

Figure S1 (S1A and S1B): Multiplex PCR assay for the detection of carbapenemase genes. On the left (S1A), assay for the detection of *blaKPC* (798 bp), *blaNDM* (621 bp), and *blaOXA-48* (438 bp) genes. L: 100 bp ladder; N: Negative control; C1: *K. pneumoniae* BAA-1705 *blaKPC* (+); C2: *K. pneumoniae* UCO-361 *blaNDM* (+); C3: *K. pneumoniae* BAA-2524 *blaOXA-48* (+). On the right (S1B), assay for the detection of the *blaIMP* (232 bp) and *blaVIM* (390 bp) genes. L: 100 bp ladder; N: Negative control; C1: *S. marcescens* UCO-143 *blaIMP* (+); C2: *P. aeruginosa* *blaVIM* (+).

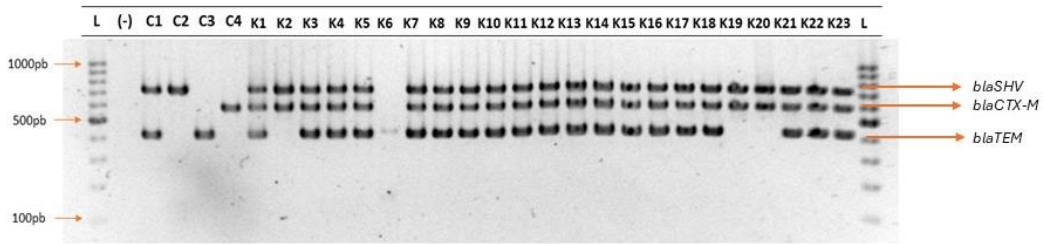


Figure S2: Multiplex PCR assay for the detection of *blaTEM* (422 bp), *blaSHV* (739 bp), and *blaCTX-M* (593 bp) genes. L: 100 bp ladder; (-): Negative control; C1: *K. pneumoniae* BAA-1705 *blaTEM* (+), *blaSHV* (+); C2: *K. pneumoniae* ATCC 700603 *blaSHV* (+); C3: *E. coli* ATCC 35218 *blaTEM* (+); C4: *E. coli* UCH-235 *blaCTX-M* (+).

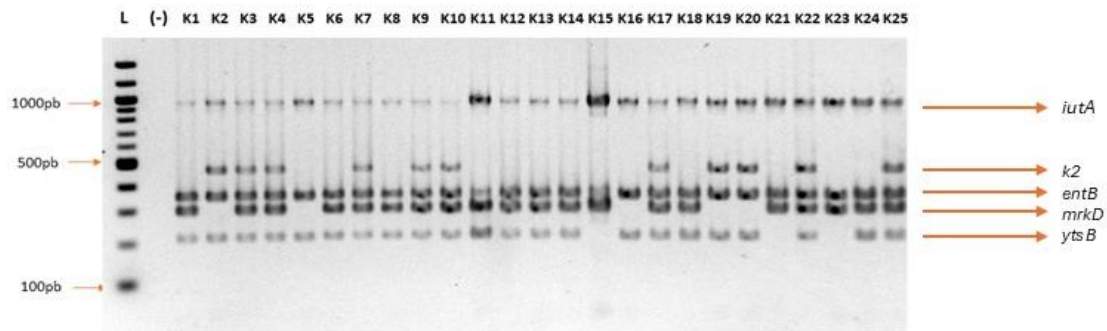


Figure S3. Multiplex PCR for virulence genes. Multiplex PCR assay for the detection of *ytsB* (242 bp), *entB* (400 bp), *iutA* (920 bp), *kfu* (638 bp), *allS* (764 bp), *mrkD* (340 bp), *rmpA* (461 bp), *k2* (531 bp), and *magA* (1283 bp) genes. L: 100 bp ladder; (-): Negative control.

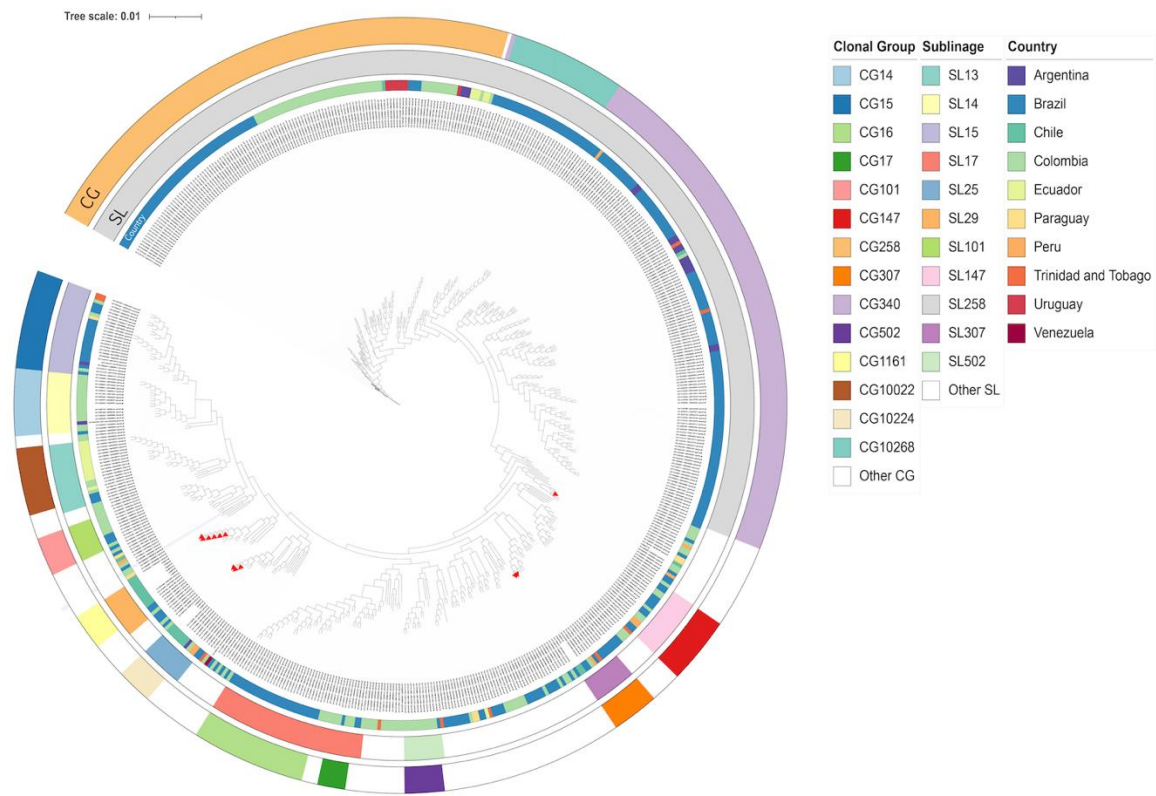


Figure S4. Phylogenetic tree of South American *K. pneumoniae* strains and the CR-Kp strains sequenced and described in this study. Red arrows indicate strains from this study. The figure was created using the IToL platform.

Table S1. Resistance genes identified in CR-Kp isolates. Compiled from the TSV file generated by the **ABRicate** and **Kleborate** platforms.

| GENE | %COVERAGE | %IDENTITY | PRODUCT | STRAIN |
|--------------------|-----------|-----------|--|--------|
| <i>blaSHV-110</i> | 100 | 100 | class A beta-lactamase SHV-110 | K2 |
| <i>fosA6</i> | 100 | 99 | fosfomycin resistance glutathione transferase FosA6 | |
| <i>qnrB19</i> | 100 | 100 | quinolone resistance pentapeptide repeat protein QnrB19 | |
| <i>oqxB17</i> | 100 | 99 | multidrug efflux RND transporter permease subunit OqxB17 | |
| <i>oqxA7</i> | 100 | 100 | multidrug efflux RND transporter periplasmic adaptor subunit OqxA7 | |
| <i>blaNDM-7</i> | 100 | 100 | subclass B1 metallo-beta-lactamase NDM-7 | |
| <i>ble-MBL</i> | 100 | 100 | bleomycin binding protein Ble-MBL | |
| <i>blaCTX-M-2</i> | 100 | 100 | class A extended-spectrum beta-lactamase CTX-M-2 | |
| <i>sul1</i> | 100 | 100 | sulfonamide-resistant dihydropteroate synthase Sul1 | |
| <i>aadA1</i> | 100 | 100 | ANT(3'')-Ia family aminoglycoside nucleotidyltransferase AadA1 | |
| <i>blaOXA-10</i> | 100 | 100 | oxacillin-hydrolyzing class D beta-lactamase OXA-10 | |
| <i>cmlA5</i> | 100 | 100 | chloramphenicol efflux MFS transporter CmlA5 | |
| <i>arr-2</i> | 100 | 100 | NAD(+)-rifampin ADP-ribosyltransferase Arr-2 | |
| <i>dfrA14</i> | 100 | 100 | trimethoprim-resistant dihydrofolate reductase DfrA14 | |
| <i>blaCTX-M-15</i> | 100 | 100 | class A extended-spectrum beta-lactamase CTX-M-15 | |
| <i>blaCTX-M-3</i> | 100.00 | 100.00 | class A extended-spectrum beta-lactamase CTX-M-3 | K5 |
| <i>blaTEM-1</i> | 100.00 | 100.00 | class A broad-spectrum beta-lactamase TEM-1 | |
| <i>blaSHV-187</i> | 100.00 | 100.00 | class A beta-lactamase SHV-187 | |

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|-------------------|--------|--------|--|--|----|
| <i>armA</i> | 100.00 | 100.00 | ArmA family 16S rRNA (guanine(1405)-N(7))-methyltransferase | | |
| <i>msr(E)</i> | 100.00 | 100.00 | ABC-F type ribosomal protection protein Msr(E) | | |
| <i>mph(E)</i> | 100.00 | 100.00 | Mph(E) family macrolide 2'-phosphotransferase | | |
| <i>aadA1</i> | 100.00 | 99.87 | ANT(3'')-Ia family aminoglycoside nucleotidyltransferase AadA1 | | |
| <i>blaOXA-10</i> | 100.00 | 100.00 | oxacillin-hydrolyzing class D beta-lactamase OXA-10 | | |
| <i>cmlA5</i> | 100.00 | 100.00 | chloramphenicol efflux MFS transporter CmlA5 | | |
| <i>arr-2</i> | 100.00 | 100.00 | NAD(+)--rifampin ADP-ribosyltransferase Arr-2 | | |
| <i>blaCTX-M-2</i> | 100.00 | 100.00 | class A extended-spectrum beta-lactamase CTX-M-2 | | |
| <i>aadA2</i> | 100.00 | 100.00 | ANT(3'')-Ia family aminoglycoside nucleotidyltransferase AadA2 | | |
| <i>dfrA12</i> | 100.00 | 100.00 | trimethoprim-resistant dihydrofolate reductase DfrA12 | | |
| <i>fosA6</i> | 100.00 | 99.29 | fosfomicin resistance glutathione transferase FosA6 | | |
| <i>blaCTX-M-3</i> | 100.00 | 100.00 | class A extended-spectrum beta-lactamase CTX-M-3 | | K6 |
| <i>blaTEM-1</i> | 100.00 | 99.88 | class A broad-spectrum beta-lactamase TEM-1 | | |
| <i>blaKPC-2</i> | 100.00 | 100.00 | carbapenem-hydrolyzing class A beta-lactamase KPC-2 | | |
| <i>mph(A)</i> | 100.00 | 99.67 | Mph(A) family macrolide 2'-phosphotransferase | | |
| <i>blaSHV-187</i> | 100.00 | 100.00 | class A beta-lactamase SHV-187 | | |
| <i>mph(E)</i> | 100.00 | 100.00 | Mph(E) family macrolide 2'-phosphotransferase | | |
| <i>msr(E)</i> | 100.00 | 100.00 | ABC-F type ribosomal protection protein Msr(E) | | |
| <i>armA</i> | 100.00 | 100.00 | ArmA family 16S rRNA (guanine(1405)-N(7))-methyltransferase | | |
| <i>aadA1</i> | 100.00 | 99.87 | ANT(3'')-Ia family aminoglycoside nucleotidyltransferase AadA1 | | |
| <i>blaOXA-10</i> | 100.00 | 100.00 | oxacillin-hydrolyzing class D beta-lactamase OXA-10 | | |
| <i>cmlA5</i> | 100.00 | 100.00 | chloramphenicol efflux MFS transporter CmlA5 | | |

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|--------------------|--------|--------|--|-----|
| <i>arr-2</i> | 100.00 | 100.00 | NAD(+)-rifampin ADP-ribosyltransferase Arr-2 | |
| <i>blaCTX-M-2</i> | 100.00 | 100.00 | class A extended-spectrum beta-lactamase CTX-M-2 | |
| <i>aadA2</i> | 100.00 | 100.00 | ANT(3'')-Ia family aminoglycoside nucleotidyltransferase AadA2 | |
| <i>dfrA12</i> | 100.00 | 100.00 | trimethoprim-resistant dihydrofolate reductase DfrA12 | |
| <i>fosA6</i> | 100.00 | 99.29 | fosfomycin resistance glutathione transferase FosA6 | |
| <i>blaSHV-110</i> | 100.00 | 99.77 | class A beta-lactamase SHV-110 | K10 |
| <i>dfrA14</i> | 100.00 | 100.00 | trimethoprim-resistant dihydrofolate reductase DfrA14 | |
| <i>blaCTX-M-30</i> | 100.00 | 99.77 | class A extended-spectrum beta-lactamase CTX-M-30 | |
| <i>qnrB19</i> | 100.00 | 100.00 | quinolone resistance pentapeptide repeat protein QnrB19 | |
| <i>blaOXA-9</i> | 100.00 | 100.00 | oxacillin-hydrolyzing class D beta-lactamase OXA-9 | |
| <i>aadA1</i> | 100.00 | 100.00 | ANT(3'')-Ia family aminoglycoside nucleotidyltransferase AadA1 | |
| <i>blaKPC-2</i> | 100.00 | 100.00 | carbapenem-hydrolyzing class A beta-lactamase KPC-2 | |
| <i>oqxB17</i> | 100.00 | 99.24 | multidrug efflux RND transporter permease subunit OqxB17 | |
| <i>oqxA7</i> | 100.00 | 99.92 | multidrug efflux RND transporter periplasmic adaptor subunit OqxA7 | |
| <i>rmtD2</i> | 100.00 | 100.00 | 16S rRNA (guanine(1405)-N(7))-methyltransferase RmtD2 | |
| <i>floR</i> | 99.84 | 85.24 | chloramphenicol/florfenicol efflux MFS transporter FloR | |
| <i>tet(G)</i> | 100.00 | 94.13 | tetracycline efflux MFS transporter Tet(G) | |
| <i>fosA6</i> | 100.00 | 99.05 | fosfomycin resistance glutathione transferase FosA6 | |
| <i>blaOXA-101</i> | 100.00 | 100.00 | OXA-10 family class D beta-lactamase OXA-101 | |
| <i>blaTEM-150</i> | 100.00 | 99.88 | class A beta-lactamase TEM-150 | |
| <i>sul1</i> | 100.00 | 100.00 | sulfonamide-resistant dihydropteroate synthase Sull | |

