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Original Article

Molecular types, genetic characteristics and phylogenomic analysis of *Staphylococcus aureus* causing infective endocarditis

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Abstract

Introduction: *Staphylococcus aureus* is a leading cause of infective endocarditis (IE), yet its molecular epidemiology remains understudied. In this study, genomic data from 285 IE-associated *S. aureus* strains wre analyzed to inform clinical strategies.

Methodology: Strains were characterized by multilocus sequence typing (MLST), *spa* typing, and SCC*mec* classification. Antibiotic resistance genes (ARGs) and virulence factors (VFs) were identified from genomic data, and phylogenetic trees were constructed.

Results: Predominant sequence types (STs) included ST45 (CC45), ST5 (CC5), ST8 (CC8), ST15 (CC15), ST30 (CC30), ST1 (CC1), and ST188 (CC1). Common spa types were t2, t8, t230, and t88. Among 46 mecA-positive strains, SCC*mec* IV (50%) and II (34.8%) predominated. *MecA* was more prevalent in ST5 and ST8 strains but less prevalent in ST45 and ST15 strains. ST45 strains lacked *splA*, *splB*, and *splE*, unlike other STs. ST45 and ST8 strains harbored higher numbers of ARGs, while ST15 and ST188 carried fewer ARGs. Similarly, ST5 and ST1 strains exhibited higher VF counts than ST15 and ST188 strains. Phylogenetic tree revealed that some clades dominated by a single ST contained insertions of strains from different STs, and closely related strains were primarily associated with different CC groups. Some CC1 and CC8 strains clustered together on a branch, indicating a close genetic relationship.

Conclusions: ST5 and ST8 clones pose high ARG or VF risks and warrant targeted therapy, whereas ST15 and ST188 may represent lower-risk lineages. The prevalence of SCC*mec* IV highlights the contribution of community-associated MRSA to IE. Phylogenetic inconsistencies reflect adaptive evolution of *S. aureus* in IE.

Key words: *Staphylococcus aureus*; infective endocarditis; multilocus sequence typing; antibiotic resistance genes; virulence genes.

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Introduction

Infective endocarditis (IE) is a severe and potentially life-threatening infection of the endocardium, primarily caused by bacterial pathogens [1]. Its incidence rate is 3-10 per 100,000 people, with a 30-day mortality rate as high as 30% [2]. *Staphylococcus aureus* is a leading causative agent of IE, responsible for a significant proportion of cases worldwide [3]. *S. aureus* IE affects the heart valves, leading to inflammation, valve damage, and life-threatening complications such as heart failure, stroke, and sepsis, which can spread to other organs and significantly increase mortality risk [4]. In addition, *S. aureus* can form biofilms on medical devices such as artificial heart valves or pacemakers. These biofilms provide a protective environment that enhances antibiotic resistance and immune system attacks [4], making IE caused by this pathogen particularly challenging to treat.

Understanding the genetic diversity, antimicrobial susceptibility patterns, and virulence determinants of *S. aureus* strains is crucial for guiding appropriate antibiotic therapy and implementing effective infection control measures. To date, several studies have investigated the molecular epidemiology of *S. aureus* in various clinical contexts, including bloodstream infections, surgical site infections, and pneumonia [5-7]. However, the molecular epidemiology of *S. aureus* strains responsible for IE remains poorly understood. Existing studies have been limited by small sample sizes [8] and a paucity of molecular epidemiological data, as this was not their primary focus [9,10]. In this study, a comprehensive molecular epidemiological investigation was conducted on *S. aureus* strains from patients diagnosed with IE. A combination of molecular typing techniques and whole-genome sequencing was used to assess the genetic diversity, virulence gene profiles, and antibiotic resistance gene profiles of these strains. The findings enhance understanding of the molecular types, genetic characteristics, and

phylogenetic relationships of IE-associated *S. aureus* strains, which may ultimately facilitate the development of more effective prevention and treatment strategies.

Methodology

Data collection

Accession numbers for whole-genome sequenced *S. aureus* strains from infective endocarditis (IE) cases were retrieved from published literature and the NCBI Pathogen Database (https://www.ncbi.nlm.nih.gov/pathogens/) using keywords including 'infective endocarditis', 'endocarditis', and 'IE'. The sole criterion for inclusion was that the strain's metadata in the database or its associated publication explicitly identified it as originating from a clinically confirmed human infective endocarditis case**.** Any strain with an ambiguous or non-human source was excluded. All analyses were performed on publicly available whole-genome sequence data from the NCBI pathogen database. Raw sequencing data or assembled genomes were downloaded from the NCBI database.

Sequence analysis

Acquired antibiotic resistance genes (ARGs) and virulence factors (VFs) were analyzed using both offline and online versions of ResFinder 4.1 and VirulenceFinder 2.0. The offline versions were applied to raw sequencing reads, whereas the online versions were used with assembled genomes. The online versions of ResFinder and VirulenceFinder were accessed through the following URLs: https://cge.food.dtu.dk/services/ResFinder/ and https://cge.food.dtu.dk/services/VirulenceFinder/, respectively. Results were reported for ≥ 90% nucleotide identity, ≥ 90% coverage of the query, and a sequence depth of ≥ 10×. ARG and VF scores were defined as the number of unique ARGs and VFs detected for each strain, respectively. Raw sequencing data were assembled into scaffolds using SPAdes version 3.13.1 [11]. For each genome, multi-locus sequence type (MLST) and the corresponding clonal complex (CC) were determined using the online PubMLST tool (https://pubmlst.org/bigsdb?db=pubmlst_saureus_seqdef&page=sequenceQuery). *spa* types and staphylococcal cassette chromosome *mec* (SCC*mec*) types were determined using spaTyper version 1.0 (https://cge.food.dtu.dk/services/spaTyper/) and SCCmecFinder version 1.2 (https://cge.food.dtu.dk/services/SCCmecFinder/), respectively.

Phylogenomic analyses

GTDB-Tk version 2.1.1 [12] was used to identify, extract, and align the bac120 marker gene set from all the assembled genomes. The resulting alignment was used to construct a maximum likelihood phylogenetic tree using IQ-TREE version 2.2.2.3 [13]. The optimal nucleotide substitution model (-MFP) was selected, and 1000 ultrafast bootstrap (UFBS) replicates were performed. The phylogenetic tree was visualized and annotated using iTOL (itol.embl.de).

Statistical analysis

Group comparisons were analyzed using the Kruskal-Wallis test or Mann-Whitney *U*-test for continuous variables, and the Chi-square or Fisher's exact test for categorical variables. A two-sided *p* value < 0.05 was considered statistically significant. All statistical analyses were performed using IBM SPSS Statistics version 27.0 (IBM Corp., Armonk, NY, USA).

Data availability

The complete lists of ARGs and VFs for each strain are available from the corresponding author upon reasonable request.

Results

Molecular types

A total of 285 non-duplicate *S. aureus* strains causing IE were identified from previous studies and NCBI pathogen database (https://www.ncbi.nlm.nih.gov/pathogens/; 18 October 2024). Among these, 52 STs and 9 CCs were identified (Supplementary Table S1). The most common ST was ST45 (belonging to CC45), accounting for 11.2% of the strains (32/285). Six other prevalent STs were identified: ST5 (CC5), ST8 (CC8), ST15 (CC15), ST30 (CC30), ST1 (CC1), and ST188 (CC1), representing 10.9%, 9.1%, 8.4%, 8.1%, 5.6%, and 4.2% of the strains, respectively. In addition, 269 strains were classified into 144 different *spa* types, whereas 16 strains could not be assigned to any known type (Supplementary Table S1). The most prevalent *spa* type was t2, which accounted for 5.6% of the strains (16/285), followed by t8 (4.6%), t230 (4.2%), and t88 (4.2%).

SCCmec typing

Among the 285 *S. aureus* strains, 46 (16.1%) carried the *mecA* gene. Of these *mecA*-positive strains, 23 (50%) carried SCC*mec* IV, with subtypes IVa (13), IV (4; subtype not assigned), IVc (3), IVg (2), and IVh

(1); 16 (34.8%) carried SCC*mec* II. The remaining *mecA*-positive strains included SCC*mec* V (2), I (1), III (1), and three with non-typable SCC*mec* (Supplementary Table 1).

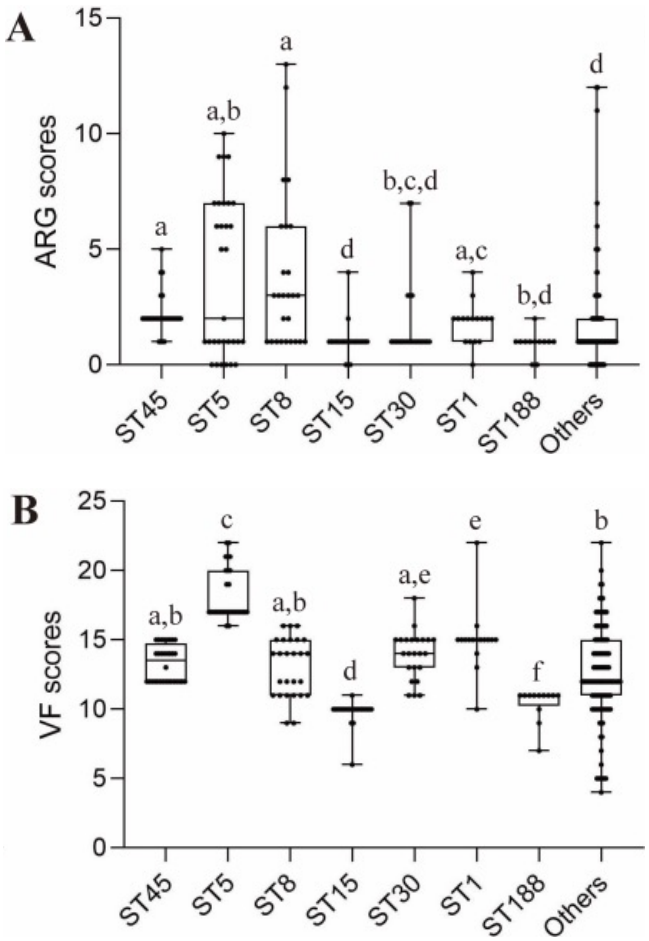
Gene (ARGs and VFs) capacity and subtype specificity

