

Protein ID	08BA2176	08S974	71193	E154	ED98	ED133	ISU935	LGA251	Newbould_305	NZ15	O11	O46	RF122	ST398	COG Accessio	COG Class	Function
APE88908.1	-	-	-	+	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein AS852_09550
APE88909.1	-	-	-	+	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein AS852_09555
APE88911.1	-	-	-	+	-	+	-	-	+	-	-	-	-	+	NA	NA	hypothetical protein AS852_09565
APE88913.1	-	-	-	+	-	-	-	-	-	-	-	-	+	+	NA	NA	hypothetical protein AS852_09575
APE88917.1	-	-	-	+	-	+	+	-	-	+	+	-	+	+	NA	NA	hypothetical protein AS852_09595
APE88918.1	-	-	-	+	-	+	-	+	-	-	-	-	+	-	NA	NA	hypothetical protein AS852_09600
APE88919.1	-	-	-	+	-	+	-	-	-	-	-	-	+	-	COG0305	L	damage-inducible protein
APE88920.1	-	-	-	+	-	+	-	+	-	-	-	+	+	-	NA	NA	hypothetical protein AS852_09610
APE88921.1	-	-	-	+	-	+	-	+	-	-	-	-	+	-	NA	NA	DnaD domain protein
APE88922.1	-	-	-	+	-	+	+	+	+	+	+	+	+	+	NA	NA	hypothetical protein AS852_09620
APE88963.1	-	-	-	+	-	-	-	-	-	-	-	+	-	-	NA	NA	hypothetical protein AS852_09870
APE88964.1	-	-	-	+	-	-	-	-	-	-	-	+	-	-	NA	NA	glucosamine-6-phosphate isomerase
AFR72383.1	+	-	+	-	+	+	-	-	-	-	-	+	-	+	NA	NA	Phage Holin
APE89083.1	-	-	-	+	-	-	+	-	-	+	+	+	-	+	COG0028	EH	acetolactate synthase, large subunit, biosynthetic type
APE89084.1	-	-	-	+	-	-	-	-	-	+	-	-	-	+	COG0440	E	acetolactate synthase I regulatory subunit
AFR72384.1	+	-	+	-	+	+	-	-	-	-	-	+	-	+	NA	NA	amidase
APE89093.1	-	-	-	+	-	-	-	-	-	+	+	+	-	-	COG1191	K	RNA polymerase sigma factor SigB
APE89094.1	-	-	-	+	-	-	-	-	-	+	+	+	-	-	COG2172	T	anti-sigma B factor RsbW
APE89095.1	-	-	-	+	-	-	-	-	-	+	+	+	-	-	COG1366	T	anti-anti-sigma factor
APE89096.1	-	-	-	+	-	-	-	-	-	+	+	+	-	-	COG2208	TK	serine/threonine protein phosphatase
APE89097.1	-	-	-	+	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein AS852_10755
APE89098.1	-	-	-	+	-	-	-	-	-	-	-	-	-	-	COG2337	V	PemK family transcriptional regulator
APE89099.1	-	-	-	+	-	-	-	-	-	+	+	-	-	-	NA	NA	antitoxin MazE
APE89100.1	-	-	-	+	-	-	-	-	-	+	+	+	-	-	COG0787	M	alanine racemase
APE89101.1	-	-	-	+	-	-	-	-	-	-	+	+	+	-	COG0736	I	holo-ACP synthase
AFR72460.1	+	-	+	-	+	+	-	+	-	-	-	-	+	+	COG0518	F	putative GMP synthase
APE89102.1	-	-	-	+	-	-	-	-	-	+	+	+	-	-	COG3402	S	hypothetical protein AS852_10780
APE89103.1	-	-	-	+	-	-	-	-	-	+	+	+	-	-	COG3428	S	hypothetical protein AS852_10785
APE89104.1	-	-	-	+	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein AS852_10790
AFR72461.1	+	-	+	-	-	+	-	+	+	-	-	-	+	+	COG0582	LX	Integrase
AFR72462.1	-	-	-	-	-	+	-	-	-	-	-	-	+	+	NA	NA	Transcriptional regulator
AFR72463.1	+	-	-	-	-	+	-	-	-	-	-	-	+	+	NA	NA	phage protein
AFR72464.1	+	-	-	-	-	+	-	-	+	-	-	-	+	+	NA	NA	pathogenicity island protein
AFR72465.1	+	-	-	-	+	+	-	+	+	-	-	-	+	+	NA	NA	hypothetical protein C248_0452
AFR72037.1	+	-	+	-	-	+	-	+	-	-	+	-	+	+	NA	NA	putative exported protein
APE89536.1	-	-	-	+	-	-	-	-	-	+	-	-	-	-	NA	NA	restriction endonuclease
AFR72466.1	+	-	-	-	+	+	-	+	+	-	-	-	+	+	NA	NA	hypothetical protein C248_0453
AFR72467.1	+	-	-	-	+	+	-	+	+	-	-	-	+	+	NA	NA	Hypothetical protein C248_0454
AD196568.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	NA	NA	conserved hypothetical protein
AD196569.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	NA	NA	putative helicase
AFR72468.1	+	-	-	-	-	+	-	+	+	-	-	-	-	+	NA	NA	putative primase
AD196570.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein SAOV_0028
AD196571.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein SAOV_0029
AD196572.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	COG2963	X	putative insertion element protein
AD196573.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	COG2801	X	putative insertion element protein
AD196575.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	NA	NA	putative transposase, truncation
AD196576.1	-	-	-	-	-	+	-	-	-	-	-	-	+	+	COG0042	J	hypothetical protein SAOV_0034
AD196577.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein SAOV_0035
AD196578.1	-	-	-	-	+	+	-	+	+	-	-	-	+	+	COG0730	S	hypothetical protein SAOV_0036
AD196579.1	-	-	-	-	+	+	-	+	+	-	-	-	+	+	COG1937	K	conserved hypothetical protein
AFR72469.1	+	-	-	-	+	+	-	+	+	-	-	-	+	+	NA	NA	hypothetical protein C248_0456

ADI96580.1	-	-	-	-	+	+	-	+	+	-	-	-	+	+	COG0425	O	conserved hypothetical protein
ADI96581.1	-	-	-	-	+	+	-	+	+	-	-	-	+	-	COG0607	P	metallo-beta-lactamase family protein
ADI96582.1	-	-	-	-	+	+	-	+	+	-	-	-	+	-	COG0446	I	conserved hypothetical protein
ADI96583.1	-	-	-	-	+	+	-	+	+	-	+	+	-	-	COG0042	J	hypothetical protein SAOV_0041
ADI96584.1	-	-	-	-	+	+	-	-	-	-	+	+	-	-	NA	NA	hypothetical protein SAOV_0042
ADI96585.1	-	-	-	-	+	+	-	+	+	-	-	+	-	-	COG3070	K	conserved hypothetical protein
ADI96586.1	-	-	-	-	+	+	-	-	+	-	+	+	-	-	NA	NA	hypothetical protein SAOV_0044
ADI96587.1	-	-	-	-	+	+	-	+	+	-	-	-	-	-	COG1112	L	hypothetical protein SAOV_0045
ADI96588.1	-	-	-	-	+	+	-	+	+	-	+	+	-	-	NA	NA	hypothetical protein SAOV_0046
AFR72470.1	+	-	-	-	-	+	-	-	+	-	-	-	-	+	NA	NA	hypothetical protein C248_0457
ADI96591.1	-	-	-	-	+	+	-	+	+	-	-	-	-	-	NA	NA	l-phosphatidylinositol phosphodiesterase
ADI96592.1	-	-	-	-	+	-	-	+	-	-	-	-	-	-	COG2207	K	putative transcriptional regulator
ADI96593.1	-	-	-	-	+	-	-	+	-	-	-	-	-	-	COG1473	R	putative peptidase
ADI96811.1	-	-	-	-	+	+	-	+	-	-	-	+	-	-	NA	NA	putative prophage integrase
ADI96812.1	-	-	-	-	-	+	-	-	-	-	-	+	-	-	COG1266	O	CAAX amino terminal protease family
ADI96813.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein SAOV_0276
ADI96814.1	-	-	-	-	-	+	-	-	-	-	-	+	-	-	NA	NA	putative lipoprotein
ADI96815.1	-	-	-	-	-	+	-	-	-	-	+	+	-	+	NA	NA	hypothetical phage-related protein
ADI96816.1	-	-	-	-	-	+	-	-	-	-	+	-	-	-	COG1396	K	phage repressor
AFR72471.1	+	-	-	-	-	+	-	-	+	-	-	-	-	+	NA	NA	hypothetical protein C248_0458
ADI96817.1	-	-	-	-	-	+	-	-	-	-	-	+	+	-	NA	NA	hypothetical phage-related protein
ADI96818.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein SAOV_0281
ADI96819.1	-	-	-	-	-	+	-	-	-	-	+	+	-	-	NA	NA	hypothetical protein SAOV_0282
ADI96824.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein SAOV_0287
ADI96825.1	-	-	-	-	-	+	-	-	-	-	+	-	-	+	NA	NA	hypothetical protein SAOV_0288
ADI96826.1	-	-	-	-	-	+	-	-	-	-	-	-	-	+	NA	NA	putative topoisomerase
AFR72472.1	+	-	-	-	-	+	-	-	+	-	-	-	-	+	NA	NA	hypothetical protein C248_0459
ADI96827.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	COG0629	L	Single-stranded DNA-binding protein, phage associated
ADI96829.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	NA	NA	Phage replication initiation
ADI96832.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	NA	NA	hypothetical phage-related protein
ADI96836.1	-	-	-	-	-	+	-	-	-	-	+	-	-	-	NA	NA	Transcriptional regulator, Cro/C1 family
AFR72473.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	adenosine deaminase
ADI96841.1	-	-	-	-	-	+	-	-	-	-	-	+	+	-	NA	NA	hypothetical protein SAOV_0304
ADI96844.1	-	-	-	-	-	+	-	-	-	-	-	+	-	-	NA	NA	hypothetical protein SAOV_0307
ADI96845.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein SAOV_0308
AFR72474.1	+	-	-	+	-	+	-	-	+	-	-	-	-	-	NA	NA	Hypothetical protein C248_0461
AFR72038.1	+	-	-	-	-	+	-	-	+	-	-	+	+	+	NA	NA	putative exported protein
AFR72476.1	+	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein C248_0463
ADI96867.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	NA	NA	Phage tail length tape-measure protein
ADI96868.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	NA	NA	Phage tail length tape-measure protein
AFR72477.1	+	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein C248_0464
ADI96877.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein SAOV_0340
ADI96880.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein SAOV_0343
ADI96881.1	-	-	-	-	-	+	-	-	+	-	-	+	+	-	NA	NA	hypothetical protein SAOV_0344
ADI96882.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein SAOV_0345
ADI96883.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	COG0657	I	hypothetical protein SAOV_0346c
ADI96884.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	COG1902	C	NADH-dependent flavin oxidoreductase
AFR72478.1	-	-	-	-	-	+	+	-	-	-	-	+	-	-	NA	NA	hypothetical protein C248_0465
ADI96955.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	NA	NA	pathogenicity island protein
AFR72479.1	+	-	-	+	-	-	-	+	-	-	-	-	-	-	NA	NA	hypothetical protein C248_0466
ADI96961.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	NA	NA	pathogenicity island protein

AD196962.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	NA	NA	pathogenicity island protein, putative terminase
AD196964.1	-	-	-	-	-	+	-	-	-	-	-	-	+	-	NA	NA	pathogenicity island protein
AD196965.1	-	-	-	-	-	+	-	+	-	-	-	-	+	-	NA	NA	pathogenicity island protein
AD196966.1	-	-	-	-	-	+	-	-	-	-	-	-	+	-	NA	NA	staphylococcal enterotoxin C-ovine
AD196967.1	-	-	-	-	-	+	+	+	-	-	-	-	+	-	NA	NA	staphylococcal enterotoxin L
AD197584.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein SAOV_1071c
AD197585.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein SAOV_1072c
AD197586.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein SAOV_1073c
AD197588.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein SAOV_1075
AD197589.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	NA	NA	hypothetical phage-related protein
AD197590.1	-	-	-	-	-	+	-	+	-	-	-	-	-	-	COG3617	X	prophage, antirepressor, putative
AD197598.1	-	-	-	-	-	+	-	+	-	+	+	+	+	-	NA	NA	hypothetical phage-related protein
AD197599.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	NA	NA	hypothetical phage-related protein
AD197606.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein SAOV_1093
AD197607.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein SAOV_1094
AFR72484.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein C248_0471
AFR72039.1	+	-	+	-	-	+	-	+	-	-	+	+	+	+	COG1235	P	metallo-beta-lactamase superfamily protein
AD197627.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	COG5412	X	Phage tail length tape-measure protein
AD197628.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	NA	NA	Phage tail length tape-measure protein
AD197632.1	-	-	-	-	-	+	+	-	-	-	+	-	-	-	NA	NA	hypothetical phage protein
AD197633.1	-	-	-	-	-	+	+	-	-	-	-	-	+	-	NA	NA	Enterotoxin, phage associated
AD197635.1	-	-	-	-	-	+	+	-	-	-	-	-	-	-	NA	NA	Phage amidase
AD197665.1	-	-	-	-	-	+	+	-	-	-	-	-	-	-	NA	NA	hypothetical protein SAOV_1152
AD197666.1	-	-	-	-	-	+	+	-	-	-	-	-	-	-	NA	NA	hypothetical protein SAOV_1153c
AD197670.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein SAOV_1157c
AD197675.1	-	-	-	-	-	+	+	-	-	+	-	-	+	-	NA	NA	hypothetical protein SAOV_1162
AD197683.1	-	-	-	-	-	+	-	-	-	-	-	-	+	-	NA	NA	probable membrane protein
AFR72489.1	+	-	+	-	-	-	-	-	-	-	-	-	-	-	NA	NA	Hypothetical protein C248_0476
AD197947.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	NA	NA	conserved hypothetical protein
AFR72491.1	+	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein C248_0478
AD198288.1	-	-	-	-	-	+	-	-	-	-	+	-	-	-	COG1131	V	ABC transporter, ATP-binding protein
AD198289.1	-	-	-	-	-	+	-	-	-	-	+	-	-	-	NA	NA	putative ABC transporter permease protein
AD198290.1	-	-	-	-	-	+	+	-	-	-	+	-	-	-	NA	NA	conserved hypothetical protein
AD198291.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein SAOV_1787
AD198295.1	-	-	-	-	-	+	-	+	-	-	-	-	-	-	NA	NA	hypothetical protein SAOV_1791
AD198296.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein SAOV_1792
AD198299.1	-	-	-	-	-	+	+	-	-	+	+	+	+	-	COG3591	E	serine proteinase
AD198300.1	-	-	-	-	-	+	+	-	-	+	-	-	+	-	COG3591	E	serine proteinase
AD198301.1	-	-	-	-	-	+	+	-	+	-	+	-	+	-	COG3591	E	serine proteinase
AD198302.1	-	-	-	-	-	+	+	-	-	+	-	-	+	-	NA	NA	beta-lactamase
AD198303.1	-	-	-	-	-	+	-	+	-	-	-	+	-	-	NA	NA	putative lantibiotic ABC transporter protein
AD198304.1	-	-	-	-	-	+	-	+	-	-	-	+	-	-	NA	NA	putative lantibiotic ABC transporter protein
AD198305.1	-	-	-	-	-	+	-	-	-	-	-	-	+	-	COG1131	V	epidermin immunity protein F
AD198306.1	-	-	-	-	-	+	-	+	-	-	-	-	+	-	COG1404	O	probable serine protease precursor
AD198307.1	-	-	-	-	-	+	-	+	-	-	-	-	+	-	COG0452	H	Epidermin biosynthesis protein epiD
AD198308.1	-	-	-	-	-	+	-	+	-	-	-	-	+	-	NA	NA	Epidermin biosynthesis protein epiC
AD198309.1	-	-	-	-	-	+	-	+	-	-	-	-	+	-	NA	NA	epidermin biosynthesis protein EpiB
AD198310.1	-	-	-	-	-	+	-	-	-	-	-	-	+	-	NA	NA	hypothetical protein SAOV_1807
AD198311.1	-	-	-	-	-	+	-	-	-	-	-	-	+	-	NA	NA	hypothetical protein SAOV_1808
AD198314.1	-	-	-	-	-	+	-	+	-	-	-	-	+	-	NA	NA	hypothetical protein SAOV_1811
AD198315.1	-	-	-	-	-	+	+	-	+	-	+	+	+	-	NA	NA	leukotoxin D subunit

ADI98316.1	-	-	-	-	+	+	+	-	+	-	-	-	+	-	NA	NA	hypothetical protein SAOV_1814
ADI98317.1	-	-	-	-	+	+	+	-	+	-	-	-	+	-	NA	NA	hypothetical protein SAOV_1815
ADI98318.1	-	-	-	-	+	+	-	-	+	-	-	-	-	-	NA	NA	hypothetical protein SAOV_1816
AFR72040.1	+	-	+	-	-	+	-	+	-	-	+	-	+	+	COG0737	FV	putative 5'-nucleotidase
ADI98372.1	-	-	-	-	+	+	+	-	+	-	+	-	+	-	NA	NA	leukocidin chain lukM precursor
ADI98373.1	-	-	-	-	-	+	-	-	-	-	+	-	-	-	NA	NA	lytic enzyme
ADI98374.1	-	-	-	-	-	+	-	-	-	-	+	+	-	-	COG5546	S	phage-associated holin
ADI98381.1	-	-	-	-	+	+	-	-	-	-	+	-	-	-	NA	NA	hypothetical protein SAOV_1919c
ADI98382.1	-	-	-	-	+	+	-	-	-	-	+	-	-	-	NA	NA	hypothetical protein SAOV_1920c
ADI98383.1	-	-	-	-	+	+	-	-	-	-	+	-	-	-	NA	NA	hypothetical protein SAOV_1921c
ADI98384.1	-	-	-	-	+	+	-	-	-	-	+	-	-	-	NA	NA	hypothetical protein SAOV_1922c
ADI98385.1	-	-	-	-	+	+	-	-	-	-	+	-	-	-	NA	NA	hypothetical phage related protein
ADI98386.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein SAOV_1924c
ADI98387.1	-	-	-	-	+	+	-	-	-	-	+	+	-	-	NA	NA	DNA packaging protein
ADI98388.1	-	-	-	-	+	+	-	-	-	-	+	+	-	-	NA	NA	hypothetical protein SAOV_1926c
ADI98389.1	-	-	-	-	+	+	-	-	-	-	+	+	-	-	NA	NA	Phage capsid protein
ADI98390.1	-	-	-	-	+	+	-	-	-	-	+	+	-	-	NA	NA	Prohead protease
ADI98391.1	-	-	-	-	+	+	-	-	-	-	+	+	-	-	NA	NA	Phage portal protein
ADI98392.1	-	-	-	-	+	+	-	-	-	-	+	+	-	-	NA	NA	phi PVL orf 3-like protein-related protein
ADI98393.1	-	-	-	-	+	+	-	-	-	-	+	+	-	-	COG4626	X	Terminase large subunit, phage associated
ADI98394.1	-	-	-	-	+	+	-	-	-	-	+	+	-	-	NA	NA	Phage Terminase Small Subunit
ADI98395.1	-	-	-	-	+	+	-	-	-	-	+	+	-	-	COG1403	V	hypothetical protein SAOV_1933c
ADI98396.1	-	-	-	-	+	+	-	-	-	-	+	+	-	-	NA	NA	hypothetical phage-related protein
AFR72498.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	putative exported protein
AFR72499.1	+	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein C248_0486
ADI98412.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	NA	NA	DNA helicase, phage-associated
ADI98416.1	-	-	-	-	-	+	-	-	-	-	+	-	-	-	NA	NA	hypothetical protein SAOV_1954c
ADI98419.1	-	-	-	-	+	+	+	+	+	-	+	+	-	-	NA	NA	hypothetical protein SAOV_1957c
ADI98420.1	-	-	-	-	+	+	+	+	+	-	+	+	-	-	NA	NA	hypothetical protein SAOV_1958c
ADI98421.1	-	-	-	-	+	+	-	-	+	-	-	-	-	-	NA	NA	hypothetical protein SAOV_1959c
ADI98423.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein SAOV_1961c
ADI98424.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein SAOV_1962c
ADI98425.1	-	-	-	-	-	+	-	-	-	-	+	-	-	-	NA	NA	hypothetical protein SAOV_1963
ADI98426.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	NA	NA	hypothetical phage-related protein
ADI98428.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein SAOV_1966
ADI98429.1	-	-	-	-	+	+	-	-	-	-	+	-	-	+	NA	NA	hypothetical protein SAOV_1967c
ADI98430.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein SAOV_1968c
ADI98431.1	-	-	-	-	+	+	-	-	+	-	-	-	-	-	NA	NA	hypothetical protein SAOV_1969c
ADI98433.1	-	-	-	-	-	+	-	-	-	-	+	-	-	-	NA	NA	hypothetical protein SAOV_1971
ADI98435.1	-	-	-	-	-	+	-	-	-	-	+	+	-	-	NA	NA	hypothetical protein SAOV_1973
ADI98436.1	-	-	-	-	+	+	+	+	-	-	+	+	-	-	NA	NA	prophage integrase
ADI98503.1	-	-	-	-	-	+	-	-	+	-	+	-	-	-	NA	NA	probable leukocidin S subunit
ADI98504.1	-	-	-	-	-	+	-	-	+	-	+	-	+	-	COG0624	E	probable succinyldiaminopimelate desuccinylase
ADI98505.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	COG0697	GER	Permease of the drug/metabolite transporter (DMT)
ADI98506.1	-	-	-	-	-	+	-	-	-	-	-	-	+	-	COG0156	H	5-aminolevulinate synthase
ADI98507.1	-	-	-	-	-	+	-	-	+	-	+	-	+	-	COG0168	P	probable sodium transport protein
ADI98508.1	-	-	-	-	-	+	-	-	-	-	-	-	+	-	NA	NA	transposase
ADI98509.1	-	-	-	-	-	+	-	-	-	-	+	+	-	-	NA	NA	phage-like protein
ADI98510.1	-	-	-	-	-	+	-	-	+	-	+	-	+	+	NA	NA	hypothetical protein SAOV_2049
ADI98511.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein SAOV_2050
ADI98517.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein SAOV_2056c

