

Table S3. List of *S. Typhi* genes identified following negative selection of mutant pool in human macrophages.

<i>Salmonella</i>		<i>Salmonella</i>		<i>Salmonella Typhi</i>		Functional class	log2	
<i>Salmonella</i>	Typhi	<i>Salmonella</i>	Typhimurium	Name	Sanger Product		output/input	P-value
Typhi	Name	Typhimurium	Name					
STY0015		STM0015		putative phage protein		Phage and insertion sequence elements	-2.54	0.00001
STY0016		STM0016		conserved hypothetical protein		Unknown	-3.13	0.00000
STY0021		STM0020		conserved hypothetical protein		Unknown	-3.57	0.00001
STY0031	<i>bcfF</i>	STM0026	<i>bcfF</i>	fimbrial subunit		Cell envelope	-2.12	0.00004
STY0039		STM0032		possible sulfatase		Small molecule metabolism	-4.00	0.00035
STY0040		STM0033		putative secreted 5'-nucleotidase		Unknown	-2.13	0.00005
STY0041		STM0034		putative exported protein		Cell envelope	-5.75	0.00001
STY0134	<i>leuO</i>	STM0115	<i>leuO</i>	probable activator protein in leuABCD operon		Amino acid biosynthesis/degradation	-2.69	0.00001
STY0207	<i>staA, yadN</i>			putative fimbrial protein		Cell envelope	-3.06	0.00002
STY0231	<i>htrA</i>	STM0209	<i>htrA</i>	protease DO precursor; heat shock protein HtrA		Protein biosynthesis/degradation	-3.69	0.00000
STY0329		STM0298		IS element transposase (pseudogene)		Phage and insertion sequence elements	-2.04	0.00015
STY0372	<i>stbB</i>	STM0339	<i>stbB</i>	fimbrial chaperone protein		Cell envelope	-3.69	0.00000
STY0419	<i>proC</i>	STM0386	<i>proC</i>	pyrroline-5-carboxylate reductase		Amino acid biosynthesis/degradation	-3.57	0.00009
STY0477		STM0437		conserved hypothetical protein		Unknown	-2.29	0.00001
STY0520	<i>acrA</i>	STM0476	<i>acrA</i>	acriflavin resistance protein A precursor		Cell envelope	-4.13	0.00014
STY0569	<i>ybbW</i>	STM0522	<i>ybbV</i>	putative allantoin permease (pseudogene)		Transport and binding proteins	-2.60	0.00011
STY0605		STM0557		putative membrane protein		Cell envelope	-4.55	0.00032
STY0651	<i>ybdO</i>	STM0606	<i>ybdO</i>	putative lysR-family transcriptional regulator		Regulatory functions	-2.91	0.00041
STY0804	<i>gpmA</i>	STM0772	<i>gpmA</i>	phosphoglycerate mutase 1		Energy metabolism	-4.71	0.00023
STY0878	<i>ybiS</i>	STM0837	<i>ybiS</i>	putative exported protein		Cell envelope	-4.52	0.00004
STY0917	<i>ulaA</i>	STM0884	<i>ulaA</i>	possible transport protein		Transport and binding proteins	-2.42	0.00008
STY0968	<i>pflA</i>	STM0970	<i>pflA</i>	pyruvate formate-lyase 1 activating enzyme		Energy metabolism	-4.12	0.00005
STY0973	<i>pflB</i>	STM0973	<i>pflB</i>	formate acetyltransferase 1		Energy metabolism	-6.02	0.00015
STY0974	<i>focA</i>	STM0974	<i>focA</i>	probable formate transporter (formate channel)		Transport and binding proteins	-6.17	0.00002

STY0977	<i>serC</i>	STM0977	<i>serC</i>	phosphoserine aminotransferase	Amino acid biosynthesis/degradation	-2.24	0.00005
STY1041				putative prophage membrane protein	Phage and insertion sequence elements	-2.33	0.00044
STY1121	<i>sigD, sopB</i>	STM1091	<i>sopB</i>	cell invasion protein	Pathogenesis	-2.08	0.00004
STY1129		STM1097		putative exported protein	Cell envelope	-2.57	0.00004
STY1157		STM1122	<i>ycdC</i>	putative transcriptional regulator	Regulatory functions	-3.16	0.00038
STY1177	<i>csgF</i>	STM1140	<i>csgF</i>	assembly/transport component in curli production	Cell envelope	-4.74	0.00041
