

Table S1. *Mycobacterium* cluster P bacteriophages included in the comparative analyses. Bacteriophages for which integration-dependent immunity systems had previously been identified through the computational identification of an *attP* site within the repressor gene are highlighted in blue.

Phage	Subcluster	Length (bp)	GC-content	# ORFs	# tRNAs	IDIS*	Accession #	Reference
Arib1	P1	46,732	67.5%	78	0	yes	NC_051736.1	unpublished
Atcoo	P1	49,075	67.0%	78	0	yes	NC_051729.1	unpublished
Bartholomew	P1	46,484	67.2%	77	0	yes	NC_051734.1	Doyle <i>et al.</i> 2018
Bogie	P1	48,639	66.9%	81	0	yes	MF133446.1	Doyle <i>et al.</i> 2018
Brusacoram	P1	47,618	67.0%	78	0	yes	NC_028747.1	Hatfull <i>et al.</i> 2016
Bunnies	P1	48,822	67.1%	81	1	yes	MN096356.1	unpublished
CactusJack	P1	48,222	67.3%	79	0	yes	MN892484.1	unpublished
Camster	P1	47,149	67.2%	80	0	yes	MW055902.1	unpublished
Donovan	P1	47,162	67.2%	78	0	yes	KF841477.1	Pope <i>et al.</i> 2015
FirstPlacePfu	P1	45,680	67.3%	82	0	yes	NC_051735.1	unpublished
Fishburne	P1	47,109	67.3%	77	0	yes	NC_021302.1	Hatfull <i>et al.</i> 2013
Glaske	P1	48,222	67.3%	78	0	yes	MN807250.1	unpublished
GreaseLightnin	P1	48,424	67.1%	80	0	yes	NC_051731.1	unpublished
HUHilltop	P1	46,896	67.2%	81	0	yes	MN010757.1	Pope <i>et al.</i> 2015
Jebeks	P1	45,580	67.3%	77	0	yes	NC_041969.1	Pope <i>et al.</i> 2015
Jung	P1	46,561	67.1%	77	0	yes	NC_051730.1	Van <i>et al.</i> 2020
KilKor	P1	48,916	67.2%	79	0	yes	NC_053209.1	unpublished
Ksquared	P1	48,699	67.1%	80	0	yes	NC_051732.1	Doyle <i>et al.</i> 2018
Majeke	P1	47,612	67.4%	81	0	yes	NC_051737.1	unpublished
Malithi	P1	46,870	67.1%	79	0	yes	KP027200.1	Pope <i>et al.</i> 2015
Mangethe	P1	47,612	67.4%	81	1	yes	MK016499.1	unpublished
Megiddo	P1	48,783	67.1%	78	0	yes	NC_051728.1	unpublished
Necropolis	P1	46,263	62.9%	76	0	yes	MK937604.1	unpublished
Phalm	P1	48,213	67.3%	79	0	yes	MN807248.1	unpublished
Phegasus	P1	47,578	67.4%	81	0	yes	ON637760	Howell, Versoza <i>et al.</i> 2022
Phineas	P1	47,229	67.2%	77	0	yes	NC_051733.1	Pope <i>et al.</i> 2015
Shipwreck	P1	48,670	66.9%	81	0	yes	NC_031261.1	Pope <i>et al.</i> 2015
StevieRay	P1	48,815	66.9%	81	1	yes	MF373843.1	unpublished
StressBall	P1	47,915	67.3%	78	0	yes	MN908683.1	unpublished
Techage	P1	47,094	67.4%	79	0	yes	MK919480.1	unpublished
Thespis	P1	47,618	67.0%	78	0	yes	MG198785.1	Bushhouse <i>et al.</i> 2017
Willsammy	P1	48,399	67.0%	80	0	yes	NC_051727.1	unpublished
Zilizebeth	P1	48,056	67.3%	83	1	yes	MK524508.1	unpublished
Tortellini	P2	49,658	65.8%	76	0	no	NC_041888.1	Doyle <i>et al.</i> 2018
Xavia	P3	49,808	65.9%	71	0	no	NC_051740.1	unpublished
BigNuz	P4	48,984	66.7%	82	0	yes	NC_023692.1	Pope <i>et al.</i> 2015
Nazo	P4	48,870	66.8%	83	0	yes	KX641262	unpublished
Phayonce	P5	49,203	66.7%	77	0	yes	KR080195	Pope <i>et al.</i> 2015
ThulaThula	P5	50,415	66.5%	80	0	no	MN234172	Wada <i>et al.</i> 2017
Purky	P6	50,513	66.4%	84	0	yes	MN096355.1	Pope <i>et al.</i> 2015