ADI98522.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	+	-	NA	NA	hypothetical protein SAOV_2061c
ADI98523.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	NA	NA	putative prophage antirepressor
ADI98524.1	-	-	-	-	+	+	-	-	-	-	-	-	-	-	-	-	NA	NA	putative transcriptional regulator
ADI98525.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	COG1396	K	putative transcriptional regulator
ADI98526.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	+	-	COG0582	LX	probable integrase
ADI98527.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	+	+	COG0459	O	60 kDa chaperonin protein
AFR72041.1	+	-	+	-	-	-	-	-	-	-	-	-	-	-	+	+	COG1576	J	hypothetical protein C248_0027
ADI98883.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	+	-	NA	NA	hypothetical protein SAOV_2443c
ADI98893.1	-	-	-	-	-	+	+	+	+	+	-	-	-	-	+	-	COG4115	V	conserved hypothetical protein
ADI98894.1	-	-	-	-	-	+	+	+	+	+	-	-	-	-	+	-	COG2161	V	hypothetical protein SAOV_2454c
ADI98980.1	-	-	-	-	-	+	+	+	+	+	-	-	-	-	-	-	NA	NA	permease, putative
ADI98990.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein SAOV_2551c
ADI98991.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein SAOV_2552c
ACY09979.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein SAAV_0030
ACY09980.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	NA	NA	conserved hypothetical protein
ACY09993.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein SAAV_0044
ACY10313.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	NA	NA	superantigen-like protein
ACY10325.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	NA	NA	putative lipoprotein
ACY10326.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	NA	NA	putative lipoprotein
ACY10327.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	+	-	NA	NA	putative lipoprotein
ACY10330.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	NA	NA	conserved hypothetical protein
ACY10703.1	-	-	-	-	-	+	-	-	-	+	-	-	-	-	-	-	COG1464	P	ABC transporter, substrate-binding protein
AFR72514.1	+	-	+	-	-	+	-	-	-	+	-	-	-	-	+	-	COG0523	R	putative cobalamin synthesis protein
ACY10705.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	NA	NA	SAP domain protein
ACY10706.1	-	-	-	-	-	+	-	-	-	+	-	-	-	-	-	-	NA	NA	conserved hypothetical protein
ACY10711.1	-	-	-	-	-	+	-	-	-	+	-	-	-	-	-	-	NA	NA	pathogenicity island protein
ACY10713.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	+	-	NA	NA	pathogenicity island protein ORF15
ACY10714.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	+	-	COG5519	S	pathogenicity island protein ORF 14/13
AFR72515.1	+	-	+	-	-	+	-	-	-	+	-	-	-	-	+	-	COG1009	CP	Putative NADH Ubiquinone plastoquinone protein
AFR72042.1	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	COG1397	O	ADP-ribosylglycohydrolase
ACY10716.1	-	-	-	-	-	+	-	-	-	+	+	-	-	-	+	-	NA	NA	pathogenicity island protein ORF11
ACY10717.1	-	-	-	-	-	+	-	-	-	+	+	-	-	-	+	-	NA	NA	pathogenicity island protein ORF10
ACY10718.1	-	-	-	-	-	+	-	-	-	-	+	-	-	-	+	-	NA	NA	pathogenicity island protein ORF9
ACY10719.1	-	-	-	-	-	+	-	-	-	-	+	-	-	-	+	-	NA	NA	pathogenicity island protein ORF8
ACY10721.1	-	-	-	-	-	+	-	-	-	+	+	-	-	-	+	-	NA	NA	pathogenicity island protein ORF6
ACY10722.1	-	-	-	-	-	+	-	-	-	+	+	-	-	-	+	-	COG3728	X	pathogenicity island protein ORF5; phage terminase
ACY10723.1	-	-	-	-	-	+	-	-	-	+	+	-	-	-	-	-	NA	NA	hypothetical protein SAAV_0806
ACY10724.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	NA	NA	conserved hypothetical protein
AFR72516.1	+	-	+	-	-	+	-	-	-	+	-	-	-	-	+	-	COG3002	S	hypothetical protein C248_0503
ACY10725.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	NA	NA	conserved hypothetical protein
ACY10727.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein SAAV_0810
ACY10728.1	-	-	-	-	-	+	-	-	-	+	+	-	-	-	-	-	COG3237	S	hypothetical protein SAAV_0811
ACY10736.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	NA	NA	DNA adenine methylase
ACY10737.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	COG0338	L	putative methylase
ACY10738.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	NA	NA	conserved hypothetical phage protein
AFR72517.1	+	-	+	-	-	+	-	-	-	+	-	-	-	-	+	-	COG5609	S	hypothetical protein C248_0504
ACY10743.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	+	-	NA	NA	conserved hypothetical phage protein
ACY10745.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	NA	NA	conserved hypothetical phage protein
ACY10746.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	NA	NA	conserved hypothetical phage protein
ACY10747.1	-	-	-	-	-	+	-	-	-	+	+	-	-	-	-	-	NA	NA	conserved hypothetical phage protein
AFR72518.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	+	-	NA	NA	putative membrane protein

ACY10753.1	-	-	-	-	+	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical phage protein
ACY10754.1	-	-	-	-	+	-	-	-	-	-	-	-	-	-	NA	NA	conserved hypothetical phage protein
ACY10755.1	-	-	-	-	+	-	-	-	-	-	-	-	-	-	NA	NA	putative phage replication protein
ACY10756.1	-	-	-	-	+	-	+	-	+	-	+	+	-	-	COG1484	L	DnaC
ACY10757.1	-	-	-	-	+	-	-	-	+	-	-	-	-	-	NA	NA	conserved hypothetical phage protein
ACY10760.1	-	-	-	-	+	-	-	-	-	-	-	-	-	-	NA	NA	PVL ORF-50 family protein
AFR72519.1	+	-	+	-	+	-	-	+	-	-	+	-	-	-	COG0671	I	putative membrane protein
ACY10761.1	-	-	-	-	+	-	-	-	-	-	-	-	-	-	NA	NA	conserved hypothetical phage protein
ACY10763.1	-	-	-	-	+	-	-	-	-	-	-	-	-	-	NA	NA	conserved hypothetical phage protein
ACY10766.1	-	-	-	-	+	-	-	-	-	-	+	+	-	-	NA	NA	conserved hypothetical phage protein
AFR72520.1	-	-	+	-	+	-	-	+	-	-	+	-	-	-	COG1647	Q	hypothetical protein C248_0507
AFR72521.1	+	-	+	-	+	-	-	+	-	-	+	-	-	-	COG0733	R	sodium:neurotransmitter symporter family protein
ACY10790.1	-	-	-	-	+	-	-	-	-	-	-	-	-	-	NA	NA	holin, SPP1 family
AFR72522.1	+	-	+	-	+	-	-	+	-	-	+	-	-	-	COG0031	E	pyridoxal-phosphate dependent enzyme
ACY10791.1	-	-	-	-	+	-	-	-	-	-	-	-	-	-	NA	NA	phage amidase
ACY10792.1	-	-	-	-	+	-	-	-	-	-	-	-	-	-	NA	NA	Ear-like protein
ACY10793.1	-	-	-	-	+	-	-	-	+	-	-	-	-	-	NA	NA	hypothetical phage protein
ACY10794.1	-	-	-	-	+	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical phage protein
ACY10795.1	-	-	-	-	+	-	-	-	+	-	-	-	-	-	NA	NA	hypothetical phage protein
AFR72523.1	+	-	+	-	+	-	-	+	-	-	+	-	-	-	COG0626	E	putative Cys/Met metabolism PLP-dependent enzyme
ACY11036.1	-	-	-	-	+	-	-	-	+	-	-	-	-	-	NA	NA	conserved hypothetical protein
ACY11038.1	-	-	-	-	+	-	-	+	-	-	-	-	-	-	COG3464	X	IS1181 transposase
AFR72524.1	+	-	+	-	+	-	-	+	-	-	+	-	-	-	COG1135	E	ABC transporter ATP-binding protein
AFR72525.1	-	-	-	-	+	-	-	-	-	-	+	-	-	-	COG2011	E	putative transport system membrane protein
AFR72043.1	+	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	putative permease
ACY11317.1	-	-	-	-	+	-	-	-	+	-	-	-	-	-	NA	NA	hypothetical protein SAAV_1415
ACY11319.1	-	-	-	-	+	-	-	-	-	-	-	-	-	-	NA	NA	surface protein, ECM binding protein-like protein
ACY11320.1	-	-	-	-	+	-	-	-	-	-	-	-	-	-	NA	NA	surface protein, ECM binding protein-like protein
ACY11321.1	-	-	-	-	+	-	-	-	-	-	-	-	-	-	COG5281	X	surface protein, ECM binding protein-like protein
ACY11701.1	-	-	-	-	+	-	-	-	-	-	-	-	-	-	COG2801	X	transposase
ACY11702.1	-	-	-	-	+	-	-	-	-	-	-	-	-	-	COG4584	X	transposase
ACY11706.1	-	-	-	-	+	-	-	-	-	-	+	-	-	-	COG3591	E	serine protease SplD, putative
ACY11709.1	-	-	-	-	+	-	-	+	+	-	+	-	-	-	COG3591	E	serine protease SplA
ACY11711.1	-	-	-	-	+	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein SAAV_1823
ACY11712.1	-	-	-	-	+	-	-	-	+	-	-	-	-	-	NA	NA	epidermin immunity protein F
ACY11713.1	-	-	-	-	+	-	-	-	+	-	-	-	-	-	NA	NA	conserved hypothetical protein
ACY11714.1	-	-	-	-	+	-	-	-	+	-	-	-	-	-	NA	NA	conserved hypothetical protein
ACY11715.1	-	-	-	-	+	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein SAAV_1827
ACY11718.1	-	-	-	-	+	-	+	-	-	-	-	-	-	-	NA	NA	hypothetical protein SAAV_1830
ACY11722.1	-	-	-	-	+	-	-	-	-	-	-	-	-	-	NA	NA	staphylococcal enterotoxin G
ACY11723.1	-	-	-	-	+	-	-	-	-	-	-	-	-	-	NA	NA	staphylococcal enterotoxin N
ACY11724.1	-	-	-	-	+	-	+	-	-	-	-	-	-	-	NA	NA	staphylococcal enterotoxin Yent1
ACY11725.1	-	-	-	-	+	-	-	-	-	-	-	-	-	-	NA	NA	staphylococcal enterotoxin Yent2
ACY11727.1	-	-	-	-	+	-	+	-	-	-	-	-	-	-	NA	NA	staphylococcal enterotoxin M
ACY11728.1	-	-	-	-	+	-	+	-	-	-	-	-	+	-	NA	NA	staphylococcal enterotoxin O
AFR72582.1	+	-	-	+	-	-	+	-	-	-	-	-	-	-	NA	NA	hypothetical protein C248_0573
ACY11887.1	-	-	-	-	+	-	-	-	-	-	-	-	-	-	NA	NA	conserved hypothetical phage protein
ACY11890.1	-	-	-	-	+	-	-	-	-	-	-	-	-	-	NA	NA	conserved hypothetical phage protein
ACY11892.1	-	-	-	-	+	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical phage protein
ACY12283.1	-	-	-	-	+	-	-	-	-	-	+	+	-	-	COG2223	P	nitrite extrusion protein
AFR72044.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	COG0524	G	putative kinase

ACY12392.1	-	-	-	-	+	-	-	-	-	-	-	-	-	-	NA	NA	LPXTG-motif protein
ACY12393.1	-	-	-	-	+	-	+	-	+	-	-	-	-	-	COG1846	K	staphylococcal accessory regulator T
ACY12394.1	-	-	-	-	+	-	-	+	-	-	-	-	-	-	COG1846	K	Staphylococcal accessory regulator U
ACY12397.1	-	-	-	-	+	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein SAAV_2567
ACY12604.1	-	-	-	-	+	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein SAAV_2775
ACY12606.1	-	-	-	-	+	-	-	-	-	-	-	-	-	-	COG1476	K	transcriptional regulator, Cro/Ci family
AFR72869.1	+	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein C248_0875
ACY12607.1	-	-	-	-	+	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein SAAV_2778
ACY12608.1	-	-	-	-	+	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein SAAV_2779
ACY12609.1	-	-	-	-	+	-	-	-	-	-	-	-	-	-	COG1475	D	ParB family chromosome partitioning protein
ACY12610.1	-	-	-	-	+	-	-	-	-	-	-	-	-	-	COG0357	J	16S rRNA methyltransferase GidB
ACY12611.1	-	-	-	-	+	-	-	-	-	-	-	-	-	-	COG0445	J	tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA
ACY12612.1	-	-	-	-	+	-	-	-	-	-	-	-	-	-	COG0486	J	tRNA modification GTPase TrmE
ACY12613.1	-	-	-	-	+	-	-	-	-	-	-	-	-	-	COG0594	J	ribonuclease P protein component
ACY12614.1	-	-	-	-	+	-	-	-	-	-	-	-	-	-	COG0230	J	50S ribosomal protein L34
AFR72870.1	-	-	-	-	+	-	-	-	-	-	-	-	-	-	NA	NA	Hypothetical protein C248_0876
ASC0314.1	-	-	-	-	-	-	+	-	-	-	-	-	-	-	COG0557	K	ribonuclease R
ASC0315.1	-	-	-	-	-	-	+	-	-	-	-	-	-	+	COG0691	O	SsrA-binding protein
ASC0316.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein A2V17_04080
ASC0317.1	-	-	-	-	-	-	+	-	+	-	-	-	-	-	NA	NA	hypothetical protein A2V17_04085
ASC0318.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein A2V17_04090
ASC0323.1	-	-	-	-	-	-	+	-	-	-	-	-	-	-	NA	NA	clumping factor A
AFR72874.1	+	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	Putative coagulase
AFR72875.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	von Willebrand factor binding protein
ASC0361.1	-	-	-	-	-	-	+	-	-	-	-	-	-	-	NA	NA	hypothetical protein A2V17_04305
ASC0362.1	-	-	-	-	-	-	+	-	-	-	-	-	-	-	COG0463	M	glycosyl transferase family A
ASC0363.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	COG1396	K	DNA-binding protein
ASC0364.1	-	-	-	-	-	-	+	-	-	-	-	-	-	-	NA	NA	transcriptional regulator
ASC52276.1	-	-	-	-	-	-	+	-	-	-	-	-	-	-	NA	NA	hypothetical protein A2V17_04325
AFR72045.1	+	-	-	-	-	-	-	-	-	-	-	-	+	+	COG3316	X	putative transposase
ASC0366.1	-	-	-	-	-	-	+	+	-	-	-	-	-	-	NA	NA	hypothetical protein A2V17_04340
ASC0375.1	-	-	-	-	-	-	-	-	-	+	+	-	-	-	NA	NA	replication protein
ASC0386.1	-	-	-	-	-	-	+	-	+	-	-	-	-	-	NA	NA	hypothetical protein A2V17_04445
AFR72879.1	+	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	Hypothetical protein C248_0885
ASC0944.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein A2V17_07350
ASC0945.1	-	-	-	-	-	-	+	-	-	-	-	-	-	-	NA	NA	hypothetical protein A2V17_07355
AFR72046.1	+	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	HMG-CoA synthase
AFR72028.1	+	-	-	+	-	-	-	-	-	-	-	-	+	-	COG2021	E	putative hydrolase
AFR72887.1	+	-	-	-	-	-	-	-	-	-	-	-	-	-	COG0406	G	phosphoglycerate mutase family protein
ASC51455.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein A2V17_10200
ASC51456.1	-	-	-	-	-	-	+	-	+	-	-	-	-	-	NA	NA	hypothetical protein A2V17_10205
ASC51569.1	-	-	-	-	-	-	+	-	-	-	-	-	-	-	COG0394	T	arsenate reductase (thioredoxin)
ASC51570.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	ATP-binding protein
ASC51571.1	-	-	-	-	-	-	+	-	-	-	-	-	-	-	COG2801	X	transposase
ASC51572.1	-	-	-	-	-	-	+	-	-	-	-	-	+	-	COG1961	L	transposon DNA-invertase
ASC51573.1	-	-	-	-	-	-	+	+	-	-	-	-	-	-	COG3682	K	penicillinase repressor BlaI
ASC51574.1	-	-	-	-	-	-	+	+	-	-	-	-	-	-	COG2602	V	BlaR1 family beta-lactam sensor/signal transducer
ASC51575.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	COG2367	V	BlaZ family class A beta-lactamase
ASC51576.1	-	-	-	-	-	-	+	-	-	-	-	-	-	-	NA	NA	hypothetical protein A2V17_10870
ASC51577.1	-	-	-	-	-	-	+	-	-	-	-	-	-	-	COG0640	K	transcriptional regulator
ASC51578.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	COG0701	S	permease

