BacAnt: the combination annotation server of antibiotic resistance gene, insertion sequences, integron, transposable elements for bacterial DNA sequences.

Running Title: combination annotation of ARG, IS, integron, Tn

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Note

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Abstract

Whole genome sequencing (WGS) of bacteria has become a routine method in diagnostic laboratories. One of the most exciting advantages of WGS is the ability to predict antimicrobial resistance genes (ARGs) and mobile genetic elements (MGEs) in a variety of bacteria, which may allow comprehensive investigations of genetic features but also serve for epidemiological studies. A plethora of softwares have been developed for the detailed annotation of DNA sequences, such as RAST (Rapid Annotation using Subsystem Technology), Resfinder, ISfinder, INTEGRALL and The Transposon Registry. Unfortunately, up to now, a reliable annotation tool of the combination of ARGs and MGEs is not available to researchers, and the generation of genbank files requires much manual input. Here, we present a new webserver which allows the annotation of ARGs, ISs, integron, and transposable elements at the same time. The algorithm generates genbank files automatically, which are compatible with easyfig for comparative genomic analysis.

Key words: BacAnt, annotation, IS, ARG, integron, Tn

Key Points

- There exist a number of software for DNA sequence annotation, RAST (Rapid Annotation using Subsystem Technology), Resfinder, ISfinder, INTEGRALL and The Transposon Registry.
- A reliable annotation tool of the combination of ARGs and MGEs is not available to researchers, and the generation of genbank files requires much manual input.
- We present a new webserver which allows the annotation of ARGs, ISs, integron, and transposable elements at the same time. The algorithm generates genbank files automatically, which are compatible with easyfig for comparative genomic analysis.

Introduction

The era of next-generation sequencing (NGS) started in 2005 with the commercial release of massively parallel pyrosequencing [1]. The NGS technology developed rapidly in the past years and has made substantial improvements in terms of quality and yield. With the rapid decrease of sequencing costs, falling by as much as 80% year over year, whole genome sequencing of bacteria has become a routine method in diagnostic laboratories [2]. To date, the most common use of NGS is for simultaneous identification, typing, and/or antimicrobial susceptibility prediction of microbial pathogens [3]. One of the most exciting advantages of NGS is the ability to predict antimicrobial resistance genes (ARGs) and mobile genetic elements (MGEs) in a variety of bacteria, which may allow comprehensive investigations of genetic features but is also of tremendous use for epidemiological studies, including the spread and distribution of resistant bacteria as part of surveillance programs [3, 4]. A massive number of bacteria genomes is being sequenced using NGS technology every day in laboratories across the globe, with genomes released at remarkable rates. With this huge amount of data available, it is important to have the ability to extract project-relevant information easily. However, in publicly available databases, most of bacterial genomes are available as contigs which have been constructed employing auto-annotation algorithms. Over the years, highly efficient methods for bacterial genome annotation have been developed, that do not require much user input.

Rapid Annotation using Subsystem Technology (RAST) is a widely used webserver for genome annotations of microbial species [5]. Although the performance using RAST-based annotation are quite useful, several important limitations remain. For example, RAST will label many Open Reading Frames (ORFs) as “hypothetical proteins”, and the performance to identify ARGs and label them as such, is fairly limited as the algorithm is not tailored towards this purpose. Based on the RAST system, the Pathosystems Resource Integration Center (PATRIC) improved the data collection of ARGs, and provided users a more powerful analysis for both genomes and individual genes [6]. Another available annotation server is Resfinder which is managed by the Center for Genomic Epidemiology; it provides a convenient way of identifying acquired ARGs in sequenced bacterial isolates [7]. In addition to annotations for ARGs, some databases specifically designed to annotate MGEs such as insertion sequences (ISfinder) and integrons (INTEGRALL) and transposable elements (The Transposon Registry) have been created [8-10]. Inter/intra-species genetic transfer events of MGEs are responsible for the emergence and rapid spread of resistance [11]. Therefore, the knowledge of MGE-associated drug resistance is crucial for the monitoring of resistance among microbial species. Unfortunately, up to now, a rapid annotation tool of the combination of ARGs and MGEs is not available, and the generation of genbank files has to be done manually. Therefore, we created a new program/algorithm called BacAnt, which rapidly and efficiently annotates ARGs, insertion sequences (ISs), integron, and transposable elements in a single step and generates a genbank file automatically, that is compatible with the easyfig program for comparative genomic analysis.

Material and methods

Reference sequences

There are four curated databases for BacAnt tool, including ResDB (resistance gene sequence database), ISDB (insertion sequence database), IntegronDB (integron sequence database), and TransposonDB (transposon sequence database). We collected 5029 sequences from NCBI Bacterial Antimicrobial Resistance Reference Gene Database (https://www.ncbi.nlm.nih.gov, version: 2019-09-06.1) into ResDB at 2019-12-01. In addition, we collected 5553 sequences from ISFINDER (https://www-is.biotoul.fr, version: 2019) into ISDB by 2019-12-01, 1094 sequences from INTEGRALL (http://integrall.bio.ua.pt, version: 2017-11-30) to be included into IntegronDB by 2019-12-01. We also collected 234 sequences from THE TRANSPOSON REGISTRY (https://transposon.lstmed.ac.uk, version: 2019-07-23) into the TransposonDB by 2019-12-01.

Program for identifying resistance genes and mobile elements

We created a python program (BacAnt) to identify resistance genes and mobile elements for bacteria nucleotide sequences with BLAST analysis. We first used the BLASTN program comparing input sequences with the reference database with an -evalue 1e-5. We then filtered the raw results by identities and coverage (blast align match length/subject length). All results that pass the identity and coverage filter are kept for further analysis. The default threshold was set to 90% for identities and to 60% for coverage. Finally, we display the filtered results in text and genbank format, while also providing a visual output. The four types of annotations for the sequences are displayed in the same figure to guide the analysis of the genomic sequence.

BacAnt has six parameters. The user has two choices regarding the input sequence file: --nucleotide (-n), fasta format or –genbank (-g), genbank format. The required output path: --resultdir (-o). --databases (-d), reference databases, select all by default. –coverages (-c), coverage threshold, 60% by default. –identities (-i), identities threshold, 90% by default. In average, it takes about 2 minutes for each run.

Website for BacAnt

For the analysis to be performed online, we developed a website which we call http://bacant.net. The algorithm running on the server is based on Python/Django, which allows the user to upload sequence files for the rapid identification of ARGs and MGEs. The output format allows the display of graphic representations of the results. A demo report can be seen here: http://bacant.net/BacAnt/demo.

Examples analysis using BacAnt

Four genome sequences from NCBI, including *Acinetobacter baumannii* (2019.11.17), *Escherichia coli* (2019.5.7), *Salmonella enterica* (2019.6.4) and *Staphylococcus aureus* (2019.6.4) were used to illustrate the capabilities of our program. The number of drug-resistance genes and insertion sequences of each sample were identified in the BacAnt analysis, and plotted as horizontal and vertical coordinates respectively. Scatter plots were created using the ggplot2 package in R (V3.6.2), together with the trend line [12].

It is also possible to create a network diagram using the analysis results of BacAnt. The tool to construct a network graph is Cytoscape (v3.7.2) [13]. Only resistance gene pairs with a distance of less than 10 kb and frequency of occurrence no less than 10 are extracted from the data to construct the network map. In addition, we also created a map from resistance genes and insertion sequence pairs with a distance of less than 10 kb and frequency of occurrence no less than 10.

Results and Discussion

BacAnt is a browser-based platform to annotate DNA sequences, and to visualize the annotation results. When using the web interface, the user first has the choice to upload DNA sequences as Fasta, Seq or GenBank files (Fig. 1A). Then, the user has the option to select one or more -or all- databases, which include ResDB, ISDB, IntegronDB or TransponsonDB for the sequence annotation. After the DNA sequence is submitted, the python-based program BacAnt will identify ARGs and MGEs in the bacterial nucleotide sequences.

The output of BacAnt commences with the summary of the annotation, followed with up to four tables including the annotation result from each database, if they have been selected in the first step. The final part of the BacAnt annotation result visualizes an annotation result which is combined from all four databases. The user can then download all annotation results obtained by running BacAnt, including figures and genbank files. The genebank files generated by BacAnt are compatible with Easyfig [14]. As an example we used *Acinetobacter baumannii* MDR-ZJ06 to display the result of the annotation by BacAnt (Fig. 1B, Fig. 1C). The annotation output of the MDR-ZJ06 strains shows that the isolate harbors 19 resistance genes, 31 insertion elements, 124 integrons and 17 transposons.

To investigate whether or not a relationship between ARGs and ISs exists, we extracted the number of ARGs and ISs from the results of BacAnt analysis of four species genome sequences from NCBI. The results show that the number of ARGs does not correlate with the number of ISs in the four species (Pearson's $R^2 < 0.8$, Fig. 2). Previously, it was reported that at least eight MGEs were associated with ARGs in *A. baumannii* [15]. Our result, however, indicates that there is a more complex relationship between ARGs and ISs. We believe that there are two reason for the "independence" (and thus "non-correlation") of the occurrence of ISs and ARGs: First, any cargo gene can be encoded by an IS, meaning that it is not limited to ARGs. Second, there are other ways for horizontal gene transfer events for ARGs which are different from ISs.

