA	23S rRNA m1G745 methyltransferase	**0.26**	0.53124
STM1836	STM1836	putative penicillin-binding protein 3	**-0.17**	0.73448
STM1836	STM1836	putative penicillin-binding protein 3	**1.39**	0.22602
STM1837	cspC	cold shock protein	**-0.37**	0.62970
STM1837	cspC	cold shock protein	**-0.36**	0.60249
STM1839	STM1839	hypothetical protein STM1839	**-0.70**	0.46915
STM1839	STM1839	hypothetical protein STM1839	**-0.78**	0.11224
STM1840	yobG	putative inner membrane protein	**-1.26**	0.03091
STM1840	yobG	putative inner membrane protein	**-1.15**	0.07318
STM1841	STM1841	hypothetical protein STM1841	**-0.05**	0.92506
STM1841	STM1841	hypothetical protein STM1841	**0.01**	0.99268
STM1842	kdgR	putative transcriptional repressor	**0.02**	0.97001
STM1842	kdgR	putative transcriptional repressor	**0.05**	0.93688
STM1843	STM1843	putative transport protein	**-0.04**	0.94016
STM1843	STM1843	putative transport protein	**-0.03**	0.95980
STM1844	htpX	heat shock protein HtpX	**-0.42**	0.24313

STM1844	htpX	heat shock protein HtpX	**0.39**	0.32967
STM1845	prc	carboxy-terminal protease	**-0.51**	0.24568
STM1845	prc	carboxy-terminal protease	**0.70**	0.19967
STM1846	proQ	putative solute/DNA competence effector	**0.15**	0.70966
STM1846	proQ	putative solute/DNA competence effector	**0.43**	0.29044
STM1847	yebR	putative nucleotide-binding protein	**-0.11**	0.77186
STM1847	yebR	putative nucleotide-binding protein	**-0.13**	0.73781
STM1848	yebS	putative inner membrane protein	**0.18**	0.67448
STM1848	yebS	putative inner membrane protein	**0.31**	0.56786
STM1849	STM1849	putative inner membrane protein	**-0.35**	0.38351
STM1849	STM1849	putative inner membrane protein	**0.09**	0.83655
STM1850	yebU	putative rRNA methyltransferase	**-0.08**	0.83191
STM1850	yebU	putative rRNA methyltransferase	**-0.14**	0.76540
STM1851	STM1851	putative cytoplasmic protein	**-0.56**	0.25454
STM1851	STM1851	putative cytoplasmic protein	**-0.24**	0.64367
STM1852	yebW	putative inner membrane lipoprotein	**-0.02**	0.97602
STM1852	yebW	putative inner membrane lipoprotein	**-0.10**	0.86207
STM1853	prpA	serine/threonine protein phosphatase	**-0.46**	0.38394
STM1853	prpA	serine/threonine protein phosphatase	**0.55**	0.61375
STM1854	STM1854	putative inner membrane protein	**-0.25**	0.65271
STM1854	STM1854	putative inner membrane protein	**0.07**	0.87096
STM1855	sopE2	type III-secreted effector protein	**0.04**	0.94329
STM1855	sopE2	type III-secreted effector protein	**0.37**	0.36942
STM1856	STM1856	putative cytoplasmic protein	**0.53**	0.22602
STM1856	STM1856	putative cytoplasmic protein	**0.34**	0.51381
STM1856,1N	STM1856,1N	hypothetical protein STM1856,1N	**-0.24**	0.64909
STM1856,1N	STM1856,1N	hypothetical protein STM1856,1N	**0.79**	0.24818
STM1857	STM1857	putative acetyltransferase	**0.20**	0.71606
STM1857	STM1857	putative acetyltransferase	**0.49**	0.24973
STM1862	pagO	integral membrane protein	**-0.26**	0.52364
STM1862	pagO	integral membrane protein	**0.12**	0.81737
STM1863	STM1863	putative inner membrane protein	**-0.54**	0.35824
STM1863	STM1863	putative inner membrane protein	**0.39**	0.64175
STM1864	STM1864	putative inner membrane protein	**-0.10**	0.91170
STM1864	STM1864	putative inner membrane protein	**0.06**	0.90513
STM1868	mig-3	phage-tail assembly-like protein	**-0.63**	0.17754
STM1868	mig-3	phage-tail assembly-like protein	**-0.28**	0.46199
STM1868,1N	STM1868,1N	hypothetical protein STM1868,1N	**-0.64**	0.23123
STM1868,1N	STM1868,1N	hypothetical protein STM1868,1N	**0.41**	0.33587
STM1868A	STM1868A	lytic enzyme	**-0.27**	0.62617
STM1868A	STM1868A	lytic enzyme	**0.50**	0.46169
STM1869	STM1869	phage-tail assembly-like protein	**-0.15**	0.81270
STM1869	STM1869	phage-tail assembly-like protein	**0.61**	0.46760
STM1870	STM1870	RecE-like protein	**-0.46**	0.49870
STM1870	STM1870	RecE-like protein	**0.13**	0.76538
STM1873	STM1873	hypothetical protein STM1873	**-0.44**	0.49299
STM1873	STM1873	hypothetical protein STM1873	**0.09**	0.86968
STM1874	STM1874	putative inner membrane protein	**0.15**	0.73846
STM1874	STM1874	putative inner membrane protein	**0.51**	0.36311
STM1875	yobA	putative copper resistance protein	**0.09**	0.89003
STM1875	yobA	putative copper resistance protein	**0.34**	0.54946
STM1876	holE	DNA polymerase III theta subunit	**-0.01**	0.98566
STM1876	holE	DNA polymerase III theta subunit	**0.00**	0.99822
STM1877	STM1877	putative amidohydrolase	**0.23**	0.72040
STM1877	STM1877	putative amidohydrolase	**0.69**	0.43982
STM1878	exoX	exodeoxyribonuclease X	**-0.13**	0.74142
STM1878	exoX	exodeoxyribonuclease X	**0.45**	0.26910
STM1879	ptrB	protease II	**-0.30**	0.55978
STM1879	ptrB	protease II	**0.19**	0.71169
STM1880	yebE	putative inner membrane protein	**-0.81**	0.14285
STM1880	yebE	putative inner membrane protein	**-0.11**	0.89542
STM1881	yebF	putative periplasmic protein	**-0.03**	0.94472
STM1881	yebF	putative periplasmic protein	**0.86**	0.17358

STM1882	yebG	DNA damage-inducible protein	**-0.16**	0.64590
STM1882	yebG	DNA damage-inducible protein	**0.42**	0.48062
STM1883	purT	5'-phosphoribosylglycinamide transformylase	**-0.22**	0.77346
STM1883	purT	5'-phosphoribosylglycinamide transformylase	**0.76**	0.39243
STM1884	eda	keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate aldolase	**-0.26**	0.58216
STM1884	eda	keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate aldolase	**0.08**	0.83443
STM1885	edd	phosphogluconate dehydratase	**-0.21**	0.64163
STM1885	edd	phosphogluconate dehydratase	**0.03**	0.96107
STM1886	zwf	glucose-6-phosphate 1-dehydrogenase	**0.24**	0.48447
STM1886	zwf	glucose-6-phosphate 1-dehydrogenase	**0.59**	0.34148
STM1887	yebK	putative transcriptional regulator	**-0.07**	0.92008
STM1887	yebK	putative transcriptional regulator	**0.59**	0.18426
STM1888	pykA	pyruvate kinase	**-0.07**	0.87518
STM1888	pykA	pyruvate kinase	**0.26**	0.45824
STM1889	msbB	lipid A biosynthesis lauroyl acyltransferase	**-0.39**	0.42940
STM1889	msbB	lipid A biosynthesis lauroyl acyltransferase	**-0.37**	0.34051
STM1890	yebA	putative peptidase	**-0.08**	0.90136
STM1890	yebA	putative peptidase	**0.08**	0.89487
STM1891	znuA	high-affinity Zn transport protein	**-0.03**	0.95747
STM1891	znuA	high-affinity Zn transport protein	**0.27**	0.54656
STM1892,S	znuC	high-affinity Zn transport protein	**-0.27**	0.61285
STM1892,S	znuC	high-affinity Zn transport protein	**0.13**	0.75437
STM1893	znuB	high-affinity Zn transport protein	**0.15**	0.83084
STM1893	znuB	high-affinity Zn transport protein	**0.04**	0.96238
STM1894	ruvB	Holliday junction DNA helicase RuvB	**-0.30**	0.50825
STM1894	ruvB	Holliday junction DNA helicase RuvB	**0.13**	0.77677
STM1895	ruvA	Holliday junction DNA helicase motor protein	**0.00**	0.99512
STM1895	ruvA	Holliday junction DNA helicase motor protein	**0.18**	0.82285
STM1896	STM1896	putative cytoplasmic protein	**0.55**	0.35466
STM1896	STM1896	putative cytoplasmic protein	**1.31**	0.20749
STM1897	yebB	putative periplasmic protein	**-0.20**	0.64730
STM1897	yebB	putative periplasmic protein	**-0.22**	0.61532
STM1898	ruvC	Holliday junction resolvase	**-0.35**	0.44812
STM1898	ruvC	Holliday junction resolvase	**-0.30**	0.41785
STM1899	yebC	hypothetical protein STM1899	**-0.52**	0.32204
STM1899	yebC	hypothetical protein STM1899	**-0.26**	0.53741
STM1900	ntpA	dATP pyrophosphohydrolase	**-0.02**	0.96568
STM1900	ntpA	dATP pyrophosphohydrolase	**-0.08**	0.83443
STM1901	aspS	aspartyl-tRNA synthetase	**-0.59**	0.26833
STM1901	aspS	aspartyl-tRNA synthetase	**-0.46**	0.28861
STM1902	yecD	putative isochorismatase	**-0.14**	0.79246
STM1902	yecD	putative isochorismatase	**0.22**	0.59820
STM1903	yecE	putative cytoplasmic protein	**-0.03**	0.95532
STM1903	yecE	putative cytoplasmic protein	**0.14**	0.74374
STM1904	yecN	putative inner membrane protein	**0.14**	0.76240
STM1904	yecN	putative inner membrane protein	**0.08**	0.85683
STM1905	yecO	putative SAM-dependent methyltransferase	**-0.11**	0.76811
STM1905	yecO	putative SAM-dependent methyltransferase	**0.18**	0.62946
STM1906	yecP	putative enzyme	**-0.28**	0.65779
STM1906	yecP	putative enzyme	**0.61**	0.31977
STM1907	cutC	copper homeostasis protein	**-0.42**	0.53124
STM1907	cutC	copper homeostasis protein	**0.42**	0.49708
STM1908	yecM	putative cytoplasmic protein	**-0.33**	0.37543
STM1908	yecM	putative cytoplasmic protein	**-0.17**	0.74361
STM1909	argS	arginyl-tRNA synthetase	**-0.56**	0.19236
STM1909	argS	arginyl-tRNA synthetase	**-0.09**	0.83843
STM1910	STM1910	putative penicillin-binding protein	**-0.11**	0.81288
STM1910	STM1910	putative penicillin-binding protein	**1.01**	0.17603
STM1911	STM1911	putative cytoplasmic protein	**-0.10**	0.87999
STM1911	STM1911	putative cytoplasmic protein	**-0.03**	0.96261
STM1912	flhE	flagellar protein	**0.26**	0.55892

STM1912	flhE	flagellar protein	**0.28**	0.70249
STM1913	flhA	flagellar biosynthesis protein	**-0.23**	0.55956
STM1913	flhA	flagellar biosynthesis protein	**-0.08**	0.86876
STM1914	flhB	flagellar biosynthesis protein	**-0.04**	0.94050
STM1914	flhB	flagellar biosynthesis protein	**0.42**	0.26910
STM1915	cheZ	chemotactic response protein	**-0.43**	0.31277
STM1915	cheZ	chemotactic response protein	**-0.06**	0.89937
STM1916	cheY	chemotaxis regulator	**-0.08**	0.88998
STM1916	cheY	chemotaxis regulator	**-0.16**	0.71113
STM1917	cheB	chemotaxis-specific methylesterase	**-0.08**	0.83109
STM1917	cheB	chemotaxis-specific methylesterase	**0.55**	0.20285
STM1918	cheR	glutamate methyltransferase	**0.26**	0.49009
STM1918	cheR	glutamate methyltransferase	**0.21**	0.59940
STM1919	cheM	methyl accepting chemotaxis protein II	**0.10**	0.82006
STM1919	cheM	methyl accepting chemotaxis protein II	**-0.07**	0.93023
STM1920	cheW	chemotaxis docking protein	**-0.14**	0.73855
STM1920	cheW	chemotaxis docking protein	**-0.12**	0.80002
STM1921	cheA	chemotaxis sensory histidine protein kinase	**0.14**	0.78973
STM1921	cheA	chemotaxis sensory histidine protein kinase	**0.27**	0.48062
STM1922	motB	flagellar motor protein	**0.14**	0.70122
STM1922	motB	flagellar motor protein	**0.31**	0.47844
STM1923	motA	flagellar motor protein	**-0.26**	0.50759
STM1923	motA	flagellar motor protein	**-0.19**	0.63156
STM1924,S	flhC	flagellar transcriptional activator	**0.13**	0.75739
STM1924,S	flhC	flagellar transcriptional activator	**0.53**	0.26512
STM1925	flhD	transcriptional activator FlhD	**0.40**	0.41154
STM1925	flhD	transcriptional activator FlhD	**0.41**	0.42277
STM1927	yecG	putative universal stress protein	**0.05**	0.93485
STM1927	yecG	putative universal stress protein	**0.26**	0.54169
STM1928	otsA	trehalose-6-phosphate synthase	**1.03**	0.29871
STM1928	otsA	trehalose-6-phosphate synthase	**1.18**	0.19843
STM1929	otsB	trehalose-6-phosphate phophatase	**-0.21**	0.71690
STM1929	otsB	trehalose-6-phosphate phophatase	**0.71**	0.25382
STM1931	araH	putative intracellular protease/amidase	**0.22**	0.86396
STM1931	araH	putative intracellular protease/amidase	**0.75**	0.13824
STM1932	ftnB	ferritin-like protein	**0.04**	0.94360
STM1932	ftnB	ferritin-like protein	**0.52**	0.44745
STM1933	STM1933	hypothetical protein STM1933	**-0.31**	0.42344
STM1933	STM1933	hypothetical protein STM1933	**0.16**	0.80406
STM1934	STM1934	putative outer membrane lipoprotein	**-0.04**	0.93811
STM1934	STM1934	putative outer membrane lipoprotein	**-0.03**	0.94060
STM1935	ftn	cytoplasmic ferritin	**-0.24**	0.61965
STM1935	ftn	cytoplasmic ferritin	**0.04**	0.96785
STM1936	yecH	putative cytoplasmic protein	**-0.44**	0.26690
STM1936	yecH	putative cytoplasmic protein	**-0.35**	0.56245
STM1937	tyrP	tyrosine-specific transport protein	**-0.20**	0.67473
STM1937	tyrP	tyrosine-specific transport protein	**-0.12**	0.78452
STM1938	yecA	putative metal-binding protein	**-0.93**	0.13645
STM1938	yecA	putative metal-binding protein	**0.00**	0.99887
STM1939	STM1939	putative glucose-6-phosphate dehydrogenase	**-0.40**	0.35824
STM1939	STM1939	putative glucose-6-phosphate dehydrogenase	**-0.64**	0.17139
STM1940	STM1940	putative cell wall-associated hydrolase	**-0.12**	0.80341
STM1940	STM1940	putative cell wall-associated hydrolase	**-0.29**	0.45800
STM1941	STM1941	putative inner membrane protein	**-0.52**	0.20271
STM1941	STM1941	putative inner membrane protein	**-0.22**	0.55956
STM1942	leuZ	STM1942	**-0.37**	0.45462
STM1942	leuZ	STM1942	**0.07**	0.93975
STM1943	cysT	STM1943	**-0.69**	0.26910
STM1943	cysT	STM1943	**-0.35**	0.48994
STM1944	glyW	STM1944	**-0.36**	0.69633
STM1944	glyW	STM1944	**-0.46**	0.56048
STM1944	glyW	STM1944	**-0.42**	0.49035
STM1944	glyW	STM1944	**-0.60**	0.31280

STM1944	glyW	STM1944	**-0.31**	0.51267
STM1944	glyW	STM1944	**-0.45**	0.37154
STM1944	glyW	STM1944	**-0.42**	0.28799
STM1944	glyW	STM1944	**-0.23**	0.58506
STM1945	pgsA	phosphatidylglycerophosphate synthetase	**-0.10**	0.80306
STM1945	pgsA	phosphatidylglycerophosphate synthetase	**0.06**	0.89624
STM1946	uvrC	excinuclease ABC subunit C	**0.04**	0.94050
STM1946	uvrC	excinuclease ABC subunit C	**0.25**	0.61679
STM1947	uvrY	response regulator	**-0.06**	0.91996
STM1947	uvrY	response regulator	**0.17**	0.70140
STM1949	yecF	putative cytoplasmic protein	**-0.42**	0.26213
STM1949	yecF	putative cytoplasmic protein	**-0.03**	0.95876
STM1950	sdiA	transcriptional regulator	**-0.27**	0.58108
STM1950	sdiA	transcriptional regulator	**-0.27**	0.47610
STM1951	yecC	putative ABC-type polar amino acid transport system ATPase	**0.05**	0.92403
STM1951	yecC	putative ABC-type polar amino acid transport system ATPase	**0.19**	0.72219
STM1952	yecS	putative ABC-type amino acid transporter permease component	**-0.59**	0.15529
STM1952	yecS	putative ABC-type amino acid transporter permease component	**-0.33**	0.41284
STM1953	yedO	D-cysteine desulfhydrase	**-0.16**	0.74436
STM1953	yedO	D-cysteine desulfhydrase	**0.64**	0.23613
STM1954	fliY	putative periplasmic binding transport protein	**0.16**	0.69776
STM1954	fliY	putative periplasmic binding transport protein	**0.33**	0.58766
STM1955	fliZ	putative FliA-regulator	**0.07**	0.94765
STM1955	fliZ	putative FliA-regulator	**0.54**	0.18140
STM1956	fliA	flagellar biosynthesis sigma factor FliA	**0.11**	0.84854
STM1956	fliA	flagellar biosynthesis sigma factor FliA	**0.60**	0.14723
STM1958	fliB	lysine-N-methylase	**0.19**	0.66310
STM1958	fliB	lysine-N-methylase	**0.27**	0.57804
STM1959	fliC	flagellar biosynthesis protein	**0.08**	0.87512
STM1959	fliC	flagellar biosynthesis protein	**0.22**	0.72247
STM1960	fliD	flagellar hook-associated protein	**0.29**	0.43731
STM1960	fliD	flagellar hook-associated protein	**0.50**	0.28024
STM1961	fliS	flagellar protein FliS	**0.30**	0.62265
STM1961	fliS	flagellar protein FliS	**-0.11**	0.91900
STM1962	fliT	possible FliD export chaperone	**-0.15**	0.68434
STM1962	fliT	possible FliD export chaperone	**0.43**	0.30422
STM1963	amyA	cytoplasmic alpha-amylase	**-0.40**	0.27753
STM1963	amyA	cytoplasmic alpha-amylase	**-0.13**	0.83443
STM1964	yedD	putative outer membrane lipoprotein	**-1.10**	0.17359
STM1964	yedD	putative outer membrane lipoprotein	**0.04**	0.94316
STM1965	yedE	hypothetical protein STM1965	**-0.01**	0.98489
STM1965	yedE	hypothetical protein STM1965	**-0.08**	0.86580
STM1966	yedF	putative transcriptional regulator	**-0.18**	0.77186
STM1966	yedF	putative transcriptional regulator	**0.19**	0.74268
STM1968	fliE	flagellar basal body protein	**0.15**	0.78665
STM1968	fliE	flagellar basal body protein	**0.25**	0.57076
STM1969	fliF	flagellar M-ring protein	**-0.30**	0.48388
STM1969	fliF	flagellar M-ring protein	**0.02**	0.97364
STM1970	fliG	flagellar motor protein	**0.08**	0.83700
STM1970	fliG	flagellar motor protein	**0.26**	0.54624
STM1971	fliH	flagellar assembly protein	**-0.14**	0.70185
STM1971	fliH	flagellar assembly protein	**0.26**	0.49870
STM1972	fliI	flagellum-specific ATP synthase	**0.01**	0.98066
STM1972	fliI	flagellum-specific ATP synthase	**0.16**	0.77818
STM1973	fliJ	flagellar protein	**-0.37**	0.41154
STM1973	fliJ	flagellar protein	**0.13**	0.75529
STM1974	fliK	flagellar hook-length control protein	**0.03**	0.95360
STM1974	fliK	flagellar hook-length control protein	**0.19**	0.63301
STM1975	fliL	flagellar biosynthesis protein	**0.10**	0.86385

STM1975	fliL	flagellar biosynthesis protein	**0.23**	0.61201
STM1976	fliM	flagellar motor switch protein	**-0.01**	0.98212
STM1976	fliM	flagellar motor switch protein	**-0.11**	0.77002
STM1977	fliN	flagellar motor switch protein	**0.05**	0.91236
STM1977	fliN	flagellar motor switch protein	**0.03**	0.96228
STM1978	fliO	flagellar biosynthetic protein	**-0.14**	0.76720
STM1978	fliO	flagellar biosynthetic protein	**-0.06**	0.91170
STM1979	fliP	flagellar biosynthesis protein	**0.19**	0.66506
STM1979	fliP	flagellar biosynthesis protein	**0.51**	0.26771
STM1980	fliQ	flagellar biosynthesis protein	**0.40**	0.34051
STM1980	fliQ	flagellar biosynthesis protein	**0.39**	0.36991
STM1981	fliR	flagellar biosynthesis protein	**-0.21**	0.64525
STM1981	fliR	flagellar biosynthesis protein	**-0.21**	0.74178
STM1982	rcsA	colanic acid capsular biosynthesis activation protein A	**0.62**	0.15589
STM1982	rcsA	colanic acid capsular biosynthesis activation protein A	**0.57**	0.53827
STM1983	dsrB	hypothetical protein STM1983	**-0.36**	0.48600
STM1983	dsrB	hypothetical protein STM1983	**0.18**	0.73473
STM1984	yodD	putative cytoplasmic protein	**0.82**	0.17603
STM1984	yodD	putative cytoplasmic protein	**0.98**	0.30018
STM1986	yedP	hypothetical protein STM1986	**0.05**	0.93841
STM1986	yedP	hypothetical protein STM1986	**0.28**	0.63101
STM1987	STM1987	putative inner membrane protein	**-0.10**	0.90776
STM1987	STM1987	putative inner membrane protein	**0.17**	0.71690
STM1988,S	STM1988,S	putative cytoplasmic protein	**0.19**	0.83998
STM1988,S	STM1988,S	putative cytoplasmic protein	**1.06**	0.55008
STM1989	yedI	putative inner membrane protein	**0.11**	0.84687
STM1989	yedI	putative inner membrane protein	**0.16**	0.76538
STM1990	yedA	putative permease	**-0.19**	0.62861
STM1990	yedA	putative permease	**0.63**	0.22060
STM1991	vsr	DNA mismatch endonuclease	**-0.36**	0.61892
STM1991	vsr	DNA mismatch endonuclease	**0.36**	0.41286
STM1992	dcm	DNA cytosine methylase	**-0.03**	0.94880
STM1992	dcm	DNA cytosine methylase	**0.95**	0.15276
STM1993	yedJ	putative hydrolase	**0.10**	0.85601
STM1993	yedJ	putative hydrolase	**-0.02**	0.97270
STM1994	STM1994	putative inner membrane protein	**-0.42**	0.37154
STM1994	STM1994	putative inner membrane protein	**-0.21**	0.58788
STM1995	ompS	putative porin	**0.13**	0.73473
STM1995	ompS	putative porin	**0.41**	0.47897
STM1996	cspB	putative cold-shock protein	**0.51**	0.38314
STM1996	cspB	putative cold-shock protein	**0.46**	0.43548
STM1997	umuC	DNA polymerase IV	**-0.37**	0.42277
STM1997	umuC	DNA polymerase IV	**-0.79**	0.39316
STM1997	umuC	DNA polymerase IV	**-0.28**	0.57089
STM1997	umuC	DNA polymerase IV	**-0.41**	0.35366
STM1998	umuD	SOS-response transcriptional repressors	**-0.25**	0.55393
STM1998	umuD	SOS-response transcriptional repressors	**0.69**	0.23892
STM1999	STM1999	putative cytoplasmic protein	**-0.42**	0.63688
STM1999	STM1999	putative cytoplasmic protein	**0.23**	0.65980
STM2000	serU	STM2000	**-0.73**	0.25561
STM2000	serU	STM2000	**-0.37**	0.60936
STM2001	yeeI	putative inner membrane protein	**0.27**	0.50811
STM2001	yeeI	putative inner membrane protein	**0.36**	0.40819
STM2005	STM2005	putative endoprotease	**-1.32**	0.11913
STM2005	STM2005	putative endoprotease	**-0.39**	0.48432
STM2007	STM2007	tetratricopeptide repeat protein	**-0.34**	0.36017
STM2007	STM2007	tetratricopeptide repeat protein	**0.43**	0.59422
STM2008	STM2008	putative periplasmic protein	**-0.50**	0.24926
STM2008	STM2008	putative periplasmic protein	**0.46**	0.48810
STM2009	amn	AMP nucleosidase	**0.03**	0.96364
STM2009	amn	AMP nucleosidase	**-0.27**	0.57568
STM2011	STM2011	putative cytoplasmic protein	**-0.40**	0.45947
STM2011	STM2011	putative cytoplasmic protein	**0.03**	0.97348

STM2013	yeeO	putative transport protein	**0.25**	0.53497
STM2013	yeeO	putative transport protein	**0.24**	0.72843
STM2014	asnU	STM2014	**-1.35**	0.10149
STM2014	asnU	STM2014	**0.07**	0.89878
STM2014	asnU	STM2014	**-0.72**	0.15276
STM2014	asnU	STM2014	**-0.96**	0.15859
STM2014	asnU	STM2014	**-0.39**	0.30956
STM2014	asnU	STM2014	**0.62**	0.32481
STM2014	asnU	STM2014	**-0.63**	0.35373
STM2014	asnU	STM2014	**-0.60**	0.32673
STM2015	erfK	putative periplasmic protein	**-0.30**	0.46267
STM2015	erfK	putative periplasmic protein	**0.02**	0.96785
STM2016	cobT	nicotinate-nucleotide--dimethylbenzimidazole	**-0.16**	0.78257
STM2016	cobT	nicotinate-nucleotide--dimethylbenzimidazole	**0.64**	0.26378
STM2017	cobS	cobalamin synthase	**0.60**	0.29044
STM2017	cobS	cobalamin synthase	**0.34**	0.67785
STM2018	cobU	adenosylcobinamide kinase	**-0.03**	0.98026
STM2018	cobU	adenosylcobinamide kinase	**0.17**	0.83525
STM2019	cbiP	cobyric acid synthase	**-0.72**	0.19398
STM2019	cbiP	cobyric acid synthase	**0.26**	0.60174
STM2020	cbiO	vitamin B12 biosynthetic protein	**-0.57**	0.21293
STM2020	cbiO	vitamin B12 biosynthetic protein	**-0.20**	0.65730
STM2021	cbiQ	vitamin B12 biosynthetic protein	**-0.17**	0.66677
STM2021	cbiQ	vitamin B12 biosynthetic protein	**-0.12**	0.78718
STM2022	cbiN	cobalt transport protein CbiN	**0.13**	0.74354
STM2022	cbiN	cobalt transport protein CbiN	**0.79**	0.11913
STM2023	cbiM	cobalt transport protein CbiM	**0.01**	0.98894
STM2023	cbiM	cobalt transport protein CbiM	**0.16**	0.86580
STM2024	cbiL	precorrin-2 methyltransferase	**-0.64**	0.29543
STM2024	cbiL	precorrin-2 methyltransferase	**0.10**	0.85433
STM2025	cbiK	vitamin B12 biosynthetic protein	**0.12**	0.77801
STM2025	cbiK	vitamin B12 biosynthetic protein	**0.29**	0.53832
STM2026	cbiJ	precorrin-6x reductase	**0.16**	0.80415
STM2026	cbiJ	precorrin-6x reductase	**0.99**	0.27834
STM2027	cbiH	precorrin-3B C17-methyltransferase	**-0.57**	0.37225
STM2027	cbiH	precorrin-3B C17-methyltransferase	**0.01**	0.98551
STM2028	cbiG	cobalamin biosynthesis protein CbiG	**-0.36**	0.56535
STM2028	cbiG	cobalamin biosynthesis protein CbiG	**0.39**	0.36341
STM2029	cbiF	vitamin B12 biosynthetic protein	**0.45**	0.75158
STM2029	cbiF	vitamin B12 biosynthetic protein	**1.49**	0.11224
STM2030	cbiT	precorrin-8w decarboxylase	**-0.10**	0.88998
STM2030	cbiT	precorrin-8w decarboxylase	**0.51**	0.59527
STM2031	cbiE	precorrin-6B methylase	**-0.11**	0.87016
STM2031	cbiE	precorrin-6B methylase	**0.04**	0.95608
STM2032	cbiD	cobalt-precorrin-6A synthase	**0.05**	0.95046
STM2032	cbiD	cobalt-precorrin-6A synthase	**0.32**	0.42591
STM2033	cbiC	precorrin-8X methylmutase	**-0.06**	0.94087
STM2033	cbiC	precorrin-8X methylmutase	**0.19**	0.64730
STM2034	cobD	cobalamin biosynthesis protein	**0.12**	0.77186
STM2034	cobD	cobalamin biosynthesis protein	**0.90**	0.18763
STM2035	cbiA	cobyrinic acid a,c-diamide synthase	**-0.14**	0.71690
STM2035	cbiA	cobyrinic acid a,c-diamide synthase	**0.15**	0.84456
STM2036	pocR	transcriptional regulator	**-0.30**	0.55956
STM2036	pocR	transcriptional regulator	**0.14**	0.84911
STM2037	pduF	propanediol diffusion facilitator	**0.17**	0.74381
STM2037	pduF	propanediol diffusion facilitator	**0.13**	0.77336
STM2038	pduA	polyhedral body protein	**-0.26**	0.76325
STM2038	pduA	polyhedral body protein	**0.54**	0.45848
STM2039	pudB	polyhedral body protein	**0.07**	0.93582
STM2039	pudB	polyhedral body protein	**0.42**	0.32673
STM2040	pduC	propanediol dehydratase large subunit	**-0.82**	0.32172
STM2040	pduC	propanediol dehydratase large subunit	**0.16**	0.86516
STM2041	pduD	propanediol dehydratase medium subunit	**-0.19**	0.83926

STM2041	pduD	propanediol dehydratase medium subunit	**0.27**	0.56103
STM2042	pduE	propanediol dehydratase small subunit	**0.28**	0.65305
STM2042	pduE	propanediol dehydratase small subunit	**-0.04**	0.93688
STM2043	pduG	propanediol dehydratase reactivation protein	**-0.56**	0.50458
STM2043	pduG	propanediol dehydratase reactivation protein	**0.41**	0.53827
STM2044	pduH	propanediol dehydratase reactivation protein	**-0.93**	0.12273
STM2044	pduH	propanediol dehydratase reactivation protein	**-0.24**	0.74807
STM2045	pduJ	polyhedral body protein	**-0.37**	0.32675
STM2045	pduJ	polyhedral body protein	**0.50**	0.39861
STM2046	pduK	polyhedral body protein	**-0.38**	0.43772
STM2046	pduK	polyhedral body protein	**0.49**	0.29796
STM2047	pduL	propanediol utilization protein	**0.09**	0.84103
STM2047	pduL	propanediol utilization protein	**1.12**	0.13645
STM2048	pduM	propanediol utilization protein	**0.14**	0.81455
STM2048	pduM	propanediol utilization protein	**0.28**	0.44208
STM2049	pduN	polyhedral body protein	**-0.25**	0.56618
STM2049	pduN	polyhedral body protein	**0.31**	0.70323
STM2050	pduO	propanediol utilization protein	**-0.19**	0.65025
STM2050	pduO	propanediol utilization protein	**0.90**	0.23398
STM2051	pduP	CoA-dependent propionaldehyde dehydrogenase	**-0.35**	0.40930
STM2051	pduP	CoA-dependent propionaldehyde dehydrogenase	**0.11**	0.87135
STM2052	pduQ	propanol dehydrogenase	**0.15**	0.84788
STM2052	pduQ	propanol dehydrogenase	**0.67**	0.35564
STM2053	pduS	polyhedral body protein	**0.09**	0.89393
STM2053	pduS	polyhedral body protein	**0.52**	0.29284
STM2054	pduT	polyhedral body protein	**0.12**	0.83443
STM2054	pduT	polyhedral body protein	**0.97**	0.19398
STM2055	pduU	polyhedral body protein	**0.85**	0.26213
STM2055	pduU	polyhedral body protein	**1.16**	0.32016
STM2056	pduV	propanediol utilization protein	**-0.16**	0.68929
STM2056	pduV	propanediol utilization protein	**0.98**	0.22602
STM2057	pduW	acetate/propionate kinase	**-0.09**	0.85288
STM2057	pduW	acetate/propionate kinase	**0.18**	0.65040
STM2058	pduX	propanediol utilization protein	**-0.50**	0.39577
STM2058	pduX	propanediol utilization protein	**0.05**	0.91917
STM2059	yeeX	hypothetical protein STM2059	**-0.24**	0.60574
STM2059	yeeX	hypothetical protein STM2059	**-0.21**	0.55978
STM2060	yeeA	putative inner membrane protein	**-0.38**	0.37310
STM2060	yeeA	putative inner membrane protein	**0.17**	0.70077
STM2061	sbmC	DNA gyrase inhibitor	**-0.13**	0.71971
STM2061	sbmC	DNA gyrase inhibitor	**0.33**	0.38668
STM2062	dacD	DD-carboxypeptidase	**-0.17**	0.76921
STM2062	dacD	DD-carboxypeptidase	**0.33**	0.45797
STM2063	phsC	thiosulfate reductase cytochrome B subunit	**-0.14**	0.74374
STM2063	phsC	thiosulfate reductase cytochrome B subunit	**0.31**	0.51952
STM2064	phsB	thiosulfate reductase electron transport protein	**-0.23**	0.61723
STM2064	phsB	thiosulfate reductase electron transport protein	**0.26**	0.67551
STM2065	phsA	thiosulfate reductase precursor	**-0.38**	0.51973
STM2065	phsA	thiosulfate reductase precursor	**0.71**	0.14928
STM2066	sopA	secreted effector protein	**0.00**	0.99887
STM2066	sopA	secreted effector protein	**0.24**	0.65305
STM2067	sbcB	exonuclease I	**-0.21**	0.65519
STM2067	sbcB	exonuclease I	**0.04**	0.95345
STM2068	yeeF	putative amino acid transport protein	**-0.46**	0.23042
STM2068	yeeF	putative amino acid transport protein	**0.09**	0.82122
STM2069	yeeY	putative transcriptional regulator	**-0.04**	0.94087
STM2069	yeeY	putative transcriptional regulator	**0.57**	0.22602
STM2070	yeeZ	putative dehydratase	**-0.34**	0.46184
STM2070	yeeZ	putative dehydratase	**-0.19**	0.65012
STM2071	hisG	ATP phosphoribosyltransferase	**-0.39**	0.41154
STM2071	hisG	ATP phosphoribosyltransferase	**0.16**	0.73010
STM2072	hisD	histidinol dehydrogenase	**-0.28**	0.58472
STM2072	hisD	histidinol dehydrogenase	**0.03**	0.95491

STM2073	hisC	histidinol-phosphate aminotransferase	**0.06**	0.92074
STM2073	hisC	histidinol-phosphate aminotransferase	**-0.01**	0.99381
STM2074	hisB	imidazole glycerol-phosphate dehydratase/histidinol phosphatase	**0.01**	0.98958
STM2074	hisB	imidazole glycerol-phosphate dehydratase/histidinol phosphatase	**0.06**	0.91021
STM2075	hisH	imidazole glycerol phosphate synthase subunit HisH	**-0.13**	0.82400
STM2075	hisH	imidazole glycerol phosphate synthase subunit HisH	**0.31**	0.47474
STM2076	hisA	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]	**-0.02**	0.96785
STM2076	hisA	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]	**0.19**	0.61654
STM2077	hisF	imidazole glycerol phosphate synthase subunit HisF	**0.00**	0.99992
STM2077	hisF	imidazole glycerol phosphate synthase subunit HisF	**-0.13**	0.79741
STM2078	hisI	bifunctional phosphoribosyl-AMP cyclohydrolase/phosphoribosyl-ATP	**-0.24**	0.52218
STM2078	hisI	bifunctional phosphoribosyl-AMP cyclohydrolase/phosphoribosyl-ATP	**0.16**	0.74906
STM2079	wzzB	lipopolysaccharide O-antigen chain length regulator	**-0.38**	0.37154
STM2079	wzzB	lipopolysaccharide O-antigen chain length regulator	**0.05**	0.93023
STM2080	udg	UDP-glucose/GDP-mannose dehydrogenase	**-0.33**	0.39962
STM2080	udg	UDP-glucose/GDP-mannose dehydrogenase	**-0.33**	0.55111
STM2081	gnd	6-phosphogluconate dehydrogenase	**0.04**	0.93420
STM2081	gnd	6-phosphogluconate dehydrogenase	**0.10**	0.80588
STM2082	rfbP	undecaprenol-phosphate galactosephosphotransferase/O-antigen	**0.17**	0.67351
STM2082	rfbP	undecaprenol-phosphate galactosephosphotransferase/O-antigen	**-0.09**	0.83897
STM2083	rfbK	phosphomannomutase	**0.01**	0.98539
STM2083	rfbK	phosphomannomutase	**0.09**	0.83545
STM2084	rfbM	mannose-1-phosphate guanylyltransferase	**-0.07**	0.91019
STM2084	rfbM	mannose-1-phosphate guanylyltransferase	**0.25**	0.65245
STM2085	rfbN	rhamnosyl transferase	**0.37**	0.40947
STM2085	rfbN	rhamnosyl transferase	**0.33**	0.35757
STM2086	rfbU	mannosyl transferase	**0.12**	0.75309
STM2086	rfbU	mannosyl transferase	**0.19**	0.60014
STM2087	rfbV	abequosyltransferase	**0.32**	0.57123
STM2087	rfbV	abequosyltransferase	**-0.23**	0.59325
STM2088	rfbX	putative O-antigen transferase	**0.22**	0.56879
STM2088	rfbX	putative O-antigen transferase	**0.07**	0.87438
STM2089	rfbJ	CDP-abequose synthase	**0.15**	0.71935
STM2089	rfbJ	CDP-abequose synthase	**0.18**	0.67473
STM2090	rfbH	CDP-6-deoxy-D-xylo-4-hexulose-3-dehydrase	**0.10**	0.84783
STM2090	rfbH	CDP-6-deoxy-D-xylo-4-hexulose-3-dehydrase	**0.10**	0.85053
STM2091	rfbG	CDP glucose 4,6-dehydratase	**-0.01**	0.99268
STM2091	rfbG	CDP glucose 4,6-dehydratase	**0.15**	0.80831
STM2092	rfbF	glucose-1-phosphate cytidylyltransferase	**-0.10**	0.82145
STM2092	rfbF	glucose-1-phosphate cytidylyltransferase	**0.08**	0.88764
STM2093	rfbI	CDP-6-deoxy-delta-3,4-glucoseen reductase	**0.44**	0.35816
STM2093	rfbI	CDP-6-deoxy-delta-3,4-glucoseen reductase	**0.07**	0.86190
STM2094	rfbC	dTDP-4,deoxyrhamnose 3,5 epimerase	**0.27**	0.53263
STM2094	rfbC	dTDP-4,deoxyrhamnose 3,5 epimerase	**0.26**	0.45111
STM2095	rfbA	dTDP-glucose pyrophosphorylase	**0.02**	0.97140
STM2095	rfbA	dTDP-glucose pyrophosphorylase	**0.73**	0.19138
STM2096	rfbD	TDP-rhamnose synthetase	**0.19**	0.74626
STM2096	rfbD	TDP-rhamnose synthetase	**0.37**	0.48199
STM2097	rfbB	dTDP-glucose 4,6-dehydratase	**0.17**	0.72247
STM2097	rfbB	dTDP-glucose 4,6-dehydratase	**0.11**	0.78982
STM2098	galF	putative glucose-1-phosphate uridylyltransferase subunit	**-0.35**	0.38317
STM2098	galF	putative glucose-1-phosphate uridylyltransferase subunit	**0.20**	0.59416
STM2099	wcaM	putative colanic acid biosynthetic protein	**-0.03**	0.97168
STM2099	wcaM	putative colanic acid biosynthetic protein	**0.26**	0.64524
STM2100	wcaL	putative glycosyl transferase	**-0.14**	0.78521

STM2100	wcaL	putative glycosyl transferase	**-0.07**	0.88211
STM2101	wcaK	putative galactokinase	**-0.39**	0.34770
STM2101	wcaK	putative galactokinase	**0.71**	0.21111
STM2102	wzxC	putative export	**-0.01**	0.97973
STM2102	wzxC	putative export	**-0.01**	0.99266
STM2103	wcaJ	UDP-glucose lipid carrier transferase/glucose-1-phosphate	**-0.30**	0.66489
STM2103	wcaJ	UDP-glucose lipid carrier transferase/glucose-1-phosphate	**-0.28**	0.66262
STM2104	cpsG	phosphomannomutase	**0.18**	0.76446
STM2104	cpsG	phosphomannomutase	**0.87**	0.24973
STM2105,S	manC	mannose-1-phosphate guanylyltransferase	**-0.14**	0.81667
STM2105,S	manC	mannose-1-phosphate guanylyltransferase	**1.19**	0.30497
STM2106	wcaI	putative glycosyl transferase	**-0.44**	0.29532
STM2106	wcaI	putative glycosyl transferase	**0.33**	0.60042
STM2107	wcaH	GDP-mannose mannosyl hydrolase	**0.08**	0.91082
STM2107	wcaH	GDP-mannose mannosyl hydrolase	**0.78**	0.21078
STM2108	wcaG	GDP-fucose synthetase	**-0.03**	0.96640
STM2108	wcaG	GDP-fucose synthetase	**-0.25**	0.56786
STM2109	gmd	GDP-D-mannose dehydratase	**-0.59**	0.58841
STM2109	gmd	GDP-D-mannose dehydratase	**0.03**	0.96251
STM2110	wcaF	putative acyltransferase	**0.17**	0.81325
STM2110	wcaF	putative acyltransferase	**0.01**	0.98427
STM2111	wcaE	putative transferase	**-0.64**	0.26910
STM2111	wcaE	putative transferase	**0.26**	0.45664
STM2112	wcaD	putative colanic acid polymerase	**-0.28**	0.43219
STM2112	wcaD	putative colanic acid polymerase	**-0.07**	0.90990
STM2113	wcaC	putative glycosyl transferase	**0.46**	0.32399
STM2113	wcaC	putative glycosyl transferase	**0.24**	0.56971
STM2114	wcaB	putative acyl transferase	**0.93**	0.11962
STM2114	wcaB	putative acyl transferase	**1.00**	0.14030
STM2115	wcaA	putative glycosyl transferase	**1.01**	0.40121
STM2115	wcaA	putative glycosyl transferase	**1.29**	0.34051
STM2116	wzc	putative tyrosine protein kinase	**0.14**	0.95650
STM2116	wzc	putative tyrosine protein kinase	**1.74**	0.29044
STM2117	wzb	putative phosphotyrosine-protein phosphatase	**-0.22**	0.82443
STM2117	wzb	putative phosphotyrosine-protein phosphatase	**0.30**	0.61341
STM2118	wza	putative outer membrane polysaccharide export protein	**-0.45**	0.38829
STM2118	wza	putative outer membrane polysaccharide export protein	**0.21**	0.62188
STM2119	yegH	putative inner membrane protein	**-0.96**	0.09135
STM2119	yegH	putative inner membrane protein	**-0.24**	0.66743
STM2120	asmA	suppressor of OmpF assembly mutants	**-0.34**	0.48814
STM2120	asmA	suppressor of OmpF assembly mutants	**0.21**	0.67351
STM2121	dcd	deoxycytidine triphosphate deaminase	**-0.41**	0.39577
STM2121	dcd	deoxycytidine triphosphate deaminase	**0.35**	0.43219
STM2122	udk	uridine kinase	**0.12**	0.75510
STM2122	udk	uridine kinase	**0.10**	0.81763
STM2123	yegE	putative diguanylate cyclase/phosphodiesterase	**-0.15**	0.73781
STM2123	yegE	putative diguanylate cyclase/phosphodiesterase	**-0.08**	0.87126
STM2124	alkA	3-methyl-adenine DNA glycosylase II	**-0.36**	0.46787
STM2124	alkA	3-methyl-adenine DNA glycosylase II	**0.11**	0.81061
STM2125	yegD	putative heat shock protein	**-0.20**	0.66881
STM2125	yegD	putative heat shock protein	**0.22**	0.68094
STM2126	STM2126	putative secretion protein	**-0.49**	0.36636
STM2126	STM2126	putative secretion protein	**-0.15**	0.72913
STM2127	yegN	putative outer membrane receptor	**-0.12**	0.81667
STM2127	yegN	putative outer membrane receptor	**0.39**	0.61201
STM2128	yegO	outer membrane putative efflux transporter	**-0.59**	0.28008
STM2128	yegO	outer membrane putative efflux transporter	**-0.03**	0.96605
STM2129	yegB	putative transport protein	**-0.38**	0.60052
STM2129	yegB	putative transport protein	**0.12**	0.74374
STM2130	baeS	sensor kinase	**-0.08**	0.91900
STM2130	baeS	sensor kinase	**-0.38**	0.48429

STM2131	baeR	response regulator	**-0.41**	0.37057
STM2131	baeR	response regulator	**0.47**	0.49374
STM2133	STM2133	putative cytoplasmic protein	**-0.31**	0.63243
STM2133	STM2133	putative cytoplasmic protein	**0.78**	0.28240
STM2134	STM2134	putative inner membrane protein	**0.00**	0.99751
STM2134	STM2134	putative inner membrane protein	**0.93**	0.22733
STM2135	STM2135	putative inner membrane protein	**-0.01**	0.98615
STM2135	STM2135	putative inner membrane protein	**0.36**	0.45462
STM2136	yegQ	putative protease	**-0.17**	0.67937
STM2136	yegQ	putative protease	**0.19**	0.59106
STM2137	STM2137	putative cytoplasmic protein	**-0.17**	0.67631
STM2137	STM2137	putative cytoplasmic protein	**-0.10**	0.85592
STM2138	STM2138	putative cytoplasmic protein	**0.16**	0.65730
STM2138	STM2138	putative cytoplasmic protein	**-0.15**	0.73250
STM2139	STM2139	putative inner membrane protein	**-0.25**	0.62988
STM2139	STM2139	putative inner membrane protein	**0.36**	0.55309
STM2139,2n	STM2139,2n	hypothetical protein STM2139,2n	**0.54**	0.35366
STM2139,2n	STM2139,2n	hypothetical protein STM2139,2n	**0.62**	0.18763
STM2140	yegS	putative diacylglycerol kinase	**0.08**	0.90513
STM2140	yegS	putative diacylglycerol kinase	**0.80**	0.24290
STM2141	fbaB	fructose-bisphosphate aldolase	**-0.56**	0.32760
STM2141	fbaB	fructose-bisphosphate aldolase	**0.56**	0.34574
STM2142	yegT	putative transport protein	**-0.25**	0.56810
STM2142	yegT	putative transport protein	**-0.34**	0.40562
STM2143	yegU	putative glycohydrolase	**-0.04**	0.95081
STM2143	yegU	putative glycohydrolase	**0.10**	0.83855
STM2144	yegV	putative sugar kinase	**0.04**	0.96018
STM2144	yegV	putative sugar kinase	**-0.06**	0.88012
STM2145	yegW	putative regulatory protein	**-0.09**	0.92840
STM2145	yegW	putative regulatory protein	**-0.23**	0.59978
STM2146	thiD	phosphomethylpyrimidine kinase	**-0.36**	0.38552
STM2146	thiD	phosphomethylpyrimidine kinase	**0.46**	0.33095
STM2147	thiM	hydroxyethylthiazole kinase	**0.01**	0.97983
STM2147	thiM	hydroxyethylthiazole kinase	**0.44**	0.49009
STM2148	STM2148	putative periplasmic protein	**-0.49**	0.27045
STM2148	STM2148	putative periplasmic protein	**0.52**	0.22602
STM2149	stcD	putative outer membrane lipoprotein	**-0.58**	0.41144
STM2149	stcD	putative outer membrane lipoprotein	**-0.09**	0.88548
STM2150	stcC	putative outer membrane protein	**-0.37**	0.46436
STM2150	stcC	putative outer membrane protein	**0.07**	0.91047
STM2151	stcB	putative periplasmic chaperone protein	**-0.90**	0.19398
STM2151	stcB	putative periplasmic chaperone protein	**0.22**	0.71902
STM2152	stcA	putative fimbrial-like protein	**-0.35**	0.65451
STM2152	stcA	putative fimbrial-like protein	**0.09**	0.88561
STM2153	yehE	putative outer membrane protein	**-0.06**	0.91047
STM2153	yehE	putative outer membrane protein	**-0.03**	0.95663
STM2154	mrp	putative ATP-binding protein	**-0.09**	0.83855
STM2154	mrp	putative ATP-binding protein	**0.22**	0.65012
STM2155	metG	methionyl-tRNA synthetase	**-0.17**	0.73207
STM2155	metG	methionyl-tRNA synthetase	**-0.23**	0.61833
STM2156	yehR	putative lipoprotein	**-0.42**	0.43365
STM2156	yehR	putative lipoprotein	**0.12**	0.85718
STM2156A	STM2156A	hypothetical protein STM2156A	**-0.44**	0.31989
STM2156A	STM2156A	hypothetical protein STM2156A	**0.10**	0.83655
STM2157	yehS	putative cytoplasmic protein	**0.28**	0.42957
STM2157	yehS	putative cytoplasmic protein	**0.43**	0.32760
STM2158	yehT	putative regulatory protein	**-0.12**	0.81455
STM2158	yehT	putative regulatory protein	**0.45**	0.31236
STM2159	yehU	putative sensor kinase	**-0.27**	0.63793
STM2159	yehU	putative sensor kinase	**0.41**	0.37920
STM2160	yehV	putative transcriptional repressor	**-0.24**	0.60950
STM2160	yehV	putative transcriptional repressor	**0.22**	0.60444

STM2162	yehW	putative ABC-type proline/glycine betaine transport system permease	**-0.07**	0.87917
STM2162	yehW	putative ABC-type proline/glycine betaine transport system permease	**-0.11**	0.79134
STM2163	yehX	putative ABC-type proline/glycine betaine transport system ATPase	**-0.31**	0.64267
STM2163	yehX	putative ABC-type proline/glycine betaine transport system ATPase	**-0.26**	0.66990
STM2164	yehY	putative ABC-type proline/glycine betaine transport system permease	**-0.37**	0.34553
STM2164	yehY	putative ABC-type proline/glycine betaine transport system permease	**0.24**	0.69624
STM2165	yehZ	putative transport protein	**-0.65**	0.16631
STM2165	yehZ	putative transport protein	**0.24**	0.59543
STM2166	bglX	periplasmic beta-D-glucoside glucohydrolase	**-0.11**	0.83188
STM2166	bglX	periplasmic beta-D-glucoside glucohydrolase	**0.36**	0.35363
STM2167	dld	D-lactate dehydrogenase	**-0.86**	0.11671
STM2167	dld	D-lactate dehydrogenase	**-0.21**	0.68136
STM2168	pbpG	D-alanyl-D-alanine endopeptidase	**-0.23**	0.65974
STM2168	pbpG	D-alanyl-D-alanine endopeptidase	**-0.32**	0.55956
STM2169	yohC	putative transport protein	**-0.23**	0.52897
STM2169	yohC	putative transport protein	**-0.09**	0.86560
STM2170	yohD	hypothetical protein STM2170	**-0.14**	0.71297
STM2170	yohD	hypothetical protein STM2170	**0.76**	0.18426
STM2171	yohF	oxidoreductase	**0.13**	0.89058
STM2171	yohF	oxidoreductase	**0.51**	0.35325
STM2172	yohG	putative outer membrane efflux protein	**0.32**	0.39791
STM2172	yohG	putative outer membrane efflux protein	**0.67**	0.37182
STM2174	yohI	putative regulatory protein	**0.06**	0.91359
STM2174	yohI	putative regulatory protein	**0.59**	0.24520
STM2175	STM2175	salicylate hydroxylase	**-0.46**	0.53453
STM2175	STM2175	salicylate hydroxylase	**0.46**	0.49633
STM2176	STM2176	putative glutathione S-transferase	**-0.33**	0.56162
STM2176	STM2176	putative glutathione S-transferase	**-0.09**	0.89578
STM2177	STM2177	putative flutathione S-transferase	**-0.44**	0.34148
STM2177	STM2177	putative flutathione S-transferase	**0.42**	0.35816
STM2178	STM2178	putative 1,2-dioxygenase	**0.26**	0.61201
STM2178	STM2178	putative 1,2-dioxygenase	**0.67**	0.20168
STM2179	STM2179	putative sugar transporter	**0.09**	0.85149
STM2179	STM2179	putative sugar transporter	**0.65**	0.23772
STM2180	STM2180	putative transcriptional regulator	**0.01**	0.98718
STM2180	STM2180	putative transcriptional regulator	**0.12**	0.80070
STM2181	yohJ	hypothetical protein STM2181	**-0.58**	0.26261
STM2181	yohJ	hypothetical protein STM2181	**-0.32**	0.57950
STM2182	yohK	hypothetical protein STM2182	**0.03**	0.96018
STM2182	yohK	hypothetical protein STM2182	**0.33**	0.41314
STM2183	cdd	cytidine deaminase	**0.09**	0.87154
STM2183	cdd	cytidine deaminase	**0.99**	0.09224
STM2184	sanA	vancomycin sensitivity	**-0.04**	0.93485
STM2184	sanA	vancomycin sensitivity	**0.23**	0.60679
STM2185	b2145	putative inner membrane protein	**-0.06**	0.91170
STM2185	b2145	putative inner membrane protein	**0.25**	0.52151
STM2186	STM2186	putative NADPH-dependent glutamate synthase beta chain	**-0.14**	0.82071
STM2186	STM2186	putative NADPH-dependent glutamate synthase beta chain	**0.66**	0.22621
STM2187	yeiA	dihydropyrimidine dehydrogenase	**-0.39**	0.37610
STM2187	yeiA	dihydropyrimidine dehydrogenase	**0.26**	0.67662
STM2188	mglC	beta-methylgalactoside transporter inner membrane component	**-0.27**	0.76811
STM2188	mglC	beta-methylgalactoside transporter inner membrane component	**1.17**	0.06780

STM2189	mglA	methyl-galactoside transport protein	**0.42**	0.51252
STM2189	mglA	methyl-galactoside transport protein	**1.19**	0.13206
STM2190	mglB	galactose transport protein	**0.28**	0.66641
STM2190	mglB	galactose transport protein	**1.21**	0.10586
STM2191	galS	mgl operon transcriptional repressor	**0.27**	0.60891
STM2191	galS	mgl operon transcriptional repressor	**0.96**	0.11690
STM2192	yeiB	putative inner membrane protein	**-0.12**	0.83223
STM2192	yeiB	putative inner membrane protein	**0.09**	0.84854
STM2193	folE	GTP cyclohydrolase I	**-0.23**	0.57465
STM2193	folE	GTP cyclohydrolase I	**0.02**	0.97333
STM2194	yeiG	putative esterase	**-0.14**	0.76381
STM2194	yeiG	putative esterase	**-0.07**	0.88959
STM2195	STM2195	putative transcriptional regulator	**-0.04**	0.94798
STM2195	STM2195	putative transcriptional regulator	**0.15**	0.74481
STM2196	STM2196	putative L-serine dehydratase	**-0.57**	0.28221
STM2196	STM2196	putative L-serine dehydratase	**0.18**	0.66310
STM2197	STM2197	putative phosphoserine phosphatase	**-0.64**	0.33452
STM2197	STM2197	putative phosphoserine phosphatase	**0.15**	0.81667
STM2198	STM2198	putative regulatory protein	**0.41**	0.45477
STM2198	STM2198	putative regulatory protein	**0.62**	0.30605
STM2199	cirA	colicin I receptor protein	**-0.41**	0.50529
STM2199	cirA	colicin I receptor protein	**0.71**	0.21671
STM2200	lysP	lysine-specific permease	**-0.04**	0.93506
STM2200	lysP	lysine-specific permease	**0.12**	0.86585
STM2201	yeiE	putative transcriptional regulator	**0.19**	0.65353
STM2201	yeiE	putative transcriptional regulator	**0.11**	0.82327
STM2202	yeiH	putative inner membrane protein	**0.05**	0.92874
STM2202	yeiH	putative inner membrane protein	**-0.07**	0.88765
STM2203	nfo	endonuclease IV	**-0.64**	0.21015
STM2203	nfo	endonuclease IV	**-0.08**	0.84862
STM2204	fruA	fructose-specific transport protein	**-0.09**	0.88561
STM2204	fruA	fructose-specific transport protein	**0.24**	0.69882
STM2205	fruK	1-phosphofructokinase	**-0.36**	0.40633
STM2205	fruK	1-phosphofructokinase	**0.07**	0.91900
STM2206	fruF	phosphoenolpyruvate-dependent sugar phosphotransferase system	**-0.17**	0.76631
STM2206	fruF	phosphoenolpyruvate-dependent sugar phosphotransferase system	**-0.09**	0.87146
STM2207	setB	proton efflux pump	**-0.49**	0.22644
STM2207	setB	proton efflux pump	**-0.09**	0.81862
STM2208	STM2208	putative inner membrane protein	**-0.50**	0.33536
STM2208	STM2208	putative inner membrane protein	**0.20**	0.79176
STM2209	STM2209	putative inner membrane protein	**0.08**	0.85766
STM2209	STM2209	putative inner membrane protein	**-0.10**	0.86958
STM2211,S	yeiP	elongation factor P	**-0.16**	0.68583
STM2211,S	yeiP	elongation factor P	**0.53**	0.21501
STM2212	yeiR	putative cobalamin biosynthetic protein	**-0.85**	0.11224
STM2212	yeiR	putative cobalamin biosynthetic protein	**-0.04**	0.95721
STM2213	yeiU	putative permease	**-0.99**	0.08783
STM2213	yeiU	putative permease	**-0.96**	0.13206
STM2214	spr	putative lipoprotein	**-0.02**	0.96785
STM2214	spr	putative lipoprotein	**-0.05**	0.92637
STM2215	rtn	hypothetical protein STM2215	**-0.17**	0.77923
STM2215	rtn	hypothetical protein STM2215	**0.02**	0.97449
STM2216	yejA	putative ABC transporter periplasmic binding protein	**-0.16**	0.73157
STM2216	yejA	putative ABC transporter periplasmic binding protein	**0.38**	0.34272
STM2217	yejB	putative ABC-type dipeptide/oligopeptide/nickel transport system	**-0.16**	0.75424
STM2217	yejB	putative ABC-type dipeptide/oligopeptide/nickel transport system	**0.01**	0.99213
STM2218	yejE	putative ABC-type dipeptide/oligopeptide/nickel transport system	**-0.08**	0.89675

STM2218	yejE	putative ABC-type dipeptide/oligopeptide/nickel transport system	**0.28**	0.49035
STM2219	yejF	putative ABC-type transport system ATPase component	**-0.11**	0.81323
STM2219	yejF	putative ABC-type transport system ATPase component	**0.09**	0.87975
STM2220	yejG	putative cytoplasmic protein	**-0.40**	0.26465
STM2220	yejG	putative cytoplasmic protein	**0.00**	0.99751
STM2221	bcr	bicyclomycin resistance protein	**-0.20**	0.58595
STM2221	bcr	bicyclomycin resistance protein	**-0.20**	0.63477
STM2222	rsuA	16S rRNA pseudouridylate 516 synthase	**-0.47**	0.32967
STM2222	rsuA	16S rRNA pseudouridylate 516 synthase	**-0.40**	0.33971
STM2223	yejH	putative ATP-dependent helicase	**-0.36**	0.39302
STM2223	yejH	putative ATP-dependent helicase	**-0.11**	0.87456
STM2224	rplY	50S ribosomal protein L25	**-0.10**	0.78990
STM2224	rplY	50S ribosomal protein L25	**0.42**	0.36311
STM2225	STM2225	putative inner membrane protein	**-0.04**	0.94426
STM2225	STM2225	putative inner membrane protein	**0.16**	0.81342
STM2226	yejK	nucleoid-associated protein NdpA	**-0.08**	0.82443
STM2226	yejK	nucleoid-associated protein NdpA	**0.78**	0.11913
STM2227	yejL	putative cytoplasmic protein	**-0.19**	0.59768
STM2227	yejL	putative cytoplasmic protein	**-0.01**	0.98793
STM2228	yejM	putative hydrolase	**0.06**	0.90797
STM2228	yejM	putative hydrolase	**-0.27**	0.46854
STM2229	tRNAPro2	STM2229	**-0.27**	0.70249
STM2229	tRNAPro2	STM2229	**0.51**	0.33813
STM2231	STM2231	virulence protein	**0.01**	0.99268
STM2231	STM2231	virulence protein	**0.67**	0.19142
STM2232	oafA	O-antigen acetylase	**-0.02**	0.97505
STM2232	oafA	O-antigen acetylase	**0.17**	0.71973
STM2233	STM2233	putative cytoplasmic protein	**-0.42**	0.32181
STM2233	STM2233	putative cytoplasmic protein	**-0.11**	0.84911
STM2234	STM2234	putative phage tail fiber assembly protein	**-0.30**	0.68313
STM2234	STM2234	putative phage tail fiber assembly protein	**-0.16**	0.80840
STM2235	STM2235	hypothetical protein STM2235	**0.34**	0.75002
STM2235	STM2235	hypothetical protein STM2235	**-0.04**	0.93991
STM2236	STM2236	hypothetical protein STM2236	**-0.39**	0.56253
STM2236	STM2236	hypothetical protein STM2236	**-0.24**	0.61930
STM2237	STM2237	putative inner membrane protein	**-0.05**	0.94739
STM2237	STM2237	putative inner membrane protein	**0.46**	0.33536
STM2238	STM2238	hypothetical protein STM2238	**-0.32**	0.56535
STM2238	STM2238	hypothetical protein STM2238	**-0.13**	0.83855
STM2240	STM2240	putative cytoplasmic protein	**-0.46**	0.46784
STM2240	STM2240	putative cytoplasmic protein	**0.02**	0.97583
STM2240	STM2240	putative cytoplasmic protein	**0.31**	0.70355
STM2240	STM2240	putative cytoplasmic protein	**-0.25**	0.67823
STM2241	sspH2	leucine-rich repeat protein	**-0.87**	0.11690
STM2241	sspH2	leucine-rich repeat protein	**-0.21**	0.55842
STM2242	STM2242	putative phage tail fiber protein	**-0.19**	0.76605
STM2242	STM2242	putative phage tail fiber protein	**0.28**	0.48814
STM2243	STM2243	putative tail fiber protein of phage	**0.03**	0.96785
STM2243	STM2243	putative tail fiber protein of phage	**0.57**	0.30497
STM2245	STM2245	putative outer membrane protein	**-0.12**	0.82431
STM2245	STM2245	putative outer membrane protein	**0.30**	0.74714
STM2246	narP	response regulator	**-0.19**	0.70084
STM2246	narP	response regulator	**-0.33**	0.52767
STM2247	ccmH	putative heme lyase subunit	**-0.16**	0.75530
STM2247	ccmH	putative heme lyase subunit	**1.02**	0.10012
STM2254	ccmA	heme exporter protein	**-0.35**	0.52511
STM2254	ccmA	heme exporter protein	**-0.16**	0.68599
STM2254	ccmA	heme exporter protein	**0.36**	0.32126
STM2254	ccmA	heme exporter protein	**0.37**	0.40227
STM2255	napC	periplasmic nitrate reductase	**-0.17**	0.68136
STM2255	napC	periplasmic nitrate reductase	**0.31**	0.41552
STM2256	napB	periplasmic nitrate reductase	**0.20**	0.64422

STM2256	napB	periplasmic nitrate reductase	**0.64**	0.40562
STM2257	napH	quinol dehydrogenase membrane component	**-0.39**	0.36465
STM2257	napH	quinol dehydrogenase membrane component	**-0.02**	0.96650
STM2258	napG	quinol dehydrogenase periplasmic component	**0.01**	0.99009
STM2258	napG	quinol dehydrogenase periplasmic component	**0.16**	0.79893
STM2259	napA	periplasmic nitrate reductase	**-0.11**	0.78755
STM2259	napA	periplasmic nitrate reductase	**0.71**	0.14030
STM2260	napD	periplasmic nitrate reductase	**-0.35**	0.61654
STM2260	napD	periplasmic nitrate reductase	**0.16**	0.76172
STM2262	eco	ecotin precursor	**-0.24**	0.57559
STM2262	eco	ecotin precursor	**0.77**	0.13206
STM2263	yojI	putative ABC-type multidrug/protein/lipid transport system ATPase	**0.18**	0.79223
STM2263	yojI	putative ABC-type multidrug/protein/lipid transport system ATPase	**0.40**	0.39136
STM2264	alkB	DNA repair system protein	**-0.10**	0.80652
STM2264	alkB	DNA repair system protein	**-0.11**	0.80833
STM2265	ada	O6-methylguanine-DNA methyltransferase/transcription	**-0.48**	0.22540
STM2265	ada	O6-methylguanine-DNA methyltransferase/transcription	**-0.19**	0.67804
STM2266	apbE	putative lipoprotein	**-0.71**	0.16281
STM2266	apbE	putative lipoprotein	**-0.33**	0.46199
STM2267	ompC	outer membrane protein C precursor	**-0.73**	0.34051
STM2267	ompC	outer membrane protein C precursor	**-0.79**	0.19843
STM2269	yojN	putative sensor kinase	**-0.19**	0.67330
STM2269	yojN	putative sensor kinase	**0.40**	0.31384
STM2270	rcsB	response regulator	**-0.27**	0.61636
STM2270	rcsB	response regulator	**-0.04**	0.95397
STM2271	rcsC	sensory histidine kinase	**-0.41**	0.28598
STM2271	rcsC	sensory histidine kinase	**0.37**	0.29543
STM2272	gyrA	DNA gyrase subunit A	**-0.38**	0.35955
STM2272	gyrA	DNA gyrase subunit A	**0.06**	0.88959
STM2273	STM2273	putative dehydratase	**0.09**	0.89736
STM2273	STM2273	putative dehydratase	**0.28**	0.54461
STM2274	STM2274	putative permease	**-0.08**	0.88937
STM2274	STM2274	putative permease	**-0.08**	0.89863
STM2275	STM2275	putative regulatory protein	**-0.24**	0.51480
STM2275	STM2275	putative regulatory protein	**0.41**	0.27636
STM2276	ubiG	3-demethylubiquinone-9 3-methyltransferase	**0.62**	0.17359
STM2276	ubiG	3-demethylubiquinone-9 3-methyltransferase	**0.89**	0.20285
STM2277	nrdA	ribonucleotide-diphosphate reductase alpha subunit	**0.14**	0.76172
STM2277	nrdA	ribonucleotide-diphosphate reductase alpha subunit	**0.30**	0.38351
STM2278	nrdB	ribonucleotide-diphosphate reductase beta subunit	**-0.27**	0.55403
STM2278	nrdB	ribonucleotide-diphosphate reductase beta subunit	**0.35**	0.38748
STM2279	yfaE	putative ferredoxin	**-0.17**	0.73129
STM2279	yfaE	putative ferredoxin	**0.04**	0.92840
STM2280	STM2280	putative permease	**-0.37**	0.52676
STM2280	STM2280	putative permease	**-0.17**	0.74528
STM2281	STM2281	putative transcriptional regulator	**0.18**	0.81667
STM2281	STM2281	putative transcriptional regulator	**0.94**	0.11224
STM2282	glpQ	periplasmic glycerophosphodiester phosphodiesterase	**0.44**	0.53362
STM2282	glpQ	periplasmic glycerophosphodiester phosphodiesterase	**0.42**	0.47610
STM2283	glpT	sn-glycerol-3-phosphate transport protein	**0.75**	0.33531
STM2283	glpT	sn-glycerol-3-phosphate transport protein	**0.92**	0.21078
STM2284	glpA	sn-glycerol-3-phosphate dehydrogenase large subunit	**0.83**	0.23187
STM2284	glpA	sn-glycerol-3-phosphate dehydrogenase large subunit	**0.90**	0.13813
STM2285	glpB	anaerobic glycerol-3-phosphate dehydrogenase subunit B	**0.36**	0.32675
STM2285	glpB	anaerobic glycerol-3-phosphate dehydrogenase subunit B	**0.62**	0.15859
STM2286	glpC	sn-glycerol-3-phosphate dehydrogenase K-small subunit	**-0.40**	0.45800
STM2286	glpC	sn-glycerol-3-phosphate dehydrogenase K-small subunit	**0.41**	0.67157
STM2287	STM2287	putative cytoplasmic protein	**-0.37**	0.37919
STM2287	STM2287	putative cytoplasmic protein	**0.02**	0.98539

STM2288	STM2288	putative cytoplasmic protein	**-0.49**	0.36842
STM2288	STM2288	putative cytoplasmic protein	**0.31**	0.62572
STM2289	STM2289	putative 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase	**-1.02**	0.11224
STM2289	STM2289	putative 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase	**0.09**	0.82956
STM2290	yfaV	putative transport protein	**-0.06**	0.91148
STM2290	yfaV	putative transport protein	**0.32**	0.66070
STM2291	yfaW	putative galactonate dehydratase	**0.03**	0.98140
STM2291	yfaW	putative galactonate dehydratase	**-0.12**	0.80475
STM2292	yfaX	putative transcriptional regulator	**-0.17**	0.76483
STM2292	yfaX	putative transcriptional regulator	**-0.14**	0.85209
STM2293	STM2293	competence damage-inducible protein A	**0.05**	0.93637
STM2293	STM2293	competence damage-inducible protein A	**0.27**	0.59325
STM2294	yfaZ	putative inner membrane protein	**0.47**	0.22788
STM2294	yfaZ	putative inner membrane protein	**0.96**	0.09991
STM2295	yfaO	putative NTP pyrophosphohydrolase	**0.01**	0.98693
STM2295	yfaO	putative NTP pyrophosphohydrolase	**-0.09**	0.85457
STM2296	ais	aluminum-inducible protein	**-0.64**	0.18265
STM2296	ais	aluminum-inducible protein	**-0.60**	0.20916
STM2297	yfbE	4-amino-4-deoxy-L-arabinose lipopolysaccharide-modifying enzyme	**-2.45**	0.00231
STM2297	yfbE	4-amino-4-deoxy-L-arabinose lipopolysaccharide-modifying enzyme	**-1.90**	0.00655
STM2298	pmrF	putative glycosyl transferase	**-1.25**	0.11690
STM2298	pmrF	putative glycosyl transferase	**-0.72**	0.24444
STM2299	yfbG	hypothetical protein STM2299	**-1.30**	0.04232
STM2299	yfbG	hypothetical protein STM2299	**-1.04**	0.06967
STM2300	STM2300	putative cytoplasmic protein	**-0.82**	0.17940
STM2300	STM2300	putative cytoplasmic protein	**-0.13**	0.88914
STM2301	pqaB	putative melittin resistance protein	**-1.43**	0.08322
STM2301	pqaB	putative melittin resistance protein	**-0.80**	0.36017
STM2302	STM2302	putative inner membrane protein	**-0.36**	0.39186
STM2302	STM2302	putative inner membrane protein	**0.54**	0.25125
STM2303	STM2303	hypothetical protein STM2303	**-0.85**	0.11690
STM2303	STM2303	hypothetical protein STM2303	**-0.42**	0.34761
STM2304	pmrD	polymyxin resistance protein B	**-0.78**	0.34719
STM2304	pmrD	polymyxin resistance protein B	**-0.83**	0.13128
STM2305	menE	O-succinylbenzoic acid--CoA ligase	**-0.37**	0.46720
STM2305	menE	O-succinylbenzoic acid--CoA ligase	**-0.04**	0.91844
STM2306	menC	O-succinylbenzoate synthase	**-0.10**	0.88599
STM2306	menC	O-succinylbenzoate synthase	**0.02**	0.96568
STM2307	menB	naphthoate synthase	**-0.63**	0.19811
STM2307	menB	naphthoate synthase	**0.02**	0.96785
STM2308	yfbB	putative enzyme	**-0.33**	0.45259
STM2308	yfbB	putative enzyme	**0.15**	0.72821
STM2309	menD	2-oxoglutarate decarboxylase	**0.76**	0.18918
STM2309	menD	2-oxoglutarate decarboxylase	**0.84**	0.28861
STM2310	menF	menaquinone-specific isochorismate synthase	**0.03**	0.96247
STM2310	menF	menaquinone-specific isochorismate synthase	**1.04**	0.20916
STM2311	elaB	putative inner membrane protein	**-0.40**	0.35937
STM2311	elaB	putative inner membrane protein	**-0.05**	0.92815
STM2312	elaA	putative acyltransferase	**0.10**	0.84657
STM2312	elaA	putative acyltransferase	**0.40**	0.51819
STM2313	elaC	ribonuclease Z	**0.06**	0.90531
STM2313	elaC	ribonuclease Z	**0.33**	0.47844
STM2314	STM2314	putative chemotaxis signal transduction protein	**0.28**	0.65145
STM2314	STM2314	putative chemotaxis signal transduction protein	**0.46**	0.25460
STM2315	yfbK	hypothetical protein STM2315	**-0.06**	0.89108
STM2315	yfbK	hypothetical protein STM2315	**0.45**	0.26239
STM2316,S	nuoN	NADH dehydrogenase subunit N	**-0.15**	0.68830
STM2316,S	nuoN	NADH dehydrogenase subunit N	**0.24**	0.48362
STM2317	nuoM	NADH dehydrogenase subunit M	**0.23**	0.58095
STM2317	nuoM	NADH dehydrogenase subunit M	**0.25**	0.51529
STM2318	nuoL	NADH dehydrogenase subunit L	**0.11**	0.87019

STM2318	nuoL	NADH dehydrogenase subunit L	**-0.01**	0.98640
STM2319	nuoK	NADH dehydrogenase kappa subunit	**0.19**	0.57950
STM2319	nuoK	NADH dehydrogenase kappa subunit	**0.02**	0.96797
STM2320	nuoJ	NADH dehydrogenase subunit J	**-0.06**	0.91203
STM2320	nuoJ	NADH dehydrogenase subunit J	**0.34**	0.60936
STM2321	nuoI	NADH dehydrogenase subunit I	**-0.25**	0.65451
STM2321	nuoI	NADH dehydrogenase subunit I	**-0.09**	0.85766
STM2322	nuoH	NADH dehydrogenase subunit H	**0.27**	0.48362
STM2322	nuoH	NADH dehydrogenase subunit H	**0.40**	0.38080
STM2323,S	nuoG	NADH dehydrogenase gamma subunit	**-0.06**	0.90587
STM2323,S	nuoG	NADH dehydrogenase gamma subunit	**0.23**	0.53734
STM2324	nuoF	NADH dehydrogenase I chain F	**0.17**	0.66893
STM2324	nuoF	NADH dehydrogenase I chain F	**0.22**	0.61679
STM2325	nuoE	ATP synthase subunit E	**-0.04**	0.95396
STM2325	nuoE	ATP synthase subunit E	**-0.02**	0.98090
STM2326	nuoC	NADH dehydrogenase I chain C/D	**0.40**	0.36856
STM2326	nuoC	NADH dehydrogenase I chain C/D	**0.32**	0.45069
STM2327	nuoB	NADH dehydrogenase beta subunit	**0.40**	0.52511
STM2327	nuoB	NADH dehydrogenase beta subunit	**0.54**	0.34148
STM2328	nuoA	NADH dehydrogenase alpha subunit	**0.42**	0.34148
STM2328	nuoA	NADH dehydrogenase alpha subunit	**0.55**	0.22104
STM2329	STM2329	putative cytoplasmic protein	**0.12**	0.76319
STM2329	STM2329	putative cytoplasmic protein	**0.18**	0.74557
STM2330	lrhA	NADH dehydrogenase transcriptional repressor	**-0.42**	0.27636
STM2330	lrhA	NADH dehydrogenase transcriptional repressor	**-0.48**	0.27312
STM2331	yfbQ	aspartate aminotransferase	**-0.09**	0.84783
STM2331	yfbQ	aspartate aminotransferase	**0.27**	0.61809
STM2332	STM2332	hypothetical protein STM2332	**-0.59**	0.22421
STM2332	STM2332	hypothetical protein STM2332	**-0.02**	0.97415
STM2333	yfbS	putative response regulator	**-0.50**	0.35151
STM2333	yfbS	putative response regulator	**-0.14**	0.81075
STM2334	yfbT	putative phosphatase	**-0.04**	0.94964
STM2334	yfbT	putative phosphatase	**0.50**	0.21777
STM2335	yfbU	hypothetical protein STM2335	**0.23**	0.53731
STM2335	yfbU	hypothetical protein STM2335	**0.17**	0.69126
STM2336	STM2336	hypothetical protein STM2336	**0.02**	0.97176
STM2336	STM2336	hypothetical protein STM2336	**-0.16**	0.75437
STM2337	ackA	acetate/propionate kinase	**-0.26**	0.60940
STM2337	ackA	acetate/propionate kinase	**-0.08**	0.90499
STM2338	pta	phosphate acetyltransferase	**-0.20**	0.57850
STM2338	pta	phosphate acetyltransferase	**-0.03**	0.95496
STM2339	yfcC	putative integral membrane protein	**0.05**	0.93924
STM2339	yfcC	putative integral membrane protein	**-0.34**	0.47610
STM2340	STM2340	putative transketolase	**0.12**	0.88508
STM2340	STM2340	putative transketolase	**0.16**	0.68961
STM2341	STM2341	putative transketolase	**-0.11**	0.91170
STM2341	STM2341	putative transketolase	**0.75**	0.13027
STM2342	ulaA	ascorbate-specific PTS system enzyme IIC	**0.41**	0.55309
STM2342	ulaA	ascorbate-specific PTS system enzyme IIC	**0.74**	0.30748
STM2343	STM2343	putative cytoplasmic protein	**0.39**	0.45861
STM2343	STM2343	putative cytoplasmic protein	**-0.11**	0.93023
STM2344	STM2344	putative phosphotransferase system enzyme II A component	**0.01**	0.99009
STM2344	STM2344	putative phosphotransferase system enzyme II A component	**1.27**	0.17359
STM2345	STM2345	putative transcriptional regulator	**-0.15**	0.77683
STM2345	STM2345	putative transcriptional regulator	**0.26**	0.56849
STM2346	STM2346	putative NTP pyrophosphohydrolase	**-0.35**	0.35937
STM2346	STM2346	putative NTP pyrophosphohydrolase	**-0.21**	0.63510
STM2347	yfcE	phosphodiesterase	**-0.33**	0.66469
STM2347	yfcE	phosphodiesterase	**1.22**	0.11913
STM2348	yfcF	putative glutathione S-transferase	**-0.13**	0.81732
STM2348	yfcF	putative glutathione S-transferase	**-0.36**	0.45082

STM2349	yfcG	putative glutathione S-transferase	**-0.04**	0.96605
STM2349	yfcG	putative glutathione S-transferase	**0.95**	0.43982
STM2350	yfcH	putative sugar nucleotide epimerase	**-0.06**	0.93916
STM2350	yfcH	putative sugar nucleotide epimerase	**0.30**	0.65181
STM2351	hisP	histidine/lysine/arginine/ornithine transport protein	**0.27**	0.66747
STM2351	hisP	histidine/lysine/arginine/ornithine transport protein	**1.31**	0.29866
STM2352	hisM	histidine/lysine/arginine/ornithine transport protein	**0.02**	0.96785
STM2352	hisM	histidine/lysine/arginine/ornithine transport protein	**0.41**	0.39186
STM2353	hisQ	histidine/lysine/arginine/ornithine transport protein	**0.00**	0.99770
STM2353	hisQ	histidine/lysine/arginine/ornithine transport protein	**0.58**	0.36942
STM2354	hisJ	histidine transport protein	**-0.50**	0.21933
STM2354	hisJ	histidine transport protein	**-0.16**	0.71169
STM2355	argT	lysine/arginine/ornithine transport protein	**0.15**	0.77346
STM2355	argT	lysine/arginine/ornithine transport protein	**0.53**	0.33452
STM2356	ubiX	3-octaprenyl-4-hydroxybenzoate carboxy-lyase	**-0.53**	0.38729
STM2356	ubiX	3-octaprenyl-4-hydroxybenzoate carboxy-lyase	**-0.15**	0.80475
STM2357	STM2357	putative amino acid transporter	**0.24**	0.54497
STM2357	STM2357	putative amino acid transporter	**0.13**	0.81667
STM2358	STM2358	putative cytoplasmic protein	**0.12**	0.83240
STM2358	STM2358	putative cytoplasmic protein	**0.39**	0.33452
STM2359	STM2359	putative amino acid transporter	**-0.61**	0.22540
STM2359	STM2359	putative amino acid transporter	**-0.38**	0.44208
STM2360	STM2360	putative diaminopimelate decarboxylase	**-0.34**	0.52934
STM2360	STM2360	putative diaminopimelate decarboxylase	**-0.19**	0.76767
STM2361	STM2361	putative regulatory protein	**0.11**	0.84503
STM2361	STM2361	putative regulatory protein	**-0.40**	0.47159
STM2362	purF	amidophosphoribosyltransferase	**-0.25**	0.61960
STM2362	purF	amidophosphoribosyltransferase	**-0.08**	0.86682
STM2363	cvpA	colicin V production protein	**0.20**	0.55338
STM2363	cvpA	colicin V production protein	**0.09**	0.82428
STM2364	dedD	putative lipoprotein	**0.04**	0.93280
STM2364	dedD	putative lipoprotein	**-0.16**	0.69882
STM2365	folC	multifunctional folylpolyglutamate synthase	**-0.15**	0.76161
STM2365	folC	multifunctional folylpolyglutamate synthase	**0.06**	0.92371
STM2366	accD	acetyl-CoA carboxylase beta subunit	**-0.28**	0.56162
STM2366	accD	acetyl-CoA carboxylase beta subunit	**-0.46**	0.47937
STM2367	dedA	hypothetical protein STM2367	**-0.10**	0.81667
STM2367	dedA	hypothetical protein STM2367	**-0.02**	0.97415
STM2368	truA	tRNA pseudouridine synthase A	**0.06**	0.90181
STM2368	truA	tRNA pseudouridine synthase A	**-0.07**	0.90430
STM2369	usg	hypothetical protein STM2369	**-0.14**	0.84783
STM2369	usg	hypothetical protein STM2369	**-0.26**	0.53459
STM2370	pdxB	erythronate-4-phosphate dehydrogenase	**-0.13**	0.74142
STM2370	pdxB	erythronate-4-phosphate dehydrogenase	**-0.28**	0.47929
STM2371	flk	flagellar protein	**0.00**	0.99887
STM2371	flk	flagellar protein	**-0.11**	0.84021
STM2372	STM2372	hypothetical protein STM2372	**-0.10**	0.82756
STM2372	STM2372	hypothetical protein STM2372	**0.41**	0.31989
STM2373	STM2373	putative cytoplasmic protein	**-0.21**	0.74361
STM2373	STM2373	putative cytoplasmic protein	**0.12**	0.81901
STM2374	STM2374	putative regulatory protein	**0.05**	0.95384
STM2374	STM2374	putative regulatory protein	**-0.02**	0.97720
STM2375	STM2375	putative cytoplasmic protein	**-0.21**	0.66561
STM2375	STM2375	putative cytoplasmic protein	**-0.15**	0.79666
STM2376	STM2376	putative periplasmic protein	**-0.25**	0.57659
STM2376	STM2376	putative periplasmic protein	**-0.02**	0.97660
STM2377	STM2377	putative inner membrane protein	**-0.09**	0.85679
STM2377	STM2377	putative inner membrane protein	**0.01**	0.98539
STM2378	fabB	3-oxoacyl-(acyl carrier protein) synthase	**-0.17**	0.70966
STM2378	fabB	3-oxoacyl-(acyl carrier protein) synthase	**-0.23**	0.56860
STM2379	STM2379	hypothetical protein STM2379	**-0.33**	0.54510
STM2379	STM2379	hypothetical protein STM2379	**-0.04**	0.96785
STM2380	yfcL	putative cytoplasmic protein	**0.15**	0.76008

STM2380	yfcL	putative cytoplasmic protein	**0.24**	0.60051
STM2381	yfcM	putative cytoplasmic protein	**-0.65**	0.16281
STM2381	yfcM	putative cytoplasmic protein	**0.24**	0.49299
STM2382	yfcA	putative permease	**0.27**	0.50255
STM2382	yfcA	putative permease	**0.75**	0.12727
STM2383	mepA	penicillin-insensitive murein endopeptidase	**-0.59**	0.31422
STM2383	mepA	penicillin-insensitive murein endopeptidase	**-0.46**	0.26833
STM2384	aroC	chorismate synthase	**-0.14**	0.81667
STM2384	aroC	chorismate synthase	**-0.05**	0.93767
STM2385	yfcB	putative methylase	**0.00**	0.99447
STM2385	yfcB	putative methylase	**-0.12**	0.79102
STM2386	yfcN	hypothetical protein STM2386	**-0.54**	0.24444
STM2386	yfcN	hypothetical protein STM2386	**-0.32**	0.38985
STM2387	sixA	phosphohistidine phosphatase	**-0.49**	0.22283
STM2387	sixA	phosphohistidine phosphatase	**-0.12**	0.78312
STM2388	yfcX	putative dehydrogenase	**-0.02**	0.96794
STM2388	yfcX	putative dehydrogenase	**0.61**	0.29064
STM2389	yfcY	acetyl-CoA acetyltransferase	**-0.33**	0.80559
STM2389	yfcY	acetyl-CoA acetyltransferase	**0.38**	0.79308
STM2390	yfcZ	putative cytoplasmic protein	**0.17**	0.72146
STM2390	yfcZ	putative cytoplasmic protein	**0.24**	0.59760
STM2391	fadL	outer membrane-bound fatty acid transporter	**-0.05**	0.92371
STM2391	fadL	outer membrane-bound fatty acid transporter	**0.22**	0.52101
STM2392	vacJ	lipoprotein precursor	**-0.06**	0.90181
STM2392	vacJ	lipoprotein precursor	**0.76**	0.12009
STM2393	yfdC	hypothetical protein STM2393	**0.30**	0.88018
STM2393	yfdC	hypothetical protein STM2393	**0.80**	0.55584
STM2394	argW	STM2394	**0.00**	0.99546
STM2394	argW	STM2394	**-0.01**	0.99009
STM2395	pgtE	outer membrane protein E precursor	**0.09**	0.84584
STM2395	pgtE	outer membrane protein E precursor	**0.16**	0.83268
STM2396	pgtA	activator	**-0.09**	0.87079
STM2396	pgtA	activator	**0.46**	0.39315
STM2397	pgtB	phosphoglycerate transport system sensor protein	**-0.34**	0.58108
STM2397	pgtB	phosphoglycerate transport system sensor protein	**-0.02**	0.98555
STM2398	pgtC	phosphoglycerate transport regulatory protein precursor	**-0.59**	0.41715
STM2398	pgtC	phosphoglycerate transport regulatory protein precursor	**0.61**	0.36311
STM2399	pgtP	transporter	**0.18**	0.70199
STM2399	pgtP	transporter	**0.50**	0.49708
STM2400	STM2400	putative inner membrane protein	**-0.15**	0.72781
STM2400	STM2400	putative inner membrane protein	**0.18**	0.69914
STM2401	ddg	lipid A biosynthesis lauroyl acyltransferase	**-0.16**	0.80110
STM2401	ddg	lipid A biosynthesis lauroyl acyltransferase	**-0.10**	0.85922
STM2402	yfdZ	hypothetical protein STM2402	**0.06**	0.90797
STM2402	yfdZ	hypothetical protein STM2402	**0.37**	0.55956
STM2403	glk	glucokinase	**-0.07**	0.89640
STM2403	glk	glucokinase	**-0.01**	0.98539
STM2404	STM2404	hypothetical protein STM2404	**-0.04**	0.94765
STM2404	STM2404	hypothetical protein STM2404	**-0.07**	0.89811
STM2405	STM2405	indolepyruvate decarboxylase	**-0.97**	0.14928
STM2405	STM2405	indolepyruvate decarboxylase	**-0.02**	0.96640
STM2406	STM2406	putative oxidoreductase	**-0.10**	0.87667
STM2406	STM2406	putative oxidoreductase	**0.04**	0.92637
STM2407	ypeC	putative periplasmic protein	**0.56**	0.35424
STM2407	ypeC	putative periplasmic protein	**1.01**	0.25460
STM2408	mntH	putative manganese transport protein MntH	**-0.56**	0.32164
STM2408	mntH	putative manganese transport protein MntH	**0.05**	0.93841
STM2409	nupC	nucleoside transport	**0.26**	0.51538
STM2409	nupC	nucleoside transport	**0.54**	0.25565
STM2410	yfeA	hypothetical protein STM2410	**-0.17**	0.77605
STM2410	yfeA	hypothetical protein STM2410	**0.28**	0.58108
STM2412	alaW	STM2412	**-0.38**	0.41541
STM2412	alaW	STM2412	**-0.45**	0.24444

STM2412	alaW	STM2412	**-0.32**	0.49319
STM2412	alaW	STM2412	**0.02**	0.97449
STM2413	yfeC	putative negative regulator	**-0.16**	0.71404
STM2413	yfeC	putative negative regulator	**0.13**	0.76319
STM2414	yfeD	putative negative regulator	**-0.04**	0.93506
STM2414	yfeD	putative negative regulator	**0.12**	0.82637
STM2415	gltX	glutamyl-tRNA synthetase	**0.03**	0.95589
STM2415	gltX	glutamyl-tRNA synthetase	**0.02**	0.97874
STM2418	valY	STM2418	**-0.33**	0.37150
STM2418	valY	STM2418	**-0.61**	0.36270
STM2418	valY	STM2418	**-0.10**	0.85893
STM2418	valY	STM2418	**-0.53**	0.42312
STM2418	valY	STM2418	**-0.37**	0.49374
STM2418	valY	STM2418	**-0.20**	0.77432
STM2418	valY	STM2418	**-0.31**	0.57659
STM2418	valY	STM2418	**-0.20**	0.70199
STM2419	lysV	STM2419	**-0.23**	0.64330
STM2419	lysV	STM2419	**-0.36**	0.52208
STM2419	lysV	STM2419	**-0.64**	0.30422
STM2419	lysV	STM2419	**-0.06**	0.91484
STM2419	lysV	STM2419	**-0.37**	0.47455
STM2419	lysV	STM2419	**-0.30**	0.51267
STM2419	lysV	STM2419	**-0.23**	0.57089
STM2419	lysV	STM2419	**-0.29**	0.52151
STM2419	lysV	STM2419	**-0.34**	0.36243
STM2419	lysV	STM2419	**-0.37**	0.30113
STM2420	xapR	XapA transcriptional regulator	**-0.38**	0.32763
STM2420	xapR	XapA transcriptional regulator	**-0.23**	0.63815
STM2420,1n	STM2420,1n	hypothetical protein STM2420,1n	**0.30**	0.61205
STM2420,1n	STM2420,1n	hypothetical protein STM2420,1n	**0.04**	0.94299
STM2421	xapB	xanthosine permease	**-0.24**	0.51604
STM2421	xapB	xanthosine permease	**-0.01**	0.98553
STM2423	yfeN	putative outer membrane protein	**-0.16**	0.74127
STM2423	yfeN	putative outer membrane protein	**-0.44**	0.47174
STM2424	yfeR	putative transcriptional regulator	**-0.05**	0.92253
STM2424	yfeR	putative transcriptional regulator	**0.88**	0.13002
STM2425	yfeH	putative Na+-dependent transporter	**-0.47**	0.40307
STM2425	yfeH	putative Na+-dependent transporter	**-0.14**	0.81697
STM2426	STM2426	putative cytoplasmic protein	**-0.14**	0.75424
STM2426	STM2426	putative cytoplasmic protein	**0.24**	0.54624
STM2427	lig	DNA ligase	**-0.69**	0.16534
STM2427	lig	DNA ligase	**0.08**	0.86703
STM2428	zipA	cell division protein ZipA	**-0.19**	0.61299
STM2428	zipA	cell division protein ZipA	**0.16**	0.70082
STM2429	cysZ	putative sulfate transport protein CysZ	**-0.24**	0.60051
STM2429	cysZ	putative sulfate transport protein CysZ	**-0.04**	0.94658
STM2430	cysK	O-acetylserine sulfhydrolase A	**-0.03**	0.95995
STM2430	cysK	O-acetylserine sulfhydrolase A	**0.11**	0.79037
STM2431	ptsH	phosphohistidinoprotein-hexose phosphotransferase	**0.03**	0.96595
STM2431	ptsH	phosphohistidinoprotein-hexose phosphotransferase	**0.39**	0.34260
STM2432	ptsI	PEP-protein phosphotransferase	**0.18**	0.66506
STM2432	ptsI	PEP-protein phosphotransferase	**0.20**	0.65451
STM2433	crr	glucose-specific PTS system enzyme IIA component	**0.03**	0.93841
STM2433	crr	glucose-specific PTS system enzyme IIA component	**0.42**	0.38425
STM2434	STM2434	putative cytoplasmic protein	**-0.43**	0.26856
STM2434	STM2434	putative cytoplasmic protein	**-0.49**	0.35824
STM2435	pdxK	pyridoxine kinase	**-0.27**	0.61201
STM2435	pdxK	pyridoxine kinase	**0.34**	0.33587
STM2436	ptsJ	putative regulatory protein	**0.98**	0.17919
STM2436	ptsJ	putative regulatory protein	**1.36**	0.16475
STM2437	yfeJ	glutamine amidotransferase	**-0.66**	0.19142
STM2437	yfeJ	glutamine amidotransferase	**0.23**	0.61481
STM2438	yfeK	putative periplasmic protein	**0.14**	0.77346

STM2438	yfeK	putative periplasmic protein	**0.17**	0.63328
STM2439	yfeL	putative membrane carboxypeptidase	**-0.43**	0.48791
STM2439	yfeL	putative membrane carboxypeptidase	**-0.29**	0.52861
STM2440	cysM	cysteine synthase B	**-0.15**	0.73568
STM2440	cysM	cysteine synthase B	**0.17**	0.71864
STM2441	cysA	sulfate permease A protein	**-0.06**	0.93264
STM2441	cysA	sulfate permease A protein	**-0.06**	0.91784
STM2442	cysW	thiosulfate permease W protein	**-0.64**	0.23613
STM2442	cysW	thiosulfate permease W protein	**0.92**	0.26378
STM2443	cysU	thiosulfate transport protein	**-0.18**	0.74344
STM2443	cysU	thiosulfate transport protein	**0.21**	0.67097
STM2444	cysP	thiosulfate transport protein	**-0.38**	0.60620
STM2444	cysP	thiosulfate transport protein	**0.47**	0.39316
STM2445	ucpA	short chain dehydrogenase	**0.06**	0.92102
STM2445	ucpA	short chain dehydrogenase	**0.31**	0.40190
STM2446	STM2446	putative iron-dependent peroxidase	**-0.21**	0.62526
STM2446	STM2446	putative iron-dependent peroxidase	**-0.30**	0.40947
STM2447	STM2447	putative outer membrane lipoprotein	**-0.20**	0.60888
STM2447	STM2447	putative outer membrane lipoprotein	**-0.22**	0.63154
STM2448	yfeZ	putative inner membrane protein	**-0.41**	0.47136
STM2448	yfeZ	putative inner membrane protein	**0.34**	0.46629
STM2449,S	STM2449,S	putative acetyltransferase	**0.09**	0.83100
STM2449,S	STM2449,S	putative acetyltransferase	**0.50**	0.32929
STM2450	amiA	N-acetylmuramoyl-l-alanine amidase I	**-0.18**	0.61634
STM2450	amiA	N-acetylmuramoyl-l-alanine amidase I	**-0.15**	0.68775
STM2451	hemF	coproporphyrinogen III oxidase	**-1.00**	0.06197
STM2451	hemF	coproporphyrinogen III oxidase	**0.14**	0.77923
STM2452	STM2452	putative inner membrane protein	**0.07**	0.87727
STM2452	STM2452	putative inner membrane protein	**0.06**	0.88937
STM2453	STM2453	putative cytoplasmic protein	**-0.44**	0.48214
STM2453	STM2453	putative cytoplasmic protein	**0.36**	0.35101
STM2454	eutR	putative ethanolamine operon regulator	**-0.13**	0.88060
STM2454	eutR	putative ethanolamine operon regulator	**0.13**	0.80093
STM2455	eutK	putative carboxysome structural protein	**-0.16**	0.66807
STM2455	eutK	putative carboxysome structural protein	**0.07**	0.90797
STM2456	eutL	putative carboxysome structural protein	**-0.25**	0.55892
STM2456	eutL	putative carboxysome structural protein	**0.45**	0.32172
STM2457	eutC	ethanolamine ammonia-lyase small subunit	**-0.48**	0.49871
STM2457	eutC	ethanolamine ammonia-lyase small subunit	**-0.18**	0.68143
STM2458	eutB	ethanolamine ammonia-lyase heavy chain	**-0.36**	0.73473
STM2458	eutB	ethanolamine ammonia-lyase heavy chain	**1.12**	0.17139
STM2459	eutA	ethanolamine utilization protein	**0.08**	0.89227
STM2459	eutA	ethanolamine utilization protein	**0.57**	0.21501
STM2460	eutH	putative transport protein	**-0.05**	0.95176
STM2460	eutH	putative transport protein	**0.92**	0.21699
STM2461	eutG	putative transport protein	**0.09**	0.94050
STM2461	eutG	putative transport protein	**-0.09**	0.84622
STM2462	eutJ	ethanolamine utilization protein	**-0.03**	0.96785
STM2462	eutJ	ethanolamine utilization protein	**0.34**	0.42507
STM2463	eutE	putative aldehyde oxidoreductase	**-0.66**	0.20065
STM2463	eutE	putative aldehyde oxidoreductase	**0.11**	0.78633
STM2464	eutN	putative detox protein	**0.18**	0.76553
STM2464	eutN	putative detox protein	**0.91**	0.15276
STM2465	eutM	putative detox protein	**0.25**	0.63235
STM2465	eutM	putative detox protein	**0.78**	0.18313
STM2466	eutD	phosphate acetyltransferase	**-0.31**	0.57945
STM2466	eutD	phosphate acetyltransferase	**0.30**	0.55661
STM2467	eutT	putative cobalamin adenosyltransferase	**-0.15**	0.84109
STM2467	eutT	putative cobalamin adenosyltransferase	**-0.32**	0.57138
STM2468	eutQ	putative ethanolamine utilization protein	**0.24**	0.72987
STM2468	eutQ	putative ethanolamine utilization protein	**0.37**	0.34193
STM2469	eutP	putative ethanolamine utilization protein	**-0.10**	0.82192
STM2469	eutP	putative ethanolamine utilization protein	**0.40**	0.45069

STM2470	eutS	putative carboxysome structural protein	**-0.23**	0.79275
STM2470	eutS	putative carboxysome structural protein	**0.74**	0.29044
STM2472	maeB	phosphate acetyltransferase	**0.05**	0.94565
STM2472	maeB	phosphate acetyltransferase	**0.15**	0.77346
STM2473	talA	transaldolase	**-0.21**	0.70155
STM2473	talA	transaldolase	**0.43**	0.37855
STM2474	tktB	transketolase	**-0.21**	0.73653
STM2474	tktB	transketolase	**-0.03**	0.97140
STM2475	STM2475	putative cytoplasmic protein	**-0.04**	0.97273
STM2475	STM2475	putative cytoplasmic protein	**0.49**	0.42312
STM2476	ypfG	putative periplasmic protein	**-0.13**	0.79371
STM2476	ypfG	putative periplasmic protein	**0.26**	0.66555
STM2477	yffH	putative pyrophosphohydrolase	**-0.01**	0.98640
STM2477	yffH	putative pyrophosphohydrolase	**0.38**	0.31344
STM2478	STM2478	hypothetical protein STM2478	**0.18**	0.72247
STM2478	STM2478	hypothetical protein STM2478	**0.25**	0.76538
STM2479	aegA	putative oxidoreductase	**0.49**	0.73175
STM2479	aegA	putative oxidoreductase	**0.50**	0.52846
STM2480	narQ	sensory histidine kinase	**-0.31**	0.44331
STM2480	narQ	sensory histidine kinase	**0.32**	0.44210
STM2481	acrD	aminoglycoside/multidrug efflux pump	**-0.21**	0.79241
STM2481	acrD	aminoglycoside/multidrug efflux pump	**0.11**	0.81737
STM2482	yffB	putative glutaredoxin	**0.11**	0.76622
STM2482	yffB	putative glutaredoxin	**-0.02**	0.95663
STM2483	dapE	succinyl-diaminopimelate desuccinylase	**-0.10**	0.84473
STM2483	dapE	succinyl-diaminopimelate desuccinylase	**0.21**	0.55482
STM2484	STM2484	putative inner membrane protein	**-0.71**	0.16534
STM2484	STM2484	putative inner membrane protein	**0.26**	0.61407
STM2485	ypfI	putative acetyltransferase	**0.04**	0.94417
STM2485	ypfI	putative acetyltransferase	**0.01**	0.99447
STM2486	STM2486	putative inner membrane protein	**0.06**	0.89004
STM2486	STM2486	putative inner membrane protein	**0.02**	0.97720
STM2487	purC	phosphoribosylaminoimidazole-succinocarboxamide synthase	**-0.08**	0.85680
STM2487	purC	phosphoribosylaminoimidazole-succinocarboxamide synthase	**0.20**	0.69192
STM2488	nlpB	lipoprotein	**0.08**	0.85718
STM2488	nlpB	lipoprotein	**0.25**	0.60052
STM2489	dapA	dihydrodipicolinate synthase	**0.02**	0.98237
STM2489	dapA	dihydrodipicolinate synthase	**0.00**	0.99829
STM2490	gcvR	gcv operon transcriptional repressor	**0.13**	0.73542
STM2490	gcvR	gcv operon transcriptional repressor	**0.41**	0.33452
STM2491	bcp	bacterioferritin comigratory protein	**0.00**	0.99929
STM2491	bcp	bacterioferritin comigratory protein	**0.42**	0.25125
STM2492	STM2492	putative glycerate kinase	**-0.47**	0.36942
STM2492	STM2492	putative glycerate kinase	**-0.01**	0.99009
STM2493	perM	putative permease	**-0.09**	0.84077
STM2493	perM	putative permease	**0.22**	0.60051
STM2494	STM2494	hypothetical protein STM2494	**-0.50**	0.25620
STM2494	STM2494	hypothetical protein STM2494	**0.06**	0.93011
STM2495	yfgD	putative arsenate reductase	**0.11**	0.86951
STM2495	yfgD	putative arsenate reductase	**0.02**	0.98212
STM2496	yfgE	DNA replication initiation factor	**-0.63**	0.23570
STM2496	yfgE	DNA replication initiation factor	**0.43**	0.42409
STM2497	uraA	uracil transport protein	**-0.39**	0.29285
STM2497	uraA	uracil transport protein	**0.13**	0.82624
STM2498	upp	uracil phosphoribosyltransferase	**-0.14**	0.75137
STM2498	upp	uracil phosphoribosyltransferase	**-0.22**	0.60249
STM2499,S	purM	phosphoribosylaminoimidazole synthetase	**-0.25**	0.55482
STM2499,S	purM	phosphoribosylaminoimidazole synthetase	**0.42**	0.36543
STM2500	purN	phosphoribosylglycinamide formyltransferase	**0.03**	0.96785
STM2500	purN	phosphoribosylglycinamide formyltransferase	**0.28**	0.49336
STM2501	ppk	polyphosphate kinase	**-0.51**	0.33587

STM2501	ppk	polyphosphate kinase	**0.21**	0.56389
STM2502	ppx	exopolyphosphatase	**-0.81**	0.19843
STM2502	ppx	exopolyphosphatase	**0.00**	0.99887
STM2503	STM2503	putative diguanylate cyclase	**-0.67**	0.19843
STM2503	STM2503	putative diguanylate cyclase	**-0.05**	0.93582
STM2506	STM2506	putative inner membrane protein	**-0.65**	0.21015
STM2506	STM2506	putative inner membrane protein	**0.42**	0.38044
STM2509	STM2509	putative transposase	**-0.71**	0.39127
STM2509	STM2509	putative transposase	**0.01**	0.99009
STM2510	guaA	bifunctional GMP synthase/glutamine amidotransferase protein	**-0.20**	0.60687
STM2510	guaA	bifunctional GMP synthase/glutamine amidotransferase protein	**0.08**	0.87126
STM2511	guaB	inositol-5-monophosphate dehydrogenase	**-0.18**	0.68032
STM2511	guaB	inositol-5-monophosphate dehydrogenase	**-0.18**	0.68961
STM2512	xseA	exodeoxyribonuclease VII large subunit	**-0.63**	0.20730
STM2512	xseA	exodeoxyribonuclease VII large subunit	**0.30**	0.63235
STM2513	shdA	AIDA autotransporter-like protein	**-0.34**	0.59821
STM2513	shdA	AIDA autotransporter-like protein	**-0.09**	0.87667
STM2514	ratB	putative outer membrane protein	**0.10**	0.86861
STM2514	ratB	putative outer membrane protein	**0.05**	0.90733
STM2515	ratA	putative outer membrane protein	**0.22**	0.61824
STM2515	ratA	putative outer membrane protein	**0.45**	0.50602
STM2516	sinI	putative outer membrane protein	**0.03**	0.96278
STM2516	sinI	putative outer membrane protein	**0.28**	0.65145
STM2517	sinH	intimin-like protein	**-0.16**	0.89487
STM2517	sinH	intimin-like protein	**0.53**	0.29848
STM2518	yfgJ	putative cytoplasmic protein	**0.11**	0.75851
STM2518	yfgJ	putative cytoplasmic protein	**0.14**	0.76502
STM2519	engA	GTP-binding protein EngA	**-0.51**	0.34633
STM2519	engA	GTP-binding protein EngA	**0.19**	0.67097
STM2520	yfgL	putative serine/threonine protein kinase	**0.00**	0.99540
STM2520	yfgL	putative serine/threonine protein kinase	**-0.25**	0.64525
STM2521	yfgM	putative inner membrane protein	**-0.08**	0.85977
STM2521	yfgM	putative inner membrane protein	**0.64**	0.16752
STM2522	hisS	histidyl-tRNA synthetase	**-0.34**	0.34666
STM2522	hisS	histidyl-tRNA synthetase	**-0.23**	0.51979
STM2523	gcpE	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	**-0.05**	0.91484
STM2523	gcpE	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	**0.17**	0.68450
STM2524	yfgA	hypothetical protein STM2524	**-0.30**	0.53827
STM2524	yfgA	hypothetical protein STM2524	**0.16**	0.66805
STM2525	yfgB	putative FeS redox enzyme	**-0.01**	0.98352
STM2525	yfgB	putative FeS redox enzyme	**0.01**	0.98398
STM2526	ndk	nucleoside diphosphate kinase	**0.19**	0.60249
STM2526	ndk	nucleoside diphosphate kinase	**0.27**	0.44568
STM2527	STM2527	putative polyferredoxin	**-0.04**	0.93916
STM2527	STM2527	putative polyferredoxin	**0.20**	0.57469
STM2528	STM2528	putative dimethylsulfoxide reductase	**0.00**	0.99929
STM2528	STM2528	putative dimethylsulfoxide reductase	**0.54**	0.22602
STM2529	STM2529	putative anaerobic dimethylsulfoxide reductase	**-0.25**	0.69882
STM2529	STM2529	putative anaerobic dimethylsulfoxide reductase	**-0.31**	0.57804
STM2530	STM2530	putative anaerobic dimethylsulfoxide reductase	**-0.29**	0.53454
STM2530	STM2530	putative anaerobic dimethylsulfoxide reductase	**0.81**	0.35010
STM2531	pbpC	penicillin-binding protein 1c	**-0.19**	0.74779
STM2531	pbpC	penicillin-binding protein 1c	**0.83**	0.17139
STM2532	STM2532	putative inner membrane lipoprotein	**-0.03**	0.96247
STM2532	STM2532	putative inner membrane lipoprotein	**0.00**	0.99997
STM2533	sseA	putative sulfurtransferase	**0.00**	0.99928
STM2533	sseA	putative sulfurtransferase	**0.16**	0.78453
STM2534	STM2534	putative cytoplasmic protein	**-0.48**	0.38596
STM2534	STM2534	putative cytoplasmic protein	**0.06**	0.91571
STM2535	sseB	enhanced serine sensitivity protein	**-0.06**	0.88404
STM2535	sseB	enhanced serine sensitivity protein	**0.03**	0.95663

STM2536	pepB	aminopeptidase B	**-0.31**	0.46915
STM2536	pepB	aminopeptidase B	**0.01**	0.99213
STM2537	yfhJ	hypothetical protein STM2537	**-0.51**	0.25759
STM2537	yfhJ	hypothetical protein STM2537	**-0.41**	0.33452
STM2538	fdx	electron carrer protein	**-0.01**	0.98348
STM2538	fdx	electron carrer protein	**0.15**	0.72135
STM2539	hscA	chaperone protein HscA	**-0.31**	0.47130
STM2539	hscA	chaperone protein HscA	**-0.12**	0.76538
STM2540	hscB	co-chaperone HscB	**-0.22**	0.52728
STM2540	hscB	co-chaperone HscB	**-0.16**	0.68232
STM2541	iscA	iron-sulfur cluster assembly protein	**-0.20**	0.66677
STM2541	iscA	iron-sulfur cluster assembly protein	**0.34**	0.52804
STM2542	nifU	NifU-like protein	**-0.35**	0.56569
STM2542	nifU	NifU-like protein	**-0.10**	0.82656
STM2543	nifS	cysteine desulfurase	**0.25**	0.55976
STM2543	nifS	cysteine desulfurase	**0.28**	0.55338
STM2544	yfhP	putative iron-sulfur cluster regulatory protein	**-0.08**	0.88018
STM2544	yfhP	putative iron-sulfur cluster regulatory protein	**0.03**	0.94050
STM2545	STM2545	putative rRNA methylase	**-0.20**	0.66594
STM2545	STM2545	putative rRNA methylase	**0.50**	0.27004
STM2546	suhB	inositol monophosphatase	**0.69**	0.22283
STM2546	suhB	inositol monophosphatase	**-0.14**	0.92716
STM2547	STM2547	putative hydrolase	**-0.16**	0.78211
STM2547	STM2547	putative hydrolase	**0.00**	0.99938
STM2548	asrA	anaerobic sulfide reductase	**-0.21**	0.55482
STM2548	asrA	anaerobic sulfide reductase	**0.26**	0.61130
STM2549	asrB	anaerobic sulfite reductase subunit B	**-0.23**	0.64742
STM2549	asrB	anaerobic sulfite reductase subunit B	**0.14**	0.82667
STM2550	asrC	anaerobic sulfide reductase	**-0.44**	0.43286
STM2550	asrC	anaerobic sulfide reductase	**0.22**	0.65130
STM2551	STM2551	putative inner membrane protein	**-0.17**	0.74374
STM2551	STM2551	putative inner membrane protein	**0.50**	0.46184
STM2552	STM2552	hypothetical protein STM2552	**-0.42**	0.26213
STM2552	STM2552	hypothetical protein STM2552	**0.44**	0.31775
STM2553	csiE	stationary phase-inducible protein	**-0.33**	0.37154
STM2553	csiE	stationary phase-inducible protein	**0.59**	0.16039
STM2554	hcaT	putative transport protein	**-0.27**	0.57696
STM2554	hcaT	putative transport protein	**-0.17**	0.68708
STM2555	glyA	serine hydroxymethyltransferase	**0.17**	0.66729
STM2555	glyA	serine hydroxymethyltransferase	**0.33**	0.55892
STM2556	hmpA	dihydropteridine reductase 2/nitric oxide dioxygenase	**-0.38**	0.44416
STM2556	hmpA	dihydropteridine reductase 2/nitric oxide dioxygenase	**0.50**	0.22049
STM2557	cadC	transcriptional activator	**-0.27**	0.46720
STM2557	cadC	transcriptional activator	**-0.27**	0.47838
STM2558	cadB	lysine/cadaverine transport protein	**-0.42**	0.32760
STM2558	cadB	lysine/cadaverine transport protein	**0.85**	0.13027
STM2559	cadA	lysine decarboxylase 1	**-0.02**	0.98855
STM2559	cadA	lysine decarboxylase 1	**-0.29**	0.64465
STM2560	yjdL	putative di-/tripeptide transport protein	**-0.22**	0.64422
STM2560	yjdL	putative di-/tripeptide transport protein	**0.67**	0.13206
STM2561	glnB	regulatory protein P-II	**0.02**	0.96785
STM2561	glnB	regulatory protein P-II	**0.15**	0.80175
STM2562	yfhA	putative transcriptional regulator	**-0.43**	0.29871
STM2562	yfhA	putative transcriptional regulator	**-0.07**	0.89140
STM2563	yfhG	putative transcriptional regulator	**-0.15**	0.79093
STM2563	yfhG	putative transcriptional regulator	**-0.13**	0.78399
STM2564	yfhK	putative sensor kinase	**-0.24**	0.60311
STM2564	yfhK	putative sensor kinase	**0.06**	0.93023
STM2565	purG	phosphoribosylformylglycinamidine synthase	**-0.88**	0.15276
STM2565	purG	phosphoribosylformylglycinamidine synthase	**-0.21**	0.71864
STM2567	yfhD	putative periplasmic amino acid-binding protein	**-0.20**	0.62216
STM2567	yfhD	putative periplasmic amino acid-binding protein	**-0.09**	0.87740
STM2568	yfhC	putative cytosine/adenosine deaminase	**-0.09**	0.83240

STM2568	yfhC	putative cytosine/adenosine deaminase	**0.45**	0.49871
STM2569	yfhB	putative phosphoserine phosphatase	**-0.25**	0.62199
STM2569	yfhB	putative phosphoserine phosphatase	**0.41**	0.34690
STM2570	STM2570	putative phosphotransferase system IIB component	**-0.15**	0.72149
STM2570	STM2570	putative phosphotransferase system IIB component	**-0.04**	0.94279
STM2571	STM2571	hypothetical protein STM2571	**-0.01**	0.98612
STM2571	STM2571	hypothetical protein STM2571	**0.22**	0.63222
STM2572	yfhH	putative transport protein	**0.01**	0.98718
STM2572	yfhH	putative transport protein	**0.19**	0.60629
STM2573	STM2573	2-dehydropantoate 2-reductase	**-0.24**	0.60574
STM2573	STM2573	2-dehydropantoate 2-reductase	**-0.07**	0.91047
STM2574	STM2574	putative permease	**-0.34**	0.52765
STM2574	STM2574	putative permease	**-0.14**	0.80539
STM2575	STM2575	putative transcriptional regulator	**-0.26**	0.55482
STM2575	STM2575	putative transcriptional regulator	**0.30**	0.69241
STM2576	yfhL	putative ferredoxin	**-0.26**	0.64880
STM2576	yfhL	putative ferredoxin	**0.10**	0.83443
STM2577	acpS	4'-phosphopantetheinyl transferase	**-0.27**	0.46629
STM2577	acpS	4'-phosphopantetheinyl transferase	**-0.29**	0.46862
STM2578	pdxJ	pyridoxal phosphate biosynthetic protein	**-0.89**	0.13509
STM2578	pdxJ	pyridoxal phosphate biosynthetic protein	**0.00**	0.99755
STM2579	recO	DNA repair protein RecO	**-0.03**	0.94529
STM2579	recO	DNA repair protein RecO	**0.00**	0.99660
STM2580	era	GTP-binding protein Era	**-0.05**	0.91389
STM2580	era	GTP-binding protein Era	**0.34**	0.36311
STM2581	rncS	ribonuclease III	**-0.18**	0.62403
STM2581	rncS	ribonuclease III	**-0.14**	0.79180
STM2582	lepB	signal peptidase I	**-0.14**	0.72247
STM2582	lepB	signal peptidase I	**-0.16**	0.64489
STM2583	lepA	GTP-binding protein LepA	**-0.21**	0.60595
STM2583	lepA	GTP-binding protein LepA	**0.03**	0.95384
STM2584	gogB	leucine-rich repeat protein [Phage Gifsy-1]	**-0.16**	0.72970
STM2584	gogB	leucine-rich repeat protein [Phage Gifsy-1]	**-0.23**	0.59675
STM2586	STM2586	phage tail assembly-like protein	**-1.08**	0.17330
STM2586	STM2586	phage tail assembly-like protein	**-0.22**	0.70229
STM2587	STM2587	phage tail assembly-like protein	**-0.85**	0.19398
STM2587	STM2587	phage tail assembly-like protein	**0.50**	0.36341
STM2588	STM2588	tail fiber-like protein	**-0.64**	0.35937
STM2588	STM2588	tail fiber-like protein	**-0.22**	0.63101
STM2589	STM2589	host specificity protein-J-like	**-0.42**	0.35853
STM2589	STM2589	host specificity protein-J-like	**-0.08**	0.87909
STM2590	STM2590	tail assembly protein I-like	**-0.18**	0.76811
STM2590	STM2590	tail assembly protein I-like	**0.56**	0.77130
STM2591	STM2591	tail assembly protein K-like	**-0.61**	0.23697
STM2591	STM2591	tail assembly protein K-like	**0.31**	0.49117
STM2592	STM2592	phage tail component L-like protein	**-0.73**	0.21855
STM2592	STM2592	phage tail component L-like protein	**0.18**	0.72518
STM2593	STM2593	phage tail component M-like protein	**-0.50**	0.35619
STM2593	STM2593	phage tail component M-like protein	**-0.02**	0.98127
STM2594	STM2594	phage tail component H-like protein	**-0.40**	0.55364
STM2594	STM2594	phage tail component H-like protein	**0.02**	0.98718
STM2595	STM2595	minor tail-like protein	**-0.59**	0.45739
STM2595	STM2595	minor tail-like protein	**0.44**	0.38668
STM2596	STM2596	minor tail-like protein	**-0.33**	0.50458
STM2596	STM2596	minor tail-like protein	**0.65**	0.17327
STM2597	STM2597	major tail-like protein	**-0.08**	0.87116
STM2597	STM2597	major tail-like protein	**1.03**	0.32016
STM2598	STM2598	hypothetical protein STM2598	**-0.83**	0.32760
STM2598	STM2598	hypothetical protein STM2598	**0.14**	0.83443
STM2599	STM2599	putative virulence protein [Phage Gifsy-1]	**-0.23**	0.67388
STM2599	STM2599	putative virulence protein [Phage Gifsy-1]	**-0.05**	0.91597
STM2600	STM2600	minor tail protein Z-like	**0.28**	0.52511
STM2600	STM2600	minor tail protein Z-like	**0.56**	0.45800

STM2601	STM2601	minor capsid protein FII	**-0.20**	0.69297
STM2601	STM2601	minor capsid protein FII	**0.57**	0.45374
STM2602	STM2602	DNA packaging-like protein	**-0.53**	0.30481
STM2602	STM2602	DNA packaging-like protein	**0.30**	0.61285
STM2603	STM2603	phage head-like protein	**-0.29**	0.63702
STM2603	STM2603	phage head-like protein	**0.00**	0.99742
STM2604	STM2604	phage head-like protein	**-0.05**	0.94087
STM2604	STM2604	phage head-like protein	**0.52**	0.52511
STM2605	STM2605	head-tail preconnector-like protein	**-0.32**	0.42674
STM2605	STM2605	head-tail preconnector-like protein	**0.94**	0.16324
STM2606	STM2606	head-tail preconnector-like protein	**0.68**	0.60034
STM2606	STM2606	head-tail preconnector-like protein	**2.02**	0.17318
STM2607	STM2607	head-to-tail joining-like protein	**-0.28**	0.81667
STM2607	STM2607	head-to-tail joining-like protein	**0.05**	0.96027
STM2608	STM2608	terminase-like large protein	**-0.65**	0.28078
STM2608	STM2608	terminase-like large protein	**-0.14**	0.81455
STM2609	STM2609	DNA packaging-like protein	**-0.54**	0.62403
STM2609	STM2609	DNA packaging-like protein	**0.88**	0.23918
STM2610	STM2610	hypothetical protein STM2610 [Phage Gifsy-1]	**-0.56**	0.38894
STM2610	STM2610	hypothetical protein STM2610 [Phage Gifsy-1]	**-0.43**	0.48063
STM2611,S	STM2611,S	endopeptidase-like protein	**-0.30**	0.55008
STM2611,S	STM2611,S	endopeptidase-like protein	**0.58**	0.23434
STM2612	STM2612	morphogenesis-like protein	**-0.28**	0.69462
STM2612	STM2612	morphogenesis-like protein	**0.17**	0.81323
STM2613	STM2613	hypothetical protein STM2613	**-0.69**	0.23879
STM2613	STM2613	hypothetical protein STM2613	**-0.35**	0.41717
STM2613	STM2613	hypothetical protein STM2613	**0.14**	0.76622
STM2613	STM2613	hypothetical protein STM2613	**0.29**	0.61960
STM2614	STM2614	hypothetical protein STM2614 [Phage Gifsy-1]	**-0.16**	0.87208
STM2614	STM2614	hypothetical protein STM2614 [Phage Gifsy-1]	**-0.17**	0.78210
STM2614	STM2614	hypothetical protein STM2614 [Phage Gifsy-1]	**0.26**	0.75387
STM2614	STM2614	hypothetical protein STM2614 [Phage Gifsy-1]	**0.36**	0.40227
STM2615	-	STM2615	**-0.88**	0.18763
STM2615	-	STM2615	**-0.53**	0.34960
STM2616	STM2616	antirepressor-like protein	**0.01**	0.98372
STM2616	STM2616	antirepressor-like protein	**0.50**	0.28030
STM2617	STM2617	antiterminator-like protein	**-1.29**	0.16490
STM2617	STM2617	antiterminator-like protein	**-0.42**	0.41422
STM2619	STM2619	hypothetical protein STM2619	**-0.53**	0.58246
STM2619	STM2619	hypothetical protein STM2619	**0.62**	0.22421
STM2621	STM2621	hypothetical protein STM2621	**-0.58**	0.23989
STM2621	STM2621	hypothetical protein STM2621	**-0.59**	0.34541
STM2621	STM2621	hypothetical protein STM2621	**0.05**	0.93656
STM2621	STM2621	hypothetical protein STM2621	**-0.42**	0.42733
STM2622	STM2622	hypothetical protein STM2622	**-0.32**	0.36818
STM2622	STM2622	hypothetical protein STM2622	**0.08**	0.87496
STM2623	STM2623	hypothetical protein STM2623	**-0.42**	0.35824
STM2623	STM2623	hypothetical protein STM2623	**-0.24**	0.62757
STM2624	STM2624	hypothetical protein STM2624	**0.02**	0.99009
STM2624	STM2624	hypothetical protein STM2624	**0.84**	0.51014
STM2625	STM2625	DNA replication protein DnaC	**-0.13**	0.75371
STM2625	STM2625	DNA replication protein DnaC	**0.09**	0.84187
STM2626	STM2626	replication protein 15-like	**-0.28**	0.76016
STM2626	STM2626	replication protein 15-like	**0.78**	0.15315
STM2630	STM2630	hypothetical protein STM2630 [Phage Gifsy-1]	**-0.15**	0.82350
STM2630	STM2630	hypothetical protein STM2630 [Phage Gifsy-1]	**-0.19**	0.71884
STM2632	STM2632	exodeoxyribonuclease VIII-like protein [Phage Gifsy-1]	**0.43**	0.53679
STM2632	STM2632	exodeoxyribonuclease VIII-like protein [Phage Gifsy-1]	**1.43**	0.13824
STM2634	STM2634	putative cytoplasmic protein [Phage Gifsy-1]	**-0.18**	0.91111
STM2634	STM2634	putative cytoplasmic protein [Phage Gifsy-1]	**0.26**	0.70472
STM2634	STM2634	putative cytoplasmic protein [Phage Gifsy-1]	**-0.34**	0.65779
STM2634	STM2634	putative cytoplasmic protein [Phage Gifsy-1]	**0.14**	0.76008
STM2634	STM2634	putative cytoplasmic protein [Phage Gifsy-1]	**-0.02**	0.96850

STM2634	STM2634	putative cytoplasmic protein [Phage Gifsy-1]	**0.09**	0.84788
STM2636	STM2636	integrase-like protein	**-0.37**	0.36465
STM2636	STM2636	integrase-like protein	**0.51**	0.29543
STM2637	rseC	sigma E regulator	**0.17**	0.67092
STM2637	rseC	sigma E regulator	**0.27**	0.66716
STM2638	rseB	periplasmic negative regulator of sigmaE	**-0.05**	0.90605
STM2638	rseB	periplasmic negative regulator of sigmaE	**-0.18**	0.62614
STM2639	rseA	anti sigma-E factor	**-0.32**	0.76240
STM2639	rseA	anti sigma-E factor	**0.71**	0.29871
STM2640	rpoE	RNA polymerase sigma-70 factor	**0.15**	0.68314
STM2640	rpoE	RNA polymerase sigma-70 factor	**0.06**	0.89132
STM2641	nadB	L-aspartate oxidase	**-0.30**	0.41996
STM2641	nadB	L-aspartate oxidase	**0.27**	0.68450
STM2642	yfiC	putative transferase	**-0.16**	0.69398
STM2642	yfiC	putative transferase	**0.00**	0.99861
STM2643	srmB	ATP-dependent RNA helicase	**-0.65**	0.18873
STM2643	srmB	ATP-dependent RNA helicase	**-0.31**	0.49369
STM2644	yfiE	putative transcriptional regulator	**-0.03**	0.95396
STM2644	yfiE	putative transcriptional regulator	**-0.16**	0.66677
STM2645	yfiK	putative transport protein	**-0.20**	0.64658
STM2645	yfiK	putative transport protein	**0.04**	0.94050
STM2646	yfiD	putative formate acetyltransferase	**-0.26**	0.61811
STM2646	yfiD	putative formate acetyltransferase	**0.65**	0.19284
STM2647	ung	uracil-DNA glycosylase	**-0.21**	0.68032
STM2647	ung	uracil-DNA glycosylase	**-0.13**	0.79772
STM2648	yfiF	putative tRNA/rRNA methyltransferase	**-0.57**	0.21015
STM2648	yfiF	putative tRNA/rRNA methyltransferase	**-0.28**	0.48214
STM2649	trxC	thioredoxin 2	**-0.30**	0.41187
STM2649	trxC	thioredoxin 2	**0.11**	0.81323
STM2650	yfiP	putative cytoplasmic protein	**-0.38**	0.33745
STM2650	yfiP	putative cytoplasmic protein	**0.15**	0.72197
STM2651	yfiQ	putative acetyl-CoA synthetase	**-0.21**	0.61809
STM2651	yfiQ	putative acetyl-CoA synthetase	**0.39**	0.37585
STM2652	pssA	phosphatidylserine synthase	**0.26**	0.47736
STM2652	pssA	phosphatidylserine synthase	**0.11**	0.86370
STM2653	yfiM	putative outer membrane lipoprotein	**-0.04**	0.95491
STM2653	yfiM	putative outer membrane lipoprotein	**0.02**	0.97994
STM2654	kgtP	alpha-ketoglutarate permease	**0.34**	0.39000
STM2654	kgtP	alpha-ketoglutarate permease	**0.09**	0.83718
STM2655	STM2655	putative cytoplasmic protein	**-0.54**	0.32760
STM2655	STM2655	putative cytoplasmic protein	**0.39**	0.45833
STM2657	rrlG	STM2657	**-0.16**	0.80655
STM2657	rrlG	STM2657	**-0.58**	0.36942
STM2660	clpB	ATP-dependent protease	**-0.27**	0.55355
STM2660	clpB	ATP-dependent protease	**-0.42**	0.35937
STM2661	yfiH	putative inner membrane protein	**-0.54**	0.22602
STM2661	yfiH	putative inner membrane protein	**-0.31**	0.43982
STM2662	rluD	ribosomal large subunit pseudouridine synthase D	**-0.31**	0.41715
STM2662	rluD	ribosomal large subunit pseudouridine synthase D	**-0.17**	0.62861
STM2663	yfiO	putative lipoprotein	**-0.63**	0.29689
STM2663	yfiO	putative lipoprotein	**0.11**	0.86190
STM2665	yfiA	ribosome stabilization factor	**-0.15**	0.75798
STM2665	yfiA	ribosome stabilization factor	**0.64**	0.28024
STM2667	pheA	chorismate mutase P/prephenate dehydratase	**-0.39**	0.35986
STM2667	pheA	chorismate mutase P/prephenate dehydratase	**0.00**	0.99907
STM2668	STM2668	putative cytoplasmic protein	**-0.20**	0.59121
STM2668	STM2668	putative cytoplasmic protein	**0.17**	0.75851
STM2669	tyrA	chorismate mutase T/prephenate dehydrogenase	**-0.30**	0.45498
STM2669	tyrA	chorismate mutase T/prephenate dehydrogenase	**0.05**	0.94475
STM2670	aroF	3-deoxy-7-phosphoheptulonate synthase	**-0.27**	0.53731
STM2670	aroF	3-deoxy-7-phosphoheptulonate synthase	**-0.04**	0.91981
STM2671	yfiR	putative periplasmic protein	**-0.40**	0.35366
STM2671	yfiR	putative periplasmic protein	**0.05**	0.95049

STM2672	yfiN	putative diguanylate cyclase/phosphodiesterase	**-0.37**	0.49871
STM2672	yfiN	putative diguanylate cyclase/phosphodiesterase	**0.01**	0.98643
STM2673	rplS	50S ribosomal protein L19	**-0.62**	0.31280
STM2673	rplS	50S ribosomal protein L19	**-0.43**	0.50759
STM2674	trmD	tRNA (guanine-N(1)-)-methyltransferase	**-0.57**	0.17139
STM2674	trmD	tRNA (guanine-N(1)-)-methyltransferase	**-0.24**	0.54169
STM2675	rimM	16S rRNA-processing protein	**0.06**	0.90057
STM2675	rimM	16S rRNA-processing protein	**0.66**	0.17754
STM2676	rpsP	30S ribosomal protein S16	**-0.03**	0.94798
STM2676	rpsP	30S ribosomal protein S16	**0.37**	0.32760
STM2677	ffh	4,5S-RNP protein	**-0.60**	0.19142
STM2677	ffh	4,5S-RNP protein	**0.05**	0.91900
STM2678	corE	hypothetical protein STM2678	**-0.08**	0.89849
STM2678	corE	hypothetical protein STM2678	**0.34**	0.61215
STM2679	yfjD	hypothetical protein STM2679	**-0.43**	0.49336
STM2679	yfjD	hypothetical protein STM2679	**0.22**	0.63562
STM2680	STM2680	putative cytoplasmic protein	**-0.14**	0.76074
STM2680	STM2680	putative cytoplasmic protein	**-0.36**	0.45423
STM2681	grpE	heat shock protein	**0.11**	0.79890
STM2681	grpE	heat shock protein	**0.22**	0.71864
STM2683	ppnK	inorganic polyphosphate/ATP-NAD kinase	**-0.23**	0.57799
STM2683	ppnK	inorganic polyphosphate/ATP-NAD kinase	**0.10**	0.83026
STM2684	recN	recombination/DNA repair protein	**-0.35**	0.42591
STM2684	recN	recombination/DNA repair protein	**0.52**	0.33587
STM2685	smpA	small membrane protein A	**-0.40**	0.29689
STM2685	smpA	small membrane protein A	**0.01**	0.98840
STM2686	yfjF	hypothetical protein STM2686	**-0.23**	0.62873
STM2686	yfjF	hypothetical protein STM2686	**0.12**	0.85698
STM2687	yfjG	putative oligoketide cyclase	**-0.18**	0.64103
STM2687	yfjG	putative oligoketide cyclase	**0.74**	0.18313
STM2688	smpB	SsrA-binding protein	**-0.35**	0.45664
STM2688	smpB	SsrA-binding protein	**0.00**	0.99938
STM2690	STM2690	putative outer membrane efflux protein	**-0.40**	0.41913
STM2690	STM2690	putative outer membrane efflux protein	**0.36**	0.58506
STM2691	STM2691	putative ABC transporter transmembrane region	**-0.34**	0.48567
STM2691	STM2691	putative ABC transporter transmembrane region	**0.02**	0.97219
STM2692	STM2692	putative HlyD family secretion protein	**0.17**	0.75437
STM2692	STM2692	putative HlyD family secretion protein	**0.21**	0.64458
STM2695	STM2695	late control-like protein	**0.31**	0.55338
STM2695	STM2695	late control-like protein	**0.23**	0.51526
STM2696	STM2696	putative phage tail protein	**-0.12**	0.85670
STM2696	STM2696	putative phage tail protein	**0.32**	0.45852
STM2697	STM2697	phage tail-like protein	**-0.18**	0.83109
STM2697	STM2697	phage tail-like protein	**0.44**	0.35564
STM2698	STM2698	gpE-like protein	**-0.18**	0.79283
STM2698	STM2698	gpE-like protein	**0.83**	0.22849
STM2699	STM2699	putative phage tail-like protein	**-0.29**	0.55833
STM2699	STM2699	putative phage tail-like protein	**0.01**	0.99024
STM2700	STM2700	phage tail fiber-like protein	**-0.77**	0.14395
STM2700	STM2700	phage tail fiber-like protein	**0.17**	0.73855
STM2701	STM2701	phage tail sheath-like protein	**-0.18**	0.65130
STM2701	STM2701	phage tail sheath-like protein	**0.64**	0.50474
STM2704	STM2704	tail fibre assembly-like protein phage Fels-2]	**-1.15**	0.19843
STM2704	STM2704	tail fibre assembly-like protein phage Fels-2]	**-0.18**	0.83688
STM2705	STM2705	hypothetical protein STM2705	**0.23**	0.77834
STM2705	STM2705	hypothetical protein STM2705	**0.66**	0.28861
STM2707	STM2707	phage tail-like protein	**0.03**	0.95591
STM2707	STM2707	phage tail-like protein	**0.78**	0.18622
STM2708	STM2708	phage tail-like protein	**0.22**	0.82667
STM2708	STM2708	phage tail-like protein	**0.41**	0.55598
STM2709	STM2709	base plate tail-like protein	**-0.63**	0.21984
STM2709	STM2709	base plate tail-like protein	**-0.14**	0.83918
STM2710	STM2710	phage baseplate assembly-like protein	**-0.55**	0.26261

STM2710	STM2710	phage baseplate assembly-like protein	**-0.18**	0.84272
STM2711	STM2711	phage tail-like protein	**-0.25**	0.58890
STM2711	STM2711	phage tail-like protein	**0.46**	0.59820
STM2712	STM2712	phage tail-like protein	**-0.15**	0.80406
STM2712	STM2712	phage tail-like protein	**-0.38**	0.55584
STM2714	STM2714	lysis-like protein	**-0.08**	0.88599
STM2714	STM2714	lysis-like protein	**0.40**	0.47610
STM2715,S	STM2715,S	probable prophage lysozyme	**1.08**	0.26785
STM2715,S	STM2715,S	probable prophage lysozyme	**1.72**	0.17359
STM2716	STM2716	phage-holin-like protein	**-0.45**	0.27959
STM2716	STM2716	phage-holin-like protein	**0.25**	0.62861
STM2717	STM2717	phage tail-like protein	**0.10**	0.92032
STM2717	STM2717	phage tail-like protein	**0.01**	0.99230
STM2718	STM2718	head completion-like protein	**0.80**	0.55483
STM2718	STM2718	head completion-like protein	**1.29**	0.29796
STM2719	STM2719	terminase-like protein	**-0.87**	0.18426
STM2719	STM2719	terminase-like protein	**0.36**	0.56860
STM2720	STM2720	major capsid-like protein	**-0.16**	0.70229
STM2720	STM2720	major capsid-like protein	**1.00**	0.15955
STM2721	STM2721	capsid scaffold-like protein	**-0.37**	0.35986
STM2721	STM2721	capsid scaffold-like protein	**0.74**	0.29796
STM2722	STM2722	terminase-like protein phage Fels-2]	**-1.02**	0.16490
STM2722	STM2722	terminase-like protein phage Fels-2]	**-0.42**	0.45926
STM2723	STM2723	portal vertex-like protein phage Fels-2]	**-0.07**	0.93089
STM2723	STM2723	portal vertex-like protein phage Fels-2]	**0.36**	0.42409
STM2727	STM2727	hypothetical protein STM2727	**-0.07**	0.96785
STM2727	STM2727	hypothetical protein STM2727	**1.08**	0.26201
STM2729	STM2729	hypothetical protein STM2729	**0.09**	0.89407
STM2729	STM2729	hypothetical protein STM2729	**0.87**	0.26213
STM2730	STM2730	DNA adenine methylase-like protein	**-0.56**	0.53827
STM2730	STM2730	DNA adenine methylase-like protein	**0.55**	0.61343
STM2732	STM2732	hypothetical protein STM2732	**-0.69**	0.19811
STM2732	STM2732	hypothetical protein STM2732	**0.67**	0.26410
STM2733	STM2733	hypothetical protein STM2733	**-0.36**	0.53813
STM2733	STM2733	hypothetical protein STM2733	**0.19**	0.79096
STM2735	STM2735	hypothetical protein STM2735	**-0.33**	0.48600
STM2735	STM2735	hypothetical protein STM2735	**0.23**	0.76312
STM2736	STM2736	hypothetical protein STM2736	**-0.03**	0.95397
STM2736	STM2736	hypothetical protein STM2736	**0.66**	0.13112
STM2737	STM2737	hypothetical protein STM2737	**-0.48**	0.26378
STM2737	STM2737	hypothetical protein STM2737	**0.04**	0.95363
STM2739	STM2739	phage tail-like protein phage Fels-2]	**-0.47**	0.37888
STM2739	STM2739	phage tail-like protein phage Fels-2]	**-0.29**	0.53840
STM2740	STM2740	integrase-like protein phage Fels-2]	**-0.17**	0.73473
STM2740	STM2740	integrase-like protein phage Fels-2]	**0.49**	0.29796
STM2740,1N	STM2740,1N	hypothetical protein STM2740,1N	**-0.64**	0.15984
STM2740,1N	STM2740,1N	hypothetical protein STM2740,1N	**0.93**	0.30113
STM2741	STM2741	putative periplasmic protein	**-0.12**	0.84842
STM2741	STM2741	putative periplasmic protein	**0.48**	0.24811
STM2742	STM2742	putative cytoplasmic protein	**-0.09**	0.82384
STM2742	STM2742	putative cytoplasmic protein	**0.53**	0.22540
STM2743	STM2743	putative cytoplasmic protein	**-0.09**	0.89487
STM2743	STM2743	putative cytoplasmic protein	**-0.18**	0.77536
STM2744	STM2744	putative cytoplasmic protein	**0.04**	0.93582
STM2744	STM2744	putative cytoplasmic protein	**0.36**	0.51979
STM2745	STM2745	putative inner membrane protein	**0.11**	0.81293
STM2745	STM2745	putative inner membrane protein	**0.02**	0.96736
STM2746	STM2746	putative ATPase	**0.21**	0.68232
STM2746	STM2746	putative ATPase	**0.22**	0.72056
STM2747	STM2747	putative cytoplasmic protein	**-0.12**	0.77923
STM2747	STM2747	putative cytoplasmic protein	**-0.34**	0.65451
STM2748	STM2748	putative transcriptional regulator	**-0.27**	0.47736
STM2748	STM2748	putative transcriptional regulator	**0.05**	0.93485

STM2749	STM2749	putative cytoplasmic protein	**-0.38**	0.58182
STM2749	STM2749	putative cytoplasmic protein	**0.59**	0.26910
STM2750	STM2750	putative PTS system glucitol/sorbitol-specific enzyme II	**-0.56**	0.21393
STM2750	STM2750	putative PTS system glucitol/sorbitol-specific enzyme II	**0.11**	0.86629
STM2751	STM2751	putative glucitol-specific PTS enzyme III	**0.66**	0.32481
STM2751	STM2751	putative glucitol-specific PTS enzyme III	**1.45**	0.15479
STM2752	STM2752	putative glucitol-specific PTS enzyme III	**0.49**	0.34936
STM2752	STM2752	putative glucitol-specific PTS enzyme III	**0.33**	0.42494
STM2753	STM2753	putative dehydrogenase	**-0.06**	0.91378
STM2753	STM2753	putative dehydrogenase	**0.72**	0.11913
STM2754	STM2754	putative hexulose 6 phosphate synthase	**-0.05**	0.93506
STM2754	STM2754	putative hexulose 6 phosphate synthase	**0.55**	0.25759
STM2755	STM2755	putative hexulose 6 phosphate synthase	**0.15**	0.84687
STM2755	STM2755	putative hexulose 6 phosphate synthase	**0.59**	0.50825
STM2756	STM2756	putative sugar phosphate aminotransferase	**0.28**	0.68969
STM2756	STM2756	putative sugar phosphate aminotransferase	**0.69**	0.26714
STM2757	STM2757	putative cytoplasmic protein	**-0.61**	0.24818
STM2757	STM2757	putative cytoplasmic protein	**0.22**	0.69578
STM2758	STM2758	putative phosphotransferase system IIC component	**0.12**	0.85718
STM2758	STM2758	putative phosphotransferase system IIC component	**-0.12**	0.81284
STM2759	STM2759	putative dipeptide/oligopeptide/nickel ABC-type transport system	**0.00**	0.99806
STM2759	STM2759	putative dipeptide/oligopeptide/nickel ABC-type transport system	**-0.07**	0.97612
STM2760	STM2760	putative integrase	**-0.51**	0.37535
STM2760	STM2760	putative integrase	**0.25**	0.72936
STM2761	STM2761	putative inner membrane protein	**-0.62**	0.34102
STM2761	STM2761	putative inner membrane protein	**0.03**	0.96850
STM2762	STM2762	putative inner membrane protein	**-0.36**	0.55008
STM2762	STM2762	putative inner membrane protein	**-0.11**	0.82667
STM2765	STM2765	putative transposase	**-0.99**	0.13813
STM2765	STM2765	putative transposase	**0.16**	0.86296
STM2767	STM2767	putative DNA/RNA helicase	**0.07**	0.85774
STM2767	STM2767	putative DNA/RNA helicase	**-0.06**	0.87826
STM2768	STM2768	putative transposase	**-0.46**	0.30644
STM2768	STM2768	putative transposase	**0.68**	0.20021
STM2769	STM2769	putative transposase	**-0.12**	0.76225
STM2769	STM2769	putative transposase	**0.53**	0.36654
STM2770	fljA	phase-1 flagellin repressor	**0.03**	0.96785
STM2770	fljA	phase-1 flagellin repressor	**-0.05**	0.91874
STM2771	fljB	flagellar biosynthesis protein	**-0.28**	0.46488
STM2771	fljB	flagellar biosynthesis protein	**0.27**	0.55167
STM2772	hin	DNA-invertase Hin	**-0.47**	0.31458
STM2772	hin	DNA-invertase Hin	**0.04**	0.94368
STM2773	iroB	putative glycosyl transferase	**-0.31**	0.64719
STM2773	iroB	putative glycosyl transferase	**0.06**	0.93699
STM2774	iroC	putative ABC transporter protein	**-0.10**	0.84913
STM2774	iroC	putative ABC transporter protein	**0.97**	0.14030
STM2775	iroD	enterochelin esterase=-like protein	**-0.09**	0.87154
STM2775	iroD	enterochelin esterase=-like protein	**0.42**	0.36856
STM2776	iroE	putative hydrolase	**-0.32**	0.68136
STM2776	iroE	putative hydrolase	**0.42**	0.39861
STM2777	iroN	TonB-dependent siderophore receptor protein	**0.44**	0.60679
STM2777	iroN	TonB-dependent siderophore receptor protein	**1.33**	0.21138
STM2780	pipB2	secreted effector protein	**-0.46**	0.45732
STM2780	pipB2	secreted effector protein	**0.17**	0.74626
STM2781	virK	virulence protein	**-1.65**	0.02425
STM2781	virK	virulence protein	**-1.04**	0.08322
STM2782	mig-14	putative transcriptional activator	**-1.87**	0.08174
STM2782	mig-14	putative transcriptional activator	**-0.26**	0.76008
STM2783	nixA	putative nickel transporter	**0.00**	0.99726
STM2783	nixA	putative nickel transporter	**-0.06**	0.94050
STM2784	tctE	regulatory protein	**0.05**	0.94675

STM2784	tctE	regulatory protein	**0.14**	0.72146
STM2785	tctD	regulatory protein	**0.42**	0.33971
STM2785	tctD	regulatory protein	**1.14**	0.11913
STM2786	STM2786	tricarboxylic transport	**-0.33**	0.61285
STM2786	STM2786	tricarboxylic transport	**-0.13**	0.74224
STM2787	STM2787	tricarboxylic transport	**-0.26**	0.54436
STM2787	STM2787	tricarboxylic transport	**0.16**	0.72521
STM2788	STM2788	tricarboxylic transport	**0.16**	0.79278
STM2788	STM2788	tricarboxylic transport	**0.14**	0.72219
STM2789	STM2789	hypothetical protein STM2789	**0.03**	0.96001
STM2789	STM2789	hypothetical protein STM2789	**0.21**	0.65305
STM2790	ygaF	putative sarcosine oxidase-like protein	**-0.32**	0.73940
STM2790	ygaF	putative sarcosine oxidase-like protein	**-1.75**	0.60942
STM2791	gabD	succinate-semialdehyde dehydrogenase I	**-0.35**	0.50764
STM2791	gabD	succinate-semialdehyde dehydrogenase I	**0.43**	0.29044
STM2792	gabT	4-aminobutyrate aminotransferase	**0.34**	0.61960
STM2792	gabT	4-aminobutyrate aminotransferase	**-0.41**	0.45800
STM2793	gabP	gamma-aminobutyrate transport protein	**-0.93**	0.19236
STM2793	gabP	gamma-aminobutyrate transport protein	**0.03**	0.97333
STM2794	ygaE	putative transcriptional repressor	**-0.26**	0.52362
STM2794	ygaE	putative transcriptional repressor	**0.08**	0.91170
STM2795	ygaU	hypothetical protein STM2795	**-0.16**	0.88018
STM2795	ygaU	hypothetical protein STM2795	**0.31**	0.57441
STM2796	yqaE	putative transport protein	**0.49**	0.24005
STM2796	yqaE	putative transport protein	**0.31**	0.58903
STM2797	STM2797	putative regulatory protein	**-0.37**	0.34070
STM2797	STM2797	putative regulatory protein	**0.48**	0.29912
STM2798	ygaP	putative rhodanese-like sulfurtransferase	**0.13**	0.74231
STM2798	ygaP	putative rhodanese-like sulfurtransferase	**0.18**	0.61735
STM2799	stpA	DNA-binding protein	**-0.60**	0.43439
STM2799	stpA	DNA-binding protein	**-0.88**	0.25720
STM2800	STM2800	putative inner membrane protein	**-0.48**	0.34936
STM2800	STM2800	putative inner membrane protein	**-0.37**	0.48432
STM2801	ygaC	putative cytoplasmic protein	**-0.81**	0.13206
STM2801	ygaC	putative cytoplasmic protein	**-0.19**	0.68032
STM2802	ygaM	putative inner membrane protein	**0.12**	0.83045
STM2802	ygaM	putative inner membrane protein	**0.32**	0.53138
STM2803	STM2803	putative regulatory protein	**0.03**	0.96966
STM2803	STM2803	putative regulatory protein	**0.20**	0.65436
STM2804	STM2804	putative cytoplasmic protein	**0.00**	0.99929
STM2804	STM2804	putative cytoplasmic protein	**0.81**	0.19967
STM2805	nrdH	glutaredoxin-like protein	**-0.02**	0.98140
STM2805	nrdH	glutaredoxin-like protein	**0.25**	0.51813
STM2806	nrdI	hypothetical protein STM2806	**-0.04**	0.93639
STM2806	nrdI	hypothetical protein STM2806	**0.97**	0.11681
STM2807	nrdE	ribonucleotide-diphosphate reductase alpha subunit	**0.35**	0.57132
STM2807	nrdE	ribonucleotide-diphosphate reductase alpha subunit	**0.74**	0.31280
STM2808	nrdF	ribonucleotide-diphosphate reductase beta subunit	**-0.15**	0.72538
STM2808	nrdF	ribonucleotide-diphosphate reductase beta subunit	**0.65**	0.46854
STM2809	proV	glycine/betaine/proline transport protein	**0.46**	0.46101
STM2809	proV	glycine/betaine/proline transport protein	**0.04**	0.93582
STM2810	proW	glycine/betaine/proline transport protein	**0.24**	0.54624
STM2810	proW	glycine/betaine/proline transport protein	**0.23**	0.54599
STM2811	proX	glycine/betaine/proline transport protein	**-0.08**	0.86702
STM2811	proX	glycine/betaine/proline transport protein	**0.65**	0.13128
STM2812	STM2812	putative inner membrane protein	**-0.19**	0.61345
STM2812	STM2812	putative inner membrane protein	**0.03**	0.95683
STM2813	emrR	emrAB operon transcriptional repressor	**-0.15**	0.74231
STM2813	emrR	emrAB operon transcriptional repressor	**-0.04**	0.94087
STM2814	emrA	multidrug resistance secretion protein	**-0.24**	0.54307
STM2814	emrA	multidrug resistance secretion protein	**-0.07**	0.88998
STM2815	emrB	putative multidrug transport protein	**0.50**	0.68313
STM2815	emrB	putative multidrug transport protein	**-0.23**	0.65549

STM2816	STM2816	putative glycoporin	**-0.08**	0.89542
STM2816	STM2816	putative glycoporin	**0.16**	0.76026
STM2817	luxS	S-ribosylhomocysteinase	**-0.87**	0.25195
STM2817	luxS	S-ribosylhomocysteinase	**-0.61**	0.40227
STM2818	gshA	glutamate--cysteine ligase	**-0.15**	0.66938
STM2818	gshA	glutamate--cysteine ligase	**-0.17**	0.71693
STM2819	yqaA	putative inner membrane protein	**0.00**	0.99518
STM2819	yqaA	putative inner membrane protein	**0.13**	0.81763
STM2820	yqaB	putative phosphoglucomutase	**-0.75**	0.32984
STM2820	yqaB	putative phosphoglucomutase	**-0.30**	0.56564
STM2824	-	STM2824	**-0.50**	0.25473
STM2824	-	STM2824	**-0.56**	0.19843
STM2824	-	STM2824	**-0.37**	0.33452
STM2824	-	STM2824	**-0.24**	0.54389
STM2824	-	STM2824	**-0.20**	0.70137
STM2824	-	STM2824	**-0.45**	0.40636
STM2824	-	STM2824	**-0.22**	0.61960
STM2824	-	STM2824	**0.00**	0.99381
STM2825	-	STM2825	**-0.10**	0.87917
STM2825	-	STM2825	**0.03**	0.96687
STM2826	csrA	carbon storage regulator	**-0.11**	0.79283
STM2826	csrA	carbon storage regulator	**-0.06**	0.91378
STM2827	alaS	alanyl-tRNA synthetase	**-0.55**	0.21393
STM2827	alaS	alanyl-tRNA synthetase	**0.28**	0.58071
STM2828	recX	RecA regulator RecX	**-0.31**	0.42525
STM2828	recX	RecA regulator RecX	**-0.21**	0.69921
STM2829	recA	recombinase A	**-0.38**	0.41154
STM2829	recA	recombinase A	**0.11**	0.85314
STM2830	ygaD	competence damage-inducible protein A	**-0.09**	0.84911
STM2830	ygaD	competence damage-inducible protein A	**0.02**	0.96851
STM2831	mltB	membrane-bound lytic murein transglycosylase B	**-0.08**	0.84930
STM2831	mltB	membrane-bound lytic murein transglycosylase B	**-0.14**	0.79635
STM2832	srlA	glucitol/sorbitol-specific enzyme IIC component	**0.27**	0.52101
STM2832	srlA	glucitol/sorbitol-specific enzyme IIC component	**0.31**	0.53827
STM2833	srlE	glucitol/sorbitol-specific enzyme IIB component	**0.21**	0.63154
STM2833	srlE	glucitol/sorbitol-specific enzyme IIB component	**0.64**	0.20065
STM2834	slrB	glucitol/sorbitol-specific enzyme IIA component	**0.09**	0.87016
STM2834	slrB	glucitol/sorbitol-specific enzyme IIA component	**0.20**	0.67233
STM2835	srlD	sorbitol-6-phosphate 2-dehydrogenase	**0.14**	0.85382
STM2835	srlD	sorbitol-6-phosphate 2-dehydrogenase	**0.25**	0.71249
STM2836	gutM	putative glucitol operon regulatory protein	**-0.35**	0.36399
STM2836	gutM	putative glucitol operon regulatory protein	**0.30**	0.48994
STM2837	srlR	transcriptional repressor for glucitol operon	**-0.31**	0.48386
STM2837	srlR	transcriptional repressor for glucitol operon	**0.55**	0.29336
STM2838,S	gutQ	putative sugar phosphate isomerase	**-0.72**	0.12727
STM2838,S	gutQ	putative sugar phosphate isomerase	**-0.20**	0.70549
STM2839	ygaA	anaerobic nitric oxide reductase transcription regulator	**0.22**	0.65984
STM2839	ygaA	anaerobic nitric oxide reductase transcription regulator	**0.42**	0.38126
STM2840	STM2840	anaerobic nitric oxide reductase flavorubredoxin	**-0.50**	0.31139
STM2840	STM2840	anaerobic nitric oxide reductase flavorubredoxin	**-0.17**	0.78335
STM2841	ygbD	nitric oxide reductase	**-0.43**	0.32770
STM2841	ygbD	nitric oxide reductase	**-0.09**	0.86385
STM2842	hypF	hydrogenase maturation protein	**0.46**	0.45240
STM2842	hypF	hydrogenase maturation protein	**0.67**	0.36399
STM2843	hydN	electron transport protein	**-0.16**	0.70848
STM2843	hydN	electron transport protein	**0.00**	0.99434
STM2844	STM2844	hypothetical protein STM2844	**-0.01**	0.98704
STM2844	STM2844	hypothetical protein STM2844	**-0.09**	0.84021
STM2845	hycI	hydrogenase 3 large subunit C-terminal protease	**0.03**	0.96673
STM2845	hycI	hydrogenase 3 large subunit C-terminal protease	**0.08**	0.89924
STM2846	hycH	hydrogenase 3 large subunit processing protein	**-0.68**	0.13645
STM2846	hycH	hydrogenase 3 large subunit processing protein	**0.12**	0.81763
STM2847	hycG	hydrogenase	**-0.05**	0.94570

STM2847	hycG	hydrogenase	**0.09**	0.86876
STM2848	hycF	hydrogenase 4 Fe-S subunit	**0.29**	0.41584
STM2848	hycF	hydrogenase 4 Fe-S subunit	**0.85**	0.19091
STM2849	hycE	hydrogenase 3 large subunit	**-0.27**	0.56786
STM2849	hycE	hydrogenase 3 large subunit	**0.07**	0.92021
STM2850	hycD	hydrogenase 3 membrane subunit	**-0.07**	0.89487
STM2850	hycD	hydrogenase 3 membrane subunit	**0.40**	0.62433
STM2851	hycC	NADH dehydrogenase subunit N	**0.16**	0.69882
STM2851	hycC	NADH dehydrogenase subunit N	**0.78**	0.16281
STM2852	hycB	hydrogenase-3 iron-sulfur subunit	**0.13**	0.82595
STM2852	hycB	hydrogenase-3 iron-sulfur subunit	**0.19**	0.69882
STM2853	hycA	transcriptional repressor	**-0.90**	0.15859
STM2853	hycA	transcriptional repressor	**-0.36**	0.41990
STM2854	hypA	hydrogenase nickel incorporation protein	**0.02**	0.96850
STM2854	hypA	hydrogenase nickel incorporation protein	**0.80**	0.14030
STM2855	hypB	hydrogenase-3 accessory protein	**0.12**	0.82956
STM2855	hypB	hydrogenase-3 accessory protein	**0.31**	0.49645
STM2856	hypC	putative hydrogenase formation protein	**0.01**	0.98592
STM2856	hypC	putative hydrogenase formation protein	**0.33**	0.42940
STM2857	hypD	putative hydrogenase formation protein	**0.04**	0.95498
STM2857	hypD	putative hydrogenase formation protein	**-0.03**	0.95532
STM2858	hypE	putative hydrogenase formation protein	**0.07**	0.90462
STM2858	hypE	putative hydrogenase formation protein	**0.03**	0.94649
STM2859	fhlA	formate hydrogen-lyase transcriptional activator	**-0.24**	0.68062
STM2859	fhlA	formate hydrogen-lyase transcriptional activator	**0.55**	0.33095
STM2860	ygbA	putative cytoplasmic protein	**0.20**	0.68923
STM2860	ygbA	putative cytoplasmic protein	**0.71**	0.21360
STM2861	sitA	putative periplasmic binding protein	**0.26**	0.60552
STM2861	sitA	putative periplasmic binding protein	**1.14**	0.08274
STM2862	sitB	putative ATP-binding protein	**0.54**	0.23495
STM2862	sitB	putative ATP-binding protein	**0.69**	0.16534
STM2863	sitC	putative permease	**-0.03**	0.95809
STM2863	sitC	putative permease	**0.65**	0.30813
STM2864	sitD	putative permease	**-0.14**	0.73270
STM2864	sitD	putative permease	**0.61**	0.35366
STM2865	avrA	secreted effector protein	**0.34**	0.46772
STM2865	avrA	secreted effector protein	**0.93**	0.25199
STM2866	sprB	transcriptional regulator	**0.16**	0.73448
STM2866	sprB	transcriptional regulator	**0.49**	0.35824
STM2867	hilC	invasion regulatory protein	**0.34**	0.41715
STM2867	hilC	invasion regulatory protein	**0.42**	0.35824
STM2868	orgC	putative cytoplasmic protein	**-0.52**	0.26261
STM2868	orgC	putative cytoplasmic protein	**-0.27**	0.56103
STM2869	orgB	needle complex export protein	**-0.95**	0.14001
STM2869	orgB	needle complex export protein	**-0.76**	0.13206
STM2870	orgA	needle complex assembly protein	**0.22**	0.58071
STM2870	orgA	needle complex assembly protein	**0.09**	0.83443
STM2871	prgK	needle complex inner membrane lipoprotein	**0.33**	0.41158
STM2871	prgK	needle complex inner membrane lipoprotein	**0.73**	0.24811
STM2872	prgJ	needle complex minor subunit	**0.37**	0.33452
STM2872	prgJ	needle complex minor subunit	**0.81**	0.13645
STM2873	prgI	needle complex major subunit	**0.31**	0.42354
STM2873	prgI	needle complex major subunit	**0.98**	0.11224
STM2874	prgH	needle complex inner membrane protein	**0.60**	0.36311
STM2874	prgH	needle complex inner membrane protein	**1.78**	0.08983
STM2875	hilD	invasion protein regulatory protein	**0.41**	0.34553
STM2875	hilD	invasion protein regulatory protein	**0.39**	0.35908
STM2876	hilA	invasion protein transcriptional activator	**0.02**	0.98309
STM2876	hilA	invasion protein transcriptional activator	**0.94**	0.15984
STM2877	iagB	invasion protein precursor	**-0.26**	0.52663
STM2877	iagB	invasion protein precursor	**0.36**	0.34756
STM2878	sptP	protein tyrosine phosphatase/GTPase activating protein	**-0.01**	0.99310
STM2878	sptP	protein tyrosine phosphatase/GTPase activating protein	**0.43**	0.48736

STM2879	sicP	secretion chaperone	**0.41**	0.34789
STM2879	sicP	secretion chaperone	**0.39**	0.26971
STM2881	iacP	acyl carrier protein	**0.36**	0.40500
STM2881	iacP	acyl carrier protein	**0.26**	0.44280
STM2882	sipA	secreted effector protein	**0.27**	0.54600
STM2882	sipA	secreted effector protein	**0.68**	0.15859
STM2883	sipD	translocation machinery component	**0.40**	0.48814
STM2883	sipD	translocation machinery component	**1.00**	0.15859
STM2884	sipC	translocation machinery component	**0.66**	0.25084
STM2884	sipC	translocation machinery component	**0.46**	0.40126
STM2885	sipB	translocation machinery component	**1.08**	0.06780
STM2885	sipB	translocation machinery component	**1.46**	0.11224
STM2886	sicA	secretion chaperone	**0.43**	0.27764
STM2886	sicA	secretion chaperone	**1.12**	0.17041
STM2887	spaS	type III secretion protein	**-0.14**	0.85893
STM2887	spaS	type III secretion protein	**0.61**	0.19142
STM2888	spaR	needle complex export protein	**0.25**	0.65916
STM2888	spaR	needle complex export protein	**-0.28**	0.63546
STM2889	spaQ	needle complex export protein	**-0.15**	0.75244
STM2889	spaQ	needle complex export protein	**0.12**	0.82956
STM2890	spaP	needle complex export protein	**0.22**	0.58178
STM2890	spaP	needle complex export protein	**0.26**	0.58207
STM2891	spaO	type III secretion protein	**0.31**	0.42455
STM2891	spaO	type III secretion protein	**0.68**	0.17765
STM2892	invJ	needle length control protein	**0.04**	0.95532
STM2892	invJ	needle length control protein	**0.99**	0.22994
STM2893	invI	needle complex assembly protein	**0.61**	0.18961
STM2893	invI	needle complex assembly protein	**1.64**	0.08015
STM2894	invC	type III secretion system ATPase	**0.85**	0.24313
STM2894	invC	type III secretion system ATPase	**0.92**	0.14374
STM2895	invB	secretion chaperone	**0.44**	0.27959
STM2895	invB	secretion chaperone	**0.66**	0.26910
STM2896	invA	needle complex export protein	**0.36**	0.40190
STM2896	invA	needle complex export protein	**0.76**	0.17754
STM2897	invE	invasion protein	**0.32**	0.37634
STM2897	invE	invasion protein	**0.55**	0.25454
STM2898	invG	outer membrane secretin precursor	**-0.13**	0.80614
STM2898	invG	outer membrane secretin precursor	**0.65**	0.37919
STM2899	invF	invasion regulatory protein	**0.18**	0.76319
STM2899	invF	invasion regulatory protein	**0.40**	0.30422
STM2900	invH	needle complex outer membrane lipoprotein precursor	**0.49**	0.24721
STM2900	invH	needle complex outer membrane lipoprotein precursor	**0.56**	0.22088
STM2902	STM2902	putative cytoplasmic protein	**-0.51**	0.34070
STM2902	STM2902	putative cytoplasmic protein	**0.17**	0.66112
STM2903	STM2903	putative cytoplasmic protein	**-0.63**	0.16534
STM2903	STM2903	putative cytoplasmic protein	**-0.24**	0.54996
STM2904	STM2904	putative ABC-type transporter	**-0.18**	0.70144
STM2904	STM2904	putative ABC-type transporter	**-0.25**	0.63154
STM2905	STM2905	putative acetyltransferase	**0.02**	0.96785
STM2905	STM2905	putative acetyltransferase	**0.00**	0.99447
STM2907	pphB	serine/threonine protein phosphatase 2	**0.09**	0.82350
STM2907	pphB	serine/threonine protein phosphatase 2	**-0.31**	0.57469
STM2909	mutS	DNA mismatch repair protein	**-0.65**	0.21062
STM2909	mutS	DNA mismatch repair protein	**0.15**	0.78846
STM2910	STM2910	putative cytoplasmic protein	**-0.47**	0.29789
STM2910	STM2910	putative cytoplasmic protein	**0.16**	0.74238
STM2911	STM2911	putative permease	**0.25**	0.68047
STM2911	STM2911	putative permease	**-0.13**	0.73855
STM2912	STM2912	putative transcriptional regulator	**0.38**	0.42525
STM2912	STM2912	putative transcriptional regulator	**0.78**	0.27312
STM2913	STM2913	putative permease	**0.03**	0.95747
STM2913	STM2913	putative permease	**0.34**	0.61359
STM2914	STM2914	putative nucleoside-diphosphate-sugar epimerase	**0.25**	0.64422

STM2914	STM2914	putative nucleoside-diphosphate-sugar epimerase	**1.04**	0.24908
STM2915	ygbM	putative endonuclease	**-0.31**	0.74483
STM2915	ygbM	putative endonuclease	**0.39**	0.36444
STM2916	ygbL	hypothetical protein STM2916	**0.19**	0.76319
STM2916	ygbL	hypothetical protein STM2916	**0.22**	0.60101
STM2917	ygbK	putative tRNA synthase	**0.38**	0.48745
STM2917	ygbK	putative tRNA synthase	**0.25**	0.68305
STM2918	ygbJ	3-hydroxyisobutyrate dehydrogenase	**-0.46**	0.40566
STM2918	ygbJ	3-hydroxyisobutyrate dehydrogenase	**0.08**	0.89935
STM2919	ygbI	putative regulatory protein	**0.01**	0.98564
STM2919	ygbI	putative regulatory protein	**0.97**	0.12986
STM2920	STM2920	putative transcriptional regulator	**-0.25**	0.49421
STM2920	STM2920	putative transcriptional regulator	**0.36**	0.40227
STM2921	STM2921	putative flavoprotein	**-0.36**	0.35911
STM2921	STM2921	putative flavoprotein	**-0.06**	0.91837
STM2922	STM2922	putative 3-polyprenyl-4-hydroxybenzoate decarboxylase	**-0.37**	0.39255
STM2922	STM2922	putative 3-polyprenyl-4-hydroxybenzoate decarboxylase	**0.13**	0.79635
STM2923	STM2923	putative cytoplasmic protein	**-1.04**	0.13509
STM2923	STM2923	putative cytoplasmic protein	**-0.11**	0.81931
STM2924	rpoS	RNA polymerase sigma factor	**0.09**	0.84788
STM2924	rpoS	RNA polymerase sigma factor	**0.07**	0.87917
STM2925	nlpD	lipoprotein	**0.44**	0.31973
STM2925	nlpD	lipoprotein	**0.68**	0.24995
STM2926	pcm	protein-L-isoaspartate O-methyltransferase	**0.15**	0.69192
STM2926	pcm	protein-L-isoaspartate O-methyltransferase	**0.38**	0.36399
STM2927	surE	acid phosphatase	**0.03**	0.95390
STM2927	surE	acid phosphatase	**-0.01**	0.97776
STM2928	ygbO	tRNA pseudouridine synthase D	**0.07**	0.87512
STM2928	ygbO	tRNA pseudouridine synthase D	**0.44**	0.28655
STM2929	ispF	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	**-0.35**	0.38080
STM2929	ispF	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	**-0.35**	0.35937
STM2930	ispD	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase	**0.00**	0.99726
STM2930	ispD	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase	**0.44**	0.31280
STM2931	ftsB	cell divison protein FtsB	**-0.55**	0.30422
STM2931	ftsB	cell divison protein FtsB	**-0.06**	0.87909
STM2932	ygbE	putative inner membrane protein	**0.33**	0.40020
STM2932	ygbE	putative inner membrane protein	**0.09**	0.86017
STM2933	cysC	adenylylsulfate kinase	**-0.22**	0.77801
STM2933	cysC	adenylylsulfate kinase	**-0.08**	0.87265
STM2934	cysN	sulfate adenylyltransferase subunit 1	**-0.46**	0.36619
STM2934	cysN	sulfate adenylyltransferase subunit 1	**0.45**	0.35770
STM2935	cysD	sulfate adenylyltransferase subunit 2	**-0.13**	0.83789
STM2935	cysD	sulfate adenylyltransferase subunit 2	**0.93**	0.17359
STM2936	iap	aminopeptidase	**-0.46**	0.72700
STM2936	iap	aminopeptidase	**0.59**	0.42909
STM2937	ygbF	putative inner membrane protein	**-0.22**	0.55892
STM2937	ygbF	putative inner membrane protein	**-0.08**	0.90277
STM2938	STM2938	putative cytoplasmic protein	**-0.31**	0.62617
STM2938	STM2938	putative cytoplasmic protein	**0.55**	0.22607
STM2939	ygcH	putative cytoplasmic protein	**0.08**	0.91079
STM2939	ygcH	putative cytoplasmic protein	**0.30**	0.62988
STM2940	STM2940	putative cytoplasmic protein	**-0.42**	0.42008
STM2940	STM2940	putative cytoplasmic protein	**0.06**	0.90237
STM2941	yghJ	putative cytoplasmic protein	**-0.27**	0.56560
STM2941	yghJ	putative cytoplasmic protein	**0.22**	0.61375
STM2942	STM2942	putative transposase	**0.01**	0.99213
STM2942	STM2942	putative transposase	**0.53**	0.38991
STM2943	STM2943	putative cytoplasmic protein	**-0.26**	0.81676
STM2943	STM2943	putative cytoplasmic protein	**-0.48**	0.33434
STM2944	ygcB	putative helicase	**-0.17**	0.77974
STM2944	ygcB	putative helicase	**0.09**	0.86017
STM2945	sopD	secreted effector protein	**0.52**	0.22087
STM2945	sopD	secreted effector protein	**0.68**	0.21360

STM2946	cysH	phosphoadenosine phosphosulfate reductase	**-0.67**	0.19967
STM2946	cysH	phosphoadenosine phosphosulfate reductase	**0.34**	0.61130
STM2947	cysI	sulfite reductase alpha subunit	**-0.60**	0.18622
STM2947	cysI	sulfite reductase alpha subunit	**0.46**	0.44969
STM2948	cysJ	sulfite reductase beta subunit	**-0.01**	0.98156
STM2948	cysJ	sulfite reductase beta subunit	**1.06**	0.38641
STM2949	ptpS	putative 6-pyruvoyl tetrahydrobiopterin synthase	**0.00**	0.99997
STM2949	ptpS	putative 6-pyruvoyl tetrahydrobiopterin synthase	**0.20**	0.58927
STM2950	STM2950	putative metal-dependent hydrolase	**-0.22**	0.80976
STM2950	STM2950	putative metal-dependent hydrolase	**0.27**	0.59015
STM2951	ygcF	hypothetical protein STM2951	**-0.23**	0.60629
STM2951	ygcF	hypothetical protein STM2951	**0.19**	0.67024
STM2952	eno	phosphopyruvate hydratase	**-0.73**	0.17152
STM2952	eno	phosphopyruvate hydratase	**-0.06**	0.91170
STM2953	pyrG	CTP synthetase	**-0.13**	0.76502
STM2953	pyrG	CTP synthetase	**-0.05**	0.92292
STM2954	mazG	putative pyrophosphatase	**0.16**	0.75101
STM2954	mazG	putative pyrophosphatase	**0.58**	0.41994
STM2954,1n	STM2954,1n	hypothetical protein STM2954,1n	**-0.11**	0.82145
STM2954,1n	STM2954,1n	hypothetical protein STM2954,1n	**-0.21**	0.62174
STM2955,S	STM2955,S	putative transcriptional regulator	**-0.84**	0.13112
STM2955,S	STM2955,S	putative transcriptional regulator	**-0.31**	0.41676
STM2956	relA	(p)ppGpp synthetase I	**-0.43**	0.49336
STM2956	relA	(p)ppGpp synthetase I	**0.18**	0.74779
STM2957	rumA	23S rRNA (uracil-5-)-methyltransferase	**-0.13**	0.74374
STM2957	rumA	23S rRNA (uracil-5-)-methyltransferase	**-0.02**	0.96630
STM2958	barA	sensor histidine kinase	**-1.17**	0.07318
STM2958	barA	sensor histidine kinase	**-0.06**	0.91900
STM2959	STM2959	putative glycerate kinase 2	**-0.05**	0.95628
STM2959	STM2959	putative glycerate kinase 2	**0.44**	0.46915
STM2960	gudD	d-glucarate dehydratase	**-0.64**	0.18918
STM2960	gudD	d-glucarate dehydratase	**0.51**	0.38075
STM2961	ygcY	putative D-glucarate dehydratase	**-0.37**	0.57026
STM2961	ygcY	putative D-glucarate dehydratase	**0.01**	0.98894
STM2962	gudT	putative D-glucarate permease	**-0.09**	0.91203
STM2962	gudT	putative D-glucarate permease	**-0.39**	0.37919
STM2963	STM2963	flavodoxin	**-0.53**	0.29871
STM2963	STM2963	flavodoxin	**0.45**	0.52685
STM2964	yqcB	putative pseudouridylate synthase	**-0.76**	0.23772
STM2964	yqcB	putative pseudouridylate synthase	**-0.11**	0.82384
STM2965	yqcC	putative cytoplasmic protein	**-0.05**	0.91082
STM2965	yqcC	putative cytoplasmic protein	**0.08**	0.85340
STM2966	csrB	STM2966	**-0.26**	0.56772
STM2966	csrB	STM2966	**0.35**	0.50825
STM2967	syd	SecY interacting protein Syd	**0.26**	0.47464
STM2967	syd	SecY interacting protein Syd	**0.06**	0.91263
STM2968	yqcD	putative GTP cyclohydrolase I	**0.12**	0.74388
STM2968	yqcD	putative GTP cyclohydrolase I	**0.08**	0.83899
STM2969	ygdH	putative nucleotide binding	**0.39**	0.29543
STM2969	ygdH	putative nucleotide binding	**0.25**	0.50190
STM2970	sdaC	putative serine transport protein	**0.65**	0.22621
STM2970	sdaC	putative serine transport protein	**0.69**	0.19843
STM2971	sdaB	L-serine dehydratase/L-threonine deaminase 2	**-0.14**	0.86176
STM2971	sdaB	L-serine dehydratase/L-threonine deaminase 2	**0.35**	0.51446
STM2972	xni	exonuclease IX	**0.34**	0.42269
STM2972	xni	exonuclease IX	**-0.01**	0.99260
STM2973	fucO	L-1,2-propanediol oxidoreductase	**-0.30**	0.48386
STM2973	fucO	L-1,2-propanediol oxidoreductase	**0.42**	0.38641
STM2974	fucA	L-fuculose phosphate aldolase	**-0.15**	0.83982
STM2974	fucA	L-fuculose phosphate aldolase	**0.10**	0.83084
STM2976	fucI	L-fucose isomerase	**0.14**	0.89546
STM2976	fucI	L-fucose isomerase	**0.40**	0.29543
STM2977	fucK	L-fuculokinase	**-0.42**	0.40947

STM2977	fucK	L-fuculokinase	**-0.11**	0.83084
STM2978	fucU	putative L-fucose-binding protein	**0.12**	0.83899
STM2978	fucU	putative L-fucose-binding protein	**0.16**	0.75190
STM2979	fucR	fuc operon positive regulator	**-0.18**	0.72146
STM2979	fucR	fuc operon positive regulator	**0.11**	0.79772
STM2980	ygdE	putative SAM-dependent methyltransferase	**-0.69**	0.37241
STM2980	ygdE	putative SAM-dependent methyltransferase	**-0.19**	0.61960
STM2981	ygdD	hypothetical protein STM2981	**-0.14**	0.73939
STM2981	ygdD	hypothetical protein STM2981	**-0.09**	0.84783
STM2982	gcvA	gcv operon regulator	**0.44**	0.85210
STM2982	gcvA	gcv operon regulator	**1.13**	0.48447
STM2983	ygdI	putative lipoprotein	**-0.42**	0.42048
STM2983	ygdI	putative lipoprotein	**0.11**	0.87727
STM2984	csdA	putative selenocysteine lyase	**-0.06**	0.92008
STM2984	csdA	putative selenocysteine lyase	**0.04**	0.93778
STM2985	ygdK	putative FeS center assembly protein	**-0.08**	0.87999
STM2985	ygdK	putative FeS center assembly protein	**0.38**	0.38068
STM2986,Sc	STM2986,Sc	putative integral membrane protein	**-0.25**	0.58196
STM2986,Sc	STM2986,Sc	putative integral membrane protein	**-0.12**	0.80055
STM2987	ygdL	putative enzyme	**-0.59**	0.20285
STM2987	ygdL	putative enzyme	**-0.04**	0.93203
STM2988	mltA	membrane-bound lytic murein transglycosylase A	**-0.15**	0.67816
STM2988	mltA	membrane-bound lytic murein transglycosylase A	**0.04**	0.94448
STM2991	amiC	N-acetylmuramoyl-L-alanine amidase	**-0.23**	0.66669
STM2991	amiC	N-acetylmuramoyl-L-alanine amidase	**0.15**	0.76172
STM2992	argA	N-acetylglutamate synthase	**-0.34**	0.37154
STM2992	argA	N-acetylglutamate synthase	**-0.04**	0.93023
STM2993	recD	exonuclease V alpha chain	**0.19**	0.69556
STM2993	recD	exonuclease V alpha chain	**0.75**	0.31800
STM2994	recB	exonuclease V beta chain	**-0.45**	0.28861
STM2994	recB	exonuclease V beta chain	**-0.41**	0.34500
STM2995	ptr	protease III	**0.23**	0.74361
STM2995	ptr	protease III	**0.14**	0.69876
STM2996	recC	exonuclease V subunit	**-0.07**	0.91595
STM2996	recC	exonuclease V subunit	**0.21**	0.61183
STM2997	ppdC	prepilin peptidase dependent protein C	**-0.24**	0.66893
STM2997	ppdC	prepilin peptidase dependent protein C	**-0.04**	0.93767
STM2998	ygdB	putative periplasmic protein	**-0.26**	0.59455
STM2998	ygdB	putative periplasmic protein	**0.47**	0.27426
STM2999	ppdB	prepilin peptidase-dependent protein B	**0.08**	0.86506
STM2999	ppdB	prepilin peptidase-dependent protein B	**0.34**	0.68521
STM3000	ppdA	prepilin peptidase-dependent protein A	**-0.04**	0.94050
STM3000	ppdA	prepilin peptidase-dependent protein A	**0.72**	0.42811
STM3001	thyA	thymidylate synthase	**-0.01**	0.98640
STM3001	thyA	thymidylate synthase	**0.08**	0.91206
STM3002	lgt	prolipoprotein diacylglyceryl transferase	**-0.40**	0.53840
STM3002	lgt	prolipoprotein diacylglyceryl transferase	**0.05**	0.95687
STM3003	ptsP	transcriptional regulator	**-0.40**	0.34553
STM3003	ptsP	transcriptional regulator	**-0.40**	0.30202
STM3004	ygdP	dinucleoside polyphosphate hydrolase	**-0.13**	0.75158
STM3004	ygdP	dinucleoside polyphosphate hydrolase	**0.61**	0.24005
STM3005	mutH	DNA mismatch repair protein	**0.05**	0.91271
STM3005	mutH	DNA mismatch repair protein	**0.30**	0.54194
STM3006	ygdQ	putative transport protein	**0.98**	0.12389
STM3006	ygdQ	putative transport protein	**1.31**	0.05817
STM3007	ygdR	putative peptide transport protein	**-0.35**	0.47366
STM3007	ygdR	putative peptide transport protein	**0.46**	0.51608
STM3009	ygeD	putative efflux protein	**0.01**	0.99075
STM3009	ygeD	putative efflux protein	**-0.19**	0.61288
STM3010	aas	2-acyl-glycerophospho-ethanolamine acyltransferase	**-0.27**	0.55019
STM3010	aas	2-acyl-glycerophospho-ethanolamine acyltransferase	**-0.18**	0.70322
STM3011	galR	galETK operon transcriptional repressor	**-0.04**	0.96630
STM3011	galR	galETK operon transcriptional repressor	**-0.30**	0.58718

STM3012	STM3012	putative transcriptional regulator	**-0.31**	0.64664
STM3012	STM3012	putative transcriptional regulator	**0.11**	0.78521
STM3013	lysA	diaminopimelate decarboxylase	**-0.13**	0.76008
STM3013	lysA	diaminopimelate decarboxylase	**0.41**	0.29848
STM3014	lysR	transcriptional regulator	**0.04**	0.95628
STM3014	lysR	transcriptional regulator	**-0.37**	0.56993
STM3015	ygeA	putative aspartate racemase	**0.12**	0.81381
STM3015	ygeA	putative aspartate racemase	**0.96**	0.14435
STM3016	araE	L-arabinose/proton symport protein	**-0.25**	0.63859
STM3016	araE	L-arabinose/proton symport protein	**-0.04**	0.96423
STM3017	kduD	2-deoxy-D-gluconate 3-dehydrogenase	**-0.43**	0.34260
STM3017	kduD	2-deoxy-D-gluconate 3-dehydrogenase	**0.16**	0.78109
STM3018	kduI	5-keto-4-deoxyuronate isomerase	**-0.24**	0.65857
STM3018	kduI	5-keto-4-deoxyuronate isomerase	**-0.04**	0.95608
STM3019	yqeF	acetyl-CoA acetyltransferase	**0.71**	0.21114
STM3019	yqeF	acetyl-CoA acetyltransferase	**1.00**	0.17754
STM3020	STM3020	putative transcriptional regulator	**-0.29**	0.61634
STM3020	STM3020	putative transcriptional regulator	**0.12**	0.73473
STM3021	STM3021	putative inner membrane protein	**-0.02**	0.97117
STM3021	STM3021	putative inner membrane protein	**0.30**	0.55978
STM3022	STM3022	putative transport protein	**0.18**	0.63148
STM3022	STM3022	putative transport protein	**0.48**	0.33452
STM3023	yohL	putative cytoplasmic protein	**-0.11**	0.77847
STM3023	yohL	putative cytoplasmic protein	**0.62**	0.17139
STM3024	yohM	putative inner membrane protein	**0.08**	0.94087
STM3024	yohM	putative inner membrane protein	**0.02**	0.97720
STM3025	STM3025	putative cytoplasmic protein	**0.15**	0.76811
STM3025	STM3025	putative cytoplasmic protein	**0.00**	0.99997
STM3025,1N	STM3025,1N	hypothetical protein STM3025,1N	**-1.23**	0.04814
STM3025,1N	STM3025,1N	hypothetical protein STM3025,1N	**0.41**	0.34070
STM3026	STM3026	putative outer membrane protein	**0.07**	0.91900
STM3026	STM3026	putative outer membrane protein	**0.19**	0.73473
STM3027	stdC	putative fimbrial chaperone	**0.23**	0.82161
STM3027	stdC	putative fimbrial chaperone	**0.23**	0.74481
STM3028	stdB	putative outer membrane usher protein	**0.22**	0.74224
STM3028	stdB	putative outer membrane usher protein	**0.76**	0.31422
STM3029,S	stdA	putative fimbrial-like protein	**-0.41**	0.46629
STM3029,S	stdA	putative fimbrial-like protein	**0.47**	0.59156
STM3030	STM3030	putative periplasmic protein	**0.17**	0.70140
STM3030	STM3030	putative periplasmic protein	**1.02**	0.19976
STM3031	STM3031	Ail/OmpX-like protein	**-0.26**	0.59455
STM3031	STM3031	Ail/OmpX-like protein	**0.37**	0.46629
STM3033	STM3033	putative nucleic acid-binding protein	**-0.26**	0.48810
STM3033	STM3033	putative nucleic acid-binding protein	**0.18**	0.70562
STM3036	STM3036	putative inner membrane protein	**0.63**	0.61299
STM3036	STM3036	putative inner membrane protein	**0.37**	0.68232
STM3037	glyU	STM3037	**1.35**	0.38601
STM3037	glyU	STM3037	**1.85**	0.16783
STM3038	STM3038	putative metalloendopeptidase	**0.39**	0.48129
STM3038	STM3038	putative metalloendopeptidase	**1.10**	0.10283
STM3039	idi	isopentenyl-diphosphate delta-isomerase	**-0.14**	0.77801
STM3039	idi	isopentenyl-diphosphate delta-isomerase	**-0.02**	0.98539
STM3040	lysS	lysyl-tRNA synthetase	**-0.08**	0.85423
STM3040	lysS	lysyl-tRNA synthetase	**0.03**	0.94050
STM3041c	prfB	peptide chain release factor 2	**-0.14**	0.75330
STM3041c	prfB	peptide chain release factor 2	**0.31**	0.56800
STM3042	recJ	single-stranded-DNA-specific exonuclease	**0.03**	0.97054
STM3042	recJ	single-stranded-DNA-specific exonuclease	**0.20**	0.73343
STM3043	dsbC	protein disulfide isomerase II	**-0.18**	0.67983
STM3043	dsbC	protein disulfide isomerase II	**0.49**	0.42580
STM3044	xerD	tyrosine recombinase	**0.17**	0.68305
STM3044	xerD	tyrosine recombinase	**0.28**	0.48270
STM3045	fldB	flavodoxin	**-0.22**	0.61205

STM3045	fldB	flavodoxin	**0.21**	0.61843
STM3046	ygfX	putative inner membrane protein	**-0.08**	0.90462
STM3046	ygfX	putative inner membrane protein	**-0.11**	0.82917
STM3047	ygfY	putative cytoplasmic protein	**-0.24**	0.54160
STM3047	ygfY	putative cytoplasmic protein	**0.05**	0.93367
STM3048	ygfZ	putative aminomethyltransferase	**-0.18**	0.64172
STM3048	ygfZ	putative aminomethyltransferase	**0.03**	0.95476
STM3049	yqfA	putative hemolysin	**-0.06**	0.88337
STM3049	yqfA	putative hemolysin	**0.09**	0.86485
STM3050	yqfB	hypothetical protein STM3050	**-0.13**	0.79049
STM3050	yqfB	hypothetical protein STM3050	**0.32**	0.48210
STM3051	bglA	6-phospho-beta-glucosidase A	**0.11**	0.78877
STM3051	bglA	6-phospho-beta-glucosidase A	**0.14**	0.87297
STM3052	STM3052	putative outer membrane protein	**-0.35**	0.40121
STM3052	STM3052	putative outer membrane protein	**-0.19**	0.70144
STM3053	gcvP	glycine dehydrogenase	**-0.54**	0.21747
STM3053	gcvP	glycine dehydrogenase	**-0.02**	0.97333
STM3054	gcvH	glycine cleavage system protein H	**0.26**	0.57400
STM3054	gcvH	glycine cleavage system protein H	**0.01**	0.98677
STM3055	gcvT	aminomethyltransferase	**0.11**	0.83610
STM3055	gcvT	aminomethyltransferase	**0.15**	0.70966
STM3056	visC	hypothetical protein STM3056	**-0.23**	0.64838
STM3056	visC	hypothetical protein STM3056	**0.01**	0.98582
STM3057	ubiH	2-octaprenyl-6-methoxyphenyl hydroxylase	**-0.19**	0.59528
STM3057	ubiH	2-octaprenyl-6-methoxyphenyl hydroxylase	**-0.10**	0.82533
STM3058	pepP	proline aminopeptidase P II	**-0.81**	0.18873
STM3058	pepP	proline aminopeptidase P II	**-0.39**	0.33082
STM3059,S	ygfB	hypothetical protein STM3059,S	**-0.44**	0.46720
STM3059,S	ygfB	hypothetical protein STM3059,S	**-0.26**	0.51545
STM3060	ygfE	putative cytoplasmic protein	**-0.22**	0.61364
STM3060	ygfE	putative cytoplasmic protein	**-0.04**	0.92351
STM3061	ygfA	putative ligase	**-0.35**	0.41422
STM3061	ygfA	putative ligase	**0.04**	0.94990
STM3062	serA	D-3-phosphoglycerate dehydrogenase	**-0.43**	0.44416
STM3062	serA	D-3-phosphoglycerate dehydrogenase	**0.46**	0.23114
STM3063	rpiA	ribose-5-phosphate isomerase A	**0.23**	0.52166
STM3063	rpiA	ribose-5-phosphate isomerase A	**0.44**	0.29532
STM3064	iciA	chromosome replication initiation inhibitor protein	**-0.04**	0.96757
STM3064	iciA	chromosome replication initiation inhibitor protein	**0.64**	0.29912
STM3065	yggE	hypothetical protein STM3065	**-0.45**	0.34449
STM3065	yggE	hypothetical protein STM3065	**0.11**	0.88765
STM3066	yggA	arginine exporter protein	**-0.09**	0.87733
STM3066	yggA	arginine exporter protein	**-0.21**	0.74231
STM3067	yggB	putative mechanosensitive channel	**-0.15**	0.72129
STM3067	yggB	putative mechanosensitive channel	**0.39**	0.30422
STM3068	fba	fructose-bisphosphate aldolase	**0.07**	0.90462
STM3068	fba	fructose-bisphosphate aldolase	**0.40**	0.43219
STM3069	pgk	phosphoglycerate kinase	**1.98**	0.52840
STM3069	pgk	phosphoglycerate kinase	**-0.13**	0.72987
STM3070	epd	D-erythrose 4-phosphate dehydrogenase	**-0.06**	0.88653
STM3070	epd	D-erythrose 4-phosphate dehydrogenase	**-0.03**	0.96107
STM3071	STM3071	putative DNA-binding protein	**0.00**	0.99806
STM3071	STM3071	putative DNA-binding protein	**0.19**	0.69398
STM3072	STM3072	putative inner membrane protein	**-0.18**	0.74481
STM3072	STM3072	putative inner membrane protein	**0.18**	0.71783
STM3073	STM3073	putative ABC-type cobalt transport system permease component	**-0.37**	0.46266
STM3073	STM3073	putative ABC-type cobalt transport system permease component	**0.30**	0.48700
STM3074	STM3074	putative ABC-type cobalt transport system ATP-binding component	**-0.24**	0.65709
STM3074	STM3074	putative ABC-type cobalt transport system ATP-binding component	**0.45**	0.55598

STM3075	STM3075	putative ABC-type cobalt transport system ATP-binding component	**-0.12**	0.86190
STM3075	STM3075	putative ABC-type cobalt transport system ATP-binding component	**-0.22**	0.62552
STM3076	tktA	transketolase	**-0.29**	0.45848
STM3076	tktA	transketolase	**-0.03**	0.94485
STM3077	yggG	putative Zn-dependent protease	**-0.22**	0.56565
STM3077	yggG	putative Zn-dependent protease	**0.32**	0.52511
STM3078	speB	agmatinase	**-0.08**	0.91019
STM3078	speB	agmatinase	**0.17**	0.68030
STM3079,S	STM3079,S	putative hydrolase/acyltransferase	**-0.33**	0.44832
STM3079,S	STM3079,S	putative hydrolase/acyltransferase	**-0.19**	0.63514
STM3080	STM3080	putative mannitol dehydrogenase	**-0.60**	0.35010
STM3080	STM3080	putative mannitol dehydrogenase	**0.14**	0.81667
STM3081	STM3081	putative malate/L-lactate dehydrogenase	**-0.56**	0.28049
STM3081	STM3081	putative malate/L-lactate dehydrogenase	**-0.17**	0.75424
STM3082	STM3082	putative zinc-binding dehydrogenase	**-0.22**	0.62860
STM3082	STM3082	putative zinc-binding dehydrogenase	**0.44**	0.36864
STM3083	STM3083	putative mannitol dehydrogenase	**-0.28**	0.55393
STM3083	STM3083	putative mannitol dehydrogenase	**0.20**	0.74361
STM3084,S	STM3084,S	putative regulatory protein	**0.01**	0.98140
STM3084,S	STM3084,S	putative regulatory protein	**0.53**	0.19398
STM3085	STM3085	putative outer membrane lipoprotein	**0.02**	0.98070
STM3085	STM3085	putative outer membrane lipoprotein	**-0.04**	0.95081
STM3086	speA	arginine decarboxylase	**-0.39**	0.37718
STM3086	speA	arginine decarboxylase	**-0.07**	0.87775
STM3087	yqgB	putative inner membrane protein	**0.18**	0.62619
STM3087	yqgB	putative inner membrane protein	**-0.02**	0.97720
STM3089	yqgD	putative inner membrane protein	**-0.02**	0.98140
STM3089	yqgD	putative inner membrane protein	**-0.05**	0.94426
STM3090	metK	S-adenosylmethionine synthetase	**-0.61**	0.30813
STM3090	metK	S-adenosylmethionine synthetase	**-0.32**	0.52419
STM3091	galP	galactose/proton symporter	**-0.45**	0.34332
STM3091	galP	galactose/proton symporter	**0.17**	0.68434
STM3092	sprT	hypothetical protein STM3092	**-0.28**	0.66677
STM3092	sprT	hypothetical protein STM3092	**0.03**	0.95703
STM3092	sprT	hypothetical protein STM3092	**0.05**	0.94087
STM3092	sprT	hypothetical protein STM3092	**0.22**	0.61679
STM3093	endA	DNA-specific endonuclease I	**-0.25**	0.61982
STM3093	endA	DNA-specific endonuclease I	**0.01**	0.98877
STM3094	yggJ	putative cytoplasmic protein	**-0.12**	0.74784
STM3094	yggJ	putative cytoplasmic protein	**0.09**	0.81872
STM3095	gshB	glutathione synthetase	**-0.22**	0.56936
STM3095	gshB	glutathione synthetase	**0.20**	0.73698
STM3096	yqgE	hypothetical protein STM3096	**0.04**	0.93924
STM3096	yqgE	hypothetical protein STM3096	**0.04**	0.94417
STM3097	yqgF	Holliday junction resolvase-like protein	**-0.01**	0.99353
STM3097	yqgF	Holliday junction resolvase-like protein	**0.17**	0.64314
STM3098	STM3098	putative transcriptional regulator	**0.05**	0.96968
STM3098	STM3098	putative transcriptional regulator	**0.39**	0.39127
STM3099	yggR	twitching motility protein	**-0.87**	0.11913
STM3099	yggR	twitching motility protein	**0.26**	0.66332
STM3100	yggS	hypothetical protein STM3100	**-0.12**	0.74087
STM3100	yggS	hypothetical protein STM3100	**-0.05**	0.91428
STM3101	yggT	putative integral membrane protein	**0.21**	0.58410
STM3101	yggT	putative integral membrane protein	**-0.03**	0.95220
STM3102	yggU	hypothetical protein STM3102	**-0.29**	0.50716
STM3102	yggU	hypothetical protein STM3102	**0.11**	0.79180
STM3103	yggV	putative deoxyribonucleotide triphosphate pyrophosphatase	**0.00**	0.99367
STM3103	yggV	putative deoxyribonucleotide triphosphate pyrophosphatase	**0.39**	0.40633
STM3104	yggW	coproporphyrinogen III oxidase	**-0.14**	0.70249

STM3104	yggW	coproporphyrinogen III oxidase	**0.00**	0.99546
STM3105	yggM	putative periplasmic protein	**0.33**	0.58822
STM3105	yggM	putative periplasmic protein	**1.09**	0.19236
STM3106	ansB	periplasmic L-asparaginase II	**0.12**	0.80490
STM3106	ansB	periplasmic L-asparaginase II	**0.16**	0.78335
STM3107	yggN	putative periplasmic protein	**-0.44**	0.25823
STM3107	yggN	putative periplasmic protein	**-0.31**	0.46674
STM3108	yggL	putative cytoplasmic protein	**-0.42**	0.27004
STM3108	yggL	putative cytoplasmic protein	**-0.16**	0.79114
STM3109	yggH	tRNA (guanine-N(7)-)-methyltransferase	**-0.06**	0.88217
STM3109	yggH	tRNA (guanine-N(7)-)-methyltransferase	**0.17**	0.65181
STM3110	mutY	adenine DNA glycosylase	**0.40**	0.63148
STM3110	mutY	adenine DNA glycosylase	**0.60**	0.42511
STM3111	yggX	hypothetical protein STM3111	**-0.71**	0.13645
STM3111	yggX	hypothetical protein STM3111	**0.01**	0.98135
STM3112	mltC	membrane-bound lytic murein transglycosylase C	**0.21**	0.60169
STM3112	mltC	membrane-bound lytic murein transglycosylase C	**0.22**	0.66969
STM3113	nupG	nucleoside transport	**0.36**	0.38389
STM3113	nupG	nucleoside transport	**1.21**	0.11690
STM3114	speC	ornithine decarboxylase isozyme	**-0.04**	0.94341
STM3114	speC	ornithine decarboxylase isozyme	**1.13**	0.14030
STM3115	yqgA	putative inner membrane protein	**-0.10**	0.83545
STM3115	yqgA	putative inner membrane protein	**0.38**	0.42935
STM3116	pheV	STM3116	**-0.68**	0.46578
STM3116	pheV	STM3116	**-0.36**	0.51381
STM3116	pheV	STM3116	**-0.05**	0.94470
STM3116	pheV	STM3116	**-0.21**	0.62503
STM3118	STM3118	putative acetyl-CoA hydrolase	**-0.63**	0.34148
STM3118	STM3118	putative acetyl-CoA hydrolase	**0.14**	0.83343
STM3119	STM3119	putative monoamine oxidase	**-0.36**	0.49336
STM3119	STM3119	putative monoamine oxidase	**0.13**	0.88018
STM3120	STM3120	putative transcriptional regulator	**-0.34**	0.41508
STM3120	STM3120	putative transcriptional regulator	**-0.01**	0.98976
STM3121	STM3121	putative transcriptional regulator	**0.03**	0.97804
STM3121	STM3121	putative transcriptional regulator	**0.19**	0.72241
STM3122	STM3122	putative arylsulfatase	**-0.35**	0.43881
STM3122	STM3122	putative arylsulfatase	**0.10**	0.88433
STM3123	STM3123	putative arylsulfatase regulator	**-0.44**	0.40808
STM3123	STM3123	putative arylsulfatase regulator	**0.32**	0.65974
STM3124	STM3124	putative response regulator	**-0.16**	0.87655
STM3124	STM3124	putative response regulator	**0.37**	0.36511
STM3125	STM3125	putative cytoplasmic protein	**-0.24**	0.62479
STM3125	STM3125	putative cytoplasmic protein	**0.37**	0.38552
STM3126	STM3126	putative amino acid transporter	**-0.16**	0.80660
STM3126	STM3126	putative amino acid transporter	**0.18**	0.73188
STM3127	STM3127	putative cytoplasmic protein	**-0.03**	0.96595
STM3127	STM3127	putative cytoplasmic protein	**-0.05**	0.93435
STM3128	STM3128	putative oxidoreductase	**0.40**	0.46629
STM3128	STM3128	putative oxidoreductase	**0.04**	0.94852
STM3129	STM3129	putative NAD-dependent aldehyde dehydrogenase	**-0.72**	0.30813
STM3129	STM3129	putative NAD-dependent aldehyde dehydrogenase	**-0.31**	0.70185
STM3131	STM3131	putative cytoplasmic protein	**0.18**	0.66482
STM3131	STM3131	putative cytoplasmic protein	**1.00**	0.23114
STM3132	STM3132	putative xylanase/chitin deacetylase	**0.50**	0.22602
STM3132	STM3132	putative xylanase/chitin deacetylase	**0.56**	0.46720
STM3133	STM3133	putative amidohydrolase	**-0.10**	0.86495
STM3133	STM3133	putative amidohydrolase	**-0.04**	0.97333
STM3134	STM3134	putative permease	**0.45**	0.35373
STM3134	STM3134	putative permease	**0.52**	0.37154
STM3135	STM3135	mannonate dehydratase	**0.60**	0.32673
STM3135	STM3135	mannonate dehydratase	**0.61**	0.22285
STM3136	STM3136	putative D-mannonate oxidoreductase	**-0.31**	0.61183
STM3136	STM3136	putative D-mannonate oxidoreductase	**0.72**	0.22540

STM3137	STM3137	uronate isomerase	**-0.07**	0.87727
STM3137	STM3137	uronate isomerase	**0.30**	0.42811
STM3138	STM3138	putative methyl-accepting chemotaxis protein	**-0.50**	0.27763
STM3138	STM3138	putative methyl-accepting chemotaxis protein	**0.24**	0.65312
STM3139	gsp	glutathionylspermidine synthetase/glutathionylspermidine amidase	**1.04**	0.18426
STM3139	gsp	glutathionylspermidine synthetase/glutathionylspermidine amidase	**1.59**	0.11690
STM3140	yghU	putative glutathione S-transferase	**-0.13**	0.83899
STM3140	yghU	putative glutathione S-transferase	**0.37**	0.38260
STM3141	STM3141	hypothetical protein STM3141	**-0.14**	0.70545
STM3141	STM3141	hypothetical protein STM3141	**0.78**	0.27378
STM3142	STM3142	putative periplasmic ferrichrome-binding protein	**-0.29**	0.51671
STM3142	STM3142	putative periplasmic ferrichrome-binding protein	**0.44**	0.47553
STM3143	hybG	chaperone-like protein	**-0.47**	0.26254
STM3143	hybG	chaperone-like protein	**0.07**	0.87707
STM3144	hypA	hydrogenase nickel incorporation protein	**-0.18**	0.62867
STM3144	hypA	hydrogenase nickel incorporation protein	**-0.03**	0.95397
STM3145	hybE	putative hydrogenase	**-0.26**	0.49336
STM3145	hybE	putative hydrogenase	**-0.07**	0.89617
STM3146	hybD	putative hydrogenase-2 processing element	**0.05**	0.92716
STM3146	hybD	putative hydrogenase-2 processing element	**0.52**	0.32481
STM3147	hybC	hydrogenase-2 large subunit	**0.35**	0.57407
STM3147	hybC	hydrogenase-2 large subunit	**0.57**	0.33618
STM3148	hybB	putative chaperone	**0.13**	0.78734
STM3148	hybB	putative chaperone	**0.40**	0.31004
STM3149	hybA	putative hydrogenase-2 component	**0.22**	0.59820
STM3149	hybA	putative hydrogenase-2 component	**0.15**	0.74272
STM3150	hypO	putative Ni/Fe hydrogenase small subunit	**-0.44**	0.39364
STM3150	hypO	putative Ni/Fe hydrogenase small subunit	**0.44**	0.44208
STM3151	yghW	putative cytoplasmic protein	**0.13**	0.75319
STM3151	yghW	putative cytoplasmic protein	**0.24**	0.62216
STM3152	STM3152	putative methyl-accepting chemotaxis protein	**0.07**	0.86654
STM3152	STM3152	putative methyl-accepting chemotaxis protein	**0.03**	0.95815
STM3153	yqhA	hypothetical protein STM3153	**0.02**	0.96785
STM3153	yqhA	hypothetical protein STM3153	**-0.12**	0.80010
STM3154	STM3154	putative ATP-dependent RNA helicase-like protein	**-0.16**	0.68450
STM3154	STM3154	putative ATP-dependent RNA helicase-like protein	**0.02**	0.96785
STM3155	STM3155	putative cytoplasmic protein	**0.15**	0.74212
STM3155	STM3155	putative cytoplasmic protein	**0.85**	0.14285
STM3156	STM3156	putative cytoplasmic protein	**0.09**	0.83897
STM3156	STM3156	putative cytoplasmic protein	**0.68**	0.16281
STM3157	yghA	oxidoreductase	**-0.02**	0.98539
STM3157	yghA	oxidoreductase	**0.29**	0.62757
STM3158	exbD	energy transduction protein	**-0.71**	0.17041
STM3158	exbD	energy transduction protein	**0.16**	0.66751
STM3159	exbB	energy transduction protein	**-0.34**	0.38260
STM3159	exbB	energy transduction protein	**0.05**	0.92529
STM3160	STM3160	putative inner membrane protein	**0.47**	0.26164
STM3160	STM3160	putative inner membrane protein	**0.25**	0.53811
STM3161	metC	cystathionine beta-lyase	**0.02**	0.97474
STM3161	metC	cystathionine beta-lyase	**0.46**	0.44214
STM3162	yghB	hypothetical protein STM3162	**-0.17**	0.67206
STM3162	yghB	hypothetical protein STM3162	**0.24**	0.52826
STM3163	yqhC	putative transcriptional regulator	**0.04**	0.96865
STM3163	yqhC	putative transcriptional regulator	**-0.15**	0.73968
STM3164	yqhD	putative alcohol dehydrogenase	**-0.05**	0.94765
STM3164	yqhD	putative alcohol dehydrogenase	**0.42**	0.31919
STM3165	yqhE	2,5-diketo-D-gluconate reductase A	**-0.20**	0.63536
STM3165	yqhE	2,5-diketo-D-gluconate reductase A	**0.89**	0.45947
STM3166,S	STM3166,S	putative cation transporter	**-0.04**	0.94004
STM3166,S	STM3166,S	putative cation transporter	**0.28**	0.58841
STM3167	STM3167	putative diadenosine tetraphosphatehydrolase	**-0.01**	0.99540

STM3167	STM3167	putative diadenosine tetraphosphatehydrolase	**0.70**	0.27753
STM3168	ygiR	hypothetical protein STM3168	**0.42**	0.69398
STM3168	ygiR	hypothetical protein STM3168	**1.00**	0.38260
STM3169	STM3169	putative periplasmic dicarboxylate-binding protein	**-0.82**	0.34719
STM3169	STM3169	putative periplasmic dicarboxylate-binding protein	**-0.11**	0.81651
STM3170	STM3170	putative inner membrane protein	**-0.12**	0.78335
STM3170	STM3170	putative inner membrane protein	**0.29**	0.52511
STM3171	ygiK	putative transporter	**0.00**	0.99887
STM3171	ygiK	putative transporter	**0.23**	0.61285
STM3172	sufI	suppressor of ftsI	**-0.16**	0.70430
STM3172	sufI	suppressor of ftsI	**0.15**	0.77931
STM3173	plsC	1-acyl-sn-glycerol-3-phosphate acyltransferase	**-0.11**	0.87208
STM3173	plsC	1-acyl-sn-glycerol-3-phosphate acyltransferase	**0.10**	0.82533
STM3174	parC	DNA topoisomerase IV subunit A	**-0.23**	0.50825
STM3174	parC	DNA topoisomerase IV subunit A	**-0.13**	0.84622
STM3175	STM3175	putative regulatory protein	**-0.08**	0.84873
STM3175	STM3175	putative regulatory protein	**0.10**	0.82637
STM3176	ygiW	putative outer membrane protein	**0.02**	0.97403
STM3176	ygiW	putative outer membrane protein	**0.65**	0.16981
STM3177	ygiX	putative transcriptional regulator	**0.10**	0.82673
STM3177	ygiX	putative transcriptional regulator	**0.24**	0.52101
STM3178	ygiY	putative sensor histidine kinase	**-0.42**	0.43219
STM3178	ygiY	putative sensor histidine kinase	**-0.02**	0.96805
STM3179	mdaB	NADPH-specific quinone oxidoreductase	**-0.18**	0.71113
STM3179	mdaB	NADPH-specific quinone oxidoreductase	**0.04**	0.94062
STM3180	ygiN	putative cytoplasmic protein	**-0.05**	0.92513
STM3180	ygiN	putative cytoplasmic protein	**0.09**	0.86247
STM3181	parE	DNA topoisomerase IV subunit B	**-0.21**	0.60051
STM3181	parE	DNA topoisomerase IV subunit B	**-0.16**	0.78211
STM3182	yqiA	putative esterase	**-0.06**	0.91917
STM3182	yqiA	putative esterase	**0.13**	0.78633
STM3183	icc	cyclic 3',5'-adenosine monophosphate phosphodiesterase	**0.02**	0.97402
STM3183	icc	cyclic 3',5'-adenosine monophosphate phosphodiesterase	**0.24**	0.58147
STM3184	yqiB	putative cytoplasmic protein	**0.18**	0.66641
STM3184	yqiB	putative cytoplasmic protein	**0.14**	0.77745
STM3185	yqiE	ADP-ribose pyrophosphatase	**-0.15**	0.78795
STM3185	yqiE	ADP-ribose pyrophosphatase	**0.27**	0.47159
STM3186	tolC	outer membrane channel precursor protein	**-0.25**	0.63887
STM3186	tolC	outer membrane channel precursor protein	**-0.43**	0.42266
STM3187	ygiB	putative inner membrane protein	**-0.14**	0.72450
STM3187	ygiB	putative inner membrane protein	**0.14**	0.74091
STM3188	ygiC	putative glutathionylspermidine synthase	**0.01**	0.99182
STM3188	ygiC	putative glutathionylspermidine synthase	**0.11**	0.83928
STM3189	ygiD	putative cytoplasmic protein	**-0.06**	0.90400
STM3189	ygiD	putative cytoplasmic protein	**0.76**	0.38729
STM3190	ygiE	zinc transporter ZupT	**-0.42**	0.29871
STM3190	ygiE	zinc transporter ZupT	**-0.19**	0.68305
STM3191	STM3191	putative arylsulfate sulfotransferase	**0.02**	0.97127
STM3191	STM3191	putative arylsulfate sulfotransferase	**0.51**	0.28799
STM3193	STM3193	putative disulfide bond formation protein	**-0.03**	0.95737
STM3193	STM3193	putative disulfide bond formation protein	**0.09**	0.89024
STM3194	STM3194	putative disulfide oxidoreductase	**-0.25**	0.67351
STM3194	STM3194	putative disulfide oxidoreductase	**0.19**	0.80077
STM3195	ribB	3,4-dihydroxy-2-butanone 4-phosphate synthase	**-0.03**	0.95538
STM3195	ribB	3,4-dihydroxy-2-butanone 4-phosphate synthase	**0.19**	0.64302
STM3196,S	yqiC	putative cytoplasmic protein	**-1.02**	0.17074
STM3196,S	yqiC	putative cytoplasmic protein	**0.05**	0.90587
STM3197	glgS	glycogen synthesis protein GlgS	**-0.22**	0.65984
STM3197	glgS	glycogen synthesis protein GlgS	**0.73**	0.16746
STM3198	STM3198	putative inner membrane protein	**-0.26**	0.55482
STM3198	STM3198	putative inner membrane protein	**0.83**	0.24520

STM3199	yqiK	hypothetical protein STM3199	**0.22**	0.56877
STM3199	yqiK	hypothetical protein STM3199	**0.50**	0.33971
STM3200	rfaE	putative ADP-L-glycero-D-manno-heptose synthase	**-0.61**	0.17139
STM3200	rfaE	putative ADP-L-glycero-D-manno-heptose synthase	**0.07**	0.86895
STM3201	glnE	adenylyl transferase for glutamine synthetase	**-0.49**	0.42277
STM3201	glnE	adenylyl transferase for glutamine synthetase	**-0.08**	0.89808
STM3202	ygiF	putative cytoplasmic protein	**-0.04**	0.95397
STM3202	ygiF	putative cytoplasmic protein	**0.40**	0.33710
STM3203	ygiM	hypothetical protein STM3203	**-0.05**	0.92183
STM3203	ygiM	hypothetical protein STM3203	**0.68**	0.14154
STM3204	cca	tRNA nucleotidyl transferase	**0.01**	0.99182
STM3204	cca	tRNA nucleotidyl transferase	**-0.49**	0.30432
STM3205	uppP	undecaprenyl pyrophosphate phosphatase	**-0.15**	0.73153
STM3205	uppP	undecaprenyl pyrophosphate phosphatase	**-0.06**	0.89487
STM3206	folB	dihydroneopterin aldolase/dihydroneopterin triphosphate	**-0.15**	0.79096
STM3206	folB	dihydroneopterin aldolase/dihydroneopterin triphosphate	**-0.21**	0.54656
STM3207	ygiH	hypothetical protein STM3207	**-0.47**	0.24376
STM3207	ygiH	hypothetical protein STM3207	**0.00**	0.99735
STM3208	gcp	putative O-sialoglycoprotein endopeptidase	**-0.35**	0.40185
STM3208	gcp	putative O-sialoglycoprotein endopeptidase	**0.57**	0.21111
STM3209	rpsU	30S ribosomal protein S21	**-0.24**	0.52383
STM3209	rpsU	30S ribosomal protein S21	**-0.12**	0.76811
STM3210	dnaG	DNA primase	**0.27**	0.44186
STM3210	dnaG	DNA primase	**0.39**	0.47479
STM3211,S	rpoD	RNA polymerase sigma factor	**-0.07**	0.87208
STM3211,S	rpoD	RNA polymerase sigma factor	**-0.04**	0.95497
STM3212	mug	G/U mismatch-specific DNA glycosylase	**-0.43**	0.32172
STM3212	mug	G/U mismatch-specific DNA glycosylase	**-0.09**	0.82384
STM3213	ileX	STM3213	**0.24**	0.65353
STM3213	ileX	STM3213	**0.32**	0.50759
STM3214	yqjH	putative transporter	**-0.31**	0.37310
STM3214	yqjH	putative transporter	**0.11**	0.78755
STM3215	yqjI	putative transcriptional regulator	**-0.05**	0.90318
STM3215	yqjI	putative transcriptional regulator	**0.14**	0.74779
STM3216	STM3216	putative methyl-accepting chemotaxis protein	**0.12**	0.94990
STM3216	STM3216	putative methyl-accepting chemotaxis protein	**-0.71**	0.49046
STM3217	aer	aerotaxis sensor receptor	**0.07**	0.86873
STM3217	aer	aerotaxis sensor receptor	**0.30**	0.42774
STM3218	oat	putative acetylornithine aminotransferase	**0.60**	0.19398
STM3218	oat	putative acetylornithine aminotransferase	**0.52**	0.35955
STM3219	fadH	2,4-dieonyl-CoA reductase	**-0.36**	0.35564
STM3219	fadH	2,4-dieonyl-CoA reductase	**0.15**	0.89405
STM3220	ygjO	putative methyltransferase	**-0.55**	0.19852
STM3220	ygjO	putative methyltransferase	**0.07**	0.89730
STM3221	ygjP	putative metal-dependent hydrolase	**-0.30**	0.41154
STM3221	ygjP	putative metal-dependent hydrolase	**0.02**	0.96653
STM3222	ygjQ	putative integral membrane protein	**0.06**	0.93596
STM3222	ygjQ	putative integral membrane protein	**1.02**	0.32984
STM3223	ygjR	putative dehydrogenase	**-0.19**	0.76043
STM3223	ygjR	putative dehydrogenase	**0.39**	0.49336
STM3224	ygjT	putative tellurite resistance protein	**-0.11**	0.80406
STM3224	ygjT	putative tellurite resistance protein	**0.20**	0.61538
STM3225	ygjU	putative dicarboxylate permease	**-0.04**	0.92637
STM3225	ygjU	putative dicarboxylate permease	**-0.01**	0.98095
STM3226	yqjA	hypothetical protein STM3226	**-0.02**	0.97090
STM3226	yqjA	hypothetical protein STM3226	**0.51**	0.23452
STM3227	yqjB	putative outer membrane protein	**-0.48**	0.22621
STM3227	yqjB	putative outer membrane protein	**0.19**	0.57512
STM3228	yqjC	putative periplasmic protein	**-0.61**	0.18622
STM3228	yqjC	putative periplasmic protein	**-0.13**	0.75077
STM3229	yqjD	putative inner membrane protein	**-0.67**	0.18464
STM3229	yqjD	putative inner membrane protein	**-0.53**	0.23114
STM3230	yqjE	putative inner membrane protein	**-0.87**	0.11224

STM3230	yqjE	putative inner membrane protein	**-0.22**	0.68308
STM3231	yqjK	putative inner membrane protein	**-0.52**	0.35010
STM3231	yqjK	putative inner membrane protein	**-0.59**	0.17139
STM3232	yqjF	hypothetical protein STM3232	**0.08**	0.85312
STM3232	yqjF	hypothetical protein STM3232	**0.66**	0.30702
STM3233	yqjG	putative glutathione S-transferase	**-0.39**	0.32016
STM3233	yqjG	putative glutathione S-transferase	**0.21**	0.68414
STM3234	yhaH	putative inner membrane protein	**0.02**	0.98539
STM3234	yhaH	putative inner membrane protein	**-0.10**	0.84263
STM3235	yhaJ	putative transcriptional regulator	**-0.88**	0.11018
STM3235	yhaJ	putative transcriptional regulator	**-0.02**	0.96692
STM3236	yhaK	putative cytoplasmic protein	**-0.55**	0.31280
STM3236	yhaK	putative cytoplasmic protein	**0.10**	0.89266
STM3237	yhaL	putative cytoplasmic protein	**0.35**	0.44997
STM3237	yhaL	putative cytoplasmic protein	**0.78**	0.36856
STM3238	yhaN	putative inner membrane protein	**-0.62**	0.16902
STM3238	yhaN	putative inner membrane protein	**0.23**	0.62861
STM3239	yhaO	putative transport protein	**-0.29**	0.61285
STM3239	yhaO	putative transport protein	**0.12**	0.84982
STM3240	tdcG	L-serine deaminase	**0.54**	0.31280
STM3240	tdcG	L-serine deaminase	**0.52**	0.55661
STM3241	tdcE	pyruvate formate-lyase 4/2-ketobutyrate formate-lyase	**0.43**	0.41913
STM3241	tdcE	pyruvate formate-lyase 4/2-ketobutyrate formate-lyase	**0.24**	0.64929
STM3242	tdcD	acetate/propionate kinase	**0.36**	0.35619
STM3242	tdcD	acetate/propionate kinase	**0.65**	0.29044
STM3243	tdcC	L-threonine/L-serine permease	**0.10**	0.89410
STM3243	tdcC	L-threonine/L-serine permease	**0.23**	0.55656
STM3244	tdcB	threonine dehydratase	**0.24**	0.52391
STM3244	tdcB	threonine dehydratase	**1.16**	0.15276
STM3245	tdcA	transcriptional activator	**-0.04**	0.95855
STM3245	tdcA	transcriptional activator	**0.28**	0.56303
STM3247	garK	glycerate kinase	**-0.59**	0.29912
STM3247	garK	glycerate kinase	**-0.19**	0.78363
STM3248	garR	tartronate semialdehyde reductase	**0.16**	0.79982
STM3248	garR	tartronate semialdehyde reductase	**-0.16**	0.82637
STM3249	garL	2-dehydro-3-deoxy-galactarate aldolase	**-0.09**	0.87019
STM3249	garL	2-dehydro-3-deoxy-galactarate aldolase	**0.33**	0.46629
STM3250	garD	galactarate dehydrogenase	**-0.71**	0.32673
STM3250	garD	galactarate dehydrogenase	**-0.22**	0.59820
STM3251	STM3251	putative sugar kinase	**-0.09**	0.88928
STM3251	STM3251	putative sugar kinase	**0.62**	0.19142
STM3252	agaR	Aga operon transcriptional repressor	**0.06**	0.91937
STM3252	agaR	Aga operon transcriptional repressor	**0.50**	0.22063
STM3253	STM3253	tagatose 1,6-diphosphate aldolase	**-0.29**	0.69833
STM3253	STM3253	tagatose 1,6-diphosphate aldolase	**0.33**	0.58934
STM3254	STM3254	putative fructose-1-phosphate kinase	**0.16**	0.79134
STM3254	STM3254	putative fructose-1-phosphate kinase	**0.04**	0.94965
STM3255	STM3255	putative phosphotransferase system fructose-specific component IIB	**-0.64**	0.26910
STM3255	STM3255	putative phosphotransferase system fructose-specific component IIB	**0.32**	0.73017
STM3256	STM3256	putative phosphotransferase system mannitol/fructose-specific IIA	**-0.08**	0.89979
STM3256	STM3256	putative phosphotransferase system mannitol/fructose-specific IIA	**-0.32**	0.67363
STM3257	STM3257	putative tagatose 6-phosphate kinase 1	**-1.08**	0.12009
STM3257	STM3257	putative tagatose 6-phosphate kinase 1	**0.09**	0.90136
STM3258	STM3258	galactitol-specific enzyme IIA	**0.39**	0.31929
STM3258	STM3258	galactitol-specific enzyme IIA	**0.83**	0.22358
STM3259	STM3259	PTS family galactitol-specific enzyme IIB	**-0.25**	0.62095
STM3259	STM3259	PTS family galactitol-specific enzyme IIB	**0.03**	0.94360
STM3260	STM3260	PTS family galactitol-specific enzyme IIC	**-0.15**	0.75544
STM3260	STM3260	PTS family galactitol-specific enzyme IIC	**0.05**	0.94050