STY1187	<i>mdoG</i>	STM1150	<i>mdoG</i>	periplasmic glucans biosynthesis protein MdoG precursor	Cellular processes	-3.16	0.00018
STY1220	<i>flgI</i>	STM1181	<i>flgI</i>	flagellar P-ring protein precursor	Cell envelope	-4.16	0.00032
STY1312	<i>cls</i>	STM1739	<i>cls</i>	cardiolipin synthetase	Cell envelope	-3.72	0.00039
STY1364				hypothetical periplasmic protein	Cell envelope	-3.47	0.00003
STY1397		STM1667		putative thiol peroxidase	Unknown	-2.33	0.00010
STY1398		STM1666		hypothetical protein	Unknown	-3.84	0.00001
STY1401		STM1663	<i>ynal</i>	putative membrane protein	Cell envelope	-2.22	0.00044
STY1408		STM1657		putative chemo-receptor protein	Cellular processes	-2.79	0.00042
STY1427	<i>acpD</i>	STM1642	<i>acpD</i>	acyl carrier protein phosphodiesterase	Small molecule metabolism	-2.37	0.00044
STY1497	<i>osmC</i>	STM1563	<i>osmC</i>	osmotically inducible protein C	Cellular processes	-3.90	0.00019
STY1523	<i>hyaA2</i>	STM1539		uptake hydrogenase small subunit	Energy metabolism	-4.89	0.00007
STY1534		STM1527		putative membrane protein	Cell envelope	-2.02	0.00002
STY1554		STM1507	<i>yfdJ</i>	putative membrane transport protein	Transport and binding proteins	-2.77	0.00021
STY1576		STM1488	<i>mlc</i>	putative regulatory protein	Regulatory functions	-2.25	0.00018
STY1585		STM1482	<i>ydgF</i>	putative conserved membrane protein	Cell envelope	-5.21	0.00002
STY1643				DNA-invertase	Phage and insertion sequence elements	-2.28	0.00008
STY1649		STM1473	<i>ompN</i>	outer membrane protein	Transport and binding proteins	-3.87	0.00005
STY1690		STM1432	<i>ydhO</i>	putative secreted protein	Cell envelope	-2.70	0.00003
STY1702	<i>ssaQ</i>	STM1418	<i>ssaQ</i>	putative type III secretion protein	Pathogenesis	-2.55	0.00048
STY1703	<i>ssaP</i>	STM1417	<i>ssaP</i>	putative type III secretion protein	Pathogenesis	-3.43	0.00028
STY1705	<i>ssaN</i>	STM1415	<i>ssaN</i>	putative type III secretion ATP synthase	Pathogenesis	-2.46	0.00023
STY1739		STM1382	<i>orf408</i>	Putative ribokinase (pseudogene)	Pathogenesis	-2.26	0.00022
STY1770	<i>btuC</i>	STM1340	<i>btuC</i>	vitamin B12 transport system permease	Transport and binding proteins	-2.25	0.00033
STY1852	<i>aroQ</i>	STM1269		putative chorismate mutase	Amino acid biosynthesis/degradation	-2.95	0.00001

STY1859		STM1261		conserved hypothetical protein	Unknown	-2.76	0.00024
STY1867		STM1254		putative lipoprotein	Cell envelope	-5.46	0.00018
STY1868		STM1253		putative cytochrome	Unknown	-4.14	0.00003
STY1869		STM1252		hypothetical protein	Unknown	-2.10	0.00042
STY1878	<i>pagC</i>	STM1246	<i>pagC</i>	outer membrane invasion protein	Pathogenesis	-2.23	0.00049
STY1886	<i>cdtB</i>			putative toxin-like protein	Pathogenesis	-3.86	0.00006
STY1910		STM1784	<i>ychF</i>	putative ATP/GTP-binding protein	Unknown	-3.28	0.00039
STY1976	<i>prc</i>	STM1845	<i>prc</i>	tail-specific protease precursor	Protein biosynthesis/degradation	-4.85	0.00016
STY2091	<i>kdgA</i>	STM1884	<i>eda</i>	multifunctional:2-keto-3-deoxygluconate 6-phosphate aldolase; 2-keto-4-hydroxyglutarate aldolase; oxaloacetate decarboxylase	Energy metabolism	-4.16	0.00003
STY2134	<i>flhD</i>	STM1925	<i>flhD</i>	flagellar transcriptional activator FlhD	Regulatory functions	-3.22	0.00043