ARG and VF scores were analyzed across different STs to assess their potential for resistance and virulence. Among the major STs, ST45 and ST8 strains carried higher numbers of ARGs, whereas ST15 and ST188 carried lower ARGs. Conversely, ST5 and ST1 strains harbored higher numbers of VFs, while ST15 and ST188 carried lower VFs (Figure 1, and Supplementary Tables 2 and 3). ST15 and ST188 strains carried fewer resistance and virulence genes overall, suggesting they may exhibit less resistant and virulent phenotypes. Associations between molecular types and the distribution of ARGs and VFs were assessed using the Chi-square or Fisher's exact test (Supplementary Table 2). For β-lactam resistance, *mecA* was more prevalent in ST5 and ST8 strains and less prevalent in ST45 and ST15 strains. For macrolide resistance, *erm*(A) was more prevalent in ST5 strains and less prevalent in ST45 strains. All ST45 strains (100%) lacked exoenzyme genes *splA*, *splB*, and *splE*, whereas other STs showed a high prevalence of at least one of these genes. All ST15 strains carried *scn* but lacked *sak*, while the remaining STs showed a high prevalence of both *scn* and *sak*. Among toxin genes, a significant proportion of the 285 *S. aureus* strains carried *lukD* (61.8%), *lukE* (62.8%), *seg* (51.6%), *sei* (52.3%), *sem* (53.0%), *sen* (50.9%), *seo* (53.3%), and *seu* (51.2%). *lukD* and *lukE* were present in all strains of ST5, ST8, ST15, ST1, and ST188 strains. In addition, *seg*, *sei*, *sem*, *sen*, *seo*, and *seu* were present in > 95% of ST45, ST5, and ST30 strains. The observed associations between molecular types and these ARGs and VFs may contribute to the resistance and virulence characteristics of the strains.

Whole-genome phylogenetic analysis

As shown in Figure 2, the 285 *S. aureus* strains formed a single phylogenetic tree with high bootstrap support, indicating high confidence in the branching pattern and low genetic divergence among strains. Branches composed of strains from the same ST occasionally contained insertions of strains from other STs. For example, a single ST6425 strain (BPH3211) was located within a clade of 12 ST188 strains, and two strains [134789 (ST573) and 76045 (ST3384)] were embedded within a clade of 16 ST1 strains. In addition, closely related strains were primarily associated with different CC groups. For instance, 42 CC45 and 9 CC22 strains formed two distinct clades with high bootstrap support. The clustering of some CC1 and CC8 strains (ST20101161, ST20100875, 113391, 106461, BPH2745, ST20110196, BSN39, BPH3540, and

Figure 1. ARG (A) and VF (B) scores according to ST types among the 285 *S. aureus* strains. ARG and VF scores were defined as the number of unique ARG and VF detected for each strain, respectively. Since the ARG and VF scores were not normally distributed, they are summarized as median and interquartile range [M (Q1, Q3)] (Supplementary Table 2). Pairwise comparisons between groups were performed using the Mann–Whitney U test. Detailed results—including *p*, effect sizes (r), and their 95% confidence intervals—are fully provided in Supplementary Table 3. In the box plots, groups that share at least one common letter are not significantly different ($p \geq 0.05$), whereas groups with no common letters are statistically significant ($p < 0.05$). ARG scores in ST45 and ST8 strains were significantly higher than in ST15, ST30, ST188 or "Others" strains, while ARG scores in ST15 and ST188 strains were significantly lower than those in ST45, ST8, and ST1 strains, with ST15 also lower than ST5 ($p < 0.05$). VF scores in ST5 strains were markedly elevated compared to the other seven groups ($p < 0.05$). Similarly, ST1 strains exhibited significantly higher VF scores than the other seven groups, with the exception of ST30 ($p < 0.05$). In contrast, ST15 and ST188 strains had significantly lower VF scores than the remaining six groups ($p < 0.05$).

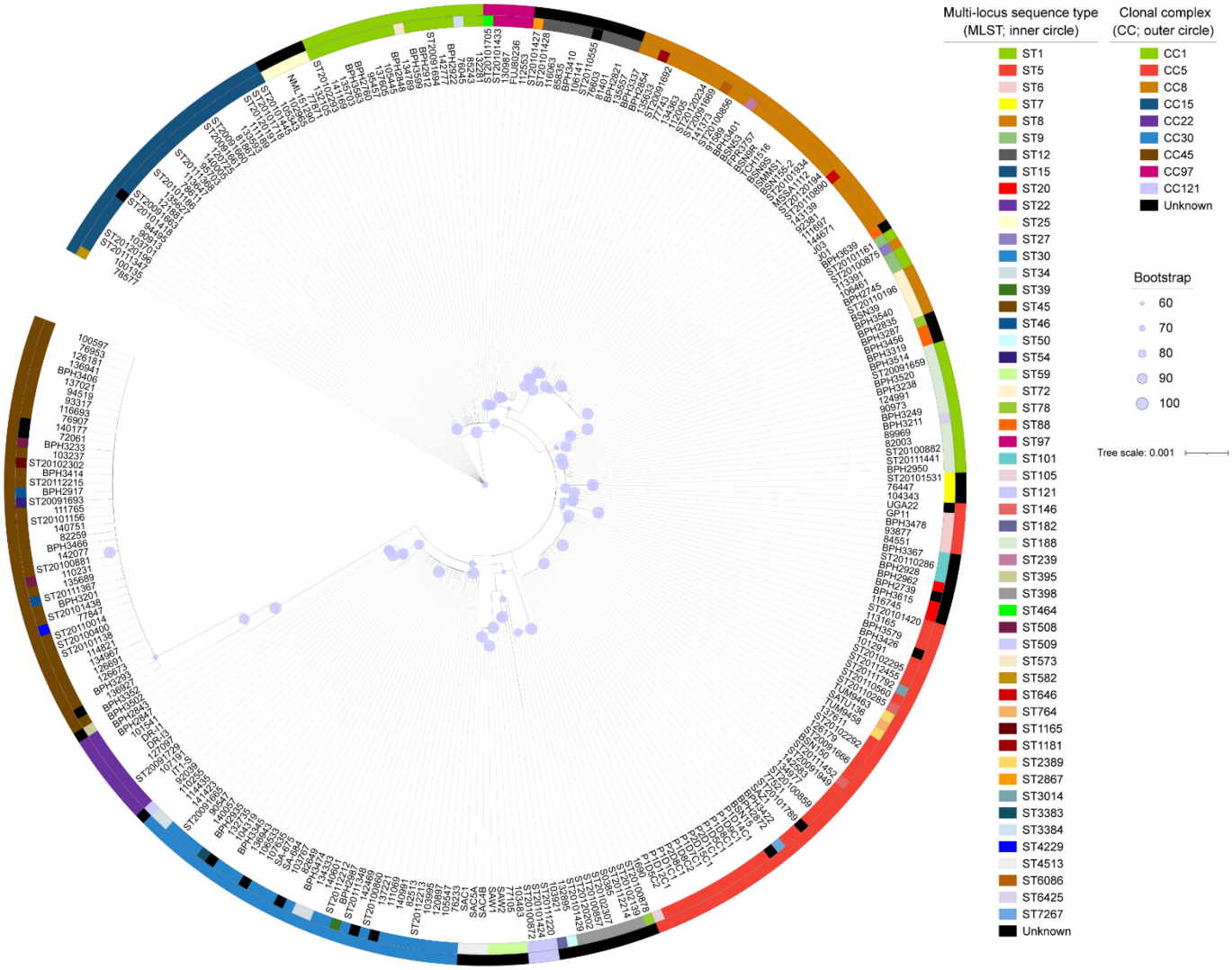


BPH2835) on the same branch suggests a close genetic relationship between them. The presence of strains with different STs within branches otherwise dominated by a single ST may be attributed to mutations, horizontal gene transfer, or hybridization, reflecting the diversity and adaptability of *S. aureus* during its evolution.

Discussion

The molecular types of *S. aureus* vary by infected site [14]. For example, in skin and soft tissue infections, the predominant methicillin-resistant *S. aureus* (MRSA) strains were ST59, ST8, and ST45 [15]. Similarly, in bone and joint infections, the predominant MRSA strains were ST59 and ST22 [16]. In this study, among 285 *S. aureus* strains causing IE, the most prevalent molecular types identified were ST45 (CC45), ST5 (CC5), ST8 (CC8), ST15 (CC15), and ST30 (CC30). The predominance of ST45 (CC45), ST5 (CC5), and ST8 (CC8) clones in IE aligns with their established pathogenic potential. ST5 (CC5) is known to be associated with healthcare-associated MRSA infections and has been linked to persistent bacteremia and poorer clinical outcomes [17]. The high prevalence of ST8 (CC8), a common community-associated MRSA clone, may reflect the evolving epidemiology of IE, in which community strains are increasingly causing severe invasive disease. The molecular types of *S. aureus* causing bacteremia and IE appear similar [9]. These findings are consistent with previous studies reporting these molecular types as common in *S. aureus* isolated from blood [9,18,19]. In addition, a diverse distribution of *spa* types was observed among the 285 *S. aureus* strains. Out of these, 269 strains were classified into 144 different *spa* types, indicating high

Figure 2. Phylogenetic analysis of 285 *S. aureus* strains causing IE. The inner and outer rings illustrate the multilocus sequence type (ST) and clonal complex (CC) for each genome, respectively.



genetic diversity within the population. 16 strains could not be assigned to any known type, suggesting the presence of novel or rare *spa* types. The identification of these molecular types highlights their potential significance in the epidemiology and pathogenesis of *S. aureus* endocarditis.