STM3261	STM3261	galactitol-1-phosphate dehydrogenase	**-0.11**	0.81697
STM3261	STM3261	galactitol-1-phosphate dehydrogenase	**0.68**	0.16534
STM3262	STM3262	galactitol utilization operon transcriptional repressor	**-0.43**	0.41024
STM3262	STM3262	galactitol utilization operon transcriptional repressor	**-0.03**	0.97660
STM3263	yraL	putative methyltransferase	**-0.02**	0.98539
STM3263	yraL	putative methyltransferase	**0.02**	0.98555
STM3264	yraM	putative transglycosylase	**-0.28**	0.46717
STM3264	yraM	putative transglycosylase	**0.61**	0.35593
STM3265	yraN	hypothetical protein STM3265	**-0.44**	0.27312
STM3265	yraN	hypothetical protein STM3265	**0.18**	0.64518
STM3266	yraO	putative phosphoheptose isomerase	**0.06**	0.90462
STM3266	yraO	putative phosphoheptose isomerase	**0.14**	0.70229
STM3267	yraP	putative periplasmic protein	**-0.08**	0.85168
STM3267	yraP	putative periplasmic protein	**0.25**	0.62023
STM3268	yraR	putative nucleoside-diphosphate-sugar epimerase	**-0.21**	0.83855
STM3268	yraR	putative nucleoside-diphosphate-sugar epimerase	**-0.21**	0.71515
STM3269	yhbO	putative intracellular proteinase	**-0.27**	0.53840
STM3269	yhbO	putative intracellular proteinase	**-0.17**	0.78534
STM3270	yhbP	hypothetical protein STM3270	**-0.32**	0.51450
STM3270	yhbP	hypothetical protein STM3270	**0.18**	0.74528
STM3271	yhbQ	hypothetical protein STM3271	**-0.12**	0.78824
STM3271	yhbQ	hypothetical protein STM3271	**-0.04**	0.94417
STM3272	yhbS	putative transport protein	**0.24**	0.63464
STM3272	yhbS	putative transport protein	**0.79**	0.26378
STM3273	yhbT	putative lipid carrier protein	**-0.12**	0.83718
STM3273	yhbT	putative lipid carrier protein	**0.54**	0.18562
STM3274	yhbU	putative protease	**-0.12**	0.78909
STM3274	yhbU	putative protease	**0.28**	0.51300
STM3275,S	yhbV	putative protease	**-0.23**	0.61205
STM3275,S	yhbV	putative protease	**1.10**	0.19425
STM3276	yhbW	putative alkanal monooxygenase	**-0.29**	0.45423
STM3276	yhbW	putative alkanal monooxygenase	**0.04**	0.95059
STM3277	STM3277	putative inner membrane protein	**-0.55**	0.30813
STM3277	STM3277	putative inner membrane protein	**0.78**	0.40190
STM3278	STM3278	putative cytoplasmic protein	**-0.56**	0.31280
STM3278	STM3278	putative cytoplasmic protein	**-0.12**	0.85152
STM3279	mtr	tryptophan-specific transport protein	**0.05**	0.93767
STM3279	mtr	tryptophan-specific transport protein	**-0.05**	0.91585
STM3280,S	deaD	cysteine sulfinate desulfinase	**-0.35**	0.50700
STM3280,S	deaD	cysteine sulfinate desulfinase	**-0.20**	0.77967
STM3281	nlpI	lipoprotein	**-0.15**	0.74374
STM3281	nlpI	lipoprotein	**-0.17**	0.68277
STM3282	pnp	polynucleotide phosphorylase	**0.08**	0.86654
STM3282	pnp	polynucleotide phosphorylase	**0.47**	0.42580
STM3283	rpsO	30S ribosomal protein S15	**-0.36**	0.35325
STM3283	rpsO	30S ribosomal protein S15	**-0.71**	0.20916
STM3284	truB	tRNA pseudouridine synthase B	**-0.15**	0.70048
STM3284	truB	tRNA pseudouridine synthase B	**0.06**	0.89979
STM3285	rbfA	ribosome-binding factor A	**-0.35**	0.42735
STM3285	rbfA	ribosome-binding factor A	**0.57**	0.18265
STM3286	infB	translation initiation factor IF-2	**0.24**	0.84514
STM3286	infB	translation initiation factor IF-2	**-0.07**	0.86680
STM3287	nusA	transcription elongation factor NusA	**0.06**	0.92262
STM3287	nusA	transcription elongation factor NusA	**0.45**	0.42591
STM3288	yhbC	hypothetical protein STM3288	**0.50**	0.30748
STM3288	yhbC	hypothetical protein STM3288	**0.61**	0.30018
STM3289	metY	STM3289	**-0.61**	0.33452
STM3289	metY	STM3289	**-0.35**	0.56129
STM3289	metY	STM3289	**-0.51**	0.26164
STM3289	metY	STM3289	**-0.07**	0.89657
STM3289	metY	STM3289	**0.04**	0.95650
STM3289	metY	STM3289	**-0.19**	0.74374
STM3290,S	argG	argininosuccinate synthase	**-0.48**	0.29539

STM3290,S	argG	argininosuccinate synthase	**0.30**	0.49117
STM3291	STM3291	putative cytoplasmic protein	**-0.02**	0.96684
STM3291	STM3291	putative cytoplasmic protein	**0.43**	0.43219
STM3292	leuU	STM3292	**-0.36**	0.37507
STM3292	leuU	STM3292	**-0.37**	0.44552
STM3293	secG	protein-export membrane protein	**-0.55**	0.36341
STM3293	secG	protein-export membrane protein	**-0.26**	0.47455
STM3294	mrsA	phosphoglucosamine mutase	**-0.30**	0.43890
STM3294	mrsA	phosphoglucosamine mutase	**0.13**	0.73859
STM3295	folP	7,8-dihydropteroate synthase	**-0.35**	0.41996
STM3295	folP	7,8-dihydropteroate synthase	**-0.08**	0.85012
STM3296	hflB	ATP-dependent zinc-metallo protease	**-0.34**	0.52101
STM3296	hflB	ATP-dependent zinc-metallo protease	**-0.24**	0.64929
STM3297	ftsJ	23S rRNA methyltransferase	**0.06**	0.87740
STM3297	ftsJ	23S rRNA methyltransferase	**0.03**	0.93841
STM3298,S	yhbY	putative RNA-binding protein	**-0.41**	0.30813
STM3298,S	yhbY	putative RNA-binding protein	**0.28**	0.55482
STM3299	greA	transcription elongation factor GreA	**-0.25**	0.48388
STM3299	greA	transcription elongation factor GreA	**-0.01**	0.99232
STM3300	dacB	D-alanyl-D-alanine carboxypeptidase	**-0.23**	0.59820
STM3300	dacB	D-alanyl-D-alanine carboxypeptidase	**0.39**	0.36270
STM3301	yhbZ	putative GTP-binding protein	**-0.19**	0.58439
STM3301	yhbZ	putative GTP-binding protein	**0.22**	0.62988
STM3303	rpmA	50S ribosomal protein L27	**0.07**	0.88288
STM3303	rpmA	50S ribosomal protein L27	**-0.05**	0.90502
STM3303	rpmA	50S ribosomal protein L27	**0.31**	0.42591
STM3303	rpmA	50S ribosomal protein L27	**0.29**	0.41153
STM3305	ispB	octaprenyl diphosphate synthase	**0.00**	0.99997
STM3305	ispB	octaprenyl diphosphate synthase	**0.21**	0.56179
STM3306	nlp	transcriptional regulator	**-0.11**	0.80960
STM3306	nlp	transcriptional regulator	**0.22**	0.66460
STM3307	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	**-0.14**	0.76538
STM3307	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	**0.43**	0.36856
STM3308	yrbA	putative transcriptional regulator	**-0.17**	0.72197
STM3308	yrbA	putative transcriptional regulator	**-0.33**	0.43341
STM3308	yrbA	putative transcriptional regulator	**-0.15**	0.69882
STM3308	yrbA	putative transcriptional regulator	**0.33**	0.35824
STM3309	yrbB	hypothetical protein STM3309	**-0.31**	0.43577
STM3309	yrbB	hypothetical protein STM3309	**-0.02**	0.96228
STM3310	yrbC	putative transport protein	**-0.37**	0.30605
STM3310	yrbC	putative transport protein	**-0.12**	0.74436
STM3311	yrbD	putative transport protein	**-0.02**	0.97508
STM3311	yrbD	putative transport protein	**0.36**	0.39861
STM3312	yrbE	putative transport protein	**0.00**	0.99938
STM3312	yrbE	putative transport protein	**-0.04**	0.93367
STM3313	yrbF	putative transport protein	**0.06**	0.88998
STM3313	yrbF	putative transport protein	**0.38**	0.38049
STM3314	yrbG	Na/Ca transport protein	**0.13**	0.77347
STM3314	yrbG	Na/Ca transport protein	**0.14**	0.75424
STM3315	yrbH	putative sugar phosphate isomerase	**0.18**	0.68070
STM3315	yrbH	putative sugar phosphate isomerase	**0.12**	0.75538
STM3316	yrbI	3-deoxy-D-manno-octulosonate 8-phosphate phosphatase	**-0.44**	0.42654
STM3316	yrbI	3-deoxy-D-manno-octulosonate 8-phosphate phosphatase	**0.06**	0.88561
STM3317	yrbK	putative inner membrane protein	**0.10**	0.85636
STM3317	yrbK	putative inner membrane protein	**0.46**	0.39186
STM3318	yhbN	putative transport protein	**-0.17**	0.67137
STM3318	yhbN	putative transport protein	**0.76**	0.16902
STM3319	yhbG	putative transport protein	**-0.48**	0.38080
STM3319	yhbG	putative transport protein	**0.06**	0.91025
STM3320	rpoN	DNA-directed RNA polymerase subunit N	**0.11**	0.81455
STM3320	rpoN	DNA-directed RNA polymerase subunit N	**0.18**	0.64335

STM3321	yhbH	putative sigma N modulation factor	**-0.21**	0.53459
STM3321	yhbH	putative sigma N modulation factor	**0.30**	0.59881
STM3322	ptsN	sugar-specific PTS family enzyme IIA	**0.20**	0.64975
STM3322	ptsN	sugar-specific PTS family enzyme IIA	**0.18**	0.71275
STM3323	yhbJ	hypothetical protein STM3323	**0.18**	0.71058
STM3323	yhbJ	hypothetical protein STM3323	**0.33**	0.52861
STM3324	ptsO	phosphocarrier protein HPr-like NPr	**0.04**	0.96627
STM3324	ptsO	phosphocarrier protein HPr-like NPr	**0.23**	0.56285
STM3325	yrbL	putative cytoplasmic protein	**-0.41**	0.40721
STM3325	yrbL	putative cytoplasmic protein	**-0.20**	0.71367
STM3326	mtgA	monofunctional biosynthetic peptidoglycan transglycosylase	**0.05**	0.91170
STM3326	mtgA	monofunctional biosynthetic peptidoglycan transglycosylase	**-0.01**	0.98840
STM3327	yhbL	sigma cross-reacting protein 27A	**-0.62**	0.17603
STM3327	yhbL	sigma cross-reacting protein 27A	**0.13**	0.73908
STM3328	arcB	sensory histidine kinase	**-0.66**	0.65762
STM3328	arcB	sensory histidine kinase	**0.37**	0.50736
STM3329	yhcC	putative FeS oxidoreductase	**-0.23**	0.64727
STM3329	yhcC	putative FeS oxidoreductase	**-0.13**	0.78829
STM3330	gltB	glutamate synthase large subunit	**-0.10**	0.83100
STM3330	gltB	glutamate synthase large subunit	**0.25**	0.53459
STM3331	gltD	glutamate synthase small subunit	**-0.11**	0.90587
STM3331	gltD	glutamate synthase small subunit	**-0.20**	0.63148
STM3332	yhcG	putative cytoplasmic protein	**-0.70**	0.20285
STM3332	yhcG	putative cytoplasmic protein	**0.56**	0.22602
STM3333	STM3333	putative purine-cytosine permease	**-0.48**	0.40412
STM3333	STM3333	putative purine-cytosine permease	**-0.31**	0.62174
STM3334	STM3334	cytosine deaminase	**-0.33**	0.48724
STM3334	STM3334	cytosine deaminase	**0.33**	0.38961
STM3335	yhcH	putative cytoplasmic protein	**-0.21**	0.72976
STM3335	yhcH	putative cytoplasmic protein	**0.10**	0.88198
STM3336	nanK	N-acetylmannosamine kinase	**0.20**	0.76720
STM3336	nanK	N-acetylmannosamine kinase	**0.41**	0.26261
STM3337	nanE	putative ManNAc-6P epimerase	**0.07**	0.93023
STM3337	nanE	putative ManNAc-6P epimerase	**1.39**	0.02875
STM3338	nanT	putative sialic acid transporter	**0.31**	0.46148
STM3338	nanT	putative sialic acid transporter	**0.93**	0.16534
STM3339	nanA	N-acetylneuraminate lyase	**-0.54**	0.31919
STM3339	nanA	N-acetylneuraminate lyase	**0.05**	0.92914
STM3340	yhcK	transcriptional regulator NanR	**-0.20**	0.57843
STM3340	yhcK	transcriptional regulator NanR	**-0.31**	0.50719
STM3341	sspB	stringent starvation protein B	**-0.29**	0.55892
STM3341	sspB	stringent starvation protein B	**0.12**	0.78641
STM3342	sspA	stringent starvation protein A	**-0.07**	0.86233
STM3342	sspA	stringent starvation protein A	**0.04**	0.92637
STM3343	STM3343	putative cytoplasmic protein	**0.12**	0.81228
STM3343	STM3343	putative cytoplasmic protein	**0.29**	0.42409
STM3344	rpsI	30S ribosomal protein S9	**-0.10**	0.85382
STM3344	rpsI	30S ribosomal protein S9	**0.18**	0.71113
STM3345	rplM	50S ribosomal protein L13	**0.19**	0.65966
STM3345	rplM	50S ribosomal protein L13	**0.88**	0.11690
STM3346	yhcM	putative ATPase	**0.02**	0.98090
STM3346	yhcM	putative ATPase	**0.30**	0.58890
STM3347	yhcB	putative periplasmic protein	**-0.47**	0.31139
STM3347	yhcB	putative periplasmic protein	**0.04**	0.93506
STM3348	degQ	serine endoprotease	**-0.10**	0.82384
STM3348	degQ	serine endoprotease	**0.12**	0.87826
STM3349	degS	periplasmic serine endoprotease	**-0.12**	0.86174
STM3349	degS	periplasmic serine endoprotease	**0.62**	0.22620
STM3350	STM3350	putative inner membrane protein	**-0.19**	0.65674
STM3350	STM3350	putative inner membrane protein	**0.08**	0.87996

STM3351	oadB	putative sodium ion pump oxaloacetate decarboxylase beta chain	**-0.10**	0.88198
STM3351	oadB	putative sodium ion pump oxaloacetate decarboxylase beta chain	**-0.33**	0.55656
STM3352	oadA	oxaloacetate decarboxylase	**0.67**	0.65730
STM3352	oadA	oxaloacetate decarboxylase	**-0.36**	0.64307
STM3352	oadA	oxaloacetate decarboxylase	**0.35**	0.49336
STM3352	oadA	oxaloacetate decarboxylase	**0.19**	0.61654
STM3352	oadA	oxaloacetate decarboxylase	**-0.01**	0.98798
STM3352	oadA	oxaloacetate decarboxylase	**0.81**	0.17074
STM3353	oadG	putative oxaloacetate decarboxylase subunit gamma	**0.03**	0.96202
STM3353	oadG	putative oxaloacetate decarboxylase subunit gamma	**0.31**	0.56566
STM3354	STM3354	L(+)-tartrate dehydratase	**-0.66**	0.24520
STM3354	STM3354	L(+)-tartrate dehydratase	**-0.36**	0.42774
STM3355	STM3355	tartrate dehydratase	**0.08**	0.91790
STM3355	STM3355	tartrate dehydratase	**0.37**	0.46169
STM3356	STM3356	putative cation transporter	**-0.10**	0.91183
STM3356	STM3356	putative cation transporter	**-0.09**	0.95980
STM3357	STM3357	putative regulatory protein	**-0.10**	0.84021
STM3357	STM3357	putative regulatory protein	**-0.06**	0.91484
STM3358	STM3358	putative regulatory protein	**0.29**	0.42486
STM3358	STM3358	putative regulatory protein	**0.16**	0.78111
STM3359	mdh	malate dehydrogenase	**0.18**	0.69785
STM3359	mdh	malate dehydrogenase	**0.61**	0.20285
STM3360	argR	arginine repressor	**0.17**	0.71103
STM3360	argR	arginine repressor	**0.57**	0.25759
STM3361	yhcN	putative outer membrane protein	**-0.14**	0.74354
STM3361	yhcN	putative outer membrane protein	**0.67**	0.18265
STM3362	STM3362	putative periplasmic protein	**-0.72**	0.33833
STM3362	STM3362	putative periplasmic protein	**-0.13**	0.79772
STM3363	yhcO	putative cytoplasmic protein	**-0.31**	0.80096
STM3363	yhcO	putative cytoplasmic protein	**0.07**	0.91047
STM3364	yhcP	putative inner membrane protein	**-0.58**	0.21747
STM3364	yhcP	putative inner membrane protein	**-0.02**	0.96782
STM3365	yhcQ	putative multidrug resistance protein	**-0.11**	0.83443
STM3365	yhcQ	putative multidrug resistance protein	**0.01**	0.99252
STM3366	yhcR	putative inner membrane protein	**-0.15**	0.79037
STM3366	yhcR	putative inner membrane protein	**-0.26**	0.67506
STM3367	yhcS	putative transcriptional regulator	**-0.04**	0.95815
STM3367	yhcS	putative transcriptional regulator	**-0.04**	0.95481
STM3368	tldD	microcin B17-processing protein	**-0.25**	0.67097
STM3368	tldD	microcin B17-processing protein	**-0.09**	0.87019
STM3369	yhdP	putative protease	**-0.45**	0.33452
STM3369	yhdP	putative protease	**0.60**	0.35373
STM3370	cafA	RNase G	**0.00**	0.99882
STM3370	cafA	RNase G	**0.22**	0.55665
STM3371	maf	Maf-like protein	**-0.22**	0.55482
STM3371	maf	Maf-like protein	**0.01**	0.97837
STM3372	mreD	rod shape-determining protein	**-0.13**	0.76387
STM3372	mreD	rod shape-determining protein	**0.17**	0.67474
STM3373	mreC	rod shape-determining protein	**-0.33**	0.49336
STM3373	mreC	rod shape-determining protein	**-0.27**	0.53678
STM3374	mreB	rod shape-determining protein	**-0.38**	0.35635
STM3374	mreB	rod shape-determining protein	**-0.31**	0.62526
STM3375	yhdA	putative diguanylate cyclase	**-0.09**	0.91170
STM3375	yhdA	putative diguanylate cyclase	**0.00**	0.99703
STM3376	yhdH	putative oxidoreductase	**-0.02**	0.97117
STM3376	yhdH	putative oxidoreductase	**0.34**	0.41836
STM3377	STM3377	hypothetical protein STM3377	**0.30**	0.46629
STM3377	STM3377	hypothetical protein STM3377	**0.42**	0.29454
STM3378	STM3378	hypothetical protein STM3378	**0.24**	0.49336
STM3378	STM3378	hypothetical protein STM3378	**0.16**	0.70033
STM3379	accB	acetyl-CoA carboxylase	**0.09**	0.82443

STM3379	accB	acetyl-CoA carboxylase	**0.28**	0.53827
STM3380	accC	acetyl-CoA carboxylase	**-0.51**	0.24991
STM3380	accC	acetyl-CoA carboxylase	**0.14**	0.73863
STM3381	yhdT	putative inner membrane protein	**-0.34**	0.40562
STM3381	yhdT	putative inner membrane protein	**-0.29**	0.59422
STM3382	panF	sodium/panthothenate symporter	**0.04**	0.93506
STM3382	panF	sodium/panthothenate symporter	**0.20**	0.61614
STM3383	prmA	ribosomal protein L11 methyltransferase	**-0.48**	0.22153
STM3383	prmA	ribosomal protein L11 methyltransferase	**-0.07**	0.89740
STM3384	yhdG	possible dehydrogenase	**-0.35**	0.35538
STM3384	yhdG	possible dehydrogenase	**0.23**	0.60891
STM3385	fis	DNA-binding protein Fis	**-0.87**	0.12727
STM3385	fis	DNA-binding protein Fis	**-0.32**	0.53064
STM3386	yhdJ	putative methyltransferase	**0.13**	0.74359
STM3386	yhdJ	putative methyltransferase	**0.33**	0.38071
STM3387	yhdU	putative periplasmic protein	**0.13**	0.73568
STM3387	yhdU	putative periplasmic protein	**0.12**	0.76981
STM3388	STM3388	putative signal transduction protein	**-0.38**	0.34051
STM3388	STM3388	putative signal transduction protein	**0.16**	0.81872
STM3389	envR	transcriptional repressor	**-0.01**	0.99182
STM3389	envR	transcriptional repressor	**0.54**	0.42591
STM3390	acrE	acriflavine resistance protein E precursor	**-0.55**	0.21919
STM3390	acrE	acriflavine resistance protein E precursor	**0.45**	0.38270
STM3391	acrF	multidrug transport protein	**-0.33**	0.54656
STM3391	acrF	multidrug transport protein	**-0.02**	0.97983
STM3392	yhdV	putative outer membrane lipoprotein	**-0.44**	0.57804
STM3392	yhdV	putative outer membrane lipoprotein	**-0.52**	0.39002
STM3394	thrV	STM3394	**-0.28**	0.64525
STM3394	thrV	STM3394	**0.10**	0.82667
STM3396	rrlD	STM3396	**-0.08**	0.89108
STM3396	rrlD	STM3396	**-0.02**	0.98140
STM3399	yrdA	putative ferripyochelin-binding protein	**-0.48**	0.29611
STM3399	yrdA	putative ferripyochelin-binding protein	**-0.07**	0.92703
STM3400	yrdB	putative periplasmic protein	**-0.14**	0.76538
STM3400	yrdB	putative periplasmic protein	**-0.30**	0.62503
STM3401	aroE	shikimate 5-dehydrogenase	**-0.53**	0.31557
STM3401	aroE	shikimate 5-dehydrogenase	**0.05**	0.91170
STM3402	yrdC	putative dsRNA-binding protein	**-0.19**	0.74268
STM3402	yrdC	putative dsRNA-binding protein	**0.11**	0.81069
STM3403	yrdD	putative DNA topoisomerase	**-0.11**	0.83443
STM3403	yrdD	putative DNA topoisomerase	**0.35**	0.39002
STM3404	smg	hypothetical protein STM3404	**0.01**	0.98749
STM3404	smg	hypothetical protein STM3404	**0.44**	0.34148
STM3405	smf	putative competence protein	**0.12**	0.80374
STM3405	smf	putative competence protein	**0.36**	0.44179
STM3406	def	peptide deformylase	**-0.09**	0.86895
STM3406	def	peptide deformylase	**-0.06**	0.92170
STM3407	fmt	methionyl-tRNA formyltransferase	**-0.19**	0.66310
STM3407	fmt	methionyl-tRNA formyltransferase	**0.09**	0.82289
STM3408	sun	putative rRNA methylase	**-0.32**	0.58445
STM3408	sun	putative rRNA methylase	**0.51**	0.23114
STM3409	trkA	potassium transporter peripheral membrane component	**-0.20**	0.66482
STM3409	trkA	potassium transporter peripheral membrane component	**0.13**	0.77967
STM3410	mscL	large-conductance mechanosensitive channel	**0.02**	0.96785
STM3410	mscL	large-conductance mechanosensitive channel	**0.28**	0.46772
STM3412	zntR	zinc-responsive transcriptional regulator	**-0.35**	0.37189
STM3412	zntR	zinc-responsive transcriptional regulator	**-0.13**	0.77190
STM3413	yhdN	putative cytoplasmic protein	**-0.24**	0.63778
STM3413	yhdN	putative cytoplasmic protein	**-0.56**	0.40227
STM3414	rplQ	50S ribosomal protein L17	**-0.38**	0.31912
STM3414	rplQ	50S ribosomal protein L17	**-0.30**	0.42486
STM3415	rpoA	DNA-directed RNA polymerase alpha subunit	**-0.18**	0.61341
STM3415	rpoA	DNA-directed RNA polymerase alpha subunit	**-0.12**	0.73515

STM3416	rpsD	30S ribosomal protein S4	**0.08**	0.86190
STM3416	rpsD	30S ribosomal protein S4	**0.07**	0.87359
STM3417	rpsK	30S ribosomal protein S11	**0.21**	0.65983
STM3417	rpsK	30S ribosomal protein S11	**0.25**	0.52543
STM3418	rpsM	30S ribosomal protein S13	**0.18**	0.65025
STM3418	rpsM	30S ribosomal protein S13	**-0.01**	0.99182
STM3420	secY	preprotein translocase SecY	**-0.01**	0.98539
STM3420	secY	preprotein translocase SecY	**0.04**	0.94004
STM3421	rplO	50S ribosomal protein L15	**0.20**	0.61201
STM3421	rplO	50S ribosomal protein L15	**0.29**	0.48668
STM3422	rpmD	50S ribosomal protein L30	**0.15**	0.73653
STM3422	rpmD	50S ribosomal protein L30	**0.16**	0.72247
STM3423	rpsE	30S ribosomal protein S5	**-0.03**	0.95218
STM3423	rpsE	30S ribosomal protein S5	**0.58**	0.16425
STM3424	rplR	50S ribosomal protein L18	**0.18**	0.66545
STM3424	rplR	50S ribosomal protein L18	**0.18**	0.66589
STM3425	rplF	50S ribosomal protein L6	**-0.02**	0.97415
STM3425	rplF	50S ribosomal protein L6	**0.15**	0.70570
STM3426	rpsH	30S ribosomal protein S8	**0.28**	0.46267
STM3426	rpsH	30S ribosomal protein S8	**0.03**	0.95532
STM3426	rpsH	30S ribosomal protein S8	**0.23**	0.60693
STM3426	rpsH	30S ribosomal protein S8	**0.11**	0.80100
STM3427,S	rpsN	30S ribosomal subunit protein S14	**0.01**	0.98239
STM3427,S	rpsN	30S ribosomal subunit protein S14	**0.45**	0.31036
STM3428	rplE	50S ribosomal protein L5	**0.23**	0.58848
STM3428	rplE	50S ribosomal protein L5	**0.20**	0.65130
STM3429	rplX	50S ribosomal protein L24	**0.00**	0.99939
STM3429	rplX	50S ribosomal protein L24	**-0.07**	0.89542
STM3429	rplX	50S ribosomal protein L24	**0.18**	0.61201
STM3429	rplX	50S ribosomal protein L24	**-0.18**	0.65974
STM3430	rplN	50S ribosomal protein L14	**0.28**	0.56179
STM3430	rplN	50S ribosomal protein L14	**0.36**	0.42764
STM3430	rplN	50S ribosomal protein L14	**0.04**	0.93772
STM3430	rplN	50S ribosomal protein L14	**0.23**	0.55008
STM3431	rpsQ	30S ribosomal protein S17	**-0.06**	0.88959
STM3431	rpsQ	30S ribosomal protein S17	**-0.02**	0.96018
STM3432	rpmC	50S ribosomal protein L29	**-0.24**	0.49064
STM3432	rpmC	50S ribosomal protein L29	**-0.34**	0.35366
STM3433	rplP	50S ribosomal protein L16	**-0.03**	0.94470
STM3433	rplP	50S ribosomal protein L16	**0.05**	0.93083
STM3434	rpsC	30S ribosomal protein S3	**-0.15**	0.70122
STM3434	rpsC	30S ribosomal protein S3	**0.59**	0.23772
STM3435	rplV	50S ribosomal protein L22	**0.07**	0.86718
STM3435	rplV	50S ribosomal protein L22	**0.39**	0.30813
STM3436	rpsS	30S ribosomal protein S19	**0.17**	0.68232
STM3436	rpsS	30S ribosomal protein S19	**0.40**	0.36872
STM3437	rplB	50S ribosomal protein L2	**0.06**	0.89546
STM3437	rplB	50S ribosomal protein L2	**0.43**	0.52208
STM3438	rplW	50S ribosomal protein L23	**0.34**	0.43731
STM3438	rplW	50S ribosomal protein L23	**0.30**	0.65730
STM3439	rplD	50S ribosomal protein L4	**0.18**	0.65916
STM3439	rplD	50S ribosomal protein L4	**0.27**	0.49633
STM3440	rplC	50S ribosomal protein L3	**0.16**	0.68617
STM3440	rplC	50S ribosomal protein L3	**0.22**	0.56618
STM3456	yheV	putative cytoplasmic protein	**-0.24**	0.60552
STM3456	yheV	putative cytoplasmic protein	**-0.17**	0.78421
STM3457	kefB	glutathione-regulated potassium-efflux system protein	**-0.35**	0.42766
STM3457	kefB	glutathione-regulated potassium-efflux system protein	**0.39**	0.40930
STM3458	yheR	glutathione-regulated potassium-efflux system ancillary protein	**-0.22**	0.66506
STM3458	yheR	glutathione-regulated potassium-efflux system ancillary protein	**-0.18**	0.67823
STM3459	yheS	putative ABC transporter ATPase component	**-0.46**	0.38363

STM3459	yheS	putative ABC transporter ATPase component	**-0.50**	0.28655
STM3461	STM3461	putative cytoplasmic protein	**-0.21**	0.70423
STM3461	STM3461	putative cytoplasmic protein	**0.25**	0.49787
STM3462	yheT	putative hydrolase	**-0.07**	0.90605
STM3462	yheT	putative hydrolase	**0.14**	0.73473
STM3463	yheU	hypothetical protein STM3463	**-0.42**	0.34260
STM3463	yheU	hypothetical protein STM3463	**-0.14**	0.79185
STM3464	prkB	putative phosphoribulokinase	**-0.57**	0.23635
STM3464	prkB	putative phosphoribulokinase	**0.17**	0.75851
STM3465	yhfA	putative inner membrane protein	**-0.10**	0.83191
STM3465	yhfA	putative inner membrane protein	**-0.05**	0.91790
STM3466	crp	catabolite activator protein	**0.11**	0.81312
STM3466	crp	catabolite activator protein	**0.49**	0.22421
STM3467	yhfK	putative inner membrane protein	**-0.19**	0.75075
STM3467	yhfK	putative inner membrane protein	**0.87**	0.11690
STM3468	argD	bifunctional	**-0.52**	0.52351
STM3468	argD	bifunctional	**-0.09**	0.84611
STM3469	pabA	para-aminobenzoate synthase component II	**-0.03**	0.96001
STM3469	pabA	para-aminobenzoate synthase component II	**0.03**	0.95564
STM3470	fic	putative cell filamentation protein	**-0.24**	0.65974
STM3470	fic	putative cell filamentation protein	**0.33**	0.49452
STM3472	ppiA	peptidyl-prolyl cis-trans isomerase A	**0.01**	0.98840
STM3472	ppiA	peptidyl-prolyl cis-trans isomerase A	**0.13**	0.73905
STM3473	yhfC	hypothetical protein STM3473	**0.12**	0.76803
STM3473	yhfC	hypothetical protein STM3473	**0.17**	0.74374
STM3474	nirB	nitrite reductase large subunit	**-0.62**	0.30813
STM3474	nirB	nitrite reductase large subunit	**-0.18**	0.68961
STM3475	nirD	nitrite reductase small subunit	**-0.42**	0.46169
STM3475	nirD	nitrite reductase small subunit	**0.11**	0.81078
STM3476	nirC	nitrite transport protein	**-0.15**	0.73448
STM3476	nirC	nitrite transport protein	**0.22**	0.77139
STM3477	cysG	siroheme synthase	**-0.46**	0.39668
STM3477	cysG	siroheme synthase	**0.36**	0.45111
STM3478	bigA	putative surface-exposed virulence protein	**0.05**	0.93804
STM3478	bigA	putative surface-exposed virulence protein	**0.29**	0.45797
STM3480	yhfL	putative outer membrane lipoprotein	**0.02**	0.96850
STM3480	yhfL	putative outer membrane lipoprotein	**0.10**	0.82485
STM3481	trpS	tryptophanyl-tRNA synthetase	**-0.30**	0.45623
STM3481	trpS	tryptophanyl-tRNA synthetase	**-0.31**	0.49009
STM3482	gph	phosphoglycolate phosphatase	**-0.33**	0.34102
STM3482	gph	phosphoglycolate phosphatase	**0.11**	0.77801
STM3483	rpe	ribulose-phosphate 3-epimerase	**-0.15**	0.72247
STM3483	rpe	ribulose-phosphate 3-epimerase	**0.55**	0.17111
STM3484	dam	DNA adenine methylase	**-0.71**	0.13206
STM3484	dam	DNA adenine methylase	**0.11**	0.83443
STM3485	damX	membrane protein DamX	**-0.10**	0.83949
STM3485	damX	membrane protein DamX	**-0.12**	0.80258
STM3486	aroB	3-dehydroquinate synthase	**0.00**	0.99372
STM3486	aroB	3-dehydroquinate synthase	**0.21**	0.56370
STM3487	aroK	shikimate kinase I	**-0.07**	0.89410
STM3487	aroK	shikimate kinase I	**0.43**	0.38792
STM3488	hofQ	putative type IV pilin assembly protein	**-0.72**	0.31677
STM3488	hofQ	putative type IV pilin assembly protein	**0.30**	0.52038
STM3489	yrfA	putative inner membrane protein	**-0.23**	0.81667
STM3489	yrfA	putative inner membrane protein	**-0.05**	0.91937
STM3490	yrfB	putative inner membrane protein	**-0.22**	0.60311
STM3490	yrfB	putative inner membrane protein	**0.73**	0.21855
STM3491	yrfC	putative inner membrane protein	**-0.01**	0.99009
STM3491	yrfC	putative inner membrane protein	**0.60**	0.18873
STM3492	yrfD	putative periplasmic protein	**-0.22**	0.57633
STM3492	yrfD	putative periplasmic protein	**0.20**	0.72185
STM3493	mrcA	penicillin-binding protein 1A	**-0.03**	0.94863
STM3493	mrcA	penicillin-binding protein 1A	**0.39**	0.38976

STM3494,S	yrfE	putative NTP pyrophosphohydrolase	**-0.14**	0.78992
STM3494,S	yrfE	putative NTP pyrophosphohydrolase	**0.39**	0.33074
STM3495	yrfF	putative inner membrane protein	**0.08**	0.85391
STM3495	yrfF	putative inner membrane protein	**0.22**	0.56452
STM3496	yrfG	putative hydrolase	**-0.63**	0.20151
STM3496	yrfG	putative hydrolase	**-0.03**	0.95608
STM3497	yrfH	heat shock protein	**-0.71**	0.13112
STM3497	yrfH	heat shock protein	**-0.20**	0.60891
STM3498	hslO	Hsp33-like chaperonin	**-0.41**	0.37580
STM3498	hslO	Hsp33-like chaperonin	**0.10**	0.84930
STM3499	yhgE	putative inner membrane protein	**-0.46**	0.42791
STM3499	yhgE	putative inner membrane protein	**0.05**	0.95532
STM3500	pckA	phosphoenolpyruvate carboxykinase	**-0.02**	0.98340
STM3500	pckA	phosphoenolpyruvate carboxykinase	**0.39**	0.41774
STM3501	envZ	osmolarity sensor protein	**-0.18**	0.70229
STM3501	envZ	osmolarity sensor protein	**-0.11**	0.80139
STM3502	ompR	osmolarity response regulator	**-0.46**	0.35557
STM3502	ompR	osmolarity response regulator	**0.03**	0.96244
STM3503	greB	transcription elongation factor GreB	**-0.30**	0.44832
STM3503	greB	transcription elongation factor GreB	**0.27**	0.55956
STM3504	yhgF	putative RNase R	**-0.10**	0.82624
STM3504	yhgF	putative RNase R	**-0.19**	0.72549
STM3505	feoA	ferrous iron transport protein A	**-0.38**	0.38490
STM3505	feoA	ferrous iron transport protein A	**-0.32**	0.34770
STM3506	feoB	ferrous iron transport protein B	**-0.74**	0.14354
STM3506	feoB	ferrous iron transport protein B	**-0.20**	0.68277
STM3507	yhgG	putative cytoplasmic protein	**-0.45**	0.27834
STM3507	yhgG	putative cytoplasmic protein	**0.16**	0.74714
STM3508	STM3508	putative cytoplasmic protein	**0.06**	0.91111
STM3508	STM3508	putative cytoplasmic protein	**0.01**	0.99447
STM3509	bioH	putative hydrolase	**-0.24**	0.54624
STM3509	bioH	putative hydrolase	**-0.01**	0.99512
STM3510	yhgH	putative amidophosphoribosyltransferase	**-0.09**	0.86317
STM3510	yhgH	putative amidophosphoribosyltransferase	**0.17**	0.71763
STM3511	yhgI	putative thioredoxin-like protein	**-0.63**	0.23724
STM3511	yhgI	putative thioredoxin-like protein	**0.00**	0.99870
STM3512	gntT	high-affinity gluconate permease	**0.55**	0.37632
STM3512	gntT	high-affinity gluconate permease	**0.47**	0.40227
STM3513	malQ	4-alpha-glucanotransferase	**-0.01**	0.98718
STM3513	malQ	4-alpha-glucanotransferase	**0.44**	0.40820
STM3514	malP	maltodextrin phosphorylase	**0.87**	0.19843
STM3514	malP	maltodextrin phosphorylase	**0.89**	0.14030
STM3515	malT	transcriptional regulator MalT	**0.50**	0.22283
STM3515	malT	transcriptional regulator MalT	**0.15**	0.75395
STM3516	STM3516	putative cytoplasmic protein	**0.28**	0.64465
STM3516	STM3516	putative cytoplasmic protein	**0.29**	0.47614
STM3517	STM3517	putative DNA-damage-inducibile protein	**0.07**	0.85053
STM3517	STM3517	putative DNA-damage-inducibile protein	**0.48**	0.25125
STM3518	rtcA	RNA 3'-terminal-phosphate cyclase	**0.30**	0.76008
STM3518	rtcA	RNA 3'-terminal-phosphate cyclase	**0.49**	0.40020
STM3519	rtcB	putative cytoplasmic protein	**-0.26**	0.61830
STM3519	rtcB	putative cytoplasmic protein	**0.15**	0.72192
STM3521	STM3521	putative ribonucleoprotein related-protein	**0.11**	0.81667
STM3521	STM3521	putative ribonucleoprotein related-protein	**0.50**	0.53045
STM3522	rtcR	sigma N	**-0.20**	0.61474
STM3522	rtcR	sigma N	**-0.24**	0.51300
STM3523	glpR	glp operon transcriptional repressor	**0.17**	0.63849
STM3523	glpR	glp operon transcriptional repressor	**0.19**	0.65974
STM3524	glpG	glp regulon protein	**-0.06**	0.89405
STM3524	glpG	glp regulon protein	**0.19**	0.64909
STM3525	glpE	thiosulfate sulfurtransferase	**-0.16**	0.76622
STM3525	glpE	thiosulfate sulfurtransferase	**0.21**	0.56759
STM3526	glpD	sn-glycerol-3-phosphate dehydrogenase	**-0.45**	0.39615

STM3526	glpD	sn-glycerol-3-phosphate dehydrogenase	**0.18**	0.64422
STM3527	STM3527	putative inner membrane protein	**0.18**	0.65196
STM3527	STM3527	putative inner membrane protein	**0.15**	0.78973
STM3528	STM3528	putative periplasmic phosphate-binding protein	**0.16**	0.69828
STM3528	STM3528	putative periplasmic phosphate-binding protein	**-0.06**	0.94050
STM3529	gldA	glycerol dehydrogenase	**-0.06**	0.91170
STM3529	gldA	glycerol dehydrogenase	**0.23**	0.52419
STM3531	STM3531	putative dihydroxyacid dehydratase	**0.06**	0.94658
STM3531	STM3531	putative dihydroxyacid dehydratase	**-0.07**	0.90721
STM3532	STM3532	putative dihydrodipicolinate synthetase	**-0.45**	0.33833
STM3532	STM3532	putative dihydrodipicolinate synthetase	**-0.36**	0.68450
STM3533	STM3533	putative transcriptional regulator	**-0.07**	0.90440
STM3533	STM3533	putative transcriptional regulator	**0.41**	0.49358
STM3534	glgP	glycogen phosphorylase	**-0.14**	0.78877
STM3534	glgP	glycogen phosphorylase	**0.59**	0.34148
STM3535	glgA	glycogen synthase	**0.07**	0.90295
STM3535	glgA	glycogen synthase	**0.32**	0.38596
STM3536	glgC	glucose-1-phosphate adenylyltransferase	**-0.12**	0.83443
STM3536	glgC	glucose-1-phosphate adenylyltransferase	**0.01**	0.99452
STM3537	glgX	glycogen debranching enzyme	**-0.10**	0.86385
STM3537	glgX	glycogen debranching enzyme	**0.51**	0.34500
STM3538	glgB	glycogen branching enzyme	**-0.19**	0.93157
STM3538	glgB	glycogen branching enzyme	**0.76**	0.55956
STM3539	asd	aspartate-semialdehyde dehydrogenase	**0.08**	0.83901
STM3539	asd	aspartate-semialdehyde dehydrogenase	**0.16**	0.76181
STM3541	gntU	low-affinity gluconate permease	**-0.28**	0.63493
STM3541	gntU	low-affinity gluconate permease	**0.15**	0.77923
STM3542	gntK	gluconate kinase 2	**0.18**	0.66743
STM3542	gntK	gluconate kinase 2	**0.49**	0.38919
STM3543	gntR	gluconate operon transcriptional repressor	**-0.17**	0.69519
STM3543	gntR	gluconate operon transcriptional repressor	**0.27**	0.48567
STM3544	yhhW	putative cytoplasmic protein	**-0.14**	0.73406
STM3544	yhhW	putative cytoplasmic protein	**0.35**	0.48214
STM3545	yhhX	putative oxidoreductase	**-0.76**	0.13645
STM3545	yhhX	putative oxidoreductase	**0.27**	0.45848
STM3546	yhhY	putative transferase	**0.28**	0.79160
STM3546	yhhY	putative transferase	**0.61**	0.26956
STM3547,Sc	STM3547,Sc	putative transcriptional regulator	**0.36**	0.45861
STM3547,Sc	STM3547,Sc	putative transcriptional regulator	**0.76**	0.23114
STM3548	STM3548	putative cytoplasmic protein	**-0.33**	0.50811
STM3548	STM3548	putative cytoplasmic protein	**0.14**	0.86576
STM3549	STM3549	putative inner membrane protein	**0.16**	0.81061
STM3549	STM3549	putative inner membrane protein	**0.30**	0.61843
STM3550	STM3550	putative phosphotriesterase	**-0.44**	0.29510
STM3550	STM3550	putative phosphotriesterase	**0.47**	0.24712
STM3551	ggt	gamma-glutamyltranspeptidase	**-0.67**	0.39052
STM3551	ggt	gamma-glutamyltranspeptidase	**0.01**	0.98894
STM3552	yhhA	putative outer membrane protein	**-0.53**	0.19398
STM3552	yhhA	putative outer membrane protein	**0.10**	0.81455
STM3553	ugpQ	cytoplasmic glycerophosphodiester phosphodiesterase	**-0.03**	0.96107
STM3553	ugpQ	cytoplasmic glycerophosphodiester phosphodiesterase	**-0.08**	0.87254
STM3554	ugpC	sn-glycerol 3-phosphate transport protein	**0.12**	0.80637
STM3554	ugpC	sn-glycerol 3-phosphate transport protein	**0.01**	0.98489
STM3555	ugpE	sn-glycerol 3-phosphate transport protein	**-0.31**	0.42811
STM3555	ugpE	sn-glycerol 3-phosphate transport protein	**0.44**	0.36777
STM3556	ugpA	sn-glycerol 3-phosphate transport protein	**-0.20**	0.76184
STM3556	ugpA	sn-glycerol 3-phosphate transport protein	**-0.17**	0.79752
STM3557	ugpB	sn-glycerol 3-phosphate transport protein	**-0.31**	0.70249
STM3557	ugpB	sn-glycerol 3-phosphate transport protein	**0.20**	0.71693
STM3558	STM3558	death-on-curing protein	**0.48**	0.72247
STM3558	STM3558	death-on-curing protein	**0.40**	0.43799
STM3559	yhhV	putative cytoplasmic protein	**-0.27**	0.50201
STM3559	yhhV	putative cytoplasmic protein	**0.44**	0.33710

STM3560	livF	high-affinity branched-chain amino acid transporter	**-0.24**	0.55403
STM3560	livF	high-affinity branched-chain amino acid transporter	**0.29**	0.65383
STM3561	livG	high-affinity branched-chain amino acid transporter	**-0.22**	0.75552
STM3561	livG	high-affinity branched-chain amino acid transporter	**0.04**	0.93841
STM3562	livM	high-affinity branched-chain amino acid transporter	**-0.52**	0.37178
STM3562	livM	high-affinity branched-chain amino acid transporter	**-0.18**	0.69988
STM3563	livH	high-affinity branched-chain amino acid transporter	**-0.31**	0.73421
STM3563	livH	high-affinity branched-chain amino acid transporter	**0.07**	0.90990
STM3564	livK	high-affinity branched-chain amino acid transporter	**-0.23**	0.70430
STM3564	livK	high-affinity branched-chain amino acid transporter	**-0.07**	0.91917
STM3565	yhhK	putative acetyltransferase	**-0.10**	0.79741
STM3565	yhhK	putative acetyltransferase	**0.42**	0.29796
STM3567	livJ	high-affinity branched-chain amino acid transporter	**-0.37**	0.43772
STM3567	livJ	high-affinity branched-chain amino acid transporter	**0.38**	0.57512
STM3568	rpoH	RNA polymerase sigma factor	**-0.18**	0.67351
STM3568	rpoH	RNA polymerase sigma factor	**0.04**	0.92637
STM3569	ftsX	putative cell division protein	**-0.09**	0.83723
STM3569	ftsX	putative cell division protein	**-0.07**	0.86334
STM3570	ftsE	putative cell division ATPase	**-0.42**	0.29912
STM3570	ftsE	putative cell division ATPase	**0.15**	0.71782
STM3571	ftsY	cell division membrane protein	**-0.01**	0.97720
STM3571	ftsY	cell division membrane protein	**-0.08**	0.85053
STM3572	yhhF	putative methyltransferase	**-0.06**	0.91170
STM3572	yhhF	putative methyltransferase	**0.17**	0.65271
STM3573	yhhL	putative inner membrane protein	**0.10**	0.80093
STM3573	yhhL	putative inner membrane protein	**0.09**	0.86385
STM3574	yhhM	putative inner membrane protein	**-0.15**	0.74368
STM3574	yhhM	putative inner membrane protein	**-0.26**	0.47205
STM3575	yhhN	putative inner membrane protein	**0.15**	0.79635
STM3575	yhhN	putative inner membrane protein	**0.63**	0.24005
STM3576	zntA	Pb/Cd/Zn/Hg-transporting ATPase	**-0.19**	0.70102
STM3576	zntA	Pb/Cd/Zn/Hg-transporting ATPase	**0.26**	0.67351
STM3577	tcp	methyl-accepting transmembrane citrate/phenol chemoreceptor	**-0.47**	0.54917
STM3577	tcp	methyl-accepting transmembrane citrate/phenol chemoreceptor	**-0.27**	0.64786
STM3578	yhhP	hypothetical protein STM3578	**0.49**	0.22602
STM3578	yhhP	hypothetical protein STM3578	**0.30**	0.66743
STM3579	yhhQ	putative integral membrane protein	**0.02**	0.97219
STM3579	yhhQ	putative integral membrane protein	**0.20**	0.65644
STM3580	STM3580	putative inner membrane lipoprotein	**-0.64**	0.30508
STM3580	STM3580	putative inner membrane lipoprotein	**0.08**	0.86680
STM3581,S	yhhS	hypothetical protein STM3581,S	**0.10**	0.79752
STM3581,S	yhhS	hypothetical protein STM3581,S	**0.17**	0.74481
STM3582	yhhT	putative permease	**-0.04**	0.95608
STM3582	yhhT	putative permease	**0.58**	0.34770
STM3583	acpT	putative phosphopantetheinyl transferase	**-0.14**	0.86385
STM3583	acpT	putative phosphopantetheinyl transferase	**0.32**	0.52364
STM3584	nikR	nickel responsive regulator	**-0.07**	0.89004
STM3584	nikR	nickel responsive regulator	**-0.03**	0.95363
STM3585	yhhJ	putative ABC transport protein	**-0.03**	0.98958
STM3585	yhhJ	putative ABC transport protein	**0.71**	0.19398
STM3586,S	yhiH	putative ABC-type multidrug transport system ATPase component	**-0.30**	0.59455
STM3586,S	yhiH	putative ABC-type multidrug transport system ATPase component	**0.30**	0.42729
STM3587	yhiI	hypothetical protein STM3587	**-0.24**	0.56129
STM3587	yhiI	hypothetical protein STM3587	**0.16**	0.68405
STM3588	yhiN	putative periplasmic protein	**-0.34**	0.56120
STM3588	yhiN	putative periplasmic protein	**0.14**	0.79278
STM3589	pitA	low-affinity phosphate transporter	**0.21**	0.63403
STM3589	pitA	low-affinity phosphate transporter	**0.36**	0.33703
STM3590	uspB	universal stress protein UspB	**0.15**	0.72821

STM3590	uspB	universal stress protein UspB	**-0.20**	0.67448
STM3591	uspA	universal stress protein A	**-0.13**	0.73473
STM3591	uspA	universal stress protein A	**-0.20**	0.62188
STM3592	yhiP	putative peptide transport protein	**-0.15**	0.78091
STM3592	yhiP	putative peptide transport protein	**-1.51**	0.61201
STM3593	yhiQ	putative SAM-dependent methyltransferase	**-0.35**	0.68062
STM3593	yhiQ	putative SAM-dependent methyltransferase	**0.10**	0.87297
STM3594	prlC	oligopeptidase A	**-0.32**	0.38236
STM3594	prlC	oligopeptidase A	**0.30**	0.43219
STM3595	STM3595	putative phosphatase	**-0.55**	0.17603
STM3595	STM3595	putative phosphatase	**-0.20**	0.61960
STM3596	yhiR	putative cytoplasmic protein	**-0.18**	0.73473
STM3596	yhiR	putative cytoplasmic protein	**0.03**	0.97168
STM3597	gor	glutathione reductase	**-0.28**	0.46629
STM3597	gor	glutathione reductase	**0.07**	0.88045
STM3598	STM3598	putative L-asparaginase	**-0.56**	0.27378
STM3598	STM3598	putative L-asparaginase	**-0.49**	0.33452
STM3599	STM3599	anaerobic C4-dicarboxylate transporter	**-0.60**	0.27658
STM3599	STM3599	anaerobic C4-dicarboxylate transporter	**0.09**	0.90733
STM3600	STM3600	putative sugar kinase	**-0.45**	0.39809
STM3600	STM3600	putative sugar kinase	**0.21**	0.71971
STM3601	STM3601	putative phosphosugar isomerase	**0.01**	0.99152
STM3601	STM3601	putative phosphosugar isomerase	**0.28**	0.56103
STM3602	STM3602	putative regulatory protein	**0.02**	0.97626
STM3602	STM3602	putative regulatory protein	**-0.04**	0.94143
STM3603	treF	cytoplasmic trehalase	**-0.10**	0.84436
STM3603	treF	cytoplasmic trehalase	**0.42**	0.28970
STM3604	STM3604	putative inner membrane protein	**-0.11**	0.81830
STM3604	STM3604	putative inner membrane protein	**0.72**	0.17139
STM3605	STM3605	putative phage endolysin	**-0.14**	0.79324
STM3605	STM3605	putative phage endolysin	**0.10**	0.84863
STM3606	yhjB	putative transcriptional regulator	**-0.32**	0.64498
STM3606	yhjB	putative transcriptional regulator	**-0.08**	0.87566
STM3607	yhjC	putative transcriptional regulator	**-0.38**	0.34156
STM3607	yhjC	putative transcriptional regulator	**0.61**	0.26910
STM3608	yhjD	putative tRNA-processing ribonuclease	**-0.25**	0.55974
STM3608	yhjD	putative tRNA-processing ribonuclease	**0.89**	0.28655
STM3609	yhjE	putative transport protein	**-0.06**	0.91170
STM3609	yhjE	putative transport protein	**0.28**	0.55618
STM3610	yhjG	putative inner membrane protein	**-0.04**	0.92351
STM3610	yhjG	putative inner membrane protein	**0.76**	0.16039
STM3611	yhjH	hypothetical protein STM3611	**0.17**	0.69042
STM3611	yhjH	hypothetical protein STM3611	**0.31**	0.49422
STM3612	kdgK	ketodeoxygluconokinase	**0.03**	0.94663
STM3612	kdgK	ketodeoxygluconokinase	**0.03**	0.95380
STM3613	yhjJ	putative Zn-dependent peptidase	**0.16**	0.89252
STM3613	yhjJ	putative Zn-dependent peptidase	**0.13**	0.83443
STM3614	dctA	C4-dicarboxylate transport protein	**0.52**	0.24520
STM3614	dctA	C4-dicarboxylate transport protein	**0.40**	0.52689
STM3615	yhjK	putative diguanylate cyclase/phosphodiesterase	**0.00**	0.99929
STM3615	yhjK	putative diguanylate cyclase/phosphodiesterase	**0.22**	0.61735
STM3616	yhjL	tetratricopeptide repeat protein	**0.13**	0.91181
STM3616	yhjL	tetratricopeptide repeat protein	**0.44**	0.30813
STM3617	STM3617	endo-1,4-D-glucanase	**0.12**	0.79093
STM3617	STM3617	endo-1,4-D-glucanase	**0.00**	0.99997
STM3618	yhjN	putative cellulose synthase	**0.10**	0.86190
STM3618	yhjN	putative cellulose synthase	**0.20**	0.62575
STM3619	yhjO	glycosyltransferase	**0.03**	0.94990
STM3619	yhjO	glycosyltransferase	**0.28**	0.48668
STM3620	yhjQ	putative chromosome partitioning ATPase	**-0.07**	0.87740
STM3620	yhjQ	putative chromosome partitioning ATPase	**0.59**	0.27378
STM3621	yhjR	putative cytoplasmic protein	**-0.07**	0.90502
STM3621	yhjR	putative cytoplasmic protein	**-0.27**	0.46720

STM3622	yhjS	putative cytoplasmic protein	**-0.31**	0.41391
STM3622	yhjS	putative cytoplasmic protein	**0.32**	0.51203
STM3623	yhjT	putative inner membrane protein	**-0.09**	0.85157
STM3623	yhjT	putative inner membrane protein	**0.15**	0.70762
STM3624	yhjU	putative inner membrane protein	**-0.49**	0.36297
STM3624	yhjU	putative inner membrane protein	**-0.52**	0.22540
STM3624A	STM3624A	cystathionine gamma-synthase	**-0.04**	0.95257
STM3624A	STM3624A	cystathionine gamma-synthase	**0.18**	0.64969
STM3625	yhjV	putative transport protein	**-0.34**	0.53459
STM3625	yhjV	putative transport protein	**0.02**	0.96640
STM3626	dppF	dipeptide transport protein	**0.13**	0.76492
STM3626	dppF	dipeptide transport protein	**0.33**	0.60936
STM3627	dppD	dipeptide transport protein	**0.21**	0.79180
STM3627	dppD	dipeptide transport protein	**0.66**	0.24908
STM3628	dppC	dipeptide transport protein 2	**-0.01**	0.98124
STM3628	dppC	dipeptide transport protein 2	**0.42**	0.33730
STM3629	dppB	dipeptide transport protein 1	**-0.29**	0.45811
STM3629	dppB	dipeptide transport protein 1	**0.57**	0.21562
STM3630	dppA	dipeptide transport protein	**-0.03**	0.95985
STM3630	dppA	dipeptide transport protein	**0.57**	0.27312
STM3631	STM3631	putative xanthine permease	**-0.33**	0.63328
STM3631	STM3631	putative xanthine permease	**0.88**	0.39069
STM3632	STM3632	hypothetical protein STM3632	**0.05**	0.89979
STM3632	STM3632	hypothetical protein STM3632	**0.22**	0.60084
STM3633	STM3633	putative regulatory protein	**-0.50**	0.32770
STM3633	STM3633	putative regulatory protein	**-0.27**	0.60891
STM3634	proK	STM3634	**0.28**	0.69828
STM3634	proK	STM3634	**0.07**	0.95608
STM3635	yhjW	putative membrane-associated metal-dependent hydrolase	**0.19**	0.70966
STM3635	yhjW	putative membrane-associated metal-dependent hydrolase	**0.45**	0.45837
STM3636	lpfE	long polar fimbrial minor protein	**0.10**	0.78521
STM3636	lpfE	long polar fimbrial minor protein	**1.16**	0.07353
STM3637	lpfD	long polar fimbrial protein	**0.07**	0.93340
STM3637	lpfD	long polar fimbrial protein	**0.57**	0.23123
STM3638	lpfC	long polar fimbrial outer membrane usher protein	**0.00**	0.99769
STM3638	lpfC	long polar fimbrial outer membrane usher protein	**-0.10**	0.89468
STM3639	lpfB	long polar fimbrial chaperone precursor	**-0.26**	0.73415
STM3639	lpfB	long polar fimbrial chaperone precursor	**0.98**	0.34480
STM3640	lpfA	long polar fimbrial protein A precursor	**-0.18**	0.73546
STM3640	lpfA	long polar fimbrial protein A precursor	**0.16**	0.70933
STM3641	yhjY	putative lipase	**-0.40**	0.40642
STM3641	yhjY	putative lipase	**0.02**	0.98090
STM3642	tag	3-methyl-adenine DNA glycosylase I	**-0.11**	0.84456
STM3642	tag	3-methyl-adenine DNA glycosylase I	**-0.03**	0.95318
STM3643	yiaC	putative acetyltransferase	**-0.36**	0.47844
STM3643	yiaC	putative acetyltransferase	**0.26**	0.65130
STM3644	bisC	biotin sulfoxide reductase	**0.03**	0.94765
STM3644	bisC	biotin sulfoxide reductase	**0.00**	0.99800
STM3645	yiaD	putative outer membrane lipoprotein	**-0.46**	0.36942
STM3645	yiaD	putative outer membrane lipoprotein	**0.14**	0.86190
STM3646	yiaE	2-hydroxyacid dehydrogenase	**-0.32**	0.37321
STM3646	yiaE	2-hydroxyacid dehydrogenase	**0.50**	0.21663
STM3647	yiaF	putative outer membrane lipoprotein	**-0.42**	0.38068
STM3647	yiaF	putative outer membrane lipoprotein	**0.11**	0.87254
STM3648	yiaG	putative transcriptional regulator	**-0.11**	0.89233
STM3648	yiaG	putative transcriptional regulator	**0.06**	0.93203
STM3649	cspA	major cold shock protein	**-0.35**	0.68830
STM3649	cspA	major cold shock protein	**0.06**	0.94050
STM3650	STM3650	hypothetical protein STM3650	**-0.56**	0.38722
STM3650	STM3650	hypothetical protein STM3650	**-0.13**	0.81270
STM3651	STM3651	putative acetyltransferase	**-0.10**	0.83134

STM3651	STM3651	putative acetyltransferase	**0.34**	0.35770
STM3652	STM3652	putative cytoplasmic protein	**-0.03**	0.95665
STM3652	STM3652	putative cytoplasmic protein	**0.17**	0.69170
STM3655	glyS	glycyl-tRNA synthetase beta subunit	**-0.41**	0.31710
STM3655	glyS	glycyl-tRNA synthetase beta subunit	**-0.34**	0.58934
STM3656	glyQ	glycyl-tRNA synthetase alpha subunit	**0.06**	0.89546
STM3656	glyQ	glycyl-tRNA synthetase alpha subunit	**-0.09**	0.84354
STM3657	STM3657	putative outer membrane lipoprotein	**-0.23**	0.52728
STM3657	STM3657	putative outer membrane lipoprotein	**-0.23**	0.62216
STM3658	yiaH	putative inner membrane protein	**-0.03**	0.95548
STM3658	yiaH	putative inner membrane protein	**0.55**	0.50825
STM3659	yiaB	putative inner membrane protein	**-0.35**	0.61285
STM3659	yiaB	putative inner membrane protein	**0.91**	0.23398
STM3660	xylB	xylulokinase	**0.17**	0.68545
STM3660	xylB	xylulokinase	**0.42**	0.40532
STM3661	xylA	xylose isomerase	**0.18**	0.71098
STM3661	xylA	xylose isomerase	**0.11**	0.92161
STM3662	xylR	xylose operon regulatory protein	**-0.34**	0.47879
STM3662	xylR	xylose operon regulatory protein	**-0.30**	0.41676
STM3663	bax	putative ATP-binding protein	**-0.36**	0.50825
STM3663	bax	putative ATP-binding protein	**-0.11**	0.79056
STM3664	malS	periplasmic alpha-amylase precursor	**0.26**	0.52381
STM3664	malS	periplasmic alpha-amylase precursor	**0.35**	0.65730
STM3665	avtA	valine--pyruvate transaminase	**-0.42**	0.52208
STM3665	avtA	valine--pyruvate transaminase	**-0.06**	0.90733
STM3666	ysaA	putative oxidoreductase	**-0.08**	0.87965
STM3666	ysaA	putative oxidoreductase	**0.01**	0.98539
STM3667	yiaJ	transcriptional repressor	**-0.36**	0.39334
STM3667	yiaJ	transcriptional repressor	**0.41**	0.39315
STM3668	yiaK	putative malate dehydrogenase	**-0.17**	0.84355
STM3668	yiaK	putative malate dehydrogenase	**0.21**	0.69668
STM3669	yiaL	putative cytoplasmic protein	**-0.58**	0.17793
STM3669	yiaL	putative cytoplasmic protein	**0.51**	0.24125
STM3670	STM3670	putative chemotaxis protein	**-0.80**	0.37154
STM3670	STM3670	putative chemotaxis protein	**0.34**	0.57731
STM3671	yiaM	putative transporter	**-0.88**	0.16281
STM3671	yiaM	putative transporter	**-0.09**	0.93011
STM3672	yiaN	hypothetical protein STM3672	**-0.53**	0.57021
STM3672	yiaN	hypothetical protein STM3672	**-0.26**	0.73542
STM3673	yiaO	putative periplasmic dicarboxylate-binding protein	**-0.11**	0.81544
STM3673	yiaO	putative periplasmic dicarboxylate-binding protein	**0.94**	0.17754
STM3674	lyxK	L-xylulose kinase	**0.15**	0.87965
STM3674	lyxK	L-xylulose kinase	**-0.15**	0.75424
STM3675	sgbH	putative 3-hexulose-6-phosphate isomerase	**-0.65**	0.18566
STM3675	sgbH	putative 3-hexulose-6-phosphate isomerase	**0.29**	0.55338
STM3676	sgbU	putative 3-hexulose-6-phosphate isomerase	**-0.78**	0.11224
STM3676	sgbU	putative 3-hexulose-6-phosphate isomerase	**0.19**	0.66893
STM3677	sgbE	L-ribulose-5-phosphate 4-epimerase	**-0.51**	0.28655
STM3677	sgbE	L-ribulose-5-phosphate 4-epimerase	**0.13**	0.82162
STM3678	STM3678	putative regulatory protein	**-0.26**	0.60444
STM3678	STM3678	putative regulatory protein	**0.15**	0.77660
STM3679	STM3679	putative cytoplasmic protein	**-0.15**	0.80798
STM3679	STM3679	putative cytoplasmic protein	**0.74**	0.34812
STM3680	aldB	aldehyde dehydrogenase B	**0.15**	0.77745
STM3680	aldB	aldehyde dehydrogenase B	**1.26**	0.06346
STM3681	STM3681	putative transcriptional regulator	**-0.38**	0.52781
STM3681	STM3681	putative transcriptional regulator	**0.44**	0.43219
STM3682	selB	selenocysteinyl-tRNA-specific translation factor	**-0.21**	0.63101
STM3682	selB	selenocysteinyl-tRNA-specific translation factor	**-0.18**	0.61824
STM3683	selA	selenocysteine synthase	**-0.21**	0.63223
STM3683	selA	selenocysteine synthase	**-0.07**	0.92170
STM3684	yibF	putative glutathione S-transferase	**-0.14**	0.75418
STM3684	yibF	putative glutathione S-transferase	**0.14**	0.76538

STM3685	mtlA	mannitol-specific enzyme IIABC component	**-0.06**	0.90247
STM3685	mtlA	mannitol-specific enzyme IIABC component	**0.34**	0.55338
STM3686	mtlD	mannitol-1-phosphate 5-dehydrogenase	**0.12**	0.79037
STM3686	mtlD	mannitol-1-phosphate 5-dehydrogenase	**0.51**	0.40562
STM3687	mtlR	mannitol operon repressor	**-0.20**	0.73157
STM3687	mtlR	mannitol operon repressor	**0.00**	0.99540
STM3688	STM3688	putative cytoplasmic protein	**-0.49**	0.38919
STM3688	STM3688	putative cytoplasmic protein	**-0.14**	0.76381
STM3689	yibL	putative cytoplasmic protein	**0.07**	0.94765
STM3689	yibL	putative cytoplasmic protein	**0.22**	0.55403
STM3690	STM3690	putative inner membrane lipoprotein	**-0.54**	0.44210
STM3690	STM3690	putative inner membrane lipoprotein	**0.17**	0.82956
STM3691	STM3691	putative inner membrane protein	**0.15**	0.83789
STM3691	STM3691	putative inner membrane protein	**0.58**	0.15736
STM3692	lldP	transporter LctP	**0.43**	0.40819
STM3692	lldP	transporter LctP	**0.43**	0.45367
STM3693	lldR	putative transcriptional regulator	**0.26**	0.70201
STM3693	lldR	putative transcriptional regulator	**0.93**	0.18265
STM3694	lldD	L-lactate dehydrogenase	**-0.01**	0.98539
STM3694	lldD	L-lactate dehydrogenase	**-0.12**	0.89151
STM3695	yibK	putative tRNA/rRNA methyltransferase	**-0.34**	0.48817
STM3695	yibK	putative tRNA/rRNA methyltransferase	**-0.06**	0.89580
STM3696	STM3696	putative transcriptional regulator	**-0.42**	0.36999
STM3696	STM3696	putative transcriptional regulator	**0.03**	0.94421
STM3697	STM3697	putative mandelate racemase	**-0.61**	0.34070
STM3697	STM3697	putative mandelate racemase	**-0.03**	0.96364
STM3698	STM3698	putative permease	**-0.08**	0.89979
STM3698	STM3698	putative permease	**-0.01**	0.98581
STM3699	cysE	serine acetyltransferase	**-0.20**	0.71169
STM3699	cysE	serine acetyltransferase	**0.37**	0.40412
STM3700	gpsA	NAD(P)H-dependent glycerol-3-phosphate dehydrogenase	**0.08**	0.89624
STM3700	gpsA	NAD(P)H-dependent glycerol-3-phosphate dehydrogenase	**0.47**	0.44150
STM3701	secB	export protein SecB	**-0.06**	0.89259
STM3701	secB	export protein SecB	**-0.06**	0.91937
STM3702	grxC	glutaredoxin 3	**0.01**	0.98546
STM3702	grxC	glutaredoxin 3	**0.27**	0.46292
STM3703	yibN	putative rhodanese-like sulfurtransferase	**-0.04**	0.94973
STM3703	yibN	putative rhodanese-like sulfurtransferase	**0.01**	0.98976
STM3704	pmgI	phosphoglyceromutase	**-0.42**	0.45372
STM3704	pmgI	phosphoglyceromutase	**-0.26**	0.45093
STM3705	yibP	hypothetical protein STM3705	**0.06**	0.89164
STM3705	yibP	hypothetical protein STM3705	**0.23**	0.57345
STM3706	yigQ	putative periplasmic protein	**-0.56**	0.23495
STM3706	yigQ	putative periplasmic protein	**0.13**	0.77186
STM3707	yibD	putative glycosyltransferase	**-0.10**	0.82656
STM3707	yibD	putative glycosyltransferase	**-0.13**	0.74354
STM3708	tdh	L-threonine 3-dehydrogenase	**-0.01**	0.99260
STM3708	tdh	L-threonine 3-dehydrogenase	**0.29**	0.59801
STM3709	kbl	2-amino-3-ketobutyrate coenzyme A ligase	**0.06**	0.89668
STM3709	kbl	2-amino-3-ketobutyrate coenzyme A ligase	**0.04**	0.91992
STM3710	rfaD	ADP-L-glycero-D-mannoheptose-6-epimerase	**0.26**	0.64590
STM3710	rfaD	ADP-L-glycero-D-mannoheptose-6-epimerase	**-0.64**	0.34201
STM3711	rfaF	ADP-heptose-LPS heptosyltransferase 1	**-0.07**	0.87368
STM3711	rfaF	ADP-heptose-LPS heptosyltransferase 1	**0.12**	0.75739
STM3712	rfaC	heptosyl transferase I	**-0.19**	0.72672
STM3712	rfaC	heptosyl transferase I	**0.13**	0.72781
STM3713	rfaL	O-antigen ligase	**0.23**	0.59509
STM3713	rfaL	O-antigen ligase	**0.42**	0.34449
STM3714	rfaK	putative hexose transferase	**-0.40**	0.27004
STM3714	rfaK	putative hexose transferase	**-0.21**	0.59455
STM3715	rfaZ	lipopolysaccharide core biosynthetic protein	**-0.23**	0.75319

STM3715	rfaZ	lipopolysaccharide core biosynthetic protein	**0.27**	0.75453
STM3716	rfaY	lipopolysaccharide core biosynthetic protein	**0.07**	0.88415
STM3716	rfaY	lipopolysaccharide core biosynthetic protein	**0.47**	0.29543
STM3717	rfaJ	lipopolysaccharide glucosyltransferase	**-0.03**	0.95059
STM3717	rfaJ	lipopolysaccharide glucosyltransferase	**0.34**	0.41193
STM3718	rfaI	lipopolysaccharide-alpha-1,3-D-galactosyltransferase	**0.15**	0.71914
STM3718	rfaI	lipopolysaccharide-alpha-1,3-D-galactosyltransferase	**0.08**	0.84354
STM3719	rfaB	lipopolysaccharide-1,6-D-galactosyltransferase	**0.30**	0.39315
STM3719	rfaB	lipopolysaccharide-1,6-D-galactosyltransferase	**0.17**	0.66636
STM3720	yibR	putative inner membrane protein	**-0.04**	0.94552
STM3720	yibR	putative inner membrane protein	**0.10**	0.81961
STM3721	rfaP	lipopolysaccharide core biosynthetic protein	**0.03**	0.96785
STM3721	rfaP	lipopolysaccharide core biosynthetic protein	**-0.14**	0.75851
STM3722	rfaG	glucosyltransferase I	**0.08**	0.88018
STM3722	rfaG	glucosyltransferase I	**0.01**	0.99381
STM3723	rfaQ	lipopolysaccharide core biosynthetic protein	**0.10**	0.80762
STM3723	rfaQ	lipopolysaccharide core biosynthetic protein	**0.16**	0.67750
STM3724	kdtA	3-deoxy-D-manno-octulosonic-acid transferase	**-0.25**	0.51526
STM3724	kdtA	3-deoxy-D-manno-octulosonic-acid transferase	**0.06**	0.88864
STM3725	kdtB	phosphopantetheine adenylyltransferase	**-0.26**	0.47159
STM3725	kdtB	phosphopantetheine adenylyltransferase	**-0.15**	0.75626
STM3726	mutM	formamidopyrimidine-DNA glycosylase	**-0.22**	0.67506
STM3726	mutM	formamidopyrimidine-DNA glycosylase	**0.18**	0.76502
STM3727	rpmG	50S ribosomal protein L33	**-0.52**	0.31195
STM3727	rpmG	50S ribosomal protein L33	**-0.32**	0.64456
STM3728	rpmB	50S ribosomal protein L28	**-0.25**	0.65779
STM3728	rpmB	50S ribosomal protein L28	**-0.07**	0.92594
STM3729	radC	DNA repair protein RadC	**-0.31**	0.46720
STM3729	radC	DNA repair protein RadC	**0.11**	0.78332
STM3730	dfp	phosphopantothenoylcysteine synthase/decarboxylase	**0.16**	0.68240
STM3730	dfp	phosphopantothenoylcysteine synthase/decarboxylase	**0.15**	0.68439
STM3731	dut	deoxyuridine 5'-triphosphate nucleotidohydrolase	**0.26**	0.45394
STM3731	dut	deoxyuridine 5'-triphosphate nucleotidohydrolase	**0.24**	0.70707
STM3732	slmA	nucleoid occlusion protein	**-0.33**	0.40531
STM3732	slmA	nucleoid occlusion protein	**-0.12**	0.79324
STM3733	pyrE	orotate phosphoribosyltransferase	**-0.48**	0.29866
STM3733	pyrE	orotate phosphoribosyltransferase	**0.15**	0.68113
STM3734	rph	ribonuclease PH	**0.38**	0.31280
STM3734	rph	ribonuclease PH	**0.78**	0.22391
STM3735	yicC	putative stress-induced protein	**-0.12**	0.82956
STM3735	yicC	putative stress-induced protein	**0.32**	0.50825
STM3736	STM3736	putative transcriptional regulator	**-0.19**	0.58694
STM3736	STM3736	putative transcriptional regulator	**0.10**	0.84245
STM3737	STM3737	putative Zn-dependent hydrolase	**-0.58**	0.34553
STM3737	STM3737	putative Zn-dependent hydrolase	**0.38**	0.43772
STM3738	yigC	putative inner membrane protein	**0.11**	0.86516
STM3738	yigC	putative inner membrane protein	**0.05**	0.91047
STM3739	yicF	DNA ligase	**-0.36**	0.32812
STM3739	yicF	DNA ligase	**0.26**	0.54625
STM3740	gmk	guanylate kinase	**0.01**	0.97664
STM3740	gmk	guanylate kinase	**0.08**	0.84456
STM3741	rpoZ	DNA-directed RNA polymerase omega subunit	**-0.40**	0.29871
STM3741	rpoZ	DNA-directed RNA polymerase omega subunit	**-0.14**	0.72677
STM3742	spoT	(p)ppGpp synthetase II/guanosine-3',5'-bis pyrophosphate	**0.09**	0.83943
STM3742	spoT	(p)ppGpp synthetase II/guanosine-3',5'-bis pyrophosphate	**0.26**	0.46565
STM3743	spoU	putative tRNA/rRNA methyltransferase	**0.02**	0.97645
STM3743	spoU	putative tRNA/rRNA methyltransferase	**-0.04**	0.95507
STM3744	recG	DNA helicase	**-0.21**	0.65709
STM3744	recG	DNA helicase	**-0.33**	0.51977
STM3745	STM3745	putative cytoplasmic protein	**-0.14**	0.75798
STM3745	STM3745	putative cytoplasmic protein	**0.55**	0.37568

STM3746	gltS	glutamate transport protein	**-0.03**	0.95650
STM3746	gltS	glutamate transport protein	**-0.33**	0.45664
STM3747	yicE	putative purine/xanthine transport protein	**-0.20**	0.70307
STM3747	yicE	putative purine/xanthine transport protein	**0.27**	0.58613
STM3748	yicH	putative inner membrane protein	**-0.21**	0.65012
STM3748	yicH	putative inner membrane protein	**0.40**	0.37342
STM3749	yicI	putative alpha xylosidase	**-0.24**	0.57409
STM3749	yicI	putative alpha xylosidase	**0.58**	0.39316
STM3750	yicJ	putative transport protein	**-0.09**	0.91641
STM3750	yicJ	putative transport protein	**-0.09**	0.87909
STM3751	selC	STM3751	**-0.14**	0.86385
STM3751	selC	STM3751	**0.05**	0.96286
STM3752	STM3752	putative cytoplasmic protein	**-0.32**	0.39470
STM3752	STM3752	putative cytoplasmic protein	**0.01**	0.99260
STM3753	sugR	ATP binding protein	**-0.09**	0.84392
STM3753	sugR	ATP binding protein	**0.60**	0.23635
STM3754	STM3754	putative cytoplasmic protein	**0.09**	0.86190
STM3754	STM3754	putative cytoplasmic protein	**0.09**	0.84873
STM3755	rhuM	putative cytoplasmic protein	**-0.31**	0.60311
STM3755	rhuM	putative cytoplasmic protein	**0.27**	0.62873
STM3756	rmbA	putative cytoplasmic protein	**0.02**	0.97117
STM3756	rmbA	putative cytoplasmic protein	**0.02**	0.95980
STM3757	misL	putative autotransporter	**0.46**	0.30326
STM3757	misL	putative autotransporter	**0.93**	0.28861
STM3758	fidL	putative inner membrane protein	**0.01**	0.98718
STM3758	fidL	putative inner membrane protein	**-1.06**	0.63076
STM3759,S	marT	putative transcriptional regulator	**-0.22**	0.71971
STM3759,S	marT	putative transcriptional regulator	**0.26**	0.61809
STM3761	slsA	putative inner membrane protein	**-0.85**	0.15859
STM3761	slsA	putative inner membrane protein	**-0.07**	0.91484
STM3762	cigR	putative inner membrane protein	**-0.52**	0.64422
STM3762	cigR	putative inner membrane protein	**-0.10**	0.83499
STM3763	mgtB	Mg2+ transporter	**-0.37**	0.34070
STM3763	mgtB	Mg2+ transporter	**0.50**	0.38425
STM3764	mgtC	Mg2+ transport protein	**-0.86**	0.25759
STM3764	mgtC	Mg2+ transport protein	**0.13**	0.75851
STM3765	yicL	putative permease	**-0.11**	0.87110
STM3765	yicL	putative permease	**0.06**	0.93491
STM3766	STM3766	putative cytoplasmic protein	**-0.68**	0.14183
STM3766	STM3766	putative cytoplasmic protein	**0.35**	0.47541
STM3767	STM3767	putative cytoplasmic protein	**-0.30**	0.49707
STM3767	STM3767	putative cytoplasmic protein	**0.36**	0.45477
STM3768	STM3768	putative selenocysteine synthase	**-0.06**	0.94050
STM3768	STM3768	putative selenocysteine synthase	**0.79**	0.33356
STM3769,S	STM3769,S	putative phosphotransferase system enzyme II	**-0.06**	0.91756
STM3769,S	STM3769,S	putative phosphotransferase system enzyme II	**0.57**	0.37678
STM3770	STM3770	putative phosphotransferase system enzyme IIC	**0.09**	0.86443
STM3770	STM3770	putative phosphotransferase system enzyme IIC	**0.08**	0.90347
STM3771	STM3771	putative phosphotransferase system enzyme IIB	**-0.32**	0.63101
STM3771	STM3771	putative phosphotransferase system enzyme IIB	**0.56**	0.32295
STM3772	STM3772	putative phosphotransferase system enzyme IIA	**0.34**	0.42591
STM3772	STM3772	putative phosphotransferase system enzyme IIA	**1.22**	0.14030
STM3773	STM3773	putative transcriptional regulator	**0.05**	0.94470
STM3773	STM3773	putative transcriptional regulator	**1.28**	0.14154
STM3774	STM3774	putative inner membrane protein	**-0.24**	0.89405
STM3774	STM3774	putative inner membrane protein	**1.29**	0.22602
STM3775	STM3775	putative glycosyl hydrolase	**-0.01**	0.99449
STM3775	STM3775	putative glycosyl hydrolase	**0.78**	0.33703
STM3776	yicM	putative transport protein	**-0.81**	0.24414
STM3776	yicM	putative transport protein	**-0.08**	0.86495
STM3777	STM3777	putative cytoplasmic protein	**-0.44**	0.26213
STM3777	STM3777	putative cytoplasmic protein	**0.41**	0.39354
STM3778	STM3778	putative DNA-binding protein	**-0.34**	0.63148

STM3778	STM3778	putative DNA-binding protein	**0.38**	0.57021
STM3779	STM3779	putative phosphotransferase system HPr protein	**-0.26**	0.57021
STM3779	STM3779	putative phosphotransferase system HPr protein	**0.20**	0.72146
STM3780	STM3780	hypothetical protein STM3780	**-1.10**	0.08174
STM3780	STM3780	hypothetical protein STM3780	**0.56**	0.25454
STM3781	STM3781	putative sugar kinase	**-0.57**	0.34201
STM3781	STM3781	putative sugar kinase	**0.23**	0.59497
STM3782	STM3782	putative PTS system galactitol-specific enzyme IIC component	**-0.47**	0.29539
STM3782	STM3782	putative PTS system galactitol-specific enzyme IIC component	**-0.34**	0.69319
STM3783	STM3783	putative periplasmic protein	**-0.30**	0.46042
STM3783	STM3783	putative periplasmic protein	**0.01**	0.99152
STM3784	STM3784	putative phosphotransferase system mannitol/fructose-specific IIA	**0.08**	0.87456
STM3784	STM3784	putative phosphotransferase system mannitol/fructose-specific IIA	**0.35**	0.45664
STM3785	STM3785	putative regulatory protein	**-0.31**	0.46385
STM3785	STM3785	putative regulatory protein	**0.17**	0.79260
STM3786	yicN	putative inner membrane protein	**-0.06**	0.88937
STM3786	yicN	putative inner membrane protein	**0.19**	0.64489
STM3787	uhpT	hexose phosphate transport protein	**-0.23**	0.59675
STM3787	uhpT	hexose phosphate transport protein	**0.37**	0.72299
STM3788	uhpC	regulatory protein	**-0.24**	0.52504
STM3788	uhpC	regulatory protein	**0.09**	0.89227
STM3789	uhpB	sensory histidine kinase	**-0.13**	0.74374
STM3789	uhpB	sensory histidine kinase	**-0.04**	0.94360
STM3790	uhpA	response regulator	**-0.39**	0.39357
STM3790	uhpA	response regulator	**-0.07**	0.86947
STM3791	STM3791	putative cytoplasmic protein	**0.23**	0.55656
STM3791	STM3791	putative cytoplasmic protein	**0.48**	0.39987
STM3792	STM3792	putative L-fucose permease	**0.16**	0.77677
STM3792	STM3792	putative L-fucose permease	**0.02**	0.95980
STM3793	STM3793	putative sugar kinase	**-0.10**	0.87016
STM3793	STM3793	putative sugar kinase	**-0.18**	0.76008
STM3794	STM3794	putative regulatory protein	**-0.14**	0.70966
STM3794	STM3794	putative regulatory protein	**0.23**	0.55008
STM3795	ilvN	acetolactate synthase small subunit	**0.01**	0.98958
STM3795	ilvN	acetolactate synthase small subunit	**0.65**	0.21933
STM3796	ilvB	acetolactate synthase large subunit	**-0.06**	0.96447
STM3796	ilvB	acetolactate synthase large subunit	**0.68**	0.42958
STM3796A,S	STM3796A,S	integral membrane protein	**0.49**	0.24722
STM3796A,S	STM3796A,S	integral membrane protein	**1.12**	0.19398
STM3797	ivbL	ilvB operon leader peptide	**-0.39**	0.47997
STM3797	ivbL	ilvB operon leader peptide	**0.38**	0.44808
STM3798	emrD	multidrug tranport protein	**-0.46**	0.45625
STM3798	emrD	multidrug tranport protein	**0.09**	0.82350
STM3799	STM3799	putative periplasmic protein	**-0.09**	0.93023
STM3799	STM3799	putative periplasmic protein	**-0.20**	0.70726
STM3800	dsdC	transcriptional activator	**0.15**	0.73862
STM3800	dsdC	transcriptional activator	**0.18**	0.67012
STM3801	dsdX	putative transport protein	**0.27**	0.46772
STM3801	dsdX	putative transport protein	**0.58**	0.22621
STM3802	dsdA	D-serine dehydratase	**-0.29**	0.44208
STM3802	dsdA	D-serine dehydratase	**0.83**	0.19398
STM3803	yidF	putative cytoplasmic protein	**0.19**	0.65753
STM3803	yidF	putative cytoplasmic protein	**0.61**	0.27312
STM3804	yidG	putative inner membrane protein	**-0.29**	0.54573
STM3804	yidG	putative inner membrane protein	**0.31**	0.51545
STM3805	yidH	putative inner membrane protein	**-0.08**	0.91170
STM3805	yidH	putative inner membrane protein	**0.15**	0.76008
STM3807	yidE	hypothetical protein STM3807	**-0.36**	0.35824
STM3807	yidE	hypothetical protein STM3807	**0.09**	0.86176

STM3808,S	ibpB	small heat shock protein	**-0.06**	0.95412
STM3808,S	ibpB	small heat shock protein	**0.94**	0.32315
STM3809,S	ibpA	small heat shock protein	**-0.60**	0.41626
STM3809,S	ibpA	small heat shock protein	**-0.67**	0.24414
STM3810	yidQ	putative outer membrane lipoprotein	**-0.80**	0.18734
STM3810	yidQ	putative outer membrane lipoprotein	**-0.48**	0.55938
STM3811	yidR	putative cytoplasmic protein	**0.04**	0.94617
STM3811	yidR	putative cytoplasmic protein	**-0.22**	0.75403
STM3812	ccmH	putative heme lyase subunit	**-0.25**	0.58613
STM3812	ccmH	putative heme lyase subunit	**0.35**	0.53840
STM3813	ccmG	heme lyase disulfide oxidoreductase	**-0.56**	0.41717
STM3813	ccmG	heme lyase disulfide oxidoreductase	**-0.25**	0.57604
STM3813	ccmG	heme lyase disulfide oxidoreductase	**-0.33**	0.46629
STM3813	ccmG	heme lyase disulfide oxidoreductase	**0.13**	0.75798
STM3814	ccmF	cytochrome c-type biogenesis protein	**0.59**	0.76720
STM3814	ccmF	cytochrome c-type biogenesis protein	**0.16**	0.94045
STM3814	ccmF	cytochrome c-type biogenesis protein	**0.71**	0.26429
STM3814	ccmF	cytochrome c-type biogenesis protein	**0.88**	0.12727
STM3815	ccmE	periplasmic heme-dependent peroxidase	**-0.57**	0.36311
STM3815	ccmE	periplasmic heme-dependent peroxidase	**-0.14**	0.72781
STM3815	ccmE	periplasmic heme-dependent peroxidase	**-0.19**	0.64331
STM3815	ccmE	periplasmic heme-dependent peroxidase	**0.42**	0.47603
STM3816	ccmD	heme exporter protein C	**-0.58**	0.59695
STM3816	ccmD	heme exporter protein C	**-0.33**	0.40701
STM3816	ccmD	heme exporter protein C	**0.26**	0.64838
STM3816	ccmD	heme exporter protein C	**0.41**	0.51446
STM3817	ccmC	heme exporter protein	**-1.03**	0.11224
STM3817	ccmC	heme exporter protein	**-1.21**	0.13206
STM3817	ccmC	heme exporter protein	**-0.60**	0.18763
STM3817	ccmC	heme exporter protein	**-0.07**	0.86414
STM3818	ccmB	heme exporter protein	**-0.78**	0.24313
STM3818	ccmB	heme exporter protein	**-0.75**	0.26910
STM3818	ccmB	heme exporter protein	**-0.32**	0.41154
STM3818	ccmB	heme exporter protein	**-0.35**	0.47838
STM3820	STM3820	putative cytochrome c peroxidase	**-0.63**	0.25020
STM3820	STM3820	putative cytochrome c peroxidase	**-0.50**	0.40972
STM3821	torD	chaperone protein TorD	**-0.50**	0.30748
STM3821	torD	chaperone protein TorD	**0.40**	0.54925
STM3822	torA	trimethylamine N-oxide reductase subunit	**-0.88**	0.13645
STM3822	torA	trimethylamine N-oxide reductase subunit	**0.51**	0.33651
STM3823	torC	trimethylamine N-oxide reductase cytochrome c-like subunit	**-0.47**	0.36399
STM3823	torC	trimethylamine N-oxide reductase cytochrome c-like subunit	**0.80**	0.39364
STM3824	torR	response regulator	**-0.15**	0.79755
STM3824	torR	response regulator	**0.08**	0.86580
STM3825	torT	periplasmic sensor	**-0.25**	0.61057
STM3825	torT	periplasmic sensor	**0.01**	0.98564
STM3826	torS	sensor kinase	**-0.28**	0.62503
STM3826	torS	sensor kinase	**1.20**	0.13645
STM3827	dgoT	D-galactonate transport protein	**0.06**	0.90605
STM3827	dgoT	D-galactonate transport protein	**0.60**	0.36414
STM3828	dgoA	2-oxo-3-deoxygalactonate 6-phosphate aldolase/galactonate	**0.74**	0.18140
STM3828	dgoA	2-oxo-3-deoxygalactonate 6-phosphate aldolase/galactonate	**1.01**	0.25759
STM3829	dgoK	2-oxo-3-deoxygalactonate kinase	**-0.20**	0.73469
STM3829	dgoK	2-oxo-3-deoxygalactonate kinase	**0.87**	0.13206
STM3830	dgoR	galactonate operon transcriptional repressor	**-0.41**	0.27312
STM3830	dgoR	galactonate operon transcriptional repressor	**0.74**	0.22087
STM3831	yidA	putative hydrolase	**-0.13**	0.76283
STM3831	yidA	putative hydrolase	**0.07**	0.91075
STM3832	STM3832	putative permease	**0.17**	0.75512

STM3832	STM3832	putative permease	**0.20**	0.63169
STM3833	STM3833	putative mandelate racemase	**-0.75**	0.19236
STM3833	STM3833	putative mandelate racemase	**-0.15**	0.72843
STM3834	STM3834	putative transcriptional regulator	**-0.34**	0.36414
STM3834	STM3834	putative transcriptional regulator	**-0.26**	0.45111
STM3835	gyrB	DNA gyrase subunit B	**-0.40**	0.46927
STM3835	gyrB	DNA gyrase subunit B	**-0.31**	0.45423
STM3836	recF	recombination protein F	**0.05**	0.90612
STM3836	recF	recombination protein F	**0.12**	0.75831
STM3837	dnaN	DNA polymerase III subunit beta	**-0.64**	0.17359
STM3837	dnaN	DNA polymerase III subunit beta	**-0.02**	0.97720
STM3838	dnaA	chromosomal replication initiation protein	**-0.23**	0.60937
STM3838	dnaA	chromosomal replication initiation protein	**-0.01**	0.99268
STM3839	rpmH	50S ribosomal protein L34	**0.20**	0.72247
STM3839	rpmH	50S ribosomal protein L34	**0.76**	0.21015
STM3840	rnpA	ribonuclease P	**0.18**	0.67816
STM3840	rnpA	ribonuclease P	**0.45**	0.33971
STM3842	yidC	inner membrane protein translocase component YidC	**-0.20**	0.61679
STM3842	yidC	inner membrane protein translocase component YidC	**0.61**	0.18873
STM3843	trmE	tRNA modification GTPase	**-0.45**	0.22087
STM3843	trmE	tRNA modification GTPase	**0.20**	0.74626
STM3845	STM3845	putative inner membrane protein	**-0.35**	0.38351
STM3845	STM3845	putative inner membrane protein	**0.02**	0.98332
STM3846,s	STM3846,s	putative reverse transcriptase	**-0.47**	0.35824
STM3846,s	STM3846,s	putative reverse transcriptase	**-0.12**	0.82642
STM3847	yidY	putative tranport protein	**-0.55**	0.35178
STM3847	yidY	putative tranport protein	**0.75**	0.15276
STM3848	yidZ	putative transcriptional regulator	**-0.09**	0.86190
STM3848	yidZ	putative transcriptional regulator	**0.80**	0.18248
STM3849	yieE	putative cytoplasmic protein	**0.00**	0.99540
STM3849	yieE	putative cytoplasmic protein	**0.16**	0.78934
STM3850	yieF	putative oxidoreductase	**-0.20**	0.65408
STM3850	yieF	putative oxidoreductase	**0.05**	0.93340
STM3851,S	yieG	hypothetical protein STM3851,S	**-0.20**	0.64590
STM3851,S	yieG	hypothetical protein STM3851,S	**0.14**	0.77719
STM3852	yieH	putative phosphatase/phosphohexomutase	**-0.35**	0.53840
STM3852	yieH	putative phosphatase/phosphohexomutase	**-0.06**	0.89546
STM3853	phoU	high-affinity phosphate uptake regulatory protein	**-0.13**	0.79096
STM3853	phoU	high-affinity phosphate uptake regulatory protein	**-0.01**	0.99213
STM3854	pstB	high-affinity phosphate transporter	**-0.54**	0.18851
STM3854	pstB	high-affinity phosphate transporter	**0.10**	0.79308
STM3855	pstA	high-affinity phosphate transporter	**0.09**	0.90534
STM3855	pstA	high-affinity phosphate transporter	**-0.04**	0.96018
STM3856	pstC	high-affinity phosphate transporter	**-0.55**	0.24319
STM3856	pstC	high-affinity phosphate transporter	**-0.28**	0.61201
STM3857	pstS	high-affinity phosphate transporter	**0.05**	0.94417
STM3857	pstS	high-affinity phosphate transporter	**0.24**	0.77025
STM3858	STM3858	putative phosphotransferase system fructose-specific component IIB	**-0.17**	0.75978
STM3858	STM3858	putative phosphotransferase system fructose-specific component IIB	**0.39**	0.37942
STM3859	aroE	shikimate 5-dehydrogenase	**0.04**	0.93525
STM3859	aroE	shikimate 5-dehydrogenase	**0.41**	0.40749
STM3860	STM3860	putative dipeptide/oligopeptide/nickel ABC-type transport system	**0.06**	0.91047
STM3860	STM3860	putative dipeptide/oligopeptide/nickel ABC-type transport system	**0.25**	0.50267
STM3861	glmS	D-fructose-6-phosphate amidotransferase	**-0.19**	0.65709
STM3861	glmS	D-fructose-6-phosphate amidotransferase	**0.18**	0.70765
STM3862	glmU	bifunctional N-acetylglucosamine-1-phosphate	**-0.13**	0.75158
STM3862	glmU	bifunctional N-acetylglucosamine-1-phosphate	**0.31**	0.51421
STM3863	STM3863	putative permease	**-0.05**	0.91055
STM3863	STM3863	putative permease	**-0.10**	0.83829

STM3864	atpC	ATP synthase subunit epsilon	**-0.57**	0.30140
STM3864	atpC	ATP synthase subunit epsilon	**-0.14**	0.74995
STM3865	atpD	ATP synthase subunit B	**-0.10**	0.79719
STM3865	atpD	ATP synthase subunit B	**0.23**	0.58694
STM3866	atpG	ATP synthase subunit C	**0.01**	0.99449
STM3866	atpG	ATP synthase subunit C	**0.58**	0.19811
STM3867	atpA	ATP synthase subunit A	**0.01**	0.98352
STM3867	atpA	ATP synthase subunit A	**0.76**	0.15438
STM3868	atpH	ATP synthase subunit D	**0.34**	0.35619
STM3868	atpH	ATP synthase subunit D	**0.40**	0.31146
STM3869	atpF	ATP synthase subunit B	**0.68**	0.23879
STM3869	atpF	ATP synthase subunit B	**0.42**	0.36942
STM3870	atpE	ATP synthase subunit C	**0.67**	0.15276
STM3870	atpE	ATP synthase subunit C	**0.58**	0.22283
STM3871	atpB	ATP synthase subunit A	**0.54**	0.19967
STM3871	atpB	ATP synthase subunit A	**0.67**	0.30715
STM3871	atpB	ATP synthase subunit A	**0.44**	0.27378
STM3871	atpB	ATP synthase subunit A	**0.54**	0.52712
STM3872	atpI	ATP synthase subunit I	**0.28**	0.47937
STM3872	atpI	ATP synthase subunit I	**0.50**	0.20202
STM3873,S	gidB	glucose-inhibited division protein B	**0.01**	0.99156
STM3873,S	gidB	glucose-inhibited division protein B	**0.39**	0.33587
STM3874	gidA	glucose-inhibited division protein A	**-0.17**	0.68232
STM3874	gidA	glucose-inhibited division protein A	**0.38**	0.31677
STM3875	mioC	flavodoxin	**-0.31**	0.38317
STM3875	mioC	flavodoxin	**0.28**	0.58445
STM3876	asnC	transcriptional regulator	**-0.24**	0.62619
STM3876	asnC	transcriptional regulator	**0.09**	0.90766
STM3877	asnA	asparagine synthetase AsnA	**-0.27**	0.52360
STM3877	asnA	asparagine synthetase AsnA	**-0.15**	0.79134
STM3878,S	yieM	putative inner membrane protein	**0.05**	0.93974
STM3878,S	yieM	putative inner membrane protein	**0.64**	0.35010
STM3879	yieN	putative regulatory protein	**0.10**	0.83899
STM3879	yieN	putative regulatory protein	**0.83**	0.11913
STM3880	kup	low-affinity potassium transport protein	**0.92**	0.17074
STM3880	kup	low-affinity potassium transport protein	**0.94**	0.14285
STM3881	rbsD	high-affinity D-ribose transport protein	**1.01**	0.19142
STM3881	rbsD	high-affinity D-ribose transport protein	**1.14**	0.12966
STM3882	rbsA	high-affinity D-ribose transport protein	**0.99**	0.19398
STM3882	rbsA	high-affinity D-ribose transport protein	**1.14**	0.25020
STM3883	rbsC	ribose high-affinity ABC transporter permease component	**1.02**	0.36654
STM3883	rbsC	ribose high-affinity ABC transporter permease component	**1.30**	0.25543
STM3884	rbsB	D-ribose transport protein	**1.00**	0.34541
STM3884	rbsB	D-ribose transport protein	**1.15**	0.25433
STM3885	rbsK	ribokinase	**0.55**	0.53399
STM3885	rbsK	ribokinase	**0.57**	0.45367
STM3886	rbsR	rbs operon transcriptional repressor	**0.49**	0.39635
STM3886	rbsR	rbs operon transcriptional repressor	**0.69**	0.20341
STM3887	yieO	putative tranport protein	**0.17**	0.65025
STM3887	yieO	putative tranport protein	**0.29**	0.45351
STM3888	yieP	putative regulatory protein	**-0.37**	0.40020
STM3888	yieP	putative regulatory protein	**-0.64**	0.22849
STM3891	rrlC	STM3891	**-0.54**	0.21880
STM3891	rrlC	STM3891	**-0.61**	0.16534
STM3895	aspT	STM3895	**-0.81**	0.21360
STM3895	aspT	STM3895	**-0.32**	0.63235
STM3895	aspT	STM3895	**-0.46**	0.35955
STM3895	aspT	STM3895	**-0.26**	0.65451
STM3895	aspT	STM3895	**-0.26**	0.62403
STM3895	aspT	STM3895	**-0.16**	0.75978
STM3896	trpT	STM3896	**-0.50**	0.24444

STM3896	trpT	STM3896	**-0.29**	0.57021
STM3897	yifA	transcriptional regulator HdfR	**-0.57**	0.19048
STM3897	yifA	transcriptional regulator HdfR	**-0.42**	0.31280
STM3898	yifE	putative transcriptional regulator	**-0.36**	0.52487
STM3898	yifE	putative transcriptional regulator	**-0.46**	0.29064
STM3899	yifB	putative magnesium chelatase subunit ChlI	**0.23**	0.74005
STM3899	yifB	putative magnesium chelatase subunit ChlI	**0.40**	0.46720
STM3901	ilvG	acetolactate synthase II large subunit	**-0.07**	0.91272
STM3901	ilvG	acetolactate synthase II large subunit	**0.19**	0.68439
STM3902	ilvM	acetolactate synthase II small subunit	**0.12**	0.80306
STM3902	ilvM	acetolactate synthase II small subunit	**0.37**	0.44208
STM3903	ilvE	branched-chain amino acid aminotransferase	**0.07**	0.87826
STM3903	ilvE	branched-chain amino acid aminotransferase	**0.97**	0.13112
STM3904	ilvD	dihydroxy-acid dehydratase	**-0.04**	0.91937
STM3904	ilvD	dihydroxy-acid dehydratase	**0.10**	0.79668
STM3905	ilvA	threonine dehydratase	**-0.45**	0.30229
STM3905	ilvA	threonine dehydratase	**-0.37**	0.33651
STM3906	STM3906	putative cytoplasmic protein	**0.08**	0.91909
STM3906	STM3906	putative cytoplasmic protein	**0.65**	0.23423
STM3907	STM3907	putative cytoplasmic protein	**-0.12**	0.83503
STM3907	STM3907	putative cytoplasmic protein	**-0.02**	0.96687
STM3908	ilvY	regulatory protein	**-0.15**	0.76883
STM3908	ilvY	regulatory protein	**-0.10**	0.86385
STM3909	ilvC	ketol-acid reductoisomerase	**-0.87**	0.11690
STM3909	ilvC	ketol-acid reductoisomerase	**-0.10**	0.91139
STM3910	ppiC	peptidyl-prolyl cis-trans isomerase C	**-0.35**	0.36703
STM3910	ppiC	peptidyl-prolyl cis-trans isomerase C	**0.44**	0.23164
STM3911	STM3911	putative inner membrane protein	**-0.15**	0.72170
STM3911	STM3911	putative inner membrane protein	**0.25**	0.59924
STM3912	rep	ATP-dependent DNA helicase rep	**-0.56**	0.17139
STM3912	rep	ATP-dependent DNA helicase rep	**-0.10**	0.84179
STM3913	gppA	guanosine pentaphosphatase/exopolyphosphatase	**-0.58**	0.22533
STM3913	gppA	guanosine pentaphosphatase/exopolyphosphatase	**0.03**	0.96785
STM3914	rhlB	ATP-dependent RNA helicase	**-0.10**	0.80987
STM3914	rhlB	ATP-dependent RNA helicase	**0.26**	0.47735
STM3915	trxA	thioredoxin	**-0.14**	0.71550
STM3915	trxA	thioredoxin	**-0.24**	0.61316
STM3917	rho	transcription termination factor Rho	**-0.18**	0.66594
STM3917	rho	transcription termination factor Rho	**0.12**	0.80077
STM3918	rfe	undecaprenyl-phosphate N-acetylglucosaminyltransferase	**-0.20**	0.63482
STM3918	rfe	undecaprenyl-phosphate N-acetylglucosaminyltransferase	**-0.11**	0.86385
STM3919	wzzE	enterobacterial common antigen chain length regulator	**-0.08**	0.84099
STM3919	wzzE	enterobacterial common antigen chain length regulator	**0.17**	0.63235
STM3920	wecB	UDP-N-acetyl glucosamine-2-epimerase	**-0.06**	0.89661
STM3920	wecB	UDP-N-acetyl glucosamine-2-epimerase	**-0.46**	0.24515
STM3921	wecC	UDP-N-acetyl-D-mannosaminuronic acid dehydrogenase	**-0.52**	0.22602
STM3921	wecC	UDP-N-acetyl-D-mannosaminuronic acid dehydrogenase	**-0.19**	0.67012
STM3922	rffG	dTDP-glucose 4,6-dehydratase	**-0.32**	0.45925
STM3922	rffG	dTDP-glucose 4,6-dehydratase	**0.00**	0.99703
STM3923	rffH	glucose-1-phosphate thymidyl transferase	**-0.10**	0.81862
STM3923	rffH	glucose-1-phosphate thymidyl transferase	**0.08**	0.87297
STM3924	wecD	lipopolysaccharide biosynthetic protein	**-0.31**	0.47880
STM3924	wecD	lipopolysaccharide biosynthetic protein	**-0.25**	0.53840
STM3925	wecE	TDP-4-oxo-6-deoxy-D-glucose transaminase	**-0.26**	0.48854
STM3925	wecE	TDP-4-oxo-6-deoxy-D-glucose transaminase	**-0.05**	0.91387
STM3926	wzxE	O-antigen translocase	**-0.04**	0.93841
STM3926	wzxE	O-antigen translocase	**0.07**	0.87871
STM3927	STM3927	4-alpha-L-fucosyltransferase	**-0.29**	0.51549
STM3927	STM3927	4-alpha-L-fucosyltransferase	**0.33**	0.40500

STM3928	wecF	putative enterobacterial common antigen polymerase	**-0.39**	0.38041
STM3928	wecF	putative enterobacterial common antigen polymerase	**0.13**	0.83552
STM3929	wecG	putative UDP-N-acetyl-D-mannosaminuronic acid transferase	**-0.07**	0.87727
STM3929	wecG	putative UDP-N-acetyl-D-mannosaminuronic acid transferase	**0.00**	0.99938
STM3930	yifK	putative amino acid transport protein	**-0.27**	0.49336
STM3930	yifK	putative amino acid transport protein	**-0.22**	0.67284
STM3931	argX	STM3931	**-0.84**	0.23032
STM3931	argX	STM3931	**-0.67**	0.21015
STM3932	hisR	STM3932	**-0.54**	0.45462
STM3932	hisR	STM3932	**-0.32**	0.57804
STM3933	leuT	STM3933	**-0.27**	0.65598
STM3933	leuT	STM3933	**-0.23**	0.70973
STM3933	leuT	STM3933	**-0.51**	0.38747
STM3933	leuT	STM3933	**-0.58**	0.39136
STM3933	leuT	STM3933	**-0.06**	0.92937
STM3933	leuT	STM3933	**-0.17**	0.81331
STM3933	leuT	STM3933	**-0.09**	0.86385
STM3933	leuT	STM3933	**-0.24**	0.67816
STM3934	proM	STM3934	**-0.33**	0.50335
STM3934	proM	STM3934	**-0.28**	0.58848
STM3935	hemY	heme biosynthetic protein	**-0.28**	0.44208
STM3935	hemY	heme biosynthetic protein	**0.08**	0.84021
STM3936	hemX	uroporphyrinogen III methylase	**0.09**	0.85758
STM3936	hemX	uroporphyrinogen III methylase	**0.13**	0.79769
STM3937	STM3937	uroporphyrinogen-III synthetase	**-0.05**	0.91170
STM3937	STM3937	uroporphyrinogen-III synthetase	**-0.34**	0.54376
STM3938	hemC	porphobilinogen deaminase	**-0.05**	0.91387
STM3938	hemC	porphobilinogen deaminase	**0.01**	0.98734
STM3939	cyaA	adenylate cyclase	**-0.47**	0.25433
STM3939	cyaA	adenylate cyclase	**0.34**	0.39315
STM3940	STM3940	putative inner membrane protein	**-0.08**	0.86968
STM3940	STM3940	putative inner membrane protein	**0.11**	0.82384
STM3941	STM3941	putative inner membrane protein	**-0.25**	0.57696
STM3941	STM3941	putative inner membrane protein	**-0.04**	0.94386
STM3943	cyaY	frataxin-like protein	**-0.67**	0.16631
STM3943	cyaY	frataxin-like protein	**0.14**	0.76245
STM3944	STM3944	putative inner membrane protein	**0.04**	0.93582
STM3944	STM3944	putative inner membrane protein	**-0.14**	0.72916
STM3946	yifL	putative outer membrane lipoprotein	**-0.25**	0.58506
STM3946	yifL	putative outer membrane lipoprotein	**0.68**	0.16490
STM3947	dapF	diaminopimelate epimerase	**0.09**	0.86064
STM3947	dapF	diaminopimelate epimerase	**0.07**	0.85825
STM3948	yigA	putative cytoplasmic protein	**-0.41**	0.40227
STM3948	yigA	putative cytoplasmic protein	**-0.11**	0.86321
STM3949	xerC	tyrosine recombinase	**0.00**	0.99939
STM3949	xerC	tyrosine recombinase	**0.43**	0.41990
STM3950	yigB	putative hydrolase	**-0.28**	0.62751
STM3950	yigB	putative hydrolase	**-0.11**	0.82871
STM3951	uvrD	DNA-dependent ATPase I/helicase II	**-0.34**	0.52934
STM3951	uvrD	DNA-dependent ATPase I/helicase II	**-0.23**	0.66902
STM3952	corA	Mg2+/Ni2+/Co2+ transport protein	**-0.22**	0.60597
STM3952	corA	Mg2+/Ni2+/Co2+ transport protein	**-0.19**	0.69519
STM3953	yigF	putative inner membrane protein	**0.07**	0.87512
STM3953	yigF	putative inner membrane protein	**0.02**	0.98090
STM3955	rarD	chloramphenicol resistance	**-0.15**	0.72149
STM3955	rarD	chloramphenicol resistance	**-0.19**	0.61201
STM3956	yigI	hypothetical protein STM3956	**-0.73**	0.15955
STM3956	yigI	hypothetical protein STM3956	**-0.25**	0.61299
STM3957	pldA	outer membrane phospholipase A precursor	**-0.29**	0.49708
STM3957	pldA	outer membrane phospholipase A precursor	**0.48**	0.30748
STM3958	recQ	ATP-dependent DNA helicase	**-0.16**	0.65301

STM3958	recQ	ATP-dependent DNA helicase	**0.33**	0.46629
STM3959	rhtC	threonine efflux protein	**-0.17**	0.71978
STM3959	rhtC	threonine efflux protein	**0.05**	0.93150
STM3960	rthB	homoserine/homoserine lactone efflux protein	**-0.18**	0.68418
STM3960	rthB	homoserine/homoserine lactone efflux protein	**0.33**	0.45423
STM3961	pldB	lysophospholipase L2	**-0.02**	0.97916
STM3961	pldB	lysophospholipase L2	**0.05**	0.91456
STM3962	yigL	putative hydrolase	**0.30**	0.42811
STM3962	yigL	putative hydrolase	**0.44**	0.26261
STM3963	yigM	putative transport protein	**0.07**	0.92727
STM3963	yigM	putative transport protein	**0.42**	0.48129
STM3964	metR	metE/metH regulator	**-0.57**	0.32481
STM3964	metR	metE/metH regulator	**0.03**	0.95985
STM3965	metE	5-methyltetrahydropteroyltriglutamate--homocysteine	**-0.37**	0.45852
STM3965	metE	5-methyltetrahydropteroyltriglutamate--homocysteine	**0.46**	0.34125
STM3966	STM3966	putative arylsulfatase regulator	**-0.59**	0.18265
STM3966	STM3966	putative arylsulfatase regulator	**0.09**	0.91783
STM3967	dlhH	putative dienelactone hydrolase	**0.26**	0.47065
STM3967	dlhH	putative dienelactone hydrolase	**0.17**	0.72219
STM3968	udp	uridine phosphorylase	**-0.19**	0.74224
STM3968	udp	uridine phosphorylase	**0.18**	0.76538
STM3969	yigN	putative inner membrane protein	**-0.32**	0.47937
STM3969	yigN	putative inner membrane protein	**0.27**	0.55825
STM3970	ubiE	ubiquinone/menaquinone biosynthesis methyltransferase	**0.09**	0.84686
STM3970	ubiE	ubiquinone/menaquinone biosynthesis methyltransferase	**0.04**	0.92520
STM3971	yigP	putative inner membrane protein	**-0.34**	0.36243
STM3971	yigP	putative inner membrane protein	**0.10**	0.84625
STM3972	aarF	putative ubiquinone biosynthesis protein UbiB	**-0.38**	0.39025
STM3972	aarF	putative ubiquinone biosynthesis protein UbiB	**-0.27**	0.46629
STM3973	tatA	twin argininte translocase protein A	**-0.15**	0.74087
STM3973	tatA	twin argininte translocase protein A	**-0.06**	0.88647
STM3974	tatB	sec-independent translocase	**0.05**	0.93387
STM3974	tatB	sec-independent translocase	**0.19**	0.66460
STM3975	tatC	Sec-independent protein secretion pathway component	**-0.69**	0.19142
STM3975	tatC	Sec-independent protein secretion pathway component	**-0.21**	0.62861
STM3976,S	yigW	putative hydrolase	**-0.64**	0.22602
STM3976,S	yigW	putative hydrolase	**-0.06**	0.93367
STM3977	rfaH	transcriptional activator RfaH	**-0.03**	0.94990
STM3977	rfaH	transcriptional activator RfaH	**0.01**	0.99512
STM3978	yigC	putative oxidoreductase	**0.08**	0.84296
STM3978	yigC	putative oxidoreductase	**0.41**	0.43591
STM3979	ubiB	NAD(P)H-flavin reductase	**-0.04**	0.93506
STM3979	ubiB	NAD(P)H-flavin reductase	**-0.09**	0.86017
STM3981	STM3981	putative cytoplasmic protein	**-0.36**	0.56535
STM3981	STM3981	putative cytoplasmic protein	**-0.05**	0.92908
STM3982	fadA	acetyl-CoA acetyltransferase	**-0.92**	0.15346
STM3982	fadA	acetyl-CoA acetyltransferase	**-0.24**	0.74779
STM3983	fadB	3-hydroxyacyl-CoA dehydrogenase	**-0.62**	0.35881
STM3983	fadB	3-hydroxyacyl-CoA dehydrogenase	**-0.18**	0.75851
STM3984	pepQ	proline dipeptidase	**-0.17**	0.65130
STM3984	pepQ	proline dipeptidase	**0.69**	0.16778
STM3985	yigZ	putative cytoplasmic protein	**-0.06**	0.87690
STM3985	yigZ	putative cytoplasmic protein	**0.01**	0.99182
STM3986	trkH	potassium transport protein	**0.15**	0.78996
STM3986	trkH	potassium transport protein	**-0.12**	0.77818
STM3987	hemG	protoporphyrin oxidase	**-0.46**	0.26663
STM3987	hemG	protoporphyrin oxidase	**0.10**	0.87512
STM3991	rrlA	STM3991	**0.02**	0.97837
STM3991	rrlA	STM3991	**0.24**	0.58903
STM3991	rrlA	STM3991	**-0.13**	0.87917
STM3991	rrlA	STM3991	**-0.43**	0.60052

STM3992	rrfA	STM3992	**-0.04**	0.96568
STM3992	rrfA	STM3992	**0.12**	0.83443
STM3992	rrfA	STM3992	**-0.01**	0.99432
STM3992	rrfA	STM3992	**-0.04**	0.95890
STM3992	rrfA	STM3992	**-0.08**	0.89142
STM3992	rrfA	STM3992	**0.04**	0.93767
STM3992	rrfA	STM3992	**0.23**	0.63683
STM3992	rrfA	STM3992	**-0.05**	0.93174
STM3992	rrfA	STM3992	**0.45**	0.43219
STM3992	rrfA	STM3992	**0.21**	0.70458
STM3993	mobB	molybdopterin-guanine dinucleotide biosynthesis protein B	**-0.20**	0.60620
STM3993	mobB	molybdopterin-guanine dinucleotide biosynthesis protein B	**-0.23**	0.57804
STM3994	mobA	molybdopterin-guanine dinucleotide biosynthesis protein A	**-0.14**	0.74878
STM3994	mobA	molybdopterin-guanine dinucleotide biosynthesis protein A	**-0.37**	0.55978
STM3995	yihD	putative cytoplasmic protein	**-0.19**	0.67908
STM3995	yihD	putative cytoplasmic protein	**-0.03**	0.93811
STM3996	yihE	putative type II homoserine kinase	**-0.33**	0.41391
STM3996	yihE	putative type II homoserine kinase	**0.00**	0.99540
STM3997	dsbA	periplasmic protein disulfide isomerase I	**-0.07**	0.87655
STM3997	dsbA	periplasmic protein disulfide isomerase I	**0.10**	0.81325
STM3998	yihG	putative endonuclease	**-0.42**	0.29848
STM3998	yihG	putative endonuclease	**-0.28**	0.53594
STM3999	polA	DNA polymerase I	**-0.35**	0.40227
STM3999	polA	DNA polymerase I	**0.15**	0.68136
STM4000	spf	STM4000	**0.22**	0.61833
STM4000	spf	STM4000	**0.17**	0.72976
STM4001	yihA	GTP-binding protein	**-0.47**	0.23724
STM4001	yihA	GTP-binding protein	**-0.29**	0.63076
STM4003	yihI	hypothetical protein STM4003	**-0.46**	0.37619
STM4003	yihI	hypothetical protein STM4003	**-0.12**	0.80915
STM4004	hemN	coproporphyrinogen III oxidase	**-0.10**	0.80077
STM4004	hemN	coproporphyrinogen III oxidase	**0.02**	0.96018
STM4005	glnG	response regulator	**0.41**	0.29393
STM4005	glnG	response regulator	**0.26**	0.76538
STM4006	glnL	sensor kinase	**0.37**	0.30422
STM4006	glnL	sensor kinase	**0.60**	0.17359
STM4007	glnA	glutamine synthetase	**0.25**	0.50801
STM4007	glnA	glutamine synthetase	**-0.04**	0.93083
STM4009	typA	GTP-binding elongation factor family protein	**-0.37**	0.37342
STM4009	typA	GTP-binding elongation factor family protein	**0.18**	0.75212
STM4010	STM4010	putative hydrolase	**-0.11**	0.80719
STM4010	STM4010	putative hydrolase	**-0.11**	0.84453
STM4011	STM4011	putative inner membrane protein	**-0.28**	0.67970
STM4011	STM4011	putative inner membrane protein	**-0.16**	0.75413
STM4012	STM4012	coproporphyrinogen III oxidase	**-0.41**	0.29796
STM4012	STM4012	coproporphyrinogen III oxidase	**-0.20**	0.62757
STM4013,S	STM4013,S	putative membrane-associated metal-dependent hydrolase	**-0.34**	0.52208
STM4013,S	STM4013,S	putative membrane-associated metal-dependent hydrolase	**0.20**	0.66902
STM4014	STM4014	putative periplasmic protein	**-0.35**	0.51587
STM4014	STM4014	putative periplasmic protein	**0.18**	0.83443
STM4015	STM4015	putative cytoplasmic protein	**-0.53**	0.38792
STM4015	STM4015	putative cytoplasmic protein	**0.59**	0.21015
STM4016	yshA	putative outer membrane protein	**-0.36**	0.59675
STM4016	yshA	putative outer membrane protein	**-0.04**	0.95081
STM4017	yihO	putative GPH family transport protein	**-0.62**	0.22602
STM4017	yihO	putative GPH family transport protein	**0.25**	0.65285
STM4018	yihP	putative GPH family transport protein	**-0.60**	0.39034

STM4018	yihP	putative GPH family transport protein	**0.27**	0.61205
STM4019	yihQ	putative alpha-xylosidase	**0.17**	0.76610
STM4019	yihQ	putative alpha-xylosidase	**0.25**	0.59821
STM4020,S	yihR	putative aldose-1-epimerase	**0.26**	0.56565
STM4020,S	yihR	putative aldose-1-epimerase	**0.13**	0.79473
STM4021	yihS	putative isomerase	**-0.33**	0.60595
STM4021	yihS	putative isomerase	**0.15**	0.74949
STM4022	yihT	putative aldolase	**-0.31**	0.61285
STM4022	yihT	putative aldolase	**0.30**	0.53497
STM4023	yihU	putative oxidoreductase	**-0.06**	0.94839
STM4023	yihU	putative oxidoreductase	**0.43**	0.59887
STM4024,S	yihV	putative sugar kinase	**0.40**	0.42613
STM4024,S	yihV	putative sugar kinase	**0.49**	0.34070
STM4025	yihW	putative glycerol-3-phosphate regulon repressor	**-0.20**	0.67363
STM4025	yihW	putative glycerol-3-phosphate regulon repressor	**0.01**	0.98546
STM4026	yihX	phosphatase	**-0.05**	0.92007
STM4026	yihX	phosphatase	**-0.06**	0.90661
STM4027	rbn	ribonuclease BN	**-0.50**	0.25382
STM4027	rbn	ribonuclease BN	**-0.29**	0.50034
STM4028	yihZ	D-tyrosyl-tRNA deacylase	**-0.54**	0.23055
STM4028	yihZ	D-tyrosyl-tRNA deacylase	**0.42**	0.34449
STM4029	yiiD	putative acetyltransferase	**0.11**	0.80661
STM4029	yiiD	putative acetyltransferase	**0.45**	0.32444
STM4030,S	STM4030,S	putative cytoplasmic protein	**-0.24**	0.52846
STM4030,S	STM4030,S	putative cytoplasmic protein	**0.48**	0.49296
STM4031	STM4031	putative cytoplasmic protein	**-0.08**	0.84687
STM4031	STM4031	putative cytoplasmic protein	**0.00**	0.99921
STM4032	STM4032	putative acetyl esterase	**-0.24**	0.66460
STM4032	STM4032	putative acetyl esterase	**0.24**	0.60051
STM4032,2N	STM4032,2N	hypothetical protein STM4032,2N	**0.00**	0.99512
STM4032,2N	STM4032,2N	hypothetical protein STM4032,2N	**0.29**	0.46184
STM4033	STM4033	putative regulatory protein	**-0.18**	0.76312
STM4033	STM4033	putative regulatory protein	**-0.19**	0.80976
STM4034	fdhE	formate dehydrogenase accessory protein FdhE	**-0.63**	0.33452
STM4034	fdhE	formate dehydrogenase accessory protein FdhE	**-0.23**	0.57797
STM4035	fdoI	formate dehydrogenase-O gamma subunit	**0.27**	0.63328
STM4035	fdoI	formate dehydrogenase-O gamma subunit	**-0.04**	0.94579
STM4036	fdoH	formate dehydrogenase-O beta subunit	**-0.49**	0.66460
STM4036	fdoH	formate dehydrogenase-O beta subunit	**0.44**	0.40774
STM4037	fdoG	formate dehydrogenase alpha subunit	**0.12**	0.83671
STM4037	fdoG	formate dehydrogenase alpha subunit	**0.82**	0.31280
STM4038	fdhD	formate dehydrogenase accessory protein	**0.77**	0.17057
STM4038	fdhD	formate dehydrogenase accessory protein	**0.87**	0.15859
STM4039	STM4039	putative inner membrane lipoprotein	**-0.42**	0.33452
STM4039	STM4039	putative inner membrane lipoprotein	**-0.16**	0.73811
STM4040	yiiG	putative cytoplasmic protein	**-0.19**	0.70966
STM4040	yiiG	putative cytoplasmic protein	**0.50**	0.53705
STM4041	STM4041	putative inner membrane protein	**-0.39**	0.33536
STM4041	STM4041	putative inner membrane protein	**-0.20**	0.72365
STM4042	STM4042	putative branched-chain amino acid permease	**-0.11**	0.79018
STM4042	STM4042	putative branched-chain amino acid permease	**0.01**	0.98894
STM4042A	STM4042A	hypothetical protein STM4042A	**0.00**	0.99822
STM4042A	STM4042A	hypothetical protein STM4042A	**-0.04**	0.93881
STM4043	yiiL	putative cytoplasmic protein	**0.33**	0.68961
STM4043	yiiL	putative cytoplasmic protein	**0.16**	0.74361
STM4044	STM4044	putative alcohol dehydrogenase	**0.52**	0.61201
STM4044	STM4044	putative alcohol dehydrogenase	**0.09**	0.85758
STM4045	rhaD	rhamnulose-1-phosphate aldolase	**-0.34**	0.58912
STM4045	rhaD	rhamnulose-1-phosphate aldolase	**0.12**	0.82664
STM4046	rhaA	L-rhamnose isomerase	**-0.04**	0.91974
STM4046	rhaA	L-rhamnose isomerase	**0.82**	0.12727
STM4047	rhaB	rhamnulokinase	**-0.89**	0.11913
STM4047	rhaB	rhamnulokinase	**0.55**	0.32016

STM4048	rhaS	L-rhamnose operon regulatory protein	**-0.19**	0.62216
STM4048	rhaS	L-rhamnose operon regulatory protein	**0.81**	0.32673
STM4049	rhaR	rhaRS operon regulatory protein	**-0.04**	0.95211
STM4049	rhaR	rhaRS operon regulatory protein	**0.35**	0.49708
STM4050	rhaT	L-rhamnose/H+ symporter protein	**-0.28**	0.71113
STM4050	rhaT	L-rhamnose/H+ symporter protein	**0.19**	0.80637
STM4051	STM4051	putative outer membrane protein	**-0.41**	0.46674
STM4051	STM4051	putative outer membrane protein	**-0.37**	0.49530
STM4052	STM4052	putative C4-dicarboxylate transport system	**-0.15**	0.78521
STM4052	STM4052	putative C4-dicarboxylate transport system	**0.10**	0.92403
STM4053	STM4053	putative C4-dicarboxylate transport system	**0.03**	0.95608
STM4053	STM4053	putative C4-dicarboxylate transport system	**0.58**	0.17402
STM4054	STM4054	putative periplasmic dicarboxylate-binding protein	**0.10**	0.80976
STM4054	STM4054	putative periplasmic dicarboxylate-binding protein	**0.38**	0.47766
STM4055	sodA	superoxide dismutase	**-0.25**	0.53062
STM4055	sodA	superoxide dismutase	**0.18**	0.70229
STM4056,S	yiiM	putative cytoplasmic protein	**-0.21**	0.62861
STM4056,S	yiiM	putative cytoplasmic protein	**0.14**	0.78755
STM4057	STM4057	putative inner membrane protein	**-0.52**	0.22283
STM4057	STM4057	putative inner membrane protein	**-0.01**	0.99213
STM4058	cpxA	two-component sensor protein	**-0.53**	0.31424
STM4058	cpxA	two-component sensor protein	**-0.04**	0.95809
STM4059	cpxR	response reguator	**-0.51**	0.31267
STM4059	cpxR	response reguator	**-0.07**	0.89340
STM4060	cpxP	periplasmic repressor	**-0.21**	0.60444
STM4060	cpxP	periplasmic repressor	**0.26**	0.50759
STM4061	fieF	ferrous iron efflux protein F	**-0.09**	0.81970
STM4061	fieF	ferrous iron efflux protein F	**-0.07**	0.86153
STM4062	pfkA	6-phosphofructokinase	**-0.87**	0.11224
STM4062	pfkA	6-phosphofructokinase	**0.27**	0.72192
STM4063	sbp	sulfate transport protein	**-0.41**	0.47407
STM4063	sbp	sulfate transport protein	**0.20**	0.79096
STM4064	ushB	CDP-diacylglycerol pyrophosphatase	**-1.39**	0.04783
STM4064	ushB	CDP-diacylglycerol pyrophosphatase	**-1.12**	0.11607
STM4065	STM4065	putative Na+/galactoside symporter	**-0.67**	0.27477
STM4065	STM4065	putative Na+/galactoside symporter	**-0.16**	0.77567
STM4066	STM4066	aminoimidazole riboside kinase	**-0.53**	0.37241
STM4066	STM4066	aminoimidazole riboside kinase	**-0.10**	0.80195
STM4067	STM4067	putative ADP-ribosylglycohydrolase	**-0.17**	0.68545
STM4067	STM4067	putative ADP-ribosylglycohydrolase	**-0.13**	0.76387
STM4068	STM4068	putative regulatory protein	**-0.12**	0.73825
STM4068	STM4068	putative regulatory protein	**0.62**	0.32390
STM4069	STM4069	putative periplasmic protein	**-0.28**	0.49871
STM4069	STM4069	putative periplasmic protein	**0.25**	0.73424
STM4070	STM4070	putative cytoplasmic protein	**-0.58**	0.22483
STM4070	STM4070	putative cytoplasmic protein	**-0.33**	0.47263
STM4071	STM4071	putative mannose-6-phosphate isomerase	**0.13**	0.80490
STM4071	STM4071	putative mannose-6-phosphate isomerase	**0.14**	0.89863
STM4072	ydeV	putative sugar kinase	**-0.48**	0.32673
STM4072	ydeV	putative sugar kinase	**0.80**	0.21094
STM4073	ydeW	putative transcriptional repressor	**0.32**	0.55338
STM4073	ydeW	putative transcriptional repressor	**-0.25**	0.70353
STM4074	ego	putative ABC-type aldose transport system ATPase component	**-0.28**	0.68313
STM4074	ego	putative ABC-type aldose transport system ATPase component	**0.47**	0.41611
STM4075	ydeY	putative sugar transport protein	**-0.63**	0.39260
STM4075	ydeY	putative sugar transport protein	**0.89**	0.14030
STM4076	ydeZ	putative sugar transport protein	**-0.31**	0.65693
STM4076	ydeZ	putative sugar transport protein	**0.33**	0.48400
STM4077	yneA	putative sugar transport protein	**-0.05**	0.94060
STM4077	yneA	putative sugar transport protein	**0.30**	0.43672
STM4078	yneB	hypothetical protein STM4078	**-0.30**	0.48879

STM4078	yneB	hypothetical protein STM4078	**0.01**	0.98539
STM4079,S	yneC	putative inner membrane protein	**-0.39**	0.34553
STM4079,S	yneC	putative inner membrane protein	**0.11**	0.82079
STM4080	STM4080	ribulose-phosphate 3-epimerase	**-0.06**	0.90356
STM4080	STM4080	ribulose-phosphate 3-epimerase	**-0.17**	0.78159
STM4081	tpiA	triosephosphate isomerase	**-0.17**	0.77186
STM4081	tpiA	triosephosphate isomerase	**-0.63**	0.32957
STM4082	yiiQ	putative periplasmic protein	**0.16**	0.67351
STM4082	yiiQ	putative periplasmic protein	**0.42**	0.30422
STM4083	yiiR	putative inner membrane protein	**-0.46**	0.24515
STM4083	yiiR	putative inner membrane protein	**0.21**	0.68830
STM4084	fpr	ferredoxin-NADP reductase	**0.33**	0.45286
STM4084	fpr	ferredoxin-NADP reductase	**0.41**	0.45423
STM4085	glpX	fructose 1,6-bisphosphatase II	**-0.29**	0.47610
STM4085	glpX	fructose 1,6-bisphosphatase II	**-0.29**	0.56511
STM4086	glpK	glycerol kinase	**0.25**	0.70430
STM4086	glpK	glycerol kinase	**0.58**	0.36311
STM4087	glpF	glycerol diffusion	**1.04**	0.17041
STM4087	glpF	glycerol diffusion	**1.12**	0.14183
STM4088	yiiU	putative cytoplasmic protein	**-0.30**	0.50272
STM4088	yiiU	putative cytoplasmic protein	**-0.06**	0.91047
STM4089	menG	ribonuclease activity regulator protein RraA	**-0.29**	0.41676
STM4089	menG	ribonuclease activity regulator protein RraA	**0.26**	0.55397
STM4090	menA	1,4-dihydroxy-2-naphthoate octaprenyltransferase,	**-0.33**	0.44208
STM4090	menA	1,4-dihydroxy-2-naphthoate octaprenyltransferase,	**-0.30**	0.45047
STM4091	hslU	ATP-dependent protease ATP-binding subunit	**-0.45**	0.22602
STM4091	hslU	ATP-dependent protease ATP-binding subunit	**-0.14**	0.69743
STM4092	hslV	ATP-dependent protease peptidase subunit	**-0.33**	0.38071
STM4092	hslV	ATP-dependent protease peptidase subunit	**-0.41**	0.28030
STM4093	ftsN	essential cell division protein	**-0.31**	0.61960
STM4093	ftsN	essential cell division protein	**-0.12**	0.78630
STM4094	cytR	transcriptional repressor	**0.40**	0.31280
STM4094	cytR	transcriptional repressor	**0.54**	0.32172
STM4095	priA	primosome assembly protein PriA	**-0.07**	0.87690
STM4095	priA	primosome assembly protein PriA	**-0.01**	0.99381
STM4097	STM4097	putative outer membrane lipoprotein	**-0.53**	0.36942
STM4097	STM4097	putative outer membrane lipoprotein	**0.20**	0.80574
STM4098	STM4098	putative arylsulfate sulfotransferase	**-0.68**	0.18464
STM4098	STM4098	putative arylsulfate sulfotransferase	**-0.09**	0.82521
STM4099	metJ	transcriptional repressor protein MetJ	**-0.58**	0.17603
STM4099	metJ	transcriptional repressor protein MetJ	**-0.26**	0.45660
STM4100	metB	cystathionine gamma-synthase	**-0.57**	0.35824
STM4100	metB	cystathionine gamma-synthase	**0.19**	0.63493
STM4101	metL	bifunctional aspartate kinase II/homoserine dehydrogenase II	**-0.28**	0.53459
STM4101	metL	bifunctional aspartate kinase II/homoserine dehydrogenase II	**0.41**	0.33167
STM4102	STM4102	putative inner membrane protein	**-0.02**	0.98372
STM4102	STM4102	putative inner membrane protein	**0.49**	0.36444
STM4103	STM4103	putative cytoplasmic protein	**0.26**	0.85658
STM4103	STM4103	putative cytoplasmic protein	**-0.71**	0.20783
STM4104	STM4104	putative 5'-nucleotidase/2',3'-cyclic phosphodiesterase	**-0.07**	0.90671
STM4104	STM4104	putative 5'-nucleotidase/2',3'-cyclic phosphodiesterase	**0.93**	0.21747
STM4105	metF	5,10-methylenetetrahydrofolate reductase	**0.23**	0.62216
STM4105	metF	5,10-methylenetetrahydrofolate reductase	**0.56**	0.35955
STM4106	katG	hydroperoxidase	**0.04**	0.96695
STM4106	katG	hydroperoxidase	**-0.16**	0.72646
STM4107	yijF	putative periplasmic protein	**-0.95**	0.19398
STM4107	yijF	putative periplasmic protein	**0.35**	0.48062
STM4108	gldA	glycerol dehydrogenase	**0.33**	0.60558
STM4108	gldA	glycerol dehydrogenase	**0.54**	0.25084
STM4109	talC	fructose-6-phosphate aldolase	**0.16**	0.76553
STM4109	talC	fructose-6-phosphate aldolase	**-0.08**	0.87126

STM4110	ptsA	PEP-protein phosphotransferase	**-0.04**	0.94658
STM4110	ptsA	PEP-protein phosphotransferase	**0.31**	0.48791
STM4112	frwC	PTS system fructose-like IIC component	**-0.47**	0.24520
STM4112	frwC	PTS system fructose-like IIC component	**0.10**	0.86412
STM4113	frwB	PTS system fructose-like IIB component 1	**0.00**	0.99822
STM4113	frwB	PTS system fructose-like IIB component 1	**0.32**	0.46787
STM4114	pflD	putative pyruvate formate lyase II	**0.08**	0.84783
STM4114	pflD	putative pyruvate formate lyase II	**0.13**	0.76921
STM4115	pflC	putative pyruvate formate lyase activating enzyme 2	**0.03**	0.95910
STM4115	pflC	putative pyruvate formate lyase activating enzyme 2	**0.55**	0.41134
STM4116	frwD	PTS system fructose-like IIB component 2	**-0.42**	0.29891
STM4116	frwD	PTS system fructose-like IIB component 2	**0.09**	0.88013
STM4117	yijO	putative regulatory protein	**-0.36**	0.47656
STM4117	yijO	putative regulatory protein	**0.26**	0.66545
STM4118	yijP	putative integral membrane protein	**-0.02**	0.98239
STM4118	yijP	putative integral membrane protein	**0.29**	0.74238
STM4119	ppc	phosphoenolpyruvate carboxylase	**-0.02**	0.96785
STM4119	ppc	phosphoenolpyruvate carboxylase	**0.06**	0.90277
STM4120	argE	acetylornithine deacetylase	**0.11**	0.81667
STM4120	argE	acetylornithine deacetylase	**0.02**	0.96785
STM4121	argC	N-acetyl-gamma-glutamyl-phosphate reductase	**0.31**	0.44331
STM4121	argC	N-acetyl-gamma-glutamyl-phosphate reductase	**0.46**	0.41314
STM4122	argB	acetylglutamate kinase	**0.12**	0.78877
STM4122	argB	acetylglutamate kinase	**0.01**	0.99079
STM4123	argH	argininosuccinate lyase	**0.10**	0.81806
STM4123	argH	argininosuccinate lyase	**0.18**	0.74142
STM4125	oxyR	oxidative stress regulatory protein	**-0.02**	0.96850
STM4125	oxyR	oxidative stress regulatory protein	**0.08**	0.86987
STM4126	udhA	soluble pyridine nucleotide transhydrogenase	**-0.07**	0.88709
STM4126	udhA	soluble pyridine nucleotide transhydrogenase	**0.08**	0.86951
STM4127	yijC	putative transcriptional repressor	**-0.43**	0.32673
STM4127	yijC	putative transcriptional repressor	**0.28**	0.49871
STM4128	yijD	putative inner membrane protein	**-0.25**	0.61614
STM4128	yijD	putative inner membrane protein	**0.12**	0.81142
STM4129	trmA	tRNA (uracil-5-)-methyltransferase	**-0.02**	0.97348
STM4129	trmA	tRNA (uracil-5-)-methyltransferase	**0.49**	0.32172
STM4130	btuB	outer membrane receptor protein precursor	**-0.07**	0.87826
STM4130	btuB	outer membrane receptor protein precursor	**0.12**	0.76240
STM4131	murI	glutamate racemase	**-0.21**	0.68032
STM4131	murI	glutamate racemase	**-0.37**	0.35816
STM4132	rrsB	STM4132	**0.08**	0.87016
STM4132	rrsB	STM4132	**0.09**	0.85909
STM4132	rrsB	STM4132	**-0.45**	0.28030
STM4132	rrsB	STM4132	**-0.22**	0.66112
STM4132	rrsB	STM4132	**-0.34**	0.41330
STM4132	rrsB	STM4132	**-0.14**	0.81727
STM4132	rrsB	STM4132	**-0.13**	0.86190
STM4132	rrsB	STM4132	**-0.26**	0.58903
STM4132	rrsB	STM4132	**-0.38**	0.46629
STM4132	rrsB	STM4132	**-0.38**	0.48590
STM4132	rrsB	STM4132	**-0.45**	0.39962
STM4132	rrsB	STM4132	**0.30**	0.58912
STM4133	ileU	STM4133	**-0.28**	0.55780
STM4133	ileU	STM4133	**-0.67**	0.21747
STM4133	ileU	STM4133	**-0.41**	0.38260
STM4133	ileU	STM4133	**-0.30**	0.51608
STM4133	ileU	STM4133	**-0.11**	0.79308
STM4133	ileU	STM4133	**0.14**	0.79242
STM4134	-	STM4134	**-0.22**	0.73129
STM4134	-	STM4134	**-0.33**	0.38317
STM4134	-	STM4134	**-0.42**	0.27763
STM4134	-	STM4134	**-0.27**	0.46199
STM4134	-	STM4134	**-0.34**	0.37161

STM4134	-	STM4134	**0.14**	0.77346
STM4135	rrlB	STM4135	**-0.05**	0.94102
STM4135	rrlB	STM4135	**0.14**	0.84354
STM4138	birA	biotin--protein ligase	**-0.11**	0.81943
STM4138	birA	biotin--protein ligase	**0.04**	0.96117
STM4139	coaA	pantothenate kinase	**-0.22**	0.65817
STM4139	coaA	pantothenate kinase	**0.14**	0.76929
STM4142	thrU	STM4142	**-0.28**	0.67097
STM4142	thrU	STM4142	**0.56**	0.22602
STM4143	tyrU	STM4143	**-0.25**	0.68147
STM4143	tyrU	STM4143	**0.44**	0.47159
STM4144	glyT	STM4144	**-0.12**	0.80128
STM4144	glyT	STM4144	**0.08**	0.84456
STM4145	thrT	STM4145	**-0.30**	0.59237
STM4145	thrT	STM4145	**-0.42**	0.45069
STM4146	tuf	elongation factor Tu	**-0.22**	0.63535
STM4146	tuf	elongation factor Tu	**0.33**	0.41913
STM4147	secE	translocase	**-0.01**	0.98117
STM4147	secE	translocase	**0.32**	0.61275
STM4148	nusG	transcription antitermination protein NusG	**-0.06**	0.89004
STM4148	nusG	transcription antitermination protein NusG	**-0.03**	0.94990
STM4149	rplK	50S ribosomal protein L11	**-0.07**	0.86190
STM4149	rplK	50S ribosomal protein L11	**0.19**	0.75437
STM4150	rplA	50S ribosomal protein L1	**0.03**	0.94765
STM4150	rplA	50S ribosomal protein L1	**0.03**	0.94990
STM4151	rplJ	50S ribosomal protein L10	**-0.09**	0.84021
STM4151	rplJ	50S ribosomal protein L10	**0.21**	0.60174
STM4152	rplL	50S ribosomal protein L7/L12	**-0.23**	0.51275
STM4152	rplL	50S ribosomal protein L7/L12	**0.25**	0.55355
STM4153	rpoB	DNA-directed RNA polymerase beta subunit	**0.00**	0.99742
STM4153	rpoB	DNA-directed RNA polymerase beta subunit	**0.44**	0.38668
STM4154	rpoC	DNA-directed RNA polymerase beta' subunit	**-0.19**	0.64174
STM4154	rpoC	DNA-directed RNA polymerase beta' subunit	**-0.62**	0.34793
STM4155	STM4155	putative inner membrane protein	**0.02**	0.96595
STM4155	STM4155	putative inner membrane protein	**0.00**	0.99513
STM4156	STM4156	putative cytoplasmic protein	**-0.30**	0.46565
STM4156	STM4156	putative cytoplasmic protein	**0.26**	0.45739
STM4157	STM4157	putative cytoplasmic protein	**-0.21**	0.63154
STM4157	STM4157	putative cytoplasmic protein	**0.13**	0.78750
STM4158	STM4158	putative cytoplasmic protein	**-0.25**	0.52767
STM4158	STM4158	putative cytoplasmic protein	**0.04**	0.95910
STM4159	thiH	thiamine biosynthesis protein ThiH	**0.02**	0.98976
STM4159	thiH	thiamine biosynthesis protein ThiH	**0.01**	0.98658
STM4160	thiG	thiazole synthase	**0.02**	0.98677
STM4160	thiG	thiazole synthase	**0.47**	0.41422
STM4161	STM4161	sulfur carrier protein ThiS	**0.12**	0.77801
STM4161	STM4161	sulfur carrier protein ThiS	**0.69**	0.24515
STM4162	thiF	thiamine biosynthesis protein ThiF	**-0.56**	0.19967
STM4162	thiF	thiamine biosynthesis protein ThiF	**0.01**	0.98640
STM4163	thiE	thiamine-phosphate pyrophosphorylase	**-0.28**	0.67024
STM4163	thiE	thiamine-phosphate pyrophosphorylase	**0.36**	0.35937
STM4164	thiC	thiamine biosynthesis protein ThiC	**0.43**	0.40930
STM4164	thiC	thiamine biosynthesis protein ThiC	**0.76**	0.19780
STM4165	rsd	anti sigma 70 factor	**-0.41**	0.35955
STM4165	rsd	anti sigma 70 factor	**0.43**	0.47656
STM4166	nudC	NADH pyrophosphatase	**-0.06**	0.90007
STM4166	nudC	NADH pyrophosphatase	**0.34**	0.45664
STM4167	hemE	uroporphyrinogen decarboxylase	**-0.15**	0.74100
STM4167	hemE	uroporphyrinogen decarboxylase	**0.05**	0.92716
STM4168	nfi	endonuclease V	**0.25**	0.52101
STM4168	nfi	endonuclease V	**0.54**	0.34201
STM4169	yjaG	putative cytoplasmic protein	**-0.09**	0.82822
STM4169	yjaG	putative cytoplasmic protein	**0.22**	0.65539

STM4170	hupA	DNA-binding protein HU-alpha	**-0.47**	0.41329
STM4170	hupA	DNA-binding protein HU-alpha	**-0.32**	0.51820
STM4171	yjaH	putative inner membrane protein	**-0.06**	0.91315
STM4171	yjaH	putative inner membrane protein	**0.09**	0.86629
STM4172	zraP	zinc-resistance associated protein	**-0.10**	0.88504
STM4172	zraP	zinc-resistance associated protein	**0.21**	0.75893
STM4173	hydH	sensor kinase	**0.03**	0.96209
STM4173	hydH	sensor kinase	**0.67**	0.23613
STM4174	hydG	response regulator	**0.09**	0.81667
STM4174	hydG	response regulator	**0.58**	0.22283
STM4175	purD	phosphoribosylamine--glycine ligase	**0.02**	0.97720
STM4175	purD	phosphoribosylamine--glycine ligase	**-0.42**	0.49870
STM4176	purH	bifunctional phosphoribosylaminoimidazolecarboxamide	**-0.09**	0.86190
STM4176	purH	bifunctional phosphoribosylaminoimidazolecarboxamide	**-0.30**	0.42486
STM4178	gltV	STM4178	**-0.93**	0.08580
STM4178	gltV	STM4178	**-0.34**	0.40020
STM4178	gltV	STM4178	**-0.66**	0.17754
STM4178	gltV	STM4178	**-0.72**	0.19909
STM4178	gltV	STM4178	**-0.42**	0.40191
STM4178	gltV	STM4178	**-0.23**	0.63454
STM4178	gltV	STM4178	**-0.44**	0.31280
STM4178	gltV	STM4178	**-0.14**	0.76483
STM4180	rrfE	STM4180	**0.20**	0.81323
STM4180	rrfE	STM4180	**-0.23**	0.84021
STM4180	rrfE	STM4180	**-0.39**	0.59908
STM4180	rrfE	STM4180	**0.20**	0.74997
STM4181	yjaB	putative acetyltransferase	**-0.23**	0.65793
STM4181	yjaB	putative acetyltransferase	**-0.13**	0.82918
STM4182	metA	homoserine O-succinyltransferase	**-0.11**	0.79356
STM4182	metA	homoserine O-succinyltransferase	**0.07**	0.89863
STM4183	aceB	malate synthase	**-0.14**	0.80840
STM4183	aceB	malate synthase	**-0.20**	0.70430
STM4184	aceA	isocitrate lyase	**-0.07**	0.88653
STM4184	aceA	isocitrate lyase	**0.37**	0.55598
STM4185	aceK	bifunctional isocitrate dehydrogenase kinase/phosphatase protein	**0.56**	0.40517
STM4185	aceK	bifunctional isocitrate dehydrogenase kinase/phosphatase protein	**0.81**	0.24520
STM4186	STM4186	putative cytoplasmic protein	**-0.15**	0.79581
STM4186	STM4186	putative cytoplasmic protein	**0.38**	0.35373
STM4187	iclR	acetate operon transcriptional repressor	**0.37**	0.35955
STM4187	iclR	acetate operon transcriptional repressor	**0.21**	0.68969
STM4188,S	metH	B12-dependent methionine synthase	**-0.65**	0.34756
STM4188,S	metH	B12-dependent methionine synthase	**0.51**	0.34936
STM4189	yjbB	putative transport protein	**-0.21**	0.67351
STM4189	yjbB	putative transport protein	**0.09**	0.83443
STM4190	pepE	peptidase E	**0.25**	0.79676
STM4190	pepE	peptidase E	**0.82**	0.11913
STM4191	STM4191	putative cytoplasmic protein	**-0.43**	0.37919
STM4191	STM4191	putative cytoplasmic protein	**0.64**	0.39385
STM4192	STM4192	putative cytoplasmic protein	**0.19**	0.66677
STM4192	STM4192	putative cytoplasmic protein	**0.11**	0.80902
STM4193	yjbC	putative pseudouridine synthase	**-0.14**	0.85988
STM4193	yjbC	putative pseudouridine synthase	**0.10**	0.87918
STM4194	yjbD	putative cytoplasmic protein	**-0.26**	0.57407
STM4194	yjbD	putative cytoplasmic protein	**0.06**	0.91294
STM4195	STM4195	putative Na+-dependent transporter	**-0.85**	0.11421
STM4195	STM4195	putative Na+-dependent transporter	**0.10**	0.80027
STM4196	STM4196	putative cytoplasmic protein	**-0.58**	0.26465
STM4196	STM4196	putative cytoplasmic protein	**0.33**	0.50190
STM4198	STM4198	putative cytoplasmic protein	**-0.65**	0.24520
STM4198	STM4198	putative cytoplasmic protein	**-0.26**	0.62604
STM4199	STM4199	putative cytoplasmic protein	**0.45**	0.61285

STM4199	STM4199	putative cytoplasmic protein	**1.64**	0.16776
STM4200	STM4200	putative phage tail fiber protein H	**-0.15**	0.77346
STM4200	STM4200	putative phage tail fiber protein H	**-0.46**	0.59455
STM4201	STM4201	putative phage tail protein	**-1.22**	0.08783
STM4201	STM4201	putative phage tail protein	**-0.37**	0.63235
STM4202	STM4202	putative phage baseplate protein	**-0.32**	0.56059
STM4202	STM4202	putative phage baseplate protein	**0.16**	0.80408
STM4203	STM4203	putative phage baseplate protein	**-0.03**	0.98140
STM4203	STM4203	putative phage baseplate protein	**0.56**	0.38049
STM4204	STM4204	putative inner membrane protein	**-0.45**	0.26261
STM4204	STM4204	putative inner membrane protein	**0.32**	0.68961
STM4205	STM4205	putative phage glycosyltransferase	**-0.13**	0.80715
STM4205	STM4205	putative phage glycosyltransferase	**0.30**	0.41626
STM4206	STM4206	putative phage glucose translocase	**-0.02**	0.98340
STM4206	STM4206	putative phage glucose translocase	**-0.13**	0.84657
STM4207	STM4207	putative phage baseplate component	**0.17**	0.79180
STM4207	STM4207	putative phage baseplate component	**0.51**	0.26856
STM4208	STM4208	putative cytoplasmic protein	**-0.09**	0.86852
STM4208	STM4208	putative cytoplasmic protein	**0.26**	0.56565
STM4209	STM4209	putative inner membrane protein	**0.00**	0.99698
STM4209	STM4209	putative inner membrane protein	**0.48**	0.34201
STM4210	STM4210	putative methyl-accepting chemotaxis protein	**-0.19**	0.69372
STM4210	STM4210	putative methyl-accepting chemotaxis protein	**0.29**	0.74361
STM4211	STM4211	putative phage tail protein	**-0.19**	0.75319
STM4211	STM4211	putative phage tail protein	**0.51**	0.40121
STM4212	STM4212	putative phage tail core protein	**-0.28**	0.40820
STM4212	STM4212	putative phage tail core protein	**0.21**	0.66888
STM4213	STM4213	putative phage tail sheath protein	**-0.09**	0.89759
STM4213	STM4213	putative phage tail sheath protein	**0.38**	0.42268
STM4214	STM4214	putative cytoplasmic protein	**-0.56**	0.38490
STM4214	STM4214	putative cytoplasmic protein	**0.28**	0.69634
STM4215	STM4215	putative cytoplasmic protein	**-1.17**	0.21091
STM4215	STM4215	putative cytoplasmic protein	**-0.32**	0.59675
STM4216	STM4216	putative inner membrane protein	**-0.59**	0.37154
STM4216	STM4216	putative inner membrane protein	**0.56**	0.52511
STM4217	STM4217	putative soluble lytic murein transglycosylase	**-0.31**	0.54624
STM4217	STM4217	putative soluble lytic murein transglycosylase	**0.31**	0.57406
STM4218	STM4218	putative inner membrane protein	**-0.25**	0.65916
STM4218	STM4218	putative inner membrane protein	**0.23**	0.61183
STM4219,S	STM4219,S	putative cytoplasmic protein	**-0.24**	0.77923
STM4219,S	STM4219,S	putative cytoplasmic protein	**0.17**	0.68649
STM4220	lysC	aspartate kinase III	**0.18**	0.82667
STM4220	lysC	aspartate kinase III	**1.01**	0.38668
STM4221	pgi	glucose-6-phosphate isomerase	**-0.57**	0.24622
STM4221	pgi	glucose-6-phosphate isomerase	**-0.47**	0.35373
STM4222,S	yjbE	putative outer membrane protein	**0.07**	0.88863
STM4222,S	yjbE	putative outer membrane protein	**0.13**	0.81656
STM4223	yjbF	putative outer membrane lipoprotein	**-0.17**	0.71404
STM4223	yjbF	putative outer membrane lipoprotein	**0.83**	0.21114
STM4224	yjbG	putative periplasmic protein	**-0.11**	0.87720
STM4224	yjbG	putative periplasmic protein	**0.48**	0.29889
STM4225	yjbH	putative outer membrane lipoprotein	**-0.05**	0.93485
STM4225	yjbH	putative outer membrane lipoprotein	**0.44**	0.37888
STM4226	yjbA	phosphate-starvation-inducible protein PsiE	**0.10**	0.85893
STM4226	yjbA	phosphate-starvation-inducible protein PsiE	**0.45**	0.36703
STM4227	malG	maltose transport protein	**0.04**	0.97005
STM4227	malG	maltose transport protein	**1.13**	0.31458
STM4228	malF	maltose transport protein	**0.11**	0.89405
STM4228	malF	maltose transport protein	**0.79**	0.17139
STM4229	malE	periplasmic maltose-binding protein	**1.10**	0.07318
STM4229	malE	periplasmic maltose-binding protein	**1.63**	0.07098
STM4230	malK	maltose transport protein/repressor	**1.65**	0.10754
STM4230	malK	maltose transport protein/repressor	**2.05**	0.01765

STM4231	lamB	maltoporin precursor	**1.89**	0.13813
STM4231	lamB	maltoporin precursor	**1.95**	0.09991
STM4232	malM	periplasmic protein precursor	**0.40**	0.40227
STM4232	malM	periplasmic protein precursor	**0.61**	0.19398
STM4233	ubiC	chorismate pyruvate lyase	**0.01**	0.98896
STM4233	ubiC	chorismate pyruvate lyase	**0.21**	0.54461
STM4234	ubiA	4-hydroxybenzoate octaprenyltransferase	**-0.30**	0.53840
STM4234	ubiA	4-hydroxybenzoate octaprenyltransferase	**-0.03**	0.94519
STM4235	plsB	glycerol-3-phosphate acyltransferase	**-0.32**	0.48791
STM4235	plsB	glycerol-3-phosphate acyltransferase	**0.16**	0.77346
STM4236	dgkA	diacylglycerol kinase	**-0.07**	0.87254
STM4236	dgkA	diacylglycerol kinase	**-0.10**	0.81284
STM4237	lexA	LexA repressor	**0.15**	0.66460
STM4237	lexA	LexA repressor	**0.45**	0.34070
STM4238	dinF	DNA-damage-inducible protein F	**-0.07**	0.88085
STM4238	dinF	DNA-damage-inducible protein F	**0.10**	0.79731
STM4240	yjbJ	putative cytoplasmic protein	**-0.53**	0.24571
STM4240	yjbJ	putative cytoplasmic protein	**-0.05**	0.91626
STM4241	zur	transcriptional repressor	**-0.17**	0.74779
STM4241	zur	transcriptional repressor	**0.08**	0.89107
STM4242	STM4242	conjugative transfer protein	**-0.46**	0.62682
STM4242	STM4242	conjugative transfer protein	**-0.09**	0.90169
STM4243	yjbN	hypothetical protein STM4243	**-0.29**	0.51034
STM4243	yjbN	hypothetical protein STM4243	**0.11**	0.77606
STM4244	pspG	phage shock protein G	**-0.55**	0.33452
STM4244	pspG	phage shock protein G	**-0.06**	0.91317
STM4245	qor	quinone oxidoreductase	**-0.13**	0.88647
STM4245	qor	quinone oxidoreductase	**-0.26**	0.58788
STM4246	dnaB	replicative DNA helicase	**-0.09**	0.82667
STM4246	dnaB	replicative DNA helicase	**-0.04**	0.92716
STM4247	alr	alanine racemase	**-0.33**	0.43219
STM4247	alr	alanine racemase	**0.13**	0.75105
STM4248	tyrB	aspartate aminotransferase	**0.29**	0.73801
STM4248	tyrB	aspartate aminotransferase	**1.17**	0.16880
STM4249	aphA	non-specific acid phosphatase/phosphotransferase	**-0.11**	0.83402
STM4249	aphA	non-specific acid phosphatase/phosphotransferase	**0.11**	0.87208
STM4250	yjbQ	putative cytoplasmic protein	**0.06**	0.92262
STM4250	yjbQ	putative cytoplasmic protein	**0.54**	0.31195
STM4251	yjbR	putative cytoplasmic protein	**0.05**	0.93811
STM4251	yjbR	putative cytoplasmic protein	**0.45**	0.38201
STM4252	STM4252	putative inner membrane protein	**-0.18**	0.66609
STM4252	STM4252	putative inner membrane protein	**0.59**	0.29543
STM4253	STM4253	putative outer membrane lipoprotein	**0.25**	0.60265
STM4253	STM4253	putative outer membrane lipoprotein	**0.74**	0.26820
STM4254	uvrA	excinuclease ABC subunit A	**0.01**	0.98290
STM4254	uvrA	excinuclease ABC subunit A	**0.32**	0.63277
STM4256	ssb	single-strand DNA-binding protein	**-0.43**	0.37872
STM4256	ssb	single-strand DNA-binding protein	**-0.19**	0.67351
STM4258	STM4258	putative methyl-accepting chemotaxis protein	**0.72**	0.17754
STM4258	STM4258	putative methyl-accepting chemotaxis protein	**1.47**	0.07388
STM4259	STM4259	putative ABC exporter outer membrane component	**1.02**	0.11224
STM4259	STM4259	putative ABC exporter outer membrane component	**1.66**	0.02875
STM4260	STM4260	predicted cation efflux pump	**1.03**	0.11268
STM4260	STM4260	predicted cation efflux pump	**1.82**	0.04510
STM4261	STM4261	putative inner membrane protein	**0.04**	0.95608
STM4261	STM4261	putative inner membrane protein	**0.08**	0.92637
STM4262	STM4262	putative ABC-type bacteriocin/lantibiotic exporter	**-0.60**	0.20996
STM4262	STM4262	putative ABC-type bacteriocin/lantibiotic exporter	**-0.08**	0.90766
STM4263	yjcB	putative inner membrane protein	**-0.64**	0.18763
STM4263	yjcB	putative inner membrane protein	**-0.21**	0.69266
STM4264	yjcC	putative diguanylate cyclase/phosphodiesterase	**-0.28**	0.74481
STM4264	yjcC	putative diguanylate cyclase/phosphodiesterase	**0.12**	0.76937
STM4265	soxS	transcriptional activator	**-0.26**	0.52712

STM4265	soxS	transcriptional activator	**0.08**	0.87126
STM4266	soxR	redox-sensing transcriptional activator	**-0.07**	0.90797
STM4266	soxR	redox-sensing transcriptional activator	**0.16**	0.83855
STM4267	STM4267	putative glutathione S-transferase	**-0.61**	0.42427
STM4267	STM4267	putative glutathione S-transferase	**-0.24**	0.68491
STM4268	yjcD	hypothetical protein STM4268	**-0.56**	0.22358
STM4268	yjcD	hypothetical protein STM4268	**-0.30**	0.56786
STM4269	yjcE	Na/H transport protein	**-0.52**	0.35325
STM4269	yjcE	Na/H transport protein	**-0.24**	0.70048
STM4270	STM4270	putative transcriptional regulator	**-0.24**	0.52408
STM4270	STM4270	putative transcriptional regulator	**0.79**	0.18763
STM4271	STM4271	putative inner membrane protein	**-0.03**	0.95608
STM4271	STM4271	putative inner membrane protein	**0.30**	0.62617
STM4272	STM4272	putative inner membrane protein	**0.19**	0.73473
STM4272	STM4272	putative inner membrane protein	**0.85**	0.15859
STM4273	actP	acetate permease	**-0.36**	0.48086
STM4273	actP	acetate permease	**0.11**	0.86702
STM4274	yjcH	putative inner membrane protein	**0.71**	0.73473
STM4274	yjcH	putative inner membrane protein	**1.47**	0.28861
STM4275	acs	acetyl-coenzyme A synthetase	**-0.04**	0.92513
STM4275	acs	acetyl-coenzyme A synthetase	**0.65**	0.18740
STM4277	nrfA	nitrite reductase periplasmic cytochrome c552	**-0.07**	0.93064
STM4277	nrfA	nitrite reductase periplasmic cytochrome c552	**0.86**	0.41422
STM4278,S	nrfB	formate-dependent nitrite reductase	**0.13**	0.74354
STM4278,S	nrfB	formate-dependent nitrite reductase	**0.92**	0.18426
STM4279	nrfC	putative formate-dependent nitrite reductase	**-0.24**	0.57568
STM4279	nrfC	putative formate-dependent nitrite reductase	**0.46**	0.36942
STM4280	nrfD	putative formate-dependent nitrate reductase	**-0.16**	0.75033
STM4280	nrfD	putative formate-dependent nitrate reductase	**0.32**	0.39499
STM4281	nrfE	formate-dependent nitrite reductase	**-0.14**	0.91443
STM4281	nrfE	formate-dependent nitrite reductase	**0.42**	0.62494
STM4282	nrfG	formate-dependent nitrite reductase component	**0.10**	0.83443
STM4282	nrfG	formate-dependent nitrite reductase component	**0.44**	0.27004
STM4283	gltP	glutamate/aspartate symport protein	**-0.48**	0.25125
STM4283	gltP	glutamate/aspartate symport protein	**0.21**	0.58095
STM4284	yjcO	tetratricopeptide repeat protein	**0.11**	0.77883
STM4284	yjcO	tetratricopeptide repeat protein	**0.30**	0.40337
STM4285	fdhF	formate dehydrogenase	**-0.32**	0.43899
STM4285	fdhF	formate dehydrogenase	**0.58**	0.40562
STM4286	lpxO	putative dioxygenase	**-0.23**	0.69358
STM4286	lpxO	putative dioxygenase	**0.40**	0.71973
STM4287,S	phnO	putative regulatory protein	**-0.30**	0.73968
STM4287,S	phnO	putative regulatory protein	**-0.29**	0.61048
STM4288	phnB	putative cytoplasmic protein	**-0.29**	0.41913
STM4288	phnB	putative cytoplasmic protein	**-0.16**	0.71169
STM4289	phnA	putative alkylphosphonate uptake protein	**-0.44**	0.38200
STM4289	phnA	putative alkylphosphonate uptake protein	**0.03**	0.97333
STM4290	proP	low-affinity proline transporter	**-0.93**	0.17211
STM4290	proP	low-affinity proline transporter	**0.02**	0.97443
STM4291	basS	sensor kinase	**-1.06**	0.10012
STM4291	basS	sensor kinase	**-1.74**	0.21393
STM4292	basR	response regulator	**-0.92**	0.09679
STM4292	basR	response regulator	**-1.00**	0.12549
STM4293	yjdB	putative integral membrane protein	**-2.27**	0.01937
STM4293	yjdB	putative integral membrane protein	**-1.64**	0.04232
STM4294	yjdE	putative putrescine/ornithine transport protein	**-1.13**	0.07318
STM4294	yjdE	putative putrescine/ornithine transport protein	**-0.98**	0.07353
STM4295	adiY	transcriptional activator	**-0.76**	0.34553
STM4295	adiY	transcriptional activator	**-0.22**	0.74091
STM4296	adi	catabolic arginine decarboxylase	**-0.44**	0.41631
STM4296	adi	catabolic arginine decarboxylase	**0.12**	0.84611
STM4297	melR	melibiose operon regulator	**0.42**	0.69882
STM4297	melR	melibiose operon regulator	**0.68**	0.45419

STM4298	melA	alpha-galactosidase	**-0.32**	0.59096
STM4298	melA	alpha-galactosidase	**1.00**	0.25102
STM4299	melB	melibiose permease II	**0.19**	0.65285
STM4299	melB	melibiose permease II	**0.77**	0.17919
STM4300	fumB	fumarase B	**-0.12**	0.79096
STM4300	fumB	fumarase B	**0.21**	0.74812
STM4301	dcuB	anaerobic C4-dicarboxylate transporter	**-0.17**	0.70249
STM4301	dcuB	anaerobic C4-dicarboxylate transporter	**-0.07**	0.88953
STM4302	STM4302	putative cytoplasmic protein	**-0.51**	0.48837
STM4302	STM4302	putative cytoplasmic protein	**0.40**	0.46385
STM4303	dcuR	response regulator	**0.00**	0.99938
STM4303	dcuR	response regulator	**-0.28**	0.60311
STM4304	dcuS	sensory histidine kinase	**-0.51**	0.27696
STM4304	dcuS	sensory histidine kinase	**-0.07**	0.90318
STM4305,S	STM4305,S	putative anaerobic dimethylsulfoxide reductase subunit A	**-0.11**	0.90671
STM4305,S	STM4305,S	putative anaerobic dimethylsulfoxide reductase subunit A	**0.51**	0.31146
STM4306	STM4306	putative anaerobic dimethylsulfoxide reductase subunit B	**-0.62**	0.31280
STM4306	STM4306	putative anaerobic dimethylsulfoxide reductase subunit B	**0.82**	0.30748
STM4307	STM4307	putative anaerobic dimethylsulfoxide reductase subunit C	**-0.21**	0.81896
STM4307	STM4307	putative anaerobic dimethylsulfoxide reductase subunit C	**0.02**	0.98013
STM4308	STM4308	putative anaerobic dehydrogenase component	**-0.70**	0.34633
STM4308	STM4308	putative anaerobic dehydrogenase component	**0.16**	0.76694
STM4309	STM4309	hypothetical protein STM4309	**-0.28**	0.43778
STM4309	STM4309	hypothetical protein STM4309	**0.64**	0.47656
STM4310	STM4310	putative inner membrane protein	**-0.92**	0.21933
STM4310	STM4310	putative inner membrane protein	**-0.35**	0.76387
STM4312	STM4312	hypothetical protein STM4312	**0.12**	0.91111
STM4312	STM4312	hypothetical protein STM4312	**-0.06**	0.94050
STM4313	STM4313	putative cytoplasmic protein	**0.03**	0.96785
STM4313	STM4313	putative cytoplasmic protein	**0.46**	0.26261
STM4314	STM4314	putative regulatory protein	**0.01**	0.98622
STM4314	STM4314	putative regulatory protein	**0.26**	0.52511
STM4315	STM4315	putative DNA-binding protein	**0.63**	0.29510
STM4315	STM4315	putative DNA-binding protein	**1.36**	0.08059
STM4317	STM4317	hypothetical protein STM4317	**-0.39**	0.33587
STM4317	STM4317	hypothetical protein STM4317	**0.14**	0.84249
STM4318	STM4318	putative acetyltransferase	**-0.57**	0.25460
STM4318	STM4318	putative acetyltransferase	**-0.51**	0.24520
STM4319	phoN	non-specific acid phosphatase	**-1.17**	0.08983
STM4319	phoN	non-specific acid phosphatase	**-0.74**	0.16281
STM4322	yjdC	putative regulatory protein	**-0.04**	0.93011
STM4322	yjdC	putative regulatory protein	**0.09**	0.86233
STM4323	dsbD	thiol:disulfide interchange protein precursor	**-0.44**	0.26910
STM4323	dsbD	thiol:disulfide interchange protein precursor	**0.10**	0.89004
STM4324	cutA	putative periplasmic divalent cation tolerance protein	**-0.07**	0.86680
STM4324	cutA	putative periplasmic divalent cation tolerance protein	**0.76**	0.17139
STM4325	dcuA	anaerobic C4-dicarboxylate transporter	**-0.21**	0.56040
STM4325	dcuA	anaerobic C4-dicarboxylate transporter	**0.00**	0.99938
STM4326	aspA	aspartate ammonia-lyase	**0.18**	0.74481
STM4326	aspA	aspartate ammonia-lyase	**0.01**	0.98976
STM4327	fxsA	suppressor of F exclusion of bacteriophage T7	**-0.37**	0.55956
STM4327	fxsA	suppressor of F exclusion of bacteriophage T7	**-0.34**	0.40947
STM4328	yjeH	putative transporter	**-0.06**	0.88998
STM4328	yjeH	putative transporter	**-0.18**	0.65762
STM4329	groES	co-chaperonin GroES	**-0.27**	0.57021
STM4329	groES	co-chaperonin GroES	**-0.13**	0.78257
STM4330	groEL	chaperonin GroEL	**-1.03**	0.13206

STM4330	groEL	chaperonin GroEL	**-1.07**	0.08174
STM4331	yjeI	putative outer membrane lipoprotein	**-0.40**	0.31280
STM4331	yjeI	putative outer membrane lipoprotein	**-0.35**	0.39238
STM4332	yjeJ	putative inner membrane protein	**-0.34**	0.34193
STM4332	yjeJ	putative inner membrane protein	**-0.21**	0.61201
STM4333	yjeK	putative aminomutase	**-0.48**	0.24995
STM4333	yjeK	putative aminomutase	**0.03**	0.96228
STM4334	efp	elongation factor P	**-0.29**	0.45676
STM4334	efp	elongation factor P	**0.24**	0.63688
STM4335	ecnA	putative entericidin A precursor	**-0.04**	0.95025
STM4335	ecnA	putative entericidin A precursor	**0.18**	0.63955
STM4337	ecnR	putative regulatory protein	**-0.43**	0.34201
STM4337	ecnR	putative regulatory protein	**-0.09**	0.88977
STM4338	sugE	putative DMT superfamily transport protein	**-0.26**	0.52543
STM4338	sugE	putative DMT superfamily transport protein	**-0.12**	0.82637
STM4339	blc	outer membrane lipoprotein precursor	**-0.04**	0.94050
STM4339	blc	outer membrane lipoprotein precursor	**0.59**	0.22602
STM4340	frdD	fumarate reductase subunit D	**-0.08**	0.87999
STM4340	frdD	fumarate reductase subunit D	**0.24**	0.56860
STM4341	frdC	fumarate reductase subunit C	**0.14**	0.74669
STM4341	frdC	fumarate reductase subunit C	**-0.09**	0.85743
STM4342	frdB	succinate dehydrogenase	**0.43**	0.36942
STM4342	frdB	succinate dehydrogenase	**0.62**	0.17754
STM4343	frdA	fumarate reductase	**0.04**	0.94180
STM4343	frdA	fumarate reductase	**0.64**	0.17139
STM4344	yjeA	lysyl-tRNA synthetase	**-0.33**	0.46184
STM4344	yjeA	lysyl-tRNA synthetase	**-0.30**	0.62682
STM4345	yjeM	putative amino-acid transport protein	**-0.32**	0.65730
STM4345	yjeM	putative amino-acid transport protein	**0.08**	0.89617
STM4346	yjeO	putative inner membrane protein	**-0.01**	0.99182
STM4346	yjeO	putative inner membrane protein	**0.00**	0.99770
STM4347	yjeP	putative periplasmic binding protein	**-0.14**	0.79176
STM4347	yjeP	putative periplasmic binding protein	**0.07**	0.87910
STM4348	psd	phosphatidylserine decarboxylase	**-0.39**	0.30501
STM4348	psd	phosphatidylserine decarboxylase	**0.07**	0.86702
STM4349	yjeQ	ribosome-associated GTPase	**0.06**	0.88705
STM4349	yjeQ	ribosome-associated GTPase	**0.15**	0.80571
STM4350	orn	oligoribonuclease	**-0.22**	0.61170
STM4350	orn	oligoribonuclease	**0.33**	0.42811
STM4351	STM4351	putative arginine-binding periplasmic protein	**-0.05**	0.93367
STM4351	STM4351	putative arginine-binding periplasmic protein	**-0.01**	0.98749
STM4355,S	yjeS	putative FeS protein	**-0.85**	0.14285
STM4355,S	yjeS	putative FeS protein	**-0.31**	0.50572
STM4356	yjeF	putative sugar kinase	**-0.26**	0.65025
STM4356	yjeF	putative sugar kinase	**0.05**	0.90733
STM4357	yjeE	putative nucleotide-binding protein	**0.01**	0.98034
STM4357	yjeE	putative nucleotide-binding protein	**0.23**	0.56565
STM4358	amiB	N-acetylmuramoyl-l-alanine amidase II	**-0.06**	0.91459
STM4358	amiB	N-acetylmuramoyl-l-alanine amidase II	**-0.05**	0.93970
STM4359	mutL	DNA mismatch repair protein	**-0.28**	0.48668
STM4359	mutL	DNA mismatch repair protein	**0.02**	0.97333
STM4360	miaA	tRNA delta(2)-isopentenylpyrophosphate transferase	**-0.05**	0.92637
STM4360	miaA	tRNA delta(2)-isopentenylpyrophosphate transferase	**0.10**	0.81359
STM4361	hfq	RNA-binding protein Hfq	**-0.11**	0.78973
STM4361	hfq	RNA-binding protein Hfq	**-0.02**	0.96018
STM4362	hflX	putative GTP-ase	**-0.04**	0.95412
STM4362	hflX	putative GTP-ase	**0.13**	0.78016
STM4363	hflK	FtsH modulator	**-0.25**	0.58624
STM4363	hflK	FtsH modulator	**-0.17**	0.81383
STM4364	hflC	FtsH modulator	**-0.16**	0.64335
STM4364	hflC	FtsH modulator	**0.13**	0.78335
STM4365	yjeT	putative inner membrane protein	**-0.35**	0.34553
STM4365	yjeT	putative inner membrane protein	**0.11**	0.77411

STM4366	purA	adenylosuccinate synthetase	**-0.47**	0.20285
STM4366	purA	adenylosuccinate synthetase	**-0.14**	0.72149
STM4367	yjeB	putative negative regulator	**-0.25**	0.51697
STM4367	yjeB	putative negative regulator	**0.24**	0.54624
STM4368	vacB	putative exoribonuclease	**-0.21**	0.64921
STM4368	vacB	putative exoribonuclease	**0.03**	0.95565
STM4369	yjfH	putative tRNA/rRNA methyltransferase	**-0.09**	0.83897
STM4369	yjfH	putative tRNA/rRNA methyltransferase	**-0.22**	0.66768
STM4370	yjfI	putative cytoplasmic protein	**-0.10**	0.86828
STM4370	yjfI	putative cytoplasmic protein	**0.46**	0.32848
STM4371	yjfJ	putative phage shock protein A	**0.40**	0.58541
STM4371	yjfJ	putative phage shock protein A	**0.98**	0.24515
STM4372	STM4372	putative potassium channels	**-0.27**	0.48590
STM4372	STM4372	putative potassium channels	**0.10**	0.82637
STM4373	yjfK	putative cytoplasmic protein	**-0.25**	0.64394
STM4373	yjfK	putative cytoplasmic protein	**0.35**	0.41541
STM4374	yjfL	putative inner membrane protein	**-0.04**	0.97333
STM4374	yjfL	putative inner membrane protein	**0.42**	0.42811
STM4375	yjfM	putative inner membrane protein	**-0.44**	0.34553
STM4375	yjfM	putative inner membrane protein	**-0.08**	0.89529
STM4376	yjfC	putative glutathionylspermidine synthase	**-0.32**	0.49932
STM4376	yjfC	putative glutathionylspermidine synthase	**0.13**	0.85465
STM4377	aidB	putative acyl-CoA dehydrogenase	**0.93**	0.52208
STM4377	aidB	putative acyl-CoA dehydrogenase	**1.69**	0.30082
STM4378	yjfN	putative inner membrane protein	**-0.15**	0.81621
STM4378	yjfN	putative inner membrane protein	**0.71**	0.17118
STM4379	yjfO	putative lipoprotein	**0.10**	0.81449
STM4379	yjfO	putative lipoprotein	**0.52**	0.27651
STM4380	yjfP	putative hydrolase	**0.05**	0.94990
STM4380	yjfP	putative hydrolase	**0.25**	0.65974
STM4381	yjfQ	putative transcriptional repressor	**-0.38**	0.55008
STM4381	yjfQ	putative transcriptional repressor	**-0.17**	0.71490
STM4382	yjfR	putative Zn-dependent hydrolase	**-0.06**	0.90071
STM4382	yjfR	putative Zn-dependent hydrolase	**-0.13**	0.78929
STM4383,S	ulaA	ascorbate-specific PTS system enzyme IIC	**0.05**	0.91584
STM4383,S	ulaA	ascorbate-specific PTS system enzyme IIC	**1.14**	0.27525
STM4384	sgaB	putative PTS enzyme II	**-0.14**	0.83102
STM4384	sgaB	putative PTS enzyme II	**0.10**	0.85372
STM4385	ptxA	putative PTS enzyme II	**-0.45**	0.27035
STM4385	ptxA	putative PTS enzyme II	**0.27**	0.79741
STM4386	sgaH	putative hexulose phosphate synthase	**0.06**	0.90797
STM4386	sgaH	putative hexulose phosphate synthase	**0.77**	0.13206
STM4387	sgaU	putative hexulose-6-phosphate isomerase	**-0.83**	0.24995
STM4387	sgaU	putative hexulose-6-phosphate isomerase	**-0.29**	0.53591
STM4388	sgaE	L-ribulose-5-phosphate 4-epimerase	**0.28**	0.42940
STM4388	sgaE	L-ribulose-5-phosphate 4-epimerase	**0.31**	0.57616
STM4389	yjfY	putative outer membrane protein	**0.02**	0.97716
STM4389	yjfY	putative outer membrane protein	**0.16**	0.74669
STM4391	rpsF	30S ribosomal protein S6	**-0.20**	0.61364
STM4391	rpsF	30S ribosomal protein S6	**-0.03**	0.94417
STM4393	rpsR	30S ribosomal protein S18	**0.18**	0.66731
STM4393	rpsR	30S ribosomal protein S18	**0.20**	0.57021
STM4394	rplI	50S ribosomal protein L9	**0.06**	0.90440
STM4394	rplI	50S ribosomal protein L9	**-0.02**	0.96805
STM4395	yifZ	putative permease	**-0.43**	0.36270
STM4395	yifZ	putative permease	**0.51**	0.26905
STM4396	ytfB	putative cell envelope opacity-associated protein A	**-0.21**	0.68136
STM4396	ytfB	putative cell envelope opacity-associated protein A	**0.14**	0.75676
STM4397	fklB	FKBP-type 22KD peptidyl-prolyl cis-trans isomerase	**-0.26**	0.55255
STM4397	fklB	FKBP-type 22KD peptidyl-prolyl cis-trans isomerase	**0.18**	0.60890
STM4398	cycA	D-alanine/D-serine/glycine transport protein	**0.17**	0.69882
STM4398	cycA	D-alanine/D-serine/glycine transport protein	**0.22**	0.62248
STM4399	ytfE	putative cell morphogenesis protein	**-0.28**	0.62867

STM4399	ytfE	putative cell morphogenesis protein	**0.30**	0.46539
STM4400	ytfF	putative cationic amino acid transporter	**0.18**	0.75479
STM4400	ytfF	putative cationic amino acid transporter	**0.66**	0.36162
STM4401	ytfG	putative reductase	**0.13**	0.85630
STM4401	ytfG	putative reductase	**0.25**	0.70229
STM4402	ytfH	putative transcriptional regulator	**-0.23**	0.54741
STM4402	ytfH	putative transcriptional regulator	**-0.14**	0.76008
STM4403	cpdB	2',3'-cyclic nucleotide 2'-phosphodiesterase/3'-nucleotidase	**-0.06**	0.91585
STM4403	cpdB	2',3'-cyclic nucleotide 2'-phosphodiesterase/3'-nucleotidase	**0.49**	0.32481
STM4404	cysQ	sulfite biosynthetic protein	**-0.40**	0.36066
STM4404	cysQ	sulfite biosynthetic protein	**0.19**	0.65431
STM4405	ytfJ	putative transcriptional regulator	**-0.38**	0.52101
STM4405	ytfJ	putative transcriptional regulator	**0.03**	0.96682
STM4406,S	ytfK	putative cytoplasmic protein	**0.19**	0.91170
STM4406,S	ytfK	putative cytoplasmic protein	**0.62**	0.61481
STM4407	ytfL	putative hemolysin-like protein	**-1.12**	0.08324
STM4407	ytfL	putative hemolysin-like protein	**-0.22**	0.70185
STM4408	msrA	methionine sulfoxide reductase A	**-0.07**	0.91387
STM4408	msrA	methionine sulfoxide reductase A	**0.16**	0.77847
STM4409	ytfM	putative outer membrane protein	**-0.07**	0.87740
STM4409	ytfM	putative outer membrane protein	**0.32**	0.45418
STM4410	ytfN	putative periplasmic protein	**0.03**	0.94426
STM4410	ytfN	putative periplasmic protein	**0.21**	0.61720
STM4411	ytfP	putative cytoplasmic protein	**-0.04**	0.93841
STM4411	ytfP	putative cytoplasmic protein	**0.01**	0.98445
STM4412	STM4412	putative permease	**-0.10**	0.86895
STM4412	STM4412	putative permease	**0.30**	0.64590
STM4413	STM4413	dihydroorotase	**-0.10**	0.90665
STM4413	STM4413	dihydroorotase	**0.18**	0.76586
STM4414	ppa	inorganic pyrophosphatase	**-0.51**	0.32859
STM4414	ppa	inorganic pyrophosphatase	**-0.29**	0.63148
STM4415	fbp	fructose-1,6-bisphosphatase	**0.20**	0.61201
STM4415	fbp	fructose-1,6-bisphosphatase	**0.23**	0.58570
STM4416	mpl	UDP-N-acetylmuramate/L-alanyl-gamma-D-glutamyl-meso-diaminopimelate	**-0.40**	0.40227
STM4416	mpl	UDP-N-acetylmuramate/L-alanyl-gamma-D-glutamyl-meso-diaminopimelate	**0.29**	0.50474
STM4417	STM4417	putative transcriptional regulator	**-0.31**	0.38552
STM4417	STM4417	putative transcriptional regulator	**0.22**	0.69797
STM4418	STM4418	sugar transporter	**-0.11**	0.81943
STM4418	STM4418	sugar transporter	**0.47**	0.45374
STM4419	STM4419	sugar transporter	**-0.38**	0.58548
STM4419	STM4419	sugar transporter	**0.77**	0.22788
STM4420	STM4420	putative inner membrane protein	**-0.24**	0.70229
STM4420	STM4420	putative inner membrane protein	**0.06**	0.94725
STM4421	STM4421	putative NAD-dependent aldehyde dehydrogenase	**-0.21**	0.74127
STM4421	STM4421	putative NAD-dependent aldehyde dehydrogenase	**0.11**	0.86861
STM4423	STM4423	putative DNA-binding protein	**-0.05**	0.94180
STM4423	STM4423	putative DNA-binding protein	**0.87**	0.22540
STM4424,S	STM4424,S	putative endonuclease	**-0.07**	0.94496
STM4424,S	STM4424,S	putative endonuclease	**0.15**	0.80002
STM4425	STM4425	putative dehydrogenase	**-0.58**	0.24520
STM4425	STM4425	putative dehydrogenase	**-0.28**	0.68136
STM4426	srfJ	lysosomal glucosyl ceramidase-like protein	**0.10**	0.84560
STM4426	srfJ	lysosomal glucosyl ceramidase-like protein	**0.51**	0.35824
STM4427	STM4427	putative endonuclease	**0.09**	0.91139
STM4427	STM4427	putative endonuclease	**0.60**	0.34541
STM4428	STM4428	hypothetical protein STM4428	**0.24**	0.56810
STM4428	STM4428	hypothetical protein STM4428	**0.35**	0.60936
STM4433	STM4433	myo-inositol 2-dehydrogenase	**-0.05**	0.95747
STM4433	STM4433	myo-inositol 2-dehydrogenase	**0.82**	0.11690

STM4434	STM4434	putative permease	**-0.40**	0.43219
STM4434	STM4434	putative permease	**0.14**	0.72580
STM4435	STM4435	putative cytoplasmic protein	**-0.28**	0.46088
STM4435	STM4435	putative cytoplasmic protein	**0.22**	0.66837
STM4436	STM4436	putative endonuclease	**-0.66**	0.19398
STM4436	STM4436	putative endonuclease	**-0.29**	0.43550
STM4437	yjgA	hypothetical protein STM4437	**-0.36**	0.53686
STM4437	yjgA	hypothetical protein STM4437	**-0.27**	0.72976
STM4438	pmbA	putative antibiotic maturation protein	**-0.12**	0.78211
STM4438	pmbA	putative antibiotic maturation protein	**-0.18**	0.72104
STM4439	cybC	cytochrome b562	**-0.40**	0.32172
STM4439	cybC	cytochrome b562	**-0.15**	0.77923
STM4440	STM4440	putative cytoplasmic protein	**-0.05**	0.92759
STM4440	STM4440	putative cytoplasmic protein	**0.02**	0.96785
STM4441	STM4441	putative cytoplasmic protein	**-0.12**	0.89445
STM4441	STM4441	putative cytoplasmic protein	**-0.24**	0.62216
STM4442	STM4442	putative cytoplasmic protein	**0.20**	0.69474
STM4442	STM4442	putative cytoplasmic protein	**0.60**	0.21501
STM4443	STM4443	putative inner membrane protein	**-0.67**	0.15276
STM4443	STM4443	putative inner membrane protein	**0.07**	0.87727
STM4444	STM4444	putative inner membrane protein	**-0.34**	0.52728
STM4444	STM4444	putative inner membrane protein	**0.50**	0.38668
STM4445	STM4445	dihydroorotase	**-0.30**	0.59509
STM4445	STM4445	dihydroorotase	**0.63**	0.30162
STM4446	STM4446	putative selenocysteine synthase	**-0.08**	0.91387
STM4446	STM4446	putative selenocysteine synthase	**0.11**	0.80672
STM4447	STM4447	putative periplasmic protein	**-0.19**	0.66969
STM4447	STM4447	putative periplasmic protein	**0.40**	0.45664
STM4448	STM4448	putative phosphotransferase system mannitol/fructose-specific IIA	**-0.24**	0.54624
STM4448	STM4448	putative phosphotransferase system mannitol/fructose-specific IIA	**0.31**	0.51973
STM4449	STM4449	putative regulatory protein	**-0.25**	0.61443
STM4449	STM4449	putative regulatory protein	**0.17**	0.76240
STM4450	STM4450	putative inner membrane protein	**-0.26**	0.52402
STM4450	STM4450	putative inner membrane protein	**0.45**	0.42732
STM4451	nrdG	anaerobic ribonucleotide reductase activating protein	**0.06**	0.91531
STM4451	nrdG	anaerobic ribonucleotide reductase activating protein	**0.24**	0.54136
STM4452	nrdD	anaerobic ribonucleoside triphosphate reductase	**-0.54**	0.22393
STM4452	nrdD	anaerobic ribonucleoside triphosphate reductase	**0.27**	0.64489
STM4452,1N	STM4452,1N	hypothetical protein STM4452,1N	**-0.09**	0.89487
STM4452,1N	STM4452,1N	hypothetical protein STM4452,1N	**0.12**	0.81323
STM4453	treC	trehalose-6-phosphate hydrolase	**-0.37**	0.46266
STM4453	treC	trehalose-6-phosphate hydrolase	**0.32**	0.65128
STM4455	treR	trehalose repressor	**0.26**	0.83190
STM4455	treR	trehalose repressor	**0.86**	0.15466
STM4456	mgtA	Mg2+ ATPase transporter	**-0.67**	0.13824
STM4456	mgtA	Mg2+ ATPase transporter	**-0.44**	0.32770
STM4457	STM4457	putative transposase	**-0.44**	0.42957
STM4457	STM4457	putative transposase	**-0.48**	0.39069
STM4458	yjgF	putative translation initiation inhibitor	**-0.15**	0.76008
STM4458	yjgF	putative translation initiation inhibitor	**0.04**	0.95608
STM4459	pyrI	aspartate carbamoyltransferase regulatory subunit	**-0.47**	0.28030
STM4459	pyrI	aspartate carbamoyltransferase regulatory subunit	**-0.19**	0.59096
STM4460	pyrB	aspartate carbamoyltransferase catalytic subunit	**-0.14**	0.76553
STM4460	pyrB	aspartate carbamoyltransferase catalytic subunit	**-0.10**	0.81709
STM4463	STM4463	putative arginine repressor	**-0.53**	0.18447
STM4463	STM4463	putative arginine repressor	**0.02**	0.97645
STM4464	STM4464	putative arginine repressor	**0.08**	0.86289
STM4464	STM4464	putative arginine repressor	**1.19**	0.18052
STM4465	STM4465	ornithine carbamoyltransferase	**0.22**	0.72413
STM4465	STM4465	ornithine carbamoyltransferase	**0.74**	0.21393
STM4466	STM4466	carbamate kinase	**0.28**	0.41715

STM4466	STM4466	carbamate kinase	**0.55**	0.29930
STM4467	STM4467	arginine deiminase	**-0.07**	0.91937
STM4467	STM4467	arginine deiminase	**0.58**	0.32481
STM4468	yjgK	putative cytoplasmic protein	**-0.22**	0.70545
STM4468	yjgK	putative cytoplasmic protein	**0.40**	0.58387
STM4469	argI	ornithine carbamoyltransferase	**-0.82**	0.34432
STM4469	argI	ornithine carbamoyltransferase	**0.02**	0.98124
STM4470	yjgD	putative cytoplasmic protein	**-0.51**	0.27043
STM4470	yjgD	putative cytoplasmic protein	**0.18**	0.63003
STM4471	miaE	hydroxylase	**-0.10**	0.82428
STM4471	miaE	hydroxylase	**0.09**	0.89130
STM4472	ytgA	putative inner membrane protein	**-0.55**	0.40820
STM4472	ytgA	putative inner membrane protein	**-0.10**	0.85718
STM4473	yjgM	putative acetyltransferase	**-0.34**	0.40020
STM4473	yjgM	putative acetyltransferase	**-0.05**	0.94453
STM4474	yjgN	putative inner membrane protein	**-0.27**	0.48447
STM4474	yjgN	putative inner membrane protein	**0.07**	0.89979
STM4475	valS	valyl-tRNA synthetase	**-0.15**	0.77801
STM4475	valS	valyl-tRNA synthetase	**0.08**	0.90797
STM4476,S	holC	DNA polymerase III subunit chi	**0.01**	0.98790
STM4476,S	holC	DNA polymerase III subunit chi	**-0.04**	0.96107
STM4477	pepA	leucyl aminopeptidase	**0.00**	0.99882
STM4477	pepA	leucyl aminopeptidase	**0.07**	0.88813
STM4479	yjgP	putative permease	**-0.18**	0.65271
STM4479	yjgP	putative permease	**-0.08**	0.86839
STM4480	yjgQ	putative permease	**-0.28**	0.46464
STM4480	yjgQ	putative permease	**-0.33**	0.55403
STM4481	idnR	L-idonate regulator	**0.00**	0.99729
STM4481	idnR	L-idonate regulator	**0.43**	0.42811
STM4482	idnT	L-idonate transport protein	**-0.34**	0.55008
STM4482	idnT	L-idonate transport protein	**0.34**	0.54656
STM4483	idnO	gluconate 5-dehydrogenase	**-0.68**	0.17139
STM4483	idnO	gluconate 5-dehydrogenase	**0.09**	0.88647
STM4484	idnD	L-idonate 5-dehydrogenase	**-0.30**	0.65549
STM4484	idnD	L-idonate 5-dehydrogenase	**0.86**	0.11913
STM4485	idnK	thermosensitive D-gluconate kinase	**0.11**	0.88339
STM4485	idnK	thermosensitive D-gluconate kinase	**0.07**	0.93485
STM4486	yjgB	putative alcohol dehydrogenase	**-0.06**	0.91653
STM4486	yjgB	putative alcohol dehydrogenase	**0.29**	0.74872
STM4487	leuX	STM4487	**-0.34**	0.38276
STM4487	leuX	STM4487	**0.33**	0.37342
STM4488	STM4488	putative integrase	**-0.26**	0.53678
STM4488	STM4488	putative integrase	**0.84**	0.21747
STM4489	STM4489	putative DNA helicases	**-0.09**	0.83524
STM4489	STM4489	putative DNA helicases	**0.08**	0.90733
STM4490	STM4490	putative restriction endonuclease	**0.02**	0.96785
STM4490	STM4490	putative restriction endonuclease	**0.31**	0.55976
STM4491	STM4491	putative ATP-dependent Lon protease	**-0.30**	0.57419
STM4491	STM4491	putative ATP-dependent Lon protease	**-0.29**	0.54461
STM4492	STM4492	putative cytoplasmic protein	**-0.02**	0.97095
STM4492	STM4492	putative cytoplasmic protein	**-0.18**	0.73093
STM4493	STM4493	putative cytoplasmic protein	**0.24**	0.64185
STM4493	STM4493	putative cytoplasmic protein	**0.33**	0.41391
STM4494	STM4494	putative ABC-type sugar/spermidine/putrescine transport system	**-0.09**	0.82192
STM4494	STM4494	putative ABC-type sugar/spermidine/putrescine transport system	**0.09**	0.87512
STM4495	STM4495	putative type II restriction enzyme methylase subunit	**-0.03**	0.96317
STM4495	STM4495	putative type II restriction enzyme methylase subunit	**0.08**	0.87078
STM4496	STM4496	putative DNA repair ATPase	**-0.28**	0.52334
STM4496	STM4496	putative DNA repair ATPase	**0.14**	0.81075
STM4497	STM4497	putative cytoplasmic protein	**0.17**	0.76240
STM4497	STM4497	putative cytoplasmic protein	**0.02**	0.96851

STM4498	STM4498	putative inner membrane protein	**0.34**	0.38351
STM4498	STM4498	putative inner membrane protein	**0.25**	0.52861
STM4499	yeeN	hypothetical protein STM4499	**-0.22**	0.65854
STM4499	yeeN	hypothetical protein STM4499	**-0.15**	0.72375
STM4500	yjhP	putative SAM-dependent methyltransferase	**-0.76**	0.23999
STM4500	yjhP	putative SAM-dependent methyltransferase	**0.01**	0.99417
STM4501	STM4501	putative cytoplasmic protein	**-0.52**	0.29562
STM4501	STM4501	putative cytoplasmic protein	**-0.12**	0.81862
STM4502	STM4502	putative cytoplasmic protein	**-0.26**	0.72120
STM4502	STM4502	putative cytoplasmic protein	**0.09**	0.85766
STM4503	STM4503	putative inner membrane protein	**0.37**	0.41812
STM4503	STM4503	putative inner membrane protein	**1.08**	0.11913
STM4504	STM4504	putative cytoplasmic protein	**-0.25**	0.66218
STM4504	STM4504	putative cytoplasmic protein	**-1.44**	0.51300
STM4505	STM4505	hypothetical protein STM4505	**-0.62**	0.26261
STM4505	STM4505	hypothetical protein STM4505	**0.09**	0.89675
STM4506	STM4506	putative dienelactone hydrolase	**-0.18**	0.77847
STM4506	STM4506	putative dienelactone hydrolase	**-0.06**	0.94811
STM4507	uxuR	uxu operon transcriptional repressor	**0.45**	0.23853
STM4507	uxuR	uxu operon transcriptional repressor	**0.80**	0.17139
STM4508	trpS2	tryptophanyl-tRNA synthetase	**-0.76**	0.19236
STM4508	trpS2	tryptophanyl-tRNA synthetase	**-0.14**	0.72143
STM4508,1N	STM4508,1N	hypothetical protein STM4508,1N	**-0.06**	0.94567
STM4508,1N	STM4508,1N	hypothetical protein STM4508,1N	**-0.17**	0.82518
STM4509,S	STM4509,S	putative cytoplasmic protein	**0.25**	0.81325
STM4509,S	STM4509,S	putative cytoplasmic protein	**0.55**	0.40008
STM4510	STM4510	putative aspartate racemase	**-0.62**	0.21015
STM4510	STM4510	putative aspartate racemase	**0.55**	0.25895
STM4511	yjiE	putative transcriptional regulator	**-0.49**	0.39260
STM4511	yjiE	putative transcriptional regulator	**1.01**	0.31280
STM4512	iadA	isoaspartyl dipeptidase	**-0.44**	0.46720
STM4512	iadA	isoaspartyl dipeptidase	**0.48**	0.34553
STM4513	yjiG	putative permease	**-0.09**	0.83497
STM4513	yjiG	putative permease	**0.18**	0.70966
STM4514,S	yjiH	putative inner membrane protein	**-0.42**	0.61811
STM4514,S	yjiH	putative inner membrane protein	**0.10**	0.85378
STM4515	yjiJ	putative sugar transporter	**-0.48**	0.25460
STM4515	yjiJ	putative sugar transporter	**-0.09**	0.89212
STM4516	yjiN	putative inner membrane protein	**0.71**	0.29796
STM4516	yjiN	putative inner membrane protein	**1.29**	0.08647
STM4517	yjiO	putative transport protein	**0.08**	0.90462
STM4517	yjiO	putative transport protein	**-0.13**	0.83103
STM4518	STM4518	putative inner membrane protein	**0.17**	0.89811
STM4518	STM4518	putative inner membrane protein	**0.85**	0.30956
STM4519	STM4519	putative NAD-dependent aldehyde dehydrogenase	**-0.06**	0.93367
STM4519	STM4519	putative NAD-dependent aldehyde dehydrogenase	**-0.04**	0.94050
STM4522	STM4522	putative inner membrane protein	**-0.82**	0.21067
STM4522	STM4522	putative inner membrane protein	**-0.20**	0.81763
STM4523	yjiW	putative SOS response protein	**-0.31**	0.36543
STM4523	yjiW	putative SOS response protein	**0.52**	0.40947
STM4524	hsdS	type I restriction enzyme specificity protein	**-0.14**	0.79233
STM4524	hsdS	type I restriction enzyme specificity protein	**0.23**	0.69189
STM4525	hsdM	DNA methylase M	**-0.41**	0.35014
STM4525	hsdM	DNA methylase M	**-0.18**	0.74583
STM4526	hsdR	endonuclease R	**-0.21**	0.61335
STM4526	hsdR	endonuclease R	**0.57**	0.26213
STM4527	mrr	restriction endonuclease	**-0.43**	0.27312
STM4527	mrr	restriction endonuclease	**0.45**	0.38596
STM4528	STM4528	putative inner membrane protein	**-0.23**	0.64371
STM4528	STM4528	putative inner membrane protein	**0.64**	0.41024
STM4529	STM4529	putative cytoplasmic protein	**-0.58**	0.23892
STM4529	STM4529	putative cytoplasmic protein	**0.06**	0.93023
STM4530	yjiA	putative cobalamin biosynthetic protein	**0.91**	0.56913

STM4530	yjiA	putative cobalamin biosynthetic protein	**-0.14**	0.94470
STM4531	yjiX	putative cytoplasmic protein	**-0.20**	0.77967
STM4531	yjiX	putative cytoplasmic protein	**0.24**	0.65730
STM4532	yjiY	putative carbon starvation protein	**0.12**	0.87727
STM4532	yjiY	putative carbon starvation protein	**0.54**	0.18622
STM4533	tsr	methyl-accepting chemotaxis protein I	**-0.48**	0.21015
STM4533	tsr	methyl-accepting chemotaxis protein I	**0.06**	0.93033
STM4534	STM4534	putative transcriptional regulator	**-0.27**	0.69963
STM4534	STM4534	putative transcriptional regulator	**0.20**	0.81929
STM4535	STM4535	putative PTS permease	**-0.03**	0.96850
STM4535	STM4535	putative PTS permease	**-0.32**	0.65730
STM4536	STM4536	putative PTS permease	**0.07**	0.94675
STM4536	STM4536	putative PTS permease	**1.37**	0.22049
STM4537	STM4537	putative PTS permease	**0.01**	0.98658
STM4537	STM4537	putative PTS permease	**0.83**	0.30560
STM4538	STM4538	putative PTS permease	**-0.94**	0.13206
STM4538	STM4538	putative PTS permease	**-0.02**	0.97513
STM4539	STM4539	putative glucosamine-fructose-6-phosphate aminotransferase	**-0.40**	0.35788
STM4539	STM4539	putative glucosamine-fructose-6-phosphate aminotransferase	**0.08**	0.87655
STM4540,S	STM4540,S	putative glucosamine-fructose-6-phosphate aminotransferase	**-0.81**	0.10754
STM4540,S	STM4540,S	putative glucosamine-fructose-6-phosphate aminotransferase	**-0.58**	0.19967
STM4541	mdoB	phosphoglycerol transferase I	**-1.72**	0.01174
STM4541	mdoB	phosphoglycerol transferase I	**-0.86**	0.15276
STM4542	yjjA	putative outer membrane protein	**-0.19**	0.65228
STM4542	yjjA	putative outer membrane protein	**-0.10**	0.79442
STM4543	dnaC	DNA replication protein DnaC	**-0.60**	0.37154
STM4543	dnaC	DNA replication protein DnaC	**0.28**	0.59704
STM4544	dnaT	primosomal protein I	**-0.27**	0.45069
STM4544	dnaT	primosomal protein I	**0.19**	0.76184
STM4545	STM4545	putative inner membrane protein	**-0.24**	0.58934
STM4545	STM4545	putative inner membrane protein	**-0.19**	0.78846
STM4546	yjjP	hypothetical protein STM4546	**-0.31**	0.46199
STM4546	yjjP	hypothetical protein STM4546	**-0.18**	0.73690
STM4547	yjjQ	putative transcriptional regulator	**-0.87**	0.25964
STM4547	yjjQ	putative transcriptional regulator	**-0.27**	0.67012
STM4548	bglJ	bgl operon transcriptional activator	**-0.08**	0.87496
STM4548	bglJ	bgl operon transcriptional activator	**-0.05**	0.94765
STM4549	STM4549	putative cytoplasmic protein	**-0.50**	0.20922
STM4549	STM4549	putative cytoplasmic protein	**0.01**	0.98894
STM4550	fhuF	ferric hydrozamate transport protein	**-0.08**	0.85257
STM4550	fhuF	ferric hydrozamate transport protein	**0.41**	0.34201
STM4551	STM4551	hypothetical protein STM4551	**-0.38**	0.52765
STM4551	STM4551	hypothetical protein STM4551	**-0.06**	0.94450
STM4552	STM4552	putative inner membrane protein	**-0.43**	0.39069
STM4552	STM4552	putative inner membrane protein	**0.19**	0.73653
STM4556	rsmC	16S ribosomal RNA m2G1207 methyltransferase	**-0.35**	0.47844
STM4556	rsmC	16S ribosomal RNA m2G1207 methyltransferase	**-0.11**	0.79275
STM4558	rimI	ribosomal-protein-alanine N-acetyltransferase	**-0.01**	0.98539
STM4558	rimI	ribosomal-protein-alanine N-acetyltransferase	**0.34**	0.36311
STM4559,S	yjjG	nucleotidase	**0.12**	0.80637
STM4559,S	yjjG	nucleotidase	**0.16**	0.73473
STM4560	prfC	peptide chain release factor 3	**-0.25**	0.58613
STM4560	prfC	peptide chain release factor 3	**0.01**	0.98551
STM4561	osmY	hyperosmotically-inducible periplasmic protein	**-0.20**	0.63380
STM4561	osmY	hyperosmotically-inducible periplasmic protein	**0.24**	0.63196
STM4562	STM4562	putative inner membrane protein	**0.05**	0.92506
STM4562	STM4562	putative inner membrane protein	**0.35**	0.35755
STM4563	yjjU	putative phosphoesterase	**-0.11**	0.85174
STM4563	yjjU	putative phosphoesterase	**-0.01**	0.99260

STM4564	yjjV	putative hydrolase	**0.04**	0.97219
STM4564	yjjV	putative hydrolase	**0.04**	0.95380
STM4565	yjjW	pyruvate formate lyase-activating enzyme	**-0.09**	0.83414
STM4565	yjjW	pyruvate formate lyase-activating enzyme	**0.76**	0.17085
STM4566	yjjI	putative cytoplasmic protein	**-0.80**	0.12889
STM4566	yjjI	putative cytoplasmic protein	**-0.07**	0.88977
STM4567	deoC	deoxyribose-phosphate aldolase	**0.34**	0.57827
STM4567	deoC	deoxyribose-phosphate aldolase	**0.34**	0.56129
STM4568	deoA	thymidine phosphorylase	**0.34**	0.41676
STM4568	deoA	thymidine phosphorylase	**0.38**	0.37342
STM4569	deoB	phosphopentomutase	**-0.17**	0.67121
STM4569	deoB	phosphopentomutase	**0.09**	0.87019
STM4570	deoD	purine nucleoside phosphorylase	**-0.64**	0.15276
STM4570	deoD	purine nucleoside phosphorylase	**-0.46**	0.29664
STM4571	STM4571	putative outer membrane protein	**-0.10**	0.87078
STM4571	STM4571	putative outer membrane protein	**-0.02**	0.97776
STM4572	stjB	putative fimbrial usher protein	**-0.52**	0.39186
STM4572	stjB	putative fimbrial usher protein	**0.02**	0.96850
STM4573	stjC	putative fimbrial chaperone	**-0.09**	0.91456
STM4573	stjC	putative fimbrial chaperone	**-0.15**	0.87909
STM4574	STM4574	putative outer membrane protein	**-0.17**	0.79816
STM4574	STM4574	putative outer membrane protein	**0.14**	0.77148
STM4575	STM4575	putative outer membrane protein	**-0.31**	0.53124
STM4575	STM4575	putative outer membrane protein	**-0.04**	0.94527
STM4576	lplA	lipoate-protein ligase A	**-0.86**	0.19142
STM4576	lplA	lipoate-protein ligase A	**-0.24**	0.73415
STM4577	smp	hypothetical protein STM4577	**0.04**	0.93410
STM4577	smp	hypothetical protein STM4577	**0.37**	0.53655
STM4578	serB	3-phosphoserine phosphatase	**-0.18**	0.79056
STM4578	serB	3-phosphoserine phosphatase	**0.24**	0.53840
STM4579	radA	putative ATP-dependent protease	**-0.01**	0.98718
STM4579	radA	putative ATP-dependent protease	**0.09**	0.86102
STM4580,S	nadR	nicotinamide-nucleotide adenylyltransferase	**-0.24**	0.55956
STM4580,S	nadR	nicotinamide-nucleotide adenylyltransferase	**0.01**	0.98855
STM4581	yjjK	putative transport protein	**-0.35**	0.34812
STM4581	yjjK	putative transport protein	**0.32**	0.46629
STM4582	slt	soluble lytic murein transglycosylase	**0.07**	0.91917
STM4582	slt	soluble lytic murein transglycosylase	**0.20**	0.69882
STM4583	trpR	Trp operon repressor	**-0.59**	0.22540
STM4583	trpR	Trp operon repressor	**-0.43**	0.26910
STM4584	yjjX	hypothetical protein STM4584	**0.13**	0.75017
STM4584	yjjX	hypothetical protein STM4584	**0.12**	0.79180
STM4585	gpmB	phosphoglycerate mutase	**-0.05**	0.91170
STM4585	gpmB	phosphoglycerate mutase	**0.25**	0.47844
STM4586	rob	transcriptional regulator	**0.20**	0.62827
STM4586	rob	transcriptional regulator	**-0.03**	0.95059
STM4587	creA	putative periplasmic protein	**0.03**	0.96278
STM4587	creA	putative periplasmic protein	**0.15**	0.75190
STM4588	creB	response regulator	**-0.20**	0.65353
STM4588	creB	response regulator	**0.38**	0.39302
STM4589	creC	sensor kinase	**0.12**	0.79308
STM4589	creC	sensor kinase	**0.56**	0.32016
STM4590	creD	colicin E2 tolerance protein	**-1.01**	0.18710
STM4590	creD	colicin E2 tolerance protein	**-0.25**	0.64330
STM4591	sthE	putative major fimbrial subunit	**-0.06**	0.95318
STM4591	sthE	putative major fimbrial subunit	**-0.23**	0.65709
STM4592	sthD	putative fimbrial subunit	**-0.31**	0.56303
STM4592	sthD	putative fimbrial subunit	**0.00**	0.99997
STM4593	sthB	putative fimbrial usher protein	**-0.82**	0.11913
STM4593	sthB	putative fimbrial usher protein	**-0.27**	0.68537
STM4594	sthA	putative fimbrial chaperone	**-0.31**	0.63777
STM4594	sthA	putative fimbrial chaperone	**0.36**	0.36304
STM4595	STM4595	putative fimbrial chaperone	**-0.13**	0.80045

STM4595	STM4595	putative fimbrial chaperone	**0.30**	0.70229
STM4596	STM4596	putative inner membrane protein	**-0.32**	0.49871
STM4596	STM4596	putative inner membrane protein	**0.39**	0.48014
STM4597	STM4597	putative periplasmic protein	**-0.34**	0.36543
STM4597	STM4597	putative periplasmic protein	**-0.39**	0.36703
STM4598	arcA	response regulator	**-0.22**	0.56222
STM4598	arcA	response regulator	**0.04**	0.92161
STM4600	lasT	putative tRNA/tRNA methyltransferase	**0.09**	0.87796
STM4600	lasT	putative tRNA/tRNA methyltransferase	**0.28**	0.45968
PSLT001	PSLT001	putative cytoplasmic protein	**-0.09**	0.83507
PSLT001	PSLT001	putative cytoplasmic protein	**0.15**	0.70144
PSLT002	PSLT002	putative phospholipase D	**-1.02**	0.21198
PSLT002	PSLT002	putative phospholipase D	**-0.38**	0.51952
PSLT006	repA	DNA replication protein	**-0.33**	0.43439
PSLT006	repA	DNA replication protein	**0.48**	0.32760
PSLT008	srgC	putative regulatory protein	**-0.68**	0.22602
PSLT008	srgC	putative regulatory protein	**-0.02**	0.96797
PSLT009	rcK	resistance to complement killing	**-0.17**	0.62988
PSLT009	rcK	resistance to complement killing	**0.01**	0.98355
PSLT010	srgB	putative outer membrane protein	**-0.83**	0.56654
PSLT010	srgB	putative outer membrane protein	**0.27**	0.81830
PSLT010	srgB	putative outer membrane protein	**0.69**	0.34051
PSLT010	srgB	putative outer membrane protein	**0.85**	0.33465
PSLT011	srgA	putative thiol-disulfide isomerase or thioredoxin	**-0.48**	0.62069
PSLT011	srgA	putative thiol-disulfide isomerase or thioredoxin	**0.23**	0.58995
PSLT012	orf7	putative bacterial regulatory protein	**-0.59**	0.36162
PSLT012	orf7	putative bacterial regulatory protein	**0.07**	0.89790
PSLT013	pefI	regulator	**-0.47**	0.37454
PSLT013	pefI	regulator	**-0.03**	0.96650
PSLT014	orf6	putative outer membrane protein	**-0.29**	0.72271
PSLT014	orf6	putative outer membrane protein	**-0.06**	0.91170
PSLT015	orf5	putative outer membrane protein	**-0.21**	0.86190
PSLT015	orf5	putative outer membrane protein	**-0.46**	0.40399
PSLT016	pefD	chaperone	**0.78**	0.22283
PSLT016	pefD	chaperone	**1.28**	0.22088
PSLT017	pefC	usher protein	**-0.21**	0.56179
PSLT017	pefC	usher protein	**-0.53**	0.42254
PSLT018	pefA	major fimbrial subunit	**-1.19**	0.11224
PSLT018	pefA	major fimbrial subunit	**-0.21**	0.66677
PSLT019	pefB	regulatory protein	**-0.15**	0.79313
PSLT019	pefB	regulatory protein	**1.12**	0.13813
PSLT023	repA2	DNA replication protein	**-0.73**	0.15736
PSLT023	repA2	DNA replication protein	**-0.15**	0.72819
PSLT025	PSLT025	putative cytoplasmic protein	**-0.20**	0.79233
PSLT025	PSLT025	putative cytoplasmic protein	**0.37**	0.44745
PSLT026	PSLT026	putative periplasmic protein	**-0.64**	0.35937
PSLT026	PSLT026	putative periplasmic protein	**0.32**	0.76838
PSLT027	ccdA	antidote	**-0.19**	0.74243
PSLT027	ccdA	antidote	**-0.08**	0.91937
PSLT028	ccdB	toxin	**-0.80**	0.19398
PSLT028	ccdB	toxin	**0.10**	0.80110
PSLT029	PSLT029	putative cytoplasmic protein	**0.50**	0.31511
PSLT029	PSLT029	putative cytoplasmic protein	**0.49**	0.32444
PSLT030	PSLT030	putative cytoplasmic protein	**-0.55**	0.27312
PSLT030	PSLT030	putative cytoplasmic protein	**-0.08**	0.86912
PSLT031	rsdB	resolvase	**-0.53**	0.28861
PSLT031	rsdB	resolvase	**-0.24**	0.55338
PSLT032	PSLT032	putative diguanylate cyclase/phosphodiesterase	**-0.43**	0.38041
PSLT032	PSLT032	putative diguanylate cyclase/phosphodiesterase	**0.26**	0.56569
PSLT032,1N	PSLT032,1N	hypothetical protein PSLT032,1N	**-0.19**	0.64664
PSLT032,1N	PSLT032,1N	hypothetical protein PSLT032,1N	**-0.09**	0.85210
PSLT033	PSLT033	putative inner membrane protein	**0.49**	0.61341
PSLT033	PSLT033	putative inner membrane protein	**0.27**	0.69184

PSLT036	PSLT036	putative transposase	**-0.64**	0.34201
PSLT036	PSLT036	putative transposase	**0.94**	0.21078
PSLT037	spvD	hydrophilic protein	**-1.02**	0.17431
PSLT037	spvD	hydrophilic protein	**-0.24**	0.77974
PSLT038	spvC	hydrophilic protein	**-0.41**	0.57950
PSLT038	spvC	hydrophilic protein	**1.12**	0.13645
PSLT039	spvB	hydrophilic protein	**-0.51**	0.51052
PSLT039	spvB	hydrophilic protein	**0.37**	0.48386
PSLT040	spvA	outer membrane protein	**-0.52**	0.30956
PSLT040	spvA	outer membrane protein	**-0.06**	0.91170
PSLT041	spvR	regulator of spv operon	**-1.07**	0.30334
PSLT041	spvR	regulator of spv operon	**-0.11**	0.81896
PSLT042	PSLT042	putative integrase protein	**-1.00**	0.11690
PSLT042	PSLT042	putative integrase protein	**-0.77**	0.21951
PSLT043	PSLT043	type II secretion system protein	**-0.33**	0.38363
PSLT043	PSLT043	type II secretion system protein	**0.18**	0.79629
PSLT044	rlgA	putative integrase protein	**-0.50**	0.39186
PSLT044	rlgA	putative integrase protein	**-0.29**	0.55403
PSLT045	PSLT045	putative resolvase	**-0.50**	0.24811
PSLT045	PSLT045	putative resolvase	**-0.48**	0.29912
PSLT046	PSLT046	putative carbonic anhydrase	**-1.81**	0.02667
PSLT046	PSLT046	putative carbonic anhydrase	**-1.54**	0.05896
PSLT047	PSLT047	putative cytoplasmic protein	**-0.58**	0.27522
PSLT047	PSLT047	putative cytoplasmic protein	**0.02**	0.97720
PSLT048	tlpA	alpha-helical coiled-coil protein	**-0.47**	0.22788
PSLT048	tlpA	alpha-helical coiled-coil protein	**0.40**	0.47484
PSLT050,1N	PSLT050,1N	hypothetical protein PSLT050,1N	**-0.79**	0.36701
PSLT050,1N	PSLT050,1N	hypothetical protein PSLT050,1N	**-0.31**	0.52712
PSLT050,2N	PSLT050,2N	hypothetical protein PSLT050,2N	**-0.02**	0.97590
PSLT050,2N	PSLT050,2N	hypothetical protein PSLT050,2N	**-0.24**	0.49336
PSLT051	PSLT051	putative cytoplasmic protein	**-0.79**	0.16063
PSLT051	PSLT051	putative cytoplasmic protein	**-0.08**	0.85918
PSLT052	parA	plasmid partition protein A	**-0.01**	0.99446
PSLT052	parA	plasmid partition protein A	**0.31**	0.49811
PSLT053	parB	plasmid partition protein B	**0.28**	0.62403
PSLT053	parB	plasmid partition protein B	**0.19**	0.75730
PSLT054	samB	DNA polymerase IV	**-0.64**	0.22540
PSLT054	samB	DNA polymerase IV	**0.11**	0.78399
PSLT055	samA	SamA	**-0.35**	0.48021
PSLT055	samA	SamA	**0.81**	0.29912
PSLT056	PSLT056	putative cytoplasmic protein	**-0.36**	0.38668
PSLT056	PSLT056	putative cytoplasmic protein	**0.15**	0.78067
PSLT057	PSLT057	putative cytoplasmic protein	**-0.16**	0.65281
PSLT057	PSLT057	putative cytoplasmic protein	**0.62**	0.40431
PSLT059	PSLT059	putative adenine-specific DNA methylase	**-0.25**	0.75294
PSLT059	PSLT059	putative adenine-specific DNA methylase	**0.11**	0.82756
PSLT060	PSLT060	putative cytoplasmic protein	**-0.10**	0.82428
PSLT060	PSLT060	putative cytoplasmic protein	**0.55**	0.60427
PSLT060,1N	PSLT060,1N	hypothetical protein PSLT060,1N	**-0.31**	0.52511
PSLT060,1N	PSLT060,1N	hypothetical protein PSLT060,1N	**0.32**	0.42312
PSLT061	PSLT061	putative inner membrane protein	**-0.38**	0.33651
PSLT061	PSLT061	putative inner membrane protein	**0.36**	0.41774
PSLT062	PSLT062	putative cytoplasmic protein	**-1.65**	0.14030
PSLT062	PSLT062	putative cytoplasmic protein	**-0.59**	0.26254
PSLT063	PSLT063	putative cytoplasmic protein	**-0.12**	0.87135
PSLT063	PSLT063	putative cytoplasmic protein	**0.30**	0.63101
PSLT064	PSLT064	putative inner membrane protein	**0.00**	0.99882
PSLT064	PSLT064	putative inner membrane protein	**0.65**	0.23114
PSLT066	ssbB	single-strand DNA binding protein	**0.08**	0.86947
PSLT066	ssbB	single-strand DNA binding protein	**0.63**	0.29537
PSLT067	PSLT067	putative cytoplasmic protein	**-0.87**	0.28655
PSLT067	PSLT067	putative cytoplasmic protein	**0.01**	0.99268
PSLT068	PSLT068	putative ParB-like nuclease	**-0.26**	0.82162

PSLT068	PSLT068	putative ParB-like nuclease	**0.94**	0.19138
PSLT069	psiB	PsiB	**-0.53**	0.48386
PSLT069	psiB	PsiB	**-1.85**	0.60759
PSLT070	psiA	PsiA	**0.34**	0.54217
PSLT070	psiA	PsiA	**1.03**	0.15276
PSLT072	PSLT072	putative transglycosylase	**-0.93**	0.17765
PSLT072	PSLT072	putative transglycosylase	**0.32**	0.51549
PSLT073	traM	mating signal protein	**0.05**	0.95563
PSLT073	traM	mating signal protein	**0.11**	0.87836
PSLT075	traJ	regulatory protein	**-0.08**	0.93767
PSLT075	traJ	regulatory protein	**-0.21**	0.72129
PSLT076	traY	DNA-binding protein	**-0.66**	0.22540
PSLT076	traY	DNA-binding protein	**0.19**	0.86895
PSLT077	traA	pilus subunit	**-0.47**	0.30806
PSLT077	traA	pilus subunit	**0.34**	0.71902
PSLT078	traL	pilus assembly protein	**-1.02**	0.18763
PSLT078	traL	pilus assembly protein	**-0.46**	0.51973
PSLT079	traE	pilus assembly protein	**-0.04**	0.92637
PSLT079	traE	pilus assembly protein	**0.53**	0.44218
PSLT080	traK	pilus assembly protein	**0.16**	0.87356
PSLT080	traK	pilus assembly protein	**0.35**	0.35536
PSLT081	traB	pilus assembly protein	**-0.52**	0.33373
PSLT081	traB	pilus assembly protein	**0.04**	0.94765
PSLT082	traP	conjugative transfer protein	**-0.29**	0.46199
PSLT082	traP	conjugative transfer protein	**0.07**	0.88012
PSLT083	trbD	conjugative transfer protein	**-0.41**	0.43837
PSLT083	trbD	conjugative transfer protein	**0.22**	0.64331
PSLT084	traV	pilus assembly protein	**-0.66**	0.19843
PSLT084	traV	pilus assembly protein	**-0.09**	0.87906
PSLT085	traR	conjugative transfer protein	**-0.80**	0.15859
PSLT085	traR	conjugative transfer protein	**-0.27**	0.62988
PSLT087	PSLT087	OrfG2	**-0.91**	0.12727
PSLT087	PSLT087	OrfG2	**-0.33**	0.52861
PSLT088	traC	ATP-binding protein	**-0.66**	0.27496
PSLT088	traC	ATP-binding protein	**0.01**	0.98428
PSLT089	trbI	pilus assembly protein	**0.35**	0.76407
PSLT089	trbI	pilus assembly protein	**-0.11**	0.78016
PSLT091	traW	pilus assembly protein	**0.84**	0.66070
PSLT091	traW	pilus assembly protein	**0.46**	0.53827
PSLT092	traU	pilus assembly protein	**-0.12**	0.74713
PSLT092	traU	pilus assembly protein	**0.06**	0.89979
PSLT094	trbC	pilus assembly protein	**-0.18**	0.66893
PSLT094	trbC	pilus assembly protein	**0.75**	0.20129
PSLT094,1N	PSLT094,1N	hypothetical protein PSLT094,1N	**-0.63**	0.28905
PSLT094,1N	PSLT094,1N	hypothetical protein PSLT094,1N	**0.29**	0.51275
PSLT095	traN	mating pair stabilization protein	**0.05**	0.92723
PSLT095	traN	mating pair stabilization protein	**1.20**	0.27557
PSLT097	traF	pilus assembly protein	**-0.74**	0.15529
PSLT097	traF	pilus assembly protein	**-0.24**	0.58506
PSLT098	traQ	pilin chaperone	**-0.73**	0.19142
PSLT098	traQ	pilin chaperone	**0.37**	0.36066
PSLT099	trbB	conjugative transfer protein	**-0.97**	0.15859
PSLT099	trbB	conjugative transfer protein	**0.41**	0.31635
PSLT100	traH	pilus assembly protein	**0.29**	0.67631
PSLT100	traH	pilus assembly protein	**0.46**	0.45811
PSLT101	traG	mating pair stabilization and pilus assembly protein	**-0.15**	0.76075
PSLT101	traG	mating pair stabilization and pilus assembly protein	**0.02**	0.96785
PSLT102	traS	entry exclusion protein	**-0.20**	0.72518
PSLT102	traS	entry exclusion protein	**0.23**	0.53263
PSLT103	traT	surface exclusion protein	**-0.78**	0.27651
PSLT103	traT	surface exclusion protein	**-0.22**	0.61809
PSLT104	traD	ATP-binding protein/DNA transporter	**-0.14**	0.73473
PSLT104	traD	ATP-binding protein/DNA transporter	**0.24**	0.57070

PSLT105	trbH	conjugative transfer protein	**-0.83**	0.28285
PSLT105	trbH	conjugative transfer protein	**-0.35**	0.62617
PSLT106	PSLT106	MvpA-like protein	**-0.36**	0.46870
PSLT106	PSLT106	MvpA-like protein	**0.17**	0.64422
PSLT107	PSLT107	putative cytoplasmic protein	**-0.34**	0.42277
PSLT107	PSLT107	putative cytoplasmic protein	**0.49**	0.49117
PSLT108	traI	oriT nickase/helicase	**-0.48**	0.45188
PSLT108	traI	oriT nickase/helicase	**-0.11**	0.82350
PSLT110	traX	pilin subunit acetylation	**0.18**	0.74889
PSLT110	traX	pilin subunit acetylation	**0.31**	0.61343
PSLT111	finO	finP binding-protein	**-0.14**	0.74957
PSLT111	finO	finP binding-protein	**0.17**	0.65709