ASC51579.1	-	-	-	-	-	-	-	+	-	-	-	-	-	-	NA	NA	methyltransferase
AFR72892.1	+	-	-	-	-	-	-	-	-	-	-	-	-	-	COG0778	C	nitroreductase family protein
AFR72964.1	-	-	-	-	-	-	-	-	-	-	-	-	+	COG0179	Q	fumarylacetoacetate (FAA) hydrolase family protein	
AFR72965.1	+	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	putative membrane protein	
ASC52030.1	-	-	-	-	-	-	-	-	+	-	-	-	-	NA	NA	hypothetical protein A2V17_13270	
ASC52031.1	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	Accumulation-associated protein	
AFR72047.1	+	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	putative membrane protein	
CCC86798.1	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	putative membrane protein	
CCC86799.1	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	putative exported protein	
CCC86800.1	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	conserved hypothetical protein	
CCC86801.1	-	-	-	-	-	-	-	-	-	-	-	-	-	COG2003	L	conserved hypothetical protein	
CCC86828.1	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	putative membrane protein	
CCC86829.1	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	hypothetical protein SARLGA251_00600	
CCC86830.1	-	-	-	-	-	-	-	+	+	-	-	-	-	NA	NA	hypothetical protein SARLGA251_00610	
AFR72967.1	+	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein C248_0973	
CCC86837.1	-	-	-	-	-	-	-	-	-	-	-	-	-	COG0589	T	hypothetical protein SARLGA251_00680	
CCC86840.1	-	-	-	-	-	-	-	+	-	-	-	-	-	COG2814	G	Major Facilitator Superfamily protein	
CCC86841.1	-	-	-	-	-	-	-	+	-	-	-	-	-	COG0655	C	conserved hypothetical protein	
AFR72969.1	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein C248_0975	
CCC86842.1	-	-	-	-	-	-	-	+	-	-	-	-	-	COG0583	K	LysR family regulatory protein	
CCC87126.1	-	-	-	-	-	-	-	+	+	-	-	-	-	COG1683	S	conserved hypothetical protein	
CCC87182.1	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	putative membrane protein	
CCC87223.1	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	hypothetical protein SARLGA251_04550	
AFR72048.1	-	-	-	-	-	-	-	-	-	-	-	-	+	COG0584	I	glycerophosphoryl diester phosphodiesterase	
CCC87516.1	-	-	-	-	-	-	-	+	-	-	-	+	-	NA	NA	pathogenicity island protein	
AFR72978.1	+	-	-	-	+	-	-	-	-	-	-	-	+	NA	NA	hypothetical protein C248_0984	
CCC87522.1	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	pathogenicity island protein	
CCC87523.1	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	pathogenicity island replication protein	
CCC87524.1	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	pathogenicity island protein	
CCC87527.1	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	pathogenicity island protein	
CCC87528.1	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	pathogenicity island protein	
CCC87536.1	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	pathogenicity island protein	
CCC87538.1	-	-	-	-	-	-	-	+	-	-	-	-	-	COG2035	S	putative membrane protein	
CCC87539.1	-	-	-	-	-	-	-	+	-	-	-	-	-	COG0396	O	ABC transporter ATP-binding protein	
CCC87540.1	-	-	-	-	-	-	-	+	-	-	-	-	-	COG0719	O	conserved hypothetical protein	
CCC87541.1	-	-	-	-	-	-	-	+	-	-	-	-	-	COG0520	E	putative selenocysteine lyase	
CCC87542.1	-	-	-	-	-	-	-	+	-	-	-	-	-	COG0822	O	NifU-like protein	
CCC87545.1	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	phage protein	
CCC87547.1	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	phage DNA-binding protein	
CCC87548.1	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	phage protein	
CCC87549.1	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	phage protein	
AFR72982.1	+	-	-	-	+	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein C248_0988	
CCC87565.1	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	phage protein	
CCC87568.1	-	-	-	-	-	-	-	+	-	+	-	-	+	NA	NA	phage protein	
CCC87582.1	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	phage protein	
CCC87589.1	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	phage protein	
AFR72986.1	+	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein C248_0992	
AFR72049.1	-	-	-	-	-	-	-	-	-	-	-	-	+	COG2030	I	acyl dehydratase	
AFR72988.1	+	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	Putative transposase	
CCC88454.1	-	-	-	-	-	-	-	+	-	-	-	-	-	COG0739	M	peptidase family M23/M37 protein	
CCC88458.1	-	-	-	-	-	-	-	+	-	+	-	-	-	COG3591	E	serine protease	

CCC88475.1	-	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	hypothetical protein SARLGA251_17100	
AFR72993.1	+	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein C248_0999	
CCC89034.1	-	-	-	-	-	-	-	-	+	+	-	-	-	-	NA	NA	putative helicase	
CCC89035.1	-	-	-	-	-	-	-	-	+	+	-	-	-	-	COG0494	V	putative NUDIX hydrolase	
AFR73173.1	+	-	-	-	-	+	+	-	+	+	-	-	-	+	+	COG0622	R	hypothetical protein C248_1181
AFR73174.1	+	-	-	+	-	+	+	-	-	-	-	-	-	+	+	NA	NA	Hypothetical protein C248_1182
AFR72050.1	+	-	-	-	-	-	-	-	+	-	-	-	-	+	+	COG0768	DM	penicillin-binding protein 2 prime
SaureusN305_00073	-	-	-	-	-	-	-	-	+	-	-	-	-	+	-	NA	NA	TSorf172 domain protein
SaureusN305_00074	-	-	-	-	-	-	-	-	+	-	-	-	-	+	-	NA	NA	hypothetical protein
AFR73175.1	+	-	-	+	-	+	+	-	+	+	-	-	-	+	+	NA	NA	putative exported protein
SaureusN305_00083	-	-	-	-	-	-	-	-	+	-	-	-	-	-	COG3591	E	Serine protease SpIC precursor	
SaureusN305_00084	-	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	Serine protease SpIC precursor	
AFR73176.1	+	-	-	+	-	+	+	-	+	+	-	-	-	+	+	NA	NA	FPRL1 inhibitory protein
AFR73177.1	+	-	-	+	-	+	+	-	+	+	-	-	-	+	+	NA	NA	putative membrane protein
SaureusN305_00161	-	-	-	-	-	-	-	-	+	-	-	+	-	+	COG0624	E	Putative dipeptidase	
SaureusN305_00368	-	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	hypothetical protein	
SaureusN305_00371	-	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	Surface protein G precursor	
AFR73178.1	+	-	+	-	+	+	-	+	+	-	-	-	-	+	+	NA	NA	fibrinogen-binding protein precursor
AFR73179.1	+	-	+	-	+	+	-	+	+	-	-	-	-	+	+	NA	NA	putative exported protein
SaureusN305_00384	-	-	-	-	-	-	-	-	+	+	-	-	-	+	-	NA	NA	hypothetical protein
SaureusN305_00385	-	-	-	-	-	-	-	-	+	-	-	-	-	+	-	NA	NA	putative sulfoacetate transporter SauU
SaureusN305_00386	-	-	-	-	-	-	-	-	+	-	-	-	-	+	-	COG0586	S	Inner membrane protein YqjA
SaureusN305_00626	-	-	-	-	-	-	-	-	+	-	-	-	-	-	COG0042	J	putative tRNA-dihydrouridine synthase	
AFR73180.1	+	-	-	-	+	+	-	+	+	-	-	-	-	+	+	NA	NA	Hypothetical protein C248_1188
SaureusN305_00637	-	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	1-phosphatidylinositol phosphodiesterase precursor	
AFR73181.1	+	-	-	-	+	+	-	+	+	-	-	-	-	+	+	NA	NA	hypothetical protein C248_1189
SaureusN305_00938	-	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	Helix-turn-helix	
SaureusN305_00939	-	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	Helix-turn-helix	
AFR73182.1	+	-	-	-	+	+	-	+	+	-	-	-	-	+	+	NA	NA	Alpha-hemolysin
SaureusN305_00948	-	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	hypothetical protein	
SaureusN305_00949	-	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	Aminodeoxyfualosine deaminase	
SaureusN305_00952	-	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	hypothetical protein	
SaureusN305_00953	-	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	hypothetical protein	
SaureusN305_00955	-	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	hypothetical protein	

AFR73183.1	+	-	+	+	+	+	-	+	+	-	-	-	+	+	NA	NA	hypothetical protein C248_1191
SaureusN305_00960	-	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	hypothetical protein
AFR73184.1	+	-	+	-	+	+	-	+	+	-	-	-	+	+	NA	NA	exotoxin
AFR72051.1	+	-	-	-	-	-	-	-	-	-	-	-	-	-	COG3316	X	Transposase for insertion sequence element IS431
AFR73185.1	+	-	+	-	+	+	-	+	+	-	-	-	+	+	NA	NA	exotoxin
SaureusN305_01293	-	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	Clumping factor A precursor
AFR73186.1	+	-	+	-	+	+	-	+	-	-	-	-	+	+	NA	NA	exotoxin
AFR73187.1	+	-	+	-	+	+	-	+	+	-	-	-	+	+	COG0078	E	ornithine carbamoyltransferase
AFR73188.1	+	-	+	-	+	+	-	+	+	-	-	-	+	+	COG0549	E	putative carbamate kinase
AFR73189.1	+	-	+	-	+	+	-	+	+	-	-	-	+	+	COG1288	R	putative membrane protein
AFR73190.1	-	-	-	-	+	-	-	+	+	-	-	-	-	-	NA	NA	putative membrane protein
SaureusN305_01842	-	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	hypothetical protein
SaureusN305_01843	-	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	hypothetical protein
SaureusN305_01851	-	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	hypothetical protein
SaureusN305_01852	-	-	-	-	-	-	-	-	+	-	-	-	-	-	COG0286	V	N-6 DNA Methylase
AFR73191.1	+	-	+	-	+	+	-	+	+	-	-	-	+	+	COG1275	V	exfoliative toxin A/B
SaureusN305_01854	-	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	hypothetical protein
SaureusN305_01856	-	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	hypothetical protein
SaureusN305_01858	-	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	hypothetical protein
SaureusN305_01860	-	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	hypothetical protein
AFR73192.1	+	-	+	-	+	+	-	+	+	-	-	-	+	+	NA	NA	putative DNA binding protein
SaureusN305_01889	-	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	Phage tail repeat like protein
SaureusN305_01890	-	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	hypothetical protein
AFR73193.1	+	-	+	-	+	+	-	+	+	-	-	-	-	+	NA	NA	antibacterial protein
SaureusN305_01962	-	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	Tyrosine recombinase XerD
SaureusN305_01963	-	-	-	-	-	-	-	-	+	-	-	-	-	-	COG0582	LX	site-specific tyrosine recombinase XerC
SaureusN305_01964	-	-	-	-	-	-	-	-	+	-	+	-	-	-	NA	NA	Host cell surface-exposed lipoprotein
SaureusN305_01965	-	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	hypothetical protein
SaureusN305_01966	-	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	transcriptional repressor DicA
SaureusN305_01968	-	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	hypothetical protein
SaureusN305_01969	-	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	hypothetical protein
SaureusN305_1970	-	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	hypothetical protein
SaureusN305_	-	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	hypothetical protein

SaureusN305_2006	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	hypothetical protein
SaureusN305_2007	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	hypothetical protein
SaureusN305_2008	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	Holin family protein
SaureusN305_2009	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	N-acetylmuramoyl-L-alanine amidase CwIA precursor
SaureusN305_2140	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	Extracellular matrix-binding protein EbhA
AFR73461.1	+	-	+	+	-	-	+	+	-	-	-	-	+	-	NA	NA	hypothetical protein C248_1471	
SaureusN305_2292	-	-	-	-	-	-	-	-	-	+	-	-	-	+	-	NA	NA	putative MFS-type transporter EfpA
SaureusN305_2293	-	-	-	-	-	-	-	-	-	+	-	-	-	+	-	NA	NA	hypothetical protein
SaureusN305_2295	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	hypothetical protein
SaureusN305_2299	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	COG0614	P	Iron(3+)-hydroxamate-binding protein PhuD precursor
SaureusN305_2300	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	COG3315	Q	Leucine carboxyl methyltransferase
SaureusN305_2303	-	-	-	-	-	-	-	-	-	+	-	+	-	-	-	NA	NA	putative leukocidin-like protein 1 precursor
SaureusN305_2309	-	-	-	-	-	-	-	-	-	+	-	+	-	-	+	COG1131	V	ABC transporter ATP-binding protein YtrB
SaureusN305_2310	-	-	-	-	-	-	-	-	-	+	-	+	-	-	+	NA	NA	hypothetical protein
SaureusN305_2312	-	-	-	-	-	-	-	-	-	+	-	+	-	-	+	NA	NA	ABC-2 family transporter protein
SaureusN305_2313	-	-	-	-	-	-	-	-	-	+	-	+	-	-	+	COG0526	O	hypothetical protein
SaureusN305_2314	-	-	-	-	-	-	-	-	-	+	-	+	-	-	+	NA	NA	hypothetical protein
SaureusN305_2315	-	-	-	-	-	-	-	-	-	+	-	+	-	-	+	NA	NA	hypothetical protein
SaureusN305_2316	-	-	-	-	-	-	-	-	-	+	-	+	-	-	-	NA	NA	hypothetical protein
SaureusN305_2317	-	-	-	-	-	-	-	-	-	+	-	+	-	-	-	COG4927	R	Acyl-coenzyme A:6-aminopenicillanic acid acyl-transferase
SaureusN305_2318	-	-	-	-	-	-	-	-	-	+	-	+	-	-	-	NA	NA	hypothetical protein
SaureusN305_2319	-	-	-	-	-	-	-	-	-	+	-	+	-	-	-	NA	NA	YolD-like protein
SaureusN305_2320	-	-	-	-	-	-	-	-	-	+	-	+	-	-	-	COG2706	G	6-phosphogluconolactonase
SaureusN305_2321	-	-	-	-	-	-	-	-	-	+	-	+	-	-	-	COG1012	C	Aldehyde dehydrogenase
SaureusN305_2322	-	-	-	-	-	-	-	-	-	+	-	+	-	-	-	COG1227	CP	putative manganese-dependent inorganic pyrophosphatase
SaureusN305_2323	-	-	-	-	-	-	-	-	-	+	-	+	-	-	-	COG1335	HR	Peroxyureidoacrylate/ureidoacrylate amidohydrolase RutB
SaureusN305_2324	-	-	-	-	-	-	-	-	-	+	-	+	-	-	-	NA	NA	Plasmin and fibronectin-binding protein A precursor

SaureusN305_2325	-	-	-	-	-	-	-	-	-	+	-	+	-	-	-	COG0471	G	Sodium-dependent dicarboxylate transporter SdcS
SaureusN305_2326	-	-	-	-	-	-	-	-	-	+	-	+	-	-	-	COG0077	E	P-protein
SaureusN305_2327	-	-	-	-	-	-	-	-	-	+	-	+	-	-	-	COG4362	P	Nitric oxide synthase oxygenase
SaureusN305_2328	-	-	-	-	-	-	-	-	-	+	-	+	-	-	-	COG1488	H	Nicotinate phosphoribosyltransferase pncB2
SaureusN305_2355	-	-	-	-	-	-	-	-	-	+	-	+	-	-	-	NA	NA	hypothetical protein
SaureusN305_2356	-	-	-	-	-	-	-	-	-	+	-	+	-	-	-	COG4758	S	hypothetical protein
SaureusN305_2357	-	-	-	-	-	-	-	-	-	+	-	+	-	-	-	COG4585	T	Sensor protein VraS
SaureusN305_2359	-	-	-	-	-	-	-	-	-	+	-	+	-	-	-	COG1295	S	hypothetical protein
SaureusN305_2360	-	-	-	-	-	-	-	-	-	+	-	+	-	-	-	NA	NA	hypothetical protein
SaureusN305_2361	-	-	-	-	-	-	-	-	-	+	-	+	+	-	-	COG0394	T	Low molecular weight protein-tyrosine-phosphatase PtpA
AFR72053.1	+	-	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	hypothetical protein C248_0039
SaureusN305_2362	-	-	-	-	-	-	-	-	-	+	-	+	+	-	-	NA	NA	hypothetical protein
SaureusN305_2363	-	-	-	-	-	-	-	-	-	+	-	+	+	-	-	COG2309	E	Aminopeptidase PepS
SaureusN305_2364	-	-	-	-	-	-	-	-	-	+	-	+	+	-	-	COG1607	I	putative acyl-CoA thioester hydrolase
SaureusN305_2365	-	-	-	-	-	-	-	-	-	+	-	+	+	-	-	COG0535	R	7-carboxy-7-deazaguanine synthase
SaureusN305_2366	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	hypothetical protein
SaureusN305_2367	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	COG0693	R	Putative cysteine protease YraA
SaureusN305_2368	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	COG0744	M	Monofunctional glycosyltransferase
SaureusN305_2369	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	COG2137	O	Regulatory protein RecX
SaureusN305_2370	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	hypothetical protein
SaureusN305_2371	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	COG1134	GM	Teichoic acids export ATP-binding protein TagH
SaureusN305_2431	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	Putative surface protein precursor
SaureusN305_2440	-	-	-	-	-	-	-	-	-	+	+	-	-	-	-	NA	NA	putative lipoprotein precursor
SaureusN305_2442	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	hypothetical protein
SaureusN305_2444	-	-	-	-	-	-	-	-	-	+	+	-	-	-	-	NA	NA	hypothetical protein
SaureusN305_2445	-	-	-	-	-	-	-	-	-	+	+	-	-	-	-	COG4221	C	putative oxidoreductase
AFR72054.1	+	-	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	hypothetical protein C248_0040
AFR73801.1	+	-	+	-	-	-	+	-	-	-	-	-	-	-	+	NA	NA	Hypothetical Protein C248_1811

SaureusNZMR 0322_01447	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	chromosome segregation protein
SaureusNZMR 0322_01754	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	ribulose-1,5-biphosphate synthetase
AFR73803.1	+	-	+	-	-	+	-	-	-	-	-	-	-	-	COG0054	H	6,7-dimethyl-8-ribityllumazine synthase	
AFR73835.1	+	-	+	-	+	+	-	-	-	-	-	-	+	+	NA	NA	putative lipoprotein	
SaureusNZMR 0322_01857	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein	
AFR73836.1	+	-	+	-	+	+	-	-	-	-	-	-	+	+	NA	NA	hypothetical protein C248_1846	
SaureusNZMR 0322_01897	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein	
SaureusNZMR 0322_02007	-	-	-	-	-	-	-	-	-	-	-	-	-	-	COG0533	J	tRNA N6-adenosine threonylcarbamoyltransferase	
SaureusNZMR 0322_02008	-	-	-	-	-	-	-	-	-	-	-	-	-	-	COG0456	J	ribosomal-protein-alanine N-acetyltransferase	
SaureusNZMR 0322_02009	-	-	-	-	-	-	-	-	-	-	-	-	-	-	COG1214	J	tRNA threonylcarbamoyladenine biosynthesis protein TsaB	
SaureusNZMR 0322_02010	-	-	-	-	-	-	-	-	-	-	-	-	-	-	COG0802	J	tRNA threonylcarbamoyladenine biosynthesis protein TsaE	
AFR73837.1	+	-	+	-	+	+	-	-	-	-	-	-	+	+	NA	NA	hypothetical protein C248_1847	
SaureusNZMR 0322_02011	-	-	-	-	-	-	-	-	-	-	-	-	-	-	COG0129	EG	Dihydroxy-acid dehydratase	
SaureusNZMR 0322_02020	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	Cell wall-associated hydrolase	
AFR73838.1	+	-	+	-	-	-	-	-	-	-	-	-	-	+	NA	NA	hypothetical protein C248_1848	
AFR73839.1	+	-	+	-	-	-	-	-	-	-	-	-	-	+	NA	NA	hypothetical protein C248_1849	
SaureusNZMR 0322_02123	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	Transposon Tn7 transposition protein TnsC	
SaureusNZMR 0322_02124	-	-	-	-	-	-	-	-	-	-	-	-	-	-	COG3464	X	Transposase	
SaureusNZMR 0322_02125	-	-	-	-	-	-	-	-	-	-	-	-	-	-	COG3666	X	Transposase DDE domain protein	
SaureusNZMR 0322_02126	-	-	-	-	-	-	-	-	-	-	-	-	-	-	COG3666	X	hypothetical protein	
AFR73840.1	+	-	+	-	-	-	-	-	-	-	-	-	-	+	NA	NA	hypothetical protein C248_1850	
AFR72055.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein C248_0041	
AFR73841.1	+	-	+	-	-	-	-	-	-	-	-	-	-	+	NA	NA	Transposase	
AFR73843.1	+	-	+	-	-	-	-	-	-	-	-	-	-	+	NA	NA	Hypothetical protein C248_1853	
SaureusNZMR 0322_02186	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein	
SaureusNZMR 0322_02187	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein	
SaureusNZMR 0322_02188	-	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	YopX protein	
AFR73844.1	+	-	+	-	+	-	-	-	-	-	-	-	+	+	NA	NA	hypothetical protein C248_1854	
AFR73845.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	putative exported protein	
SaureusNZMR 0322_02211	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein	
SaureusNZMR 0322_02212	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein	
AFR73846.1	+	-	+	-	-	-	-	-	-	-	-	-	+	+	NA	NA	hyaluronate lyase precursor 1	
AFR73847.1	+	-	+	-	+	+	-	-	-	-	-	-	+	+	NA	NA	putative exported protein	
SaureusNZMR	-	-	-	-	-	-	-	-	-	-	-	-	-	-	COG1251	C	Nitrite reductase (NAD(P)H)	