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|-------------------|--------|--------|--|-----|
| <i>blaCTX-M-3</i> | 100.00 | 100.00 | class A extended-spectrum beta-lactamase CTX-M-3 | K16 |
| <i>blaCTX-M-2</i> | 100.00 | 100.00 | class A extended-spectrum beta-lactamase CTX-M-2 | |
| <i>blaTEM-1</i> | 100.00 | 100.00 | class A broad-spectrum beta-lactamase TEM-1 | |
| <i>blaSHV-187</i> | 100.00 | 100.00 | class A beta-lactamase SHV-187 | |
| <i>armA</i> | 100.00 | 100.00 | ArmA family 16S rRNA (guanine(1405)-N(7))-methyltransferase | |
| <i>msr(E)</i> | 100.00 | 100.00 | ABC-F type ribosomal protection protein Msr(E) | |
| <i>mph(E)</i> | 100.00 | 100.00 | Mph(E) family macrolide 2'-phosphotransferase | |
| <i>aadA1</i> | 100.00 | 99.87 | ANT(3'')-Ia family aminoglycoside nucleotidyltransferase AadA1 | |
| <i>blaOXA-10</i> | 100.00 | 100.00 | oxacillin-hydrolyzing class D beta-lactamase OXA-10 | |
| <i>cmlA5</i> | 100.00 | 100.00 | chloramphenicol efflux MFS transporter CmlA5 | |
| <i>arr-2</i> | 100.00 | 100.00 | NAD(+)-rifampin ADP-ribosyltransferase Arr-2 | |
| <i>dfrA12</i> | 100.00 | 100.00 | trimethoprim-resistant dihydrofolate reductase DfrA12 | |
| <i>aadA2</i> | 100.00 | 100.00 | ANT(3'')-Ia family aminoglycoside nucleotidyltransferase AadA2 | |
| <i>fosA6</i> | 100.00 | 99.29 | fosfomycin resistance glutathione transferase FosA6 | |
| <i>blaSHV-187</i> | 100.00 | 100.00 | class A beta-lactamase SHV-187 | K24 |
| <i>blaKPC-2</i> | 100.00 | 100.00 | carbapenem-hydrolyzing class A beta-lactamase KPC-2 | |
| <i>armA</i> | 100.00 | 100.00 | ArmA family 16S rRNA (guanine(1405)-N(7))-methyltransferase | |
| <i>msr(E)</i> | 100.00 | 100.00 | ABC-F type ribosomal protection protein Msr(E) | |
| <i>mph(E)</i> | 100.00 | 100.00 | Mph(E) family macrolide 2'-phosphotransferase | |
| <i>blaCTX-M-2</i> | 100.00 | 100.00 | class A extended-spectrum beta-lactamase CTX-M-2 | |
| <i>blaCTX-M-3</i> | 100.00 | 100.00 | class A extended-spectrum beta-lactamase CTX-M-3 | |

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|--------------------|--------|--------|--|-----|
| <i>aadA1</i> | 100.00 | 99.87 | ANT(3'')-Ia family aminoglycoside nucleotidyltransferase AadA1 | |
| <i>blaOXA-10</i> | 100.00 | 100.00 | oxacillin-hydrolyzing class D beta-lactamase OXA-10 | |
| <i>cmlA5</i> | 100.00 | 100.00 | chloramphenicol efflux MFS transporter CmlA5 | |
| <i>arr-2</i> | 100.00 | 100.00 | NAD(+)-rifampin ADP-ribosyltransferase Arr-2 | |
| <i>aadA2</i> | 100.00 | 100.00 | ANT(3'')-Ia family aminoglycoside nucleotidyltransferase AadA2 | |
| <i>dfrA12</i> | 100.00 | 100.00 | trimethoprim-resistant dihydrofolate reductase DfrA12 | |
| <i>blaOXA-9</i> | 100.00 | 99.88 | oxacillin-hydrolyzing class D beta-lactamase OXA-9 | |
| <i>blaTEM-1</i> | 100.00 | 99.77 | class A broad-spectrum beta-lactamase TEM-1 | |
| <i>fosA6</i> | 100.00 | 99.29 | fosfomycin resistance glutathione transferase FosA6 | |
| <i>blaSHV-106</i> | 100.00 | 99.88 | class A extended-spectrum beta-lactamase SHV-106 | K26 |
| <i>mph(E)</i> | 100.00 | 100.00 | Mph(E) family macrolide 2'-phosphotransferase | |
| <i>msr(E)</i> | 100.00 | 100.00 | ABC-F type ribosomal protection protein Msr(E) | |
| <i>armA</i> | 100.00 | 100.00 | ArmA family 16S rRNA (guanine(1405)-N(7))-methyltransferase | |
| <i>sul1</i> | 100.00 | 100.00 | sulfonamide-resistant dihydropteroate synthase Sul1 | |
| <i>aadA2</i> | 100.00 | 100.00 | ANT(3'')-Ia family aminoglycoside nucleotidyltransferase AadA2 | |
| <i>dfrA12</i> | 100.00 | 100.00 | trimethoprim-resistant dihydrofolate reductase DfrA12 | |
| <i>tet(A)</i> | 100.00 | 100.00 | tetracycline efflux MFS transporter Tet(A) | |
| <i>qnrB1</i> | 100.00 | 100.00 | quinolone resistance pentapeptide repeat protein QnrB1 | |
| <i>dfrA14</i> | 100.00 | 100.00 | trimethoprim-resistant dihydrofolate reductase DfrA14 | |
| <i>aph(6)-Id</i> | 100.00 | 100.00 | aminoglycoside O-phosphotransferase APH(6)-Id | |
| <i>aph(3'')-Ib</i> | 100.00 | 100.00 | aminoglycoside O-phosphotransferase APH(3'')-Ib | |
| <i>sul2</i> | 100.00 | 100.00 | sulfonamide-resistant dihydropteroate synthase Sul2 | |
| <i>aac(3)-Ile</i> | 100.00 | 99.77 | aminoglycoside N-acetyltransferase AAC(3)-Ile | |

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|-------------------------|--------|--------|--|-----|
| <i>blaOXA-1</i> | 100.00 | 100.00 | oxacillin-hydrolyzing class D beta-lactamase OXA-1 | |
| <i>aac(6')-Ib-D181Y</i> | 100.00 | 99.82 | AAC(6')-Ib family aminoglycoside 6'-N-acetyltransferase | |
| <i>oqxB19</i> | 100.00 | 99.40 | multidrug efflux RND transporter permease subunit OqxB19 | |
| <i>oqxA5</i> | 100.00 | 99.41 | multidrug efflux RND transporter periplasmic adaptor subunit OqxA5 | |
| <i>blaCTX-M-3</i> | 100.00 | 100.00 | class A extended-spectrum beta-lactamase CTX-M-3 | |
| <i>blaTEM-1</i> | 100.00 | 100.00 | class A broad-spectrum beta-lactamase TEM-1 | |
| <i>fosA6</i> | 100.00 | 99.76 | fosfomycin resistance glutathione transferase FosA6 | |
| <i>blaSHV-106</i> | 100.00 | 99.88 | class A extended-spectrum beta-lactamase SHV-106 | K28 |
| <i>dfrA12</i> | 100.00 | 100.00 | trimethoprim-resistant dihydrofolate reductase DfrA12 | |
| <i>aadA2</i> | 100.00 | 100.00 | ANT(3'')-Ia family aminoglycoside nucleotidyltransferase AadA2 | |
| <i>sul1</i> | 100.00 | 100.00 | sulfonamide-resistant dihydropteroate synthase Sul1 | |
| <i>armA</i> | 100.00 | 100.00 | ArmA family 16S rRNA (guanine(1405)-N(7))-methyltransferase | |
| <i>msr(E)</i> | 100.00 | 100.00 | ABC-F type ribosomal protection protein Msr(E) | |
| <i>mph(E)</i> | 100.00 | 100.00 | Mph(E) family macrolide 2'-phosphotransferase | |
| <i>tet(A)</i> | 100.00 | 100.00 | tetracycline efflux MFS transporter Tet(A) | |
| <i>qnrB1</i> | 100.00 | 100.00 | quinolone resistance pentapeptide repeat protein QnrB1 | |
| <i>dfrA14</i> | 100.00 | 100.00 | trimethoprim-resistant dihydrofolate reductase DfrA14 | |
| <i>sul2</i> | 100.00 | 100.00 | sulfonamide-resistant dihydropteroate synthase Sul2 | |
| <i>aph(3'')-Ib</i> | 100.00 | 100.00 | aminoglycoside O-phosphotransferase APH(3'')-Ib | |
| <i>aph(6)-Id</i> | 100.00 | 100.00 | aminoglycoside O-phosphotransferase APH(6)-Id | |
| <i>aac(3)-Ile</i> | 100.00 | 99.77 | aminoglycoside N-acetyltransferase AAC(3)-Ile | |

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|-------------------------|--------|--------|--|-----|
| <i>aac(6')-Ib-D181Y</i> | 100.00 | 99.82 | AAC(6')-Ib family aminoglycoside 6'-N-acetyltransferase | |
| <i>blaOXA-1</i> | 100.00 | 100.00 | oxacillin-hydrolyzing class D beta-lactamase OXA-1 | |
| <i>blaCTX-M-3</i> | 100.00 | 100.00 | class A extended-spectrum beta-lactamase CTX-M-3 | |
| <i>oqxA5</i> | 100.00 | 99.41 | multidrug efflux RND transporter periplasmic adaptor subunit OqxA5 | |
| <i>oqxB19</i> | 100.00 | 99.40 | multidrug efflux RND transporter permease subunit OqxB19 | |
| <i>blaTEM-1</i> | 100.00 | 100.00 | class A broad-spectrum beta-lactamase TEM-1 | |
| <i>fosA6</i> | 100.00 | 99.76 | fosfomycin resistance glutathione transferase FosA6 | |
| <i>blaSHV-110</i> | 100.00 | 99.77 | class A beta-lactamase SHV-110 | K29 |
| <i>fosA6</i> | 100.00 | 99.05 | fosfomycin resistance glutathione transferase FosA6 | |
| <i>dfrA14</i> | 100.00 | 100.00 | trimethoprim-resistant dihydrofolate reductase DfrA14 | |
| <i>oqxA7</i> | 100.00 | 99.92 | multidrug efflux RND transporter periplasmic adaptor subunit OqxA7 | |
| <i>oqxB17</i> | 100.00 | 99.24 | multidrug efflux RND transporter permease subunit OqxB17 | |
| <i>blaCTX-M-2</i> | 100.00 | 100.00 | class A extended-spectrum beta-lactamase CTX-M-2 | |
| <i>sul1</i> | 100.00 | 100.00 | sulfonamide-resistant dihydropteroate synthase Sul1 | |
| <i>aadA1</i> | 100.00 | 99.87 | ANT(3'')-Ia family aminoglycoside nucleotidyltransferase AadA1 | |
| <i>blaOXA-10</i> | 100.00 | 100.00 | oxacillin-hydrolyzing class D beta-lactamase OXA-10 | |
| <i>cmlA5</i> | 100.00 | 100.00 | chloramphenicol efflux MFS transporter CmlA5 | |
| <i>arr-2</i> | 100.00 | 100.00 | NAD(+)-rifampin ADP-ribosyltransferase Arr-2 | |
| <i>qnrB19</i> | 100.00 | 100.00 | quinolone resistance pentapeptide repeat protein QnrB19 | |
| <i>tet(A)</i> | 100.00 | 100.00 | tetracycline efflux MFS transporter Tet(A) | |
| <i>aph(3'')-Ib</i> | 95.17 | 100.00 | aminoglycoside O-phosphotransferase APH(3'')-Ib | |

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|-------------------------|--------|--------|--|-----|
| <i>aph(6)-Id</i> | 100.00 | 100.00 | aminoglycoside O-phosphotransferase APH(6)-Id | |
| <i>blaTEM-1</i> | 100.00 | 100.00 | class A broad-spectrum beta-lactamase TEM-1 | |
| <i>qnrB1</i> | 100.00 | 100.00 | quinolone resistance pentapeptide repeat protein QnrB1 | |
| <i>aac(3)-Ile</i> | 100.00 | 99.77 | aminoglycoside N-acetyltransferase AAC(3)-Ile | |
| <i>blaOXA-1</i> | 100.00 | 100.00 | oxacillin-hydrolyzing class D beta-lactamase OXA-1 | |
| <i>aac(6')-Ib-D181Y</i> | 100.00 | 99.82 | AAC(6')-Ib family aminoglycoside 6'-N-acetyltransferase | |
| <i>sul2</i> | 100.00 | 100.00 | sulfonamide-resistant dihydropteroate synthase Sul2 | |
| <i>blaCTX-M-3</i> | 100.00 | 100.00 | class A extended-spectrum beta-lactamase CTX-M-3 | K39 |
| <i>blaTEM-1</i> | 100.00 | 100.00 | class A broad-spectrum beta-lactamase TEM-1 | |
| <i>blaSHV-187</i> | 100.00 | 100.00 | class A beta-lactamase SHV-187 | |
| <i>mph(E)</i> | 100.00 | 100.00 | Mph(E) family macrolide 2'-phosphotransferase | |
| <i>msr(E)</i> | 100.00 | 100.00 | ABC-F type ribosomal protection protein Msr(E) | |
| <i>armA</i> | 100.00 | 100.00 | ArmA family 16S rRNA (guanine(1405)-N(7))-methyltransferase | |
| <i>arr-2</i> | 100.00 | 100.00 | NAD(+)-rifampin ADP-ribosyltransferase Arr-2 | |
| <i>cmlA5</i> | 100.00 | 100.00 | chloramphenicol efflux MFS transporter CmlA5 | |
| <i>blaOXA-10</i> | 100.00 | 100.00 | oxacillin-hydrolyzing class D beta-lactamase OXA-10 | |
| <i>aadA1</i> | 100.00 | 99.87 | ANT(3'')-Ia family aminoglycoside nucleotidyltransferase AadA1 | |
| <i>blaCTX-M-2</i> | 100.00 | 100.00 | class A extended-spectrum beta-lactamase CTX-M-2 | |
| <i>aadA2</i> | 100.00 | 100.00 | ANT(3'')-Ia family aminoglycoside nucleotidyltransferase AadA2 | |
| <i>dfrA12</i> | 100.00 | 100.00 | trimethoprim-resistant dihydrofolate reductase DfrA12 | |

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|-------------------------|--------|--------|---|-------|
| <i>fosA6</i> | 100.00 | 99.29 | fosfomycin resistance glutathione transferase FosA6 | |
| <i>blaSHV-145</i> | 100.00 | 99.88 | class A beta-lactamase SHV-145 | K43.1 |
| <i>dfrA14</i> | 100.00 | 100.00 | trimethoprim-resistant dihydrofolate reductase DfrA14 | |
| <i>aac(3)-Ile</i> | 100.00 | 99.77 | aminoglycoside N-acetyltransferase AAC(3)-Ile | |
| <i>qnrB1</i> | 100.00 | 100.00 | quinolone resistance pentapeptide repeat protein QnrB1 | |
| <i>sul2</i> | 100.00 | 100.00 | sulfonamide-resistant dihydropteroate synthase Sul2 | |
| <i>aph(3'')-Ib</i> | 100.00 | 100.00 | aminoglycoside O-phosphotransferase APH(3'')-Ib | |
| <i>aph(6)-Id</i> | 100.00 | 100.00 | aminoglycoside O-phosphotransferase APH(6)-Id | |
| <i>blaTEM-1</i> | 100.00 | 100.00 | class A broad-spectrum beta-lactamase TEM-1 | |
| <i>blaOXA-1</i> | 100.00 | 100.00 | oxacillin-hydrolyzing class D beta-lactamase OXA-1 | |
| <i>aac(6')-Ib-D181Y</i> | 100.00 | 99.82 | AAC(6')-Ib family aminoglycoside 6'-N-acetyltransferase | |
| <i>blaCTX-M-15</i> | 100.00 | 100.00 | class A extended-spectrum beta-lactamase CTX-M-15 | |
| <i>oqxA11</i> | 100.00 | 99.66 | multidrug efflux RND transporter periplasmic adaptor subunit OqxA11 | |
| <i>oqxB20</i> | 100.00 | 99.11 | multidrug efflux RND transporter permease subunit OqxB20 | |
| <i>fosA_gen</i> | 100.00 | 100.00 | FosA family fosfomycin resistance glutathione transferase | |
| <i>blaCTX-M-3</i> | 100.00 | 100.00 | class A extended-spectrum beta-lactamase CTX-M-3 | K43.3 |
| <i>blaTEM-1</i> | 100.00 | 100.00 | class A broad-spectrum beta-lactamase TEM-1 | |
| <i>blaSHV-187</i> | 100.00 | 100.00 | class A beta-lactamase SHV-187 | |
| <i>mph(E)</i> | 100.00 | 100.00 | Mph(E) family macrolide 2'-phosphotransferase | |

| | | | |
|-------------------|--------|--------|--|
| <i>msr(E)</i> | 100.00 | 100.00 | ABC-F type ribosomal protection protein Msr(E) |
| <i>armA</i> | 100.00 | 100.00 | ArmA family 16S rRNA (guanine(1405)-N(7))-methyltransferase |
| <i>arr-2</i> | 100.00 | 100.00 | NAD(+)--rifampin ADP-ribosyltransferase Arr-2 |
| <i>cmlA5</i> | 100.00 | 100.00 | chloramphenicol efflux MFS transporter CmlA5 |
| <i>blaOXA-10</i> | 100.00 | 100.00 | oxacillin-hydrolyzing class D beta-lactamase OXA-10 |
| <i>aadA1</i> | 100.00 | 99.87 | ANT(3'')-Ia family aminoglycoside nucleotidyltransferase AadA1 |
| <i>blaCTX-M-2</i> | 100.00 | 100.00 | class A extended-spectrum beta-lactamase CTX-M-2 |
| <i>aadA2</i> | 100.00 | 100.00 | ANT(3'')-Ia family aminoglycoside nucleotidyltransferase AadA2 |
| <i>dfrA12</i> | 100.00 | 100.00 | trimethoprim-resistant dihydrofolate reductase DfrA12 |
| <i>fosA6</i> | 100.00 | 99.29 | fosfomycin resistance glutathione transferase FosA6 |

