

## 8 Appendices

### 8.1 Chapter 2

#### 8.1.1 CD\_001

Perl script genBank2pathologic.pl can be found upon the accompanying CD.

### 8.2 Chapter 3

#### 8.2.1 Biolog phenotypes for PM-1

Substrate on plate PM1	Typhi	Gallinarum	Typhimurium
negative control	35	37	44
L-arabinose	68	<b>275</b>	<b>151</b>
N-acetyl-D-glucosamine	<b>132</b>	<b>302</b>	<b>196</b>
D-saccharic acid	25	29	<b>208</b>
succinic acid	42	59	<b>206</b>
D-galactose	<b>180</b>	<b>319</b>	<b>230</b>
L-aspartic acid	38	35	<b>223</b>
L-proline	<b>142</b>	<b>130</b>	<b>201</b>
D-alanine	37	<b>120</b>	75
D-trehalose	<b>182</b>	<b>291</b>	<b>203</b>
D-mannose	<b>152</b>	<b>310</b>	<b>152</b>
dulcitol	49	90	88
D-serine	<b>132</b>	<b>271</b>	<b>292</b>
D-sorbitol	<b>120</b>	27	<b>188</b>
glycerol	<b>151</b>	<b>264</b>	<b>115</b>
L-fucose	21	25	98
D-glucuronic acid	99	<b>268</b>	<b>253</b>
D-gluconic acid	<b>164</b>	<b>313</b>	<b>249</b>
D,L-alpha-glycerol-phosphate	80	<b>264</b>	<b>152</b>
D-xylose	85	40	50
L-lactic acid	<b>194</b>	<b>269</b>	<b>274</b>
formic acid	20	27	38
D-mannitol	<b>217</b>	<b>317</b>	<b>214</b>
L-glutamic acid	<b>103</b>	99	<b>245</b>
D-glucose-6-phosphate	<b>198</b>	<b>312</b>	<b>302</b>
D-galatonic acid-gamma-lactone	23	33	<b>141</b>
D,L-malic acid	37	18	<b>228</b>

D-ribose	68	<b>265</b>	<b>215</b>
tween 20	20	63	78
L-rhamnose	12	23	<b>146</b>
D-fructose	<b>130</b>	<b>297</b>	<b>177</b>
acetic acid	52	87	<b>172</b>
alpha-D-glucose	<b>150</b>	<b>299</b>	<b>188</b>
maltose	<b>115</b>	<b>221</b>	<b>226</b>
D-melibiose	<b>115</b>	39	<b>197</b>
thymidine	<b>120</b>	<b>314</b>	<b>209</b>
L-asparagine	54	47	<b>204</b>
D-aspartic acid	31	19	<b>155</b>
D-glucosaminic acid	20	22	<b>232</b>
1,2-propanediol	20	24	32
tween 40	18	35	72
alpha-keto-glutaric acid	18	21	31
alpha-keto-butyric acid	62	25	<b>196</b>
alpha-methyl-D-galactoside	<b>170</b>	22	<b>264</b>
alpha-D-lactose	25	29	44
lactulose	30	41	51
sucrose	<b>146</b>	34	<b>140</b>
uridine	<b>112</b>	<b>300</b>	<b>163</b>
L-glutamine	55	48	<b>190</b>
M-tartric acid	22	22	28
D-glucose-1-phosphate	<b>191</b>	<b>293</b>	<b>263</b>
D-fructose-6-phosphate	<b>162</b>	<b>263</b>	<b>238</b>
tween 80	24	39	94
alpha-hydroxy-glutaric acid-gamme-lactone	22	46	58
alpha-hydroxy butyric acid	<b>131</b>	39	<b>211</b>
beta-methyl-D-glucoside	<b>107</b>	35	<b>218</b>
adonitol	23	28	38
maltotriose	<b>178</b>	<b>289</b>	<b>229</b>
2-deoxy adenosine	<b>118</b>	<b>304</b>	<b>254</b>
adenosine	<b>150</b>	<b>321</b>	<b>273</b>
glycyl-L-aspartic acid	80	<b>140</b>	<b>257</b>
citric acid	26	34	77
M-inositol	62	22	41
D-threonine	21	39	77
fumaric acid	37	26	<b>197</b>
bromo succinic acid	28	24	<b>161</b>
propionic acid	95	<b>111</b>	<b>219</b>
mucic acid	26	32	<b>227</b>
glycolic acid	23	27	30
glyoxylic acid	24	34	29
D-cellibiose	77	48	<b>161</b>
inosine	<b>139</b>	<b>299</b>	<b>241</b>
glycyl-L-glutamic acid	97	<b>238</b>	<b>227</b>
tricarballic acid	72	32	40
L-serine	<b>146</b>	<b>268</b>	<b>230</b>
L-threonine	95	34	72
L-alanine	29	<b>136</b>	<b>175</b>

L-alanyl-glycine	55	<b>204</b>	<b>212</b>
acetoacetic acid	25	43	34
N-acetyl-beta-D-mannosamine	<b>182</b>	<b>290</b>	<b>224</b>
mono methyl succinate	34	62	<b>114</b>
methyl pyruvate	<b>111</b>	<b>290</b>	<b>159</b>
D-malic acid	36	41	36
L-malic acid	57	81	<b>228</b>
glycyl-L-proline	<b>102</b>	<b>233</b>	<b>201</b>
p-hydroxy phenyl acetic acid	40	43	<b>152</b>
m-hydroxy phenyl acetic acid	36	37	<b>127</b>
tyramine	42	40	<b>119</b>
d-palacose	41	50	57
L-lyxose	62	73	79
glucuronamide	45	<b>117</b>	59
pyruvic acid	<b>119</b>	<b>233</b>	<b>184</b>
L-galactonic acid-gamma-lactone	36	48	47
D-galacturonic acid	71	77	<b>171</b>
phenylethylamine	39	53	51
2-aminoethanol	54	68	61

Substrates are listed in the order they appear in plate PM1 (wells A1-12, B1-12 etc). Values are the integer average of three replicates and those in bold exceed the 100 cutoff, indicating a positive metabolic phenotype for that substrate.

## 8.2.2 Biolog phenotypes for PM-2A

Substrate on plate PM2	Typhi	Gallinarum	Typhimurium
negative control	57	64	61
chondroitin sulfate C	47	47	52
alpha-cyclodextrin	39	45	42
beta-cyclodextrin	41	48	52
gamma-cyclodextrin	35	38	37
dextrin	54	<b>186</b>	<b>167</b>
gelatin	37	43	47
glycogen	42	62	83
inulin	37	44	47
laminarin	43	57	59
mannan	45	57	60
pectin	92	<b>122</b>	<b>128</b>
N-acetyl-D-galactosamine	47	53	55
N-acetyl-neuraminic acid	<b>152</b>	<b>296</b>	<b>223</b>
beta-D-allose	16	17	19
amygdalin	26	30	29
D-arabinose	32	41	39
D-arabitol	26	33	32
L-arabitol	23	26	26
arbutin	27	32	32
2-deoxy-D-ribose	56	<b>116</b>	40
L-erythritol	23	29	26

D-fucose	30	34	36
3-O-beta-D-galactopyranosyl-D-arabinose	50	52	79
gentiobiose	<b>141</b>	44	80
L-glucose	27	27	29
lactitol	19	20	22
D-melizitose	24	25	29
maltitol	24	31	32
alpha-methyl-D-glucoside	21	24	26
beta-methyl-D-galactoside	21	27	35
3-methyl glucose	23	25	32
beta-methyl-D-glucuronic acid	25	26	38
alpha-methyl-D-mannoside	26	32	35
beta-methyl-D-xyloside	26	28	35
palatinose	45	52	54
D-raffinose	88	44	86
salicin	22	23	26
deoxyheptulosan	18	18	24
L-sorbose	49	26	64
stachyose	19	21	26
D-tagatose	22	28	<b>185</b>
turanose	24	41	51
xylitol	18	21	24
N-acetyl-D-glucosaminitol	20	22	32
gamma-amino butyric acid	26	31	35
delta-amino valeric acid	23	29	27
butyric acid	42	44	44
capric acid	44	50	43
caproic acid	28	29	32
citraconic acid	20	23	26
citramelic acid	23	26	27
D-glucosamine	<b>219</b>	<b>323</b>	<b>233</b>
2-hydroxy benzoic acid	14	17	26
4-hydroxy benzoic acid	15	17	22
beta-hydroxy butyric acid	17	21	38
gamma-hydroxy butyric acid	24	26	27
alpha-keto valeric acid	24	33	32
itaconic acid	25	33	63
5-keto-D-gluconic acid	53	<b>231</b>	75
D-lactic acid methyl ester	<b>124</b>	55	<b>213</b>
malonic acid	24	21	33
melibiononic acid	81	28	<b>196</b>
oxalic acid	24	29	27
oxalomalic acid	22	22	23
quinic acid	21	22	25
D-ribono-1,4-lactone	21	30	36
sabacic acid	18	22	25
sorbic acid	33	37	44
succinamic acid	24	51	63
D-tartric acid	29	33	<b>231</b>
L-tartric acid	45	47	58

acetamide	33	39	35
L-alaninamide	32	41	57
N-acetyl-L-glutamic acid	17	18	32
L-arginine	21	23	26
glycine	28	23	44
L-histidine	16	56	82
L-homoserine	16	22	23
Hydroxy-L-proline	21	22	35
L-isoleucine	23	27	27
L-leucine	19	24	35
L-lysine	24	27	33
L-methionine	45	50	60
L-ornithine	31	38	38
L-phenylalanine	24	26	26
L-pyroglutamic acid	22	22	24
L-valine	24	26	33
D,L-carnitine	16	20	18
sec-butylamine	7	6	10
D,L-octopamine	23	24	26
putrescine	22	21	28
dihydroxyacetone	77	90	83
2,3-butanediol	23	41	43
2,3-butanone	49	63	83
3-hydroxy 2-butanone	41	57	69

Substrates are listed in the order they appear in plate PM-2A (wells A1-12, B1-12 etc). Values are the integer average of three replicates and those in bold exceed the 100 cutoff, indicating a positive metabolic phenotype for that substrate.

## 8.3 Chapter 4

### 8.3.1 CD\_002

Perl script removeTn5\_new.pl can be found upon the accompanying CD.

### 8.3.2 CD\_003

Excel table of TraDIS results for Typhi can be found on the accompanying CD.

### 8.3.3 Typhi essential genes

Total inserts	Total reads	Gene length	Insertion index	Gene name	Ty2 unique ID	CT18 unique ID	Start	End	Strand	LLR*	P-value for no inserts
0	0	683	0	-	t1702	STY1258	1767132	1767815	-	-174.95588	6.63E-23
0	0	1151	0	-	t1621	STY1343	1676999	1678150	-	-174.95588	4.22E-38
0	0	164	0	-	t1947	STY0989	1995908	1996072	-	-174.95588	4.73E-06
0	0	134	0	-	t0535	STY2559	609653	609787	+	-174.95588	4.45E-05
0	0	212	0	-	t1378	STY1610	1432097	1432309	-	-174.95588	1.31E-07
0	0	209	0	-	t3166	none	3257647	3257856	-	-174.95588	1.63E-07
0	0	1319	0	-	t3211	STY3472	3302434	3303753	-	-174.95588	1.48E-43
0	0	29	0	-	t2621	STY2853	2699223	2699252	+	-174.95588	0.1143721
0	0	995	0	-	t3128	STY3387	3215818	3216813	-	-174.95588	4.91E-33
0	0	707	0	-	t3236	STY3498	3323667	3324374	+	-174.95588	1.10E-23
0	0	1454	0	-	t0337	STY2764	387679	389133	+	-174.95588	6.11E-48
0	0	1082	0	-	t4513	STY4817	4661340	4662422	+	-174.95588	7.34E-36
0	0	941	0	accA	t0233	STY0255	269925	270866	+	-174.95588	2.78E-31
0	0	452	0	accB	t3294	STY3559	3389201	3389653	+	-174.95588	2.10E-15
0	0	362	0	acpS	t0280	STY2823	318329	318691	+	-174.95588	1.76E-12
0	0	626	0	adk	t2372	STY0532	2441400	2442026	-	-174.95588	4.71E-21
0	0	2612	0	alaS	t2728	STY2948	2810136	2812748	-	-174.95588	1.53E-85
0	0	1715	0	argS	t0968	STY2117	1057200	1058915	-	-174.95588	2.05E-56
0	0	1088	0	asd	t3981	STY4271	4120832	4121920	+	-174.95588	4.69E-36
0	0	1382	0	asnS	t1934	STY1004	1977691	1979073	+	-174.95588	1.33E-45
0	0	1754	0	aspS	t0976	STY2109	1064648	1066402	+	-174.95588	1.11E-57
0	0	614	0	cl	t4337	STY4644	4489204	4489818	+	-174.95588	1.15E-20

0	0	461	0	coaD	t3793	STY4069	3912702	3913163	-	-174.95588	1.07E-15
0	0	167	0	csrA	t2727	STY2947	2809716	2809883	-	-174.95588	3.78E-06
0	0	1367	0	cysS	t2324	STY0585	2387383	2388750	-	-174.95588	4.08E-45
0	0	806	0	dapD	t0214	STY0236	246298	247104	-	-174.95588	6.73E-27
0	0	1109	0	dapE	t0376	STY2721	445724	446833	-	-174.95588	9.75E-37
0	0	1205	0	dfp	t3788	STY4064	3909064	3910269	-	-174.95588	7.44E-40
0	0	1382	0	dnaA	t3681	STY3940	3790627	3792009	+	-174.95588	1.33E-45
0	0	719	0	dnaC	t4586	STY4896	4742290	4743009	-	-174.95588	4.50E-24
0	0	3464	0	dnaE	t0232	STY0254	266430	269894	+	-174.95588	3.30E-113
0	0	1727	0	dnaG	t3130	STY3389	3217510	3219237	+	-174.95588	8.34E-57
0	0	713	0	dnaQ	t2601	STY0285	2678132	2678845	-	-174.95588	7.04E-24
0	0	521	0	dnaT	t4587	STY4897	4743030	4743551	-	-174.95588	1.21E-17
0	0	437	0	dut	t3787	STY4063	3908628	3909065	-	-174.95588	6.45E-15
0	0	1178	0	dxr	t0221	STY0243	254731	255909	+	-174.95588	5.60E-39
0	0	716	0	fabG	t1725	STY1234	1791565	1792281	-	-174.95588	5.63E-24
0	0	437	0	fabZ	t0228	STY0250	263418	263855	+	-174.95588	6.45E-15
0	0	344	0	folB	t3126	STY3385	3214491	3214835	-	-174.95588	6.76E-12
0	0	650	0	folE	t0662	STY2427	747254	747904	+	-174.95588	7.82E-22
0	0	1244	0	ftsA	t0136	STY0152	155775	157019	+	-174.95588	4.03E-41
0	0	650	0	ftsE	t3952	STY4241	4091910	4092560	+	-174.95588	7.82E-22
0	0	1748	0	ftsl	t0126	STY0142	143141	144889	+	-174.95588	1.74E-57
0	0	1100	0	gcpE	t0333	STY2768	383234	384334	+	-174.95588	1.91E-36
0	0	560	0	gmhA	t2540	STY0355	2615917	2616477	-	-174.95588	6.54E-19
0	0	275	0	groES	t4381	STY4689	4534179	4534454	+	-174.95588	1.18E-09
0	0	1238	0	hemA	t1099	STY1902	1183829	1185067	+	-174.95588	6.31E-41
0	0	1046	0	hemE	t3464	STY3718	3552993	3554039	-	-174.95588	1.08E-34
0	0	527	0	hemG	t3311	STY3573	3409489	3410016	-	-174.95588	7.72E-18
0	0	605	0	hemM	t1098	STY1904	1182892	1183497	-	-174.95588	2.26E-20
0	0	2816	0	ileS	t0048	STY0055	53861	56677	+	-174.95588	3.63E-92
0	0	200	0	infA	t1980	STY0951	2039984	2040184	+	-174.95588	3.20E-07
0	0	524	0	infC	t1214	STY1777	1282586	1283110	+	-174.95588	9.66E-18
0	0	833	0	ipk	t1097	STY1905	1182044	1182877	-	-174.95588	8.93E-28
0	0	953	0	ispB	t3222	STY3484	3313375	3314328	+	-174.95588	1.13E-31
0	0	728	0	kdsB	t1946	STY0990	1995165	1995893	-	-174.95588	2.29E-24
0	0	2564	0	leuS	t2219	STY0699	2284624	2287188	+	-174.95588	5.53E-84
0	0	857	0	lgt	t2911	STY3143	3000970	3001827	-	-174.95588	1.49E-28
0	0	1997	0	ligA	t0431	STY2663	503096	505093	+	-174.95588	1.43E-65
0	0	596	0	lolA	t1973	STY0959	2028390	2028986	-	-174.95588	4.43E-20
0	0	770	0	lpxA	t0229	STY0251	263877	264647	+	-174.95588	9.93E-26
0	0	482	0	lspA	t0049	STY0056	56695	57177	+	-174.95588	2.23E-16
0	0	1064	0	mraY	t0129	STY0145	147730	148794	+	-174.95588	2.82E-35
0	0	1094	0	mrdB	t2228	STY0690	2294311	2295405	+	-174.95588	2.99E-36
0	0	1025	0	mreB	t3289	STY3554	3382621	3383646	-	-174.95588	5.21E-34
0	0	1730	0	msbA	t1950	STY0985	1998392	2000122	-	-174.95588	6.67E-57
0	0	1304	0	mukF	t1942	STY0994	1991051	1992355	-	-174.95588	4.54E-43
0	0	1457	0	murC	t0133	STY0149	152558	154015	+	-174.95588	4.88E-48

