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| **Table S1 Profiles of antimicrobial resistance gene in F11 chromosome of *Klebsiella pnenmoniae*** |
| **Antimicrobial resistance gene** | **Identity (%)** | **Position (bp)** | **Antimicrobial resistance category** |
| *oqxB* | 98.45 | 1184025..1187177 | quinolone |
| *oqxA* | 99.15 | 1187201..1188376 | quinolone |
| *bla*SHV-187 | 99.88 | 2769227..2770093 | beta-lactam |
| *fosA* | 98.81 | 4537851..4538270 | fosfomycin |

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| **Table 2 Profiles of virlence gene in F11 chromosome of *Klebsiella pnenmoniae*** |
| **Virulence gene** | **Identity (%)** | **Position (bp)** | **Functional annotation** |
| **Adherence** |  |
|  | *fimK* | 98.87 | 861339..862580 | transcriptional regulator |
|  | *fimH* | 99.12 | 862748..863656 | type 1 fimbrial adhesin precursor |
|  | *fimG* | 99.4 | 863671..864171 | type 1 fimbrial minor component |
|  | *fimF* | 99.44 | 864184..864714 | type 1 fimbrial minor component |
|  | *fimD* | 99.7 | 864722..867367 | outer membrane usher protein |
|  | *fimC* | 99.86 | 867416..868141 | periplasmic chaperone |
|  | *fimI* | 99.37 | 868170..868805 | type 1 pilus biosynthesis fimbrial protein |
|  | *fimA* | 99.64 | 868777..869325 | type 1 major fimbrial subunit precursor |
|  | *fimE* | 99.01 | 869805..870413 | tyrosine recombinase |
|  | *fimB* | 99.5 | 870879..871484 | tyrosine recombinase |
| **Biofilm** |  |
|  | *mrkA* | 99.67 | 876150..876758 | type 3 fimbrial major pilin subunit MrkA |
|  | *mrkB* | 99.72 | 876854..877555 | fimbrial chaperone protein MrkB precursor |
|  | *mrkC* | 99.56 | 877567..880053 | fimbrial biogenesis outer membrane usher protein MrkC precursor |
|  | *mrkD* | 99.7 | 880044..881039 | fimbrial adhesin protein precursor MrkD |
|  | *mrkF* | 100 | 881053..881688 | type 3 fimbrial minor pilin subunit MrkF |
|  | *mrkJ* | 99.72 | 881723..882439 | phosphodiesterase |
|  | *mrkI* | 99.49 | 882583..883167 | LuxR family regulatory protein |
|  | *mrkH* | 99.86 | 883173..883883 | transcriptional activator |
| **Regulation** |  |
|  | *rcsB* | 100 | 1617043..1617693 | transcriptional regulator RcsB |
|  | *rcsA* | 100 | 1920312..1920935 | transcriptional activator for ctr capsule biosynthesis |
| **Immune modulation** |  |
|  | *gnd* | 97.07 | 1790127..1791491 | 6-phosphogluconate dehydrogenase |
|  | *ugd* | 97.51 | 1798298..1799422 | UDP-glucose 6-dehydrogenase |
|  | *galF* | 98.77 | 1768594..1769490 | UTP-glucose-1-phosphate uridylyltransferase subunit GalF |
|  | *cpsACP* | 91.17 | 1769883..1770481 | phosphatase PAP2 family protein |
|  | *wbbM* | 98.15 | 1805967..1807862 | glycosyltransferase |
|  | *wbbN* | 97.65 | 1809029..1809922 | glycosyltransferase |
|  | *glf* | 98.44 | 1807878..1809032 | UDP-galactopyranose mutase |
|  | *wbbO* | 97.71 | 1809935..1811025 | glycosyltransferase family 1 protein |
| **Type VI secretion system (T6SS)** |  |
|  | *sciN/tssJ* | 100 | 2968688..2969230 | type VI secretion system lipoprotein TssJ |
|  | *tssG* | 99.08 | 2969208..2970293 | type VI secretion system baseplate subunit TssG |
|  | *tssF* | 99.37 | 2970257..2972011 | type VI secretion system baseplate subunit TssF |
|  | *impA/tssA* | 96.8 | 2973278..2973683 | type VI secretion system protein TssA |
|  | *icmF/tssM* | 98.76 | 2973685..2976754 | type VI secretion protein TssM |
|  | *clpV/tssH* | 99.1 | 2985267..2987921 | type VI secretion system ATPase TssH |
|  | *hcp/tssD* | 100 | 2988186..2988677 | type VI secretion system protein, Hcp family |
|  | *dotU/tssL* | 99.42 | 2990385..2991074 | type VI secretion system protein, DotU/TssL family |
|  | *vasE/tssK* | 99.33 | 2991071..2992414 | type VI secretion system baseplate subunit TssK |
