

Research Article

# Genomic islands and the evolution of livestock-associated *Staphylococcus aureus* genomes

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**Background:** Genomic Islands (GIs) are commonly believed to be relics of horizontal transfer and associated with specific metabolic capacities, including virulence of the strain. Horizontal gene transfer (HGT) plays a vital role in the acquisition of GIs and the evolution and adaptation of bacterial genomes.

**Objective:** The present study was designed to predict the GIs and role of HGT in evolution of livestock-associated *Staphylococcus aureus* (LA-SA).

**Methods:** GIs were predicted with two methods namely, Ensemble algorithm for Genomic Island Detection (EGID) tool, and Seq word Sniffer script. Functional characterization of GI elements was performed with clustering of orthologs. The putative donor predictions of GIs was done with the aid of the pre\_GI database.

**Results:** The present study predicted a pan of 46 GIs across the LA-SA genomes. Functional characterization of GI sequences revealed few unique results like the presence of metabolic operons like *leuABCD* and *folPK* genes in GIs and showed the importance of GIs in the adaptation to the host niche. The developed framework for GI donor prediction results revealed *Rickettsia* and *Mycoplasma* as the major donors of GI elements.

**Conclusions:** The role of GIs during the evolutionary race of LA-SA could be concluded from the present study. Niche adaptation of LA-SA enhanced presumably due to these GIs. Future studies could focus on the evolutionary relationships between *Rickettsia* and *Mycoplasma* sp. with *S. aureus* and also the evolution of Leucine/Isoleucine mosaic operon (*leuABCD*).

## Introduction

The gene transfer between the different bacterial species has a great impact on the evolution and transformation of bacterial pathogens. Genomic Islands (GIs) are unfamiliar gene blocks present in pathogenic and non-pathogenic prokaryotic genomes apart from the core genome [1]. They play a role in determining accessory functions, such as antibiotic resistance, secondary metabolic activities, symbiosis and other special functions related to sustaining during adverse environmental conditions. These GIs supposedly associate with the virulence of the pathogenic bacteria and are known as pathogenicity islands (PAIs) [2]. GIs have evidence of horizontal origins, i.e. Horizontal Gene Transfer (HGT), which means that an interchange of genetic information between phylogenetically distant organisms takes place [3]. The advantage of acquisition of GIs has an evolutionary edge and that is a large number of genes can be transferred and incorporated into the recipient genome. This transfer may lead to dramatic changes in an organism and ultimately result in a quantum leap in evolution [4].

During the evolution, many bacteria have equipped their genomes with DNA from other bacterial species or even genus with the help of mobile genetic elements (MGEs). These MGEs also referred to as

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accessory genetic elements, are therefore a potential resource for bacteria that provide adaptive strengths to improve the fitness and, potentially, pathogenicity and drug resistance [5].

For instance, in *Pseudomonas aeruginosa*, accessory gene elements have enhanced the virulence toward invertebrate *Caenorhabditis elegans* [6]. GIs' another class of accessory gene elements contribute to the evolution and adaptation to the niche. *Staphylococcus aureus* also possesses several MGEs, including GIs but the knowledge on GIs of livestock-associated *S. aureus* (LA-SA) is limited.

Computational analysis of whole-genome sequences of several bacterial strains predicted that GIs are present in any given strain [7]. In the present genomic era, the number of sequenced bacterial whole genomes is increasing rapidly. Comparative genomic studies became the initial step in analyzing the microbial genomics and it helps in deciphering the evolutionary relationships [8]. Public accessibility of data of whole-genome sequences and development of bioinformatics methods makes it possible to study the evolution of bacteria, pathogenicity and other associated characteristics. Recognition and analysis of GIs contribute toward a better understanding of the evolution of the disease and the development of bacterial pathogenicity and even in understanding the evolution of host-specific strains [4,9]. Moreover, zoonotic transfer of *S. aureus* is becoming a major possible way of spreading resistant *S. aureus*. Hence, it is imperative to predict and analyze the evolution of the GIs in the livestock-associated strains, to comprehend the evolutionary developments. Pertaining to this context, the present study was planned-out in order to predict the GIs and the genetic elements' coding by GIs in the available completed genomes of *S. aureus* which have livestock-association. Furthermore, an in-depth bioinformatics comparative analysis of predicted GIs and their functions was performed.

## Materials and methods

### Acquisition of genome sequences

Complete genome sequences of *S. aureus* strains available at NCBI's FTP server ([ftp://ftp.ncbi.nlm.nih.gov/genomes/genbank/bacteria/Staphylococcus\\_aureus](ftp://ftp.ncbi.nlm.nih.gov/genomes/genbank/bacteria/Staphylococcus_aureus)) were retrieved only after manual verification of the Livestock association or origin. Chromosomal sequences alone were analyzed and annotated with Prokka: rapid prokaryotic genome annotation tool in local machine [10] for maintaining uniformity in the annotation files. The details of genome sequences were presented as supplementary data (Supplementary Table S1).

### Prediction of GIs

Initial comparative analysis was done with GView Server [11], to draw circular chromosomes based on the BLAST-core to check the similarity. The following existing methods were deployed to predict GIs of the genomes. These methods are Ensemble algorithm for Genomic Island Detection ((EGID)—[12]), and SeqWord Sniffer-python language script [13]. EGID: a tool for improved GI detection in genomic sequences, is based on the predicted results of five existing GI programs, namely Alien Hunter [14], COLOMBO SIGI-HMM [15], INDeGenIUS [16], IslandPath [17] and PAI-DA [18]. The framework of this program includes (i) collection of prediction results from existing five programs; (ii) analysis and filtering of predicted results; and (iii) generating final consensus GI results. SeqWord Gene Island Sniffer program is based on the analysis of oligonucleotide usage variations in DNA sequences and detects putative horizontally transferred gene clusters. Chromosomal sequences alone were analyzed in the present study as GIs were integrated part of chromosomes.

### Clusters of orthologous group enrichment analysis

Clusters of Orthologous Group (COG) of proteins enrichment analysis was performed in order to establish the functional characterization of GIs. COG categorization was carried out online using the Batch version of Conserved Domain Database [19], searching against the COG database while using other default parameters. 'NA' was used instead when the genes did not match any COG accession numbers.

### Virulent genes analysis

To identify possible virulence factors, the curated and experimentally validated virulence factors of Virulence Factors Database (VFDB) were aligned with the ORF protein sequences. BLAST-based virulence gene analysis was performed in local machine, and virulence factor protein sequences were downloaded from VFDB (<http://www.mgc.ac.cn/VFs/> [20]). A local database was built in the local machine with VFDB.SetA (curated and validated) protein sequences. Proteins encoded by GIs were aligned against this database with minimum e-value as  $1e^{-10}$  using Blastp and were filtered with 75% identity and 95% aligned length.

## Distribution analysis of GIs

The predicted GI elements clustering analysis was performed with ClustAGE software [21] as described in the manual of the software. Heat map of Bray–Curtis (BC) [22] similarity values to the neighbor-joining tree were visualized in the online tree visualization software Interactive Tree Of Life [23].

## Credible donors of predicted GIs

A novel framework was proposed and developed to detect the GIs with the aid of the concept of island ontology and proposed island flow from the pre\_GI database [24]. Initially, all available Oligonucleotide Usage Pattern (OUP) neighbors data, i.e. proposed host, compositional similarity (CS) and island distance (D) for Query Island were retrieved from the pre\_GI database, except the data for the proposed island flow from the query to subject with the compositional similarity cutoff of 80%. The values of D were normalized and the data with values  $> 0$  were removed from the analysis ( $x_i > 0$ , regarded as false positives); lower D values indicate the most probable donor. The finalized data were manually curated and the bacterial donors were removed with which there is no possible interaction, e.g. marine thermophiles and archaea have a low possibility of terrestrial bacteria to interact. Finally, all the probable donors were grouped into three categories based on the normalized values of D. Group I was regarded as potent probable neighbors, Group II had moderately probable neighbors and group III had the least probable donors (Supplementary Data S2). The credible donor relationship was established by comparing the two GIs [Query and Subject (probable donor)] with LingvoCom [24].

## Results

### Properties and comparative studies of genomes

All the points of interest of the genomes used as a part of the present study have been classified (Table 1). Among these strains, *S. aureus* ST398 has the large genome with the size of 2.87 Mb, which has bovine origin but isolated from human and the smallest genome is of *S. aureus* 71193 strain with 2.71 Mb. The genomes demonstrated a noteworthy deviation in size from one another and the GC content of all genomes appeared to be same with an estimation of 33%.

GView server, a BLAST-based approach, for genome comparisons was employed in order to further analyze the collinearity between genomes. It demonstrated a similarity between genomes at approximately 90–98% on sequence level and can be seen in Figure 1. Similar results of Mauve analysis were repeated here with a better understanding of the unique regions of genomes when compared with that of the reference genome. The loss and gain of genes could be seen from the whole-genome BLAST results, wherein ED133 strain had much more similar nucleotide content while RF122 strain had the least similarity. The regions around 1.8 and 2.1 Mb were unique to the majority of strains in the study. The GView server results of Blast-based comparisons were similar to the results obtained from Mauve alignment.

### Prediction of GIs

GIs were predicted with the EGID tool, and then followed by the SeqWord Gene Island Sniffer and. EGID uses the resulted GI coordinates of five existing GI prediction programs mentioned in the methods section, followed by filtering statistically significant and consensus GI coordinates [12]. SeqWord Gene Island Sniffer program analyzes the oligonucleotide usage variations in DNA sequences and detects putative horizontally transferred gene clusters [13]. The overlapping GIs from these methods was removed manually and examined the HGT mechanisms of GIs based on the annotations. Further, the coordinates of GIs were adjusted on the basis of the HGT mechanism. Additionally, the false-positive predicted GIs (e.g. ribosomal genes) and essential genes were removed from the analyses.

It was concluded that 46 different GIs prevailed across the study genomes, most GIs were 17 in number as observed in *S. aureus* ST398 strain and least were only 11 in number as found in 08S00974 strain, in spite of its larger genome-size elevated coverage by the GIs was also in accordance with the predicted number of GIs and was found to be 15.5% in whole-genome sequence and 15.3% in proteome in case of *S. aureus* ST398 (large genome) strain, whereas the least coverage was seen in *S. aureus* 08S00974 (Table 1). LA-SA strains possess an average of 13 GIs in their genomes and the least number of GIs was 11.

