



1
2 **Figure S1. The M1-CovS- Y39H strain lasts more than the M1-CovS-WT mutant strain**
3 **in mouse throat.** Mice were infected with M1-CovS-WT and M1-CovS-Y39H strains.
4 intranasally (n = 6) with 5×10^8 and 1.2×10^9 cfus, respectively. Intranasal and throat swabs
5 were carried out daily until day 5. *S. pyogenes*, as attested by numbering cfus on plates, were
6 found in both intranasally and in the throat (not shown for the intranasal samplings). Then only
7 throat swabs were done, every other day until day 14 and then weekly. **A)** Swabs from days 1
8 to 14, **B)** swabs from days 1 to 41, indicating only the weekly values. Median values are
9 indicated by, a red dash for the M1-CovS-WT strain and a blue one for the M1-CovS-Y39H
10 strain.
11

12 **Table S1. Primer sequences**

Oligonucleotides	Sequence (5'→3')	Target gene
gyrA1	GCCATGAGTGTTCATTGTGGC	<i>gyrA</i>
gyrA2	GGCGATAACTCCACCACTGA	
speA1	CGCAAGAGGTATTTGCTCAA	<i>speA</i>
speA2	GCCATCTCTTGGTTCTTAAG	
speB1	CCGCTGGTAGAGTATCCTA	<i>speB</i>
speB2	GCTAACCCAGTATTTGCCG	
grab3	GGCCGTAATATTACTTTTCGGAG	<i>grab</i>
grab4	GCTACAGTTTATAATAGCTTGAAAGAC	
has1	GGAACATCAACTGTAGGAATTTAT	<i>hasA</i>
has2	GCATCTGTGTTTGA ACTCC	
skal	GCACTGCTGTTTGCATTAAC	<i>ska</i>
ska2	GCAAATGGTTTTGATTTTGGACT	
gasslo_F	ACCGTATCAGCAAACCTTCCT	<i>slo</i>
gasslo_R	ACTAAAGGCCGCTTCAACATC	
CovSF	<i>CGACTCTAGAGGATCCGGGTTAGAACTGCTTTGGA</i>	<i>covR</i>
CovSR	<i>CCATGATTACGAATTCCGGTGTTTCGTAATTCATGG</i>	<i>covS</i>
F_Cov	CGCTAGAAGACTATTTGACCA	<i>covR</i>
R_Cov	CCTTGTACGCGAATCATGT	<i>covS</i>

13 The letters in italic correspond to the nucleotide required for the “In fusion” cloning.

14

15 **Table S2. RNAseq analysis of *Streptococcus pyogenes* M1-CovS-WT and M1-Cov-Y39H**
 16 **transcript abundance in THY broth or THY supplemented by 15 mM Mg⁺⁺.**

17 a) Genes differentially expressed in M1-CovS-Y39H/ M1-CovS-WT comparisons (un-supplemented THY)
 18 with Foldchange (FC) >2 and adjusted p-values < 0.05

