**Frequency of the Genes Isolated from Animals**

The most frequent genes in **animal samples** are: **mepA (11.6%)** - Efflux pump associated with antimicrobial resistance. **tet(38) (11.2%)** - Tetracycline resistance gene. **blaI (9.8%), blaZ (9.3%), blaR1 (7.3%)** - β-lactam resistance genes.**mecA (9.3%)** - The key methicillin resistance gene in MRSA. Other resistance genes like **fosB (4.5%) (Fosfomycin resistance), erm(C) (3%) (Macrolide resistance), tet(K) (2.6%) (Tetracycline resistance)** were present at lower frequencies. This table highlights that MRSA in animals harbors a significant number of antibiotic resistance genes, particularly against β-lactams, tetracyclines, and macrolides.

Table 1. Frequency of the genes isolated from the animal

| Gene | Count | Percentage | N (%) |
| --- | --- | --- | --- |
| mepA | 57 | 11.6 | 57 (11.6%) |
| tet(38) | 55 | 11.2 | 55 (11.2%) |
| blaI | 48 | 9.8 | 48 (9.8%) |
| blaZ | 46 | 9.3 | 46 (9.3%) |
| mecA | 46 | 9.3 | 46 (9.3%) |
| blaR1 | 36 | 7.3 | 36 (7.3%) |
| fosB | 22 | 4.5 | 22 (4.5%) |
| tet(M) | 17 | 3.5 | 17 (3.5%) |
| erm(C) | 15 | 3.0 | 15 (3%) |
| aac(6')-Ie/aph(2'')-Ia | 14 | 2.8 | 14 (2.8%) |
| tet(K) | 13 | 2.6 | 13 (2.6%) |
| ant(6)-Ia | 12 | 2.4 | 12 (2.4%) |
| aph(3')-IIIa | 11 | 2.2 | 11 (2.2%) |
| dfrK | 11 | 2.2 | 11 (2.2%) |
| sat4 | 11 | 2.2 | 11 (2.2%) |
| aadD1 | 7 | 1.4 | 7 (1.4%) |
| tet(L) | 6 | 1.2 | 6 (1.2%) |
| dfrS1 | 5 | 1.0 | 5 (1%) |
| msr(A) | 5 | 1.0 | 5 (1%) |
| Other genes | 55 | 11.2 | 55 (11.2%) |

Other genes include genes less than 5 counts in occurrence: fexA, mph(C), ant(9)-Ia, blaPC1, dfrG, erm(A), mecC, mecI, str, vga(A), catA, lsa(E), spd, spw, ant(6)-Ia, blaR1b,blaR1nm, erm(c), fosB=C, lnu(B), mph (C), mupA, parC\_S80Y, tet(M),HMM, tet(M) point, vga(E), vga€.

Figure 1. The distribution of the gene isolated from the animals

**Frequency of the Mutations Isolated from Animals**

The most common mutations found in **animal MRSA isolates**: **murA\_E291D (15%) & murA\_D278E (11.6%)** - These mutations suggest fosfomycin resistance. **glpT\_A100V (14.5%) & glpT\_F3I (11.6%)** - Possibly affecting bacterial metabolism. **gyrA\_S84L (6.9%) & parC\_S80F (6.9%)** - Associated with fluoroquinolone resistance. This table suggests fluoroquinolone resistance and fosfomycin resistance are increasing in animal MRSA isolates.

Table 2. Frequency of the mutations isolated from the animal

| Mutation | Count | Percentage | N (%) |
| --- | --- | --- | --- |
| murA\_E291D | 26 | 15.0 | 26 (15%) |
| glpT\_A100V | 25 | 14.5 | 25 (14.5%) |
| glpT\_F3I | 20 | 11.6 | 20 (11.6%) |
| murA\_D278E | 20 | 11.6 | 20 (11.6%) |
| NA | 13 | 7.5 | 13 (7.5%) |
| gyrA\_S84L | 12 | 6.9 | 12 (6.9%) |
| parC\_S80F | 12 | 6.9 | 12 (6.9%) |
| pbp4\_R200L | 9 | 5.2 | 9 (5.2%) |
| parC\_S80Y | 6 | 3.5 | 6 (3.5%) |
| murA\_G257D | 5 | 2.9 | 5 (2.9%) |
| murA\_T396N | 5 | 2.9 | 5 (2.9%) |
| Other mutations | 20 | 11.6 | 20 (11.6%) |

**Frequency of the Genes Isolated from the Environment**

The most common genes found in **environmental samples**: **mepA (8.2%), mecA (8.1%), tet(38) (8%), blaI (7.7%), blaR1 (7.5%), blaZ (7.2%)**.These genes show a similar trend to those found in **animal isolates**, suggesting **environmental reservoirs play a key role in MRSA transmission**. **fosB (6.8%)** appears at a **higher frequency** compared to **animal samples**, indicating a potential environmental selection pressure for fosfomycin resistance. This table suggests that the environment is a major reservoir for resistance genes and plays a role in spreading MRSA between animals and humans.

