Table S2. Genes downregulated in ΩCvfA compared to the wild type control

Locus[1]	Gene[2]	Gene product[2]	COG[3]	Fold change[4]
SPy0003	*dnaN*	beta subunit of DNA polymerase III	L	-2.08
SPy0013	-	putative cell-cycle protein	D	-2.38
SPy0074	*adk*	adenylate kinase	F	-2.73
SPy0075	*infA*	putative translation initiation factor IF-1	J	-3.59
SPy0076	*rpmJ*	50S ribosomal protein B	J	-3.34
SPy0077	*rpsM*	30S ribosomal protein S13	J	-2.96
SPy0078	*rpsK*	30S ribosomal protein S11	J	-2.07
SPy0080	*rpoA*	DNA-directed RNA polymerase alpha subunit	K	-2.71
SPy0116	-	hypothetical protein	-	-4.86
SPy0185	*polA*	DNA-directed DNA polymerase I	L	-3.73
SPy0186	-	conserved hypothetical protein	R	-2.08
SPy0187	*spf*	Ferric transport regulator protein	P	-2.24
SPy0198	-	putative transposase, IS861	L	-9.84
SPy0227	-	hypothetical protein	-	-5.26
SPy0233	-	conserved hypothetical protein	S	-2.42
SPy0242	-	putative histidine kinase, possibly involved in competence	T	-2.17
SPy0246	*rnpA*	putative ribonuclease P protein component	J	-3.02
SPy0250	*rpmH*	50S ribosomal protein L34	J	-2.10
SPy0258	-	putative glucose kinase	K	-2.23
SPy0285	-	putative ABC transporter (ATP-binding protein)	O	-2.00
SPy0330	*lemA*	putative cytoplasmic membrane protein	S	-3.31
SPy0340	*dnaI*	putative primosome component (helicase loader)	L	-3.42
SPy0342	*snf*	putative SNF helicase	K	-3.79
SPy0343	-	hypothetical protein	-	-3.10
SPy0364	-	conserved hypothetical protein	R	-2.10
SPy0370	-	conserved hypothetical protein	S	-2.03
SPy0476	*era*	GTP-binding protein (GTPase)	R	-3.84
SPy0477	-	conserved hypothetical protein	L	-2.25
SPy0501	-	putative multi-drug resistance efflux pump	G	-2.08
SPy0502	-	hypothetical protein	U	-4.79
SPy0521	-	conserved hypothetical protein	R	-2.42
SPy0559	-	hypothetical protein	J	-3.61
SPy0560	-	conserved hypothetical protein	I	-3.45
SPy0581	-	conserved hypothetical protein	S	-3.69
SPy0596	-	conserved hypothetical protein	R	-4.51
SPy0599	-	putative transcription regulator	S	-2.76
SPy0622	-	hypothetical protein	-	-2.42
SPy0653	-	conserved hypothetical protein	S	-2.34
SPy0721	-	putative flavodoxin	C	-3.21
SPy0738	*sagA*	streptolysin S associated protein	-	-4.36
SPy0739	*sagB*	streptolysin S associated ORF	C	-2.92
SPy0740	*sagC*	streptolysin S associated ORF	-	-2.72
SPy0741	*sagD*	hypothetical protein	-	-2.83
SPy0742	*sagE*	hypothetical protein	R	-3.06
SPy0743	*sagF*	hypothetical protein	-	-3.30
SPy0744	*sagG*	putative ABC transporter (ATP-binding protein)	V	-4.50
SPy0745	*sagH*	ABC transporter (ATP-binding protein) - streptolysin S associated ORF	V	-2.75
SPy0757	*atpH*	putative proton-translocating ATPase, delta subunit	C	-2.18
SPy0761	*atpC*	putative proton-translocating ATPase, epsiron subunit	C	-2.11
SPy0778	-	putative ABC transporter (substrate-binding protein)	E	-2.17
SPy0779	*rpsU*	30S ribosomal protein S21	J	-2.92
SPy0780	*mscL*	putative large conductance mechanosensitive channel	M	-2.38
SPy0792	*rgpFc*	possibly involved in cell wall localization and side chain formation of rhamnose-glucose polysaccharide	M	-2.21
SPy0793	-	conserved hypothetical protein	M	-3.10
SPy0797	-	conserved hypothetical protein	R	-3.05
SPy0806	*rplT*	50S ribosomal protein L20	J	-2.22
SPy0830	*pyrR*	putative pyrimidine regulatory protein	F	-2.21

