

Table S1. Repressed genes for *letS*^{T311M} vs. WT at OD₆₀₀ = 2 and OD₆₀₀ = 3

Gene ID	Name	Paris ID	Lens ID	Description	OD2 ¹	OD3 ¹
<i>lpg1219</i>	<i>flgE</i>	<i>lpp1227</i>	<i>lp11227</i>	flagellar hook protein	-6.1	-
<i>lpg1225</i>	<i>flgK</i>	<i>lpp1233</i>	<i>lp11233</i>	flagellar hook-associated protein	-4.9	-
<i>lpg1226</i>	<i>flgL</i>	<i>lpp1234</i>	<i>lp11234</i>	flagellar hook-associated protein	-4.4	-
<i>lpg1220</i>	<i>flgF</i>	<i>lpp1228</i>	<i>lp11228</i>	flagellar biosynthesis protein	-4.3	-
<i>lpg0901</i>	-	<i>lpp0962</i>	<i>lp10932</i>	unknown	-3.8	-
<i>lpg0902</i>	-	<i>lpp0963</i>	<i>lp10933</i>	unknown	-3.6	-
<i>lpg0669</i>	-	<i>lpp0725</i>	<i>lp10705</i>	unknown	-3.6	-
<i>lpg1168</i>	-	<i>lpp1170</i>	<i>lp11176</i>	regulatory protein (GGDEF and EAL domains)	-3.4	-
<i>lpg1454</i>	-	<i>lpp1410</i>	<i>lp11590</i>	multidrug efflux protein	-3.2	-
<i>lpg0277</i>	-	<i>lpp0351</i>	<i>lp10329</i>	regulatory protein (EAL domain)	-3.2	-
<i>lpg1370</i>	<i>fis2</i>	<i>lpp1324</i>	<i>lp11321</i>	similar to DNA-binding protein Fis	-3.1	-
<i>lpg1055</i>	-	<i>lpp2327</i>	-	unknown	-3.0	-
<i>lpg2028</i>	<i>hemE</i>	<i>lpp2010</i>	<i>lp12005</i>	uroporphyrinogen decarboxylase	-2.9	-
<i>lpg2622</i>	-	<i>lpp2675</i>	<i>lp12547</i>	weakly similar to cysteine protease	-2.9	-
<i>lpg1223</i>	<i>flgI</i>	<i>lpp1231</i>	<i>lp11231</i>	flagellar P-ring protein precursor	-2.9	-
<i>lpg0426</i>	<i>cspD</i>	<i>lpp0493</i>	<i>lp10469</i>	cold shock-like protein	-2.9	-
<i>lpg2105</i>	-	-	-	transmembrane protein	-2.8	-
<i>lpg0560</i>	<i>phaB1</i>	<i>lpp0620</i>	<i>lp10603</i>	acetoacetyl-CoA reductase	-2.8	-
<i>lpg2106</i>	-	-	-	unknown	-2.7	-
<i>lpg1224</i>	<i>flgJ</i>	<i>lpp1232</i>	<i>lp11232</i>	flagellar biosynthesis protein	-2.6	-
<i>lpg1667</i>	-	<i>lpp1638</i>	<i>lp11632</i>	similar to metallo-endopeptidases	-2.6	-
<i>lpg0737</i>	-	<i>lpp0802</i>	<i>lp10773</i>	putative secreted protein	-2.6	-
<i>lpg2579</i>	-	<i>lpp2631</i>	<i>lp12501</i>	unknown	-2.5	-
<i>lpg2732</i>	<i>lqsR</i>	<i>lpp2788</i>	<i>lp12657</i>	LqsR response regulator	-2.5	-
<i>lpg2837</i>	-	<i>lpp2894</i>	<i>lp12749</i>	similar to lysophospholipase A	-2.5	-
<i>lpg2457</i>	-	<i>lpp2523</i>	<i>lp12376</i>	two-component response regulator (crystallized)	-2.4	-
<i>lpg1908</i>	<i>gst</i>	<i>lpp1883</i>	<i>lp11874</i>	glutathione S-transferase	-2.4	-
<i>lpg1218</i>	<i>flgD</i>	<i>lpp1226</i>	<i>lp11226</i>	flagellar basal-body rod modification protein	-2.4	-
<i>lpg0733</i>	-	<i>lpp0799</i>	<i>lp10770</i>	unknown	-2.3	-
<i>lpg1222</i>	<i>flgH</i>	<i>lpp1230</i>	<i>lp11230</i>	flagellar L-ring protein precursor	-2.3	-
<i>lpg1059</i>	<i>phaB3</i>	<i>lpp2322</i>	<i>lp11056</i>	acetoacetyl-CoA reductase	-2.2	-
<i>lpg2237</i>	-	<i>lpp2190</i>	<i>lp12163</i>	ABC-type multidrug transport system, ATPase and permease components	-2.2	-
<i>lpg2950a</i> ²	-	<i>lpp3021</i>	<i>lp12878</i>	unknown	-2.2	-
<i>lpg2328</i>	-	<i>lpp2276</i>	<i>lp12248</i>	unknown - N-terminal similar to <i>Legionella</i> 33 kDa polypeptide	-2.2	-
<i>lpg2258</i>	-	<i>lpp2212</i>	<i>lp12184</i>	unknown	-2.1	-
<i>lpg1221</i>	<i>flgG</i>	<i>lpp1229</i>	<i>lp11229</i>	flagellar biosynthesis protein	-2.1	-
<i>lpg0874</i>	<i>pntB</i>	<i>lpp0937</i>	<i>lp10907</i>	NAD(P) transhydrogenase subunit beta	-2.0	-
<i>lpg0953</i>	-	<i>lpp1015</i>	<i>lp10982</i>	long-chain acyl-CoA synthetases (AMP-forming)	-2.0	-
<i>lpg1655</i>	-	<i>lpp1626</i>	<i>lp11620</i>	LasB-like zinc metalloprotease (elastase)	-2.0	-
<i>lpg1174a</i> ²	-	<i>lpp1177</i>	<i>lp11183</i>	unknown	-5.8	-8.5
<i>lpg0012</i>	-	<i>lpp0012</i>	<i>lp10012</i>	unknown	-3.2	-2.6
<i>lpg0632</i>	-	<i>lpp0686</i>	<i>lp10669</i>	type IV fimbrial pilin related protein	-	-7.5
<i>lpg2803</i>	-	<i>lpp2849</i>	<i>lp12718</i>	unknown	-	-6.4
<i>lpg1895</i>	-	<i>lpp1864</i>	<i>lp11859</i>	unknown	-	-6.0
<i>lpg2569</i>	-	-	-	unknown	-	-5.9
<i>lpg0741</i>	-	<i>lpp0806</i>	<i>lp10777</i>	unknown	-	-5.5
<i>lpg0586</i>	-	<i>lpp0636</i>	<i>lp10620</i>	putative transcriptional regulator	-	-5.4
<i>lpg2315</i>	-	<i>lpp2263</i>	<i>lp12235</i>	unknown	-	-4.8
<i>lpg0259</i>	-	<i>lpp0329</i>	<i>lp10312</i>	unknown	-	-4.7
<i>lpg2187</i>	-	<i>lpp2137</i>	<i>lp12112</i>	unknown	-	-4.5
<i>lpg1686</i>	-	-	-	unknown	-	-4.3
<i>lpg2862</i>	<i>legC8</i>	-	-	cytotoxic glucosyltransferase	-	-4.3
<i>lpg2990</i>	-	<i>lpp3061</i>	<i>lp12918</i>	unknown	-	-4.1
<i>lpg1340</i>	<i>flaA</i>	<i>lpp1294</i>	<i>lp11293</i>	flagellin	-	-4.0

