Supplementary data

Genomic characterization of four novel bacteriophages infecting the clinical pathogen *Klebsiella pneumonia*

Boris Estrada Bonilla, Ana Rita Costa, Teunke van Rossum, Stefan Hagedoorn, Hielke Walinga, Minfeng Xiao, Wenchen Song, Pieter-Jan Haas, Franklin L. Nobrega, Stan J. J. Brouns

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Supplementary Table S1. List of protein homologs to the tubulin spindle protein of phage 201phi2-1 found by psi-Blast and Hmmer search and used to build the tubulin spindle phylogenetic tree.

Phage	**Genome size**	**psi-Blast**			**Hmmer E value**	**Protein accession number**	**Ref**
		Coverage (%)	**E-value**	**Identity (%)**			
Aeromonas phage CF8	238,150	100	5.0E-55	24.46	-	QDB70454.1	-
Aeromonas phage D3	262,372	98	6.0E-50	18.61	-	QDJ97033.1	-
Aeromonas phage D6	259,831	98	5.0E-49	18.93	-	QDJ97195.1	-
Aeromonas phage D9	260,857	98	6.0E-50	18.61	-	QEP52339.1	-
Aeromonas phage LAh10	260,310	98	5.0E-49	18.93	-	QDH47086.1	-
Aeromonas phage PS1	237,367	99	1.0E-47	20.56	-	QDJ96797.1	-
Bacillus virus G	497,513	94	7.0E-53	12.28	-	YP_009015441.1	-
Clostridium phage c-st	185,683	95	4.0E-65	15.00	-	4XCQ_A	-
Edwardsiella phage pEt-SU	276,734	99	2.0E-58	25.39	3.0E-18	YP_009822177.1	-
Erwinia phage Ea35-70	271,084	100	3.0E-56	23.46	1.0E-21	YP_009005002.1	-
Erwinia phage PhiEaH1	218,339	98	7.0E-49	23.84	2.6E-15	YP_009010087.1	-
Erwinia phage vB_EamM_Deimos-Minion	273,501	-	-	-	1.0E-21	ANH52315	-
Erwinia phage vB_EamM_Joad	235,374	-	-	-	1.2E-06	ASU03898	-
Erwinia phage vB_EamM_RisingSun	235,108	99	2.0E-48	16.92	-	YP_009612761.1	-
Erwinia phage vB_EamM_Special G	273,224	-	-	-	1.0E-21	ANJ65024	-
Escherichia phage vB_EcoM_Goslar	237,307	99	2.0E-55	22.77	1.3E-12	YP_009820885.1	-
Halocynthia phage JM-2012	167,292	99	2.0E-43	20.81	6.3E-09	YP_006383382.1	-
Klebsiella phage Miami	253,383	98	2.0E-44	18.81	-	QPB09366.1	-
Klebsiella phage N1M2	253,367	99	8.0E-60	21.81	-	QGH71890.1	-
Photobacterium phage PDCC-1	237,509	98	6.0E-52	19.44	-	YP_009853560.1	-
Proteus phage 10	223,209	100	6.0E-61	25.00	-	QMP24134.1	-
Pseudomonas phage 201phi2-1	316,674	99	8.0E-57	100.00	5.1E-208	3J5V_a	[1]
Pseudomonas phage EL	211,215	91	3.0E-45	16.72	-	YP_418049.1	-
Pseudomonas phage fnug	278,899	99	3.0E-63	29.85	-	QJB22689.1	-
Pseudomonas phage KTN4	279,593	99	2.0E-63	29.85	-	ANM44810.1	-
Pseudomonas phage Noxifer	278,136	99	4.0E-46	26.93	1.9E-26	YP_009608946.1	-
Pseudomonas phage OBP	284,757	99	3.0E-49	22.12	2.0E-14	YP_004957954.1	-
Pseudomonas phage PA02	279,095	99	2.0E-64	30.46	-	BBI55877.1	-
Pseudomonas phage PA1C	304,671	99	2.0E-76	48.73	7.1E-88	QBX32179.1	-
Pseudomonas phage Phabio	309,157	99	6.0E-52	29.84	2.7E-39	ARV76677.1	-
Pseudomonas phage PhiPA3	309,208	99	6.0E-73	45.86	2.0E-86	YP_009217111.1	[1]

Pseudomonas phage Psa21	305,260	99	8.0E-54	31.95	1.5E-46	QBJ02557.1	-
Pseudomonas phage SL2	279,696	99	3.0E-63	29.85	-	YP_009619864.1	-
Pseudomonas virus phiKZ	278,899	99	2.0E-63	29.85	2.8E-44	3ZBP_A	[1]
Ralstonia phage RP12	279,845	96	3.0E-51	19.62	2.0E-09	YP_009598707.1	-
Ralstonia phage RP31	276,958	96	2.0E-51	19.94	1.9E-09	BAW19276.1	-
Ralstonia phage RSF1	222,888	91	5.0E-48	20.76	1.3E-12	YP_009207815.1	-
Ralstonia phage RSL2	223,932	91	9.0E-51	22.15	1.1E-13	BAQ02539.2	-
Salmonella phage vB_SalM_SA002	288,012	100	9.0E-59	24.54	-	QKE54534.1	-
Serratia phage 2050HW	276,025	99	2.0E-56	22.50	1.6E-16	YP_009833975.1	[2]
Serratia phage PCH45	212,807	90	2.0E-51	18.47	-	QFP93107.1	-
Vibrio phage 2 TSL-2019	242,446	98	2.0E-51	19.44	-	YP_009843109.1	-
Vibrio phage Aphrodite1	237,722	98	8.0E-54	21.25	3.5E-13	YP_009622183.1	-
Vibrio phage BONAISHI	288,967	98	2.0E-49	20.24	1.7E-11	AXH70800.1	-

Supplementary Table S2. List of protein homologs to the nucleus shell protein of phage 201phi2-1 found by psi-Blast and Hmmer search and used to build the nucleus shell phylogenetic tree.

Phage	**Genome size**	**psi-Blast**			**Hmmer E value**	**Protein accession number**	**Ref**
		Coverage (%)	**E-value**	**Identity (%)**			
Aeromonas phage CF8	238,150	97	5.0E-77	14.01	-	QDB70465.1	-
Aeromonas phage D3	262,372	96	6.0E-90	13.73	-	QDJ97041.1	-
Aeromonas phage LAh10	260,310	96	1.0E-89	13.27	-	QDH47031.1	-
Aeromonas phage PS1	237,367	93	3.0E-94	13.90	-	QDJ96807.1	-
Cronobacter phage CR5	223,989	95	2.0E-96	13.76	-	YP_008125763.1	-
Edwardsiella phage pEt-SU	276,734	92	2.0E-96	13.29	-	YP_009821902.1	-
Erwinia phage Ea35-70	271,084	96	1.0E-116	20.79	3.6E-12	YP_009005014.1	-
Erwinia phage PhiEaH1	218,339	98	7.0E-91	16.25	-	YP_009010075.1	-
Erwinia phage phiEaH2	243,050	90	5.0E-115	12.48	-	YP_007237854.1	-
Erwinia phage vB_EamM_Asesino	246,290	99	7.0E-117	11.85	-	YP_009290657.1	-
Erwinia phage vB_EamM_Caitlin	241,147	90	3.0E-104	12.88	-	YP_009292105.1	-
Erwinia phage vB_EamM_ChrisDB	244,840	89	4.0E-103	13.14	-	YP_009292727.1	-
Erwinia phage vB_EamM_Deimos-Minion	273,501	-	-	-	3.6E-12	ANH52327	-
Erwinia phage vB_EamM_EarlPhillipIV	223,935	95	8.0E-96	13.85	-	YP_009278336.1	-
Erwinia phage vB_EamM_Huxley	240,761	96	5.0E-105	11.73	-	YP_009293007.1	-
Erwinia phage vB_EamM_Kwan	246,390	90	2.0E-91	12.01	-	YP_009278639.1	-
Erwinia phage vB_EamM_Phobos	229,501	95	3.0E-94	13.76	-	YP_009283513.1	-
Erwinia phage vB_EamM_RisingSun	235,108	94	7.0E-76	12.98	-	YP_009612772.1	-
Erwinia phage vB_EamM_Simmy50	271,088	93	5.0E-116	21.39	-	YP_009606010.1	-
Erwinia phage vB_EamM_Special G	273,224	-	-	-	3.6E-12	ANJ65036	-
Escherichia phage vB_EcoM_Goslar	237,307	100	2.0E-131	18.18	2.8E-07	YP_009820873.1	-
Halocynthia phage JM-2012	167,292	94	4.0E-55	14.77	-	YP_006383413.1	-
Klebsiella phage Miami	253,383	95	5.0E-80	15.76	-	QPB09376.1	-
Klebsiella phage N1M2	253,367	92	7.0E-95	15.24	-	QGH71899.1	-
Photobacterium phage PDCC-1	237,509	99	5.0E-91	15.06	-	YP_009853356.1	-

