

Supplementary Table 1. LSMMG-regulated genes for wild type *S. Typhimurium* relative to control cultures*

Gene	Fold Change	Description	Gene	Fold Change	Description
SPI-1			Motility and chemotaxis		
<i>prgI</i>	4.508	EscF/YscF/HrpA family type III secretion system needle major subunit	<i>flgA</i>	7.531	Flagella basal body P-ring formation protein FlgA
<i>sipC</i>	3.776	Pathogenicity island 1 effector protein	<i>flgB</i>	15.541	Flagellar basal body rod protein FlgB
<i>sipB</i>	5.502	Pathogenicity island 1 effector protein	<i>flgC</i>	10.086	Flagellar basal body rod protein FlgC
<i>sicA</i>	4.306	CesD/SycD/LcrH family type III secretion system chaperone	<i>flgD</i>	25.596	Flagellar basal body rod modification protein
<i>invA</i>	3.701	EscV/YscV/HrcV family type III secretion system export apparatus protein	<i>flgE</i>	16.166	Flagellar hook protein FlgE
<i>invG</i>	6.662	EscC/YscC/HrcC family type III secretion system outer membrane ring protein	<i>flgF</i>	8.133	Flagellar biosynthesis protein FlgF
<i>invF</i>	7.976	Invasion protein	<i>flgG</i>	5.626	Flagellar basal-body rod protein FlgG
<i>sitA</i>	-3.745	Iron ABC transporter substrate-binding protein	<i>flgI</i>	5.608	Flagellar biosynthesis protein FlgA
<i>sitB</i>	-4.450	Manganese/iron transporter ATP-binding protein	<i>flgJ</i>	5.518	Flagellar rod assembly protein/muramidase FlgJ
<i>sitC</i>	-4.971	Iron ABC transporter permease	<i>flgL</i>	3.908	Flagellar hook-filament junction protein FlgL
<i>sitD</i>	-6.206	Iron ABC transporter permease	<i>motB</i>	3.393	Flagellar motor protein MotB
<i>iagB</i>	-3.796	Invasion protein IagB	<i>motA</i>	3.556	Flagellar motor stator protein MotA
<i>spaR</i>	-4.689	EscT/YscT/HrcT family type III secretion system export apparatus	<i>fliZ</i>	6.106	Flagellar regulatory protein FliZ
SPI-2			<i>fliA</i>	5.428	RNA polymerase sigma factor FliA
<i>sifA</i>	-3.947	Effector protein SifA	<i>fliC</i>	4.098	Flagellin
<i>sifB</i>	-9.792	Effector protein SifB	<i>fliD</i>	6.044	Flagellar filament-capping protein FliD
<i>ssaL</i>	-4.582	secretion system apparatus protein	<i>fliS</i>	6.622	Flagellar export chaperone FliS
<i>ssaM</i>	-11.888	type III secretion system protein SsaM	<i>fliT</i>	5.373	Flagellar biosynthesis protein FliT
<i>ssaV</i>	-4.448	EscV/YscV/HrcV family type III secretion system export apparatus protein	<i>fliF</i>	5.605	Flagellar M-ring protein FliF
<i>sseJ</i>	-5.512	Pathogenicity island 2 effector SseJ	<i>fliJ</i>	12.874	Flagellar biosynthesis chaperone FliJ
STM1698	-5.016	Secreted effector kinase SteC	<i>fliL</i>	7.342	Flagellar basal body-associated protein FliL
<i>sseL</i>	-5.239	Effector protein SseL; Deubiquitinase for macrophage killing and virulence	<i>fliM</i>	7.345	Flagellar motor switch protein FliM
SPI-4			<i>fliN</i>	18.490	Flagellar motor switch protein FliN
STM4262	-9.845	Antibiotic ABC transporter ATP-binding protein, SiiF	<i>cheZ</i>	4.474	Protein phosphatase CheZ
SPI-5			<i>cheY</i>	4.428	Two-component system response regulator