AFR72057.1	+	-	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	hypothetical protein C248_0043
ATV03361.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	Putative deoxyadenosine kinase protein
AFR74023.1	-	-	-	+	-	-	-	-	-	-	+	+	-	-	+	COG2183	K	putative RNA binding protein
ATV04437.1	-	-	-	-	-	-	-	-	-	-	-	+	+	-	-	NA	NA	Hypothetical protein SaO11_01611
ATV04473.1	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	NA	NA	hypothetical protein SaO11_01647
ATV04475.1	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	NA	NA	Putative membrane protein
ATV04477.1	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	NA	NA	NTPase
ATV04535.1	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	NA	NA	Phage protein
ATV04562.1	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	NA	NA	Phage protein
ATV04567.1	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	NA	NA	hypothetical protein SaO11_01741
ATV04572.1	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	NA	NA	hypothetical protein SaO11_01746
AFR72058.1	+	-	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	Hypothetical protein C248_0044
ATV04584.1	-	-	-	-	-	-	-	-	-	-	-	+	+	-	-	NA	NA	hypothetical protein SaO11_01758
AFR74376.1	+	-	+	+	-	-	-	-	-	-	-	+	-	-	+	COG5504	S	hypothetical protein C248_2436
ATV04604.1	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	COG0024	J	Putative metalloproteinase
ATV04605.1	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	COG4129	S	Putative membrane protein
ATV04606.1	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	NA	NA	Hypothetical protein SaO11_01780
ATV04607.1	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	COG3442	R	Hypothetical protein SaO11_01781
ATV04608.1	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	COG0769	M	Mur ligase family protein
ATV04609.1	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	COG1528	P	Ferritin
ATV04610.1	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	COG0847	L	Putative exonuclease
ATV04611.1	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	COG0389	L	ImpB/MucB/SamB family protein
ATV04612.1	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	NA	NA	Putative membrane protein
ATV04613.1	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	COG2265	J	Putative RNA methyltransferase
ATV04614.1	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	COG1597	IR	Hypothetical protein SaO11_01788
ATV04615.1	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	NA	NA	hypothetical protein SaO11_01789
ATV04616.1	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	COG0064	J	Glutamyl-tRNA amidotransferase subunit B
ATV04617.1	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	COG0154	J	Glutamyl-tRNA amidotransferase subunit A
ATV04618.1	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	COG0721	J	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit C
ATV04619.1	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	COG0591	E	High affinity proline permease
ATV04620.1	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	COG1733	K	Transcriptional regulator
ATV04621.1	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	COG2070	R	Nitronate monooxygenase
ATV04622.1	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	COG4851	R	Putative lipoprotein
ATV04623.1	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	COG0272	L	DNA ligase
ATV04624.1	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	COG0210	L	ATP-dependent DNA helicase
ATV04625.1	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	COG1646	I	PerB family protein
ATV04626.1	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	COG4496	S	hypothetical protein SaO11_01800
ATV04627.1	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	COG0015	F	Adenylosuccinate lyase
ATV04628.1	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	NA	NA	Staphopain A
ATV04629.1	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	COG4843	S	hypothetical protein SaO11_01803
ATV04630.1	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	COG0171	H	NAD(+) synthetase
ATV04638.1	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	NA	NA	hypothetical protein SaO11_01812
ATV04652.1	-	-	-	-	-	-	-	-	-	-	-	+	-	-	+	COG1725	K	GntR family transcriptional regulator
ATV04653.1	-	-	-	-	-	-	-	-	-	-	-	+	-	-	+	NA	NA	hypothetical protein SaO11_01827
ATV04654.1	-	-	-	-	-	-	-	-	-	-	-	+	-	-	+	COG0436	E	Hypothetical protein SaO11_01828
ATV04655.1	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	NA	NA	Extracellular adherence protein Eap/Map
ATV04656.1	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	NA	NA	Extracellular adherence protein of broad specificity
ATV04661.1	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	NA	NA	hypothetical protein SaO11_01835
ATV04666.1	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	COG0234	O	10 kDa chaperonin
ATV04667.1	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	COG1266	O	Putative membrane protein
ATV04668.1	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	NA	NA	Serine-aspartate repeat family protein, SdrH

ATV04669.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	COG3560	R	Hypothetical protein SaO11_01843
ATV04670.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	COG0388	R	Putative carbon-nitrogen hydrolase
ATV04671.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	Delta-hemolysin
ATV04672.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	Accessory regulator protein B
ATV04673.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	AgrD protein
ATV04674.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	Autoinducer sensor AgrC
ATV04675.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	COG3279	KT	DNA-binding response regulator
ATV04676.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	COG0524	G	hypothetical protein SaO11_01850
ATV04677.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	COG1621	G	Invertase
ATV04678.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	COG1609	K	Sucrose operon repressor
AFR72059.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein C248_0045
ATV04679.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	COG0004	P	Ammonium transporter family protein
ATV04680.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	COG0425	O	SirA family protein
ATV04681.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	COG2391	R	Membrane protein
ATV04682.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	COG2344	K	Hypothetical protein SaO11_01856
ATV04683.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	ABC transporter ATP-binding protein
ATV04684.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	COG0249	L	Putative membrane protein
ATV04691.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	Acetolactate synthase 1 regulatory subunit
ATV04704.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	COG2337	V	Endoribonuclease MazF
ATV05031.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	Addiction module antitoxin
AUG72740.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein SAO46_00265
AUG72752.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	Nuclease
AFR74393.1	+	-	-	-	-	+	+	+	+	-	-	-	-	-	-	COG0803	P	putative solute binding lipoprotein
AUG72754.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein SAO46_00280
AUG72755.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	PVL ORF-50-like family protein
AFR74394.1	+	-	-	-	-	+	+	+	+	-	-	-	-	-	-	COG1651	O	putative lipoprotein
AFR72060.1	-	-	-	-	-	-	+	+	+	-	-	-	-	-	-	COG1961	L	Recombinase CcrC
AUG72767.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein SAO46_00293
AFR74395.1	+	-	-	-	-	+	+	+	+	-	-	-	-	-	-	NA	NA	putative lipoprotein
AFR74488.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	COG1109	G	putative phosphomannomutase
AUG72787.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	Phage protein
AUG72790.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	Phage-like protein
AUG72791.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	XkdX family protein
AFR74489.1	+	-	-	+	+	+	-	+	+	+	-	+	+	-	-	NA	NA	putative exported protein
AFR74490.1	-	-	-	+	+	-	-	-	+	+	-	-	+	+	-	NA	NA	putative membrane protein
AFR74491.1	+	-	-	+	+	+	+	+	+	+	-	+	+	+	-	COG1210	M	UTP--glucose-1-phosphate uridylyltransferase
AFR74492.1	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	Fibronectin-binding protein A
AUG74185.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	Nitrogen regulation protein NIFR3
AFR74494.1	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	Fibronectin binding protein precursor
AFR74493.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	Hypothetical protein C248_2553
AFR74495.1	+	-	-	+	+	+	+	+	+	+	-	+	+	+	-	NA	NA	Fibronectin-binding protein A
AUG74243.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	Phage protein
AFR74496.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	Hypothetical protein C248_2556
AFR72061.1	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	Hypothetical protein C248_0047
AUG74246.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein SAO46_01835
AUG74249.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein SAO46_01838
AUG74250.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	COG0305	L	DNA helicase, phage-associated
AFR74497.1	-	-	-	-	+	+	+	+	+	+	-	+	+	+	-	COG2610	GR	putative gluconate permease
AUG74263.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein SAO46_01852
AFR74498.1	+	-	-	+	+	+	+	+	+	+	-	+	+	+	-	COG1070	G	putative gluconokinase
AUG74264.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein SAO46_01853

AFR74499.1	+	-	+	+	-	+	-	+	+	+	-	+	+	+	COG1802	K	gluconate operon transcriptional repressor
AFR74500.1	+	-	+	+	-	+	-	-	+	+	+	+	+	+	COG0789	K	MerR family regulatory protein
AFR74501.1	-	-	+	+	-	+	-	-	+	+	-	+	+	+	COG2357	FT	hypothetical protein C248_2561
AFR74502.1	+	-	+	+	-	-	-	-	+	+	-	+	+	+	COG4876	S	hypothetical protein C248_2562
AFR74503.1	+	-	+	+	-	-	-	-	+	+	-	+	+	+	COG1289	S	putative membrane protein
AFR72480.1	+	+	+	-	+	-	-	+	+	+	-	-	-	+	COG2963	X	Transposase
AFR72481.1	+	+	+	-	+	-	-	+	+	-	-	-	-	-	NA	NA	hypothetical protein C248_0468
AFR72482.1	-	+	-	-	+	-	-	-	+	+	-	-	-	-	COG3759	S	Hypothetical Protein C248_0469
AFR72062.1	+	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	hypothetical protein C248_0048
CAI79713.1	-	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	conserved hypothetical protein
CAI79714.1	-	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	probable enterotoxin protein
AFR72483.1	+	+	+	-	+	-	-	+	+	-	-	-	-	-	COG0702	R	hypothetical protein C248_0470
CAI79911.1	-	-	-	-	-	-	-	-	-	-	-	-	-	+	COG4842	S	conserved hypothetical protein
CAI79912.1	-	-	-	-	-	-	-	-	-	-	-	-	-	+	COG1511	S	probable membrane protein
CAI79914.1	-	-	-	-	-	-	-	-	-	-	-	-	-	+	COG5417	S	conserved hypothetical protein
CAI79915.1	-	-	-	-	-	-	-	-	-	-	-	-	-	+	COG4499	S	probable membrane protein
CAI79916.1	-	-	-	-	-	-	-	-	-	-	-	-	-	+	COG1674	D	probable DNA segregation ATPase and related
CAI79917.1	-	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	hypothetical protein SAB0229
CAI79918.1	-	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	hypothetical protein SAB0230
CAI79919.1	-	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	hypothetical protein SAB0231
CAI79920.1	-	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	hypothetical protein SAB0232
AFR72485.1	+	+	+	-	+	-	-	+	+	-	-	-	-	-	NA	NA	superantigen-like protein
CAI79922.1	-	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	conserved hypothetical protein
CAI79923.1	-	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	hypothetical protein SAB0235
CAI79924.1	-	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	truncated hypothetical protein
CAI79929.1	-	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	probable membrane protein
CAI79930.1	-	-	-	-	-	-	-	-	-	-	-	-	-	+	COG2116	P	probable formate/nitrite transport protein
CAI79931.1	-	-	-	-	-	-	-	-	-	-	-	-	-	+	COG1114	E	probable branched-chain amino acid transport system
AFR72486.1	+	+	+	-	+	-	-	+	+	-	-	-	-	-	NA	NA	exotoxin
CAI80035.1	-	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	hypothetical bovine pathogenicity island protein
CAI80036.1	-	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	bovine pathogenicity island protein Orf17
AFR72487.1	-	+	-	-	+	-	-	-	+	+	-	-	-	-	NA	NA	exotoxin
CAI80042.1	-	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	bovine pathogenicity island protein Orf10
AFR72488.1	+	+	+	-	+	-	-	+	+	-	-	-	-	-	NA	NA	Exotoxin
CAI80078.1	-	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	probable lipoprotein
CAI80079.1	-	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	hypothetical protein SAB0391
AFR72490.1	+	+	+	-	+	-	-	+	+	-	-	-	-	-	NA	NA	superantigen-like protein
AFR72492.1	+	+	+	-	+	-	-	+	+	-	-	-	-	-	NA	NA	exotoxin 1
AFR72493.1	+	+	+	-	+	-	-	+	+	-	-	-	-	-	NA	NA	exotoxin 5
CAI80428.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein SAB0740
AFR72494.1	+	+	+	-	+	+	-	+	+	-	-	-	-	+	NA	NA	exotoxin 4
CAI80432.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	truncated clumping factor
AFR72495.1	-	+	+	-	+	+	-	+	+	-	-	-	-	+	COG0286	V	putative type I restriction enzyme modification
AFR72063.1	+	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	hypothetical protein C248_0049
CAI80711.1	-	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	probable membrane protein
AFR72496.1	+	+	+	-	+	+	-	+	+	-	-	-	-	+	COG0732	V	Restriction modification system DNA specificity subunit
AFR72497.1	+	+	+	-	+	-	-	+	+	-	+	-	-	-	NA	NA	Exotoxin type C
CAI80726.1	-	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	hypothetical protein SAB1038
CAI80978.1	-	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	truncated cell surface fibronectin-binding protein
Saureus08S 00974_00415	-	+	+	-	+	-	-	+	+	-	+	+	+	+	NA	NA	hypothetical protein
CAI80979.1	-	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	truncated cell surface fibronectin-binding protein

CAI80980.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	NA	NA	truncated cell surface fibronectin-binding protein
CAI80981.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	NA	NA	truncated cell surface fibronectin-binding protein
CAI80982.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	NA	NA	truncated cell surface fibronectin-binding protein
CAI80984.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	NA	NA	hypothetical protein SABI295
CAI80985.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	COG0604	CR	probable alcohol dehydrogenase
CAI80986.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	COG1846	K	conserved hypothetical protein
CAI80989.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	NA	NA	truncated cell surface fibronectin-binding protein
AFR72500.1	-	+	+	-	-	+	-	-	-	-	-	-	-	+	+	-	NA	NA	putative exported protein
AFR72501.1	+	+	+	-	+	-	-	-	+	-	-	-	-	-	+	-	NA	NA	putative lipoprotein
CAI81349.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	NA	NA	conserved hypothetical protein
CAI81350.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	NA	NA	conserved hypothetical protein
AFR72502.1	+	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	putative lipoprotein
CAI81359.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	COG3591	E	serine proteinase
CAI81363.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	NA	NA	hypothetical protein SABI674c, partial
AFR72503.1	+	+	+	+	+	-	-	-	+	+	-	-	-	-	+	+	NA	NA	putative lipoprotein
AFR72504.1	-	+	+	-	-	+	+	-	-	+	+	-	-	-	+	-	NA	NA	putative lipoprotein
CAI81377.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	NA	NA	hypothetical protein SABI688
CAI81378.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	NA	NA	hypothetical protein SABI689c
CAI81381.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	NA	NA	hypothetical protein SABI692
CAI81384.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	NA	NA	hypothetical protein SABI695
CAI81385.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	NA	NA	enterotoxin G
AFR72505.1	+	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	putative lipoprotein
CAI81387.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	NA	NA	enterotoxin type C variant
CAI81391.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	NA	NA	hypothetical protein SABI702c
CAI81394.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	NA	NA	phage-related tail fiber
AFR72506.1	+	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	putative lipoprotein
AFR72064.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein C248_0050
AFR72507.1	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	putative lipoprotein
CAI81413.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	NA	NA	hypothetical phage-related protein
CAI81416.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	COG3728	X	hypothetical mobile-element-associated protein
AFR72508.1	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	putative lipoprotein
CAI81420.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	NA	NA	hypothetical phage-related protein
AFR72509.1	+	+	+	-	+	-	-	-	+	-	-	-	-	-	+	-	NA	NA	putative lipoprotein
AFR72510.1	+	+	+	-	-	-	-	-	+	-	-	-	-	-	+	-	NA	NA	hypothetical protein C248_0497
CAI81439.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	NA	NA	hypothetical protein SABI750c
CAI81441.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	NA	NA	hypothetical protein SABI752c
CAI81444.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	NA	NA	phage anti-repressor protein
CAI81445.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	NA	NA	hypothetical phage-related protein
CAI81447.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	NA	NA	hypothetical protein SABI758
AFR72511.1	-	+	+	-	-	+	-	-	-	-	-	-	-	-	+	-	NA	NA	hypothetical protein C248_0498
CAI81448.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	NA	NA	hypothetical protein SABI759
CAI81450.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	NA	NA	hypothetical protein SABI761c
CAI81452.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	COG1232	H	protoporphyrinogen oxidase
CAI81453.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	COG0276	H	ferrochelatase
CAI81454.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	COG0407	H	uroporphyrinogen decarboxylase
CAI81567.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	NA	NA	truncated hypothetical protein
CAI81568.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	COG0697	GER	hypothetical protein SABI879c
AFR72512.1	-	-	-	-	-	+	-	-	-	-	-	-	-	-	+	-	NA	NA	hypothetical protein C248_0499
CAI81570.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	NA	NA	hypothetical protein SABI881c
CAI81577.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	NA	NA	hypothetical protein SABI888c
CAI81579.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	NA	NA	hypothetical protein SABI890