Table S2. Kleborate-predicted porin alterations in WGS isolates.

| Strain | OmpK35 alteration | OmpK36 alteration |
|---------------|--------------------------|--------------------------|
| K2 | OmpK35-7% | OmpK36GD |
| K5 | OmpK35-40% | OmpK36GD |
| K6 | OmpK35-40% | OmpK36GD |
| K10 | OmpK35-0% | OmpK36GD |
| K16 | OmpK35-40% | OmpK36GD |
| K24 | OmpK35-40% | OmpK36GD |
| K26 | - | - |
| K28 | - | - |
| K29 | OmpK35-7% | OmpK36GD |
| K39 | OmpK35-40% | - |
| K43.1 | OmpK35-17% | OmpK36-75% |
| K43.3 | OmpK35-40% | OmpK36GD |

Porin alterations in **OmpK35** and **OmpK36** were extracted from Kleborate output for the 12 WGS draft assemblies. Kleborate reports putative truncation/partial hits as a percentage of the expected amino-acid length recovered from the start codon (e.g., **OmpK35-40%** indicates a partial/disrupted locus of ~40% of the expected length). Values close to 0% are consistent with gene loss or severe disruption; however, partial calls can also reflect contig fragmentation in draft assemblies. **OmpK36GD** denotes the Gly-Asp (GD) insertion in the OmpK36 loop 3 (L3) constriction region, which narrows the pore and can reduce β -lactam (including carbapenem) influx. A dash (–) indicates that no porin alteration was flagged by Kleborate for that isolate.

Table S3. K-locus and O-locus assignment of sequenced isolates. Compiled from the TSV file generated by the Kleborate platform.

| Code | K_locus | K_type | O_locus | O_type |
|-------|---------|--------|---------|--------|
| K10 | KL2 | K2 | O1/O2v2 | O1 |
| K16 | KL19 | K19 | O1/O2v2 | O2afg |
| K2 | KL2 | K2 | O1/O2V2 | O4 |
| K24 | KL19 | K19 | O1/O2v2 | O2a |
| K26 | KL102 | KL102 | O1/O2v2 | O4 |
| K28 | KL102 | KL102 | O1/O2v2 | O4 |
| K29 | KL2 | K2 | O1/O2v2 | O4 |
| K39 | KL19 | K19 | O1/O2v2 | O1 |
| K43.1 | KL62 | K62 | O1/O2v1 | O4 |
| K43.3 | KL19 | K19 | O1/O2v2 | O2afg |
| K5 | KL19 | K19 | O1/O2v2 | O2a |
| K6 | KL19 | K19 | O1/O2v2 | O4 |

Table S4. Clinical and epidemiological characterization of 26 patients included in this study.

| Age (years) | n (%) |
|------------------------------|--------------|
| Mean \pm SD (years) | 59 \pm 16 |
| < 45 years | 7 (27) |
| 45-75 years | 13 (50) |
| > 75 years | 6 (23) |
| Sex | n (%) |
| Male | 14 (54) |
| Female | 12 (46) |
| Prior hospitalization | n (%) |
| Same facility | 3 (50) |
| Different facility | 3 (50) |
| Length of stay (days) | n (%) |
| Mean \pm SD | 85 \pm 60 |
| Originating unit | n (%) |
| ICU-2C | 31 |
| ICU-3A | 3 |
| IMCU | 3 |
| ISCU | 5 |
| Acute Stroke Unit | 1 |
| Internal Medicine Unit | 1 |
| Emergency Room | 1 |
| Specimen Source | n (%) |
| Endotracheal Aspirate | 5 (11) |
| Rectal Swab | 27 (60) |
| Blood Culture | 2 (4) |
| Urine Culture | 4 (9) |
| Oropharyngeal Aspirate | 4 (9) |
| IAC | 1 (2) |
| Fomite | 1 (2) |
| Ascitic fluid | 1 (2) |
| Comorbidities | n (%) |
| Arterial hypertension | 12 (46) |
| Type 2 diabetes mellitus | 5 (19) |
| Chronic kidney disease | 5 (19) |
| Dyslipidemia | 1 (4) |
| Obesity | 1 (4) |
| Hypothyroidism | 1 (4) |
| Stroke | 3 (12) |
| Coronary artery disease | 1 (4) |
| Chronic liver disease | 4 (15) |

| | |
|---------------------------------|--------------|
| Chronic GI conditions | 2 (8) |
| COPD | 3 (12) |
| Asthma | 1 (4) |
| Immunodeficiencies | 2 (8) |
| Cancer | 3 (12) |
| Substance abuse | 2 (8) |
| Invasive Procedures | n (%) |
| Surgery | 13 (50) |
| Enteroscopy | 5 (19) |
| Bronchoalveolar lavage | 2 (8) |
| Invasive Medical Devices | n (%) |
| Endotracheal/tracheostomy tube | 23 (88) |
| CVC/PICCl ine | 25 (96) |
| Drains / Ostomies | 7 (27) |
| Indwelling urinary catheter | 25 (96) |
| Antibiotic Treatment | n (%) |
| Yes | 26 (100) |
| No | 0 (0) |
| Outcome | n (%) |
| Survived | 18 (69) |
| Died | 8 (31) |

Abbreviations: SD, Standard deviation; ICU, Intensive care unit; IMCU, Intermediate medical care unit; ISCU, Intermediate surgical care unit; IAC, Intra-abdominal collection; GI, Gastrointestinal; COPD, Chronic obstructive pulmonary disease; CVC, Central venous catheter.

Table S5. Extract of Fisher's exact test results. Statistical significance level: p -value < 0.05. Compiled from the CSV file generated in RStudio, version 2024.09.0+375.

| Factor | <i>blaTEM</i> (-) | <i>blaTEM</i> (+) | <i>p</i>-value |
|------------------------|--------------------------|--------------------------|-----------------------|
| Surgery | 0 (0%) | 20 (51%) | 0.053 |
| Bronchoalveolar lavage | 1 (20%) | 4 (10%) | 0.47 |
| Enteroscopy | 3 (60%) | 6 (15%) | 0.050 |

Table S6. Antibiotics used for susceptibility testing.

| Antibiotic family | Antibiotic name | Abbreviations |
|--------------------------|---|----------------------|
| Cephalosporins | Cefazolin | KZ |
| | Ceftazidime | CAZ |
| | Cefotaxime | CTX |
| | Ceftazidime/Clavulanic acid (for ESBL test) | CAL |
| | Cefotaxime /Clavulanic acid (for ESBL test) | CLT |
| Fluoroquinolones | Ciprofloxacin | CIP |
| | Levofloxacin | LEV |
| Sulfonamides | Trimethoprim/Sulfamethoxazole | SXT |
| Aminoglycosides | Amikacin | AK |
| | Gentamicin | CN |
| Penicillins | Ampicillin/Sulbactam | SAM |
| | Piperacillin/Tazobactam | TZP |
| Carbapenems | Imipenem | IMI |
| | Ertapenem | ETP |
| | Meropenem | MEM |
| Tetracyclines | Tetracycline | TE |

Table S7. Primers for carbapenemase gene detection (adapted from Candan & Aksöz, 2015; Poirel *et al.*, 2011).

| Primers | Sequence (5' a 3') | Amplicon size |
|-------------------|---------------------------|----------------------|
| <i>blaKPC_F</i> | CGTCTAGTTCTGCTGTCTTG | 798 pb |
| <i>blaKPC_R</i> | CTTGTCATCCTTGTTAGGCG | |
| <i>blaNDM_F</i> | GGTTTGGCGATCTGGTTTTC | 621 pb |
| <i>blaNDM_R</i> | CGGAATGGCTCATCACGATC | |
| <i>blaOXA48_F</i> | GCGTGGTTAAGGATGAACAC | 438 pb |
| <i>blaOXA48_R</i> | CATCAAGTTCAACCCAACCG | |
| <i>blaIMP_F</i> | GGAATAGAGTGGCTTAAYTCTC | 232 pb |
| <i>blaIMP_R</i> | GGTTTAAAYAAAACAACCACC | |
| <i>blaVIM_F</i> | GATGGTGGTTTGGTCGCATA | 390 pb |
| <i>blaVIM_R</i> | CGAATGCGCAGCACCAG | |

Table S8. Primers for ESBL gene detection (adapted from Trung *et al.*, 2015).

| Primers | Sequences (5' a 3') | Amplicon size |
|-------------------|-------------------------------------|----------------------|
| <i>blaCTX-M_F</i> | ATGTGCAGYACCAGTAARGTKATGGC | 590 pb |
| <i>blaCTX-M_R</i> | GGTRAARTARGTSACCAGAAAYCAGCGG | |
| <i>blaTEM_F</i> | TCGCCGCATACACTATTCTCAGAATGAC | 422 pb |
| <i>blaTEM_R</i> | CAGCAATAAACCAGCCAGCCGGAAG | |
| <i>blaSHV_F</i> | TGTATTATCTC(C/T)CTGTTAGCC(A/G)CCCTG | 739 pb |
| <i>blaSHV_R</i> | GCTCTGCTTTGTTATTCGGGCCAAGC | |

Table S9. Primers used in this study for the detection frequency of genes identified as virulence factors in *K. pneumoniae* (adapted from Compain *et al.*, 2014).

| Primer | Sequence (5' to 3') | Gene Product/Function | Amplicon Size |
|---------------|------------------------------|--|----------------------|
| <i>ybtS_F</i> | GACGGAAACAGCACGGTAAA | Siderophore (yersiniabactin) | 242 pb |
| <i>ybtS_R</i> | GAGCATAATAAGGCGAAAGA | | |
| <i>entB_F</i> | GTCAACTGGGCCTTTGAGCCGTC | Siderophore (enterobactin) | 400 pb |
| <i>entB_R</i> | TATGGGCGTAAACGCCGGTGAT | | |
| <i>iutA_F</i> | GGGAAAGGCTTCTCTGCCAT | Siderophore (aerobactin) | 920 pb |
| <i>iutA_R</i> | TTATTCGCCACCACGCTCTT | | |
| <i>kfu_F</i> | GGCCTTTGTCCAGAGCTACG | Iron transport and phosphotransferase function | 638 pb |
| <i>kfu_R</i> | GGGTCTGGCGCAGAGTATGC | | |
| <i>mrkD_F</i> | AAGCTATCGCTGTACTTCCGGCA | Type 3 fimbrial adhesin | 340 pb |
| <i>mrkD_R</i> | GGCGTTGGCGCTCAGATAGG | | |
| <i>allS_F</i> | CATTACGCACCTTTGTCAGC | Allantoin metabolism | 764 pb |
| <i>allS_R</i> | GAATGTGTCGGCGATCAGCTT | | |
| <i>rmpA_F</i> | CATAAGAGTATTGGTTGACAG | Regulator of mucoid phenotype A | 461 pb |
| <i>rmpA_R</i> | CTTGCATGAGCCATCTTTCA | | |
| <i>k2_F</i> | CAACCATGGTGGTCGATTAG | Capsular serotype K2 | 531 pb |
| <i>k2_R</i> | TGGTAGCCATATCCCTTTGG | | |
| <i>magA_F</i> | GGTGCTCTTTACATCATTGC | Capsular serotype K1 | 1238 pb |
| <i>magA_R</i> | GCAATGGCCATTTGCGTTAG | | |

Table S10. RefSeq genomes included in the regional *Klebsiella pneumoniae* phylogenetic analyses. Genomes were retrieved from the NCBI RefSeq database. “ID” corresponds to the file/label used in downstream analyses (e.g., FASTA filename), whereas “Assembly accession” corresponds to the RefSeq assembly accession. cgLIN codes were assigned using the cgMLST-based hierarchical nomenclature framework (Hennart et al., 2022).

| ID | Assembly accession | Country | cgLIN code | Species |
|---|--------------------|-----------|-------------------------|------------------------------|
| GCF_000316265.2_MTE1_ImprovedAssembly_genomic | GCF_000316265.2 | Argentina | 0 0 1 1 0 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_000512165.1_ASM51216v1_genomic | GCF_000512165.1 | Brazil | 0 0 152 0 0 0 1 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_000807515.1_ASM80751v2_genomic | GCF_000807515.1 | Colombia | 0 0 197 0 25 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_001701895.1_ASM170189v1_genomic | GCF_001701895.1 | Brazil | 0 0 105 0 0 0 1 1 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_001701915.1_ASM170191v1_genomic | GCF_001701915.1 | Brazil | 0 0 105 1 1 1 7 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_001718115.2_ASM171811v2_genomic | GCF_001718115.2 | Brazil | 0 0 105 0 11 0 0 0 1 0 | <i>Klebsiella pneumoniae</i> |
| GCF_001718175.1_ASM171817v1_genomic | GCF_001718175.1 | Brazil | 0 0 105 0 11 0 0 8 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_001907955.1_ASM190795v1_genomic | GCF_001907955.1 | Brazil | 0 0 407 0 0 0 0 1 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002104175.1_ASM210417v1_genomic | GCF_002104175.1 | Brazil | 0 0 105 0 11 0 6 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002104185.1_ASM210418v1_genomic | GCF_002104185.1 | Brazil | 0 0 105 6 0 0 69 0 1 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002104215.1_ASM210421v1_genomic | GCF_002104215.1 | Brazil | 0 0 105 0 0 0 1 2 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002104255.1_ASM210425v1_genomic | GCF_002104255.1 | Brazil | 0 0 105 0 11 0 12 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002104265.1_ASM210426v1_genomic | GCF_002104265.1 | Brazil | 0 0 105 6 0 0 69 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002104295.1_ASM210429v1_genomic | GCF_002104295.1 | Brazil | 0 0 105 6 0 0 69 0 1 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002104315.1_ASM210431v1_genomic | GCF_002104315.1 | Brazil | 0 0 105 0 0 0 2 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002104355.1_ASM210435v1_genomic | GCF_002104355.1 | Brazil | 0 0 105 0 0 0 10 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002104365.1_ASM210436v1_genomic | GCF_002104365.1 | Brazil | 0 0 105 0 11 0 12 0 1 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002119885.1_ASM211988v1_genomic | GCF_002119885.1 | Colombia | 0 0 105 6 0 0 17 58 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002119895.1_ASM211989v1_genomic | GCF_002119895.1 | Colombia | 0 0 105 6 0 0 26 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002119955.1_ASM211995v1_genomic | GCF_002119955.1 | Colombia | 0 0 1 1 0 1 1 0 0 2 | <i>Klebsiella pneumoniae</i> |
| GCF_002120065.1_ASM212006v1_genomic | GCF_002120065.1 | Colombia | 0 0 105 6 0 0 77 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002120105.1_ASM212010v1_genomic | GCF_002120105.1 | Colombia | 0 0 105 6 0 0 17 57 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002154825.1_ASM215482v1_genomic | GCF_002154825.1 | Brazil | 0 0 105 0 11 0 5 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002157345.1_ASM215734v1_genomic | GCF_002157345.1 | Brazil | 0 0 407 0 0 0 0 0 1 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002192975.1_ASM219297v1_genomic | GCF_002192975.1 | Brazil | 0 0 105 0 11 0 6 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002241035.1_ASM224103v1_genomic | GCF_002241035.1 | Brazil | 0 0 407 0 0 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002251715.1_ASM225171v1_genomic | GCF_002251715.1 | Brazil | 0 0 105 1 1 1 4 1 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002283495.1_ASM228349v1_genomic | GCF_002283495.1 | Colombia | 0 0 369 0 0 0 0 0 20 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002529065.1_ASM252906v1_genomic | GCF_002529065.1 | Brazil | 0 0 105 0 0 0 7 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002529075.1_ASM252907v1_genomic | GCF_002529075.1 | Brazil | 0 0 105 0 0 0 1 0 1 0 | <i>Klebsiella pneumoniae</i> |

