Supplementary Table 1. Tobramycin MICs (μg/mL) for evolved populations in the presence or absence of increasing inhibitory concentrations of tobramycin in rich laboratory medium (MH), urine or SCFM.

| Environment          | Replicate | 5 days | 10 days | 15 days | 20 days | 25 days | 30 days |
|----------------------|-----------|--------|---------|---------|---------|---------|---------|
|                      |           | 1      | 6       | 6       | 12      | 16      | 24      | 24      |
| MH                   |           | 2      | 4       | 4       | 8       | 8       | 24      | 24      |
|                      |           | 3      | 4       | 4       | 6       | 12      | 16      | 32      |
|                      |           | 4      | 4       | 6       | 12      | 16      | 24      | 32      |
| Tobramycin           |           | 1      | 4       | 6       | 6       | 24      | 24      | 64      |
|                      |           | 2      | 8       | 8       | 8       | 24      | 32      | 64      |
|                      |           | 3      | 4       | 8       | 8       | 24      | 32      | 64      |
|                      |           | 4      | 4       | 6       | 6       | 32      | 32      | 64      |
| Urine                |           | 1      | 3       | 12      | 12      | 12      | 32      | 64      |
| Tobramycin           |           | 2      | 4       | 8       | 12      | 12      | 48      | 48      |
|                      |           | 3      | 3       | 8       | 6       | 6       | 24      | 48      |
|                      |           | 4      | 4       | 8       | 8       | 8       | 12      | 64      |
| SCFM                 |           | 1      | 1       | 1       | 1.5     | 1       | 1       | 1       |
| Tobramycin           |           | 2      | 1       | 1       | 1.5     | 1       | 1       | 1.5     |
|                      |           | 3      | 1       | 1.5     | 1.5     | 1.5     | 1       | 1.5     |
|                      |           | 4      | 1.5     | 1       | 1.5     | 1.5     | 1       | 1.5     |
| MH without           |           | 1      | 1.5     | 1.5     | 1       | 1.5     | 1       | 2       |
| antibiotic           |           | 2      | 1.5     | 1.5     | 1       | 1.5     | 0.75    | 1.5     |
|                      |           | 3      | 1       | 1.5     | 1       | 1       | 1.5     | 2       |
| Urine without        |           | 1      | 1.5     | 1.5     | 1       | 1.5     | 1       | 2       |
| antibiotic           |           | 2      | 1.5     | 1.5     | 1       | 1.5     | 0.75    | 1.5     |
|                      |           | 3      | 1       | 1.5     | 1       | 1       | 1.5     | 2       |
| SCFM without antibiotic | 1   | 0.75 | 0.75 | 1   | 0.75 | 0.75 | 1  |
|-------------------------|-----|------|------|-----|------|------|----|
|                         | 2   | 0.75 | 0.75 | 1   | 0.75 | 0.75 | 1  |
|                         | 3   | 0.75 | 1    | 1   | 0.75 | 0.75 | 1  |
|                         | 4   | 0.75 | 1    | 1   | 0.75 | 1    | 1.5|
**Supplementary Table 2. Ceftazidime MICs (μg/mL) for evolved populations in the presence or absence of increasing inhibitory concentrations of ceftazidime alone or in combination with 4 μg/mL of avibactam in rich laboratory medium (LB), urine or SCFM.**

| Environment | Replicate | 5 days | 10 days | 15 days | 20 days | 25 days | 30 days |
|-------------|-----------|--------|---------|---------|---------|---------|---------|
| LB          |           |        |         |         |         |         |         |
| Ceftazidime | 1         | 16     | 48      | 96      | ≥256    | ≥256    | ≥256    |
|             | 2         | 16     | 48      | 64      | ≥256    | ≥256    | ≥256    |
|             | 3         | 16     | 64      | 64      | ≥256    | ≥256    | -       |
|             | 4         | 12     | 32      | 64      | ≥256    | ≥256    | ≥256    |
| Urine       |           |        |         |         |         |         |         |
| Ceftazidime | 1         | 3      | 6       | 4       | 6       | 32      | 32      |
|             | 2         | 2      | 3       | 6       | 12      | 16      | 48      |
|             | 3         | 3      | 3       | 16      | 8       | 64      | 96      |
|             | 4         | 2      | 3       | 3       | 8       | 96      | 96      |
| SCFM        |           |        |         |         |         |         |         |
| Ceftazidime | 1         | 1.5    | 2       | 6       | 24      | 96      | ≥256    |
|             | 2         | 1.5    | 2       | 12      | 32      | 64      | 64      |
|             | 3         | 1.5    | 2       | 8       | 32      | 96      | ≥256    |
|             | 4         | 1.5    | 2       | 8       | 32      | 128     | ≥256    |
| LB          |           |        |         |         |         |         |         |
| Ceftazidime-Avibactam | 1 | 16 | 48 | 48 | ≥256 | ≥256 | ≥256 |
|             | 2         | 12     | 32      | 48      | ≥256    | -       | -       |
|             | 3         | 12     | 32      | 64      | ≥256    | ≥256    | -       |
|             | 4         | 16     | 48      | 64      | ≥256    | -       | -       |
| Urine       |           |        |         |         |         |         |         |
| Avibactam   | 1         | 2      | 3       | 12      | 12      | 32      | 32      |
|             | 2         | 2      | 4       | 6       | 12      | 12      | 64      |
|                  | Urine Ceftazidime-Avibactam | SCFM Ceftazidime-Avibactam | LB without antibiotic | Urine without antibiotic | SCFM without antibiotic |
|------------------|-----------------------------|----------------------------|-----------------------|--------------------------|--------------------------|
|                  | 3  2  4  3  3  32  32       | 1  6  6  24  48  192  ≥256 | 2  6  8  24  64  192  ≥256 | 3  6  8  16  48  128  ≥256 | 4  6  24  96  192  ≥256  ≥256 |
|                  | 4  1.5  4  8  8  12  64     | 1  0.75  0.75  0.75  0.75  0.75  1 | 2  1  0.75  0.75  0.75  0.75  1 | 3  1  1  0.75  0.75  0.75  0.75  0.75 | 4  1  1  0.75  0.75  0.75  0.75  0.75 |
|                  |                             |                            |                       |                          |                          |
|                  |                             | 1  1  1.5  0.75  1.5  1.5  2 | 2  1.5  1.5  1  1.5  1  2 | 3  1  1.5  1  1.5  1.5  2 | 4  1  1  0.75  1  1.5  2 |
|                  |                             |                            |                       |                          |                          |
|                  |                             | 1  1  1  0.75  1  1  1 | 2  0.75  0.75  0.75  1  1  1 | 3  0.75  0.75  0.75  1  1  1 | 4  0.75  0.75  0.75  1.5  1.5  1.5 |