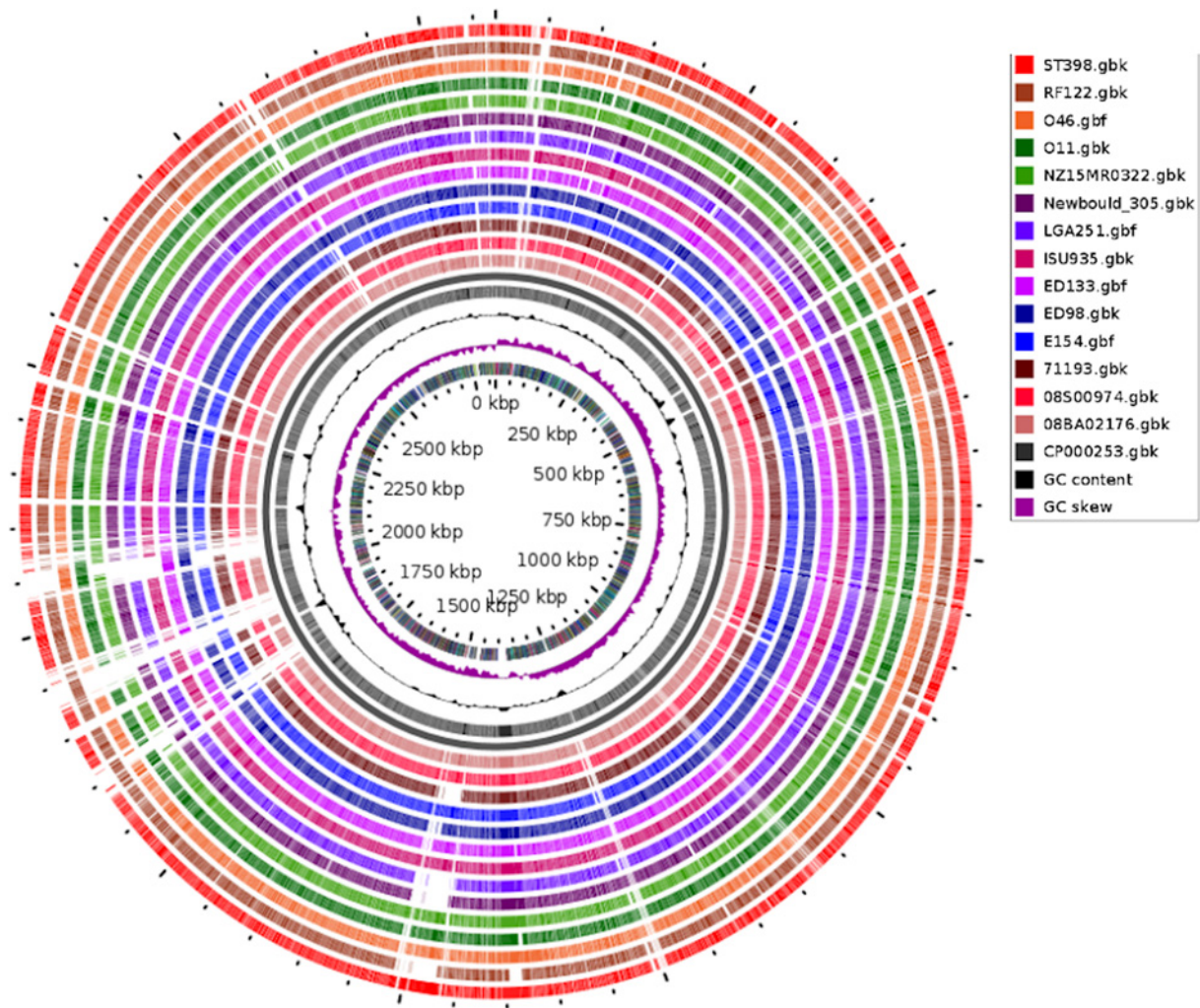
Some of the known islands from other *S. aureus* strains were identified in the LA-SA genomes and represented in Table 2. They were regarded as PAIs since these Islands coded for virulence factors like enterotoxins and clumping factors [25]. The visualization of GIs of 08BA02176, RF122 and ST398 strains was done with *DNAplotter*, a Java-based program [26] as seen in Figure 2.

**Table 1** Characteristic features and properties of LA-SA genomes selected for the present study

Strain/Feature	08BA02176	08S00974	71193	E154	ED98	ED133	ISU935	LGA251	Newbould.305	NZ15MR0322	O11	O46	RF122	ST398
Sequence type	st398	st398	st398	st398	st5	st133	st5	st130	st115	st398	st130	st130	st151	st398
Size (Mb)	2.78	2.8	2.71	2.83	2.82	2.83	2.86	2.75	2.8	2.83	2.76	2.79	2.74	2.87
Genes	2593	2613	2531	2671	2681	2710	2683	2564	2662	2750	2596	2614	2656	2738
CDS	2532	2551	2472	2609	2618	2649	2621	2501	2601	2688	2569	2562	2594	2676
tRNA genes	58	61	58	61	62	60	61	61	59	61	29	51	61	61
tmRNA genes	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Repeat regions	2	0	0	0	0	0	0	0	1	0	0	0	0	0
GC%	32.94	32.94	32.93	33	32.84	32.92	32.91	32.96	32.92	32.86	32.78	32.83	32.78	32.92
Predicted GIs	14	11	13	13	12	13	13	14	13	12	11	11	14	17
Coverage in genome (%)	14.3	9.63	9.96	11.4	11.16	13.97	11.42	14.13	13.96	10.9	14.1	10.59	13.64	15.55
Coverage in proteome (%)	13.57	6.97	10.5	8.34	11.76	15.31	9.35	12.24	13.14	9.89	13.04	9.41	13.67	15.23

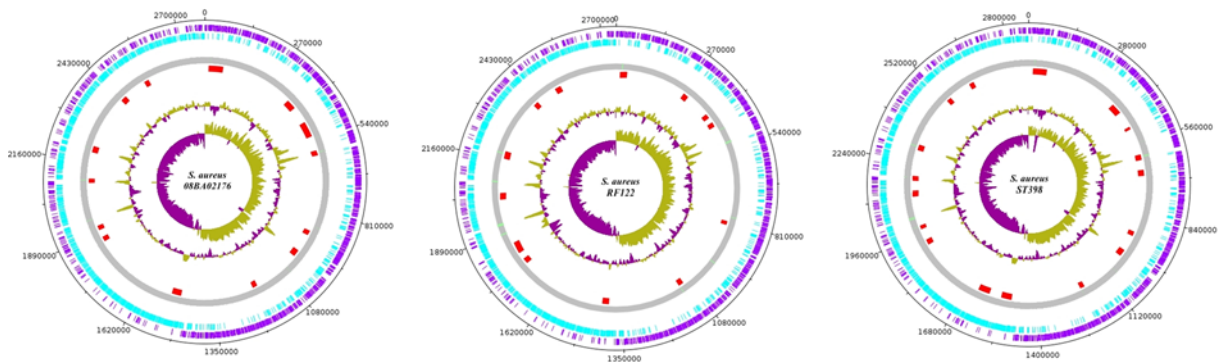
Abbreviation: CDS, Conserved Domain Search.





**Figure 1. BLAST-based comparative genome maps**

The comparative genome map generated with the GView server using *S. aureus* NCTC8325 as a reference sequence to other *S. aureus* genomes. The outermost ring depicts the genes of a reference strain followed by the genomes of other strains based on the BLAST similarity. The genome sequences are colored differently, and regions without colors are absent from the respective strain, and highlight differences in the accessory gene content.



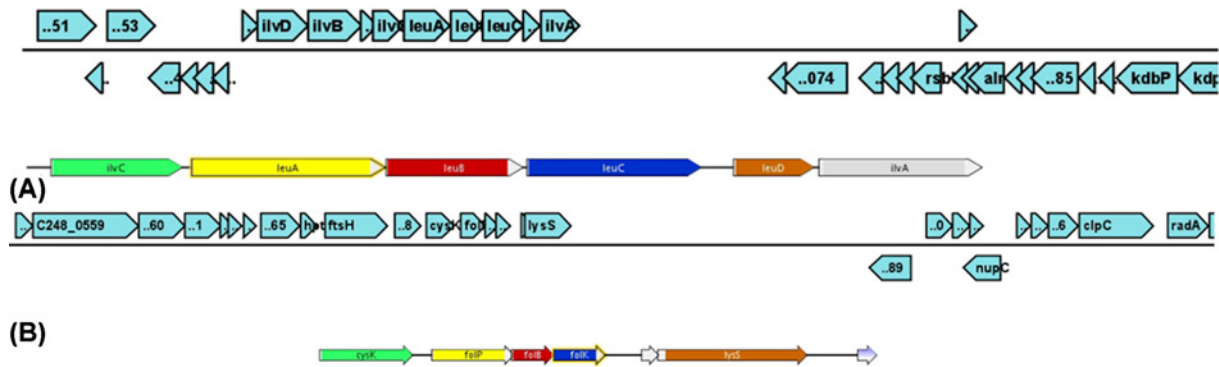
**Figure 2. Location of GI coordinates on the circular genome**

The circular genome of *S. aureus* strains represent the predicted GI locations. The inner circle represents the GC skew and the next represents the GC content plot and the red dots represent the predicted GI location on the circular genome (plotted by *DNAplotter*).

**Table 2** Previously published Staphylococcal GIs predicted in these LA-SA' genomes\*

GI	LASA-GI	Coordinates	Function	08BA20716	08S00974	71193	E154	ED98	ED133	ISU935	LGA251	N305 <sup>†</sup>	NZ15	O11	O46	RF122	ST398
φSa2	08BA02176_GI2	354723-392677	Virulence	+	+	-	+	+	+	+	-	+	+	+	+	-	+
νSaβ	LGA251_GI11	1870085-1902095	Virulence	-	-	-	-	-	+	-	+	-	-	-	-	+	-
φSa3	77193_GI10	1934043-1976257	Virulence	-	-	+	-	-	+	-	-	-	-	+	+	-	-
νSaγ	08BA02176_GI7	1182896-1202263	Virulence	+	-	+	-	+	+	-	+	+	-	-	-	+	+
Salbov	08BA02176_GI3	458784-517982	Virulence	+	+	+	-	+	+	-	+	+	-	-	-	+	+
Type-V SSCmec	08BA02176_GI1	16107-72549	Resistance	+	+	+	-	-	+	-	+	-	-	-	-	+	+

\*From PAI-DB [32].  
<sup>†</sup>Newbould\_305.



**Figure 3. Genetic maps of the operons present in the GIs**

Gene maps of GIs indicating the presence of genes involved in metabolism (A) 08BA02176\_GI11 with *leuABCD*, (B) 08BA02176\_GI14 with folic acid biosynthesis genes.

