

Supplemental table 1. Features of pKPI-6 ORFs (GenBank accession no. AB616660)

| ORF | Position (bp) | | Strand | Gene | Length | | Description | Identity (%) | Overlap ^b | | Function/product |
|-----|---------------|-------|--------|------------------------------|-------------------|---|--|--------------|----------------------|---------------|---|
| | start | stop | | | (aa) ^a | Source | | | (aa) | Accession no. | |
| 1 | 1 | 720 | + | <i>repA</i> | 239 | <i>K. pneumoniae</i> (plasmid 12) | Initiator Replication protein | 100 | 239/239 | YP_002286934 | Initiation of plasmid replication |
| 2 | 2417 | 2986 | - | <i>resP</i> | 189 | <i>K. pneumoniae</i> subsp. <i>ozaenae</i> (pK06) | resolvase, Site-specific recombinases | 100 | 189/189 | AGW99991 | Resolvase |
| 3 | 3379 | 4392 | - | <i>intI1</i> | 337 | <i>Shigella flexneri</i> 2b (plasmid R100) | IntI (E2) integrases, site-specific tyrosine recombinases | 100 | 337/337 | NP_052698 | Class 1 integrase |
| 4 | 4494 | 5114 | + | <i>aacA4'</i> | 210 | uncultured bacterium (pKSP212) | aminoglycoside (6')-N-acetyltransferase | 97 | 204/210 | ADC80806 | Aminoglycoside acetyltransferase |
| 5 | 5191 | 5931 | + | <i>bla_{IMP-6}</i> | 246 | <i>Serratia marcescens</i> | metallo-β-lactamase | 100 | 246/246 | BAB15941 | Metallo-β-lactamase |
| 6 | 6076 | 6855 | + | <i>aadA2</i> | 267 | Gammaproteobacteria | Streptomycin 3'-adenyltransferase | 100 | 267/267 | WP_000729308 | Aminoglycoside adenytransferase |
| 7 | 6996 | 8111 | + | <i>tnpA</i> of IS91 family | 371 | <i>Psychromonas ossibalaenae</i> | <i>tnpA</i> of IS91 family | 55 | 198/359 | WP_019617277 | Transposase of IS91 family |
| 8 | 8481 | 8828 | + | <i>qacEA1</i> | 115 | <i>Citrobacter freundii</i> (pT-OXA-181) | Quaternary ammonium compound resistance | 100 | 115/115 | AGE11240 | Quaternary ammonium compound resistance |
| 9 | 8822 | 9661 | + | <i>sulI</i> | 279 | <i>Shigella flexneri</i> 2b (plasmid R100) | dihydropteroate synthase | 100 | 279/279 | NP_052895 | Dihydropteroate synthase |
| 10 | 9789 | 10289 | + | <i>orf5</i> | 166 | <i>Desulfurispirillum indicum</i> S5 | GCN5-like N-acetyltransferase | 100 | 166/166 | YP_004111325 | Unknown |
| 11 | 10766 | 11560 | + | <i>tnpA</i> of IS6100 | 264 | <i>E. coli</i> (pEK499) | transposase for insertion sequence IS6100 | 100 | 264/264 | YP_003108355 | Transposase of IS6100 |
| 12 | 11821 | 13035 | + | <i>EcoRII</i> | 404 | <i>K. pneumoniae</i> NK245 (pK245) | N-terminal domain of type IIE restriction endonuclease <i>EcoRII</i> | 100 | 404/404 | YP_001966230 | Restriction endonuclease type II |