Among the 46 *mecA*-positive *S. aureus* strains, SCC*mec* type IV was the most prevalent, followed by type II. SCC*mec* types I, II and III are the most frequent among hospital acquired-MRSA, whereas types IV and V are associated with community acquired-MRSA [20]. The predominance of SCC*mec* IV in the MRSA strains analyzed here carries significant therapeutic implications. While traditionally associated with community settings, its prevalence in IE underscores the need to reconsider empirical antibiotic regimens. Although the background of these strains was not specified, IE is generally more prevalent in hospital settings, which aligns with the literature cited above. Additionally, SCC*mec* type IV MRSA is associated with frequent bloodstream infections, and the SCC*mec* type IV clone exhibits a higher ability to form plasma biofilm compared to the SCC*mec* type II [21]. The prevalence of SCC*mec* IV and II suggests the need for ongoing monitoring and investigation into their clinical relevance.

Analysis of ARG and VF scores revealed differences in resistance and virulence gene capacity among different molecular types. Specifically, ST45 and ST8 strains had a higher number of ARGs, while ST15 and ST188 strains had a lower number of ARGs. On the other hand, ST5 and ST1 strains harbored a higher number of VFs compared to other molecular types. Direct comparisons with other studies are challenging, as few reports have quantified ARG and VF scores. The present findings contradict a previous report indicating that CC8 harbored a significantly higher number of exoenzyme and toxin genes than other CCs [22]. Differences in sample sizes and sources between studies may contribute to this discrepancy. Overall, these findings indicate potential differences in resistance and virulence among *S. aureus* strains causing IE. In addition, a comparative analysis based on molecular types further elucidated associations between specific ARGs and VFs with different STs. For instance, the *mecA* gene, which confers β-lactam resistance, was more prevalent in ST5 and ST8 strains. This observation is consistent with previous studies reporting higher rates of methicillin resistance in ST5 and ST8 strains [23,24]. The *erm*(A) gene, associated with macrolide resistance, was more prevalent in ST5 strains, partially aligning with a previous report that *erm*(A) was mainly present in MRSA ST5 and ST8 [25]. Additionally, all ST45 (CC45) strains lacked the exoenzyme genes *splA*, *splB*, and *splE*, whereas other STs showed a high prevalence of at least one of these genes (Supplementary Table S2). This genetic profile is consistent with previous reports characterizing CC45 by the absence of these three genes [26], suggesting that it may be a characteristic feature of this lineage. Regarding leukotoxin genes, leukotoxin ED (LukED) genes (*lukD* and *lukE*) were present in all strains of certain STs, including ST5 (CC5), ST8 (CC8), ST15 (CC15), ST1 (CC1), and ST188 (CC1) (Supplementary Table S2). This observation partially aligns with a previous report that associated *lukD* and *lukE* with CC8 and CC97 [22]. The universal presence of *lukED* across major lineages is particularly relevant for IE pathogenesis, as this toxin directly damages endothelial cells and promotes vegetation formation [27]. Only 5 ST8 strains carried the Panton-Valentine leukocidin (LukSF-PV) genes (*lukF-PV* and *lukS-PV*) (Supplementary Table S2). This low prevalence may correlate with more severe disease manifestations, which is consistent with the known role of this toxin in causing tissue necrosis and intense inflammation [28].

Whole-genome phylogenetic analysis demonstrated a close genetic relationship among the *S. aureus* strains causing IE. The presence of insertions of strains from different STs within branches otherwise dominated by a single ST suggests possible genetic recombination or horizontal gene transfer. This finding is consistent with previous studies reporting genetic diversity and genomic plasticity in *S. aureus* [29,30]. The clustering of CC1 and CC8 strains on the same branch indicates a close genetic relationship between these two clonal complexes.

This study has several limitations. Its retrospective nature and reliance on public database data precluded access to detailed clinical metadata, such as primary infection sites, patient comorbidities, and treatment outcomes, which prevented in-depth statistical analysis. The strain collection may harbor selection bias, potentially over- or under-representing certain clones. Furthermore, the findings are based on genotypic predictions without phenotypic validation of antimicrobial resistance or virulence. Finally, although the sample size is substantial, it may still be insufficient to capture the full genetic diversity of *S. aureus* causing IE.

Conclusions

This study provides valuable information on the molecular types, ARGs, VFs, and phylogenomic

characteristics of *S. aureus* strains causing IE. ST5 and ST8 clones pose high ARG or VF risks, warranting targeted therapy, while ST15 and ST188 may represent lower-risk lineages. The prevalence of SCC*mec* IV highlights the contribution of community-associated MRSA to IE. Phylogenetic inconsistencies reflect the adaptive evolution of *S. aureus* in IE. Strain-specific management and surveillance of high-risk clones are imperative for improving outcomes. These findings may contribute to the development of targeted interventions for preventing and treating *S. aureus* endocarditis.

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Authors' contributions

All authors made a significant contribution to the work. Xiujuan Wu, Yitao Duan, and Chuanyu Gao designed the study. Xiujuan Wu and Weili Liu collected and analyzed the data. Xiujuan Wu drafted the paper. Yitao Duan and Chuanyu Gao revised the paper.

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Conflict of interest

No conflict of interest is declared.

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Annex – Supplementary Items

Supplementary Table 1. General information about 285 *S. aureus* strains causing IE.