1 - Populations unable to grow after an increase in the antibiotic concentration.
Supplementary Table 3. MICs (µg/mL) of antibiotics from different structural families for final populations submitted to ALE in the presence or absence of tobramycin, ceftazidime or ceftazidime-avibactam in rich laboratory medium (MH or LB, as indicated), urine or SCFM.

| Replicate | TGC | TET | CAZ | ATM | IPM | CIP | NOR | TOB | AK | CHL | ERY | FOF |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|----|-----|-----|-----|
| PA14      | 4   | 24  | 0.75| 2   | 1   | 0.064| 0.25| 0.75| 2  | 32  | 32  | 48  |
| MH Tobramycin |     |     |     |     |     |     |     |     |    |     |     |     |
| 1         | 64  | 48  | 1.5 | 3   | 0.75| 0.5 | 0.25| 32  | 256| 24  | 256 | 1   |
| 2         | 24  | 32  | 1.5 | 4   | 1   | 0.5 | 0.25| 24  | 192| 32  | 64  | 1   |
| 3         | 12  | 24  | 1.5 | 4   | 0.75| 0.19| 0.25| 8   | 128| 24  | 32  | 1   |
| 4         | 32  | 24  | 1.5 | 3   | 1.5 | 0.5 | 0.25| 32  | 256| 24  | 256 | 1.5 |
| Urine Tobramycin |     |     |     |     |     |     |     |     |    |     |     |     |
| 1         | 24  | 16  | 1.5 | 2   | 0.25| 0.25| 1   | 64  | ≥256| 32 | 96  | 32  |
| 2         | 24  | 24  | 2   | 2   | 0.19| 0.25| 1.5 | 64  | ≥256| 32 | ≥256| 96  |
| 3         | 32  | 16  | 2   | 3   | 0.5 | 0.25| 1.5 | 64  | ≥256| 32 | 128 | 32  |
| 4         | 24  | 24  | 1.5 | 2   | 0.25| 0.25| 1.5 | 64  | ≥256| 32 | ≥256| 32  |
| SCFM Tobramycin |     |     |     |     |     |     |     |     |    |     |     |     |

|          | TGC | TET | CAZ | ATM | IPM | CIP | NOR | TOB | AK | CHL | ERY | FOF |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|----|-----|-----|-----|
|            |     |     |     |     |     |     |     |     |    |     |     |     |
|   | 16 | 16 | 1.5 | 2   | 0.75 | 0.38 | 1.5 | 64 | ≥256 | 32 | ≥256 | 32 |
|---|----|----|-----|-----|------|------|-----|----|------|----|------|----|
| 2 | 24 | 16 | 1.5 | 2   | 0.75 | 0.25 | 1.5 | 48 | ≥256 | 32 | ≥256 | 32 |
| 3 | 24 | 16 | 1.5 | 2   | 0.75 | 0.38 | 1.5 | 48 | ≥256 | 32 | ≥256 | 32 |
| 4 | 16 | 16 | 1.5 | 2   | 0.75 | 0.19 | 1.5 | 64 | ≥256 | 32 | ≥256 | 32 |

**LB Ceftazidime**

|   | 2  | 32 | ≥256 | ≥256 | 8   | 0.19 | 1.5 | 1  | 1   | ≥256 | ≥256 | 4  |
|---|----|----|------|------|-----|------|-----|----|-----|------|------|----|
| 2 | 1.5| 24 | ≥256 | ≥256 | 4   | 0.19 | 1  | 1  | 0.5 | ≥256 | ≥256 | 1.5|
| 3 | 2  | 16 | ≥256 | ≥256 | 2   | 0.19 | 1  | 1  | 0.75| ≥256 | ≥256 | 4  |
| 4 | 2  | 16 | ≥256 | ≥256 | 3   | 0.19 | 1  | 1  | 0.5 | ≥256 | ≥256 | 2  |

**Urine Ceftazidime**

|   | 16 | 12 | 32  | 24  | 2   | 0.064| 0.25| 2  | 4   | 48  | 96  | 16 |
|---|----|----|-----|-----|-----|------|------|----|-----|-----|-----|----|
| 2 | 16 | 16 | 48  | 32  | 2   | 0.094| 0.38| 4  | 48  | 48  | 128 | 8  |
| 3 | 8  | 12 | 96  | 96  | 1   | 0.032| 0.19| 1  | 2   | 32  | 32  | 16 |
| 4 | 12 | 12 | 96  | 64  | 1.5 | 0.032| 0.125| 1 | 2   | 32  | 32  | 24 |

**SCFM Ceftazidime**

|   | 8  | 16 | ≥256| 16  | 1.5 | 0.064| 0.38| 1.5| 4   | 96  | ≥256| 24 |
|---|----|----|-----|-----|-----|------|------|----|-----|-----|------|----|
|   | LB Ceftazidime-Avibactam |   |   |   |   |   |   |   |   |   |   |   |   |   |
|---|--------------------------|---|---|---|---|---|---|---|---|---|---|---|---|---|
|   |                          |   |   |   |   |   |   |   |   |   |   |   |   |   |
| 2 | 6                        | 12| 64| 32| 4 | 0.047| 0.19| 1.5| 4 | ≥256| ≥256| 6 |   |   |
| 3 | 6                        | 16| ≥256| ≥256| 3 | 0.064| 0.38| 1.5| 4 | 96  | ≥256| 16|   |   |
| 4 | 8                        | 12| ≥256| ≥256| 3 | 0.064| 0.38| 1.5| 4 | 96  | ≥256| 16|   |   |
|   | LB Ceftazidime-Avibactam |   |   |   |   |   |   |   |   |   |   |   |   |   |
| 1 | 0.75                     | 4 | ≥256| ≥256| 32| 0.094| 0.25| 1  | 0.75| ≥256| ≥256| 3 |   |   |
| 2 | 0.5                      | 4 | ≥256| ≥256| 3 | 0.094| 0.25| 1  | 1   | ≥256| ≥256| 4 |   |   |
| 3 | 0.38                     | 4 | ≥256| 96  | 32| 0.094| 0.25| 1  | 2   | ≥256| ≥256| 6 |   |   |
| 4 | 0.75                     | 8 | ≥256| ≥256| 4 | 0.094| 0.75| 1  | 0.75| ≥256| ≥256| 4 |   |   |
|   | Urine Ceftazidime-Avibactam |   |   |   |   |   |   |   |   |   |   |   |   |   |
| 1 | 24                       | 16| 32 | 48 | 1.5| 0.38 | 2   | 0.75| 1   | ≥256| 32  | 12|   |   |
| 2 | 16                       | 24| 64 | 48 | 2  | 0.19 | 1   | 0.75| 1.5 | ≥256| 48  | 12|   |   |
| 3 | 16                       | 16| 32 | 24 | 2  | 0.094| 0.38| 2   | 8   | 32  | 48  | 12|   |   |
| 4 | 24                       | 16| 64 | 48 | 2  | 0.064| 0.38| 2   | 8   | 48  | 64  | 3 |   |   |
|   | SCFM Ceftazidime-Avibactam |   |   |   |   |   |   |   |   |   |   |   |   |   |
|   |                          |   |   |   |   |   |   |   |   |   |   |   |   |   |
|   | 16 | 16 | ≥256 | ≥256 | 3  | 0.064 | 0.38 | 3  | 6  | ≥256 | ≥256 | 3  |
|---|----|----|------|------|----|-------|------|----|----|------|------|----|
| 1 | 16 | 16 | ≥256 | ≥256 | 1.5| 0.094 | 0.5  | 3  | 8  | ≥256 | ≥256 | 1.5|
| 2 | 16 | 16 | ≥256 | ≥256 | 4  | 0.094 | 0.38 | 4  | 8  | ≥256 | ≥256 | 2  |
| 3 | 12 | 6  | 128  | 8    | 0.064 | 0.38 | 1    | 3  | ≥256 | ≥256 | 3  |