AFR72513.1	+	+	-	-	+	-	-	+	-	-	+	-	-	NA	NA	putative membrane protein
CAI81582.1	-	-	-	-	-	-	-	-	-	-	-	+	-	NA	NA	hypothetical protein SAB1893c
CAI81589.1	-	-	-	-	-	-	-	-	-	-	-	+	-	NA	NA	hypothetical protein SAB1900c
CAI81590.1	-	-	-	-	-	-	-	-	-	-	-	+	-	NA	NA	hypothetical protein SAB1901c
Saureus08S 00974_00487	-	+	+	-	-	-	-	-	-	+	-	-	-	COG0037	J	tRNA(Ile)-lysidine synthase
AFR72575.1	+	+	-	+	-	-	-	-	+	+	-	-	-	COG0634	F	putative hypoxanthine phosphoribosyltransferase
AFR72576.1	-	+	-	+	-	-	-	-	+	+	-	-	+	COG0465	O	putative cell division protein
AFR72065.1	+	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	type I restriction-modification system restriction subunit
CAI81734.1	-	-	-	-	-	-	-	-	-	-	-	+	-	COG3464	X	transposase
CAI81735.1	-	-	-	-	-	-	-	-	-	-	-	+	-	COG3464	X	probable transposase
CAI81740.1	-	-	-	-	-	-	-	-	-	-	-	+	-	COG1272	U	probable hemolysin
AFR72577.1	+	+	+	+	-	-	-	+	+	+	-	-	+	COG1281	O	putative chaperonin
AFR72578.1	+	+	+	+	-	-	+	+	+	+	-	-	+	COG0031	E	Cysteine synthase
CAI82058.1	-	-	-	-	-	-	-	-	-	-	-	+	-	NA	NA	hypothetical protein SAB2370c
AFR72579.1	-	+	-	+	-	-	-	-	+	+	-	-	+	COG0294	H	dihydropteroate synthase
CAI82064.1	-	-	-	-	-	-	-	-	-	-	-	+	-	NA	NA	hypothetical protein SAB2376c
AFR72580.1	+	+	+	+	-	-	+	+	+	+	-	-	+	COG1539	H	dihydroneopterin aldolase
CAI82075.1	-	-	-	-	-	-	-	-	-	-	-	+	-	NA	NA	hypothetical protein SAB2387
AFR72581.1	+	+	+	+	-	-	+	+	+	+	-	-	+	COG0801	H	putative 2-amino-4-hydroxy-6-hydroxymethylidihydropteridine pyrophosphokinase
YP_005732836	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	conserved hypothetical protein
YP_00573283	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	conserved hypothetical protein
AFR72583.1	+	+	+	+	-	-	+	+	+	+	-	-	+	COG1190	J	lysyl-tRNA synthetase
YP_00573283	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	conserved hypothetical protein
YP_005732840	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	conserved hypothetical protein
YP_005732842	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	conserved hypothetical protein
YP_005732844	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	conserved hypothetical protein
YP_005732846	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	conserved hypothetical protein
YP_005732847	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	conserved hypothetical protein
AFR72584.1	+	+	+	+	-	-	+	+	+	+	-	-	+	COG1167	KE	GntR family regulatory protein
YP_005732849	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	probable HMG-CoA synthase
Saureus08S 00974_00545	-	+	+	+	-	+	-	+	+	+	+	-	+	COG0590	J	tRNA-specific adenosine deaminase
YP_005732865	-	-	-	-	-	-	-	-	-	-	-	-	+	COG0550	L	DNA topoisomerase III
YP_005732866	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	conserved hypothetical protein
YP_005732867	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	cassette chromosome recombinase A
YP_005732868	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	conserved hypothetical protein
AFR72991.1	-	-	-	-	-	-	-	-	-	-	-	-	-	COG0561	HR	putative haloacid dehalogenase-like hydrolase
YP_005732869	-	-	-	-	-	-	-	-	-	-	-	-	+	COG2217	P	cadmium-translocating P-type ATPase
YP_005732870	-	-	-	-	-	-	-	-	-	-	-	-	+	COG0607	P	metallo-beta-lactamase family protein
YP_005732871	-	-	-	-	-	-	-	-	-	-	-	-	+	COG0491	R	metallo-beta-lactamase family protein
YP_005732875	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	copper P-type ATPase AtkB
YP_005732876	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	lipoprotein, putative
Saureus08S 00974_00547	-	+	+	+	-	+	-	+	+	+	+	-	+	COG0431	C	FMN-dependent NADPH-azoreductase
AFR72066.1	-	-	-	-	-	-	-	-	-	-	-	-	-	COG1518	V	CasI family protein
AFR72030.1	+	-	+	-	-	+	-	+	-	-	-	+	+	COG3887	T	putative membrane protein
YP_005733149	-	-	-	-	-	-	-	-	-	-	-	-	+	COG1396	K	repressor
YP_005733150	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	conserved hypothetical protein
YP_005733151	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	phage regulatory protein, Rha family
YP_005733153	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	conserved hypothetical protein

YP_005733155	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	conserved hypothetical protein
Saureus08S 00974_00548	-	+	+	+	-	+	-	-	-	-	-	-	-	-	-	+	NA	NA	Serine-aspartate repeat-containing protein C precursor
Saureus08S 00974_00549	-	+	+	+	-	+	-	-	-	-	-	-	-	-	-	+	NA	NA	Serine-aspartate repeat-containing protein D precursor
YP_005733169	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	conserved hypothetical protein
Saureus08S 00974_00550	-	+	+	+	-	+	-	-	-	-	-	-	-	-	-	+	NA	NA	Serine-aspartate repeat-containing protein E precursor
Saureus08S 00974_00551	-	+	+	+	-	+	-	-	-	-	-	-	-	-	-	+	COG0438	M	putative poly(glycerol-phosphate) alpha-glucosyltransferase
YP_005733195	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	prophage L54a, tail tape measure protein,
Saureus08S 00974_00552	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	+	COG2826	X	Integrase core domain protein
Saureus08S 00974_00553	-	+	+	+	-	+	-	-	-	-	-	-	-	-	-	+	COG0438	M	putative poly(glycerol-phosphate) alpha-glucosyltransferase
Saureus08S 00974_00554	-	+	-	-	-	-	-	-	-	-	+	-	-	-	-	+	COG1469	H	GTP cyclohydrolase FofE2
Saureus08S 00974_00555	-	+	-	-	-	-	-	-	-	-	+	-	-	-	-	+	COG2120	G	Mycothiol S-conjugate amidase
Saureus08S 00974_00556	-	+	-	-	-	-	-	-	-	-	-	+	-	-	-	+	NA	NA	hypothetical protein
YP_005733447	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	COG0546	C	indigoidine synthesis protein
Saureus08S 00974_00557	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	+	COG0363	G	Glucosamine-6-phosphate deaminase
AFR72067.1	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	CRISPR-associated protein Cas2
YP_005733664	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	clumping factor A
YP_005733665	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	hypothetical protein SAPIG0865
YP_005733666	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	lpxtg-motif cell wall anchor domain
Saureus08S 00974_00558	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	+	COG0269	G	3-hexulose-6-phosphate synthase
Saureus08S 00974_00559	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	+	COG0794	GM	3-hexulose-6-phosphate isomerase
YP_005733749	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	COG1074	L	recombination helicase AddA
AFR72867.1	-	+	+	+	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	hypothetical protein C248_0873
AFR72868.1	+	+	+	+	-	-	+	-	+	+	-	-	+	+	+	+	NA	NA	putative lipoprotein
YP_005733767	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	conjugative transposon protein
YP_005733949	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	hypothetical protein SAPIG1152
AFR72871.1	+	+	+	+	-	-	+	-	+	+	-	-	+	+	+	+	NA	NA	putative membrane protein
AFR72872.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	COG3153	R	putative acetyltransferase
AFR72873.1	+	+	+	+	-	-	-	-	-	-	+	-	-	-	-	-	NA	NA	clumping factor
YP_005734281	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	conserved hypothetical protein
AFR72475.1	-	-	-	+	-	+	-	-	+	+	-	-	+	+	+	+	NA	NA	secreted von Willebrand factor-binding protein precursor
YP_005734284	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	conserved hypothetical protein
YP_005734285	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	hypothetical protein SAPIG1489
YP_005734286	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	conserved hypothetical protein
AFR72876.1	+	+	+	+	-	-	+	-	+	+	-	-	+	+	+	+	NA	NA	putative exported protein
YP_005734292	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	conserved hypothetical protein
YP_005734293	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	hypothetical phage-related protein
AFR72877.1	+	+	+	+	-	-	+	-	+	+	-	-	+	+	+	+	NA	NA	hypothetical protein C248_0883
AFR72068.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	COG1353	V	CRISPR-associated Csm1 family protein
AFR72878.1	+	+	+	+	-	-	+	-	+	+	-	-	+	+	+	+	COG1525	L	thermonuclease precursor
AFR72880.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	COG1278	K	putative cold shock protein

AFR72881.1	+	+	+	+	-	-	+	-	+	+	-	-	-	NA	NA	hypothetical protein C248_0887
AFR72882.1	+	+	+	+	-	-	+	-	+	+	-	-	+	NA	NA	hypothetical protein C248_0888
YP_005734599	-	-	-	-	-	-	-	-	-	-	-	-	+	COG0115	EH	D-amino acid aminotransferase
AFR72883.1	+	+	+	+	-	-	+	-	+	+	-	-	+	NA	NA	putative exported protein
AFR72884.1	+	+	+	+	-	-	+	-	+	+	-	-	+	NA	NA	Hypothetical protein C248_0890
Saureus08S 00974_00791	-	+	+	+	-	-	+	-	+	+	-	-	-	NA	NA	hypothetical protein
YP_005734680	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	conserved hypothetical protein
YP_005734789	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	conserved hypothetical protein
YP_005734790	-	-	-	-	-	-	-	-	-	-	-	-	+	COG2826	X	transposase InsI for insertion sequence element
AFR72885.1	+	+	+	+	-	-	+	-	+	+	-	-	+	NA	NA	hypothetical protein C248_0891
YP_005734791	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	N-region of transposase of
YP_005734793	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	conserved hypothetical protein
YP_005734794	-	-	-	-	-	-	-	-	-	-	-	-	+	COG3942	M	transfer complex protein TraG
YP_005734795	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	membrane protein, putative
YP_005734796	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	ftsk/spoiii family protein
YP_005734797	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	ftsk/spoiii family protein
YP_005734798	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	conserved hypothetical protein
YP_005734799	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	conserved hypothetical protein
YP_005734800	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	conserved hypothetical protein
AFR72886.1	+	+	+	+	-	-	+	-	+	+	-	-	+	NA	NA	Hypothetical protein C248_0892
YP_005734801	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	conserved hypothetical protein
YP_005734802	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	replication initiation factor family protein
YP_005734803	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	replication initiation factor family protein
YP_005734804	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	conserved hypothetical protein
YP_005734805	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	conserved hypothetical protein
YP_005734806	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	conserved hypothetical protein
YP_005734807	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	conserved hypothetical protein
Saureus08S 00974_00794	-	+	+	+	-	-	+	-	+	+	-	-	+	COG0406	G	Putative phosphoserine phosphatase 2
AFR72069.1	+	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	CRISPR-associated Csm2 protein
AFR72888.1	+	+	+	+	-	-	+	-	+	+	-	-	+	COG1279	E	putative LysE type translocator protein
YP_005734970	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	transcriptional antiterminator, BglG family/DNA-binding protein
AFR72889.1	+	+	+	+	-	-	+	-	+	+	-	-	+	COG1670	JO	hypothetical protein C248_0895
AFR72890.1	+	+	+	+	-	-	+	-	+	+	-	-	+	COG1764	V	OsmC-like protein
AFR72891.1	+	+	+	+	-	-	+	-	+	+	-	-	+	COG0710	E	putative type I 3-dehydroquinase
AFR72966.1	+	+	+	+	-	-	+	-	+	+	-	-	+	NA	NA	Putative transposon integrase
AFR72968.1	+	+	+	+	-	-	+	-	+	+	-	-	+	NA	NA	Hypothetical protein C248_0974
AFR72970.1	+	+	+	+	-	-	+	-	+	+	-	-	+	NA	NA	hypothetical protein C248_0976
AFR72971.1	+	+	+	+	-	-	+	-	+	+	-	-	+	NA	NA	hypothetical protein C248_0977
AFR72972.1	+	+	+	+	-	-	+	-	+	+	-	-	+	COG1396	K	transcriptional regulator, putative
AFR72973.1	+	+	+	+	-	-	+	-	+	+	-	-	+	COG0480	J	tetracycline resistance protein
AFR72070.1	+	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	CRISPR-associated RAMP protein, Csm3 family
AFR72974.1	+	+	+	+	-	-	+	-	+	+	-	-	+	NA	NA	Hypothetical protein C248_0980
AFR72975.1	+	+	+	+	-	-	+	-	+	+	-	-	+	COG0791	M	hypothetical protein C248_0981
AFR72976.1	+	+	+	+	-	-	+	-	+	+	-	-	+	NA	NA	Hypothetical protein C248_0982
AFR72977.1	+	+	+	+	-	-	+	-	+	+	-	-	+	COG0433	L	hypothetical protein C248_0983
AFR72979.1	+	+	+	+	-	-	+	-	+	+	-	-	+	NA	NA	Antirestriction protein
AFR72980.1	+	+	+	+	-	-	+	-	+	+	-	-	+	NA	NA	hypothetical protein C248_0986
AFR72981.1	+	+	+	+	-	-	+	-	+	+	-	-	+	NA	NA	Transcriptional regulator
AFR72983.1	+	+	+	+	-	-	+	-	+	+	-	-	+	COG1674	D	hypothetical protein C248_0989
AFR72984.1	+	+	+	+	-	-	+	-	+	+	-	-	+	NA	NA	hypothetical protein C248_0990

AFR72985.1	+	+	-	+	-	-	-	-	-	+	-	-	-	-	NA	NA	hypothetical protein C248_0991
AFR72071.1	+	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	CRISPR-associated RAMP protein
AFR72987.1	-	-	+	-	-	-	-	-	-	+	-	-	-	+	COG3666	X	putative transposase
AFR72989.1	+	-	-	-	-	-	-	-	-	+	-	-	-	+	NA	NA	Putative transposase
AFR72990.1	+	+	-	+	-	-	-	-	-	+	-	-	-	+	COG0446	I	coenzyme A disulfide reductase
AFR72992.1	+	+	-	+	-	-	-	-	-	+	-	-	-	-	COG2151	O	hypothetical protein C248_0998
AFR72994.1	+	+	-	+	-	-	-	-	-	+	-	-	-	-	NA	NA	putative membrane protein
AFR72995.1	-	+	+	+	-	-	-	-	-	+	-	-	-	-	COG0542	O	putative ATPase subunit of an ATP-dependent
AFR73458.1	+	+	+	+	+	+	+	+	+	-	+	+	+	+	NA	NA	hypothetical protein C248_1468
AFR73459.1	+	+	+	+	+	+	+	+	+	-	+	+	+	+	COG1413	R	Conserved virulence factor C
AFR73460.1	-	+	+	+	+	+	+	+	+	-	+	+	+	+	NA	NA	hypothetical protein C248_1470
AFR72072.1	+	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	CRISPR-associated RAMP protein, Csm5 family
AFR73462.1	+	+	+	+	+	+	+	+	+	-	+	+	+	+	COG1738	S	putative membrane protein
AFR73463.1	+	+	+	+	+	+	+	+	+	-	+	+	+	+	COG0328	L	hypothetical protein C248_1473
AFR73464.1	+	+	+	+	-	-	-	-	+	-	-	-	-	+	NA	NA	Extracellular matrix-binding protein ebbB
Saureus08S 00974_01342	-	+	+	+	+	+	+	+	+	+	-	+	+	+	NA	NA	Quinolone resistance protein NorB
Saureus08S 00974_01343	-	+	+	+	+	+	+	+	+	+	-	+	+	+	COG0531	E	Serine/threonine exchanger SteT
Saureus08S 00974_01344	-	+	+	+	+	+	+	+	+	+	-	+	+	+	COG1171	E	L-threonine dehydratase catabolic TdcB
Saureus08S 00974_01345	-	+	+	-	+	+	+	+	+	-	+	-	-	+	COG0686	E	Alanine dehydrogenase 1
Saureus08S 00974_01346	-	+	-	-	-	-	-	-	+	-	-	-	-	-	COG0258	L	5'-3' exonuclease
Saureus08S 00974_01397	-	+	-	+	-	+	+	+	+	+	-	-	+	+	NA	NA	Bacteriophage holin
AFR72382.1	-	-	+	+	+	+	+	+	+	+	+	+	+	+	NA	NA	putative phage protein
AFR72073.1	+	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	CRISPR-associated protein, Csm6 family
AFR72381.1	+	+	-	+	+	+	+	+	+	+	-	-	-	+	NA	NA	putative phage protein
AFR72380.1	+	+	-	+	+	+	+	+	+	+	-	-	-	+	NA	NA	putative phage protein
AFR72379.1	+	+	-	+	+	+	+	+	+	+	-	+	-	+	NA	NA	putative phage protein
AFR72378.1	-	+	+	+	+	+	+	+	+	+	+	+	+	+	NA	NA	putative phage protein
AFR72377.1	+	+	-	-	+	+	+	+	+	+	-	-	-	+	NA	NA	putative phage protein
AFR72376.1	+	+	-	-	+	+	+	+	+	+	+	+	-	+	NA	NA	putative phage protein
AFR72375.1	-	+	-	-	+	+	+	+	+	+	-	-	-	+	NA	NA	putative phage protein
AFR72374.1	+	+	-	-	+	-	+	-	-	+	+	+	-	+	NA	NA	putative phage protein
AFR72373.1	+	+	-	-	+	+	+	+	+	+	+	+	-	+	NA	NA	hypothetical protein C248_0360
AFR72372.1	+	+	-	-	+	+	+	+	+	+	+	+	-	+	NA	NA	hypothetical protein C248_0359
AFR72074.1	+	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	CRISPR-associated protein C
AFR72371.1	-	+	-	-	+	+	+	+	+	+	+	+	-	+	COG5492	R	major tail protein
AFR73789.1	+	+	+	-	-	+	+	+	+	+	-	-	+	-	NA	NA	putative exported protein
AFR73790.1	+	+	+	+	+	+	+	+	+	+	-	+	+	+	COG1187	J	RNA pseudouridine synthase
AFR73791.1	-	-	+	+	+	+	+	+	+	+	+	+	+	+	COG2244	M	Polysaccharide biosynthesis protein
AFR73792.1	+	+	+	+	+	+	+	+	+	+	+	+	+	+	COG2081	R	putative exported protein
AFR73793.1	+	+	+	+	-	-	-	+	+	+	+	+	-	+	NA	NA	putative surface anchored protein
AFR73794.1	+	+	+	+	+	+	+	+	+	+	+	+	+	+	COG0607	P	hypothetical protein C248_1804
AFR73795.1	+	+	+	+	+	+	+	+	+	+	+	+	+	+	COG0495	J	leucyl-tRNA synthetase
AFR73796.1	-	+	+	+	+	+	+	+	+	+	+	+	+	+	COG2814	G	putative membrane protein
AFR73797.1	+	+	+	+	+	+	+	+	+	+	+	+	+	+	COG1242	R	hypothetical protein C248_1807
AFR72075.1	+	-	+	+	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein C248_0061
AFR73798.1	-	-	+	+	+	+	+	+	+	+	-	+	+	+	COG0500	QR	hypothetical protein C248_1808

