| Strain | Organism       | Genotype beta-lactams (genes identified by WGS) | Genotype aminoglycosides (PROTEINS and genes identified by WGS) | Beta-lactam and aminoglycoside [GEN, TOB, NET, AMI only]) | BMD PLZ MIC (µg/mL) |
|--------|----------------|-----------------------------------------------|---------------------------------------------------------------|----------------------------------------------------------|---------------------|
| 1      | *Citrobacter koseri* | *bla*<sub>TEM-110</sub> *bla*<sub>MAL-CKO</sub> | AAC(3)-Ila APH(3')-Ib APH(6)-id ANT(3'')-Ia | Acquired Pase Aminoglycoside resistant (AME*) | 2                   |
| 2      | *Citrobacter koseri* | *bla*<sub>TEM-1</sub> *bla*<sub>MAL-CKO</sub> | AAC(6')-Ib like ANT(3')-Ia | ESBL Aminoglycoside resistant (AME) | 0.25                |
| 3      | *Klebsiella aerogenes* | *bla*<sub>TEM-1</sub> | AAC(3)-Ila AAC(6')-Ib like ANT(3')-Ia APH(3')-Ib APH(6)-id | Carbapenem Resistant (impermeability) Aminoglycoside Resistant (AME) | 0.5                  |
| 4      | *Enterobacter cloacae* | *bla*<sub>MIR</sub> | None | Carbapenem Resistant (impermeability) Aminoglycoside wild | 0.25                |
| 5      | *Escherichia coli* | *bla*<sub>TEM-2</sub> | APH(3')-Ib | Acquired Pase Aminoglycoside wild | 0.25                |
| 6      | *Klebsiella pneumoniae* | *bla*<sub>TEM-11</sub> *bla*<sub>SV-83</sub> | AAC(3)-Ila ANT(3')-Ia | ESBL and/or SHV hyperproduction Aminoglycoside Resistant (AME) | 0.25                |
| 7      | *Escherichia coli* | *bla*<sub>TEM-21</sub> | AAC(3)-Ila AAC(6')-Ib like | ESBL Aminoglycoside Resistant (AME) | 1                   |
| 8      | *Escherichia coli* | *bla*<sub>TEM-20</sub> *bla*<sub>CTX-M</sub> | AAC(3)-Ila ANT(3')-Ia APH(3')-Ib APH(6)-id | ESBL Aminoglycoside Resistant (AME) | 0.5                  |
| 9      | *Klebsiella aerogenes* | *bla*<sub>TEM-24</sub> *bla*<sub>APC</sub> | AAC(6')-Ib like ANT(3')-Ia | ESBL Aminoglycoside Resistant (AME) | 1                   |
| 10     | *Citrobacter freundii* | *bla*<sub>CMY-2</sub> *bla*<sub>TEM-1</sub> *bla*<sub>32A-10</sub> | AAC(3)-Ila AAC(6')-Ib like AAC(6')-If ANT(3')-Ia | ESBL Aminoglycoside Resistant (AME) | 0.5                  |
| 11     | *Klebsiella pneumoniae* | *bla*<sub>TEM-1</sub> *bla<sub>SHV</sub> (multiple alleles including one for an ESBL) *bla*<sub>KPC</sub> *bla*<sub>ESCA-0</sub> *bla*<sub>FOX</sub> *bla*<sub>CARB-1</sub> | AAC(3)-Iva AAC(6')-Ib like ANT(2')-Ia ANT(3')-Ia APH(3')-Ia APH(4)-Ia | ESBL + Acquired Case + Carbapenemase (KPC) Aminoglycoside Resistant (AME) | 0.25                |
| 12     | *Citrobacter freundii* | *bla*<sub>CMY-2</sub> like | None | High level Case Aminoglycoside wild | 1                   |
| Strain | Organism          | Genotype beta-lactams (genes identified by WGS) | Genotype aminoglycosides (PROTEINS and genes identified by WGS) | Beta-lactam and aminoglycoside [GEN, TOB, NET, AMI only]) | BMD PLZ MIC (µg/mL) |
|--------|-------------------|-----------------------------------------------|---------------------------------------------------------------|-------------------------------------------------------------|---------------------|
| 13     | *Escherichia coli*| *bla*TEM-1, *bla*VIM, *bla*OXA-1 like          | AAC(6')-Ic, ANT(3'')-Ia, APH(3'')-Ib, APH(6)-Id               | Carbapenemase (KPC) Aminoglycoside Resistant (AME)            | 2                   |