Gene ID	Name	Paris ID	Lens ID	Description	OD2 ¹	OD3 ¹
<i>lpg1577</i>	<i>rpoE</i>	<i>lpp1535</i>	<i>lpl1448</i>	sigma factor RpoE (σ^{24})	-	-3.9
<i>lpg0631</i>	-	<i>lpp0685</i>	<i>lpl0668</i>	type IV fimbrial biogenesis protein PilV	-	-3.8
<i>lpg1386</i>	<i>enhA3</i>	<i>lpp1341</i>	<i>lpl1337</i>	similar to enhanced entry protein EnhA	-	-3.8
<i>lpg0910</i>	<i>enhA2</i>	<i>lpp0972</i>	<i>lpl0942</i>	similar to enhanced entry protein EnhA	-	-3.7
<i>lpg2603</i>	-	<i>lpp2656</i>	<i>lpl2526</i>	unknown	-	-3.6
<i>lpg0672</i>	-	<i>lpp0728</i>	<i>lpl0708</i>	acetoacetate decarboxylase (crystallized)	-	-3.6
<i>lpg2582a²</i>	-	<i>lpp2636</i>	<i>lpl2506</i>	unknown	-	-3.5
<i>lpg2520</i>	-	<i>lpp2588</i>	<i>lpl2442</i>	unknown	-	-3.5
<i>lpg2364</i>	-	-	-	weakly similar to NAD-dependent DNA ligase	-	-3.5
<i>lpg0628</i>	-	<i>lpp0682</i>	<i>lpl0665</i>	type IV fimbrial biogenesis PilY1-related protein	-	-3.4
<i>lpg1121</i>	-	<i>lpp1121</i>	<i>lpl1126</i>	unknown	-	-3.3
<i>lpg0286a²</i>	-	<i>lpp0364</i>	<i>lpl0339</i>	unknown - signal peptide predicted	-	-3.1
<i>lpg2157</i>	<i>sdeA</i>	<i>lpp2096</i>	<i>lpl2085</i>	SdeA - substrate of the Dot/Icm T4SS	-	-3.1
<i>lpg0898</i>	-	<i>lpp0959</i>	<i>lpl0929</i>	unknown	-	-3.0
<i>lpg1491</i>	-	<i>lpp1447</i>	-	some similarity with eukaryotic proteins	-	-3.0
<i>lpg1339</i>	-	<i>lpp1293</i>	<i>lpl1292</i>	unknown	-	-3.0
<i>lpg0620</i>	-	<i>lpp0674</i>	<i>lpl0657</i>	unknown	-	-3.0
<i>lpg1158</i>	-	<i>lpp1160</i>	-	some similarity with eukaryotic proteins	-	-3.0
<i>lpg1669</i>	-	<i>lpp1641</i>	<i>lpl1634</i>	unknown - α -amylase domain	-	-3.0
<i>lpg2524</i>	-	-	-	LuxR family transcriptional regulator	-	-2.9
<i>lpg1355</i>	<i>sidG</i>	<i>lpp1309</i>	-	SidG - substrate of the Dot/Icm T4SS	-	-2.9
<i>lpg2145</i>	-	<i>lpp2083</i>	<i>lpl2073</i>	putative two-component response regulator	-	-2.9
<i>lpg0629</i>	-	<i>lpp0683</i>	<i>lpl0666</i>	Tfp pilus assembly protein PilX	-	-2.9
<i>lpg0088</i>	-	<i>lpp0102</i>	<i>lpl0087</i>	similar to arginine-binding periplasmic protein	-	-2.9
<i>lpg2521</i>	-	<i>lpp2589</i>	<i>lpl2443</i>	unknown - transmembrane protein	-	-2.8
<i>lpg2527</i>	-	<i>lpp2592</i>	<i>lpl2447</i>	unknown	-	-2.8
<i>lpg0625</i>	-	<i>lpp0679</i>	<i>lpl0662</i>	similar to unknown eukaryotic proteins	-	-2.8