<i>sigE</i>	5.650	Class IA chaperone involved in stability, secretion, and translocation of SopB	<i>cheB</i>	4.425	Chemotaxis response regulator protein-glutamate methyltransferase
<i>sopB</i>	4.965	Inositol phosphatase	<i>cheM</i>	3.932	Methyl-accepting chemotaxis protein II
Plasmid			<i>cheW</i>	2.881	Chemotaxis protein CheW
<i>parB</i>	3.110	Plasmid partition protein B	<i>cheA</i>	3.605	Sensory histidine protein kinase
PSLT034	-4.650	Putative adhesin	<i>tcp</i>	5.305	Methyl-accepting chemotaxis protein II
<i>spvD</i>	-14.285	putative transposase	<i>aer</i>	2.800	Aerotaxis receptor
<i>spvB</i>	-8.355	Salmonella plasmid virulence: hydrophilic protein	STM3152	-8.083	McpB; putative methyl-accepting chemotaxis protein
<i>spvR</i>	-8.004	Salmonella plasmid virulence: regulation of spv operon, lysR family	<i>ymdF</i>	-9.904	Involved in flagella-dependent motility
<i>tlpA</i>	-6.472	Alpha-helical coiled coil protein	<i>yciG</i>	-3.600	Involved in flagella-dependent motility
PSLT049	-7.424	Putative DNA polymerase III epsilon subunit (3'-5' exonuclease)	Transport		
PSLT050.1N	-12.599		<i>gltL</i>	3.584	Arginine transporter ATP-binding subunit
PSLT050.2N	-8.624		<i>nagE</i>	2.680	PTS N-acetyl glucosamine transporter subunit IIABC
<i>traJ</i>	-6.796	Conjugative transfer: regulation	<i>cydC</i>	2.672	Cysteine/glutathione ABC transporter ATP-binding protein/permease CydC
<i>traD</i>	-5.250	Conjugative transfer: DNA transport	STM1613	2.973	PTS sugar transporter subunit IIB

Fimbrial proteins/Adhesins		
<i>fimA</i>	6.086	Type-1 fimbrial protein subunit A
<i>fimC</i>	5.006	Fimbrial chaperone protein FimC
<i>fimZ</i>	3.142	DNA-binding response regulator
<i>bcfA</i>	-3.734	Fimbrial protein
<i>stiB</i>	-26.512	Long polar fimbrial chaperone LpfB
<i>safB</i>	-3.780	Putative fimbriae assembly chaperone
<i>lpfA</i>	-19.085	Long polar fimbria
<i>stjB</i>	-3.677	Fimbrial assembly protein
<i>stjC</i>	-5.093	Fimbrial chaperone protein
STM4593	-12.124	Putative fimbrial usher protein
STM4594	-14.483	Fimbrial assembly chaperone SthB
STM4595	-11.698	Fimbrial protein SthA
STM0551	-11.770	Diguanylate cyclase
<i>stcD</i>	-6.945	Adhesin
<i>stcB</i>	-12.995	Putative fimbrial chaperone protein

Transcriptional regulators		
<i>araC</i>	3.169	DNA-binding transcriptional regulator AraC
STM2361	3.083	Sigma-54-dependent Fis family transcriptional regulator
STM3124	2.857	Helix-turn-helix transcriptional regulator
STM3678	3.522	AraC family transcriptional regulator
<i>melR</i>	3.162	Transcriptional regulator MelR
STM4315	8.265	AraC family transcriptional regulator
STM0029	-83.659	Transcriptional regulator
<i>sinR</i>	-3.205	Transcriptional regulator
<i>marR</i>	-3.775	Transcriptional regulator
<i>rcsA</i>	-4.100	Helix-turn-helix transcriptional regulator
<i>ygaE</i>	-5.758	Transcriptional regulator
STM2797	-6.135	Transcriptional regulator
STM3098	-3.628	Putative transcriptional regulator
<i>envR</i>	-42.880	acrEF/envCD operon transcriptional regulator
<i>rmbA</i>	-33.603	Transcriptional regulator

Metabolism		