S119	SF370	locus	M1-CovS-Y39H/ M1-CovS-WT (Log2 FC)	M1-CovS-Y39H/ M1-CovS-WT (adj pvalue)	M1-CovS-WT: Mg ²⁺ /THY (Log2 FC)	M1-CovS-WT: Mg ²⁺ /THY (adj pvalue)	M1-CovS-Y39H: Mg ²⁺ /THY (Log2 FC)	M1-CovS-Y39H: Mg ²⁺ /THY (adj pvalue)	Hypothetical/proposed function
SP119_0139	SPy_0167	<i>slo</i>	-2.9	2.43E-06	-3.1	1.59E-09	0.0	1.00	streptolysin O
SP119_1170	—	<i>spd3</i>	-2.4	0.0003	-2.6	5.57E-06	-0.4	0.93	DNase
SP119_1403	SPy_1718	—	-2.0	0.0140	-1.8	0.0037	0.0	1.00	alpha/beta hydrolase fold family protein
SP119_1480	SPy_1743	<i>accA</i>	-1.7	0.0002	-1.9	1.75E-06	-0.2	0.96	acetyl-CoA carboxylase, carboxyl transferase, alpha subunit
SP119_1665	SPy_1979	<i>ska</i>	-1.7	0.0007	-1.2	0.0052	-0.5	0.79	streptokinase C
SP119_1694	—	<i>sic</i>	-1.6	0.0024	-3.3	5.20E-13	0.3	0.95	sic family protein
SP119_0578	—	—	-1.5	0.0006	-2.0	8.88E-09	0.2	0.96	transposase IS116/IS110/IS902 family protein
SP119_1078	SPy_1316	<i>glnQ</i>	-1.4	0.0037	-1.4	0.0019	-0.7	0.65	ABC transporter family protein
SP119_1686	SPy_2004	<i>dppE</i>	-1.4	0.0002	-1.3	0.0001	-0.3	0.89	ABC transporter family protein
SP119_0579	—	—	-1.4	0.0494	-1.4	0.0108	0.1	0.99	hypothetical protein
SP119_1691	SPy_2009	<i>fbxA</i>	-1.4	0.0002	-2.5	2.37E-15	-0.2	0.96	LPXTG-motif cell wall anchor domain protein
SP119_1683	SPy_2001	<i>dppB</i>	-1.4	0.0009	-1.4	0.0001	-0.1	0.98	binding--dependent transport system inner membrane component family protein
SP119_1692	SPy_2010	<i>scpA</i>	-1.3	0.0018	-2.0	3.72E-08	-0.6	0.70	C5a peptidase
SP119_0581	—	—	-1.3	0.0166	-1.5	0.0014	-0.5	0.79	mga helix-turn-helix domain protein
SP119_0333b	—	<i>spyB</i>	-1.3	0.0472	-2.4	2.84E-06	0.6	0.79	hypothetical protein
SP119_1077	SPy_1315	<i>glnP</i>	-1.3	0.0009	-1.2	0.0007	-0.8	0.41	amino ABC transporter, permease, 3-TM region, His/Glu/Gln/Arg/opine family domain protein
SP119_1684	SPy_2002	<i>dppC</i>	-1.3	0.0112	-1.7	0.0001	-0.1	0.99	binding--dependent transport system inner membrane component family protein
SP119_1481	SPy_1744	<i>accD</i>	-1.3	0.0004	-1.6	6.51E-07	-0.6	0.61	acetyl-CoA carboxylase, carboxyl transferase, beta subunit
SP119_0333	SPy_0428	<i>spyA</i>	-1.2	0.0318	-2.5	8.01E-08	0.5	0.75	clostridial binary toxin A family protein
SP119_0580	—	—	-1.2	0.0106	-1.4	0.0003	-0.1	0.99	transcriptional regulator
SP119_1588	SPy_1877	<i>glnA</i>	-1.2	0.0119	-1.1	0.0137	-0.5	0.72	glutamine synthetase, type I
SP119_1827	SPy_2206	<i>guaB</i>	-1.2	5.10E-07	-1.1	8.59E-07	0.5	0.41	inosine-5'-monophosphate dehydrogenase
SP119_1241	SPy_1510	<i>mutT</i>	-1.1	0.0498	-1.4	0.0019	-0.1	0.99	mutT/nudix family protein
SP119_1271	SPy_1544	<i>arcB</i>	-1.1	0.0017	0.7	0.0583	-0.3	0.75	ornithine carbamoyltransferase
SP119_1715	SPy_2045	—	-1.1	0.0174	-0.8	0.0767	0.7	0.61	low temperature requirement C
SP119_1682	SPy_2000	<i>dppA</i>	-1.1	0.0012	-0.3	0.4170	-0.8	0.31	bacterial extracellular solute-binding s, 5 Middle family protein
SP119_0176	SPy_0210	—	-1.1	0.0389	-1.0	0.0196	0.1	0.99	transglutaminase-like superfamily protein
SP119_0450	SPy_0577	—	-1.1	0.0497	-0.8	0.1169	0.6	0.71	hypothetical protein
SP119_0804	SPy_1070	—	-1.0	0.0040	-0.6	0.1516	0.2	0.89	dipeptidase PepV
SP119_1551	SPy_1833	<i>mutY</i>	-1.0	0.0115	-1.0	0.0064	0.0	1.00	A/G-specific adenine glycosylase
SP119_1752	SPy_2095	<i>pepO</i>	-1.0	0.0027	-0.7	0.0505	-0.2	0.90	endopeptidase
SP119_0401	SPy_0516	—	-1.0	0.0172	-0.5	0.2601	0.1	0.99	glycosyl transferases group 1 family protein
SP119_1634	SPy_1936	<i>degV</i>	-1.0	0.0321	-1.5	9.55E-05	0.6	0.62	EDD, DegV family domain protein
SP119_0933	SPy_1214	<i>lplA</i>	1.0	0.0416	2.0	3.72E-08	-0.6	0.61	lipoyltransferase and lipolate-ligase family protein