| 14     | *Enterobacter cloacae* | *bla*VIM                                      | AAC(6')-II, ANT(3'')-Ia, APH(3'')-Ia, APH(3'')-Ib, APH(6)-Id | Carbapenemase (MBL) Aminoglycoside Resistant (AME)            | 0.5                 |
| 15     | *Enterobacter cloacae* | *bla*IMP, *bla*OXA-1 like, *bla*OXA-2        | AAC(6')-Ib like                                             | Carbapenemase (MBL) Aminoglycoside Resistant (AME)            | 0.25                |
| 16     | *Serratia marcescens* | *bla*TEM, *bla*XCU                           | AAC(6')-Ic, AAC(6')-II, ANT(3'')-Ia                       | Carbapenemase (MBL) Aminoglycoside Resistant (AME)            | 1                   |
| 17     | *Serratia marcescens* | *bla*IMP, *bla*XCU                           | AAC(6')-Ic, AAC(6')-II, ANT(3'')-Ia                       | Carbapenemase (MBL) Aminoglycoside Resistant (AME)            | 1                   |
| 18     | *Klebsiella pneumoniae* | *bla*TEM-1, *bla*XCU, *bla*CMY-2 like, *bla*NDM, *bla*OXA-1 like, *bla*CTX-M | AAC(6')-II, AAC(6')-I, ANT(3'')-I, APH(2'')-Ia, APH(3'')-Ia, APH(6)-Id | ESBL + Acquired Case + Carbapenemase (MBL) Aminoglycoside Resistant (AME) | 0.5                 |
| 19     | *Klebsiella pneumoniae* | *bla*TEM-1, *bla*XCU, *bla*CMY-2 like, *bla*NDM, *bla*OXA-1 like, *bla*CTX-M | AAC(6')-Ib like, ANT(3'')-Ia                              | ESBL + Carbapenemase (KPC) Aminoglycoside Resistant (AME)     | 0.25                |
| 20     | *Citrobacter freundii* | *bla*TEM-2, *bla*OXA-10 like, *bla*CTX-M | AAC(3)-I, AAC(6')-Ib like, ANT(2'')-Ia, ANT(3'')-Ia | ESBL + Carbapenemase (MBL) Aminoglycoside Resistant (AME)     | 0.5                 |
| 21     | *Citrobacter freundii* | *bla*TEM-2, *bla*OXA-10 like, *bla*CTX-M | AAC(3)-I, ANT(3'')-Ia                                      | Acquired Pase Aminoglycoside Resistant (AME)                   | 0.25                |
| 22     | *Klebsiella pneumoniae* | *bla*TEM-1, *bla*OHA-1, *bla*OXA-4B           | None                                                        | Carbapenemase (OXA-4B) Aminoglycoside wild                    | 0.25                |
| 23     | *Klebsiella pneumoniae* | *bla*TEM-1, *bla*OHA-1, *bla*OXA-4B           | AAC(3)-I, AAC(6')-Ib like, ANT(3'')-Ia                   | ESBL + Carbapenemase (MBL) Aminoglycoside Resistant (AME)     | 0.25                |
| Strain | Organism          | Genotype beta-lactams (genes identified by WGS) | Genotype aminoglycosides (PROTEINS and genes identified by WGS) | Beta-lactam and aminoglycoside [GEN, TOB, NET, AMI only]) | BMD PLZ MIC (µg/mL) |
|---------|-------------------|------------------------------------------------|---------------------------------------------------------------|-----------------------------------------------------------|---------------------|
| 24      | *Klebsiella pneumoniae* | *blaCTX-M* | AAC(3)-Ila AAC(6’)-lb like truncated APH(3’)-lb APH(6)-Id armA | ESBL + Carbapenemase (MBL) Aminoglycoside Resistant (AME and RNA methylase armA) | >256                |
| 25      | *Providencia stuartii* | *blaTEM-1* | AAC(2’)-la APH(3’)-la APH(3’)-VI APH(3’)-lb APH(6)-Id ? ANT(3’)-la rmTC | ESBL + Acquired Case Carbapenemase (MBL) Aminoglycoside Resistant (AME and RNA methylase rmC) | 256                 |
| 26      | *Klebsiella pneumoniae* | *blaCTX-M* | AAC(3)-Ila AAC(6’)-lb like truncated AAC(6’)-lb-cr truncated ANT(3’)-la APH(3’)-la APH(3’)-lb APH(6)-Id rmF | ESBL + Carbapenemase (OXA-181) Aminoglycoside resistant (AME and RNA methylase rmF) | >256                |
