

Supplementary Table 1. Primers used to complete the genome sequences reported in this study.

Primers used to complete phage genome sequences			
Primer name	Primer direction	sequence (5' -> 3')	
C2P21/24	FWD	CTAGGACAACCTGTGCGTCGCC	
C2P21/24	REV	CCAGGAATTAAGCAGTTTGCACG	
AB-Navy1	FWD	GCATGTGGAGCTAATACTGAGGA	
AB-Navy1	REV	GTAGAGCACTACGATGGTGACA	
AB-Navy4	FWD	GCCGGATAATTTTAAACCTGCA	
AB-Navy4	REV	GCACCAGTAACAGTTGCAGTAA	
AB-Navy71	FWD	TTTGATTCGAAAATCAAATCGATCAAAG	
AB-Navy71	REV	CCTTAATTGCTGCATTAGCTG	
AB-Navy97	FWD	GAAGGCCATATTTTCTAGTGCC	
AB-Navy97	REV	CCTGATAGTTCTGCGCTTAATG	
AB-TP3Φ1	FWD	AGAGCGAATGCATAGAAAGAC	
AB-TP3Φ1	REV	GAACATCACTCAGAGAGTGT	

Primers used to complete bacterial genome sequences			
TP1			
Primer name	Primer direction	sequence (5' -> 3')	location on TP1 genome
JDC F1 TP1 C1-2	FWD	TTGGGAACCGCTTTCACCAT	1377633
JDC F1 TP1 C5-1	REV	GGCTGCACAGTGGTTTTCTG	1379144
TP1_gap3_FWD	FWD	TGGTCCACATACAGTGGCTG	837881
TP1_gap3_REV	REV	GCGAGATCTGTGAAAAGTCGC	843014
TP1_gap5_FWD	FWD	TTGGGCTGTGATTCGTTTCGT	1381828
TP1_gap5_REV	REV	CCGTGGTTCTGGGTTTTTGC	1382823

TP2			
Primer name	Primer direction	sequence (5' -> 3')	location on TP1 genome
TP2_end_FWD2	FWD	TTCTGGCTTCCCGCAATGAG	2492088
TP2_end_REV2	REV	GCACAAGGTAAGCGTAGAGC	2492860
TP2_FWD	FWD	ATATGCACCGCCAGACAAGG	2543120
TP2_REV	REV	AAGCGGCTGAGCAAGGAAAT	2492807

TP3			
Primer name	Primer direction	sequence (5' -> 3')	location on TP1 genome
TP3_end_FWD2	FWD	ACCAAGCCAACCTCCCACGAA	1965094
TP3_end_REV2	REV	GGCAGCGGAAGAGCCAATTC	2024403
TP3_ends_FWD1	FWD	CACAATTAGGGGGCGTAAAAATCA	2023907
TP3_ends_REV1	REV	CATGCTCGGCCAGAAATTCG	1965873
TP3_gap1_FWD1	FWD	AGACTGAGGCTGAGGAGGAG	547097
TP3_gap1_REV1	REV	TCCAAAGCCCCTTCTGCATT	558195
TP3_gap1_REV2	REV	ATAAGCTCCTCCTGCCGTTG	547700

Supplementary Table 2. Antibiotic susceptibility of some strains collected from the patient during phage treatment.