We identified commonly found ARG-IS pairs or ARG pairs that were in close proximity to the insertion sequence (< 10 kb apart), which allows to detect gene cassettes that may play an import role in evolution, regulation and ARG exchange. ARG cassettes are generally small (2-7) and specific for the species we investigated (Fig. 3). The ARG cassettes for Gram-negative bacteria were larger and more stable than the cassettes in Gram-positive bacteria, which confirms a previously published observation [16]. In case of *A. baumannii*, we identified two ARG cassettes, with one containing the genes *tet(B)*, *sul2*, *aph(3")-Ib* and *aph(6)-Id*, and the other one encoding the genes *mph(E)*, *msr(E)*, *armA*, *aadA1*, *sul1*, *aac(6')-Ib'* and *catB8*. The ARG cassette which contained *mph(E)*, *msr(E)* and *armA* was described previously [16]. For *E. coli*, the program identified a stable small cassette that shows overlap with that of *A. baumannii*, including *sul2*, *aph(3")-Ib* and *aph(6)-Id*. When analyzing genomes of *S. aureus*, the program BacAnt found three ARG cassettes; the first one contained the genes *blaZ*, *blaR1* and *blaI_of_Z*, while the second one encoded for *ant(6)-Ia*, *aph(3')-IIIa* and *sat4*. The third ARG cassette in *S. aureus* includes the genes for *mecA*, *mecR1*, *mecI_of_mecA*, *ant(9)-Ia* and *erm(A)*. The identified ARGs were clearly linked to prevalent, dominant *E. coli* clones, illustrated by the link between *bla*$_{\text{CTX-M-15}}$ and ST131 [17]. Other ARGs, however, show a higher degree of diversity, like *bla*$_{\text{NDM-1}}$ [18]. The species-specific occurrence of ARG cassettes may be due to differences in evolutionary pathways when acquiring genes for multi-drug resistance.

For the ARG-IS pairs, *mecA* with diverse IS are the top nine ARG-IS pairs in *S. aureus* (Fig. 4D). In *A. baumannii,* IS*Vsa3* containing the genes *aph(6)-Id*, *aph(3")-Ib* and *tet(B)* comprise the top three ARG-IS pairs (Fig. 4A). In *E. coli*, IS*26* was the most abundant IS (Fig. 4B). It appears that the ISs are specific to species. As previously reported, we also observed notable differences between the important MGE in Gram-negative bacteria compared to Gram-positive bacteria [19].

In order to be able to extract the maximum amount of information from whole genome sequence data, we need the improve annotation and analysis methods of MGEs [19]. In this work, we created a webserver that allows the annotation of ARGs, ISs, integron, and transposable elements at the same time. The algorithm generates genbank files automatically, which are compatible with easyfig for comparative genomic analysis.

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Figure legends:

Fig 1

Screenshots of the BacAnt web interface. A) Users upload an assembled file from their local personal computer and select the desired annotation database. B) BacAnt annotation result for *Acinetobacter baumannii* MDR-ZJ06. C) BacAnt graphic representations of the results for *Acinetobacter baumannii* MDR-ZJ06.

Fig 2

The relationship between the number of drug-resistant genes and insertion sequences from four species (*Acinetobacter baumannii*, *Escherichia coli*, *Salmonella enterica* and *Staphylococcus aureus*). The number of drug-resistant genes and insertion sequences of each sample were extracted from the results of BacAnt analysis, and the number of them was taken as the horizontal and vertical coordinates respectively. The scatter plot was drawn with ggplot2 package in R (V3.6.2), and the trend line was generated.

Fig 3

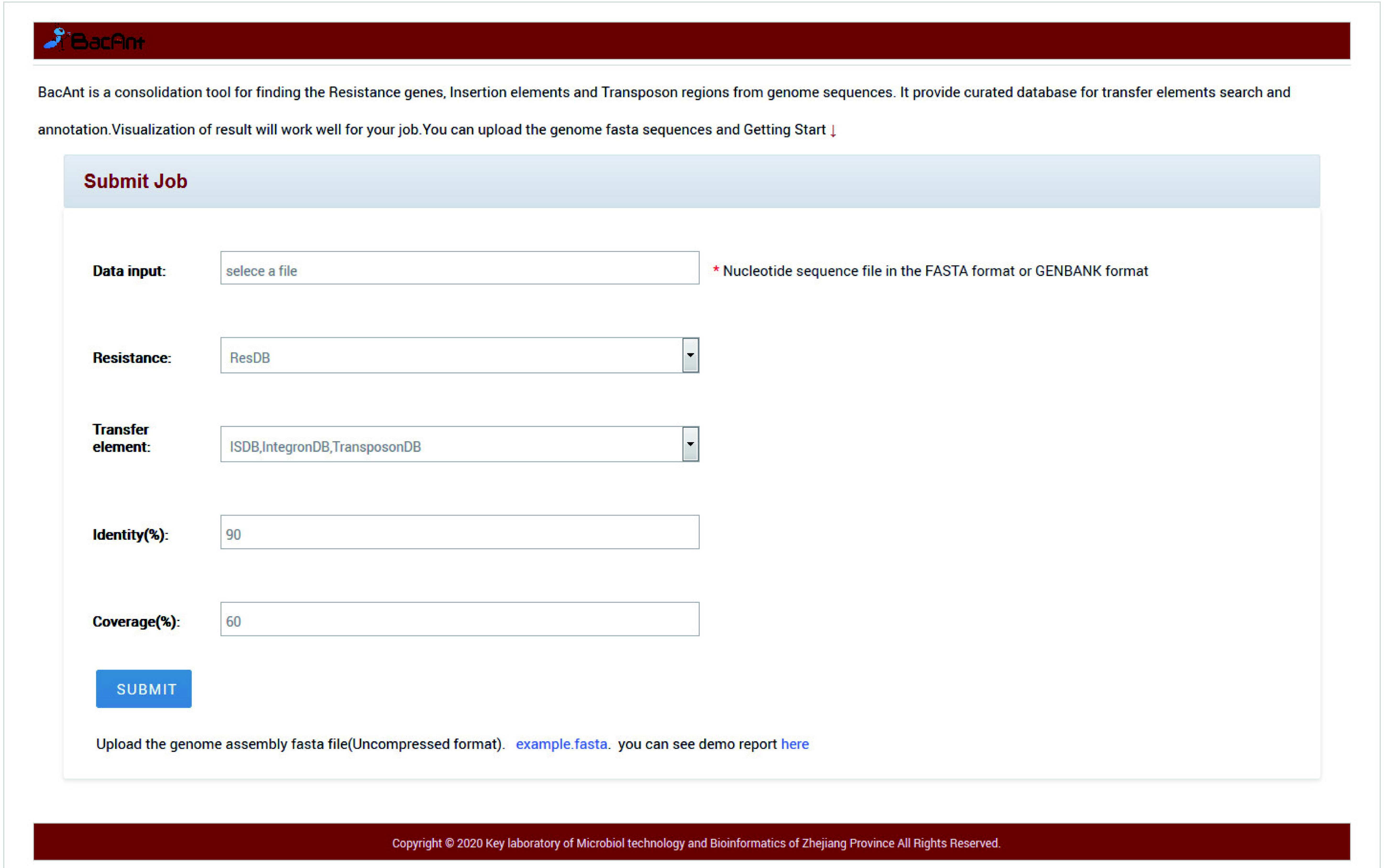
Genomic proximity of antibiotic resistance gene and Insertion sequences in four species (*Acinetobacter baumannii*, *Escherichia coli*, *Salmonella enterica* and *Staphylococcus aureus*). The resistance gene pairs with a distance of less than 10 kb and frequency of occurrence no less than 10 were screened to construct the network. Diamond nodes are used to represent antibiotic resistance genes, solid lines are used to represent gene pairs whose frequency is not less than 80% of the total number and labeled as pink, dotted lines represent gene pairs with frequency less than 80% of the total number and are marked as gray, and the width of the line indicates the frequency. Different antibiotics are displayed in different colors, corresponding to the drug-resistant genes.

Fig 4

Genomic proximity of antibiotic resistance gene and Insertion sequences in four species: A) *Acinetobacter baumannii*, B) *Escherichia coli*, C) *Salmonella enterica* and D) *Staphylococcus aureus*. The resistance genes and insertion sequence pairs with a distance of less than 10 kb and frequency of occurrence no less than 10 were screened to construct the network. The diamond node is used to represent the drug-resistant gene, the circle is the insertion sequence. The solid line is the gene pair whose frequency is not less than 80% of the total number and labeled as orange, the dotted line represents the gene pair whose frequency is less than 80% of the total number and labeled as sky blue, and the width of the line indicates the frequency. Different colors are assigned to the antibiotics corresponding to the drug-resistant genes, the insertion sequences are displayed in gray.

References:

1. Goodwin S, McPherson JD, McCombie WR. Coming of age: ten years of next-generation sequencing technologies. Nat Rev Genet 2016; 17(6): 333-51.
2. Didelot X, Bowden R, Wilson DJ, et al. Transforming clinical microbiology with bacterial genome sequencing. Nat Rev Genet 2012; 13(9): 601-612.
3. Mitchell SL, Simner PJ. Next-Generation Sequencing in Clinical Microbiology: Are We There Yet? Clin Lab Med 2019; 39(3): 405-418.
4. Zhou K, Lokate M, Deurenberg RH, et al. Characterization of a CTX-M-15 Producing Klebsiella Pneumoniae Outbreak Strain Assigned to a Novel Sequence Type (1427). Front Microbiol 2015; 6: 1250.
5. Aziz RK, Bartels D, Best AA, et al. The RAST Server: rapid annotations using subsystems technology. BMC Genomics 2008; 9: 75.
6. Wattam AR, Brettin T, Davis JJ, et al. Assembly, Annotation, and Comparative Genomics in PATRIC, the All Bacterial Bioinformatics Resource Center. Methods Mol Biol 2018; 1704: 79-101.
7. Zankari E, Hasman H, Cosentino S, et al. Identification of acquired antimicrobial resistance genes. J Antimicrob Chemother 2012; 67(11): 2640-4.
8. Siguier P, Perochon J, Lestrade L, et al. ISfinder: the reference centre for bacterial insertion sequences. Nucleic Acids Res 2006; 34(Database issue): D32-6.
9. Moura A, Soares M, Pereira C, et al. INTEGRALL: a database and search engine for integrons, integrases and gene cassettes. Bioinformatics 2009; 25(8): 1096-8.
10. Tansirichaiya S, Rahman MA, Roberts AP. The Transposon Registry. Mob DNA 2019; 10: 40.
11. Subedi D, Vijay AK, Willcox M. Overview of mechanisms of antibiotic resistance in Pseudomonas aeruginosa: an ocular perspective. Clin Exp Optom 2018; 101(2): 162-171.
12. Wickham H. ggplot2: Elegant Graphics for Data Analysis. Springer-Verlag New York 2016. ISBN 978-3-319-24277-4, https://ggplot2.tidyverse.org.
13. Shannon P, Markiel A, Ozier O, et al. Cytoscape: a software environment for integrated models of biomolecular interaction networks. Genome Res 2003; 13(11): 2498-504.
14. Sullivan MJ, Petty NK, Beatson SA. Easyfig: a genome comparison visualizer. Bioinformatics 2011; 27(7): 1009-10.
15. Leal NC, Campos TL, Rezende AM, et al. Comparative Genomics of Acinetobacter baumannii Clinical Strains From Brazil Reveals Polyclonal Dissemination and Selective Exchange of Mobile Genetic Elements Associated With Resistance Genes. Front Microbiol 2020; 11: 1176.
16. Chng KR, Li C, Bertrand D, et al. Cartography of opportunistic pathogens and antibiotic resistance genes in a tertiary hospital environment. Nat Med 2020; 26(6): 941-951.
17. Mathers AJ, Peirano G, Pitout JD. The role of epidemic resistance plasmids and international high-risk clones in the spread of multidrug-resistant Enterobacteriaceae. Clin Microbiol Rev 2015; 28(3): 565-91.
18. Wu W, Feng Y, Tang G, et al. NDM Metallo-β-Lactamases and Their Bacterial Producers in Health Care Settings. Clin Microbiol Rev 2019; 32(2).
19. Partridge SR, Kwong SM, Firth N, et al. Mobile Genetic Elements Associated with Antimicrobial Resistance. Clin Microbiol Rev 2018; 31(4).



BacAnt is a consolidation tool for finding the Resistance genes, Insertion elements and Transposon regions from genome sequences. It provide curated database for transfer elements search and annotation.Visualization of result will work well for your job.You can upload the genome fasta sequences and Getting Start ↓

Submit Job

Data input: selece a file * Nucleotide sequence file in the FASTA format or GENBANK format

Resistance: ResDB

Transfer element: ISDB,IntegronDB,TransposonDB

Identity(%): 90

Coverage(%): 60

Upload the genome assembly fasta file(Uncompressed format). example.fasta. you can see demo report here

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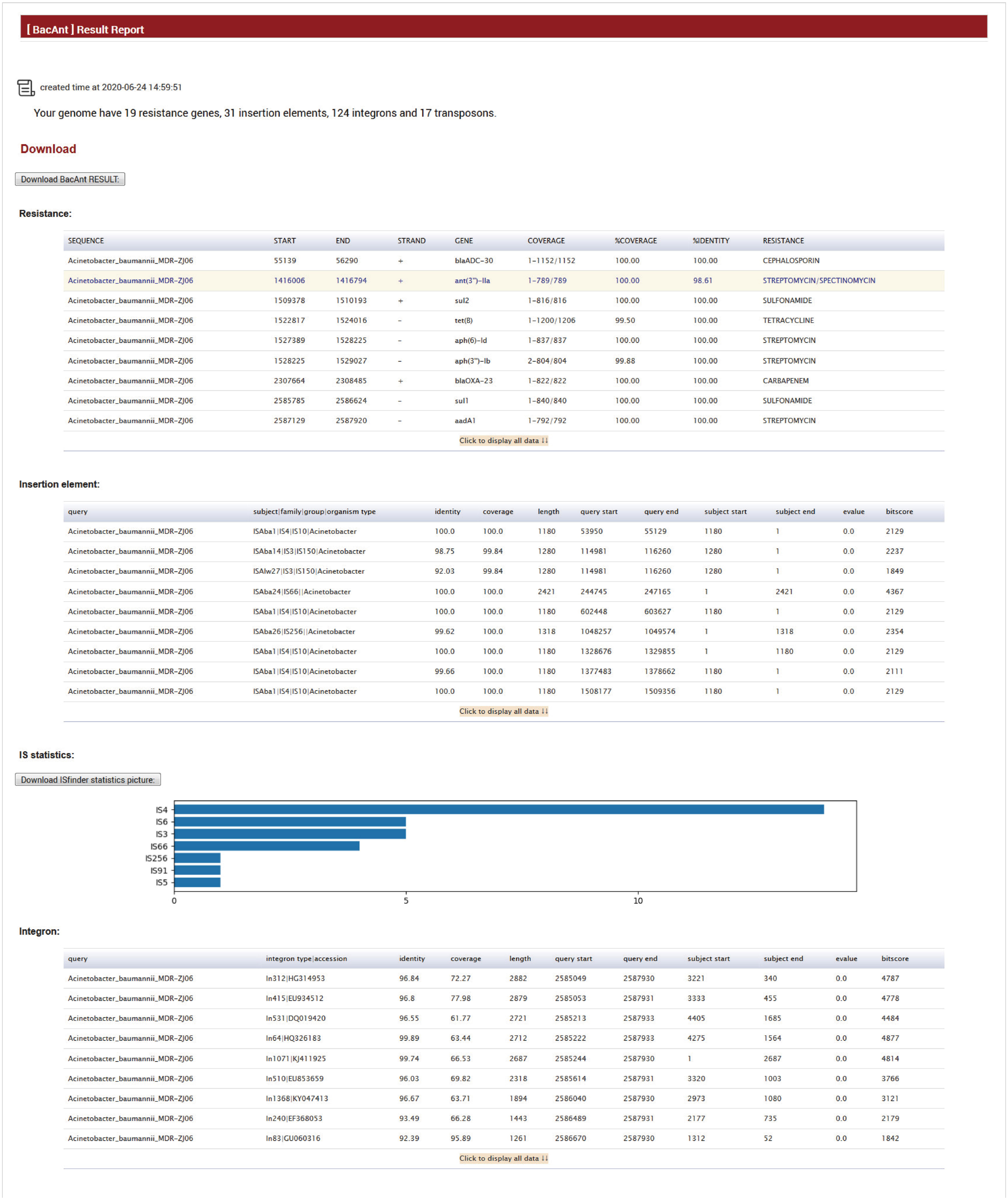


[BacAnt] Result Report

created time at 2020-06-24 14:59:51

Your genome have 19 resistance genes, 31 insertion elements, 124 integrons and 17 transposons.

Download

Resistance:

SEQUENCE	START	END	STRAND	GENE	COVERAGE	%COVERAGE	%IDENTITY	RESISTANCE
Acinetobacter_baumannii_MDR-ZJ06	55139	56290	+	blaADC-30	1-1152/1152	100.00	100.00	CEPHALOSPORIN
Acinetobacter_baumannii_MDR-ZJ06	1416006	1416794	+	ant(3")-IIa	1-789/789	100.00	98.61	STREPTOMYCIN/SPECTINOMYCIN
Acinetobacter_baumannii_MDR-ZJ06	1509378	1510193	+	sul2	1-816/816	100.00	100.00	SULFONAMIDE
Acinetobacter_baumannii_MDR-ZJ06	1522817	1524016	-	tet(B)	1-1200/1206	99.50	100.00	TETRACYCLINE
Acinetobacter_baumannii_MDR-ZJ06	1527389	1528225	-	aph(6)-Id	1-837/837	100.00	100.00	STREPTOMYCIN
Acinetobacter_baumannii_MDR-ZJ06	1528225	1529027	-	aph(3")-Ib	2-804/804	99.88	100.00	STREPTOMYCIN
Acinetobacter_baumannii_MDR-ZJ06	2307664	2308485	+	blaOXA-23	1-822/822	100.00	100.00	CARBAPENEM
Acinetobacter_baumannii_MDR-ZJ06	2585785	2586624	-	sul1	1-840/840	100.00	100.00	SULFONAMIDE
Acinetobacter_baumannii_MDR-ZJ06	2587129	2587920	-	aadA1	1-792/792	100.00	100.00	STREPTOMYCIN