AFR73799.1	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	COG1846	K	Toxin repressor
AFR73800.1	+	+	+	+	+	+	+	+	+	-	-	+	+	+	+	COG2267	I	hypothetical protein C248_1810
AFR73802.1	-	-	-	-	-	+	-	-	-	-	+	-	+	+	COG0506	E	proline dehydrogenase	
Saureus08S 00974_01807	+	-	-	+	-	-	-	-	-	-	+	-	+	-	-	COG0219	J	tRNA (cytidine(34)-2'-O)-methyltransferase
Saureus08S 00974_01808	-	+	-	+	-	-	+	-	-	-	+	-	+	-	-	COG1600	J	Epoxyqueuosine reductase
Saureus08S 00974_01809	-	+	-	+	-	-	+	-	-	+	+	+	+	+	+	COG1126	E	L-cystine import ATP-binding protein TcyC
Saureus08S 00974_01810	-	+	-	+	-	-	+	-	-	-	+	-	+	-	-	COG0834	ET	Arginine transport system permease protein ArtQ
Saureus08S 00974_01811	-	+	-	+	-	-	+	-	-	-	+	-	+	-	-	COG3641	S	Phosphotransferase system, EIIC
Saureus08S 00974_01841	-	+	-	+	-	-	+	-	-	+	+	-	+	-	-	COG0735	P	Peroxide-responsive repressor PerR
AFR72076.1	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	Putative transposase
AFR72031.1	-	-	-	-	-	+	-	-	-	-	-	-	-	+	+	COG0359	J	50S ribosomal protein L9
Saureus08S00974_01	-	+	-	+	-	-	+	-	-	+	+	-	+	-	-	COG0111	HR	Glyoxylate/hydroxyppyruvate reductase B
Saureus08S 00974_01843	-	+	-	+	-	-	+	-	-	+	+	-	+	-	-	COG1225	O	Putative peroxiredoxin bep
Saureus08S 00974_01844	-	+	-	+	-	-	+	-	-	+	+	-	+	-	-	COG0001	H	Glutamate-1-semialdehyde 2,1-aminomutase 2
Saureus08S 00974_01845	-	+	-	+	-	-	+	-	-	+	+	-	+	-	-	COG4129	S	Fusaric acid resistance protein family protein
Saureus08S 00974_01846	-	+	-	+	-	-	+	-	-	+	+	-	+	-	-	COG1132	V	Putative multidrug export ATP-binding/permease protein
Saureus08S 00974_01847	-	+	-	+	-	-	+	-	-	+	+	-	+	-	-	COG3557	S	hypothetical protein
Saureus08S 00974_01848	-	+	-	+	-	-	+	-	-	+	+	-	+	-	-	COG1194	L	putative A/G-specific adenine glycosylase YfbQ
Saureus08S 00974_01849	-	+	-	+	-	-	+	-	-	+	+	-	+	-	-	COG1988	R	hypothetical protein
Saureus08S 00974_02069	-	+	-	-	-	+	-	-	-	-	-	-	-	-	-	COG3666	X	Transposase DDE domain protein
Saureus08S 00974_02070	-	+	-	-	-	-	-	-	-	-	+	-	-	-	-	COG0449	M	Glutamine--fructose-6-phosphate aminotransferase
AFR72077.1	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	COG4584	X	Hypothetical protein C248_0063
Saureus08S 00974_02071	-	+	+	-	-	-	+	-	-	-	+	+	-	+	-	COG2213	G	PTS system mannitol-specific EIICB component
AFR74134.1	+	+	+	-	-	-	+	-	-	-	+	+	+	+	-	COG1762	GT	putative transcriptional antiterminator
AFR74135.1	-	+	+	+	-	-	+	-	-	-	+	+	-	+	+	COG4668	G	PTS system, mannitol-specific IIA component
AFR74136.1	+	+	+	+	-	-	+	+	-	-	+	+	+	+	+	COG0246	G	putative mannitol-1-phosphate 5-dehydrogenase
AFR74137.1	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	NA	NA	fntB protein
AFR74138.1	+	+	+	+	-	-	+	+	-	-	+	+	+	+	+	COG1109	G	putative phosphoglucosamine mutase
AFR74139.1	+	+	+	+	-	-	+	+	-	-	+	+	+	+	+	COG4856	S	putative exported protein
AFR74140.1	+	+	+	+	-	-	+	+	-	-	+	+	+	+	+	COG1624	T	putative membrane protein
AFR74141.1	+	+	+	+	-	-	+	+	-	-	+	+	+	+	+	COG0010	E	arginase
AFR74142.1	+	+	+	+	-	-	+	+	-	-	+	+	+	+	+	NA	NA	hypothetical protein C248_2202
AFR72078.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	putative transposase
AFR74143.1	+	+	+	-	-	-	-	-	-	-	+	-	-	+	+	COG2814	G	Putative multidrug resistance transporter
Saureus08S 00974_02088	-	+	-	-	-	-	-	-	-	-	-	-	-	+	-	NA	NA	Multidrug resistance efflux pump SepA
Saureus08S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	COG0477	GFBR	Multidrug resistance protein 3

00974_02089																COG077	CLASS	putative membrane protein
AFR74377.1	+	+	-	-	+	+	+	-	-	+	-	-	+	+	COG0789	K	HTH-type transcriptional activator tipA	
AFR74378.1	-	-	-	-	+	+	-	-	+	+	+	-	+	+	COG2197	TK	putative response regulator	
AFR74379.1	+	+	-	-	+	+	+	+	-	+	+	+	+	+	COG4585	T	putative histidine kinase	
AFR74380.1	+	+	-	-	+	+	-	+	-	+	+	+	+	+	COG2203	T	hypothetical protein C248_2440	
AFR74381.1	+	+	-	-	+	+	+	+	-	+	+	+	+	+	COG2181	CP	putative nitrate reductase gamma chain	
AFR74382.1	+	+	-	-	+	+	+	+	-	+	+	+	+	+	COG2180	CPO	respiratory nitrate reductase delta chain	
AFR74383.1	-	+	-	-	+	+	-	-	-	+	+	-	+	+	COG1140	CP	nitrate reductase beta chain	
AFR72079.1	+	-	-	+	-	-	-	-	-	-	-	-	-	+	COG1484	L	IstB-like ATP binding protein	
AFR74384.1	+	+	-	-	+	+	+	+	-	+	+	+	+	+	COG5013	CP	nitrate reductase alpha chain	
AFR74385.1	-	+	-	-	+	+	-	-	-	+	+	+	+	+	COG0007	H	Tetrapyrrole methyltransferase	
AFR74386.1	+	+	-	-	+	+	+	+	-	+	+	+	+	+	COG2146	PQ	assimilatory nitrite reductase small subunit	
AFR74387.1	+	+	-	-	+	+	-	+	-	+	+	+	+	+	COG1251	C	nitrite reductase large subunit	
AFR74388.1	+	+	-	-	+	+	+	+	-	+	+	+	+	+	COG2138	H	Regulatory protein	
AFR74389.1	+	+	-	-	+	+	+	+	-	+	+	+	+	+	NA	NA	acetyltransferase GNAT family protein	
AFR74390.1	-	+	-	-	+	+	-	-	-	+	+	+	+	+	COG2116	P	putative nitrite transporter	
AFR74391.1	+	+	-	-	+	+	+	+	-	+	+	+	+	+	NA	NA	putative membrane protein	
AFR74392.1	+	+	-	-	+	+	+	+	-	-	+	+	+	+	COG3832	S	hypothetical protein C248_2452	
AFR72080.1	-	-	-	+	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein C248_0066	
AFH68375.1	-	-	+	-	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein ST398NM01_2800	
AFH68381.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein ST398NM01_2801	
AFR72081.1	+	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	Transposase	
AFH68713.1	-	-	+	-	-	-	-	-	-	-	-	-	-	-	NA	NA	Hypothetical protein ST398NM01_2819	
AFR72336.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	putative phage protein	
AFH68721.1	-	-	+	-	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein ST398NM01_2821	
AFR72337.1	+	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein C248_0324	
AFR72338.1	-	-	-	-	+	+	-	-	-	-	-	-	-	+	NA	NA	putative DNA-binding protein	
AFR72339.1	+	-	+	-	-	+	+	-	+	+	+	+	-	-	NA	NA	putative phage protein	
AFH68744.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein ST398NM01_0516	
AFH68746.1	-	-	+	-	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein ST398NM01_2822	
AFH68747.1	-	-	+	-	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein ST398NM01_2823	
AFR72340.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	putative phage protein	
AFR72032.1	+	-	+	-	-	+	-	+	-	-	-	-	+	+	COG0305	L	DnaB-like helicase	
AFH68763.1	-	-	+	-	-	+	-	-	-	-	+	-	+	-	NA	NA	Acetyltransferase	
AFH68764.1	-	-	-	-	-	-	-	-	-	-	+	-	+	-	COG5438	S	putative membrane spanning protein	
AFH68765.1	-	-	+	-	-	-	+	-	-	-	+	+	+	-	COG5438	S	putative membrane spanning protein	
AFH68766.1	-	-	+	-	-	-	-	-	-	-	+	+	+	-	COG0583	K	Glc	
AFH68767.1	-	-	+	-	-	-	+	-	-	-	+	+	-	-	COG0070	E	Glutamate synthase [NADPH] large chain	
AFR72341.1	+	-	-	-	-	-	-	-	-	-	-	+	-	+	NA	NA	putative phage protein	
AFH68768.1	-	-	-	-	-	-	-	-	-	-	-	+	-	-	COG0493	ER	Glutamate synthase [NADPH] small chain	
AFH68769.1	-	-	-	+	-	-	+	-	-	-	-	+	+	-	COG1264	G	PTS system, trehalose-specific IIBC component	
AFH68770.1	-	-	-	+	-	-	+	-	-	-	-	+	+	-	COG0366	G	Trehalose-6-phosphate hydrolase	
AFH68771.1	-	-	+	-	-	-	-	-	-	-	-	-	+	-	COG2188	K	Trehalose operon transcriptional repressor	
AFH68772.1	-	-	-	+	-	-	+	-	-	-	-	+	+	-	COG3153	R	Acetyltransferase	
AFH68773.1	-	-	-	+	-	-	+	-	-	-	-	+	+	-	COG2812	L	DNA polymerase III subunit gamma/tau	
AFH68774.1	-	-	+	+	-	-	+	+	-	-	-	+	+	-	COG0718	R	putative transcriptional regulatory protein	
AFH68775.1	-	-	+	+	-	-	+	+	-	-	-	+	-	-	COG0353	L	RecR	
AFH68776.1	-	-	-	+	-	-	-	-	-	-	-	-	-	-	NA	NA	Arginine decarboxylase	
AFH68777.1	-	-	+	+	-	-	+	+	-	-	-	-	-	-	COG0125	F	Thymidylate kinase	
AFR72342.1	+	-	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	putative phage protein	
AFH68778.1	-	-	-	+	-	-	-	-	-	-	-	-	-	-	COG3870	S	putative cytosolic protein	

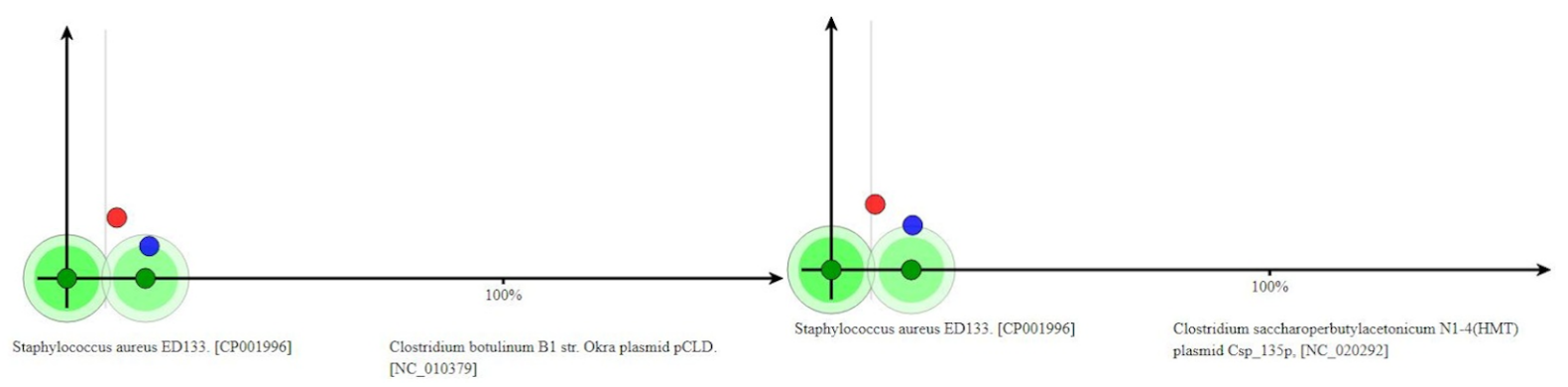
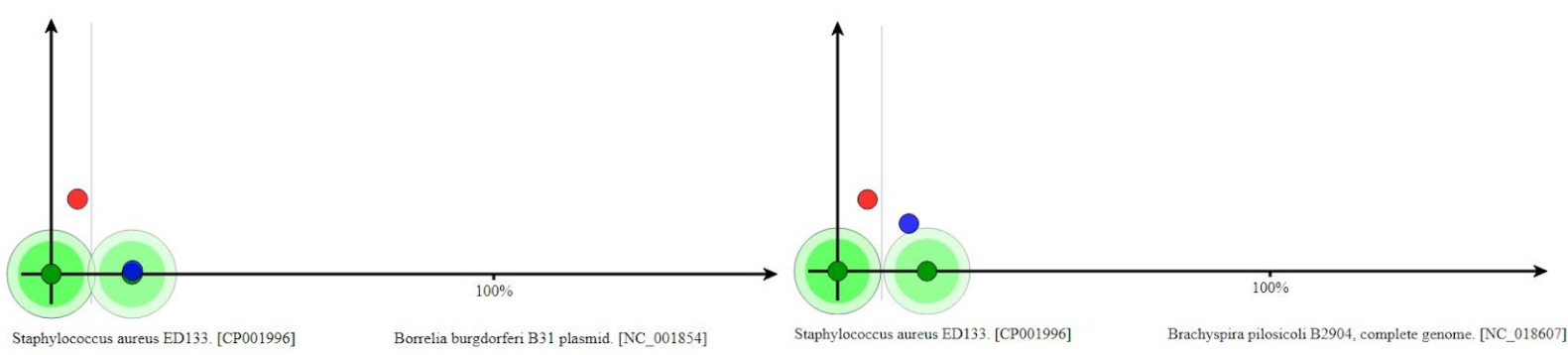
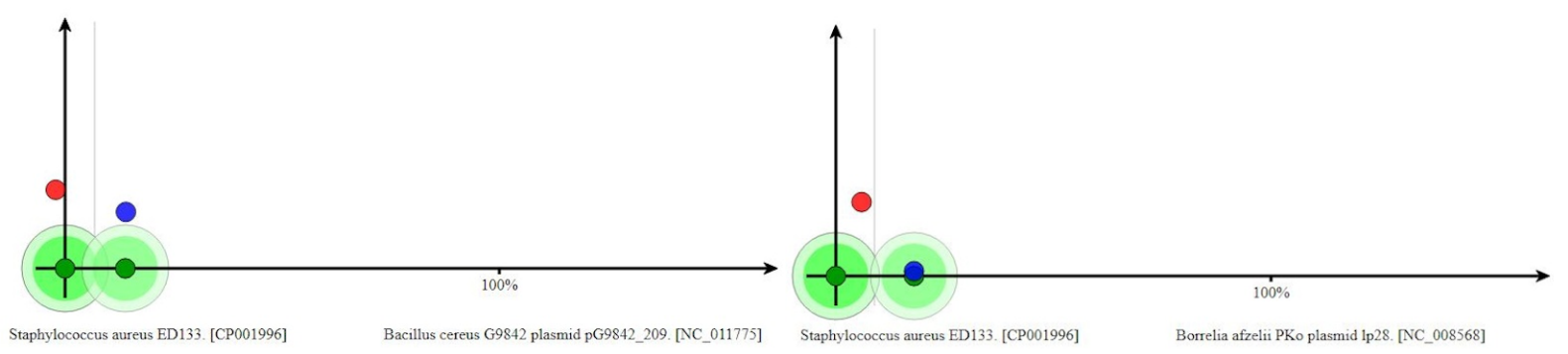
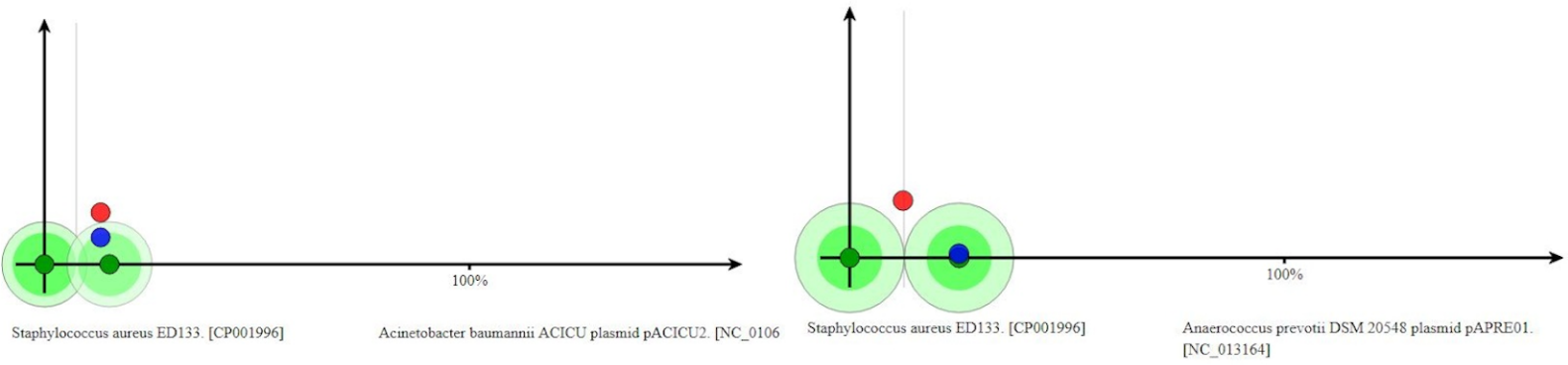
AFH68779.1	-	-	+	+	-	-	-	+	-	-	-	-	-	NA	NA	DNA polymerase III, delta' subunit
AFH68780.1	-	-	+	+	-	-	-	+	-	-	-	-	-	COG1774	T	Phosphorelay inhibitor
AFH68781.1	-	-	+	+	-	-	-	-	-	-	-	-	-	COG4467	L	Initiation-control protein
AFR72343.1	+	-	-	-	-	-	-	-	-	-	+	-	+	NA	NA	putative phage protein
AFH68815.1	-	-	-	+	-	-	-	+	-	-	-	-	+	COG0214	H	Pyridoxine biosynthesis protein
AFH68816.1	-	-	-	+	-	-	+	-	-	+	-	-	-	COG0311	H	Pyridoxine biosynthesis amidotransferase
AFH68817.1	-	-	+	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein ST398NM01_2825
AFH68818.1	-	-	-	-	-	-	-	-	-	-	-	-	-	COG1972	F	hypothetical protein ST398NM01_0596
AFH68819.1	-	-	+	-	-	-	-	-	-	-	-	-	-	COG4463	K	CtsR
AFH68820.1	-	-	+	-	-	-	-	-	-	-	-	-	-	COG3880	O	ClpC ATPase
AFH68850.1	-	-	+	-	-	-	-	+	-	+	-	-	-	COG1069	G	L-ribulokinase
AFH68851.1	-	-	-	+	-	-	+	-	+	+	-	-	-	COG0451	M	L-threonine 3-dhydrogenase
AFR72344.1	+	-	-	-	-	-	-	-	-	-	-	-	+	NA	NA	putative DNA polymerase
AFH68852.1	-	-	+	-	-	+	-	+	-	+	-	-	+	COG0115	EH	Branched-chain amino acid aminotransferase
AFH68853.1	-	-	+	-	-	+	-	+	-	+	-	-	+	COG0546	C	Putative phosphatase
AFH68854.1	-	-	-	+	-	-	+	-	+	-	-	-	+	COG1428	F	Deoxyadenosine kinase
AFH68855.1	-	-	+	+	-	+	-	+	-	+	-	-	+	COG1428	F	Deoxyguanosine kinase
AFR72345.1	+	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	Hypothetical protein C248_0332
AFH69094.1	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein ST398NM01_2845
AFR72346.1	+	-	-	+	+	+	+	+	-	+	+	+	-	NA	NA	Hypothetical Protein C248_0333
AFR72347.1	+	-	-	+	+	+	+	+	-	+	-	-	+	NA	NA	PVL ORF-50-like family
AFR72348.1	+	-	+	+	-	+	+	+	+	+	+	+	+	NA	NA	putative phage protein
AFH69378.1	-	-	+	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein ST398NM01_2861
AFH69379.1	-	-	-	-	+	-	-	-	-	-	-	+	-	NA	NA	hypothetical protein ST398NM01_2862
AFR72349.1	+	-	+	+	+	+	+	+	-	+	-	-	+	NA	NA	PVL orf 52-like protein
AFR72350.1	+	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	Putative dUTP pyrophosphatase
AFR72033.1	-	-	-	-	-	+	-	-	-	-	+	+	+	COG0104	F	putative adenylosuccinate synthetase
AFR72351.1	+	-	-	-	-	-	+	-	-	-	-	-	-	NA	NA	concerned hypothetical protein
AFR72352.1	+	-	-	+	-	-	-	-	+	-	-	-	-	NA	NA	hypothetical protein C248_0339
AFR72353.1	+	-	+	+	+	-	-	-	-	-	-	-	+	NA	NA	putative phage protein
AFR72354.1	+	-	+	+	-	+	+	+	-	+	+	+	+	NA	NA	Transcriptional activator RinB
AFH70181.1	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein ST398NM01_1156
AFH70182.1	-	-	+	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein ST398NM01_2911
AFH70183.1	-	-	+	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein ST398NM01_2912
AFH70185.1	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	Chemotaxis-inhibiting protein
AFH70188.1	-	-	+	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein ST398NM01_2914
AFR72355.1	+	-	-	-	+	+	-	-	-	+	+	+	+	NA	NA	Hypothetical protein C248_0342
AFH70190.1	-	-	+	-	-	+	-	-	-	+	+	-	-	NA	NA	hypothetical protein ST398NM01_2915
AFH70191.1	-	-	+	-	-	+	-	-	-	+	-	-	-	NA	NA	hypothetical protein ST398NM01_2916
AFH70192.1	-	-	-	-	+	+	-	-	-	+	+	-	-	NA	NA	Phage-related protein
AFH70193.1	-	-	+	-	+	+	-	-	-	+	+	-	-	NA	NA	Phage-related protein
AFH70194.1	-	-	+	-	-	+	-	-	-	+	+	-	-	COG0739	M	hypothetical protein ST398NM01_2919
AFH70195.1	-	-	-	-	-	+	-	-	-	-	-	-	-	NA	NA	hypothetical protein ST398NM01_2920
AFH70196.1	-	-	+	-	-	+	-	-	-	+	-	-	-	NA	NA	hypothetical protein ST398NM01_2921
AFH70197.1	-	-	+	-	-	+	-	-	-	-	-	-	-	NA	NA	Phage protein
AFH70198.1	-	-	+	-	-	+	-	-	-	+	-	-	-	NA	NA	prophage pi2 protein 39
AFH70199.1	-	-	+	-	-	+	-	-	-	+	-	-	-	NA	NA	hypothetical protein ST398NM01_2924
AFR72356.1	-	-	-	-	-	+	-	-	-	-	-	-	+	NA	NA	E family protein
AFH70201.1	-	-	+	-	-	+	-	-	-	+	-	-	-	NA	NA	Phage protein
AFH70202.1	-	-	+	-	-	+	-	-	-	+	-	-	-	NA	NA	Gp6 protein
AFH70203.1	-	-	-	-	-	+	-	-	-	+	-	-	+	NA	NA	Phage protein