NO.	Strain	NCBI Accession numbers	BioSample numbers	Isolation date	Geographical origin (Country)	CCa	MLST[a]	spa type[a]	SCCmec[a]	References[c]
1	UGA22	GCA_003850085.1	SAMN07666475	2003-01-01	Kenya	5	Unknown	t701	ND[b]	-
2	J01	GCA_005889995.1	SAMN11823229	2011	Sakoulas	8	8	t64	IVg(2B)	-
3	MSSA1112	GCA_009729825.1	SAMN13381878	1997-10	Switzerland	8	8	t8	ND	-
4	FUJ80236	GCA_021029565.1	SAMN22072579	2020-06-03	Japan	97	97	t267	IVc(2B)	[1]
5	P1D9C1	GCA_009739735.1	SAMN10374691	2017-05-12	Israel	5	5	t88	II(2A)	-
6	P1D8C2	GCA_009739755.1	SAMN10374690	2017-05-11	Israel	5	5	t88	II(2A)	-
7	P1D8C1	GCA_009739775.1	SAMN10374689	2017-05-11	Israel	5	5	t88	II(2A)	-
8	P1D7C1	GCA_009739795.1	SAMN10374688	2017-05-10	Israel	5	5	t88	II(2A)	-
9	P1D5C1	GCA_009739825.1	SAMN10374686	2017-05-08	Israel	5	5	t88	II(2A)	-
10	P1D1C1	GCA_009739845.1	SAMN10374685	2017-05-04	Israel	5	5	t88	II(2A)	-
11	P1D14C1	GCA_009739865.1	SAMN10374693	2017-05-17	Israel	5	5	t88	II(2A)	-
12	P1D12C1	GCA_009739885.1	SAMN10374692	2017-05-15	Israel	5	5	t88	II(2A)	-
13	P1D5C2	GCA_009740205.1	SAMN10374687	2017-05-08	Israel	5	5	t88	II(2A)	-
14	P2D8C1	GCA_009739675.1	SAMN10374695	2017-10-10	Israel	5	5	t88	II(2A)	-
15	P2D1C1	GCA_009739695.1	SAMN10374694	2017-10-03	Israel	5	5	t88	II(2A)	-
16	P2D15C1	GCA_009739715.1	SAMN10374696	2017-10-17	Israel	5	5	t88	II(2A)	-
17	BSN9S	GCA_007954445.1	SAMN12476135	2018-08-08	USA	8	8	t8	IVa(2B)	-
18	BSN9R	GCA_007954465.1	SAMN12476193	2018-08-08	USA	8	8	t8	IVa(2B)	-
19	1690	GCA_002608455.1	SAMN03838904	2014-06-30	USA	5	105	t2	ND	-
20	TUM9458	AP019305.1	SAMD00148192	2008-10-20	Japan	5	2389	t539	ND	[2]
21	TUM9463	AP019306.1	SAMD00148193	2009-11-27	Japan	5	2389	t539	II(2A)	[2]
22	S0385	AM990992-AM990995	SAMEA2272644	2006	Dutch	Unknown	398	t11	Vc(5C2&5)	[3]
23	DR-I1	SRR7702578	SAMN09843589	2015-07-25	Austria	22	22	t709	ND	[4]
24	DR-I3	SRR7702580	SAMN09843591	2016-04-01	Austria	22	22	t709	ND	[4]
25	NML151290	MEGZ00000000	SAMN05605119	2015-11	Canada	Unknown	25	t1054	ND	[5]
26	IT1-S	CP028468-CP028469	SAMN08580535	2013-4-30	Italy	22	22	t223	ND	[6]
27	SAZ1	GCA_009873715.1	SAMN13021438	2017-09-25	China	5	5	t311	II(2A)	[7]
28	SAW1	GCA_009914455.1	SAMN13025165	2018-01-25	China	Unknown	59	t172	IVa(2B)	[7]
29	SAW2	GCA_009873795.1	SAMN13021434	2018-01-29	China	Unknown	59	t172	IVa(2B)	[7]
30	SAC1	GCA_009873875.1	SAMN13021426	2017-11-21	China	Unknown	4513	t437	IVa(2B)	[7]
31	SAC4B	GCA_009873815.1	SAMN13021430	2018-01-04	China	Unknown	4513	t437	IVa(2B)	[7]
32	SAC5A	GCA_009873735.1	SAMN13021431	2018-04-28	China	Unknown	4513	t437	IVa(2B)	[7]
33	USA300-ISMMS1 (ISMMS1)	CP007176-CP007178	SAMN03081531	Unknown	USA	8	8	t8	IVa(2B)	[8]
34	USA300_TCH1516 (TCH1516)	NC_010079	SAMN00253845	Unknown	USA	8	8	t622	IVa(2B)	[9]
35	USA300_FPR3757 (FPR3757)	NC_007793	SAMN02604150	Unknown	USA	8	8	t8	IVa(2B)	[9]
36	72061	ERR2026690	SAMEA104152168	2009-01-01—2010-08-31	Denmark	45	Unknown	t230	ND	[10]
37	76045	ERR2026454	SAMEA104152169	2009-01-01—2010-08-31	Denmark	1	3384	t127	ND	[10]
38	76233	ERR2026455	SAMEA104152170	2009-01-01—2010-08-31	Denmark	30	30	t12	ND	[10]
39	76447	ERR2026456	SAMEA104152171	2009-01-01—2010-08-31	Denmark	Unknown	7	t1943	ND	[10]
40	76603	ERR2026457	SAMEA104152172	2009-01-01—2010-08-31	Denmark	Unknown	12	t160	ND	[10]
41	76907	ERR2026458	SAMEA104152173	2009-01-01—2010-08-31	Denmark	45	45	t2948	ND	[10]
42	76953	ERR2026459	SAMEA104152174	2009-01-01—2010-08-31	Denmark	45	45	t230	ND	[10]
43	77105	ERR2026460	SAMEA104152175	2009-01-01—2010-08-31	Denmark	Unknown	59	t3999	ND	[10]
44	77521	ERR2026461	SAMEA104152176	2009-01-01—2010-08-31	Denmark	5	5	t2	ND	[10]
45	77743	ERR2026462	SAMEA104152177	2009-01-01—2010-08-31	Denmark	8	8	t112	ND	[10]
46	77847	ERR2026463	SAMEA104152178	2009-01-01—2010-08-31	Denmark	45	4229	t5775	ND	[10]
47	77871	ERR2026464	SAMEA104152179	2009-01-01—2010-08-31	Denmark	Unknown	25	t78	ND	[10]
48	78577	ERR2026465	SAMEA104152180	2009-01-01—2010-08-31	Denmark	15	582	t84	ND	[10]
49	78611	ERR2026466	SAMEA104152181	2009-01-01—2010-08-31	Denmark	15	15	t94	ND	[10]
50	81401	ERR2026467	SAMEA104152182	2009-01-01—2010-08-31	Denmark	Unknown	12	t156	ND	[10]
51	81867	ERR2026468	SAMEA104152183	2009-01-01—2010-08-31	Denmark	15	15	t94	ND	[10]
52	82003	ERR2026469	SAMEA104152184	2009-01-01—2010-08-31	Denmark	1	188	t2883	ND	[10]
53	82259	ERR2026470	SAMEA104152185	2009-01-01—2010-08-31	Denmark	45	45	t1402	ND	[10]
54	82513	ERR2026471	SAMEA104152186	2009-01-01—2010-08-31	Denmark	30	30	t21	ND	[10]
55	82649	ERR2026472	SAMEA104152187	2009-01-01—2010-08-31	Denmark	30	30	t300	ND	[10]
56	84551	ERR2026473	SAMEA104152188	2009-01-01—2010-08-31	Denmark	5	6	t2360	ND	[10]
57	85243	ERR2026474	SAMEA104152189	2009-01-01—2010-08-31	Denmark	1	1	t693	ND	[10]
58	85835	ERR2026475	SAMEA104152190	2009-01-01—2010-08-31	Denmark	Unknown	12	t160	ND	[10]
59	89969	ERR2026476	SAMEA104152191	2009-01-01—2010-08-31	Denmark	1	188	t189	ND	[10]
60	90547	ERR2026477	SAMEA104152192	2009-01-01—2010-08-31	Denmark	30	30	t363	ND	[10]
61	90913	ERR2026478	SAMEA104152193	2009-01-01—2010-08-31	Denmark	15	15	t2119	ND	[10]
62	90973	ERR2026479	SAMEA104152194	2009-01-01—2010-08-31	Denmark	1	188	t189	ND	[10]
63	91589	ERR2026480	SAMEA104152195	2009-01-01—2010-08-31	Denmark	8	8	t8	ND	[10]
64	92039	ERR2026481	SAMEA104152196	2009-01-01—2010-08-31	Denmark	Unknown	509	t1691	ND	[10]
65	92381	ERR2026482	SAMEA104152197	2009-01-01—2010-08-31	Denmark	8	8	Unknown	ND	[10]
66	93317	ERR2026483	SAMEA104152198	2009-01-01—2010-08-31	Denmark	45	45	t630	ND	[10]
67	93877	ERR2026484	SAMEA104152199	2009-01-01—2010-08-31	Denmark	5	6	t5777	ND	[10]
68	94495	ERR2026485	SAMEA104152200	2009-01-01—2010-08-31	Denmark	15	15	t181	ND	[10]
69	94519	ERR2026486	SAMEA104152201	2009-01-01—2010-08-31	Denmark	45	45	t15	ND	[10]
70	95457	ERR2026487	SAMEA104152202	2009-01-01—2010-08-31	Denmark	1	1	t127	ND	[10]
71	95703	ERR2026488	SAMEA104152203	2009-01-01—2010-08-31	Denmark	15	15	t84	ND	[10]
72	100135	ERR2026489	SAMEA104152204	2002-10-1—2005-08-31	Denmark	15	15	t94	ND	[10]
73	100597	ERR2026490	SAMEA104152205	2002-10-1—2005-08-31	Denmark	45	45	t230	ND	[10]
74	101291	ERR2026491	SAMEA104152206	2002-10-1—2005-08-31	Denmark	5	5	t2	ND	[10]
75	101541	ERR2026492	SAMEA104152207	2002-10-1—2005-08-31	Denmark	22	22	t32	IV(2B)	[10]
76	102965	ERR2026493	SAMEA104152208	2002-10-1—2005-08-31	Denmark	Unknown	25	t18776	ND	[10]
77	103237	ERR2026494	SAMEA104152209	2002-10-1—2005-08-31	Denmark	45	45	t4	ND	[10]
78	103483	ERR2026495	SAMEA104152210	2002-10-1—2005-08-31	Denmark	Unknown	59	t216	ND	[10]
79	103701	ERR2026496	SAMEA104152211	2002-10-1—2005-08-31	Denmark	15	15	t94	ND	[10]
80	103767	ERR2026497	SAMEA104152212	2002-10-1—2005-08-31	Denmark	30	Unknown	t631	ND	[10]
81	103921	ERR2026498	SAMEA104152213	2002-10-1—2005-08-31	Denmark	Unknown	182	t493	ND	[10]
82	103995	ERR2026499	SAMEA104152214	2002-10-1—2005-08-31	Denmark	30	30	t268	ND	[10]
83	104319	ERR2026500	SAMEA104152215	2002-10-1—2005-08-31	Denmark	30	30	t12	ND	[10]
84	104343	ERR2026501	SAMEA104152216	2002-10-1—2005-08-31	Denmark	Unknown	7	t1943	ND	[10]
85	105343	ERR2026502	SAMEA104152217	2002-10-1—2005-08-31	Denmark	Unknown	25	t227	ND	[10]
86	105445	ERR2026503	SAMEA104152218	2002-10-1—2005-08-31	Denmark	1	1	t8824	ND	[10]
87	105547	ERR2026504	SAMEA104152219	2002-10-1—2005-08-31	Denmark	30	30	t21	ND	[10]
88	106141	ERR2026505	SAMEA104152220	2002-10-1—2005-08-31	Denmark	Unknown	12	t909	ND	[10]