0	0	1298	0	murD	t0130	STY0146	148815	150113	+	-174.95588	7.11E-43
0	0	1469	0	murE	t0127	STY0143	144894	146363	+	-174.95588	1.99E-48
0	0	809	0	nadE	t1189	STY1803	1258005	1258814	-	-174.95588	5.38E-27
0	0	2267	0	nrdA	t0587	STY2506	663376	665643	-	-174.95588	2.44E-74
0	0	527	0	orn	t4402	STY4710	4554290	4554817	+	-174.95588	7.72E-18
0	0	1874	0	parE	t3102	STY3359	3186968	3188842	-	-174.95588	1.41E-61
0	0	530	0	pgsA	t0931	STY2153	1025903	1026433	+	-174.95588	6.17E-18
0	0	26	0	pheM	t1217	STY1774	1283949	1283975	+	-174.95588	0.1431315
0	0	965	0	pheS	t1218	STY1773	1284130	1285095	+	-174.95588	4.62E-32
0	0	2369	0	pheT	t1219	STY1772	1285129	1287498	+	-174.95588	1.19E-77
0	0	719	0	plsC	t3094	STY3350	3178960	3179679	-	-174.95588	4.50E-24
0	0	512	0	ppa	t4468	STY4773	4616745	4617257	-	-174.95588	2.37E-17
0	0	1064	0	prfA	t1100	STY1901	1185126	1186190	+	-174.95588	2.82E-35
0	0	1080	0	prfB	t2959	STY3197	3048772	3049852	-	-174.95588	8.52E-36
0	0	296	0	priB	t4443	STY4748	4589371	4589667	+	-174.95588	2.45E-10
0	0	929	0	prsA	t1096	STY1906	1180831	1181760	-	-174.95588	6.82E-31
0	0	1337	0	pssA	t0258	STY2845	295248	296585	-	-174.95588	3.85E-44
0	0	707	0	pyrH	t0219	STY0241	253160	253867	+	-174.95588	1.10E-23
0	0	920	0	ribF	t0047	STY0054	52878	53798	+	-174.95588	1.34E-30
0	0	452	0	ribH	t2446	STY0456	2517395	2517847	-	-174.95588	2.10E-15
0	0	803	0	rplB	t4068	STY4361	4219535	4220338	+	-174.95588	8.42E-27
0	0	521	0	rplE	t4077	STY4370	4223460	4223981	+	-174.95588	1.21E-17
0	0	515	0	rplF	t4080	STY4373	4224758	4225273	+	-174.95588	1.89E-17
0	0	347	0	rplL	t3475	STY3733	3571291	3571638	-	-174.95588	5.40E-12
0	0	410	0	rplM	t3261	STY3525	3351928	3352338	-	-174.95588	4.86E-14
0	0	353	0	rplN	t4075	STY4368	4222749	4223102	+	-174.95588	3.45E-12
0	0	416	0	rplO	t4084	STY4377	4226359	4226775	+	-174.95588	3.10E-14
0	0	392	0	rplP	t4072	STY4365	4221730	4222122	+	-174.95588	1.87E-13
0	0	335	0	rplR	t4081	STY4374	4225301	4225636	+	-174.95588	1.32E-11
0	0	338	0	rplT	t1216	STY1775	1283472	1283810	+	-174.95588	1.06E-11
0	0	293	0	rplU	t3221	STY3483	3312805	3313098	-	-174.95588	3.06E-10
0	0	314	0	rplV	t4070	STY4363	4220666	4220980	+	-174.95588	6.37E-11
0	0	284	0	rplW	t4067	STY4360	4219215	4219499	+	-174.95588	6.00E-10
0	0	296	0	rplX	t4076	STY4369	4223131	4223427	+	-174.95588	2.45E-10
0	0	239	0	rpmA	t3220	STY3482	3312528	3312767	-	-174.95588	1.73E-08
0	0	218	0	rpmB	t3790	STY4066	3911343	3911561	+	-174.95588	8.34E-08
0	0	173	0	rpmC	t4073	STY4366	4222140	4222313	+	-174.95588	2.41E-06
0	0	161	0	rpmD	t4083	STY4376	4226176	4226337	+	-174.95588	5.92E-06
0	0	122	0	rpmH	t3680	STY3939A	3789826	3789948	-	-174.95588	0.0001093
0	0	179	0	rpmI	t1215	STY1776	1283224	1283403	+	-174.95588	1.54E-06
0	0	971	0	rpoA	t4090	STY4383	4229869	4230840	+	-174.95588	2.95E-32
0	0	683	0	rpsC	t4071	STY4364	4221016	4221699	+	-174.95588	6.63E-23
0	0	602	0	rpsD	t4089	STY4382	4229223	4229825	+	-174.95588	2.83E-20
0	0	485	0	rpsE	t4082	STY4375	4225669	4226154	+	-174.95588	1.78E-16
0	0	377	0	rpsF	t4442	STY4747	4588969	4589346	+	-174.95588	5.73E-13
0	0	452	0	rpsG	t4058	STY4351	4211920	4212372	+	-174.95588	2.10E-15



0	0	374	0	rpsH	t4079	STY4372	4224353	4224727	+	-174.95588	7.17E-13
0	0	293	0	rpsJ	t4064	STY4357	4217629	4217922	+	-174.95588	3.06E-10
0	0	371	0	rpsK	t4088	STY4381	4228800	4229171	+	-174.95588	8.97E-13
0	0	356	0	rpsL	t4057	STY4350	4211450	4211806	+	-174.95588	2.75E-12
0	0	338	0	rpsM	t4087	STY4380	4228427	4228765	+	-174.95588	1.06E-11
0	0	287	0	rpsN	t4078	STY4371	4224014	4224301	+	-174.95588	4.79E-10
0	0	230	0	rpsP	t2631	STY2863	2707753	2707983	-	-174.95588	3.40E-08
0	0	236	0	rpsQ	t4074	STY4367	4222331	4222567	+	-174.95588	2.17E-08
0	0	260	0	rpsS	t4069	STY4362	4220373	4220633	+	-174.95588	3.61E-09
0	0	512	0	ssb	t4161	STY4451	4306069	4306581	+	-174.95588	2.37E-17
0	0	1910	0	thrS	t1213	STY1778	1280654	1282564	+	-174.95588	9.53E-63
0	0	623	0	tmk	t1720	STY1239	1787263	1787886	-	-174.95588	5.89E-21
0	0	833	0	tsf	t0218	STY0240	252164	252997	+	-174.95588	8.93E-28
0	0	1256	0	tyrS	t1317	STY1673	1377902	1379158	+	-174.95588	1.64E-41
0	0	737	0	ubiE	t3327	STY3589	3427124	3427861	-	-174.95588	1.17E-24
0	0	2837	0	valS	t4510	STY4814	4655999	4658836	-	-174.95588	7.55E-93
0	0	530	0	yfjA	t2630	STY2862	2707186	2707716	-	-174.95588	6.17E-18
0	0	461	0	ygbB	t2830	STY3054	2905705	2906166	-	-174.95588	1.07E-15
0	0	1460	0	yigC	t3319	STY3581	3420094	3421554	-	-174.95588	3.90E-48
1	2	2396	4E-04	gyrB	t3684	STY3943	3794432	3796828	+	-43.368975	1.58E-78
1	9	2240	4E-04	parC	t3095	STY3351	3179954	3182194	-	-42.651896	1.83E-73
1	1	2180	5E-04	priA	t3523	STY3775	3625523	3627703	+	-42.362453	1.63E-71
1	2	1844	5E-04	dxs	t2441	STY0461	2512409	2514253	+	-40.574479	1.32E-60
1	4	1628	6E-04	groEL	t4382	STY4690	4534516	4536144	+	-39.239302	1.37E-53
1	7	1628	6E-04	yidC	t3678	STY3938	3787580	3789208	-	-39.239302	1.37E-53
1	2	1499	7E-04	lysS	t2958	STY3196	3047245	3048744	-	-38.352224	2.11E-49
3	6	4448	7E-04	mukB	t1940	STY0996	1985900	1990348	-	-38.234347	3.68E-145
1	1	1409	7E-04	lpdA	t0160	STY0177	184153	185562	+	-37.685548	1.77E-46
1	1	1397	7E-04	dnaB	t4152	STY4442	4296374	4297771	+	-37.593361	4.34E-46
1	4	1352	7E-04	glmU	t3657	STY3916	3762297	3763649	+	-37.240239	1.25E-44
1	4	1340	7E-04	murF	t0128	STY0144	146378	147718	+	-37.144026	3.08E-44
3	6	4010	7E-04	rpoB	t3474	STY3732	3566945	3570955	-	-37.117142	6.14E-131
1	1	1334	7E-04	yaeL	t0224	STY0246	257880	259214	+	-37.095586	4.82E-44
1	6	1331	8E-04	accC	t3295	STY3560	3389682	3391013	+	-37.071281	6.03E-44
1	5	1313	8E-04	priA	t4085	STY4378	4226801	4228114	+	-36.924257	2.32E-43
2	4	2618	8E-04	gyrA	t0592	STY2499	670713	673331	+	-36.891302	9.75E-86
1	1	1274	8E-04	serS	t1971	STY0961	2025486	2026760	-	-36.598437	4.28E-42
1	6	1241	8E-04	murA	t3224	STY3486	3314925	3316166	-	-36.314593	5.04E-41
1	1	1241	8E-04	rho	t3380	STY3638	3480453	3481694	-	-36.314593	5.04E-41
1	1	1226	8E-04	-	t1701	STY1259	1765888	1767114	-	-36.182984	1.55E-40
2	10	2336	9E-04	imp	t0096	STY0108	105614	107950	-	-35.657933	1.40E-76
1	1	1133	9E-04	ftsZ	t0137	STY0153	157098	158231	+	-35.327864	1.62E-37
1	29	1130	9E-04	lpxB	t0230	STY0252	264665	265795	+	-35.299082	2.03E-37
1	2	1112	9E-04	nrdB	t0586	STY2507	662133	663245	-	-35.124709	7.79E-37
1	1	1082	9E-04	dnaN	t3682	STY3941	3792032	3793114	+	-34.827474	7.34E-36
1	1	1061	9E-04	fba	t2987	STY3226	3078251	3079312	-	-34.614273	3.53E-35

1	1	1049	1E-03	murG	t0132	STY0148	151372	152421	+	-34.490466	8.65E-35
2	6	1964	0.001	rpoD	t3131	STY3390	3219270	3221234	+	-33.770948	1.68E-64
1	3	977	0.001	gapA	t1169	STY1825	1236581	1237558	-	-33.715218	1.88E-32
1	1	968	0.001	-	t0429	STY2664	502038	503006	+	-33.614149	3.69E-32
1	3	959	0.001	lpxK	t1949	STY0986	1997418	1998377	-	-33.512096	7.24E-32
1	1	956	0.001	hemB	t2492	STY0404	2564895	2565851	+	-33.477856	9.06E-32
1	2	944	0.001	hemH	t2371	STY0533	2440208	2441152	-	-33.339766	2.22E-31
1	5	911	0.001	fabD	t1726	STY1233	1792312	1793223	-	-32.950356	2.62E-30
3	9	2660	0.001	infB	t3204	STY3467	3294925	3297585	-	-32.653651	4.22E-87
1	11	881	0.001	ispA	t2440	STY0462	2511486	2512367	+	-32.583332	2.47E-29
1	6	860	0.001	dapA	t0370	STY2727	439626	440486	+	-32.318545	1.19E-28
1	4	860	0.001	yfjB	t2637	STY2869	2713443	2714303	+	-32.318545	1.19E-28
2	10	1700	0.001	proS	t0245	STY0269	280765	282465	-	-32.190065	6.28E-56
1	30	836	0.001	kdsA	t1104	STY1897	1188278	1189114	+	-32.007506	7.14E-28
1	10	836	0.001	rpoH	t3954	STY4243	4093872	4094708	+	-32.007506	7.14E-28
1	1	803	0.001	dapB	t0066	STY0073	74022	74825	+	-31.564172	8.42E-27
3	13	2402	0.001	plsB	t4141	STY4431	4285962	4288364	-	-31.532104	1.01E-78
3	6	2393	0.001	yaeT	t0225	STY0247	259264	261657	+	-31.490729	1.97E-78
2	12	1520	0.001	Int	t2207	STY0711	2272626	2274146	+	-30.95685	4.40E-50
1	9	740	0.001	-	t0222	STY0244	256240	256980	+	-30.661925	9.35E-25
2	24	1457	0.001	ftsY	t3951	STY4240	4090432	4091889	+	-30.48851	4.88E-48
1	13	722	0.001	hemD	t3360	STY3622	3461587	3462309	+	-30.38921	3.59E-24
1	11	719	0.001	-	t2619	STY2852	2697772	2698491	+	-30.34306	4.50E-24
1	3	704	0.001	ybbF	t2326	STY0583	2389438	2390142	+	-30.109215	1.38E-23
1	1	644	0.002	yadF	t0176	STY0193	203598	204242	-	-29.117947	1.23E-21
1	1	638	0.002	pdxH	t1316	STY1674	1377119	1377757	+	-29.01347	1.92E-21
2	22	1256	0.002	hisS	t0334	STY2767	384463	385719	+	-28.836997	1.64E-41
3	19	1883	0.002	pbpA	t2227	STY0691	2292407	2294290	+	-28.831064	7.17E-62
1	1	623	0.002	ribE	t1294	STY1696	1357967	1358590	+	-28.747636	5.89E-21
1	7	614	0.002	-	t3620	STY3880	3721114	3721728	+	-28.584844	1.15E-20
1	1	611	0.002	rplC	t4065	STY4358	4217973	4218584	+	-28.530014	1.44E-20
1	1	602	0.002	yacE	t0146	STY0162	166354	166956	-	-28.363786	2.83E-20
2	15	1196	0.002	fabB	t0486	STY2609	559866	561062	+	-28.289054	1.46E-39
2	8	1190	0.002	sucB	t2139	STY0780	2200547	2201737	-	-28.232654	2.28E-39
1	2	587	0.002	rplD	t4066	STY4359	4218613	4219200	+	-28.080756	8.69E-20
2	2	1145	0.002	pgk	t2988	STY3227	3079432	3080577	-	-27.799715	6.61E-38
1	5	572	0.002	ribA	t1624	STY1340	1679593	1680165	+	-27.789888	2.67E-19
1	6	572	0.002	rlpB	t2220	STY0698	2287221	2287793	+	-27.789888	2.67E-19
2	8	1136	0.002	metK	t3002	STY3243	3092881	3094017	+	-27.710944	1.29E-37
1	12	557	0.002	rpoE	t0270	STY2833	309252	309809	+	-27.49074	8.19E-19
1	3	554	0.002	yrdC	t4102	STY4395	4239498	4240052	+	-27.429875	1.02E-18
5	18	2768	0.002	polA	t3621	STY3881	3722082	3724850	-	-27.421733	1.31E-90
2	6	1088	0.002	trmU	t1686	STY1274	1749012	1750100	+	-27.224407	4.69E-36
3	11	1619	0.002	pyrG	t2854	STY3082	2931600	2933219	-	-27.134108	2.68E-53
1	1	539	0.002	frr	t0220	STY0242	254032	254571	+	-27.120147	3.15E-18
2	12	1064	0.002	-	t4514	STY4818	4662440	4663504	+	-26.972424	2.82E-35

1	6	527	0.002	nusG	t3479	STY3737	3573930	3574457	-	-26.865623	7.72E-18
4	13	2096	0.002	fusA	t4059	STY4352	4212487	4214583	+	-26.801017	8.70E-69
4	10	2051	0.002	glyS	t3864	STY4144	3991761	3993812	+	-26.55515	2.51E-67
1	1	500	0.002	fabA	t1853	STY1088	1913358	1913858	+	-26.269371	5.81E-17
3	9	1475	0.002	mviN	t1750	STY1209	1814380	1815855	-	-26.078304	1.27E-48
1	1	491	0.002	fms	t4098	STY4391	4236714	4237205	-	-26.062867	1.14E-16
2	2	971	0.002	fepG	t2277	STY0635	2344426	2345397	+	-25.934647	2.95E-32
3	9	1415	0.002	waaE	t3120	STY3379	3205564	3206979	-	-25.605074	1.13E-46
4	8	1871	0.002	aceF	t0159	STY0176	182065	183936	+	-25.509857	1.76E-61
2	2	935	0.002	fabH	t1727	STY1232	1793257	1794192	-	-25.50375	4.35E-31
2	30	929	0.002	fmt	t4097	STY4390	4235751	4236680	-	-25.430187	6.82E-31
2	6	923	0.002	hemC	t3359	STY3621	3460649	3461572	+	-25.356108	1.07E-30
4	11	1829	0.002	secD	t2456	STY0445	2524726	2526555	-	-25.250262	4.07E-60
2	3	914	0.002	waaD	t3809	STY4085	3928396	3929310	-	-25.244002	2.09E-30
3	6	1352	0.002	purB	t1688	STY1272	1750850	1752202	+	-25.084175	1.25E-44
2	7	893	0.002	glyQ	t3863	STY4143	3990840	3991733	+	-24.977688	1.01E-29
1	1	443	0.002	yjeE	t4408	STY4714	4559146	4559589	+	-24.8874	4.12E-15
2	3	854	0.002	ubiA	t4140	STY4430	4284991	4285845	+	-24.464509	1.86E-28
3	117	1259	0.002	kdtA	t3794	STY4070	3913190	3914449	-	-24.264867	1.31E-41
2	2	839	0.002	cdsA	t0223	STY0245	257011	257850	+	-24.260285	5.70E-28
3	5	1250	0.002	folC	t0499	STY2596	571079	572329	+	-24.182093	2.57E-41
1	9	410	0.002	rplK	t3478	STY3736	3573344	3573754	-	-23.995793	4.86E-14
2	12	812	0.002	ftsQ	t0135	STY0151	154948	155760	+	-23.882413	4.30E-27
2	10	806	0.002	dapF	t3350	STY3612	3452074	3452880	-	-23.796571	6.73E-27
1	2	386	0.003	-	t1920	STY1020	1965700	1966086	+	-23.296494	2.92E-13
2	7	770	0.003	fabI	t1613	STY1352	1667618	1668388	+	-23.266327	9.93E-26
1	4	383	0.003	rbfA	t3203	STY3466	3294303	3294686	-	-23.205733	3.66E-13
5	11	1910	0.003	dnaX	t2376	STY0528	2445425	2447335	-	-23.175306	9.53E-63
5	10	1898	0.003	dnaK	t0012	STY0012	11603	13501	+	-23.10192	2.34E-62
7	11	2645	0.003	aceE	t0158	STY0175	179387	182032	+	-23.048307	1.30E-86
2	10	749	0.003	trmD	t2629	STY2861	2706374	2707123	-	-22.944262	4.77E-25
1	1	371	0.003	yadR	t0205	STY0226	237127	237498	+	-22.834688	8.97E-13
1	2	365	0.003	rplQ	t4091	STY4384	4230899	4231264	+	-22.644164	1.41E-12
1	5	365	0.003	secE	t3480	STY3738	3574477	3574842	-	-22.644164	1.41E-12
3	26	1085	0.003	ribD	t2447	STY0455	2517954	2519039	-	-22.536815	5.86E-36
2	21	710	0.003	ubiG	t0588	STY2505	666016	666726	-	-22.318791	8.81E-24
2	16	707	0.003	rpsB	t0217	STY0239	251181	251888	+	-22.269111	1.10E-23
1	2	347	0.003	ftsL	t0125	STY0141	142760	143107	+	-22.051091	5.40E-12
1	6	341	0.003	rnpA	t3679	STY3939	3789450	3789791	-	-21.845778	8.46E-12
2	20	677	0.003	-	t1057	STY1950	1141081	1141758	+	-21.759042	1.04E-22
5	9	1622	0.003	aarF	t3325	STY3587	3424872	3426494	-	-21.256089	2.14E-53
2	11	635	0.003	ribB	t3115	STY3373	3200858	3201493	-	-21.000987	2.40E-21
2	26	623	0.003	-	t2222	STY0696	2288844	2289467	+	-20.77406	5.89E-21
3	32	932	0.003	lytB	t0051	STY0058	57802	58734	+	-20.742155	5.45E-31
4	24	1223	0.003	cca	t3124	STY3383	3212226	3213449	+	-20.551938	1.94E-40
3	8	899	0.003	lpxC	t0138	STY0154	158350	159249	+	-20.311769	6.43E-30