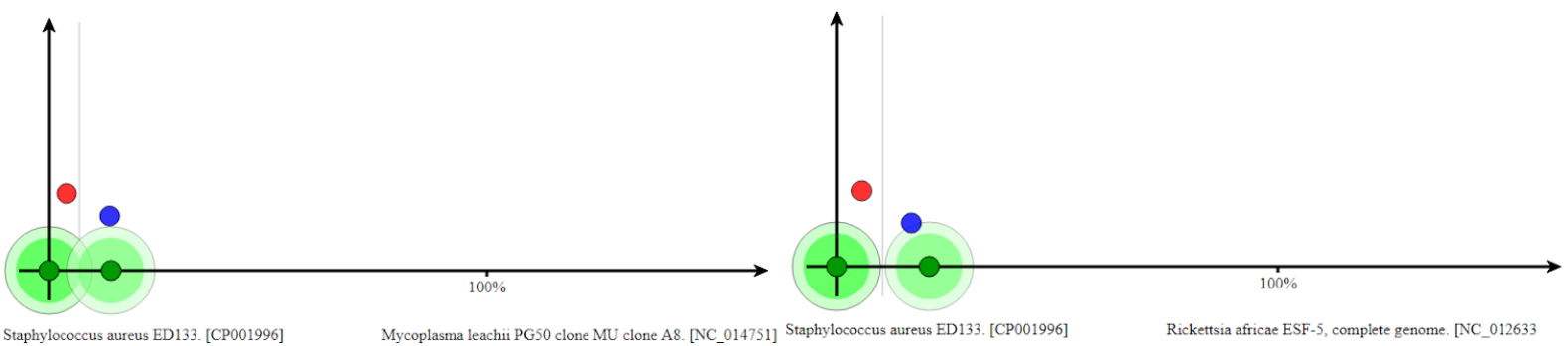
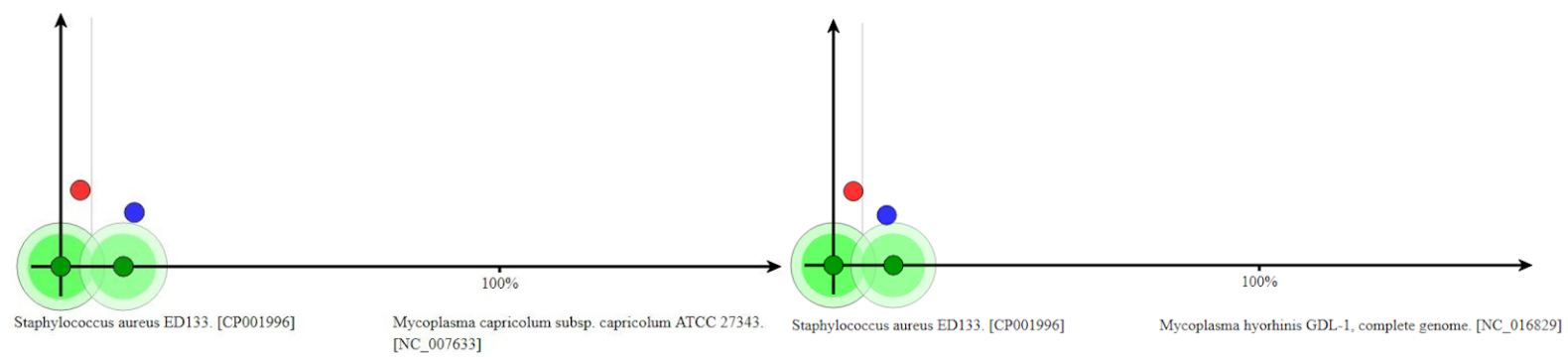
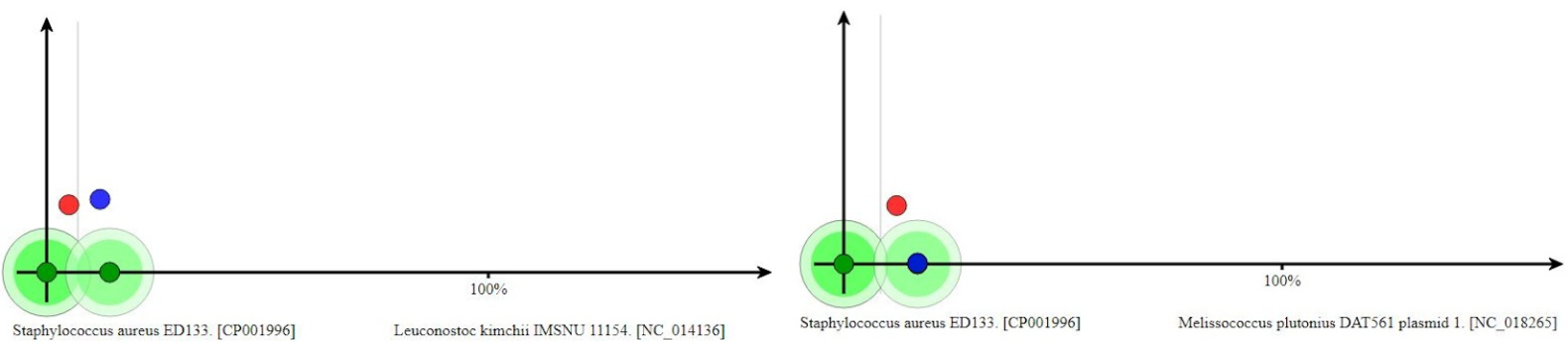
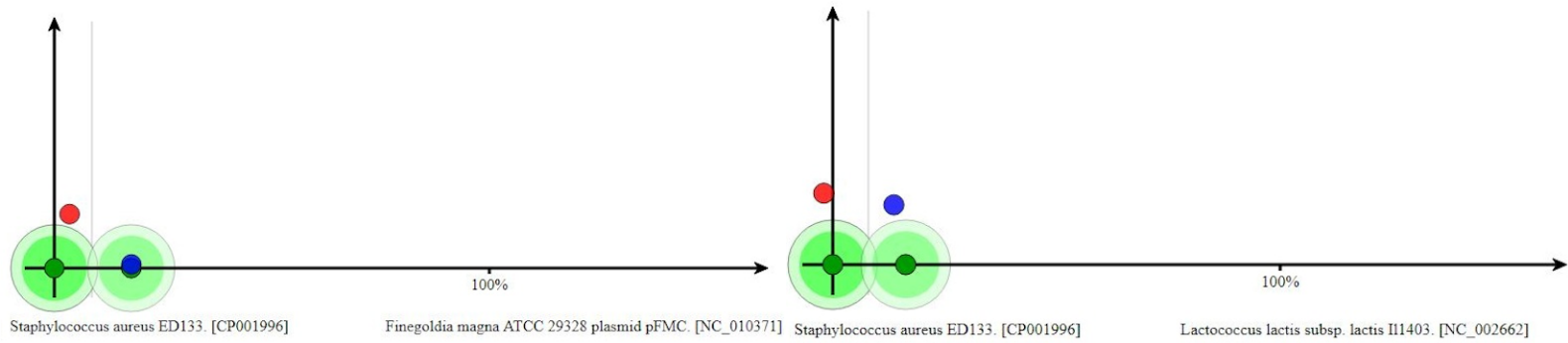
AFH70204.1	-	-	+	-	-	+	-	-	-	+	-	-	-	-	NA	NA	Major capsid protein
AFH70205.1	-	-	+	-	-	+	-	-	-	+	-	-	-	-	COG0740	O	CipP
AFH70206.1	-	-	+	-	-	+	-	-	-	+	-	-	-	-	NA	NA	Portal protein
AFH70208.1	-	-	+	-	-	+	-	-	-	+	-	-	-	-	NA	NA	Phage-related protein
AFH70209.1	-	-	+	-	-	+	-	-	-	+	-	-	-	-	NA	NA	hypothetical protein ST398NM01_2932
AFR72357.1	+	-	-	-	-	+	-	-	-	-	-	+	-	+	NA	NA	hypothetical protein C248_0344
AFH70210.1	-	-	+	-	-	+	-	-	-	+	-	-	-	-	COG1403	V	HNH endonuclease family protein
AFH70211.1	-	-	-	-	+	+	-	-	-	+	-	-	-	-	NA	NA	Phage transcriptional activator
AFH70215.1	-	-	+	+	+	+	+	+	-	+	+	+	+	+	NA	NA	hypothetical protein ST398NM01_0362
AFH70216.1	-	-	+	-	+	+	-	+	-	-	-	-	-	-	NA	NA	Deoxyuridine 5'-triphosphate nucleotidohydrolase
AFH70217.1	-	-	+	-	-	-	-	-	+	-	-	-	-	-	NA	NA	hypothetical protein ST398NM01_2936
AFH70218.1	-	-	+	+	+	+	+	+	-	-	+	+	+	+	NA	NA	Phage protein
AFH70219.1	-	-	+	-	-	-	-	-	-	-	-	-	-	-	NA	NA	Hypothetical protein ST398NM01_2937
AFR72358.1	+	-	-	-	-	+	-	-	-	-	-	+	-	+	COG0553	KL	putative phage protein
AFH70222.1	-	-	+	+	+	+	-	-	-	-	-	-	-	-	NA	NA	Phage protein
AFH70223.1	-	-	+	-	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein ST398NM01_2940
AFH70224.1	-	-	+	-	-	-	-	-	+	-	-	-	-	-	NA	NA	Phage protein
AFH70225.1	-	-	+	-	+	+	+	+	+	-	+	+	+	-	COG0629	L	Single-strand DNA binding protein
AFH70226.1	-	-	+	-	-	-	-	-	-	-	-	-	-	-	NA	NA	Metal-dependent hydrolase
AFH70227.1	-	-	+	-	-	-	-	-	-	-	-	-	-	-	NA	NA	Rect
AFH70228.1	-	-	+	-	-	-	-	-	-	-	-	-	-	-	NA	NA	Hypothetical protein ST398NM01_2945
AFH70229.1	-	-	+	-	-	-	-	-	+	-	-	-	-	-	NA	NA	hypothetical protein ST398NM01_2946
AFR72359.1	+	-	-	-	-	+	+	+	-	-	+	+	+	+	NA	NA	phage regulatory protein
AFH70230.1	-	-	+	-	-	+	+	+	+	+	+	+	+	-	NA	NA	putative cytosolic protein
AFH70231.1	-	-	+	-	-	+	+	+	-	+	-	-	+	-	NA	NA	putative cytosolic protein
AFH70232.1	-	-	+	-	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein ST398NM01_2949
AFH70234.1	-	-	+	-	-	-	-	-	-	+	-	-	-	-	COG4707	X	Hypothetical protein ST398NM01_2951
AFH70235.1	-	-	+	-	-	-	-	-	-	+	-	-	-	-	NA	NA	hypothetical protein ST398NM01_2952
AFH70236.1	-	-	+	-	-	+	-	-	-	+	-	+	-	-	NA	NA	Phage protein
AFH70237.1	-	-	+	-	+	+	+	+	+	+	+	+	+	-	COG3645	X	Phage antirepressor protein
AFH70238.1	-	-	+	-	-	-	-	-	-	-	-	-	-	-	NA	NA	Phage protein
AFH70239.1	-	-	+	-	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein ST398NM01_2956
AFR72360.1	+	-	-	-	+	+	-	-	-	-	+	+	-	+	COG1403	V	HNH endonuclease family protein
AFR72034.1	+	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	Hypothetical Protein C248_0020
AFH70240.1	-	-	+	-	-	-	-	-	-	-	-	-	-	-	NA	NA	Phage transcriptional regulator, Cro/C1 family
AFH70241.1	-	-	+	-	+	+	-	-	-	+	-	+	+	-	COG1396	K	Phage transcriptional repressor
AFH70242.1	-	-	+	-	-	-	-	-	-	-	-	-	-	-	NA	NA	DNA polymerase III alpha subunit
AFH70243.1	-	-	+	-	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein ST398NM01_2959
AFH70244.1	-	-	+	-	-	-	-	-	-	+	+	-	-	-	NA	NA	putative cytosolic protein
AFH70247.1	-	-	+	-	-	-	-	-	+	-	+	-	-	-	NA	NA	Sphingomyelin phosphodiesterase
AFR72361.1	+	-	-	-	+	+	+	+	-	+	+	+	-	+	NA	NA	terminase small subunit
AFH70405.1	-	-	+	-	-	-	-	-	-	-	-	-	-	-	NA	NA	Mannitol-1-phosphate 5-dehydrogenase
AFH70412.1	-	-	+	-	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein ST398NM01_2970
AFH70413.1	-	-	+	-	-	-	-	-	-	-	-	-	-	-	COG0489	D	ApoC
AFR72362.1	+	-	+	-	+	+	-	-	-	+	-	+	-	+	COG4626	X	terminase large subunit
AFH70762.1	-	-	+	+	-	-	-	-	-	+	-	-	+	-	NA	NA	Type II restriction-modification system methylation subunit
AFH70769.1	-	-	+	+	-	-	-	-	-	+	-	-	+	-	NA	NA	Fibronectin-binding protein
AFR72363.1	-	-	+	-	+	+	-	-	-	+	+	-	-	-	NA	NA	portal protein
APE87178.1	-	-	-	+	-	-	-	-	-	-	-	-	-	+	NA	NA	hypothetical protein AS852_00350
APE87179.1	-	-	-	+	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein AS852_00355
APE87181.1	-	-	-	+	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein AS852_00365