NO.	Strain	NCBI Accession numbers	BioSample numbers	Isolation date	Geographical origin (Country)	CCa	MLST[a]	spa type[a]	SCCmec[a]	References[c]
89	106461	ERR2026506	SAMEA104152221	2002-10-1—2005-08-31	Denmark	1	9	t4812	ND	[10]
90	106533	ERR2026507	SAMEA104152222	2002-10-1—2005-08-31	Denmark	30	Unknown	t3687	ND	[10]
91	107191	ERR2026508	SAMEA104152223	2002-10-1—2005-08-31	Denmark	22	22	Unknown	ND	[10]
92	107635	ERR2026509	SAMEA104152224	2002-10-1—2005-08-31	Denmark	30	30	t860	ND	[10]
93	110231	ERR2026510	SAMEA104152225	2002-10-1—2005-08-31	Denmark	45	508	t50	ND	[10]
94	110255	ERR2026511	SAMEA104152226	2002-10-1—2005-08-31	Denmark	30	34	t3653	ND	[10]
95	111069	ERR2026512	SAMEA104152227	2002-10-1—2005-08-31	Denmark	30	30	t871	ND	[10]
96	111189	ERR2026513	SAMEA104152228	2002-10-1—2005-08-31	Denmark	15	15	t18776	ND	[10]
97	111697	ERR2026514	SAMEA104152229	2002-10-1—2005-08-31	Denmark	8	8	t2985	ND	[10]
98	111765	ERR2026515	SAMEA104152230	2002-10-1—2005-08-31	Denmark	45	45	t2989	ND	[10]
99	112005	ERR2026516	SAMEA104152231	2002-10-1—2005-08-31	Denmark	8	8	t8	ND	[10]
100	112553	ERR2026517	SAMEA104152232	2002-10-1—2005-08-31	Denmark	97	97	t1200	ND	[10]
101	113165	ERR2026518	SAMEA104152233	2002-10-1—2005-08-31	Denmark	5	5	t2	ND	[10]
102	113391	ERR2026519	SAMEA104152234	2002-10-1—2005-08-31	Denmark	1	9	t4812	ND	[10]
103	113647	ERR2026520	SAMEA104152235	2002-10-1—2005-08-31	Denmark	15	15	t3348	ND	[10]
104	114435	ERR2026521	SAMEA104152236	2002-10-1—2005-08-31	Denmark	30	34	t89	ND	[10]
105	114821	ERR2026522	SAMEA104152237	2002-10-1—2005-08-31	Denmark	45	45	t302	ND	[10]
106	116063	ERR2026523	SAMEA104152238	2002-10-1—2005-08-31	Denmark	Unknown	12	t888	ND	[10]
107	116693	ERR2026524	SAMEA104152239	2002-10-1—2005-08-31	Denmark	45	45	t230	ND	[10]
108	116745	ERR2026525	SAMEA104152240	2002-10-1—2005-08-31	Denmark	Unknown	20	t164	ND	[10]
109	120725	ERR2026526	SAMEA104152241	2002-10-1—2005-08-31	Denmark	15	15	t853	ND	[10]
110	120897	ERR2026527	SAMEA104152242	2002-10-1—2005-08-31	Denmark	30	30	t37	ND	[10]
111	121881	ERR2026528	SAMEA104152243	2002-10-1—2005-08-31	Denmark	15	15	t181	ND	[10]
112	124991	ERR2026531	SAMEA104152246	2002-10-1—2005-08-31	Denmark	1	188	t189	ND	[10]
113	126179	ERR2026533	SAMEA104152248	2002-10-1—2005-08-31	Denmark	5	5	t2	ND	[10]
114	126181	ERR2026534	SAMEA104152249	2002-10-1—2005-08-31	Denmark	45	45	t230	ND	[10]
115	126673	ERR2026535	SAMEA104152250	2002-10-1—2005-08-31	Denmark	45	45	Unknown	ND	[10]
116	126691	ERR2026536	SAMEA104152251	2002-10-1—2005-08-31	Denmark	45	45	t5051	ND	[10]
117	127097	ERR2026537	SAMEA104152252	2002-10-1—2005-08-31	Denmark	22	22	t902	ND	[10]
118	130987	ERR2026542	SAMEA104152257	2002-10-1—2005-08-31	Denmark	97	97	t521	ND	[10]
119	132105	ERR2026548	SAMEA104152263	2002-10-1—2005-08-31	Denmark	Unknown	25	t78	ND	[10]
120	132281	ERR2026549	SAMEA104152264	2002-10-1—2005-08-31	Denmark	1	1	t948	ND	[10]
121	132735	ERR2026552	SAMEA104152267	2002-10-1—2005-08-31	Denmark	30	Unknown	t37	ND	[10]
122	132895	ERR2026555	SAMEA104152270	2002-10-1—2005-08-31	Denmark	Unknown	50	t246	ND	[10]
123	133593	ERR2026558	SAMEA104152273	2002-10-1—2005-08-31	Denmark	15	15	t94	ND	[10]
124	134333	ERR2026562	SAMEA104152277	2002-10-1—2005-08-31	Denmark	30	34	t3906	ND	[10]
125	134363	ERR2026564	SAMEA104152279	2002-10-1—2005-08-31	Denmark	8	8	t8	ND	[10]
126	134789	ERR2026569	SAMEA104152284	2002-10-1—2005-08-31	Denmark	1	573	t345	ND	[10]
127	134967	ERR2026570	SAMEA104152285	2002-10-1—2005-08-31	Denmark	45	45	t15	ND	[10]
128	134977	ERR2026572	SAMEA104152287	2002-10-1—2005-08-31	Denmark	5	5	t2	ND	[10]
129	135557	ERR2026578	SAMEA104152293	2002-10-1—2005-08-31	Denmark	Unknown	12	t160	ND	[10]
130	135627	ERR2026579	SAMEA104152294	2002-10-1—2005-08-31	Denmark	15	15	t84	ND	[10]
131	135633	ERR2026581	SAMEA104152296	2002-10-1—2005-08-31	Denmark	8	1181	t334	ND	[10]
132	135689	ERR2026583	SAMEA104152298	2002-10-1—2005-08-31	Denmark	45	45	t15	ND	[10]
133	135703	ERR2026584	SAMEA104152299	2002-10-1—2005-08-31	Denmark	1	1	t114	ND	[10]
134	136927	ERR2026609	SAMEA104152324	2002-10-1—2005-08-31	Denmark	45	Unknown	t230	ND	[10]
135	136941	ERR2026611	SAMEA104152326	2002-10-1—2005-08-31	Denmark	45	45	t230	ND	[10]
136	136943	ERR2026612	SAMEA104152327	2002-10-1—2005-08-31	Denmark	30	30	Unknown	ND	[10]
137	137021	ERR2026614	SAMEA104152329	2002-10-1—2005-08-31	Denmark	45	45	t230	ND	[10]
138	137221	ERR2026619	SAMEA104152334	2002-10-1—2005-08-31	Denmark	30	Unknown	t1945	ND	[10]
139	137605	ERR2026626	SAMEA104152341	2002-10-1—2005-08-31	Denmark	1	1	t127	ND	[10]
140	137611	ERR2026629	SAMEA104152344	2002-10-1—2005-08-31	Denmark	5	5	t6356	ND	[10]
141	140005	ERR2026637	SAMEA104152352	2002-10-1—2005-08-31	Denmark	15	15	t84	ND	[10]
142	140057	ERR2026638	SAMEA104152353	2002-10-1—2005-08-31	Denmark	30	30	t1988	ND	[10]
143	140177	ERR2026643	SAMEA104152358	2002-10-1—2005-08-31	Denmark	45	Unknown	t230	ND	[10]
144	140601	ERR2026647	SAMEA104152362	2002-10-1—2005-08-31	Denmark	30	30	t363	ND	[10]
145	140751	ERR2026649	SAMEA104152364	2002-10-1—2005-08-31	Denmark	45	45	t230	ND	[10]
146	140991	ERR2026656	SAMEA104152371	2002-10-1—2005-08-31	Denmark	30	30	t6600	ND	[10]
147	141169	ERR2026660	SAMEA104152375	2002-10-1—2005-08-31	Denmark	1	1	Unknown	ND	[10]
148	141373	ERR2026661	SAMEA104152376	2002-10-1—2005-08-31	Denmark	8	6086	t211	ND	[10]
149	141423	ERR2026663	SAMEA104152378	2002-10-1—2005-08-31	Denmark	30	30	t6566	ND	[10]
150	142077	ERR2026671	SAMEA104152386	2002-10-1—2005-08-31	Denmark	45	45	Unknown	ND	[10]
151	142469	ERR2026676	SAMEA104152391	2002-10-1—2005-08-31	Denmark	30	Unknown	t136	ND	[10]
152	142583	ERR2026677	SAMEA104152392	2002-10-1—2005-08-31	Denmark	5	5	t105	ND	[10]
153	142777	ERR2026679	SAMEA104152394	2002-10-1—2005-08-31	Denmark	1	1	t174	ND	[10]
154	143139	ERR2026681	SAMEA104152396	2002-10-1—2005-08-31	Denmark	8	8	t8	ND	[10]
155	144671	ERR2026686	SAMEA104152405	2002-10-1—2005-08-31	Denmark	8	8	t24	ND	[10]
156	SATU136	SRR16971212	SAMN23247394	2014-01-29	Thailand	5	764	t45	II(2A)	[11]
157	SA-675	CP156984-CP156985	SAMN35547081	1990-10	USA	30	30	t19	ND	[12]
158	SA-684	CP156695-CP156696	SAMN35547000	1990-10	USA	30	30	t19	ND	[12]
159	BSN15	CP158581-CP158585	SAMN15016621	2018-12-14	USA	5	Unknown	t2	II(2A)	-
160	BSN39	GCA_036628495.1	SAMN39896512	2020-09-12	USA	8	72	t148	ND	-
161	BSN53	CP152409-CP152411	SAMN38334799	2018-10-21	USA	8	8	t8	IVa(2B)	-
162	BSN150	CP148047	SAMN38637729	2021-11-03	USA	5	5	t179	ND	-
163	BSN155-2	CP148079-CP148080	SAMN38637735	2022-01-07	USA	8	8	t24	IVa(2B)	-
164	J03	CP168442-CP168444	SAMN43213423	2011	USA	8	8	t64	IVg(2B)	[13]
165	GP11	CP139867-CP139868	SAMN38397519	2021-03	Spain	5	6	t4285	ND	-
166	BPH2739	ERR2137051	SAMEA104317351	2011	Australia	Unknown	Unknown	t164	ND	[14]
167	BPH2745	ERR2137057	SAMEA104317357	2011	Australia	8	72	t148	ND	[14]
168	BPH2760	ERR2137072	SAMEA104317372	2011	Australia	1	1	t286	ND	[14]
169	BPH2821	ERR2137128	SAMEA104317428	2011	Australia	Unknown	12	t160	ND	[14]
170	BPH2835	ERR2137140	SAMEA104317440	2012	Australia	8	72	t148	ND	[14]
171	BPH2843	ERR2137148	SAMEA104317448	2012	Australia	22	22	t717	IV(2B)	[14]
172	BPH2847	ERR2137152	SAMEA104317452	2012	Australia	22	22	t4274	IV(2B)	[14]
173	BPH2848	ERR2137153	SAMEA104317453	2012	Australia	1	1	t127	ND	[14]
174	BPH2854	ERR2137158	SAMEA104317458	2012	Australia	8	8	t986	IVa(2B)	[14]
175	BPH2872	ERR2137175	SAMEA104317475	2012	Australia	5	7267	t2	ND	[14]
176	BPH2912	ERR2137213	SAMEA104317513	2012	Australia	1	1	t693	ND	[14]
177	BPH2917	ERR2137218	SAMEA104317518	2012	Australia	45	46	t370	ND	[14]
178	BPH2922	ERR2137223	SAMEA104317523	2012	Australia	1	1	t591	ND	[14]
179	BPH2928	ERR2137225	SAMEA104317525	2012	Australia	Unknown	101	t2078	ND	[14]
180	BPH2935	ERR2137232	SAMEA104317532	2012	Australia	30	3383	t459	ND	[14]
181	BPH2950	ERR2137247	SAMEA104317547	2012	Australia	1	188	t189	ND	[14]