| 13 | 13069 | 14502 | - | <i>EcoRIImet</i> | 477 | <i>E. coli</i> (pMUR050) | DNA cytosine methylase | 100 | 477/477 | YP_724464 | DNA methylase |
| 14 | 14884 | 15090 | - | hypothetical protein | 68 | <i>K. pneumoniae</i> (plasmid 12) | hypothetical protein | 100 | 68/68 | YP_002287015 | Unknown |
| 15 | 15095 | 15604 | - | <i>mrr</i> | 169 | <i>E. coli</i> (pNDM-BTR) | Restriction endonuclease | 100 | 169/169 | YP_008574960 | Restriction endonuclease |
| 16 | 15792 | 16103 | - | hypothetical protein | 103 | <i>Salmonella typhimurium</i> (plasmid R46) | unknown | 100 | 103/103 | NP_511182 | Unknown |
| 17 | 16139 | 16453 | - | <i>kikA</i> | 104 | <i>K. pneumoniae</i> (plasmid 12) | conjugal transfer protein TrbM | 100 | 104/104 | YP_002287012 | Killing of <i>Klebsiella</i> during conjugation |
| 18 | 16450 | 16794 | - | hypothetical protein | 114 | <i>K. pneumoniae</i> (plasmid 12) | unknown | 100 | 114/114 | YP_002287011 | Unknown |
| 19 | 16810 | 17115 | - | <i>korB</i> | 101 | <i>E. coli</i> 517-2H1 (pLEW517) | histone-like proteins of HNS family | 100 | 101/101 | YP_001096375 | Initiation of kik mediated killing |
| 20 | 17224 | 17958 | + | <i>traL</i> | 244 | <i>K. pneumoniae</i> (plasmid 12) | Lytic Transglycosylase | 100 | 244/244 | YP_002287009 | Conjugal transfer |
| 21 | 17955 | 18248 | + | <i>korA</i> | 97 | <i>K. oxytoca</i> KOX105 (pKOX105) | Initiation of kik mediated killing | 100 | 97/97 | YP_003675738 | Initiation of kik mediated killing |
| 22 | 18258 | 18551 | + | <i>traM</i> | 97 | <i>K. pneumoniae</i> (plasmid 9) | Conjugal transfer | 100 | 97/97 | YP_002286912 | Conjugal transfer |
| 23 | 18601 | 18918 | + | <i>traA</i> | 78 | <i>E. coli</i> L46 (pEC_L46) | Type IV secretory pathway | 100 | 78/78 | YP_003829295 | Conjugal transfer |
| 24 | 18918 | 21518 | + | <i>traB</i> | 866 | <i>K. pneumoniae</i> KP96 (pKP96) | conjugal transfer protein | 100 | 866/866 | YP_002332880 | Conjugal transfer |
| 25 | 21536 | 22249 | + | <i>traC</i> | 237 | <i>K. pneumoniae</i> (plasmid 9) | Type IV secretion system proteins | 100 | 237/237 | YP_002286909 | Conjugal transfer |
| 26 | 22257 | 22484 | + | <i>eex</i> | 75 | <i>E. coli</i> L46 (pEC_L46) | entry exclusion protein | 100 | 75/75 | YP_003829298 | Entry exclusion |
| 27 | 22500 | 23540 | + | <i>traD</i> | 346 | <i>K. pneumoniae</i> (plasmid 12) | TrbL/VirB6 plasmid conjugal transfer protein | 100 | 346/346 | YP_002286993 | Conjugal transfer |
| 28 | 23611 | 23769 | + | <i>traN</i> | 52 | <i>K. pneumoniae</i> (plasmid 12) | metallophosphatase superfamily | 100 | 52/52 | YP_002286992 | Conjugal transfer |