| | | | | |
|-------------------------------------|-----------------|----------|--------------------------|------------------------------|
| GCF_002631045.1_ASM263104v1_genomic | GCF_002631045.1 | Brazil | 0 0 152 0 0 1 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002834285.1_ASM283428v1_genomic | GCF_002834285.1 | Peru | 0 0 105 0 11 2 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002850795.1_ASM285079v1_genomic | GCF_002850795.1 | Colombia | 0 0 419 0 0 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002850805.1_ASM285080v1_genomic | GCF_002850805.1 | Colombia | 0 0 1 1 0 1 1 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002850835.1_ASM285083v1_genomic | GCF_002850835.1 | Colombia | 0 0 108 3 0 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002850845.1_ASM285084v1_genomic | GCF_002850845.1 | Colombia | 0 0 13 11 0 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002850875.1_ASM285087v1_genomic | GCF_002850875.1 | Colombia | 0 0 22 30 0 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002850885.1_ASM285088v1_genomic | GCF_002850885.1 | Colombia | 0 0 1 1 0 1 1 0 0 3 | <i>Klebsiella pneumoniae</i> |
| GCF_002850915.1_ASM285091v1_genomic | GCF_002850915.1 | Colombia | 0 0 107 0 1 4 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002850935.1_ASM285093v1_genomic | GCF_002850935.1 | Colombia | 0 0 1 1 0 1 1 0 0 1 | <i>Klebsiella pneumoniae</i> |
| GCF_002850955.1_ASM285095v1_genomic | GCF_002850955.1 | Colombia | 0 0 1 1 9 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002850965.1_ASM285096v1_genomic | GCF_002850965.1 | Colombia | 0 0 147 1 0 4 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002850995.1_ASM285099v1_genomic | GCF_002850995.1 | Colombia | 0 0 127 1 0 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002851015.1_ASM285101v1_genomic | GCF_002851015.1 | Colombia | 0 0 0 0 16 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002851035.1_ASM285103v1_genomic | GCF_002851035.1 | Colombia | 0 0 105 6 0 0 17 114 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002851055.1_ASM285105v1_genomic | GCF_002851055.1 | Colombia | 0 0 123 1 0 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002851115.1_ASM285111v1_genomic | GCF_002851115.1 | Colombia | 0 0 276 0 0 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002851135.1_ASM285113v1_genomic | GCF_002851135.1 | Colombia | 0 0 111 0 5 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002851155.1_ASM285115v1_genomic | GCF_002851155.1 | Colombia | 0 0 152 0 2 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002851175.1_ASM285117v1_genomic | GCF_002851175.1 | Colombia | 0 0 105 10 0 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002851195.1_ASM285119v1_genomic | GCF_002851195.1 | Colombia | 0 0 98 0 1 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002851215.1_ASM285121v1_genomic | GCF_002851215.1 | Colombia | 0 0 300 1 0 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002851245.1_ASM285124v1_genomic | GCF_002851245.1 | Colombia | 0 0 104 0 0 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002851275.1_ASM285127v1_genomic | GCF_002851275.1 | Colombia | 0 0 94 2 1 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002851335.1_ASM285133v1_genomic | GCF_002851335.1 | Colombia | 0 0 41 0 0 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002851345.1_ASM285134v1_genomic | GCF_002851345.1 | Colombia | 0 0 84 0 8 0 0 9 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002851375.1_ASM285137v1_genomic | GCF_002851375.1 | Colombia | 0 0 105 0 6 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002851395.1_ASM285139v1_genomic | GCF_002851395.1 | Colombia | 0 0 107 2 0 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002851435.1_ASM285143v1_genomic | GCF_002851435.1 | Colombia | 0 0 1 1 0 1 1 0 2 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002851455.1_ASM285145v1_genomic | GCF_002851455.1 | Colombia | 0 0 22 24 1 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002851475.1_ASM285147v1_genomic | GCF_002851475.1 | Colombia | 0 0 137 0 1 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002851495.1_ASM285149v1_genomic | GCF_002851495.1 | Colombia | 0 0 46 8 0 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002851515.1_ASM285151v1_genomic | GCF_002851515.1 | Colombia | 0 0 250 0 4 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002851525.1_ASM285152v1_genomic | GCF_002851525.1 | Colombia | 0 0 361 0 0 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |

| | | | | |
|-------------------------------------|-----------------|----------|-------------------------|------------------------------|
| GCF 002851555.1 ASM285155v1 genomic | GCF 002851555.1 | Colombia | 0 0 1 1 0 1 1 0 2 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002851575.1 ASM285157v1 genomic | GCF 002851575.1 | Colombia | 0 0 260 0 0 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002851615.1 ASM285161v1 genomic | GCF 002851615.1 | Colombia | 0 0 240 0 0 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002853565.1 ASM285356v1 genomic | GCF 002853565.1 | Colombia | 0 0 67 0 0 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002853595.1 ASM285359v1 genomic | GCF 002853595.1 | Colombia | 0 0 220 7 4 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002853725.1 ASM285372v1 genomic | GCF 002853725.1 | Colombia | 0 0 47 0 2 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002853735.1 ASM285373v1 genomic | GCF 002853735.1 | Colombia | 0 0 131 1 23 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002853795.1 ASM285379v1 genomic | GCF 002853795.1 | Colombia | 0 0 237 1 0 1 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002853815.1 ASM285381v1 genomic | GCF 002853815.1 | Colombia | 0 0 22 2 16 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002853825.1 ASM285382v1 genomic | GCF 002853825.1 | Colombia | 0 0 22 24 10 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002853895.1 ASM285389v1 genomic | GCF 002853895.1 | Colombia | 0 0 29 1 0 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002853915.1 ASM285391v1 genomic | GCF 002853915.1 | Colombia | 0 0 334 0 1 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002853935.1 ASM285393v1 genomic | GCF 002853935.1 | Colombia | 0 0 194 0 0 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002853955.1 ASM285395v1 genomic | GCF 002853955.1 | Colombia | 0 0 23 0 0 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002853975.1 ASM285397v1 genomic | GCF 002853975.1 | Colombia | 0 0 1 1 14 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002854015.1 ASM285401v1 genomic | GCF 002854015.1 | Colombia | 0 0 1 1 0 1 1 0 1 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002854035.1 ASM285403v1 genomic | GCF 002854035.1 | Colombia | 0 0 116 0 0 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002854055.1 ASM285405v1 genomic | GCF 002854055.1 | Colombia | 0 0 108 4 0 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002854085.1 ASM285408v1 genomic | GCF 002854085.1 | Colombia | 0 0 98 0 5 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002854115.1 ASM285411v1 genomic | GCF 002854115.1 | Colombia | 0 0 253 0 0 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002854135.1 ASM285413v1 genomic | GCF 002854135.1 | Colombia | 0 0 28 0 0 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002854145.1 ASM285414v1 genomic | GCF 002854145.1 | Colombia | 0 0 253 0 0 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002854175.1 ASM285417v1 genomic | GCF 002854175.1 | Colombia | 0 0 238 0 0 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002854195.1 ASM285419v1 genomic | GCF 002854195.1 | Colombia | 0 0 197 0 4 0 0 0 1 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002854215.1 ASM285421v1 genomic | GCF 002854215.1 | Colombia | 0 0 0 0 2 1 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002854235.1 ASM285423v1 genomic | GCF 002854235.1 | Colombia | 0 0 105 6 0 0 17 42 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002854255.1 ASM285425v1 genomic | GCF 002854255.1 | Colombia | 0 0 28 0 1 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002854275.1 ASM285427v1 genomic | GCF 002854275.1 | Colombia | 0 0 105 6 0 0 17 16 8 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002854285.1 ASM285428v1 genomic | GCF 002854285.1 | Colombia | 0 0 22 30 1 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002854295.1 ASM285429v1 genomic | GCF 002854295.1 | Colombia | 0 0 105 6 0 0 17 16 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002854335.1 ASM285433v1 genomic | GCF 002854335.1 | Colombia | 0 0 105 6 0 0 17 16 9 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002854355.1 ASM285435v1 genomic | GCF 002854355.1 | Colombia | 0 0 84 0 8 0 3 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002854375.1 ASM285437v1 genomic | GCF 002854375.1 | Colombia | 0 0 105 6 0 0 17 16 7 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002854385.1 ASM285438v1 genomic | GCF 002854385.1 | Colombia | 0 0 105 6 0 0 17 16 0 0 | <i>Klebsiella pneumoniae</i> |

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|-------------------------------------|-----------------|----------|-------------------------|------------------------------|
| GCF 002854415.1 ASM285441v1 genomic | GCF 002854415.1 | Colombia | 0 0 105 6 0 0 17 16 2 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002854435.1 ASM285443v1 genomic | GCF 002854435.1 | Colombia | 0 0 105 6 0 0 17 41 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002854455.1 ASM285445v1 genomic | GCF 002854455.1 | Colombia | 0 0 105 6 0 0 17 53 1 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002854465.1 ASM285446v1 genomic | GCF 002854465.1 | Colombia | 0 0 105 6 0 0 17 16 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002854495.1 ASM285449v1 genomic | GCF 002854495.1 | Colombia | 0 0 105 6 0 0 17 16 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002854515.1 ASM285451v1 genomic | GCF 002854515.1 | Colombia | 0 0 197 0 4 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002854525.1 ASM285452v1 genomic | GCF 002854525.1 | Colombia | 0 0 105 6 0 0 17 53 1 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002854575.1 ASM285457v1 genomic | GCF 002854575.1 | Colombia | 0 0 1 1 0 1 1 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002854585.1 ASM285458v1 genomic | GCF 002854585.1 | Colombia | 0 0 158 8 0 0 7 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002854635.1 ASM285463v1 genomic | GCF 002854635.1 | Colombia | 0 0 158 8 0 0 5 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002854655.1 ASM285465v1 genomic | GCF 002854655.1 | Colombia | 0 0 197 0 0 0 0 2 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002854675.1 ASM285467v1 genomic | GCF 002854675.1 | Colombia | 0 0 22 24 7 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002854695.1 ASM285469v1 genomic | GCF 002854695.1 | Colombia | 0 0 84 0 8 0 0 9 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002854715.1 ASM285471v1 genomic | GCF 002854715.1 | Colombia | 0 0 84 0 8 0 0 9 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002854735.1 ASM285473v1 genomic | GCF 002854735.1 | Colombia | 0 0 105 6 0 0 17 16 1 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002854745.1 ASM285474v1 genomic | GCF 002854745.1 | Colombia | 0 0 94 1 2 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002854815.1 ASM285481v1 genomic | GCF 002854815.1 | Colombia | 0 0 197 0 0 0 0 1 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002854835.1 ASM285483v1 genomic | GCF 002854835.1 | Colombia | 0 0 23 1 4 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002854855.1 ASM285485v1 genomic | GCF 002854855.1 | Colombia | 0 0 52 4 1 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002854865.1 ASM285486v1 genomic | GCF 002854865.1 | Colombia | 0 0 105 6 0 0 17 16 6 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002854895.1 ASM285489v1 genomic | GCF 002854895.1 | Colombia | 0 0 105 6 0 0 17 16 5 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002854915.1 ASM285491v1 genomic | GCF 002854915.1 | Colombia | 0 0 98 0 5 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002854935.1 ASM285493v1 genomic | GCF 002854935.1 | Colombia | 0 0 23 0 0 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002854955.1 ASM285495v1 genomic | GCF 002854955.1 | Colombia | 0 0 84 0 8 0 3 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002854975.1 ASM285497v1 genomic | GCF 002854975.1 | Colombia | 0 0 105 6 0 0 17 16 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002854995.1 ASM285499v1 genomic | GCF 002854995.1 | Colombia | 0 0 105 6 0 0 17 16 4 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002855015.1 ASM285501v1 genomic | GCF 002855015.1 | Colombia | 0 0 410 0 3 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002855035.1 ASM285503v1 genomic | GCF 002855035.1 | Colombia | 0 0 105 6 0 0 17 16 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002855045.1 ASM285504v1 genomic | GCF 002855045.1 | Colombia | 0 0 105 6 0 0 17 16 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002855075.1 ASM285507v1 genomic | GCF 002855075.1 | Colombia | 0 0 105 6 0 0 17 16 3 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002855115.1 ASM285511v1 genomic | GCF 002855115.1 | Colombia | 0 0 105 6 0 0 17 16 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002855125.1 ASM285512v1 genomic | GCF 002855125.1 | Colombia | 0 0 105 6 0 0 17 16 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002855155.1 ASM285515v1 genomic | GCF 002855155.1 | Colombia | 0 0 108 3 0 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 002855175.1 ASM285517v1 genomic | GCF 002855175.1 | Colombia | 0 0 22 2 19 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |

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| GCF_002855195.1_ASM285519v1_genomic | GCF_002855195.1 | Colombia | 0 0 105 6 0 0 17 16 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002855215.1_ASM285521v1_genomic | GCF_002855215.1 | Colombia | 0 0 105 6 0 0 17 56 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002855255.1_ASM285525v1_genomic | GCF_002855255.1 | Colombia | 0 0 1 1 0 1 1 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002855275.1_ASM285527v1_genomic | GCF_002855275.1 | Colombia | 0 0 105 6 0 0 87 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002855295.1_ASM285529v1_genomic | GCF_002855295.1 | Colombia | 0 0 1 1 0 1 1 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002855315.1_ASM285531v1_genomic | GCF_002855315.1 | Colombia | 0 0 84 0 8 0 0 9 1 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002855375.1_ASM285537v1_genomic | GCF_002855375.1 | Colombia | 0 0 48 0 0 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002855395.1_ASM285539v1_genomic | GCF_002855395.1 | Colombia | 0 0 22 24 7 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002887435.2_ASM288743v2_genomic | GCF_002887435.2 | Brazil | 0 0 105 0 11 0 0 13 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002929175.1_ASM292917v1_genomic | GCF_002929175.1 | Brazil | 0 0 6 0 1 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002951555.1_ASM295155v1_genomic | GCF_002951555.1 | Brazil | 0 0 105 1 1 1 0 15 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_002951595.1_ASM295159v1_genomic | GCF_002951595.1 | Brazil | 0 0 105 1 1 1 0 1 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_003095455.1_ASM309545v1_genomic | GCF_003095455.1 | Brazil | 0 0 105 6 0 90 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_003095475.1_ASM309547v1_genomic | GCF_003095475.1 | Brazil | 0 0 388 1 32 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_003095495.1_ASM309549v1_genomic | GCF_003095495.1 | Brazil | 0 0 105 6 0 0 373 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_003095515.1_ASM309551v1_genomic | GCF_003095515.1 | Brazil | 0 0 105 6 0 0 374 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_003095615.1_ASM309561v1_genomic | GCF_003095615.1 | Brazil | 0 0 152 0 14 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_003097475.1_ASM309747v1_genomic | GCF_003097475.1 | Brazil | 0 0 366 0 0 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_003194695.1_ASM319469v1_genomic | GCF_003194695.1 | Brazil | 0 0 369 0 0 0 0 20 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_003194705.1_ASM319470v1_genomic | GCF_003194705.1 | Brazil | 0 0 369 0 0 0 0 6 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_003284835.1_ASM328483v1_genomic | GCF_003284835.1 | Brazil | 0 0 105 0 0 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_003318315.1_ASM331831v1_genomic | GCF_003318315.1 | Brazil | 0 0 109 1 19 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_003321095.1_ASM332109v1_genomic | GCF_003321095.1 | Brazil | 0 0 22 27 5 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_003321135.1_ASM332113v1_genomic | GCF_003321135.1 | Brazil | 0 0 105 6 0 0 69 0 2 0 | <i>Klebsiella pneumoniae</i> |
| GCF_003321155.1_ASM332115v1_genomic | GCF_003321155.1 | Brazil | 0 0 105 0 0 0 0 1 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_003321195.1_ASM332119v1_genomic | GCF_003321195.1 | Brazil | 0 0 105 0 25 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_003321215.1_ASM332121v1_genomic | GCF_003321215.1 | Brazil | 0 0 105 0 0 0 0 2 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_003321225.1_ASM332122v1_genomic | GCF_003321225.1 | Brazil | 0 0 105 0 24 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_003321235.1_ASM332123v1_genomic | GCF_003321235.1 | Brazil | 0 0 105 0 24 0 3 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_003321255.1_ASM332125v1_genomic | GCF_003321255.1 | Brazil | 0 0 105 0 11 0 12 0 2 0 | <i>Klebsiella pneumoniae</i> |
| GCF_003321295.1_ASM332129v1_genomic | GCF_003321295.1 | Brazil | 0 0 105 0 0 0 8 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_003321305.1_ASM332130v1_genomic | GCF_003321305.1 | Brazil | 0 0 105 0 11 0 6 0 1 0 | <i>Klebsiella pneumoniae</i> |
| GCF_003321315.1_ASM332131v1_genomic | GCF_003321315.1 | Brazil | 0 0 105 0 0 0 9 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_003321335.1_ASM332133v1_genomic | GCF_003321335.1 | Brazil | 0 0 105 0 11 0 6 0 0 0 | <i>Klebsiella pneumoniae</i> |

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| GCF_003321375.1_ASM332137v1_genomic | GCF_003321375.1 | Brazil | 0 0 105 0 11 0 6 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_003321385.1_ASM332138v1_genomic | GCF_003321385.1 | Brazil | 0 0 105 0 11 0 0 12 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_003325525.1_ASM332552v1_genomic | GCF_003325525.1 | Brazil | 0 0 152 0 1 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_003326285.1_ASM332628v1_genomic | GCF_003326285.1 | Brazil | 0 0 105 6 7 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_003326295.1_ASM332629v1_genomic | GCF_003326295.1 | Brazil | 0 0 105 0 0 3 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_003326305.1_ASM332630v1_genomic | GCF_003326305.1 | Brazil | 0 0 105 6 0 0 70 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_003326315.1_ASM332631v1_genomic | GCF_003326315.1 | Brazil | 0 0 105 6 0 0 69 1 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_003326365.1_ASM332636v1_genomic | GCF_003326365.1 | Brazil | 0 0 105 6 0 15 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_003326375.1_ASM332637v1_genomic | GCF_003326375.1 | Brazil | 0 0 105 1 2 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_003326385.1_ASM332638v1_genomic | GCF_003326385.1 | Brazil | 0 0 105 0 0 10 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_003326395.1_ASM332639v1_genomic | GCF_003326395.1 | Brazil | 0 0 22 27 3 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_003327585.1_ASM332758v1_genomic | GCF_003327585.1 | Brazil | 0 0 105 0 11 0 0 4 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_003574335.1_ASM357433v1_genomic | GCF_003574335.1 | Uruguay | 0 0 105 6 0 0 0 93 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_003576025.1_ASM357602v1_genomic | GCF_003576025.1 | Brazil | 0 0 105 0 11 0 10 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_004284565.1_ASM428456v1_genomic | GCF_004284565.1 | Brazil | 0 0 105 0 11 3 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_005222595.1_ASM522259v1_genomic | GCF_005222595.1 | Brazil | 0 0 0 0 2 0 163 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_006152045.1_ASM615204v1_genomic | GCF_006152045.1 | Brazil | 0 0 137 6 0 0 0 0 3 0 | <i>Klebsiella pneumoniae</i> |
| GCF_006152055.2_ASM615205v2_genomic | GCF_006152055.2 | Brazil | 0 0 751 0 0 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_006152075.1_ASM615207v1_genomic | GCF_006152075.1 | Brazil | 0 0 137 6 0 0 0 0 3 1 | <i>Klebsiella pneumoniae</i> |
| GCF_006335135.1_ASM633513v1_genomic | GCF_006335135.1 | Chile | 0 0 105 6 0 0 375 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_006517515.1_ASM651751v1_genomic | GCF_006517515.1 | Brazil | 0 0 105 0 9 0 0 28 1 0 | <i>Klebsiella pneumoniae</i> |
| GCF_008123385.1_ASM812338v1_genomic | GCF_008123385.1 | Chile | 0 0 137 8 0 0 1 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_009184435.1_ASM918443v1_genomic | GCF_009184435.1 | Brazil | 0 0 944 0 0 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_009184445.1_ASM918444v1_genomic | GCF_009184445.1 | Brazil | 0 0 122 28 0 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_009184455.1_ASM918445v1_genomic | GCF_009184455.1 | Brazil | 0 0 520 0 2 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_009758275.2_ASM975827v2_genomic | GCF_009758275.2 | Brazil | 0 0 197 0 74 0 3 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_009898155.1_ASM989815v1_genomic | GCF_009898155.1 | Brazil | 0 0 197 0 25 0 0 0 15 0 | <i>Klebsiella pneumoniae</i> |
| GCF_009928565.1_ASM992856v1_genomic | GCF_009928565.1 | Argentina | 0 0 105 6 0 0 378 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_009928615.1_ASM992861v1_genomic | GCF_009928615.1 | Argentina | 0 0 0 0 7 3 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_010671585.1_ASM1067158v1_genomic | GCF_010671585.1 | Chile | 0 0 137 8 0 0 0 1 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011008735.1_ASM1100873v1_genomic | GCF_011008735.1 | Chile | 0 0 388 0 1 0 14 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011008795.1_ASM1100879v1_genomic | GCF_011008795.1 | Chile | 0 0 105 0 20 1 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011008835.1_ASM1100883v1_genomic | GCF_011008835.1 | Chile | 0 0 388 0 1 0 9 0 9 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011008895.1_ASM1100889v1_genomic | GCF_011008895.1 | Chile | 0 0 388 0 1 0 9 12 0 0 | <i>Klebsiella pneumoniae</i> |

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|--------------------------------------|-----------------|--------|------------------------|------------------------------|
| GCF_011037215.1_ASM1103721v1_genomic | GCF_011037215.1 | Brazil | 0 0 105 0 75 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011037225.1_ASM1103722v1_genomic | GCF_011037225.1 | Brazil | 0 0 105 1 1 1 19 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011037245.1_ASM1103724v1_genomic | GCF_011037245.1 | Brazil | 0 0 105 1 1 1 19 0 1 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011037275.1_ASM1103727v1_genomic | GCF_011037275.1 | Brazil | 0 0 105 1 1 1 19 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011037295.1_ASM1103729v1_genomic | GCF_011037295.1 | Brazil | 0 0 105 1 1 1 19 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011037315.1_ASM1103731v1_genomic | GCF_011037315.1 | Brazil | 0 0 105 1 1 1 19 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011037335.1_ASM1103733v1_genomic | GCF_011037335.1 | Brazil | 0 0 105 1 1 7 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011037345.1_ASM1103734v1_genomic | GCF_011037345.1 | Brazil | 0 0 105 1 1 1 0 0 3 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011037375.1_ASM1103737v1_genomic | GCF_011037375.1 | Brazil | 0 0 105 1 1 1 19 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011037395.1_ASM1103739v1_genomic | GCF_011037395.1 | Brazil | 0 0 105 1 1 7 0 0 1 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011037415.1_ASM1103741v1_genomic | GCF_011037415.1 | Brazil | 0 0 105 1 1 1 19 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011037435.1_ASM1103743v1_genomic | GCF_011037435.1 | Brazil | 0 0 105 1 1 1 19 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011037455.1_ASM1103745v1_genomic | GCF_011037455.1 | Brazil | 0 0 105 0 0 0 1 8 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011037475.1_ASM1103747v1_genomic | GCF_011037475.1 | Brazil | 0 0 105 0 9 0 0 28 1 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011037495.1_ASM1103749v1_genomic | GCF_011037495.1 | Brazil | 0 0 105 0 0 0 1 9 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011037515.1_ASM1103751v1_genomic | GCF_011037515.1 | Brazil | 0 0 105 0 0 0 1 10 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011037535.1_ASM1103753v1_genomic | GCF_011037535.1 | Brazil | 0 0 105 0 0 0 1 1 2 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011037555.1_ASM1103755v1_genomic | GCF_011037555.1 | Brazil | 0 0 105 0 9 0 0 28 1 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011037575.1_ASM1103757v1_genomic | GCF_011037575.1 | Brazil | 0 0 105 0 9 0 0 28 1 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011037595.1_ASM1103759v1_genomic | GCF_011037595.1 | Brazil | 0 0 105 0 0 0 1 11 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011037615.1_ASM1103761v1_genomic | GCF_011037615.1 | Brazil | 0 0 105 0 0 0 1 1 1 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011037635.1_ASM1103763v1_genomic | GCF_011037635.1 | Brazil | 0 0 105 0 0 0 1 12 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011037655.1_ASM1103765v1_genomic | GCF_011037655.1 | Brazil | 0 0 105 0 0 0 1 7 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011037675.1_ASM1103767v1_genomic | GCF_011037675.1 | Brazil | 0 0 105 0 0 0 13 1 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011037685.1_ASM1103768v1_genomic | GCF_011037685.1 | Brazil | 0 0 105 0 9 0 19 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011037715.1_ASM1103771v1_genomic | GCF_011037715.1 | Brazil | 0 0 105 0 0 0 1 4 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011037755.1_ASM1103775v1_genomic | GCF_011037755.1 | Brazil | 0 0 105 0 0 0 0 1 1 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011037775.1_ASM1103777v1_genomic | GCF_011037775.1 | Brazil | 0 0 105 0 0 0 0 1 2 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011037865.1_ASM1103786v1_genomic | GCF_011037865.1 | Brazil | 0 0 105 6 0 0 69 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011037885.1_ASM1103788v1_genomic | GCF_011037885.1 | Brazil | 0 0 105 6 0 0 69 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011037925.1_ASM1103792v1_genomic | GCF_011037925.1 | Brazil | 0 0 105 6 0 0 69 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011037945.1_ASM1103794v1_genomic | GCF_011037945.1 | Brazil | 0 0 105 6 0 0 69 0 6 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011037955.1_ASM1103795v1_genomic | GCF_011037955.1 | Brazil | 0 0 105 6 0 0 69 0 8 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011037995.1_ASM1103799v1_genomic | GCF_011037995.1 | Brazil | 0 0 105 6 0 0 69 0 0 0 | <i>Klebsiella pneumoniae</i> |

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| GCF_011038015.1_ASM1103801v1_genomic | GCF_011038015.1 | Brazil | 0 0 105 6 0 0 69 0 9 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011038035.1_ASM1103803v1_genomic | GCF_011038035.1 | Brazil | 0 0 105 6 0 0 69 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011038055.1_ASM1103805v1_genomic | GCF_011038055.1 | Brazil | 0 0 105 6 0 0 69 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011038095.1_ASM1103809v1_genomic | GCF_011038095.1 | Brazil | 0 0 105 6 0 0 69 0 10 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011038115.1_ASM1103811v1_genomic | GCF_011038115.1 | Brazil | 0 0 105 6 0 0 69 0 11 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011038135.1_ASM1103813v1_genomic | GCF_011038135.1 | Brazil | 0 0 105 6 0 0 69 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011038155.1_ASM1103815v1_genomic | GCF_011038155.1 | Brazil | 0 0 22 27 0 0 0 120 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011038175.1_ASM1103817v1_genomic | GCF_011038175.1 | Brazil | 0 0 22 27 0 0 0 0 27 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011038195.1_ASM1103819v1_genomic | GCF_011038195.1 | Brazil | 0 0 22 27 0 0 0 0 28 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011038215.1_ASM1103821v1_genomic | GCF_011038215.1 | Brazil | 0 0 22 27 0 0 84 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011038235.1_ASM1103823v1_genomic | GCF_011038235.1 | Brazil | 0 0 22 27 0 0 0 0 29 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011038255.1_ASM1103825v1_genomic | GCF_011038255.1 | Brazil | 0 0 22 27 0 0 0 0 30 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011038265.1_ASM1103826v1_genomic | GCF_011038265.1 | Brazil | 0 0 22 27 0 0 0 121 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011038295.1_ASM1103829v1_genomic | GCF_011038295.1 | Brazil | 0 0 22 27 0 0 0 0 31 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011038315.1_ASM1103831v1_genomic | GCF_011038315.1 | Brazil | 0 0 22 27 0 9 1 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011038335.1_ASM1103833v1_genomic | GCF_011038335.1 | Brazil | 0 0 22 27 0 0 0 0 32 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011038355.1_ASM1103835v1_genomic | GCF_011038355.1 | Brazil | 0 0 22 27 0 0 0 122 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011038365.1_ASM1103836v1_genomic | GCF_011038365.1 | Brazil | 0 0 22 27 0 0 0 0 33 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011038395.1_ASM1103839v1_genomic | GCF_011038395.1 | Brazil | 0 0 22 27 0 0 0 0 34 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011038415.1_ASM1103841v1_genomic | GCF_011038415.1 | Brazil | 0 0 22 27 0 0 0 0 35 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011038425.1_ASM1103842v1_genomic | GCF_011038425.1 | Brazil | 0 0 22 27 0 0 0 0 36 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011038455.1_ASM1103845v1_genomic | GCF_011038455.1 | Brazil | 0 0 22 27 0 0 0 0 37 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011038475.1_ASM1103847v1_genomic | GCF_011038475.1 | Brazil | 0 0 22 27 0 0 0 0 38 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011038495.1_ASM1103849v1_genomic | GCF_011038495.1 | Brazil | 0 0 22 27 0 0 0 123 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011038515.1_ASM1103851v1_genomic | GCF_011038515.1 | Brazil | 0 0 22 27 0 0 0 0 39 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011601045.1_ASM1160104v1_genomic | GCF_011601045.1 | Brazil | 0 0 105 6 0 0 69 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_011684055.1_ASM1168405v1_genomic | GCF_011684055.1 | Brazil | 0 0 1302 0 0 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_012102235.1_ASM1210223v1_genomic | GCF_012102235.1 | Brazil | 0 0 105 6 0 0 69 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_012102535.1_ASM1210253v1_genomic | GCF_012102535.1 | Brazil | 0 0 322 0 1 0 1 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_012241505.1_ASM1224150v1_genomic | GCF_012241505.1 | Peru | 0 0 197 0 4 30 0 1 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_012241595.1_ASM1224159v1_genomic | GCF_012241595.1 | Brazil | 0 0 0 0 2 0 0 31 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_012955865.1_ASM1295586v1_genomic | GCF_012955865.1 | Brazil | 0 0 105 0 0 11 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_012955875.1_ASM1295587v1_genomic | GCF_012955875.1 | Brazil | 0 0 105 0 0 0 25 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_012955905.1_ASM1295590v1_genomic | GCF_012955905.1 | Brazil | 0 0 105 0 9 0 0 28 1 0 | <i>Klebsiella pneumoniae</i> |