Bacterial strains			Antibiotic sensitivity														
CPT Strain name	Date of sample collection	Source	Amikacin	Ampicillin/Sulbactam	Cefepime	Ceftazidime	Ceftriaxone	Ciprofloxacin	Colistin	Gentamicin	Meropenem	Tetracycline	Tigecycline	Tobramycin	Doripenem	Minocycline	Trimethoprim/Sulfamethoxazole
TP1	2/10/2016		R	ND	R	R	R	R	ND	R	R	R	ND	R	ND	ND	S
AB-SD2	3/14/2016																
Start of phage therapy: March 15th																	
AB-SD4	3/17/2016	Abscess- Drain 3	R	ND	R	R	R	R	ND	R	R	R	ND	R	ND	ND	R
AB-2392	3/17/2016		R	ND	R	R	R	R	ND	R	R	R	ND	R	ND	ND	S
AB-2399	3/17/2016	Drain 3															
AB-SD1	3/19/2016	Drain 5															
AB-SD3	3/19/2016	Drain 3															
AB-2755	3/19/2016	Drain 1	R	ND	R	R	R	R	4ug/ml	R	R	R	I	R	R	ND	R
TP2	3/21/2016	Drainage 1	I	S	ND	R	I	S	ND	R	S	R	ND	I	ND	ND	S
AB-SD5	3/21/2016	Bronchial wash															
TP3	3/23/2016	Drain 1	R	ND	R	R	R	R	ND	R	R	R	ND	R	ND	ND	R
AB-0280	3/31/2016		R	R	R	R	R	R	ND	R	R	R	ND	R	ND	ND	S
AB-1485	5/9/2016	Drain 3	R	R	R	R	R	R	2ug/ml	R	R	R	6ug/ml	R	ND	R	S
AB-3804	5/9/2016	Drain 1	R	R	R	R	R	R	4ug/ml	R	R	R	8ug/ml	R	ND	R	S
AB-3819	5/9/2016	Drain 3 (2nd sample)	R	R	R	R	R	R	2ug/ml	R	R	R	6ug/ml	R	ND	R	S
AB-3847	5/9/2016	Drain 5	R	R	R	R	R	R	4ug/ml	R	R	R	8ug/ml	R	ND	R	S
AB-0214	5/16/2016	Drain 5	R	R	R	R	R	R	ND	R	R	R	ND	R	ND	ND	S
AB-0779	5/16/2016	Drain 1	R	R	R	R	R	R	ND	R	R	R	ND	R	ND	ND	S
AB-0780	5/16/2016		R	R	R	R	R	R	ND	R	R	R	ND	R	ND	ND	S

Note: (1) Antibiotic resistance profiles were determined at the UCSD clinical laboratory. (2) Strains are determined to be either sensitive (S), resistant (R) or have an intermediate (I) phenotype. Sensitivity to some antibiotics was not determined (ND). Isolates with blank rows were not tested for AMR.

Supplementary Table 3. Locations of K locus and prophages in *A. baumannii* strains TP1, TP2, TP3.

K Locus

	start position	end position	length (bp)	genes	Best match locus	Coverage	Identity
TP1	3774031	3794556	20526	17	KL116	100%	97.4%
TP2	3780056	3800575	20520	17	KL116	100%	97.4%
TP3	3781228	3801747	20520	17	KL116	100%	97.4%

Prophages in strain TP1 (NZ_CP056784.2)*

	start position	end position	length (bp)	att sequence
Prophage 1	2671137	2723699	52563	tgaacttaggggtcaagggtacgacatgcagcggcatctcggagcattatttttaa
Prophage 2	2895491	2938252	42762	gtatttggggagatggcgggagttgaac

*same prophages are identified in TP2 and TP3

Supplementary Table 4. Genomic changes in *A. baumannii* TP2 compared to TP1.

Genome ref	Mutation type	Position in TP1	Length	Position in TP2	Mutation	TP2 Genes affected	Notes
TP1	insertion	111357	6673	111361	large IS element insertion	APH(3')-VI family aminoglycoside-O-phosphotransferase, IS30-like element ISAbal25 family transposase, subclass B1 metallo-beta-lactamase, bleomycin binding protein Ble-MBL, phosphoribosylanthranilate isomerase, protein-disulfide reductase DsbD N-terminal domain-containing protein, divalent-cation tolerance protein CutA, IS3-like element ISAbal4 family transposase, all inserted.	8 new genes
TP1	SNP	768428	1	775105	cA, Ala to Glu	two-component system sensor histidine kinase PmrB	
TP1	SNP	848350	1	854712	aT	intergenic	
TP1	deletion	1356493	1090	1362854	IS element lost	IS30 family transposase is lost in TP2	
TP1	insertion	1381905	1845	1387177	IS element insertion	IS6-like element IS26 family transposase, aminoglycoside O-phosphotransferase APH(3')-Ia"	2 new genes
TP1	deletion	1679979	1189	1687155	IS element lost	IS4 family transposase ISAbal1 is lost in TP2	
TP1	insertion	2520267	1091	2526319	IS element insertion	inserted a IS30 family transposase in TP2	
TP1	SNP	2840989	1	2848094	cC, Ile to Thr	hypothetical protein	
TP1	deletion	3143593	1094	3150708	IS element lost	IS30 family transposase is lost in TP2	
TP1	deletion	3786215	6	3792200	2 AA deleted in frame	glycosyltransferase	Same mutation found in in vitro mutants

