

Supplementary

Table S1. Genomic features of *E. coli* and *K. pneumoniae* isolates

ID	PubMLST	Biosample	Contigs	Genome Length	GC Content	CDS	tRNA	rRNA	N50	Median coverage depth
1EE	<i>E. coli</i>	SAMN22568277	<u>897</u>	5475233	50.47	<u>6032</u>	67	2	19330	218
4EE	<i>E. coli</i>	SAMN22568278	<u>550</u>	5140546	50.39	<u>5302</u>	34	5	28232	223
6EE	<i>E. coli</i>	SAMN22568279	<u>102</u>	4933387	50.95	<u>4873</u>	38	8	185511	223
7EE	<i>E. coli</i>	SAMN22568280	<u>118</u>	4813344	50.73	<u>4762</u>	75	3	151269	272
11EE	<i>E. coli</i>	SAMN22568280	322	4738655	50.7	<u>4800</u>	40	5	40928	202
13EE	<i>E. coli</i>	SAMN22568282	256	4582345	50.9	<u>2326</u>	<u>21</u>	2	56438	185
14EE	<i>E. coli</i>	SAMN22568283	323	4888694	50.67	<u>4143</u>	<u>34</u>	4	195936	239
16EE	<i>E. coli</i>	SAMN22568284	100	4856794	50.69	<u>4783</u>	<u>77</u>	4	162048	308
1EP	<i>E. coli</i>	SAMN22568285	891	4954601	50.84	<u>5413</u>	39	4	28399	147
5EP	<i>E. coli</i>	SAMN22568286	186	5350986	50.45	<u>5358</u>	<u>87</u>	<u>5</u>	150097	185
8EP	<i>E. coli</i>	SAMN22568287	645	5273033	50.56	<u>5475</u>	46	5	105067	138
10EP	<i>E. coli</i>	SAMN22568288	193	4767339	50.83	<u>4798</u>	76	2	78177	238
11EP	<i>E. coli</i>	SAMN22568289	633	5425295	50.37	<u>5728</u>	<u>46</u>	<u>3</u>	70463	133
12EP	<i>E. coli</i>	SAMN22568290	<u>308</u>	4662795	50.79	<u>4651</u>	41	5	238555	293
15EP	<i>E. coli</i>	SAMN22568291	87	4989418	50.48	<u>4895</u>	<u>79</u>	4	331963	292
20EP	<i>E. coli</i>	SAMN22568292	603	5161678	50.68	<u>5357</u>	43	5	44314	156
24EP	<i>E. coli</i>	SAMN22568293	711	5211395	50.6	<u>5490</u>	44	4	53114	88
25EP	<i>E. coli</i>	SAMN22568294	631	5159300	50.68	<u>5373</u>	43	4	41360	148
26EP	<i>E. coli</i>	SAMN22860965	139	5182400	50.55	<u>5222</u>	86	4	163013	326
27EP	<i>E. coli</i>	SAMN22568295	486	4951868	50.69	<u>5083</u>	44	7	41947	135
28EP	<i>E. coli</i>	SAMN22568296	367	4930045	50.58	<u>4994</u>	45	4	46893	126
30EP	<i>E. coli</i>	SAMN22568297	149	5227267	50.6	<u>2960</u>	41	2	105971	241
1KE	<i>K. pneumoniae</i>	SAMN22857709	64	5415845	57.08	<u>5337</u>	75	3	264164	269
2KE	<i>K. pneumoniae</i>	SAMN22857710	307	5287854	57.24	<u>5340</u>	37	6	38144	197
7KE	<i>K. pneumoniae</i>	SAMN22857714	379	5357423	57.27	<u>5468</u>	40	5	58874	169
8KE	<i>K. pneumoniae</i>	SAMN22857716	263	5258392	57.88	<u>5231</u>	38	4	50455	190
11KE	<i>K. pneumoniae</i>	SAMN22857717	66	5404444	57.27	<u>4460</u>	63	2	236656	247
12KE	<i>K. pneumoniae</i>	SAMN22857718	540	5762894	56.77	<u>5941</u>	39	7	38802	166

15KE	<i>K. pneumoniae</i>	SAMN22857726	91	5488393	56.99	<u>5405</u>	75	3	350278	311
16KE	<i>K. pneumoniae</i>	SAMN22857722	44	5671546b	56.96	<u>5569</u>	76	5	451883	292
17KE	<i>K. pneumoniae</i>	SAMN22857723	156	5415843	57.22	<u>5342</u>	76	4	125571	369
19KE	<i>K. pneumoniae</i>	SAMN22857724	65	5458400	57.16	<u>5353</u>	75	5	357556	321
20KE	<i>K. pneumoniae</i>	SAMN22857725	108	5310880	57.4	<u>5214</u>	<u>76</u>	4	189136	540
21KE	<i>K. pneumoniae</i>	SAMN22857727	21	5294801	57.43	<u>5148</u>	76	5	272625	290
23KE	<i>K. pneumoniae</i>	SAMN22857728	31	5211037	57.48	<u>5052</u>	74	4	373869	285
3KP	<i>K. pneumoniae</i>	SAMN22857711	360	5454149	57.23	<u>5491</u>	34	6	51712	191
5KP	<i>K. pneumoniae</i>	SAMN22857712	387	5535606	57.02	<u>5634</u>	40	5	51948	148
6KP	<i>K. pneumoniae</i>	SAMN22857713	386	5535420	57.02	<u>5628</u>	41	5	54815	168
7KP	<i>K. pneumoniae</i>	SAMN22857715	391	5534264	57.03	<u>5631</u>	42	6	56535	135
12KP	<i>K. pneumoniae</i>	SAMN22857719	465	5603818	56.77	<u>5720</u>	50	10	58941	128
13KP	<i>K. pneumoniae</i>	SAMN22857720	379	5535338	57.03	<u>5618</u>	39	4	56449	108
14KP	<i>K. pneumoniae</i>	SAMN22857721	494	5535678	57.03	<u>5704</u>	40	4	30293	169

Table S2: Point mutations associated with antibiotic resistance

Isolate ID	Species	beta-lactam antibiotics	Fosfomycin			Pulvomycin	MDR	fluoroquinolone		
		PBP3	cyaA	UhpT	GlpT	EF-Tu	acrR	parC	gyrA	marR
1EE	<i>E. coli</i>	D350N, S357N	-	-	E448K	R234F	-	-	-	Y137H, G103S
4EE	<i>E. coli</i>	D350N, S357N	-	-	E448K	R234F	-	-	-	Y137H, G103S
6EE	<i>E. coli</i>	-	-	E350Q	E448K	-	-	-	-	Y137H, G103S
7EE	<i>E. coli</i>	-	-	-	E448K	R234F	-	-	-	Y137H, G103S
11EE	<i>E. coli</i>	-	-	-	E448K	R234F	-	-	-	Y137H, G103S
13EE	<i>E. coli</i>	-	-	-	E448K	R234F	-	-	-	Y137H, G103S
14EE	<i>E. coli</i>	-	-	-	-	-	-	-	-	-
16EE	<i>E. coli</i>	D350N, S357N	-	-	E448K	-	-	-	-	Y137H, G103S