NO.	Strain	NCBI Accession numbers	BioSample numbers	Isolation date	Geographical origin (Country)	CCa	MLST[a]	spa type[a]	SCCmec[a]	References[c]
182	BPH2962	ERR2137259	SAMEA104317559	2012	Australia	Unknown	20	t164	ND	[14]
183	BPH2987	ERR2137284	SAMEA104317584	2012	Australia	30	39	t4242	ND	[14]
184	BPH3201	ERR2137293	SAMEA104317593	2007	Australia	45	45	Unknown	ND	[14]
185	BPH3211	ERR2137303	SAMEA104317603	2008	Australia	1	6425	t5229	ND	[14]
186	BPH3233	ERR2137325	SAMEA104317625	2007	Australia	45	508	Unknown	ND	[14]
187	BPH3238	ERR2137330	SAMEA104317630	2007	Australia	1	188	t189	ND	[14]
188	BPH3249	ERR2137341	SAMEA104317641	2008	Australia	1	188	t189	ND	[14]
189	BPH3287	ERR2137379	SAMEA104317679	2008	Australia	Unknown	78	t786	ND	[14]
190	BPH3293	ERR2137385	SAMEA104317685	2008	Australia	45	45	t282	ND	[14]
191	BPH3319	ERR2137411	SAMEA104317711	2007	Australia	Unknown	88	t9873	ND	[14]
192	BPH3337	ERR2137429	SAMEA104317729	2007	Australia	8	8	t2068	ND	[14]
193	BPH3345	ERR2137437	SAMEA104317737	2008	Australia	30	30	t12	ND	[14]
194	BPH3352	ERR2137444	SAMEA104317744	2008	Australia	45	45	t1081	Vc(5C2&5)	[14]
195	BPH3367	ERR2137459	SAMEA104317759	2007	Australia	Unknown	101	t2645	ND	[14]
196	BPH3401	ERR2137491	SAMEA104317791	2007	Australia	8	239	t37	III(3A)	[14]
197	BPH3406	ERR2137495	SAMEA104317795	2008	Australia	45	45	t230	ND	[14]
198	BPH3410	ERR2137499	SAMEA104317799	2008	Australia	Unknown	12	t160	ND	[14]
199	BPH3414	ERR2137503	SAMEA104317803	2007	Australia	45	45	t230	ND	[14]
200	BPH3422	ERR2137511	SAMEA104317811	2008	Australia	5	5	t548	ND	[14]
201	BPH3426	ERR2137515	SAMEA104317815	2007	Australia	5	Unknown	t688	ND	[14]
202	BPH3456	ERR2137544	SAMEA104317844	2008	Australia	Unknown	88	t186	ND	[14]
203	BPH3466	ERR2137554	SAMEA104317854	2007	Australia	45	45	Unknown	ND	[14]
204	BPH3474	ERR2137562	SAMEA104317862	2007	Australia	30	34	t89	ND	[14]
205	BPH3478	ERR2137566	SAMEA104317866	2008	Australia	5	6	t701	ND	[14]
206	BPH3502	ERR2137589	SAMEA104317889	2008	Australia	Unknown	395	t4842	ND	[14]
207	BPH3514	ERR2137601	SAMEA104317901	2007	Australia	1	188	t189	ND	[14]
208	BPH3520	ERR2137607	SAMEA104317907	2007	Australia	1	188	t189	ND	[14]
209	BPH3540	ERR2137627	SAMEA104317927	2008	Australia	8	72	t870	ND	[14]
210	BPH3579	ERR2137666	SAMEA104317966	2007	Australia	5	5	t10	IV(2B)	[14]
211	BPH3583	ERR2137670	SAMEA104317970	2008	Australia	1	1	t127	IVh(2B)	[14]
212	BPH3599	ERR2137686	SAMEA104317986	2007	Australia	1	1	t127	ND	[14]
213	BPH3615	ERR2145129	SAMEA104325170	2007	Australia	Unknown	20	t164	ND	[14]
214	BPH3639	ERR2145152	SAMEA104325193	2007	Australia	Unknown	88	t12157	ND	[14]
215	ST20091659	ERR7681390	SAMEA11604076	2009	France	1	188	t189	ND	[14]
216	ST20091660	ERR7162648	SAMEA10030915	2009	France	15	15	t85	ND	[14]
217	ST20091661	ERR7162649	SAMEA10030916	2009	France	15	15	t254	ND	[14]
218	ST20091663	ERR7681391	SAMEA11604077	2009	France	15	15	t85	ND	[14]
219	ST20091665	ERR7162650	SAMEA10030917	2009	France	30	30	t338	ND	[14]
220	ST20091666	ERR7162651	SAMEA10030919	2009	France	5	5	t71	ND	[14]
221	ST20091669	ERR7162652	SAMEA10030920	2009	France	8	8	t8	ND	[14]
222	ST20091692	ERR7162653	SAMEA10030921	2009	France	8	8	t8	ND	[14]
223	ST20091693	ERR7162654	SAMEA10030922	2009	France	45	54	t26	ND	[14]
224	ST20091694	ERR7681392	SAMEA11604078	2009	France	1	1	t127	ND	[14]
225	ST20091729	ERR7162655	SAMEA10030923	2009	France	22	22	Unknown	ND	[14]
226	ST20091949	ERR7681393	SAMEA11604079	2009	France	5	5	t2	ND	[14]
227	ST20100400	ERR7681394	SAMEA11604080	2010	France	45	45	t1575	ND	[14]
228	ST20100856	ERR7162656	SAMEA10030924	2010	France	8	8	t569	IVc(2B)	[14]
229	ST20100857	ERR7681395	SAMEA11604081	2010	France	Unknown	398	Unknown	ND	[14]
230	ST20100859	ERR7681396	SAMEA11604082	2010	France	5	5	t688	ND	[14]
231	ST20100860	ERR7681397	SAMEA11604083	2010	France	30	30	t275	ND	[14]
232	ST20100872	ERR7681398	SAMEA11604084	2010	France	121	121	t645	ND	[14]
233	ST20100875	ERR7681399	SAMEA11604085	2010	France	8	27	t6830	ND	[14]
234	ST20100878	ERR7162657	SAMEA10030925	2010	France	Unknown	78	t186	ND	[14]
235	ST20100881	ERR7162658	SAMEA10030926	2010	France	45	45	t5020	ND	[14]
236	ST20100882	ERR7162659	SAMEA10030927	2010	France	1	188	t7099	ND	[14]
237	ST20101138	ERR7162660	SAMEA10030928	2010	France	45	45	t779	ND	[14]
238	ST20101156	ERR7162661	SAMEA10030929	2010	France	45	45	t73	ND	[14]
239	ST20101161	ERR7162662	SAMEA10030930	2010	France	1	9	t587	ND	[14]
240	ST20101186	ERR7162663	SAMEA10030931	2010	France	15	15	Unknown	ND	[14]
241	ST20101418	ERR7162664	SAMEA10030932	2010	France	15	Unknown	Unknown	ND	[14]
242	ST20101420	ERR7162665	SAMEA10030933	2010	France	5	5	t2	I(1B)	[14]
243	ST20101424	ERR7162666	SAMEA10030934	2010	France	121	121	t159	ND	[14]
244	ST20101427	ERR7681400	SAMEA11604086	2010	France	Unknown	2867	t2016	ND	[14]
245	ST20101428	ERR7162667	SAMEA10030935	2010	France	Unknown	12	t156	ND	[14]
246	ST20101429	ERR7162668	SAMEA10030936	2010	France	Unknown	398	Unknown	ND	[14]
247	ST20101433	ERR7681401	SAMEA11604087	2010	France	97	97	t267	ND	[14]
248	ST20101438	ERR7162669	SAMEA10030937	2010	France	45	45	t10553	ND	[14]
249	ST20101445	ERR7681402	SAMEA11604088	2010	France	15	15	t94	ND	[14]
250	ST20101531	ERR7162670	SAMEA10030938	2010	France	Unknown	7	t867	ND	[14]
251	ST20101705	ERR7681403	SAMEA11604089	2010	France	97	464	t224	ND	[14]
252	ST20101718	ERR7162671	SAMEA10030939	2010	France	15	15	t84	ND	[14]
253	ST20101789	ERR7162697	SAMEA10030965	2012	France	5	Unknown	t2	ND	[14]
254	ST20101934	ERR7162672	SAMEA10030940	2010	France	8	8	t723	IVc(2B)	[14]
255	ST20102139	ERR7162673	SAMEA10030941	2010	France	Unknown	398	Unknown	ND	[14]
256	ST20102292	ERR7162674	SAMEA10030942	2010	France	5	5	t2	ND	[14]
257	ST20102293	ERR7162675	SAMEA10030943	2010	France	1	1	t127	ND	[14]
258	ST20102295	ERR7162676	SAMEA10030944	2010	France	5	5	t45	ND	[14]
259	ST20102302	ERR7681404	SAMEA11604090	2010	France	45	1165	t2539	ND	[14]
260	ST20102307	ERR7681405	SAMEA11604091	2010	France	Unknown	398	t1451	ND	[14]
261	ST20110014	ERR7162677	SAMEA10030945	2011	France	45	45	Unknown	ND	[14]
262	ST20110196	ERR7162678	SAMEA10030946	2011	France	8	72	t148	ND	[14]
263	ST20110285	ERR7162679	SAMEA10030947	2011	France	5	146	t2	ND	[14]
264	ST20110286	ERR7162680	SAMEA10030948	2011	France	Unknown	101	t569	ND	[14]
265	ST20110555	ERR7681407	SAMEA11604093	2011	France	Unknown	Unknown	t160	ND	[14]
266	ST20110560	ERR7681408	SAMEA11604094	2011	France	5	5	t45	ND	[14]
267	ST20110890	ERR7162681	SAMEA10030949	2011	France	8	646	t190	ND	[14]
268	ST20111220	ERR7162682	SAMEA10030950	2011	France	121	121	t269	ND	[14]
269	ST20111347	ERR7162683	SAMEA10030951	2011	France	15	15	t84	ND	[14]
270	ST20111348	ERR7162684	SAMEA10030952	2011	France	30	30	t21	ND	[14]
271	ST20111367	ERR7162685	SAMEA10030953	2011	France	45	46	t6566	ND	[14]
272	ST20111368	ERR7681409	SAMEA11604095	2011	France	15	15	t85	ND	[14]
273	ST20111441	ERR7162686	SAMEA10030954	2011	France	1	188	t3887	ND	[14]
274	ST20111452	ERR7162687	SAMEA10030955	2011	France	5	146	t2	ND	[14]