3	11	896	0.003	accD	t0498	STY2597	570097	570993	+	-20.271765	8.04E-30
2	6	590	0.003	lexA	t4143	STY4433	4289030	4289620	+	-20.123779	6.95E-20
1	2	293	0.003	-	t2832	STY3056	2906913	2907206	-	-20.042182	3.06E-10
4	27	1157	0.003	yleB	t2202	STY0717	2267106	2268263	-	-19.88748	2.69E-38
5	14	1397	0.004	gltX	t0442	STY2654	512533	513930	+	-19.470078	4.34E-46
6	80	1649	0.004	glnS	t2189	STY0724	2256012	2257661	-	-19.270865	2.85E-54
7	60	1916	0.004	ftsH	t3213	STY3474	3304717	3306633	-	-19.221475	6.08E-63
10	30	2687	0.004	secA	t0140	STY0156	160107	162794	+	-18.99731	5.60E-88
5	35	1343	0.004	ffh	t2632	STY2864	2708345	2709688	-	-18.992791	2.46E-44
2	9	533	0.004	yfhC	t0289	STY2814	326228	326761	+	-18.89745	4.93E-18
1	1	266	0.004	rplY	t0630	STY2461	711619	711885	-	-18.874624	2.30E-09
4	16	1037	0.004	ftsX	t3953	STY4242	4092571	4093608	+	-18.56159	2.12E-34
3	11	776	0.004	map	t0216	STY0238	249937	250713	-	-18.534102	6.34E-26
3	5	776	0.004	thyA	t2910	STY3142	3000169	3000945	-	-18.534102	6.34E-26
2	24	512	0.004	fldA	t2181	STY0732	2247436	2247948	+	-18.407531	2.37E-17
5	16	1274	0.004	mesJ	t0238	STY0261	276262	277536	+	-18.350082	4.28E-42
4	21	1013	0.004	holA	t2221	STY0697	2287811	2288824	+	-18.275415	1.28E-33
4	10	1007	0.004	lpxD	t0227	STY0249	262287	263294	+	-18.202657	2.00E-33
1	3	251	0.004	rpsO	t3201	STY3464	3292939	3293190	-	-18.166092	7.07E-09
4	29	986	0.004	holB	t1719	STY1240	1786262	1787248	-	-17.944031	9.61E-33
5	12	1226	0.004	ftsW	t0131	STY0147	150131	151357	+	-17.879012	1.55E-40
3	45	722	0.004	-	t3415	STY3673	3511820	3512542	+	-17.649137	3.59E-24
4	10	959	0.004	-	t2444	STY0458	2515899	2516858	-	-17.602049	7.24E-32
4	27	956	0.004	lepB	t0275	STY2828	314016	314972	+	-17.563368	9.06E-32
4	21	950	0.004	psd	t4400	STY4708	4552071	4553021	-	-17.485583	1.42E-31
4	23	935	0.004	waaC	t3807	STY4083	3926394	3927329	-	-17.288614	4.35E-31
4	102	932	0.004	coaA	t3487	STY3740	3577233	3578165	+	-17.248782	5.45E-31
3	16	692	0.004	ygbP	t2831	STY3055	2906184	2906876	-	-17.123905	3.39E-23
4	11	887	0.005	era	t0276	STY2826	315941	316828	+	-16.632838	1.58E-29
3	20	659	0.005	mukE	t1941	STY0995	1990366	1991025	-	-16.514792	3.99E-22
1	8	218	0.005	acpP	t1724	STY1235	1791173	1791391	-	-16.419413	8.34E-08
6	53	1292	0.005	-	t1703	STY1257	1767826	1769118	-	-16.265024	1.11E-42
4	24	848	0.005	fold	t2321	STY0588	2385580	2386428	+	-16.068868	2.91E-28
5	25	1034	0.005	mreC	t3288	STY3553	3381504	3382538	-	-15.755546	2.66E-34
3	7	608	0.005	ftsJ	t3214	STY3475	3306755	3307363	-	-15.49983	1.81E-20
2	16	401	0.005	nusB	t2445	STY0457	2516955	2517356	-	-15.363324	9.52E-14
2	7	398	0.005	-	t3009	STY3250	3099855	3100253	+	-15.267798	1.19E-13
14	38	2783	0.005	sucA	t2140	STY0779	2201770	2204553	-	-15.254083	4.28E-91
1	1	197	0.005	rpsU	t3129	STY3388	3217059	3217256	+	-15.139102	4.01E-07
4	27	785	0.005	suhB	t0310	STY2792	355508	356293	-	-15.090443	3.23E-26
3	10	587	0.005	yigP	t3326	STY3588	3426509	3427096	-	-15.052445	8.69E-20
12	116	2336	0.005	lon	t2410	STY0492	2481066	2483402	-	-14.986994	1.40E-76
4	4	776	0.005	fepC	t2278	STY0634	2345412	2346188	+	-14.943138	6.34E-26
6	14	1160	0.005	visB	t2975	STY3213	3066494	3067654	-	-14.899104	2.15E-38
4	36	764	0.005	murl	t3494	STY3743	3586120	3586884	-	-14.743558	1.55E-25
2	4	374	0.005	rpsI	t3260	STY3524	3351520	3351894	-	-14.471595	7.17E-13

9	28	1655	0.005	rpsA	t1953	STY0981	2003111	2004766	-	-14.255247	1.82E-54
3	70	551	0.005	cl	t3402	STY3660	3502585	3503136	-	-14.239627	1.28E-18
6	50	1052	0.006	degS	t3265	STY3529	3355989	3357041	+	-13.63705	6.91E-35
2	6	338	0.006	yheM	t4055	STY4348	4210673	4211011	+	-13.155678	1.06E-11
10	16	1622	0.006	pgm	t2177	STY0736	2243696	2245318	-	-12.614041	2.14E-53
6	55	962	0.006	-	t2966	STY3204	3054944	3055906	+	-12.460539	5.78E-32
4	11	641	0.006	rpiA	t2981	STY3219	3072806	3073447	-	-12.453636	1.53E-21
8	64	1280	0.006	eno	t2853	STY3081	2930219	2931499	-	-12.4329	2.73E-42
3	12	473	0.006	mreD	t3287	STY3552	3381013	3381486	-	-12.23745	4.37E-16
2	3	311	0.006	-	t1835	STY1111	1896895	1897206	+	-12.052786	7.97E-11
13	29	1973	0.007	tklA	t2996	STY3236	3085841	3087814	-	-11.72735	8.58E-65
4	6	605	0.007	gmk	t3778	STY4052	3900085	3900690	-	-11.681284	2.26E-20
7	16	1043	0.007	recA	t2730	STY2950	2813619	2814662	-	-11.479405	1.36E-34
9	47	1340	0.007	rffT	t3369	STY3627	3468163	3469503	-	-11.469339	3.08E-44
3	22	440	0.007	yabB	t0123	STY0139	141362	141802	+	-11.266065	5.16E-15
1	7	146	0.007	-	t3157	STY3417	3244748	3244894	+	-11.204345	1.82E-05
4	23	572	0.007	grpE	t2636	STY2868	2712729	2713301	-	-10.922251	2.67E-19
7	14	992	0.007	ruvB	t0983	STY2102	1070786	1071778	+	-10.799114	6.14E-33
5	73	707	0.007	phoU	t3670	STY3930	3779243	3779950	+	-10.768804	1.10E-23
7	104	953	0.007	secF	t2455	STY0446	2523744	2524697	-	-10.249101	1.13E-31
1	6	131	0.008	-	t4531	STY4834	4677894	4678025	+	-9.716011	5.57E-05
16	34	2006	0.008	rep	t3384	STY3642	3485509	3487515	-	-9.102176	7.27E-66
4	13	500	0.008	-	t3235	STY3497	3323142	3323642	+	-9.0600298	5.81E-17
8	13	989	0.008	fepD	t2276	STY0636	2343419	2344408	+	-8.904122	7.68E-33
4	12	491	0.008	crr	t0424	STY2670	496734	497225	-	-8.8037667	1.14E-16
35	903	4205	0.008	rpoC	t3473	STY3731	3562645	3566850	-	-8.499316	2.86E-137
4	16	479	0.008	rplJ	t3476	STY3734	3571723	3572202	-	-8.4527162	2.79E-16
17	85	2015	0.008	metG	t0701	STY2384	786592	788607	-	-8.3066892	3.71E-66
8	29	932	0.009	miaA	t4411	STY4717	4562802	4563734	+	-8.0596268	5.45E-31
10	63	1154	0.009	-	t3218	STY3480	3310245	3311399	-	-7.9234155	3.37E-38
11	32	1262	0.009	hemL	t0203	STY0223	234219	235481	-	-7.8392958	1.05E-41
9	13	1028	0.009	waaF	t3808	STY4084	3927347	3928375	-	-7.7757289	4.16E-34
4	26	455	0.009	-	t2205	STY0714	2271097	2271552	+	-7.7159689	1.68E-15
2	3	227	0.009	yhhP	t3944	STY4233	4083902	4084129	+	-7.684203	4.26E-08
1	5	113	0.009	malY	t1332	STY1657a	1392721	1392834	-	-7.6204025	0.0002141
3	12	329	0.009	rplS	t2628	STY2860	2705986	2706315	-	-7.1856346	2.07E-11
11	58	1196	0.009	-	t0313	STY2789	358078	359274	+	-7.0600413	1.46E-39
10	48	1058	0.009	yjeQ	t4401	STY4709	4553131	4554189	-	-6.6595492	4.41E-35
4	23	419	0.01	holD	t4600	STY4907	4751767	4752186	+	-6.5123984	2.48E-14
2	23	209	0.01	rpsR	t4444	STY4749	4589690	4589899	+	-6.4770815	1.63E-07
12	54	1235	0.01	glyA	t0301	STY2802	345824	347059	+	-6.2508403	7.90E-41
9	70	923	0.01	yabC	t0124	STY0140	141822	142745	+	-6.1986095	1.07E-30
4	21	404	0.01	-	t3206	STY3469	3299158	3299562	-	-5.9708564	7.61E-14
9	37	902	0.01	htrB	t1765	STY1192	1827380	1828282	+	-5.8552635	5.13E-30
2	21	200	0.01	samA	t4339	STY4598	4457355	4457555	-	-5.8220224	3.20E-07
1	2	98	0.01	rpmJ	t4086	STY4379	4228164	4228262	+	-5.5184538	0.0006573

3	13	290	0.01	-	t1622	STY1342	1678175	1678465	-	-5.3115433	3.83E-10
10	36	938	0.011	fepB	t2274	STY0638	2341045	2341983	+	-4.8537461	3.48E-31
5	8	458	0.011	-	t2641	STY2873	2717001	2717459	-	-4.4897471	1.34E-15
1	2	89	0.011	-	t0694	STY2391	781098	781187	-	-4.0443813	0.0012883
14	37	1232	0.011	icdA	t1682	STY1278	1746072	1747304	-	-3.8684681	9.88E-41
17	75	1484	0.011	nusA	t3205	STY3468	3297628	3299112	-	-3.742686	6.49E-49
38	176	3185	0.012	rne	t1734	STY1226	1798647	1801832	+	-3.1024484	3.78E-104
8	15	665	0.012	cmk	t1954	STY0980	2004898	2005563	-	-2.9710588	2.55E-22
21	53	1703	0.012	cydC	t1978	STY0954	2037202	2038905	+	-2.5763481	5.02E-56
3	15	239	0.013	-	t2724	none	2809238	2809477	+	-2.2904746	1.73E-08
7	101	557	0.013	-	t3234	STY3496	3322562	3323119	+	-2.2711705	8.19E-19
4	34	314	0.013	yajC	t2457	STY0444	2526601	2526915	-	-2.0518214	6.37E-11

\*LLR, log-likelihood ratio.

### 8.3.4 CD\_004

Excel table of TraDIS results for Typhimurium can be found on the accompanying CD.

### 8.3.5 Typhimurium essential genes

Total inserts	Total reads	Gene length	Insertion index	Gene name	SL unique ID	CT18 unique ID	Ty2 unique ID	Start	End	Strand	LLR	P-value for no inserts
0	0	623	0	-	SL0633	STY0696	t2222	706265	706888	-	-174.35924	2.83E-31
0	0	323	0	-	SL0950	-	-	1061626	1061949	-	-174.35924	1.45E-16
0	0	683	0	-	SL1155	STY1258	t1702	1260022	1260705	+	-174.35924	3.23E-34
0	0	677	0	-	SL1749	STY1950	t1057	1875339	1876016	-	-174.35924	6.36E-34
0	0	959	0	-	SL2695	-	-	2877254	2878213	-	-174.35924	9.46E-48
0	0	743	0	-*	SL0916*	STY0979	t1955	1020636	1021379	+	-174.35924	3.69E-37
0	0	452	0	accB	SL3352	STY3559	t3294	3571524	3571976	+	-174.35924	6.86E-23
0	0	218	0	acpP	SL1133	STY1235	t1724	1236264	1236482	+	-174.35924	2.04E-11
0	0	362	0	acpS	SL2539	STY2823	t0280	2719788	2720150	-	-174.35924	1.78E-18
0	0	626	0	adk	SL0481	STY0532	t2372	545538	546164	+	-174.35924	2.02E-31
0	0	2612	0	alaS	SL2807	STY2948	t2728	2993956	2996568	-	-174.35924	8.36E-129
0	0	1715	0	argS	SL1844	STY2117	t0968	1960173	1961888	+	-174.35924	8.06E-85
0	0	557	0	cl	SL2708	STY4644	t4337	2886929	2887486	+	-174.35924	4.87E-28
0	0	1367	0	cysS	SL0530	STY0585	t2324	598632	599999	+	-174.35924	9.34E-68
0	0	1382	0	dnaA	SL3805	STY3940	t3681	4064947	4066329	-	-174.35924	1.72E-68
0	0	1082	0	dnaN	SL3804	STY3941	t3682	4063842	4064924	-	-174.35924	8.81E-54
0	0	521	0	dnaT	SL4475	STY4897	t4587	4824124	4824645	-	-174.35924	2.84E-26
0	0	1844	0	dxs	SL0416	STY0461	t2441	474125	475969	-	-174.35924	3.81E-91
0	0	1454	0	engA	SL2481	STY2764	t0337	2649182	2650636	-	-174.35924	5.06E-72
0	0	716	0	fabG	SL1132	STY1234	t1725	1235374	1236090	+	-174.35924	7.79E-36
0	0	770	0	fabI	SL1631	STY1352	t1613	1748998	1749768	+	-174.35924	1.75E-38
0	0	461	0	folA	SL0088	STY0102	t0090	100851	101312	+	-174.35924	2.48E-23
0	0	539	0	frr	SL0220	STY0242	t0220	257153	257692	+	-174.35924	3.72E-27
0	0	1133	0	ftsZ	SL0133	STY0153	t0137	155695	156828	+	-174.35924	2.78E-56
0	0	977	0	gapA	SL1225	STY1825	t1169	1325555	1326532	-	-174.35924	1.24E-48
0	0	1100	0	gcpE	SL2485	STY2768	t0333	2653981	2655081	-	-174.35924	1.15E-54
0	0	275	0	groES	SL4266	STY4689	t4381	4595364	4595639	+	-174.35924	3.28E-14
0	0	956	0	hemB	SL0367	STY0404	t2492	423173	424129	-	-174.35924	1.33E-47
0	0	605	0	hemM	SL1706	STY1904	t1098	1832886	1833491	+	-174.35924	2.16E-30
0	0	2816	0	ileS	SL0047	STY0055	t0048	53864	56680	+	-174.35924	8.31E-139
0	0	416	0	infC	SL1268	STY1777	t1214	1371104	1371520	+	-174.35924	4.00E-21
0	0	833	0	ipk	SL1707	STY1905	t1097	1833506	1834339	+	-174.35924	1.43E-41
0	0	836	0	kdsA	SL1700	STY1897	t1104	1827269	1828105	-	-174.35924	1.02E-41
0	0	728	0	kdsB	SL0925	STY0990	t1946	1031240	1031968	+	-174.35924	2.01E-36
0	0	2564	0	leuS	SL0636	STY0699	t2219	708544	711108	-	-174.35924	1.89E-126
0	0	770	0	lpxA	SL0229	STY0251	t0229	267000	267770	+	-174.35924	1.75E-38
0	0	1499	0	lysS	SL3016	STY3196	t2958	3219948	3221447	-	-174.35924	3.14E-74
0	0	1730	0	msbA	SL0921	STY0985	t1950	1027011	1028741	+	-174.35924	1.48E-85
0	0	530	0	pgsA	SL1875	STY2153	t0931	1993390	1993920	-	-174.35924	1.03E-26
0	0	965	0	pheS	SL1271	STY1773	t1218	1372540	1373505	+	-174.35924	4.81E-48
0	0	2369	0	pheT	SL1272	STY1772	t1219	1373539	1375908	+	-174.35924	6.88E-117
0	0	863	0	prfB	SL3017	STY3197	t2959	3221475	3222338	-	-174.35924	4.82E-43
0	0	1337	0	pssA	SL2616	STY2845	t0258	2793077	2794414	+	-174.35924	2.76E-66
0	0	707	0	pyrH	SL0219	STY0241	t0219	256281	256988	+	-174.35924	2.15E-35
0	0	572	0	ribA	SL1643	STY1340	t1624	1760971	1761543	+	-174.35924	8.96E-29