Supplementary Table 5. Genomic changes in *A. baumannii* TP3 compared to TP1.

Genome_ref	Mutation type	Position in TP1	Length	Position in TP3	Mutation	TP3 Genes affected	Notes
TP1	insertion	111357	6673	111359	large IS element insertion	ARG cassette: APH(3')-VI family aminoglycoside O-phosphotransferase, IS30-like element ISAb125 family transposase, subclass B1 metallo-beta-lactamase, bleomycin binding protein Ble-MBL, phosphoribosylanthranilate isomerase, protein-disulfide reductase DsbD N-terminal domain-containing protein, divalent-cation tolerance protein CutA, IS3-like element	8 new genes.
TP1	deletion	1356492	1090	1362845	IS element lost	IS30 family transposase is lost in TP3	
TP1	insertion	1381905	1886	1387168	IS element insertion	IS6-like element IS26 family transposase and aminoglycoside O-phosphotransferase APH(3')-Ia	2 new genes
TP1	SNP	2840989	1	2848220	cC, Ile to Thr	hypothetical protein	
TP1	insertion	2880890	1090	2888121	IS element insertion	IS30-like element ISAb125 family transposase	
TP1	deletion	3143593	1090	3151919	IS element lost	IS30 family transposase is lost in TP3	
TP1	deletion	3786204	6	3793401	2 AA deleted in frame	glycosyltransferase	Same mutation found in in vitro mutants


```

AB-Navy4      1 MALDPPNRIKFLRSTAGAKPTTAAIQPGEIAINLADRTLYSTDGNAIDIQFGLGQSVNPIINATQIISTNDFLYSKYQFSUNSETADGRISLYGNYTASNLPSYGLAMAATSKYGTGAVGSSHATYLTINSGTNRWIFNYNGTTNVAISISGTIATFARVDPALNQNANTATKLOSARNINQVL 102
AB-Navy1      1 MALDPPNRIKFLRSTAGAKPTTAAIQPGEIAINLADRTLYSTDGNAIDIQFGLGQSVNPIINATQIISTNDFLYSKYQFSUNSETADGRISLYGNYTASNLPSYGLAMAATSKYGTGAVGSSHATYLTINSGTNRWIFNYNGTTNVAISISGTIATFARVDPALNQNANTATKLOSARNINQVL 102
AB-Navy97     1 MALDPPNRIKFLRSTAGAKPTTAAIQPGEIAINLADRTLYSTDGNAIDIQFGLGQSVNPIINATQIISTNDFLYSKYQFSUNSETADGRISLYGNYTASNLPSYGLAMAATSKYGTGAVGSSHATYLTINSGTNRWIFNYNGTTNVAISISGTIATFARVDPALNQNANTATKLOSARNINQVL 102
Maestro      1 MALDPPNRIKFLRSTAGAKPTTAAIQPGEIAINLADRTLYSTDGNAIDIQFGLGQSVNPIINATQIISTNDFLYSKYQFSUNSETADGRISLYGNYTASNLPSYGLAMAATSKYGTGAVGSSHATYLTINSGTNRWIFNYNGTTNVAISISGTIATFARVDPALNQNANTATKLOSARNINQVL 101