| 27      | *Escherichia coli*    | *blaTEM-1* | APH(3’)-la APH(6)-Id ANT(3’)-la rmTB | ESBL Aminoglycoside resistant (RNA methylase rmB) | >256                |
| 28      | *Escherichia coli*    | *blaTEM-1* | AAC(6’)-lb like truncated APH(3’)-lb APH(6)-Id ANT(2’)-la ANT(3’)-la armA | ESBL + Carbapenemase (MBL) Aminoglycoside Resistant (AME and RNA methylase armA) | >256                |
| 29      | *Klebsiella pneumoniae* | *blaCTX-M* | AAC(3)-Ila AAC(6’)-lb-cr APH(3’)-la APH(3’)-lb APH(6)-Id | ESBL + Carbapenemase (OXA-48) Aminoglycoside Resistant (AME) | 0.25                |
| 30      | *Escherichia coli*    | *blaCTX-M* | AAC(3)-Ila ANT(3’)-la APH(3’)-lb APH(6)-Id | ESBL + Carbapenemase (OXA-48) Aminoglycoside Resistant (AME) | 0.5                 |
| 31      | *Citrobacter koseri*  | *blaMAL_CED18* | None | Pase Aminoglycoside wild | 0.25                |
| 32      | *Klebsiella oxytoca*  | *blaOXY* | APH(3’)-la truncated | Beta lactam and Aminoglycoside wild | 0.5                 |
| Strain | Organism     | Genotype beta-lactams (genes identified by WGS) | Genotype aminoglycosides (PROTEINS and genes identified by WGS) | Beta-lactam and aminoglycoside [GEN, TOB, NET, AMI only]) | BMD PLZ MIC (µg/mL) |
|--------|--------------|-----------------------------------------------|-------------------------------------------------|---------------------------------------------------------|---------------------|
| 33     | *Klebsiella oxytoca* | bl*TEM-1* bl*OXA-2 like truncated bl*OXY* | AAC(6’)-Ic ANT(2’’)-b truncated APH(3’)-la APH(3’)-lb APH(6)-Id | Carbapenem Resistant (impermeability) Aminoglycoside Resistant (AME) | 1                   |
| 34     | *Klebsiella pneumoniae* | bl*TEM-1* bl*SHV-12* bl*OXA-48* bl*OXY* | AAC(3’)-Ila AAC(6’)-lb-cr ANT(3’’)-la | ESBL + Carbapenemase (OXA-48) Aminoglycoside Resistant (AME) | 0.5                 |
| 35     | *Klebsiella oxytoca* | bl*TEM-1* bl*KPC* bl*OXA-9 like* bl*OXY* | AAC(6’)-Ib like ANT(3’’)-la APH(3’)-la truncated APH(3’)-lb APH(6)-Id truncated | Carbapenemase (KPC) Aminoglycoside Resistant (AME) | 0.5                 |
| 36     | *Klebsiella oxytoca* | bl*TEM-1* bl*KPC* bl*OXA-9 like* bl*OXY* | AAC(6’)-Ib like ANT(3’’)-la APH(3’)-la truncated APH(3’)-lb APH(6)-Id truncated | Carbapenemase (KPC) Aminoglycoside Resistant (AME) | 0.25                |
| 37     | *Klebsiella oxytoca* | bl*TEM-1* bl*KPC* bl*OXA-9 like* bl*OXY* | AAC(6’)-Ib like ANT(3’’)-la APH(3’)-la truncated APH(3’)-lb APH(6)-Id truncated | Carbapenemase (KPC) Aminoglycoside Resistant (AME) | 0.25                |
| 38     | *Klebsiella oxytoca* | bl*OXY* | None | High level natural Pase (K1) Aminoglycoside wild | 0.25                |
| 39     | Enterobacter cloacae | bl*TEM-1* bl*SHV-12* bl*OXA-48* bl*OXY* bl*ACT* | AAC(3’)-Ila AAC(6’)-lb-cr ANT(3’’)-la APH(3’)-lb truncated APH(6)-Id | ESBL + Carbapenemase (OXA-48) Aminoglycoside Resistant (AME) | 0.25                |
| 40     | Enterobacter cloacae | bl*SHV-12* bl*SHV-12* bl*ACT* | AAC(6’)-Ib like ANT(3’’)-la | ESBL + Carbapenemase (MBL) Aminoglycoside Resistant (AME) | 0.25                |
| 41     | Escherichia coli | bl*TEM-1* bl*SHV-12* bl*OXA-48* bl*ACT* | AAC(3’)-Ila AAC(6’)-lb like truncated AAC(6’)-lb-cr truncated ANT(3’’)-la armA | ESBL + Carbapenemase (MBL) Aminoglycoside resistant (AME and RNA methylase armA) | >256                |
| 42     | Klebsiella aerogenes | bl*TEM-24* | AAC(6’)-Ib like truncated ANT(3’’)-la | ESBL Aminoglycoside Resistant (AME) | 0.5                 |
