

Table S1: Comparison of TviA-regulated genes in *S. Typhi* and *S. Typhimurium*

Cluster	Annotation in microarray	Gene Symbol	S. Typhimurium	S. Typhi
			IR715 (pTVIA1) / IR715 (pWSK29)	Δ tviB-vexE / Δ viaB
			Fold change	Fold change
1	major type 1 subunit fimbrin (pilin)	<i>fimA</i>	0.133	0.323
	putative outer membrane lipoprotein	STM1934	0.148	0.341
	flagellar biosynthesis, basal-body outer-membrane L (lipopolysaccharide layer)	<i>flgH</i>	0.143	0.385
	flagellar biosynthesis	<i>fliQ</i>	0.129	0.400
	flagellar protein FliO	<i>fliO</i>	0.124	0.403
	flagellar hook-length control protein	<i>fliK</i>	0.136	0.423
	putative Flagellar hook-basal body protein	<i>fliE</i>	0.113	0.336
	flagellar biosynthesis, cell-proximal portion of basal-body rod	<i>flgB</i>	0.113	0.331
	flagellar protein	<i>fliJ</i>	0.110	0.332
	flagellar biosynthesis basal-body MS(membrane and supramembrane)-ring and	<i>fliF</i>	0.106	0.345
	flagellar biosynthesis, component of motor switch and	<i>fliN</i>	0.109	0.321
	flagellar biosynthesis, component of motor switch and	<i>fliM</i>	0.108	0.380
	putative flagella basal body protein	<i>flgI</i>	0.105	0.364
	flagellar biosynthesis	<i>fliL</i>	0.103	0.385
	flagellar biosynthesis	<i>flgJ</i>	0.105	0.311
	flagellar biosynthesis possible export of flagellar proteins	<i>fliH</i>	0.102	0.294
	flagellar basal body rod modification protein	<i>flgD</i>	0.093	0.339
	flagellar biosynthesis, hook protein	<i>flgE</i>	0.105	0.274
	flagellar biosynthesis, cell-proximal portion of basal-body rod	<i>flgF</i>	0.094	0.285
	flagellar basal body rod protein	<i>flgC</i>	0.089	0.300
	flagellar biosynthesis, cell-distal portion of basal-body rod	<i>flgG</i>	0.088	0.379
	flagellum-specific ATP synthase	<i>fliI</i>	0.111	0.468
	putative inner membrane protein	<i>ycgR</i>	0.079	0.285
	putative cytoplasmic protein	STM3156	0.113	0.236
	hypothetical protein	t1775	0.161	0.274
	putative cytoplasmic protein	STM3155	0.165	0.288
	ssrAB activated gene	<i>srfB</i>	0.175	0.294
	putative ATP-dependent RNA helicase-like	STM3154	0.181	0.356

protein			
ssrAB activated gene: predicted coiled-coil structure	<i>srfC</i>	0.192	0.343
aerotaxis sensor receptor, senses cellular redox state	<i>aer</i>	0.120	0.206
flagellar biosynthesis assembly of basal-body periplasmic P	<i>flgA</i>	0.184	0.429
FliZ protein	<i>fliZ</i>	0.083	0.225
putative periplasmic protein	<i>ymdA</i>	0.201	0.398
ssrAB activated gene	<i>srfA</i>	0.195	0.435
putative periplasmic protein	STM1300	0.199	0.257
invasion protein	<i>invE</i>	0.157	0.198
invasion genes transcription activator	<i>hilA</i>	0.171	0.198
putative AraC-type DNA-binding domain-containing protein	STM4315	0.231	0.274
putative outer membrane protein	STM1328	0.248	0.252
invasion protein	<i>invA</i>	0.258	0.360
flagellar protein	<i>flhE</i>	0.186	0.592
putative outer membrane or exported	STM1841	0.096	0.630
putative methyl-accepting chemotaxis protein	STM3152	0.122	0.155
flagellar biosynthesis hook-filament junction protein	<i>flgL</i>	0.066	0.222
flagella synthesis protein FlgN	<i>flgN</i>	0.064	0.207
transcriptional regulator of ftsQAZ gene cluster (LuxR/UhpA	<i>sdiA</i>	0.294	0.254
flagellar biosynthesis repressor of class 3a and	<i>fliS</i>	0.056	0.244
hypothetical protein	t3059	0.055	0.227
flagellar biosynthesis possible export chaperone for FliD	<i>fliT</i>	0.057	0.205
chemotaxis regulator, transmits chemoreceptor signals to flagellar	<i>cheY</i>	0.055	0.192
anti-FliA (anti-sigma) factor also known as RfiB	<i>flgM</i>	0.050	0.221
flagellar biosynthesis filament capping protein	<i>fliD</i>	0.054	0.180
regulator of flagellar biosynthesis, acts on class	<i>flhD</i>	0.316	0.318
methyl esterase, response regulator for chemotaxis (cheA	<i>cheB</i>	0.046	0.209
flagellar biosynthesis, hook-filament junction protein 1	<i>flgK</i>	0.048	0.178
chemotactic response CheY protein phosphatase	<i>cheZ</i>	0.043	0.198
regulator of flagellar biosynthesis, acts on class	<i>flhC</i>	0.301	0.497
cell invasion protein cytoplasmic	<i>prgI</i>	0.213	0.128
invasion protein	<i>invH</i>	0.356	0.305
transcriptional regulator	<i>sprB</i>	0.367	0.324
surface presentation of antigens secretory proteins	<i>spaP</i>	0.306	0.161