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| GCF_012955925.1_ASM1295592v1_genomic | GCF_012955925.1 | Brazil | 0 0 105 0 76 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_012956605.1_ASM1295660v1_genomic | GCF_012956605.1 | Brazil | 0 0 105 6 0 0 379 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_012956625.1_ASM1295662v1_genomic | GCF_012956625.1 | Brazil | 0 0 105 6 0 0 69 3 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_012956645.1_ASM1295664v1_genomic | GCF_012956645.1 | Brazil | 0 0 105 6 0 0 380 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_013002785.1_ASM1300278v1_genomic | GCF_013002785.1 | Brazil | 0 0 105 0 24 0 0 0 3 0 | <i>Klebsiella pneumoniae</i> |
| GCF_013155005.1_ASM1315500v1_genomic | GCF_013155005.1 | Chile | 0 0 137 8 0 0 0 2 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_013169065.1_ASM1316906v1_genomic | GCF_013169065.1 | Colombia | 0 0 283 0 0 0 1 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_013169115.1_ASM1316911v1_genomic | GCF_013169115.1 | Colombia | 0 0 22 24 7 1 2 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_013169725.1_ASM1316972v1_genomic | GCF_013169725.1 | Colombia | 0 0 22 25 10 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_013169765.1_ASM1316976v1_genomic | GCF_013169765.1 | Colombia | 0 0 105 6 0 0 17 53 75 0 | <i>Klebsiella pneumoniae</i> |
| GCF_013169775.1_ASM1316977v1_genomic | GCF_013169775.1 | Colombia | 0 0 105 6 0 0 17 16 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_013169865.1_ASM1316986v1_genomic | GCF_013169865.1 | Colombia | 0 0 219 0 0 0 0 1 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_013169875.1_ASM1316987v1_genomic | GCF_013169875.1 | Colombia | 0 0 22 24 7 1 0 1 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_013170105.1_ASM1317010v1_genomic | GCF_013170105.1 | Colombia | 0 0 29 5 0 0 0 0 2 0 | <i>Klebsiella pneumoniae</i> |
| GCF_013170115.1_ASM1317011v1_genomic | GCF_013170115.1 | Colombia | 0 0 105 6 0 0 17 53 65 0 | <i>Klebsiella pneumoniae</i> |
| GCF_013170165.1_ASM1317016v1_genomic | GCF_013170165.1 | Colombia | 0 0 0 0 23 1 6 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_013170205.1_ASM1317020v1_genomic | GCF_013170205.1 | Colombia | 0 0 105 6 0 0 17 53 76 0 | <i>Klebsiella pneumoniae</i> |
| GCF_013170215.1_ASM1317021v1_genomic | GCF_013170215.1 | Colombia | 0 0 388 0 5 0 1 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_013170325.1_ASM1317032v1_genomic | GCF_013170325.1 | Colombia | 0 0 28 0 0 0 0 1 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_013170385.1_ASM1317038v1_genomic | GCF_013170385.1 | Colombia | 0 0 219 0 0 0 0 2 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_013170405.1_ASM1317040v1_genomic | GCF_013170405.1 | Colombia | 0 0 219 0 0 0 0 3 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_013170425.1_ASM1317042v1_genomic | GCF_013170425.1 | Colombia | 0 0 472 0 4 0 0 1 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_013170435.1_ASM1317043v1_genomic | GCF_013170435.1 | Colombia | 0 0 84 0 0 6 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_013170445.1_ASM1317044v1_genomic | GCF_013170445.1 | Colombia | 0 0 219 0 0 0 0 4 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_013170455.1_ASM1317045v1_genomic | GCF_013170455.1 | Colombia | 0 0 219 0 0 0 0 5 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_013170505.1_ASM1317050v1_genomic | GCF_013170505.1 | Colombia | 0 0 472 0 4 0 0 0 1 0 | <i>Klebsiella pneumoniae</i> |
| GCF_013170535.1_ASM1317053v1_genomic | GCF_013170535.1 | Colombia | 0 0 219 0 0 0 0 6 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_013170565.1_ASM1317056v1_genomic | GCF_013170565.1 | Colombia | 0 0 219 0 0 0 0 7 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_013170595.1_ASM1317059v1_genomic | GCF_013170595.1 | Colombia | 0 0 219 0 0 0 0 8 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_013170625.1_ASM1317062v1_genomic | GCF_013170625.1 | Colombia | 0 0 219 0 0 0 0 9 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_013170645.1_ASM1317064v1_genomic | GCF_013170645.1 | Colombia | 0 0 219 0 0 0 0 10 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_013303005.1_ASM1330300v1_genomic | GCF_013303005.1 | Brazil | 0 0 105 0 9 0 0 28 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_013372785.1_ASM1337278v1_genomic | GCF_013372785.1 | Brazil | 0 0 22 27 0 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_014323585.1_ASM1432358v1_genomic | GCF_014323585.1 | Brazil | 0 0 105 1 1 1 0 0 0 0 | <i>Klebsiella pneumoniae</i> |

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| GCF_014323625.1_ASM1432362v1_genomic | GCF_014323625.1 | Brazil | 0 0 105 6 0 0 17 182 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_014323715.1_ASM1432371v1_genomic | GCF_014323715.1 | Brazil | 0 0 105 0 0 0 1 13 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_014451135.1_ASM1445113v1_genomic | GCF_014451135.1 | Brazil | 0 0 220 0 0 0 11 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_014451175.1_ASM1445117v1_genomic | GCF_014451175.1 | Brazil | 0 0 220 0 0 0 12 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_014451185.1_ASM1445118v1_genomic | GCF_014451185.1 | Brazil | 0 0 220 0 8 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_014451215.1_ASM1445121v1_genomic | GCF_014451215.1 | Brazil | 0 0 0 0 80 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_014451235.1_ASM1445123v1_genomic | GCF_014451235.1 | Brazil | 0 0 105 1 1 1 4 3 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_014451245.1_ASM1445124v1_genomic | GCF_014451245.1 | Brazil | 0 0 105 6 0 0 69 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_014451255.1_ASM1445125v1_genomic | GCF_014451255.1 | Brazil | 0 0 105 1 1 1 3 1 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_014451275.1_ASM1445127v1_genomic | GCF_014451275.1 | Brazil | 0 0 0 0 2 0 165 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_014451315.1_ASM1445131v1_genomic | GCF_014451315.1 | Brazil | 0 0 105 6 0 0 69 4 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_014490685.2_ASM1449068v2_genomic | GCF_014490685.2 | Peru | 0 0 197 0 4 30 1 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_014500765.1_ASM1450076v1_genomic | GCF_014500765.1 | Brazil | 0 0 0 0 2 0 0 0 67 0 | <i>Klebsiella pneumoniae</i> |
| GCF_014500785.1_ASM1450078v1_genomic | GCF_014500785.1 | Brazil | 0 0 0 0 2 0 0 227 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_014500805.1_ASM1450080v1_genomic | GCF_014500805.1 | Brazil | 0 0 0 0 2 0 0 0 68 0 | <i>Klebsiella pneumoniae</i> |
| GCF_014500815.1_ASM1450081v1_genomic | GCF_014500815.1 | Brazil | 0 0 0 0 2 0 0 0 69 0 | <i>Klebsiella pneumoniae</i> |
| GCF_014500865.1_ASM1450086v1_genomic | GCF_014500865.1 | Brazil | 0 0 0 0 2 0 125 1 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_014524525.1_ASM1452452v1_genomic | GCF_014524525.1 | Brazil | 0 0 0 0 2 0 0 0 70 0 | <i>Klebsiella pneumoniae</i> |
| GCF_014788765.1_ASM1478876v1_genomic | GCF_014788765.1 | Chile | 0 0 388 0 1 0 9 2 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_014833135.1_Kp14U04_genomic | GCF_014833135.1 | Brazil | 0 0 0 0 2 0 166 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_014883955.1_ASM1488395v1_genomic | GCF_014883955.1 | Colombia | 0 0 128 9 2 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_015666295.1_ASM1566629v1_genomic | GCF_015666295.1 | Brazil | 0 0 105 0 3 0 1 13 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_015666325.1_ASM1566632v1_genomic | GCF_015666325.1 | Brazil | 0 0 105 0 0 0 13 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_015666395.1_ASM1566639v1_genomic | GCF_015666395.1 | Brazil | 0 0 0 0 37 1 0 1 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_015666405.1_ASM1566640v1_genomic | GCF_015666405.1 | Brazil | 0 0 105 0 3 0 28 2 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_015666415.1_ASM1566641v1_genomic | GCF_015666415.1 | Brazil | 0 0 105 0 0 0 13 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_015666445.1_ASM1566644v1_genomic | GCF_015666445.1 | Brazil | 0 0 105 0 0 0 13 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_015666485.1_ASM1566648v1_genomic | GCF_015666485.1 | Brazil | 0 0 105 0 3 0 63 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_015666525.1_ASM1566652v1_genomic | GCF_015666525.1 | Brazil | 0 0 124 0 0 2 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_015666585.1_ASM1566658v1_genomic | GCF_015666585.1 | Brazil | 0 0 105 0 3 0 28 3 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_015666595.1_ASM1566659v1_genomic | GCF_015666595.1 | Brazil | 0 0 105 6 0 0 69 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_015666615.1_ASM1566661v1_genomic | GCF_015666615.1 | Brazil | 0 0 369 0 0 0 0 380 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_015666635.1_ASM1566663v1_genomic | GCF_015666635.1 | Brazil | 0 0 194 0 0 0 2 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_015666685.1_ASM1566668v1_genomic | GCF_015666685.1 | Brazil | 0 0 419 0 0 0 2 0 0 0 | <i>Klebsiella pneumoniae</i> |

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| GCF_015826235.1_ASM1582623v1_genomic | GCF_015826235.1 | Brazil | 0 0 395 0 59 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_015826265.1_ASM1582626v1_genomic | GCF_015826265.1 | Brazil | 0 0 395 0 60 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_015912475.1_ASM1591247v1_genomic | GCF_015912475.1 | Uruguay | 0 0 105 6 0 0 381 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_015912485.1_ASM1591248v1_genomic | GCF_015912485.1 | Uruguay | 0 0 105 6 0 0 382 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_015912585.1_ASM1591258v1_genomic | GCF_015912585.1 | Uruguay | 0 0 105 6 0 0 383 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016054805.1_ASM1605480v1_genomic | GCF_016054805.1 | Brazil | 0 0 105 0 9 0 0 56 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016054825.1_ASM1605482v1_genomic | GCF_016054825.1 | Brazil | 0 0 106 0 0 2 3 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016054895.1_ASM1605489v1_genomic | GCF_016054895.1 | Brazil | 0 0 94 0 0 0 0 1 1 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016054935.1_ASM1605493v1_genomic | GCF_016054935.1 | Brazil | 0 0 124 0 0 3 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016054995.1_ASM1605499v1_genomic | GCF_016054995.1 | Brazil | 0 0 124 0 0 4 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016055215.1_ASM1605521v1_genomic | GCF_016055215.1 | Brazil | 0 0 211 0 39 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016055235.1_ASM1605523v1_genomic | GCF_016055235.1 | Brazil | 0 0 105 0 0 0 13 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016055275.1_ASM1605527v1_genomic | GCF_016055275.1 | Brazil | 0 0 105 0 0 0 1 14 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016055295.1_ASM1605529v1_genomic | GCF_016055295.1 | Brazil | 0 0 194 0 0 0 3 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016055305.1_ASM1605530v1_genomic | GCF_016055305.1 | Brazil | 0 0 323 0 1 0 1 1 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016055345.1_ASM1605534v1_genomic | GCF_016055345.1 | Brazil | 0 0 197 0 25 0 0 23 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016055395.1_ASM1605539v1_genomic | GCF_016055395.1 | Brazil | 0 0 105 0 3 0 28 1 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016055435.1_ASM1605543v1_genomic | GCF_016055435.1 | Brazil | 0 0 369 0 0 0 0 0 1 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016055445.1_ASM1605544v1_genomic | GCF_016055445.1 | Brazil | 0 0 197 0 25 0 0 23 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016055495.1_ASM1605549v1_genomic | GCF_016055495.1 | Brazil | 0 0 105 6 0 0 69 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016055535.1_ASM1605553v1_genomic | GCF_016055535.1 | Brazil | 0 0 105 6 0 0 69 0 12 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016055575.1_ASM1605557v1_genomic | GCF_016055575.1 | Brazil | 0 0 22 27 0 0 0 106 3 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016055605.1_ASM1605560v1_genomic | GCF_016055605.1 | Brazil | 0 0 197 0 4 0 1 3 4 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016055635.1_ASM1605563v1_genomic | GCF_016055635.1 | Brazil | 0 0 197 0 0 0 20 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016055655.1_ASM1605565v1_genomic | GCF_016055655.1 | Brazil | 0 0 22 24 7 1 3 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016055675.1_ASM1605567v1_genomic | GCF_016055675.1 | Brazil | 0 0 105 6 0 0 69 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016055695.1_ASM1605569v1_genomic | GCF_016055695.1 | Brazil | 0 0 105 0 0 0 13 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016055755.1_ASM1605575v1_genomic | GCF_016055755.1 | Brazil | 0 0 105 0 0 0 1 15 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016055795.1_ASM1605579v1_genomic | GCF_016055795.1 | Brazil | 0 0 323 0 1 0 1 2 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016055885.1_ASM1605588v1_genomic | GCF_016055885.1 | Brazil | 0 0 105 0 0 0 1 16 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016055895.1_ASM1605589v1_genomic | GCF_016055895.1 | Brazil | 0 0 105 0 3 0 28 1 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016055935.1_ASM1605593v1_genomic | GCF_016055935.1 | Brazil | 0 0 84 0 8 0 4 8 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016055975.1_ASM1605597v1_genomic | GCF_016055975.1 | Brazil | 0 0 107 0 4 0 1 9 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016055995.1_ASM1605599v1_genomic | GCF_016055995.1 | Brazil | 0 0 105 0 0 0 1 17 0 0 | <i>Klebsiella pneumoniae</i> |