<i>lpg2146</i>	<i>stuC</i>	<i>lpp2084</i>	<i>lpl2074</i>	sensor histidine kinase	-	-2.8
<i>lpg1290</i>	-	<i>lpp1253</i>	-	unknown	-	-2.8
<i>lpg1963</i>	-	-	-	unknown	-	-2.8
<i>lpg2498a²</i>	-	<i>lpp2567</i>	<i>lpl2421</i>	unknown	-	-2.7
<i>lpg0673</i>	-	<i>lpp0729</i>	<i>lpl0709</i>	unknown - signal peptide protein	-	-2.7
<i>lpg1207</i>	-	<i>lpp1209</i>	<i>lpl1215</i>	similar to YbaK/prolyl-tRNA synthetase associated region	-	-2.7
<i>lpg2877</i>	-	<i>lpp2936</i>	<i>lpl2790</i>	unknown	-	-2.7
<i>lpg0627</i>	<i>pilE</i>	<i>lpp0681</i>	<i>lpl0664</i>	type IV pilin	-	-2.6
<i>lpg0589</i>	-	<i>lpp0639</i>	<i>lpl0623</i>	unknown	-	-2.6
<i>lpg1968a²</i>	-	<i>lpp1951</i>	<i>lpl1940</i>	unknown	-	-2.6
<i>lpg0871</i>	-	<i>lpp0934</i>	<i>lpl0903</i>	unknown	-	-2.6
<i>lpg0614</i>	-	<i>lpp0665</i>	<i>lpl0649</i>	unknown	-	-2.6
<i>lpg1485</i>	-	<i>lpp1441</i>	<i>lpl1543</i>	unknown	-	-2.5
<i>lpg2181</i>	<i>arcB</i>	<i>lpp2133</i>	<i>lpl2108</i>	putative histidine kinase/response regulator	-	-2.5
<i>lpg0037</i>	<i>artJ1</i>	<i>lpp0036</i>	<i>lpl0037</i>	similar to arginine 3rd transport system periplasmic binding protein	-	-2.5
<i>lpg1115</i>	<i>kaiC2</i>	<i>lpp1116</i>	<i>lpl1120a</i>	putative circadian clock protein KaiC	-	-2.5
<i>lpg0258</i>	-	<i>lpp0328</i>	<i>lpl0311</i>	unknown	-	-2.5
<i>lpg2132</i>	-	<i>lpp2071</i>	<i>lpl2061</i>	regulatory protein (GGDEF domain)	-	-2.5
<i>lpg1113</i>	-	<i>lpp1113</i>	<i>lpl1117</i>	unknown	-	-2.4
<i>lpg2147</i>	-	<i>lpp2086</i>	<i>lpl2075</i>	unknown	-	-2.4
<i>lpg1496</i>	-	<i>lpp1453</i>	<i>lpl1530</i>	some similarities with sidE protein	-	-2.4
<i>lpg1080</i>	-	-	-	putative deoxyguanosine triphosphate triphosphohydrolase	-	-2.4
<i>lpg2907</i>	-	<i>lpp2976</i>	<i>lpl2824</i>	unknown	-	-2.4
<i>lpg2049</i>	-	<i>lpp2032</i>	<i>lpl2027</i>	unknown	-	-2.4
<i>lpg2719</i>	-	<i>lpp2776</i>	<i>lpl2647</i>	unknown	-	-2.4
<i>lpg0671</i>	<i>ndh</i>	<i>lpp0727</i>	<i>lpl0707</i>	NADH dehydrogenase	-	-2.3
<i>lpg2268</i>	-	<i>lpp2222</i>	<i>lpl2194</i>	unknown	-	-2.3
<i>lpg2246</i>	-	<i>lpp2200</i>	<i>lpl2172</i>	unknown	-	-2.2
<i>lpg0039</i>	-	<i>lpp0040</i>	<i>lpl0039</i>	unknown	-	-2.2
<i>lpg0587</i>	<i>yqgF</i>	<i>lpp0637</i>	<i>lpl0621</i>	Holliday junction resolvase-like protein	-	-2.2
<i>lpg1112</i>	-	<i>lpp0639</i>	<i>lpl1116</i>	unknown	-	-2.2