## Mechanisms involved in the transfer of GIs

The three common mechanisms mainly meant for HGT are through Phage integrase (Transduction), Transposon – Transposase (Insertion Sequences) and tRNA [27]. Mostly, phage-related integrase genes are present on these predicted GIs, suggesting that they are integrated and excised in a method similar to prophages. *S. aureus* Pathogenicity Island (SaPI) is mobilizable with the assistance of the transducing phages [28]. The majority of the predicted GIs (13/46) were noted to flank by transposon – transposase genes and followed by phage integrases suggesting that transposase is majorly responsible for the acquisition of GIs (Supplementary Table S2). The present study also suggests that transducing phages are responsible for the acquisition of GIs. Finally, it was concluded that from the mechanisms involved in gene transfer, transposon – transposase and phage infections are important mechanisms involved in the HGT events of the studied genomes.

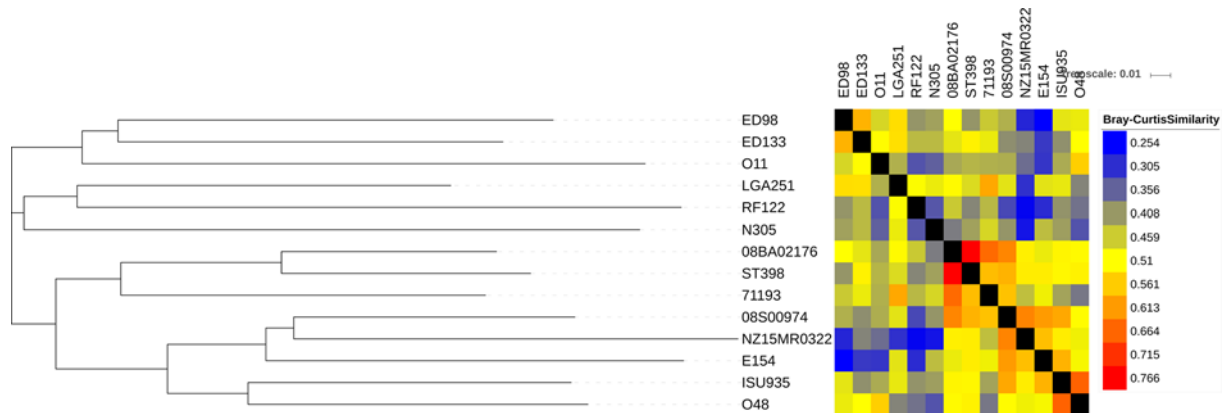
## Homologous GIs

Homologs from the predicted GIs were retrieved with GET\_HOMOLOGUES software [29], for understanding the relationship among LA-SA genomes, and also for performing comparative analysis. Further, the conserved domain superfamily analysis was also carried out for the retrieved homologs representing each strain [19]. These findings showed that only eight ORFs of all GIs are common to all strains under the study. Unique proteins of each strain are majorly noted as hypothetical proteins that belong to an unknown family of proteins. The common proteins are mainly Phage proteins and virulent proteins. The Conserved Domain Search (CDS) analysis also showed that many hypothetical proteins are assigned to the unknown family and other hypothetical proteins belong to proteins. The presence of phage proteins indicates frequent phage infections. RF122 strain's GIs harbor the highest unique ORFs and lowest in 08S00974.

## Functional categorization and COG enrichment analysis

Based on the annotation results of genomes, the predicted GIs mostly possess phage and hypothetical proteins (Supplementary Data S1). Besides the usual hypothetical proteins, several GIs encode for some virulent proteins, and also confer antibiotic resistance, as expected. Apart from these functions, some GIs encode for metabolism-related functions as well, e.g. LASA-GI4 genomes encode genes for folate synthesis and LASA-GI19 encodes for trehalose metabolism. This unique finding from the study shows the mosaic operon cluster transfer of LASA-GI11, encoding for Leucine/Isoleucine biosynthesis (Figure 3).

It was found that potent toxin genes like enterotoxins and exotoxins genes were associated with GIs and were found to have HGT origin because of their anomalous GC content (Supplementary Data S1). Phage infections were responsible for the transfer of these toxin genes. The other important genes, which have a horizontal origin, are fibronectin-binding proteins. Fibronectin-binding proteins are adhesins, cell wall-associated proteins involved in critical host–pathogen interactions [30]. These genes, found across all GIs of the study genomes and other putative fibronectin-binding proteins, are also associated with GIs. Furthermore, these proteins were reported to evolve in *S. aureus* in the ruminant host habitat [31]. When we compare the GIs including PAIs of other *S. aureus* strains (human pathogenic *S. aureus*) published in PAI-DB [32], it was observed that the GIs majorly encoded for toxins and antibiotic resistance genes but not for fibronectin-binding proteins in major. Since all the strain genomes used in the



**Figure 4. Cluster analysis of GI elements**

BC distances (d) calculated for every pair-wise comparison of shared GI element content between strains. Neighbor-joining tree (left) is a consensus across 1000 bootstrap resampling of distributions. The heatmap shows relative pairwise similarity (1 - d) between strains.

present study have animal association, the association of fibronectin-binding proteins with GIs is significant in the view of evolutionary strategies adopted by *S. aureus*.

For approximately 1250 homologous protein sequences representing the overall GI elements of LA-SA genomes of the present study, only 440 sequences were assigned with COG accession numbers and categorized into different functional groups (Supplementary Data S1), since the majority of the sequences are annotated as hypothetical proteins which do not belong to the existing functional classes. Hence, the number of sequences assigned to the COG functional class was less. The overall enrichment analysis resulted in the GI elements that were with molecular functions-related elements like replication, transcription and translation regulatory proteins (25%), followed by general prediction class and proteins with unknown functions (COG class R and S - 14%), amino acid transport and metabolism-related proteins (COG class E - 9%), Phage-related elements (COG class X - 8%) and Defense-related proteins (COG class V - 5%).

## Virulent genes across the GIs

The Blastp analysis of GIs against VFDB resulted in identifying the major genes contributing the virulence in LA-SA (Supplementary Table S3). The enrichment analysis against a database indicated that these GIs carried important virulent genes. This analysis identified that the GIs predominantly encode for toxin genes, especially different kinds of enterotoxins followed by adherence-related genes like fibronectin and fibrinogen binding proteins, serine-aspartate rich fibrinogen-binding proteins (*sdr* genes) and clumping factor. Exotoxins and Type VII Secretion System (T7SS) genes that have been associated with virulence in *S. aureus* were also part of GIs. These results suggested that the genes associated with virulence in LA-SA were hustled through HGT mechanisms.

## The GI elements distribution and their relatedness

The homologous GI elements were distributed among the *S. aureus* genomes in the present study. The distribution and relatedness of these GI elements help to understand the implications of GIs on the strain-based relatedness, and the evolution of LA-SA genomes. The sequence similarity and the distribution of related GI elements among the LA-SA genomes were depicted in Figure 4 with BC distance-based heat map and Neighbor-joining tree. The heat map based results suggested that the GI elements among the LA-SA genomes have intermediate relatedness. During clustering, the GI elements resulted in BC distance ranging only from 0.25 to 0.76. This was presumably due to the differences in the composition of GI elements. The highest BC (0.766) similarity was seen between 08BA20176 and ST398, presumably, because they both belonged to st398 type. But the average BC similarity coefficient was found to be only 0.5, a moderate similarity coefficient likely due to different phage infections (frequency of certain phage groups varied between *S. aureus* Clonal Lineages - [33]), barriers such as restriction-modification systems (R-M systems) and niche separation reducing the opportunities for HGT [34]. Sequence-type based clustering was not observed when the phylogenetic tree was constructed with GI elements; and this observation suggests similar HGT events that were, presumably, not dependent on STs of strains. The highest BC similarity was seen between 08BA20176 and



ST398 strains while least was found in between E154 and ED98 strains and also in NZ15MR0322 and RF122 strains. These results indicated the uniqueness of GI composition of each strain.

## Credible donors of GI elements

From the above results, it was obvious that HGT played an important role in the acquisition of GIs and the evolution of virulence and adaptation of LA-SA strains. Thus, it is practically significant to explore the donors of GIs in order to understand the interactions with donors, as well as to interpret the HGT events. Predictions were performed for all 14 genomes of the present study and all the results were cumulated for understanding the donors for LA-SA GIs better. The donor–recipient island ontology further confirmed with LingvoCom (Supplementary Data S3).

This framework predicted several probable donors of GIs and the data were plotted as a network with gephi tool [35]. The results showed that *Rickettsia* sp. and *Mycoplasma* sp. were over-represented as donors of GI elements (Figure 5A). The family-level representation of the donors' list resulted in the same observation that Rickettsiaceae followed by Mycoplasmataceae were dominant donors of the GI elements of the LA-SA strains (Supplementary Figure S1). Further, these results compared with donors of GI elements of human-associated *S. aureus* (HA-SA), revealed that these strains presented with *Mycobacterium* sp. were also part of donors while some species of *Rickettsia* and *Mycoplasma* were absent from donors list of HA-SA (Figure 5B). These results suggested LA-SA and HA-SA strains were presented with diverse GIs, in the due course of evolution.