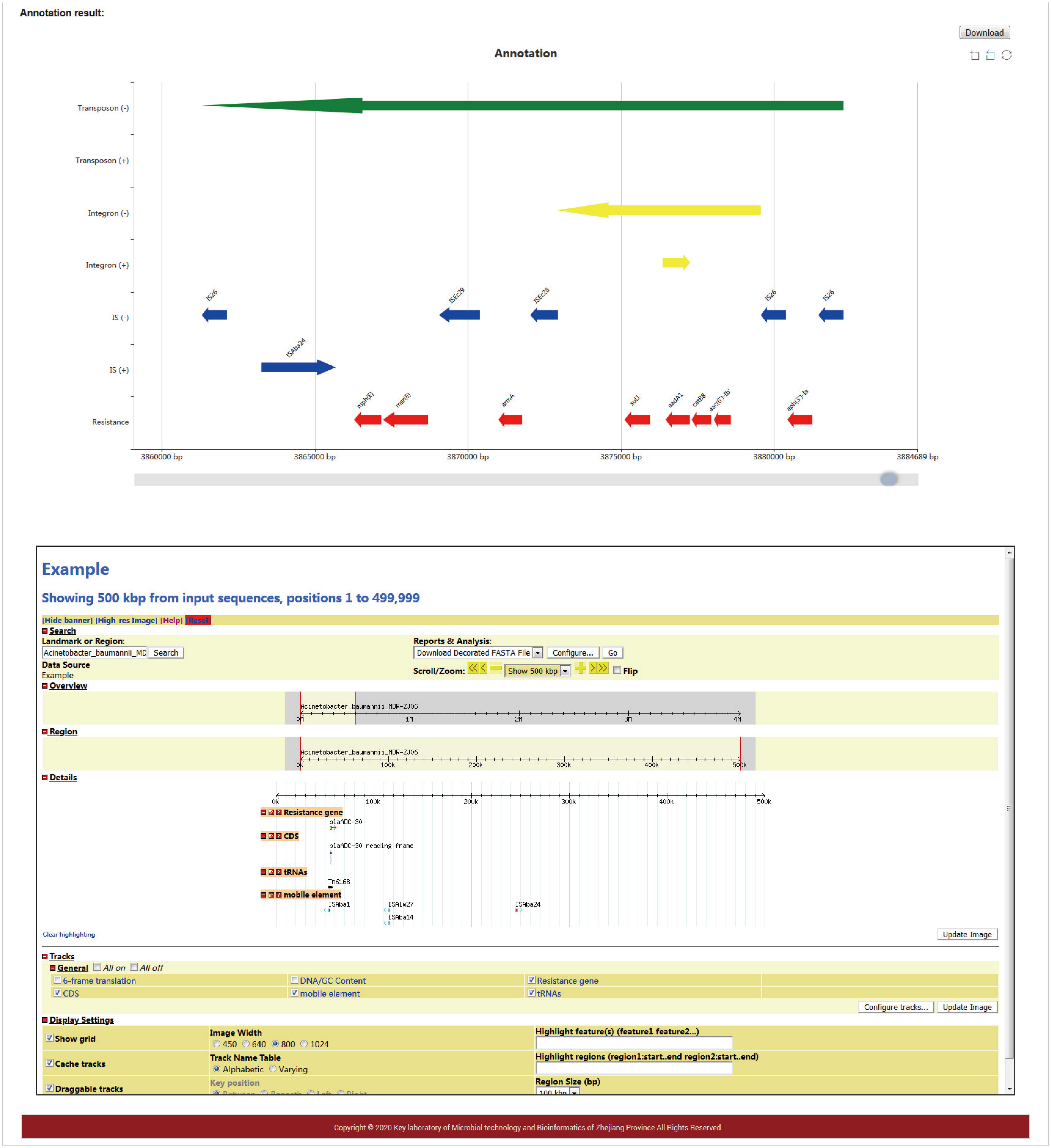
Insertion element:

query	subject|family|group|organism type	identity	coverage	length	query start	query end	subject start	subject end	evalue	bitscore
Acinetobacter_baumannii_MDR-ZJ06	ISAba1|IS4|IS10|Acinetobacter	100.0	100.0	1180	53950	55129	1180	1	0.0	2129
Acinetobacter_baumannii_MDR-ZJ06	ISAba14|IS3|IS150|Acinetobacter	98.75	99.84	1280	114981	116260	1280	1	0.0	2237
Acinetobacter_baumannii_MDR-ZJ06	ISAlw27|IS3|IS150|Acinetobacter	92.03	99.84	1280	114981	116260	1280	1	0.0	1849
Acinetobacter_baumannii_MDR-ZJ06	ISAba24|IS66||Acinetobacter	100.0	100.0	2421	244745	247165	1	2421	0.0	4367
Acinetobacter_baumannii_MDR-ZJ06	ISAba1|IS4|IS10|Acinetobacter	100.0	100.0	1180	602448	603627	1180	1	0.0	2129
Acinetobacter_baumannii_MDR-ZJ06	ISAba26|IS256||Acinetobacter	99.62	100.0	1318	1048257	1049574	1	1318	0.0	2354
Acinetobacter_baumannii_MDR-ZJ06	ISAba1|IS4|IS10|Acinetobacter	100.0	100.0	1180	1328676	1329855	1	1180	0.0	2129
Acinetobacter_baumannii_MDR-ZJ06	ISAba1|IS4|IS10|Acinetobacter	99.66	100.0	1180	1377483	1378662	1180	1	0.0	2111
Acinetobacter_baumannii_MDR-ZJ06	ISAba1|IS4|IS10|Acinetobacter	100.0	100.0	1180	1508177	1509356	1180	1	0.0	2129

IS statistics:

Integron:

query	integron type|accession	identity	coverage	length	query start	query end	subject start	subject end	evalue	bitscore
Acinetobacter_baumannii_MDR-ZJ06	In312|HG314953	96.84	72.27	2882	2585049	2587930	3221	340	0.0	4787
Acinetobacter_baumannii_MDR-ZJ06	In415|EU934512	96.8	77.98	2879	2585053	2587931	3333	455	0.0	4778
Acinetobacter_baumannii_MDR-ZJ06	In531|DQ019420	96.55	61.77	2721	2585213	2587933	4405	1685	0.0	4484
Acinetobacter_baumannii_MDR-ZJ06	In64|HQ326183	99.89	63.44	2712	2585222	2587933	4275	1564	0.0	4877
Acinetobacter_baumannii_MDR-ZJ06	In1071|KJ411925	99.74	66.53	2687	2585244	2587930	1	2687	0.0	4814
Acinetobacter_baumannii_MDR-ZJ06	In510|EU853659	96.03	69.82	2318	2585614	2587931	3320	1003	0.0	3766
Acinetobacter_baumannii_MDR-ZJ06	In1368|KY047413	96.67	63.71	1894	2586040	2587930	2973	1080	0.0	3121
Acinetobacter_baumannii_MDR-ZJ06	In240|EF368053	93.49	66.28	1443	2586489	2587931	2177	735	0.0	2179
Acinetobacter_baumannii_MDR-ZJ06	In83|GU060316	92.39	95.89	1261	2586670	2587930	1312	52	0.0	1842



Annotation result:

Download
Annotation
Transposon (-)
Transposon (+)
Integron (-)
Integron (+)
IS (-)
IS (+)
Resistance
IS26
ISEc29
ISEc28
IS26
IS26
ISAba24
mph(E)
msr(E)
armA
sul1
aadA1
catB8
aac(6')-Ib'
aph(3')-Ia
3860000 bp
3865000 bp
3870000 bp
3875000 bp
3880000 bp
3884689 bp

Example

Showing 500 kbp from input sequences, positions 1 to 499,999

[Hide banner] [High-res Image] [Help] [Reset]
Search

Landmark or Region: Acinetobacter_baumannii_MD

Search

Reports & Analysis: Download Decorated FASTA File

Configure...
Go

Data Source
Example

Scroll/Zoom: Show 500 kbp ☐ **Flip**

Overview
Acinetobacter_baumannii_MDR-ZJ06
0M
1M
2M
3M
4M
Region
Acinetobacter_baumannii_MDR-ZJ06
0k
100k
200k
300k
400k
500k
Details
0k
100k
200k
300k
400k
500k
Resistance gene
blaADC-30
CDS
blaADC-30 reading frame
tRNAs
Tn6168
mobile element
ISAba1
ISAlw27
ISAba14
ISAba24
Clear highlighting
Update Image
Tracks

General ☐ *All on* ☐ *All off*

☐ 6-frame translation
☐ DNA/GC Content
☑ Resistance gene
☑ CDS
☑ mobile element
☑ tRNAs

Configure tracks...
Update Image
Display Settings

☑ **Show grid**

Image Width
○ 450 ○ 640 ● 800 ○ 1024

Highlight feature(s) (feature1 feature2...)

☑ **Cache tracks**

Track Name Table
● Alphabetic ○ Varying

Highlight regions (region1:start..end region2:start..end)

☑ **Draggable tracks**

Key position

Region Size (bp)