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
PSLT001	PSLT001	putative cytoplasmic protein	**1.20**	0.17334	**0.99**	0.00620	**1.07**	0.01183
PSLT001	PSLT001	putative cytoplasmic protein	**3.71**	0.00541	**1.03**	0.01011	**2.17**	0.00286
PSLT002	PSLT002	putative phospholipase D	**0.47**	0.49160	**0.95**	0.01972	**-0.94**	0.27630
PSLT002	PSLT002	putative phospholipase D	**1.20**	0.28598	**1.13**	0.01602	**0.03**	0.96184
PSLT006	repA	DNA replication protein	**3.02**	0.00660	**2.15**	0.00060	**3.28**	0.00030
PSLT006	repA	DNA replication protein	**2.81**	0.04089	**1.13**	0.01170	**1.71**	0.00234
PSLT007	-	putative outer membrane protein	**2.18**	0.19185	**-0.36**	0.19276	**0.27**	0.72025
PSLT007	-	putative outer membrane protein	**3.38**	0.09362	**-0.93**	0.06593	**0.55**	0.32803
PSLT008	srgC	putative regulatory protein	**2.32**	0.03113	**1.30**	0.00477	**0.48**	0.35423
PSLT008	srgC	putative regulatory protein	**3.58**	0.02831	**1.29**	0.00722	**1.83**	0.00193
PSLT009	rcK	resistance to complement killing	**1.68**	0.08513	**1.58**	0.00134	**-0.02**	0.97608
PSLT009	rcK	resistance to complement killing	**2.77**	0.00581	**1.29**	0.00329	**0.77**	0.10007
PSLT010	srgB	putative outer membrane protein	**0.65**	0.57569	**0.22**	0.53304	**-0.19**	0.85064
PSLT010	srgB	putative outer membrane protein	**3.62**	0.02818	**-0.49**	0.17868	**1.95**	0.02013
PSLT011	srgA	putative thiol-disulfide isomerase or thioredoxin	**1.36**	0.16559	**1.39**	0.00387	**1.86**	0.01320
PSLT011	srgA	putative thiol-disulfide isomerase or thioredoxin	**3.46**	0.00595	**1.28**	0.00995	**2.71**	0.00815
PSLT012	orf7	putative bacterial regulatory protein	**0.38**	0.47153	**1.58**	0.00543	**-0.67**	0.17075
PSLT012	orf7	putative bacterial regulatory protein	**0.92**	0.06678	**1.31**	0.00291	**-0.63**	0.09756
PSLT013	pefI	regulator	**0.77**	0.16257	**1.84**	0.00070	**-0.63**	0.24091
PSLT013	pefI	regulator	**3.00**	0.00546	**1.69**	0.00075	**-0.06**	0.91926
PSLT014	orf6	putative outer membrane protein	**-0.04**	0.96378	**2.13**	0.00177	**0.53**	0.47040
PSLT014	orf6	putative outer membrane protein	**0.84**	0.19442	**2.28**	0.00024	**0.10**	0.82181
PSLT015	orf5	putative outer membrane protein	**-1.04**	0.23254	**0.64**	0.43319	**-0.26**	0.77618
PSLT015	orf5	putative outer membrane protein	**0.49**	0.61036	**0.59**	0.10180	**-0.72**	0.10506
PSLT016	pefD	chaperone	**1.74**	0.30757	**-1.33**	0.00278	**-0.61**	0.37275
PSLT016	pefD	chaperone	**2.29**	0.12357	**-1.62**	0.00592	**-0.05**	0.95480
PSLT017	pefC	usher protein	**0.40**	0.67561	**0.68**	0.03019	**-0.10**	0.91879
PSLT017	pefC	usher protein	**1.00**	0.19413	**0.52**	0.15462	**0.24**	0.71092
PSLT018	pefA	major fimbrial subunit	**0.35**	0.72937	**0.72**	0.19462	**-1.15**	0.04682
PSLT018	pefA	major fimbrial subunit	**1.93**	0.01908	**0.46**	0.12243	**-0.06**	0.88693
PSLT019	pefB	regulatory protein	**0.32**	0.58595	**-0.69**	0.07574	**-0.95**	0.06200
PSLT019	pefB	regulatory protein	**1.01**	0.06224	**-1.56**	0.01660	**0.93**	0.08442
PSLT023	repA2	DNA replication protein	**-0.35**	0.56890	**0.75**	0.08263	**-0.94**	0.10942
PSLT023	repA2	DNA replication protein	**0.44**	0.57909	**0.66**	0.08897	**-0.35**	0.46990
PSLT025	PSLT025	putative cytoplasmic protein	**0.92**	0.16016	**1.69**	0.00173	**0.99**	0.22008
PSLT025	PSLT025	putative cytoplasmic protein	**2.68**	0.00689	**1.38**	0.00932	**0.89**	0.07452
PSLT026	PSLT026	putative periplasmic protein	**1.77**	0.02838	**3.83**	0.00005	**0.76**	0.15236
PSLT026	PSLT026	putative periplasmic protein	**2.28**	0.02545	**3.71**	0.00014	**2.48**	0.00588
PSLT027	ccdA	antidote	**1.40**	0.04321	**1.57**	0.00914	**-0.06**	0.90592
PSLT027	ccdA	antidote	**2.30**	0.01336	**1.88**	0.00093	**0.06**	0.90250
PSLT028	ccdB	toxin	**0.41**	0.61765	**1.24**	0.01034	**-1.26**	0.04960
PSLT028	ccdB	toxin	**1.51**	0.04086	**1.32**	0.00350	**-0.35**	0.38080
PSLT029	PSLT029	putative cytoplasmic protein	**2.83**	0.01390	**0.36**	0.31019	**0.37**	0.53126
PSLT029	PSLT029	putative cytoplasmic protein	**2.60**	0.01497	**0.75**	0.05984	**0.46**	0.41973
PSLT030	PSLT030	putative cytoplasmic protein	**0.21**	0.68193	**1.28**	0.00845	**-0.57**	0.26997
PSLT030	PSLT030	putative cytoplasmic protein	**1.35**	0.13641	**1.41**	0.01488	**-0.40**	0.36429
PSLT031	rsdB	resolvase	**0.11**	0.84429	**1.13**	0.02172	**-0.34**	0.36764
PSLT031	rsdB	resolvase	**1.32**	0.04674	**1.04**	0.01003	**-0.38**	0.36710
PSLT032	PSLT032	putative diguanylate cyclase/phosphodiesterase	**-0.17**	0.81801	**1.33**	0.00753	**-1.34**	0.00572
PSLT032	PSLT032	putative diguanylate cyclase/phosphodiesterase	**1.56**	0.29023	**0.92**	0.06397	**-0.78**	0.20327
PSLT032,1N	PSLT032,1N	hypothetical protein PSLT032,1N	**0.42**	0.37991	**1.57**	0.00188	**-1.15**	0.02725
PSLT032,1N	PSLT032,1N	hypothetical protein PSLT032,1N	**1.28**	0.02615	**2.15**	0.00021	**-0.41**	0.29101
PSLT033	PSLT033	putative inner membrane protein	**0.89**	0.53670	**1.38**	0.00173	**0.35**	0.73071
PSLT033	PSLT033	putative inner membrane protein	**0.92**	0.22457	**2.43**	0.00077	**-0.92**	0.06064
PSLT036	PSLT036	putative transposase	**0.54**	0.70368	**0.44**	0.16031	**-0.45**	0.40240
PSLT036	PSLT036	putative transposase	**2.14**	0.09243	**0.05**	0.93145	**1.12**	0.01307
PSLT037	spvD	hydrophilic protein	**3.85**	0.01309	**2.29**	0.00012	**2.73**	0.00124
PSLT037	spvD	hydrophilic protein	**3.70**	0.06970	**1.93**	0.00145	**2.91**	0.00143
PSLT038	spvC	hydrophilic protein	**2.24**	0.02219	**1.41**	0.00520	**0.74**	0.16686
PSLT038	spvC	hydrophilic protein	**4.11**	0.00800	**0.52**	0.20189	**2.46**	0.00080
PSLT039	spvB	hydrophilic protein	**3.10**	0.16215	**2.97**	0.00004	**3.51**	0.00814
PSLT039	spvB	hydrophilic protein	**4.39**	0.00512	**3.20**	0.00008	**3.62**	0.00095
PSLT040	spvA	outer membrane protein	**2.09**	0.02148	**3.54**	0.00002	**1.23**	0.02278
PSLT040	spvA	outer membrane protein	**3.52**	0.00512	**2.98**	0.00004	**1.42**	0.01023
PSLT041	spvR	regulator of spv operon	**0.52**	0.57962	**2.29**	0.00057	**1.60**	0.05052
PSLT041	spvR	regulator of spv operon	**2.38**	0.05710	**1.62**	0.00065	**1.90**	0.00667
PSLT042	PSLT042	putative integrase protein	**0.45**	0.48857	**1.91**	0.00035	**0.24**	0.58025
PSLT042	PSLT042	putative integrase protein	**2.23**	0.05384	**2.98**	0.00004	**1.95**	0.04263
PSLT043	PSLT043	type II secretion system protein	**2.49**	0.03490	**2.78**	0.00005	**0.58**	0.12211
PSLT043	PSLT043	type II secretion system protein	**3.56**	0.02251	**2.72**	0.00048	**1.82**	0.00246

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
PSLT044	rlgA	putative integrase protein	**1.32**	0.02351	**3.64**	0.00006	**0.63**	0.13477
PSLT044	rlgA	putative integrase protein	**1.72**	0.01443	**3.26**	0.00002	**0.76**	0.11919
PSLT045	PSLT045	putative resolvase	**2.88**	0.00918	**3.38**	0.00002	**0.08**	0.83743
PSLT045	PSLT045	putative resolvase	**3.40**	0.00673	**3.30**	0.00003	**0.25**	0.53219
PSLT046	mig-5	putative carbonic anhydrase	**2.61**	0.00826	**1.62**	0.00134	**0.73**	0.17144
PSLT046	mig-5	putative carbonic anhydrase	**3.02**	0.00547	**1.85**	0.00082	**0.89**	0.05827
PSLT047	PSLT047	putative cytoplasmic protein	**3.09**	0.00829	**3.33**	0.00002	**2.75**	0.00098
PSLT047	PSLT047	putative cytoplasmic protein	**3.05**	0.00546	**2.83**	0.00029	**2.60**	0.00021
PSLT048	tlpA	alpha-helical coiled-coil protein	**1.23**	0.06459	**2.26**	0.00013	**-0.84**	0.11191
PSLT048	tlpA	alpha-helical coiled-coil protein	**1.22**	0.03323	**1.81**	0.00290	**-1.12**	0.01276
PSLT050,1N	PSLT050,1N	hypothetical protein PSLT050,1N	**0.13**	0.87510	**2.49**	0.00015	**0.41**	0.61895
PSLT050,1N	PSLT050,1N	hypothetical protein PSLT050,1N	**1.02**	0.10226	**2.63**	0.00029	**0.01**	0.97927
PSLT050,2N	PSLT050,2N	hypothetical protein PSLT050,2N	**0.87**	0.08901	**2.32**	0.00039	**1.56**	0.01035
PSLT050,2N	PSLT050,2N	hypothetical protein PSLT050,2N	**2.24**	0.01293	**2.90**	0.00010	**1.54**	0.00223
PSLT051	PSLT051	putative cytoplasmic protein	**1.30**	0.12019	**2.71**	0.00012	**2.71**	0.00043
PSLT051	PSLT051	putative cytoplasmic protein	**1.85**	0.02373	**2.38**	0.00013	**3.06**	0.00010
PSLT052	parA	plasmid partition protein A	**0.61**	0.29264	**1.23**	0.00678	**-0.59**	0.25462
PSLT052	parA	plasmid partition protein A	**1.35**	0.13351	**0.98**	0.01126	**0.12**	0.77789
PSLT053	parB	plasmid partition protein B	**0.27**	0.58603	**0.12**	0.81688	**-0.34**	0.67714
PSLT053	parB	plasmid partition protein B	**0.41**	0.38106	**0.00**	0.99619	**-0.28**	0.49299
PSLT054	samB	DNA polymerase IV	**-0.04**	0.95366	**0.94**	0.01752	**-0.13**	0.77015
PSLT054	samB	DNA polymerase IV	**1.00**	0.13486	**0.37**	0.24145	**0.29**	0.45178
PSLT055	samA	SamA	**1.33**	0.05014	**1.43**	0.00182	**0.45**	0.32940
PSLT055	samA	SamA	**1.35**	0.03223	**0.63**	0.19780	**1.55**	0.00592
PSLT056	PSLT056	putative cytoplasmic protein	**1.52**	0.29869	**0.13**	0.70944	**0.48**	0.35510
PSLT056	PSLT056	putative cytoplasmic protein	**2.52**	0.04376	**-0.33**	0.24643	**1.18**	0.06469
PSLT057	PSLT057	putative cytoplasmic protein	**1.17**	0.20957	**-0.05**	0.88732	**0.04**	0.94286
PSLT057	PSLT057	putative cytoplasmic protein	**2.56**	0.08204	**-0.42**	0.39020	**0.48**	0.50310
PSLT059	PSLT059	putative adenine-specific DNA methylase	**1.87**	0.08551	**1.11**	0.02796	**0.24**	0.69970
PSLT059	PSLT059	putative adenine-specific DNA methylase	**3.36**	0.03288	**1.01**	0.01639	**0.69**	0.08003
PSLT060	PSLT060	putative cytoplasmic protein	**2.57**	0.06463	**2.30**	0.00046	**1.55**	0.00428
PSLT060	PSLT060	putative cytoplasmic protein	**4.03**	0.01319	**2.13**	0.03496	**2.52**	0.00043
PSLT060,1N	PSLT060,1N	hypothetical protein PSLT060,1N	**1.35**	0.20692	**1.31**	0.01422	**-1.09**	0.21321
PSLT060,1N	PSLT060,1N	hypothetical protein PSLT060,1N	**2.17**	0.06409	**1.23**	0.00809	**0.02**	0.97313
PSLT061	PSLT061	putative inner membrane protein	**1.09**	0.06755	**0.86**	0.05034	**-0.18**	0.61985
PSLT061	PSLT061	putative inner membrane protein	**2.97**	0.00547	**-0.13**	0.68202	**0.64**	0.16926
PSLT062	PSLT062	putative cytoplasmic protein	**-0.56**	0.56735	**0.89**	0.08894	**-0.71**	0.33136
PSLT062	PSLT062	putative cytoplasmic protein	**1.85**	0.21940	**0.54**	0.10855	**0.92**	0.09703
PSLT063	PSLT063	putative cytoplasmic protein	**1.74**	0.15567	**1.00**	0.01945	**0.45**	0.37584
PSLT063	PSLT063	putative cytoplasmic protein	**3.66**	0.00546	**0.85**	0.09599	**1.60**	0.00459
PSLT064	PSLT064	putative inner membrane protein	**-0.60**	0.22608	**-1.25**	0.02009	**-0.86**	0.19448
PSLT064	PSLT064	putative inner membrane protein	**0.07**	0.93703	**-2.32**	0.00026	**-1.62**	0.00634
PSLT066	ssbB	single-strand DNA binding protein	**3.54**	0.04568	**0.45**	0.24287	**0.81**	0.06023
PSLT066	ssbB	single-strand DNA binding protein	**4.19**	0.02652	**-0.28**	0.50555	**1.36**	0.00916
PSLT067	PSLT067	putative cytoplasmic protein	**0.54**	0.53887	**0.46**	0.17681	**0.08**	0.90200
PSLT067	PSLT067	putative cytoplasmic protein	**1.84**	0.13291	**-0.02**	0.95605	**0.35**	0.53690
PSLT068	PSLT068	putative ParB-like nuclease	**1.19**	0.19865	**1.56**	0.00182	**1.10**	0.20380
PSLT068	PSLT068	putative ParB-like nuclease	**2.31**	0.06201	**-0.79**	0.03549	**1.05**	0.06646
PSLT069	psiB	PsiB	**0.78**	0.30297	**0.02**	0.94003	**-1.09**	0.06451
PSLT069	psiB	PsiB	**1.87**	0.04008	**1.46**	0.34046	**0.31**	0.54533
PSLT070	psiA	PsiA	**2.27**	0.05203	**0.09**	0.84028	**-0.15**	0.75248
PSLT070	psiA	PsiA	**2.65**	0.02098	**-0.60**	0.10223	**1.00**	0.06570
PSLT072	PSLT072	putative transglycosylase	**2.33**	0.00991	**1.71**	0.00235	**1.40**	0.05658
PSLT072	PSLT072	putative transglycosylase	**3.67**	0.01136	**1.60**	0.00202	**2.08**	0.00103
PSLT073	traM	mating signal protein	**4.91**	0.00547	**3.68**	0.00026	**6.08**	0.00009
PSLT073	traM	mating signal protein	**4.31**	0.00547	**2.41**	0.00916	**6.19**	0.00010
PSLT075	traJ	regulatory protein	**-0.55**	0.35858	**-1.14**	0.12973	**-0.69**	0.32226
PSLT075	traJ	regulatory protein	**-0.52**	0.64143	**-0.92**	0.03099	**0.21**	0.70282
PSLT076	traY	DNA-binding protein	**1.30**	0.04746	**0.80**	0.03484	**2.52**	0.00044
PSLT076	traY	DNA-binding protein	**2.26**	0.10377	**0.27**	0.72652	**2.34**	0.00033
PSLT077	traA	pilus subunit	**0.56**	0.44435	**-0.59**	0.30478	**-1.05**	0.02297
PSLT077	traA	pilus subunit	**1.67**	0.16842	**-1.27**	0.04376	**0.01**	0.98253
PSLT078	traL	pilus assembly protein	**-0.89**	0.22737	**-0.18**	0.88768	**-2.00**	0.00409
PSLT078	traL	pilus assembly protein	**-0.07**	0.94539	**-1.02**	0.01198	**-0.62**	0.29870
PSLT079	traE	pilus assembly protein	**2.61**	0.03896	**0.04**	0.89699	**1.28**	0.07731
PSLT079	traE	pilus assembly protein	**2.80**	0.01946	**-0.31**	0.54928	**2.26**	0.00150
PSLT080	traK	pilus assembly protein	**0.22**	0.73688	**-0.48**	0.50919	**-0.15**	0.83942
PSLT080	traK	pilus assembly protein	**2.06**	0.12389	**0.39**	0.17569	**-0.24**	0.54172
PSLT081	traB	pilus assembly protein	**2.77**	0.01405	**0.77**	0.07269	**0.52**	0.65342
PSLT081	traB	pilus assembly protein	**2.98**	0.01199	**0.40**	0.30069	**1.41**	0.02200

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
PSLT082	traP	conjugative transfer protein	**1.45**	0.33131	**0.64**	0.07714	**0.75**	0.16277
PSLT082	traP	conjugative transfer protein	**2.32**	0.24076	**1.19**	0.00643	**0.96**	0.15101
PSLT083	trbD	conjugative transfer protein	**1.63**	0.01844	**2.63**	0.00020	**1.73**	0.05780
PSLT083	trbD	conjugative transfer protein	**3.05**	0.00552	**2.00**	0.00213	**2.51**	0.01395
PSLT084	traV	pilus assembly protein	**-0.50**	0.66698	**0.46**	0.44103	**-0.47**	0.35698
PSLT084	traV	pilus assembly protein	**2.19**	0.01813	**0.94**	0.01259	**0.42**	0.38273
PSLT085	traR	conjugative transfer protein	**0.83**	0.13547	**1.09**	0.27176	**0.79**	0.29557
PSLT085	traR	conjugative transfer protein	**0.51**	0.64635	**0.16**	0.61622	**0.12**	0.89078
PSLT087	PSLT087	OrfG2	**0.79**	0.50995	**0.80**	0.14052	**0.41**	0.64142
PSLT087	PSLT087	OrfG2	**3.71**	0.00547	**2.02**	0.03244	**2.64**	0.01222
PSLT088	traC	ATP-binding protein	**1.43**	0.14806	**0.67**	0.09577	**0.28**	0.54242
PSLT088	traC	ATP-binding protein	**2.95**	0.01363	**0.49**	0.15812	**1.14**	0.01681
PSLT089	trbI	pilus assembly protein	**-0.17**	0.87553	**-0.99**	0.09587	**-0.13**	0.90141
PSLT089	trbI	pilus assembly protein	**0.84**	0.28413	**0.08**	0.79941	**-0.38**	0.50840
PSLT091	traW	pilus assembly protein	**1.27**	0.44740	**-0.67**	0.25321	**1.70**	0.19524
PSLT091	traW	pilus assembly protein	**3.16**	0.02226	**-0.14**	0.74176	**1.00**	0.30923
PSLT092	traU	pilus assembly protein	**1.90**	0.03651	**0.58**	0.12628	**0.93**	0.05510
PSLT092	traU	pilus assembly protein	**2.63**	0.00927	**0.62**	0.07251	**0.84**	0.18542
PSLT094	trbC	pilus assembly protein	**1.86**	0.20564	**0.28**	0.39215	**-0.25**	0.64906
PSLT094	trbC	pilus assembly protein	**2.18**	0.07022	**-0.84**	0.05729	**0.19**	0.64347
PSLT094,1N	PSLT094,1N	hypothetical protein PSLT094,1N	**0.36**	0.51734	**-0.01**	0.97910	**-1.41**	0.04280
PSLT094,1N	PSLT094,1N	hypothetical protein PSLT094,1N	**1.48**	0.11489	**-0.38**	0.35432	**0.38**	0.37158
PSLT095	traN	mating pair stabilization protein	**1.43**	0.11638	**0.11**	0.75781	**0.64**	0.35403
PSLT095	traN	mating pair stabilization protein	**1.59**	0.03477	**-0.81**	0.21059	**2.06**	0.00524
PSLT097	traF	pilus assembly protein	**0.52**	0.30837	**1.14**	0.03443	**-1.29**	0.01661
PSLT097	traF	pilus assembly protein	**2.31**	0.01964	**1.42**	0.00268	**0.94**	0.03770
PSLT098	traQ	pilin chaperone	**1.65**	0.04720	**1.28**	0.00588	**0.99**	0.26020
PSLT098	traQ	pilin chaperone	**3.47**	0.00546	**0.70**	0.02785	**2.32**	0.00043
PSLT099	trbB	conjugative transfer protein	**0.11**	0.86910	**0.84**	0.06195	**-0.62**	0.15591
PSLT099	trbB	conjugative transfer protein	**1.55**	0.07945	**0.12**	0.70633	**0.21**	0.69062
PSLT100	traH	pilus assembly protein	**1.08**	0.22862	**0.68**	0.07788	**0.71**	0.29948
PSLT100	traH	pilus assembly protein	**2.53**	0.08533	**0.38**	0.35584	**0.21**	0.63608
PSLT101	traG	mating pair stabilization and pilus assembly protein	**2.02**	0.06999	**3.03**	0.00018	**2.45**	0.00090
PSLT101	traG	mating pair stabilization and pilus assembly protein	**2.73**	0.02974	**2.90**	0.00010	**2.58**	0.00017
PSLT102	traS	entry exclusion protein	**1.56**	0.03932	**3.66**	0.00003	**1.09**	0.04710
PSLT102	traS	entry exclusion protein	**1.73**	0.02320	**3.81**	0.00002	**1.87**	0.00142
PSLT103	traT	surface exclusion protein	**0.88**	0.31057	**4.62**	0.00001	**1.90**	0.01709
PSLT103	traT	surface exclusion protein	**1.44**	0.19050	**4.32**	0.00002	**1.49**	0.01680
PSLT104	traD	ATP-binding protein/DNA transporter	**2.87**	0.00739	**3.20**	0.00007	**0.79**	0.06377
PSLT104	traD	ATP-binding protein/DNA transporter	**4.31**	0.01449	**3.38**	0.00004	**1.53**	0.00517
PSLT105	trbH	conjugative transfer protein	**1.67**	0.05345	**3.60**	0.00011	**0.47**	0.39537
PSLT105	trbH	conjugative transfer protein	**2.04**	0.03231	**3.13**	0.00011	**0.06**	0.91584
PSLT106	PSLT106	MvpA-like protein	**2.56**	0.00925	**3.32**	0.00006	**-0.04**	0.93102
PSLT106	PSLT106	MvpA-like protein	**4.05**	0.00547	**3.23**	0.00006	**0.99**	0.01955
PSLT107	PSLT107	putative cytoplasmic protein	**4.36**	0.00512	**5.23**	0.00000	**2.05**	0.00081
PSLT107	PSLT107	putative cytoplasmic protein	**4.89**	0.00514	**4.80**	0.00007	**2.63**	0.00034
PSLT108	traI	oriT nickase/helicase	**1.83**	0.03408	**1.59**	0.00401	**-0.24**	0.71818
PSLT108	traI	oriT nickase/helicase	**3.37**	0.02352	**1.55**	0.00319	**-0.06**	0.88780
PSLT110	traX	pilin subunit acetylation	**-0.11**	0.83532	**-1.00**	0.03395	**-1.11**	0.09646
PSLT110	traX	pilin subunit acetylation	**1.60**	0.02277	**-0.56**	0.09908	**-0.36**	0.50024
PSLT111	finO	finP binding-protein	**1.50**	0.18017	**1.21**	0.01336	**-0.55**	0.13805
PSLT111	finO	finP binding-protein	**2.12**	0.11468	**0.92**	0.01273	**0.24**	0.53450
STM0002	thrA	bifunctional aspartokinase I/homeserine dehydrogenase I	**0.37**	0.62845	**-0.54**	0.11836	**-1.81**	0.00963
STM0002	thrA	bifunctional aspartokinase I/homeserine dehydrogenase I	**0.32**	0.64452	**-0.15**	0.64847	**-2.17**	0.00140
STM0003	thrB	homoserine kinase	**-1.30**	0.18742	**-0.06**	0.84412	**-0.77**	0.08797
STM0003	thrB	homoserine kinase	**1.02**	0.06251	**-0.35**	0.24131	**-1.07**	0.03493
STM0004	thrC	threonine synthase	**-1.33**	0.03916	**-0.57**	0.09294	**-1.27**	0.07834
STM0004	thrC	threonine synthase	**0.80**	0.22006	**0.32**	0.43538	**-1.45**	0.02807
STM0005	yaaA	hypothetical protein STM0005	**-1.05**	0.12753	**-0.38**	0.18228	**-1.30**	0.01063
STM0005	yaaA	hypothetical protein STM0005	**-0.55**	0.31077	**-0.37**	0.22720	**-0.48**	0.19818
STM0006	yaaJ	putative alanine/glycine transport protein	**-1.38**	0.08984	**-1.07**	0.00735	**-1.66**	0.00295
STM0006	yaaJ	putative alanine/glycine transport protein	**0.01**	0.99547	**-1.66**	0.00056	**-0.94**	0.03485
STM0007	talB	transaldolase	**-1.64**	0.02576	**0.14**	0.70954	**-0.88**	0.11601
STM0007	talB	transaldolase	**-0.64**	0.16904	**0.17**	0.65154	**-0.38**	0.35457
STM0008	mogA	molybdenum cofactor biosynthesis protein	**-1.97**	0.01977	**-0.90**	0.01659	**-1.43**	0.02038
STM0008	mogA	molybdenum cofactor biosynthesis protein	**-0.46**	0.55708	**-0.38**	0.36682	**-1.11**	0.01360
STM0009	yaaH	putative regulatory protein	**-0.51**	0.68300	**-0.08**	0.91349	**1.71**	0.00339
STM0009	yaaH	putative regulatory protein	**-0.17**	0.88807	**0.38**	0.47781	**1.91**	0.00306
STM0010	htgA	positive regulator	**-1.44**	0.05309	**-0.37**	0.25043	**-0.30**	0.47113
STM0010	htgA	positive regulator	**-2.52**	0.00871	**-1.54**	0.00261	**-3.61**	0.00071

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM0011	yaaI	putative periplasmic protein	**-0.85**	0.22408	**-1.09**	0.01036	**-0.36**	0.58626
STM0011	yaaI	putative periplasmic protein	**0.40**	0.43196	**-0.78**	0.03244	**-0.80**	0.14249
STM0012	dnaK	molecular chaperone DnaK	**-1.65**	0.05569	**0.28**	0.42555	**-1.60**	0.00305
STM0012	dnaK	molecular chaperone DnaK	**-0.63**	0.24615	**0.31**	0.42764	**-1.17**	0.00805
STM0013	dnaJ	heat shock protein	**-1.20**	0.04310	**0.10**	0.73282	**-1.66**	0.00259
STM0013	dnaJ	heat shock protein	**0.19**	0.68209	**-0.46**	0.10333	**-1.52**	0.00333
STM0014	STM0014	putative transcriptional regulator	**-1.39**	0.03028	**-0.32**	0.48259	**0.05**	0.90354
STM0014	STM0014	putative transcriptional regulator	**-1.23**	0.17298	**-0.87**	0.09566	**-1.62**	0.14034
STM0015	STM0015	putative bacteriophage protein	**-0.43**	0.42520	**-1.54**	0.02284	**-0.83**	0.24642
STM0015	STM0015	putative bacteriophage protein	**-0.16**	0.88591	**-1.35**	0.00195	**-1.73**	0.04162
STM0016	STM0016	hypothetical protein STM0016	**0.07**	0.92280	**-1.10**	0.00976	**-0.09**	0.92277
STM0016	STM0016	hypothetical protein STM0016	**1.25**	0.07942	**0.03**	0.93480	**-0.41**	0.55782
STM0017	STM0017	hypothetical protein STM0017	**0.88**	0.23256	**-0.51**	0.44867	**0.49**	0.39691
STM0017	STM0017	hypothetical protein STM0017	**2.62**	0.02064	**-0.33**	0.50077	**0.55**	0.42002
STM0018	STM0018	putative exochitinase	**-0.36**	0.45159	**0.12**	0.83650	**-0.71**	0.26906
STM0018	STM0018	putative exochitinase	**0.60**	0.21115	**-0.97**	0.05172	**-0.15**	0.77563
STM0019	STM0019	putative hydroxymethyltransferase	**1.64**	0.22475	**-0.52**	0.24083	**-0.74**	0.19391
STM0019	STM0019	putative hydroxymethyltransferase	**2.22**	0.13309	**-1.31**	0.00232	**0.11**	0.79316
STM0020	STM0020	putative cytoplasmic protein	**0.16**	0.72937	**-0.22**	0.54919	**-0.94**	0.05154
STM0020	STM0020	putative cytoplasmic protein	**1.90**	0.05566	**-0.85**	0.10963	**0.09**	0.83437
STM0021	bcfA	fimbrial subunit	**-0.29**	0.74272	**-0.29**	0.38775	**-0.02**	0.97120
STM0021	bcfA	fimbrial subunit	**0.38**	0.66856	**-0.95**	0.07685	**-0.05**	0.90096
STM0022	bcfB	fimbrial chaparone	**0.14**	0.75900	**-0.60**	0.10797	**-0.07**	0.92086
STM0022	bcfB	fimbrial chaparone	**0.78**	0.19598	**-0.43**	0.24913	**1.07**	0.04189
STM0023	bcfC	fimbrial usher	**-0.37**	0.52059	**-0.64**	0.17303	**-0.53**	0.56299
STM0023	bcfC	fimbrial usher	**0.32**	0.46003	**-1.97**	0.00442	**0.54**	0.44090
STM0024	bcfD	fimbrial subunit	**0.15**	0.78012	**-0.13**	0.76206	**-1.08**	0.02545
STM0024	bcfD	fimbrial subunit	**2.37**	0.01219	**-0.36**	0.53988	**0.21**	0.84131
STM0025	bcfE	fimbrial subunit	**-0.36**	0.51479	**-0.52**	0.42998	**-0.72**	0.56023
STM0025	bcfE	fimbrial subunit	**-0.76**	0.27018	**-0.98**	0.02728	**-0.62**	0.35626
STM0026	bcfF	fimbrial subunit	**-0.40**	0.60177	**0.43**	0.67211	**0.02**	0.96386
STM0026	bcfF	fimbrial subunit	**-1.55**	0.03535	**-1.06**	0.01750	**-0.40**	0.73457
STM0027	bcfG	fimbrial chaparone	**-0.14**	0.82901	**0.18**	0.60282	**-0.24**	0.66117
STM0027	bcfG	fimbrial chaparone	**0.39**	0.34512	**0.61**	0.13135	**0.33**	0.43711
STM0028	bcfH	putative thiol-disulfide isomerase	**-0.46**	0.34898	**-0.23**	0.57080	**-0.62**	0.37462
STM0028	bcfH	putative thiol-disulfide isomerase	**-0.19**	0.82430	**-0.28**	0.48091	**-2.41**	0.08252
STM0028,1n	STM0028,1n	hypothetical protein STM0028,1n	**0.01**	0.97757	**0.10**	0.73971	**0.26**	0.50041
STM0028,1n	STM0028,1n	hypothetical protein STM0028,1n	**-0.63**	0.23911	**-0.49**	0.34500	**0.25**	0.63757
STM0029	STM0029	putative transcriptional regulator	**0.97**	0.12856	**-0.22**	0.52902	**0.44**	0.47578
STM0029	STM0029	putative transcriptional regulator	**2.33**	0.00795	**-0.24**	0.63567	**1.30**	0.01499
STM0030	STM0030	putative transcriptional regulator	**-0.14**	0.80152	**0.01**	0.98835	**0.18**	0.74824
STM0030	STM0030	putative transcriptional regulator	**-0.35**	0.58781	**0.33**	0.56029	**0.19**	0.70875
STM0031	STM0031	putative transcriptional regulator	**1.44**	0.05971	**-0.07**	0.89715	**2.69**	0.00431
STM0031	STM0031	putative transcriptional regulator	**3.17**	0.00547	**0.79**	0.32740	**3.19**	0.00022
STM0032	STM0032	putative arylsulfatase	**-0.39**	0.42641	**0.77**	0.05165	**-0.12**	0.88032
STM0032	STM0032	putative arylsulfatase	**0.71**	0.27883	**-0.22**	0.59904	**0.40**	0.45322
STM0033	STM0033	putative 5'-nucleotidase	**-0.59**	0.37229	**0.15**	0.75972	**-0.17**	0.79506
STM0033	STM0033	putative 5'-nucleotidase	**0.51**	0.40306	**0.41**	0.36597	**0.64**	0.09905
STM0034	STM0034	putative outer membrane/exported protein	**-0.48**	0.32287	**-1.70**	0.00357	**0.04**	0.95985
STM0034	STM0034	putative outer membrane/exported protein	**6.46**	0.00595	**0.86**	0.27176	**1.89**	0.01197
STM0035	STM0035	putative arylsulfatase	**0.26**	0.65824	**0.32**	0.34348	**-0.03**	0.96342
STM0035	STM0035	putative arylsulfatase	**1.73**	0.01408	**0.14**	0.72026	**0.99**	0.04902
STM0036	STM0036	putative arylsulfatase regulator	**-0.02**	0.97698	**-1.00**	0.01685	**-0.73**	0.13499
STM0036	STM0036	putative arylsulfatase regulator	**0.70**	0.27232	**0.83**	0.50980	**1.34**	0.00487
STM0037	STM0037	putative cytoplasmic protein	**-0.25**	0.60019	**-0.57**	0.37644	**-0.30**	0.58972
STM0037	STM0037	putative cytoplasmic protein	**2.22**	0.05139	**-0.54**	0.14646	**0.84**	0.16779
STM0038	STM0038	putative arylsulfatase	**-1.39**	0.03517	**-0.43**	0.28451	**-0.72**	0.19757
STM0038	STM0038	putative arylsulfatase	**0.14**	0.83865	**0.17**	0.54768	**0.19**	0.65697
STM0039	nhaA	Na+/H antiporter	**-0.78**	0.11374	**1.27**	0.01909	**-1.42**	0.00459
STM0039	nhaA	Na+/H antiporter	**-0.42**	0.40578	**1.19**	0.00536	**-1.29**	0.05368
STM0040	nhaR	transcriptional activator	**-0.32**	0.46736	**1.48**	0.00764	**-1.74**	0.01832
STM0040	nhaR	transcriptional activator	**0.72**	0.32145	**1.64**	0.00101	**-0.43**	0.40198
STM0041	STM0041	putative glycosyl hydrolase	**-0.50**	0.32184	**1.48**	0.02752	**-1.38**	0.01739
STM0041	STM0041	putative glycosyl hydrolase	**0.77**	0.14788	**1.72**	0.00249	**0.19**	0.82855
STM0042	STM0042	putative sodium galactoside symporter	**-0.57**	0.35761	**-0.49**	0.18616	**0.36**	0.58027
STM0042	STM0042	putative sodium galactoside symporter	**1.26**	0.08722	**-0.39**	0.33210	**1.21**	0.01914
STM0043	rpsT	30S ribosomal protein S20	**-3.57**	0.02952	**-1.89**	0.00939	**-3.41**	0.00006
STM0043	rpsT	30S ribosomal protein S20	**-3.16**	0.08305	**-2.04**	0.00550	**-4.38**	0.00417
STM0044	yaaY	putative cytoplasmic protein	**-2.28**	0.01999	**-1.08**	0.01801	**-1.65**	0.00259
STM0044	yaaY	putative cytoplasmic protein	**-1.95**	0.01033	**-1.51**	0.00177	**-1.21**	0.17932

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM0045	ribF	hypothetical protein STM0045	**-1.51**	0.09468	**-0.87**	0.01196	**-2.83**	0.00014
STM0045	ribF	hypothetical protein STM0045	**-0.96**	0.06414	**-0.20**	0.48678	**-2.37**	0.00110
STM0046	ileS	isoleucyl-tRNA synthetase	**-2.56**	0.00829	**-0.57**	0.12575	**-3.04**	0.00014
STM0046	ileS	isoleucyl-tRNA synthetase	**-1.64**	0.04580	**-0.69**	0.06061	**-2.46**	0.00382
STM0047	lspA	signal peptidase II	**-1.98**	0.01400	**-0.28**	0.34032	**-2.88**	0.00014
STM0047	lspA	signal peptidase II	**-1.85**	0.04338	**-0.07**	0.83295	**-2.94**	0.00159
STM0048	slpA	FKBP-type peptidyl-prolyl cis-trans isomerase	**-1.40**	0.02149	**-0.59**	0.07725	**-2.00**	0.00510
STM0048	slpA	FKBP-type peptidyl-prolyl cis-trans isomerase	**0.64**	0.71993	**-0.98**	0.02587	**-1.36**	0.06469
STM0049	lytB	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	**-2.41**	0.00639	**0.23**	0.80106	**-2.52**	0.00187
STM0049	lytB	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	**-1.58**	0.02996	**-0.58**	0.06964	**-1.94**	0.01268
STM0050	STM0050	putative nitrite reductase	**-0.84**	0.16492	**0.24**	0.37753	**-0.38**	0.50663
STM0050	STM0050	putative nitrite reductase	**-0.01**	0.98974	**0.06**	0.86757	**-0.01**	0.99158
STM0051	rihC	putative purine nucleoside hydrolase	**0.04**	0.92542	**0.69**	0.05580	**-0.73**	0.07037
STM0051	rihC	putative purine nucleoside hydrolase	**1.05**	0.08725	**0.71**	0.09218	**-0.16**	0.66436
STM0052	STM0052	putative transcriptional regulator	**0.23**	0.62974	**-0.15**	0.66649	**-0.33**	0.56325
STM0052	STM0052	putative transcriptional regulator	**1.12**	0.04908	**-0.24**	0.51672	**0.52**	0.25040
STM0053	STM0053	putative transcriptional regulator	**0.52**	0.31521	**-0.28**	0.78598	**-0.33**	0.72283
STM0053	STM0053	putative transcriptional regulator	**-1.35**	0.11657	**0.44**	0.32008	**-0.90**	0.27960
STM0054	STM0054	putative oxalacetate decarboxylase subunit beta	**1.62**	0.20087	**0.58**	0.49522	**-0.36**	0.46816
STM0054	STM0054	putative oxalacetate decarboxylase subunit beta	**1.84**	0.17699	**0.40**	0.31199	**-0.15**	0.75383
STM0054	STM0054	putative oxalacetate decarboxylase subunit beta	**2.08**	0.21134	**-0.73**	0.08172	**-0.08**	0.86572
STM0054	STM0054	putative oxalacetate decarboxylase subunit beta	**3.17**	0.01479	**-0.09**	0.79545	**0.26**	0.65347
STM0056	STM0056	putative oxaloacetate decarboxylase subunit gamma	**3.11**	0.01114	**-1.41**	0.00437	**-1.64**	0.01079
STM0056	STM0056	putative oxaloacetate decarboxylase subunit gamma	**3.60**	0.01210	**-1.78**	0.00067	**-0.19**	0.76309
STM0057	STM0057	putative citrate-sodium symporter	**0.78**	0.37575	**-1.36**	0.14807	**0.32**	0.44242
STM0057	STM0057	putative citrate-sodium symporter	**1.38**	0.11807	**-1.45**	0.01105	**0.39**	0.44235
STM0058	citC2	putative citrate lyase synthetase	**-1.08**	0.23064	**0.58**	0.45095	**-0.64**	0.14173
STM0058	citC2	putative citrate lyase synthetase	**-0.29**	0.65494	**-0.50**	0.13285	**-0.61**	0.22401
STM0059	citD2	putative citrate lyase acyl carrier protein gamma chain	**0.67**	0.56507	**0.08**	0.82309	**-0.45**	0.62904
STM0059	citD2	putative citrate lyase acyl carrier protein gamma chain	**1.32**	0.15259	**-0.21**	0.62973	**-0.50**	0.48583
STM0060	citE2	putative citrate lyase beta chain	**0.90**	0.08701	**0.17**	0.65706	**0.14**	0.83480
STM0060	citE2	putative citrate lyase beta chain	**1.27**	0.12228	**-0.63**	0.06702	**1.17**	0.12646
STM0061	citF2	putative citrate lyase alpha chain/citrate-ACP transferase	**-0.01**	0.97472	**-0.56**	0.11593	**-0.57**	0.34869
STM0061	citF2	putative citrate lyase alpha chain/citrate-ACP transferase	**2.35**	0.01479	**-0.71**	0.24847	**-1.04**	0.11693
STM0062	citX2	putative cytoplasmic protein	**-0.07**	0.89872	**-0.21**	0.48097	**-0.65**	0.39419
STM0062	citX2	putative cytoplasmic protein	**0.79**	0.49472	**-0.51**	0.15162	**0.22**	0.77436
STM0063	citG2	triphosphoribosyl-dephospho-CoA synthase	**-0.73**	0.12104	**-0.32**	0.55031	**1.89**	0.10304
STM0063	citG2	triphosphoribosyl-dephospho-CoA synthase	**-0.06**	0.90690	**-0.81**	0.01940	**1.29**	0.00765
STM0064	dapB	dihydrodipicolinate reductase	**-0.31**	0.63234	**0.11**	0.78951	**-1.10**	0.09255
STM0064	dapB	dihydrodipicolinate reductase	**-0.57**	0.36958	**-0.49**	0.37333	**-2.12**	0.04235
STM0066	carA	carbamoyl-phosphate synthase small subunit	**-1.19**	0.03541	**1.05**	0.00926	**-1.70**	0.00269
STM0066	carA	carbamoyl-phosphate synthase small subunit	**-1.19**	0.03781	**0.90**	0.03406	**-0.74**	0.12409
STM0067	carB	carbamoyl-phosphate synthase large subunit	**-1.33**	0.06815	**0.06**	0.89964	**-1.00**	0.26081
STM0067	carB	carbamoyl-phosphate synthase large subunit	**-0.44**	0.38011	**0.51**	0.13929	**-1.89**	0.13456
STM0068	caiF	of cai/fix operon transcriptional regulator	**3.59**	0.09758	**3.86**	0.00062	**5.01**	0.00139
STM0068	caiF	of cai/fix operon transcriptional regulator	**1.07**	0.13027	**-0.01**	0.98617	**2.19**	0.00543
STM0069	caiE	carnitine racemase stimulation factor	**0.61**	0.40578	**0.23**	0.59715	**0.29**	0.60389
STM0069	caiE	carnitine racemase stimulation factor	**2.37**	0.00778	**-0.35**	0.40099	**2.43**	0.00070
STM0070	caiD	carnitinyl-CoA dehydratase	**0.66**	0.48186	**0.59**	0.36682	**-0.24**	0.58410
STM0070	caiD	carnitinyl-CoA dehydratase	**1.61**	0.06391	**0.19**	0.65555	**0.31**	0.50482
STM0071	caiC	crotonobetaine/carnitine-CoA ligase	**-0.24**	0.76010	**-0.28**	0.33278	**-0.85**	0.03868
STM0071	caiC	crotonobetaine/carnitine-CoA ligase	**1.55**	0.08653	**-0.83**	0.02054	**1.07**	0.02852
STM0072	caiB	crotonobetainyl-CoA:carnitineCoA-transferase	**-0.06**	0.90024	**1.26**	0.00463	**0.24**	0.61710
STM0072	caiB	crotonobetainyl-CoA:carnitineCoA-transferase	**0.46**	0.37580	**0.39**	0.27983	**-0.21**	0.67653
STM0073	caiA	crotonobetainyl-CoA dehydrogenase	**-0.19**	0.77241	**-0.31**	0.53139	**-0.79**	0.48295
STM0073	caiA	crotonobetainyl-CoA dehydrogenase	**0.56**	0.18533	**0.25**	0.56616	**0.00**	0.99713
STM0074	caiT	L-carnitine/gamma-butyrobetaine antiporter	**-0.65**	0.23325	**0.39**	0.63234	**-0.29**	0.64856
STM0074	caiT	L-carnitine/gamma-butyrobetaine antiporter	**-0.89**	0.48762	**-1.86**	0.00203	**-0.82**	0.14725
STM0075	fixA	putative electron transfer flavoprotein subunit beta	**0.73**	0.22719	**0.27**	0.50308	**0.32**	0.59771
STM0075	fixA	putative electron transfer flavoprotein subunit beta	**1.58**	0.14269	**0.23**	0.78809	**2.13**	0.00875
STM0076	fixB	putative electron transfer flavoprotein subunit alpha	**-1.75**	0.12773	**-1.58**	0.04857	**-0.64**	0.37862
STM0076	fixB	putative electron transfer flavoprotein subunit alpha	**0.80**	0.18729	**-1.59**	0.00577	**-0.65**	0.42962
STM0077	fixC	flavoprotein	**0.89**	0.21242	**-0.99**	0.07104	**0.47**	0.47046
STM0077	fixC	flavoprotein	**1.23**	0.05424	**-0.22**	0.55100	**1.51**	0.01049
STM0078	fixX	putative ferredoxin	**0.88**	0.48195	**1.03**	0.12011	**1.46**	0.01854
STM0078	fixX	putative ferredoxin	**1.97**	0.08866	**-1.25**	0.01081	**0.31**	0.76913
STM0079	yaaU	putative transport protein	**0.43**	0.41983	**0.29**	0.40413	**0.49**	0.19913
STM0079	yaaU	putative transport protein	**1.71**	0.14696	**-0.65**	0.17629	**1.20**	0.01098
STM0080	STM0080	putative outer membrane lipoprotein	**0.72**	0.46194	**1.23**	0.00715	**1.68**	0.00292
STM0080	STM0080	putative outer membrane lipoprotein	**1.98**	0.06031	**-0.08**	0.83611	**2.88**	0.00030

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM0081	STM0081	putative secreted protein	**1.80**	0.02092	**0.70**	0.05058	**1.03**	0.05335
STM0081	STM0081	putative secreted protein	**3.40**	0.00547	**0.72**	0.06259	**1.09**	0.03182
STM0082	STM0082	putative secreted protein	**0.52**	0.45600	**1.91**	0.03948	**0.46**	0.30457
STM0082	STM0082	putative secreted protein	**1.95**	0.14379	**0.55**	0.20631	**1.38**	0.03937
STM0084	STM0084	putative sulfatase	**-0.77**	0.31810	**0.42**	0.43889	**-1.23**	0.01511
STM0084	STM0084	putative sulfatase	**0.13**	0.81488	**-0.32**	0.30738	**-0.45**	0.29026
STM0085	yabF	glutathione-regulated potassium-efflux system ancillary	**-1.09**	0.06515	**-0.45**	0.21424	**0.49**	0.26256
STM0085	yabF	glutathione-regulated potassium-efflux system ancillary	**-0.52**	0.46474	**-1.00**	0.05044	**0.96**	0.12083
STM0086	kefC	glutathione-regulated potassium-efflux system protein	**1.10**	0.39268	**-1.45**	0.00848	**-0.61**	0.29443
STM0086	kefC	glutathione-regulated potassium-efflux system protein	**1.58**	0.03542	**-1.14**	0.03773	**-0.51**	0.28469
STM0087	folA	dihydrofolate reductase type I	**0.74**	0.09758	**-0.12**	0.73016	**-1.34**	0.00750
STM0087	folA	dihydrofolate reductase type I	**0.54**	0.31133	**-0.05**	0.88176	**-0.93**	0.07373
STM0088	apaH	diadenosinetetraphosphatase	**-0.03**	0.95350	**0.06**	0.87002	**-0.72**	0.08439
STM0088	apaH	diadenosinetetraphosphatase	**0.44**	0.32853	**-0.03**	0.92774	**-0.03**	0.94140
STM0089	apaG	hypothetical protein STM0089	**-2.02**	0.06218	**0.39**	0.30002	**-0.22**	0.67188
STM0089	apaG	hypothetical protein STM0089	**-1.65**	0.01827	**-0.29**	0.46796	**-0.66**	0.09243
STM0090	ksgA	dimethyladenosine transferase	**-2.64**	0.00567	**-1.19**	0.00667	**-1.20**	0.01207
STM0090	ksgA	dimethyladenosine transferase	**-1.63**	0.01993	**-0.69**	0.05957	**-0.91**	0.06178
STM0091	pdxA	4-hydroxythreonine-4-phosphate dehydrogenase	**-3.34**	0.00947	**-2.10**	0.00019	**-2.26**	0.00039
STM0091	pdxA	4-hydroxythreonine-4-phosphate dehydrogenase	**-3.52**	0.00547	**-2.09**	0.00042	**-1.81**	0.04647
STM0092	surA	peptidyl-prolyl cis-trans isomerase	**-2.57**	0.01092	**-1.02**	0.00765	**-3.42**	0.00011
STM0092	surA	peptidyl-prolyl cis-trans isomerase	**-1.46**	0.05313	**-1.34**	0.00564	**-2.92**	0.00010
STM0093	imp	organic solvent tolerance protein precursor	**-1.96**	0.01855	**-0.77**	0.06119	**-1.88**	0.00118
STM0093	imp	organic solvent tolerance protein precursor	**-1.95**	0.02226	**-0.81**	0.02145	**-1.93**	0.00075
STM0094	djlA	Dna-J like membrane chaperone protein	**0.65**	0.21114	**-0.24**	0.46930	**1.70**	0.01491
STM0094	djlA	Dna-J like membrane chaperone protein	**1.63**	0.01534	**-0.18**	0.64266	**2.29**	0.00270
STM0095	rluA	23S rRNA pseudouridylate 746 synthase	**-1.97**	0.01123	**-0.68**	0.04738	**-1.36**	0.03579
STM0095	rluA	23S rRNA pseudouridylate 746 synthase	**1.10**	0.05101	**-0.10**	0.84249	**1.12**	0.06059
STM0096	hepA	ATP-dependent helicase HepA	**-1.61**	0.01494	**-1.39**	0.00377	**-3.23**	0.00040
STM0096	hepA	ATP-dependent helicase HepA	**-1.26**	0.04091	**-1.20**	0.00766	**-1.82**	0.00364
STM0097	polB	DNA polymerase II	**-1.34**	0.13827	**-1.46**	0.02763	**-0.45**	0.21169
STM0097	polB	DNA polymerase II	**0.13**	0.75456	**-1.28**	0.00835	**1.06**	0.11222
STM0098	STM0098	putative secreted protein	**-0.51**	0.38699	**-0.70**	0.08758	**-1.41**	0.01867
STM0098	STM0098	putative secreted protein	**0.76**	0.15745	**-0.02**	0.94723	**0.02**	0.97519
STM0100	STM0100	putative cytoplasmic protein	**0.42**	0.45509	**0.10**	0.72185	**-0.64**	0.18964
STM0100	STM0100	putative cytoplasmic protein	**2.52**	0.00817	**-0.04**	0.88750	**0.23**	0.64428
STM0101	araD	L-ribulose-5-phosphate 4-epimerase	**0.38**	0.48253	**1.32**	0.01174	**1.04**	0.08506
STM0101	araD	L-ribulose-5-phosphate 4-epimerase	**0.33**	0.65552	**-0.09**	0.83291	**0.75**	0.14173
STM0102	araA	L-arabinose isomerase	**-0.32**	0.70353	**0.15**	0.69520	**-0.77**	0.12622
STM0102	araA	L-arabinose isomerase	**0.94**	0.08196	**-0.68**	0.04352	**0.20**	0.81672
STM0103	araB	ribulokinase	**1.80**	0.03878	**3.84**	0.00021	**-0.08**	0.92978
STM0103	araB	ribulokinase	**2.58**	0.01808	**3.52**	0.00012	**2.41**	0.02447
STM0104	araC	arabinose operon transcriptional regulator	**-0.24**	0.59380	**0.94**	0.09980	**-0.42**	0.27345
STM0104	araC	arabinose operon transcriptional regulator	**3.51**	0.00547	**-0.09**	0.84969	**1.92**	0.00608
STM0105	yabI	hypothetical protein STM0105	**-1.33**	0.03523	**0.02**	0.96273	**-0.55**	0.41742
STM0105	yabI	hypothetical protein STM0105	**-0.41**	0.48837	**-0.22**	0.63997	**-0.62**	0.09769
STM0106	yabJ	putative ABC transporter protein	**-1.37**	0.04570	**-0.11**	0.78792	**-0.55**	0.34746
STM0106	yabJ	putative ABC transporter protein	**0.70**	0.16246	**0.21**	0.45990	**-0.69**	0.08660
STM0107	thiP	thiamin ABC transporter membrane component	**0.24**	0.68187	**0.53**	0.11608	**0.73**	0.19688
STM0107	thiP	thiamin ABC transporter membrane component	**-0.02**	0.97845	**0.03**	0.95522	**2.04**	0.00237
STM0108	tbpA	thiamine-binding periplasmic protein	**-0.47**	0.74114	**0.81**	0.03860	**-1.79**	0.00592
STM0108	tbpA	thiamine-binding periplasmic protein	**0.23**	0.87190	**0.82**	0.02599	**-1.02**	0.01609
STM0109	yabN	putative periplasmic binding protein	**-1.23**	0.03518	**-0.18**	0.66076	**-0.10**	0.85499
STM0109	yabN	putative periplasmic binding protein	**-0.30**	0.56128	**-0.38**	0.26161	**-0.53**	0.24122
STM0110	leuD	isopropylmalate isomerase small subunit	**-0.34**	0.54963	**0.72**	0.09445	**-0.53**	0.42989
STM0110	leuD	isopropylmalate isomerase small subunit	**-0.70**	0.37875	**0.28**	0.35851	**-2.47**	0.07998
STM0111	leuC	isopropylmalate isomerase large subunit	**2.08**	0.15162	**1.12**	0.01144	**-1.24**	0.06251
STM0111	leuC	isopropylmalate isomerase large subunit	**2.12**	0.01001	**0.57**	0.10346	**0.70**	0.34548
STM0112	leuB	3-isopropylmalate dehydrogenase	**-0.73**	0.28577	**0.74**	0.02964	**-1.06**	0.09933
STM0112	leuB	3-isopropylmalate dehydrogenase	**-0.67**	0.26495	**0.80**	0.03980	**-1.02**	0.03910
STM0113	leuA	2-isopropylmalate synthase	**1.47**	0.02729	**2.00**	0.00047	**3.12**	0.00018
STM0113	leuA	2-isopropylmalate synthase	**1.77**	0.01479	**2.00**	0.00088	**3.40**	0.00007
STM0115	leuO	leucine transcriptional activator	**0.27**	0.57932	**-1.56**	0.10443	**-0.49**	0.42429
STM0115	leuO	leucine transcriptional activator	**0.26**	0.65987	**-1.74**	0.01222	**-0.31**	0.77401
STM0116	ilvI	acetolactate synthase III large subunit	**1.28**	0.06957	**0.90**	0.01313	**-0.77**	0.15262
STM0116	ilvI	acetolactate synthase III large subunit	**1.32**	0.03161	**0.82**	0.04996	**0.05**	0.92588
STM0117	ilvH	acetolactate synthase small subunit	**-0.12**	0.84406	**0.20**	0.57517	**-0.65**	0.14243
STM0117	ilvH	acetolactate synthase small subunit	**1.05**	0.37870	**0.17**	0.58063	**0.11**	0.81731
STM0118	fruR	fru operon transcriptional repressor	**-1.35**	0.11970	**-1.00**	0.04758	**-0.87**	0.18712
STM0118	fruR	fru operon transcriptional repressor	**-0.83**	0.09202	**-1.35**	0.02585	**-0.28**	0.46519

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM0119	yabB	hypothetical protein STM0119	**-1.22**	0.03367	**-0.58**	0.11340	**-1.77**	0.00115
STM0119	yabB	hypothetical protein STM0119	**-0.94**	0.06238	**-0.43**	0.24520	**-1.39**	0.01188
STM0120	mraW	S-adenosyl-methyltransferase	**-1.34**	0.03984	**-0.65**	0.06197	**-1.07**	0.02821
STM0120	mraW	S-adenosyl-methyltransferase	**-0.98**	0.05490	**-0.18**	0.58785	**-0.56**	0.14446
STM0121	ftsL	cell division protein	**-1.24**	0.17600	**-0.52**	0.12338	**-0.94**	0.02714
STM0121	ftsL	cell division protein	**-0.01**	0.99747	**-0.79**	0.01940	**0.08**	0.88312
STM0122	ftsI	division specific transpeptidase	**-0.09**	0.88701	**-1.07**	0.01854	**-0.39**	0.37697
STM0122	ftsI	division specific transpeptidase	**0.90**	0.20602	**-1.17**	0.00841	**0.00**	0.99713
STM0123	murE	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-	**-2.65**	0.00547	**-2.15**	0.00037	**-3.15**	0.00011
STM0123	murE	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-	**-1.91**	0.01479	**-2.25**	0.00038	**-2.76**	0.00031
STM0124	murF	D-alanine-D-alanine ligase	**-2.54**	0.00796	**-2.56**	0.00079	**-2.98**	0.00099
STM0124	murF	D-alanine-D-alanine ligase	**-2.51**	0.00811	**-2.53**	0.00019	**-4.46**	0.00509
STM0125	mraY	phospho-N-acetylmuramoyl-pentapeptide-transferase	**-1.68**	0.03792	**-2.24**	0.00028	**-3.27**	0.00011
STM0125	mraY	phospho-N-acetylmuramoyl-pentapeptide-transferase	**-1.64**	0.02137	**-2.17**	0.00049	**-2.01**	0.00316
STM0126	murD	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase	**-0.10**	0.95303	**-0.32**	0.58425	**-1.44**	0.00635
STM0126	murD	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase	**-1.15**	0.14806	**-1.56**	0.00150	**-1.89**	0.01488
STM0127	ftsW	essential cell division gene	**-1.91**	0.00921	**-1.82**	0.00050	**-1.90**	0.00134
STM0127	ftsW	essential cell division gene	**-2.65**	0.02148	**-2.07**	0.00022	**-1.89**	0.00106
STM0128	murG	N-acetylglucosaminyl transferase	**-2.37**	0.00900	**-1.57**	0.00150	**-1.34**	0.04650
STM0128	murG	N-acetylglucosaminyl transferase	**-2.25**	0.01052	**-1.61**	0.00060	**-2.16**	0.00839
STM0129	murC	UDP-N-acetylmuramate--L-alanine ligase	**-2.89**	0.02069	**-1.87**	0.00035	**-2.47**	0.00032
STM0129	murC	UDP-N-acetylmuramate--L-alanine ligase	**-2.00**	0.00831	**-1.43**	0.00218	**-2.42**	0.00021
STM0130	ddl	D-alanylalanine synthetase	**-2.37**	0.00753	**-0.68**	0.04334	**-2.23**	0.00219
STM0130	ddl	D-alanylalanine synthetase	**-0.92**	0.18246	**-0.30**	0.40176	**-2.57**	0.00019
STM0131	ftsQ	cell division protein	**-0.62**	0.45920	**-0.01**	0.97867	**-2.83**	0.00015
STM0131	ftsQ	cell division protein	**0.37**	0.46250	**0.19**	0.53261	**-1.75**	0.00352
STM0132	ftsA	cell division protein	**-2.31**	0.02665	**-0.21**	0.44586	**-2.36**	0.00038
STM0132	ftsA	cell division protein	**-0.61**	0.17603	**-0.42**	0.16069	**-1.62**	0.00294
STM0133	ftsZ	cell division protein FtsZ	**-1.90**	0.02603	**0.35**	0.37251	**-2.15**	0.00038
STM0133	ftsZ	cell division protein FtsZ	**-1.12**	0.07292	**0.33**	0.27061	**-2.35**	0.00158
STM0134	lpxC	UDP-3-O-	**-1.15**	0.03211	**1.37**	0.00185	**1.35**	0.00506
STM0134	lpxC	UDP-3-O-	**-0.27**	0.56888	**1.16**	0.00325	**1.61**	0.00251
STM0135	yacA	SecA regulator SecM	**-1.19**	0.04632	**-1.07**	0.06327	**-1.00**	0.01623
STM0135	yacA	SecA regulator SecM	**-0.89**	0.18641	**-0.93**	0.01883	**-1.05**	0.03581
STM0136	secA	translocase	**-1.01**	0.06312	**-0.99**	0.00862	**-2.00**	0.00203
STM0136	secA	translocase	**-0.05**	0.93930	**-0.34**	0.26328	**-0.70**	0.12099
STM0137	mutT	7,8-dihydro-8-oxoguanine-triphosphatase	**-1.42**	0.02162	**-0.26**	0.52576	**-1.26**	0.08762
STM0137	mutT	7,8-dihydro-8-oxoguanine-triphosphatase	**-0.13**	0.82377	**-0.80**	0.05036	**-1.33**	0.10743
STM0138	yacG	zinc-binding protein	**-0.97**	0.06283	**-0.68**	0.07960	**-1.00**	0.02907
STM0138	yacG	zinc-binding protein	**-0.18**	0.66459	**-0.95**	0.01921	**-0.39**	0.39507
STM0139	yacF	hypothetical protein STM0139	**-1.37**	0.02040	**-1.07**	0.01548	**-1.48**	0.01135
STM0139	yacF	hypothetical protein STM0139	**-0.30**	0.45568	**-1.07**	0.01094	**-1.52**	0.01089
STM0140	coaE	dephospho-CoA kinase	**-1.17**	0.11448	**-0.86**	0.09063	**-2.33**	0.00034
STM0140	coaE	dephospho-CoA kinase	**-0.51**	0.34231	**-0.28**	0.39983	**-1.32**	0.01208
STM0141	guaC	guanosine 5'-monophosphate oxidoreductase	**-1.16**	0.07767	**-0.06**	0.87834	**-0.15**	0.76776
STM0141	guaC	guanosine 5'-monophosphate oxidoreductase	**-0.41**	0.52984	**-0.12**	0.67712	**0.44**	0.42591
STM0142	hofC	putative type IV pilin assembly protein	**-1.69**	0.02148	**-0.95**	0.09738	**-0.95**	0.09115
STM0142	hofC	putative type IV pilin assembly protein	**-0.96**	0.14835	**-0.26**	0.42709	**-1.68**	0.00264
STM0143	hofB	putative type IV fimbrial biosynthetic protein	**-0.17**	0.74962	**-1.50**	0.00095	**-0.91**	0.35583
STM0143	hofB	putative type IV fimbrial biosynthetic protein	**2.08**	0.01065	**0.37**	0.25016	**-0.58**	0.34871
STM0144	ppdD	putative type IV pilin major component	**0.53**	0.33606	**-0.80**	0.02173	**-1.27**	0.12729
STM0144	ppdD	putative type IV pilin major component	**0.46**	0.29520	**0.02**	0.95835	**-0.38**	0.56516
STM0145	nadC	nicotinate-nucleotide pyrophosphorylase	**-0.64**	0.23453	**-0.75**	0.06488	**-0.22**	0.66979
STM0145	nadC	nicotinate-nucleotide pyrophosphorylase	**-0.25**	0.61931	**-0.73**	0.06480	**-0.21**	0.64347
STM0146	ampD	N-acetyl-anhydromuramyl-L-alanine amidase	**-0.35**	0.43030	**0.84**	0.03795	**-0.30**	0.38880
STM0146	ampD	N-acetyl-anhydromuramyl-L-alanine amidase	**0.21**	0.64076	**0.90**	0.04557	**-0.09**	0.87760
STM0147	ampE	putative beta lactamase regulator	**-0.32**	0.67877	**0.27**	0.35540	**-0.20**	0.78649
STM0147	ampE	putative beta lactamase regulator	**-0.06**	0.88801	**0.62**	0.05201	**-0.59**	0.13616
STM0148	STM0148	putative cytoplasmic protein	**-0.19**	0.65904	**0.37**	0.17725	**0.13**	0.81762
STM0148	STM0148	putative cytoplasmic protein	**-0.53**	0.24565	**-0.83**	0.06542	**0.47**	0.51676
STM0149	STM0149	Na+/galactoside symporter	**0.95**	0.07167	**0.55**	0.09014	**-0.85**	0.18172
STM0149	STM0149	Na+/galactoside symporter	**1.54**	0.04119	**-0.32**	0.52204	**0.90**	0.04855
STM0150	aroP	aromatic amino acid transporter	**0.51**	0.62330	**-0.60**	0.11575	**-0.31**	0.36039
STM0150	aroP	aromatic amino acid transporter	**0.89**	0.22132	**-0.86**	0.03576	**0.31**	0.39826
STM0151	pdhR	transcriptional regulator of pyruvate dehydrogenase	**-1.93**	0.01497	**-1.36**	0.00130	**-3.09**	0.00010
STM0151	pdhR	transcriptional regulator of pyruvate dehydrogenase	**-0.48**	0.48976	**-0.77**	0.02173	**-2.50**	0.00165
STM0152	aceE	pyruvate dehydrogenase E1 component	**-3.66**	0.01611	**-0.71**	0.05077	**-2.64**	0.01633
STM0152	aceE	pyruvate dehydrogenase E1 component	**-2.30**	0.00947	**-0.43**	0.29102	**-3.06**	0.00011
STM0153	aceF	dihydrolipoamide acetyltransferase	**-2.97**	0.02399	**-2.15**	0.00103	**-3.19**	0.00010
STM0153	aceF	dihydrolipoamide acetyltransferase	**-2.82**	0.06375	**-1.51**	0.01367	**-4.58**	0.00141

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM0154	lpdA	dihydrolipoamide dehydrogenase	**-3.28**	0.00541	**-0.85**	0.01565	**-3.35**	0.00030
STM0154	lpdA	dihydrolipoamide dehydrogenase	**-2.62**	0.01590	**-0.64**	0.06067	**-2.72**	0.00015
STM0155	STM0155	putative outer membrane protein	**-0.78**	0.24824	**-1.68**	0.00112	**-2.03**	0.00143
STM0155	STM0155	putative outer membrane protein	**0.41**	0.60635	**-1.74**	0.00306	**-1.02**	0.01698
STM0156	STM0156	putative periplasmic protein	**-1.57**	0.01635	**-1.34**	0.00817	**-1.54**	0.00764
STM0156	STM0156	putative periplasmic protein	**-0.14**	0.76088	**-1.74**	0.00052	**-1.38**	0.00522
STM0157	yacH	putative outer membrane protein	**-1.64**	0.03224	**-0.53**	0.11422	**-1.77**	0.01277
STM0157	yacH	putative outer membrane protein	**-1.50**	0.03865	**-2.30**	0.02309	**-1.84**	0.00197
STM0158	acnB	aconitate hydratase	**-1.19**	0.03235	**-0.38**	0.24036	**-1.07**	0.01726
STM0158	acnB	aconitate hydratase	**-1.10**	0.07086	**-0.29**	0.35851	**-0.77**	0.12743
STM0159	STM0159	putative restriction endonuclease	**1.82**	0.02971	**1.32**	0.00473	**3.59**	0.00008
STM0159	STM0159	putative restriction endonuclease	**2.06**	0.02560	**0.41**	0.17739	**3.96**	0.00014
STM0160	yacL	hypothetical protein STM0160	**0.78**	0.10129	**-0.69**	0.12094	**-0.13**	0.74336
STM0160	yacL	hypothetical protein STM0160	**0.12**	0.80084	**-0.59**	0.18238	**-0.39**	0.60097
STM0161	kdgT	2-keto-3-deoxygluconate permease	**1.75**	0.04701	**-0.33**	0.43348	**0.71**	0.19326
STM0161	kdgT	2-keto-3-deoxygluconate permease	**2.11**	0.02172	**0.25**	0.54004	**1.22**	0.01058
STM0162	STM0162	putative inner membrane protein	**0.24**	0.82987	**0.05**	0.90971	**-0.31**	0.37157
STM0162	STM0162	putative inner membrane protein	**1.33**	0.03242	**0.06**	0.90798	**0.65**	0.15954
STM0163	STM0163	4-hydroxythreonine-4-phosphate dehydrogenase	**-0.28**	0.55339	**0.40**	0.24417	**1.16**	0.01609
STM0163	STM0163	4-hydroxythreonine-4-phosphate dehydrogenase	**0.51**	0.35321	**-0.20**	0.52190	**2.15**	0.09216
STM0164	STM0164	putative transcriptional regulator	**-1.05**	0.05741	**-0.67**	0.06025	**-1.86**	0.00225
STM0164	STM0164	putative transcriptional regulator	**-1.71**	0.03861	**-0.61**	0.07259	**-1.42**	0.00806
STM0165	speD	S-adenosylmethionine decarboxylase proenzyme	**-1.97**	0.01172	**-1.04**	0.02692	**-1.74**	0.02647
STM0165	speD	S-adenosylmethionine decarboxylase proenzyme	**-0.70**	0.20638	**-1.54**	0.00269	**-1.97**	0.01056
STM0166	speE	spermidine synthase	**-4.00**	0.00512	**-2.52**	0.00043	**-5.00**	0.00002
STM0166	speE	spermidine synthase	**-3.83**	0.02059	**-2.19**	0.00019	**-5.24**	0.00243
STM0167	yacC	putative periplasmic protein	**-1.57**	0.02011	**-1.04**	0.00961	**-2.97**	0.00111
STM0167	yacC	putative periplasmic protein	**-1.16**	0.04785	**-0.23**	0.78932	**-1.67**	0.01104
STM0168	cueO	putative multicopper oxidase	**-0.22**	0.61744	**0.99**	0.01561	**0.25**	0.55906
STM0168	cueO	putative multicopper oxidase	**-0.19**	0.67877	**0.51**	0.10235	**0.56**	0.19002
STM0169	gcd	glucose dehydrogenase	**-0.12**	0.86951	**1.14**	0.00358	**-0.05**	0.96795
STM0169	gcd	glucose dehydrogenase	**0.53**	0.32685	**1.13**	0.00744	**0.20**	0.83162
STM0170	hpt	hypoxanthine-guanine phosphoribosyltransferase	**-2.32**	0.00991	**-0.06**	0.90120	**-2.99**	0.00011
STM0170	hpt	hypoxanthine-guanine phosphoribosyltransferase	**-1.55**	0.01706	**0.18**	0.58832	**-2.59**	0.00026
STM0171	yadF	putative carbonic anhydrase	**1.19**	0.67671	**0.83**	0.03824	**2.11**	0.01446
STM0171	yadF	putative carbonic anhydrase	**1.76**	0.01258	**1.18**	0.00622	**1.33**	0.16994
STM0172	yadG	putative ABC-type multidrug transport system ATPase	**-0.67**	0.15766	**-1.17**	0.29909	**-0.62**	0.43077
STM0172	yadG	putative ABC-type multidrug transport system ATPase	**-0.26**	0.67884	**-0.43**	0.27790	**-1.08**	0.12296
STM0173	yadH	putative transport protein	**1.78**	0.01352	**-0.71**	0.03178	**-0.26**	0.56146
STM0173	yadH	putative transport protein	**0.60**	0.19382	**-0.85**	0.07643	**-0.70**	0.19060
STM0174	stiH	putative fimbrial protein precurosr	**1.28**	0.03103	**-0.18**	0.51273	**-0.69**	0.14679
STM0174	stiH	putative fimbrial protein precurosr	**1.26**	0.06896	**-0.49**	0.26981	**0.50**	0.29649
STM0175	stiC	putativie fimbrial usher	**-0.03**	0.95651	**0.89**	0.07341	**0.59**	0.20316
STM0175	stiC	putativie fimbrial usher	**1.16**	0.09686	**-0.64**	0.11229	**0.03**	0.98468
STM0176	stiB	putative fimbrial chaparone	**0.57**	0.40903	**1.13**	0.15696	**1.73**	0.10063
STM0176	stiB	putative fimbrial chaparone	**0.17**	0.76997	**-0.81**	0.22561	**0.16**	0.83198
STM0177	stiA	putative fimbrial subunit	**-0.52**	0.40679	**-0.79**	0.12586	**-0.33**	0.72911
STM0177	stiA	putative fimbrial subunit	**-0.96**	0.20600	**-1.21**	0.00297	**-0.20**	0.60043
STM0178	yadI	putative PTS enzyme	**-0.60**	0.19506	**0.63**	0.14178	**1.25**	0.05716
STM0178	yadI	putative PTS enzyme	**0.28**	0.50886	**0.30**	0.56098	**2.50**	0.01387
STM0179	yadE	putative xylanase/chitin deacetylase	**-1.34**	0.02615	**-0.65**	0.06862	**-1.56**	0.00557
STM0179	yadE	putative xylanase/chitin deacetylase	**-0.16**	0.74536	**0.01**	0.97910	**-1.42**	0.01304
STM0180	panD	aspartate 1-decarboxylase precursor	**-0.85**	0.13019	**-0.12**	0.75336	**-0.77**	0.11787
STM0180	panD	aspartate 1-decarboxylase precursor	**-0.45**	0.29048	**0.05**	0.92069	**0.58**	0.14561
STM0181	panC	pantoate--beta-alanine ligase	**-1.92**	0.01425	**-1.54**	0.00278	**-2.95**	0.00032
STM0181	panC	pantoate--beta-alanine ligase	**-1.78**	0.05049	**-1.18**	0.00456	**-2.13**	0.01726
STM0182	panB	3-methyl-2-oxobutanoate hydroxymethyltransferase	**-1.47**	0.01595	**-1.44**	0.00188	**-1.12**	0.04977
STM0182	panB	3-methyl-2-oxobutanoate hydroxymethyltransferase	**-1.00**	0.10554	**-1.20**	0.00594	**-1.65**	0.02833
STM0183	folK	7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase	**-2.06**	0.02980	**-1.31**	0.01651	**-1.07**	0.03085
STM0183	folK	7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase	**-0.82**	0.38100	**-1.30**	0.00237	**-1.21**	0.04854
STM0184	pcnB	polyA polymerase I	**-2.34**	0.01066	**-1.29**	0.00388	**-3.86**	0.00033
STM0184	pcnB	polyA polymerase I	**-1.20**	0.07564	**-1.32**	0.00222	**-3.76**	0.00010
STM0185	yadB	glutamyl-tRNA synthetase	**-1.56**	0.02373	**-1.69**	0.00145	**-1.61**	0.00656
STM0185	yadB	glutamyl-tRNA synthetase	**-0.59**	0.25571	**-0.75**	0.03937	**-1.50**	0.01863
STM0186	dksA	dnaK suppressor protein	**-1.61**	0.01938	**-0.87**	0.03384	**-0.29**	0.50292
STM0186	dksA	dnaK suppressor protein	**-0.47**	0.25658	**-0.08**	0.81896	**-0.36**	0.34588
STM0187	sfsA	sugar fermentation stimulation protein	**-1.19**	0.10582	**0.35**	0.28541	**3.06**	0.00011
STM0187	sfsA	sugar fermentation stimulation protein	**-1.23**	0.15305	**0.23**	0.45813	**3.57**	0.00006
STM0188	ligT	2'-5' RNA ligase	**-1.59**	0.01570	**-0.79**	0.04928	**-0.93**	0.03094
STM0188	ligT	2'-5' RNA ligase	**-1.65**	0.01666	**-0.91**	0.01115	**-1.06**	0.02320

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM0189	hrpB	ATP-dependent helicase	**-0.91**	0.11322	**-0.22**	0.75947	**-2.14**	0.00150
STM0189	hrpB	ATP-dependent helicase	**0.22**	0.61452	**-0.49**	0.16310	**-1.11**	0.01225
STM0190	mrcB	penicillin-binding protein 1b	**-1.70**	0.05095	**-0.83**	0.02640	**-2.18**	0.00194
STM0190	mrcB	penicillin-binding protein 1b	**-0.52**	0.46574	**-0.25**	0.45112	**-1.57**	0.00410
STM0191	fhuA	outer membrane ferrichrome receptor protein precursor	**-2.24**	0.02265	**-0.27**	0.34266	**-0.93**	0.02441
STM0191	fhuA	outer membrane ferrichrome receptor protein precursor	**-2.60**	0.02102	**-0.50**	0.10365	**-1.33**	0.00590
STM0192	fhuC	hydroxymate-dependent iron transport protein	**-1.32**	0.02226	**-0.59**	0.15673	**-2.05**	0.00073
STM0192	fhuC	hydroxymate-dependent iron transport protein	**-0.20**	0.63219	**-0.86**	0.03935	**-1.09**	0.03404
STM0193	fhuD	hydroxamate-dependent iron uptake protein	**-1.37**	0.03561	**-1.42**	0.00258	**-3.33**	0.00011
STM0193	fhuD	hydroxamate-dependent iron uptake protein	**-0.86**	0.14703	**-1.20**	0.00258	**-1.58**	0.05979
STM0194	fhuB	hydroxamate-dependent iron uptake protein	**-1.69**	0.02148	**-1.38**	0.01249	**-0.38**	0.47144
STM0194	fhuB	hydroxamate-dependent iron uptake protein	**-0.65**	0.40479	**-1.38**	0.00190	**-1.41**	0.00710
STM0195	stfA	putative fimbrial subunit	**0.71**	0.36404	**0.79**	0.11438	**-0.32**	0.60398
STM0195	stfA	putative fimbrial subunit	**1.85**	0.07952	**0.31**	0.28832	**-0.40**	0.36764
STM0196	stfC	putative fimbrial outer membrane usher	**-0.02**	0.97596	**-0.83**	0.15376	**-0.90**	0.03405
STM0196	stfC	putative fimbrial outer membrane usher	**0.11**	0.81851	**-1.23**	0.01079	**-0.14**	0.78971
STM0197	stfD	putative periplasmic fimbrial chaperone	**-0.45**	0.49833	**1.33**	0.05774	**-0.89**	0.15014
STM0197	stfD	putative periplasmic fimbrial chaperone	**2.21**	0.00864	**0.63**	0.03937	**0.66**	0.21277
STM0198	stfE	putative minor fimbrial subunit	**-0.35**	0.46437	**-0.22**	0.63116	**-0.50**	0.51121
STM0198	stfE	putative minor fimbrial subunit	**-0.51**	0.74253	**-0.01**	0.98193	**0.78**	0.22642
STM0199	stfF	putative minor fimbrial subunit	**0.62**	0.39267	**0.37**	0.33353	**-0.07**	0.91311
STM0199	stfF	putative minor fimbrial subunit	**1.54**	0.09659	**-1.03**	0.01044	**2.51**	0.02535
STM0200	stfG	putative minor fimbrial subunit	**-1.11**	0.13857	**-1.64**	0.00128	**-1.53**	0.01161
STM0200	stfG	putative minor fimbrial subunit	**-0.86**	0.35224	**-1.14**	0.00882	**-0.72**	0.26344
STM0201	STM0201	putative outer membrane protein	**-1.22**	0.05376	**-1.21**	0.00844	**-0.59**	0.21063
STM0201	STM0201	putative outer membrane protein	**-0.39**	0.36919	**-0.71**	0.04318	**0.06**	0.89430
STM0202	hemL	glutamate-1-semialdehyde aminotransferase	**-0.81**	0.10662	**-1.16**	0.01119	**-1.79**	0.00181
STM0202	hemL	glutamate-1-semialdehyde aminotransferase	**-0.69**	0.12844	**-1.16**	0.02372	**-0.90**	0.03658
STM0203	yadQ	chloride channel protein	**-0.77**	0.19312	**-0.03**	0.92477	**-0.61**	0.19128
STM0203	yadQ	chloride channel protein	**0.54**	0.37178	**-0.45**	0.13873	**-0.40**	0.36342
STM0204,S	yadR	hypothetical protein STM0204,S	**-1.91**	0.03141	**-0.15**	0.62142	**-1.52**	0.00282
STM0204,S	yadR	hypothetical protein STM0204,S	**-1.80**	0.12446	**-0.22**	0.46641	**-2.21**	0.03996
STM0205	yadS	putative inner membrane protein	**-0.39**	0.49575	**1.00**	0.01160	**-2.19**	0.00056
STM0205	yadS	putative inner membrane protein	**0.35**	0.46968	**0.91**	0.03141	**-1.69**	0.01052
STM0206	btuF	vitamin B12-transporter protein BtuF	**-1.03**	0.06605	**-0.08**	0.79854	**-1.72**	0.00377
STM0206	btuF	vitamin B12-transporter protein BtuF	**-0.36**	0.53945	**0.27**	0.35862	**-2.03**	0.00391
STM0207	pfs	5'-methylthioadenosine/S-adenosylhomocysteine	**-1.50**	0.02443	**-0.15**	0.64878	**-2.52**	0.00046
STM0207	pfs	5'-methylthioadenosine/S-adenosylhomocysteine	**-0.65**	0.27146	**-0.38**	0.29361	**-1.23**	0.00850
STM0208	dgt	deoxyguanosinetriphosphate triphosphohydrolase	**-0.88**	0.17613	**0.68**	0.14116	**-0.87**	0.11740
STM0208	dgt	deoxyguanosinetriphosphate triphosphohydrolase	**0.60**	0.35386	**0.63**	0.09727	**-0.17**	0.79673
STM0209	htrA	high temperature requirement A protein precursor	**-0.45**	0.61992	**1.88**	0.00297	**0.69**	0.06469
STM0209	htrA	high temperature requirement A protein precursor	**0.33**	0.46383	**2.01**	0.00110	**0.53**	0.21919
STM0210	cdaR	putative inner membrane protein	**-0.42**	0.44585	**1.39**	0.00176	**0.85**	0.05323
STM0210	cdaR	putative inner membrane protein	**0.34**	0.65270	**1.36**	0.00989	**1.24**	0.01261
STM0211	yaeH	putative cytoplasmic protein	**-0.77**	0.15577	**0.62**	0.14317	**0.68**	0.13431
STM0211	yaeH	putative cytoplasmic protein	**0.18**	0.86042	**0.92**	0.01071	**1.56**	0.01420
STM0212	STM0212	putative inner membrane protein	**-1.63**	0.04594	**-0.21**	0.45642	**-0.66**	0.07640
STM0212	STM0212	putative inner membrane protein	**-0.68**	0.14494	**0.05**	0.90159	**-0.34**	0.36764
STM0213	dapD	2,3,4,5-tetrahydropyridine-2-carboxylate N-	**-0.84**	0.16295	**0.86**	0.02520	**-1.05**	0.02617
STM0213	dapD	2,3,4,5-tetrahydropyridine-2-carboxylate N-	**-0.45**	0.57963	**1.11**	0.01129	**-0.39**	0.31440
STM0214	glnD	PII uridylyl-transferase	**-1.98**	0.00889	**-0.29**	0.69989	**-1.24**	0.01101
STM0214	glnD	PII uridylyl-transferase	**-0.39**	0.78379	**-0.95**	0.02042	**-3.55**	0.00433
STM0215	map	methionine aminopeptidase	**-2.62**	0.00757	**-0.61**	0.04476	**-2.01**	0.00278
STM0215	map	methionine aminopeptidase	**-0.04**	0.96628	**-0.14**	0.61464	**-0.77**	0.06361
STM0216	rpsB	30S ribosomal protein S2	**-2.62**	0.00750	**-0.84**	0.05990	**-4.09**	0.00011
STM0216	rpsB	30S ribosomal protein S2	**-1.78**	0.02836	**-1.18**	0.02550	**-5.33**	0.00002
STM0217	tsf	elongation factor Ts	**-2.78**	0.00547	**-1.44**	0.01198	**-4.49**	0.00003
STM0217	tsf	elongation factor Ts	**-1.50**	0.02347	**-1.19**	0.01338	**-3.89**	0.00004
STM0218	pyrH	uridylate kinase	**-2.57**	0.09231	**-0.72**	0.07513	**-0.22**	0.59391
STM0218	pyrH	uridylate kinase	**-0.33**	0.80696	**-2.41**	0.00076	**-0.70**	0.06997
STM0219	frr	ribosome releasing factor	**-1.96**	0.00955	**-0.27**	0.33908	**-1.37**	0.00486
STM0219	frr	ribosome releasing factor	**-1.34**	0.03176	**-0.29**	0.41231	**-0.93**	0.09859
STM0220	dxr	1-deoxy-D-xylulose 5-phosphate reductoisomerase	**-2.34**	0.00755	**-1.68**	0.00096	**-2.01**	0.00182
STM0220	dxr	1-deoxy-D-xylulose 5-phosphate reductoisomerase	**-1.46**	0.02172	**-1.20**	0.00528	**-2.26**	0.00226
STM0221	uppS	undecaprenyl pyrophosphate synthetase	**-2.15**	0.00717	**-1.03**	0.01669	**-2.30**	0.00040
STM0221	uppS	undecaprenyl pyrophosphate synthetase	**-0.91**	0.10631	**-1.15**	0.01305	**-2.43**	0.00069
STM0222	cdsA	CDP-diglyceride synthase	**-0.05**	0.97440	**-1.06**	0.00871	**-2.27**	0.00082
STM0222	cdsA	CDP-diglyceride synthase	**-1.77**	0.01562	**-0.71**	0.05282	**-1.44**	0.04339
STM0223	yaeL	putative membrane-associated Zn-dependent protease	**-0.76**	0.13363	**-0.51**	0.15324	**-1.49**	0.00449
STM0223	yaeL	putative membrane-associated Zn-dependent protease	**-0.62**	0.61663	**-0.74**	0.02107	**-1.92**	0.00118

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM0224	yaeT	putative outer membrane protein precursor	**-3.71**	0.00537	**-1.68**	0.00310	**-3.98**	0.00130
STM0224	yaeT	putative outer membrane protein precursor	**-2.87**	0.00567	**-1.53**	0.00212	**-3.53**	0.00010
STM0225	hlpA	outer membrane protein H precursor	**-4.56**	0.01041	**-2.62**	0.00034	**-4.87**	0.00003
STM0225	hlpA	outer membrane protein H precursor	**-3.82**	0.00595	**-1.38**	0.00459	**-5.05**	0.00002
STM0226	lpxD	UDP-3-O-	**-2.60**	0.00955	**-0.46**	0.13893	**-2.22**	0.00296
STM0226	lpxD	UDP-3-O-	**-2.61**	0.01171	**-0.49**	0.20583	**-2.13**	0.00246
STM0227	fabZ	(3R)-hydroxymyristoyl ACP dehydratase	**-0.87**	0.15305	**-0.54**	0.12848	**-2.28**	0.00077
STM0227	fabZ	(3R)-hydroxymyristoyl ACP dehydratase	**-0.82**	0.28394	**-0.39**	0.20516	**-2.47**	0.00043
STM0228	lpxA	UDP-N-acetylglucosamine acyltransferase	**-0.92**	0.10850	**-0.65**	0.12912	**-1.61**	0.00215
STM0228	lpxA	UDP-N-acetylglucosamine acyltransferase	**-0.77**	0.14184	**-0.17**	0.62607	**-2.04**	0.00151
STM0229	lpxB	lipid-A-disaccharide synthase	**-1.88**	0.01041	**-1.27**	0.00374	**-2.76**	0.00016
STM0229	lpxB	lipid-A-disaccharide synthase	**-1.29**	0.04522	**-1.50**	0.00145	**-2.11**	0.00393
STM0230	rnhB	ribonuclease HII	**-3.24**	0.00547	**-1.94**	0.00060	**-2.99**	0.00045
STM0230	rnhB	ribonuclease HII	**-2.66**	0.00889	**-1.96**	0.00030	**-2.72**	0.00395
STM0231	dnaE	DNA polymerase III subunit alpha	**-2.21**	0.04403	**-1.60**	0.00160	**-3.08**	0.00009
STM0231	dnaE	DNA polymerase III subunit alpha	**-2.46**	0.01311	**-1.68**	0.00058	**-2.56**	0.00024
STM0232	accA	acetyl-CoA carboxylase alpha subunit	**-2.84**	0.00562	**-1.09**	0.03399	**-2.70**	0.00039
STM0232	accA	acetyl-CoA carboxylase alpha subunit	**-1.64**	0.02217	**-1.46**	0.00257	**-1.26**	0.11040
STM0233	STM0233	putative endochitinase	**-0.92**	0.09910	**-0.93**	0.07997	**0.08**	0.88988
STM0233	STM0233	putative endochitinase	**0.15**	0.83890	**-0.87**	0.07620	**-0.79**	0.18051
STM0234	ldcC	lysine decarboxylase 2	**-0.70**	0.28591	**0.17**	0.65577	**-0.92**	0.10652
STM0234	ldcC	lysine decarboxylase 2	**0.19**	0.76451	**0.20**	0.45852	**0.39**	0.27456
STM0235	yaeR	putative lactoylglutathione lyase	**-0.03**	0.96567	**-0.54**	0.08941	**0.17**	0.74204
STM0235	yaeR	putative lactoylglutathione lyase	**0.62**	0.56681	**0.11**	0.86520	**0.77**	0.24607
STM0236	mesJ	cell cycle protein	**-0.93**	0.08440	**-0.93**	0.01001	**-1.40**	0.03582
STM0236	mesJ	cell cycle protein	**0.49**	0.37352	**-0.72**	0.02890	**0.16**	0.71863
STM0237	rof	Rho-dependent transcription termination modulator	**-1.10**	0.05312	**-0.55**	0.10878	**-1.10**	0.01499
STM0237	rof	Rho-dependent transcription termination modulator	**-0.18**	0.67678	**-0.48**	0.09489	**-0.46**	0.38319
STM0238	yaeP	hypothetical protein STM0238	**-1.58**	0.04652	**-0.58**	0.06192	**-0.09**	0.83791
STM0238	yaeP	hypothetical protein STM0238	**-1.30**	0.05496	**0.06**	0.85155	**-0.07**	0.88163
STM0239	yaeQ	putative cytoplasmic protein	**-1.47**	0.12485	**-0.96**	0.01376	**-0.64**	0.42310
STM0239	yaeQ	putative cytoplasmic protein	**-1.07**	0.05056	**-1.70**	0.00057	**-1.74**	0.00322
STM0240	yaeJ	hypothetical protein STM0240	**-1.07**	0.06218	**-0.09**	0.78792	**-0.65**	0.07569
STM0240	yaeJ	hypothetical protein STM0240	**0.33**	0.76451	**-0.03**	0.95605	**0.35**	0.33281
STM0242	proS	prolyl-tRNA synthetase	**-0.10**	0.87043	**-1.88**	0.00108	**-1.32**	0.02684
STM0242	proS	prolyl-tRNA synthetase	**-0.10**	0.90313	**-2.36**	0.00678	**-0.22**	0.70170
STM0243	yaeB	putative regulatory protein	**-1.17**	0.25779	**-0.83**	0.01733	**-2.36**	0.00113
STM0243	yaeB	putative regulatory protein	**-0.09**	0.95054	**-1.00**	0.01222	**-1.81**	0.00780
STM0244	rcsF	colanic acid synthesis regulator	**-2.60**	0.00571	**-1.54**	0.00130	**-2.07**	0.00118
STM0244	rcsF	colanic acid synthesis regulator	**-1.40**	0.02655	**-1.04**	0.03556	**-1.61**	0.00278
STM0245	yaeC	putative outer membrane lipoprotein	**-1.46**	0.12963	**-0.36**	0.34109	**-1.29**	0.02347
STM0245	yaeC	putative outer membrane lipoprotein	**-0.24**	0.65131	**-0.34**	0.21026	**-1.27**	0.00528
STM0246	yaeE	putative transport protein	**-1.87**	0.01164	**-0.71**	0.02321	**-0.63**	0.18491
STM0246	yaeE	putative transport protein	**-1.26**	0.02667	**0.40**	0.37103	**-0.30**	0.59876
STM0247	abc	putative transport protein	**-1.81**	0.03508	**-0.95**	0.01006	**-0.75**	0.08104
STM0247	abc	putative transport protein	**-0.98**	0.41696	**-0.89**	0.00927	**-0.44**	0.21695
STM0248	yaeD	hypothetical protein STM0248	**1.31**	0.03167	**0.37**	0.24386	**0.35**	0.45257
STM0248	yaeD	hypothetical protein STM0248	**1.15**	0.12056	**0.16**	0.67323	**1.23**	0.03977
STM0249	rrsH	STM0249	**-1.59**	0.21078	**0.93**	0.03369	**0.26**	0.61903
STM0249	rrsH	STM0249	**-1.37**	0.43159	**0.69**	0.06921	**0.06**	0.92607
STM0250	ileV	STM0250	**0.95**	0.26794	**0.51**	0.16730	**1.26**	0.02305
STM0250	ileV	STM0250	**1.66**	0.02121	**0.84**	0.06829	**1.19**	0.02045
STM0251	alaV	STM0251	**0.75**	0.34691	**0.25**	0.52399	**0.73**	0.10246
STM0251	alaV	STM0251	**1.55**	0.02400	**0.87**	0.02044	**0.65**	0.08377
STM0252	rrlH	STM0252	**-2.35**	0.04570	**0.75**	0.17038	**0.24**	0.69099
STM0252	rrlH	STM0252	**-2.08**	0.03561	**1.16**	0.01083	**0.06**	0.91555
STM0253	rrfH	STM0253	**0.21**	0.69382	**-0.15**	0.68981	**0.25**	0.62768
STM0253	rrfH	STM0253	**0.51**	0.32123	**-0.17**	0.67976	**0.46**	0.24875
STM0254	aspU	STM0254	**-0.60**	0.33366	**0.70**	0.21886	**0.10**	0.83871
STM0254	aspU	STM0254	**-0.30**	0.61544	**0.41**	0.36782	**0.07**	0.87206
STM0255	yafB	2,5-diketo-D-gluconate reductase B	**-1.18**	0.15583	**-0.95**	0.01203	**0.12**	0.83312
STM0255	yafB	2,5-diketo-D-gluconate reductase B	**0.20**	0.62843	**-1.14**	0.03527	**0.71**	0.12468
STM0256	yafC	putative transcriptional regulator	**-1.47**	0.04976	**-1.20**	0.00536	**0.23**	0.67001
STM0256	yafC	putative transcriptional regulator	**-1.52**	0.02281	**-1.33**	0.00215	**0.30**	0.48583
STM0257	STM0257	putative drug efflux protein	**-0.30**	0.49184	**-0.33**	0.27638	**-0.26**	0.72025
STM0257	STM0257	putative drug efflux protein	**-1.48**	0.09447	**-0.86**	0.02722	**-1.55**	0.09804
STM0258	yafD	hypothetical protein STM0258	**-0.84**	0.08154	**0.72**	0.03620	**-0.34**	0.56742
STM0258	yafD	hypothetical protein STM0258	**-0.44**	0.37352	**0.73**	0.02700	**0.35**	0.59886
STM0259	yafE	putative methyltransferase	**-0.17**	0.70976	**1.36**	0.02815	**-1.00**	0.01911
STM0259	yafE	putative methyltransferase	**0.45**	0.31724	**1.48**	0.00209	**-0.17**	0.70148

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM0260	dniR	transcriptional regulator	**3.15**	0.11193	**2.31**	0.00015	**2.04**	0.00894
STM0260	dniR	transcriptional regulator	**-0.54**	0.82326	**2.00**	0.00204	**0.19**	0.76232
STM0261	gloB	hydroxyacylglutathione hydrolase	**-0.83**	0.11463	**1.10**	0.02026	**-1.62**	0.01551
STM0261	gloB	hydroxyacylglutathione hydrolase	**0.35**	0.57498	**0.97**	0.01275	**-0.18**	0.80729
STM0262	yafS	putative SAM-dependent methyltransferase	**-0.87**	0.21374	**0.08**	0.83238	**0.74**	0.52255
STM0262	yafS	putative SAM-dependent methyltransferase	**0.02**	0.97285	**-0.53**	0.09094	**-0.12**	0.84461
STM0263	rnhA	ribonuclease H	**0.63**	0.22844	**0.19**	0.69786	**-1.15**	0.01504
STM0263	rnhA	ribonuclease H	**0.58**	0.20626	**-0.09**	0.81152	**-0.72**	0.16683
STM0264	dnaQ	DNA polymerase III subunit epsilon	**-1.31**	0.03369	**-0.82**	0.03891	**-0.54**	0.16054
STM0264	dnaQ	DNA polymerase III subunit epsilon	**1.70**	0.06090	**-0.58**	0.11251	**0.27**	0.56839
STM0265	aspV	STM0265	**-1.25**	0.04812	**0.17**	0.72668	**0.19**	0.68125
STM0265	aspV	STM0265	**-0.65**	0.27981	**0.12**	0.82375	**-0.01**	0.97874
STM0266	STM0266	putative cytoplasmic protein	**-0.34**	0.63111	**-0.50**	0.18123	**-0.92**	0.02623
STM0266	STM0266	putative cytoplasmic protein	**-0.51**	0.25707	**-0.75**	0.06273	**-0.52**	0.17408
STM0267	STM0267	putative cytoplasmic protein	**-0.98**	0.05245	**-0.25**	0.47940	**-0.27**	0.52711
STM0267	STM0267	putative cytoplasmic protein	**-1.06**	0.13291	**-1.42**	0.01072	**-0.22**	0.85842
STM0268	STM0268	putative cytoplasmic protein	**0.24**	0.71380	**-2.76**	0.00056	**-1.16**	0.10461
STM0268	STM0268	putative cytoplasmic protein	**0.18**	0.78595	**-2.70**	0.00014	**-0.31**	0.69836
STM0269	STM0269	putative cytoplasmic protein	**-0.24**	0.80094	**-0.42**	0.24775	**-1.37**	0.03153
STM0269	STM0269	putative cytoplasmic protein	**0.19**	0.87813	**-0.38**	0.34761	**-0.77**	0.45935
STM0270	STM0270	putative cytoplasmic protein	**-0.59**	0.24713	**-0.44**	0.46632	**-0.16**	0.68490
STM0270	STM0270	putative cytoplasmic protein	**-1.19**	0.34585	**-0.71**	0.03755	**-0.47**	0.24787
STM0271	STM0271	putative cytoplasmic protein	**-0.15**	0.86361	**0.69**	0.05346	**-0.22**	0.67096
STM0271	STM0271	putative cytoplasmic protein	**1.20**	0.19282	**0.40**	0.33762	**1.44**	0.02860
STM0272	STM0272	putative chaperone ATPase	**0.12**	0.88887	**-0.52**	0.14676	**-0.43**	0.41248
STM0272	STM0272	putative chaperone ATPase	**0.47**	0.44347	**0.55**	0.18273	**0.73**	0.16331
STM0273	STM0273	putative cytoplasmic protein	**0.14**	0.82796	**-0.16**	0.75985	**-0.62**	0.40503
STM0273	STM0273	putative cytoplasmic protein	**0.43**	0.55466	**-0.22**	0.45944	**0.44**	0.43448
STM0274	STM0274	putative cytoplasmic protein	**-0.09**	0.89074	**-0.07**	0.85978	**0.93**	0.11443
STM0274	STM0274	putative cytoplasmic protein	**-0.75**	0.47036	**-0.96**	0.19130	**-0.28**	0.57478
STM0275,s	STM0275,s	putative cytoplasmic protein	**-0.20**	0.83452	**0.34**	0.38822	**-0.66**	0.32583
STM0275,s	STM0275,s	putative cytoplasmic protein	**-1.40**	0.02492	**-1.23**	0.04708	**0.15**	0.79506
STM0276	STM0276	putative cytoplasmic protein	**1.24**	0.08296	**0.47**	0.15971	**-0.56**	0.13422
STM0276	STM0276	putative cytoplasmic protein	**3.14**	0.06234	**-0.42**	0.47184	**0.21**	0.70830
STM0277	STM0277	putative cytoplasmic protein	**1.01**	0.09208	**-0.13**	0.81126	**-0.23**	0.73603
STM0277	STM0277	putative cytoplasmic protein	**0.71**	0.20867	**0.08**	0.86757	**0.36**	0.61774
STM0278	STM0278	putative periplasmic protein	**0.03**	0.96378	**0.34**	0.45657	**0.55**	0.40716
STM0278	STM0278	putative periplasmic protein	**0.69**	0.36030	**1.12**	0.02793	**1.95**	0.00905
STM0279	STM0279	putative cytoplasmic protein	**3.03**	0.06140	**-1.71**	0.00234	**0.19**	0.76157
STM0279	STM0279	putative cytoplasmic protein	**3.46**	0.01388	**-1.78**	0.00438	**-0.03**	0.96217
STM0280	STM0280	putative outer membrane lipoprotein	**1.88**	0.03111	**0.22**	0.48490	**2.64**	0.00216
STM0280	STM0280	putative outer membrane lipoprotein	**2.65**	0.00727	**-0.04**	0.92332	**3.05**	0.00130
STM0281	STM0281	putative cytoplasmic protein	**1.45**	0.22065	**-0.48**	0.09951	**1.77**	0.05066
STM0281	STM0281	putative cytoplasmic protein	**2.18**	0.01600	**0.66**	0.53636	**1.28**	0.01955
STM0282	STM0282	hypothetical protein STM0282	**-0.49**	0.27290	**-0.03**	0.94723	**-0.35**	0.59002
STM0282	STM0282	hypothetical protein STM0282	**0.45**	0.44254	**-0.85**	0.09595	**0.05**	0.94872
STM0283	STM0283	putative inner membrane protein	**-0.73**	0.14984	**-0.13**	0.91349	**-0.04**	0.94651
STM0283	STM0283	putative inner membrane protein	**0.45**	0.51450	**-0.61**	0.11555	**-0.37**	0.50024
STM0284	STM0284	putative Shiga-like toxin A subunit	**-0.86**	0.08168	**0.79**	0.05693	**0.42**	0.39961
STM0284	STM0284	putative Shiga-like toxin A subunit	**-1.35**	0.04270	**-0.10**	0.78725	**-0.17**	0.79099
STM0285	STM0285	putative inner membrane protein	**-0.73**	0.41786	**-0.70**	0.10642	**-1.01**	0.06193
STM0285	STM0285	putative inner membrane protein	**0.12**	0.82875	**-0.87**	0.05324	**0.45**	0.52733
STM0286	STM0286	putative cytoplasmic protein	**1.08**	0.05582	**0.67**	0.04705	**0.76**	0.28422
STM0286	STM0286	putative cytoplasmic protein	**1.76**	0.01982	**0.07**	0.88217	**2.64**	0.00072
STM0287	STM0287	putative periplasmic protein	**0.71**	0.19529	**0.79**	0.02667	**0.36**	0.41923
STM0287	STM0287	putative periplasmic protein	**1.15**	0.06515	**0.83**	0.07614	**-0.05**	0.95596
STM0288	STM0288	putative cytoplasmic protein	**0.71**	0.21068	**-0.94**	0.05962	**-1.22**	0.14647
STM0288	STM0288	putative cytoplasmic protein	**1.18**	0.03861	**-0.96**	0.04492	**-0.40**	0.59886
STM0289	STM0289	putative cytoplasmic protein	**0.80**	0.22435	**-0.52**	0.23106	**0.28**	0.77070
STM0289	STM0289	putative cytoplasmic protein	**1.76**	0.03422	**-0.57**	0.26038	**0.78**	0.07951
STM0290	STM0290	putative cytoplasmic protein	**-0.65**	0.36920	**-1.33**	0.00432	**-0.53**	0.39278
STM0290	STM0290	putative cytoplasmic protein	**1.48**	0.03382	**-2.06**	0.00022	**-0.10**	0.78315
STM0291	STM0291	putative RHS-like protein	**0.14**	0.79237	**1.71**	0.00397	**0.97**	0.03993
STM0291	STM0291	putative RHS-like protein	**1.31**	0.05665	**1.78**	0.00100	**1.12**	0.00912
STM0292	STM0292	putative RHS-like protein	**-1.19**	0.03861	**0.86**	0.03785	**-0.64**	0.31811
STM0292	STM0292	putative RHS-like protein	**0.86**	0.12988	**1.71**	0.00054	**0.58**	0.13643
STM0293	STM0293	putative cytoplasmic protein	**0.27**	0.56983	**1.55**	0.00666	**-0.73**	0.15615
STM0293	STM0293	putative cytoplasmic protein	**0.30**	0.70725	**0.93**	0.02180	**0.00**	0.99701
STM0294	STM0294	putative cytoplasmic protein	**0.70**	0.19847	**1.10**	0.02842	**1.08**	0.01426
STM0294	STM0294	putative cytoplasmic protein	**1.39**	0.03379	**0.84**	0.06553	**1.20**	0.06200

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM0294,1N	STM0294,1N	hypothetical protein STM0294,1N	**3.26**	0.00645	**1.15**	0.03290	**3.76**	0.00010
STM0294,1N	STM0294,1N	hypothetical protein STM0294,1N	**3.33**	0.00546	**-0.13**	0.93191	**3.62**	0.00008
STM0295	STM0295	putative cytoplasmic protein	**3.90**	0.00546	**2.83**	0.00138	**5.03**	0.00005
STM0295	STM0295	putative cytoplasmic protein	**3.27**	0.00547	**1.66**	0.01776	**5.44**	0.00002
STM0300	safB	putative fimbrial assembly chaparone	**0.31**	0.62076	**1.05**	0.05189	**0.17**	0.83006
STM0300	safB	putative fimbrial assembly chaparone	**1.78**	0.01765	**0.51**	0.42233	**1.70**	0.00335
STM0301	safC	putative fimbrial usher	**0.46**	0.47324	**0.07**	0.94679	**0.83**	0.09407
STM0301	safC	putative fimbrial usher	**0.99**	0.05377	**1.85**	0.00065	**-0.55**	0.15834
STM0302	safD	putative fimbrial subunit	**0.30**	0.58485	**1.67**	0.00110	**-1.07**	0.03475
STM0302	safD	putative fimbrial subunit	**0.73**	0.12519	**1.31**	0.01103	**-0.06**	0.94646
STM0303	ybeJ	putative xylanase/chitin deacetylase	**0.79**	0.26284	**-0.64**	0.30216	**-0.69**	0.15956
STM0303	ybeJ	putative xylanase/chitin deacetylase	**1.20**	0.27549	**-0.69**	0.14608	**0.18**	0.75788
STM0304	sinR	transcriptional regulator	**-0.56**	0.24692	**-1.11**	0.01113	**-0.71**	0.16517
STM0304	sinR	transcriptional regulator	**-0.76**	0.47550	**-0.63**	0.11518	**-0.33**	0.38859
STM0306	STM0306	SapA-like protein	**0.66**	0.31507	**0.29**	0.49921	**-2.02**	0.01290
STM0306	STM0306	SapA-like protein	**1.71**	0.01479	**0.37**	0.47297	**-0.18**	0.71302
STM0307	STM0307	VirG-like protein	**-1.07**	0.07040	**1.14**	0.00695	**-0.41**	0.49271
STM0307	STM0307	VirG-like protein	**1.11**	0.05865	**1.28**	0.00256	**1.69**	0.00843
STM0308	yafV	putative amidohydrolase	**-0.26**	0.70034	**0.14**	0.61349	**-0.96**	0.04719
STM0308	yafV	putative amidohydrolase	**1.87**	0.01155	**0.80**	0.03824	**0.49**	0.21204
STM0309	fadE	acyl-CoA dehydrogenase	**0.58**	0.54856	**0.74**	0.04259	**1.13**	0.01597
STM0309	fadE	acyl-CoA dehydrogenase	**0.67**	0.48874	**0.78**	0.03242	**1.60**	0.00877
STM0310	ghmA	phosphoheptose isomerase	**-2.38**	0.00831	**0.19**	0.75160	**-1.13**	0.01175
STM0310	ghmA	phosphoheptose isomerase	**-1.29**	0.05247	**-0.54**	0.07016	**-0.88**	0.05385
STM0311	yafJ	putative glutamine amidotransferase	**-0.85**	0.07461	**-0.08**	0.81482	**-1.14**	0.13273
STM0311	yafJ	putative glutamine amidotransferase	**-0.98**	0.06241	**-0.19**	0.56737	**-0.62**	0.18303
STM0312	yafK	putative periplasmic protein	**-2.23**	0.01027	**-0.62**	0.05446	**-1.97**	0.00228
STM0312	yafK	putative periplasmic protein	**-1.54**	0.02655	**-0.69**	0.04908	**-2.63**	0.00034
STM0313	dinP	DNA polymerase IV	**0.81**	0.33161	**0.53**	0.28850	**0.25**	0.80874
STM0313	dinP	DNA polymerase IV	**2.24**	0.00992	**-0.29**	0.72704	**0.76**	0.16277
STM0315	prfH	peptide chain release factor 2	**-0.44**	0.41885	**0.47**	0.24038	**-2.49**	0.00058
STM0315	prfH	peptide chain release factor 2	**-0.34**	0.41696	**0.87**	0.02865	**-1.92**	0.00476
STM0316	pepD	aminoacyl-histidine dipeptidase	**-1.30**	0.04378	**1.08**	0.01086	**-1.39**	0.01254
STM0316	pepD	aminoacyl-histidine dipeptidase	**-0.57**	0.22379	**1.67**	0.00349	**-1.02**	0.04449
STM0317	gpt	xanthine phosphoribosyltransferase	**-1.50**	0.01645	**-0.97**	0.02499	**-1.73**	0.00147
STM0317	gpt	xanthine phosphoribosyltransferase	**-0.47**	0.35799	**-1.26**	0.00959	**-0.95**	0.04027
STM0318	yafA	hypothetical protein STM0318	**-1.09**	0.05948	**-0.37**	0.28109	**-0.36**	0.40030
STM0318	yafA	hypothetical protein STM0318	**-0.45**	0.45611	**-0.49**	0.22238	**0.58**	0.11876
STM0319	crl	transcriptional regulator	**-0.60**	0.65388	**-0.74**	0.06799	**-0.62**	0.17055
STM0319	crl	transcriptional regulator	**0.66**	0.19039	**-0.34**	0.33532	**-0.74**	0.06840
STM0320	phoE	outer membrane pore protein E precursor	**-1.48**	0.04758	**-0.23**	0.56825	**-0.49**	0.39379
STM0320	phoE	outer membrane pore protein E precursor	**-0.22**	0.82735	**-0.53**	0.14809	**-0.23**	0.57695
STM0321	proB	gamma-glutamyl kinase	**-1.72**	0.01699	**-0.42**	0.26171	**-3.13**	0.00027
STM0321	proB	gamma-glutamyl kinase	**-0.71**	0.12316	**-0.61**	0.11876	**-2.11**	0.00050
STM0322	proA	gamma-glutamyl phosphate reductase	**-0.77**	0.17969	**-0.16**	0.58424	**-0.69**	0.11179
STM0322	proA	gamma-glutamyl phosphate reductase	**0.23**	0.73216	**-0.29**	0.32295	**0.19**	0.78771
STM0323	thrW	STM0323	**-2.02**	0.01047	**-1.57**	0.01373	**3.03**	0.00045
STM0323	thrW	STM0323	**-0.40**	0.49299	**-1.07**	0.05854	**3.25**	0.00008
STM0325	STM0325	putative truncated IS3 transposase	**-0.29**	0.69395	**-0.58**	0.15359	**-1.23**	0.06104
STM0325	STM0325	putative truncated IS3 transposase	**1.26**	0.09878	**-0.81**	0.03968	**-0.13**	0.79044
STM0327	STM0327	putative cytoplasmic protein	**0.21**	0.78079	**1.29**	0.00411	**1.30**	0.01238
STM0327	STM0327	putative cytoplasmic protein	**1.25**	0.22810	**1.22**	0.00990	**3.05**	0.00431
STM0328,s	STM0328,s	putative permease	**0.05**	0.93975	**-1.24**	0.08373	**-0.48**	0.32071
STM0328,s	STM0328,s	putative permease	**1.54**	0.01788	**-1.03**	0.02604	**1.14**	0.01145
STM0329	STM0329	isopropylmalate isomerase large subunit	**1.08**	0.24833	**1.15**	0.01395	**2.41**	0.00071
STM0329	STM0329	isopropylmalate isomerase large subunit	**1.06**	0.22639	**0.52**	0.33447	**2.79**	0.00024
STM0330	STM0330	putative 3-isopropylmalate isomerase	**0.83**	0.17735	**-1.39**	0.00764	**0.48**	0.60754
STM0330	STM0330	putative 3-isopropylmalate isomerase	**0.59**	0.26511	**-1.41**	0.00509	**1.81**	0.01230
STM0331	STM0331	putative fumarylacetoacetate hydrolase	**-0.97**	0.12003	**-0.17**	0.85326	**-0.66**	0.38370
STM0331	STM0331	putative fumarylacetoacetate hydrolase	**0.75**	0.18876	**-0.95**	0.01882	**0.80**	0.36586
STM0332	STM0332	putative hydrolase/acyltransferase	**-0.20**	0.72557	**0.30**	0.40732	**1.46**	0.00840
STM0332	STM0332	putative hydrolase/acyltransferase	**0.89**	0.53618	**-1.63**	0.02217	**-2.06**	0.01095
STM0333	STM0333	putative transcriptional regulator	**-0.32**	0.72201	**-1.92**	0.00244	**-1.07**	0.29558
STM0333	STM0333	putative transcriptional regulator	**-0.16**	0.80777	**-0.80**	0.04075	**-0.67**	0.25586
STM0335	STM0335	putative outer membrane protein	**-0.45**	0.41950	**-0.67**	0.39209	**-0.67**	0.22619
STM0335	STM0335	putative outer membrane protein	**0.00**	0.99756	**-0.84**	0.14928	**0.57**	0.31962
STM0336	stbE	putative fimbrial chaparone	**0.33**	0.54847	**1.49**	0.33479	**-0.34**	0.60390
STM0336	stbE	putative fimbrial chaparone	**0.81**	0.09401	**-0.90**	0.05330	**0.63**	0.13122
STM0337	stbD	putative fimbrial usher	**0.10**	0.88435	**0.62**	0.08758	**0.83**	0.08784
STM0337	stbD	putative fimbrial usher	**1.85**	0.09788	**0.21**	0.67955	**2.19**	0.00233

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM0338	stbC	putative fimbrial usher	**1.25**	0.03578	**1.06**	0.04902	**-0.31**	0.47459
STM0338	stbC	putative fimbrial usher	**2.21**	0.01336	**1.18**	0.05327	**1.22**	0.06140
STM0339	stbB	putative fimbrial chaperone	**4.72**	0.08359	**-0.84**	0.04037	**2.87**	0.02488
STM0339	stbB	putative fimbrial chaperone	**2.29**	0.05250	**0.32**	0.47985	**1.58**	0.28613
STM0340	stbA	putative fimbrial major subunit	**-0.20**	0.87933	**1.29**	0.01047	**2.26**	0.00168
STM0340	stbA	putative fimbrial major subunit	**-0.31**	0.86173	**0.87**	0.07749	**2.59**	0.00030
STM0341	STM0341	putative inner membrane protein	**0.05**	0.91382	**0.17**	0.78293	**-0.20**	0.72994
STM0341	STM0341	putative inner membrane protein	**0.48**	0.64858	**1.03**	0.17739	**-0.33**	0.54924
STM0342	STM0342	putative periplasmic protein	**0.18**	0.74416	**0.20**	0.76403	**1.48**	0.01320
STM0342	STM0342	putative periplasmic protein	**0.40**	0.35321	**0.12**	0.74224	**0.87**	0.07936
STM0343	STM0343	hypothetical protein STM0343	**0.04**	0.94323	**0.88**	0.02001	**-0.05**	0.93137
STM0343	STM0343	hypothetical protein STM0343	**0.71**	0.30754	**0.56**	0.23766	**-0.09**	0.83862
STM0344	STM0344	putative response regulator	**-0.67**	0.14382	**0.64**	0.28290	**-0.26**	0.61128
STM0344	STM0344	putative response regulator	**0.80**	0.63756	**-0.05**	0.91856	**-0.70**	0.17998
STM0345	STM0345	putative inner membrane protein	**0.77**	0.55647	**0.46**	0.13101	**-0.97**	0.03020
STM0345	STM0345	putative inner membrane protein	**1.03**	0.31051	**0.02**	0.97149	**-0.15**	0.72283
STM0346	STM0346	putative outer membrane protein	**-0.07**	0.89465	**0.67**	0.14174	**0.11**	0.91210
STM0346	STM0346	putative outer membrane protein	**0.32**	0.49792	**0.09**	0.83752	**0.68**	0.24360
STM0347	STM0347	putative response regulator	**-0.82**	0.19700	**0.01**	0.98453	**-0.60**	0.13475
STM0347	STM0347	putative response regulator	**0.39**	0.41995	**-0.75**	0.14794	**0.21**	0.59460
STM0348	STM0348	putative inner membrane protein	**-0.66**	0.35386	**0.50**	0.34699	**-0.76**	0.25011
STM0348	STM0348	putative inner membrane protein	**-0.24**	0.80754	**0.45**	0.36784	**0.34**	0.59911
STM0349	STM0349	putative outer membrane lipoprotein	**0.37**	0.60319	**0.48**	0.14151	**-1.05**	0.21976
STM0349	STM0349	putative outer membrane lipoprotein	**1.42**	0.20580	**0.52**	0.15098	**0.60**	0.31004
STM0350,S	STM0350,S	outer membrane efflux-like protein	**0.43**	0.39843	**0.19**	0.59541	**-0.97**	0.03253
STM0350,S	STM0350,S	outer membrane efflux-like protein	**1.31**	0.05440	**-0.48**	0.13950	**0.76**	0.22280
STM0351	STM0351	putative cation efflux system protein	**0.03**	0.95941	**-0.23**	0.62123	**0.64**	0.20976
STM0351	STM0351	putative cation efflux system protein	**0.64**	0.30327	**-0.87**	0.04930	**0.24**	0.76688
STM0352,S	STM0352,S	putative cation efflux pump	**0.46**	0.62037	**-0.57**	0.16945	**-0.69**	0.15456
STM0352,S	STM0352,S	putative cation efflux pump	**1.71**	0.10692	**-0.33**	0.28209	**1.13**	0.05318
STM0353	STM0353	putative cation transport ATPase	**0.75**	0.19430	**0.59**	0.11111	**0.18**	0.63925
STM0353	STM0353	putative cation transport ATPase	**1.99**	0.01067	**-0.06**	0.92546	**1.08**	0.02143
STM0354	STM0354	putative transcriptional regulator	**0.38**	0.48937	**-0.57**	0.22710	**-0.42**	0.46990
STM0354	STM0354	putative transcriptional regulator	**0.80**	0.21947	**-0.63**	0.06172	**0.84**	0.19111
STM0355	STM0355	putative copper chaperone	**0.79**	0.16748	**0.10**	0.82392	**-0.24**	0.48750
STM0355	STM0355	putative copper chaperone	**0.84**	0.09758	**-0.29**	0.35977	**1.29**	0.01732
STM0356	STM0356	putative inner membrane protein	**-1.07**	0.04939	**-1.17**	0.01510	**-0.97**	0.10275
STM0356	STM0356	putative inner membrane protein	**-1.92**	0.10952	**-1.21**	0.06340	**-0.97**	0.31024
STM0357	mod	DNA methylase	**-0.62**	0.20931	**-1.19**	0.00960	**-0.74**	0.16277
STM0357	mod	DNA methylase	**-0.57**	0.24382	**-1.40**	0.01337	**-0.47**	0.28060
STM0358,S	res	DNA restriction enzyme	**-0.98**	0.05113	**-0.27**	0.41360	**0.06**	0.90427
STM0358,S	res	DNA restriction enzyme	**0.47**	0.50015	**-0.96**	0.01421	**0.42**	0.31469
STM0359	STM0359	putative cytoplasmic protein	**2.08**	0.14351	**-1.47**	0.00273	**3.01**	0.01520
STM0359	STM0359	putative cytoplasmic protein	**2.05**	0.03893	**-1.62**	0.01412	**3.93**	0.00072
STM0360	STM0360	cytochrome BD2 subunit I	**-0.78**	0.24636	**0.82**	0.06534	**3.46**	0.00019
STM0360	STM0360	cytochrome BD2 subunit I	**-0.88**	0.54588	**0.85**	0.02025	**3.79**	0.00010
STM0361	STM0361	cytochrome BD2 subunit II	**-0.72**	0.17613	**0.22**	0.56804	**1.83**	0.00458
STM0361	STM0361	cytochrome BD2 subunit II	**0.35**	0.56791	**0.58**	0.06470	**2.15**	0.00176
STM0363	STM0363	putative transcriptional regulator	**-0.62**	0.26997	**-0.17**	0.66465	**-0.41**	0.23553
STM0363	STM0363	putative transcriptional regulator	**-0.10**	0.87342	**0.98**	0.39743	**0.07**	0.91391
STM0364	foxA	ferrioxamine receptor	**-0.09**	0.83569	**0.22**	0.52151	**-0.19**	0.67083
STM0364	foxA	ferrioxamine receptor	**0.21**	0.85322	**0.68**	0.11127	**0.04**	0.95808
STM0365	yahN	putative transport protein	**-0.08**	0.92540	**0.65**	0.08386	**0.38**	0.39159
STM0365	yahN	putative transport protein	**0.75**	0.22959	**1.25**	0.02962	**0.41**	0.44043
STM0366	yahO	putative periplasmic protein	**1.28**	0.08459	**2.60**	0.00091	**4.47**	0.00003
STM0366	yahO	putative periplasmic protein	**2.24**	0.04942	**1.97**	0.01350	**5.20**	0.00009
STM0367	prpR	prp operon regulator	**-0.53**	0.47718	**1.36**	0.00441	**2.68**	0.00049
STM0367	prpR	prp operon regulator	**-0.15**	0.91131	**1.52**	0.00289	**3.10**	0.00035
STM0368	prpB	putative carboxyphosphonoenolpyruvate mutase	**0.72**	0.23286	**1.18**	0.00959	**0.63**	0.41099
STM0368	prpB	putative carboxyphosphonoenolpyruvate mutase	**2.69**	0.00720	**0.92**	0.02356	**2.37**	0.00075
STM0369	prpC	citrate synthase	**1.29**	0.02585	**-0.09**	0.78135	**-0.35**	0.66558
STM0369	prpC	citrate synthase	**2.07**	0.08093	**-0.17**	0.69980	**-1.32**	0.08818
STM0370	prpD	2-methylcitrate dehydratase	**-0.30**	0.54425	**0.34**	0.35860	**0.47**	0.19903
STM0370	prpD	2-methylcitrate dehydratase	**0.36**	0.55398	**-0.95**	0.06849	**-1.42**	0.01993
STM0371	prpE	putative acetyl-CoA synthetase	**-0.66**	0.13892	**-0.04**	0.90002	**-1.52**	0.01242
STM0371	prpE	putative acetyl-CoA synthetase	**-0.36**	0.44254	**0.04**	0.91712	**-0.22**	0.69226
STM0372	hemB	delta-aminolevulinic acid dehydratase	**-1.31**	0.03755	**0.16**	0.73906	**-0.19**	0.84397
STM0372	hemB	delta-aminolevulinic acid dehydratase	**-0.95**	0.09910	**-0.03**	0.92781	**-0.43**	0.36642
STM0373	yaiU	flagellar protein	**0.31**	0.47264	**0.96**	0.01854	**0.24**	0.68844
STM0373	yaiU	flagellar protein	**2.24**	0.00983	**0.56**	0.25810	**1.66**	0.00415

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM0374	yaiV	putative inner membrane protein	**0.48**	0.37490	**1.33**	0.01781	**1.55**	0.00673
STM0374	yaiV	putative inner membrane protein	**-0.56**	0.43412	**0.63**	0.14517	**0.58**	0.37964
STM0375	ampH	penicillin-binding protein	**0.26**	0.62250	**0.92**	0.05004	**1.03**	0.04274
STM0375	ampH	penicillin-binding protein	**0.02**	0.97079	**0.17**	0.66878	**0.27**	0.61356
STM0376	sbmA	putative ABC transporter membrane protein	**-1.23**	0.15783	**-0.34**	0.36871	**-1.79**	0.00293
STM0376	sbmA	putative ABC transporter membrane protein	**-0.26**	0.60234	**-0.17**	0.58742	**-0.43**	0.39057
STM0377	yaiW	putative outer membrane lipoprotein	**1.53**	0.03932	**1.40**	0.01677	**0.00**	0.99713
STM0377	yaiW	putative outer membrane lipoprotein	**2.32**	0.02126	**1.09**	0.01329	**1.88**	0.01071
STM0378	yaiY	putative inner membrane protein	**-0.12**	0.79332	**1.31**	0.00628	**1.84**	0.00087
STM0378	yaiY	putative inner membrane protein	**1.73**	0.03822	**0.75**	0.06684	**2.75**	0.00031
STM0379	yaiZ	putative inner membrane protein	**-1.21**	0.06705	**-0.50**	0.09943	**-1.09**	0.04261
STM0379	yaiZ	putative inner membrane protein	**0.53**	0.41805	**-0.71**	0.04103	**0.49**	0.26081
STM0380	ddl	D-alanylalanine synthetase	**-1.31**	0.05992	**-0.27**	0.38705	**-1.29**	0.00903
STM0380	ddl	D-alanylalanine synthetase	**0.01**	0.98879	**-0.31**	0.42032	**-0.29**	0.41955
STM0381	STM0381	putative inner membrane protein	**-0.17**	0.75541	**0.13**	0.73603	**0.58**	0.14917
STM0381	STM0381	putative inner membrane protein	**1.31**	0.19524	**-0.77**	0.15969	**3.01**	0.00026
STM0382	STM0382	putative permease	**-0.46**	0.35773	**-0.15**	0.66753	**-0.04**	0.93616
STM0382	STM0382	putative permease	**0.80**	0.21751	**0.25**	0.49031	**0.56**	0.17554
STM0383	yaiB	putative cytoplasmic protein	**0.03**	0.97750	**0.80**	0.01928	**-1.66**	0.00357
STM0383	yaiB	putative cytoplasmic protein	**0.91**	0.24565	**0.57**	0.06592	**-1.84**	0.01260
STM0384	psiF	phosphate starvation-inducible protein	**0.29**	0.52490	**1.17**	0.01119	**1.59**	0.00827
STM0384	psiF	phosphate starvation-inducible protein	**1.26**	0.06515	**1.64**	0.00188	**1.85**	0.00359
STM0385	yaiC	hypothetical protein STM0385	**-1.18**	0.06356	**1.19**	0.00363	**-1.65**	0.00322
STM0385	yaiC	hypothetical protein STM0385	**0.24**	0.62132	**1.58**	0.00129	**-0.44**	0.27981
STM0386	proC	pyrroline-5-carboxylate reductase	**-1.23**	0.04896	**0.80**	0.02245	**-0.87**	0.07639
STM0386	proC	pyrroline-5-carboxylate reductase	**-0.34**	0.56070	**1.50**	0.00265	**-0.35**	0.37083
STM0387	yaiI	hypothetical protein STM0387	**-0.85**	0.28662	**0.01**	0.97744	**-1.63**	0.00204
STM0387	yaiI	hypothetical protein STM0387	**0.00**	0.99790	**-0.20**	0.61719	**-0.63**	0.11432
STM0388	aroL	shikimate kinase II	**-0.38**	0.41100	**-0.13**	0.65590	**-0.11**	0.81576
STM0388	aroL	shikimate kinase II	**0.32**	0.65088	**0.07**	0.84409	**0.07**	0.89292
STM0389	yaiA	putative cytoplasmic protein	**0.72**	0.43575	**-0.14**	0.80186	**3.03**	0.00324
STM0389	yaiA	putative cytoplasmic protein	**0.23**	0.75116	**-0.12**	0.77446	**3.69**	0.00008
STM0390	aroM	aro operon protein	**-0.50**	0.29095	**0.72**	0.05247	**0.03**	0.95793
STM0390	aroM	aro operon protein	**-0.67**	0.14999	**0.44**	0.13791	**0.27**	0.51909
STM0391	yaiE	putative cytoplasmic protein	**-0.88**	0.16390	**-0.12**	0.78205	**-0.47**	0.21728
STM0391	yaiE	putative cytoplasmic protein	**-0.37**	0.62629	**-0.73**	0.03131	**-0.69**	0.16286
STM0392	rdgC	recombination associated protein	**1.36**	0.35142	**-0.03**	0.94295	**-1.19**	0.01343
STM0392	rdgC	recombination associated protein	**1.73**	0.13709	**-0.14**	0.70522	**-0.60**	0.11037
STM0393	yajF	putative sugar kinase/transcriptional regulator	**0.59**	0.40496	**-0.08**	0.87789	**-0.39**	0.44329
STM0393	yajF	putative sugar kinase/transcriptional regulator	**1.18**	0.05112	**-0.04**	0.90114	**0.73**	0.08988
STM0394	araJ	arabinose polymer transporter	**-1.51**	0.03561	**-0.24**	0.74633	**-0.28**	0.67325
STM0394	araJ	arabinose polymer transporter	**0.20**	0.79689	**-0.51**	0.20349	**-0.45**	0.30991
STM0395	sbcC	ATP-dependent dsDNA exonuclease	**1.55**	0.03520	**-0.45**	0.18879	**1.78**	0.06039
STM0395	sbcC	ATP-dependent dsDNA exonuclease	**2.67**	0.01099	**-0.02**	0.97848	**4.12**	0.00635
STM0396	sbcD	ATP-dependent dsDNA exonuclease	**-1.49**	0.09643	**-2.38**	0.00576	**-1.58**	0.04926
STM0396	sbcD	ATP-dependent dsDNA exonuclease	**-0.09**	0.92838	**-1.15**	0.00651	**-1.65**	0.00910
STM0397	phoB	response regulator	**0.13**	0.87342	**-0.05**	0.89573	**-0.99**	0.03567
STM0397	phoB	response regulator	**1.19**	0.14307	**-0.21**	0.73019	**0.52**	0.36562
STM0398	phoR	sensor kinase	**-0.77**	0.22922	**-0.34**	0.27983	**-0.47**	0.67615
STM0398	phoR	sensor kinase	**-0.18**	0.72860	**-0.06**	0.86476	**-0.60**	0.17762
STM0399	brnQ	branched-chain amino acid transporter	**1.02**	0.09456	**-1.01**	0.04569	**-1.31**	0.06961
STM0399	brnQ	branched-chain amino acid transporter	**1.50**	0.03517	**-1.59**	0.00165	**-0.10**	0.85584
STM0400	proY	putative proline transporter	**-2.21**	0.00929	**-1.85**	0.00082	**-1.91**	0.01077
STM0400	proY	putative proline transporter	**-1.98**	0.00845	**-1.59**	0.00121	**-1.53**	0.02184
STM0401	malZ	maltodextrin glucosidase	**-1.31**	0.03042	**0.37**	0.20977	**-1.47**	0.00292
STM0401	malZ	maltodextrin glucosidase	**-0.67**	0.19588	**0.25**	0.53890	**-1.67**	0.00211
STM0402	STM0402	putative thiol-alkyl hydroperoxide reductase	**-0.64**	0.19752	**0.01**	0.98144	**-2.01**	0.00193
STM0402	STM0402	putative thiol-alkyl hydroperoxide reductase	**-0.31**	0.56776	**0.31**	0.35953	**-1.98**	0.00804
STM0403	yajB	putative cytoplasmic protein	**-1.07**	0.03991	**0.74**	0.05244	**-1.28**	0.00750
STM0403	yajB	putative cytoplasmic protein	**-1.04**	0.07611	**0.82**	0.02284	**-1.23**	0.03288
STM0404	queA	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	**-1.61**	0.04046	**-1.66**	0.00178	**-2.33**	0.01152
STM0404	queA	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	**-1.33**	0.02904	**-1.75**	0.00068	**-2.43**	0.00032
STM0405	tgt	queuine tRNA-ribosyltransferase	**-2.46**	0.00652	**-0.70**	0.06767	**-3.02**	0.00012
STM0405	tgt	queuine tRNA-ribosyltransferase	**-1.70**	0.01523	**-0.57**	0.11741	**-2.69**	0.00024
STM0406	yajC	preprotein translocase subunit YajC	**-2.93**	0.04386	**-1.38**	0.00480	**-2.86**	0.00040
STM0406	yajC	preprotein translocase subunit YajC	**-2.85**	0.00660	**-1.34**	0.00225	**-3.37**	0.00011
STM0407	secD	protein export protein SecD	**-2.71**	0.00547	**-0.98**	0.01240	**-3.11**	0.00009
STM0407	secD	protein export protein SecD	**-1.71**	0.01601	**-0.70**	0.04112	**-3.50**	0.00006
STM0408	secF	protein export protein SecF	**-0.43**	0.57393	**-1.16**	0.01685	**-1.46**	0.01917
STM0408	secF	protein export protein SecF	**-0.21**	0.70070	**-0.96**	0.00879	**-0.70**	0.27077

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM0409	STM0409	hypothetical protein STM0409	**-1.37**	0.02652	**-0.01**	0.97893	**-0.81**	0.04710
STM0409	STM0409	hypothetical protein STM0409	**-0.91**	0.06679	**-0.92**	0.01559	**-1.59**	0.00299
STM0410	STM0410	putative regulatory protein	**-0.48**	0.29487	**-0.47**	0.10751	**-1.34**	0.03748
STM0410	STM0410	putative regulatory protein	**0.58**	0.63775	**-1.44**	0.00325	**-2.07**	0.00139
STM0411	yajD	putative cytoplasmic protein	**0.37**	0.52230	**0.11**	0.74098	**0.16**	0.76508
STM0411	yajD	putative cytoplasmic protein	**0.69**	0.14806	**-0.29**	0.33644	**0.27**	0.42529
STM0413	tsx	nucleoside channel	**-1.01**	0.16045	**-3.11**	0.00005	**-1.81**	0.00468
STM0413	tsx	nucleoside channel	**-1.47**	0.03564	**-3.37**	0.00003	**-2.03**	0.00449
STM0415	ybaD	hypothetical protein STM0415	**1.05**	0.27648	**-0.69**	0.03275	**-2.54**	0.00030
STM0415	ybaD	hypothetical protein STM0415	**0.04**	0.93748	**-0.67**	0.02875	**-1.84**	0.00115
STM0416	ribD	pyrimidine deaminase/reductase	**-0.69**	0.21970	**0.17**	0.62193	**-2.58**	0.00077
STM0416	ribD	pyrimidine deaminase/reductase	**0.65**	0.18603	**0.07**	0.82835	**-2.19**	0.00046
STM0417	ribH	riboflavin synthase subunit beta	**-1.95**	0.04683	**-1.00**	0.01317	**-2.21**	0.00041
STM0417	ribH	riboflavin synthase subunit beta	**-1.57**	0.12435	**-0.91**	0.00958	**-1.67**	0.00288
STM0418	nusB	transcription antitermination protein NusB	**-1.64**	0.16132	**-0.89**	0.01870	**-0.77**	0.06251
STM0418	nusB	transcription antitermination protein NusB	**-0.52**	0.52776	**-0.18**	0.56126	**-1.37**	0.00484
STM0419	thiL	thiamine monophosphate kinase	**-1.87**	0.02344	**-1.10**	0.02389	**-1.47**	0.03016
STM0419	thiL	thiamine monophosphate kinase	**-0.41**	0.62911	**-0.69**	0.06640	**-1.00**	0.02164
STM0420	pgpA	phosphatidylglycerophosphatase A	**1.35**	0.22971	**-0.76**	0.02560	**1.30**	0.28701
STM0420	pgpA	phosphatidylglycerophosphatase A	**-0.20**	0.69574	**-0.72**	0.05669	**2.04**	0.07640
STM0421	yajO	putative oxidoreductase	**-1.42**	0.07255	**0.56**	0.08398	**0.64**	0.18087
STM0421	yajO	putative oxidoreductase	**0.52**	0.36796	**-0.49**	0.11018	**0.83**	0.03721
STM0422	dxs	1-deoxy-D-xylulose-5-phosphate synthase	**-1.24**	0.02764	**-0.47**	0.11313	**-0.34**	0.33091
STM0422	dxs	1-deoxy-D-xylulose-5-phosphate synthase	**-0.68**	0.15730	**-0.46**	0.29246	**0.26**	0.60289
STM0423	ispA	geranyltranstransferase	**-3.00**	0.00562	**-0.95**	0.06729	**-2.95**	0.00157
STM0423	ispA	geranyltranstransferase	**-1.48**	0.03472	**-0.66**	0.12181	**-2.01**	0.00120
STM0424	xseB	exodeoxyribonuclease VII small subunit	**-2.45**	0.00686	**-0.93**	0.02038	**-2.56**	0.00016
STM0424	xseB	exodeoxyribonuclease VII small subunit	**-2.55**	0.11638	**-1.09**	0.01617	**-1.52**	0.04031
STM0425	thiI	thiamine biosynthesis protein ThiI	**-1.38**	0.02981	**-1.96**	0.01470	**-1.71**	0.05944
STM0425	thiI	thiamine biosynthesis protein ThiI	**-1.19**	0.03368	**-1.95**	0.00177	**-1.05**	0.06469
STM0426	phnV	2-aminoethylphosphonate transporter	**-0.44**	0.42560	**-0.19**	0.56652	**-0.47**	0.42059
STM0426	phnV	2-aminoethylphosphonate transporter	**0.70**	0.27648	**-0.10**	0.75076	**-0.25**	0.64205
STM0427	phnU	2-aminoethylphosphonate transporter	**0.43**	0.35443	**-0.90**	0.01472	**-0.49**	0.31629
STM0427	phnU	2-aminoethylphosphonate transporter	**1.33**	0.10320	**-0.58**	0.23974	**0.13**	0.85046
STM0428	phnT	2-aminoethylphosphonate transporter	**-0.07**	0.89100	**-0.82**	0.11819	**-0.13**	0.83871
STM0428	phnT	2-aminoethylphosphonate transporter	**2.07**	0.18821	**0.04**	0.90708	**-0.54**	0.50224
STM0429	phnS	2-aminoethylphosphonate transporter	**-0.70**	0.16453	**0.19**	0.69823	**-0.48**	0.21286
STM0429	phnS	2-aminoethylphosphonate transporter	**-0.29**	0.63974	**-0.63**	0.16425	**-0.44**	0.48253
STM0430	phnR	2-aminoethylphosphonate transport protein	**0.98**	0.06603	**0.20**	0.61067	**0.95**	0.04051
STM0430	phnR	2-aminoethylphosphonate transport protein	**1.83**	0.01196	**-0.23**	0.46667	**-0.24**	0.62725
STM0431	phnW	2-aminoethylphosphonate transport	**-0.94**	0.07579	**1.43**	0.00158	**1.96**	0.00395
STM0431	phnW	2-aminoethylphosphonate transport	**0.17**	0.87614	**1.70**	0.02399	**2.96**	0.00040
STM0432	phnX	2-aminoethylphosphonate transport	**-0.36**	0.64858	**-0.67**	0.13146	**-0.60**	0.12932
STM0432	phnX	2-aminoethylphosphonate transport	**0.97**	0.05384	**-0.59**	0.23567	**0.66**	0.08244
STM0433	thiJ	4-methyl-5(beta-hydroxyethyl)-thiazole synthesis	**-0.38**	0.39644	**-0.07**	0.91723	**-0.76**	0.22760
STM0433	thiJ	4-methyl-5(beta-hydroxyethyl)-thiazole synthesis	**0.71**	0.31214	**-1.13**	0.00925	**0.62**	0.27486
STM0434	apbA	2-dehydropantoate 2-reductase	**-0.15**	0.81981	**0.11**	0.73090	**1.45**	0.04323
STM0434	apbA	2-dehydropantoate 2-reductase	**-0.63**	0.40342	**0.40**	0.26213	**0.43**	0.42137
STM0435	yajQ	hypothetical protein STM0435	**0.42**	0.62257	**-0.16**	0.70071	**0.18**	0.73640
STM0435	yajQ	hypothetical protein STM0435	**1.29**	0.18327	**0.33**	0.41103	**0.60**	0.16953
STM0436,S	yajR	putative transport protein	**-0.56**	0.38349	**0.79**	0.01940	**0.22**	0.62089
STM0436,S	yajR	putative transport protein	**0.15**	0.81805	**0.30**	0.35602	**1.14**	0.04051
STM0437	STM0437	putative periplasmic protein	**-0.56**	0.19427	**-0.18**	0.55274	**-0.80**	0.14345
STM0437	STM0437	putative periplasmic protein	**0.80**	0.24508	**0.25**	0.53204	**0.31**	0.53309
STM0438	STM0438	tetratricopeptide repeat protein	**-1.37**	0.13407	**-2.09**	0.00015	**-1.28**	0.01750
STM0438	STM0438	tetratricopeptide repeat protein	**-2.30**	0.00686	**-1.95**	0.00033	**-1.77**	0.00150
STM0439	cyoE	protoheme IX farnesyltransferase	**-3.45**	0.00593	**-2.78**	0.00012	**-1.21**	0.00885
STM0439	cyoE	protoheme IX farnesyltransferase	**-2.53**	0.00674	**-2.68**	0.00005	**-1.30**	0.01233
STM0440	cyoD	cytochrome o ubiquinol oxidase subunit IV	**-4.68**	0.00500	**-2.68**	0.00006	**-2.00**	0.00140
STM0440	cyoD	cytochrome o ubiquinol oxidase subunit IV	**-4.30**	0.00512	**-2.36**	0.00020	**-2.03**	0.00093
STM0441	cyoC	cytochrome o ubiquinol oxidase subunit III	**-3.80**	0.00547	**-3.20**	0.00003	**-1.91**	0.00252
STM0441	cyoC	cytochrome o ubiquinol oxidase subunit III	**-4.01**	0.00514	**-3.12**	0.00004	**-1.84**	0.00264
STM0442	cyoB	cytochrome o ubiquinol oxidase subunit I	**-3.65**	0.00547	**-2.07**	0.00033	**-1.59**	0.01098
STM0442	cyoB	cytochrome o ubiquinol oxidase subunit I	**-2.67**	0.00750	**-2.12**	0.00038	**-1.28**	0.00467
STM0443	cyoA	cytochrome o ubiquinol oxidase subunit II	**-3.56**	0.00623	**-1.25**	0.00986	**-1.04**	0.01961
STM0443	cyoA	cytochrome o ubiquinol oxidase subunit II	**-2.42**	0.00971	**-1.38**	0.00406	**-0.68**	0.08398
STM0444	ampG	muropeptide transporter	**-1.39**	0.07746	**-2.08**	0.00024	**-1.87**	0.00256
STM0444	ampG	muropeptide transporter	**-1.04**	0.05496	**-2.01**	0.00048	**-0.69**	0.18435
STM0445	yajG	putative lipoprotein	**-3.46**	0.00727	**-1.27**	0.00257	**-2.00**	0.00079
STM0445	yajG	putative lipoprotein	**-2.53**	0.00719	**-1.67**	0.00054	**-2.14**	0.00199

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM0446	bolA	putative regulatory protein	**-1.83**	0.01091	**-1.43**	0.00151	**0.79**	0.03927
STM0446	bolA	putative regulatory protein	**-2.32**	0.00711	**-1.41**	0.00152	**0.65**	0.07893
STM0447	tig	trigger factor	**-3.34**	0.01443	**-1.25**	0.01031	**-3.66**	0.00168
STM0447	tig	trigger factor	**-1.21**	0.54601	**-1.07**	0.01142	**-1.42**	0.00578
STM0448	clpP	ATP-dependent Clp protease proteolytic subunit	**-1.27**	0.08555	**0.40**	0.31174	**-1.25**	0.00587
STM0448	clpP	ATP-dependent Clp protease proteolytic subunit	**-0.88**	0.09171	**0.64**	0.07852	**-0.76**	0.07265
STM0449	clpX	ATP-dependent protease ATP-binding subunit	**-0.92**	0.06522	**0.25**	0.42355	**-0.47**	0.17588
STM0449	clpX	ATP-dependent protease ATP-binding subunit	**-0.28**	0.55401	**0.27**	0.43078	**0.29**	0.52429
STM0450	lon	ATP-dependent protease Lon	**-2.51**	0.03408	**0.01**	0.96580	**-1.70**	0.00185
STM0450	lon	ATP-dependent protease Lon	**-1.77**	0.03005	**0.15**	0.64580	**-1.96**	0.00082
STM0451	hupB	DNA-binding protein HU-beta	**-1.63**	0.05468	**0.64**	0.08965	**-2.64**	0.00031
STM0451	hupB	DNA-binding protein HU-beta	**-1.31**	0.09445	**0.42**	0.24847	**-1.92**	0.00328
STM0452	cypD	peptidyl-prolyl isomerase	**0.61**	0.76451	**-1.35**	0.03050	**-0.11**	0.85903
STM0452	cypD	peptidyl-prolyl isomerase	**-0.95**	0.49184	**-1.17**	0.06810	**-0.65**	0.38265
STM0453	ybaV	putative DNA uptake protein	**0.18**	0.79350	**-0.29**	0.37488	**-0.53**	0.27915
STM0453	ybaV	putative DNA uptake protein	**1.63**	0.02541	**-0.07**	0.81944	**0.89**	0.20339
STM0454	ybaW	putative esterase	**0.62**	0.30493	**-0.55**	0.18269	**1.44**	0.00815
STM0454	ybaW	putative esterase	**1.48**	0.02260	**-0.53**	0.17418	**2.01**	0.00274
STM0455	ybaX	putative aluminum resistance protein	**-0.81**	0.23242	**-0.21**	0.46588	**-0.79**	0.24881
STM0455	ybaX	putative aluminum resistance protein	**0.54**	0.21875	**-0.99**	0.03721	**0.20**	0.74006
STM0456	ybaE	putative ABC transporter periplasmic binding protein	**0.53**	0.36089	**-1.23**	0.05097	**-0.19**	0.78401
STM0456	ybaE	putative ABC transporter periplasmic binding protein	**0.98**	0.05591	**-0.26**	0.39323	**0.80**	0.09927
STM0457	cof	putative hydrolase	**-0.98**	0.08544	**0.21**	0.63320	**0.05**	0.94087
STM0457	cof	putative hydrolase	**1.43**	0.03770	**1.82**	0.00813	**3.22**	0.00142
STM0458	STM0458	putative cysteine synthase/cystathionine beta-synthase	**0.68**	0.48579	**0.88**	0.04255	**-0.37**	0.41225
STM0458	STM0458	putative cysteine synthase/cystathionine beta-synthase	**1.75**	0.01184	**0.14**	0.76386	**0.66**	0.44676
STM0459	ybaO	putative transcriptional regulator	**1.43**	0.21280	**0.18**	0.61387	**0.95**	0.10017
STM0459	ybaO	putative transcriptional regulator	**1.29**	0.08322	**0.95**	0.01173	**-0.10**	0.81397
STM0460	mdlA	ATP-binding component	**-0.36**	0.45621	**-0.13**	0.69598	**-1.14**	0.01102
STM0460	mdlA	ATP-binding component	**-0.17**	0.74986	**-0.20**	0.55604	**-1.39**	0.01206
STM0461	mdlB	putative transporter	**0.83**	0.27794	**0.14**	0.66751	**0.57**	0.25040
STM0461	mdlB	putative transporter	**2.82**	0.01081	**-0.10**	0.74627	**1.50**	0.12110
STM0462	glnK	nitrogen regulatory protein P-II 2	**-1.83**	0.03095	**-0.42**	0.19130	**-0.49**	0.26255
STM0462	glnK	nitrogen regulatory protein P-II 2	**-0.75**	0.13497	**-1.77**	0.00232	**0.92**	0.05677
STM0463	amtB	putative ammonium transport protein	**0.24**	0.78825	**0.20**	0.51983	**0.40**	0.52786
STM0463	amtB	putative ammonium transport protein	**1.11**	0.04102	**-0.62**	0.11222	**0.29**	0.53505
STM0464	tesB	acyl-CoA thioesterase II	**-0.45**	0.61561	**0.32**	0.41528	**0.33**	0.32882
STM0464	tesB	acyl-CoA thioesterase II	**0.14**	0.78214	**0.00**	0.99752	**1.16**	0.00999
STM0465	ybaY	hypothetical protein STM0465	**-0.25**	0.72164	**2.73**	0.00074	**4.18**	0.00003
STM0465	ybaY	hypothetical protein STM0465	**2.13**	0.34198	**2.62**	0.00014	**4.80**	0.00004
STM0466	ybaZ	putative methyltransferase	**-1.37**	0.18480	**0.22**	0.64511	**0.59**	0.37515
STM0466	ybaZ	putative methyltransferase	**0.97**	0.21801	**-0.20**	0.59214	**1.42**	0.00653
STM0467	ffs	STM0467	**-0.87**	0.24494	**0.83**	0.07668	**3.69**	0.00132
STM0467	ffs	STM0467	**-0.42**	0.43492	**0.82**	0.12560	**4.21**	0.00024
STM0468	ylaB	hypothetical protein STM0468	**0.98**	0.37989	**1.39**	0.16175	**1.68**	0.01522
STM0468	ylaB	hypothetical protein STM0468	**0.73**	0.29186	**-0.22**	0.51177	**1.96**	0.00066
STM0469	rpmE2	50S ribosomal protein L31	**-0.54**	0.24474	**-0.14**	0.67544	**-0.20**	0.58283
STM0469	rpmE2	50S ribosomal protein L31	**-0.60**	0.37992	**-0.11**	0.75037	**0.78**	0.05040
STM0470	rpmJ2	50S ribosomal protein L36	**-0.52**	0.44035	**0.21**	0.49106	**0.59**	0.20668
STM0470	rpmJ2	50S ribosomal protein L36	**0.11**	0.85417	**0.70**	0.06235	**1.24**	0.00591
STM0471	ylaC	putative inner membrane protein	**-1.14**	0.27274	**-0.80**	0.04069	**-0.90**	0.06021
STM0471	ylaC	putative inner membrane protein	**-1.77**	0.01445	**-1.42**	0.00296	**-0.77**	0.04247
STM0472	maa	maltose O-acetyltransferase	**-0.86**	0.07678	**0.42**	0.19865	**-0.32**	0.60846
STM0472	maa	maltose O-acetyltransferase	**-0.10**	0.82483	**0.36**	0.20794	**0.10**	0.81283
STM0473	hha	hemolysin expression-modulating protein	**-1.60**	0.07375	**-1.03**	0.02929	**-0.28**	0.53127
STM0473	hha	hemolysin expression-modulating protein	**-0.15**	0.75132	**-0.02**	0.95396	**0.37**	0.31439
STM0474	ybaJ	putative cytoplasmic protein	**-2.31**	0.01652	**-1.22**	0.00834	**0.06**	0.91578
STM0474	ybaJ	putative cytoplasmic protein	**-1.92**	0.05319	**-1.10**	0.00389	**-0.26**	0.58898
STM0475	acrB	acridine efflux pump	**-1.49**	0.02459	**-0.94**	0.08090	**-1.53**	0.02990
STM0475	acrB	acridine efflux pump	**0.46**	0.64534	**-0.97**	0.02165	**-1.85**	0.00714
STM0476	acrA	acridine efflux pump	**-1.80**	0.03476	**-0.74**	0.04481	**-2.40**	0.00033
STM0476	acrA	acridine efflux pump	**-0.34**	0.46047	**-0.55**	0.11596	**-1.90**	0.00333
STM0477	acrR	acrAB operon repressor	**-0.52**	0.22121	**-1.49**	0.00110	**-1.05**	0.01384
STM0477	acrR	acrAB operon repressor	**0.70**	0.26456	**-0.98**	0.01674	**0.03**	0.94831
STM0478	aefA	putative small-conductance mechanosensitive channel	**1.80**	0.02522	**0.33**	0.34862	**0.14**	0.83913
STM0478	aefA	putative small-conductance mechanosensitive channel	**2.69**	0.01799	**-0.29**	0.39550	**2.18**	0.00463
STM0479	STM0479	putative transposase	**0.85**	0.42371	**0.69**	0.06615	**-0.49**	0.20005
STM0479	STM0479	putative transposase	**1.27**	0.29343	**0.63**	0.04154	**0.11**	0.81189
STM0480	ybaM	putative inner membrane protein	**-1.47**	0.06354	**0.62**	0.10056	**-0.21**	0.75170
STM0480	ybaM	putative inner membrane protein	**-0.46**	0.28111	**-0.37**	0.22915	**-0.08**	0.89430

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM0481	priC	primosomal replication protein N	**-0.30**	0.57315	**1.07**	0.00990	**-0.75**	0.05478
STM0481	priC	primosomal replication protein N	**1.30**	0.04229	**0.85**	0.01515	**1.14**	0.11713
STM0482	ybaN	hypothetical protein STM0482	**0.32**	0.68267	**-0.35**	0.25079	**-0.84**	0.04148
STM0482	ybaN	hypothetical protein STM0482	**0.02**	0.98029	**0.15**	0.65535	**-0.38**	0.53861
STM0483	apt	adenine phosphoribosyltransferase	**-0.87**	0.08286	**-1.49**	0.00166	**-1.78**	0.00430
STM0483	apt	adenine phosphoribosyltransferase	**1.33**	0.41844	**-1.66**	0.00167	**-1.31**	0.05483
STM0484	dnaX	DNA polymerase III subunits gamma and tau	**-2.83**	0.00547	**-1.29**	0.00340	**-3.17**	0.00013
STM0484	dnaX	DNA polymerase III subunits gamma and tau	**-1.52**	0.02586	**-0.91**	0.01829	**-2.15**	0.00128
STM0485	ybaB	hypothetical protein STM0485	**-2.57**	0.01382	**-1.70**	0.00145	**-2.96**	0.00011
STM0485	ybaB	hypothetical protein STM0485	**-2.82**	0.00673	**-1.87**	0.00078	**-2.60**	0.00024
STM0486	recR	recombination protein RecR	**-3.28**	0.00547	**-1.55**	0.02177	**-3.83**	0.00010
STM0486	recR	recombination protein RecR	**-2.06**	0.00800	**-1.45**	0.00269	**-3.99**	0.00004
STM0487,S	htpG	heat shock protein 90	**-2.39**	0.00689	**-0.32**	0.27253	**-2.23**	0.01239
STM0487,S	htpG	heat shock protein 90	**-1.26**	0.06338	**-0.85**	0.02174	**-2.20**	0.01544
STM0488	adk	adenylate kinase	**-1.45**	0.01955	**-2.12**	0.00021	**-3.06**	0.00092
STM0488	adk	adenylate kinase	**-0.60**	0.47566	**-1.73**	0.00099	**-4.42**	0.00195
STM0489	hemH	ferrochelatase	**-1.22**	0.03417	**-1.20**	0.02350	**-0.19**	0.67500
STM0489	hemH	ferrochelatase	**-1.27**	0.24964	**-0.94**	0.03016	**-0.09**	0.84640
STM0490	aes	acetyl esterase	**-1.21**	0.02988	**-1.16**	0.04585	**-0.65**	0.22399
STM0490	aes	acetyl esterase	**-0.12**	0.88003	**-1.55**	0.00149	**-0.35**	0.45824
STM0491	gsk	inosine-guanosine kinase	**-0.96**	0.06515	**-0.51**	0.17363	**-1.95**	0.00158
STM0491	gsk	inosine-guanosine kinase	**-0.08**	0.91869	**-0.30**	0.37457	**-0.93**	0.02125
STM0492	ybaL	putative transport protein	**0.19**	0.75846	**0.10**	0.78133	**-1.37**	0.03100
STM0492	ybaL	putative transport protein	**0.46**	0.26563	**-0.32**	0.27097	**-0.56**	0.25414
STM0493	fsr	putative transport protein	**-0.38**	0.36488	**-1.22**	0.00624	**-0.90**	0.17558
STM0493	fsr	putative transport protein	**0.38**	0.46285	**-0.83**	0.02997	**-0.61**	0.35381
STM0494	ushA	UDP-sugar hydrolase/5'-nucleotidase	**2.51**	0.02702	**-0.75**	0.05975	**-1.46**	0.04472
STM0494	ushA	UDP-sugar hydrolase/5'-nucleotidase	**2.46**	0.01620	**-0.47**	0.15303	**-1.66**	0.00462
STM0495	ybaK	putative cytoplasmic protein	**-1.55**	0.02952	**-0.68**	0.16386	**-0.94**	0.07773
STM0495	ybaK	putative cytoplasmic protein	**-2.46**	0.01196	**-0.73**	0.03607	**-2.32**	0.00904
STM0496	ybaP	putative cytoplasmic protein	**-0.42**	0.38345	**0.04**	0.90424	**-1.86**	0.01077
STM0496	ybaP	putative cytoplasmic protein	**-0.19**	0.68727	**0.15**	0.68815	**-0.55**	0.35226
STM0497	STM0497	putative periplasmic protein	**0.03**	0.96628	**0.79**	0.03108	**0.05**	0.90469
STM0497	STM0497	putative periplasmic protein	**0.71**	0.14817	**-0.41**	0.31168	**-0.32**	0.67714
STM0498	copA	putative copper-transporting ATPase	**-0.14**	0.77241	**-0.28**	0.50433	**0.72**	0.26761
STM0498	copA	putative copper-transporting ATPase	**0.67**	0.22605	**-0.62**	0.05812	**1.07**	0.34919
STM0499	cueR	putative heavy metal transcriptional repressor	**-0.22**	0.58088	**0.64**	0.07248	**0.44**	0.24645
STM0499	cueR	putative heavy metal transcriptional repressor	**-0.19**	0.76786	**0.10**	0.73996	**1.42**	0.00692
STM0500	ybbJ	hypothetical protein STM0500	**-0.15**	0.73633	**0.16**	0.73681	**0.36**	0.35142
STM0500	ybbJ	hypothetical protein STM0500	**1.21**	0.29259	**-0.15**	0.67909	**-0.03**	0.93900
STM0501	ybbK	putative inner membrane protein	**-1.18**	0.04212	**-0.42**	0.16007	**-0.48**	0.40701
STM0501	ybbK	putative inner membrane protein	**-0.18**	0.75358	**-0.49**	0.13098	**0.09**	0.85584
STM0502	ybbL	putative ABC-type sugar/spermidine/putrescine transport	**0.48**	0.28178	**-0.67**	0.03317	**0.00**	0.99711
STM0502	ybbL	putative ABC-type sugar/spermidine/putrescine transport	**0.39**	0.34102	**-0.48**	0.15103	**-0.09**	0.84786
STM0503	ybbM	putative transport protein	**-2.35**	0.00686	**-0.43**	0.16536	**-1.11**	0.10361
STM0503	ybbM	putative transport protein	**-1.42**	0.03975	**-0.35**	0.20042	**-1.32**	0.01414
STM0504	ybbN	putative thioredoxin protein	**-1.52**	0.03330	**-1.10**	0.02570	**-2.28**	0.00091
STM0504	ybbN	putative thioredoxin protein	**-0.74**	0.15162	**-0.33**	0.27368	**-2.38**	0.00051
STM0505	ybbO	short chain dehydrogenase	**-1.08**	0.07769	**0.06**	0.86854	**-2.57**	0.00217
STM0505	ybbO	short chain dehydrogenase	**-0.64**	0.18323	**0.29**	0.36230	**-1.81**	0.00186
STM0506	tesA	multifunctional acyl-CoA thioesterase I	**-0.53**	0.32756	**-0.15**	0.63567	**-1.39**	0.00563
STM0506	tesA	multifunctional acyl-CoA thioesterase I	**-0.33**	0.53112	**-0.53**	0.11520	**-1.04**	0.03728
STM0507	ybbA	putative transporter	**0.80**	0.12256	**1.99**	0.00120	**-0.79**	0.04422
STM0507	ybbA	putative transporter	**2.35**	0.02110	**1.96**	0.00304	**-0.72**	0.22406
STM0508	ybbP	putative inner membrane protein	**0.77**	0.35080	**0.01**	0.98165	**-1.28**	0.00808
STM0508	ybbP	putative inner membrane protein	**1.73**	0.05730	**-0.42**	0.19331	**0.04**	0.92782
STM0509	STM0509	putative outer membrane protein	**-0.47**	0.33859	**0.05**	0.90452	**0.28**	0.62089
STM0509	STM0509	putative outer membrane protein	**0.31**	0.58887	**0.54**	0.06736	**1.14**	0.04685
STM0510	sfbA	putative ABC-type transport system ATPase component	**0.10**	0.86862	**2.07**	0.00078	**-0.69**	0.21938
STM0510	sfbA	putative ABC-type transport system ATPase component	**1.47**	0.13620	**1.92**	0.00363	**0.98**	0.03295
STM0511	sfbB	putative ABC-type transport system ATPase component	**-0.27**	0.50374	**0.71**	0.03792	**-0.38**	0.45514
STM0511	sfbB	putative ABC-type transport system ATPase component	**-0.30**	0.48170	**0.47**	0.34067	**0.47**	0.19372
STM0512	sfbC	putative ABC transporter permease component	**-1.23**	0.14813	**0.07**	0.84941	**-1.03**	0.14038
STM0512	sfbC	putative ABC transporter permease component	**0.02**	0.97265	**0.31**	0.43844	**-0.44**	0.24222
STM0513	ybbB	putative ATPase	**-1.47**	0.03666	**-0.28**	0.47269	**-0.49**	0.34280
STM0513	ybbB	putative ATPase	**-0.34**	0.44779	**-0.14**	0.68835	**-1.20**	0.00930
STM0514	ybbS	putative transcriptional regulator	**0.36**	0.42780	**0.37**	0.38981	**-0.45**	0.43356
STM0514	ybbS	putative transcriptional regulator	**1.01**	0.10271	**0.45**	0.24760	**0.57**	0.19098
STM0515	allA	ureidoglycolate hydrolase	**0.77**	0.15347	**0.24**	0.52222	**-0.67**	0.49644
STM0515	allA	ureidoglycolate hydrolase	**1.21**	0.10913	**0.43**	0.19802	**0.73**	0.10364

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM0516	allR	putative regulatory protein	**1.21**	0.13705	**0.43**	0.16351	**-0.44**	0.38396
STM0516	allR	putative regulatory protein	**2.27**	0.00738	**0.83**	0.02896	**1.15**	0.03238
STM0517	gcl	glyoxylate carboligase	**0.52**	0.26680	**0.57**	0.09286	**0.76**	0.17998
STM0517	gcl	glyoxylate carboligase	**2.69**	0.00661	**-0.26**	0.47601	**2.27**	0.00065
STM0518	gip	glyoxylate-induced protein	**-0.71**	0.22921	**-0.68**	0.14741	**0.24**	0.84467
STM0518	gip	glyoxylate-induced protein	**-0.32**	0.68440	**-0.04**	0.94003	**-0.20**	0.61903
STM0519	glxR	tartronic semialdehyde reductase	**0.36**	0.61745	**-0.11**	0.87322	**0.93**	0.06654
STM0519	glxR	tartronic semialdehyde reductase	**0.18**	0.81771	**-1.41**	0.01696	**1.97**	0.00427
STM0520	STM0520	putative permease	**-0.16**	0.82172	**-0.96**	0.06167	**-0.12**	0.87234
STM0520	STM0520	putative permease	**-0.53**	0.65942	**-0.93**	0.06469	**0.63**	0.13627
STM0522	allP	putative allantoin transport protein	**0.24**	0.70143	**0.41**	0.23284	**1.46**	0.00487
STM0522	allP	putative allantoin transport protein	**0.38**	0.76831	**0.35**	0.38897	**1.61**	0.00203
STM0523	allB	allantoinase	**2.74**	0.02948	**0.53**	0.41443	**3.00**	0.05401
STM0523	allB	allantoinase	**0.98**	0.26266	**-0.68**	0.07647	**0.56**	0.50812
STM0524	ybbY	putative transport protein	**2.52**	0.35102	**-0.34**	0.50368	**1.17**	0.24937
STM0524	ybbY	putative transport protein	**0.00**	0.99547	**-1.30**	0.03098	**1.80**	0.11140
STM0525	glxK	glycerate kinase II	**-0.14**	0.81959	**-0.52**	0.18066	**-0.25**	0.75248
STM0525	glxK	glycerate kinase II	**0.74**	0.37124	**0.26**	0.45127	**0.97**	0.05149
STM0526	ylbA	putative glyoxylate utilization protein	**-0.07**	0.90565	**0.52**	0.25879	**0.70**	0.23461
STM0526	ylbA	putative glyoxylate utilization protein	**0.40**	0.49677	**0.05**	0.93285	**1.31**	0.05415
STM0527	allC	N-carbamoyl-L-amino acid amidohydrolase	**-0.73**	0.32788	**0.64**	0.07208	**0.07**	0.90141
STM0527	allC	N-carbamoyl-L-amino acid amidohydrolase	**-0.15**	0.83365	**-0.50**	0.27371	**-0.48**	0.51990
STM0528	allD	ureidoglycolate dehydrogenase	**-0.64**	0.40835	**1.17**	0.43951	**-1.52**	0.03319
STM0528	allD	ureidoglycolate dehydrogenase	**-0.05**	0.95219	**-1.22**	0.06472	**-3.05**	0.01922
STM0529	fdrA	succinyl-CoA synthetase alpha subunit	**0.00**	0.99384	**-0.45**	0.40379	**-1.56**	0.00483
STM0529	fdrA	succinyl-CoA synthetase alpha subunit	**0.20**	0.75398	**-0.74**	0.13601	**-0.39**	0.39919
STM0530	ylbE	putative cytoplasmic protein	**-0.10**	0.91393	**0.29**	0.35918	**-0.17**	0.85436
STM0530	ylbE	putative cytoplasmic protein	**1.25**	0.08396	**-1.03**	0.02481	**-0.24**	0.74614
STM0531	ylbF	putative cytoplasmic protein	**0.95**	0.06025	**-0.24**	0.61580	**-0.29**	0.45763
STM0531	ylbF	putative cytoplasmic protein	**0.57**	0.52175	**-1.90**	0.00108	**-0.23**	0.71846
STM0532	arcC	carbamate kinase	**-0.25**	0.73570	**-0.25**	0.46255	**-1.04**	0.12583
STM0532	arcC	carbamate kinase	**0.33**	0.54912	**-0.15**	0.60706	**-0.59**	0.18003
STM0533	purK	phosphoribosylaminoimidazole carboxylase	**0.70**	0.17147	**0.97**	0.02133	**-0.98**	0.03042
STM0533	purK	phosphoribosylaminoimidazole carboxylase	**1.13**	0.03453	**0.78**	0.05866	**0.26**	0.50557
STM0534	purE	phosphoribosylaminoimidazole carboxylase catalytic subunit	**-0.24**	0.62990	**1.15**	0.01622	**-2.55**	0.00061
STM0534	purE	phosphoribosylaminoimidazole carboxylase catalytic subunit	**-0.19**	0.67020	**1.16**	0.01465	**-1.81**	0.03452
STM0535	lpxH	UDP-2,3-diacylglucosamine hydrolase	**-1.33**	0.05948	**-0.95**	0.00725	**-1.93**	0.00801
STM0535	lpxH	UDP-2,3-diacylglucosamine hydrolase	**-0.49**	0.36946	**-1.43**	0.00190	**-2.11**	0.00920
STM0536	ppiB	peptidyl-prolyl cis-trans isomerase B	**-2.56**	0.02357	**-0.95**	0.01911	**-1.62**	0.00487
STM0536	ppiB	peptidyl-prolyl cis-trans isomerase B	**-0.56**	0.25111	**-0.28**	0.37825	**-1.23**	0.00704
STM0537	cysS	cysteinyl-tRNA synthetase	**-0.41**	0.40887	**-0.58**	0.13350	**-0.93**	0.03299
STM0537	cysS	cysteinyl-tRNA synthetase	**-0.50**	0.30358	**-0.22**	0.62437	**-0.72**	0.07980
STM0538	STM0538	putative outer membrane protein	**-1.30**	0.02934	**-1.85**	0.00376	**-2.01**	0.01362
STM0538	STM0538	putative outer membrane protein	**0.15**	0.79511	**-1.90**	0.00234	**-1.79**	0.01435
STM0539	STM0539	putative inner membrane protein	**0.25**	0.70217	**0.07**	0.87327	**-0.48**	0.40593
STM0539	STM0539	putative inner membrane protein	**0.18**	0.86644	**-1.20**	0.00678	**-0.79**	0.51545
STM0540	ybcI	putative membrane-bound metal-dependent hydrolase	**-0.74**	0.13488	**-1.51**	0.02564	**-1.04**	0.13575
STM0540	ybcI	putative membrane-bound metal-dependent hydrolase	**-0.64**	0.47141	**-0.64**	0.10872	**0.00**	0.99937
STM0541	ybcJ	putative cytoplasmic protein	**-0.03**	0.97248	**0.13**	0.67873	**-0.96**	0.06932
STM0541	ybcJ	putative cytoplasmic protein	**0.75**	0.37638	**0.17**	0.56566	**0.04**	0.95072
STM0542	folD	5,10-methylene-tetrahydrofolate	**-1.15**	0.05275	**-0.57**	0.06573	**-1.32**	0.04845
STM0542	folD	5,10-methylene-tetrahydrofolate	**-1.67**	0.05440	**-0.55**	0.07746	**-2.54**	0.03530
STM0543	fimA	fimbrin	**2.19**	0.14571	**1.32**	0.01752	**-0.50**	0.23491
STM0543	fimA	fimbrin	**1.48**	0.25983	**0.76**	0.03438	**-0.12**	0.86540
STM0544	fimI	fimbrial protein	**-0.13**	0.74520	**-0.01**	0.99286	**0.70**	0.06552
STM0544	fimI	fimbrial protein	**1.09**	0.36007	**-0.37**	0.22441	**0.76**	0.11386
STM0545	fimC	periplasmic chaperone	**0.33**	0.54374	**0.10**	0.84409	**0.00**	0.99899
STM0545	fimC	periplasmic chaperone	**-0.20**	0.82751	**-1.36**	0.00688	**-0.73**	0.49698
STM0546	fimD	outer membrane usher protein precursor	**0.13**	0.76521	**0.00**	0.99835	**-0.58**	0.34841
STM0546	fimD	outer membrane usher protein precursor	**0.57**	0.29352	**-1.40**	0.02204	**-1.02**	0.02633
STM0547	fimH	minor fimbrial subunit	**-0.57**	0.23646	**0.08**	0.88821	**-0.08**	0.88786
STM0547	fimH	minor fimbrial subunit	**0.77**	0.16053	**-0.69**	0.08821	**-0.33**	0.47927
STM0548	fimF	putative fimbrial protein	**2.93**	0.06503	**1.97**	0.02643	**6.37**	0.00014
STM0548	fimF	putative fimbrial protein	**3.11**	0.00747	**-1.37**	0.00623	**0.81**	0.40058
STM0549	fimZ	fimbrial protein Z	**0.22**	0.73174	**0.48**	0.21497	**-0.37**	0.39919
STM0549	fimZ	fimbrial protein Z	**-0.05**	0.93638	**-0.16**	0.75939	**-0.32**	0.60849
STM0550	fimY	putative regulatory protein	**1.91**	0.15180	**0.28**	0.60675	**2.90**	0.09300
STM0550	fimY	putative regulatory protein	**0.89**	0.09192	**-0.94**	0.07351	**0.99**	0.37862
STM0551	STM0551	hypothetical protein STM0551	**-0.53**	0.41555	**-0.11**	0.85557	**1.02**	0.49423
STM0551	STM0551	hypothetical protein STM0551	**0.58**	0.74962	**-1.12**	0.02116	**0.26**	0.71679

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM0552	fimW	putative fimbrial protein	**0.35**	0.62872	**0.09**	0.90038	**-0.30**	0.69836
STM0552	fimW	putative fimbrial protein	**2.16**	0.01549	**-0.04**	0.92004	**1.13**	0.03798
STM0553	argU	STM0553	**-2.96**	0.00705	**-1.38**	0.00651	**-1.63**	0.00725
STM0553	argU	STM0553	**-0.78**	0.36425	**-1.36**	0.00325	**-0.62**	0.35595
STM05559.T1	-	STM05559.T1	**-1.90**	0.01355	**-1.75**	0.00095	**-2.12**	0.00708
STM05559.T1	-	STM05559.T1	**-0.42**	0.52824	**-1.60**	0.01560	**-1.51**	0.00897
STM0557	STM0557	putative inner membrane protein	**1.06**	0.12960	**0.68**	0.04608	**0.01**	0.99014
STM0557	STM0557	putative inner membrane protein	**1.71**	0.01741	**0.09**	0.84235	**1.76**	0.00598
STM0558	yfdH	putative glycosyltransferase	**-0.76**	0.36222	**-0.79**	0.09265	**-0.88**	0.23980
STM0558	yfdH	putative glycosyltransferase	**-0.33**	0.54152	**-0.80**	0.38382	**-0.74**	0.31788
STM0559	rfbI	putative glycosyl translocase	**-1.79**	0.01707	**-0.51**	0.34347	**-0.42**	0.63786
STM0559	rfbI	putative glycosyl translocase	**-0.45**	0.57560	**-1.51**	0.00579	**-0.58**	0.31532
STM0561	STM0561	sensor kinase	**6.16**	0.01215	**0.26**	0.41874	**1.67**	0.33113
STM0561	STM0561	sensor kinase	**7.72**	0.00190	**0.28**	0.63116	**4.47**	0.03898
STM0563	STM0563	putative transcriptional regulator	**0.31**	0.51363	**0.62**	0.15334	**-0.49**	0.35891
STM0563	STM0563	putative transcriptional regulator	**2.50**	0.16181	**0.22**	0.44171	**-0.72**	0.39910
STM0564	STM0564	pyridine nucleotide-disulfide oxidoreductase	**-0.25**	0.62257	**0.81**	0.06768	**0.45**	0.21619
STM0564	STM0564	pyridine nucleotide-disulfide oxidoreductase	**0.36**	0.41919	**-0.01**	0.98628	**0.98**	0.24330
STM0565	STM0565	putative periplasmic protein	**-0.14**	0.82541	**0.32**	0.41542	**0.17**	0.77857
STM0565	STM0565	putative periplasmic protein	**0.50**	0.49387	**-0.61**	0.30560	**1.06**	0.05618
STM0566	STM0566	putative inner membrane protein	**-0.33**	0.58428	**-1.10**	0.03955	**-1.78**	0.01984
STM0566	STM0566	putative inner membrane protein	**0.10**	0.85201	**-0.73**	0.04175	**-1.37**	0.03581
STM0567	STM0567	putative DNA repair ATPase	**0.31**	0.78079	**-0.94**	0.02957	**-1.14**	0.08589
STM0567	STM0567	putative DNA repair ATPase	**0.95**	0.13084	**0.04**	0.89655	**-0.20**	0.70174
STM0568	pheP	phenylalanine transporter	**-1.10**	0.06139	**-0.60**	0.17307	**-0.60**	0.18599
STM0568	pheP	phenylalanine transporter	**-0.76**	0.15670	**-0.66**	0.25140	**-1.15**	0.14242
STM0569	ybdG	hypothetical protein STM0569	**-2.15**	0.01569	**-1.23**	0.00454	**-2.35**	0.04678
STM0569	ybdG	hypothetical protein STM0569	**-0.81**	0.20982	**-0.67**	0.03954	**-0.68**	0.22267
STM0570	apeE	outer membrane esterase	**0.64**	0.13961	**1.58**	0.00082	**0.26**	0.59065
STM0570	apeE	outer membrane esterase	**1.08**	0.04751	**1.93**	0.00033	**-0.01**	0.98652
STM0571	STM0571	putative inner membrane protein	**-1.43**	0.07035	**0.37**	0.30338	**-0.60**	0.21752
STM0571	STM0571	putative inner membrane protein	**-1.51**	0.03778	**-0.68**	0.06177	**0.14**	0.83143
STM0572	STM0572	putative phosphosugar isomerase	**0.20**	0.81835	**-0.52**	0.28782	**0.72**	0.27952
STM0572	STM0572	putative phosphosugar isomerase	**0.34**	0.77318	**-1.11**	0.03087	**0.23**	0.81360
STM0573	STM0573	putative inner membrane protein	**0.51**	0.39064	**-0.47**	0.57372	**0.16**	0.87445
STM0573	STM0573	putative inner membrane protein	**1.10**	0.06366	**-2.49**	0.00060	**-0.87**	0.13162
STM0574	STM0574	putative PTS system mannose-specific enzyme IID	**2.42**	0.20471	**-0.22**	0.57766	**0.32**	0.46715
STM0574	STM0574	putative PTS system mannose-specific enzyme IID	**0.85**	0.16675	**-0.24**	0.53636	**1.03**	0.04298
STM0575	STM0575	putative inner membrane protein	**-0.29**	0.58682	**-0.22**	0.65154	**1.16**	0.07709
STM0575	STM0575	putative inner membrane protein	**1.00**	0.07536	**-0.62**	0.26241	**0.69**	0.09521
STM0576	STM0576	putative PTS system mannose-specific enzyme IIAB	**-1.20**	0.18659	**-0.93**	0.05070	**-0.04**	0.97461
STM0576	STM0576	putative PTS system mannose-specific enzyme IIAB	**-0.12**	0.82672	**-1.32**	0.04367	**0.27**	0.59002
STM0577	STM0577	putative PTS system mannose-specific enzyme IIAB	**1.98**	0.02179	**1.22**	0.02195	**1.79**	0.05886
STM0577	STM0577	putative PTS system mannose-specific enzyme IIAB	**2.91**	0.03954	**0.84**	0.37999	**2.53**	0.00502
STM0578	nfnB	dihydropteridine reductase/oxygen-insensitive NAD(P)H	**-1.84**	0.01162	**-0.50**	0.13241	**-1.96**	0.00440
STM0578	nfnB	dihydropteridine reductase/oxygen-insensitive NAD(P)H	**-0.94**	0.17294	**-0.68**	0.04577	**-0.60**	0.25847
STM0579	ybdF	putative cytoplasmic protein	**1.46**	0.42407	**-0.03**	0.97003	**-0.18**	0.78357
STM0579	ybdF	putative cytoplasmic protein	**-0.43**	0.31823	**-0.59**	0.13171	**-0.39**	0.34604
STM0580	STM0580	putative regulatory protein	**-1.36**	0.03126	**-0.74**	0.10176	**-1.82**	0.03921
STM0580	STM0580	putative regulatory protein	**-0.37**	0.46968	**-0.86**	0.04534	**-1.39**	0.00903
STM0581	STM0581	putative regulatory protein	**2.06**	0.01170	**2.33**	0.00023	**0.97**	0.02036
STM0581	STM0581	putative regulatory protein	**2.09**	0.01397	**1.75**	0.00184	**2.10**	0.00152
STM0582	ybdJ	putative inner membrane protein	**-0.31**	0.64876	**0.84**	0.03035	**0.20**	0.72385
STM0582	ybdJ	putative inner membrane protein	**0.18**	0.76557	**0.71**	0.04696	**0.21**	0.58718
STM0583	ybdK	putative cytoplasmic protein	**0.32**	0.50687	**0.37**	0.24294	**0.90**	0.05748
STM0583	ybdK	putative cytoplasmic protein	**0.78**	0.16883	**0.54**	0.19337	**1.79**	0.00657
STM0584	entD	enterochelin synthetase component D	**-0.26**	0.71993	**-0.26**	0.77157	**0.96**	0.17062
STM0584	entD	enterochelin synthetase component D	**-1.18**	0.21673	**-1.01**	0.39282	**-1.64**	0.00892
STM0585	fepA	outer membrane ferric enterobactin receptor precursor	**0.18**	0.72379	**2.68**	0.00008	**-0.07**	0.90972
STM0585	fepA	outer membrane ferric enterobactin receptor precursor	**1.02**	0.08071	**2.47**	0.00033	**0.69**	0.23057
STM0586	fes	enterochelin esterase	**-0.20**	0.65452	**1.73**	0.00277	**-0.16**	0.73110
STM0586	fes	enterochelin esterase	**0.55**	0.31819	**1.92**	0.00049	**-1.27**	0.01159
STM0587	ybdZ	putative cytoplasmic protein	**0.55**	0.18694	**2.71**	0.00033	**-1.89**	0.00071
STM0587	ybdZ	putative cytoplasmic protein	**0.71**	0.13171	**2.74**	0.00014	**-0.62**	0.31131
STM0588	entF	enterobactin synthetase component F	**-1.87**	0.02407	**1.67**	0.00167	**-1.49**	0.00820
STM0588	entF	enterobactin synthetase component F	**-0.14**	0.74302	**1.55**	0.00353	**-0.75**	0.18102
STM0589	fepE	ferric enterobactin/enterochelin transporter	**-0.80**	0.20900	**-0.66**	0.10203	**-1.13**	0.03972
STM0589	fepE	ferric enterobactin/enterochelin transporter	**2.34**	0.13171	**0.09**	0.76763	**-0.33**	0.53248
STM0590	fepC	enterobactin transporter	**-1.03**	0.07951	**-0.25**	0.66242	**-1.22**	0.01267
STM0590	fepC	enterobactin transporter	**-0.68**	0.13223	**-0.58**	0.08212	**-0.07**	0.88009

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM0591	fepG	ferric enterobactin transporter	**-1.52**	0.01961	**-1.34**	0.00636	**-2.28**	0.00072
STM0591	fepG	ferric enterobactin transporter	**-1.34**	0.03088	**-1.26**	0.00630	**-1.85**	0.00193
STM0592	fepD	ferric enterobactin/enterochelin transporter	**-0.80**	0.33525	**-1.11**	0.01733	**-0.71**	0.20933
STM0592	fepD	ferric enterobactin/enterochelin transporter	**0.02**	0.96779	**-1.60**	0.00070	**0.05**	0.97275
STM0593	entS	putative transport protein	**0.05**	0.94133	**-0.03**	0.95207	**-0.56**	0.24989
STM0593	entS	putative transport protein	**1.18**	0.37789	**-0.06**	0.91422	**0.79**	0.27996
STM0594	fepB	ferric enterobactin transporter	**-1.33**	0.02633	**-0.11**	0.71564	**-0.56**	0.25552
STM0594	fepB	ferric enterobactin transporter	**-1.46**	0.17236	**-0.22**	0.59598	**-1.15**	0.03483
STM0595	entC	isochorismate synthase	**-1.94**	0.02369	**-0.20**	0.53218	**-0.98**	0.08398
STM0595	entC	isochorismate synthase	**-1.02**	0.04447	**0.33**	0.29105	**-2.07**	0.00044
STM0596	entE	2,3-dihydroxybenzoate-AMP ligase	**-1.25**	0.07277	**0.97**	0.01267	**-1.28**	0.01548
STM0596	entE	2,3-dihydroxybenzoate-AMP ligase	**-0.30**	0.61551	**0.81**	0.04306	**-1.40**	0.02102
STM0597	entB	2,3-dihydro-2,3-dihydroxybenzoate synthetase	**-0.54**	0.24490	**1.41**	0.00143	**0.90**	0.48950
STM0597	entB	2,3-dihydro-2,3-dihydroxybenzoate synthetase	**0.84**	0.32861	**1.31**	0.00916	**0.74**	0.27715
STM0598	entA	2,3-dihydroxybenzoate-2,3-dehydrogenase	**-1.66**	0.01473	**1.18**	0.01578	**-1.89**	0.00546
STM0598	entA	2,3-dihydroxybenzoate-2,3-dehydrogenase	**0.10**	0.85422	**1.50**	0.00182	**-0.70**	0.10540
STM0599	ybdB	hypothetical protein STM0599	**-0.22**	0.60606	**1.23**	0.00989	**-1.53**	0.00511
STM0599	ybdB	hypothetical protein STM0599	**0.69**	0.21674	**0.97**	0.00834	**-0.28**	0.51510
STM0600	cstA	carbon starvation protein	**0.16**	0.72041	**1.68**	0.00079	**0.73**	0.09049
STM0600	cstA	carbon starvation protein	**1.39**	0.05136	**1.52**	0.00204	**1.89**	0.00151
STM0601	ybdD	putative cytoplasmic protein	**-0.52**	0.39217	**0.20**	0.58397	**1.01**	0.05921
STM0601	ybdD	putative cytoplasmic protein	**0.44**	0.35237	**1.35**	0.00382	**1.36**	0.00742
STM0602	ybdH	putative glycerol dehydrogenase	**0.56**	0.20388	**0.54**	0.10127	**0.18**	0.63287
STM0602	ybdH	putative glycerol dehydrogenase	**-0.42**	0.60031	**0.59**	0.11275	**0.81**	0.07059
STM0603	ybdL	putative aminotransferase	**-1.37**	0.03584	**-0.19**	0.60615	**-1.11**	0.01841
STM0603	ybdL	putative aminotransferase	**-0.27**	0.54542	**-0.09**	0.76711	**-0.85**	0.03130
STM0604	ybdM	putative transcriptional regulator	**0.22**	0.64076	**0.85**	0.04280	**-0.72**	0.08252
STM0604	ybdM	putative transcriptional regulator	**0.69**	0.13900	**0.64**	0.12375	**0.51**	0.30118
STM0605	ybdN	putative 3'-phosphoadenosine 5'-phosphosulfate	**0.46**	0.39131	**0.70**	0.04446	**0.67**	0.17308
STM0605	ybdN	putative 3'-phosphoadenosine 5'-phosphosulfate	**1.42**	0.08198	**-0.20**	0.75158	**1.42**	0.00510
STM0606	ybdO	putative transcriptional regulator	**-0.71**	0.14412	**0.07**	0.87339	**-1.02**	0.06186
STM0606	ybdO	putative transcriptional regulator	**-0.52**	0.65199	**0.37**	0.33283	**-0.01**	0.98279
STM0607	dsbG	periplasmic disulfide isomerase/thiol-disulphide oxidase	**-1.00**	0.10008	**1.29**	0.00619	**0.17**	0.81268
STM0607	dsbG	periplasmic disulfide isomerase/thiol-disulphide oxidase	**0.69**	0.26167	**1.35**	0.00936	**1.15**	0.06200
STM0608	ahpC	alkyl hydroperoxide reductase C22 subunit	**-1.08**	0.08918	**-0.13**	0.66630	**-1.18**	0.01013
STM0608	ahpC	alkyl hydroperoxide reductase C22 subunit	**-0.52**	0.34691	**-0.20**	0.47759	**-0.96**	0.03313
STM0609	ahpF	alkyl hydroperoxide reductase F52a subunit	**-0.84**	0.10140	**-0.89**	0.03879	**-2.82**	0.00093
STM0609	ahpF	alkyl hydroperoxide reductase F52a subunit	**0.48**	0.34370	**-0.28**	0.40554	**-1.62**	0.00274
STM0610	STM0610	putative anaerobic dehydrogenase component	**-0.82**	0.29091	**-1.80**	0.00544	**-1.17**	0.03988
STM0610	STM0610	putative anaerobic dehydrogenase component	**1.11**	0.25354	**-2.18**	0.00814	**1.49**	0.25541
STM0611	STM0611	putative oxidoreductase protein	**0.92**	0.14047	**-0.84**	0.01601	**-0.71**	0.19893
STM0611	STM0611	putative oxidoreductase protein	**-0.45**	0.48454	**-1.91**	0.00215	**0.90**	0.15094
STM0612	STM0612	putative hydrogenase protein	**-0.21**	0.65942	**-0.86**	0.02480	**-0.33**	0.56076
STM0612	STM0612	putative hydrogenase protein	**-0.35**	0.61495	**0.07**	0.85600	**-0.70**	0.32969
STM0613	STM0613	putative hydrogenase protein	**-1.10**	0.05758	**0.05**	0.88634	**0.72**	0.36755
STM0613	STM0613	putative hydrogenase protein	**0.36**	0.79260	**0.43**	0.29864	**1.12**	0.09781
STM0614	ybdQ	putative universal stress protein	**0.28**	0.61184	**0.97**	0.00980	**1.50**	0.00537
STM0614	ybdQ	putative universal stress protein	**-1.39**	0.52540	**0.45**	0.28378	**2.18**	0.00118
STM0615	ybdR	putative dehydrogenase	**0.32**	0.48123	**-0.13**	0.74099	**1.11**	0.01760
STM0615	ybdR	putative dehydrogenase	**1.72**	0.02017	**-0.10**	0.73821	**1.99**	0.00152
STM0616	rnk	nucleoside diphosphate kinase regulator	**-0.34**	0.50056	**-0.10**	0.73817	**0.01**	0.98713
STM0616	rnk	nucleoside diphosphate kinase regulator	**0.62**	0.26857	**-0.87**	0.01853	**0.12**	0.79703
STM0617	rna	RNase I	**0.23**	0.62673	**0.26**	0.44901	**-0.60**	0.17000
STM0617	rna	RNase I	**0.67**	0.15588	**0.50**	0.13723	**-0.32**	0.44707
STM0618	citT	citrate/succinate transport antiport protein	**-0.43**	0.34794	**0.28**	0.40449	**-0.03**	0.95090
STM0618	citT	citrate/succinate transport antiport protein	**0.83**	0.14190	**-0.20**	0.52701	**-0.64**	0.10077
STM0619	citG	triphosphoribosyl-dephospho-CoA synthase	**-0.36**	0.42371	**0.30**	0.68760	**-0.11**	0.87248
STM0619	citG	triphosphoribosyl-dephospho-CoA synthase	**-0.69**	0.49024	**0.43**	0.32584	**-1.10**	0.36023
STM0620	citX	2'-(5'-triphosphoribosyl)-3'-dephospho-CoA:apo-citrate lyase	**-0.47**	0.47834	**0.26**	0.41497	**-0.92**	0.16345
STM0620	citX	2'-(5'-triphosphoribosyl)-3'-dephospho-CoA:apo-citrate lyase	**1.01**	0.08701	**0.79**	0.06579	**-0.08**	0.87847
STM0621	citF	citrate lyase alpha chain/citrate-ACP transferase	**0.56**	0.21468	**1.42**	0.00862	**-1.09**	0.06640
STM0621	citF	citrate lyase alpha chain/citrate-ACP transferase	**1.75**	0.11370	**1.65**	0.00419	**0.10**	0.90200
STM0622	citE	citrate lyase beta chain	**0.36**	0.52290	**2.28**	0.00115	**0.54**	0.13623
STM0622	citE	citrate lyase beta chain	**0.37**	0.60637	**1.52**	0.00407	**0.06**	0.92608
STM0623	citD	citrate lyase acyl carrier protein gamma chain	**-0.85**	0.22471	**1.39**	0.00997	**-0.12**	0.84080
STM0623	citD	citrate lyase acyl carrier protein gamma chain	**0.04**	0.93135	**0.90**	0.04952	**0.83**	0.30674
STM0624	citC	citrate lyase synthetase	**-0.44**	0.31176	**1.23**	0.01414	**-0.79**	0.04917
STM0624	citC	citrate lyase synthetase	**1.38**	0.03323	**0.49**	0.24285	**0.74**	0.49423
STM0625	dpiB	sensory histidine kinase	**-0.29**	0.47673	**0.98**	0.01367	**-0.14**	0.71772
STM0625	dpiB	sensory histidine kinase	**2.34**	0.02162	**0.99**	0.02657	**2.21**	0.00222

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM0626	dpiA	response regulator	**0.77**	0.23414	**0.88**	0.08142	**-0.40**	0.51869
STM0626	dpiA	response regulator	**0.91**	0.26685	**-0.89**	0.02156	**-0.70**	0.41261
STM0627	dcuC	dicarboxylate transporter	**-0.97**	0.15840	**0.27**	0.62318	**-0.72**	0.24382
STM0627	dcuC	dicarboxylate transporter	**-0.21**	0.71319	**-0.06**	0.91587	**1.04**	0.04164
STM0628	pagP	PhoPQ-activated gene	**-1.47**	0.11671	**-1.77**	0.23041	**-0.76**	0.07554
STM0628	pagP	PhoPQ-activated gene	**-1.35**	0.03618	**-0.46**	0.36364	**-0.80**	0.13642
STM0629	cspE	cold shock protein E	**-3.07**	0.01046	**0.19**	0.81691	**1.40**	0.01627
STM0629	cspE	cold shock protein E	**-1.72**	0.01589	**0.45**	0.41960	**2.05**	0.00087
STM0630	ccrB	camphor resistance protein CrcB	**-2.11**	0.02481	**-1.02**	0.02991	**-0.35**	0.34414
STM0630	ccrB	camphor resistance protein CrcB	**-1.27**	0.41844	**-0.63**	0.07389	**-0.13**	0.83030
STM0631	ybeM	putative hydrolase	**-1.65**	0.06312	**-0.08**	0.78615	**-0.60**	0.11071
STM0631	ybeM	putative hydrolase	**-0.46**	0.45618	**-0.35**	0.33116	**0.44**	0.29326
STM0632	tatE	twin argininte translocase protein A	**0.39**	0.47283	**0.07**	0.83423	**1.16**	0.04008
STM0632	tatE	twin argininte translocase protein A	**1.63**	0.03088	**0.82**	0.02957	**1.35**	0.01056
STM0633	lipA	lipoyl synthase	**-1.62**	0.09639	**-1.14**	0.00310	**-1.42**	0.00415
STM0633	lipA	lipoyl synthase	**-0.92**	0.49059	**-1.21**	0.00257	**0.02**	0.96664
STM0634	ybeF	putative transcriptional regulator	**-1.09**	0.12464	**-0.59**	0.06862	**-0.56**	0.31503
STM0634	ybeF	putative transcriptional regulator	**-0.23**	0.62263	**-0.82**	0.04035	**0.09**	0.85831
STM0635,S	lipB	lipoyltransferase	**-1.88**	0.02102	**-0.57**	0.05922	**-1.12**	0.01790
STM0635,S	lipB	lipoyltransferase	**-1.50**	0.05644	**-0.95**	0.01071	**-1.68**	0.00360
STM0636	ybeD	hypothetical protein STM0636	**-1.61**	0.01813	**0.85**	0.02387	**-1.48**	0.01432
STM0636	ybeD	hypothetical protein STM0636	**-0.38**	0.36340	**0.94**	0.01120	**-1.37**	0.00365
STM0637	dacA	D-alanyl-D-alanine carboxypeptidase	**-2.87**	0.00571	**-1.44**	0.00190	**-2.19**	0.00047
STM0637	dacA	D-alanyl-D-alanine carboxypeptidase	**-1.78**	0.01848	**-1.73**	0.00076	**-2.67**	0.01419
STM0638	rlpA	minor lipoprotein	**-1.91**	0.04784	**-1.36**	0.02099	**-2.86**	0.00016
STM0638	rlpA	minor lipoprotein	**-0.66**	0.46953	**-1.10**	0.01023	**-2.27**	0.00288
STM0639	mrdB	rod shape-determining membrane protein	**-1.03**	0.06705	**-0.67**	0.09596	**-1.99**	0.00125
STM0639	mrdB	rod shape-determining membrane protein	**-0.26**	0.56027	**-0.89**	0.02064	**-1.19**	0.01110
STM0640	mrdA	cell elongation-specific transpeptidase	**0.01**	0.99053	**-1.30**	0.00347	**-0.94**	0.03291
STM0640	mrdA	cell elongation-specific transpeptidase	**1.41**	0.14061	**-1.51**	0.00295	**-1.02**	0.06418
STM0641	ybeA	hypothetical protein STM0641	**-2.56**	0.03787	**-0.36**	0.22393	**-3.17**	0.00409
STM0641	ybeA	hypothetical protein STM0641	**-1.12**	0.03498	**-0.92**	0.03417	**-3.24**	0.00117
STM0642	ybeB	hypothetical protein STM0642	**-1.99**	0.02579	**-0.15**	0.67904	**-2.47**	0.00476
STM0642	ybeB	hypothetical protein STM0642	**-0.90**	0.15567	**-0.26**	0.44618	**-0.76**	0.59002
STM0643	cobC	alpha ribazole-5'-P phosphatase	**-1.05**	0.09741	**-1.18**	0.00270	**-1.96**	0.00202
STM0643	cobC	alpha ribazole-5'-P phosphatase	**0.33**	0.46618	**-0.44**	0.12647	**-0.96**	0.02681
STM0644	cobD	threonine-phosphate decarboxylase	**-0.86**	0.13361	**-0.44**	0.17277	**-0.28**	0.65658
STM0644	cobD	threonine-phosphate decarboxylase	**-0.77**	0.09664	**-1.23**	0.00510	**-1.14**	0.40645
STM0645	nadD	nicotinic acid mononucleotide adenyltransferase	**0.40**	0.70958	**-1.00**	0.03579	**-1.32**	0.02668
STM0645	nadD	nicotinic acid mononucleotide adenyltransferase	**0.77**	0.49312	**-0.47**	0.11407	**-0.61**	0.26915
STM0646	holA	DNA polymerase III subunit delta	**-1.06**	0.04270	**-1.11**	0.01247	**-1.53**	0.03761
STM0646	holA	DNA polymerase III subunit delta	**-1.17**	0.03732	**-1.12**	0.00838	**-2.92**	0.02755
STM0647	rlpB	minor lipoprotein	**-2.56**	0.01198	**-1.10**	0.01395	**-2.24**	0.00050
STM0647	rlpB	minor lipoprotein	**-2.20**	0.00814	**-0.89**	0.02289	**-2.03**	0.00084
STM0648	leuS	leucyl-tRNA synthetase	**-3.44**	0.00537	**-0.69**	0.04804	**-1.16**	0.00869
STM0648	leuS	leucyl-tRNA synthetase	**-2.22**	0.01426	**-0.57**	0.06247	**-1.72**	0.00200
STM0649,S	STM0649,S	putative hydrolase	**0.96**	0.15782	**-0.71**	0.05022	**1.29**	0.08286
STM0649,S	STM0649,S	putative hydrolase	**0.70**	0.17462	**-1.42**	0.00139	**1.19**	0.05468
STM0650	STM0650	putative hydrolas	**1.41**	0.07300	**1.07**	0.15154	**1.75**	0.01624
STM0650	STM0650	putative hydrolas	**3.22**	0.08960	**2.17**	0.09098	**4.18**	0.00010
STM0651	STM0651	2-keto-3-deoxygluconate permease	**1.49**	0.08671	**-0.45**	0.20631	**0.68**	0.46889
STM0651	STM0651	2-keto-3-deoxygluconate permease	**3.53**	0.04090	**-0.48**	0.50209	**1.74**	0.26963
STM0652	STM0652	putative sigma-54 dependent transcriptional regulator	**1.17**	0.09448	**-0.46**	0.22633	**0.56**	0.47382
STM0652	STM0652	putative sigma-54 dependent transcriptional regulator	**2.49**	0.01055	**-0.51**	0.20817	**1.69**	0.01069
STM0653	ybeL	putative cytoplasmic protein	**-0.11**	0.88600	**0.38**	0.24629	**3.34**	0.00048
STM0653	ybeL	putative cytoplasmic protein	**1.56**	0.03083	**1.77**	0.03119	**4.19**	0.00007
STM0654	ybeQ	tetratricopeptide repeat protein	**0.02**	0.96450	**1.40**	0.00203	**2.24**	0.00250
STM0654	ybeQ	tetratricopeptide repeat protein	**1.48**	0.06702	**0.99**	0.02034	**2.97**	0.00080
STM0655	ybeR	putative cytoplasmic protein	**1.06**	0.21331	**-0.09**	0.82574	**-0.70**	0.18043
STM0655	ybeR	putative cytoplasmic protein	**2.10**	0.02043	**-0.12**	0.76429	**0.44**	0.47230
STM0656	ybeS	putative molecular chaperone	**-0.18**	0.73161	**0.14**	0.66126	**0.16**	0.68157
STM0656	ybeS	putative molecular chaperone	**1.01**	0.16050	**-0.62**	0.24214	**0.81**	0.35007
STM0657	ybeU	putative cytoplasmic protein	**-0.64**	0.24587	**-0.58**	0.57212	**0.87**	0.16409
STM0657	ybeU	putative cytoplasmic protein	**-0.27**	0.77607	**-0.09**	0.88464	**-0.58**	0.16686
STM0657	ybeU	putative cytoplasmic protein	**0.53**	0.74253	**-2.10**	0.00169	**-0.58**	0.68811
STM0657	ybeU	putative cytoplasmic protein	**0.71**	0.23679	**-0.98**	0.15141	**-0.49**	0.33875
STM0658	ybeV	putative molecular chaperone	**-0.72**	0.49497	**-0.33**	0.26806	**-0.86**	0.13383
STM0658	ybeV	putative molecular chaperone	**0.74**	0.27643	**1.24**	0.34786	**0.65**	0.21328
STM0659	hscC	putative heatshock protein	**1.47**	0.02098	**-0.26**	0.46426	**-0.14**	0.81857
STM0659	hscC	putative heatshock protein	**2.36**	0.02443	**0.01**	0.98646	**-0.41**	0.45322

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM0660	STM0660	putative cytoplasmic protein	**-0.35**	0.66670	**-0.80**	0.23186	**1.00**	0.10913
STM0660	STM0660	putative cytoplasmic protein	**0.22**	0.71179	**-2.66**	0.00020	**0.42**	0.68650
STM0661	ybeK	putative purine nucleoside hydrolase	**-0.49**	0.36750	**-0.88**	0.06258	**-0.21**	0.68426
STM0661	ybeK	putative purine nucleoside hydrolase	**-0.77**	0.67151	**-0.79**	0.02354	**-0.15**	0.85108
STM0662	gltL	glutamate/aspartate transporter	**3.37**	0.00547	**1.42**	0.08867	**1.16**	0.03331
STM0662	gltL	glutamate/aspartate transporter	**3.41**	0.00789	**0.91**	0.02172	**1.81**	0.00496
STM0663	gltK	glutamate/aspartate transporter	**0.88**	0.37753	**1.17**	0.00389	**0.80**	0.07641
STM0663	gltK	glutamate/aspartate transporter	**0.72**	0.13462	**0.73**	0.06531	**1.73**	0.00838
STM0664	gltJ	glutamate/aspartate transporter	**-2.14**	0.18943	**0.27**	0.66754	**0.92**	0.33471
STM0664	gltJ	glutamate/aspartate transporter	**1.15**	0.18541	**-1.26**	0.00954	**1.58**	0.05910
STM0665	gltI	glutamate/aspartate transporter	**0.77**	0.14412	**4.91**	0.00000	**4.09**	0.00005
STM0665	gltI	glutamate/aspartate transporter	**0.84**	0.07268	**4.02**	0.00039	**4.95**	0.00003
STM0666	lnt	apolipoprotein N-acyltransferase	**-1.38**	0.02500	**0.69**	0.06803	**0.40**	0.31480
STM0666	lnt	apolipoprotein N-acyltransferase	**-0.20**	0.65033	**1.34**	0.00226	**0.81**	0.05508
STM0667	ybeX	putative transport protein	**-0.75**	0.13407	**0.66**	0.42712	**-1.50**	0.00612
STM0667	ybeX	putative transport protein	**-0.42**	0.32224	**-0.70**	0.05258	**-0.58**	0.22858
STM0668	ybeY	hypothetical protein STM0668	**-2.17**	0.00950	**-0.65**	0.04168	**-0.49**	0.17172
STM0668	ybeY	hypothetical protein STM0668	**-1.60**	0.01679	**0.39**	0.18150	**-0.74**	0.05235
STM0669	phoL	putative phosphate starvation-inducible protein	**-1.02**	0.13540	**0.00**	0.99037	**-1.82**	0.00129
STM0669	phoL	putative phosphate starvation-inducible protein	**0.00**	0.99687	**-0.02**	0.96545	**-1.32**	0.00732
STM0670	miaB	rRNA modification protein	**-1.64**	0.04739	**-1.65**	0.00249	**-2.59**	0.00147
STM0670	miaB	rRNA modification protein	**-0.93**	0.08664	**-1.34**	0.00278	**-1.82**	0.00594
STM0671	ubiF	2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinol	**-1.20**	0.03758	**-1.88**	0.00180	**-0.54**	0.24973
STM0671	ubiF	2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinol	**-1.63**	0.04574	**-1.60**	0.00164	**-0.81**	0.11544
STM0672	STM0672	putative inner membrane protein	**-1.97**	0.01034	**-1.87**	0.00037	**-0.84**	0.06134
STM0672	STM0672	putative inner membrane protein	**-1.90**	0.01646	**-2.16**	0.00054	**-0.91**	0.04899
STM0673	glnX	STM0673	**-1.14**	0.06276	**-1.36**	0.05912	**2.81**	0.00115
STM0673	glnX	STM0673	**-0.04**	0.93222	**-1.23**	0.05816	**2.96**	0.00014
STM0674	glnV	STM0674	**-1.14**	0.07505	**-2.05**	0.00210	**2.45**	0.00062
STM0674	glnV	STM0674	**-1.02**	0.13109	**-2.42**	0.00099	**2.77**	0.00018
STM0675	metU	STM0675	**-3.20**	0.01946	**-1.86**	0.00336	**1.34**	0.05510
STM0675	metU	STM0675	**-1.80**	0.01788	**-1.73**	0.00161	**2.01**	0.00112
STM0676	glnW	STM0676	**-1.45**	0.04072	**-1.12**	0.04059	**2.65**	0.00033
STM0676	glnW	STM0676	**-1.58**	0.03539	**-1.59**	0.01448	**2.42**	0.00093
STM0677	glnU	STM0677	**-2.19**	0.01710	**-1.44**	0.03275	**1.65**	0.00975
STM0677	glnU	STM0677	**-1.66**	0.02251	**-2.16**	0.00214	**1.61**	0.00487
STM0678	leuW	STM0678	**-4.65**	0.00512	**-3.46**	0.00002	**-2.50**	0.00022
STM0678	leuW	STM0678	**-4.33**	0.00547	**-3.66**	0.00002	**-2.89**	0.00016
STM0679	metT	STM0679	**-3.03**	0.00991	**-1.86**	0.00053	**1.33**	0.02127
STM0679	metT	STM0679	**-2.24**	0.00901	**-1.90**	0.00184	**1.54**	0.00537
STM0680	asnB	asparagine synthetase B	**-0.47**	0.26120	**-0.47**	0.23744	**-1.00**	0.02623
STM0680	asnB	asparagine synthetase B	**-0.47**	0.64483	**-1.75**	0.00074	**-2.44**	0.02020
STM0681	nagD	putative phosphatase	**-0.84**	0.20762	**-0.01**	0.98671	**-0.89**	0.02944
STM0681	nagD	putative phosphatase	**0.74**	0.26729	**-0.48**	0.19966	**-0.68**	0.16346
STM0682	nagC	N-acetylglucosamine operon transcriptional repressor	**-1.05**	0.05760	**-0.84**	0.01730	**-1.99**	0.00473
STM0682	nagC	N-acetylglucosamine operon transcriptional repressor	**-1.08**	0.27453	**-0.92**	0.01604	**-0.52**	0.25902
STM0683	nagA	N-acetylglucosamine-6-phosphate deacetylase	**-1.10**	0.03938	**-0.14**	0.68826	**-0.80**	0.06086
STM0683	nagA	N-acetylglucosamine-6-phosphate deacetylase	**-0.09**	0.92245	**0.26**	0.44499	**-0.36**	0.34506
STM0684	nagB	glucosamine-6-phosphate deaminase	**-2.34**	0.01385	**-0.06**	0.86434	**0.15**	0.72626
STM0684	nagB	glucosamine-6-phosphate deaminase	**-1.79**	0.01443	**-0.30**	0.37149	**1.16**	0.01740
STM0685	nagE	N-acetylglucosamine-specific enzyme IIABC	**-0.91**	0.05926	**-0.37**	0.72539	**-0.79**	0.19777
STM0685	nagE	N-acetylglucosamine-specific enzyme IIABC	**-1.27**	0.19202	**-1.11**	0.00432	**-0.95**	0.21029
STM0686	glnS	glutaminyl-tRNA synthetase	**-0.58**	0.42724	**-0.80**	0.04936	**-1.27**	0.04089
STM0686	glnS	glutaminyl-tRNA synthetase	**0.50**	0.37575	**-1.00**	0.02250	**-0.52**	0.36968
STM0687	ybfM	putative outer membrane protein	**1.00**	0.19322	**-0.11**	0.78133	**-0.41**	0.29300
STM0687	ybfM	putative outer membrane protein	**1.71**	0.03236	**0.13**	0.72635	**0.74**	0.20492
STM0688	ybfN	putative lipoprotein	**2.36**	0.01041	**0.67**	0.13074	**1.35**	0.03659
STM0688	ybfN	putative lipoprotein	**2.05**	0.05312	**-0.35**	0.38408	**0.62**	0.19504
STM0689	citA	citrate-proton symporter	**-0.71**	0.18541	**-0.60**	0.26172	**-0.66**	0.27527
STM0689	citA	citrate-proton symporter	**-0.20**	0.78983	**-0.45**	0.17115	**-0.76**	0.13636
STM0690	citB	citrate utilization protein b	**1.08**	0.16800	**0.52**	0.21076	**0.25**	0.63480
STM0690	citB	citrate utilization protein b	**2.18**	0.02067	**-0.04**	0.91666	**0.69**	0.31592
STM0691	STM0691	hypothetical protein STM0691	**0.40**	0.43737	**-0.20**	0.57900	**1.43**	0.03073
STM0691	STM0691	hypothetical protein STM0691	**1.17**	0.09934	**-0.86**	0.04417	**0.63**	0.15950
STM0692	STM0692	putative transcriptional regulator	**-0.33**	0.45282	**-0.97**	0.03406	**-2.03**	0.00220
STM0692	STM0692	putative transcriptional regulator	**0.32**	0.55064	**-1.10**	0.01701	**-0.57**	0.26761
STM0693	fur	ferric uptake regulator	**-1.90**	0.05343	**-1.28**	0.00550	**-1.75**	0.03031
STM0693	fur	ferric uptake regulator	**-0.97**	0.15272	**-1.15**	0.00556	**-1.70**	0.00146
STM0694	fldA	flavodoxin	**-3.42**	0.00595	**-1.04**	0.01336	**-2.82**	0.00014
STM0694	fldA	flavodoxin	**-1.12**	0.06702	**-0.76**	0.03250	**-1.62**	0.00591

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM0695	ybfE	putative SOS response protein	**-2.56**	0.00812	**-1.92**	0.00070	**-2.47**	0.00108
STM0695	ybfE	putative SOS response protein	**-2.25**	0.06218	**-2.13**	0.00014	**-3.98**	0.00007
STM0696	ybfF	putative enzyme	**-1.50**	0.01835	**-1.61**	0.00164	**-3.44**	0.00027
STM0696	ybfF	putative enzyme	**-1.37**	0.02780	**-1.15**	0.00596	**-1.97**	0.00386
STM0697	seqA	sequestration protein A	**-3.16**	0.01460	**-0.96**	0.01456	**-2.29**	0.00119
STM0697	seqA	sequestration protein A	**-1.32**	0.02636	**-1.16**	0.00549	**-1.68**	0.00801
STM0698	pgm	phosphoglucomutase	**0.45**	0.50518	**-0.14**	0.62234	**1.52**	0.00555
STM0698	pgm	phosphoglucomutase	**0.88**	0.54856	**-0.08**	0.82951	**2.29**	0.00160
STM0699	STM0699	putative cytoplasmic protein	**-0.85**	0.15487	**-1.75**	0.00055	**-1.61**	0.02160
STM0699	STM0699	putative cytoplasmic protein	**0.68**	0.21280	**-1.09**	0.01689	**-0.93**	0.08360
STM0700	potE	putrescine/ornithine antiporter	**0.60**	0.72265	**-0.53**	0.10489	**-1.17**	0.06716
STM0700	potE	putrescine/ornithine antiporter	**3.32**	0.01067	**0.09**	0.85269	**2.43**	0.00395
STM0701	speF	ornithine decarboxylase isozyme	**-0.52**	0.35022	**-1.06**	0.01544	**-0.03**	0.95416
STM0701	speF	ornithine decarboxylase isozyme	**1.49**	0.04005	**-0.89**	0.03645	**0.91**	0.07426
STM0702	kdpE	response regulator	**1.66**	0.02201	**-0.32**	0.32054	**0.00**	0.99486
STM0702	kdpE	response regulator	**2.91**	0.00686	**-0.14**	0.64912	**0.57**	0.25809
STM0703	kdpD	sensor kinase	**-1.49**	0.01590	**-0.39**	0.60308	**-1.09**	0.19448
STM0703	kdpD	sensor kinase	**1.32**	0.36846	**-0.12**	0.75579	**0.19**	0.83020
STM0704	kdpC	potassium-transporting ATPase subunit C	**0.65**	0.41695	**0.42**	0.17843	**-1.14**	0.11745
STM0704	kdpC	potassium-transporting ATPase subunit C	**-0.05**	0.95941	**-0.02**	0.96249	**-0.80**	0.17768
STM0705	kdpB	potassium-transporting ATPase subunit B	**-0.85**	0.32123	**0.03**	0.97838	**-1.32**	0.00981
STM0705	kdpB	potassium-transporting ATPase subunit B	**-0.48**	0.48560	**-0.62**	0.18663	**-1.08**	0.08205
STM0706	kdpA	potassium-transporting ATPase subunit A	**-0.34**	0.67328	**-1.62**	0.00688	**0.32**	0.79018
STM0706	kdpA	potassium-transporting ATPase subunit A	**-0.35**	0.53193	**-1.42**	0.00139	**-0.91**	0.44761
STM0708	ybfA	putative periplasmic protein	**0.63**	0.22157	**1.76**	0.00325	**0.49**	0.20494
STM0708	ybfA	putative periplasmic protein	**1.78**	0.02936	**1.38**	0.02972	**1.14**	0.01667
STM0709	phrB	deoxyribodipyrimidine photolyase	**-0.69**	0.15040	**0.33**	0.46473	**-0.56**	0.31837
STM0709	phrB	deoxyribodipyrimidine photolyase	**-0.25**	0.84585	**0.16**	0.70841	**0.13**	0.71804
STM0710	ybgH	putative POT family transport protein	**-0.73**	0.14053	**0.64**	0.09245	**-0.66**	0.41067
STM0710	ybgH	putative POT family transport protein	**0.50**	0.51800	**0.07**	0.80321	**-0.07**	0.86528
STM0711	ybgI	putative cytoplasmic protein	**-1.09**	0.06636	**0.46**	0.14203	**-1.21**	0.00957
STM0711	ybgI	putative cytoplasmic protein	**-0.36**	0.55006	**0.12**	0.72335	**0.16**	0.66951
STM0712	ybgJ	putative carboxylase	**-1.52**	0.02075	**0.11**	0.77317	**-1.94**	0.00109
STM0712	ybgJ	putative carboxylase	**-0.63**	0.18330	**0.13**	0.67941	**-1.10**	0.03277
STM0713	ybgK	putative carboxylase	**-1.80**	0.01479	**-0.85**	0.14836	**-0.81**	0.05729
STM0713	ybgK	putative carboxylase	**-0.99**	0.05106	**-0.58**	0.07972	**-1.25**	0.00501
STM0714	ybgL	hypothetical protein STM0714	**-0.63**	0.32776	**-0.26**	0.72277	**-1.79**	0.05254
STM0714	ybgL	hypothetical protein STM0714	**-1.20**	0.27923	**-0.42**	0.17513	**-1.35**	0.10030
STM0715	STM0715	putative cytoplasmic protein	**0.38**	0.62471	**-0.05**	0.95206	**0.03**	0.97258
STM0715	STM0715	putative cytoplasmic protein	**1.22**	0.07865	**-0.03**	0.94131	**0.32**	0.65167
STM0716	NT_FimBE_C	putative phage integrase	**-0.41**	0.50674	**0.52**	0.09523	**-0.06**	0.93289
STM0716	NT_FimBE_C	putative phage integrase	**1.73**	0.01215	**0.24**	0.42544	**1.29**	0.01963
STM0719	STM0719	putative UDP-galactopyranose mutase	**-0.10**	0.86520	**-0.04**	0.93704	**-0.86**	0.12396
STM0719	STM0719	putative UDP-galactopyranose mutase	**0.55**	0.49910	**0.54**	0.72511	**-0.08**	0.91566
STM0719	STM0719	putative UDP-galactopyranose mutase	**0.77**	0.14135	**0.97**	0.01604	**0.94**	0.05275
STM0719	STM0719	putative UDP-galactopyranose mutase	**2.10**	0.01001	**-0.79**	0.04306	**0.56**	0.13535
STM0719	STM0719	putative UDP-galactopyranose mutase	**2.60**	0.02059	**-1.14**	0.11142	**-0.51**	0.63740
STM0719	STM0719	putative UDP-galactopyranose mutase	**0.46**	0.58858	**-0.20**	0.50625	**0.96**	0.15024
STM0720	STM0720	putative glycosyl transferase	**-0.86**	0.08127	**-0.85**	0.04600	**-0.03**	0.94145
STM0720	STM0720	putative glycosyl transferase	**0.09**	0.91100	**-0.03**	0.96876	**0.74**	0.33069
STM0721	STM0721	putative glycosyl transferase	**-0.06**	0.90542	**0.23**	0.75781	**0.66**	0.30228
STM0721	STM0721	putative glycosyl transferase	**-0.11**	0.88986	**-2.04**	0.00289	**-2.42**	0.02497
STM0722	STM0722	putative ABC transporter permease protein	**-0.54**	0.32546	**-0.09**	0.86466	**0.00**	0.99701
STM0722	STM0722	putative ABC transporter permease protein	**-0.11**	0.85422	**-1.26**	0.02111	**-0.12**	0.82079
STM0723	STM0723	putative ABC-type polysaccharide/polyol phosphate	**-0.71**	0.27249	**0.29**	0.36866	**-0.77**	0.09346
STM0723	STM0723	putative ABC-type polysaccharide/polyol phosphate	**0.52**	0.30252	**-0.62**	0.26531	**0.73**	0.14090
STM0724	STM0724	putative glycosyltransferase	**-0.72**	0.33717	**-0.40**	0.35162	**0.38**	0.44761
STM0724	STM0724	putative glycosyltransferase	**0.59**	0.32060	**-1.13**	0.25279	**-0.54**	0.59941
STM0725	STM0725	putative glycosyltransferase	**-0.94**	0.34639	**-0.61**	0.17391	**-0.42**	0.33093
STM0725	STM0725	putative glycosyltransferase	**1.25**	0.09938	**-0.11**	0.83068	**1.23**	0.13471
STM0726	STM0726	putative glycosyl transferase	**1.39**	0.02441	**0.90**	0.01561	**1.50**	0.01562
STM0726	STM0726	putative glycosyl transferase	**2.61**	0.01041	**0.10**	0.85978	**3.04**	0.00018
STM0728	nei	endonuclease VIII	**-0.06**	0.92487	**0.31**	0.29160	**-0.30**	0.39974
STM0728	nei	endonuclease VIII	**0.09**	0.82416	**-0.07**	0.86108	**0.67**	0.27073
STM0729	abrB	putative transport protein	**-1.38**	0.10067	**-1.01**	0.05843	**-0.62**	0.20262
STM0729	abrB	putative transport protein	**-0.64**	0.37382	**-0.87**	0.01619	**-1.14**	0.06062
STM0730	gltA	citrate synthase	**1.99**	0.55094	**1.00**	0.04577	**-0.44**	0.23261
STM0730	gltA	citrate synthase	**-1.37**	0.09118	**1.84**	0.00623	**0.13**	0.77280
STM0732	sdhC	succinate dehydrogenase cytochrome b556 large	**-2.86**	0.01580	**-1.02**	0.02651	**-0.82**	0.06667
STM0732	sdhC	succinate dehydrogenase cytochrome b556 large	**-2.28**	0.00924	**-1.23**	0.00321	**-1.47**	0.00415