## Discussion

### GIs and their importance in LA-SA genomes

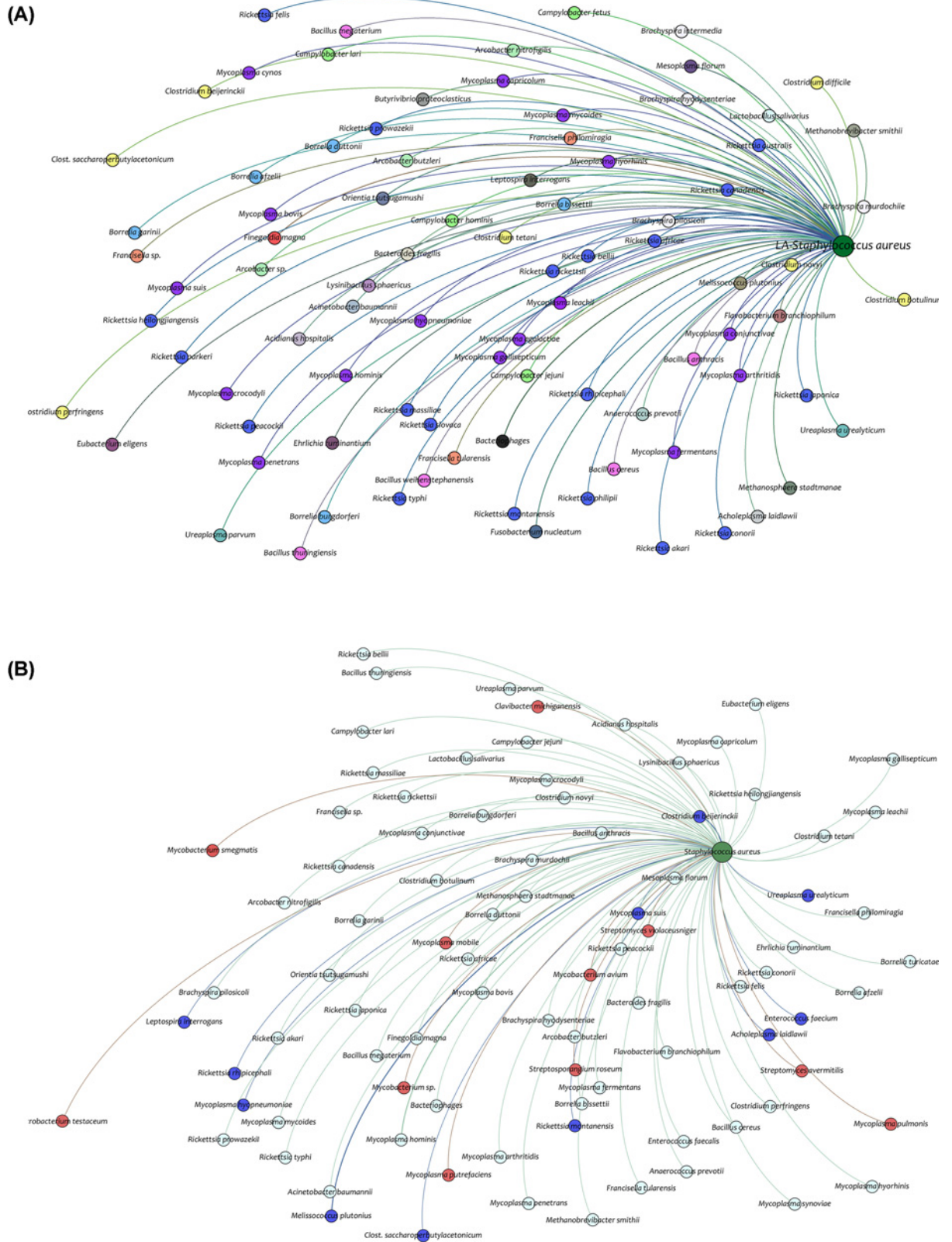
To have a better idea of the evolution of LA-SA, the roles of the accessory genome, and HGT events in pathogenicity, drug resistance and epidemiological information, GI prediction, and functional categorization were carried out with the available LA-SA's 14 complete genomes. Several studies emphasized the importance of HGT and GIs in the evolution of *S. aureus* and identified GIs including PAIs [36,37]. A different study reported the detection of 13 known GIs including PAIs across the 5 MRSA strains [38], comparable with the present study where 13 GIs have been predicted, on average, in the 14 LA-SA strains. Some GIs were widely distributed across these 14 LA-SA genomes while some were confined to two or three strains (Supplementary Data S1). This was so perhaps due to the barriers such as DNA R–M systems and niche separation which reduce the opportunities for HGT [34].

Phages and Transposon – Transposases were found to be predominantly involved in the exchange of genetic material through HGT in LA-SA genomes in the present study. Moon et al. [39] in 2016 suggested that phages involved in mediating GIs which confers virulence and resistance in some *S. aureus* strains. While transposons are not able to transpose within the bacterium, but they are capable to integrate with various sites of the other host's genome and are therefore able to transpose in the host genome [40]. Primarily, Transposon – Transposase-mediated GIs confer resistance to host strains [34]; but here we report that Transposon – Transposase-mediated GIs were predicted to encode virulence and some metabolism-related functions, apart from antibiotic resistance. A recent study by Jani et al. [38] also reported the Transposase-mediated GIs.

Functional characterization of GIs revealed that apart from the virulence and antibiotic resistance functions, certain GIs encode some metabolism-related functions. The Leucine/Isoleucine biosynthesis genes are a mosaic *leuABCD* operon and known to have horizontal transfer origin and probable source would be archaea [41]. This operon in *S. aureus* is involved in leucine and pyruvate metabolism. There were no available reports on the acquisition of *leuABCD* operon through HGT in *S. aureus*. The folic acid synthesis genes in *S. aureus* also seem to be a part of HGT events. The genes *folP*, *folB* and *folK*, involved in folate synthesis in *S. aureus*, were encoded by a GI in LA-SA genomes. This functional characterization of GIs also suggests the role of HGT in host-niche adaptation and the similar finding was well established in *Prochlorococcus* spp. and *Klebsiella pneumoniae* as well [42,43]. Another recent study on *S. aureus* also suggests the importance of GIs in the host specificity [44].

Even though many genes encoded by GIs were hypothetical proteins and phage-related protein, COG enrichment analysis revealed that certain genes encoding vital molecular functions, such as transcriptional regulatory genes, were enriched in GIs. These genes were primarily flanked with phage elements like integrase and capsid proteins, suggesting that temperate phages may responsible for this enrichment. Apart from these regulatory functions, phage proteins are known to increase the virulence of host bacterium, through regulation of expression of the virulence genes [45].

The other important genes which have horizontal origin are fibronectin-binding proteins. Fibronectin-binding proteins are adhesins, cell wall-associated proteins, involved in critical host–pathogen interactions [30]. The insights into the predicted GIs of strains clearly state that important virulence factors are associated with GIs. Sui et al. [46] reported that GIs inconsistently harbor greater number of virulence factors than the rest of the host genome, and



**Figure 5. Representation of GI donors in the network model**

**(A)** Donors of GIs of LA-SA strains and each colored node represent a different genus. **(B)** This network depicts the GI donors of both LA-SA strains and HA-SA strains. The red color nodes represent the unique donors to HA-SA strains while blue color for LA-SA strains and cyan colored nodes represents the common donors.

are enriched for proteins like toxins or hypothetical pathogen-associated genes. Similar results were obtained in the present study, which located proximity to the earlier studies. Analyzing the closely related pathogenic genomes have suggested that genes involved in virulence are apparently associated with PAIs, a subset of GIs [9,46]. This again supports the notion of the role that GIs play in the transformation of non- virulent strain to virulent strain.

## GIs and their credible donors

GIs played a vital role in adaptation, survival and virulence of strains but which organisms contributed to acquiring such traits was yet to discover in the field of accessory genomics of bacteria. In the present study, an attempt was made to predict the donors of such traits, and also the relationships between host and donors. Predictions were performed for the 14 genomes of the present study and *Rickettsia* sp. and *Mycoplasma* sp. were found to have been over-represented as donors. Wan and Che [47] in 2014, also developed a similar kind of approach to predict the GI donors. They reported that *Gordonia*, *Nocardia* and *Rhodopseudomonas* species as major donors of GI elements of *Mycobacterium tuberculosis*. The predicted donor results also suggested the frequent phage infections and incorporated phage related genes in the genomes of LA-SA strains. There were few unique donors for LA-SA GIs and HA-SA GIs, presumably, because of niche separation.

There were not enough literature or reports available to support these findings of GI donors. While previous experimental research suggested that capsular polysaccharide genes of *S. aureus* were found to have homologs in the *Rickettsia* genome [48]. And there could be a possible membrane fusion between *Mycoplasma* and *S. aureus*, *Bacillus subtilis* for facilitating the transfer of conjugative elements between hosts and recipient cells [49,50]. The other plausible reasons for these results could be the interactions between *S. aureus* and other donors (or part of the microbiome of hosts) during the due course of infection. It was also reported that *Mycoplasma* and *S. aureus* are believed to coexist and cause bovine mastitis [51]. This study paves the way to realize a need to understand the evolutionary relationships with other bacterial species and in particular between *Rickettsia* and *Mycoplasma* sp. with *S. aureus*.

## Conclusions

In conclusion, the established the fact that GIs plays a vital role in niche adaptation and evolution of LA-SA strains. The predicted GIs were observed to enhance the virulence capacity of strain as they primarily encoded for adherence-related proteins, like the fibronectin-binding proteins, clumping factors and also for most of the toxin genes, like entero- and exotoxins. The GIs functional enrichment and horizontal transfer of *leuABCD* mosaic operon and folic acid biosynthesis genes (*folBPK*) in *S. aureus* suggests their role in the niche adaptation. The donor prediction results of GI elements showed that *Rickettsia* sp. and *Mycoplasma* sp., over-represented as donors of GI elements in LA-SA strains and *Mycobacterium* sp., were unique donors for the HA-SA associated GI elements. Based on these findings, future studies could focus on the evolutionary relationships between *Rickettsia* and *Mycoplasma* sp. with *S. aureus*, and also the evolution of Leucine/Isoleucine mosaic operon (*leuABCD*) in *S. aureus*.

## Competing Interests

The authors declare that there are no competing interests associated with the manuscript.

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## Author Contribution

R.T.R. and S.S. conceived and designed the experiments. R.T.R. conducted the experiments, and R.T.R. and S.S. analyzed the data. R.T.R. wrote the manuscript. S.S., N.S., and K.J. corrected and revised the manuscript.

