

**Table S1** Allele number and MLST types of 90 *K. pneumoniae*

Panda code	Isolated time	<i>gapA</i>	<i>infB</i>	<i>mdh</i>	<i>pgi</i>	<i>phoE</i>	<i>rpoB</i>	<i>tonB</i>	MLST
No. 09	18.05.28~18.05.31	2	1	1	1	3	1	9	1933
No. 03		2	1	62	1	10	4	110	2286
No. 47		2	1	1	2	2	1	43	4680
No. 46		2	1	1	1	9	1	93	323
No. 21		2	1	2	1	4	4	8	60
No. 50		2	9	2	1	13	45	16	37
No. 05		2	1	62	3	10	4	110	405
No. 04		2	1	1	1	9	4	4	631
No. 52		2	1	1	2	2	1	43	4680
No. 07		2	1	62	3	10	4	110	405
No. 16		2	2	2	1	1	4	34	1017
No. 56		4	114	1	1	13	70	12	4659
No. 10		2	115	114	166	2	146	140	2890
No. 20		2	3	2	2	6	4	4	29
No. 01		2	3	1	8	12	1	22	4790
No. 22		2	1	62	3	10	4	4	4845
No. 02		3	1	1	1	9	4	177	839
No. 48		2	9	2	1	13	1	38	896
No. 14		2	1	2	2	10	4	9	458
No. 13		2	1	2	1	12	1	68	200
No. 51		2	1	62	3	10	4	110	405
No. 15		2	1	2	1	12	1	68	200
No. 23		2	1	5	2	7	4	23	314
No. 40		16	18	43	49	47	30	75	2462
No. 53		2	1	1	2	2	1	43	4680
No. 24		2	1	1	2	2	1	43	4680
No. 58		38	19	53	58	73	21	130	526
No. 54		43	3	1	1	1	4	91	4881
No. 55		4	114	1	1	13	70	12	4659
No. 57		2	1	1	2	2	1	43	4680
No. 08		4	1	6	1	12	5	30	1558
No. 11		2	1	1	1	9	4	4	631
No. 12		16	24	36	27	29	22	105	1562
No. 49		2	1	62	3	10	4	4	4845
No. 39		4	1	6	1	12	5	30	1558
No. 17		2	1	62	3	10	4	110	405
No. 06	18.9.11~18.9.14	16	1	21	76	47	22	152	615
No. 06		2	9	2	1	13	1	16	37
No. 14		2	9	2	1	13	1	16	37
No. 19		2	1	2	1	7	1	7	36
No. 43		2	1	2	4	9	1	16	39
No. 15		2	9	1	1	13	1	2	617
No. 30		120	9	2	1	13	1	16	4522
No. 05		4	1	2	1	1	4	62	983
No. 38		2	9	1	1	13	1	2	617
No. 42		10	3	2	1	4	1	4	1440
No. 17		2	1	65	1	10	11	2	1362
No. 02		2	1	1	2	16	4	337	2219
No. 12		18	22	18	16	25	13	165	1584
No. 25		4	3	1	36	9	10	14	661
No. 27		18	15	18	61	93	37	99	894
No. 59		18	15	18	22	31	13	51	1840
No. 60		2	5	118	1	179	1	13	1303
No. 61		2	1	1	1	7	2	12	1106
No. 01		2	1	1	1	4	4	4	17
No. 62		3	1	1	1	27	5	25	626
No. 29		2	5	118	1	10	1	13	1886
No. 09		18	15	18	61	93	37	99	894
No. 11		2	3	1	8	12	1	22	4790
No. 31		2	3	2	1	7	4	12	2938
No. 32		2	1	1	1	48	1	46	4683
No. 37		18	15	18	22	31	13	51	1840
No. 33		4	5	1	3	12	4	46	1078
No. 18		2	1	2	1	1	7	13	403
No. 03		2	1	2	1	7	45	7	36