1EP	<i>E. coli</i>	D350N, S357N	-	-	E448K	R234F	-	-	-	Y137H, G103S
5EP	<i>E. coli</i>	-	S352T	-	E448K	R234F	-	-	-	Y137H, G103S
8EP	<i>E. coli</i>	-	S352T	-	E448K	R234F	-	S80I	D87N, S83L	Y137H, G103S
10EP	<i>E. coli</i>	-	S352T	-	E448K	R234F	-	S80I	D87N, S83L	-
11EP	<i>E. coli</i>	-	S352T	-	E448K	R234F	-	S80I	D87N, S83L	Y137H, G103S
12EP	<i>E. coli</i>	-	-	-	E448K	R234F	-	-	-	Y137H, G103S
15EP	<i>E. coli</i>	-	-	-	E448K	R234F	-	-	-	Y137H, G103S
20EP	<i>E. coli</i>	-	S352T	-	E448K	R234F	-	S80I	D87N, S83L	-
24EP	<i>E. coli</i>	-	S352T	-	E448K	R234F	-	S80I	D87N, S83L	Y137H, G103S
25EP	<i>E. coli</i>	-	S352T	-	E448K	R234F	-	S80I	-	-
26EP	<i>E. coli</i>	-	-	E350Q	E448K	R234F	-	-	-	Y137H, G103S
27EP	<i>E. coli</i>	-	-	-	-	R234F	-		S83L	-
28EP	<i>E. coli</i>	-	-	-	E448K	R234F	-	S80I	D87N, S83L	Y137H, G103S
30EP	<i>E. coli</i>	-	S352T		E448K	R234F	-	S80I	D87N, S83L	-
1KE	<i>K. pneumoniae</i>	-	-	E350Q	-	-	-		-	-
2KE	<i>K. pneumoniae</i>	-	-	E350Q	-	R234F	-		-	-
7KE	<i>K. pneumoniae</i>	-	-	E350Q	-	R234F	-		-	-
8KE	<i>K. pneumoniae</i>	-	-	E350Q	-	-	Y114F, V165I	-	-	-
11KE	<i>K. pneumoniae</i>	-	-	E350Q	-	R234F	-		-	-
12KE	<i>K. pneumoniae</i>	-	-	E350Q	-	R234F	-		-	-
15KE	<i>K. pneumoniae</i>	-	-	E350Q	-	R234F	-		-	-
16KE	<i>K. pneumoniae</i>	-	-	E350Q	-	-	-	-	-	-
17KE	<i>K. pneumoniae</i>	-	-	E350Q	-	-	-	-	-	-
19KE	<i>K. pneumoniae</i>	-	-	nil	-	-	-	-	-	-

20KE	<i>K. pneumoniae</i>	-	-	nil	-	-	-	-	-	-
21KE	<i>K. pneumoniae</i>	-	-	nil	-	-	-	-	-	-
23KE	<i>K. pneumoniae</i>	-	-	E350Q	-	-	-	-	-	-
3KP	<i>K. pneumoniae</i>	-	-	E350Q	-	-	-	-	-	-
5KP	<i>K. pneumoniae</i>	-	-	E350Q	-	-	-	-	-	-
6KP	<i>K. pneumoniae</i>	-	-	E350Q	-	-	-	-	-	-
7KP	<i>K. pneumoniae</i>	-	-	E350Q	-	-	-	-	-	-
12KP	<i>K. pneumoniae</i>	-	-	E350Q	-	-	-	-	-	-
13KP	<i>K. pneumoniae</i>	-	-	E350Q	-	-	-	-	-	-
14KP	<i>K. pneumoniae</i>	-	-	E350Q	-	-	-	-	-	-

Table S3. Genes associated with antibiotic efflux, antibiotic target alteration and protection

ID	Species	Source	Gene
1EE	<i>E. coli</i>	Community	acrB, msbA, emrR, emrB, mdtG, AcrE, cpxA, H-NS, marA, evgA, mdtE, TolC, sul2, emrA, CRP, bacA, mdtH, AcrF, AcrS
4EE	<i>E. coli</i>	Community	mdtG, mdtH, marA, msbA, acrB, <i>E. coli</i> acrA, AcrE, <i>E. coli</i> ampH beta-lactamase, evgA, cpxA, emrB, emrR, TolC, mdtE, H-NS, baeR, <i>E. coli</i> emrE
6EE	<i>E. coli</i>	Community	AcrE, TolC, H-NS, mdtG, baeS, acrB, <i>E. coli</i> acrA, mdtE, msbA, emrR, emrB, evgA, cpxA, marA
7EE	<i>E. coli</i>	Community	evgA, baeR, baeS, mdtG, mdtH, H-NS, marA, acrB, <i>E. coli</i> acrA, emrR, TolC, cpxA, msbA, mdtE, AcrE
11EE	<i>E. coli</i>	Community	<i>E. coli</i> acrA, H-NS, bacA, msbA, mdtG, mdtH, AcrS, AcrE, mdtC, YojI, PmrF, emrB, mdtN, TolC, gadX, mdtF, mdtE, evgA, emrK, marA
13EE	<i>E. coli</i>	Community	acrB, <i>E. coli</i> acrA, mdtH, mdtG, emrY, evgA, msbA, PmrF, TolC, cpxA, emrB, AcrE, AcrS, mdtE, H-NS, baeS, marA
14EE	<i>E. coli</i>	Community	baeS, PmrF, evgA, TolC, AcrE, mdtG, H-NS, emrR, emrB, mdtE, <i>E. coli</i> acrA, acrB, <i>E. coli</i> ampH beta-lactamase, msbA, cpxA, marA