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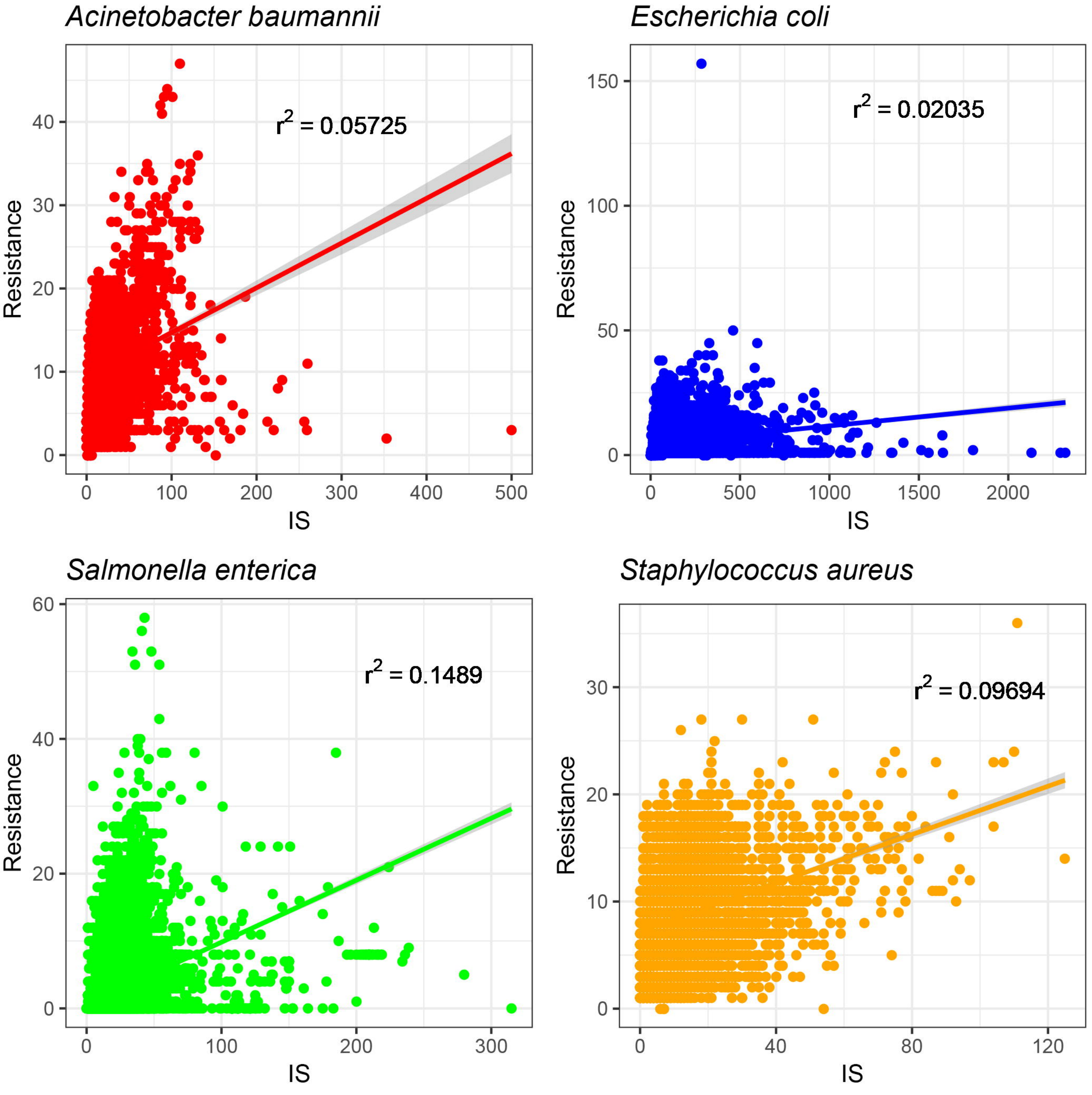
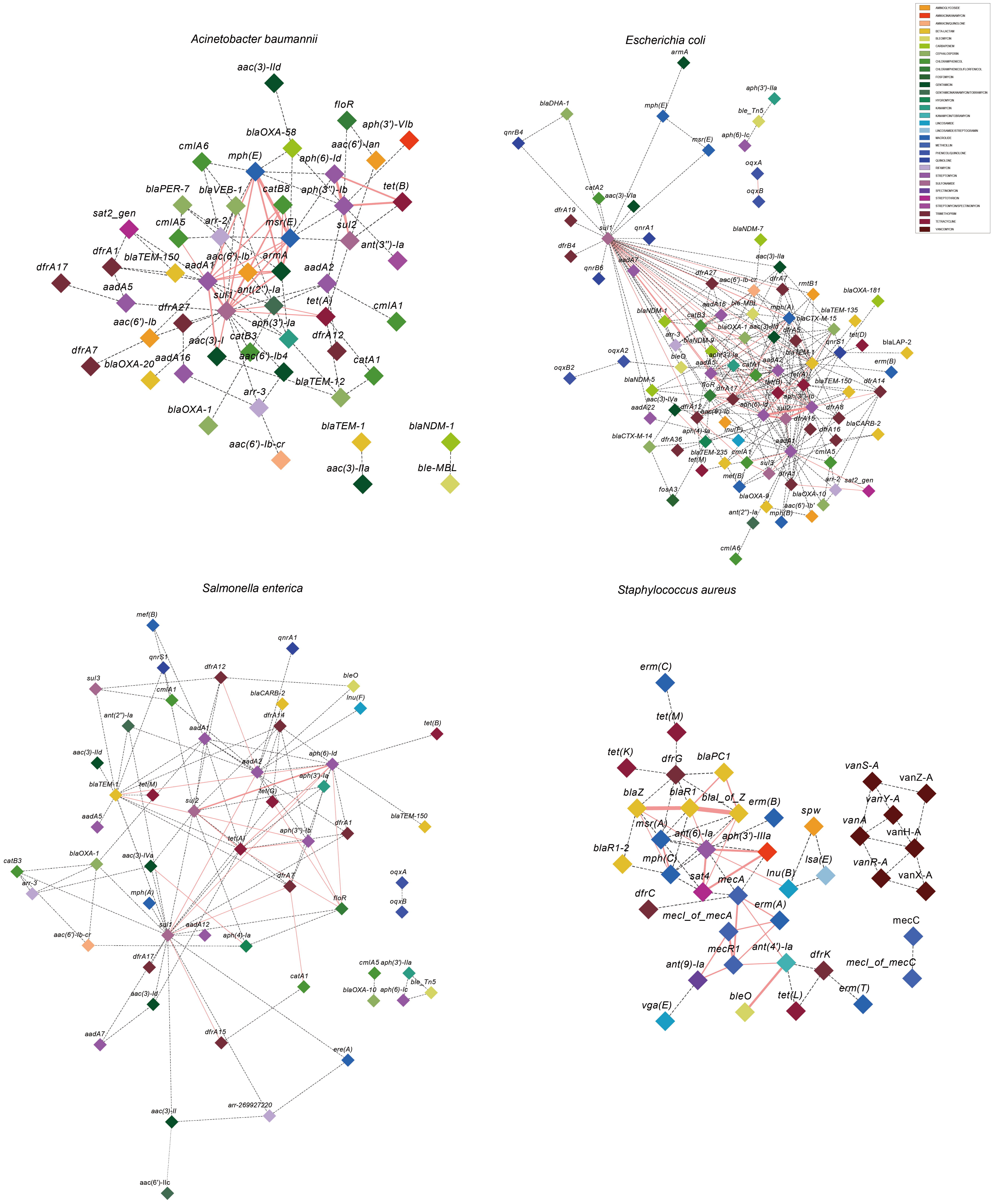
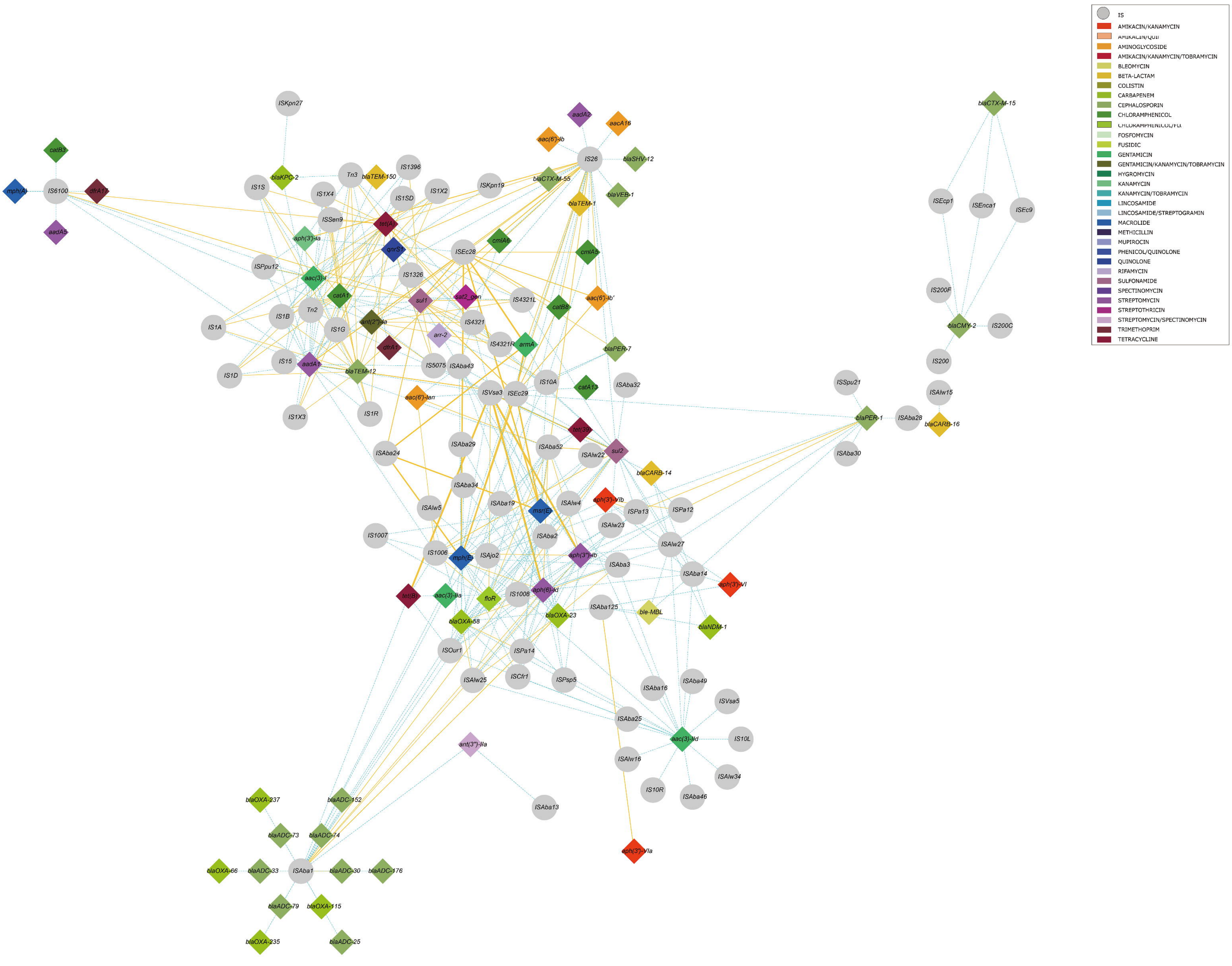
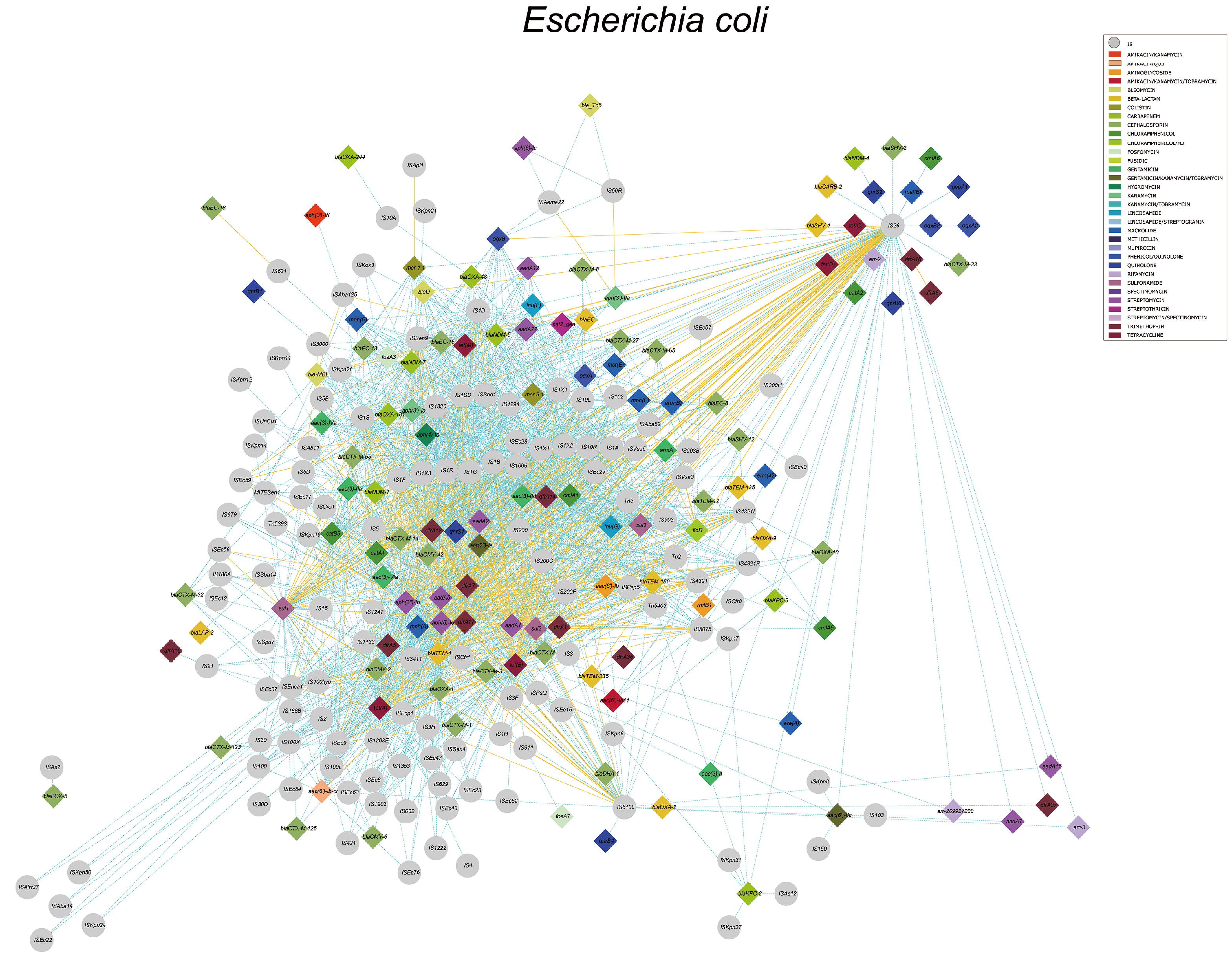

