Table S1. Genes upregulated in ΩCvfA compared to the wild type control

Locus[1]	Gene[2]	Gene product[2]	COG[3]	Fold change[4]
SPy0019	-	putative secreted protein	R	2.32
SPy0020	*prsA.2*	putative ribose-phosphate pyrophosphokinase	F	3.30
SPy0022	*plsX*	putative fatty acid/phospholipid synthesis protein	I	2.46
SPy0028	*purN*	Phosphoribosylglycinamide formyltransferase	F	3.56
SPy0049	*rplC*	50S ribosomal protein L3	J	2.18
SPy0050	*rplD*	50S ribosomal protein L4	J	2.49
SPy0052	*rplB*	50S ribosomal protein L2	J	2.02
SPy0057	*rplP*	50S ribosomal protein L16	J	2.11
SPy0060	*rpsQ*	30S ribosomal protein S17	J	2.10
SPy0061	-	50S ribosomal protein L14	J	2.69
SPy0062	*rplX*	50S ribosomal protein L24	J	2.34
SPy0065	*rpsH*	30S ribosomal protein S8	J	2.55
SPy0066	*rplF*	50S ribosomal protein L6	J	3.94
SPy0067	*rplR*	50S ribosomal protein L18	J	3.89
SPy0069	*rpsE*	30S ribosomal protein S5	J	2.85
SPy0094	*adcB*	putative ABC transporter (permease)	P	3.70
SPy0097	*pbp1b*	putative penicillin-binding protein 1b	M	2.72
SPy0098	*rpoB*	putative DNA-dependent RNA polymerase subunit beta	K	3.22
SPy0099	*rpoC*	DNA-dependent RNA polymerase, B' subunit	K	3.15
SPy0112	*proC*	putative pyrroline carboxylate reductase	E	2.43
SPy0144	-	conserved hypothetical protein	S	2.82
SPy0146	-	putative regulatory protein	G	2.28
SPy0149	*ntpK*	putative V-type Na+ -ATPase subunit K	C	2.50
SPy0150	*ntpE*	putative V-type Na+ -ATPase subunit E	-	2.38
SPy0151	*ntpC*	putative V-type Na+ -ATPase subunit C	C	2.69
SPy0154	*ntpA*	putative V-type Na+ -ATPase alpha subunit	C	2.58
SPy0155	*ntpB*	putative V-type Na+ -ATPase subunit B	C	3.20
SPy0157	*ntpD*	putative V-type Na+ -ATPase subunit D	C	3.78
SPy0158	-	putative toxic anion resistance protein	P	3.64
SPy0165	*nga/spn*	nicotine adenine dinucleotide glycohydrolase precursor	-	2.43
SPy0166	-	hypothetical protein	-	2.02
SPy0167	*slo*	streptolysin O precursor	-	3.82
SPy0174	-	conserved hypothetical protein	S	3.58
SPy0175	-	conserved hypothetical protein	G	2.27
SPy0176	-	conserved hypothetical protein	G	2.70
SPy0177	-	putative hexulose-6-phosphate synthase	G	6.06
SPy0178	-	putative hexulose-6-phosphate isomerase	G	3.95
SPy0179	*araD*	putative L-ribulose 5-phosphate 4-epimerase	G	2.73
SPy0182	-	conserved hypothetical protein	R	3.60
SPy0195	-	conserved hypothetical protein	L	2.54
SPy0212	*speG*	exotoxin G precursor	-	6.24
SPy0215	*pgi*	glucose-6-phosphate isomerase	G	6.88
SPy0224	*hasC.2*	putative UDP-glucose pyrophosphorylase	M	2.12
SPy0226	*gpsA*	putative NAD(P)H-dependent glycerol-3-phosphate dehydrogenase	C	3.38
SPy0247	-	conserved hypothetical protein	U	2.05
SPy0269	*prgA*	putative surface exclusion protein	-	2.30
SPy0272	*rpsG*	30S ribosomal protein S7	J	2.20
SPy0273	*fus*	translation elongation factor G, EF-G	J	2.62
SPy0280	*bacA*	putative undecaprenol kinase (bacitracin resistance protein)	V	4.22
SPy0319	-	conserved hypothetical protein	P	2.14
SPy0320	-	putative ABC transporter (ATP-binding protein)h	P	2.47
SPy0321	-	putative ABC transporter (permease protein)	P	3.45

