

## SUPPLEMENTARY TABLES FOR:

### **Genomic surveillance for hypervirulence and multi-drug resistance in invasive *Klebsiella pneumoniae* from south and southeast Asia**

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**Table S2: Characteristics of non-*Kp* BSI isolate genomes**

	<i>K. quasipneumoniae</i> subsp. <i>quasipneumoniae</i>	<i>K. quasipneumoniae</i> subsp. <i>similipneumoniae</i>	<i>K. variicola</i>
<b>N</b>	5	20	9
<b># STs</b>	4: 2 Vietnam 1 India 1 Nepal	17: 7 Cambodia 6 Vietnam 5 Laos	9: 3 Hong Kong 2 Cambodia 1 India 1 Laos 1 Nepal 1 Vietnam
<b>Common STs<sup>a</sup></b>	ST1118-3LV (40%)	ST1191 (10%) ST1124 (10%) ST334 (10%)	-
<b># K loci</b>	3	15	9
<b>Common K loci<sup>a</sup></b>	KL107 (60%)	KL60 (15%) KL10 (10%) KL13 (10%) KL103 (10%)	-
<b># O types</b>	2	4	4
<b>Common O types<sup>a</sup></b>	O3/O3a (80%)	O5 (55%) O3/O3a (30%) O12 (10%)	O3/O3a (44%) O5 (33%)
<b>% ESBL+</b>	0	65%	0
<b>ESBL genes</b>	-	CTX-M-15 (35%) CTX-M-27 (10%) SHV-2a (10%) CTX-M-14 (5%) CTX-M-9 (5%)	-
<b>% Carb+</b>	20%	0	0
<b>Virulence determinants</b>	-	ICE <i>Kp3</i> + <i>iuc1</i> + <i>iro1</i> + <i>rmpA</i> + <i>peg-344</i> (n=1 ST367 from Vietnam)	<i>ybt</i> plasmid lineage (n=1 ST209-1LV from Cambodia)

<sup>a</sup> Only O types detected in >1 genome are shown.

**Table S3: K locus prevalence among *K. pneumoniae sensu stricto*.**

	K locus	Prevalence (%)								
		Cambodia	Hong Kong	India	Laos	Nepal	Vietnam	Mean	ESBL+	Carb+
1	KL2	12	11	2	11	6	10	9	3	0
2	KL1	2	7	2	16	0	19	8	2	0
3	KL24	5	7	1	23	0	1	6	11	2
4	KL51	0	0	22	2	3	3	5	11	23
5	KL62	7	11	5	0	0	5	5	4	4
6	KL112	0	0	2	0	22	0	4	6	11
7	KL57	0	7	2	7	0	6	4	1	0
8	KL10	5	0	1	7	3	5	3	6	0
9	KL23	7	4	0	2	3	4	3	2	0
10	KL13	2	0	0	0	16	0	3	3	0
11	KL64	0	0	18	0	0	0	3	3	21
12	KL102	7	4	0	3	0	3	3	2	0
13	KL117	0	7	4	0	3	0	2	2	4
14	KL54	2	7	1	2	0	1	2	1	0
15	KL122	10	0	0	0	0	1	2	3	0
16	KL105	0	0	0	0	9	1	2	2	5
17	KL3	0	4	0	2	3	1	2	3	0
18	KL149	0	4	1	0	0	3	1	1	2
19	KL19	0	0	4	0	0	4	1	3	2
20	KL52	2	0	0	2	3	0	1	1	0
21	KL39	0	4	0	0	3	0	1	1	0
22	KL7	5	0	0	2	0	0	1	1	0
23	KL17	2	0	2	2	0	0	1	1	4
24	KL5	0	4	0	0	0	3	1	0	0
25	KL25	5	0	0	0	0	1	1	1	0
26	KL28	5	0	0	0	0	1	1	2	0
27	KL27	2	0	0	0	3	0	1	1	0
28	KL125	0	4	0	2	0	0	1	0	0
29	KL21	2	0	0	2	0	1	1	1	0
30	KL103	0	4	0	0	0	1	1	1	0
31	KL12	0	4	0	0	0	1	1	1	0
32	KL20	0	0	1	0	0	4	1	0	0
33	KL9	0	4	1	0	0	0	1	0	0
34	KL107	0	0	0	0	3	1	1	1	0
35	KL45	0	0	0	2	0	3	1	1	2
36	KL15	2	0	0	2	0	0	1	2	0
37	KL114	0	4	0	0	0	0	1	0	0
38	KL106	0	0	0	3	0	0	1	1	0
39	KL148	0	0	0	3	0	0	1	1	0
40	KL162	0	0	0	0	0	3	0	0	0
41	KL163	0	0	0	0	0	3	0	1	2
42	KL31	0	0	1	0	0	1	0	0	2
43	KL34	2	0	0	0	0	0	0	0	0
44	KL111	2	0	0	0	0	0	0	0	0
45	KL135	2	0	0	0	0	0	0	1	0
46	KL157	2	0	0	0	0	0	0	1	0
47	KL35	2	0	0	0	0	0	0	0	0
48	KL8	2	0	0	0	0	0	0	1	0
49	KL128	0	0	0	2	0	0	0	0	0
50	KL136	0	0	0	2	0	0	0	1	0
51	KL30	0	0	0	2	0	0	0	1	2
52	KL56	0	0	0	2	0	0	0	0	0
53	KL63	0	0	0	2	0	0	0	0	0
54	KL142	0	0	0	0	0	1	0	1	0
55	KL127	0	0	0	0	0	1	0	0	0

56	KL164	0	0	0	0	0	1	0	0	0
57	KL22	0	0	0	0	0	1	0	0	0
58	KL42	0	0	0	0	0	1	0	0	0
59	KL81	0	0	0	0	0	1	0	0	0
60	KL124	0	0	1	0	0	0	0	1	0
61	KL33	0	0	1	0	0	0	0	0	0
62	KL43	0	0	1	0	0	0	0	0	0
63	KL50	0	0	1	0	0	0	0	1	0
	Unk	0	0	24	0	19	4	8	11	18

K-loci are ordered by highest to lowest mean prevalence across all sites. Note that the Thai site is excluded from these calculations due to small sample size (n=4). Unk; unknown.

**Table S4: Predicted O type prevalence among *K. pneumoniae sensu stricto*.**

O type	Prevalence (%)								
	Cambodia	Hong Kong	India	Laos	Nepal	Vietnam	Mean	ESBL+	Carb+
O1	67	48	35	69	66	50	56	55	44
O2	12	26	15	8	16	15	15	13	16
O1/O2 <sup>a</sup>	0	4	11	0	0	3	3	5	7
O3b	10	11	6	10	3	9	8	6	4
O4	2	4	0	2	3	4	2	3	0
O5	7	4	0	0	0	4	2	1	0
O3/O3a	0	0	0	8	0	3	2	3	0
OL101	2	0	0	0	6	1	2	1	0
OL103	0	4	0	2	0	1	1	1	0
OL104	0	0	2	0	0	0	0	1	2
OL102	0	0	0	0	0	1	0	0	0
Unk	0	0	31	2	6	10	8	12	28

Predicted O types are ordered by highest to lowest mean prevalence across all sites. Note that the Thai site is excluded from these calculations due to small sample size (n=4).

<sup>a</sup> It was not possible to confidently distinguish between O1 and O2 for a minority of genomes (n=12 in total). The prevalence of these genomes is shown here by site and among ESBL+/Carb+ isolates. These values are added at the second position in the cumulative prevalence plot (**Figure 2B**). Unk; unknown