| 29 | 23759 | 24457 | + | <i>traE</i> | 232 | <i>K. pneumoniae</i> (plasmid 9) | VirB8 protein | 100 | 232/232 | YP_002286905 | Conjugal transfer |
| 30 | 24468 | 25352 | + | <i>traO</i> | 294 | <i>E. coli</i> L46 (pEC_L46) | type IV conjugative transfer system protein | 100 | 294/294 | YP_003829302 | Conjugal transfer |
| 31 | 25352 | 26512 | + | <i>traF</i> | 386 | <i>Photobacterium damsela</i> subsp. <i>piscicida</i> PT99-018 (pP99-018) | Bacterial conjugation TrbI-like protein | 100 | 386/386 | YP_908595 | Conjugal transfer |
| 32 | 26554 | 27549 | + | <i>traG</i> | 331 | <i>E. coli</i> (pMUR050) | conjugation | 100 | 331/331 | YP_724501 | Conjugal transfer |
| 33 | 27549 | 28082 | + | <i>nuc</i> | 177 | <i>K. oxytoca</i> E718 (pKOX_R1) | endonuclease | 100 | 177/177 | YP_006501590 | Periplasmic endonuclease |
| 34 | 28256 | 28750 | - | <i>ΔfipA</i> (1) | | <i>E. coli</i> 345-2RfC (plasmid N3) | fertility inhibition of IncP plasmids protein | | | YP_004558188 | Fertility inhibition of IncP plasmids (truncated) |
| 35 | 29019 | 29261 | + | <i>relaxase</i> | 80 | <i>E. coli</i> A2363 (pAPEC-O2-R) | relaxase | 100 | 80/80 | YP_190207 | Unknown |
| 36 | 29293 | 29919 | + | <i>tetR</i> | 208 | <i>Providencia stuartii</i> MRSN 2154 (pMR0211) | tetracycline repressor protein | 100 | 208/208 | YP_005351739 | tetracycline resistant regulatory protein |
| 37 | 30049 | 31248 | + | <i>tetA</i> | 399 | <i>K. pneumoniae</i> KP96 (pKP96) | tetracycline resistance protein | 100 | 399/399 | YP_002332890 | tetracycline resistant protein A |
| 38 | 31280 | 31978 | - | <i>pecM</i> | 232 | <i>E. coli</i> (pHKU1) | EamA-like transporter family | 100 | 232/232 | YP_008574853 | Unknown |
| 39 | 32165 | 32301 | - | <i>ΔfipA</i> (2) | | <i>E. coli</i> 345-2RfC (plasmid N3) | fertility inhibition of IncP plasmids protein | | | YP_004558188 | Fertility inhibition of IncP plasmids (truncated) |
| 40 | 32301 | 35543 | - | <i>traI</i> | 1080 | <i>K. pneumoniae</i> KP96 (pKP96) | conjugal transfer protein | 100 | 1080/1080 | YP_002332893 | Conjugal transfer |
| 41 | 35543 | 37072 | - | <i>traJ</i> | 509 | <i>K. pneumoniae</i> KP96 (pKP96) | conjugal transfer protein | 100 | 509/509 | YP_002332894 | Conjugal transfer |
| 42 | 37074 | 37490 | - | <i>traK</i> | 138 | <i>K. pneumoniae</i> (plasmid 12) | conjugal transfer protein | 100 | 138/138 | YP_002286951 | Conjugal transfer |
| 43 | 38020 | 38400 | + | <i>stbA</i> | 126 | <i>K. pneumoniae</i> (plasmid 12) | prevention of the induction of SOS-responses | 99 | 125/126 | YP_002286950 | Prevention of SOS response |