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM0733	sdhD	succinate dehydrogenase cytochrome b556 small	**-2.00**	0.02762	**-2.02**	0.00036	**-1.89**	0.00157
STM0733	sdhD	succinate dehydrogenase cytochrome b556 small	**-2.46**	0.02948	**-1.52**	0.00422	**-1.60**	0.00694
STM0734	sdhA	succinate dehydrogenase catalytic subunit	**-2.56**	0.00753	**-1.92**	0.05244	**-1.53**	0.00903
STM0734	sdhA	succinate dehydrogenase catalytic subunit	**-3.13**	0.00577	**-2.92**	0.00013	**-2.09**	0.00068
STM0735	sdhB	succinate dehydrogenase catalytic subunit	**-2.07**	0.01263	**-1.86**	0.00069	**-2.25**	0.00070
STM0735	sdhB	succinate dehydrogenase catalytic subunit	**-0.82**	0.15516	**-1.38**	0.00273	**-1.71**	0.00467
STM0736	sucA	2-oxoglutarate dehydrogenase	**-3.84**	0.00565	**-1.74**	0.00525	**-2.83**	0.00496
STM0736	sucA	2-oxoglutarate dehydrogenase	**-1.41**	0.05957	**-1.59**	0.01622	**-3.84**	0.00277
STM0737	sucB	dihydrolipoamide acetyltransferase	**-3.85**	0.01032	**-0.22**	0.48519	**-2.69**	0.00102
STM0737	sucB	dihydrolipoamide acetyltransferase	**-2.43**	0.00824	**-0.12**	0.75985	**-2.96**	0.00019
STM0738	sucC	succinyl-CoA synthetase subunit beta	**-0.58**	0.58701	**0.83**	0.03027	**-1.32**	0.04466
STM0738	sucC	succinyl-CoA synthetase subunit beta	**-0.78**	0.39473	**1.00**	0.01853	**-1.51**	0.03381
STM0739	sucD	succinyl-CoA synthetase alpha subunit	**-0.94**	0.06974	**0.79**	0.06439	**-1.04**	0.02689
STM0739	sucD	succinyl-CoA synthetase alpha subunit	**0.35**	0.58334	**0.32**	0.40572	**-0.52**	0.21359
STM0740	cydA	cytochrome d terminal oxidase polypeptide subunit I	**-1.93**	0.01520	**-0.86**	0.02910	**-2.48**	0.00074
STM0740	cydA	cytochrome d terminal oxidase polypeptide subunit I	**-0.87**	0.24054	**-0.84**	0.04321	**-2.60**	0.00108
STM0741	cydB	cytochrome d terminal oxidase polypeptide subunit II	**-1.93**	0.01967	**0.00**	0.99632	**-1.79**	0.00125
STM0741	cydB	cytochrome d terminal oxidase polypeptide subunit II	**-1.61**	0.05901	**-0.59**	0.08550	**-2.06**	0.00072
STM0742	ybgT	putative outer membrane lipoprotein	**0.45**	0.83532	**-0.86**	0.02378	**-1.56**	0.37275
STM0742	ybgT	putative outer membrane lipoprotein	**0.05**	0.94496	**-0.39**	0.24183	**-1.70**	0.05156
STM0743	ybgE	putative inner membrane lipoprotein	**-1.65**	0.01298	**-1.17**	0.00546	**-2.44**	0.00024
STM0743	ybgE	putative inner membrane lipoprotein	**-2.34**	0.01228	**-1.15**	0.01094	**-2.07**	0.10919
STM0744	ybgC	putative esterase	**-2.37**	0.00796	**-1.09**	0.01848	**-1.98**	0.00174
STM0744	ybgC	putative esterase	**-1.39**	0.03086	**-1.04**	0.00889	**-1.38**	0.04617
STM0745	tolQ	Tol import system inner membrane protein	**-0.72**	0.61970	**-1.30**	0.00241	**-2.52**	0.00026
STM0745	tolQ	Tol import system inner membrane protein	**0.42**	0.41697	**-1.66**	0.00212	**-2.32**	0.00036
STM0746	tolR	Tol import sytem inner membrane protein	**-2.09**	0.01417	**-1.08**	0.01804	**-3.35**	0.00009
STM0746	tolR	Tol import sytem inner membrane protein	**-1.41**	0.02695	**-0.69**	0.03536	**-2.05**	0.03137
STM0747	tolA	cell envelope integrity inner membrane protein TolA	**-2.20**	0.01028	**-0.54**	0.07765	**-2.39**	0.00075
STM0747	tolA	cell envelope integrity inner membrane protein TolA	**-0.65**	0.26216	**-0.53**	0.08928	**-1.84**	0.00133
STM0748	tolB	translocation protein TolB precursor	**-2.83**	0.00630	**-0.28**	0.35231	**-2.31**	0.00035
STM0748	tolB	translocation protein TolB precursor	**-1.49**	0.01813	**-0.26**	0.49971	**-1.57**	0.01078
STM0749	pal	peptidoglycan-associated lipoprotein precursor	**-3.96**	0.01114	**-1.13**	0.00764	**-3.14**	0.00012
STM0749	pal	peptidoglycan-associated lipoprotein precursor	**-2.70**	0.03569	**-1.24**	0.00312	**-3.02**	0.00017
STM0750	ybgF	putative periplasmic protein	**-1.20**	0.03054	**-0.35**	0.34076	**-2.03**	0.00094
STM0750	ybgF	putative periplasmic protein	**-0.99**	0.04688	**-0.10**	0.74063	**-1.23**	0.02240
STM0751	lysT	STM0751	**-1.40**	0.13314	**-1.14**	0.00365	**0.17**	0.72924
STM0751	lysT	STM0751	**-0.03**	0.94878	**-1.01**	0.00958	**0.15**	0.70823
STM0752	valT	STM0752	**-1.21**	0.23088	**-1.25**	0.00251	**-1.16**	0.04265
STM0752	valT	STM0752	**-0.86**	0.33859	**-1.29**	0.00295	**-0.95**	0.04567
STM0753	lysW	STM0753	**-2.29**	0.01032	**-1.19**	0.00681	**0.33**	0.46715
STM0753	lysW	STM0753	**-1.01**	0.40767	**-1.27**	0.00387	**0.26**	0.54700
STM0754	lysY	STM0754	**-2.17**	0.04984	**-1.49**	0.00185	**-0.56**	0.19527
STM0754	lysY	STM0754	**-1.00**	0.35870	**-1.33**	0.00165	**-0.03**	0.94081
STM0755	lysZ	STM0755	**-2.01**	0.08764	**-0.81**	0.02815	**0.09**	0.85588
STM0755	lysZ	STM0755	**-1.00**	0.31834	**-0.56**	0.08203	**0.41**	0.31813
STM0756	nadA	quinolinate synthetase	**-0.81**	0.12327	**-0.21**	0.55702	**0.50**	0.26028
STM0756	nadA	quinolinate synthetase	**0.01**	0.97962	**-0.08**	0.85235	**0.73**	0.09216
STM0757	pnuC	nucleoside/purine/pyrimidine transporter	**-0.94**	0.19282	**0.68**	0.06361	**0.95**	0.03662
STM0757	pnuC	nucleoside/purine/pyrimidine transporter	**-0.34**	0.48245	**-0.29**	0.41102	**0.62**	0.12853
STM0758	ybgR	zinc transporter ZitB	**-0.94**	0.07746	**-0.11**	0.71949	**0.84**	0.03772
STM0758	ybgR	zinc transporter ZitB	**-1.54**	0.09878	**0.09**	0.83521	**0.91**	0.09524
STM0759	ybgS	hypothetical protein STM0759	**2.77**	0.00660	**3.30**	0.00009	**8.46**	0.00001
STM0759	ybgS	hypothetical protein STM0759	**-0.73**	0.81615	**3.11**	0.00006	**9.52**	0.00001
STM0760	aroG	3-deoxy-7-phosphoheptulonate synthase	**-0.32**	0.56239	**-0.02**	0.96131	**1.12**	0.11817
STM0760	aroG	3-deoxy-7-phosphoheptulonate synthase	**1.52**	0.03893	**0.62**	0.09448	**1.43**	0.00789
STM0761	STM0761	fumarate hydratase	**-0.14**	0.76189	**0.02**	0.95799	**-0.13**	0.78809
STM0761	STM0761	fumarate hydratase	**3.16**	0.01549	**0.49**	0.19623	**0.71**	0.15834
STM0762	STM0762	fumarate hydratase	**0.92**	0.28285	**-0.39**	0.30926	**0.85**	0.07664
STM0762	STM0762	fumarate hydratase	**1.23**	0.18639	**0.43**	0.39019	**0.28**	0.55428
STM0763,s	STM0763,s	transcriptional regulator	**2.69**	0.00567	**1.89**	0.00643	**3.12**	0.00020
STM0763,s	STM0763,s	transcriptional regulator	**3.16**	0.00719	**1.73**	0.01187	**3.56**	0.00017
STM0764	STM0764	transcriptional regulator	**-0.51**	0.40431	**-0.31**	0.49949	**0.13**	0.85258
STM0764	STM0764	transcriptional regulator	**-0.48**	0.43042	**-1.17**	0.04245	**-0.26**	0.62912
STM0765	STM0765	putative cation transporter	**-0.42**	0.53080	**-1.04**	0.01483	**0.00**	0.99713
STM0765	STM0765	putative cation transporter	**-0.38**	0.70846	**-1.34**	0.02847	**0.11**	0.85705
STM0766	dcoC	putative oxaloacetate decarboxylase subunit gamma	**2.20**	0.15371	**-0.56**	0.23268	**-1.09**	0.06348
STM0766	dcoC	putative oxaloacetate decarboxylase subunit gamma	**2.85**	0.07824	**-0.86**	0.02614	**-0.10**	0.83931
STM0769	STM0769	putative cytoplasmic protein	**-0.98**	0.25928	**0.53**	0.51841	**-1.57**	0.02006
STM0769	STM0769	putative cytoplasmic protein	**0.80**	0.09098	**0.06**	0.85837	**-0.31**	0.42033

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM0770	STM0770	putative ABC transport protein	**-1.15**	0.04630	**0.64**	0.04612	**0.33**	0.52347
STM0770	STM0770	putative ABC transport protein	**-0.44**	0.45468	**0.32**	0.32758	**0.37**	0.31515
STM0771	STM0771	putative ABC-type cobalamin/Fe3+-siderophore transport	**-1.11**	0.06459	**1.18**	0.00410	**0.06**	0.90191
STM0771	STM0771	putative ABC-type cobalamin/Fe3+-siderophore transport	**0.68**	0.39100	**2.27**	0.00022	**0.64**	0.11767
STM0772	gpmA	phosphoglyceromutase	**-0.47**	0.29947	**2.26**	0.00014	**0.85**	0.03706
STM0772	gpmA	phosphoglyceromutase	**0.86**	0.08950	**2.37**	0.00017	**1.50**	0.01346
STM0773	galM	galactose-1-epimerase	**-1.45**	0.01801	**0.37**	0.30677	**-0.61**	0.10903
STM0773	galM	galactose-1-epimerase	**-1.01**	0.05261	**0.82**	0.04350	**-0.32**	0.47937
STM0774	galK	galactokinase	**-0.81**	0.08485	**-0.24**	0.53525	**-0.91**	0.04600
STM0774	galK	galactokinase	**0.00**	0.99279	**-0.07**	0.84384	**-0.45**	0.19446
STM0775	galT	galactose-1-phosphate uridylyltransferase	**-1.77**	0.04119	**-1.59**	0.00590	**-1.53**	0.00301
STM0775	galT	galactose-1-phosphate uridylyltransferase	**-1.43**	0.06694	**-1.11**	0.00911	**-1.31**	0.00570
STM0776	galE	UDP-galactose 4-epimerase	**1.16**	0.66633	**-0.81**	0.02064	**2.85**	0.01103
STM0776	galE	UDP-galactose 4-epimerase	**0.45**	0.81180	**-0.65**	0.05645	**1.60**	0.17138
STM0777	STM0777	putative inner membrane protein	**0.47**	0.26806	**-0.65**	0.11001	**-0.10**	0.80547
STM0777	STM0777	putative inner membrane protein	**2.99**	0.00773	**-0.44**	0.54396	**1.52**	0.01210
STM0778	modF	putative molybdenum transporter	**-0.55**	0.22891	**-0.29**	0.29361	**-0.52**	0.67240
STM0778	modF	putative molybdenum transporter	**0.18**	0.83865	**-0.02**	0.96395	**-0.49**	0.44905
STM0779	modE	molybdate uptake operon transcriptional repressor	**-1.44**	0.10095	**-0.09**	0.82309	**-1.74**	0.00995
STM0779	modE	molybdate uptake operon transcriptional repressor	**-0.37**	0.55169	**0.57**	0.11433	**-1.29**	0.02660
STM0781	modA	molybdate transporter	**-1.63**	0.01426	**1.17**	0.00276	**-3.49**	0.00144
STM0781	modA	molybdate transporter	**-1.51**	0.04257	**1.48**	0.00130	**-3.24**	0.00091
STM0782	modB	molybdate transport permease protein	**-1.29**	0.02828	**0.12**	0.69790	**-2.38**	0.00051
STM0782	modB	molybdate transport permease protein	**-0.50**	0.58841	**-0.24**	0.49843	**-1.35**	0.01770
STM0783	modC	molybdate transporter	**-1.37**	0.03235	**-0.43**	0.16945	**-2.50**	0.00161
STM0783	modC	molybdate transporter	**-1.42**	0.01976	**-0.31**	0.26612	**-1.03**	0.16591
STM0784	ybhA	putative hydrolase	**0.14**	0.74642	**0.29**	0.47565	**0.93**	0.08458
STM0784	ybhA	putative hydrolase	**-0.46**	0.71380	**-0.12**	0.71950	**-1.65**	0.18597
STM0785	ybhE	putative 3-carboxymuconate cyclase	**-0.80**	0.17278	**0.20**	0.51437	**-0.54**	0.21735
STM0785	ybhE	putative 3-carboxymuconate cyclase	**0.21**	0.85257	**-0.01**	0.98144	**-0.19**	0.65066
STM0786	ybhC	putative pectinesterase	**-0.85**	0.16839	**-0.47**	0.12213	**-0.84**	0.38052
STM0786	ybhC	putative pectinesterase	**-0.48**	0.46251	**-1.30**	0.00419	**-0.98**	0.19818
STM0787	hutI	imidazolonepropionase	**-0.74**	0.27874	**0.50**	0.18597	**-0.69**	0.13879
STM0787	hutI	imidazolonepropionase	**0.37**	0.68282	**-0.09**	0.79523	**0.77**	0.05525
STM0788	hutG	formimidoylglutamase	**-0.55**	0.31023	**-0.85**	0.02410	**-0.80**	0.03793
STM0788	hutG	formimidoylglutamase	**0.50**	0.27957	**-0.26**	0.42611	**0.20**	0.70055
STM0789	hutC	histidine utilization repressor	**-1.19**	0.03508	**-1.33**	0.00322	**0.59**	0.67098
STM0789	hutC	histidine utilization repressor	**-1.27**	0.03158	**-1.62**	0.14685	**-1.44**	0.00992
STM0791	hutH	histidine ammonia-lyase	**-0.22**	0.72937	**0.37**	0.34689	**0.77**	0.07556
STM0791	hutH	histidine ammonia-lyase	**-0.98**	0.11344	**-0.11**	0.75508	**-1.23**	0.09196
STM0792	ybhB	putative phospholipid-binding protein	**0.32**	0.74820	**0.70**	0.04361	**0.39**	0.31997
STM0792	ybhB	putative phospholipid-binding protein	**1.19**	0.12999	**0.63**	0.07962	**1.22**	0.01499
STM0793	bioA	adenosylmethionine--8-amino-7-oxononanoate	**-0.78**	0.18239	**1.45**	0.00187	**-0.86**	0.05953
STM0793	bioA	adenosylmethionine--8-amino-7-oxononanoate	**0.38**	0.39271	**1.55**	0.00094	**0.21**	0.58027
STM0794	bioB	biotin synthetase	**0.97**	0.29048	**3.97**	0.00009	**-0.17**	0.81930
STM0794	bioB	biotin synthetase	**1.74**	0.24403	**2.93**	0.00027	**0.07**	0.95719
STM0795	bioF	8-amino-7-oxononanoate synthase	**0.82**	0.37389	**-0.49**	0.42246	**-0.56**	0.68128
STM0795	bioF	8-amino-7-oxononanoate synthase	**0.24**	0.88427	**-1.08**	0.05509	**0.00**	0.99968
STM0796	bioC	biotin biosynthetic protein	**0.23**	0.76572	**2.01**	0.00056	**-1.27**	0.02940
STM0796	bioC	biotin biosynthetic protein	**1.84**	0.01530	**1.86**	0.00136	**0.27**	0.54311
STM0797	bioD	dithiobiotin synthetase	**0.05**	0.93655	**-0.59**	0.14314	**-1.44**	0.01558
STM0797	bioD	dithiobiotin synthetase	**0.67**	0.21970	**-0.54**	0.18443	**-0.27**	0.51805
STM0798	uvrB	excinuclease ABC subunit B	**-0.88**	0.19252	**0.00**	0.99632	**0.52**	0.26405
STM0798	uvrB	excinuclease ABC subunit B	**0.14**	0.81485	**0.26**	0.41103	**-0.20**	0.67210
STM0800	slrP	leucine-rich repeat protein	**0.14**	0.79305	**0.75**	0.07310	**0.56**	0.37201
STM0800	slrP	leucine-rich repeat protein	**1.17**	0.04629	**0.29**	0.37230	**0.94**	0.04324
STM0801	ybhK	putative cytoplasmic protein	**-0.36**	0.49898	**0.03**	0.95969	**-0.08**	0.90227
STM0801	ybhK	putative cytoplasmic protein	**0.96**	0.13892	**0.77**	0.05814	**0.54**	0.35049
STM0802	moaA	molybdenum cofactor biosynthesis protein A	**-1.85**	0.01305	**-1.02**	0.01167	**-0.61**	0.09036
STM0802	moaA	molybdenum cofactor biosynthesis protein A	**-0.42**	0.46345	**-0.90**	0.02722	**0.75**	0.12561
STM0803	moaB	molybdopterin biosynthetic protein B	**-1.82**	0.01408	**0.11**	0.73846	**-0.69**	0.10917
STM0803	moaB	molybdopterin biosynthetic protein B	**-0.34**	0.40507	**0.19**	0.58861	**-0.46**	0.27630
STM0804	moaC	molybdenum cofactor biosynthesis protein C	**-0.97**	0.19898	**-1.62**	0.00314	**-1.42**	0.01273
STM0804	moaC	molybdenum cofactor biosynthesis protein C	**-1.70**	0.04692	**-1.14**	0.00761	**-1.51**	0.01177
STM0805	moaD	molybdopterin biosynthetic protein	**-0.39**	0.48121	**-1.52**	0.00521	**-1.37**	0.03212
STM0805	moaD	molybdopterin biosynthetic protein	**-1.34**	0.05364	**-1.99**	0.00083	**-1.53**	0.04263
STM0806	moaE	molybdopterin converting factor subunit 2	**-1.55**	0.04254	**-1.31**	0.00302	**-0.53**	0.18748
STM0806	moaE	molybdopterin converting factor subunit 2	**-0.91**	0.19658	**-0.64**	0.04258	**-0.45**	0.21976
STM0807	ybhL	putative permease	**-1.13**	0.03387	**0.09**	0.79460	**1.28**	0.00561
STM0807	ybhL	putative permease	**-0.30**	0.52769	**0.17**	0.60388	**1.82**	0.00227

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM0808	ybhM	putative integral membrane protein	**-1.61**	0.01616	**-1.33**	0.07752	**0.94**	0.05562
STM0808	ybhM	putative integral membrane protein	**-1.06**	0.21280	**-0.69**	0.29718	**0.22**	0.55880
STM0809	STM0809	putative inner membrane protein	**0.86**	0.25808	**-0.42**	0.48517	**0.37**	0.30764
STM0809	STM0809	putative inner membrane protein	**1.08**	0.22297	**-0.98**	0.04804	**0.36**	0.50578
STM0810	STM0810	putative inner membrane protein	**-0.09**	0.91090	**-0.72**	0.17242	**0.45**	0.44712
STM0810	STM0810	putative inner membrane protein	**1.09**	0.15154	**-0.80**	0.12908	**1.48**	0.08681
STM0811	ybhN	hypothetical protein STM0811	**1.92**	0.11444	**-1.01**	0.02281	**0.65**	0.37764
STM0811	ybhN	hypothetical protein STM0811	**2.95**	0.04243	**-1.29**	0.00843	**2.06**	0.00257
STM0812	ybhO	cardiolipin synthase	**2.79**	0.04229	**-0.39**	0.42647	**0.66**	0.12855
STM0812	ybhO	cardiolipin synthase	**2.33**	0.02172	**-0.23**	0.73632	**1.16**	0.03045
STM0813	ybhP	putative cytoplasmic protein	**-1.44**	0.04220	**-0.08**	0.89527	**0.11**	0.85965
STM0813	ybhP	putative cytoplasmic protein	**0.65**	0.22022	**-0.21**	0.61214	**0.62**	0.17046
STM0814	ybhQ	putative inner membrane protein	**-0.82**	0.15344	**0.78**	0.06912	**2.65**	0.00071
STM0814	ybhQ	putative inner membrane protein	**0.42**	0.42163	**1.50**	0.00363	**2.62**	0.00056
STM0815	ybhR	putative transport protein	**-0.89**	0.27929	**0.15**	0.77904	**1.05**	0.05011
STM0815	ybhR	putative transport protein	**-0.22**	0.72148	**0.53**	0.23126	**1.02**	0.01504
STM0816	ybhS	putative transport protein	**-0.75**	0.20812	**-0.40**	0.41793	**-0.63**	0.09411
STM0816	ybhS	putative transport protein	**-0.29**	0.50429	**-0.97**	0.01924	**0.16**	0.79242
STM0817	ybhF	putative ABC-type multidrug transport system ATPase	**-0.28**	0.50461	**0.50**	0.08959	**0.46**	0.20309
STM0817	ybhF	putative ABC-type multidrug transport system ATPase	**0.65**	0.49654	**-0.50**	0.22603	**-0.08**	0.86863
STM0818	STM0818	hypothetical protein STM0818	**-0.35**	0.63316	**0.34**	0.33294	**0.05**	0.91503
STM0818	STM0818	hypothetical protein STM0818	**-0.55**	0.30483	**-0.75**	0.06330	**0.21**	0.72966
STM0819	ybiH	putative transcriptional repressor	**-0.91**	0.16634	**0.01**	0.98084	**-0.10**	0.79213
STM0819	ybiH	putative transcriptional repressor	**-0.36**	0.50004	**0.08**	0.79385	**0.67**	0.18852
STM0820	rhlE	putative ATP-dependent RNA helicase	**-1.05**	0.04517	**-1.51**	0.00238	**-2.57**	0.00325
STM0820	rhlE	putative ATP-dependent RNA helicase	**0.32**	0.67685	**-0.92**	0.02693	**-1.99**	0.00206
STM0821	dinG	SOS repair enzyme	**-0.35**	0.41466	**-0.47**	0.13256	**-0.04**	0.93002
STM0821	dinG	SOS repair enzyme	**0.09**	0.94322	**-1.27**	0.00365	**0.04**	0.93002
STM0822	ybiB	hypothetical protein STM0822	**-0.74**	0.49480	**-0.08**	0.79321	**0.30**	0.72700
STM0822	ybiB	hypothetical protein STM0822	**0.67**	0.49952	**-0.32**	0.41378	**-0.24**	0.60466
STM0823	ybiJ	putative periplasmic protein	**-1.10**	0.05689	**-0.08**	0.85133	**0.07**	0.89180
STM0823	ybiJ	putative periplasmic protein	**0.12**	0.79518	**0.11**	0.77302	**0.36**	0.30509
STM0825	ybiI	hypothetical protein STM0825	**0.75**	0.27289	**0.47**	0.18345	**2.08**	0.00378
STM0825	ybiI	hypothetical protein STM0825	**0.62**	0.22160	**0.23**	0.54286	**2.22**	0.00107
STM0826	ybiN	putative SAM-dependent methyltransferase	**-0.44**	0.54856	**-1.01**	0.04241	**-0.30**	0.54316
STM0826	ybiN	putative SAM-dependent methyltransferase	**1.96**	0.01709	**-0.57**	0.11023	**-0.11**	0.86528
STM0827	ybiO	putative transport protein	**-0.79**	0.19981	**-0.60**	0.06708	**-0.69**	0.15406
STM0827	ybiO	putative transport protein	**0.41**	0.42557	**-0.79**	0.05922	**-0.89**	0.04142
STM0828	glnQ	glutamine ABC transporter ATP-binding component	**-0.35**	0.49076	**-0.91**	0.01141	**-1.56**	0.00541
STM0828	glnQ	glutamine ABC transporter ATP-binding component	**-0.46**	0.73458	**-1.15**	0.00336	**-1.93**	0.00386
STM0829	glnP	glutamine ABC transporter permease component	**-2.72**	0.00654	**-1.87**	0.00141	**-1.05**	0.07198
STM0829	glnP	glutamine ABC transporter permease component	**0.05**	0.96615	**-1.21**	0.01886	**-1.70**	0.00156
STM0830	glnH	glutamine ABC transporter periplasmic-binding protein	**-2.45**	0.00864	**-0.26**	0.38005	**-1.25**	0.01095
STM0830	glnH	glutamine ABC transporter periplasmic-binding protein	**-2.56**	0.03748	**-0.51**	0.17739	**-1.69**	0.00197
STM0831	dps	DNA protection during starvation conditions	**-1.33**	0.02858	**2.58**	0.00015	**5.89**	0.00012
STM0831	dps	DNA protection during starvation conditions	**-0.26**	0.64662	**2.79**	0.00031	**6.38**	0.00002
STM0832	ybiF	putative permease	**-1.00**	0.16202	**-0.54**	0.12564	**1.27**	0.01979
STM0832	ybiF	putative permease	**-0.89**	0.24695	**0.02**	0.93942	**1.85**	0.00594
STM0833	ompX	outer membrane protein X	**-2.19**	0.01443	**-1.23**	0.01313	**0.45**	0.23607
STM0833	ompX	outer membrane protein X	**-0.83**	0.12861	**-0.92**	0.01081	**0.63**	0.09371
STM0834	ybiP	putative Integral membrane protein	**0.02**	0.97161	**-1.16**	0.01109	**0.71**	0.07865
STM0834	ybiP	putative Integral membrane protein	**0.38**	0.59869	**-0.57**	0.12223	**1.02**	0.01647
STM0835	STM0835	putative Mn-dependent transcriptional regulator	**-0.03**	0.96078	**0.14**	0.66481	**-0.51**	0.23395
STM0835	STM0835	putative Mn-dependent transcriptional regulator	**-0.61**	0.17818	**-0.09**	0.78935	**0.13**	0.76918
STM0836	ybiR	putative transporter	**-0.52**	0.22605	**-0.72**	0.03904	**0.10**	0.79934
STM0836	ybiR	putative transporter	**1.09**	0.09758	**-0.51**	0.09628	**0.19**	0.62087
STM0837	ybiS	putative periplasmic protein	**-0.94**	0.09011	**-0.56**	0.13393	**-0.62**	0.10497
STM0837	ybiS	putative periplasmic protein	**1.33**	0.05743	**-1.23**	0.00307	**-1.55**	0.03610
STM0838	ybiT	putative ABC transporter ATPase component	**0.23**	0.78453	**1.04**	0.00500	**-0.91**	0.19485
STM0838	ybiT	putative ABC transporter ATPase component	**0.84**	0.27015	**1.52**	0.00339	**-1.08**	0.04007
STM0839	STM0839	putative inner membrane protein	**-0.08**	0.85597	**0.96**	0.03644	**-0.42**	0.55002
STM0839	STM0839	putative inner membrane protein	**-0.52**	0.54376	**0.11**	0.75188	**-0.45**	0.73380
STM0840	ybiV(2)	putative hydrolase	**-1.79**	0.02177	**-0.02**	0.96375	**-1.79**	0.00421
STM0840	ybiV(2)	putative hydrolase	**-0.77**	0.12699	**-0.46**	0.42042	**-0.52**	0.20117
STM0841	ybiU	putative cytoplasmic protein	**0.23**	0.55991	**1.16**	0.01013	**-0.66**	0.10868
STM0841	ybiU	putative cytoplasmic protein	**1.97**	0.02160	**1.30**	0.00215	**0.60**	0.15298
STM0842	ybiV(1)	putative hydrolase	**-0.56**	0.41616	**-1.38**	0.00640	**-1.62**	0.03631
STM0842	ybiV(1)	putative hydrolase	**1.71**	0.34493	**-0.73**	0.05189	**-0.33**	0.68698
STM0843	pflF	putative pyruvate formate lyase	**-0.27**	0.63515	**0.40**	0.33625	**-0.27**	0.64834
STM0843	pflF	putative pyruvate formate lyase	**0.45**	0.45778	**-0.38**	0.22833	**0.71**	0.35121

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM0844	pflE	putative pyruvate formate lyase activating enzyme	**-0.83**	0.40613	**-0.35**	0.43823	**-1.45**	0.01557
STM0844	pflE	putative pyruvate formate lyase activating enzyme	**0.49**	0.38161	**-0.67**	0.13499	**1.02**	0.13838
STM0845	moeB	molybdopterin biosynthesis protein MoeB	**-0.29**	0.64755	**-0.59**	0.08349	**-1.47**	0.01144
STM0845	moeB	molybdopterin biosynthesis protein MoeB	**0.95**	0.46345	**-0.41**	0.21876	**-1.13**	0.06355
STM0846	moeA	molybdopterin biosynthesis protein	**-1.23**	0.02821	**-0.54**	0.10700	**-0.96**	0.19355
STM0846	moeA	molybdopterin biosynthesis protein	**-0.24**	0.62471	**-0.71**	0.04900	**1.51**	0.01768
STM0847	ybiK	putative asparaginase	**-1.80**	0.04570	**-0.53**	0.08690	**-1.26**	0.04339
STM0847	ybiK	putative asparaginase	**0.57**	0.34702	**0.04**	0.92574	**0.01**	0.98561
STM0848	yliA	putative ABC transporter ATPase components	**-0.50**	0.22544	**-0.98**	0.08155	**-1.52**	0.00672
STM0848	yliA	putative ABC transporter ATPase components	**-0.44**	0.33126	**-1.38**	0.00257	**-1.10**	0.05677
STM0849	yliB	putative ABC transporter periplasmic binding protein	**-0.89**	0.09059	**0.10**	0.82055	**0.13**	0.74089
STM0849	yliB	putative ABC transporter periplasmic binding protein	**-1.21**	0.30361	**-0.01**	0.97207	**-1.05**	0.08837
STM0850	yliC	putative ABC transporter periplasmic binding protein	**-1.45**	0.07325	**-0.44**	0.15452	**-1.63**	0.00631
STM0850	yliC	putative ABC transporter periplasmic binding protein	**-0.10**	0.81828	**-1.32**	0.00867	**-0.94**	0.16139
STM0851	yliD	putative ABC transporter inner membrane component	**-1.80**	0.01038	**-1.11**	0.00853	**-1.09**	0.15326
STM0851	yliD	putative ABC transporter inner membrane component	**-0.59**	0.57209	**-1.18**	0.00650	**-1.38**	0.01489
STM0852	yliG	putative FeS oxidoreductase	**-1.80**	0.02181	**-1.00**	0.01547	**-2.09**	0.00526
STM0852	yliG	putative FeS oxidoreductase	**-0.66**	0.16795	**-2.00**	0.00031	**-1.35**	0.04534
STM0853	yliH	putative cytoplasmic protein	**-0.35**	0.47149	**1.89**	0.00077	**6.49**	0.00001
STM0853	yliH	putative cytoplasmic protein	**-1.19**	0.04983	**2.01**	0.00024	**6.40**	0.00001
STM0854	STM0854	putative cytoplasmic protein	**0.28**	0.69620	**0.30**	0.46696	**1.75**	0.00568
STM0854	STM0854	putative cytoplasmic protein	**1.26**	0.03242	**0.17**	0.81126	**2.59**	0.00068
STM0855	STM0855	putative electron transfer protein beta subunit	**0.11**	0.87642	**-0.09**	0.79574	**-0.79**	0.08954
STM0855	STM0855	putative electron transfer protein beta subunit	**0.62**	0.31930	**0.42**	0.29415	**1.11**	0.06873
STM0856	STM0856	putative electron transfer protein alpha subunit	**0.09**	0.89999	**0.04**	0.92012	**-0.93**	0.04692
STM0856	STM0856	putative electron transfer protein alpha subunit	**1.10**	0.09525	**0.02**	0.96521	**0.01**	0.98461
STM0857	STM0857	putative acyl-CoA dehydrogenase	**1.37**	0.31205	**-0.12**	0.75579	**-0.17**	0.85119
STM0857	STM0857	putative acyl-CoA dehydrogenase	**1.32**	0.07584	**0.34**	0.36979	**2.42**	0.04497
STM0858	STM0858	putative dehydrogenase	**0.89**	0.07050	**0.42**	0.35765	**0.05**	0.96299
STM0858	STM0858	putative dehydrogenase	**2.59**	0.00791	**0.50**	0.17200	**2.49**	0.00125
STM0859	STM0859	putative transcriptional regulator	**-0.17**	0.76043	**-0.54**	0.20971	**0.21**	0.64024
STM0859	STM0859	putative transcriptional regulator	**-0.49**	0.40170	**0.08**	0.85622	**-1.87**	0.02240
STM0860	STM0860	putative inner membrane protein	**-0.31**	0.45012	**1.03**	0.04224	**0.12**	0.76280
STM0860	STM0860	putative inner membrane protein	**0.75**	0.16362	**0.57**	0.19652	**0.21**	0.62768
STM0862	yliJ	putative glutathione S-transferase	**-0.71**	0.16521	**0.92**	0.01542	**-0.68**	0.14952
STM0862	yliJ	putative glutathione S-transferase	**-0.11**	0.88091	**1.48**	0.00341	**-0.50**	0.35846
STM0863	dacC	D-alanyl-D-alanine carboxypeptidase	**-0.52**	0.20626	**0.41**	0.28451	**-0.12**	0.81762
STM0863	dacC	D-alanyl-D-alanine carboxypeptidase	**-0.76**	0.13555	**-0.11**	0.76620	**-0.28**	0.72924
STM0864	deoR	deoxyribose operon transcriptional repressor	**1.09**	0.35237	**0.39**	0.29360	**0.23**	0.80029
STM0864	deoR	deoxyribose operon transcriptional repressor	**0.88**	0.41626	**0.07**	0.85600	**-0.51**	0.31442
STM0865	ybjG	putative permease	**-1.00**	0.05298	**-0.24**	0.49611	**-1.05**	0.06086
STM0865	ybjG	putative permease	**0.34**	0.76280	**-0.45**	0.21875	**-0.82**	0.27042
STM0866	mdfA	multidrug translocase	**-0.99**	0.10451	**-0.77**	0.04658	**-1.40**	0.03620
STM0866	mdfA	multidrug translocase	**-0.21**	0.82751	**-1.21**	0.01282	**-0.65**	0.17806
STM0867	STM0867	putative hydrolase	**-0.33**	0.64833	**-0.37**	0.29805	**-0.63**	0.24396
STM0867	STM0867	putative hydrolase	**0.31**	0.61744	**-0.07**	0.85046	**-0.27**	0.61014
STM0868	STM0868	putative transport protein/regulator	**0.96**	0.06012	**-0.32**	0.40616	**0.05**	0.93258
STM0868	STM0868	putative transport protein/regulator	**1.02**	0.10070	**-0.41**	0.43103	**1.11**	0.16689
STM0869	STM0869	putative regulatory protein	**-0.87**	0.20928	**0.40**	0.24294	**-0.30**	0.66060
STM0869	STM0869	putative regulatory protein	**-0.97**	0.42579	**-0.90**	0.03751	**-0.13**	0.76404
STM0870	STM0870	hypothetical protein STM0870	**-0.97**	0.19975	**-0.99**	0.00848	**-2.37**	0.00100
STM0870	STM0870	hypothetical protein STM0870	**0.08**	0.89608	**-0.76**	0.10808	**-0.61**	0.35839
STM0871	ybjM	putative inner membrane protein	**-1.53**	0.03988	**0.26**	0.48678	**-0.42**	0.42170
STM0871	ybjM	putative inner membrane protein	**-0.52**	0.39936	**0.48**	0.12184	**-1.20**	0.01635
STM0872	grxA	glutaredoxin 1	**-0.98**	0.11670	**0.30**	0.48187	**-0.81**	0.18102
STM0872	grxA	glutaredoxin 1	**0.67**	0.13529	**0.48**	0.27176	**0.62**	0.15897
STM0873	ybjC	putative inner membrane protein	**-0.83**	0.43042	**-0.17**	0.58715	**-1.53**	0.00573
STM0873	ybjC	putative inner membrane protein	**-0.66**	0.17044	**-0.32**	0.33555	**0.53**	0.44021
STM0874	mdaA	oxygen-insensitive NADPH nitroreductase	**-0.23**	0.60031	**0.05**	0.89029	**-1.13**	0.02981
STM0874	mdaA	oxygen-insensitive NADPH nitroreductase	**-0.01**	0.98763	**-0.19**	0.54022	**-0.73**	0.08846
STM0875	rimK	ribosomal protein S6 modification protein	**-1.06**	0.09512	**-0.71**	0.08858	**-0.89**	0.08828
STM0875	rimK	ribosomal protein S6 modification protein	**-0.74**	0.12906	**-0.73**	0.06909	**-1.92**	0.00074
STM0876	ybjN	putative cytoplasmic protein	**-1.67**	0.02635	**-0.84**	0.05810	**-2.15**	0.00428
STM0876	ybjN	putative cytoplasmic protein	**-0.90**	0.07573	**-0.58**	0.10273	**-1.27**	0.05414
STM0877	potF	putrescine transporter	**0.68**	0.13498	**0.80**	0.04238	**0.84**	0.03362
STM0877	potF	putrescine transporter	**1.60**	0.08078	**0.87**	0.03303	**0.78**	0.11804
STM0878	potG	putrescine transporter	**0.88**	0.36741	**-0.56**	0.25993	**-0.82**	0.33959
STM0878	potG	putrescine transporter	**2.37**	0.00956	**-1.84**	0.00324	**0.42**	0.33734
STM0879	potH	putrescine transporter	**-1.47**	0.26495	**-1.67**	0.00631	**-1.22**	0.08955
STM0879	potH	putrescine transporter	**-1.21**	0.17879	**-2.30**	0.01570	**-1.34**	0.07016

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM0880	potI	putrescine transporter	**0.01**	0.98861	**0.12**	0.81308	**-0.57**	0.24241
STM0880	potI	putrescine transporter	**1.01**	0.08765	**-0.24**	0.41497	**0.50**	0.26967
STM0881	ybjO	putative inner membrane protein	**-1.94**	0.01562	**-0.25**	0.55465	**-0.89**	0.09474
STM0881	ybjO	putative inner membrane protein	**-0.87**	0.27512	**-1.18**	0.00656	**-0.40**	0.45561
STM0882	ybjF	23S rRNA (uracil-5-)-methyltransferase	**-0.69**	0.21998	**-0.62**	0.23793	**-0.12**	0.85588
STM0882	ybjF	23S rRNA (uracil-5-)-methyltransferase	**2.30**	0.35495	**-0.75**	0.08871	**-0.31**	0.42713
STM0884	ulaA	ascorbate-specific PTS system enzyme IIC	**0.45**	0.64341	**0.55**	0.49988	**-0.68**	0.19903
STM0884	ulaA	ascorbate-specific PTS system enzyme IIC	**1.53**	0.04046	**-1.56**	0.05640	**-2.23**	0.00194
STM0885	STM0885	putative inner membrane protein	**-0.98**	0.19499	**-1.09**	0.00611	**-1.50**	0.11386
STM0885	STM0885	putative inner membrane protein	**0.19**	0.71609	**-0.98**	0.03673	**-0.91**	0.06968
STM0886	STM0886	putative sulfatase	**0.60**	0.31855	**0.47**	0.38937	**0.70**	0.19859
STM0886	STM0886	putative sulfatase	**1.29**	0.03310	**1.11**	0.00700	**0.78**	0.11698
STM0887	artJ	arginine transport system component	**0.22**	0.74788	**1.81**	0.00341	**0.93**	0.06005
STM0887	artJ	arginine transport system component	**0.30**	0.59477	**1.41**	0.00554	**0.85**	0.04175
STM0888	artM	arginine transport system component	**-1.42**	0.02605	**-0.24**	0.51415	**-0.87**	0.10506
STM0888	artM	arginine transport system component	**-0.19**	0.63111	**0.28**	0.31690	**0.24**	0.52054
STM0889	artQ	arginine transport system component	**-1.67**	0.01773	**-0.85**	0.02057	**-3.54**	0.00190
STM0889	artQ	arginine transport system component	**-0.53**	0.36190	**-0.52**	0.12037	**-1.69**	0.00350
STM0890	artI	arginine transport system	**-0.99**	0.04923	**-0.16**	0.58707	**-1.42**	0.01057
STM0890	artI	arginine transport system	**-1.54**	0.02888	**-0.06**	0.86760	**-1.48**	0.01186
STM0891	artP	arginine transport system	**-0.39**	0.45134	**0.14**	0.67136	**-1.00**	0.02377
STM0891	artP	arginine transport system	**-0.84**	0.10008	**0.50**	0.09368	**-0.24**	0.58171
STM0892	ybjP	putative lipoprotein	**-0.94**	0.29599	**0.28**	0.47627	**-0.40**	0.27265
STM0892	ybjP	putative lipoprotein	**-0.23**	0.69232	**0.11**	0.82309	**0.29**	0.49911
STM0893	STM0893	putative integrase	**-1.44**	0.02031	**-0.68**	0.04303	**-1.16**	0.07300
STM0893	STM0893	putative integrase	**-1.83**	0.05667	**-0.95**	0.01684	**-1.76**	0.04318
STM0898	STM0898	putative transcriptional regulator	**-0.40**	0.37430	**0.96**	0.01175	**-0.64**	0.14675
STM0898	STM0898	putative transcriptional regulator	**0.09**	0.82483	**0.62**	0.08212	**0.54**	0.47864
STM0906	STM0906	hypothetical protein STM0906	**1.12**	0.04735	**0.32**	0.64151	**-0.13**	0.80083
STM0906	STM0906	hypothetical protein STM0906	**2.04**	0.01428	**0.14**	0.69426	**0.26**	0.57306
STM0907	STM0907	putative chitinase	**1.17**	0.13687	**0.77**	0.03596	**-0.15**	0.83913
STM0907	STM0907	putative chitinase	**2.55**	0.05946	**0.29**	0.47297	**1.59**	0.03962
STM0908	STM0908	hypothetical protein STM0908	**2.58**	0.05170	**1.11**	0.01948	**4.05**	0.00147
STM0908	STM0908	hypothetical protein STM0908	**2.81**	0.00661	**0.18**	0.51632	**3.57**	0.00007
STM0930	orfB	hypothetical protein STM0930	**0.35**	0.46502	**1.30**	0.00481	**0.41**	0.26187
STM0930	orfB	hypothetical protein STM0930	**1.23**	0.07261	**1.06**	0.00954	**1.25**	0.01490
STM0931	ybjR	putative aminidase	**-0.48**	0.49835	**-0.74**	0.09631	**-0.81**	0.19238
STM0931	ybjR	putative aminidase	**0.32**	0.59828	**-0.15**	0.58441	**-0.40**	0.36237
STM0932	STM0932	putative nucleoside-diphosphate-sugar epimerase	**-0.29**	0.62319	**0.11**	0.77531	**-2.10**	0.00469
STM0932	STM0932	putative nucleoside-diphosphate-sugar epimerase	**0.76**	0.28474	**-0.04**	0.92343	**-0.99**	0.05456
STM0933	ybjT	putative nucleoside-diphosphate-sugar epimerase	**-0.08**	0.86817	**-0.35**	0.28887	**-0.14**	0.89389
STM0933	ybjT	putative nucleoside-diphosphate-sugar epimerase	**2.75**	0.11638	**-0.42**	0.28895	**-1.22**	0.04261
STM0934	ltaA	L-allo-threonine aldolase	**-1.49**	0.02193	**-0.49**	0.15578	**-1.45**	0.00343
STM0934	ltaA	L-allo-threonine aldolase	**-0.98**	0.08071	**-0.82**	0.03137	**-0.84**	0.13643
STM0935	poxB	pyruvate dehydrogenase	**-0.97**	0.15104	**0.99**	0.04330	**1.89**	0.00791
STM0935	poxB	pyruvate dehydrogenase	**-0.23**	0.76369	**1.30**	0.00239	**2.00**	0.00059
STM0936	hcr	NADH oxidoreductase	**-0.77**	0.39570	**0.66**	0.21217	**-0.27**	0.55140
STM0936	hcr	NADH oxidoreductase	**1.18**	0.14061	**0.20**	0.48678	**-0.14**	0.87683
STM0937	hcp	hydroxylamine reductase	**-1.23**	0.04911	**0.35**	0.37724	**0.06**	0.91566
STM0937	hcp	hydroxylamine reductase	**0.18**	0.66039	**0.50**	0.27490	**-0.22**	0.70723
STM0938	ybjE	putative inner membrane protein	**-0.42**	0.47100	**-0.53**	0.15935	**-0.92**	0.05732
STM0938	ybjE	putative inner membrane protein	**0.18**	0.71116	**1.07**	0.12842	**0.13**	0.78570
STM0939	ybjD	hypothetical protein STM0939	**-2.69**	0.01436	**-0.29**	0.48875	**-2.22**	0.00110
STM0939	ybjD	hypothetical protein STM0939	**-1.34**	0.02346	**-0.88**	0.01639	**-2.34**	0.00026
STM0940	ybjX	VirK-like protein	**-2.40**	0.00791	**0.01**	0.98646	**-3.00**	0.00010
STM0940	ybjX	VirK-like protein	**-1.34**	0.02148	**-0.34**	0.32708	**-2.18**	0.00186
STM0941	ybjY	hypothetical protein STM0941	**0.95**	0.10106	**0.93**	0.01880	**-0.65**	0.20262
STM0941	ybjY	hypothetical protein STM0941	**1.32**	0.02347	**1.11**	0.00756	**0.05**	0.89836
STM0942	ybjZ	putative transport protein	**1.22**	0.33309	**0.50**	0.21501	**0.27**	0.49985
STM0942	ybjZ	putative transport protein	**0.05**	0.91057	**0.86**	0.01981	**0.95**	0.03923
STM0943	cspD	stress response protein	**-0.61**	0.36178	**3.26**	0.00004	**2.37**	0.00048
STM0943	cspD	stress response protein	**-0.04**	0.95007	**2.98**	0.00047	**3.23**	0.00021
STM0944	clpS	ATP-dependent Clp protease adaptor protein ClpS	**0.11**	0.83854	**2.09**	0.00027	**0.83**	0.03810
STM0944	clpS	ATP-dependent Clp protease adaptor protein ClpS	**0.82**	0.35348	**1.67**	0.00068	**1.40**	0.01099
STM0945	clpA	ATP-binding subunit of serine protease	**1.16**	0.04832	**1.11**	0.00521	**1.99**	0.00318
STM0945	clpA	ATP-binding subunit of serine protease	**2.08**	0.00851	**1.11**	0.00671	**2.97**	0.00019
STM0947	STM0947	putative integrase	**-0.32**	0.59866	**0.63**	0.61227	**0.39**	0.44793
STM0947	STM0947	putative integrase	**1.08**	0.17495	**-0.20**	0.50397	**1.28**	0.00563
STM0948	STM0948	putative cytoplasmic protein	**0.79**	0.22160	**0.80**	0.02355	**1.41**	0.00808
STM0948	STM0948	putative cytoplasmic protein	**2.13**	0.01399	**0.39**	0.33010	**3.24**	0.00023

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM0949	serW	STM0949	**-0.19**	0.75051	**-1.18**	0.00758	**1.65**	0.00167
STM0949	serW	STM0949	**0.95**	0.08508	**-1.16**	0.05633	**2.13**	0.00091
STM0950	STM0950	SlsA	**0.00**	0.99547	**0.92**	0.01314	**2.82**	0.00029
STM0950	STM0950	SlsA	**0.00**	0.99568	**0.85**	0.01252	**3.00**	0.00011
STM0951	STM0951	putative cytoplasmic protein	**-0.37**	0.68802	**1.05**	0.01467	**2.08**	0.00612
STM0951	STM0951	putative cytoplasmic protein	**1.63**	0.02953	**0.99**	0.02051	**2.72**	0.00156
STM0952	STM0952	putative transcriptional regulator	**-1.13**	0.05254	**-0.55**	0.09679	**-2.36**	0.00477
STM0952	STM0952	putative transcriptional regulator	**-0.07**	0.88427	**0.06**	0.88217	**-1.42**	0.00677
STM0953	infA	translation initiation factor IF-1	**-2.58**	0.00689	**-1.05**	0.01609	**-3.19**	0.00103
STM0953	infA	translation initiation factor IF-1	**-0.20**	0.79237	**-0.81**	0.03405	**-2.32**	0.00111
STM0955	aat	leucyl/phenylalanyl-tRNA--protein transferase	**-1.51**	0.05330	**-0.87**	0.01277	**-1.36**	0.00958
STM0955	aat	leucyl/phenylalanyl-tRNA--protein transferase	**-1.36**	0.04864	**-1.40**	0.00173	**-0.44**	0.54234
STM0956	cydC	cytochrome-related transporter	**-1.45**	0.02504	**-1.20**	0.00783	**-1.69**	0.00342
STM0956	cydC	cytochrome-related transporter	**-3.16**	0.01468	**-1.04**	0.01019	**-1.71**	0.00502
STM0957	cydD	cytochrome-related transporter	**-2.01**	0.01272	**-1.97**	0.00048	**-2.76**	0.00033
STM0957	cydD	cytochrome-related transporter	**-2.04**	0.01417	**-1.62**	0.00123	**-2.38**	0.00271
STM0958	trxB	thioredoxin reductase	**-1.51**	0.06815	**-0.82**	0.01693	**-3.48**	0.00009
STM0958	trxB	thioredoxin reductase	**-0.45**	0.62331	**-0.86**	0.02518	**-2.87**	0.00020
STM0959	lrp	leucine-responsive regulatory protein	**-0.29**	0.63973	**0.86**	0.01958	**-2.05**	0.00055
STM0959	lrp	leucine-responsive regulatory protein	**-0.49**	0.32903	**0.59**	0.06483	**-0.33**	0.39670
STM0960	ftsK	cell division protein	**-1.03**	0.22155	**-0.71**	0.02911	**-1.60**	0.02043
STM0960	ftsK	cell division protein	**-0.46**	0.69990	**-0.17**	0.61458	**-1.38**	0.02263
STM0961	lolA	outer-membrane lipoprotein carrier protein precursor	**-1.24**	0.03024	**0.31**	0.34573	**-0.96**	0.02077
STM0961	lolA	outer-membrane lipoprotein carrier protein precursor	**-0.99**	0.06325	**0.50**	0.09663	**-0.08**	0.87700
STM0962	ycaJ	hypothetical protein STM0962	**-1.36**	0.03884	**-0.71**	0.06866	**-1.58**	0.02649
STM0962	ycaJ	hypothetical protein STM0962	**-0.63**	0.70308	**-1.78**	0.08891	**-2.02**	0.04082
STM0963	serS	seryl-tRNA synthetase	**-1.76**	0.01136	**-0.47**	0.11864	**-2.35**	0.00280
STM0963	serS	seryl-tRNA synthetase	**-2.15**	0.02143	**-0.70**	0.03503	**-1.83**	0.07370
STM0964	dmsA	anaerobic dimethyl sulfoxide reductase subunit A	**0.70**	0.48015	**-0.17**	0.68774	**-0.50**	0.55732
STM0964	dmsA	anaerobic dimethyl sulfoxide reductase subunit A	**0.92**	0.15588	**-0.49**	0.20295	**-0.16**	0.81438
STM0965	dmsB	anaerobic dimethyl sulfoxide reductase subunit B	**2.58**	0.03093	**1.28**	0.08917	**0.70**	0.36322
STM0965	dmsB	anaerobic dimethyl sulfoxide reductase subunit B	**3.54**	0.06319	**-0.23**	0.56064	**2.27**	0.00608
STM0966	dmsC	anaerobic dimethyl sulfoxide reductase subunit C	**0.81**	0.17553	**0.18**	0.65309	**0.72**	0.20825
STM0966	dmsC	anaerobic dimethyl sulfoxide reductase subunit C	**3.89**	0.00654	**0.18**	0.52033	**2.97**	0.00113
STM0968	ycaD	putative MFS family transporter protein	**-0.49**	0.38902	**-1.98**	0.00023	**-1.23**	0.04127
STM0968	ycaD	putative MFS family transporter protein	**1.20**	0.04570	**-1.00**	0.02011	**-0.10**	0.87903
STM0969	ycaM	putative amino-acid transporter	**2.83**	0.21328	**-0.23**	0.53380	**0.26**	0.75411
STM0969	ycaM	putative amino-acid transporter	**0.69**	0.22201	**-0.07**	0.90341	**-0.31**	0.54878
STM0970	pflA	pyruvate formate lyase-activating enzyme 1	**-1.15**	0.06013	**0.47**	0.14121	**-0.66**	0.12057
STM0970	pflA	pyruvate formate lyase-activating enzyme 1	**0.26**	0.59975	**0.08**	0.80079	**0.41**	0.32667
STM0972	STM0972	SopD-like protein	**-0.34**	0.50703	**4.60**	0.00001	**0.92**	0.06878
STM0972	STM0972	SopD-like protein	**0.30**	0.56229	**4.87**	0.00001	**0.80**	0.03685
STM0973	pflB	pyruvate formate lyase I	**-1.76**	0.02268	**1.09**	0.00432	**0.19**	0.73211
STM0973	pflB	pyruvate formate lyase I	**-0.08**	0.91364	**1.40**	0.01182	**0.20**	0.69334
STM0974	focA	putative formate transporter	**-1.99**	0.01068	**-0.13**	0.74894	**0.98**	0.05334
STM0974	focA	putative formate transporter	**-1.37**	0.04595	**-0.13**	0.65882	**0.96**	0.02842
STM0975	ycaO	putative cytoplasmic protein	**-1.77**	0.04685	**-2.23**	0.00016	**-1.77**	0.00109
STM0975	ycaO	putative cytoplasmic protein	**-1.93**	0.01479	**-2.60**	0.00019	**-1.37**	0.00928
STM0976	ycaP	putative inner membrane protein	**-1.50**	0.02537	**-0.48**	0.20794	**-2.48**	0.00416
STM0976	ycaP	putative inner membrane protein	**-0.75**	0.10634	**1.65**	0.34632	**-1.34**	0.02331
STM0977	serC	phosphoserine aminotransferase	**-2.07**	0.01067	**-0.14**	0.69727	**-2.64**	0.00018
STM0977	serC	phosphoserine aminotransferase	**0.39**	0.49027	**0.25**	0.50209	**-2.38**	0.00276
STM0978	aroA	3-phosphoshikimate 1-carboxyvinyltransferase	**-2.38**	0.00779	**-0.78**	0.03622	**-2.68**	0.00195
STM0978	aroA	3-phosphoshikimate 1-carboxyvinyltransferase	**-0.64**	0.17633	**-0.42**	0.14526	**-1.79**	0.00190
STM0979	ycaL	putative Zn-dependent protease	**-1.19**	0.07276	**-0.33**	0.43058	**0.16**	0.66271
STM0979	ycaL	putative Zn-dependent protease	**-0.74**	0.34117	**-1.25**	0.04554	**0.01**	0.98468
STM0980	cmk	cytidylate kinase	**-1.78**	0.01403	**-1.41**	0.00170	**-1.91**	0.00072
STM0980	cmk	cytidylate kinase	**-1.67**	0.01835	**-1.29**	0.00459	**-1.63**	0.00283
STM0981	rpsA	30S ribosomal protein S1	**-2.42**	0.01040	**-1.90**	0.00036	**-3.02**	0.00019
STM0981	rpsA	30S ribosomal protein S1	**-1.84**	0.01907	**-1.69**	0.00129	**-3.32**	0.00024
STM0982	himD	integration host factor beta subunit	**-2.76**	0.03614	**-1.55**	0.00309	**-0.24**	0.51907
STM0982	himD	integration host factor beta subunit	**-2.58**	0.02687	**-1.70**	0.00260	**-0.24**	0.51833
STM0983	ycaI	putative recombination protein	**-0.77**	0.28070	**-0.02**	0.95644	**0.02**	0.95577
STM0983	ycaI	putative recombination protein	**-2.22**	0.04101	**-0.95**	0.01243	**-1.02**	0.03191
STM0984	msbA	transport protein	**-3.21**	0.01545	**-1.26**	0.00490	**-2.11**	0.00051
STM0984	msbA	transport protein	**-1.81**	0.01834	**-1.74**	0.00049	**-1.50**	0.02198
STM0985	lpxK	tetraacyldisaccharide 4'-kinase	**-0.75**	0.33269	**-0.96**	0.02432	**-1.55**	0.00824
STM0985	lpxK	tetraacyldisaccharide 4'-kinase	**-0.26**	0.56451	**-1.40**	0.00265	**-1.98**	0.00554
STM0986	ycaQ	putative cytoplasmic protein	**-0.54**	0.38106	**-1.18**	0.12750	**0.92**	0.13691
STM0986	ycaQ	putative cytoplasmic protein	**0.21**	0.76050	**-0.37**	0.28813	**-0.58**	0.23274

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM0987	ycaR	putative inner membrane protein	**0.24**	0.56765	**0.32**	0.31212	**0.77**	0.04252
STM0987	ycaR	putative inner membrane protein	**-0.22**	0.78992	**0.17**	0.54325	**0.78**	0.05288
STM0988	kdsB	3-deoxy-manno-octulosonate cytidylyltransferase	**-1.18**	0.15863	**-0.97**	0.08212	**-0.83**	0.15723
STM0988	kdsB	3-deoxy-manno-octulosonate cytidylyltransferase	**-0.29**	0.67322	**-0.87**	0.01166	**-1.18**	0.01421
STM0989	STM0989	hypothetical protein STM0989	**1.68**	0.39739	**0.44**	0.24847	**0.97**	0.42473
STM0989	STM0989	hypothetical protein STM0989	**-0.23**	0.71354	**-0.48**	0.49362	**0.91**	0.10848
STM0990	ycbC	putative KicA-like protein	**-0.59**	0.27346	**-0.29**	0.33573	**-0.30**	0.43224
STM0990	ycbC	putative KicA-like protein	**0.33**	0.58706	**-0.27**	0.57978	**0.82**	0.07488
STM0991	smtA	S-adenosylmethionine-dependent methyltransferase	**-1.99**	0.01731	**-0.57**	0.06690	**-2.00**	0.00093
STM0991	smtA	S-adenosylmethionine-dependent methyltransferase	**0.58**	0.38973	**-0.85**	0.02896	**-0.85**	0.04187
STM0992	mukF	condesin subunit F	**-1.85**	0.01178	**-1.16**	0.00357	**-1.28**	0.00567
STM0992	mukF	condesin subunit F	**-2.33**	0.00756	**-1.28**	0.00332	**-1.56**	0.00286
STM0993	mukE	condesin subunit E	**-1.37**	0.02018	**-0.89**	0.01056	**-1.39**	0.01056
STM0993	mukE	condesin subunit E	**-0.36**	0.45276	**-0.99**	0.00763	**-1.25**	0.01846
STM0994	mukB	condesin subunit B	**-1.94**	0.00834	**-1.35**	0.00562	**-2.34**	0.00409
STM0994	mukB	condesin subunit B	**-0.77**	0.56917	**-1.45**	0.00108	**-2.09**	0.06149
STM0995	ycbB	putative periplasmic protein	**-1.25**	0.03444	**0.18**	0.58425	**-0.79**	0.04065
STM0995	ycbB	putative periplasmic protein	**-0.99**	0.23205	**0.38**	0.24643	**0.16**	0.72973
STM0996	ycbK	putative outer membrane protein	**-1.58**	0.02776	**0.78**	0.03079	**-1.90**	0.00151
STM0996	ycbK	putative outer membrane protein	**-1.97**	0.01904	**0.91**	0.01594	**-2.59**	0.00073
STM0997	ycbL	putative metallo-beta-lactamase	**-2.78**	0.00654	**-0.24**	0.56196	**-2.28**	0.00038
STM0997	ycbL	putative metallo-beta-lactamase	**-1.81**	0.01088	**-0.14**	0.65511	**-2.38**	0.00033
STM0998	aspC	aspartate aminotransferase	**-1.69**	0.03222	**-0.13**	0.73485	**-1.64**	0.00352
STM0998	aspC	aspartate aminotransferase	**-0.91**	0.21656	**0.54**	0.10772	**-2.12**	0.00087
STM0999	ompF	outer membrane protein F precursor	**-0.07**	0.95371	**0.94**	0.01809	**-1.82**	0.00176
STM0999	ompF	outer membrane protein F precursor	**-1.01**	0.05758	**0.98**	0.02304	**-1.67**	0.01097
STM1000	asnS	asparaginyl-tRNA synthetase	**-2.42**	0.00700	**-0.79**	0.11130	**-2.56**	0.00144
STM1000	asnS	asparaginyl-tRNA synthetase	**-2.39**	0.03417	**-0.86**	0.01085	**-2.24**	0.00173
STM1001	STM1001	putative leucine response regulator	**-1.62**	0.01907	**-0.48**	0.15736	**-0.46**	0.28954
STM1001	STM1001	putative leucine response regulator	**-1.37**	0.15466	**-0.96**	0.01575	**-0.15**	0.90503
STM1002	STM1002	diaminopropionate ammonia-lyase	**0.05**	0.92673	**0.09**	0.79385	**1.26**	0.28389
STM1002	STM1002	diaminopropionate ammonia-lyase	**-1.06**	0.09548	**-0.60**	0.27211	**0.53**	0.42861
STM1003	STM1003	putative transcriptional regulator	**-1.05**	0.04734	**-0.32**	0.42219	**0.20**	0.59774
STM1003	STM1003	putative transcriptional regulator	**0.05**	0.96378	**0.25**	0.68767	**-0.44**	0.35361
STM1004	pncB	nicotinate phosphoribosyltransferase	**-0.45**	0.41404	**-0.48**	0.23315	**-0.08**	0.91050
STM1004	pncB	nicotinate phosphoribosyltransferase	**-0.70**	0.14348	**-0.38**	0.21235	**-0.96**	0.03902
STM1005	STM1005	integrase	**-0.72**	0.57095	**-0.05**	0.89061	**-0.74**	0.23733
STM1005	STM1005	integrase	**0.33**	0.66546	**0.01**	0.98614	**0.14**	0.76739
STM1006	STM1006	excisionase	**2.32**	0.01523	**0.77**	0.05032	**2.89**	0.00578
STM1006	STM1006	excisionase	**2.80**	0.00547	**-0.09**	0.77180	**3.52**	0.00008
STM1008,S	STM1008,S	hypothetical protein STM1008,S	**1.01**	0.08068	**2.03**	0.00077	**1.34**	0.04741
STM1008,S	STM1008,S	hypothetical protein STM1008,S	**1.17**	0.39210	**-0.23**	0.58112	**1.28**	0.28070
STM1008,S	STM1008,S	hypothetical protein STM1008,S	**1.78**	0.19671	**0.69**	0.04457	**1.32**	0.04691
STM1008,S	STM1008,S	hypothetical protein STM1008,S	**3.16**	0.02945	**-0.94**	0.04712	**2.09**	0.00525
STM1010,1n	STM1010,1n	hypothetical protein STM1010,1n	**1.77**	0.03932	**0.43**	0.15021	**1.07**	0.22560
STM1010,1n	STM1010,1n	hypothetical protein STM1010,1n	**2.69**	0.00595	**0.19**	0.64154	**2.99**	0.00032
STM1020	STM1020	hypothetical protein STM1020	**0.04**	0.94225	**0.10**	0.87638	**-0.71**	0.16824
STM1020	STM1020	hypothetical protein STM1020	**2.61**	0.04979	**0.33**	0.32740	**-0.11**	0.84981
STM1020	STM1020	hypothetical protein STM1020	**2.26**	0.05213	**0.84**	0.01693	**0.11**	0.77409
STM1020	STM1020	hypothetical protein STM1020	**3.14**	0.02573	**0.54**	0.09359	**0.32**	0.63268
STM1021	STM1021	hypothetical protein STM1021	**2.39**	0.10387	**0.99**	0.00958	**0.34**	0.62353
STM1021	STM1021	hypothetical protein STM1021	**3.05**	0.03475	**0.47**	0.20679	**0.86**	0.06169
STM1022	STM1022	putative molecular chaperone	**0.94**	0.35906	**-0.01**	0.98033	**0.11**	0.86032
STM1022	STM1022	putative molecular chaperone	**1.90**	0.01951	**-0.89**	0.06624	**0.62**	0.34398
STM1028	STM1028	lysozyme	**1.43**	0.23505	**0.43**	0.27473	**-0.26**	0.56271
STM1028	STM1028	lysozyme	**1.31**	0.05496	**-0.23**	0.57507	**-0.01**	0.97446
STM1029	STM1029	hypothetical protein STM1029	**1.00**	0.14077	**-0.26**	0.37081	**0.63**	0.11004
STM1029	STM1029	hypothetical protein STM1029	**2.30**	0.01358	**-0.98**	0.14886	**0.89**	0.39842
STM1030	STM1030	hypothetical protein STM1030	**0.71**	0.15783	**-0.64**	0.15109	**0.20**	0.82339
STM1030	STM1030	hypothetical protein STM1030	**1.75**	0.07536	**-0.96**	0.01966	**3.26**	0.00147
STM1031	STM1031	hypothetical protein STM1031	**1.68**	0.03459	**0.39**	0.20227	**1.42**	0.01325
STM1031	STM1031	hypothetical protein STM1031	**2.49**	0.04599	**-0.30**	0.77038	**2.72**	0.00038
STM1032	STM1032	hypothetical protein STM1032	**0.49**	0.62241	**-0.81**	0.09602	**-0.75**	0.38617
STM1032	STM1032	hypothetical protein STM1032	**-0.20**	0.89893	**-2.59**	0.02338	**-0.63**	0.35901
STM1033	STM1033	Clp protease-like protein	**-0.45**	0.53746	**1.21**	0.00261	**0.58**	0.40881
STM1033	STM1033	Clp protease-like protein	**0.53**	0.40414	**-0.12**	0.77686	**0.67**	0.17113
STM1034	STM1034	putative RecA/RadA recombinase	**1.15**	0.05709	**-0.51**	0.24589	**-1.06**	0.08306
STM1034	STM1034	putative RecA/RadA recombinase	**2.39**	0.00661	**-0.35**	0.22068	**0.53**	0.20425
STM1035	STM1035	ATP-binding sugar transporter-like protein	**-0.22**	0.70138	**0.83**	0.03970	**0.00**	0.99462
STM1035	STM1035	ATP-binding sugar transporter-like protein	**-0.50**	0.55440	**-0.12**	0.79056	**-0.02**	0.96217

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM1036	STM1036	probable minor tail protein	**0.83**	0.10291	**0.40**	0.26730	**0.96**	0.10728
STM1036	STM1036	probable minor tail protein	**-0.27**	0.67290	**0.44**	0.24706	**0.77**	0.24726
STM1037	STM1037	probable minor tail protein	**1.36**	0.04983	**0.67**	0.17518	**1.37**	0.02046
STM1037	STM1037	probable minor tail protein	**3.75**	0.00541	**0.35**	0.47402	**2.91**	0.00839
STM1038	STM1038	probable major tail protein	**1.94**	0.05381	**-2.00**	0.00309	**1.44**	0.09427
STM1038	STM1038	probable major tail protein	**1.57**	0.05745	**-2.55**	0.00239	**2.32**	0.03175
STM1039	STM1039	probable minor tail protein	**-0.43**	0.54972	**0.48**	0.31136	**0.61**	0.29567
STM1039	STM1039	probable minor tail protein	**0.71**	0.30245	**0.13**	0.78057	**0.98**	0.12787
STM1040	STM1040	probable minor tail protein	**0.48**	0.46629	**0.63**	0.15275	**1.56**	0.02816
STM1040	STM1040	probable minor tail protein	**1.61**	0.03088	**0.59**	0.07875	**1.18**	0.03849
STM1041	STM1041	probable minor tail protein	**2.23**	0.05171	**0.24**	0.61370	**-0.28**	0.73581
STM1041	STM1041	probable minor tail protein	**2.25**	0.06648	**-1.67**	0.00153	**-0.27**	0.63823
STM1042	STM1042	probable minor tail protein	**-0.08**	0.92997	**0.64**	0.10474	**1.86**	0.00276
STM1042	STM1042	probable minor tail protein	**1.58**	0.02667	**0.85**	0.05917	**1.23**	0.02158
STM1043	STM1043	attachment/invasion protein	**0.48**	0.40136	**0.72**	0.07379	**0.05**	0.92946
STM1043	STM1043	attachment/invasion protein	**0.38**	0.49079	**-0.16**	0.71883	**-0.94**	0.38020
STM1044	sodC	superoxide dismutase precursor	**0.49**	0.29112	**0.78**	0.21507	**-0.45**	0.21078
STM1044	sodC	superoxide dismutase precursor	**2.02**	0.00949	**0.15**	0.66674	**-0.19**	0.61705
STM1045	STM1045	probable minor tail protein	**-0.20**	0.72806	**-2.33**	0.00080	**-1.62**	0.01906
STM1045	STM1045	probable minor tail protein	**0.83**	0.22544	**-1.97**	0.00223	**0.51**	0.39032
STM1046	STM1046	probable tail assembly protein	**1.30**	0.05709	**1.06**	0.00690	**0.68**	0.11238
STM1046	STM1046	probable tail assembly protein	**1.20**	0.13484	**0.66**	0.09387	**0.82**	0.11068
STM1047	STM1047	probable tail assembly protein	**1.98**	0.03256	**-0.99**	0.01741	**0.39**	0.53590
STM1047	STM1047	probable tail assembly protein	**2.32**	0.01828	**-1.24**	0.05608	**0.98**	0.05608
STM1048	STM1048	host specificity protein J	**2.67**	0.01336	**0.91**	0.01701	**2.69**	0.00040
STM1048	STM1048	host specificity protein J	**2.15**	0.36871	**-0.28**	0.74644	**1.78**	0.00605
STM1049	STM1049	probable tail fiber protein	**2.22**	0.01090	**2.44**	0.00021	**2.17**	0.00161
STM1049	STM1049	probable tail fiber protein	**3.44**	0.00537	**1.42**	0.00489	**2.49**	0.00096
STM1050	STM1050	tail fiber assembly like-protein	**1.51**	0.09165	**1.63**	0.00070	**1.13**	0.03757
STM1050	STM1050	tail fiber assembly like-protein	**1.79**	0.04439	**1.13**	0.02359	**0.28**	0.59655
STM1051	sseI	secreted effector protein	**0.91**	0.34711	**5.43**	0.00001	**2.24**	0.01053
STM1051	sseI	secreted effector protein	**0.08**	0.90746	**5.94**	0.00001	**1.66**	0.01123
STM1053	STM1053	hypothetical protein STM1053	**0.32**	0.62331	**2.69**	0.00011	**0.29**	0.57912
STM1053	STM1053	hypothetical protein STM1053	**2.70**	0.01417	**2.47**	0.00071	**1.12**	0.09489
STM1055	STM1055	hypothetical protein STM1055	**-0.74**	0.22682	**0.92**	0.04497	**-0.54**	0.23566
STM1055	STM1055	hypothetical protein STM1055	**3.25**	0.00613	**1.70**	0.00697	**1.31**	0.01671
STM1056	STM1056	MsgA-like protein	**0.39**	0.51000	**1.10**	0.04569	**1.54**	0.04737
STM1056	STM1056	MsgA-like protein	**1.99**	0.02573	**0.79**	0.05114	**1.77**	0.02582
STM1057	pepN	aminopeptidase N	**1.56**	0.02456	**-0.29**	0.33010	**-0.86**	0.18695
STM1057	pepN	aminopeptidase N	**1.48**	0.04046	**0.55**	0.16069	**0.14**	0.79186
STM1058	pyrD	dihydroorotate dehydrogenase	**-0.37**	0.39909	**-0.76**	0.09120	**-0.90**	0.13937
STM1058	pyrD	dihydroorotate dehydrogenase	**1.42**	0.07190	**0.59**	0.29639	**1.26**	0.01056
STM1059	ycbW	putative cytoplasmic protein	**-0.29**	0.63074	**1.04**	0.01462	**-0.60**	0.20557
STM1059	ycbW	putative cytoplasmic protein	**0.98**	0.05371	**1.39**	0.02453	**0.53**	0.31467
STM1060	STM1060	putative iron-sulfur protein	**1.48**	0.07067	**1.24**	0.00303	**0.04**	0.93346
STM1060	STM1060	putative iron-sulfur protein	**3.09**	0.00750	**1.49**	0.00345	**1.76**	0.02199
STM1061	ycbY	putative N6-adenine-specific DNA methylase	**-0.16**	0.88453	**-1.55**	0.00320	**-1.78**	0.03680
STM1061	ycbY	putative N6-adenine-specific DNA methylase	**0.03**	0.97778	**-0.88**	0.02382	**-1.86**	0.00423
STM1062	uup	putative ABC transporter ATPase component	**0.42**	0.51519	**-0.47**	0.10824	**0.20**	0.76035
STM1062	uup	putative ABC transporter ATPase component	**1.54**	0.02522	**-0.94**	0.02883	**-0.10**	0.80345
STM1063	pqiA	paraquat-inducible protein A	**-1.35**	0.02743	**-0.53**	0.13102	**-0.60**	0.11243
STM1063	pqiA	paraquat-inducible protein A	**-0.75**	0.20530	**-0.69**	0.04263	**-0.72**	0.11017
STM1064	pqiB	paraquat-inducible protein B	**0.82**	0.12321	**-0.06**	0.86785	**1.57**	0.01795
STM1064	pqiB	paraquat-inducible protein B	**2.05**	0.00889	**-0.15**	0.65080	**2.45**	0.00035
STM1065	ymbA	putative outer membrane protein	**-0.70**	0.30866	**-0.19**	0.57542	**0.37**	0.32772
STM1065	ymbA	putative outer membrane protein	**0.12**	0.77992	**-0.28**	0.42544	**0.54**	0.47861
STM1067	fabA	3-hydroxydecanoyl-ACP dehydratase	**-1.88**	0.01356	**-1.53**	0.00130	**-2.23**	0.00156
STM1067	fabA	3-hydroxydecanoyl-ACP dehydratase	**-1.15**	0.10780	**-1.53**	0.00185	**-1.75**	0.00116
STM1068	lonH	putative protease	**-2.57**	0.00654	**-1.25**	0.01495	**-2.40**	0.00059
STM1068	lonH	putative protease	**-1.11**	0.05758	**-1.66**	0.00083	**-2.33**	0.00246
STM1069	ycbG	hypothetical protein STM1069	**-1.37**	0.05401	**0.39**	0.36780	**-0.51**	0.17957
STM1069	ycbG	hypothetical protein STM1069	**-1.30**	0.11699	**0.26**	0.53334	**-0.16**	0.68022
STM1070	ompA	putative hydrogenase membrane component precurosr	**-3.70**	0.01199	**0.45**	0.34003	**-0.68**	0.07463
STM1070	ompA	putative hydrogenase membrane component precurosr	**-3.83**	0.01016	**0.21**	0.46168	**-1.71**	0.00782
STM1071	sulA	cell division inhibitor	**-3.52**	0.00719	**-0.52**	0.28212	**-0.91**	0.07260
STM1071	sulA	cell division inhibitor	**-2.36**	0.04973	**-0.19**	0.72335	**-1.32**	0.03937
STM1074	yccF	putative inner membrane protein	**-1.10**	0.04932	**-0.90**	0.06835	**-1.07**	0.01239
STM1074	yccF	putative inner membrane protein	**-0.15**	0.75631	**-0.87**	0.01545	**-0.48**	0.28567
STM1075	helD	DNA helicase IV	**-0.93**	0.23375	**-0.04**	0.91467	**-0.43**	0.57586
STM1075	helD	DNA helicase IV	**0.57**	0.28808	**-0.40**	0.24801	**-0.63**	0.22723

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM1076	mgsA	methylglyoxal synthase	**-1.02**	0.06349	**0.02**	0.96273	**-0.57**	0.17778
STM1076	mgsA	methylglyoxal synthase	**-0.12**	0.81326	**0.16**	0.63793	**0.64**	0.24662
STM1077	yccT	hypothetical protein STM1077	**-0.15**	0.83294	**0.17**	0.68305	**0.19**	0.65706
STM1077	yccT	hypothetical protein STM1077	**0.34**	0.53583	**-0.65**	0.09740	**0.17**	0.69970
STM1078	STM1078	putative cytoplasmic protein	**0.89**	0.54370	**2.10**	0.00080	**1.24**	0.07108
STM1078	STM1078	putative cytoplasmic protein	**1.16**	0.38527	**2.27**	0.00013	**1.70**	0.00638
STM1079	yccV	putative inner membrane protein	**-0.84**	0.10506	**-0.06**	0.90452	**0.46**	0.26108
STM1079	yccV	putative inner membrane protein	**-0.79**	0.25538	**-0.05**	0.89653	**1.60**	0.01106
STM1080	yccW	putative SAM-dependent methyltransferase	**-0.52**	0.39937	**-0.78**	0.02864	**0.57**	0.36524
STM1080	yccW	putative SAM-dependent methyltransferase	**-2.33**	0.01549	**-0.65**	0.03673	**0.12**	0.80093
STM1081	STM1081	putative outer membrane protein	**-1.17**	0.06140	**0.39**	0.16357	**-0.89**	0.20543
STM1081	STM1081	putative outer membrane protein	**0.57**	0.34818	**0.44**	0.17817	**-0.19**	0.73468
STM1082	STM1082	bacterial regulatory protein	**-0.67**	0.25908	**0.50**	0.09704	**0.26**	0.52138
STM1082	STM1082	bacterial regulatory protein	**1.52**	0.22243	**0.66**	0.07854	**1.82**	0.00476
STM1083	yccX	putative phosphohydrolase	**-0.31**	0.46038	**1.06**	0.01128	**0.65**	0.09217
STM1083	yccX	putative phosphohydrolase	**0.22**	0.74697	**0.85**	0.03451	**0.86**	0.07286
STM1084	yccK	putative sulfite reductase gamma subunit	**0.25**	0.59869	**1.05**	0.00764	**1.05**	0.01843
STM1084	yccK	putative sulfite reductase gamma subunit	**2.00**	0.05709	**0.41**	0.32326	**1.38**	0.02615
STM1085	yccA	putative transport protein	**0.27**	0.65886	**1.78**	0.00075	**2.28**	0.00035
STM1085	yccA	putative transport protein	**0.16**	0.75467	**2.05**	0.00093	**2.65**	0.00058
STM1086	serT	STM1086	**-2.30**	0.02539	**-0.76**	0.19079	**3.08**	0.00022
STM1086	serT	STM1086	**-1.11**	0.06801	**-0.60**	0.30007	**3.45**	0.00027
STM1087	pipA	pathogenicity island-encoded protein A	**0.09**	0.87200	**3.44**	0.00002	**1.34**	0.23820
STM1087	pipA	pathogenicity island-encoded protein A	**0.75**	0.09424	**3.33**	0.00008	**1.27**	0.00518
STM1088	pipB	secreted effector protein	**2.57**	0.03083	**8.57**	0.00000	**0.09**	0.91584
STM1088	pipB	secreted effector protein	**2.24**	0.01261	**8.12**	0.00000	**1.40**	0.04351
STM1090	pipC	pathogenicity island-encoded protein C	**-0.79**	0.13459	**-0.22**	0.64548	**-1.12**	0.01825
STM1090	pipC	pathogenicity island-encoded protein C	**-0.62**	0.20028	**0.17**	0.77831	**-0.39**	0.35208
STM1091	sopB	secreted effector protein	**2.50**	0.01203	**-0.62**	0.06909	**-0.76**	0.30334
STM1091	sopB	secreted effector protein	**2.79**	0.01259	**-0.88**	0.03320	**0.88**	0.23384
STM1094	pipD	pathogenicity island-encoded protein D	**0.20**	0.76061	**-0.27**	0.66213	**-0.05**	0.93387
STM1094	pipD	pathogenicity island-encoded protein D	**2.06**	0.03925	**-0.77**	0.03280	**0.87**	0.09667
STM1095	copS	copper resistance protein	**-0.28**	0.55865	**-0.08**	0.87599	**0.49**	0.38566
STM1095	copS	copper resistance protein	**1.00**	0.05673	**-0.42**	0.29975	**0.06**	0.90497
STM1096	copR	copper resistance protein	**0.41**	0.34481	**0.76**	0.04364	**0.74**	0.24491
STM1096	copR	copper resistance protein	**1.63**	0.02003	**0.73**	0.07612	**1.13**	0.02622
STM1097	STM1097	hypothetical protein STM1097	**-0.51**	0.30019	**1.15**	0.01220	**0.62**	0.20558
STM1097	STM1097	hypothetical protein STM1097	**0.84**	0.28373	**2.09**	0.00028	**2.61**	0.00674
STM1098	hpaC	4-hydroxyphenylacetate catabolism	**0.12**	0.84287	**1.34**	0.00410	**-0.46**	0.53047
STM1098	hpaC	4-hydroxyphenylacetate catabolism	**1.30**	0.22802	**1.82**	0.00203	**-1.13**	0.01986
STM1099	hpaB	4-hydroxyphenylacetate catabolism	**-0.39**	0.50635	**-0.56**	0.11596	**-0.60**	0.44829
STM1099	hpaB	4-hydroxyphenylacetate catabolism	**1.09**	0.05741	**-0.39**	0.34589	**1.14**	0.05508
STM1100	hpaR	4-hydroxyphenylacetate catabolism	**-0.80**	0.64009	**-0.32**	0.50209	**0.91**	0.04020
STM1100	hpaR	4-hydroxyphenylacetate catabolism	**1.91**	0.02573	**0.19**	0.83889	**0.46**	0.50489
STM1101	hpaG	4-hydroxyphenylacetate catabolism	**0.26**	0.68566	**1.14**	0.00361	**0.59**	0.25088
STM1101	hpaG	4-hydroxyphenylacetate catabolism	**1.07**	0.04923	**0.85**	0.07806	**1.78**	0.00589
STM1102	hpaE	4-hydroxyphenylacetate catabolism	**-0.37**	0.55997	**0.02**	0.97103	**-0.62**	0.29269
STM1102	hpaE	4-hydroxyphenylacetate catabolism	**0.16**	0.79084	**0.91**	0.26310	**0.25**	0.70417
STM1103	hpaD	4-hydroxyphenylacetate catabolism	**-0.72**	0.39423	**0.25**	0.39310	**0.42**	0.52111
STM1103	hpaD	4-hydroxyphenylacetate catabolism	**-0.32**	0.61184	**-1.24**	0.03058	**0.20**	0.68805
STM1104	hpaF	4-hydroxyphenylacetate catabolism	**0.05**	0.95350	**1.23**	0.01167	**0.44**	0.43336
STM1104	hpaF	4-hydroxyphenylacetate catabolism	**1.48**	0.34196	**-0.32**	0.53262	**1.00**	0.04600
STM1105	hpaH	4-hydroxyphenylacetate catabolism	**0.43**	0.39007	**-1.03**	0.04721	**-0.32**	0.63670
STM1105	hpaH	4-hydroxyphenylacetate catabolism	**0.98**	0.23189	**-1.02**	0.06084	**1.38**	0.07806
STM1106	hpaI	4-hydroxyphenylacetate catabolism	**-0.71**	0.31214	**-0.56**	0.23287	**-0.01**	0.98546
STM1106	hpaI	4-hydroxyphenylacetate catabolism	**0.27**	0.59869	**-0.53**	0.38496	**0.28**	0.55218
STM1107	hpaX	4-hydroxyphenylacetate catabolism	**-0.39**	0.56239	**-0.45**	0.34067	**-0.34**	0.53850
STM1107	hpaX	4-hydroxyphenylacetate catabolism	**1.07**	0.21050	**-0.23**	0.54128	**0.11**	0.80608
STM1108	hpaA	4-hydroxyphenylacetate catabolism	**-0.27**	0.58841	**-2.17**	0.08685	**0.79**	0.35901
STM1108	hpaA	4-hydroxyphenylacetate catabolism	**0.02**	0.98561	**-0.90**	0.06234	**-1.56**	0.14367
STM1109	STM1109	putative periplasmic protein	**0.28**	0.51100	**0.22**	0.47069	**0.31**	0.43806
STM1109	STM1109	putative periplasmic protein	**0.65**	0.55212	**-0.79**	0.11551	**1.58**	0.05159
STM1111	yccD	putative cytoplasmic protein	**-1.09**	0.04414	**0.44**	0.34768	**0.24**	0.50461
STM1111	yccD	putative cytoplasmic protein	**-0.66**	0.16721	**0.44**	0.32362	**0.88**	0.06994
STM1112	cbpA	DNA-binding protein	**-1.31**	0.06965	**0.32**	0.33227	**0.37**	0.32940
STM1112	cbpA	DNA-binding protein	**-0.62**	0.14918	**0.61**	0.11281	**0.64**	0.14035
STM1113	scsA	suppression of copper sensitivity protein A	**-0.23**	0.68827	**1.13**	0.10812	**-0.48**	0.20564
STM1113	scsA	suppression of copper sensitivity protein A	**0.49**	0.29994	**0.37**	0.49730	**0.21**	0.68841
STM1114	scsB	suppression of copper sensitivity protein	**-0.10**	0.88088	**1.03**	0.03827	**0.67**	0.32261
STM1114	scsB	suppression of copper sensitivity protein	**0.75**	0.45900	**0.42**	0.29544	**0.69**	0.27345

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM1115	scsC	suppression of copper sensitivity protein	**1.35**	0.04372	**1.49**	0.00847	**0.96**	0.03722
STM1115	scsC	suppression of copper sensitivity protein	**3.36**	0.08514	**1.27**	0.00574	**2.14**	0.00079
STM1116	scsD	suppression of copper sensitivity protein	**-0.46**	0.45507	**-0.25**	0.39277	**-0.17**	0.80945
STM1116	scsD	suppression of copper sensitivity protein	**1.25**	0.07399	**0.24**	0.42172	**0.61**	0.18295
STM1117	agp	glucose-1-phosphatase	**-0.11**	0.78992	**3.22**	0.00007	**2.63**	0.00025
STM1117	agp	glucose-1-phosphatase	**0.42**	0.33525	**3.59**	0.00002	**3.31**	0.00019
STM1118	yccJ	putative cytoplasmic protein	**1.20**	0.05800	**2.28**	0.00047	**4.09**	0.00022
STM1118	yccJ	putative cytoplasmic protein	**1.73**	0.02442	**2.28**	0.00049	**5.31**	0.00002
STM1119	wraB	TrpR binding protein WrbA	**0.42**	0.50162	**3.12**	0.00006	**5.47**	0.00002
STM1119	wraB	TrpR binding protein WrbA	**1.28**	0.07428	**3.21**	0.00015	**5.39**	0.00020
STM1121	ymdF	putative cytoplasmic protein	**0.86**	0.12381	**2.60**	0.00012	**7.21**	0.00002
STM1121	ymdF	putative cytoplasmic protein	**2.48**	0.00635	**2.69**	0.00010	**8.99**	0.00001
STM1122	ycdC	putative transcriptional repressor	**-0.87**	0.20836	**0.47**	0.15006	**1.15**	0.00929
STM1122	ycdC	putative transcriptional repressor	**-0.17**	0.77174	**0.29**	0.36153	**1.37**	0.00468
STM1123	STM1123	putative periplasmic protein	**-0.64**	0.57394	**-2.81**	0.00041	**-0.73**	0.18895
STM1123	STM1123	putative periplasmic protein	**-0.15**	0.89576	**-2.46**	0.00070	**-0.87**	0.28474
STM1125	putP	major sodium/proline symporter	**0.36**	0.44366	**0.28**	0.48330	**-0.87**	0.03999
STM1125	putP	major sodium/proline symporter	**0.26**	0.53359	**0.19**	0.57025	**-0.82**	0.07171
STM1127	STM1127	putative transcriptional regulator	**-0.66**	0.25920	**0.29**	0.42507	**0.47**	0.19850
STM1127	STM1127	putative transcriptional regulator	**-0.14**	0.78220	**-0.44**	0.22185	**0.58**	0.18304
STM1128	STM1128	putative sodium/glucose cotransporter	**-1.27**	0.04747	**-0.67**	0.06637	**-0.97**	0.06294
STM1128	STM1128	putative sodium/glucose cotransporter	**0.56**	0.58028	**-0.45**	0.28692	**-0.47**	0.35902
STM1129	STM1129	putative inner membrane protein	**-0.08**	0.89999	**0.96**	0.50789	**-0.16**	0.70360
STM1129	STM1129	putative inner membrane protein	**-0.45**	0.41542	**-0.05**	0.94003	**-2.49**	0.01908
STM1130	STM1130	putative inner membrane protein	**-0.05**	0.94606	**0.82**	0.18809	**1.23**	0.10272
STM1130	STM1130	putative inner membrane protein	**0.35**	0.65239	**-0.31**	0.61540	**-0.47**	0.66789
STM1131	STM1131	putative outer membrane protein	**0.13**	0.78367	**0.25**	0.47216	**1.24**	0.01677
STM1131	STM1131	putative outer membrane protein	**0.91**	0.16859	**0.28**	0.53131	**1.54**	0.01179
STM1132	STM1132	putative sialic acid transporter	**-0.93**	0.06515	**-0.35**	0.50013	**-0.22**	0.55781
STM1132	STM1132	putative sialic acid transporter	**-0.77**	0.12640	**0.33**	0.34076	**0.51**	0.40701
STM1133	STM1133	putative dehydrogenase	**-1.44**	0.02262	**0.45**	0.13935	**0.41**	0.39322
STM1133	STM1133	putative dehydrogenase	**0.04**	0.96242	**1.26**	0.00419	**1.23**	0.01159
STM1134	serX	STM1134	**0.90**	0.14620	**-1.29**	0.00514	**2.15**	0.00093
STM1134	serX	STM1134	**1.64**	0.03289	**-1.01**	0.02681	**2.57**	0.00055
STM1135	ycdW	putative oxidoreductase	**0.28**	0.51096	**-0.68**	0.07251	**-0.95**	0.07011
STM1135	ycdW	putative oxidoreductase	**1.42**	0.02573	**-0.40**	0.16189	**0.19**	0.75669
STM1136	ycdX	hypothetical protein STM1136	**-1.85**	0.00991	**-0.82**	0.01998	**-0.93**	0.02855
STM1136	ycdX	hypothetical protein STM1136	**-1.33**	0.03111	**-0.51**	0.14652	**-0.29**	0.44030
STM1137	ycdY	putative oxidoreductase component	**0.12**	0.89962	**-0.09**	0.77248	**-0.82**	0.03881
STM1137	ycdY	putative oxidoreductase component	**1.35**	0.10510	**-0.04**	0.89742	**1.11**	0.01631
STM1138	ycdZ	putative inner membrane protein	**-0.90**	0.14219	**-0.99**	0.00982	**-1.39**	0.00733
STM1138	ycdZ	putative inner membrane protein	**0.36**	0.50612	**-0.97**	0.01342	**0.01**	0.97989
STM1139	csgG	putative curli operon transcriptional regulator	**0.96**	0.06146	**-1.01**	0.04316	**0.63**	0.44299
STM1139	csgG	putative curli operon transcriptional regulator	**1.85**	0.05385	**-0.88**	0.03921	**0.62**	0.29466
STM1140	csgF	curli production assembly/transport component	**1.55**	0.02633	**0.85**	0.04641	**1.14**	0.22330
STM1140	csgF	curli production assembly/transport component	**3.16**	0.00541	**0.71**	0.06483	**3.66**	0.00212
STM1141	csgE	curli production assembly/transport component	**1.79**	0.12594	**3.41**	0.00008	**3.75**	0.00011
STM1141	csgE	curli production assembly/transport component	**3.14**	0.15151	**2.48**	0.02135	**4.46**	0.00096
STM1142	csgD	putative transcriptional regulator	**-0.67**	0.42423	**0.77**	0.15400	**2.59**	0.01019
STM1142	csgD	putative transcriptional regulator	**1.79**	0.14654	**-0.84**	0.02246	**1.49**	0.08465
STM1143	csgB	minor curlin subunit precursor	**0.20**	0.89893	**-0.13**	0.80331	**0.73**	0.43281
STM1143	csgB	minor curlin subunit precursor	**0.65**	0.28620	**0.04**	0.97004	**1.03**	0.07429
STM1144	csgA	major curlin subunit precursor	**-1.04**	0.09155	**0.51**	0.18434	**-0.54**	0.23926
STM1144	csgA	major curlin subunit precursor	**1.30**	0.03644	**0.09**	0.82370	**1.21**	0.01550
STM1145	csgC	putative curli production protein precursor	**0.32**	0.45778	**-0.04**	0.92921	**0.10**	0.89293
STM1145	csgC	putative curli production protein precursor	**1.13**	0.08198	**0.14**	0.79910	**0.39**	0.40867
STM1146	ymdA	putative periplasmic protein	**-0.76**	0.15099	**-0.45**	0.19139	**-0.71**	0.22330
STM1146	ymdA	putative periplasmic protein	**-0.78**	0.26249	**-0.91**	0.05452	**-0.23**	0.64697
STM1147	STM1147	hypothetical protein STM1147	**-0.65**	0.53267	**-0.63**	0.15124	**0.10**	0.84838
STM1147	STM1147	hypothetical protein STM1147	**1.21**	0.12119	**-1.25**	0.02614	**0.67**	0.40243
STM1148,S	ymdC	putative phospholipase	**-0.05**	0.93290	**-0.27**	0.53139	**0.01**	0.99131
STM1148,S	ymdC	putative phospholipase	**-0.27**	0.53193	**-0.26**	0.49389	**-0.79**	0.42420
STM1149	mdoC	glucans biosynthesis protein	**-0.96**	0.06265	**-0.31**	0.50364	**-1.17**	0.02414
STM1149	mdoC	glucans biosynthesis protein	**-0.08**	0.85069	**-0.98**	0.00925	**-0.64**	0.16963
STM1150	mdoG	periplasmic glucans biosynthesis protein	**-0.92**	0.20599	**-0.52**	0.15086	**-1.11**	0.03939
STM1150	mdoG	periplasmic glucans biosynthesis protein	**0.69**	0.35080	**0.09**	0.80960	**-1.25**	0.06066
STM1151	mdoH	glucosyltransferase MdoH	**-2.15**	0.01449	**-0.54**	0.60988	**-0.58**	0.21151
STM1151	mdoH	glucosyltransferase MdoH	**-0.62**	0.29377	**-0.64**	0.10181	**-0.13**	0.75917
STM1152	yceK	putative outer membrane lipoprotein	**0.23**	0.71992	**-0.43**	0.21799	**1.20**	0.00935
STM1152	yceK	putative outer membrane lipoprotein	**0.82**	0.08921	**0.42**	0.20552	**2.08**	0.00177

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM1153	msyB	acidic protein	**0.91**	0.15734	**1.51**	0.00182	**2.57**	0.00019
STM1153	msyB	acidic protein	**2.63**	0.00757	**1.35**	0.00848	**2.83**	0.00036
STM1154	yceE	putative transport protein	**1.15**	0.04642	**0.13**	0.65822	**1.49**	0.00554
STM1154	yceE	putative transport protein	**0.60**	0.20774	**-0.12**	0.78293	**1.73**	0.00180
STM1155	htrB	lipid A biosynthesis lauroyl acyltransferase	**0.04**	0.96478	**0.51**	0.19689	**1.05**	0.05714
STM1155	htrB	lipid A biosynthesis lauroyl acyltransferase	**-0.96**	0.08591	**1.34**	0.24959	**-0.14**	0.71477
STM1156	yceA	hypothetical protein STM1156	**-1.37**	0.06077	**-0.57**	0.12575	**-1.69**	0.01455
STM1156	yceA	hypothetical protein STM1156	**-0.77**	0.29799	**-0.69**	0.09349	**-0.45**	0.44129
STM1157	yceI	hypothetical protein STM1157	**-1.11**	0.03905	**0.15**	0.64171	**-1.08**	0.01512
STM1157	yceI	hypothetical protein STM1157	**0.25**	0.66258	**-0.10**	0.73506	**-0.94**	0.05015
STM1158	STM1158	putative inner membrane protein	**-0.56**	0.22379	**1.08**	0.01468	**0.25**	0.49466
STM1158	STM1158	putative inner membrane protein	**0.67**	0.28930	**0.67**	0.07308	**1.03**	0.12732
STM1159	yceO	putative inner membrane protein	**-1.03**	0.06965	**0.07**	0.90424	**0.31**	0.49552
STM1159	yceO	putative inner membrane protein	**-0.93**	0.15633	**-1.04**	0.01296	**-0.75**	0.16413
STM1160	solA	putative sarcosine oxidase	**-0.29**	0.60632	**-0.70**	0.08143	**-0.71**	0.16107
STM1160	solA	putative sarcosine oxidase	**-1.00**	0.09268	**-0.60**	0.21882	**-0.06**	0.90141
STM1161,S	yceP	putative cytoplasmic protein	**-0.19**	0.84231	**-0.71**	0.05519	**-0.46**	0.34632
STM1161,S	yceP	putative cytoplasmic protein	**1.02**	0.11276	**-0.70**	0.13604	**0.50**	0.27415
STM1162	dinI	DNA damage-inducible protein I	**-0.93**	0.11919	**-0.53**	0.11130	**-1.99**	0.00132
STM1162	dinI	DNA damage-inducible protein I	**0.21**	0.70846	**-0.10**	0.74028	**-1.32**	0.00728
STM1163	pyrC	dihydroorotase	**-0.79**	0.20430	**-0.11**	0.72185	**-0.68**	0.24227
STM1163	pyrC	dihydroorotase	**-0.93**	0.30487	**0.06**	0.88289	**-0.88**	0.09577
STM1164	yceB	putative outer membrane lipoprotein	**1.49**	0.06207	**1.11**	0.00517	**2.22**	0.00264
STM1164	yceB	putative outer membrane lipoprotein	**1.51**	0.08560	**1.03**	0.06483	**3.38**	0.00012
STM1165	grxB	glutaredoxin 2	**-1.61**	0.03383	**2.53**	0.00011	**4.81**	0.00003
STM1165	grxB	glutaredoxin 2	**-1.36**	0.02648	**2.38**	0.00017	**5.05**	0.00003
STM1166	yceL	putative transport protein	**-0.66**	0.21058	**-0.31**	0.62309	**1.26**	0.01357
STM1166	yceL	putative transport protein	**-0.26**	0.63700	**0.13**	0.69793	**1.51**	0.01355
STM1167	rimJ	acetylatase	**-1.48**	0.09162	**-0.21**	0.42946	**-0.20**	0.64931
STM1167	rimJ	acetylatase	**0.02**	0.97778	**-0.29**	0.41161	**-0.80**	0.11922
STM1168	yceH	putative cytoplasmic protein	**-1.32**	0.02281	**-0.04**	0.92231	**-1.99**	0.00186
STM1168	yceH	putative cytoplasmic protein	**-0.76**	0.09447	**-0.21**	0.59685	**-1.17**	0.02040
STM1169	mviM	putative virulence protein	**1.22**	0.09283	**-1.35**	0.01310	**-0.85**	0.10550
STM1169	mviM	putative virulence protein	**1.61**	0.02080	**-1.29**	0.02640	**0.15**	0.76309
STM1170	mviN	putative virulence protein	**-2.22**	0.00900	**-3.01**	0.00389	**-2.19**	0.00162
STM1170	mviN	putative virulence protein	**-2.36**	0.01487	**-2.14**	0.00027	**-2.21**	0.00182
STM1171	flgN	putative FlgK/FlgL export chaperone	**-1.55**	0.02729	**-2.84**	0.00004	**-2.38**	0.00032
STM1171	flgN	putative FlgK/FlgL export chaperone	**-1.22**	0.14283	**-2.50**	0.00023	**-2.56**	0.00063
STM1172	flgM	anti-FliA factor	**-1.48**	0.01741	**-2.99**	0.00005	**-1.04**	0.04723
STM1172	flgM	anti-FliA factor	**-0.62**	0.31320	**-2.79**	0.00008	**-0.81**	0.09838
STM1173	flgA	flagellar basal body P-ring biosynthesis protein	**-3.72**	0.00541	**-2.74**	0.00024	**-1.47**	0.02499
STM1173	flgA	flagellar basal body P-ring biosynthesis protein	**-2.66**	0.00654	**-2.86**	0.00003	**-1.46**	0.00257
STM1174	flgB	flagellar basal body rod protein	**-3.88**	0.00512	**-3.10**	0.00005	**-4.68**	0.00008
STM1174	flgB	flagellar basal body rod protein	**-3.20**	0.00546	**-3.05**	0.00008	**-4.41**	0.00036
STM1175	flgC	flagellar basal body rod protein	**-3.48**	0.00775	**-3.07**	0.00011	**-5.88**	0.00079
STM1175	flgC	flagellar basal body rod protein	**-2.10**	0.00900	**-3.18**	0.00006	**-4.15**	0.00007
STM1176	flgD	flagellar basal body rod modification protein	**-3.15**	0.00673	**-2.90**	0.00017	**-3.43**	0.00024
STM1176	flgD	flagellar basal body rod modification protein	**-1.61**	0.02200	**-2.95**	0.00051	**-3.20**	0.03101
STM1177	flgE	flagellar hook protein	**-3.55**	0.00638	**-4.13**	0.00001	**-3.20**	0.00024
STM1177	flgE	flagellar hook protein	**-2.30**	0.00727	**-3.38**	0.00004	**-3.52**	0.00020
STM1178	flgF	cell-proximal portion of basal-body rod	**-2.31**	0.01326	**-3.15**	0.00022	**-2.61**	0.00058
STM1178	flgF	cell-proximal portion of basal-body rod	**-0.70**	0.29448	**-3.00**	0.00003	**-1.95**	0.00176
STM1179	flgG	flagellar basal-body rod protein	**-1.90**	0.01712	**-2.76**	0.00005	**-2.80**	0.00145
STM1179	flgG	flagellar basal-body rod protein	**-0.86**	0.37508	**-2.83**	0.00016	**-2.44**	0.00148
STM1180	flgH	flagellar L-ring protein precursor	**0.37**	0.51564	**-3.51**	0.00002	**-2.39**	0.00275
STM1180	flgH	flagellar L-ring protein precursor	**0.17**	0.89679	**-3.84**	0.00001	**-2.14**	0.01023
STM1181	flgI	flagellar P-ring protein precursor	**-2.80**	0.00626	**-3.17**	0.00014	**-3.69**	0.00024
STM1181	flgI	flagellar P-ring protein precursor	**-3.64**	0.00650	**-2.84**	0.00024	**-4.10**	0.00341
STM1182	flgJ	flagellar biosynthesis protein	**-1.12**	0.11805	**-1.94**	0.00102	**-0.48**	0.18479
STM1182	flgJ	flagellar biosynthesis protein	**-0.91**	0.24987	**-2.83**	0.00027	**-0.29**	0.54946
STM1183	flgK	flagellar hook-associated protein	**-3.26**	0.00547	**-3.75**	0.00006	**-4.52**	0.00041
STM1183	flgK	flagellar hook-associated protein	**-3.25**	0.00537	**-3.20**	0.00002	**-3.69**	0.00018
STM1184	flgL	flagellar hook-associated protein	**-2.45**	0.00686	**-2.22**	0.00024	**-3.05**	0.00022
STM1184	flgL	flagellar hook-associated protein	**-1.39**	0.06207	**-2.21**	0.00036	**-2.03**	0.00126
STM1185	rne	RNase E	**-1.44**	0.04050	**-0.16**	0.70393	**-2.16**	0.01192
STM1185	rne	RNase E	**-0.71**	0.25977	**-0.35**	0.33318	**-2.27**	0.01739
STM1187	rluC	23S rRNA pseudouridylate synthase	**-1.50**	0.01850	**-0.78**	0.04236	**-1.02**	0.01979
STM1187	rluC	23S rRNA pseudouridylate synthase	**-2.43**	0.01914	**-1.77**	0.00126	**-2.41**	0.00042
STM1188	STM1188	putative inner membrane lipoprotein	**-0.87**	0.28560	**-0.98**	0.00811	**-1.28**	0.00997
STM1188	STM1188	putative inner membrane lipoprotein	**0.50**	0.78024	**-0.92**	0.01800	**-0.57**	0.14314

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM1189	maf	Maf-like protein	**-1.89**	0.00927	**-1.62**	0.05633	**-1.93**	0.00120
STM1189	maf	Maf-like protein	**-0.88**	0.13943	**-0.93**	0.01137	**-1.11**	0.09595
STM1190	yceD	putative metal-binding protein	**-4.19**	0.00595	**-0.63**	0.07115	**-5.15**	0.00002
STM1190	yceD	putative metal-binding protein	**-3.62**	0.00512	**-0.56**	0.10488	**-4.87**	0.00003
STM1192	plsX	fatty acid/phospholipid synthesis protein	**-2.01**	0.01382	**-1.07**	0.01019	**-2.72**	0.00021
STM1192	plsX	fatty acid/phospholipid synthesis protein	**-1.03**	0.06731	**-0.38**	0.19474	**-2.74**	0.00018
STM1193	fabH	3-oxoacyl-(acyl carrier protein) synthase	**-2.54**	0.00789	**-1.70**	0.00108	**-3.37**	0.00040
STM1193	fabH	3-oxoacyl-(acyl carrier protein) synthase	**-2.28**	0.01125	**-0.99**	0.01654	**-3.45**	0.00006
STM1194	fabD	acyl carrier protein S-malonyltransferase	**-1.05**	0.08484	**-0.49**	0.26487	**-0.55**	0.14294
STM1194	fabD	acyl carrier protein S-malonyltransferase	**-2.27**	0.02977	**-1.17**	0.02811	**-4.17**	0.00004
STM1194	fabD	acyl carrier protein S-malonyltransferase	**-1.04**	0.11320	**-0.56**	0.05767	**0.58**	0.53322
STM1194	fabD	acyl carrier protein S-malonyltransferase	**-1.18**	0.05377	**-0.72**	0.03219	**-3.99**	0.00006
STM1195	fabG	3-ketoacyl-(acyl-carrier-protein) reductase	**-3.50**	0.00545	**-1.84**	0.00438	**-3.11**	0.00018
STM1195	fabG	3-ketoacyl-(acyl-carrier-protein) reductase	**-3.43**	0.00537	**-1.60**	0.00210	**-3.67**	0.00005
STM1196	acpP	acyl carrier protein	**-2.05**	0.04704	**0.47**	0.16195	**-1.51**	0.00261
STM1196	acpP	acyl carrier protein	**0.07**	0.92939	**0.29**	0.35037	**-0.84**	0.03493
STM1197	fabF	3-oxoacyl-(acyl carrier protein) synthase	**-2.89**	0.00547	**-1.23**	0.01173	**-2.96**	0.00126
STM1197	fabF	3-oxoacyl-(acyl carrier protein) synthase	**-2.36**	0.02202	**-0.17**	0.67751	**-3.51**	0.00588
STM1198	pabC	4-amino-4-deoxychorismate lyase	**-0.33**	0.81891	**-0.12**	0.72955	**-1.34**	0.00581
STM1198	pabC	4-amino-4-deoxychorismate lyase	**-0.25**	0.74644	**-0.70**	0.02836	**-1.27**	0.04371
STM1199	yceG	putative periplasmic solute-binding protein	**-0.10**	0.84317	**0.14**	0.68302	**-1.25**	0.01255
STM1199	yceG	putative periplasmic solute-binding protein	**-0.31**	0.78250	**-0.35**	0.36495	**-0.19**	0.67238
STM1200	tmk	thymidylate kinase	**-2.43**	0.01199	**-1.15**	0.20610	**-1.63**	0.01435
STM1200	tmk	thymidylate kinase	**-2.17**	0.09987	**-1.99**	0.00033	**-1.92**	0.00206
STM1201	holB	DNA polymerase III subunit delta	**-2.27**	0.02062	**-1.77**	0.00180	**-2.47**	0.00028
STM1201	holB	DNA polymerase III subunit delta	**-1.92**	0.01798	**-1.45**	0.00170	**-2.72**	0.00064
STM1202	ycfH	putative metal-dependent hydrolase	**-2.04**	0.05687	**-1.85**	0.00045	**-1.77**	0.00124
STM1202	ycfH	putative metal-dependent hydrolase	**-1.20**	0.03725	**-1.56**	0.00199	**-1.25**	0.02633
STM1203	ptsG	glucose-specific IIBC component	**-2.33**	0.00822	**-1.02**	0.00778	**-1.87**	0.00618
STM1203	ptsG	glucose-specific IIBC component	**-0.36**	0.44116	**-0.93**	0.01367	**-1.25**	0.01458
STM1204	fhuE	outer membrane receptor protein precursor	**-1.14**	0.21328	**-0.25**	0.55836	**-0.06**	0.93644
STM1204	fhuE	outer membrane receptor protein precursor	**-0.20**	0.86396	**0.40**	0.25713	**-0.21**	0.63854
STM1205	ycfF	putative protein kinase C inhibitor	**-2.66**	0.03447	**-0.25**	0.39902	**-0.56**	0.17630
STM1205	ycfF	putative protein kinase C inhibitor	**-2.29**	0.01479	**-0.24**	0.42846	**-0.83**	0.04927
STM1206	ycfL	putative outer membrane lipoprotein	**-1.28**	0.03186	**0.62**	0.08589	**-0.68**	0.06501
STM1206	ycfL	putative outer membrane lipoprotein	**-1.07**	0.04020	**0.78**	0.04469	**-0.14**	0.79381
STM1207	ycfM	putative outer membrane lipoprotein	**-1.27**	0.04403	**0.33**	0.28016	**-0.91**	0.07048
STM1207	ycfM	putative outer membrane lipoprotein	**-0.18**	0.76451	**0.77**	0.02382	**-0.01**	0.97790
STM1208	ycfN	putative cytoplasmic protein	**-1.79**	0.01297	**-1.24**	0.00316	**-1.42**	0.01093
STM1208	ycfN	putative cytoplasmic protein	**-0.70**	0.27805	**-0.56**	0.07566	**-1.31**	0.00576
STM1209	nagZ	beta-hexosaminidase	**-0.99**	0.10289	**-0.30**	0.28109	**-0.25**	0.60259
STM1209	nagZ	beta-hexosaminidase	**-1.15**	0.11970	**0.30**	0.34944	**-0.27**	0.52982
STM1210	ycfP	hypothetical protein STM1210	**-1.18**	0.07112	**0.82**	0.01483	**0.07**	0.85584
STM1210	ycfP	hypothetical protein STM1210	**-0.69**	0.39109	**0.90**	0.02115	**0.14**	0.78683
STM1211	ndh	respiratory NADH dehydrogenase 2	**-0.50**	0.40724	**0.06**	0.85963	**-0.75**	0.08000
STM1211	ndh	respiratory NADH dehydrogenase 2	**0.09**	0.83296	**0.02**	0.95569	**0.43**	0.32911
STM1212	ycfJ	putative outer membrane lipoprotein	**-0.71**	0.32144	**0.81**	0.02560	**2.37**	0.00188
STM1212	ycfJ	putative outer membrane lipoprotein	**0.49**	0.31047	**1.31**	0.00376	**2.67**	0.00016
STM1213	ycfQ	putative transcriptional repressor	**3.94**	0.08857	**1.06**	0.02131	**2.38**	0.06440
STM1213	ycfQ	putative transcriptional repressor	**1.09**	0.06074	**1.68**	0.00494	**2.15**	0.00085
STM1214	ycfR	putative outer membrane protein	**1.40**	0.03457	**4.75**	0.00001	**1.48**	0.00656
STM1214	ycfR	putative outer membrane protein	**2.38**	0.01013	**4.74**	0.00001	**2.28**	0.00139
STM1215	ycfS	putative periplasmic protein	**-0.52**	0.43730	**2.80**	0.00009	**0.48**	0.25502
STM1215	ycfS	putative periplasmic protein	**1.00**	0.12267	**2.94**	0.00007	**1.09**	0.04898
STM1216	mfd	transcription-repair coupling factor	**-0.72**	0.34609	**0.36**	0.36876	**-0.88**	0.05453
STM1216	mfd	transcription-repair coupling factor	**-0.26**	0.55064	**-0.55**	0.35270	**-0.58**	0.12666
STM1217,S	ycfU	integral membrane protein	**-1.73**	0.02067	**-1.37**	0.00203	**-2.12**	0.00089
STM1217,S	ycfU	integral membrane protein	**-1.93**	0.01842	**-1.98**	0.00020	**-1.49**	0.00538
STM1218	ycfV	ATP-binding protein	**-1.59**	0.02670	**-1.63**	0.00286	**-3.53**	0.00187
STM1218	ycfV	ATP-binding protein	**-1.88**	0.01214	**-1.86**	0.00052	**-2.07**	0.00095
STM1219	ycfW	integral membrane protein	**1.88**	0.02673	**2.72**	0.00109	**-2.01**	0.00319
STM1219	ycfW	integral membrane protein	**2.67**	0.00719	**3.26**	0.00049	**-1.97**	0.00340
STM1220	ycfX	putative regulatory protein	**-0.28**	0.71501	**-0.03**	0.94477	**-1.39**	0.00720
STM1220	ycfX	putative regulatory protein	**-0.61**	0.29939	**-0.16**	0.64293	**-0.55**	0.58972
STM1221	cobB	NAD-dependent deacetylase	**-1.78**	0.02872	**2.29**	0.00015	**-2.34**	0.01703
STM1221	cobB	NAD-dependent deacetylase	**-0.75**	0.25111	**2.85**	0.00013	**-2.04**	0.00427
STM1222	potD	spermidine/putrescine ABC transporter periplasmic	**-0.66**	0.27015	**3.81**	0.00002	**-0.94**	0.04839
STM1222	potD	spermidine/putrescine ABC transporter periplasmic	**-0.54**	0.50018	**3.60**	0.00007	**-1.79**	0.02445
STM1223	potC	spermidine/putrescine ABC transporter membrane	**-1.06**	0.09734	**2.85**	0.00014	**-2.73**	0.00025
STM1223	potC	spermidine/putrescine ABC transporter membrane	**-1.26**	0.03991	**3.17**	0.00012	**-1.63**	0.01481

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM1224	sifA	secreted effector protein	**-1.19**	0.07943	**3.57**	0.00005	**-0.20**	0.65210
STM1224	sifA	secreted effector protein	**-1.02**	0.19173	**4.02**	0.00009	**0.48**	0.22113
STM1225	potB	spermidine/putrescine ABC transporter membrane	**-1.67**	0.01487	**0.86**	0.03644	**-0.04**	0.93346
STM1225	potB	spermidine/putrescine ABC transporter membrane	**-1.34**	0.03892	**1.38**	0.00468	**-1.24**	0.02326
STM1226	potA	putrescine/spermidine ABC transporter ATPase	**-0.57**	0.21998	**-0.72**	0.03100	**1.44**	0.11656
STM1226	potA	putrescine/spermidine ABC transporter ATPase	**-0.21**	0.71833	**-0.76**	0.02818	**0.63**	0.10917
STM1227	pepT	peptidase T	**0.19**	0.78623	**1.02**	0.00594	**0.22**	0.62184
STM1227	pepT	peptidase T	**0.06**	0.92304	**0.48**	0.12874	**0.84**	0.11623
STM1228	STM1228	putative periplasmic protein	**-1.31**	0.03466	**-0.47**	0.14722	**-1.03**	0.05594
STM1228	STM1228	putative periplasmic protein	**-0.17**	0.82608	**-0.51**	0.16069	**-0.45**	0.32032
STM1229	ycfD	putative cytoplasmic protein	**0.03**	0.96020	**0.12**	0.89875	**-1.36**	0.01446
STM1229	ycfD	putative cytoplasmic protein	**1.44**	0.03862	**-0.26**	0.42325	**-0.46**	0.22580
STM1230	phoQ	sensor kinase protein	**-1.13**	0.04050	**-0.68**	0.18388	**0.69**	0.25829
STM1230	phoQ	sensor kinase protein	**0.05**	0.92973	**0.08**	0.80333	**-0.97**	0.39673
STM1231	phoP	response regulator	**-0.16**	0.79826	**0.80**	0.05120	**-0.94**	0.02478
STM1231	phoP	response regulator	**1.16**	0.06218	**0.52**	0.17419	**-0.38**	0.34435
STM1232	purB	adenylosuccinate lyase	**-1.76**	0.02009	**0.74**	0.08377	**-2.36**	0.00257
STM1232	purB	adenylosuccinate lyase	**0.15**	0.80373	**1.19**	0.00849	**-1.65**	0.00271
STM1233	ycfC	hypothetical protein STM1233	**-2.06**	0.00749	**0.06**	0.86562	**-2.31**	0.00171
STM1233	ycfC	hypothetical protein STM1233	**-1.61**	0.01710	**0.11**	0.75865	**-3.05**	0.00075
STM1234,S	trmU	tRNA (5-methylaminomethyl-2-thiouridylate)-	**-1.60**	0.07463	**-0.23**	0.63112	**-2.46**	0.00606
STM1234,S	trmU	tRNA (5-methylaminomethyl-2-thiouridylate)-	**-2.24**	0.04748	**-0.86**	0.02230	**-2.59**	0.00064
STM1235	ymfB	putative MutT-like protein	**-1.24**	0.02803	**-0.76**	0.02099	**-0.73**	0.06609
STM1235	ymfB	putative MutT-like protein	**-0.88**	0.07453	**-0.66**	0.06503	**-1.01**	0.05834
STM1236	STM1236	putative periplasmic protein	**-0.68**	0.13167	**0.66**	0.06013	**-0.08**	0.84222
STM1236	STM1236	putative periplasmic protein	**-0.27**	0.55997	**0.50**	0.12049	**0.49**	0.26965
STM1237	ymfC	putative ribosomal large subunit pseudouridine synthase	**-1.25**	0.04338	**0.09**	0.78751	**0.35**	0.36950
STM1237	ymfC	putative ribosomal large subunit pseudouridine synthase	**0.83**	0.51078	**0.13**	0.77307	**1.73**	0.00430
STM1238	icdA	isocitrate dehydrogenase	**0.32**	0.50178	**1.98**	0.00033	**0.01**	0.99021
STM1238	icdA	isocitrate dehydrogenase	**1.09**	0.10533	**2.11**	0.00033	**0.30**	0.46670
STM1239	STM1239	putative cytoplasmic protein	**-0.41**	0.42933	**-1.14**	0.00628	**-1.13**	0.02259
STM1239	STM1239	putative cytoplasmic protein	**-0.08**	0.87827	**-0.22**	0.46533	**0.20**	0.70420
STM1240	envF	putative envelope lipoprotein	**2.55**	0.00595	**2.59**	0.00034	**3.56**	0.00007
STM1240	envF	putative envelope lipoprotein	**3.87**	0.00512	**1.60**	0.02012	**4.38**	0.00004
STM1241	msgA	macrophage survival protein	**1.32**	0.04762	**1.46**	0.00117	**0.87**	0.06411
STM1241	msgA	macrophage survival protein	**1.97**	0.01338	**1.53**	0.00793	**1.20**	0.01305
STM1242	envE	putative envelope protein	**1.01**	0.16597	**1.33**	0.00266	**-1.21**	0.03497
STM1242	envE	putative envelope protein	**2.02**	0.01336	**0.80**	0.03395	**-0.53**	0.50644
STM1246	pagC	virulence membrane protein PAGC precursor	**2.25**	0.03476	**-0.32**	0.41810	**0.21**	0.74983
STM1246	pagC	virulence membrane protein PAGC precursor	**3.23**	0.00567	**0.09**	0.87638	**0.47**	0.21424
STM1247	-	STM1247	**0.16**	0.88701	**-1.93**	0.00201	**-1.09**	0.20564
STM1247	-	STM1247	**0.81**	0.15411	**-0.71**	0.03494	**-0.60**	0.18270
STM1249	STM1249	putative periplasmic protein	**2.18**	0.01405	**1.65**	0.00556	**1.89**	0.00449
STM1249	STM1249	putative periplasmic protein	**1.94**	0.01686	**1.36**	0.00999	**1.23**	0.04890
STM1250	STM1250	putative cytoplasmic protein	**-0.31**	0.72379	**4.03**	0.00001	**1.02**	0.05310
STM1250	STM1250	putative cytoplasmic protein	**1.85**	0.04021	**4.66**	0.00007	**-0.56**	0.62607
STM1251	STM1251	putative molecular chaperone	**2.56**	0.00822	**2.22**	0.00612	**3.94**	0.00008
STM1251	STM1251	putative molecular chaperone	**2.93**	0.00547	**2.44**	0.00151	**5.00**	0.00002
STM1252	STM1252	putative cytoplasmic protein	**-0.24**	0.69442	**0.06**	0.87217	**-0.90**	0.10467
STM1252	STM1252	putative cytoplasmic protein	**0.76**	0.16872	**-0.10**	0.78795	**-0.33**	0.45390
STM1253	STM1253	putative inner membrane protein	**0.38**	0.44694	**0.51**	0.21874	**-1.08**	0.03795
STM1253	STM1253	putative inner membrane protein	**0.46**	0.45939	**0.16**	0.61565	**-0.37**	0.56263
STM1254	STM1254	putative outer membrane lipoprotein	**1.28**	0.07541	**-0.33**	0.37130	**-1.28**	0.02264
STM1254	STM1254	putative outer membrane lipoprotein	**1.54**	0.02838	**0.40**	0.21470	**-0.81**	0.11620
STM1255	STM1255	putative ABC transporter periplasmic binding protein	**0.48**	0.30354	**0.21**	0.54205	**-0.72**	0.11283
STM1255	STM1255	putative ABC transporter periplasmic binding protein	**1.77**	0.02262	**0.49**	0.20234	**1.21**	0.04578
STM1256	STM1256	putative ABC transporter protein	**0.62**	0.20618	**-0.36**	0.33250	**-0.19**	0.81438
STM1256	STM1256	putative ABC transporter protein	**0.33**	0.62623	**-0.51**	0.21436	**-0.48**	0.45088
STM1257	STM1257	putative ABC transporter protein	**1.32**	0.21088	**-0.17**	0.70369	**-0.73**	0.08855
STM1257	STM1257	putative ABC transporter protein	**-0.10**	0.93065	**-0.51**	0.43613	**0.77**	0.09992
STM1258	STM1258	putative ABC-type transport system ATPase component	**0.72**	0.15198	**1.32**	0.00190	**-0.10**	0.84763
STM1258	STM1258	putative ABC-type transport system ATPase component	**2.47**	0.00719	**0.37**	0.55517	**-0.08**	0.91510
STM1259	STM1259	putative ABC-type transport system ATPase component	**-0.33**	0.60114	**-0.28**	0.45487	**-0.10**	0.86177
STM1259	STM1259	putative ABC-type transport system ATPase component	**0.49**	0.45004	**-0.44**	0.33811	**0.16**	0.79018
STM1260	STM1260	putative inner membrane protein	**1.28**	0.12218	**0.24**	0.43855	**2.51**	0.00167
STM1260	STM1260	putative inner membrane protein	**2.71**	0.00674	**0.68**	0.06102	**3.74**	0.00012
STM1261	STM1261	putative cytoplasmic protein	**0.09**	0.85065	**0.45**	0.16033	**2.05**	0.00053
STM1261	STM1261	putative cytoplasmic protein	**1.02**	0.16661	**0.37**	0.19460	**3.05**	0.00011
STM1262	-	STM1262	**0.01**	0.99034	**1.36**	0.01427	**1.64**	0.03857
STM1262	-	STM1262	**0.85**	0.13564	**1.83**	0.00047	**2.33**	0.00070

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM1263	STM1263	putative periplasmic protein	**-0.49**	0.23895	**0.81**	0.02710	**0.87**	0.04291
STM1263	STM1263	putative periplasmic protein	**-0.12**	0.83757	**-0.40**	0.29806	**1.58**	0.17193
STM1264	aadA	aminoglycoside adenyltransferase	**0.34**	0.44306	**0.30**	0.48722	**-0.39**	0.37601
STM1264	aadA	aminoglycoside adenyltransferase	**1.86**	0.03785	**-0.01**	0.97910	**2.02**	0.07942
STM1265	STM1265	putative response regulator	**0.00**	0.99678	**0.18**	0.52384	**0.46**	0.52618
STM1265	STM1265	putative response regulator	**1.09**	0.05652	**0.24**	0.48493	**0.57**	0.31828
STM1266	STM1266	putative transcriptional regulator	**0.18**	0.66131	**0.25**	0.55604	**0.41**	0.31551
STM1266	STM1266	putative transcriptional regulator	**1.74**	0.02617	**0.55**	0.10179	**0.55**	0.28780
STM1267	STM1267	putative cytoplasmic protein	**-0.61**	0.36105	**0.22**	0.62745	**1.34**	0.02608
STM1267	STM1267	putative cytoplasmic protein	**-0.75**	0.11866	**-0.08**	0.83378	**1.77**	0.00119
STM1268	STM1268	putative cytoplasmic protein	**-0.97**	0.20321	**1.41**	0.00437	**-0.04**	0.95858
STM1268	STM1268	putative cytoplasmic protein	**2.02**	0.06385	**0.64**	0.39981	**0.49**	0.17630
STM1269	STM1269	chorismate mutase	**-0.20**	0.65687	**-0.33**	0.59520	**-0.96**	0.01993
STM1269	STM1269	chorismate mutase	**1.20**	0.32861	**-0.44**	0.22601	**-0.34**	0.65948
STM1270	yeaS	putative transport protein	**-0.19**	0.67397	**2.46**	0.30328	**0.33**	0.49708
STM1270	yeaS	putative transport protein	**-0.29**	0.56553	**-0.25**	0.40398	**-0.65**	0.12855
STM1271	yeaR	putative cytoplasmic protein	**-0.52**	0.29183	**2.31**	0.00020	**-0.07**	0.94774
STM1271	yeaR	putative cytoplasmic protein	**0.28**	0.81117	**2.49**	0.00018	**-0.96**	0.05455
STM1273	STM1273	putative nitric oxide reductase	**1.25**	0.03752	**-0.21**	0.54976	**-0.13**	0.83398
STM1273	STM1273	putative nitric oxide reductase	**2.31**	0.01691	**-0.56**	0.07259	**2.08**	0.01456
STM1273,1n	STM1273,1n	hypothetical protein STM1273,1n	**-0.76**	0.11322	**1.05**	0.00892	**-0.65**	0.16648
STM1273,1n	STM1273,1n	hypothetical protein STM1273,1n	**-0.49**	0.50359	**1.25**	0.00682	**0.49**	0.21359
STM1274	yeaQ	putative inner membrane protein	**0.20**	0.69024	**2.90**	0.00005	**0.76**	0.08879
STM1274	yeaQ	putative inner membrane protein	**1.09**	0.36091	**3.18**	0.00009	**1.56**	0.01254
STM1275	yaoF	putative hemolysin	**0.54**	0.41455	**0.47**	0.18419	**0.03**	0.95374
STM1275	yaoF	putative hemolysin	**1.64**	0.02898	**0.91**	0.03200	**0.80**	0.07226
STM1276	STM1276	putative periplasmic protein	**0.23**	0.80825	**1.19**	0.00401	**-0.83**	0.06642
STM1276	STM1276	putative periplasmic protein	**0.97**	0.05093	**0.91**	0.01386	**-0.38**	0.33404
STM1277	yeaO	putative cytoplasmic protein	**-0.04**	0.94519	**1.43**	0.00414	**-0.49**	0.25715
STM1277	yeaO	putative cytoplasmic protein	**1.21**	0.03748	**1.50**	0.00190	**0.85**	0.07567
STM1278	yeaN	putative amino acid/amine transport protein	**0.18**	0.71609	**0.25**	0.45135	**0.48**	0.52218
STM1278	yeaN	putative amino acid/amine transport protein	**1.01**	0.08843	**0.51**	0.17619	**1.05**	0.20167
STM1279	yeaM	putative regulatory protein	**-0.23**	0.58746	**1.32**	0.00325	**0.31**	0.41205
STM1279	yeaM	putative regulatory protein	**0.22**	0.63876	**0.52**	0.17681	**0.53**	0.37012
STM1280	yeaL	putative inner membrane protein	**-0.53**	0.55837	**-0.58**	0.26544	**-0.11**	0.87393
STM1280	yeaL	putative inner membrane protein	**0.95**	0.13751	**0.24**	0.40613	**-0.06**	0.90427
STM1282	yeaK	putative cytoplasmic protein	**1.48**	0.09689	**0.01**	0.98874	**0.51**	0.46393
STM1282	yeaK	putative cytoplasmic protein	**-0.33**	0.75016	**-1.13**	0.03001	**-2.09**	0.00881
STM1283	yeaJ	putative methyl-accepting chemotaxis protein	**-0.16**	0.83569	**1.06**	0.03559	**-0.87**	0.09237
STM1283	yeaJ	putative methyl-accepting chemotaxis protein	**0.56**	0.27249	**0.62**	0.09599	**0.53**	0.22622
STM1284	yeaH	hypothetical protein STM1284	**4.62**	0.00758	**3.65**	0.00074	**4.77**	0.00004
STM1284	yeaH	hypothetical protein STM1284	**5.57**	0.00512	**2.68**	0.00196	**2.57**	0.00060
STM1285	yeaG	putative serine protein kinase	**-0.04**	0.94487	**3.95**	0.00014	**3.06**	0.00019
STM1285	yeaG	putative serine protein kinase	**1.59**	0.02143	**4.00**	0.00001	**3.58**	0.00012
STM1286	mipA	MltA-interacting protein A	**-2.43**	0.00613	**1.10**	0.01222	**-2.65**	0.00077
STM1286	mipA	MltA-interacting protein A	**-1.41**	0.02499	**1.40**	0.00529	**-2.70**	0.00018
STM1287	STM1287	arylsulfatase regulator	**-0.35**	0.56391	**0.48**	0.18265	**1.16**	0.06180
STM1287	STM1287	arylsulfatase regulator	**-0.65**	0.33297	**-0.48**	0.12496	**-0.21**	0.87206
STM1288	STM1288	putative aldehyde reductase	**-1.28**	0.05655	**-0.13**	0.68812	**0.41**	0.62353
STM1288	STM1288	putative aldehyde reductase	**-0.63**	0.17499	**-0.91**	0.01800	**-0.59**	0.15139
STM1289	yeaD	aldose 1-epimerase	**-1.59**	0.01491	**-0.53**	0.13731	**-1.58**	0.00554
STM1289	yeaD	aldose 1-epimerase	**-1.49**	0.06005	**-0.43**	0.18641	**-1.50**	0.00744
STM1290	gapA	glyceraldehyde-3-phosphate dehydrogenase	**-0.48**	0.74592	**-0.99**	0.08487	**-1.60**	0.03770
STM1290	gapA	glyceraldehyde-3-phosphate dehydrogenase	**-1.99**	0.01630	**-0.57**	0.17197	**-1.69**	0.00461
STM1291	yeaA	methionine sulfoxide reductase B	**-2.35**	0.01394	**0.03**	0.93728	**-1.03**	0.02939
STM1291	yeaA	methionine sulfoxide reductase B	**-0.72**	0.12226	**0.22**	0.58424	**-0.47**	0.26460
STM1292	yeaC	putative cytoplasmic protein	**-1.01**	0.04885	**-0.12**	0.69795	**-1.00**	0.04087
STM1292	yeaC	putative cytoplasmic protein	**-0.51**	0.46682	**-0.08**	0.80873	**-0.25**	0.62270
STM1293	pncA	nicotinamidase/pyrazinamidase	**-0.58**	0.32769	**-1.21**	0.00518	**-1.49**	0.00395
STM1293	pncA	nicotinamidase/pyrazinamidase	**0.07**	0.88427	**-1.37**	0.00125	**-0.71**	0.09115
STM1294	ansA	cytoplasmic asparaginase I	**-2.88**	0.01725	**-1.38**	0.00255	**-2.48**	0.00033
STM1294	ansA	cytoplasmic asparaginase I	**-0.41**	0.33309	**-1.28**	0.00185	**-1.42**	0.00753
STM1295	sppA	protease IV	**-2.16**	0.00747	**-1.36**	0.00536	**-2.78**	0.00019
STM1295	sppA	protease IV	**-1.65**	0.02087	**-1.15**	0.00892	**-2.52**	0.00027
STM1296	ydjA	putative oxidoreductase	**-0.65**	0.17908	**-0.35**	0.27249	**-1.55**	0.00588
STM1296	ydjA	putative oxidoreductase	**-0.16**	0.68653	**-0.51**	0.16615	**-0.53**	0.16114
STM1297	selD	selenophosphate synthetase	**2.56**	0.00678	**-1.27**	0.00437	**-1.74**	0.00788
STM1297	selD	selenophosphate synthetase	**2.99**	0.00541	**-1.71**	0.00160	**-1.25**	0.01145
STM1298	topB	DNA topoisomerase III	**0.96**	0.13716	**-0.67**	0.04596	**1.34**	0.06126
STM1298	topB	DNA topoisomerase III	**1.59**	0.01941	**0.21**	0.46212	**1.46**	0.01775

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM1299	gdhA	glutamate dehydrogenase	**-1.16**	0.04125	**0.73**	0.09836	**-0.97**	0.02288
STM1299	gdhA	glutamate dehydrogenase	**0.37**	0.64897	**0.22**	0.44084	**-1.13**	0.02352
STM1300	STM1300	putative periplasmic protein	**0.68**	0.22375	**-0.54**	0.07852	**-0.98**	0.09479
STM1300	STM1300	putative periplasmic protein	**-0.48**	0.37311	**-0.79**	0.03205	**0.20**	0.59738
STM1301	STM1301	putative mutator protein	**-1.41**	0.03236	**-0.61**	0.05292	**-0.57**	0.14728
STM1301	STM1301	putative mutator protein	**-1.25**	0.08231	**-0.84**	0.01844	**-1.12**	0.04150
STM1302	xthA	exonuclease III	**-0.92**	0.14798	**0.03**	0.94859	**-1.22**	0.01918
STM1302	xthA	exonuclease III	**0.02**	0.97915	**0.30**	0.33309	**-0.44**	0.33425
STM1303	argD	bifunctional	**-0.21**	0.63449	**1.52**	0.00793	**1.63**	0.01201
STM1303	argD	bifunctional	**-0.63**	0.46283	**0.69**	0.06467	**0.66**	0.19531
STM1304	astA	arginine succinyltransferase	**-0.51**	0.41169	**2.21**	0.00085	**1.67**	0.00216
STM1304	astA	arginine succinyltransferase	**0.29**	0.52381	**2.35**	0.00045	**2.74**	0.00041
STM1305	astD	aldehyde dehyrogenase	**-0.10**	0.90813	**1.71**	0.00046	**3.02**	0.00801
STM1305	astD	aldehyde dehyrogenase	**0.97**	0.05140	**2.72**	0.00087	**2.47**	0.00024
STM1306	astB	succinylarginine dihydrolase	**-0.49**	0.45562	**1.42**	0.00152	**1.13**	0.02535
STM1306	astB	succinylarginine dihydrolase	**0.68**	0.43401	**0.82**	0.03531	**1.40**	0.01341
STM1307	astE	succinylglutamate desuccinylase	**-0.79**	0.10350	**0.75**	0.06199	**0.01**	0.97072
STM1307	astE	succinylglutamate desuccinylase	**-0.16**	0.74222	**-0.28**	0.40611	**0.97**	0.02706
STM1308	spy	putative stress response protein	**-0.20**	0.76637	**1.23**	0.01697	**3.65**	0.00033
STM1308	spy	putative stress response protein	**1.72**	0.05543	**1.31**	0.00600	**4.32**	0.00004
STM1309	STM1309	putative excinuclease subunit	**1.51**	0.02219	**1.04**	0.00867	**2.02**	0.00077
STM1309	STM1309	putative excinuclease subunit	**0.81**	0.09959	**0.91**	0.00929	**2.42**	0.00078
STM1310	nadE	NAD(+) synthetase	**-0.85**	0.09059	**2.04**	0.00037	**2.62**	0.00928
STM1310	nadE	NAD(+) synthetase	**0.36**	0.53333	**1.55**	0.00173	**2.37**	0.00032
STM1311	osmE	transcriptional activator	**-0.41**	0.33257	**3.21**	0.00006	**4.96**	0.00002
STM1311	osmE	transcriptional activator	**1.04**	0.29367	**2.66**	0.00044	**5.76**	0.00002
STM1312	celA	sugar-specific enzyme IIB	**-0.08**	0.89868	**-0.18**	0.88334	**1.60**	0.00265
STM1312	celA	sugar-specific enzyme IIB	**0.53**	0.30358	**0.06**	0.84086	**1.35**	0.00976
STM1313	celB	sugar-specific enzyme II	**2.47**	0.00778	**2.00**	0.00024	**4.19**	0.00003
STM1313	celB	sugar-specific enzyme II	**3.03**	0.00719	**1.15**	0.01669	**4.89**	0.00007
STM1314	celC	sugar-specific enzyme III	**-0.23**	0.75846	**1.67**	0.00097	**1.53**	0.00567
STM1314	celC	sugar-specific enzyme III	**0.09**	0.84243	**1.64**	0.00240	**2.31**	0.01217
STM1315	celD	transcriptional repressor of cel operon	**-0.54**	0.40174	**0.47**	0.18164	**0.47**	0.60915
STM1315	celD	transcriptional repressor of cel operon	**0.55**	0.28227	**0.73**	0.03575	**0.20**	0.85369
STM1316	celF	phospho-beta-glucosidase/cellobiose-6-phosphate	**-1.09**	0.09627	**1.84**	0.00044	**-0.28**	0.54985
STM1316	celF	phospho-beta-glucosidase/cellobiose-6-phosphate	**0.48**	0.44127	**1.44**	0.00269	**0.50**	0.18738
STM1317	celG	hypothetical protein STM1317	**0.07**	0.88576	**1.64**	0.00146	**2.74**	0.01190
STM1317	celG	hypothetical protein STM1317	**0.84**	0.40835	**1.37**	0.00199	**2.39**	0.00095
STM1318	katE	hydroperoxidase HPII	**0.23**	0.75196	**0.81**	0.03290	**2.11**	0.00300
STM1318	katE	hydroperoxidase HPII	**1.48**	0.08594	**0.36**	0.40818	**3.11**	0.00156
STM1319	cedA	cell division modulator protein	**-0.13**	0.80322	**0.12**	0.73906	**0.66**	0.10370
STM1319	cedA	cell division modulator protein	**0.46**	0.44109	**0.86**	0.02231	**1.12**	0.02781
STM1320	ydjN	kinase/transporter-like protein	**-0.94**	0.07992	**0.36**	0.29674	**-0.30**	0.52459
STM1320	ydjN	kinase/transporter-like protein	**0.25**	0.57393	**0.91**	0.02585	**0.15**	0.69838
STM1321	ydjM	putative SOS response protein	**-0.44**	0.32454	**0.06**	0.88799	**0.10**	0.79881
STM1321	ydjM	putative SOS response protein	**0.06**	0.94424	**-0.58**	0.24066	**0.35**	0.39676
STM1322	yniC	putative enzyme	**0.23**	0.77906	**0.22**	0.45541	**-0.99**	0.02569
STM1322	yniC	putative enzyme	**0.21**	0.63940	**0.04**	0.88839	**-0.19**	0.66318
STM1323	yniB	putative regulatory protein	**-1.13**	0.04277	**0.26**	0.34173	**-0.13**	0.73110
STM1323	yniB	putative regulatory protein	**-0.83**	0.22043	**0.57**	0.09708	**0.44**	0.23649
STM1324	STM1324	putative cytoplasmic protein	**-1.27**	0.03916	**1.14**	0.01899	**0.85**	0.05880
STM1324	STM1324	putative cytoplasmic protein	**0.79**	0.11724	**1.55**	0.00592	**1.39**	0.00394
STM1325	ydiZ	putative cytoplasmic protein	**-0.41**	0.45317	**1.76**	0.00084	**1.01**	0.02212
STM1325	ydiZ	putative cytoplasmic protein	**0.67**	0.14582	**1.86**	0.00074	**1.89**	0.00243
STM1326	pfkB	6-phosphofructokinase II	**-0.06**	0.92235	**2.05**	0.00027	**2.69**	0.00071
STM1326	pfkB	6-phosphofructokinase II	**-0.37**	0.41466	**2.76**	0.00018	**2.92**	0.00018
STM1327	ydiY	putative outer membrane protein	**-1.49**	0.04399	**-1.27**	0.00495	**-0.91**	0.06535
STM1327	ydiY	putative outer membrane protein	**-1.29**	0.09096	**-1.71**	0.00067	**-1.31**	0.00650
STM1328	STM1328	putative outer membrane protein	**-0.83**	0.17600	**-1.48**	0.00540	**-0.96**	0.03813
STM1328	STM1328	putative outer membrane protein	**-0.09**	0.93333	**-1.35**	0.00478	**-0.37**	0.66335
STM1329	STM1329	putative inner membrane protein	**3.72**	0.00512	**1.86**	0.00876	**4.20**	0.00016
STM1329	STM1329	putative inner membrane protein	**2.18**	0.02367	**0.92**	0.11191	**2.77**	0.00062
STM1330	STM1330	putative DNA/RNA non-specific endonuclease	**0.15**	0.73344	**-0.25**	0.41172	**0.47**	0.31263
STM1330	STM1330	putative DNA/RNA non-specific endonuclease	**1.15**	0.03471	**-1.20**	0.00510	**0.24**	0.63196
STM1332	rfc	O-antigen polymerase	**-1.12**	0.13497	**0.21**	0.63706	**-0.47**	0.29041
STM1332	rfc	O-antigen polymerase	**-0.76**	0.12247	**-0.57**	0.34338	**0.20**	0.67059
STM1333	thrS	threonyl-tRNA synthetase	**-2.47**	0.02031	**-0.13**	0.73357	**-3.38**	0.00011
STM1333	thrS	threonyl-tRNA synthetase	**-1.77**	0.02953	**-0.06**	0.86842	**-3.05**	0.00011
STM1334,c	infC	translation initiation factor IF-3	**-2.87**	0.01523	**0.40**	0.18356	**-4.84**	0.00005
STM1334,c	infC	translation initiation factor IF-3	**-2.53**	0.00869	**0.62**	0.06483	**-4.40**	0.00009

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM1335	rpmI	50S ribosomal protein L35	**-2.50**	0.00876	**0.48**	0.14609	**-4.50**	0.00004
STM1335	rpmI	50S ribosomal protein L35	**-1.38**	0.05591	**0.83**	0.03619	**-4.36**	0.00006
STM1336	rplT	50S ribosomal protein L20	**-2.92**	0.00577	**-1.95**	0.14971	**-4.09**	0.00003
STM1336	rplT	50S ribosomal protein L20	**-0.99**	0.46276	**-0.03**	0.94723	**-3.81**	0.00009
STM1337	pheS	phenylalanyl-tRNA synthetase alpha subunit	**-2.05**	0.01357	**-1.49**	0.00229	**-2.89**	0.00011
STM1337	pheS	phenylalanyl-tRNA synthetase alpha subunit	**-1.82**	0.01079	**-1.54**	0.01870	**-2.72**	0.00083
STM1338	pheT	phenylalanyl-tRNA synthetase beta subunit	**-1.78**	0.01725	**0.23**	0.44994	**-0.37**	0.29127
STM1338	pheT	phenylalanyl-tRNA synthetase beta subunit	**-0.79**	0.09281	**0.50**	0.10840	**0.31**	0.48258
STM1339	himA	integration host factor alpha subunit	**-1.69**	0.02654	**0.70**	0.09666	**0.28**	0.43791
STM1339	himA	integration host factor alpha subunit	**-0.49**	0.34794	**1.16**	0.00710	**0.97**	0.03656
STM1340	btuC	vtamin B12-transporter permease	**-1.45**	0.04561	**-0.95**	0.04506	**-1.10**	0.04524
STM1340	btuC	vtamin B12-transporter permease	**-0.70**	0.21884	**-1.17**	0.00359	**-0.88**	0.02996
STM1341	btuE	vitamin B12 transport protein	**-0.97**	0.14642	**0.71**	0.02453	**0.69**	0.07893
STM1341	btuE	vitamin B12 transport protein	**-0.36**	0.42006	**0.38**	0.33083	**2.07**	0.00197
STM1342	btuD	vitamin B12-transporter ATPase	**-0.66**	0.18601	**0.55**	0.10203	**0.83**	0.04076
STM1342	btuD	vitamin B12-transporter ATPase	**0.68**	0.29666	**0.82**	0.02978	**1.31**	0.03378
STM1343	nlpC	lipoprotein	**-1.35**	0.04799	**0.89**	0.01617	**-0.43**	0.40552
STM1343	nlpC	lipoprotein	**-0.07**	0.87984	**1.24**	0.00467	**0.19**	0.73863
STM1344	ydiV	hypothetical protein STM1344	**-0.24**	0.61730	**0.17**	0.69520	**0.17**	0.73154
STM1344	ydiV	hypothetical protein STM1344	**0.45**	0.35434	**-0.15**	0.62643	**1.05**	0.05011
STM1345	ydiU	hypothetical protein STM1345	**0.90**	0.19914	**1.63**	0.00117	**2.04**	0.01105
STM1345	ydiU	hypothetical protein STM1345	**1.22**	0.08124	**1.00**	0.01547	**1.55**	0.00372
STM1346	ydiE	putative cytoplasmic protein	**0.29**	0.53066	**1.28**	0.00528	**-0.11**	0.79461
STM1346	ydiE	putative cytoplasmic protein	**2.12**	0.04649	**0.87**	0.06217	**-0.48**	0.18312
STM1347	aroH	3-deoxy-7-phosphoheptulonate synthase	**-0.94**	0.15487	**-0.20**	0.46124	**-0.74**	0.14217
STM1347	aroH	3-deoxy-7-phosphoheptulonate synthase	**-0.89**	0.17599	**-0.35**	0.41361	**0.05**	0.90250
STM1348	ydiA	hypothetical protein STM1348	**-0.08**	0.94487	**1.24**	0.00502	**-0.06**	0.89746
STM1348	ydiA	hypothetical protein STM1348	**0.09**	0.90521	**1.36**	0.00839	**0.34**	0.51390
STM1349	pps	phosphoenolpyruvate synthase	**-0.55**	0.47025	**1.29**	0.00467	**0.05**	0.91503
STM1349	pps	phosphoenolpyruvate synthase	**0.58**	0.18462	**1.12**	0.00536	**1.06**	0.02059
STM1350	ydiD	hypothetical protein STM1350	**0.29**	0.56943	**1.04**	0.02528	**-0.22**	0.69105
STM1350	ydiD	hypothetical protein STM1350	**2.88**	0.03916	**1.54**	0.00213	**0.44**	0.53505
STM1351	ydiT	putative ferredoxin	**1.83**	0.04414	**-0.41**	0.30794	**0.04**	0.93297
STM1351	ydiT	putative ferredoxin	**3.63**	0.00541	**-0.30**	0.54822	**1.68**	0.03638
STM1352	ydiS	flavoprotein	**-0.93**	0.12963	**-0.16**	0.76763	**-1.12**	0.14679
STM1352	ydiS	flavoprotein	**0.13**	0.77241	**-0.30**	0.58742	**-1.39**	0.25937
STM1353	ydiR	putative electron transfer flavoprotein subunit alpha	**0.77**	0.46748	**-1.11**	0.19393	**-0.86**	0.10643
STM1353	ydiR	putative electron transfer flavoprotein subunit alpha	**1.56**	0.05502	**-0.43**	0.15039	**0.56**	0.27129
STM1354	ydiQ	putative electron transfer flavoprotein subunit beta	**1.42**	0.02710	**0.38**	0.50156	**0.39**	0.47473
STM1354	ydiQ	putative electron transfer flavoprotein subunit beta	**2.78**	0.00889	**0.14**	0.67477	**1.44**	0.02980
STM1355	ydiP	putative transcriptional regulator	**0.28**	0.52797	**1.49**	0.00610	**0.94**	0.01982
STM1355	ydiP	putative transcriptional regulator	**0.63**	0.21726	**-0.20**	0.72129	**0.04**	0.92467
STM1356	ydiO	crotonobetainyl-CoA dehydrogenase	**-3.11**	0.09819	**-1.81**	0.04267	**-2.88**	0.01767
STM1356	ydiO	crotonobetainyl-CoA dehydrogenase	**0.03**	0.97992	**-4.34**	0.00003	**-2.83**	0.01437
STM1357,S	ydiF	putative acetyl-CoA/acetoacetyl-CoA transferase beta	**0.01**	0.99004	**0.11**	0.69823	**-0.91**	0.13688
STM1357,S	ydiF	putative acetyl-CoA/acetoacetyl-CoA transferase beta	**0.00**	0.99756	**-0.01**	0.97270	**0.85**	0.13399
STM1358	aroD	3-dehydroquinate dehydratase	**-1.00**	0.05579	**0.68**	0.08222	**-1.25**	0.16683
STM1358	aroD	3-dehydroquinate dehydratase	**1.44**	0.12587	**0.18**	0.57535	**-0.15**	0.84242
STM1359	aroE	shikimate 5-dehydrogenase	**0.15**	0.83879	**0.48**	0.17725	**-0.08**	0.87763
STM1359	aroE	shikimate 5-dehydrogenase	**2.28**	0.10387	**0.88**	0.08673	**0.68**	0.44125
STM1360	ydiN	putative transport protein	**1.56**	0.14212	**-0.26**	0.59389	**-0.20**	0.63917
STM1360	ydiN	putative transport protein	**1.78**	0.02991	**-0.68**	0.42724	**0.46**	0.30764
STM1361	ydiM	putative transport protein	**-0.68**	0.17462	**-0.76**	0.26309	**-0.75**	0.12609
STM1361	ydiM	putative transport protein	**1.71**	0.01311	**-1.47**	0.00222	**0.75**	0.09087
STM1362	ydiL	putative cytoplasmic protein	**0.04**	0.97228	**0.81**	0.07005	**0.88**	0.13931
STM1362	ydiL	putative cytoplasmic protein	**1.12**	0.13708	**1.40**	0.08418	**1.23**	0.02453
STM1363	rprA	STM1363	**-0.73**	0.18572	**0.43**	0.73152	**1.31**	0.01193
STM1363	rprA	STM1363	**-0.29**	0.48991	**0.37**	0.50325	**0.62**	0.11226
STM1364	ydiK	putative permease	**1.17**	0.04037	**0.73**	0.03415	**1.70**	0.00512
STM1364	ydiK	putative permease	**2.28**	0.00845	**0.55**	0.07624	**2.31**	0.00092
STM1365	ydiJ	putative oxidase	**-1.64**	0.03112	**0.11**	0.70924	**-1.19**	0.02884
STM1365	ydiJ	putative oxidase	**-1.09**	0.05145	**-0.05**	0.88331	**-0.39**	0.64280
STM1366	STM1366	hypothetical protein STM1366	**-0.79**	0.12349	**0.38**	0.27999	**-1.25**	0.14240
STM1366	STM1366	hypothetical protein STM1366	**0.18**	0.80932	**0.71**	0.03128	**-0.27**	0.46990
STM1367	ydiH	putative cytoplasmic protein	**2.48**	0.37169	**1.29**	0.00226	**1.31**	0.11674
STM1367	ydiH	putative cytoplasmic protein	**0.12**	0.89762	**3.32**	0.01399	**0.85**	0.51772
STM1368	STM1368	putative Na+-dicarboxylate symporter	**-0.38**	0.55963	**-0.05**	0.91173	**-0.60**	0.19008
STM1368	STM1368	putative Na+-dicarboxylate symporter	**0.06**	0.90575	**-0.33**	0.31309	**0.09**	0.87266
STM1369	sufA	iron-sulfur cluster assembly scaffold protein	**0.57**	0.31260	**4.77**	0.00001	**1.31**	0.00449
STM1369	sufA	iron-sulfur cluster assembly scaffold protein	**1.39**	0.03585	**4.89**	0.00001	**2.05**	0.00103

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM1370	sufB	putative ABC transporter protein	**-0.49**	0.33903	**3.26**	0.00005	**0.22**	0.56077
STM1370	sufB	putative ABC transporter protein	**0.39**	0.35181	**4.89**	0.00083	**1.66**	0.00357
STM1371	sufC	putative transport protein	**-0.50**	0.42520	**3.94**	0.00001	**0.97**	0.08588
STM1371	sufC	putative transport protein	**0.91**	0.12491	**4.31**	0.00001	**1.37**	0.01082
STM1372	sufD	cysteine desulfurase modulator	**-0.66**	0.19374	**3.01**	0.00016	**0.54**	0.17932
STM1372	sufD	cysteine desulfurase modulator	**-0.31**	0.45525	**3.60**	0.00002	**0.89**	0.03952
STM1373	sufS	selenocysteine lyase	**0.81**	0.09298	**4.57**	0.00000	**1.39**	0.00954
STM1373	sufS	selenocysteine lyase	**1.64**	0.02109	**4.50**	0.00001	**2.44**	0.00208
STM1374	ynhA	cysteine desufuration protein SufE	**0.28**	0.78890	**2.98**	0.00006	**0.82**	0.06840
STM1374	ynhA	cysteine desufuration protein SufE	**0.28**	0.56699	**3.06**	0.00003	**1.05**	0.02387
STM1375	ynhG	hypothetical protein STM1375	**-1.73**	0.01878	**-0.47**	0.20601	**0.14**	0.73607
STM1375	ynhG	hypothetical protein STM1375	**-1.05**	0.07388	**0.21**	0.54275	**0.39**	0.32036
STM1376	lppB	putative methyl-accepting chemotaxis protein	**-2.78**	0.02659	**-2.17**	0.00023	**-1.12**	0.08642
STM1376	lppB	putative methyl-accepting chemotaxis protein	**-2.27**	0.01417	**-1.68**	0.00140	**-0.81**	0.09541
STM1377	lpp	murein lipoprotein	**-3.96**	0.00627	**-0.86**	0.12941	**-2.54**	0.00085
STM1377	lpp	murein lipoprotein	**-3.43**	0.00541	**-0.98**	0.02356	**-2.19**	0.00059
STM1378	pykF	pyruvate kinase	**-3.38**	0.00613	**-0.83**	0.03403	**-1.50**	0.00493
STM1378	pykF	pyruvate kinase	**-2.48**	0.00778	**-0.47**	0.11784	**-0.98**	0.01884
STM1379	orf48	putative amino acid permease	**-0.91**	0.25025	**-0.52**	0.31257	**-0.13**	0.78781
STM1379	orf48	putative amino acid permease	**0.20**	0.86605	**-1.37**	0.00556	**-0.84**	0.29650
STM1380	orf32	putative proline iminopeptidase	**-0.41**	0.37503	**-1.21**	0.14355	**1.03**	0.12537
STM1380	orf32	putative proline iminopeptidase	**-0.79**	0.12063	**0.09**	0.81029	**-0.72**	0.10580
STM1381	orf245	putative cytoplasmic protein	**1.94**	0.09625	**-0.49**	0.42867	**3.90**	0.00025
STM1381	orf245	putative cytoplasmic protein	**1.83**	0.27822	**-0.14**	0.71610	**1.58**	0.01819
STM1382	orf408	putative regulatory protein	**-0.90**	0.08440	**0.64**	0.43604	**-0.40**	0.60680
STM1382	orf408	putative regulatory protein	**-0.90**	0.22468	**-0.52**	0.20693	**0.32**	0.36301
STM1383	ttrA	tetrathionate reductase complex subunit A	**-0.35**	0.61544	**-1.54**	0.04038	**-0.93**	0.19406
STM1383	ttrA	tetrathionate reductase complex subunit A	**0.45**	0.55942	**-1.36**	0.00399	**-0.52**	0.37373
STM1384	ttrC	tetrathionate reductase complex subunit C	**0.05**	0.90910	**0.30**	0.32596	**1.10**	0.01942
STM1384	ttrC	tetrathionate reductase complex subunit C	**0.25**	0.71361	**-0.55**	0.43017	**0.19**	0.87319
STM1385	ttrB	tetrathionate reductase complex subunit B	**-0.78**	0.17300	**-0.33**	0.63124	**1.14**	0.05316
STM1385	ttrB	tetrathionate reductase complex subunit B	**0.19**	0.76190	**-1.26**	0.00994	**0.06**	0.89137
STM1386	ttrS	sensory histidine kinase	**0.69**	0.36618	**0.00**	0.99977	**0.37**	0.64149
STM1386	ttrS	sensory histidine kinase	**-0.41**	0.64683	**-1.27**	0.03153	**-0.31**	0.39613
STM1387	ttrR	response regulator	**-0.68**	0.19975	**0.79**	0.02497	**1.07**	0.02411
STM1387	ttrR	response regulator	**0.14**	0.82161	**1.03**	0.01894	**1.84**	0.00213
STM1388	orf70	putative cytoplasmic protein	**-1.36**	0.03420	**0.61**	0.09802	**0.06**	0.90284
STM1388	orf70	putative cytoplasmic protein	**-0.67**	0.13712	**0.24**	0.48035	**0.67**	0.07723
STM1389	orf319	putative inner membrane protein	**-0.30**	0.78300	**0.80**	0.02321	**1.77**	0.00542
STM1389	orf319	putative inner membrane protein	**-1.62**	0.11017	**0.89**	0.06663	**2.03**	0.00744
STM1390	orf242	putative regulatory protein	**0.03**	0.95648	**1.60**	0.00249	**0.45**	0.35141
STM1390	orf242	putative regulatory protein	**1.02**	0.04702	**1.16**	0.01870	**1.98**	0.00186
STM1391	ssrB	transcriptional activator	**1.13**	0.11425	**3.15**	0.00020	**0.33**	0.65164
STM1391	ssrB	transcriptional activator	**1.14**	0.08076	**3.76**	0.00002	**-0.12**	0.86177
STM1392	ssrA	sensor kinase	**1.15**	0.28308	**1.90**	0.00151	**1.00**	0.21279
STM1392	ssrA	sensor kinase	**2.72**	0.01686	**1.31**	0.03140	**2.90**	0.00688
STM1394	ssaC	outer membrane secretin precursor	**0.86**	0.28849	**5.69**	0.00001	**0.98**	0.06077
STM1394	ssaC	outer membrane secretin precursor	**1.47**	0.08825	**5.86**	0.00001	**1.57**	0.00516
STM1395	ssaD	virulence protein	**1.26**	0.11839	**6.25**	0.00000	**0.84**	0.33994
STM1395	ssaD	virulence protein	**1.19**	0.05754	**7.17**	0.00000	**0.12**	0.87683
STM1396	ssaE	secretion system effector	**0.66**	0.45642	**7.15**	0.00000	**1.04**	0.18380
STM1396	ssaE	secretion system effector	**1.47**	0.03584	**6.48**	0.00000	**0.85**	0.06779
STM1398	sseB	translocation machinery component	**2.89**	0.01428	**9.16**	0.00000	**-0.12**	0.84857
STM1398	sseB	translocation machinery component	**2.92**	0.01580	**8.63**	0.00000	**-1.04**	0.33661
STM1399	sscA	secretion system chaparone	**3.16**	0.01072	**9.45**	0.00000	**1.49**	0.04008
STM1399	sscA	secretion system chaparone	**4.21**	0.00512	**8.99**	0.00000	**2.61**	0.00201
STM1400	sseC	translocation machinery component	**1.21**	0.07710	**6.94**	0.00000	**-0.48**	0.51383
STM1400	sseC	translocation machinery component	**2.48**	0.00686	**7.51**	0.00001	**1.64**	0.00444
STM1401	sseD	translocation machinery component	**1.98**	0.01634	**6.25**	0.00000	**0.13**	0.90484
STM1401	sseD	translocation machinery component	**2.47**	0.01424	**7.06**	0.00000	**1.24**	0.29438
STM1402	sseE	secreted effector protein	**2.39**	0.00776	**7.54**	0.00000	**0.83**	0.18923
STM1402	sseE	secreted effector protein	**3.51**	0.00546	**6.56**	0.00001	**1.48**	0.00887
STM1403	sscB	secretion system chaparone	**1.68**	0.03822	**5.56**	0.00001	**0.37**	0.58493
STM1403	sscB	secretion system chaparone	**2.46**	0.00727	**5.64**	0.00001	**1.07**	0.08950
STM1404	sseF	secreted effector protein	**-0.34**	0.42972	**3.70**	0.00008	**-0.78**	0.21389
STM1404	sseF	secreted effector protein	**1.36**	0.02148	**3.60**	0.00007	**0.88**	0.51138
STM1405	sseG	secreted effector protein	**-0.02**	0.97778	**3.41**	0.00058	**0.08**	0.83418
STM1405	sseG	secreted effector protein	**1.31**	0.18196	**3.76**	0.00006	**0.88**	0.17308
STM1406	ssaG	type III secretion system apparatus protein	**1.44**	0.03572	**6.29**	0.00000	**0.21**	0.60482
STM1406	ssaG	type III secretion system apparatus protein	**2.33**	0.01595	**6.49**	0.00001	**1.05**	0.16484

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM1407	ssaH	type III secretion system apparatus protein	**0.81**	0.18888	**7.19**	0.00000	**-0.93**	0.11788
STM1407	ssaH	type III secretion system apparatus protein	**1.52**	0.04437	**7.53**	0.00000	**-0.27**	0.69196
STM1408	ssaI	type III secretion system apparatus protein	**1.58**	0.06552	**8.44**	0.00000	**-0.80**	0.09562
STM1408	ssaI	type III secretion system apparatus protein	**2.70**	0.00845	**7.85**	0.00000	**1.09**	0.12342
STM1409	ssaJ	needle complex inner membrane lipoprotein	**1.40**	0.10224	**7.34**	0.00000	**0.18**	0.75170
STM1409	ssaJ	needle complex inner membrane lipoprotein	**2.82**	0.00566	**7.63**	0.00000	**1.35**	0.00805
STM1410	STM1410	putative cytoplasmic protein	**1.65**	0.32110	**5.98**	0.00001	**1.22**	0.06740
STM1410	STM1410	putative cytoplasmic protein	**0.91**	0.30790	**6.04**	0.00207	**-0.53**	0.44620
STM1411	ssaK	type III secretion system apparatus protein	**-0.33**	0.61449	**6.06**	0.00001	**0.71**	0.15533
STM1411	ssaK	type III secretion system apparatus protein	**1.63**	0.02124	**6.84**	0.00000	**1.35**	0.02821
STM1412	ssaL	type III secretion system apparatus protein	**1.16**	0.04183	**7.55**	0.00000	**-0.55**	0.54480
STM1412	ssaL	type III secretion system apparatus protein	**2.57**	0.02000	**7.48**	0.00000	**-0.14**	0.87683
STM1413	ssaM	type III secretion system apparatus protein	**1.04**	0.08899	**5.82**	0.00000	**2.04**	0.00057
STM1413	ssaM	type III secretion system apparatus protein	**0.67**	0.16275	**6.11**	0.00000	**1.98**	0.00138
STM1414	ssaV	type III secretion system apparatus protein	**-0.22**	0.82541	**4.84**	0.00002	**-1.00**	0.29981
STM1414	ssaV	type III secretion system apparatus protein	**2.86**	0.02908	**5.74**	0.00000	**0.10**	0.87781
STM1415	ssaN	type III secretion system ATPase	**-0.47**	0.44016	**5.30**	0.00000	**-1.14**	0.12417
STM1415	ssaN	type III secretion system ATPase	**1.35**	0.04999	**6.13**	0.00000	**0.45**	0.55236
STM1416	ssaO	type III secretion system apparatus protein	**-0.37**	0.52554	**5.54**	0.00001	**0.60**	0.13250
STM1416	ssaO	type III secretion system apparatus protein	**-0.40**	0.43816	**5.76**	0.00001	**0.78**	0.30262
STM1417	ssaP	type III secretion system apparatus protein	**-0.74**	0.21542	**4.15**	0.00007	**-0.19**	0.74372
STM1417	ssaP	type III secretion system apparatus protein	**0.13**	0.82672	**4.33**	0.00001	**-1.57**	0.10194
STM1418	ssaQ	type III secretion protein	**-0.15**	0.71442	**5.16**	0.00001	**-0.98**	0.26312
STM1418	ssaQ	type III secretion protein	**0.92**	0.30734	**5.18**	0.00001	**0.84**	0.05181
STM1419	ssaR	needle complex export protein	**2.59**	0.12157	**5.31**	0.00001	**0.95**	0.18394
STM1419	ssaR	needle complex export protein	**3.01**	0.17156	**5.57**	0.00001	**1.39**	0.35185
STM1421	ssaT	type III secretion system apparatus protein	**0.68**	0.38952	**3.92**	0.00002	**0.79**	0.34671
STM1421	ssaT	type III secretion system apparatus protein	**0.60**	0.45331	**4.22**	0.00002	**0.60**	0.20802
STM1422	ssaU	type III secretion system apparatus protein	**-1.39**	0.05278	**1.70**	0.00170	**-0.55**	0.20621
STM1422	ssaU	type III secretion system apparatus protein	**-0.90**	0.25983	**1.67**	0.00325	**0.11**	0.84838
STM1423	valW	STM1423	**0.33**	0.52554	**-1.05**	0.01963	**0.23**	0.62904
STM1423	valW	STM1423	**0.46**	0.40701	**-0.67**	0.18357	**1.14**	0.05041
STM1424	valV	STM1424	**-0.87**	0.25983	**-0.58**	0.45914	**-0.39**	0.57706
STM1424	valV	STM1424	**-0.77**	0.26216	**-0.76**	0.05832	**-0.21**	0.75098
STM1425	ydhE	multidrug efflux protein NorA	**-1.47**	0.02080	**0.33**	0.28023	**-0.42**	0.26434
STM1425	ydhE	multidrug efflux protein NorA	**-1.32**	0.07431	**0.23**	0.45514	**-0.39**	0.84249
STM1426	ribE	riboflavin synthase subunit alpha	**-0.29**	0.47428	**0.03**	0.92002	**-0.41**	0.34527
STM1426	ribE	riboflavin synthase subunit alpha	**0.03**	0.96815	**0.29**	0.46795	**0.15**	0.79610
STM1427	cfa	cyclopropane fatty acyl phospholipid synthase	**-0.29**	0.66164	**0.06**	0.87217	**0.84**	0.03182
STM1427	cfa	cyclopropane fatty acyl phospholipid synthase	**-0.82**	0.10156	**0.59**	0.06166	**0.93**	0.02509
STM1428	ydhC	putative transport protein	**-1.68**	0.01894	**-1.12**	0.00521	**-0.28**	0.53219
STM1428	ydhC	putative transport protein	**1.23**	0.34362	**0.00**	0.99850	**2.10**	0.10743
STM1429	ydhB	putative transcriptional regulator	**-0.65**	0.22696	**-0.50**	0.31693	**-0.53**	0.40769
STM1429	ydhB	putative transcriptional regulator	**-0.74**	0.14685	**-0.26**	0.51501	**-0.19**	0.70707
STM1430	purR	pur regulon transcriptional repressor	**-1.05**	0.11951	**-0.57**	0.06662	**-0.12**	0.75912
STM1430	purR	pur regulon transcriptional repressor	**-0.93**	0.24529	**-0.19**	0.50383	**-1.10**	0.02175
STM1431	sodB	superoxide dismutase	**-0.77**	0.10974	**-0.58**	0.07986	**-1.98**	0.00395
STM1431	sodB	superoxide dismutase	**-0.53**	0.22279	**-0.62**	0.10859	**-1.50**	0.01003
STM1432	ydhO	putative cell wall-associated hydrolase	**-0.62**	0.32370	**-0.11**	0.78795	**-1.99**	0.00750
STM1432	ydhO	putative cell wall-associated hydrolase	**0.19**	0.63316	**-0.09**	0.81278	**-1.10**	0.02077
STM1433	ydhD	putative glutaredoxin protein	**-1.61**	0.08203	**-0.50**	0.13788	**-1.64**	0.02855
STM1433	ydhD	putative glutaredoxin protein	**1.36**	0.61146	**-0.77**	0.03379	**-2.35**	0.00360
STM1434	rnt	ribonuclease T	**-1.16**	0.05312	**-0.72**	0.02418	**-2.34**	0.00419
STM1434	rnt	ribonuclease T	**-0.49**	0.26894	**-0.27**	0.36110	**-1.54**	0.02284
STM1435	gloA	glyoxalase I	**-0.64**	0.16086	**0.74**	0.04507	**0.03**	0.93511
STM1435	gloA	glyoxalase I	**-0.45**	0.43816	**0.48**	0.20475	**0.72**	0.09560
STM1436	nemA	N-ethylmaleimide reductase	**-0.90**	0.10477	**-0.44**	0.17897	**-1.81**	0.00271
STM1436	nemA	N-ethylmaleimide reductase	**-1.18**	0.07418	**-1.06**	0.01951	**-1.06**	0.02181
STM1437	ydhM	putative transcriptional repressor	**-2.34**	0.00673	**-1.51**	0.00301	**-1.11**	0.01590
STM1437	ydhM	putative transcriptional repressor	**-1.25**	0.11484	**-1.58**	0.00222	**-1.46**	0.00500
STM1438	ydhL	putative oxidoreductase	**-1.79**	0.02538	**0.29**	0.80561	**0.74**	0.06851
STM1438	ydhL	putative oxidoreductase	**0.46**	0.68087	**-0.56**	0.11296	**-1.87**	0.08222
STM1439	ydhF	putative aldo/keto reductase	**-1.66**	0.04245	**-0.68**	0.02724	**0.47**	0.24881
STM1439	ydhF	putative aldo/keto reductase	**-2.12**	0.00757	**-0.74**	0.04217	**-0.11**	0.76981
STM1440	sodC	copper/zinc superoxide dismutase	**-0.49**	0.28018	**0.95**	0.02075	**2.50**	0.00090
STM1440	sodC	copper/zinc superoxide dismutase	**-0.39**	0.46700	**1.33**	0.00358	**3.03**	0.00047
STM1441	STM1441	putative inner membrane protein	**-0.76**	0.19443	**2.41**	0.00046	**2.85**	0.00018
STM1441	STM1441	putative inner membrane protein	**-0.13**	0.82222	**2.58**	0.00015	**3.26**	0.00010
STM1442	ydhJ	putative multidrug resistance efflux pump	**-0.58**	0.30358	**-0.57**	0.13092	**-1.12**	0.01116
STM1442	ydhJ	putative multidrug resistance efflux pump	**-0.24**	0.57902	**-1.22**	0.00700	**-0.13**	0.76211

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM1444	slyA	transcriptional regulator SlyA	**-0.53**	0.41661	**0.26**	0.42635	**-0.29**	0.42598
STM1444	slyA	transcriptional regulator SlyA	**-0.32**	0.55908	**0.47**	0.13041	**-0.06**	0.91445
STM1445	slyB	putative outer membrane lipoprotein	**-0.66**	0.42811	**0.91**	0.02157	**0.88**	0.03622
STM1445	slyB	putative outer membrane lipoprotein	**-0.09**	0.93129	**0.60**	0.06221	**1.48**	0.00236
STM1446	ydhH	putative cytoplasmic protein	**-1.70**	0.03047	**-0.30**	0.49991	**-0.43**	0.45192
STM1446	ydhH	putative cytoplasmic protein	**-0.21**	0.67685	**-0.38**	0.61316	**0.06**	0.92298
STM1447	ydhA	putative outer membrane lipoprotein	**-0.03**	0.96020	**-0.30**	0.28657	**-0.87**	0.06475
STM1447	ydhA	putative outer membrane lipoprotein	**-0.13**	0.78367	**0.13**	0.68229	**-0.09**	0.87084
STM1448	pdxH	pyridoxamine 5'-phosphate oxidase	**-2.79**	0.00627	**-1.49**	0.00091	**-2.93**	0.00042
STM1448	pdxH	pyridoxamine 5'-phosphate oxidase	**-0.47**	0.61745	**-1.15**	0.00610	**-3.78**	0.00018
STM1449	tyrS	tyrosyl-tRNA synthetase	**0.79**	0.63473	**-0.68**	0.04262	**-1.31**	0.00507
STM1449	tyrS	tyrosyl-tRNA synthetase	**0.28**	0.68617	**-1.03**	0.00517	**-1.15**	0.03917
STM1450	pdxY	pyridoxine kinase	**0.47**	0.31499	**0.12**	0.69896	**-0.65**	0.35949
STM1450	pdxY	pyridoxine kinase	**0.87**	0.09801	**-0.30**	0.27006	**-0.60**	0.34818
STM1451	gst	glutathionine S-transferase	**-0.80**	0.09058	**0.57**	0.12559	**-0.90**	0.05849
STM1451	gst	glutathionine S-transferase	**-3.03**	0.04587	**1.13**	0.00813	**-0.07**	0.87159
STM1452	ydgR	putative peptide transport protein	**-0.21**	0.64359	**0.55**	0.11054	**-1.93**	0.00412
STM1452	ydgR	putative peptide transport protein	**0.55**	0.29302	**0.38**	0.26641	**-0.96**	0.02045
STM1453	nth	endonuclease III	**-0.79**	0.28425	**-0.07**	0.91278	**-0.01**	0.98922
STM1453	nth	endonuclease III	**-0.58**	0.34358	**-1.23**	0.00695	**-2.99**	0.00257
STM1454	ydgQ	NADH-ubiquinone oxidoreductase	**-1.70**	0.01467	**-0.36**	0.25651	**-1.46**	0.05894
STM1454	ydgQ	NADH-ubiquinone oxidoreductase	**-0.57**	0.33377	**-1.13**	0.00433	**-1.10**	0.09600
STM1455	ydgP	electron transport complex protein RnfG	**-0.03**	0.94995	**-0.58**	0.10407	**-1.38**	0.00451
STM1455	ydgP	electron transport complex protein RnfG	**0.94**	0.07241	**-0.54**	0.10608	**-0.71**	0.26973
STM1456	rnfD	electron transport complex protein RnfD	**-1.35**	0.05496	**-1.49**	0.08128	**-1.40**	0.03643
STM1456	rnfD	electron transport complex protein RnfD	**-0.45**	0.27113	**-1.07**	0.01994	**-2.45**	0.00027
STM1457	STM1457	electron transport complex protein RnfC	**-0.76**	0.13758	**-0.63**	0.09013	**-1.97**	0.00223
STM1457	STM1457	electron transport complex protein RnfC	**-1.45**	0.03015	**-0.84**	0.01707	**-1.24**	0.01522
STM1458	ydgM	electron transport complex protein RnfB	**-1.75**	0.01740	**-0.08**	0.77559	**-1.52**	0.17762
STM1458	ydgM	electron transport complex protein RnfB	**-0.55**	0.48181	**-0.15**	0.69024	**-0.86**	0.21737
STM1459	STM1459	Na(+)-translocating NADH-quinone reductase subunit E	**-1.57**	0.01982	**-0.63**	0.09908	**-1.62**	0.04377
STM1459	STM1459	Na(+)-translocating NADH-quinone reductase subunit E	**-0.74**	0.26629	**-0.33**	0.33256	**-1.66**	0.01837
STM1460	ydgK	putative inner membrane protein	**-1.05**	0.21054	**0.03**	0.95356	**-1.51**	0.03021
STM1460	ydgK	putative inner membrane protein	**-0.31**	0.60292	**0.27**	0.51093	**-2.25**	0.01328
STM1461,S	ydgT	putative cytoplasmic protein	**-1.20**	0.03228	**-0.02**	0.95179	**-1.96**	0.00406
STM1461,S	ydgT	putative cytoplasmic protein	**-0.07**	0.87330	**0.22**	0.43092	**-1.86**	0.01473
STM1462,S	ydgJ	putative oxidoreductase	**-1.24**	0.04260	**-0.01**	0.98336	**-0.29**	0.47996
STM1462,S	ydgJ	putative oxidoreductase	**0.78**	0.24861	**-0.17**	0.56399	**-0.24**	0.52137
STM1463	add	adenosine deaminase	**-1.32**	0.02344	**-0.41**	0.30992	**-1.03**	0.10508
STM1463	add	adenosine deaminase	**-0.19**	0.63124	**-0.43**	0.27345	**-0.55**	0.33884
STM1466	ydgA	putative periplasmic protein	**-2.30**	0.00753	**-1.56**	0.00086	**-1.08**	0.02292
STM1466	ydgA	putative periplasmic protein	**-2.11**	0.02070	**-1.49**	0.00150	**-0.71**	0.31251
STM1467	manA	mannose-6-phosphate isomerase	**-0.89**	0.12290	**-1.55**	0.00169	**-1.35**	0.00585
STM1467	manA	mannose-6-phosphate isomerase	**-0.66**	0.16839	**-1.13**	0.01191	**-0.98**	0.04561
STM1468	fumA	fumarase A	**-1.94**	0.01028	**-0.28**	0.38561	**-0.90**	0.08894
STM1468	fumA	fumarase A	**-1.58**	0.20668	**0.03**	0.93816	**-0.84**	0.09820
STM1469	fumC	fumarate hydratase	**0.47**	0.61733	**0.76**	0.03126	**1.80**	0.03915
STM1469	fumC	fumarate hydratase	**0.83**	0.21671	**0.99**	0.05137	**1.40**	0.00732
STM1470	tus	DNA replication terminus site-binding protein	**-0.41**	0.41886	**0.68**	0.09170	**1.21**	0.02188
STM1470	tus	DNA replication terminus site-binding protein	**-0.67**	0.24318	**0.68**	0.05087	**1.24**	0.01376
STM1471	rstB	sensory histidine kinase	**-0.26**	0.74562	**-0.97**	0.02041	**-0.75**	0.24340
STM1471	rstB	sensory histidine kinase	**1.84**	0.07008	**-1.67**	0.00301	**0.38**	0.59894
STM1472	STM1472	putative periplasmic protein	**-1.84**	0.10079	**-0.52**	0.26988	**-0.02**	0.96982
STM1472	STM1472	putative periplasmic protein	**-0.25**	0.72148	**-0.03**	0.95323	**0.89**	0.03121
STM1473	ompN	outer membrane protein N precursor	**-2.18**	0.07451	**-1.84**	0.00623	**-1.20**	0.26322
STM1473	ompN	outer membrane protein N precursor	**-1.83**	0.10628	**-2.10**	0.00650	**-2.42**	0.01510
STM1475	rstA	response regulator	**-1.75**	0.01217	**-0.86**	0.01807	**-1.58**	0.00554
STM1475	rstA	response regulator	**-1.17**	0.04102	**-0.93**	0.01262	**-2.40**	0.00058
STM1476	ydgC	putative inner membrane protein	**-1.16**	0.03111	**-1.05**	0.01654	**-1.09**	0.09531
STM1476	ydgC	putative inner membrane protein	**0.34**	0.51716	**-1.08**	0.04089	**-0.53**	0.19903
STM1477	ydgI	putative amino acid transporter	**-0.59**	0.33321	**-0.70**	0.13969	**-0.03**	0.94551
STM1477	ydgI	putative amino acid transporter	**0.63**	0.26164	**-1.11**	0.01547	**-0.46**	0.22307
STM1478	ydgH	putative periplasmic protein	**-3.13**	0.00778	**-1.43**	0.00145	**-2.56**	0.00094
STM1478	ydgH	putative periplasmic protein	**-1.73**	0.07314	**-1.47**	0.00190	**-3.29**	0.00026
STM1479	pntA	NAD(P) transhydrogenase subunit alpha	**-2.02**	0.01146	**-0.37**	0.46994	**-1.52**	0.00254
STM1479	pntA	NAD(P) transhydrogenase subunit alpha	**-1.65**	0.02339	**-0.89**	0.02204	**-1.40**	0.01876
STM1480	pntB	pyridine nucleotide transhydrogenase	**-1.21**	0.13754	**0.15**	0.65688	**-0.52**	0.15139
STM1480	pntB	pyridine nucleotide transhydrogenase	**-0.81**	0.19313	**-0.23**	0.52151	**-0.05**	0.93414
STM1481	STM1481	putative transport protein	**0.18**	0.65232	**0.40**	0.36312	**-1.13**	0.07707
STM1481	STM1481	putative transport protein	**0.45**	0.39805	**0.12**	0.69904	**-0.38**	0.49775

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM1482	ydgF	putative cationic transporter	**-0.41**	0.56254	**0.63**	0.12500	**0.16**	0.77436
STM1482	ydgF	putative cationic transporter	**-0.11**	0.84760	**0.10**	0.75143	**0.54**	0.23194
STM1483	ydgE	putative cationic transporter	**-0.86**	0.15118	**1.09**	0.03021	**-0.34**	0.54263
STM1483	ydgE	putative cationic transporter	**0.27**	0.69063	**0.63**	0.09080	**-0.74**	0.12609
STM1484	STM1484	putative protease	**0.14**	0.78379	**0.32**	0.48171	**0.33**	0.36724
STM1484	STM1484	putative protease	**-0.45**	0.43508	**-0.06**	0.88944	**-1.58**	0.00328
STM1486	ynfM	putative transport protein	**0.41**	0.50483	**-0.89**	0.03061	**1.61**	0.00539
STM1486	ynfM	putative transport protein	**2.72**	0.14463	**-1.12**	0.07138	**2.41**	0.00024
STM1487	ynfL	putative transcriptional regulator	**-0.44**	0.46239	**0.05**	0.93083	**0.32**	0.48128
STM1487	ynfL	putative transcriptional regulator	**0.86**	0.08266	**0.22**	0.45674	**2.39**	0.00033
STM1488	mlc	pts operon transcriptional repressor	**-0.33**	0.63291	**0.05**	0.89030	**-0.64**	0.12410
STM1488	mlc	pts operon transcriptional repressor	**-0.61**	0.56239	**-1.23**	0.02289	**-1.32**	0.00922
STM1489	bioD	dithiobiotin synthetase	**-0.90**	0.08416	**-0.31**	0.47398	**0.72**	0.49222
STM1489	bioD	dithiobiotin synthetase	**0.10**	0.83951	**-0.03**	0.92361	**0.57**	0.19111
STM1490	STM1490	putative voltage-gated ClC-type chloride channel ClcB	**0.26**	0.52154	**0.34**	0.34555	**0.51**	0.41186
STM1490	STM1490	putative voltage-gated ClC-type chloride channel ClcB	**0.62**	0.21597	**0.07**	0.86096	**1.07**	0.05049
STM1491	STM1491	proline/glycine betaine transport systems	**0.11**	0.86966	**0.88**	0.02239	**0.61**	0.16687
STM1491	STM1491	proline/glycine betaine transport systems	**0.19**	0.76187	**0.01**	0.98144	**0.72**	0.12430
STM1492	STM1492	putative ABC transporter permease component	**0.16**	0.78750	**0.53**	0.25302	**0.99**	0.05715
STM1492	STM1492	putative ABC transporter permease component	**-0.43**	0.39937	**0.40**	0.18483	**1.28**	0.07454
STM1493	STM1493	putative ABC transporter periplasmic component	**0.72**	0.16697	**1.24**	0.01108	**1.83**	0.00257
STM1493	STM1493	putative ABC transporter periplasmic component	**1.21**	0.10897	**0.58**	0.21848	**2.43**	0.00024
STM1494	STM1494	putative transport system permease component	**-0.19**	0.72634	**1.01**	0.02096	**0.94**	0.03519
STM1494	STM1494	putative transport system permease component	**0.38**	0.39345	**0.58**	0.34288	**1.54**	0.01236
STM1495	ynfI	putative anaerobic dehydrogenase component	**-0.70**	0.35232	**0.07**	0.85557	**0.80**	0.16547
STM1495	ynfI	putative anaerobic dehydrogenase component	**-0.73**	0.15588	**0.61**	0.12328	**-0.64**	0.25218
STM1496	STM1496	putative dimethylsulfoxide reductase	**-0.75**	0.13717	**0.16**	0.70261	**-1.37**	0.00930
STM1496	STM1496	putative dimethylsulfoxide reductase	**-0.65**	0.16295	**0.16**	0.64391	**-1.00**	0.02990
STM1497	STM1497	putative dimethyl sulphoxide reductase	**1.61**	0.10808	**0.56**	0.34094	**0.45**	0.42975
STM1497	STM1497	putative dimethyl sulphoxide reductase	**2.05**	0.01067	**-0.34**	0.58788	**0.51**	0.77850
STM1498	STM1498	putative dimethyl sulphoxide reductase	**0.68**	0.12455	**-0.36**	0.46396	**-0.40**	0.49035
STM1498	STM1498	putative dimethyl sulphoxide reductase	**1.54**	0.05178	**-0.64**	0.12696	**0.85**	0.40178
STM1499	STM1499	putative dimethyl sulphoxide reductase chain A1	**4.09**	0.00796	**0.50**	0.15826	**1.45**	0.05807
STM1499	STM1499	putative dimethyl sulphoxide reductase chain A1	**3.96**	0.06602	**0.07**	0.93816	**1.39**	0.37065
STM1500	ynfD	putative outer membrane protein	**-0.48**	0.52691	**0.57**	0.08393	**0.82**	0.05871
STM1500	ynfD	putative outer membrane protein	**0.65**	0.54784	**0.26**	0.55810	**1.68**	0.00453
STM1501	ynfC	hypothetical protein STM1501	**-0.39**	0.35668	**-0.22**	0.50703	**-0.55**	0.13876
STM1501	ynfC	hypothetical protein STM1501	**-0.52**	0.36796	**-0.46**	0.15006	**-1.02**	0.04461
STM1502	speG	spermidine N1-acetyltransferase	**-0.60**	0.37359	**0.25**	0.49269	**-1.12**	0.00925
STM1502	speG	spermidine N1-acetyltransferase	**-0.52**	0.36902	**0.19**	0.60797	**-0.61**	0.31551
STM1503	ynfB	putative periplasmic protein	**-0.75**	0.30739	**-0.25**	0.49971	**-2.32**	0.00061
STM1503	ynfB	putative periplasmic protein	**-0.44**	0.38764	**0.28**	0.43255	**-1.72**	0.00344
STM1504	ynfA	hypothetical protein STM1504	**-0.31**	0.48660	**-1.08**	0.02060	**-1.00**	0.08388
STM1504	ynfA	hypothetical protein STM1504	**0.14**	0.77240	**-1.19**	0.01474	**-0.78**	0.20117
STM1505	rspA	putative dehydratase	**-0.45**	0.40268	**0.92**	0.04869	**-1.41**	0.01352
STM1505	rspA	putative dehydratase	**0.59**	0.21555	**1.28**	0.02012	**0.48**	0.23360
STM1506	rspB	putative dehydrogenase	**-0.25**	0.58469	**2.15**	0.00177	**0.48**	0.25584
STM1506	rspB	putative dehydrogenase	**2.17**	0.08918	**2.19**	0.00020	**-0.09**	0.88212
STM1508	ydfI	putative mannitol dehydrogenase	**1.10**	0.05175	**-0.31**	0.36782	**-0.56**	0.51636
STM1508	ydfI	putative mannitol dehydrogenase	**1.81**	0.01730	**-0.50**	0.13258	**1.07**	0.06285
STM1510	ydfH	putative regulatory protein	**3.10**	0.04151	**-0.43**	0.40078	**2.46**	0.00068
STM1510	ydfH	putative regulatory protein	**2.37**	0.03083	**-0.05**	0.95763	**2.42**	0.00122
STM1511	ydfG	putative oxidoreductase	**-1.24**	0.07186	**0.23**	0.44814	**-0.48**	0.26579
STM1511	ydfG	putative oxidoreductase	**-0.42**	0.68440	**0.48**	0.14488	**0.08**	0.85420
STM1512	dcp	dipeptidyl carboxypeptidase II	**0.17**	0.73728	**0.86**	0.01835	**1.36**	0.00410
STM1512	dcp	dipeptidyl carboxypeptidase II	**0.28**	0.50901	**0.74**	0.05427	**1.35**	0.00554
STM1514	ydeJ	competence damage-inducible protein A	**1.97**	0.01145	**0.73**	0.09009	**3.87**	0.00007
STM1514	ydeJ	competence damage-inducible protein A	**1.28**	0.35494	**0.84**	0.04008	**4.79**	0.00002
STM1515	ydeI	putative periplasmic protein	**1.33**	0.11448	**2.92**	0.00007	**3.83**	0.00011
STM1515	ydeI	putative periplasmic protein	**2.73**	0.00796	**3.17**	0.00046	**5.20**	0.00002
STM1516	ydeE	putative transport protein	**0.36**	0.46980	**0.34**	0.27712	**1.80**	0.03979
STM1516	ydeE	putative transport protein	**1.11**	0.08383	**0.52**	0.17260	**1.15**	0.02046
STM1517	ydeD	putative permease	**-0.83**	0.13620	**0.87**	0.05888	**-0.14**	0.80148
STM1517	ydeD	putative permease	**-0.14**	0.72927	**0.26**	0.51103	**-0.03**	0.94846
STM1518	marB	multiple antibiotic resistance protein	**-0.39**	0.52984	**0.80**	0.01917	**-0.51**	0.48750
STM1518	marB	multiple antibiotic resistance protein	**0.63**	0.21170	**1.17**	0.01959	**-0.12**	0.86380
STM1519,S	marA	transcriptional activator	**-0.26**	0.69072	**0.32**	0.28007	**-1.30**	0.06115
STM1519,S	marA	transcriptional activator	**0.85**	0.09815	**0.47**	0.22949	**-0.22**	0.61613
STM1520	marR	marRAB operon repressor	**-0.43**	0.34012	**0.13**	0.68202	**-0.21**	0.73624
STM1520	marR	marRAB operon repressor	**1.26**	0.03408	**0.71**	0.03479	**1.00**	0.02426

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM1521	marC	multiple antibiotic resistance transporter	**0.07**	0.87379	**1.16**	0.02072	**0.63**	0.11114
STM1521	marC	multiple antibiotic resistance transporter	**1.43**	0.09269	**0.91**	0.01662	**1.07**	0.02941
STM1522	ydeA	sugar efflux transporter	**-0.03**	0.96762	**0.32**	0.40803	**-0.35**	0.57801
STM1522	ydeA	sugar efflux transporter	**0.77**	0.16474	**-0.01**	0.99011	**0.24**	0.71298
STM1523	yneJ	putative transcriptional regulator	**0.05**	0.92833	**-0.02**	0.96296	**-0.83**	0.07077
STM1523	yneJ	putative transcriptional regulator	**1.01**	0.10160	**-0.57**	0.26118	**1.11**	0.06321
STM1524	yneI	putative succinate-semialdehyde dehydrogenase	**-1.13**	0.05366	**-0.52**	0.41852	**-1.41**	0.03229
STM1524	yneI	putative succinate-semialdehyde dehydrogenase	**-0.46**	0.27870	**-0.89**	0.02179	**-1.13**	0.01696
STM1525	yneH	glutaminase	**-0.68**	0.14494	**-1.40**	0.00786	**-1.65**	0.00337
STM1525	yneH	glutaminase	**1.56**	0.09446	**-0.86**	0.06664	**0.41**	0.40580
STM1526	yneG	putative cytoplasmic protein	**-0.02**	0.96762	**-0.08**	0.85492	**0.13**	0.81045
STM1526	yneG	putative cytoplasmic protein	**2.72**	0.00686	**0.30**	0.50717	**0.77**	0.15744
STM1527	STM1527	putative inner membrane protein	**-1.90**	0.00961	**-0.49**	0.26547	**-1.64**	0.03707
STM1527	STM1527	putative inner membrane protein	**-0.83**	0.11638	**-0.87**	0.01877	**-1.16**	0.03204
STM1528	STM1528	putative outer membrane protein	**-0.41**	0.32925	**-1.06**	0.01612	**-2.41**	0.00033
STM1528	STM1528	putative outer membrane protein	**0.08**	0.91982	**-0.96**	0.01415	**-1.60**	0.03041
STM1530	STM1530	putative outer membrane protein	**-0.19**	0.65199	**-0.88**	0.03355	**-0.72**	0.15472
STM1530	STM1530	putative outer membrane protein	**0.71**	0.15868	**-1.36**	0.00193	**0.43**	0.42756
STM1531	STM1531	putative hydrogenase	**-0.64**	0.28619	**0.29**	0.52916	**-0.78**	0.08463
STM1531	STM1531	putative hydrogenase	**0.67**	0.18831	**-0.85**	0.04936	**0.62**	0.20246
STM1532	STM1532	putative dehydrogenase protein	**-1.17**	0.07385	**0.18**	0.56467	**-0.16**	0.77687
STM1532	STM1532	putative dehydrogenase protein	**0.19**	0.70717	**0.90**	0.02145	**0.72**	0.28099
STM1533	STM1533	putative hydrogenase	**0.02**	0.97024	**0.91**	0.02185	**1.12**	0.02808
STM1533	STM1533	putative hydrogenase	**-0.42**	0.37718	**-0.03**	0.94244	**0.44**	0.32549
STM1534	STM1534	putative hydrogenase	**-0.59**	0.18763	**0.58**	0.15199	**0.38**	0.35900
STM1534	STM1534	putative hydrogenase	**4.23**	0.04782	**-0.52**	0.31195	**1.05**	0.32969
STM1535	STM1535	putative hydrogenase protein	**2.86**	0.01386	**3.53**	0.00019	**4.01**	0.00416
STM1535	STM1535	putative hydrogenase protein	**3.96**	0.01363	**3.62**	0.00061	**5.18**	0.00018
STM1536	STM1536	putative hydrogenase maturation protease	**-0.59**	0.22882	**0.06**	0.87241	**-1.13**	0.01240
STM1536	STM1536	putative hydrogenase maturation protease	**-0.42**	0.53066	**0.42**	0.17344	**0.03**	0.94628
STM1537	STM1537	putative Ni/Fe hydrogenase 1 b-type cytochrome subunit	**0.07**	0.91111	**0.88**	0.02192	**1.38**	0.29775
STM1537	STM1537	putative Ni/Fe hydrogenase 1 b-type cytochrome subunit	**0.70**	0.28909	**0.71**	0.25332	**2.03**	0.00056
STM1538	STM1538	putative hydrogenase-1 large subunit	**-0.45**	0.45200	**-1.96**	0.00043	**-1.07**	0.23861
STM1538	STM1538	putative hydrogenase-1 large subunit	**0.34**	0.64515	**-1.34**	0.00421	**-0.10**	0.89368
STM1539	STM1539	putative hydrogenase-1 small subunit	**1.61**	0.03167	**0.56**	0.16970	**2.76**	0.00070
STM1539	STM1539	putative hydrogenase-1 small subunit	**2.50**	0.01199	**0.45**	0.27223	**4.14**	0.00011
STM1540	STM1540	putative hydrolase	**0.14**	0.75644	**1.18**	0.00572	**0.03**	0.96501
STM1540	STM1540	putative hydrolase	**0.54**	0.23498	**0.40**	0.22094	**0.55**	0.71621
STM1541	STM1541	putative regulatory protein	**-0.44**	0.43816	**-0.14**	0.70071	**-1.15**	0.16921
STM1541	STM1541	putative regulatory protein	**1.13**	0.07255	**0.37**	0.43514	**-0.63**	0.15775
STM1542	STM1542	putative zinc-binding dehydrogenase	**-0.63**	0.17126	**0.22**	0.52399	**-0.04**	0.96274
STM1542	STM1542	putative zinc-binding dehydrogenase	**-0.21**	0.74980	**-0.25**	0.41398	**-0.02**	0.98515
STM1543	STM1543	putative transport protein	**-0.54**	0.45690	**-0.56**	0.06749	**-0.66**	0.26963
STM1543	STM1543	putative transport protein	**0.26**	0.61303	**-0.97**	0.06141	**-0.33**	0.54909
STM1544	pqaA	PhoPQ-regulated protein	**1.49**	0.36075	**-0.53**	0.38661	**4.46**	0.00007
STM1544	pqaA	PhoPQ-regulated protein	**2.10**	0.01423	**0.28**	0.39541	**1.68**	0.01131
STM1545	STM1545	putative multidrug efflux protein	**-1.16**	0.05515	**0.06**	0.95580	**-0.15**	0.82386
STM1545	STM1545	putative multidrug efflux protein	**-0.05**	0.94323	**-0.83**	0.05633	**-0.26**	0.68954
STM1546	STM1546	hypothetical protein STM1546	**0.16**	0.87984	**0.73**	0.17278	**2.34**	0.00033
STM1546	STM1546	hypothetical protein STM1546	**-0.04**	0.97145	**1.28**	0.00379	**2.10**	0.00086
STM1547	STM1547	putative transcriptional regulator	**-0.68**	0.53089	**0.44**	0.24065	**-0.65**	0.18212
STM1547	STM1547	putative transcriptional regulator	**-0.06**	0.90171	**0.45**	0.61067	**-0.36**	0.42907
STM1548,s	STM1548,s	putative S-adenosylmethionine/tRNA-ribosyltransferase-	**-0.14**	0.76703	**1.12**	0.03228	**-0.12**	0.76580
STM1548,s	STM1548,s	putative S-adenosylmethionine/tRNA-ribosyltransferase-	**1.05**	0.07165	**0.69**	0.03687	**0.09**	0.86189
STM1549	STM1549	putative translation initiation inhibitor	**-0.83**	0.13871	**0.30**	0.39659	**-0.73**	0.08768
STM1549	STM1549	putative translation initiation inhibitor	**0.91**	0.09777	**0.03**	0.94227	**-2.28**	0.04355
STM1551	STM1551	putative cytoplasmic protein	**-0.20**	0.71423	**1.73**	0.00151	**-0.29**	0.45946
STM1551	STM1551	putative cytoplasmic protein	**0.71**	0.17877	**1.43**	0.00162	**0.37**	0.40482
STM1551,1n	STM1551,1n	hypothetical protein STM1551,1n	**-0.89**	0.29994	**0.05**	0.95900	**-0.87**	0.11740
STM1551,1n	STM1551,1n	hypothetical protein STM1551,1n	**0.45**	0.54889	**-0.73**	0.16386	**-1.64**	0.02940
STM1552	STM1552	putative cytoplasmic protein	**-0.78**	0.22942	**-0.63**	0.10115	**-0.17**	0.71053
STM1552	STM1552	putative cytoplasmic protein	**-0.77**	0.17565	**-0.99**	0.03131	**-0.03**	0.97028
STM1554	STM1554	putative coiled-coil protein	**-0.55**	0.30875	**-0.01**	0.98161	**-1.95**	0.03837
STM1554	STM1554	putative coiled-coil protein	**0.34**	0.42046	**-0.03**	0.93418	**0.51**	0.15860
STM1555	STM1555	putative transcriptional regulator	**-0.70**	0.24394	**0.11**	0.76943	**-0.97**	0.21310
STM1555	STM1555	putative transcriptional regulator	**0.12**	0.88688	**-0.99**	0.14756	**-0.49**	0.38106
STM1556	STM1556	putative Na+/H+ antiporter	**-0.52**	0.41231	**0.60**	0.09379	**0.09**	0.91116
STM1556	STM1556	putative Na+/H+ antiporter	**0.77**	0.22411	**1.10**	0.05093	**0.76**	0.30573
STM1557	STM1557	putative aminotransferase	**0.77**	0.18990	**0.55**	0.08841	**1.37**	0.01833
STM1557	STM1557	putative aminotransferase	**2.20**	0.01549	**0.71**	0.19622	**3.06**	0.00045

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM1558	STM1558	putative glycosyl hydrolase	**-0.39**	0.46236	**0.28**	0.54022	**0.16**	0.75896
STM1558	STM1558	putative glycosyl hydrolase	**0.35**	0.58858	**-0.62**	0.06645	**0.81**	0.19987
STM1559	STM1559	putative glycosyl hydrolase	**0.67**	0.18955	**-0.38**	0.38142	**1.00**	0.03020
STM1559	STM1559	putative glycosyl hydrolase	**1.55**	0.06276	**-0.54**	0.26541	**1.53**	0.03627
STM1560	STM1560	putative alpha amylase	**-0.49**	0.47210	**0.78**	0.52121	**0.57**	0.24388
STM1560	STM1560	putative alpha amylase	**1.04**	0.17638	**0.24**	0.47297	**1.73**	0.00335
STM1561	STM1561	putative lipoprotein	**-0.03**	0.95785	**-0.05**	0.93243	**0.10**	0.87102
STM1561	STM1561	putative lipoprotein	**-0.20**	0.76178	**-1.04**	0.07778	**0.23**	0.67780
STM1562	STM1562	putative periplasmic transport protein	**-0.06**	0.89257	**2.42**	0.03251	**0.51**	0.39728
STM1562	STM1562	putative periplasmic transport protein	**1.38**	0.02552	**0.98**	0.01298	**1.33**	0.00986
STM1563	osmC	putative envelope protein	**-0.40**	0.46387	**4.34**	0.00001	**4.42**	0.00011
STM1563	osmC	putative envelope protein	**0.22**	0.77505	**4.02**	0.00001	**4.35**	0.00008
STM1564	yddX	putative cytoplasmic protein	**-1.11**	0.07052	**1.01**	0.01938	**2.46**	0.00066
STM1564	yddX	putative cytoplasmic protein	**1.54**	0.02776	**0.61**	0.12613	**3.43**	0.00014
STM1565	rpsV	30S ribosomal subunit protein S22	**0.22**	0.69215	**1.39**	0.00505	**2.21**	0.01537
STM1565	rpsV	30S ribosomal subunit protein S22	**-0.54**	0.43488	**0.59**	0.11093	**2.58**	0.00145
STM1566	sfcA	NAD-linked malate dehydrogenase	**-1.81**	0.01497	**-0.20**	0.49522	**-0.10**	0.81048
STM1566	sfcA	NAD-linked malate dehydrogenase	**-0.85**	0.10460	**-0.65**	0.24706	**0.23**	0.71053
STM1567	adhP	alcohol dehydrogenase	**-0.51**	0.25142	**3.32**	0.00003	**2.23**	0.00035
STM1567	adhP	alcohol dehydrogenase	**0.83**	0.08071	**2.74**	0.00020	**3.00**	0.00012
STM1568	fdnI	formate dehydrogenase-N gamma subunit	**2.73**	0.00547	**1.82**	0.00036	**4.36**	0.00004
STM1568	fdnI	formate dehydrogenase-N gamma subunit	**3.40**	0.00520	**1.58**	0.00532	**5.26**	0.00003
STM1569	fdnH	formate dehydrogenase-N beta subunit	**-0.08**	0.88657	**0.22**	0.59971	**0.42**	0.34679
STM1569	fdnH	formate dehydrogenase-N beta subunit	**0.61**	0.20252	**0.17**	0.55776	**0.77**	0.06232
STM1570	fdnG	formate dehydorgenase-N alpha subunit	**-0.97**	0.10333	**-1.69**	0.00048	**-1.68**	0.01596
STM1570	fdnG	formate dehydorgenase-N alpha subunit	**0.52**	0.31023	**-1.69**	0.00062	**-1.32**	0.01444
STM1571	yddG	putative permease	**0.91**	0.11468	**-2.27**	0.00017	**-2.60**	0.00026
STM1571	yddG	putative permease	**0.11**	0.87420	**-2.34**	0.00036	**-2.43**	0.00090
STM1572	nmpC	putative outer membrane porin precursor	**-3.69**	0.00541	**-2.52**	0.00031	**-5.46**	0.00009
STM1572	nmpC	putative outer membrane porin precursor	**-2.09**	0.01206	**-1.98**	0.00030	**-5.00**	0.00002
STM1573,Sc	STM1573,Sc	putative cytoplasmic protein	**-1.21**	0.10900	**-1.55**	0.00213	**-2.90**	0.00165
STM1573,Sc	STM1573,Sc	putative cytoplasmic protein	**-0.61**	0.37481	**-2.05**	0.00204	**-3.66**	0.00040
STM1574	smvA	methyl viologen resistance	**-2.34**	0.01207	**-1.74**	0.00046	**-2.26**	0.00081
STM1574	smvA	methyl viologen resistance	**-1.09**	0.07067	**-1.93**	0.00110	**-2.82**	0.00040
STM1575	STM1575	putative transcriptional regulator	**-0.78**	0.13384	**-0.97**	0.02449	**-0.98**	0.03407
STM1575	STM1575	putative transcriptional regulator	**-0.95**	0.27166	**-0.41**	0.17247	**-0.61**	0.44536
STM1576	narU	nitrate extrusion protein	**1.41**	0.35020	**0.75**	0.03577	**1.31**	0.08371
STM1576	narU	nitrate extrusion protein	**1.28**	0.09874	**0.37**	0.31546	**1.95**	0.02167
STM1577	narZ	nitrate reductase 2 alpha subunit	**2.91**	0.01056	**0.69**	0.04236	**3.91**	0.00018
STM1577	narZ	nitrate reductase 2 alpha subunit	**4.53**	0.00520	**0.60**	0.08306	**5.68**	0.00004
STM1578	narY	nitrate reductase 2 beta subunit	**1.35**	0.46087	**-1.48**	0.19856	**-5.06**	0.01514
STM1578	narY	nitrate reductase 2 beta subunit	**1.61**	0.23558	**-3.16**	0.00108	**-3.01**	0.02351
STM1579	narW	nitrate reductase 2 delta subunit	**0.11**	0.90818	**-0.72**	0.14329	**2.29**	0.08336
STM1579	narW	nitrate reductase 2 delta subunit	**2.09**	0.01263	**0.17**	0.64847	**0.74**	0.14292
STM1580	narV	nitrate reductase 2 gamma subunit	**0.90**	0.34059	**0.55**	0.16350	**0.60**	0.10951
STM1580	narV	nitrate reductase 2 gamma subunit	**1.64**	0.01642	**-0.07**	0.90767	**2.00**	0.00065
STM1581	yddE	putative phenazine biosynthetic protein	**0.26**	0.72167	**-1.39**	0.10208	**-0.17**	0.84834
STM1581	yddE	putative phenazine biosynthetic protein	**-0.30**	0.70111	**-0.15**	0.69007	**-0.75**	0.48402
STM1582	nhoA	putative arylamine N-acetyltransferase	**-1.16**	0.06396	**-0.39**	0.17341	**-1.37**	0.01689
STM1582	nhoA	putative arylamine N-acetyltransferase	**-0.32**	0.63344	**-0.64**	0.05150	**0.00**	0.99606
STM1583	STM1583	putative cytoplasmic protein	**0.93**	0.18378	**0.53**	0.52253	**0.11**	0.83517
STM1583	STM1583	putative cytoplasmic protein	**1.80**	0.07719	**-0.61**	0.59677	**1.73**	0.04472
STM1584	ansP	L-asparagine transport protein	**-0.96**	0.13671	**-0.57**	0.08858	**-0.69**	0.23949
STM1584	ansP	L-asparagine transport protein	**-0.94**	0.05562	**-0.45**	0.16005	**-1.34**	0.03077
STM1585	STM1585	putative outer membrane lipoprotein	**2.04**	0.13717	**0.65**	0.05282	**0.64**	0.27152
STM1585	STM1585	putative outer membrane lipoprotein	**2.19**	0.07329	**1.46**	0.01233	**1.39**	0.01832
STM1586	STM1586	putative periplasmic protein	**-0.09**	0.89761	**0.80**	0.43928	**-1.39**	0.03092
STM1586	STM1586	putative periplasmic protein	**0.40**	0.44435	**1.88**	0.00031	**-0.09**	0.85035
STM1587	yncD	putative outer membrane receptor	**-0.25**	0.66676	**0.62**	0.20037	**0.91**	0.02685
STM1587	yncD	putative outer membrane receptor	**-1.48**	0.06811	**0.31**	0.33283	**0.02**	0.96475
STM1588	yncC	putative regulatory protein	**1.20**	0.02766	**0.75**	0.04460	**1.45**	0.01058
STM1588	yncC	putative regulatory protein	**2.33**	0.01834	**0.73**	0.04506	**2.58**	0.00023
STM1589	yncB	putative NADP-dependent oxidoreductase	**-0.57**	0.49519	**0.13**	0.89389	**1.34**	0.05302
STM1589	yncB	putative NADP-dependent oxidoreductase	**1.34**	0.04720	**0.91**	0.03417	**1.57**	0.01117
STM1590	yncA	putative acyltransferase	**-0.47**	0.52477	**0.20**	0.61415	**-1.02**	0.01890
STM1590	yncA	putative acyltransferase	**-0.22**	0.64455	**0.09**	0.81217	**-0.39**	0.34632
STM1591	ydcZ	putative inner membrane protein	**-0.86**	0.13901	**-0.01**	0.97286	**-0.61**	0.10898
STM1591	ydcZ	putative inner membrane protein	**-0.18**	0.91522	**-0.77**	0.05635	**-1.29**	0.02003
STM1592	ydcY	putative cytoplasmic protein	**4.13**	0.00753	**-0.38**	0.53277	**1.47**	0.06061
STM1592	ydcY	putative cytoplasmic protein	**1.84**	0.13687	**-1.51**	0.10295	**0.81**	0.33884

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM1593	srfA	putative virulence protein	-1.12	0.16928	-2.16	0.00064	-2.17	0.00122
STM1593	srfA	putative virulence protein	-0.96	0.05659	-2.57	0.00036	-1.63	0.00651
STM1594	srfB	putative virulence protein	-1.42	0.02181	-2.23	0.00071	-1.76	0.00355
STM1594	srfB	putative virulence protein	-1.16	0.04220	-2.50	0.00043	-0.81	0.11111
STM1595	srfC	putative virulence protein	-1.08	0.11005	-0.59	0.16356	-1.32	0.01135
STM1595	srfC	putative virulence protein	-0.21	0.65193	-0.67	0.08004	-0.99	0.02349
STM1596	ydcX	putative inner membrane protein	-1.40	0.08966	-1.26	0.00303	-1.27	0.01398
STM1596	ydcX	putative inner membrane protein	-0.90	0.12247	-1.16	0.00589	-0.86	0.16637
STM1597	ydcW	putative aldehyde dehydrogenase	0.03	0.97285	1.26	0.01590	1.95	0.00098
STM1597	ydcW	putative aldehyde dehydrogenase	1.42	0.17631	0.70	0.04587	2.99	0.00058
STM1598	ydcR	putative regulatory protein	-0.62	0.18603	0.22	0.63032	-0.10	0.80954
STM1598	ydcR	putative regulatory protein	0.58	0.25068	0.35	0.32539	1.29	0.00926
STM1599	pdgL	periplasmic dipeptidase precursor	-0.12	0.81589	0.20	0.86854	-0.89	0.05874
STM1599	pdgL	periplasmic dipeptidase precursor	0.98	0.08238	-0.49	0.28230	0.55	0.25187
STM1601	ugtL	hypothetical protein STM1601	0.16	0.75196	0.94	0.01841	-0.23	0.65290
STM1601	ugtL	hypothetical protein STM1601	1.79	0.04722	1.32	0.01230	1.37	0.05310
STM1602	sifB	secreted effector protein	0.59	0.35920	4.90	0.00001	0.72	0.19653
STM1602	sifB	secreted effector protein	1.66	0.03871	4.58	0.00004	1.26	0.02343
STM1603	yncJ	putative periplasmic protein	0.99	0.07851	3.37	0.00002	0.64	0.22912
STM1603	yncJ	putative periplasmic protein	1.16	0.02992	3.75	0.00001	1.50	0.00722
STM1604	ydcP	putative collagenase	0.05	0.94155	-0.23	0.42735	-1.25	0.01313
STM1604	ydcP	putative collagenase	-0.50	0.40544	0.32	0.37708	-1.17	0.06733
STM1605	ydcN	putative repressor	-0.17	0.70215	0.11	0.71105	-0.43	0.44697
STM1605	ydcN	putative repressor	0.80	0.11459	0.03	0.93074	0.18	0.63574
STM1606	STM1606	putative benzoate membrane transport protein	-0.32	0.45043	0.15	0.62769	-0.95	0.02830
STM1606	STM1606	putative benzoate membrane transport protein	0.89	0.19780	0.85	0.01554	0.32	0.36938
STM1607	STM1607	putative outer membrane lipoprotein	-0.67	0.26183	1.51	0.00215	-0.07	0.91283
STM1607	STM1607	putative outer membrane lipoprotein	0.33	0.63233	1.24	0.00374	0.38	0.35900
STM1608	tehB	putative methyltransferase	-0.52	0.30295	1.10	0.00441	-1.04	0.02039
STM1608	tehB	putative methyltransferase	0.10	0.87990	1.09	0.01146	-0.89	0.07640
STM1609	tehA	K+-tellurite ethidium and proflavin transport protein	-0.39	0.53193	1.16	0.00999	-1.88	0.01007
STM1609	tehA	K+-tellurite ethidium and proflavin transport protein	-1.28	0.17542	1.33	0.01368	-0.62	0.11432
STM1610	ydcK	putative nucleoside-diphosphate-sugar pyrophosphorylase	-0.38	0.67039	1.00	0.01348	-0.51	0.33330
STM1610	ydcK	putative nucleoside-diphosphate-sugar pyrophosphorylase	1.55	0.02623	0.63	0.21179	0.83	0.06915
STM1611	rimL	acetyl transferase	0.33	0.43816	1.33	0.00419	0.60	0.24877
STM1611	rimL	acetyl transferase	0.73	0.26129	1.50	0.00501	1.33	0.02837
STM1612	STM1612	putative cellulase protein	0.20	0.80772	2.10	0.00103	1.93	0.03312
STM1612	STM1612	putative cellulase protein	2.04	0.04353	3.05	0.00016	3.08	0.00181
STM1613	STM1613	putative PTS system enzymeIIB component	-0.10	0.92542	2.09	0.00095	0.59	0.39706
STM1613	STM1613	putative PTS system enzymeIIB component	0.43	0.36007	2.64	0.00177	1.16	0.02969
STM1614	STM1614	putative PTS system enzyme IIC component	0.33	0.55671	1.33	0.01013	-0.08	0.91117
STM1614	STM1614	putative PTS system enzyme IIC component	-0.73	0.11697	0.42	0.21010	-0.08	0.91587
STM1615	STM1615	putative nucleoside triphosphatase	-0.22	0.70958	0.27	0.71894	0.14	0.76913
STM1615	STM1615	putative nucleoside triphosphatase	-0.66	0.71609	-0.89	0.03682	-0.70	0.43761
STM1616	STM1616	putative sugar-specific PTS enzyme II	-0.10	0.84287	0.68	0.05081	0.64	0.08973
STM1616	STM1616	putative sugar-specific PTS enzyme II	0.17	0.77290	0.42	0.28791	1.30	0.04449
STM1617	STM1617	ribulose-phosphate 3-epimerase	-0.36	0.81801	-1.71	0.00395	-0.05	0.96438
STM1617	STM1617	ribulose-phosphate 3-epimerase	0.28	0.70640	-1.54	0.00851	-0.11	0.87470
STM1618	STM1618	putative transcriptional repressor of sgc operon	1.45	0.02104	1.06	0.04498	0.04	0.91658
STM1618	STM1618	putative transcriptional repressor of sgc operon	1.50	0.11284	1.60	0.00397	1.52	0.03378
STM1619	STM1619	cryptic aminoglycoside resistance gene	0.55	0.57930	0.13	0.84363	0.51	0.44761
STM1619	STM1619	cryptic aminoglycoside resistance gene	2.19	0.01041	0.14	0.69727	0.77	0.06414
STM1620	STM1620	putative oxidase	0.96	0.07169	0.82	0.11245	0.91	0.05629
STM1620	STM1620	putative oxidase	2.15	0.04747	0.19	0.65721	2.13	0.00431
STM1621	STM1621	putative periplasmic protein	1.08	0.07541	0.96	0.07100	1.78	0.00267
STM1621	STM1621	putative periplasmic protein	0.21	0.82543	-0.44	0.42969	1.14	0.27220
STM1622	ydcG	putative MDO biosynthetic protein	-0.73	0.14680	-0.12	0.76129	-1.34	0.00827
STM1622	ydcG	putative MDO biosynthetic protein	0.32	0.63876	-0.92	0.02564	-1.03	0.14813
STM1623	STM1623	putative carboxylesterase	-1.59	0.12536	-1.22	0.00536	-0.78	0.22159
STM1623	STM1623	putative carboxylesterase	-0.74	0.13497	-0.98	0.02307	-1.58	0.02766
STM1624	STM1624	putative cytoplasmic protein	-0.41	0.31997	-0.26	0.53412	1.87	0.00108
STM1624	STM1624	putative cytoplasmic protein	0.37	0.58858	0.49	0.18575	2.50	0.00062
STM1625	ydcI	putative transcriptional regulator	-1.30	0.03038	0.36	0.38197	-1.68	0.01430
STM1625	ydcI	putative transcriptional regulator	1.78	0.15252	0.38	0.22398	0.59	0.39650
STM1626	trg	methyl-accepting chemotaxis protein III	-1.02	0.15994	-0.18	0.53261	0.12	0.83871
STM1626	trg	methyl-accepting chemotaxis protein III	-0.85	0.09981	-0.59	0.06877	-0.58	0.58409
STM1627	STM1627	alcohol dehydrogenase class III	-1.08	0.04331	-0.69	0.13068	-1.27	0.00954
STM1627	STM1627	alcohol dehydrogenase class III	0.04	0.96627	-0.04	0.91235	-0.39	0.41520
STM1628	STM1628	putative cytoplasmic protein	-1.85	0.07172	-0.18	0.64133	-1.74	0.00425
STM1628	STM1628	putative cytoplasmic protein	-0.68	0.20611	0.09	0.79292	-2.70	0.00952

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM1630	STM1630	putative inner membrane protein	**-0.92**	0.27928	**-0.07**	0.87343	**0.11**	0.89732
STM1630	STM1630	putative inner membrane protein	**-1.52**	0.05747	**-0.42**	0.50120	**0.39**	0.44819
STM1631	sseJ	secreted effector protein	**0.48**	0.54187	**6.60**	0.00000	**0.64**	0.27668
STM1631	sseJ	secreted effector protein	**2.31**	0.01196	**6.36**	0.00017	**1.91**	0.00403
STM1632	STM1632	putative inner membrane protein	**-0.16**	0.72483	**4.05**	0.00035	**0.22**	0.67215
STM1632	STM1632	putative inner membrane protein	**1.41**	0.02948	**4.27**	0.00001	**0.99**	0.03547
STM1633	STM1633	putative periplasmic binding protein	**-0.30**	0.53819	**1.08**	0.00550	**0.29**	0.61305
STM1633	STM1633	putative periplasmic binding protein	**1.97**	0.04122	**1.97**	0.00146	**1.12**	0.06253
STM1634	STM1634	putative ABC transporter permease component	**-0.30**	0.61184	**0.23**	0.70904	**-0.64**	0.45142
STM1634	STM1634	putative ABC transporter permease component	**-0.40**	0.71442	**0.80**	0.04068	**1.30**	0.13646
STM1635	STM1635	putative ABC-type polar amino acid transport system	**-1.16**	0.28978	**-0.98**	0.02865	**-0.65**	0.10112
STM1635	STM1635	putative ABC-type polar amino acid transport system	**0.06**	0.90746	**0.08**	0.88540	**0.48**	0.62129
STM1636	STM1636	putative ABC-type transport system membrane component	**-0.14**	0.76098	**-0.68**	0.12306	**-1.07**	0.02386
STM1636	STM1636	putative ABC-type transport system membrane component	**0.62**	0.40841	**-0.99**	0.12618	**0.01**	0.98561
STM1637	STM1637	putative inner membrane protein	**0.06**	0.89675	**1.50**	0.01338	**0.08**	0.90484
STM1637	STM1637	putative inner membrane protein	**1.13**	0.21880	**1.27**	0.00762	**0.76**	0.30835
STM1638	STM1638	putative SAM-dependent methyltransferase	**0.38**	0.74464	**0.44**	0.24308	**-1.44**	0.00743
STM1638	STM1638	putative SAM-dependent methyltransferase	**-0.81**	0.37351	**1.19**	0.00404	**0.09**	0.94483
STM1639	cybB	cytochrome b561	**-1.25**	0.02560	**0.21**	0.43528	**-0.76**	0.04316
STM1639	cybB	cytochrome b561	**-1.33**	0.07413	**0.10**	0.87638	**-0.58**	0.38739
STM1640	ydcF	putative inner membrane protein	**-0.93**	0.22845	**-0.30**	0.30992	**-1.14**	0.08329
STM1640	ydcF	putative inner membrane protein	**-0.48**	0.42965	**-0.34**	0.28136	**-0.81**	0.10652
STM1641	hrpA	ATP-dependent helicase	**-1.35**	0.02829	**-0.28**	0.32126	**-0.68**	0.11285
STM1641	hrpA	ATP-dependent helicase	**-0.09**	0.85794	**-0.15**	0.67904	**0.28**	0.60951
STM1642	acpD	acyl carrier protein phosphodiesterase	**-1.22**	0.07777	**0.29**	0.45624	**-0.26**	0.64639
STM1642	acpD	acyl carrier protein phosphodiesterase	**0.20**	0.66546	**0.70**	0.06652	**-0.21**	0.59561
STM1643	STM1643	putative inner membrane protein	**-0.70**	0.13555	**0.92**	0.03865	**-0.03**	0.94245
STM1643	STM1643	putative inner membrane protein	**0.48**	0.44306	**0.83**	0.04427	**1.24**	0.01526
STM1644	ydbL	putative periplasmic protein	**-0.06**	0.90441	**-0.10**	0.74266	**-0.21**	0.62851
STM1644	ydbL	putative periplasmic protein	**0.94**	0.05468	**-0.53**	0.24274	**1.27**	0.01142
STM1645	ynbE	putative outer membrane lipoprotein	**0.72**	0.13497	**0.42**	0.19802	**0.83**	0.05748
STM1645	ynbE	putative outer membrane lipoprotein	**0.52**	0.37752	**-0.08**	0.80911	**1.25**	0.02617
STM1646	ydbH	putative periplasmic protein	**-0.91**	0.12530	**-0.98**	0.01195	**-0.30**	0.55730
STM1646	ydbH	putative periplasmic protein	**-0.72**	0.18585	**-0.35**	0.27937	**-0.67**	0.14240
STM1647	ldhA	D-lactate dehydrogenase	**-0.18**	0.68590	**-0.34**	0.29079	**0.14**	0.74145
STM1647	ldhA	D-lactate dehydrogenase	**0.14**	0.78563	**-0.18**	0.59190	**1.13**	0.00918
STM1648	hslJ	heat shock protein hslJ	**-0.87**	0.15610	**0.01**	0.97623	**-0.34**	0.59003
STM1648	hslJ	heat shock protein hslJ	**0.68**	0.24718	**0.13**	0.78896	**0.39**	0.60389
STM1649	STM1649	putative cytoplasmic protein	**-0.40**	0.75996	**0.10**	0.73720	**-1.75**	0.05880
STM1649	STM1649	putative cytoplasmic protein	**-1.62**	0.01924	**0.10**	0.72529	**-1.73**	0.02341
STM1651	nifJ	putative pyruvate-flavodoxin oxidoreductase	**-1.11**	0.04676	**-0.31**	0.34347	**-0.74**	0.05241
STM1651	nifJ	putative pyruvate-flavodoxin oxidoreductase	**1.06**	0.06656	**-0.86**	0.01433	**0.24**	0.64119
STM1652	ynaF	putative universal stress protein	**-0.75**	0.13364	**0.43**	0.30810	**-0.26**	0.53950
STM1652	ynaF	putative universal stress protein	**-0.34**	0.50056	**0.73**	0.09388	**-1.62**	0.37041
STM1654	ydaO	putative ATPase	**-2.17**	0.01630	**-1.19**	0.00677	**-1.78**	0.02482
STM1654	ydaO	putative ATPase	**-0.49**	0.52932	**-0.84**	0.04416	**-2.04**	0.03389
STM1655	dbpA	ATP-dependent RNA helicase	**1.41**	0.01858	**0.83**	0.02153	**3.02**	0.00010
STM1655	dbpA	ATP-dependent RNA helicase	**2.19**	0.00756	**0.03**	0.95135	**2.97**	0.00079
STM1656	STM1656	putative Zn transport protein	**-0.36**	0.46998	**-0.52**	0.23971	**0.24**	0.55262
STM1656	STM1656	putative Zn transport protein	**-0.24**	0.72641	**-1.10**	0.01806	**0.98**	0.05059
STM1657	STM1657	putative methyl-accepting chemotaxis protein	**0.07**	0.88446	**-0.45**	0.23257	**-0.69**	0.25304
STM1657	STM1657	putative methyl-accepting chemotaxis protein	**-0.65**	0.17495	**-0.65**	0.06122	**-0.80**	0.13876
STM1658	ydaL	hypothetical protein STM1658	**0.22**	0.64103	**1.77**	0.00169	**0.45**	0.25829
STM1658	ydaL	hypothetical protein STM1658	**1.01**	0.05991	**1.52**	0.00188	**1.50**	0.00504
STM1659	ogt	O-6-alkylguanine-DNA/cysteine-protein methyltransferase	**-0.36**	0.41841	**0.40**	0.27824	**-0.46**	0.41434
STM1659	ogt	O-6-alkylguanine-DNA/cysteine-protein methyltransferase	**0.32**	0.53602	**0.83**	0.04666	**0.64**	0.11222
STM1660,S	fnr	transcriptional regulator	**-0.41**	0.40854	**0.14**	0.66794	**-0.29**	0.41531
STM1660,S	fnr	transcriptional regulator	**-0.40**	0.33144	**0.25**	0.47554	**0.30**	0.40067
STM1661	ydaA	putative universal stress protein	**-0.04**	0.92334	**0.68**	0.03027	**1.05**	0.02280
STM1661	ydaA	putative universal stress protein	**-1.95**	0.19270	**1.13**	0.02253	**1.16**	0.03823
STM1662	ynaJ	putative inner membrane protein	**-0.73**	0.43818	**1.07**	0.01332	**1.15**	0.01240
STM1662	ynaJ	putative inner membrane protein	**-0.59**	0.55612	**1.02**	0.01389	**0.76**	0.06475
STM1663	ynaI	putative integral membrane protein	**-1.47**	0.02479	**0.40**	0.43886	**-0.83**	0.12587
STM1663	ynaI	putative integral membrane protein	**0.15**	0.89449	**-0.33**	0.45749	**0.05**	0.91884
STM1664	STM1664	putative transcriptional regulator	**-0.96**	0.19533	**0.40**	0.39143	**-1.48**	0.02468
STM1664	STM1664	putative transcriptional regulator	**0.01**	0.98812	**-0.16**	0.73016	**-0.62**	0.27844
STM1665	STM1665	putative cytoplasmic protein	**2.07**	0.10533	**0.68**	0.09770	**0.96**	0.14822
STM1665	STM1665	putative cytoplasmic protein	**-0.19**	0.66786	**0.36**	0.42512	**0.79**	0.07519
STM1667	STM1667	putative thiol peroxidase	**-0.51**	0.37772	**-0.18**	0.65492	**-0.41**	0.46262
STM1667	STM1667	putative thiol peroxidase	**-0.18**	0.74592	**0.44**	0.27151	**0.52**	0.35137