NO.	Strain	NCBI Accession numbers	BioSample numbers	Isolation date	Geographical origin (Country)	CCa	MLST[a]	spa type[a]	SCCmec[a]	References[c]
275	ST20111792	ERR7162688	SAMEA10030956	2011	France	5	3014	t2	ND	[14]
276	ST20112212	ERR7681410	SAMEA11604096	2011	France	30	30	t12	ND	[14]
277	ST20112213	ERR7162689	SAMEA10030957	2011	France	30	30	t12	ND	[14]
278	ST20112214	ERR7162690	SAMEA10030958	2011	France	Unknown	398	t1451	ND	[14]
279	ST20112215	ERR7162691	SAMEA10030959	2011	France	45	45	t26	ND	[14]
280	ST20112455	ERR7681411	SAMEA11604097	2011	France	5	5	t2	ND	[14]
281	ST20120191	ERR7162692	SAMEA10030960	2012	France	15	15	t1038	ND	[14]
282	ST20120194	ERR7162693	SAMEA10030961	2012	France	8	8	t1882	ND	[14]
283	ST20120196	ERR7162694	SAMEA10030962	2012	France	15	15	t2119	ND	[14]
284	ST20120202	ERR7162695	SAMEA10030963	2012	France	Unknown	398	t6587	ND	[14]
285	ST20120234	ERR7162696	SAMEA10030964	2012	France	8	8	t8	ND	[14]

[a]Raw reads were assembled into scaffolds using SPAdes v 3.13.1. For each genome, we determined the multi-locus sequence type (MLST), including the clonal complex (CC) to which it belongs, using the online PubMLST tool (https://pubmlst.org/bigsdb?db=pubmlst_saureus_seqdef&page=sequenceQuery). Additionally, we determined the spa type and staphylococcal cassette chromosome mec (SCCmec) type using spaTyper version 1.0 (https://cge.food.dtu.dk/services/spaTyper/) and SCCmecFinder version 1.2 (https://cge.food.dtu.dk/services/SCCmecFinder/), respectively. [b]"ND" stands for "not detected.

[c]References

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Supplementary Table 2. Differential ARGs and VFs according to ST types among the 285 S. aureus strains causing IE.