SPy0324	-	putative sodium/dicarboxylate symporter	E	2.13
SPy0326	-	conserved hypothetical protein	P	2.53
SPy0373	-	conserved hypothetical protein	S	2.62
SPy0378	*hlyX*	putative hemolysin	R	3.76
SPy0407	-	hypothetical protein	-	7.36
SPy0408	-	hypothetical protein (similar to Human CGI-32 protein	P	2.06
SPy0412	*exoA*	putative 3'-exo-deoxyribonuclease	L	2.24
SPy0414	*lctO*	putative lactate oxidase	C	2.56
SPy0416	*prtS*	putative cell envelope proteinase	O	2.21
SPy0427	*nrdE.1*	ribonucleoside-diphosphate reductase, large chain	F	2.23
SPy0444	-	conserved hypothetical protein	L	2.17
SPy0457	-	putative cyclophilin-type protein	O	3.00
SPy0458	-	conserved hypothetical protein	D	2.47
SPy0460	*rplK*	50S ribosomal protein L11	J	2.29
SPy0492	-	hypothetical protein	-	2.12
SPy0511	*gloA*	putative lactoylglutathione lyase	E	5.08
SPy0512	-	putative NAD(P)H-flavin oxidoreductase	C	3.53
SPy0513	*pepQ*	putative XAA-PRO dipeptidase; X-PRO dipeptidase	E	3.49
SPy0517	*thrS*	putative threonyl-tRNA synthetase 1	J	9.16
SPy0530	*vicX*	conserved hypothetical protein	R	4.34
SPy0568	-	conserved hypothetical protein	R	2.18
SPy0569	*ftsY*	putative signal recognition particle (docking protein)	U	4.90
SPy0591	-	putative protease	O	2.63
SPy0595	*lysS*	putative lysyl-tRNA synthetase	J	2.24
SPy0603	-	hypothetical protein	-	2.06
SPy0605	*bsaA*	putative glutathione peroxidase	O	2.89
SPy0606	*pepF*	putative oligopeptidase	E	3.96
SPy0611	*tufA*	putative translation elongation factor EF-Tu	J	3.88
SPy0621	-	conserved hypothetical protein	R	3.32
SPy0627	*regR*	putative transcriptional regulator (LacI family)	K	3.79
SPy0630	*agaW*	putative PTS dependent N-acetyl-galactosamine-IIC component	G	2.21
SPy0714	*adcA*	putative adhesion protein	R	2.87
SPy0731	*eno*	putative enolase	G	2.68
SPy0752	-	conserved hypothetical protein	I	2.38
SPy0770	-	hypothetical protein	-	2.08
SPy0803	*cmk*	putative cytidylate kinase	F	2.71
SPy0813	*gor*	putative glutathione reductase (GR)	C	2.11
SPy0822	*rpmA*	50S ribosomal protein L27	J	2.31
SPy0857	*mur1.2*	putative peptidoglycan hydrolase	N	2.00
SPy0913	-	putative ribosomal protein S1-like DNA-binding protein	J	2.03
SPy0919	-	hypothetical protein	-	3.94
SPy0936	*cpsFQ*	putative dTDP-glucose-4,6-dehydratase	M	3.14
SPy1011	-	conserved hypothetical protein	R	3.10
SPy1012	-	conserved hypothetical protein	R	7.08
SPy1020	-	conserved hypothetical protein	R	2.24
SPy1029	*acoC*	putative dihydrolipoamide S-acetyltransferase	C	2.37
SPy1031	*acoL*	putative dihydrolipoamide dehydrogenase, component E3	C	4.33
SPy1036	-	conserved hypothetical protein	S	4.95
SPy1037	-	conserved hypothetical protein	S	7.45
SPy1038	-	putative phospho-sugar mutase	G	5.53
SPy1054	-	putative collagen-like protein	-	3.65
SPy1057	-	hypothetical protein	G	2.02
SPy1058	-	putative phosphotransferase system (PTS), enzyme II component B	G	2.06
SPy1059	-	putative phospotransferase system (PTS), enzyme II, component C	G	6.22
SPy1060	-	putative phospotransferase system (PTS), enzyme II component D	G	6.36
SPy1070	-	putative dipeptidase	E	4.52