| MH |
|----|
| 1  | 2  | 12  | 1.5  | 2   | 1   | 0.094 | 0.25 | 1  | 4  | 24  | 32  | 32 |
| 2  | 2  | 8   | 1    | 2   | 1   | 0.19  | 0.25 | 1  | 2  | 16  | 32  | 32 |
| 3  | 1.5| 12  | 1    | 2   | 1   | 0.094 | 0.25 | 1  | 3  | 32  | 32  | 32 |
| 4  | 2  | 12  | 1.5  | 2   | 1   | 0.125 | 0.25 | 0.75 | 3 | 16  | 32  | 32 |

| LB |
|----|
| 1  | 3  | 12  | 1    | 1.5 | 0.75 | 0.094 | 0.25 | 1  | 1.5| 24  | 32  | 24 |
| 2  | 3  | 12  | 1    | 1.5 | 0.5  | 0.094 | 0.25 | 1  | 1.5| 24  | 32  | 24 |
| 3  | 3  | 12  | 1    | 1   | 0.75 | 0.094 | 0.25 | 1  | 1.5| 24  | 32  | 16 |
| 4  | 3  | 16  | 1    | 1   | 0.75 | 0.094 | 0.38 | 1  | 1.5| 24  | 32  | 12 |

| Urine |
|-------|
| 1  | 16 | 24  | 2    | 4   | 1   | 0.094 | 0.38 | 2  | 6  | 32  | 32  | 48 |
|   |   |   |   |   |   |   |   |   |   |
|---|---|---|---|---|---|---|---|---|---|
| 2 | 16 | 24 | 2 | 3 | 1.5 | 0.094 | 0.38 | 1.5 | 6 |
| 3 | 16 | 24 | 2 | 3 | 0.75 | 0.094 | 0.38 | 2 | 6 |
| 4 | 16 | 24 | 2 | 3 | 1 | 0.094 | 0.38 | 2 | 6 |

| SCFM |
|---|---|---|---|---|---|---|---|---|---|
| 1 | 3 | 12 | 1 | 3 | 1 | 0.047 | 0.19 | 0.75 | 2 |
| 2 | 4 | 12 | 1 | 3 | 1 | 0.064 | 0.38 | 1 | 3 |
| 3 | 6 | 16 | 1 | 2 | 1 | 0.047 | 0.19 | 1 | 2 |
| 4 | 12 | 12 | 1.5 | 4 | 1 | 0.064 | 0.25 | 1.5 | 3 |

TGC, tigecycline; TET, tetracycline; CAZ, ceftazidime; ATM, aztreonam; IPM, imipenem; CIP, ciprofloxacin; NOR, norfloxacin; TOB, tobramycin; AMK, amikacin; CHL, chloramphenicol; ERY, erythromycin; FOF, fosfomycin.
Supplementary Table 4. Newly genetic events acquired after 30 days of ALE in SCFM, urine or rich laboratory medium in the presence of tobramycin, ceftazidime or ceftazidime-avibactam.