| 44 | 38409 | 39125 | + | <i>stbB</i> | 238 | <i>K. pneumoniae</i> (plasmid 12) | plasmid stability protein | 100 | 238/238 | YP_002286949 | Stable plasmid inheritance |
| 45 | 39127 | 39495 | + | <i>stbC</i> | 122 | <i>Salmonella typhimurium</i> (plasmid R46) | stable plasmid inheritance | 100 | 122/122 | NP_511206 | Stable plasmid inheritance |
| 46 | 39677 | 40021 | + | <i>orfD</i> | 114 | <i>Salmonella typhimurium</i> (plasmid R46) | hypothetical protein | 100 | 114/114 | NP_511207 | Unknown |
| 47 | 40132 | 40452 | - | <i>cagAII</i> | 106 | <i>K. pneumoniae</i> (plasmid 12) | member of CUP-controlled regulon; similar to RecX | 100 | 106/106 | YP_002286945 | Prevention of RecA overproduction |
| 48 | 40530 | 40769 | - | <i>cagEIII</i> | 79 | <i>Salmonella typhimurium</i> (plasmid R46) | member of CUP-controlled regulon | 100 | 79/79 | NP_511213 | Unknown |
| 49 | 40779 | 41183 | - | <i>ardR</i> | 134 | <i>E. coli</i> L46 (pEC_L46) | antirestriction protein | 100 | 134/134 | YP_003829321 | Regulation of <i>cag</i> genes |
| 50 | 41241 | 41666 | - | <i>ardB</i> | 141 | <i>E. coli</i> L46 (pEC_L46) | Antirestriction protein | 100 | 141/141 | YP_003829320 | Inhibition of host type I restriction enzymes |
| 51 | 42348 | 43223 | - | <i>bla_{CTX-M-2}</i> | 291 | <i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Typhimurium | Beta-lactamase | 100 | 291/291 | P74841 | Extended-spectrum-β-lactamase |
| 52 | 43480 | 44742 | - | <i>tnpA</i> | 420 | <i>E. coli</i> L46 (pEC_L46) | IS <i>Ecp1</i> transposase | 100 | 420/420 | YP_003829282 | Transposase of IS <i>Ecp1</i> |
| 53 | 45005 | 45379 | + | <i>ΔmucB</i> | 124 | <i>K. pneumoniae</i> | DNA polymerase V subunit | 99 | 123/124 | WP_020320119 | UV protection (truncated) |
| 54 | 45494 | 46321 | + | <i>mpr</i> | 275 | <i>K. oxytoca</i> KOX105 (pKOX105) | zinc metalloproteinase | 100 | 275/275 | YP_003675760 | Unknown |
| 55 | 46336 | 46677 | - | <i>ardK</i> | 113 | <i>Salmonella typhimurium</i> (plasmid R46) | control of expression of genes fused to CUP sequences | 100 | 113/113 | NP_511219 | Regulation of <i>cag</i> genes |
| 56 | 46761 | 46952 | - | hypothetical protein | 63 | Enterobacteriaceae | unknown | 100 | 63/63 | WP_016750023 | Unknown |

^a aa, amino acids.^b Overlap indicates the number of overlapping amino acids/total number of amino acids.

Supplemental table 2. Primers used in this study.

| Primer set No. | Primer | Sequence | Amplicon size (bp) | References |