* integration-dependent immunity system, comprised of an immunity repressor flanked by an integrase, an excise gene, and an anti-repressor

Table S2. Bacteriophages included in the comparative analyses for which integration-dependent immunity systems had previously been identified (green: experimentally validated; blue: computationally predicted).

Phage Name	Subcluster	Length (bp)	GC-content	# ORFs	# tRNAs	Accession #	Reference
BPs	G1	41,901	66.6%	63	0	EU568876	Sampson <i>et al.</i> 2009
Cedarsite	G1	41,901	66.6%	63	0	KT355472	Hatfull <i>et al.</i> 2016
Halo	G1	42,289	66.7%	64	0	NC_008202.2	Sampson <i>et al.</i> 2009
Island3	I1	47,287	66.8%	76	0	HM152765.1	Pope <i>et al.</i> 2011
Babsiella	I1	48,420	67.1%	78	0	NC_023697.1	Hatfull <i>et al.</i> 2012
Brujita	I1	47,057	66.8%	74	0	NC_011291.1	Hatfull <i>et al.</i> 2010
Charcharodon	N	43,680	66.2%	71	0	KM588359	Hatfull <i>et al.</i> 2016
Charlie	N	43,036	66.3%	69	0	NC_023729.1	Hatfull <i>et al.</i> 2012
MichelleMyBell	N	42,240	66.0%	70	0	KF986246	Hatfull <i>et al.</i> 2016
Panchino	N	43,516	65.9%	66	0	KU935727	Hatfull <i>et al.</i> 2016
Phrann	N	44,872	66.3%	67	0	KU935731	Hatfull <i>et al.</i> 2016
Pipsqueaks	N	43,679	66.3%	73	0	KU935730	Hatfull <i>et al.</i> 2016
Redi	N	42,594	66.1%	70	0	NC_023730.1	Hatfull <i>et al.</i> 2012
SkinnyPete	N	43,478	66.4%	67	0	KU935729	Hatfull <i>et al.</i> 2016
Xeno	N	42,395	66.8%	69	0	KU935728	Hatfull <i>et al.</i> 2016
Xerxes	N	43,698	66.3%	72	0	KU935726	Hatfull <i>et al.</i> 2016

Table S3. *Mycobacteria* included in the comparative analyses.

<i>Mycobacterium</i>	# Genes	Length (kb)	GC-content	Accession #	Reference
<i>M. abscessus</i>	4,957	4,618	64.2%	CP004374	Kim <i>et al.</i> 2013
<i>M. africanum</i>	4,069	4,493	65.1%	CP014617	Hurtado <i>et al.</i> 2016
<i>M. avium</i>	3,935	3,981	69.3%	AE016958	Li <i>et al.</i> 2005
<i>M. bovis</i>	3,952	3,972	65.6%	AM408590	Brosch <i>et al.</i> 2007
<i>M. canetti</i>	4,139	4,482	65.6%	HE572590	Bentley <i>et al.</i> 2012
<i>M. chelonae</i>	4,943	5,061	64.0%	CP050145	Gu <i>et al.</i> 2020
<i>M. fortuitum</i>	6,023	6,255	66.2%	CP011269	Costa <i>et al.</i> 2015
<i>M. gilvum</i>	5,139	5,077	67.9%	CP002385	Kallimanis <i>et al.</i> 2011
<i>M. intracellulare</i>	5,143	4,936	68.1%	CP003322	Kim <i>et al.</i> 2012
<i>M. leprae</i>	1,604	1,620	57.8%	AL450380	Cole <i>et al.</i> 2001
<i>M. marinum</i>	5,422	5,973	65.2%	CP000854	Stinear <i>et al.</i> 2008
<i>M. smegmatis</i>	6,692	6,508	67.4%	CP001663	Deshayes <i>et al.</i> 2007
<i>M. tuberculosis</i>	3,935	3,981	65.6%	AL123456	Cole <i>et al.</i> 1998
<i>M. ulcerans</i>	4,159	4,074	65.4%	CP000325	Stinear <i>et al.</i> 2007