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM1668	STM1668	hypothetical protein STM1668	**0.37**	0.49079	**0.69**	0.09337	**0.95**	0.09747
STM1668	STM1668	hypothetical protein STM1668	**1.62**	0.13871	**0.02**	0.96036	**1.64**	0.00522
STM1669	STM1669	invasin-like protein	**1.09**	0.04560	**0.44**	0.23307	**1.11**	0.01468
STM1669	STM1669	invasin-like protein	**2.30**	0.00789	**0.14**	0.86101	**2.18**	0.00613
STM1670	STM1670	putative lipoprotein	**0.10**	0.89045	**-0.09**	0.87873	**-0.72**	0.23424
STM1670	STM1670	putative lipoprotein	**0.99**	0.06395	**-0.79**	0.08825	**0.50**	0.33333
STM1671	STM1671	putative regulatory protein	**-0.18**	0.72462	**-1.29**	0.16667	**0.00**	0.99551
STM1671	STM1671	putative regulatory protein	**-1.14**	0.14696	**0.91**	0.13041	**-0.12**	0.81076
STM1673	STM1673	putative outer membrane lipoprotein	**-0.20**	0.74341	**0.06**	0.84575	**-0.55**	0.23076
STM1673	STM1673	putative outer membrane lipoprotein	**0.60**	0.28785	**0.82**	0.01673	**0.96**	0.06130
STM1674	STM1674	putative regulatory protein	**0.52**	0.56134	**-0.11**	0.73971	**0.08**	0.84201
STM1674	STM1674	putative regulatory protein	**1.52**	0.04427	**0.00**	0.99752	**1.93**	0.02164
STM1675	STM1675	oxidoreductase	**-0.42**	0.42614	**-0.71**	0.05331	**-1.07**	0.01218
STM1675	STM1675	oxidoreductase	**0.35**	0.49783	**-0.99**	0.05817	**-0.79**	0.32923
STM1676	STM1676	putative aldo/keto reductase	**-0.36**	0.43816	**-0.52**	0.19673	**-0.86**	0.05789
STM1676	STM1676	putative aldo/keto reductase	**0.27**	0.62210	**-0.50**	0.24218	**0.26**	0.52778
STM1677	STM1677	putative transcriptional regulator	**0.37**	0.58374	**-0.18**	0.69795	**0.44**	0.24665
STM1677	STM1677	putative transcriptional regulator	**0.93**	0.08254	**-0.08**	0.84905	**1.35**	0.00723
STM1678	STM1678	putative 2'-hydroxyisoflavone reductase	**0.15**	0.85165	**1.26**	0.00544	**-0.35**	0.68811
STM1678	STM1678	putative 2'-hydroxyisoflavone reductase	**0.37**	0.48816	**1.15**	0.00817	**0.02**	0.96960
STM1679	mppA	periplasmic murein tripeptide transport protein	**-1.04**	0.05440	**0.58**	0.07695	**-0.73**	0.05531
STM1679	mppA	periplasmic murein tripeptide transport protein	**-0.12**	0.83998	**0.97**	0.00804	**-0.18**	0.70609
STM1680	ycjI	putative carboxypeptidase	**-0.55**	0.29898	**1.09**	0.00550	**0.37**	0.31313
STM1680	ycjI	putative carboxypeptidase	**0.68**	0.20801	**0.55**	0.10346	**-0.42**	0.41515
STM1681	ycjG	putative chloromuconate cycloisomerase	**-0.33**	0.56308	**0.59**	0.12594	**-0.21**	0.74239
STM1681	ycjG	putative chloromuconate cycloisomerase	**1.63**	0.07790	**0.51**	0.11648	**-0.71**	0.11225
STM1682	tpx	thiol peroxidase	**-1.88**	0.01079	**0.53**	0.15289	**-2.49**	0.00093
STM1682	tpx	thiol peroxidase	**-1.31**	0.06226	**0.88**	0.01457	**-2.75**	0.00032
STM1683	tyrR	transcriptional regulator	**-1.41**	0.06501	**0.40**	0.25556	**-1.42**	0.00983
STM1683	tyrR	transcriptional regulator	**-1.46**	0.02259	**0.62**	0.08758	**-1.81**	0.00084
STM1684	ycjF	hypothetical protein STM1684	**-0.09**	0.83532	**1.10**	0.00516	**0.85**	0.09187
STM1684	ycjF	hypothetical protein STM1684	**-0.45**	0.51104	**0.66**	0.12039	**1.47**	0.27653
STM1685	ycjX	putative ATPase	**-0.67**	0.28111	**2.13**	0.00113	**-0.56**	0.31674
STM1685	ycjX	putative ATPase	**0.35**	0.48090	**2.20**	0.00129	**-1.21**	0.01733
STM1686	pspE	phage shock protein	**2.04**	0.01951	**3.99**	0.00007	**0.17**	0.67325
STM1686	pspE	phage shock protein	**3.12**	0.00582	**4.10**	0.00002	**0.31**	0.47971
STM1687	pspD	phage shock protein	**1.85**	0.01067	**4.22**	0.00005	**-0.44**	0.36487
STM1687	pspD	phage shock protein	**3.12**	0.00541	**4.59**	0.00001	**-0.21**	0.62362
STM1688	pspC	phage shock protein	**3.22**	0.04188	**4.65**	0.00002	**0.60**	0.13302
STM1688	pspC	phage shock protein	**3.83**	0.00537	**4.84**	0.00001	**0.26**	0.50165
STM1689	pspB	phage shock protein B	**4.46**	0.00567	**5.84**	0.00000	**0.71**	0.06451
STM1689	pspB	phage shock protein B	**5.81**	0.00308	**5.39**	0.00001	**1.66**	0.00354
STM1690	pspA	phage shock protein	**4.41**	0.00581	**5.70**	0.00000	**2.30**	0.00081
STM1690	pspA	phage shock protein	**5.27**	0.00512	**5.54**	0.00000	**2.85**	0.00028
STM1691	pspF	transcription activator	**1.69**	0.22926	**0.35**	0.41085	**0.54**	0.53652
STM1691	pspF	transcription activator	**1.26**	0.06541	**0.29**	0.38885	**0.20**	0.70819
STM1692	sapA	peptide transport protein	**-1.55**	0.06900	**-0.30**	0.67697	**-0.69**	0.11488
STM1692	sapA	peptide transport protein	**0.07**	0.90537	**-1.49**	0.00120	**-0.84**	0.22880
STM1693	sapB	peptide transport protein	**-2.15**	0.01601	**-1.42**	0.00319	**-1.55**	0.01817
STM1693	sapB	peptide transport protein	**-0.82**	0.37797	**-1.16**	0.02688	**-0.75**	0.05163
STM1694	sapC	peptide transport protein	**-1.77**	0.05032	**-1.31**	0.00200	**-1.44**	0.02066
STM1694	sapC	peptide transport protein	**-1.25**	0.10628	**-2.04**	0.00074	**-1.91**	0.01187
STM1695	sapD	peptide transport protein	**-0.99**	0.17383	**-0.70**	0.06219	**-1.56**	0.00289
STM1695	sapD	peptide transport protein	**-0.87**	0.30631	**-0.54**	0.22603	**-1.45**	0.02231
STM1696	sapF	peptide transport protein	**-0.33**	0.44726	**0.97**	0.02519	**-1.16**	0.01504
STM1696	sapF	peptide transport protein	**0.33**	0.54425	**1.43**	0.00380	**0.10**	0.86723
STM1697	STM1697	hypothetical protein STM1697	**0.44**	0.32307	**1.53**	0.00129	**-0.36**	0.52398
STM1697	STM1697	hypothetical protein STM1697	**0.75**	0.14119	**2.07**	0.00019	**-0.09**	0.87295
STM1698	STM1698	putative inner membrane protein	**-0.50**	0.28856	**5.77**	0.00000	**-1.55**	0.01035
STM1698	STM1698	putative inner membrane protein	**1.01**	0.06323	**6.34**	0.00001	**-0.15**	0.71969
STM1700	fabI	enoyl-(acyl carrier protein) reductase	**-2.06**	0.00922	**-0.02**	0.96753	**-1.66**	0.00204
STM1700	fabI	enoyl-(acyl carrier protein) reductase	**-0.99**	0.09502	**0.57**	0.06750	**-1.58**	0.04737
STM1701	yciW	putative cytoplasmic protein	**-1.34**	0.06399	**-0.79**	0.02039	**-1.53**	0.02715
STM1701	yciW	putative cytoplasmic protein	**-0.93**	0.06238	**-0.24**	0.44860	**-1.24**	0.01017
STM1702	rnb	exoribonuclease II	**-1.27**	0.04582	**-0.70**	0.02865	**-1.55**	0.01145
STM1702	rnb	exoribonuclease II	**-0.80**	0.10733	**-1.11**	0.00438	**-0.60**	0.11910
STM1703	yciR	putative diguanylate cyclase/phosphodiesterase	**-0.12**	0.90732	**0.80**	0.02281	**0.96**	0.35445
STM1703	yciR	putative diguanylate cyclase/phosphodiesterase	**1.70**	0.02137	**0.79**	0.02667	**0.32**	0.49412
STM1704	yciT	putative regulatory protein	**-1.33**	0.02655	**-0.08**	0.82407	**-0.37**	0.34719
STM1704	yciT	putative regulatory protein	**0.16**	0.85117	**-0.86**	0.02816	**0.00**	0.99213

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM1705	osmB	lipoprotein B	**1.93**	0.02064	**2.20**	0.00035	**4.40**	0.00014
STM1705	osmB	lipoprotein B	**1.18**	0.03236	**1.90**	0.00099	**4.74**	0.00002
STM1706	yciH	hypothetical protein STM1706	**1.17**	0.11648	**0.24**	0.43113	**0.33**	0.39346
STM1706	yciH	hypothetical protein STM1706	**1.44**	0.01740	**-0.15**	0.72294	**1.48**	0.00349
STM1707	pyrF	orotidine 5'-phosphate decarboxylase	**-2.35**	0.01566	**-1.17**	0.00474	**-0.60**	0.17104
STM1707	pyrF	orotidine 5'-phosphate decarboxylase	**-0.43**	0.43189	**-1.14**	0.01053	**-0.52**	0.22146
STM1708	yciM	putative N-acetylglucosaminyl transferase	**-0.73**	0.39846	**0.08**	0.86854	**-0.12**	0.85406
STM1708	yciM	putative N-acetylglucosaminyl transferase	**-1.34**	0.03037	**0.05**	0.86597	**-1.21**	0.01534
STM1709	yciS	putative inner membrane protein	**-1.94**	0.01101	**-0.29**	0.39221	**-1.88**	0.00142
STM1709	yciS	putative inner membrane protein	**-1.03**	0.05800	**0.32**	0.28549	**-2.06**	0.00052
STM1710	pgpB	phosphatidylglycerophosphate phosphatase B	**-0.74**	0.12384	**1.20**	0.01783	**0.04**	0.92925
STM1710	pgpB	phosphatidylglycerophosphate phosphatase B	**-0.40**	0.35034	**0.99**	0.01295	**1.11**	0.02434
STM1711	ribA	GTP cyclohydrolase II protein	**0.06**	0.95465	**-0.39**	0.24800	**0.49**	0.43554
STM1711	ribA	GTP cyclohydrolase II protein	**0.25**	0.87141	**0.26**	0.40432	**0.95**	0.16683
STM1712	acnA	aconitate hydratase	**-0.16**	0.69471	**0.18**	0.64442	**0.44**	0.20630
STM1712	acnA	aconitate hydratase	**0.41**	0.32552	**-0.07**	0.83266	**1.25**	0.01767
STM1713	cysB	transcriptional regulator for cysteine regulon	**1.93**	0.26717	**-0.11**	0.77260	**-0.76**	0.28800
STM1713	cysB	transcriptional regulator for cysteine regulon	**1.03**	0.05056	**0.43**	0.15936	**0.54**	0.17064
STM1714	topA	DNA topoisomerase I	**0.52**	0.44116	**0.08**	0.81422	**0.13**	0.85441
STM1714	topA	DNA topoisomerase I	**2.15**	0.03517	**0.12**	0.73817	**0.87**	0.05322
STM1715	yciN	putative cytoplasmic protein	**-0.85**	0.27646	**-1.31**	0.00269	**-0.46**	0.37033
STM1715	yciN	putative cytoplasmic protein	**-0.03**	0.95489	**-1.22**	0.00331	**-0.84**	0.03691
STM1716	sohB	putative peptidase	**0.50**	0.60914	**-0.24**	0.46854	**-1.52**	0.00398
STM1716	sohB	putative peptidase	**0.84**	0.24166	**0.01**	0.96715	**-1.31**	0.01609
STM1717	yciK	short chain dehydrogenase	**-1.81**	0.01032	**0.55**	0.23828	**-1.16**	0.01435
STM1717	yciK	short chain dehydrogenase	**-0.42**	0.36133	**0.83**	0.02504	**0.45**	0.23874
STM1718	btuR	cob(I)yrinic acid a,c-diamide adenosyltransferase	**-1.88**	0.02908	**-0.44**	0.12628	**-1.70**	0.00839
STM1718	btuR	cob(I)yrinic acid a,c-diamide adenosyltransferase	**-1.64**	0.04326	**-0.48**	0.10115	**-2.10**	0.05765
STM1719	yciL	putative ribosomal large subunit pseudouridine synthase	**-1.66**	0.01391	**-0.79**	0.04869	**-2.51**	0.00032
STM1719	yciL	putative ribosomal large subunit pseudouridine synthase	**-1.52**	0.01753	**-0.90**	0.04537	**-1.80**	0.00276
STM1720	yciO	putative dsRNA-binding protein	**-0.13**	0.83105	**-0.13**	0.72481	**-1.41**	0.00481
STM1720	yciO	putative dsRNA-binding protein	**0.75**	0.18460	**0.32**	0.37035	**-1.08**	0.07843
STM1721	trpH	hypothetical protein STM1721	**-1.68**	0.01741	**0.51**	0.14837	**-1.09**	0.01731
STM1721	trpH	hypothetical protein STM1721	**-1.07**	0.09108	**0.79**	0.03202	**-0.36**	0.47944
STM1723	trpE	anthranilate synthase component I	**-0.50**	0.29099	**1.27**	0.01393	**0.24**	0.54835
STM1723	trpE	anthranilate synthase component I	**-0.50**	0.69462	**1.28**	0.00760	**0.40**	0.31776
STM1724	trpD	anthranilate phosphoribosyltransferase	**-1.03**	0.13709	**1.25**	0.03782	**-1.08**	0.01220
STM1724	trpD	anthranilate phosphoribosyltransferase	**0.24**	0.76454	**1.59**	0.00387	**0.30**	0.45535
STM1725	trpC	bifunctional indole-3-glycerol phosphate	**-0.86**	0.10403	**1.61**	0.00243	**0.15**	0.72044
STM1725	trpC	bifunctional indole-3-glycerol phosphate	**-0.22**	0.88887	**1.57**	0.00075	**-0.76**	0.12196
STM1726	trpB	tryptophan synthase subunit beta	**0.49**	0.54784	**2.12**	0.00055	**0.77**	0.14447
STM1726	trpB	tryptophan synthase subunit beta	**-1.83**	0.06773	**2.26**	0.00022	**0.19**	0.67664
STM1727	trpA	tryptophan synthase subunit alpha	**-0.33**	0.59371	**0.39**	0.48880	**0.49**	0.37174
STM1727	trpA	tryptophan synthase subunit alpha	**0.35**	0.38726	**-0.14**	0.73291	**1.37**	0.00810
STM1728	yciG	putative cytoplasmic protein	**0.57**	0.34131	**2.73**	0.00016	**9.56**	0.00001
STM1728	yciG	putative cytoplasmic protein	**1.22**	0.04764	**2.92**	0.00033	**9.94**	0.00001
STM1729	yciF	putative cytoplasmic protein	**1.98**	0.01722	**-0.58**	0.18907	**4.65**	0.00006
STM1729	yciF	putative cytoplasmic protein	**2.54**	0.01257	**-0.79**	0.10049	**5.82**	0.00006
STM1730	yciE	putative cytoplasmic protein	**0.09**	0.87489	**1.05**	0.03714	**4.92**	0.00008
STM1730	yciE	putative cytoplasmic protein	**1.21**	0.13003	**0.76**	0.10295	**5.32**	0.00009
STM1731	STM1731	putative catalase	**2.73**	0.00627	**1.09**	0.32533	**3.42**	0.00160
STM1731	STM1731	putative catalase	**3.07**	0.00541	**-0.08**	0.88876	**3.70**	0.00015
STM1732	ompW	outer membrane protein W precursor	**1.12**	0.14828	**0.37**	0.36876	**0.88**	0.08351
STM1732	ompW	outer membrane protein W precursor	**2.84**	0.07400	**0.15**	0.72730	**1.86**	0.00482
STM1733	STM1733	putative ferredoxin	**-0.48**	0.26894	**0.92**	0.01800	**-0.52**	0.15550
STM1733	STM1733	putative ferredoxin	**0.38**	0.47513	**1.44**	0.00152	**0.54**	0.28659
STM1734	yciC	hypothetical protein STM1734	**-1.16**	0.12984	**-0.19**	0.57388	**-1.17**	0.01815
STM1734	yciC	hypothetical protein STM1734	**-0.44**	0.30885	**-0.19**	0.51869	**-0.95**	0.23475
STM1735	yciB	putative intracellular septation protein	**-0.05**	0.96137	**-0.29**	0.33283	**-0.45**	0.44697
STM1735	yciB	putative intracellular septation protein	**-0.13**	0.86652	**0.09**	0.84064	**-1.49**	0.20119
STM1736	yciA	putative Acyl-CoA hydrolase	**-0.27**	0.65402	**-0.02**	0.96348	**-1.24**	0.02160
STM1736	yciA	putative Acyl-CoA hydrolase	**-0.49**	0.36774	**0.48**	0.11014	**-1.12**	0.05123
STM1737	tonB	periplasmic protein	**0.16**	0.80250	**0.77**	0.02678	**-0.88**	0.15765
STM1737	tonB	periplasmic protein	**0.11**	0.79059	**0.76**	0.04650	**-0.41**	0.32946
STM1738	yciI	putative cytoplasmic protein	**-0.44**	0.36401	**0.46**	0.16730	**-1.05**	0.02255
STM1738	yciI	putative cytoplasmic protein	**-0.47**	0.28742	**0.61**	0.06548	**-0.54**	0.23646
STM1739	cls	cardiolipin synthetase	**-0.68**	0.11908	**-0.11**	0.76820	**-0.55**	0.17285
STM1739	cls	cardiolipin synthetase	**0.66**	0.15487	**0.24**	0.48035	**0.04**	0.95099
STM1741	STM1741	putative voltage-gated potassium channel	**-0.20**	0.68092	**0.10**	0.78745	**-0.08**	0.88181
STM1741	STM1741	putative voltage-gated potassium channel	**0.85**	0.59115	**-0.80**	0.02257	**0.27**	0.54480

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM1742	oppF	oligopeptide transport protein	**-1.17**	0.09992	**0.62**	0.06337	**0.69**	0.08426
STM1742	oppF	oligopeptide transport protein	**-0.16**	0.75688	**0.32**	0.34189	**-0.15**	0.76744
STM1743	oppD	oligopeptide transporter ATP-binding component	**0.23**	0.81712	**0.50**	0.11869	**-0.29**	0.74442
STM1743	oppD	oligopeptide transporter ATP-binding component	**2.51**	0.00747	**0.69**	0.04822	**-0.18**	0.81252
STM1744	oppC	oligopeptide transport protein	**-0.78**	0.18217	**0.39**	0.30700	**0.03**	0.95920
STM1744	oppC	oligopeptide transport protein	**0.28**	0.68556	**0.61**	0.07138	**-0.17**	0.73163
STM1745	oppB	oligopeptide permease ABC transporter membrane	**-1.54**	0.03905	**0.43**	0.58382	**-1.47**	0.01667
STM1745	oppB	oligopeptide permease ABC transporter membrane	**-0.30**	0.61000	**-0.31**	0.41915	**-0.17**	0.84393
STM1746,S	oppA	oligopeptide transport protein	**-0.09**	0.92192	**2.34**	0.00023	**-0.15**	0.74177
STM1746,S	oppA	oligopeptide transport protein	**0.22**	0.78556	**2.82**	0.00009	**-0.53**	0.17375
STM1748	ychE	putative integral membrane protein	**1.41**	0.04933	**-0.24**	0.55886	**1.60**	0.06407
STM1748	ychE	putative integral membrane protein	**1.37**	0.02845	**-0.58**	0.14276	**-0.61**	0.23261
STM1749	adhE	iron-dependent alcohol dehydrogenase	**0.78**	0.11427	**0.78**	0.03074	**1.77**	0.00129
STM1749	adhE	iron-dependent alcohol dehydrogenase	**1.28**	0.02838	**1.15**	0.00530	**2.33**	0.00110
STM1750	tdk	thymidine kinase	**0.07**	0.89997	**-0.51**	0.11302	**-0.74**	0.05032
STM1750	tdk	thymidine kinase	**1.58**	0.03552	**0.05**	0.89029	**0.16**	0.79147
STM1751	hns	DNA-binding protein HLP-II	**-0.46**	0.54118	**0.70**	0.04936	**-0.02**	0.95416
STM1751	hns	DNA-binding protein HLP-II	**0.31**	0.57278	**0.77**	0.03407	**-0.03**	0.95904
STM1752	galU	glucose-1-phosphate uridylyltransferase	**-1.19**	0.03293	**1.05**	0.00653	**-0.79**	0.11420
STM1752	galU	glucose-1-phosphate uridylyltransferase	**-0.21**	0.71082	**0.71**	0.03824	**-0.56**	0.16215
STM1753	hnr	response regulator	**-0.12**	0.89255	**-0.46**	0.20794	**-0.41**	0.41451
STM1753	hnr	response regulator	**-0.03**	0.97323	**-0.89**	0.14427	**1.13**	0.03238
STM1754	ychK	putative phosphoesterase	**-1.24**	0.04313	**-0.74**	0.05451	**-0.95**	0.10252
STM1754	ychK	putative phosphoesterase	**-0.79**	0.12276	**-0.68**	0.03335	**0.32**	0.51476
STM1755	ychJ	hypothetical protein STM1755	**-1.84**	0.01963	**-0.68**	0.03694	**-1.26**	0.10996
STM1755	ychJ	hypothetical protein STM1755	**-1.31**	0.06828	**-0.73**	0.02381	**-0.87**	0.06998
STM1756	purU	formyltetrahydrofolate deformylase	**-3.20**	0.00541	**-1.06**	0.01496	**-1.54**	0.00309
STM1756	purU	formyltetrahydrofolate deformylase	**-1.49**	0.11036	**-1.21**	0.00229	**-1.41**	0.04852
STM1757	tyrT	STM1757	**-0.50**	0.60869	**-1.65**	0.00173	**-0.69**	0.16121
STM1757	tyrT	STM1757	**0.27**	0.65110	**-1.01**	0.00832	**-0.70**	0.08626
STM1758	rtT	STM1758	**-0.73**	0.22585	**-1.83**	0.00042	**-2.44**	0.00028
STM1758	rtT	STM1758	**-1.06**	0.06025	**-1.17**	0.00791	**-1.78**	0.00296
STM1759	tyrV	STM1759	**-0.49**	0.50198	**-1.88**	0.00109	**-0.10**	0.84748
STM1759	tyrV	STM1759	**-0.21**	0.69393	**-1.62**	0.00134	**-0.63**	0.13548
STM1760	STM1760	tetratricopeptide repeat protein	**0.20**	0.78328	**-0.73**	0.03511	**0.61**	0.28682
STM1760	STM1760	tetratricopeptide repeat protein	**1.63**	0.03715	**-0.22**	0.43148	**0.70**	0.12451
STM1761	narI	nitrate reductase 1 gamma subunit	**-0.15**	0.70958	**-0.10**	0.72195	**-0.65**	0.09943
STM1761	narI	nitrate reductase 1 gamma subunit	**0.29**	0.68360	**-0.42**	0.14427	**-0.56**	0.23680
STM1762	narJ	nitrate reductase 1 delta subunit	**0.84**	0.31460	**-0.25**	0.42695	**-0.75**	0.08184
STM1762	narJ	nitrate reductase 1 delta subunit	**1.54**	0.02588	**-0.75**	0.02000	**-0.06**	0.90592
STM1763	narH	nitrate reductase 1 beta subunit	**-0.60**	0.37870	**0.22**	0.51046	**-1.19**	0.04827
STM1763	narH	nitrate reductase 1 beta subunit	**0.96**	0.26990	**-0.47**	0.15199	**0.56**	0.36023
STM1764	narG	nitrate reductase 1 alpha subunit	**0.32**	0.60323	**-0.30**	0.54197	**0.56**	0.34026
STM1764	narG	nitrate reductase 1 alpha subunit	**1.16**	0.03756	**0.03**	0.94280	**1.49**	0.00486
STM1765	narK	nitrite extrusion protein	**-1.17**	0.11156	**-0.06**	0.92834	**-1.08**	0.05136
STM1765	narK	nitrite extrusion protein	**0.17**	0.72937	**-0.33**	0.50308	**0.06**	0.91035
STM1766	narX	sensory histidine kinase	**-0.67**	0.35595	**1.22**	0.07274	**-0.71**	0.27027
STM1766	narX	sensory histidine kinase	**0.23**	0.61190	**1.02**	0.01052	**-0.56**	0.23529
STM1767	narL	response regulator	**1.13**	0.24890	**1.53**	0.03402	**0.71**	0.50372
STM1767	narL	response regulator	**2.53**	0.06690	**3.16**	0.00989	**3.57**	0.01880
STM1768	ychP	putative invasin	**-1.11**	0.10387	**-0.43**	0.62945	**0.53**	0.37940
STM1768	ychP	putative invasin	**-0.10**	0.84920	**0.75**	0.03423	**-0.20**	0.63608
STM1769	ychN	putative sulfur reduction protein	**-0.76**	0.13795	**0.97**	0.03683	**-0.07**	0.88173
STM1769	ychN	putative sulfur reduction protein	**0.05**	0.90987	**0.72**	0.03615	**0.60**	0.12086
STM1770	chaB	cation transport regulator	**-0.19**	0.81928	**1.84**	0.00129	**3.22**	0.00011
STM1770	chaB	cation transport regulator	**1.05**	0.10071	**1.40**	0.00409	**3.59**	0.00014
STM1771	chaA	sodium-calcium/proton antiporter	**-0.18**	0.70066	**-0.10**	0.78276	**-1.62**	0.00722
STM1771	chaA	sodium-calcium/proton antiporter	**-0.09**	0.83664	**0.08**	0.82502	**-0.83**	0.06413
STM1772	kdsA	2-dehydro-3-deoxyphosphooctonate aldolase	**-0.97**	0.06005	**0.02**	0.96249	**-2.30**	0.00315
STM1772	kdsA	2-dehydro-3-deoxyphosphooctonate aldolase	**-0.11**	0.85232	**0.15**	0.63173	**-0.85**	0.14915
STM1773	ychA	putative transcriptional regulator	**-2.33**	0.00660	**-1.31**	0.00265	**-2.23**	0.00274
STM1773	ychA	putative transcriptional regulator	**-1.35**	0.07992	**-1.00**	0.01545	**-2.30**	0.00030
STM1774	sirC	transcriptional regulator	**-2.26**	0.00747	**-1.66**	0.00075	**-2.78**	0.00077
STM1774	sirC	transcriptional regulator	**-2.16**	0.02605	**-0.93**	0.00989	**-2.51**	0.01183
STM1775	hemK	N5-glutamine S-adenosyl-L-methionine-dependent	**-1.74**	0.01289	**-1.75**	0.00069	**-1.77**	0.00155
STM1775	hemK	N5-glutamine S-adenosyl-L-methionine-dependent	**-0.69**	0.13620	**-1.73**	0.00804	**-0.59**	0.11017
STM1776	prfA	peptide chain release factor 1	**-0.79**	0.11797	**-1.97**	0.00035	**-2.45**	0.00178
STM1776	prfA	peptide chain release factor 1	**0.39**	0.57568	**-1.47**	0.00157	**-2.11**	0.01443
STM1777	hemA	glutamyl-tRNA reductase	**-2.97**	0.00957	**-2.22**	0.00016	**-2.28**	0.00053
STM1777	hemA	glutamyl-tRNA reductase	**-2.25**	0.01041	**-1.85**	0.00073	**-2.30**	0.00143

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM1778	lolB	outer membrane lipoprotein LolB precursor	**-2.46**	0.00645	**-0.40**	0.24496	**-1.84**	0.00403
STM1778	lolB	outer membrane lipoprotein LolB precursor	**-1.10**	0.06843	**-0.07**	0.85187	**-0.97**	0.02512
STM1779	ipk	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase	**-3.30**	0.01562	**-0.80**	0.01544	**-4.11**	0.00007
STM1779	ipk	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase	**-2.98**	0.02506	**-0.58**	0.07712	**-3.43**	0.00008
STM1780	prsA	ribose-phosphate pyrophosphokinase	**-1.14**	0.06232	**0.11**	0.70659	**-1.96**	0.00518
STM1780	prsA	ribose-phosphate pyrophosphokinase	**-0.22**	0.71993	**0.68**	0.04325	**-1.12**	0.13122
STM1781	ychM	putative transport protein	**-0.52**	0.20702	**-0.24**	0.59609	**-0.69**	0.06285
STM1781	ychM	putative transport protein	**0.25**	0.60061	**-0.47**	0.12426	**0.55**	0.31447
STM1782	ychH	putative inner membrane protein	**-0.16**	0.71523	**0.38**	0.17560	**0.16**	0.70952
STM1782	ychH	putative inner membrane protein	**0.07**	0.94318	**0.10**	0.79449	**1.20**	0.01833
STM1783,S	pth	peptidyl-tRNA hydrolase	**-1.68**	0.03082	**-0.47**	0.22548	**-1.90**	0.00068
STM1783,S	pth	peptidyl-tRNA hydrolase	**-0.93**	0.06648	**-0.69**	0.05422	**-0.98**	0.01832
STM1784	ychF	putative GTP-binding protein	**0.29**	0.53344	**-0.36**	0.28464	**0.80**	0.24472
STM1784	ychF	putative GTP-binding protein	**1.41**	0.01970	**-0.34**	0.33869	**2.35**	0.00027
STM1785	STM1785	putative cytoplasmic protein	**-0.73**	0.17732	**-0.44**	0.16042	**-0.66**	0.12110
STM1785	STM1785	putative cytoplasmic protein	**-0.23**	0.69641	**-0.50**	0.13595	**-0.10**	0.81893
STM1786	STM1786	hydrogenase-1 small subunit	**2.72**	0.01063	**0.99**	0.05130	**3.40**	0.00643
STM1786	STM1786	hydrogenase-1 small subunit	**4.66**	0.00512	**0.49**	0.40512	**4.27**	0.00012
STM1787	STM1787	hydrogenase-1 large subunit	**0.70**	0.25720	**-2.83**	0.00025	**-0.43**	0.49349
STM1787	STM1787	hydrogenase-1 large subunit	**0.93**	0.25394	**-2.49**	0.00201	**1.14**	0.02782
STM1788	STM1788	putative Ni/Fe hydrogenase 1 b-type cytochrome subunit	**-0.18**	0.81579	**-0.93**	0.10958	**-0.36**	0.37158
STM1788	STM1788	putative Ni/Fe hydrogenase 1 b-type cytochrome subunit	**0.78**	0.12984	**-0.04**	0.94701	**0.56**	0.19159
STM1789	STM1789	putative hydrogenase maturation protease	**1.56**	0.04270	**1.74**	0.00160	**2.45**	0.00093
STM1789	STM1789	putative hydrogenase maturation protease	**1.72**	0.02601	**0.26**	0.74343	**2.36**	0.00090
STM1790	STM1790	putative chaperone	**-0.29**	0.72124	**-1.65**	0.02894	**-0.65**	0.44194
STM1790	STM1790	putative chaperone	**1.87**	0.04212	**-0.79**	0.09950	**-1.43**	0.01239
STM1791	STM1791	putative hydrogenase-1 protein	**0.11**	0.81981	**-1.00**	0.01035	**-1.40**	0.02488
STM1791	STM1791	putative hydrogenase-1 protein	**0.59**	0.22078	**-1.13**	0.00602	**0.09**	0.87274
STM1792	STM1792	putative cytochrome oxidase subunit I	**-0.49**	0.30493	**-2.56**	0.00071	**-1.28**	0.14497
STM1792	STM1792	putative cytochrome oxidase subunit I	**0.54**	0.21536	**-1.06**	0.05380	**-0.22**	0.64205
STM1793	STM1793	putative cytochrome oxidase subunit II	**0.55**	0.32854	**0.07**	0.91626	**0.10**	0.79361
STM1793	STM1793	putative cytochrome oxidase subunit II	**5.37**	0.02043	**0.16**	0.72937	**2.62**	0.02852
STM1795	STM1795	putative glutamic dehyrogenase-like protein	**-0.19**	0.82084	**0.88**	0.02982	**0.39**	0.29354
STM1795	STM1795	putative glutamic dehyrogenase-like protein	**-0.29**	0.71427	**1.29**	0.00667	**1.40**	0.00765
STM1796	treA	trehalase	**-0.31**	0.64480	**1.44**	0.00210	**1.77**	0.00602
STM1796	treA	trehalase	**0.97**	0.14957	**1.67**	0.00055	**2.95**	0.00011
STM1797	ymgE	putative transglycosylase-associated protein	**0.19**	0.66258	**1.05**	0.07722	**2.27**	0.00118
STM1797	ymgE	putative transglycosylase-associated protein	**0.61**	0.23679	**0.58**	0.08296	**2.11**	0.00176
STM1798	ycgR	putative inner membrane protein	**-0.90**	0.09175	**-0.62**	0.07502	**-1.03**	0.03239
STM1798	ycgR	putative inner membrane protein	**-0.52**	0.40921	**-0.89**	0.01630	**-0.74**	0.11684
STM1799	emtA	membrane-bound lytic murein transglycosylase E	**-0.94**	0.06614	**-1.17**	0.02011	**-0.52**	0.15994
STM1799	emtA	membrane-bound lytic murein transglycosylase E	**-0.61**	0.19018	**-1.00**	0.01030	**-1.18**	0.01113
STM1800	ycgQ	putative microcin C7 resistance protein	**-0.86**	0.19542	**0.30**	0.45792	**-0.03**	0.96386
STM1800	ycgQ	putative microcin C7 resistance protein	**-1.21**	0.19673	**-0.31**	0.38885	**-0.77**	0.06160
STM1801	ycgO	cell volume regulation protein CvrA	**0.72**	0.13459	**-0.03**	0.93046	**0.65**	0.37379
STM1801	ycgO	cell volume regulation protein CvrA	**1.80**	0.01836	**-0.07**	0.87209	**2.23**	0.00156
STM1802	alr	alanine racemase	**-1.31**	0.03064	**0.04**	0.90454	**-0.67**	0.48750
STM1802	alr	alanine racemase	**0.83**	0.59024	**-0.25**	0.55009	**0.70**	0.24995
STM1803	dadA	D-amino acid dehydrogenase small subunit	**-0.81**	0.48179	**1.27**	0.00892	**0.87**	0.07753
STM1803	dadA	D-amino acid dehydrogenase small subunit	**-0.62**	0.58469	**1.15**	0.02172	**0.66**	0.25984
STM1804,S	ycgB	putative cytoplasmic protein	**1.31**	0.03224	**2.10**	0.00036	**1.95**	0.00140
STM1804,S	ycgB	putative cytoplasmic protein	**1.73**	0.01244	**2.29**	0.00063	**2.73**	0.00024
STM1805	fadR	fatty acid metabolism regulator	**-1.11**	0.09684	**1.29**	0.00433	**-0.07**	0.87046
STM1805	fadR	fatty acid metabolism regulator	**1.41**	0.23122	**0.96**	0.02151	**0.73**	0.06349
STM1806	nhaB	Na+/H+ antiporter	**-0.03**	0.96020	**-0.10**	0.81370	**-1.56**	0.00471
STM1806	nhaB	Na+/H+ antiporter	**0.07**	0.88091	**-0.15**	0.69958	**-0.33**	0.39997
STM1807	dsbB	disulfide bond formation protein B	**-1.23**	0.03425	**1.08**	0.01799	**-0.72**	0.07700
STM1807	dsbB	disulfide bond formation protein B	**0.32**	0.61958	**0.89**	0.01119	**0.19**	0.64438
STM1808	STM1808	putative cytoplasmic protein	**1.69**	0.04085	**3.62**	0.00003	**1.28**	0.00524
STM1808	STM1808	putative cytoplasmic protein	**1.27**	0.02586	**3.82**	0.00009	**2.60**	0.00022
STM1810	STM1810	putative cytoplasmic protein	**0.29**	0.67888	**1.51**	0.00156	**3.97**	0.00009
STM1810	STM1810	putative cytoplasmic protein	**0.63**	0.32776	**1.36**	0.00521	**4.45**	0.00004
STM1811	ycgN	hypothetical protein STM1811	**-1.30**	0.03961	**0.26**	0.49000	**0.11**	0.79934
STM1811	ycgN	hypothetical protein STM1811	**-0.63**	0.15884	**0.08**	0.83569	**-0.08**	0.83262
STM1812	ycgM	putative fumarylacetoacetate hydrolase	**-1.02**	0.05333	**0.69**	0.09742	**-0.43**	0.23526
STM1812	ycgM	putative fumarylacetoacetate hydrolase	**0.55**	0.43120	**0.75**	0.02354	**-0.01**	0.98546
STM1813	ycgL	putative cytoplasmic protein	**-1.90**	0.00908	**0.00**	0.99904	**-0.13**	0.78971
STM1813	ycgL	putative cytoplasmic protein	**-0.78**	0.10017	**-0.28**	0.46133	**0.24**	0.55218
STM1814	minC	septum formation inhibitor	**-1.87**	0.02504	**-0.33**	0.28451	**-1.24**	0.00621
STM1814	minC	septum formation inhibitor	**-1.14**	0.08868	**-0.19**	0.51062	**-1.11**	0.01020

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM1815	minD	cell division inhibitor protein	**-2.06**	0.00949	**-0.03**	0.93083	**-1.32**	0.01032
STM1815	minD	cell division inhibitor protein	**-1.08**	0.04573	**-0.04**	0.90120	**-0.21**	0.81712
STM1816	minE	cell division topological specificity factor MinE	**-2.18**	0.00829	**-0.45**	0.15984	**-0.82**	0.04265
STM1816	minE	cell division topological specificity factor MinE	**-1.39**	0.04046	**-1.14**	0.03417	**-0.27**	0.60201
STM1817	rnd	RNase D	**-1.47**	0.05699	**-0.49**	0.15021	**-0.77**	0.30331
STM1817	rnd	RNase D	**-1.12**	0.08626	**-1.23**	0.00292	**-0.95**	0.10889
STM1818	fadD	acyl-CoA synthase	**0.09**	0.85422	**0.06**	0.84687	**0.68**	0.11386
STM1818	fadD	acyl-CoA synthase	**0.66**	0.41995	**0.06**	0.86434	**1.43**	0.00482
STM1819	slp	putative outer membrane protein	**-1.78**	0.01426	**-0.31**	0.49020	**-0.46**	0.42850
STM1819	slp	putative outer membrane protein	**-1.71**	0.02945	**-1.07**	0.00885	**-2.47**	0.00122
STM1820	yeaZ	putative molecular chaperone	**-1.68**	0.01397	**-0.23**	0.41061	**-1.87**	0.00104
STM1820	yeaZ	putative molecular chaperone	**-1.39**	0.02009	**-0.07**	0.83443	**-1.29**	0.02447
STM1821	yoaA	putative DNA helicase	**-1.78**	0.02346	**-0.44**	0.67323	**-0.70**	0.21693
STM1821	yoaA	putative DNA helicase	**-0.92**	0.10364	**-1.38**	0.00229	**-1.68**	0.01567
STM1822	yoaB	putative translation initiation inhibitor	**-0.87**	0.23076	**0.22**	0.52929	**-0.11**	0.83480
STM1822	yoaB	putative translation initiation inhibitor	**-2.06**	0.00979	**0.04**	0.89101	**-0.45**	0.24961
STM1823	yoaH	hypothetical protein STM1823	**-1.20**	0.08057	**-0.23**	0.43148	**-1.69**	0.00419
STM1823	yoaH	hypothetical protein STM1823	**0.32**	0.56470	**0.09**	0.82375	**-0.83**	0.03964
STM1824	pabB	para-aminobenzoate synthase component I	**-1.85**	0.02510	**-0.01**	0.98768	**-0.52**	0.40643
STM1824	pabB	para-aminobenzoate synthase component I	**-0.45**	0.60804	**-0.26**	0.43148	**-1.70**	0.00221
STM1825	yeaB	putative NTP pyrophosphohydrolase	**-0.49**	0.33086	**-1.44**	0.04264	**-0.81**	0.23439
STM1825	yeaB	putative NTP pyrophosphohydrolase	**-1.35**	0.06974	**-1.30**	0.00377	**-3.16**	0.02669
STM1826	sdaA	L-serine deaminase I/L-threonine deaminase I	**1.55**	0.02725	**-0.24**	0.52090	**-0.29**	0.61485
STM1826	sdaA	L-serine deaminase I/L-threonine deaminase I	**1.89**	0.01451	**-0.16**	0.70446	**0.34**	0.49610
STM1827,S	STM1827,S	putative diguanylate cyclase/phosphodiesterase	**0.10**	0.85094	**-0.57**	0.19818	**0.06**	0.89351
STM1827,S	STM1827,S	putative diguanylate cyclase/phosphodiesterase	**0.55**	0.37699	**-0.77**	0.03949	**0.83**	0.07569
STM1828	yoaE	putative inner membrane protein	**-0.30**	0.62437	**-0.71**	0.05230	**-0.10**	0.87503
STM1828	yoaE	putative inner membrane protein	**0.23**	0.67110	**-0.31**	0.33624	**0.62**	0.11668
STM1830	manX	mannose-specific enzyme IIAB	**-1.72**	0.03912	**0.38**	0.31259	**-1.29**	0.02506
STM1830	manX	mannose-specific enzyme IIAB	**-0.44**	0.38785	**0.53**	0.13884	**-0.80**	0.09267
STM1831	manY	mannose-specific enzyme IIC	**-1.60**	0.07767	**-0.26**	0.41177	**-1.07**	0.04237
STM1831	manY	mannose-specific enzyme IIC	**-1.27**	0.04769	**0.48**	0.22729	**-0.76**	0.05771
STM1832	manZ	mannose-specific enzyme IID	**-0.99**	0.06717	**-0.52**	0.16760	**-0.33**	0.38154
STM1832	manZ	mannose-specific enzyme IID	**-0.34**	0.42403	**-0.45**	0.12965	**-0.90**	0.02696
STM1833	STM1833	hypothetical protein STM1833	**-1.34**	0.04725	**-0.35**	0.37591	**-1.10**	0.01657
STM1833	STM1833	hypothetical protein STM1833	**0.65**	0.29204	**-0.21**	0.59312	**1.54**	0.00243
STM1834	yebN	putative transport protein	**-0.35**	0.75933	**0.25**	0.46986	**-0.44**	0.28174
STM1834	yebN	putative transport protein	**0.30**	0.64337	**0.11**	0.71105	**-0.94**	0.03025
STM1835	rrmA	23S rRNA m1G745 methyltransferase	**-1.06**	0.06501	**-0.13**	0.66016	**0.09**	0.87248
STM1835	rrmA	23S rRNA m1G745 methyltransferase	**0.02**	0.97348	**0.00**	0.99977	**-1.35**	0.02245
STM1836	STM1836	putative penicillin-binding protein 3	**-0.14**	0.82886	**0.19**	0.65303	**-0.48**	0.28586
STM1836	STM1836	putative penicillin-binding protein 3	**0.35**	0.40927	**-0.98**	0.21643	**0.46**	0.18300
STM1837	cspC	cold shock protein	**-3.63**	0.00755	**-1.15**	0.09337	**-0.74**	0.06473
STM1837	cspC	cold shock protein	**-2.05**	0.00821	**-0.74**	0.13284	**-0.50**	0.16188
STM1839	STM1839	hypothetical protein STM1839	**-0.87**	0.64098	**-1.00**	0.04875	**0.12**	0.89908
STM1839	STM1839	hypothetical protein STM1839	**1.03**	0.04754	**-1.29**	0.00442	**-0.60**	0.30898
STM1840	yobG	putative inner membrane protein	**-0.72**	0.19770	**-0.79**	0.01902	**-0.14**	0.80699
STM1840	yobG	putative inner membrane protein	**-0.97**	0.13075	**-0.93**	0.03027	**-0.97**	0.27698
STM1841	STM1841	hypothetical protein STM1841	**-1.11**	0.10448	**-1.17**	0.00631	**-0.19**	0.63989
STM1841	STM1841	hypothetical protein STM1841	**0.22**	0.69822	**-0.26**	0.44521	**-0.02**	0.97999
STM1842	kdgR	putative transcriptional repressor	**-2.08**	0.01228	**-0.17**	0.76216	**-1.42**	0.05107
STM1842	kdgR	putative transcriptional repressor	**-1.24**	0.22569	**-0.53**	0.16025	**-1.55**	0.02513
STM1843	STM1843	putative transport protein	**-0.85**	0.26308	**-0.20**	0.71216	**-0.23**	0.62668
STM1843	STM1843	putative transport protein	**0.34**	0.51786	**0.88**	0.01533	**0.14**	0.73607
STM1844	htpX	heat shock protein HtpX	**1.05**	0.06251	**2.34**	0.00010	**1.48**	0.00270
STM1844	htpX	heat shock protein HtpX	**1.79**	0.01417	**1.91**	0.00128	**2.60**	0.00021
STM1845	prc	carboxy-terminal protease	**0.65**	0.34370	**0.52**	0.08354	**-0.24**	0.58229
STM1845	prc	carboxy-terminal protease	**1.89**	0.01731	**-0.16**	0.65018	**0.71**	0.07771
STM1846	proQ	putative solute/DNA competence effector	**-3.60**	0.02148	**-1.51**	0.00188	**-3.56**	0.00009
STM1846	proQ	putative solute/DNA competence effector	**-2.90**	0.01102	**-1.37**	0.00140	**-4.51**	0.00163
STM1847	yebR	putative nucleotide-binding protein	**-3.12**	0.00932	**-1.50**	0.00316	**-2.67**	0.00020
STM1847	yebR	putative nucleotide-binding protein	**-1.95**	0.18439	**-1.48**	0.00293	**-3.08**	0.00143
STM1848	yebS	putative inner membrane protein	**-1.28**	0.03725	**-0.97**	0.01712	**-0.07**	0.87847
STM1848	yebS	putative inner membrane protein	**1.23**	0.07213	**-0.43**	0.13836	**1.44**	0.01622
STM1849	STM1849	putative inner membrane protein	**-0.08**	0.85530	**-0.13**	0.70041	**-0.16**	0.76703
STM1849	STM1849	putative inner membrane protein	**1.27**	0.32499	**0.38**	0.54376	**1.04**	0.01772
STM1850	yebU	putative rRNA methyltransferase	**-1.13**	0.05160	**-0.49**	0.10650	**0.03**	0.93658
STM1850	yebU	putative rRNA methyltransferase	**-1.30**	0.03486	**-0.48**	0.18218	**0.23**	0.73581
STM1851	STM1851	putative cytoplasmic protein	**-0.84**	0.18861	**0.47**	0.14193	**1.76**	0.00269
STM1851	STM1851	putative cytoplasmic protein	**-0.30**	0.71390	**0.25**	0.44193	**1.87**	0.00243

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM1852	yebW	putative inner membrane lipoprotein	**-0.09**	0.94318	**0.97**	0.01618	**2.42**	0.00023
STM1852	yebW	putative inner membrane lipoprotein	**-0.48**	0.68800	**1.25**	0.01120	**2.27**	0.00035
STM1853	prpA	serine/threonine protein phosphatase	**-0.62**	0.21115	**0.10**	0.77806	**0.57**	0.16687
STM1853	prpA	serine/threonine protein phosphatase	**0.66**	0.13418	**-0.10**	0.90452	**1.79**	0.00130
STM1854	STM1854	putative inner membrane protein	**0.76**	0.26577	**-0.99**	0.32335	**0.19**	0.65782
STM1854	STM1854	putative inner membrane protein	**1.82**	0.01337	**-0.21**	0.64761	**0.35**	0.57935
STM1855	sopE2	type III-secreted effector protein	**-1.15**	0.04188	**-0.60**	0.26022	**0.06**	0.92946
STM1855	sopE2	type III-secreted effector protein	**1.04**	0.39698	**-0.66**	0.08631	**0.98**	0.03911
STM1856	STM1856	putative cytoplasmic protein	**0.00**	0.99756	**-1.25**	0.00617	**-0.01**	0.98975
STM1856	STM1856	putative cytoplasmic protein	**0.62**	0.55723	**0.72**	0.13437	**-0.65**	0.15222
STM1856,1N	STM1856,1N	hypothetical protein STM1856,1N	**-0.14**	0.88020	**-0.21**	0.60479	**-1.39**	0.02263
STM1856,1N	STM1856,1N	hypothetical protein STM1856,1N	**1.51**	0.07036	**-0.23**	0.57302	**-0.07**	0.90484
STM1857	STM1857	putative acetyltransferase	**-1.14**	0.04794	**0.67**	0.07107	**-0.83**	0.16527
STM1857	STM1857	putative acetyltransferase	**-0.15**	0.85913	**0.64**	0.05332	**-0.80**	0.04702
STM1862	pagO	integral membrane protein	**0.84**	0.08901	**-0.10**	0.81073	**-0.49**	0.37291
STM1862	pagO	integral membrane protein	**3.44**	0.04484	**0.76**	0.06617	**1.78**	0.00120
STM1863	STM1863	putative inner membrane protein	**2.17**	0.10685	**0.99**	0.04344	**2.63**	0.00096
STM1863	STM1863	putative inner membrane protein	**1.95**	0.06312	**0.07**	0.91744	**3.80**	0.00011
STM1864	STM1864	putative inner membrane protein	**0.32**	0.64305	**1.11**	0.58424	**0.09**	0.92833
STM1864	STM1864	putative inner membrane protein	**-0.03**	0.94892	**-1.09**	0.03586	**-1.51**	0.14983
STM1868	mig-3	phage-tail assembly-like protein	**3.84**	0.00512	**2.56**	0.00020	**2.42**	0.01269
STM1868	mig-3	phage-tail assembly-like protein	**4.72**	0.00512	**2.15**	0.00173	**3.31**	0.00227
STM1868,1N	STM1868,1N	hypothetical protein STM1868,1N	**1.84**	0.01814	**1.73**	0.00085	**1.44**	0.09105
STM1868,1N	STM1868,1N	hypothetical protein STM1868,1N	**2.79**	0.00673	**1.75**	0.00061	**2.06**	0.00182
STM1868A	STM1868A	lytic enzyme	**0.34**	0.61112	**4.42**	0.00001	**2.61**	0.00186
STM1868A	STM1868A	lytic enzyme	**1.39**	0.10320	**3.97**	0.00008	**-0.10**	0.88432
STM1869	STM1869	phage-tail assembly-like protein	**5.63**	0.00512	**2.60**	0.00115	**2.47**	0.00190
STM1869	STM1869	phage-tail assembly-like protein	**2.63**	0.01462	**2.26**	0.00261	**2.91**	0.00570
STM1870	STM1870	RecE-like protein	**0.45**	0.56732	**-0.26**	0.57058	**0.63**	0.34915
STM1870	STM1870	RecE-like protein	**2.58**	0.05410	**-0.11**	0.70668	**3.19**	0.00334
STM1873	STM1873	hypothetical protein STM1873	**-0.95**	0.12653	**0.16**	0.60377	**-0.59**	0.29164
STM1873	STM1873	hypothetical protein STM1873	**-0.70**	0.18021	**-0.33**	0.41212	**0.54**	0.20027
STM1874	STM1874	putative inner membrane protein	**-1.12**	0.04842	**0.64**	0.05785	**-1.04**	0.03539
STM1874	STM1874	putative inner membrane protein	**-0.19**	0.74567	**0.73**	0.03854	**-0.65**	0.14903
STM1875	yobA	putative copper resistance protein	**-0.14**	0.72496	**0.31**	0.46715	**1.82**	0.05659
STM1875	yobA	putative copper resistance protein	**1.02**	0.09516	**0.58**	0.12153	**0.83**	0.06344
STM1876	holE	DNA polymerase III theta subunit	**-1.39**	0.10817	**-0.39**	0.30610	**-0.08**	0.92980
STM1876	holE	DNA polymerase III theta subunit	**0.04**	0.94969	**1.30**	0.01056	**0.64**	0.68554
STM1877	STM1877	putative amidohydrolase	**-0.13**	0.84826	**-0.68**	0.06537	**-0.98**	0.07416
STM1877	STM1877	putative amidohydrolase	**0.06**	0.91683	**-0.64**	0.30956	**0.28**	0.53860
STM1878	exoX	exodeoxyribonuclease X	**0.53**	0.21339	**1.68**	0.00064	**0.58**	0.12857
STM1878	exoX	exodeoxyribonuclease X	**0.23**	0.71556	**1.24**	0.00296	**0.43**	0.27486
STM1879	ptrB	protease II	**-1.13**	0.06705	**1.03**	0.03417	**-0.69**	0.10342
STM1879	ptrB	protease II	**1.02**	0.07746	**0.99**	0.02051	**0.55**	0.18104
STM1880	yebE	putative inner membrane protein	**1.38**	0.08296	**3.49**	0.00006	**2.72**	0.00026
STM1880	yebE	putative inner membrane protein	**2.25**	0.02603	**3.44**	0.00003	**3.37**	0.00046
STM1881	yebF	putative periplasmic protein	**0.58**	0.47178	**2.43**	0.00012	**1.09**	0.01219
STM1881	yebF	putative periplasmic protein	**0.69**	0.51936	**2.28**	0.00090	**1.59**	0.00777
STM1882	yebG	DNA damage-inducible protein	**2.11**	0.01091	**2.46**	0.00013	**1.09**	0.01398
STM1882	yebG	DNA damage-inducible protein	**2.87**	0.01545	**2.70**	0.00019	**1.97**	0.00281
STM1883	purT	5'-phosphoribosylglycinamide transformylase	**3.02**	0.00743	**1.13**	0.00564	**4.00**	0.00027
STM1883	purT	5'-phosphoribosylglycinamide transformylase	**3.25**	0.00558	**0.43**	0.39177	**4.70**	0.00004
STM1884	eda	keto-hydroxyglutarate-aldolase/keto-deoxy-	**-0.69**	0.19051	**-0.05**	0.89573	**-2.22**	0.00091
STM1884	eda	keto-hydroxyglutarate-aldolase/keto-deoxy-	**0.61**	0.19050	**0.47**	0.09592	**-1.43**	0.01638
STM1885	edd	phosphogluconate dehydratase	**-1.01**	0.09487	**-0.19**	0.61557	**-2.30**	0.00054
STM1885	edd	phosphogluconate dehydratase	**-0.01**	0.97537	**0.12**	0.67595	**-2.02**	0.00099
STM1886	zwf	glucose-6-phosphate 1-dehydrogenase	**-0.72**	0.12200	**-0.20**	0.52151	**-1.12**	0.01993
STM1886	zwf	glucose-6-phosphate 1-dehydrogenase	**1.05**	0.13203	**-0.01**	0.97851	**-0.09**	0.87168
STM1887	yebK	putative transcriptional regulator	**-0.95**	0.14579	**0.40**	0.29174	**0.08**	0.91754
STM1887	yebK	putative transcriptional regulator	**0.33**	0.47263	**0.04**	0.90527	**0.86**	0.03093
STM1888	pykA	pyruvate kinase	**-0.76**	0.17822	**-0.77**	0.05138	**-1.33**	0.00470
STM1888	pykA	pyruvate kinase	**-0.96**	0.05424	**-0.49**	0.10315	**-0.42**	0.33028
STM1889	msbB	lipid A biosynthesis lauroyl acyltransferase	**-1.29**	0.06515	**-0.93**	0.03416	**-0.72**	0.12561
STM1889	msbB	lipid A biosynthesis lauroyl acyltransferase	**-0.13**	0.86139	**-0.30**	0.39724	**-0.09**	0.84249
STM1890	yebA	putative peptidase	**-1.04**	0.13234	**-0.02**	0.96555	**-0.59**	0.15751
STM1890	yebA	putative peptidase	**-0.74**	0.14975	**-0.47**	0.18168	**-1.28**	0.08634
STM1891	znuA	high-affinity Zn transport protein	**-1.16**	0.10292	**0.77**	0.03417	**-0.58**	0.17232
STM1891	znuA	high-affinity Zn transport protein	**0.11**	0.81005	**0.96**	0.01350	**-0.06**	0.88311
STM1892,S	znuC	high-affinity Zn transport protein	**-0.80**	0.32005	**0.12**	0.81238	**-2.02**	0.00130
STM1892,S	znuC	high-affinity Zn transport protein	**-0.18**	0.85345	**-0.62**	0.04372	**-0.78**	0.07178

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM1893	znuB	high-affinity Zn transport protein	**0.21**	0.69269	**-0.40**	0.41534	**-0.87**	0.12063
STM1893	znuB	high-affinity Zn transport protein	**2.35**	0.06965	**0.19**	0.63567	**-1.00**	0.10763
STM1894	ruvB	Holliday junction DNA helicase RuvB	**-0.66**	0.19208	**-0.54**	0.08898	**-1.45**	0.01077
STM1894	ruvB	Holliday junction DNA helicase RuvB	**0.66**	0.16914	**-0.09**	0.82055	**-0.81**	0.08815
STM1895	ruvA	Holliday junction DNA helicase motor protein	**-0.46**	0.26712	**0.36**	0.31213	**-1.69**	0.00458
STM1895	ruvA	Holliday junction DNA helicase motor protein	**0.50**	0.43590	**0.40**	0.35577	**-1.32**	0.02497
STM1896	STM1896	putative cytoplasmic protein	**0.45**	0.60796	**-2.60**	0.00025	**-0.64**	0.18380
STM1896	STM1896	putative cytoplasmic protein	**1.39**	0.04624	**-2.49**	0.01065	**0.77**	0.13039
STM1897	yebB	putative periplasmic protein	**-1.08**	0.11510	**-0.64**	0.08374	**-2.09**	0.00217
STM1897	yebB	putative periplasmic protein	**-0.61**	0.15195	**-0.61**	0.08556	**-1.81**	0.00130
STM1898	ruvC	Holliday junction resolvase	**-1.31**	0.04312	**-0.57**	0.07316	**-1.46**	0.00903
STM1898	ruvC	Holliday junction resolvase	**-1.55**	0.01547	**-0.26**	0.34032	**-1.90**	0.00103
STM1899	yebC	hypothetical protein STM1899	**-1.97**	0.03039	**-1.00**	0.01326	**-2.69**	0.00189
STM1899	yebC	hypothetical protein STM1899	**-0.26**	0.63739	**-0.79**	0.06829	**-2.05**	0.01183
STM1900	ntpA	dATP pyrophosphohydrolase	**-2.75**	0.03103	**-0.83**	0.02165	**-2.80**	0.00020
STM1900	ntpA	dATP pyrophosphohydrolase	**-1.78**	0.01808	**-0.76**	0.03152	**-3.52**	0.00419
STM1901	aspS	aspartyl-tRNA synthetase	**-2.35**	0.00753	**-0.31**	0.46401	**-3.70**	0.00008
STM1901	aspS	aspartyl-tRNA synthetase	**-1.04**	0.04983	**-0.12**	0.70432	**-3.29**	0.00008
STM1902	yecD	putative isochorismatase	**-1.10**	0.04151	**-0.40**	0.20524	**-1.26**	0.00564
STM1902	yecD	putative isochorismatase	**0.28**	0.50253	**-0.04**	0.88848	**-0.40**	0.40102
STM1903	yecE	putative cytoplasmic protein	**-0.98**	0.05901	**-1.03**	0.00754	**-0.75**	0.05454
STM1903	yecE	putative cytoplasmic protein	**-0.10**	0.83590	**-1.39**	0.00955	**-0.12**	0.92529
STM1904	yecN	putative inner membrane protein	**-1.67**	0.02124	**-0.97**	0.02354	**-1.75**	0.00811
STM1904	yecN	putative inner membrane protein	**-1.01**	0.05001	**-0.73**	0.02933	**-1.90**	0.00126
STM1905	yecO	putative SAM-dependent methyltransferase	**-2.30**	0.00689	**-0.97**	0.00834	**-2.22**	0.00035
STM1905	yecO	putative SAM-dependent methyltransferase	**-2.20**	0.00766	**-1.17**	0.00446	**-2.13**	0.00053
STM1906	yecP	putative enzyme	**-0.10**	0.85599	**-0.13**	0.70537	**0.18**	0.86159
STM1906	yecP	putative enzyme	**-0.12**	0.88354	**-0.85**	0.08590	**-0.04**	0.95259
STM1907	cutC	copper homeostasis protein	**0.16**	0.83879	**0.55**	0.10650	**1.24**	0.02189
STM1907	cutC	copper homeostasis protein	**0.93**	0.13232	**0.08**	0.85765	**1.85**	0.00145
STM1908	yecM	putative cytoplasmic protein	**-1.40**	0.03953	**-0.31**	0.63837	**-1.41**	0.00412
STM1908	yecM	putative cytoplasmic protein	**-1.25**	0.06811	**-1.06**	0.01963	**-0.95**	0.04177
STM1909	argS	arginyl-tRNA synthetase	**-1.17**	0.05944	**0.08**	0.76642	**-0.88**	0.21366
STM1909	argS	arginyl-tRNA synthetase	**-0.74**	0.29367	**-0.56**	0.06202	**-1.57**	0.00712
STM1910	STM1910	putative penicillin-binding protein	**0.11**	0.84070	**-0.24**	0.57934	**-0.18**	0.70266
STM1910	STM1910	putative penicillin-binding protein	**1.34**	0.10547	**-0.21**	0.70208	**2.03**	0.01824
STM1911	STM1911	putative cytoplasmic protein	**-0.67**	0.20370	**0.31**	0.48885	**1.26**	0.07759
STM1911	STM1911	putative cytoplasmic protein	**0.41**	0.64286	**0.20**	0.54813	**0.72**	0.12023
STM1912	flhE	flagellar protein	**-1.39**	0.07470	**-2.09**	0.00603	**-1.62**	0.02020
STM1912	flhE	flagellar protein	**-1.23**	0.24936	**-1.98**	0.00086	**-1.82**	0.04888
STM1913	flhA	flagellar biosynthesis protein	**-1.83**	0.01114	**-1.75**	0.01786	**-0.85**	0.04600
STM1913	flhA	flagellar biosynthesis protein	**-0.40**	0.74417	**-2.20**	0.00052	**-1.55**	0.00219
STM1914	flhB	flagellar biosynthesis protein	**-2.35**	0.00661	**-3.89**	0.01093	**-3.06**	0.00035
STM1914	flhB	flagellar biosynthesis protein	**-0.35**	0.54812	**-2.92**	0.00019	**-1.06**	0.01651
STM1915	cheZ	chemotactic response protein	**-3.21**	0.00546	**-3.58**	0.00003	**-3.18**	0.00013
STM1915	cheZ	chemotactic response protein	**-1.08**	0.13203	**-3.98**	0.00001	**-2.82**	0.00024
STM1916	cheY	chemotaxis regulator	**-5.49**	0.00512	**-5.08**	0.00000	**-5.28**	0.00006
STM1916	cheY	chemotaxis regulator	**-3.66**	0.00537	**-4.53**	0.00002	**-4.42**	0.00006
STM1917	cheB	chemotaxis-specific methylesterase	**-4.75**	0.00512	**-5.07**	0.00000	**-5.74**	0.00001
STM1917	cheB	chemotaxis-specific methylesterase	**-3.90**	0.00541	**-5.48**	0.00000	**-5.02**	0.00005
STM1918	cheR	glutamate methyltransferase	**-1.09**	0.03878	**-4.12**	0.00001	**-3.12**	0.00235
STM1918	cheR	glutamate methyltransferase	**-2.14**	0.00774	**-4.72**	0.00003	**-3.02**	0.00439
STM1919	cheM	methyl accepting chemotaxis protein II	**-3.22**	0.00547	**-4.48**	0.00001	**-3.08**	0.00025
STM1919	cheM	methyl accepting chemotaxis protein II	**-1.73**	0.04036	**-3.45**	0.00004	**-3.75**	0.00014
STM1920	cheW	chemotaxis docking protein	**-1.93**	0.02171	**-1.45**	0.09455	**-1.69**	0.00256
STM1920	cheW	chemotaxis docking protein	**-1.67**	0.18852	**-3.32**	0.00004	**-3.19**	0.00602
STM1921	cheA	chemotaxis sensory histidine protein kinase	**-3.61**	0.00753	**-4.08**	0.00006	**-3.61**	0.00007
STM1921	cheA	chemotaxis sensory histidine protein kinase	**-3.19**	0.00818	**-3.89**	0.00001	**-4.12**	0.00004
STM1922	motB	flagellar motor protein	**-2.77**	0.00689	**-2.97**	0.01120	**-4.39**	0.00050
STM1922	motB	flagellar motor protein	**-2.58**	0.01319	**-3.71**	0.00008	**-4.72**	0.00553
STM1923	motA	flagellar motor protein	**-1.72**	0.03161	**-2.43**	0.00013	**-2.03**	0.01060
STM1923	motA	flagellar motor protein	**-0.42**	0.57773	**-2.92**	0.00008	**-1.11**	0.02639
STM1924,S	flhC	flagellar transcriptional activator	**-2.57**	0.00768	**-1.22**	0.00277	**-0.91**	0.05584
STM1924,S	flhC	flagellar transcriptional activator	**-1.39**	0.05350	**-1.64**	0.00478	**-0.77**	0.11140
STM1925	flhD	transcriptional activator FlhD	**-1.46**	0.04296	**0.39**	0.28718	**-0.97**	0.05594
STM1925	flhD	transcriptional activator FlhD	**-0.50**	0.36030	**0.55**	0.15826	**-1.18**	0.11698
STM1927	yecG	putative universal stress protein	**-0.25**	0.70286	**0.06**	0.88193	**0.66**	0.09479
STM1927	yecG	putative universal stress protein	**0.06**	0.90764	**0.05**	0.88515	**1.19**	0.01015
STM1928	otsA	trehalose-6-phosphate synthase	**2.06**	0.07172	**-1.43**	0.00418	**1.63**	0.11118
STM1928	otsA	trehalose-6-phosphate synthase	**1.50**	0.07863	**-1.54**	0.00109	**1.89**	0.06818

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM1929	otsB	trehalose-6-phosphate phophatase	**0.90**	0.16362	**2.95**	0.00009	**3.51**	0.00014
STM1929	otsB	trehalose-6-phosphate phophatase	**1.83**	0.06001	**2.74**	0.00034	**5.27**	0.00003
STM1931	araH	putative intracellular protease/amidase	**-0.84**	0.28542	**-0.08**	0.85737	**2.36**	0.00621
STM1931	araH	putative intracellular protease/amidase	**0.75**	0.25242	**-1.00**	0.01533	**3.04**	0.00016
STM1932	ftnB	ferritin-like protein	**-0.04**	0.94879	**0.80**	0.04298	**0.06**	0.91352
STM1932	ftnB	ferritin-like protein	**1.83**	0.07329	**0.91**	0.04772	**1.24**	0.03940
STM1933	STM1933	hypothetical protein STM1933	**0.82**	0.15894	**0.46**	0.10373	**0.76**	0.08841
STM1933	STM1933	hypothetical protein STM1933	**1.45**	0.02435	**0.56**	0.17100	**1.28**	0.01647
STM1934	STM1934	putative outer membrane lipoprotein	**-1.16**	0.05040	**-1.16**	0.15093	**-0.87**	0.09520
STM1934	STM1934	putative outer membrane lipoprotein	**-0.75**	0.31231	**-1.55**	0.00254	**-1.31**	0.06191
STM1935	ftn	cytoplasmic ferritin	**-1.86**	0.01713	**-1.57**	0.00147	**-2.68**	0.00135
STM1935	ftn	cytoplasmic ferritin	**-1.04**	0.13364	**-1.32**	0.00189	**-2.24**	0.00881
STM1936	yecH	putative cytoplasmic protein	**-1.41**	0.02108	**-0.54**	0.24399	**-0.96**	0.04041
STM1936	yecH	putative cytoplasmic protein	**-1.30**	0.16100	**-1.97**	0.00751	**-2.75**	0.00255
STM1937	tyrP	tyrosine-specific transport protein	**-0.93**	0.18749	**0.25**	0.37591	**-0.01**	0.98406
STM1937	tyrP	tyrosine-specific transport protein	**-0.35**	0.53849	**-0.25**	0.39589	**-1.33**	0.11111
STM1938	yecA	putative metal-binding protein	**0.34**	0.46969	**0.62**	0.06956	**-0.56**	0.27532
STM1938	yecA	putative metal-binding protein	**1.37**	0.07476	**0.77**	0.03337	**0.78**	0.07118
STM1939	STM1939	putative glucose-6-phosphate dehydrogenase	**0.28**	0.70745	**-0.96**	0.12341	**-1.94**	0.00074
STM1939	STM1939	putative glucose-6-phosphate dehydrogenase	**0.87**	0.07451	**-0.01**	0.97347	**-0.74**	0.24139
STM1940	STM1940	putative cell wall-associated hydrolase	**0.00**	0.99251	**3.43**	0.00004	**1.06**	0.12800
STM1940	STM1940	putative cell wall-associated hydrolase	**1.06**	0.24690	**0.09**	0.89964	**1.64**	0.03331
STM1941	STM1941	putative inner membrane protein	**-0.44**	0.28122	**-0.93**	0.20359	**-1.47**	0.00297
STM1941	STM1941	putative inner membrane protein	**-1.34**	0.12742	**-1.59**	0.00060	**-1.30**	0.02050
STM1942	leuZ	STM1942	**-1.70**	0.01363	**-0.95**	0.02199	**-0.07**	0.85763
STM1942	leuZ	STM1942	**0.53**	0.59985	**-1.15**	0.02253	**0.41**	0.40102
STM1943	cysT	STM1943	**-2.80**	0.00789	**-0.72**	0.21819	**2.92**	0.00020
STM1943	cysT	STM1943	**-2.90**	0.02344	**-0.99**	0.02486	**3.12**	0.00009
STM1944	glyW	STM1944	**-1.12**	0.13062	**-0.34**	0.46927	**0.23**	0.61447
STM1944	glyW	STM1944	**-1.15**	0.04748	**-0.64**	0.10969	**0.32**	0.46475
STM1945	pgsA	phosphatidylglycerophosphate synthetase	**-1.80**	0.02394	**-0.70**	0.05138	**-1.48**	0.00291
STM1945	pgsA	phosphatidylglycerophosphate synthetase	**-1.86**	0.05448	**-0.70**	0.06206	**-1.00**	0.05703
STM1946	uvrC	excinuclease ABC subunit C	**1.75**	0.41865	**0.08**	0.82326	**0.62**	0.59806
STM1946	uvrC	excinuclease ABC subunit C	**-0.18**	0.76118	**0.05**	0.90780	**1.71**	0.12190
STM1947	uvrY	response regulator	**-1.84**	0.01854	**0.31**	0.40413	**-0.60**	0.19330
STM1947	uvrY	response regulator	**-0.83**	0.15665	**0.09**	0.75820	**0.02**	0.97275
STM1949	yecF	putative cytoplasmic protein	**-0.22**	0.68166	**-1.17**	0.00399	**-1.07**	0.08450
STM1949	yecF	putative cytoplasmic protein	**1.36**	0.05716	**-0.91**	0.02138	**-0.54**	0.25165
STM1950	sdiA	transcriptional regulator	**-0.91**	0.22810	**-0.79**	0.03083	**0.24**	0.65697
STM1950	sdiA	transcriptional regulator	**-0.15**	0.73008	**-0.47**	0.22962	**-0.62**	0.22460
STM1951	yecC	putative ABC-type polar amino acid transport system	**-1.56**	0.03603	**0.90**	0.25757	**0.11**	0.79744
STM1951	yecC	putative ABC-type polar amino acid transport system	**1.17**	0.52384	**-0.91**	0.40241	**-1.67**	0.01906
STM1952	yecS	putative ABC-type amino acid transporter permease	**-1.15**	0.04196	**0.50**	0.10280	**-0.29**	0.54205
STM1952	yecS	putative ABC-type amino acid transporter permease	**0.46**	0.30160	**0.92**	0.01549	**0.81**	0.09468
STM1953	yedO	D-cysteine desulfhydrase	**0.33**	0.50245	**0.56**	0.09165	**-0.03**	0.95407
STM1953	yedO	D-cysteine desulfhydrase	**1.57**	0.03961	**-0.02**	0.96131	**1.31**	0.03680
STM1954	fliY	putative periplasmic binding transport protein	**-0.94**	0.08929	**1.52**	0.29593	**-0.05**	0.93013
STM1954	fliY	putative periplasmic binding transport protein	**-0.46**	0.52776	**0.00**	0.99871	**0.74**	0.14946
STM1955	fliZ	putative FliA-regulator	**-1.23**	0.13486	**-1.22**	0.03049	**-0.76**	0.36878
STM1955	fliZ	putative FliA-regulator	**0.44**	0.30631	**-2.39**	0.00020	**-1.34**	0.03545
STM1956	fliA	flagellar biosynthesis sigma factor FliA	**-2.64**	0.03029	**-2.82**	0.00011	**-4.22**	0.00004
STM1956	fliA	flagellar biosynthesis sigma factor FliA	**-1.83**	0.02655	**-3.21**	0.00005	**-3.91**	0.00011
STM1958	fliB	lysine-N-methylase	**-2.57**	0.00661	**-2.53**	0.00015	**-2.59**	0.00691
STM1958	fliB	lysine-N-methylase	**-2.52**	0.02729	**-2.68**	0.00034	**-2.65**	0.02959
STM1959	fliC	flagellar biosynthesis protein	**-4.90**	0.00512	**-4.95**	0.00000	**-5.78**	0.00001
STM1959	fliC	flagellar biosynthesis protein	**-3.82**	0.00541	**-4.95**	0.00002	**-5.44**	0.00002
STM1960	fliD	flagellar hook-associated protein	**-1.25**	0.53960	**-3.82**	0.00012	**-3.44**	0.00021
STM1960	fliD	flagellar hook-associated protein	**0.78**	0.46604	**-4.48**	0.00001	**-5.31**	0.00003
STM1961	fliS	flagellar protein FliS	**-2.74**	0.00673	**-3.06**	0.00005	**-3.59**	0.00257
STM1961	fliS	flagellar protein FliS	**-3.64**	0.01615	**-3.06**	0.00007	**-4.30**	0.00018
STM1962	fliT	possible FliD export chaperone	**-2.66**	0.01808	**-3.21**	0.00002	**-4.19**	0.00004
STM1962	fliT	possible FliD export chaperone	**-2.57**	0.03538	**-3.38**	0.00003	**-2.44**	0.01808
STM1963	amyA	cytoplasmic alpha-amylase	**-0.95**	0.07738	**-0.62**	0.07315	**-1.50**	0.00773
STM1963	amyA	cytoplasmic alpha-amylase	**0.67**	0.17278	**-0.48**	0.14895	**-0.31**	0.45592
STM1964	yedD	putative outer membrane lipoprotein	**-0.35**	0.59076	**0.06**	0.89765	**-1.55**	0.01557
STM1964	yedD	putative outer membrane lipoprotein	**1.04**	0.08929	**-0.64**	0.14162	**-0.18**	0.67204
STM1965	yedE	hypothetical protein STM1965	**-2.05**	0.01028	**-1.17**	0.02840	**-1.43**	0.03369
STM1965	yedE	hypothetical protein STM1965	**-1.35**	0.02896	**-1.80**	0.00043	**-1.01**	0.03130
STM1966	yedF	putative transcriptional regulator	**-0.89**	0.10029	**-1.19**	0.00838	**-1.85**	0.01010
STM1966	yedF	putative transcriptional regulator	**0.53**	0.55509	**-0.94**	0.01679	**-1.31**	0.01758

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM1968	fliE	flagellar basal body protein	**-0.79**	0.13730	**-2.16**	0.00735	**-2.20**	0.01114
STM1968	fliE	flagellar basal body protein	**-0.65**	0.19351	**-2.59**	0.00009	**-1.96**	0.00098
STM1969	fliF	flagellar M-ring protein	**-3.40**	0.00623	**-4.07**	0.00006	**-4.11**	0.00012
STM1969	fliF	flagellar M-ring protein	**-2.24**	0.00930	**-4.73**	0.00000	**-4.31**	0.00007
STM1970	fliG	flagellar motor protein	**-3.03**	0.01085	**-4.05**	0.00011	**-3.52**	0.00014
STM1970	fliG	flagellar motor protein	**-3.89**	0.00512	**-4.79**	0.00005	**-4.56**	0.00006
STM1971	fliH	flagellar assembly protein	**-4.84**	0.00547	**-4.41**	0.00001	**-5.34**	0.00006
STM1971	fliH	flagellar assembly protein	**-3.13**	0.00757	**-5.40**	0.00001	**-4.45**	0.00234
STM1972	fliI	flagellum-specific ATP synthase	**-2.85**	0.00547	**-2.37**	0.00011	**-2.20**	0.00976
STM1972	fliI	flagellum-specific ATP synthase	**-1.37**	0.10932	**-3.61**	0.00004	**-2.37**	0.00046
STM1973	fliJ	flagellar protein	**-1.76**	0.01975	**-2.67**	0.00014	**-0.80**	0.35689
STM1973	fliJ	flagellar protein	**0.03**	0.96004	**-2.65**	0.00047	**-0.20**	0.80480
STM1974	fliK	flagellar hook-length control protein	**-2.84**	0.00547	**-2.88**	0.00325	**-2.40**	0.00057
STM1974	fliK	flagellar hook-length control protein	**-2.33**	0.00819	**-3.13**	0.00017	**-3.07**	0.00052
STM1975	fliL	flagellar biosynthesis protein	**-2.53**	0.00643	**-2.99**	0.00021	**-2.90**	0.00012
STM1975	fliL	flagellar biosynthesis protein	**-2.31**	0.01418	**-3.63**	0.00003	**-2.39**	0.00053
STM1976	fliM	flagellar motor switch protein	**-3.97**	0.00512	**-2.62**	0.00012	**-2.79**	0.00034
STM1976	fliM	flagellar motor switch protein	**-2.85**	0.00955	**-3.20**	0.00004	**-4.28**	0.00012
STM1977	fliN	flagellar motor switch protein	**-2.77**	0.01420	**-3.70**	0.00372	**-2.70**	0.00012
STM1977	fliN	flagellar motor switch protein	**-3.07**	0.00803	**-3.40**	0.00005	**-3.70**	0.00008
STM1978	fliO	flagellar biosynthetic protein	**-3.02**	0.00627	**-2.74**	0.00020	**-2.83**	0.00078
STM1978	fliO	flagellar biosynthetic protein	**-2.02**	0.01392	**-3.50**	0.00005	**-3.18**	0.00022
STM1979	fliP	flagellar biosynthesis protein	**-0.32**	0.55245	**-1.51**	0.00101	**-1.41**	0.08574
STM1979	fliP	flagellar biosynthesis protein	**0.30**	0.73607	**-1.79**	0.00111	**-0.90**	0.13107
STM1980	fliQ	flagellar biosynthesis protein	**-1.34**	0.02584	**-1.85**	0.00412	**-1.46**	0.00500
STM1980	fliQ	flagellar biosynthesis protein	**-1.64**	0.01466	**-1.98**	0.00139	**-2.98**	0.03959
STM1981	fliR	flagellar biosynthesis protein	**-1.53**	0.02172	**-0.76**	0.50503	**-1.23**	0.00930
STM1981	fliR	flagellar biosynthesis protein	**-0.78**	0.18114	**-1.18**	0.00448	**-0.96**	0.10506
STM1982	rcsA	colanic acid capsular biosynthesis activation protein A	**0.27**	0.51266	**-0.68**	0.05500	**0.77**	0.19154
STM1982	rcsA	colanic acid capsular biosynthesis activation protein A	**0.53**	0.43958	**0.04**	0.94075	**0.80**	0.20262
STM1983	dsrB	hypothetical protein STM1983	**-0.52**	0.37624	**0.19**	0.61509	**1.33**	0.01567
STM1983	dsrB	hypothetical protein STM1983	**-0.08**	0.88368	**-0.22**	0.57598	**1.41**	0.00732
STM1984	yodD	putative cytoplasmic protein	**-0.96**	0.25101	**-0.24**	0.47380	**3.72**	0.00018
STM1984	yodD	putative cytoplasmic protein	**-0.33**	0.78325	**0.43**	0.25930	**3.96**	0.00064
STM1986	yedP	hypothetical protein STM1986	**-0.12**	0.82471	**0.29**	0.49860	**0.28**	0.54826
STM1986	yedP	hypothetical protein STM1986	**1.57**	0.04632	**0.72**	0.09752	**2.38**	0.00195
STM1987	STM1987	putative inner membrane protein	**0.33**	0.61141	**0.25**	0.47812	**1.18**	0.05517
STM1987	STM1987	putative inner membrane protein	**-0.06**	0.92304	**0.49**	0.11199	**1.39**	0.04990
STM1988,S	STM1988,S	putative cytoplasmic protein	**0.99**	0.08311	**0.08**	0.88335	**2.85**	0.00022
STM1988,S	STM1988,S	putative cytoplasmic protein	**1.53**	0.09758	**-0.48**	0.64502	**3.47**	0.00014
STM1989	yedI	putative inner membrane protein	**-0.36**	0.49561	**0.42**	0.22710	**0.32**	0.49610
STM1989	yedI	putative inner membrane protein	**-1.47**	0.06452	**-0.61**	0.06710	**-0.02**	0.97030
STM1990	yedA	putative permease	**-1.21**	0.06088	**-0.02**	0.95244	**-0.93**	0.08999
STM1990	yedA	putative permease	**-0.21**	0.72668	**-0.71**	0.02954	**0.01**	0.99365
STM1991	vsr	DNA mismatch endonuclease	**-0.03**	0.96201	**-0.21**	0.57979	**-0.97**	0.04971
STM1991	vsr	DNA mismatch endonuclease	**1.26**	0.10585	**-0.34**	0.27843	**0.12**	0.80133
STM1992	dcm	DNA cytosine methylase	**0.07**	0.91561	**0.64**	0.07789	**-0.13**	0.77584
STM1992	dcm	DNA cytosine methylase	**0.77**	0.46368	**-0.60**	0.06460	**0.98**	0.04488
STM1993	yedJ	putative hydrolase	**0.12**	0.86827	**-0.54**	0.15812	**-1.62**	0.00817
STM1993	yedJ	putative hydrolase	**0.03**	0.96503	**0.01**	0.97326	**-0.04**	0.94189
STM1994	STM1994	putative inner membrane protein	**-0.48**	0.29599	**0.18**	0.59651	**-1.05**	0.03649
STM1994	STM1994	putative inner membrane protein	**1.65**	0.04067	**0.59**	0.20981	**0.83**	0.11879
STM1995	ompS	putative porin	**-1.04**	0.33309	**-1.70**	0.00348	**-0.86**	0.31440
STM1995	ompS	putative porin	**-0.36**	0.46188	**-0.79**	0.03205	**-0.73**	0.49256
STM1996	cspB	putative cold-shock protein	**-0.41**	0.58917	**-0.70**	0.06498	**-0.35**	0.43177
STM1996	cspB	putative cold-shock protein	**-0.48**	0.73377	**-1.51**	0.08962	**-0.33**	0.44707
STM1997	umuC	DNA polymerase IV	**-0.54**	0.26298	**1.98**	0.00067	**0.53**	0.33530
STM1997	umuC	DNA polymerase IV	**0.69**	0.49838	**0.95**	0.03033	**-0.17**	0.81749
STM1997	umuC	DNA polymerase IV	**0.38**	0.61086	**1.58**	0.00214	**-0.20**	0.72506
STM1997	umuC	DNA polymerase IV	**1.33**	0.12158	**0.87**	0.03681	**0.19**	0.73031
STM1998	umuD	SOS-response transcriptional repressors	**-0.32**	0.43811	**0.18**	0.54118	**0.06**	0.91533
STM1998	umuD	SOS-response transcriptional repressors	**1.54**	0.02776	**0.53**	0.12121	**0.36**	0.48339
STM1999	STM1999	putative cytoplasmic protein	**0.47**	0.56946	**1.69**	0.00121	**0.30**	0.71528
STM1999	STM1999	putative cytoplasmic protein	**2.70**	0.01392	**1.81**	0.00093	**1.35**	0.00882
STM2000	serU	STM2000	**-1.84**	0.01267	**-0.17**	0.69598	**0.49**	0.23040
STM2000	serU	STM2000	**-0.49**	0.40521	**0.12**	0.76912	**1.17**	0.02753
STM2001	yeeI	putative inner membrane protein	**0.11**	0.80250	**-0.30**	0.30158	**0.14**	0.73511
STM2001	yeeI	putative inner membrane protein	**0.93**	0.06092	**0.15**	0.66614	**-0.04**	0.95431
STM2002	asnT	STM2002	**0.77**	0.54711	**1.22**	0.00356	**3.67**	0.00007
STM2002	asnT	STM2002	**1.37**	0.33225	**0.84**	0.28533	**4.48**	0.00008

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM2004	asnT	STM2004	**-0.07**	0.92472	**-0.12**	0.74485	**0.75**	0.07059
STM2004	asnT	STM2004	**0.30**	0.68440	**-0.18**	0.67904	**1.02**	0.02500
STM2005	STM2005	putative endoprotease	**-1.23**	0.07501	**-0.23**	0.60608	**-1.48**	0.01726
STM2005	STM2005	putative endoprotease	**-0.29**	0.55444	**-0.70**	0.09291	**0.01**	0.99449
STM2007	STM2007	tetratricopeptide repeat protein	**0.94**	0.25633	**-0.55**	0.13103	**0.80**	0.37065
STM2007	STM2007	tetratricopeptide repeat protein	**3.50**	0.01496	**-0.67**	0.17151	**2.06**	0.01818
STM2008	STM2008	putative periplasmic protein	**-0.34**	0.40482	**0.65**	0.10654	**0.36**	0.32479
STM2008	STM2008	putative periplasmic protein	**-0.14**	0.80777	**-0.20**	0.54016	**0.47**	0.42861
STM2009	amn	AMP nucleosidase	**-0.70**	0.22701	**0.19**	0.56497	**-0.37**	0.50722
STM2009	amn	AMP nucleosidase	**-0.33**	0.55231	**1.29**	0.00479	**0.77**	0.51989
STM2011	STM2011	putative cytoplasmic protein	**-0.46**	0.36706	**0.67**	0.06553	**-0.34**	0.42059
STM2011	STM2011	putative cytoplasmic protein	**0.20**	0.72539	**0.13**	0.75062	**0.19**	0.72200
STM2012	asnW	STM2012	**-0.43**	0.64742	**0.06**	0.88759	**0.69**	0.08989
STM2012	asnW	STM2012	**0.49**	0.34197	**-0.16**	0.71622	**1.24**	0.01088
STM2013	yeeO	putative transport protein	**0.67**	0.36618	**-0.67**	0.04724	**0.66**	0.31613
STM2013	yeeO	putative transport protein	**-0.54**	0.47205	**-0.60**	0.21356	**0.50**	0.53624
STM2014	asnU	STM2014	**-1.06**	0.12047	**-0.39**	0.27037	**0.39**	0.36462
STM2014	asnU	STM2014	**0.49**	0.30701	**-0.44**	0.23357	**1.21**	0.00684
STM2015	erfK	putative periplasmic protein	**-0.53**	0.28413	**1.12**	0.03316	**0.40**	0.30919
STM2015	erfK	putative periplasmic protein	**0.46**	0.27055	**1.29**	0.00489	**1.07**	0.02018
STM2016	cobT	nicotinate-nucleotide--dimethylbenzimidazole	**0.89**	0.09989	**0.33**	0.28442	**0.21**	0.63741
STM2016	cobT	nicotinate-nucleotide--dimethylbenzimidazole	**1.82**	0.13375	**0.01**	0.96917	**0.77**	0.12516
STM2017	cobS	cobalamin synthase	**0.21**	0.74886	**-1.30**	0.00682	**0.33**	0.70148
STM2017	cobS	cobalamin synthase	**0.15**	0.87296	**-1.13**	0.00610	**-0.29**	0.76667
STM2018	cobU	adenosylcobinamide kinase	**1.86**	0.07400	**-1.22**	0.00551	**-1.51**	0.02386
STM2018	cobU	adenosylcobinamide kinase	**1.94**	0.04021	**-1.47**	0.00245	**-1.11**	0.03187
STM2019	cbiP	cobyric acid synthase	**-0.19**	0.85702	**0.38**	0.22603	**-0.78**	0.07073
STM2019	cbiP	cobyric acid synthase	**0.31**	0.46499	**-0.10**	0.79321	**0.04**	0.93971
STM2020	cbiO	vitamin B12 biosynthetic protein	**0.51**	0.33041	**0.88**	0.01233	**0.83**	0.22770
STM2020	cbiO	vitamin B12 biosynthetic protein	**1.84**	0.01748	**0.92**	0.01606	**0.73**	0.16613
STM2021	cbiQ	vitamin B12 biosynthetic protein	**-0.31**	0.47566	**0.27**	0.43113	**-0.75**	0.31527
STM2021	cbiQ	vitamin B12 biosynthetic protein	**1.35**	0.03731	**0.47**	0.10955	**-0.16**	0.72575
STM2022	cbiN	cobalt transport protein CbiN	**0.05**	0.90743	**-0.15**	0.61889	**-0.57**	0.23296
STM2022	cbiN	cobalt transport protein CbiN	**0.50**	0.30921	**-0.61**	0.12881	**-0.19**	0.81438
STM2023	cbiM	cobalt transport protein CbiM	**0.25**	0.70476	**-0.11**	0.76889	**0.23**	0.58025
STM2023	cbiM	cobalt transport protein CbiM	**0.38**	0.61349	**-0.01**	0.98464	**-0.16**	0.77856
STM2024	cbiL	precorrin-2 methyltransferase	**-0.36**	0.64478	**0.01**	0.98505	**-0.96**	0.09789
STM2024	cbiL	precorrin-2 methyltransferase	**-0.32**	0.60881	**-0.30**	0.34094	**0.24**	0.70417
STM2025	cbiK	vitamin B12 biosynthetic protein	**-0.48**	0.36320	**-0.84**	0.05169	**-1.28**	0.02638
STM2025	cbiK	vitamin B12 biosynthetic protein	**-0.06**	0.89255	**-0.36**	0.25473	**-0.52**	0.27257
STM2026	cbiJ	precorrin-6x reductase	**-0.04**	0.94628	**-0.92**	0.06386	**-2.03**	0.04543
STM2026	cbiJ	precorrin-6x reductase	**0.86**	0.18354	**-1.30**	0.03264	**-0.52**	0.30938
STM2027	cbiH	precorrin-3B C17-methyltransferase	**-0.02**	0.96816	**1.07**	0.01984	**0.59**	0.14117
STM2027	cbiH	precorrin-3B C17-methyltransferase	**1.31**	0.06902	**0.61**	0.10867	**0.21**	0.74751
STM2028	cbiG	cobalamin biosynthesis protein CbiG	**-0.27**	0.61337	**1.05**	0.02622	**0.13**	0.79608
STM2028	cbiG	cobalamin biosynthesis protein CbiG	**1.13**	0.17809	**0.63**	0.07523	**0.08**	0.89035
STM2029	cbiF	vitamin B12 biosynthetic protein	**-0.39**	0.75543	**-1.15**	0.06886	**-0.85**	0.24916
STM2029	cbiF	vitamin B12 biosynthetic protein	**1.91**	0.01790	**-2.56**	0.00016	**-0.43**	0.51181
STM2030	cbiT	precorrin-8w decarboxylase	**0.47**	0.43011	**-0.08**	0.85580	**-0.61**	0.19725
STM2030	cbiT	precorrin-8w decarboxylase	**0.89**	0.28507	**-0.01**	0.98941	**0.50**	0.42229
STM2031	cbiE	precorrin-6B methylase	**0.67**	0.56436	**0.23**	0.54825	**-0.96**	0.20944
STM2031	cbiE	precorrin-6B methylase	**-0.35**	0.55318	**0.24**	0.47525	**-0.74**	0.18300
STM2032	cbiD	cobalt-precorrin-6A synthase	**-1.22**	0.04794	**0.11**	0.89417	**-1.08**	0.08800
STM2032	cbiD	cobalt-precorrin-6A synthase	**0.67**	0.21880	**-0.36**	0.28896	**-0.07**	0.91479
STM2033	cbiC	precorrin-8X methylmutase	**-1.34**	0.06199	**0.05**	0.90455	**0.11**	0.83564
STM2033	cbiC	precorrin-8X methylmutase	**-1.15**	0.15884	**-0.33**	0.51066	**-0.28**	0.50498
STM2034	cobD	cobalamin biosynthesis protein	**0.45**	0.32918	**0.22**	0.46090	**0.51**	0.20108
STM2034	cobD	cobalamin biosynthesis protein	**1.65**	0.02633	**0.13**	0.73224	**2.01**	0.00102
STM2035	cbiA	cobyrinic acid a,c-diamide synthase	**-0.52**	0.29937	**0.02**	0.96443	**-0.85**	0.07085
STM2035	cbiA	cobyrinic acid a,c-diamide synthase	**0.52**	0.52906	**-0.14**	0.74199	**-0.61**	0.31492
STM2036	pocR	transcriptional regulator	**0.02**	0.97064	**1.51**	0.00892	**0.15**	0.73854
STM2036	pocR	transcriptional regulator	**1.05**	0.47388	**-0.43**	0.16566	**0.13**	0.87119
STM2037	pduF	propanediol diffusion facilitator	**0.83**	0.30734	**0.04**	0.91923	**-0.28**	0.62842
STM2037	pduF	propanediol diffusion facilitator	**0.40**	0.50087	**0.46**	0.13623	**0.15**	0.78956
STM2038	pduA	polyhedral body protein	**2.00**	0.06522	**1.11**	0.21933	**3.04**	0.04737
STM2038	pduA	polyhedral body protein	**1.31**	0.09846	**-0.86**	0.18661	**1.90**	0.02647
STM2039	pudB	polyhedral body protein	**0.34**	0.71993	**-1.04**	0.01938	**1.46**	0.34691
STM2039	pudB	polyhedral body protein	**-0.02**	0.98974	**-1.81**	0.04862	**0.77**	0.15598
STM2040	pduC	propanediol dehydratase large subunit	**0.82**	0.40458	**-0.71**	0.14155	**-0.35**	0.59391
STM2040	pduC	propanediol dehydratase large subunit	**3.56**	0.18512	**-0.36**	0.62694	**0.69**	0.48950

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM2041	pduD	propanediol dehydratase medium subunit	**0.85**	0.69269	**-0.87**	0.06776	**0.76**	0.26259
STM2041	pduD	propanediol dehydratase medium subunit	**1.62**	0.45345	**-2.33**	0.00780	**-0.80**	0.19750
STM2042	pduE	propanediol dehydratase small subunit	**-0.56**	0.25990	**-1.43**	0.06372	**0.00**	0.99518
STM2042	pduE	propanediol dehydratase small subunit	**0.27**	0.70405	**-1.58**	0.00098	**-0.07**	0.90111
STM2043	pduG	propanediol dehydratase reactivation protein	**-0.15**	0.83489	**-0.79**	0.05881	**0.05**	0.94846
STM2043	pduG	propanediol dehydratase reactivation protein	**1.04**	0.08410	**-0.80**	0.19493	**1.73**	0.01663
STM2044	pduH	propanediol dehydratase reactivation protein	**-0.28**	0.57930	**-0.16**	0.63458	**0.12**	0.73802
STM2044	pduH	propanediol dehydratase reactivation protein	**1.13**	0.11528	**-0.44**	0.36955	**0.98**	0.02603
STM2045	pduJ	polyhedral body protein	**0.05**	0.90377	**-0.07**	0.93612	**-0.79**	0.10985
STM2045	pduJ	polyhedral body protein	**2.36**	0.06636	**-0.08**	0.85772	**0.49**	0.55912
STM2046	pduK	polyhedral body protein	**-0.45**	0.33191	**-0.43**	0.42395	**-0.81**	0.11856
STM2046	pduK	polyhedral body protein	**0.66**	0.45612	**-0.91**	0.03554	**0.29**	0.72150
STM2047	pduL	propanediol utilization protein	**0.37**	0.35949	**-0.54**	0.08853	**-0.19**	0.79610
STM2047	pduL	propanediol utilization protein	**0.85**	0.14190	**-1.04**	0.02848	**1.22**	0.11745
STM2048	pduM	propanediol utilization protein	**-0.61**	0.17542	**0.63**	0.62438	**-0.61**	0.34691
STM2048	pduM	propanediol utilization protein	**-0.29**	0.59371	**-1.11**	0.01031	**-0.61**	0.61017
STM2049	pduN	polyhedral body protein	**0.50**	0.54377	**-0.70**	0.13248	**-0.25**	0.59945
STM2049	pduN	polyhedral body protein	**-0.57**	0.21536	**-0.72**	0.19459	**-0.82**	0.10781
STM2050	pduO	propanediol utilization protein	**-0.22**	0.59927	**0.42**	0.29820	**0.13**	0.77763
STM2050	pduO	propanediol utilization protein	**1.54**	0.24107	**-1.33**	0.03986	**0.41**	0.40800
STM2051	pduP	CoA-dependent propionaldehyde dehydrogenase	**-0.71**	0.22006	**-0.59**	0.19320	**-1.24**	0.01698
STM2051	pduP	CoA-dependent propionaldehyde dehydrogenase	**1.97**	0.13716	**-1.10**	0.02644	**-0.68**	0.31379
STM2052	pduQ	propanol dehydrogenase	**1.07**	0.09751	**-1.42**	0.00591	**0.02**	0.97553
STM2052	pduQ	propanol dehydrogenase	**0.93**	0.16786	**-1.16**	0.02249	**0.87**	0.18597
STM2053	pduS	polyhedral body protein	**-0.46**	0.39776	**-0.69**	0.06866	**-0.69**	0.40116
STM2053	pduS	polyhedral body protein	**-0.77**	0.13062	**-1.10**	0.03508	**-1.37**	0.20625
STM2054	pduT	polyhedral body protein	**2.14**	0.01491	**-1.10**	0.01099	**0.38**	0.32226
STM2054	pduT	polyhedral body protein	**2.58**	0.01652	**-1.26**	0.02872	**1.72**	0.01192
STM2055	pduU	polyhedral body protein	**0.82**	0.32287	**-1.95**	0.00385	**-0.11**	0.83342
STM2055	pduU	polyhedral body protein	**0.95**	0.27415	**-2.35**	0.00612	**0.89**	0.32940
STM2056	pduV	propanediol utilization protein	**-0.79**	0.08929	**-0.61**	0.16207	**0.20**	0.74333
STM2056	pduV	propanediol utilization protein	**-0.09**	0.86228	**-1.46**	0.01214	**0.47**	0.32479
STM2057	pduW	acetate/propionate kinase	**-0.43**	0.49096	**-0.67**	0.39735	**-0.95**	0.07208
STM2057	pduW	acetate/propionate kinase	**-0.02**	0.96450	**0.46**	0.32465	**-0.03**	0.95469
STM2058	pduX	propanediol utilization protein	**-1.67**	0.03038	**0.11**	0.80605	**-1.89**	0.00939
STM2058	pduX	propanediol utilization protein	**0.76**	0.43560	**-0.23**	0.54244	**-0.91**	0.08999
STM2059	yeeX	hypothetical protein STM2059	**-1.66**	0.10867	**-0.33**	0.45891	**-1.23**	0.01144
STM2059	yeeX	hypothetical protein STM2059	**-1.76**	0.05543	**0.12**	0.70889	**-1.25**	0.01833
STM2060	yeeA	putative inner membrane protein	**-0.41**	0.36207	**0.97**	0.00717	**0.03**	0.95195
STM2060	yeeA	putative inner membrane protein	**0.08**	0.84977	**0.60**	0.11864	**0.13**	0.74708
STM2061	sbmC	DNA gyrase inhibitor	**0.49**	0.59477	**1.76**	0.00130	**2.91**	0.00009
STM2061	sbmC	DNA gyrase inhibitor	**1.10**	0.06456	**1.47**	0.00471	**3.67**	0.00005
STM2062	dacD	DD-carboxypeptidase	**-1.14**	0.09991	**0.02**	0.95330	**-0.17**	0.73391
STM2062	dacD	DD-carboxypeptidase	**0.06**	0.90910	**-0.64**	0.08151	**-0.04**	0.94836
STM2063	phsC	thiosulfate reductase cytochrome B subunit	**0.15**	0.79511	**-0.45**	0.28607	**-0.61**	0.11071
STM2063	phsC	thiosulfate reductase cytochrome B subunit	**0.42**	0.40446	**-0.69**	0.07180	**0.48**	0.52339
STM2064	phsB	thiosulfate reductase electron transport protein	**-0.08**	0.87808	**0.30**	0.31347	**0.20**	0.68157
STM2064	phsB	thiosulfate reductase electron transport protein	**-0.18**	0.68598	**-0.43**	0.35898	**0.27**	0.50290
STM2065	phsA	thiosulfate reductase precursor	**0.26**	0.69493	**0.52**	0.22785	**-0.79**	0.08184
STM2065	phsA	thiosulfate reductase precursor	**1.63**	0.02423	**-0.77**	0.07599	**0.67**	0.12104
STM2066	sopA	secreted effector protein	**-0.84**	0.12856	**-0.76**	0.03245	**-1.13**	0.06556
STM2066	sopA	secreted effector protein	**2.15**	0.21798	**-0.49**	0.25358	**-0.08**	0.90141
STM2067	sbcB	exonuclease I	**0.00**	0.99465	**-1.01**	0.00699	**0.26**	0.73618
STM2067	sbcB	exonuclease I	**0.22**	0.84620	**-0.91**	0.02793	**0.85**	0.04607
STM2068	yeeF	putative amino acid transport protein	**-2.76**	0.00839	**-1.56**	0.00083	**-2.93**	0.00042
STM2068	yeeF	putative amino acid transport protein	**-1.36**	0.02364	**-2.09**	0.00037	**-2.10**	0.00072
STM2069	yeeY	putative transcriptional regulator	**-1.00**	0.08959	**-0.54**	0.10542	**1.35**	0.16811
STM2069	yeeY	putative transcriptional regulator	**-0.99**	0.07354	**-1.94**	0.00036	**0.64**	0.46536
STM2070	yeeZ	putative dehydratase	**-1.38**	0.02181	**1.24**	0.01298	**2.26**	0.00046
STM2070	yeeZ	putative dehydratase	**-0.37**	0.53951	**1.39**	0.00197	**2.72**	0.00026
STM2071	hisG	ATP phosphoribosyltransferase	**-1.23**	0.04100	**1.57**	0.00226	**-1.68**	0.01608
STM2071	hisG	ATP phosphoribosyltransferase	**-0.31**	0.48950	**1.54**	0.00175	**-1.59**	0.00386
STM2072	hisD	histidinol dehydrogenase	**-0.84**	0.08333	**1.77**	0.00158	**-2.70**	0.00265
STM2072	hisD	histidinol dehydrogenase	**0.22**	0.76436	**1.67**	0.00220	**-1.04**	0.14339
STM2073	hisC	histidinol-phosphate aminotransferase	**-1.36**	0.05655	**0.37**	0.23796	**-1.01**	0.13751
STM2073	hisC	histidinol-phosphate aminotransferase	**-0.55**	0.46005	**0.70**	0.06137	**-1.24**	0.01145
STM2074	hisB	imidazole glycerol-phosphate dehydratase/histidinol	**-1.62**	0.01572	**0.68**	0.05181	**-1.61**	0.00194
STM2074	hisB	imidazole glycerol-phosphate dehydratase/histidinol	**-1.25**	0.03457	**0.74**	0.05963	**-2.72**	0.00845
STM2075	hisH	imidazole glycerol phosphate synthase subunit HisH	**0.80**	0.11955	**1.26**	0.00849	**-2.17**	0.00097
STM2075	hisH	imidazole glycerol phosphate synthase subunit HisH	**0.90**	0.07710	**1.15**	0.00629	**-0.88**	0.07039

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM2076	hisA	1-(5-phosphoribosyl)-5-	**-2.18**	0.01834	**0.31**	0.35289	**-1.72**	0.01479
STM2076	hisA	1-(5-phosphoribosyl)-5-	**-1.93**	0.00950	**0.39**	0.23994	**-2.73**	0.03631
STM2077	hisF	imidazole glycerol phosphate synthase subunit HisF	**-1.99**	0.04201	**0.08**	0.82442	**-1.03**	0.06148
STM2077	hisF	imidazole glycerol phosphate synthase subunit HisF	**-1.15**	0.05557	**1.15**	0.00430	**-1.07**	0.03394
STM2078	hisI	bifunctional phosphoribosyl-AMP	**-0.11**	0.81793	**0.00**	0.98906	**-1.00**	0.02623
STM2078	hisI	bifunctional phosphoribosyl-AMP	**0.26**	0.64095	**-0.07**	0.85765	**-0.70**	0.19325
STM2079	wzzB	lipopolysaccharide O-antigen chain length regulator	**-0.82**	0.07968	**0.59**	0.08860	**0.47**	0.31812
STM2079	wzzB	lipopolysaccharide O-antigen chain length regulator	**-0.24**	0.55715	**0.41**	0.27131	**0.93**	0.02540
STM2080	udg	UDP-glucose/GDP-mannose dehydrogenase	**-0.17**	0.68969	**1.11**	0.16941	**-0.47**	0.45768
STM2080	udg	UDP-glucose/GDP-mannose dehydrogenase	**-0.18**	0.89257	**0.06**	0.88515	**-3.03**	0.00336
STM2081	gnd	6-phosphogluconate dehydrogenase	**-1.83**	0.01114	**-0.81**	0.01371	**-0.49**	0.27913
STM2081	gnd	6-phosphogluconate dehydrogenase	**0.12**	0.91058	**-0.41**	0.29246	**-0.83**	0.19132
STM2082	rfbP	undecaprenol-phosphate galactosephosphotransferase/O-	**-2.95**	0.00582	**-1.42**	0.00683	**-3.10**	0.00062
STM2082	rfbP	undecaprenol-phosphate galactosephosphotransferase/O-	**-3.06**	0.00613	**-1.21**	0.02512	**-2.29**	0.00043
STM2083	rfbK	phosphomannomutase	**-1.61**	0.01752	**-1.49**	0.00955	**-1.82**	0.01655
STM2083	rfbK	phosphomannomutase	**-1.06**	0.12640	**-1.32**	0.00737	**-1.68**	0.01863
STM2084	rfbM	mannose-1-phosphate guanylyltransferase	**0.40**	0.54840	**-0.92**	0.02713	**-1.67**	0.00611
STM2084	rfbM	mannose-1-phosphate guanylyltransferase	**1.25**	0.11003	**-0.80**	0.11800	**-0.75**	0.10258
STM2085	rfbN	rhamnosyl transferase	**-2.53**	0.00775	**-2.33**	0.00011	**-1.67**	0.01191
STM2085	rfbN	rhamnosyl transferase	**-3.93**	0.00593	**-2.26**	0.00026	**-2.87**	0.00086
STM2086	rfbU	mannosyl transferase	**-1.82**	0.02162	**-1.37**	0.00364	**-1.76**	0.00371
STM2086	rfbU	mannosyl transferase	**-2.60**	0.00637	**-1.85**	0.00052	**-2.03**	0.00113
STM2087	rfbV	abequosyltransferase	**-4.02**	0.00537	**-2.05**	0.00052	**-3.09**	0.00024
STM2087	rfbV	abequosyltransferase	**-2.75**	0.00757	**-2.14**	0.00081	**-5.12**	0.00002
STM2088	rfbX	putative O-antigen transferase	**-0.72**	0.40315	**-1.87**	0.00303	**-1.69**	0.00395
STM2088	rfbX	putative O-antigen transferase	**-0.89**	0.59119	**-2.23**	0.00027	**-0.84**	0.04572
STM2089	rfbJ	CDP-abequose synthase	**-1.63**	0.19791	**-0.54**	0.08212	**-3.96**	0.00008
STM2089	rfbJ	CDP-abequose synthase	**-2.89**	0.00547	**-0.42**	0.15065	**-3.99**	0.00253
STM2090	rfbH	CDP-6-deoxy-D-xylo-4-hexulose-3-dehydrase	**-3.00**	0.01013	**-1.15**	0.01045	**-2.30**	0.03063
STM2090	rfbH	CDP-6-deoxy-D-xylo-4-hexulose-3-dehydrase	**-2.89**	0.00927	**-1.35**	0.00392	**-3.75**	0.00007
STM2091	rfbG	CDP glucose 4,6-dehydratase	**-2.13**	0.00849	**-1.09**	0.00430	**-3.53**	0.00008
STM2091	rfbG	CDP glucose 4,6-dehydratase	**-1.48**	0.03408	**-0.79**	0.03487	**-3.15**	0.00058
STM2092	rfbF	glucose-1-phosphate cytidylyltransferase	**-2.83**	0.01479	**-0.78**	0.02150	**-3.02**	0.00037
STM2092	rfbF	glucose-1-phosphate cytidylyltransferase	**-1.30**	0.05125	**-0.58**	0.08068	**-2.29**	0.00035
STM2093	rfbI	CDP-6-deoxy-delta-3,4-glucoseen reductase	**-2.55**	0.00841	**-2.06**	0.00130	**-2.41**	0.00031
STM2093	rfbI	CDP-6-deoxy-delta-3,4-glucoseen reductase	**-1.49**	0.07767	**-1.93**	0.00046	**-2.33**	0.00076
STM2094	rfbC	dTDP-4,deoxyrhamnose 3,5 epimerase	**-2.83**	0.00607	**-1.94**	0.00024	**-3.47**	0.00009
STM2094	rfbC	dTDP-4,deoxyrhamnose 3,5 epimerase	**-3.04**	0.00541	**-1.43**	0.00293	**-3.75**	0.00018
STM2095	rfbA	dTDP-glucose pyrophosphorylase	**-1.91**	0.01198	**-0.77**	0.02846	**-1.75**	0.21592
STM2095	rfbA	dTDP-glucose pyrophosphorylase	**-1.50**	0.05136	**-1.02**	0.00782	**-2.22**	0.00232
STM2096	rfbD	TDP-rhamnose synthetase	**-2.59**	0.01235	**-0.76**	0.11538	**-3.48**	0.00026
STM2096	rfbD	TDP-rhamnose synthetase	**-1.35**	0.03748	**-0.83**	0.04003	**-2.80**	0.00095
STM2097	rfbB	dTDP-glucose 4,6-dehydratase	**0.38**	0.46227	**-0.01**	0.96891	**1.51**	0.00284
STM2097	rfbB	dTDP-glucose 4,6-dehydratase	**0.84**	0.08259	**-0.16**	0.63279	**2.02**	0.00134
STM2098	galF	putative glucose-1-phosphate uridylyltransferase subunit	**-1.77**	0.01993	**-0.54**	0.09991	**-0.43**	0.21919
STM2098	galF	putative glucose-1-phosphate uridylyltransferase subunit	**-0.32**	0.63744	**-0.55**	0.07366	**0.46**	0.27669
STM2099	wcaM	putative colanic acid biosynthetic protein	**-0.92**	0.13284	**-1.30**	0.01313	**0.34**	0.63431
STM2099	wcaM	putative colanic acid biosynthetic protein	**0.12**	0.80011	**-1.67**	0.00682	**0.39**	0.44994
STM2100	wcaL	putative glycosyl transferase	**0.60**	0.56160	**0.49**	0.15290	**1.89**	0.00332
STM2100	wcaL	putative glycosyl transferase	**0.63**	0.36178	**-0.28**	0.33945	**1.75**	0.00198
STM2101	wcaK	putative galactokinase	**1.16**	0.05496	**-0.98**	0.02326	**-0.23**	0.69832
STM2101	wcaK	putative galactokinase	**1.76**	0.02645	**-0.56**	0.16993	**1.58**	0.00174
STM2102	wzxC	putative export	**0.05**	0.92457	**-1.24**	0.03855	**0.47**	0.39181
STM2102	wzxC	putative export	**0.58**	0.35952	**-0.34**	0.30297	**0.89**	0.06536
STM2103	wcaJ	UDP-glucose lipid carrier transferase/glucose-1-phosphate	**0.13**	0.83489	**0.47**	0.30026	**1.72**	0.00745
STM2103	wcaJ	UDP-glucose lipid carrier transferase/glucose-1-phosphate	**1.14**	0.15590	**0.58**	0.20062	**1.99**	0.00336
STM2104	cpsG	phosphomannomutase	**2.17**	0.02101	**0.03**	0.95492	**0.34**	0.58727
STM2104	cpsG	phosphomannomutase	**1.87**	0.05468	**-0.65**	0.08131	**0.44**	0.65192
STM2105,S	manC	mannose-1-phosphate guanylyltransferase	**1.07**	0.30326	**-0.95**	0.01825	**-0.21**	0.66375
STM2105,S	manC	mannose-1-phosphate guanylyltransferase	**1.46**	0.07059	**-0.86**	0.21909	**1.07**	0.03749
STM2106	wcaI	putative glycosyl transferase	**-0.10**	0.83853	**0.51**	0.14483	**0.78**	0.10018
STM2106	wcaI	putative glycosyl transferase	**0.50**	0.34308	**-0.30**	0.53832	**0.51**	0.49698
STM2107	wcaH	GDP-mannose mannosyl hydrolase	**-0.37**	0.57239	**-0.46**	0.48906	**-0.50**	0.44942
STM2107	wcaH	GDP-mannose mannosyl hydrolase	**0.70**	0.46968	**-1.38**	0.00499	**-1.84**	0.00192
STM2108	wcaG	GDP-fucose synthetase	**-0.33**	0.58484	**0.33**	0.26256	**0.34**	0.54335
STM2108	wcaG	GDP-fucose synthetase	**0.43**	0.30977	**1.17**	0.03279	**0.29**	0.50098
STM2109	gmd	GDP-D-mannose dehydratase	**0.78**	0.41794	**0.74**	0.06680	**-0.49**	0.57673
STM2109	gmd	GDP-D-mannose dehydratase	**1.69**	0.11408	**0.67**	0.12329	**0.73**	0.53380
STM2110	wcaF	putative acyltransferase	**-0.32**	0.58728	**-0.18**	0.68415	**-0.80**	0.21279
STM2110	wcaF	putative acyltransferase	**-0.54**	0.59128	**0.48**	0.12561	**-0.68**	0.40914

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM2111	wcaE	putative transferase	**0.97**	0.30150	**0.75**	0.05018	**-0.15**	0.79632
STM2111	wcaE	putative transferase	**0.89**	0.11427	**0.89**	0.01538	**1.05**	0.01404
STM2112	wcaD	putative colanic acid polymerase	**0.05**	0.90734	**-0.55**	0.19529	**-0.57**	0.39253
STM2112	wcaD	putative colanic acid polymerase	**0.78**	0.31928	**-0.82**	0.04041	**0.69**	0.26644
STM2113	wcaC	putative glycosyl transferase	**-0.50**	0.34416	**-0.12**	0.77342	**0.95**	0.07034
STM2113	wcaC	putative glycosyl transferase	**-0.06**	0.95493	**-0.86**	0.07565	**-0.94**	0.20138
STM2114	wcaB	putative acyl transferase	**1.69**	0.01955	**-0.64**	0.03772	**0.44**	0.27933
STM2114	wcaB	putative acyl transferase	**0.83**	0.14061	**-1.29**	0.00513	**-1.17**	0.08710
STM2115	wcaA	putative glycosyl transferase	**1.28**	0.19084	**-2.91**	0.00016	**-1.73**	0.04631
STM2115	wcaA	putative glycosyl transferase	**0.82**	0.30301	**-4.08**	0.00069	**-0.28**	0.72975
STM2116	wzc	putative tyrosine protein kinase	**0.94**	0.62974	**0.40**	0.38233	**2.05**	0.14996
STM2116	wzc	putative tyrosine protein kinase	**4.41**	0.01215	**-0.78**	0.02570	**3.30**	0.00620
STM2117	wzb	putative phosphotyrosine-protein phosphatase	**-0.27**	0.64924	**1.54**	0.45058	**-0.48**	0.58638
STM2117	wzb	putative phosphotyrosine-protein phosphatase	**0.59**	0.27425	**-0.73**	0.10346	**-0.90**	0.56077
STM2118	wza	putative outer membrane polysaccharide export protein	**0.02**	0.97884	**0.23**	0.53437	**0.61**	0.17427
STM2118	wza	putative outer membrane polysaccharide export protein	**0.19**	0.66101	**-0.06**	0.94639	**0.44**	0.52411
STM2119	yegH	putative inner membrane protein	**-0.33**	0.54243	**0.96**	0.00700	**-0.18**	0.80377
STM2119	yegH	putative inner membrane protein	**0.70**	0.26560	**0.77**	0.04257	**0.02**	0.97769
STM2120	asmA	suppressor of OmpF assembly mutants	**-0.43**	0.33887	**0.71**	0.04371	**-0.64**	0.12855
STM2120	asmA	suppressor of OmpF assembly mutants	**0.46**	0.41040	**0.64**	0.08785	**0.32**	0.49090
STM2121	dcd	deoxycytidine triphosphate deaminase	**-1.35**	0.03288	**0.26**	0.46715	**-1.92**	0.00169
STM2121	dcd	deoxycytidine triphosphate deaminase	**-0.50**	0.43697	**-0.14**	0.73857	**-1.24**	0.04086
STM2122	udk	uridine kinase	**-1.59**	0.03218	**-1.12**	0.00516	**-1.56**	0.01353
STM2122	udk	uridine kinase	**-2.68**	0.02540	**-0.84**	0.02601	**-3.56**	0.01540
STM2123	yegE	putative diguanylate cyclase/phosphodiesterase	**-0.68**	0.15610	**-0.56**	0.45714	**-0.10**	0.80148
STM2123	yegE	putative diguanylate cyclase/phosphodiesterase	**0.83**	0.09627	**0.22**	0.48449	**0.88**	0.05528
STM2124	alkA	3-methyl-adenine DNA glycosylase II	**-0.67**	0.27727	**-0.49**	0.32436	**-0.69**	0.15680
STM2124	alkA	3-methyl-adenine DNA glycosylase II	**-0.31**	0.79511	**0.34**	0.26927	**1.73**	0.07327
STM2125	yegD	putative heat shock protein	**-0.52**	0.23359	**0.43**	0.69583	**-0.92**	0.20873
STM2125	yegD	putative heat shock protein	**-1.15**	0.16568	**-1.19**	0.00726	**-2.15**	0.17160
STM2126	STM2126	putative secretion protein	**-0.37**	0.46474	**-0.09**	0.82048	**0.88**	0.10886
STM2126	STM2126	putative secretion protein	**0.64**	0.25246	**-0.67**	0.04376	**0.98**	0.06021
STM2127	yegN	putative outer membrane receptor	**0.37**	0.74562	**-0.45**	0.68972	**-0.38**	0.30636
STM2127	yegN	putative outer membrane receptor	**0.85**	0.35598	**-0.54**	0.09656	**0.64**	0.40929
STM2128	yegO	outer membrane putative efflux transporter	**-0.53**	0.28785	**0.46**	0.38083	**-1.09**	0.33210
STM2128	yegO	outer membrane putative efflux transporter	**0.48**	0.34079	**-0.88**	0.02715	**-0.16**	0.77219
STM2129	yegB	putative transport protein	**-0.67**	0.45246	**0.71**	0.08377	**0.40**	0.50361
STM2129	yegB	putative transport protein	**0.60**	0.16917	**0.31**	0.47781	**0.42**	0.25525
STM2130	baeS	sensor kinase	**-1.20**	0.05959	**-0.58**	0.31397	**0.05**	0.93387
STM2130	baeS	sensor kinase	**-0.15**	0.84241	**-0.19**	0.56804	**-0.68**	0.16086
STM2131	baeR	response regulator	**-0.26**	0.61888	**-0.22**	0.47462	**-0.69**	0.11080
STM2131	baeR	response regulator	**1.34**	0.04539	**0.07**	0.87931	**0.16**	0.77687
STM2133	STM2133	putative cytoplasmic protein	**0.46**	0.34101	**0.17**	0.59387	**0.53**	0.34874
STM2133	STM2133	putative cytoplasmic protein	**0.81**	0.19208	**-1.09**	0.02179	**0.45**	0.38014
STM2134	STM2134	putative inner membrane protein	**-0.29**	0.53846	**-0.29**	0.79652	**-0.42**	0.61163
STM2134	STM2134	putative inner membrane protein	**-0.28**	0.78571	**-0.34**	0.50278	**-1.14**	0.25884
STM2135	STM2135	putative inner membrane protein	**-0.79**	0.22802	**-1.77**	0.00115	**-1.33**	0.01410
STM2135	STM2135	putative inner membrane protein	**0.63**	0.19917	**-1.15**	0.02825	**-0.61**	0.33187
STM2136	yegQ	putative protease	**-1.39**	0.05224	**-1.19**	0.00289	**-2.18**	0.00049
STM2136	yegQ	putative protease	**-0.89**	0.11322	**-1.12**	0.00502	**-1.41**	0.00500
STM2137	STM2137	putative cytoplasmic protein	**2.29**	0.00900	**3.62**	0.00005	**1.76**	0.03578
STM2137	STM2137	putative cytoplasmic protein	**0.61**	0.62274	**3.85**	0.00002	**1.50**	0.00812
STM2138	STM2138	putative cytoplasmic protein	**3.10**	0.00541	**5.10**	0.00003	**3.01**	0.00038
STM2138	STM2138	putative cytoplasmic protein	**2.74**	0.00595	**4.83**	0.00001	**2.60**	0.00051
STM2139	STM2139	putative inner membrane protein	**0.47**	0.44035	**5.91**	0.00001	**0.53**	0.51217
STM2139	STM2139	putative inner membrane protein	**1.60**	0.03086	**5.91**	0.00001	**0.71**	0.16107
STM2139,2n	STM2139,2n	hypothetical protein STM2139,2n	**2.07**	0.02240	**1.13**	0.01607	**1.79**	0.01111
STM2139,2n	STM2139,2n	hypothetical protein STM2139,2n	**2.04**	0.00800	**1.76**	0.00347	**2.45**	0.00025
STM2140	yegS	putative diacylglycerol kinase	**-0.70**	0.17625	**1.27**	0.00528	**1.76**	0.00245
STM2140	yegS	putative diacylglycerol kinase	**0.83**	0.18059	**1.18**	0.01245	**2.59**	0.00106
STM2141	fbaB	fructose-bisphosphate aldolase	**0.41**	0.46047	**4.05**	0.00001	**3.74**	0.00008
STM2141	fbaB	fructose-bisphosphate aldolase	**2.24**	0.01431	**3.48**	0.00008	**4.63**	0.00003
STM2142	yegT	putative transport protein	**-0.39**	0.45912	**0.18**	0.56067	**0.53**	0.24553
STM2142	yegT	putative transport protein	**0.46**	0.39581	**0.18**	0.55009	**0.83**	0.07452
STM2143	yegU	putative glycohydrolase	**-0.33**	0.60637	**-0.66**	0.32045	**-1.32**	0.03094
STM2143	yegU	putative glycohydrolase	**1.00**	0.07033	**-0.71**	0.02493	**-0.58**	0.19781
STM2144	yegV	putative sugar kinase	**-0.17**	0.85117	**-0.18**	0.61477	**0.94**	0.18476
STM2144	yegV	putative sugar kinase	**-1.93**	0.02357	**-0.31**	0.42194	**-1.50**	0.05910
STM2145	yegW	putative regulatory protein	**-0.80**	0.31859	**0.68**	0.04630	**-0.39**	0.61159
STM2145	yegW	putative regulatory protein	**0.04**	0.93135	**1.07**	0.01062	**-0.43**	0.47598

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM2146	thiD	phosphomethylpyrimidine kinase	**0.32**	0.49007	**3.93**	0.00002	**0.01**	0.98233
STM2146	thiD	phosphomethylpyrimidine kinase	**0.78**	0.11322	**3.74**	0.00003	**1.21**	0.02584
STM2147	thiM	hydroxyethylthiazole kinase	**-0.58**	0.21687	**3.28**	0.00003	**-0.35**	0.57688
STM2147	thiM	hydroxyethylthiazole kinase	**1.13**	0.14205	**3.42**	0.00006	**-0.39**	0.51345
STM2148	STM2148	putative periplasmic protein	**-0.10**	0.83116	**0.16**	0.61534	**-0.27**	0.44088
STM2148	STM2148	putative periplasmic protein	**1.24**	0.04148	**0.12**	0.67697	**0.49**	0.20118
STM2149	stcD	putative outer membrane lipoprotein	**0.60**	0.25571	**0.85**	0.07414	**0.18**	0.69757
STM2149	stcD	putative outer membrane lipoprotein	**0.60**	0.36771	**0.66**	0.12751	**0.25**	0.57027
STM2150	stcC	putative outer membrane protein	**-0.51**	0.49324	**0.01**	0.97436	**-1.54**	0.02899
STM2150	stcC	putative outer membrane protein	**1.34**	0.05962	**0.23**	0.71785	**0.54**	0.20240
STM2151	stcB	putative periplasmic chaperone protein	**0.20**	0.79922	**0.65**	0.08774	**0.32**	0.49292
STM2151	stcB	putative periplasmic chaperone protein	**0.27**	0.57682	**-0.59**	0.35042	**0.79**	0.23842
STM2152	stcA	putative fimbrial-like protein	**0.13**	0.87730	**-0.22**	0.72795	**-0.16**	0.81580
STM2152	stcA	putative fimbrial-like protein	**1.13**	0.41632	**-0.08**	0.87789	**1.07**	0.02245
STM2153	yehE	putative outer membrane protein	**-1.14**	0.05303	**-0.41**	0.16554	**-0.23**	0.67281
STM2153	yehE	putative outer membrane protein	**-0.48**	0.35322	**-0.37**	0.24900	**-0.75**	0.08267
STM2154	mrp	putative ATP-binding protein	**-1.07**	0.23434	**-0.47**	0.11993	**-0.89**	0.06344
STM2154	mrp	putative ATP-binding protein	**-0.83**	0.11754	**-0.34**	0.23845	**-0.82**	0.09859
STM2155	metG	methionyl-tRNA synthetase	**-0.64**	0.39473	**-0.63**	0.04330	**0.20**	0.66322
STM2155	metG	methionyl-tRNA synthetase	**-0.33**	0.60635	**-1.10**	0.00597	**-1.10**	0.03641
STM2156	yehR	putative lipoprotein	**1.30**	0.06959	**0.05**	0.91828	**1.77**	0.00280
STM2156	yehR	putative lipoprotein	**2.05**	0.04208	**-0.09**	0.85092	**2.19**	0.00099
STM2156A	STM2156A	hypothetical protein STM2156A	**-0.84**	0.11953	**0.06**	0.85622	**-0.66**	0.10811
STM2156A	STM2156A	hypothetical protein STM2156A	**-0.38**	0.49605	**-0.48**	0.15583	**-0.32**	0.40622
STM2157	yehS	putative cytoplasmic protein	**-1.12**	0.06568	**-0.65**	0.07129	**-1.47**	0.00457
STM2157	yehS	putative cytoplasmic protein	**0.74**	0.63875	**-0.81**	0.09540	**-1.26**	0.19350
STM2158	yehT	putative regulatory protein	**-1.26**	0.11400	**-0.32**	0.34305	**-0.43**	0.26108
STM2158	yehT	putative regulatory protein	**-1.11**	0.08517	**-0.84**	0.01645	**-0.33**	0.65860
STM2159	yehU	putative sensor kinase	**-0.99**	0.08078	**-0.43**	0.27289	**-1.40**	0.01040
STM2159	yehU	putative sensor kinase	**1.29**	0.05515	**-0.84**	0.02857	**-0.08**	0.84514
STM2160	yehV	putative transcriptional repressor	**2.38**	0.00755	**1.25**	0.00277	**2.46**	0.00047
STM2160	yehV	putative transcriptional repressor	**3.14**	0.00547	**1.44**	0.00214	**3.12**	0.00035
STM2162	yehW	putative ABC-type proline/glycine betaine transport system	**-1.14**	0.03561	**-0.14**	0.66490	**0.97**	0.01931
STM2162	yehW	putative ABC-type proline/glycine betaine transport system	**-0.12**	0.82172	**0.86**	0.03395	**1.34**	0.00592
STM2163	yehX	putative ABC-type proline/glycine betaine transport system	**0.46**	0.45509	**-0.72**	0.03244	**-0.69**	0.16137
STM2163	yehX	putative ABC-type proline/glycine betaine transport system	**0.99**	0.19975	**-0.02**	0.95677	**-0.16**	0.72025
STM2164	yehY	putative ABC-type proline/glycine betaine transport system	**-0.78**	0.17944	**-0.12**	0.70638	**-0.75**	0.12030
STM2164	yehY	putative ABC-type proline/glycine betaine transport system	**0.11**	0.80508	**0.15**	0.76429	**0.11**	0.84249
STM2165	yehZ	putative transport protein	**0.08**	0.89893	**2.15**	0.00049	**1.16**	0.02418
STM2165	yehZ	putative transport protein	**1.28**	0.02652	**2.04**	0.00039	**2.78**	0.00017
STM2166	bglX	periplasmic beta-D-glucoside glucohydrolase	**-1.01**	0.12210	**-1.02**	0.02447	**0.02**	0.96216
STM2166	bglX	periplasmic beta-D-glucoside glucohydrolase	**-0.06**	0.89679	**-1.26**	0.00500	**0.51**	0.26344
STM2167	dld	D-lactate dehydrogenase	**-0.60**	0.23262	**0.19**	0.53204	**-0.08**	0.85719
STM2167	dld	D-lactate dehydrogenase	**1.22**	0.03095	**-0.48**	0.13437	**0.46**	0.27866
STM2168	pbpG	D-alanyl-D-alanine endopeptidase	**-0.42**	0.40158	**-1.28**	0.00413	**-1.06**	0.05240
STM2168	pbpG	D-alanyl-D-alanine endopeptidase	**-0.60**	0.29275	**-1.20**	0.00858	**-1.44**	0.01309
STM2169	yohC	putative transport protein	**-0.78**	0.09128	**0.42**	0.19221	**4.10**	0.00004
STM2169	yohC	putative transport protein	**0.16**	0.73728	**0.55**	0.06501	**4.57**	0.00005
STM2170	yohD	hypothetical protein STM2170	**0.62**	0.20480	**1.27**	0.02674	**1.36**	0.00642
STM2170	yohD	hypothetical protein STM2170	**1.31**	0.13262	**-0.40**	0.50034	**-0.16**	0.83179
STM2171	yohF	oxidoreductase	**0.06**	0.93292	**0.90**	0.00963	**2.62**	0.00215
STM2171	yohF	oxidoreductase	**2.23**	0.02991	**1.09**	0.00785	**3.73**	0.00008
STM2172	yohG	putative outer membrane efflux protein	**-0.35**	0.58596	**0.72**	0.20750	**1.42**	0.00343
STM2172	yohG	putative outer membrane efflux protein	**1.64**	0.36222	**-1.16**	0.10395	**-0.57**	0.45068
STM2174	yohI	putative regulatory protein	**0.72**	0.36007	**0.40**	0.29907	**1.16**	0.10705
STM2174	yohI	putative regulatory protein	**1.15**	0.06881	**-0.48**	0.14966	**1.75**	0.01429
STM2175	STM2175	salicylate hydroxylase	**-0.92**	0.18217	**0.24**	0.60967	**-0.55**	0.36296
STM2175	STM2175	salicylate hydroxylase	**-0.86**	0.10292	**-0.67**	0.22043	**0.90**	0.08345
STM2176	STM2176	putative glutathione S-transferase	**-0.68**	0.18762	**0.27**	0.43190	**-0.47**	0.48976
STM2176	STM2176	putative glutathione S-transferase	**0.74**	0.33947	**1.82**	0.01809	**0.58**	0.14412
STM2177	STM2177	putative flutathione S-transferase	**0.34**	0.45264	**-0.03**	0.94963	**-0.20**	0.59330
STM2177	STM2177	putative flutathione S-transferase	**0.30**	0.50620	**-0.20**	0.56704	**0.99**	0.03578
STM2178	STM2178	putative 1,2-dioxygenase	**0.05**	0.91861	**0.38**	0.27726	**0.67**	0.15094
STM2178	STM2178	putative 1,2-dioxygenase	**0.24**	0.79088	**0.56**	0.09539	**0.82**	0.08422
STM2179	STM2179	putative sugar transporter	**-0.11**	0.88250	**-0.37**	0.31387	**-0.68**	0.10540
STM2179	STM2179	putative sugar transporter	**2.23**	0.00889	**-0.62**	0.10608	**1.31**	0.07482
STM2180	STM2180	putative transcriptional regulator	**0.47**	0.46283	**-0.21**	0.57303	**0.68**	0.07886
STM2180	STM2180	putative transcriptional regulator	**2.07**	0.03182	**-0.47**	0.23708	**0.93**	0.02949
STM2181	yohJ	hypothetical protein STM2181	**0.15**	0.70320	**1.04**	0.01722	**0.78**	0.06727
STM2181	yohJ	hypothetical protein STM2181	**0.41**	0.40670	**0.88**	0.07178	**0.96**	0.03761

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM2182	yohK	hypothetical protein STM2182	**-0.27**	0.65007	**0.50**	0.08184	**-0.67**	0.09708
STM2182	yohK	hypothetical protein STM2182	**0.48**	0.26308	**0.43**	0.19652	**0.38**	0.27692
STM2183	cdd	cytidine deaminase	**-0.56**	0.49254	**-0.64**	0.07355	**-1.66**	0.01308
STM2183	cdd	cytidine deaminase	**-0.53**	0.44659	**-1.30**	0.00387	**-1.17**	0.15468
STM2184	sanA	vancomycin sensitivity	**-1.22**	0.03253	**-0.72**	0.03665	**-1.18**	0.13878
STM2184	sanA	vancomycin sensitivity	**-0.61**	0.20560	**-1.09**	0.03531	**-0.78**	0.33514
STM2185	b2145	putative inner membrane protein	**-0.58**	0.31205	**-1.23**	0.00609	**-0.78**	0.08336
STM2185	b2145	putative inner membrane protein	**-1.04**	0.31106	**-1.20**	0.00696	**-0.17**	0.67083
STM2186	STM2186	putative NADPH-dependent glutamate synthase beta chain	**-0.74**	0.21372	**-0.65**	0.09080	**-0.82**	0.14199
STM2186	STM2186	putative NADPH-dependent glutamate synthase beta chain	**0.58**	0.24030	**-0.94**	0.06107	**0.32**	0.43094
STM2187	yeiA	dihydropyrimidine dehydrogenase	**0.15**	0.84786	**0.98**	0.04908	**1.56**	0.09609
STM2187	yeiA	dihydropyrimidine dehydrogenase	**0.71**	0.40751	**-0.11**	0.82048	**-0.55**	0.60212
STM2188	mglC	beta-methylgalactoside transporter inner membrane	**0.47**	0.52834	**-0.01**	0.97385	**-0.16**	0.82029
STM2188	mglC	beta-methylgalactoside transporter inner membrane	**2.28**	0.00704	**-1.20**	0.01095	**0.32**	0.39483
STM2189	mglA	methyl-galactoside transport protein	**0.08**	0.91368	**0.44**	0.24553	**0.31**	0.53258
STM2189	mglA	methyl-galactoside transport protein	**1.61**	0.26359	**0.66**	0.06811	**0.82**	0.27981
STM2190	mglB	galactose transport protein	**-0.12**	0.81450	**1.89**	0.00151	**0.21**	0.61858
STM2190	mglB	galactose transport protein	**0.26**	0.62017	**1.79**	0.00111	**0.90**	0.03674
STM2191	galS	mgl operon transcriptional repressor	**0.23**	0.57178	**0.93**	0.03442	**-0.66**	0.25364
STM2191	galS	mgl operon transcriptional repressor	**1.43**	0.02344	**1.24**	0.01013	**1.41**	0.01056
STM2192	yeiB	putative inner membrane protein	**-0.48**	0.28744	**0.08**	0.82326	**-0.18**	0.67398
STM2192	yeiB	putative inner membrane protein	**-0.32**	0.47999	**-0.45**	0.11413	**-0.10**	0.83630
STM2193	folE	GTP cyclohydrolase I	**-1.70**	0.01215	**0.23**	0.46008	**-0.35**	0.35981
STM2193	folE	GTP cyclohydrolase I	**-0.73**	0.14131	**0.05**	0.86885	**-0.70**	0.20262
STM2194	yeiG	putative esterase	**-0.43**	0.45204	**-0.09**	0.78476	**-0.02**	0.95904
STM2194	yeiG	putative esterase	**0.50**	0.29330	**0.81**	0.02251	**-0.04**	0.93710
STM2195	STM2195	putative transcriptional regulator	**-0.51**	0.31125	**-0.45**	0.21820	**-1.04**	0.04572
STM2195	STM2195	putative transcriptional regulator	**0.32**	0.54395	**0.27**	0.31587	**-0.61**	0.14129
STM2196	STM2196	putative L-serine dehydratase	**-0.35**	0.50018	**0.72**	0.04091	**-0.08**	0.87342
STM2196	STM2196	putative L-serine dehydratase	**1.21**	0.09173	**0.23**	0.45541	**-0.47**	0.20668
STM2197	STM2197	putative phosphoserine phosphatase	**0.34**	0.59791	**1.16**	0.01497	**1.08**	0.09494
STM2197	STM2197	putative phosphoserine phosphatase	**1.57**	0.03206	**-0.58**	0.26256	**1.41**	0.01165
STM2198	STM2198	putative regulatory protein	**0.45**	0.29310	**1.93**	0.00150	**-0.20**	0.73391
STM2198	STM2198	putative regulatory protein	**0.98**	0.09173	**2.19**	0.00049	**0.62**	0.24183
STM2199	cirA	colicin I receptor protein	**-0.54**	0.34217	**2.25**	0.00043	**-0.69**	0.15440
STM2199	cirA	colicin I receptor protein	**0.81**	0.12984	**2.06**	0.00056	**1.35**	0.02565
STM2200	lysP	lysine-specific permease	**-2.02**	0.00796	**-0.20**	0.80599	**-0.96**	0.16577
STM2200	lysP	lysine-specific permease	**-1.05**	0.16316	**-0.91**	0.39695	**0.34**	0.76710
STM2201	yeiE	putative transcriptional regulator	**0.03**	0.94155	**0.24**	0.50029	**0.83**	0.05988
STM2201	yeiE	putative transcriptional regulator	**-0.16**	0.70999	**0.41**	0.32147	**-0.31**	0.41189
STM2202	yeiH	putative inner membrane protein	**-1.08**	0.06140	**-1.74**	0.01430	**-2.01**	0.00471
STM2202	yeiH	putative inner membrane protein	**-0.46**	0.34372	**-0.72**	0.03899	**-1.42**	0.03886
STM2203	nfo	endonuclease IV	**-2.15**	0.00747	**-1.06**	0.01126	**-1.88**	0.01287
STM2203	nfo	endonuclease IV	**-1.51**	0.02766	**-1.61**	0.00128	**-2.18**	0.00069
STM2204	fruA	fructose-specific transport protein	**-1.47**	0.02567	**-1.01**	0.05812	**-3.19**	0.00038
STM2204	fruA	fructose-specific transport protein	**-0.49**	0.43235	**-1.59**	0.00396	**-2.65**	0.00042
STM2205	fruK	1-phosphofructokinase	**-2.52**	0.00741	**-1.18**	0.00603	**-2.14**	0.00391
STM2205	fruK	1-phosphofructokinase	**-2.00**	0.01468	**-1.25**	0.00675	**-2.72**	0.00123
STM2206	fruF	phosphoenolpyruvate-dependent sugar phosphotransferase	**-2.48**	0.00753	**-1.94**	0.00054	**-4.32**	0.00009
STM2206	fruF	phosphoenolpyruvate-dependent sugar phosphotransferase	**-2.35**	0.05069	**-1.49**	0.00517	**-3.15**	0.00016
STM2207	setB	proton efflux pump	**-0.68**	0.21565	**-0.06**	0.86398	**-1.09**	0.01158
STM2207	setB	proton efflux pump	**-0.08**	0.86838	**-1.26**	0.02469	**-0.29**	0.41603
STM2208	STM2208	putative inner membrane protein	**-0.18**	0.73115	**0.45**	0.34537	**-0.24**	0.58025
STM2208	STM2208	putative inner membrane protein	**1.00**	0.45246	**-0.24**	0.54928	**-1.25**	0.03627
STM2209	STM2209	putative inner membrane protein	**-0.38**	0.45785	**0.23**	0.48899	**0.32**	0.52541
STM2209	STM2209	putative inner membrane protein	**0.32**	0.78985	**-0.70**	0.14270	**-0.03**	0.96190
STM2211,S	yeiP	elongation factor P	**-1.07**	0.04399	**-1.23**	0.00384	**-1.77**	0.00513
STM2211,S	yeiP	elongation factor P	**-0.27**	0.57072	**-1.54**	0.00281	**-1.00**	0.06830
STM2212	yeiR	putative cobalamin biosynthetic protein	**-1.01**	0.07361	**-0.25**	0.40398	**-0.55**	0.15176
STM2212	yeiR	putative cobalamin biosynthetic protein	**0.38**	0.61142	**-0.33**	0.41528	**0.39**	0.35037
STM2213	yeiU	putative permease	**-1.61**	0.02885	**-0.12**	0.69778	**-2.36**	0.02649
STM2213	yeiU	putative permease	**-1.89**	0.02116	**-0.80**	0.02259	**-2.65**	0.00623
STM2214	spr	putative lipoprotein	**-2.26**	0.00727	**-1.20**	0.00425	**-2.37**	0.00041
STM2214	spr	putative lipoprotein	**-1.82**	0.01083	**-0.64**	0.09602	**-1.93**	0.00175
STM2215	rtn	hypothetical protein STM2215	**-0.80**	0.18171	**-0.59**	0.18268	**-0.28**	0.56675
STM2215	rtn	hypothetical protein STM2215	**0.11**	0.87510	**-0.83**	0.06001	**0.70**	0.10251
STM2216	yejA	putative ABC transporter periplasmic binding protein	**-0.23**	0.65039	**0.28**	0.35851	**-0.31**	0.51429
STM2216	yejA	putative ABC transporter periplasmic binding protein	**-0.17**	0.70804	**-0.29**	0.34632	**0.50**	0.57927
STM2217	yejB	putative ABC-type dipeptide/oligopeptide/nickel transport	**-1.50**	0.03436	**-0.58**	0.14400	**-0.76**	0.15863
STM2217	yejB	putative ABC-type dipeptide/oligopeptide/nickel transport	**0.31**	0.72602	**-0.48**	0.25939	**-0.14**	0.79443

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM2218	yejE	putative ABC-type dipeptide/oligopeptide/nickel transport	**-0.52**	0.41195	**-0.88**	0.01440	**-0.59**	0.38971
STM2218	yejE	putative ABC-type dipeptide/oligopeptide/nickel transport	**-0.49**	0.34691	**-0.62**	0.03970	**-0.03**	0.94619
STM2219	yejF	putative ABC-type transport system ATPase component	**-0.05**	0.91880	**0.34**	0.34103	**-1.41**	0.03173
STM2219	yejF	putative ABC-type transport system ATPase component	**1.43**	0.12247	**-0.04**	0.91733	**-0.55**	0.39283
STM2220	yejG	putative cytoplasmic protein	**-0.34**	0.56778	**0.33**	0.31238	**-0.79**	0.05275
STM2220	yejG	putative cytoplasmic protein	**0.40**	0.43513	**0.17**	0.60834	**-0.48**	0.16687
STM2221	bcr	bicyclomycin resistance protein	**-1.08**	0.04212	**-0.31**	0.30933	**-0.22**	0.55646
STM2221	bcr	bicyclomycin resistance protein	**-0.89**	0.10850	**-0.60**	0.07502	**-0.70**	0.14341
STM2222	rsuA	16S rRNA pseudouridylate 516 synthase	**-0.55**	0.54459	**-1.13**	0.01655	**-1.44**	0.07473
STM2222	rsuA	16S rRNA pseudouridylate 516 synthase	**-1.04**	0.06216	**-0.89**	0.02019	**-1.51**	0.00733
STM2223	yejH	putative ATP-dependent helicase	**-0.26**	0.66164	**-0.36**	0.47004	**-0.97**	0.13523
STM2223	yejH	putative ATP-dependent helicase	**-0.20**	0.77775	**-0.66**	0.04306	**-1.41**	0.03152
STM2224	rplY	50S ribosomal protein L25	**-0.75**	0.18441	**-0.79**	0.02635	**-3.73**	0.00020
STM2224	rplY	50S ribosomal protein L25	**0.06**	0.93319	**-0.84**	0.02532	**-2.10**	0.00093
STM2225	STM2225	putative inner membrane protein	**-1.77**	0.02597	**-0.32**	0.39332	**-0.52**	0.17595
STM2225	STM2225	putative inner membrane protein	**-0.48**	0.61958	**-0.35**	0.44186	**-0.34**	0.40201
STM2226	yejK	nucleoid-associated protein NdpA	**1.52**	0.15968	**-0.11**	0.70369	**-0.26**	0.81357
STM2226	yejK	nucleoid-associated protein NdpA	**2.95**	0.00547	**-0.51**	0.10664	**-1.01**	0.05476
STM2227	yejL	putative cytoplasmic protein	**-2.27**	0.00694	**-1.27**	0.00647	**-2.29**	0.00051
STM2227	yejL	putative cytoplasmic protein	**-2.20**	0.01164	**-1.05**	0.02570	**-1.79**	0.00335
STM2228	yejM	putative hydrolase	**-0.72**	0.16482	**-0.55**	0.31309	**0.39**	0.46274
STM2228	yejM	putative hydrolase	**-1.29**	0.09097	**-0.33**	0.31491	**-0.33**	0.37884
STM2229	tRNAPro2	STM2229	**-0.11**	0.84899	**0.41**	0.49686	**2.75**	0.00038
STM2229	tRNAPro2	STM2229	**0.22**	0.61745	**-0.95**	0.01646	**2.71**	0.00020
STM2231	STM2231	virulence protein	**-0.60**	0.52776	**-1.49**	0.03522	**-0.25**	0.72346
STM2231	STM2231	virulence protein	**0.35**	0.48093	**-1.10**	0.02543	**0.11**	0.79951
STM2232	oafA	O-antigen acetylase	**-1.24**	0.06314	**-1.11**	0.00918	**-0.50**	0.41963
STM2232	oafA	O-antigen acetylase	**-2.34**	0.04995	**-1.35**	0.00569	**-0.90**	0.04268
STM2233	STM2233	putative cytoplasmic protein	**-0.58**	0.27959	**2.36**	0.00046	**-0.49**	0.47075
STM2233	STM2233	putative cytoplasmic protein	**0.53**	0.24220	**2.15**	0.00070	**0.00**	0.99365
STM2234	STM2234	putative phage tail fiber assembly protein	**-1.26**	0.07773	**3.67**	0.00011	**-1.02**	0.17398
STM2234	STM2234	putative phage tail fiber assembly protein	**-0.12**	0.87029	**4.21**	0.00003	**-0.07**	0.88099
STM2235	STM2235	hypothetical protein STM2235	**-0.55**	0.42968	**2.02**	0.00504	**2.27**	0.00251
STM2235	STM2235	hypothetical protein STM2235	**-1.31**	0.02540	**1.00**	0.01929	**1.52**	0.00872
STM2236	STM2236	hypothetical protein STM2236	**0.90**	0.28500	**4.74**	0.00001	**-0.17**	0.78946
STM2236	STM2236	hypothetical protein STM2236	**1.94**	0.10271	**4.83**	0.00001	**0.00**	0.99691
STM2237	STM2237	putative inner membrane protein	**0.83**	0.12840	**3.79**	0.00008	**-1.45**	0.01017
STM2237	STM2237	putative inner membrane protein	**1.93**	0.01530	**4.01**	0.00002	**0.54**	0.33187
STM2238	STM2238	hypothetical protein STM2238	**0.53**	0.35162	**-1.05**	0.00790	**0.39**	0.57961
STM2238	STM2238	hypothetical protein STM2238	**0.80**	0.20880	**-0.73**	0.08212	**1.24**	0.02912
STM2240	STM2240	putative cytoplasmic protein	**-0.33**	0.62438	**2.19**	0.00061	**-0.45**	0.40243
STM2240	STM2240	putative cytoplasmic protein	**0.37**	0.72951	**2.38**	0.00066	**-0.53**	0.34160
STM2240	STM2240	putative cytoplasmic protein	**-0.15**	0.83479	**1.54**	0.00273	**-1.01**	0.11342
STM2240	STM2240	putative cytoplasmic protein	**0.43**	0.64924	**2.96**	0.00005	**0.61**	0.26953
STM2241	sspH2	leucine-rich repeat protein	**0.08**	0.87990	**4.67**	0.00001	**-1.31**	0.01435
STM2241	sspH2	leucine-rich repeat protein	**1.41**	0.02339	**4.62**	0.00002	**0.26**	0.56064
STM2242	STM2242	putative phage tail fiber protein	**1.71**	0.08975	**3.09**	0.00005	**0.35**	0.62494
STM2242	STM2242	putative phage tail fiber protein	**2.23**	0.02598	**2.85**	0.00013	**1.41**	0.00754
STM2243	STM2243	putative tail fiber protein of phage	**0.83**	0.17511	**0.73**	0.03986	**-1.05**	0.13751
STM2243	STM2243	putative tail fiber protein of phage	**1.11**	0.05633	**0.83**	0.07107	**0.52**	0.19851
STM2245	pagL	putative outer membrane protein	**0.91**	0.36919	**0.06**	0.94382	**0.83**	0.11003
STM2245	pagL	putative outer membrane protein	**2.94**	0.00764	**-0.95**	0.06988	**0.99**	0.08957
STM2246	narP	response regulator	**-0.27**	0.59556	**-0.70**	0.08853	**-1.05**	0.02477
STM2246	narP	response regulator	**0.79**	0.13786	**0.23**	0.51552	**-1.27**	0.09215
STM2247	ccmH	putative heme lyase subunit	**-0.64**	0.20774	**0.02**	0.95605	**-1.12**	0.08795
STM2247	ccmH	putative heme lyase subunit	**0.21**	0.68969	**-1.85**	0.05051	**0.63**	0.13706
STM2248	ccmG	heme lyase disulfide oxidoreductase	**1.03**	0.26164	**-0.41**	0.28788	**-0.26**	0.49893
STM2248	ccmG	heme lyase disulfide oxidoreductase	**2.24**	0.08505	**-0.76**	0.04859	**0.82**	0.09755
STM2249	ccmF	cytochrome c-type biogenesis protein	**0.50**	0.32538	**-1.43**	0.00433	**0.16**	0.73863
STM2249	ccmF	cytochrome c-type biogenesis protein	**0.55**	0.43044	**-1.92**	0.00067	**0.03**	0.96969
STM2250	ccmE	periplasmic heme-dependent peroxidase	**2.49**	0.01566	**-0.19**	0.53261	**0.04**	0.95174
STM2250	ccmE	periplasmic heme-dependent peroxidase	**2.85**	0.00547	**-0.16**	0.72481	**1.27**	0.02640
STM2251	ccmD	heme exporter protein C	**0.84**	0.10045	**-0.42**	0.23096	**-1.51**	0.03785
STM2251	ccmD	heme exporter protein C	**1.11**	0.04359	**-0.59**	0.14400	**-0.19**	0.64894
STM2252	ccmC	heme exporter protein	**0.70**	0.12362	**-0.18**	0.54864	**-0.75**	0.13159
STM2252	ccmC	heme exporter protein	**1.59**	0.10625	**-0.26**	0.35113	**-0.55**	0.25217
STM2253	ccmB	heme exporter protein	**-0.65**	0.14224	**0.40**	0.20797	**-2.13**	0.00490
STM2253	ccmB	heme exporter protein	**0.29**	0.70460	**1.20**	0.01168	**-0.61**	0.15735
STM2254	ccmA	heme exporter protein	**-0.76**	0.14539	**-0.62**	0.14501	**-1.05**	0.08578
STM2254	ccmA	heme exporter protein	**0.23**	0.64477	**-1.13**	0.00910	**-1.70**	0.00288

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM2255	napC	periplasmic nitrate reductase	**-1.00**	0.07227	**-0.24**	0.43484	**-1.26**	0.00968
STM2255	napC	periplasmic nitrate reductase	**0.32**	0.70396	**-0.47**	0.11030	**-0.39**	0.32749
STM2256	napB	periplasmic nitrate reductase	**-0.17**	0.74341	**-1.38**	0.00341	**-1.14**	0.01301
STM2256	napB	periplasmic nitrate reductase	**0.33**	0.61038	**-1.82**	0.01250	**0.18**	0.72410
STM2257	napH	quinol dehydrogenase membrane component	**-0.34**	0.41155	**-0.56**	0.13103	**0.69**	0.25266
STM2257	napH	quinol dehydrogenase membrane component	**1.91**	0.00913	**-0.54**	0.10343	**0.51**	0.43987
STM2258	napG	quinol dehydrogenase periplasmic component	**0.96**	0.17809	**-1.57**	0.00290	**-1.06**	0.19461
STM2258	napG	quinol dehydrogenase periplasmic component	**0.91**	0.27065	**-1.27**	0.00391	**-0.25**	0.60418
STM2259	napA	periplasmic nitrate reductase	**-1.84**	0.04720	**-0.64**	0.09183	**-1.47**	0.01045
STM2259	napA	periplasmic nitrate reductase	**-1.60**	0.04102	**-1.38**	0.00561	**-0.34**	0.54496
STM2260	napD	periplasmic nitrate reductase	**-0.62**	0.40888	**-0.48**	0.28124	**-0.13**	0.86528
STM2260	napD	periplasmic nitrate reductase	**1.11**	0.29898	**-0.94**	0.02769	**0.30**	0.58804
STM2262	eco	ecotin precursor	**-0.32**	0.63756	**0.79**	0.02179	**0.60**	0.14488
STM2262	eco	ecotin precursor	**0.19**	0.87395	**0.17**	0.59337	**1.82**	0.00121
STM2263	yojI	putative ABC-type multidrug/protein/lipid transport system	**-0.96**	0.10377	**-0.21**	0.56986	**-1.32**	0.02803
STM2263	yojI	putative ABC-type multidrug/protein/lipid transport system	**0.21**	0.68411	**-0.37**	0.30681	**-0.55**	0.20212
STM2264	alkB	DNA repair system protein	**-0.03**	0.97915	**-0.58**	0.09507	**-1.01**	0.04136
STM2264	alkB	DNA repair system protein	**-0.20**	0.73302	**-0.37**	0.24728	**1.53**	0.28456
STM2265	ada	O6-methylguanine-DNA methyltransferase/transcription	**-1.15**	0.03585	**-0.30**	0.36784	**-0.73**	0.07142
STM2265	ada	O6-methylguanine-DNA methyltransferase/transcription	**-0.09**	0.90246	**-0.89**	0.01316	**-0.31**	0.54122
STM2266	apbE	putative lipoprotein	**-1.27**	0.11924	**-0.99**	0.01203	**-1.45**	0.01816
STM2266	apbE	putative lipoprotein	**-0.50**	0.40084	**-1.06**	0.00475	**-1.44**	0.00731
STM2267	ompC	outer membrane protein C precursor	**-4.48**	0.00673	**-1.61**	0.00405	**-3.81**	0.02273
STM2267	ompC	outer membrane protein C precursor	**-3.54**	0.00579	**-0.90**	0.01098	**-4.71**	0.00010
STM2269	yojN	putative sensor kinase	**-1.40**	0.02148	**0.37**	0.36364	**-0.58**	0.10972
STM2269	yojN	putative sensor kinase	**-0.80**	0.11472	**0.00**	0.99505	**-0.40**	0.29601
STM2270	rcsB	response regulator	**-1.13**	0.18196	**-0.36**	0.29979	**-1.56**	0.00317
STM2270	rcsB	response regulator	**0.11**	0.82377	**-0.09**	0.81837	**-0.94**	0.07653
STM2271	rcsC	sensory histidine kinase	**-0.99**	0.06276	**-0.45**	0.13167	**-1.07**	0.02850
STM2271	rcsC	sensory histidine kinase	**-0.11**	0.90505	**-0.63**	0.06483	**-0.27**	0.46715
STM2272	gyrA	DNA gyrase subunit A	**-0.25**	0.61320	**-0.30**	0.32575	**-1.30**	0.02230
STM2272	gyrA	DNA gyrase subunit A	**0.37**	0.39809	**-0.43**	0.15033	**-0.31**	0.57488
STM2273	STM2273	putative dehydratase	**0.14**	0.84977	**-0.26**	0.41378	**0.40**	0.46115
STM2273	STM2273	putative dehydratase	**0.70**	0.31214	**-0.39**	0.24385	**0.50**	0.30028
STM2274	STM2274	putative permease	**-1.22**	0.03642	**-1.31**	0.00755	**-0.09**	0.85872
STM2274	STM2274	putative permease	**-0.74**	0.63313	**-0.85**	0.05528	**-0.03**	0.96613
STM2275	STM2275	putative regulatory protein	**-1.15**	0.03253	**-0.38**	0.21527	**-0.59**	0.11207
STM2275	STM2275	putative regulatory protein	**1.94**	0.01257	**-0.72**	0.02737	**-0.29**	0.43344
STM2276	ubiG	3-demethylubiquinone-9 3-methyltransferase	**-1.73**	0.18201	**-1.14**	0.01021	**-0.86**	0.08950
STM2276	ubiG	3-demethylubiquinone-9 3-methyltransferase	**1.18**	0.35364	**-0.92**	0.01245	**-0.89**	0.08343
STM2277	nrdA	ribonucleotide-diphosphate reductase alpha subunit	**-2.18**	0.01725	**-1.34**	0.00176	**-3.59**	0.00010
STM2277	nrdA	ribonucleotide-diphosphate reductase alpha subunit	**-1.79**	0.01661	**-1.08**	0.00532	**-3.42**	0.00198
STM2278	nrdB	ribonucleotide-diphosphate reductase beta subunit	**-2.14**	0.00901	**-0.65**	0.09868	**-3.07**	0.00053
STM2278	nrdB	ribonucleotide-diphosphate reductase beta subunit	**-0.82**	0.17816	**-0.67**	0.04883	**-1.85**	0.00433
STM2279	yfaE	putative ferredoxin	**-2.01**	0.03095	**-1.68**	0.00164	**-2.57**	0.01509
STM2279	yfaE	putative ferredoxin	**-1.04**	0.18307	**-1.10**	0.00739	**-1.72**	0.00170
STM2280	STM2280	putative permease	**-1.48**	0.03575	**-0.96**	0.05574	**-3.51**	0.00006
STM2280	STM2280	putative permease	**-0.31**	0.60796	**-0.99**	0.02363	**-0.67**	0.20545
STM2281	STM2281	putative transcriptional regulator	**1.06**	0.25851	**0.25**	0.58842	**1.59**	0.38254
STM2281	STM2281	putative transcriptional regulator	**-0.07**	0.86624	**0.35**	0.41793	**0.56**	0.29954
STM2282	glpQ	periplasmic glycerophosphodiester phosphodiesterase	**0.98**	0.23289	**1.24**	0.04741	**0.40**	0.49672
STM2282	glpQ	periplasmic glycerophosphodiester phosphodiesterase	**-0.38**	0.74777	**0.33**	0.45942	**-2.40**	0.04053
STM2283	glpT	sn-glycerol-3-phosphate transport protein	**-1.42**	0.15626	**-0.15**	0.66071	**-0.57**	0.31407
STM2283	glpT	sn-glycerol-3-phosphate transport protein	**-0.53**	0.36796	**0.20**	0.55564	**-0.92**	0.08164
STM2284	glpA	sn-glycerol-3-phosphate dehydrogenase large subunit	**-0.60**	0.30050	**0.61**	0.20149	**0.91**	0.03777
STM2284	glpA	sn-glycerol-3-phosphate dehydrogenase large subunit	**1.44**	0.02541	**1.09**	0.00759	**2.62**	0.00063
STM2285	glpB	anaerobic glycerol-3-phosphate dehydrogenase subunit B	**2.05**	0.09378	**1.08**	0.01944	**0.49**	0.19382
STM2285	glpB	anaerobic glycerol-3-phosphate dehydrogenase subunit B	**2.35**	0.04440	**0.90**	0.04428	**0.70**	0.12082
STM2286	glpC	sn-glycerol-3-phosphate dehydrogenase K-small subunit	**0.03**	0.95272	**1.55**	0.00231	**1.14**	0.03408
STM2286	glpC	sn-glycerol-3-phosphate dehydrogenase K-small subunit	**1.25**	0.05536	**1.26**	0.03549	**1.62**	0.00716
STM2287	sseL	putative cytoplasmic protein	**-0.10**	0.92457	**4.87**	0.00003	**1.35**	0.01071
STM2287	sseL	putative cytoplasmic protein	**-0.87**	0.19770	**5.52**	0.00004	**0.33**	0.69132
STM2288	STM2288	putative cytoplasmic protein	**-0.42**	0.39064	**3.63**	0.00004	**0.37**	0.54437
STM2288	STM2288	putative cytoplasmic protein	**0.38**	0.44447	**3.42**	0.00023	**-0.07**	0.90785
STM2289	STM2289	putative 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase	**-0.45**	0.54585	**2.47**	0.00249	**0.19**	0.76378
STM2289	STM2289	putative 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase	**1.16**	0.15446	**2.39**	0.00020	**0.70**	0.21130
STM2290	yfaV	putative transport protein	**0.03**	0.96815	**0.00**	0.99979	**-1.00**	0.03638
STM2290	yfaV	putative transport protein	**0.51**	0.38023	**-0.36**	0.42618	**-0.20**	0.73009
STM2291	yfaW	putative galactonate dehydratase	**2.16**	0.03081	**0.38**	0.66467	**1.52**	0.02694
STM2291	yfaW	putative galactonate dehydratase	**1.10**	0.26489	**0.24**	0.68081	**1.14**	0.35151

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM2292	yfaX	putative transcriptional regulator	**-0.04**	0.93799	**0.09**	0.83587	**1.44**	0.00896
STM2292	yfaX	putative transcriptional regulator	**1.11**	0.15717	**0.33**	0.52296	**1.33**	0.00845
STM2293	STM2293	competence damage-inducible protein A	**0.45**	0.36277	**3.12**	0.00010	**-0.23**	0.68166
STM2293	STM2293	competence damage-inducible protein A	**1.14**	0.10961	**3.70**	0.00004	**-0.46**	0.38839
STM2294	yfaZ	putative inner membrane protein	**-2.83**	0.01426	**-2.13**	0.00980	**-3.34**	0.00012
STM2294	yfaZ	putative inner membrane protein	**0.68**	0.64281	**-2.49**	0.00715	**-0.67**	0.29061
STM2295	yfaO	putative NTP pyrophosphohydrolase	**-0.73**	0.24212	**-0.02**	0.96453	**-0.74**	0.36215
STM2295	yfaO	putative NTP pyrophosphohydrolase	**-0.24**	0.60670	**-0.03**	0.94295	**-1.17**	0.04353
STM2296	ais	aluminum-inducible protein	**-1.40**	0.02124	**1.11**	0.08769	**-0.43**	0.42791
STM2296	ais	aluminum-inducible protein	**-1.23**	0.07935	**-0.48**	0.31390	**-2.89**	0.00148
STM2297	yfbE	4-amino-4-deoxy-L-arabinose lipopolysaccharide-modifying	**-1.41**	0.02606	**0.01**	0.97933	**-2.25**	0.01070
STM2297	yfbE	4-amino-4-deoxy-L-arabinose lipopolysaccharide-modifying	**-0.35**	0.41685	**-0.04**	0.93584	**-1.50**	0.00728
STM2298	pmrF	putative glycosyl transferase	**-0.52**	0.40522	**-0.02**	0.96917	**-0.54**	0.42038
STM2298	pmrF	putative glycosyl transferase	**0.94**	0.12380	**-0.56**	0.16391	**-0.83**	0.17724
STM2299	yfbG	hypothetical protein STM2299	**-1.33**	0.02838	**-1.15**	0.02524	**-2.74**	0.00086
STM2299	yfbG	hypothetical protein STM2299	**-1.20**	0.10684	**-0.30**	0.36534	**-1.77**	0.06311
STM2300	STM2300	putative cytoplasmic protein	**1.02**	0.41946	**-1.22**	0.01998	**-0.83**	0.47703
STM2300	STM2300	putative cytoplasmic protein	**1.16**	0.06677	**-1.46**	0.01841	**-0.57**	0.16290
STM2301	pqaB	putative melittin resistance protein	**-0.44**	0.45879	**0.27**	0.37724	**-0.99**	0.05147
STM2301	pqaB	putative melittin resistance protein	**1.03**	0.17298	**-0.05**	0.94007	**0.01**	0.99462
STM2302	STM2302	putative inner membrane protein	**0.71**	0.11464	**-0.50**	0.27870	**-0.87**	0.04585
STM2302	STM2302	putative inner membrane protein	**1.49**	0.01777	**-1.03**	0.03319	**0.61**	0.26595
STM2303	STM2303	hypothetical protein STM2303	**0.37**	0.39641	**-0.52**	0.16845	**-1.57**	0.00444
STM2303	STM2303	hypothetical protein STM2303	**1.25**	0.03426	**-0.54**	0.11509	**-0.45**	0.27220
STM2304	pmrD	polymyxin resistance protein B	**1.09**	0.36222	**0.51**	0.27031	**-0.24**	0.65319
STM2304	pmrD	polymyxin resistance protein B	**0.70**	0.63012	**-0.36**	0.21523	**-2.94**	0.00050
STM2305	menE	O-succinylbenzoic acid--CoA ligase	**-0.29**	0.57958	**0.11**	0.73999	**0.52**	0.27262
STM2305	menE	O-succinylbenzoic acid--CoA ligase	**-0.13**	0.84649	**-0.10**	0.75320	**0.16**	0.75788
STM2306	menC	O-succinylbenzoate synthase	**-1.90**	0.03088	**-0.77**	0.25036	**-0.81**	0.10062
STM2306	menC	O-succinylbenzoate synthase	**-0.81**	0.10899	**-1.33**	0.00976	**-1.16**	0.04096
STM2307	menB	naphthoate synthase	**-1.47**	0.02070	**-0.33**	0.36876	**-2.15**	0.00075
STM2307	menB	naphthoate synthase	**0.23**	0.59072	**-0.50**	0.13924	**-1.46**	0.01013
STM2308	yfbB	putative enzyme	**-1.32**	0.02316	**-0.02**	0.94882	**-1.37**	0.02497
STM2308	yfbB	putative enzyme	**0.40**	0.39108	**0.43**	0.22324	**-0.18**	0.68482
STM2309	menD	2-oxoglutarate decarboxylase	**-1.55**	0.16184	**-2.41**	0.00029	**-1.25**	0.04377
STM2309	menD	2-oxoglutarate decarboxylase	**-1.29**	0.45145	**-2.23**	0.00077	**-2.03**	0.06469
STM2310	menF	menaquinone-specific isochorismate synthase	**0.05**	0.94275	**0.41**	0.67756	**0.42**	0.36837
STM2310	menF	menaquinone-specific isochorismate synthase	**1.47**	0.16959	**-2.41**	0.04006	**0.70**	0.37584
STM2311	elaB	putative inner membrane protein	**0.47**	0.59827	**2.36**	0.00041	**3.92**	0.00006
STM2311	elaB	putative inner membrane protein	**0.92**	0.38379	**2.31**	0.00023	**4.30**	0.00007
STM2312	elaA	putative acyltransferase	**-0.43**	0.31406	**0.66**	0.08996	**1.18**	0.00914
STM2312	elaA	putative acyltransferase	**0.47**	0.43045	**1.23**	0.00389	**2.10**	0.00244
STM2313	elaC	ribonuclease Z	**-0.94**	0.06182	**-0.88**	0.08758	**-0.53**	0.14342
STM2313	elaC	ribonuclease Z	**-0.06**	0.90126	**-0.83**	0.04758	**-0.26**	0.60025
STM2314	STM2314	putative chemotaxis signal transduction protein	**-1.30**	0.07573	**-2.90**	0.00006	**-1.14**	0.09687
STM2314	STM2314	putative chemotaxis signal transduction protein	**-0.81**	0.11720	**-2.41**	0.00015	**-1.23**	0.01188
STM2315	yfbK	hypothetical protein STM2315	**-0.89**	0.17930	**-1.63**	0.00071	**-1.21**	0.00900
STM2315	yfbK	hypothetical protein STM2315	**-1.83**	0.07979	**-0.86**	0.29760	**-0.18**	0.64269
STM2316,S	nuoN	NADH dehydrogenase subunit N	**-1.89**	0.01237	**-2.51**	0.00008	**-3.08**	0.00011
STM2316,S	nuoN	NADH dehydrogenase subunit N	**-0.85**	0.12114	**-2.61**	0.00092	**-1.89**	0.00156
STM2317	nuoM	NADH dehydrogenase subunit M	**-3.91**	0.00571	**-3.69**	0.00002	**-4.07**	0.00003
STM2317	nuoM	NADH dehydrogenase subunit M	**-4.87**	0.00512	**-3.85**	0.00002	**-4.77**	0.00009
STM2318	nuoL	NADH dehydrogenase subunit L	**-3.74**	0.00546	**-3.72**	0.00006	**-4.25**	0.00003
STM2318	nuoL	NADH dehydrogenase subunit L	**-2.24**	0.01041	**-3.42**	0.00055	**-4.10**	0.00010
STM2319	nuoK	NADH dehydrogenase kappa subunit	**-3.43**	0.00547	**-3.51**	0.00006	**-3.01**	0.00174
STM2319	nuoK	NADH dehydrogenase kappa subunit	**-2.16**	0.02394	**-3.41**	0.00003	**-3.40**	0.00007
STM2320	nuoJ	NADH dehydrogenase subunit J	**0.76**	0.13309	**-1.74**	0.04853	**-2.77**	0.00538
STM2320	nuoJ	NADH dehydrogenase subunit J	**0.72**	0.12918	**-2.79**	0.00021	**-2.51**	0.00021
STM2321	nuoI	NADH dehydrogenase subunit I	**-1.38**	0.02653	**-3.40**	0.00003	**-1.64**	0.02821
STM2321	nuoI	NADH dehydrogenase subunit I	**-0.19**	0.68827	**-3.45**	0.00003	**-0.94**	0.02225
STM2322	nuoH	NADH dehydrogenase subunit H	**-3.58**	0.00512	**-4.23**	0.00001	**-3.91**	0.00004
STM2322	nuoH	NADH dehydrogenase subunit H	**-2.48**	0.00747	**-4.18**	0.00002	**-2.48**	0.00318
STM2323,S	nuoG	NADH dehydrogenase gamma subunit	**-2.12**	0.00861	**-3.11**	0.00005	**-2.55**	0.00078
STM2323,S	nuoG	NADH dehydrogenase gamma subunit	**-2.08**	0.01866	**-4.03**	0.00003	**-2.06**	0.00132
STM2324	nuoF	NADH dehydrogenase I chain F	**-3.95**	0.00512	**-3.73**	0.00001	**-4.18**	0.00006
STM2324	nuoF	NADH dehydrogenase I chain F	**-2.69**	0.00650	**-3.21**	0.00002	**-3.38**	0.00010
STM2325	nuoE	ATP synthase subunit E	**-4.29**	0.00512	**-3.47**	0.00003	**-3.69**	0.00034
STM2325	nuoE	ATP synthase subunit E	**-2.49**	0.02139	**-3.32**	0.00006	**-3.64**	0.00007
STM2326	nuoC	NADH dehydrogenase I chain C/D	**-3.52**	0.00654	**-3.80**	0.00002	**-3.32**	0.00007
STM2326	nuoC	NADH dehydrogenase I chain C/D	**-3.47**	0.00541	**-3.94**	0.00001	**-3.33**	0.00042

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM2327	nuoB	NADH dehydrogenase beta subunit	**-3.50**	0.00635	**-3.60**	0.00016	**-3.75**	0.00021
STM2327	nuoB	NADH dehydrogenase beta subunit	**-2.21**	0.07824	**-3.28**	0.00008	**-3.33**	0.00021
STM2328	nuoA	NADH dehydrogenase alpha subunit	**-3.78**	0.00512	**-3.60**	0.00004	**-2.77**	0.00017
STM2328	nuoA	NADH dehydrogenase alpha subunit	**-2.67**	0.09923	**-3.94**	0.00002	**-2.90**	0.00018
STM2329	STM2329	putative cytoplasmic protein	**-2.24**	0.01067	**-0.42**	0.66287	**-2.09**	0.00218
STM2329	STM2329	putative cytoplasmic protein	**-1.22**	0.09359	**-1.67**	0.00201	**-1.66**	0.01366
STM2330	lrhA	NADH dehydrogenase transcriptional repressor	**-1.49**	0.07463	**-1.09**	0.00824	**-1.10**	0.12850
STM2330	lrhA	NADH dehydrogenase transcriptional repressor	**-0.06**	0.91149	**-0.75**	0.05608	**-0.86**	0.07300
STM2331	yfbQ	aspartate aminotransferase	**-0.54**	0.27400	**-0.88**	0.01888	**-1.70**	0.00264
STM2331	yfbQ	aspartate aminotransferase	**-0.03**	0.95842	**-0.69**	0.07252	**-0.66**	0.28751
STM2332	STM2332	hypothetical protein STM2332	**-0.12**	0.77958	**0.33**	0.33086	**-0.64**	0.08961
STM2332	STM2332	hypothetical protein STM2332	**0.95**	0.12117	**0.24**	0.43092	**-0.02**	0.96800
STM2333	yfbS	putative response regulator	**-0.11**	0.86650	**0.47**	0.11110	**-0.95**	0.05051
STM2333	yfbS	putative response regulator	**-0.12**	0.90635	**-0.58**	0.15240	**-0.62**	0.32920
STM2334	yfbT	putative phosphatase	**-0.82**	0.07892	**-0.15**	0.70889	**-0.44**	0.21966
STM2334	yfbT	putative phosphatase	**-0.06**	0.91689	**-0.05**	0.88582	**0.23**	0.63009
STM2335	yfbU	hypothetical protein STM2335	**-1.63**	0.02148	**-0.02**	0.95323	**-0.71**	0.06990
STM2335	yfbU	hypothetical protein STM2335	**-0.42**	0.39063	**0.39**	0.21702	**-0.47**	0.28849
STM2336	STM2336	hypothetical protein STM2336	**-1.53**	0.01801	**-0.67**	0.03824	**0.30**	0.48805
STM2336	STM2336	hypothetical protein STM2336	**-0.78**	0.23242	**-0.38**	0.27243	**0.26**	0.55899
STM2337	ackA	acetate/propionate kinase	**-4.41**	0.00512	**-2.23**	0.00036	**-3.47**	0.00011
STM2337	ackA	acetate/propionate kinase	**-3.85**	0.00512	**-1.97**	0.00224	**-3.44**	0.00008
STM2338	pta	phosphate acetyltransferase	**-1.40**	0.03905	**-0.49**	0.67136	**-2.14**	0.00163
STM2338	pta	phosphate acetyltransferase	**-1.09**	0.04496	**-1.45**	0.00258	**-1.66**	0.00644
STM2339	yfcC	putative integral membrane protein	**-1.22**	0.08508	**0.00**	0.99395	**-0.47**	0.50013
STM2339	yfcC	putative integral membrane protein	**-0.52**	0.34627	**-0.33**	0.33283	**-1.31**	0.00609
STM2340	STM2340	putative transketolase	**-0.41**	0.58595	**0.24**	0.48529	**0.92**	0.12789
STM2340	STM2340	putative transketolase	**1.38**	0.02217	**1.35**	0.04008	**3.16**	0.01077
STM2341	STM2341	putative transketolase	**-0.29**	0.60249	**0.46**	0.34032	**-0.31**	0.51384
STM2341	STM2341	putative transketolase	**0.77**	0.25119	**0.16**	0.59448	**0.43**	0.37839
STM2342	ulaA	ascorbate-specific PTS system enzyme IIC	**0.98**	0.11805	**0.68**	0.11502	**1.56**	0.04016
STM2342	ulaA	ascorbate-specific PTS system enzyme IIC	**1.93**	0.02024	**0.86**	0.03197	**2.41**	0.00153
STM2343	STM2343	putative cytoplasmic protein	**0.34**	0.42177	**0.34**	0.34941	**0.24**	0.61436
STM2343	STM2343	putative cytoplasmic protein	**0.73**	0.33259	**0.90**	0.03590	**0.03**	0.96777
STM2344	STM2344	putative phosphotransferase system enzyme II A	**0.96**	0.19706	**0.59**	0.17728	**-0.17**	0.75178
STM2344	STM2344	putative phosphotransferase system enzyme II A	**1.58**	0.06280	**-0.04**	0.92633	**1.51**	0.11764
STM2345	STM2345	putative transcriptional regulator	**-0.28**	0.51958	**-0.24**	0.45104	**-0.48**	0.37964
STM2345	STM2345	putative transcriptional regulator	**0.20**	0.63587	**0.11**	0.73838	**0.67**	0.14216
STM2346	STM2346	putative NTP pyrophosphohydrolase	**0.82**	0.26877	**-0.23**	0.52902	**-1.57**	0.00374
STM2346	STM2346	putative NTP pyrophosphohydrolase	**2.48**	0.00900	**0.04**	0.89755	**-1.00**	0.02141
STM2347	yfcE	phosphodiesterase	**-0.34**	0.74113	**0.21**	0.55780	**2.00**	0.00057
STM2347	yfcE	phosphodiesterase	**-0.43**	0.77775	**0.23**	0.55752	**2.14**	0.00079
STM2348	yfcF	putative glutathione S-transferase	**-0.96**	0.07941	**0.23**	0.78417	**0.46**	0.46225
STM2348	yfcF	putative glutathione S-transferase	**0.32**	0.61172	**-0.40**	0.17705	**0.60**	0.34298
STM2349	yfcG	putative glutathione S-transferase	**-1.06**	0.27200	**0.38**	0.36702	**1.40**	0.01064
STM2349	yfcG	putative glutathione S-transferase	**-0.60**	0.49397	**-0.30**	0.71425	**1.90**	0.00380
STM2350	yfcH	putative sugar nucleotide epimerase	**-0.04**	0.94628	**0.58**	0.17424	**0.78**	0.12234
STM2350	yfcH	putative sugar nucleotide epimerase	**1.90**	0.06648	**0.67**	0.10464	**1.45**	0.02096
STM2351	hisP	histidine/lysine/arginine/ornithine transport protein	**1.58**	0.02439	**-0.62**	0.11909	**-0.12**	0.81963
STM2351	hisP	histidine/lysine/arginine/ornithine transport protein	**2.37**	0.01041	**-0.80**	0.25635	**1.77**	0.00253
STM2352	hisM	histidine/lysine/arginine/ornithine transport protein	**-1.21**	0.06916	**-0.09**	0.78832	**-1.59**	0.00325
STM2352	hisM	histidine/lysine/arginine/ornithine transport protein	**-0.28**	0.61038	**0.10**	0.78594	**0.45**	0.27366
STM2353	hisQ	histidine/lysine/arginine/ornithine transport protein	**-0.27**	0.74257	**0.28**	0.40807	**-0.14**	0.86591
STM2353	hisQ	histidine/lysine/arginine/ornithine transport protein	**2.05**	0.01057	**-0.74**	0.36778	**0.04**	0.95985
STM2354	hisJ	histidine transport protein	**-1.31**	0.02665	**1.34**	0.00215	**-0.89**	0.06409
STM2354	hisJ	histidine transport protein	**-0.02**	0.96468	**1.30**	0.00293	**-0.66**	0.11313
STM2355	argT	lysine/arginine/ornithine transport protein	**-0.72**	0.17944	**2.13**	0.00015	**1.05**	0.03740
STM2355	argT	lysine/arginine/ornithine transport protein	**0.23**	0.57930	**1.49**	0.00409	**1.29**	0.01694
STM2356	ubiX	3-octaprenyl-4-hydroxybenzoate carboxy-lyase	**-0.74**	0.22540	**-0.35**	0.28481	**0.19**	0.79417
STM2356	ubiX	3-octaprenyl-4-hydroxybenzoate carboxy-lyase	**0.35**	0.45345	**-0.33**	0.36347	**0.91**	0.22632
STM2357	STM2357	putative amino acid transporter	**-1.34**	0.02260	**0.15**	0.69962	**-0.37**	0.31812
STM2357	STM2357	putative amino acid transporter	**-0.03**	0.94585	**0.34**	0.41796	**0.20**	0.64637
STM2358	STM2358	putative cytoplasmic protein	**-0.50**	0.29722	**-0.48**	0.46640	**0.72**	0.20262
STM2358	STM2358	putative cytoplasmic protein	**1.19**	0.22062	**-0.46**	0.30384	**-0.29**	0.81063
STM2359	STM2359	putative amino acid transporter	**0.29**	0.71063	**0.26**	0.40205	**-0.42**	0.54889
STM2359	STM2359	putative amino acid transporter	**1.46**	0.16264	**0.38**	0.34917	**0.48**	0.63664
STM2360	STM2360	putative diaminopimelate decarboxylase	**-0.06**	0.89647	**-0.32**	0.53243	**0.07**	0.94831
STM2360	STM2360	putative diaminopimelate decarboxylase	**0.59**	0.46474	**0.49**	0.44945	**0.26**	0.80174
STM2361	STM2361	putative regulatory protein	**0.88**	0.19533	**0.69**	0.03074	**1.88**	0.01988
STM2361	STM2361	putative regulatory protein	**0.36**	0.53160	**1.04**	0.00918	**0.99**	0.13323

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM2362	purF	amidophosphoribosyltransferase	**-0.96**	0.21279	**0.63**	0.06258	**0.60**	0.24800
STM2362	purF	amidophosphoribosyltransferase	**0.19**	0.78623	**1.12**	0.00405	**0.73**	0.07198
STM2363	cvpA	colicin V production protein	**-1.86**	0.08236	**0.10**	0.75781	**-2.27**	0.00135
STM2363	cvpA	colicin V production protein	**-1.25**	0.02573	**-0.01**	0.97286	**-2.71**	0.01310
STM2364	dedD	putative lipoprotein	**-0.94**	0.14152	**-0.69**	0.04168	**-0.91**	0.02645
STM2364	dedD	putative lipoprotein	**-0.87**	0.27113	**-0.01**	0.97699	**-1.52**	0.02463
STM2365	folC	multifunctional folylpolyglutamate synthase	**-0.79**	0.12856	**0.35**	0.33003	**-1.68**	0.01081
STM2365	folC	multifunctional folylpolyglutamate synthase	**-0.02**	0.96829	**0.30**	0.37747	**-0.86**	0.06099
STM2366	accD	acetyl-CoA carboxylase beta subunit	**-1.19**	0.04910	**-1.49**	0.00117	**-3.27**	0.00037
STM2366	accD	acetyl-CoA carboxylase beta subunit	**0.01**	0.98765	**-0.52**	0.11404	**-3.27**	0.00041
STM2367	dedA	hypothetical protein STM2367	**-1.68**	0.01196	**-0.34**	0.43706	**-1.00**	0.01643
STM2367	dedA	hypothetical protein STM2367	**-2.03**	0.01305	**-1.17**	0.00475	**-2.56**	0.00361
STM2368	truA	tRNA pseudouridine synthase A	**-1.04**	0.04403	**-0.34**	0.30331	**-1.67**	0.00571
STM2368	truA	tRNA pseudouridine synthase A	**-0.68**	0.19583	**-0.28**	0.42919	**-1.79**	0.00744
STM2369	usg	hypothetical protein STM2369	**-0.81**	0.28355	**-0.19**	0.69980	**-2.08**	0.00687
STM2369	usg	hypothetical protein STM2369	**-0.43**	0.34391	**-0.22**	0.53090	**-2.14**	0.00077
STM2370	pdxB	erythronate-4-phosphate dehydrogenase	**-3.42**	0.00512	**-1.99**	0.00166	**-3.46**	0.00038
STM2370	pdxB	erythronate-4-phosphate dehydrogenase	**-3.34**	0.00547	**-2.47**	0.00316	**-4.11**	0.00006
STM2371	flk	flagellar protein	**-0.70**	0.11628	**0.46**	0.38095	**-1.46**	0.01198
STM2371	flk	flagellar protein	**0.28**	0.59866	**0.57**	0.14801	**-1.33**	0.01306
STM2372	STM2372	hypothetical protein STM2372	**-0.85**	0.10017	**0.94**	0.01978	**-1.76**	0.01468
STM2372	STM2372	hypothetical protein STM2372	**-0.21**	0.73688	**1.20**	0.00473	**-0.93**	0.09755
STM2373	STM2373	putative cytoplasmic protein	**-0.41**	0.49835	**-0.77**	0.09660	**-0.49**	0.41176
STM2373	STM2373	putative cytoplasmic protein	**1.11**	0.04243	**-0.33**	0.44968	**1.06**	0.14151
STM2374	STM2374	putative regulatory protein	**-0.84**	0.14512	**-0.35**	0.40839	**-0.33**	0.64309
STM2374	STM2374	putative regulatory protein	**0.83**	0.17531	**-0.79**	0.12605	**0.13**	0.79578
STM2375	STM2375	putative cytoplasmic protein	**-0.27**	0.62241	**-0.83**	0.03399	**-1.30**	0.02944
STM2375	STM2375	putative cytoplasmic protein	**0.11**	0.80786	**-0.90**	0.02204	**-0.02**	0.96274
STM2376	STM2376	putative periplasmic protein	**-1.02**	0.12841	**-0.81**	0.15969	**-0.84**	0.09594
STM2376	STM2376	putative periplasmic protein	**0.38**	0.62210	**-0.92**	0.02062	**-1.42**	0.01320
STM2377	STM2377	putative inner membrane protein	**-0.93**	0.07033	**-0.83**	0.03341	**-0.40**	0.30862
STM2377	STM2377	putative inner membrane protein	**-0.70**	0.13970	**-0.95**	0.04900	**0.00**	0.99711
STM2378	fabB	3-oxoacyl-(acyl carrier protein) synthase	**-1.62**	0.02782	**-0.74**	0.07408	**-2.04**	0.00202
STM2378	fabB	3-oxoacyl-(acyl carrier protein) synthase	**-1.06**	0.04061	**-0.34**	0.40495	**-1.76**	0.00389
STM2379	STM2379	hypothetical protein STM2379	**-0.58**	0.28308	**-0.36**	0.35289	**-0.18**	0.65188
STM2379	STM2379	hypothetical protein STM2379	**-1.71**	0.11459	**-1.35**	0.02518	**-0.76**	0.10194
STM2380	yfcL	putative cytoplasmic protein	**-0.83**	0.10850	**-1.17**	0.00532	**-1.48**	0.04600
STM2380	yfcL	putative cytoplasmic protein	**-1.80**	0.02389	**-0.96**	0.02354	**-1.44**	0.06628
STM2381	yfcM	putative cytoplasmic protein	**-0.62**	0.29410	**-0.60**	0.06608	**-2.02**	0.00708
STM2381	yfcM	putative cytoplasmic protein	**0.17**	0.68007	**-0.78**	0.01798	**-0.40**	0.52736
STM2382	yfcA	putative permease	**-1.93**	0.01093	**-1.38**	0.06223	**-2.34**	0.00232
STM2382	yfcA	putative permease	**-0.69**	0.43001	**-1.93**	0.03236	**-1.51**	0.07532
STM2383	mepA	penicillin-insensitive murein endopeptidase	**2.04**	0.22834	**1.15**	0.00778	**-1.24**	0.02255
STM2383	mepA	penicillin-insensitive murein endopeptidase	**2.20**	0.09382	**1.32**	0.01722	**-1.07**	0.04573
STM2384	aroC	chorismate synthase	**-1.25**	0.15068	**-0.33**	0.52833	**-2.09**	0.00165
STM2384	aroC	chorismate synthase	**-0.70**	0.11755	**-0.38**	0.26709	**-1.71**	0.00577
STM2385	yfcB	putative methylase	**-2.09**	0.01555	**-0.80**	0.07640	**-2.44**	0.00034
STM2385	yfcB	putative methylase	**-1.72**	0.01326	**-0.88**	0.02722	**-2.32**	0.00118
STM2386	yfcN	hypothetical protein STM2386	**-0.62**	0.20762	**0.47**	0.10504	**-0.56**	0.16274
STM2386	yfcN	hypothetical protein STM2386	**-0.11**	0.82987	**0.92**	0.02219	**-0.46**	0.24766
STM2387	sixA	phosphohistidine phosphatase	**-1.05**	0.06350	**0.65**	0.03787	**-0.07**	0.87085
STM2387	sixA	phosphohistidine phosphatase	**0.04**	0.96889	**0.97**	0.00818	**0.55**	0.24227
STM2388	yfcX	putative dehydrogenase	**-0.60**	0.20375	**2.69**	0.00022	**0.35**	0.32940
STM2388	yfcX	putative dehydrogenase	**1.14**	0.07325	**2.83**	0.00006	**0.98**	0.09062
STM2389	yfcY	acetyl-CoA acetyltransferase	**1.64**	0.09574	**-0.58**	0.28877	**-0.13**	0.90096
STM2389	yfcY	acetyl-CoA acetyltransferase	**2.71**	0.03664	**-2.15**	0.00031	**0.35**	0.72207
STM2390	yfcZ	putative cytoplasmic protein	**0.29**	0.73507	**-1.52**	0.08869	**-0.80**	0.09309
STM2390	yfcZ	putative cytoplasmic protein	**-1.41**	0.11037	**-0.19**	0.53594	**-0.55**	0.37957
STM2391	fadL	outer membrane-bound fatty acid transporter	**-2.09**	0.00971	**-0.97**	0.01237	**-0.99**	0.03055
STM2391	fadL	outer membrane-bound fatty acid transporter	**-0.60**	0.39998	**-0.69**	0.03437	**1.24**	0.01979
STM2392	vacJ	lipoprotein precursor	**-0.89**	0.34544	**-0.61**	0.13673	**-0.91**	0.03598
STM2392	vacJ	lipoprotein precursor	**-0.04**	0.97265	**-0.80**	0.03203	**0.03**	0.94353
STM2393	yfdC	hypothetical protein STM2393	**4.12**	0.03086	**-1.43**	0.00277	**2.10**	0.07556
STM2393	yfdC	hypothetical protein STM2393	**3.08**	0.01235	**-2.07**	0.01020	**2.60**	0.00358
STM2394	argW	STM2394	**-0.02**	0.98369	**0.73**	0.11202	**0.83**	0.10090
STM2394	argW	STM2394	**-0.16**	0.85377	**-0.35**	0.42291	**-1.88**	0.00360
STM2395	pgtE	outer membrane protein E precursor	**0.63**	0.21328	**-0.26**	0.41048	**-0.25**	0.53505
STM2395	pgtE	outer membrane protein E precursor	**1.30**	0.07631	**0.12**	0.81857	**2.10**	0.00963
STM2396	pgtA	activator	**1.63**	0.01855	**0.70**	0.05111	**-0.57**	0.19906
STM2396	pgtA	activator	**0.84**	0.13970	**0.74**	0.06223	**0.10**	0.84280

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM2397	pgtB	phosphoglycerate transport system sensor protein	**-1.66**	0.02573	**-0.24**	0.64803	**-1.17**	0.05230
STM2397	pgtB	phosphoglycerate transport system sensor protein	**-0.91**	0.16626	**-0.29**	0.56804	**0.08**	0.89925
STM2398	pgtC	phosphoglycerate transport regulatory protein precursor	**0.61**	0.27624	**0.80**	0.06850	**0.49**	0.37262
STM2398	pgtC	phosphoglycerate transport regulatory protein precursor	**2.80**	0.01196	**0.69**	0.20228	**1.71**	0.01284
STM2399	pgtP	transporter	**-0.36**	0.43816	**0.02**	0.95121	**-0.26**	0.70875
STM2399	pgtP	transporter	**1.32**	0.34909	**-0.59**	0.10087	**-0.37**	0.63860
STM2400	STM2400	putative inner membrane protein	**-0.10**	0.88482	**-0.24**	0.50625	**1.41**	0.12985
STM2400	STM2400	putative inner membrane protein	**1.41**	0.02096	**0.13**	0.81881	**2.26**	0.00210
STM2401	ddg	lipid A biosynthesis lauroyl acyltransferase	**-0.46**	0.32563	**-0.13**	0.79256	**-1.12**	0.07580
STM2401	ddg	lipid A biosynthesis lauroyl acyltransferase	**0.47**	0.51183	**-0.08**	0.77252	**-0.43**	0.44919
STM2402	yfdZ	hypothetical protein STM2402	**-0.35**	0.63473	**0.13**	0.71776	**-0.49**	0.17351
STM2402	yfdZ	hypothetical protein STM2402	**0.05**	0.93773	**0.39**	0.22222	**0.07**	0.91503
STM2403	glk	glucokinase	**-0.82**	0.47591	**-0.17**	0.67919	**1.34**	0.00890
STM2403	glk	glucokinase	**-1.04**	0.04252	**-0.28**	0.36466	**-0.02**	0.96589
STM2404	STM2404	hypothetical protein STM2404	**-0.69**	0.19590	**0.36**	0.22845	**2.11**	0.00225
STM2404	STM2404	hypothetical protein STM2404	**-0.07**	0.90161	**0.77**	0.13118	**2.04**	0.00119
STM2405	STM2405	indolepyruvate decarboxylase	**-0.78**	0.10885	**0.71**	0.05275	**2.07**	0.00155
STM2405	STM2405	indolepyruvate decarboxylase	**0.79**	0.30002	**0.81**	0.03886	**3.22**	0.00013
STM2406	STM2406	putative oxidoreductase	**-0.67**	0.25983	**0.36**	0.33718	**0.23**	0.65384
STM2406	STM2406	putative oxidoreductase	**0.03**	0.94505	**0.31**	0.48082	**0.44**	0.24968
STM2407	ypeC	putative periplasmic protein	**0.41**	0.43614	**1.14**	0.00525	**1.43**	0.01204
STM2407	ypeC	putative periplasmic protein	**0.22**	0.74802	**0.60**	0.13130	**1.33**	0.04071
STM2408	mntH	putative manganese transport protein MntH	**0.10**	0.93436	**2.10**	0.00057	**0.91**	0.03650
STM2408	mntH	putative manganese transport protein MntH	**0.49**	0.54890	**2.15**	0.00029	**1.08**	0.02914
STM2409	nupC	nucleoside transport	**-1.90**	0.02347	**-1.24**	0.00824	**-0.98**	0.01727
STM2409	nupC	nucleoside transport	**-1.39**	0.02124	**-1.69**	0.00104	**-0.90**	0.07488
STM2410	yfeA	hypothetical protein STM2410	**-0.15**	0.78528	**-0.66**	0.10976	**-0.90**	0.04045
STM2410	yfeA	hypothetical protein STM2410	**0.84**	0.10993	**-1.29**	0.01752	**-0.13**	0.76334
STM2411	alaX	STM2412	**1.60**	0.02908	**1.11**	0.00796	**1.01**	0.01646
STM2411	alaX	STM2412	**2.09**	0.04581	**1.14**	0.00288	**1.41**	0.00943
STM2412	alaW	STM2412	**1.13**	0.14440	**0.85**	0.05285	**0.72**	0.09135
STM2412	alaW	STM2412	**1.96**	0.02887	**0.94**	0.01159	**1.32**	0.00847
STM2413	yfeC	putative negative regulator	**-1.15**	0.09699	**-0.88**	0.02653	**-0.32**	0.36407
STM2413	yfeC	putative negative regulator	**-0.29**	0.62257	**-0.74**	0.03948	**-0.09**	0.83162
STM2414	yfeD	putative negative regulator	**0.08**	0.95570	**-0.58**	0.15341	**-0.93**	0.03373
STM2414	yfeD	putative negative regulator	**0.56**	0.39937	**-0.57**	0.11947	**-0.71**	0.10453
STM2415	gltX	glutamyl-tRNA synthetase	**-1.17**	0.04050	**-1.21**	0.00508	**-0.93**	0.07016
STM2415	gltX	glutamyl-tRNA synthetase	**-0.34**	0.55731	**-1.23**	0.00529	**-0.92**	0.07668
STM2416	valU	STM2416	**-1.09**	0.08078	**-0.80**	0.02875	**-1.02**	0.02717
STM2416	valU	STM2416	**-0.91**	0.22411	**-1.00**	0.01129	**-1.35**	0.01330
STM2417	valX	STM2417	**-1.22**	0.16839	**-1.27**	0.00310	**-1.00**	0.02548
STM2417	valX	STM2417	**-0.88**	0.31586	**-1.21**	0.00496	**-0.96**	0.05939
STM2418	valY	STM2418	**0.39**	0.63651	**-1.21**	0.00418	**-0.79**	0.09479
STM2418	valY	STM2418	**0.33**	0.60637	**-1.14**	0.01141	**-0.64**	0.25940
STM2419	lysV	STM2419	**-1.38**	0.09879	**-1.09**	0.01270	**0.60**	0.21976
STM2419	lysV	STM2419	**-0.83**	0.24636	**-1.01**	0.01693	**0.27**	0.46326
STM2420	xapR	XapA transcriptional regulator	**-0.98**	0.04842	**-1.49**	0.00386	**-1.77**	0.00162
STM2420	xapR	XapA transcriptional regulator	**-2.10**	0.04811	**-2.09**	0.00057	**-1.99**	0.00088
STM2420,1n	STM2420,1n	hypothetical protein STM2420,1n	**-1.03**	0.08599	**-1.22**	0.03929	**-0.86**	0.06952
STM2420,1n	STM2420,1n	hypothetical protein STM2420,1n	**-0.65**	0.25322	**-1.48**	0.00309	**-0.55**	0.27459
STM2421	xapB	xanthosine permease	**-1.05**	0.04930	**-1.22**	0.00385	**-0.99**	0.02091
STM2421	xapB	xanthosine permease	**-1.25**	0.04123	**-1.81**	0.00200	**-0.68**	0.11937
STM2423	yfeN	putative outer membrane protein	**-0.43**	0.31843	**0.10**	0.89357	**0.02**	0.96274
STM2423	yfeN	putative outer membrane protein	**-0.87**	0.34934	**0.33**	0.35857	**-0.27**	0.67592
STM2424	yfeR	putative transcriptional regulator	**0.92**	0.16623	**-0.10**	0.87324	**-0.91**	0.09155
STM2424	yfeR	putative transcriptional regulator	**1.84**	0.14452	**-1.15**	0.01058	**0.31**	0.54797
STM2425	yfeH	putative Na+-dependent transporter	**-0.87**	0.17403	**-0.01**	0.98617	**-0.46**	0.36137
STM2425	yfeH	putative Na+-dependent transporter	**-0.65**	0.30731	**-0.11**	0.72335	**-0.05**	0.94027
STM2426	STM2426	putative cytoplasmic protein	**-0.89**	0.09758	**0.16**	0.83257	**-0.94**	0.04315
STM2426	STM2426	putative cytoplasmic protein	**-0.53**	0.62724	**-0.94**	0.01436	**-3.31**	0.00297
STM2427	lig	DNA ligase	**-1.51**	0.02479	**-0.28**	0.35472	**-0.85**	0.20130
STM2427	lig	DNA ligase	**-1.52**	0.02039	**-0.50**	0.15953	**-1.62**	0.00470
STM2428	zipA	cell division protein ZipA	**-0.88**	0.06375	**-0.28**	0.35520	**-0.96**	0.07349
STM2428	zipA	cell division protein ZipA	**-0.49**	0.27829	**-0.28**	0.40583	**-0.40**	0.46879
STM2429	cysZ	putative sulfate transport protein CysZ	**-1.57**	0.01850	**-0.03**	0.94882	**-1.43**	0.00349
STM2429	cysZ	putative sulfate transport protein CysZ	**-1.10**	0.05264	**-0.30**	0.36784	**-1.28**	0.02627
STM2430	cysK	O-acetylserine sulfhydrolase A	**-1.90**	0.01102	**0.80**	0.02654	**-1.51**	0.00466
STM2430	cysK	O-acetylserine sulfhydrolase A	**-0.90**	0.06385	**1.03**	0.00549	**-0.95**	0.04348
STM2431	ptsH	phosphohistidinoprotein-hexose phosphotransferase	**-3.58**	0.01196	**-0.17**	0.68107	**-1.18**	0.00723
STM2431	ptsH	phosphohistidinoprotein-hexose phosphotransferase	**-1.74**	0.01622	**-0.05**	0.90712	**-0.38**	0.34387

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM2432	ptsI	PEP-protein phosphotransferase	**-2.90**	0.02163	**0.26**	0.42253	**0.16**	0.69801
STM2432	ptsI	PEP-protein phosphotransferase	**-2.12**	0.01982	**0.15**	0.68292	**0.51**	0.19949
STM2433	crr	glucose-specific PTS system enzyme IIA component	**-2.15**	0.02009	**-0.37**	0.32299	**0.25**	0.46740
STM2433	crr	glucose-specific PTS system enzyme IIA component	**-1.74**	0.03993	**-0.23**	0.53525	**0.67**	0.10219
STM2434	STM2434	putative cytoplasmic protein	**-1.06**	0.05492	**-0.14**	0.75004	**-0.11**	0.85489
STM2434	STM2434	putative cytoplasmic protein	**0.58**	0.49779	**-0.25**	0.46854	**-0.49**	0.28709
STM2435	pdxK	pyridoxine kinase	**-0.05**	0.91992	**-0.13**	0.69823	**-0.67**	0.11243
STM2435	pdxK	pyridoxine kinase	**0.28**	0.50156	**-0.20**	0.51646	**-0.25**	0.49674
STM2436	ptsJ	putative regulatory protein	**0.60**	0.64036	**-2.74**	0.00024	**-0.50**	0.50389
STM2436	ptsJ	putative regulatory protein	**0.17**	0.91415	**-3.45**	0.00006	**-0.68**	0.44312
STM2437	yfeJ	glutamine amidotransferase	**-0.64**	0.21801	**0.08**	0.82763	**-1.22**	0.03347
STM2437	yfeJ	glutamine amidotransferase	**1.13**	0.05101	**-0.01**	0.97744	**0.20**	0.61246
STM2438	yfeK	putative periplasmic protein	**-0.52**	0.25933	**1.00**	0.57443	**-0.68**	0.35595
STM2438	yfeK	putative periplasmic protein	**-1.20**	0.08683	**-0.52**	0.09079	**-0.06**	0.90050
STM2439	yfeL	putative membrane carboxypeptidase	**-1.08**	0.13864	**0.24**	0.49627	**-0.52**	0.40439
STM2439	yfeL	putative membrane carboxypeptidase	**-0.32**	0.61544	**0.11**	0.73559	**0.12**	0.80435
STM2440	cysM	cysteine synthase B	**-1.49**	0.01787	**-0.82**	0.04882	**-1.64**	0.01690
STM2440	cysM	cysteine synthase B	**-0.21**	0.73458	**-0.94**	0.03937	**-1.14**	0.03985
STM2441	cysA	sulfate permease A protein	**-0.05**	0.93891	**-0.59**	0.16682	**-1.30**	0.03550
STM2441	cysA	sulfate permease A protein	**1.13**	0.07468	**0.30**	0.36909	**0.04**	0.94267
STM2442	cysW	thiosulfate permease W protein	**1.04**	0.12356	**0.92**	0.01844	**1.92**	0.00122
STM2442	cysW	thiosulfate permease W protein	**2.92**	0.00547	**0.48**	0.34195	**2.91**	0.00017
STM2443	cysU	thiosulfate transport protein	**-0.84**	0.14420	**-0.03**	0.94302	**-1.70**	0.04497
STM2443	cysU	thiosulfate transport protein	**2.01**	0.01040	**0.20**	0.59312	**0.19**	0.80766
STM2444	cysP	thiosulfate transport protein	**-0.36**	0.63817	**-0.56**	0.12647	**-2.41**	0.00371
STM2444	cysP	thiosulfate transport protein	**1.05**	0.28221	**-0.98**	0.01057	**-1.50**	0.00591
STM2445	ucpA	short chain dehydrogenase	**-0.83**	0.43370	**-0.52**	0.17677	**-0.58**	0.17829
STM2445	ucpA	short chain dehydrogenase	**-0.34**	0.65904	**-0.41**	0.34046	**0.27**	0.43956
STM2446	STM2446	putative iron-dependent peroxidase	**-1.10**	0.04296	**-0.16**	0.67206	**-1.26**	0.01049
STM2446	STM2446	putative iron-dependent peroxidase	**1.19**	0.41194	**-0.16**	0.71091	**-0.65**	0.09859
STM2447	STM2447	putative outer membrane lipoprotein	**-1.16**	0.03954	**-0.07**	0.82184	**0.23**	0.53652
STM2447	STM2447	putative outer membrane lipoprotein	**0.33**	0.55541	**0.24**	0.43948	**-0.62**	0.25370
STM2448	yfeZ	putative inner membrane protein	**-0.39**	0.64567	**0.25**	0.49455	**-1.16**	0.07524
STM2448	yfeZ	putative inner membrane protein	**0.90**	0.33717	**0.24**	0.48164	**0.25**	0.54480
STM2449,S	STM2449,S	putative acetyltransferase	**-0.56**	0.24241	**-0.01**	0.98824	**-1.22**	0.01095
STM2449,S	STM2449,S	putative acetyltransferase	**-0.15**	0.82613	**0.41**	0.55616	**0.13**	0.75522
STM2450	amiA	N-acetylmuramoyl-l-alanine amidase I	**-0.43**	0.34366	**-1.33**	0.00288	**-2.12**	0.00188
STM2450	amiA	N-acetylmuramoyl-l-alanine amidase I	**-1.89**	0.05899	**-1.54**	0.00477	**-1.99**	0.00244
STM2451	hemF	coproporphyrinogen III oxidase	**-1.10**	0.17096	**-1.05**	0.10307	**-3.06**	0.00014
STM2451	hemF	coproporphyrinogen III oxidase	**0.90**	0.47183	**-1.35**	0.00432	**-1.46**	0.00824
STM2452	STM2452	putative inner membrane protein	**0.02**	0.97285	**-1.97**	0.00199	**-0.68**	0.27344
STM2452	STM2452	putative inner membrane protein	**-2.01**	0.03471	**-1.96**	0.00546	**-1.34**	0.03953
STM2453	STM2453	putative cytoplasmic protein	**0.88**	0.41577	**-0.10**	0.73911	**-0.29**	0.57253
STM2453	STM2453	putative cytoplasmic protein	**2.29**	0.01595	**-0.25**	0.39595	**1.83**	0.01244
STM2454	eutR	putative ethanolamine operon regulator	**-1.92**	0.01900	**-0.49**	0.31269	**-0.22**	0.71783
STM2454	eutR	putative ethanolamine operon regulator	**-0.08**	0.91550	**-0.70**	0.15418	**0.01**	0.98252
STM2455	eutK	putative carboxysome structural protein	**0.46**	0.28978	**1.15**	0.00761	**0.08**	0.91610
STM2455	eutK	putative carboxysome structural protein	**0.68**	0.18821	**1.98**	0.04342	**1.05**	0.13575
STM2456	eutL	putative carboxysome structural protein	**-0.18**	0.74341	**0.45**	0.17897	**0.25**	0.59552
STM2456	eutL	putative carboxysome structural protein	**1.38**	0.14267	**0.09**	0.82712	**0.93**	0.06300
STM2457	eutC	ethanolamine ammonia-lyase small subunit	**0.14**	0.82994	**1.02**	0.05871	**1.43**	0.03347
STM2457	eutC	ethanolamine ammonia-lyase small subunit	**1.79**	0.10321	**0.95**	0.01264	**1.37**	0.02677
STM2458	eutB	ethanolamine ammonia-lyase heavy chain	**1.23**	0.15459	**0.21**	0.66614	**0.38**	0.61421
STM2458	eutB	ethanolamine ammonia-lyase heavy chain	**2.69**	0.02617	**-0.70**	0.06120	**1.47**	0.01675
STM2459	eutA	ethanolamine utilization protein	**0.59**	0.21912	**0.23**	0.59365	**-0.25**	0.64334
STM2459	eutA	ethanolamine utilization protein	**0.60**	0.23857	**-0.04**	0.92483	**0.01**	0.97990
STM2460	eutH	putative transport protein	**0.99**	0.07851	**0.94**	0.03743	**0.49**	0.30914
STM2460	eutH	putative transport protein	**2.53**	0.05095	**-0.76**	0.04238	**0.62**	0.22406
STM2461	eutG	putative transport protein	**3.30**	0.04188	**-0.54**	0.35344	**0.68**	0.49698
STM2461	eutG	putative transport protein	**3.18**	0.00541	**0.04**	0.90639	**1.43**	0.14505
STM2462	eutJ	ethanolamine utilization protein	**0.40**	0.44416	**-0.69**	0.07806	**0.06**	0.92963
STM2462	eutJ	ethanolamine utilization protein	**1.56**	0.02540	**-0.35**	0.26924	**0.19**	0.71862
STM2463	eutE	putative aldehyde oxidoreductase	**-0.16**	0.79281	**0.24**	0.59214	**-1.27**	0.00634
STM2463	eutE	putative aldehyde oxidoreductase	**1.01**	0.05175	**0.00**	0.99206	**-0.07**	0.87683
STM2464	eutN	putative detox protein	**0.64**	0.38106	**-0.06**	0.90526	**-0.22**	0.68811
STM2464	eutN	putative detox protein	**1.49**	0.02735	**-0.84**	0.01679	**-0.12**	0.83048
STM2465	eutM	putative detox protein	**0.89**	0.07395	**0.06**	0.90672	**0.08**	0.89732
STM2465	eutM	putative detox protein	**1.27**	0.06091	**-0.34**	0.29483	**-0.12**	0.90653
STM2466	eutD	phosphate acetyltransferase	**-0.16**	0.71638	**-0.15**	0.79193	**0.20**	0.68707
STM2466	eutD	phosphate acetyltransferase	**0.88**	0.18742	**-0.85**	0.02397	**2.21**	0.00757

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM2467	eutT	putative cobalamin adenosyltransferase	**-1.19**	0.09242	**-0.94**	0.00734	**-0.24**	0.71589
STM2467	eutT	putative cobalamin adenosyltransferase	**-0.17**	0.71355	**-0.61**	0.16443	**-0.16**	0.71797
STM2468	eutQ	putative ethanolamine utilization protein	**-0.37**	0.48685	**-0.77**	0.09566	**0.63**	0.24602
STM2468	eutQ	putative ethanolamine utilization protein	**-0.31**	0.73224	**-1.16**	0.01184	**-0.38**	0.33123
STM2469	eutP	putative ethanolamine utilization protein	**0.55**	0.24318	**0.91**	0.01975	**1.13**	0.11837
STM2469	eutP	putative ethanolamine utilization protein	**2.03**	0.01835	**0.87**	0.02602	**1.30**	0.01732
STM2470	eutS	putative carboxysome structural protein	**4.11**	0.00595	**-0.12**	0.78961	**-0.51**	0.43994
STM2470	eutS	putative carboxysome structural protein	**4.65**	0.00512	**-0.75**	0.08481	**1.56**	0.05942
STM2472	maeB	phosphate acetyltransferase	**-0.63**	0.31460	**-0.40**	0.30992	**-1.50**	0.01769
STM2472	maeB	phosphate acetyltransferase	**0.24**	0.69773	**-0.23**	0.52124	**0.00**	0.99947
STM2473	talA	transaldolase	**-0.91**	0.14205	**2.54**	0.00014	**2.92**	0.00040
STM2473	talA	transaldolase	**0.14**	0.78825	**2.74**	0.00022	**3.97**	0.00009
STM2474	tktB	transketolase	**-0.43**	0.46384	**1.00**	0.00806	**1.32**	0.01739
STM2474	tktB	transketolase	**-0.09**	0.89334	**0.89**	0.08179	**1.65**	0.01029
STM2475	STM2475	putative cytoplasmic protein	**5.91**	0.00512	**1.66**	0.09200	**5.30**	0.00034
STM2475	STM2475	putative cytoplasmic protein	**7.10**	0.00512	**1.63**	0.02306	**4.63**	0.00638
STM2476	ypfG	putative periplasmic protein	**0.70**	0.12740	**-0.32**	0.50325	**-0.12**	0.73003
STM2476	ypfG	putative periplasmic protein	**1.14**	0.25396	**-0.19**	0.62704	**1.31**	0.02610
STM2477	yffH	putative pyrophosphohydrolase	**-0.57**	0.24162	**-0.26**	0.41028	**-0.38**	0.31066
STM2477	yffH	putative pyrophosphohydrolase	**0.04**	0.92982	**0.44**	0.40748	**-0.22**	0.86413
STM2478	STM2478	hypothetical protein STM2478	**0.32**	0.66672	**1.26**	0.02811	**0.98**	0.05212
STM2478	STM2478	hypothetical protein STM2478	**1.35**	0.04568	**1.75**	0.00374	**1.66**	0.01460
STM2479	aegA	putative oxidoreductase	**-0.03**	0.97445	**0.44**	0.44562	**0.53**	0.55238
STM2479	aegA	putative oxidoreductase	**1.61**	0.03896	**0.27**	0.60479	**0.23**	0.61223
STM2480	narQ	sensory histidine kinase	**0.72**	0.12155	**-0.13**	0.65558	**0.01**	0.98379
STM2480	narQ	sensory histidine kinase	**2.60**	0.19438	**-0.71**	0.04969	**1.18**	0.04097
STM2481	acrD	aminoglycoside/multidrug efflux pump	**0.86**	0.47388	**0.44**	0.41151	**2.83**	0.07952
STM2481	acrD	aminoglycoside/multidrug efflux pump	**0.64**	0.25320	**-0.58**	0.11383	**0.26**	0.58333
STM2482	yffB	putative glutaredoxin	**-1.90**	0.00994	**-1.30**	0.00272	**-2.13**	0.00040
STM2482	yffB	putative glutaredoxin	**-1.82**	0.01405	**-1.52**	0.00133	**-2.48**	0.00146
STM2483	dapE	succinyl-diaminopimelate desuccinylase	**-2.44**	0.00650	**-0.17**	0.55660	**0.26**	0.48911
STM2483	dapE	succinyl-diaminopimelate desuccinylase	**-1.22**	0.03925	**-0.10**	0.74912	**0.49**	0.20093
STM2484	STM2484	putative inner membrane protein	**-0.63**	0.28111	**0.49**	0.12500	**1.06**	0.02482
STM2484	STM2484	putative inner membrane protein	**0.18**	0.69529	**0.02**	0.95751	**1.56**	0.00391
STM2485	ypfI	putative acetyltransferase	**-1.63**	0.04376	**-1.45**	0.17728	**-0.17**	0.76199
STM2485	ypfI	putative acetyltransferase	**-0.10**	0.90467	**-0.35**	0.41172	**-0.23**	0.60435
STM2486	STM2486	putative inner membrane protein	**-0.47**	0.37554	**0.59**	0.06206	**0.57**	0.13235
STM2486	STM2486	putative inner membrane protein	**-0.08**	0.91393	**1.05**	0.00843	**1.38**	0.01386
STM2487	purC	phosphoribosylaminoimidazole-succinocarboxamide	**-1.23**	0.03188	**0.73**	0.03596	**-1.87**	0.00508
STM2487	purC	phosphoribosylaminoimidazole-succinocarboxamide	**-1.26**	0.05496	**0.97**	0.00845	**-0.84**	0.15732
STM2488	nlpB	lipoprotein	**-1.50**	0.01652	**-0.78**	0.02349	**-3.20**	0.00041
STM2488	nlpB	lipoprotein	**-0.30**	0.57122	**0.06**	0.86466	**-2.56**	0.00024
STM2489	dapA	dihydrodipicolinate synthase	**-2.91**	0.01235	**-1.66**	0.00373	**-3.02**	0.00026
STM2489	dapA	dihydrodipicolinate synthase	**-3.32**	0.00796	**-0.59**	0.13865	**-4.40**	0.00002
STM2490	gcvR	gcv operon transcriptional repressor	**-1.74**	0.03887	**0.09**	0.76403	**-1.92**	0.00461
STM2490	gcvR	gcv operon transcriptional repressor	**-0.92**	0.08960	**0.12**	0.70110	**-1.43**	0.05661
STM2491	bcp	bacterioferritin comigratory protein	**-1.08**	0.10468	**-0.12**	0.69250	**-0.62**	0.09186
STM2491	bcp	bacterioferritin comigratory protein	**0.51**	0.45136	**-0.12**	0.71909	**-0.47**	0.23768
STM2492	STM2492	putative glycerate kinase	**0.14**	0.87292	**0.42**	0.17924	**-1.71**	0.00676
STM2492	STM2492	putative glycerate kinase	**-0.47**	0.29898	**0.32**	0.33962	**-0.06**	0.90111
STM2493	perM	putative permease	**-1.56**	0.02456	**-0.32**	0.29487	**-1.05**	0.04176
STM2493	perM	putative permease	**-0.13**	0.83855	**-0.60**	0.07526	**-1.04**	0.07865
STM2494	STM2494	hypothetical protein STM2494	**-0.27**	0.79064	**1.27**	0.00952	**-0.39**	0.30625
STM2494	STM2494	hypothetical protein STM2494	**-0.54**	0.29945	**1.02**	0.02951	**0.35**	0.52152
STM2495	yfgD	putative arsenate reductase	**-0.95**	0.14828	**0.25**	0.40572	**0.49**	0.46857
STM2495	yfgD	putative arsenate reductase	**-0.50**	0.33719	**0.72**	0.09717	**-0.68**	0.10682
STM2496	yfgE	DNA replication initiation factor	**-1.22**	0.04685	**0.82**	0.03760	**-1.16**	0.02414
STM2496	yfgE	DNA replication initiation factor	**0.08**	0.85963	**0.60**	0.10464	**0.16**	0.68201
STM2497	uraA	uracil transport protein	**0.27**	0.69215	**-1.23**	0.00270	**-1.03**	0.01607
STM2497	uraA	uracil transport protein	**1.27**	0.07740	**-0.50**	0.09013	**-0.29**	0.54611
STM2498	upp	uracil phosphoribosyltransferase	**-0.41**	0.39332	**-0.47**	0.29303	**1.15**	0.39419
STM2498	upp	uracil phosphoribosyltransferase	**-0.76**	0.11941	**-1.00**	0.02257	**-2.85**	0.04051
STM2499,S	purM	phosphoribosylaminoimidazole synthetase	**0.57**	0.29842	**1.73**	0.00102	**1.03**	0.08629
STM2499,S	purM	phosphoribosylaminoimidazole synthetase	**1.14**	0.07421	**1.65**	0.00332	**1.89**	0.00232
STM2500	purN	phosphoribosylglycinamide formyltransferase	**-0.90**	0.07984	**0.06**	0.89351	**1.46**	0.02326
STM2500	purN	phosphoribosylglycinamide formyltransferase	**-0.27**	0.71247	**-0.18**	0.55733	**0.77**	0.22267
STM2501	ppk	polyphosphate kinase	**-2.45**	0.00747	**-0.25**	0.46196	**-1.63**	0.00337
STM2501	ppk	polyphosphate kinase	**-1.18**	0.03006	**-0.69**	0.07732	**-0.72**	0.12142
STM2502	ppx	exopolyphosphatase	**-0.74**	0.38726	**-0.53**	0.17879	**-1.53**	0.02705
STM2502	ppx	exopolyphosphatase	**0.19**	0.76815	**-0.55**	0.13579	**-0.73**	0.13691