|----------------------------|--------------------------------------|---|--------------------|---|
| For PCR scanning of In722 | | | | |
| A | intl1-1014R intl1-F | CTACCTCTCACTAGTGAGGG GCATCCTCGGTTTTCTGG | 644 | Kouda <i>et al.</i> Kouda <i>et al.</i> |
| B | intl1-501R aac6'lb-R aac6'lb-F | CACGATGATCGTGCCGTGAT CCCAAGCCTTTGCCAGTTG GAGTGGTGGGGCGGAGAAGA | 1009 | Kouda <i>et al.</i> Kouda <i>et al.</i> Kouda <i>et al.</i> |
| C | imp-6-500R | GGCAACCAAACCACTACGTT | 1038 | this study |
| D | imp-1-381F aadA2-447R | CGGTAAGGTTCAAGCCACAA AGCTTCAAGGTTTCCCTC | 1009 | Kouda <i>et al.</i> this study |
| E | aadA2-212F transposase-315R | AATTTCGAACCAACTATCAGAG AAAGACTCCGCAGAGATG | 1083 | this study this study |
| F | transposase-81F tamspase-1241R | TTCACCATCAAGTGTAGCTG GCCGCTATTCGTTCTGTG | 1153 | this study this study |
| G | transposase-569F qacEdelta1-R | GCGTCGCTAAATATTTAGCTC AGCAATTATGAGCCCATAC | 1043 | this study Kouda <i>et al.</i> |
| H | qacEdelta1-269F sul1-527R | GTATGGGGCTCATAATTGCT ATCCCGGATCGAGGATGAG | 600 | Kouda <i>et al.</i> Kouda <i>et al.</i> |
| I | sul1-435F orf5-107R | GCTCGACGAGATTGTGCGGT GTTCCCTTGGCGGACATCCA | 640 | Kouda <i>et al.</i> Kouda <i>et al.</i> |
| J | sul1-815F orf5-R | GAGACCGAGGGTTAGATCAT ATTTGAGTTCTAGGCGTTC | 650 | Kouda <i>et al.</i> Kouda <i>et al.</i> |
| For PCR scanning of pKPI-6 | | | | |
| 1 | repA-40F resP-51F | GTCTAACGAGCTTACCGAAG CCAGGTTGACGAACTAACAA | 2898 | Aurora <i>et al.</i> this study |
| 2 | resP-237R imp-1-500R | TAATGACTTGACCCAATGAAC GGCAGCCAAACCACTACGTT | 2942 | this study Kouda <i>et al.</i> |
| 3 | imp-1-381F qacEdelta1-R | CGGTAAGGTTCAAGCCACAA AGCAATTATGAGCCCATAC | 3259 | Kouda <i>et al.</i> Kouda <i>et al.</i> |
| 4 | qacEdelta1-269F IS6100-631R | GTATGGGGCTCATAATTGCT ATCCCTTGATCGTGGCATAG | 2639 | Kouda <i>et al.</i> this study |
| 5 | Sul815F EcoRIIm1325F | GAGACCGAGGGTTAGATCAT AGTTCGGTAACTCCGTAGTGG | 3703 | Kouda <i>et al.</i> this study |
| 6 | EcoRII-686F kikA-248F | TTCTATTGGTTGAGGAACTGC GCGAAGGTGGAAGTAACCAG | 3701 | this study this study |
| 7 | mrr-kikA-F traL-593R | CCATAGAATAAGGTTTTCTGTAGTG CCCTTCGCTGTTTCTGTCT | 2254 | this study this study |
| 8 | traL-173F traB-2574R | ATAATTTAGTGGGCCTGGGTC GAGCCATACTTCAGGGTC | 3961 | this study this study |
| 9 | traB-2360F traO-305R | TGTCGATTACCGAACACTC ATCACCAGGTTGGTATCACTC | 3476 | this study this study |
| 10 | traE516F nuc526R | AGCAACGATACGCTTTACTAC TGGAACGGTAGTCTCTCC | 3806 | this study this study |
| 11 | nuc-321F tetA-888R | TACTGACAGTGATTTCCCTATCC GAAGGCAAGCAGGATGTAGC | 3068 | this study this study |