Proteus phage 10	223,209	97	3.0E-113	20.60	-	QMP24145.1	-
Pseudomonas phage 201phi2-1	316,674	100	2.0E-175	100.00	0.0E+00	YP_001956829.1	[1]
Pseudomonas phage EL	211,215	97	2.0E-68	11.11	-	YP_418056.1	-
Pseudomonas phage KTN4	279,593	100	2.0E-146	39.59	-	ANM44831.1	-
Pseudomonas phage Noxifer	278,136	96	3.0E-142	35.90	1.7E-111	YP_009608965.1	-
Pseudomonas phage OBP	284,757	93	4.0E-102	14.38	-	YP_004957964.1	-
Pseudomonas phage PA02	279,095	100	2.0E-145	39.59	-	BBI55859.1	-
Pseudomonas phage PA1C	304,671	100	1.0E-164	51.35	1.1E-201	QBX32206.1	-
Pseudomonas phage PA7	266,743	100	2.0E-145	39.44	-	YP_009617618.1	-
Pseudomonas phage Phabio	309,157	100	1.0E-156	52.52	7.8E-206	ARV76713.1	-
Pseudomonas phage PhiPA3	309,208	95	5.0E-172	51.41	6.2E-196	YP_009217136.1	[1]
Pseudomonas phage Psa21	305,260	100	3.0E-139	41.13	4.8E-144	QBJ02586.1	-
Pseudomonas phage SL2	279,696	100	3.0E-145	39.28	-	YP_009619844.1	-
Pseudomonas phage vB_PaeM_kmuB	266,592	100	1.0E-146	39.59	-	QOV07924.1	-
Pseudomonas phage vB_PaeM_PS119XW	301,543	100	2.0E-166	51.35	-	QEM41783.1	-
Pseudomonas virus phiKZ	278,899	100	5.0E-146	39.75	2.1E-133	NP_803620.1	[1]
Ralstonia phage RP12	279,845	99	1.0E-95	18.88	8.1E-15	YP_009598981.1	-
Ralstonia phage RP31	276,958	99	5.0E-93	18.82	5.2E-15	BAW19549.1	-
Ralstonia phage RSF1	222,888	97	2.0E-118	17.67	6.9E-07	YP_009208033.2	-
Ralstonia phage RSL2	223,932	97	9.0E-117	17.80	1.5E-07	YP_009213072.1	-
Salmonella phage pSal-SNUABM-04	239,626	94	2.0E-103	11.49	-	QOC54489.1	-
Salmonella phage STsAS	197,215	99	2.0E-108	13.64	-	AWN08967.1	-
Salmonella phage vB_SalM_SA002	288,012	95	6.0E-120	20.29	-	QKE54546.1	-
Serratia phage 2050HW	276,025	37	1.0E-21	14.57	-	YP_009833990.1	[2]
Serratia phage Moabite	273,933	90	6.0E-84	16.47	-	YP_009849136.1	-
Serratia phage PCH45	212,807	95	6.0E-85	13.94	-	QFP93061.1	-
Vibrio phage 2 TSL-2019	242,446	99	7.0E-90	15.06	-	YP_009843316.1	-
Vibrio phage Aphrodite1	237,722	99	2.0E-87	15.21	-	YP_009622192.1	-
Vibrio phage BONAISHI	288,967	99	3.0E-88	14.85	-	AXH70812.1	-
Vibrio phage pTD1	239,276	94	8.0E-92	14.93	-	YP_009599417.1	-
Vibrio phage pVa-21	231,998	93	4.0E-82	13.79	-	AQT28149.1	-
Vibrio phage USC-1	238,099	99	2.0E-87	15.21	-	YP_009847864.1	-
Vibrio phage vB_pir03	286,284	98	2.0E-70	15.85	-	QNI21050.1	-
Vibrio phage vB_VmeM-Yong XC31	290,532	97	2.0E-78	15.24	-	QAX96061.1	-
Vibrio phage VP4B	236,053	99	5.0E-96	16.01	-	YP_009626053.1	-
Xanthomonas phage Xoo-sp14	232,104	99	1.0E-105	19.82	-	QNR51901.1	-

Supplementary Table S3. Genome annotations of *Klebsiella pneumoniae* phage vB_KpP_FBKp16.

Locus_tag	**Direction**	**Min**	**Max**	**Product**	**Notes**	**Function**
gp001	+	13	729	hypothetical protein		
gp002	+	739	1,086	peptidase	contains peptidase M15 domain	cell lysis
gp003	+	1,079	1,201	hypothetical protein		
gp004	+	1,198	1,344	hypothetical protein		
gp005	+	1,413	1,628	hypothetical protein		
gp006	+	1,949	3,694	hypothetical protein		
gp007	+	5,005	5,205	hypothetical protein		
gp008	-	5,479	5,709	hypothetical protein		
gp009	+	5,774	5,968	hypothetical protein		
gp010	+	6,023	6,541	hypothetical protein		
gp011	+	6,737	7,642	hypothetical protein		
gp012	+	7,711	10,344	phage DNA-directed RNA polymerase	contains DNA-directed RNA polymerase N-terminal and DNA-dependent RNA polymerase domains	transcription
gp013	+	10,594	10,770	hypothetical protein		
gp014	+	10,773	12,776	DNA primase/helicase	DnaB-like helicase C terminal domain	DNA replication
gp015	+	12,840	13,535	hypothetical protein		
gp016	+	13,532	13,759	hypothetical protein		
gp017	+	13,752	13,964	hypothetical protein		
gp018	+	14,030	14,125	hypothetical protein		
gp019	+	14,109	16,655	phage DNA-directed DNA polymerase	contains DNA polymerase family A domain	DNA replication
gp020	+	16,666	16,887	hypothetical protein		
gp021	+	17,026	17,832	hypothetical protein		
gp022	+	17,832	18,047	hypothetical protein		
gp023	+	18,345	18,716	hypothetical protein		

Locus_tag	Direction	Min	Max	Product	Notes	Function
gp024	+	18,796	19,242	hypothetical protein		
gp025	+	19,310	19,633	hypothetical protein		
gp026	+	19,615	20,550	phage exonuclease		DNA replication
gp027	+	20,535	20,936	endonuclease	contains recombination endonuclease VII domain	DNA repair
gp028	+	20,937	21,944	phage phosphoesterase		
gp029	+	22,061	22,468	hypothetical protein		
gp030	+	22,465	22,668	hypothetical protein		
gp031	+	22,665	23,618	phage-associated ATP-dependent DNA ligase	contains DNA ligase OB-like domain	DNA replication and repair
gp032	+	23,611	23,796	hypothetical protein		
gp033	+	23,783	24,211	HNH endonuclease		DNA metabolism
gp034	+	24,238	24,387	hypothetical protein		
gp035	+	24,384	24,845	putative N-acetyltransferase	contains acetyltransferase (GNAT) family domain	
gp036	+	24,854	25,060	hypothetical protein		
gp037	+	25,062	26,630	phage collar, head-to-tail connector protein	contains bacteriophage head to tail connecting protein domain	structural components
gp038	+	26,630	27,481	phage capsid assembly scaffolding protein		structural components
gp039	+	27,557	28,648	major capsid protein		structural components
gp040	+	28,800	29,525	phage non-contractile tail tubular protein A	contains tail tubular protein domain	structural components
gp041	+	29,525	31,909	phage non-contractile tail tubular protein B		structural components
gp042	+	31,909	32,577	internal virion protein		structural components
gp043	+	32,578	35,514	hypothetical protein		
gp044	+	35,584	39,396	phage DNA ejectosome component Gp16, peptidoglycan lytic exotransglycosylase (EC 4.2.2.n1)		structural components

Locus_tag	Direction	Min	Max	Product	Notes	Function
gp045	+	39,396	40,382	tail fiber	contains phage T7 tail fibre protein domain; coiledstalk of trimeric autotransporter adhesin domain	structural components
gp046	+	40,391	40,579	holin	contains phage holin T7 family, holin superfamily II domain	cell lysis
gp047	+	40,569	40,868	phage terminase, small subunit		DNA packaging
gp048	+	40,868	42,766	phage terminase large subunit		
gp049	+	42,917	43,183	hypothetical protein		
gp050	+	43,197	43,463	hypothetical protein		
gp051	+	43,474	44,010	hypothetical protein	possible neck whiskers protein	

Supplementary Table S4. Genome annotations of *Klebsiella pneumoniae* phage vB_KpP_FBKp27.

Locus_tag	**Direction**	**Min**	**Max**	**Product**	**Notes**	**Function**	**Cluster**
gp001	-	46	744	hypothetical protein	putative tail protein	structural components	F
gp002	+	834	1,595	thymidylate synthase thyX		DNA metabolism	A
gp003	+	1,683	2,747	ribonucleotide reductase, small subunit		DNA metabolism	A
gp004	+	2,750	4,480	ribonucleotide reductase of class Ia (aerobic), alpha subunit		DNA metabolism	A
gp005	+	4,538	5,017	hypothetical protein			A
gp006	+	4,995	5,969	hypothetical protein			A
gp007	+	5,978	8,137	hypothetical protein	DNA primase		A
gp008	+	8,207	8,938	hypothetical protein	AAA-domain protein		A
gp009	+	8,935	9,465	putative HNH endonuclease		DNA metabolism	A
gp010	+	9,467	10,207	hypothetical protein	putative single-stranded DNA-binding protein		A
gp011	+	10,250	10,573	hypothetical protein			A
gp012	+	10,536	11,099	hypothetical protein			A
gp013	+	11,102	11,782	hypothetical protein			A
gp014	+	11,793	11,966	hypothetical protein			A
gp015	-	12,002	22,642	RNA polymerase		transcription	B
gp016	-	22,687	23,745	hypothetical protein			B
gp017	-	23,749	24,174	hypothetical protein			B
gp018	-	24,183	26,897	hypothetical protein			B
gp019	-	26,954	27,772	hypothetical protein			B
gp020	-	27,782	28,324	hypothetical protein			B
gp021	-	28,408	29,580	major capsid protein		structural components	B
gp022	-	29,595	30,755	putative tail tape measure protein		structural components	B
gp023	-	30,759	31,073	hypothetical protein			B

Locus_tag	Direction	Min	Max	Product	Notes	Function	Cluster
gp024	-	31,143	33,404	portal protein		structural components	B
gp025	+	33,461	34,075	putative nucleoside triphosphate pyrophosphohydrolase		regulation	C
tRNA	+	34,455	34,529	tRNA-Asn-GTT			C
tRNA	+	34,535	34,609	tRNA-Asp-GTC			C
tRNA	+	34,617	34,693	tRNA-Pro-TGG			C
tRNA	+	34,699	34,785	tRNA-Tyr-GTA			C
tRNA	+	34,792	34,881	tRNA-Ser-TGA			C
tRNA	+	34,955	35,031	tRNA-Gln-TTG			C
gp026	+	35,311	35,622	hypothetical protein			C
gp027	+	35,619	36,038	hypothetical protein			C
gp028	-	36,068	36,949	hypothetical protein			D
gp029	-	36,959	38,563	terminase large subunit		DNA packaging	D
gp030	-	38,665	39,360	hypothetical protein			D
gp031	+	39,445	39,840	hypothetical protein			D
gp032	-	39,873	40,067	hypothetical protein			D
gp033	+	40,591	40,818	hypothetical protein			E
gp034	+	41,445	41,588	hypothetical protein			E
gp035	+	41,596	41,748	hypothetical protein			E
gp036	+	41,752	41,943	hypothetical protein			E
gp037	+	41,959	42,222	hypothetical protein			E
gp038	+	42,264	42,536	hypothetical protein			E
gp039	+	42,816	43,019	hypothetical protein			E
gp040	+	43,006	43,245	hypothetical protein			E
gp041	+	43,666	44,007	hypothetical protein			E
gp042	+	44,007	44,135	hypothetical protein			E