Table 3. Frequency of the genes isolated from the environment

| Gene | Count | Percentage | N (%) |
| --- | --- | --- | --- |
| mepA | 87 | 8.2 | 87 (8.2%) |
| mecA | 86 | 8.1 | 86 (8.1%) |
| tet(38) | 85 | 8.0 | 85 (8%) |
| blaI | 82 | 7.7 | 82 (7.7%) |
| blaR1 | 79 | 7.5 | 79 (7.5%) |
| blaZ | 76 | 7.2 | 76 (7.2%) |
| fosB | 72 | 6.8 | 72 (6.8%) |
| aadD1 | 40 | 3.8 | 40 (3.8%) |
| mph(C) | 40 | 3.8 | 40 (3.8%) |
| msr(A) | 40 | 3.8 | 40 (3.8%) |
| ant(9)-Ia | 37 | 3.5 | 37 (3.5%) |
| erm(A) | 36 | 3.4 | 36 (3.4%) |
| mecR1 | 36 | 3.4 | 36 (3.4%) |
| aph(3')-IIIa | 35 | 3.3 | 35 (3.3%) |
| bleO | 35 | 3.3 | 35 (3.3%) |
| mecI | 35 | 3.3 | 35 (3.3%) |
| sat4 | 34 | 3.2 | 34 (3.2%) |
| erm(C) | 16 | 1.5 | 16 (1.5%) |
| tet(K) | 13 | 1.2 | 13 (1.2%) |
| dfrG | 12 | 1.1 | 12 (1.1%) |
| ant(6)-Ia | 10 | 0.9 | 10 (0.9%) |
| tet(M) | 9 | 0.8 | 9 (0.8%) |
| Other genes | 55 | 5.2 | 55 (5.2%) |

Other genes include genes less than 9 counts in occurrence: aac(6')-Ie/aph(2'')-Ia, lnu(B), fosY, lsa(E), spw, fexA, blaPC1, dfrS1, gyrA\_S84L, ant(6)-Ia=PARTIAL, cfr, dfrF, dfrK, lsa (E), mapA, mpc(C), mph(C)l, mph©, mupA, sr(A), str, tet(38) MISTRANSLATION, tet(38) point

Figure 2. The distribution of the gene isolated from the environment

**Table 4: Frequency of the Mutations Isolated from the Environment**

The most frequent mutations in **environmental MRSA isolates**: **gyrA\_S84L (21.6%) & parC\_S80Y (21%)** - Strong indicators of fluoroquinolone resistance. **murA\_G257D (8.9%) & murA\_E291D (3.8%)** - Associated with fosfomycin resistance. Other mutations such as **glpT\_A100V (4.1%)** indicate bacterial adaptations. This suggests that MRSA in the environment is evolving resistance to fluoroquinolones at a high rate.

Table 4. Frequency of the mutations isolated from the environment

| Mutation | Count | Percentage | Display |
| --- | --- | --- | --- |
| gyrA\_S84L | 63 | 21.6 | 63 (21.6%) |
| parC\_S80Y | 61 | 21.0 | 61 (21%) |
| parC\_E84G | 30 | 10.3 | 30 (10.3%) |
| murA\_G257D | 26 | 8.9 | 26 (8.9%) |
| glpT\_A100V | 12 | 4.1 | 12 (4.1%) |
| murA\_E291D | 11 | 3.8 | 11 (3.8%) |
| glpT\_F3I | 9 | 3.1 | 9 (3.1%) |
| murA\_D278E | 9 | 3.1 | 9 (3.1%) |
| gyrA\_S85P | 7 | 2.4 | 7 (2.4%) |
| NA | 7 | 2.4 | 7 (2.4%) |
| gyrA\_E88K | 6 | 2.1 | 6 (2.1%) |
| parC\_S80F | 5 | 1.7 | 5 (1.7%) |
| Other mutations | 45 | 15.5 | 45 (15.5%) |

**Frequency of the Genes Isolated from Humans**

The most common **human MRSA genes**: **mepA (8.6%), mecA (8.3%), tet(38) (8.3%), blaI (7.9%), fosB (7.5%)**. There are higher frequencies of macrolide resistance genes **(mph(C), msr(A), erm(A))** in human samples compared to animals and the environment. This suggests a higher antibiotic selection pressure in humans, possibly due to frequent antibiotic use. This indicates that **human MRSA isolates show a broader spectrum of resistance genes**, reflecting exposure to multiple antibiotic classes.