16EE	<i>E. coli</i>	Community	baeS, PmrF, H-NS, msbA, emrY, evgA, AcrE, <i>E. coli</i> acrA, acrB, TolC, cpxA, marA, emrB, emrR
1EP	<i>E. coli</i>	Clinical	marA, acrA, acrB, evgA, QnrB4, DHA-1, sul1, mphA, H-NS, cpxA, msbA, mdtG, mdtH, AcrE, ampH, emrR, PmrF, mdtE, bacA, mdtP, mdtO, mdtN, baeRbaeS
5EP	<i>E. coli</i>	Clinical	TolC, baeR, marA, msbA, emrB, emrR, evgA, emrK, mdtH, mdtG, mdtF, H-NS, cpxA
8EP	<i>E. coli</i>	Clinical	mdtH, TolC, marA, evgA, emrK, emrY, baeR, msbA, emrR, emrB, H-NS, sul2, dfrA17, qacEdelta1, sul1
10EP	<i>E. coli</i>	Clinical	mdtG, mdtH, H-NS, msbA, acrD, <i>E. coli</i> acrA, acrB, evgS, evgA, emrK, PmrF, YojI, bacA, TolC, mdtP, mdtN, marA, emrR, emrB, mdtE, gadX, dfrA17, qacEdelta1
11EP	<i>E. coli</i>	Clinical	mdtG, marA, cpxA, TolC, emrY, evgA, msbA, acrB, <i>E. coli</i> ampH beta-lactamase, kdpE, baeR, mphA, sul1, qacEdelta1, aadA5, dfrA17, H-NS
12EP	<i>E. coli</i>	Clinical	baeS, PmrF, emrY, evgA, mdtG, H-NS, emrR, emrB, marA, AcrE, TolC, msbA, mdtE, <i>E. coli</i> acrA, cpxA
15EP	<i>E. coli</i>	Clinical	evgA, baeR, emrR, H-NS, gadW, cpxA, mdtH
20EP	<i>E. coli</i>	Clinical	emrK, emrY, H-NS, mdtG, mdtH, baeR, emrR, TolC, sul2, evgA, rmtB, marA, msbA, catI, QepA4, sul1, qacEdelta1, dfrA12, emrB
24EP	<i>E. coli</i>	Clinical	baeR, H-NS, mdtH, mdtG, TolC, marA, emrY, emrK, evgA, sul2, emrR, msbA, emrB, QepA4, sul1, qacEdelta1, dfrA12, rmtB
25EP	<i>E. coli</i>	Clinical	marA, emrK, evgA, mdtG, mdtH, msbA, H-NS, emrR, dfrA12, qacEdelta1, sul1, BRP(MBL), emrB, TolC, baeR, sul2, rmtB, catI, QepA4
26EP	<i>E. coli</i>	Clinical	emrB, emrR, mdtH, cpxA, H-NS, marA, evgA, emrK, emrY, sul2
27EP	<i>E. coli</i>	Clinical	<i>E. coli</i> acrA, acrB, <i>E. coli</i> ampH beta-lactamase, YojI, PmrF, evgA, kdpE, TolC, msbA, baeS, mdtG, mdtP, mdtN, AcrS, AcrE, emrA, emrB, H-NS, mdtF, gadX, marA, cpxA, bacA, mdtH
28EP	<i>E. coli</i>	Clinical	mdtG, evgA, AcrE, AcrS, emrR, msbA, TolC, marA, <i>E. coli</i> acrA, acrB, mdtB, cpxA, mdtE, H-NS,
30EP	<i>E. coli</i>	Clinical	evgA, emrK, emrY, TolC, msbA, emrB, emrR, baeR, mdtG, mdtH, H-NS, marA
1KE	<i>K. pneumoniae</i>	Community	LptD, oqxA, <i>K. pneumoniae</i> KpnF, QnrS1, <i>K. pneumoniae</i> KpnH, <i>K. pneumoniae</i> KpnG, emrR, OmpA, CRP, ArnT, eptB, <i>K. pneumoniae</i> OmpK37
2KE	<i>K. pneumoniae</i>	Community	<i>K. pneumoniae</i> KpnF, marA, adeF, LptD, H-NS, msbA, OmpA, ArnT, CRP, oqxA, adeF, emrR, <i>K. pneumoniae</i> KpnG, <i>K. pneumoniae</i> KpnH, <i>K. pneumoniae</i> KpnE, <i>K. pneumoniae</i> OmpK37, eptB, baeR
7KE	<i>K. pneumoniae</i>	Community	<i>K. pneumoniae</i> KpnF, LptD, <i>K. pneumoniae</i> KpnE, <i>K. pneumoniae</i> OmpK37, <i>K. pneumoniae</i> KpnH, <i>K. pneumoniae</i> KpnG, emrR, adeF, oqxA, CRP, msbA, baeR, adeF, H-NS, ArnT, marA, tet(A), <i>K. pneumoniae</i> OmpK37, oqxA, adeF, emrR, <i>K. pneumoniae</i> KpnG, <i>K. pneumoniae</i> KpnH, H-NS,
8KE	<i>K. pneumoniae</i>	Community	LptD, eptB, CRP, marA, <i>K. pneumoniae</i> KpnF, <i>K. pneumoniae</i> KpnE, msbA, OmpA, adeF, ArnT, oqxA, LptD, <i>K. pneumoniae</i> KpnF, marA, emrR, <i>K. pneumoniae</i> KpnG, <i>K. pneumoniae</i> KpnH, adeF, eptB, ArnT, CRP, baeR, msbA, OmpA, <i>K. pneumoniae</i> OmpK37, H-NS, <i>K. pneumoniae</i> KpnE
11KE	<i>K. pneumoniae</i>	Community	LptD, oqxA, <i>K. pneumoniae</i> KpnF, <i>K. pneumoniae</i> OmpK37, marA, ArnT, OmpA, msbA, eptB, CRP, adeF, baeR, <i>K. pneumoniae</i> KpnH, <i>K. pneumoniae</i> KpnG, emrR, H-NS
12KE	<i>K. pneumoniae</i>	Community	

15KE	<i>K. pneumoniae</i>	Community	LptD, K. pneumoniae KpnF, baeR, H-NS, K. pneumoniae Kpn, H, K. pneumoniae KpnG, emrR, oqxA, adeF, ompA, msbA, K. pneumoniae KpnE, K. pneumoniae ompK37, ArnT, CRP, eptB, marA
16KE	<i>K. pneumoniae</i>	Community	K. pneumoniae ompK37, K. pneumoniae KpnE, K. pneumoniae KpnF, marA, H-NS, msbA, baeR, adeF, K. pneumoniae KpnH, K. pneumoniae KpnG, emrR, oqxA, LptD, eptB, ArnT, CRP
17KE	<i>K. pneumoniae</i>	Community	K. pneumoniae KpnE, K. pneumoniae KpnF, H-NS, msbA, ompA, ArnT, eptB, K. pneumoniae KpnG, emrR, adeF, oqxA, baeR, K. pneumoniae ompK37, CRP, marA, LptD
19KE	<i>K. pneumoniae</i>	Community	LptD, K. pneumoniae KpnF, baeR, H-NS, marA, K. pneumoniae KpnG, ArnT, CRP, K. pneumoniae KpnE, eptB
20KE	<i>K. pneumoniae</i>	Community	K. pneumoniae KpnF, LptD, K. pneumoniae KpnE, eptB, ArnT, CRP, ompA, oqxA, K. pneumoniae KpnG, K. pneumoniae KpnH
21KE	<i>K. pneumoniae</i>	Community	K. pneumoniae KpnF, LptD, oqxA, K. pneumoniae KpnG, K. pneumoniae KpnE, K. pneumoniae ompK37, H-NS, CRP, ArnT
23KE	<i>K. pneumoniae</i>	Community	LptD, K. pneumoniae KpnF, K. pneumoniae KpnE, K. pneumoniae ompK37, K. pneumoniae KpnG, oqxA, CRP, ArnT
3KP	<i>K. pneumoniae</i>	Clinical	oxqA, LptD, K. pneumoniae KpnF, K. pneumoniae KpnG, eptB, ompA, CRP, ArnT, K. pneumoniae KpnE, K. pneumoniae ompK37
5KP	<i>K. pneumoniae</i>	Clinical	QnrB1, LptD, dfrA14, K. pneumoniae KpnF, sul2, CRP, eptB, oqxA, adeF, emrR, K. pneumoniae KpnG, K. pneumoniae KpnH, ompA, msbA, ArnT, baeR
6KP	<i>K. pneumoniae</i>	Clinical	LptD, K. pneumoniae KpnF, dfrA14, sul2, QnrB1, ArnT, H-NS, ompA, msbA, marA, baeR, K. pneumoniae KpnE, CRP, K. pneumoniae KpnH, K. pneumoniae KpnG, oqxA, K. pneumoniae ompK37
7KP	<i>K. pneumoniae</i>	Clinical	K. pneumoniae KpnF, LptD, dfrA14, QnrB1, oqxA, adeF, emrR, K. pneumoniae KpnG, K. pneumoniae KpnH, baeR, ArnT, H-NS, K. pneumoniae KpnE, marA, CRP, eptB, ompA, K. pneumoniae ompK37
12KP	<i>K. pneumoniae</i>	Clinical	LptD, K. pneumoniae KpnF, sul2, QnrB1, dfrA14, CRP, ArnT, eptB, oqxA, K. pneumoniae KpnG, ompA, K. pneumoniae KpnE, H-NS, K. pneumoniae ompK37
13KP	<i>K. pneumoniae</i>	Clinical	QnrB1, LptD, K. pneumoniae KpnF, dfrA14, sul2, msbA, oqxA, adeF, emrR, K. pneumoniae KpnG, K. pneumoniae KpnH, marA, baeR, K. pneumoniae ompK37, ompA, eptB, ArnT, K. pneumoniae KpnE, H-NS, CRP
14KP	<i>K. pneumoniae</i>	Clinical	LptD, QnrB1, sul2, dfrA14, K. pneumoniae KpnF, emrR, K. pneumoniae KpnG, K. pneumoniae KpnH, eptB, K. pneumoniae ompK37, marA, ompA, msbA, CRP, adeF, oqxA, baeR, K. pneumoniae KpnE

