

S1 table. Description of potential SPase substrates as predicted by LipoP software.

Gene symbol	Gene description
<i>SSA_0012</i>	Beta-lactamase class A, putative
<i>SSA_0015</i>	Membrane ATPase FtsH, degrades sigma32 (integral membrane cell-division Zn metallo-peptidase), putative
<i>SSA_0017</i>	Cell shape determining protein MreC, putative
<i>SSA_0019</i>	Secreted antigen GbpB/SagA; peptidoglycan hydrolase; PcsB protein precursor, putative
<i>SSA_0021</i>	hypothetical protein SSA_0021
<i>SSA_0036</i>	Secreted protein, possible function in cell-wall metabolism (amidase), putative
<i>SSA_0094</i>	Cell wall metabolism, LysM type protein, putative
<i>SSA_0140</i>	Copper-translocating P-type ATPase, putative
<i>SSA_0146</i>	DNA repair ATPase, putative
<i>SSA_0157</i>	hypothetical protein SSA_0157
<i>SSA_0165</i>	hypothetical protein SSA_0165
<i>SSA_0167</i>	Hypothetical protein (Asparagine/proline-rich)
<i>SSA_0173</i>	23S rRNA m1G745 methyltransferase, putative
<i>SSA_0175</i>	Penicillin-binding protein 1B, putative
<i>SSA_0181</i>	Glycosyltransferase (vectorial glycosyl polymerization (VGP) family), putative
<i>SSA_0186</i>	Competence protein ComYC, putative
<i>SSA_0187</i>	Competence protein ComYD, putative
<i>SSA_0189</i>	Competence protein ComGF, putative
<i>SSA_0210</i>	hypothetical protein SSA_0210
<i>SSA_0215</i>	Periplasmic sugar-binding protein (ribose porter), putative
<i>SSA_0218</i>	Sugar-binding periplasmic protein, putative
<i>SSA_0227</i>	Collagen-binding surface protein, putative
<i>SSA_0243</i>	2',3'-cyclic nucleotide 2'-phosphodiesterase/3'-nucleotidase bifunctional periplasmic precursor protein
<i>SSA_0257</i>	N-acetylmuramidase/lysin, putative
<i>SSA_0273</i>	hypothetical protein SSA_0273
<i>SSA_0291</i>	short chain dehydrogenase

<i>SSA_0301</i>	hypothetical protein SSA_0301
<i>SSA_0303</i>	surface protein C
<i>SSA_0304</i>	Bacterial cell wall degradation (CHAP/LysM domains), putative
<i>SSA_0351</i>	Signal peptidase I, putative
<i>SSA_0396</i>	hypothetical protein SSA_0396
<i>SSA_0398</i>	hypothetical protein SSA_0398
<i>SSA_0400</i>	hypothetical protein SSA_0400
<i>SSA_0424</i>	Exopolysaccharide biosynthesis protein, putative
<i>SSA_0453</i>	Type II secretory pathway, pullulanase PulaA glycosidase, putative
<i>SSA_0477</i>	Cobalamin biosynthesis protein CbiM (ABC-type cobalt transporter), putative
<i>SSA_0478</i>	Cobalt transport protein cbiN, putative
<i>SSA_0498</i>	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components, putative
<i>SSA_0500</i>	Peptide ABC transporter, permease protein, putative
<i>SSA_0521</i>	Ethanolamine utilization protein EutL, putative
<i>SSA_0565</i>	hypothetical protein SSA_0565
<i>SSA_0607</i>	ABC transporter, permease component, putative
<i>SSA_0610</i>	LemA-like protein, putative
<i>SSA_0613</i>	Glucosyltransferase, putative
<i>SSA_0684</i>	Fibril-like structure subunit FibA, putative
<i>SSA_0689</i>	Penicillin-binding protein 2B, putative
<i>SSA_0723</i>	hypothetical protein SSA_0723
<i>SSA_0726</i>	FmtA-like protein, putative
<i>SSA_0747</i>	DD-carboxypeptidase, putative
<i>SSA_0793</i>	DNA-entry nuclease, putative
<i>SSA_0801</i>	Mur ligase family protein, putative
<i>SSA_0803</i>	hypothetical protein SSA_0803
<i>SSA_0805</i>	Collagen-binding surface protein, putative
<i>SSA_0871</i>	Cell division protein FtsX, putative
<i>SSA_0881</i>	Lipoprotein, putative
<i>SSA_0897</i>	Two component system histidine kinase, putative
<i>SSA_0904</i>	CshA-like fibrillar surface protein A