Table 5. Frequency of the genes isolated from the human

| Gene | Count | Percentage | Display |
| --- | --- | --- | --- |
| mepA | 129 | 8.6 | 129 (8.6%) |
| mecA | 125 | 8.3 | 125 (8.3%) |
| tet(38) | 125 | 8.3 | 125 (8.3%) |
| blaI | 119 | 7.9 | 119 (7.9%) |
| fosB | 112 | 7.5 | 112 (7.5%) |
| blaR1 | 110 | 7.3 | 110 (7.3%) |
| blaZ | 105 | 7.0 | 105 (7%) |
| mph(C) | 72 | 4.8 | 72 (4.8%) |
| msr(A) | 64 | 4.3 | 64 (4.3%) |
| aph(3')-IIIa | 56 | 3.7 | 56 (3.7%) |
| mecI | 51 | 3.4 | 51 (3.4%) |
| ant(9)-Ia | 50 | 3.3 | 50 (3.3%) |
| mecR1 | 50 | 3.3 | 50 (3.3%) |
| erm(A) | 49 | 3.3 | 49 (3.3%) |
| sat4 | 48 | 3.2 | 48 (3.2%) |
| aadD1 | 46 | 3.1 | 46 (3.1%) |
| bleO | 44 | 2.9 | 44 (2.9%) |
| erm(C) | 33 | 2.2 | 33 (2.2%) |
| tet(K) | 11 | 0.7 | 11 (0.7%) |
| aac(6')-Ie/aph(2'')-Ia | 9 | 0.6 | 9 (0.6%) |
| Other genes | 69 | 4.6 | 69 (4.6%) |

Other genes include genes less than 9 counts in occurrence: mupA, tet(M), blaPC1, dfrG, fexA, dfrS1, dfrK, cfr, catA, fosY, tet(38, vga(A), blaR1=HMM, dfrB\_F99Y, dfrF, fosBmecA, gyrA\_S84L mecAmecR, pbp2m, str, tet(38) pont, tet(38)mepA, tet(M) mecA, tet(W)

Figure 3. Frequency of the genes isolated from the human

**Frequency of the Mutations Isolated from Humans**

The most common mutations in human MRSA isolates: **gyrA\_S84L (20.5%) & parC\_S80Y (17.3%)** - Indicate high-level fluoroquinolone resistance. **murA\_G257D (10.2%)** - Shows fosfomycin resistance.Other mutations such as **parC\_E84G (8.5%)** further reinforce quinolone resistance.Human MRSA isolates show the highest fluoroquinolone resistance levels, suggesting strong antibiotic selection pressure in medical settings.

Table 6. Frequency of the mutations isolated from the human

| Mutation | Count | Percentage | Display |
| --- | --- | --- | --- |
| gyrA\_S84L | 84 | 20.5 | 84 (20.5%) |
| parC\_S80Y | 71 | 17.3 | 71 (17.3%) |
| murA\_G257D | 42 | 10.2 | 42 (10.2%) |
| parC\_E84G | 35 | 8.5 | 35 (8.5%) |
| parC\_S80F | 21 | 5.1 | 21 (5.1%) |
| NA | 16 | 3.9 | 16 (3.9%) |
| glpT\_A100V | 13 | 3.2 | 13 (3.2%) |
| murA\_E291D | 13 | 3.2 | 13 (3.2%) |
| gyrA\_E88K | 9 | 2.2 | 9 (2.2%) |
| ileS\_V588F | 8 | 2.0 | 8 (2%) |
| parE\_P585S | 8 | 2.0 | 8 (2%) |
| murA\_T396N | 7 | 1.7 | 7 (1.7%) |
| gyrA\_S85P | 6 | 1.5 | 6 (1.5%) |
| murA\_D278E | 6 | 1.5 | 6 (1.5%) |
| Other mutations | 59 | 14.4 | 59 (14.4%) |

**The Distribution of MRSA Genes in the Environment, Human and Animals Across Selected Locations**

Highest MRSA gene detection in the USA (Baltimore, MD) compared to other locations. Genes like **mecA, blaI, blaR1, blaZ, tet(38), mepA** are common across different countries. Some resistance genes **(ant(9)-Ia, dfrG, aadD1, mecR1, mph(C))** appear at higher frequencies in the USA. This suggests geographical differences in MRSA gene distribution, possibly due to differences in antibiotic use policies and environmental conditions.