Locus_tag	Direction	Min	Max	Product	Notes	Function	Cluster
gp043	+	44,137	44,391	hypothetical protein			E
gp044	+	44,378	44,671	hypothetical protein			E
gp045	+	44,668	44,928	hypothetical protein			E
gp046	+	45,011	45,301	hypothetical protein			E
gp047	+	45,350	45,661	hypothetical protein			E
gp048	+	45,651	45,929	hypothetical protein			E
gp049	+	45,929	46,936	RNA polymerase small subunit		transcription	E
gp050	+	46,954	47,187	hypothetical protein			E
gp051	+	47,177	48,451	RNA polymerase large subunit		transcription	E
gp052	+	48,438	48,572	hypothetical protein			E
gp053	+	48,618	48,839	hypothetical protein			E
gp054	+	48,830	49,078	hypothetical protein			E
gp055	+	49,084	49,473	hypothetical protein			E
gp056	+	49,525	49,809	hypothetical protein			E
gp057	+	50,361	50,609	hypothetical protein			E
gp058	+	50,602	50,763	hypothetical protein			E
gp059	+	50,738	51,400	hypothetical protein			E
gp060	+	51,421	51,591	hypothetical protein			E
gp061	+	51,588	52,130	hypothetical protein			E
gp062	+	52,114	52,302	hypothetical protein			E
gp063	+	52,265	52,630	putative HNH endonuclease		DNA metabolism	E
gp064	+	52,627	52,959	hypothetical protein			E
gp065	+	52,943	53,128	hypothetical protein			E
gp066	+	53,125	53,298	hypothetical protein			E
gp067	+	53,355	53,552	hypothetical protein			E

Locus_tag	**Direction**	**Min**	**Max**	**Product**	**Notes**	**Function**	**Cluster**
gp068	+	53,555	54,226	hypothetical protein			E
gp069	+	54,236	54,475	hypothetical protein			E
gp070	+	54,477	55,529	putative ATPase		DNA replication	E
gp071	+	55,539	56,720	hypothetical protein			E
gp072	+	56,859	58,142	DNA helicase		DNA replication	E
gp073	+	58,139	58,660	hypothetical protein			E
gp074	+	58,657	59,031	hypothetical protein			E
gp075	+	59,031	59,399	hypothetical protein			E
gp076	+	59,356	59,535	hypothetical protein			E
gp077	+	59,606	62,083	RIIA-like protein		DNA replication	E
gp078	+	62,080	63,930	RIIB-like protein		DNA replication	E
gp079	+	63,983	66,607	DNA polymerase I		DNA replication	E
gp080	+	66,600	67,100	hypothetical protein	putative avirulence protein		E
gp081	+	67,094	67,468	hypothetical protein			E
gp082	+	67,513	67,836	hypothetical protein			E
gp083	+	67,877	68,215	hypothetical protein			E
gp084	+	68,232	69,131	methyl-directed repair DNA adenine methylase		DNA repair	E
gp085	+	69,128	69,358	hypothetical protein			E
gp086	-	69,583	70,026	putative tail protein		structural components	F
gp087	-	70,103	70,612	endopeptidase Rz		cell lysis	F
gp088	-	70,593	70,814	hypothetical protein	possible holin		F
gp089	-	70,811	71,299	lysozyme		cell lysis	F
gp090	-	71,339	71,533	hypothetical protein			F
gp091	-	71,537	73,384	tail fiber family protein		structural components	F
gp092	-	73,455	73,742	hypothetical protein			F

Locus_tag	**Direction**	**Min**	**Max**	**Product**	**Notes**	**Function**	**Cluster**
gp093	-	73,754	76,339	tail spike protein	contains tail spike TSP1/Gp66 receptor binding N-terminal domain domain, and pectate lyase superfamily protein domain	structural components	F

Supplementary Table S5. Genome annotations of *Klebsiella pneumoniae* phage vB_KpM_FBKp34.

Locus_tag	**Direction**	**Min**	**Max**	**Product**	**Notes**	**Function**	**Cluster**
gp001	+	44	238	hypothetical protein			D
gp002	+	344	1,012	putative recombinase, resolvase family protein	contains resolvase, N terminal domain; similar to Phi92_gp052	DNA recombination	D
gp003	+	1,020	1,232	hypothetical protein			D
gp004	+	1,309	1,554	hypothetical protein			D
gp005	+	1,616	1,948	hypothetical protein	contains domain of unknown function DUF4326		D
gp006	+	1,948	2,232	hypothetical protein			D
gp007	+	2,225	2,470	hypothetical protein			D
gp008	+	2,470	2,718	hypothetical protein	contains domain of unknown function DUF4236		D
gp009	+	2,727	2,819	hypothetical protein			D
gp010	+	2,932	3,402	hypothetical protein			D
gp011	+	3,406	3,729	hypothetical protein			D
gp012	+	3,726	4,265	hypothetical protein	contains domain of unknown function DUF1768		D
gp013	+	4,279	4,458	hypothetical protein			D
gp014	+	4,593	4,805	hypothetical protein			D
gp015	+	4,802	5,152	hypothetical protein			D
gp016	+	5,149	5,370	hypothetical protein			D
gp017	+	5,398	5,973	hypothetical protein			D
gp018	+	5,966	6,415	hypothetical protein			D
gp019	+	6,408	6,695	hypothetical protein			D
gp020	+	6,685	7,011	hypothetical protein			D
gp021	+	6,998	7,525	hypothetical protein			D
gp022	+	7,522	7,764	hypothetical protein			D
gp023	+	7,773	8,141	hypothetical protein			D

Locus_tag	Direction	Min	Max	Product	Notes	Function	Cluster
gp024	+	8,143	8,370	hypothetical protein			D
gp025	+	8,376	8,687	hypothetical protein			D
gp026	+	8,695	8,943	hypothetical protein			D
gp027	+	8,940	9,362	hypothetical protein			D
gp028	+	9,369	9,548	hypothetical protein			D
gp029	+	9,558	9,797	hypothetical protein	contains restriction alleviation protein Lar domain		D
gp030	+	9,863	10,240	hypothetical protein			D
gp031	+	10,331	10,585	hypothetical protein			D
gp032	+	10,582	10,863	hypothetical protein			D
gp033	+	11,052	11,312	hypothetical protein			D
gp034	+	11,322	11,543	hypothetical protein			D
gp035	+	11,540	11,974	hypothetical protein			D
gp036	+	11,977	12,144	hypothetical protein			D
gp037	+	12,160	12,567	hypothetical protein			D
gp038	-	13,697	13,855	hypothetical protein			A
gp039	-	14,339	14,707	hypothetical protein	contains phage GP30.8 protein domain		A
gp040	-	14,776	15,144	hypothetical protein			A
gp041	-	15,605	15,892	hypothetical protein			A
gp042	-	15,903	16,088	hypothetical protein			A
gp043	-	16,134	16,493	hypothetical protein			A
gp044	-	16,579	16,962	hypothetical protein			A
gp045	-	16,977	17,111	hypothetical protein			A
gp046	-	17,185	17,535	hypothetical protein			A
gp047	-	17,539	17,832	hypothetical protein			A
gp048	-	17,878	18,177	hypothetical protein			A

Locus_tag	**Direction**	**Min**	**Max**	**Product**	**Notes**	**Function**	**Cluster**
gp049	-	18,268	18,516	hypothetical protein			A
gp050	-	18,578	18,802	hypothetical protein			A
gp051	-	18,892	19,350	hypothetical protein			A
gp052	-	19,689	19,850	hypothetical protein			A
gp053	-	19,847	20,149	hypothetical protein			A
gp054	-	20,149	20,409	hypothetical protein			A
gp055	-	20,543	20,674	hypothetical protein			A
gp056	-	20,677	20,967	hypothetical protein			A
gp057	-	20,985	21,377	hypothetical protein			A
gp058	-	21,456	21,800	hypothetical protein			A
gp059	-	21,804	21,953	hypothetical protein			A
gp060	-	22,009	22,359	hypothetical protein			A
gp061	-	22,449	22,706	hypothetical protein			A
gp062	-	22,752	22,973	hypothetical protein			A
gp063	-	23,049	23,213	hypothetical protein			A
gp064	-	23,291	23,533	hypothetical protein			A
gp065	-	23,597	24,133	hypothetical protein			A
gp066	-	24,223	24,444	hypothetical protein			A
gp067	-	25,705	25,818	putative DNA methylase		DNA methylation	A
gp068	-	25,812	26,318	HNH endonuclease	contains HNH endonuclease domain	DNA metabolism	A
gp069	-	26,324	27,016	DNA cytosine methyltransferase		DNA methylation	A
gp070	-	27,013	27,360	hypothetical protein			A
gp071	-	27,350	27,751	hypothetical protein			A
gp072	-	27,752	27,997	hypothetical protein			A

Locus_tag	Direction	Min	Max	Product	Notes	Function	Cluster
gp073	-	28,001	29,545	putative DNA helicase	contains AAA domain and UvrD-like helicase C-terminal domain	DNA replication	A
gp074	-	29,542	29,949	hypothetical protein			A
gp075	-	29,946	30,263	hypothetical protein			A
gp076	-	30,379	30,888	hypothetical protein			A
gp077	-	30,899	32,182	hypothetical protein			A
gp078	-	32,378	32,614	hypothetical protein	contains restriction alleviation protein Lar domain		A
gp079	-	32,752	34,104	hypothetical protein			A
gp080	-	34,117	34,437	hypothetical protein			A
gp081	-	34,444	34,692	hypothetical protein			A
gp082	-	34,701	34,895	hypothetical protein			A
gp083	-	34,892	35,089	hypothetical protein			A
gp084	-	35,086	35,241	hypothetical protein			A
gp085	-	35,241	35,336	hypothetical protein			A
gp086	-	35,329	35,550	hypothetical protein			A
gp087	-	35,550	35,918	hypothetical protein			A
gp088	-	35,946	36,413	hypothetical protein			A
gp089	-	36,424	36,558	hypothetical protein			A
gp090	-	36,571	36,858	hypothetical protein			A
gp091	-	36,842	37,396	putative metal dependent phosphohydrolase			A
gp092	+	37,516	37,878	hypothetical protein			B
gp093	+	37,881	38,252	hypothetical protein			B
gp094	+	38,326	38,478	hypothetical protein			B
gp095	+	38,478	38,801	hypothetical protein			B