No. 26		2	1	1	17	4	16	4	774
No. 07		2	9	2	1	13	1	10	309
No. 16		2	3	2	1	7	4	12	2938
No. 44		4	3	1	36	9	10	14	661
No. 04		6	3	1	1	12	45	4	12
No. 28		6	3	1	1	12	45	4	12
No. 08		2	1	2	1	1	1	7	298
No. 41		2	51	1	4	17	15	355	2473
No. 10		2	6	1	3	8	1	44	110
No. 13		4	3	1	36	9	10	14	661
No. 63		2	1	1	1	4	4	4	17
No. 34		2	1	33	1	1	4	56	730
No. 35	18.12.12~18.12.14	2	3	1	1	56	1	110	13
No. 39		2	1	2	1	4	4	8	60
No. 03		2	1	2	1	4	4	8	60
No. 37		2	1	2	1	9	1	112	412
No. 18		2	1	1	1	4	4	4	17
No. 01		16	115	370	166	47	146	606	2368
No. 07		2	3	2	2	6	4	4	29
No. 19		3	5	1	134	10	4	4	1798
No. 05		3	5	1	134	10	4	4	1798
No. 04		3	5	1	134	10	4	4	1798
No. 06		2	1	2	17	27	1	39	107
No. 02		2	1	4	14	1	5	30	1558
No. 38		2	1	4	14	1	5	30	1558

**Table S2** Primer sequence information of housekeeping gene of *K. pneumoniae*

Housekeeping Gene	abbreviate	Primer Sequence	Length (bp)
beta-subunit of RNA polymerase	rpoB	F: Vic3oF: GTTTTCCCAGTCACGACGTTGTAGGCGAAATGGCWGAGAACCA	501
		R: Vic2oR: TTGTGAGCGGATAACAATTTTCGAGTCTTCGAAGTTGTAACC	
glyceraldehyde 3-phosphate dehydrogenase	gapA	F: gapA173oF: GTTTTCCCAGTCACGACGTTGTATGAAATATGACTCCACTCACGG	450
		R: gapA181oR: TTGTGAGCGGATAACAATTTCTTCAGAAAGCGGCTTTGATGGCTT	
malate dehydrogenase	mdh	F: mdh130oF: GTTTTCCCAGTCACGACGTTGTACCCAACCTCGCTTCAGGTTTCAG	477
		R: mdh867oR: TTGTGAGCGGATAACAATTTCCCGTTTTTCCCCAGCAGCAG	
phosphoglucose isomerase	pgi	F: pgi1FoF: GTTTTCCCAGTCACGACGTTGTAGAGAAAAACCTGCCTGTACTGCTGGC	432
		R: pgi1RoR: TTGTGAGCGGATAACAATTTCCGCGCCACGCTTTATAGCGGTTAAT	
phosphorine E	phoE	F: phoE604.1oF: GTTTTCCCAGTCACGACGTTGTAACCTACCGCAACACCGACTTCTTCGG	420
		R: phoE604.2oR: TTGTGAGCGGATAACAATTTCTGATCAGAACTGGTAGGTGAT	
translation initiation fact or 2	infB	F: infB1FoF: GTTTTCCCAGTCACGACGTTGTACTCGCTGCTGGACTATATTCG	318
		R: infB1RoR: TTGTGAGCGGATAACAATTTCCGCTTTCAGCTCAAGAACTTC	
periplasmic energy transducer	tonB	F: tonB1FoF: GTTTTCCCAGTCACGACGTTGTACTTTATACCTCGGTACATCAGGTT	414
		R: tonB2RoR: TTGTGAGCGGATAACAATTTTCATTCGCCGGCTGRGCRGAGAG	