<i>sdhC</i>	3.522	Succinate dehydrogenase, cytochrome b556
<i>sdhD</i>	3.563	Succinate dehydrogenase, hydrophobic membrane anchor protein
<i>sdhA</i>	5.231	Succinate dehydrogenase flavoprotein subunit
<i>sdhB</i>	4.949	Succinate dehydrogenase, Fe-S protein
<i>sucA</i>	4.243	2-oxoglutarate dehydrogenase E1 component
<i>sucB</i>	3.706	Dihydrolipoamide succinyltransferase
<i>sucD</i>	3.059	Succinate--CoA ligase subunit alpha
<i>cydB</i>	3.490	Cytochrome d ubiquinol oxidase subunit II
<i>prpR</i>	3.667	Propionate catabolism operon regulatory protein PrpR
<i>ushA</i>	2.925	Bifunctional UDP-sugar hydrolase/5'-nucleotidase
<i>cstA</i>	3.498	Carbon starvation protein A

Transport (continued)		
<i>mglB</i>	2.879	Methyl-galactoside ABC transporter substrate-binding protein
<i>glpT</i>	3.882	Glycerol-3-phosphate transporter
<i>cysA</i>	10.840	Sulfate ABC transporter ATP-binding protein
<i>cysW</i>	8.936	Sulfate ABC transporter permease subunit CysW
<i>cysP</i>	7.737	Thiosulfate transporter subunit
STM3134	2.780	MFS transporter
STM3169	4.314	C4-dicarboxylate ABC transporter substrate-binding protein
STM3170	3.518	C4-dicarboxylate ABC transporter permease
<i>nanT</i>	3.966	MFS transporter
<i>dgoT</i>	7.721	MFS transporter
<i>rbsC</i>	3.139	ribose ABC transporter permease
STM4065	11.036	MFS transporter
<i>putA</i>	4.491	Trifunctional transcriptional regulator/proline dehydrogenase
<i>putP</i>	2.979	Sodium/proline symporter
<i>glpF</i>	3.280	Aquaporin
STM0520	-15.981	MFS transporter
<i>allP</i>	-81.265	Putative NCS1 family, allantoin transport protein
<i>ybbY</i>	-4.277	Uracil/xanthine transporter
STM0718	-22.290	Transport protein
STM0722	-16.337	ABC transporter permease
STM0723	-4.223	Sugar ABC transporter ATP-binding protein
STM0765	-15.373	Putative cation transporter
<i>ybiR</i>	-4.716	Anion transporter
<i>ulaA</i>	-8.690	PTS system ascorbate-specific transporter subunit IIC
<i>macA</i>	-2.858	Macrolide transporter subunit MacA
STM1128	-3.315	Acetylneuraminate ABC transporter
<i>potC</i>	-3.645	Spermidine/putrescine ABC transporter permease PotC
STM1256	-4.197	Peptide ABC transporter permease
<i>ydiM</i>	-5.436	MFS transporter
STM1634	-3.491	Amino acid ABC transporter ATP-binding protein
STM1668	-8.566	ZirS protein, secreted by zirT
STM1669	-8.730	ZirT, outer membrane protein, secretes zirS; homology to invasins of Yersinia
<i>narK</i>	-8.501	Nitrate/nitrite transporter
<i>pagO</i>	-20.129	EamA family transporter
<i>znuB</i>	-2.870	Zinc ABC transporter permease
<i>tyrP</i>	-7.342	Tyrosine transporter TyrP
<i>yedA</i>	-3.994	Drug/metabolite exporter YedA
<i>setB</i>	-13.870	Sugar efflux transporter SetB
<i>yefE</i>	-4.099	Microcin ABC transporter permease
<i>yefF</i>	-2.967	Microcin C ABC transporter ATP-binding protein YefF
<i>yojI</i>	-3.619	Multidrug ABC transporter permease/ATP-binding protein
STM2274	-8.369	MFS transporter
<i>xapB</i>	-6.945	MFS transporter
<i>sinH</i>	-8.029	Intimin-like inverse autotransporter protein
STM2574	-10.500	MFS transporter

Metabolism (continued)			Transport (continued)		