Acinetobacter baumannii
r² = 0.05725
Resistance
IS
0
10
20
30
40
0
100
200
300
400
500
Escherichia coli
r² = 0.02035
Resistance
IS
0
50
100
150
0
500
1000
1500
2000
Salmonella enterica
r² = 0.1489
Resistance
IS
0
20
40
60
0
100
200
300
Staphylococcus aureus
r² = 0.09694
Resistance
IS
0
10
20
30
0
40
80
120

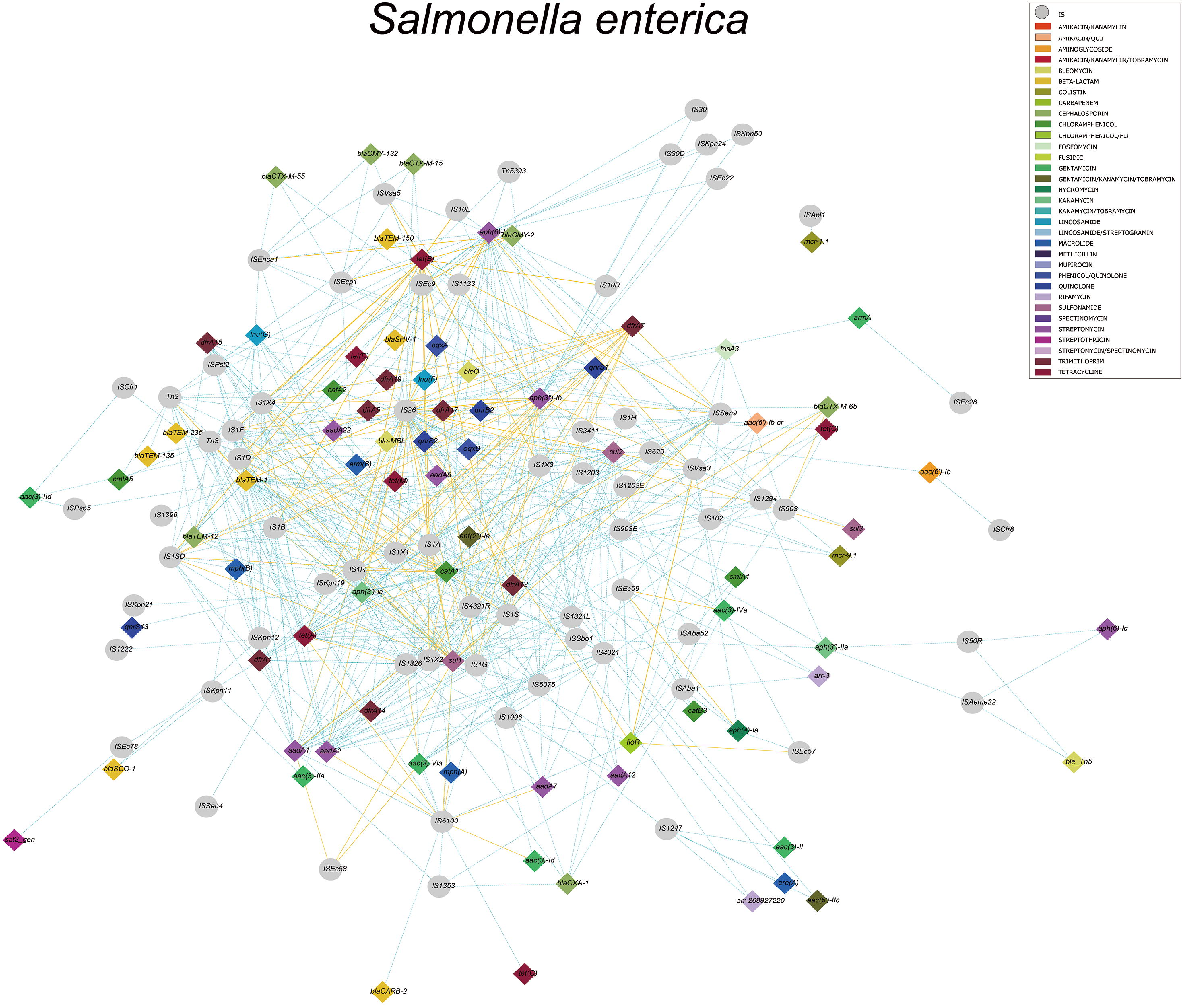

Acinetobacter baumannii
aac(3)-IId
floR
aph(3')-VIb
blaOXA-58
aac(6')-Ian
cmlA6
mph(E)
aph(6)-Id
tet(B)
blaPER-7
blaVEB-1
catB8
aph(3'')-Ib
sat2_gen
cmlA5
arr-2
msr(E)
sul2
ant(3'')-Ia
dfrA1
blaTEM-150
aac(6')-Ib'
armA
dfrA17
aadA1
aadA2
aadA5
sul1
ant(2'')-Ia
tet(A)
cmlA1
dfrA27
aac(6')-Ib
aph(3')-Ia
aac(3)-I
catB3
dfrA12
dfrA7
blaOXA-20
aadA16
aac(6')-Ib4
catA1
blaTEM-12
arr-3
blaOXA-1
blaTEM-1
blaNDM-1
aac(6')-Ib-cr
aac(3)-IIa
ble-MBL
Escherichia coli
armA
aph(3')-IIa
blaDHA-1
mph(E)
ble_Tn5
qnrB4
msr(E)
aph(6)-Ic
oqxA
oqxB
catA2
aac(3)-VIa
dfrA19
sul1
qnrA1
blaNDM-7
dfrB4
aac(3)-IIa
aadA7
qnrB6
dfrA27
aac(6')-Ib-cr
dfrA7
rmtB1
blaOXA-181
aadA16
ble-MBL
mph(A)
blaNDM-1
catB3
blaTEM-135
blaCTX-M-15
blaOXA-1
aac(3)-IId
dfrA5
arr-3
blaNDM-9
tet(D)
qnrS1
blaLAP-2
oqxA2
aph(3')-Ia
blaTEM-1
bleO
aadA5
catA1
aadA2
erm(B)
oqxB2
tet(A)
blaNDM-5
floR
dfrA17
tet(B)
blaTEM-150
dfrA14
aac(3)-IVa
aph(3'')-Ib
aadA22
dfrA12
aac(6')-Ib
aph(6)-Id
sul2
dfrA8
dfrA15
blaCARB-2
aph(4)-Ia
lnu(F)
dfrA16
blaCTX-M-14
dfrA36
aadA1
blaTEM-235
cmlA1
cmlA5
tet(M)
sul3
mef(B)
dfrA1
fosA3
arr-2
sat2_gen
blaOXA-9
blaOXA-10
aac(6')-Ib'
ant(2'')-Ia
mph(B)
cmlA6
AMINOGLYCOSIDE
AMIKACIN/KANAMYCIN
AMIKACIN/QUINOLONE
BETA-LACTAM
BLEOMYCIN
CARBAPENEM
CEPHALOSPORIN
CHLORAMPHENICOL
CHLORAMPHENICOL/FLORFENICOL
FOSFOMYCIN
GENTAMICIN
GENTAMICIN/KANAMYCIN/TOBRAMYCIN
HYGROMYCIN
KANAMYCIN
KANAMYCIN/TOBRAMYCIN
LINCOSAMIDE
LINCOSAMIDE/STREPTOGRAMIN
MACROLIDE
METHICILLIN
PHENICOL/QUINOLONE
QUINOLONE
RIFAMYCIN
STREPTOMYCIN
SULFONAMIDE
SPECTINOMYCIN
STREPTOTHRICIN
STREPTOMYCIN/SPECTINOMYCIN
TRIMETHOPRIM
TETRACYCLINE
VANCOMYCIN
Salmonella enterica
mef(B)
qnrA1
qnrS1
dfrA12
sul3
bleO
cmlA1
blaCARB-2
lnu(F)
ant(2'')-Ia
dfrA14
tet(B)
aadA1
aac(3)-IId
aadA2
aph(6)-Id
aph(3')-Ia
blaTEM-1
tet(M)
tet(G)
sul2
blaTEM-150
aadA5
aph(3'')-Ib
dfrA1
tet(A)
catB3
blaOXA-1
aac(3)-IVa
dfrA7
arr-3
oqxA
mph(A)
floR
oqxB
sul1
aadA12
aac(6')-Ib-cr
aph(4)-Ia
dfrA17
cmlA5
aph(3')-IIa
catA1
blaOXA-10
aph(6)-Ic
ble_Tn5
aac(3)-Id
aadA7
dfrA15
ere(A)
aac(3)-II
arr-269927220
aac(6')-IIc
Staphylococcus aureus
erm(C)
tet(M)
tet(K)
dfrG
blaPC1
vanS-A
vanZ-A
blaZ
blaR1
blaI_of_Z
erm(B)
vanY-A
spw
msr(A)
vanA
ant(6)-Ia
aph(3')-IIIa
vanH-A
blaR1-2
mph(C)
lsa(E)
vanR-A
sat4
mecA
lnu(B)
vanX-A
dfrC
erm(A)
mecI_of_mecA
mecC
mecR1
ant(4')-Ia
dfrK
ant(9)-Ia
mecI_of_mecC
erm(T)
vga(E)
bleO
tet(L)