**Table S3** Determination criteria for antibiotic resistance profiles

Types	Antibiotics	Content (μg/tablet)	Diameter (mm)		
			Resistance (R)	Intermediate (I)	Sensitivity (S)
β-lactams	cefotaxime (CTX)	30	≤14	15-17	≥18
	cefaclor (CEC)	30	≤14	15-17	≥18
	meropenem (MEM)	10	≤28	29-37	≥38
	Cefradine (CE)	30	≤14	15-17	≥18
	ampicillin (AMP)	10	≤13	14-16	≥17
Aminoglycosides	Amikacin (AK)	30	≤14	15-16	≥17
	neomycin (N)	30	≤12	13-16	≥17
Quinolones	Ciprofloxacin (CIP)	5	≤15	16-22	≥23
	enrofloxacin (ENR)	10	≤21	22-28	≥29
Tetracyclines	tetracycline (TE)	30	≤14	15-18	≥19
	doxycycline (DOX)	30	≤12	13-15	≥16
Others	Compound sulfamethoxazole (SXT)	24	≤23	24-32	≥33
	rifampicin (RD)	5	≤16	17-19	≥20
	azithromycin (AZM)	15	≤13	14-17	≥18

Florfenicol (FON)	30	≤12	13-17	≥18
Polymyxin B (PB)	300	≤7	8-11	≥12

**Table S4** Primers information of antibiotic resistance genes (ARGs)

Classification	Gene	Forward primer	Reverse primer
aminoglycoside	<i>aac</i>	CCCTGCGTTGTGGCTATGT	TGGCCACGCCAATCC
aminoglycoside	<i>aac(3)-I</i>	ACCTACTCCCAACATCAGCC	ATATAGATCTCACTACGCGC
aminoglycoside	<i>aac(6')I1</i>	GACCGGATTAAGGCCGATG	CTTGCCITGATATTCAGTTTTTATAACCA
aminoglycoside	<i>aac(6')-Ib(aka aacA4)-01</i>	GTTTGAGAGGCAAGGTACCGTAA	GAATGCCTGGCGTGTGTTGA
aminoglycoside	<i>aac(6')-Ib(aka aacA4)-02</i>	CGTCGCCGAGCAACTTG	CGGTACCTTGCCCTCTCAAACC
aminoglycoside	<i>aac(6')-Ib(aka aacA4)-03</i>	AGAAGCACGCCCGACACTT	GCTCTCCATTTCAGCATTGCA
aminoglycoside	<i>aac(6')-II</i>	CGACCCGACTCCGAACAA	GCACGAATCCTGCCTTCTCA
aminoglycoside	<i>aac(6')-Iy</i>	GCTTTGCGGATGCCTCAAT	GGAGAACAAAAATACCTTCAAGGAAA
aminoglycoside	<i>ant (3')-I</i>	TGATTTGCTGGTTACGGTGAC	CGCTATGTTCTCTTGCTTTTC
aminoglycoside	<i>aph</i>	TTTCAGCAAGTTGGATCATGTTAAAAAT	CCAAGCTGTTTCCACTGTTTTTC
aminoglycoside	<i>aph(2')-Id-01</i>	TGAGCAGTATCATAAGTTGAGTGAAAAAG	GACAGAACAATCAATCTCTATGGAATG
aminoglycoside	<i>aph6ia</i>	CCCATCCCATGTGTAAGGAAA	GCCACCGCTTCTGCTGTAC
aminoglycoside	<i>aphA1(aka kanR)</i>	TGAACAAGTCTGGAAAGAAATGCA	CCTATTAATTTCCCTCTCGTCAAAAA
aminoglycoside	<i>aphA3-01</i>	TGACGATCCGAGGAGTATC	AGCTGGTGAACGTACTAC
aminoglycoside	<i>aphA3-02</i>	CAATCGGATCGTCAAGCGATC	ATGCTACTTGAGCTTAGGCGAAA
fca	<i>acrA-03</i>	CAGACCCGATCGCATATT	CGACAATTTCCGCTCATG
integron	<i>intl-1</i>	CGAACGAGTGCGCGAGGGTG	TACCCGAGAGCTTGGCACCCA
integron	<i>Int12-01</i>	GACGAATAATCGTGACGACGAT	ACTTTCTCGGTCTGCCATGAG
integron	<i>Int12-02</i>	AACGTAGCTCTGAAAACGCAGTT	TATGTGACCTGGCGATGATTGAC
integron	<i>Int13-01</i>	CCGAAAAGAAGGGATTAAGCGAG	AACGGTTTACGGAACGTACGACC
integron	<i>Int13-02</i>	ATCGGAAATCGATTCCGACT	ATGGCAATCGATCGAATTCA
MLSB	<i>ermA</i>	TTGAGAAGGGGATTGCGAAAAAG	ATATCCATCTCCACCATAATAGTAAACC
MLSB	<i>ermB</i>	TAAAGGGCATTTAACGACGAAACT	TTTATACCTCTGTTGTAGGGAATTGAA
