

Table 2. *Salmonella typhimurium* genes differentially-regulated during spaceflight mission STS-115

UP-regulated

<u>Gene number</u>	<u>Fold change</u>	<u>Gene name</u>	<u>Known or putative function</u>
<u>Secreted proteins:</u>			
STM1959	2.10	fliC	flagellar biosynthesis; flagellin, filament structural protein
STM2066	2.31	sopA	Secreted effector protein of <i>Salmonella dublin</i>
STM2883	2.57	sipD	cell invasion protein
STM2884	6.28	sipC	cell invasion protein
<u>Membrane proteins:</u>			
STM0374	2.04	yaiV	putative inner membrane protein
STM1070	2.05	ompA	putative hydrogenase, membrane component
STM1572	3.34	ompD	outer membrane protein; bacterial porin
STM2267	2.44	ompC	outer membrane protein 1b (ib;c), porin
STM3420	3.12	secY	preprotein translocase of IISP family, putative membrane ATPase
<u>Other function:</u>			
STM0152	2.18	aceE	pyruvate dehydrogenase, decarboxylase component
STM0182	2.21	panB	3-methyl-2-oxobutanoate hydroxymethyltransferase
STM0240	2.02	yaeJ	putative-tRNA hydrolase domain
STM0272	2.36		putative ATPase with chaperone activity; homologue of <i>Yersinia clpB</i>
STM0596	2.24	entE	2,3-dihydroxybenzoate-AMP ligase
STM0730	4.75	gltA	citrate synthase
STM1040	2.12		Gifsy-2 prophage; probable minor tail protein
STM1290	7.67	gapA	glyceraldehyde-3-phosphate dehydrogenase A
STM1749	4.76	adhE	iron-dependent alcohol dehydrogenase of <i>AdhE</i>
STM2106	2.07	wcaI	putative glycosyl transferase in colanic acid biosynthesis
STM2118	2.30	wza	putative polysaccharide export protein, outer membrane
STM2181	2.06	yohJ	putative effector of murein hydrolase <i>LrgA</i>
STM2282	2.58	glpQ	glycerophosphodiester phosphodiesterase, periplasmic
STM2314	2.58		putative chemotaxis signal transduction protein
STM2708	2.03		Fels-2 prophage: similar to tail fiber protein (gpI) in phage P2
STM2719	2.12		Fels-2 prophage: similar to gpR in phage 186
STM2843	2.03	hydN	electron transport protein (FeS sender) from formate to hydrogen
STM2846	2.26	hycH	processing of <i>HycE</i> (part of the FHL complex)
STM2855	3.25	hypB	hydrogenase-3 accessory protein, assembly of metallocenter
STM4311	3.58	tnpA	IS200 transposase
STM4325	6.39	dcuA	Dcu family, anaerobic dicarboxylate transport protein
STM4415	2.71	fbp	fructose-bisphosphatase
STM4466	4.07		putative carbamate kinase
SSL_2286	2.97	orf36	putative phage replicase

Putative, unknown function:

STM0289	2.08	putative cytoplasmic protein
STM0699	2.76	putative cytoplasmic protein
STM2744	2.44	putative cytoplasmic protein
STM3752	2.05	putative cytoplasmic protein
SSL_T1747	4.06	putative cytoplasmic protein

Plasmid genes:

Plasmid 1 (pSLT):

PSLT011	2.20	srgA	sdiA-regulated gene; putative thiol-disulfide isomerase or thioredoxin
PSLT015	4.44	orf5	putative outer membrane protein
PSLT039	2.21	spvB	Salmonella plasmid virulence: hydrophilic protein
PSLT043	4.21		putative phosphoribulokinase / uridine kinase family
PSLT044	4.43		putative integrase protein
PSLT054	2.37	samB	mutagenesis by UV and mutagens; related to umuDC operon
PSLT068	2.04		putative ParB-like nuclease domain
PSLT072	2.11		putative transglycosylase
PSLT081	4.71	traB	conjugative transfer: assembly
PSLT095	4.24	traN	conjugative transfer: aggregate stability
PSLT099	2.32	trbB	conjugative transfer
PSLT100	2.59	traH	conjugative transfer: assembly
PSLT101	2.20	traG	conjugative transfer: assembly abd aggregate stability
PSLT104	2.87	traD	conjugative transfer: DNA transport
PSLT110	2.37	traX	conjugative transfer: fimbrial acetylation