|  | *vipB/tssC* | 98.9 | 2992424..2993968 | type VI secretion system contractile sheath large subunit VipB |
|  | *vipA/tssB* | 99.19 | 2994011..2994502 | type VI secretion system contractile sheath small subunit VipA |
| **Siderophore uptake system** |  |
|  | *iroE* | 99.04 | 2692381..2693316 | siderophore esterase IroE |
|  | *fepB* | 99.58 | 3758936..3759895 | iron-enterobactin transporter periplasmic binding protein |
|  | *fepD* | 99.7 | 3761629..3762636 | iron-enterobactin transporter membrane protein |
|  | *fepG* | 98.69 | 3762633..3763625 | iron-enterobactin transporter permease |
|  | *fepA* | 99.28 | 3770072..3772300 | outer membrane receptor FepA |
|  | *entA* | 98.34 | 3754336..3755120 | 2,3-dihydroxybenzoate-2,3-dehydrogenase |
|  | *entB* | 98.23 | 3755094..3755941 | 2,3-dihydro-2,3-dihydroxybenzoate synthetase, isochroismatase |
|  | *entE* | 97.89 | 3755955..3757562 | enterobactin synthase subunit E |
|  | *entD* | 99.21 | 3772367..3772996 | enterochelin synthetase component D |
|  | *entC* | 99.41 | 3757572..3758759 | isochorismate synthase |
|  | *entF* | 99.05 | 3764481..3768362 | enterobactin synthase subunit F |
|  | *fes* | 98.92 | 3768604..3769812 | enterobactin/ferric enterobactin esterase |
|  | *ybdA* | 99.36 | 3760275..3761516 | enterobactin exporter EntS |
| **Antimicrobial activity** |  |
|  | *acrA* | 99.92 | 3961789..3962982 | acriflavine resistance protein A |
|  | *acrB* | 99.59 | 3963005..3966151 | acriflavine resistance protein B |
| ***E. coli*** common pilus |  |
|  | *yagW/ecpD* | 89.44 | 4116072..4117672 | polymerized tip adhesin of ECP fibers |
|  | *yagX/ecpC* | 87.48 | 4117705..4120211 | *E. coli* common pilus usher EcpC |
|  | *yagY/ecpB* | 88.89 | 4120256..4120876 | *E. coli* common pilus chaperone EcpB |
|  | *yagZ/ecpA* | 90.07 | 4120987..4121570 | *E. coli* common pilus structural subunit EcpA |
|  | *ykgK/ecpR* | 86.75 | 4121645..4122225 | regulator protein EcpR |

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| **Table S3 Sequence analysis for In1765 from plasmid\_pA\_F11 and In27 from plasmid\_pB\_F11** |
| **Integron Number** | **In1765** |  | **In27** |
| Pc variant | PcW | "-10": 112,032-112,037 bp |  | PcW | "-10": 33,092-33,097 bp |
| "-35": 112,055-112,060 bp | "-35": 33,069-33,074 bp |
| P2 promoter | Absent | Absent |
| PintI1 | OK | "-10": 111,913-111,918 bp | OK | "-10": 33,211-33,216 bp |
| "-35": 111,890-111,895 bp | "-35": 33,234-33,239 bp |
| 19 bp ORF11 dupl. | Yes | No |
| *IntI1* | IntI1P32\_H39 | 111,945-112,958 bp | IntI1P32\_H39 | 32,171-33,184 bp |
| *attI1* | 111,784-111,864 bp | 33,265-33,326 bp |
| Array of gene cassettes | *fosE*(111,328-111,789)-*attC*(111,322-111,381)-*gcu206*(111,050-111,327)-*attC*(111,044-111,104)-*bla*OXA-1Δ(110,979-111,049)-*ipaH*(109,645-110,978)- *bla*OXA-1Δ(108,708-109,649)-*attC*(108,702-108,791)-*catB3*(107,993-108,707)-*attC*(107,987-108,046)-3'CS | *dfrA12*(33,321-33,904)-*attC*(33,821- 33,910)-*gcuF*(33,905-34,224)-*attC*(34,171-34,230)-*aadA2*(34,225-35,080) -*attC*(35,027-35,086)-3'CS |
| 5'-CS | 111790-111830 bp | 33,280-33,320 bp |
| CDS of GC | fosE(111,376-111,780) /*gcu206*(None) /*bla*OXA-1(108,811-109,641) /*catB3*(108,041-108,673) | *dfrA12*(33,329-33,826) /*gcuF*(33,938-34,228) /*aadA2*(34,234-35,025) |
| *attC* | *attC*fosE(111,784-111,789; 111,328-111,381) /*attC*gcu206(111,322-111,327; 111,050-111,104) /*attCbla*OXA-1(111,044-111,049; 108,708-108,791) /*attC*catB3(108,702-108,707; 107,993-108,046) | *attC*dfrA12(33,321-33,326; 33,821-33,904) /*attC*gcuF(33,905-33,910; 34,171-34,224) /*attC*aadA(34,225-34,230; 35,027-35,080) |
| 3'-CS | 107,499-107,992 bp | 35,081-35,574 bp |
| GenBank accession number: Plasmid\_pA\_F11 (CP092902.1), Plasmid\_pB\_F11 (CP092903.1). |