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## Abbreviations

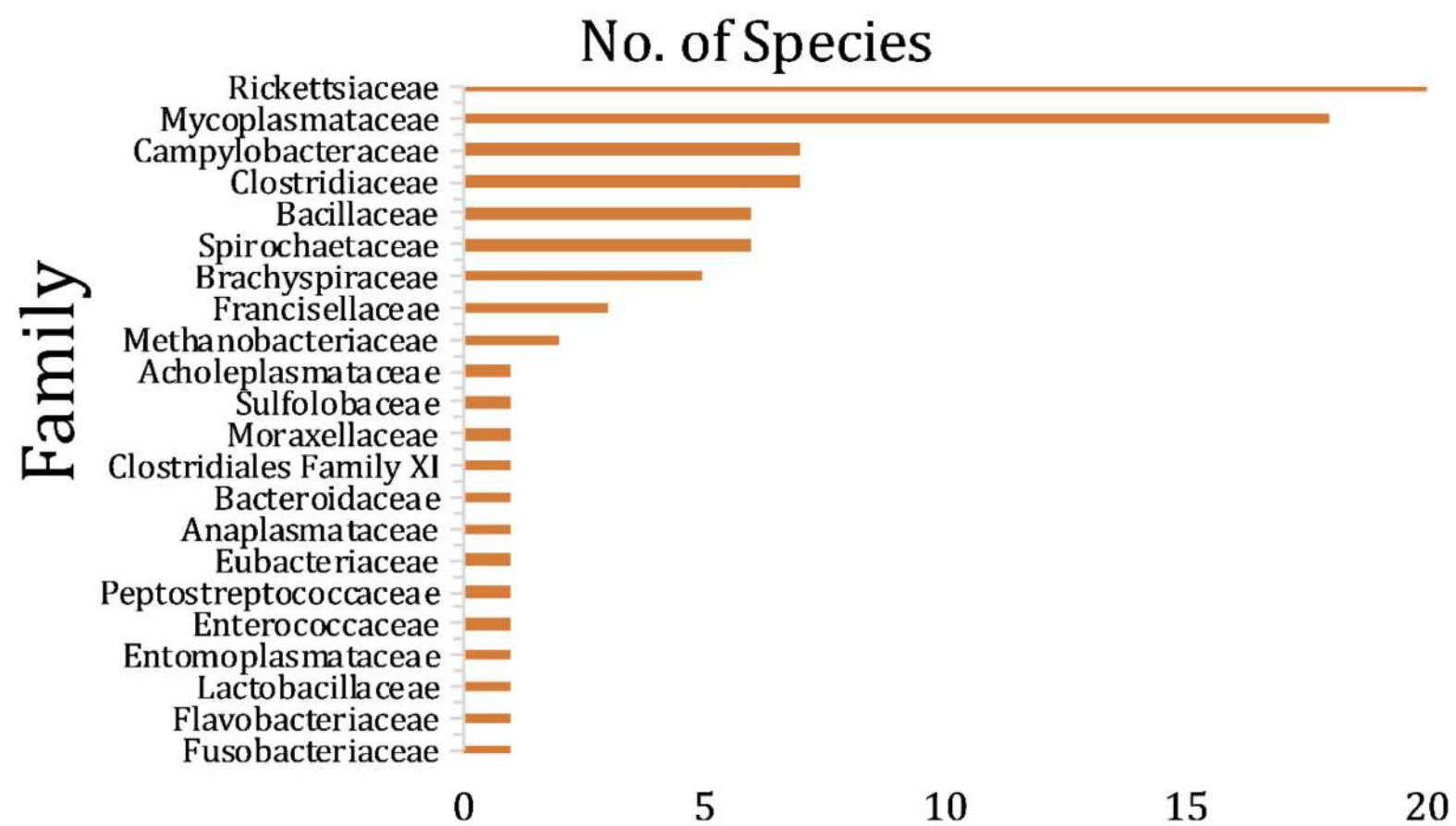
BC, Bray–Curtis; COG, Cluster of Orthologous Group; EGID, Ensemble algorithm for Genomic Island Detection; GI, genomic island; HA-SA, human-associated *Staphylococcus aureus*; HGT, horizontal gene transfer; LA-SA, livestock-associated *Staphylococcus aureus*; MGE, mobile genetic element; PAI, pathogenicity island; R–M system, restriction–modification system; VFDB, Virulence Factors Database.

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**Figure S1** Categorization of GI element donors based on their family

**Figure S1 Categorization of GI element donors based on their family.** The predicted donors of LA-SA GIs' were grouped as family, and the number of species from that family was represented by the length of bars.

Table S1. General Properties of the 14 Livestock-Associated *Staphylococcus aureus* genomes retrieved from NCBI

Strain	Sequence Type	Accession Number	Sequencing Technology	Host
08BA02176	ST398	CP003808	GS FLX Titanium pyrosequencing	Cattle
08S00974	ST398	CP020019	Illumina MiSeq	Cattle
71193	ST398	CP003045	Roche genome sequencer	Cattle
E154	ST398	CP013218	--	Chicken
ED98	ST5	CP001781	454 pyrosequencing	Chicken
ED133	ST133	CP001996	454 pyrosequencing	Small Ruminants
ISU935	ST5	CP017090	--	Swine
LGA251	ST130	FR821779	454 pyrosequencing	Cattle
Newbould_305	ST115	AKYW010000	Illumina HiSeq	Cattle
NZ15MR0322	ST398	LT699704	PacBio	Cattle
O11	ST130	CP024649	Illumina Genome Analyzer GAII	Small Ruminants
O46	ST130	CP025395	Illumina Genome Analyzer GAII	Small Ruminants
RF122	ST398	AJ938182	Shotgun Sequencing	Cattle
ST398	ST398	AM990992	Pyrophosphate Sequencing	Cattle

Table S2. Distribution patterns of GIs across the fourteen LA-SA genomes

GI	08BA2176	08S974	71193	E154	ED98	ED133	ISU935	LGA251	Newboul	NZ1	O11	O46	RF122	ST398	GC Content	Mechanism	Major Contributions
LASA-G11	+	-	+	-	-	+	-	+	-	-	-	-	+	+	31.6797477	Transposon	Immunity and antibiotic resistance
LASA-G12	+	-	+	-	-	-	-	-	-	-	-	-	-	-	33.7610328	Phage	Hypothetical Proteins
LASA-G13	+	+	+	-	+	+	-	+	+	-	-	-	+	+	32.2944644	Transposon	Toxins-Pathogenicity
LASA-G14	+	+	-	+	-	+	+	+	-	+	-	-	-	-	39.6454862	tRNA	Folate Synthesis
LASA-G15	+	+	+	+	+	-	+	-	-	-	-	-	-	-	30.7276935	NA	Virulence
LASA-G16	+	-	-	+	-	-	-	-	-	+	-	-	-	-	36.167112	NA	Virulence and antibiotic resistance
LASA-G17	+	-	+	-	+	+	-	+	+	-	-	-	-	+	30.1321768	NA	Virulence – Adherence
LASA-G18	+	-	-	-	-	-	-	-	-	-	-	-	-	-	35.7181749	tRNA	Virulence
LASA-G19	+	+	+	+	+	+	-	+	+	+	+	+	+	+	33.36027	tRNA	Antibiotic resistance
LASA-G110	+	-	+	+	-	-	-	-	-	-	-	-	-	-	29.5847244	Transposon	NA
LASA-G111	+	-	-	-	-	-	+	-	-	+	+	+	-	+	38.8052363	NA	Leucine/isoleucine biosynthesis
LASA-G112	+	+	+	+	-	-	+	+	+	+	+	+	-	+	37.2816085	NA	Virulence – Adherence
LASA-G113	+	-	-	-	+	-	+	+	+	+	+	+	+	+	34.3597446	NA	Virulence – Iron Acquisition
LASA-G114	+	-	+	+	+	-	+	+	+	+	+	+	+	+	34.3101279	NA	Virulence and antibiotic resistance
LASA-G115	-	+	+	+	-	+	-	+	-	+	-	-	-	+	31.205944	NA	Virulence – Adherence
LASA-G116	-	+	+	+	+	+	+	+	+	+	+	+	-	-	39.9966572	NA	Virulence and antibiotic resistance
LASA-G117	-	+	-	-	-	-	-	-	-	-	-	-	-	-	30.64652	Phage	Hypothetical Proteins
LASA-G118	-	+	-	+	-	-	-	-	-	+	-	+	-	-	36.5712591	NA	Antibiotic resistance
LASA-G119	-	-	+	+	+	+	+	+	+	+	+	+	+	-	37.2173272	Phage	Hypothetical Proteins
LASA-G120	-	-	-	+	-	-	+	-	-	-	-	+	+	-	39.6322739	tRNA	Trehalose metabolism
LASA-G121	-	-	-	-	+	-	-	-	-	-	-	-	-	-	26.8541583	NA	Antibiotic resistance
LASA-G122	-	-	-	-	+	+	-	-	-	-	+	-	-	-	36.8922605	Transposon	Hypothetical Proteins
LASA-G123	-	-	-	-	+	+	-	+	+	-	+	-	-	-	40.0605816	NA	Virulence – Toxins
LASA-G124	-	-	-	-	+	-	+	-	+	-	-	-	-	-	32.0237296	Phage	Hypothetical Proteins
LASA-G125	-	-	-	-	+	-	-	-	-	-	-	-	-	-	30.7045269	NA	NA
LASA-G126	-	-	-	-	-	+	-	-	-	-	-	-	-	-	34.6094074	tRNA	Virulence – Toxins
LASA-G127	-	-	-	-	-	+	-	-	-	-	-	-	-	-	29.8438981	Phage	Hypothetical Proteins
LASA-G128	-	-	-	-	-	+	-	-	-	-	-	-	-	-	35.1715317	Phage	Toxins-Pathogenicity
LASA-G129	-	-	-	-	-	-	+	-	-	-	-	-	-	-	29.8652591	NA	Toxins-Pathogenicity
LASA-G130	-	-	-	-	-	-	+	+	-	-	-	-	-	-	35.3210565	Transposon	Virulence and antibiotic resistance
LASA-G131	-	-	-	-	-	-	-	+	-	-	-	-	-	-	37.1447325	NA	NA
LASA-G132	-	-	-	-	-	-	-	-	+	-	-	-	-	-	40.4467135	Transposon	NA
LASA-G133	-	-	-	-	-	-	-	-	+	-	-	-	-	-	31.2197022	NA	Hypothetical Proteins
LASA-G134	-	-	-	-	-	-	-	-	+	-	-	-	-	-	34.989423	NA	NA
LASA-G135	-	-	-	-	-	-	-	-	+	-	-	-	-	-	35.1886396	Transposon	Virulence
LASA-G136	-	-	-	-	-	-	-	-	-	+	-	+	-	+	30.722953	Phage	Hypothetical Proteins
LASA-G137	-	-	-	-	-	-	-	-	-	-	+	-	-	-	36.8259804	Transposon	Toxins-Pathogenicity
LASA-G138	-	-	-	-	-	-	-	-	-	-	+	-	-	+	30.2064079	NA	Metabolism related
LASA-G139	-	-	-	-	-	-	-	-	-	-	-	+	-	-	35.419869	Transposon	Metabolism related
LASA-G140	-	-	-	-	-	-	-	-	-	-	-	-	+	-	35.8041138	NA	Virulence
LASA-G141	-	-	-	-	-	-	-	-	-	-	-	-	+	-	31.1702718	NA	Hypothetical Proteins
LASA-G142	-	-	-	-	-	-	-	-	-	-	-	-	+	-	29.6798588	Transposon	Virulence
LASA-G143	-	-	-	-	-	-	-	-	-	-	-	-	+	-	30.295941	NA	Virulence – Adherence
LASA-G144	-	-	-	-	-	-	-	-	-	-	-	-	+	-	35.8607324	Transposon	Metabolism related
LASA-G145	-	-	-	-	-	-	-	-	-	-	-	-	-	+	40.7430506	Transposon	Hypothetical Proteins
LASA-G146	-	-	-	-	-	-	-	-	-	-	-	-	-	+	37.5417913	Phage	Hypothetical Proteins