<i>SSA_0905</i>	CshA-like fibrillar surface protein B
<i>SSA_0906</i>	CshA-like fibrillar surface protein C
<i>SSA_0908</i>	ABC-type uncharacterized transport system, periplasmic component, putative
<i>SSA_0947</i>	hypothetical protein <i>SSA_0947</i>
<i>SSA_0956</i>	surface protein D
<i>SSA_0963</i>	Peptidoglycan N-acetylglucosamine deacetylase A, putative
<i>SSA_0967</i>	hypothetical protein <i>SSA_0967</i>
<i>SSA_0970</i>	hypothetical protein <i>SSA_0970</i>
<i>SSA_0991</i>	Deoxyribonuclease, putative
<i>SSA_1018</i>	Zinc metalloprotease <i>zmpC</i> precursor, putative
<i>SSA_1019</i>	Collagen-binding surface protein, putative
<i>SSA_1023</i>	Von Willebrand factor-binding protein precursor, putative
<i>SSA_1042</i>	Xylanase/chitin deacetylase, putative
<i>SSA_1051</i>	Spermidine/putrescine ABC transporter, spermidine/putrescine-binding protein, putative
<i>SSA_1052</i>	hypothetical protein <i>SSA_1052</i>
<i>SSA_1063</i>	Peptidoglycan-binding domain-containing protein, putative
<i>SSA_1064</i>	hypothetical protein <i>SSA_1064</i>
<i>SSA_1065</i>	Beta-hexosamidase A, putative
<i>SSA_1095</i>	Peptidoglycan hydrolase, putative
<i>SSA_1106</i>	IgA-specific metalloendopeptidase
<i>SSA_1112</i>	Cell wall surface anchor family protein, putative
<i>SSA_1118</i>	Peptide methionine sulfoxide reductase, putative
<i>SSA_1130</i>	Iron-dependent peroxidase, putative
<i>SSA_1132</i>	TatC, sec-independent protein translocase, putative
<i>SSA_1148</i>	Beta-glucosides PTS, EIIC, putative
<i>SSA_1158</i>	hypothetical protein <i>SSA_1158</i>
<i>SSA_1161</i>	hypothetical protein <i>SSA_1161</i>
<i>SSA_1219</i>	Sortase, putative
<i>SSA_1221</i>	L-lactate dehydrogenase
<i>SSA_1234</i>	5'-nucleotidase, putative
<i>SSA_1274</i>	hypothetical protein <i>SSA_1274</i>
<i>SSA_1301</i>	Conserved uncharacterized protein, possible surface protein
<i>SSA_1339</i>	Pneumococcal histidine triad protein D