SP119_0681	SPy_0854	<i>pfkB</i>	1.0	1.56E-05	1.6	2.37E-15	-0.4	0.60	1-phosphofructokinase
SP119_0029	SPy_0034	<i>purK</i>	1.0	0.0302	0.2	0.7158	0.6	0.68	phosphoribosylaminoimidazole carboxylase, ATPase subunit
SP119_1688	SPy_2006	—	1.1	0.0050	1.3	4.05E-05	0.1	0.98	hypothetical protein
SP119_0022	SPy_0026	<i>purF</i>	1.1	0.0107	0.8	0.0578	-0.1	0.98	amidophosphoribosyltransferase
SP119_0492	SPy_0632	<i>ugl</i>	1.1	0.0321	-0.1	0.8369	0.0	1.00	unsaturated glucuronyl hydrolase
SP119_0326	SPy_0416	<i>prtS</i>	1.1	0.0112	1.4	0.0001	-0.3	0.85	hypothetical protein
SP119_0631	SPy_0794	—	1.1	0.0389	1.0	0.0315	-0.1	0.99	glycosyl transferase 2 family protein
SP119_1105	SPy_1355	—	1.2	0.0275	0.6	0.2792	-0.2	0.98	CBS domain pair family protein
SP119_1661	SPy_1972	<i>pulL</i>	1.2	0.0028	2.0	6.83E-10	-0.4	0.72	putative pullulanase
SP119_0024	SPy_0028	<i>purN</i>	1.2	0.0020	0.4	0.3075	0.0	0.99	phosphoribosylglycinamide formyltransferase
SP119_0034	SPy_0039	—	1.2	0.0435	0.5	0.3830	0.0	1.00	low molecular weight phosphotyrosine phosphatase family protein
SP119_0446	SPy_0572	<i>bgIP</i>	1.2	0.0140	1.5	0.0005	0.3	0.92	PTS system, beta-glucoside-specific IIABC component family protein
SP119_1778	SPy_2149	—	1.2	0.0498	0.4	0.6099	-0.6	0.75	hypothetical protein
SP119_0629	SPy_0792	<i>rgpF</i>	1.2	0.0140	0.7	0.1467	-0.1	0.99	rhamnan synthesis F family protein
SP119_1067	—	<i>amyA</i>	1.2	0.0112	0.2	0.7483	-0.1	0.99	cyclomalto-dextrin glucanotransferase
SP119_1493	SPy_1759	<i>dnaJ</i>	1.3	0.0112	0.4	0.4924	-0.2	0.97	chaperone protein DnaJ
SP119_0062	SPy_0074	<i>adk</i>	1.3	0.0106	1.0	0.0310	-0.6	0.68	adenylate kinase
SP119_1095	SPy_1340	—	1.3	0.0002	1.0	0.0031	0.5	0.71	sugar (and other) transporter family protein
SP119_0023	SPy_0027	<i>purM</i>	1.4	2.02E-05	1.0	0.0009	0.0	1.00	phosphoribosylformylglycinamide cyclo-ligase
SP119_1058	SPy_1292	<i>malQ</i>	1.4	0.0009	1.8	1.13E-07	0.1	0.99	4-alpha-glucanotransferase
SP119_0632	SPy_0796	—	1.4	0.0429	0.6	0.3668	-0.1	0.99	putative membrane protein
SP119_0445	SPy_0571	<i>licT</i>	1.4	0.0101	1.2	0.0122	0.2	0.94	transcription antiterminator LicT
SP119_0661	SPy_0831	<i>pyrP</i>	1.4	0.0078	1.6	0.0014	-0.2	0.99	uracil permease
SP119_1069	—	<i>malX</i>	1.4	0.0174	0.1	0.8749	-0.8	0.71	maltose/maltodextrin-binding protein
SP119_1057	SPy_1291	<i>glgP</i>	1.5	0.0040	2.3	2.20E-08	-0.4	0.84	glycogen/starch/alpha-glucan phosphorylases family protein
SP119_0660	SPy_0830	<i>pyrR</i>	1.5	0.0015	1.7	1.92E-05	-0.1	0.99	bifunctional protein pyrR
SP119_0949	SPy_1232	—	1.5	0.0127	0.8	0.2160	0.3	0.96	methyltransferase small domain protein
SP119_0106	SPy_0129	<i>srIB</i>	1.6	0.0017	1.3	0.0059	0.2	0.95	sortase, SrtB family
SP119_0125	SPy_0149	<i>ntpK</i>	1.6	0.0392	2.5	8.46E-06	0.1	0.99	V-type sodium ATPase subunit K
SP119_0103	—	<i>cpaI</i>	1.7	6.05E-07	1.3	0.0002	0.0	1.00	ancillary protein I
SP119_0105	—	—	1.7	0.0078	1.4	0.0221	-0.1	0.99	pilin
SP119_0720	SPy_0900	<i>pyrF</i>	1.7	2.63E-06	1.2	0.0011	-0.4	0.71	orotidine 5'-phosphate decarboxylase
SP119_0860	—	—	1.8	0.0038	1.1	0.0701	0.7	0.71	putative short-chain dehydrogenase domain protein
SP119_0695	SPy_0872	—	1.8	0.0010	-0.3	0.6842	0.9	0.60	calcineurin-like phosphoesterase family protein
SP119_0721	SPy_0901	<i>pyrE</i>	1.8	2.88E-05	1.3	0.0035	-0.4	0.79	orate phosphoribosyltransferase
SP119_1621	SPy_1917	<i>lacE</i>	1.9	0.0027	1.5	0.0151	0.3	0.93	PTS system lactose-specific EIICB component
SP119_1107	SPy_1357	<i>grab</i>	1.9	8.59E-08	2.0	6.83E-10	-0.3	0.85	immunoglobulin G-binding protein G