Plasmid 2:

SSL_36	2.02	colIb	colicin Ib protein
SSL_T3	2.68	trbC	conjugative transfer
SSL_T5	3.14	trbA	conjugative transfer
SSL_T12	2.34	traT	conjugative transfer
SSL_T20	2.91	traK	conjugative transfer
SSL_T24	2.10	traF	conjugative transfer
SSL_T35	3.03	pilL	lipoprotein
SSL_T45	2.32	yagA	unknown function
SSL_T52	2.17	stbA	plasmid stability
SSL_T53	5.31	orf05	unknown function
SSL_T66	2.93	ygbA	unknown function

Plasmid 3:

SSL_T69	2.39	tnpB	putative transposase
SSL_T70	14.1	strB	streptomycin resistance
SSL_T71	3.55	strA	streptomycin resistance
SSL_T72	7.43	sulII	sulphonamide resistance
SSL_5085	2.08	repA	plasmid replication

DOWN-regulated

Protein secretion:

STM1153	0.342	msyB	suppresses protein export mutants
STM2895	0.417	invB	surface presentation of antigens; secretory proteins
STM3293	0.432	secG	preprotein translocase IISPF family
STM3701	0.473	secB	molecular chaperone in protein export
STM3974	0.445	tatB	component of Sec-independent protein secretion pathway
STM4147	0.392	secE	preprotein translocase IISPF family, membrane subunit

Flagella:

STM1916	0.458	cheY	chemotaxis regulator, transmits signals to flagellar motor
STM1925	0.356	flhD	regulator of flagellar biosynthesis, acts on class 2 operons
STM1962	0.443	fliT	flagellar biosynthesis; possible export chaperone for FliD

Fimbrial:

STM0543	0.434	fimA	major type 1 subunit fimbrin (pilin)
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Stress proteins:

STM0831	0.273	dps	stress response DNA-binding protein
STM1652	0.200	ynaF	putative universal stress protein

Regulatory:

STM_sRNA	0.458	RFN	putative small regulatory RNA
STM_sRNA	0.499	rne5	putative small regulatory RNA
STM_sRNA	0.318	csrB	regulatory RNA
STM0473	0.389	hha	hemolysin expression modulating protein
STM0606	0.493	ybdO	putative transcriptional regulator, LysR family
STM0959	0.415	lrp	regulator for lrp regulon (AsnC family)
STM1444	0.391	slyA	transcriptional regulator for hemolysin (MarR family)
STM1660	0.494	fnr	transcriptional regulator
STM2640	0.402	rpoE	sigma E (sigma 24) factor of RNA polymerase
STM3466	0.438	crp	catabolite activator protein (CAP), cyclic AMP protein (CRP family)
STM4315	0.445	rtsA	AraC-type DNA-binding domain-containing protein
STM4361	0.298	hfq	host factor I for bacteriophage Q beta replication

Ribosomal:

STM0216	0.344	rpsB	30S ribosomal subunit protein S2
STM0469	0.474	rpmE2	putative 50S ribosomal protein L31 (second copy)
STM2675	0.356	rimM	16S rRNA processing protein
STM3345	0.310	rplM	50S ribosomal subunit protein L13
STM3425	0.403	rplF	50S ribosomal subunit protein L6
STM3428	0.438	rplE	50S ribosomal subunit protein L5
STM3430	0.182	rplN	50S ribosomal subunit protein L14
STM3433	0.422	rplP	50S ribosomal subunit protein L16
STM3436	0.289	rpsS	30S ribosomal subunit protein S19
STM3438	0.457	rplW	50S ribosomal subunit protein L23
STM3439	0.393	rplD	50S ribosomal subunit protein L4, regulates S10 expression

STM3448	0.250	rpsL	30S ribosomal subunit protein S12
STM4150	0.423	rplA	50S ribosomal subunit protein L1, regulates L1 and L11
STM4391	0.401	rpsF	30S ribosomal subunit protein S6

Membrane/periplasmic proteins:

STM1164	0.340	yceB	putative outer membrane lipoprotein
STM1249	0.443		putative periplasmic protein
STM1432	0.464	ydhO	putative cell wall-associated hydrolase
STM1460	0.408	ydgK	putative inner membrane protein
STM1732	0.276	ompW	outer membrane protein W; colicin S4 receptor
STM1798	0.471	ycgR	putative inner membrane protein
STM2505	0.410		putative inner membrane protein
STM2685	0.411	smpA	small membrane protein A
STM2802	0.453	ygaM	putative inner membrane protein
STM2870	0.462		putative inner membrane protein
STM3107	0.460	yggN	putative periplasmic protein
STM3228	0.378	yqjC	putative periplasmic protein
STM3229	0.485	yqjD	putative inner membrane protein
STM3231	0.457	yqjK	putative inner membrane protein
STM3347	0.393	yhcB	putative periplasmic protein
STM4378	0.328	yjfN	putative inner membrane protein
STM4561	0.319	osmY	hyperosmotically inducible periplasmic protein

Other function:

STM0186	0.406	dksA	dnaK suppressor protein
STM0368	0.386	prpB	putative carboxyphosphoenolpyruvate mutase
STM0369	0.403	prpC	putative citrate synthase
STM0417	0.382	ribH	riboflavin synthase, beta chain
STM0536	0.483	ppiB	peptidyl-prolyl cis-trans isomerase B (rotamase B)
STM0665	0.480	gltI	ABC superfamily (bind_prot), glutamate/aspartate transporter
STM0759	0.492	ybgS	putative homeobox protein
STM0803	0.408	moaB	molybdopterin biosynthesis, protein B
STM0966	0.497	dmsC	anaerobic dimethyl sulfoxide reductase, subunit C
STM1196	0.336	acpP	acyl carrier protein
STM1291	0.474	yeaA	putative peptide methionine sulfoxide reductase
STM1569	0.458	fdnH	formate dehydrogenase-N, Fe-S beta subunit, nitrate-inducible
STM1783	0.478	pth	peptidyl-tRNA hydrolase
STM2488	0.436	nlpB	lipoprotein-34
STM2542	0.495	nifU	NifU homologs involved in Fe-S cluster formation
STM2549	0.460	asrB	anaerobic sulfide reductase
STM2646	0.294	yfiD	putative formate acetyltransferase
STM2746	0.344		putative Excinuclease ATPase subunit
STM2767	0.491		putative Superfamily I DNA and RNA helicase
STM3039	0.455	idi	isopentenylidiphosphate isomerase
STM3054	0.431	gcvH	glycine cleavage complex protein H
STM3241	0.458	tdcE	pyruvate formate-lyase 4/ 2-ketobutyrate formate-lyase
STM3443	0.404	bfr	bacterioferrin, an iron storage homoprotein
STM3702	0.453	grxC	glutaredoxin 3

STM3703	0.321	yibN	putative Rhodanese-related sulfurtransferases
STM3870	0.484	atpE	membrane-bound ATP synthase, F0 sector, subunit c
STM3915	0.492	trxA	thioredoxin 1, redox factor
STM4341	0.411	frdC	fumarate reductase, anaerobic, membrane anchor polypeptide
STM4414	0.475	ppa	inorganic pyrophosphatase

Putative ORF, unknown function:

STM0474	0.435	ybaJ	putative cytoplasmic protein
STM1367	0.378	ydiH	putative cytoplasmic protein
STM1583	0.441		putative cytoplasmic protein
STM2390	0.290	yfcZ	putative cytoplasmic protein
STM2801	0.451	ygaC	putative cytoplasmic protein
STM3461	0.493		putative cytoplasmic protein
STM3654	0.341		pseudogene; in-frame stop following codon 23
STM3995	0.459	yihD	putative cytoplasmic protein
STM4002	0.172		putative cytoplasmic protein
STM4088	0.357	yiiU	putative cytoplasmic protein
STM4239	0.334		putative cytoplasmic protein
STM4240	0.411	yjbJ	putative cytoplasmic protein
STM4250	0.422	yjbQ	putative cytoplasmic protein
STM4499	0.494	yeeN	putative cytoplasmic protein