<i>rihA</i>	2.598	Pyrimidine-specific ribonucleoside hydrolase RihA	STM2752	-13.745	PTS sorbitol transporter subunit IIB
<i>hutH</i>	2.770	Histidine ammonia-lyase	<i>nixA</i>	-6.989	High-affinity nickel-transport protein, NixA
<i>bioC</i>	3.482	Malonyl-ACP O-methyltransferase BioC	STM3022	-5.009	Transporter
<i>dmsA</i>	4.412	Dimethylsulfoxide reductase subunit A	STM3771	-6.221	PTS sugar transporter subunit IIB
<i>dmsB</i>	5.643	Dimethylsulfoxide reductase, chain B	<i>pstS</i>	-6.189	Phosphate ABC transporter substrate-binding protein PstS
<i>dmsC</i>	6.421	Dimethyl sulfoxide reductase	<i>yigM</i>	-5.799	EamA family transporter
<i>hpaE</i>	3.643	5-carboxymethyl-2-hydroxymuconate semialdehyde dehydrogenase	<i>ompL</i>	-13.351	Outer membrane porin L
<i>hpaD</i>	3.305	3,4-dihydroxyphenylacetate 2,3-dioxygenase	<i>yabF</i>	-56.706	glutathione-regulated potassium-efflux system ancillary protein KefF
<i>hpaF</i>	2.744	5-carboxymethyl-2-hydroxymuconate delta-isomerase	STM4206	-7.260	translocase
<i>selD</i>	3.168	Selenophosphate synthase	<i>yjeM</i>	-7.303	Glutamate/gamma-aminobutyrate family transporter YjeM
<i>nemA</i>	2.711	N-ethylmaleimide reductase	<i>yifZ</i>	-3.884	EamA family transporter
<i>fumA</i>	3.819	Fumarate hydratase	Hypothetical, unknown function and pseudogenes		
<i>rspB</i>	3.575	Zn-dependent oxidoreductase	STM0989	3.616	Hypothetical protein
<i>pykA</i>	3.114	Pyruvate kinase	<i>ygbK</i>	3.962	Hypothetical protein
<i>phsA</i>	3.298	Thiosulfate reductase PhsA	STM3604	4.505	Hypothetical protein
<i>yeiA</i>	3.309	Dihydropyrimidine dehydrogenase subunit B	STM04675	16.686	
<i>glpQ</i>	3.504	Glycerophosphodiester phosphodiesterase	<i>yegU</i>	3.263	Hypothetical protein
<i>glpA</i>	3.516	sn-glycerol-3-phosphate dehydrogenase subunit A	<i>hutU</i>	2.846	Pseudogene
<i>glpB</i>	4.781	Anaerobic glycerol-3-phosphate dehydrogenase subunit B	<i>ygbJ</i>	3.704	3-hydroxyisobutyrate dehydrogenase
<i>glpC</i>	3.625	sn-glycerol-3-phosphate dehydrogenase subunit C	<i>fucP</i>	3.283	Pseudogene
<i>fabB</i>	2.929	Beta-ketoacyl-[acyl-carrier-protein] synthase I	STM3828.1N	6.636	
<i>cysK</i>	3.215	Cysteine synthase A	STM4305.S	3.040	
<i>hypB</i>	3.448	Hydrogenase accessory protein HypB	STM0020	-5.359	Hypothetical protein
STM2914	8.327	Putative nucleoside-diphosphate-sugar epimerase	STM0034	-59.511	Hypothetical protein
<i>cysN</i>	10.282	Sulfate adenylyltransferase subunit CysN	STM0305	-10.623	Hypothetical protein
<i>cysD</i>	10.187	Sulfate adenylyltransferase small subunit	STM0348	-14.671	Hypothetical protein
<i>cysH</i>	6.869	Phosphoadenosine phosphosulfate reductase	STM0373	-3.008	yaiU; Similar to 3rd module of ATP-binding components of transporters
<i>cysI</i>	4.905	Sulfite reductase subunit beta	<i>ylaC</i>	-3.750	Hypothetical protein
STM3082	5.627	Galactonate oxidoreductase	STM0777	-5.300	Hypothetical protein
STM3136	5.367	Fructuronate reductase	STM0719	-151.463	putative UDP-galactopyranose mutase
STM3137	4.627	Glucuronate isomerase	STM0726	-37.734	Putative glycosyl transferase