Among the samples isolated from humans, the highest prevalence of MRSA genes in the USA **(Baltimore, MD and Torrance, CA)**. Other locations (Brazil, Colombia, Tanzania) show lower MRSA gene frequency. The presence of **mecA, mecI, mecR1, mph(C), fosB, tet(38)** is common across countries. This suggests a global spread of MRSA resistance genes, with the USA showing the highest rates.

Among the samples isolated from animals, the higher resistance gene diversity in France, China, and India. Lower resistance gene detection in Australia, Norway, and Sweden. Common genes across countries: **mecA, blaI, tet(38), mepA, fosB**. This suggests variations in MRSA resistance based on geography, antibiotic usage, and healthcare practices.

Table 7. The distribution of the genes isolated from the environment according to locations

| Complete MRSA genes detected | China | Italy: Bari | Netherlands | Serbia | USA:Baltimore, MD |
| --- | --- | --- | --- | --- | --- |
| blaI | 2 (16.7%) | 1 (9.1%) | 1 (6.7%) | 9 (7.4%) | 68 (7.6%) |
| blaR1 | 2 (16.7%) | 1 (9.1%) | 1 (6.7%) | 9 (7.4%) | 65 (7.3%) |
| blaZ | 2 (16.7%) | 1 (9.1%) | 0 (0%) | 9 (7.4%) | 64 (7.2%) |
| mecA | 2 (16.7%) | 1 (9.1%) | 1 (6.7%) | 10 (8.3%) | 71 (8%) |
| mepA | 2 (16.7%) | 1 (9.1%) | 0 (0%) | 10 (8.3%) | 73 (8.2%) |
| tet(38) | 2 (16.7%) | 1 (9.1%) | 1 (6.7%) | 10 (8.3%) | 70 (7.8%) |
| ant(6)-Ia | 0 (0%) | 1 (9.1%) | 0 (0%) | 8 (6.6%) | 0 (0%) |
| aph(3')-IIIa | 0 (0%) | 1 (9.1%) | 0 (0%) | 2 (1.7%) | 31 (3.5%) |
| erm(C) | 0 (0%) | 1 (9.1%) | 0 (0%) | 3 (2.5%) | 12 (1.3%) |
| sat4 | 0 (0%) | 1 (9.1%) | 0 (0%) | 2 (1.7%) | 30 (3.4%) |
| tet(K) | 0 (0%) | 1 (9.1%) | 1 (6.7%) | 8 (6.6%) | 3 (0.3%) |
| Other Genes | 0 (0%) | 0 (0%) | 7 (46.7%) | 23 (19%) | 24 (2.7%) |
| ant(9)-Ia | 0 (0%) | 0 (0%) | 1 (6.7%) | 0 (0%) | 35 (3.9%) |
| dfrG | 0 (0%) | 0 (0%) | 1 (6.7%) | 6 (5%) | 5 (0.6%) |
| tet(M) | 0 (0%) | 0 (0%) | 1 (6.7%) | 6 (5%) | 2 (0.2%) |
| aadD1 | 0 (0%) | 0 (0%) | 0 (0%) | 6 (5%) | 34 (3.8%) |
| bleO | 0 (0%) | 0 (0%) | 0 (0%) | 0 (0%) | 35 (3.9%) |
| erm(A) | 0 (0%) | 0 (0%) | 0 (0%) | 0 (0%) | 35 (3.9%) |
| fosB | 0 (0%) | 0 (0%) | 0 (0%) | 0 (0%) | 71 (8%) |
| mecI | 0 (0%) | 0 (0%) | 0 (0%) | 0 (0%) | 35 (3.9%) |
| mecR1 | 0 (0%) | 0 (0%) | 0 (0%) | 0 (0%) | 36 (4%) |
| mph(C) | 0 (0%) | 0 (0%) | 0 (0%) | 0 (0%) | 40 (4.5%) |
| msr(A) | 0 (0%) | 0 (0%) | 0 (0%) | 0 (0%) | 40 (4.5%) |