| Treatment | Replicate | Gene annotation         | Gene | Genetic event | Aminoacid change |
|-----------|-----------|-------------------------|------|---------------|------------------|
| LB        | 1         | DNA-directed RNA polymerase subunit β | *rpoB* | 1562G>A       | Gly521Asp        |
|           |           | Transcriptional regulator MvfR | *myfR* | 62T>C         | Ile21Thr         |
|           | 2         | Transcriptional regulator MvfR | *myfR* | 527A>C        | His176Pro        |
|           |           | Transcriptional regulator   | *psdR* | 58A>C         | Thr20Pro         |
|           |           | Elongation factor G         | *fusA* | 1082G>C       | Gly361Ala        |
|           |           | Malic enzyme               | *maeB* | 407T>C        | Asp136Gly        |
| LB        | 3         | Transcriptional regulator MvfR | *myfR* | 73G>A         | Ala25Thr         |
|           |           | Transcriptional regulator MvfR | *myfR* | 727G>T        | Glu243*          |
|           | 4         | Transcriptional regulator MvfR | *myfR* | 94C>T         | His32Tyr         |
| Transcriptional regulator MvfR | myfR | 133G>A | Asp45Asn |
|--------------------------------|------|--------|----------|
| Elongation factor G | fusA | 1082G>C | Gly361Ala |
| 1 | LuxR family transcriptional regulator | lasR | 667_668delGA | Ser223fs |
| 2 | LuxR family transcriptional regulator | lasR | 667_668delGA | Ser223fs |
| MH | DNA-directed RNA polymerase subunit β | rpoB | 1562G>A | Gly521Asp |
| 3 | LuxR family transcriptional regulator | lasR | 667_668delGA | Ser223fs |
| 4 | LuxR family transcriptional regulator | lasR | 667_668delGA | Ser223fs |
| 1 | DNA-directed RNA polymerase subunit alpha | rpoA | 867G>T | Leu289Phe |
| 2 | LuxR family transcriptional regulator | lasR | 349delG | Pro117fs |
| SCFM | DNA-directed RNA polymerase subunit alpha | rpoA | 867G>T | Leu289Phe |
| 3 | LuxR family transcriptional regulator | lasR | 680C>T | Ala227Val |
| 4 | Helix-turn-helix domain-containing protein | pcaR | 499A>C | Met167Leu |
| Genes/Termini | Gene | Mutation | Effect |
|---------------|------|----------|--------|
| Formylglycine-generating enzyme family protein | pvdO | 794A>G | Asn265Ser |
| LuxR family transcriptional regulator | lasR | 349delG | Pro117fs |
| Transcriptional regulator FleQ | fleQ | 617T>C | Ile206Thr |
| UDP-N-acetyl-D-mannosamine dehydrogenase | orfH | 1186G>T | Asp396Tyr |
| Transcriptional regulator FleQ | fleQ | 779G>T | Arg260Leu |
| Transcriptional regulator FleQ | fleQ | 1092A>T | Glu364Asp |
| Transcriptional regulator FleQ | fleQ | 809T>G | Val270Gly |
| LuxR family transcriptional regulator | lasR | 323_336delCCGTCCTGGTGTATinsACAGCCAGGACTAC | AlaGlyLeuVal108AAspSerGlnAsp |
| Transcriptional regulator FleQ | fleQ | 905A>G | Asp302Gly |
| TOB MH | orfN | 148delG | Val50fs |
| Protein Name                                      | Gene | Mutation       | Effect          |
|--------------------------------------------------|------|----------------|----------------|
| Two-component regulator system signal sensor kinase PmrB | pmrB | 772C>A         | Leu28Met       |
| Elongation factor G                               | fusA | 2011A>G        | Thr671Ala      |
| Glycosyltransferase family 4 protein              | orfN | 148delG        | Val50fs        |
| Two-component regulator system signal sensor kinase PmrB | pmrB | 22T>G          | Ser8Ala        |
| Elongation factor G                               | fusA | 1783G>C        | Ala595Pro      |
| Transcriptional regulator FleQ                    | fleQ | 721T>G         | Thr241Pro      |
| Phosphoenolpyruvate--protein phosphotransferase   | ptsP | 2029G>T        | Asp720fs       |
| Glycosyltransferase family 4 protein              | orfN | 148delG        | Val50fs        |
| Two-component regulator system signal sensor kinase PmrB | pmrB | 853G>C         | Val285Leu      |
| Elongation factor G                               | fusA | 1634G>A        | Gly545Asp      |
| Protein/Function                              | Gene | Mutation          | Amino Acid Change |
|----------------------------------------------|------|-------------------|-------------------|
| Transcriptional regulator FleQ               | fleQ | 2156delG          | Glu677fs          |
| Glycosyltransferase family 4 protein         | orfN | 148dupG           | Val50fs           |
| Two-component regulator system signal sensor kinase | pmrB | 110T>C            | Leu37Pro          |
| Elongation factor G                          | fusA | 2038C>T           | Arg680Cys         |
| Elongation factor G                          | fusA | 2011A>G           | Thr671Ala         |
| UDP-N-acetyl-D-mannosamine dehydrogenase     | orfH | 792delG           | His265fs          |
| Hypothetical protein                         | PA14_44650 | 32_33insC  | Val12fs           |
| TOB SCFM                                     | ispE | 724G>A            | Gly242Arg         |
| Elongation factor G                          | fusA | 2011A>G           | Thr671Ala         |
| 1-deoxy-D-xylulose-5-phosphate synthase      | dcs  | 1284_1286delGGTinsCGG | Val429Gly         |
| 1-deoxy-D-xylulose-5-phosphate reductoisomerase | dxr | 1019C>T           | Ala340Val         |
| Protein Name                                                                 | Gene | Mutation   | Change     |
|------------------------------------------------------------------------------|------|------------|------------|
| UDP-N-acetyl-D-mannosamine dehydrogenase                                      | orfH | 628delA    | Met210fs   |
| Phosphoenolpyruvate--protein phosphotransferase                              | ptsP | 520C>T     | Gln174*    |
| Elongation factor G                                                          | fusA | 2033A>T    | Gln678Leu  |
| UDP-N-acetylglucosamine 2-epimerase                                          | orfK | 646C>T     | Arg216Cys  |
| Multidrug efflux RND transporter permease subunit                            | mexY | 2723A>T    | His908Leu  |
| Multidrug efflux RND transporter permease subunit                            | mexY | 2729T>C     | Val910Ala  |
| Phosphoenolpyruvate--protein phosphotransferase                              | ptsP | 1135dupG   | Ala379fs   |
| Elongation factor G                                                          | fusA | 2038C>T    | Arg680Cys  |
| UDP-N-acetyl-D-mannosamine dehydrogenase                                      | orfH | 286C>T     | Arg96*     |
| UDP-N-acetyl-D-mannosamine dehydrogenase                                      | orfH | 792delG    | His265fs   |
| TOB Urine                                                                    |      |            |            |
| Elongation factor G                                                          | fusA | 2011A>G    | Thr671Ala  |
| Gene Name                                           | Gene Symbol | Mutation | Protein Change |
|----------------------------------------------------|-------------|----------|----------------|
| UDP-N-acetylglucosamine 2-epimerase                | orfK        | 355G>A   | Glu119Lys      |
| Sigma-54-dependent Fis family transcriptional regulator | pilR        | 301T>C   | Phe101Leu      |
| Elongation factor G                                | fusA        | 2011A>G  | Thr671Ala      |
| UDP-N-acetylglucosamine 2-epimerase                | orfK        | 355G>A   | Glu119Lys      |
| NADH-quinone oxidoreductase subunit C/D            | nuoD        | 183_184insC | Lys63fs       |
| Elongation factor G                                | fusA        | 1366A>G  | Thr456Ala      |
| UDP-N-acetyl-D-mannosamine dehydrogenase           | orfH        | 68C>A    | Ala23Asp       |
| Glycosyltransferase family 4 protein               | orfN        | 148delG  | Val50fs        |
| LysR family transcriptional regulator              | mexT        | 833G>T   | Arg278Leu      |
| Elongation factor G                                | fusA        | 2011A>G  | Thr671Ala      |
| UDP-N-acetylglucosamine 2-epimerase                | orfK        | 355G>A   | Glu119Lys      |
| Gene/Protein Name                                      | Gene/Protein ID | Mutation Type   | Mutation Description | Impact          |
|-------------------------------------------------------|-----------------|-----------------|-----------------------|-----------------|
| NADH-quinone oxidoreductase subunit C/D               | *nuoD*          | 183_184insC     |                       | Lys63fs         |
| Malto-oligosyltrehalose synthase                      | *PA14_36605*    | 2754C>G         |                       | Tyr918*         |
| Multidrug resistance operon repressor MexR           | *mexR*          | 80_81insA       |                       | Glu27fs         |
| RND multidrug efflux transporter MexB                 | *mexB*          | 1126C>G         |                       | Leu376Val       |