0	0	803	0	rplB	SL3404	STY4361	t4068	3615294	3616097	-	-174.35924	4.22E-40
0	0	521	0	rplE	SL3395	STY4370	t4077	3611651	3612172	-	-174.35924	2.84E-26
0	0	410	0	rplK	SL4088	STY3736	t3478	4384445	4384855	+	-174.35924	7.87E-21
0	0	347	0	rplL	SL4091	STY3733	t3475	4386565	4386912	+	-174.35924	9.66E-18
0	0	353	0	rplN	SL3397	STY4368	t4075	3612530	3612883	-	-174.35924	4.91E-18
0	0	416	0	rplO	SL3388	STY4377	t4084	3608857	3609273	-	-174.35924	4.00E-21
0	0	392	0	rplP	SL3400	STY4365	t4072	3613510	3613902	-	-174.35924	6.01E-20
0	0	365	0	rplQ	SL3381	STY4384	t4091	3604368	3604733	-	-174.35924	1.27E-18
0	0	257	0	rplR	SL3391	STY4374	t4081	3609996	3610253	-	-174.35924	2.50E-13
0	0	338	0	rplT	SL1270	STY1775	t1216	1371882	1372220	+	-174.35924	2.67E-17
0	0	314	0	rplV	SL3402	STY4363	t4070	3614652	3614966	-	-174.35924	4.01E-16
0	0	284	0	rplW	SL3405	STY4360	t4067	3616133	3616417	-	-174.35924	1.19E-14
0	0	296	0	rplX	SL3396	STY4369	t4076	3612205	3612501	-	-174.35924	3.06E-15
0	0	239	0	rpmA	SL3275	STY3482	t3220	3493927	3494166	-	-174.35924	1.91E-12
0	0	218	0	rpmB	SL3694	STY4066	t3790	3943549	3943767	-	-174.35924	2.04E-11
0	0	173	0	rpmC	SL3399	STY4366	t4073	3613319	3613492	-	-174.35924	3.29E-09
0	0	161	0	rpmD	SL3389	STY4376	t4083	3609295	3609456	-	-174.35924	1.27E-08
0	0	122	0	rpmH	SL3806	STY3939A	t3680	4067008	4067130	+	-174.35924	1.04E-06
0	0	179	0	rpmI	SL1269	STY1776	t1215	1371634	1371813	+	-174.35924	1.67E-09
0	0	683	0	rpsC	SL3401	STY4364	t4071	3613933	3614616	-	-174.35924	3.23E-34
0	0	485	0	rpsE	SL3390	STY4375	t4082	3609478	3609963	-	-174.35924	1.65E-24
0	0	374	0	rpsH	SL3393	STY4372	t4079	3610905	3611279	-	-174.35924	4.58E-19
0	0	314	0	rpsK	SL3384	STY4381	t4088	3606461	3606775	-	-174.35924	4.01E-16
0	0	356	0	rpsL	SL3415	STY4350	t4057	3623826	3624182	-	-174.35924	3.50E-18
0	0	338	0	rpsM	SL3385	STY4380	t4087	3606867	3607205	-	-174.35924	2.67E-17
0	0	272	0	rpsN	SL3394	STY4371	t4078	3611331	3611603	-	-174.35924	4.60E-14
0	0	260	0	rpsS	SL3403	STY4362	t4069	3614999	3615259	-	-174.35924	1.78E-13
0	0	1910	0	thrS	SL1267	STY1778	t1213	1369064	1370974	+	-174.35924	2.21E-94
0	0	1256	0	tyrS	SL1381	STY1673	t1317	1480348	1481604	+	-174.35924	2.59E-62
0	0	326	0	yadR	SL0205	STY0226	t0205	240169	240495	+	-174.35924	1.03E-16
0	0	860	0	yfiB	SL2655	STY2869	t2637	2833497	2834357	+	-174.35924	6.77E-43
1	2	3464	0.0002887	dnaE	SL0232	STY0254	t0232	269553	273017	+	-36.20768	1.40E-170
1	3	2396	0.0004174	yaeT	SL0225	STY0247	t0225	262384	264780	+	-33.37681	3.26E-118
1	1	2051	0.0004876	glyS	SL3620	STY4144	t3864	3861094	3863145	-	-32.17801	2.70E-101
1	2	1628	0.0006143	groEL	SL4267	STY4690	t4382	4595701	4597329	+	-30.39024	1.49E-80
1	2	1469	0.0006807	murE	SL0123	STY0143	t0127	143491	144960	+	-29.59172	9.30E-73
1	1	1457	0.0006863	murC	SL0129	STY0149	t0133	151155	152612	+	-29.52790	3.61E-72
1	23	1397	0.0007158	dnaB	SL4182	STY4442	t4152	4487892	4489289	+	-29.20046	3.16E-69
1	7	1382	0.0007236	asnS	SL0937	STY1004	t1934	1048055	1049437	-	-29.11634	1.72E-68
1	10	1352	0.0007396	glmU	SL3829	STY3916	t3657	4092373	4093725	-	-28.94525	5.08E-67
1	1	1319	0.0007582	-	SL3265	STY3472	t3211	3483121	3484440	-	-28.75248	2.11E-65
1	5	1298	0.0007704	murD	SL0126	STY0146	t0130	147412	148710	+	-28.62721	2.26E-64
1	3	1274	0.0007849	serS	SL0901	STY0961	t1971	1000368	1001642	+	-28.48146	3.39E-63
1	4	1244	0.0008039	ftsA	SL0132	STY0152	t0136	154372	155616	+	-28.29524	1.00E-61
1	6	1241	0.0008058	murA	SL3279	STY3486	t3224	3496321	3497562	-	-28.27636	1.41E-61
1	1	1241	0.0008058	rho	SL3876	STY3638	t3380	4147138	4148379	+	-28.27636	1.41E-61
1	5	1238	0.0008078	hemA	SL1705	STY1902	t1099	1831316	1832554	-	-28.25744	1.97E-61
2	8	2396	0.0008347	gyrB	SL3802	STY3943	t3684	4060178	4062574	-	-28.00050	3.26E-118
1	7	1193	0.0008382	tyrP	SL1870	STY2145	t0941	1987977	1989170	+	-27.96777	3.18E-59
1	4	1181	0.0008467	-	SL1154	STY1257	t1703	1258830	1260011	+	-27.88862	1.23E-58
1	6	1136	0.0008803	metK	SL3065	STY3243	t3002	3272404	3273540	+	-27.58421	1.98E-56
1	1	1109	0.0009017	dapE	SL2446	STY2721	t0376	2595419	2596528	+	-27.39553	4.18E-55



1	7	1088	0.0009191	asd	SL3506	STY4271	t3981	3729959	3731047	-	-27.24546	4.47E-54
1	1	1007	0.000993	lpxD	SL0227	STY0249	t0227	265410	266417	+	-26.63708	4.19E-50
2	23	1997	0.0010015	ligA	SL2390	STY2663	t0431	2536726	2538723	-	-26.57031	1.20E-98
1	15	971	0.0010299	rpoA	SL3382	STY4383	t4090	3604792	3605763	-	-26.35019	2.44E-48
2	6	1910	0.0010471	dnaX	SL0477	STY0528	t2376	540404	542314	+	-26.21912	2.21E-94
1	4	953	0.0010493	msbB	SL1823	STY2097	t0988	1941569	1942522	-	-26.20257	1.86E-47
1	6	929	0.0010764	prsA	SL1708	STY1906	t1096	1834623	1835552	+	-26.00117	2.80E-46
2	5	1829	0.0010935	rpoD	SL3185	STY3390	t3131	3397115	3398944	+	-25.87685	2.07E-90
1	34	911	0.0010977	fabD	SL1131	STY1233	t1726	1234432	1235343	+	-25.84653	2.14E-45
1	6	902	0.0011086	htrB	SL1092	STY1192	t1765	1198766	1199668	-	-25.76801	5.90E-45
1	1	893	0.0011198	glyQ	SL3621	STY4143	t3863	3863173	3864066	-	-25.68867	1.63E-44
5	29	4448	0.0011241	mukB	SL0931	STY0996	t1940	1036785	1041233	+	-25.65848	7.86E-219
1	10	860	0.0011628	dapA	SL2452	STY2727	t0370	2601768	2602628	-	-25.39045	6.77E-43
1	20	857	0.0011669	lgt	SL2980	STY3143	t2911	3180289	3181146	-	-25.36275	9.50E-43
1	1	809	0.0012361	nadE	SL1245	STY1803	t1189	1346981	1347790	-	-24.90520	2.14E-40
1	34	803	0.0012453	dapB	SL0065	STY0073	t0066	74029	74832	+	-24.84601	4.22E-40
1	2	776	0.0012887	thyA	SL2979	STY3142	t2910	3179488	3180264	-	-24.57383	8.90E-39
1	9	740	0.0013514	-	SL0222	STY0244	t0222	259360	260100	+	-24.19503	5.18E-37
1	5	719	0.0013908	dnaC	SL4474	STY4896	t4586	4823384	4824103	-	-23.96502	5.55E-36
1	1	719	0.0013908	plsC	SL3147	STY3350	t3094	3356666	3357385	-	-23.96502	5.55E-36
1	1	713	0.0014025	dnaQ	SL0259	STY0285	t2601	303402	304115	+	-23.89800	1.09E-35
1	9	710	0.0014085	ubiG	SL2245	STY2505	t0588	2378041	2378751	+	-23.86427	1.53E-35
4	12	2837	0.0014099	valS	SL4405	STY4814	t4510	4737605	4740442	-	-23.85581	7.76E-140
1	1	704	0.0014205	ybbF	SL0528	STY0583	t2326	597240	597944	-	-23.79635	3.02E-35
2	12	1406	0.0014225	lpdA	SL0154	STY0177	t0160	181020	182426	+	-23.78497	1.14E-69
1	3	698	0.0014327	-	SL1560	-	-	1677013	1677711	-	-23.72782	5.94E-35
2	28	1313	0.0015232	prlA	SL3387	STY4378	t4085	3607518	3608831	-	-23.23609	4.15E-65
2	2	1304	0.0015337	mukF	SL0929	STY0994	t1942	1034778	1036082	+	-23.18081	1.15E-64
1	1	650	0.0015385	folE	SL2170	STY2427	t0662	2288169	2288819	-	-23.15611	1.34E-32
1	4	623	0.0016051	ribE	SL1358	STY1696	t1294	1460413	1461036	+	-22.81455	2.83E-31
1	4	623	0.0016051	tmk	SL1137	STY1239	t1720	1239775	1240398	+	-22.81455	2.83E-31
1	1	611	0.0016367	rplC	SL3407	STY4358	t4065	3617048	3617659	-	-22.65768	1.10E-30
1	2	596	0.0016779	lolA	SL0899	STY0959	t1973	998142	998738	+	-22.45692	5.96E-30
1	7	587	0.0017036	rplD	SL3406	STY4359	t4066	3616432	3617019	-	-22.33387	1.65E-29
3	12	1754	0.0017104	aspS	SL1836	STY2109	t0976	1952687	1954441	-	-22.30165	9.86E-87
3	17	1748	0.0017162	ftsI	SL0122	STY0142	t0126	141738	143486	+	-22.27391	1.94E-86
2	3	1085	0.0018433	ribD	SL0410	STY0455	t2447	469339	470424	+	-21.69438	6.28E-54
2	6	1082	0.0018484	-	SL4409	STY4817	t4513	4742946	4744028	+	-21.67186	8.81E-54
3	4	1619	0.001853	pyrG	SL2932	STY3082	t2854	3120217	3121836	-	-21.65178	4.11E-80
2	14	1049	0.0019066	murG	SL0128	STY0148	t0132	149969	151018	+	-21.41962	3.66E-52
1	6	500	0.002	fabA	SL1007	STY1088	t1853	1114239	1114739	-	-21.02896	3.04E-25
3	19	1457	0.002059	ftsY	SL3536	STY4240	t3951	3760077	3761534	-	-20.79076	3.61E-72
4	18	1874	0.0021345	parE	SL3155	STY3359	t3102	3364675	3366549	-	-20.49531	1.29E-92
2	8	935	0.002139	fabH	SL1130	STY1232	t1727	1233463	1234398	+	-20.47774	1.42E-46
3	40	1397	0.0021475	gltX	SL2381	STY2654	t0442	2527888	2529285	-	-20.44543	3.16E-69
4	11	1811	0.0022087	glmS	SL3828	STY3917	t3658	4090355	4092166	-	-20.21378	1.58E-89
1	3	452	0.0022124	ribH	SL0411	STY0456	t2446	470531	470983	+	-20.20012	6.86E-23
1	4	452	0.0022124	rpsG	SL3414	STY4351	t4058	3623260	3623712	-	-20.20012	6.86E-23
3	15	1340	0.0022388	murF	SL0124	STY0144	t0128	144975	146315	+	-20.10220	1.97E-66
1	8	437	0.0022883	dut	SL3697	STY4063	t3787	3946045	3946482	+	-19.92146	3.73E-22
1	1	437	0.0022883	fabZ	SL0228	STY0250	t0228	266541	266978	+	-19.92146	3.73E-22
4	36	1727	0.0023162	dnaG	SL3184	STY3389	t3130	3395220	3396947	+	-19.82148	2.08E-85

4	27	1700	0.0023529	proS	SL0243	STY0269	t0245	282467	284167	-	-19.69097	4.38E-84
3	73	1256	0.0023885	hisS	SL2484	STY2767	t0334	2652596	2653852	-	-19.56645	2.59E-62
3	7	1226	0.002447	-	SL1156	STY1259	t1701	1260723	1261949	+	-19.36562	7.66E-61
2	4	815	0.002454	-	SL0707	STY0767	t2151	790305	791120	+	-19.34184	1.09E-40
3	8	1205	0.0024896	dfp	SL3696	STY4064	t3788	3944841	3946046	+	-19.22182	8.20E-60
10	41	4010	0.0024938	rpoB	SL4092	STY3732	t3474	4387248	4391258	+	-19.20798	2.36E-197
3	3	1178	0.0025467	dxr	SL0221	STY0243	t0221	257851	259029	+	-19.03287	1.73E-58
3	8	1157	0.0025929	yleB	SL0660	STY0717	t2202	735475	736632	+	-18.88261	1.85E-57
3	14	1139	0.0026339	ftsW	SL0127	STY0147	t0131	148815	149954	+	-18.75142	1.41E-56
1	7	377	0.0026525	rpsF	SL4324	STY4747	t4442	4651103	4651480	+	-18.69238	3.27E-19
1	5	365	0.0027397	secE	SL4086	STY3738	t3480	4383357	4383722	+	-18.42092	1.27E-18
3	24	1064	0.0028195	mraY	SL0125	STY0145	t0129	146327	147391	+	-18.17918	6.72E-53
3	8	1061	0.0028275	fba	SL3044	STY3226	t2987	3250240	3251301	-	-18.15537	9.43E-53
3	13	995	0.0030151	-	SL3182	STY3387	t3128	3393528	3394523	-	-17.61203	1.63E-49
5	29	1649	0.0030321	glnS	SL0668	STY0724	t2189	746841	748490	+	-17.56410	1.39E-81
3	17	959	0.0031283	lpxK	SL0922	STY0986	t1949	1028756	1029715	+	-17.29857	9.46E-48
2	12	635	0.0031496	ribB	SL3168	STY3373	t3115	3378565	3379200	-	-17.24058	7.30E-32
3	17	941	0.0031881	accA	SL0233	STY0255	t0233	273048	273989	+	-17.13690	7.22E-47
4	19	1241	0.0032232	accC	SL3353	STY3560	t3295	3572095	3573336	+	-17.04330	1.41E-61
3	6	920	0.0032609	ribF	SL0046	STY0054	t0047	52881	53801	+	-16.94388	7.73E-46
6	22	1829	0.0032805	secD	SL0402	STY0445	t2456	461826	463655	+	-16.89251	2.07E-90
2	32	605	0.0033058	gmk	SL3706	STY4052	t3778	3954421	3955026	+	-16.82664	2.16E-30
4	18	1196	0.0033445	fabB	SL2347	STY2609	t0486	2486347	2487543	-	-16.72675	2.26E-59
1	5	296	0.0033784	-	SL1264	STY1782	t1209	1365082	1365378	+	-16.64009	3.06E-15
8	27	2342	0.0034159	imp	SL0094	STY0108	t0096	105822	108164	-	-16.54509	1.45E-115
6	35	1622	0.0036991	aarF	SL3926	STY3587	t3325	4200212	4201834	+	-15.85577	2.93E-80
4	21	1064	0.0037594	prfA	SL1704	STY1901	t1100	1830193	1831257	-	-15.71509	6.72E-53
1	2	266	0.0037594	rplY	SL2201	STY2461	t0630	2324158	2324424	+	-15.71509	9.05E-14
2	12	530	0.0037736	rimM	SL2648	STY2862	t2630	2827270	2827800	-	-15.68226	1.03E-26
10	50	2618	0.0038197	gyrA	SL2241	STY2499	t0592	2371436	2374054	-	-15.57624	4.25E-129
2	5	515	0.0038835	rplF	SL3392	STY4373	t4080	3610359	3610874	-	-15.43145	5.59E-26
2	3	512	0.0039063	fldA	SL0676	STY0732	t2181	756548	757060	-	-15.38030	7.84E-26
6	52	1520	0.0039474	Int	SL0655	STY0711	t2207	729592	731112	-	-15.28851	2.94E-75
5	19	1265	0.0039526	aroA*	SL0915*	STY0978	t1956	1019210	1020475	+	-15.27696	9.37E-63
9	77	2240	0.0040179	parC	SL3148	STY3351	t3095	3357660	3359900	-	-15.13306	1.46E-110
1	5	248	0.0040323	minE	SL1744	STY1946	t1061	1870496	1870744	+	-15.10159	6.91E-13
3	13	737	0.0040706	ubiE	SL3924	STY3589	t3327	4198845	4199582	+	-15.01837	7.27E-37
1	2	236	0.0042373	rpsQ	SL3398	STY4367	t4074	3613065	3613301	-	-14.66373	2.68E-12
3	15	707	0.0042433	-	SL3291	STY3498	t3236	3505063	3505770	+	-14.65120	2.15E-35
4	26	932	0.0042918	coaA	SL4083	STY3740	t3487	4380034	4380966	-	-14.55027	2.00E-46
1	5	230	0.0043478	rpsP	SL2649	STY2863	t2631	2827837	2828067	-	-14.43513	5.27E-12
1	3	230	0.0043478	ssal	SL1342	STY1712	t1276	1446893	1447123	+	-14.43513	5.27E-12
5	27	1145	0.0043668	pgk	SL3045	STY3227	t2988	3251421	3252566	-	-14.39637	7.17E-57
5	60	1130	0.0044248	lpxB	SL0230	STY0252	t0230	267788	268918	+	-14.27890	3.90E-56
3	27	677	0.0044313	-	SL1967	-	-	2072253	2072930	+	-14.26574	6.36E-34
4	25	887	0.0045096	era	SL2542	STY2826	t0276	2721651	2722538	-	-14.10938	3.21E-44
6	79	1280	0.0046875	eno	SL2931	STY3081	t2853	3118836	3120116	-	-13.76231	1.72E-63
6	58	1274	0.0047096	wbaX	SL2065	STY2297	t0785	2166349	2167623	-	-13.72002	3.39E-63
4	22	839	0.0047676	cdsA	SL0223	STY0245	t0223	260131	260970	+	-13.60971	7.25E-42
4	21	836	0.0047847	-	SL0831	-	-	925884	926720	+	-13.57738	1.02E-41
4	42	833	0.0048019	murl	SL4080	STY3743	t3494	4371346	4372179	+	-13.54492	1.43E-41
4	24	833	0.0048019	tsf	SL0218	STY0240	t0218	255285	256118	+	-13.54492	1.43E-41