Gene ID	Name	Paris ID	Lens ID	Description	OD2 ¹	OD3 ¹
<i>lpg0245</i>	-	<i>lpp0315</i>	<i>lp10299</i>	NAD-glutamate dehydrogenase	-	-2.2
<i>lpg2759</i>	-	<i>lpp2807</i>	<i>lp12676</i>	unknown	-	-2.2
<i>lpg2093</i>	-	-	-	unknown	-	-2.2
<i>lpg2108</i>	-	-	-	unknown	-	-2.2
<i>lpg0121</i>	-	<i>lpp0134</i>	<i>lp10119</i>	ABC transporter, permease protein	-	-2.2
<i>lpg0514a</i> ²	-	<i>lpp0577</i>	<i>lp10553</i>	unknown	-	-2.1
<i>lpg1793</i>	-	<i>lpp1757</i>	<i>lp11757</i>	unknown	-	-2.1
<i>lpg0645</i>	-	-	-	truncated structural toxin protein RtxA	-	-2.1
<i>lpg2907</i>	-	<i>lpp2976</i>	<i>lp12824</i>	unknown	-	-2.1
<i>lpg0527</i>	-	<i>lpp0592</i>	<i>lp10573</i>	signal transduction protein	-	-2.1
<i>lpg2351</i>	-	<i>lpp2300</i>	<i>lp12273</i>	unknown	-	-2.1
<i>lpg1114a</i> ²	-	<i>lpp1115</i>	<i>lp11119</i>	KaiB-like circadian clock protein	-	-2.1
<i>lpg1796</i>	-	<i>lpp1760</i>	<i>lp11760</i>	LysR family transcriptional regulator	-	-2.0
<i>lpg2075</i>	-	-	-	DNA adenine methylase	-	-2.0

¹Fold Change (FC) at the corresponding OD₆₀₀. If no FC is indicated, the gene was either not differentially expressed or the statistical analyses failed due to FC variability.

²These genes were not predicted in the Philadelphia strain. Their ID therefore became the ID of the gene located upstream on the chromosome followed by “a”. For the exact location and orientation of these genes see Table S2.

Table S2. Implementation of the Philadelphia strain annotation

Gene ID	Description	Strand	Start coordinates	Stop coordinates	Length (aa)
<i>lpg0286a</i>	unknown - signal peptide predicted	+	341722	341952	77
<i>lpg0514a</i>	unknown	+	556062	556325	88
<i>lpg1174a</i>	unknown	+	1299590	1299835	82
<i>lpg2498a</i>	unknown	+	2816627	2816851	75
<i>lpg2582a</i>	unknown	+	2912984	2913163	60
<i>lpg1114a</i>	unknown	-	1221307	1221035	91
<i>lpg1968a</i>	unknown	-	2208173	2207934	80
<i>lpg2950a</i>	unknown	-	3339455	3339189	89