SP119_0662	SPy_0832	<i>pyrB</i>	2.0	2.26E-05	2.0	4.00E-06	-0.8	0.61	aspartate carbamoyltransferase
SP119_0107	SPy_0130	—	2.0	0.0009	1.6	0.0046	0.0	1.00	LPXTG-motif cell wall anchor domain protein
SP119_0104	SPy_0127	<i>lepB</i>	2.1	0.0037	1.7	0.0154	-0.2	0.99	signal peptidase I
SP119_0664	SPy_0835	<i>carB</i>	2.2	8.59E-08	1.8	2.61E-06	-0.5	0.75	carbamoyl-phosphate synthase, large subunit
SP119_0663	SPy_0833	<i>carA</i>	2.2	8.59E-08	2.1	8.01E-08	-0.4	0.75	carbamoyl-phosphate synthase, small subunit
SP119_1709	SPy_2038	<i>spi</i>	2.4	5.16E-05	3.7	2.49E-12	0.8	0.71	streptopain domain protein
SP119_1710	SPy_2039	<i>speB</i>	2.4	0.0002	4.0	1.92E-12	0.6	0.79	pyrogenic exotoxin B
SP119_1623	SPy_1919	<i>lacD</i>	2.5	0.0002	1.9	0.0029	-0.2	0.99	tagatose 1,6-diphosphate aldolase
SP119_1620	SPy_1916	<i>lacG</i>	3.1	2.43E-06	2.1	0.0010	-0.2	0.99	6-phospho-beta-galactosidase
SP119_1712	—	—	3.3	0.0014	2.0	0.0678	1.3	0.60	hypothetical protein