Table S3 Virulent genes associated with predicted Gis of *LASA'* genomes

Protein ID	VFDB Accession No.	Related genes	Virulence Factors	VF Class
ACY11319.1; ACY11320.1; ACY11321.1; AFR3846.1; ATV04656.1; CAI80978.1; CAI80979.1; CAI80980.1; CAI80981.1; CAI80982.1; CAI80989.1; SaureusN305_02140	VFG004506(gi:15927015)	<i>ebh</i>	Cell wall associated fibronectin binding protein	Adherence
ACY12392.1; AFR73793.1; ASC52031.1; SaureusN305_00371; SaureusN305_02431	VFG043588(gi:57651004)	<i>sasG</i>	cell wall surface anchor family protein	
AFR72873.1; ASC50323.1; CAI80432.1; SaureusN305_01293; YP_005733664.1	VFG004638(gi:87160156)	<i>clfA</i>	Clumping factor A	
AFR73178.1	VFG004496(gi:49483319)	<i>efb</i>	Fibrinogen binding protein	
AFR74495.1	VFG001283(gb/NP_647238)	<i>fnbA</i>	Fibronectin binding proteins	
AFR74492.1; AFR74494.1; ATV04655.1; SaureusNZMR0322_02541; SaureusNZMR0322_02542	VFG004615(gi:15928081)	<i>fnbB</i>		
Saureus08S00974_00548	VFG004606(gi:49482791)	<i>sdrC</i>		
Saureus08S00974_00549	VFG017111(gi:148267022)	<i>sdrD</i>	Ser-Asp rich fibrinogen-binding proteins	
Saureus08S00974_00550	VFG017226(gi:151220737)	<i>sdrE</i>		
AFR72875.1	VFG002418(gb/YP_001331791)	<i>vwbp</i>	secreted von Willebrand factor-binding protein precursor	
AFR72876.1	VFG043451(gi:57650133)	<i>emp</i>	secretory extracellular matrix and plasma binding protein	
AFR72040.1	VFG002420(gb/NP_644838)	<i>adsA</i>	Adenosine synthase A	Enzyme
AFR73846.1	VFG004744(gi:15927782)	<i>hysA</i>	Hyaluronate lyase	
ACY11709.1	VFG004703(gi:15927387)	<i>splA</i>	Serine Protease	
ADI98301.1; ATV02856.1	VFG004694(gi:82751395)	<i>splB</i>		
ADI98300.1; SaureusN305_00083; SaureusN305_00084	VFG004685(gi:82751394)	<i>splC</i>		
ACY11706.1	VFG004678(gi:87160514)	<i>splD</i>	thermonuclease precursor	
CAI81359.1; CCC88458.1	VFG004674(gi:82751393)	<i>splE</i>		
ADI98299.1	VFG004665(gi:82751392)	<i>splF</i>		
AFR72878.1	VFG004737(gi:49483047)	<i>nuc</i>		
AFH70185.1	VFG002422(gb/YP_001332911)	<i>chb</i>	chemotaxis-inhibiting protein	
CAI79911.1	VFG002405(gb/NP_645073)	<i>esxA</i>	Type VII Secretion System	Secretion System
CAI79912.1	VFG018114(gi:82749989)	<i>esxA</i>		
CAI79914.1	VFG002407(gb/NP_645076)	<i>esxB</i>		
CAI79915.1	VFG002408(gb/NP_645078)	<i>esxB</i>		
CAI79916.1	VFG018165(gi:82749992)	<i>esxC</i>		
CAI79917.1	VFG018167(gi:156978617)	<i>esxC</i>		
CAI79918.1	VFG018189(gi:82749994)	<i>esxB</i>		
AFR73182.1	VFG001293(gb/NP_645861)	<i>hly</i>	Alpha hemolysin	Toxin
AFH70247.1	VFG001798(gb/YP_186826)	<i>hlyB</i>	beta-hemolysin	
ATV03271.1; ATV04671.1	VFG043452(gi:57651346)	<i>hlyD</i>	Delta hemolysin	
ADI96966.1	VFG005006(gi:82750124)	<i>sec</i>	Enterotoxin C-bovine	
ACY11722.1; CAI81385.1	VFG005003(gi:15927398)	<i>seg</i>	Enterotoxin G	
ADI96967.1	VFG004988(gi:82750125)	<i>sell</i>	Enterotoxin-like L	
ACY11727.1	VFG004985(gi:15927403)	<i>selm</i>	Enterotoxin-like M	
ACY11723.1	VFG004982(gi:15927399)	<i>seln</i>	Enterotoxin-like N	
ACY11728.1	VFG004978(gi:15927404)	<i>selo</i>	Enterotoxin-like O	
ADI97633.1	VFG005013(gi:15924938)	<i>selp</i>	Enterotoxin-like P	
CAI81387.1	VFG004970(gi:82751420)	<i>selU</i>	Enterotoxin-like U	
ACY11724.1	VFG004966(gi:15927400)	<i>yent2</i>	Enterotoxin Yent2	
ACY11725.1	VFG004968(gi:15927401)	<i>yent1</i>	Enterotoxin Yent1	
AFR73191.1	VFG004877(gi:82750780)	<i>eta</i>	Exfoliative toxin type A	
ACY10313.1	VFG004942(gi:15926105)	<i>set12</i>	exotoxin	
AFR72485.1	VFG004959(gi:15926099)	<i>set6</i>		
AFR72486.1	VFG004956(gi:15926100)	<i>set7</i>		
AFR72487.1; AFR72488.1	VFG004964(gi:49482653)	<i>set2</i>		
AFR72490.1	VFG004963(gi:49482655)	<i>set10</i>		
AFR72492.1	VFG004965(gi:49482656)	<i>set11</i>		
AFR72493.1	VFG004961(gi:49482657)	<i>set13</i>		
AFR72494.1	VFG004962(gi:49482658)	<i>set14</i>		
AFR72497.1	VFG004901(gi:82750145)	<i>set15</i>		
ADI98315.1	VFG004862(gi:82751408)	<i>lukD</i>		
ADI98372.1	VFG004852(gi:82750532)	<i>lukE</i>	Leukotoxin E	
ADI98503.1; SaureusN305_02303	VFG044014(gi:87162038)	<i>lukH</i>	leukocidin family protein	



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/CI 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)

0322_02438																			COG1251	C	Nitrite reductase [NAD(P)H]
SaureusNZMR 0322_02439	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	COG1251	C	Nitrite reductase [NAD(P)H]
AFR73848.1	+	-	+	-	-	-	-	-	+	-	-	-	-	-	+			NA	NA	putative exported protein	
SaureusNZMR 0322_02445	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	COG0803	P	Metal-binding protein ZinT precursor
SaureusNZMR 0322_02446	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	NA	NA	High-affinity zinc uptake system binding-protein ZnuA
SaureusNZMR 0322_02449	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	COG2348	M	Aminoacyltransferase FemA
SaureusNZMR 0322_02522	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	COG2963	X	Transposase
SaureusNZMR 0322_02523	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein
AFR73849.1	+	-	-	-	-	-	-	-	-	-	-	-	-	-	+			NA	NA	hypothetical protein C248_1859	
AFR72056.1	+	-	-	-	-	-	-	-	-	-	-	-	-	-	+			NA	NA	hypothetical protein C248_0042	
AFR72029.1	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-			COG4241	S	putative membrane protein	
SaureusNZMR 0322_02541	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	NA	NA	Fibronectin-binding protein A precursor
SaureusNZMR 0322_02542	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	NA	NA	Fibronectin-binding protein A precursor
AFR73851.1	-	-	-	+	-	-	-	-	-	-	-	-	-	-	+			COG4584	X	Putative transposase	
AFR73852.1	+	-	+	+	-	-	-	-	-	+	-	-	-	-	+			NA	NA	putative lipoprotein	
ATV02856.1	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	COG3591	E	Serine protease
AFR73853.1	+	-	-	-	+	+	+	+	+	+	+	+	+	+	+			COG3545	R	hypothetical protein C248_1871	
ATV02866.1	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	NA	NA	hypothetical protein SaO11_00040
ATV02868.1	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	NA	NA	hypothetical protein SaO11_00042
ATV02869.1	-	-	-	-	-	-	-	-	-	-	+	+	-	-	-	-	-	-	NA	NA	DNA helicase protein
ATV02874.1	-	-	-	-	-	-	-	-	-	-	+	+	-	-	-	-	-	-	NA	NA	BioC protein
AFR74016.1	-	-	-	+	-	-	-	-	-	+	+	-	-	-	+			COG0059	EH	ketol-acid reductoisomerase	
ATV02876.1	-	-	-	-	-	-	-	-	-	-	+	+	-	-	-	-	-	-	COG3208	Q	Iron acquisition yersiniabactin synthesis enzyme (YbT,resembles
ATV02877.1	-	-	-	-	-	-	-	-	-	-	+	+	-	-	-	-	-	-	NA	NA	4'-phosphopantetheinyl transferase
ATV02878.1	-	-	-	-	-	-	-	-	-	-	+	+	-	-	-	-	-	-	NA	NA	2,3-dihydroxybenzoate-AMP ligase
ATV02879.1	-	-	-	-	-	-	-	-	-	-	+	+	-	-	-	-	-	-	NA	NA	Non-ribosomal peptide synthetase
ATV02880.1	-	-	-	-	-	-	-	-	-	-	+	+	-	-	-	-	-	-	NA	NA	Polyketide synthase
ATV02881.1	-	-	-	-	-	-	-	-	-	-	+	+	-	-	-	-	-	-	NA	NA	hypothetical protein SaO11_00055
ATV02882.1	-	-	-	-	-	-	-	-	-	-	+	+	-	-	-	-	-	-	COG1020	Q	Iron acquisition yersiniabactin synthesis enzyme (Irp2)
ATV02883.1	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	NA	NA	Substrate-specific component of ECF transporter
ATV02884.1	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	COG0619	H	Transmembrane component of energizing module of
ATV02885.1	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	COG1122	PR	Duplicated ATPase component of energizing module
AFR74017.1	+	-	-	+	-	-	+	-	-	+	+	+	-	+	+			COG0119	E	2-isopropylmalate synthase	
AFR74018.1	+	-	-	+	-	-	+	-	-	+	+	+	-	+	+			COG0473	CE	3-isopropylmalate dehydrogenase	
ATV03138.1	-	-	-	-	-	-	-	-	-	-	+	+	-	-	-	-	-	-	NA	NA	Phage tail protein
AFR74019.1	+	-	-	+	-	-	+	-	-	+	+	+	-	+	+			COG0065	E	3-isopropylmalate dehydratase large subunit	
AFR74020.1	+	-	-	+	-	-	+	-	-	+	+	+	-	+	+			COG0066	E	3-isopropylmalate dehydratase small subunit	
ATV03255.1	-	-	-	-	-	-	-	-	-	-	+	+	-	-	-	-	-	-	NA	NA	hypothetical protein SaO11_00429
AFR74021.1	+	-	-	+	-	-	+	-	-	+	+	+	-	+	+			COG1171	E	threonine dehydratase biosynthetic	
ATV03264.1	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	NA	NA	hypothetical protein SaO11_00438
ATV03271.1	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	COG1388	M	N-acetylmuramoyl-L-alanine amidase sle1
ATV03272.1	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	NA	NA	hypothetical protein SaO11_00446
ATV03273.1	-	-	-	-	-	-	-	-	-	-	+	-	-	+	-	-	-	-	COG0494	V	MutT domain containing protein
AFR74022.1	+	-	-	+	-	-	+	-	-	+	+	+	-	+	+			COG3091	R	hypothetical protein C248_2073	