| 43     | Enterobacter cloacae | bl*TEM-1* bl*SHV-12* bl*ACT* | AAC(6’)-Ib like AAC(6’)-Ic ANT(3’’)-la APH(3’)-lb APH(6)-Id | ESBL Aminoglycoside Resistant (AME) | 0.5                 |
| Strain | Organism          | Genotype beta-lactams (genes identified by WGS) | Genotype aminoglycosides (PROTEINS and genes identified by WGS) | Beta-lactam and aminoglycoside [(GEN, TOB, NET, AMI only)] | BMD PLZ MIC (µg/mL) |
|--------|-------------------|-------------------------------------------------|-----------------------------------------------------------------|----------------------------------------------------------|---------------------|
| 44     | *Enterobacter cloacae* | blαCTX-M, blαOXA-1 like, blαACT                | AAC(3)-Ila AAC(6')-Ib-cr ANT(3')-Ia APH(3')-Ib APH(6)-Id          | ESBL Aminoglycoside Resistant (AME)                        | 0.5                 |
| 45     | *Enterobacter cloacae* | blαCTX-M, blαSHV-12, blαACT                        | AAC(6')-Ib like ANT(2'')-Ia ANT(3')-Ia                               | ESBL Aminoglycoside Resistant (AME)                        | 0.25                |
| 46     | *Enterobacter cloacae* | blαACT                                               | None                                                             | High Level Case Aminoglycoside wild                       | 0.5                 |
| 47     | *Enterobacter cloacae* | blαACT                                               | None                                                             | Beta lactam and Aminoglycoside wild                       | 0.5                 |
| 48     | *Providencia stuartii* | blαTEM-1, blαECO, blαACC                           | AAC(2'')-Ia APH(3')-Ia APH(3')-Ib APH(6)-Id ANT(3')-Ia             | Undetermined for beta-lactams Aminoglycoside wild         | 1                   |
| 49     | *Citrobacter freundii* | blαCMY-2 like                                         | None                                                             | High Level Case Aminoglycoside wild                       | 0.5                 |
| 50     | *Klebsiella aerogenes* | None                                                 | None                                                             | High Level Case Aminoglycoside wild                       | 0.5                 |
| 51     | *Klebsiella pneumoniae* | blαTEM-1, blαSHV-11, blαCTX-M, blαOXA-2 like, blαOXA-48 | AAC(3)-Ila AAC(6')-Ib-cr                                         | ESBL + Carbapenemase (OXA-48) Aminoglycoside Resistant (AME) | 8                   |
| 52     | *Klebsiella pneumoniae* | blαTEM-1, blαSHV-11, blαCTX-M, blαOXA-2 like, blαOXA-48 | AAC(3)-Ila AAC(6')-Ib-cr                                         | ESBL + Carbapenemase (OXA-48) Aminoglycoside Resistant (AME) | 16                  |
| 53     | *Proteus mirabilis* | blαTEM-1, blαSHV-12                                  | APH(3')-Ia APH(3')-Ib APH(6)-Id ANT(3')-Ia                       | ESBL Aminoglycoside wild                                  | 32                  |
| 54     | *Klebsiella aerogenes* | None                                                 | None                                                             | Undetermined                                             | 8                   |
| 55     | *Morganella morganii* | blαOXA                                              | None                                                             | Undetermined                                             | 16                  |