SPy0831	*pyrP*	putative uracil permease	F	-3.65
SPy0832	*pyrB*	putative aspartate transcarbamoylase	F	-3.62
SPy0833	*carA*	putative carbamoyl phosphate synthetase small subunit	E	-3.43
SPy0835	*carB*	putative carbamoylphosphate synthetase	E	-4.12
SPy0840	*rpsP*	30S ribosomal protein S16	J	-3.88
SPy0841	-	conserved hypothetical protein	R	-3.77
SPy0845	*czcD*	putative cation-efflux system membrane protein	P	-8.00
SPy0846	-	conserved hypothetical protein	K	-3.28
SPy0870	*fms*	putative polypeptide deformylase	J	-3.66
SPy0885	*clpX*	putative ATP-dependent Clp protease subunit X	O	-2.25
SPy0887	-	hypothetical protein	-	-3.86
SPy0895	-	histidine protein kinase	-	-2.32
SPy0912	-	hypothetical protein	-	-10.68
SPy0914	-	hypothetical protein	-	-4.11
SPy0921	*miaA*	putative tRNA isopentenylpyrophosphate transferase	J	-2.71
SPy0928	-	conserved hypothetical protein	L	-2.25
SPy0929	*nth*	putative endonuclease III (DNA repair)	L	-2.19
SPy1010	*mutX*	putative 7,8-dihydro-8-oxoguanine-triphosphatase	L	-2.01
SPy1019	-	putative ABC transporter (ATP-binding protein)	R	-2.89
SPy1024	-	hypothetical protein	-	-2.38
SPy1026	*acoA*	putative acetoin dehydrogenase (TPP-dependent) alpha chain	C	-2.32
SPy1056	-	conserved hypothetical protein	S	-2.02
SPy1096	*folC.1*	putative folyl-polyglutamate synthetase	H	-2.31
SPy1115	-	hypothetical protein	E	-2.81
SPy1117	-	hypothetical protein	R	-2.28
SPy1119	-	conserved hypothetical protein	R	-3.88
SPy1140	*tdk2*	putative thymidine kinase	F	-2.36
SPy1141	*prfA*	putative peptide chain release factor 1	J	-2.11
SPy1142	*hemK*	putative protoporphyrinogen oxidase	J	-3.01
SPy1143	-	hypothetical protein	J	-4.13
SPy1144	-	hypothetical protein	K	-3.24
SPy1147	-	conserved hypothetical protein	M	-2.89
SPy1148	-	putative ABC transporter (ATP-binding protein)	V	-2.43
SPy1156	-	hypothetical protein	-	-2.33
SPy1161	-	conserved hypothetical protein	R	-2.98
SPy1162	*rnh*	putative ribonuclease HII	L	-2.27
SPy1164	*topA*	putative DNA topoisomerase I	L	-2.12
SPy1175	-	hypothetical protein	-	-4.13
SPy1179	-	putative transcriptional regulator	K	-2.48
SPy1196	-	putative integrase/recombinase	L	-5.09
SPy1198	-	putative repressor protein	K	-3.23
SPy1206	-	putative ABC transporter (ATP-binding protein)	R	-2.88
SPy1209	*pdxK*	putative pyridoxal kinase	H	-3.70
SPy1215	-	hypothetical protein	K	-2.44
SPy1218	-	conserved hypothetical protein	C	-2.69
SPy1219	-	putative trimethylamine dehydrogenase	C	-2.35
SPy1220	-	conserved hypothetical protein	H	-2.46
SPy1232	-	conserved hypothetical protein	J	-4.87
SPy1233	*coaA*	putative pantothenate kinase	H	-4.05
SPy1234	*rpsT*	30S ribosomal protein S20	J	-5.10
SPy1237	-	putative response regulator	T	-2.18
SPy1239	*pepN*	putative lysyl-aminopeptidase; aminopeptidase N	E	-2.99
SPy1240	*phoU*	putative phosphate uptake regulatory protein	P	-2.99
SPy1243	*pstC*	putative phosphate ABC transporter (permease protein)	P	-2.40
SPy1251	*truB*	putative tRNA pseudouridine 55 synthase	J	-2.78
SPy1253	-	conserved hypothetical protein	S	-4.61
SPy1254	-	hypothetical protein	V	-2.97
SPy1259	-	putative transcriptional regulator	K	-2.55
SPy1265	-	conserved hypothetical protein	S	-3.80
SPy1274	-	putative amino acid ABC transporter, periplasmic amino acid-binding protein	E	-3.39
SPy1277	-	conserved hypothetical protein	P	-5.54