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/hydroxypyruvate 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	FUNCTIONAL DESCRIPTION
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	GlcC	
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	



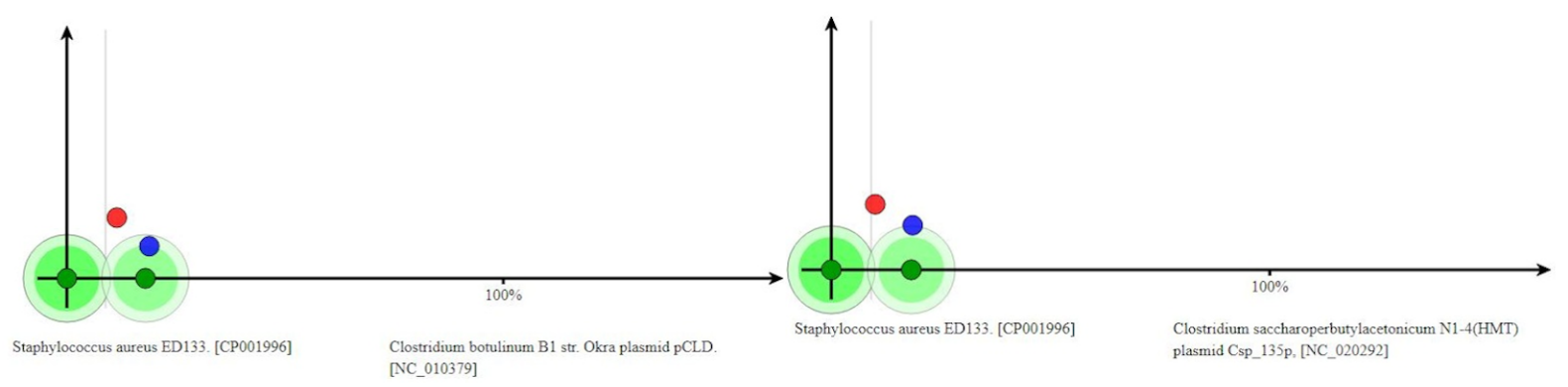
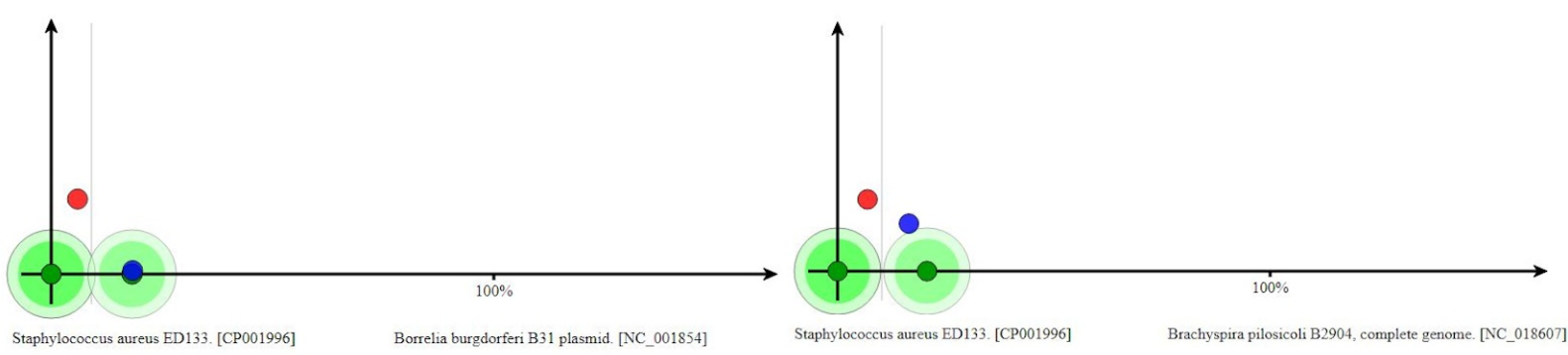
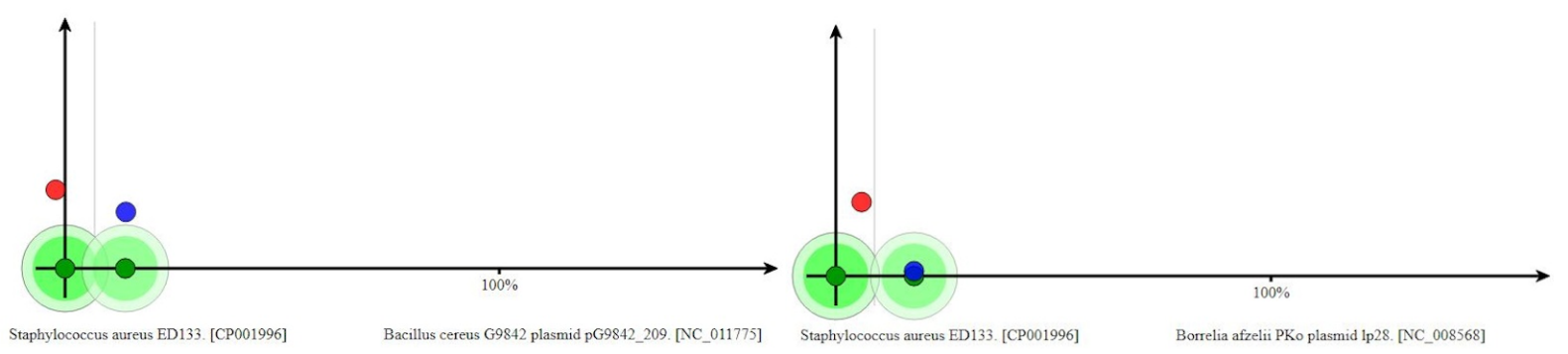
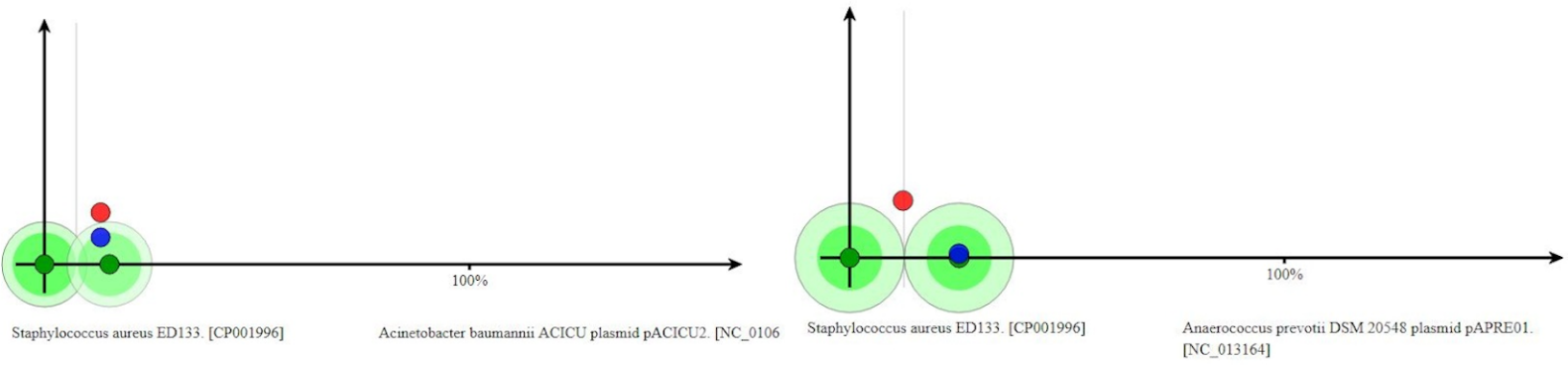
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AFH68780.1	-	-	+	+	-	-	-	+	-	-	-	-	-	-	COG1774	T	Phosphorelay inhibitor
AFH68781.1	-	-	+	+	-	-	-	-	-	-	-	-	-	-	COG4467	L	Initiation-control protein
AFR72343.1	+	-	-	-	-	-	-	-	-	-	+	-	+	-	NA	NA	putative phage protein
AFH68815.1	-	-	-	+	-	-	-	+	-	-	-	-	+	-	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
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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
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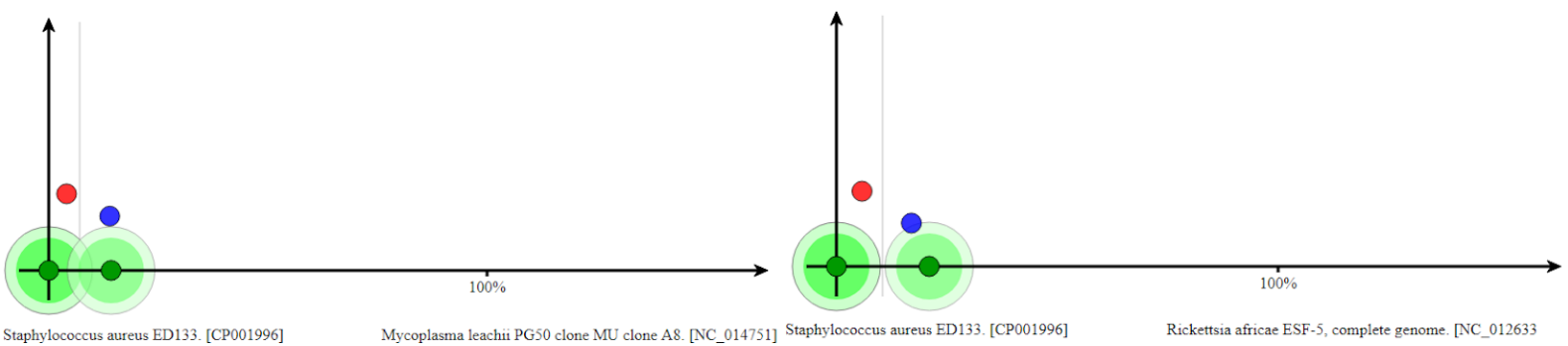
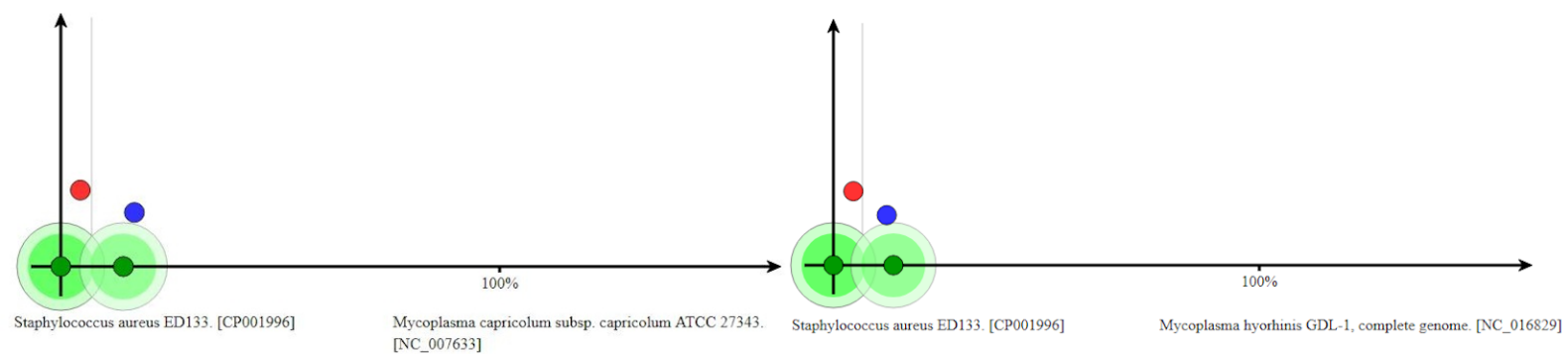
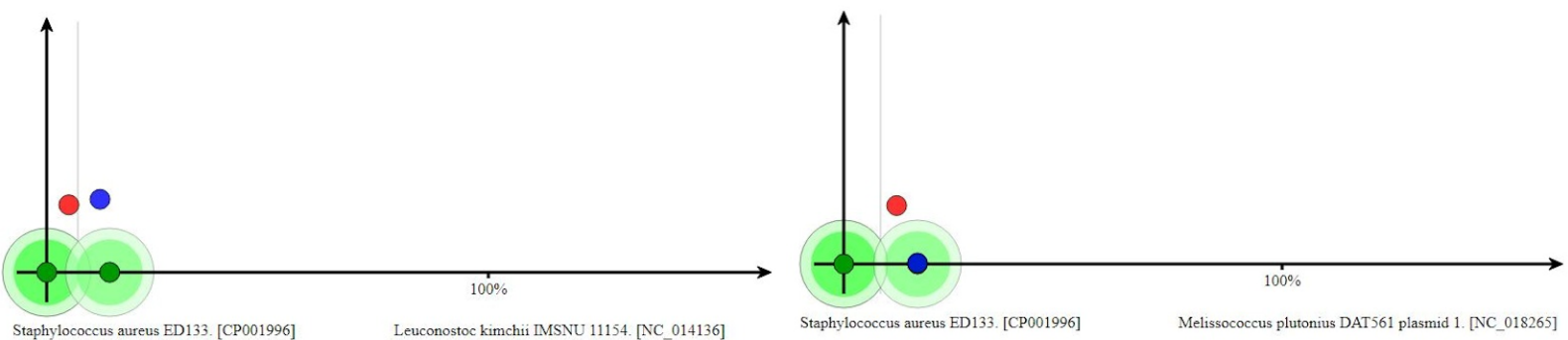
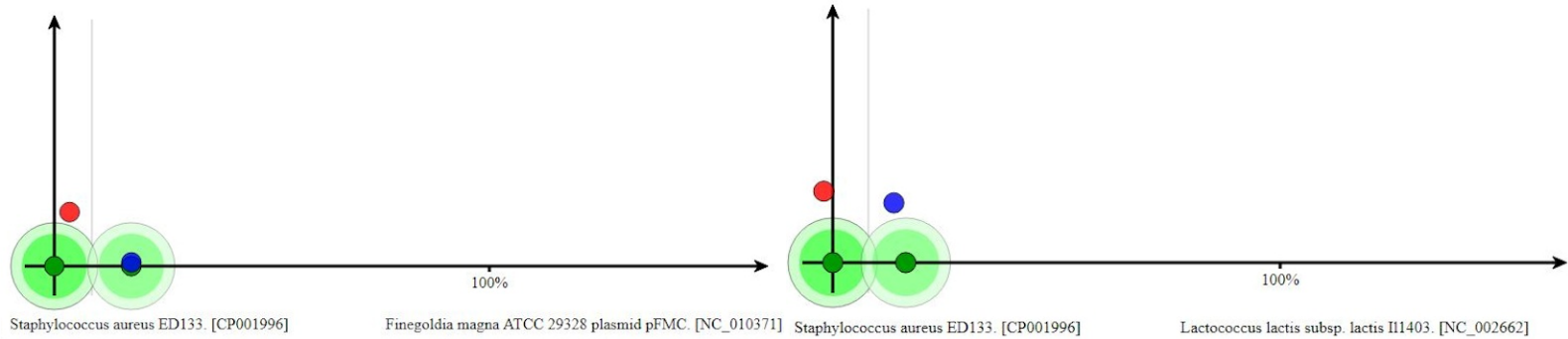
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AFH70206.1	-	-	+	-	-	+	-	-	-	+	-	-	-	-	NA	NA	Portal protein
AFH70208.1	-	-	+	-	-	+	-	-	-	+	-	-	-	-	NA	NA	Phage-related protein
AFH70209.1	-	-	+	-	-	+	-	-	-	+	-	-	-	-	NA	NA	hypothetical protein ST398NM01_2932
AFR72357.1	+	-	-	-	-	+	-	-	-	-	-	+	-	+	NA	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