SPy1072	*rplJ*	50S ribosomal protein L10	J	2.52
SPy1073	*rplL*	50S ribosomal protein L7/L12	J	4.24
SPy1093	-	putative D,D-carboxypeptidase, penicillin-binding protein	M	2.56
SPy1106	-	putative two-component response regulator	K	2.18
SPy1109	*malP*	putative L-malate permease	C	3.41
SPy1128	*pta*	putative phosphotransacetylase	C	2.00
SPy1151	*ldh*	putative L-lactate dehydrogenase	C	2.21
SPy1190	*citX*	conserved hypothetical protein	H	4.44
SPy1191	*oadA*	putative oxaloacetate decarboxylase alpha chain	C	3.74
SPy1228	-	putative lipoprotein	R	2.31
SPy1230	*cdd*	putative cytidine deaminase	F	3.30
SPy1247	-	putative myo-inositol-1(or 4)-monophosphatase	G	2.09
SPy1250	*mreA*	putative macrolide-efflux protein	H	2.63
SPy1273	*cfa*	CAMP factor	-	5.29
SPy1282	*pyk*	putative pyruvate kinase	G	2.45
SPy1283	*pfk*	putative 6-phosphofructokinase	G	2.28
SPy1316	-	putative ABC transporter (ATP-binding protein)	E	4.32
SPy1344	-	conserved hypothetical protein	Q	3.59
SPy1346	-	putative RNA methyltransferase	J	2.05
SPy1359	*metK*	S-adenosylmethionine synthetase	H	2.61
SPy1370	-	putative deacetylase	G	3.77
SPy1402	-	hypothetical protein	-	2.56
SPy1410	-	putative 1-acylglycerol-3-phosphate O-acyltransferase	I	2.01
SPy1425	-	hypothetical protein	-	3.75
SPy1427	-	putative transcriptional regulator	R	5.22
SPy1429	*gpmA*	putative phosphoglycerate mutase	G	2.90
SPy1489	*hlpA*	histone-like DNA-binding protein	L	4.29
SPy1494	-	hypothetical protein	-	3.27
SPy1510	*mutT*	putative mutator protein	L	2.80
SPy1513	*ileS*	putative isoleucyl-tRNA synthetase	J	4.51
SPy1527	-	putative GTP-binding protein TypA/BipA (tyrosine phosphorylated protein A)	T	2.19
SPy1528	-	conserved hypothetical protein	P	2.74
SPy1529	*glcK*	glucose kinase	K	2.56
SPy1541	*arcC*	putative carbamate kinase	E	5.54
SPy1542	-	putative Xaa-His dipeptidase	E	4.93
SPy1543	-	conserved hypothetical protein	S	2.98
SPy1544	*arcB*	putative ornithine transcarbamylase	E	5.69
SPy1546	-	hypothetical protein	K	4.84
SPy1547	*sagP*	streptococcal antitumor protein (possible arginine deiminase)	E	2.14
SPy1568	*valS*	putative valine-tRNA ligase	J	3.30
SPy1569	-	hypothetical protein	-	2.43
SPy1605	-	putative two-component responsible histidine kinase	T	2.20
SPy1638	*atoD.1*	putative Acetyl-CoA:acetoacetyl-CoA transferase A subunit	I	2.13
SPy1639	*atoA*	putative Acetyl-CoA:acetoacetyl-CoA transferase b subunit	I	3.18
SPy1640	-	putative oxidoreductase	Q	3.04
SPy1643	-	hypothetical protein	-	5.04
SPy1644	-	conserved hypothetical protein	L	5.69
SPy1646	-	conserved hypothetical protein	D	5.34
SPy1651	*pepC*	putative cysteine aminopeptidase C	E	2.27
SPy1652	*nadE*	putative NAD+ synthase	H	2.23
SPy1654	*aapA*	putative amino acid permease	E	2.25
SPy1676	*tkt*	putative transketolase	G	5.63
SPy1678	-	putative transaldolase	G	3.09
SPy1700	-	conserved hypothetical protein	R	2.54
SPy1737	-	conserved hypothetical protein	R	2.98
SPy1739	*manM*	putative mannose-specific phosphotransferase system component IIC	G	3.24

SPy1740	*manN*	putative mannose-specific phosphotransferase system component IID	G	4.95