	putative cytoplasmic protein	<i>yghW</i>	0.214	0.790
	purine-binding chemotaxis protein regulation	<i>cheW</i>	0.041	0.179
	proton conductor component of motor, torque generator	<i>motA</i>	0.039	0.206
	possible AraC-family regulatory protein	<i>invF</i>	0.180	0.101
	surface presentation of antigens secretory proteins	<i>spaO</i>	0.381	0.188
	cell invasion protein	<i>prgH</i>	0.258	0.113
	methyl-accepting transmembrane citrate/phenol chemoreceptor	<i>tcp</i>	0.040	0.149
	N-methylation of lysine residues in flagellin	<i>fliB</i>	0.086	ND
	putative bacterial regulatory proteins, luxR family	STM4314	0.104	ND
	putative cytoplasmic protein	STM4313	0.166	ND
	30S ribosomal protein S19	<i>rpsS</i>	0.176	0.995
	methyl-accepting chemotaxis protein III, ribose and galactose	<i>trg</i>	0.089	ND
	putative flagellar biosynthetic protein	<i>fliR</i>	0.117	1.065
	putative 50S ribosomal protein	STM1967	0.074	ND
	putative methyl-accepting chemotaxis protein	STM3216	0.234	ND
	putative Diguanylate cyclase/phosphodiesterase domain 3	<i>yhjH</i>	0.034	0.396
2	Pathogenicity island encoded protein: homologous to ipgE	<i>pipC</i>	0.644	0.075
	cell invasion protein	<i>sipC</i>	0.537	0.097
	surface presentation of antigens secretory proteins	<i>sicA</i>	0.525	0.107
	cell invasion protein	<i>sipB</i>	0.647	0.106
	putative inner membrane protein	STM2870	0.466	0.120
	Salmonella outer protein: homologous to ipgD of	<i>sopB</i>	0.387	0.116
	putative flagellar biosynthesis/type III secretory pathway protein	<i>orgA</i>	0.423	0.154
	cell invasion protein lipoprotein, may link inner	<i>prgK</i>	0.331	0.099
	cell invasion protein	<i>sipA</i>	0.550	0.178
	cell invasion protein cytoplasmic	<i>prgJ</i>	0.328	0.074
	surface presentation of antigens secretory proteins	<i>invI</i>	0.289	0.064
	virulence-associated secretory protein	<i>spak</i>	0.243	0.082
	invasion protein outer membrane	<i>invG</i>	0.238	0.077
	surface presentation of antigens secretory proteins	<i>invC</i>	0.235	0.078
	surface presentation of antigens secretory proteins	<i>invJ</i>	0.276	0.060
	flagellar biosynthesis protein	<i>fliC</i>	ND	0.089
	pathogenicity island 1 effector protein	<i>sipD</i>	ND	0.143

	hypothetical protein	t0349	ND	0.145
	hypothetical protein	t1865	ND	0.148
	putative receptor/regulator protein	t0549	ND	0.148
	methyl-accepting chemotaxis protein II	<i>cheM</i>	ND	0.167
	putative cytoplasmic protein	STM2868	0.557	0.250
	regulatory helix-turn-helix proteins, araC family	<i>hilD</i>	0.493	0.283
	bacterial regulatory helix-turn-helix proteins, araC family	<i>hilC</i>	0.465	0.293
3	flagellar biosynthesis flagellin, filament structural protein	<i>fliC</i>	0.014	ND
	Flagellar synthesis: phase 2 flagellin (filament structural	<i>fliB</i>	0.056	ND
	putative chemotaxis signal transduction protein	STM2314	0.059	ND
4	invasion-associated secreted protein.	<i>sopE</i>	ND	0.030
5	glutamate methyltransferase, response regulator for chemotaxis	<i>cheR</i>	0.031	0.177
	methyl-accepting chemotaxis protein I, serine sensor receptor	<i>tsr</i>	0.029	0.182
	methyl accepting chemotaxis protein II, aspartate sensor-receptor	<i>cheM</i>	0.025	0.174
	flagellar motor protein	<i>motB</i>	0.029	0.247
	sensory histidine protein kinase, transduces signal between	<i>cheA</i>	0.035	0.131
6	Vi polysaccharide biosynthesis protein	<i>tviA</i>	8.174	14.630
7	putative aspartate racemase	STM4510	12.313	1.050
	isoaspartyl dipeptidase	<i>iadA</i>	10.505	1.330
	hypothetical protein	t4563	7.295	1.128
	putative transcriptional regulator, LysR family	<i>yjiE</i>	7.190	0.947
	putative inner membrane protein	<i>yjiH</i>	5.156	1.180