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21 b) Genes differentially expressed in Mg²⁺ supplemented THY in M1-CovS-WT strain (FC>2 and adjusted
 22 p-values ≤ 0.05) and with adjusted p-values < 0.05 but FC< 2 in M1-CovS-Y39H/ M1-CovS-WT
 23 comparisons

M1-CovS-WT (S119)	SF370	locus	M1-Cov-Y39H/ M1-CovS-WT (Log2 FC)	M1-Cov-Y39H/ M1-CovS-WT (adj pvalue)	M1-CovS-WT: Mg ²⁺ /THY (Log2 FC)	M1-CovS-WT: Mg ²⁺ /THY (adj pvalue)	M1-Cov-Y39H : Mg ²⁺ /THY (Log2 FC)	M1-Cov-Y39H : Mg ²⁺ /THY (adj pvalue)	Hypothetical/proposed function
SP119_1696	SPy_2019	<i>mga</i>	-0.9	0.0064	-1.5	3.85E-08	-0.2	0.96	M trans-acting positive regulator (MGA) PRD domain protein
SP119_0236	SPy_0291	<i>php7</i>	-0.9	0.0062	-1.4	1.74E-07	-0.1	0.99	D-alanyl-D-alanine carboxypeptidase family protein
SP119_1368	SPy_1673	—	-0.9	0.0190	-1.2	0.0002	0.1	0.98	putative membrane protein
SP119_1485	SPy_1748	<i>fabF</i>	-0.7	0.0117	-1.1	1.11E-05	-0.7	0.34	3-oxoacyl-[acyl-carrier-protein] synthase 2
SP119_1484	SPy_1747	<i>accB</i>	-0.7	0.0088	-1.2	1.45E-07	-0.7	0.25	acetyl-CoA carboxylase, biotin carboxyl carrier protein
SP119_1482	SPy_1745	<i>accC</i>	-0.7	0.0221	-1.2	1.74E-06	-0.6	0.34	acetyl-CoA carboxylase, biotin carboxylase
SP119_0859	—	<i>ydfG</i>	0.7	0.0284	1.2	3.51E-06	0.1	0.99	NADP-dependent 3-hydroxy acid dehydrogenase YdfG
SP119_0447	SPy_0574	<i>bgIH</i>	0.8	0.0078	1.7	3.35E-13	0.1	0.98	aryl-phospho-beta-D-glucosidase BgIH
SP119_1235	SPy_1503	<i>pgm</i>	0.8	0.0197	1.7	3.22E-09	-0.6	0.60	phosphoglucomutase/phosphomannomutase, alpha/beta/alpha domain I family protein
SP119_0680	SPy_0853	<i>fruR</i>	0.9	0.0060	1.3	5.99E-06	-0.3	0.75	deoR-like helix-turn-helix domain protein

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26 c) Genes differentially expressed in Mg²⁺ supplemented THY in M1-CovS-WT strain (FC>2 and adjusted
 27 p-values ≤ 0.05) and not differentially expressed in M1-CovS-Y39H/ M1-CovS-WT comparisons (FC <2
 28 and adjusted p-values >0.05)