Table S4. Mycobacteriophage integration systems and putative integration sites of *Mycobacterium* cluster P bacteriophages in *M. chelonae* Myco3a (*attB* location: tRNA^{Thr} ; 447,412–447,737 bp), *M. leprae* TN (*attB* location: tRNA^{Thr} ; 271,936–271,975 bp), and *M. smegmatis* mc² (*attB* location: tRNA^{Thr} ; 6,222,599–6,222,637 bp).

Phage	BLASTn percent identity		
	<i>M. chelonae</i>	<i>M. leprae</i>	<i>M. smegmatis</i>
Arib1	38/40 (95%)	40/40 (100%)	39/39 (100%)
Atcoo	38/40 (95%)	40/40 (100%)	41/42 (98%)
Bartholomew	38/40 (95%)	40/40 (100%)	39/39 (100%)
Bogie	38/40 (95%)	40/40 (100%)	39/39 (100%)
Brusacoram	38/40 (95%)	40/40 (100%)	41/42 (98%)
Bunnies	38/40 (95%)	40/40 (100%)	41/42 (98%)
CactusJack	38/40 (95%)	40/40 (100%)	41/42 (98%)
Camster	38/40 (95%)	40/40 (100%)	41/42 (98%)
Donovan	38/40 (95%)	40/40 (100%)	39/39 (100%)
FirstPlacePfu	38/40 (95%)	40/40 (100%)	39/39 (100%)
Fishburne	38/40 (95%)	40/40 (100%)	39/39 (100%)
Glasko	38/40 (95%)	40/40 (100%)	41/42 (98%)
GreaseLightnin	38/40 (95%)	40/40 (100%)	41/42 (98%)
HUHilltop	38/40 (95%)	40/40 (100%)	39/39 (100%)
Jebeks	38/40 (95%)	40/40 (100%)	39/39 (100%)
Jung	38/40 (95%)	40/40 (100%)	41/42 (98%)
KilKor	38/40 (95%)	40/40 (100%)	41/42 (98%)
Ksquared	38/40 (95%)	40/40 (100%)	41/42 (98%)
Majeke	38/40 (95%)	40/40 (100%)	39/39 (100%)
Malithi	38/40 (95%)	40/40 (100%)	41/42 (98%)
Mangethe	38/40 (95%)	40/40 (100%)	39/39 (100%)
Megiddo	38/40 (95%)	40/40 (100%)	41/42 (98%)
Necropolis	38/40 (95%)	40/40 (100%)	39/39 (100%)
Phalm	38/40 (95%)	40/40 (100%)	41/42 (98%)
Phegasus	38/40 (95%)	40/40 (100%)	39/39 (100%)
Phineas	38/40 (95%)	40/40 (100%)	39/39 (100%)
Shipwreck	38/40 (95%)	40/40 (100%)	39/39 (100%)
StevieRay	38/40 (95%)	40/40 (100%)	41/42 (98%)
StressBall	38/40 (95%)	40/40 (100%)	41/42 (98%)
Techage	38/40 (95%)	40/40 (100%)	39/39 (100%)
Thespis	38/40 (95%)	40/40 (100%)	41/42 (98%)
Willsammy	38/40 (95%)	40/40 (100%)	41/42 (98%)
Zilizebeth	38/40 (95%)	40/40 (100%)	39/39 (100%)
BigNuz	38/40 (95%)	40/40 (100%)	39/39 (100%)
Nazo	38/40 (95%)	40/40 (100%)	39/39 (100%)
Phayonce	42/45 (93%)	44/45 (98%)	43/44 (98%)
Purky	39/41 (95%)	41/41 (100%)	42/43 (98%)

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