AC4          1 MALDPPNRIKFLRSTAGAKPTTAAIQPGEIAINLADRTLYSTDGNAIDIQFGLGQSVNPIINATQIISTNDFLYSKYQFSUNSETADGRISLYGNYTASNLPSYGLAMAATSKYGTGAVGSSHATYLTINSGTNRWIFNYNGTTNVAISISGTIATFARVDPALNQNANTATKLOSARNINQVL 101
AB-Navy71    1 MALDPPNRIKFLRSTAGAKPTTAAIQPGEIAINLADRTLYSTDGNAIDIQFGLGQSVNPIINATQIISTNDFLYSKYQFSUNSETADGRISLYGNYTASNLPSYGLAMAATSKYGTGAVGSSHATYLTINSGTNRWIFNYNGTTNVAISISGTIATFARVDPALNQNANTATKLOSARNINQVL 101

AB-Navy4      103 FDGTDSDINTPAIDVVVSFNRTVKP.....SDVRNKAMGVYFSSKAGLNGAANDNYGDFLSLSTYDGGTGGKNGLYFKNLSREILHYQD.....LNSNSWGTPTKIAYDSSITGMAAS..ATRLQARTINGTAFDQ...TANIINV..NATYSEFIPDGANLNDYKTPGLYDPTDAGAATQLNL 363
AB-Navy1      103 FDGTDSDINTPAIDVVVSFNRTVKP.....SDVRNKAMGVYFSSKAGLNGAANDNYGDFLSLSTYDGGTGGKNGLYFKNLSREILHYQD.....LNSNSWGTPTKIAYDSSITGMAAS..ATRLQARTINGTAFDQ...TANIINV..NATYSEFIPDGANLNDYKTPGLYDPTDAGAATQLNL 363
AB-Navy97     103 FDGTDSDINTPAIDVVVSFNRTVKP.....SDVRNKAMGVYFSSKAGLNGAANDNYGDFLSLSTYDGGTGGKNGLYFKNLSREILHYQD.....LNSNSWGTPTKIAYDSSITGMAAS..ATRLQARTINGTAFDQ...TANIINV..NATYSEFIPDGANLNDYKTPGLYDPTDAGAATQLNL 363
Maestro      102 FDGTRDITIEDSTKLYENLVLTASDSSRVIKRVATTIRAMGIT.....VNGALII.....HLPKAAR.....NASTMMKIIIGDFDYSPROATSSNWSVDISQYNTTAAWISYQAIISQSPAPFDIWRWSGADHCVIILGEEA.....GASPSWSYNIISIEKIYLT..SNNTALYDNDP..... 261
AC4          102 FDGTRDITIEDSTKLYENLVLTASDSSRVIKRVATTIRAMGIT.....VNGALII.....HLPKAAR.....NASTMMKIIIGDFDYSPROATSSNWSVDISQYNTTAAWISYQAIISQSPAPFDIWRWSGADHCVIILGEEA.....GASPSWSYNIISIEKIYLT..SNNTALYDNDP..... 261
AB-Navy71    102 FDGTRDITIEDSTKLYENLVLTASDSSRVIKRVATTIRAMGIT.....VNGALII.....HLPKAAR.....NASTMMKIIIGDFDYSPROATSSNWSVDISQYNTTAAWISYQAIISQSPAPFDIWRWSGADHCVIILGEEA.....GASPSWSYNIISIEKIYLT..SNNTALYDNDP..... 265

AB-Navy4      394 PFSNAYSLFVERHAGIKOTIQYATNKTFIRKFYNGYDNRQLAFLDPSDKFTENITLEKASS..AIIKVKSTTGSSELISLNGKNTASVLTLDGSGFIICDSTRSSFAFTFDPGVQVILNSKLLINTPASLVNLTGGTFEAVTGGESSPIRFKII..NRGGAITINSPTVGVSSIPHAIISFNWYNTIEWI 552