M1-CovS-WT (S119)	SF370	locus	M1-Cov-Y39H/ M1-CovS-WT (Log2 FC)	M1-Cov-Y39H/ M1-CovS-WT (adj pvalue)	M1-CovS-WT: Mg ²⁺ /THY (Log2 FC)	M1-CovS-WT: Mg ²⁺ /THY (adj pvalue)	M1-Cov-Y39H : Mg ²⁺ /THY (Log2 FC)	M1-Cov-Y39H : Mg ²⁺ /THY (adj pvalue)	Hypothetical/proposed function
SP119_1668	SPy_1983	<i>sclA</i>	-3.0	NA	-3.5	0.0006	1.5	0.709	LPXTG-motif cell wall anchor domain protein
SP119_1707	SPy_2036	—	-0.7	0.4683	-3.4	2.98E-07	0.7	0.790	hypothetical protein
SP119_1171	—	—	-1.7	NA	-2.6	0.0482	0.1	0.999	hypothetical protein
SP119_0906	SPy_1180	<i>citN</i>	-0.5	0.4606	-2.3	4.66E-06	0.4	0.915	citrate transporter
SP119_0146	SPy_0174	<i>ulaA</i>	-0.1	0.8699	-2.1	0.0010	0.2	0.993	ascorbate-specific permease IIC component ulaA
SP119_1552	SPy_1834	—	-0.3	NA	-2.0	0.0494	1.4	0.708	helix-turn-helix family protein
SP119_1094	SPy_1339	—	-0.7	0.2181	-2.0	5.99E-06	0.9	0.604	thioesterase superfamily protein
SP119_1469	SPy_1731	—	-0.9	0.0660	-1.8	6.25E-07	0.5	0.730	hypothetical protein
SP119_0583	SPy_0738	<i>sagA</i>	-0.8	0.1731	-1.8	0.0002	0.8	0.610	bacteriocin protoxin, streptolysin S family protein
SP119_1388	SPy_1699	<i>acrR</i>	-0.8	0.2006	-1.7	0.0007	0.7	0.677	bacterial regulatory s, tetR family protein
SP119_1468	SPy_1730	<i>hit</i>	-0.3	0.6465	-1.7	0.0010	0.6	0.746	protein hit
SP119_0888	SPy_1160	—	-0.7	0.1175	-1.7	6.25E-07	0.4	0.710	hypothetical protein
SP119_1215	—	—	-0.6	0.3144	-1.5	0.0015	0.8	0.609	hypothetical protein
SP119_0356	SPy_0459	—	-0.5	0.4477	-1.4	0.0096	1.0	0.604	putative membrane protein
SP119_0909	SPy_1184	<i>gcdB</i>	-0.1	0.8878	-1.4	0.0031	0.2	0.978	glutaconyl-CoA decarboxylase subunit beta
SP119_1411	—	<i>sdaD2/ sdaI</i>	-1.0	0.0855	-1.4	0.0031	0.0	0.999	streptodornase SdaD2
SP119_1706	SPy_2034	—	-0.4	0.5367	-1.4	0.0034	0.2	0.978	hypothetical protein
SP119_1693	—	—	-0.9	0.0551	-1.3	0.0007	0.3	0.854	transposase
SP119_1829	—	—	-0.7	0.2289	-1.3	0.0087	1.2	0.340	hypothetical protein
SP119_1747	SPy_2089	<i>hutH</i>	-0.6	0.4222	-1.3	0.0194	0.5	0.790	histidine ammonia-lyase
SP119_0350	SPy_0450	<i>scar</i>	-0.3	0.6725	-1.3	0.0390	0.7	0.709	Mn-dependent transcriptional regulator
SP119_1795	SPy_2169	—	-0.8	0.0796	-1.3	0.0011	0.6	0.642	hypothetical protein
SP119_1126	SPy_1379	—	0.1	0.8615	-1.3	0.0413	0.6	0.763	voltage gated chloride channel family protein
SP119_0181	SPy_0216	<i>rivR</i>	-0.3	0.6176	-1.3	0.0045	0.6	0.682	M trans-acting positive regulator (MGA) PRD domain protein
SP119_0737	—	—	-0.7	0.3714	-1.3	0.0465	1.1	0.524	hypothetical protein
SP119_0868	SPy_1139	—	-0.6	0.3079	-1.3	0.0172	1.2	0.340	tautomerase enzyme family protein
SP119_0887	SPy_1159	<i>hlyIII</i>	-0.3	0.5914	-1.3	0.0081	0.5	0.718	channel, hemolysin III family protein
SP119_0133	SPy_0159	<i>sihA</i>	-0.7	0.0956	-1.2	0.0009	0.0	0.994	putative membrane associated protein
SP119_0718	SPy_0898	<i>cpsY</i>	-0.4	0.4199	-1.2	0.0003	0.5	0.677	bacterial regulatory helix-turn-helix, lysR family protein
SP119_0458	SPy_0589	—	-0.6	0.2319	-1.2	0.0081	1.0	0.340	hypothetical protein
SP119_1748	SPy_2090	<i>hutG</i>	-0.3	0.7226	-1.2	0.0266	0.7	0.678	formimidoylglutamate
SP119_0037	SPy_0042	—	-0.8	0.0578	-1.2	0.0005	0.0	1.000	aldehyde-alcohol dehydrogenase 2
SP119_0463	—	—	-0.3	0.6603	-1.2	0.0342	0.6	0.710	putative membrane protein
SP119_1115	SPy_1366	—	-0.2	0.7451	-1.2	0.0143	0.8	0.604	putative membrane protein
SP119_0364	SPy_0469	—	-0.6	0.2090	-1.2	0.0037	0.2	0.978	lysM domain protein
SP119_1770	SPy_2115	<i>spxA</i>	-0.9	0.1321	-1.2	0.0480	0.9	0.609	regulatory protein spx
SP119_1386	SPy_1697	—	-0.5	0.4145	-1.2	0.0081	0.2	0.960	putative lipoprotein
SP119_1796	SPy_2170	—	0.2	0.8116	-1.2	0.0466	0.6	0.748	NUDIX domain protein

