

TABLE S1. Coding DNA bound by Rgg in the post-exponential phase of growth

Category & Spy49 no. ^{a,b}	Gene ^e	Description	ChIP-chip fold enrichment ^c	Transcript fold change (<i>rgg</i> /wt) ^{d,f}
Virulence associated				
830	<i>sclB</i>	collagen like surface protein	2.66	3
1084	<i>inlA</i>	internalin	2.30	-
146	<i>slo</i>	streptolysin O	2.21	28
Transcriptional regulator				
1153	(-)	repressor protein	2.90	-
122c	(-)	LysR family regulatory protein	2.24	-
Transport				
1402	<i>fhuB2</i>	ferrichrome transport system permease protein	4.11	-
1397	(-)	permease component BL0695 of the <i>cbiOQ</i> -type ABC transporter	3.0	-
974	(-)	lipoprotein	2.66	-
1021	(-)	ABC transporter	2.54	-
1249	<i>comFA</i>	comF operon protein 1	2.35	-
1729	(-)	putative cationic amino acid transporter protein	2.21	58
1162	(-)	amino acid ABC transporter	2.08	-5
1611	(-)	PTS system, IIB component	2.07	3
Synthesis				
1064	<i>rsuA</i>	16S pseudouridylate synthase	2.54	-
1638	<i>prmA</i>	ribosomal protein L11 methyltransferase	2.52	-
1615	<i>def</i>	peptide deformylase	2.28	-
905	<i>gyrA</i>	DNA gyrase subunit A	2.05	-
Metabolism				
234	<i>plr</i>	NAD-dependent glyceraldehyde-3-phosphate dehydrogenase	2.13	-
399	<i>phoH</i>	phosphate starvation-induced protein	2.15	-
Repair				

1439	<i>recD</i>	exodeoxyribonuclease V alpha chain	3.99	-
Hypothetical				
1006	(-)	hypothetical protein	3.54	-
426	(-)	hypothetical protein	3.36	-
1200	(-)	hypothetical protein	3.27	-
1048	(-)	hypothetical protein	3.20	-
410	(-)	hypothetical protein	3.12	-
502	(-)	hypothetical protein	2.28	-
202	(-)	hypothetical protein	2.28	-3
117	(-)	hypothetical protein	2.05	-
371	(-)	hypothetical protein	2.03	-
400	(-)	hypothetical protein	2.02	-

^a Genes are categorized based on KEGG genome annotations.

^b Spy49 numbers are the open reading frames based on the *S. pyogenes* strain NZ131 genome annotation [23].

^c ChIP-chip fold enrichment was calculated as a ratio of signal intensity between the *rggmyc+* and *rgg-*.

^d Fold change in the transcript level is from [16].

^e Hyphen indicates unnamed gene.

^f Hyphen indicates no changes in the transcript level was observed.