4	30	806	0.0049628	dapD	SL0214	STY0236	t0214	249294	250100	-	-13.24654	3.01E-40
3	47	602	0.0049834	coaE	SL0140	STY0162	t0146	163220	163822	-	-13.20890	3.03E-30
3	28	602	0.0049834	rpsD	SL3383	STY4382	t4089	3605807	3606409	-	-13.20890	3.03E-30
1	3	200	0.005	infA	SL0891	STY0951	t1980	986893	987093	-	-13.17866	1.56E-10
8	34	1556	0.0051414	mviN	SL1107	STY1209	t1750	1211114	1212670	+	-12.92454	5.04E-77
7	91	1343	0.0052122	ffh	SL2650	STY2864	t2632	2828399	2829742	-	-12.79943	1.40E-66
11	132	2096	0.0052481	fusA	SL3413	STY4352	t4059	3621049	3623145	-	-12.73658	1.68E-103
4	44	761	0.0052562	ssaT	SL1355	STY1699	t1289	1456516	1457277	+	-12.72235	4.84E-38
5	16	947	0.0052798	lipA	SL0621	STY0683	t2234	694359	695306	-	-12.68128	3.67E-47
5	8	944	0.0052966	hemH	SL0482	STY0533	t2371	546411	547355	+	-12.65216	5.15E-47
3	15	566	0.0053004	pth	SL1711	STY1909	t1093	1837979	1838545	+	-12.64567	1.76E-28
7	35	1250	0.0056	folC	SL2334	STY2596	t0499	2475079	2476329	-	-12.13821	5.09E-62
3	13	533	0.0056285	yfhC	SL2530	STY2814	t0289	2711718	2712251	-	-12.09108	7.32E-27
6	59	1064	0.0056391	-	SL4410	STY4818	t4514	4744046	4745110	+	-12.07365	6.72E-53
14	115	2402	0.0058285	plsB	SL4172	STY4431	t4141	4477481	4479883	-	-11.76599	1.66E-118
1	1	167	0.005988	csrA	SL2806	STY2947	t2727	2993536	2993703	-	-11.51303	6.48E-09
16	78	2660	0.006015	infB	SL3259	STY3467	t3204	3474324	3476984	-	-11.47074	3.70E-131
6	41	986	0.0060852	holB	SL1138	STY1240	t1719	1240413	1241399	+	-11.36162	4.49E-49
1	5	164	0.0060976	-	SL1659	STY1323	t1640	1782420	1782584	+	-11.34249	9.09E-09
6	46	968	0.0061983	-	SL2391	STY2664	t0429	2538813	2539781	-	-11.18773	3.43E-48
6	21	959	0.0062565	-	SL0413	STY0458	t2444	471520	472479	+	-11.09933	9.46E-48
6	35	932	0.0064378	sifB	SL1532	STY1462	t1511	1649043	1649975	+	-10.82802	2.00E-46
3	18	461	0.0065076	coaD	SL3691	STY4069	t3793	3941947	3942408	+	-10.72512	2.48E-23
3	12	461	0.0065076	ispF	SL2908	STY3054	t2830	3092836	3093297	-	-10.72512	2.48E-23
5	28	749	0.0066756	trmD	SL2647	STY2861	t2629	2826458	2827207	-	-10.48112	1.88E-37
3	9	443	0.006772	yjeE	SL4291	STY4714	t4408	4620476	4620919	+	-10.34321	1.90E-22
4	20	590	0.0067797	lexA	SL4174	STY4433	t4143	4480549	4481139	+	-10.33234	1.17E-29
2	16	293	0.0068259	rpsJ	SL3408	STY4357	t4064	3617710	3618003	-	-10.26677	4.29E-15
5	14	731	0.0068399	ssaJ	SL1343	STY1711	t1277	1447138	1447869	+	-10.24699	1.43E-36
5	44	719	0.0069541	-	SL2623	STY2852	t2619	2807081	2807800	+	-10.08698	5.55E-36
12	80	1655	0.0072508	rpsA	SL0918	STY0981	t1953	1022367	1024022	+	-9.68054	7.05E-82
9	80	1223	0.007359	cca	SL3177	STY3383	t3124	3389935	3391158	+	-9.53552	1.07E-60
19	110	2579	0.0073672	topA	SL1646	STY1336	t1627	1766654	1769233	-	-9.52454	3.47E-127
31	405	4205	0.0073722	rpoC	SL4093	STY3731	t3473	4391353	4395558	+	-9.51791	6.47E-207
5	22	674	0.0074184	-	SL1069	STY1168	t1789	1176998	1177672	+	-9.45654	8.93E-34
7	65	938	0.0074627	hemC	SL3893	STY3621	t3359	4166603	4167541	-	-9.39802	1.01E-46
3	34	401	0.0074813	nusB	SL0412	STY0457	t2445	471022	471423	+	-9.37350	2.17E-20
9	57	1193	0.007544	mesJ	SL0237	STY0261	t0238	278756	279949	+	-9.29125	3.18E-59
1	1	131	0.0076336	-	SL1203	STY1853	t1146	1306483	1306614	-	-9.17465	3.77E-07
6	46	785	0.0076433	suhB	SL2508	STY2792	t0310	2682161	2682946	+	-9.16206	3.22E-39
6	49	776	0.007732	map	SL0216	STY0238	t0216	253057	253833	-	-9.04782	8.90E-39
7	66	899	0.0077864	lpxC	SL0134	STY0154	t0138	156947	157846	+	-8.97811	8.28E-45
7	42	896	0.0078125	accD	SL2335	STY2597	t0498	2476415	2477311	-	-8.94488	1.16E-44
4	7	512	0.0078125	ppa	SL4347	STY4773	t4468	4675331	4675843	-	-8.94488	7.84E-26
5	44	629	0.0079491	-	SL1564	STY1437	t1537	1681521	1682150	+	-8.77210	1.44E-31
3	9	377	0.0079576	-	SL1785	STY1988	t1022	1910995	1911372	+	-8.76151	3.27E-19
9	26	1121	0.0080285	cydB	SL0723	STY0787	t2135	810533	811654	+	-8.67270	1.08E-55
9	61	1115	0.0080717	-	SL0703	STY0761	t2155	785494	786609	+	-8.61894	2.12E-55
11	51	1352	0.0081361	purB	SL1170	STY1272	t1688	1276349	1277701	-	-8.53927	5.08E-67
4	35	491	0.0081466	def	SL3373	STY4391	t4098	3598427	3598918	+	-8.52626	8.40E-25
2	12	245	0.0081633	rpsT	SL0044	STY0052	t0045	52289	52534	-	-8.50578	9.70E-13
7	49	848	0.0082547	folD	SL0535	STY0588	t2321	602199	603047	-	-8.39364	2.62E-42

9	30	1088	0.0082721	trmU	SL1172	STY1274	t1686	1278451	1279539	-	-8.37248	4.47E-54
10	39	1193	0.0083822	kdtA	SL3690	STY4070	t3794	3940727	3941920	+	-8.23883	3.18E-59
13	69	1550	0.0083871	cydA	SL0722	STY0786	t2136	808949	810499	+	-8.23296	9.93E-77
2	6	236	0.0084746	-	SL0514	-	-	581902	582138	+	-8.12782	2.68E-12
6	34	707	0.0084866	rpsB	SL0217	STY0239	t0217	254302	255009	+	-8.11348	2.15E-35
15	67	1760	0.0085227	-	SL0706	STY0765	t2152	788334	790094	+	-8.07029	5.01E-87
14	155	1628	0.0085995	yidC	SL3809	STY3938	t3678	4067748	4069376	+	-7.97906	1.49E-80
9	90	1046	0.0086042	hemE	SL4106	STY3718	t3464	4405485	4406531	+	-7.97350	5.13E-52
8	44	929	0.0086114	fmt	SL3374	STY4390	t4097	3598952	3599881	+	-7.96497	2.80E-46
6	30	692	0.0086705	ispD	SL2909	STY3055	t2831	3093315	3094007	-	-7.89522	1.17E-34
2	4	230	0.0086957	-	SL1480	-	-	1583701	1583931	-	-7.86567	5.27E-12
5	31	572	0.0087413	rlpB	SL0635	STY0698	t2220	707939	708511	-	-7.81221	8.96E-29
4	149	449	0.0089087	-	SL2593	STY2066	-	2768375	2768824	+	-7.61769	9.63E-23
9	149	1010	0.0089109	murB	SL4081	STY3742	t3489	4378012	4379022	+	-7.61515	2.99E-50
18	105	2015	0.008933	metG	SL2132	STY2384	t0701	2247464	2249479	+	-7.58967	1.57E-99
20	82	2180	0.0091743	priA	SL4044	STY3775	t3523	4324808	4326988	-	-7.31454	1.27E-107
6	36	641	0.0093604	rpiA	SL3039	STY3219	t2981	3245506	3246147	-	-7.10600	3.71E-32
9	62	953	0.0094439	ispB	SL3277	STY3484	t3222	3494773	3495726	+	-7.01340	1.86E-47
11	115	1160	0.0094828	visB	SL3033	STY3213	t2975	3239194	3240354	-	-6.97046	1.32E-57
5	20	527	0.0094877	hemG	SL3940	STY3573	t3311	4216690	4217217	+	-6.96506	1.44E-26
2	5	209	0.0095694	-	SL1341	STY1713	t1275	1446654	1446863	+	-6.87530	5.65E-11
8	35	836	0.0095694	rpoH	SL3533	STY4243	t3954	3757258	3758094	-	-6.87530	1.02E-41
4	18	410	0.0097561	rplM	SL3317	STY3525	t3261	3534240	3534650	-	-6.67227	7.87E-21
10	87	1013	0.0098717	holA	SL0634	STY0697	t2221	706908	707921	-	-6.54799	2.13E-50
17	67	1703	0.0099824	cydC	SL0894	STY0954	t1978	988172	989875	-	-6.42992	3.12E-84
9	27	896	0.0100446	pagO	SL1793	STY2000	t1016	1917084	1917980	+	-6.36393	1.16E-44
4	21	398	0.0100503	-	SL3072	STY3250	t3009	3279377	3279775	+	-6.35800	3.05E-20
10	57	983	0.0101729	wbaV	SL2064	STY2296	t0786	2165343	2166326	-	-6.22886	6.30E-49
7	24	686	0.0102041	mukE	SL0930	STY0995	t1941	1036081	1036767	+	-6.19626	2.30E-34
10	146	977	0.0102354	-	SL2633	-	-	2816812	2817789	-	-6.16352	1.24E-48
7	37	680	0.0102941	mtn	SL0208	STY0229	t0208	242067	242747	-	-6.10239	4.54E-34
6	26	581	0.010327	-	SL3948	STY3880	t3620	4230699	4231280	-	-6.06823	3.24E-29
7	31	662	0.010574	rnc	SL2543	STY2827	t0277	2722553	2723215	-	-5.81424	3.46E-33
10	90	932	0.0107296	lytB	SL0050	STY0058	t0051	57805	58737	+	-5.65638	2.00E-46
7	67	650	0.0107692	ftsE	SL3535	STY4241	t3952	3759406	3760056	-	-5.61644	1.34E-32
16	64	1460	0.0109589	yigC	SL3932	STY3581	t3319	4205152	4206612	+	-5.42663	2.57E-72
9	140	812	0.0110837	ftsQ	SL0131	STY0151	t0135	153545	154357	+	-5.30295	1.53E-40
30	247	2687	0.0111649	secA	SL0136	STY0156	t0140	158702	161389	+	-5.22309	1.76E-132
6	35	536	0.0111194	-	SL3290	STY3497	t3235	3504502	3505038	+	-5.19448	5.22E-27
6	49	527	0.0113852	nusG	SL4087	STY3737	t3479	4383742	4384269	+	-5.00820	1.44E-26
10	64	878	0.0113895	-	SL0702	STY0760	t2156	784585	785463	+	-5.00401	8.87E-44
20	69	1748	0.0114416	cydD	SL0895	STY0955	t1977	989894	991642	-	-4.95361	1.94E-86
11	43	956	0.0115063	lepB	SL2544	STY2828	t0275	2723507	2724463	-	-4.89133	1.33E-47
4	28	344	0.0116279	folB	SL3179	STY3385	t3126	3392200	3392544	-	-4.77477	1.36E-17
5	26	422	0.0118483	-	SL0032	STY0038	t0033	34385	34807	-	-4.56562	2.03E-21
2	9	164	0.0121951	-	SL0924	STY0989	t1947	1031061	1031225	+	-4.24187	9.09E-09
23	102	1883	0.0122146	mrdA	SL0628	STY0691	t2227	701442	703325	-	-4.22391	4.66E-93
6	28	482	0.0124481	lspA	SL0048	STY0056	t0049	56698	57180	+	-4.00954	2.32E-24
12	85	962	0.012474	-	SL3024	STY3204	t2966	3227647	3228609	+	-3.98595	6.75E-48
6	46	479	0.0125261	rplJ	SL4090	STY3734	t3476	4386001	4386480	+	-3.93859	3.26E-24
7	67	554	0.0126354	yrdC	SL3369	STY4395	t4102	3595580	3596134	-	-3.83962	6.84E-28
12	56	944	0.0127119	birA	SL4082	STY3741	t3488	4379037	4379981	+	-3.77070	5.15E-47

6	19	458	0.0131004	-	SL2659	STY2873	t2641	2837055	2837513	-	-3.42470	3.49E-23
16	174	1208	0.013245	sseJ	SL1561	STY1439a	-	1678155	1679363	+	-3.29767	5.84E-60
10	44	743	0.013459	-	SL1563	STY1438	t1536	1680753	1681496	+	-3.11139	3.69E-37
4	15	293	0.0136519	rplU	SL3276	STY3483	t3221	3494204	3494497	-	-2.94503	4.29E-15
26	91	1871	0.0138963	aceF	SL0153	STY0176	t0159	178931	180802	+	-2.73643	1.81E-92
19	92	1355	0.0140221	-	SL1628	STY1353	t1612	1747019	1748374	-	-2.62996	3.62E-67
12	73	854	0.0140515	ubiA	SL4171	STY4430	t4140	4476510	4477364	+	-2.60519	1.33E-42
15	155	1061	0.0141376	wbaG	SL2068	STY2301	t0781	2169990	2171051	-	-2.53280	9.43E-53
7	29	491	0.0142566	crr	SL2396	STY2670	t0424	2544385	2544876	+	-2.43318	8.40E-25
11	75	770	0.0142857	envF	SL1179	-	-	1285051	1285821	-	-2.40891	1.75E-38
3	34	209	0.0143541	-	SL2549	-	-	2730709	2730918	+	-2.35201	5.65E-11
18	123	1250	0.0144	-	SL0742	-	-	827815	829065	+	-2.31387	5.09E-62
5	52	347	0.0144092	ftsL	SL0121	STY0141	t0125	141357	141704	+	-2.30622	9.66E-18
9	36	623	0.0144462	lipB	SL0623	STY0686	t2232	696785	697408	-	-2.27556	2.83E-31
16	70	1094	0.0146252	mrdB	SL0627	STY0690	t2228	700327	701421	-	-2.12796	2.27E-54

\*SL0916 and *aroA* are (partly) deleted in the strain of Typhimurium used

### 8.3.6 Shared essential genes

Total inserts Tm	Total reads Tm	Total inserts Ty	Total reads Ty	Unique Tm ID	Unique Ty Ty2 ID	Unique Ty CT18 ID	Gene name	Gene length Tm	Gene length Ty
3	6	0	0	SL0046	t0047	STY0054	ribF	920	920
0	0	0	0	SL0047	t0048	STY0055	ileS	2816	2816
6	28	0	0	SL0048	t0049	STY0056	lspA	482	482
10	90	3	32	SL0050	t0051	STY0058	lytB	932	932
1	34	1	1	SL0065	t0066	STY0073	dapB	803	803
8	27	2	10	SL0094	t0096	STY0108	imp	2342	2336
5	52	1	2	SL0121	t0125	STY0141	ftsL	347	347
3	17	0	0	SL0122	t0126	STY0142	ftsI	1748	1748
1	2	0	0	SL0123	t0127	STY0143	murE	1469	1469
3	15	1	4	SL0124	t0128	STY0144	murF	1340	1340
3	24	0	0	SL0125	t0129	STY0145	mraY	1064	1064
1	5	0	0	SL0126	t0130	STY0146	murD	1298	1298
3	14	5	12	SL0127	t0131	STY0147	ftsW	1139	1226
2	14	1	1	SL0128	t0132	STY0148	murG	1049	1049
1	1	0	0	SL0129	t0133	STY0149	murC	1457	1457
9	140	2	12	SL0131	t0135	STY0151	ftsQ	812	812
1	4	0	0	SL0132	t0136	STY0152	ftsA	1244	1244
0	0	1	1	SL0133	t0137	STY0153	ftsZ	1133	1133
7	66	3	8	SL0134	t0138	STY0154	lpxC	899	899
30	247	10	30	SL0136	t0140	STY0156	secA	2687	2687
3	47	1	1	SL0140	t0146	STY0162	yacE	602	602
26	91	4	8	SL0153	t0159	STY0176	aceF	1871	1871
2	12	1	1	SL0154	t0160	STY0177	lpdA	1406	1409
0	0	1	1	SL0205	t0205	STY0226	yadR	326	371
4	30	0	0	SL0214	t0214	STY0236	dapD	806	806
6	49	3	11	SL0216	t0216	STY0238	map	776	776
6	34	2	16	SL0217	t0217	STY0239	rpsB	707	707
4	24	0	0	SL0218	t0218	STY0240	tsf	833	833
0	0	0	0	SL0219	t0219	STY0241	pyrH	707	707
0	0	1	1	SL0220	t0220	STY0242	frr	539	539
3	3	0	0	SL0221	t0221	STY0243	dxr	1178	1178
1	9	1	9	SL0222	t0222	STY0244	-	740	740
4	22	2	2	SL0223	t0223	STY0245	cdsA	839	839
1	3	3	6	SL0225	t0225	STY0247	yaeT	2396	2393
1	1	4	10	SL0227	t0227	STY0249	lpxD	1007	1007
1	1	0	0	SL0228	t0228	STY0250	fabZ	437	437
0	0	0	0	SL0229	t0229	STY0251	lpxA	770	770
5	60	1	29	SL0230	t0230	STY0252	lpxB	1130	1130
1	2	0	0	SL0232	t0232	STY0254	dnaE	3464	3464
3	17	0	0	SL0233	t0233	STY0255	accA	941	941
9	57	5	16	SL0237	t0238	STY0261	mesJ	1193	1274
4	27	2	10	SL0243	t0245	STY0269	proS	1700	1700
1	1	0	0	SL0259	t2601	STY0285	dnaQ	713	713
0	0	1	1	SL0367	t2492	STY0404	hemB	956	956
6	22	4	11	SL0402	t2456	STY0445	secD	1829	1829
8	137	7	104	SL0403	t2455	STY0446	secF	953	953

2	3	3	26	SL0410	t2447	STY0455	ribD	1085	1085
1	3	0	0	SL0411	t2446	STY0456	ribH	452	452
3	34	2	16	SL0412	t2445	STY0457	nusB	401	401
6	21	4	10	SL0413	t2444	STY0458	-	959	959
0	0	1	2	SL0416	t2441	STY0461	dxs	1844	1844
2	6	5	11	SL0477	t2376	STY0528	dnaX	1910	1910
0	0	0	0	SL0481	t2372	STY0532	adk	626	626
5	8	1	2	SL0482	t2371	STY0533	hemH	944	944
1	1	1	3	SL0528	t2326	STY0583	ybbF	704	704
0	0	0	0	SL0530	t2324	STY0585	cysS	1367	1367
7	49	4	24	SL0535	t2321	STY0588	folD	848	848
16	70	0	0	SL0627	t2228	STY0690	mrdB	1094	1094
23	102	3	19	SL0628	t2227	STY0691	pbpA	1883	1883
0	0	2	26	SL0633	t2222	STY0696	-	623	623
10	87	4	21	SL0634	t2221	STY0697	holA	1013	1013
5	31	1	6	SL0635	t2220	STY0698	rlpB	572	572
0	0	0	0	SL0636	t2219	STY0699	leuS	2564	2564
6	52	2	12	SL0655	t2207	STY0711	Int	1520	1520
3	8	4	27	SL0660	t2202	STY0717	yleB	1157	1157
5	29	6	80	SL0668	t2189	STY0724	glnS	1649	1649
2	3	2	24	SL0676	t2181	STY0732	fldA	512	512
1	3	0	0	SL0891	t1980	STY0951	infA	200	200
17	67	21	53	SL0894	t1978	STY0954	cydC	1703	1703
1	2	0	0	SL0899	t1973	STY0959	lolA	596	596
1	3	1	1	SL0901	t1971	STY0961	serS	1274	1274
12	80	9	28	SL0918	t1953	STY0981	rpsA	1655	1655
0	0	0	0	SL0921	t1950	STY0985	msbA	1730	1730
3	17	1	3	SL0922	t1949	STY0986	lpxK	959	959
2	9	0	0	SL0924	t1947	STY0989	-	164	164
0	0	0	0	SL0925	t1946	STY0990	kdsB	728	728
2	2	0	0	SL0929	t1942	STY0994	mukF	1304	1304
7	24	3	20	SL0930	t1941	STY0995	mukE	686	659
5	29	3	6	SL0931	t1940	STY0996	mukB	4448	4448
1	7	0	0	SL0937	t1934	STY1004	asnS	1382	1382
1	6	1	1	SL1007	t1853	STY1088	fabA	500	500
1	6	9	37	SL1092	t1765	STY1192	htrB	902	902
8	34	3	9	SL1107	t1750	STY1209	mviN	1556	1475
2	8	2	2	SL1130	t1727	STY1232	fabH	935	935
1	34	1	5	SL1131	t1726	STY1233	fabD	911	911
0	0	0	0	SL1132	t1725	STY1234	fabG	716	716
0	0	1	8	SL1133	t1724	STY1235	acpP	218	218
1	4	0	0	SL1137	t1720	STY1239	tmk	623	623
6	41	4	29	SL1138	t1719	STY1240	holB	986	986
1	4	6	53	SL1154	t1703	STY1257	-	1181	1292
0	0	0	0	SL1155	t1702	STY1258	-	683	683
3	7	1	1	SL1156	t1701	STY1259	-	1226	1226
11	51	3	6	SL1170	t1688	STY1272	purB	1352	1352
9	30	2	6	SL1172	t1686	STY1274	trmU	1088	1088
0	0	1	3	SL1225	t1169	STY1825	gapA	977	977
1	1	0	0	SL1245	t1189	STY1803	nadE	809	809
0	0	0	0	SL1267	t1213	STY1778	thrS	1910	1910
0	0	0	0	SL1268	t1214	STY1777	infC	416	524