<i>nanK</i>	4.152	N-acetylmannosamine kinase	STM0759	-4.617	Uncharacterized protein ybgS
STM3697	3.906	Mandelate racemase/muconate lactonizing protein	<i>ybhM</i>	-38.365	Hypothetical protein
<i>dgoA</i>	10.879	2-oxo-3-deoxygalactonate 6-phosphate aldolase	STM0839	-5.720	putative inner membrane protein
<i>dgoK</i>	5.456	2-oxo-3-deoxygalactonate kinase	STM0860	-7.203	Hypothetical protein
<i>glnA</i>	3.310	Type I glutamate--ammonia ligase	<i>ycdF</i>	-10.756	pseudogene
<i>fdoH</i>	2.859	Formate dehydrogenase subunit beta	STM1131	-8.775	Hypothetical protein
<i>fdoG</i>	3.071	Formate dehydrogenase	<i>ydhI</i>	-5.845	Hypothetical protein
STM4066	13.452	Aminoimidazole riboside kinase	<i>ynfM</i>	-5.384	Hypothetical protein
STM4067	8.502	Putative ADP-ribosylglycohydrolase	STM1379	-3.576	Putative amino acid permease
<i>glpK</i>	3.232	Glycerol kinase	STM1380	-4.504	Putative hydrolase or acyltransferase
<i>aceB</i>	5.166	Malate synthase A	STM1552	-3.395	putative cytoplasmic protein
<i>aceA</i>	6.004	Isocitrate lyase	STM1553	-8.088	pseudogene
<i>aceK</i>	4.136	Bifunctional isocitrate dehydrogenase kinase/phosphatase	STM1637	-4.423	Hypothetical protein
<i>yjhP</i>	2.926	Putative SAM-dependent methyltransferase	STM1665	-6.556	Hypothetical protein
<i>araD</i>	-11.692	L-ribulose-5-phosphate 4-epimerase	STM1666	-5.941	pseudo
STM0018	-8.786	Chitinase	STM1671	-9.440	putative bacterial regulatory helix-turn-helix protein, araC family
STM0019	-3.682	Chitinase	STM1863	-4.692	putative inner membrane protein

Metabolism (continued)			Hypothetical, unknown function and pseudogenes (continued)		
STM0330	-10.818	3-isopropylmalate dehydratase small subunit	STM1866	-4.565	pseudo
STM0361	-4.488	Cytochrome BD2 subunit II	STM1896	-8.206	putative cytoplasmic protein
STM0855	-3.253	Putative electron transfer flavoprotein beta subunit	STM1999	-7.247	Hypothetical protein
STM0856	-10.576	Electron transfer flavoprotein subunit alpha	STM2008	-3.013	Hypothetical protein
STM1002	-5.423	Diaminopropionate ammonia-lyase	STM2137	-5.298	putative cytoplasmic protein
STM1269	-8.294	Putative chorismate mutase	STM2156A	-4.139	Hypothetical protein
<i>celF</i>	-8.047	6-phospho-beta-glucosidase	STM2208	-10.759	Hypothetical protein
STM1620	-6.441	lactate oxidase	STM2245	-7.368	putative outer membrane protein
<i>udg</i>	-5.249	UDP-glucose 6-dehydrogenase	STM2508	-21.030	putative cytoplasmic protein
<i>wcaF</i>	-53.368	Colanic acid biosynthesis acetyltransferase WcaF	STM2509	-7.155	Hypothetical protein
STM05445	-18.670	Purine nucleoside phosphorylase	<i>yfgJ</i>	-5.463	Hypothetical protein
<i>eutE</i>	-5.686	Aldehyde dehydrogenase EutE	STM2534	-4.594	DUF5066 domain-containing protein
<i>eutQ</i>	-25.510	Ethanolamine utilization protein EutQ	STM2906	-7.104	putative cytoplasmic protein
<i>yfiN</i>	-4.165	Diguanylate cyclase	STM2908	-18.953	Hypothetical protein
STM3123	-4.760	Anaerobic sulfatase maturase	STM2954.1n	-3.379	Hypothetical protein
STM3532	-4.183	Dihydrodipicolinate synthase family protein	STM3026	-13.558	Hypothetical protein