Table 8. The distribution of the genes isolated from humans according to locations

| Complete MRSA genes detected | Brazil: Rio de Janeiro | Colombia: Putumayo | Tanzania | USA: Baltimore, MD | USA: Torrance, CA |
| --- | --- | --- | --- | --- | --- |
| aadD1 | 1 (6.7%) | 2 (5.1%) | 3 (3.4%) | 21 (2%) | 19 (6.1%) |
| ant(9)-Ia | 1 (6.7%) | 2 (5.1%) | 2 (2.3%) | 29 (2.8%) | 16 (5.2%) |
| aph(3')-IIIa | 1 (6.7%) | 2 (5.1%) | 3 (3.4%) | 36 (3.4%) | 14 (4.5%) |
| blaI | 1 (6.7%) | 2 (5.1%) | 6 (6.9%) | 91 (8.6%) | 19 (6.1%) |
| blaR1 | 1 (6.7%) | 2 (5.1%) | 5 (5.7%) | 85 (8.1%) | 17 (5.5%) |
| bleO | 1 (6.7%) | 2 (5.1%) | 1 (1.1%) | 21 (2%) | 19 (6.1%) |
| erm(A) | 1 (6.7%) | 2 (5.1%) | 2 (2.3%) | 29 (2.8%) | 15 (4.8%) |
| fosB | 1 (6.7%) | 2 (5.1%) | 5 (5.7%) | 86 (8.2%) | 18 (5.8%) |
| mepA | 1 (6.7%) | 2 (5.1%) | 7 (8%) | 100 (9.5%) | 19 (6.1%) |
| mph(C) | 1 (6.7%) | 2 (5.1%) | 3 (3.4%) | 51 (4.8%) | 15 (4.8%) |
| msr(A) | 1 (6.7%) | 2 (5.1%) | 3 (3.4%) | 46 (4.4%) | 12 (3.9%) |
| sat4 | 1 (6.7%) | 2 (5.1%) | 2 (2.3%) | 28 (2.7%) | 15 (4.8%) |
| tet(38) | 1 (6.7%) | 2 (5.1%) | 7 (8%) | 96 (9.1%) | 19 (6.1%) |
| aac(6')-Ie/aph(2'')-Ia | 0 (0%) | 2 (5.1%) | 7 (8%) | 0 (0%) | 0 (0%) |
| blaZ | 0 (0%) | 2 (5.1%) | 5 (5.7%) | 79 (7.5%) | 19 (6.1%) |
| erm(C) | 0 (0%) | 1 (2.6%) | 2 (2.3%) | 24 (2.3%) | 6 (1.9%) |
| mecA | 0 (0%) | 2 (5.1%) | 6 (6.9%) | 98 (9.3%) | 19 (6.1%) |
| mecI | 0 (0%) | 2 (5.1%) | 3 (3.4%) | 29 (2.8%) | 17 (5.5%) |
| mecR1 | 0 (0%) | 2 (5.1%) | 2 (2.3%) | 29 (2.8%) | 17 (5.5%) |
| tet(K) | 0 (0%) | 0 (0%) | 0 (0%) | 10 (0.9%) | 1 (0.3%) |
| Other Genes | 2 (13.3%) | 2 (5.1%) | 11 (12.6%) | 47 (4.5%) | 7 (2.3%) |

Table 9. The distribution of the genes isolated from humans according to locations