SPy1742	*serS*	putative seryl-tRNA synthetase	J	2.40
SPy1743	*accA*	putative acetyl-CoA carboxylase alpha subunit	I	2.81
SPy1782	*asnB*	putative L-asparaginase	E	5.31
SPy1805	*secA*	putative preprotein translocase binding subunit (ATPase)	U	2.69
SPy1823	*comEB*	putative late competence protein required for DNA binding	F	3.29
SPy1824	*pepP*	putative aminopeptidase P; XAA-pro aminopeptidase	E	5.96
SPy1825	*uvrA*	putative excinuclease ABC (subunit A)	L	2.53
SPy1841	-	putative ribonuclease HIII	L	2.98
SPy1842	*spi*	putative signal peptidase I	U	2.31
SPy1844	-	putative exodeoxyribonuclease V (alpha subunit)	L	3.74
SPy1846	*dinP*	putative DNA-damage-inducible protein P	L	3.74
SPy1849	*pfl*	putative pyruvate formate-lyase	C	2.75
SPy1858	*pepXP*	putative X-Pro dipeptidyl-peptidase IV	-	2.39
SPy1861	-	putative repressor	K	2.01
SPy1862	-	conserved hypothetical protein	S	2.25
SPy1863	-	putative transcriptional activator regulator protein	K	3.21
SPy1864	*dnaQ*	putative DNA polymerase III epsilon subunit	L	2.21
SPy1866	-	conserved hypothetical protein	R	3.98
SPy1871	*rpsN2*	30S ribosomal protein S14	J	18.13
SPy1877	*glnA*	putative glutamine synthetase	E	2.59
SPy1896	*ropA*	transcription regulator - (trigger factor (prolyl isomerase))	O	2.48
SPy1906	*hsdM*	putative type I site-specific deoxyribonuclease	V	2.45
SPy1931	*rpsI*	ribosomal protein S9	J	2.25
SPy1932	*rplM*	50S ribosomal protein L13	J	3.58
SPy1934	-	putative transcription regulator	K	3.41
SPy1955	*rpsO*	30S ribosomal protein S15	J	2.90
SPy1962	*proS*	putative prolyl-tRNA synthetase	J	5.38
SPy1964	*cdsA*	putative phosphatidate cytidylyltransferase (CDP-diglyceride synthase)	I	2.66
SPy1972	*pulA*	putative pullulanase	G	2.34
SPy1979	*ska*	streptokinase A precursor	-	9.28
SPy1980	-	conserved hypothetical protein	J	2.66
SPy1981	*relA*	(p)ppGpp synthetase	T	3.16
SPy1992	-	conserved hypothetical protein	L	2.48
SPy2018	*emm1*	M protein type 1	-	3.74
SPy2034	-	conversed hypothetical protein	-	2.18
SPy2045	-	protein low temperature requirement C	I	2.41
SPy2047	*gldA*	putative glycerol dehydrogenase	C	2.80
SPy2059	*pbp2A*	penicillin-binding protein 2a	M	3.47
SPy2088	-	putative cationic amino acid transporter protein	E	2.96
SPy2091	-	putative regulatory protein	R	6.21
SPy2092	*rpsB*	30S ribosomal protein S2	J	12.19
SPy2093	*tsf*	putative elongation factor TS	J	16.54
SPy2095	*pepO*	putative endopeptidase O	O	3.77
SPy2097	-	putative PTS system enzyme II	G	2.58
SPy2111	-	hypothetical protein	-	2.91
SPy2119	*ruvA*	putative Holiday junction DNA helicase	L	2.12
SPy2151	*argS*	putative arginyl-tRNA synthetase	J	2.91
SPy2156	*aspS*	putative aspartyl-tRNA synthetase	J	2.96
SPy2188	-	putative tRNA-(5-methylaminomethyl-2-thiouridylate)	J	2.64
SPy2189	*sdhB*	putative L-serine dehydratase beta subunit	E	2.16
SPy2190	*sdhA*	putative L-serine dehydratase alpha subunit	E	8.41
SPy2191	-	hypothetical protein	-	2.11
SPy2206	*guaB*	inosine monophosphate dehydrogenase	R	3.20
SPy2216	*htrA*	putative serine protease	O	3.35

[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.