| Penicillin binding protein 3 FtsI                     | *ftsI*          | 1510G>A         |                       | Arg504Cys       |
| ATP-dependent Clp protease                            | *clpA*          | 515delA         |                       | His172fs        |
| CAZ LB del 220701 bp                                  |                 | Δ                | del *PA14_36910* −   |                 |
|                                                       |                 |                 | *PA14_39440*          |                 |
| UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-        | *mpl*           | 1305_1313delCGGC |                       | Phe438_Gly440del|
| meso-diaminopimelate ligase                          |                 | GGCT T          |                       |                 |
| 2                                                     |                 | 371T>G          |                       | Val124Gly       |
| UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-        | *mpl*           |                 |                       |                 |
| meso-diaminopimelate ligase                          |                 |                 |                       |                 |
| Glycosyltransferase family 4 protein                  | *orfN*          | 148dupG         |                       | Val50fs         |
| Gene/Locus Description                                      | Gene/Protein | Candidate SNP | Protein Change |
|------------------------------------------------------------|--------------|---------------|----------------|
| Translation initiation factor IF-2                        | infB         | 2407C>T       | Val803Ile      |
| Phosphate transporter PitA                                 | pitA         | 133A>C        | Thr45Pro       |
| del 299658 bp                                               | Δ            | del PA14_35950 – PA14_39320 |
| Multidrug resistance operon repressor MexR                 | mexR         | 126_128delAAT | Leu43del       |
| Heat shock protein GrpE                                     | grpE         | 39delG        | Glu14fs        |
| ATP-dependent Clp protease proteolytic subunit              | clpP         | 365delC       | Gly122fs       |
| Molecular chaperone DnaK                                    | dnaK         | 1115G>A       | Ala372Val      |
| RND multidrug efflux transporter MexB                       | mexB         | 2300T>G       | Val767Gly      |
| del 258271 bp                                               | Δ            | del PA14_36050 – PA14_38910 |
| UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase | mpl          | 416T>G        | Val139Gly      |
| Genes/Proteins                                                                 | Genotypes                                                                 | Mutations/Replacements                                                                 |
|------------------------------------------------------------------------------|---------------------------------------------------------------------------|----------------------------------------------------------------------------------------|
| Phosphate transporter PitA                                                    | *pitA*                                                                    | 367A>C                                                                                 | Thr123Pro                                                                 |
| DNA-directed RNA polymerase subunit β                                        | *rpoB*                                                                    | 2867_2878delTGCAACTC GACC                                                            | Met956_Gln960delinsLys                                                    |
| D-alanyl-D-alanine carboxypeptidase/D-alanyl-D-alanine-endopeptidase           | *dacB*                                                                    | 343C>T                                                                                 | Gly115Ser                                                                 |
| Multidrug resistance operon repressor NalD                                   | *nalD*                                                                    | 32G>T                                                                                  | Gly115Ser                                                                 |
| del 299658 bp                                                                | Δ                                                                          | del *PA14_35950* – *PA14_39320*                                                       |                                                                           |
| Class C β-lactamase PDC-34                                                    | *ampC*                                                                    | 742G>A                                                                                 | Gly248Ser                                                                 |
| Class C β-lactamase PDC-34                                                    | *ampC*                                                                    | 716T>G                                                                                 | Val239Gly                                                                 |
| CAZ SCFM                                                                      | 1                                                                         |                                                                                        |                                                                           |
| UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase    | *mpl*                                                                    | 1151T>G                                                                                 | Val384Gly                                                                 |
| D-alanyl-D-alanine carboxypeptidase/D-alanyl-D-alanine-endopeptidase           | *dacB*                                                                    | 1169G>A                                                                                 | Ser390Asn                                                                 |
| Location | Gene | Mutation  | Protein   |
|----------|------|-----------|-----------|
| 1511 G>A | ftsI | Arg504His | Penicillin binding protein 3 FtsI |
| 2230 T>G | gyrB | Leu744Val | DNA topoisomerase (ATP-hydrolyzing) subunit B |
| 1151 T>G | mpl | Val384Gly | UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase |
| 270 C>G | dacB | Tyr90* | D-alanyl-D-alanine carboxypeptidase/D-alanyl-D-alanine-endopeptidase |
| 706 A>C | mpl | Thr236Pro | UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase |
| 326 G>A | dacB | Gly109Asp | D-alanyl-D-alanine carboxypeptidase/D-alanyl-D-alanine-endopeptidase |
| 248 A>C | clpS | Gln83Pro | ATP-dependent Clp protease adapter ClpS |
| 1510 C>T | ftsI | Arg504Cys | Penicillin binding protein 3 FtsI |
| 337 G>T | mpl | Gly113Cys | UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase |
| Gene/Protein Name                                                                 | Gene Symbol | SNP Change       | Amino Acid Change       |
|---------------------------------------------------------------------------------|-------------|------------------|-------------------------|
| D-alanyl-D-alanine carboxypeptidase/D-alanyl-D-alanine-endopeptidase                | dacB        | 1114C>T          | Gln372*                 |
| ATP-dependent Clp protease adapter ClpS                                          | clpS        | 288delC          | Glu97fs                 |
| Penicillin binding protein 3 FtsI                                                | ftsI        | 1445C>T          | Ala482Val               |
| Penicillin binding protein 3 FtsI                                                | ftsI        | 1244C>T          | Ala415Val               |
| Anhydro-N-acetylmuramic acid kinase                                              | anmK        | 695G>A           | Gly232Asp               |
| UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase       | mpl         | 111dupC          | Met38fs                 |
| 1 Glycosyltransferase family 4 protein                                           | orfN        | 148dupG          | Val50fs                 |
| CAZ Urine                                                                        |             |                  |                         |
| Pyoverdine export/recycling transporter periplasmic adaptor subunit PvdR         | pvdR        | 669G>A           | Met223Ile               |
| Amino-acid N-acetyltransferase                                                   | argA        | 1208T>C          | Phe403Ser               |