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SP119_0108			-0.5	0.3447	-1.1	0.0046	0.3	0.892	transposase IS66
SP119_1463			0.5	0.5052	-1.1	0.0485	1.0	0.604	site-specific integrase
SP119_0484	SPy_0621		-0.8	0.0834	-1.1	0.0059	0.5	0.709	HD domain protein
SP119_1284			-1.0	0.0990	-1.1	0.0485	0.4	0.899	CRISPR-associated protein CasI
SP119_1483	SPy_1746	<i>fabZ</i>	-0.7	0.0516	-1.1	5.75E-05	-0.5	0.604	beta-hydroxyacyl-(acyl-carrier-protein) dehydratase FabZ
SP119_1581	SPy_1870		0.5	0.4452	-1.1	0.0346	0.8	0.604	bacterial regulatory s_gntR family protein
SP119_0172	SPy_0205		-0.5	0.2249	-1.1	0.0004	0.7	0.464	putative membrane protein
SP119_0324	SPy_0414	<i>lctO</i>	-0.4	0.2433	-1.1	9.35E-06	-0.2	0.846	L-lactate oxidase
SP119_1056	SPy_1290		-0.3	0.6872	-1.1	0.0230	0.4	0.832	DUF3862 domain-containing protein
SP119_1479	SPy_1742	<i>serS</i>	-0.9	0.0554	-1.1	0.0139	0.7	0.610	seryl-tRNA synthetase
SP119_0903	SPy_1177		-0.2	0.7018	-1.1	0.0053	0.4	0.791	glutaconyl-CoA decarboxylase subunit beta
SP119_0650	SPy_0815		-0.5	0.2631	-1.0	0.0062	0.2	0.945	hypothetical protein
SP119_0408	SPy_0527		-0.3	0.5724	-1.0	0.0018	0.6	0.604	putative cytoplasmic protein
SP119_0570	SPy_0722		-0.5	0.2433	-1.0	0.0042	0.1	0.993	chorismate mutase
SP119_0948	SPy_1230	<i>cdt</i>	0.7	0.1480	1.0	0.0267	0.1	0.993	cytidine deaminase
SP119_0932	SPy_1213	<i>fhsI</i>	0.5	0.0701	1.0	1.29E-06	-0.2	0.779	formate-tetrahydrofolate ligase I
SP119_0155	SPy_0184	<i>busAB</i>	0.0	0.9936	1.0	5.12E-05	0.0	0.993	betaine ABC transporter permease and substrate binding protein
SP119_0630	SPy_0793		1.0	0.0516	1.0	0.0318	-0.2	0.960	sulfatase family protein
SP119_0715	SPy_0892	<i>punA</i>	0.1	0.8494	1.0	0.0027	-0.6	0.609	purine nucleoside phosphorylase I, inosine and guanosine-specific
SP119_0552			0.6	0.1902	1.0	0.0029	-0.1	0.975	
SP119_0633	SPy_0797	<i>amrA</i>	0.7	0.1297	1.0	0.0058	-0.1	0.984	polysaccharide biosynthesis family protein
SP119_1402	SPy_1717	<i>copY</i>	0.1	0.8840	1.1	0.0049	0.2	0.930	Negative transcriptional regulator-copper transport operon
SP119_0073	SPy_0092	<i>adcR</i>	0.3	0.6165	1.1	0.0045	-0.4	0.748	transcriptional repressor AdcR
SP119_0931	SPy_1212	<i>cls</i>	0.5	0.2646	1.1	0.0031	-0.5	0.708	phospholipase D Active site motif family protein
SP119_0682	SPy_0855	<i>fruA</i>	0.3	0.4199	1.1	0.0001	0.0	0.995	PTS system, fructose subfamily, IIA component domain protein
SP119_0745	SPy_0928		0.1	0.9325	1.1	0.0465	-0.8	0.609	hypothetical protein
SP119_0301	SPy_0379	<i>pflA</i>	0.5	0.2319	1.1	0.0031	-0.5	0.708	pyruvate formate-lyase I-activating enzyme
SP119_0795	SPy_1061		0.1	0.8245	1.2	0.0002	-0.3	0.806	histidine kinase family protein
SP119_0683	SPy_0856	<i>murI</i>	0.9	0.1829	1.2	0.0414	0.2	0.975	mannosyl-glycoendo-beta-N-acetylglucosaminidase family protein
SP119_0864	SPy_1135	<i>guaC</i>	0.5	0.3447	1.2	0.0017	0.1	0.993	guanosine monophosphate reductase
SP119_0405	SPy_0521	<i>gacY</i>	0.7	0.1920	1.2	0.0053	0.3	0.913	ABC-type multidrug transport system, permease component
SP119_1417			-0.1	0.9151	1.2	0.0008	0.2	0.934	hypothetical protein
SP119_0938	SPy_1219	<i>yqiG</i>	0.5	0.1485	1.2	1.38E-05	-0.4	0.708	NADH:flavin oxidoreductase / NADH oxidase family protein
SP119_1420			0.6	0.2836	1.2	0.0083	-0.1	0.993	peptidase
SP119_0791	SPy_1057		0.2	0.7740	1.2	0.0005	-0.6	0.604	PTS system fructose IIA component family protein
SP119_0196	SPy_0244	<i>fasC</i>	0.9	0.1421	1.2	0.0215	-0.4	0.882	sensor histidine kinase FasC
SP119_1060	SPy_1294	<i>malE</i>	-0.1	0.9081	1.2	0.0170	-0.2	0.962	bacterial extracellular solute-binding family protein
SP119_1412		<i>amiD9</i>	-0.3	0.6931	1.3	0.0049	0.3	0.934	phage associated protein
SP119_1425			-0.1	0.9290	1.3	0.0021	0.4	0.779	phage major tail protein, TP901-1 family
SP119_1059	SPy_1293	<i>malR</i>	0.7	0.1256	1.3	0.0004	-0.6	0.642	bacterial regulatory s_lacI family protein
SP119_0947	SPy_1228	<i>tmbC</i>	0.6	0.2191	1.3	0.0004	-0.5	0.709	basic membrane family protein
SP119_1689	SPy_2007	<i>lmb</i>	0.7	0.1099	1.3	0.0002	-0.2	0.935	laminin binding protein
SP119_1229	SPy_1496	<i>argR3</i>	0.8	0.1286	1.3	0.0040	-0.8	0.604	arginine repressor, DNA binding domain protein
SP119_1418			0.3	0.7445	1.3	0.0188	0.1	0.993	hypothetical protein
SP119_1415			0.1	0.8775	1.3	6.17E-05	0.0	0.993	hypothetical protein
SP119_1306	SPy_1592		1.1	0.1495	1.3	0.0396	-0.7	0.718	bacterial extracellular solute-binding family protein
SP119_1662	SPy_1973	<i>dexB</i>	0.3	0.6396	1.3	0.0005	-0.1	0.993	glucan 1,6-alpha-glucosidase
SP119_0544			0.4	0.6480	1.3	0.0072	0.1	0.993	
SP119_0936	SPy_1217	<i>gcvH2</i>	0.5	0.2579	1.4	7.04E-05	-0.2	0.957	glycine cleavage H-family protein
SP119_0955	SPy_1240	<i>phoU</i>	1.2	0.0505	1.4	0.0064	-0.7	0.682	phosphate transport system regulatory protein PhoU
SP119_0844	SPy_1113	<i>aphA</i>	0.9	0.0736	1.4	0.0004	-0.2	0.957	class B acid phosphatase
SP119_0404	SPy_0519		0.7	0.2133	1.4	0.0020	-0.1	0.993	hypothetical protein
SP119_1421			0.4	0.5975	1.4	0.0025	0.0	1.000	hypothetical protein
SP119_0935	SPy_1216		0.6	0.1421	1.4	1.98E-05	-0.2	0.894	macro domain protein
SP119_0403	SPy_0518	<i>tagH</i>	0.7	0.1047	1.4	9.50E-05	-0.4	0.790	ABC transporter family protein
SP119_1578	SPy_1867	<i>deoC</i>	0.8	0.0740	1.4	3.58E-05	-0.9	0.340	deoxyribose-phosphate aldolase
SP119_1414			0.5	0.4560	1.4	0.0027	0.2	0.951	hypothetical protein
SP119_0937	SPy_1218		0.4	0.4211	1.5	3.65E-06	-0.6	0.604	luciferase oxidoreductase, group I family protein
SP119_0543			1.0	0.1050	1.5	0.0036	-0.2	0.984	
SP119_0549			0.3	0.7022	1.5	0.0031	0.3	0.866	
SP119_1413			0.3	0.6176	1.5	0.0003	0.3	0.891	hypothetical protein
SP119_1426			0.2	0.8373	1.5	0.0082	0.6	0.741	hypothetical protein
SP119_0793	SPy_1059	<i>ptsC</i>	0.5	0.2266	1.5	4.96E-06	-0.3	0.844	PTS system sorbose-specific iic component family protein
SP119_0792	SPy_1058	<i>ptsB</i>	0.3	0.6080	1.5	5.12E-05	-0.7	0.604	PTS system, mannose/fructose family IIB component
SP119_0934	SPy_1215		0.5	0.2677	1.5	6.25E-07	-0.5	0.694	SIR2 family protein
SP119_0545			1.7	NA	1.6	0.0497	0.4	0.936	
SP119_1431			0.3	0.6065	1.6	1.13E-06	0.0	0.993	DUF4355 domain-containing protein
SP119_1429			0.3	0.7121	1.6	0.0054	0.0	1.000	hypothetical protein
SP119_1423			0.0	NA	1.6	0.0483	-0.8	0.748	hypothetical protein
SP119_1430			0.2	0.6745	1.7	2.96E-09	0.3	0.748	hypothetical protein
SP119_1434			1.2	0.0592	1.7	0.0005	0.7	0.642	phage head morphogenesis protein
SP119_1443			1.6	0.0528	1.7	0.0187	0.2	0.993	ATP-dependent helicase
SP119_0538			1.0	NA	1.7	0.0417	0.3	0.948	
SP119_1419			0.9	0.0834	1.7	1.29E-06	0.1	0.993	hypothetical protein
SP119_0536			0.4	NA	1.7	0.0342	-0.1	0.993	
SP119_1428			0.6	0.4701	1.7	0.0014	-0.3	0.934	hypothetical protein
SP119_1435			0.8	0.4591	1.8	0.0194	0.5	0.870	phage portal protein
SP119_0794	SPy_1060	<i>ptsD</i>	0.4	0.3816	1.8	8.59E-07	-0.3	0.846	PTS system mannose/fructose/sorbose IID component family protein
SP119_0129	SPy_0154	<i>ntpA</i>	0.6	0.0958	1.8	1.98E-10	-0.1	0.960	V-type sodium ATPase catalytic subunit A
SP119_1270	SPy_1543		0.0	0.9868	1.8	3.51E-08	-0.2	0.893	C4-dicarboxylate anaerobic carrier family protein
SP119_0796	SPy_1062		1.0	0.2643	1.9	0.0057	-0.2	0.993	response regulator