<i>yibD</i>	-66.592	Putative glycosyltransferase	STM3035	-43.269	Hypothetical protein
STM4205	-3.610	Glycosyltransferase	<i>yghW</i>	-4.934	Hypothetical protein
STM4433	-4.250	Inositol 2-dehydrogenase	STM3153	-3.546	Hypothetical protein
STM4467	-8.310	Putative arginine deiminase	STM3166.S	-25.720	putative cation transporter pseudogene
Other functions			<i>yhbE</i>	-3.296	Hypothetical protein
<i>yfiA</i>	3.528	Ribosomal subunit interface protein	STM3906	-4.579	Hypothetical protein
STM2693	3.489	tmRNA, 10Sa RNA, ssrA	STM3907	-3.685	Hypothetical protein
STM0084	-9.981	AslA sulfatase	STM3941	-127.454	Hypothetical protein
<i>polB</i>	-3.152	DNA polymerase II	STM3942	-7.917	Hypothetical protein
STM0291	-3.817	Putative RHS-family protein	STM4013.S	-4.456	
STM0294	-14.389	Phosphotriesterase	STM4014	-39.694	Putative periplasmic protein
STM0295	-18.732	Putative cytoplasmic protein	STM4015	-4.020	Hypothetical protein
STM0721	-16.973	Glycosyltransferase family 1 protein	STM4039	-5.528	Hypothetical protein
STM0724	-24.169	Glycosyl transferase	<i>yiiG</i>	-6.952	putative cytoplasmic protein
STM0725	-13.694	Glycosyl transferase	STM4197	-17.380	putative inner membrane protein
STM0854	-7.482	CoA ester lyase	STM4219.S	-3.984	
<i>ybeV</i>	-9.211	Molecular chaperone DnaJ	<i>yjcB</i>	-6.270	Hypothetical protein
<i>pagC</i>	-5.866	Virulence membrane protein PagC	<i>yjeJ</i>	-4.361	Hypothetical protein
STM1267	-3.849	Histidine kinase	STM4472	-5.140	Hypothetical protein
<i>marB</i>	-5.510	Multiple antibiotic resistance regulatory periplasmic protein MarB	STM4504	-8.830	Hypothetical protein
STM1530	-3.655	phosphoprotein PhoE	STM4575	-7.204	Hypothetical protein
STM1836	-3.714	Peptidoglycan synthase, penicillin-binding protein 3	Phage/Prophage proteins		
<i>pphA</i>	-3.742	Phosphoprotein phosphatase	STM0908	-6.070	Fels-1 prophage protein
<i>umuD</i>	-4.279	DNA polymerase V subunit UmuD	<i>mig-3</i>	-6.254	Phage tail protein
<i>engA</i>	-4.930	Ribosome biogenesis GTPase Der	STM2585	-16.099	SarA/PagJ, <i>Salmonella</i> -anti-inflammatory response activator; Gifsy-1 prophage protein
<i>pphB</i>	-17.053	Serine/threonine protein phosphatase	STM2585A	-56.599	Gifsy-1 prophage protein, PagK2
<i>rpsU</i>	-26.663	30S ribosomal protein S21	STM2586	-35.924	Gifsy-1 prophage protein
<i>hopD</i>	-3.725	Prepilin peptidase	STM2587	-72.380	Gifsy-1 prophage protein
<i>yrfD</i>	-22.854	DNA utilization protein HofM	STM2608	-3.747	Gifsy-1 prophage protein
<i>dinF</i>	-3.303	DNA-damage-inducible protein F	STM2620	-4.292	Gifsy-1 prophage protein
			STM2702	-40.059	Fels-2 prophage protein
			STM2722	-21.560	Fels-2 prophage protein

* Significant differences between the LSMMG and control cultures were determined according to an FDR < 0.05 and a minimum logFC of 1 or -1 (corresponding to a 2-fold increase or decrease in expression, respectively). LogFC values were converted to fold change. Red shading indicates upregulation in the LSMMG culture, blue shading downregulation in the LSMMG culture.