| 2 UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase     | mpl         | 111dupC          | Met38fs                 |
| Protein                                             | Gene | Mutation   | Change        |
|-----------------------------------------------------|------|------------|---------------|
| Glycosyltransferase family 4 protein                | *orfN* | 148dupG    | Val50fs       |
| Glutamate 5-kinase                                  | *proB* | 866C>T     | Ala289Val     |
| 50S ribosomal protein L27                           | *rpmA* | 10delA     | Ala6fs        |
| UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase | *mpl* | 353C>G     | Thr118Ser     |
| Cell division protein FtsL                          | *ftsL* | 176G>A     | Gly59Asp      |
| UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase | *mpl* | 353C>G     | Thr118Ser     |
| Cell division protein FtsL                          | *ftsL* | 176G>A     | Gly59Asp      |
| Chaperone protein DnaJ                              | *dnaJ* | 1081G>A    | Pro361Ser     |
| Multidrug efflux RND transporter permease subunit   | *PA14_45890* | 1001G>A | Ser334Leu     |
| Penicillin binding protein 3 FtsI                   | *ftsI* | 1567C>T    | Val523Met     |
| Penicillin binding protein 3 FtsI                   | *ftsI* | 1511C>T    | Arg504His     |
| Protein/Protein Domain                       | Gene | SNP          | Protein Effect                      |
|---------------------------------------------|------|--------------|------------------------------------|
| ATP-dependent Clp protease                  | clpA | 1634A>G      | Tyr545Cys                           |
| del 220701 bp                               | Δ    | del PA14_36910 – PA14_39440 |
| Leucyl aminopeptidase                       | pepA | 1439C>T      | Gly480Asp                           |
| Carboxyl-terminal processing protease        | ctpA | 971G>A       | Ser324Asn                           |
| PII uridylyl-transferase                    | glnD | 2466_2467insG | Asp823fs                            |
| Flagellar basal body rod protein FlgF       | flgF | 676C>A       | Glu226*                             |
| Multidrug resistance operon repressor NalD  | nalD | 32G>T        | Gly115Ser                           |
| RND multidrug efflux transporter MexB       | mexB | 1345C>T      | Leu449Phe                           |
| del 55009 bp                                | Δ    | del PA14_37950 – PA14_38580 |
| Two component response regulator            | PA14_45880 | 159C>A   | Met53Ile                            |
| Multidrug efflux RND transporter permease subunit | PA14_45890 | 836G>A | Pro279Leu                           |
| Gene/Protein                        | Symbol | Mutation | Description |
|------------------------------------|--------|----------|-------------|
| Multidrug efflux RND transporter permease subunit | PA14_45890 | 830G>A   | Ala277Val |
| del 442741 bp                      | Δ      | del PA14_35970 – PA14_40880 |
| Protein-L-isoaspartate O-methyltransferase | pcm     | 530_531insG | Arg180fs |
| Guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase | spoT   | 931T>C   | Phe311Leu |
| Multidrug resistance operon repressor NalD | nalD   | 32G>T   | Gly115Ser |
| RND multidrug efflux transporter MexB | mexB   | 1693C>T  | Pro565Ser |
| Penicillin binding protein 3 FtsI   | ftsI   | 851C>T   | Arg284Gln |
| del 55009 bp                       | Δ      | del PA14_37950 – PA14_38580 |
| class C β-lactamase PDC-34         | ampC   | 716T>C   | Val239Ala |
| CAZ-AVI SCFM                       | mpl    | 111dupC | Met38fs |
| UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase |      |          |            |
| Protein/Enzyme/Pathway                                                                 | Gene | Reference | Mutation   | Change   |
|----------------------------------------------------------------------------------------|------|-----------|------------|----------|
| D-alanyl-D-alanine carboxypeptidase                                                      | dacC | 688A>G    |            | Thr230Ala|
| D-alanyl-D-alanine carboxypeptidase                                                      | dacC | 697G>A    |            | Ala233Thr|
| DNA mismatch repair protein MutS                                                         | mutS | 2026A>C   |            | Thr676Pro |
| Glycosyltransferase family 4 protein                                                    | orfN | 148delG   |            | Val50fs  |
| D-alanyl-D-alanine carboxypeptidase/D-alanyl-D-alanine-endopeptidase                    | dacB | 1048T>C   |            | Trp350Arg|
| Cell division protein ZipA                                                              | zipA | 76C>T     |            | Arg26Trp |
| UDP-N-acetylglucosamine--D-alanyl-D-alanine ligase                                       | murF | 574A>G    |            | Thr192Ala|
| Class C β-lactamase PDC-34                                                              | ampC | 1040A>G   |            | Asn347Ser|
| LysR family transcriptional regulator AmpR                                              | ampR | 275A>G    |            | Tyr92Cys |
| Class C β-lactamase PDC-34                                                              | ampC | 716T>C    |            | Val239Ala|
| Gene | Protein Name | Mutation | amino acid change |
|------|--------------|----------|-------------------|
| mpl  | UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase | 111dupC | Met38fs |
| dacC | D-alanyl-D-alanine carboxypeptidase | 688A>G | Thr230Ala |
| mutS | DNA mismatch repair protein MutS | 2026A>C | Thr676Pro |
| orfN | Glycosyltransferase family 4 protein | 148delG | Val50fs |
| zipA | Cell division protein ZipA | 76C>T | Arg26Trp |
| anmK | Anhydro-N-acetylmuramic acid kinase | 197G>A | Trp66* |
| mpl  | UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase | 111delC | Met38fs |
| mpl  | UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase | 104A>C | Tyr35Ser |
| PA14_45880 | Two component response regulator | 1255C>T | Arg419Cys |
| PA14_45890 | Multidrug efflux RND transporter permease subunit | 830C>T | Ala277Val |
| Gene/Protein                                      | Gene/Protein Family | Reference (Accession) | Mutation Type | Description |
|--------------------------------------------------|---------------------|-----------------------|---------------|-------------|
| Multidrug efflux RND transporter permease subunit | PA14_45890          | 1787A>G               | Asn596Ser     |             |
| Penicillin binding protein 3 FtsI                 | ftsI                | 1511G>A               | Arg504His     |             |
| UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase | mpl                  | 111dupC               | Met38fs       |             |
| Efflux system transcriptional repressor NalC     | nalC                | 442_443insC           | His150fs      |             |
| Cell division protein FtsB                       | ftsB                | 121A>G                | Ile41Val      |             |
| UDP-N-acetyl-D-mannosamine dehydrogenase         | orfH                | 792dupG               | His265fs      |             |
| DNA mismatch repair endonuclease MutL            | mutL                | 1306A>C               | Ser436Arg     |             |
| UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase | mpl                  | 742C>T                | Gln248*       |             |
| UDP-N-acetyl-D-mannosamine dehydrogenase         | orfH                | 561_565delGGCAGinsAG  | Ala189Ser     |             |
| Glycosyltransferase family 4 protein             | orfN                | 148delG               | Val50fs       |             |
| Gene/Protein                        | Symbol  | Mutation     | Amino Acid Change   |
|------------------------------------|---------|--------------|---------------------|
| Cell division protein FtsL         | ftsL    | 176G>A       | Gly59Asp            |
| Class C β-lactamase PDC-34         | ampC    | 1040A>G      | Asn347Ser           |
| UDP-N-acetylMuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase | mpl     | 111dupC      | Met38fs             |
| Efflux system transcriptional repressor NalC | nalC    | 442_443insC  | His150fs            |
| Cell division protein FtsB         | ftsB    | 119_121delAGAinsTGG | GlnIle40LeuVal     |
| UDP-N-acetyl-D-mannosamine dehydrogenase | orfH    | 792dupG      | His265fs            |
| DNA mismatch repair endonuclease MutL | mutL    | 1306A>C      | Ser436Arg           |
| UDP-N-acetylMuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase | mpl     | 742C>T       | Gln248*             |
| Glycosyltransferase family 4 protein | orfN    | 148dupG      | Val50fs             |
| Cell division protein FtsL         | ftsL    | 176G>A       | Gly59Asp            |
| Transcriptional regulator          | lrp     | 103G>T       | Glu35*              |
* The amino acid led to a stop codon