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM2503	STM2503	putative diguanylate cyclase	**-0.36**	0.72496	**0.58**	0.07414	**-0.35**	0.49120
STM2503	STM2503	putative diguanylate cyclase	**-0.01**	0.97962	**-0.84**	0.03602	**-0.99**	0.03262
STM2506	STM2506	putative inner membrane protein	**0.58**	0.51063	**2.08**	0.00029	**1.10**	0.01844
STM2506	STM2506	putative inner membrane protein	**1.36**	0.07367	**1.82**	0.00161	**2.22**	0.00251
STM2509	STM2509	putative transposase	**1.07**	0.13872	**0.49**	0.21170	**0.52**	0.57169
STM2509	STM2509	putative transposase	**2.50**	0.02108	**0.47**	0.23868	**1.77**	0.01211
STM2510	guaA	bifunctional GMP synthase/glutamine amidotransferase	**-1.76**	0.01114	**-0.58**	0.06449	**-1.74**	0.01114
STM2510	guaA	bifunctional GMP synthase/glutamine amidotransferase	**-0.67**	0.39345	**-0.39**	0.23227	**-1.22**	0.00943
STM2511	guaB	inositol-5-monophosphate dehydrogenase	**-1.63**	0.01696	**0.05**	0.89875	**-1.22**	0.01311
STM2511	guaB	inositol-5-monophosphate dehydrogenase	**-1.52**	0.02828	**0.47**	0.13604	**-1.65**	0.00221
STM2512	xseA	exodeoxyribonuclease VII large subunit	**-0.33**	0.47370	**-0.80**	0.01975	**-0.10**	0.81935
STM2512	xseA	exodeoxyribonuclease VII large subunit	**0.63**	0.15497	**-0.96**	0.04036	**0.49**	0.28341
STM2513	shdA	AIDA autotransporter-like protein	**-0.31**	0.58029	**-0.52**	0.19050	**0.83**	0.08941
STM2513	shdA	AIDA autotransporter-like protein	**0.55**	0.24390	**-0.45**	0.25086	**-0.89**	0.06126
STM2514	ratB	putative outer membrane protein	**0.66**	0.28745	**-1.13**	0.11782	**2.84**	0.01746
STM2514	ratB	putative outer membrane protein	**1.99**	0.02703	**0.29**	0.34258	**1.20**	0.16994
STM2515	ratA	putative outer membrane protein	**-0.22**	0.63301	**0.22**	0.47604	**-0.23**	0.66056
STM2515	ratA	putative outer membrane protein	**0.21**	0.66516	**0.28**	0.53260	**0.00**	0.99711
STM2516	sinI	putative outer membrane protein	**0.42**	0.34927	**-1.30**	0.00487	**0.22**	0.56831
STM2516	sinI	putative outer membrane protein	**0.99**	0.30603	**-0.91**	0.04293	**0.51**	0.18300
STM2517	sinH	intimin-like protein	**1.09**	0.17565	**1.29**	0.06645	**1.39**	0.04187
STM2517	sinH	intimin-like protein	**0.95**	0.34855	**0.08**	0.90455	**1.54**	0.10951
STM2518	yfgJ	putative cytoplasmic protein	**-1.01**	0.05615	**-0.57**	0.07126	**-0.99**	0.01519
STM2518	yfgJ	putative cytoplasmic protein	**0.06**	0.93581	**-0.92**	0.01495	**-0.78**	0.10007
STM2519	engA	GTP-binding protein EngA	**0.36**	0.42438	**-0.03**	0.94293	**-0.22**	0.68707
STM2519	engA	GTP-binding protein EngA	**0.95**	0.12321	**-0.39**	0.17490	**0.61**	0.17963
STM2520	yfgL	putative serine/threonine protein kinase	**-2.42**	0.00969	**-1.83**	0.00067	**-2.13**	0.00034
STM2520	yfgL	putative serine/threonine protein kinase	**-2.40**	0.03832	**-1.70**	0.00097	**-2.27**	0.00051
STM2521	yfgM	putative inner membrane protein	**-2.80**	0.04120	**-0.83**	0.02826	**-2.69**	0.00037
STM2521	yfgM	putative inner membrane protein	**-1.55**	0.28755	**-1.10**	0.00515	**-2.08**	0.00200
STM2522	hisS	histidyl-tRNA synthetase	**-2.23**	0.00689	**-1.12**	0.00511	**-3.10**	0.00020
STM2522	hisS	histidyl-tRNA synthetase	**-1.04**	0.04373	**-0.69**	0.03240	**-2.72**	0.00014
STM2523	gcpE	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	**-3.06**	0.00778	**-1.41**	0.00437	**-0.98**	0.01917
STM2523	gcpE	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	**-2.14**	0.00735	**-0.93**	0.01539	**-0.68**	0.10506
STM2524	yfgA	hypothetical protein STM2524	**-1.52**	0.03239	**0.01**	0.97856	**-1.01**	0.02234
STM2524	yfgA	hypothetical protein STM2524	**-0.44**	0.55171	**-0.16**	0.60724	**-0.31**	0.50391
STM2525	yfgB	putative FeS redox enzyme	**-2.51**	0.00673	**-1.66**	0.00080	**-3.22**	0.00023
STM2525	yfgB	putative FeS redox enzyme	**-2.54**	0.03017	**-1.36**	0.00234	**-3.07**	0.00022
STM2526	ndk	nucleoside diphosphate kinase	**-2.91**	0.00546	**-2.64**	0.00005	**-3.46**	0.00006
STM2526	ndk	nucleoside diphosphate kinase	**-2.00**	0.01041	**-2.65**	0.00013	**-3.03**	0.00020
STM2527	STM2527	putative polyferredoxin	**-0.98**	0.35982	**-1.50**	0.00240	**-1.40**	0.00693
STM2527	STM2527	putative polyferredoxin	**0.01**	0.97845	**-1.20**	0.00536	**1.82**	0.00137
STM2528	STM2528	putative dimethylsulfoxide reductase	**0.33**	0.69128	**-0.46**	0.58775	**-1.13**	0.14266
STM2528	STM2528	putative dimethylsulfoxide reductase	**-0.67**	0.39843	**-2.12**	0.00805	**-0.84**	0.24363
STM2529	STM2529	putative anaerobic dimethylsulfoxide reductase	**-0.10**	0.87872	**-0.38**	0.43148	**0.16**	0.81005
STM2529	STM2529	putative anaerobic dimethylsulfoxide reductase	**-1.24**	0.20710	**-0.69**	0.04103	**-0.41**	0.52582
STM2530	STM2530	putative anaerobic dimethylsulfoxide reductase	**0.28**	0.57176	**-0.61**	0.12291	**0.97**	0.05617
STM2530	STM2530	putative anaerobic dimethylsulfoxide reductase	**1.35**	0.04050	**-0.76**	0.19376	**1.64**	0.00802
STM2531	pbpC	penicillin-binding protein 1c	**0.12**	0.78453	**-0.42**	0.28109	**-0.80**	0.17991
STM2531	pbpC	penicillin-binding protein 1c	**1.11**	0.19353	**-0.56**	0.19402	**0.25**	0.57743
STM2532	STM2532	putative inner membrane lipoprotein	**-1.16**	0.03541	**-0.80**	0.05063	**-0.98**	0.13645
STM2532	STM2532	putative inner membrane lipoprotein	**-0.19**	0.83479	**-0.22**	0.47540	**-0.54**	0.15742
STM2533	sseA	putative sulfurtransferase	**-1.29**	0.13871	**-0.63**	0.05193	**-0.10**	0.83741
STM2533	sseA	putative sulfurtransferase	**-0.30**	0.51664	**-0.47**	0.24399	**0.50**	0.22319
STM2534	STM2534	putative cytoplasmic protein	**-0.81**	0.16678	**0.14**	0.73817	**0.48**	0.26256
STM2534	STM2534	putative cytoplasmic protein	**0.03**	0.95570	**-0.28**	0.37640	**0.93**	0.02525
STM2535	sseB	enhanced serine sensitivity protein	**-1.15**	0.04451	**-1.27**	0.06349	**-1.09**	0.01689
STM2535	sseB	enhanced serine sensitivity protein	**-0.66**	0.14600	**-1.28**	0.00306	**-2.19**	0.00031
STM2536	pepB	aminopeptidase B	**-1.87**	0.01027	**-1.82**	0.00165	**-3.40**	0.00006
STM2536	pepB	aminopeptidase B	**-1.81**	0.01536	**-2.21**	0.00017	**-2.90**	0.00025
STM2537	yfhJ	hypothetical protein STM2537	**-3.52**	0.00991	**-1.99**	0.00049	**-2.27**	0.00040
STM2537	yfhJ	hypothetical protein STM2537	**-4.72**	0.00541	**-1.89**	0.00036	**-3.65**	0.00034
STM2538	fdx	electron carrer protein	**-3.00**	0.00840	**-1.82**	0.00155	**-4.22**	0.00006
STM2538	fdx	electron carrer protein	**-1.86**	0.01024	**-1.75**	0.00165	**-3.60**	0.00005
STM2539	hscA	chaperone protein HscA	**-3.00**	0.00546	**-1.67**	0.00141	**-3.78**	0.00006
STM2539	hscA	chaperone protein HscA	**-1.99**	0.01201	**-1.44**	0.00130	**-2.74**	0.00186
STM2540	hscB	co-chaperone HscB	**-2.82**	0.02284	**-0.96**	0.01230	**-2.34**	0.00114
STM2540	hscB	co-chaperone HscB	**-0.98**	0.05112	**-0.59**	0.10650	**-2.54**	0.00036
STM2541	iscA	iron-sulfur cluster assembly protein	**-1.70**	0.03623	**-0.13**	0.71894	**-1.24**	0.01002
STM2541	iscA	iron-sulfur cluster assembly protein	**-1.08**	0.04528	**-0.41**	0.32082	**-0.86**	0.04274

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM2542	nifU	NifU-like protein	**-1.37**	0.02710	**-0.21**	0.61113	**-0.93**	0.02782
STM2542	nifU	NifU-like protein	**-0.41**	0.31537	**0.16**	0.62704	**-0.33**	0.49928
STM2543	nifS	cysteine desulfurase	**-2.64**	0.01068	**-1.18**	0.00434	**-1.54**	0.01343
STM2543	nifS	cysteine desulfurase	**-2.10**	0.02007	**-0.59**	0.06274	**-0.98**	0.05395
STM2544	yfhP	putative iron-sulfur cluster regulatory protein	**-1.35**	0.10533	**1.27**	0.00508	**-0.13**	0.78047
STM2544	yfhP	putative iron-sulfur cluster regulatory protein	**-0.35**	0.50831	**1.34**	0.00160	**0.27**	0.43247
STM2545	STM2545	putative rRNA methylase	**-0.39**	0.43976	**0.84**	0.01819	**-1.49**	0.01515
STM2545	STM2545	putative rRNA methylase	**-0.37**	0.36741	**0.52**	0.13047	**-1.20**	0.01517
STM2546	suhB	inositol monophosphatase	**2.31**	0.41602	**1.33**	0.00148	**3.90**	0.00011
STM2546	suhB	inositol monophosphatase	**-0.43**	0.78300	**0.03**	0.94512	**2.33**	0.00231
STM2547	STM2547	putative hydrolase	**-1.03**	0.10141	**-1.13**	0.00426	**-1.43**	0.00960
STM2547	STM2547	putative hydrolase	**-0.11**	0.87983	**-0.87**	0.06229	**-0.52**	0.50024
STM2548	asrA	anaerobic sulfide reductase	**0.70**	0.11657	**-0.79**	0.05133	**-1.13**	0.02145
STM2548	asrA	anaerobic sulfide reductase	**1.19**	0.09078	**-1.37**	0.00722	**0.24**	0.55140
STM2549	asrB	anaerobic sulfite reductase subunit B	**0.43**	0.42560	**0.13**	0.69981	**-0.25**	0.59945
STM2549	asrB	anaerobic sulfite reductase subunit B	**1.40**	0.05195	**0.24**	0.40329	**0.35**	0.53146
STM2550	asrC	anaerobic sulfide reductase	**-0.20**	0.80487	**0.12**	0.70961	**-1.07**	0.07805
STM2550	asrC	anaerobic sulfide reductase	**0.73**	0.23621	**0.33**	0.35270	**-0.35**	0.41761
STM2551	STM2551	putative inner membrane protein	**-0.78**	0.14209	**0.03**	0.91960	**-0.57**	0.31440
STM2551	STM2551	putative inner membrane protein	**-1.31**	0.03906	**-0.70**	0.15065	**0.58**	0.23926
STM2552	STM2552	hypothetical protein STM2552	**1.16**	0.06515	**0.60**	0.06301	**-0.44**	0.29002
STM2552	STM2552	hypothetical protein STM2552	**1.49**	0.04273	**-0.02**	0.95130	**0.55**	0.20093
STM2553	csiE	stationary phase-inducible protein	**0.42**	0.30207	**0.57**	0.09238	**1.39**	0.00484
STM2553	csiE	stationary phase-inducible protein	**0.00**	0.99635	**0.18**	0.50146	**1.80**	0.00274
STM2554	hcaT	putative transport protein	**-1.12**	0.08469	**0.13**	0.75947	**0.20**	0.66676
STM2554	hcaT	putative transport protein	**-1.01**	0.13068	**-0.17**	0.59738	**-0.75**	0.13930
STM2555	glyA	serine hydroxymethyltransferase	**-1.74**	0.01850	**0.49**	0.13681	**-1.87**	0.00211
STM2555	glyA	serine hydroxymethyltransferase	**0.38**	0.67702	**0.90**	0.03172	**-0.92**	0.04460
STM2556	hmpA	dihydropteridine reductase 2/nitric oxide dioxygenase	**-0.26**	0.72937	**3.93**	0.00002	**-1.01**	0.02212
STM2556	hmpA	dihydropteridine reductase 2/nitric oxide dioxygenase	**0.22**	0.71140	**3.51**	0.00009	**-0.38**	0.40864
STM2557	cadC	transcriptional activator	**-1.69**	0.01655	**0.13**	0.82662	**-0.08**	0.84118
STM2557	cadC	transcriptional activator	**-1.82**	0.05154	**-0.46**	0.32327	**-0.80**	0.29650
STM2558	cadB	lysine/cadaverine transport protein	**-0.43**	0.56945	**-0.47**	0.14579	**-0.44**	0.37403
STM2558	cadB	lysine/cadaverine transport protein	**1.02**	0.12247	**-0.63**	0.22939	**0.71**	0.08587
STM2559	cadA	lysine decarboxylase 1	**0.49**	0.62602	**0.63**	0.23478	**1.06**	0.07771
STM2559	cadA	lysine decarboxylase 1	**0.81**	0.34370	**0.79**	0.07390	**-0.14**	0.83324
STM2560	yjdL	putative di-/tripeptide transport protein	**0.18**	0.68473	**0.56**	0.10603	**-0.63**	0.45734
STM2560	yjdL	putative di-/tripeptide transport protein	**-0.31**	0.44542	**0.16**	0.63942	**1.87**	0.00774
STM2561	glnB	regulatory protein P-II	**-1.31**	0.04183	**-0.25**	0.42986	**-2.20**	0.00766
STM2561	glnB	regulatory protein P-II	**-0.18**	0.76815	**0.75**	0.06332	**-2.18**	0.01007
STM2562	yfhA	putative transcriptional regulator	**-0.56**	0.41681	**0.75**	0.04708	**-0.54**	0.45227
STM2562	yfhA	putative transcriptional regulator	**0.05**	0.91347	**0.72**	0.04238	**-0.63**	0.09536
STM2563	yfhG	putative transcriptional regulator	**-1.18**	0.04832	**-0.59**	0.10286	**-0.90**	0.03342
STM2563	yfhG	putative transcriptional regulator	**-0.14**	0.73458	**0.02**	0.96835	**-0.74**	0.06065
STM2564	yfhK	putative sensor kinase	**-1.18**	0.06406	**0.24**	0.46337	**-0.51**	0.17508
STM2564	yfhK	putative sensor kinase	**-0.12**	0.84160	**0.46**	0.24979	**-0.72**	0.16686
STM2565	purG	phosphoribosylformylglycinamidine synthase	**0.12**	0.81191	**2.51**	0.00016	**-1.63**	0.01819
STM2565	purG	phosphoribosylformylglycinamidine synthase	**1.33**	0.06276	**2.15**	0.00020	**-0.15**	0.75178
STM2567	yfhD	putative periplasmic amino acid-binding protein	**-0.59**	0.36108	**-0.45**	0.14887	**-0.17**	0.65079
STM2567	yfhD	putative periplasmic amino acid-binding protein	**0.53**	0.44435	**-0.25**	0.49171	**0.95**	0.16466
STM2568	yfhC	putative cytosine/adenosine deaminase	**0.47**	0.26894	**-1.00**	0.01295	**-1.56**	0.02925
STM2568	yfhC	putative cytosine/adenosine deaminase	**1.06**	0.11438	**-0.97**	0.02173	**-1.04**	0.09722
STM2569	yfhB	putative phosphoserine phosphatase	**-0.78**	0.15474	**0.06**	0.87599	**0.09**	0.84838
STM2569	yfhB	putative phosphoserine phosphatase	**-0.23**	0.64901	**-0.23**	0.50794	**0.94**	0.04911
STM2570	STM2570	putative phosphotransferase system IIB component	**-0.80**	0.25727	**0.11**	0.76920	**0.44**	0.29644
STM2570	STM2570	putative phosphotransferase system IIB component	**-0.18**	0.71493	**0.26**	0.42640	**0.50**	0.26788
STM2571	STM2571	hypothetical protein STM2571	**0.28**	0.57682	**-0.81**	0.06005	**-0.85**	0.05934
STM2571	STM2571	hypothetical protein STM2571	**0.43**	0.46005	**-0.60**	0.07904	**0.02**	0.96184
STM2572	yfhH	putative transport protein	**-0.17**	0.73305	**-0.86**	0.08971	**-0.88**	0.12228
STM2572	yfhH	putative transport protein	**0.94**	0.05571	**-0.62**	0.09616	**-0.20**	0.70805
STM2573	STM2573	2-dehydropantoate 2-reductase	**-0.42**	0.47067	**0.07**	0.86101	**-0.98**	0.04240
STM2573	STM2573	2-dehydropantoate 2-reductase	**-0.37**	0.70170	**0.28**	0.38159	**-0.25**	0.61895
STM2574	STM2574	putative permease	**-0.43**	0.44976	**-0.68**	0.10203	**-0.96**	0.08771
STM2574	STM2574	putative permease	**-0.72**	0.29666	**-1.08**	0.01487	**-0.84**	0.11942
STM2575	STM2575	putative transcriptional regulator	**0.93**	0.07818	**0.28**	0.45872	**0.12**	0.81583
STM2575	STM2575	putative transcriptional regulator	**0.92**	0.09617	**-0.21**	0.65126	**0.65**	0.26165
STM2576	yfhL	putative ferredoxin	**-1.65**	0.02650	**-0.30**	0.35584	**-1.79**	0.03503
STM2576	yfhL	putative ferredoxin	**-0.61**	0.30853	**-0.28**	0.53099	**-2.08**	0.11040
STM2577	acpS	4'-phosphopantetheinyl transferase	**-0.74**	0.11083	**-0.61**	0.10700	**-1.34**	0.07942
STM2577	acpS	4'-phosphopantetheinyl transferase	**-1.18**	0.12841	**-0.29**	0.36784	**0.35**	0.84292

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM2578	pdxJ	pyridoxal phosphate biosynthetic protein	**-2.42**	0.02148	**-0.31**	0.44794	**-2.00**	0.00852
STM2578	pdxJ	pyridoxal phosphate biosynthetic protein	**-1.49**	0.02018	**-1.18**	0.00355	**-2.29**	0.00027
STM2579	recO	DNA repair protein RecO	**-0.33**	0.41886	**-0.64**	0.04072	**-1.10**	0.22921
STM2579	recO	DNA repair protein RecO	**-0.36**	0.49654	**-1.34**	0.00409	**-1.30**	0.08620
STM2580	era	GTP-binding protein Era	**-1.58**	0.01479	**-1.62**	0.00190	**-2.62**	0.00063
STM2580	era	GTP-binding protein Era	**-1.90**	0.03368	**-1.61**	0.00092	**-1.97**	0.00059
STM2581	rncS	ribonuclease III	**-2.51**	0.00613	**-0.94**	0.01653	**-2.55**	0.00038
STM2581	rncS	ribonuclease III	**-1.92**	0.02003	**-1.19**	0.01329	**-2.14**	0.00195
STM2582	lepB	signal peptidase I	**-1.90**	0.01885	**-0.89**	0.02521	**-1.47**	0.01492
STM2582	lepB	signal peptidase I	**-0.54**	0.20699	**-0.40**	0.15583	**-1.05**	0.06827
STM2583	lepA	GTP-binding protein LepA	**-2.29**	0.00796	**-1.30**	0.00374	**-2.44**	0.00069
STM2583	lepA	GTP-binding protein LepA	**-1.36**	0.02967	**-1.00**	0.00651	**-2.54**	0.00032
STM2584	gogB	leucine-rich repeat protein	**0.64**	0.31928	**1.33**	0.00359	**1.44**	0.00309
STM2584	gogB	leucine-rich repeat protein	**1.72**	0.02039	**0.96**	0.02537	**0.96**	0.03649
STM2586	STM2586	phage tail assembly-like protein	**2.23**	0.05145	**1.95**	0.00829	**0.20**	0.82188
STM2586	STM2586	phage tail assembly-like protein	**3.39**	0.00595	**1.82**	0.00087	**2.96**	0.00592
STM2587	STM2587	phage tail assembly-like protein	**0.42**	0.46047	**1.77**	0.00258	**0.59**	0.33243
STM2587	STM2587	phage tail assembly-like protein	**2.50**	0.02089	**1.20**	0.02635	**1.42**	0.00447
STM2588	STM2588	tail fiber-like protein	**1.43**	0.18229	**1.29**	0.00652	**0.86**	0.15469
STM2588	STM2588	tail fiber-like protein	**2.30**	0.02878	**1.29**	0.00293	**0.93**	0.08891
STM2589	STM2589	host specificity protein-J-like	**1.20**	0.17191	**0.94**	0.14574	**1.50**	0.01378
STM2589	STM2589	host specificity protein-J-like	**2.22**	0.05238	**0.73**	0.08544	**0.59**	0.19773
STM2590	STM2590	tail assembly protein I-like	**1.05**	0.27646	**-0.21**	0.62948	**1.17**	0.34975
STM2590	STM2590	tail assembly protein I-like	**2.10**	0.18507	**-0.84**	0.38761	**1.49**	0.06451
STM2591	STM2591	tail assembly protein K-like	**1.23**	0.14497	**0.67**	0.06143	**0.42**	0.31208
STM2591	STM2591	tail assembly protein K-like	**1.83**	0.01382	**0.51**	0.15313	**0.08**	0.93658
STM2592	STM2592	phage tail component L-like protein	**0.12**	0.87793	**0.60**	0.12202	**-0.47**	0.50695
STM2592	STM2592	phage tail component L-like protein	**4.16**	0.01842	**0.44**	0.17032	**0.92**	0.06605
STM2593	STM2593	phage tail component M-like protein	**0.02**	0.97408	**0.42**	0.20044	**-0.62**	0.13198
STM2593	STM2593	phage tail component M-like protein	**0.58**	0.26993	**0.18**	0.66125	**0.57**	0.33837
STM2594	STM2594	phage tail component H-like protein	**0.69**	0.34584	**0.73**	0.11518	**0.95**	0.10488
STM2594	STM2594	phage tail component H-like protein	**2.42**	0.01423	**-0.15**	0.73817	**1.24**	0.04270
STM2595	STM2595	minor tail-like protein	**1.01**	0.16242	**1.56**	0.01465	**-0.22**	0.77851
STM2595	STM2595	minor tail-like protein	**2.14**	0.01314	**0.99**	0.01058	**0.69**	0.13942
STM2596	STM2596	minor tail-like protein	**0.89**	0.22802	**1.39**	0.00389	**0.90**	0.18964
STM2596	STM2596	minor tail-like protein	**0.41**	0.31152	**0.00**	0.99707	**0.96**	0.01762
STM2597	STM2597	major tail-like protein	**1.00**	0.23605	**-0.93**	0.01460	**-0.68**	0.10072
STM2597	STM2597	major tail-like protein	**0.47**	0.29638	**-1.07**	0.10752	**-0.40**	0.37381
STM2598	STM2598	hypothetical protein STM2598	**0.70**	0.34702	**1.16**	0.00975	**1.46**	0.03772
STM2598	STM2598	hypothetical protein STM2598	**2.14**	0.08303	**0.74**	0.06234	**1.87**	0.00567
STM2599	STM2599	putative virulence protein	**-0.87**	0.14274	**0.75**	0.09869	**-0.03**	0.96589
STM2599	STM2599	putative virulence protein	**-1.62**	0.03920	**0.30**	0.35037	**-0.91**	0.04587
STM2600	STM2600	minor tail protein Z-like	**-0.54**	0.53128	**-0.04**	0.91349	**0.10**	0.89079
STM2600	STM2600	minor tail protein Z-like	**0.41**	0.42422	**0.30**	0.56539	**-0.11**	0.85769
STM2601	STM2601	minor capsid protein FII	**1.77**	0.02396	**0.45**	0.26914	**0.79**	0.24473
STM2601	STM2601	minor capsid protein FII	**2.06**	0.01568	**0.25**	0.52124	**1.09**	0.05094
STM2602	STM2602	DNA packaging-like protein	**0.61**	0.56348	**1.05**	0.00700	**-0.29**	0.48246
STM2602	STM2602	DNA packaging-like protein	**1.74**	0.01630	**1.08**	0.02060	**0.75**	0.17580
STM2603	STM2603	phage head-like protein	**-0.34**	0.43996	**0.75**	0.13601	**-0.42**	0.38173
STM2603	STM2603	phage head-like protein	**0.95**	0.51039	**1.14**	0.00892	**0.19**	0.77927
STM2604	STM2604	phage head-like protein	**-0.03**	0.96157	**1.53**	0.00226	**0.31**	0.44849
STM2604	STM2604	phage head-like protein	**0.06**	0.94683	**0.82**	0.05642	**-1.43**	0.05116
STM2605	STM2605	head-tail preconnector-like protein	**0.84**	0.14371	**2.18**	0.00026	**0.30**	0.46673
STM2605	STM2605	head-tail preconnector-like protein	**1.22**	0.10724	**1.56**	0.00656	**2.25**	0.00087
STM2606	STM2606	head-tail preconnector-like protein	**0.98**	0.30717	**-0.65**	0.14203	**1.20**	0.13343
STM2606	STM2606	head-tail preconnector-like protein	**0.90**	0.50061	**-2.33**	0.00607	**1.05**	0.14177
STM2607	STM2607	head-to-tail joining-like protein	**-0.13**	0.89804	**0.09**	0.82450	**-0.44**	0.59391
STM2607	STM2607	head-to-tail joining-like protein	**1.52**	0.09924	**0.45**	0.25531	**0.50**	0.40318
STM2608	STM2608	terminase-like large protein	**0.54**	0.61014	**0.50**	0.21846	**1.16**	0.02509
STM2608	STM2608	terminase-like large protein	**2.86**	0.00643	**1.42**	0.12184	**2.12**	0.00984
STM2609	STM2609	DNA packaging-like protein	**0.11**	0.91113	**2.05**	0.00038	**1.55**	0.06734
STM2609	STM2609	DNA packaging-like protein	**0.52**	0.66105	**0.06**	0.89875	**1.84**	0.02143
STM2610	STM2610	hypothetical protein STM2610	**-0.14**	0.83532	**0.57**	0.22949	**0.38**	0.50325
STM2610	STM2610	hypothetical protein STM2610	**0.53**	0.32861	**1.08**	0.03892	**0.79**	0.14272
STM2611,S	STM2611,S	endopeptidase-like protein	**3.65**	0.03449	**1.24**	0.00414	**2.25**	0.00114
STM2611,S	STM2611,S	endopeptidase-like protein	**3.14**	0.00627	**1.18**	0.16031	**2.30**	0.00176
STM2612	STM2612	morphogenesis-like protein	**0.86**	0.32833	**-0.23**	0.58609	**-0.26**	0.71077
STM2612	STM2612	morphogenesis-like protein	**1.68**	0.14152	**-0.24**	0.60608	**0.30**	0.40607
STM2613	STM2613	hypothetical protein STM2613	**0.11**	0.89200	**0.01**	0.98167	**-0.60**	0.22406
STM2613	STM2613	hypothetical protein STM2613	**0.79**	0.30638	**-0.17**	0.55592	**0.20**	0.66682

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM2613	STM2613	hypothetical protein STM2613	**1.80**	0.03078	**-0.23**	0.46396	**0.70**	0.14632
STM2613	STM2613	hypothetical protein STM2613	**1.24**	0.15446	**-0.49**	0.11526	**0.77**	0.16121
STM2614	STM2614	hypothetical protein STM2614	**0.53**	0.66548	**1.25**	0.03728	**-0.84**	0.24346
STM2614	STM2614	hypothetical protein STM2614	**1.00**	0.11000	**0.63**	0.04220	**1.24**	0.03857
STM2614	STM2614	hypothetical protein STM2614	**0.61**	0.68672	**-0.06**	0.87241	**-1.15**	0.23556
STM2614	STM2614	hypothetical protein STM2614	**3.78**	0.01420	**0.59**	0.23752	**2.49**	0.00073
STM2615	STM2615	STM2615	**-0.40**	0.42140	**2.64**	0.00011	**2.23**	0.01499
STM2615	STM2615	STM2615	**0.40**	0.57062	**2.28**	0.00023	**2.18**	0.00212
STM2616	STM2616	antirepressor-like protein	**-0.13**	0.88509	**-0.67**	0.16297	**-1.17**	0.01079
STM2616	STM2616	antirepressor-like protein	**1.02**	0.28256	**-0.86**	0.15681	**-0.36**	0.38971
STM2617	STM2617	antiterminator-like protein	**-0.69**	0.20679	**1.13**	0.12212	**-0.63**	0.41531
STM2617	STM2617	antiterminator-like protein	**0.03**	0.96659	**-0.59**	0.10561	**-0.66**	0.13527
STM2619	STM2619	hypothetical protein STM2619	**0.67**	0.43614	**1.06**	0.00562	**0.26**	0.80322
STM2619	STM2619	hypothetical protein STM2619	**2.28**	0.10160	**-0.01**	0.98084	**0.16**	0.70401
STM2621	STM2621	hypothetical protein STM2621	**2.42**	0.00635	**2.29**	0.00036	**1.40**	0.22405
STM2621	STM2621	hypothetical protein STM2621	**0.12**	0.87745	**1.72**	0.00082	**-0.42**	0.36115
STM2621	STM2621	hypothetical protein STM2621	**2.64**	0.01001	**2.44**	0.00080	**3.44**	0.01643
STM2621	STM2621	hypothetical protein STM2621	**0.48**	0.56654	**1.36**	0.00139	**0.26**	0.65504
STM2622	STM2622	hypothetical protein STM2622	**-0.92**	0.22242	**0.78**	0.07640	**-0.37**	0.37087
STM2622	STM2622	hypothetical protein STM2622	**0.05**	0.92780	**0.73**	0.08547	**0.16**	0.69524
STM2623	STM2623	hypothetical protein STM2623	**-0.34**	0.50125	**0.73**	0.06010	**-1.21**	0.10899
STM2623	STM2623	hypothetical protein STM2623	**0.51**	0.41383	**0.67**	0.06534	**-0.97**	0.19045
STM2624	STM2624	hypothetical protein STM2624	**1.96**	0.03795	**-0.69**	0.10365	**1.08**	0.10756
STM2624	STM2624	hypothetical protein STM2624	**2.84**	0.01578	**-1.48**	0.04696	**1.94**	0.00966
STM2625	STM2625	DNA replication protein DnaC	**-1.17**	0.03453	**-0.29**	0.45852	**-0.38**	0.58267
STM2625	STM2625	DNA replication protein DnaC	**-0.13**	0.82161	**-0.46**	0.36235	**-0.17**	0.76659
STM2626	STM2626	replication protein 15-like	**-0.62**	0.37311	**1.51**	0.40978	**-1.63**	0.08531
STM2626	STM2626	replication protein 15-like	**0.97**	0.17974	**-0.92**	0.03074	**0.87**	0.07856
STM2630	STM2630	hypothetical protein STM2630	**-0.83**	0.19262	**0.46**	0.34768	**0.06**	0.93217
STM2630	STM2630	hypothetical protein STM2630	**0.48**	0.69773	**0.59**	0.08468	**-0.03**	0.96708
STM2632	STM2632	exodeoxyribonuclease VIII-like protein	**2.70**	0.02992	**0.27**	0.60665	**1.57**	0.01388
STM2632	STM2632	exodeoxyribonuclease VIII-like protein	**3.82**	0.00660	**-0.43**	0.30394	**4.12**	0.00207
STM2634	STM2634	putative cytoplasmic protein	**0.69**	0.57536	**0.94**	0.04908	**0.93**	0.33123
STM2634	STM2634	putative cytoplasmic protein	**0.59**	0.23635	**0.54**	0.31042	**0.67**	0.18886
STM2634	STM2634	putative cytoplasmic protein	**1.42**	0.25049	**1.05**	0.00581	**1.54**	0.01911
STM2634	STM2634	putative cytoplasmic protein	**1.97**	0.11370	**0.59**	0.34467	**0.39**	0.39379
STM2634	STM2634	putative cytoplasmic protein	**2.37**	0.21374	**0.74**	0.03037	**0.80**	0.06134
STM2634	STM2634	putative cytoplasmic protein	**2.46**	0.08918	**1.33**	0.00430	**1.32**	0.03398
STM2636	STM2636	integrase-like protein	**-0.93**	0.18512	**0.25**	0.53784	**-0.10**	0.91769
STM2636	STM2636	integrase-like protein	**0.66**	0.16953	**-0.81**	0.02896	**0.17**	0.88181
STM2637	rseC	sigma E regulator	**-0.18**	0.67685	**-0.85**	0.04386	**-0.26**	0.64451
STM2637	rseC	sigma E regulator	**-0.27**	0.61495	**-0.49**	0.30553	**-1.77**	0.35137
STM2638	rseB	periplasmic negative regulator of sigmaE	**-1.46**	0.09211	**0.11**	0.77002	**-0.56**	0.16069
STM2638	rseB	periplasmic negative regulator of sigmaE	**-0.30**	0.46543	**0.13**	0.65395	**-0.71**	0.06788
STM2639	rseA	anti sigma-E factor	**0.90**	0.20017	**0.67**	0.08292	**0.78**	0.17790
STM2639	rseA	anti sigma-E factor	**0.72**	0.35081	**0.15**	0.69717	**1.14**	0.01904
STM2640	rpoE	RNA polymerase sigma-70 factor	**0.12**	0.93334	**2.15**	0.00043	**2.42**	0.00058
STM2640	rpoE	RNA polymerase sigma-70 factor	**1.52**	0.02235	**1.97**	0.00038	**2.67**	0.00015
STM2641	nadB	L-aspartate oxidase	**1.44**	0.01823	**-0.14**	0.72900	**-0.83**	0.03800
STM2641	nadB	L-aspartate oxidase	**1.02**	0.38027	**-0.15**	0.70841	**-0.42**	0.47910
STM2642	yfiC	putative transferase	**0.69**	0.22926	**-0.44**	0.14475	**-1.08**	0.22774
STM2642	yfiC	putative transferase	**0.95**	0.14813	**-0.70**	0.05069	**0.16**	0.80762
STM2643	srmB	ATP-dependent RNA helicase	**0.36**	0.68802	**-0.07**	0.86476	**0.84**	0.26162
STM2643	srmB	ATP-dependent RNA helicase	**1.58**	0.02838	**-0.57**	0.10328	**2.00**	0.00587
STM2644	yfiE	putative transcriptional regulator	**-2.02**	0.00957	**-0.67**	0.05432	**-0.88**	0.10101
STM2644	yfiE	putative transcriptional regulator	**-0.87**	0.10643	**-0.80**	0.02411	**-1.13**	0.04068
STM2645	yfiK	putative transport protein	**-0.01**	0.98547	**-0.42**	0.16899	**-0.25**	0.52152
STM2645	yfiK	putative transport protein	**0.63**	0.30358	**-0.36**	0.31206	**0.45**	0.36411
STM2646	yfiD	putative formate acetyltransferase	**0.07**	0.95350	**-0.34**	0.78792	**-1.18**	0.01495
STM2646	yfiD	putative formate acetyltransferase	**1.16**	0.26666	**-0.20**	0.87217	**-0.02**	0.96438
STM2647	ung	uracil-DNA glycosylase	**-1.00**	0.05366	**-0.79**	0.07621	**-0.66**	0.16812
STM2647	ung	uracil-DNA glycosylase	**0.82**	0.16476	**-0.44**	0.16350	**0.13**	0.73165
STM2648	yfiF	putative tRNA/rRNA methyltransferase	**-1.69**	0.01703	**-1.15**	0.00574	**-1.51**	0.00764
STM2648	yfiF	putative tRNA/rRNA methyltransferase	**-0.62**	0.25374	**-1.04**	0.00814	**-0.49**	0.25102
STM2649	trxC	thioredoxin 2	**-1.64**	0.01745	**-1.09**	0.00402	**-0.32**	0.39526
STM2649	trxC	thioredoxin 2	**-1.49**	0.01624	**-1.42**	0.00224	**0.30**	0.40137
STM2650	yfiP	putative cytoplasmic protein	**-0.98**	0.11839	**-0.42**	0.13980	**-1.09**	0.06063
STM2650	yfiP	putative cytoplasmic protein	**0.25**	0.74145	**-0.55**	0.10906	**-0.41**	0.28842
STM2651	yfiQ	putative acetyl-CoA synthetase	**-1.79**	0.01257	**-0.10**	0.77040	**0.33**	0.40927
STM2651	yfiQ	putative acetyl-CoA synthetase	**-0.97**	0.23254	**-0.56**	0.10282	**0.69**	0.09556

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM2652	pssA	phosphatidylserine synthase	**-0.32**	0.46047	**-1.28**	0.00665	**-0.50**	0.24898
STM2652	pssA	phosphatidylserine synthase	**-0.10**	0.85370	**-1.37**	0.01119	**0.39**	0.66100
STM2653	yfiM	putative outer membrane lipoprotein	**-2.39**	0.02159	**-1.24**	0.08976	**-0.41**	0.32342
STM2653	yfiM	putative outer membrane lipoprotein	**0.26**	0.88701	**-2.16**	0.02159	**-0.95**	0.26264
STM2654	kgtP	alpha-ketoglutarate permease	**-0.70**	0.22701	**-1.54**	0.00137	**-0.46**	0.23107
STM2654	kgtP	alpha-ketoglutarate permease	**0.04**	0.96095	**-1.22**	0.00377	**0.05**	0.92231
STM2655	STM2655	putative cytoplasmic protein	**0.77**	0.16178	**0.06**	0.89652	**0.78**	0.04914
STM2655	STM2655	putative cytoplasmic protein	**0.23**	0.79523	**-0.17**	0.62868	**1.68**	0.00252
STM2656	rrfG	STM2656	**0.27**	0.65576	**0.14**	0.68500	**0.62**	0.16215
STM2656	rrfG	STM2656	**1.40**	0.03492	**0.40**	0.37637	**1.12**	0.01423
STM2657	rrlG	STM2657	**-0.70**	0.14472	**1.05**	0.10536	**1.85**	0.04140
STM2657	rrlG	STM2657	**-0.97**	0.16482	**1.34**	0.03501	**0.33**	0.49379
STM2658	gltW	STM2658	**1.36**	0.05587	**0.82**	0.02726	**1.14**	0.01484
STM2658	gltW	STM2658	**2.01**	0.01747	**0.94**	0.03119	**1.48**	0.00652
STM2659	rrsG	STM2659	**-2.55**	0.01145	**-0.50**	0.19771	**0.23**	0.65342
STM2659	rrsG	STM2659	**-2.10**	0.05345	**0.66**	0.04129	**-0.24**	0.57253
STM2660	clpB	ATP-dependent protease	**-1.81**	0.08755	**0.44**	0.20316	**1.58**	0.00589
STM2660	clpB	ATP-dependent protease	**-0.80**	0.10029	**0.81**	0.04758	**1.27**	0.04422
STM2661	yfiH	putative inner membrane protein	**-0.31**	0.43433	**0.28**	0.41162	**-0.67**	0.06432
STM2661	yfiH	putative inner membrane protein	**-0.54**	0.28404	**0.20**	0.52779	**-0.54**	0.17724
STM2662	rluD	ribosomal large subunit pseudouridine synthase D	**-2.17**	0.03345	**-1.44**	0.00258	**-1.79**	0.00094
STM2662	rluD	ribosomal large subunit pseudouridine synthase D	**-0.91**	0.11624	**-1.51**	0.00080	**-1.52**	0.00233
STM2663	yfiO	putative lipoprotein	**-0.54**	0.31162	**-0.06**	0.90586	**-0.57**	0.20186
STM2663	yfiO	putative lipoprotein	**0.12**	0.78750	**-0.34**	0.29169	**-0.68**	0.11044
STM2665	yfiA	ribosome stabilization factor	**1.56**	0.04365	**3.36**	0.00004	**4.96**	0.00002
STM2665	yfiA	ribosome stabilization factor	**1.92**	0.00971	**3.21**	0.00031	**5.62**	0.00001
STM2667	pheA	chorismate mutase P/prephenate dehydratase	**-0.32**	0.56439	**-0.05**	0.87263	**-0.38**	0.30108
STM2667	pheA	chorismate mutase P/prephenate dehydratase	**0.02**	0.97919	**0.22**	0.43933	**-0.11**	0.80121
STM2668	STM2668	putative cytoplasmic protein	**-1.09**	0.06906	**-0.04**	0.91744	**-0.49**	0.19716
STM2668	STM2668	putative cytoplasmic protein	**-0.03**	0.95833	**0.36**	0.24622	**-0.05**	0.91910
STM2669	tyrA	chorismate mutase T/prephenate dehydrogenase	**-0.82**	0.09014	**0.53**	0.14867	**-0.24**	0.61246
STM2669	tyrA	chorismate mutase T/prephenate dehydrogenase	**0.68**	0.26399	**0.95**	0.01860	**0.88**	0.07796
STM2670	aroF	3-deoxy-7-phosphoheptulonate synthase	**-1.04**	0.18898	**1.75**	0.00054	**-0.21**	0.69409
STM2670	aroF	3-deoxy-7-phosphoheptulonate synthase	**-0.39**	0.42965	**1.70**	0.00270	**-0.65**	0.17552
STM2671	yfiR	putative periplasmic protein	**-0.80**	0.11959	**0.87**	0.01705	**-0.17**	0.66365
STM2671	yfiR	putative periplasmic protein	**-0.60**	0.28960	**0.34**	0.28464	**-0.16**	0.73154
STM2672	yfiN	putative diguanylate cyclase/phosphodiesterase	**0.50**	0.30670	**-0.05**	0.89106	**1.08**	0.15516
STM2672	yfiN	putative diguanylate cyclase/phosphodiesterase	**1.72**	0.01314	**-0.08**	0.80907	**1.71**	0.00156
STM2673	rplS	50S ribosomal protein L19	**-3.44**	0.00791	**-1.24**	0.07086	**-2.58**	0.01370
STM2673	rplS	50S ribosomal protein L19	**-2.54**	0.01203	**-0.67**	0.18357	**-4.03**	0.00035
STM2674	trmD	tRNA (guanine-N(1)-)-methyltransferase	**-1.94**	0.01215	**-0.26**	0.41554	**-3.39**	0.00025
STM2674	trmD	tRNA (guanine-N(1)-)-methyltransferase	**-1.42**	0.04570	**-0.12**	0.68995	**-3.03**	0.00019
STM2675	rimM	16S rRNA-processing protein	**-2.49**	0.01381	**-0.69**	0.05276	**-4.55**	0.00002
STM2675	rimM	16S rRNA-processing protein	**-1.58**	0.02953	**-0.70**	0.02627	**-4.08**	0.00005
STM2676	rpsP	30S ribosomal protein S16	**-2.41**	0.01429	**-1.46**	0.00353	**-4.95**	0.00002
STM2676	rpsP	30S ribosomal protein S16	**-1.79**	0.03563	**-1.40**	0.00126	**-4.54**	0.00004
STM2677	ffh	4,5S-RNP protein	**-0.84**	0.09313	**-0.34**	0.22292	**-1.98**	0.00140
STM2677	ffh	4,5S-RNP protein	**0.11**	0.84698	**0.18**	0.54813	**-1.44**	0.00447
STM2678	corE	hypothetical protein STM2678	**0.91**	0.08253	**-0.59**	0.16544	**-1.75**	0.00381
STM2678	corE	hypothetical protein STM2678	**0.57**	0.43662	**-0.46**	0.31136	**-1.17**	0.10075
STM2679	yfjD	hypothetical protein STM2679	**1.74**	0.01227	**0.48**	0.26365	**1.88**	0.00676
STM2679	yfjD	hypothetical protein STM2679	**2.41**	0.01287	**0.23**	0.45765	**2.50**	0.00112
STM2680	STM2680	putative cytoplasmic protein	**0.42**	0.59866	**1.04**	0.00597	**1.37**	0.01008
STM2680	STM2680	putative cytoplasmic protein	**1.39**	0.02965	**1.29**	0.00427	**1.17**	0.02596
STM2681	grpE	heat shock protein	**-0.05**	0.93345	**0.44**	0.15848	**-0.74**	0.10020
STM2681	grpE	heat shock protein	**0.42**	0.50544	**1.15**	0.01187	**0.14**	0.81340
STM2683	ppnK	inorganic polyphosphate/ATP-NAD kinase	**-0.02**	0.97635	**-0.14**	0.65569	**-0.81**	0.05758
STM2683	ppnK	inorganic polyphosphate/ATP-NAD kinase	**-0.02**	0.97962	**-0.45**	0.20779	**-0.06**	0.87234
STM2684	recN	recombination/DNA repair protein	**0.70**	0.32838	**0.09**	0.81512	**-0.64**	0.12015
STM2684	recN	recombination/DNA repair protein	**1.08**	0.08019	**-0.08**	0.82668	**0.29**	0.49523
STM2685	smpA	small membrane protein A	**-1.94**	0.02172	**0.07**	0.83257	**-1.76**	0.01085
STM2685	smpA	small membrane protein A	**-1.06**	0.04774	**0.46**	0.23929	**-0.22**	0.76719
STM2686	yfjF	hypothetical protein STM2686	**-0.04**	0.96906	**0.53**	0.13342	**-0.97**	0.04901
STM2686	yfjF	hypothetical protein STM2686	**-0.98**	0.11529	**0.42**	0.25402	**-0.83**	0.13055
STM2687	yfjG	putative oligoketide cyclase	**-0.37**	0.61745	**1.09**	0.00655	**-0.18**	0.60829
STM2687	yfjG	putative oligoketide cyclase	**0.28**	0.69493	**0.74**	0.05749	**1.51**	0.00253
STM2688	smpB	SsrA-binding protein	**1.25**	0.04719	**0.21**	0.51130	**1.50**	0.04683
STM2688	smpB	SsrA-binding protein	**1.24**	0.05285	**0.03**	0.92605	**2.04**	0.00093
STM2690	STM2690	putative outer membrane efflux protein	**-0.25**	0.68566	**-0.07**	0.84821	**0.53**	0.47547
STM2690	STM2690	putative outer membrane efflux protein	**2.77**	0.00839	**-0.30**	0.38745	**1.22**	0.07978

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM2691	STM2691	putative ABC transporter transmembrane region	**-0.15**	0.82961	**0.02**	0.96285	**1.31**	0.00579
STM2691	STM2691	putative ABC transporter transmembrane region	**0.93**	0.12760	**0.20**	0.45436	**1.21**	0.02305
STM2692	STM2692	putative HlyD family secretion protein	**-0.63**	0.25982	**1.49**	0.00169	**2.40**	0.00072
STM2692	STM2692	putative HlyD family secretion protein	**0.37**	0.49079	**2.11**	0.00022	**2.95**	0.00018
STM2695	STM2695	late control-like protein	**-1.12**	0.03429	**1.80**	0.00347	**2.55**	0.00018
STM2695	STM2695	late control-like protein	**1.25**	0.20103	**2.00**	0.00027	**2.87**	0.00023
STM2696	STM2696	putative phage tail protein	**-0.99**	0.12550	**-0.23**	0.53641	**0.33**	0.54270
STM2696	STM2696	putative phage tail protein	**0.28**	0.53276	**-0.53**	0.26860	**1.20**	0.01096
STM2697	STM2697	phage tail-like protein	**0.72**	0.48739	**1.56**	0.00416	**2.90**	0.00048
STM2697	STM2697	phage tail-like protein	**1.24**	0.53282	**1.27**	0.00350	**2.54**	0.00024
STM2698	STM2698	gpE-like protein	**0.78**	0.22800	**-0.75**	0.09139	**-0.51**	0.30444
STM2698	STM2698	gpE-like protein	**0.15**	0.75518	**-1.76**	0.01058	**-0.05**	0.93157
STM2699	STM2699	putative phage tail-like protein	**0.26**	0.76828	**-0.52**	0.32953	**-0.92**	0.05699
STM2699	STM2699	putative phage tail-like protein	**1.40**	0.04632	**-0.35**	0.25687	**0.29**	0.54593
STM2700	STM2700	phage tail fiber-like protein	**0.09**	0.85646	**0.15**	0.73115	**0.30**	0.59207
STM2700	STM2700	phage tail fiber-like protein	**1.61**	0.02969	**-0.41**	0.29876	**0.95**	0.05388
STM2701	STM2701	phage tail sheath-like protein	**-0.17**	0.70958	**-0.32**	0.41085	**-0.23**	0.81483
STM2701	STM2701	phage tail sheath-like protein	**0.46**	0.48579	**-0.56**	0.37236	**0.16**	0.82747
STM2704	STM2704	tail fibre assembly-like protein	**0.50**	0.45508	**0.62**	0.13265	**0.14**	0.84467
STM2704	STM2704	tail fibre assembly-like protein	**1.88**	0.07498	**0.58**	0.08899	**1.01**	0.10568
STM2705	STM2705	hypothetical protein STM2705	**0.10**	0.87808	**3.46**	0.00325	**-0.13**	0.88243
STM2705	STM2705	hypothetical protein STM2705	**2.39**	0.02003	**2.33**	0.00032	**-0.33**	0.67780
STM2707	STM2707	phage tail-like protein	**2.37**	0.15840	**0.13**	0.84941	**0.30**	0.75058
STM2707	STM2707	phage tail-like protein	**1.38**	0.14472	**-1.20**	0.00910	**-1.08**	0.02330
STM2708	STM2708	phage tail-like protein	**-0.22**	0.78321	**-1.30**	0.00536	**0.02**	0.97888
STM2708	STM2708	phage tail-like protein	**1.03**	0.32638	**-1.58**	0.00886	**-0.27**	0.52301
STM2709	STM2709	base plate tail-like protein	**3.14**	0.15588	**0.33**	0.33822	**3.30**	0.00018
STM2709	STM2709	base plate tail-like protein	**1.38**	0.46005	**-0.78**	0.08389	**1.55**	0.32312
STM2710	STM2710	phage baseplate assembly-like protein	**1.30**	0.04857	**0.29**	0.37029	**1.63**	0.06115
STM2710	STM2710	phage baseplate assembly-like protein	**1.87**	0.17574	**-1.49**	0.12242	**1.56**	0.08957
STM2711	STM2711	phage tail-like protein	**0.59**	0.47345	**-0.68**	0.14563	**-0.88**	0.06364
STM2711	STM2711	phage tail-like protein	**1.64**	0.09199	**-1.04**	0.08315	**0.51**	0.43018
STM2712	STM2712	phage tail-like protein	**-0.19**	0.69393	**-0.06**	0.93057	**0.07**	0.90511
STM2712	STM2712	phage tail-like protein	**0.00**	0.99561	**-0.79**	0.22274	**-0.69**	0.19771
STM2714	STM2714	lysis-like protein	**-0.96**	0.13861	**-1.51**	0.00411	**-1.45**	0.06530
STM2714	STM2714	lysis-like protein	**0.94**	0.31215	**-1.72**	0.00171	**-0.64**	0.23094
STM2715,S	STM2715,S	probable prophage lysozyme	**1.29**	0.12760	**-1.53**	0.00156	**1.59**	0.15409
STM2715,S	STM2715,S	probable prophage lysozyme	**2.14**	0.06060	**-1.90**	0.00304	**2.86**	0.00956
STM2716	STM2716	phage-holin-like protein	**0.34**	0.40710	**-1.32**	0.02099	**-0.97**	0.02614
STM2716	STM2716	phage-holin-like protein	**0.81**	0.13798	**-0.78**	0.05763	**0.11**	0.83652
STM2717	STM2717	phage tail-like protein	**-0.22**	0.78112	**-0.35**	0.64645	**1.39**	0.04183
STM2717	STM2717	phage tail-like protein	**0.54**	0.42147	**-0.90**	0.01350	**0.62**	0.57253
STM2718	STM2718	head completion-like protein	**0.37**	0.72539	**-3.77**	0.00004	**-1.60**	0.16503
STM2718	STM2718	head completion-like protein	**0.70**	0.42564	**-2.92**	0.00043	**0.16**	0.85179
STM2719	STM2719	terminase-like protein	**0.80**	0.25208	**1.16**	0.01697	**1.56**	0.00900
STM2719	STM2719	terminase-like protein	**1.67**	0.01638	**-1.20**	0.02622	**1.75**	0.11102
STM2720	STM2720	major capsid-like protein	**1.41**	0.21225	**-0.29**	0.35953	**0.49**	0.18455
STM2720	STM2720	major capsid-like protein	**2.20**	0.03512	**-1.15**	0.03228	**1.46**	0.01025
STM2721	STM2721	capsid scaffold-like protein	**0.12**	0.83262	**-0.87**	0.03016	**-0.32**	0.41952
STM2721	STM2721	capsid scaffold-like protein	**1.50**	0.06765	**-1.14**	0.04818	**1.01**	0.03898
STM2722	STM2722	terminase-like protein	**0.03**	0.96650	**0.50**	0.38154	**-0.32**	0.59456
STM2722	STM2722	terminase-like protein	**1.19**	0.17054	**-0.14**	0.69954	**0.04**	0.92666
STM2723	STM2723	portal vertex-like protein	**-0.82**	0.21144	**-0.24**	0.63469	**-0.54**	0.45037
STM2723	STM2723	portal vertex-like protein	**-0.22**	0.71386	**-0.27**	0.48517	**0.22**	0.90641
STM2727	STM2727	hypothetical protein STM2727	**1.71**	0.10377	**-0.45**	0.22495	**1.02**	0.19909
STM2727	STM2727	hypothetical protein STM2727	**2.15**	0.00789	**-1.06**	0.07309	**1.50**	0.00988
STM2729	STM2729	hypothetical protein STM2729	**1.04**	0.05139	**0.04**	0.93535	**1.04**	0.19025
STM2729	STM2729	hypothetical protein STM2729	**4.12**	0.01426	**-0.25**	0.61822	**1.45**	0.05032
STM2730	STM2730	DNA adenine methylase-like protein	**0.24**	0.71798	**0.97**	0.05959	**0.97**	0.18300
STM2730	STM2730	DNA adenine methylase-like protein	**0.42**	0.57501	**-1.75**	0.02193	**-0.36**	0.68786
STM2732	STM2732	hypothetical protein STM2732	**0.02**	0.99193	**0.07**	0.84293	**-0.70**	0.33459
STM2732	STM2732	hypothetical protein STM2732	**2.13**	0.00753	**-0.48**	0.19657	**1.20**	0.29470
STM2733	STM2733	hypothetical protein STM2733	**1.08**	0.05897	**-0.36**	0.68418	**-0.80**	0.24527
STM2733	STM2733	hypothetical protein STM2733	**2.12**	0.02191	**-0.26**	0.59197	**1.92**	0.00303
STM2735	STM2735	hypothetical protein STM2735	**2.22**	0.00814	**0.06**	0.89060	**0.64**	0.44206
STM2735	STM2735	hypothetical protein STM2735	**4.05**	0.00547	**-0.06**	0.93768	**2.37**	0.01121
STM2736	STM2736	hypothetical protein STM2736	**1.85**	0.03631	**-0.31**	0.61286	**0.35**	0.40988
STM2736	STM2736	hypothetical protein STM2736	**0.81**	0.10154	**-1.21**	0.00478	**1.37**	0.00416
STM2737	STM2737	hypothetical protein STM2737	**-1.07**	0.05430	**-0.66**	0.07119	**-1.24**	0.01055
STM2737	STM2737	hypothetical protein STM2737	**0.35**	0.57102	**-1.00**	0.03384	**0.18**	0.67927

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM2739	STM2739	phage tail-like protein	**-0.66**	0.17908	**0.22**	0.59210	**0.00**	0.99405
STM2739	STM2739	phage tail-like protein	**-0.07**	0.88800	**0.58**	0.10070	**0.31**	0.59981
STM2740	STM2740	integrase-like protein	**0.81**	0.29937	**1.39**	0.01126	**0.98**	0.02237
STM2740	STM2740	integrase-like protein	**1.62**	0.04803	**1.10**	0.02055	**1.99**	0.00820
STM2740,1N	STM2740,1N	hypothetical protein STM2740,1N	**-0.19**	0.71319	**1.25**	0.00496	**-0.20**	0.62276
STM2740,1N	STM2740,1N	hypothetical protein STM2740,1N	**1.67**	0.02053	**0.49**	0.41705	**1.24**	0.02090
STM2741	STM2741	putative periplasmic protein	**-0.65**	0.22678	**-0.68**	0.06490	**-0.01**	0.98262
STM2741	STM2741	putative periplasmic protein	**0.15**	0.76912	**-1.14**	0.03930	**-0.05**	0.92980
STM2742	STM2742	putative cytoplasmic protein	**-0.53**	0.23163	**-0.10**	0.78725	**-1.02**	0.06255
STM2742	STM2742	putative cytoplasmic protein	**0.99**	0.08886	**-0.44**	0.23082	**0.71**	0.09825
STM2743	STM2743	putative cytoplasmic protein	**2.24**	0.00991	**0.24**	0.44748	**2.15**	0.00976
STM2743	STM2743	putative cytoplasmic protein	**1.95**	0.03984	**1.22**	0.03478	**1.90**	0.00487
STM2744	STM2744	putative cytoplasmic protein	**0.51**	0.33353	**-1.93**	0.00051	**0.12**	0.84656
STM2744	STM2744	putative cytoplasmic protein	**3.28**	0.11724	**-1.30**	0.00793	**1.87**	0.02943
STM2745	STM2745	putative inner membrane protein	**-0.98**	0.06894	**-0.60**	0.47160	**-0.99**	0.07820
STM2745	STM2745	putative inner membrane protein	**1.19**	0.17736	**-1.07**	0.01146	**0.99**	0.16585
STM2746	STM2746	putative ATPase	**0.60**	0.30866	**-0.67**	0.25202	**0.19**	0.71871
STM2746	STM2746	putative ATPase	**0.50**	0.61411	**-0.67**	0.08898	**2.07**	0.00105
STM2747	STM2747	putative cytoplasmic protein	**-1.45**	0.02777	**0.08**	0.89250	**-0.65**	0.08700
STM2747	STM2747	putative cytoplasmic protein	**-1.32**	0.08055	**-0.35**	0.36074	**-0.82**	0.12911
STM2748	STM2748	putative transcriptional regulator	**1.96**	0.45553	**-0.56**	0.11878	**-0.17**	0.92217
STM2748	STM2748	putative transcriptional regulator	**-0.37**	0.46285	**-0.53**	0.11177	**-1.00**	0.07016
STM2749	STM2749	putative cytoplasmic protein	**0.71**	0.30575	**2.27**	0.00199	**0.04**	0.96985
STM2749	STM2749	putative cytoplasmic protein	**3.31**	0.00673	**1.49**	0.02139	**2.86**	0.00026
STM2750	STM2750	putative PTS system glucitol/sorbitol-specific enzyme II	**0.43**	0.65179	**0.30**	0.44380	**-0.28**	0.57711
STM2750	STM2750	putative PTS system glucitol/sorbitol-specific enzyme II	**2.22**	0.13268	**-0.65**	0.09742	**0.26**	0.53505
STM2751	STM2751	putative glucitol-specific PTS enzyme III	**2.69**	0.02845	**-1.22**	0.01612	**-0.61**	0.17935
STM2751	STM2751	putative glucitol-specific PTS enzyme III	**1.65**	0.06801	**-1.65**	0.01305	**0.64**	0.32899
STM2752	STM2752	putative glucitol-specific PTS enzyme III	**0.41**	0.50249	**-0.26**	0.32335	**0.11**	0.86863
STM2752	STM2752	putative glucitol-specific PTS enzyme III	**1.85**	0.02319	**0.52**	0.07804	**0.13**	0.79924
STM2753	STM2753	putative dehydrogenase	**0.86**	0.11993	**0.59**	0.08740	**-1.59**	0.03458
STM2753	STM2753	putative dehydrogenase	**1.33**	0.03559	**0.60**	0.04762	**0.09**	0.89836
STM2754	STM2754	putative hexulose 6 phosphate synthase	**-0.38**	0.40058	**0.02**	0.97377	**0.69**	0.07601
STM2754	STM2754	putative hexulose 6 phosphate synthase	**0.66**	0.18639	**-0.87**	0.05922	**0.53**	0.18678
STM2755	STM2755	putative hexulose 6 phosphate synthase	**0.21**	0.69114	**0.17**	0.82048	**-0.97**	0.36028
STM2755	STM2755	putative hexulose 6 phosphate synthase	**-0.04**	0.96829	**-0.63**	0.27907	**-0.69**	0.28702
STM2756	STM2756	putative sugar phosphate aminotransferase	**-0.16**	0.78433	**-0.75**	0.07952	**-0.35**	0.67946
STM2756	STM2756	putative sugar phosphate aminotransferase	**0.95**	0.14274	**-0.98**	0.00800	**1.40**	0.01765
STM2757	STM2757	putative cytoplasmic protein	**-0.32**	0.60038	**-0.79**	0.04610	**-0.79**	0.13879
STM2757	STM2757	putative cytoplasmic protein	**0.59**	0.34328	**-1.10**	0.02954	**0.32**	0.64239
STM2758	STM2758	putative phosphotransferase system IIC component	**0.03**	0.94960	**-0.88**	0.30050	**-0.29**	0.55038
STM2758	STM2758	putative phosphotransferase system IIC component	**-0.18**	0.81252	**-0.40**	0.28286	**0.03**	0.94719
STM2759	STM2759	putative dipeptide/oligopeptide/nickel ABC-type transport	**-0.81**	0.09456	**0.11**	0.80333	**0.19**	0.83831
STM2759	STM2759	putative dipeptide/oligopeptide/nickel ABC-type transport	**0.74**	0.38253	**-0.94**	0.29674	**1.67**	0.05079
STM2760	STM2760	putative integrase	**0.50**	0.54351	**-0.21**	0.79439	**-0.37**	0.63711
STM2760	STM2760	putative integrase	**1.86**	0.01624	**-1.09**	0.23082	**0.69**	0.13487
STM2761	STM2761	putative inner membrane protein	**-0.47**	0.44374	**0.83**	0.03246	**0.30**	0.56915
STM2761	STM2761	putative inner membrane protein	**0.22**	0.65919	**-1.12**	0.02586	**0.28**	0.52098
STM2762	STM2762	putative inner membrane protein	**0.16**	0.91223	**0.66**	0.59990	**1.46**	0.01172
STM2762	STM2762	putative inner membrane protein	**1.37**	0.04441	**-0.33**	0.61473	**0.71**	0.24775
STM2765	STM2765	putative transposase	**0.74**	0.15557	**1.26**	0.00447	**2.29**	0.01846
STM2765	STM2765	putative transposase	**1.03**	0.05358	**-0.12**	0.86267	**1.46**	0.02277
STM2767	STM2767	putative DNA/RNA helicase	**-2.24**	0.01580	**-0.52**	0.26485	**-1.91**	0.00128
STM2767	STM2767	putative DNA/RNA helicase	**-2.24**	0.02277	**-0.61**	0.13041	**-2.25**	0.00122
STM2768	STM2768	putative transposase	**0.30**	0.71054	**-0.70**	0.03009	**-0.02**	0.97431
STM2768	STM2768	putative transposase	**-0.18**	0.68575	**-1.40**	0.00724	**-0.24**	0.65192
STM2769	STM2769	putative transposase	**1.69**	0.04345	**-0.59**	0.05733	**-0.33**	0.45862
STM2769	STM2769	putative transposase	**1.25**	0.03993	**-0.99**	0.04372	**0.46**	0.25786
STM2770	fljA	phase-1 flagellin repressor	**-2.82**	0.00720	**-3.53**	0.00003	**-3.01**	0.00283
STM2770	fljA	phase-1 flagellin repressor	**-2.43**	0.08953	**-2.58**	0.00036	**-2.05**	0.00659
STM2771	fljB	flagellar biosynthesis protein	**-4.11**	0.00574	**-4.47**	0.00003	**-4.62**	0.00006
STM2771	fljB	flagellar biosynthesis protein	**-3.21**	0.00546	**-4.86**	0.00001	**-4.73**	0.00003
STM2772	hin	DNA-invertase Hin	**-1.16**	0.11522	**-1.10**	0.01689	**-1.08**	0.03240
STM2772	hin	DNA-invertase Hin	**-0.37**	0.52193	**-1.01**	0.01438	**-0.50**	0.23880
STM2773	iroB	putative glycosyl transferase	**-0.15**	0.74693	**4.74**	0.00006	**-1.03**	0.07218
STM2773	iroB	putative glycosyl transferase	**1.55**	0.01904	**5.20**	0.00001	**-0.54**	0.16215
STM2774	iroC	putative ABC transporter protein	**-0.22**	0.74749	**4.53**	0.00001	**0.27**	0.70092
STM2774	iroC	putative ABC transporter protein	**0.33**	0.60292	**4.30**	0.00002	**1.02**	0.02390
STM2775	iroD	enterochelin esterase=-like protein	**0.51**	0.25814	**3.90**	0.00003	**-1.05**	0.07743
STM2775	iroD	enterochelin esterase=-like protein	**1.38**	0.03310	**3.83**	0.00002	**0.32**	0.48893

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM2776	iroE	putative hydrolase	**0.50**	0.45142	**6.36**	0.00001	**1.58**	0.21327
STM2776	iroE	putative hydrolase	**3.05**	0.01849	**6.33**	0.00000	**4.11**	0.00171
STM2777	iroN	TonB-dependent siderophore receptor protein	**2.54**	0.12025	**5.52**	0.00000	**0.34**	0.56617
STM2777	iroN	TonB-dependent siderophore receptor protein	**3.83**	0.00546	**5.56**	0.00007	**0.64**	0.54613
STM2780	pipB2	secreted effector protein	**1.82**	0.01443	**10.64**	0.00000	**-0.19**	0.74488
STM2780	pipB2	secreted effector protein	**2.93**	0.00743	**9.87**	0.00000	**1.65**	0.04847
STM2781	virK	virulence protein	**1.05**	0.05879	**2.05**	0.00040	**-0.33**	0.60435
STM2781	virK	virulence protein	**2.43**	0.00660	**1.83**	0.00055	**2.01**	0.00545
STM2782	mig-14	putative transcriptional activator	**0.80**	0.30237	**0.59**	0.19422	**-0.75**	0.11487
STM2782	mig-14	putative transcriptional activator	**2.28**	0.02122	**-0.46**	0.45262	**1.35**	0.01405
STM2783	nixA	putative nickel transporter	**-0.15**	0.81771	**0.50**	0.25714	**1.27**	0.00948
STM2783	nixA	putative nickel transporter	**-0.29**	0.61132	**-0.09**	0.86794	**-0.49**	0.63387
STM2784	tctE	regulatory protein	**0.28**	0.59495	**-0.38**	0.25939	**0.28**	0.53370
STM2784	tctE	regulatory protein	**0.15**	0.72860	**-0.04**	0.92269	**-1.29**	0.15298
STM2785	tctD	regulatory protein	**0.69**	0.32343	**0.59**	0.09346	**-0.17**	0.64572
STM2785	tctD	regulatory protein	**1.58**	0.05056	**0.45**	0.21528	**1.16**	0.04270
STM2786	STM2786	tricarboxylic transport	**1.96**	0.02654	**2.78**	0.00006	**2.19**	0.00494
STM2786	STM2786	tricarboxylic transport	**2.47**	0.00908	**3.49**	0.00005	**2.24**	0.00197
STM2787	STM2787	tricarboxylic transport	**1.54**	0.04893	**1.53**	0.00185	**-0.88**	0.03646
STM2787	STM2787	tricarboxylic transport	**1.88**	0.01136	**1.78**	0.00080	**0.38**	0.30620
STM2788	STM2788	tricarboxylic transport	**-0.54**	0.36741	**0.82**	0.01715	**0.20**	0.73758
STM2788	STM2788	tricarboxylic transport	**1.54**	0.41886	**0.76**	0.02343	**-0.37**	0.57278
STM2789	STM2789	hypothetical protein STM2789	**0.56**	0.27110	**3.17**	0.00005	**0.40**	0.35891
STM2789	STM2789	hypothetical protein STM2789	**1.63**	0.01715	**3.55**	0.00002	**1.39**	0.00776
STM2790	ygaF	putative sarcosine oxidase-like protein	**-1.05**	0.53887	**0.17**	0.84941	**2.01**	0.00432
STM2790	ygaF	putative sarcosine oxidase-like protein	**2.45**	0.41986	**2.74**	0.11673	**2.43**	0.00140
STM2791	gabD	succinate-semialdehyde dehydrogenase I	**-0.60**	0.35051	**1.90**	0.00029	**0.65**	0.12130
STM2791	gabD	succinate-semialdehyde dehydrogenase I	**-0.70**	0.21362	**1.77**	0.00154	**1.27**	0.03634
STM2792	gabT	4-aminobutyrate aminotransferase	**-0.28**	0.66432	**1.51**	0.00263	**1.22**	0.04854
STM2792	gabT	4-aminobutyrate aminotransferase	**0.37**	0.51255	**3.67**	0.00014	**1.27**	0.01174
STM2793	gabP	gamma-aminobutyrate transport protein	**1.72**	0.03496	**1.00**	0.05377	**-0.03**	0.95177
STM2793	gabP	gamma-aminobutyrate transport protein	**2.70**	0.00674	**0.77**	0.02259	**1.69**	0.00855
STM2794	ygaE	putative transcriptional repressor	**-1.55**	0.01600	**-0.10**	0.84576	**2.12**	0.00186
STM2794	ygaE	putative transcriptional repressor	**-0.39**	0.43078	**0.60**	0.24160	**2.87**	0.00030
STM2795	ygaU	hypothetical protein STM2795	**0.46**	0.54458	**2.68**	0.00035	**4.46**	0.00024
STM2795	ygaU	hypothetical protein STM2795	**1.61**	0.02573	**2.99**	0.00006	**5.50**	0.00004
STM2796	yqaE	putative transport protein	**-0.17**	0.79342	**1.15**	0.01055	**5.62**	0.00001
STM2796	yqaE	putative transport protein	**0.52**	0.36089	**1.53**	0.00419	**5.09**	0.00005
STM2797	STM2797	putative regulatory protein	**1.00**	0.06941	**3.22**	0.00005	**1.62**	0.00160
STM2797	STM2797	putative regulatory protein	**1.40**	0.02339	**3.39**	0.00010	**2.43**	0.00052
STM2798	ygaP	putative rhodanese-like sulfurtransferase	**0.38**	0.37363	**2.82**	0.00035	**-0.14**	0.72603
STM2798	ygaP	putative rhodanese-like sulfurtransferase	**1.21**	0.03218	**2.80**	0.00026	**0.14**	0.72307
STM2799	stpA	DNA-binding protein	**-1.82**	0.11797	**-0.42**	0.17260	**-3.15**	0.00079
STM2799	stpA	DNA-binding protein	**-1.09**	0.20593	**0.02**	0.96691	**-2.85**	0.00072
STM2800	STM2800	putative inner membrane protein	**-1.13**	0.05468	**-0.02**	0.97250	**0.47**	0.35197
STM2800	STM2800	putative inner membrane protein	**-1.80**	0.02762	**-0.72**	0.08081	**-0.84**	0.11558
STM2801	ygaC	putative cytoplasmic protein	**-0.88**	0.11378	**0.81**	0.07874	**0.36**	0.30165
STM2801	ygaC	putative cytoplasmic protein	**0.19**	0.67883	**0.40**	0.20463	**1.03**	0.06090
STM2802	ygaM	putative inner membrane protein	**-0.05**	0.94474	**0.23**	0.61822	**4.25**	0.00008
STM2802	ygaM	putative inner membrane protein	**2.35**	0.05615	**0.31**	0.37405	**4.95**	0.00002
STM2803	STM2803	putative regulatory protein	**0.80**	0.25394	**-0.54**	0.27859	**1.97**	0.00380
STM2803	STM2803	putative regulatory protein	**-0.20**	0.64775	**0.17**	0.57843	**2.94**	0.00433
STM2804	STM2804	putative cytoplasmic protein	**-0.12**	0.81773	**2.08**	0.00061	**-0.28**	0.44194
STM2804	STM2804	putative cytoplasmic protein	**0.92**	0.06712	**2.09**	0.00166	**0.63**	0.12404
STM2805	nrdH	glutaredoxin-like protein	**0.89**	0.23356	**4.36**	0.00001	**0.62**	0.30176
STM2805	nrdH	glutaredoxin-like protein	**1.95**	0.00886	**4.68**	0.00001	**0.66**	0.08117
STM2806	nrdI	hypothetical protein STM2806	**1.12**	0.26115	**4.85**	0.00000	**1.02**	0.01403
STM2806	nrdI	hypothetical protein STM2806	**2.00**	0.17171	**4.35**	0.00002	**1.51**	0.00309
STM2807	nrdE	ribonucleotide-diphosphate reductase alpha subunit	**-0.14**	0.83664	**3.45**	0.00005	**-0.68**	0.22942
STM2807	nrdE	ribonucleotide-diphosphate reductase alpha subunit	**0.89**	0.18453	**3.97**	0.00006	**0.08**	0.90781
STM2808	nrdF	ribonucleotide-diphosphate reductase beta subunit	**-0.23**	0.59965	**3.92**	0.00002	**-0.65**	0.10606
STM2808	nrdF	ribonucleotide-diphosphate reductase beta subunit	**0.80**	0.27069	**3.97**	0.00041	**-0.13**	0.85901
STM2809	proV	glycine/betaine/proline transport protein	**-0.80**	0.22379	**1.00**	0.01536	**0.24**	0.70272
STM2809	proV	glycine/betaine/proline transport protein	**-0.75**	0.26604	**1.75**	0.00048	**-0.21**	0.65585
STM2810	proW	glycine/betaine/proline transport protein	**-0.50**	0.25507	**0.54**	0.09274	**-0.60**	0.10520
STM2810	proW	glycine/betaine/proline transport protein	**-0.94**	0.06249	**1.02**	0.01022	**-1.06**	0.26122
STM2811	proX	glycine/betaine/proline transport protein	**0.24**	0.56647	**1.07**	0.01724	**-0.40**	0.62512
STM2811	proX	glycine/betaine/proline transport protein	**0.55**	0.41383	**0.17**	0.56882	**-2.13**	0.00103
STM2812	STM2812	putative inner membrane protein	**-0.73**	0.11387	**-0.34**	0.28779	**-0.52**	0.28330
STM2812	STM2812	putative inner membrane protein	**-0.49**	0.29507	**-1.12**	0.00789	**-0.70**	0.22018

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM2813	emrR	emrAB operon transcriptional repressor	**-1.61**	0.01694	**-1.10**	0.00605	**-3.53**	0.00154
STM2813	emrR	emrAB operon transcriptional repressor	**-0.12**	0.84287	**-1.00**	0.01870	**-3.44**	0.00031
STM2814	emrA	multidrug resistance secretion protein	**0.22**	0.67830	**-0.70**	0.07112	**-2.40**	0.00204
STM2814	emrA	multidrug resistance secretion protein	**0.03**	0.95819	**-1.24**	0.00300	**-2.97**	0.00835
STM2815	emrB	putative multidrug transport protein	**-0.11**	0.91742	**-0.14**	0.76429	**-0.74**	0.50663
STM2815	emrB	putative multidrug transport protein	**0.39**	0.44708	**-0.36**	0.29184	**-0.03**	0.97474
STM2816	STM2816	putative glycoporin	**1.83**	0.02009	**-0.17**	0.61868	**0.38**	0.49153
STM2816	STM2816	putative glycoporin	**2.77**	0.00595	**0.02**	0.95244	**1.45**	0.06252
STM2817	luxS	S-ribosylhomocysteinase	**-1.81**	0.02198	**0.81**	0.09868	**0.60**	0.13204
STM2817	luxS	S-ribosylhomocysteinase	**-0.70**	0.16726	**1.28**	0.01404	**1.49**	0.00915
STM2818	gshA	glutamate--cysteine ligase	**-0.77**	0.26606	**-0.29**	0.34338	**-0.81**	0.03187
STM2818	gshA	glutamate--cysteine ligase	**-0.39**	0.56069	**0.20**	0.49797	**-0.31**	0.51217
STM2819	yqaA	putative inner membrane protein	**-0.81**	0.12162	**-0.55**	0.07948	**-1.40**	0.01074
STM2819	yqaA	putative inner membrane protein	**0.57**	0.56439	**-0.38**	0.25106	**-0.24**	0.62768
STM2820	yqaB	putative phosphoglucomutase	**1.12**	0.33154	**0.05**	0.87434	**-1.91**	0.00820
STM2820	yqaB	putative phosphoglucomutase	**0.92**	0.24458	**-0.06**	0.86224	**-1.59**	0.00358
STM2821	-	STM2821	**-1.69**	0.04591	**-1.80**	0.00114	**-2.15**	0.00355
STM2821	-	STM2821	**-1.25**	0.14668	**-1.99**	0.00109	**-2.05**	0.00096
STM2822	-	STM2822	**-2.01**	0.04614	**-2.14**	0.00020	**-2.74**	0.00025
STM2822	-	STM2822	**-1.13**	0.18667	**-2.27**	0.00016	**-2.53**	0.00043
STM2823	-	STM2823	**-2.61**	0.00650	**-2.45**	0.00016	**-2.64**	0.00026
STM2823	-	STM2823	**-1.50**	0.09331	**-2.16**	0.00019	**-2.27**	0.00430
STM2824	-	STM2824	**-2.83**	0.00550	**-2.43**	0.00010	**-2.60**	0.00033
STM2824	-	STM2824	**-1.47**	0.10091	**-2.24**	0.00045	**-2.20**	0.00177
STM2825	-	STM2825	**-2.25**	0.01142	**-1.89**	0.00379	**0.02**	0.96274
STM2825	-	STM2825	**-1.29**	0.03678	**-1.46**	0.00175	**-0.09**	0.84292
STM2826	csrA	carbon storage regulator	**-2.40**	0.00643	**-1.30**	0.00292	**-0.71**	0.05966
STM2826	csrA	carbon storage regulator	**-2.47**	0.02573	**-1.06**	0.00837	**-0.43**	0.39744
STM2827	alaS	alanyl-tRNA synthetase	**-2.66**	0.00581	**-0.43**	0.15091	**-2.73**	0.00014
STM2827	alaS	alanyl-tRNA synthetase	**-1.99**	0.00864	**-0.66**	0.08000	**-1.79**	0.00098
STM2828	recX	RecA regulator RecX	**-1.50**	0.02389	**-0.29**	0.62367	**-2.58**	0.00018
STM2828	recX	RecA regulator RecX	**-0.55**	0.28920	**-0.13**	0.72481	**-1.86**	0.00538
STM2829	recA	recombinase A	**0.51**	0.28880	**1.10**	0.02558	**-1.17**	0.01144
STM2829	recA	recombinase A	**1.20**	0.05747	**1.01**	0.02815	**-0.36**	0.38617
STM2830	ygaD	competence damage-inducible protein A	**-0.92**	0.19163	**-0.94**	0.01019	**-0.83**	0.06971
STM2830	ygaD	competence damage-inducible protein A	**-0.43**	0.31276	**-0.02**	0.96048	**-0.81**	0.04560
STM2831	mltB	membrane-bound lytic murein transglycosylase B	**-1.80**	0.02018	**-0.41**	0.45792	**-1.12**	0.01141
STM2831	mltB	membrane-bound lytic murein transglycosylase B	**-1.07**	0.21742	**-1.54**	0.00317	**-2.81**	0.00049
STM2832	srlA	glucitol/sorbitol-specific enzyme IIC component	**-0.52**	0.27660	**0.12**	0.72227	**-1.54**	0.05832
STM2832	srlA	glucitol/sorbitol-specific enzyme IIC component	**-0.75**	0.32639	**0.02**	0.96465	**-1.27**	0.12494
STM2833	srlE	glucitol/sorbitol-specific enzyme IIB component	**-0.18**	0.73809	**-0.12**	0.72017	**-0.39**	0.31625
STM2833	srlE	glucitol/sorbitol-specific enzyme IIB component	**0.32**	0.59824	**-0.04**	0.95522	**0.04**	0.95237
STM2834	slrB	glucitol/sorbitol-specific enzyme IIA component	**0.33**	0.69343	**-0.75**	0.05500	**-0.56**	0.22228
STM2834	slrB	glucitol/sorbitol-specific enzyme IIA component	**1.82**	0.01423	**-0.65**	0.14568	**-0.19**	0.60435
STM2835	srlD	sorbitol-6-phosphate 2-dehydrogenase	**-0.41**	0.59899	**0.21**	0.56782	**1.33**	0.17783
STM2835	srlD	sorbitol-6-phosphate 2-dehydrogenase	**0.28**	0.50087	**0.54**	0.30321	**1.13**	0.01746
STM2836	gutM	putative glucitol operon regulatory protein	**-0.63**	0.25618	**0.46**	0.11891	**-0.90**	0.13191
STM2836	gutM	putative glucitol operon regulatory protein	**1.52**	0.02380	**0.72**	0.02277	**-0.26**	0.70170
STM2837	srlR	transcriptional repressor for glucitol operon	**1.14**	0.04517	**0.04**	0.92124	**0.63**	0.19128
STM2837	srlR	transcriptional repressor for glucitol operon	**1.90**	0.01066	**-0.16**	0.64814	**1.66**	0.01876
STM2838,S	gutQ	putative sugar phosphate isomerase	**0.05**	0.92278	**-0.31**	0.34041	**-0.51**	0.19229
STM2838,S	gutQ	putative sugar phosphate isomerase	**0.57**	0.19533	**-0.64**	0.08218	**-0.18**	0.71447
STM2839	ygaA	anaerobic nitric oxide reductase transcription regulator	**0.01**	0.97992	**-0.72**	0.05103	**-1.91**	0.01393
STM2839	ygaA	anaerobic nitric oxide reductase transcription regulator	**0.36**	0.49299	**-0.66**	0.09762	**-0.56**	0.42695
STM2840	STM2840	anaerobic nitric oxide reductase flavorubredoxin	**1.40**	0.03665	**-0.03**	0.93725	**0.09**	0.90469
STM2840	STM2840	anaerobic nitric oxide reductase flavorubredoxin	**1.54**	0.03293	**-0.33**	0.61214	**1.13**	0.06812
STM2841	ygbD	nitric oxide reductase	**-0.08**	0.92513	**-0.48**	0.11589	**-0.06**	0.93734
STM2841	ygbD	nitric oxide reductase	**0.89**	0.29762	**-0.18**	0.59083	**0.11**	0.82912
STM2842	hypF	hydrogenase maturation protein	**1.38**	0.04434	**-1.23**	0.00257	**-1.19**	0.10215
STM2842	hypF	hydrogenase maturation protein	**0.33**	0.67020	**-1.64**	0.00282	**-1.67**	0.22901
STM2843	hydN	electron transport protein	**-0.23**	0.72792	**-0.24**	0.63942	**-1.34**	0.09005
STM2843	hydN	electron transport protein	**0.45**	0.34889	**-0.66**	0.03786	**0.25**	0.85525
STM2844	STM2844	hypothetical protein STM2844	**-0.17**	0.71581	**-1.08**	0.00876	**-0.01**	0.98388
STM2844	STM2844	hypothetical protein STM2844	**0.03**	0.95428	**-0.55**	0.21505	**-0.32**	0.56241
STM2845	hycI	hydrogenase 3 large subunit C-terminal protease	**-0.21**	0.63891	**-1.17**	0.10263	**-1.01**	0.23611
STM2845	hycI	hydrogenase 3 large subunit C-terminal protease	**0.85**	0.11826	**-0.84**	0.08839	**-0.35**	0.44711
STM2846	hycH	hydrogenase 3 large subunit processing protein	**-0.75**	0.25855	**-0.17**	0.55066	**-0.81**	0.09217
STM2846	hycH	hydrogenase 3 large subunit processing protein	**2.02**	0.21125	**-0.62**	0.05897	**0.01**	0.98279
STM2847	hycG	hydrogenase	**-0.35**	0.55325	**-0.66**	0.37488	**-0.49**	0.29993
STM2847	hycG	hydrogenase	**1.17**	0.03084	**0.49**	0.36497	**1.07**	0.06532

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM2848	hycF	hydrogenase 4 Fe-S subunit	**-0.97**	0.05006	**-1.36**	0.00597	**-0.47**	0.50989
STM2848	hycF	hydrogenase 4 Fe-S subunit	**0.75**	0.25327	**-1.49**	0.00331	**-1.35**	0.03522
STM2849	hycE	hydrogenase 3 large subunit	**0.38**	0.37124	**0.18**	0.65595	**-0.21**	0.78195
STM2849	hycE	hydrogenase 3 large subunit	**1.77**	0.02316	**2.25**	0.00092	**2.27**	0.00103
STM2850	hycD	hydrogenase 3 membrane subunit	**-0.02**	0.97058	**-1.01**	0.15969	**-0.72**	0.12017
STM2850	hycD	hydrogenase 3 membrane subunit	**0.76**	0.35641	**-2.16**	0.00773	**-1.51**	0.08815
STM2851	hycC	NADH dehydrogenase subunit N	**0.85**	0.19774	**-0.62**	0.20794	**-0.63**	0.08415
STM2851	hycC	NADH dehydrogenase subunit N	**1.16**	0.07225	**-0.85**	0.06297	**0.55**	0.24353
STM2852	hycB	hydrogenase-3 iron-sulfur subunit	**-0.57**	0.37508	**0.11**	0.72851	**0.15**	0.78178
STM2852	hycB	hydrogenase-3 iron-sulfur subunit	**-1.14**	0.16085	**-1.30**	0.00651	**-1.25**	0.17629
STM2853	hycA	transcriptional repressor	**-0.82**	0.11173	**0.14**	0.71237	**-0.67**	0.37572
STM2853	hycA	transcriptional repressor	**0.46**	0.58086	**-0.75**	0.04145	**-0.02**	0.96184
STM2854	hypA	hydrogenase nickel incorporation protein	**-0.14**	0.74592	**-0.55**	0.13499	**-0.50**	0.25011
STM2854	hypA	hydrogenase nickel incorporation protein	**1.43**	0.02948	**-0.77**	0.13075	**1.21**	0.01293
STM2855	hypB	hydrogenase-3 accessory protein	**0.03**	0.95585	**-0.83**	0.01730	**-0.19**	0.68762
STM2855	hypB	hydrogenase-3 accessory protein	**0.18**	0.68574	**-1.14**	0.01609	**-0.15**	0.75357
STM2856	hypC	putative hydrogenase formation protein	**-0.11**	0.82751	**-0.09**	0.87539	**-1.63**	0.05449
STM2856	hypC	putative hydrogenase formation protein	**-0.68**	0.16482	**-0.83**	0.01854	**-0.96**	0.10525
STM2857	hypD	putative hydrogenase formation protein	**-1.42**	0.02720	**-0.74**	0.11234	**-0.95**	0.28744
STM2857	hypD	putative hydrogenase formation protein	**-0.55**	0.28623	**-0.63**	0.05474	**-0.46**	0.23202
STM2858	hypE	putative hydrogenase formation protein	**-1.00**	0.08378	**-0.22**	0.69504	**-0.25**	0.55541
STM2858	hypE	putative hydrogenase formation protein	**-1.96**	0.01999	**-0.86**	0.03065	**-3.28**	0.00164
STM2859	fhlA	formate hydrogen-lyase transcriptional activator	**-0.07**	0.89762	**2.96**	0.00028	**2.11**	0.00265
STM2859	fhlA	formate hydrogen-lyase transcriptional activator	**2.49**	0.02407	**3.12**	0.00023	**3.14**	0.00018
STM2860	ygbA	putative cytoplasmic protein	**0.73**	0.17133	**4.16**	0.00002	**3.40**	0.00015
STM2860	ygbA	putative cytoplasmic protein	**1.89**	0.03064	**3.44**	0.00017	**3.89**	0.00009
STM2861	sitA	putative periplasmic binding protein	**2.76**	0.00700	**7.26**	0.00000	**6.83**	0.00001
STM2861	sitA	putative periplasmic binding protein	**3.27**	0.00547	**6.79**	0.00001	**7.38**	0.00001
STM2862	sitB	putative ATP-binding protein	**0.68**	0.20506	**5.27**	0.00000	**5.46**	0.00002
STM2862	sitB	putative ATP-binding protein	**2.24**	0.00942	**5.77**	0.00001	**6.40**	0.00002
STM2863	sitC	putative permease	**1.17**	0.19675	**4.67**	0.00001	**1.88**	0.02480
STM2863	sitC	putative permease	**1.86**	0.05977	**4.72**	0.00003	**2.41**	0.01054
STM2864	sitD	putative permease	**0.25**	0.55141	**4.51**	0.00002	**3.70**	0.00006
STM2864	sitD	putative permease	**1.47**	0.15478	**4.46**	0.00005	**4.34**	0.00003
STM2865	avrA	secreted effector protein	**2.80**	0.01715	**2.66**	0.00016	**1.87**	0.00131
STM2865	avrA	secreted effector protein	**2.80**	0.02246	**2.23**	0.00077	**2.21**	0.00321
STM2866	sprB	transcriptional regulator	**0.51**	0.41383	**1.02**	0.01445	**0.29**	0.57163
STM2866	sprB	transcriptional regulator	**0.79**	0.15984	**1.06**	0.00609	**0.72**	0.12410
STM2867	hilC	invasion regulatory protein	**0.68**	0.39882	**0.27**	0.46659	**0.54**	0.46539
STM2867	hilC	invasion regulatory protein	**0.89**	0.09193	**-0.25**	0.49860	**-0.16**	0.67349
STM2868	orgC	putative cytoplasmic protein	**-0.05**	0.94279	**-0.44**	0.16375	**-0.82**	0.04673
STM2868	orgC	putative cytoplasmic protein	**0.17**	0.72227	**-0.52**	0.19337	**-0.19**	0.70541
STM2869	orgB	needle complex export protein	**-0.80**	0.49835	**-0.39**	0.43190	**-0.43**	0.37967
STM2869	orgB	needle complex export protein	**-0.91**	0.34131	**-0.54**	0.07929	**-0.73**	0.05805
STM2870	orgA	needle complex assembly protein	**-0.09**	0.95415	**-0.69**	0.04145	**-1.37**	0.15466
STM2870	orgA	needle complex assembly protein	**0.54**	0.63793	**-0.30**	0.28355	**-0.51**	0.60625
STM2871	prgK	needle complex inner membrane lipoprotein	**-0.07**	0.86752	**0.04**	0.91171	**0.13**	0.76817
STM2871	prgK	needle complex inner membrane lipoprotein	**-0.13**	0.83332	**0.20**	0.53363	**-0.36**	0.52011
STM2872	prgJ	needle complex minor subunit	**-1.69**	0.02981	**-0.21**	0.46015	**-0.01**	0.99035
STM2872	prgJ	needle complex minor subunit	**-0.78**	0.13130	**-0.38**	0.16506	**-1.13**	0.01722
STM2873	prgI	needle complex major subunit	**-0.87**	0.10193	**0.24**	0.46714	**-2.26**	0.00792
STM2873	prgI	needle complex major subunit	**-0.28**	0.62037	**-0.17**	0.61067	**-1.33**	0.09788
STM2874	prgH	needle complex inner membrane protein	**1.31**	0.04434	**-0.38**	0.25544	**0.18**	0.77611
STM2874	prgH	needle complex inner membrane protein	**1.27**	0.06357	**-1.04**	0.03312	**1.14**	0.07722
STM2875	hilD	invasion protein regulatory protein	**-0.11**	0.80975	**-0.59**	0.06753	**-0.12**	0.86068
STM2875	hilD	invasion protein regulatory protein	**1.66**	0.02633	**0.50**	0.12485	**1.29**	0.01860
STM2876	hilA	invasion protein transcriptional activator	**0.17**	0.78568	**0.12**	0.78826	**-0.37**	0.42989
STM2876	hilA	invasion protein transcriptional activator	**0.97**	0.07214	**0.03**	0.95479	**1.20**	0.01813
STM2877	iagB	invasion protein precursor	**1.11**	0.04255	**0.72**	0.04123	**1.45**	0.01255
STM2877	iagB	invasion protein precursor	**1.80**	0.04322	**0.22**	0.46396	**1.60**	0.00475
STM2878	sptP	protein tyrosine phosphatase/GTPase activating protein	**0.43**	0.44698	**0.09**	0.80211	**-1.51**	0.02756
STM2878	sptP	protein tyrosine phosphatase/GTPase activating protein	**1.54**	0.01488	**0.19**	0.72073	**-0.20**	0.58454
STM2879	sicP	secretion chaparone	**-1.46**	0.02037	**-0.49**	0.08979	**-2.10**	0.00672
STM2879	sicP	secretion chaparone	**-1.55**	0.02040	**-0.33**	0.24775	**-2.30**	0.00030
STM2881	iacP	acyl carrier protein	**-0.88**	0.14548	**-0.22**	0.51044	**-0.88**	0.04188
STM2881	iacP	acyl carrier protein	**-0.85**	0.07366	**-0.51**	0.13874	**-1.31**	0.01296
STM2882	sipA	secreted effector protein	**-0.87**	0.08732	**-0.33**	0.30524	**-1.50**	0.01355
STM2882	sipA	secreted effector protein	**0.57**	0.37965	**-0.08**	0.79941	**-0.06**	0.89732
STM2883	sipD	translocation machinery component	**-0.51**	0.35898	**0.13**	0.81954	**0.44**	0.55303
STM2883	sipD	translocation machinery component	**0.45**	0.36207	**-0.30**	0.46541	**-0.14**	0.79243

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM2884	sipC	translocation machinery component	**-0.87**	0.36963	**-0.68**	0.05852	**-0.23**	0.75680
STM2884	sipC	translocation machinery component	**0.54**	0.44680	**0.42**	0.43230	**0.13**	0.88979
STM2885	sipB	translocation machinery component	**-0.46**	0.37294	**-0.25**	0.67941	**-2.60**	0.00197
STM2885	sipB	translocation machinery component	**0.58**	0.19958	**-0.22**	0.62420	**-0.46**	0.56848
STM2886	sicA	secretion chaperone	**1.03**	0.04883	**0.20**	0.57136	**1.07**	0.26778
STM2886	sicA	secretion chaperone	**1.39**	0.06896	**-0.17**	0.61349	**2.10**	0.01158
STM2887	spaS	type III secretion protein	**0.44**	0.46942	**-0.16**	0.71702	**-0.15**	0.85064
STM2887	spaS	type III secretion protein	**1.21**	0.03914	**-0.19**	0.63567	**1.18**	0.02788
STM2888	spaR	needle complex export protein	**-0.04**	0.96031	**1.44**	0.00297	**2.52**	0.00027
STM2888	spaR	needle complex export protein	**-0.37**	0.76178	**1.45**	0.00947	**2.67**	0.00016
STM2889	spaQ	needle complex export protein	**-0.87**	0.11992	**-0.12**	0.72465	**-0.28**	0.54128
STM2889	spaQ	needle complex export protein	**-0.64**	0.30866	**-1.96**	0.00032	**-0.10**	0.85901
STM2890	spaP	needle complex export protein	**-1.20**	0.04933	**-0.25**	0.39122	**-0.12**	0.81731
STM2890	spaP	needle complex export protein	**-1.86**	0.03584	**-1.60**	0.00369	**-0.65**	0.25303
STM2891	spaO	type III secretion protein	**-0.12**	0.90111	**-0.28**	0.48180	**-0.45**	0.49926
STM2891	spaO	type III secretion protein	**-1.13**	0.12587	**-1.26**	0.00867	**0.60**	0.20052
STM2892	invJ	needle length control protein	**2.85**	0.00678	**-0.12**	0.78961	**1.59**	0.03125
STM2892	invJ	needle length control protein	**3.34**	0.00547	**0.13**	0.81389	**1.97**	0.00200
STM2893	invI	needle complex assembly protein	**2.95**	0.01210	**0.20**	0.53718	**2.68**	0.00021
STM2893	invI	needle complex assembly protein	**3.22**	0.00546	**-0.43**	0.29342	**3.46**	0.00026
STM2894	invC	type III secretion system ATPase	**1.03**	0.20566	**-0.48**	0.18047	**0.22**	0.66749
STM2894	invC	type III secretion system ATPase	**1.56**	0.09268	**-0.81**	0.05674	**-0.16**	0.73040
STM2895	invB	secretion chaperone	**0.01**	0.98038	**-0.84**	0.02934	**-0.90**	0.31314
STM2895	invB	secretion chaperone	**0.33**	0.52864	**-0.34**	0.47621	**-0.17**	0.79603
STM2896	invA	needle complex export protein	**0.38**	0.37797	**-0.11**	0.91051	**0.13**	0.91529
STM2896	invA	needle complex export protein	**1.71**	0.22352	**-0.98**	0.01667	**1.04**	0.46740
STM2897	invE	invasion protein	**-0.61**	0.15553	**0.83**	0.32976	**-0.31**	0.62551
STM2897	invE	invasion protein	**0.54**	0.54456	**-1.40**	0.09309	**-1.57**	0.00681
STM2898	invG	outer membrane secretin precursor	**-0.65**	0.32904	**-0.06**	0.85409	**0.20**	0.71730
STM2898	invG	outer membrane secretin precursor	**2.54**	0.00694	**-0.37**	0.49843	**1.19**	0.01183
STM2899	invF	invasion regulatory protein	**-0.32**	0.55318	**0.19**	0.52785	**0.52**	0.47307
STM2899	invF	invasion regulatory protein	**-0.20**	0.64684	**0.18**	0.64464	**0.25**	0.58246
STM2900	invH	needle complex outer membrane lipoprotein precursor	**1.37**	0.02245	**-0.05**	0.93004	**-0.78**	0.25931
STM2900	invH	needle complex outer membrane lipoprotein precursor	**1.35**	0.02725	**0.09**	0.78021	**0.92**	0.12048
STM2902	STM2902	putative cytoplasmic protein	**-0.95**	0.17278	**0.40**	0.23082	**-1.50**	0.00943
STM2902	STM2902	putative cytoplasmic protein	**-0.06**	0.91468	**-0.07**	0.84062	**-0.61**	0.12993
STM2903	STM2903	putative cytoplasmic protein	**3.71**	0.00547	**2.14**	0.00087	**2.80**	0.00462
STM2903	STM2903	putative cytoplasmic protein	**3.58**	0.00541	**1.35**	0.01405	**2.66**	0.00350
STM2904	STM2904	putative ABC-type transporter	**1.15**	0.06148	**2.78**	0.00005	**0.01**	0.97267
STM2904	STM2904	putative ABC-type transporter	**1.77**	0.04480	**2.58**	0.00008	**0.92**	0.04114
STM2905	STM2905	putative acetyltransferase	**0.06**	0.91869	**1.96**	0.00069	**0.59**	0.17099
STM2905	STM2905	putative acetyltransferase	**0.45**	0.34307	**1.86**	0.00075	**-0.09**	0.87903
STM2907	pphB	serine/threonine protein phosphatase 2	**-0.74**	0.16772	**-0.53**	0.14134	**-0.89**	0.03920
STM2907	pphB	serine/threonine protein phosphatase 2	**1.66**	0.05585	**0.83**	0.09094	**1.24**	0.30415
STM2909	mutS	DNA mismatch repair protein	**-1.18**	0.04752	**-0.12**	0.86895	**-0.80**	0.11996
STM2909	mutS	DNA mismatch repair protein	**-0.05**	0.94061	**-1.41**	0.00177	**-0.73**	0.13358
STM2910	STM2910	putative cytoplasmic protein	**0.66**	0.31214	**-0.22**	0.56448	**1.12**	0.16256
STM2910	STM2910	putative cytoplasmic protein	**1.27**	0.02726	**-0.71**	0.12156	**0.99**	0.05834
STM2911	STM2911	putative permease	**0.51**	0.54930	**-0.21**	0.81056	**1.40**	0.01141
STM2911	STM2911	putative permease	**1.44**	0.21225	**0.72**	0.06195	**0.11**	0.79508
STM2912	STM2912	putative transcriptional regulator	**0.15**	0.77481	**-1.09**	0.00605	**-0.80**	0.22292
STM2912	STM2912	putative transcriptional regulator	**1.23**	0.03894	**-1.24**	0.02092	**-0.21**	0.78566
STM2913	STM2913	putative permease	**-0.14**	0.82858	**-0.85**	0.03719	**-1.05**	0.07059
STM2913	STM2913	putative permease	**1.48**	0.04650	**-0.30**	0.53064	**0.55**	0.26033
STM2914	STM2914	putative nucleoside-diphosphate-sugar epimerase	**-0.50**	0.32224	**-1.30**	0.00376	**-0.86**	0.05846
STM2914	STM2914	putative nucleoside-diphosphate-sugar epimerase	**0.13**	0.82021	**-2.47**	0.00617	**0.59**	0.29354
STM2915	ygbM	putative endonuclease	**0.28**	0.83908	**0.26**	0.42775	**0.84**	0.24654
STM2915	ygbM	putative endonuclease	**3.15**	0.00595	**-0.42**	0.26220	**0.70**	0.07964
STM2916	ygbL	hypothetical protein STM2916	**-0.60**	0.45278	**-0.89**	0.05216	**-1.32**	0.10020
STM2916	ygbL	hypothetical protein STM2916	**0.95**	0.21896	**-0.79**	0.01862	**-0.27**	0.59738
STM2917	ygbK	putative tRNA synthase	**-0.46**	0.36461	**-0.59**	0.08490	**-0.19**	0.79099
STM2917	ygbK	putative tRNA synthase	**-0.81**	0.22906	**-0.47**	0.17868	**-1.00**	0.43603
STM2918	ygbJ	3-hydroxyisobutyrate dehydrogenase	**-1.18**	0.05655	**-0.07**	0.93755	**-0.67**	0.14679
STM2918	ygbJ	3-hydroxyisobutyrate dehydrogenase	**-0.22**	0.70460	**-1.27**	0.00421	**-0.86**	0.10638
STM2919	ygbI	putative regulatory protein	**-0.26**	0.55759	**-0.10**	0.78855	**-0.89**	0.12743
STM2919	ygbI	putative regulatory protein	**0.27**	0.73922	**-0.75**	0.03381	**0.32**	0.63741
STM2920	STM2920	putative transcriptional regulator	**-1.86**	0.03242	**0.08**	0.86983	**0.21**	0.54727
STM2920	STM2920	putative transcriptional regulator	**-0.86**	0.14061	**-0.40**	0.24066	**-0.71**	0.17645
STM2921	STM2921	putative flavoprotein	**-1.07**	0.05126	**-0.08**	0.89699	**-0.45**	0.25257
STM2921	STM2921	putative flavoprotein	**0.58**	0.48181	**-0.94**	0.01776	**-1.01**	0.18188

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM2922	STM2922	putative 3-polyprenyl-4-hydroxybenzoate decarboxylase	**-0.69**	0.15634	**2.08**	0.00710	**0.78**	0.11205
STM2922	STM2922	putative 3-polyprenyl-4-hydroxybenzoate decarboxylase	**0.40**	0.33154	**2.59**	0.00019	**1.79**	0.00146
STM2923	STM2923	putative cytoplasmic protein	**-0.97**	0.25134	**2.51**	0.00355	**0.66**	0.28701
STM2923	STM2923	putative cytoplasmic protein	**0.27**	0.74619	**2.38**	0.00011	**0.78**	0.16736
STM2924	rpoS	RNA polymerase sigma factor	**-1.35**	0.27138	**3.29**	0.00004	**3.18**	0.00180
STM2924	rpoS	RNA polymerase sigma factor	**-1.52**	0.35714	**3.77**	0.00001	**3.38**	0.00050
STM2925	nlpD	lipoprotein	**0.50**	0.26606	**3.70**	0.00003	**2.43**	0.00026
STM2925	nlpD	lipoprotein	**1.37**	0.04182	**4.07**	0.00001	**3.00**	0.00115
STM2926	pcm	protein-L-isoaspartate O-methyltransferase	**-1.37**	0.02338	**-0.30**	0.45792	**-1.39**	0.00477
STM2926	pcm	protein-L-isoaspartate O-methyltransferase	**-1.43**	0.04414	**0.15**	0.63116	**-1.65**	0.00859
STM2927	surE	acid phosphatase	**-2.95**	0.01391	**-1.54**	0.00077	**-2.01**	0.00125
STM2927	surE	acid phosphatase	**-2.16**	0.00829	**-1.47**	0.00134	**-2.40**	0.00028
STM2928	ygbO	tRNA pseudouridine synthase D	**-0.91**	0.35386	**-1.64**	0.00094	**-1.07**	0.08555
STM2928	ygbO	tRNA pseudouridine synthase D	**-0.62**	0.17012	**-1.68**	0.00057	**-0.50**	0.52742
STM2929	ispF	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	**-2.51**	0.00613	**-1.83**	0.00042	**-2.64**	0.00042
STM2929	ispF	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	**-1.50**	0.01545	**-1.44**	0.00168	**-2.73**	0.00011
STM2930	ispD	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase	**-2.68**	0.00581	**-1.38**	0.01031	**-3.25**	0.00018
STM2930	ispD	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase	**-1.09**	0.55813	**-1.98**	0.00036	**-4.51**	0.00260
STM2931	ftsB	cell divison protein FtsB	**-0.23**	0.65388	**-1.32**	0.00454	**-4.12**	0.00004
STM2931	ftsB	cell divison protein FtsB	**1.12**	0.12065	**-1.15**	0.01093	**-2.97**	0.00041
STM2932	ygbE	putative inner membrane protein	**-1.86**	0.01028	**-1.18**	0.00579	**-1.85**	0.00150
STM2932	ygbE	putative inner membrane protein	**-1.08**	0.11472	**-1.07**	0.00592	**-0.99**	0.15561
STM2933	cysC	adenylylsulfate kinase	**-1.70**	0.06792	**0.41**	0.26801	**-1.68**	0.03742
STM2933	cysC	adenylylsulfate kinase	**-0.15**	0.89576	**0.81**	0.01999	**-0.95**	0.02950
STM2934	cysN	sulfate adenylyltransferase subunit 1	**-0.15**	0.75850	**1.86**	0.00084	**-0.61**	0.32047
STM2934	cysN	sulfate adenylyltransferase subunit 1	**0.85**	0.17118	**1.80**	0.00197	**0.93**	0.09568
STM2935	cysD	sulfate adenylyltransferase subunit 2	**2.08**	0.01217	**2.90**	0.00011	**1.60**	0.02467
STM2935	cysD	sulfate adenylyltransferase subunit 2	**3.36**	0.00541	**2.22**	0.00096	**0.31**	0.64309
STM2936	iap	aminopeptidase	**0.16**	0.86161	**-1.07**	0.05311	**-0.38**	0.63830
STM2936	iap	aminopeptidase	**2.07**	0.03367	**-1.94**	0.00049	**0.69**	0.30882
STM2937	ygbF	putative inner membrane protein	**-0.12**	0.82344	**0.30**	0.45604	**-0.79**	0.04937
STM2937	ygbF	putative inner membrane protein	**-0.06**	0.90577	**0.16**	0.72465	**0.15**	0.75832
STM2938	STM2938	putative cytoplasmic protein	**0.73**	0.38484	**0.53**	0.09592	**-0.37**	0.56284
STM2938	STM2938	putative cytoplasmic protein	**1.10**	0.31261	**-0.57**	0.08234	**-0.50**	0.45021
STM2939	ygcH	putative cytoplasmic protein	**-0.92**	0.08322	**-0.39**	0.22319	**-0.89**	0.14039
STM2939	ygcH	putative cytoplasmic protein	**1.11**	0.30769	**-0.27**	0.49976	**0.32**	0.45406
STM2940	STM2940	putative cytoplasmic protein	**-0.67**	0.28679	**0.15**	0.68251	**-0.85**	0.11004
STM2940	STM2940	putative cytoplasmic protein	**-0.16**	0.72937	**-0.74**	0.04497	**-0.22**	0.68291
STM2941	yghJ	putative cytoplasmic protein	**1.05**	0.49835	**-0.22**	0.56308	**-0.75**	0.36411
STM2941	yghJ	putative cytoplasmic protein	**0.27**	0.62447	**-0.14**	0.71963	**-0.12**	0.76099
STM2942	STM2942	putative transposase	**0.13**	0.85864	**-0.32**	0.46714	**-1.48**	0.01993
STM2942	STM2942	putative transposase	**0.88**	0.10533	**-0.44**	0.30330	**-0.21**	0.63737
STM2943	STM2943	putative cytoplasmic protein	**2.69**	0.03383	**1.97**	0.00185	**4.83**	0.00045
STM2943	STM2943	putative cytoplasmic protein	**2.93**	0.00626	**1.94**	0.01807	**4.84**	0.00006
STM2944	ygcB	putative helicase	**-0.03**	0.96631	**-0.29**	0.52035	**-1.20**	0.05165
STM2944	ygcB	putative helicase	**0.64**	0.35507	**-0.55**	0.16994	**-0.24**	0.61526
STM2945	sopD	secreted effector protein	**0.16**	0.69832	**-0.26**	0.40979	**0.61**	0.37924
STM2945	sopD	secreted effector protein	**1.20**	0.06803	**-0.11**	0.78370	**0.91**	0.27648
STM2946	cysH	phosphoadenosine phosphosulfate reductase	**0.48**	0.34817	**1.12**	0.00801	**0.33**	0.66582
STM2946	cysH	phosphoadenosine phosphosulfate reductase	**1.92**	0.02314	**0.19**	0.63084	**0.87**	0.19653
STM2947	cysI	sulfite reductase alpha subunit	**0.40**	0.69215	**0.70**	0.03893	**-1.53**	0.00519
STM2947	cysI	sulfite reductase alpha subunit	**1.66**	0.13710	**0.61**	0.11646	**-0.58**	0.30591
STM2948	cysJ	sulfite reductase beta subunit	**0.46**	0.30250	**1.36**	0.00156	**0.15**	0.77472
STM2948	cysJ	sulfite reductase beta subunit	**0.70**	0.23325	**0.87**	0.28895	**1.11**	0.04207
STM2949	ptpS	putative 6-pyruvoyl tetrahydrobiopterin synthase	**-0.87**	0.17832	**-1.13**	0.00363	**-1.91**	0.00140
STM2949	ptpS	putative 6-pyruvoyl tetrahydrobiopterin synthase	**-0.09**	0.87411	**-0.54**	0.08354	**-1.22**	0.10271
STM2950	STM2950	putative metal-dependent hydrolase	**-0.59**	0.42296	**-0.41**	0.44162	**-1.25**	0.07628
STM2950	STM2950	putative metal-dependent hydrolase	**0.67**	0.14032	**-0.97**	0.03027	**-0.90**	0.08184
STM2951	ygcF	hypothetical protein STM2951	**-1.30**	0.04794	**-0.60**	0.04440	**-0.95**	0.04152
STM2951	ygcF	hypothetical protein STM2951	**-1.04**	0.05440	**-0.80**	0.03626	**-0.77**	0.08442
STM2952	eno	phosphopyruvate hydratase	**-1.08**	0.04933	**-1.08**	0.02674	**-0.84**	0.08201
STM2952	eno	phosphopyruvate hydratase	**-0.16**	0.81928	**-0.82**	0.02638	**-0.40**	0.26395
STM2953	pyrG	CTP synthetase	**-3.17**	0.00546	**-0.58**	0.13574	**-1.17**	0.00948
STM2953	pyrG	CTP synthetase	**-2.58**	0.00747	**-0.35**	0.21455	**-0.75**	0.08950
STM2954	mazG	putative pyrophosphatase	**1.79**	0.01824	**-0.81**	0.02172	**1.82**	0.00722
STM2954	mazG	putative pyrophosphatase	**2.36**	0.02897	**-0.44**	0.41715	**2.44**	0.00046
STM2954,1n	STM2954,1n	hypothetical protein STM2954,1n	**0.25**	0.76779	**0.55**	0.21683	**-0.15**	0.79129
STM2954,1n	STM2954,1n	hypothetical protein STM2954,1n	**-0.18**	0.86272	**0.28**	0.34110	**-0.54**	0.60536
STM2955,S	STM2955,S	putative transcriptional regulator	**-0.20**	0.64143	**0.71**	0.03202	**0.12**	0.78971
STM2955,S	STM2955,S	putative transcriptional regulator	**0.59**	0.19486	**0.68**	0.03640	**0.87**	0.05801

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM2956	relA	(p)ppGpp synthetase I	**0.45**	0.41205	**-0.63**	0.12297	**-1.68**	0.00591
STM2956	relA	(p)ppGpp synthetase I	**0.90**	0.16748	**-0.91**	0.01016	**-0.67**	0.19230
STM2957	rumA	23S rRNA (uracil-5-)-methyltransferase	**-1.62**	0.05303	**-0.70**	0.05120	**-2.10**	0.00036
STM2957	rumA	23S rRNA (uracil-5-)-methyltransferase	**-1.00**	0.10399	**-0.55**	0.10115	**-1.98**	0.00133
STM2958	barA	sensor histidine kinase	**-1.04**	0.21645	**0.45**	0.18658	**-0.48**	0.26079
STM2958	barA	sensor histidine kinase	**0.95**	0.17589	**0.50**	0.09810	**0.62**	0.13160
STM2959	STM2959	putative glycerate kinase 2	**0.06**	0.90196	**0.31**	0.51093	**-0.19**	0.74716
STM2959	STM2959	putative glycerate kinase 2	**0.90**	0.58533	**-0.64**	0.08703	**-0.26**	0.69838
STM2960	gudD	d-glucarate dehydratase	**0.25**	0.66927	**0.95**	0.01199	**-0.15**	0.77436
STM2960	gudD	d-glucarate dehydratase	**0.57**	0.30591	**0.24**	0.60307	**1.05**	0.07954
STM2961	ygcY	putative D-glucarate dehydratase	**0.20**	0.75580	**0.43**	0.34483	**0.05**	0.92862
STM2961	ygcY	putative D-glucarate dehydratase	**1.36**	0.27724	**0.47**	0.15631	**0.57**	0.23179
STM2962	gudT	putative D-glucarate permease	**-1.31**	0.06653	**-0.48**	0.33389	**-1.20**	0.11677
STM2962	gudT	putative D-glucarate permease	**-1.05**	0.39076	**-0.22**	0.46588	**-0.91**	0.05575
STM2963	STM2963	flavodoxin	**0.63**	0.39749	**-0.03**	0.91738	**-0.87**	0.13787
STM2963	STM2963	flavodoxin	**1.15**	0.25202	**-0.71**	0.10650	**0.28**	0.52972
STM2964	yqcB	putative pseudouridylate synthase	**0.29**	0.82173	**0.01**	0.96756	**0.05**	0.93282
STM2964	yqcB	putative pseudouridylate synthase	**1.79**	0.03030	**-0.24**	0.43484	**0.81**	0.03948
STM2965	yqcC	putative cytoplasmic protein	**-1.02**	0.08684	**0.36**	0.42523	**1.10**	0.01177
STM2965	yqcC	putative cytoplasmic protein	**0.02**	0.96886	**0.40**	0.27371	**1.42**	0.00876
STM2966	csrB	STM2966	**-0.84**	0.40178	**0.24**	0.60199	**3.27**	0.00138
STM2966	csrB	STM2966	**1.37**	0.02147	**0.83**	0.05733	**4.24**	0.00003
STM2967	syd	SecY interacting protein Syd	**-1.24**	0.05440	**-0.42**	0.25132	**1.32**	0.01362
STM2967	syd	SecY interacting protein Syd	**-0.44**	0.37335	**0.16**	0.66454	**0.68**	0.25570
STM2968	yqcD	putative GTP cyclohydrolase I	**-1.37**	0.02827	**-1.60**	0.00065	**-0.89**	0.05407
STM2968	yqcD	putative GTP cyclohydrolase I	**-1.27**	0.02432	**-1.55**	0.00115	**-0.02**	0.97990
STM2969	ygdH	putative nucleotide binding	**-1.66**	0.06625	**-1.39**	0.00208	**-1.42**	0.00647
STM2969	ygdH	putative nucleotide binding	**-1.51**	0.02153	**-1.34**	0.00203	**-1.39**	0.03751
STM2970	sdaC	putative serine transport protein	**-3.38**	0.00546	**-1.96**	0.00161	**-3.02**	0.00013
STM2970	sdaC	putative serine transport protein	**-2.93**	0.00929	**-1.72**	0.00119	**-2.72**	0.00048
STM2971	sdaB	L-serine dehydratase/L-threonine deaminase 2	**-0.88**	0.26511	**-0.83**	0.03193	**-2.16**	0.00257
STM2971	sdaB	L-serine dehydratase/L-threonine deaminase 2	**-0.62**	0.23356	**-0.78**	0.02614	**-0.60**	0.25889
STM2972	xni	exonuclease IX	**-0.21**	0.70630	**-0.01**	0.98802	**0.80**	0.23993
STM2972	xni	exonuclease IX	**-0.58**	0.24454	**-1.02**	0.04007	**-1.20**	0.02636
STM2973	fucO	L-1,2-propanediol oxidoreductase	**-0.23**	0.64858	**-1.06**	0.05922	**-1.38**	0.03921
STM2973	fucO	L-1,2-propanediol oxidoreductase	**0.50**	0.35507	**-0.63**	0.05975	**-0.56**	0.22383
STM2974	fucA	L-fuculose phosphate aldolase	**-0.93**	0.12044	**-0.26**	0.61796	**0.25**	0.62768
STM2974	fucA	L-fuculose phosphate aldolase	**-0.74**	0.49521	**-0.26**	0.47781	**0.04**	0.94831
STM2976	fucI	L-fucose isomerase	**-0.30**	0.78037	**0.10**	0.80743	**-0.03**	0.97853
STM2976	fucI	L-fucose isomerase	**0.39**	0.42840	**0.11**	0.89459	**0.98**	0.04801
STM2977	fucK	L-fuculokinase	**-0.56**	0.20360	**0.66**	0.11995	**-2.13**	0.00073
STM2977	fucK	L-fuculokinase	**1.07**	0.06252	**0.75**	0.03180	**0.24**	0.65412
STM2978	fucU	putative L-fucose-binding protein	**-0.25**	0.56768	**0.51**	0.31190	**-0.08**	0.90250
STM2978	fucU	putative L-fucose-binding protein	**0.19**	0.86747	**0.28**	0.41565	**-0.05**	0.92913
STM2979	fucR	fuc operon positive regulator	**2.01**	0.13364	**-0.96**	0.05099	**0.03**	0.95480
STM2979	fucR	fuc operon positive regulator	**-0.85**	0.11623	**-1.21**	0.00289	**-0.58**	0.32882
STM2980	ygdE	putative SAM-dependent methyltransferase	**-0.92**	0.24817	**-0.30**	0.34434	**-1.23**	0.08029
STM2980	ygdE	putative SAM-dependent methyltransferase	**0.82**	0.12778	**-0.09**	0.78533	**-1.44**	0.00471
STM2981	ygdD	hypothetical protein STM2981	**2.36**	0.21565	**-1.17**	0.00768	**-0.78**	0.47411
STM2981	ygdD	hypothetical protein STM2981	**3.08**	0.22457	**-1.43**	0.00152	**-0.70**	0.64751
STM2982	gcvA	gcv operon regulator	**1.40**	0.30712	**-1.77**	0.01553	**0.23**	0.86026
STM2982	gcvA	gcv operon regulator	**2.36**	0.07572	**-2.23**	0.00519	**1.37**	0.16185
STM2983	ygdI	putative lipoprotein	**0.93**	0.07223	**1.36**	0.00542	**4.43**	0.00003
STM2983	ygdI	putative lipoprotein	**1.88**	0.02655	**1.17**	0.02601	**5.30**	0.00002
STM2984	csdA	putative selenocysteine lyase	**-1.19**	0.04778	**-0.58**	0.14302	**-0.12**	0.78570
STM2984	csdA	putative selenocysteine lyase	**-1.09**	0.11040	**-1.22**	0.00550	**-0.87**	0.05445
STM2985	ygdK	putative FeS center assembly protein	**-0.34**	0.65172	**-0.13**	0.73248	**-0.81**	0.09188
STM2985	ygdK	putative FeS center assembly protein	**0.54**	0.30479	**-1.30**	0.00338	**-1.31**	0.21979
STM2986,Sc	STM2986,Sc	putative integral membrane protein	**-0.36**	0.45509	**-0.73**	0.10936	**0.40**	0.42025
STM2986,Sc	STM2986,Sc	putative integral membrane protein	**0.61**	0.17278	**-0.88**	0.01896	**-0.03**	0.94413
STM2987	ygdL	putative enzyme	**-1.47**	0.01997	**-0.24**	0.53454	**-1.65**	0.00303
STM2987	ygdL	putative enzyme	**-0.05**	0.90565	**-1.06**	0.00848	**-1.24**	0.02305
STM2988	mltA	membrane-bound lytic murein transglycosylase A	**-1.96**	0.11195	**-0.63**	0.07020	**-1.09**	0.04255
STM2988	mltA	membrane-bound lytic murein transglycosylase A	**-0.43**	0.35870	**-1.31**	0.00377	**-0.88**	0.10351
STM2989	metZ	STM2989	**0.78**	0.36511	**0.98**	0.01062	**3.12**	0.00020
STM2989	metZ	STM2989	**1.62**	0.02640	**0.48**	0.12982	**3.42**	0.00009
STM2990	metW	STM2990	**1.10**	0.15292	**0.80**	0.03335	**3.36**	0.00016
STM2990	metW	STM2990	**2.53**	0.05850	**1.21**	0.00522	**4.06**	0.00007
STM2991	amiC	N-acetylmuramoyl-L-alanine amidase	**-0.99**	0.06859	**0.54**	0.15151	**1.09**	0.01895
STM2991	amiC	N-acetylmuramoyl-L-alanine amidase	**0.27**	0.66787	**0.04**	0.93480	**1.61**	0.00175

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM2992	argA	N-acetylglutamate synthase	**0.13**	0.88576	**1.41**	0.00113	**1.39**	0.01145
STM2992	argA	N-acetylglutamate synthase	**0.10**	0.89485	**1.07**	0.00510	**0.01**	0.98560
STM2993	recD	exonuclease V alpha chain	**0.61**	0.19052	**-0.37**	0.33250	**-0.71**	0.13143
STM2993	recD	exonuclease V alpha chain	**0.74**	0.11138	**-0.94**	0.13609	**0.05**	0.94551
STM2994	recB	exonuclease V beta chain	**-0.93**	0.07395	**-0.82**	0.04898	**-1.65**	0.00249
STM2994	recB	exonuclease V beta chain	**0.67**	0.37359	**-1.18**	0.00347	**-2.22**	0.00506
STM2995	ptr	protease III	**-1.03**	0.13647	**-0.76**	0.05812	**0.16**	0.85847
STM2995	ptr	protease III	**-0.74**	0.15041	**-1.19**	0.00851	**-1.23**	0.00592
STM2996	recC	exonuclease V subunit	**-0.86**	0.09103	**0.09**	0.90852	**-0.73**	0.13966
STM2996	recC	exonuclease V subunit	**0.42**	0.44314	**-0.29**	0.51940	**-0.06**	0.91110
STM2997	ppdC	prepilin peptidase dependent protein C	**-0.12**	0.82430	**-0.82**	0.07121	**0.16**	0.71113
STM2997	ppdC	prepilin peptidase dependent protein C	**1.44**	0.02695	**-0.78**	0.03652	**0.24**	0.65920
STM2998	ygdB	putative periplasmic protein	**-0.79**	0.09758	**-0.97**	0.27379	**0.35**	0.40482
STM2998	ygdB	putative periplasmic protein	**0.72**	0.43648	**-0.35**	0.48995	**-0.09**	0.94692
STM2999	ppdB	prepilin peptidase-dependent protein B	**-1.12**	0.05531	**0.37**	0.20674	**-0.75**	0.23872
STM2999	ppdB	prepilin peptidase-dependent protein B	**0.72**	0.65388	**-1.37**	0.07890	**-1.89**	0.06538
STM3000	ppdA	prepilin peptidase-dependent protein A	**-0.26**	0.82796	**-1.32**	0.02309	**-0.29**	0.45372
STM3000	ppdA	prepilin peptidase-dependent protein A	**0.29**	0.61864	**-1.96**	0.00952	**-1.15**	0.01597
STM3001	thyA	thymidylate synthase	**-1.46**	0.04097	**-1.83**	0.00038	**-2.33**	0.00186
STM3001	thyA	thymidylate synthase	**-1.09**	0.05175	**-1.89**	0.00550	**-3.07**	0.00031
STM3002	lgt	prolipoprotein diacylglyceryl transferase	**0.28**	0.82423	**-0.98**	0.01544	**-2.54**	0.00163
STM3002	lgt	prolipoprotein diacylglyceryl transferase	**-0.78**	0.32717	**-1.16**	0.02069	**-1.72**	0.00297
STM3003	ptsP	transcriptional regulator	**-1.56**	0.01447	**-0.49**	0.18690	**-2.41**	0.00056
STM3003	ptsP	transcriptional regulator	**0.08**	0.92754	**-0.65**	0.05568	**-1.42**	0.00429
STM3004	ygdP	dinucleoside polyphosphate hydrolase	**-0.52**	0.62853	**-0.23**	0.41172	**-1.41**	0.00517
STM3004	ygdP	dinucleoside polyphosphate hydrolase	**-0.17**	0.72168	**-0.39**	0.28894	**-0.19**	0.65530
STM3005	mutH	DNA mismatch repair protein	**-0.99**	0.05136	**-0.73**	0.07079	**-1.73**	0.02823
STM3005	mutH	DNA mismatch repair protein	**-0.23**	0.70353	**-0.73**	0.04584	**-1.25**	0.01117
STM3006	ygdQ	putative transport protein	**-0.94**	0.13248	**-0.99**	0.00955	**0.73**	0.36770
STM3006	ygdQ	putative transport protein	**-1.21**	0.04277	**-1.32**	0.00354	**-1.57**	0.01800
STM3007	ygdR	putative peptide transport protein	**0.22**	0.61163	**0.39**	0.22967	**1.78**	0.00201
STM3007	ygdR	putative peptide transport protein	**1.15**	0.05742	**-0.03**	0.95044	**2.56**	0.00068
STM3009	ygeD	putative efflux protein	**-0.87**	0.12491	**-0.63**	0.13946	**-0.74**	0.10947
STM3009	ygeD	putative efflux protein	**0.81**	0.43322	**-0.30**	0.27212	**0.50**	0.24034
STM3010	aas	2-acyl-glycerophospho-ethanolamine acyltransferase	**-1.45**	0.02471	**-1.44**	0.00269	**-2.16**	0.00692
STM3010	aas	2-acyl-glycerophospho-ethanolamine acyltransferase	**-0.40**	0.41384	**-0.69**	0.02964	**-1.32**	0.01166
STM3011	galR	galETK operon transcriptional repressor	**-1.20**	0.12179	**-0.89**	0.03188	**-0.51**	0.43682
STM3011	galR	galETK operon transcriptional repressor	**-0.54**	0.23660	**0.15**	0.70261	**0.18**	0.72486
STM3012	STM3012	putative transcriptional regulator	**-1.02**	0.15779	**1.06**	0.00619	**0.23**	0.69105
STM3012	STM3012	putative transcriptional regulator	**0.08**	0.88793	**0.59**	0.08821	**-0.29**	0.46831
STM3013	lysA	diaminopimelate decarboxylase	**-0.70**	0.12638	**0.18**	0.56566	**-0.67**	0.17185
STM3013	lysA	diaminopimelate decarboxylase	**0.76**	0.55339	**-0.23**	0.42200	**-0.08**	0.94366
STM3014	lysR	transcriptional regulator	**3.19**	0.13471	**-0.53**	0.50717	**0.21**	0.80789
STM3014	lysR	transcriptional regulator	**0.70**	0.17809	**-0.48**	0.24559	**0.09**	0.92111
STM3015	ygeA	putative aspartate racemase	**1.54**	0.03827	**0.13**	0.76190	**0.72**	0.44825
STM3015	ygeA	putative aspartate racemase	**0.46**	0.51127	**-0.35**	0.26374	**-0.59**	0.59602
STM3016	araE	L-arabinose/proton symport protein	**0.79**	0.18340	**0.65**	0.09391	**0.62**	0.31491
STM3016	araE	L-arabinose/proton symport protein	**1.46**	0.02831	**0.96**	0.06759	**1.66**	0.00394
STM3017	kduD	2-deoxy-D-gluconate 3-dehydrogenase	**-0.30**	0.46292	**-1.56**	0.00287	**-0.57**	0.29067
STM3017	kduD	2-deoxy-D-gluconate 3-dehydrogenase	**0.25**	0.60568	**-0.77**	0.06963	**0.12**	0.82064
STM3018	kduI	5-keto-4-deoxyuronate isomerase	**0.56**	0.23361	**-0.35**	0.34076	**0.82**	0.07691
STM3018	kduI	5-keto-4-deoxyuronate isomerase	**0.47**	0.74145	**-0.92**	0.07581	**1.83**	0.07335
STM3019	yqeF	acetyl-CoA acetyltransferase	**0.10**	0.84441	**-0.89**	0.02331	**-0.32**	0.65081
STM3019	yqeF	acetyl-CoA acetyltransferase	**0.69**	0.24172	**-1.19**	0.01276	**0.20**	0.76136
STM3020	STM3020	putative transcriptional regulator	**1.08**	0.07421	**-0.05**	0.91745	**0.93**	0.20863
STM3020	STM3020	putative transcriptional regulator	**1.31**	0.02316	**0.16**	0.59312	**0.63**	0.19060
STM3021	STM3021	putative inner membrane protein	**-0.28**	0.69860	**-1.82**	0.00791	**-1.29**	0.02711
STM3021	STM3021	putative inner membrane protein	**0.01**	0.98801	**-1.93**	0.00190	**-0.86**	0.07470
STM3022	STM3022	putative transport protein	**-0.96**	0.12050	**-0.71**	0.02510	**-1.98**	0.00544
STM3022	STM3022	putative transport protein	**-0.79**	0.59066	**-0.96**	0.02010	**-2.47**	0.01843
STM3023	yohL	putative cytoplasmic protein	**0.08**	0.90413	**0.81**	0.02251	**-0.74**	0.14679
STM3023	yohL	putative cytoplasmic protein	**0.50**	0.31432	**0.65**	0.09421	**0.64**	0.08954
STM3024	yohM	putative inner membrane protein	**-0.39**	0.65886	**1.02**	0.14854	**1.73**	0.02986
STM3024	yohM	putative inner membrane protein	**-0.95**	0.20634	**-0.60**	0.10119	**-0.06**	0.90250
STM3025	STM3025	putative cytoplasmic protein	**0.30**	0.54661	**-0.59**	0.05064	**-0.68**	0.12328
STM3025	STM3025	putative cytoplasmic protein	**1.02**	0.14230	**0.61**	0.11140	**-0.03**	0.97999
STM3025,1N	STM3025,1N	hypothetical protein STM3025,1N	**1.25**	0.08868	**1.24**	0.00297	**2.05**	0.00178
STM3025,1N	STM3025,1N	hypothetical protein STM3025,1N	**2.99**	0.00673	**0.82**	0.02257	**4.28**	0.00006
STM3026	STM3026	putative outer membrane protein	**0.77**	0.13471	**-0.08**	0.84934	**-0.41**	0.45587
STM3026	STM3026	putative outer membrane protein	**1.14**	0.03587	**0.22**	0.58022	**-0.24**	0.80148

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM3027	stdC	putative fimbrial chaparone	**0.05**	0.94879	**-0.33**	0.47177	**-0.53**	0.40606
STM3027	stdC	putative fimbrial chaparone	**-0.27**	0.64103	**-0.39**	0.32335	**-0.48**	0.42195
STM3028	stdB	putative outer membrane usher protein	**0.58**	0.41131	**-0.02**	0.98357	**-0.26**	0.70170
STM3028	stdB	putative outer membrane usher protein	**1.90**	0.02998	**0.62**	0.75137	**-0.01**	0.99357
STM3029,S	stdA	putative fimbrial-like protein	**1.15**	0.08950	**0.39**	0.25242	**0.55**	0.36724
STM3029,S	stdA	putative fimbrial-like protein	**2.65**	0.02603	**0.02**	0.97250	**1.87**	0.00458
STM3030	STM3030	putative periplasmic protein	**3.00**	0.29764	**-0.18**	0.61604	**0.66**	0.55436
STM3030	STM3030	putative periplasmic protein	**0.97**	0.49299	**-1.70**	0.12480	**-0.61**	0.27873
STM3031	STM3031	Ail/OmpX-like protein	**0.84**	0.32702	**0.46**	0.22335	**-0.64**	0.17672
STM3031	STM3031	Ail/OmpX-like protein	**0.00**	0.99561	**-0.08**	0.85285	**-0.31**	0.69757
STM3033	STM3033	putative nucleic acid-binding protein	**-0.04**	0.95779	**0.57**	0.09230	**-2.02**	0.00063
STM3033	STM3033	putative nucleic acid-binding protein	**-0.05**	0.92869	**0.77**	0.03367	**-1.56**	0.01961
STM3036	STM3036	putative inner membrane protein	**-0.51**	0.66812	**0.11**	0.87339	**2.21**	0.00434
STM3036	STM3036	putative inner membrane protein	**0.58**	0.69625	**0.40**	0.55189	**3.75**	0.00089
STM3037	glyU	STM3037	**-2.17**	0.14118	**-2.32**	0.00224	**3.24**	0.00601
STM3037	glyU	STM3037	**-2.64**	0.13309	**-2.48**	0.00048	**3.16**	0.00119
STM3038	STM3038	putative metalloendopeptidase	**2.85**	0.00654	**-0.63**	0.06054	**1.10**	0.04890
STM3038	STM3038	putative metalloendopeptidase	**1.92**	0.04166	**-1.12**	0.01057	**1.08**	0.05027
STM3039	idi	isopentenyl-diphosphate delta-isomerase	**-0.88**	0.09574	**-0.40**	0.20241	**-1.19**	0.03063
STM3039	idi	isopentenyl-diphosphate delta-isomerase	**-0.42**	0.61184	**-0.34**	0.28582	**-0.69**	0.10375
STM3040	lysS	lysyl-tRNA synthetase	**-1.49**	0.02536	**-0.98**	0.00790	**-1.67**	0.00268
STM3040	lysS	lysyl-tRNA synthetase	**-0.88**	0.12079	**-0.52**	0.11489	**-1.65**	0.00728
STM3041c	prfB	peptide chain release factor 2	**-2.66**	0.00676	**-0.65**	0.07738	**-4.21**	0.00005
STM3041c	prfB	peptide chain release factor 2	**-0.73**	0.11625	**-0.71**	0.05760	**-3.44**	0.00011
STM3042	recJ	single-stranded-DNA-specific exonuclease	**-1.34**	0.06354	**-0.84**	0.10650	**-2.20**	0.00114
STM3042	recJ	single-stranded-DNA-specific exonuclease	**-0.73**	0.12186	**-0.35**	0.31257	**-1.51**	0.00943
STM3043	dsbC	protein disulfide isomerase II	**-0.45**	0.34702	**0.28**	0.39829	**-0.86**	0.04600
STM3043	dsbC	protein disulfide isomerase II	**-0.06**	0.92351	**-0.01**	0.98628	**0.91**	0.10743
STM3044	xerD	tyrosine recombinase	**-0.93**	0.08960	**-0.07**	0.82168	**-1.52**	0.00283
STM3044	xerD	tyrosine recombinase	**-0.32**	0.77041	**0.00**	0.99058	**-1.21**	0.01344
STM3045	fldB	flavodoxin	**-1.06**	0.05808	**-0.23**	0.48885	**-0.53**	0.29269
STM3045	fldB	flavodoxin	**-0.98**	0.10559	**-0.45**	0.18632	**-1.17**	0.03173
STM3046	ygfX	putative inner membrane protein	**-0.88**	0.13319	**0.09**	0.79550	**-0.91**	0.24973
STM3046	ygfX	putative inner membrane protein	**-0.75**	0.13204	**-0.10**	0.76936	**-1.02**	0.11492
STM3047	ygfY	putative cytoplasmic protein	**-1.19**	0.09502	**0.01**	0.97300	**-1.09**	0.05620
STM3047	ygfY	putative cytoplasmic protein	**-0.19**	0.73305	**-0.02**	0.96157	**-1.24**	0.02308
STM3048	ygfZ	putative aminomethyltransferase	**-0.95**	0.07710	**-0.18**	0.55009	**-0.65**	0.07641
STM3048	ygfZ	putative aminomethyltransferase	**-0.68**	0.27378	**-0.48**	0.14641	**-0.73**	0.05748
STM3049	yqfA	putative hemolysin	**-0.78**	0.11605	**0.64**	0.05318	**-1.01**	0.06086
STM3049	yqfA	putative hemolysin	**-0.08**	0.93290	**0.28**	0.37964	**-0.42**	0.45121
STM3050	yqfB	hypothetical protein STM3050	**-0.35**	0.48699	**1.24**	0.00416	**-0.15**	0.74560
STM3050	yqfB	hypothetical protein STM3050	**0.69**	0.29343	**0.97**	0.01674	**0.71**	0.10352
STM3051	bglA	6-phospho-beta-glucosidase A	**0.60**	0.16310	**-0.49**	0.12222	**-0.54**	0.42054
STM3051	bglA	6-phospho-beta-glucosidase A	**0.25**	0.81928	**0.01**	0.97933	**-1.10**	0.08195
STM3052	STM3052	putative outer membrane protein	**2.19**	0.00716	**0.79**	0.02678	**2.84**	0.00025
STM3052	STM3052	putative outer membrane protein	**3.94**	0.07023	**0.69**	0.10484	**3.24**	0.00012
STM3053	gcvP	glycine dehydrogenase	**-1.50**	0.03449	**0.89**	0.01510	**-0.43**	0.37654
STM3053	gcvP	glycine dehydrogenase	**0.06**	0.94176	**1.16**	0.00836	**0.34**	0.56519
STM3054	gcvH	glycine cleavage system protein H	**-2.37**	0.01027	**0.59**	0.07857	**-2.23**	0.00247
STM3054	gcvH	glycine cleavage system protein H	**-1.80**	0.02479	**1.38**	0.00346	**-3.05**	0.00026
STM3055	gcvT	aminomethyltransferase	**-2.13**	0.02668	**0.44**	0.33447	**-1.27**	0.04297
STM3055	gcvT	aminomethyltransferase	**-2.76**	0.00700	**0.66**	0.15130	**-2.62**	0.00172
STM3056	visC	hypothetical protein STM3056	**-0.50**	0.35237	**-0.14**	0.67758	**-0.76**	0.06200
STM3056	visC	hypothetical protein STM3056	**0.57**	0.21234	**0.14**	0.72803	**0.23**	0.64791
STM3057	ubiH	2-octaprenyl-6-methoxyphenyl hydroxylase	**-1.87**	0.00971	**-0.82**	0.27785	**-1.09**	0.02438
STM3057	ubiH	2-octaprenyl-6-methoxyphenyl hydroxylase	**-1.65**	0.02906	**-0.92**	0.02253	**-1.52**	0.03128
STM3058	pepP	proline aminopeptidase P II	**1.33**	0.44352	**0.37**	0.18957	**-1.59**	0.00860
STM3058	pepP	proline aminopeptidase P II	**1.10**	0.51827	**0.35**	0.20404	**-1.15**	0.01575
STM3059,S	ygfB	hypothetical protein STM3059,S	**-0.47**	0.71936	**-0.18**	0.68418	**-1.48**	0.00787
STM3059,S	ygfB	hypothetical protein STM3059,S	**0.55**	0.60456	**0.61**	0.04425	**-0.92**	0.03191
STM3060	ygfE	putative cytoplasmic protein	**2.57**	0.23789	**0.19**	0.56202	**0.80**	0.05390
STM3060	ygfE	putative cytoplasmic protein	**3.20**	0.02435	**0.28**	0.34862	**1.78**	0.00170
STM3061	ygfA	putative ligase	**-1.01**	0.05601	**-0.15**	0.75352	**0.25**	0.60978
STM3061	ygfA	putative ligase	**0.30**	0.45509	**-0.19**	0.62159	**0.75**	0.06347
STM3062	serA	D-3-phosphoglycerate dehydrogenase	**0.38**	0.43948	**0.75**	0.03992	**-1.21**	0.01500
STM3062	serA	D-3-phosphoglycerate dehydrogenase	**2.01**	0.01827	**0.63**	0.05166	**0.09**	0.84705
STM3063	rpiA	ribose-5-phosphate isomerase A	**-0.97**	0.07730	**-0.41**	0.18396	**-0.45**	0.21110
STM3063	rpiA	ribose-5-phosphate isomerase A	**-0.87**	0.09446	**0.09**	0.77185	**-0.30**	0.58753
STM3064	iciA	chromosome replication initiation inhibitor protein	**-0.57**	0.29318	**-0.55**	0.10190	**-0.27**	0.53888
STM3064	iciA	chromosome replication initiation inhibitor protein	**-0.09**	0.84025	**-0.86**	0.04593	**0.61**	0.14495

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM3065	yggE	hypothetical protein STM3065	**0.12**	0.90330	**-0.05**	0.87638	**0.41**	0.46489
STM3065	yggE	hypothetical protein STM3065	**1.00**	0.06328	**-0.33**	0.37569	**0.85**	0.06457
STM3066	yggA	arginine exporter protein	**-1.65**	0.01970	**-0.37**	0.70123	**-0.66**	0.10077
STM3066	yggA	arginine exporter protein	**-0.71**	0.55347	**-0.83**	0.01346	**-0.60**	0.18970
STM3067	yggB	putative mechanosensitive channel	**-1.17**	0.03242	**0.53**	0.11771	**-1.15**	0.01443
STM3067	yggB	putative mechanosensitive channel	**-1.11**	0.04986	**0.23**	0.54497	**-0.73**	0.15778
STM3068	fba	fructose-bisphosphate aldolase	**-2.34**	0.01590	**-0.14**	0.66071	**-1.31**	0.00617
STM3068	fba	fructose-bisphosphate aldolase	**-1.63**	0.04650	**-0.45**	0.22939	**-0.98**	0.04408
STM3069	pgk	phosphoglycerate kinase	**-2.01**	0.37533	**-1.42**	0.00229	**0.31**	0.86528
STM3069	pgk	phosphoglycerate kinase	**-4.20**	0.01280	**-1.10**	0.01072	**-1.97**	0.00823
STM3070	epd	D-erythrose 4-phosphate dehydrogenase	**-2.71**	0.00925	**-0.34**	0.25391	**-0.32**	0.37054
STM3070	epd	D-erythrose 4-phosphate dehydrogenase	**-1.49**	0.02479	**-0.30**	0.34689	**0.10**	0.82264
STM3071	STM3071	putative DNA-binding protein	**-1.15**	0.05197	**-1.60**	0.00321	**0.03**	0.94864
STM3071	STM3071	putative DNA-binding protein	**-0.17**	0.84154	**-1.99**	0.00055	**-0.40**	0.28731
STM3072	STM3072	putative inner membrane protein	**-0.78**	0.18060	**-1.64**	0.01866	**-1.14**	0.04263
STM3072	STM3072	putative inner membrane protein	**-0.08**	0.90940	**-1.04**	0.00532	**-0.75**	0.23311
STM3073	STM3073	putative ABC-type cobalt transport system permease	**-0.22**	0.70999	**-1.00**	0.02182	**-0.89**	0.03519
STM3073	STM3073	putative ABC-type cobalt transport system permease	**0.75**	0.14693	**-0.91**	0.02761	**-0.15**	0.76913
STM3074	STM3074	putative ABC-type cobalt transport system ATP-binding	**0.58**	0.18678	**-0.90**	0.11696	**-0.72**	0.13114
STM3074	STM3074	putative ABC-type cobalt transport system ATP-binding	**0.43**	0.35512	**-0.53**	0.27785	**-0.71**	0.23649
STM3075	STM3075	putative ABC-type cobalt transport system ATP-binding	**-1.29**	0.10535	**-0.93**	0.01854	**-0.93**	0.32842
STM3075	STM3075	putative ABC-type cobalt transport system ATP-binding	**-0.51**	0.45920	**-0.67**	0.09009	**-0.86**	0.08388
STM3076	tktA	transketolase	**-1.29**	0.02805	**-0.65**	0.03719	**-1.91**	0.00074
STM3076	tktA	transketolase	**-1.48**	0.02445	**-0.51**	0.18868	**-1.22**	0.02685
STM3077	yggG	putative Zn-dependent protease	**-1.42**	0.04586	**-1.21**	0.02660	**-1.78**	0.00202
STM3077	yggG	putative Zn-dependent protease	**0.25**	0.84059	**-1.66**	0.00379	**-1.38**	0.00846
STM3078	speB	agmatinase	**-1.24**	0.09433	**-1.30**	0.00512	**-1.77**	0.03473
STM3078	speB	agmatinase	**-0.37**	0.43011	**-2.21**	0.00022	**-1.59**	0.01379
STM3079,S	STM3079,S	putative hydrolase/acyltransferase	**-1.63**	0.01598	**-1.09**	0.01908	**-1.69**	0.00207
STM3079,S	STM3079,S	putative hydrolase/acyltransferase	**-1.36**	0.02277	**-1.15**	0.01180	**-1.45**	0.00966
STM3080	STM3080	putative mannitol dehydrogenase	**-0.68**	0.30864	**-0.50**	0.33007	**-0.50**	0.30967
STM3080	STM3080	putative mannitol dehydrogenase	**0.30**	0.63565	**-0.79**	0.09727	**0.55**	0.30807
STM3081	STM3081	putative malate/L-lactate dehydrogenase	**-0.91**	0.10365	**0.42**	0.18698	**0.21**	0.72463
STM3081	STM3081	putative malate/L-lactate dehydrogenase	**0.39**	0.48903	**0.06**	0.87925	**0.63**	0.22715
STM3082	STM3082	putative zinc-binding dehydrogenase	**2.24**	0.00931	**0.59**	0.12537	**1.99**	0.01620
STM3082	STM3082	putative zinc-binding dehydrogenase	**1.69**	0.01227	**0.27**	0.47063	**1.70**	0.00413
STM3083	STM3083	putative mannitol dehydrogenase	**4.81**	0.08308	**0.93**	0.24559	**2.30**	0.01271
STM3083	STM3083	putative mannitol dehydrogenase	**8.76**	0.00190	**3.00**	0.00068	**6.96**	0.00006
STM3084,S	STM3084,S	putative regulatory protein	**-0.94**	0.11862	**0.69**	0.25714	**0.19**	0.64309
STM3084,S	STM3084,S	putative regulatory protein	**0.16**	0.92741	**-0.44**	0.24170	**-1.15**	0.25525
STM3085	STM3085	putative outer membrane lipoprotein	**-0.88**	0.09574	**-0.90**	0.05877	**-0.68**	0.36411
STM3085	STM3085	putative outer membrane lipoprotein	**0.24**	0.62922	**-0.63**	0.04120	**-0.27**	0.52851
STM3086	speA	arginine decarboxylase	**-1.27**	0.02944	**-1.03**	0.01538	**0.34**	0.35142
STM3086	speA	arginine decarboxylase	**-1.61**	0.02516	**-1.10**	0.01548	**-1.40**	0.00357
STM3087	yqgB	putative inner membrane protein	**-2.91**	0.00595	**-2.37**	0.00122	**-2.75**	0.00012
STM3087	yqgB	putative inner membrane protein	**-2.57**	0.00814	**-2.19**	0.00019	**-2.52**	0.00039
STM3089	yqgD	putative inner membrane protein	**-2.51**	0.00818	**-1.37**	0.00289	**-1.94**	0.02242
STM3089	yqgD	putative inner membrane protein	**0.07**	0.96762	**-1.56**	0.00093	**-2.11**	0.00348
STM3090	metK	S-adenosylmethionine synthetase	**-2.18**	0.01761	**-0.79**	0.09349	**-3.16**	0.00118
STM3090	metK	S-adenosylmethionine synthetase	**-1.72**	0.03720	**-0.44**	0.28269	**-2.98**	0.00500
STM3091	galP	galactose/proton symporter	**-0.48**	0.37789	**-0.53**	0.12754	**-0.54**	0.19172
STM3091	galP	galactose/proton symporter	**0.65**	0.22300	**-0.40**	0.17306	**0.19**	0.65684
STM3092	sprT	hypothetical protein STM3092	**-0.91**	0.21330	**-1.12**	0.04600	**-2.13**	0.00172
STM3092	sprT	hypothetical protein STM3092	**-1.39**	0.08950	**-0.98**	0.01625	**-0.97**	0.12985
STM3092	sprT	hypothetical protein STM3092	**-0.16**	0.72232	**-0.88**	0.03268	**-1.28**	0.01966
STM3092	sprT	hypothetical protein STM3092	**-2.50**	0.02585	**-0.93**	0.01299	**-2.43**	0.01412
STM3093	endA	DNA-specific endonuclease I	**-3.68**	0.00541	**-2.79**	0.00010	**-3.48**	0.00092
STM3093	endA	DNA-specific endonuclease I	**-3.15**	0.03180	**-3.23**	0.00003	**-4.28**	0.00256
STM3094	yggJ	putative cytoplasmic protein	**-2.42**	0.00632	**-1.37**	0.00315	**-2.78**	0.00011
STM3094	yggJ	putative cytoplasmic protein	**-1.87**	0.03577	**-1.50**	0.00358	**-2.03**	0.00210
STM3095	gshB	glutathione synthetase	**-2.50**	0.00755	**-2.18**	0.03263	**-2.40**	0.02939
STM3095	gshB	glutathione synthetase	**-1.77**	0.02172	**-0.70**	0.10970	**-2.55**	0.00967
STM3096	yqgE	hypothetical protein STM3096	**-0.76**	0.16584	**0.67**	0.38620	**-2.06**	0.00336
STM3096	yqgE	hypothetical protein STM3096	**-1.31**	0.06100	**0.34**	0.34094	**-2.03**	0.00389
STM3097	yqgF	Holliday junction resolvase-like protein	**-0.97**	0.06515	**0.75**	0.45824	**-1.78**	0.01844
STM3097	yqgF	Holliday junction resolvase-like protein	**-1.77**	0.02451	**-0.39**	0.16803	**-3.38**	0.04091
STM3098	STM3098	putative transcriptional regulator	**-0.35**	0.75567	**0.33**	0.40619	**-0.18**	0.84449
STM3098	STM3098	putative transcriptional regulator	**0.59**	0.21114	**-0.53**	0.11720	**-0.83**	0.04339
STM3099	yggR	twitching motility protein	**0.05**	0.94591	**-0.78**	0.12767	**-0.69**	0.11589
STM3099	yggR	twitching motility protein	**0.84**	0.09675	**-1.64**	0.00495	**0.11**	0.78851

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM3100	yggS	hypothetical protein STM3100	**-2.78**	0.00567	**-0.54**	0.09346	**-2.39**	0.00037
STM3100	yggS	hypothetical protein STM3100	**-1.84**	0.01041	**-0.67**	0.05857	**-2.28**	0.00050
STM3101	yggT	putative integral membrane protein	**-0.52**	0.27182	**-0.33**	0.42246	**-1.97**	0.00229
STM3101	yggT	putative integral membrane protein	**0.34**	0.80777	**-0.24**	0.51970	**-2.93**	0.00026
STM3102	yggU	hypothetical protein STM3102	**-1.56**	0.03465	**-0.16**	0.63673	**-1.57**	0.03839
STM3102	yggU	hypothetical protein STM3102	**-0.35**	0.62320	**-0.14**	0.69958	**-1.95**	0.01284
STM3103	yggV	putative deoxyribonucleotide triphosphate pyrophosphatase	**-1.79**	0.02123	**-1.02**	0.00547	**-3.42**	0.00139
STM3103	yggV	putative deoxyribonucleotide triphosphate pyrophosphatase	**-1.19**	0.27616	**-1.18**	0.01295	**-4.05**	0.00007
STM3104	yggW	coproporphyrinogen III oxidase	**-0.90**	0.43436	**-0.32**	0.25079	**-1.03**	0.26747
STM3104	yggW	coproporphyrinogen III oxidase	**-1.00**	0.04803	**-0.97**	0.02179	**-0.87**	0.09779
STM3105	yggM	putative periplasmic protein	**-0.98**	0.53249	**0.42**	0.18688	**1.99**	0.00093
STM3105	yggM	putative periplasmic protein	**-0.89**	0.61862	**0.12**	0.83985	**2.50**	0.00120
STM3106	ansB	periplasmic L-asparaginase II	**2.14**	0.29889	**0.19**	0.68961	**1.63**	0.00754
STM3106	ansB	periplasmic L-asparaginase II	**3.83**	0.00546	**0.06**	0.88895	**2.98**	0.00056
STM3107	yggN	putative periplasmic protein	**-0.40**	0.59931	**0.65**	0.10986	**0.96**	0.13110
STM3107	yggN	putative periplasmic protein	**-0.47**	0.45245	**0.51**	0.09768	**-0.04**	0.91391
STM3108	yggL	putative cytoplasmic protein	**-3.09**	0.01040	**-0.33**	0.28705	**-1.98**	0.00075
STM3108	yggL	putative cytoplasmic protein	**-1.48**	0.02526	**-0.39**	0.27884	**-1.83**	0.00132
STM3109	yggH	tRNA (guanine-N(7)-)-methyltransferase	**-2.47**	0.01005	**-0.47**	0.16885	**-1.84**	0.00106
STM3109	yggH	tRNA (guanine-N(7)-)-methyltransferase	**-1.86**	0.13657	**-0.38**	0.20826	**-1.30**	0.00708
STM3110	mutY	adenine DNA glycosylase	**0.00**	0.99985	**-2.31**	0.00083	**-0.38**	0.47193
STM3110	mutY	adenine DNA glycosylase	**-0.21**	0.72794	**-2.99**	0.00032	**0.23**	0.83538
STM3111	yggX	hypothetical protein STM3111	**-1.39**	0.02908	**0.39**	0.29616	**-1.46**	0.00827
STM3111	yggX	hypothetical protein STM3111	**-0.46**	0.39064	**0.33**	0.30610	**-0.71**	0.07451
STM3112	mltC	membrane-bound lytic murein transglycosylase C	**-1.13**	0.06424	**-1.19**	0.00567	**1.20**	0.08843
STM3112	mltC	membrane-bound lytic murein transglycosylase C	**0.02**	0.97285	**-0.91**	0.05082	**-0.37**	0.41205
STM3113	nupG	nucleoside transport	**-0.40**	0.51096	**-1.63**	0.00072	**-1.33**	0.00841
STM3113	nupG	nucleoside transport	**0.36**	0.54043	**-1.90**	0.00377	**-0.81**	0.52739
STM3114	speC	ornithine decarboxylase isozyme	**-0.68**	0.13925	**-0.28**	0.35209	**0.19**	0.66720
STM3114	speC	ornithine decarboxylase isozyme	**1.35**	0.32833	**-0.83**	0.10070	**1.17**	0.03582
STM3115	yqgA	putative inner membrane protein	**0.28**	0.55698	**-0.55**	0.11803	**-1.21**	0.00938
STM3115	yqgA	putative inner membrane protein	**0.87**	0.24298	**-0.51**	0.10968	**0.44**	0.63830
STM3116	pheV	STM3116	**-1.39**	0.02747	**-0.93**	0.11203	**4.24**	0.00006
STM3116	pheV	STM3116	**-1.62**	0.02803	**-1.62**	0.00677	**4.47**	0.00007
STM3118	STM3118	putative acetyl-CoA hydrolase	**-0.57**	0.21439	**0.67**	0.24385	**-0.13**	0.76234
STM3118	STM3118	putative acetyl-CoA hydrolase	**1.28**	0.06677	**0.56**	0.06102	**1.07**	0.04516
STM3119	STM3119	putative monoamine oxidase	**0.39**	0.49636	**1.22**	0.03210	**0.11**	0.87950
STM3119	STM3119	putative monoamine oxidase	**0.17**	0.87036	**-0.19**	0.67564	**-1.99**	0.00802
STM3120	STM3120	putative transcriptional regulator	**-0.24**	0.62903	**0.64**	0.06726	**0.49**	0.22373
STM3120	STM3120	putative transcriptional regulator	**-0.45**	0.50245	**-0.44**	0.29461	**-0.86**	0.19078
STM3121	STM3121	putative transcriptional regulator	**2.96**	0.01645	**-0.77**	0.17482	**0.13**	0.81799
STM3121	STM3121	putative transcriptional regulator	**1.85**	0.32468	**-0.77**	0.02864	**0.01**	0.99350
STM3122	STM3122	putative arylsulfatase	**-0.71**	0.33541	**-0.25**	0.45384	**-0.72**	0.11208
STM3122	STM3122	putative arylsulfatase	**0.53**	0.42475	**0.27**	0.33114	**1.78**	0.08061
STM3123	STM3123	putative arylsulfatase regulator	**0.37**	0.40908	**0.04**	0.92755	**-0.26**	0.53567
STM3123	STM3123	putative arylsulfatase regulator	**1.21**	0.14071	**-0.46**	0.42089	**1.12**	0.14117
STM3124	STM3124	putative response regulator	**0.18**	0.81970	**-0.53**	0.16805	**0.33**	0.71302
STM3124	STM3124	putative response regulator	**0.35**	0.49733	**-0.58**	0.21987	**-0.31**	0.55579
STM3125	STM3125	putative cytoplasmic protein	**0.90**	0.11460	**-0.19**	0.79256	**0.70**	0.26420
STM3125	STM3125	putative cytoplasmic protein	**1.23**	0.04295	**-0.08**	0.81944	**0.24**	0.73382
STM3126	STM3126	putative amino acid transporter	**1.88**	0.01950	**1.14**	0.05056	**2.51**	0.00090
STM3126	STM3126	putative amino acid transporter	**2.00**	0.07951	**0.72**	0.21002	**2.44**	0.00023
STM3127	STM3127	putative cytoplasmic protein	**-0.76**	0.26824	**0.37**	0.37677	**0.15**	0.85872
STM3127	STM3127	putative cytoplasmic protein	**-0.51**	0.28189	**-0.18**	0.61509	**0.13**	0.82517
STM3128	STM3128	putative oxidoreductase	**0.85**	0.09625	**0.95**	0.04433	**1.58**	0.00297
STM3128	STM3128	putative oxidoreductase	**-1.64**	0.03512	**0.57**	0.22967	**-0.35**	0.72626
STM3129	STM3129	putative NAD-dependent aldehyde dehydrogenase	**-0.31**	0.74567	**-0.34**	0.48409	**-0.30**	0.66289
STM3129	STM3129	putative NAD-dependent aldehyde dehydrogenase	**-0.15**	0.83951	**-0.15**	0.67282	**-0.49**	0.42191
STM3131	STM3131	putative cytoplasmic protein	**1.74**	0.03017	**-0.21**	0.57420	**0.16**	0.71302
STM3131	STM3131	putative cytoplasmic protein	**2.38**	0.03315	**-0.03**	0.93155	**0.74**	0.31934
STM3132	STM3132	putative xylanase/chitin deacetylase	**0.06**	0.88925	**-1.75**	0.04386	**0.04**	0.92086
STM3132	STM3132	putative xylanase/chitin deacetylase	**0.70**	0.14114	**-1.13**	0.07382	**0.41**	0.33075
STM3133	STM3133	putative amidohydrolase	**2.33**	0.01669	**0.12**	0.89183	**4.01**	0.00020
STM3133	STM3133	putative amidohydrolase	**2.66**	0.00720	**0.86**	0.15021	**3.21**	0.00229
STM3134	STM3134	putative permease	**0.77**	0.21535	**0.36**	0.40846	**-0.36**	0.51519
STM3134	STM3134	putative permease	**1.96**	0.01572	**1.20**	0.20341	**0.49**	0.45638
STM3135	STM3135	mannonate dehydratase	**0.22**	0.74749	**0.28**	0.45291	**0.32**	0.52165
STM3135	STM3135	mannonate dehydratase	**1.77**	0.01064	**1.18**	0.01434	**0.83**	0.04716
STM3136	STM3136	putative D-mannonate oxidoreductase	**0.41**	0.44795	**0.93**	0.06329	**0.10**	0.85570
STM3136	STM3136	putative D-mannonate oxidoreductase	**1.89**	0.02344	**0.88**	0.02982	**1.43**	0.01573

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM3137	STM3137	uronate isomerase	**-0.04**	0.92542	**0.28**	0.40380	**-1.03**	0.03292
STM3137	STM3137	uronate isomerase	**0.10**	0.87586	**0.30**	0.36054	**-0.01**	0.97853
STM3138	STM3138	putative methyl-accepting chemotaxis protein	**-0.30**	0.65495	**-0.19**	0.58497	**-0.92**	0.07300
STM3138	STM3138	putative methyl-accepting chemotaxis protein	**0.90**	0.09689	**-0.24**	0.48875	**-0.19**	0.64021
STM3139	gsp	glutathionylspermidine synthetase/glutathionylspermidine	**1.50**	0.02339	**-1.79**	0.00182	**-0.37**	0.60531
STM3139	gsp	glutathionylspermidine synthetase/glutathionylspermidine	**1.63**	0.07547	**-2.01**	0.00145	**0.64**	0.28054
STM3140	yghU	putative glutathione S-transferase	**0.29**	0.66192	**0.63**	0.13486	**-0.06**	0.91420
STM3140	yghU	putative glutathione S-transferase	**1.38**	0.06565	**0.83**	0.02981	**0.84**	0.04513
STM3141	STM3141	hypothetical protein STM3141	**0.45**	0.28946	**1.31**	0.00171	**0.36**	0.35984
STM3141	STM3141	hypothetical protein STM3141	**1.31**	0.04295	**1.42**	0.05398	**1.66**	0.00581
STM3142	STM3142	putative periplasmic ferrichrome-binding protein	**0.11**	0.83464	**1.68**	0.00244	**-0.22**	0.76913
STM3142	STM3142	putative periplasmic ferrichrome-binding protein	**1.61**	0.03715	**1.74**	0.00071	**0.96**	0.05880
STM3143	hybG	chaperone-like protein	**0.14**	0.75567	**-0.13**	0.66912	**-1.27**	0.10786
STM3143	hybG	chaperone-like protein	**1.20**	0.06503	**-0.56**	0.14867	**-0.55**	0.42608
STM3144	hypA	hydrogenase nickel incorporation protein	**-1.57**	0.01955	**-0.41**	0.29806	**-0.81**	0.04874
STM3144	hypA	hydrogenase nickel incorporation protein	**0.09**	0.95833	**-1.14**	0.01326	**-1.09**	0.02219
STM3145	hybE	putative hydrogenase	**-1.30**	0.07223	**-1.13**	0.01552	**-1.50**	0.00234
STM3145	hybE	putative hydrogenase	**-1.18**	0.04517	**-1.63**	0.00171	**-1.96**	0.00308
STM3146	hybD	putative hydrogenase-2 processing element	**-1.23**	0.03088	**-0.80**	0.02258	**-1.50**	0.06175
STM3146	hybD	putative hydrogenase-2 processing element	**-0.72**	0.24680	**-1.16**	0.00910	**-1.20**	0.08851
STM3147	hybC	hydrogenase-2 large subunit	**-0.15**	0.77479	**-1.51**	0.00157	**-0.87**	0.35541
STM3147	hybC	hydrogenase-2 large subunit	**-0.34**	0.54425	**-1.49**	0.00250	**-0.23**	0.72522
STM3148	hybB	putative chaperone	**0.00**	0.99687	**-0.68**	0.06274	**-0.76**	0.04912
STM3148	hybB	putative chaperone	**0.45**	0.30002	**-0.96**	0.03657	**0.06**	0.92925
STM3149	hybA	putative hydrogenase-2 component	**-0.71**	0.13387	**-0.81**	0.08483	**-1.42**	0.00415
STM3149	hybA	putative hydrogenase-2 component	**-0.68**	0.66289	**-0.81**	0.03205	**-0.67**	0.32113
STM3150	hypO	putative Ni/Fe hydrogenase small subunit	**0.51**	0.51519	**-1.00**	0.02286	**-1.22**	0.04287
STM3150	hypO	putative Ni/Fe hydrogenase small subunit	**0.14**	0.76412	**-1.30**	0.00958	**-0.46**	0.32650
STM3151	yghW	putative cytoplasmic protein	**-1.98**	0.00825	**-2.34**	0.01701	**-1.84**	0.04653
STM3151	yghW	putative cytoplasmic protein	**-2.00**	0.01104	**-1.31**	0.00882	**-2.01**	0.01356
STM3152	STM3152	putative methyl-accepting chemotaxis protein	**-2.36**	0.00694	**-2.51**	0.00172	**-1.71**	0.00549
STM3152	STM3152	putative methyl-accepting chemotaxis protein	**-1.82**	0.01275	**-3.02**	0.00008	**-1.99**	0.04098
STM3153	yqhA	hypothetical protein STM3153	**-1.52**	0.01496	**-0.65**	0.09372	**-1.27**	0.08475
STM3153	yqhA	hypothetical protein STM3153	**-0.75**	0.24608	**-0.54**	0.09583	**-1.24**	0.02134
STM3154	STM3154	putative ATP-dependent RNA helicase-like protein	**-0.63**	0.49544	**0.16**	0.57666	**-1.18**	0.01114
STM3154	STM3154	putative ATP-dependent RNA helicase-like protein	**0.34**	0.61745	**0.37**	0.18646	**-0.25**	0.61170
STM3155	STM3155	putative cytoplasmic protein	**1.24**	0.04691	**-0.11**	0.83656	**1.18**	0.02696
STM3155	STM3155	putative cytoplasmic protein	**1.83**	0.02124	**-1.21**	0.01405	**0.78**	0.28735
STM3156	STM3156	putative cytoplasmic protein	**-0.84**	0.11528	**-1.31**	0.00238	**-0.20**	0.64032
STM3156	STM3156	putative cytoplasmic protein	**-0.57**	0.23001	**-1.44**	0.00379	**0.39**	0.38168
STM3157	yghA	oxidoreductase	**1.10**	0.10156	**0.11**	0.73817	**1.62**	0.00641
STM3157	yghA	oxidoreductase	**1.50**	0.03038	**0.32**	0.40847	**1.99**	0.00155
STM3158	exbD	energy transduction protein	**-1.53**	0.07209	**0.94**	0.00790	**0.02**	0.97431
STM3158	exbD	energy transduction protein	**0.02**	0.97707	**0.76**	0.02988	**0.44**	0.26670
STM3159	exbB	energy transduction protein	**-0.68**	0.14494	**1.04**	0.00793	**-1.67**	0.00361
STM3159	exbB	energy transduction protein	**0.44**	0.53036	**1.50**	0.00225	**-1.18**	0.02477
STM3160	STM3160	putative inner membrane protein	**-1.01**	0.04986	**0.59**	0.07663	**0.99**	0.02618
STM3160	STM3160	putative inner membrane protein	**-0.80**	0.10063	**0.70**	0.02749	**-0.64**	0.18019
STM3161	metC	cystathionine beta-lyase	**-0.32**	0.52587	**0.05**	0.88634	**-0.66**	0.07383
STM3161	metC	cystathionine beta-lyase	**0.49**	0.47667	**0.11**	0.80391	**0.68**	0.12503
STM3162	yghB	hypothetical protein STM3162	**0.62**	0.65614	**0.36**	0.20665	**-0.45**	0.38422
STM3162	yghB	hypothetical protein STM3162	**0.89**	0.06739	**-0.17**	0.55336	**-0.25**	0.56047
STM3163	yqhC	putative transcriptional regulator	**0.86**	0.26183	**0.13**	0.70884	**0.06**	0.92981
STM3163	yqhC	putative transcriptional regulator	**0.52**	0.27250	**0.62**	0.07806	**-0.58**	0.15256
STM3164	yqhD	putative alcohol dehydrogenase	**-1.13**	0.04718	**-1.16**	0.00940	**-0.70**	0.09275
STM3164	yqhD	putative alcohol dehydrogenase	**-0.36**	0.50560	**-1.52**	0.00095	**0.59**	0.10738
STM3165	yqhE	2,5-diketo-D-gluconate reductase A	**-0.38**	0.41720	**-0.44**	0.17603	**1.14**	0.00961
STM3165	yqhE	2,5-diketo-D-gluconate reductase A	**-0.14**	0.76966	**-1.12**	0.14161	**2.17**	0.00129
STM3166,S	STM3166,S	putative cation transporter	**0.17**	0.84418	**-1.51**	0.02186	**-0.42**	0.48230
STM3166,S	STM3166,S	putative cation transporter	**0.96**	0.06850	**-0.45**	0.22248	**0.31**	0.42747
STM3167	STM3167	putative diadenosine tetraphosphatehydrolase	**-0.28**	0.65674	**0.47**	0.32679	**-0.56**	0.35807
STM3167	STM3167	putative diadenosine tetraphosphatehydrolase	**0.34**	0.77034	**0.57**	0.11518	**0.65**	0.24596
STM3168	ygiR	hypothetical protein STM3168	**-1.43**	0.10241	**-2.20**	0.00107	**-1.27**	0.08607
STM3168	ygiR	hypothetical protein STM3168	**-0.33**	0.64949	**-3.95**	0.00019	**-1.57**	0.08096
STM3169	STM3169	putative periplasmic dicarboxylate-binding protein	**-0.81**	0.23420	**-0.64**	0.24824	**-0.47**	0.42388
STM3169	STM3169	putative periplasmic dicarboxylate-binding protein	**0.82**	0.15801	**-0.11**	0.79566	**1.64**	0.00571
STM3170	STM3170	putative inner membrane protein	**0.77**	0.48579	**-0.78**	0.06175	**0.75**	0.46889
STM3170	STM3170	putative inner membrane protein	**3.02**	0.01546	**-0.64**	0.08366	**1.37**	0.17531
STM3171	ygiK	putative transporter	**-0.33**	0.47552	**-1.22**	0.00355	**0.02**	0.96049
STM3171	ygiK	putative transporter	**0.03**	0.96628	**-1.21**	0.00561	**0.14**	0.81388

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM3172	sufI	suppressor of ftsI	**-1.20**	0.03417	**-0.88**	0.02061	**-1.56**	0.00219
STM3172	sufI	suppressor of ftsI	**-0.67**	0.16236	**-0.65**	0.09673	**-1.46**	0.00572
STM3173	plsC	1-acyl-sn-glycerol-3-phosphate acyltransferase	**0.77**	0.18366	**-0.98**	0.01328	**0.29**	0.58065
STM3173	plsC	1-acyl-sn-glycerol-3-phosphate acyltransferase	**0.72**	0.19152	**-0.72**	0.13481	**0.45**	0.20440
STM3174	parC	DNA topoisomerase IV subunit A	**-3.12**	0.00541	**-2.19**	0.00013	**-2.96**	0.00370
STM3174	parC	DNA topoisomerase IV subunit A	**-0.94**	0.06146	**-1.60**	0.00665	**-2.56**	0.00018
STM3175	STM3175	putative regulatory protein	**-0.42**	0.57498	**-1.26**	0.00325	**-1.40**	0.00724
STM3175	STM3175	putative regulatory protein	**0.01**	0.99163	**-0.97**	0.01183	**-1.55**	0.00737
STM3176	ygiW	putative outer membrane protein	**-0.69**	0.43457	**0.40**	0.17043	**0.08**	0.84348
STM3176	ygiW	putative outer membrane protein	**-0.66**	0.54930	**0.09**	0.80184	**0.68**	0.11389
STM3177	ygiX	putative transcriptional regulator	**-0.81**	0.27101	**-0.38**	0.25997	**0.16**	0.78781
STM3177	ygiX	putative transcriptional regulator	**-1.49**	0.12384	**-0.75**	0.06148	**-1.21**	0.15116
STM3178	ygiY	putative sensor histidine kinase	**-1.11**	0.11230	**0.26**	0.46308	**0.14**	0.81045
STM3178	ygiY	putative sensor histidine kinase	**0.36**	0.40214	**-0.36**	0.29368	**-0.04**	0.93507
STM3179	mdaB	NADPH-specific quinone oxidoreductase	**-2.22**	0.01348	**-0.13**	0.69378	**-1.00**	0.02689
STM3179	mdaB	NADPH-specific quinone oxidoreductase	**-2.18**	0.00876	**-0.82**	0.02008	**-0.32**	0.48084
STM3180	ygiN	putative cytoplasmic protein	**-1.35**	0.04605	**-0.34**	0.40080	**-1.46**	0.02630
STM3180	ygiN	putative cytoplasmic protein	**-0.26**	0.61848	**-0.42**	0.22949	**-2.36**	0.05706
STM3181	parE	DNA topoisomerase IV subunit B	**-1.08**	0.06236	**-0.85**	0.02981	**-1.37**	0.06464
STM3181	parE	DNA topoisomerase IV subunit B	**0.42**	0.46541	**-0.73**	0.03166	**-0.65**	0.16686
STM3182	yqiA	putative esterase	**-2.25**	0.00884	**-0.71**	0.05932	**-1.68**	0.00476
STM3182	yqiA	putative esterase	**-1.63**	0.01572	**-0.60**	0.08787	**-1.88**	0.00673
STM3183	icc	cyclic 3',5'-adenosine monophosphate phosphodiesterase	**-2.01**	0.01083	**-0.62**	0.12402	**-3.15**	0.00014
STM3183	icc	cyclic 3',5'-adenosine monophosphate phosphodiesterase	**-1.98**	0.01835	**-0.74**	0.06740	**-2.75**	0.10925
STM3184	yqiB	putative cytoplasmic protein	**-1.92**	0.01266	**-0.15**	0.61522	**-0.82**	0.17890
STM3184	yqiB	putative cytoplasmic protein	**-0.48**	0.41696	**0.22**	0.54396	**-1.15**	0.01906
STM3185	yqiE	ADP-ribose pyrophosphatase	**-0.29**	0.62664	**-0.10**	0.81517	**-1.22**	0.02854
STM3185	yqiE	ADP-ribose pyrophosphatase	**0.17**	0.79451	**0.16**	0.63784	**-0.10**	0.87445
STM3186	tolC	outer membrane channel precursor protein	**0.77**	0.62495	**0.00**	0.99871	**-0.40**	0.34361
STM3186	tolC	outer membrane channel precursor protein	**0.89**	0.41890	**0.43**	0.22843	**-0.44**	0.20795
STM3187	ygiB	putative inner membrane protein	**-2.71**	0.01186	**0.21**	0.51090	**0.35**	0.35207
STM3187	ygiB	putative inner membrane protein	**-1.12**	0.07232	**-0.06**	0.85643	**0.84**	0.04553
STM3188	ygiC	putative glutathionylspermidine synthase	**-0.64**	0.17299	**0.08**	0.80911	**-0.57**	0.13782
STM3188	ygiC	putative glutathionylspermidine synthase	**1.18**	0.04933	**0.21**	0.55292	**0.93**	0.16687
STM3189	ygiD	putative cytoplasmic protein	**0.77**	0.17366	**0.47**	0.14165	**0.50**	0.18434
STM3189	ygiD	putative cytoplasmic protein	**1.11**	0.11348	**-0.31**	0.60931	**1.16**	0.01934
STM3190	ygiE	zinc transporter ZupT	**-0.88**	0.16362	**0.18**	0.57229	**-0.82**	0.03886
STM3190	ygiE	zinc transporter ZupT	**0.66**	0.39131	**0.33**	0.32309	**0.08**	0.85148
STM3191	STM3191	putative arylsulfate sulfotransferase	**0.60**	0.21730	**0.44**	0.25895	**0.17**	0.76819
STM3191	STM3191	putative arylsulfate sulfotransferase	**2.33**	0.01536	**0.24**	0.41746	**0.13**	0.88341
STM3193	STM3193	putative disulfide bond formation protein	**-0.64**	0.14485	**0.50**	0.14681	**0.47**	0.34784
STM3193	STM3193	putative disulfide bond formation protein	**0.19**	0.91091	**-0.24**	0.46635	**0.59**	0.22776
STM3194	STM3194	putative disulfide oxidoreductase	**-0.66**	0.25631	**-1.03**	0.02677	**-1.10**	0.03331
STM3194	STM3194	putative disulfide oxidoreductase	**0.20**	0.80928	**-1.04**	0.01597	**1.52**	0.05741
STM3195	ribB	3,4-dihydroxy-2-butanone 4-phosphate synthase	**-0.98**	0.08236	**-0.14**	0.70316	**0.46**	0.33776
STM3195	ribB	3,4-dihydroxy-2-butanone 4-phosphate synthase	**-1.23**	0.05179	**-0.48**	0.16673	**0.25**	0.78851
STM3196,S	yqiC	putative cytoplasmic protein	**0.53**	0.76383	**0.93**	0.05037	**-0.04**	0.95069
STM3196,S	yqiC	putative cytoplasmic protein	**1.68**	0.30019	**0.71**	0.02857	**1.20**	0.03347
STM3197	glgS	glycogen synthesis protein GlgS	**-0.47**	0.36389	**0.05**	0.87851	**-0.20**	0.62892
STM3197	glgS	glycogen synthesis protein GlgS	**1.74**	0.10150	**-0.36**	0.28431	**1.11**	0.01726
STM3198	STM3198	putative inner membrane protein	**-0.71**	0.14009	**-0.33**	0.40080	**-1.07**	0.02693
STM3198	STM3198	putative inner membrane protein	**1.16**	0.03295	**-0.92**	0.13103	**1.10**	0.02626
STM3199	yqiK	hypothetical protein STM3199	**-2.23**	0.02407	**-0.76**	0.02064	**-0.93**	0.03749
STM3199	yqiK	hypothetical protein STM3199	**-1.70**	0.13359	**-0.78**	0.03020	**-1.37**	0.01702
STM3200	rfaE	putative ADP-L-glycero-D-manno-heptose synthase	**-0.91**	0.06069	**-0.59**	0.06749	**-0.62**	0.30659
STM3200	rfaE	putative ADP-L-glycero-D-manno-heptose synthase	**-1.16**	0.06618	**-1.03**	0.00591	**-0.96**	0.05277
STM3201	glnE	adenylyl transferase for glutamine synthetase	**-1.46**	0.14543	**-1.04**	0.02410	**-1.38**	0.02765
STM3201	glnE	adenylyl transferase for glutamine synthetase	**-1.16**	0.17459	**-1.02**	0.02041	**-1.51**	0.00654
STM3202	ygiF	putative cytoplasmic protein	**-1.22**	0.04979	**-0.68**	0.05562	**-1.43**	0.01957
STM3202	ygiF	putative cytoplasmic protein	**1.30**	0.08166	**-1.01**	0.01012	**-0.40**	0.30309
STM3203	ygiM	hypothetical protein STM3203	**0.51**	0.22891	**0.48**	0.17025	**-1.31**	0.00536
STM3203	ygiM	hypothetical protein STM3203	**0.89**	0.10248	**0.18**	0.53139	**-0.52**	0.27866
STM3204	cca	tRNA nucleotidyl transferase	**-0.44**	0.40706	**-0.18**	0.81645	**-0.23**	0.71037
STM3204	cca	tRNA nucleotidyl transferase	**-0.33**	0.53333	**-0.26**	0.34046	**-0.39**	0.34770
STM3205	uppP	undecaprenyl pyrophosphate phosphatase	**0.05**	0.94799	**-0.50**	0.24548	**-0.09**	0.87188
STM3205	uppP	undecaprenyl pyrophosphate phosphatase	**0.56**	0.37183	**-0.70**	0.17343	**0.76**	0.57927
STM3206	folB	dihydroneopterin aldolase/dihydroneopterin triphosphate	**-0.70**	0.15969	**-1.28**	0.00258	**-1.29**	0.01107
STM3206	folB	dihydroneopterin aldolase/dihydroneopterin triphosphate	**0.09**	0.85581	**-1.10**	0.00802	**-2.19**	0.00040
STM3207	ygiH	hypothetical protein STM3207	**-0.32**	0.68193	**0.09**	0.77806	**1.10**	0.01356
STM3207	ygiH	hypothetical protein STM3207	**0.44**	0.43987	**-0.23**	0.39124	**1.15**	0.01243

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM3208	gcp	putative O-sialoglycoprotein endopeptidase	**-0.83**	0.30712	**-0.60**	0.09770	**-1.40**	0.00692
STM3208	gcp	putative O-sialoglycoprotein endopeptidase	**0.10**	0.92458	**-0.98**	0.00839	**0.61**	0.21007
STM3209	rpsU	30S ribosomal protein S21	**-3.12**	0.00884	**-1.11**	0.01920	**-4.13**	0.00009
STM3209	rpsU	30S ribosomal protein S21	**-2.41**	0.00753	**-1.15**	0.00609	**-3.91**	0.00009
STM3210	dnaG	DNA primase	**-0.76**	0.09268	**-0.33**	0.36977	**-1.04**	0.01984
STM3210	dnaG	DNA primase	**-0.35**	0.51894	**0.25**	0.40003	**-0.53**	0.28459
STM3211,S	rpoD	RNA polymerase sigma factor	**-0.21**	0.63074	**0.61**	0.08780	**-0.85**	0.05027
STM3211,S	rpoD	RNA polymerase sigma factor	**0.49**	0.34050	**0.81**	0.03092	**-0.31**	0.46166
STM3212	mug	G/U mismatch-specific DNA glycosylase	**0.22**	0.78992	**0.74**	0.02430	**1.49**	0.00564
STM3212	mug	G/U mismatch-specific DNA glycosylase	**0.35**	0.51087	**0.87**	0.01329	**1.23**	0.00574
STM3213	ileX	STM3213	**-0.51**	0.36065	**-1.14**	0.00536	**0.60**	0.36955
STM3213	ileX	STM3213	**-1.10**	0.36108	**-1.08**	0.00437	**0.72**	0.31519
STM3214	yqjH	putative transporter	**-1.00**	0.05595	**-0.15**	0.67352	**-0.83**	0.04129
STM3214	yqjH	putative transporter	**-0.01**	0.97919	**-0.19**	0.51012	**0.03**	0.96438
STM3215	yqjI	putative transcriptional regulator	**-0.94**	0.06553	**-1.44**	0.00239	**-2.08**	0.00100
STM3215	yqjI	putative transcriptional regulator	**-0.10**	0.89154	**-1.43**	0.00130	**-1.56**	0.00503
STM3216	STM3216	putative methyl-accepting chemotaxis protein	**-1.83**	0.07348	**-1.91**	0.00592	**-0.39**	0.70170
STM3216	STM3216	putative methyl-accepting chemotaxis protein	**2.27**	0.28018	**-2.36**	0.00643	**-0.18**	0.82611
STM3217	aer	aerotaxis sensor receptor	**-1.60**	0.01817	**-3.33**	0.00102	**-2.03**	0.00408
STM3217	aer	aerotaxis sensor receptor	**-1.67**	0.03504	**-4.38**	0.00008	**-2.61**	0.01163
STM3218	oat	putative acetylornithine aminotransferase	**0.79**	0.10559	**0.16**	0.58109	**2.65**	0.00022
STM3218	oat	putative acetylornithine aminotransferase	**0.05**	0.93261	**0.31**	0.41220	**2.30**	0.00236
STM3219	fadH	2,4-dieonyl-CoA reductase	**-0.18**	0.67365	**-0.42**	0.31257	**-2.33**	0.00266
STM3219	fadH	2,4-dieonyl-CoA reductase	**0.76**	0.30144	**-1.03**	0.09811	**-0.65**	0.12113
STM3220	ygjO	putative methyltransferase	**-0.85**	0.07935	**-0.43**	0.23992	**-1.14**	0.02103
STM3220	ygjO	putative methyltransferase	**0.19**	0.64833	**-0.64**	0.06478	**-0.51**	0.22654
STM3221	ygjP	putative metal-dependent hydrolase	**-0.90**	0.11370	**-0.85**	0.02066	**-1.48**	0.00593
STM3221	ygjP	putative metal-dependent hydrolase	**0.50**	0.30886	**-0.36**	0.32375	**-0.41**	0.25850
STM3222	ygjQ	putative integral membrane protein	**0.20**	0.67951	**-0.89**	0.05487	**-0.60**	0.15976
STM3222	ygjQ	putative integral membrane protein	**1.63**	0.06274	**-1.50**	0.02645	**0.75**	0.28004
STM3223	ygjR	putative dehydrogenase	**0.48**	0.56791	**0.11**	0.73846	**-0.19**	0.75741
STM3223	ygjR	putative dehydrogenase	**1.21**	0.11173	**0.61**	0.11564	**1.74**	0.04639
STM3224	ygjT	putative tellurite resistance protein	**0.53**	0.37920	**3.03**	0.00032	**0.36**	0.45317
STM3224	ygjT	putative tellurite resistance protein	**0.29**	0.71798	**3.02**	0.00021	**1.27**	0.03328
STM3225	ygjU	putative dicarboxylate permease	**-0.69**	0.14762	**0.16**	0.59904	**-0.01**	0.98279
STM3225	ygjU	putative dicarboxylate permease	**-0.96**	0.08229	**0.71**	0.03130	**-0.02**	0.97030
STM3226	yqjA	hypothetical protein STM3226	**-1.03**	0.27496	**-1.21**	0.00560	**-1.28**	0.01123
STM3226	yqjA	hypothetical protein STM3226	**0.89**	0.29339	**-1.22**	0.00873	**-0.36**	0.40198
STM3227	yqjB	putative outer membrane protein	**-1.25**	0.03392	**-0.11**	0.79139	**-0.13**	0.77101
STM3227	yqjB	putative outer membrane protein	**0.18**	0.78824	**-0.36**	0.18816	**0.47**	0.20093
STM3228	yqjC	putative periplasmic protein	**0.65**	0.15162	**2.00**	0.00082	**3.55**	0.00009
STM3228	yqjC	putative periplasmic protein	**0.91**	0.16124	**2.01**	0.00028	**4.17**	0.00016
STM3229	yqjD	putative inner membrane protein	**-0.68**	0.26249	**2.11**	0.00032	**1.15**	0.02265
STM3229	yqjD	putative inner membrane protein	**0.41**	0.63739	**2.14**	0.00055	**1.95**	0.00139
STM3230	yqjE	putative inner membrane protein	**-1.43**	0.02585	**2.14**	0.00017	**0.22**	0.54971
STM3230	yqjE	putative inner membrane protein	**-0.81**	0.20026	**2.46**	0.00024	**0.91**	0.09228
STM3231	yqjK	putative inner membrane protein	**-0.94**	0.09874	**2.47**	0.00036	**0.53**	0.20093
STM3231	yqjK	putative inner membrane protein	**-0.32**	0.58374	**2.75**	0.00011	**0.42**	0.25525
STM3232	yqjF	hypothetical protein STM3232	**-0.43**	0.53986	**0.12**	0.67735	**0.27**	0.51836
STM3232	yqjF	hypothetical protein STM3232	**3.40**	0.02501	**-0.10**	0.76817	**1.69**	0.02423
STM3233	yqjG	putative glutathione S-transferase	**0.07**	0.87342	**0.24**	0.57107	**1.15**	0.02967
STM3233	yqjG	putative glutathione S-transferase	**-0.32**	0.54856	**-0.27**	0.35311	**1.39**	0.00625
STM3234	yhaH	putative inner membrane protein	**-1.34**	0.05566	**-0.35**	0.71583	**-0.44**	0.36546
STM3234	yhaH	putative inner membrane protein	**-0.51**	0.34022	**-0.68**	0.03640	**-1.03**	0.03005
STM3235	yhaJ	putative transcriptional regulator	**-0.42**	0.46152	**0.98**	0.01594	**0.46**	0.55272
STM3235	yhaJ	putative transcriptional regulator	**0.76**	0.15238	**0.73**	0.02104	**0.32**	0.45236
STM3236	yhaK	putative cytoplasmic protein	**0.27**	0.78455	**-0.11**	0.78140	**-0.67**	0.17263
STM3236	yhaK	putative cytoplasmic protein	**0.89**	0.17766	**0.15**	0.72482	**0.33**	0.57927
STM3237	yhaL	putative cytoplasmic protein	**1.99**	0.02436	**0.13**	0.74425	**0.97**	0.04335
STM3237	yhaL	putative cytoplasmic protein	**2.05**	0.01972	**-0.07**	0.89974	**1.62**	0.01132
STM3238	yhaN	putative inner membrane protein	**-0.44**	0.29238	**0.03**	0.93550	**-1.02**	0.04685
STM3238	yhaN	putative inner membrane protein	**-0.17**	0.72602	**-0.48**	0.12844	**-0.66**	0.33018
STM3239	yhaO	putative transport protein	**-0.94**	0.11453	**-0.76**	0.08038	**-1.42**	0.01278
STM3239	yhaO	putative transport protein	**1.63**	0.08799	**-1.24**	0.00387	**0.38**	0.38502
STM3240	tdcG	L-serine deaminase	**-0.32**	0.65088	**-1.30**	0.00999	**-0.36**	0.54635
STM3240	tdcG	L-serine deaminase	**1.45**	0.21947	**-1.27**	0.00946	**-1.25**	0.06798
STM3241	tdcE	pyruvate formate-lyase 4/2-ketobutyrate formate-lyase	**-1.12**	0.07186	**-0.75**	0.17278	**-0.20**	0.80590
STM3241	tdcE	pyruvate formate-lyase 4/2-ketobutyrate formate-lyase	**-0.26**	0.86747	**-0.88**	0.01938	**0.12**	0.84076
STM3242	tdcD	acetate/propionate kinase	**0.36**	0.41018	**-1.13**	0.02837	**0.11**	0.85828
STM3242	tdcD	acetate/propionate kinase	**1.00**	0.11259	**-0.53**	0.23101	**0.26**	0.68588

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM3243	tdcC	L-threonine/L-serine permease	**0.59**	0.62738	**-0.17**	0.78795	**0.91**	0.19341
STM3243	tdcC	L-threonine/L-serine permease	**0.67**	0.33831	**0.16**	0.75820	**0.06**	0.96274
STM3244	tdcB	threonine dehydratase	**0.32**	0.46345	**-0.06**	0.86983	**0.11**	0.77399
STM3244	tdcB	threonine dehydratase	**1.10**	0.12655	**-0.36**	0.65756	**-0.11**	0.90484
STM3245	tdcA	transcriptional activator	**-0.35**	0.63432	**-1.59**	0.00471	**-1.15**	0.04696
STM3245	tdcA	transcriptional activator	**1.05**	0.06769	**-0.58**	0.47619	**0.07**	0.94781
STM3247	garK	glycerate kinase	**0.53**	0.28930	**1.49**	0.00462	**-1.12**	0.02578
STM3247	garK	glycerate kinase	**1.99**	0.05111	**1.83**	0.00107	**-0.52**	0.35691
STM3248	garR	tartronate semialdehyde reductase	**-0.46**	0.38661	**0.12**	0.75024	**-0.34**	0.56192
STM3248	garR	tartronate semialdehyde reductase	**0.63**	0.28849	**0.13**	0.74871	**-0.83**	0.11534
STM3249	garL	2-dehydro-3-deoxy-galactarate aldolase	**0.04**	0.95007	**0.33**	0.51268	**-0.83**	0.17935
STM3249	garL	2-dehydro-3-deoxy-galactarate aldolase	**0.65**	0.41986	**0.30**	0.36784	**0.35**	0.47513
STM3250	garD	galactarate dehydrogenase	**-0.72**	0.33270	**-0.28**	0.53854	**-0.95**	0.16372
STM3250	garD	galactarate dehydrogenase	**1.57**	0.14815	**-0.34**	0.43019	**0.20**	0.78965
STM3251	STM3251	putative sugar kinase	**-0.79**	0.16262	**0.16**	0.72305	**-0.40**	0.62936
STM3251	STM3251	putative sugar kinase	**0.78**	0.14187	**-0.66**	0.05485	**0.09**	0.80705
STM3252	agaR	Aga operon transcriptional repressor	**0.12**	0.80365	**0.14**	0.70514	**2.06**	0.05619
STM3252	agaR	Aga operon transcriptional repressor	**0.67**	0.46472	**0.00**	0.99819	**1.90**	0.12440
STM3253	STM3253	tagatose 1,6-diphosphate aldolase	**1.68**	0.03376	**1.10**	0.01969	**1.75**	0.06260
STM3253	STM3253	tagatose 1,6-diphosphate aldolase	**2.53**	0.01106	**0.02**	0.94974	**2.46**	0.00168
STM3254	STM3254	putative fructose-1-phosphate kinase	**-0.39**	0.49422	**-1.13**	0.01899	**-0.60**	0.19949
STM3254	STM3254	putative fructose-1-phosphate kinase	**0.62**	0.32051	**-0.16**	0.63957	**0.13**	0.73869
STM3255	STM3255	putative phosphotransferase system fructose-specific	**0.66**	0.34178	**1.60**	0.00239	**0.25**	0.64232
STM3255	STM3255	putative phosphotransferase system fructose-specific	**1.88**	0.12411	**-0.35**	0.58424	**0.31**	0.51115
STM3256	STM3256	putative phosphotransferase system mannitol/fructose-	**3.34**	0.14914	**-0.31**	0.76008	**2.09**	0.05757
STM3256	STM3256	putative phosphotransferase system mannitol/fructose-	**1.54**	0.09032	**-0.61**	0.14612	**0.98**	0.54459
STM3257	STM3257	putative tagatose 6-phosphate kinase 1	**-1.59**	0.02435	**0.51**	0.55810	**-0.42**	0.54228
STM3257	STM3257	putative tagatose 6-phosphate kinase 1	**0.17**	0.81981	**-1.24**	0.01678	**-0.58**	0.20197
STM3258	STM3258	galactitol-specific enzyme IIA	**0.52**	0.25925	**0.21**	0.74069	**-0.42**	0.27648
STM3258	STM3258	galactitol-specific enzyme IIA	**1.46**	0.36682	**-1.45**	0.02479	**-1.36**	0.04605
STM3259	STM3259	PTS family galactitol-specific enzyme IIB	**-0.01**	0.98200	**0.20**	0.54466	**1.20**	0.01665
STM3259	STM3259	PTS family galactitol-specific enzyme IIB	**-0.08**	0.87342	**-0.30**	0.53218	**0.93**	0.04242
STM3260	STM3260	PTS family galactitol-specific enzyme IIC	**0.06**	0.92640	**-0.72**	0.10687	**0.35**	0.39744
STM3260	STM3260	PTS family galactitol-specific enzyme IIC	**-0.64**	0.46897	**-1.50**	0.01968	**0.49**	0.46025
STM3261	STM3261	galactitol-1-phosphate dehydrogenase	**-1.24**	0.30190	**-0.80**	0.11600	**-1.02**	0.13879
STM3261	STM3261	galactitol-1-phosphate dehydrogenase	**1.83**	0.09954	**-0.36**	0.32281	**-0.65**	0.42685
STM3262	STM3262	galactitol utilization operon transcriptional repressor	**0.11**	0.87796	**-0.37**	0.31257	**0.97**	0.05242
STM3262	STM3262	galactitol utilization operon transcriptional repressor	**0.60**	0.38660	**-0.39**	0.27622	**0.68**	0.50355
STM3263	yraL	putative methyltransferase	**0.23**	0.66772	**-0.39**	0.27797	**0.14**	0.89115
STM3263	yraL	putative methyltransferase	**1.38**	0.03284	**-0.40**	0.37767	**0.00**	0.99379
STM3264	yraM	putative transglycosylase	**-1.37**	0.05579	**-0.23**	0.47184	**-1.71**	0.00638
STM3264	yraM	putative transglycosylase	**-0.24**	0.78589	**-0.58**	0.17868	**-0.91**	0.09526
STM3265	yraN	hypothetical protein STM3265	**-1.48**	0.01858	**0.01**	0.97466	**-1.32**	0.00537
STM3265	yraN	hypothetical protein STM3265	**-0.63**	0.37572	**-0.50**	0.14450	**-0.64**	0.19142
STM3266	yraO	putative phosphoheptose isomerase	**-0.60**	0.25480	**-0.24**	0.45133	**-1.47**	0.00683
STM3266	yraO	putative phosphoheptose isomerase	**0.53**	0.22043	**0.11**	0.70134	**0.08**	0.82353
STM3267	yraP	putative periplasmic protein	**-0.10**	0.82172	**-0.19**	0.60338	**-0.79**	0.04207
STM3267	yraP	putative periplasmic protein	**0.43**	0.43573	**-0.05**	0.86456	**-0.24**	0.60259
STM3268	yraR	putative nucleoside-diphosphate-sugar epimerase	**-0.33**	0.67298	**0.07**	0.85159	**0.89**	0.21737
STM3268	yraR	putative nucleoside-diphosphate-sugar epimerase	**0.54**	0.27378	**0.47**	0.22393	**0.71**	0.07520
STM3269	yhbO	putative intracellular proteinase	**-0.51**	0.28433	**0.03**	0.94131	**1.50**	0.00518
STM3269	yhbO	putative intracellular proteinase	**0.54**	0.34628	**0.56**	0.09242	**2.37**	0.00197
STM3270	yhbP	hypothetical protein STM3270	**0.06**	0.92872	**0.45**	0.26657	**1.39**	0.00521
STM3270	yhbP	hypothetical protein STM3270	**0.91**	0.11315	**0.38**	0.26788	**2.14**	0.00084
STM3271	yhbQ	hypothetical protein STM3271	**-1.01**	0.05873	**-0.15**	0.67224	**-0.30**	0.45089
STM3271	yhbQ	hypothetical protein STM3271	**-0.94**	0.06515	**-0.59**	0.15041	**-1.21**	0.01612
STM3272	yhbS	putative transport protein	**-0.96**	0.23558	**-0.86**	0.01198	**-1.39**	0.01345
STM3272	yhbS	putative transport protein	**-0.63**	0.51958	**-1.10**	0.02258	**-0.81**	0.26354
STM3273	yhbT	putative lipid carrier protein	**-0.84**	0.18180	**0.53**	0.12848	**0.54**	0.14887
STM3273	yhbT	putative lipid carrier protein	**-0.86**	0.15039	**-0.04**	0.90488	**0.07**	0.85525
STM3274	yhbU	putative protease	**-0.86**	0.25205	**-0.83**	0.03646	**-0.44**	0.36411
STM3274	yhbU	putative protease	**-0.12**	0.77958	**-1.77**	0.00309	**-0.23**	0.59627
STM3275,S	yhbV	putative protease	**0.32**	0.48347	**-0.51**	0.09309	**-0.79**	0.26020
STM3275,S	yhbV	putative protease	**0.20**	0.78300	**-2.11**	0.00409	**0.92**	0.03567
STM3276	yhbW	putative alkanal monooxygenase	**-0.73**	0.18812	**-0.46**	0.15628	**0.53**	0.19103
STM3276	yhbW	putative alkanal monooxygenase	**0.28**	0.51104	**0.30**	0.45381	**0.98**	0.03871
STM3277	STM3277	putative inner membrane protein	**0.61**	0.29137	**1.26**	0.03035	**0.44**	0.34171
STM3277	STM3277	putative inner membrane protein	**1.21**	0.04221	**-0.40**	0.50510	**1.46**	0.02428
STM3278	STM3278	putative cytoplasmic protein	**-1.08**	0.06471	**-0.32**	0.33639	**-0.38**	0.39346
STM3278	STM3278	putative cytoplasmic protein	**0.17**	0.88749	**0.23**	0.61617	**0.12**	0.83480

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM3279	mtr	tryptophan-specific transport protein	**-0.65**	0.18348	**-0.18**	0.57576	**-0.50**	0.47498
STM3279	mtr	tryptophan-specific transport protein	**0.55**	0.27080	**-0.15**	0.65735	**-0.13**	0.85656
STM3280,S	deaD	cysteine sulfinate desulfinase	**-0.35**	0.51990	**0.96**	0.08756	**-1.65**	0.00812
STM3280,S	deaD	cysteine sulfinate desulfinase	**-1.01**	0.10236	**0.14**	0.78618	**-1.29**	0.02277
STM3281	nlpI	lipoprotein	**-1.70**	0.03038	**0.33**	0.29919	**-2.98**	0.00022
STM3281	nlpI	lipoprotein	**1.46**	0.03950	**0.87**	0.02076	**-2.98**	0.00169
STM3282	pnp	polynucleotide phosphorylase	**0.43**	0.41267	**-1.28**	0.00518	**-0.23**	0.84247
STM3282	pnp	polynucleotide phosphorylase	**-1.48**	0.37922	**-1.38**	0.00644	**-0.16**	0.90846
STM3283	rpsO	30S ribosomal protein S15	**-2.42**	0.02363	**-0.68**	0.10095	**-2.25**	0.00075
STM3283	rpsO	30S ribosomal protein S15	**-2.67**	0.05615	**-0.47**	0.20794	**-4.64**	0.00047
STM3284	truB	tRNA pseudouridine synthase B	**-1.49**	0.04046	**-0.05**	0.92605	**-2.85**	0.00014
STM3284	truB	tRNA pseudouridine synthase B	**-0.92**	0.08124	**0.05**	0.92338	**-2.32**	0.00058
STM3285	rbfA	ribosome-binding factor A	**-2.14**	0.05741	**-0.77**	0.04138	**-2.43**	0.00027
STM3285	rbfA	ribosome-binding factor A	**-1.10**	0.37241	**-1.12**	0.00573	**-1.57**	0.00449
STM3286	infB	translation initiation factor IF-2	**-1.50**	0.07268	**-0.11**	0.81565	**-2.24**	0.00493
STM3286	infB	translation initiation factor IF-2	**-0.64**	0.15577	**-0.01**	0.97889	**-1.56**	0.09553
STM3287	nusA	transcription elongation factor NusA	**-1.07**	0.07031	**-0.78**	0.06402	**-3.66**	0.00064
STM3287	nusA	transcription elongation factor NusA	**-0.31**	0.63051	**-0.61**	0.12468	**-4.03**	0.00025
STM3288	yhbC	hypothetical protein STM3288	**-1.94**	0.15195	**-0.67**	0.09737	**0.42**	0.24990
STM3288	yhbC	hypothetical protein STM3288	**1.45**	0.47667	**-1.62**	0.00799	**0.08**	0.87004
STM3289	metY	STM3289	**1.50**	0.06416	**1.06**	0.00812	**4.22**	0.00004
STM3289	metY	STM3289	**2.35**	0.01298	**1.10**	0.00833	**4.42**	0.00006
STM3290,S	argG	argininosuccinate synthase	**-0.98**	0.13555	**-0.14**	0.67681	**-0.99**	0.08531
STM3290,S	argG	argininosuccinate synthase	**0.23**	0.60713	**-0.14**	0.66320	**0.68**	0.34515
STM3291	STM3291	putative cytoplasmic protein	**-0.45**	0.33541	**-0.37**	0.19553	**-0.17**	0.69375
STM3291	STM3291	putative cytoplasmic protein	**-0.05**	0.94734	**-0.44**	0.33246	**0.97**	0.03607
STM3292	leuU	STM3292	**-1.58**	0.01380	**-0.83**	0.34390	**-0.87**	0.07042
STM3292	leuU	STM3292	**-2.24**	0.00869	**-1.33**	0.00550	**-1.02**	0.02284
STM3293	secG	protein-export membrane protein	**-1.70**	0.02449	**-0.88**	0.03435	**-2.52**	0.00073
STM3293	secG	protein-export membrane protein	**-1.19**	0.02903	**-0.72**	0.04149	**-1.96**	0.00190
STM3294	mrsA	phosphoglucosamine mutase	**-2.68**	0.01134	**-1.18**	0.00483	**-2.86**	0.00030
STM3294	mrsA	phosphoglucosamine mutase	**-0.92**	0.10662	**-1.40**	0.00234	**-2.44**	0.00022
STM3295	folP	7,8-dihydropteroate synthase	**-0.11**	0.81330	**-0.98**	0.01011	**-1.77**	0.00383
STM3295	folP	7,8-dihydropteroate synthase	**0.35**	0.56489	**-0.92**	0.00955	**-1.31**	0.00697
STM3296	hflB	ATP-dependent zinc-metallo protease	**-0.93**	0.18123	**-0.08**	0.82326	**-1.68**	0.01025
STM3296	hflB	ATP-dependent zinc-metallo protease	**-0.51**	0.49059	**0.85**	0.02899	**-1.15**	0.03449
STM3297	ftsJ	23S rRNA methyltransferase	**-2.10**	0.02655	**0.01**	0.98739	**-2.02**	0.00097
STM3297	ftsJ	23S rRNA methyltransferase	**-2.00**	0.03444	**0.23**	0.44559	**-2.03**	0.00064
STM3298,S	yhbY	putative RNA-binding protein	**-1.49**	0.01588	**0.59**	0.06270	**-2.70**	0.00022
STM3298,S	yhbY	putative RNA-binding protein	**-0.73**	0.22891	**0.22**	0.60308	**-2.22**	0.00248
STM3299	greA	transcription elongation factor GreA	**-2.13**	0.00918	**-0.21**	0.57075	**-2.22**	0.00661
STM3299	greA	transcription elongation factor GreA	**-0.84**	0.09820	**0.31**	0.34347	**-2.19**	0.00048
STM3300	dacB	D-alanyl-D-alanine carboxypeptidase	**-1.34**	0.04246	**-0.13**	0.66693	**-1.25**	0.01361
STM3300	dacB	D-alanyl-D-alanine carboxypeptidase	**0.72**	0.34597	**0.05**	0.87217	**0.21**	0.60525
STM3301	yhbZ	putative GTP-binding protein	**0.66**	0.28273	**0.66**	0.08234	**0.45**	0.30860
STM3301	yhbZ	putative GTP-binding protein	**1.47**	0.01989	**0.74**	0.03418	**1.50**	0.01034
STM3303	rpmA	50S ribosomal protein L27	**-2.68**	0.07992	**-0.37**	0.27846	**-3.90**	0.00035
STM3303	rpmA	50S ribosomal protein L27	**-1.72**	0.07343	**-0.19**	0.66385	**-3.06**	0.00010
STM3303	rpmA	50S ribosomal protein L27	**-1.48**	0.06597	**-0.61**	0.06483	**-3.60**	0.00016
STM3303	rpmA	50S ribosomal protein L27	**-1.29**	0.10651	**-0.31**	0.28918	**-3.01**	0.00014
STM3305	ispB	octaprenyl diphosphate synthase	**-1.27**	0.04025	**-0.67**	0.07165	**-2.98**	0.00186
STM3305	ispB	octaprenyl diphosphate synthase	**0.86**	0.55316	**-0.66**	0.03421	**-2.49**	0.00053
STM3306	nlp	transcriptional regulator	**-0.02**	0.96628	**-0.62**	0.06010	**-0.73**	0.17836
STM3306	nlp	transcriptional regulator	**0.89**	0.10535	**-0.83**	0.02378	**0.18**	0.64347
STM3307	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	**-1.90**	0.00991	**-1.31**	0.00427	**-3.83**	0.00004
STM3307	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	**-1.32**	0.02693	**-1.40**	0.00447	**-3.48**	0.00011
STM3308	yrbA	putative transcriptional regulator	**-1.96**	0.01782	**-1.43**	0.00350	**-2.45**	0.00146
STM3308	yrbA	putative transcriptional regulator	**-1.50**	0.03368	**-1.29**	0.00435	**-2.72**	0.00035
STM3308	yrbA	putative transcriptional regulator	**-1.21**	0.07678	**-1.21**	0.00613	**-3.21**	0.00011
STM3308	yrbA	putative transcriptional regulator	**-1.92**	0.06959	**-1.76**	0.00055	**-3.13**	0.00008
STM3309	yrbB	hypothetical protein STM3309	**-1.82**	0.01091	**-0.31**	0.34597	**-2.11**	0.00066
STM3309	yrbB	hypothetical protein STM3309	**-0.95**	0.06500	**-0.43**	0.19431	**-1.46**	0.00527
STM3310	yrbC	putative transport protein	**-1.63**	0.01536	**0.24**	0.48187	**-0.87**	0.08773
STM3310	yrbC	putative transport protein	**-0.65**	0.13367	**0.75**	0.02820	**-0.65**	0.07454
STM3311	yrbD	putative transport protein	**-0.85**	0.09691	**-0.01**	0.97904	**-0.59**	0.12180
STM3311	yrbD	putative transport protein	**-0.48**	0.30390	**-0.16**	0.71564	**0.17**	0.64347
STM3312	yrbE	putative transport protein	**-1.05**	0.07464	**-0.53**	0.39179	**-1.19**	0.06414
STM3312	yrbE	putative transport protein	**-1.91**	0.01120	**-1.31**	0.00448	**-2.22**	0.01208
STM3313	yrbF	putative transport protein	**-1.76**	0.01136	**-1.65**	0.00099	**-2.65**	0.00527
STM3313	yrbF	putative transport protein	**-1.51**	0.03020	**-1.42**	0.00268	**-3.17**	0.00184

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM3314	yrbG	Na/Ca transport protein	**-2.33**	0.00660	**-1.14**	0.00610	**-2.95**	0.00024
STM3314	yrbG	Na/Ca transport protein	**-1.64**	0.04587	**-1.25**	0.00644	**-2.52**	0.00187
STM3315	yrbH	putative sugar phosphate isomerase	**-1.90**	0.01155	**-1.23**	0.00590	**-2.53**	0.00074
STM3315	yrbH	putative sugar phosphate isomerase	**-1.08**	0.08755	**-1.03**	0.00650	**-1.73**	0.01327
STM3316	yrbI	3-deoxy-D-manno-octulosonate 8-phosphate phosphatase	**-1.93**	0.01435	**-0.44**	0.32824	**-1.18**	0.01458
STM3316	yrbI	3-deoxy-D-manno-octulosonate 8-phosphate phosphatase	**-0.82**	0.17650	**-0.55**	0.12647	**-0.41**	0.22957
STM3317	yrbK	putative inner membrane protein	**-2.13**	0.01205	**0.38**	0.75558	**-1.34**	0.01206
STM3317	yrbK	putative inner membrane protein	**-1.69**	0.06312	**-0.76**	0.02704	**-1.03**	0.06367
STM3318	yhbN	putative transport protein	**-0.85**	0.08090	**-0.21**	0.51185	**-1.13**	0.01202
STM3318	yhbN	putative transport protein	**-0.56**	0.65685	**-0.97**	0.01546	**-0.56**	0.18143
STM3319	yhbG	putative transport protein	**-1.78**	0.02080	**-0.18**	0.62701	**-1.84**	0.00156
STM3319	yhbG	putative transport protein	**-1.37**	0.02992	**-0.34**	0.33927	**-1.34**	0.02020
STM3320	rpoN	DNA-directed RNA polymerase subunit N	**-1.58**	0.08661	**0.74**	0.05812	**-0.63**	0.17933
STM3320	rpoN	DNA-directed RNA polymerase subunit N	**0.72**	0.17687	**1.22**	0.01031	**0.46**	0.39311
STM3321	yhbH	putative sigma N modulation factor	**-1.46**	0.05169	**1.03**	0.00466	**-0.31**	0.41184
STM3321	yhbH	putative sigma N modulation factor	**-0.66**	0.21775	**1.00**	0.02306	**0.41**	0.36645
STM3322	ptsN	sugar-specific PTS family enzyme IIA	**-0.74**	0.20339	**-0.26**	0.54630	**1.23**	0.00833
STM3322	ptsN	sugar-specific PTS family enzyme IIA	**-1.66**	0.02423	**0.30**	0.33639	**0.93**	0.03074
STM3323	yhbJ	hypothetical protein STM3323	**-1.99**	0.00956	**-0.92**	0.01725	**-1.41**	0.00541
STM3323	yhbJ	hypothetical protein STM3323	**-1.56**	0.04243	**-0.64**	0.06225	**-0.62**	0.27329
STM3324	ptsO	phosphocarrier protein HPr-like NPr	**-1.66**	0.07261	**-1.70**	0.00218	**-1.34**	0.03801
STM3324	ptsO	phosphocarrier protein HPr-like NPr	**-1.30**	0.02655	**-1.68**	0.00065	**-1.10**	0.02158
STM3325	yrbL	putative cytoplasmic protein	**-1.06**	0.09643	**-0.56**	0.29806	**0.93**	0.07295
STM3325	yrbL	putative cytoplasmic protein	**-1.11**	0.07329	**-1.23**	0.01373	**1.44**	0.01034
STM3326	mtgA	monofunctional biosynthetic peptidoglycan transglycosylase	**-1.56**	0.01970	**-1.35**	0.13891	**0.05**	0.89601
STM3326	mtgA	monofunctional biosynthetic peptidoglycan transglycosylase	**-1.21**	0.12158	**-0.93**	0.01800	**-0.29**	0.50589
STM3327	yhbL	sigma cross-reacting protein 27A	**-1.21**	0.17567	**-0.76**	0.03484	**-2.27**	0.00038
STM3327	yhbL	sigma cross-reacting protein 27A	**-0.18**	0.84760	**-1.02**	0.00534	**-1.60**	0.00236
STM3328	arcB	sensory histidine kinase	**0.05**	0.98038	**-0.76**	0.04023	**0.71**	0.52736
STM3328	arcB	sensory histidine kinase	**2.29**	0.19540	**-1.71**	0.00048	**1.03**	0.16471
STM3329	yhcC	putative FeS oxidoreductase	**-0.06**	0.88959	**-1.27**	0.02151	**-1.30**	0.05515
STM3329	yhcC	putative FeS oxidoreductase	**1.36**	0.02883	**-0.07**	0.81313	**0.18**	0.75552
STM3330	gltB	glutamate synthase large subunit	**-1.41**	0.02415	**-0.57**	0.18458	**-2.11**	0.00122
STM3330	gltB	glutamate synthase large subunit	**0.31**	0.74962	**-0.56**	0.08958	**-0.86**	0.12472
STM3331	gltD	glutamate synthase small subunit	**-0.53**	0.30879	**-1.17**	0.02064	**-1.40**	0.01819
STM3331	gltD	glutamate synthase small subunit	**0.68**	0.20353	**-1.01**	0.04687	**-0.92**	0.11313
STM3332	yhcG	putative cytoplasmic protein	**-0.74**	0.27541	**1.00**	0.01195	**-1.05**	0.06604
STM3332	yhcG	putative cytoplasmic protein	**0.12**	0.77174	**-0.26**	0.51756	**2.33**	0.09870
STM3333	STM3333	putative purine-cytosine permease	**-1.40**	0.03916	**-0.04**	0.92605	**-1.99**	0.00496
STM3333	STM3333	putative purine-cytosine permease	**-0.07**	0.96214	**0.07**	0.86576	**-1.46**	0.00863
STM3334	STM3334	cytosine deaminase	**0.41**	0.65448	**0.08**	0.83023	**-0.64**	0.13338
STM3334	STM3334	cytosine deaminase	**1.42**	0.13961	**0.13**	0.69749	**-0.18**	0.77376
STM3335	yhcH	putative cytoplasmic protein	**0.77**	0.34092	**0.57**	0.15184	**-0.05**	0.94453
STM3335	yhcH	putative cytoplasmic protein	**1.11**	0.05377	**-0.37**	0.43103	**0.03**	0.96352
STM3336	nanK	N-acetylmannosamine kinase	**0.27**	0.69114	**0.63**	0.06324	**1.38**	0.03354
STM3336	nanK	N-acetylmannosamine kinase	**-1.03**	0.30135	**0.33**	0.29169	**1.08**	0.03003
STM3337	nanE	putative ManNAc-6P epimerase	**3.01**	0.31521	**0.41**	0.38963	**1.04**	0.15608
STM3337	nanE	putative ManNAc-6P epimerase	**1.93**	0.25113	**0.49**	0.18868	**1.51**	0.04042
STM3338	nanT	putative sialic acid transporter	**0.60**	0.25202	**0.76**	0.07704	**0.97**	0.02131
STM3338	nanT	putative sialic acid transporter	**1.04**	0.08960	**0.68**	0.05873	**1.62**	0.03327
STM3339	nanA	N-acetylneuraminate lyase	**-0.76**	0.15567	**0.48**	0.22512	**1.14**	0.03666
STM3339	nanA	N-acetylneuraminate lyase	**0.64**	0.37031	**0.18**	0.76022	**1.26**	0.00591
STM3340	yhcK	transcriptional regulator NanR	**3.57**	0.09429	**-0.42**	0.25618	**1.31**	0.01416
STM3340	yhcK	transcriptional regulator NanR	**1.61**	0.04403	**-0.26**	0.43103	**1.83**	0.04675
STM3341	sspB	stringent starvation protein B	**-0.67**	0.37872	**-0.22**	0.50209	**-2.53**	0.00026
STM3341	sspB	stringent starvation protein B	**-0.05**	0.93053	**-0.47**	0.10951	**-1.11**	0.02977
STM3342	sspA	stringent starvation protein A	**-2.14**	0.00929	**-1.41**	0.00190	**-2.48**	0.00028
STM3342	sspA	stringent starvation protein A	**-1.93**	0.00886	**-1.78**	0.00039	**-2.28**	0.00079
STM3343	STM3343	putative cytoplasmic protein	**0.16**	0.76786	**-1.29**	0.00710	**-1.37**	0.06674
STM3343	STM3343	putative cytoplasmic protein	**0.67**	0.29999	**-0.90**	0.01247	**-1.48**	0.00482
STM3344	rpsI	30S ribosomal protein S9	**-1.10**	0.06060	**-1.14**	0.10806	**-1.19**	0.02689
STM3344	rpsI	30S ribosomal protein S9	**-1.16**	0.03788	**-1.05**	0.01323	**-1.34**	0.03769
STM3345	rplM	50S ribosomal protein L13	**-0.70**	0.27024	**-0.35**	0.29748	**-3.82**	0.00007
STM3345	rplM	50S ribosomal protein L13	**-0.02**	0.97228	**-0.94**	0.03280	**-2.56**	0.00560
STM3346	yhcM	putative ATPase	**-3.41**	0.00661	**-1.72**	0.00145	**-3.97**	0.00022
STM3346	yhcM	putative ATPase	**-2.27**	0.01762	**-1.44**	0.00694	**-3.14**	0.00022
STM3347	yhcB	putative periplasmic protein	**-1.12**	0.04229	**-0.16**	0.61713	**-2.28**	0.00053
STM3347	yhcB	putative periplasmic protein	**-1.20**	0.02888	**-0.20**	0.54383	**-1.59**	0.01141
STM3348	degQ	serine endoprotease	**-1.45**	0.02320	**-0.23**	0.47066	**-1.03**	0.01573
STM3348	degQ	serine endoprotease	**-0.41**	0.45069	**-0.31**	0.50017	**-0.69**	0.11163