Acinetobacter baumannii

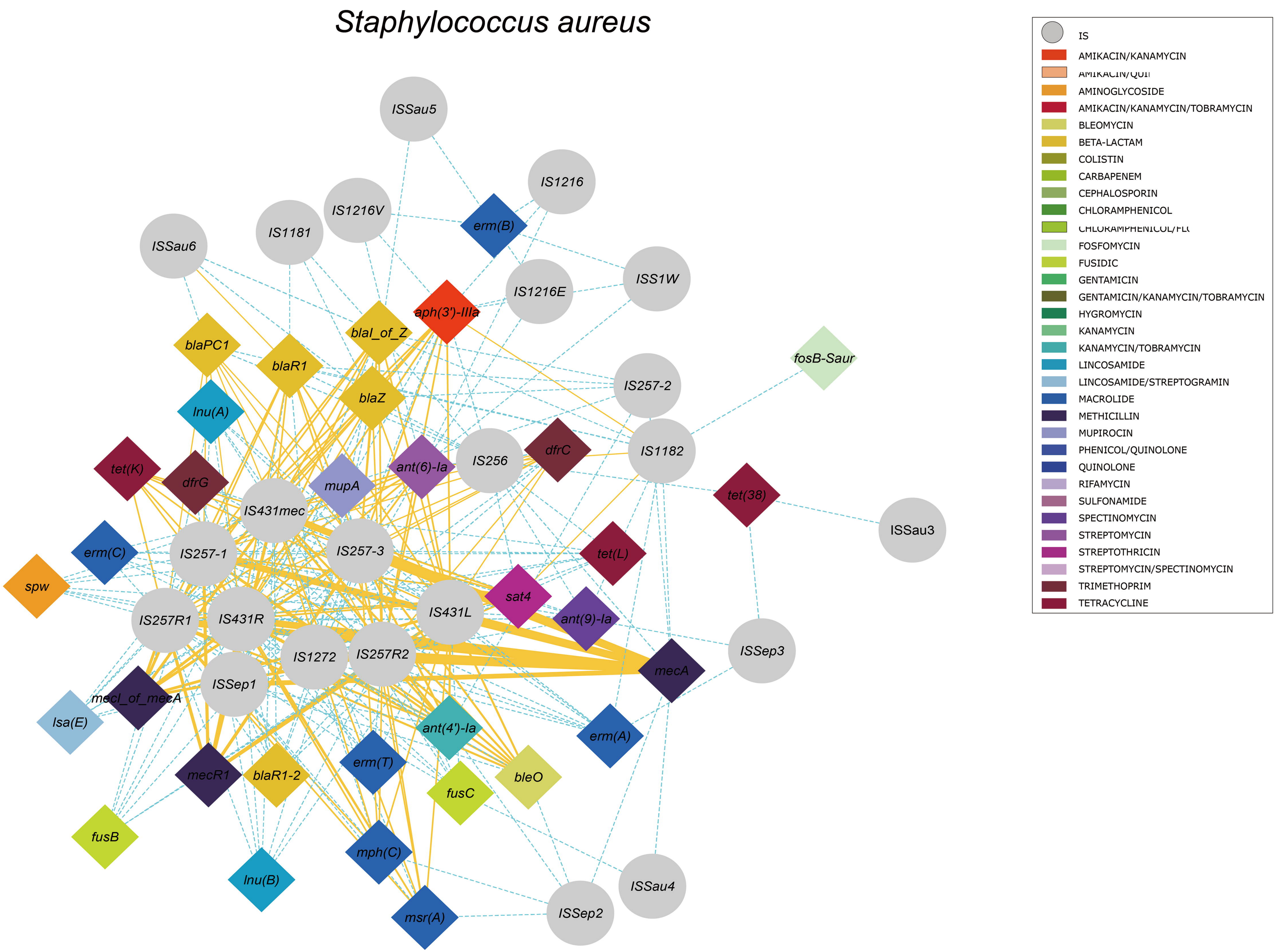

IS
AMIKACIN/KANAMYCIN
AMIKACIN/QUI
AMINOGLYCOSIDE
AMIKACIN/KANAMYCIN/TOBRAMYCIN
BLEOMYCIN
BETA-LACTAM
COLISTIN
CARBAPENEM
CEPHALOSPORIN
CHLORAMPHENICOL
CHLORAMPHENICOL/FL
FOSFOMYCIN
FUSIDIC
GENTAMICIN
GENTAMICIN/KANAMYCIN/TOBRAMYCIN
HYGROMYCIN
KANAMYCIN
KANAMYCIN/TOBRAMYCIN
LINCOSAMIDE
LINCOSAMIDE/STREPTOGRAMIN
MACROLIDE
METHICILLIN
MUPIROCIN
PHENICOL/QUINOLONE
QUINOLONE
RIFAMYCIN
SULFONAMIDE
SPECTINOMYCIN
STREPTOMYCIN
STREPTOTHRICIN
STREPTOMYCIN/SPECTINOMYCIN
TRIMETHOPRIM
TETRACYCLINE
ISKpn27
catB3
mph(A)
IS6100
dfrA17
aadA5
blaKPC-2
Tn3
blaTEM-150
IS1396
IS1S
IS1X4
IS1SD
IS1X2
ISKpn19
aadA2
aacA16
aac(6')-Ib
IS26
blaSHV-12
blaCTX-M-55
blaVEB-1
blaTEM-1
ISSen9
tet(A)
aph(3')-Ia
qnrS1
ISEc28
cmlA6
cmlA5
ISPpu12
aac(3)-I
IS1326
catA1
sul1
sat2_gen
IS4321L
catB8
aac(6')-Ib'
IS1A
IS1B
Tn2
IS1G
ant(2'')-Ia
arr-2
IS4321
IS4321R
armA
blaPER-7
dfrA1
IS15
aadA1
blaTEM-12
IS5075
ISAba43
IS1D
IS10A
catA13
ISAba32
ISVsa3
ISEc29
aac(6')-Ian
IS1X3
IS1R
tet(39)
ISAba24
ISAba29
ISAba52
ISAlw22
sul2
blaCARB-14
ISAba34
ISAlw5
ISAba19
msr(E)
ISAlw4
aph(3')-VIb
ISPa13
ISPa12
IS1007
ISAlw23
ISAba2
IS1006
mph(E)
ISAjo2
aph(3'')-Ib
ISAlw27
ISAba3
ISAba14
aph(3')-VI
tet(B)
aac(3)-IIa
floR
IS1008
aph(6)-Id
blaOXA-58
blaOXA-23
ISAba125
ble-MBL
blaNDM-1
ISOur1
ISPa14
ISAlw25
ISCfr1
ISPsp5
ISAba16
ISAba49
ISVsa5
ISAba25
aac(3)-IId
IS10L
ant(3'')-IIa
ISAlw16
ISAlw34
IS10R
ISAba46
ISAba13
aph(3')-VIa
blaOXA-237
blaADC-152
blaADC-73
blaADC-74
blaOXA-66
blaADC-33
ISAba1
blaADC-30
blaADC-176
blaADC-79
blaOXA-115
blaOXA-235
blaADC-25
blaCTX-M-15
ISEcp1
ISEnca1
ISEc9
IS200F
blaCMY-2
IS200C
IS200
ISAlw15
ISSpu21
blaPER-1
ISAba28
blaCARB-16
ISAba30