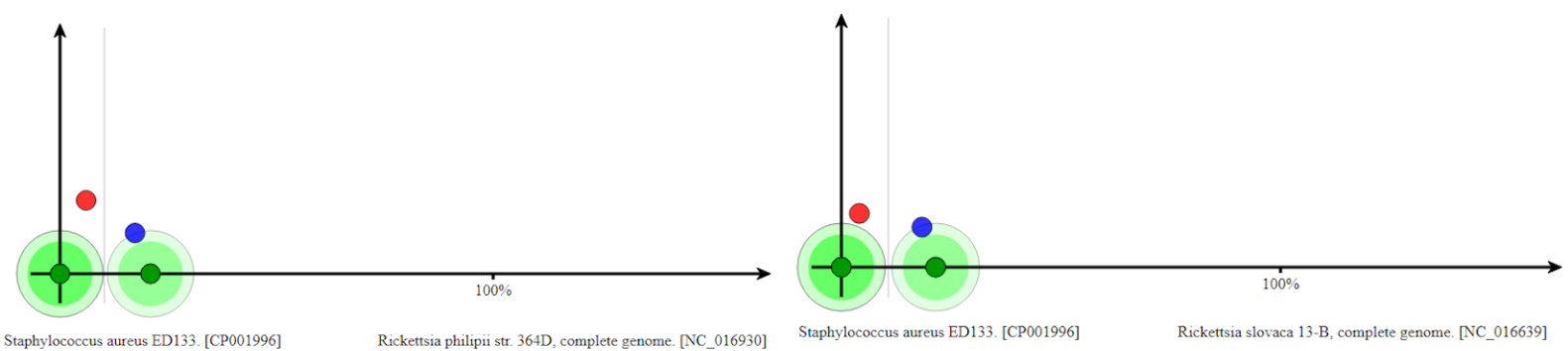
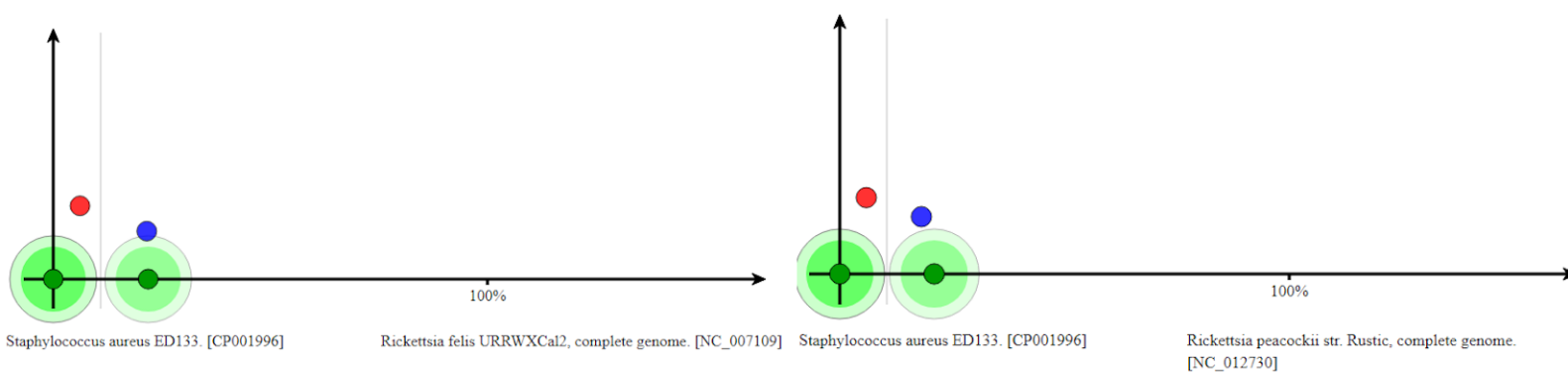
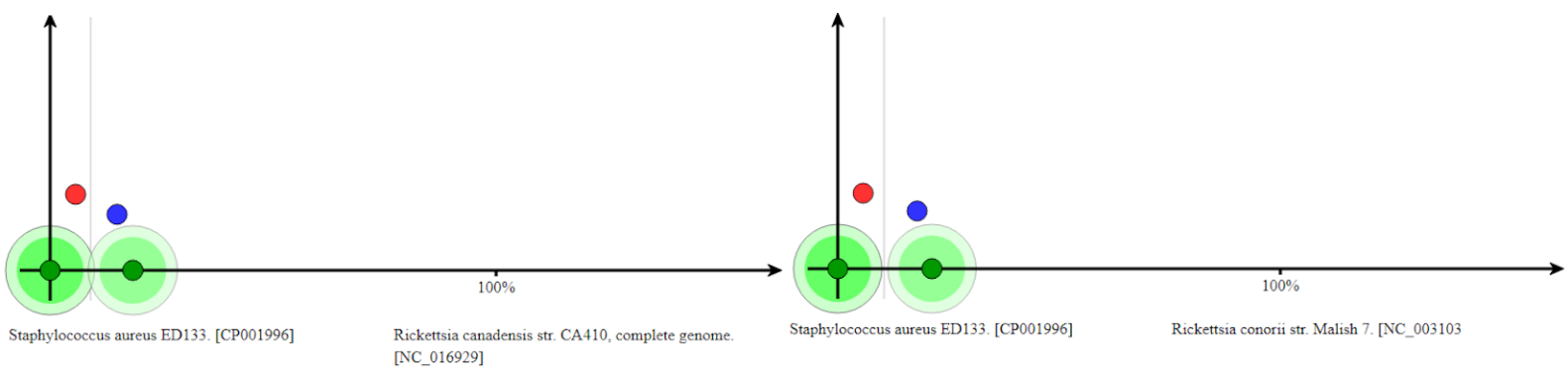
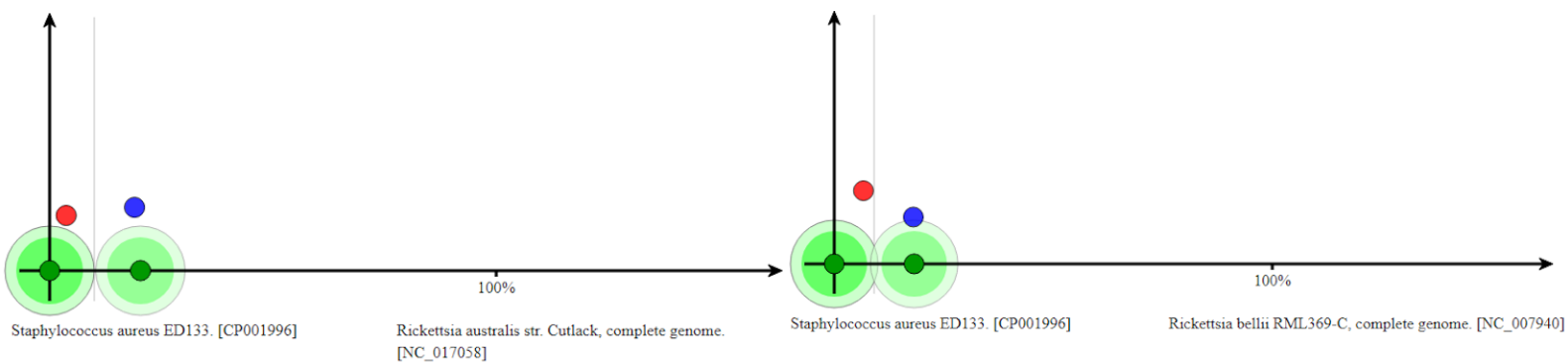
AFR72364.1	+	-	-	-	+	+	+	-	-	+	+	+	-	+	COG0740	O	phage protease
APE87185.1	-	-	-	+	-	-	-	-	-	-	-	-	-	-	NA	NA	transposase
APE87186.1	-	-	-	+	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein AS852_00395
APE87187.1	-	-	-	+	-	-	-	-	-	-	-	-	-	-	NA	NA	hydratase
APE87188.1	-	-	-	+	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein AS852_00405
AFR72365.1	+	-	-	-	+	+	+	-	-	+	+	+	-	+	NA	NA	putative phage capsid protein
APE87533.1	-	-	-	+	-	-	+	-	-	-	-	-	-	-	NA	NA	hypothetical protein AS852_02250
APE89767.1	-	-	-	+	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein AS852_02310
AFR72366.1	+	-	-	-	+	+	+	-	-	+	+	+	-	+	NA	NA	putative phage protein
APE87544.1	-	-	-	+	-	-	-	-	-	-	-	-	-	-	COG4123	J	hypothetical protein AS852_02330
APE87545.1	-	-	-	+	-	-	-	-	-	-	-	-	-	-	COG2827	L	hypothetical protein AS852_02335
APE87546.1	-	-	-	+	-	-	-	-	-	-	-	-	-	-	COG0313	J	16S rRNA (cytidine(1402)-2'-O)-methyltransferase
APE87547.1	-	-	-	+	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein AS852_02345
APE87548.1	-	-	-	+	-	-	-	-	-	-	-	-	-	-	COG0073	J	methionine--tRNA ligase
APE87549.1	-	-	-	+	-	-	-	-	-	-	-	-	-	-	COG0084	N	hydrolase TatD
APE87550.1	-	-	-	+	-	-	-	-	-	-	-	-	-	-	COG1658	J	ribonuclease M5
APE89768.1	-	-	-	+	-	-	-	-	-	-	-	-	-	-	COG0030	J	16S rRNA (adenine(1518)-N(6)/adenine(1519)-N(6))-dimethyltransferase
AFR72367.1	+	-	-	-	+	+	+	-	-	+	+	+	-	+	NA	NA	putative phage protein
APE87551.1	-	-	-	+	-	-	-	-	-	-	-	-	-	-	COG4466	S	hypothetical protein AS852_02370
AFR72368.1	+	-	+	-	+	+	+	-	-	+	+	+	-	+	NA	NA	putative phage protein
AFR72369.1	+	-	-	-	+	+	+	-	-	+	+	+	-	+	NA	NA	putative phage protein
AFR72370.1	+	-	-	-	+	+	+	-	-	+	+	+	-	+	NA	NA	major tail protein
AFR72035.1	+	-	+	-	-	+	-	+	-	-	+	-	+	+	COG0745	TK	response regulator protein
APE87872.1	-	-	-	+	-	-	-	+	-	-	-	-	-	+	COG0778	C	nitroreductase
APE8873.1	-	-	-	+	-	-	-	+	-	-	-	-	+	+	NA	NA	autolysin
APE8875.1	-	-	-	+	-	-	-	+	-	-	-	-	-	-	NA	NA	phage tail protein
APE8876.1	-	-	-	+	-	-	-	+	-	-	-	-	+	-	COG4193	G	cell wall hydrolase
APE8880.1	-	-	-	+	-	-	+	+	-	-	-	-	+	-	NA	NA	hypothetical protein AS852_09410
APE8882.1	-	-	-	+	-	-	-	+	+	-	-	-	+	-	NA	NA	peptidase
APE8883.1	-	-	-	+	-	-	+	+	-	-	-	-	-	-	NA	NA	phage tail protein
APE8884.1	-	-	-	+	-	-	+	+	-	-	-	-	+	-	NA	NA	terminase
APE8885.1	-	-	-	+	-	-	-	+	+	-	-	-	-	-	NA	NA	hypothetical protein AS852_09435
APE8886.1	-	-	-	+	-	-	+	+	-	-	-	-	-	-	NA	NA	hypothetical protein AS852_09440
APE8887.1	-	-	-	+	-	-	+	+	-	-	-	-	-	-	NA	NA	phage tail protein
APE8888.1	-	-	-	+	-	-	-	+	-	-	-	-	-	-	NA	NA	hypothetical protein AS852_09450
APE8889.1	-	-	-	+	-	-	+	+	-	-	-	-	-	-	NA	NA	hypothetical protein AS852_09455
APE8890.1	-	-	-	+	-	-	-	+	+	-	-	-	-	-	NA	NA	phage head-tail adapter protein
APE8891.1	-	-	-	+	-	-	+	+	-	-	-	-	-	-	NA	NA	phage head-tail adapter protein
APE8892.1	-	-	-	+	-	-	+	+	-	-	-	-	+	-	NA	NA	major capsid protein
APE8893.1	-	-	-	+	-	-	-	+	-	-	-	-	-	-	NA	NA	hypothetical protein AS852_09475
APE8894.1	-	-	-	+	-	-	+	-	-	-	-	-	-	-	NA	NA	hypothetical protein AS852_09480
APE8895.1	-	-	-	+	-	-	+	+	-	-	-	-	-	-	NA	NA	phage head morphogenesis protein
APE8896.1	-	-	-	+	-	-	-	+	-	-	-	-	+	-	NA	NA	phage portal protein
APE8897.1	-	-	-	+	-	-	+	+	-	-	-	-	-	-	NA	NA	terminase
APE8898.1	-	-	-	+	-	-	+	+	-	-	-	-	-	-	NA	NA	terminase
APE8899.1	-	-	-	+	+	+	-	-	-	-	+	+	-	-	NA	NA	hypothetical protein AS852_09505
APE8900.1	-	-	-	+	-	-	+	+	-	-	-	-	-	-	NA	NA	hypothetical protein AS852_09510
APE8901.1	-	-	-	+	-	-	-	+	-	-	-	-	-	-	NA	NA	hypothetical protein AS852_09515
APE8906.1	-	-	-	+	+	+	+	-	+	+	+	+	+	+	NA	NA	dUTPase
AFR72036.1	+	-	+	-	-	+	-	+	-	-	+	-	+	+	COG5002	T	sensor kinase protein

Source	Target	Distance	Group
<i>Borrelia burgdorferi</i>	<i>Staphylococcus aureus</i> LA*	7.51763	I
<i>Clostridium botulinum</i>	<i>Staphylococcus aureus</i> LA*	8.32624	I
<i>Borrelia afzelii</i>	<i>Staphylococcus aureus</i> LA*	8.60591	I
<i>Clostridium tetani</i>	<i>Staphylococcus aureus</i> LA*	9.93434	I
<i>Rickettsia africae</i>	<i>Staphylococcus aureus</i> LA*	10.1228	I
<i>Rickettsia akari</i>	<i>Staphylococcus aureus</i> LA*	10.3842	I
<i>Mycoplasma hyorhinis</i>	<i>Staphylococcus aureus</i> LA*	10.6426	I
<i>Anaerococcus prevotii</i>	<i>Staphylococcus aureus</i> LA*	10.9594	I
<i>Finegoldia magna</i>	<i>Staphylococcus aureus</i> LA*	11.0287	I
<i>Rickettsia prowazekii</i>	<i>Staphylococcus aureus</i> LA*	11.0743	I
<i>Rickettsia heilongjiangensis</i>	<i>Staphylococcus aureus</i> LA*	11.3296	I
<i>Rickettsia felis</i>	<i>Staphylococcus aureus</i> LA*	11.3418	I
<i>Rickettsia japonica</i>	<i>Staphylococcus aureus</i> LA*	11.3844	I
<i>Rickettsia philipii</i>	<i>Staphylococcus aureus</i> LA*	11.5516	I
<i>Rickettsia canadensis</i>	<i>Staphylococcus aureus</i> LA*	11.5637	I
<i>Melissococcus plutonius</i>	<i>Staphylococcus aureus</i> LA*	11.5759	I
<i>Rickettsia conorii</i>	<i>Staphylococcus aureus</i> LA*	11.582	I
<i>Rickettsia rickettsii</i>	<i>Staphylococcus aureus</i> LA*	11.5911	I
<i>Clostridium saccharoperbutylacetonicum</i>	<i>Staphylococcus aureus</i> LA*	11.6458	I
<i>Mycoplasma mycoides</i> subsp. <i>mycoides</i>	<i>Staphylococcus aureus</i> LA*	11.6473	I
<i>Brachyspira pilosicoli</i>	<i>Staphylococcus aureus</i> LA*	11.6488	I
<i>Rickettsia typhi</i>	<i>Staphylococcus aureus</i> LA*	11.6701	I
<i>Mycoplasma leachii</i>	<i>Staphylococcus aureus</i> LA*	11.7461	I
<i>Rickettsia australis</i>	<i>Staphylococcus aureus</i> LA*	11.8191	I
<i>Mycoplasma capricolum</i> subsp. <i>capricolum</i>	<i>Staphylococcus aureus</i> LA*	11.8616	I
<i>Rickettsia peacockii</i>	<i>Staphylococcus aureus</i> LA*	11.9022	I
<i>Bacillus cereus</i>	<i>Staphylococcus aureus</i> LA*	11.9376	I
<i>Acinetobacter baumannii</i>	<i>Staphylococcus aureus</i> LA*	12.0547	I
<i>Rickettsia slovaca</i>	<i>Staphylococcus aureus</i> LA*	12.0623	I
<i>Rickettsia bellii</i>	<i>Staphylococcus aureus</i> LA*	12.0957	I
<i>Ureaplasma parvum</i>	<i>Staphylococcus aureus</i> LA*	12.2051	I
<i>Mycoplasma bovis</i>	<i>Staphylococcus aureus</i> LA*	12.2355	II
<i>Rickettsia rhipicephali</i>	<i>Staphylococcus aureus</i> LA*	12.2659	II
<i>Rickettsia massiliae</i>	<i>Staphylococcus aureus</i> LA*	12.2842	II
<i>Brachyspira murdochi</i>	<i>Staphylococcus aureus</i> LA*	12.2902	II
<i>Mycoplasma hominis</i>	<i>Staphylococcus aureus</i> LA*	12.3043	II
<i>Mycoplasma cynos</i>	<i>Staphylococcus aureus</i> LA*	12.3085	II
<i>Borrelia bissettii</i>	<i>Staphylococcus aureus</i> LA*	12.3814	II
<i>Brachyspira hyodysenteriae</i>	<i>Staphylococcus aureus</i> LA*	12.4027	II
<i>Borrelia garinii</i>	<i>Staphylococcus aureus</i> LA*	12.4554	II
<i>Ureaplasma urealyticum</i>	<i>Staphylococcus aureus</i> LA*	12.4696	II
<i>Arcobacter nitrofigilis</i>	<i>Staphylococcus aureus</i> LA*	12.6246	II
<i>Mycoplasma crocodyli</i>	<i>Staphylococcus aureus</i> LA*	12.6297	II
<i>Brachyspira intermedia</i>	<i>Staphylococcus aureus</i> LA*	12.7857	II

<i>Mycoplasma fermentans</i>	<i>Staphylococcus aureus</i> LA*	12.8003	II
<i>Bacteroides fragilis</i>	<i>Staphylococcus aureus</i> LA*	12.8055	II
<i>Bacillus thuringiensis</i>	<i>Staphylococcus aureus</i> LA*	12.8192	II
<i>Rickettsia parkeri</i>	<i>Staphylococcus aureus</i> LA*	12.8496	II
<i>Brachyspira pilosicoli</i>	<i>Staphylococcus aureus</i> LA*	12.9165	II
<i>Mycoplasma penetrans</i>	<i>Staphylococcus aureus</i> LA*	13.0269	II
<i>Methanosphaera stadtmanae</i>	<i>Staphylococcus aureus</i> LA*	13.0441	II
<i>Arcobacter butzleri</i>	<i>Staphylococcus aureus</i> LA*	13.0563	II
<i>Campylobacter jejuni</i> subsp. <i>jejuni</i>	<i>Staphylococcus aureus</i> LA*	13.0563	II
<i>Mycoplasma conjunctivae</i>	<i>Staphylococcus aureus</i> LA*	13.1723	II
<i>Lysinibacillus sphaericus</i>	<i>Staphylococcus aureus</i> LA*	13.2174	II
<i>Mycoplasma arthritidis</i>	<i>Staphylococcus aureus</i> LA*	13.2554	II
<i>Arcobacter</i> sp.	<i>Staphylococcus aureus</i> LA*	13.2964	II
<i>Rickettsia montanensis</i>	<i>Staphylococcus aureus</i> LA*	13.5771	II
<i>Lactobacillus salivarius</i>	<i>Staphylococcus aureus</i> LA*	13.7372	II
<i>Mycoplasma agalactiae</i>	<i>Staphylococcus aureus</i> LA*	13.8436	II
<i>Orientia tsutsugamushi</i>	<i>Staphylococcus aureus</i> LA*	13.8588	II
<i>Mesoplasma florum</i>	<i>Staphylococcus aureus</i> LA*	13.9014	II
<i>Francisella tularensis</i>	<i>Staphylococcus aureus</i> LA*	13.9652	II
<i>Campylobacter lari</i>	<i>Staphylococcus aureus</i> LA*	14.0412	II
<i>Mycoplasma hyopneumoniae</i>	<i>Staphylococcus aureus</i> LA*	14.2373	II
<i>Bacillus anthracis</i>	<i>Staphylococcus aureus</i> LA*	14.3981	II
<i>Mycoplasma suis</i>	<i>Staphylococcus aureus</i> LA*	14.5805	II
<i>Mycoplasma gallisepticum</i>	<i>Staphylococcus aureus</i> LA*	14.6705	II
<i>Campylobacter hominis</i>	<i>Staphylococcus aureus</i> LA*	14.9501	II
<i>Ehrlichia ruminantium</i>	<i>Staphylococcus aureus</i> LA*	15.0292	II
<i>Leptospira interrogans</i>	<i>Staphylococcus aureus</i> LA*	15.0687	II
<i>Clostridium novyi</i>	<i>Staphylococcus aureus</i> LA*	15.1325	II
<i>Clostridium perfringens</i>	<i>Staphylococcus aureus</i> LA*	15.4517	II
<i>Flavobacterium branchiophilum</i>	<i>Staphylococcus aureus</i> LA*	15.5622	II
<i>Francisella</i> sp.	<i>Staphylococcus aureus</i> LA*	15.5916	II
<i>Methanobrevibacter smithii</i>	<i>Staphylococcus aureus</i> LA*	15.6955	II
<i>Clostridium beijerinckii</i>	<i>Staphylococcus aureus</i> LA*	15.8074	II
<i>Butyrivibrio proteoclasticus</i>	<i>Staphylococcus aureus</i> LA*	15.8196	II
<i>Eubacterium eligens</i>	<i>Staphylococcus aureus</i> LA*	15.853	II
<i>Bacillus weihenstephanensis</i>	<i>Staphylococcus aureus</i> LA*	15.8682	II
<i>Acidianus hospitalis</i>	<i>Staphylococcus aureus</i> LA*	15.8864	II
<i>Clostridium difficile</i>	<i>Staphylococcus aureus</i> LA*	15.9807	II
<i>Acholeplasma laidlawii</i>	<i>Staphylococcus aureus</i> LA*	15.9898	II
<i>Campylobacter fetus</i> subsp. <i>fetus</i>	<i>Staphylococcus aureus</i> LA*	15.9924	II
<i>Fusobacterium nucleatum</i> subsp. <i>nucleatum</i>	<i>Staphylococcus aureus</i> LA*	16.1296	II
<i>Borrelia duttonii</i>	<i>Staphylococcus aureus</i> LA*	16.2056	II
<i>Bacillus megaterium</i>	<i>Staphylococcus aureus</i> LA*	16.3059	II
<i>Francisella philomiragia</i> subsp. <i>philomiragia</i>	<i>Staphylococcus aureus</i> LA*	16.3272	II







SUPPLEMENTARY DATA. These figures depicts the proposed GI donor-recipient relationship with the aid of Lingvocom 2D projection utility. Two dark green spots on the plots represent OUP of *S. aureus* ED133 (at centre point) and proposed donors (on principal axis). Light green circle depicts 1/2 of the distance between patterns calculated for chromosomes/plasmids. The island of *S. aureus* is shown as a red small circle and that of other donors as a blue circle. Islands were plotted along the second principal axis according to distance values between OUP of islands and host chromosome.