Table S4. Virulence and transposases genes detected in *K. pneumonia* and *E. coli* isolates

ID	Human pathogen probability	Virulence	Transposases
1EE	90	hra, gad, terC, astA, lpfA, terC	MITEEc1, MITEEc1, Tn6024, MITEEc1, ISPpu12, ISEc11, MITEEc1, IS30, ISKpn8, IS4, IS421, IS629, ISKpn14.
4EE	88	terC, fyuA, irp2, lpfA, cia, iss, iss, ompT, gad, gad, terC, capU	ISSfl10, IS26, MITEEc1, MITEEc1, IS30, IS30, ISEc40, ISEc40, ISEc38, IS421, ISEc53, IS903, IS903
6EE	93	terC, lpfA, gad	MITEEc1, MITEEc1, IS421, MITEEc1, IS30, ISEsa1, IS609, MITEEc1
7EE	94	astA, terC, gad, iss, terC, lpfA	MITEEc1, MITEEc1, IS102, MITEEc1, MITEEc1, IS102, MITEEc1, ISEc31
11EE	94	terC	MITEEc1, ISKpn8, IS421, ISEsa1,
13EE	94	ompT, gad, lpfA, terC, iss	MITEEc1, ISEc17,
14EE	94	terC, etsC, papC, iss, iroN, lpfA, gad, iss, mchF	MITEEc1, IS679, ISKpn24, ISKpn24, IS682, IS30, cn_51933_IS679, ISEc46
16EE	94	terC, cia, gad, gad, lpfA	ISVsa3, ISKpn19, MITEEc1, IS102, ISEsa1, IS609, ISEam1, IS30, IS26
1EP	93	sitA, terC, senB, cea, lpfA, astA, capU, traT, iss, fyuA, irp2, ompT, iutA, iucC, cia, iss, terC	IS911, ISEc38, ISKpn24, ISEc30,
5EP	91	sitA, irp2, fyuA, kpsMII_K5, kpsE, aggC, ORF4, aatA, aggR, terC, gad, iss, eilA, air, chuA, capU, hra, traT	MITEEc1, ISVsa3, IS6100, ISEc46, ISEc9, ISEc38, IS30, MITEEc1, IS609, IS609, ISEc31, ISEc38, IS100, IS5075, IS5075, SEc48.
8EP	93	sitA, terC, eilA, kpsMII_K4, terC, hra, irp2, fyuA, sat, kpsE, iutA, iucC, senB, gad, traT, chuA, papA_F43	IS6100, ISEc9, Tn5403, IS421, ISKpn8, ISKpn8, ISEc38,
10EP	89	gad, kpsE, kpsMII_K1, irp2, fyuA, papC, papA_F12, terC, traT, iss	IS6100, ISEc43, ISEc38, ISEcB1, ISKox3, ISEc30, ISEc1, IS682, IS421, IS26, MITEEc1
11EP	93	sitA, iucC, traT, lpfA, air, fyuA, irp2, eilA, eilA, gad, chuA, terC, kpsE, yfcV, terC	IS6100, ISEc81, ISKpn8, ISEc38, ISEc30, IS421, ISEc45,
12EP	93	lpfA, terC, iss, ompT, terC	IS3, MITEEc1, ISSen4,
15EP	93	sitA, cnf1, fyuA, clbB, gad, focCsfA, sfaD, chuA, iss, pic, vat, hra, terC, iss, iroN, kpsE, yfcV, cea, mchF, kpsMII_K23, usp, tcpC	ISEc42, MITEEc1, ISEc17, ICEEcIHE3034-1, ISEc38, ISEc13, ISEc41, IS100, ISEc38, ISEc31

20EP	93	cia, kpsE, kpsMII_K5, gad, eilA, traT, irp2, hra, chuA, papA_F19, terC, fyuA	Tn2, IS4, ISEc30, IS100, IS26
24EP	93	traT, kpsMII_K5, kpsE, eilA, terC, chuA, irp2, fyuA, cia, gad, hra, terC	IS6100, IS4, ISEc30, IS100, ISKpn8, IS26,
25EP	93	terC, eilA, hra, kpsE, kpsE, irp2, fyuA, chuA, papA_F19, gad, cia, traT	Tn2, IS4, IS100, ISEc30, IS26,
26EP	94	astA, afaD, eilA, air, aap, ORF3, iutA, iucC, capU, terC, hra, traT, chuA	MITEEc1, ISSpu2, IS629 cn_7104_IS629, IS911, IS682, ISEc30, MITEEc1, ISEc1, IS609, IS100, ISEc31, ISEc38, ISEc46
27EP	93	iha, iha, traT, terC, afaC, afaD, iss, fyuA, irp2, gad, terC, hra	IS6100, MITEEc1, ISKpn8, IS609, ISEc45, IS30, IS421, ISEc10, IS3, IS102, ISKox3
28EP	93	traT, gad, gad, irp2, fyuA, terC	IS6100, MITEEc1, ISKpn8, IS4, IS30, IS3, ISKpn26, IS26
30EP	93	eilA, air, chuA, fyuA, irp2, terC, kpsE, gad, terC, traT	IS102, , ISEc38, ISEc17, Tn5403, MITEEc1, ISEc1, IS609, IS4, cn_3324_ISEc1, ISEc30, ISKpn8, IS5075
1KE	90	iutA, terC, traT	ISEc9, IS6100, ISKpn24, ISEc30, ISKox1, ISEsa1, ISSm1, IS5075, ISKpn28, IS26, Tn3
2KE	91	iutA	ISSty2, ISSen4, ISKpn43, ISSpu2,
7KE	92	iutA, terC, traT	S903, SEc15, SKpn21, SKpn1, Tn3
8KE	92	iutA	SKox1, SEc52,
11ke	90	iutA, traT	SSty2, SEc52, SKpn14, SKpn24, SKpn38, SKpn28, SKpn1,
12ke	89	iutA, terC, traT	Tn6082, ISKpn43, Tn5403, ISEhe3, ISKpn38, ISEsa1, ISSty2
15ke	91	iutA, terC	ISEsa1, ISKpn14, ISKpn47, ISKpn43, IS102, ISKpn26, ISCfr26, ISKpn28
16ke	80	iutA	ISKpn41, ISKpn28,
17ke	90	iutA	ISSty2, ISKpn43, IS5075,
19ke	90	irp2, fyuA, iutA, traT	ICEEcoED1a-1, ISKpn26, IS26, ISEam1, ISKpn14, ISKpn1
20ke	90	iutA, traT	ISEhe3, ISKpn8, IS26, ISSen4, ISKpn34
21ke	90	iutA	NIL
23ke	89	iutA	ISEc33, ISEc52, ISSty2, ISKpn1,
3KP	92	iutA, traT	SEhe3, SSm1, S5075, SKpn42, SKpn14, SKpn21, SKpn38, SKpn43
5KP	92	iutA, traT	S5075, SEc9, SEhe3, SEcl1, SKpn1, SEc15, S6100, Tn3
6KP	90	iutA, traT	S5075, SEc9, SEc15, SKpn1, SEhe3, SEcl1, S6100, Tn3
7KP	89	iutA, traT	S5075, SEc9, SKpn1, SEhe3, SEcl1, SEc15