Locus_tag	Direction	Min	Max	Product	Notes	Function	Cluster
gp096	+	38,798	39,007	hypothetical protein			B
gp097	+	39,000	39,341	hypothetical protein			B
gp098	+	39,351	39,587	hypothetical protein			B
gp099	+	39,590	40,288	hypothetical protein			B
gp100	+	40,281	40,475	hypothetical protein	contains RNA repair pathway DNA polymerase beta family domain		B
gp101	+	40,476	41,237	putative thioredoxin		DNA metabolism	B
gp102	+	41,234	41,515	hypothetical protein			B
gp103	+	41,699	42,076	hypothetical protein			B
gp104	+	42,091	42,753	hypothetical protein			B
gp105	+	42,762	43,277	putative phosphatase			B
gp106	+	43,287	44,216	anti-sigma factor			B
gp107	+	44,213	44,332	hypothetical protein			B
gp108	+	44,336	44,746	hypothetical protein			B
gp109	+	44,759	45,196	hypothetical protein			B
gp110	+	45,224	45,661	hypothetical protein			B
gp111	+	45,699	46,985	poly [ADP-ribose] polymerase	contains WGR domain; Poly(ADP-ribose) polymerase, regulatory domain; and Poly(ADP-ribose) polymerase catalytic domain	DNA repair	B
gp112	+	47,003	47,470	hypothetical protein			B
gp113	+	47,483	47,890	hypothetical protein	contains Yqey-like protein domain		B
gp114	+	47,975	50,992	ribonucleotide reductase of class III (anaerobic), large subunit	contains ATP cone domain and anaerobic ribonucleoside-triphosphate reductase domains	DNA metabolism	B
gp115	+	51,002	51,253	hypothetical protein			B

Locus_tag	**Direction**	**Min**	**Max**	**Product**	**Notes**	**Function**	**Cluster**
gp116	+	51,253	51,732	ribonucleotide reductase of class III (anaerobic), activating protein	contains 4Fe-4S single cluster domain	DNA metabolism	B
gp117	+	51,713	52,096	hypothetical protein			B
gp118	+	52,106	52,288	hypothetical protein			B
gp119	+	52,281	52,703	NinX	contains DUF2591 domain		B
gp120	+	52,711	52,929	hypothetical protein			B
gp121	+	52,926	53,258	hypothetical protein			B
gp122	+	53,267	53,458	bacterioferritin-associated ferredoxin	contains BFD-like [2Fe-2S] binding domain		B
gp123	+	53,466	53,624	hypothetical protein			B
gp124	+	53,653	54,630	integral membrane protein TerC	contains integral membrane protein TerC family domain		B
gp125	+	54,675	55,037	hypothetical protein			B
gp126	+	55,180	55,353	hypothetical protein			B
gp127	+	55,343	55,528	hypothetical protein			B
gp128	+	55,529	55,732	hypothetical protein			B
gp129	+	55,719	55,976	hypothetical protein			B
gp130	+	55,976	56,308	hypothetical protein			B
gp131	+	56,329	57,042	putative tellurium resistance protein	contains vWA found in TerF C terminus domain		B
gp132	+	57,110	57,691	TerD family protein	contains TerD domain		B
gp133	+	57,753	58,334	TerD family protein	contains TerD domain		B
gp134	+	58,393	59,271	hypothetical protein			B
gp135	+	59,282	60,358	toxic anion (tellurite) resistance protein	contains toxic anion resistance protein (TelA) domain		B
gp136	+	60,423	60,932	cell wall hydrolase	contains cell wall hydrolase domain		B
gp137	+	60,945	61,196	hypothetical protein			B
gp138	+	61,193	61,783	hypothetical protein			B
gp139	+	61,815	62,117	hypothetical protein			B

Locus_tag	Direction	Min	Max	Product	Notes	Function	Cluster
gp140	+	62,120	62,395	hypothetical protein			B
gp141	+	62,395	63,045	hypothetical protein	putative hydrolase		B
gp142	+	63,045	63,869	hypothetical protein	contains PRTase ComF-like domain		B
gp143	+	63,879	64,298	hypothetical protein			B
gp144	+	64,291	64,551	hypothetical protein			B
gp145	+	64,544	64,963	hypothetical protein			B
gp146	+	64,960	65,139	hypothetical protein			B
gp147	+	65,136	65,552	putative Eaa1			B
gp148	+	65,549	66,055	hypothetical protein			B
gp149	+	66,030	66,677	hypothetical protein			B
gp150	+	66,714	66,965	hypothetical protein			B
gp151	+	66,973	67,671	hypothetical protein			B
gp152	+	67,685	69,484	DNA primase/helicase	contains Toprim-like domain and DnaB-like helicase C terminal domain	DNA replication	B
gp153	+	69,501	71,717	phage DNA polymerase I	contains DNA polymerase family A domain	DNA replication	B
gp154	+	71,810	72,670	hypothetical protein			B
gp155	-	72,832	76,431	hypothetical protein	contains chaperone of endosialidase domain		C
gp156	-	76,431	76,916	hypothetical protein			C
gp157	-	76,946	77,272	hypothetical protein			C
gp158	-	77,274	77,762	hypothetical protein	possible tail fiber assembly protein		C
gp159	-	77,764	78,792	hypothetical protein			C
gp160	-	78,805	79,428	hypothetical protein			C
gp161	-	79,438	80,922	putative baseplate	contains baseplate J-like protein domain	structural components	C
gp162	-	80,915	81,196	putative membrane protein			C
gp163	-	81,210	81,734	hypothetical protein			C

Locus_tag	**Direction**	**Min**	**Max**	**Product**	**Notes**	**Function**	**Cluster**
gp164	-	81,737	82,390	baseplate central spike	contains phage protein gp137 N-terminal domain	structural components	C
gp165	-	82,391	83,356	hypothetical protein			C
gp166	-	83,366	83,704	hypothetical protein			C
gp167	-	83,716	84,417	hypothetical protein			C
gp168	-	84,422	86,365	putative cell envelope integrity protein TolA			C
gp169	-	86,377	86,598	hypothetical protein			C
gp170	-	86,619	87,110	hypothetical protein			C
gp171	-	87,187	87,654	hypothetical protein			C
gp172	-	87,697	89,064	putative tail sheath protein	contains DUF3383 domain	structural components	C
gp173	-	89,082	89,657	hypothetical protein			C
gp174	-	89,650	90,069	hypothetical protein			C
gp175	-	90,115	90,585	hypothetical protein			C
gp176	-	90,585	91,091	hypothetical protein			C
gp177	-	91,094	91,504	hypothetical protein			C
gp178	-	91,571	92,569	major capsid protein	contains phage major capsid protein E domain	structural components	C
gp179	-	92,587	92,988	putative head stabilization/decoration protein		structural components	C
gp180	-	93,004	94,344	hypothetical protein	possible scaffold protein		C
gp181	-	94,344	94,820	hypothetical protein	contains putative phage serine protease XkdF domain		C
gp182	-	94,968	96,548	hypothetical protein			C
gp183	-	96,686	98,230	putative terminase large subunit	contains terminase-like family domain and terminaseRNaseH-like domain	DNA packaging	C
gp184	-	98,352	98,651	hypothetical protein			C
tRNA	-	98,756	98,833	tRNA-Lys-TTT			C

Locus_tag	Direction	Min	Max	Product	Notes	Function	Cluster
gp185	-	98,841	98,957	hypothetical protein			C
tRNA	-	98,980	99,055	tRNA-Arg-TCT			C
gp186	-	99,071	99,250	hypothetical protein	possible lysin		C
tRNA	-	99,267	99,342	tRNA-Gly-TCC			C
tRNA	-	99,647	99,723	tRNA-His-GTG			C
tRNA	-	99,964	100,055	tRNA-Leu-TAA			C
tRNA	-	100,067	100,141	tRNA-Ile2-CAT			C
gp187	-	100,446	100,868	hypothetical protein	possible Rz spanin		C
gp188	-	101,442	102,566	IS200/IS605 family element transposase accessory protein TnpB	contains helix-turn-helix domain; probable transposase domain; and putative transposase DNA-binding domain	DNA integration	C
gp189	-	102,999	103,373	hypothetical protein			C
gp190	-	103,459	104,154	hypothetical protein			C
gp191	-	104,273	104,596	hypothetical protein			C
tRNA	-	104,784	104,857	tRNA-Trp-CCA			C
tRNA	-	104,866	104,941	tRNA-Phe-GAA			C
tRNA	-	104,947	105,021	tRNA-Asn-GTT			C
gp192	-	105,022	105,216	hypothetical protein			C
tRNA	-	105,263	105,340	tRNA-Pro-TGG			C
tRNA	-	105,347	105,421	tRNA-Cys-GCA			C
tRNA	-	105,596	105,671	tRNA-Ile-GAT			C
tRNA	-	105,678	105,763	tRNA-Ser-GCT			C
tRNA	-	105,844	105,929	tRNA-Ser-TGA			C
tRNA	-	105,936	106,013	tRNA-Leu-TAG			C
tRNA	-	106,024	106,101	tRNA-Glu-TTC			C
tRNA	-	106,110	106,223	tRNA-Asp-GTC			C