** When hypermutators emerged, only those genetic events that may be involved in β-lactam resistance were included to simplify the analysis.
Supplementary Table 5. Genetic variations previously reported in clinical *P. aeruginosa* isolates or in experimental *in vitro* studies and leading to antibiotic resistance.

| Gene (Amino acid modification) | Population          | Studies                | References |
|--------------------------------|---------------------|------------------------|------------|
| *mexY* (His908Leu)            | TOB SCFM 3          |                        | (1)        |
| *fusA* (Thr671Ala)           | TOB RM 1            |                        |            |
|                                | TOB SCFM 1          |                        |            |
|                                | TOB SCFM 2          |                        |            |
|                                | TOB U 1             |                        |            |
|                                | TOB U 2             |                        |            |
|                                | TOB U 4             |                        |            |
| *fusA* (Gln678Leu)           | TOB SCFM 3          |                        | (1)        |
| *fusA* (Arg680Cys)           | TOB RM 4            |                        | (1, 3)     |
|                                | TOB SCFM 4          |                        |            |
| *fusA* (Thr456Ala)           | TOB U 3             |                        | (1)        |
| *ampC* (Val239Gly)           | CAZ SCFM 1          |                        | (1, 4)     |
| *anmK* (Gly232Asp)           | CAZ U 1             |                        | (1)        |
| *mpl* (Met38fs)              | CAZ U 1             |                        | (1, 4)     |
|                                | CAZ U 2             |                        |            |
|                                | CAZ-AVI SCFM 1      |                        |            |
|                                | CAZ-AVI SCFM 2      |                        |            |
| Gene | Mutation | Strains | Reference(s) |
|------|----------|---------|--------------|
| mpl (Val384Gly) | CAZ-AVI SCFM 3, CAZ-AVI U 1, CAZ-AVI U 3 | (1) |
| mpl (Val124Gly) | CAZ SCFM 1, CAZ SCFM 2 | (4) |
| mpl (Tyr35Ser) | CAZ-AVI SCFM 3 | (1) |
| dacB (Gln372*) | CAZ SCFM 4 | (1) |
| dacB (Trp350Arg) | CAZ-AVI SCFM 1 | (4) |
| fisI (Arg504His) | CAZ SCFM 1, CAZ-AVI RM 1, CAZ-AVI SCFM 4 | (1, 5, 6) |
| fisI (Ala482Val) | CAZ SCFM 4 | (7) |
| fisL (Gly59Asp) | CAZ U 3, CAZ U 4, CAZ-AVI U 2, CAZ-AVI U 4 | (1) |
| fusA (Thr671Ala) | TOB RM 1, TOB SCFM 1, Experimental studies | (8) |
| Gene          | Mutations                      | Resistance Markers                      | References |
|--------------|--------------------------------|-----------------------------------------|------------|
| fusA         | (Gln678Leu)                    | TOB SCFM 2, TOB U 1, TOB U 2, TOB U 4 | (8)        |
| fusA         | (Arg680Cys)                    | TOB SCFM 3                             |            |
| fusA         | (Thr456Ala)                    | TOB RM 4, TOB SCFM 4                   | (8)        |
| ftsI         | (Arg504His)                    | CAZ SCFM 1, CAZ-AVI RM 1, CAZ-AVI SCFM 4 | (9)        |
| orfN         | (Val50fs)                      | TOB RM 1, TOB RM 2, TOB RM 3, TOB RM 4, TOB U 3, CAZ RM 2, CAZ U 1, CAZ U 2, CAZ-AVI SCFM 1, CAZ-AVI SCFM 2, CAZ-AVI U 4 | (8, 10, 11) |

