

Table S1. Coding regions bound by Rgg in the exponential phase of growth.

Category & Spy49 no. ^a	Gene ^b	Description	ChIP-chip fold enrichment ^c	Transcript fold change (<i>rgg</i> /wt) ^d
Synthesis				
1132	<i>deaD1</i>	ATP-dependent RNA helicase	2.65	-2
14	(-)	amino acid permease	2.55	-2
1788	<i>dnaC</i>	replicative DNA helicase	2.51	-
60	<i>rpsN.1</i>	small subunit ribosomal protein S14 (S29e)	2.48	-2
536	<i>prfB</i>	peptide chain release factor 2	2.33	-
940	<i>citC</i>	citrate (pro-3S)-lyase ligase	2.31	2
27	<i>purD</i>	phosphoribosylamine--glycine ligase	2.22	-2
Metabolism				
390	<i>pyrH</i>	uridylate kinase	2.92	-
1724	<i>hutU</i>	urocanate hydratase	2.90	4
158	<i>araD</i>	L-ribulose-5-phosphate 4-epimerase	2.67	-5
1413	<i>scrK</i>	Fructokinase	2.64	-2
108	(-)	deoxyadenosine kinase/deoxyguanosine kinase	2.49	2
1369	<i>fabH</i>	3-oxoacyl-(acyl carrier protein) synthase III	2.45	-
1621	<i>cdsA</i>	phosphatidate cytidyltransferase	2.46	2
788	(-)	glycine reductase	2.24	-
821	(-)	4-nitrophenyl phosphatase	2.16	-
1282	<i>nadE</i>	nicotinate phosphoribosyltransferase	2.14	2
637	<i>gor</i>	glutathione reductase	2.13	-2
965	(-)	trimethylamine dehydrogenase	2.01	3
Transport				
1205	(-)	thiol:disulfide interchange protein	3.45	-
579	(-)	membrane protein	2.21	-
590	(-)	membrane protein	2.05	-
969	(-)	integral membrane protein	2.04	2
1098	(-)	receptor protein kinase	2.04	-

Repair 1160c	<i>phr</i>	deoxyribodipyrimidine photolyase	5.9	3
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^a Genes are categorized based on KEGG genome annotations. Spy49 numbers are the open reading frames based on the *S. pyogenes* strain NZ131 genome annotation [23].

^b A dash within parentheses indicates that the gene is not named.

^c ChIP-chip fold enrichment was calculated as a ratio of signal intensity between the SA5 and *rgg* mutant strains.

^d Fold change in the transcript level is from the current study and [16]. A dash indicates no change in the transcript level was observed.