SP119_1269	SPy_1542	<i>arcT</i>	0.4	0.4477	2.0	9.76E-09	-0.4	0.748	dipeptidase, family protein
SP119_0130	SPy_0155	<i>ntpB</i>	0.4	0.4053	2.1	9.37E-11	-0.3	0.854	V-type sodium ATPase subunit B
SP119_1424	—	—	0.8	0.5241	2.1	0.0066	-0.7	0.779	hypothetical protein
SP119_0127	SPy_0151	<i>ntpC</i>	0.7	0.1942	2.2	9.89E-09	-0.2	0.975	ATP synthase (C/AC39) subunit
SP119_0124	SPy_0148	<i>ntpI</i>	0.8	0.2272	2.2	5.57E-06	0.1	0.993	V-type ATPase 116kDa subunit
SP119_0131	SPy_0157	<i>ntpD</i>	0.8	0.3759	2.5	9.33E-05	-0.1	0.993	V-type ATPase, D subunit
SP119_1268	SPy_1541	<i>arcC</i>	0.7	0.2733	2.5	1.41E-08	-0.6	0.694	carbamate kinase
SP119_1416	—	—	0.6	NA	2.6	0.0267	-0.4	0.975	Ribosome maturation factor RimP
SP119_0128	SPy_0152 na	<i>ntpF</i>	1.0	NA	2.7	0.0030	-0.6	0.844	ATP synthase (F/14-kDa) subunit
SP119_0126	SPy_0150	<i>ntpE</i>	0.7	NA	2.9	8.25E-05	0.1	0.993	V-type sodium ATP synthase subunit E
SP119_0546	—	—	1.0	NA	2.9	0.0450	0.4	0.978	
SP119_1179	—	—	0.1	NA	3.0	0.0295	0.8	0.810	hypothetical protein
SP119_0123	SPy_0147	—	2.2	NA	3.9	0.0137	-0.5	0.957	hypothetical protein
SP119_1189	—	—	0.0	NA	4.8	0.0066	0.7	0.902	DUF4355 domain-containing protein
SP119_1188	—	—	0.0	NA	5.0	0.0066	0.3	0.993	hypothetical protein

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32 The results are expressed as log₂ fold changes.

33 The corresponding p-values, after multiple testing adjustment procedure are indicated

34 green, genes that are under expressed in at least one of the conditions; orange, genes that are

35 overexpressed in at least one of the conditions

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