



Supplemental Material to:

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**Identification and characterization of ϕ H111-1:
A novel myovirus with broad activity against clinical
isolates of *Burkholderia cenocepacia***

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1 Table S1: ϕ H111-1 host range

Category	<i>Burkholderia</i> species	Strain or isolate	Lysis
Strain panel ^{22,23}	<i>B. cepacia</i>	LMG 18821	-
		ATCC 17759	-
	<i>B. multivorans</i>	ATCC 17616	+
		C5274	+
		C5393	-
		C3430	-
	<i>B. cenocepacia</i>	C6433	+
		715J	+
		J2315	+
		K56-2	+
		C1257	+
		C5424	+
		PC184	+
		C4455	-
		CEP511	-
		<i>B. stabilis</i>	LMG 14294
	LMG 18870		-
	<i>B. vietnamiensis</i>	LMG 10929	-
		LMG 18835	-
		DBO1	-
	<i>B. dolosa</i>	LMG 18943	-
		LMG 21443	-
	<i>B. ambifaria</i>	LMG 17828	-
LMG 19182		-	
LMG 19467		-	
<i>B. anthina</i>	LMG 16670	-	
<i>B. pyrrocinia</i>	LMG 14191	-	
Clinical isolates ¹³	<i>B. multivorans</i>	M1512	-
		M1865	-

		R810	-
		R1159	-
	<i>B. cenocepacia</i>	R161	+
		R452	+
		R750	+
		R1284	+
		R1285	+
		R1314	+
		R1434	+
		R1619	+
		R1882	+
		R1883	+
		R1884	+
		R2314	+
		S11528	+
LPS mutants ^{11,12}	<i>B. cenocepacia</i> (all K56-2)	wildtype	+
		RSF19	+
		XOA7	+
		XOA15	+
		XOA17	+
		XOA8	-
		CCB1	-

3 Table S2: ϕ H111-1 HHpred analysis

Protein	Motif of closest relative	Motif definition	Percent probability	E-value
gp2	1zn6_A	Phage-related conserved hypothetical protein	100	7.10e ⁻⁵⁸
gp10	2g1p_A	DNA adenine methylase	100	8.00e ⁻⁶⁰
gp12	2ikb_A	Hypothetical protein NMB1012	100	1.10e ⁻⁵⁹
gp14	3d37_A	Tail protein, 43 kDa	100	5.40e ⁻⁴⁰
gp15	2djp_A	Hypothetical protein SB145	99.48	1.70e ⁻¹⁴
gp20	3j2m_U	Tail sheath protein GP18	100	1.10e ⁻⁵⁵
gp21	2kz6_A	Uncharacterized protein	98.09	8.50e ⁻⁶
gp22	2xgf_A	Long tail fiber protein P37	100	2.70e ⁻³⁷
gp24	3h2t_A	Baseplate structural protein GP6	99.02	4.30e ⁻⁹
gp25	2ia7_A	Tail lysozyme, putative	99.93	2.80e ⁻²⁵
gp27	3qr8_A	GPV, baseplate assembly protein V	100	9.50e ⁻⁴³
gp28	2gfv_A	Putative cytoplasmic protein	95.21	0.39
gp30	1k0h_A	Gpfii	99.97	7.10e ⁻³⁴
gp31	3bqw_A	Putative capsid protein of prophage	100	8.40e ⁻⁵²
gp32	1td4_A	Head decoration protein	97.78	0.00013
gp33	1tg6_A	Putative ATP-dependent CLP protease proteolytic S	99.96	3.80e ⁻²⁹
gp34	2jes_A	Portal protein	98.31	3.90e ⁻⁵
gp35	1hyw_A	GPW, head-TO-tail joining protein W	99.77	7.80e ⁻¹⁹
gp36	2o0j_A	Terminase, DNA packaging protein GP17	98.9	8.70e ⁻⁹
gp37	1j9i_A	GPNU1 DBD	97.73	2.60e ⁻⁵
gp39	1nlt_A	Protein YDJ1, mitochondrial protein import protein MAS5	99.93	3.60e ⁻²⁶
gp40	1nui_A	DNA primase/helicase	99.38	8.90e ⁻¹³
gp42	3e7l_A	Transcriptional regulator (NTRC family)	91.04	0.37
gp43	3bd1_A	CRO protein	99.8	4.60e ⁻²⁰
gp44	3bs3_A	Putative DNA-binding protein	99.79	5.90e ⁻²⁰
gp47	1vz0_A	PARB, chromosome partitioning protein PARB	99.96	2.60e ⁻²⁸
gp50	1z4h_A	TORI, TOR inhibition protein	99.66	1.60e ⁻¹⁶
gp51	3ubt_Y	Modification methylase HAEIII	100	8.40e ⁻⁷³
gp52	4f0q_A	Restriction endonuclease	91.41	0.81
gp53	1vz0_A	PARB, chromosome partitioning protein PARB	99.97	3.70e ⁻³¹
gp54	1z1b_A	Integrase	100	2.70e ⁻³⁹

4 HHpred hits with $\geq 90\%$ probability have been listed.

5 Table S3: BLASTN and PHAST analysis of nucleotide sequences closely related to ϕ H111-1

<i>Burkholderia</i> strain (all chromosome 1)	BLASTN query coverage (%)	BLASTN E-value	BLASTN alignment region	PHAST prediction
<i>B. gladioli</i> BSR3	78	0	3,123,511-3,138,769	intact prophage; 3,108,388-3,134,134
<i>B. glumae</i> BGR1	70	0	3,096,940-3,109,799	intact prophage; 3,075,378-3,102,996
<i>B. ambifaria</i> AMMD	69	0	2,058,351-2,065,877	intact prophage; 2,023,987-2,070,156
<i>B. pseudomallei</i> BPC006	65	0	1,113,292-1,124,344	intact prophage; 1,099,056-1,147,321
<i>B. pseudomallei</i> 1026b	64	0	1,175,535-1,186,832	intact prophage; 1,176,397-1,201,823
<i>B. pseudomallei</i> MSHR346	62	0	2,640,168-2,651,467	intact prophage; 2,625,992-2,650,729

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