STY2167	<i>fliC, flaG</i>	STM1959	<i>fliC</i>	flagellin	Cell envelope	-2.72	0.00000
STY2168	<i>fliD</i>	STM1960	<i>fliD</i>	flagellar hook associated protein 2	Cell envelope	-7.08	0.00009
STY2171	<i>amyA</i>	STM1963	<i>amyA</i>	cytoplasmic alpha-amylase	Macromolecule metabolism	-2.18	0.00042
STY2251	<i>pduK</i>	STM2046	<i>pduK</i>	putative propanediol utilization protein PduK	Small molecule metabolism	-2.10	0.00008
STY2276	<i>sbcB</i>	STM2067	<i>sbcB</i>	exodeoxyribonuclease I	DNA/RNA replication, degradation, modification	-2.04	0.00003
STY2289	<i>ugd, udg</i>	STM2080	<i>udg</i>	UDP-glucose 6-dehydrogenase	Small molecule metabolism	-2.54	0.00001
STY2303	<i>rfbI</i>	STM2093	<i>rfbI</i>	putative reductase RfbI	Cell envelope	-2.87	0.00024
STY2304	<i>rfbC</i>	STM2094	<i>rfbC</i>	dTDP-4-dehydrorhamnose 3,5-epimerase	Cell envelope	-3.48	0.00009
STY2346		STM2133		hypothetical protein	Unknown	-4.47	0.00035
STY2347		STM2134		hypothetical protein	Unknown	-2.40	0.00004
STY2378	<i>stcD, yehA</i>	STM2149	<i>stcD</i>	putative exported protein	Cell envelope	-2.85	0.00002
STY2403		STM2173		hypothetical protein	Unknown	-3.61	0.00001
STY2432		STM2198		putative transport protein (pseudogene)	Transport and binding proteins	-2.19	0.00004
STY2444		STM2208		putative membrane protein	Cell envelope	-4.39	0.00039
STY2469		STM2243		putative bacteriophage tail protein (pseudogene)	Unknown	-2.50	0.00003
STY2501		STM2274		putative transmembrane transpot protein (pseudogene)	Transport and binding proteins	-3.76	0.00016
STY2504		STM2275		putative transcriptional regulator (pseudogene)	Regulatory functions	-2.33	0.00002
STY2509		STM2280		putative transmembrane transport protein	Transport and binding proteins	-2.44	0.00026
STY2574		STM2344		putative sugar phosphotransferase component II A	Small molecule metabolism	-2.06	0.00010
STY2582	<i>hisM</i>	STM2352	<i>hisM</i>	histidine transport system permease	Transport and binding proteins	-2.61	0.00003
STY2607		STM2376		putative lipoprotein	Cell envelope	-2.15	0.00013

STY2608		STM2377		conserved hypothetical protein	Unknown	-2.76	0.00016
STY2621	<i>fadL</i>	STM2389	<i>yfcY</i>	putative 3-ketoacyl-CoA thiolase	Small molecule metabolism	-2.11	0.00009
STY2632	<i>pgtE, prtA</i>	STM2395	<i>pgtE</i>	outer membrane protease E, protease VII precursor	Cell envelope	-3.20	0.00038
STY2725	<i>purC</i>	STM2487	<i>purC</i>	phosphoribosylaminoimidazole-succinocarboxamide synthase	DNA/RNA replication, degradation, modification	-2.73	0.00020
STY2762	<i>sivH, sinH</i>	STM2517	<i>sinH</i>	putative intimin (pseudogene)	Pathogenesis	-2.32	0.00017
STY2820		STM2574		putative transmembrane transport protein	Transport and binding proteins	-2.57	0.00001
STY2860	<i>rplS</i>	STM2673	<i>rplS</i>	50S ribosomal subunit protein L19	Protein biosynthesis/degradation	-2.42	0.00008
STY2982	<i>ygbA</i>	STM2860	<i>ygbA</i>	conserved hypothetical protein	Unknown	-2.89	0.00010
STY2988	<i>sprA, hilC</i>	STM2867	<i>hilC</i>	possible AraC-family transcriptional regulator	Pathogenesis	-3.90	0.00002
STY2994	<i>prgI</i>	STM2873	<i>prgI</i>	pathogenicity 1 island effector protein	Pathogenesis	-3.42	0.00024
STY3004	<i>sipF</i>	STM2881	<i>iacP</i>	probable acyl carrier protein	Pathogenesis	-5.00	0.00003
STY3007	<i>sipC, sspC</i>	STM2884	<i>sipC</i>	pathogenicity island 1 effector protein	Pathogenesis	-2.01	0.00010