SPy1288	-	hypothetical protein	S	-2.35
SPy1289	-	hypothetical protein	S	-2.50
SPy1291	*glgP*	putative glycogen phosphorylase	G	-2.97
SPy1292	*malM*	putative 4-alpha-glucanotransferase	G	-3.84
SPy1293	*malR*	putative maltose operon transcriptional repressor	K	-2.82
SPy1294	-	putative maltose/maltodextrin-binding protein	G	-5.38
SPy1312	*dltA*	putative D-alanine-D-alanyl carrier protein ligase	Q	-2.79
SPy1314	*uvrB*	putative excinuclease ABC (subunit B)	L	-2.47
SPy1332	-	hypothetical protein	-	-2.05
SPy1337	*rsuA*	putative 16S pseudouridylate synthase	J	-2.50
SPy1353	-	conserved hypothetical protein	S	-2.86
SPy1354	*map*	putative methionine aminopeptidase	J	-3.03
SPy1355	-	conserved hypothetical protein	K	-2.11
SPy1364	*dnaX*	DNA polymerase III subunits gamma / tau	L	-2.25
SPy1372	*pstI*	putative phosphoenolpyruvate:sugar phosphotransferase system enzyme I	G	-3.54
SPy1378	*nrdF.2*	ribonucleotide diphosphate reductase small subunit	F	-2.41
SPy1395	-	putative transcription factor	R	-2.39
SPy1398	-	putative 16S pseudouridylate synthetase	J	-3.86
SPy1399	*nagB*	putative N-acetylglucosamine-6-phosphate isomerase	G	-5.61
SPy1406	*sodA*	superoxide dismutase (Fe/Mn)	P	-5.75
SPy1407	*holA*	DNA polymerase III delta subunit	L	-2.02
SPy1508	-	hypothetical protein	S	-5.12
SPy1514	*divIVAS*	cell-division initiation protein (septum placement)	D	-2.57
SPy1515	-	conserved hypothetical protein	S	-2.71
SPy1519	-	conserved hypothetical protein	R	-2.62
SPy1520	*ftsZ*	putative cell division protein	D	-3.18
SPy1533	-	conserved hypothetical protein	R	-2.15
SPy1534	-	hypothetical protein	S	-2.83
SPy1548	-	hypothetical protein	T	-2.13
SPy1580	-	putative acetate kinase	S	-2.63
SPy1584	*aroE*	putative shikimate 5-dehydrogenase	E	-2.79
SPy1587	-	putative two-component sensor response regulator	T	-8.06
SPy1588	-	putative two-component sensor histidine kinase	T	-16.33
SPy1589	-	conserved hypothetical protein	-	-17.01
SPy1591	-	hypothetical protein	G	-7.75
SPy1592	-	conserved hypothetical protein	G	-8.05
SPy1593	-	putative sugar-binding transport protein	G	-5.11
SPy1595	-	putative sugar-binding transport protein	G	-8.66
SPy1596	-	putative transcriptional regulator	K	-2.97
SPy1602	-	putative transcription regulator	K	-2.83
SPy1604	-	conserved hypothetical protein	G	-2.20
SPy1619	-	putative polyribonucleotide nucleotidyltransferase (general stress protein)	J	-2.03
SPy1628	*fmt*	putative methionyl tRNA formyltransferase	J	-8.40
SPy1633	-	conserved hypothetical protein	R	-3.90
SPy1657	-	putative amino acid ABC transport system (ATP-binding protein)	E	-3.07
SPy1666	-	conserved hypothetical protein	M	-2.32
SPy1694	*nagA*	putative N-acetylglucosamine-6-phosphate deacetylase	G	-2.31
SPy1721	*infB*	putative initiation factor 2	J	-3.72
SPy1722	-	putative ribosomal protein	J	-3.21
SPy1723	-	conserved hypothetical protein	K	-3.03
SPy1724	*nusA*	transcription termination-antitermination factor	K	-4.36
SPy1725	-	conserved hypothetical protein	S	-7.92
SPy1726	-	conserved hypothetical protein	R	-2.34
SPy1727	-	conserved hypothetical protein	M	-2.10
SPy1729	-	putative ABC transporter (ATP-binding protein)	V	-2.34
SPy1746	*fabZ*	putative beta-hydroxyacyl-ACP dehydratase	I	-2.08
SPy1753	*acpP*	putative acyl carrier protein	I	-2.37
SPy1761	*grpE*	putative Hsp-70 cofactor	O	-5.21
SPy1763	*hrcA*	putative heat shock transcription repressor protein	K	-4.97
SPy1811	*scrK*	putative fructokinase	K	-4.03
SPy1813	-	hypothetical protein	-	-11.58