0	0	0	0	SL1269	t1215	STY1776	rpmI	179	179
0	0	0	0	SL1270	t1216	STY1775	rplT	338	338
0	0	0	0	SL1271	t1218	STY1773	pheS	965	965
0	0	0	0	SL1272	t1219	STY1772	pheT	2369	2369
1	4	1	1	SL1358	t1294	STY1696	ribE	623	623
0	0	0	0	SL1381	t1317	STY1673	tyrS	1256	1256
0	0	2	7	SL1631	t1613	STY1352	fabI	770	770
0	0	1	5	SL1643	t1624	STY1340	ribA	572	572
0	0	1	30	SL1700	t1104	STY1897	kdsA	836	836
4	21	0	0	SL1704	t1100	STY1901	prfA	1064	1064
1	5	0	0	SL1705	t1099	STY1902	hemA	1238	1238
0	0	0	0	SL1706	t1098	STY1904	hemM	605	605
0	0	0	0	SL1707	t1097	STY1905	ipk	833	833
1	6	0	0	SL1708	t1096	STY1906	prsA	929	929
0	0	2	20	SL1749	t1057	STY1950	-	677	677
3	12	0	0	SL1836	t0976	STY2109	aspS	1754	1754
0	0	0	0	SL1844	t0968	STY2117	argS	1715	1715
0	0	0	0	SL1875	t0931	STY2153	pgsA	530	530
18	105	17	85	SL2132	t0701	STY2384	metG	2015	2015
1	1	0	0	SL2170	t0662	STY2427	folE	650	650
1	2	1	1	SL2201	t0630	STY2461	rplY	266	266
10	50	2	4	SL2241	t0592	STY2499	gyrA	2618	2618
1	9	2	21	SL2245	t0588	STY2505	ubiG	710	710
7	35	3	5	SL2334	t0499	STY2596	folC	1250	1250
7	42	3	11	SL2335	t0498	STY2597	accD	896	896
4	18	2	15	SL2347	t0486	STY2609	fabB	1196	1196
3	40	5	14	SL2381	t0442	STY2654	gltX	1397	1397
2	23	0	0	SL2390	t0431	STY2663	ligA	1997	1997
6	46	1	1	SL2391	t0429	STY2664	-	968	968
7	29	4	12	SL2396	t0424	STY2670	crr	491	491
1	1	0	0	SL2446	t0376	STY2721	dapE	1109	1109
1	10	1	6	SL2452	t0370	STY2727	dapA	860	860
0	0	0	0	SL2481	t0337	STY2764	-	1454	1454
3	73	2	22	SL2484	t0334	STY2767	hisS	1256	1256
0	0	0	0	SL2485	t0333	STY2768	gcpE	1100	1100
6	46	4	27	SL2508	t0310	STY2792	suhB	785	785
3	13	2	9	SL2530	t0289	STY2814	yfhC	533	533
0	0	0	0	SL2539	t0280	STY2823	acpS	362	362
4	25	4	11	SL2542	t0276	STY2826	era	887	887
11	43	4	27	SL2544	t0275	STY2828	lepB	956	956
0	0	0	0	SL2616	t0258	STY2845	pssA	1337	1337
5	44	1	11	SL2623	t2619	STY2852	-	719	719
5	28	2	10	SL2647	t2629	STY2861	trmD	749	749
2	12	0	0	SL2648	t2630	STY2862	yfjA	530	530
1	5	0	0	SL2649	t2631	STY2863	rpsP	230	230
7	91	5	35	SL2650	t2632	STY2864	ffh	1343	1343
0	0	1	4	SL2655	t2637	STY2869	yfjB	860	860
6	19	5	8	SL2659	t2641	STY2873	-	458	458
0	0	0	0	SL2708	t4337	STY4644	cl	557	614
1	1	0	0	SL2806	t2727	STY2947	csrA	167	167
0	0	0	0	SL2807	t2728	STY2948	alaS	2612	2612
3	12	0	0	SL2908	t2830	STY3054	ygbB	461	461



6	30	3	16	SL2909	t2831	STY3055	ygbP	692	692
6	79	8	64	SL2931	t2853	STY3081	eno	1280	1280
3	4	3	11	SL2932	t2854	STY3082	pyrG	1619	1619
1	2	3	5	SL2979	t2910	STY3142	thyA	776	776
1	20	0	0	SL2980	t2911	STY3143	lgt	857	857
0	0	1	2	SL3016	t2958	STY3196	lysS	1499	1499
0	0	0	0	SL3017	t2959	STY3197	prfB	863	1080
12	85	6	55	SL3024	t2966	STY3204	-	962	962
11	115	6	14	SL3033	t2975	STY3213	visB	1160	1160
6	36	4	11	SL3039	t2981	STY3219	rpiA	641	641
3	8	1	1	SL3044	t2987	STY3226	fba	1061	1061
5	27	2	2	SL3045	t2988	STY3227	pgk	1145	1145
1	6	2	8	SL3065	t3002	STY3243	metK	1136	1136
4	21	2	7	SL3072	t3009	STY3250	-	398	398
1	1	0	0	SL3147	t3094	STY3350	plsC	719	719
9	77	1	9	SL3148	t3095	STY3351	parC	2240	2240
4	18	0	0	SL3155	t3102	STY3359	parE	1874	1874
2	12	2	11	SL3168	t3115	STY3373	ribB	635	635
9	80	4	24	SL3177	t3124	STY3383	cca	1223	1223
4	28	0	0	SL3179	t3126	STY3385	folB	344	344
3	13	0	0	SL3182	t3128	STY3387	-	995	995
4	36	0	0	SL3184	t3130	STY3389	dnaG	1727	1727
2	5	2	6	SL3185	t3131	STY3390	rpoD	1829	1964
16	78	3	9	SL3259	t3204	STY3467	infB	2660	2660
1	1	0	0	SL3265	t3211	STY3472	-	1319	1319
0	0	0	0	SL3275	t3220	STY3482	rpmA	239	239
4	15	0	0	SL3276	t3221	STY3483	rplU	293	293
9	62	0	0	SL3277	t3222	STY3484	ispB	953	953
1	6	1	6	SL3279	t3224	STY3486	murA	1241	1241
6	35	4	13	SL3290	t3235	STY3497	-	536	500
3	15	0	0	SL3291	t3236	STY3498	-	707	707
4	18	0	0	SL3317	t3261	STY3525	rplM	410	410
0	0	0	0	SL3352	t3294	STY3559	accB	452	452
4	19	1	6	SL3353	t3295	STY3560	accC	1241	1331
7	67	1	3	SL3369	t4102	STY4395	yrnC	554	554
4	35	1	1	SL3373	t4098	STY4391	fms	491	491
8	44	2	30	SL3374	t4097	STY4390	fmt	929	929
0	0	1	2	SL3381	t4091	STY4384	rplQ	365	365
1	15	0	0	SL3382	t4090	STY4383	rpoA	971	971
3	28	0	0	SL3383	t4089	STY4382	rpsD	602	602
0	0	0	0	SL3384	t4088	STY4381	rpsK	314	371
0	0	0	0	SL3385	t4087	STY4380	rpsM	338	338
2	28	1	5	SL3387	t4085	STY4378	prlA	1313	1313
0	0	0	0	SL3388	t4084	STY4377	rplO	416	416
0	0	0	0	SL3389	t4083	STY4376	rpmD	161	161
0	0	0	0	SL3390	t4082	STY4375	rpsE	485	485
0	0	0	0	SL3391	t4081	STY4374	rplR	257	335
2	5	0	0	SL3392	t4080	STY4373	rplF	515	515
0	0	0	0	SL3393	t4079	STY4372	rpsH	374	374
0	0	0	0	SL3394	t4078	STY4371	rpsN	272	287
0	0	0	0	SL3395	t4077	STY4370	rplE	521	521
0	0	0	0	SL3396	t4076	STY4369	rplX	296	296

0	0	0	0	SL3397	t4075	STY4368	rplN	353	353
1	2	0	0	SL3398	t4074	STY4367	rpsQ	236	236
0	0	0	0	SL3399	t4073	STY4366	rpmC	173	173
0	0	0	0	SL3400	t4072	STY4365	rplP	392	392
0	0	0	0	SL3401	t4071	STY4364	rpsC	683	683
0	0	0	0	SL3402	t4070	STY4363	rplV	314	314
0	0	0	0	SL3403	t4069	STY4362	rpsS	260	260
0	0	0	0	SL3404	t4068	STY4361	rplB	803	803
0	0	0	0	SL3405	t4067	STY4360	rplW	284	284
1	7	1	2	SL3406	t4066	STY4359	rplD	587	587
1	1	1	1	SL3407	t4065	STY4358	rplC	611	611
2	16	0	0	SL3408	t4064	STY4357	rpsJ	293	293
11	132	4	13	SL3413	t4059	STY4352	fusA	2096	2096
1	4	0	0	SL3414	t4058	STY4351	rpsG	452	452
0	0	0	0	SL3415	t4057	STY4350	rpsL	356	356
1	7	0	0	SL3506	t3981	STY4271	asd	1088	1088
8	35	1	10	SL3533	t3954	STY4243	rpoH	836	836
7	67	0	0	SL3535	t3952	STY4241	ftsE	650	650
3	19	2	24	SL3536	t3951	STY4240	ftsY	1457	1457
1	1	4	10	SL3620	t3864	STY4144	glyS	2051	2051
1	1	2	7	SL3621	t3863	STY4143	glyQ	893	893
10	39	3	117	SL3690	t3794	STY4070	kdtA	1193	1259
3	18	0	0	SL3691	t3793	STY4069	coaD	461	461
0	0	0	0	SL3694	t3790	STY4066	rpmB	218	218
3	8	0	0	SL3696	t3788	STY4064	dfp	1205	1205
1	8	0	0	SL3697	t3787	STY4063	dut	437	437
2	32	4	6	SL3706	t3778	STY4052	gmk	605	605
2	8	1	2	SL3802	t3684	STY3943	gyrB	2396	2396
0	0	1	1	SL3804	t3682	STY3941	dnaN	1082	1082
0	0	0	0	SL3805	t3681	STY3940	dnaA	1382	1382
0	0	0	0	SL3806	t3680	STY3939A	rpmH	122	122
14	155	1	7	SL3809	t3678	STY3938	yidC	1628	1628
1	10	1	4	SL3829	t3657	STY3916	glmU	1352	1352
1	1	1	1	SL3876	t3380	STY3638	rho	1241	1241
7	65	2	6	SL3893	t3359	STY3621	hemC	938	923
3	13	0	0	SL3924	t3327	STY3589	ubiE	737	737
6	35	5	9	SL3926	t3325	STY3587	aarF	1622	1622
16	64	0	0	SL3932	t3319	STY3581	yigC	1460	1460
5	20	0	0	SL3940	t3311	STY3573	hemG	527	527
6	26	1	7	SL3948	t3620	STY3880	-	581	614
20	82	1	1	SL4044	t3523	STY3775	priA	2180	2180
4	42	4	36	SL4080	t3494	STY3743	murI	833	764
4	26	4	102	SL4083	t3487	STY3740	coaA	932	932
1	5	1	5	SL4086	t3480	STY3738	secE	365	365
6	49	1	6	SL4087	t3479	STY3737	nusG	527	527
0	0	1	9	SL4088	t3478	STY3736	rplK	410	410
6	46	4	16	SL4090	t3476	STY3734	rplJ	479	479
0	0	0	0	SL4091	t3475	STY3733	rplL	347	347
10	41	3	6	SL4092	t3474	STY3732	rpoB	4010	4010
31	405	35	903	SL4093	t3473	STY3731	rpoC	4205	4205
9	90	0	0	SL4106	t3464	STY3718	hemE	1046	1046
12	73	2	3	SL4171	t4140	STY4430	ubiA	854	854

14	115	3	13	SL4172	t4141	STY4431	plsB	2402	2402
4	20	2	6	SL4174	t4143	STY4433	lexA	590	590
1	23	1	1	SL4182	t4152	STY4442	dnaB	1397	1397
0	0	0	0	SL4266	t4381	STY4689	groES	275	275
1	2	1	4	SL4267	t4382	STY4690	groEL	1628	1628
3	9	1	1	SL4291	t4408	STY4714	yjeE	443	443
1	7	0	0	SL4324	t4442	STY4747	rpsF	377	377
4	7	0	0	SL4347	t4468	STY4773	ppa	512	512
4	12	0	0	SL4405	t4510	STY4814	valS	2837	2837
2	6	0	0	SL4409	t4513	STY4817	-	1082	1082
6	59	2	12	SL4410	t4514	STY4818	-	1064	1064
1	5	0	0	SL4474	t4586	STY4896	dnaC	719	719
0	0	0	0	SL4475	t4587	STY4897	dnaT	521	521

Ty, Typhi; Tm, Typhimurium.

### 8.3.7 Core gene functions in Typhimurium

Biological process	Sub-process	Essential genes	Non-essential genes
<b>Cell division</b>		<b><i>ftsALQWYZ, minE, mukB, SL2391</i></b>	<b><i>ftsHJK*NX*, minCD, sdiA, cedA, sulA</i></b>
<b>DNA replication</b>	Polymerases I, II and III	<b><i>dnaENQX, holAB</i></b>	<b><i>polAB, holCDE</i></b>
	Supercoiling	<b><i>gyrAB, parCE</i></b>	
	Primosome-associated	<b><i>dnaBCGT, priA</i></b>	<b><i>priBC, rep, ssb*</i></b>
<b>Transcription</b>	RNA polymerase	<b><i>rpoABC</i></b>	
	Sigma, elongation, anti- and termination factors	<b><i>nusBG, rpoDH, rho</i></b>	<b><i>nusA, rpoENS</i></b>
<b>Translation</b>	tRNA-synthetases	<b><i>alaS, argS, asnS, aspS, cysS, glnS, gltX, glyQS, hisS, ileS, leuS, lysS, metG, pheST, proS, serS, thrS, tyrS, valS,</i></b>	<b><i>trpS, trpS2</i></b>
	Ribosome components	<b><i>rpIB CDE FJ KLMNOPQRTU VWXY, rpmABCDHI, rpsABCDEF GHIJ KLMNPQ ST</i></b>	<b><i>rplAIS*, rpmEE2, rpmFGJJ2, rpsI*ORU*V</i></b>
	Initiation, elongation and peptide chain release factors	<b><i>fusA, infABC, prfAB, tsf, yrdC</i></b>	<b><i>efp, prfCH, selB, tuf</i></b>
Biosynthetic pathways			
<b>Peptidoglycan</b>		<b><i>murABCDEFGHI,</i></b>	<b><i>ddl, ddlA</i></b>
<b>Fatty acids</b>		<b><i>accABCD, fabABDGHIZ</i></b>	<b>-</b>

Gene names in bold are also essential in Typhi. \*Unassigned gene due to LR between -2 and 2.

### 8.3.8 Essential genes omitted from comparison

Five essential Typhi were omitted from the comparison with Typhimurium. Two (t1217 and t2621) were too short (26bp and 29bp, respectively) for accurate comparison. A further two (t2724 and t3166) are annotated in the Ty2 genome as coding sequences, but comparison with SL1344 indicates that these actually represent RNA genes, and therefore

were not relevant to the analysis. Lastly, t4339 is a gene only present in Typhi that has been disrupted by the insertion of a phage; it is therefore not an essential gene in Typhi.