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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
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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
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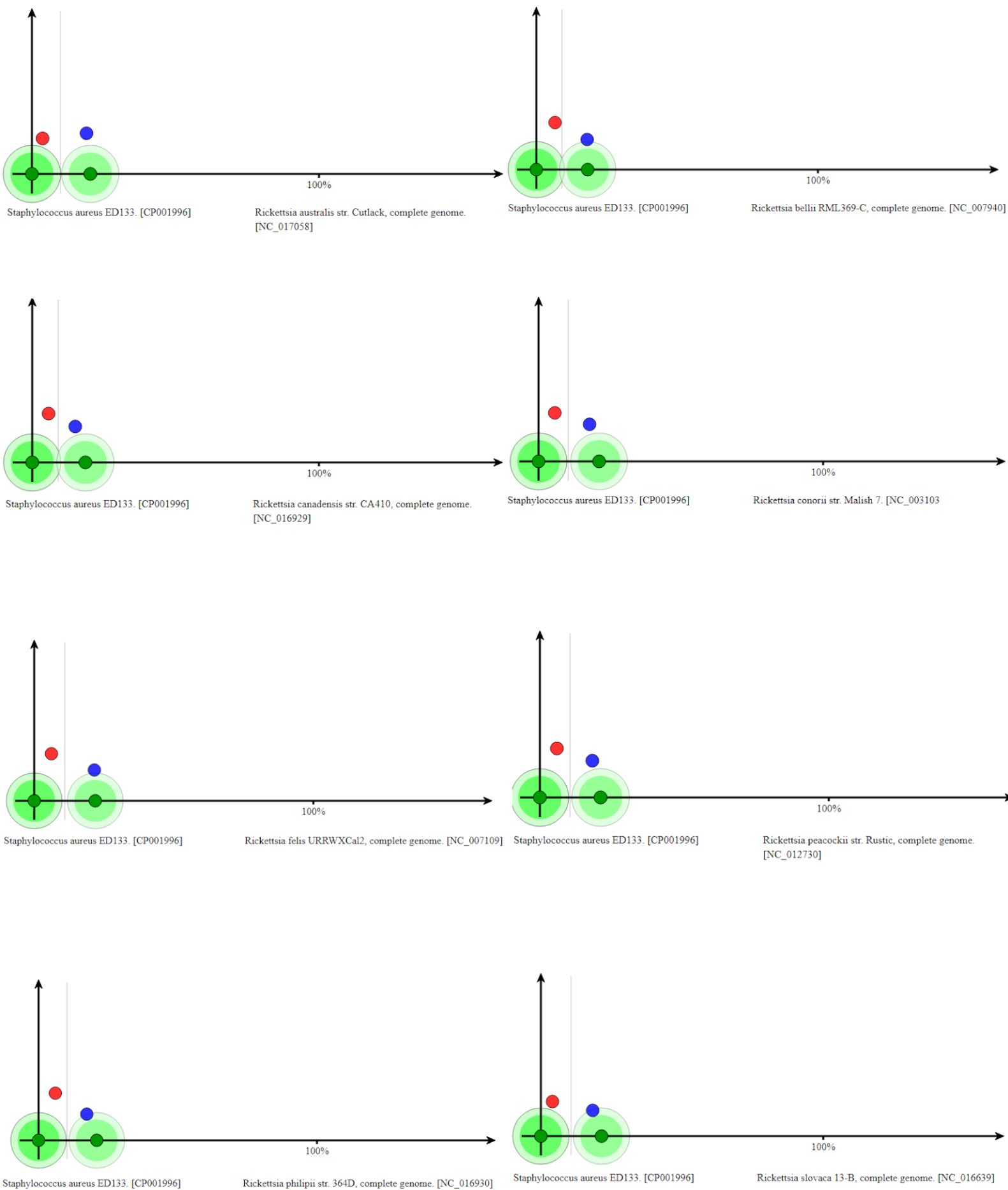
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APE87185.1	-	-	-	+	-	-	-	-	-	-	-	-	-	-	NA	NA	transposase
APE87186.1	-	-	-	+	-	-	-	-	-	-	-	-	-	-	NA	NA	hypothetical protein AS852_00395
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APE87533.1	-	-	-	+	-	-	+	-	-	-	-	-	-	-	NA	NA	hypothetical protein AS852_02250
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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
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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
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APE8875.1	-	-	-	+	-	-	-	+	-	-	-	-	-	-	NA	NA	phage tail protein
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APE8880.1	-	-	-	+	-	-	+	+	-	-	-	-	+	-	NA	NA	hypothetical protein AS852_09410
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APE8883.1	-	-	-	+	-	-	+	+	-	-	-	-	-	-	NA	NA	phage tail protein
APE8884.1	-	-	-	+	-	-	+	+	-	-	-	-	+	-	NA	NA	terminase
APE8885.1	-	-	-	+	-	-	-	+	+	-	-	-	-	-	NA	NA	hypothetical protein AS852_09435
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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.