MLSB	<i>ermC</i>	TTTGAAATCGGCTCAGGAAAA	ATGGTCTATTTCATGGCAGTTACG
MLSB	<i>mcr1</i>	CGCGATGCTACTGATACCA	GGTCGTATCATAGACCGTGCC
MLSB	<i>mcr2</i>	AATCGTACCCAAGTAATC	TAGGCTGAAACTGTCTAAATCG
MLSB	<i>msrA-01</i>	CTGCTAACACAAGTACGATTCCAAAT	TCAAGTAAAGTTGTCTTACCTACACCATT
other	<i>IS26</i>	TACCGTAAGGCTACAACGT	AACTGAGCTAGCTCCTTTACGGC
other	<i>IS3</i>	TCCGGCTAGTCAATTTCGGACCGA	TACGTAAAGGCTAGCTTACG
other	<i>IS613</i>	AGGTTTCGGACTCAATGCAACA	TTCAGCACATACCGCCTTGAT
other	<i>ISCR1</i>	ACTGGCAAACGGTCATCG	ACTGTCCGATCCCTTACTGAAACT
other/efflux	<i>qacA</i>	TGGCAATAGGAGCTATGGTGTTT	AAGGTAACACTATTTTCGGTCCAAATC
other/efflux	<i>qacEdelta1-01</i>	TCGCAACATCCGCATTAAAA	ATGGATTTTCAAGAACAGAGAAAGAAA
other/efflux	<i>qacEdelta1-02</i>	CCCCTTCCGCCGTTGT	CGACCAGACTGCATAAGCAACA
other/efflux	<i>qacH-01</i>	GTGGCAGCTATCGCTTGGAT	CCAACGAACGCCACAA
other/efflux	<i>qacH-02</i>	GTGGCAGCTATCGCTTGGAT	TGAACGCCCAGAAGCTAGTTTTT
quinilone	<i>acrA-01</i>	CAACGATCGGACGGGTTTC	TGGCGATGCCACCGTACT
quinilone	<i>acrA-02</i>	GGTCTATCACCTACGCGCTATC	GCGCGCACGAACATACC
quinilone	<i>acrB-01</i>	AGTCGGTGTTTCGCCGTTAAC	CAAGGAAACGAACGCAATACC
quinilone	<i>qnrA</i>	AGGATTTCTCACGCCAGGATT	CCGCTTTCAATGAAACTGCCAA
tetracycline	<i>tcrB</i>	GCAACTGCTAGTACGCTTAACG	GGCATGTGGTCAAGCCTTAC
tetracycline	<i>tetA-01</i>	GCTGTTTGTTCTGCCGAAA	GGTTAAGTTCCTTGAACGCAAACT
tetracycline	<i>tetA-02</i>	CTCACCAGCCTGACCTCGAT	CACGTTGTTATAGAAGCCGCATAG
tetracycline	<i>tetB-01</i>	AGTGCGCTTTGGATGCTGTA	AGCCCCAGTAGCTCCTGTGA
tetracycline	<i>tetB-02</i>	GCCCAGTGCTGTTGTGTCAT	TGAAAGCAAACGGCCTAAATACA
vancomycin	<i>vanA</i>	AAAAGGCTCTGAAAACGCAGTTAT	CGGCCGTTATCTTGTA AAAACAT
vancomycin	<i>vanB-01</i>	TTGTCCGCGAAGTGGATCA	AGCCTTTTTCCGGCTCGTT
vancomycin	<i>vanC-01</i>	ACAGGGATTGGCTATGAACCAT	TGACTGGCGATGATTTGACTATG
β-lactamase	<i>blaCMY2-01</i>	AAAGCCTCAT GGGTGCAATAA	ATAGCTTTTGTGTTGCCAGCATCA
β-lactamase	<i>blaCMY2-02</i>	GCGAGCAGCCTGAAGCA	CGGATGGGCTTGTCCTCTT
β-lactamase	<i>blaCTX-M-01</i>	GGAGGCGTGACGGCTTTT	TTCAGTGCGATCCAGACGAA
β-lactamase	<i>blaCTX-M-02</i>	GCCGCGGTGCTGAAGA	ATCGGATTATAGTTAACAGGTCAGATT
β-lactamase	<i>blaCTX-M-03</i>	CGATACCACCACGCCGTTA	GCATTGCCCAACGTGAGATT
β-lactamase	<i>blaCTX-M-04</i>	CTTGCGGTTGCGGTGAT	CGTTCATCGGCACGGTAGA
β-lactamase	<i>blaCTX-M-05</i>	GCGATAACGTGGCGATGAAT	GTCGAGACGGAACGTTTCGT
β-lactamase	<i>blaCTX-M-06</i>	CACAGTTGGTGACGTGGCTTAA	CTCCGCTGCCGGTTTTATC
β-lactamase	<i>blaGES</i>	GCAATGTGCTCAACGTTC AAG	GTGCTGAGTCAATTCTTTCAAAG
β-lactamase	<i>blaIMP-01</i>	AACACGGTTTGGTGGTTCTTGTA	GCGCTCCACAAACCAATTG
β-lactamase	<i>blaKPC</i>	ATGTCACTGTATCGCCGTCTA	TACTGCCCGTTGACGCCCAA
β-lactamase	<i>blaMOX/blaCMY</i>	CTATGTCAATGTGCCGAAGCA	GGCTTGCTCTCTTCGAATAGC
β-lactamase	<i>BlaNDM</i>	CTTGAGGTTGCTTGCCG	AGCGTCAGAAATTGCCCATAC