### 8.3.9 Putative essential genes

#### 8.3.9.1 *Typhi*

Total inserts Ty	Total reads Ty	Total inserts Tm	Total reads Tm	Unique Ty Ty2 ID	Unique Ty CT18 ID	Unique Tm ID	Gene name	Gene length Ty	Gene length Tm
4	23	59	408	t3807	STY4083	SL3678	waaC	935	935
5	73	76	604	t3670	STY3930	SL3820	phoU	707	707
7	11	76	336	t0158	STY0175	SL0152	aceE	2645	2645
9	70	61	537	t0124	STY0140	SL0120	yabC	923	923
1	2	49	250	t0586	STY2507	SL2247	nrdB	1112	1112
3	7	42	263	t3214	STY3475	SL3269	ftsJ	608	608
7	60	64	393	t3213	STY3474	SL3268	ftsH	1916	1916
5	10	35	231	t0012	STY0012	SL0012	dnaK	1898	1898
17	75	45	424	t3205	STY3468	SL3260	nusA	1484	1484
0	0	42	193	t1621	STY1343	SL1640	-	1151	1097
2	8	44	207	t2139	STY0780	SL0719	sucB	1190	1190
2	3	28	166	t3809	STY4085	SL3676	waaD	914	914
14	37	41	248	t1682	STY1278	SL1176	icdA	1232	1232
12	54	62	260	t0301	STY2802	SL2517	glyA	1235	1235
2	10	28	152	t3350	STY3612	SL3901	dapF	806	809
3	12	24	144	t3287	STY3552	SL3344	mreD	473	473
0	0	9	116	t4161	STY4451	SL4192	ssb	512	512
1	1	22	117	t1316	STY1674	SL1380	pdxH	638	638
0	0	27	114	t3289	STY3554	SL3346	mreB	1025	1025
4	21	20	157	t3206	STY3469	SL3261	-	404	404
2	6	25	114	t4055	STY4348	SL3417	yheM	338	338
1	11	23	122	t2440	STY0462	SL0417	ispA	881	881
9	47	21	190	t3369	STY3627	SL3887	rffT	1340	1340
1	13	12	121	t3360	STY3622	SL3892	hemD	722	722
0	0	23	89	t2540	STY0355	SL0306	gmhA	560	560
1	3	12	94	t3201	STY3464	SL3256	rpsO	251	251
4	16	17	118	t3953	STY4242	SL3534	ftsX	1037	1037
5	25	31	132	t3288	STY3553	SL3345	mreC	1034	1034
7	14	26	111	t0983	STY2102	SL1828	ruvB	992	911
4	34	17	146	t2457	STY0444	SL0401	yajC	314	314
2	3	15	89	t3944	STY4233	SL3543	yhhP	227	227
4	21	16	119	t4400	STY4708	SL4285	psd	950	950
1	7	13	91	t3157	STY3417	SL3209	-	146	113
10	63	25	187	t3218	STY3480	SL3273	-	1154	1154

11	58	22	165	t0313	STY2789	SL2505	-	1196	1196
1	4	14	69	t3203	STY3466	SL3258	rbfA	383	383
0	0	7	61	t4443	STY4748	SL4325	priB	296	296
38	176	58	328	t1734	STY1226	SL1122	rne	3185	3185
3	13	12	75	t1622	STY1342	SL1641	-	290	290
4	23	18	88	t4600	STY4907	SL4485	holD	419	419
4	23	9	84	t2636	STY2868	SL2654	grpE	572	572
2	23	5	82	t4444	STY4749	SL4326	rpsR	209	209
7	101	20	194	t3234	STY3496	SL3289	-	557	557
1	2	6	43	t2832	STY3056	SL2910	-	293	293
8	15	11	59	t1954	STY0980	SL0917	cmk	665	665
3	12	6	54	t2628	STY2860	SL2646	rplS	329	329
1	6	7	45	t3679	STY3939	SL3807	rnpA	341	341
1	2	6	34	t4086	STY4379	SL3386	rpmJ	98	98
0	0	10	30	t4402	STY4710	SL4287	orn	527	527
2	4	6	35	t3260	STY3524	SL3316	rpsI	374	374
1	5	4	35	t1332	STY1657a	SL4528	malY	113	113
1	1	12	28	t0176	STY0193	SL0172	yadF	644	644
1	2	3	26	t0694	STY2391	SL2139	-	89	89
2	3	6	22	t1835	STY1111	SL1024	-	311	311
1	1	3	18	t3129	STY3388	SL3183	rpsU	197	197
4	26	10	47	t2205	STY0714	SL0657	-	455	455
0	0	3	15	t0535	STY2559	SL2298	-	134	134
10	48	16	70	t4401	STY4709	SL4286	yjeQ	1058	1058

Ty, Typhi; Tm, Typhimurium

### 8.3.9.2 *Typhimurium*

Total inserts Ty	Total reads Ty	Total inserts Tm	Total reads Tm	Unique Ty Ty2 ID	Unique Ty CT18 ID	Unique Tm ID	Gene name	Gene length Ty	Gene length Tm
17	104	0	0	t0090	STY0102	SL0088	folA	461	461
65	413	15	155	t0781	STY2301	SL2068	rfbG	1061	1061
23	129	7	37	t0208	STY0229	SL0208	mtn	680	680
19	107	9	26	t2135	STY0787	SL0723	cydB	1121	1121
14	145	12	56	t3488	STY3741	SL4082	birA	944	944
61	216	19	110	t1627	STY1336	SL1646	topA	2579	2579
17	61	1	7	t0941	STY2145	SL1870	tyrP	1193	1193
13	274	9	149	t3489	STY3742	SL4081	murB	1010	1010
16	53	5	16	t2234	STY0683	SL0621	lipA	947	947
8	47	3	15	t1093	STY1909	SL1711	pth	590	566
29	114	20	69	t1977	STY0955	SL0895	cydD	1748	1748
5	22	1	5	t1061	STY1946	SL1744	minE	248	248
4	19	2	12	t0045	STY0052	SL0044	rpsT	245	245
15	37	7	31	t0277	STY2827	SL2543	rnc	662	662

Ty, Typhi; Tm, Typhimurium

### 8.3.10      **Attempted construction of a Typhi *recA* mutant**

This work was performed by Jana Haase.

The suicide vector allelic-exchange method involves introducing, by homologous recombination, mutant sequences ligated to a suicide vector into the target gene to generate partial merodiploids. In this particular case, the structure of the *recA*-suicide vector construct was such that, depending on the point of cross-over, the merodiploids may be either wild-type or mutant for *recA*, and for a non-essential gene, one would expect to obtain approximately equal numbers of each. During the attempted construction of the *recA* mutant in Typhi, 19 out of 19 partial merodiploids were recombinants of the type possessing a wild-type copy of *recA*, a strong indication that *recA* is essential. The next stage involves processing of the *recA*-suicide vector recombinant for loss of the suicide vector which occurs by homologous recombination between the merodiploid sequences, resulting in either reversion or incorporation of the mutation. Again, depending on the point of crossover this process would be expected to generate approximately equal numbers of wild-type (revertant) and mutant derivatives, for a non-essential gene. In this particular case, on three independent occasions a total of 39 out of 39 derivatives were *recA* revertants, providing additional strong evidence that the *recA* gene in Typhi is essential.

## 8.4 Chapter 5

### 8.4.1 Typhimurium genes essential for macrophage infection

Inserts (input)	Reads (input)	Inserts (p.i.)	Reads (p.i.)	ID	Gene	Start	End	Strand	Log <sub>2</sub> FC	P-value
38	1850	0.35	26	SL0093	surA	104482	105750	-	-7.67	6.01E-10
30	1307	0.00	0	SL2482	-	2650773	2651933	-	-7.61	8.37E-10
11	1149	0.04	8	SL1860	flhD	1979293	1979625	-	-7.37	2.72E-09
13	1011	0.00	0	SL1622	sapA	1740541	1742172	+	-7.24	5.14E-09
29	1374	0.44	24	SL1774	prc	1898711	1900741	-	-7.16	7.75E-09
16	1190	0.31	17	SL0275	-	319216	319734	+	-7.09	1.07E-08
14	723	0.00	0	SL1904	fliL	2020640	2021089	+	-6.76	4.80E-08
19	793	0.15	26	SL1517	-	1629447	1630490	-	-6.69	6.72E-08
11	702	0.04	8	SL1466	hyaC2	1568164	1568889	-	-6.67	7.31E-08
16	1323	0.96	47	SL1772	-	1896215	1897570	+	-6.66	7.65E-08
13	1334	0.98	46	SL1082	-	1188296	1188604	+	-6.66	7.69E-08
38	1270	0.92	63	SL1428	dmsA2	1531281	1533698	-	-6.63	8.71E-08
17	896	0.38	17	SL0185	pcnB	213879	215279	-	-6.60	9.66E-08
16	966	0.55	16	SL1374	-	1475447	1476325	-	-6.54	1.26E-07
15	1150	0.86	18	SL1884	fliZ	2001714	2002247	-	-6.53	1.35E-07
8	636	0.04	8	SL1180	msgA	1286328	1286549	-	-6.53	1.36E-07
42	1738	2.10	55	SL1898	fliF	2014116	2015780	+	-6.39	2.47E-07
14	587	0.07	16	SL1634	-	1753404	1755368	+	-6.36	2.75E-07
2	537	0.00	0	SL4326	rpsR	4651824	4652033	+	-6.34	3.06E-07
17	735	0.37	17	SL1123	rluC	1228282	1229223	+	-6.33	3.13E-07
13	837	0.59	26	SL0996	gtgF	1099854	1100027	-	-6.30	3.50E-07
38	1431	1.75	58	SL3287	-	3502388	3503356	+	-6.28	3.84E-07
30	1327	1.56	25	SL0318	proA	366917	368149	+	-6.27	3.99E-07
10	574	0.12	9	SL1108	flgN	1212770	1213174	-	-6.27	4.03E-07
2	496	0.00	0	SL3543	yhhP	3767840	3768067	-	-6.22	4.91E-07
14	944	0.90	18	SL3454	aroK	3663755	3664258	-	-6.21	5.10E-07
9	510	0.04	8	SL1769	-	1894496	1894621	-	-6.21	5.17E-07
1	491	0.00	0	SL1210	-	1310000	1310230	+	-6.21	5.21E-07
19	656	0.35	18	SL1857	motB	1976774	1977685	-	-6.19	5.75E-07
22	481	0.00	0	SL3433	cap	3637137	3637751	+	-6.18	5.88E-07
24	1130	1.34	51	SL2872	spaM	3058841	3059266	-	-6.17	6.05E-07
2	475	0.00	0	SL0707	-	790305	791120	+	-6.16	6.33E-07
10	490	0.04	8	SL3809	yidC	4067748	4069376	+	-6.15	6.54E-07
23	1114	1.38	41	SL1885	fliA	2002324	2003025	-	-6.13	7.23E-07
2	469	0.04	8	SL1439	-	1544465	1544650	-	-6.09	8.43E-07
7	450	0.00	0	SL4281	yjeA	4606685	4607644	+	-6.08	8.67E-07
25	1137	1.52	38	SL1964	-	2069158	2069958	-	-6.08	9.00E-07
9	757	0.72	55	SL1478	-	1582867	1583238	-	-6.05	1.01E-06
13	584	0.33	8	SL2232	eco	2357784	2358260	+	-6.04	1.02E-06
2	408	0.00	0	SL0810	-	901541	901996	+	-5.95	1.52E-06



14	489	0.21	29	SL0746	-	832602	833282	+	-5.93	1.61E-06
8	522	0.30	21	SL1595	-	1714751	1715335	-	-5.92	1.67E-06
5	404	0.04	8	SL1354	ssaS	1456249	1456497	+	-5.88	1.97E-06
12	633	0.62	38	SL1146	nagZ	1248758	1249765	+	-5.88	1.99E-06
9	398	0.04	8	SL1111	flgB	1214398	1214796	+	-5.86	2.14E-06
13	406	0.08	9	SL1585	-	1704171	1705088	+	-5.83	2.40E-06
25	666	0.77	24	SL2843	sitC	3030688	3031530	+	-5.82	2.48E-06
9	504	0.38	21	SL1987	-	2090681	2090989	-	-5.79	2.83E-06
11	816	1.25	24	SL2207	-	2329217	2329489	+	-5.77	3.06E-06
12	358	0.00	0	SL1312	pykF	1416787	1418127	-	-5.76	3.13E-06
12	588	0.63	54	SL1621	pspF	1739449	1740411	+	-5.76	3.14E-06
12	569	0.59	18	SL0780	moaC	871428	871895	+	-5.75	3.25E-06
9	474	0.33	16	SL2603	rseA	2779168	2779800	-	-5.75	3.29E-06
28	1404	2.97	71	SL4323	-	4650826	4651014	+	-5.72	3.60E-06
9	362	0.04	8	SL2835	hypB	3022808	3023662	+	-5.72	3.60E-06
11	1300	2.68	77	SL1874	-	1992357	1992671	-	-5.72	3.63E-06
8	400	0.15	8	SL1297	-	1401165	1401506	-	-5.72	3.65E-06
11	599	0.73	17	SL0666	-	743551	744171	-	-5.70	3.93E-06
4	342	0.00	0	SL3134	-	3341448	3341579	-	-5.70	4.02E-06
11	340	0.00	0	SL1577	ldhA	1696891	1697862	+	-5.69	4.14E-06
24	554	0.63	29	SL1900	fliH	2016779	2017468	+	-5.68	4.31E-06
13	500	0.47	38	SL2571	-	2753096	2753281	-	-5.67	4.35E-06
6	333	0.00	0	SL1584	-	1703916	1704101	+	-5.66	4.63E-06
11	918	1.73	75	SL0978	-	1081781	1082161	+	-5.66	4.67E-06
26	1541	3.65	80	SL0536	fimA	603627	604151	+	-5.63	5.16E-06
21	951	1.90	42	SL2052	hisH	2151782	2152357	+	-5.62	5.41E-06
21	711	1.18	70	SL0684	kdpE	765759	766418	-	-5.62	5.44E-06
13	423	0.31	9	SL1163	potA	1268181	1269299	-	-5.60	5.71E-06
8	677	1.10	48	SL2502	hscB	2677785	2678282	-	-5.60	5.86E-06
10	708	1.21	51	SL1946	-	2055079	2055261	-	-5.59	6.05E-06
18	820	1.56	38	SL2148	yohD	2265082	2265660	+	-5.58	6.11E-06
11	469	0.48	16	SL2337	truA	2478187	2478981	-	-5.58	6.18E-06
17	324	0.04	8	SL2123	thiD	2237986	2238768	-	-5.57	6.52E-06
8	912	1.90	46	SL1257	-	1359202	1359852	-	-5.56	6.76E-06
12	425	0.37	25	SL1651	-	1772666	1773523	-	-5.54	7.08E-06
2	388	0.26	21	SL0473	ybaM	538432	538581	-	-5.54	7.10E-06
5	307	0.00	0	SL1625	sapD	1744029	1745003	+	-5.54	7.13E-06
2	303	0.00	0	SL1738	-	1866793	1866912	-	-5.52	7.64E-06
36	1170	2.86	32	SL1848	flhA	1965788	1967848	-	-5.50	8.29E-06
4	310	0.04	9	SL2116	-	2231538	2231636	-	-5.50	8.33E-06
9	735	1.45	29	SL1866	-	1985499	1986119	-	-5.49	8.55E-06
2	304	0.04	8	SL1107	mviN	1211114	1212670	+	-5.48	9.09E-06
8	310	0.06	13	SL1827	yebI	1945767	1946534	+	-5.47	9.29E-06
5	302	0.04	8	SL2191	-	2311383	2311937	+	-5.47	9.41E-06
19	759	1.61	8	SL2671	-	2860782	2861279	-	-5.45	1.02E-05
1	285	0.00	0	SL1264	-	1365082	1365378	+	-5.44	1.05E-05
8	757	1.64	38	SL1252	-	1353174	1353914	+	-5.43	1.09E-05
2	282	0.00	0	SL0714	sdhC	797412	797783	+	-5.42	1.11E-05
12	599	1.10	9	SL0528	ybbF	597240	597944	-	-5.42	1.11E-05
18	1022	2.63	83	SL3119	hybE	3328524	3328994	-	-5.40	1.22E-05

102	2437	7.73	178	SL3810	thdF	4069524	4070882	+	-5.38	1.30E-05
13	633	1.29	38	SL1607	-	1726810	1727697	-	-5.38	1.31E-05
5	485	0.77	30	SL1921	yedJ	2033410	2034087	-	-5.37	1.35E-05
5	309	0.14	21	SL0730	tolB	815384	816658	+	-5.36	1.37E-05
16	1437	4.23	113	SL4400	-	4733509	4733907	+	-5.36	1.40E-05
14	649	1.37	21	SL1530	pcgL	1646816	1647568	-	-5.36	1.40E-05
2	267	0.00	0	SL3039	rpiA	3245506	3246147	-	-5.35	1.46E-05
8	471	0.76	46	SL1511	narV	1623522	1624184	+	-5.33	1.54E-05
8	264	0.00	0	SL0853	-	946829	947287	+	-5.33	1.55E-05
21	1133	3.21	76	SL4327	rplI	4652093	4652524	+	-5.33	1.56E-05
17	262	0.00	0	SL1537	-	1654400	1655050	-	-5.32	1.61E-05
6	252	0.00	0	SL1208	-	1309044	1309667	+	-5.26	1.96E-05
4	252	0.00	0	SL1236	-	1337315	1337713	-	-5.26	1.96E-05
5	250	0.00	0	SL2883	-	3069469	3069558	+	-5.25	2.03E-05
14	660	1.62	59	SL1064	phoH	1170647	1171483	+	-5.24	2.13E-05
14	256	0.04	8	SL2473	xseA	2623804	2625135	+	-5.24	2.17E-05
13	443	0.78	17	SL3295	-	3508234	3509070	+	-5.23	2.21E-05
2	263	0.07	16	SL1989	-	2091713	2091862	+	-5.22	2.27E-05
4	244	0.00	0	SL1186	-	1291954	1292208	+	-5.22	2.29E-05
18	794	2.21	62	SL1648	-	1769947	1770975	-	-5.21	2.34E-05
12	342	0.40	16	SL3883	rffC	4154664	4155194	+	-5.21	2.40E-05
20	689	1.80	33	SL0658	ybeZ	732656	733723	-	-5.20	2.41E-05
21	410	0.68	25	SL1339	sseG	1445615	1446286	+	-5.20	2.44E-05
15	381	0.58	43	SL1589	-	1709704	1710249	-	-5.19	2.52E-05
7	495	1.05	25	SL1009	-	1116772	1117206	+	-5.19	2.57E-05
28	864	2.56	63	SL0812	ybiS	903167	904069	-	-5.18	2.59E-05
13	991	3.08	49	SL2113	-	2229221	2230249	+	-5.18	2.61E-05
7	269	0.13	29	SL1057	-	1161306	1161515	-	-5.18	2.68E-05
9	897	2.73	29	SL1350	ssaO	1453856	1454215	+	-5.17	2.73E-05
3	244	0.04	8	SL1979	-	2082182	2082637	+	-5.17	2.75E-05
12	492	1.06	16	SL1510	narW	1622830	1623507	+	-5.17	2.75E-05
6	324	0.38	21	SL2162	-	2278668	2278895	+	-5.16	2.83E-05
11	357	0.52	33	SL2110	-	2224455	2225153	+	-5.16	2.86E-05
2	233	0.00	0	SL1207	-	1308632	1308796	+	-5.15	2.87E-05
10	322	0.39	9	SL1401	tus	1502262	1503173	-	-5.13	3.11E-05
27	1016	3.35	93	SL0277	-	321096	322382	+	-5.13	3.18E-05
15	573	1.48	38	SL1841	-	1957394	1958347	+	-5.12	3.23E-05
5	227	0.00	0	SL1090	msyB	1196941	1197297	-	-5.12	3.26E-05
4	226	0.00	0	SL2389	ypeB	2536506	2536715	-	-5.11	3.33E-05
3	224	0.00	0	SL0012	dnaK	11602	13500	+	-5.10	3.48E-05
4	233	0.04	9	SL0462	rpmE2	525849	526091	+	-5.10	3.48E-05
18	753	2.31	16	SL4431	-	4776169	4776408	-	-5.09	3.56E-05
14	809	2.58	49	SL1050	yccD	1155025	1155312	-	-5.08	3.69E-05
3	221	0.00	0	SL4295	hfq	4625165	4625455	+	-5.08	3.71E-05
11	711	2.18	29	SL4193	-	4499158	4499772	+	-5.07	3.90E-05
13	557	1.51	59	SL1633	rnb	1751208	1753124	+	-5.06	3.97E-05
25	565	1.56	50	SL3952	glnG	4234304	4235695	-	-5.05	4.06E-05
1	249	0.15	8	SL0800	ybil	890271	890519	-	-5.05	4.11E-05
16	312	0.43	27	SL1307	-	1413046	1414248	+	-5.05	4.15E-05
32	1134	4.15	97	SL3220	-	3435924	3437051	-	-5.04	4.27E-05