12kp	81	iutA, traT	IS5075, ISEc9, ISKpn1, IS6100, ISEc15, ISEhe3, ISEcl1
13kp	90	iutA, traT	IS5075, ISEc9, IS6100, ISEhe3, ISKpn1, ISEcl1, ISEc15, Tn3
14kp	90	iutA, traT	IS5075, ISEc9, ISEcl1, ISEhe3, ISEc15, IS6100, Tn3

Table S5. Co-occurrence of antimicrobial-resistance genes and transposases.

ID	Sample Source	Contig number	Contig length (Coverage)	ARG		IS/Tn		Plasmid	
				Name	position	Name	Position	Name	Position
1EP	Wound of postoperative infection	33	15007 (124)	<i>qnrB4</i>	1044-400	IS6100	10897-11776		
				<i>mph(A)</i>	14034-14939				
				<i>qacE</i>	7614-7824				
				<i>sul1</i>	7884-8723G				
				<i>blaDHA-1</i>	5168-6307				
8EP	UTI	652	9813 (30)	<i>dfrA17</i>	1224-751	IS6100	5703-6582		
				<i>qacE</i>	2349-2630				
				<i>mph(A)</i>	8840-9745				
				<i>sul1</i>	2690-3529				
				<i>aadA5</i>	1355-2143				
		381	5965 (31)	<i>bla</i> _{CTX-M-15}	2453-3328	ISEc9	749-2404	IncFII(29)	6928-7186
		131	17556 (264)			Tn5403	47-3694		
10EP	Wound of postoperative infection	79	9975 (457)	<i>mph(A)</i>	9004-9906	IS6100	5855-6734		
				<i>dfrA17</i>	1376-903				

				<i>sul1</i>	2842-3681				
				<i>aadA5</i>	1507-2295				
11EP	Wound of	257	9949 (100)	<i>qacE</i>	7231-7512	IS6100	3279-4158		
	postoperative infection			<i>dfrA17</i>	8637-9110				
				<i>mph(A)</i>	1021-116				
				<i>sul1</i>	6332-7171				
				<i>aadA5</i>	7718-8506				
14EE	Water	13	126908 (264)			IS679	72830-75533	IncFII	121336-121595
						ISKpn24	79321-81774		
						IS682	24433-26966		
						IS30	10801-12021		
						cn_51933 IS679	23600-75533		
16EE	Water	45	5269 (231)	<i>qnrS1</i>	3599-4255	ISKpn19	1-2850		
		48	3983 (254)	<i>floR</i>	1541-328	ISVsa3	2660-3636		
		42	13543 (230)			IS102	37-1092	p0111	2936-3820
20EP	Urine (Chronic Kidney Disease)	224	8722 (222)	<i>rmtB</i>	1461-706	Tn2	1484-6433		
				<i>bla</i> _{TEM-1B}	1631-2491				
24EP	sepsis	1370	4166 (41)	<i>mph(A)</i>	3195-4097	IS6100	46-925		

25EP	Urine (Chronic Kidney Disease)	401	8726 (142)	<i>rmtB</i>	1461-706	Tn2	1484-6433		
				<i>bla</i> _{TEM-1B}	1631-2491				
27EP	UTI	580	11125 (169)	<i>mph(A)</i>	1022-117	IS6100	3280-4159		
				<i>qacE</i>	7232-7513				
				<i>dfrA17</i>	8638-9111				
				<i>sul1</i>	6333-7172				
				<i>aadA5</i>	7719-8507				
28EP	Recurrent UTI	165	21847 (142)	<i>mph(A)</i>	1023-118	IS6100	3281-4160		
				<i>bla</i> _{TEM-35}	5141-6001				

30EP	UTI	77	6551 (306.4)	tet(B)	1898-3103	IS102	3114-4170		
		66	11302 (252.7)			Tn5403	506-4169	IncFII	7404-7664

1KE	Vegetables	33	12084 (250.6)	<i>bla</i> _{TEM-1D}	6334-7194	IS1380-like, ISKra4-like, Tn3	3562-5217 7400-8400 1-2350	PRIA4b ORF3	9050-9650
				<i>qnrS1</i>	10976-11632				
				<i>bla</i> _{CTX-M-15}	2638-3513				
		34	5958 (241.1)	<i>mph(A)</i>	4984-5889	IS6100	1847-2726		

2KE	Surface	16	130723 (310.9)	<i>OqxB</i>	10870-7718	ISSty2	2245-3503		
				<i>OqxA</i>	6519-7694				
5KP	Neonatal sepsis	361	2832 (183)	<i>sul2</i>	1982-2797	IS5075	223-1549		
				<i>aph(6)-Ia</i>		IS91			
				<i>aph(3'')-Ib</i>					
		334	5415 (178)	<i>bla</i> _{CTX-M-15}	2506-3381	ISEc9, Tn3	802-2457 3786 -6005		

6KP	Neonatal sepsis	522	5098 (163)	<i>aph(6)-Id</i>	3661-4497	IS5075	223-1549		
				<i>aph(3'')-Ib</i>	2858-3661	IS91			
				<i>sul2</i>	1982-2797				
		281	6016 (171)	<i>bla</i> _{CTX-M-15}	2684-3559	ISEc9	3608-5263		
						Tn3	2279 - 60		
7KP	Sepsis	140	5098 (197)	<i>aph(6)-Id</i>	1486-650	IS5075	3598-4924		
				<i>aph(3'')-Ib</i>	1486-2289	IS91			
				<i>sul2</i>	2350-3165				
		68	1641 (301)	<i>bla</i> _{CTX-M-15}	2684-3559	ISEc9	3608-5263		
						Tn3	1-2275		

11KE Vegetables 1 501618 (228) *bla*_{SHV-1} 27779-28645 **ISSty2** 459960-461218

12KE	Fruits	303	13004 (100)	<i>aph(3'')-Ib</i>	8477-9279	Tn3,	1100-3900, 10100-12900		
				<i>aph(6)-Id</i>	7641-8477	IS110			
13KP	Neonatal sepsis	210	5098 (193)	<i>aph(6)-Id</i>	1486-650	IS5075	3598-4924		
				<i>aph(3'')-Ib</i>	1486-2289	IS91			
				<i>sul2</i>	2350-3165				