| MRSA gene | Australia: Melbourne | Canada | China | China:Shaanxi | France | Germany | India: Assam | India: Veraval, Gujarat | Norway | Sweden | Thailand: Kanchanaburi |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Other Genes | 3 (50%) | 2 (20%) | 7 (28%) | 5 (29.4%) | 15 (10.6%) | 15 (28.8%) | 0 (0%) | 0 (0%) | 0 (0%) | 7 (6.1%) | 3 (27.3%) |
| fosB | 1 (16.7%) | 1 (10%) | 1 (4%) | 1 (5.9%) | 0 (0%) | 4 (7.7%) | 1 (14.3%) | 1 (33.3%) | 0 (0%) | 12 (10.5%) | 0 (0%) |
| mepA | 1 (16.7%) | 1 (10%) | 2 (8%) | 1 (5.9%) | 16 (11.3%) | 8 (15.4%) | 0 (0%) | 1 (33.3%) | 10 (9.3%) | 16 (14%) | 1 (9.1%) |
| tet(38) | 1 (16.7%) | 1 (10%) | 2 (8%) | 1 (5.9%) | 16 (11.3%) | 7 (13.5%) | 1 (14.3%) | 1 (33.3%) | 9 (8.3%) | 15 (13.2%) | 1 (9.1%) |
| aac(6')-Ie/aph(2'')-Ia | 0 (0%) | 1 (10%) | 1 (4%) | 1 (5.9%) | 10 (7.1%) | 0 (0%) | 0 (0%) | 0 (0%) | 0 (0%) | 0 (0%) | 1 (9.1%) |
| blaI | 0 (0%) | 1 (10%) | 2 (8%) | 1 (5.9%) | 16 (11.3%) | 2 (3.8%) | 1 (14.3%) | 0 (0%) | 10 (9.3%) | 14 (12.3%) | 1 (9.1%) |
| dfrS1 | 0 (0%) | 1 (10%) | 0 (0%) | 0 (0%) | 4 (2.8%) | 0 (0%) | 0 (0%) | 0 (0%) | 0 (0%) | 0 (0%) | 0 (0%) |
| mecA | 0 (0%) | 1 (10%) | 2 (8%) | 1 (5.9%) | 16 (11.3%) | 0 (0%) | 1 (14.3%) | 0 (0%) | 10 (9.3%) | 14 (12.3%) | 1 (9.1%) |
| tet(M) | 0 (0%) | 1 (10%) | 0 (0%) | 0 (0%) | 14 (9.9%) | 1 (1.9%) | 0 (0%) | 0 (0%) | 0 (0%) | 0 (0%) | 1 (9.1%) |
| aadD1 | 0 (0%) | 0 (0%) | 1 (4%) | 1 (5.9%) | 1 (0.7%) | 4 (7.7%) | 0 (0%) | 0 (0%) | 0 (0%) | 0 (0%) | 0 (0%) |
| blaR1 | 0 (0%) | 0 (0%) | 3 (12%) | 1 (5.9%) | 4 (2.8%) | 2 (3.8%) | 1 (14.3%) | 0 (0%) | 10 (9.3%) | 14 (12.3%) | 1 (9.1%) |
| blaZ | 0 (0%) | 0 (0%) | 2 (8%) | 1 (5.9%) | 15 (10.6%) | 0 (0%) | 1 (14.3%) | 0 (0%) | 10 (9.3%) | 16 (14%) | 1 (9.1%) |
| tet(K) | 0 (0%) | 0 (0%) | 1 (4%) | 0 (0%) | 1 (0.7%) | 0 (0%) | 0 (0%) | 0 (0%) | 9 (8.3%) | 2 (1.8%) | 0 (0%) |
| tet(L) | 0 (0%) | 0 (0%) | 1 (4%) | 1 (5.9%) | 0 (0%) | 4 (7.7%) | 0 (0%) | 0 (0%) | 0 (0%) | 0 (0%) | 0 (0%) |
| ant(6)-Ia | 0 (0%) | 0 (0%) | 0 (0%) | 1 (5.9%) | 0 (0%) | 0 (0%) | 0 (0%) | 0 (0%) | 10 (9.3%) | 1 (0.9%) | 0 (0%) |
| erm(C) | 0 (0%) | 0 (0%) | 0 (0%) | 1 (5.9%) | 1 (0.7%) | 1 (1.9%) | 1 (14.3%) | 0 (0%) | 10 (9.3%) | 1 (0.9%) | 0 (0%) |
| dfrK | 0 (0%) | 0 (0%) | 0 (0%) | 0 (0%) | 11 (7.8%) | 0 (0%) | 0 (0%) | 0 (0%) | 0 (0%) | 0 (0%) | 0 (0%) |
| msr(A) | 0 (0%) | 0 (0%) | 0 (0%) | 0 (0%) | 1 (0.7%) | 4 (7.7%) | 0 (0%) | 0 (0%) | 0 (0%) | 0 (0%) | 0 (0%) |
| aph(3')-IIIa | 0 (0%) | 0 (0%) | 0 (0%) | 0 (0%) | 0 (0%) | 0 (0%) | 0 (0%) | 0 (0%) | 10 (9.3%) | 1 (0.9%) | 0 (0%) |
| sat4 | 0 (0%) | 0 (0%) | 0 (0%) | 0 (0%) | 0 (0%) | 0 (0%) | 0 (0%) | 0 (0%) | 10 (9.3%) | 1 (0.9%) | 0 (0%) |