| 56     | *Klebsiella pneumoniae* | blαTEM-1, blαSHV-11, blαOxa                       | AAC(6')-Ib like APH(3')-Ib APH(6)-Id ANT(3')-Ia                  | Carbapenemase (KPC) Aminoglycoside Resistant (AME)        | 2                   |
| 57     | *Klebsiella aerogenes* | blαSHV-12                                             | AAC(6')-Ib like APH(6)-Ic ANT(3')-Ia                             | ESBL + Carbapenem Resistant (impermeability) Aminoglycoside Resistant (AME) | 1                   |
| Strain | Organism                   | Genotype beta-lactams (genes identified by WGS) | Genotype aminoglycosides (PROTEINS and genes identified by WGS) | Beta-lactam and aminoglycoside [GEN, TOB, NET, AMI only]) | BMD PLZ MIC (µg/mL) |
|--------|----------------------------|-----------------------------------------------|---------------------------------------------------------------|-------------------------------------------------------------|---------------------|
| 58     | Citrobacter freundii       | bla<sub>2CEX-2</sub>                           | None                                                         | Beta lactam and Aminoglycoside wild                        | 0.5                |
| 59     | Morganella morganii        | bla<sub>RNA</sub>                              | None                                                         | High Level Case Aminoglycoside wild                        | 8                  |
| 60     | Morganella morganii        | bla<sub>RNA</sub>                              | None                                                         | Beta lactam and Aminoglycoside wild                        | 2                  |
| 61     | Proteus mirabilis          | bla<sub>TEM-1</sub>, bla<sub>2CEX-2</sub>, bla<sub>2DNA-1</sub> | AAC(3)-Ila, AAC(6')-Ib like ANT(3")-Ia                        | ESBL + Acquired Case Aminoglycoside Resistant (AME)         | 8                  |
| 62     | Proteus vulgaris group     | None                                          | None                                                         | Undetermined for beta-lactams Aminoglycoside Resistant (AME) | 4                  |
| 63     | Serratia marcescens        | None                                          | AAC(6')-Ic                                                   | ESBL + Carbapenem Resistant (impermeability) Aminoglycoside | 1                  |
| 64     | Klebsiella pneumoniae      | bla<sub>TEM-1</sub> (multiple alleles including one for an ESBL) bla<sub>2DNA-1</sub> | APH(3")-Ib, APH(6)-Id truncated ANT(3")-Ia truncated         | ESBL + Carbapenem Resistant (impermeability) Aminoglycoside | 8                  |
| 65     | Serratia marcescens        | bla<sub>SCP</sub>                              | None                                                         | Beta lactam and Aminoglycoside wild                        | 1                  |
| 66     | Proteus vulgaris group     | None                                          | None                                                         | Acquired Pase or wild (cefuroximase) Aminoglycoside wild    | 4                  |
| 67     | Proteus vulgaris group     | None                                          | None                                                         | Acquired Pase Aminoglycoside wild                          | 2                  |