| 12 | tetR-179R tral-1110F | ACCGAATGCGTATGATTCTC ACCTGAAGGCGGTACAGAAG | 4258 | this study this study |
| 13 | tral-1773R traK-286F | GCGAGCGTTATGCTTCTC TGCATGAATCACTCGCTATTG | 3434 | this study this study |
| 14 | traJ-135R cagAII-195F | TAACCAGATACGGAATCAGG ATTTGACTATCTGACCCAAGAC | 3322 | this study this study |
| 15 | cagAII-282R ISEcpl-470F | ATTACGCTCAATACCGTGG CCTAAGAACTGGGAAACCG | 4122 | this study this study |
| 16 | ISEcpl-1117R repA-553R | AGTCCAAGGAATCAAACCTTG ACGGTCATTTAACCAAGCATG | 4163 | this study Aurora <i>et al.</i> |

Supplemental table 3. Result of susceptibility testing

| Strain | Name | Place | Year | ABPC | PIPC | CEZ | CAZ | CPR | CMZ | CPDX | AZT | IPM | MEPM | A/C | C/S | P/T | AMK | GM | MINO | CPFX | IPM [#] | MEPM [#] | PAPM [#] | BIPM [#] | DRPM [#] |
|----------------------|--------|------------|------|------|------|-----|-----|-----|-----|------|-----|------|------|-----|-----|-----|-----|----|------|-------|------------------|-------------------|-------------------|-------------------|-------------------|
| <i>K. pneumoniae</i> | a26 | Hiroshima | 2009 | >16 | >64 | >16 | >16 | >16 | >32 | >4 | >16 | 1 | >8 | 16 | >32 | ≤16 | ≤4 | 4 | >8 | >2 | 1 | 32 | 1 | 1 | 32 |
| <i>K. pneumoniae</i> | MS5263 | Amagasaki | 2011 | >16 | >64 | >16 | >16 | >16 | >32 | >4 | >16 | 2 | >8 | >16 | >32 | >64 | ≤4 | >8 | >8 | ≤0.25 | 2 | 256 | 8 | 2 | 256 |
| <i>K. pneumoniae</i> | MS5265 | Amagasaki | 2011 | >16 | >64 | >16 | 16 | >16 | >32 | >4 | 16 | ≤0.5 | 8 | 16 | >32 | ≤16 | ≤4 | 2 | 8 | >2 | 0.25 | 32 | 0.5 | ≤0.125 | 64 |
| <i>K. pneumoniae</i> | MS5266 | Amagasaki | 2011 | >16 | >64 | >16 | 16 | >16 | >32 | >4 | 8 | 2 | >8 | 16 | >32 | ≤16 | 8 | 2 | 8 | ≤0.25 | 1 | 32 | 2 | 1 | 64 |
| <i>K. pneumoniae</i> | MS5283 | Kinki area | 2006 | >16 | >64 | >16 | >16 | >16 | >32 | >4 | >16 | 2 | >8 | >16 | >32 | >64 | ≤4 | >8 | >8 | ≤0.25 | 2 | 128 | 8 | 0.5 | 128 |
| <i>K. pneumoniae</i> | MS5287 | Kinki area | 2008 | >16 | >64 | >16 | 16 | >16 | >32 | >4 | 4 | ≤0.5 | 8 | 16 | >32 | ≤16 | ≤4 | 4 | 8 | >2 | 0.5 | 32 | 1 | 1 | 32 |
| <i>K. pneumoniae</i> | MS5288 | Kinki area | 2009 | >16 | >64 | >16 | 8 | >16 | 32 | >4 | 8 | ≤0.5 | >8 | 8 | 32 | ≤16 | ≤4 | 4 | 4 | ≤0.25 | 0.5 | 16 | 0.5 | 0.5 | 8 |
| <i>K. pneumoniae</i> | MS5289 | Kinki area | 2010 | >16 | >64 | >16 | >16 | >16 | >32 | >4 | >16 | 1 | >8 | 16 | >32 | ≤16 | ≤4 | 4 | 8 | >2 | 1 | 32 | 1 | 0.5 | 32 |
| <i>K. pneumoniae</i> | MS5290 | Kinki area | 2010 | >16 | >64 | >16 | >16 | >16 | >32 | >4 | 16 | 1 | >8 | 16 | >32 | ≤16 | ≤4 | 8 | 4 | >2 | 1 | 64 | 4 | 2 | 32 |