STY3010	<i>spaS</i>	STM2887	<i>spaS</i>	secretory protein (associated with virulence)	Pathogenesis	-2.05	0.00045
STY3047		STM2922		conserved hypothetical protein	Unknown	-3.08	0.00019
STY3167		STM3022		probable amino acid transport protein	Transport and binding proteins	-2.06	0.00043
STY3309		STM3138		hypothetical protein	Unknown	-2.43	0.00001
STY3331	<i>exbD</i>	STM3158	<i>exbD</i>	biopolymer transport ExbD protein	Transport and binding proteins	-6.04	0.00010
STY3332	<i>exbB</i>	STM3159	<i>exbB</i>	biopolymer transport ExbB protein	Transport and binding proteins	-3.53	0.00012
STY3340		STM3166.S		possible membrane transport protein	Transport and binding proteins	-2.58	0.00044
STY3456		STM3273	<i>yhbT</i>	conserved hypothetical protein	Unknown	-2.07	0.00027
STY3537		STM3357		possible transcriptional regulator	Regulatory functions	-4.71	0.00021
STY3605		STM3954	<i>yigG</i>	conserved hypothetical protein	Unknown	-3.03	0.00046
STY3862	<i>ompL</i>	STM4016	<i>ompL, yshA</i>	conserved hypothetical protein	Unknown	-2.78	0.00010
STY3871	<i>typA</i>	STM4009	<i>typA, bipA</i>	GTP-binding protein	Regulatory functions	-2.94	0.00049
STY4049	<i>trmH, spoU</i>	STM3743	<i>spoU</i>	tRNA (guanosine-2'-O)-methyltransferase	Protein biosynthesis/degradation	-2.53	0.00033
STY4072	<i>waaG, rfaG</i>	STM3722	<i>rfaG</i>	lipopolysaccharide core biosynthesis protein	Cell envelope	-3.25	0.00001
STY4077	<i>waal, rfal</i>	STM3718	<i>rfal</i>	lipopolysaccharide 1,3-galactosyltransferase	Cell envelope	-6.82	0.00005
STY4081	<i>waaK, rfak</i>	STM3714	<i>rfak</i>	lipopolysaccharide 1,2-N-acetylglucosaminetransferase	Cell envelope	-2.31	0.00007
STY4082	<i>waaL, rfaL, rfbT</i>	STM3713	<i>rfaL</i>	O-antigen ligase	Cell envelope	-2.26	0.00002
STY4106		STM3690		putative lipoprotein	Cell envelope	-4.77	0.00031

STY4264		STM3547.Sc		putative ribokinase	Unknown	-3.09	0.00022
STY4400	<i>metA</i>	STM4182	<i>metA</i>	homoserine O-succinyltransferase	Amino acid biosynthesis/degradation	-2.27	0.00015
STY4426	<i>malK</i>	STM4230	<i>malK</i>	maltose/maltodextrin transport ATP-binding protein	Transport and binding proteins	-2.01	0.00026
STY4453		STM4258	<i>siIB</i>	putative integral membrane protein	Pathogenesis	-3.55	0.00020
STY4456		STM4259	<i>siIC</i>	putative type-I secretion protein	Pathogenesis	-3.43	0.00002
STY4458		STM4261	<i>siIE</i>	large repetitive protein (pseudogene)	Pathogenesis	-2.35	0.00004
STY4582				possible exported protein	Pathogenesis	-2.89	0.00038
STY4679				putative membrane protein	Pathogenesis	-3.33	0.00001
STY4725	<i>rnr</i>	STM4368	<i>vacB</i>	ribonuclease R (RNase R)	DNA/RNA replication, degradation, modification	-3.84	0.00009
STY4728	<i>yifJ</i>	STM4371	<i>yifJ</i>	conserved hypothetical protein (pseudogene)	Unknown	-3.37	0.00004
STY4805		STM4467		arginine deiminase	Amino acid biosynthesis/degradation	-3.06	0.00024
STY4842				probable regulatory protein	Pathogenesis	-3.74	0.00000
STY4863	<i>trpS2</i>	STM4508	<i>trpS2</i>	probable tryptophanyl-tRNA synthetase	Protein biosynthesis/degradation	-2.85	0.00015
STY4881	<i>hsdS</i>	STM4524	<i>hsdS</i>	subunit S of type I restriction - modification system	DNA/RNA replication, degradation, modification	-2.51	0.00006
STY4899		STM4546	<i>yijP</i>	putative membrane protein	Cell envelope	-2.96	0.00035