Escherichia coli
IS
AMIKACIN/KANAMYCIN
AMIKACIN/QUI
AMINOGLYCOSIDE
AMIKACIN/KANAMYCIN/TOBRAMYCIN
BLEOMYCIN
BETA-LACTAM
COLISTIN
CARBAPENEM
CEPHALOSPORIN
CHLORAMPHENICOL
CHLORAMPHENICOL/FL
FOSFOMYCIN
FUSIDIC
GENTAMICIN
GENTAMICIN/KANAMYCIN/TOBRAMYCIN
HYGROMYCIN
KANAMYCIN
KANAMYCIN/TOBRAMYCIN
LINCOSAMIDE
LINCOSAMIDE/STREPTOGRAMIN
MACROLIDE
METHICILLIN
MUPIROCIN
PHENICOL/QUINOLONE
QUINOLONE
RIFAMYCIN
SULFONAMIDE
SPECTINOMYCIN
STREPTOMYCIN
STREPTOTHRICIN
STREPTOMYCIN/SPECTINOMYCIN
TRIMETHOPRIM
TETRACYCLINE
ble_Tn5
aph(6)-Ic
blaOXA-244
ISApl1
IS50R
ISAeme22
blaEC-18
aph(3')-VI
IS10A
ISKpn21
oqxB
blaNDM-4
blaSHV-2
cmlA6
blaCARB-2
qnrS2
mef(B)
qepA1
blaSHV-1
tet(C)
IS26
oqxB2
oqxA2
tet(D)
arr-2
dfrA16
blaCTX-M-33
catA2
qnrB6
dfrA8
IS621
ISKox3
mcr-1.1
blaOXA-48
aadA12
blaCTX-M-8
qnrB1
ISAba125
bleO
aph(3')-IIa
IS1D
lnu(F)
cat2_gen
blaEC
mph(B)
ISSen9
blaEC-15
tet(M)
blaNDM-5
aadA22
ISEc57
IS3000
blaEC-13
fosA3
blaNDM-7
blaCTX-M-27
blaCTX-M-65
ISKpn11
ISKpn26
ble-MBL
msr(E)
oqxA
ISKpn12
IS5B
IS1SD
ISSbo1
mcr-9.1
IS1X1
IS10L
IS102
mph(E)
erm(B)
blaEC-8
IS200H
ISUnCu1
aac(3)-IVa
IS1S
blaOXA-181
aph(3')-Ia
IS1326
IS1294
ISAba52
ISKpn14
ISAba1
aph(4)-Ia
ISEc28
IS1X4
IS1X2
IS10R
IS1A
ISVsa5
armA
IS903B
blaSHV-12
blaCTX-M-55
IS1B
IS1006
ISEc40
IS5D
IS1R
IS1G
ISEc29
erm(42)
ISEc59
IS1X3
IS1F
ISVsa3
blaTEM-135
MITESen1
aac(3)-IIa
blaNDM-1
aac(3)-IId
dfrA14
cmlA1
Tn3
blaTEM-12
ISEc17
ISCro1
IS4321L
IS679
Tn5393
IS903
ISKpn19
catB3
IS5
dfrA12
qnrS1
aadA2
IS200
lnu(G)
sul3
floR
blaOXA-9
blaCTX-M-14
ISEc58
catA1
blaCMY-42
ant(2'')-Ia
IS200C
Tn2
IS4321R
blaOXA-10
IS186A
ISSba14
aac(3)-VIa
dfrA7
blaCTX-M-32
ISEc12
IS200F
aac(6')-Ib
ISPsp5
blaTEM-150
IS4321
sul1
IS15
aph(3'')-Ib
aadA5
IS1247
Tn5403
rmtB1
ISCfr8
blaKPC-3
blaLAP-2
mph(A)
aph(6)-Id
dfrA17
aadA1
sul2
dfrA1
IS5075
cmlA5
ISSpu7
IS1133
dfrA5
ISKpn7
dfrA15
IS91
IS3411
blaTEM-1
ISCfr1
blaCTX-M-
IS3
dfrA36
blaCMY-2
blaCTX-M-3
tet(B)
blaTEM-235
ISEc37
ISEnca1
IS100kyp
blaOXA-1
IS3F
ISPst2
aac(6')-Ib11
ISEc15
IS186B
tet(A)
ISEcp1
IS2
IS3H
blaCTX-M-1
ere(A)
IS1H
ISKpn6
IS30
IS100X
ISEc9
IS1203E
blaCTX-M-123
ISSen4
IS911
ISEc47
IS100
IS100L
IS1353
ISAs2
blaDHA-1
aac(3)-II
aadA16
ISKpn8
ISEc84
aac(6')-Ib-cr
ISEc63
ISEc8
IS629
ISEc23
blaFOX-5
IS30D
IS1203
ISEc52
IS682
ISEc43
fosA7
IS6100
blaOXA-2
aac(6')-IIc
IS103
arr-269927220
dfrA27
aadA7
arr-3
blaCTX-M-125
IS421
blaCMY-6
qnrB4
IS1222
IS150
ISKpn50
IS4
ISKpn31
ISEc76
ISAlw27
blaKPC-2
ISAs12
ISAba14
ISKpn24
ISKpn27
ISEc22

Salmonella enterica



● IS
🟥 AMIKACIN/KANAMYCIN
AMIKACIN/QUI
AMINOGLYCOSIDE
AMIKACIN/KANAMYCIN/TOBRAMYCIN
BLEOMYCIN
BETA-LACTAM
COLISTIN
CARBAPENEM
CEPHALOSPORIN
CHLORAMPHENICOL
CHLORAMPHENICOL/FL
FOSFOMYCIN
FUSIDIC
GENTAMICIN
GENTAMICIN/KANAMYCIN/TOBRAMYCIN
HYGROMYCIN
KANAMYCIN
KANAMYCIN/TOBRAMYCIN
LINCOSAMIDE
LINCOSAMIDE/STREPTOGRAMIN
MACROLIDE
METHICILLIN
MUPIROCIN
PHENICOL/QUINOLONE
QUINOLONE
RIFAMYCIN
SULFONAMIDE
SPECTINOMYCIN
STREPTOMYCIN
STREPTOTHRICIN
STREPTOMYCIN/SPECTINOMYCIN
TRIMETHOPRIM
TETRACYCLINE
IS30
ISKpn50
ISKpn24
IS30D
ISEc22
blaCMY-132
blaCTX-M-15
blaCTX-M-55
Tn5393
ISVsa5
IS10L
ISApl1
aph(6)-I
blaCMY-2
blaTEM-150
mcr-1.1
ISEnca1
tet(B)
ISEcp1
ISEc9
IS1133
IS10R
armA
dfrA7
fosA3
lnu(G)
blaSHV-1
dfrA15
oqxA
tet(D)
qnrS1
ISPst2
bleO
dfrA19
lnu(F)
ISCfr1
catA2
aph(3'')-Ib
blaCTX-M-65
ISEc28
Tn2
IS1X4
dfrA5
IS26
dfrA17
qnrB2
ISSen9
IS1H
aac(6')-Ib-cr
IS1F
aadA22
IS3411
tet(C)
blaTEM-235
Tn3
ble-MBL
qnrS2
oqxB
sul2
IS629
IS1D
blaTEM-135
erm(B)
IS1X3
ISVsa3
aac(6')-Ib
cmlA5
blaTEM-1
tet(M)
aadA5
IS1203
IS1203E
aac(3)-IId
ISPsp5
IS1294
IS1396
IS903
IS102
sul3
IS1B
IS903B
ISCfr8
blaTEM-12
ant(2'')-Ia
IS1A
IS1SD
IS1X1
mcr-9.1
mph(B)
IS1R
catA1
cmlA1
ISKpn19
dfrA12
ISEc59
aph(3')-Ia
ISKpn21
IS4321R
aac(3)-IVa
IS1S
qnrS13
IS4321L
aph(6)-Ic
ISAba52
ISKpn12
tet(A)
ISSbo1
IS50R
IS1222
IS4321
aph(3')-IIa
IS1X2
dfrA1
IS1326
sul1
IS1G
arr-3
IS5075
ISKpn11
ISAba1
ISAeme22
dfrA14
catB3
IS1006
aph(4)-Ia
ISEc78
floR
aadA1
aadA2
ISEc57
ble_Tn5
blaSCO-1
aac(3)-VIa
mph(A)
aac(3)-IIa
aadA12
aadA7
ISSen4
IS6100
IS1247
sat2_gen
aac(3)-II
aac(3)-Id
ISEc58
blaOXA-1
ere(A)
IS1353
arr-269927220
aac(6')-IIc
tet(G)
blaCARB-2


Staphylococcus aureus
ISSau5
IS1216
IS1216V
erm(B)
IS1181
ISSau6
IS1216E
ISS1W
aph(3')-IIIa
blaI_of_Z
blaPC1
blaR1
blaZ
IS257-2
fosB-Saur
lnu(A)
IS1182
dfrC
IS256
ant(6)-Ia
tet(K)
dfrG
mupA
IS431mec
tet(38)
ISSau3
erm(C)
IS257-1
IS257-3
tet(L)
spw
sat4
IS257R1
IS431R
IS431L
ant(9)-Ia
ISSep3
IS1272
IS257R2
mecA
mecI_of_mecA
ISSep1
lsa(E)
ant(4')-Ia
erm(A)
mecR1
blaR1-2
erm(T)
bleO
fusC
fusB
mph(C)
lnu(B)
ISSau4
msr(A)
ISSep2
IS
AMIKACIN/KANAMYCIN
AMIKACIN/QUI
AMINOGLYCOSIDE
AMIKACIN/KANAMYCIN/TOBRAMYCIN
BLEOMYCIN
BETA-LACTAM
COLISTIN
CARBAPENEM
CEPHALOSPORIN
CHLORAMPHENICOL
CHLORAMPHENICOL/FL
FOSFOMYCIN
FUSIDIC
GENTAMICIN
GENTAMICIN/KANAMYCIN/TOBRAMYCIN
HYGROMYCIN
KANAMYCIN
KANAMYCIN/TOBRAMYCIN
LINCOSAMIDE
LINCOSAMIDE/STREPTOGRAMIN
MACROLIDE
METHICILLIN
MUPIROCIN
PHENICOL/QUINOLONE
QUINOLONE
RIFAMYCIN
SULFONAMIDE
SPECTINOMYCIN
STREPTOMYCIN
STREPTOTHRICIN
STREPTOMYCIN/SPECTINOMYCIN
TRIMETHOPRIM
TETRACYCLINE