| <i>K. pneumoniae</i> | MS5291 | Kinki area | 2010 | >16 | 16 | >16 | >16 | ≤8 | >32 | >4 | ≤1 | 2 | >8 | 16 | >32 | ≤16 | ≤4 | 4 | 8 | >2 | 1 | 128 | 8 | 4 | 64 |
| <i>K. pneumoniae</i> | MS5292 | Kinki area | 2010 | >16 | >64 | >16 | 4 | >16 | 32 | >4 | 4 | 1 | >8 | 8 | >32 | ≤16 | ≤4 | 4 | 4 | ≤0.25 | 0.5 | 16 | 0.5 | 0.5 | 8 |
| <i>K. pneumoniae</i> | MS5293 | Kinki area | 2009 | >16 | >64 | >16 | >16 | >16 | >32 | >4 | >16 | 1 | >8 | >16 | >32 | ≤16 | ≤4 | 2 | >8 | >2 | 0.5 | 32 | 1 | 1 | 16 |
| <i>K. pneumoniae</i> | MS5294 | Kinki area | 2009 | >16 | >64 | >16 | >16 | >16 | >32 | >4 | >16 | ≤0.5 | >8 | 16 | >32 | ≤16 | ≤4 | 4 | 4 | >2 | 2 | 32 | 4 | 0.25 | 32 |
| <i>K. pneumoniae</i> | MS5295 | Kinki area | 2010 | >16 | >64 | >16 | >16 | >16 | >32 | >4 | 16 | ≤0.5 | >8 | 16 | >32 | ≤16 | ≤4 | 4 | 4 | >2 | 1 | 32 | 2 | 0.5 | 32 |
| <i>K. oxytoca</i> | MS5282 | Kinki area | 2009 | >16 | >64 | >16 | >16 | >16 | >32 | >4 | >16 | 1 | >8 | 16 | >32 | ≤16 | 8 | 8 | >8 | >2 | 0.5 | 32 | 1 | 0.25 | 16 |
| <i>E. coli</i> | MS5264 | Amagasaki | 2011 | >16 | >64 | >16 | >16 | >16 | >32 | >4 | >16 | 1 | >8 | >16 | >32 | >64 | ≤4 | >8 | 2 | >2 | 0.5 | 32 | 1 | 0.25 | 64 |
| <i>E. coli</i> | MS5267 | Amagasaki | 2011 | >16 | >64 | >16 | 16 | >16 | >32 | >4 | >16 | 1 | 8 | 16 | >32 | ≤16 | 8 | 8 | 8 | >2 | 0.25 | 8 | 0.25 | 0.25 | 4 |
| <i>E. coli</i> | MS5275 | Kinki area | 2006 | >16 | >64 | >16 | >16 | >16 | >32 | >4 | >16 | 1 | >8 | 16 | >32 | ≤16 | ≤4 | ≤1 | 4 | >2 | 0.25 | 16 | 0.5 | ≤0.125 | 8 |
| <i>E. coli</i> | MS5276 | Kinki area | 2006 | >16 | >64 | >16 | >16 | >16 | >32 | >4 | >16 | 1 | >8 | >16 | >32 | ≤16 | ≤4 | ≤1 | >8 | >2 | 0.5 | 16 | 0.5 | ≤0.125 | 8 |
| <i>E. coli</i> | MS5277 | Kinki area | 2009 | >16 | >64 | >16 | 16 | >16 | >32 | >4 | >16 | 1 | >8 | 16 | >32 | ≤16 | ≤4 | 4 | 4 | 0.5 | 0.5 | 16 | 1 | ≤0.125 | 8 |
| <i>E. coli</i> | MS5278 | Kinki area | 2010 | >16 | >64 | >16 | 8 | >16 | >32 | >4 | >16 | 1 | 8 | 16 | >32 | ≤16 | ≤4 | 8 | 2 | ≤0.25 | 0.25 | 2 | ≤0.125 | ≤0.125 | 1 |

Susceptibility tests were performed by MicroScan WalkAway (Siemens Healthcare Diagnostics, Tokyo, Japan), NMIC6.31J.

Susceptibility tests were performed by the microdilution method (7).

ABPC; Ampicillin, PIPC; Piperacillin, CEZ; Cefazolin, CAZ; Ceftazidime, CPR; Cefpirome, CMZ; Cefmetazole, CPDX; Cefpodoxime, AZT; Aztreonam, IPM; Imipenem, MEPM; Meropenem, A/C; Amoxicillin/Clavulanate, C/S; Cefoperazone/Sulbactam, P/T; Piperacillin/Tazobactam, AMK; Amikacin, GM; Gentamicin, MINO; Minocycline, CPFX; Ciprofloxacin, PAPM; Panipenem, BIPM; Biapenem, DRPM; Doripenem