**Table S1**: Detailed location of the genomic regions found in accessory genome of the *K. pneumoniae* isolates.

Genomic	Contig nº (bp location) 1		
region	Kp703	Kp45	Kp2948
1	14 (33420-78461)		
2	17 (31818-73195)		
3	19 (1-3882)		
4	40 (583642-589716)		
5	74 (34702-47865)		
6	121 (1-57266)		
7	8 (85065-97181)		
8	11 (27681-29438)	52 (1-1271)	
9	28 (1-11937); 3 (1-3191)	35 (57896-71598)	
10	56 (191811-227997)		
11	·	17 (43644-79326)	
12		18 (1-12394)	33 (1-14831)
13		30 (131058-168299)	·
14		34 (1-43459)	
15	20 (74425-131652)		105 (64308-97514); 227 (1-18761); 191 (1-869);
	,		176 (1-718); 193 (1-2953)
16	26 (1-1856)		70 (1-1696); 94 (520)
17		46 (145706-158835)	184 (1-12343)
18		73 (1-6909)	21 (7549); 217 (1714); 76 (1-375)
19		108 (18731-29947)	
20		108 (144770-183310)	
21		, 	110 (217714-234854)
22			137 (239588-250991)
23			8 (40463-77928); 137 (367234-368894)
24			150 (1-25438)
25			256 (106917-144254)
26			158 (15631-27237)
27			72 (2392-7596)
28			2 (1-27296)
29			24 (1-1133)
30			195 (35740-64378); 29 (1071); 61 (61399-72132)
31			47 (1-3700)
32			9 (1-16630)
33			79 (1-22765)
34			12 (1-4894)
35			140 (1-846)
36			51 (1-2703)
37			87 (1-1962)
38			78 (1-1442)

<sup>&</sup>lt;sup>1</sup>Some genomic regions assembled in a single contig for a given isolate were found to be completed but fragmented in several contigs in the genome of other isolate.