| 68     | Klebsiella pneumoniae      | bla<sub>TEM-1</sub>, bla<sub>TEM-1</sub> (multiple alleles including one for an ESBL) bla<sub>2DNA-1</sub> | AAC(6')-Ib like APH(3")-Ia APH(3")-Ib APH(6)-Id ANT(2")-Ia ANT(3")-Ia rmtB | ESBL Aminoglycoside Resistant (AME and RNA methylase rmtB) | >256               |
| 69     | Escherichia coli           | bla<sub>TEM-1</sub>                           | APH(3")-Ib, APH(6)-Id                                        | Acquired Pase Aminoglycoside undetermined                   | 4                  |
| 70     | Proteus vulgaris group     | None                                          | None                                                         | Undetermined                                               | 2                  |
| 71     | Klebsiella pneumoniae      | bla<sub>HV-11</sub>                           | None                                                         | Acquired Pase Aminoglycoside undetermined                   | 4                  |
| 72     | Proteus mirabilis          | bla<sub>TEM-1</sub>                           | APH(3")-Ia, APH(3")-Ib APH(6)-Id ANT(3")-Ia                 | Acquired Pase Aminoglycoside wild                          | 4                  |
| Strain | Organism                 | Genotype beta-lactams (genes identified by WGS) | Genotype aminoglycosides (PROTEINS and genes identified by WGS) | Beta-lactam and aminoglycoside [GEN, TOB, NET, AMI only] | BMD PLZ MIC (µg/mL) |
|--------|-------------------------|-----------------------------------------------|---------------------------------------------------------------|----------------------------------------------------------|----------------------|
| 73     | Klebsiella oxytoca      | blαTEM-1                                      | ANT(3'')-Ia                                                  | High level Natural Pase (K1) Aminoglycoside undetermined | 2                    |
| 74     | Proteus vulgaris group  | None                                          | None                                                         | High level cefuroximase Aminoglycoside wild              | 4                    |
| 75     | Escherichia coli        | blαTEM-1                                      | None                                                         | Acquired Pase Aminoglycoside undetermined                | 4                    |
| 76     | Proteus mirabilis       | blαTEM-1                                      | AAC(3)-Id                                                   | Inhibitor resistant Pase Aminoglycoside Resistant (AME)   | 2                    |
| 77     | Klebsiella pneumoniae   | blαMOV-1                                      | armA                                                        | Carbapenemase (KPC) Aminoglycoside Resistant (RNA methylase armA) | >256                |
| 78     | Escherichia coli        | blαTEM-1                                      | AAC(3)-Ila                                                  | ESBL Aminoglycoside Resistant (AME and RNA methylase rmtB) | >256                |
| 79     | Escherichia coli        | blαCTX-M                                      | AAC(3)-Ila                                                  | ESBL Aminoglycoside Resistant (AME and RNA methylase rmtB) | >256                |
| 80     | Escherichia coli        | blαTEM-1                                      | AAC(3)-Ila                                                  | ESBL Aminoglycoside Resistant (AME)                      | 1                    |

2 *AME = Aminoglycoside Modifying Enzymes
3 Pase = penicillinase
4 Case = cephalosporinase