8	424	0.96	25	SL1336	sseE	1443918	1444316	+	-5.03	4.45E-05
19	704	2.25	33	SL2534	yfhH	2715314	2716144	+	-5.02	4.53E-05
10	211	0.00	0	SL1134	fabF	1236586	1237809	+	-5.02	4.62E-05
40	1406	5.56	96	SL0441	tig	501160	502440	+	-5.00	4.87E-05
1	247	0.18	8	SL1433	-	1538169	1538492	-	-4.99	4.98E-05
15	675	2.21	46	SL0756	modE	843705	844475	-	-4.98	5.20E-05
18	548	1.62	35	SL1105	-	1209277	1209906	+	-4.98	5.30E-05
16	599	1.87	33	SL0852	rimK	945830	946714	+	-4.97	5.41E-05
3	204	0.00	0	SL1340	ssaG	1446398	1446595	+	-4.97	5.42E-05
12	453	1.19	33	SL2190	-	2310250	2310951	+	-4.97	5.47E-05
8	350	0.70	8	SL3678	rfaC	3928620	3929555	+	-4.97	5.47E-05
6	349	0.69	38	SL1617	pspD	1737726	1737926	-	-4.96	5.49E-05
1	203	0.00	0	SL0221	dxr	257851	259029	+	-4.96	5.55E-05
14	504	1.46	29	SL0541	fimF	609189	609689	+	-4.95	5.82E-05
25	803	2.91	33	SL2194	yejB	2315759	2316835	+	-4.94	5.88E-05
4	253	0.25	29	SL3535	ftsE	3759406	3760056	-	-4.94	5.90E-05
17	875	3.28	46	SL2120	-	2235264	2236250	+	-4.94	6.04E-05
15	1038	4.13	113	SL2214	-	2335549	2336862	+	-4.92	6.39E-05
10	444	1.22	29	SL1751	-	1878133	1878459	+	-4.92	6.45E-05
12	550	1.75	52	SL1199	aadA	1303458	1304228	+	-4.91	6.61E-05
3	243	0.24	9	SL2334	folC	2475079	2476329	-	-4.91	6.62E-05
7	218	0.11	17	SL0478	ybaB	542378	542689	+	-4.91	6.64E-05
12	405	1.06	16	SL1551	-	1665918	1666475	-	-4.89	7.03E-05
6	321	0.65	17	SL1183	pagD	1288038	1288283	-	-4.89	7.13E-05
43	1988	9.13	117	SL4377	-	4709292	4710014	+	-4.87	7.49E-05
2	190	0.00	0	SL4090	rplJ	4386001	4386480	+	-4.87	7.53E-05
9	344	0.78	29	SL3170	glgS	3380028	3380219	-	-4.87	7.55E-05
7	230	0.22	8	SL2234	alkB	2360206	2360838	-	-4.85	8.03E-05
8	186	0.00	0	SL2290	nuoI	2428088	2428612	-	-4.84	8.30E-05
3	184	0.00	0	SL0719	sucB	803981	805171	+	-4.82	8.72E-05
8	546	1.90	46	SL1080	csgB	1187282	1187719	+	-4.82	8.73E-05
23	828	3.38	79	SL2944	-	3136548	3136979	-	-4.82	8.79E-05
10	183	0.00	0	SL1871	yecA	1989263	1989910	-	-4.82	8.94E-05
12	512	1.74	47	SL0789	ybhP	877614	878354	-	-4.82	8.97E-05
13	361	0.99	16	SL3900	-	4173576	4173761	+	-4.78	0.000101
11	266	0.48	8	SL1018	-	1126241	1126639	+	-4.78	0.000101
9	178	0.00	0	SL1276	btuD	1378056	1378787	+	-4.78	0.000101
2	177	0.00	0	SL2394	ptsH	2542311	2542550	+	-4.77	0.000104
6	392	1.17	42	SL1698	chaB	1825618	1825830	-	-4.77	0.000104
8	229	0.29	29	SL2834	hypA	3022383	3022721	+	-4.77	0.000105
10	440	1.46	26	SL0492	cueR	560053	560451	+	-4.76	0.000109
18	724	3.03	68	SL2147	yohC	2264363	2264932	-	-4.75	0.000111
3	210	0.20	9	SL1531	ugtL	1648108	1648488	-	-4.75	0.000111
5	181	0.04	8	SL1890	fliS	2008397	2008786	+	-4.75	0.000111
8	696	2.89	38	SL2946	yqcC	3137798	3138109	-	-4.75	0.000113
12	598	2.35	81	SL0445	hupB	507600	507854	+	-4.74	0.000113
5	173	0.00	0	SL0892	-	987039	987404	-	-4.74	0.000115
4	172	0.00	0	SL1897	fliE	2013585	2013881	-	-4.73	0.000118
6	172	0.00	0	SL4114	purD	4412501	4413772	-	-4.73	0.000118
15	618	2.50	50	SL1126	-	1230642	1231208	-	-4.73	0.000119

3	341	0.96	30	SL1202	-	1306156	1306386	-	-4.72	0.000123
6	170	0.00	0	SL3813	-	4073660	4074577	+	-4.71	0.000124
23	763	3.40	29	SL1115	flgF	1217191	1217928	+	-4.70	0.00013
9	876	4.05	68	SL3026	-	3229566	3229859	-	-4.70	0.00013
12	353	1.06	32	SL1935	-	2046003	2046518	-	-4.70	0.000132
16	698	3.06	49	SL1993	cobS	2096124	2096849	-	-4.69	0.000134
11	687	3.00	77	SL0888	-	984225	984884	-	-4.69	0.000136
3	262	0.55	17	SL0121	ftsL	141357	141704	+	-4.69	0.000137
7	452	1.66	72	SL3839	atpI	4101496	4101858	-	-4.68	0.00014
3	163	0.00	0	SL0152	aceE	176253	178898	+	-4.66	0.00015
8	438	1.63	21	SL1895	yedF	2012581	2012796	+	-4.65	0.000152
4	160	0.00	0	SL1275	btuE	1377505	1378038	+	-4.63	0.000162
11	259	0.59	17	SL1157	-	1261996	1262889	+	-4.63	0.000162
27	613	2.72	59	SL1119	flgJ	1220604	1221536	+	-4.63	0.000163
21	520	2.20	24	SL3885	-	4156349	4157581	+	-4.61	0.000171
13	707	3.33	41	SL4303	yjfl	4635045	4635431	+	-4.61	0.000171
23	347	1.15	42	SL1903	fliK	2019318	2020517	+	-4.61	0.000172
9	188	0.18	16	SL0398	yajB	458380	458943	-	-4.61	0.000172
15	459	1.83	26	SL2005	cblF	2105484	2106239	-	-4.61	0.000173
9	893	4.54	72	SL1939	-	2050978	2051286	-	-4.59	0.000183
7	205	0.30	13	SL2025	pduN	2122653	2122910	+	-4.59	0.000183
25	1055	5.54	159	SL0811	ybiR	902011	903105	+	-4.59	0.000183
13	167	0.07	8	SL0215	glnD	250148	252802	-	-4.59	0.000185
14	393	1.47	38	SL2017	pduD	2117357	2118013	+	-4.59	0.000186
17	2254	13.06	100	SL2745	-	2924055	2925911	+	-4.58	0.000191
4	153	0.00	0	SL1308	-	1414279	1414677	+	-4.57	0.000197
24	240	0.55	8	SL4505	serB	4853813	4854763	+	-4.56	0.000199
19	212	0.38	39	SL1452	sotB	1555764	1556936	-	-4.56	0.0002
4	152	0.00	0	SL2903	rpoS	3088064	3089038	-	-4.56	0.000202
5	150	0.00	0	SL1801	-	1922089	1922334	-	-4.54	0.000214
4	178	0.18	8	SL3289	-	3503958	3504515	+	-4.54	0.000218
15	983	5.37	41	SL0546	-	613247	613573	-	-4.53	0.000222
1	148	0.00	0	SL1370	-	1471645	1471866	+	-4.52	0.000226
9	147	0.00	0	SL3020	xerD	3225154	3226032	-	-4.51	0.000233
19	577	2.84	90	SL3051	-	3256422	3257060	+	-4.50	0.000244
17	304	1.04	55	SL2040	phsB	2135806	2136366	-	-4.50	0.000244
2	145	0.00	0	SL1415	-	1518921	1519187	-	-4.49	0.000247
7	174	0.20	9	SL3411	yheA	3619414	3619590	-	-4.49	0.000252
9	337	1.28	21	SL0251	yafC	295893	296789	-	-4.49	0.000253
7	507	2.41	29	SL0382	yail	439700	440137	+	-4.49	0.000254
24	949	5.37	148	SL3019	dsbC	3224417	3225073	-	-4.48	0.000259
14	511	2.49	55	SL1383	gst	1482601	1483188	-	-4.46	0.000272
15	512	2.51	55	SL1811	-	1927969	1928607	+	-4.46	0.000276
21	430	1.97	17	SL1396	-	1496062	1497552	-	-4.45	0.000281
11	669	3.61	51	SL2857	iagB	3044120	3044584	+	-4.45	0.000286
22	877	5.03	71	SL1734	nhaB	1863690	1865216	+	-4.45	0.000287
21	1179	7.11	106	SL3042	-	3248318	3248935	-	-4.44	0.00029
9	494	2.43	35	SL1306	-	1411778	1413031	+	-4.44	0.000292
12	439	2.05	51	SL2786	-	2971894	2972214	+	-4.44	0.000292
19	1097	6.57	76	SL2195	yejE	2316853	2317860	+	-4.44	0.000294

15	492	2.44	63	SL2258	-	2393765	2394550	-	-4.43	0.0003
3	138	0.00	0	SL2528	-	2709889	2710104	+	-4.43	0.000304
9	175	0.26	16	SL4004	sodA	4287986	4288588	+	-4.43	0.000304
7	270	0.92	24	SL1850	cheZ	1969204	1969830	-	-4.42	0.000306
6	370	1.62	26	SL1926	umuD	2038740	2039141	-	-4.42	0.000311
13	532	2.75	82	SL1289	-	1392599	1393471	+	-4.42	0.000313
12	385	1.73	30	SL1932	-	2044512	2045015	-	-4.41	0.000316
7	136	0.00	0	SL1541	rimL	1657904	1658425	-	-4.41	0.000322
21	1043	6.39	109	SL1106	mviM	1209926	1210831	+	-4.40	0.000329
4	135	0.00	0	SL0637	-	711414	711686	+	-4.40	0.000332
28	1113	6.99	91	SL1230	sppA	1329772	1331610	-	-4.38	0.000349
19	457	2.33	64	SL4226	phnA	4551468	4551785	-	-4.37	0.000359
14	347	1.57	17	SL0301	-	349161	349358	+	-4.36	0.000376
4	160	0.22	21	SL1386	rnfE	1486053	1486727	-	-4.35	0.000386
12	475	2.52	29	SL0279	-	323381	323794	+	-4.34	0.000388
9	419	2.12	29	SL1052	scsA	1156485	1156829	+	-4.34	0.000392
7	226	0.71	18	SL2222	narP	2344427	2345056	+	-4.34	0.000392
7	254	0.92	17	SL1256	-	1358465	1359046	-	-4.33	0.0004
8	824	5.13	29	SL4251	-	4581471	4582328	-	-4.33	0.000403
1	158	0.22	8	SL2931	eno	3118836	3120116	-	-4.33	0.000409
5	138	0.07	8	SL0529	ppiB	597965	598441	-	-4.32	0.000411
1	184	0.42	21	SL2332	cvpA	2473616	2474086	-	-4.32	0.000416
4	461	2.48	63	SL1809	-	1927119	1927481	-	-4.32	0.000417
9	334	1.54	80	SL4379	relB	4712040	4712264	+	-4.32	0.000418
4	146	0.15	8	SL2504	nifU	2678848	2679216	-	-4.31	0.000433
7	223	0.73	24	SL2271	-	2408414	2408653	+	-4.30	0.000442
6	146	0.16	9	SL1127	-	1231424	1231927	+	-4.29	0.00045
14	404	2.15	29	SL1416	-	1519564	1520799	-	-4.28	0.000472
11	210	0.67	17	SL3450	rpe	3659523	3660182	-	-4.27	0.000483
5	174	0.40	16	SL1217	-	1314579	1315079	-	-4.26	0.000499
10	200	0.61	38	SL0933	-	1043697	1044227	+	-4.26	0.000499
42	1024	7.01	109	SL0371	sbmA	429956	431056	+	-4.26	0.0005
17	1229	8.64	62	SL1095	yceJ	1201582	1202136	-	-4.25	0.000509
17	862	5.79	122	SL1762	-	1888853	1889293	+	-4.25	0.000513
3	184	0.50	17	SL2247	nrdB	2381523	2382635	+	-4.24	0.000523
6	232	0.88	34	SL2020	pduH	2120399	2120731	+	-4.24	0.000526
7	357	1.86	38	SL0575	ybdZ	644744	644944	+	-4.24	0.000529
16	541	3.32	59	SL0349	-	400355	400801	+	-4.24	0.000533
17	1218	8.70	122	SL2400	-	2547535	2548236	+	-4.23	0.000542
9	462	2.73	72	SL1743	minD	1869680	1870474	+	-4.22	0.00055
4	441	2.58	38	SL1330A	-	1366420	1366605	+	-4.22	0.000565
4	118	0.00	0	SL3699	pyrE	3947282	3947905	-	-4.21	0.00057
17	563	3.58	109	SL1715	-	1842805	1844580	+	-4.21	0.000574
22	1358	10.00	64	SL4440	-	4784233	4784661	+	-4.20	0.000583
12	554	3.52	55	SL0137	mutT	161559	161936	+	-4.20	0.000584
5	212	0.77	38	SL1235	-	1337080	1337337	+	-4.20	0.000586
16	469	2.87	105	SL0928	smtA	1033982	1034767	+	-4.19	0.000604
5	116	0.00	0	SL2021	pduJ	2120768	2121025	+	-4.19	0.00061
15	511	3.31	42	SL0500	ybbA	565936	566604	+	-4.16	0.000665
5	387	2.28	55	SL1566	-	1682921	1683583	+	-4.16	0.000668

7	325	1.77	55	SL3181	-	3393352	3393606	+	-4.15	0.000677
8	219	0.91	30	SL4392	pyrL	4725533	4725616	-	-4.14	0.000708
6	419	2.60	29	SL1697	-	1825185	1825520	+	-4.13	0.000714
6	475	3.09	29	SL1367	gloA	1469311	1469700	-	-4.13	0.000721
7	380	2.31	51	SL2588	-	2764956	2765408	-	-4.12	0.000742
23	702	5.10	85	SL3490	-	3708204	3708518	-	-4.11	0.000761
13	484	3.23	38	SL2037	gyrI	2133129	2133578	-	-4.11	0.000768
3	141	0.27	9	SL0620	tatE	694070	694255	+	-4.11	0.000771
5	109	0.00	0	SL1909	fliQ	2023650	2023901	+	-4.10	0.000775
11	241	1.16	29	SL4100	thiS	4400264	4400446	-	-4.09	0.000797
29	1274	10.14	140	SL2796	proX	2980865	2981842	+	-4.09	0.000798
18	776	5.91	41	SL0804	glnP	894731	895372	-	-4.07	0.000844
5	131	0.22	8	SL2790	nrdH	2974442	2974669	+	-4.07	0.000856
1	106	0.00	0	SL2508	suhB	2682161	2682946	+	-4.07	0.000862
20	375	2.40	38	SL4011	pfkA	4293777	4294721	+	-4.06	0.000873
6	230	1.11	17	SL1726	-	1854130	1854846	+	-4.06	0.000874
16	772	5.94	93	SL2154	-	2271357	2272040	-	-4.06	0.000877
31	1656	13.82	101	SL2177	lysP	2296613	2298064	-	-4.06	0.000879
8	402	2.68	60	SL2902	-	3087783	3088001	+	-4.04	0.000914
14	787	6.19	89	SL3380	yhdN	3603892	3604242	-	-4.04	0.000937
31	1959	16.83	122	SL3229	-	3446539	3447327	+	-4.03	0.000943
2	115	0.11	8	SL0136	secA	158702	161389	+	-4.03	0.000962
6	441	3.09	25	SL0670	-	750410	750724	+	-4.02	0.00097
22	1524	13.00	101	SL1996	cbiO	2098923	2099720	-	-4.02	0.000973
18	567	4.27	71	SL4277	frdD	4603069	4603410	-	-4.02	0.000988
4	102	0.00	0	SL1059	-	1162535	1162684	+	-4.01	0.000996

p.i. post infection; reads and inserts from post infection are the combined values of the 30 minute, 2 hour and 4 hour timepoints, normalised for sequencing yield per sample.

## 8.4.2 Typhi genes required for macrophage infection (original assay)

Inserts (input)	Reads (input)	Inserts (p.i.)	Reads (p.i.)	ID	Gene	Start	End	Strand	Log <sub>2</sub> FC	P-value
14	117	0.27	5	t3623	dsbA	3726177	3726782	-	-3.79	7.96E-09
18	184	1.01	10	t1975	lrp	2033312	2033788	-	-3.75	1.07E-08
19	87	0.00	0	t0336	-	386382	387542	+	-3.74	1.22E-08
32	120	0.59	13	t2980	serA	3071308	3072522	-	-3.50	8.23E-08
87	740	10.35	81	t3645	gidA	3750936	3752807	+	-3.22	6.60E-07
11	47	0.00	0	t3214	ftsJ	3306755	3307363	-	-2.94	4.74E-06
58	1173	21.08	93	t1033	prc	1116361	1118391	+	-2.92	5.29E-06
9	71	0.55	5	t2131	tolQ	2192191	2192865	-	-2.84	9.02E-06
5	104	1.22	19	t1068	-	1149801	1149956	+	-2.83	9.78E-06
12	41	0.00	0	t3505	ppc	3598965	3601598	+	-2.77	1.43E-05
18	86	1.00	9	t4411	miaA	4562802	4563734	+	-2.72	1.93E-05
6	282	5.64	20	t4378	-	4531819	4531923	-	-2.63	3.43E-05
6	32	0.00	0	t4623	yjiX	4776185	4776502	-	-2.47	8.68E-05
21	83	1.42	21	t3372	rffA	3471846	3472958	-	-2.40	0.0001282

11	160	3.51	13	t1070	dsbB	1150495	1151007	-	-2.39	0.0001331
4	40	0.27	9	t2628	rplS	2705986	2706315	-	-2.39	0.0001358
5	50	0.59	9	t3210	secG	3301879	3302193	-	-2.34	0.000175
5	213	5.17	24	t1054	-	1138452	1138613	+	-2.34	0.0001819
75	561	15.15	59	t3797	waaP	3917060	3917839	+	-2.32	0.0002015
4	28	0.00	0	t0879	-	981038	981181	+	-2.31	0.0002074
5	36	0.23	4	t4579	-	4733209	4733493	+	-2.31	0.0002075
6	53	0.73	9	t4643	ssrA	2734390	2734838	+	-2.30	0.0002231
13	87	1.71	17	t0732	-	813181	813642	+	-2.30	0.0002248
9	79	1.50	9	t2916	-	3007291	3007491	+	-2.29	0.000239
1	44	0.49	10	t1719	holB	1786262	1787248	-	-2.28	0.000246
7	44	0.52	12	t2365	-	2432203	2432664	+	-2.25	0.0002899
26	80	1.60	8	t0317	hscA	360783	362615	+	-2.25	0.0002942
3	25	0.00	0	t0045	rpsT	52286	52531	-	-2.18	0.0004114
2	24	0.00	0	t2130	tolR	2191759	2192169	-	-2.14	0.0005204
11	110	2.88	17	t0887	vsr	988540	988992	+	-2.10	0.0006378
8	30	0.23	4	t1312	slyA	1374300	1374716	+	-2.10	0.0006429
7	23	0.00	0	t1974	ftsK	2029146	2033159	-	-2.09	0.0006605
6	30	0.26	6	t0606	napG	691360	692037	+	-2.06	0.0007736

p.i. post infection; reads and inserts from post infection are the combined values of the 30 minute, 2 hour and 4 hour timepoints, normalised for sequencing yield per sample.