156 6016 (249) *bla*_{CTX-M-15} 2684-3559 **ISEc9** 3608-5263,
Tn3 5077 -3815

14KP	Neonatal sepsis	211	5098 (267)	<i>aph(6)-Id</i>	3661-4497	IS5075,	223-1549		
				<i>aph(3'')-Ib</i>	2858-3661	IS91			

				<i>sul2</i>	1982-2797				
		256	3312 (277)	<i>bla</i> _{CTX-M-15}	1-855	ISEc9Tn3	904-2559		
15KE	Surface in Market	35	10536 (306)			ISKpn14	3140-3907	IncHI1B	8736-9305
16KE	Surface in Market	11	133532 (143)			ISKpn41	4042-5467	IncFIB(Ma r)	36801- 37239
20KE	vegetables	34	38475 (784)			ISEhe3	35866- 37094	repA	31937- 32627

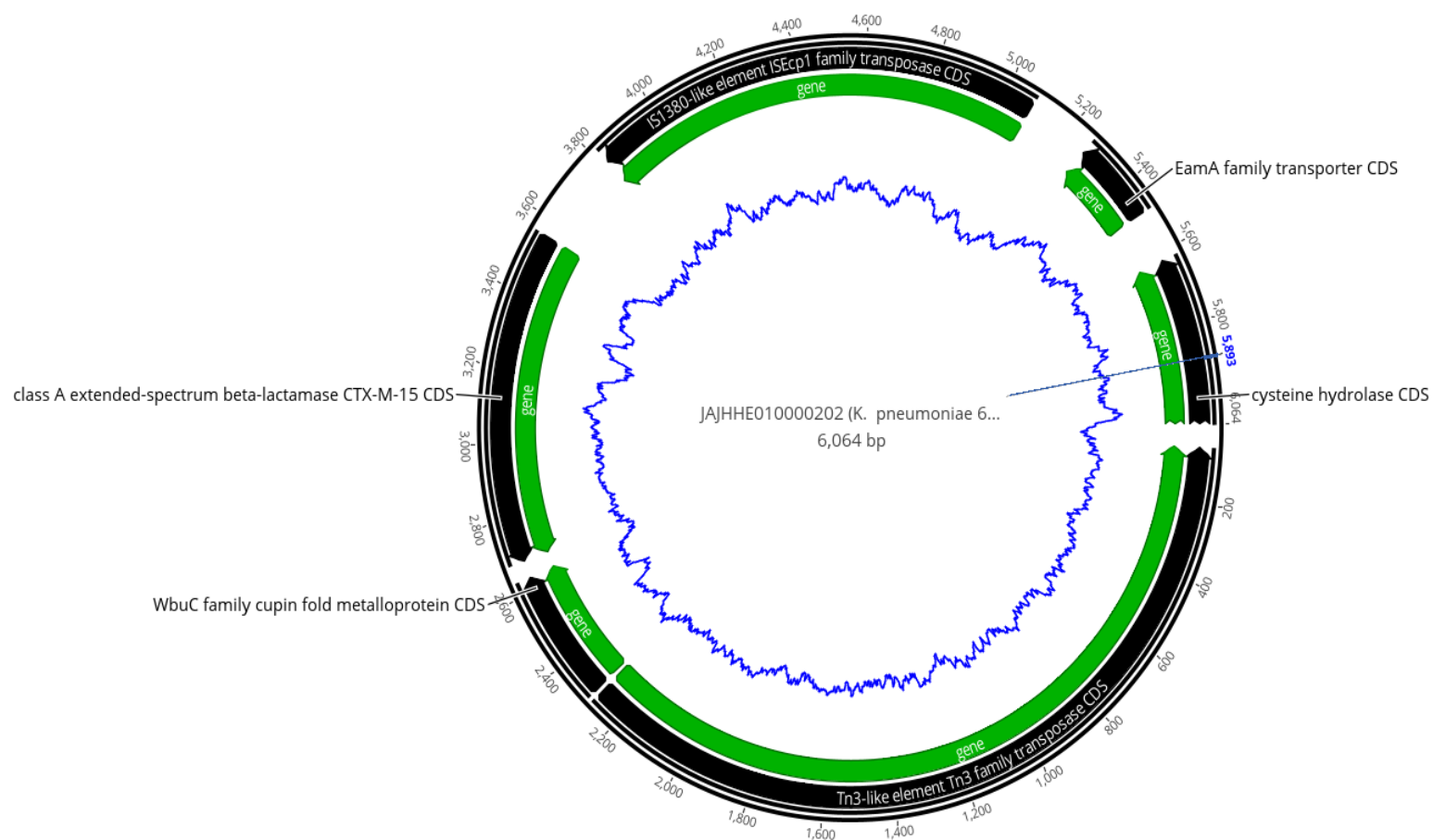


Figure S1. Map of different antibiotic-resistant genes, transposases, and plasmid, clustered in contig 202 of clinical *K. pneumoniae* (5KP) isolate. Showing an example for the presence of *CTX-M-15* gene between two transposases. The outer black circle indicates for the length of the contig, black arrows indicate for coding sequences (CDS), green arrows indicate genes, and blue inner zigzag circle indicates GC content.