Locus_tag	**Direction**	**Min**	**Max**	**Product**	**Notes**	**Function**	**Cluster**
tRNA	-	106,230	106,306	tRNA-Asp-GTC			C
gp193	-	106,786	108,225	hypothetical protein	contains DUF2828 domain		C
gp194	-	108,308	108,550	hypothetical protein			C
gp195	-	108,624	109,478	hypothetical protein			C
gp196	-	109,568	111,253	nicotinamide phosphoribosyltransferase	contains DUF5598 domain and nicotinate phosphoribosyltransferase (NAPRTase) family domain		C
gp197	-	111,243	111,836	HNH homing endonuclease	contains NUMOD4 motif and HNH endonuclease domain	DNA metabolism	C
gp198	-	111,802	112,647	ribose-phosphate pyrophosphokinase	contains N-terminal domain of ribose phosphate pyrophosphokinase and a phosphoribosyl transferase domain	DNA metabolism	C
gp199	-	112,644	113,027	hypothetical protein			C
gp200	+	113,366	113,662	hypothetical protein			D
gp201	+	113,662	114,708	ribosylnicotinamide kinase	contains cytidylyltransferase-like domain and AAA domain		D
gp202	+	114,723	114,908	hypothetical protein			D
gp203	+	114,905	115,603	nicotinamide mononucleotide transport	contains nicotinamide mononucleotide transporter domain		D
gp204	+	115,633	115,950	hypothetical protein			D
gp205	+	115,950	116,231	hypothetical protein			D
gp206	+	116,484	117,119	hypothetical protein			D
gp207	+	117,116	117,469	hypothetical protein	possible restriction nuclease		D
gp208	+	117,469	117,960	hypothetical protein			D
gp209	+	117,962	118,519	hypothetical protein	possible metallophosphoesterase		D
gp210	+	118,678	119,598	RNA ligase	contains RNA ligase domain		D
gp211	+	119,598	119,942	hypothetical protein			D
gp212	+	119,952	120,377	hypothetical protein	contains AAA domain		D

Locus_tag	Direction	Min	Max	Product	Notes	Function	Cluster
gp213	+	120,386	120,598	hypothetical protein			D
gp214	+	120,598	121,374	NAD-dependent protein deacetylase of SIR2 family	contains Sir2 family domain		D
gp215	+	121,379	121,564	hypothetical protein			D
gp216	+	121,567	121,785	hypothetical protein			D
gp217	+	121,794	122,012	hypothetical protein			D
gp218	+	122,009	123,370	DNA ligase	contains ATP dependent DNA ligase domain	DNA replication and repair	D
gp219	+	123,372	124,031	hypothetical protein	contains phosphoribosyl-ATP pyrophosphohydrolase domain		D
gp220	+	124,039	124,146	hypothetical protein			D
gp221	+	124,140	124,412	hypothetical protein			D
gp222	+	124,425	125,360	DNA recombination-dependent growth factor RdgC	contains putative exonuclease RdgC domain	DNA repair	D
gp223	+	125,418	125,645	hypothetical protein			D
gp224	+	125,720	126,757	exonuclease		DNA replication	D
gp225	+	126,853	127,386	hypothetical protein			D
gp226	+	127,350	127,934	packaging and recombination endonuclease VII	contains recombination endonuclease VII domain	DNA repair	D
gp227	+	127,921	128,124	hypothetical protein			D
gp228	+	128,121	129,059	exonuclease	contains RNase_H superfamily domain	DNA replication	D
gp229	+	129,097	129,474	hypothetical protein			D
gp230	+	129,474	129,641	hypothetical protein			D
gp231	+	129,635	130,213	hypothetical protein	contains 5' nucleotidase, deoxy (Pyrimidine), cytosolic type C protein (NT5C) domain		D

Locus_tag	**Direction**	**Min**	**Max**	**Product**	**Notes**	**Function**	**Cluster**
gp232	+	130,210	130,533	hypothetical protein			D
gp233	+	130,534	131,505	putative thymidylate synthase	contains thymidylate synthase complementing protein domain	DNA metabolism	D
gp234	+	131,577	132,047	hypothetical protein			D
gp235	+	132,061	132,312	hypothetical protein			D
gp236	+	132,332	134,629	ribonucleoside-diphosphate reductase	contains ATP cone domain and ribonucleotide reductase, barrel domain	DNA replication	D
gp237	+	134,671	135,771	ribonucleotide-diphosphate reductase subunit beta	contains ribonucleotide reductase, small chain domain	DNA replication	D
gp238	+	135,784	136,038	glutaredoxin	contains glutaredoxin domain	DNA metabolism	D
gp239	+	136,047	136,187	hypothetical protein			D
gp240	+	136,187	136,588	hypothetical protein			D
gp241	+	136,598	137,092	lysozyme	contains phage lysozyme domain	cell lysis	D
gp242	+	137,170	137,916	PhoH-like protein	contains PhoH-like protein domain		D
gp243	+	137,923	138,384	hypothetical protein			D
gp244	+	138,422	139,336	hypothetical protein			D
gp245	+	139,290	140,063	serine/threonine-protein phosphatase	contains calcineurin-like phosphoesterase domain	DNA repair	D
gp246	+	140,063	140,329	hypothetical protein			D
gp247	+	140,326	140,892	hypothetical protein			D
gp248	+	141,029	141,376	putative DNA N-6-adenine methyltransferase		DNA methylation	D

Supplementary Table S6. Genome annotations of *Klebsiella pneumoniae* phage vB_KpM_FBKp24.

Locus_tag	Direction	Min	Max	Product	Notes	Function
gp001	-	1	561	hypothetical protein		
gp002	+	619	2,178	putative helicase		DNA replication
gp003	-	2,262	2,627	hypothetical protein		
gp004	-	2,633	2,812	hypothetical protein		
gp005	-	2,895	3,533	hypothetical protein		
gp006	-	3,670	4,113	hypothetical protein	N-acetyltransferase domain-containing protein	
gp007	-	4,221	5,564	virion structural protein		structural components
gp008	-	5,564	6,184	hypothetical protein		
gp009	-	6,184	7,557	virion structural protein		structural components
gp010	-	7,570	9,111	hypothetical protein		
gp011	-	9,180	10,103	hypothetical protein		
gp012	-	10,186	11,415	hypothetical protein		
gp013	-	11,425	12,666	hypothetical protein		
gp014	-	12,681	14,129	hypothetical protein		
gp015	-	14,221	16,647	hypothetical protein		
gp016	-	16,673	17,200	putative virion structural protein		structural components
gp017	-	17,206	18,111	putative virion structural protein		structural components
gp018	-	18,129	19,370	virion structural protein		structural components
gp019	+	19,407	20,582	virion structural protein		structural components
gp020	+	20,582	23,488	virion structural protein		structural components
gp021	-	23,532	24,764	hypothetical protein		
gp022	-	24,733	25,773	hypothetical protein		
gp023	-	25,784	26,242	hypothetical protein		
gp024	-	26,256	27,563	putative virion structural protein		structural components

Locus_tag	Direction	Min	Max	Product	Notes	Function
gp025	+	27,694	29,430	putative DNA polymerase		DNA replication
gp026	-	29,477	30,844	putative DNA-directed RNA polymerase beta subunit		transcription
gp027	-	30,837	31,676	hypothetical protein		
gp028	+	31,757	32,185	hypothetical protein		
gp029	+	32,178	33,893	hypothetical protein		
gp030	+	33,911	34,273	hypothetical protein		
gp031	+	34,288	34,926	hypothetical protein		
gp032	-	34,983	35,966	hypothetical protein		
gp033	+	36,038	38,032	putative SNF2 domain/DEAD-like helicase		transcription
gp034	-	38,094	38,477	hypothetical protein		
gp035	-	38,508	39,044	hypothetical protein		
gp036	-	39,126	39,314	hypothetical protein		
gp037	-	39,358	39,627	hypothetical protein	possible DNA primase	
gp038	-	39,828	40,016	hypothetical protein		
gp039	-	40,013	40,489	GNAT family N-acetyltransferase		
gp040	-	40,683	40,835	hypothetical protein		
tRNA	-	41,672	41,761	tRNA-Ser-GCT		
tRNA	-	41,771	41,844	tRNA-Asn-GTT		
tRNA	-	41,851	41,925	tRNA-Asp-GTC		
tRNA	-	42,043	42,116	tRNA-Gln-TTG		
tRNA	-	42,125	42,208	tRNA-Tyr-GTA		
gp041	-	42,392	42,751	hypothetical protein		
tRNA	-	42,834	42,907	tRNA-Arg-TCT		
tRNA	-	42,913	42,997	tRNA-Leu-TAA		
tRNA	-	43,003	43,078	tRNA-Ile2-CAT		

Locus_tag	Direction	Min	Max	Product	Notes	Function
gp042	-	43,130	43,294	hypothetical protein		
gp043	-	43,298	44,155	TRAP transporter solute receptor, TAXI family	contains a NMT1-like family domain	
gp044	+	44,395	44,652	hypothetical protein		
gp045	-	44,667	44,837	hypothetical protein		
gp046	-	44,849	45,736	hypothetical protein		
gp047	-	45,806	45,922	hypothetical protein		
tRNA	-	46,041	46,120	tRNA-Sup-TTA		
gp048	-	46,370	47,137	hypothetical protein		
gp049	-	47,244	47,825	hypothetical protein		
gp050	-	47,883	48,305	hypothetical protein		
gp051	-	48,431	48,721	hypothetical protein		
gp052	-	48,733	49,902	hypothetical protein	AAA domain-containing protein	
gp053	-	50,010	50,351	hypothetical protein		
gp054	-	50,438	51,706	hypothetical protein	AAA domain-containing protein, putative ATP-binding protein	
gp055	-	51,735	52,370	hypothetical protein		
gp056	-	52,386	52,757	hypothetical protein	putative tRNA nuclease WapA	
gp057	-	52,768	53,118	hypothetical protein		
gp058	-	53,151	53,510	hypothetical protein		
gp059	-	53,489	53,965	hypothetical protein		
gp060	-	53,976	54,578	hypothetical protein		
gp061	-	54,619	54,921	hypothetical protein		
gp062	-	55,283	56,239	hypothetical protein		
gp063	-	56,236	56,484	hypothetical protein		
gp064	-	56,510	56,875	hypothetical protein		

Locus_tag	**Direction**	**Min**	**Max**	**Product**	**Notes**	**Function**
gp065	-	56,891	57,337	macro domain containing protein		
gp066	-	57,815	58,279	GNAT family N-acetyltransferase		
gp067	-	58,503	60,017	putative helicase		DNA replication
gp068	-	60,173	62,140	RNA polymerase beta subunit	putative ATP-dependent DNA helicase	transcription
gp069	-	62,140	64,413	Putative DNA-directed RNA polymerase beta subunit	RNA_pol_Rpb2_6 domain-containing protein	transcription
gp070	+	64,527	64,877	hypothetical protein		
gp071	-	64,970	65,203	hypothetical protein		
gp072	-	65,263	66,489	hypothetical protein		
gp073	-	66,519	68,042	hypothetical protein		
gp074	-	68,070	69,611	hypothetical protein		
gp075	-	69,714	70,499	hypothetical protein		
gp076	-	70,570	71,415	hypothetical protein		
gp077	-	71,427	71,654	hypothetical protein		
gp078	-	71,657	72,778	putative nuclease SbcCD D subunit		DNA repair
gp079	-	72,768	73,325	hypothetical protein		
gp080	-	73,318	73,716	hypothetical protein		
gp081	-	73,809	74,429	hypothetical protein		
gp082	-	74,426	75,880	Bifunctional DNA-directed RNA polymerase subunit beta-beta', RpoBC		transcription
gp083	-	75,965	77,866	hypothetical protein	low similarity (62% query cover, 24% ident, 2e-11 e-value) to nuclear shell protein gp104 from Pseudomonas phage 201phi2-1	
gp084	-	79,189	81,405	putative T4-like DNA polymerase		DNA replication
gp085	-	81,517	81,939	hypothetical protein		
gp086	-	82,242	82,670	hypothetical protein		