AB-Navy1      394 PFSNAYSLFVERHAGIKOTIQYATNKTFIRKFYNGYDNRQLAFLDPSDKFTENITLEKASS..AIIKVKSTTGSSELISLNGKNTASVLTLDGSGFIICDSTRSSFAFTFDPGVQVILNSKLLINTPASLVNLTGGTFEAVTGGESSPIRFKII..NRGGAITINSPTVGVSSIPHAIISFNWYNTIEWI 552
AB-Navy97     394 PFSNAYSLFVERHAGIKOTIQYATNKTFIRKFYNGYDNRQLAFLDPSDKFTENITLEKASS..AIIKVKSTTGSSELISLNGKNTASVLTLDGSGFIICDSTRSSFAFTFDPGVQVILNSKLLINTPASLVNLTGGTFEAVTGGESSPIRFKII..NRGGAITINSPTVGVSSIPHAIISFNWYNTIEWI 552
Maestro      296 .....IYL.....TIEDSLPNTLQVLT.....PL.....EGV.....NLAKSLRKRFTFTFDATGSLAFDGTANVSTALTINSATTGQ..... 331
AC4          296 .....IYL.....TIEDSLPNTLQVLT.....PL.....EGV.....NLAKSLRKRFTFTFDATGSLAFDGTANVSTALTINSATTGQ..... 327
AB-Navy71    296 .....IYL.....TIEDSLPNTLQVLT.....PL.....EGV.....NLAKSLRKRFTFTFDATGSLAFDGTANVSTALTINSATTGQ..... 327

AB-Navy4      653 GNVRDGSSTGVGFIITGNNTLVWRHGNMTMNY..GNISNTGQ.....ISTGDDISSNGLSTAGSISGDSLIRTRGRIAPTSTYHYLDIGRGGDITTVGGYGGAFRVVDSNGATSFYVDPVDAKFSGKIITTKPVTFYWNVTDLGNSTAAITVPDAIAPMCKTGYAPFIIHGSVQTD 735
AB-Navy1      653 GNVRDGSSTGVGFIITGNNTLVWRHGNMTMNY..GNISNTGQ.....ISTGDDISSNGLSTAGSISGDSLIRTRGRIAPTSTYHYLDIGRGGDITTVGGYGGAFRVVDSNGATSFYVDPVDAKFSGKIITTKPVTFYWNVTDLGNSTAAITVPDAIAPMCKTGYAPFIIHGSVQTD 744
AB-Navy97     653 GNVRDGSSTGVGFIITGNNTLVWRHGNMTMNY..GNISNTGQ.....ISTGDDISSNGLSTAGSISGDSLIRTRGRIAPTSTYHYLDIGRGGDITTVGGYGGAFRVVDSNGATSFYVDPVDAKFSGKIITTKPVTFYWNVTDLGNSTAAITVPDAIAPMCKTGYAPFIIHGSVQTD 743
Maestro      332 .....A.....GLVKLNTLTSVTEALTAAGKALDQTKVNRSGDIIISGR.....LVVTGQII.....TTPSISNDVTP..ISFLGSPVNN..SNAAGIRVRNLEVINNYQVATRAFGIIS.....KE.....DIIAAGSASLASDIOGNINIPFKVUNTWLVTTFVDFLGGHVS 479
AC4          332 .....A.....GLVKLNTLTSVTEALTAAGKALDQTKVNRSGDIIISGR.....LVVTGQII.....TTPSISNDVTP..ISFLGSPVNN..SNAAGIRVRNLEVINNYQVATRAFGIIS.....KE.....DIIAAGSASLASDIOGNINIPFKVUNTWLVTTFVDFLGGHVS 479
AB-Navy71    332 .....A.....GLVKLNTLTSVTEALTAAGKALDQTKVNRSGDIIISGR.....LVVTGQII.....TTPSISNDVTP..ISFLGSPVNN..SNAAGIRVRNLEVINNYQVATRAFGIIS.....KE.....DIIAAGSASLASDIOGNINIPFKVUNTWLVTTFVDFLGGHVS 479