	precursor, putative
<i>SSA_1359</i>	Arginine/histidine ABC transporter, permease component, putative
<i>SSA_1363</i>	FmtA-like protein, putative
<i>SSA_1365</i>	FmtA-like protein, putative
<i>SSA_1368</i>	hypothetical protein SSA_1368
<i>SSA_1369</i>	FmtA-like protein, putative
<i>SSA_1371</i>	FmtA-like protein, putative
<i>SSA_1372</i>	hypothetical protein SSA_1372
<i>SSA_1390</i>	hypothetical protein SSA_1390
<i>SSA_1391</i>	hypothetical protein SSA_1391
<i>SSA_1408</i>	hypothetical protein SSA_1408
<i>SSA_1415</i>	Oxidoreductase, putative
<i>SSA_1434</i>	Conserved uncharacterized Firmicutes protein
<i>SSA_1481</i>	FmtA-like protein, putative
<i>SSA_1489</i>	hypothetical protein SSA_1489
<i>SSA_1525</i>	Lysozyme M1 (1,4-beta-N- acetylmuramidase), putative
<i>SSA_1532</i>	Membrane-fusion protein / periplasmic component of efflux system, putative
<i>SSA_1544</i>	Conserved uncharacterized protein
<i>SSA_1567</i>	Polar amino acid ABC transporter, amino acid-binding protein, putative
<i>SSA_1588</i>	Conserved ABC-type antimicrobial permease-like protein, putative
<i>SSA_1591</i>	Dipeptidase, putative
<i>SSA_1593</i>	Dipeptidase, putative
<i>SSA_1594</i>	Metalloendopeptidase, putative
<i>SSA_1596</i>	hypothetical protein SSA_1596
<i>SSA_1597</i>	hypothetical protein SSA_1597
<i>SSA_1598</i>	hypothetical protein SSA_1598
<i>SSA_1599</i>	hypothetical protein SSA_1599
<i>SSA_1626</i>	DNA translocase ftsK, putative
<i>SSA_1631</i>	Sortase-like protein, putative
<i>SSA_1632</i>	Surface protein, putative
<i>SSA_1633</i>	FimA fimbrial subunit-like protein, putative
<i>SSA_1634</i>	Heme utilization/adhesion exoprotein, putative
<i>SSA_1635</i>	hypothetical protein SSA_1635
<i>SSA_1649</i>	hypothetical protein SSA_1649
<i>SSA_1650</i>	3-ketoacyl-(acyl-carrier-protein) reductase
<i>SSA_1653</i>	hypothetical protein SSA_1653
<i>SSA_1663</i>	Collagen-binding protein A

<i>SSA_1671</i>	hypothetical protein SSA_1671
<i>SSA_1673</i>	hypothetical protein SSA_1673
<i>SSA_1680</i>	ABC-type bacitracin resistance protein A, permease component, putative
<i>SSA_1692</i>	Phospho-B-galactosidase LacG, putative
<i>SSA_1744</i>	Iron compound ABC transporter, permease protein, putative
<i>SSA_1750</i>	Extracellular nuclease, putative
<i>SSA_1793</i>	Histidine kinase (sensor protein), putative
<i>SSA_1871</i>	Penicillin-binding protein 2X, putative
<i>SSA_1882</i>	Subtilisin-like serine proteases, putative
<i>SSA_1909</i>	Transcriptional attenuator LytR, putative
<i>SSA_1951</i>	Penicillin-binding protein 3, putative
<i>SSA_1960</i>	hypothetical protein SSA_1960
<i>SSA_1961</i>	Amino acid ABC transporter, amino acid- binding protein/permease protein, putative
<i>SSA_1984</i>	Cell surface SD repeat antigen precursor, putative
<i>SSA_1985</i>	hypothetical protein SSA_1985
<i>SSA_1991</i>	Pneumococcal histidine triad protein A, putative
<i>SSA_2004</i>	Zinc metalloprotease zmpB precursor, putative
<i>SSA_2014</i>	D-alanyl-D-alanine carboxypeptidase, putative
<i>SSA_2020</i>	hypothetical protein SSA_2020
<i>SSA_2023</i>	Fructan beta-fructosidase precursor, putative
<i>SSA_2056</i>	Cinnamoyl ester hydrolase, putative
<i>SSA_2060</i>	Arabinose efflux permease, putative
<i>SSA_2074</i>	preprotein translocase subunit YajC
<i>SSA_2101</i>	Amino acid ABC transporter, periplasmic amino acid-binding protein, putative
<i>SSA_2103</i>	hypothetical protein SSA_2103
<i>SSA_2121</i>	Cell wall surface anchor family protein, putative
<i>SSA_2169</i>	Glucose-1-phosphate uridylyltransferase, putative
<i>SSA_2248</i>	hypothetical protein SSA_2248
<i>SSA_2250</i>	ABC-type antimicrobial peptide transporter, permease component, putative
<i>SSA_2264</i>	hypothetical protein SSA_2264
<i>SSA_2269</i>	hypothetical protein SSA_2269
<i>SSA_2281</i>	hypothetical protein SSA_2281
<i>SSA_2282</i>	Phage infection protein, putative