Locus_tag	**Direction**	**Min**	**Max**	**Product**	**Notes**	**Function**
gp087	-	82,664	83,128	hypothetical protein		
gp088	-	83,137	83,562	hypothetical protein		
gp089	-	83,543	83,794	hypothetical protein		
gp090	-	83,907	84,182	hypothetical protein		
gp091	-	84,250	84,753	hypothetical protein		
gp092	-	84,765	85,169	hypothetical protein		
gp093	-	85,484	85,873	hypothetical protein		
gp094	-	86,120	87,088	putative tubulin like protein		
gp095	+	87,174	88,004	hypothetical protein		
gp096	-	88,049	88,882	hypothetical protein		
gp097	-	88,911	89,369	hypothetical protein		
gp098	-	89,398	90,018	hypothetical protein		
gp099	-	89,999	90,526	hypothetical protein		
gp100	-	90,587	91,141	hypothetical protein		
gp101	-	91,160	91,633	hypothetical protein		
gp102	-	91,620	92,111	hypothetical protein		
gp103	-	92,140	92,481	hypothetical protein		
gp104	-	92,551	93,231	putative lytic transglycosidase		
gp105	-	93,326	93,976	hypothetical protein		
gp106	-	94,186	94,596	hypothetical protein		
gp107	-	94,692	95,057	hypothetical protein		
gp108	-	95,047	95,412	hypothetical protein		
gp109	-	95,458	95,847	hypothetical protein		
gp110	-	95,888	96,208	hypothetical protein		
gp111	-	96,270	96,593	hypothetical protein		

Locus_tag	Direction	Min	Max	Product	Notes	Function
gp112	+	96,728	97,972	putative head structural protein		structural components
gp113	-	98,019	99,065	hypothetical protein		
gp114	-	99,169	101,343	terminase large subunit		DNA packaging
gp115	-	101,432	103,141	putative virion structural protein		structural components
gp116	-	103,143	105,692	putative virion structural protein		structural components
gp117	-	105,710	106,648	virion structural protein		structural components
gp118	+	106,812	108,881	putative tail sheath protein		structural components
gp119	+	108,874	109,749	putative virion structural protein	putative baseplate wedge protein	structural components
gp120	+	109,880	110,524	lytic transglycosylase		
gp121	+	110,535	110,648	hypothetical protein		
gp122	-	110,703	111,299	hypothetical protein		
gp123	-	111,296	111,799	hypothetical protein		
gp124	-	111,771	112,715	putative phosphohydrolase		
gp125	-	112,771	113,019	hypothetical protein		
gp126	-	113,016	113,366	hypothetical protein		
gp127	-	113,463	113,864	hypothetical protein		
gp128	-	114,075	114,479	hypothetical protein		
gp129	-	114,543	114,725	hypothetical protein		
gp130	-	114,844	115,314	hypothetical protein		
gp131	-	115,405	115,683	hypothetical protein		
gp132	-	115,716	116,054	hypothetical protein		
gp133	-	116,075	116,635	hypothetical protein		
gp134	-	116,632	116,946	hypothetical protein		
gp135	-	117,340	117,687	hypothetical protein		
gp136	-	117,771	117,887	hypothetical protein		

Locus_tag	Direction	Min	Max	Product	Notes	Function
gp137	-	117,887	118,057	hypothetical protein		
gp138	-	118,072	118,230	hypothetical protein		
gp139	+	118,389	118,928	hypothetical protein		
gp140	-	118,969	119,388	hypothetical protein		
gp141	-	119,460	119,951	hypothetical protein		
gp142	-	120,012	120,416	hypothetical protein		
gp143	-	120,400	120,771	hypothetical protein		
gp144	-	120,839	121,255	hypothetical protein		
gp145	-	121,397	121,660	hypothetical protein		
gp146	-	121,743	122,186	hypothetical protein		
gp147	-	122,192	122,383	hypothetical protein		
gp148	-	122,383	122,715	hypothetical protein		
gp149	-	122,699	122,920	hypothetical protein		
gp150	-	122,926	123,333	hypothetical protein		
gp151	-	123,330	123,827	hypothetical protein		
gp152	-	123,796	124,494	guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase / GTP pyrophosphokinase, (p)ppGpp synthetase II		regulation
gp153	-	124,602	125,225	hypothetical protein		
gp154	-	125,281	126,555	hypothetical protein		
gp155	+	126,744	128,039	hypothetical protein		
gp156	-	128,095	128,460	hypothetical protein		
gp157	-	128,482	128,835	hypothetical protein		
gp158	-	128,838	129,581	hypothetical protein		
gp159	-	129,589	130,161	hypothetical protein		
gp160	-	130,163	130,426	hypothetical protein		

Locus_tag	Direction	Min	Max	Product	Notes	Function
gp161	-	130,428	131,018	thymidine kinase		DNA metabolism
gp162	-	131,020	131,295	hypothetical protein		
gp163	-	131,292	131,651	hypothetical protein		
gp164	-	131,705	132,310	hypothetical protein		
gp165	-	132,315	132,683	hypothetical protein		
gp166	-	132,680	133,267	hypothetical protein		
gp167	-	133,281	133,568	hypothetical protein		
gp168	+	133,771	136,416	hypothetical protein		
gp169	-	136,450	136,710	hypothetical protein		
gp170	-	136,707	137,111	hypothetical protein		
gp171	-	137,166	137,978	phosphate starvation-inducible protein PhoH, predicted ATPase		
gp172	-	138,073	138,420	hypothetical protein		
gp173	-	138,499	138,861	hypothetical protein		
gp174	-	138,874	139,173	hypothetical protein		
gp175	-	139,225	139,692	hypothetical protein		
gp176	+	139,828	141,288	glycosyltransferase		
gp177	+	141,307	141,897	hypothetical protein		
gp178	-	141,959	142,372	hypothetical protein		
gp179	-	142,694	143,161	hypothetical protein		
gp180	-	143,180	143,707	DUF1190 domain containing protein		
gp181	-	143,786	144,178	hypothetical protein		
gp182	-	144,175	144,624	hypothetical protein		
gp183	-	144,677	144,976	hypothetical protein		
gp184	-	144,969	145,424	hypothetical protein		

Locus_tag	**Direction**	**Min**	**Max**	**Product**	**Notes**	**Function**
gp185	-	145,421	145,873	hypothetical protein		
gp186	-	145,875	146,459	DUF1653 domain-containing protein		
gp187	-	146,532	147,173	hypothetical protein		
gp188	-	147,177	147,596	hypothetical protein		
gp189	-	147,627	148,154	hypothetical protein		
gp190	-	148,199	149,713	hypothetical protein		
gp191	-	149,772	150,050	hypothetical protein		
gp192	-	150,082	150,450	hypothetical protein		
gp193	-	150,591	152,348	nicotinamide phosphoribosyltransferase		
gp194	-	152,345	153,208	ribose-phosphate pyrophosphokinase		
gp195	-	153,257	153,796	dihydrofolate reductase		
gp196	+	153,978	155,960	putative tail fiber protein	contains head binding domain of P22 tailspike	structural components
gp197	-	156,038	156,760	HigA family addiction module antidote protein	contains helix-turn-helix domain	
gp198	-	156,816	157,229	hypothetical protein		
gp199	-	157,271	157,666	hypothetical protein		
gp200	-	157,668	158,078	hypothetical protein		
gp201	-	158,091	158,456	hypothetical protein		
gp202	-	158,588	159,394	hypothetical protein		
gp203	-	159,510	160,040	hypothetical protein		
gp204	-	160,059	160,499	hypothetical protein		
gp205	-	160,496	160,876	hypothetical protein		
gp206	-	160,942	162,630	hypothetical protein		
gp207	-	162,685	163,278	hypothetical protein		
gp208	-	163,268	163,636	hypothetical protein		
gp209	-	163,640	163,969	hypothetical protein		

Locus_tag	Direction	Min	Max	Product	Notes	Function
gp210	-	164,007	164,783	hypothetical protein		
gp211	-	164,811	165,143	hypothetical protein		
gp212	-	165,240	165,713	hypothetical protein		
gp213	-	165,732	166,067	hypothetical protein		
gp214	-	166,079	166,405	hypothetical protein		
gp215	-	166,406	166,630	hypothetical protein		
gp216	-	166,620	167,009	hypothetical protein		
gp217	-	167,012	167,455	hypothetical protein		
gp218	-	167,455	168,429	hypothetical protein		
gp219	-	168,416	168,979	hypothetical protein		
gp220	-	169,006	169,194	hypothetical protein		
gp221	-	169,211	169,486	hypothetical protein		
gp222	-	169,486	169,746	hypothetical protein		
gp223	-	169,756	170,079	hypothetical protein		
gp224	-	170,082	170,588	hypothetical protein		
gp225	-	170,725	172,029	AAA family ATPase		
gp226	-	172,147	172,497	hypothetical protein		
gp227	-	172,494	172,949	hypothetical protein		
gp228	-	172,949	173,257	hypothetical protein		
gp229	-	173,261	174,952	hypothetical protein		
gp230	-	174,955	176,199	putative tRNA-splicing ligase RtcB		RNA repair
gp231	-	176,214	176,933	hypothetical protein		
gp232	-	176,952	177,515	hypothetical protein		
gp233	-	177,518	177,787	hypothetical protein		
gp234	-	177,777	178,289	hypothetical protein		