AB-Navy4      726 EGVITNHSIGARNSNTSSGAYIAIGNDNYTTEDFRMTGGYIGTSOGLTLGLTLNAR.....LAED.....PANADNITY..TEEF.....YDCTNAVAKITNG..PFTGGAFELVRTAGVKTFTIYSPS..... 808
AB-Navy1      745 EGYRTNVSIGAWRSNTSSGAYIAIGNDNYTTEDFRMTGGYIGTSOGLTLGLTLNAR.....LAED.....PANADNITY..TEEF.....YDCTNAVAKITNG..PFTGGAFELVRTAGVKTFTIYSPS..... 828
AB-Navy97     744 EGYRTNVSIGAWRSNTSSGAYIAIGNDNYTTEDFRMTGGYIGTSOGLTLGLTLNAR.....LAED.....PANADNITY..TEEF.....YDCTNAVAKITNG..PFTGGAFELVRTAGVKTFTIYSPS..... 828
Maestro      480 ELOYMNVISIGVYRPPRNDNSOMYSI..GANDNYSTEAFLEKDRTEINTNRI..LKNADSKATKOTPRITNGVAFDQTSNRIIG.....DLAED.....PANADNITY..TEEF.....YDCTNAVAKITNG..PFTGGAFELVRTAGVKTFTIYSPS..... 608
AC4          476 SSGVYRTTISIGVYRPPRNDNSOMYSI..GANDNYSTEAFLEKDRTEINTNRI..LKNADSKATKOTPRITNGVAFDQTSNRIIG.....DLAED.....PANADNITY..TEEF.....YDCTNAVAKITNG..PFTGGAFELVRTAGVKTFTIYSPS..... 608
AB-Navy71    480 SSGVYRTTISIGVYRPPRNDNSOMYSI..GANDNYSTEAFLEKDRTEINTNRI..LKNADSKATKOTPRITNGVAFDQTSNRIIG.....DLAED.....PANADNITY..TEEF.....YDCTNAVAKITNG..PFTGGAFELVRTAGVKTFTIYSPS..... 608

AB-Navy4      780 .....TINS.....TTFNVQ 798
AB-Navy1      808 .....TINS.....TTFNVQ 817
AB-Navy97     807 .....TINS.....TTFNVQ 816
Maestro      629 ..SRTWIRNIIYGGTDAWRE.....VAV.....TD.....AFTTGAAGRTGAL.....TVNG.....INTNTLNSNDLRSOSYLGNOQTELOIGTASQVYIDFHSGSNIIDYDARIMSSGGTIAINGALSIIAASHAFNRVDDGLIS.....ASTGLG 700
AC4          666 YQTSWVKDFQYTAOAKPDGAVDYYVNTLDLSDPEVFGAIFTKNSVATPAKNTFEYTKLSMIPPHTGQ..GTWLHRLNDTSTAIEYIIKYGPTPVLRMDSQVTVYATLRNSGATLGNQMLGNQVATPVYIDFHSGSNIIDYDARIMSSGGTIAINGALSIIAASHAFNRVDDGLIS.....ASTGLG 851
AB-Navy71    667 YQTSWVKDFQYTAOAKPDGAVDYYVNTLDLSDPEVFGAIFTKNSVATPAKNTFEYTKLSMIPPHTGQ..GTWLHRLNDTSTAIEYIIKYGPTPVLRMDSQVTVYATLRNSGATLGNQMLGNQVATPVYIDFHSGSNIIDYDARIMSSGGTIAINGALSIIAASHAFNRVDDGLIS.....ASTGLG 852

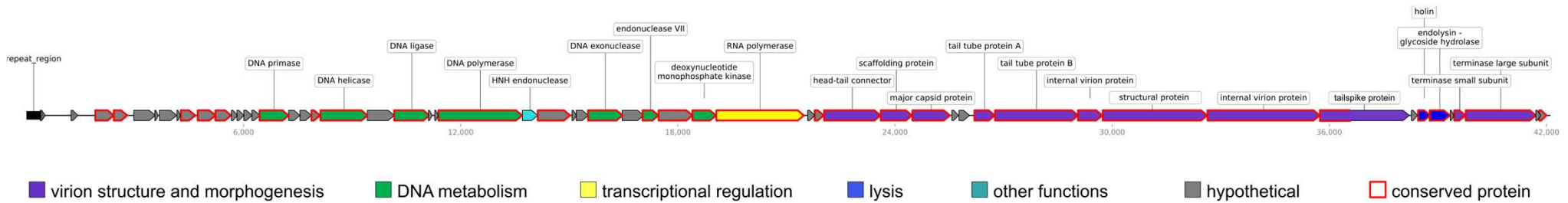
AB-Navy4      799 TINSITVHVASNLCFSTF..FELNG..IYNGND.....GATLANALDIAHYBLGIDKLNLR.....NIVNSRTEIGTRGV..IRIGNTS..AETLLINDSHQI..L..TSGRAK.....DIAAGVLA.....SDAYA 816