Characteristic		No. (%) of strains									*p*
		All (n = 285)	ST45 (n = 32)	ST5 (n = 31)	ST8 (n = 26)	ST15 (n = 24)	ST30 (n = 23)	ST1 (n = 16)	ST188 (n = 12)	Others[a] (n = 121)	
ARGs											
Aminocyclitol	*ant(9)-Ia*	30 (10.5%)	0[b] (0.0%)	14[b] (45.2%)	2 (7.7%)	0 (0.0%)	4 (17.4%)	1 (6.3%)	0 (0.0%)	9 (7.4%)	< 0.001
	aadD	14 (4.9%)	1 (3.1%)	5[b] (16.1%)	2 (7.7%)	1 (4.2%)	2 (8.7%)	0 (0.0%)	1 (8.3%)	2[b] (1.7%)	0.032
Aminoglycoside	*ant(6)-Ia*	7 (2.5%)	0 (0.0%)	0 (0.0%)	5[b] (19.2%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	2 (1.7%)	0.008
	aph(3')-III	8 (2.8%)	1 (3.1%)	0 (0.0%)	5[b] (19.2%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	2 (1.7%)	0.013
	bleO	13 (4.6%)	1 (3.1%)	5[b] (16.1%)	2 (7.7%)	1 (4.2%)	2 (8.7%)	0 (0.0%)	0 (0.0%)	2[b] (1.7%)	0.038
Amphenicol	*cat*	12 (4.2%)	0 (0.0%)	12[b] (38.7%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0[b] (0.0%)	< 0.001
Beta-lactam	*mecA*	46 (16.1%)	1[b] (3.1%)	15[b] (48.4%)	12[b] (46.2%)	0[b] (0.0%)	2 (8.7%)	1 (6.3%)	0 (0.0%)	15 (12.4%)	< 0.001
	blaZ	212 (74.4%)	27 (84.4%)	15[b] (48.4%)	19 (73.1%)	20 (83.3%)	23[b] (100.0%)	13 (81.3%)	10 (83.3%)	85 (70.2%)	< 0.001
Fusidic acid	*fusC*	14 (4.9%)	0 (0.0%)	1 (3.2%)	1 (3.8%)	0 (0.0%)	0 (0.0%)	10[b] (62.5%)	0 (0.0%)	2[b] (1.7%)	< 0.001
Lincosamide/macrolide/streptogramin B	*erm(A)*	31 (10.9%)	0[b] (0.0%)	14[b] (45.2%)	3 (11.5%)	0 (0.0%)	4 (17.4%)	1 (6.3%)	0 (0.0%)	9 (7.4%)	< 0.001
	msr(A)	8 (2.8%)	0 (0.0%)	0 (0.0%)	6[b] (23.1%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	2 (1.7%)	< 0.001
	mph(C)	7 (2.5%)	0 (0.0%)	0 (0.0%)	6[b] (23.1%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (0.8%)	< 0.001
Pseudomonic acid	*mupA*	3 (1.1%)	0 (0.0%)	0 (0.0%)	2[b] (7.7%)	0 (0.0%)	0 (0.0%)	1 (6.3%)	0 (0.0%)	0 (0.0%)	0.022
Quinolone	*grlA (p.I45M)*	40 (14.0%)	31[b] (96.9%)	0[b] (0.0%)	0[b] (0.0%)	0[b] (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	9[b] (7.4%)	< 0.001
	grlA (p.S80F)	31 (10.9%)	1 (3.1%)	13[b] (41.9%)	8[b] (30.8%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	9 (7.4%)	< 0.001
	gyrA (p.S84L)	33 (11.6%)	2 (6.3%)	13[b] (41.9%)	9[b] (34.6%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	9 (7.4%)	< 0.001
Rifamycin	*rpoB (p.S486L)*	4 (1.4%)	0 (0.0%)	4[b] (12.9%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0.002
ARG score, median (IQR)[c]		1 (1.0-2.0)	2[b] (2.0-2.0)	2[b] (1.0-7.0)	3[b] (1.0-6.0)	1[b] (1.0-1.0)	1 (1.0-1.0)	2 (1.0-2.0)	1[b] (1.0-1.0)	1[b] (1.0-2.0)	< 0.001
VFs											
Exoenzyme genes	*splA*	170 (59.6%)	0[b] (0.0%)	31[b] (100.0%)	26[b] (100.0%)	23[b] (95.8%)	1[b] (4.3%)	16[b] (100.0%)	11[b] (91.7%)	62[b] (51.2%)	< 0.001
	splB	168 (58.9%)	0[b] (0.0%)	31[b] (100.0%)	26[b] (100.0%)	23[b] (95.8%)	1[b] (4.3%)	16[b] (100.0%)	12[b] (100.0%)	59[b] (48.8%)	< 0.001
	splE	137 (48.1%)	0[b] (0.0%)	0[b] (0.0%)	22[b] (84.6%)	23[b] (95.8%)	20[b] (87.0%)	13[b] (81.3%)	10[b] (83.3%)	49[b] (40.5%)	< 0.001
	sak	232 (81.4%)	32[b] (100.0%)	31[b] (100.0%)	25 (96.2%)	0[b] (0.0%)	18 (78.3%)	15 (93.8%)	10 (83.3%)	101 (83.5%)	< 0.001
Hostimm	*scn*	266 (93.3%)	32 (100.0%)	31 (100.0%)	25 (96.2%)	24 (100.0%)	18[b] (78.3%)	15 (93.8%)	10 (83.3%)	111 (91.7%)	0.016
	ACME	11 (3.9%)	0 (0.0%)	3 (9.7%)	7[b] (26.9%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1[b] (0.8%)	< 0.001
	lukD	176 (61.8%)	0[b] (0.0%)	31[b] (100.0%)	26[b] (100.0%)	24[b] (100.0%)	1[b] (4.3%)	16[b] (100.0%)	12[b] (100.0%)	66[b] (54.5%)	< 0.001
	lukE	179 (62.8%)	0[b] (0.0%)	31[b] (100.0%)	26[b] (100.0%)	24[b] (100.0%)	1[b] (4.3%)	16[b] (100.0%)	12[b] (100.0%)	69 (57.0%)	< 0.001
	lukF-PV	5 (1.8%)	0 (0.0%)	0 (0.0%)	5[b] (19.2%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	< 0.001
	lukS-PV	5 (1.8%)	0 (0.0%)	0 (0.0%)	5[b] (19.2%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	< 0.001
	sea	50 (17.5%)	0[b] (0.0%)	1[b] (3.2%)	7 (26.9%)	0[b] (0.0%)	13[b] (56.5%)	14[b] (87.5%)	0 (0.0%)	15 (12.4%)	< 0.001
	seb	22 (7.7%)	0 (0.0%)	1 (3.2%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	2 (12.5%)	0 (0.0%)	19[b] (15.7%)	0.004
	sec	24 (8.4%)	8[b] (25.0%)	4 (12.9%)	1 (3.8%)	0 (0.0%)	1 (4.3%)	0 (0.0%)	0 (0.0%)	10 (8.3%)	0.032
	sec3	25 (8.4%)	16[b] (50.0%)	1 (3.2%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (6.3%)	0 (0.0%)	7 (5.8%)	< 0.001
	sed	16 (5.6%)	0 (0.0%)	7[b] (22.6%)	5[b] (19.2%)	0 (0.0%)	0 (0.0%)	1 (6.3%)	0 (0.0%)	3 (2.5%)	< 0.001
	seg	147 (51.6%)	32[b] (100.0%)	31[b] (100.0%)	0[b] (0.0%)	0[b] (0.0%)	22[b] (95.7%)	1[b] (6.3%)	0[b] (0.0%)	61 (50.4%)	< 0.001
	seh	23 (8.1%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	16[b] (100.0%)	0 (0.0%)	7 (5.8%)	< 0.001
Toxin	*sei*	149 (52.3%)	32[b] (100.0%)	30[b] (96.8%)	0[b] (0.0%)	0[b] (0.0%)	23[b] (100.0%)	1[b] (6.3%)	0[b] (0.0%)	63 (52.1%)	< 0.001
	sej	17 (6.0%)	1 (3.1%)	7[b] (22.6%)	5[b] (19.2%)	0 (0.0%)	0 (0.0%)	1 (6.3%)	0 (0.0%)	3[b] (2.5%)	< 0.001
	sek	32 (11.2%)	0[b] (0.0%)	1 (3.2%)	6 (23.1%)	0 (0.0%)	0 (0.0%)	14[b] (87.5%)	0 (0.0%)	11 (9.1%)	< 0.001
	sel	41 (14.4%)	16[b] (50.0%)	6 (19.4%)	2 (7.7%)	0[b] (0.0%)	1 (4.3%)	1 (6.3%)	0 (0.0%)	15 (12.4%)	< 0.001
	sem	151 (53.0%)	32[b] (100.0%)	31[b] (100.0%)	0[b] (0.0%)	0[b] (0.0%)	23[b] (100.0%)	1[b] (6.3%)	0[b] (0.0%)	64 (52.9%)	< 0.001
	sen	145 (50.9%)	32[b] (100.0%)	30[b] (96.8%)	0[b] (0.0%)	0[b] (0.0%)	23[b] (100.0%)	0[b] (0.0%)	0[b] (0.0%)	60 (49.6%)	< 0.001
	seo	152 (53.3%)	32[b] (100.0%)	31[b] (100.0%)	0[b] (0.0%)	0[b] (0.0%)	23[b] (100.0%)	0[b] (0.0%)	0[b] (0.0%)	66 (54.5%)	< 0.001
	sep	44 (15.4%)	0[b] (0.0%)	24[b] (77.4%)	4 (15.4%)	0[b] (0.0%)	0[b] (0.0%)	1 (6.3%)	0 (0.0%)	15 (12.4%)	< 0.001
	seq	32 (11.2%)	0[b] (0.0%)	1 (3.2%)	6 (23.1%)	0 (0.0%)	0 (0.0%)	14[b] (87.5%)	0 (0.0%)	11 (9.1%)	< 0.001
	ser	17 (6.0%)	1 (3.1%)	7[b] (22.6%)	5[b] (19.2%)	0 (0.0%)	0 (0.0%)	1 (6.3%)	0 (0.0%)	3[b] (2.5%)	< 0.001
	seu	146 (51.2%)	31[b] (96.9%)	31[b] (100.0%)	0[b] (0.0%)	0[b] (0.0%)	23[b] (100.0%)	0[b] (0.0%)	0[b] (0.0%)	61 (50.4%)	< 0.001
	tst	37 (13.0%)	0[b] (0.0%)	3 (9.7%)	2 (7.7%)	0 (0.0%)	17 (73.9%)	0 (0.0%)	0 (0.0%)	15 (12.4%)	< 0.001
VF score, median (IQR)[c]		13 (11.0-15.0)	13.5 (12.0-14.8)	17[b] (17.0-20.0)	14 (11.0-15.0)	10[b] (10.0-10.0)	14 (13.0-15.0)	15[b] (15.0-15.0)	11[b] (10.3-11.0)	12[b] (11.0-15.0)	< 0.001

[a]Please see the Supplementary Table 1 for details. [b]*P* value was < 0.05 in comparison with all of the other strains. [c]ARG and VF scores were defined as the number of unique ARG and VF detected for each strain, respectively. IQR, interquartile range.

Supplementary Table 3. Pairwise comparison of ARG and VF scores across ST types in 285 *S. aureus* strains.

Groups	Vs. ST45	Vs. ST5	Vs. ST8	Vs. ST15	Vs. ST30	Vs. ST1	Vs. ST188
	P/r [95% CI][a]	*P*/r [95% CI]	*P*/r [95% CI]	*P*/r [95% CI]	*P*/r [95% CI]	*P*/r [95% CI]	*P*/r [95% CI]
				ARG score			
ST5	0.819/0.030 [-0.220, 0.275]						
ST8	0.165/0.183 [-0.079, 0.421]	0.671/0.057 [-0.207, 0.313]					
ST15	< **0.001**/0.720 [0.564, 0.826]	**0.015**/0.325 [0.065, 0.543]	< **0.001**/0.601 [0.387, 0.753]				
ST30	< **0.001**/0.456 [0.217, 0.643]	0.190/0.180 [-0.092, 0.427]	**0.003**/0.416 [0.153, 0.624]	0.050/0.286 [-0.001, 0.530]			
ST1	0.201/0.191 [-0.098, 0.451]	0.479/0.105 [-0.188, 0.381]	0.071/0.279 [-0.027, 0.537]	< **0.001**/0.532 [0.264, 0.724]	0.080/0.277 [-0.042, 0.545]		
ST188	< **0.001**/0.699 [0.507, 0.825]	0.050/0.302 [0.002, 0.552]	< **0.001**/0.570 [0.306, 0.753]	0.859/0.046 [-0.287, 0.369]	0.064/0.312 [-0.024, 0.584]	**0.003**/0.555 [0.229, 0.769]	
Others[b]	< **0.001**/0.373 [0.228, 0.502]	**0.012**/0.204 [0.046, 0.352]	< **0.001**/0.347 [0.196, 0.482]	0.302/0.086 [-0.078, 0.246]	0.408/0.069 [-0.096, 0.230]	**0.021**/0.195 [0.028, 0.351]	0.320/0.087 [-0.084, 0.253]
				VF score			
ST5	< **0.001**/0.879 [0.807, 0.925]						
ST8	0.633/0.064 [-0.198, 0.317]	< **0.001**/0.867 [0.783, 0.920]					
ST15	< **0.001**/0.881 [0.805, 0.929]	< **0.001**/0.892 [0.821, 0.936]	< **0.001**/0.755 [0.603, 0.854]				
ST30	0.153/0.194 [-0.075, 0.437]	< **0.001**/0.816 [0.702, 0.890]	0.213/0.179 [-0.107, 0.439]	< **0.001**/0.890 [0.810, 0.938]			
ST1	< **0.001**/0.504 [0.256, 0.689]	< **0.001**/0.741 [0.576, 0.848]	**0.009**/0.401 [0.110, 0.628]	< **0.001**/0.865 [0.757, 0.927]	0.050/0.314 [-0.001, 0.573]		
ST188	< **0.001**/0.787 [0.639, 0.878]	< **0.001**/0.808 [0.670, 0.892]	< **0.001**/0.570 [0.307, 0.753]	< **0.001**/0.529 [0.242, 0.730]	< **0.001**/0.753 [0.560, 0.868]	< **0.001**/0.797 [0.603, 0.902]	
Others	0.100/0.133 [-0.026, 0.286]	< **0.001**/0.603 [0.491, 0.695]	0.441/0.064 [-0.099, 0.224]	< **0.001**/0.425 [0.281, 0.550]	**0.020**/0.192 [0.030, 0.345]	**0.001**/0.266 [0.102 , 0.415]	**0.003**/0.255 [0.088, 0.407]

[a]Effect sizes are presented as r (calculated as |Z|/√N) with 95% confidence intervals (CI) derived via Fisher's z-transformation. [b]Please see the Supplementary Table 1 for details.