Locus_tag	Direction	Min	Max	Product	Notes	Function
gp235	-	178,289	178,663	hypothetical protein		
gp236	-	178,665	179,048	hypothetical protein		
gp237	-	179,045	179,290	hypothetical protein		
gp238	+	179,325	179,657	putative ammonia monooxygenase		
gp239	-	179,705	181,096	AAA family ATPase		
gp240	-	181,194	181,358	hypothetical protein		
gp241	-	181,418	181,801	hypothetical protein		
gp242	-	181,802	182,167	hypothetical protein		
gp243	-	182,173	182,646	hypothetical protein	macro domain containing protein	
gp244	-	182,665	183,282	hypothetical protein		
gp245	-	183,288	183,887	hypothetical protein		
gp246	-	183,897	184,304	hypothetical protein		
gp247	-	184,308	185,525	hypothetical protein		
gp248	-	185,585	185,893	hypothetical protein		
gp249	-	185,893	186,024	hypothetical protein		
gp250	-	186,021	187,412	thymidylate synthase		DNA metabolism
gp251	-	187,409	187,642	hypothetical protein		
gp252	-	187,636	188,031	hypothetical protein		
gp253	-	188,021	188,536	hypothetical protein		
gp254	-	188,610	189,209	tail protein		structural components
gp255	-	189,214	189,699	hypothetical protein		
gp256	-	189,723	190,133	hypothetical protein		
gp257	-	190,193	190,555	hypothetical protein		
gp258	-	190,552	191,109	hypothetical protein		
gp259	-	191,106	191,669	RNA 2'-phosphotransferase		

Locus_tag	Direction	Min	Max	Product	Notes	Function
gp260	-	191,662	192,180	hypothetical protein		
gp261	-	192,180	192,455	hypothetical protein		
gp262	-	192,442	193,161	hypothetical protein		
gp263	-	193,154	193,867	hypothetical protein		
gp264	-	193,867	194,355	hypothetical protein		
gp265	-	194,470	194,877	hypothetical protein		
gp266	-	194,958	195,506	hypothetical protein		
gp267	-	195,507	195,851	hypothetical protein		
gp268	-	195,916	197,055	hypothetical protein		
gp269	-	197,052	197,240	hypothetical protein		
gp270	-	197,261	197,665	hypothetical protein		
gp271	-	197,667	198,602	hypothetical protein		
gp272	-	198,613	198,960	hypothetical protein		
gp273	-	199,043	199,555	hypothetical protein		
gp274	-	199,572	200,021	membrane protease subunit		
gp275	-	200,021	200,272	hypothetical protein		
gp276	-	200,300	200,989	nicotinamide mononucleotide transporter		
gp277	-	200,986	201,138	hypothetical protein		
gp278	-	201,152	202,366	multifunctional transcriptional regulator/nicotinamide-nucleotide adenylyltransferase/ribosylnicotinamide kinase NadR		
gp279	-	202,386	202,697	hypothetical protein		
gp280	-	202,710	203,105	hypothetical protein		
gp281	-	203,114	203,347	hypothetical protein		
gp282	-	203,357	203,917	hypothetical protein		

Locus_tag	**Direction**	**Min**	**Max**	**Product**	**Notes**	**Function**
gp283	-	203,918	204,178	hypothetical protein		
gp284	-	204,189	204,314	hypothetical protein		
gp285	-	204,379	205,014	hypothetical protein		
gp286	-	205,011	205,304	hypothetical protein		
gp287	-	205,301	205,735	hypothetical protein		
gp288	-	205,760	206,251	hypothetical protein		
gp289	-	206,229	206,507	hypothetical protein		
gp290	-	206,509	206,736	hypothetical protein		
gp291	-	206,747	207,154	hypothetical protein		
gp292	-	207,142	207,570	hypothetical protein		
gp293	-	207,589	208,176	deoxyuridine 5'-triphosphate nucleotidohydrolase		DNA metabolism
gp294	-	208,276	210,345	bifunctional tail protein		structural components
gp295	-	210,361	212,400	bifunctional tail protein		structural components
gp296	-	212,532	212,933	hypothetical protein		
gp297	-	212,930	213,259	hypothetical protein		
gp298	+	213,383	213,595	hypothetical protein		
gp299	-	213,638	213,883	hypothetical protein		
gp300	-	214,060	215,856	putative tail fiber protein	contains beta-helix domain	structural components
gp301	-	215,902	218,649	hypothetical protein	tail spike N-terminal domain containing protein	
gp302	-	218,757	218,951	hypothetical protein		
gp303	-	218,951	220,936	putative tail fiber protein		structural components
gp304	-	221,011	223,278	putative tail fiber protein		structural components
gp305	-	223,346	223,639	hypothetical protein		
gp306	-	223,651	226,302	putative tail fiber protein		structural components
gp307	-	226,470	228,698	hypothetical protein	beta-helix domain containing protein	

Locus_tag	Direction	Min	Max	Product	Notes	Function
gp308	+	228,908	231,121	hypothetical protein	putative tail fiber or spike with GTPase (hydrolase) activity	
gp309	+	231,199	233,454	hypothetical protein	exopolysaccharide biosynthesis protein; putative tail fiber	
gp310	+	233,520	235,559	hypothetical protein	peptidase S74 domain-containing protein; putative tail fiber	
gp311	+	235,573	235,794	hypothetical protein		
gp312	+	235,874	237,868	hypothetical protein	putative tail spike protein	
gp313	+	237,880	239,541	hypothetical protein		
gp314	-	239,593	240,159	hypothetical protein	putative virion structural protein	
gp315	-	240,210	240,596	hypothetical protein		
gp316	-	240,660	241,184	hypothetical protein		
gp317	-	241,239	241,790	hypothetical protein		
gp318	-	241,883	242,344	hypothetical protein		
gp319	-	242,505	243,155	hypothetical protein		
gp320	-	243,227	243,958	hypothetical protein		
gp321	-	244,085	244,246	hypothetical protein		
gp322	-	244,285	244,974	hypothetical protein		
gp323	-	245,080	245,826	virion structural protein	possible prohead core protein protease	structural components
gp324	-	245,830	246,558	hypothetical protein		
gp325	-	246,560	247,285	hypothetical protein		
gp326	-	247,297	248,829	hypothetical protein		
gp327	-	248,829	249,020	hypothetical protein		
gp328	-	249,101	253,579	RNA polymerase beta subunit		transcription
gp329	-	253,596	255,227	putative DNA-directed RNA polymerase beta subunit		transcription

Locus_tag	Direction	Min	Max	Product	Notes	Function
gp330	+	255,274	261,879	hypothetical protein	putative tail fiber with transglycosylase activity	
gp331	+	261,933	264,077	hypothetical protein		
gp332	-	264,119	264,463	hypothetical protein		
gp333	-	264,547	265,614	hypothetical protein		
gp334	-	265,605	265,898	hypothetical protein		
gp335	-	265,980	266,735	hypothetical protein		
gp336	-	266,748	267,266	hypothetical protein		
gp337	+	267,395	267,916	hypothetical protein		
gp338	-	267,956	268,657	hypothetical protein		
gp339	-	268,654	269,130	hypothetical protein		
gp340	-	269,135	269,806	virion structural protein		structural components
gp341	-	270,182	270,469	hypothetical protein		
gp342	-	270,488	271,903	UvsX DNA recombinase		DNA replication and repair
gp343	+	272,012	272,884	hypothetical protein		
gp344	-	272,927	273,304	hypothetical protein		
gp345	-	273,301	274,899	RnhA ribonuclease HI		DNA replication
gp346	-	274,956	275,384	hypothetical protein		
gp347	+	275,443	276,744	putative virion structural protein		structural components
gp348	+	276,747	277,349	hypothetical protein		
gp349	-	277,424	277,675	hypothetical protein		
gp350	-	277,783	278,028	hypothetical protein		
gp351	-	278,030	278,353	hypothetical protein		
gp352	-	278,343	278,984	hypothetical protein		
gp353	-	279,077	281,548	nuclease SbcCD subunit C		DNA repair

Locus_tag	Direction	Min	Max	Product	Notes	Function
gp354	+	281,627	282,616	hypothetical protein		
gp355	-	282,660	283,190	hypothetical protein		
gp356	-	283,206	284,561	YomR		
gp357	-	284,575	286,806	putative tail fiber protein		structural components
gp358	+	286,872	288,116	putative virion structural protein		structural components
gp359	+	288,119	288,718	putative spanin		cell lysis
gp360	-	288,763	289,380	hypothetical protein		
gp361	-	289,380	289,997	thymidylate kinase		DNA metabolism
gp362	-	290,010	290,591	hypothetical protein	possible RuvC-like resolvase	
gp363	-	290,677	291,822	hypothetical protein		
gp364	-	291,837	292,754	virion structural protein		structural components
gp365	-	292,864	293,406	hypothetical protein		
gp366	-	293,440	294,282	putative virion structural protein		structural components
gp367	-	294,362	296,806	virion structural protein		structural components
gp368	+	296,871	299,660	virion structural protein		structural components
gp369	-	299,732	301,936	hypothetical protein		
gp370	-	301,967	303,577	hypothetical protein	putative RNA polymerase beta subunit	
gp371	-	303,599	304,594	hypothetical protein		
gp372	-	304,809	307,097	major head protein		structural components

Supplementary Table S7. Analysis of codon usage of phages vB_KpP_FBKp27, vB_KpM_FBKp34, vB_KpM_FBKp24 and *Klebsiella pneumoniae* HS11286 using Cusp from EMBOSS.