SPy1815	*scrA*	putative sucrose-specific PTS permease, enzyme II	G	-8.74
SPy1816	*scrB*	putative sucrose-6-phosphate hydrolase	G	-2.84
SPy1817	*scrR*	putative sucrose operon repressor	K	-3.67
SPy1840	-	hypothetical protein	-	-2.03
SPy1852	-	hypothetical protein	-	-3.07
SPy1869	*udp*	putative uridine phosphorylase	F	-2.25
SPy1874	-	putative glycoprotein endopeptidase	O	-2.75
SPy1886	*asp*	putative alkaline-shock protein	S	-2.12
SPy1888	*rpmB*	50S ribosomal protein L28	J	-5.17
SPy1895	*rpoE*	putative DNA-directed RNA polymerase (delta subunit)	K	-2.53
SPy1898	-	conserved hypothetical protein	S	-2.93
SPy1899	-	conserved hypothetical protein	S	-2.76
SPy1900	*thiD*	putative phosphomethylpyrimidine kinase	H	-2.80
SPy1901	*truA*	putative tRNA pseudouridine synthase A (pseudouridylate synthase I)	J	-2.27
SPy1911	*salY*	putative ABC transporter (permease) associated with salivaricin lantibiotic	V	-2.50
SPy1914	*salB*	putative salivaricin A modification enzyme; amino acid dehydration	V	-4.86
SPy1923	*lacA.2*	galactosidase acetyltransferase	G	-3.30
SPy1924	*lacR.2*	putative lactose phosphotransferase system repressor protein	K	-2.43
SPy1926	-	hypothetical protein	-	-2.01
SPy1940	-	conserved hypothetical proteins	S	-3.07
SPy1958	*def*	putative polypeptide deformylase	J	-2.15
SPy1959	-	conserved hypothetical protein	R	-2.28
SPy2013	-	transposase - IS1562	L	-2.03
SPy2023	-	hypothetical protein (Mga-associated)	-	-2.60
SPy2025	*isp*	immunogenic secreted protein precursor	R	-2.53
SPy2026	-	putative histidine kinase	T	-4.00
SPy2027	-	putative two-component response regulator	T	-4.89
SPy2029	-	putative ABC transporter (ATP-binding protein)	V	-4.90
SPy2031	-	putative ABC transporter (ATP-binding protein)	V	-10.41
SPy2032	-	putative ATP-binding cassette transporter-like protein	M	-12.00
SPy2033	-	hypothetical protein	-	-10.95
SPy2037	-	conserved hypothetical	O	-36.50
SPy2039	*speB*	pyrogenic exotoxin B	-	-130.54
SPy2040	-	hypothetical protein	-	-77.51
SPy2043	*mf*	mitogenic factor	-	-3.17
SPy2052	-	putative PTS system, enzyme III	G	-3.73
SPy2053	-	putative transcriptional regulator	K	-3.33
SPy2105	*nrdG*	putative anaerobic ribonucleotide reductase activator	O	-2.16
SPy2112	-	conserved hypothetical protein	S	-2.79
SPy2113	-	conserved hypothetical protein	L	-3.55
SPy2114	-	hypothetical protein	S	-3.28
SPy2115	-	conserved hypothetical proteins	P	-2.26
SPy2152	-	conserved hypothetical protein	-	-2.59
SPy2159	*rpmF*	50S ribosomal protein L32	J	-2.12
SPy2169	-	conserved hypothetical protein	S	-6.73
SPy2177	-	putative transcriptional regulator (TetR/AcrR family)	K	-3.08
SPy2181	-	hypothetical protein	S	-2.40
SPy2186	-	hypothetical protein	L	-2.31
SPy2204	*recF*	RecF protein	L	-4.17

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[1] SPy numbers are assigned based on genome of serotype M1 GAS strain SF370.

[2] Assignment based on annotation of serotype M1 GAS strain SF370 ORFs (http://www.ncbi.nlm.nih.gov/genomes/altik.cgi?gi=178&db=Genome).

[3] Cluster of Othologous Groups (http://www.ncbi.nlm.nih.gov/sutils/coxik.cgi?gi=178)

[4] Average of a data set consisting of 18 total microarray hybridizations with 2 independently prepared RNA samples. The values here fulfilled the following criteria: the estimated false discovery rate at the 90th percentile in SAM (Significance Analysis of Microarrays) analysis was ≤ 0.1%, and the fold-change value was at least ±2.0.