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| GCF_016056105.1_ASM1605610v1_genomic | GCF_016056105.1 | Brazil | 0 0 105 1 1 1 3 2 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016056175.1_ASM1605617v1_genomic | GCF_016056175.1 | Brazil | 0 0 369 0 0 0 0 0 104 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016056195.1_ASM1605619v1_genomic | GCF_016056195.1 | Brazil | 0 0 0 0 2 0 0 0 72 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016801375.1_ASM1680137v1_genomic | GCF_016801375.1 | Colombia | 0 0 105 6 0 0 0 17 722 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016805425.1_ASM1680542v1_genomic | GCF_016805425.1 | Ecuador | 0 0 98 0 5 0 0 2 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016805435.1_ASM1680543v1_genomic | GCF_016805435.1 | Ecuador | 0 0 98 0 5 0 0 3 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016805465.1_ASM1680546v1_genomic | GCF_016805465.1 | Ecuador | 0 0 98 0 5 0 0 0 7 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016805485.1_ASM1680548v1_genomic | GCF_016805485.1 | Ecuador | 0 0 98 0 5 0 0 4 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016805505.1_ASM1680550v1_genomic | GCF_016805505.1 | Ecuador | 0 0 98 0 5 0 0 5 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016805525.1_ASM1680552v1_genomic | GCF_016805525.1 | Ecuador | 0 0 98 0 5 0 0 0 8 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016805545.1_ASM1680554v1_genomic | GCF_016805545.1 | Ecuador | 0 0 98 0 5 0 0 6 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016805565.1_ASM1680556v1_genomic | GCF_016805565.1 | Ecuador | 0 0 105 6 43 0 0 0 1 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016805585.1_ASM1680558v1_genomic | GCF_016805585.1 | Ecuador | 0 0 105 6 43 0 2 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016805625.1_ASM1680562v1_genomic | GCF_016805625.1 | Ecuador | 0 0 105 6 43 0 0 4 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016805635.1_ASM1680563v1_genomic | GCF_016805635.1 | Ecuador | 0 0 98 0 5 0 1 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016805665.1_ASM1680566v1_genomic | GCF_016805665.1 | Ecuador | 0 0 98 0 5 0 0 0 9 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016805685.1_ASM1680568v1_genomic | GCF_016805685.1 | Ecuador | 0 0 98 0 5 0 0 0 10 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016805705.1_ASM1680570v1_genomic | GCF_016805705.1 | Ecuador | 0 0 98 0 5 0 2 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016805715.1_ASM1680571v1_genomic | GCF_016805715.1 | Ecuador | 0 0 98 0 5 0 0 0 11 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016805745.1_ASM1680574v1_genomic | GCF_016805745.1 | Ecuador | 0 0 395 0 12 0 4 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016805765.1_ASM1680576v1_genomic | GCF_016805765.1 | Ecuador | 0 0 105 6 43 0 0 1 1 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016805785.1_ASM1680578v1_genomic | GCF_016805785.1 | Ecuador | 0 0 105 6 43 0 0 5 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016836885.1_ASM1683688v1_genomic | GCF_016836885.1 | Paraguay | 0 0 848 0 0 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016836905.1_ASM1683690v1_genomic | GCF_016836905.1 | Paraguay | 0 0 261 0 0 0 0 8 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016836965.1_ASM1683696v1_genomic | GCF_016836965.1 | Paraguay | 0 0 0 0 2 58 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016837025.1_ASM1683702v1_genomic | GCF_016837025.1 | Paraguay | 0 0 158 7 1 2 1 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016837045.1_ASM1683704v1_genomic | GCF_016837045.1 | Paraguay | 0 0 123 1 5 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_016887985.1_ASM1688798v1_genomic | GCF_016887985.1 | Paraguay | 0 0 158 7 1 2 2 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_017309465.1_ASM1730946v1_genomic | GCF_017309465.1 | Paraguay | 0 0 88 0 0 0 2 5 1 0 | <i>Klebsiella pneumoniae</i> |
| GCF_017655225.1_ASM1765522v1_genomic | GCF_017655225.1 | Peru | 0 0 369 0 0 0 0 0 100 0 | <i>Klebsiella pneumoniae</i> |
| GCF_018109905.1_ASM1810990v1_genomic | GCF_018109905.1 | Brazil | 0 0 0 0 2 0 75 2 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_018359185.1_ASM1835918v1_genomic | GCF_018359185.1 | Colombia | 0 0 95 1 3 0 2 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_018359195.1_ASM1835919v1_genomic | GCF_018359195.1 | Colombia | 0 0 105 6 0 0 17 689 1 0 | <i>Klebsiella pneumoniae</i> |
| GCF_018359205.1_ASM1835920v1_genomic | GCF_018359205.1 | Colombia | 0 0 105 6 0 0 17 689 1 0 | <i>Klebsiella pneumoniae</i> |

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| GCF_018359245.1_ASM1835924v1_genomic | GCF_018359245.1 | Colombia | 0 0 95 1 3 0 3 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_018359255.1_ASM1835925v1_genomic | GCF_018359255.1 | Colombia | 0 0 105 6 0 0 17 689 1 0 | <i>Klebsiella pneumoniae</i> |
| GCF_018359285.1_ASM1835928v1_genomic | GCF_018359285.1 | Colombia | 0 0 105 6 0 0 17 16 6 0 | <i>Klebsiella pneumoniae</i> |
| GCF_018359295.1_ASM1835929v1_genomic | GCF_018359295.1 | Colombia | 0 0 80 8 0 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_018359305.1_ASM1835930v1_genomic | GCF_018359305.1 | Colombia | 0 0 105 6 43 0 0 1 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_018359345.1_ASM1835934v1_genomic | GCF_018359345.1 | Colombia | 0 0 105 6 0 0 17 16 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_018359365.1_ASM1835936v1_genomic | GCF_018359365.1 | Colombia | 0 0 105 6 0 0 17 697 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_018359385.1_ASM1835938v1_genomic | GCF_018359385.1 | Colombia | 0 0 105 6 0 0 17 16 6 0 | <i>Klebsiella pneumoniae</i> |
| GCF_018359405.1_ASM1835940v1_genomic | GCF_018359405.1 | Colombia | 0 0 105 6 0 0 17 16 6 0 | <i>Klebsiella pneumoniae</i> |
| GCF_018359425.1_ASM1835942v1_genomic | GCF_018359425.1 | Colombia | 0 0 105 6 0 0 17 16 6 0 | <i>Klebsiella pneumoniae</i> |
| GCF_018359445.1_ASM1835944v1_genomic | GCF_018359445.1 | Colombia | 0 0 105 6 0 0 17 16 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_018359455.1_ASM1835945v1_genomic | GCF_018359455.1 | Colombia | 0 0 105 6 0 0 17 16 35 0 | <i>Klebsiella pneumoniae</i> |
| GCF_018359485.1_ASM1835948v1_genomic | GCF_018359485.1 | Colombia | 0 0 1 1 0 1 1 0 0 6 | <i>Klebsiella pneumoniae</i> |
| GCF_018359505.1_ASM1835950v1_genomic | GCF_018359505.1 | Colombia | 0 0 1 1 0 1 1 0 0 7 | <i>Klebsiella pneumoniae</i> |
| GCF_018359525.1_ASM1835952v1_genomic | GCF_018359525.1 | Colombia | 0 0 1 1 0 1 1 0 5 0 | <i>Klebsiella pneumoniae</i> |
| GCF_018359545.1_ASM1835954v1_genomic | GCF_018359545.1 | Colombia | 0 0 105 6 0 0 17 16 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_018359565.1_ASM1835956v1_genomic | GCF_018359565.1 | Colombia | 0 0 1 1 0 1 1 0 0 8 | <i>Klebsiella pneumoniae</i> |
| GCF_018359585.1_ASM1835958v1_genomic | GCF_018359585.1 | Colombia | 0 0 105 6 0 0 17 16 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_018359605.1_ASM1835960v1_genomic | GCF_018359605.1 | Colombia | 0 0 105 6 0 0 17 16 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_018359625.1_ASM1835962v1_genomic | GCF_018359625.1 | Colombia | 0 0 105 6 0 0 17 16 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_018359645.1_ASM1835964v1_genomic | GCF_018359645.1 | Colombia | 0 0 105 6 0 0 17 53 1 0 | <i>Klebsiella pneumoniae</i> |
| GCF_018423625.1_ASM1842362v1_genomic | GCF_018423625.1 | Brazil | 0 0 105 0 0 0 1 18 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_018423645.1_ASM1842364v1_genomic | GCF_018423645.1 | Brazil | 0 0 105 1 1 1 19 1 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_018423665.1_ASM1842366v1_genomic | GCF_018423665.1 | Brazil | 0 0 105 0 0 0 1 19 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_018423675.1_ASM1842367v1_genomic | GCF_018423675.1 | Brazil | 0 0 105 0 24 0 0 5 1 0 | <i>Klebsiella pneumoniae</i> |
| GCF_018423705.1_ASM1842370v1_genomic | GCF_018423705.1 | Brazil | 0 0 105 1 1 1 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_018423715.1_ASM1842371v1_genomic | GCF_018423715.1 | Brazil | 0 0 105 0 0 0 3 0 1 0 | <i>Klebsiella pneumoniae</i> |
| GCF_018423745.1_ASM1842374v1_genomic | GCF_018423745.1 | Brazil | 0 0 105 0 0 0 1 1 1 0 | <i>Klebsiella pneumoniae</i> |
| GCF_018423765.1_ASM1842376v1_genomic | GCF_018423765.1 | Brazil | 0 0 105 0 24 0 0 0 4 0 | <i>Klebsiella pneumoniae</i> |
| GCF_018423775.1_ASM1842377v1_genomic | GCF_018423775.1 | Brazil | 0 0 105 1 1 1 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_018423805.1_ASM1842380v1_genomic | GCF_018423805.1 | Brazil | 0 0 105 0 0 0 1 20 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_018423815.1_ASM1842381v1_genomic | GCF_018423815.1 | Brazil | 0 0 105 1 1 1 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_018423825.1_ASM1842382v1_genomic | GCF_018423825.1 | Brazil | 0 0 22 27 0 0 0 0 41 0 | <i>Klebsiella pneumoniae</i> |
| GCF_018423865.1_ASM1842386v1_genomic | GCF_018423865.1 | Brazil | 0 0 105 1 1 5 0 2 0 0 | <i>Klebsiella pneumoniae</i> |

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| GCF 018423905.1 ASM1842390v1 genomic | GCF 018423905.1 | Brazil | 0 0 105 1 1 1 0 0 4 0 | <i>Klebsiella pneumoniae</i> |
| GCF 018423915.1 ASM1842391v1 genomic | GCF 018423915.1 | Brazil | 0 0 105 1 1 1 4 0 1 0 | <i>Klebsiella pneumoniae</i> |
| GCF 018920475.1 ASM1892047v1 genomic | GCF 018920475.1 | Brazil | 0 0 395 5 0 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 019038575.1 ASM1903857v1 genomic | GCF 019038575.1 | Brazil | 0 0 883 0 0 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 019334205.1 ASM1933420v1 genomic | GCF 019334205.1 | Brazil | 0 0 219 4 0 0 1 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 019837225.1 ASM1983722v1 genomic | GCF 019837225.1 | Brazil | 0 0 105 0 85 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 019928625.2 ASM1992862v2 genomic | GCF 019928625.2 | Peru | 0 0 146 0 2 1 0 1 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 019928665.1 ASM1992866v1 genomic | GCF 019928665.1 | Peru | 0 0 374 0 2 1 1 1 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 020589615.1 ASM2058961v1 genomic | GCF 020589615.1 | Brazil | 0 0 105 0 11 0 12 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 020589635.1 ASM2058963v1 genomic | GCF 020589635.1 | Brazil | 0 0 105 0 11 0 12 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 020589645.1 ASM2058964v1 genomic | GCF 020589645.1 | Brazil | 0 0 194 0 0 0 4 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 020589755.1 ASM2058975v1 genomic | GCF 020589755.1 | Brazil | 0 0 309 0 2 1 1 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 020589795.1 ASM2058979v1 genomic | GCF 020589795.1 | Brazil | 0 0 22 12 38 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 020589815.1 ASM2058981v1 genomic | GCF 020589815.1 | Brazil | 0 0 407 0 0 0 0 0 2 0 | <i>Klebsiella pneumoniae</i> |
| GCF 020589835.1 ASM2058983v1 genomic | GCF 020589835.1 | Brazil | 0 0 407 0 0 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 020589895.1 ASM2058989v1 genomic | GCF 020589895.1 | Brazil | 0 0 193 3 3 0 1 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 020589935.1 ASM2058993v1 genomic | GCF 020589935.1 | Brazil | 0 0 407 0 0 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 020615425.1 ASM2061542v1 genomic | GCF 020615425.1 | Brazil | 0 0 197 0 4 0 31 9 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 020615495.1 ASM2061549v1 genomic | GCF 020615495.1 | Brazil | 0 0 105 0 0 0 6 1 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 020615575.1 ASM2061557v1 genomic | GCF 020615575.1 | Brazil | 0 0 98 2 17 1 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 020615655.1 ASM2061565v1 genomic | GCF 020615655.1 | Brazil | 0 0 105 0 0 0 6 2 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 020615675.1 ASM2061567v1 genomic | GCF 020615675.1 | Brazil | 0 0 98 2 17 2 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 021011315.1 ASM2101131v1 genomic | GCF 021011315.1 | Argentina | 0 0 105 0 11 0 0 24 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 021020725.1 ASM2102072v1 genomic | GCF 021020725.1 | Brazil | 0 0 105 1 1 7 0 1 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 021020735.1 ASM2102073v1 genomic | GCF 021020735.1 | Brazil | 0 0 105 0 3 0 1 13 3 0 | <i>Klebsiella pneumoniae</i> |
| GCF 021020745.1 ASM2102074v1 genomic | GCF 021020745.1 | Brazil | 0 0 105 6 0 0 69 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 021020815.1 ASM2102081v1 genomic | GCF 021020815.1 | Brazil | 0 0 105 6 0 0 69 0 13 0 | <i>Klebsiella pneumoniae</i> |
| GCF 021020835.1 ASM2102083v1 genomic | GCF 021020835.1 | Brazil | 0 0 105 6 0 0 69 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 021020855.1 ASM2102085v1 genomic | GCF 021020855.1 | Brazil | 0 0 105 6 0 0 69 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 021020865.1 ASM2102086v1 genomic | GCF 021020865.1 | Brazil | 0 0 105 0 3 0 64 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 021020875.1 ASM2102087v1 genomic | GCF 021020875.1 | Brazil | 0 0 105 0 9 0 0 58 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 021020915.1 ASM2102091v1 genomic | GCF 021020915.1 | Brazil | 0 0 105 6 0 0 69 0 14 0 | <i>Klebsiella pneumoniae</i> |
| GCF 021020935.1 ASM2102093v1 genomic | GCF 021020935.1 | Brazil | 0 0 105 6 0 0 69 0 15 0 | <i>Klebsiella pneumoniae</i> |
| GCF 021020955.1 ASM2102095v1 genomic | GCF 021020955.1 | Brazil | 0 0 105 6 0 0 69 0 0 0 | <i>Klebsiella pneumoniae</i> |