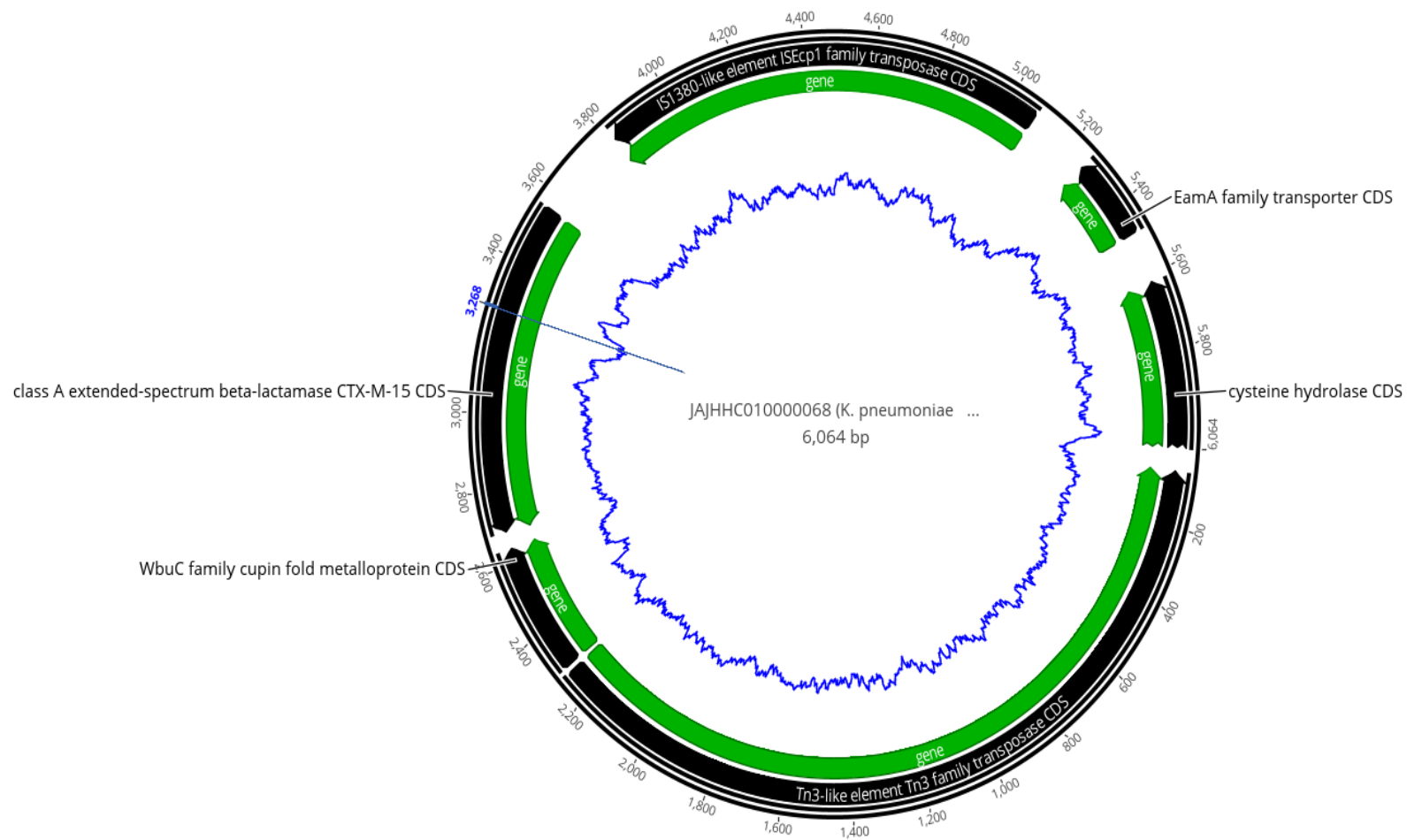


Figure S2. Map of different antibiotic resistant genes, transposases, and plasmid, clustered in contig 68 of clinical *K. pneumoniae* (7KP) isolate. Showing an example for the presence of *CTX-M-15* gene between two transposases. The outer black circle indicates for the length of the contig, black arrows indicate for coding sequences (CDS), green arrows indicate genes, and blue inner zigzag circle indicates GC content

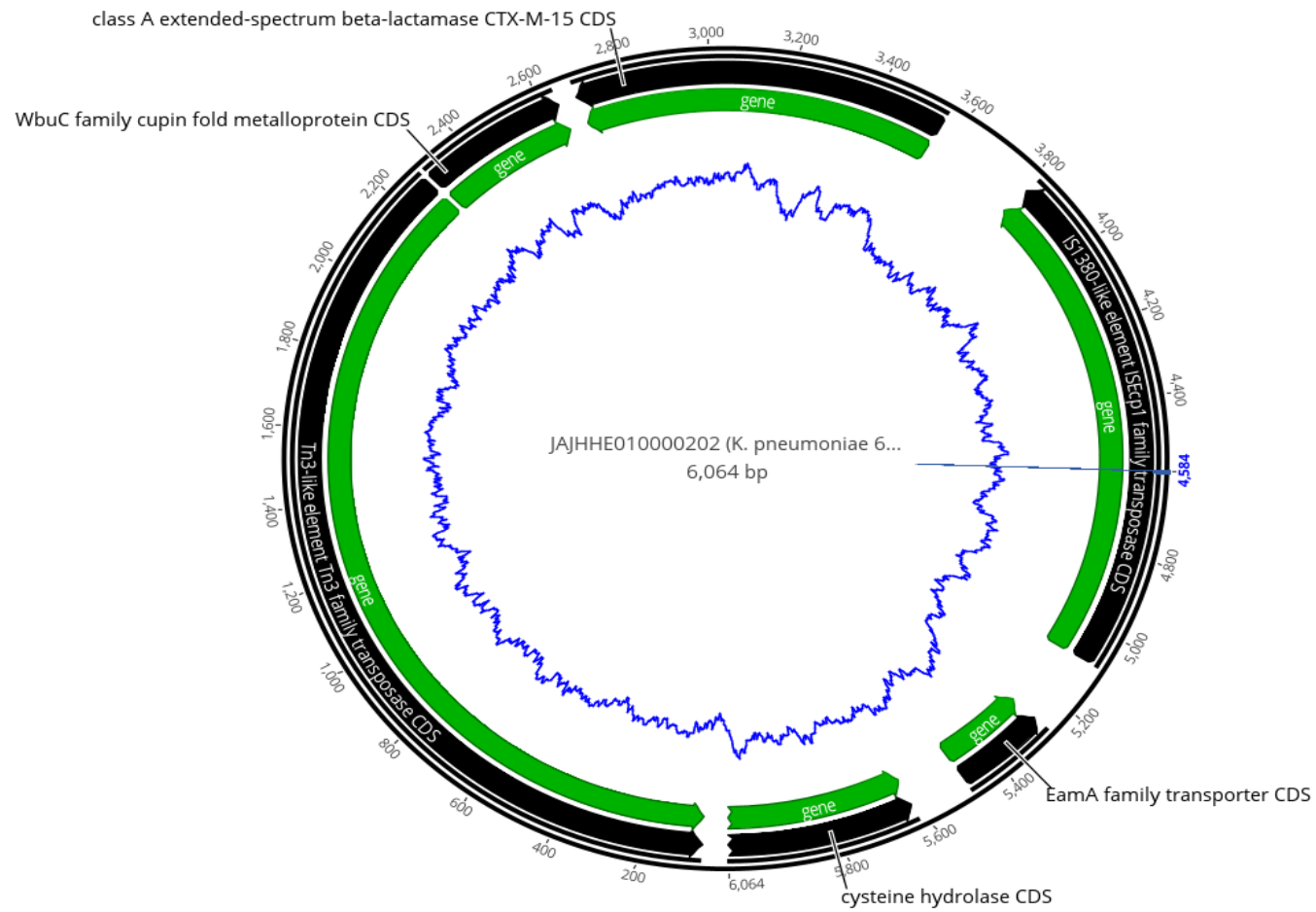


Figure S3. Map of different antibiotic resistant genes, transposases, and plasmid, clustered in contig 202 of clinical *K. pneumonia* (6KP) isolate. Showing an example for the presence of *CTX-M-15* gene between two transposases. The outer black circle indicates for the length of the contig, black arrows indicate for coding sequences (CDS), green arrows indicate genes, and blue inner zigzag circle indicates GC content