β-lactamase	<i>blaOCH</i>	GGCGACTTGCGCCGTAT	TTTTCTGCTCGGCCATGAG
β-lactamase	<i>blaOXA1/blaOXA30</i>	CGGATGGTTTGAAGGGTTATTAT	TCTTGGCTTTTATGCTTGATGTAA
β-lactamase	<i>blaOXA10-01</i>	CGCAATTATCGGCCTAGAAACT	TGGCTTTCCGTCCCATTT
β-lactamase	<i>blaOXA10-02</i>	CGCAATTATCGGCCTAGAAACT	TGGCTTTCCGTCCCATTT
β-lactamase	<i>blaOXY</i>	CGTTCAGGCGGCAGGT	GCCGCGATATAAGATTTGAGAATT
β-lactamase	<i>blaPER</i>	TGCTGGTTGCTGTTTTGTGA	CCTGCGCAATGATAGCTTCAT
β-lactamase	<i>blaSHV-01</i>	TCCCATGATGAGCACCTTTAAA	TTCGTCACCGGCATCCA
β-lactamase	<i>blaSHV-02</i>	CTTCCCATGATGAGCACCTTT	TCCTGCTGGCGATAGTGGAT
β-lactamase	<i>blaTEM</i>	AGCATCTTACGGATGGCATGA	TCCTCCGATCGTTGTCAGAAAGT
β-lactamase	<i>blaVEB</i>	CCCGATGCAAAGCGTTATG	GAAAGATTCCCTTTATCTATCTCAGACAA
β-lactamase	<i>blaVIM</i>	GCACTTCTCGCGGAGATTG	CGACGGTGATGCGTACGTT