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM3349	degS	periplasmic serine endoprotease	**0.58**	0.58858	**-0.76**	0.06184	**-0.44**	0.52228
STM3349	degS	periplasmic serine endoprotease	**1.06**	0.09097	**-1.26**	0.00630	**-0.31**	0.54067
STM3350	STM3350	putative inner membrane protein	**-1.05**	0.05466	**-1.32**	0.00306	**-1.93**	0.01540
STM3350	STM3350	putative inner membrane protein	**0.48**	0.29330	**-0.85**	0.03228	**0.29**	0.53425
STM3351	oadB	putative sodium ion pump oxaloacetate decarboxylase beta	**1.62**	0.12602	**0.72**	0.52995	**-0.09**	0.89495
STM3351	oadB	putative sodium ion pump oxaloacetate decarboxylase beta	**1.67**	0.27954	**-0.12**	0.71994	**-0.33**	0.46990
STM3352	oadA	oxaloacetate decarboxylase	**0.49**	0.71993	**-0.60**	0.36290	**0.86**	0.46716
STM3352	oadA	oxaloacetate decarboxylase	**1.05**	0.30366	**0.38**	0.40758	**0.01**	0.99365
STM3352	oadA	oxaloacetate decarboxylase	**1.92**	0.09167	**0.11**	0.83578	**0.79**	0.06524
STM3352	oadA	oxaloacetate decarboxylase	**1.69**	0.22352	**0.01**	0.98967	**0.39**	0.49753
STM3352	oadA	oxaloacetate decarboxylase	**2.56**	0.09231	**-0.01**	0.98010	**0.95**	0.02625
STM3352	oadA	oxaloacetate decarboxylase	**3.00**	0.05810	**-0.58**	0.09836	**1.56**	0.01917
STM3353	oadG	putative oxaloacetate decarboxylase subunit gamma	**1.00**	0.11849	**-0.29**	0.36059	**1.30**	0.00602
STM3353	oadG	putative oxaloacetate decarboxylase subunit gamma	**1.01**	0.10405	**-0.79**	0.17191	**0.54**	0.25124
STM3354	STM3354	L(+)-tartrate dehydratase	**-0.34**	0.52834	**0.01**	0.98628	**0.29**	0.74554
STM3354	STM3354	L(+)-tartrate dehydratase	**0.78**	0.34233	**-0.52**	0.36682	**0.77**	0.31828
STM3355	STM3355	tartrate dehydratase	**0.46**	0.45778	**-0.53**	0.16032	**0.59**	0.52471
STM3355	STM3355	tartrate dehydratase	**0.73**	0.46005	**-0.83**	0.08417	**0.78**	0.29951
STM3356	STM3356	putative cation transporter	**0.88**	0.34838	**-0.39**	0.43153	**-0.17**	0.77436
STM3356	STM3356	putative cation transporter	**0.62**	0.20111	**1.07**	0.46899	**3.93**	0.00023
STM3357	STM3357	putative regulatory protein	**-0.91**	0.07367	**-0.61**	0.26719	**0.62**	0.34975
STM3357	STM3357	putative regulatory protein	**-1.63**	0.01885	**-1.22**	0.01961	**-0.46**	0.40607
STM3358	STM3358	putative regulatory protein	**-1.99**	0.01067	**-0.54**	0.15070	**-0.60**	0.14996
STM3358	STM3358	putative regulatory protein	**-1.12**	0.06385	**0.05**	0.90579	**-0.78**	0.21507
STM3359	mdh	malate dehydrogenase	**-2.60**	0.00660	**1.17**	0.00611	**-1.78**	0.00178
STM3359	mdh	malate dehydrogenase	**-0.87**	0.16915	**1.09**	0.00851	**-1.27**	0.01553
STM3360	argR	arginine repressor	**-0.01**	0.97285	**-0.40**	0.26025	**-1.00**	0.03070
STM3360	argR	arginine repressor	**-0.37**	0.41619	**-0.63**	0.15126	**-0.28**	0.61476
STM3361	yhcN	putative outer membrane protein	**-0.67**	0.17113	**-0.80**	0.02672	**-0.83**	0.10655
STM3361	yhcN	putative outer membrane protein	**0.32**	0.43436	**-0.79**	0.03137	**0.22**	0.71804
STM3362	STM3362	putative periplasmic protein	**0.29**	0.79237	**-0.14**	0.81481	**-0.42**	0.29615
STM3362	STM3362	putative periplasmic protein	**1.34**	0.12988	**-0.06**	0.83378	**0.53**	0.21479
STM3363	yhcO	putative cytoplasmic protein	**-0.25**	0.84353	**0.93**	0.01867	**2.38**	0.01612
STM3363	yhcO	putative cytoplasmic protein	**1.09**	0.16050	**0.49**	0.15240	**1.79**	0.00187
STM3364	yhcP	putative inner membrane protein	**-0.32**	0.43508	**-0.38**	0.30994	**-0.10**	0.79033
STM3364	yhcP	putative inner membrane protein	**1.01**	0.07220	**-0.37**	0.20601	**0.30**	0.41079
STM3365	yhcQ	putative multidrug resistance protein	**0.37**	0.61648	**-0.63**	0.13074	**-1.13**	0.10243
STM3365	yhcQ	putative multidrug resistance protein	**-0.24**	0.60402	**-0.36**	0.31174	**-0.79**	0.11036
STM3366	yhcR	putative inner membrane protein	**-1.00**	0.10199	**-0.88**	0.04386	**-0.54**	0.21297
STM3366	yhcR	putative inner membrane protein	**-0.86**	0.34084	**-1.24**	0.00516	**-1.04**	0.09953
STM3367	yhcS	putative transcriptional regulator	**-0.38**	0.65121	**0.50**	0.30331	**1.05**	0.11815
STM3367	yhcS	putative transcriptional regulator	**-1.52**	0.04570	**-0.68**	0.10936	**-1.62**	0.00331
STM3368	tldD	microcin B17-processing protein	**-0.39**	0.40395	**-0.41**	0.36283	**-0.34**	0.59806
STM3368	tldD	microcin B17-processing protein	**0.14**	0.78409	**-0.47**	0.15837	**-0.19**	0.70132
STM3369	yhdP	putative protease	**-0.58**	0.41542	**-0.93**	0.03630	**-1.32**	0.01759
STM3369	yhdP	putative protease	**0.23**	0.64839	**-1.37**	0.00635	**-0.66**	0.22262
STM3370	cafA	RNase G	**-0.79**	0.13003	**-0.73**	0.03050	**0.12**	0.80333
STM3370	cafA	RNase G	**-1.30**	0.02567	**-1.10**	0.00635	**0.27**	0.63357
STM3371	maf	Maf-like protein	**-2.38**	0.00660	**-0.98**	0.01317	**-2.13**	0.00188
STM3371	maf	Maf-like protein	**-1.34**	0.08658	**-0.97**	0.00649	**-2.52**	0.00024
STM3372	mreD	rod shape-determining protein	**-2.34**	0.05421	**-1.54**	0.00193	**-3.30**	0.00035
STM3372	mreD	rod shape-determining protein	**-1.80**	0.10017	**-2.09**	0.00022	**-1.68**	0.00650
STM3373	mreC	rod shape-determining protein	**-2.56**	0.01417	**-2.38**	0.00041	**-3.09**	0.00056
STM3373	mreC	rod shape-determining protein	**-1.81**	0.01575	**-2.09**	0.00015	**-2.66**	0.00035
STM3374	mreB	rod shape-determining protein	**-2.73**	0.00720	**-2.39**	0.00017	**-4.12**	0.00006
STM3374	mreB	rod shape-determining protein	**-1.52**	0.04277	**-2.00**	0.00163	**-5.11**	0.00002
STM3375	yhdA	putative diguanylate cyclase	**-0.73**	0.18201	**-0.75**	0.02860	**-1.01**	0.04472
STM3375	yhdA	putative diguanylate cyclase	**-1.18**	0.14711	**-0.94**	0.01445	**-1.50**	0.06013
STM3376	yhdH	putative oxidoreductase	**0.07**	0.90441	**0.06**	0.87322	**-0.77**	0.07936
STM3376	yhdH	putative oxidoreductase	**-0.09**	0.90413	**-0.26**	0.44427	**-0.72**	0.11398
STM3377	STM3377	hypothetical protein STM3377	**-1.31**	0.08580	**-0.24**	0.50026	**1.19**	0.01334
STM3377	STM3377	hypothetical protein STM3377	**-1.49**	0.15336	**-0.31**	0.28464	**0.36**	0.33800
STM3378	STM3378	hypothetical protein STM3378	**-2.43**	0.00627	**-1.16**	0.01910	**-0.91**	0.03575
STM3378	STM3378	hypothetical protein STM3378	**-0.61**	0.33999	**-0.93**	0.03113	**-1.00**	0.04082
STM3379	accB	acetyl-CoA carboxylase	**-0.84**	0.70795	**-1.81**	0.00033	**-4.37**	0.00007
STM3379	accB	acetyl-CoA carboxylase	**-2.06**	0.01636	**-1.12**	0.00338	**-2.52**	0.04027
STM3380	accC	acetyl-CoA carboxylase	**-1.62**	0.02548	**-1.14**	0.00590	**-1.90**	0.00935
STM3380	accC	acetyl-CoA carboxylase	**-0.83**	0.44369	**-1.64**	0.00076	**-0.58**	0.13937
STM3381	yhdT	putative inner membrane protein	**-1.58**	0.02677	**-1.23**	0.00297	**-2.97**	0.00062
STM3381	yhdT	putative inner membrane protein	**-0.92**	0.10669	**-1.67**	0.00190	**-2.09**	0.00181

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM3382	panF	sodium/panthothenate symporter	**-0.80**	0.10464	**-1.80**	0.00043	**-0.87**	0.21154
STM3382	panF	sodium/panthothenate symporter	**-0.52**	0.27065	**-1.48**	0.00123	**0.05**	0.90808
STM3383	prmA	ribosomal protein L11 methyltransferase	**-1.48**	0.02102	**-0.73**	0.02259	**-0.10**	0.88656
STM3383	prmA	ribosomal protein L11 methyltransferase	**-1.27**	0.07006	**-1.29**	0.00347	**-0.89**	0.07947
STM3384	yhdG	possible dehydrogenase	**-3.74**	0.00547	**-1.90**	0.00060	**-5.82**	0.00012
STM3384	yhdG	possible dehydrogenase	**-3.37**	0.01572	**-1.94**	0.00091	**-5.08**	0.00003
STM3385	fis	DNA-binding protein Fis	**-3.60**	0.00652	**-1.23**	0.02744	**-3.80**	0.00016
STM3385	fis	DNA-binding protein Fis	**-2.09**	0.01319	**-1.06**	0.01830	**-2.85**	0.00085
STM3386	yhdJ	putative methyltransferase	**-0.02**	0.97719	**-1.43**	0.03512	**0.64**	0.62782
STM3386	yhdJ	putative methyltransferase	**0.23**	0.89107	**-0.45**	0.64225	**2.70**	0.00271
STM3387	yhdU	putative periplasmic protein	**-0.54**	0.20028	**-0.95**	0.01495	**-0.81**	0.13667
STM3387	yhdU	putative periplasmic protein	**-0.49**	0.34656	**-0.99**	0.01579	**-0.25**	0.52606
STM3388	STM3388	putative signal transduction protein	**-1.39**	0.13015	**-0.04**	0.94974	**-1.19**	0.02497
STM3388	STM3388	putative signal transduction protein	**-1.31**	0.13706	**-0.78**	0.07774	**1.66**	0.29870
STM3389	envR	transcriptional repressor	**-0.25**	0.67940	**-0.56**	0.18625	**-0.27**	0.56046
STM3389	envR	transcriptional repressor	**0.48**	0.30879	**-0.56**	0.33116	**0.32**	0.51662
STM3390	acrE	acriflavine resistance protein E precursor	**0.00**	0.99568	**-0.51**	0.19196	**-0.19**	0.76633
STM3390	acrE	acriflavine resistance protein E precursor	**0.44**	0.33830	**-1.41**	0.00338	**-0.44**	0.31526
STM3391	acrF	multidrug transport protein	**-0.59**	0.25510	**-1.17**	0.01096	**-0.35**	0.37615
STM3391	acrF	multidrug transport protein	**0.47**	0.26727	**-0.95**	0.02064	**0.61**	0.12663
STM3392	yhdV	putative outer membrane lipoprotein	**0.25**	0.83819	**-0.33**	0.27468	**-0.18**	0.80357
STM3392	yhdV	putative outer membrane lipoprotein	**0.45**	0.71254	**-0.26**	0.47083	**-0.64**	0.23296
STM3393	rrfF	STM3393	**0.39**	0.65080	**-0.13**	0.86476	**0.30**	0.68816
STM3393	rrfF	STM3393	**1.32**	0.13685	**-0.15**	0.79185	**0.12**	0.84461
STM3394	thrV	STM3394	**-1.56**	0.04856	**-1.34**	0.00612	**-1.10**	0.02940
STM3394	thrV	STM3394	**-0.46**	0.30809	**-1.22**	0.00354	**-0.65**	0.19622
STM3396	rrlD	STM3396	**-2.94**	0.01045	**-0.28**	0.62868	**-2.16**	0.01145
STM3396	rrlD	STM3396	**-2.04**	0.01834	**0.14**	0.81438	**-1.43**	0.03094
STM3397	-	STM3397	**1.17**	0.17624	**0.64**	0.03571	**1.13**	0.02755
STM3397	-	STM3397	**1.82**	0.01571	**0.47**	0.11340	**1.24**	0.00837
STM3398	rrsD	STM3398	**-1.48**	0.28608	**0.61**	0.16337	**0.07**	0.89430
STM3398	rrsD	STM3398	**-1.51**	0.12503	**0.00**	0.99442	**0.70**	0.19050
STM3399	yrdA	putative ferripyochelin-binding protein	**-0.44**	0.31122	**-0.07**	0.83626	**0.54**	0.12254
STM3399	yrdA	putative ferripyochelin-binding protein	**0.16**	0.74962	**0.30**	0.39981	**0.74**	0.12344
STM3400	yrdB	putative periplasmic protein	**-1.11**	0.06618	**-0.09**	0.82255	**0.55**	0.13114
STM3400	yrdB	putative periplasmic protein	**-0.40**	0.47211	**-0.16**	0.68023	**0.98**	0.02457
STM3401	aroE	shikimate 5-dehydrogenase	**-0.98**	0.09360	**0.10**	0.80248	**0.07**	0.86712
STM3401	aroE	shikimate 5-dehydrogenase	**-0.01**	0.97698	**-0.34**	0.33005	**0.44**	0.36840
STM3402	yrdC	putative dsRNA-binding protein	**-1.61**	0.04050	**-1.18**	0.01585	**-0.87**	0.02782
STM3402	yrdC	putative dsRNA-binding protein	**-1.36**	0.02232	**-1.43**	0.00176	**-0.49**	0.19956
STM3403	yrdD	putative DNA topoisomerase	**-1.29**	0.07241	**-0.19**	0.67941	**-0.17**	0.83020
STM3403	yrdD	putative DNA topoisomerase	**-1.20**	0.12661	**-0.61**	0.09806	**-0.66**	0.10520
STM3404	smg	hypothetical protein STM3404	**-1.06**	0.06614	**1.06**	0.00548	**0.79**	0.06189
STM3404	smg	hypothetical protein STM3404	**-0.40**	0.37797	**1.03**	0.00999	**1.48**	0.00881
STM3405	smf	putative competence protein	**-0.09**	0.89129	**1.45**	0.00258	**1.84**	0.00157
STM3405	smf	putative competence protein	**0.11**	0.81152	**1.87**	0.00036	**2.42**	0.00084
STM3406	def	peptide deformylase	**-1.71**	0.02604	**-0.26**	0.46273	**-0.79**	0.04379
STM3406	def	peptide deformylase	**-0.54**	0.60472	**-0.20**	0.56737	**0.71**	0.16686
STM3407	fmt	methionyl-tRNA formyltransferase	**-1.45**	0.02265	**-0.32**	0.32042	**-0.45**	0.30913
STM3407	fmt	methionyl-tRNA formyltransferase	**-1.03**	0.07835	**-0.85**	0.02791	**-0.81**	0.10554
STM3408	sun	putative rRNA methylase	**-0.28**	0.64934	**-0.70**	0.05442	**-0.42**	0.30210
STM3408	sun	putative rRNA methylase	**-0.16**	0.78371	**-1.96**	0.00077	**-0.72**	0.16341
STM3409	trkA	potassium transporter peripheral membrane component	**-1.65**	0.02526	**-1.31**	0.00493	**-1.59**	0.00333
STM3409	trkA	potassium transporter peripheral membrane component	**-1.03**	0.06207	**-0.80**	0.03140	**-1.05**	0.06882
STM3410	mscL	large-conductance mechanosensitive channel	**-1.37**	0.02998	**-0.75**	0.04418	**-0.76**	0.08841
STM3410	mscL	large-conductance mechanosensitive channel	**-1.42**	0.03667	**-0.63**	0.06054	**-0.89**	0.06050
STM3412	zntR	zinc-responsive transcriptional regulator	**-1.24**	0.03561	**-0.12**	0.75425	**-0.93**	0.02894
STM3412	zntR	zinc-responsive transcriptional regulator	**-0.15**	0.73218	**0.40**	0.27257	**-0.63**	0.09329
STM3413	yhdN	putative cytoplasmic protein	**-2.13**	0.00787	**-0.80**	0.07129	**-1.65**	0.00351
STM3413	yhdN	putative cytoplasmic protein	**-0.87**	0.12362	**0.34**	0.45215	**-1.80**	0.00186
STM3414	rplQ	50S ribosomal protein L17	**-4.07**	0.01449	**-1.92**	0.00987	**-5.21**	0.00002
STM3414	rplQ	50S ribosomal protein L17	**-3.86**	0.00985	**-1.13**	0.01447	**-5.81**	0.00002
STM3415	rpoA	DNA-directed RNA polymerase alpha subunit	**-2.30**	0.02000	**-0.48**	0.12500	**-6.28**	0.00001
STM3415	rpoA	DNA-directed RNA polymerase alpha subunit	**-1.40**	0.05644	**-0.47**	0.10840	**-6.59**	0.00001
STM3416	rpsD	30S ribosomal protein S4	**-1.42**	0.11466	**-0.27**	0.67988	**-5.64**	0.00005
STM3416	rpsD	30S ribosomal protein S4	**-0.98**	0.13007	**-0.12**	0.74224	**-6.31**	0.00002
STM3417	rpsK	30S ribosomal protein S11	**-2.21**	0.03577	**-0.84**	0.03398	**-6.24**	0.00002
STM3417	rpsK	30S ribosomal protein S11	**-2.22**	0.01423	**-0.36**	0.33350	**-6.14**	0.00002
STM3418	rpsM	30S ribosomal protein S13	**-1.71**	0.02344	**-0.72**	0.28230	**-5.62**	0.00002
STM3418	rpsM	30S ribosomal protein S13	**-1.81**	0.01301	**-0.15**	0.61713	**-6.00**	0.00002

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM3420	secY	preprotein translocase SecY	**-2.50**	0.02124	**-0.66**	0.21065	**-5.34**	0.00002
STM3420	secY	preprotein translocase SecY	**-2.63**	0.00720	**-0.43**	0.15166	**-5.26**	0.00003
STM3421	rplO	50S ribosomal protein L15	**-2.07**	0.01765	**-0.60**	0.07129	**-6.06**	0.00002
STM3421	rplO	50S ribosomal protein L15	**-1.65**	0.01328	**-0.60**	0.13637	**-6.47**	0.00001
STM3422	rpmD	50S ribosomal protein L30	**-2.83**	0.00750	**-1.22**	0.00732	**-5.63**	0.00002
STM3422	rpmD	50S ribosomal protein L30	**-2.82**	0.03306	**-0.54**	0.09229	**-6.15**	0.00003
STM3423	rpsE	30S ribosomal protein S5	**-1.43**	0.14047	**0.61**	0.08848	**-5.33**	0.00002
STM3423	rpsE	30S ribosomal protein S5	**-0.93**	0.06959	**0.19**	0.53226	**-4.86**	0.00006
STM3424	rplR	50S ribosomal protein L18	**-1.96**	0.01355	**-0.52**	0.36695	**-5.58**	0.00001
STM3424	rplR	50S ribosomal protein L18	**-1.68**	0.01578	**0.08**	0.84293	**-5.77**	0.00005
STM3425	rplF	50S ribosomal protein L6	**-0.22**	0.65450	**-0.45**	0.25023	**-6.00**	0.00001
STM3425	rplF	50S ribosomal protein L6	**-1.05**	0.12786	**-0.18**	0.63702	**-6.47**	0.00002
STM3426	rpsH	30S ribosomal protein S8	**-2.72**	0.00595	**-1.09**	0.06002	**-6.42**	0.00001
STM3426	rpsH	30S ribosomal protein S8	**-1.56**	0.07619	**-0.60**	0.08935	**-6.65**	0.00002
STM3426	rpsH	30S ribosomal protein S8	**-2.65**	0.00688	**-1.23**	0.01868	**-6.87**	0.00001
STM3426	rpsH	30S ribosomal protein S8	**-0.86**	0.09879	**-0.07**	0.84438	**-6.28**	0.00002
STM3427,S	rpsN	30S ribosomal subunit protein S14	**-2.87**	0.00888	**-0.66**	0.08892	**-7.72**	0.00001
STM3427,S	rpsN	30S ribosomal subunit protein S14	**-1.44**	0.02561	**-0.02**	0.96048	**-6.55**	0.00002
STM3428	rplE	50S ribosomal protein L5	**-3.22**	0.00571	**-1.05**	0.06428	**-5.63**	0.00003
STM3428	rplE	50S ribosomal protein L5	**-3.16**	0.00541	**-1.02**	0.02699	**-6.59**	0.00002
STM3429	rplX	50S ribosomal protein L24	**-4.28**	0.01377	**-1.46**	0.00846	**-6.21**	0.00002
STM3429	rplX	50S ribosomal protein L24	**-3.03**	0.01435	**-1.28**	0.02860	**-5.90**	0.00002
STM3429	rplX	50S ribosomal protein L24	**-2.89**	0.00743	**-1.33**	0.00236	**-5.91**	0.00002
STM3429	rplX	50S ribosomal protein L24	**-2.95**	0.00547	**-0.93**	0.01631	**-6.29**	0.00002
STM3430	rplN	50S ribosomal protein L14	**-3.49**	0.01509	**-1.96**	0.00482	**-5.86**	0.00002
STM3430	rplN	50S ribosomal protein L14	**-2.26**	0.04528	**-1.06**	0.02958	**-5.87**	0.00002
STM3430	rplN	50S ribosomal protein L14	**-3.83**	0.01172	**-1.88**	0.00043	**-6.48**	0.00001
STM3430	rplN	50S ribosomal protein L14	**-2.34**	0.00673	**-0.95**	0.03834	**-6.15**	0.00002
STM3431	rpsQ	30S ribosomal protein S17	**-2.83**	0.00547	**-1.04**	0.04786	**-5.35**	0.00002
STM3431	rpsQ	30S ribosomal protein S17	**-2.50**	0.01117	**-1.18**	0.00459	**-4.76**	0.00003
STM3432	rpmC	50S ribosomal protein L29	**-2.82**	0.03417	**-0.70**	0.14203	**-4.57**	0.00002
STM3432	rpmC	50S ribosomal protein L29	**-1.33**	0.02747	**-0.44**	0.27468	**-4.87**	0.00002
STM3433	rplP	50S ribosomal protein L16	**-1.46**	0.04812	**-0.15**	0.69391	**-5.31**	0.00002
STM3433	rplP	50S ribosomal protein L16	**-0.21**	0.64092	**0.18**	0.57928	**-5.08**	0.00003
STM3434	rpsC	30S ribosomal protein S3	**-1.29**	0.15305	**0.55**	0.06738	**-5.71**	0.00002
STM3434	rpsC	30S ribosomal protein S3	**-0.71**	0.13497	**0.32**	0.30992	**-5.11**	0.00003
STM3435	rplV	50S ribosomal protein L22	**-1.52**	0.03475	**-0.30**	0.33313	**-6.95**	0.00001
STM3435	rplV	50S ribosomal protein L22	**-1.26**	0.06701	**-0.27**	0.42704	**-6.61**	0.00001
STM3436	rpsS	30S ribosomal protein S19	**-1.56**	0.02998	**0.07**	0.83611	**-4.05**	0.00631
STM3436	rpsS	30S ribosomal protein S19	**-0.72**	0.12160	**0.28**	0.37635	**-5.31**	0.00014
STM3437	rplB	50S ribosomal protein L2	**-2.09**	0.03587	**-0.11**	0.70446	**-4.82**	0.00018
STM3437	rplB	50S ribosomal protein L2	**-1.67**	0.02460	**-0.46**	0.11360	**-5.21**	0.00002
STM3438	rplW	50S ribosomal protein L23	**-1.34**	0.15487	**0.25**	0.46639	**-6.35**	0.00002
STM3438	rplW	50S ribosomal protein L23	**-0.87**	0.22324	**0.09**	0.75138	**-6.86**	0.00004
STM3439	rplD	50S ribosomal protein L4	**-0.50**	0.30358	**0.02**	0.96866	**-7.04**	0.00002
STM3439	rplD	50S ribosomal protein L4	**-0.88**	0.08481	**0.02**	0.95522	**-7.83**	0.00001
STM3440	rplC	50S ribosomal protein L3	**-2.31**	0.04409	**-0.77**	0.03609	**-6.87**	0.00001
STM3440	rplC	50S ribosomal protein L3	**-1.15**	0.03984	**-0.56**	0.16031	**-6.51**	0.00002
STM3456	yheV	putative cytoplasmic protein	**0.54**	0.23442	**0.19**	0.50607	**-0.75**	0.08415
STM3456	yheV	putative cytoplasmic protein	**-0.12**	0.89465	**0.25**	0.47059	**-0.70**	0.06727
STM3457	kefB	glutathione-regulated potassium-efflux system protein	**0.19**	0.82818	**0.81**	0.02599	**-0.54**	0.17491
STM3457	kefB	glutathione-regulated potassium-efflux system protein	**0.77**	0.14129	**0.69**	0.16945	**0.31**	0.42791
STM3458	yheR	glutathione-regulated potassium-efflux system ancillary	**-0.96**	0.18619	**-0.16**	0.70641	**-1.34**	0.04752
STM3458	yheR	glutathione-regulated potassium-efflux system ancillary	**-1.05**	0.25384	**-0.50**	0.16531	**-2.81**	0.00369
STM3459	yheS	putative ABC transporter ATPase component	**-0.71**	0.16181	**-0.42**	0.27106	**-0.60**	0.32930
STM3459	yheS	putative ABC transporter ATPase component	**0.11**	0.79537	**-0.02**	0.95438	**-1.22**	0.02931
STM3461	STM3461	putative cytoplasmic protein	**-1.03**	0.06064	**0.69**	0.06222	**0.10**	0.82501
STM3461	STM3461	putative cytoplasmic protein	**0.02**	0.96475	**1.07**	0.00717	**0.38**	0.27889
STM3462	yheT	putative hydrolase	**-1.98**	0.01479	**-1.23**	0.00288	**-0.59**	0.20443
STM3462	yheT	putative hydrolase	**-1.00**	0.05058	**-0.61**	0.05922	**-1.01**	0.02853
STM3463	yheU	hypothetical protein STM3463	**-0.73**	0.18395	**-0.26**	0.46294	**-1.30**	0.00694
STM3463	yheU	hypothetical protein STM3463	**-0.38**	0.42879	**-0.21**	0.48124	**-0.16**	0.85658
STM3464	prkB	putative phosphoribulokinase	**-1.22**	0.13268	**-0.03**	0.93074	**0.23**	0.82944
STM3464	prkB	putative phosphoribulokinase	**-0.12**	0.86170	**-0.24**	0.50611	**-1.05**	0.04106
STM3465	yhfA	putative inner membrane protein	**-1.35**	0.03016	**-0.76**	0.13274	**-0.50**	0.33093
STM3465	yhfA	putative inner membrane protein	**-1.71**	0.02037	**-0.78**	0.02908	**-0.74**	0.21366
STM3466	crp	catabolite activator protein	**-1.46**	0.03369	**-0.38**	0.22710	**0.36**	0.29990
STM3466	crp	catabolite activator protein	**-1.56**	0.01609	**-0.65**	0.04781	**1.03**	0.02458
STM3467	yhfK	putative inner membrane protein	**0.48**	0.59927	**0.47**	0.14251	**-0.72**	0.19663
STM3467	yhfK	putative inner membrane protein	**0.47**	0.32529	**0.00**	0.99245	**1.69**	0.00177

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM3468	argD	bifunctional	**-0.43**	0.63577	**0.67**	0.12795	**-0.07**	0.91566
STM3468	argD	bifunctional	**0.48**	0.52824	**0.63**	0.04218	**-0.37**	0.39283
STM3469	pabA	para-aminobenzoate synthase component II	**0.27**	0.69320	**0.12**	0.75531	**-0.84**	0.10465
STM3469	pabA	para-aminobenzoate synthase component II	**-0.04**	0.94155	**0.70**	0.02713	**-0.01**	0.99115
STM3470	fic	putative cell filamentation protein	**-0.63**	0.19255	**0.93**	0.01310	**1.12**	0.01814
STM3470	fic	putative cell filamentation protein	**-0.28**	0.59387	**0.82**	0.01673	**1.33**	0.01623
STM3472	ppiA	peptidyl-prolyl cis-trans isomerase A	**-0.73**	0.39937	**0.75**	0.02530	**-0.76**	0.14767
STM3472	ppiA	peptidyl-prolyl cis-trans isomerase A	**0.88**	0.09689	**0.78**	0.03179	**-0.54**	0.26035
STM3473	yhfC	hypothetical protein STM3473	**-1.32**	0.04652	**-2.34**	0.00047	**-2.13**	0.00531
STM3473	yhfC	hypothetical protein STM3473	**-1.09**	0.03924	**-2.78**	0.00068	**-1.58**	0.01119
STM3474	nirB	nitrite reductase large subunit	**-0.56**	0.27302	**-0.45**	0.27937	**-0.92**	0.29073
STM3474	nirB	nitrite reductase large subunit	**0.90**	0.28793	**-0.34**	0.30199	**0.32**	0.39679
STM3475	nirD	nitrite reductase small subunit	**3.63**	0.00686	**-1.08**	0.02775	**-1.12**	0.00984
STM3475	nirD	nitrite reductase small subunit	**3.62**	0.00649	**-0.13**	0.69230	**0.78**	0.06357
STM3476	nirC	nitrite transport protein	**-0.39**	0.50370	**-0.34**	0.30677	**-0.95**	0.03460
STM3476	nirC	nitrite transport protein	**-0.72**	0.19975	**-0.78**	0.11302	**-1.38**	0.09479
STM3477	cysG	siroheme synthase	**-1.33**	0.03584	**-0.37**	0.29496	**-1.20**	0.02302
STM3477	cysG	siroheme synthase	**0.28**	0.57995	**-0.41**	0.25850	**-0.35**	0.34475
STM3478	bigA	putative surface-exposed virulence protein	**-0.17**	0.82482	**-0.81**	0.06742	**-0.90**	0.14447
STM3478	bigA	putative surface-exposed virulence protein	**0.47**	0.36425	**-0.36**	0.18105	**0.03**	0.95841
STM3480	yhfL	putative outer membrane lipoprotein	**-1.92**	0.01801	**-1.68**	0.00106	**-2.39**	0.00904
STM3480	yhfL	putative outer membrane lipoprotein	**-0.81**	0.12658	**-2.23**	0.00037	**-2.47**	0.00040
STM3481	trpS	tryptophanyl-tRNA synthetase	**-2.81**	0.00796	**-2.39**	0.00027	**-2.56**	0.00026
STM3481	trpS	tryptophanyl-tRNA synthetase	**-1.83**	0.01576	**-2.15**	0.00022	**-2.60**	0.00016
STM3482	gph	phosphoglycolate phosphatase	**-3.45**	0.00512	**-1.78**	0.00081	**-2.99**	0.00009
STM3482	gph	phosphoglycolate phosphatase	**-2.72**	0.00673	**-1.90**	0.00076	**-2.40**	0.00094
STM3483	rpe	ribulose-phosphate 3-epimerase	**-1.94**	0.06216	**-1.08**	0.00562	**-1.56**	0.00250
STM3483	rpe	ribulose-phosphate 3-epimerase	**-1.62**	0.21234	**-1.51**	0.00332	**-0.94**	0.02531
STM3484	dam	DNA adenine methylase	**-2.38**	0.01572	**-1.01**	0.01898	**-2.79**	0.00129
STM3484	dam	DNA adenine methylase	**-1.28**	0.12631	**-1.44**	0.00334	**-1.90**	0.00238
STM3485	damX	membrane protein DamX	**-2.93**	0.00547	**-2.15**	0.00043	**-2.89**	0.00034
STM3485	damX	membrane protein DamX	**-1.50**	0.06407	**-1.51**	0.00389	**-2.93**	0.00011
STM3486	aroB	3-dehydroquinate synthase	**-2.50**	0.00595	**-1.23**	0.01004	**-3.06**	0.00020
STM3486	aroB	3-dehydroquinate synthase	**-2.56**	0.00845	**-1.07**	0.00822	**-2.56**	0.00020
STM3487	aroK	shikimate kinase I	**-3.28**	0.01041	**-1.54**	0.00229	**-3.03**	0.00053
STM3487	aroK	shikimate kinase I	**-3.00**	0.00796	**-1.82**	0.00114	**-3.01**	0.00012
STM3488	hofQ	putative type IV pilin assembly protein	**-0.19**	0.79541	**-0.64**	0.08377	**-1.38**	0.06065
STM3488	hofQ	putative type IV pilin assembly protein	**2.04**	0.01240	**-1.03**	0.04103	**0.07**	0.86859
STM3489	yrfA	putative inner membrane protein	**-0.88**	0.29292	**0.52**	0.12364	**0.43**	0.53809
STM3489	yrfA	putative inner membrane protein	**0.68**	0.24833	**0.59**	0.57173	**-0.15**	0.71950
STM3490	yrfB	putative inner membrane protein	**-0.66**	0.14629	**-1.68**	0.00123	**-0.46**	0.38154
STM3490	yrfB	putative inner membrane protein	**1.03**	0.17351	**-2.78**	0.00006	**0.07**	0.91630
STM3491	yrfC	putative inner membrane protein	**3.09**	0.34200	**1.60**	0.03397	**3.71**	0.00050
STM3491	yrfC	putative inner membrane protein	**6.85**	0.01572	**2.70**	0.00097	**6.37**	0.00008
STM3492	yrfD	putative periplasmic protein	**-0.14**	0.80217	**-1.22**	0.05860	**-1.18**	0.05973
STM3492	yrfD	putative periplasmic protein	**0.76**	0.19650	**-2.09**	0.00016	**0.03**	0.97036
STM3493	mrcA	penicillin-binding protein 1A	**0.02**	0.96137	**-0.17**	0.61286	**0.58**	0.33672
STM3493	mrcA	penicillin-binding protein 1A	**1.60**	0.01425	**-0.64**	0.10706	**1.34**	0.20240
STM3494,S	yrfE	putative NTP pyrophosphohydrolase	**-0.12**	0.80373	**-0.99**	0.01250	**-1.47**	0.03920
STM3494,S	yrfE	putative NTP pyrophosphohydrolase	**0.89**	0.07006	**-0.76**	0.03908	**0.02**	0.96065
STM3495	yrfF	putative inner membrane protein	**-1.53**	0.01479	**0.79**	0.63620	**-1.29**	0.01926
STM3495	yrfF	putative inner membrane protein	**0.13**	0.89099	**-1.11**	0.00599	**-2.79**	0.03345
STM3496	yrfG	putative hydrolase	**-2.01**	0.00994	**-0.40**	0.20224	**-2.91**	0.00011
STM3496	yrfG	putative hydrolase	**-1.02**	0.05101	**-0.45**	0.18827	**-2.36**	0.00049
STM3497	yrfH	heat shock protein	**-0.18**	0.67327	**-0.08**	0.84454	**-1.89**	0.00623
STM3497	yrfH	heat shock protein	**0.29**	0.49059	**-0.14**	0.63156	**-2.05**	0.00482
STM3498	hslO	Hsp33-like chaperonin	**-1.42**	0.02101	**-0.77**	0.04391	**-3.30**	0.00017
STM3498	hslO	Hsp33-like chaperonin	**-0.32**	0.46688	**-0.91**	0.03131	**-2.28**	0.00035
STM3499	yhgE	putative inner membrane protein	**-0.38**	0.47761	**-0.07**	0.91015	**-1.03**	0.09597
STM3499	yhgE	putative inner membrane protein	**0.41**	0.82613	**-0.95**	0.05908	**-0.86**	0.28567
STM3500	pckA	phosphoenolpyruvate carboxykinase	**-0.58**	0.35838	**0.38**	0.80377	**-1.40**	0.08958
STM3500	pckA	phosphoenolpyruvate carboxykinase	**0.46**	0.31782	**-0.92**	0.02516	**-0.84**	0.06873
STM3501	envZ	osmolarity sensor protein	**0.08**	0.86166	**-0.55**	0.16014	**-1.35**	0.00880
STM3501	envZ	osmolarity sensor protein	**1.17**	0.10434	**-0.04**	0.93074	**-0.36**	0.44030
STM3502	ompR	osmolarity response regulator	**-1.26**	0.03751	**-0.54**	0.09961	**-1.30**	0.07020
STM3502	ompR	osmolarity response regulator	**-0.08**	0.87320	**-0.81**	0.02864	**-1.14**	0.02890
STM3503	greB	transcription elongation factor GreB	**-1.14**	0.07710	**-0.85**	0.02591	**-1.55**	0.00246
STM3503	greB	transcription elongation factor GreB	**0.52**	0.33087	**-0.85**	0.02287	**-1.02**	0.05272
STM3504	yhgF	putative RNase R	**-0.14**	0.82290	**-0.35**	0.64603	**-1.71**	0.01320
STM3504	yhgF	putative RNase R	**-1.30**	0.06233	**-1.69**	0.00500	**-2.46**	0.00221

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM3505	feoA	ferrous iron transport protein A	**-0.45**	0.51135	**-0.31**	0.30892	**-2.14**	0.00119
STM3505	feoA	ferrous iron transport protein A	**-0.64**	0.66707	**-0.15**	0.67595	**-2.61**	0.00122
STM3506	feoB	ferrous iron transport protein B	**-2.20**	0.00747	**-0.45**	0.20042	**-3.10**	0.00612
STM3506	feoB	ferrous iron transport protein B	**-0.03**	0.97698	**-0.46**	0.18646	**-0.98**	0.16190
STM3507	yhgG	putative cytoplasmic protein	**-1.41**	0.11096	**-0.78**	0.02289	**-2.30**	0.00048
STM3507	yhgG	putative cytoplasmic protein	**-0.71**	0.13705	**-1.22**	0.00742	**-0.64**	0.14597
STM3508	STM3508	putative cytoplasmic protein	**0.33**	0.46761	**-0.69**	0.12218	**-0.87**	0.08938
STM3508	STM3508	putative cytoplasmic protein	**0.81**	0.27387	**-0.12**	0.70431	**0.29**	0.56284
STM3509	bioH	putative hydrolase	**-1.25**	0.04117	**-0.11**	0.77755	**-1.60**	0.00372
STM3509	bioH	putative hydrolase	**0.05**	0.95651	**-0.31**	0.46473	**-1.27**	0.05524
STM3510	yhgH	putative amidophosphoribosyltransferase	**-2.59**	0.01041	**-1.69**	0.00115	**-2.30**	0.00080
STM3510	yhgH	putative amidophosphoribosyltransferase	**-2.05**	0.00818	**-1.77**	0.00154	**0.15**	0.83658
STM3511	yhgI	putative thioredoxin-like protein	**-1.40**	0.09590	**0.27**	0.40068	**-2.63**	0.00024
STM3511	yhgI	putative thioredoxin-like protein	**-0.55**	0.46541	**-0.05**	0.89425	**-2.10**	0.00096
STM3512	gntT	high-affinity gluconate permease	**-2.44**	0.01376	**-3.45**	0.00007	**-2.48**	0.00048
STM3512	gntT	high-affinity gluconate permease	**-1.85**	0.02645	**-3.24**	0.00010	**-1.59**	0.00623
STM3513	malQ	4-alpha-glucanotransferase	**1.12**	0.03757	**-0.87**	0.01589	**2.08**	0.00217
STM3513	malQ	4-alpha-glucanotransferase	**1.76**	0.04582	**-1.02**	0.02668	**2.15**	0.00176
STM3514	malP	maltodextrin phosphorylase	**0.52**	0.74788	**-0.29**	0.55701	**2.29**	0.02073
STM3514	malP	maltodextrin phosphorylase	**-0.70**	0.20566	**-0.72**	0.06210	**1.23**	0.01404
STM3515	malT	transcriptional regulator MalT	**-1.51**	0.03832	**-0.98**	0.02055	**-0.41**	0.29081
STM3515	malT	transcriptional regulator MalT	**-0.97**	0.05998	**-0.49**	0.11433	**-1.23**	0.01007
STM3516	STM3516	putative cytoplasmic protein	**0.29**	0.70807	**1.64**	0.00928	**2.02**	0.02539
STM3516	STM3516	putative cytoplasmic protein	**-0.54**	0.36389	**0.51**	0.23483	**-0.86**	0.05147
STM3517	STM3517	putative DNA-damage-inducibile protein	**0.28**	0.58533	**1.15**	0.00417	**1.08**	0.01491
STM3517	STM3517	putative DNA-damage-inducibile protein	**0.39**	0.43648	**0.86**	0.01829	**1.48**	0.00608
STM3518	rtcA	RNA 3'-terminal-phosphate cyclase	**0.69**	0.13168	**-0.47**	0.42811	**-1.06**	0.14787
STM3518	rtcA	RNA 3'-terminal-phosphate cyclase	**1.78**	0.02146	**0.02**	0.97528	**-0.06**	0.89807
STM3519	rtcB	putative cytoplasmic protein	**0.72**	0.12247	**1.23**	0.00769	**-0.02**	0.95532
STM3519	rtcB	putative cytoplasmic protein	**1.25**	0.07388	**1.33**	0.00218	**0.54**	0.22998
STM3521	STM3521	putative ribonucleoprotein related-protein	**-0.10**	0.83479	**2.34**	0.00014	**-0.86**	0.14413
STM3521	STM3521	putative ribonucleoprotein related-protein	**0.82**	0.26862	**2.47**	0.00048	**0.06**	0.93090
STM3522	rtcR	sigma N	**-2.24**	0.00720	**-1.18**	0.00824	**-1.63**	0.00386
STM3522	rtcR	sigma N	**-0.83**	0.13203	**-0.74**	0.04531	**-1.26**	0.01062
STM3523	glpR	glp operon transcriptional repressor	**-1.29**	0.17944	**-1.92**	0.00040	**-2.29**	0.00038
STM3523	glpR	glp operon transcriptional repressor	**-0.55**	0.47591	**-1.68**	0.00203	**-1.59**	0.00740
STM3524	glpG	glp regulon protein	**-1.92**	0.01177	**-1.22**	0.00268	**-0.88**	0.05474
STM3524	glpG	glp regulon protein	**-1.32**	0.15306	**-1.46**	0.00270	**-1.35**	0.00694
STM3525	glpE	thiosulfate sulfurtransferase	**-2.46**	0.00660	**-1.57**	0.00209	**0.17**	0.67281
STM3525	glpE	thiosulfate sulfurtransferase	**-1.55**	0.02148	**-1.03**	0.01103	**0.56**	0.13771
STM3526	glpD	sn-glycerol-3-phosphate dehydrogenase	**-1.60**	0.03103	**1.63**	0.00240	**2.17**	0.00048
STM3526	glpD	sn-glycerol-3-phosphate dehydrogenase	**-0.44**	0.33225	**1.38**	0.00220	**2.78**	0.00041
STM3527	STM3527	putative inner membrane protein	**-2.26**	0.00947	**0.31**	0.41870	**1.65**	0.00251
STM3527	STM3527	putative inner membrane protein	**-0.19**	0.72718	**0.96**	0.02113	**2.03**	0.00115
STM3528	STM3528	putative periplasmic phosphate-binding protein	**-0.98**	0.07739	**0.09**	0.81126	**1.19**	0.01612
STM3528	STM3528	putative periplasmic phosphate-binding protein	**0.46**	0.70228	**0.26**	0.51910	**1.53**	0.00210
STM3529	gldA	glycerol dehydrogenase	**0.86**	0.09484	**-2.08**	0.00143	**-0.65**	0.28012
STM3529	gldA	glycerol dehydrogenase	**2.46**	0.00660	**-1.35**	0.02911	**0.35**	0.48258
STM3531	STM3531	putative dihydroxyacid dehydratase	**-0.28**	0.70969	**0.14**	0.82426	**0.79**	0.21804
STM3531	STM3531	putative dihydroxyacid dehydratase	**0.43**	0.38733	**-0.27**	0.50209	**0.39**	0.26074
STM3532	STM3532	putative dihydrodipicolinate synthetase	**0.64**	0.20778	**-0.33**	0.42232	**0.20**	0.63347
STM3532	STM3532	putative dihydrodipicolinate synthetase	**1.05**	0.16421	**-0.16**	0.79961	**-0.64**	0.13286
STM3533	STM3533	putative transcriptional regulator	**-0.13**	0.80836	**0.08**	0.82574	**-1.47**	0.02552
STM3533	STM3533	putative transcriptional regulator	**0.31**	0.65238	**0.13**	0.69958	**-1.45**	0.06520
STM3534	glgP	glycogen phosphorylase	**-0.42**	0.54550	**-0.08**	0.85609	**0.55**	0.18597
STM3534	glgP	glycogen phosphorylase	**1.58**	0.27112	**0.44**	0.34003	**1.06**	0.20367
STM3535	glgA	glycogen synthase	**-0.83**	0.10464	**1.00**	0.00546	**0.57**	0.16052
STM3535	glgA	glycogen synthase	**-0.10**	0.83254	**1.08**	0.00579	**0.86**	0.03189
STM3536	glgC	glucose-1-phosphate adenylyltransferase	**-0.57**	0.53960	**1.27**	0.00372	**0.95**	0.05884
STM3536	glgC	glucose-1-phosphate adenylyltransferase	**-0.41**	0.69269	**1.36**	0.00202	**1.08**	0.02680
STM3537	glgX	glycogen debranching enzyme	**-0.96**	0.17998	**0.93**	0.02127	**0.00**	0.99405
STM3537	glgX	glycogen debranching enzyme	**0.57**	0.19566	**0.74**	0.07369	**0.94**	0.02806
STM3538	glgB	glycogen branching enzyme	**-0.71**	0.58445	**-1.99**	0.01685	**-2.97**	0.01841
STM3538	glgB	glycogen branching enzyme	**-0.73**	0.52711	**-3.55**	0.00006	**-2.52**	0.01809
STM3539	asd	aspartate-semialdehyde dehydrogenase	**-0.35**	0.42804	**-0.12**	0.65689	**-0.71**	0.11913
STM3539	asd	aspartate-semialdehyde dehydrogenase	**1.38**	0.11193	**0.39**	0.26260	**0.32**	0.61721
STM3541	gntU	low-affinity gluconate permease	**-0.57**	0.45214	**-0.50**	0.16073	**-0.80**	0.37964
STM3541	gntU	low-affinity gluconate permease	**0.41**	0.42672	**-0.32**	0.39875	**-0.33**	0.34465
STM3542	gntK	gluconate kinase 2	**-0.88**	0.10574	**-1.76**	0.00261	**-1.60**	0.01353
STM3542	gntK	gluconate kinase 2	**-0.24**	0.72148	**-2.18**	0.00319	**-0.85**	0.20928

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM3543	gntR	gluconate operon transcriptional repressor	**-1.09**	0.04548	**-0.99**	0.02466	**-1.42**	0.02074
STM3543	gntR	gluconate operon transcriptional repressor	**-0.47**	0.28048	**-1.10**	0.10477	**-0.83**	0.05032
STM3544	yhhW	putative cytoplasmic protein	**-0.68**	0.14190	**-0.39**	0.26118	**0.46**	0.36050
STM3544	yhhW	putative cytoplasmic protein	**1.17**	0.15688	**-0.73**	0.21172	**0.35**	0.41422
STM3545	yhhX	putative oxidoreductase	**0.32**	0.45046	**0.09**	0.81981	**-0.24**	0.50112
STM3545	yhhX	putative oxidoreductase	**0.70**	0.24803	**-0.32**	0.33116	**1.35**	0.04710
STM3546	yhhY	putative transferase	**-0.33**	0.75563	**0.47**	0.27018	**0.20**	0.83143
STM3546	yhhY	putative transferase	**0.80**	0.16140	**-0.64**	0.11782	**0.65**	0.44233
STM3547,Sc	STM3547,Sc	putative transcriptional regulator	**-0.97**	0.49348	**-0.99**	0.01691	**0.23**	0.71910
STM3547,Sc	STM3547,Sc	putative transcriptional regulator	**2.94**	0.00753	**0.29**	0.38602	**2.61**	0.00319
STM3548	STM3548	putative cytoplasmic protein	**1.22**	0.52384	**0.27**	0.46280	**-1.64**	0.01188
STM3548	STM3548	putative cytoplasmic protein	**0.28**	0.67877	**-0.46**	0.32674	**-0.58**	0.29650
STM3549	STM3549	putative inner membrane protein	**0.37**	0.49184	**-0.08**	0.83702	**0.32**	0.72474
STM3549	STM3549	putative inner membrane protein	**0.99**	0.12877	**-0.07**	0.89485	**0.30**	0.60178
STM3550	STM3550	putative phosphotriesterase	**-0.05**	0.91401	**0.95**	0.01881	**0.44**	0.20725
STM3550	STM3550	putative phosphotriesterase	**0.75**	0.30712	**0.84**	0.03304	**1.64**	0.00664
STM3551	ggt	gamma-glutamyltranspeptidase	**0.19**	0.83757	**2.16**	0.00016	**1.81**	0.03983
STM3551	ggt	gamma-glutamyltranspeptidase	**0.67**	0.41249	**1.25**	0.00437	**1.74**	0.00357
STM3552	yhhA	putative outer membrane protein	**1.14**	0.17300	**3.35**	0.00008	**4.72**	0.00003
STM3552	yhhA	putative outer membrane protein	**1.89**	0.15061	**3.12**	0.00006	**5.67**	0.00003
STM3553	ugpQ	cytoplasmic glycerophosphodiester phosphodiesterase	**-0.22**	0.71326	**2.11**	0.00058	**3.90**	0.00006
STM3553	ugpQ	cytoplasmic glycerophosphodiester phosphodiesterase	**2.48**	0.18287	**2.59**	0.00032	**4.25**	0.00005
STM3554	ugpC	sn-glycerol 3-phosphate transport protein	**-0.63**	0.19001	**0.96**	0.02475	**0.11**	0.78783
STM3554	ugpC	sn-glycerol 3-phosphate transport protein	**0.13**	0.80007	**1.13**	0.00552	**0.78**	0.08020
STM3555	ugpE	sn-glycerol 3-phosphate transport protein	**0.27**	0.57100	**1.55**	0.00126	**1.86**	0.10506
STM3555	ugpE	sn-glycerol 3-phosphate transport protein	**0.42**	0.39851	**1.61**	0.00090	**0.64**	0.26594
STM3556	ugpA	sn-glycerol 3-phosphate transport protein	**-0.35**	0.56465	**0.80**	0.05574	**-0.05**	0.94036
STM3556	ugpA	sn-glycerol 3-phosphate transport protein	**-0.91**	0.31093	**0.72**	0.06187	**-0.45**	0.30091
STM3557	ugpB	sn-glycerol 3-phosphate transport protein	**0.10**	0.85641	**4.07**	0.00009	**2.19**	0.00458
STM3557	ugpB	sn-glycerol 3-phosphate transport protein	**1.86**	0.01519	**4.40**	0.00002	**2.68**	0.00020
STM3558	STM3558	death-on-curing protein	**4.75**	0.01114	**1.11**	0.03230	**1.40**	0.19577
STM3558	STM3558	death-on-curing protein	**4.49**	0.00512	**1.46**	0.00223	**0.78**	0.15374
STM3559	yhhV	putative cytoplasmic protein	**1.30**	0.21827	**1.40**	0.00479	**0.57**	0.13870
STM3559	yhhV	putative cytoplasmic protein	**1.19**	0.39416	**1.21**	0.00528	**1.20**	0.00890
STM3560	livF	high-affinity branched-chain amino acid transporter	**-0.33**	0.52677	**-0.39**	0.18987	**-0.82**	0.12032
STM3560	livF	high-affinity branched-chain amino acid transporter	**1.14**	0.10566	**0.26**	0.52399	**-0.26**	0.62655
STM3561	livG	high-affinity branched-chain amino acid transporter	**0.78**	0.51827	**-0.17**	0.64724	**-0.54**	0.31770
STM3561	livG	high-affinity branched-chain amino acid transporter	**1.98**	0.10004	**0.22**	0.43604	**0.47**	0.25508
STM3562	livM	high-affinity branched-chain amino acid transporter	**-0.10**	0.91891	**0.46**	0.25593	**-0.57**	0.26266
STM3562	livM	high-affinity branched-chain amino acid transporter	**0.98**	0.19734	**-0.12**	0.72596	**0.35**	0.57912
STM3563	livH	high-affinity branched-chain amino acid transporter	**0.40**	0.76732	**-0.44**	0.29370	**-0.12**	0.86464
STM3563	livH	high-affinity branched-chain amino acid transporter	**0.64**	0.15955	**-1.23**	0.01565	**-0.35**	0.51233
STM3564	livK	high-affinity branched-chain amino acid transporter	**-1.12**	0.08009	**-0.46**	0.34745	**-1.26**	0.08572
STM3564	livK	high-affinity branched-chain amino acid transporter	**-0.46**	0.42507	**-0.55**	0.16827	**-0.51**	0.22426
STM3565	yhhK	putative acetyltransferase	**-0.14**	0.87497	**-0.56**	0.18350	**-0.76**	0.07576
STM3565	yhhK	putative acetyltransferase	**-0.66**	0.43305	**-1.32**	0.00270	**-3.43**	0.00024
STM3567	livJ	high-affinity branched-chain amino acid transporter	**-0.53**	0.39473	**0.50**	0.19402	**-0.11**	0.84807
STM3567	livJ	high-affinity branched-chain amino acid transporter	**1.19**	0.46005	**1.08**	0.18105	**3.84**	0.00006
STM3568	rpoH	RNA polymerase sigma factor	**0.94**	0.06625	**1.67**	0.00537	**-1.00**	0.02091
STM3568	rpoH	RNA polymerase sigma factor	**2.43**	0.00901	**2.61**	0.00036	**-0.11**	0.75966
STM3569	ftsX	putative cell division protein	**-0.80**	0.14212	**-0.36**	0.44499	**-2.46**	0.00048
STM3569	ftsX	putative cell division protein	**-1.27**	0.04285	**-0.30**	0.28895	**-1.29**	0.04394
STM3570	ftsE	putative cell division ATPase	**-1.98**	0.01172	**-1.04**	0.00898	**-2.80**	0.00012
STM3570	ftsE	putative cell division ATPase	**-1.21**	0.28620	**-0.99**	0.02034	**-2.25**	0.00035
STM3571	ftsY	cell division membrane protein	**-2.27**	0.01171	**-1.19**	0.00358	**-2.15**	0.00038
STM3571	ftsY	cell division membrane protein	**-1.67**	0.02299	**-0.77**	0.03523	**-1.07**	0.04187
STM3572	yhhF	putative methyltransferase	**-1.76**	0.01908	**-1.13**	0.02134	**-2.63**	0.00023
STM3572	yhhF	putative methyltransferase	**-0.51**	0.24950	**-1.18**	0.00375	**-1.76**	0.00500
STM3573	yhhL	putative inner membrane protein	**0.19**	0.64308	**-0.16**	0.79553	**-0.24**	0.71719
STM3573	yhhL	putative inner membrane protein	**-1.04**	0.05517	**-0.73**	0.07013	**-1.32**	0.05310
STM3574	yhhM	putative inner membrane protein	**-0.95**	0.07418	**-0.09**	0.80914	**-0.51**	0.46122
STM3574	yhhM	putative inner membrane protein	**-0.83**	0.09954	**0.02**	0.95587	**-1.02**	0.03152
STM3575	yhhN	putative inner membrane protein	**-0.55**	0.22704	**0.21**	0.51971	**0.08**	0.87984
STM3575	yhhN	putative inner membrane protein	**0.76**	0.17908	**-0.68**	0.08462	**0.18**	0.72188
STM3576	zntA	Pb/Cd/Zn/Hg-transporting ATPase	**-0.10**	0.87305	**0.85**	0.04575	**-1.07**	0.05609
STM3576	zntA	Pb/Cd/Zn/Hg-transporting ATPase	**-0.49**	0.62964	**0.94**	0.03802	**-1.42**	0.13854
STM3577	tcp	methyl-accepting transmembrane citrate/phenol	**-1.03**	0.14495	**-0.30**	0.33936	**-1.33**	0.12680
STM3577	tcp	methyl-accepting transmembrane citrate/phenol	**1.17**	0.31088	**-1.05**	0.01299	**-1.57**	0.01412
STM3578	yhhP	hypothetical protein STM3578	**-0.68**	0.24145	**-1.60**	0.00095	**-2.36**	0.00035
STM3578	yhhP	hypothetical protein STM3578	**-1.40**	0.21975	**-1.16**	0.01299	**-2.07**	0.00449

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM3579	yhhQ	putative integral membrane protein	**-0.62**	0.20826	**-0.63**	0.09192	**-1.42**	0.00517
STM3579	yhhQ	putative integral membrane protein	**-0.04**	0.92137	**-0.64**	0.05009	**-0.41**	0.32603
STM3580	STM3580	putative inner membrane lipoprotein	**0.08**	0.86536	**-0.08**	0.84438	**-0.08**	0.88000
STM3580	STM3580	putative inner membrane lipoprotein	**0.92**	0.15734	**-0.18**	0.52818	**0.46**	0.36005
STM3581,S	yhhS	hypothetical protein STM3581,S	**-0.75**	0.23689	**-0.69**	0.06483	**-1.19**	0.01817
STM3581,S	yhhS	hypothetical protein STM3581,S	**0.07**	0.92137	**-0.50**	0.18762	**-0.86**	0.08201
STM3582	yhhT	putative permease	**1.88**	0.01814	**-0.25**	0.76700	**0.63**	0.60776
STM3582	yhhT	putative permease	**0.80**	0.15459	**-1.21**	0.01129	**-0.17**	0.71291
STM3583	acpT	putative phosphopantetheinyl transferase	**3.08**	0.19917	**-0.75**	0.05929	**0.86**	0.37291
STM3583	acpT	putative phosphopantetheinyl transferase	**0.45**	0.69269	**-1.26**	0.00525	**-0.52**	0.29769
STM3584	nikR	nickel responsive regulator	**-0.54**	0.29437	**0.39**	0.21455	**-2.39**	0.00341
STM3584	nikR	nickel responsive regulator	**-0.52**	0.33225	**-0.12**	0.72185	**-0.71**	0.35738
STM3585	yhhJ	putative ABC transport protein	**-0.08**	0.94892	**-1.12**	0.04646	**-0.85**	0.31442
STM3585	yhhJ	putative ABC transport protein	**0.01**	0.98229	**-1.69**	0.00075	**-0.27**	0.48077
STM3586,S	yhiH	putative ABC-type multidrug transport system ATPase	**-0.07**	0.88528	**0.07**	0.89335	**-0.87**	0.24317
STM3586,S	yhiH	putative ABC-type multidrug transport system ATPase	**-0.11**	0.86483	**-1.24**	0.00796	**-0.59**	0.22619
STM3587	yhiI	hypothetical protein STM3587	**-0.87**	0.09567	**-0.60**	0.05200	**-0.54**	0.14930
STM3587	yhiI	hypothetical protein STM3587	**0.20**	0.80007	**-0.89**	0.02329	**0.48**	0.34686
STM3588	yhiN	putative periplasmic protein	**-0.50**	0.34131	**-0.98**	0.01633	**-0.90**	0.08629
STM3588	yhiN	putative periplasmic protein	**0.37**	0.62264	**-1.42**	0.00226	**-0.67**	0.24548
STM3589	pitA	low-affinity phosphate transporter	**-1.00**	0.08528	**-0.89**	0.02519	**-1.23**	0.01084
STM3589	pitA	low-affinity phosphate transporter	**-0.76**	0.30885	**-0.72**	0.04035	**-0.22**	0.58025
STM3590	uspB	universal stress protein UspB	**-0.92**	0.05888	**0.20**	0.57880	**1.07**	0.02167
STM3590	uspB	universal stress protein UspB	**0.90**	0.12765	**0.75**	0.04939	**1.82**	0.00484
STM3591	uspA	universal stress protein A	**-2.29**	0.02316	**0.53**	0.17418	**0.74**	0.04585
STM3591	uspA	universal stress protein A	**-1.37**	0.02423	**1.03**	0.03672	**1.31**	0.00625
STM3592	yhiP	putative peptide transport protein	**-1.27**	0.08730	**-1.05**	0.03391	**-1.82**	0.00685
STM3592	yhiP	putative peptide transport protein	**0.28**	0.69139	**0.84**	0.59387	**-0.50**	0.30575
STM3593	yhiQ	putative SAM-dependent methyltransferase	**-1.23**	0.17650	**-1.07**	0.00579	**-1.13**	0.13695
STM3593	yhiQ	putative SAM-dependent methyltransferase	**-1.24**	0.05920	**-0.53**	0.18764	**-2.01**	0.00626
STM3594	prlC	oligopeptidase A	**-1.68**	0.01212	**-0.73**	0.04956	**-0.86**	0.03378
STM3594	prlC	oligopeptidase A	**-0.72**	0.20634	**-0.67**	0.05349	**0.09**	0.83143
STM3595	STM3595	putative phosphatase	**-0.67**	0.14161	**-0.60**	0.06645	**-2.17**	0.00038
STM3595	STM3595	putative phosphatase	**-0.06**	0.89465	**-0.68**	0.04174	**-1.47**	0.00714
STM3596	yhiR	putative cytoplasmic protein	**-2.06**	0.02394	**-0.84**	0.04882	**-2.71**	0.00121
STM3596	yhiR	putative cytoplasmic protein	**-0.77**	0.15787	**-0.71**	0.06536	**-2.21**	0.00063
STM3597	gor	glutathione reductase	**-1.18**	0.04720	**-0.05**	0.87339	**-0.54**	0.28709
STM3597	gor	glutathione reductase	**-0.76**	0.38860	**-0.35**	0.32622	**0.16**	0.93356
STM3598	STM3598	putative L-asparaginase	**-1.62**	0.04923	**-0.22**	0.56841	**-2.17**	0.00210
STM3598	STM3598	putative L-asparaginase	**0.22**	0.65246	**-0.06**	0.86476	**-1.74**	0.00404
STM3599	STM3599	anaerobic C4-dicarboxylate transporter	**1.47**	0.10017	**0.75**	0.13448	**-0.99**	0.06223
STM3599	STM3599	anaerobic C4-dicarboxylate transporter	**1.14**	0.14590	**0.74**	0.11673	**0.57**	0.31515
STM3600	STM3600	putative sugar kinase	**-0.22**	0.63301	**-0.90**	0.02561	**-1.25**	0.03141
STM3600	STM3600	putative sugar kinase	**0.51**	0.43483	**-1.57**	0.00383	**0.34**	0.63350
STM3601	STM3601	putative phosphosugar isomerase	**0.31**	0.61449	**0.47**	0.29431	**-0.40**	0.36349
STM3601	STM3601	putative phosphosugar isomerase	**0.94**	0.07565	**0.42**	0.20221	**0.75**	0.06536
STM3602	STM3602	putative regulatory protein	**0.58**	0.37554	**1.67**	0.00280	**1.51**	0.01188
STM3602	STM3602	putative regulatory protein	**0.21**	0.75166	**0.24**	0.54396	**0.39**	0.42219
STM3603	treF	cytoplasmic trehalase	**-0.55**	0.25906	**0.35**	0.27764	**0.51**	0.25754
STM3603	treF	cytoplasmic trehalase	**-0.02**	0.96815	**-0.45**	0.10092	**0.41**	0.32535
STM3604	STM3604	putative inner membrane protein	**0.82**	0.10890	**0.04**	0.92774	**-0.46**	0.51260
STM3604	STM3604	putative inner membrane protein	**2.01**	0.01019	**-0.41**	0.20001	**0.74**	0.07085
STM3605	STM3605	putative phage endolysin	**-1.34**	0.02909	**-0.35**	0.58314	**-1.79**	0.00518
STM3605	STM3605	putative phage endolysin	**0.28**	0.66545	**1.03**	0.06017	**-1.42**	0.01436
STM3606	yhjB	putative transcriptional regulator	**-0.15**	0.83625	**0.89**	0.02005	**1.75**	0.01421
STM3606	yhjB	putative transcriptional regulator	**1.02**	0.18692	**0.83**	0.10482	**1.59**	0.09535
STM3607	yhjC	putative transcriptional regulator	**0.70**	0.33719	**0.48**	0.31019	**-0.32**	0.53394
STM3607	yhjC	putative transcriptional regulator	**1.07**	0.14326	**0.58**	0.24386	**0.95**	0.06382
STM3608	yhjD	putative tRNA-processing ribonuclease	**-0.43**	0.49184	**-0.26**	0.45604	**-1.23**	0.01311
STM3608	yhjD	putative tRNA-processing ribonuclease	**0.90**	0.36043	**-0.99**	0.01753	**-0.39**	0.53138
STM3609	yhjE	putative transport protein	**-0.43**	0.32444	**-0.01**	0.98628	**0.37**	0.37700
STM3609	yhjE	putative transport protein	**1.01**	0.56646	**0.12**	0.77342	**0.73**	0.10351
STM3610	yhjG	putative inner membrane protein	**-0.63**	0.19533	**1.34**	0.05619	**1.71**	0.00322
STM3610	yhjG	putative inner membrane protein	**0.90**	0.47086	**-0.29**	0.48388	**1.11**	0.29146
STM3611	yhjH	hypothetical protein STM3611	**-1.16**	0.27983	**-2.82**	0.00131	**-0.12**	0.82498
STM3611	yhjH	hypothetical protein STM3611	**-1.27**	0.09362	**-0.09**	0.92012	**-0.33**	0.65347
STM3612	kdgK	ketodeoxygluconokinase	**-1.26**	0.03893	**-0.96**	0.00978	**-0.71**	0.11151
STM3612	kdgK	ketodeoxygluconokinase	**-1.43**	0.02303	**-0.48**	0.11555	**-2.02**	0.00155
STM3613	yhjJ	putative Zn-dependent peptidase	**-0.81**	0.46481	**-1.25**	0.00355	**-0.84**	0.30373
STM3613	yhjJ	putative Zn-dependent peptidase	**-0.12**	0.78280	**-0.73**	0.05922	**-1.00**	0.05468

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM3614	dctA	C4-dicarboxylate transport protein	**-1.28**	0.03218	**-1.20**	0.02972	**-2.63**	0.00645
STM3614	dctA	C4-dicarboxylate transport protein	**-0.33**	0.49704	**-0.53**	0.20143	**0.24**	0.80516
STM3615	yhjK	putative diguanylate cyclase/phosphodiesterase	**-0.76**	0.19221	**0.14**	0.71333	**0.33**	0.43281
STM3615	yhjK	putative diguanylate cyclase/phosphodiesterase	**-0.09**	0.85980	**0.59**	0.46930	**0.16**	0.70871
STM3616	yhjL	tetratricopeptide repeat protein	**0.18**	0.83757	**-0.89**	0.05044	**-0.97**	0.17427
STM3616	yhjL	tetratricopeptide repeat protein	**-0.10**	0.86668	**-1.29**	0.00177	**-0.45**	0.35814
STM3617	STM3617	endo-1,4-D-glucanase	**-2.37**	0.00747	**-1.49**	0.00513	**-1.03**	0.07731
STM3617	STM3617	endo-1,4-D-glucanase	**-1.37**	0.02258	**-0.99**	0.01671	**-0.99**	0.08841
STM3618	yhjN	putative cellulose synthase	**-1.68**	0.01337	**-0.86**	0.04189	**-1.37**	0.00649
STM3618	yhjN	putative cellulose synthase	**-2.88**	0.01636	**-1.33**	0.00221	**-4.20**	0.00009
STM3619	yhjO	glycosyltransferase	**-1.34**	0.02526	**-1.20**	0.00269	**-2.62**	0.00136
STM3619	yhjO	glycosyltransferase	**-0.47**	0.67071	**-1.61**	0.00070	**-1.86**	0.01077
STM3620	yhjQ	putative chromosome partitioning ATPase	**-0.68**	0.17875	**-0.11**	0.87427	**-1.94**	0.00111
STM3620	yhjQ	putative chromosome partitioning ATPase	**0.29**	0.63895	**-1.18**	0.00701	**-1.05**	0.02888
STM3621	yhjR	putative cytoplasmic protein	**-1.00**	0.09937	**-0.48**	0.21341	**-1.25**	0.02077
STM3621	yhjR	putative cytoplasmic protein	**-0.07**	0.91699	**-0.25**	0.39449	**-0.98**	0.04885
STM3622	yhjS	putative cytoplasmic protein	**-2.03**	0.00802	**-0.88**	0.05632	**-0.97**	0.03475
STM3622	yhjS	putative cytoplasmic protein	**-0.24**	0.72641	**-1.03**	0.00506	**-0.78**	0.12691
STM3623	yhjT	putative inner membrane protein	**-1.93**	0.01279	**-1.21**	0.01875	**-1.30**	0.03798
STM3623	yhjT	putative inner membrane protein	**0.57**	0.63041	**-1.27**	0.01167	**0.02**	0.97512
STM3624	yhjU	putative inner membrane protein	**-2.43**	0.00921	**-0.80**	0.06054	**-2.23**	0.00102
STM3624	yhjU	putative inner membrane protein	**-1.19**	0.08078	**-0.38**	0.24818	**-1.74**	0.00157
STM3624A	STM3624A	cystathionine gamma-synthase	**-1.54**	0.03083	**-0.50**	0.20843	**-2.00**	0.01439
STM3624A	STM3624A	cystathionine gamma-synthase	**-0.70**	0.14011	**-0.86**	0.05743	**-0.98**	0.21358
STM3625	yhjV	putative transport protein	**3.22**	0.00704	**-1.39**	0.00703	**3.30**	0.00013
STM3625	yhjV	putative transport protein	**1.88**	0.03379	**-1.56**	0.00137	**0.99**	0.26122
STM3626	dppF	dipeptide transport protein	**0.00**	0.99180	**-0.59**	0.07242	**0.94**	0.02688
STM3626	dppF	dipeptide transport protein	**0.41**	0.59763	**-0.46**	0.53863	**-0.55**	0.68835
STM3627	dppD	dipeptide transport protein	**0.17**	0.72937	**-0.06**	0.95696	**0.29**	0.59962
STM3627	dppD	dipeptide transport protein	**1.15**	0.26685	**-0.93**	0.05633	**1.56**	0.05037
STM3628	dppC	dipeptide transport protein 2	**-1.07**	0.05303	**-0.59**	0.16726	**-0.68**	0.29622
STM3628	dppC	dipeptide transport protein 2	**0.19**	0.79719	**-0.95**	0.02354	**-0.35**	0.59986
STM3629	dppB	dipeptide transport protein 1	**0.05**	0.93391	**0.28**	0.43925	**0.12**	0.82986
STM3629	dppB	dipeptide transport protein 1	**1.39**	0.05865	**0.37**	0.41568	**2.51**	0.00088
STM3630	dppA	dipeptide transport protein	**-1.00**	0.09445	**2.36**	0.00044	**1.01**	0.04132
STM3630	dppA	dipeptide transport protein	**1.60**	0.19621	**2.12**	0.00016	**0.85**	0.18122
STM3631	STM3631	putative xanthine permease	**0.06**	0.96120	**0.36**	0.30026	**1.31**	0.13645
STM3631	STM3631	putative xanthine permease	**1.00**	0.43980	**-0.38**	0.51353	**1.73**	0.08142
STM3632	STM3632	hypothetical protein STM3632	**-0.37**	0.52914	**-0.62**	0.05563	**0.05**	0.90808
STM3632	STM3632	hypothetical protein STM3632	**-1.16**	0.28741	**-1.39**	0.00185	**-0.24**	0.57254
STM3633	STM3633	putative regulatory protein	**-0.64**	0.30115	**-0.82**	0.04869	**-2.38**	0.00594
STM3633	STM3633	putative regulatory protein	**-0.53**	0.32756	**-0.46**	0.19105	**-1.03**	0.07769
STM3634	proK	STM3634	**0.73**	0.29898	**-1.67**	0.00663	**0.03**	0.95596
STM3634	proK	STM3634	**0.39**	0.67601	**-1.24**	0.00407	**0.08**	0.92513
STM3635	yhjW	putative membrane-associated metal-dependent hydrolase	**0.77**	0.26729	**0.39**	0.55009	**0.10**	0.84748
STM3635	yhjW	putative membrane-associated metal-dependent hydrolase	**1.46**	0.05704	**0.61**	0.07982	**0.36**	0.44761
STM3636	lpfE	long polar fimbrial minor protein	**0.11**	0.78589	**-0.22**	0.53425	**-0.40**	0.30176
STM3636	lpfE	long polar fimbrial minor protein	**2.07**	0.02352	**-0.47**	0.14971	**0.84**	0.50804
STM3637	lpfD	long polar fimbrial protein	**-0.85**	0.16697	**-0.63**	0.22494	**0.09**	0.92078
STM3637	lpfD	long polar fimbrial protein	**0.06**	0.89601	**-0.98**	0.01227	**-0.65**	0.50497
STM3638	lpfC	long polar fimbrial outer membrane usher protein	**-0.22**	0.74962	**-0.83**	0.01996	**-0.79**	0.09289
STM3638	lpfC	long polar fimbrial outer membrane usher protein	**1.16**	0.26729	**0.04**	0.90753	**-0.16**	0.75232
STM3639	lpfB	long polar fimbrial chaperone precursor	**-0.60**	0.39885	**0.01**	0.97076	**0.79**	0.16977
STM3639	lpfB	long polar fimbrial chaperone precursor	**1.94**	0.16050	**-0.15**	0.86643	**2.78**	0.00032
STM3640	lpfA	long polar fimbrial protein A precursor	**2.16**	0.06092	**0.18**	0.80656	**1.49**	0.01034
STM3640	lpfA	long polar fimbrial protein A precursor	**2.10**	0.00935	**0.19**	0.67843	**1.50**	0.00488
STM3641	yhjY	putative lipase	**-1.05**	0.06721	**-0.35**	0.31929	**-1.10**	0.04176
STM3641	yhjY	putative lipase	**-0.08**	0.86346	**-0.03**	0.94687	**0.41**	0.39325
STM3642	tag	3-methyl-adenine DNA glycosylase I	**-0.28**	0.75688	**0.15**	0.62123	**-0.37**	0.42919
STM3642	tag	3-methyl-adenine DNA glycosylase I	**1.21**	0.15341	**0.26**	0.34862	**-0.64**	0.09842
STM3643	yiaC	putative acetyltransferase	**2.18**	0.13710	**-1.02**	0.02286	**-0.95**	0.22236
STM3643	yiaC	putative acetyltransferase	**0.80**	0.13228	**-1.25**	0.01093	**-0.07**	0.92963
STM3644	bisC	biotin sulfoxide reductase	**-1.34**	0.04345	**-1.05**	0.02230	**-0.49**	0.31358
STM3644	bisC	biotin sulfoxide reductase	**-0.19**	0.69462	**-0.73**	0.03027	**-0.52**	0.53435
STM3645	yiaD	putative outer membrane lipoprotein	**0.70**	0.17300	**0.55**	0.09641	**-0.93**	0.10506
STM3645	yiaD	putative outer membrane lipoprotein	**1.65**	0.12475	**0.56**	0.15750	**-0.47**	0.25744
STM3646	yiaE	2-hydroxyacid dehydrogenase	**0.22**	0.82206	**0.37**	0.24254	**1.16**	0.01495
STM3646	yiaE	2-hydroxyacid dehydrogenase	**0.27**	0.82543	**-0.09**	0.77796	**1.76**	0.00193
STM3647	yiaF	putative outer membrane lipoprotein	**-1.85**	0.01955	**-0.48**	0.12765	**-1.72**	0.00991
STM3647	yiaF	putative outer membrane lipoprotein	**-0.33**	0.52349	**-0.60**	0.08862	**-0.68**	0.13943

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM3648	yiaG	putative transcriptional regulator	**-0.18**	0.67877	**0.98**	0.04450	**2.91**	0.00011
STM3648	yiaG	putative transcriptional regulator	**0.08**	0.88221	**1.20**	0.01200	**4.03**	0.00005
STM3649	cspA	major cold shock protein	**0.07**	0.94960	**0.32**	0.54635	**-1.31**	0.19053
STM3649	cspA	major cold shock protein	**-0.95**	0.10848	**0.36**	0.51733	**-1.57**	0.00241
STM3650	STM3650	hypothetical protein STM3650	**-0.72**	0.24896	**0.30**	0.49170	**-0.22**	0.60042
STM3650	STM3650	hypothetical protein STM3650	**0.81**	0.21015	**0.76**	0.05739	**-0.11**	0.76124
STM3651	STM3651	putative acetyltransferase	**1.27**	0.02737	**1.58**	0.00195	**-1.05**	0.02520
STM3651	STM3651	putative acetyltransferase	**1.65**	0.02087	**1.60**	0.00100	**-1.24**	0.05461
STM3652	STM3652	putative cytoplasmic protein	**0.13**	0.90917	**1.31**	0.00524	**-0.13**	0.76393
STM3652	STM3652	putative cytoplasmic protein	**0.15**	0.86821	**1.06**	0.01242	**-1.87**	0.01893
STM3655	glyS	glycyl-tRNA synthetase beta subunit	**-1.66**	0.05333	**-0.02**	0.98411	**-0.70**	0.07686
STM3655	glyS	glycyl-tRNA synthetase beta subunit	**-1.72**	0.01765	**-1.21**	0.02560	**-1.41**	0.02127
STM3656	glyQ	glycyl-tRNA synthetase alpha subunit	**-3.02**	0.01145	**-1.93**	0.00042	**-3.74**	0.00016
STM3656	glyQ	glycyl-tRNA synthetase alpha subunit	**-2.11**	0.02509	**-1.31**	0.02255	**-3.73**	0.00008
STM3657	STM3657	putative outer membrane lipoprotein	**-1.90**	0.00942	**-0.46**	0.12276	**-1.23**	0.00939
STM3657	STM3657	putative outer membrane lipoprotein	**-1.31**	0.04151	**-0.36**	0.23782	**-1.40**	0.01259
STM3658	yiaH	putative inner membrane protein	**-1.21**	0.12128	**0.14**	0.74098	**-0.90**	0.06181
STM3658	yiaH	putative inner membrane protein	**-1.13**	0.08216	**-1.42**	0.08181	**-0.12**	0.89709
STM3659	yiaB	putative inner membrane protein	**0.62**	0.30073	**-0.80**	0.04511	**-0.50**	0.57201
STM3659	yiaB	putative inner membrane protein	**2.14**	0.01082	**-1.08**	0.09039	**2.15**	0.00040
STM3660	xylB	xylulokinase	**-0.82**	0.45996	**-0.83**	0.08582	**-0.15**	0.80590
STM3660	xylB	xylulokinase	**-0.51**	0.64686	**-0.39**	0.22080	**0.27**	0.68216
STM3661	xylA	xylose isomerase	**-0.32**	0.51063	**0.18**	0.65154	**0.39**	0.50693
STM3661	xylA	xylose isomerase	**5.87**	0.00567	**1.38**	0.07216	**1.61**	0.03680
STM3662	xylR	xylose operon regulatory protein	**-1.31**	0.03457	**1.20**	0.00507	**-0.23**	0.57253
STM3662	xylR	xylose operon regulatory protein	**-0.38**	0.43235	**1.52**	0.00077	**0.51**	0.18553
STM3663	bax	putative ATP-binding protein	**-1.64**	0.02101	**1.49**	0.00296	**0.82**	0.15579
STM3663	bax	putative ATP-binding protein	**-0.78**	0.17020	**2.05**	0.00026	**0.81**	0.05441
STM3664	malS	periplasmic alpha-amylase precursor	**-0.17**	0.78300	**-0.83**	0.22093	**-0.11**	0.89991
STM3664	malS	periplasmic alpha-amylase precursor	**1.51**	0.07277	**-1.03**	0.03365	**0.71**	0.19111
STM3665	avtA	valine--pyruvate transaminase	**-0.40**	0.53192	**-1.06**	0.01622	**-0.27**	0.68201
STM3665	avtA	valine--pyruvate transaminase	**1.17**	0.04582	**-0.88**	0.03599	**0.34**	0.69818
STM3666	ysaA	putative oxidoreductase	**-1.23**	0.04161	**-1.39**	0.00489	**-0.99**	0.08442
STM3666	ysaA	putative oxidoreductase	**-0.31**	0.54425	**-0.75**	0.05356	**-1.44**	0.00982
STM3667	yiaJ	transcriptional repressor	**-1.01**	0.12518	**-0.32**	0.28405	**-0.98**	0.04336
STM3667	yiaJ	transcriptional repressor	**-0.04**	0.96762	**-0.93**	0.08234	**0.07**	0.86700
STM3668	yiaK	putative malate dehydrogenase	**-0.17**	0.86752	**-0.67**	0.07738	**-0.51**	0.42495
STM3668	yiaK	putative malate dehydrogenase	**0.43**	0.57639	**-0.76**	0.02771	**0.12**	0.79784
STM3669	yiaL	putative cytoplasmic protein	**-0.69**	0.26979	**-0.38**	0.26161	**-1.50**	0.00871
STM3669	yiaL	putative cytoplasmic protein	**-0.10**	0.90565	**-0.38**	0.23132	**0.38**	0.45088
STM3670	STM3670	putative chemotaxis protein	**-0.55**	0.49214	**0.19**	0.61574	**-0.99**	0.14874
STM3670	STM3670	putative chemotaxis protein	**0.72**	0.59477	**-0.94**	0.11132	**0.27**	0.57504
STM3671	yiaM	putative transporter	**-0.81**	0.14738	**0.17**	0.62367	**0.20**	0.64223
STM3671	yiaM	putative transporter	**-0.50**	0.43575	**-0.58**	0.18482	**0.10**	0.86801
STM3672	yiaN	hypothetical protein STM3672	**-0.52**	0.58781	**-0.06**	0.87675	**-0.83**	0.17618
STM3672	yiaN	hypothetical protein STM3672	**-1.03**	0.19634	**-0.64**	0.27846	**-0.20**	0.65684
STM3673	yiaO	putative periplasmic dicarboxylate-binding protein	**0.33**	0.68248	**0.27**	0.46732	**-0.83**	0.17093
STM3673	yiaO	putative periplasmic dicarboxylate-binding protein	**1.49**	0.04933	**-1.59**	0.00090	**-0.39**	0.77925
STM3674	lyxK	L-xylulose kinase	**0.50**	0.56239	**0.30**	0.39743	**1.77**	0.02463
STM3674	lyxK	L-xylulose kinase	**1.21**	0.12256	**0.69**	0.05828	**0.97**	0.06867
STM3675	sgbH	putative 3-hexulose-6-phosphate isomerase	**-0.12**	0.78220	**0.55**	0.29224	**-0.07**	0.88009
STM3675	sgbH	putative 3-hexulose-6-phosphate isomerase	**2.30**	0.00689	**-0.88**	0.06350	**-0.02**	0.96603
STM3676	sgbU	putative 3-hexulose-6-phosphate isomerase	**-0.12**	0.81631	**0.34**	0.45954	**-0.88**	0.03016
STM3676	sgbU	putative 3-hexulose-6-phosphate isomerase	**1.13**	0.05204	**-0.08**	0.82309	**0.70**	0.11118
STM3677	sgbE	L-ribulose-5-phosphate 4-epimerase	**0.22**	0.69987	**0.55**	0.45382	**-0.40**	0.54441
STM3677	sgbE	L-ribulose-5-phosphate 4-epimerase	**0.83**	0.27565	**-0.11**	0.71246	**0.29**	0.54250
STM3678	STM3678	putative regulatory protein	**0.54**	0.34438	**-0.09**	0.80553	**-0.62**	0.12695
STM3678	STM3678	putative regulatory protein	**0.88**	0.29860	**-0.20**	0.63301	**1.11**	0.21130
STM3679	STM3679	putative cytoplasmic protein	**0.37**	0.68543	**1.10**	0.00637	**2.69**	0.00107
STM3679	STM3679	putative cytoplasmic protein	**0.76**	0.14152	**1.22**	0.03130	**3.45**	0.00012
STM3680	aldB	aldehyde dehydrogenase B	**1.30**	0.20013	**3.54**	0.00005	**5.75**	0.00002
STM3680	aldB	aldehyde dehydrogenase B	**1.77**	0.06102	**2.85**	0.00016	**6.67**	0.00001
STM3681	STM3681	putative transcriptional regulator	**0.05**	0.94155	**-0.28**	0.74213	**0.90**	0.06811
STM3681	STM3681	putative transcriptional regulator	**0.72**	0.22727	**-1.47**	0.00309	**1.24**	0.01474
STM3682	selB	selenocysteinyl-tRNA-specific translation factor	**-2.05**	0.00796	**-0.50**	0.18265	**-0.44**	0.30244
STM3682	selB	selenocysteinyl-tRNA-specific translation factor	**-0.93**	0.18607	**-0.30**	0.39889	**0.47**	0.18300
STM3683	selA	selenocysteine synthase	**-1.83**	0.04098	**-0.96**	0.02714	**-1.84**	0.06733
STM3683	selA	selenocysteine synthase	**-0.90**	0.07276	**-0.64**	0.10840	**-0.91**	0.09709
STM3684	yibF	putative glutathione S-transferase	**0.45**	0.70804	**0.64**	0.08085	**0.84**	0.03225
STM3684	yibF	putative glutathione S-transferase	**2.85**	0.25396	**0.81**	0.05000	**1.45**	0.00342

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM3685	mtlA	mannitol-specific enzyme IIABC component	**0.62**	0.17298	**0.23**	0.51814	**0.26**	0.56325
STM3685	mtlA	mannitol-specific enzyme IIABC component	**-0.33**	0.54389	**0.40**	0.26156	**0.91**	0.03977
STM3686	mtlD	mannitol-1-phosphate 5-dehydrogenase	**0.98**	0.11427	**-0.32**	0.27468	**-0.42**	0.54393
STM3686	mtlD	mannitol-1-phosphate 5-dehydrogenase	**1.66**	0.02357	**-1.07**	0.00990	**0.23**	0.68573
STM3687	mtlR	mannitol operon repressor	**-1.73**	0.06644	**-0.63**	0.06689	**1.31**	0.01776
STM3687	mtlR	mannitol operon repressor	**-1.27**	0.13520	**-0.61**	0.11045	**2.09**	0.00151
STM3688	STM3688	putative cytoplasmic protein	**-0.92**	0.10994	**0.50**	0.14568	**3.10**	0.00015
STM3688	STM3688	putative cytoplasmic protein	**0.42**	0.48054	**0.25**	0.45330	**2.91**	0.00013
STM3689	yibL	putative cytoplasmic protein	**-0.75**	0.26894	**-1.37**	0.00520	**-0.52**	0.39419
STM3689	yibL	putative cytoplasmic protein	**0.03**	0.95954	**-1.39**	0.00142	**0.08**	0.86211
STM3690	STM3690	putative inner membrane lipoprotein	**0.67**	0.28285	**0.54**	0.48256	**2.10**	0.00575
STM3690	STM3690	putative inner membrane lipoprotein	**2.48**	0.01046	**0.00**	0.99628	**1.53**	0.00944
STM3691	STM3691	putative inner membrane protein	**0.87**	0.27828	**-0.07**	0.87640	**-0.23**	0.77868
STM3691	STM3691	putative inner membrane protein	**0.71**	0.36177	**-0.59**	0.09009	**0.01**	0.99083
STM3692	lldP	transporter LctP	**-0.69**	0.15552	**-0.97**	0.01811	**-0.36**	0.55203
STM3692	lldP	transporter LctP	**-1.16**	0.12316	**-0.89**	0.01612	**-1.76**	0.15597
STM3693	lldR	putative transcriptional regulator	**1.03**	0.11705	**-0.99**	0.02146	**-0.49**	0.44620
STM3693	lldR	putative transcriptional regulator	**1.66**	0.01761	**-1.23**	0.02012	**0.16**	0.74216
STM3694	lldD	L-lactate dehydrogenase	**-0.70**	0.36089	**-0.42**	0.55181	**0.43**	0.30914
STM3694	lldD	L-lactate dehydrogenase	**-0.43**	0.63321	**-1.03**	0.24832	**0.07**	0.91584
STM3695	yibK	putative tRNA/rRNA methyltransferase	**-0.75**	0.19304	**-0.80**	0.11469	**-1.97**	0.00236
STM3695	yibK	putative tRNA/rRNA methyltransferase	**0.51**	0.50087	**-0.77**	0.02363	**-0.47**	0.21289
STM3696	STM3696	putative transcriptional regulator	**-0.34**	0.50555	**0.15**	0.82139	**-0.89**	0.04636
STM3696	STM3696	putative transcriptional regulator	**-0.50**	0.24590	**-0.07**	0.86051	**-0.16**	0.81045
STM3697	STM3697	putative mandelate racemase	**-1.37**	0.05886	**0.38**	0.51543	**-0.97**	0.07254
STM3697	STM3697	putative mandelate racemase	**0.03**	0.95678	**0.01**	0.98570	**-0.71**	0.18787
STM3698	STM3698	putative permease	**-1.21**	0.13573	**-0.44**	0.15802	**-1.01**	0.03548
STM3698	STM3698	putative permease	**-0.25**	0.54206	**-0.31**	0.28715	**-1.40**	0.00391
STM3699	cysE	serine acetyltransferase	**-0.52**	0.28151	**0.23**	0.59682	**-1.78**	0.00526
STM3699	cysE	serine acetyltransferase	**-0.07**	0.87793	**0.59**	0.08758	**-1.16**	0.02842
STM3700	gpsA	NAD(P)H-dependent glycerol-3-phosphate dehydrogenase	**-1.37**	0.02592	**-0.36**	0.28483	**-1.87**	0.00419
STM3700	gpsA	NAD(P)H-dependent glycerol-3-phosphate dehydrogenase	**-1.37**	0.08765	**-0.18**	0.55502	**-1.88**	0.00977
STM3701	secB	export protein SecB	**-1.26**	0.16694	**-0.70**	0.03291	**-1.79**	0.00100
STM3701	secB	export protein SecB	**-1.19**	0.04297	**-0.15**	0.68936	**-1.24**	0.02064
STM3702	grxC	glutaredoxin 3	**-2.60**	0.00567	**-1.10**	0.02225	**-3.45**	0.00030
STM3702	grxC	glutaredoxin 3	**-2.17**	0.00969	**-1.13**	0.00418	**-3.24**	0.00035
STM3703	yibN	putative rhodanese-like sulfurtransferase	**-3.55**	0.00547	**-1.44**	0.00421	**-3.53**	0.00010
STM3703	yibN	putative rhodanese-like sulfurtransferase	**-1.91**	0.01317	**-1.01**	0.00813	**-2.83**	0.00018
STM3704	pmgI	phosphoglyceromutase	**-0.13**	0.79153	**-1.51**	0.00297	**-1.15**	0.03017
STM3704	pmgI	phosphoglyceromutase	**-0.62**	0.27013	**-1.59**	0.00170	**-1.36**	0.01793
STM3705	yibP	hypothetical protein STM3705	**-2.12**	0.00908	**-2.00**	0.00041	**-1.89**	0.00852
STM3705	yibP	hypothetical protein STM3705	**-3.36**	0.01926	**-1.79**	0.00043	**-3.06**	0.01722
STM3706	yigQ	putative periplasmic protein	**0.62**	0.36453	**-1.11**	0.00517	**-0.82**	0.20163
STM3706	yigQ	putative periplasmic protein	**1.18**	0.49254	**-1.20**	0.00300	**-0.18**	0.62268
STM3707	yibD	putative glycosyltransferase	**-1.26**	0.04836	**-1.62**	0.00876	**-1.16**	0.09393
STM3707	yibD	putative glycosyltransferase	**-1.43**	0.06091	**-1.43**	0.01644	**-1.68**	0.00273
STM3708	tdh	L-threonine 3-dehydrogenase	**-0.88**	0.16077	**-0.72**	0.05504	**-1.30**	0.01780
STM3708	tdh	L-threonine 3-dehydrogenase	**-0.09**	0.90608	**-0.22**	0.44568	**-0.46**	0.34478
STM3709	kbl	2-amino-3-ketobutyrate coenzyme A ligase	**-3.08**	0.00541	**-1.71**	0.00074	**-2.89**	0.00011
STM3709	kbl	2-amino-3-ketobutyrate coenzyme A ligase	**-2.32**	0.01061	**-1.48**	0.00257	**-2.86**	0.00020
STM3710	rfaD	ADP-L-glycero-D-mannoheptose-6-epimerase	**0.88**	0.50971	**1.16**	0.04910	**4.02**	0.00007
STM3710	rfaD	ADP-L-glycero-D-mannoheptose-6-epimerase	**0.49**	0.65614	**1.55**	0.00432	**2.96**	0.00025
STM3711	rfaF	ADP-heptose-LPS heptosyltransferase 1	**-3.26**	0.00546	**-1.60**	0.00188	**-1.59**	0.00257
STM3711	rfaF	ADP-heptose-LPS heptosyltransferase 1	**-2.84**	0.01081	**-1.71**	0.00110	**-1.93**	0.00145
STM3712	rfaC	heptosyl transferase I	**-1.52**	0.02646	**-1.36**	0.01178	**-1.60**	0.02536
STM3712	rfaC	heptosyl transferase I	**-2.95**	0.00660	**-1.72**	0.00088	**-2.02**	0.00115
STM3713	rfaL	O-antigen ligase	**-1.87**	0.02026	**-1.92**	0.00045	**-2.99**	0.00139
STM3713	rfaL	O-antigen ligase	**-2.60**	0.01636	**-2.13**	0.00041	**-2.30**	0.02390
STM3714	rfaK	putative hexose transferase	**-0.88**	0.06399	**-0.56**	0.13730	**0.15**	0.77058
STM3714	rfaK	putative hexose transferase	**-0.57**	0.19236	**-0.22**	0.54056	**-0.28**	0.42192
STM3715	rfaZ	lipopolysaccharide core biosynthetic protein	**-0.09**	0.95056	**1.22**	0.00469	**2.62**	0.00025
STM3715	rfaZ	lipopolysaccharide core biosynthetic protein	**1.82**	0.52914	**0.19**	0.76828	**3.16**	0.00012
STM3716	rfaY	lipopolysaccharide core biosynthetic protein	**-2.06**	0.00922	**-1.82**	0.00057	**-2.24**	0.00729
STM3716	rfaY	lipopolysaccharide core biosynthetic protein	**-1.75**	0.03523	**-2.31**	0.00027	**-3.14**	0.00510
STM3717	rfaJ	lipopolysaccharide glucosyltransferase	**-2.22**	0.00735	**-1.93**	0.00047	**-2.59**	0.00116
STM3717	rfaJ	lipopolysaccharide glucosyltransferase	**-1.25**	0.25989	**-2.48**	0.00007	**-2.03**	0.00226
STM3718	rfaI	lipopolysaccharide-alpha-1,3-D-galactosyltransferase	**-2.92**	0.00979	**-2.84**	0.00006	**-2.68**	0.00079
STM3718	rfaI	lipopolysaccharide-alpha-1,3-D-galactosyltransferase	**-3.39**	0.01007	**-2.64**	0.00042	**-2.68**	0.00141
STM3719	rfaB	lipopolysaccharide-1,6-D-galactosyltransferase	**-3.02**	0.01491	**-2.54**	0.00058	**-3.15**	0.00062
STM3719	rfaB	lipopolysaccharide-1,6-D-galactosyltransferase	**-1.39**	0.07341	**-2.20**	0.00015	**-1.61**	0.00721

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM3720	yibR	putative inner membrane protein	**0.82**	0.09758	**0.17**	0.54338	**2.37**	0.00084
STM3720	yibR	putative inner membrane protein	**0.69**	0.20931	**0.12**	0.78223	**2.99**	0.00010
STM3721	rfaP	lipopolysaccharide core biosynthetic protein	**-0.76**	0.28479	**-0.73**	0.06667	**0.15**	0.84396
STM3721	rfaP	lipopolysaccharide core biosynthetic protein	**-0.61**	0.37797	**-1.23**	0.00663	**0.08**	0.95861
STM3722	rfaG	glucosyltransferase I	**-1.93**	0.01918	**-1.46**	0.00262	**-2.64**	0.00038
STM3722	rfaG	glucosyltransferase I	**-0.44**	0.32838	**-1.29**	0.00581	**-1.85**	0.00149
STM3723	rfaQ	lipopolysaccharide core biosynthetic protein	**-2.88**	0.00547	**-1.77**	0.00051	**-2.62**	0.00115
STM3723	rfaQ	lipopolysaccharide core biosynthetic protein	**-2.33**	0.06948	**-1.72**	0.00132	**-2.56**	0.00245
STM3724	kdtA	3-deoxy-D-manno-octulosonic-acid transferase	**-2.24**	0.01319	**-1.10**	0.00609	**-3.39**	0.00010
STM3724	kdtA	3-deoxy-D-manno-octulosonic-acid transferase	**-0.92**	0.14255	**-1.03**	0.01041	**-2.85**	0.00101
STM3725	kdtB	phosphopantetheine adenylyltransferase	**-1.60**	0.04475	**-0.81**	0.01520	**-2.23**	0.00287
STM3725	kdtB	phosphopantetheine adenylyltransferase	**-1.07**	0.04268	**-0.83**	0.02537	**-1.94**	0.00942
STM3726	mutM	formamidopyrimidine-DNA glycosylase	**-1.87**	0.01896	**-0.56**	0.18357	**-2.86**	0.00093
STM3726	mutM	formamidopyrimidine-DNA glycosylase	**-0.58**	0.27024	**-0.77**	0.05632	**-2.07**	0.00238
STM3727	rpmG	50S ribosomal protein L33	**-3.17**	0.00547	**-1.98**	0.00185	**-3.25**	0.00011
STM3727	rpmG	50S ribosomal protein L33	**-2.25**	0.00841	**-1.79**	0.00571	**-2.73**	0.00028
STM3728	rpmB	50S ribosomal protein L28	**-4.10**	0.00900	**-3.01**	0.00055	**-5.24**	0.00004
STM3728	rpmB	50S ribosomal protein L28	**-3.39**	0.00541	**-2.20**	0.00102	**-4.37**	0.00003
STM3729	radC	DNA repair protein RadC	**-3.19**	0.00541	**-2.00**	0.00061	**-1.92**	0.00415
STM3729	radC	DNA repair protein RadC	**-1.65**	0.02592	**-2.13**	0.00047	**-2.13**	0.00038
STM3730	dfp	phosphopantothenoylcysteine synthase/decarboxylase	**-1.61**	0.01402	**-0.03**	0.93669	**-2.46**	0.00093
STM3730	dfp	phosphopantothenoylcysteine synthase/decarboxylase	**-0.25**	0.71986	**-0.60**	0.09317	**-2.23**	0.00228
STM3731	dut	deoxyuridine 5'-triphosphate nucleotidohydrolase	**-0.53**	0.21107	**-1.31**	0.00452	**-1.74**	0.03236
STM3731	dut	deoxyuridine 5'-triphosphate nucleotidohydrolase	**0.03**	0.95840	**-1.43**	0.00842	**-1.60**	0.02418
STM3732	slmA	nucleoid occlusion protein	**-0.42**	0.47264	**-0.60**	0.45514	**-1.12**	0.04483
STM3732	slmA	nucleoid occlusion protein	**-1.33**	0.02680	**-1.41**	0.00423	**-1.00**	0.07951
STM3733	pyrE	orotate phosphoribosyltransferase	**-1.01**	0.06558	**-0.87**	0.01533	**-0.36**	0.51047
STM3733	pyrE	orotate phosphoribosyltransferase	**-0.13**	0.79062	**-0.56**	0.22755	**-0.47**	0.33808
STM3734	rph	ribonuclease PH	**0.35**	0.45374	**-1.01**	0.02340	**-1.44**	0.05229
STM3734	rph	ribonuclease PH	**1.04**	0.20818	**-0.82**	0.02466	**-1.04**	0.09931
STM3735	yicC	putative stress-induced protein	**-1.96**	0.01405	**-0.71**	0.13103	**-1.11**	0.01387
STM3735	yicC	putative stress-induced protein	**0.62**	0.17439	**0.04**	0.95712	**1.84**	0.04130
STM3736	STM3736	putative transcriptional regulator	**-1.40**	0.04964	**-0.65**	0.09709	**-1.41**	0.00335
STM3736	STM3736	putative transcriptional regulator	**-0.92**	0.06409	**-1.10**	0.01929	**-0.57**	0.10354
STM3737	STM3737	putative Zn-dependent hydrolase	**-0.69**	0.15901	**-0.32**	0.42852	**-1.43**	0.01082
STM3737	STM3737	putative Zn-dependent hydrolase	**0.68**	0.14878	**-0.50**	0.27176	**-0.47**	0.24037
STM3738	yigC	putative inner membrane protein	**-0.60**	0.58966	**-1.02**	0.00630	**-1.10**	0.07277
STM3738	yigC	putative inner membrane protein	**-2.10**	0.06415	**-2.43**	0.00069	**-2.47**	0.01667
STM3739	yicF	DNA ligase	**-1.24**	0.08779	**-0.36**	0.34452	**-1.22**	0.02593
STM3739	yicF	DNA ligase	**-1.21**	0.28305	**-0.61**	0.04289	**-1.00**	0.16676
STM3740	gmk	guanylate kinase	**-1.65**	0.01262	**-0.74**	0.06206	**-1.34**	0.00400
STM3740	gmk	guanylate kinase	**-1.85**	0.08055	**-0.83**	0.01292	**-1.16**	0.01254
STM3741	rpoZ	DNA-directed RNA polymerase omega subunit	**-2.97**	0.00547	**-0.85**	0.01870	**-2.79**	0.00016
STM3741	rpoZ	DNA-directed RNA polymerase omega subunit	**-1.12**	0.04181	**-0.73**	0.02760	**-2.16**	0.00045
STM3742	spoT	(p)ppGpp synthetase II/guanosine-3',5'-bis pyrophosphate	**-3.18**	0.00547	**-2.46**	0.00013	**-2.03**	0.02860
STM3742	spoT	(p)ppGpp synthetase II/guanosine-3',5'-bis pyrophosphate	**-3.10**	0.01945	**-2.77**	0.00005	**-3.51**	0.00442
STM3743	spoU	putative tRNA/rRNA methyltransferase	**-1.23**	0.07835	**-2.59**	0.00014	**-3.36**	0.00073
STM3743	spoU	putative tRNA/rRNA methyltransferase	**-1.82**	0.04683	**-1.97**	0.00061	**-3.68**	0.00010
STM3744	recG	DNA helicase	**-0.95**	0.13497	**-0.47**	0.45197	**-0.16**	0.80952
STM3744	recG	DNA helicase	**0.65**	0.24810	**-0.46**	0.11498	**-1.01**	0.07923
STM3745	STM3745	putative cytoplasmic protein	**-0.40**	0.44035	**-0.30**	0.34920	**-2.82**	0.00046
STM3745	STM3745	putative cytoplasmic protein	**0.58**	0.30531	**-0.29**	0.58208	**-1.06**	0.05149
STM3746	gltS	glutamate transport protein	**-1.70**	0.01834	**-0.42**	0.34014	**-1.47**	0.01651
STM3746	gltS	glutamate transport protein	**-0.38**	0.47324	**-0.10**	0.80656	**-1.77**	0.00400
STM3747	yicE	putative purine/xanthine transport protein	**0.19**	0.68951	**0.34**	0.33319	**-1.54**	0.01141
STM3747	yicE	putative purine/xanthine transport protein	**0.84**	0.11138	**0.10**	0.73903	**-0.49**	0.34255
STM3748	yicH	putative inner membrane protein	**0.59**	0.16839	**-0.16**	0.65571	**-1.25**	0.01147
STM3748	yicH	putative inner membrane protein	**2.44**	0.01259	**-0.29**	0.31693	**0.52**	0.24471
STM3749	yicI	putative alpha xylosidase	**-0.48**	0.26642	**0.21**	0.50584	**-0.95**	0.13034
STM3749	yicI	putative alpha xylosidase	**0.74**	0.16462	**-0.21**	0.57107	**-0.32**	0.50308
STM3750	yicJ	putative transport protein	**0.15**	0.86652	**0.48**	0.30981	**1.42**	0.07039
STM3750	yicJ	putative transport protein	**1.05**	0.09643	**0.03**	0.94280	**1.50**	0.00999
STM3751	selC	STM3751	**-0.63**	0.38500	**0.28**	0.68933	**1.22**	0.05437
STM3751	selC	STM3751	**-0.80**	0.50075	**0.15**	0.80391	**0.43**	0.41547
STM3752	STM3752	putative cytoplasmic protein	**-0.94**	0.11013	**-0.48**	0.21884	**-0.49**	0.25088
STM3752	STM3752	putative cytoplasmic protein	**-0.18**	0.75031	**-0.74**	0.02726	**-0.20**	0.75334
STM3753	sugR	ATP binding protein	**-0.01**	0.97702	**-0.07**	0.83068	**-0.04**	0.93346
STM3753	sugR	ATP binding protein	**0.23**	0.61957	**-0.60**	0.09251	**1.16**	0.25040
STM3754	STM3754	putative cytoplasmic protein	**-0.74**	0.13062	**0.06**	0.85235	**1.23**	0.05453
STM3754	STM3754	putative cytoplasmic protein	**-1.14**	0.05440	**-0.43**	0.27368	**0.29**	0.42191

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM3755	rhuM	putative cytoplasmic protein	**0.23**	0.71753	**0.18**	0.71413	**0.19**	0.73589
STM3755	rhuM	putative cytoplasmic protein	**1.63**	0.01638	**0.39**	0.21994	**0.61**	0.25473
STM3756	rmbA	putative cytoplasmic protein	**-0.59**	0.22702	**-0.86**	0.04479	**-0.43**	0.47254
STM3756	rmbA	putative cytoplasmic protein	**1.03**	0.04270	**-1.38**	0.00673	**0.17**	0.65412
STM3757	misL	putative autotransporter	**1.40**	0.21414	**-0.06**	0.88634	**1.14**	0.24183
STM3757	misL	putative autotransporter	**0.28**	0.83883	**-0.43**	0.13311	**-0.54**	0.57822
STM3758	fidL	putative inner membrane protein	**-0.35**	0.48762	**-0.46**	0.12310	**-0.51**	0.25896
STM3758	fidL	putative inner membrane protein	**1.22**	0.18946	**0.68**	0.53774	**0.47**	0.34698
STM3759,S	marT	putative transcriptional regulator	**-0.13**	0.82925	**-0.25**	0.55429	**0.74**	0.25749
STM3759,S	marT	putative transcriptional regulator	**1.42**	0.07231	**-0.16**	0.77545	**0.24**	0.59886
STM3761	slsA	putative inner membrane protein	**0.09**	0.89905	**1.80**	0.00122	**-0.32**	0.45592
STM3761	slsA	putative inner membrane protein	**1.77**	0.01376	**2.00**	0.00079	**0.94**	0.02636
STM3762	cigR	putative inner membrane protein	**-0.48**	0.63662	**1.12**	0.00469	**-0.51**	0.55305
STM3762	cigR	putative inner membrane protein	**1.49**	0.02758	**2.05**	0.00091	**0.09**	0.81388
STM3763	mgtB	Mg2+ transporter	**1.77**	0.03109	**-1.02**	0.05850	**-1.39**	0.08794
STM3763	mgtB	Mg2+ transporter	**2.49**	0.01330	**-0.34**	0.53462	**0.63**	0.30355
STM3764	mgtC	Mg2+ transport protein	**4.25**	0.00541	**0.33**	0.35977	**-0.67**	0.24396
STM3764	mgtC	Mg2+ transport protein	**5.18**	0.00512	**-0.27**	0.35387	**0.68**	0.28243
STM3765	yicL	putative permease	**-0.84**	0.23926	**0.05**	0.88268	**-0.15**	0.83030
STM3765	yicL	putative permease	**-0.23**	0.72233	**-0.39**	0.25062	**-0.38**	0.60729
STM3766	STM3766	putative cytoplasmic protein	**0.93**	0.26007	**0.90**	0.01305	**0.66**	0.12786
STM3766	STM3766	putative cytoplasmic protein	**1.38**	0.11644	**0.39**	0.29907	**0.49**	0.30355
STM3767	STM3767	putative cytoplasmic protein	**1.08**	0.09412	**0.68**	0.09170	**0.12**	0.79125
STM3767	STM3767	putative cytoplasmic protein	**1.51**	0.01731	**0.18**	0.60282	**1.02**	0.05994
STM3768	STM3768	putative selenocysteine synthase	**0.08**	0.87052	**-0.27**	0.51347	**-0.51**	0.41237
STM3768	STM3768	putative selenocysteine synthase	**1.07**	0.10226	**-1.62**	0.00836	**0.11**	0.81425
STM3769,S	STM3769,S	putative phosphotransferase system enzyme II	**-0.14**	0.77029	**-0.21**	0.48523	**0.78**	0.12494
STM3769,S	STM3769,S	putative phosphotransferase system enzyme II	**0.95**	0.13828	**-0.61**	0.05305	**0.23**	0.73110
STM3770	STM3770	putative phosphotransferase system enzyme IIC	**-0.48**	0.31009	**-0.31**	0.52126	**-1.02**	0.16242
STM3770	STM3770	putative phosphotransferase system enzyme IIC	**2.63**	0.01067	**0.25**	0.67904	**2.40**	0.01124
STM3771	STM3771	putative phosphotransferase system enzyme IIB	**-0.33**	0.59332	**-0.49**	0.22412	**-0.94**	0.13456
STM3771	STM3771	putative phosphotransferase system enzyme IIB	**0.65**	0.23607	**-0.77**	0.05844	**-0.04**	0.93149
STM3772	STM3772	putative phosphotransferase system enzyme IIA	**0.65**	0.23038	**-0.30**	0.44649	**-0.05**	0.94651
STM3772	STM3772	putative phosphotransferase system enzyme IIA	**0.61**	0.22959	**-0.40**	0.36314	**1.36**	0.08054
STM3773	STM3773	putative transcriptional regulator	**0.26**	0.61745	**-1.11**	0.02122	**-0.80**	0.19111
STM3773	STM3773	putative transcriptional regulator	**-0.02**	0.97323	**-0.99**	0.13403	**0.87**	0.23871
STM3774	STM3774	putative inner membrane protein	**4.30**	0.01844	**0.07**	0.88824	**2.40**	0.04983
STM3774	STM3774	putative inner membrane protein	**3.75**	0.09229	**-1.37**	0.00239	**3.10**	0.03017
STM3775	STM3775	putative glycosyl hydrolase	**0.21**	0.72704	**-0.67**	0.05767	**-0.34**	0.68420
STM3775	STM3775	putative glycosyl hydrolase	**0.45**	0.53505	**-1.05**	0.02957	**-0.21**	0.74539
STM3776	yicM	putative transport protein	**-1.27**	0.08333	**-0.16**	0.67323	**-0.45**	0.50852
STM3776	yicM	putative transport protein	**1.52**	0.13027	**0.11**	0.83199	**1.11**	0.00975
STM3777	STM3777	putative cytoplasmic protein	**0.65**	0.18164	**2.09**	0.00021	**1.63**	0.00186
STM3777	STM3777	putative cytoplasmic protein	**2.01**	0.00935	**1.76**	0.00072	**2.73**	0.00022
STM3778	STM3778	putative DNA-binding protein	**0.72**	0.29713	**1.52**	0.00562	**1.21**	0.02811
STM3778	STM3778	putative DNA-binding protein	**1.85**	0.09620	**1.53**	0.00591	**1.70**	0.01478
STM3779	STM3779	putative phosphotransferase system HPr protein	**0.18**	0.68656	**0.88**	0.10811	**2.21**	0.04987
STM3779	STM3779	putative phosphotransferase system HPr protein	**0.13**	0.80753	**0.50**	0.31174	**1.42**	0.00705
STM3780	STM3780	hypothetical protein STM3780	**0.14**	0.83105	**0.16**	0.60282	**-0.59**	0.11989
STM3780	STM3780	hypothetical protein STM3780	**1.56**	0.02423	**0.06**	0.87913	**1.43**	0.06087
STM3781	STM3781	putative sugar kinase	**-0.33**	0.48168	**1.15**	0.03409	**-1.40**	0.01622
STM3781	STM3781	putative sugar kinase	**1.97**	0.05095	**-0.08**	0.80429	**1.60**	0.00594
STM3782	STM3782	putative PTS system galactitol-specific enzyme IIC	**0.24**	0.56913	**0.29**	0.67599	**0.10**	0.89746
STM3782	STM3782	putative PTS system galactitol-specific enzyme IIC	**-0.82**	0.24390	**-0.03**	0.96010	**-1.07**	0.07095
STM3783	STM3783	putative periplasmic protein	**0.71**	0.60249	**1.51**	0.00526	**0.61**	0.09991
STM3783	STM3783	putative periplasmic protein	**-0.85**	0.19627	**0.94**	0.01100	**0.56**	0.21853
STM3784	STM3784	putative phosphotransferase system mannitol/fructose-	**-0.41**	0.36342	**0.37**	0.19345	**0.06**	0.90469
STM3784	STM3784	putative phosphotransferase system mannitol/fructose-	**-1.22**	0.07862	**0.60**	0.11555	**0.18**	0.76228
STM3785	STM3785	putative regulatory protein	**-0.06**	0.89515	**0.98**	0.05621	**-0.73**	0.09239
STM3785	STM3785	putative regulatory protein	**3.11**	0.01818	**0.16**	0.62607	**0.54**	0.30445
STM3786	yicN	putative inner membrane protein	**-0.90**	0.12653	**-0.56**	0.15867	**-1.45**	0.00440
STM3786	yicN	putative inner membrane protein	**1.02**	0.06919	**-0.42**	0.17240	**-0.82**	0.04514
STM3787	uhpT	hexose phosphate transport protein	**0.60**	0.22345	**0.70**	0.22380	**1.10**	0.01447
STM3787	uhpT	hexose phosphate transport protein	**1.94**	0.01497	**0.08**	0.92377	**0.29**	0.81708
STM3788	uhpC	regulatory protein	**-0.25**	0.67870	**-1.45**	0.00585	**-1.61**	0.00413
STM3788	uhpC	regulatory protein	**0.59**	0.52554	**-1.45**	0.00536	**-0.77**	0.24881
STM3789	uhpB	sensory histidine kinase	**0.36**	0.77049	**-1.41**	0.00612	**0.66**	0.07979
STM3789	uhpB	sensory histidine kinase	**0.29**	0.71508	**-1.50**	0.02348	**-0.05**	0.91117
STM3790	uhpA	response regulator	**-2.04**	0.01402	**0.05**	0.94058	**-1.71**	0.04076
STM3790	uhpA	response regulator	**-1.03**	0.19350	**-1.02**	0.01096	**-1.73**	0.02221

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM3791	STM3791	putative cytoplasmic protein	**-0.33**	0.63069	**-0.95**	0.00961	**-0.35**	0.49423
STM3791	STM3791	putative cytoplasmic protein	**0.97**	0.20670	**-1.05**	0.03548	**0.79**	0.18203
STM3792	STM3792	putative L-fucose permease	**-0.84**	0.22279	**-0.68**	0.07449	**0.25**	0.75282
STM3792	STM3792	putative L-fucose permease	**0.46**	0.53467	**-0.51**	0.11302	**-0.96**	0.09847
STM3793	STM3793	putative sugar kinase	**-0.91**	0.13970	**0.04**	0.93196	**-0.70**	0.16113
STM3793	STM3793	putative sugar kinase	**-0.34**	0.51992	**0.69**	0.14320	**1.97**	0.02257
STM3794	STM3794	putative regulatory protein	**-0.85**	0.19429	**0.49**	0.16069	**1.95**	0.00672
STM3794	STM3794	putative regulatory protein	**0.49**	0.26513	**0.82**	0.02133	**3.49**	0.01089
STM3795	ilvN	acetolactate synthase small subunit	**-0.17**	0.73579	**0.22**	0.44567	**-0.94**	0.23691
STM3795	ilvN	acetolactate synthase small subunit	**1.81**	0.02331	**0.40**	0.26988	**1.58**	0.09568
STM3796	ilvB	acetolactate synthase large subunit	**1.81**	0.04734	**-0.05**	0.88176	**0.25**	0.70681
STM3796	ilvB	acetolactate synthase large subunit	**0.47**	0.70958	**-0.55**	0.27598	**0.75**	0.06311
STM3796A,S	STM3796A,S	integral membrane protein	**1.62**	0.06501	**-1.05**	0.00626	**-0.26**	0.57568
STM3796A,S	STM3796A,S	integral membrane protein	**2.39**	0.04338	**-1.50**	0.00209	**0.66**	0.25108
STM3797	ivbL	ilvB operon leader peptide	**0.26**	0.66916	**0.82**	0.04063	**0.27**	0.60247
STM3797	ivbL	ilvB operon leader peptide	**1.44**	0.03158	**1.00**	0.01167	**1.56**	0.02970
STM3798	emrD	multidrug tranport protein	**-1.21**	0.11752	**-0.51**	0.39845	**-1.14**	0.13460
STM3798	emrD	multidrug tranport protein	**-0.41**	0.37359	**-0.21**	0.47621	**-0.73**	0.05969
STM3799	STM3799	putative periplasmic protein	**-0.18**	0.80736	**-0.13**	0.70027	**0.18**	0.80831
STM3799	STM3799	putative periplasmic protein	**0.86**	0.29573	**-0.26**	0.37985	**-0.11**	0.83998
STM3800	dsdC	transcriptional activator	**-1.43**	0.02009	**-1.70**	0.09962	**-1.52**	0.12434
STM3800	dsdC	transcriptional activator	**-0.76**	0.17650	**-1.15**	0.01544	**-1.18**	0.17055
STM3801	dsdX	putative transport protein	**0.13**	0.76750	**-0.65**	0.03986	**-0.81**	0.03319
STM3801	dsdX	putative transport protein	**1.21**	0.05758	**-0.95**	0.01174	**0.45**	0.20090
STM3802	dsdA	D-serine dehydratase	**1.24**	0.16210	**-0.30**	0.34904	**-0.24**	0.62494
STM3802	dsdA	D-serine dehydratase	**0.34**	0.49299	**-1.16**	0.01401	**0.58**	0.18861
STM3803	yidF	putative cytoplasmic protein	**0.24**	0.60093	**-0.59**	0.08498	**-1.83**	0.02162
STM3803	yidF	putative cytoplasmic protein	**0.92**	0.20818	**-0.71**	0.24274	**-0.32**	0.54879
STM3804	yidG	putative inner membrane protein	**-1.03**	0.23413	**-0.31**	0.47676	**-0.35**	0.40236
STM3804	yidG	putative inner membrane protein	**0.89**	0.45963	**-0.40**	0.40058	**0.63**	0.12342
STM3805	yidH	putative inner membrane protein	**-0.84**	0.14245	**-0.11**	0.77694	**-0.58**	0.26108
STM3805	yidH	putative inner membrane protein	**0.27**	0.70994	**-0.52**	0.16883	**-1.38**	0.12110
STM3807	yidE	hypothetical protein STM3807	**-0.61**	0.18239	**-0.76**	0.04230	**-1.69**	0.01384
STM3807	yidE	hypothetical protein STM3807	**1.10**	0.12153	**-0.85**	0.01449	**-0.33**	0.45115
STM3808,S	ibpB	small heat shock protein	**2.54**	0.00747	**1.45**	0.01014	**-0.36**	0.48594
STM3808,S	ibpB	small heat shock protein	**3.17**	0.00994	**1.68**	0.00586	**0.98**	0.14033
STM3809,S	ibpA	small heat shock protein	**1.40**	0.10716	**3.09**	0.00011	**0.12**	0.85533
STM3809,S	ibpA	small heat shock protein	**2.55**	0.01196	**3.85**	0.00002	**-0.23**	0.64447
STM3810	yidQ	putative outer membrane lipoprotein	**4.69**	0.00567	**1.06**	0.01473	**3.18**	0.01146
STM3810	yidQ	putative outer membrane lipoprotein	**0.69**	0.44289	**0.96**	0.03019	**1.37**	0.22271
STM3811	yidR	putative cytoplasmic protein	**0.73**	0.12179	**0.78**	0.03288	**-0.31**	0.40105
STM3811	yidR	putative cytoplasmic protein	**0.04**	0.93891	**1.21**	0.01719	**-0.33**	0.44666
STM3812	ccmH	putative heme lyase subunit	**1.46**	0.03960	**0.22**	0.52942	**-0.61**	0.27999
STM3812	ccmH	putative heme lyase subunit	**1.66**	0.03599	**0.07**	0.83807	**0.00**	0.99711
STM3813	ccmG	heme lyase disulfide oxidoreductase	**0.16**	0.85218	**-0.35**	0.42611	**-0.70**	0.18881
STM3813	ccmG	heme lyase disulfide oxidoreductase	**1.21**	0.24390	**-0.56**	0.07358	**-0.12**	0.80802
STM3814	ccmF	cytochrome c-type biogenesis protein	**-0.24**	0.88783	**-1.15**	0.08914	**-0.17**	0.89908
STM3814	ccmF	cytochrome c-type biogenesis protein	**0.40**	0.71810	**-0.82**	0.34067	**-0.25**	0.82466
STM3815	ccmE	periplasmic heme-dependent peroxidase	**2.37**	0.01609	**0.38**	0.52684	**0.17**	0.76831
STM3815	ccmE	periplasmic heme-dependent peroxidase	**2.44**	0.00635	**0.06**	0.83199	**0.25**	0.55009
STM3816	ccmD	heme exporter protein C	**-0.40**	0.69343	**0.41**	0.15790	**-0.57**	0.44245
STM3816	ccmD	heme exporter protein C	**0.59**	0.23605	**-0.22**	0.54491	**-1.67**	0.00413
STM3817	ccmC	heme exporter protein	**-0.17**	0.73147	**0.71**	0.04804	**-0.70**	0.15656
STM3817	ccmC	heme exporter protein	**-0.07**	0.93334	**-0.03**	0.92849	**-1.73**	0.02963
STM3818	ccmB	heme exporter protein	**-1.19**	0.03637	**0.78**	0.06956	**-0.98**	0.25892
STM3818	ccmB	heme exporter protein	**0.90**	0.30295	**1.09**	0.00660	**-1.49**	0.01801
STM3819	ccmA	heme exporter protein	**0.45**	0.28070	**-1.23**	0.00736	**-0.76**	0.05852
STM3819	ccmA	heme exporter protein	**0.96**	0.07710	**-0.79**	0.02134	**-0.27**	0.51699
STM3820	STM3820	putative cytochrome c peroxidase	**-1.96**	0.02162	**-0.14**	0.88067	**-1.04**	0.04449
STM3820	STM3820	putative cytochrome c peroxidase	**-0.50**	0.37118	**-0.85**	0.04537	**-0.53**	0.36414
STM3821	torD	chaperone protein TorD	**-0.06**	0.90452	**0.00**	0.99930	**-0.03**	0.95488
STM3821	torD	chaperone protein TorD	**1.48**	0.01578	**0.00**	0.99835	**2.28**	0.00032
STM3822	torA	trimethylamine N-oxide reductase subunit	**0.35**	0.47183	**-0.22**	0.48587	**-1.25**	0.04006
STM3822	torA	trimethylamine N-oxide reductase subunit	**0.94**	0.21494	**-1.45**	0.00594	**-0.06**	0.93102
STM3823	torC	trimethylamine N-oxide reductase cytochrome c-like subunit	**2.10**	0.12917	**0.42**	0.19555	**1.91**	0.00167
STM3823	torC	trimethylamine N-oxide reductase cytochrome c-like subunit	**3.78**	0.06773	**-0.06**	0.93270	**2.71**	0.00040
STM3824	torR	response regulator	**-1.31**	0.05585	**-1.05**	0.00669	**-1.52**	0.02567
STM3824	torR	response regulator	**0.24**	0.69732	**-0.59**	0.09943	**0.30**	0.52967
STM3825	torT	periplasmic sensor	**-0.78**	0.18562	**0.17**	0.68515	**-1.14**	0.01694
STM3825	torT	periplasmic sensor	**-0.14**	0.77519	**-0.27**	0.36212	**-0.67**	0.13415

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM3826	torS	sensor kinase	**-0.10**	0.85721	**0.22**	0.55038	**0.12**	0.78230
STM3826	torS	sensor kinase	**0.15**	0.83532	**-1.53**	0.01104	**0.40**	0.29616
STM3827	dgoT	D-galactonate transport protein	**0.69**	0.18080	**-0.77**	0.02025	**0.38**	0.66972
STM3827	dgoT	D-galactonate transport protein	**3.14**	0.00546	**-0.59**	0.26241	**0.21**	0.68835
STM3828	dgoA	2-oxo-3-deoxygalactonate 6-phosphate	**1.92**	0.01997	**1.00**	0.03968	**3.00**	0.00014
STM3828	dgoA	2-oxo-3-deoxygalactonate 6-phosphate	**1.99**	0.03449	**1.23**	0.00695	**3.27**	0.00122
STM3829	dgoK	2-oxo-3-deoxygalactonate kinase	**1.03**	0.11936	**1.38**	0.00216	**2.93**	0.00066
STM3829	dgoK	2-oxo-3-deoxygalactonate kinase	**3.07**	0.03097	**1.05**	0.01667	**4.08**	0.00006
STM3830	dgoR	galactonate operon transcriptional repressor	**1.20**	0.02730	**0.88**	0.03735	**2.87**	0.00012
STM3830	dgoR	galactonate operon transcriptional repressor	**2.36**	0.01099	**0.81**	0.03644	**3.56**	0.00009
STM3831	yidA	putative hydrolase	**-0.56**	0.33214	**-0.24**	0.45514	**0.67**	0.24256
STM3831	yidA	putative hydrolase	**0.42**	0.45678	**1.18**	0.17170	**1.67**	0.02227
STM3832	STM3832	putative permease	**-0.37**	0.41666	**-0.28**	0.56384	**-0.67**	0.32018
STM3832	STM3832	putative permease	**0.74**	0.35844	**-0.61**	0.23227	**-0.19**	0.75724
STM3833	STM3833	putative mandelate racemase	**0.39**	0.61086	**0.30**	0.47781	**-0.51**	0.48407
STM3833	STM3833	putative mandelate racemase	**1.44**	0.04995	**-0.03**	0.95598	**1.60**	0.02422
STM3834	STM3834	putative transcriptional regulator	**-2.19**	0.01001	**-1.62**	0.00071	**-2.88**	0.00052
STM3834	STM3834	putative transcriptional regulator	**-1.20**	0.03925	**-1.64**	0.00054	**-2.70**	0.00048
STM3835	gyrB	DNA gyrase subunit B	**-2.60**	0.02946	**-1.89**	0.00064	**-3.56**	0.00011
STM3835	gyrB	DNA gyrase subunit B	**-0.38**	0.53467	**-1.59**	0.00075	**-3.04**	0.00017
STM3836	recF	recombination protein F	**-2.68**	0.00613	**-1.81**	0.00223	**-2.17**	0.00159
STM3836	recF	recombination protein F	**-3.28**	0.00635	**-1.89**	0.00033	**-2.42**	0.00074
STM3837	dnaN	DNA polymerase III subunit beta	**-2.20**	0.02665	**-1.11**	0.00749	**-3.56**	0.00006
STM3837	dnaN	DNA polymerase III subunit beta	**-1.04**	0.19012	**-0.80**	0.03512	**-2.27**	0.00157
STM3838	dnaA	chromosomal replication initiation protein	**-2.25**	0.03987	**-0.79**	0.05991	**-2.04**	0.01314
STM3838	dnaA	chromosomal replication initiation protein	**-1.33**	0.03218	**-0.92**	0.02159	**-2.66**	0.00014
STM3839	rpmH	50S ribosomal protein L34	**0.23**	0.66512	**-1.70**	0.00441	**-2.95**	0.00504
STM3839	rpmH	50S ribosomal protein L34	**-1.70**	0.11670	**-1.80**	0.00151	**-3.41**	0.00008
STM3840	rnpA	ribonuclease P	**-3.30**	0.02007	**-2.16**	0.00067	**-5.67**	0.00007
STM3840	rnpA	ribonuclease P	**-1.97**	0.17750	**-1.98**	0.00270	**-2.86**	0.00056
STM3842	yidC	inner membrane protein translocase component YidC	**-1.99**	0.03179	**-2.02**	0.00031	**-2.08**	0.00064
STM3842	yidC	inner membrane protein translocase component YidC	**0.16**	0.91601	**-2.02**	0.00023	**-1.32**	0.02205
STM3843	trmE	tRNA modification GTPase	**0.03**	0.95334	**-0.60**	0.08796	**-0.72**	0.12689
STM3843	trmE	tRNA modification GTPase	**0.78**	0.12389	**-0.27**	0.52429	**0.71**	0.10658
STM3845	STM3845	putative inner membrane protein	**1.02**	0.06515	**-0.06**	0.88330	**2.18**	0.00072
STM3845	STM3845	putative inner membrane protein	**1.59**	0.05468	**-0.34**	0.50787	**2.80**	0.00041
STM3846,s	STM3846,s	putative reverse transcriptase	**-1.47**	0.03405	**-0.07**	0.86576	**-0.35**	0.43126
STM3846,s	STM3846,s	putative reverse transcriptase	**-2.27**	0.02538	**0.03**	0.96131	**0.52**	0.23886
STM3847	yidY	putative tranport protein	**2.01**	0.06546	**-0.12**	0.80561	**0.19**	0.74208
STM3847	yidY	putative tranport protein	**2.26**	0.00743	**0.33**	0.64803	**0.44**	0.64753
STM3848	yidZ	putative transcriptional regulator	**-0.82**	0.29785	**-1.22**	0.03074	**-1.51**	0.01981
STM3848	yidZ	putative transcriptional regulator	**-0.21**	0.72602	**-1.64**	0.00295	**-0.02**	0.97929
STM3849	yieE	putative cytoplasmic protein	**-0.58**	0.26606	**-0.47**	0.12834	**-0.09**	0.86651
STM3849	yieE	putative cytoplasmic protein	**1.22**	0.09130	**-1.08**	0.01244	**-0.24**	0.61492
STM3850	yieF	putative oxidoreductase	**-1.58**	0.01896	**-0.36**	0.19503	**-1.66**	0.00845
STM3850	yieF	putative oxidoreductase	**-0.14**	0.82430	**0.12**	0.70053	**-0.67**	0.11995
STM3851,S	yieG	hypothetical protein STM3851,S	**-0.28**	0.76178	**0.26**	0.37554	**-1.16**	0.02380
STM3851,S	yieG	hypothetical protein STM3851,S	**0.23**	0.81252	**0.21**	0.56497	**-0.28**	0.51048
STM3852	yieH	putative phosphatase/phosphohexomutase	**-0.35**	0.50703	**-0.50**	0.15361	**-1.54**	0.00995
STM3852	yieH	putative phosphatase/phosphohexomutase	**0.85**	0.42386	**0.02**	0.96264	**-0.75**	0.05581
STM3853	phoU	high-affinity phosphate uptake regulatory protein	**-0.18**	0.82145	**0.14**	0.71905	**-1.88**	0.00187
STM3853	phoU	high-affinity phosphate uptake regulatory protein	**-0.05**	0.94753	**-0.10**	0.80656	**-1.66**	0.05763
STM3854	pstB	high-affinity phosphate transporter	**1.82**	0.01955	**0.84**	0.02416	**-0.58**	0.28744
STM3854	pstB	high-affinity phosphate transporter	**2.97**	0.08560	**0.87**	0.01203	**1.76**	0.09205
STM3855	pstA	high-affinity phosphate transporter	**-0.13**	0.91393	**1.13**	0.01024	**1.62**	0.00521
STM3855	pstA	high-affinity phosphate transporter	**-1.50**	0.06522	**0.36**	0.47462	**0.55**	0.28060
STM3856	pstC	high-affinity phosphate transporter	**-0.46**	0.49307	**0.60**	0.07975	**-1.68**	0.00532
STM3856	pstC	high-affinity phosphate transporter	**1.00**	0.14379	**0.63**	0.06643	**-0.48**	0.29394
STM3857	pstS	high-affinity phosphate transporter	**1.85**	0.01177	**2.85**	0.00010	**0.13**	0.80746
STM3857	pstS	high-affinity phosphate transporter	**2.21**	0.00789	**2.98**	0.00033	**0.63**	0.12630
STM3858	STM3858	putative phosphotransferase system fructose-specific	**-0.68**	0.14786	**0.36**	0.43313	**-0.91**	0.03627
STM3858	STM3858	putative phosphotransferase system fructose-specific	**1.05**	0.05012	**0.17**	0.59650	**-0.69**	0.09372
STM3859	aroE	shikimate 5-dehydrogenase	**-0.77**	0.13713	**-1.21**	0.02627	**-0.76**	0.10841
STM3859	aroE	shikimate 5-dehydrogenase	**-0.16**	0.83463	**-1.47**	0.00158	**0.73**	0.10782
STM3860	STM3860	putative dipeptide/oligopeptide/nickel ABC-type transport	**-2.01**	0.00984	**-1.90**	0.00057	**-3.47**	0.00008
STM3860	STM3860	putative dipeptide/oligopeptide/nickel ABC-type transport	**-1.86**	0.12680	**-1.20**	0.00325	**-1.92**	0.00537
STM3861	glmS	D-fructose-6-phosphate amidotransferase	**-1.14**	0.05655	**-0.81**	0.02108	**-2.69**	0.00021
STM3861	glmS	D-fructose-6-phosphate amidotransferase	**-0.69**	0.45900	**-1.19**	0.00418	**-3.07**	0.00021
STM3862	glmU	bifunctional N-acetylglucosamine-1-phosphate	**-1.84**	0.02576	**-2.14**	0.00024	**-3.05**	0.00041
STM3862	glmU	bifunctional N-acetylglucosamine-1-phosphate	**-2.15**	0.02058	**-2.28**	0.00057	**-2.31**	0.00063

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM3863	STM3863	putative permease	**-1.95**	0.02538	**-1.31**	0.06079	**-1.19**	0.01509
STM3863	STM3863	putative permease	**-2.05**	0.01038	**-2.00**	0.00042	**-1.70**	0.01003
STM3864	atpC	ATP synthase subunit epsilon	**-2.29**	0.03348	**-1.29**	0.00601	**-2.72**	0.00289
STM3864	atpC	ATP synthase subunit epsilon	**-1.83**	0.03441	**-1.39**	0.00127	**-3.91**	0.00012
STM3865	atpD	ATP synthase subunit B	**-2.77**	0.00595	**-1.26**	0.00213	**-3.99**	0.00004
STM3865	atpD	ATP synthase subunit B	**-0.85**	0.14585	**-1.07**	0.01188	**-3.20**	0.00041
STM3866	atpG	ATP synthase subunit C	**-2.04**	0.01397	**-1.98**	0.00100	**-4.45**	0.00005
STM3866	atpG	ATP synthase subunit C	**-1.78**	0.01114	**-1.78**	0.00079	**-3.71**	0.00007
STM3867	atpA	ATP synthase subunit A	**-3.90**	0.01262	**-2.40**	0.00012	**-4.54**	0.00010
STM3867	atpA	ATP synthase subunit A	**-3.01**	0.01716	**-2.69**	0.00015	**-4.84**	0.00006
STM3868	atpH	ATP synthase subunit D	**-3.47**	0.00512	**-2.90**	0.00010	**-5.02**	0.00002
STM3868	atpH	ATP synthase subunit D	**-3.17**	0.00722	**-2.61**	0.00006	**-5.24**	0.00003
STM3869	atpF	ATP synthase subunit B	**-5.00**	0.02665	**-3.45**	0.00006	**-4.81**	0.00003
STM3869	atpF	ATP synthase subunit B	**-3.65**	0.01448	**-2.53**	0.00017	**-5.49**	0.00002
STM3870	atpE	ATP synthase subunit C	**-3.26**	0.00537	**-3.19**	0.00003	**-5.15**	0.00003
STM3870	atpE	ATP synthase subunit C	**-2.57**	0.01056	**-2.79**	0.00010	**-5.47**	0.00005
STM3871	atpB	ATP synthase subunit A	**-3.74**	0.00512	**-2.98**	0.00019	**-4.71**	0.00007
STM3871	atpB	ATP synthase subunit A	**-2.00**	0.01447	**-2.03**	0.00142	**-2.36**	0.00112
STM3871	atpB	ATP synthase subunit A	**-3.44**	0.00512	**-2.74**	0.00010	**-4.53**	0.00006
STM3871	atpB	ATP synthase subunit A	**-1.98**	0.03067	**-1.70**	0.00301	**-2.88**	0.00095
STM3872	atpI	ATP synthase subunit I	**-3.46**	0.00512	**-2.50**	0.00009	**-3.88**	0.00006
STM3872	atpI	ATP synthase subunit I	**-2.42**	0.00876	**-2.92**	0.00006	**-4.15**	0.00010
STM3873,S	gidB	glucose-inhibited division protein B	**-1.52**	0.02655	**-1.41**	0.01852	**-2.51**	0.00024
STM3873,S	gidB	glucose-inhibited division protein B	**-0.68**	0.14889	**-2.06**	0.00023	**-1.86**	0.00258
STM3874	gidA	glucose-inhibited division protein A	**-1.59**	0.09492	**-1.10**	0.00423	**-2.30**	0.00066
STM3874	gidA	glucose-inhibited division protein A	**-1.02**	0.18683	**-1.32**	0.00394	**-1.73**	0.03264
STM3875	mioC	flavodoxin	**-2.69**	0.01363	**-0.93**	0.01334	**-3.27**	0.00009
STM3875	mioC	flavodoxin	**-1.08**	0.21141	**-0.90**	0.02931	**-2.40**	0.00037
STM3876	asnC	transcriptional regulator	**-1.00**	0.13857	**-0.62**	0.09352	**-2.07**	0.00683
STM3876	asnC	transcriptional regulator	**0.61**	0.31766	**-0.60**	0.11392	**-1.32**	0.01198
STM3877	asnA	asparagine synthetase AsnA	**-0.65**	0.17442	**0.69**	0.40875	**-0.52**	0.26545
STM3877	asnA	asparagine synthetase AsnA	**-0.01**	0.98974	**0.02**	0.96117	**-0.88**	0.20195
STM3878,S	yieM	putative inner membrane protein	**-0.12**	0.84673	**1.02**	0.01175	**-0.01**	0.97744
STM3878,S	yieM	putative inner membrane protein	**0.95**	0.12941	**1.00**	0.04081	**1.63**	0.00382
STM3879	yieN	putative regulatory protein	**-0.31**	0.52193	**-0.04**	0.91326	**0.27**	0.60752
STM3879	yieN	putative regulatory protein	**-0.38**	0.53843	**-0.65**	0.06158	**-1.29**	0.12410
STM3880	kup	low-affinity potassium transport protein	**-1.14**	0.16023	**-3.30**	0.00144	**-1.63**	0.00389
STM3880	kup	low-affinity potassium transport protein	**0.41**	0.50186	**-2.96**	0.00004	**-1.48**	0.02089
STM3881	rbsD	high-affinity D-ribose transport protein	**-2.03**	0.01449	**-4.58**	0.00001	**-2.29**	0.00326
STM3881	rbsD	high-affinity D-ribose transport protein	**-1.62**	0.03130	**-4.40**	0.00001	**-1.90**	0.00854
STM3882	rbsA	high-affinity D-ribose transport protein	**-1.47**	0.05064	**-3.68**	0.00005	**-2.88**	0.00037
STM3882	rbsA	high-affinity D-ribose transport protein	**-0.33**	0.69269	**-4.18**	0.00003	**-2.56**	0.00186
STM3883	rbsC	ribose high-affinity ABC transporter permease component	**-2.38**	0.07521	**-3.16**	0.00054	**-2.73**	0.00193
STM3883	rbsC	ribose high-affinity ABC transporter permease component	**-1.80**	0.09334	**-3.34**	0.00033	**-1.90**	0.01429
STM3884	rbsB	D-ribose transport protein	**-1.57**	0.10461	**-0.78**	0.11302	**-0.86**	0.18831
STM3884	rbsB	D-ribose transport protein	**-0.63**	0.37989	**-0.45**	0.35439	**-0.09**	0.87905
STM3885	rbsK	ribokinase	**-1.89**	0.04427	**-2.16**	0.00031	**-1.60**	0.11040
STM3885	rbsK	ribokinase	**-0.38**	0.62494	**-1.94**	0.00083	**-0.68**	0.18600
STM3886	rbsR	rbs operon transcriptional repressor	**-0.33**	0.54428	**-2.09**	0.00033	**-1.03**	0.03788
STM3886	rbsR	rbs operon transcriptional repressor	**-0.28**	0.53036	**-2.32**	0.00025	**-0.48**	0.28714
STM3887	yieO	putative tranport protein	**0.08**	0.85656	**-1.91**	0.00026	**-0.08**	0.83189
STM3887	yieO	putative tranport protein	**0.49**	0.24958	**-2.44**	0.00168	**0.36**	0.56077
STM3888	yieP	putative regulatory protein	**-2.17**	0.01479	**-0.60**	0.07988	**-0.01**	0.97553
STM3888	yieP	putative regulatory protein	**-0.53**	0.33155	**-0.07**	0.84078	**0.54**	0.23461
STM3889	rrsC	STM3889	**-2.53**	0.06106	**1.13**	0.04074	**-0.86**	0.09052
STM3889	rrsC	STM3889	**-2.08**	0.11630	**0.73**	0.15735	**-0.27**	0.66500
STM3890	gltU	STM3890	**1.25**	0.09657	**0.94**	0.03791	**0.99**	0.02175
STM3890	gltU	STM3890	**1.45**	0.03649	**0.37**	0.27631	**1.73**	0.00404
STM3891	rrlC	STM3891	**-2.04**	0.19558	**0.57**	0.08831	**0.12**	0.80086
STM3891	rrlC	STM3891	**-1.46**	0.37729	**0.82**	0.02627	**0.98**	0.05524
STM3894	rrfC	STM3894	**0.55**	0.55441	**0.17**	0.72464	**0.80**	0.13327
STM3894	rrfC	STM3894	**1.20**	0.06515	**0.43**	0.24930	**1.09**	0.03784
STM3895	aspT	STM3895	**-1.47**	0.02440	**0.27**	0.58656	**0.20**	0.63830
STM3895	aspT	STM3895	**-0.53**	0.40523	**0.68**	0.18740	**0.30**	0.52364
STM3896	trpT	STM3896	**-1.16**	0.03339	**-0.18**	0.53582	**1.69**	0.00686
STM3896	trpT	STM3896	**-0.49**	0.31954	**-0.11**	0.81422	**2.16**	0.01256
STM3897	yifA	transcriptional regulator HdfR	**-1.11**	0.08539	**0.47**	0.13462	**1.00**	0.01562
STM3897	yifA	transcriptional regulator HdfR	**-0.09**	0.82622	**0.65**	0.04857	**1.52**	0.00416
STM3898	yifE	putative transcriptional regulator	**-3.02**	0.01262	**-2.07**	0.00201	**-1.44**	0.00339
STM3898	yifE	putative transcriptional regulator	**-1.56**	0.02790	**-1.59**	0.00368	**-1.15**	0.01316

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM3899	yifB	putative magnesium chelatase subunit ChlI	**-1.06**	0.40170	**-0.45**	0.22949	**0.55**	0.19244
STM3899	yifB	putative magnesium chelatase subunit ChlI	**-1.14**	0.35943	**-1.77**	0.01009	**-1.67**	0.25266
STM3901	ilvG	acetolactate synthase II large subunit	**-0.79**	0.13484	**0.61**	0.14228	**-1.72**	0.00271
STM3901	ilvG	acetolactate synthase II large subunit	**0.69**	0.22160	**0.64**	0.07113	**0.35**	0.58913
STM3902	ilvM	acetolactate synthase II small subunit	**0.16**	0.71390	**0.74**	0.05133	**-1.36**	0.00661
STM3902	ilvM	acetolactate synthase II small subunit	**0.52**	0.42109	**0.77**	0.03814	**0.24**	0.55906
STM3903	ilvE	branched-chain amino acid aminotransferase	**0.30**	0.81994	**0.58**	0.06503	**-0.67**	0.18380
STM3903	ilvE	branched-chain amino acid aminotransferase	**1.78**	0.15901	**0.17**	0.69529	**0.52**	0.48325
STM3904	ilvD	dihydroxy-acid dehydratase	**-2.85**	0.00748	**-0.49**	0.08968	**-2.26**	0.00228
STM3904	ilvD	dihydroxy-acid dehydratase	**1.19**	0.03614	**-0.82**	0.02505	**-2.85**	0.02077
STM3905	ilvA	threonine dehydratase	**0.93**	0.15335	**0.58**	0.07933	**1.71**	0.00386
STM3905	ilvA	threonine dehydratase	**0.61**	0.19804	**0.42**	0.20997	**0.20**	0.58716
STM3906	STM3906	putative cytoplasmic protein	**1.45**	0.07710	**2.48**	0.00055	**0.79**	0.08594
STM3906	STM3906	putative cytoplasmic protein	**1.72**	0.03490	**2.42**	0.00024	**1.86**	0.00255
STM3907	STM3907	putative cytoplasmic protein	**0.41**	0.60864	**0.81**	0.05608	**0.77**	0.28378
STM3907	STM3907	putative cytoplasmic protein	**4.05**	0.00623	**1.17**	0.02110	**1.58**	0.01606
STM3908	ilvY	regulatory protein	**-0.39**	0.43614	**1.03**	0.06866	**-1.23**	0.01562
STM3908	ilvY	regulatory protein	**0.39**	0.46005	**0.61**	0.15984	**-0.61**	0.15109
STM3909	ilvC	ketol-acid reductoisomerase	**0.09**	0.87678	**1.02**	0.00599	**-0.97**	0.03080
STM3909	ilvC	ketol-acid reductoisomerase	**1.05**	0.33302	**0.46**	0.20599	**-0.09**	0.86413
STM3910	ppiC	peptidyl-prolyl cis-trans isomerase C	**-1.38**	0.02655	**-0.30**	0.28308	**-1.85**	0.00804
STM3910	ppiC	peptidyl-prolyl cis-trans isomerase C	**0.12**	0.78940	**-0.49**	0.08468	**-1.40**	0.05017
STM3911	STM3911	putative inner membrane protein	**-0.49**	0.43156	**-1.28**	0.00511	**-1.89**	0.00294
STM3911	STM3911	putative inner membrane protein	**0.28**	0.50275	**-0.74**	0.06480	**-0.37**	0.39181
STM3912	rep	ATP-dependent DNA helicase rep	**0.06**	0.88684	**0.40**	0.27271	**0.00**	0.99711
STM3912	rep	ATP-dependent DNA helicase rep	**0.97**	0.06914	**0.18**	0.52871	**0.62**	0.14039
STM3913	gppA	guanosine pentaphosphatase/exopolyphosphatase	**-0.76**	0.26777	**-0.06**	0.85712	**-1.54**	0.09029
STM3913	gppA	guanosine pentaphosphatase/exopolyphosphatase	**-0.51**	0.28081	**-0.29**	0.41088	**-0.99**	0.06134
STM3914	rhlB	ATP-dependent RNA helicase	**-2.53**	0.00581	**-1.59**	0.00082	**-2.43**	0.00061
STM3914	rhlB	ATP-dependent RNA helicase	**-2.20**	0.00700	**-1.88**	0.00047	**-2.49**	0.00025
STM3915	trxA	thioredoxin	**-2.47**	0.00700	**-1.31**	0.00165	**-2.26**	0.00039
STM3915	trxA	thioredoxin	**-1.99**	0.02039	**-1.08**	0.00529	**-2.47**	0.00088
STM3917	rho	transcription termination factor Rho	**-0.92**	0.06414	**-0.59**	0.07369	**-1.80**	0.04523
STM3917	rho	transcription termination factor Rho	**-0.75**	0.09664	**-0.68**	0.06196	**-2.29**	0.00046
STM3918	rfe	undecaprenyl-phosphate N-acetylglucosaminyltransferase	**-1.72**	0.02002	**-0.94**	0.03288	**-1.85**	0.00149
STM3918	rfe	undecaprenyl-phosphate N-acetylglucosaminyltransferase	**-1.18**	0.08204	**-0.78**	0.02277	**-2.28**	0.00224
STM3919	wzzE	enterobacterial common antigen chain length regulator	**-1.67**	0.01536	**-1.59**	0.00073	**-2.12**	0.00064
STM3919	wzzE	enterobacterial common antigen chain length regulator	**-1.28**	0.02654	**-1.60**	0.00055	**-1.53**	0.00314
STM3920	wecB	UDP-N-acetyl glucosamine-2-epimerase	**-1.76**	0.18480	**-1.82**	0.00108	**-1.37**	0.01003
STM3920	wecB	UDP-N-acetyl glucosamine-2-epimerase	**-1.66**	0.04606	**-1.89**	0.00040	**-1.69**	0.02918
STM3921	wecC	UDP-N-acetyl-D-mannosaminuronic acid dehydrogenase	**-2.23**	0.01321	**-2.12**	0.00024	**-3.36**	0.00015
STM3921	wecC	UDP-N-acetyl-D-mannosaminuronic acid dehydrogenase	**-1.62**	0.08941	**-1.78**	0.00111	**-3.56**	0.00008
STM3922	rffG	dTDP-glucose 4,6-dehydratase	**-1.47**	0.13182	**-1.85**	0.00303	**-2.13**	0.01282
STM3922	rffG	dTDP-glucose 4,6-dehydratase	**-0.76**	0.44770	**-2.05**	0.00043	**-1.75**	0.00194
STM3923	rffH	glucose-1-phosphate thymidyl transferase	**-2.06**	0.01099	**-1.05**	0.02613	**-2.54**	0.00031
STM3923	rffH	glucose-1-phosphate thymidyl transferase	**-2.05**	0.01578	**-1.99**	0.00055	**-3.86**	0.00111
STM3924	wecD	lipopolysaccharide biosynthetic protein	**-2.37**	0.00719	**-2.16**	0.00019	**-2.97**	0.00021
STM3924	wecD	lipopolysaccharide biosynthetic protein	**0.26**	0.54785	**-1.89**	0.00052	**-2.58**	0.00141
STM3925	wecE	TDP-4-oxo-6-deoxy-D-glucose transaminase	**-1.35**	0.12290	**-2.01**	0.00142	**-2.16**	0.00131
STM3925	wecE	TDP-4-oxo-6-deoxy-D-glucose transaminase	**-1.65**	0.01445	**-2.18**	0.00063	**-1.83**	0.00140
STM3926	wzxE	O-antigen translocase	**-1.63**	0.02326	**-1.57**	0.00239	**-1.03**	0.01689
STM3926	wzxE	O-antigen translocase	**-1.56**	0.02177	**-2.05**	0.00046	**-1.82**	0.00097
STM3927	STM3927	4-alpha-L-fucosyltransferase	**-0.99**	0.11338	**-1.85**	0.00039	**-1.97**	0.00297
STM3927	STM3927	4-alpha-L-fucosyltransferase	**0.16**	0.73737	**-1.59**	0.00222	**0.05**	0.92626
STM3928	wecF	putative enterobacterial common antigen polymerase	**-0.60**	0.45204	**-1.32**	0.00325	**-0.41**	0.30030
STM3928	wecF	putative enterobacterial common antigen polymerase	**-0.39**	0.46748	**-1.59**	0.01214	**-0.87**	0.07894
STM3929	wecG	putative UDP-N-acetyl-D-mannosaminuronic acid	**-1.59**	0.01425	**-1.20**	0.07891	**-0.79**	0.07793
STM3929	wecG	putative UDP-N-acetyl-D-mannosaminuronic acid	**-1.78**	0.02840	**-1.81**	0.00080	**-1.93**	0.10444
STM3930	yifK	putative amino acid transport protein	**-1.99**	0.01428	**-1.81**	0.00062	**-0.36**	0.31998
STM3930	yifK	putative amino acid transport protein	**-1.21**	0.08383	**-1.50**	0.00286	**-0.36**	0.42770
STM3931	argX	STM3931	**-3.91**	0.00783	**-0.70**	0.27037	**1.43**	0.04292
STM3931	argX	STM3931	**-2.72**	0.00547	**-0.48**	0.39038	**1.97**	0.00098
STM3932	hisR	STM3932	**-1.00**	0.09655	**0.03**	0.96561	**2.92**	0.00050
STM3932	hisR	STM3932	**-0.09**	0.83951	**0.23**	0.74090	**3.86**	0.00007
STM3933	leuT	STM3933	**-1.47**	0.03896	**-2.34**	0.00048	**-0.07**	0.87028
STM3933	leuT	STM3933	**-0.97**	0.07431	**-2.36**	0.00060	**-0.56**	0.16042
STM3934	proM	STM3934	**-2.20**	0.04107	**-1.34**	0.01056	**0.83**	0.14679
STM3934	proM	STM3934	**-2.12**	0.06218	**-1.99**	0.00130	**0.62**	0.21366
STM3935	hemY	heme biosynthetic protein	**-2.03**	0.08177	**-1.54**	0.00128	**-1.96**	0.00078
STM3935	hemY	heme biosynthetic protein	**-0.65**	0.66936	**-1.89**	0.00052	**-1.62**	0.00228

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM3936	hemX	uroporphyrinogen III methylase	**-2.39**	0.00648	**-1.71**	0.00214	**-2.21**	0.00098
STM3936	hemX	uroporphyrinogen III methylase	**-1.61**	0.05040	**-1.75**	0.00098	**-2.48**	0.00196
STM3937	STM3937	uroporphyrinogen-III synthetase	**-3.02**	0.00689	**-1.72**	0.00046	**-1.37**	0.00664
STM3937	STM3937	uroporphyrinogen-III synthetase	**-2.08**	0.01194	**-1.27**	0.01062	**-1.55**	0.00890
STM3938	hemC	porphobilinogen deaminase	**-2.66**	0.01024	**-1.95**	0.00091	**-1.62**	0.00224
STM3938	hemC	porphobilinogen deaminase	**-3.03**	0.00674	**-2.11**	0.00084	**-2.50**	0.01413
STM3939	cyaA	adenylate cyclase	**-0.10**	0.90452	**-0.28**	0.32585	**-0.13**	0.83180
STM3939	cyaA	adenylate cyclase	**0.07**	0.90762	**-0.55**	0.07975	**1.55**	0.10916
STM3940	STM3940	putative inner membrane protein	**-0.60**	0.20600	**-0.33**	0.33152	**-0.23**	0.58513
STM3940	STM3940	putative inner membrane protein	**-0.89**	0.08022	**-0.50**	0.13284	**-0.41**	0.31828
STM3941	STM3941	putative inner membrane protein	**-1.37**	0.10686	**0.08**	0.95389	**-1.21**	0.01793
STM3941	STM3941	putative inner membrane protein	**-0.77**	0.12940	**-0.67**	0.07873	**-0.92**	0.08864
STM3943	cyaY	frataxin-like protein	**-1.31**	0.02603	**0.00**	0.99589	**-0.85**	0.05086
STM3943	cyaY	frataxin-like protein	**-0.18**	0.72631	**-0.91**	0.01462	**-0.81**	0.06418
STM3944	STM3944	putative inner membrane protein	**-0.28**	0.51146	**-0.12**	0.71831	**-0.86**	0.04384
STM3944	STM3944	putative inner membrane protein	**0.17**	0.69393	**-0.08**	0.82689	**-0.18**	0.73273
STM3946	yifL	putative outer membrane lipoprotein	**-0.41**	0.64560	**0.05**	0.88176	**-0.43**	0.31649
STM3946	yifL	putative outer membrane lipoprotein	**0.18**	0.66916	**-0.31**	0.37745	**-0.14**	0.74824
STM3947	dapF	diaminopimelate epimerase	**-2.27**	0.01032	**-0.63**	0.05305	**-1.53**	0.00231
STM3947	dapF	diaminopimelate epimerase	**-1.84**	0.05742	**-0.53**	0.10203	**-1.10**	0.12656
STM3948	yigA	putative cytoplasmic protein	**-2.23**	0.01263	**-0.78**	0.05574	**-2.59**	0.00257
STM3948	yigA	putative cytoplasmic protein	**-0.93**	0.36920	**-1.10**	0.00932	**-1.88**	0.00375
STM3949	xerC	tyrosine recombinase	**-2.04**	0.00913	**-1.13**	0.00513	**-2.66**	0.00332
STM3949	xerC	tyrosine recombinase	**1.01**	0.64120	**-1.10**	0.03798	**-2.54**	0.00437
STM3950	yigB	putative hydrolase	**-1.03**	0.07572	**-1.19**	0.02626	**-0.37**	0.34979
STM3950	yigB	putative hydrolase	**-0.55**	0.39392	**-0.59**	0.07629	**-0.52**	0.24526
STM3951	uvrD	DNA-dependent ATPase I/helicase II	**-1.56**	0.03367	**-0.13**	0.71310	**-0.94**	0.12985
STM3951	uvrD	DNA-dependent ATPase I/helicase II	**-0.36**	0.60323	**-0.27**	0.41161	**-0.51**	0.42843
STM3952	corA	Mg2+/Ni2+/Co2+ transport protein	**0.95**	0.27365	**-0.13**	0.68515	**-1.07**	0.46256
STM3952	corA	Mg2+/Ni2+/Co2+ transport protein	**0.28**	0.64804	**0.10**	0.78944	**0.60**	0.25873
STM3953	yigF	putative inner membrane protein	**0.93**	0.13409	**0.06**	0.88334	**1.10**	0.02478
STM3953	yigF	putative inner membrane protein	**1.63**	0.07360	**0.50**	0.21299	**0.31**	0.68330
STM3955	rarD	chloramphenicol resistance	**-0.88**	0.08479	**-1.53**	0.00096	**-1.57**	0.00575
STM3955	rarD	chloramphenicol resistance	**0.93**	0.35003	**-1.08**	0.00665	**-1.38**	0.01440
STM3956	yigI	hypothetical protein STM3956	**-0.95**	0.11026	**0.85**	0.01893	**-0.05**	0.95646
STM3956	yigI	hypothetical protein STM3956	**1.04**	0.31379	**0.98**	0.01581	**-0.30**	0.41871
STM3957	pldA	outer membrane phospholipase A precursor	**-1.29**	0.04995	**-0.55**	0.09861	**-0.81**	0.10386
STM3957	pldA	outer membrane phospholipase A precursor	**0.00**	0.99561	**-0.57**	0.18368	**0.75**	0.09055
STM3958	recQ	ATP-dependent DNA helicase	**-0.94**	0.05421	**-0.34**	0.25132	**-1.22**	0.12391
STM3958	recQ	ATP-dependent DNA helicase	**0.51**	0.32229	**-0.65**	0.13583	**-1.01**	0.02803
STM3959	rhtC	threonine efflux protein	**0.53**	0.56060	**0.51**	0.54688	**-0.43**	0.42791
STM3959	rhtC	threonine efflux protein	**-0.02**	0.97348	**0.24**	0.55478	**-2.11**	0.00852
STM3960	rthB	homoserine/homoserine lactone efflux protein	**-0.35**	0.46766	**-0.19**	0.58513	**-1.42**	0.01705
STM3960	rthB	homoserine/homoserine lactone efflux protein	**1.64**	0.07165	**-0.58**	0.08198	**0.02**	0.98928
STM3961	pldB	lysophospholipase L2	**-1.08**	0.04983	**0.30**	0.58636	**-0.30**	0.48125
STM3961	pldB	lysophospholipase L2	**-1.07**	0.04588	**-0.28**	0.34214	**-1.94**	0.06030
STM3962	yigL	putative hydrolase	**-0.86**	0.10271	**-0.68**	0.02982	**-0.75**	0.47113
STM3962	yigL	putative hydrolase	**-1.00**	0.23662	**-0.38**	0.27194	**-1.87**	0.17802
STM3963	yigM	putative transport protein	**-0.52**	0.46474	**-0.32**	0.76294	**0.51**	0.49646
STM3963	yigM	putative transport protein	**0.11**	0.87420	**-0.12**	0.74912	**-0.57**	0.34682
STM3964	metR	metE/metH regulator	**-0.19**	0.77738	**1.12**	0.03198	**-1.57**	0.09021
STM3964	metR	metE/metH regulator	**1.24**	0.05468	**0.87**	0.01115	**-0.12**	0.78846
STM3965	metE	5-methyltetrahydropteroyltriglutamate--homocysteine	**0.69**	0.34225	**0.19**	0.52451	**-0.81**	0.13941
STM3965	metE	5-methyltetrahydropteroyltriglutamate--homocysteine	**1.78**	0.18692	**-0.19**	0.51353	**0.40**	0.63186
STM3966	STM3966	putative arylsulfatase regulator	**1.15**	0.23325	**0.93**	0.03113	**0.69**	0.50244
STM3966	STM3966	putative arylsulfatase regulator	**1.15**	0.08901	**0.65**	0.15015	**1.12**	0.07985
STM3967	dlhH	putative dienelactone hydrolase	**0.47**	0.29231	**1.10**	0.00590	**0.62**	0.48150
STM3967	dlhH	putative dienelactone hydrolase	**0.88**	0.09242	**1.48**	0.00277	**0.96**	0.03876
STM3968	udp	uridine phosphorylase	**-1.60**	0.04050	**-2.99**	0.00006	**-2.36**	0.00413
STM3968	udp	uridine phosphorylase	**-0.42**	0.69155	**-2.80**	0.00031	**-1.85**	0.00198
STM3969	yigN	putative inner membrane protein	**-0.67**	0.22605	**-0.16**	0.67409	**-0.70**	0.12558
STM3969	yigN	putative inner membrane protein	**-0.59**	0.24403	**-0.39**	0.19676	**-0.49**	0.23279
STM3970	ubiE	ubiquinone/menaquinone biosynthesis methyltransferase	**-1.08**	0.04057	**-0.32**	0.27987	**-1.82**	0.00252
STM3970	ubiE	ubiquinone/menaquinone biosynthesis methyltransferase	**-0.07**	0.91057	**0.08**	0.80415	**-1.28**	0.00732
STM3971	yigP	putative inner membrane protein	**-1.04**	0.08483	**0.16**	0.62572	**-1.64**	0.00191
STM3971	yigP	putative inner membrane protein	**-0.51**	0.28373	**0.13**	0.67904	**-0.73**	0.06767
STM3972	aarF	putative ubiquinone biosynthesis protein UbiB	**0.55**	0.41354	**-0.32**	0.34570	**-2.04**	0.00134
STM3972	aarF	putative ubiquinone biosynthesis protein UbiB	**1.45**	0.06236	**0.30**	0.34195	**-0.81**	0.06952
STM3973	tatA	twin argininte translocase protein A	**-0.28**	0.53432	**0.09**	0.79439	**0.09**	0.87700
STM3973	tatA	twin argininte translocase protein A	**0.67**	0.21314	**0.09**	0.79507	**0.65**	0.13425

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM3974	tatB	sec-independent translocase	**-1.73**	0.02339	**-0.66**	0.07189	**-1.86**	0.00465
STM3974	tatB	sec-independent translocase	**0.80**	0.17075	**-0.14**	0.73593	**-1.26**	0.01835
STM3975	tatC	Sec-independent protein secretion pathway component	**-0.66**	0.25154	**-0.51**	0.24706	**-1.37**	0.01632
STM3975	tatC	Sec-independent protein secretion pathway component	**0.74**	0.32441	**-0.41**	0.16350	**-0.50**	0.19515
STM3976,S	yigW	putative hydrolase	**-1.27**	0.06140	**0.14**	0.69566	**-1.76**	0.01105
STM3976,S	yigW	putative hydrolase	**-1.25**	0.07276	**-0.63**	0.04139	**-1.51**	0.02207
STM3977	rfaH	transcriptional activator RfaH	**-1.64**	0.01882	**-1.07**	0.00871	**-0.71**	0.16189
STM3977	rfaH	transcriptional activator RfaH	**-1.11**	0.10070	**-0.85**	0.04398	**-1.28**	0.01959
STM3978	yigC	putative oxidoreductase	**-1.46**	0.01667	**-0.95**	0.01445	**-2.50**	0.00030
STM3978	yigC	putative oxidoreductase	**-0.25**	0.68920	**-0.54**	0.07593	**-2.30**	0.00428
STM3979	ubiB	NAD(P)H-flavin reductase	**-1.44**	0.07329	**-1.35**	0.00192	**-0.87**	0.07679
STM3979	ubiB	NAD(P)H-flavin reductase	**-0.85**	0.12130	**-1.40**	0.00200	**-1.02**	0.03813
STM3981	STM3981	putative cytoplasmic protein	**-0.36**	0.49858	**-0.06**	0.88945	**-0.22**	0.64867
STM3981	STM3981	putative cytoplasmic protein	**1.02**	0.06085	**0.44**	0.13343	**0.47**	0.25343
STM3982	fadA	acetyl-CoA acetyltransferase	**-0.78**	0.15154	**1.54**	0.01422	**0.61**	0.20106
STM3982	fadA	acetyl-CoA acetyltransferase	**0.27**	0.68802	**0.77**	0.03962	**0.43**	0.42162
STM3983	fadB	3-hydroxyacyl-CoA dehydrogenase	**-0.48**	0.51786	**1.08**	0.02173	**-0.33**	0.45010
STM3983	fadB	3-hydroxyacyl-CoA dehydrogenase	**0.53**	0.35194	**1.09**	0.00445	**0.64**	0.26245
STM3984	pepQ	proline dipeptidase	**-0.57**	0.36015	**-0.32**	0.25554	**-0.07**	0.86623
STM3984	pepQ	proline dipeptidase	**0.16**	0.75196	**-0.59**	0.09504	**0.97**	0.03082
STM3985	yigZ	putative cytoplasmic protein	**-1.37**	0.02087	**-0.91**	0.00791	**-0.76**	0.05003
STM3985	yigZ	putative cytoplasmic protein	**-0.76**	0.10556	**-0.78**	0.02962	**-0.14**	0.70371
STM3986	trkH	potassium transport protein	**-1.27**	0.05571	**-0.23**	0.55435	**0.94**	0.02730
STM3986	trkH	potassium transport protein	**0.16**	0.86483	**-0.19**	0.49015	**0.49**	0.32226
STM3987	hemG	protoporphyrin oxidase	**0.06**	0.88427	**0.71**	0.06032	**0.82**	0.03858
STM3987	hemG	protoporphyrin oxidase	**0.56**	0.37031	**0.41**	0.26311	**1.75**	0.00304
STM3988	rrsA	STM3988	**-2.05**	0.04832	**-0.16**	0.68667	**0.00**	0.99426
STM3988	rrsA	STM3988	**-2.12**	0.06312	**0.25**	0.55810	**-0.52**	0.17551
STM3989	ileT	STM3989	**1.18**	0.05779	**0.48**	0.17115	**1.16**	0.00899
STM3989	ileT	STM3989	**1.20**	0.10314	**0.10**	0.77598	**1.21**	0.00967
STM3990	alaT	STM3990	**1.41**	0.03789	**0.71**	0.03235	**0.45**	0.19319
STM3990	alaT	STM3990	**1.67**	0.01305	**0.86**	0.01423	**0.25**	0.49040
STM3991	rrlA	STM3991	**-2.25**	0.01765	**0.04**	0.94642	**-0.83**	0.10546
STM3991	rrlA	STM3991	**-2.94**	0.01193	**-0.04**	0.95207	**-1.95**	0.00902
STM3992	rrfA	STM3992	**0.35**	0.59927	**0.00**	0.99252	**0.28**	0.64647
STM3992	rrfA	STM3992	**1.46**	0.02765	**0.34**	0.53369	**0.44**	0.23593
STM3993	mobB	molybdopterin-guanine dinucleotide biosynthesis protein B	**-0.93**	0.06399	**-0.23**	0.46292	**1.32**	0.00600
STM3993	mobB	molybdopterin-guanine dinucleotide biosynthesis protein B	**-0.84**	0.21626	**-0.03**	0.94003	**1.68**	0.00304
STM3994	mobA	molybdopterin-guanine dinucleotide biosynthesis protein A	**-1.25**	0.12921	**-0.28**	0.45318	**1.22**	0.03331
STM3994	mobA	molybdopterin-guanine dinucleotide biosynthesis protein A	**-0.40**	0.40310	**-0.25**	0.54693	**1.21**	0.01266
STM3995	yihD	putative cytoplasmic protein	**-1.27**	0.09313	**-1.02**	0.01654	**0.20**	0.61485
STM3995	yihD	putative cytoplasmic protein	**-0.03**	0.95887	**-0.99**	0.00622	**0.55**	0.12619
STM3996	yihE	putative type II homoserine kinase	**1.79**	0.06196	**-0.25**	0.42753	**0.12**	0.89294
STM3996	yihE	putative type II homoserine kinase	**2.32**	0.24165	**-0.47**	0.20970	**0.89**	0.62768
STM3997	dsbA	periplasmic protein disulfide isomerase I	**-1.95**	0.02729	**-0.42**	0.16845	**-0.62**	0.25030
STM3997	dsbA	periplasmic protein disulfide isomerase I	**-0.76**	0.27015	**-0.27**	0.38604	**-0.97**	0.01856
STM3998	yihG	putative endonuclease	**-1.62**	0.04342	**-0.51**	0.15812	**-1.76**	0.00280
STM3998	yihG	putative endonuclease	**-1.32**	0.03179	**-0.58**	0.06667	**-1.13**	0.02343
STM3999	polA	DNA polymerase I	**-1.15**	0.04845	**-0.33**	0.37800	**-0.91**	0.04195
STM3999	polA	DNA polymerase I	**0.24**	0.79237	**-0.64**	0.03798	**-0.44**	0.25218
STM4000	spf	STM4000	**-1.34**	0.06267	**-0.73**	0.02260	**-0.56**	0.23647
STM4000	spf	STM4000	**-1.15**	0.35912	**-1.59**	0.00085	**-0.45**	0.26782
STM4001	yihA	GTP-binding protein	**-1.42**	0.02309	**0.54**	0.38599	**-0.44**	0.33178
STM4001	yihA	GTP-binding protein	**-1.52**	0.05036	**-0.41**	0.15825	**-0.67**	0.22460
STM4003	yihI	hypothetical protein STM4003	**-1.08**	0.04501	**-1.25**	0.00505	**-0.21**	0.58267
STM4003	yihI	hypothetical protein STM4003	**-0.49**	0.27849	**-1.05**	0.00638	**0.15**	0.71025
STM4004	hemN	coproporphyrinogen III oxidase	**-1.15**	0.04692	**-1.12**	0.00596	**-1.51**	0.00372
STM4004	hemN	coproporphyrinogen III oxidase	**-1.34**	0.28131	**-0.63**	0.05044	**-1.71**	0.02700
STM4005	glnG	response regulator	**-0.44**	0.45046	**-1.42**	0.00617	**-0.40**	0.52656
STM4005	glnG	response regulator	**0.06**	0.94866	**-0.83**	0.04176	**-0.75**	0.30355
STM4006	glnL	sensor kinase	**-1.27**	0.02468	**-1.99**	0.00067	**-1.87**	0.03443
STM4006	glnL	sensor kinase	**-0.46**	0.34561	**-2.05**	0.00075	**-1.29**	0.01945
STM4007	glnA	glutamine synthetase	**-1.28**	0.02828	**-0.45**	0.11340	**-3.45**	0.00742
STM4007	glnA	glutamine synthetase	**-0.90**	0.07165	**-0.28**	0.36719	**-4.71**	0.00005
STM4009	typA	GTP-binding elongation factor family protein	**-1.17**	0.07746	**-0.30**	0.37315	**-0.79**	0.08578
STM4009	typA	GTP-binding elongation factor family protein	**-0.68**	0.21612	**-0.14**	0.68034	**-0.98**	0.09006
STM4010	STM4010	putative hydrolase	**-1.62**	0.01515	**-0.35**	0.31644	**-1.15**	0.07556
STM4010	STM4010	putative hydrolase	**-1.75**	0.09713	**-0.72**	0.07250	**-1.19**	0.01184
STM4011	STM4011	putative inner membrane protein	**-1.51**	0.07626	**-0.96**	0.01132	**-1.78**	0.00777
STM4011	STM4011	putative inner membrane protein	**-0.61**	0.21459	**-1.02**	0.00619	**-1.02**	0.03509

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM4012	STM4012	coproporphyrinogen III oxidase	**-0.84**	0.09801	**-0.61**	0.04301	**-0.03**	0.94719
STM4012	STM4012	coproporphyrinogen III oxidase	**1.51**	0.02872	**-0.34**	0.50397	**0.83**	0.23023
STM4013,S	STM4013,S	putative membrane-associated metal-dependent hydrolase	**-0.26**	0.72446	**-0.45**	0.49389	**0.35**	0.44786
STM4013,S	STM4013,S	putative membrane-associated metal-dependent hydrolase	**0.31**	0.51992	**-2.23**	0.00013	**0.40**	0.42189
STM4014	STM4014	putative periplasmic protein	**5.83**	0.02347	**4.51**	0.00010	**4.31**	0.02752
STM4014	STM4014	putative periplasmic protein	**6.92**	0.01085	**2.60**	0.00147	**4.65**	0.00152
STM4015	STM4015	putative cytoplasmic protein	**-1.09**	0.07354	**0.59**	0.08305	**-0.11**	0.87922
STM4015	STM4015	putative cytoplasmic protein	**-0.44**	0.58682	**-0.74**	0.05634	**0.63**	0.22380
STM4016	yshA	putative outer membrane protein	**1.59**	0.22022	**-0.86**	0.06592	**1.55**	0.05455
STM4016	yshA	putative outer membrane protein	**-0.52**	0.58781	**-1.41**	0.00591	**0.43**	0.40102
STM4017	yihO	putative GPH family transport protein	**0.26**	0.59615	**-0.45**	0.58946	**1.30**	0.01817
STM4017	yihO	putative GPH family transport protein	**1.37**	0.18880	**-0.95**	0.03726	**0.38**	0.45667
STM4018	yihP	putative GPH family transport protein	**1.43**	0.10004	**1.54**	0.00195	**1.82**	0.01004
STM4018	yihP	putative GPH family transport protein	**2.18**	0.01592	**1.16**	0.15953	**2.52**	0.00166
STM4019	yihQ	putative alpha-xylosidase	**0.73**	0.32129	**0.62**	0.20321	**0.28**	0.54516
STM4019	yihQ	putative alpha-xylosidase	**0.59**	0.16511	**-0.39**	0.31014	**1.07**	0.15764
STM4020,S	yihR	putative aldose-1-epimerase	**-0.13**	0.76966	**-0.58**	0.11501	**-0.41**	0.46330
STM4020,S	yihR	putative aldose-1-epimerase	**0.04**	0.94061	**-0.15**	0.77871	**-0.64**	0.43580
STM4021	yihS	putative isomerase	**-0.74**	0.20774	**-0.13**	0.84552	**0.79**	0.10436
STM4021	yihS	putative isomerase	**0.27**	0.53332	**-1.13**	0.01191	**-0.24**	0.54752
STM4022	yihT	putative aldolase	**-0.83**	0.10358	**0.19**	0.67976	**0.31**	0.75314
STM4022	yihT	putative aldolase	**0.17**	0.71798	**-0.71**	0.18193	**-0.16**	0.75671
STM4023	yihU	putative oxidoreductase	**-0.03**	0.96450	**-1.54**	0.03813	**-0.50**	0.69334
STM4023	yihU	putative oxidoreductase	**0.46**	0.71390	**-0.80**	0.05216	**0.15**	0.89697
STM4024,S	yihV	putative sugar kinase	**-0.25**	0.68769	**-0.70**	0.03533	**-0.42**	0.53854
STM4024,S	yihV	putative sugar kinase	**0.07**	0.91699	**-1.13**	0.03252	**-0.55**	0.77559
STM4025	yihW	putative glycerol-3-phosphate regulon repressor	**-0.47**	0.43401	**-0.66**	0.09379	**-0.24**	0.56691
STM4025	yihW	putative glycerol-3-phosphate regulon repressor	**-0.33**	0.55995	**-0.37**	0.17436	**0.76**	0.28271
STM4026	yihX	phosphatase	**-1.06**	0.20924	**-0.94**	0.04699	**-0.38**	0.40873
STM4026	yihX	phosphatase	**-0.28**	0.58838	**-0.40**	0.19431	**0.19**	0.59501
STM4027	rbn	ribonuclease BN	**-0.29**	0.53542	**-0.64**	0.05651	**-1.14**	0.09484
STM4027	rbn	ribonuclease BN	**0.45**	0.52695	**-0.67**	0.05172	**-0.44**	0.32665
STM4028	yihZ	D-tyrosyl-tRNA deacylase	**-0.74**	0.41626	**-0.75**	0.04802	**-1.50**	0.00720
STM4028	yihZ	D-tyrosyl-tRNA deacylase	**0.16**	0.75541	**-1.01**	0.02376	**-0.69**	0.08498
STM4029	yiiD	putative acetyltransferase	**0.27**	0.71508	**0.51**	0.15834	**0.12**	0.74768
STM4029	yiiD	putative acetyltransferase	**1.27**	0.06815	**0.95**	0.01450	**1.33**	0.05815
STM4030,S	STM4030,S	putative cytoplasmic protein	**1.16**	0.03562	**2.01**	0.00034	**0.06**	0.87641
STM4030,S	STM4030,S	putative cytoplasmic protein	**1.26**	0.03293	**1.86**	0.00213	**1.04**	0.04022
STM4031	STM4031	putative cytoplasmic protein	**0.98**	0.29260	**2.50**	0.00033	**0.15**	0.73863
STM4031	STM4031	putative cytoplasmic protein	**2.58**	0.00753	**2.91**	0.00014	**0.45**	0.24534
STM4032	STM4032	putative acetyl esterase	**-1.09**	0.25320	**-0.35**	0.27740	**-0.22**	0.64230
STM4032	STM4032	putative acetyl esterase	**1.13**	0.37126	**-0.01**	0.97647	**0.85**	0.09665
STM4032,2N	STM4032,2N	hypothetical protein STM4032,2N	**0.74**	0.12508	**3.00**	0.00503	**0.97**	0.09899
STM4032,2N	STM4032,2N	hypothetical protein STM4032,2N	**1.25**	0.06553	**0.82**	0.03442	**1.50**	0.00523
STM4033	STM4033	putative regulatory protein	**-0.60**	0.25777	**-0.23**	0.49843	**-1.03**	0.07300
STM4033	STM4033	putative regulatory protein	**0.27**	0.67110	**-0.19**	0.53694	**-0.62**	0.25100
STM4034	fdhE	formate dehydrogenase accessory protein FdhE	**1.43**	0.23254	**0.32**	0.26915	**-0.92**	0.07806
STM4034	fdhE	formate dehydrogenase accessory protein FdhE	**0.76**	0.25707	**0.41**	0.17242	**-0.60**	0.11769
STM4035	fdoI	formate dehydrogenase-O gamma subunit	**-0.45**	0.39109	**-1.39**	0.00163	**-1.65**	0.01882
STM4035	fdoI	formate dehydrogenase-O gamma subunit	**0.43**	0.38774	**-0.76**	0.03652	**-1.27**	0.02233
STM4036	fdoH	formate dehydrogenase-O beta subunit	**-0.81**	0.61242	**-2.33**	0.00032	**-0.93**	0.20093
STM4036	fdoH	formate dehydrogenase-O beta subunit	**2.35**	0.00720	**-3.04**	0.00011	**0.06**	0.94140
STM4037	fdoG	formate dehydrogenase alpha subunit	**-3.06**	0.00942	**-2.42**	0.00023	**-2.62**	0.00037
STM4037	fdoG	formate dehydrogenase alpha subunit	**-2.23**	0.01479	**-1.38**	0.12073	**-1.97**	0.00683
STM4038	fdhD	formate dehydrogenase accessory protein	**0.30**	0.71888	**-2.12**	0.00130	**-1.50**	0.07443
STM4038	fdhD	formate dehydrogenase accessory protein	**-0.94**	0.68827	**-1.83**	0.00235	**-2.27**	0.08782
STM4039	STM4039	putative inner membrane lipoprotein	**-0.82**	0.11505	**-0.33**	0.25566	**-0.67**	0.13021
STM4039	STM4039	putative inner membrane lipoprotein	**0.80**	0.50324	**0.26**	0.61191	**-0.55**	0.36837
STM4040	yiiG	putative cytoplasmic protein	**-0.39**	0.57800	**-0.09**	0.91681	**0.23**	0.58171
STM4040	yiiG	putative cytoplasmic protein	**0.52**	0.22243	**-0.24**	0.70774	**1.08**	0.01416
STM4041	STM4041	putative inner membrane protein	**-1.39**	0.04742	**-0.60**	0.41640	**-1.14**	0.03208
STM4041	STM4041	putative inner membrane protein	**-0.11**	0.81924	**-0.82**	0.05080	**-0.77**	0.20167
STM4042	STM4042	putative branched-chain amino acid permease	**0.62**	0.35370	**-0.10**	0.76452	**-1.23**	0.01032
STM4042	STM4042	putative branched-chain amino acid permease	**0.32**	0.45618	**0.20**	0.57714	**-0.13**	0.82800
STM4042A	STM4042A	hypothetical protein STM4042A	**-1.12**	0.13520	**-0.46**	0.35851	**-0.65**	0.25749
STM4042A	STM4042A	hypothetical protein STM4042A	**-0.09**	0.88349	**0.33**	0.22727	**-0.70**	0.12834
STM4043	yiiL	putative cytoplasmic protein	**-0.88**	0.17538	**-0.19**	0.69497	**0.26**	0.63548
STM4043	yiiL	putative cytoplasmic protein	**-1.99**	0.03518	**-0.18**	0.57362	**-2.07**	0.00150
STM4044	STM4044	putative alcohol dehydrogenase	**0.54**	0.55868	**-0.46**	0.26237	**0.51**	0.55918
STM4044	STM4044	putative alcohol dehydrogenase	**1.40**	0.02424	**0.27**	0.42002	**0.31**	0.40425

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM4045	rhaD	rhamnulose-1-phosphate aldolase	**-1.01**	0.17542	**-0.04**	0.89492	**-0.37**	0.52036
STM4045	rhaD	rhamnulose-1-phosphate aldolase	**0.41**	0.48015	**-0.43**	0.47304	**-0.31**	0.39788
STM4046	rhaA	L-rhamnose isomerase	**-0.04**	0.93940	**-0.60**	0.31869	**-0.14**	0.79443
STM4046	rhaA	L-rhamnose isomerase	**1.38**	0.45414	**0.09**	0.92902	**0.49**	0.43067
STM4047	rhaB	rhamnulokinase	**-0.49**	0.28373	**0.73**	0.03800	**-0.46**	0.26256
STM4047	rhaB	rhamnulokinase	**0.99**	0.05606	**-0.93**	0.04103	**1.86**	0.22418
STM4048	rhaS	L-rhamnose operon regulatory protein	**0.03**	0.97293	**-0.74**	0.06553	**-0.29**	0.53173
STM4048	rhaS	L-rhamnose operon regulatory protein	**2.02**	0.01171	**-0.52**	0.31476	**0.39**	0.52048
STM4049	rhaR	rhaRS operon regulatory protein	**0.36**	0.47883	**0.29**	0.48492	**0.92**	0.12070
STM4049	rhaR	rhaRS operon regulatory protein	**1.07**	0.15459	**0.58**	0.08734	**0.24**	0.66786
STM4050	rhaT	L-rhamnose/H+ symporter protein	**-0.72**	0.39262	**-0.07**	0.89101	**-0.85**	0.16042
STM4050	rhaT	L-rhamnose/H+ symporter protein	**0.89**	0.21547	**0.07**	0.89754	**0.30**	0.49025
STM4051	STM4051	putative outer membrane protein	**-0.49**	0.29163	**0.35**	0.59493	**-0.15**	0.74693
STM4051	STM4051	putative outer membrane protein	**0.38**	0.45198	**0.05**	0.93932	**1.72**	0.10947
STM4052	STM4052	putative C4-dicarboxylate transport system	**-0.40**	0.68170	**0.47**	0.52674	**0.25**	0.57818
STM4052	STM4052	putative C4-dicarboxylate transport system	**0.84**	0.40315	**-1.04**	0.04612	**-1.26**	0.10410
STM4053	STM4053	putative C4-dicarboxylate transport system	**0.37**	0.42988	**0.29**	0.32828	**0.84**	0.10552
STM4053	STM4053	putative C4-dicarboxylate transport system	**0.46**	0.53577	**-1.38**	0.00448	**0.09**	0.85047
STM4054	STM4054	putative periplasmic dicarboxylate-binding protein	**-0.55**	0.20566	**-0.71**	0.05932	**0.07**	0.90503
STM4054	STM4054	putative periplasmic dicarboxylate-binding protein	**0.26**	0.59741	**-1.63**	0.00341	**-0.10**	0.82029
STM4055	sodA	superoxide dismutase	**-3.04**	0.01305	**-1.42**	0.00168	**-0.08**	0.84039
STM4055	sodA	superoxide dismutase	**-1.93**	0.02552	**-1.46**	0.00358	**-0.18**	0.61424
STM4056,S	yiiM	putative cytoplasmic protein	**-1.05**	0.06500	**-0.33**	0.25839	**-0.09**	0.81963
STM4056,S	yiiM	putative cytoplasmic protein	**-0.44**	0.35495	**-0.58**	0.06780	**-0.16**	0.69549
STM4057	STM4057	putative inner membrane protein	**-1.46**	0.03991	**-0.70**	0.05328	**-1.38**	0.01526
STM4057	STM4057	putative inner membrane protein	**-0.17**	0.83693	**-0.64**	0.18856	**0.02**	0.97405
STM4058	cpxA	two-component sensor protein	**-1.27**	0.04517	**-0.22**	0.58486	**-1.77**	0.00515
STM4058	cpxA	two-component sensor protein	**0.25**	0.70219	**-0.03**	0.93731	**-0.64**	0.11757
STM4059	cpxR	response reguator	**-1.66**	0.01551	**0.19**	0.62673	**-1.77**	0.00112
STM4059	cpxR	response reguator	**-1.18**	0.06677	**0.42**	0.28241	**-1.42**	0.01622
STM4060	cpxP	periplasmic repressor	**1.58**	0.03329	**4.60**	0.00003	**4.01**	0.00005
STM4060	cpxP	periplasmic repressor	**2.67**	0.00757	**4.36**	0.00002	**4.64**	0.00002
STM4061	fieF	ferrous iron efflux protein F	**-0.58**	0.20939	**0.06**	0.88334	**-1.11**	0.01105
STM4061	fieF	ferrous iron efflux protein F	**-0.39**	0.33295	**0.58**	0.06380	**-0.57**	0.15345
STM4062	pfkA	6-phosphofructokinase	**-0.87**	0.13734	**0.56**	0.09313	**-0.27**	0.54533
STM4062	pfkA	6-phosphofructokinase	**0.28**	0.51135	**0.09**	0.85933	**0.62**	0.12974
STM4063	sbp	sulfate transport protein	**1.12**	0.16023	**0.46**	0.26241	**0.31**	0.39572
STM4063	sbp	sulfate transport protein	**-0.46**	0.43083	**-0.88**	0.10516	**-0.43**	0.34931
STM4064	ushB	CDP-diacylglycerol pyrophosphatase	**-1.24**	0.07059	**-0.78**	0.02935	**-2.85**	0.00086
STM4064	ushB	CDP-diacylglycerol pyrophosphatase	**-1.29**	0.05707	**-0.45**	0.21299	**-4.82**	0.00021
STM4065	STM4065	putative Na+/galactoside symporter	**-0.75**	0.19941	**-1.33**	0.01260	**-1.22**	0.10342
STM4065	STM4065	putative Na+/galactoside symporter	**0.03**	0.95456	**-0.69**	0.05415	**0.58**	0.38668
STM4066	STM4066	aminoimidazole riboside kinase	**-0.82**	0.12861	**-0.24**	0.53919	**-0.65**	0.28054
STM4066	STM4066	aminoimidazole riboside kinase	**0.10**	0.91824	**-0.78**	0.07882	**-0.68**	0.23094
STM4067	STM4067	putative ADP-ribosylglycohydrolase	**-2.17**	0.03218	**-0.64**	0.05000	**-1.55**	0.00725
STM4067	STM4067	putative ADP-ribosylglycohydrolase	**-1.08**	0.05100	**-0.92**	0.01562	**-1.83**	0.00214
STM4068	STM4068	putative regulatory protein	**-1.36**	0.02480	**-1.09**	0.01594	**-1.28**	0.00711
STM4068	STM4068	putative regulatory protein	**-0.92**	0.20996	**-0.63**	0.07701	**-0.75**	0.19553
STM4069	STM4069	putative periplasmic protein	**-0.13**	0.78098	**0.16**	0.66130	**-0.68**	0.12435
STM4069	STM4069	putative periplasmic protein	**-0.41**	0.65156	**-0.91**	0.05282	**-0.83**	0.28045
STM4070	STM4070	putative cytoplasmic protein	**-0.51**	0.35856	**0.55**	0.09869	**-1.10**	0.18300
STM4070	STM4070	putative cytoplasmic protein	**0.38**	0.51327	**0.63**	0.10331	**-0.85**	0.23194
STM4071	STM4071	putative mannose-6-phosphate isomerase	**0.28**	0.68170	**-0.59**	0.13300	**-1.37**	0.01062
STM4071	STM4071	putative mannose-6-phosphate isomerase	**1.66**	0.05591	**-0.09**	0.88764	**0.75**	0.13643
STM4072	ydeV	putative sugar kinase	**0.02**	0.97602	**1.44**	0.00431	**-0.14**	0.75671
STM4072	ydeV	putative sugar kinase	**2.22**	0.02748	**1.06**	0.02698	**2.31**	0.00073
STM4073	ydeW	putative transcriptional repressor	**-0.26**	0.69112	**0.53**	0.11219	**0.60**	0.26871
STM4073	ydeW	putative transcriptional repressor	**-0.20**	0.74986	**1.28**	0.03672	**0.24**	0.67630
STM4074	ego	putative ABC-type aldose transport system ATPase	**-0.79**	0.17299	**0.10**	0.80248	**-0.12**	0.86113
STM4074	ego	putative ABC-type aldose transport system ATPase	**-0.17**	0.84070	**-0.05**	0.88990	**-1.22**	0.23194
STM4075	ydeY	putative sugar transport protein	**2.41**	0.01578	**0.12**	0.77446	**1.49**	0.01597
STM4075	ydeY	putative sugar transport protein	**3.51**	0.00541	**0.53**	0.41061	**3.62**	0.00045
STM4076	ydeZ	putative sugar transport protein	**0.33**	0.69292	**2.27**	0.00067	**2.48**	0.00634
STM4076	ydeZ	putative sugar transport protein	**0.75**	0.22906	**1.96**	0.00427	**1.92**	0.01640
STM4077	yneA	putative sugar transport protein	**-0.60**	0.37789	**1.60**	0.00131	**1.05**	0.18165
STM4077	yneA	putative sugar transport protein	**0.91**	0.09243	**2.04**	0.00019	**1.53**	0.00453
STM4078	yneB	hypothetical protein STM4078	**-0.38**	0.53400	**0.99**	0.00925	**-0.61**	0.15222
STM4078	yneB	hypothetical protein STM4078	**0.34**	0.73633	**0.81**	0.02073	**0.61**	0.11611
STM4079,S	yneC	putative inner membrane protein	**-1.38**	0.06919	**0.98**	0.00972	**-0.18**	0.70360
STM4079,S	yneC	putative inner membrane protein	**-0.37**	0.68379	**0.39**	0.18503	**-0.28**	0.52152

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM4080	STM4080	ribulose-phosphate 3-epimerase	**-1.51**	0.03538	**-0.54**	0.16350	**-2.33**	0.00164
STM4080	STM4080	ribulose-phosphate 3-epimerase	**-1.24**	0.09721	**-0.21**	0.52151	**-2.27**	0.00126
STM4081	tpiA	triosephosphate isomerase	**-3.12**	0.01336	**0.07**	0.84582	**-1.24**	0.02390
STM4081	tpiA	triosephosphate isomerase	**-1.98**	0.02010	**0.61**	0.07987	**-1.48**	0.00694
STM4082	yiiQ	putative periplasmic protein	**-2.25**	0.00727	**-1.48**	0.00248	**-2.49**	0.00041
STM4082	yiiQ	putative periplasmic protein	**-1.29**	0.12619	**-1.12**	0.00427	**-2.64**	0.00896
STM4083	yiiR	putative inner membrane protein	**0.32**	0.54012	**-0.24**	0.38734	**0.41**	0.40607
STM4083	yiiR	putative inner membrane protein	**1.10**	0.08266	**-0.14**	0.65714	**1.27**	0.02811
STM4084	fpr	ferredoxin-NADP reductase	**2.31**	0.01044	**-0.05**	0.95273	**1.18**	0.03112
STM4084	fpr	ferredoxin-NADP reductase	**3.16**	0.10971	**-0.66**	0.08486	**1.00**	0.02386
STM4085	glpX	fructose 1,6-bisphosphatase II	**-2.38**	0.01319	**-0.46**	0.11724	**-1.88**	0.00237
STM4085	glpX	fructose 1,6-bisphosphatase II	**-1.05**	0.13556	**-0.18**	0.63676	**-1.99**	0.00108
STM4086	glpK	glycerol kinase	**-2.24**	0.02838	**2.12**	0.00059	**0.86**	0.06611
STM4086	glpK	glycerol kinase	**-0.66**	0.22927	**2.24**	0.00038	**1.59**	0.00692
STM4087	glpF	glycerol diffusion	**-2.20**	0.01261	**1.28**	0.00624	**1.53**	0.01044
STM4087	glpF	glycerol diffusion	**-2.30**	0.01999	**1.50**	0.00232	**1.96**	0.00693
STM4088	yiiU	putative cytoplasmic protein	**-0.83**	0.14605	**0.00**	0.99267	**-0.12**	0.76309
STM4088	yiiU	putative cytoplasmic protein	**0.31**	0.44306	**0.05**	0.88013	**0.81**	0.08351
STM4089	menG	ribonuclease activity regulator protein RraA	**-0.80**	0.11613	**0.63**	0.04334	**-0.07**	0.86891
STM4089	menG	ribonuclease activity regulator protein RraA	**0.09**	0.83507	**0.72**	0.03695	**0.98**	0.02944
STM4090	menA	1,4-dihydroxy-2-naphthoate octaprenyltransferase,	**-1.24**	0.03645	**-0.72**	0.07960	**-1.03**	0.03798
STM4090	menA	1,4-dihydroxy-2-naphthoate octaprenyltransferase,	**-1.39**	0.27994	**-1.09**	0.00831	**-2.17**	0.03629
STM4091	hslU	ATP-dependent protease ATP-binding subunit	**-1.04**	0.16127	**-1.06**	0.00631	**-1.61**	0.00200
STM4091	hslU	ATP-dependent protease ATP-binding subunit	**-0.55**	0.68331	**-1.00**	0.01173	**-2.22**	0.01230
STM4092	hslV	ATP-dependent protease peptidase subunit	**-2.78**	0.00547	**-0.51**	0.09576	**-2.14**	0.00078
STM4092	hslV	ATP-dependent protease peptidase subunit	**-2.02**	0.00849	**-0.02**	0.96015	**-1.61**	0.01541
STM4093	ftsN	essential cell division protein	**-1.26**	0.08035	**-1.49**	0.00270	**-2.12**	0.00553
STM4093	ftsN	essential cell division protein	**2.36**	0.01941	**-0.90**	0.02631	**-1.24**	0.16486
STM4094	cytR	transcriptional repressor	**-1.16**	0.03872	**-2.34**	0.00017	**-1.80**	0.00166
STM4094	cytR	transcriptional repressor	**-1.57**	0.02682	**-2.38**	0.00098	**-2.11**	0.00914
STM4095	priA	primosome assembly protein PriA	**-1.74**	0.01522	**-1.70**	0.00185	**-2.08**	0.00840
STM4095	priA	primosome assembly protein PriA	**-2.06**	0.12984	**-1.90**	0.00301	**-1.47**	0.00930
STM4097	STM4097	putative outer membrane lipoprotein	**-1.28**	0.03584	**-0.74**	0.08032	**-1.31**	0.01528
STM4097	STM4097	putative outer membrane lipoprotein	**-0.57**	0.33166	**0.05**	0.96225	**-0.25**	0.54480
STM4098	STM4098	putative arylsulfate sulfotransferase	**0.02**	0.97908	**0.64**	0.04081	**-1.53**	0.01361
STM4098	STM4098	putative arylsulfate sulfotransferase	**0.54**	0.30782	**0.40**	0.19595	**0.09**	0.81281
STM4099	metJ	transcriptional repressor protein MetJ	**-0.71**	0.11468	**-0.82**	0.03405	**-0.45**	0.31697
STM4099	metJ	transcriptional repressor protein MetJ	**-0.56**	0.46998	**-0.44**	0.12208	**0.04**	0.91503
STM4100	metB	cystathionine gamma-synthase	**-1.52**	0.02018	**-0.38**	0.30164	**-1.54**	0.00354
STM4100	metB	cystathionine gamma-synthase	**0.07**	0.86862	**-0.61**	0.05038	**-0.90**	0.07640
STM4101	metL	bifunctional aspartate kinase II/homoserine dehydrogenase	**-1.07**	0.23646	**0.27**	0.46856	**-1.73**	0.00677
STM4101	metL	bifunctional aspartate kinase II/homoserine dehydrogenase	**0.15**	0.75518	**-1.17**	0.00389	**-2.20**	0.02134
STM4102	STM4102	putative inner membrane protein	**0.93**	0.10817	**-0.72**	0.10203	**-1.04**	0.05084
STM4102	STM4102	putative inner membrane protein	**1.15**	0.07261	**-0.45**	0.19321	**0.00**	0.99449
STM4103	STM4103	putative cytoplasmic protein	**4.43**	0.02104	**3.49**	0.00544	**3.25**	0.04848
STM4103	STM4103	putative cytoplasmic protein	**0.88**	0.22379	**0.69**	0.28895	**2.53**	0.01350
STM4104	STM4104	putative 5'-nucleotidase/2',3'-cyclic phosphodiesterase	**0.28**	0.75518	**0.73**	0.10307	**0.66**	0.28233
STM4104	STM4104	putative 5'-nucleotidase/2',3'-cyclic phosphodiesterase	**0.84**	0.49312	**-0.37**	0.47317	**1.19**	0.05832
STM4105	metF	5,10-methylenetetrahydrofolate reductase	**-0.08**	0.92235	**0.43**	0.13424	**0.35**	0.60694
STM4105	metF	5,10-methylenetetrahydrofolate reductase	**0.09**	0.89675	**0.87**	0.04497	**0.12**	0.88502
STM4106	katG	hydroperoxidase	**1.91**	0.02423	**-0.29**	0.58425	**1.83**	0.03761
STM4106	katG	hydroperoxidase	**2.33**	0.02096	**2.79**	0.02536	**1.41**	0.33431
STM4107	yijF	putative periplasmic protein	**-0.09**	0.90034	**-0.10**	0.79430	**-1.67**	0.01254
STM4107	yijF	putative periplasmic protein	**1.28**	0.13882	**-0.76**	0.10356	**1.00**	0.02197
STM4108	gldA	glycerol dehydrogenase	**-0.74**	0.28305	**-0.98**	0.11014	**-0.37**	0.49523
STM4108	gldA	glycerol dehydrogenase	**0.10**	0.88368	**-0.72**	0.15462	**0.07**	0.86869
STM4109	talC	fructose-6-phosphate aldolase	**-0.04**	0.94059	**0.30**	0.34917	**0.50**	0.21322
STM4109	talC	fructose-6-phosphate aldolase	**-0.09**	0.89059	**0.60**	0.05346	**0.74**	0.06912
STM4110	ptsA	PEP-protein phosphotransferase	**0.16**	0.87027	**-0.11**	0.81837	**-0.34**	0.42713
STM4110	ptsA	PEP-protein phosphotransferase	**1.01**	0.44190	**-0.18**	0.67697	**0.80**	0.05871
STM4112	frwC	PTS system fructose-like IIC component	**-0.71**	0.20853	**0.37**	0.32228	**-0.81**	0.13481
STM4112	frwC	PTS system fructose-like IIC component	**0.59**	0.22927	**0.21**	0.53646	**0.01**	0.98686
STM4113	frwB	PTS system fructose-like IIB component 1	**0.46**	0.30181	**-0.27**	0.41946	**-0.12**	0.79316
STM4113	frwB	PTS system fructose-like IIB component 1	**1.01**	0.05615	**0.17**	0.56448	**0.72**	0.12561
STM4114	pflD	putative pyruvate formate lyase II	**-0.81**	0.08949	**-0.40**	0.19420	**-0.31**	0.39883
STM4114	pflD	putative pyruvate formate lyase II	**0.20**	0.65612	**0.25**	0.42078	**-0.37**	0.39159
STM4115	pflC	putative pyruvate formate lyase activating enzyme 2	**0.71**	0.15588	**0.51**	0.07613	**0.40**	0.36913
STM4115	pflC	putative pyruvate formate lyase activating enzyme 2	**0.48**	0.67136	**0.12**	0.80056	**0.58**	0.20776
STM4116	frwD	PTS system fructose-like IIB component 2	**0.52**	0.74131	**0.25**	0.44103	**0.33**	0.54311
STM4116	frwD	PTS system fructose-like IIB component 2	**-0.12**	0.82473	**-0.26**	0.42158	**1.31**	0.23647

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM4117	yijO	putative regulatory protein	**-0.35**	0.42383	**0.53**	0.24559	**0.64**	0.44638
STM4117	yijO	putative regulatory protein	**-0.19**	0.81152	**-0.26**	0.50555	**0.76**	0.59189
STM4118	yijP	putative integral membrane protein	**-1.68**	0.07680	**-0.87**	0.10414	**-0.75**	0.25130
STM4118	yijP	putative integral membrane protein	**-1.75**	0.06325	**-1.94**	0.00408	**-3.77**	0.00797
STM4119	ppc	phosphoenolpyruvate carboxylase	**-1.47**	0.01942	**-1.39**	0.00307	**-1.82**	0.01256
STM4119	ppc	phosphoenolpyruvate carboxylase	**-0.77**	0.32640	**-1.25**	0.00526	**-2.03**	0.00381
STM4120	argE	acetylornithine deacetylase	**-1.48**	0.03113	**0.12**	0.78905	**-0.95**	0.12918
STM4120	argE	acetylornithine deacetylase	**-2.08**	0.02178	**0.28**	0.44435	**-1.92**	0.04876
STM4121	argC	N-acetyl-gamma-glutamyl-phosphate reductase	**-0.41**	0.35323	**-0.81**	0.03476	**-0.38**	0.34729
STM4121	argC	N-acetyl-gamma-glutamyl-phosphate reductase	**0.14**	0.80932	**-0.55**	0.11136	**-0.35**	0.51477
STM4122	argB	acetylglutamate kinase	**-1.11**	0.05095	**0.08**	0.82055	**-0.22**	0.64867
STM4122	argB	acetylglutamate kinase	**-1.02**	0.05737	**0.57**	0.13571	**-0.36**	0.64280
STM4123	argH	argininosuccinate lyase	**-0.10**	0.87265	**-0.67**	0.05719	**-0.11**	0.87393
STM4123	argH	argininosuccinate lyase	**1.15**	0.10559	**0.10**	0.78792	**0.63**	0.15094
STM4125	oxyR	oxidative stress regulatory protein	**-0.47**	0.25608	**0.57**	0.10851	**-1.42**	0.00320
STM4125	oxyR	oxidative stress regulatory protein	**0.38**	0.57728	**0.94**	0.00886	**-1.00**	0.03057
STM4126	udhA	soluble pyridine nucleotide transhydrogenase	**-1.75**	0.03453	**0.37**	0.33122	**-0.75**	0.17244
STM4126	udhA	soluble pyridine nucleotide transhydrogenase	**-0.84**	0.07734	**0.72**	0.07803	**-0.83**	0.06313
STM4127	yijC	putative transcriptional repressor	**-2.16**	0.01314	**0.42**	0.16645	**-1.67**	0.02252
STM4127	yijC	putative transcriptional repressor	**-0.69**	0.52039	**0.07**	0.82309	**-0.37**	0.32284
STM4128	yijD	putative inner membrane protein	**-1.51**	0.03013	**-0.70**	0.04662	**-2.48**	0.00154
STM4128	yijD	putative inner membrane protein	**0.46**	0.50506	**-0.05**	0.89183	**-1.49**	0.00780
STM4129	trmA	tRNA (uracil-5-)-methyltransferase	**1.14**	0.21875	**-0.93**	0.01975	**-1.16**	0.06111
STM4129	trmA	tRNA (uracil-5-)-methyltransferase	**2.67**	0.01982	**0.66**	0.50209	**1.51**	0.19547
STM4130	btuB	outer membrane receptor protein precursor	**-0.83**	0.10740	**-0.96**	0.01045	**0.02**	0.96386
STM4130	btuB	outer membrane receptor protein precursor	**-1.48**	0.02109	**-1.13**	0.02518	**0.60**	0.11767
STM4131	murI	glutamate racemase	**-1.83**	0.03325	**-0.19**	0.61715	**0.89**	0.06486
STM4131	murI	glutamate racemase	**-0.34**	0.49224	**0.20**	0.55350	**1.54**	0.00589
STM4132	rrsB	STM4132	**-2.49**	0.04718	**0.42**	0.23151	**-0.60**	0.22763
STM4132	rrsB	STM4132	**-1.89**	0.13788	**0.81**	0.07672	**-0.01**	0.98634
STM4133	ileU	STM4133	**0.63**	0.30527	**0.47**	0.13924	**0.83**	0.05675
STM4133	ileU	STM4133	**1.23**	0.05078	**0.32**	0.26541	**0.86**	0.05020
STM4134	-	STM4134	**1.36**	0.02504	**0.46**	0.16993	**0.21**	0.56805
STM4134	-	STM4134	**0.88**	0.20103	**0.24**	0.45960	**0.39**	0.29573
STM4135	rrlB	STM4135	**-2.70**	0.00558	**-0.78**	0.20062	**-1.69**	0.00854
STM4135	rrlB	STM4135	**-2.65**	0.01227	**-0.18**	0.78792	**-2.04**	0.00601
STM4135	rrlB	STM4135	**-2.74**	0.00817	**-0.13**	0.84235	**-1.90**	0.00336
STM4135	rrlB	STM4135	**-2.96**	0.00818	**-0.25**	0.68415	**-1.54**	0.00872
STM4136	rrfB	STM4136	**0.55**	0.52763	**0.36**	0.56399	**0.97**	0.09893
STM4136	rrfB	STM4136	**1.49**	0.02973	**-0.09**	0.83378	**0.92**	0.04801
STM4138	birA	biotin--protein ligase	**-1.02**	0.08090	**-1.33**	0.00216	**-1.34**	0.00515
STM4138	birA	biotin--protein ligase	**-0.90**	0.06424	**-1.56**	0.00590	**-0.26**	0.59003
STM4139	coaA	pantothenate kinase	**-1.94**	0.01038	**-2.20**	0.00054	**-1.79**	0.00112
STM4139	coaA	pantothenate kinase	**-1.39**	0.01950	**-2.06**	0.00073	**-0.92**	0.02314
STM4142	thrU	STM4142	**-3.69**	0.01468	**-1.09**	0.06149	**1.29**	0.08325
STM4142	thrU	STM4142	**-2.98**	0.00727	**-0.65**	0.20189	**1.59**	0.00437
STM4143	tyrU	STM4143	**-0.52**	0.47818	**-1.15**	0.01051	**-0.37**	0.47468
STM4143	tyrU	STM4143	**1.15**	0.05553	**-1.16**	0.03039	**0.39**	0.45535
STM4144	glyT	STM4144	**-4.73**	0.00512	**-3.11**	0.00070	**-3.31**	0.00020
STM4144	glyT	STM4144	**-4.48**	0.00512	**-3.19**	0.00004	**-3.71**	0.00007
STM4145	thrT	STM4145	**-1.54**	0.07016	**-1.64**	0.00338	**-1.76**	0.00233
STM4145	thrT	STM4145	**-1.57**	0.04630	**-1.57**	0.00071	**-1.89**	0.00250
STM4146	tuf	elongation factor Tu	**-2.89**	0.00931	**-1.26**	0.00239	**-5.22**	0.00002
STM4146	tuf	elongation factor Tu	**-2.05**	0.05255	**-1.57**	0.00160	**-4.47**	0.00007
STM4147	secE	translocase	**3.40**	0.00747	**-0.99**	0.03607	**1.79**	0.15625
STM4147	secE	translocase	**2.31**	0.30135	**-1.41**	0.00411	**-0.50**	0.61721
STM4148	nusG	transcription antitermination protein NusG	**-2.94**	0.00554	**-2.03**	0.01654	**-3.19**	0.00008
STM4148	nusG	transcription antitermination protein NusG	**-2.39**	0.00753	**-1.62**	0.00116	**-3.69**	0.00004
STM4149	rplK	50S ribosomal protein L11	**-3.32**	0.01041	**-1.47**	0.00098	**-5.17**	0.00002
STM4149	rplK	50S ribosomal protein L11	**-2.24**	0.00962	**-1.31**	0.00203	**-4.97**	0.00002
STM4150	rplA	50S ribosomal protein L1	**-3.73**	0.00547	**-2.43**	0.00015	**-6.17**	0.00002
STM4150	rplA	50S ribosomal protein L1	**-3.81**	0.00512	**-2.27**	0.00047	**-6.77**	0.00001
STM4151	rplJ	50S ribosomal protein L10	**-2.84**	0.00747	**-1.15**	0.02335	**-5.37**	0.00002
STM4151	rplJ	50S ribosomal protein L10	**-2.61**	0.01193	**-0.59**	0.05150	**-5.20**	0.00002
STM4152	rplL	50S ribosomal protein L7/L12	**-0.79**	0.23318	**0.67**	0.19117	**-3.32**	0.00009
STM4152	rplL	50S ribosomal protein L7/L12	**-0.19**	0.72937	**0.70**	0.03140	**-3.34**	0.00008
STM4153	rpoB	DNA-directed RNA polymerase beta subunit	**-2.63**	0.00574	**-1.36**	0.00477	**-3.98**	0.00007
STM4153	rpoB	DNA-directed RNA polymerase beta subunit	**-3.71**	0.00747	**-1.22**	0.00323	**-4.09**	0.00027
STM4154	rpoC	DNA-directed RNA polymerase beta' subunit	**-1.96**	0.06201	**-0.71**	0.04063	**-1.30**	0.01833
STM4154	rpoC	DNA-directed RNA polymerase beta' subunit	**-1.61**	0.13830	**-0.64**	0.08277	**-1.17**	0.02758

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM4155	STM4155	putative inner membrane protein	**-1.36**	0.02636	**-1.18**	0.01124	**-1.10**	0.01789
STM4155	STM4155	putative inner membrane protein	**-1.01**	0.13154	**-1.07**	0.00623	**-1.15**	0.04242
STM4156	STM4156	putative cytoplasmic protein	**-1.13**	0.06702	**-1.37**	0.00872	**-1.47**	0.00416
STM4156	STM4156	putative cytoplasmic protein	**-0.70**	0.12999	**-0.86**	0.02000	**-0.69**	0.17351
STM4157	STM4157	putative cytoplasmic protein	**-0.52**	0.22459	**-0.71**	0.06040	**-0.94**	0.06238
STM4157	STM4157	putative cytoplasmic protein	**-0.12**	0.81119	**-0.33**	0.35648	**-0.28**	0.71695
STM4158	STM4158	putative cytoplasmic protein	**0.10**	0.82716	**-1.29**	0.04804	**-1.82**	0.00275
STM4158	STM4158	putative cytoplasmic protein	**1.80**	0.08923	**-0.30**	0.55660	**-0.54**	0.23368
STM4159	thiH	thiamine biosynthesis protein ThiH	**0.23**	0.87330	**0.72**	0.14228	**0.13**	0.85588
STM4159	thiH	thiamine biosynthesis protein ThiH	**1.68**	0.02844	**1.42**	0.00835	**-0.63**	0.33828
STM4160	thiG	thiazole synthase	**0.07**	0.91539	**1.90**	0.00087	**-0.37**	0.54635
STM4160	thiG	thiazole synthase	**2.12**	0.06532	**2.16**	0.00038	**-0.40**	0.28789
STM4161	STM4161	sulfur carrier protein ThiS	**0.72**	0.13328	**1.76**	0.00244	**-0.90**	0.11552
STM4161	STM4161	sulfur carrier protein ThiS	**0.89**	0.11238	**2.09**	0.00119	**-1.57**	0.08828
STM4162	thiF	thiamine biosynthesis protein ThiF	**0.47**	0.47931	**2.90**	0.00007	**-1.50**	0.00614
STM4162	thiF	thiamine biosynthesis protein ThiF	**0.88**	0.36979	**2.68**	0.00058	**-0.34**	0.40687
STM4163	thiE	thiamine-phosphate pyrophosphorylase	**-0.23**	0.72937	**1.82**	0.00058	**-0.18**	0.72522
STM4163	thiE	thiamine-phosphate pyrophosphorylase	**0.58**	0.20774	**1.93**	0.00077	**-0.15**	0.68608
STM4164	thiC	thiamine biosynthesis protein ThiC	**-0.64**	0.22926	**1.73**	0.00258	**-1.46**	0.05783
STM4164	thiC	thiamine biosynthesis protein ThiC	**-0.02**	0.97602	**1.89**	0.00364	**-1.59**	0.00875
STM4165	rsd	anti sigma 70 factor	**0.76**	0.12475	**1.55**	0.00180	**1.04**	0.01756
STM4165	rsd	anti sigma 70 factor	**1.02**	0.09819	**1.40**	0.00216	**1.65**	0.00841
STM4166	nudC	NADH pyrophosphatase	**-0.76**	0.19642	**-0.61**	0.04858	**-0.67**	0.14623
STM4166	nudC	NADH pyrophosphatase	**-0.68**	0.17077	**-0.85**	0.01839	**-0.96**	0.04086
STM4167	hemE	uroporphyrinogen decarboxylase	**-1.12**	0.09625	**-0.67**	0.05034	**-1.85**	0.00772
STM4167	hemE	uroporphyrinogen decarboxylase	**-1.30**	0.04449	**-0.59**	0.11725	**-1.29**	0.01971
STM4168	nfi	endonuclease V	**-0.47**	0.29809	**-0.92**	0.01413	**-1.46**	0.00277
STM4168	nfi	endonuclease V	**0.07**	0.92982	**-0.66**	0.23977	**-1.59**	0.03030
STM4169	yjaG	putative cytoplasmic protein	**-1.39**	0.02655	**-0.82**	0.03468	**-2.65**	0.00070
STM4169	yjaG	putative cytoplasmic protein	**-0.18**	0.74302	**-0.55**	0.09153	**-1.86**	0.00324
STM4170	hupA	DNA-binding protein HU-alpha	**-3.99**	0.00643	**-2.74**	0.00070	**-4.10**	0.00004
STM4170	hupA	DNA-binding protein HU-alpha	**-4.57**	0.00558	**-2.53**	0.00039	**-4.96**	0.00002
STM4171	yjaH	putative inner membrane protein	**5.03**	0.01679	**-0.05**	0.89366	**1.34**	0.24346
STM4171	yjaH	putative inner membrane protein	**0.73**	0.20978	**0.06**	0.86854	**0.45**	0.77058
STM4172	zraP	zinc-resistance associated protein	**-0.82**	0.08227	**0.89**	0.06663	**-0.93**	0.14140
STM4172	zraP	zinc-resistance associated protein	**-0.17**	0.78339	**0.81**	0.03583	**-0.96**	0.19575
STM4173	hydH	sensor kinase	**-1.14**	0.04050	**-0.62**	0.13335	**-1.44**	0.01010
STM4173	hydH	sensor kinase	**-0.27**	0.51616	**-0.70**	0.10206	**-0.81**	0.12119
STM4174	hydG	response regulator	**-0.68**	0.27054	**-0.26**	0.49934	**-0.82**	0.05429
STM4174	hydG	response regulator	**-0.24**	0.87663	**-1.02**	0.02008	**-2.52**	0.01166
STM4175	purD	phosphoribosylamine--glycine ligase	**-1.07**	0.13812	**-0.72**	0.03332	**-1.28**	0.02500
STM4175	purD	phosphoribosylamine--glycine ligase	**-0.38**	0.40255	**0.00**	0.99257	**-1.19**	0.00771
STM4176	purH	bifunctional phosphoribosylaminoimidazolecarboxamide	**-1.44**	0.02265	**0.42**	0.33003	**-0.17**	0.70282
STM4176	purH	bifunctional phosphoribosylaminoimidazolecarboxamide	**0.62**	0.54043	**0.87**	0.01267	**0.06**	0.87186
STM4177	rrsE	STM4177	**-2.10**	0.05093	**0.16**	0.75138	**0.01**	0.99237
STM4177	rrsE	STM4177	**-1.62**	0.08918	**0.61**	0.20240	**0.75**	0.11360
STM4178	gltV	STM4178	**1.69**	0.02338	**0.91**	0.03050	**1.11**	0.01089
STM4178	gltV	STM4178	**1.76**	0.01219	**0.72**	0.05946	**1.28**	0.01643
STM4180	rrfE	STM4180	**0.32**	0.68656	**-0.40**	0.35270	**0.39**	0.46380
STM4180	rrfE	STM4180	**0.65**	0.17418	**-0.63**	0.12250	**0.27**	0.51783
STM4181	yjaB	putative acetyltransferase	**-0.83**	0.20050	**-0.46**	0.16554	**1.47**	0.01145
STM4181	yjaB	putative acetyltransferase	**-1.48**	0.33047	**0.08**	0.83570	**1.26**	0.01331
STM4182	metA	homoserine O-succinyltransferase	**-0.61**	0.19107	**-0.83**	0.02370	**0.21**	0.60212
STM4182	metA	homoserine O-succinyltransferase	**-0.61**	0.35495	**-1.20**	0.00296	**0.17**	0.71709
STM4183	aceB	malate synthase	**3.02**	0.05608	**2.01**	0.00121	**4.98**	0.00071
STM4183	aceB	malate synthase	**1.25**	0.13407	**1.96**	0.00041	**4.65**	0.00607
STM4184	aceA	isocitrate lyase	**0.43**	0.47494	**1.33**	0.00414	**1.98**	0.00087
STM4184	aceA	isocitrate lyase	**1.00**	0.10845	**1.11**	0.02490	**2.64**	0.00306
STM4185	aceK	bifunctional isocitrate dehydrogenase kinase/phosphatase	**2.40**	0.02663	**-0.43**	0.17441	**0.12**	0.85907
STM4185	aceK	bifunctional isocitrate dehydrogenase kinase/phosphatase	**1.77**	0.02830	**-0.90**	0.01822	**1.10**	0.11389
STM4186	STM4186	putative cytoplasmic protein	**-0.03**	0.97301	**-0.38**	0.43230	**-0.41**	0.39558
STM4186	STM4186	putative cytoplasmic protein	**0.98**	0.30727	**-0.64**	0.05732	**0.82**	0.13878
STM4187	iclR	acetate operon transcriptional repressor	**-1.56**	0.08578	**-1.73**	0.00095	**-0.30**	0.60322
STM4187	iclR	acetate operon transcriptional repressor	**1.32**	0.48347	**-1.62**	0.00277	**-0.57**	0.25639
STM4188,S	metH	B12-dependent methionine synthase	**-0.40**	0.52494	**0.01**	0.97944	**0.09**	0.87159
STM4188,S	metH	B12-dependent methionine synthase	**1.79**	0.03732	**-1.00**	0.01354	**0.43**	0.32953
STM4189	yjbB	putative transport protein	**-0.79**	0.20982	**-0.18**	0.62607	**0.07**	0.89389
STM4189	yjbB	putative transport protein	**-0.04**	0.96062	**-0.64**	0.13091	**0.24**	0.57857
STM4190	pepE	peptidase E	**1.36**	0.08658	**-1.31**	0.00700	**-1.37**	0.03580
STM4190	pepE	peptidase E	**1.94**	0.01034	**-1.33**	0.00342	**0.10**	0.81829

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM4191	STM4191	putative cytoplasmic protein	**-0.29**	0.51301	**-0.52**	0.14327	**-0.22**	0.67847
STM4191	STM4191	putative cytoplasmic protein	**1.06**	0.05343	**-0.92**	0.11459	**0.71**	0.13228
STM4192	STM4192	putative cytoplasmic protein	**-1.68**	0.01417	**-0.83**	0.01890	**-1.66**	0.00964
STM4192	STM4192	putative cytoplasmic protein	**-1.16**	0.03429	**-0.81**	0.02913	**-1.19**	0.01617
STM4193	yjbC	putative pseudouridine synthase	**-1.24**	0.08393	**-0.53**	0.17550	**-0.83**	0.23342
STM4193	yjbC	putative pseudouridine synthase	**-0.49**	0.39885	**-0.76**	0.04987	**-0.95**	0.05165
STM4194	yjbD	putative cytoplasmic protein	**-1.06**	0.07052	**-0.31**	0.46008	**-0.99**	0.04268
STM4194	yjbD	putative cytoplasmic protein	**-0.26**	0.69193	**-0.73**	0.03037	**-1.09**	0.03457
STM4195	STM4195	putative Na+-dependent transporter	**-0.21**	0.70070	**1.06**	0.00597	**0.29**	0.52459
STM4195	STM4195	putative Na+-dependent transporter	**1.88**	0.00998	**1.05**	0.00539	**0.72**	0.12647
STM4196	STM4196	putative cytoplasmic protein	**0.31**	0.55995	**0.39**	0.24308	**0.06**	0.87634
STM4196	STM4196	putative cytoplasmic protein	**1.81**	0.01228	**0.36**	0.26389	**1.48**	0.00659
STM4198	STM4198	putative cytoplasmic protein	**0.47**	0.51664	**0.07**	0.88895	**-0.16**	0.73380
STM4198	STM4198	putative cytoplasmic protein	**1.20**	0.13695	**0.20**	0.62650	**0.98**	0.28421
STM4199	STM4199	putative cytoplasmic protein	**1.61**	0.06919	**-1.53**	0.00165	**-0.97**	0.12985
STM4199	STM4199	putative cytoplasmic protein	**1.99**	0.05707	**-2.05**	0.00141	**0.31**	0.65232
STM4200	STM4200	putative phage tail fiber protein H	**-0.15**	0.86599	**-0.44**	0.19945	**-0.66**	0.24859
STM4200	STM4200	putative phage tail fiber protein H	**0.80**	0.21801	**-0.12**	0.78417	**0.16**	0.80855
STM4201	STM4201	putative phage tail protein	**-0.69**	0.35215	**0.85**	0.04470	**-0.99**	0.01869
STM4201	STM4201	putative phage tail protein	**0.50**	0.34672	**-0.51**	0.33936	**-0.23**	0.63239
STM4202	STM4202	putative phage baseplate protein	**0.16**	0.77593	**0.31**	0.47759	**-0.04**	0.94831
STM4202	STM4202	putative phage baseplate protein	**1.47**	0.01972	**-0.35**	0.35297	**0.56**	0.42791
STM4203	STM4203	putative phage baseplate protein	**0.62**	0.36909	**-0.20**	0.82949	**-0.58**	0.44017
STM4203	STM4203	putative phage baseplate protein	**1.49**	0.04658	**-1.24**	0.00328	**-0.32**	0.67526
STM4204	STM4204	putative inner membrane protein	**0.18**	0.72134	**0.07**	0.82168	**0.37**	0.35846
STM4204	STM4204	putative inner membrane protein	**0.67**	0.17278	**-0.63**	0.34675	**1.61**	0.00777
STM4205	STM4205	putative phage glycosyltransferase	**3.94**	0.09035	**-1.03**	0.02982	**1.85**	0.02050
STM4205	STM4205	putative phage glycosyltransferase	**2.65**	0.00778	**-0.45**	0.46930	**2.01**	0.00084
STM4206	STM4206	putative phage glucose translocase	**-1.18**	0.05376	**-0.87**	0.04993	**-0.64**	0.24726
STM4206	STM4206	putative phage glucose translocase	**-1.15**	0.08194	**-1.31**	0.00834	**-1.11**	0.07640
STM4207	STM4207	putative phage baseplate component	**0.09**	0.91568	**1.04**	0.51355	**-0.55**	0.19128
STM4207	STM4207	putative phage baseplate component	**2.35**	0.09054	**0.51**	0.42559	**0.17**	0.70671
STM4208	STM4208	putative cytoplasmic protein	**1.02**	0.38079	**-0.52**	0.18999	**-0.31**	0.48726
STM4208	STM4208	putative cytoplasmic protein	**1.43**	0.10082	**-0.50**	0.12913	**0.32**	0.53049
STM4209	STM4209	putative inner membrane protein	**0.80**	0.16405	**-0.35**	0.37676	**-0.29**	0.59568
STM4209	STM4209	putative inner membrane protein	**0.59**	0.20729	**-0.14**	0.83471	**1.23**	0.00809
STM4210	STM4210	putative methyl-accepting chemotaxis protein	**-0.23**	0.61858	**-0.36**	0.40347	**-0.71**	0.40856
STM4210	STM4210	putative methyl-accepting chemotaxis protein	**-0.11**	0.87933	**-1.26**	0.01975	**-1.04**	0.24665
STM4211	STM4211	putative phage tail protein	**0.15**	0.77288	**-0.93**	0.01938	**-1.01**	0.14793
STM4211	STM4211	putative phage tail protein	**1.15**	0.21572	**-1.41**	0.00239	**-0.21**	0.70823
STM4212	STM4212	putative phage tail core protein	**-0.14**	0.74633	**0.07**	0.88193	**-0.07**	0.92589
STM4212	STM4212	putative phage tail core protein	**-1.13**	0.27954	**-0.43**	0.12072	**0.15**	0.85553
STM4213	STM4213	putative phage tail sheath protein	**0.03**	0.96122	**-1.24**	0.02182	**-1.02**	0.12272
STM4213	STM4213	putative phage tail sheath protein	**1.17**	0.07413	**0.03**	0.91349	**0.09**	0.92766
STM4214	STM4214	putative cytoplasmic protein	**0.97**	0.13486	**0.45**	0.17126	**0.68**	0.34563
STM4214	STM4214	putative cytoplasmic protein	**3.27**	0.00895	**0.16**	0.72305	**1.70**	0.00534
STM4215	STM4215	putative cytoplasmic protein	**1.38**	0.12596	**0.30**	0.52587	**-0.34**	0.61895
STM4215	STM4215	putative cytoplasmic protein	**2.47**	0.00889	**0.02**	0.96002	**0.52**	0.27368
STM4216	STM4216	putative inner membrane protein	**0.35**	0.51566	**0.86**	0.03021	**0.21**	0.67325
STM4216	STM4216	putative inner membrane protein	**1.87**	0.04345	**0.63**	0.41919	**2.51**	0.00096
STM4217	STM4217	putative soluble lytic murein transglycosylase	**-0.30**	0.63908	**-1.36**	0.04891	**-1.05**	0.03631
STM4217	STM4217	putative soluble lytic murein transglycosylase	**0.64**	0.30002	**-0.94**	0.19282	**1.04**	0.24140
STM4218	STM4218	putative inner membrane protein	**-1.40**	0.03599	**-1.54**	0.02582	**-1.41**	0.09679
STM4218	STM4218	putative inner membrane protein	**-0.33**	0.45553	**-2.06**	0.00350	**-1.31**	0.01498
STM4219,S	STM4219,S	putative cytoplasmic protein	**-0.65**	0.35130	**0.44**	0.24643	**-0.80**	0.24764
STM4219,S	STM4219,S	putative cytoplasmic protein	**0.68**	0.21044	**0.37**	0.21976	**0.61**	0.08820
STM4220	lysC	aspartate kinase III	**-0.48**	0.30747	**-0.19**	0.67544	**-1.19**	0.01408
STM4220	lysC	aspartate kinase III	**1.75**	0.14412	**-0.33**	0.66381	**-0.65**	0.58500
STM4221	pgi	glucose-6-phosphate isomerase	**-3.54**	0.00547	**-0.43**	0.36283	**-1.44**	0.00601
STM4221	pgi	glucose-6-phosphate isomerase	**-4.34**	0.00672	**-0.12**	0.74569	**-3.04**	0.00154
STM4222,S	yjbE	putative outer membrane protein	**-0.16**	0.71667	**-1.09**	0.00597	**-1.44**	0.01405
STM4222,S	yjbE	putative outer membrane protein	**0.35**	0.59233	**-1.36**	0.00447	**-0.81**	0.30166
STM4223	yjbF	putative outer membrane lipoprotein	**0.17**	0.71027	**0.11**	0.75947	**0.10**	0.83913
STM4223	yjbF	putative outer membrane lipoprotein	**1.50**	0.01595	**-0.61**	0.14344	**0.67**	0.30882
STM4224	yjbG	putative periplasmic protein	**1.23**	0.04436	**-1.03**	0.17115	**-0.83**	0.26427
STM4224	yjbG	putative periplasmic protein	**1.65**	0.02435	**-1.25**	0.01713	**0.18**	0.72802
STM4225	yjbH	putative outer membrane lipoprotein	**0.25**	0.74962	**0.15**	0.62620	**-0.79**	0.22330
STM4225	yjbH	putative outer membrane lipoprotein	**2.32**	0.01311	**0.62**	0.11150	**0.16**	0.81438
STM4226	yjbA	phosphate-starvation-inducible protein PsiE	**-0.14**	0.84241	**-0.44**	0.30082	**0.04**	0.93247
STM4226	yjbA	phosphate-starvation-inducible protein PsiE	**0.21**	0.71993	**-0.96**	0.02356	**-0.20**	0.70783