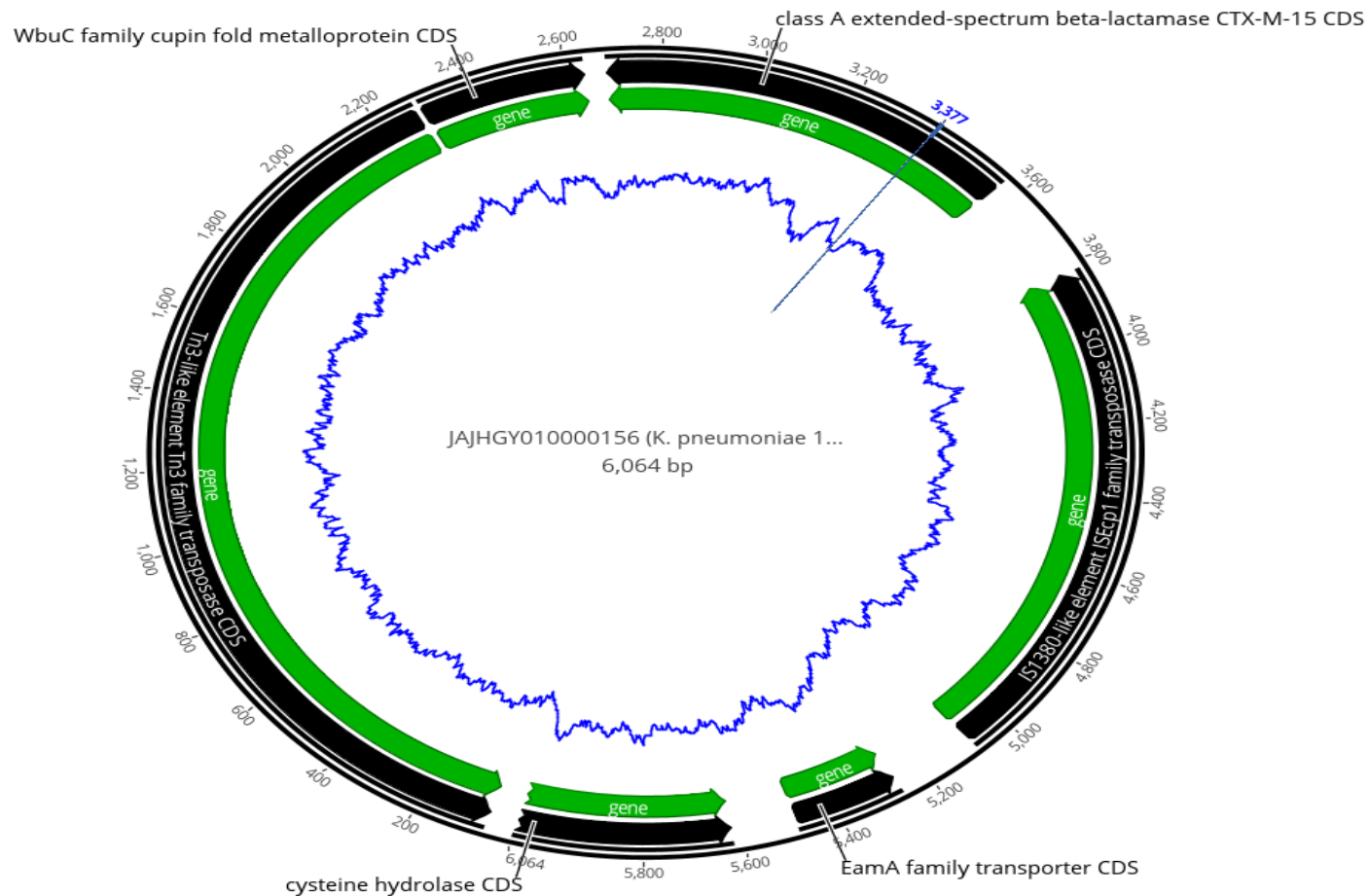


Figure S4. Map of different antibiotic resistant genes, transposases, and plasmid, clustered in contig 156 of clinical *K. pneumoniae* (13KP) isolate. Showing an example for the presence of CTX-M-15 gene between two transposases. The outer black circle indicates for the length of the contig, black arrows indicate for coding sequences (CDS), green arrows indicate genes, and blue inner zigzag circle indicates GC content.

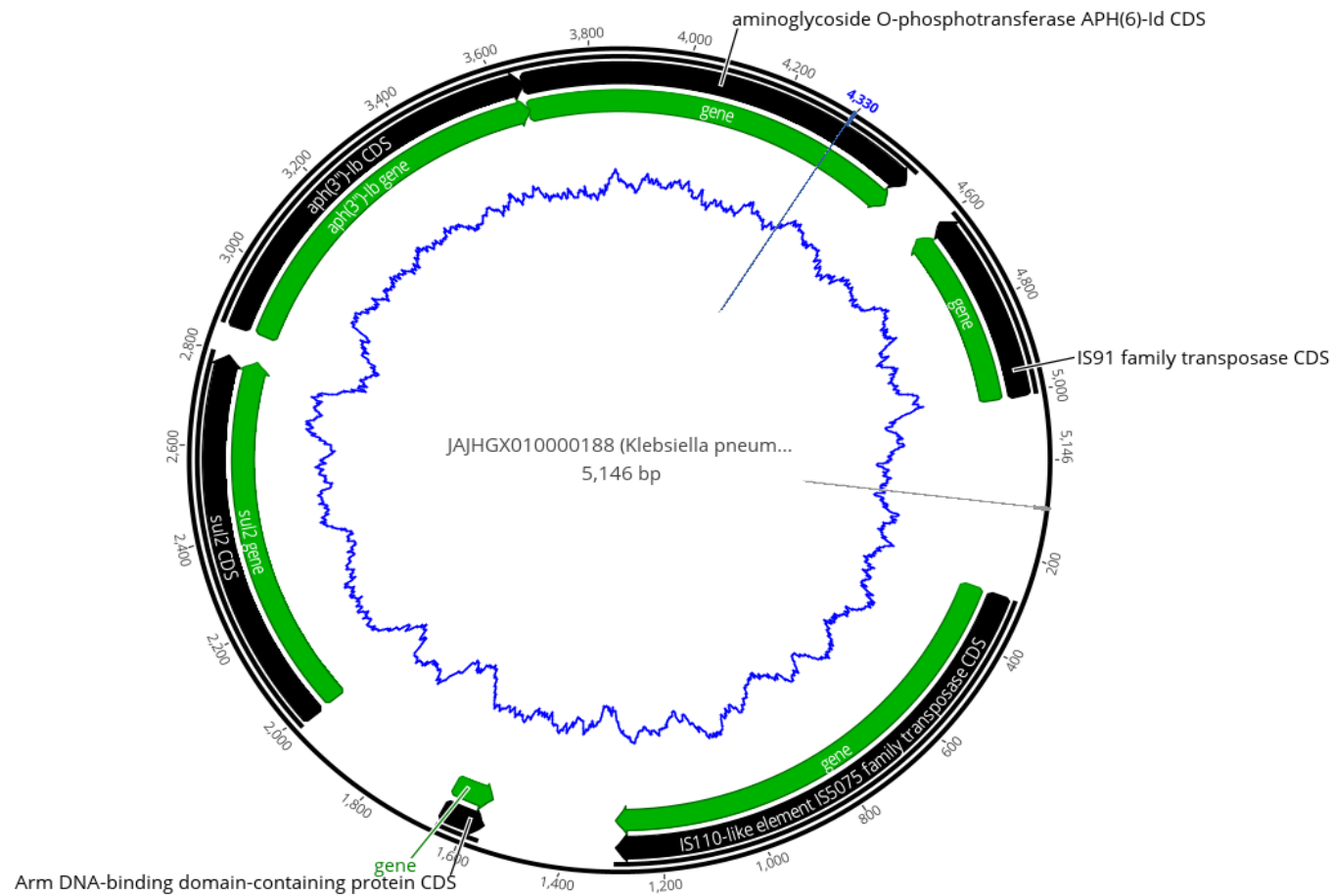


Figure S5. Map of different antibiotic resistant genes, transposases, and plasmid, clustered in contig 156 of clinical *K. pneumoniae* (14KP) isolate. Showing an example for the presence of aminoglycosides genes flanked by transposases. The outer black circle indicates for the length of the contig, black arrows indicate for coding sequences (CDS), green arrows indicate genes, and blue inner zigzag circle indicates GC content