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|--------------------------------------|-----------------|-----------|--------------------------|------------------------------|
| GCF 021020985.1 ASM2102098v1 genomic | GCF 021020985.1 | Brazil | 0 0 105 6 0 0 69 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 021021015.1 ASM2102101v1 genomic | GCF 021021015.1 | Brazil | 0 0 105 6 0 0 69 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 021021035.1 ASM2102103v1 genomic | GCF 021021035.1 | Brazil | 0 0 105 6 0 0 69 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 021021055.1 ASM2102105v1 genomic | GCF 021021055.1 | Brazil | 0 0 105 6 0 0 69 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 021021075.1 ASM2102107v1 genomic | GCF 021021075.1 | Brazil | 0 0 105 6 0 0 69 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 021021095.1 ASM2102109v1 genomic | GCF 021021095.1 | Brazil | 0 0 105 6 0 0 69 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 021021115.1 ASM2102111v1 genomic | GCF 021021115.1 | Brazil | 0 0 105 6 0 0 69 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 021021135.1 ASM2102113v1 genomic | GCF 021021135.1 | Brazil | 0 0 105 6 0 0 69 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 021021155.1 ASM2102115v1 genomic | GCF 021021155.1 | Brazil | 0 0 105 6 0 0 69 0 16 0 | <i>Klebsiella pneumoniae</i> |
| GCF 021021175.1 ASM2102117v1 genomic | GCF 021021175.1 | Brazil | 0 0 105 6 0 0 69 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 021021195.1 ASM2102119v1 genomic | GCF 021021195.1 | Brazil | 0 0 105 0 3 0 16 0 5 0 | <i>Klebsiella pneumoniae</i> |
| GCF 021021255.1 ASM2102125v1 genomic | GCF 021021255.1 | Brazil | 0 0 105 6 0 0 69 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 021206795.1 ASM2120679v1 genomic | GCF 021206795.1 | Brazil | 0 0 22 27 0 0 0 124 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 021245835.1 ASM2124583v1 genomic | GCF 021245835.1 | Brazil | 0 0 22 27 0 0 0 125 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 021496095.1 ASM2149609v1 genomic | GCF 021496095.1 | Brazil | 0 0 105 0 11 0 0 0 1 0 | <i>Klebsiella pneumoniae</i> |
| GCF 021568735.1 ASM2156873v1 genomic | GCF 021568735.1 | Brazil | 0 0 84 0 8 0 4 1 2 0 | <i>Klebsiella pneumoniae</i> |
| GCF 021648785.1 ASM2164878v1 genomic | GCF 021648785.1 | Brazil | 0 0 0 0 2 0 0 0 39 0 | <i>Klebsiella pneumoniae</i> |
| GCF 022359595.1 ASM2235959v1 genomic | GCF 022359595.1 | Brazil | 0 0 98 0 6 1 1 1 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 022544755.1 ASM2254475v1 genomic | GCF 022544755.1 | Brazil | 0 0 105 0 0 0 1 0 2 0 | <i>Klebsiella pneumoniae</i> |
| GCF 022568215.1 ASM2256821v1 genomic | GCF 022568215.1 | Brazil | 0 0 197 0 25 0 0 0 20 0 | <i>Klebsiella pneumoniae</i> |
| GCF 022698265.1 ASM2269826v1 genomic | GCF 022698265.1 | Argentina | 0 0 388 0 5 0 2 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 022848935.1 ASM2284893v1 genomic | GCF 022848935.1 | Uruguay | 0 0 105 6 0 0 385 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 022848985.1 ASM2284898v1 genomic | GCF 022848985.1 | Uruguay | 0 0 105 6 0 0 386 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 022848995.1 ASM2284899v1 genomic | GCF 022848995.1 | Uruguay | 0 0 105 6 0 0 387 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 022849125.1 ASM2284912v1 genomic | GCF 022849125.1 | Uruguay | 0 0 105 6 0 0 388 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 023059255.1 ASM2305925v1 genomic | GCF 023059255.1 | Brazil | 0 0 105 0 3 0 28 1 2 0 | <i>Klebsiella pneumoniae</i> |
| GCF 023059265.1 ASM2305926v1 genomic | GCF 023059265.1 | Brazil | 0 0 105 6 0 0 17 0 98 0 | <i>Klebsiella pneumoniae</i> |
| GCF 023059275.1 ASM2305927v1 genomic | GCF 023059275.1 | Brazil | 0 0 84 0 8 0 4 1 2 0 | <i>Klebsiella pneumoniae</i> |
| GCF 023059285.1 ASM2305928v1 genomic | GCF 023059285.1 | Brazil | 0 0 105 0 3 0 1 13 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 023059435.1 ASM2305943v1 genomic | GCF 023059435.1 | Brazil | 0 0 105 0 3 0 16 0 6 0 | <i>Klebsiella pneumoniae</i> |
| GCF 023060075.1 ASM2306007v1 genomic | GCF 023060075.1 | Brazil | 0 0 105 6 0 0 17 731 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 023060155.1 ASM2306015v1 genomic | GCF 023060155.1 | Brazil | 0 0 105 0 11 0 0 33 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 023060175.1 ASM2306017v1 genomic | GCF 023060175.1 | Brazil | 0 0 22 27 0 0 0 0 44 0 | <i>Klebsiella pneumoniae</i> |
| GCF 023060205.1 ASM2306020v1 genomic | GCF 023060205.1 | Brazil | 0 0 124 0 0 5 0 0 0 0 | <i>Klebsiella pneumoniae</i> |

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|--------------------------------------|-----------------|-----------|-------------------------|------------------------------|
| GCF 023060255.1 ASM2306025v1 genomic | GCF 023060255.1 | Brazil | 0 0 124 0 0 6 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 023060305.1 ASM2306030v1 genomic | GCF 023060305.1 | Brazil | 0 0 83 3 6 0 1 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 023060355.1 ASM2306035v1 genomic | GCF 023060355.1 | Brazil | 0 0 80 8 0 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 023060505.1 ASM2306050v1 genomic | GCF 023060505.1 | Brazil | 0 0 197 0 17 0 9 1 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 023060995.1 ASM2306099v1 genomic | GCF 023060995.1 | Brazil | 0 0 105 6 0 0 17 0 99 0 | <i>Klebsiella pneumoniae</i> |
| GCF 023061015.1 ASM2306101v1 genomic | GCF 023061015.1 | Brazil | 0 0 105 6 0 0 69 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 023061095.1 ASM2306109v1 genomic | GCF 023061095.1 | Brazil | 0 0 105 0 0 0 1 21 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 023221815.1 ASM2322181v1 genomic | GCF 023221815.1 | Argentina | 0 0 105 0 37 0 1 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 023221835.1 ASM2322183v1 genomic | GCF 023221835.1 | Argentina | 0 0 105 0 37 0 1 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 023221875.1 ASM2322187v1 genomic | GCF 023221875.1 | Argentina | 0 0 105 0 37 0 1 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 023276595.1 ASM2327659v1 genomic | GCF 023276595.1 | Brazil | 0 0 369 0 0 0 0 295 1 0 | <i>Klebsiella pneumoniae</i> |
| GCF 023276605.1 ASM2327660v1 genomic | GCF 023276605.1 | Brazil | 0 0 197 0 4 0 31 10 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 023276615.1 ASM2327661v1 genomic | GCF 023276615.1 | Brazil | 0 0 0 0 2 0 0 0 39 0 | <i>Klebsiella pneumoniae</i> |
| GCF 023554495.1 ASM2355449v1 genomic | GCF 023554495.1 | Chile | 0 0 88 5 0 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 023572235.1 ASM2357223v1 genomic | GCF 023572235.1 | Brazil | 0 0 105 0 11 0 0 0 2 0 | <i>Klebsiella pneumoniae</i> |
| GCF 023572325.1 ASM2357232v1 genomic | GCF 023572325.1 | Brazil | 0 0 413 1 3 0 0 0 1 0 | <i>Klebsiella pneumoniae</i> |
| GCF 023572345.1 ASM2357234v1 genomic | GCF 023572345.1 | Brazil | 0 0 22 27 0 0 86 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 023572385.1 ASM2357238v1 genomic | GCF 023572385.1 | Brazil | 0 0 105 0 0 0 13 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 023572615.1 ASM2357261v1 genomic | GCF 023572615.1 | Brazil | 0 0 105 6 0 0 69 5 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 024494945.1 ASM2449494v1 genomic | GCF 024494945.1 | Peru | 0 0 548 0 0 0 0 1 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 024495065.1 ASM2449506v1 genomic | GCF 024495065.1 | Peru | 0 0 388 1 5 0 3 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 024495515.1 ASM2449551v1 genomic | GCF 024495515.1 | Peru | 0 0 388 1 5 0 4 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 024534275.1 ASM2453427v1 genomic | GCF 024534275.1 | Argentina | 0 0 105 0 9 0 0 28 3 0 | <i>Klebsiella pneumoniae</i> |
| GCF 024534295.1 ASM2453429v1 genomic | GCF 024534295.1 | Argentina | 0 0 105 6 0 0 0 0 2 0 | <i>Klebsiella pneumoniae</i> |
| GCF 024734055.1 ASM2473405v1 genomic | GCF 024734055.1 | Argentina | 0 0 105 0 11 0 0 24 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 024742235.1 ASM2474223v1 genomic | GCF 024742235.1 | Argentina | 0 0 105 0 9 0 0 28 4 0 | <i>Klebsiella pneumoniae</i> |
| GCF 024742255.1 ASM2474225v1 genomic | GCF 024742255.1 | Argentina | 0 0 105 0 9 0 0 28 5 0 | <i>Klebsiella pneumoniae</i> |
| GCF 024813565.1 ASM2481356v1 genomic | GCF 024813565.1 | Brazil | 0 0 369 0 0 0 0 0 1 0 | <i>Klebsiella pneumoniae</i> |
| GCF 024813735.1 ASM2481373v1 genomic | GCF 024813735.1 | Brazil | 0 0 105 0 3 0 1 0 43 0 | <i>Klebsiella pneumoniae</i> |
| GCF 024813765.1 ASM2481376v1 genomic | GCF 024813765.1 | Brazil | 0 0 105 0 9 0 0 28 1 0 | <i>Klebsiella pneumoniae</i> |
| GCF 024813785.1 ASM2481378v1 genomic | GCF 024813785.1 | Brazil | 0 0 105 6 0 0 69 0 17 0 | <i>Klebsiella pneumoniae</i> |
| GCF 024813815.1 ASM2481381v1 genomic | GCF 024813815.1 | Brazil | 0 0 105 0 9 0 0 28 1 0 | <i>Klebsiella pneumoniae</i> |
| GCF 024813855.1 ASM2481385v1 genomic | GCF 024813855.1 | Brazil | 0 0 105 1 1 1 4 4 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 024813875.1 ASM2481387v1 genomic | GCF 024813875.1 | Brazil | 0 0 105 0 11 0 0 0 3 0 | <i>Klebsiella pneumoniae</i> |

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|--------------------------------------|-----------------|---------------------|-------------------------|------------------------------|
| GCF 024814275.1 ASM2481427v1 genomic | GCF 024814275.1 | Brazil | 0 0 0 0 84 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 024919375.1 ASM2491937v1 genomic | GCF 024919375.1 | Ecuador | 0 0 98 0 5 0 0 0 12 0 | <i>Klebsiella pneumoniae</i> |
| GCF 025395495.1 ASM2539549v1 genomic | GCF 025395495.1 | Brazil | 0 0 19 1 14 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 025395535.1 ASM2539553v1 genomic | GCF 025395535.1 | Brazil | 0 0 237 1 0 0 0 0 1 0 | <i>Klebsiella pneumoniae</i> |
| GCF 025399265.1 ASM2539926v1 genomic | GCF 025399265.1 | Argentina | 0 0 105 6 0 0 0 0 2 0 | <i>Klebsiella pneumoniae</i> |
| GCF 025399355.1 ASM2539935v1 genomic | GCF 025399355.1 | Argentina | 0 0 105 0 37 0 0 0 5 0 | <i>Klebsiella pneumoniae</i> |
| GCF 025399375.1 ASM2539937v1 genomic | GCF 025399375.1 | Argentina | 0 0 105 0 9 0 0 28 6 0 | <i>Klebsiella pneumoniae</i> |
| GCF 025399395.1 ASM2539939v1 genomic | GCF 025399395.1 | Argentina | 0 0 105 0 0 0 26 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 025399535.1 ASM2539953v1 genomic | GCF 025399535.1 | Argentina | 0 0 105 0 0 0 27 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 025399555.1 ASM2539955v1 genomic | GCF 025399555.1 | Argentina | 0 0 105 0 37 0 0 0 6 0 | <i>Klebsiella pneumoniae</i> |
| GCF 025818935.1 ASM2581893v1 genomic | GCF 025818935.1 | Trinidad and Tobago | 0 0 0 0 2 0 168 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 025818955.1 ASM2581895v1 genomic | GCF 025818955.1 | Trinidad and Tobago | 0 0 253 0 0 0 0 1 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 025819035.1 ASM2581903v1 genomic | GCF 025819035.1 | Trinidad and Tobago | 0 0 395 0 11 0 0 1 1 0 | <i>Klebsiella pneumoniae</i> |
| GCF 025819055.1 ASM2581905v1 genomic | GCF 025819055.1 | Trinidad and Tobago | 0 0 105 0 3 0 1 0 36 0 | <i>Klebsiella pneumoniae</i> |
| GCF 025819065.1 ASM2581906v1 genomic | GCF 025819065.1 | Trinidad and Tobago | 0 0 230 0 4 1 0 0 1 0 | <i>Klebsiella pneumoniae</i> |
| GCF 025819155.1 ASM2581915v1 genomic | GCF 025819155.1 | Trinidad and Tobago | 0 0 369 0 0 0 0 0 7 0 | <i>Klebsiella pneumoniae</i> |
| GCF 025819195.1 ASM2581919v1 genomic | GCF 025819195.1 | Trinidad and Tobago | 0 0 371 2 1 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 025819235.1 ASM2581923v1 genomic | GCF 025819235.1 | Trinidad and Tobago | 0 0 0 0 2 0 0 240 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 025819355.1 ASM2581935v1 genomic | GCF 025819355.1 | Trinidad and Tobago | 0 0 221 1 96 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 026191785.1 ASM2619178v1 genomic | GCF 026191785.1 | Brazil | 0 0 105 0 0 0 1 22 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 026191935.1 ASM2619193v1 genomic | GCF 026191935.1 | Brazil | 0 0 105 0 24 0 0 0 1 0 | <i>Klebsiella pneumoniae</i> |
| GCF 026191975.1 ASM2619197v1 genomic | GCF 026191975.1 | Brazil | 0 0 105 0 3 0 28 1 3 0 | <i>Klebsiella pneumoniae</i> |
| GCF 026222835.1 ASM2622283v1 genomic | GCF 026222835.1 | Brazil | 0 0 105 0 9 0 0 28 1 0 | <i>Klebsiella pneumoniae</i> |
| GCF 026222865.1 ASM2622286v1 genomic | GCF 026222865.1 | Brazil | 0 0 410 0 11 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 026223155.1 ASM2622315v1 genomic | GCF 026223155.1 | Brazil | 0 0 541 4 0 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 026223235.1 ASM2622323v1 genomic | GCF 026223235.1 | Brazil | 0 0 105 0 3 0 16 1 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 026223255.1 ASM2622325v1 genomic | GCF 026223255.1 | Brazil | 0 0 105 0 3 0 16 1 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 026223265.1 ASM2622326v1 genomic | GCF 026223265.1 | Brazil | 0 0 0 0 2 0 75 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 026620175.1 ASM2662017v1 genomic | GCF 026620175.1 | Brazil | 0 0 22 21 2 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 027124715.1 ASM2712471v1 genomic | GCF 027124715.1 | Brazil | 0 0 105 0 0 0 1 23 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 027890995.1 ASM2789099v1 genomic | GCF 027890995.1 | Brazil | 0 0 105 0 0 0 1 0 3 0 | <i>Klebsiella pneumoniae</i> |
| GCF 027891035.1 ASM2789103v1 genomic | GCF 027891035.1 | Brazil | 0 0 105 0 0 0 1 0 4 0 | <i>Klebsiella pneumoniae</i> |
| GCF 027945645.1 ASM2794564v1 genomic | GCF 027945645.1 | Brazil | 0 0 22 27 0 0 0 126 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF 028067495.1 ASM2806749v1 genomic | GCF 028067495.1 | Trinidad and Tobago | 0 0 105 0 9 0 0 0 0 0 | <i>Klebsiella pneumoniae</i> |

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|--|-----------------|-----------|------------------------|------------------------------|
| GCF_029076025.1_ASM2907602v1_genomic | GCF_029076025.1 | Brazil | 0 0 105 0 0 0 1 4 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_029079265.1_ASM2907926v1_genomic | GCF_029079265.1 | Brazil | 0 0 105 0 11 0 0 0 4 0 | <i>Klebsiella pneumoniae</i> |
| GCF_029079765.1_ASM2907976v1_genomic | GCF_029079765.1 | Brazil | 0 0 105 6 0 0 69 0 1 0 | <i>Klebsiella pneumoniae</i> |
| GCF_029193615.1_ASM2919361v1_genomic | GCF_029193615.1 | Chile | 0 0 429 0 25 0 1 1 0 0 | <i>Klebsiella pneumoniae</i> |
| GCF_928375135.1_BB1542_assembly_hybrid_genomic | GCF_928375135.1 | Venezuela | 0 0 107 0 1 9 3 0 1 0 | <i>Klebsiella pneumoniae</i> |