Codon	**AA**[a]	**ϕKp27**				**ϕKp34**				**ϕKp24**				***K. pneumoniae* HS11286**		
		Fraction[b]	**Frequency**	**No.**	**Ratio to bacteria**	**Fraction**	**Frequency**	**No.**	**Ratio to bacteria**	**Fraction**	**Frequency**	**No.**	**Ratio to bacteria**	**Fraction**	**Frequency**	**No.**
GCA	A	0.25	23.25	549	2.93	0.43	25.15	1061	3.17	0.25	16.80	1597	2.12	0.08	7.94	12537
GCC	A	0.16	14.70	347	0.34	0.11	6.38	269	0.15	0.21	14.36	1365	0.33	0.42	43.25	68298
GCG	A	0.03	2.50	59	0.06	0.08	4.46	188	0.10	0.31	21.04	2000	0.49	0.41	42.99	67889
GCT	A	0.56	51.04	1205	5.06	0.38	22.07	931	2.19	0.24	16.26	1545	1.61	0.10	10.09	15928
TGC	C	0.34	3.18	75	0.40	0.25	3.34	141	0.42	0.42	3.63	345	0.46	0.73	7.98	12595
TGT	C	0.66	6.14	145	2.03	0.75	10.12	427	3.35	0.58	5.06	481	1.67	0.28	3.03	4777
GAC	D	0.28	16.60	392	0.70	0.23	14.53	613	0.61	0.45	26.95	2561	1.13	0.47	23.82	37612
GAT	D	0.72	43.63	1030	1.64	0.77	49.87	2104	1.88	0.56	33.62	3195	1.26	0.53	26.60	42007
GAA	E	0.64	40.92	966	1.49	0.72	53.59	2261	1.96	0.68	44.74	4252	1.63	0.51	27.39	43255
GAG	E	0.36	22.91	541	0.86	0.28	20.93	883	0.79	0.32	20.65	1963	0.77	0.49	26.66	42100
TTC	F	0.55	19.65	464	1.01	0.30	13.51	570	0.70	0.49	23.30	2214	1.20	0.51	19.42	30677
TTT	F	0.46	16.39	387	0.87	0.70	31.62	1334	1.68	0.51	23.92	2273	1.27	0.49	18.81	29712
GGA	G	0.10	6.27	148	1.06	0.25	14.84	626	2.52	0.17	10.66	1013	1.81	0.08	5.89	9306
GGC	G	0.19	12.41	293	0.29	0.11	6.87	290	0.16	0.21	13.09	1244	0.31	0.56	42.48	67081
GGG	G	0.14	9.06	214	0.63	0.11	6.80	287	0.47	0.25	16.11	1531	1.11	0.19	14.47	22847
GGT	G	0.57	36.98	873	2.84	0.53	31.91	1346	2.45	0.38	24.11	2291	1.85	0.17	13.00	20537
CAC	H	0.40	6.99	165	0.62	0.30	5.67	239	0.50	0.48	7.77	738	0.69	0.50	11.34	17901
CAT	H	0.60	10.46	247	0.92	0.71	13.54	571	1.19	0.52	8.55	813	0.75	0.50	11.41	18018
ATA	I	0.08	4.41	104	1.43	0.16	10.95	462	3.55	0.10	6.53	621	2.12	0.06	3.09	4877
ATC	I	0.45	25.03	591	0.78	0.24	16.40	692	0.51	0.43	27.66	2629	0.86	0.58	32.23	50902
ATT	I	0.47	26.05	615	1.28	0.60	40.30	1700	1.98	0.47	30.78	2925	1.51	0.37	20.34	32115
AAA	K	0.58	37.32	881	1.51	0.74	61.56	2597	2.49	0.73	41.80	3973	1.69	0.64	24.68	38981
AAG	K	0.42	27.02	638	1.96	0.26	21.50	907	1.56	0.28	15.88	1509	1.15	0.36	13.77	21748

Codon	**AA**[a]	**ϕKp27**				**ϕKp34**				**ϕKp24**				***K. pneumoniae* HS11286**		
		Fraction[b]	**Frequency**	**No.**	**Ratio to bacteria**	**Fraction**	**Frequency**	**No.**	**Ratio to bacteria**	**Fraction**	**Frequency**	**No.**	**Ratio to bacteria**	**Fraction**	**Frequency**	**No.**
CTA	L	0.06	4.83	114	1.62	0.09	7.70	325	2.58	0.06	5.52	525	1.85	0.03	2.98	4711
CTC	L	0.11	9.40	222	0.61	0.05	4.39	185	0.29	0.16	14.03	1333	0.91	0.14	15.35	24245
CTG	L	0.41	35.32	834	0.49	0.12	10.00	422	0.14	0.22	19.37	1841	0.27	0.65	71.38	112738
CTT	L	0.18	15.54	367	2.00	0.28	23.09	974	2.97	0.17	15.00	1426	1.93	0.07	7.79	12296
TTA	L	0.16	14.23	336	2.27	0.31	25.60	1080	4.08	0.24	21.55	2048	3.43	0.06	6.28	9910
TTG	L	0.09	7.50	177	1.11	0.15	12.40	523	1.84	0.16	13.95	1326	2.07	0.06	6.74	10649
ATG	M	1.00	29.10	687	1.09	1.00	24.34	1027	0.91	1.00	21.21	2016	0.79	1.00	26.77	42285
AAC	N	0.53	27.95	660	1.27	0.30	16.14	681	0.73	0.53	28.19	2679	1.28	0.65	21.98	34709
AAT	N	0.47	24.65	582	2.04	0.70	37.26	1572	3.08	0.47	25.12	2387	2.08	0.36	12.09	19101
CCA	P	0.31	12.20	288	3.05	0.41	12.14	512	3.04	0.19	7.50	713	1.88	0.09	4.00	6310
CCC	P	0.10	3.73	88	0.49	0.05	1.54	65	0.20	0.15	5.87	558	0.77	0.16	7.59	11987
CCG	P	0.09	3.60	85	0.12	0.09	2.77	117	0.09	0.37	14.55	1383	0.48	0.65	30.15	47615
CCT	P	0.50	19.61	463	4.18	0.45	13.39	565	2.86	0.29	11.65	1107	2.48	0.10	4.69	7406
CAA	Q	0.38	17.41	411	2.52	0.68	22.02	929	3.19	0.54	17.69	1681	2.56	0.15	6.91	10906
CAG	Q	0.62	28.67	677	0.75	0.32	10.31	435	0.27	0.46	15.32	1456	0.40	0.85	38.05	60087
AGA	R	0.10	4.36	103	2.62	0.35	13.44	567	8.06	0.12	6.02	572	3.61	0.03	1.67	2632
AGG	R	0.06	2.41	57	1.45	0.10	3.67	155	2.20	0.05	2.75	261	1.65	0.03	1.67	2636
CGA	R	0.08	3.56	84	1.35	0.09	3.56	150	1.35	0.13	6.82	648	2.59	0.04	2.63	4151
CGC	R	0.09	3.69	87	0.12	0.06	2.42	102	0.08	0.21	10.60	1007	0.34	0.52	31.08	49083
CGG	R	0.04	1.61	38	0.16	0.04	1.40	59	0.14	0.13	6.49	617	0.65	0.17	9.91	15656
CGT	R	0.63	26.68	630	2.04	0.36	13.63	575	1.04	0.36	18.49	1757	1.41	0.22	13.08	20659
AGC	S	0.14	8.77	207	0.40	0.09	5.57	235	0.26	0.13	8.83	839	0.40	0.38	21.83	34478
AGT	S	0.19	11.48	271	2.62	0.25	16.31	688	3.72	0.21	14.03	1333	3.20	0.08	4.39	6929
TCA	S	0.17	10.55	249	2.63	0.22	14.06	593	3.51	0.14	9.05	860	2.26	0.07	4.01	6333
TCC	S	0.13	7.96	188	0.72	0.06	4.10	173	0.37	0.15	9.81	932	0.89	0.19	11.05	17449
TCG	S	0.04	2.33	55	0.20	0.03	1.71	72	0.15	0.15	9.93	944	0.86	0.20	11.56	18263

Codon	**AA**[a]	**ϕKp27**				**ϕKp34**				**ϕKp24**				***K. pneumoniae* HS11286**		
		Fraction[b]	**Frequency**	**No.**	**Ratio to bacteria**	**Fraction**	**Frequency**	**No.**	**Ratio to bacteria**	**Fraction**	**Frequency**	**No.**	**Ratio to bacteria**	**Fraction**	**Frequency**	**No.**
TCT	S	0.33	19.95	471	4.46	0.35	22.68	957	5.07	0.22	14.92	1418	3.34	0.08	4.47	7062
ACA	T	0.18	11.65	275	4.35	0.40	22.14	934	8.27	0.19	12.65	1202	4.73	0.05	2.68	4226
ACC	T	0.27	18.04	426	0.58	0.12	6.87	290	0.22	0.31	20.25	1925	0.65	0.61	31.30	49424
ACG	T	0.05	3.47	82	0.27	0.06	3.46	146	0.27	0.24	16.04	1524	1.24	0.25	12.94	20435
ACT	T	0.50	33.16	783	6.94	0.42	23.61	996	4.94	0.26	17.25	1639	3.61	0.09	4.78	7550
GTA	V	0.38	23.42	553	3.42	0.33	21.90	924	3.20	0.22	15.32	1456	2.24	0.10	6.85	10811
GTC	V	0.12	7.16	169	0.34	0.10	6.28	265	0.30	0.26	17.53	1666	0.83	0.30	21.08	33297
GTG	V	0.20	11.99	283	0.37	0.12	7.94	335	0.25	0.18	12.44	1182	0.39	0.46	32.30	51014
GTT	V	0.30	18.59	439	1.80	0.45	29.70	1253	2.87	0.34	23.25	2210	2.25	0.15	10.33	16318
TGG	W	1.00	12.75	301	0.80	1.00	14.58	615	0.91	1.00	13.54	1287	0.85	1.00	15.96	25204
TAC	Y	0.39	14.02	331	1.08	0.26	12.11	511	0.93	0.54	21.70	2062	1.67	0.48	13.03	20574
TAT	Y	0.61	21.81	515	1.54	0.74	33.99	1434	2.39	0.46	18.66	1773	1.31	0.52	14.21	22439
TAA	*[c]	0.70	2.75	65	1.39	0.59	3.46	146	1.75	0.66	2.57	244	1.30	0.52	1.97	3117
TAG	*	0.07	0.25	6	0.49	0.10	0.57	24	1.11	0.10	0.38	36	0.74	0.13	0.51	811
TGA	*	0.24	0.93	22	0.70	0.32	1.85	78	1.39	0.25	0.97	92	0.73	0.35	1.34	2108
TAA	*	0.70	2.75	65	-	-	-	-	-	-	-	-	-	-	-	-
TAG	*	0.07	0.25	6	-	-	-	-	-	-	-	-	-	-	-	-
TGA	*	0.24	0.93	22	-	-	-	-	-	-	-	-	-	-	-	-

[a] AA, amino acid

[b] Fraction, proportion of usage of the codon among the set of codons which code for this codon's amino acid; Frequency, number of specific codon divided by total number of codons in the sequence; No, total number of times the specific codon is observed in the sequence.

[c] *, stop codon

References

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