

Supplementary Information

Whole Genome Sequencing of Extended Spectrum β -lactamase (ESBL)-producing *Klebsiella pneumoniae* Isolated from Hospitalized Patients in KwaZulu-Natal, South Africa

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Table S1. Distribution of intact prophage regions among the ESBL-producing *K. pneumoniae* strains. a: Intact prophage region; b: Region length of intact prophage; c: Phage with the highest number of CDS in the region and the number of gene counts in brackets.

Isolate name	ST	Region ^a	Length ^b (kb)	No CDS	GC%	Phage (hit genes count) ^c
A105R2B2	ST607	2	31.2	42	54.83	Salmon SEN5 (19)
		4	41.8	19	52.69	Entero P4 (5)
		5	48.6	45	51.90	Pseudo JBD44 (11)
		6	14.6	20	56.63	Entero fiAA91 ss (16)
A111R1B2	ST17	1	31.2	43	53.10	Salmon Fels 2 (32)
		7	47.1	42	53.33	Entero mEp235 (9)
		9	15.1	19	55.81	Entero P88 (12)
A105R1B5	ST983	1	60.1	44	52.80	Salmon 118970 sal4 (14)
ED01500733	ST983	2	57.2	45	53.62	Salmon 118970 (15)
		3	54.6	78	49.24	Klebsi JD001 (46)
G702R3B2	ST152	1	17.5	20	55.37	Entero P88 (12)
		2	30.4	33	50.48	Salmon 118970 (7)
		3	40.1	39	52.46	Klebsi phiKO2 (22)
ED01503757	ST152	1	38.1	38	53.37	Entero mEp235 (8)
		2	15.1	19	55.80	Entero P88 (11)
		3	40.7	31	52.84	Klebsi phiKO2 (20)
G702R1B5	ST152	1	22.1	26	52.68	Entero P88 (10)
		2	33.1	39	51.39	Bacill SP 15 (10)
		3	30.1	15	54.19	Entero P88 (6)
G702R2B5	ST152	1	43.4	51	51.99	Klebsi PKP126 (9)
		2	63.3	34	50.90	Salmon SSU5 (19)
		3	23.3	33	50.32	Salmon SSU5 (11)
		4	23.2	29	54.61	Salmon Fels 2 (22)