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM4227	malG	maltose transport protein	**0.41**	0.51518	**-1.46**	0.00551	**-2.14**	0.01601
STM4227	malG	maltose transport protein	**1.04**	0.19569	**-2.45**	0.00046	**-0.50**	0.45561
STM4228	malF	maltose transport protein	**-0.31**	0.56172	**-0.72**	0.14317	**-0.52**	0.47434
STM4228	malF	maltose transport protein	**0.26**	0.55026	**-0.67**	0.08994	**0.35**	0.35370
STM4229	malE	periplasmic maltose-binding protein	**-0.88**	0.09172	**-1.50**	0.00526	**-0.96**	0.05617
STM4229	malE	periplasmic maltose-binding protein	**0.19**	0.77338	**-1.79**	0.00169	**-0.62**	0.14711
STM4230	malK	maltose transport protein/repressor	**-0.55**	0.44551	**-2.04**	0.00108	**-1.51**	0.05629
STM4230	malK	maltose transport protein/repressor	**0.39**	0.66786	**-1.56**	0.03074	**-0.56**	0.42402
STM4231	lamB	maltoporin precursor	**-0.74**	0.35142	**-1.56**	0.00344	**-1.16**	0.08164
STM4231	lamB	maltoporin precursor	**0.40**	0.51167	**-1.30**	0.01020	**-0.84**	0.16815
STM4232	malM	periplasmic protein precursor	**-1.73**	0.01569	**-1.25**	0.03235	**-0.43**	0.34388
STM4232	malM	periplasmic protein precursor	**-0.26**	0.55443	**-1.50**	0.00580	**0.19**	0.65958
STM4233	ubiC	chorismate pyruvate lyase	**-1.47**	0.03614	**-1.29**	0.00510	**0.97**	0.02859
STM4233	ubiC	chorismate pyruvate lyase	**0.41**	0.68735	**-0.96**	0.01141	**2.11**	0.00047
STM4234	ubiA	4-hydroxybenzoate octaprenyltransferase	**-1.17**	0.06172	**-0.75**	0.07432	**-0.71**	0.07703
STM4234	ubiA	4-hydroxybenzoate octaprenyltransferase	**-0.07**	0.87790	**-0.52**	0.13723	**0.35**	0.34612
STM4235	plsB	glycerol-3-phosphate acyltransferase	**-1.47**	0.04692	**-1.31**	0.00409	**-1.36**	0.00646
STM4235	plsB	glycerol-3-phosphate acyltransferase	**-0.28**	0.56186	**-1.08**	0.01014	**-0.09**	0.87248
STM4236	dgkA	diacylglycerol kinase	**-0.90**	0.06241	**-0.93**	0.02614	**-1.52**	0.00250
STM4236	dgkA	diacylglycerol kinase	**-0.87**	0.11147	**-0.65**	0.05857	**-1.30**	0.00692
STM4237	lexA	LexA repressor	**-0.86**	0.07358	**0.29**	0.32666	**-1.18**	0.03662
STM4237	lexA	LexA repressor	**0.63**	0.23062	**-0.11**	0.72305	**-0.47**	0.30170
STM4238	dinF	DNA-damage-inducible protein F	**-0.96**	0.09569	**0.66**	0.06058	**2.55**	0.00059
STM4238	dinF	DNA-damage-inducible protein F	**0.01**	0.98765	**0.51**	0.08698	**2.53**	0.00028
STM4240	yjbJ	putative cytoplasmic protein	**1.11**	0.04411	**2.29**	0.00023	**8.06**	0.00001
STM4240	yjbJ	putative cytoplasmic protein	**1.95**	0.00884	**2.22**	0.00017	**8.78**	0.00001
STM4241	zur	transcriptional repressor	**-0.53**	0.25756	**0.73**	0.02943	**4.22**	0.00004
STM4241	zur	transcriptional repressor	**0.15**	0.73728	**1.06**	0.01181	**4.48**	0.00003
STM4242	STM4242	conjugative transfer protein	**1.40**	0.09078	**0.28**	0.43230	**1.21**	0.08873
STM4242	STM4242	conjugative transfer protein	**1.64**	0.01536	**-0.72**	0.08366	**0.72**	0.13139
STM4243	yjbN	hypothetical protein STM4243	**-1.08**	0.05945	**0.19**	0.60724	**0.47**	0.19859
STM4243	yjbN	hypothetical protein STM4243	**-1.02**	0.11657	**-0.44**	0.33459	**0.09**	0.84292
STM4244	pspG	phage shock protein G	**0.20**	0.73277	**1.08**	0.01924	**0.43**	0.53514
STM4244	pspG	phage shock protein G	**1.26**	0.06023	**1.09**	0.01316	**1.30**	0.01316
STM4245	qor	quinone oxidoreductase	**-0.01**	0.98806	**0.53**	0.15290	**3.00**	0.02944
STM4245	qor	quinone oxidoreductase	**0.86**	0.11716	**0.99**	0.01654	**1.95**	0.00168
STM4246	dnaB	replicative DNA helicase	**-1.63**	0.01796	**-0.69**	0.03729	**-0.86**	0.13114
STM4246	dnaB	replicative DNA helicase	**-2.47**	0.00711	**-1.69**	0.00657	**-1.16**	0.06536
STM4247	alr	alanine racemase	**-0.23**	0.66255	**0.34**	0.24399	**-1.13**	0.08297
STM4247	alr	alanine racemase	**0.08**	0.93347	**-0.14**	0.65316	**-0.34**	0.40859
STM4248	tyrB	aspartate aminotransferase	**0.56**	0.32788	**-1.17**	0.01238	**0.07**	0.92717
STM4248	tyrB	aspartate aminotransferase	**0.64**	0.26148	**-1.19**	0.04600	**1.67**	0.07296
STM4249	aphA	non-specific acid phosphatase/phosphotransferase	**-0.85**	0.09208	**0.67**	0.08115	**-1.67**	0.00210
STM4249	aphA	non-specific acid phosphatase/phosphotransferase	**-0.15**	0.78321	**0.71**	0.08734	**-0.32**	0.56623
STM4250	yjbQ	putative cytoplasmic protein	**0.17**	0.73386	**1.77**	0.00222	**1.39**	0.00500
STM4250	yjbQ	putative cytoplasmic protein	**0.51**	0.28726	**1.61**	0.00110	**2.08**	0.00181
STM4251	yjbR	putative cytoplasmic protein	**-0.39**	0.42564	**1.28**	0.00717	**0.22**	0.69093
STM4251	yjbR	putative cytoplasmic protein	**0.25**	0.72774	**1.00**	0.01731	**-0.02**	0.97527
STM4252	STM4252	putative inner membrane protein	**-0.34**	0.39935	**1.20**	0.00427	**0.15**	0.69459
STM4252	STM4252	putative inner membrane protein	**0.37**	0.49130	**0.83**	0.03294	**0.65**	0.12985
STM4253	STM4253	putative outer membrane lipoprotein	**-0.08**	0.90669	**-0.48**	0.18914	**-0.97**	0.17970
STM4253	STM4253	putative outer membrane lipoprotein	**0.63**	0.40701	**-0.20**	0.56695	**-0.25**	0.68157
STM4254	uvrA	excinuclease ABC subunit A	**-0.85**	0.07343	**-0.18**	0.54266	**-1.27**	0.00594
STM4254	uvrA	excinuclease ABC subunit A	**1.12**	0.09643	**-0.19**	0.69618	**-1.49**	0.04001
STM4256	ssb	single-strand DNA-binding protein	**-0.72**	0.51731	**0.44**	0.18463	**-1.25**	0.01403
STM4256	ssb	single-strand DNA-binding protein	**-0.08**	0.92834	**0.73**	0.09194	**-0.25**	0.55066
STM4258	STM4258	putative methyl-accepting chemotaxis protein	**-0.31**	0.51925	**-1.36**	0.00173	**-1.24**	0.01077
STM4258	STM4258	putative methyl-accepting chemotaxis protein	**0.24**	0.67110	**-1.61**	0.00503	**-0.30**	0.51708
STM4259	STM4259	putative ABC exporter outer membrane component	**-0.32**	0.50506	**-1.03**	0.01839	**-0.72**	0.13978
STM4259	STM4259	putative ABC exporter outer membrane component	**0.27**	0.58700	**-1.25**	0.00290	**-0.89**	0.19607
STM4260	STM4260	predicted cation efflux pump	**-0.71**	0.24717	**-0.99**	0.01622	**-0.74**	0.48235
STM4260	STM4260	predicted cation efflux pump	**0.44**	0.45509	**-1.85**	0.01444	**-0.14**	0.85581
STM4261	STM4261	putative inner membrane protein	**-0.50**	0.32622	**-0.27**	0.51338	**-0.45**	0.42883
STM4261	STM4261	putative inner membrane protein	**-0.16**	0.83116	**0.38**	0.38567	**-0.23**	0.76913
STM4262	STM4262	putative ABC-type bacteriocin/lantibiotic exporter	**1.39**	0.06863	**0.49**	0.21555	**-1.20**	0.04413
STM4262	STM4262	putative ABC-type bacteriocin/lantibiotic exporter	**2.65**	0.00675	**0.47**	0.24294	**-0.36**	0.40182
STM4263	yjcB	putative inner membrane protein	**0.57**	0.26597	**2.18**	0.00258	**-1.16**	0.02148
STM4263	yjcB	putative inner membrane protein	**1.43**	0.03635	**1.93**	0.00329	**-0.48**	0.26736
STM4264	yjcC	putative diguanylate cyclase/phosphodiesterase	**-0.97**	0.20042	**0.18**	0.69471	**-0.06**	0.93258
STM4264	yjcC	putative diguanylate cyclase/phosphodiesterase	**-0.80**	0.15767	**0.29**	0.42986	**-0.71**	0.08467

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM4265	soxS	transcriptional activator	**-1.18**	0.09548	**0.82**	0.03892	**-0.33**	0.55394
STM4265	soxS	transcriptional activator	**-0.03**	0.96862	**0.84**	0.03316	**0.57**	0.44412
STM4266	soxR	redox-sensing transcriptional activator	**-0.35**	0.46353	**0.42**	0.14410	**0.10**	0.81089
STM4266	soxR	redox-sensing transcriptional activator	**-0.39**	0.39767	**0.56**	0.22900	**0.56**	0.16150
STM4267	STM4267	putative glutathione S-transferase	**-0.55**	0.45246	**1.03**	0.00841	**0.33**	0.61153
STM4267	STM4267	putative glutathione S-transferase	**0.71**	0.38601	**1.12**	0.00887	**1.05**	0.03777
STM4268	yjcD	hypothetical protein STM4268	**-0.71**	0.15688	**0.06**	0.84144	**-1.31**	0.00982
STM4268	yjcD	hypothetical protein STM4268	**-0.70**	0.15801	**0.07**	0.83681	**-0.57**	0.21828
STM4269	yjcE	Na/H transport protein	**1.37**	0.06323	**0.90**	0.01449	**1.62**	0.02918
STM4269	yjcE	Na/H transport protein	**1.65**	0.03541	**0.35**	0.27141	**1.21**	0.07568
STM4270	STM4270	putative transcriptional regulator	**-0.99**	0.20251	**-0.64**	0.16112	**-1.38**	0.00402
STM4270	STM4270	putative transcriptional regulator	**-0.66**	0.16332	**-1.28**	0.04633	**-0.23**	0.76913
STM4271	STM4271	putative inner membrane protein	**0.64**	0.30707	**-1.23**	0.00874	**0.36**	0.45591
STM4271	STM4271	putative inner membrane protein	**0.76**	0.10182	**-1.67**	0.00508	**1.28**	0.19392
STM4272	STM4272	putative inner membrane protein	**0.34**	0.52405	**-0.47**	0.15444	**-0.18**	0.77436
STM4272	STM4272	putative inner membrane protein	**3.11**	0.00547	**-0.82**	0.04425	**0.07**	0.85420
STM4273	actP	acetate permease	**-0.42**	0.50558	**-0.66**	0.03395	**-0.52**	0.35231
STM4273	actP	acetate permease	**1.27**	0.04517	**0.22**	0.53313	**0.55**	0.30509
STM4274	yjcH	putative inner membrane protein	**2.27**	0.11221	**-0.82**	0.15504	**0.23**	0.85675
STM4274	yjcH	putative inner membrane protein	**0.93**	0.46799	**-1.80**	0.01061	**0.96**	0.21130
STM4275	acs	acetyl-coenzyme A synthetase	**1.05**	0.12783	**3.42**	0.00004	**1.73**	0.00208
STM4275	acs	acetyl-coenzyme A synthetase	**2.47**	0.05962	**3.37**	0.00012	**2.26**	0.00331
STM4277	nrfA	nitrite reductase periplasmic cytochrome c552	**0.19**	0.73336	**-0.95**	0.04037	**-0.57**	0.42685
STM4277	nrfA	nitrite reductase periplasmic cytochrome c552	**1.14**	0.06709	**-2.14**	0.00611	**0.58**	0.26344
STM4278,S	nrfB	formate-dependent nitrite reductase	**0.12**	0.79544	**-0.90**	0.03026	**-0.82**	0.28232
STM4278,S	nrfB	formate-dependent nitrite reductase	**1.57**	0.03711	**-1.06**	0.02972	**-0.53**	0.27459
STM4279	nrfC	putative formate-dependent nitrite reductase	**-0.04**	0.96122	**-1.01**	0.05791	**-0.66**	0.11816
STM4279	nrfC	putative formate-dependent nitrite reductase	**1.55**	0.02037	**-0.11**	0.78689	**0.47**	0.29003
STM4280	nrfD	putative formate-dependent nitrate reductase	**-0.53**	0.29599	**-1.58**	0.02799	**-1.52**	0.06770
STM4280	nrfD	putative formate-dependent nitrate reductase	**1.96**	0.00849	**-1.55**	0.00760	**-0.28**	0.65684
STM4281	nrfE	formate-dependent nitrite reductase	**-0.09**	0.91536	**-2.05**	0.01542	**-2.17**	0.01034
STM4281	nrfE	formate-dependent nitrite reductase	**1.73**	0.23325	**-3.07**	0.00007	**-1.37**	0.06416
STM4282	nrfG	formate-dependent nitrite reductase component	**-0.79**	0.17278	**-0.74**	0.15673	**-1.20**	0.12813
STM4282	nrfG	formate-dependent nitrite reductase component	**0.10**	0.90326	**-0.16**	0.58297	**-1.13**	0.02854
STM4283	gltP	glutamate/aspartate symport protein	**-0.18**	0.85762	**-0.12**	0.77119	**-1.11**	0.02613
STM4283	gltP	glutamate/aspartate symport protein	**0.62**	0.24636	**-0.49**	0.11535	**-0.36**	0.43831
STM4284	yjcO	tetratricopeptide repeat protein	**-0.75**	0.15588	**-0.96**	0.00808	**-1.27**	0.06961
STM4284	yjcO	tetratricopeptide repeat protein	**-0.47**	0.37928	**-0.67**	0.04383	**-1.34**	0.04209
STM4285	fdhF	formate dehydrogenase	**0.56**	0.46644	**0.13**	0.70432	**0.11**	0.84080
STM4285	fdhF	formate dehydrogenase	**1.31**	0.10045	**-0.01**	0.98160	**0.88**	0.17455
STM4286	lpxO	putative dioxygenase	**0.84**	0.48324	**-0.78**	0.02012	**-1.28**	0.02896
STM4286	lpxO	putative dioxygenase	**0.54**	0.76912	**-0.71**	0.13679	**-0.53**	0.54835
STM4287,S	phnO	putative regulatory protein	**-1.09**	0.14622	**-0.57**	0.33467	**-0.56**	0.56340
STM4287,S	phnO	putative regulatory protein	**0.38**	0.50915	**-0.29**	0.56428	**0.16**	0.77764
STM4288	phnB	putative cytoplasmic protein	**-0.87**	0.13459	**-0.08**	0.80980	**0.77**	0.03940
STM4288	phnB	putative cytoplasmic protein	**1.02**	0.06446	**0.48**	0.14850	**2.09**	0.00087
STM4289	phnA	putative alkylphosphonate uptake protein	**-0.83**	0.08480	**0.23**	0.59002	**-0.44**	0.27394
STM4289	phnA	putative alkylphosphonate uptake protein	**-0.23**	0.74878	**0.28**	0.43230	**0.18**	0.62168
STM4290	proP	low-affinity proline transporter	**-0.64**	0.28940	**0.60**	0.10525	**-0.17**	0.74904
STM4290	proP	low-affinity proline transporter	**-0.27**	0.55411	**0.20**	0.62607	**0.79**	0.10838
STM4291	basS	sensor kinase	**-0.67**	0.15625	**0.15**	0.65536	**-1.02**	0.04422
STM4291	basS	sensor kinase	**-0.15**	0.75318	**1.22**	0.07248	**-0.31**	0.46740
STM4292	basR	response regulator	**-1.81**	0.01028	**-0.67**	0.10082	**-1.25**	0.01053
STM4292	basR	response regulator	**-0.15**	0.73509	**-0.51**	0.20601	**-0.98**	0.04692
STM4293	yjdB	putative integral membrane protein	**-1.07**	0.08755	**0.99**	0.06209	**-1.88**	0.00125
STM4293	yjdB	putative integral membrane protein	**0.02**	0.97265	**1.28**	0.00516	**-0.94**	0.03347
STM4294	yjdE	putative putrescine/ornithine transport protein	**-0.97**	0.16933	**0.61**	0.21404	**-0.78**	0.09703
STM4294	yjdE	putative putrescine/ornithine transport protein	**0.00**	0.99621	**0.60**	0.15392	**-0.35**	0.40067
STM4295	adiY	transcriptional activator	**0.35**	0.58469	**0.22**	0.63045	**-0.88**	0.09937
STM4295	adiY	transcriptional activator	**1.35**	0.05345	**0.12**	0.78422	**-0.12**	0.77687
STM4296	adi	catabolic arginine decarboxylase	**-0.56**	0.21537	**0.38**	0.36784	**-0.10**	0.80762
STM4296	adi	catabolic arginine decarboxylase	**0.98**	0.30297	**0.14**	0.68780	**0.67**	0.17121
STM4297	melR	melibiose operon regulator	**-0.61**	0.58361	**-0.14**	0.74912	**0.87**	0.29940
STM4297	melR	melibiose operon regulator	**0.36**	0.69114	**-1.22**	0.00631	**-0.27**	0.86615
STM4298	melA	alpha-galactosidase	**-0.60**	0.36052	**-0.44**	0.25199	**-0.80**	0.10351
STM4298	melA	alpha-galactosidase	**0.25**	0.73458	**-1.46**	0.01177	**-0.82**	0.20084
STM4299	melB	melibiose permease II	**-0.59**	0.28111	**-0.14**	0.81329	**-0.73**	0.09215
STM4299	melB	melibiose permease II	**1.31**	0.23493	**-1.31**	0.00197	**-0.91**	0.07596
STM4300	fumB	fumarase B	**-0.36**	0.84418	**-0.10**	0.79398	**-0.42**	0.30322
STM4300	fumB	fumarase B	**0.80**	0.59302	**0.55**	0.14047	**0.19**	0.75058

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM4301	dcuB	anaerobic C4-dicarboxylate transporter	-0.41	0.55541	-0.64	0.16752	-0.61	0.14242
STM4301	dcuB	anaerobic C4-dicarboxylate transporter	-0.30	0.76483	-0.92	0.08914	-0.32	0.53265
STM4302	STM4302	putative cytoplasmic protein	0.06	0.91430	0.77	0.11555	1.82	0.16572
STM4302	STM4302	putative cytoplasmic protein	1.51	0.02002	-1.27	0.01027	1.55	0.20972
STM4303	dcuR	response regulator	-1.23	0.07432	0.61	0.62159	0.10	0.79830
STM4303	dcuR	response regulator	0.29	0.89481	-1.64	0.11656	-2.66	0.00188
STM4304	dcuS	sensory histidine kinase	-1.58	0.03996	0.13	0.66864	-0.46	0.24501
STM4304	dcuS	sensory histidine kinase	-1.22	0.03639	-0.65	0.12443	-0.92	0.07481
STM4305,S	STM4305,S	putative anaerobic dimethylsulfoxide reductase subunit A	0.34	0.55541	1.65	0.02138	-0.01	0.99449
STM4305,S	STM4305,S	putative anaerobic dimethylsulfoxide reductase subunit A	0.67	0.44031	-0.92	0.03640	0.04	0.95985
STM4306	STM4306	putative anaerobic dimethylsulfoxide reductase subunit B	1.03	0.11427	-0.84	0.04983	-0.62	0.31552
STM4306	STM4306	putative anaerobic dimethylsulfoxide reductase subunit B	1.88	0.02885	-1.76	0.00185	1.11	0.04519
STM4307	STM4307	putative anaerobic dimethylsulfoxide reductase subunit C	-0.34	0.71703	-0.56	0.14320	-1.49	0.09521
STM4307	STM4307	putative anaerobic dimethylsulfoxide reductase subunit C	1.40	0.19982	-0.65	0.14373	-0.68	0.16781
STM4308	STM4308	putative anaerobic dehydrogenase component	-0.41	0.59547	-0.62	0.34660	-0.75	0.22235
STM4308	STM4308	putative anaerobic dehydrogenase component	0.41	0.49844	-0.62	0.11417	-0.38	0.41179
STM4309	STM4309	hypothetical protein STM4309	1.42	0.04345	0.13	0.71408	0.91	0.09368
STM4309	STM4309	hypothetical protein STM4309	1.63	0.01813	-0.18	0.75972	1.76	0.00651
STM4310	STM4310	putative inner membrane protein	2.31	0.01622	0.12	0.74224	0.91	0.21540
STM4310	STM4310	putative inner membrane protein	1.73	0.23216	-0.33	0.67411	1.54	0.01104
STM4312	STM4312	hypothetical protein STM4312	0.41	0.66616	0.65	0.35712	1.53	0.03663
STM4312	STM4312	hypothetical protein STM4312	1.25	0.03223	1.19	0.08757	1.21	0.02349
STM4313	STM4313	putative cytoplasmic protein	-0.20	0.72562	0.20	0.69504	1.49	0.01329
STM4313	STM4313	putative cytoplasmic protein	0.82	0.25745	0.99	0.34689	1.26	0.08837
STM4314	STM4314	putative regulatory protein	-1.29	0.07722	0.64	0.34970	-0.45	0.28459
STM4314	STM4314	putative regulatory protein	0.09	0.91750	0.45	0.23925	-0.18	0.73248
STM4315	STM4315	putative DNA-binding protein	1.60	0.04695	-1.10	0.01365	1.50	0.01746
STM4315	STM4315	putative DNA-binding protein	1.91	0.02827	-1.42	0.00571	2.92	0.00155
STM4317	STM4317	hypothetical protein STM4317	0.65	0.23260	1.44	0.00185	-0.95	0.02326
STM4317	STM4317	hypothetical protein STM4317	1.28	0.14108	1.39	0.01081	0.26	0.67159
STM4318	STM4318	putative acetyltransferase	-0.10	0.90149	0.94	0.01456	0.23	0.72716
STM4318	STM4318	putative acetyltransferase	0.78	0.11865	0.31	0.33852	-0.84	0.11181
STM4319	phoN	non-specific acid phosphatase	2.41	0.01072	0.82	0.02637	0.00	0.99925
STM4319	phoN	non-specific acid phosphatase	3.43	0.00512	0.55	0.08740	1.04	0.01823
STM4321	pheR	STM4321	-1.67	0.02143	0.06	0.96541	3.37	0.00069
STM4321	pheR	STM4321	-0.67	0.66016	-1.65	0.00349	3.61	0.00032
STM4322	yjdC	putative regulatory protein	-0.55	0.19546	-0.31	0.35583	-0.32	0.40873
STM4322	yjdC	putative regulatory protein	0.96	0.08505	0.17	0.64628	0.20	0.67714
STM4323	dsbD	thiol:disulfide interchange protein precursor	-1.26	0.07763	0.00	0.99809	-1.40	0.00515
STM4323	dsbD	thiol:disulfide interchange protein precursor	0.33	0.59340	0.52	0.16340	-0.89	0.04161
STM4324	cutA	putative periplasmic divalent cation tolerance protein	1.29	0.24404	0.12	0.70053	-0.77	0.12977
STM4324	cutA	putative periplasmic divalent cation tolerance protein	1.69	0.18155	0.02	0.96010	1.26	0.06361
STM4325	dcuA	anaerobic C4-dicarboxylate transporter	-0.12	0.76848	-0.29	0.47413	0.30	0.47297
STM4325	dcuA	anaerobic C4-dicarboxylate transporter	-0.51	0.30586	-1.08	0.03399	-0.29	0.57723
STM4326	aspA	aspartate ammonia-lyase	-0.55	0.26560	0.77	0.05527	0.32	0.41632
STM4326	aspA	aspartate ammonia-lyase	-0.25	0.71508	0.68	0.04708	0.16	0.79124
STM4327	fxsA	suppressor of F exclusion of bacteriophage T7	-2.37	0.02105	-0.90	0.01657	-2.39	0.00850
STM4327	fxsA	suppressor of F exclusion of bacteriophage T7	-1.29	0.45278	-0.67	0.03163	-0.70	0.07254
STM4328	yjeH	putative transporter	-1.67	0.07090	-0.80	0.02910	-1.48	0.00431
STM4328	yjeH	putative transporter	-0.60	0.71819	-1.42	0.00848	-2.43	0.01706
STM4329	groES	co-chaperonin GroES	-0.25	0.76102	0.87	0.03502	-3.26	0.00010
STM4329	groES	co-chaperonin GroES	0.16	0.85372	0.89	0.03037	-3.08	0.00021
STM4330	groEL	chaperonin GroEL	-1.48	0.02146	0.66	0.09251	-2.41	0.00030
STM4330	groEL	chaperonin GroEL	-1.03	0.08218	1.32	0.00327	-3.13	0.00037
STM4331	yjeI	putative outer membrane lipoprotein	-0.92	0.06902	0.27	0.35236	-1.22	0.01049
STM4331	yjeI	putative outer membrane lipoprotein	-0.47	0.27011	0.83	0.02524	-0.71	0.08075
STM4332	yjeJ	putative inner membrane protein	-1.39	0.02948	-0.44	0.14211	-2.51	0.00019
STM4332	yjeJ	putative inner membrane protein	-0.26	0.55721	0.10	0.76711	-2.26	0.00065
STM4333	yjeK	putative aminomutase	-0.24	0.77088	-0.74	0.07079	-1.94	0.00130
STM4333	yjeK	putative aminomutase	0.39	0.54239	-0.82	0.02120	-1.21	0.01357
STM4334	efp	elongation factor P	-2.18	0.01279	-1.62	0.00077	-2.65	0.00016
STM4334	efp	elongation factor P	-2.31	0.00789	-1.72	0.00174	-2.44	0.00034
STM4335	ecnA	putative entericidin A precursor	-0.97	0.07537	-1.49	0.00132	-0.76	0.13400
STM4335	ecnA	putative entericidin A precursor	0.09	0.89142	-2.02	0.00027	-1.22	0.00974
STM4337	ecnR	putative regulatory protein	-1.55	0.05238	-0.55	0.11554	0.22	0.56340
STM4337	ecnR	putative regulatory protein	-1.22	0.04444	-0.99	0.01864	0.07	0.86160
STM4338	sugE	putative DMT superfamily transport protein	-1.46	0.02565	0.01	0.98874	0.00	0.99729
STM4338	sugE	putative DMT superfamily transport protein	-0.40	0.41243	-0.11	0.75373	-0.23	0.59651
STM4339	blc	outer membrane lipoprotein precursor	-0.12	0.80800	-0.28	0.45716	0.66	0.06913
STM4339	blc	outer membrane lipoprotein precursor	1.09	0.03896	-0.09	0.82890	1.73	0.00246

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM4340	frdD	fumarate reductase subunit D	**-1.07**	0.05094	**-1.13**	0.00823	**-1.20**	0.01037
STM4340	frdD	fumarate reductase subunit D	**-0.14**	0.72937	**-1.08**	0.01113	**-0.30**	0.42802
STM4341	frdC	fumarate reductase subunit C	**-1.63**	0.03447	**-0.94**	0.01009	**-0.02**	0.96963
STM4341	frdC	fumarate reductase subunit C	**-0.67**	0.48816	**-0.44**	0.52306	**-0.98**	0.16139
STM4342	frdB	succinate dehydrogenase	**-1.37**	0.02730	**-1.19**	0.02627	**-1.05**	0.07270
STM4342	frdB	succinate dehydrogenase	**-0.45**	0.48729	**-1.26**	0.01245	**-2.71**	0.02859
STM4343	frdA	fumarate reductase	**0.39**	0.65917	**-1.04**	0.02828	**-0.30**	0.60390
STM4343	frdA	fumarate reductase	**1.18**	0.11384	**-1.13**	0.00536	**0.41**	0.37675
STM4344	yjeA	lysyl-tRNA synthetase	**2.57**	0.40806	**-1.39**	0.00494	**-0.27**	0.57912
STM4344	yjeA	lysyl-tRNA synthetase	**0.99**	0.32838	**-1.60**	0.00176	**0.04**	0.96501
STM4345	yjeM	putative amino-acid transport protein	**-1.01**	0.18155	**-0.58**	0.19139	**-0.94**	0.11017
STM4345	yjeM	putative amino-acid transport protein	**0.78**	0.13216	**-1.55**	0.00303	**-0.57**	0.36200
STM4346	yjeO	putative inner membrane protein	**-0.83**	0.09932	**-1.15**	0.00969	**-1.23**	0.03849
STM4346	yjeO	putative inner membrane protein	**0.23**	0.76786	**-1.21**	0.00687	**-1.50**	0.00677
STM4347	yjeP	putative periplasmic binding protein	**-1.08**	0.03808	**-1.66**	0.00202	**-2.12**	0.01645
STM4347	yjeP	putative periplasmic binding protein	**0.57**	0.19350	**-1.60**	0.00353	**-0.22**	0.73248
STM4348	psd	phosphatidylserine decarboxylase	**0.42**	0.63656	**-0.28**	0.41512	**-1.58**	0.00233
STM4348	psd	phosphatidylserine decarboxylase	**0.91**	0.20138	**-0.54**	0.06609	**-0.73**	0.10643
STM4349	yjeQ	ribosome-associated GTPase	**-0.81**	0.36452	**-1.07**	0.00529	**-0.67**	0.09517
STM4349	yjeQ	ribosome-associated GTPase	**-1.69**	0.02138	**-1.13**	0.01440	**-0.86**	0.03716
STM4350	orn	oligoribonuclease	**-0.69**	0.20912	**-0.66**	0.05619	**-0.80**	0.07409
STM4350	orn	oligoribonuclease	**0.23**	0.63940	**-1.01**	0.01006	**-0.55**	0.18077
STM4351	STM4351	putative arginine-binding periplasmic protein	**-1.35**	0.02567	**-0.51**	0.22080	**-1.40**	0.03772
STM4351	STM4351	putative arginine-binding periplasmic protein	**-1.64**	0.06801	**-0.75**	0.04671	**-2.06**	0.00734
STM4352	glyV	STM4352	**-1.85**	0.03678	**-0.70**	0.11233	**0.49**	0.33355
STM4352	glyV	STM4352	**-0.24**	0.77158	**0.12**	0.72566	**0.85**	0.04280
STM4353	glyX	STM4353	**-0.65**	0.34889	**-0.40**	0.27196	**0.59**	0.15751
STM4353	glyX	STM4353	**-0.26**	0.70958	**-0.03**	0.93083	**0.59**	0.10122
STM4354	glyY	STM4354	**-0.60**	0.36425	**-0.12**	0.66967	**0.88**	0.06652
STM4354	glyY	STM4354	**0.10**	0.88044	**-0.01**	0.97823	**1.06**	0.01379
STM4355,S	yjeS	putative FeS protein	**-1.51**	0.03113	**-0.51**	0.10383	**-1.12**	0.05170
STM4355,S	yjeS	putative FeS protein	**0.10**	0.86472	**-0.57**	0.06736	**-0.65**	0.27015
STM4356	yjeF	putative sugar kinase	**2.63**	0.08578	**0.15**	0.70657	**0.28**	0.63740
STM4356	yjeF	putative sugar kinase	**2.41**	0.41383	**0.19**	0.53225	**1.55**	0.36325
STM4357	yjeE	putative nucleotide-binding protein	**-1.19**	0.03218	**-0.28**	0.31803	**-1.26**	0.01141
STM4357	yjeE	putative nucleotide-binding protein	**-0.88**	0.08147	**-0.51**	0.11108	**-1.20**	0.01629
STM4358	amiB	N-acetylmuramoyl-l-alanine amidase II	**-2.49**	0.00648	**-0.88**	0.06814	**-1.81**	0.00119
STM4358	amiB	N-acetylmuramoyl-l-alanine amidase II	**-1.52**	0.02438	**-0.27**	0.48490	**-1.44**	0.01520
STM4359	mutL	DNA mismatch repair protein	**-0.04**	0.92939	**1.30**	0.01015	**-0.75**	0.04791
STM4359	mutL	DNA mismatch repair protein	**0.09**	0.83760	**1.41**	0.00224	**-0.25**	0.51902
STM4360	miaA	tRNA delta(2)-isopentenylpyrophosphate transferase	**-2.57**	0.01391	**-0.13**	0.78476	**-1.70**	0.00213
STM4360	miaA	tRNA delta(2)-isopentenylpyrophosphate transferase	**-1.48**	0.01993	**0.17**	0.58284	**-1.38**	0.00925
STM4361	hfq	RNA-binding protein Hfq	**-2.89**	0.03111	**-0.72**	0.06663	**-2.12**	0.00061
STM4361	hfq	RNA-binding protein Hfq	**-1.72**	0.01349	**-0.52**	0.07625	**-1.94**	0.00075
STM4362	hflX	putative GTP-ase	**-0.93**	0.10688	**0.57**	0.13679	**-1.36**	0.01049
STM4362	hflX	putative GTP-ase	**0.03**	0.95398	**0.76**	0.04406	**-0.57**	0.21377
STM4363	hflK	FtsH modulator	**-0.13**	0.76773	**0.58**	0.15126	**-2.52**	0.00019
STM4363	hflK	FtsH modulator	**0.79**	0.22394	**0.90**	0.02372	**-2.27**	0.00266
STM4364	hflC	FtsH modulator	**-0.21**	0.66101	**0.67**	0.15969	**-2.09**	0.00440
STM4364	hflC	FtsH modulator	**1.08**	0.04903	**0.56**	0.24620	**-1.94**	0.00156
STM4365	yjeT	putative inner membrane protein	**-0.91**	0.17044	**-0.43**	0.18368	**-2.73**	0.00043
STM4365	yjeT	putative inner membrane protein	**-0.20**	0.71609	**-0.39**	0.18095	**-1.56**	0.00310
STM4366	purA	adenylosuccinate synthetase	**-1.67**	0.01285	**0.35**	0.48159	**-0.63**	0.16381
STM4366	purA	adenylosuccinate synthetase	**-1.42**	0.07348	**-0.34**	0.21332	**-1.60**	0.03735
STM4367	yjeB	putative negative regulator	**-1.32**	0.07237	**0.46**	0.16574	**-0.20**	0.59568
STM4367	yjeB	putative negative regulator	**-0.91**	0.06792	**0.12**	0.69024	**-0.04**	0.93658
STM4368	vacB	putative exoribonuclease	**0.39**	0.45780	**-0.10**	0.79545	**0.35**	0.46118
STM4368	vacB	putative exoribonuclease	**1.14**	0.04437	**-0.01**	0.97552	**0.95**	0.12532
STM4369	yjfH	putative tRNA/rRNA methyltransferase	**-1.11**	0.04515	**-0.60**	0.08028	**-0.88**	0.03017
STM4369	yjfH	putative tRNA/rRNA methyltransferase	**-0.21**	0.76637	**-0.52**	0.15678	**-0.85**	0.05602
STM4370	yjfI	putative cytoplasmic protein	**0.06**	0.95235	**-0.53**	0.13185	**-0.53**	0.48717
STM4370	yjfI	putative cytoplasmic protein	**-0.21**	0.68653	**-1.24**	0.02247	**0.09**	0.87818
STM4371	yjfJ	putative phage shock protein A	**0.68**	0.27450	**-1.86**	0.02404	**-1.27**	0.02305
STM4371	yjfJ	putative phage shock protein A	**0.37**	0.66194	**-1.80**	0.07238	**-0.26**	0.71030
STM4372	STM4372	putative potassium channels	**0.52**	0.58469	**0.17**	0.56399	**0.98**	0.01701
STM4372	STM4372	putative potassium channels	**1.59**	0.06252	**0.09**	0.76973	**1.01**	0.05935
STM4373	yjfK	putative cytoplasmic protein	**-0.33**	0.52859	**0.28**	0.49942	**-0.08**	0.84467
STM4373	yjfK	putative cytoplasmic protein	**1.23**	0.07945	**0.25**	0.64790	**-0.33**	0.66302
STM4374	yjfL	putative inner membrane protein	**0.17**	0.78589	**-0.13**	0.81169	**0.66**	0.18629
STM4374	yjfL	putative inner membrane protein	**2.29**	0.05767	**-0.51**	0.20287	**0.28**	0.64753

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM4375	yjfM	putative inner membrane protein	**0.07**	0.92872	**0.41**	0.16818	**-1.64**	0.00388
STM4375	yjfM	putative inner membrane protein	**1.07**	0.11592	**0.28**	0.47621	**0.02**	0.97409
STM4376	yjfC	putative glutathionylspermidine synthase	**0.54**	0.45879	**0.91**	0.02145	**0.17**	0.75498
STM4376	yjfC	putative glutathionylspermidine synthase	**0.83**	0.26685	**1.08**	0.01605	**0.45**	0.32056
STM4377	aidB	putative acyl-CoA dehydrogenase	**2.47**	0.04877	**-1.41**	0.00289	**0.31**	0.76104
STM4377	aidB	putative acyl-CoA dehydrogenase	**2.52**	0.05964	**-1.96**	0.00463	**1.42**	0.17750
STM4378	yjfN	putative inner membrane protein	**1.91**	0.05424	**2.89**	0.00005	**3.74**	0.00010
STM4378	yjfN	putative inner membrane protein	**1.32**	0.04680	**2.44**	0.00060	**3.30**	0.00012
STM4379	yjfO	putative lipoprotein	**-0.55**	0.23414	**1.18**	0.00950	**2.81**	0.00036
STM4379	yjfO	putative lipoprotein	**-0.11**	0.82541	**0.93**	0.01508	**3.03**	0.00020
STM4380	yjfP	putative hydrolase	**0.84**	0.10112	**0.18**	0.68360	**-0.35**	0.39162
STM4380	yjfP	putative hydrolase	**0.85**	0.14884	**0.17**	0.55224	**0.38**	0.60829
STM4381	yjfQ	putative transcriptional repressor	**-1.21**	0.17164	**-0.63**	0.07419	**-1.61**	0.02022
STM4381	yjfQ	putative transcriptional repressor	**0.43**	0.43433	**0.44**	0.20307	**-0.55**	0.22252
STM4382	yjfR	putative Zn-dependent hydrolase	**-0.29**	0.50431	**-1.19**	0.04088	**-0.68**	0.14880
STM4382	yjfR	putative Zn-dependent hydrolase	**-0.48**	0.44635	**-1.13**	0.02721	**-0.15**	0.91103
STM4383,S	ulaA	ascorbate-specific PTS system enzyme IIC	**0.28**	0.58797	**-1.65**	0.00772	**-0.57**	0.20443
STM4383,S	ulaA	ascorbate-specific PTS system enzyme IIC	**0.74**	0.18694	**-0.71**	0.43133	**0.11**	0.89189
STM4384	sgaB	putative PTS enzyme II	**0.31**	0.53299	**0.58**	0.37301	**0.59**	0.55415
STM4384	sgaB	putative PTS enzyme II	**1.49**	0.02838	**-0.09**	0.75345	**1.08**	0.04275
STM4385	ptxA	putative PTS enzyme II	**0.86**	0.16770	**-0.31**	0.39830	**-0.52**	0.45148
STM4385	ptxA	putative PTS enzyme II	**0.74**	0.43590	**-1.43**	0.01809	**0.06**	0.93750
STM4386	sgaH	putative hexulose phosphate synthase	**0.54**	0.29455	**-1.45**	0.03755	**-1.00**	0.27629
STM4386	sgaH	putative hexulose phosphate synthase	**0.47**	0.59479	**-1.38**	0.00987	**-2.12**	0.03835
STM4387	sgaU	putative hexulose-6-phosphate isomerase	**-0.52**	0.35772	**-0.90**	0.05480	**-0.97**	0.06379
STM4387	sgaU	putative hexulose-6-phosphate isomerase	**1.59**	0.10178	**0.50**	0.48785	**2.57**	0.00125
STM4388	sgaE	L-ribulose-5-phosphate 4-epimerase	**-2.21**	0.00753	**-1.24**	0.06264	**-2.74**	0.01325
STM4388	sgaE	L-ribulose-5-phosphate 4-epimerase	**-2.50**	0.01155	**-1.69**	0.00143	**-2.19**	0.00943
STM4389	yjfY	putative outer membrane protein	**-2.38**	0.00660	**-1.59**	0.00142	**-1.59**	0.00802
STM4389	yjfY	putative outer membrane protein	**-0.52**	0.65219	**-1.47**	0.00639	**-1.60**	0.00202
STM4391	rpsF	30S ribosomal protein S6	**-4.51**	0.01761	**-2.10**	0.00130	**-5.86**	0.00021
STM4391	rpsF	30S ribosomal protein S6	**-4.73**	0.02177	**-2.06**	0.00018	**-7.68**	0.00001
STM4393	rpsR	30S ribosomal protein S18	**-3.27**	0.00795	**-1.59**	0.00613	**-4.31**	0.00004
STM4393	rpsR	30S ribosomal protein S18	**-2.01**	0.02268	**-1.41**	0.00885	**-4.98**	0.00002
STM4394	rplI	50S ribosomal protein L9	**-3.24**	0.02532	**-1.28**	0.02098	**-4.98**	0.00026
STM4394	rplI	50S ribosomal protein L9	**-2.66**	0.00661	**-0.53**	0.24878	**-5.00**	0.00003
STM4395	yifZ	putative permease	**-0.59**	0.20924	**-1.02**	0.02845	**-1.55**	0.00749
STM4395	yifZ	putative permease	**0.30**	0.76409	**-1.05**	0.01926	**-1.00**	0.02554
STM4396	ytfB	putative cell envelope opacity-associated protein A	**-0.72**	0.21612	**-0.75**	0.04526	**-0.24**	0.52642
STM4396	ytfB	putative cell envelope opacity-associated protein A	**-0.19**	0.75685	**-0.49**	0.13098	**0.31**	0.41123
STM4397	fklB	FKBP-type 22KD peptidyl-prolyl cis-trans isomerase	**-1.64**	0.01319	**-1.68**	0.00128	**-3.74**	0.00007
STM4397	fklB	FKBP-type 22KD peptidyl-prolyl cis-trans isomerase	**-0.85**	0.15091	**-1.89**	0.00070	**-2.93**	0.00047
STM4398	cycA	D-alanine/D-serine/glycine transport protein	**-0.28**	0.61990	**0.69**	0.07780	**-0.99**	0.08477
STM4398	cycA	D-alanine/D-serine/glycine transport protein	**1.63**	0.11370	**0.87**	0.01876	**-0.86**	0.08837
STM4399	ytfE	putative cell morphogenesis protein	**0.75**	0.21940	**1.58**	0.00273	**-0.12**	0.77834
STM4399	ytfE	putative cell morphogenesis protein	**2.16**	0.01401	**1.42**	0.00683	**0.28**	0.46740
STM4400	ytfF	putative cationic amino acid transporter	**1.60**	0.03453	**0.34**	0.27031	**-0.24**	0.54835
STM4400	ytfF	putative cationic amino acid transporter	**1.62**	0.08941	**-0.56**	0.16967	**0.21**	0.69836
STM4401	ytfG	putative reductase	**1.11**	0.35384	**0.65**	0.08645	**-0.07**	0.91566
STM4401	ytfG	putative reductase	**2.99**	0.00780	**-0.97**	0.09029	**-0.28**	0.78671
STM4402	ytfH	putative transcriptional regulator	**0.63**	0.39473	**0.44**	0.16412	**-0.03**	0.95290
STM4402	ytfH	putative transcriptional regulator	**0.23**	0.65326	**0.26**	0.42051	**0.45**	0.30017
STM4403	cpdB	2',3'-cyclic nucleotide 2'-phosphodiesterase/3'-nucleotidase	**1.32**	0.49426	**0.55**	0.10127	**0.58**	0.39711
STM4403	cpdB	2',3'-cyclic nucleotide 2'-phosphodiesterase/3'-nucleotidase	**0.49**	0.40371	**0.26**	0.45719	**0.53**	0.32047
STM4404	cysQ	sulfite biosynthetic protein	**-1.32**	0.02464	**0.30**	0.30994	**1.24**	0.00668
STM4404	cysQ	sulfite biosynthetic protein	**-0.17**	0.78079	**0.55**	0.10725	**1.70**	0.00264
STM4405	ytfJ	putative transcriptional regulator	**-0.05**	0.95272	**0.65**	0.07040	**1.27**	0.01578
STM4405	ytfJ	putative transcriptional regulator	**0.25**	0.69232	**0.74**	0.05447	**1.78**	0.00129
STM4406,S	ytfK	putative cytoplasmic protein	**2.32**	0.50755	**0.69**	0.29702	**2.60**	0.00314
STM4406,S	ytfK	putative cytoplasmic protein	**-0.41**	0.74558	**1.07**	0.00959	**2.30**	0.00784
STM4407	ytfL	putative hemolysin-like protein	**-1.07**	0.10500	**-0.40**	0.18585	**0.59**	0.14409
STM4407	ytfL	putative hemolysin-like protein	**0.48**	0.40754	**0.12**	0.72798	**1.62**	0.00484
STM4408	msrA	methionine sulfoxide reductase A	**-0.45**	0.49835	**0.63**	0.18118	**0.50**	0.39283
STM4408	msrA	methionine sulfoxide reductase A	**0.67**	0.18353	**0.52**	0.21528	**0.69**	0.11659
STM4409	ytfM	putative outer membrane protein	**-1.34**	0.04301	**-0.48**	0.21987	**-1.72**	0.00732
STM4409	ytfM	putative outer membrane protein	**-0.36**	0.40544	**-0.18**	0.56539	**-0.81**	0.07616
STM4410	ytfN	putative periplasmic protein	**-2.56**	0.00929	**-0.19**	0.61050	**-2.40**	0.00020
STM4410	ytfN	putative periplasmic protein	**-1.82**	0.01131	**-0.21**	0.53844	**-1.91**	0.00340
STM4411	ytfP	putative cytoplasmic protein	**-2.28**	0.01048	**-0.51**	0.12789	**-1.03**	0.05849
STM4411	ytfP	putative cytoplasmic protein	**-0.72**	0.45200	**-0.21**	0.53540	**-1.48**	0.00300

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM4412	STM4412	putative permease	**-0.57**	0.55858	**-0.72**	0.04875	**-0.45**	0.54494
STM4412	STM4412	putative permease	**0.96**	0.15645	**-0.65**	0.14488	**-0.02**	0.96883
STM4413	STM4413	dihydroorotase	**0.66**	0.31535	**1.02**	0.02314	**1.37**	0.06998
STM4413	STM4413	dihydroorotase	**-0.55**	0.47667	**-0.16**	0.73838	**-0.20**	0.81672
STM4414	ppa	inorganic pyrophosphatase	**-2.62**	0.00547	**-1.48**	0.00605	**-1.73**	0.00131
STM4414	ppa	inorganic pyrophosphatase	**-1.57**	0.05780	**-0.98**	0.01248	**-2.04**	0.00155
STM4415	fbp	fructose-1,6-bisphosphatase	**-2.38**	0.00704	**-1.08**	0.01170	**-2.41**	0.00023
STM4415	fbp	fructose-1,6-bisphosphatase	**-2.05**	0.01162	**-0.58**	0.06816	**-1.73**	0.00808
STM4416	mpl	UDP-N-acetylmuramate/L-alanyl-gamma-D-glutamyl-meso-	**-0.16**	0.79102	**-0.33**	0.37733	**-1.45**	0.01057
STM4416	mpl	UDP-N-acetylmuramate/L-alanyl-gamma-D-glutamyl-meso-	**0.04**	0.95696	**-0.12**	0.70649	**-0.79**	0.12058
STM4417	STM4417	putative transcriptional regulator	**0.05**	0.91651	**-0.19**	0.58019	**-0.65**	0.12186
STM4417	STM4417	putative transcriptional regulator	**1.42**	0.02652	**-0.60**	0.10309	**0.36**	0.43627
STM4418	STM4418	sugar transporter	**3.13**	0.00547	**2.11**	0.00406	**4.51**	0.00008
STM4418	STM4418	sugar transporter	**3.24**	0.00643	**0.99**	0.09579	**4.78**	0.00002
STM4419	STM4419	sugar transporter	**0.75**	0.19139	**-0.38**	0.42248	**0.38**	0.56843
STM4419	STM4419	sugar transporter	**1.41**	0.02636	**-0.55**	0.14785	**1.33**	0.04039
STM4420	STM4420	putative inner membrane protein	**-0.24**	0.70070	**0.00**	0.99977	**1.81**	0.01231
STM4420	STM4420	putative inner membrane protein	**2.33**	0.01251	**0.99**	0.10599	**1.02**	0.08506
STM4421	STM4421	putative NAD-dependent aldehyde dehydrogenase	**-0.56**	0.33069	**0.17**	0.62505	**-2.78**	0.00139
STM4421	STM4421	putative NAD-dependent aldehyde dehydrogenase	**1.76**	0.05330	**0.95**	0.03824	**0.57**	0.14325
STM4423	STM4423	putative DNA-binding protein	**0.00**	0.99786	**-0.12**	0.87816	**-0.48**	0.44311
STM4423	STM4423	putative DNA-binding protein	**1.71**	0.11970	**-0.82**	0.12962	**2.21**	0.00166
STM4424,S	STM4424,S	putative endonuclease	**0.70**	0.28567	**-0.51**	0.26924	**0.97**	0.22780
STM4424,S	STM4424,S	putative endonuclease	**2.22**	0.01869	**0.45**	0.15435	**1.77**	0.00709
STM4425	STM4425	putative dehydrogenase	**0.66**	0.17086	**0.99**	0.02012	**-0.07**	0.89059
STM4425	STM4425	putative dehydrogenase	**0.51**	0.39670	**1.15**	0.00517	**0.42**	0.56340
STM4426	srfJ	lysosomal glucosyl ceramidase-like protein	**0.12**	0.76451	**2.31**	0.00070	**-0.26**	0.52301
STM4426	srfJ	lysosomal glucosyl ceramidase-like protein	**-0.47**	0.62065	**2.59**	0.00016	**0.04**	0.96528
STM4427	STM4427	putative endonuclease	**1.97**	0.02765	**1.21**	0.01884	**-0.98**	0.06850
STM4427	STM4427	putative endonuclease	**1.73**	0.02754	**1.05**	0.01486	**1.40**	0.01135
STM4428	STM4428	hypothetical protein STM4428	**-1.07**	0.05338	**-0.11**	0.75927	**-0.68**	0.22957
STM4428	STM4428	hypothetical protein STM4428	**-0.52**	0.66787	**-1.57**	0.00528	**-2.51**	0.00072
STM4433	STM4433	myo-inositol 2-dehydrogenase	**1.86**	0.02605	**-0.78**	0.38110	**-0.08**	0.92944
STM4433	STM4433	myo-inositol 2-dehydrogenase	**2.61**	0.01503	**-0.26**	0.62420	**1.42**	0.01459
STM4434	STM4434	putative permease	**-0.27**	0.59899	**0.44**	0.41871	**0.68**	0.10727
STM4434	STM4434	putative permease	**-0.09**	0.94814	**-1.46**	0.00718	**0.15**	0.72414
STM4435	STM4435	putative cytoplasmic protein	**-0.11**	0.79237	**-0.03**	0.94410	**-0.05**	0.93679
STM4435	STM4435	putative cytoplasmic protein	**1.12**	0.06092	**0.65**	0.05992	**0.42**	0.46599
STM4436	STM4436	putative endonuclease	**-0.27**	0.71090	**-0.59**	0.11525	**-0.34**	0.47247
STM4436	STM4436	putative endonuclease	**0.71**	0.15772	**-0.46**	0.11222	**0.16**	0.71053
STM4437	yjgA	hypothetical protein STM4437	**-1.09**	0.12902	**-1.11**	0.00846	**-0.83**	0.09888
STM4437	yjgA	hypothetical protein STM4437	**-1.96**	0.02908	**-0.91**	0.01564	**-0.77**	0.16608
STM4438	pmbA	putative antibiotic maturation protein	**-2.76**	0.00932	**-0.63**	0.04068	**-0.86**	0.03859
STM4438	pmbA	putative antibiotic maturation protein	**-1.53**	0.08698	**-0.44**	0.15874	**-0.73**	0.11052
STM4439	cybC	cytochrome b562	**1.47**	0.15162	**-1.06**	0.00556	**-2.13**	0.00100
STM4439	cybC	cytochrome b562	**1.75**	0.14472	**-0.87**	0.01569	**-1.68**	0.00562
STM4440	STM4440	putative cytoplasmic protein	**-0.02**	0.98022	**-0.39**	0.24138	**0.83**	0.41390
STM4440	STM4440	putative cytoplasmic protein	**0.38**	0.56314	**-0.29**	0.42682	**2.64**	0.09979
STM4441	STM4441	putative cytoplasmic protein	**-0.21**	0.73745	**-0.03**	0.95079	**1.48**	0.01940
STM4441	STM4441	putative cytoplasmic protein	**0.30**	0.61957	**-0.13**	0.70440	**0.39**	0.38402
STM4442	STM4442	putative cytoplasmic protein	**0.14**	0.80816	**-0.62**	0.12641	**-0.06**	0.91989
STM4442	STM4442	putative cytoplasmic protein	**0.88**	0.16192	**-0.23**	0.50017	**0.84**	0.22702
STM4443	STM4443	putative inner membrane protein	**-0.75**	0.10900	**-0.16**	0.69562	**-0.65**	0.34220
STM4443	STM4443	putative inner membrane protein	**0.67**	0.12279	**-0.35**	0.30610	**0.54**	0.11976
STM4444	STM4444	putative inner membrane protein	**-0.04**	0.96131	**-0.01**	0.96803	**-0.37**	0.53139
STM4444	STM4444	putative inner membrane protein	**0.72**	0.25763	**-0.48**	0.17200	**-0.13**	0.88786
STM4445	STM4445	dihydroorotase	**0.51**	0.46194	**-0.59**	0.08971	**-0.24**	0.67086
STM4445	STM4445	dihydroorotase	**2.01**	0.09831	**-1.09**	0.00836	**0.83**	0.30974
STM4446	STM4446	putative selenocysteine synthase	**0.37**	0.51492	**0.24**	0.57965	**-0.06**	0.92706
STM4446	STM4446	putative selenocysteine synthase	**0.45**	0.44637	**0.36**	0.21404	**-0.41**	0.33458
STM4447	STM4447	putative periplasmic protein	**-0.67**	0.26164	**0.24**	0.68599	**-0.63**	0.14917
STM4447	STM4447	putative periplasmic protein	**0.36**	0.44337	**-1.04**	0.03226	**0.31**	0.43580
STM4448	STM4448	putative phosphotransferase system mannitol/fructose-	**0.07**	0.89154	**-0.63**	0.04336	**-0.57**	0.23461
STM4448	STM4448	putative phosphotransferase system mannitol/fructose-	**0.88**	0.08057	**-0.23**	0.53718	**0.04**	0.94554
STM4449	STM4449	putative regulatory protein	**-0.68**	0.30079	**0.91**	0.06015	**-0.14**	0.81708
STM4449	STM4449	putative regulatory protein	**0.89**	0.06825	**0.50**	0.27535	**0.62**	0.24787
STM4450	STM4450	putative inner membrane protein	**0.32**	0.47363	**0.84**	0.02517	**-0.40**	0.28702
STM4450	STM4450	putative inner membrane protein	**1.11**	0.35933	**0.59**	0.20984	**-0.30**	0.56516
STM4451	nrdG	anaerobic ribonucleotide reductase activating protein	**-0.51**	0.22993	**0.62**	0.09737	**-0.48**	0.47075
STM4451	nrdG	anaerobic ribonucleotide reductase activating protein	**0.64**	0.19900	**1.11**	0.00814	**-0.96**	0.03287

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM4452	nrdD	anaerobic ribonucleoside triphosphate reductase	**0.06**	0.92334	**0.86**	0.02151	**-0.46**	0.19236
STM4452	nrdD	anaerobic ribonucleoside triphosphate reductase	**0.66**	0.15082	**0.71**	0.08933	**1.32**	0.00623
STM4452,1N	STM4452,1N	hypothetical protein STM4452,1N	**1.92**	0.01655	**0.43**	0.28464	**2.20**	0.01040
STM4452,1N	STM4452,1N	hypothetical protein STM4452,1N	**3.16**	0.00541	**0.64**	0.06755	**3.26**	0.00017
STM4453	treC	trehalose-6-phosphate hydrolase	**-2.01**	0.02281	**-1.14**	0.00742	**-1.93**	0.00117
STM4453	treC	trehalose-6-phosphate hydrolase	**1.01**	0.36150	**-0.76**	0.01877	**-1.19**	0.03224
STM4455	treR	trehalose repressor	**-0.90**	0.28978	**-1.19**	0.05962	**0.58**	0.39283
STM4455	treR	trehalose repressor	**-0.74**	0.13710	**-1.94**	0.00261	**-0.07**	0.90484
STM4456	mgtA	Mg2+ ATPase transporter	**-0.88**	0.08960	**-0.74**	0.05804	**-1.20**	0.00748
STM4456	mgtA	Mg2+ ATPase transporter	**-0.58**	0.18697	**-0.45**	0.14971	**-0.90**	0.07888
STM4457	STM4457	putative transposase	**-1.00**	0.30207	**-0.08**	0.89061	**-0.01**	0.98607
STM4457	STM4457	putative transposase	**-1.23**	0.12157	**-1.03**	0.03634	**-1.14**	0.13128
STM4458	yjgF	putative translation initiation inhibitor	**-2.68**	0.01423	**-1.87**	0.00070	**-1.93**	0.00148
STM4458	yjgF	putative translation initiation inhibitor	**-2.09**	0.02726	**-1.34**	0.01016	**-2.71**	0.00036
STM4459	pyrI	aspartate carbamoyltransferase regulatory subunit	**-1.79**	0.01426	**0.00**	0.99456	**-2.25**	0.00053
STM4459	pyrI	aspartate carbamoyltransferase regulatory subunit	**-1.09**	0.03729	**0.18**	0.53521	**-1.49**	0.00241
STM4460	pyrB	aspartate carbamoyltransferase catalytic subunit	**-1.23**	0.11961	**-0.35**	0.19902	**-1.44**	0.05562
STM4460	pyrB	aspartate carbamoyltransferase catalytic subunit	**-0.61**	0.34597	**0.04**	0.92293	**-1.60**	0.00428
STM4463	STM4463	putative arginine repressor	**-0.91**	0.08555	**-0.80**	0.08492	**-1.30**	0.03020
STM4463	STM4463	putative arginine repressor	**0.35**	0.56647	**-0.78**	0.02795	**-0.59**	0.23556
STM4464	STM4464	putative arginine repressor	**-0.46**	0.27957	**-0.57**	0.08890	**-1.57**	0.01114
STM4464	STM4464	putative arginine repressor	**1.51**	0.07731	**-1.32**	0.00424	**-0.60**	0.38437
STM4465	STM4465	ornithine carbamoyltransferase	**0.51**	0.58404	**-0.58**	0.20316	**-0.15**	0.81283
STM4465	STM4465	ornithine carbamoyltransferase	**3.64**	0.00955	**-0.46**	0.32576	**1.22**	0.01889
STM4466	STM4466	carbamate kinase	**0.62**	0.19981	**-2.14**	0.04886	**-0.84**	0.11769
STM4466	STM4466	carbamate kinase	**0.78**	0.14460	**-1.17**	0.00551	**-0.12**	0.84572
STM4467	STM4467	arginine deiminase	**2.76**	0.00901	**0.45**	0.43367	**-0.63**	0.27257
STM4467	STM4467	arginine deiminase	**3.73**	0.02948	**-0.50**	0.16512	**0.25**	0.61153
STM4468	yjgK	putative cytoplasmic protein	**0.63**	0.38692	**0.24**	0.56650	**-0.35**	0.38962
STM4468	yjgK	putative cytoplasmic protein	**1.49**	0.01838	**0.19**	0.69158	**0.16**	0.75966
STM4469	argI	ornithine carbamoyltransferase	**1.49**	0.09629	**2.38**	0.00463	**-0.09**	0.93458
STM4469	argI	ornithine carbamoyltransferase	**1.88**	0.02805	**1.49**	0.00453	**1.20**	0.01202
STM4470	yjgD	putative cytoplasmic protein	**-1.18**	0.33147	**0.15**	0.60724	**0.17**	0.78401
STM4470	yjgD	putative cytoplasmic protein	**0.39**	0.60472	**-0.44**	0.13030	**0.46**	0.28606
STM4471	miaE	hydroxylase	**-0.23**	0.60216	**-0.23**	0.58568	**-0.40**	0.35726
STM4471	miaE	hydroxylase	**-0.68**	0.27849	**-1.47**	0.00325	**-0.50**	0.44378
STM4472	ytgA	putative inner membrane protein	**0.21**	0.72232	**-0.33**	0.57759	**2.65**	0.03914
STM4472	ytgA	putative inner membrane protein	**1.01**	0.36412	**0.18**	0.70905	**2.21**	0.09822
STM4473	yjgM	putative acetyltransferase	**-0.57**	0.18716	**-0.36**	0.25402	**-1.23**	0.02509
STM4473	yjgM	putative acetyltransferase	**-0.56**	0.38065	**-1.06**	0.01707	**-0.88**	0.10248
STM4474	yjgN	putative inner membrane protein	**0.47**	0.50860	**-0.98**	0.01565	**-0.11**	0.83277
STM4474	yjgN	putative inner membrane protein	**0.22**	0.82290	**-0.95**	0.01497	**-0.09**	0.95615
STM4475	valS	valyl-tRNA synthetase	**-1.35**	0.09858	**-1.22**	0.00574	**-1.63**	0.04895
STM4475	valS	valyl-tRNA synthetase	**0.03**	0.96386	**-0.85**	0.02232	**-1.39**	0.02865
STM4476,S	holC	DNA polymerase III subunit chi	**-2.94**	0.01785	**-1.43**	0.00118	**-2.19**	0.00062
STM4476,S	holC	DNA polymerase III subunit chi	**-1.30**	0.02914	**-1.03**	0.09507	**-2.28**	0.00074
STM4477	pepA	leucyl aminopeptidase	**-4.12**	0.00512	**-2.40**	0.00036	**-3.28**	0.00018
STM4477	pepA	leucyl aminopeptidase	**-4.07**	0.00546	**-2.13**	0.00075	**-2.70**	0.00015
STM4479	yjgP	putative permease	**-2.20**	0.00818	**-0.76**	0.02815	**-1.68**	0.00589
STM4479	yjgP	putative permease	**0.01**	0.98746	**-0.90**	0.01178	**-1.26**	0.01134
STM4480	yjgQ	putative permease	**-1.47**	0.01823	**0.12**	0.92655	**-0.75**	0.06952
STM4480	yjgQ	putative permease	**-1.28**	0.04794	**-0.95**	0.01024	**-0.87**	0.07511
STM4481	idnR	L-idonate regulator	**0.22**	0.80421	**-0.43**	0.22222	**-0.70**	0.16202
STM4481	idnR	L-idonate regulator	**-0.16**	0.81457	**-0.46**	0.39828	**-0.71**	0.19505
STM4482	idnT	L-idonate transport protein	**-0.89**	0.08618	**-0.34**	0.74485	**0.47**	0.34137
STM4482	idnT	L-idonate transport protein	**-0.85**	0.29367	**-1.06**	0.00844	**-1.17**	0.08517
STM4483	idnO	gluconate 5-dehydrogenase	**-1.03**	0.20636	**0.34**	0.34708	**-0.90**	0.08572
STM4483	idnO	gluconate 5-dehydrogenase	**0.17**	0.78300	**-0.34**	0.26379	**-0.15**	0.74370
STM4484	idnD	L-idonate 5-dehydrogenase	**-0.63**	0.27871	**1.23**	0.42529	**-1.36**	0.04876
STM4484	idnD	L-idonate 5-dehydrogenase	**1.33**	0.03973	**-1.55**	0.00208	**0.03**	0.96029
STM4485	idnK	thermosensitive D-gluconate kinase	**-1.18**	0.05743	**0.39**	0.62947	**0.31**	0.46326
STM4485	idnK	thermosensitive D-gluconate kinase	**-0.20**	0.71132	**-0.22**	0.54571	**0.42**	0.42103
STM4486	yjgB	putative alcohol dehydrogenase	**-0.24**	0.69340	**1.87**	0.00111	**1.75**	0.00327
STM4486	yjgB	putative alcohol dehydrogenase	**1.08**	0.12781	**2.03**	0.00931	**2.29**	0.00348
STM4487	leuX	STM4487	**-1.62**	0.01609	**-0.12**	0.78205	**2.79**	0.00056
STM4487	leuX	STM4487	**-0.58**	0.27794	**-0.26**	0.50156	**3.23**	0.00022
STM4488	STM4488	putative integrase	**1.55**	0.10141	**-0.32**	0.29161	**1.15**	0.03740
STM4488	STM4488	putative integrase	**3.17**	0.01024	**-0.99**	0.03370	**2.72**	0.00031
STM4489	STM4489	putative DNA helicases	**-1.30**	0.02443	**0.24**	0.47940	**-0.35**	0.43454
STM4489	STM4489	putative DNA helicases	**-0.55**	0.56833	**0.21**	0.51768	**-0.50**	0.40452

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM4490	STM4490	putative restriction endonuclease	**-0.70**	0.16266	**0.16**	0.59207	**-0.84**	0.09105
STM4490	STM4490	putative restriction endonuclease	**-0.28**	0.67668	**0.35**	0.25721	**-0.47**	0.33830
STM4491	STM4491	putative ATP-dependent Lon protease	**-1.22**	0.06709	**-0.04**	0.92942	**-0.20**	0.71092
STM4491	STM4491	putative ATP-dependent Lon protease	**-0.68**	0.37429	**0.21**	0.43148	**-0.49**	0.25088
STM4492	STM4492	putative cytoplasmic protein	**-0.89**	0.46047	**-0.56**	0.07105	**-0.69**	0.38106
STM4492	STM4492	putative cytoplasmic protein	**-0.54**	0.23076	**-0.60**	0.09868	**-1.02**	0.06317
STM4493	STM4493	putative cytoplasmic protein	**-2.34**	0.01813	**-1.54**	0.14679	**-2.29**	0.01326
STM4493	STM4493	putative cytoplasmic protein	**-2.82**	0.02197	**-1.42**	0.00273	**-4.71**	0.00042
STM4494	STM4494	putative ABC-type sugar/spermidine/putrescine transport	**-1.37**	0.08082	**-0.25**	0.37209	**-0.49**	0.46838
STM4494	STM4494	putative ABC-type sugar/spermidine/putrescine transport	**-0.75**	0.14307	**-0.90**	0.02737	**-1.03**	0.03980
STM4495	STM4495	putative type II restriction enzyme methylase subunit	**-0.35**	0.54785	**-1.12**	0.07345	**-0.87**	0.14834
STM4495	STM4495	putative type II restriction enzyme methylase subunit	**-0.45**	0.29028	**-1.32**	0.00447	**-1.15**	0.05094
STM4496	STM4496	putative DNA repair ATPase	**-1.75**	0.01490	**-0.98**	0.01153	**-2.65**	0.00072
STM4496	STM4496	putative DNA repair ATPase	**-0.13**	0.76787	**-1.30**	0.00615	**-1.24**	0.03631
STM4497	STM4497	putative cytoplasmic protein	**-0.66**	0.54662	**-1.12**	0.01326	**0.22**	0.82830
STM4497	STM4497	putative cytoplasmic protein	**-2.80**	0.00766	**-2.32**	0.00054	**-3.57**	0.00008
STM4498	STM4498	putative inner membrane protein	**-2.73**	0.00811	**-1.98**	0.00059	**-2.65**	0.00297
STM4498	STM4498	putative inner membrane protein	**-2.07**	0.01091	**-2.20**	0.00033	**-2.60**	0.03088
STM4499	yeeN	hypothetical protein STM4499	**-1.54**	0.07409	**-0.76**	0.08260	**-1.25**	0.00884
STM4499	yeeN	hypothetical protein STM4499	**-1.98**	0.03206	**-1.15**	0.00538	**-1.71**	0.00183
STM4500	yjhP	putative SAM-dependent methyltransferase	**1.08**	0.12984	**0.35**	0.55292	**-0.68**	0.23362
STM4500	yjhP	putative SAM-dependent methyltransferase	**2.52**	0.00747	**0.76**	0.03519	**0.58**	0.22942
STM4501	STM4501	putative cytoplasmic protein	**-0.11**	0.87190	**-0.30**	0.42969	**-1.34**	0.02026
STM4501	STM4501	putative cytoplasmic protein	**1.32**	0.09063	**-0.18**	0.59323	**0.16**	0.77578
STM4502	STM4502	putative cytoplasmic protein	**-0.42**	0.61303	**-0.43**	0.22658	**-1.12**	0.12206
STM4502	STM4502	putative cytoplasmic protein	**1.04**	0.12316	**0.14**	0.73784	**0.48**	0.34019
STM4503	STM4503	putative inner membrane protein	**0.54**	0.35802	**-0.67**	0.04038	**-0.23**	0.66365
STM4503	STM4503	putative inner membrane protein	**0.33**	0.71355	**-0.59**	0.13241	**0.63**	0.25087
STM4504	STM4504	putative cytoplasmic protein	**-0.35**	0.50561	**-0.42**	0.30986	**-0.37**	0.40732
STM4504	STM4504	putative cytoplasmic protein	**-0.21**	0.64857	**0.91**	0.43581	**-0.16**	0.67534
STM4505	STM4505	hypothetical protein STM4505	**-0.72**	0.18157	**0.49**	0.15151	**0.13**	0.80148
STM4505	STM4505	hypothetical protein STM4505	**1.36**	0.02953	**0.29**	0.44901	**1.51**	0.00772
STM4506	STM4506	putative dienelactone hydrolase	**-0.48**	0.58533	**0.98**	0.03058	**0.30**	0.58446
STM4506	STM4506	putative dienelactone hydrolase	**-0.38**	0.72686	**0.18**	0.71739	**-2.57**	0.00289
STM4507	uxuR	uxu operon transcriptional repressor	**0.04**	0.91878	**0.01**	0.97910	**0.27**	0.54419
STM4507	uxuR	uxu operon transcriptional repressor	**2.09**	0.03082	**0.21**	0.49667	**0.99**	0.07727
STM4508	trpS2	tryptophanyl-tRNA synthetase	**0.66**	0.41036	**1.16**	0.04255	**0.35**	0.56939
STM4508	trpS2	tryptophanyl-tRNA synthetase	**1.70**	0.01186	**1.17**	0.00274	**1.54**	0.00206
STM4508,1N	STM4508,1N	hypothetical protein STM4508,1N	**0.47**	0.41805	**0.04**	0.94075	**0.70**	0.25051
STM4508,1N	STM4508,1N	hypothetical protein STM4508,1N	**0.42**	0.51924	**0.22**	0.59493	**0.83**	0.12510
STM4509,S	STM4509,S	putative cytoplasmic protein	**-0.40**	0.61730	**-1.23**	0.02149	**0.33**	0.61447
STM4509,S	STM4509,S	putative cytoplasmic protein	**0.59**	0.17543	**-0.99**	0.04525	**-0.59**	0.21048
STM4510	STM4510	putative aspartate racemase	**0.15**	0.84395	**0.08**	0.79364	**-0.75**	0.05569
STM4510	STM4510	putative aspartate racemase	**0.82**	0.09088	**-0.89**	0.02010	**0.44**	0.42861
STM4511	yjiE	putative transcriptional regulator	**-0.01**	0.98487	**-0.01**	0.98374	**-1.40**	0.04452
STM4511	yjiE	putative transcriptional regulator	**0.74**	0.19476	**-1.03**	0.09077	**-0.23**	0.80333
STM4512	iadA	isoaspartyl dipeptidase	**-1.13**	0.07935	**-0.92**	0.02411	**-1.98**	0.01056
STM4512	iadA	isoaspartyl dipeptidase	**0.06**	0.89580	**-1.10**	0.01965	**-0.18**	0.64989
STM4513	yjiG	putative permease	**-0.90**	0.13699	**-0.79**	0.10545	**-1.78**	0.00287
STM4513	yjiG	putative permease	**-1.93**	0.06717	**-0.87**	0.05534	**-1.00**	0.09460
STM4514,S	yjiH	putative inner membrane protein	**0.69**	0.44323	**0.46**	0.18770	**1.69**	0.02569
STM4514,S	yjiH	putative inner membrane protein	**1.58**	0.02729	**-0.93**	0.16749	**0.41**	0.31796
STM4515	yjiJ	putative sugar transporter	**-0.63**	0.28070	**0.04**	0.94477	**-0.40**	0.42033
STM4515	yjiJ	putative sugar transporter	**0.19**	0.70217	**-0.24**	0.44715	**-0.14**	0.77368
STM4516	yjiN	putative inner membrane protein	**0.88**	0.15034	**-0.57**	0.07960	**0.38**	0.35208
STM4516	yjiN	putative inner membrane protein	**0.27**	0.54056	**-1.60**	0.00136	**0.81**	0.14324
STM4517	yjiO	putative transport protein	**-0.43**	0.49156	**0.39**	0.47083	**-0.59**	0.44769
STM4517	yjiO	putative transport protein	**0.91**	0.21565	**-0.02**	0.95835	**-0.45**	0.38913
STM4518	STM4518	putative inner membrane protein	**-0.11**	0.89213	**-0.67**	0.17657	**0.55**	0.41169
STM4518	STM4518	putative inner membrane protein	**-0.21**	0.75179	**-0.76**	0.07870	**0.91**	0.12410
STM4519	STM4519	putative NAD-dependent aldehyde dehydrogenase	**-0.53**	0.23646	**0.38**	0.38822	**2.47**	0.00030
STM4519	STM4519	putative NAD-dependent aldehyde dehydrogenase	**0.79**	0.40785	**0.59**	0.10495	**3.06**	0.00010
STM4522	STM4522	putative inner membrane protein	**0.74**	0.31482	**1.36**	0.00570	**2.43**	0.00246
STM4522	STM4522	putative inner membrane protein	**1.68**	0.09435	**2.14**	0.00056	**4.44**	0.00021
STM4523	yjiW	putative SOS response protein	**0.12**	0.78605	**-0.20**	0.50910	**0.63**	0.14152
STM4523	yjiW	putative SOS response protein	**0.51**	0.27339	**-1.33**	0.01308	**1.88**	0.00576
STM4524	hsdS	type I restriction enzyme specificity protein	**1.33**	0.47149	**-1.09**	0.02271	**0.18**	0.72352
STM4524	hsdS	type I restriction enzyme specificity protein	**2.33**	0.10533	**-0.94**	0.01079	**0.59**	0.43897
STM4525	hsdM	DNA methylase M	**-1.09**	0.19652	**-1.68**	0.00425	**-2.00**	0.00119
STM4525	hsdM	DNA methylase M	**0.05**	0.96762	**-2.31**	0.00075	**-2.39**	0.00038

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	Gene	Product	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value	log2Ratio (M)	*p* value
STM4526	hsdR	endonuclease R	**-1.09**	0.16213	**-1.46**	0.00316	**-2.03**	0.00096
STM4526	hsdR	endonuclease R	**-0.04**	0.92457	**-1.39**	0.00856	**1.57**	0.01514
STM4527	mrr	restriction endonuclease	**-0.44**	0.32184	**-0.05**	0.88331	**-1.58**	0.01034
STM4527	mrr	restriction endonuclease	**0.19**	0.66101	**0.33**	0.47252	**0.41**	0.29099
STM4528	STM4528	putative inner membrane protein	**1.60**	0.11374	**1.55**	0.00187	**1.03**	0.08590
STM4528	STM4528	putative inner membrane protein	**1.22**	0.05393	**1.39**	0.02907	**1.70**	0.00388
STM4529	STM4529	putative cytoplasmic protein	**1.20**	0.03938	**1.71**	0.00203	**0.04**	0.93102
STM4529	STM4529	putative cytoplasmic protein	**2.35**	0.04252	**1.84**	0.00161	**1.29**	0.01268
STM4530	yjiA	putative cobalamin biosynthetic protein	**0.20**	0.90987	**0.97**	0.01793	**3.69**	0.00656
STM4530	yjiA	putative cobalamin biosynthetic protein	**0.11**	0.93472	**1.28**	0.13745	**2.91**	0.00021
STM4531	yjiX	putative cytoplasmic protein	**-0.61**	0.30207	**0.33**	0.40862	**-0.57**	0.25048
STM4531	yjiX	putative cytoplasmic protein	**0.77**	0.13539	**0.24**	0.52479	**-0.30**	0.46857
STM4532	yjiY	putative carbon starvation protein	**-0.66**	0.36449	**-1.38**	0.00281	**-1.68**	0.01307
STM4532	yjiY	putative carbon starvation protein	**0.42**	0.57777	**-0.81**	0.01816	**-0.11**	0.76437
STM4533	tsr	methyl-accepting chemotaxis protein I	**-2.14**	0.01146	**-3.64**	0.00001	**-3.48**	0.00014
STM4533	tsr	methyl-accepting chemotaxis protein I	**-1.18**	0.04024	**-4.08**	0.00003	**-3.17**	0.00080
STM4534	STM4534	putative transcriptional regulator	**2.27**	0.15459	**1.01**	0.13882	**4.04**	0.00043
STM4534	STM4534	putative transcriptional regulator	**0.95**	0.56507	**-1.02**	0.22427	**-0.89**	0.12941
STM4535	STM4535	putative PTS permease	**1.75**	0.02585	**0.22**	0.81909	**2.64**	0.00092
STM4535	STM4535	putative PTS permease	**1.64**	0.01731	**1.03**	0.04120	**2.18**	0.01355
STM4536	STM4536	putative PTS permease	**1.87**	0.04620	**-0.79**	0.05585	**-0.42**	0.49988
STM4536	STM4536	putative PTS permease	**0.86**	0.28785	**-2.28**	0.00399	**1.32**	0.05852
STM4537	STM4537	putative PTS permease	**0.42**	0.51858	**0.90**	0.01590	**0.13**	0.83010
STM4537	STM4537	putative PTS permease	**1.23**	0.22938	**-1.03**	0.10414	**0.87**	0.29544
STM4538	STM4538	putative PTS permease	**-0.65**	0.32104	**0.83**	0.05666	**-0.94**	0.04274
STM4538	STM4538	putative PTS permease	**0.50**	0.36015	**0.02**	0.94914	**0.71**	0.12583
STM4539	STM4539	putative glucosamine-fructose-6-phosphate	**-0.90**	0.10271	**0.43**	0.17560	**-0.51**	0.20551
STM4539	STM4539	putative glucosamine-fructose-6-phosphate	**0.12**	0.80932	**0.37**	0.29161	**0.19**	0.72603
STM4540,S	STM4540,S	putative glucosamine-fructose-6-phosphate	**-1.14**	0.03293	**0.56**	0.06054	**-0.16**	0.66848
STM4540,S	STM4540,S	putative glucosamine-fructose-6-phosphate	**-1.04**	0.05158	**0.16**	0.59333	**-0.50**	0.30418
STM4541	mdoB	phosphoglycerol transferase I	**-0.39**	0.37993	**0.77**	0.02548	**-0.14**	0.75282
STM4541	mdoB	phosphoglycerol transferase I	**0.17**	0.69052	**0.32**	0.29952	**-0.10**	0.78397
STM4542	yjjA	putative outer membrane protein	**0.18**	0.80130	**0.79**	0.04308	**-0.56**	0.13379
STM4542	yjjA	putative outer membrane protein	**1.18**	0.16904	**1.05**	0.03113	**0.06**	0.89078
STM4543	dnaC	DNA replication protein DnaC	**0.71**	0.38042	**0.41**	0.27622	**-0.89**	0.14647
STM4543	dnaC	DNA replication protein DnaC	**0.69**	0.19277	**0.22**	0.56202	**-0.18**	0.75154
STM4544	dnaT	primosomal protein I	**-1.65**	0.01391	**-0.33**	0.25307	**-2.31**	0.00121
STM4544	dnaT	primosomal protein I	**-0.75**	0.20928	**-0.71**	0.07330	**-1.14**	0.01723
STM4545	STM4545	putative inner membrane protein	**-0.52**	0.27378	**-0.72**	0.17617	**-0.31**	0.62362
STM4545	STM4545	putative inner membrane protein	**0.45**	0.43576	**-0.88**	0.01574	**-1.02**	0.08316
STM4546	yjjP	hypothetical protein STM4546	**-0.76**	0.10952	**0.38**	0.34523	**0.25**	0.50795
STM4546	yjjP	hypothetical protein STM4546	**-1.54**	0.09359	**-0.93**	0.01367	**-0.56**	0.30735
STM4547	yjjQ	putative transcriptional regulator	**0.12**	0.90146	**0.71**	0.10203	**-0.85**	0.27459
STM4547	yjjQ	putative transcriptional regulator	**0.42**	0.50971	**0.77**	0.04063	**0.32**	0.59735
STM4548	bglJ	bgl operon transcriptional activator	**0.52**	0.25728	**0.97**	0.01100	**-1.64**	0.03831
STM4548	bglJ	bgl operon transcriptional activator	**0.58**	0.32630	**1.42**	0.00344	**-1.41**	0.03000
STM4549	STM4549	putative cytoplasmic protein	**0.42**	0.59119	**1.03**	0.02099	**-0.35**	0.34408
STM4549	STM4549	putative cytoplasmic protein	**0.80**	0.11786	**0.81**	0.03622	**-1.21**	0.01559
STM4550	fhuF	ferric hydrozamate transport protein	**-0.31**	0.49184	**0.86**	0.01793	**-0.88**	0.04036
STM4550	fhuF	ferric hydrozamate transport protein	**0.66**	0.53018	**0.74**	0.06057	**-0.51**	0.28325
STM4551	STM4551	hypothetical protein STM4551	**-0.22**	0.65238	**0.94**	0.05464	**-0.50**	0.22282
STM4551	STM4551	hypothetical protein STM4551	**2.31**	0.19487	**0.59**	0.18819	**0.32**	0.53264
STM4552	STM4552	putative inner membrane protein	**0.17**	0.76033	**2.21**	0.00014	**1.82**	0.00188
STM4552	STM4552	putative inner membrane protein	**0.95**	0.06717	**2.47**	0.00014	**2.83**	0.00043
STM4553	leuV	STM4553	**-1.05**	0.20025	**-2.11**	0.00087	**-0.05**	0.90354
STM4553	leuV	STM4553	**-0.17**	0.74672	**-2.19**	0.00092	**-0.20**	0.66456
STM4554	leuP	STM4554	**-0.26**	0.77318	**-1.71**	0.00055	**0.23**	0.59945
STM4554	leuP	STM4554	**0.95**	0.20082	**-1.65**	0.00056	**0.83**	0.04732
STM4555	leuQ	STM4555	**-1.07**	0.07902	**-2.26**	0.00268	**-0.53**	0.25525
STM4555	leuQ	STM4555	**-0.83**	0.14404	**-2.30**	0.00056	**-0.40**	0.32607
STM4556	rsmC	16S ribosomal RNA m2G1207 methyltransferase	**-0.93**	0.09618	**-1.09**	0.00518	**-1.36**	0.02158
STM4556	rsmC	16S ribosomal RNA m2G1207 methyltransferase	**-1.23**	0.02908	**-0.89**	0.05197	**-0.83**	0.04207
STM4558	rimI	ribosomal-protein-alanine N-acetyltransferase	**-1.36**	0.02289	**0.04**	0.90202	**-1.43**	0.01054
STM4558	rimI	ribosomal-protein-alanine N-acetyltransferase	**0.12**	0.91761	**-0.29**	0.31472	**-1.31**	0.01831
STM4559,S	yjjG	nucleotidase	**-2.44**	0.00747	**-1.11**	0.00528	**-2.06**	0.00453
STM4559,S	yjjG	nucleotidase	**-0.89**	0.07511	**-1.03**	0.01594	**-2.19**	0.01484
STM4560	prfC	peptide chain release factor 3	**-1.36**	0.02904	**0.14**	0.62082	**0.77**	0.10427
STM4560	prfC	peptide chain release factor 3	**-1.45**	0.02479	**-0.21**	0.52471	**-0.14**	0.71886
STM4561	osmY	hyperosmotically-inducible periplasmic protein	**1.93**	0.02823	**3.95**	0.00001	**5.73**	0.00002
STM4561	osmY	hyperosmotically-inducible periplasmic protein	**2.21**	0.01013	**4.01**	0.00003	**6.64**	0.00002

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM4562	STM4562	putative inner membrane protein	**-0.51**	0.34388	**1.41**	0.00353	**2.53**	0.00035
STM4562	STM4562	putative inner membrane protein	**1.53**	0.09713	**1.75**	0.00047	**3.65**	0.00009
STM4563	yjjU	putative phosphoesterase	**-0.74**	0.17783	**-0.22**	0.58486	**-0.73**	0.05713
STM4563	yjjU	putative phosphoesterase	**-0.30**	0.48347	**0.21**	0.58853	**-0.31**	0.50011
STM4564	yjjV	putative hydrolase	**0.50**	0.51151	**0.40**	0.38752	**1.44**	0.13388
STM4564	yjjV	putative hydrolase	**0.48**	0.40763	**0.88**	0.19798	**0.66**	0.25601
STM4565	yjjW	pyruvate formate lyase-activating enzyme	**0.21**	0.79552	**-0.45**	0.26173	**-0.01**	0.97999
STM4565	yjjW	pyruvate formate lyase-activating enzyme	**0.17**	0.74509	**-0.58**	0.20552	**0.42**	0.61072
STM4566	yjjI	putative cytoplasmic protein	**-0.28**	0.71423	**-0.50**	0.17114	**-0.28**	0.75048
STM4566	yjjI	putative cytoplasmic protein	**1.27**	0.16530	**-0.66**	0.09650	**1.03**	0.07184
STM4567	deoC	deoxyribose-phosphate aldolase	**-1.08**	0.05743	**-1.44**	0.00407	**-2.25**	0.00093
STM4567	deoC	deoxyribose-phosphate aldolase	**0.13**	0.84287	**-1.20**	0.00609	**-1.44**	0.01221
STM4568	deoA	thymidine phosphorylase	**-3.01**	0.00686	**-2.30**	0.00170	**-1.30**	0.00497
STM4568	deoA	thymidine phosphorylase	**-1.80**	0.01237	**-1.50**	0.00478	**-1.26**	0.00714
STM4569	deoB	phosphopentomutase	**-3.33**	0.00547	**-1.68**	0.00116	**-1.11**	0.03008
STM4569	deoB	phosphopentomutase	**-1.76**	0.03039	**-1.16**	0.00864	**-0.90**	0.10129
STM4570	deoD	purine nucleoside phosphorylase	**-2.43**	0.00650	**-1.36**	0.09258	**-2.85**	0.00049
STM4570	deoD	purine nucleoside phosphorylase	**-1.13**	0.05582	**-1.50**	0.00097	**-1.90**	0.00159
STM4571	STM4571	putative outer membrane protein	**-0.72**	0.13002	**-1.50**	0.00265	**-0.98**	0.09367
STM4571	STM4571	putative outer membrane protein	**-0.24**	0.70460	**-1.40**	0.00259	**-0.60**	0.19870
STM4572	stjB	putative fimbrial usher protein	**1.17**	0.05004	**-0.18**	0.69710	**1.49**	0.04142
STM4572	stjB	putative fimbrial usher protein	**1.09**	0.04333	**-1.16**	0.08690	**1.27**	0.03277
STM4573	stjC	putative fimbrial chaparone	**-0.49**	0.41282	**0.24**	0.66349	**1.88**	0.00848
STM4573	stjC	putative fimbrial chaparone	**0.00**	0.99986	**-0.72**	0.07141	**-0.43**	0.47000
STM4574	STM4574	putative outer membrane protein	**0.08**	0.87265	**-0.36**	0.58303	**-0.30**	0.37744
STM4574	STM4574	putative outer membrane protein	**0.87**	0.10480	**0.56**	0.20511	**0.40**	0.42975
STM4575	STM4575	putative outer membrane protein	**-1.20**	0.05468	**0.31**	0.39858	**-0.41**	0.35514
STM4575	STM4575	putative outer membrane protein	**-0.48**	0.28149	**-0.02**	0.95492	**0.72**	0.09571
STM4576	lplA	lipoate-protein ligase A	**-0.81**	0.23162	**0.63**	0.10323	**0.10**	0.86645
STM4576	lplA	lipoate-protein ligase A	**-0.58**	0.33225	**-0.62**	0.11905	**-0.22**	0.67615
STM4577	smp	hypothetical protein STM4577	**-1.28**	0.02526	**-0.90**	0.01539	**-2.15**	0.00289
STM4577	smp	hypothetical protein STM4577	**0.04**	0.94606	**-0.89**	0.01438	**-1.55**	0.02364
STM4578	serB	3-phosphoserine phosphatase	**-1.30**	0.13494	**-1.50**	0.00222	**-2.69**	0.00076
STM4578	serB	3-phosphoserine phosphatase	**-1.89**	0.01303	**-1.11**	0.00828	**-1.76**	0.00146
STM4579	radA	putative ATP-dependent protease	**-1.74**	0.01211	**-1.13**	0.00772	**-1.91**	0.00087
STM4579	radA	putative ATP-dependent protease	**-0.36**	0.74257	**-0.78**	0.02497	**-1.09**	0.03950
STM4580,S	nadR	nicotinamide-nucleotide adenylyltransferase	**0.65**	0.47550	**0.15**	0.68778	**0.18**	0.83509
STM4580,S	nadR	nicotinamide-nucleotide adenylyltransferase	**2.42**	0.10737	**-0.29**	0.39018	**-0.77**	0.07846
STM4581	yjjK	putative transport protein	**-1.27**	0.03742	**-0.73**	0.02607	**-1.06**	0.03328
STM4581	yjjK	putative transport protein	**-1.04**	0.15713	**-0.88**	0.03109	**-0.83**	0.08296
STM4582	slt	soluble lytic murein transglycosylase	**-0.99**	0.18729	**-1.09**	0.00529	**-1.27**	0.01077
STM4582	slt	soluble lytic murein transglycosylase	**-0.52**	0.22999	**-0.85**	0.03437	**-1.52**	0.05914
STM4583	trpR	Trp operon repressor	**-1.76**	0.01545	**-0.11**	0.72914	**-0.66**	0.11583
STM4583	trpR	Trp operon repressor	**-0.56**	0.54664	**-0.16**	0.55870	**-0.95**	0.02958
STM4584	yjjX	hypothetical protein STM4584	**-0.70**	0.22379	**-0.79**	0.02172	**-1.11**	0.01698
STM4584	yjjX	hypothetical protein STM4584	**-0.79**	0.09675	**-1.10**	0.00592	**-0.13**	0.73603
STM4585	gpmB	phosphoglycerate mutase	**-1.73**	0.01479	**-0.67**	0.03986	**-1.14**	0.01076
STM4585	gpmB	phosphoglycerate mutase	**-1.71**	0.01386	**-0.87**	0.01313	**-1.17**	0.00732
STM4586	rob	transcriptional regulator	**-0.63**	0.60678	**-0.34**	0.45371	**-0.25**	0.73668
STM4586	rob	transcriptional regulator	**-0.72**	0.26199	**-0.43**	0.16658	**-0.82**	0.06420
STM4587	creA	putative periplasmic protein	**0.40**	0.68944	**0.96**	0.01997	**-0.66**	0.11080
STM4587	creA	putative periplasmic protein	**0.86**	0.09777	**1.51**	0.00083	**-0.05**	0.92298
STM4588	creB	response regulator	**0.08**	0.94601	**-0.02**	0.94063	**-1.50**	0.00750
STM4588	creB	response regulator	**0.39**	0.53946	**0.08**	0.84363	**-1.55**	0.25424
STM4589	creC	sensor kinase	**-0.04**	0.93815	**-0.71**	0.24110	**-0.52**	0.39251
STM4589	creC	sensor kinase	**-1.68**	0.14669	**-0.57**	0.10785	**-0.33**	0.62275
STM4590	creD	colicin E2 tolerance protein	**-1.16**	0.07101	**0.54**	0.31693	**-1.08**	0.02939
STM4590	creD	colicin E2 tolerance protein	**0.30**	0.52038	**0.40**	0.61565	**0.12**	0.84355
STM4591	sthE	putative major fimbrial subunit	**0.47**	0.47919	**-0.71**	0.24578	**0.83**	0.16468
STM4591	sthE	putative major fimbrial subunit	**2.12**	0.01341	**0.16**	0.64424	**1.01**	0.03287
STM4592	sthD	putative fimbrial subunit	**-0.60**	0.35172	**0.32**	0.42050	**1.06**	0.09376
STM4592	sthD	putative fimbrial subunit	**0.45**	0.41430	**-0.39**	0.52151	**0.58**	0.41166
STM4593	sthB	putative fimbrial usher protein	**0.19**	0.84696	**0.44**	0.13690	**0.38**	0.57393
STM4593	sthB	putative fimbrial usher protein	**0.68**	0.24508	**0.28**	0.53239	**0.21**	0.73530
STM4594	sthA	putative fimbrial chaparone	**-0.57**	0.33531	**-1.15**	0.01367	**4.55**	0.00026
STM4594	sthA	putative fimbrial chaparone	**1.38**	0.03235	**-0.39**	0.40971	**4.63**	0.00049
STM4595	STM4595	putative fimbrial chaparone	**-0.51**	0.44185	**0.05**	0.87789	**-1.13**	0.03982
STM4595	STM4595	putative fimbrial chaparone	**1.09**	0.09989	**-0.46**	0.36939	**-0.72**	0.18725
STM4596	STM4596	putative inner membrane protein	**-1.18**	0.03651	**0.10**	0.75820	**-0.29**	0.42642
STM4596	STM4596	putative inner membrane protein	**0.76**	0.11826	**-0.12**	0.82352	**0.79**	0.07660

Table S2. Genome-wide expression of *Salmonella enterica* serovar Typhimurium inside fibroblasts

			Intracellular WT 24 h p.i.		Intracellular *phoP* 24 h p.i.		Extracellular WT stationary phase	
			Relative to WT exponential LB		Relative to *phoP* exponential LB		Relative to WT exponential LB	
Systematic name	**Gene**	**Product**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**	**log2Ratio (M)**	***p* value**
STM4597	STM4597	putative periplasmic protein	**-0.90**	0.06702	**-0.07**	0.82550	**-0.67**	0.33708
STM4597	STM4597	putative periplasmic protein	**-1.44**	0.02864	**-0.26**	0.41282	**-1.08**	0.05322
STM4598	arcA	response regulator	**-0.81**	0.10347	**0.43**	0.15848	**-0.31**	0.42081
STM4598	arcA	response regulator	**-0.71**	0.49101	**0.45**	0.13807	**0.25**	0.47818
STM4600	lasT	putative tRNA/tRNA methyltransferase	**-0.81**	0.19752	**-0.60**	0.19090	**-0.85**	0.10204
STM4600	lasT	putative tRNA/tRNA methyltransferase	**0.79**	0.14061	**-0.48**	0.10392	**0.65**	0.10518

Table S3. *S.* Typhimurium genes differentially expressed **(log2ratio ≤ -2 or ≥ 2)** in **intracellular WT bacteria compared to exponential LB bacteria**

Systematic name	Gene	Product	log2Ratio (M)
PSLT006	repA	DNA replication protein	**3.02**
PSLT006	repA	DNA replication protein	**2.81**
PSLT008	srgC	putative regulatory protein	**3.58**
PSLT008	srgC	putative regulatory protein	**2.32**
PSLT010	srgB	putative outer membrane protein	**3.62**
PSLT010	srgB	putative outer membrane protein	**3.38**
PSLT029	PSLT029	putative cytoplasmic protein	**2.83**
PSLT029	PSLT029	putative cytoplasmic protein	**2.6**
PSLT037	spvD	hydrophilic protein	**3.85**
PSLT037	spvD	hydrophilic protein	**3.7**
PSLT038	spvC	hydrophilic protein	**4.11**
PSLT038	spvC	hydrophilic protein	**2.24**
PSLT040	spvA	outer membrane protein	**3.52**
PSLT040	spvA	outer membrane protein	**2.09**
PSLT043	PSLT043	type II secretion system protein	**3.56**
PSLT043	PSLT043	type II secretion system protein	**2.49**
PSLT045	PSLT045	putative resolvase	**3.4**
PSLT045	PSLT045	putative resolvase	**2.88**
PSLT046	PSLT046	putative carbonic anhydrase	**3.02**
PSLT046	PSLT046	putative carbonic anhydrase	**2.61**
PSLT047	PSLT047	putative cytoplasmic protein	**3.09**
PSLT047	PSLT047	putative cytoplasmic protein	**3.05**
PSLT060	PSLT060	putative cytoplasmic protein	**4.03**
PSLT060	PSLT060	putative cytoplasmic protein	**2.57**
PSLT066	ssbB	single-strand DNA binding protein	**4.19**
PSLT066	ssbB	single-strand DNA binding protein	**3.54**
PSLT070	psiA	PsiA	**2.65**
PSLT070	psiA	PsiA	**2.27**
PSLT072	PSLT072	putative transglycosylase	**3.67**
PSLT072	PSLT072	putative transglycosylase	**2.33**
PSLT073	traM	mating signal protein	**4.91**
PSLT073	traM	mating signal protein	**4.31**
PSLT079	traE	pilus assembly protein	**2.8**
PSLT079	traE	pilus assembly protein	**2.61**
PSLT081	traB	pilus assembly protein	**2.98**
PSLT081	traB	pilus assembly protein	**2.77**
PSLT101	traG	mating pair stabilization and pilus assembly protein	**2.73**
PSLT101	traG	mating pair stabilization and pilus assembly protein	**2.02**
PSLT104	traD	ATP-binding protein/DNA transporter	**4.31**
PSLT104	traD	ATP-binding protein/DNA transporter	**2.87**
PSLT106	PSLT106	MvpA-like protein	**4.05**
PSLT106	PSLT106	MvpA-like protein	**2.56**
PSLT107	PSLT107	putative cytoplasmic protein	**4.89**
PSLT107	PSLT107	putative cytoplasmic protein	**4.36**
STM0043	rpsT	30S ribosomal protein S20	**-3.57**
STM0043	rpsT	30S ribosomal protein S20	**-3.16**
STM0056	STM0056	putative oxaloacetate decarboxylase subunit gamma	**3.6**

STM0056	STM0056	putative oxaloacetate decarboxylase subunit gamma	**3.11**
STM0091	pdxA	4-hydroxythreonine-4-phosphate dehydrogenase	**-3.52**
STM0091	pdxA	4-hydroxythreonine-4-phosphate dehydrogenase	**-3.34**
STM0124	murF	D-alanine-D-alanine ligase	**-2.54**
STM0124	murF	D-alanine-D-alanine ligase	**-2.51**
STM0128	murG	N-acetylglucosaminyl transferase	**-2.37**
STM0128	murG	N-acetylglucosaminyl transferase	**-2.25**
STM0152	aceE	pyruvate dehydrogenase E1 component	**-3.66**
STM0152	aceE	pyruvate dehydrogenase E1 component	**-2.30**
STM0153	aceF	dihydrolipoamide acetyltransferase	**-2.97**
STM0153	aceF	dihydrolipoamide acetyltransferase	**-2.82**
STM0154	lpdA	dihydrolipoamide dehydrogenase	**-3.28**
STM0154	lpdA	dihydrolipoamide dehydrogenase	**-2.62**
STM0166	speE	spermidine synthase	**-4.00**
STM0166	speE	spermidine synthase	**-3.83**
STM0191	fhuA	outer membrane ferrichrome receptor protein precursor	**-2.60**
STM0191	fhuA	outer membrane ferrichrome receptor protein precursor	**-2.24**
STM0224	yaeT	putative outer membrane protein precursor	**-3.71**
STM0224	yaeT	putative outer membrane protein precursor	**-2.87**
STM0225	hlpA	outer membrane protein H precursor	**-4.56**
STM0225	hlpA	outer membrane protein H precursor	**-3.82**
STM0226	lpxD	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	**-2.61**
STM0226	lpxD	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	**-2.60**
STM0230	rnhB	ribonuclease HII	**-3.24**
STM0230	rnhB	ribonuclease HII	**-2.66**
STM0231	dnaE	DNA polymerase III subunit alpha	**-2.46**
STM0231	dnaE	DNA polymerase III subunit alpha	**-2.21**
STM0252	rrlH	STM0252	**-2.35**
STM0252	rrlH	STM0252	**-2.08**
STM0279	STM0279	putative cytoplasmic protein	**3.46**
STM0279	STM0279	putative cytoplasmic protein	**3.03**
STM0294,1N	STM0294,1N	hypothetical protein STM0294,1N	**3.33**
STM0294,1N	STM0294,1N	hypothetical protein STM0294,1N	**3.26**
STM0295	STM0295	putative cytoplasmic protein	**3.9**
STM0295	STM0295	putative cytoplasmic protein	**3.27**
STM0339	stbB	putative fimbrial chaperone	**4.72**
STM0339	stbB	putative fimbrial chaperone	**2.29**
STM0406	yajC	preprotein translocase subunit YajC	**-2.93**
STM0406	yajC	preprotein translocase subunit YajC	**-2.85**
STM0439	cyoE	protoheme IX farnesyltransferase	**-3.45**
STM0439	cyoE	protoheme IX farnesyltransferase	**-2.53**
STM0440	cyoD	cytochrome o ubiquinol oxidase subunit IV	**-4.68**
STM0440	cyoD	cytochrome o ubiquinol oxidase subunit IV	**-4.30**
STM0441	cyoC	cytochrome o ubiquinol oxidase subunit III	**-4.01**
STM0441	cyoC	cytochrome o ubiquinol oxidase subunit III	**-3.80**
STM0442	cyoB	cytochrome o ubiquinol oxidase subunit I	**-3.65**
STM0442	cyoB	cytochrome o ubiquinol oxidase subunit I	**-2.67**
STM0443	cyoA	cytochrome o ubiquinol oxidase subunit II	**-3.56**
STM0443	cyoA	cytochrome o ubiquinol oxidase subunit II	**-2.42**
STM0445	yajG	putative lipoprotein	**-3.46**
STM0445	yajG	putative lipoprotein	**-2.53**

STM0485	ybaB	hypothetical protein STM0485	**-2.82**
STM0485	ybaB	hypothetical protein STM0485	**-2.57**
STM0486	recR	recombination protein RecR	**-3.28**
STM0486	recR	recombination protein RecR	**-2.06**
STM0494	ushA	UDP-sugar hydrolase/5'-nucleotidase	**2.51**
STM0494	ushA	UDP-sugar hydrolase/5'-nucleotidase	**2.46**
STM0548	fimF	putative fimbrial protein	**3.11**
STM0548	fimF	putative fimbrial protein	**2.93**
STM0561	STM0561	sensor kinase	**7.72**
STM0561	STM0561	sensor kinase	**6.16**
STM0581	STM0581	putative regulatory protein	**2.09**
STM0581	STM0581	putative regulatory protein	**2.06**
STM0647	rlpB	minor lipoprotein	**-2.56**
STM0647	rlpB	minor lipoprotein	**-2.20**
STM0648	leuS	leucyl-tRNA synthetase	**-3.44**
STM0648	leuS	leucyl-tRNA synthetase	**-2.22**
STM0662	gltL	glutamate/aspartate transporter	**3.41**
STM0662	gltL	glutamate/aspartate transporter	**3.37**
STM0678	leuW	STM0678	**-4.65**
STM0678	leuW	STM0678	**-4.33**
STM0679	metT	STM0679	**-3.20**
STM0679	metT	STM0679	**-3.03**
STM0688	ybfN	putative lipoprotein	**2.36**
STM0688	ybfN	putative lipoprotein	**2.05**
STM0695	ybfE	putative SOS response protein	**-2.56**
STM0695	ybfE	putative SOS response protein	**-2.25**
STM0719	STM0719	putative UDP-galactopyranose mutase	**2.6**
STM0719	STM0719	putative UDP-galactopyranose mutase	**2.1**
STM0732	sdhC	succinate dehydrogenase cytochrome b556 large membrane sul	**-2.86**
STM0732	sdhC	succinate dehydrogenase cytochrome b556 large membrane sul	**-2.28**
STM0734	sdhA	succinate dehydrogenase catalytic subunit	**-3.13**
STM0734	sdhA	succinate dehydrogenase catalytic subunit	**-2.56**
STM0737	sucB	dihydrolipoamide acetyltransferase	**-3.85**
STM0737	sucB	dihydrolipoamide acetyltransferase	**-2.43**
STM0749	pal	peptidoglycan-associated lipoprotein precursor	**-3.96**
STM0749	pal	peptidoglycan-associated lipoprotein precursor	**-2.70**
STM0763,s	STM0763,s	transcriptional regulator	**3.16**
STM0763,s	STM0763,s	transcriptional regulator	**2.69**
STM0812	ybhO	cardiolipin synthase	**2.79**
STM0812	ybhO	cardiolipin synthase	**2.33**
STM0830	glnH	glutamine ABC transporter periplasmic-binding protein	**-2.56**
STM0830	glnH	glutamine ABC transporter periplasmic-binding protein	**-2.45**
STM0908	STM0908	hypothetical protein STM0908 [Phage Fels-1]	**2.81**
STM0908	STM0908	hypothetical protein STM0908 [Phage Fels-1]	**2.58**
STM0957	cydD	cytochrome-related transporter	**-2.04**
STM0957	cydD	cytochrome-related transporter	**-2.01**
STM0965	dmsB	anaerobic dimethyl sulfoxide reductase subunit B	**3.54**
STM0965	dmsB	anaerobic dimethyl sulfoxide reductase subunit B	**2.58**
STM0982	himD	integration host factor beta subunit	**-2.76**
STM0982	himD	integration host factor beta subunit	**-2.58**
STM1000	asnS	asparaginyl-tRNA synthetase	**-2.42**

STM1000	asnS	asparaginyl-tRNA synthetase	**-2.39**
STM1006	STM1006	excisionase	**2.8**
STM1006	STM1006	excisionase	**2.32**
STM1020	STM1020	hypothetical protein STM1020 [Phage Gifsy-2]	**3.14**
STM1020	STM1020	hypothetical protein STM1020 [Phage Gifsy-2]	**2.61**
STM1041	STM1041	probable minor tail protein [Phage Gifsy-2]	**2.25**
STM1041	STM1041	probable minor tail protein [Phage Gifsy-2]	**2.23**
STM1049	STM1049	probable tail fiber protein [Phage Gifsy-2]	**3.44**
STM1049	STM1049	probable tail fiber protein [Phage Gifsy-2]	**2.22**
STM1070	ompA	putative hydrogenase membrane component precursor	**-2.80**
STM1070	ompA	putative hydrogenase membrane component precursor	**-2.78**
STM1071	sulA	cell division inhibitor	**-3.52**
STM1071	sulA	cell division inhibitor	**-2.36**
STM1088	**pipB**	**secreted effector protein**	**2.57**
STM1088	**pipB**	**secreted effector protein**	**2.24**
STM1091	**sopB**	**secreted effector protein**	**2.79**
STM1091	**sopB**	**secreted effector protein**	**2.5**
STM1170	mviN	putative virulence protein	**-2.36**
STM1170	mviN	putative virulence protein	**-2.22**
STM1173	flgA	flagellar basal body P-ring biosynthesis protein	**-3.72**
STM1173	flgA	flagellar basal body P-ring biosynthesis protein	**-2.66**
STM1174	flgB	flagellar basal body rod protein	**-3.88**
STM1174	flgB	flagellar basal body rod protein	**-3.20**
STM1175	flgC	flagellar basal body rod protein	**-3.48**
STM1175	flgC	flagellar basal body rod protein	**-2.10**
STM1177	flgE	flagellar hook protein	**-3.55**
STM1177	flgE	flagellar hook protein	**-2.30**
STM1181	flgI	flagellar P-ring protein precursor	**-3.64**
STM1181	flgI	flagellar P-ring protein precursor	**-2.80**
STM1183	flgK	flagellar hook-associated protein	**-3.26**
STM1183	flgK	flagellar hook-associated protein	**-3.25**
STM1190	yceD	putative metal-binding protein	**-4.19**
STM1190	yceD	putative metal-binding protein	**-3.62**
STM1193	fabH	3-oxoacyl-(acyl carrier protein) synthase	**-2.54**
STM1193	fabH	3-oxoacyl-(acyl carrier protein) synthase	**-2.28**
STM1195	fabG	3-ketoacyl-(acyl-carrier-protein) reductase	**-3.50**
STM1195	fabG	3-ketoacyl-(acyl-carrier-protein) reductase	**-3.43**
STM1197	fabF	3-oxoacyl-(acyl carrier protein) synthase	**-2.89**
STM1197	fabF	3-oxoacyl-(acyl carrier protein) synthase	**-2.36**
STM1200	tmk	thymidylate kinase	**-2.43**
STM1200	tmk	thymidylate kinase	**-2.17**
STM1205	ycfF	putative protein kinase C inhibitor	**-2.66**
STM1205	ycfF	putative protein kinase C inhibitor	**-2.29**
STM1240	envF	putative envelope lipoprotein	**3.87**
STM1240	envF	putative envelope lipoprotein	**2.55**
STM1246	**pagC**	**virulence membrane protein PAGC precursor**	**3.23**
STM1246	**pagC**	**virulence membrane protein PAGC precursor**	**2.25**
STM1251	STM1251	putative molecular chaperone	**2.93**
STM1251	STM1251	putative molecular chaperone	**2.56**
STM1284	yeaH	hypothetical protein STM1284	**5.57**
STM1284	yeaH	hypothetical protein STM1284	**4.62**

STM1297	selD	selenophosphate synthetase	**2.99**
STM1297	selD	selenophosphate synthetase	**2.56**
STM1313	celB	sugar-specific enzyme II	**3.03**
STM1313	celB	sugar-specific enzyme II	**2.47**
STM1329	STM1329	putative inner membrane protein	**3.72**
STM1329	STM1329	putative inner membrane protein	**2.18**
STM1334,c	infC	translation initiation factor IF-3	**-2.87**
STM1334,c	infC	translation initiation factor IF-3	**-2.53**
STM1376	lppB	putative methyl-accepting chemotaxis protein	**-2.78**
STM1376	lppB	putative methyl-accepting chemotaxis protein	**-2.27**
STM1377	lpp	murein lipoprotein	**-3.96**
STM1377	lpp	murein lipoprotein	**-3.43**
STM1378	pykF	pyruvate kinase	**-3.38**
STM1378	pykF	pyruvate kinase	**-2.48**
STM1398	**sseB**	**translocation machinery component**	**2.92**
STM1398	**sseB**	**translocation machinery component**	**2.89**
STM1399	**sscA**	**secretion system chaperone**	**4.21**
STM1399	**sscA**	**secretion system chaperone**	**3.16**
STM1402	**sseE**	**secreted effector protein**	**3.51**
STM1402	**sseE**	**secreted effector protein**	**2.39**
STM1466	ydgA	putative periplasmic protein	**-2.30**
STM1466	ydgA	putative periplasmic protein	**-2.11**
STM1499	STM1499	putative dimethyl sulphoxide reductase chain A1	**4.09**
STM1499	STM1499	putative dimethyl sulphoxide reductase chain A1	**3.96**
STM1510	ydfH	putative regulatory protein	**3.1**
STM1510	ydfH	putative regulatory protein	**2.37**
STM1535	STM1535	putative hydrogenase protein	**3.96**
STM1535	STM1535	putative hydrogenase protein	**2.86**
STM1568	fdnI	formate dehydrogenase-N gamma subunit	**3.4**
STM1568	fdnI	formate dehydrogenase-N gamma subunit	**2.73**
STM1572	nmpC	putative outer membrane porin precursor	**-3.69**
STM1572	nmpC	putative outer membrane porin precursor	**-2.09**
STM1577	narZ	nitrate reductase 2 alpha subunit	**4.53**
STM1577	narZ	nitrate reductase 2 alpha subunit	**2.91**
STM1686	pspE	phage shock protein	**3.12**
STM1686	pspE	phage shock protein	**2.04**
STM1688	pspC	phage shock protein	**3.83**
STM1688	pspC	phage shock protein	**3.22**
STM1689	pspB	phage shock protein B	**5.81**
STM1689	pspB	phage shock protein B	**4.46**
STM1690	pspA	phage shock protein	**5.27**
STM1690	pspA	phage shock protein	**4.41**
STM1731	STM1731	putative catalase	**3.07**
STM1731	STM1731	putative catalase	**2.73**
STM1774	sirC	transcriptional regulator	**-2.26**
STM1774	sirC	transcriptional regulator	**-2.16**
STM1777	hemA	glutamyl-tRNA reductase	**-2.97**
STM1777	hemA	glutamyl-tRNA reductase	**-2.25**
STM1779	ipk	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase	**-3.30**
STM1779	ipk	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase	**-2.98**
STM1786	STM1786	hydrogenase-1 small subunit	**4.66**

STM1786	STM1786	hydrogenase-1 small subunit	**2.72**
STM1837	cspC	cold shock protein	**-3.63**
STM1837	cspC	cold shock protein	**-2.05**
STM1846	proQ	putative solute/DNA competence effector	**-3.60**
STM1846	proQ	putative solute/DNA competence effector	**-2.90**
STM1868	**mig-3**	**phage-tail assembly-like protein**	**4.72**
STM1868	**mig-3**	**phage-tail assembly-like protein**	**3.84**
STM1869	STM1869	phage-tail assembly-like protein	**5.63**
STM1869	STM1869	phage-tail assembly-like protein	**2.63**
STM1882	yebG	DNA damage-inducible protein	**2.87**
STM1882	yebG	DNA damage-inducible protein	**2.11**
STM1883	purT	5'-phosphoribosylglycinamide transformylase	**3.25**
STM1883	purT	5'-phosphoribosylglycinamide transformylase	**3.02**
STM1905	yecO	putative SAM-dependent methyltransferase	**-2.30**
STM1905	yecO	putative SAM-dependent methyltransferase	**-2.20**
STM1916	cheY	chemotaxis regulator	**-5.49**
STM1916	cheY	chemotaxis regulator	**-3.66**
STM1917	cheB	chemotaxis-specific methylesterase	**-4.75**
STM1917	cheB	chemotaxis-specific methylesterase	**-3.90**
STM1921	cheA	chemotaxis sensory histidine protein kinase	**-3.61**
STM1921	cheA	chemotaxis sensory histidine protein kinase	**-3.19**
STM1922	motB	flagellar motor protein	**-2.77**
STM1922	motB	flagellar motor protein	**-2.58**
STM1943	cysT	STM1943	**-2.90**
STM1943	cysT	STM1943	**-2.80**
STM1958	fliB	lysine-N-methylase	**-2.57**
STM1958	fliB	lysine-N-methylase	**-2.52**
STM1959	fliC	flagellar biosynthesis protein	**-4.90**
STM1959	fliC	flagellar biosynthesis protein	**-3.82**
STM1961	fliS	flagellar protein FliS	**-3.64**
STM1961	fliS	flagellar protein FliS	**-2.74**
STM1962	fliT	possible FliD export chaperone	**-2.66**
STM1962	fliT	possible FliD export chaperone	**-2.57**
STM1969	fliF	flagellar M-ring protein	**-3.40**
STM1969	fliF	flagellar M-ring protein	**-2.24**
STM1970	fliG	flagellar motor protein	**-3.89**
STM1970	fliG	flagellar motor protein	**-3.03**
STM1971	fliH	flagellar assembly protein	**-4.84**
STM1971	fliH	flagellar assembly protein	**-3.13**
STM1974	fliK	flagellar hook-length control protein	**-2.84**
STM1974	fliK	flagellar hook-length control protein	**-2.33**
STM1975	fliL	flagellar biosynthesis protein	**-2.53**
STM1975	fliL	flagellar biosynthesis protein	**-2.31**
STM1976	fliM	flagellar motor switch protein	**-3.97**
STM1976	fliM	flagellar motor switch protein	**-2.85**
STM1977	fliN	flagellar motor switch protein	**-3.07**
STM1977	fliN	flagellar motor switch protein	**-2.77**
STM1978	fliO	flagellar biosynthetic protein	**-3.02**
STM1978	fliO	flagellar biosynthetic protein	**-2.02**
STM2054	pduT	polyhedral body protein	**2.58**
STM2054	pduT	polyhedral body protein	**2.14**

STM2082	rfbP	undecaprenol-phosphate galactosephosphotransferase/O-antige	**-3.06**
STM2082	rfbP	undecaprenol-phosphate galactosephosphotransferase/O-antige	**-2.95**
STM2085	rfbN	rhamnosyl transferase	**-3.93**
STM2085	rfbN	rhamnosyl transferase	**-2.53**
STM2087	rfbV	abequosyltransferase	**-4.02**
STM2087	rfbV	abequosyltransferase	**-2.75**
STM2090	rfbH	CDP-6-deoxy-D-xylo-4-hexulose-3-dehydrase	**-3.00**
STM2090	rfbH	CDP-6-deoxy-D-xylo-4-hexulose-3-dehydrase	**-2.89**
STM2094	rfbC	dTDP-4,deoxyrhamnose 3,5 epimerase	**-3.04**
STM2094	rfbC	dTDP-4,deoxyrhamnose 3,5 epimerase	**-2.83**
STM2138	STM2138	putative cytoplasmic protein	**3.1**
STM2138	STM2138	putative cytoplasmic protein	**2.74**
STM2139,2n	STM2139,2n	hypothetical protein STM2139,2n	**2.07**
STM2139,2n	STM2139,2n	hypothetical protein STM2139,2n	**2.04**
STM2160	yehV	putative transcriptional repressor	**3.14**
STM2160	yehV	putative transcriptional repressor	**2.38**
STM2206	fruF	phosphoenolpyruvate-dependent sugar phosphotransferase syst	**-2.48**
STM2206	fruF	phosphoenolpyruvate-dependent sugar phosphotransferase syst	**-2.35**
STM2227	yejL	putative cytoplasmic protein	**-2.27**
STM2227	yejL	putative cytoplasmic protein	**-2.20**
STM2267	ompC	outer membrane protein C precursor	**-4.48**
STM2267	ompC	outer membrane protein C precursor	**-3.54**
STM2285	glpB	anaerobic glycerol-3-phosphate dehydrogenase subunit B	**2.35**
STM2285	glpB	anaerobic glycerol-3-phosphate dehydrogenase subunit B	**2.05**
STM2317	nuoM	NADH dehydrogenase subunit M	**-4.87**
STM2317	nuoM	NADH dehydrogenase subunit M	**-3.91**
STM2318	nuoL	NADH dehydrogenase subunit L	**-3.74**
STM2318	nuoL	NADH dehydrogenase subunit L	**-2.24**
STM2319	nuoK	NADH dehydrogenase kappa subunit	**-3.43**
STM2319	nuoK	NADH dehydrogenase kappa subunit	**-2.16**
STM2322	nuoH	NADH dehydrogenase subunit H	**-3.58**
STM2322	nuoH	NADH dehydrogenase subunit H	**-2.48**
STM2323,S	nuoG	NADH dehydrogenase gamma subunit	**-2.12**
STM2323,S	nuoG	NADH dehydrogenase gamma subunit	**-2.08**
STM2324	nuoF	NADH dehydrogenase I chain F	**-3.95**
STM2324	nuoF	NADH dehydrogenase I chain F	**-2.69**
STM2325	nuoE	ATP synthase subunit E	**-4.29**
STM2325	nuoE	ATP synthase subunit E	**-2.49**
STM2326	nuoC	NADH dehydrogenase I chain C/D	**-3.52**
STM2326	nuoC	NADH dehydrogenase I chain C/D	**-3.47**
STM2327	nuoB	NADH dehydrogenase beta subunit	**-3.50**
STM2327	nuoB	NADH dehydrogenase beta subunit	**-2.21**
STM2328	nuoA	NADH dehydrogenase alpha subunit	**-3.78**
STM2328	nuoA	NADH dehydrogenase alpha subunit	**-2.67**
STM2337	ackA	acetate/propionate kinase	**-4.41**
STM2337	ackA	acetate/propionate kinase	**-3.85**
STM2370	pdxB	erythronate-4-phosphate dehydrogenase	**-3.42**
STM2370	pdxB	erythronate-4-phosphate dehydrogenase	**-3.34**
STM2393	yfdC	hypothetical protein STM2393	**4.12**
STM2393	yfdC	hypothetical protein STM2393	**3.08**
STM2419	lysV	STM2419	**-2.29**

STM2419	lysV	STM2419	**-2.17**
STM2432	ptsI	PEP-protein phosphotransferase	**-2.90**
STM2432	ptsI	PEP-protein phosphotransferase	**-2.12**
STM2461	eutG	putative transport protein	**3.3**
STM2461	eutG	putative transport protein	**3.18**
STM2470	eutS	putative carboxysome structural protein	**4.65**
STM2470	eutS	putative carboxysome structural protein	**4.11**
STM2475	STM2475	putative cytoplasmic protein	**7.1**
STM2475	STM2475	putative cytoplasmic protein	**5.91**
STM2489	dapA	dihydrodipicolinate synthase	**-3.32**
STM2489	dapA	dihydrodipicolinate synthase	**-2.91**
STM2520	yfgL	putative serine/threonine protein kinase	**-2.42**
STM2520	yfgL	putative serine/threonine protein kinase	**-2.40**
STM2523	gcpE	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	**-3.06**
STM2523	gcpE	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	**-2.14**
STM2525	yfgB	putative FeS redox enzyme	**-2.54**
STM2525	yfgB	putative FeS redox enzyme	**-2.51**
STM2537	yfhJ	hypothetical protein STM2537	**-4.72**
STM2537	yfhJ	hypothetical protein STM2537	**-3.52**
STM2543	nifS	cysteine desulfurase	**-2.64**
STM2543	nifS	cysteine desulfurase	**-2.10**
STM2586	STM2586	phage tail assembly-like protein	**3.39**
STM2586	STM2586	phage tail assembly-like protein	**2.23**
STM2611,S	STM2611,S	endopeptidase-like protein	**3.65**
STM2611,S	STM2611,S	endopeptidase-like protein	**3.14**
STM2621	STM2621	hypothetical protein STM2621	**2.64**
STM2621	STM2621	hypothetical protein STM2621	**2.42**
STM2632	STM2632	exodeoxyribonuclease VIII-like protein [Phage Gifsy-1]	**3.82**
STM2632	STM2632	exodeoxyribonuclease VIII-like protein [Phage Gifsy-1]	**2.7**
STM2673	rplS	50S ribosomal protein L19	**-3.44**
STM2673	rplS	50S ribosomal protein L19	**-2.54**
STM2735	STM2735	hypothetical protein STM2735	**4.05**
STM2735	STM2735	hypothetical protein STM2735	**2.22**
STM2767	STM2767	putative DNA/RNA helicase	**-2.24**
STM2767	STM2767	putative DNA/RNA helicase	**-2.24**
STM2770	fljA	phase-1 flagellin repressor	**-2.82**
STM2770	fljA	phase-1 flagellin repressor	**-2.43**
STM2771	fljB	flagellar biosynthesis protein	**-4.11**
STM2771	fljB	flagellar biosynthesis protein	**-3.21**
STM2824	-	STM2824	**-2.83**
STM2824	-	STM2824	**-2.61**
STM2826	csrA	carbon storage regulator	**-2.47**
STM2826	csrA	carbon storage regulator	**-2.40**
STM2861	sitA	putative periplasmic binding protein	**3.27**
STM2861	sitA	putative periplasmic binding protein	**2.76**
STM2865	**avrA**	**secreted effector protein**	**2.8**
STM2865	**avrA**	**secreted effector protein**	**2.8**
STM2892	**invJ**	**needle length control protein**	**3.34**
STM2892	**invJ**	**needle length control protein**	**2.85**
STM2893	**invI**	**needle complex assembly protein**	**3.22**
STM2893	**invI**	**needle complex assembly protein**	**2.95**

STM2903	STM2903	putative cytoplasmic protein	**3.71**
STM2903	STM2903	putative cytoplasmic protein	**3.58**
STM2927	surE	acid phosphatase	**-2.95**
STM2927	surE	acid phosphatase	**-2.16**
STM2935	cysD	sulfate adenylyltransferase subunit 2	**3.36**
STM2935	cysD	sulfate adenylyltransferase subunit 2	**2.08**
STM2943	STM2943	putative cytoplasmic protein	**2.93**
STM2943	STM2943	putative cytoplasmic protein	**2.69**
STM2953	pyrG	CTP synthetase	**-3.17**
STM2953	pyrG	CTP synthetase	**-2.58**
STM2970	sdaC	putative serine transport protein	**-3.38**
STM2970	sdaC	putative serine transport protein	**-2.93**
STM3052	STM3052	putative outer membrane protein	**3.94**
STM3052	STM3052	putative outer membrane protein	**2.19**
STM3055	gcvT	aminomethyltransferase	**-2.76**
STM3055	gcvT	aminomethyltransferase	**-2.13**
STM3083	STM3083	putative mannitol dehydrogenase	**8.76**
STM3083	STM3083	putative mannitol dehydrogenase	**4.81**
STM3087	yqgB	putative inner membrane protein	**-2.91**
STM3087	yqgB	putative inner membrane protein	**-2.57**
STM3093	endA	DNA-specific endonuclease I	**-3.68**
STM3093	endA	DNA-specific endonuclease I	**-3.15**
STM3133	STM3133	putative amidohydrolase	**2.66**
STM3133	STM3133	putative amidohydrolase	**2.33**
STM3179	mdaB	NADPH-specific quinone oxidoreductase	**-2.22**
STM3179	mdaB	NADPH-specific quinone oxidoreductase	**-2.18**
STM3209	rpsU	30S ribosomal protein S21	**-3.12**
STM3209	rpsU	30S ribosomal protein S21	**-2.41**
STM3283	rpsO	30S ribosomal protein S15	**-2.67**
STM3283	rpsO	30S ribosomal protein S15	**-2.42**
STM3289	metY	STM3289	**2.53**
STM3289	metY	STM3289	**2.35**
STM3346	yhcM	putative ATPase	**-3.41**
STM3346	yhcM	putative ATPase	**-2.27**
STM3352	oadA	oxaloacetate decarboxylase	**3**
STM3352	oadA	oxaloacetate decarboxylase	**2.56**
STM3384	yhdG	possible dehydrogenase	**-3.74**
STM3384	yhdG	possible dehydrogenase	**-3.37**
STM3385	fis	DNA-binding protein Fis	**-3.60**
STM3385	fis	DNA-binding protein Fis	**-2.09**
STM3396	rrlD	STM3396	**-2.94**
STM3396	rrlD	STM3396	**-2.04**
STM3414	rplQ	50S ribosomal protein L17	**-4.07**
STM3414	rplQ	50S ribosomal protein L17	**-3.86**
STM3417	rpsK	30S ribosomal protein S11	**-2.22**
STM3417	rpsK	30S ribosomal protein S11	**-2.21**
STM3420	secY	preprotein translocase SecY	**-2.63**
STM3420	secY	preprotein translocase SecY	**-2.50**
STM3422	rpmD	50S ribosomal protein L30	**-2.83**
STM3422	rpmD	50S ribosomal protein L30	**-2.82**
STM3426	rpsH	30S ribosomal protein S8	**-2.72**

STM3426	rpsH	30S ribosomal protein S8	**-2.65**
STM3428	rplE	50S ribosomal protein L5	**-3.22**
STM3428	rplE	50S ribosomal protein L5	**-3.16**
STM3429	rplX	50S ribosomal protein L24	**-4.28**
STM3429	rplX	50S ribosomal protein L24	**-3.03**
STM3429	rplX	50S ribosomal protein L24	**-2.95**
STM3429	rplX	50S ribosomal protein L24	**-2.89**
STM3430	rplN	50S ribosomal protein L14	**-3.83**
STM3430	rplN	50S ribosomal protein L14	**-3.49**
STM3430	rplN	50S ribosomal protein L14	**-2.34**
STM3430	rplN	50S ribosomal protein L14	**-2.26**
STM3431	rpsQ	30S ribosomal protein S17	**-2.83**
STM3431	rpsQ	30S ribosomal protein S17	**-2.50**
STM3475	nirD	nitrite reductase small subunit	**3.63**
STM3475	nirD	nitrite reductase small subunit	**3.62**
STM3482	gph	phosphoglycolate phosphatase	**-3.45**
STM3482	gph	phosphoglycolate phosphatase	**-2.72**
STM3486	aroB	3-dehydroquinate synthase	**-2.56**
STM3486	aroB	3-dehydroquinate synthase	**-2.50**
STM3487	aroK	shikimate kinase I	**-3.28**
STM3487	aroK	shikimate kinase I	**-3.00**
STM3510	yhgH	putative amidophosphoribosyltransferase	**-2.59**
STM3510	yhgH	putative amidophosphoribosyltransferase	**-2.05**
STM3558	STM3558	death-on-curing protein	**4.75**
STM3558	STM3558	death-on-curing protein	**4.49**
STM3640	lpfA	long polar fimbrial protein A precursor	**2.16**
STM3640	lpfA	long polar fimbrial protein A precursor	**2.1**
STM3656	glyQ	glycyl-tRNA synthetase alpha subunit	**-3.02**
STM3656	glyQ	glycyl-tRNA synthetase alpha subunit	**-2.11**
STM3702	grxC	glutaredoxin 3	**-2.60**
STM3702	grxC	glutaredoxin 3	**-2.17**
STM3705	yibP	hypothetical protein STM3705	**-3.36**
STM3705	yibP	hypothetical protein STM3705	**-2.12**
STM3709	kbl	2-amino-3-ketobutyrate coenzyme A ligase	**-3.08**
STM3709	kbl	2-amino-3-ketobutyrate coenzyme A ligase	**-2.32**
STM3711	rfaF	ADP-heptose-LPS heptosyltransferase 1	**-3.26**
STM3711	rfaF	ADP-heptose-LPS heptosyltransferase 1	**-2.84**
STM3718	rfaI	lipopolysaccharide-alpha-1,3-D-galactosyltransferase	**-3.39**
STM3718	rfaI	lipopolysaccharide-alpha-1,3-D-galactosyltransferase	**-2.92**
STM3723	rfaQ	lipopolysaccharide core biosynthetic protein	**-2.88**
STM3723	rfaQ	lipopolysaccharide core biosynthetic protein	**-2.33**
STM3727	rpmG	50S ribosomal protein L33	**-3.17**
STM3727	rpmG	50S ribosomal protein L33	**-2.25**
STM3728	rpmB	50S ribosomal protein L28	**-4.10**
STM3728	rpmB	50S ribosomal protein L28	**-3.39**
STM3742	spoT	(p)ppGpp synthetase II/guanosine-3',5'-bis pyrophosphate	**-3.18**
STM3742	spoT	(p)ppGpp synthetase II/guanosine-3',5'-bis pyrophosphate	**-3.10**
STM3764	**mgtC**	**Mg2+ transport protein**	**5.18**
STM3764	**mgtC**	**Mg2+ transport protein**	**4.25**
STM3774	STM3774	putative inner membrane protein	**4.3**
STM3774	STM3774	putative inner membrane protein	**3.75**

STM3808,S	ibpB	small heat shock protein	**3.17**
STM3808,S	ibpB	small heat shock protein	**2.54**
STM3815	ccmE	periplasmic heme-dependent peroxidase	**2.85**
STM3815	ccmE	periplasmic heme-dependent peroxidase	**2.49**
STM3815	ccmE	periplasmic heme-dependent peroxidase	**2.44**
STM3815	ccmE	periplasmic heme-dependent peroxidase	**2.37**
STM3836	recF	recombination protein F	**-3.28**
STM3836	recF	recombination protein F	**-2.68**
STM3847	yidY	putative tranport protein	**2.26**
STM3847	yidY	putative tranport protein	**2.01**
STM3867	atpA	ATP synthase subunit A	**-3.90**
STM3867	atpA	ATP synthase subunit A	**-3.01**
STM3868	atpH	ATP synthase subunit D	**-3.47**
STM3868	atpH	ATP synthase subunit D	**-3.17**
STM3869	atpF	ATP synthase subunit B	**-5.00**
STM3869	atpF	ATP synthase subunit B	**-3.65**
STM3870	atpE	ATP synthase subunit C	**-3.26**
STM3870	atpE	ATP synthase subunit C	**-2.57**
STM3871	atpB	ATP synthase subunit A	**-3.74**
STM3871	atpB	ATP synthase subunit A	**-3.44**
STM3872	atpI	ATP synthase subunit I	**-3.46**
STM3872	atpI	ATP synthase subunit I	**-2.42**
STM3914	rhlB	ATP-dependent RNA helicase	**-2.53**
STM3914	rhlB	ATP-dependent RNA helicase	**-2.20**
STM3923	rffH	glucose-1-phosphate thymidyl transferase	**-2.06**
STM3923	rffH	glucose-1-phosphate thymidyl transferase	**-2.05**
STM3931	argX	STM3931	**-3.91**
STM3931	argX	STM3931	**-2.72**
STM3934	proM	STM3934	**-2.20**
STM3934	proM	STM3934	**-2.12**
STM3937	STM3937	uroporphyrinogen-III synthetase	**-3.02**
STM3937	STM3937	uroporphyrinogen-III synthetase	**-2.08**
STM3938	hemC	porphobilinogen deaminase	**-3.03**
STM3938	hemC	porphobilinogen deaminase	**-2.66**
STM3991	rrlA	STM3991	**-2.94**
STM3991	rrlA	STM3991	**-2.70**
STM3991	rrlA	STM3991	**-2.65**
STM3991	rrlA	STM3991	**-2.25**
STM4014	STM4014	putative periplasmic protein	**6.92**
STM4014	STM4014	putative periplasmic protein	**5.83**
STM4037	fdoG	formate dehydrogenase alpha subunit	**-3.06**
STM4037	fdoG	formate dehydrogenase alpha subunit	**-2.23**
STM4075	ydeY	putative sugar transport protein	**3.51**
STM4075	ydeY	putative sugar transport protein	**2.41**
STM4087	glpF	glycerol diffusion	**-2.30**
STM4087	glpF	glycerol diffusion	**-2.20**
STM4092	hslV	ATP-dependent protease peptidase subunit	**-2.78**
STM4092	hslV	ATP-dependent protease peptidase subunit	**-2.02**
STM4132	rrsB	STM4132	**-2.55**
STM4132	rrsB	STM4132	**-2.53**
STM4132	rrsB	STM4132	**-2.49**

STM4132	rrsB	STM4132	**-2.12**
STM4132	rrsB	STM4132	**-2.10**
STM4132	rrsB	STM4132	**-2.10**
STM4135	rrlB	STM4135	**-2.96**
STM4135	rrlB	STM4135	**-2.74**
STM4142	thrU	STM4142	**-3.69**
STM4142	thrU	STM4142	**-2.98**
STM4144	glyT	STM4144	**-4.73**
STM4144	glyT	STM4144	**-4.48**
STM4146	tuf	elongation factor Tu	**-2.89**
STM4146	tuf	elongation factor Tu	**-2.05**
STM4148	nusG	transcription antitermination protein NusG	**-2.94**
STM4148	nusG	transcription antitermination protein NusG	**-2.39**
STM4149	rplK	50S ribosomal protein L11	**-3.32**
STM4149	rplK	50S ribosomal protein L11	**-2.24**
STM4150	rplA	50S ribosomal protein L1	**-3.81**
STM4150	rplA	50S ribosomal protein L1	**-3.73**
STM4151	rplJ	50S ribosomal protein L10	**-2.84**
STM4151	rplJ	50S ribosomal protein L10	**-2.61**
STM4153	rpoB	DNA-directed RNA polymerase beta subunit	**-3.71**
STM4153	rpoB	DNA-directed RNA polymerase beta subunit	**-2.63**
STM4170	hupA	DNA-binding protein HU-alpha	**-4.57**
STM4170	hupA	DNA-binding protein HU-alpha	**-3.99**
STM4205	STM4205	putative phage glycosyltransferase	**3.94**
STM4205	STM4205	putative phage glycosyltransferase	**2.65**
STM4221	pgi	glucose-6-phosphate isomerase	**-4.34**
STM4221	pgi	glucose-6-phosphate isomerase	**-3.54**
STM4319	**phoN**	**non-specific acid phosphatase**	**3.43**
STM4319	**phoN**	**non-specific acid phosphatase**	**2.41**
STM4334	efp	elongation factor P	**-2.31**
STM4334	efp	elongation factor P	**-2.18**
STM4377	aidB	putative acyl-CoA dehydrogenase	**2.52**
STM4377	aidB	putative acyl-CoA dehydrogenase	**2.47**
STM4388	sgaE	L-ribulose-5-phosphate 4-epimerase	**-2.50**
STM4388	sgaE	L-ribulose-5-phosphate 4-epimerase	**-2.21**
STM4391	rpsF	30S ribosomal protein S6	**-4.73**
STM4391	rpsF	30S ribosomal protein S6	**-4.51**
STM4393	rpsR	30S ribosomal protein S18	**-3.27**
STM4393	rpsR	30S ribosomal protein S18	**-2.01**
STM4394	rplI	50S ribosomal protein L9	**-3.24**
STM4394	rplI	50S ribosomal protein L9	**-2.66**
STM4415	fbp	fructose-1,6-bisphosphatase	**-2.38**
STM4415	fbp	fructose-1,6-bisphosphatase	**-2.05**
STM4418	STM4418	sugar transporter	**3.24**
STM4418	STM4418	sugar transporter	**3.13**
STM4458	yjgF	putative translation initiation inhibitor	**-2.68**
STM4458	yjgF	putative translation initiation inhibitor	**-2.09**
STM4467	STM4467	arginine deiminase	**3.73**
STM4467	STM4467	arginine deiminase	**2.76**
STM4477	pepA	leucyl aminopeptidase	**-4.12**
STM4477	pepA	leucyl aminopeptidase	**-4.07**

STM4493	STM4493	putative cytoplasmic protein	**-2.82**
STM4493	STM4493	putative cytoplasmic protein	**-2.34**
STM4498	STM4498	putative inner membrane protein	**-2.73**
STM4498	STM4498	putative inner membrane protein	**-2.07**

Table S4. *S.* Typhimurium genes significantly **up-regulated (log2M ≥ 2) in intracellular WT** at 24 h p.i. inside fibroblasts **(51 genes, see Fig. 2A)**

Systematic name	Gene	Product
PSLT006	repA	DNA replication protein
PSLT008	srgC	putative regulatory protein
PSLT010	srgB	putative outer membrane protein
PSLT029	PSLT029	putative cytoplasmic protein
PSLT038	spvC	hydrophilic protein
PSLT046	PSLT046	putative carbonic anhydrase
PSLT066	ssbB	single-strand DNA binding protein
PSLT070	psiA	PsiA
PSLT072	PSLT072	putative transglycosylase
PSLT079	traE	pilus assembly protein
PSLT081	traB	pilus assembly protein
STM0056	STM0056	putative oxaloacetate decarboxylase subunit gamma
STM0279	STM0279	putative cytoplasmic protein
STM0339	stbB	putative fimbrial chaperone
STM0494	ushA	UDP-sugar hydrolase/5'-nucleotidase
STM0548	fimF	putative fimbrial protein
STM0561	STM0561	sensor kinase
STM0581	STM0581	putative regulatory protein
STM0662	gltL	glutamate/aspartate transporter
STM0688	ybfN	putative lipoprotein
STM0719	STM0719	putative UDP-galactopyranose mutase
STM0812	ybhO	cardiolipin synthase
STM0965	dmsB	anaerobic dimethyl sulfoxide reductase subunit B
STM1020	STM1020	hypothetical protein STM1020 [Phage Gifsy-2]
STM1041	STM1041	probable minor tail protein [Phage Gifsy-2]
STM1091	**sopB**	**secreted effector protein**
STM1246	**pagC**	**virulence membrane protein PAGC precursor**
STM1297	selD	selenophosphate synthetase
STM1499	STM1499	putative dimethyl sulphoxide reductase chain A1
STM2054	pduT	polyhedral body protein
STM2139,2n	STM2139,2n	hypothetical protein STM2139,2n
STM2285	glpB	anaerobic glycerol-3-phosphate dehydrogenase subunit B
STM2461	eutG	putative transport protein
STM2470	eutS	putative carboxysome structural protein
STM2586	STM2586	phage tail assembly-like protein
STM2632	STM2632	exodeoxyribonuclease VIII-like protein [Phage Gifsy-1]
STM2735	STM2735	hypothetical protein STM2735
STM2892	**invJ**	**needle length control protein**
STM3352	oadA	oxaloacetate decarboxylase
STM3475	nirD	nitrite reductase small subunit
STM3558	STM3558	death-on-curing protein
STM3640	lpfA	long polar fimbrial protein A precursor
STM3764	**mgtC**	**Mg2+ transport protein**
STM3808,S	ibpB	small heat shock protein
STM3815	ccmE	periplasmic heme-dependent peroxidase
STM3847	yidY	putative tranport protein
STM4075	ydeY	putative sugar transport protein
STM4205	STM4205	putative phage glycosyltransferase
STM4319	**phoN**	**non-specific acid phosphatase**
STM4377	aidB	putative acyl-CoA dehydrogenase
STM4467	STM4467	arginine deiminase

Table S5. *S.* Typhimurium genes **significantly down-regulated (log2M ≤ - 2)** in **intracellular WT** at 24 h p.i. inside fibroblasts **(48 genes, see Fig. 2A)**

Systematic name	Gene	Product
STM0128	murG	N-acetylglucosaminyl transferase
STM0191	fhuA	outer membrane ferrichrome receptor protein precursor
STM0252	rrlH	STM0252
STM0443	cyoA	cytochrome o ubiquinol oxidase subunit II
STM0445	yajG	putative lipoprotein
STM0648	leuS	leucyl-tRNA synthetase
STM0679	metT	STM0679
STM0732	sdhC	succinate dehydrogenase cytochrome b556 large membrane subunit
STM0734	sdhA	succinate dehydrogenase catalytic subunit
STM0830	glnH	glutamine ABC transporter periplasmic-binding protein
STM0982	himD	integration host factor beta subunit
STM1070	ompA	putative hydrogenase membrane component precurosr
STM1071	sulA	cell division inhibitor
STM1200	tmk	thymidylate kinase
STM1205	ycfF	putative protein kinase C inhibitor
STM1376	lppB	putative methyl-accepting chemotaxis protein
STM1378	pykF	pyruvate kinase
STM1466	ydgA	putative periplasmic protein
STM1837	cspC	cold shock protein
STM1943	cysT	STM1943
STM2227	yejL	putative cytoplasmic protein
STM2419	lysV	STM2419
STM2432	ptsI	PEP-protein phosphotransferase
STM2523	gcpE	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase
STM2543	nifS	cysteine desulfurase
STM2767	STM2767	putative DNA/RNA helicase
STM2826	csrA	carbon storage regulator
STM2953	pyrG	CTP synthetase
STM3055	gcvT	aminomethyltransferase
STM3179	mdaB	NADPH-specific quinone oxidoreductase
STM3396	rrlD	STM3396
STM3510	yhgH	putative amidophosphoribosyltransferase
STM3705	yibP	hypothetical protein STM3705
STM3711	rfaF	ADP-heptose-LPS heptosyltransferase 1
STM3931	argX	STM3931
STM3934	proM	STM3934
STM3937	STM3937	uroporphyrinogen-III synthetase
STM3938	hemC	porphobilinogen deaminase
STM3991	rrlA	STM3991
STM4037	fdoG	formate dehydrogenase alpha subunit
STM4087	glpF	glycerol diffusion
STM4092	hslV	ATP-dependent protease peptidase subunit
STM4132	rrsB	STM4132
STM4135	rrlB	STM4135
STM4142	thrU	STM4142
STM4415	fbp	fructose-1,6-bisphosphatase
STM4458	yjgF	putative translation initiation inhibitor

Table S6. *S.* Typhimurium genes **differentially expressed (log2ratio ≤ -2 or ≥ 2)** in **extracellular WT bacteria in stationary phase compared to intracellular WT (160 genes, see Fig. 3 A)**

Systematic name	Gene	Product	log2Ratio (M)	*p* value
PSLT016	pefD	chaperone	**-2.18**	0.07287299
PSLT016	pefD	chaperone	**-2.41**	0.01437791
PSLT029	PSLT029	putative cytoplasmic protein	**-2.36**	0.00246363
PSLT029	PSLT029	putative cytoplasmic protein	**-2.58**	0.00257278
PSLT045	PSLT045	putative resolvase	**-2.78**	0.00036755
PSLT045	PSLT045	putative resolvase	**-3.1**	0.00031166
PSLT066	ssbB	single-strand DNA binding protein	**-3.04**	0.01241746
PSLT066	ssbB	single-strand DNA binding protein	**-3.09**	0.01055103
PSLT106	PSLT106	MvpA-like protein	**-2.34**	0.00120928
PSLT106	PSLT106	MvpA-like protein	**-3.13**	0.00019839
PSLT107	PSLT107	putative cytoplasmic protein	**-2.68**	0.00039112
PSLT107	PSLT107	putative cytoplasmic protein	**-2.76**	0.00070774
STM0054	STM0054	putative oxalacetate decarboxylase subunit beta	**-2.11**	0.05745692
STM0054	STM0054	putative oxalacetate decarboxylase subunit beta	**-2.81**	0.0027331
STM0056	STM0056	putative oxaloacetate decarboxylase subunit gamma	**-3.63**	0.00027368
STM0056	STM0056	putative oxaloacetate decarboxylase subunit gamma	**-4.24**	0.00013461
STM0187	sfsA	sugar fermentation stimulation protein	**3.62**	0.00006678
STM0187	sfsA	sugar fermentation stimulation protein	**3.55**	0.00008693
STM0252	rrlH	STM0252	**2.53**	0.00296176
STM0252	rrlH	STM0252	**2.22**	0.00427693
STM0279	STM0279	putative cytoplasmic protein	**-2.74**	0.010131
STM0279	STM0279	putative cytoplasmic protein	**-3.44**	0.00073691
STM0323	thrW	STM0323	**4.86**	0.00001511
STM0323	thrW	STM0323	**3.03**	0.00011401
STM0340	stbA	putative fimbrial major subunit	**2.79**	0.03280989
STM0340	stbA	putative fimbrial major subunit	**2.1**	0.02989434
STM0360	STM0360	cytochrome BD2 subunit I	**3.11**	0.0101547
STM0360	STM0360	cytochrome BD2 subunit I	**2.71**	0.00106081
STM0367	prpR	prp operon regulator	**2.11**	0.01219415
STM0367	prpR	prp operon regulator	**2.01**	0.00533247
STM0392	rdgC	recombination associated protein	**-2.12**	0.01498377
STM0392	rdgC	recombination associated protein	**-2.13**	0.0443021
STM0440	cyoD	cytochrome o ubiquinol oxidase subunit IV	**2.26**	0.00157766
STM0440	cyoD	cytochrome o ubiquinol oxidase subunit IV	**2.03**	0.00294961
STM0446	bolA	putative regulatory protein	**2.52**	0.00042446
STM0446	bolA	putative regulatory protein	**2.43**	0.00075362
STM0467	ffs	STM0467	**3.91**	0.00015488
STM0467	ffs	STM0467	**3.54**	0.00029433
STM0494	ushA	UDP-sugar hydrolase/5'-nucleotidase	**-3.31**	0.00138578
STM0494	ushA	UDP-sugar hydrolase/5'-nucleotidase	**-3.49**	0.00017357
STM0561	STM0561	sensor kinase	**-3.75**	0.01980445
STM0561	STM0561	sensor kinase	**-5.48**	0.01381041
STM0629	cspE	cold shock protein E	**3.63**	0.00008701
STM0629	cspE	cold shock protein E	**3.14**	0.000138
STM0665	gltI	glutamate/aspartate transporter	**2.73**	0.0010145
STM0665	gltI	glutamate/aspartate transporter	**2.72**	0.00043043
STM0674	glnV	STM0674	**3.25**	0.0001947
STM0674	glnV	STM0674	**2.99**	0.00013932
STM0677	glnU	STM0677	**4.08**	0.00001818
STM0677	glnU	STM0677	**3.95**	0.0000344
STM0679	metT	STM0679	**4.28**	0.00001009
STM0679	metT	STM0679	**4.17**	0.00001541
STM0679	metT	STM0679	**3.69**	0.0000295
STM0679	metT	STM0679	**3.39**	0.00005216
STM0759	ybgS	hypothetical protein STM0759	**8.15**	0.00091043
STM0759	ybgS	hypothetical protein STM0759	**4.01**	0.00001493

STM0766	dcoC	putative oxaloacetate decarboxylase subunit gamma	**-2.63**	0.01637511
STM0766	dcoC	putative oxaloacetate decarboxylase subunit gamma	**-2.9**	0.01379665
STM0831	dps	DNA protection during starvation conditions	**5.97**	0.00001038
STM0831	dps	DNA protection during starvation conditions	**5.64**	0.00000307
STM0832	ybiF	putative permease	**2.68**	0.0006542
STM0832	ybiF	putative permease	**2.06**	0.00403773
STM0853	yliH	putative cytoplasmic protein	**5.47**	0.00000227
STM0853	yliH	putative cytoplasmic protein	**5.02**	0.0000039
STM0935	poxB	pyruvate dehydrogenase	**2.39**	0.00137279
STM0935	poxB	pyruvate dehydrogenase	**2.1**	0.0027414
STM0943	cspD	stress response protein	**2.74**	0.00082814
STM0943	cspD	stress response protein	**2.53**	0.00064768
STM0974	focA	putative formate transporter	**2.95**	0.0010292
STM0974	focA	putative formate transporter	**2.28**	0.00138251
STM1020	STM1020	hypothetical protein STM1020 [Phage Gifsy-2]	**-2.13**	0.01269025
STM1020	STM1020	hypothetical protein STM1020 [Phage Gifsy-2]	**-2.43**	0.00977943
STM1041	STM1041	probable minor tail protein [Phage Gifsy-2]	**-2.37**	0.01020351
STM1041	STM1041	probable minor tail protein [Phage Gifsy-2]	**-2.53**	0.00067491
STM1070	ompA	putative hydrogenase membrane component precursor	**2.86**	0.00185039
STM1070	ompA	putative hydrogenase membrane component precurosr	**2.4**	0.00076521
STM1086	serT	STM1086	**3.97**	0.00003516
STM1086	serT	STM1086	**3.29**	0.0000993
STM1117	agp	glucose-1-phosphatase	**2.69**	0.00058935
STM1117	agp	glucose-1-phosphatase	**2.53**	0.00093164
STM1119	wraB	TrpR binding protein WrbA	**3.56**	0.00005044
STM1119	wraB	TrpR binding protein WrbA	**2.9**	0.00096607
STM1121	ymdF	putative cytoplasmic protein	**4.91**	0.00000634
STM1121	ymdF	putative cytoplasmic protein	**4.9**	0.00002082
STM1165	grxB	glutaredoxin 2	**5.18**	0.00000281
STM1165	grxB	glutaredoxin 2	**4.85**	0.00000557
STM1219	ycfW	integral membrane protein	**-3.33**	0.00019499
STM1219	ycfW	integral membrane protein	**-3.96**	0.00002406
STM1246	**pagC**	**virulence membrane protein PAGC precursor**	**-2.24**	**0.00427591**
STM1246	**pagC**	**virulence membrane protein PAGC precursor**	**-2.93**	**0.00015551**
STM1254	STM1254	putative outer membrane lipoprotein	**-2.28**	0.00142488
STM1254	STM1254	putative outer membrane lipoprotein	**-2.3**	0.00209251
STM1297	selD	selenophosphate synthetase	**-3.38**	0.00008989
STM1297	selD	selenophosphate synthetase	**-3.62**	0.00009374
STM1311	osmE	transcriptional activator	**4.54**	0.00001187
STM1311	osmE	transcriptional activator	**3.62**	0.00236844
STM1398	**sseB**	**translocation machinery component**	**-3.01**	**0.00065038**
STM1398	**sseB**	**translocation machinery component**	**-4.01**	**0.00080884**
STM1440	sodC	copper/zinc superoxide dismutase	**2.94**	0.0016901
STM1440	sodC	copper/zinc superoxide dismutase	**2.94**	0.00057536
STM1441	STM1441	putative inner membrane protein	**2.91**	0.00029651
STM1441	STM1441	putative inner membrane protein	**2.81**	0.00150997
STM1499	STM1499	putative dimethyl sulphoxide reductase chain A1	**-3.05**	0.00031022
STM1499	STM1499	putative dimethyl sulphoxide reductase chain A1	**-3.69**	0.05096653
STM1563	osmC	putative envelope protein	**3.64**	0.00020283
STM1563	osmC	putative envelope protein	**3.52**	0.00005014
STM1565	rpsV	30S ribosomal subunit protein S22	**2.24**	0.00122943
STM1565	rpsV	30S ribosomal subunit protein S22	**2.02**	0.02920271
STM1578	narY	nitrate reductase 2 beta subunit	**-3.39**	0.00222554
STM1578	narY	nitrate reductase 2 beta subunit	**-6.01**	0.0012047
STM1686	pspE	phage shock protein	**-2.16**	0.00113288
STM1686	pspE	phage shock protein	**-2.62**	0.00075228
STM1687	pspD	phage shock protein	**-2.1**	0.00290842
STM1687	pspD	phage shock protein	**-3.03**	0.00016011
STM1688	pspC	phage shock protein	**-2.51**	0.00288137
STM1688	pspC	phage shock protein	**-3.26**	0.00006888
STM1689	pspB	phage shock protein B	**-3.46**	0.00011906

STM1689	pspB	phage shock protein B	**-3.82**	0.00005121
STM1690	pspA	phage shock protein	**-2.01**	0.00504211
STM1690	pspA	phage shock protein	**-2.12**	0.00284104
STM1728	yciG	putative cytoplasmic protein	**7.51**	0.00000055
STM1728	yciG	putative cytoplasmic protein	**7.32**	0.00000061
STM1730	yciE	putative cytoplasmic protein	**3.66**	0.00018435
STM1730	yciE	putative cytoplasmic protein	**3.36**	0.00008374
STM1810	STM1810	putative cytoplasmic protein	**2.7**	0.00127111
STM1810	STM1810	putative cytoplasmic protein	**2.4**	0.00276636
STM1851	STM1851	putative cytoplasmic protein	**2.32**	0.00276425
STM1851	STM1851	putative cytoplasmic protein	**2.06**	0.02158256
STM1868	**mig-3**	**phage-tail assembly-like protein**	**-2.05**	**0.01679018**
STM1868	**mig-3**	**phage-tail assembly-like protein**	**-2.09**	**0.01176625**
STM1943	cysT	STM1943	**5.09**	0.00002034
STM1943	cysT	STM1943	**4.87**	0.00000932
STM1984	yodD	putative cytoplasmic protein	**2.97**	0.00148684
STM1984	yodD	putative cytoplasmic protein	**2.47**	0.00237065
STM2018	cobU	adenosylcobinamide kinase	**-2.65**	0.00072362
STM2018	cobU	adenosylcobinamide kinase	**-2.91**	0.00093439
STM2070	yeeZ	putative dehydratase	**2.81**	0.00051622
STM2070	yeeZ	putative dehydratase	**2.6**	0.00069078
STM2169	yohC	putative transport protein	**3.89**	0.0000189
STM2169	yohC	putative transport protein	**3.49**	0.00015189
STM2311	elaB	putative inner membrane protein	**2.63**	0.00218604
STM2311	elaB	putative inner membrane protein	**2.34**	0.01075296
STM2320	nuoJ	NADH dehydrogenase subunit J	**-2.56**	0.00037133
STM2320	nuoJ	NADH dehydrogenase subunit J	**-2.8**	0.00188233
STM2346	STM2346	putative NTP pyrophosphohydrolase	**-2.12**	0.00222384
STM2346	STM2346	putative NTP pyrophosphohydrolase	**-3.02**	0.00015889
STM2383	mepA	penicillin-insensitive murein endopeptidase	**-3.2**	0.01842099
STM2383	mepA	penicillin-insensitive murein endopeptidase	**-3.24**	0.00310117
STM2389	yfcY	acetyl-CoA acetyltransferase	**-2.05**	0.00793967
STM2389	yfcY	acetyl-CoA acetyltransferase	**-2.56**	0.00293803
STM2404	STM2404	hypothetical protein STM2404	**2.15**	0.00577782
STM2404	STM2404	hypothetical protein STM2404	**2.09**	0.00193913
STM2432	ptsI	PEP-protein phosphotransferase	**2.15**	0.00561373
STM2432	ptsI	PEP-protein phosphotransferase	**2.06**	0.00444152
STM2433	crr	glucose-specific PTS system enzyme IIA component	**2.28**	0.00164827
STM2433	crr	glucose-specific PTS system enzyme IIA component	**2.08**	0.0040012
STM2461	eutG	putative transport protein	**-2.1**	0.01543712
STM2461	eutG	putative transport protein	**-2.44**	0.01883584
STM2470	eutS	putative carboxysome structural protein	**-3.07**	0.00084878
STM2470	eutS	putative carboxysome structural protein	**-4.04**	0.00004399
STM2473	talA	transaldolase	**3.33**	0.00015402
STM2473	talA	transaldolase	**3.33**	0.00070937
STM2475	STM2475	putative cytoplasmic protein	**-2.61**	0.00756605
STM2475	STM2475	putative cytoplasmic protein	**-4.58**	0.00111129
STM2665	yfiA	ribosome stabilization factor	**2.72**	0.00038244
STM2665	yfiA	ribosome stabilization factor	**2.39**	0.00325806
STM2777	iroN	TonB-dependent siderophore receptor protein	**-2.08**	0.03092316
STM2777	iroN	TonB-dependent siderophore receptor protein	**-2.94**	0.00274672
STM2794	ygaE	putative transcriptional repressor	**2.69**	0.00091477
STM2794	ygaE	putative transcriptional repressor	**2.47**	0.00087266
STM2795	ygaU	hypothetical protein STM2795	**2.83**	0.0005377
STM2795	ygaU	hypothetical protein STM2795	**2.69**	0.00349097
STM2796	yqaE	putative transport protein	**4.28**	0.00000992
STM2796	yqaE	putative transport protein	**3.53**	0.00007786
STM2814	emrA	multidrug resistance secretion protein	**-2.43**	0.00187205
STM2814	emrA	multidrug resistance secretion protein	**-2.54**	0.00345941
STM2820	yqaB	putative phosphoglucomutase	**-2.05**	0.00749202
STM2820	yqaB	putative phosphoglucomutase	**-2.54**	0.007235

STM2826	csrA	carbon storage regulator	**2.28**	0.00616268
STM2826	csrA	carbon storage regulator	**2.05**	0.00509878
STM2861	sitA	putative periplasmic binding protein	**2.9**	0.00025842
STM2861	sitA	putative periplasmic binding protein	**2.77**	0.00052514
STM2862	sitB	putative ATP-binding protein	**3.76**	0.00004077
STM2862	sitB	putative ATP-binding protein	**2.85**	0.0006307
STM2864	sitD	putative permease	**3.35**	0.00021357
STM2864	sitD	putative permease	**2.2**	0.02180086
STM2924	rpoS	RNA polymerase sigma factor	**3.82**	0.00121417
STM2924	rpoS	RNA polymerase sigma factor	**3.44**	0.00074868
STM2931	ftsB	cell divison protein FtsB	**-3.24**	0.00033269
STM2931	ftsB	cell divison protein FtsB	**-3.26**	0.00008825
STM2966	csrB	STM2966	**3.2**	0.00141763
STM2966	csrB	STM2966	**2.39**	0.00057253
STM2981	ygdD	hypothetical protein STM2981	**-3.11**	0.02369411
STM2981	ygdD	hypothetical protein STM2981	**-3.81**	0.05596069
STM2983	ygdI	putative lipoprotein	**2.62**	0.00148756
STM2983	ygdI	putative lipoprotein	**2.6**	0.00047514
STM3036	STM3036	putative inner membrane protein	**2.22**	0.01351523
STM3036	STM3036	putative inner membrane protein	**2.08**	0.01452092
STM3037	glyU	STM3037	**4.81**	0.00018842
STM3037	glyU	STM3037	**4.03**	0.00005118
STM3058	pepP	proline aminopeptidase P II	**-2.06**	0.09676337
STM3058	pepP	proline aminopeptidase P II	**-2.74**	0.03774392
STM3083	STM3083	putative mannitol dehydrogenase	**-2.4**	0.13115437
STM3083	STM3083	putative mannitol dehydrogenase	**-3.39**	0.00026555
STM3105	yggM	putative periplasmic protein	**3.26**	0.02151901
STM3105	yggM	putative periplasmic protein	**2.91**	0.02179864
STM3116	pheV	STM3116	**4.85**	0.00000453
STM3116	pheV	STM3116	**4.51**	0.0000078
STM3228	yqjC	putative periplasmic protein	**2.09**	0.00431422
STM3228	yqjC	putative periplasmic protein	**2.02**	0.00312354
STM3289	metY	STM3289	**2.53**	0.0013469
STM3289	metY	STM3289	**2.16**	0.00660214
STM3415	rpoA	DNA-directed RNA polymerase alpha subunit	**-3.21**	0.00027501
STM3415	rpoA	DNA-directed RNA polymerase alpha subunit	**-3.88**	0.00006827
STM3416	rpsD	30S ribosomal protein S4	**-3.2**	0.00073899
STM3416	rpsD	30S ribosomal protein S4	**-3.98**	0.00006663
STM3417	rpsK	30S ribosomal protein S11	**-2.7**	0.00087088
STM3417	rpsK	30S ribosomal protein S11	**-2.86**	0.00092828
STM3418	rpsM	30S ribosomal protein S13	**-3.12**	0.00015551
STM3418	rpsM	30S ribosomal protein S13	**-3.33**	0.00017039
STM3420	secY	preprotein translocase SecY	**-2.15**	0.00236988
STM3420	secY	preprotein translocase SecY	**-2.49**	0.0015754
STM3421	rplO	50S ribosomal protein L15	**-3.35**	0.00014769
STM3421	rplO	50S ribosomal protein L15	**-3.94**	0.00001734
STM3422	rpmD	50S ribosomal protein L30	**-2.25**	0.00152199
STM3422	rpmD	50S ribosomal protein L30	**-2.43**	0.0031407
STM3423	rpsE	30S ribosomal protein S5	**-2.77**	0.00054569
STM3423	rpsE	30S ribosomal protein S5	**-2.87**	0.00074293
STM3424	rplR	50S ribosomal protein L18	**-2.82**	0.00024221
STM3424	rplR	50S ribosomal protein L18	**-3.27**	0.00021192
STM3425	rplF	50S ribosomal protein L6	**-4.18**	0.00004365
STM3425	rplF	50S ribosomal protein L6	**-4.45**	0.00001026
STM3426	rpsH	30S ribosomal protein S8	**-3.7**	0.00015346
STM3426	rpsH	30S ribosomal protein S8	**-3.78**	0.00008389
STM3427,S	rpsN	30S ribosomal subunit protein S14	**-3.55**	0.0001182
STM3427,S	rpsN	30S ribosomal subunit protein S14	**-3.62**	0.00007016
STM3429	rplX	50S ribosomal protein L24	**-2.06**	0.00267683
STM3429	rplX	50S ribosomal protein L24	**-2.22**	0.00434639
STM3430	rplN	50S ribosomal protein L14	**-2.82**	0.0009757

STM3430	rplN	50S ribosomal protein L14	**-2.93**	0.00023018
STM3433	rplP	50S ribosomal protein L16	**-3.04**	0.00027042
STM3433	rplP	50S ribosomal protein L16	**-3.68**	0.00004338
STM3434	rpsC	30S ribosomal protein S3	**-3.36**	0.00013017
STM3434	rpsC	30S ribosomal protein S3	**-3.38**	0.00029707
STM3435	rplV	50S ribosomal protein L22	**-3.84**	0.00004986
STM3435	rplV	50S ribosomal protein L22	**-4.2**	0.00003383
STM3436	rpsS	30S ribosomal protein S19	**-2.07**	0.04999861
STM3436	rpsS	30S ribosomal protein S19	**-3.33**	0.00031366
STM3438	rplW	50S ribosomal protein L23	**-3.71**	0.00031872
STM3438	rplW	50S ribosomal protein L23	**-4.53**	0.00003111
STM3439	rplD	50S ribosomal protein L4	**-5.13**	0.0000125
STM3439	rplD	50S ribosomal protein L4	**-5.39**	0.0000043
STM3440	rplC	50S ribosomal protein L3	**-3.58**	0.00014162
STM3440	rplC	50S ribosomal protein L3	**-3.92**	0.00004085
STM3475	nirD	nitrite reductase small subunit	**-2.86**	0.00041574
STM3475	nirD	nitrite reductase small subunit	**-4.2**	0.00003085
STM3526	glpD	sn-glycerol-3-phosphate dehydrogenase	**3.46**	0.00005561
STM3526	glpD	sn-glycerol-3-phosphate dehydrogenase	**2.77**	0.00043337
STM3552	yhhA	putative outer membrane protein	**2.56**	0.00189164
STM3552	yhhA	putative outer membrane protein	**2.26**	0.02218511
STM3558	STM3558	death-on-curing protein	**-3.17**	0.00077266
STM3558	STM3558	death-on-curing protein	**-3.59**	0.00014679
STM3648	yiaG	putative transcriptional regulator	**3.55**	0.0000935
STM3648	yiaG	putative transcriptional regulator	**2.62**	0.00040073
STM3651	STM3651	putative acetyltransferase	**-2.33**	0.00129385
STM3651	STM3651	putative acetyltransferase	**-2.55**	0.00079589
STM3679	STM3679	putative cytoplasmic protein	**2.21**	0.00150556
STM3679	STM3679	putative cytoplasmic protein	**2.12**	0.00285911
STM3680	aldB	aldehyde dehydrogenase B	**3.95**	0.0001015
STM3680	aldB	aldehyde dehydrogenase B	**3.15**	0.00089176
STM3687	mtlR	mannitol operon repressor	**2.63**	0.00085804
STM3687	mtlR	mannitol operon repressor	**2.41**	0.00172229
STM3763	**mgtB**	**Mg2+ transporter**	**-2.06**	**0.01016394**
STM3763	**mgtB**	**Mg2+ transporter**	**-2.61**	**0.00182337**
STM3764	**mgtC**	**Mg2+ transport protein**	**-4.2**	**0.00010524**
STM3764	**mgtC**	**Mg2+ transport protein**	**-4.36**	**0.00001691**
STM3794	STM3794	putative regulatory protein	**2.09**	0.03483971
STM3794	STM3794	putative regulatory protein	**2.06**	0.00790423
STM3808,S	ibpB	small heat shock protein	**-2.19**	0.00336363
STM3808,S	ibpB	small heat shock protein	**-2.78**	0.00038379
STM3815	ccmE	periplasmic heme-dependent peroxidase	**-2.14**	0.00152393
STM3815	ccmE	periplasmic heme-dependent peroxidase	**-2.49**	0.00345587
STM3815	ccmE	periplasmic heme-dependent peroxidase	**-2.22**	0.0042699
STM3815	ccmE	periplasmic heme-dependent peroxidase	**-2.49**	0.00345587
STM3891	rrlC	STM3891	**2.41**	0.04740536
STM3891	rrlC	STM3891	**2.23**	0.04881141
STM3931	argX	STM3931	**4.35**	0.00011295
STM3931	argX	STM3931	**3.93**	0.00002488
STM3932	hisR	STM3932	**3.63**	0.00003443
STM3932	hisR	STM3932	**3.53**	0.00005251
STM3934	proM	STM3934	**2.61**	0.0061852
STM3934	proM	STM3934	**2.56**	0.00493238
STM4014	STM4014	putative periplasmic protein	**-2.43**	0.18947529
STM4014	STM4014	putative periplasmic protein	**-3.48**	0.02798201
STM4087	glpF	glycerol diffusion	**3.23**	0.00072139
STM4087	glpF	glycerol diffusion	**2.66**	0.00124042
STM4132	rrsB	STM4132	**2.11**	0.00348869
STM4132	rrsB	STM4132	**2.02**	0.01656088
STM4142	thrU	STM4142	**5.22**	0.00000417
STM4142	thrU	STM4142	**4.86**	0.00000502

STM4147	secE	translocase	**-2.28**	0.07150837
STM4147	secE	translocase	**-3.13**	0.05971099
STM4150	rplA	50S ribosomal protein L1	**-2.07**	0.00296166
STM4150	rplA	50S ribosomal protein L1	**-2.28**	0.00143387
STM4240	yjbJ	putative cytoplasmic protein	**5.4**	0.00000424
STM4240	yjbJ	putative cytoplasmic protein	**5.12**	0.00000283
STM4241	zur	transcriptional repressor	**3.56**	0.00005361
STM4241	zur	transcriptional repressor	**3.53**	0.00009324
STM4262	STM4262	putative ABC-type bacteriocin/lantibiotic exporter	**-2.54**	0.00097513
STM4262	STM4262	putative ABC-type bacteriocin/lantibiotic exporter	**-2.64**	0.00033775
STM4319	**phoN**	**non-specific acid phosphatase**	**-2.21**	**0.00643769**
STM4319	**phoN**	**non-specific acid phosphatase**	**-2.43**	**0.00052389**
STM4329	groES	co-chaperonin GroES	**-2.24**	0.00336571
STM4329	groES	co-chaperonin GroES	**-2.52**	0.00245909
STM4439	cybC	cytochrome b562	**-2.77**	0.00462414
STM4439	cybC	cytochrome b562	**-2.84**	0.00598646
STM4467	STM4467	arginine deiminase	**-3.13**	0.00051824
STM4467	STM4467	arginine deiminase	**-3.25**	0.0032668
STM4487	leuX	STM4487	**3.3**	0.00025458
STM4487	leuX	STM4487	**3.29**	0.00026436
STM4561	osmY	hyperosmotically-inducible periplasmic protein	**2.85**	0.00091792
STM4561	osmY	hyperosmotically-inducible periplasmic protein	**2.5**	0.00083246
STM4594	sthA	putative fimbrial chaparone	**3.96**	0.00013256
STM4594	sthA	putative fimbrial chaparone	**2.58**	0.00527714

Table S7. *S.* Typhimurium genes **differentially expressed (log2ratio ≤ -2 or ≥ 2) in intracellular *phoP* mutant compared to intracellular WT (270 genes, see Fig. 3 A)**

Systematic name	Gene	Product	log2Ratio (M)	*p* value
PSLT010	srgB	putative outer membrane protein	**-3.18**	0.00208817
PSLT010	srgB	putative outer membrane protein	**-3.02**	0.02466669
PSLT016	pefD	chaperone	**-2.45**	0.01994782
PSLT016	pefD	chaperone	**-2.25**	0.06055057
PSLT037	**spvD**	**hydrophilic protein**	**-2.79**	**0.00262265**
PSLT037	**spvD**	**hydrophilic protein**	**-2.08**	**0.09473559**
PSLT046	PSLT046	putative carbonic anhydrase	**-2.65**	0.00033436
PSLT046	PSLT046	putative carbonic anhydrase	**-2.58**	0.00022134
PSLT066	ssbB	single-strand DNA binding protein	**-3.76**	0.00276691
PSLT066	ssbB	single-strand DNA binding protein	**-3.09**	0.00826867
PSLT073	traM	mating signal protein	**-3.26**	0.00185036
PSLT073	traM	mating signal protein	**-2.9**	0.00074686
PSLT079	traE	pilus assembly protein	**-2.56**	0.00597349
PSLT079	traE	pilus assembly protein	**-2.5**	0.00202572
PSLT081	traB	pilus assembly protein	**-2.38**	0.00214648
PSLT081	traB	pilus assembly protein	**-2.34**	0.00095841
STM0019	STM0019	putative hydroxymethyltransferase	**-2.89**	0.00760328
STM0019	STM0019	putative hydroxymethyltransferase	**-2.31**	0.02302336
STM0054	STM0054	putative oxalacetate decarboxylase subunit beta	**-2.81**	0.00136381
STM0054	STM0054	putative oxalacetate decarboxylase subunit beta	**-2.43**	0.04319258
STM0056	STM0056	putative oxaloacetate decarboxylase subunit gamma	**-3.99**	0.00008835
STM0056	STM0056	putative oxaloacetate decarboxylase subunit gamma	**-3.98**	0.0001113
STM0057	STM0057	putative citrate-sodium symporter	**-2.24**	0.00536981
STM0057	STM0057	putative citrate-sodium symporter	**-2.1**	0.03929914
STM0066	carA	carbamoyl-phosphate synthase small subunit	**2.06**	0.00182754
STM0066	carA	carbamoyl-phosphate synthase small subunit	**2.29**	0.00051241
STM0081	STM0081	putative secreted protein	**-2.8**	0.00019809
STM0081	STM0081	putative secreted protein	**-2.05**	0.00147181
STM0086	kefC	glutathione-regulated potassium-efflux system protein	**-2.13**	0.00169706
STM0086	kefC	glutathione-regulated potassium-efflux system protein	**-2.07**	0.03287109
STM0152	aceE	pyruvate dehydrogenase E1 component	**2.27**	0.0013473
STM0152	aceE	pyruvate dehydrogenase E1 component	**2.72**	0.00065841
STM0154	lpdA	dihydrolipoamide dehydrogenase	**2.45**	0.00034098
STM0154	lpdA	dihydrolipoamide dehydrogenase	**2.72**	0.00409701
STM0225	hlpA	outer membrane protein H precursor	**2.76**	0.00118281
STM0225	hlpA	outer membrane protein H precursor	**2.8**	0.0010174
STM0252	rrlH	STM0252	**2.63**	0.00123993
STM0252	rrlH	STM0252	**2.75**	0.00037284
STM0279	STM0279	putative cytoplasmic protein	**-3.96**	0.00043721
STM0279	STM0279	putative cytoplasmic protein	**-3.52**	0.00228343
STM0294,1N	STM0294,1N	hypothetical protein STM0294,1N	**-3.34**	0.00062355
STM0294,1N	STM0294,1N	hypothetical protein STM0294,1N	**-2.62**	0.0012345
STM0295	STM0295	putative cytoplasmic protein	**-2.72**	0.00130299
STM0295	STM0295	putative cytoplasmic protein	**-2.11**	0.01007301
STM0339	stbB	putative fimbrial chaperone	**-6.4**	0.00633031
STM0339	stbB	putative fimbrial chaperone	**-2.31**	0.0029537
STM0359	STM0359	putative cytoplasmic protein	**-3.05**	0.00019532
STM0359	STM0359	putative cytoplasmic protein	**-2.56**	0.00028772
STM0399	brnQ	branched-chain amino acid transporter	**-2.38**	0.00054961
STM0399	brnQ	branched-chain amino acid transporter	**-2.06**	0.00349507
STM0440	cyoD	cytochrome o ubiquinol oxidase subunit IV	**2.78**	0.00017006
STM0440	cyoD	cytochrome o ubiquinol oxidase subunit IV	**2.84**	0.00016865
STM0441	cyoC	cytochrome o ubiquinol oxidase subunit III	**2.26**	0.00053702
STM0441	cyoC	cytochrome o ubiquinol oxidase subunit III	**2.35**	0.00063882
STM0494	ushA	UDP-sugar hydrolase/5'-nucleotidase	**-2.97**	0.00252084
STM0494	ushA	UDP-sugar hydrolase/5'-nucleotidase	**-2.87**	0.00100254

STM0561	STM0561	sensor kinase	**-7.03**	0.0000032
STM0561	STM0561	sensor kinase	**-6.84**	0.00085124
STM0588	entF	enterobactin synthetase component F	**2.28**	0.00041442
STM0588	entF	enterobactin synthetase component F	**3.59**	0.00009751
STM0595	entC	isochorismate synthase	**2.25**	0.00069291
STM0595	entC	isochorismate synthase	**2.74**	0.00034396
STM0623	citD	citrate lyase acyl carrier protein gamma chain	**2.25**	0.00126591
STM0623	citD	citrate lyase acyl carrier protein gamma chain	**2.42**	0.00063602
STM0629	cspE	cold shock protein E	**2.32**	0.00211458
STM0629	cspE	cold shock protein E	**2.95**	0.0022006
STM0648	leuS	leucyl-tRNA synthetase	**2.11**	0.00260697
STM0648	leuS	leucyl-tRNA synthetase	**2.61**	0.00081754
STM0649,S	STM0649,S	putative hydrolase	**-2.25**	0.00710432
STM0649,S	STM0649,S	putative hydrolase	**-2.02**	0.00127746
STM0651	STM0651	2-keto-3-deoxygluconate permease	**-3.87**	0.00861325
STM0651	STM0651	2-keto-3-deoxygluconate permease	**-2.78**	0.00026846
STM0662	gltL	glutamate/aspartate transporter	**-2.86**	0.00097199
STM0662	gltL	glutamate/aspartate transporter	**-2.52**	0.00978681
STM0665	gltI	glutamate/aspartate transporter	**3.13**	0.0000636
STM0665	gltI	glutamate/aspartate transporter	**3.19**	0.00007599
STM0684	nagB	glucosamine-6-phosphate deaminase	**2.09**	0.00134158
STM0684	nagB	glucosamine-6-phosphate deaminase	**2.57**	0.00044589
STM0702	kdpE	response regulator	**-2.17**	0.00074017
STM0702	kdpE	response regulator	**-2.04**	0.00085302
STM0719	STM0719	putative UDP-galactopyranose mutase	**-2.95**	0.00147277
STM0719	STM0719	putative UDP-galactopyranose mutase	**-2.2**	0.00094491
STM0737	sucB	dihydrolipoamide acetyltransferase	**2.86**	0.00018248
STM0737	sucB	dihydrolipoamide acetyltransferase	**3.96**	0.00004456
STM0766	dcoC	putative oxaloacetate decarboxylase subunit gamma	**-3.03**	0.00717617
STM0766	dcoC	putative oxaloacetate decarboxylase subunit gamma	**-2.89**	0.01095986
STM0773	galM	galactose-1-epimerase	**2.07**	0.00161487
STM0773	galM	galactose-1-epimerase	**2.07**	0.00241803
STM0781	modA	molybdate transporter	**2.56**	0.00022561
STM0781	modA	molybdate transporter	**2.84**	0.00034502
STM0811	ybhN	hypothetical protein STM0811	**-2.97**	0.00437005
STM0811	ybhN	hypothetical protein STM0811	**-2.47**	0.00599068
STM0812	ybhO	cardiolipin synthase	**-3.24**	0.00172939
STM0812	ybhO	cardiolipin synthase	**-2.17**	0.00481047
STM0830	glnH	glutamine ABC transporter periplasmic-binding protein	**2.29**	0.00044011
STM0830	glnH	glutamine ABC transporter periplasmic-binding protein	**2.4**	0.00077764
STM0831	dps	DNA protection during starvation conditions	**2.67**	0.0005568
STM0831	dps	DNA protection during starvation conditions	**3.7**	0.00012534
STM0943	cspD	stress response protein	**2.64**	0.00083825
STM0943	cspD	stress response protein	**2.71**	0.00084167
STM0972	**STM0972**	**SopD-like protein**	**3.09**	**0.00019758**
STM0972	**STM0972**	**SopD-like protein**	**3.32**	**0.00007222**
STM0996	ycbK	putative outer membrane protein	**2.2**	0.0028001
STM0996	ycbK	putative outer membrane protein	**2.52**	0.00059467
STM1006	STM1006	excisionase	**-2.47**	0.00029918
STM1006	STM1006	excisionase	**-2.1**	0.00166951
STM1020	STM1020	hypothetical protein STM1020 [Phage Gifsy-2]	**-2.12**	0.01200463
STM1020	STM1020	hypothetical protein STM1020 [Phage Gifsy-2]	**-2.04**	0.00776133
STM1034	STM1034	putative RecA/RadA recombinase [Phage Gifsy-2]	**-2.46**	0.00024539
STM1034	STM1034	putative RecA/RadA recombinase [Phage Gifsy-2]	**-2.21**	0.00106711
STM1038	STM1038	probable major tail protein [Phage Gifsy-2]	**-3.06**	0.00013482
STM1038	STM1038	probable major tail protein [Phage Gifsy-2]	**-2.54**	0.00114258
STM1047	STM1047	probable tail assembly protein [Phage Gifsy-2]	**-2.62**	0.00129675
STM1047	STM1047	probable tail assembly protein [Phage Gifsy-2]	**-2.05**	0.00177558
STM1051	**sseI**	**secreted effector protein [Phage Gifsy-2]**	**3.14**	**0.00017455**
STM1051	**sseI**	**secreted effector protein [Phage Gifsy-2]**	**4.12**	**0.00001652**
STM1070	ompA	putative hydrogenase membrane component precurosr	**3.45**	0.00012132

STM1070	ompA	putative hydrogenase membrane component precurosr	**3.95**	0.00006087
STM1071	sulA	cell division inhibitor	**2.84**	0.00181142
STM1071	sulA	cell division inhibitor	**2.85**	0.00288504
STM1088	**pipB**	**secreted effector protein**	**3.95**	**0.0003397**
STM1088	**pipB**	**secreted effector protein**	**5.1**	**0.00001679**
STM1091	**sopB**	**secreted effector protein**	**-2.85**	**0.00014078**
STM1091	**sopB**	**secreted effector protein**	**-2.49**	**0.00075115**
STM1117	agp	glucose-1-phosphatase	**2.2**	0.00066021
STM1117	agp	glucose-1-phosphatase	**2.37**	0.00033657
STM1139	csgG	putative curli operon transcriptional regulator	**-2.65**	0.00539909
STM1139	csgG	putative curli operon transcriptional regulator	**-2.07**	0.00220809
STM1165	grxB	glutaredoxin 2	**2.83**	0.00027749
STM1165	grxB	glutaredoxin 2	**3.6**	0.00004657
STM1180	flgH	flagellar L-ring protein precursor	**-3.17**	0.00027324
STM1180	flgH	flagellar L-ring protein precursor	**-2.38**	0.01926802
STM1190	yceD	putative metal-binding protein	**3.62**	0.00003781
STM1190	yceD	putative metal-binding protein	**3.74**	0.00015263
STM1195	fabG	3-ketoacyl-(acyl-carrier-protein) reductase	**2.68**	0.00024281
STM1195	fabG	3-ketoacyl-(acyl-carrier-protein) reductase	**2.74**	0.00025172
STM1205	ycfF	putative protein kinase C inhibitor	**2.16**	0.00092177
STM1205	ycfF	putative protein kinase C inhibitor	**2.16**	0.00117658
STM1221	cobB	NAD-dependent deacetylase	**2.86**	0.00160945
STM1221	cobB	NAD-dependent deacetylase	**3.31**	0.0000782
STM1222	potD	spermidine/putrescine ABC transporter periplasmic substrate-binding	**3.74**	0.00017764
STM1222	potD	spermidine/putrescine ABC transporter periplasmic substrate-binding	**3.85**	0.00013198
STM1223	potC	spermidine/putrescine ABC transporter membrane component	**3.44**	0.00009492
STM1223	potC	spermidine/putrescine ABC transporter membrane component	**4.38**	0.00002438
STM1224	**sifA**	**secreted effector protein**	**3.65**	**0.00002309**
STM1224	**sifA**	**secreted effector protein**	**3.75**	**0.00004153**
STM1234,S	trmU	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	**2.38**	0.01438858
STM1234,S	trmU	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	**2.66**	0.01629126
STM1246	**pagC**	**virulence membrane protein PAGC precursor**	**-3.07**	**0.00015468**
STM1246	**pagC**	**virulence membrane protein PAGC precursor**	**-2.78**	**0.0010781**
STM1286	mipA	MltA-interacting protein A	**2.7**	0.00031956
STM1286	mipA	MltA-interacting protein A	**3.19**	0.00006704
STM1297	selD	selenophosphate synthetase	**-3.54**	0.00010878
STM1297	selD	selenophosphate synthetase	**-3.46**	0.00013555
STM1329	STM1329	putative inner membrane protein	**-2.11**	0.00842382
STM1329	STM1329	putative inner membrane protein	**-2.05**	0.01431392
STM1334,c	infC	translation initiation factor IF-3	**3.17**	0.00004917
STM1334,c	infC	translation initiation factor IF-3	**3.57**	0.00023303
STM1335	rpmI	50S ribosomal protein L35	**2.17**	0.00320161
STM1335	rpmI	50S ribosomal protein L35	**2.73**	0.00021719
STM1351	ydiT	putative ferredoxin	**-2.94**	0.00043273
STM1351	ydiT	putative ferredoxin	**-2.41**	0.00205984
STM1360	ydiN	putative transport protein	**-2.72**	0.00625632
STM1360	ydiN	putative transport protein	**-2.21**	0.02138386
STM1369	sufA	iron-sulfur cluster assembly scaffold protein	**3.19**	0.00014842
STM1369	sufA	iron-sulfur cluster assembly scaffold protein	**3.27**	0.00010246
STM1370	sufB	putative ABC transporter protein	**3.03**	0.00019382
STM1370	sufB	putative ABC transporter protein	**3.48**	0.00018798
STM1371	sufC	putative transport protein	**2.82**	0.00014908
STM1371	sufC	putative transport protein	**3.52**	0.00010183
STM1372	sufD	cysteine desulfurase modulator	**3.19**	0.00011382
STM1372	sufD	cysteine desulfurase modulator	**3.24**	0.00007001
STM1373	sufS	selenocysteine lyase	**2.72**	0.00070724
STM1373	sufS	selenocysteine lyase	**2.86**	0.00013721
STM1377	lpp	murein lipoprotein	**2.27**	0.00057743
STM1377	lpp	murein lipoprotein	**2.89**	0.00152994
STM1381	orf245	putative cytoplasmic protein	**-2.14**	0.01197883
STM1381	orf245	putative cytoplasmic protein	**-2.13**	0.11588606

STM1394	ssaC	outer membrane secretin precursor	3.37	0.00046613
STM1394	ssaC	outer membrane secretin precursor	3.58	0.00017923
STM1395	ssaD	virulence protein	3.25	0.00418513
STM1395	ssaD	virulence protein	4.28	0.00001227
STM1396	ssaE	secretion system effector	3.26	0.00010416
STM1396	ssaE	secretion system effector	3.86	0.00010788
STM1398	sseB	translocation machinery component	4.25	0.0000405
STM1398	sseB	translocation machinery component	4.35	0.00015807
STM1399	sscA	secretion system chaparone	4.07	0.00002031
STM1399	sscA	secretion system chaparone	4.56	0.00006366
STM1400	sseC	translocation machinery component	4.25	0.00000742
STM1400	sseC	translocation machinery component	4.32	0.00001983
STM1401	sseD	translocation machinery component	2.42	0.00066079
STM1401	sseD	translocation machinery component	3.34	0.00018099
STM1402	sseE	secreted effector protein	3.12	0.00009862
STM1402	sseE	secreted effector protein	3.26	0.00004894
STM1403	sscB	secretion system chaparone	2.89	0.00015205
STM1403	sscB	secretion system chaparone	3.05	0.00014194
STM1405	sseG	secreted effector protein	2.25	0.01245671
STM1405	sseG	secreted effector protein	2.91	0.00135565
STM1406	ssaG	type III secretion system apparatus protein	3.27	0.00013073
STM1406	ssaG	type III secretion system apparatus protein	3.71	0.00006084
STM1407	ssaH	type III secretion system apparatus protein	4.65	0.00000598
STM1407	ssaH	type III secretion system apparatus protein	4.72	0.00001127
STM1408	ssaI	type III secretion system apparatus protein	4.96	0.00000492
STM1408	ssaI	type III secretion system apparatus protein	5.08	0.00002379
STM1409	ssaJ	needle complex inner membrane lipoprotein	3.51	0.00003693
STM1409	ssaJ	needle complex inner membrane lipoprotein	4.61	0.0000835
STM1410	STM1410	putative cytoplasmic protein	2.6	0.03534368
STM1410	STM1410	putative cytoplasmic protein	3.78	0.00006511
STM1411	ssaK	type III secretion system apparatus protein	3.91	0.00002663
STM1411	ssaK	type III secretion system apparatus protein	5.15	0.0000028
STM1412	ssaL	type III secretion system apparatus protein	4.36	0.00015022
STM1412	ssaL	type III secretion system apparatus protein	4.87	0.00000573
STM1413	ssaM	type III secretion system apparatus protein	2.74	0.00019541
STM1413	ssaM	type III secretion system apparatus protein	3.11	0.00008665
STM1415	ssaN	type III secretion system ATPase	3.62	0.0000402
STM1415	ssaN	type III secretion system ATPase	4.39	0.00001451
STM1416	ssaO	type III secretion system apparatus protein	4.74	0.00009017
STM1416	ssaO	type III secretion system apparatus protein	4.93	0.000004
STM1417	ssaP	type III secretion system apparatus protein	3.51	0.00002964
STM1417	ssaP	type III secretion system apparatus protein	4.8	0.00003915
STM1418	ssaQ	type III secretion protein	3.27	0.00008707
STM1418	ssaQ	type III secretion protein	4.05	0.00002425
STM1421	ssaT	type III secretion system apparatus protein	3.37	0.00106647
STM1421	ssaT	type III secretion system apparatus protein	3.44	0.00219839
STM1422	ssaU	type III secretion system apparatus protein	2.35	0.00070822
STM1422	ssaU	type III secretion system apparatus protein	2.37	0.00063712
STM1441	STM1441	putative inner membrane protein	**2.24**	0.00509263
STM1441	STM1441	putative inner membrane protein	**2.8**	0.00021185
STM1499	STM1499	putative dimethyl sulphoxide reductase chain A1	**-4.81**	0.0000045
STM1499	STM1499	putative dimethyl sulphoxide reductase chain A1	**-4.37**	0.01547094
STM1563	osmC	putative envelope protein	**2.95**	0.0003636
STM1563	osmC	putative envelope protein	**3.2**	0.00018166
STM1567	adhP	alcohol dehydrogenase	**2.27**	0.00153444
STM1567	adhP	alcohol dehydrogenase	**2.91**	0.00020573
STM1577	narZ	nitrate reductase 2 alpha subunit	**-3.28**	0.00006686
STM1577	narZ	nitrate reductase 2 alpha subunit	**-2.86**	0.00075468
STM1578	narY	nitrate reductase 2 beta subunit	**-3.33**	0.00037125
STM1578	narY	nitrate reductase 2 beta subunit	**-3.05**	0.03160668
STM1631	sseJ	secreted effector protein	3.93	0.00006637

STM1631	**sseJ**	**secreted effector protein**	**5.52**	**0.00000197**
STM1632	STM1632	putative inner membrane protein	**2.08**	0.00134945
STM1632	STM1632	putative inner membrane protein	**2.96**	0.00032502
STM1682	tpx	thiol peroxidase	**2.16**	0.00207697
STM1682	tpx	thiol peroxidase	**2.7**	0.00016658
STM1698	STM1698	putative inner membrane protein	**3.97**	0.00004381
STM1698	STM1698	putative inner membrane protein	**4.58**	0.00000775
STM1721	trpH	hypothetical protein STM1721	**2.06**	0.0025311
STM1721	trpH	hypothetical protein STM1721	**2.46**	0.00118688
STM1729	yciF	putative cytoplasmic protein	**-3.17**	0.0001057
STM1729	yciF	putative cytoplasmic protein	**-2.75**	0.00085738
STM1779	ipk	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase	**3.01**	0.00182133
STM1779	ipk	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase	**3.18**	0.00078491
STM1846	proQ	putative solute/DNA competence effector	**2.41**	0.00557119
STM1846	proQ	putative solute/DNA competence effector	**2.46**	0.00971398
STM1868	**mig-3**	**phage-tail assembly-like protein**	**-3.23**	**0.00058721**
STM1868	**mig-3**	**phage-tail assembly-like protein**	**-2.27**	**0.00060968**
STM1868A	STM1868A	lytic enzyme	**2.7**	0.00290682
STM1868A	STM1868A	lytic enzyme	**3.24**	0.00012564
STM1883	purT	5'-phosphoribosylglycinamide transformylase	**-2.39**	0.00033123
STM1883	purT	5'-phosphoribosylglycinamide transformylase	**-2.29**	0.00052374
STM1896	STM1896	putative cytoplasmic protein	**-2.5**	0.00127198
STM1896	STM1896	putative cytoplasmic protein	**-2.28**	0.00447879
STM1928	otsA	trehalose-6-phosphate synthase	**-2.73**	0.00244253
STM1928	otsA	trehalose-6-phosphate synthase	**-2.07**	0.00098858
STM2018	cobU	adenosylcobinamide kinase	**-2.65**	0.00283954
STM2018	cobU	adenosylcobinamide kinase	**-2.65**	0.00136304
STM2040	pduC	propanediol dehydratase large subunit	**-3.69**	0.0556512
STM2040	pduC	propanediol dehydratase large subunit	**-2.55**	0.00145277
STM2041	pduD	propanediol dehydratase medium subunit	**-4.23**	0.00277785
STM2041	pduD	propanediol dehydratase medium subunit	**-2.04**	0.13665821
STM2054	pduT	polyhedral body protein	**-2.59**	0.00092324
STM2054	pduT	polyhedral body protein	**-2.47**	0.00180795
STM2076	hisA	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]	**2.51**	0.00066996
STM2076	hisA	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]	**2.79**	0.00174145
STM2077	hisF	imidazole glycerol phosphate synthase subunit HisF	**2.02**	0.00168014
STM2077	hisF	imidazole glycerol phosphate synthase subunit HisF	**2.32**	0.00177104
STM2090	rfbH	CDP-6-deoxy-D-xylo-4-hexulose-3-dehydrase	**2.09**	0.00104502
STM2090	rfbH	CDP-6-deoxy-D-xylo-4-hexulose-3-dehydrase	**2.38**	0.00237548
STM2115	wcaA	putative glycosyl transferase	**-2.87**	0.00045075
STM2115	wcaA	putative glycosyl transferase	**-2.65**	0.00069574
STM2139	STM2139	putative inner membrane protein	**3.41**	0.00010978
STM2139	STM2139	putative inner membrane protein	**4**	0.00006499
STM2146	thiD	phosphomethylpyrimidine kinase	**2.48**	0.00050886
STM2146	thiD	phosphomethylpyrimidine kinase	**2.55**	0.00058286
STM2190	mglB	galactose transport protein	**2.06**	0.00299997
STM2190	mglB	galactose transport protein	**2.18**	0.00067938
STM2234	STM2234	putative phage tail fiber assembly protein	**3.71**	0.0000822
STM2234	STM2234	putative phage tail fiber assembly protein	**4.27**	0.00001374
STM2236	STM2236	hypothetical protein STM2236	**2.12**	0.02461811
STM2236	STM2236	hypothetical protein STM2236	**2.68**	0.00180781
STM2267	ompC	outer membrane protein C precursor	**2.27**	0.00051115
STM2267	ompC	outer membrane protein C precursor	**2.76**	0.00040796
STM2287	STM2287	putative cytoplasmic protein	**3.94**	0.0003949
STM2287	STM2287	putative cytoplasmic protein	**4.76**	0.00000591
STM2288	STM2288	putative cytoplasmic protein	**2.98**	0.00044689
STM2288	STM2288	putative cytoplasmic protein	**3.06**	0.00009553
STM2293	STM2293	competence damage-inducible protein A	**2.16**	0.0017009
STM2293	STM2293	competence damage-inducible protein A	**2.33**	0.00072358
STM2300	STM2300	putative cytoplasmic protein	**-2.58**	0.01150278
STM2300	STM2300	putative cytoplasmic protein	**-2.45**	0.00146707

STM2320	nuoJ	NADH dehydrogenase subunit J	**-2.39**	0.00032134
STM2320	nuoJ	NADH dehydrogenase subunit J	**-2.07**	0.0154217
STM2389	yfcY	acetyl-CoA acetyltransferase	**-4.05**	0.00001781
STM2389	yfcY	acetyl-CoA acetyltransferase	**-2.64**	0.00059258
STM2393	yfdC	hypothetical protein STM2393	**-4.85**	0.00008007
STM2393	yfdC	hypothetical protein STM2393	**-4.1**	0.00001732
STM2431	ptsH	phosphohistidinoprotein-hexose phosphotransferase	**2.26**	0.00162993
STM2431	ptsH	phosphohistidinoprotein-hexose phosphotransferase	**3.09**	0.00094848
STM2432	ptsI	PEP-protein phosphotransferase	**2.7**	0.00110859
STM2432	ptsI	PEP-protein phosphotransferase	**3.27**	0.00034859
STM2436	ptsJ	putative regulatory protein	**-2.31**	0.01314675
STM2436	ptsJ	putative regulatory protein	**-2.3**	0.0296621
STM2461	eutG	putative transport protein	**-3.8**	0.00202109
STM2461	eutG	putative transport protein	**-3.18**	0.00006155
STM2470	eutS	putative carboxysome structural protein	**-4.67**	0.00000376
STM2470	eutS	putative carboxysome structural protein	**-4.54**	0.00001942
STM2473	talA	transaldolase	**2.45**	0.00153515
STM2473	talA	transaldolase	**2.73**	0.00038584
STM2475	STM2475	putative cytoplasmic protein	**-5.89**	0.00002122
STM2475	STM2475	putative cytoplasmic protein	**-5.53**	0.00015157
STM2487	purC	phosphoribosylaminoimidazole-succinocarboxamide synthase	**2.09**	0.00142964
STM2487	purC	phosphoribosylaminoimidazole-succinocarboxamide synthase	**2.7**	0.00055121
STM2523	gcpE	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	**2.03**	0.0011791
STM2523	gcpE	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	**2.67**	0.00584651
STM2556	hmpA	dihydropteridine reductase 2/nitric oxide dioxygenase	**3.14**	0.00119879
STM2556	hmpA	dihydropteridine reductase 2/nitric oxide dioxygenase	**3.22**	0.00057629
STM2624	STM2624	hypothetical protein STM2624	**-3.63**	0.00013692
STM2624	STM2624	hypothetical protein STM2624	**-2.75**	0.00024484
STM2673	rplS	50S ribosomal protein L19	**2.01**	0.00624823
STM2673	rplS	50S ribosomal protein L19	**2.36**	0.00379298
STM2679	yfjD	hypothetical protein STM2679	**-2.38**	0.0011824
STM2679	yfjD	hypothetical protein STM2679	**-2.16**	0.00090812
STM2709	STM2709	base plate tail-like protein	**-3.81**	0.00341942
STM2709	STM2709	base plate tail-like protein	**-2.14**	0.11474776
STM2719	STM2719	terminase-like protein	**-2.33**	0.00091195
STM2719	STM2719	terminase-like protein	**-2.23**	0.00433155
STM2727	STM2727	hypothetical protein STM2727	**-2.33**	0.00036158
STM2727	STM2727	hypothetical protein STM2727	**-2.18**	0.00094832
STM2735	STM2735	hypothetical protein STM2735	**-3.9**	0.00030183
STM2735	STM2735	hypothetical protein STM2735	**-2.45**	0.0007428
STM2773	iroB	putative glycosyl transferase	**2.84**	0.00011769
STM2773	iroB	putative glycosyl transferase	**3.59**	0.00010718
STM2774	iroC	putative ABC transporter protein	**3.52**	0.00014256
STM2774	iroC	putative ABC transporter protein	**3.68**	0.00023694
STM2776	iroE	putative hydrolase	**2.21**	0.00695419
STM2776	iroE	putative hydrolase	**4.05**	0.00002948
STM2780	**pipB2**	**secreted effector protein**	**5.96**	**0.00000185**
STM2780	**pipB2**	**secreted effector protein**	**7.51**	**0.00000075**
STM2782	**mig-14**	**putative transcriptional activator**	**-2.89**	**0.00130858**
STM2782	**mig-14**	**putative transcriptional activator**	**-2.29**	**0.00207058**
STM2805	nrdH	glutaredoxin-like protein	**2.14**	0.00138596
STM2805	nrdH	glutaredoxin-like protein	**2.57**	0.00041432
STM2806	nrdI	hypothetical protein STM2806	**2.28**	0.05656411
STM2806	nrdI	hypothetical protein STM2806	**2.88**	0.00656825
STM2807	nrdE	ribonucleotide-diphosphate reductase alpha subunit	**2.8**	0.0007938
STM2807	nrdE	ribonucleotide-diphosphate reductase alpha subunit	**3.47**	0.00034699
STM2808	nrdF	ribonucleotide-diphosphate reductase beta subunit	**3.18**	0.00106201
STM2808	nrdF	ribonucleotide-diphosphate reductase beta subunit	**3.36**	0.00015369
STM2809	proV	glycine/betaine/proline transport protein	**2.68**	0.00047378
STM2809	proV	glycine/betaine/proline transport protein	**2.78**	0.00558156
STM2816	STM2816	putative glycoporin	**-2.64**	0.00021154

STM2816	STM2816	putative glycoporin	**-2.18**	0.00136455
STM2827	alaS	alanyl-tRNA synthetase	**2.29**	0.00069283
STM2827	alaS	alanyl-tRNA synthetase	**2.37**	0.00046892
STM2861	sitA	putative periplasmic binding protein	**3.64**	0.00005617
STM2861	sitA	putative periplasmic binding protein	**3.69**	0.00011751
STM2862	sitB	putative ATP-binding protein	**3.17**	0.00021296
STM2862	sitB	putative ATP-binding protein	**4.22**	0.0000541
STM2863	sitC	putative permease	**2.28**	0.00624157
STM2863	sitC	putative permease	**2.38**	0.00685852
STM2864	sitD	putative permease	**2.88**	0.00495998
STM2864	sitD	putative permease	**3.21**	0.00004849
STM2892	**invJ**	**needle length control protein**	**-2.84**	**0.00038248**
STM2892	**invJ**	**needle length control protein**	**-2.36**	**0.00095244**
STM2893	**invI**	**needle complex assembly protein**	**-2.43**	**0.00187374**
STM2893	**invI**	**needle complex assembly protein**	**-2.34**	**0.00050402**
STM2903	STM2903	putative cytoplasmic protein	**-3.5**	0.00057252
STM2903	STM2903	putative cytoplasmic protein	**-3.29**	0.00158855
STM2924	**rpoS**	**RNA polymerase sigma factor**	**3.85**	**0.0007221**
STM2924	**rpoS**	**RNA polymerase sigma factor**	**3.88**	**0.00064526**
STM2925	nlpD	lipoprotein	**2.52**	0.00031686
STM2925	nlpD	lipoprotein	**2.84**	0.00010425
STM2953	pyrG	CTP synthetase	**2.41**	0.00041108
STM2953	pyrG	CTP synthetase	**2.52**	0.00050896
STM2954	mazG	putative pyrophosphatase	**-2.65**	0.00044685
STM2954	mazG	putative pyrophosphatase	**-2.28**	0.01113471
STM2970	sdaC	putative serine transport protein	**2.26**	0.00236957
STM2970	sdaC	putative serine transport protein	**2.63**	0.00021973
STM2981	ygdD	hypothetical protein STM2981	**-4.24**	0.02103544
STM2981	ygdD	hypothetical protein STM2981	**-3.16**	0.01779525
STM2982	gcvA	gcv operon regulator	**-3.32**	0.00021151
STM2982	gcvA	gcv operon regulator	**-3.04**	0.00272736
STM3054	gcvH	glycine cleavage system protein H	**2.51**	0.00175757
STM3054	gcvH	glycine cleavage system protein H	**2.9**	0.0001349
STM3055	gcvT	aminomethyltransferase	**2.48**	0.00175234
STM3055	gcvT	aminomethyltransferase	**2.83**	0.00013338
STM3060	ygfE	putative cytoplasmic protein	**-2.84**	0.07234064
STM3060	ygfE	putative cytoplasmic protein	**-2.77**	0.00183828
STM3068	fba	fructose-bisphosphate aldolase	**2.01**	0.0036419
STM3068	fba	fructose-bisphosphate aldolase	**2.52**	0.00125064
STM3069	pgk	phosphoglycerate kinase	**2.9**	0.00037909
STM3069	pgk	phosphoglycerate kinase	**3.05**	0.00012765
STM3083	STM3083	putative mannitol dehydrogenase	**-6.6**	0.00000136
STM3083	STM3083	putative mannitol dehydrogenase	**-4.26**	0.02578489
STM3133	STM3133	putative amidohydrolase	**-2.15**	0.00922321
STM3133	STM3133	putative amidohydrolase	**-2.13**	0.00149006
STM3139	gsp	glutathionylspermidine synthetase/glutathionylspermidine amidase	**-2.1**	0.00072402
STM3139	gsp	glutathionylspermidine synthetase/glutathionylspermidine amidase	**-2.06**	0.00385049
STM3230	yqjE	putative inner membrane protein	**2.28**	0.00097518
STM3230	yqjE	putative inner membrane protein	**2.65**	0.00106973
STM3231	yqjK	putative inner membrane protein	**2.01**	0.00175817
STM3231	yqjK	putative inner membrane protein	**2.01**	0.00287037
STM3256	STM3256	putative phosphotransferase system mannitol/fructose-specific IIA	**-3.67**	0.04508451
STM3256	STM3256	putative phosphotransferase system mannitol/fructose-specific IIA	**-2.4**	0.0022652
STM3297	ftsJ	23S rRNA methyltransferase	**2.45**	0.00288919
STM3297	ftsJ	23S rRNA methyltransferase	**2.46**	0.0030232
STM3340	yhcK	transcriptional regulator NanR	**-4.06**	0.01094254
STM3340	yhcK	transcriptional regulator NanR	**-2.21**	0.00172865
STM3352	oadA	oxaloacetate decarboxylase	**-2.36**	0.0338194
STM3352	oadA	oxaloacetate decarboxylase	**-2.34**	0.03631579
STM3359	mdh	malate dehydrogenase	**2.69**	0.0008298
STM3359	mdh	malate dehydrogenase	**3.62**	0.00002707

STM3384	yhdG	possible dehydrogenase	**2.14**	0.00379067
STM3384	yhdG	possible dehydrogenase	**2.8**	0.01111311
STM3396	rrlD	STM3396	**2.04**	0.00343004
STM3396	rrlD	STM3396	**2.28**	0.00151463
STM3414	rplQ	50S ribosomal protein L17	**2.48**	0.00640917
STM3414	rplQ	50S ribosomal protein L17	**2.84**	0.00468764
STM3420	secY	preprotein translocase SecY	**2.01**	0.00358742
STM3420	secY	preprotein translocase SecY	**2.09**	0.00298328
STM3422	rpmD	50S ribosomal protein L30	**2.3**	0.00341094
STM3422	rpmD	50S ribosomal protein L30	**2.73**	0.00337918
STM3426	rpsH	30S ribosomal protein S8	**2.15**	0.00151041
STM3426	rpsH	30S ribosomal protein S8	**2.31**	0.00092471
STM3427,S	rpsN	30S ribosomal subunit protein S14	**2.3**	0.00367159
STM3427,S	rpsN	30S ribosomal subunit protein S14	**2.33**	0.00037658
STM3428	rplE	50S ribosomal protein L5	**2.62**	0.00031398
STM3428	rplE	50S ribosomal protein L5	**2.85**	0.00030526
STM3429	rplX	50S ribosomal protein L24	**2.05**	0.00506956
STM3429	rplX	50S ribosomal protein L24	**3.14**	0.00087033
STM3430	rplN	50S ribosomal protein L14	**2.25**	0.00817837
STM3430	rplN	50S ribosomal protein L14	**2.36**	0.00797996
STM3475	nirD	nitrite reductase small subunit	**-4.81**	0.00002589
STM3475	nirD	nitrite reductase small subunit	**-3.71**	0.00015368
STM3487	aroK	shikimate kinase I	**2.12**	0.00502696
STM3487	aroK	shikimate kinase I	**2.42**	0.00185474
STM3491	yrfC	putative inner membrane protein	**-4.53**	0.00550804
STM3491	yrfC	putative inner membrane protein	**-2.42**	0.32373041
STM3529	gldA	glycerol dehydrogenase	**-3.33**	0.00030641
STM3529	gldA	glycerol dehydrogenase	**-2.42**	0.00077633
STM3558	STM3558	death-on-curing protein	**-3.25**	0.00010692
STM3558	STM3558	death-on-curing protein	**-3.06**	0.00015577
STM3625	yhjV	putative transport protein	**-4.49**	0.00000756
STM3625	yhjV	putative transport protein	**-3.02**	0.00085096
STM3640	lpfA	long polar fimbrial protein A precursor	**-2.41**	0.03430451
STM3640	lpfA	long polar fimbrial protein A precursor	**-2.04**	0.00278326
STM3663	bax	putative ATP-binding protein	**2.23**	0.00094204
STM3663	bax	putative ATP-binding protein	**2.6**	0.00024869
STM3763	**mgtB**	**Mg2+ transporter**	**-2.82**	**0.00142542**
STM3763	**mgtB**	**Mg2+ transporter**	**-2.18**	**0.00405442**
STM3764	**mgtC**	**Mg2+ transport protein**	**-5.45**	**0.0000026**
STM3764	**mgtC**	**Mg2+ transport protein**	**-4.77**	**0.0000053**
STM3774	STM3774	putative inner membrane protein	**-4.52**	0.00006488
STM3774	STM3774	putative inner membrane protein	**-3.62**	0.01412864
STM3796A,S	STM3796A,S	integral membrane protein	**-2.66**	0.00282556
STM3796A,S	STM3796A,S	integral membrane protein	**-2.18**	0.00463003
STM3815	ccmE	periplasmic heme-dependent peroxidase	**-2.71**	0.00069098
STM3815	ccmE	periplasmic heme-dependent peroxidase	**-2.38**	0.00040588
STM3815	ccmE	periplasmic heme-dependent peroxidase	**-2.31**	0.00382767
STM3815	ccmE	periplasmic heme-dependent peroxidase	**-2.26**	0.00041495
STM3823	torC	trimethylamine N-oxide reductase cytochrome c-like subunit	**-2.98**	0.03454245
STM3823	torC	trimethylamine N-oxide reductase cytochrome c-like subunit	**-2.01**	0.06711761
STM3931	argX	STM3931	**2.03**	0.00487878
STM3931	argX	STM3931	**2.9**	0.00133522
STM3991	rrlA	STM3991	**2.27**	0.00174246
STM3991	rrlA	STM3991	**2.39**	0.00168728
STM3996	yihE	putative type II homoserine kinase	**-2.86**	0.08200201
STM3996	yihE	putative type II homoserine kinase	**-2.39**	0.00247131
STM4014	STM4014	putative periplasmic protein	**-4.93**	0.00167434
STM4014	STM4014	putative periplasmic protein	**-2.64**	0.0758244
STM4075	ydeY	putative sugar transport protein	**-2.83**	0.0007394
STM4075	ydeY	putative sugar transport protein	**-2.45**	0.00252911
STM4081	tpiA	triosephosphate isomerase	**2.3**	0.00146889

STM4081	tpiA	triosephosphate isomerase	**3.37**	0.0001407
STM4086	glpK	glycerol kinase	**3.21**	0.00015461
STM4086	glpK	glycerol kinase	**3.5**	0.00006553
STM4087	glpF	glycerol diffusion	**3.87**	0.00002304
STM4087	glpF	glycerol diffusion	**4.58**	0.00004127
STM4132	rrsB	STM4132	**2.14**	0.01233411
STM4132	rrsB	STM4132	**2.17**	0.01331303
STM4132	rrsB	STM4132	**2.31**	0.00452344
STM4132	rrsB	STM4132	**2.31**	0.00166054
STM4135	rrlB	STM4135	**2.39**	0.00140246
STM4135	rrlB	STM4135	**2.67**	0.00053681
STM4142	thrU	STM4142	**2.25**	0.00348061
STM4142	thrU	STM4142	**2.49**	0.00135255
STM4144	glyT	STM4144	**2.19**	0.00103988
STM4144	glyT	STM4144	**2.49**	0.00161938
STM4147	secE	translocase	**-3.84**	0.00019228
STM4147	secE	translocase	**-2.9**	0.07178946
STM4151	rplJ	50S ribosomal protein L10	**2.2**	0.00140693
STM4151	rplJ	50S ribosomal protein L10	**2.27**	0.00316853
STM4164	thiC	thiamine biosynthesis protein ThiC	**2.26**	0.0016935
STM4164	thiC	thiamine biosynthesis protein ThiC	**2.26**	0.00645563
STM4190	pepE	peptidase E	**-2.16**	0.00084024
STM4190	pepE	peptidase E	**-2.1**	0.0012666
STM4199	STM4199	putative cytoplasmic protein	**-2.44**	0.00074091
STM4199	STM4199	putative cytoplasmic protein	**-2.22**	0.00304671
STM4205	STM4205	putative phage glycosyltransferase	**-5.01**	0.00686021
STM4205	STM4205	putative phage glycosyltransferase	**-2.86**	0.00203825
STM4215	STM4215	putative cytoplasmic protein	**-2.61**	0.00038097
STM4215	STM4215	putative cytoplasmic protein	**-2.02**	0.00928817
STM4221	pgi	glucose-6-phosphate isomerase	**2.1**	0.0058492
STM4221	pgi	glucose-6-phosphate isomerase	**3.59**	0.00009483
STM4224	yjbG	putative periplasmic protein	**-2.14**	0.0081934
STM4224	yjbG	putative periplasmic protein	**-2.03**	0.00121823
STM4306	STM4306	putative anaerobic dimethylsulfoxide reductase subunit B	**-2.41**	0.00031877
STM4306	STM4306	putative anaerobic dimethylsulfoxide reductase subunit B	**-2.18**	0.00107852
STM4310	STM4310	putative inner membrane protein	**-3.32**	0.00005275
STM4310	STM4310	putative inner membrane protein	**-2.89**	0.00808688
STM4315	STM4315	putative DNA-binding protein	**-2.65**	0.00061895
STM4315	STM4315	putative DNA-binding protein	**-2.31**	0.00064164
STM4319	**phoN**	**non-specific acid phosphatase**	**-3.66**	**0.00001894**
STM4319	**phoN**	**non-specific acid phosphatase**	**-2.66**	**0.0004933**
STM4344	yjeA	lysyl-tRNA synthetase	**-4.11**	0.05005005
STM4344	yjeA	lysyl-tRNA synthetase	**-2.53**	0.00440508
STM4356	yjeF	putative sugar kinase	**-2.49**	0.01786272
STM4356	yjeF	putative sugar kinase	**-2.04**	0.29520582
STM4377	aidB	putative acyl-CoA dehydrogenase	**-2.76**	0.00035924
STM4377	aidB	putative acyl-CoA dehydrogenase	**-2.71**	0.00144918
STM4391	rpsF	30S ribosomal protein S6	**2.59**	0.00816442
STM4391	rpsF	30S ribosomal protein S6	**2.67**	0.00502477
STM4415	fbp	fructose-1,6-bisphosphatase	**2.19**	0.00087833
STM4415	fbp	fructose-1,6-bisphosphatase	**2.46**	0.00048795
STM4439	cybC	cytochrome b562	**-2.26**	0.01461133
STM4439	cybC	cytochrome b562	**-2.23**	0.00980011
STM4467	STM4467	arginine deiminase	**-3.73**	0.00188589
STM4467	STM4467	arginine deiminase	**-2.32**	0.00435046
STM4477	pepA	leucyl aminopeptidase	**2.48**	0.00029537
STM4477	pepA	leucyl aminopeptidase	**3.55**	0.00046738
STM4488	STM4488	putative integrase	**-3.23**	0.00049586
STM4488	STM4488	putative integrase	**-2.36**	0.00311026
STM4524	hsdS	type I restriction enzyme specificity protein	**-2.71**	0.01188847
STM4524	hsdS	type I restriction enzyme specificity protein	**-2.27**	0.08012223

TABLE S8. Plasmids and oligonucleotides used for chromosome epitope tagging.

Plasmid / primer	Plasmid function / oligonucleotide sequence (5'-3') [a]	Reference
pSUB11	Template plasmid used to amplify the 3'-end of the gene fused to a 3xFLAG tag and the Kan cassette.	(1)
pSU315	Template plasmid used to amplify the 3'-end of the gene fused to an HA tag and the Kan cassette.	(1)
pKD46	Plasmid expressing the lambda Red recombinase.	(1)
pagC-flag1	AAAAATAAACGGCTTCAACGTCGGGGTTGGATACCGTTTC**GACTACAAAGACCATGACGG**	This study
pagC-flag2	GGCGGTGCGGAAGGCGAACCTTCCGCATAGCTTATGCTTT**CATATGAATATCCTCCTTAG**	This study
mgtC-flag1	CGATAATATCACCGCAATTCACTGGAGCATTGATAGTCAA**GACTACAAAGACCATGACGG**	This study
mgtC-flag2	TTATACGCCTGGCGTAATGTTGCAATTGAATAAAAAACTA**CATATGAATATCCTCCTTAG**	This study
virK-Fw	GCTATCATATTCTGGATACAATAATACAAGAGGTCAACAGCCTCTCCCGG**GACTACAAAGACCATGACGG**	This study
virK-Rv	AAGATCCGCTGAACGGTAGCAGGATCTGCACATCCGCGTATGAAATAGTT**CATATGAATATCCTCCTTAG**	This study
pagP-Fw	GTTCGTATAACAACGGAAACGTCTATTTCGCCTGGATGCGTTTCCAGTTT**GACTACAAAGACCATGACGG**	This study
pagP-Rv	TATTGTTTTTTAAGACTTTTTAATTCACAACTGAAGCATACCCTTCCCCA**CATATGAATATCCTCCTTAG**	This study
pagN-Fw	ACACAAAGGCTGCCTCCAATGACTTCATGCTCGGCATTACTTACGCCTTT**GACTACAAAGACCATGACGG**	This study
pagN-Rv	TCCATTGCGCCTTCGGGAACCCACAGGACCAGCTATTTTACCGATAGTGT**CATATGAATATCCTCCTTAG**	This study

a) Sequences artificially introduced in the primers corresponding to the FLAG- or HA-tag sequences are indicated in bold.

Reference:

1. **Uzzau, S., N. Figueroa-Bossi, S. Rubino, and L. Bossi.** 2001. Epitope tagging of chromosomal genes in *Salmonella*. Proc. Natl. Acad. Sci. U S A **98:**15264-15269.