<i>SSA_2301</i>	S-layer protein/ peptidoglycan endo-beta-N-acetylglucosaminidase, putative
<i>SSA_2307</i>	hypothetical protein SSA_2307
<i>SSA_2313</i>	hypothetical protein SSA_2313
<i>SSA_2320</i>	hypothetical protein SSA_2320
<i>SSA_2321</i>	Cation (Co/Zn/Cd) efflux protein, putative
<i>SSA_2338</i>	Conserved uncharacterized protein
<i>SSA_2340</i>	hypothetical protein SSA_2340
<i>SSA_2364</i>	Immunodominant staphylococcal antigen A precursor, putative
<i>SSA_2381</i>	DegP protein, putative

S2 table. Microtitter plate readings for wild type and mutant strains before (upper table) and after (lower table) crystal violet staining.

	WT	Δ0849	Δ0351	Δ0291	Δ0371	Δ1948	Δ1950	Δ2141	Δ2142
read # 1	0.846	0.82	0.886	0.915	0.733	0.885	0.915	0.81	0.831
read # 2	0.909	0.889	0.888	0.867	0.761	0.927	0.962	0.799	0.849
read # 3	0.905	0.88	0.937	0.963	0.83	0.88	1.061	0.745	0.904
read # 4	0.965	0.909	0.785	0.96	0.772	0.872	1	0.843	0.906
read # 5	0.911	0.902	0.956	0.904	0.839	0.87	1.071	0.741	0.86
read # 6	0.896	0.852	0.955	0.988	0.919	0.966	1.079	0.973	0.96
read # 7	0.879	0.897	0.963	0.904	0.872	0.929	1.093	0.819	0.902
read # 8	0.84	0.852	0.919	0.859	0.763	0.871	0.991	0.827	0.923
average	0.893875	0.875125	0.911125	0.92	0.811125	0.9	1.0215	0.819625	0.891875
P-value		0.31073	0.504805	0.247684	0.00793	0.751848	0.00029	0.023165	0.924001

	WT	Δ0849	Δ0351	Δ0291	Δ0371	Δ1948	Δ1950	Δ2141	Δ2142
read # 1	1.028	2.168	0.132	0.107	0.105	0.126	0.11	0.109	0.166
read # 2	1.46	1.99	0.091	0.101	0.103	0.105	0.095	0.101	0.095
read # 3	1.55	1.982	0.097	0.107	0.118	0.107	0.102	0.107	0.108
read # 4	1.303	2.169	0.104	0.103	0.118	0.107	0.113	0.083	0.113
read # 5	1.776	2.108	0.106	0.098	0.105	0.115	0.089	0.098	0.111
read # 6	1.755	1.821	0.105	0.093	0.104	0.103	0.102	0.096	0.111
read # 7	1.463	1.85	0.098	0.095	0.103	0.113	0.09	0.109	0.102
read # 8	1.327	1.622	0.106	0.108	0.141	0.124	0.136	0.119	0.123
average	1.45775	1.96375	0.104875	0.1015	0.112125	0.1125	0.104625	0.10275	0.116125
P-value		0.000418	3.21E-10	3.07E-10	3.46E-10	3.43E-10	3.23E-10	3.13E-10	3.72E-10