AB-Navy1      816 TIVNTINIAQGSIVMSAAPGSGRS..MYTNGD.....GASFSTCIDIGSHWBLGFKNLGNR.....NIPDTRAGNASFGS..IRIGASFA..DETOLLPTNSQLQI..L..TSGGAR.....NISTGQVLA.....SDAYA 936
AB-Navy97     817 TIVNTINIAQGSIVMSAAPGSGRS..MYTNGD.....GASFSTCIDIGSHWBLGFKNLGNR.....NIPDTRAGNASFGS..IRIGASFA..DETOLLPTNSQLQI..L..TSGGAR.....NISTGQVLA.....SDAYA 936
Maestro      787 IANTSITVLAQSLV..GASQSKNYITF..ASTGNAGTGHQDDLNASWAVVLTGATAGAEKRGWIFORSNDNTNVAISITHEVLSNTHIQTLNDNTMINVGNKDLAKVRSKAFIDVAMPTFVSQSKNANWDDPTHTFTLFTFUSAGVNAVGETEETESGENTHISLISLGNKASATLLO 958
AC4          852 ISNTSITVLAQSLV..GASQSKNYITF..ASTGNAGTGHQDDLNASWAVVLTGATAGAEKRGWIFORSNDNTNVAISITHEVLSNTHIQTLNDNTMINVGNKDLAKVRSKAFIDVAMPTFVSQSKNANWDDPTHTFTLFTFUSAGVNAVGETEETESGENTHISLISLGNKASATLLO 1039
AB-Navy71    853 ISNTSITVLAQSLV..GASQSKNYITF..ASTGNAGTGHQDDLNASWAVVLTGATAGAEKRGWIFORSNDNTNVAISITHEVLSNTHIQTLNDNTMINVGNKDLAKVRSKAFIDVAMPTFVSQSKNANWDDPTHTFTLFTFUSAGVNAVGETEETESGENTHISLISLGNKASATLLO 1044

AB-Navy4      916 BWNVVPVNGIWSKDIKT.....S..T.....WYASKFIDRTG..SDGMDGNANTATRLQARTFOITGGIITNAVVSFDGQNVLTASNVDGSKVSVVPEAV.....KAQTLAVTPQKNAKLVASWKGITLQSMPTPLTIVDANTLVRRLADDPNSRNLVLRNVKI 1009
AB-Navy1      937 DASKVPVNGIYKSDIIC.....SS.....YVACRYVIGITGPNITGFDGNANTATRLQARTFOITGGIITNAVVSFDGQNVLTASNVDGSKVSVVPEAV.....KAQTLAVTPQKNAKLVASWKGITLQSMPTPLTIVDANTLVRRLADDPNSRNLVLRNVKI 1002
AB-Navy97     936 DASKVPVNGIYKSDIIC.....S.....YVACRYVIGITGPNITGFDGNANTATRLQARTFOITGGIITNAVVSFDGQNVLTASNVDGSKVSVVPEAV.....KAQTLAVTPQKNAKLVASWKGITLQSMPTPLTIVDANTLVRRLADDPNSRNLVLRNVKI 1009
Maestro      105 TARAIGITSGASGVS.....FDGSONNIPLSVATGATANTNTIATTFVQ.....NVMVETASAYAVRLKTPRSFOITGGIITNAVVSFDGQNVLTASNVDGSKVSVVPEAV.....KAQTLAVTPQKNAKLVASWKGITLQSMPTPLTIVDANTLVRRLADDPNSRNLVLRNVKI 1187
AC4          1040 FSVIHAQVGSSEVERLQANYTEENTIASALHWNSSO.....YQVQITLKL..LAI..I..ADNVASATKLTARTFOITGGIITNAVVSFDGQNVLTASNVDGSKVSVVPEAV.....KAQTLAVTPQKNAKLVASWKGITLQSMPTPLTIVDANTLVRRLADDPNSRNLVLRNVKI 1215