References:
8, 10, 11
Supplementary Table 6. Genes reported to be mutated in clinical *P. aeruginosa* isolates or in experimental *in vitro* studies although the genetic variations are different.

| Gene | Population | Studies | References |
|------|------------|---------|------------|
| *mexR* | CAZ RM 1, CAZ RM 3 | | (4, 7, 12) |
| *clpA* | CAZ RM 1, CAZ-AVI RM 1 | | (7) |
| *nalD* | CAZ RM 4, CAZ-AVI RM 2, CAZ-AVI RM 4, | | (7, 12) |
| *gyrB* | CAZ SCFM 2 | Clinical studies | (13) |
| *ampR* | CAZ-AVI SCFM 2 | | (14) |
| *mexB* | CAZ RM 1, CAZ RM 3, CAZ-AVI RM 2, CAZ-AVI RM 4 | | (4, 15) |
| *mutL* | CAZ-AVI U 1, CAZ-AVI U 3 | | (4) |
| *mutS* | CAZ-AVI SCFM 1, | | (4) |
| Gene   | Strains                                      | References |
|--------|---------------------------------------------|------------|
| mexT   | TOB U 3                                     | (4)        |
| pmrB   | TOB RM 1, TOB RM 2, TOB RM 3, TOB RM 4     | (4)        |
| ptsP   | TOB RM 2, TOB SCFM 3, TOB SCFM 4           | (8)        |
| pmrB   | TOB RM 1, TOB RM 2, TOB RM 3, TOB RM 4     | (8, 16)    |
| orfH   | TOB SCFM 1, TOBSCFM 2, TOB SCFM 4, TOB U 3, CAZ-AVI U 1, CAZ-AVI U 2, CAZ-AVI U 3 | (8)        |
| orfK   | TOB SCFM 3,                                | (8)        |
| Gene | Strains |
|------|---------|
| mexR | CAZ RM 1, CAZ RM 3 | (7) |
| clpA | CAZ RM 1, CAZ-AVI RM 1 | (7) |
| ampC | CAZ SCFM 1, CAZ-AVI SCFM 1, CAZ-AVI SCFM 2, CAZ-AVI SCFM 3 | (7) |
| nalD | CAZ RM 4, CAZ-AVI RM 2, CAZ-AVI RM 4 | (7) |
| pepA | CAZ-AVI RM 2 | (7) |
| dacB | CAZ RM 4, CAZ SCFM 1, CAZ SCFM 2, CAZ SCFM 3, | (7, 9) |
|       | CAZ SCFM 4, CAZ-AVI SCFM 1 |       |       |
|-------|-----------------------------|-------|-------|
| *nalC* | CAZ-AVI U 1, CAZ-AVI U 3    |       | (7)   |
| Gene  | Genetic modification | Primer Fw (5’-3’)       | Primer Rv (5’-3’)       |
|-------|----------------------|-------------------------|-------------------------|
| fusA  | 2038C>T              | CGGTAAGGTTATTCTGTGCCG   | TTTTAACCAGCGCTTCGACG    |
| fusA  | 2011A>G              |                         |                         |
| fusA  | 1634G>A              | GGACGAGAAGGGCAACATCA    | CATGATCGGCTCGAGCACCT    |
| ptsP  | 1135dupG             | CTACCCGGAGCAGACCATC     | TAGCCATCGACGATCAGGTC    |
| ptsP  | 2156delG             | TGCTGCATGCCTGAAGAGAG    | AGCGAGCTGTGGATGACCTG    |
| pmrB  | 853G>C               | GCCGAACGCCGACTGACCG     | AATTGCTCCAGACGGCGTC     |
| orfN  | 148delG              | ATGGGAGCTCTCAAATGCCCG   | CCGCCAGAATCGGAAAAAC     |
| orfH  | 286C>T               | CATGCAGCTCGACTGACTTG    | GAATTACAAATCGCCCGCT     |
| orfH  | 561_565delGGCAAGinsAGCTT | CCAGAGTCACGGAGATGCTT    | TAGCTTGACACATTCAGCGG     |
| orfH  | 792delG              | AGCTGATCCGACTCGCTAAAT   | ATTCGCTTCGAGAAAACTCCG   |
| orfK  | 355G>A               | CTTGTCATGGGCGTACACG     | GGAGCAAGTGAAAGACAGGC    |
| nuoD  | 183_184insC          | TTACAAGGCAAGCAGGACCAGG  | GTAGAAGACGCTGAAAGTCGG   |
| anmK  | 197G>A               | GAAGACATCCTCGCCCTGT     | TTTGACCGTGACTGCGATA     |
| Gene | Position | Change | Sequence 1 | Sequence 2 |
|------|----------|--------|------------|------------|
| mpl | 111 | delC | CATCTGCGGGACCTTCATG | TTGCGATCACTACCAGGTC |
| mpl | 104 | A>C | CGAGGGGCCTGATCATTCGC | GTTGTGCAGGCCGGTCAG |
| mpl | 706 | A>C | CGAGGGGCCTGATCATTCGC | GTTGTGCAGGCCGGTCAG |
| mpl | 742 | C>T | CGAGGGGCCTGATCATTCGC | GTTGTGCAGGCCGGTCAG |
| mpl | 353 | C>G | CGAGGGGCCTGATCATTCGC | GTTGTGCAGGCCGGTCAG |
| mpl | 416 | T>G | CGAGGGGCCTGATCATTCGC | GTTGTGCAGGCCGGTCAG |
| fisI | 1510 | C>T | ATGCTGCAACAAGTGGTCG | CGAAGTAGCCCGCCTTG |
| fisI | 1511 | C>T | ATGCTGCAACAAGTGGTCG | CGAAGTAGCCCGCCTTG |
| fisI | 1567 | C>T | ATGCTGCAACAAGTGGTCG | CGAAGTAGCCCGCCTTG |
| fisL | 176 | G>A | CGGCAGCTTCTCTATGTTG | CATGCAGCAACTGTTCCACC |
| dacB | 326 | G>A | ACCTATGCGCCCTGGAAA | CGTCGTTGAATACCGGCAA |
| dacB | 343 | C>T | ACCTATGCGCCCTGGAAA | CGTCGTTGAATACCGGCAA |
| clpS | 248 | A>C | GGTGGTCACTGTTCGACC | CCCGTGCACTGTTCGACC |
| clpA | 1634 | A>G | TCGTTTCCTTCTCGGCAGGT | CGTGGTGACGCCGTCAGG |
| dnaJ | 1081 | G>A | AAGCTGTTCCGCTGCG | ATAAAACCACCTCCACCG |
|       |        |       |       |       |       |
|-------|--------|-------|-------|-------|-------|
| PA14_45890 | 1001G>A | GCCAACGACCAGTTGTTCAA | ACGTACGACGATCGAGGTT |
| Del 299648 bp | Del 3200274-3499932 | GCTTCACCAGGTTCCGCTGAAG | TCAGTCAATCGCCGCCCA |
|         |        | CTGTTGAGATCGTGAAGGGG | TTCGAACCTCTTCTCTCTTGA |
| Del 220701 bp | Del 3288650-3509351 | ATGCAACACAGCCAAGTGT | TCAGAACGGTTTGGTCGGCA |
|         |        | CTGTTGAGATCGTGAAGGGG | TTCGAACCTCTTCTCTCTTGA |
| nalD   | 32G>T  | AATACCTCGAGTCCGCCC | TTGAGCATCTCGTTGAAACAG |
| pitA   | 367A>C | ATGTTGCAGTCTTTTCAGCGG | CGCGATGTCGATCGCCTT |
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