AB-Navy71    1046 TARAIGITSGASGVS.....FDGSONNIPLSVATGATANTNTIATTFVQ.....NVMVETASAYAVRLKTPRSFOITGGIITNAVVSFDGQNVLTASNVDGSKVSVVPEAV.....KAQTLAVTPQKNAKLVASWKGITLQSMPTPLTIVDANTLVRRLADDPNSRNLVLRNVKI 1224

AB-Navy4      1070 GTVYHLAFSDTMLPILIN.....GTVTRVETG..LTTWEVDLNSPHHGLVGTGNGVNUMAITYSAYGYFEGSISDIIIGTGPQDSOWAYVLKLSNPTDATTNLSGSSQSDVNM..ADKNIWYLNPAQPVITAGAMI..SPDRLNFFAADTDAI..RMRNSNMVTAQIWDIV 1227
AB-Navy1      1093 GTVYHLAFSDTMLPILIN.....GTVTRVETG..LTTWEVDLNSPHHGLVGTGNGVNUMAITYSAYGYFEGSISDIIIGTGPQDSOWAYVLKLSNPTDATTNLSGSSQSDVNM..WDKDIWYLNPAQPVITAGAMI..SPDRLNFFAADTDAI..RMRNSNMVTAQIWDIV 1250
AB-Navy97     1090 GTVYHLAFSDTMLPILIN.....GTVTRVETG..LTTWEVDLNSPHHGLVGTGNGVNUMAITYSAYGYFEGSISDIIIGTGPQDSOWAYVLKLSNPTDATTNLSGSSQSDVNM..WDKDIWYLNPAQPVITAGAMI..SPDRLNFFAADTDAI..RMRNSNMVTAQIWDIV 1247
Maestro      1136 SIVHFTFTGTCQ.....IISITISITAD..NSFLKQRLSPPAHMGSGGGLKLLAIITYSAYGYFEGTASTLNT..NONGSENSMLRLTEVNDPTNLSGSSQNS..RTFTNTQIMFLDHSQPVVLTGMSANRNFHTSDSDSAGAMPSSMWTIWDIV 1204
AC4          1216 SLLHGVFAGSTGWSNLSGRI..IDVITNRVSGVDAIVEIPIHSIPGNVTSF..IWLAVTYSNNSF..IGNIAAYAKDLGADSAWSLLRTSTAINNPSVSIISGDVATDRDLQGLWLSGKNI..IASSETMINSCTNFI..VSDNNNDVANSNGYISIDIVDVM 1380
AB-Navy71    1225 GNCLHVFAAGSTGWSNLSGRI..IDVITNRVSGVDAIVEIPIHSIPGNVTSF..IWLAVTYSNNSF..IGNIAAYAKDLGADSAWSLLRTSTAINNPSVSIISGDVATDRDLQGLWLSGKNI..IASSETMINSCTNFI..VSDNNNDVANSNGYISIDIVDVM 1388

```

Supplemental Figure 2. Multiple sequence alignment of the long tail fiber protein sequences of the myophages used in this study. The black box denotes the regions with homology to T4 gp37.



Supplementary Figure 3. Genome map of AbTP3Phi1. Predicted genes are represented by blocks, with blocks pointing to the right genes encoded on the forward strand, and blocks pointing to the left are on the reverse strand. The ruler below the genomes indicates scale in bp. Genes are color coded based on functions according to the legend; genes outlined in red are conserved in a set of 16 species representatives of the genus *Friunavirus*.