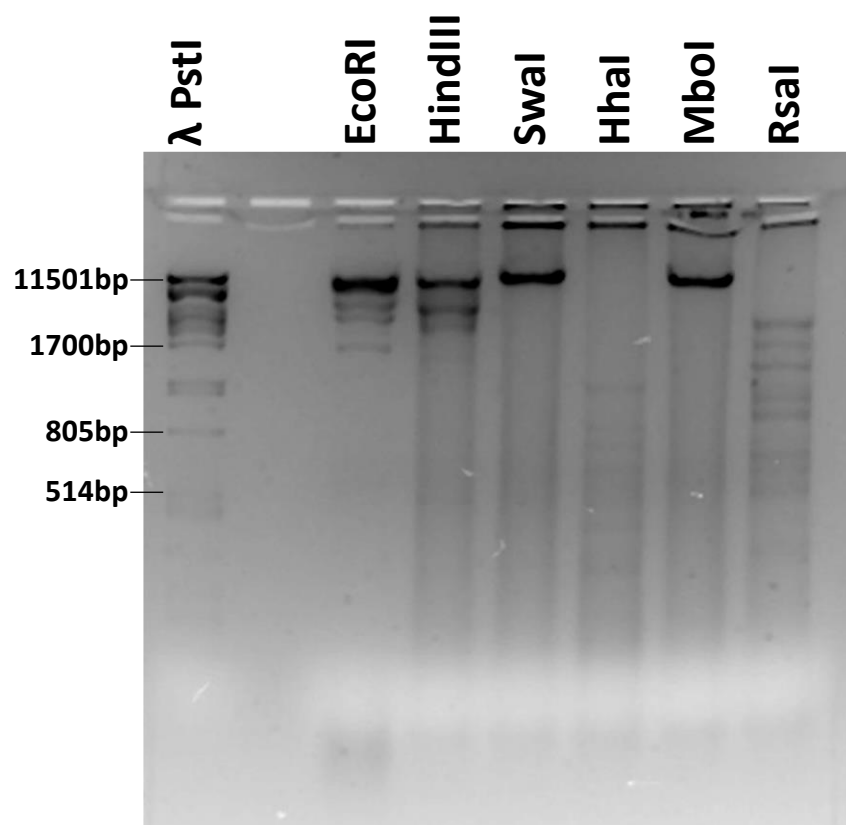
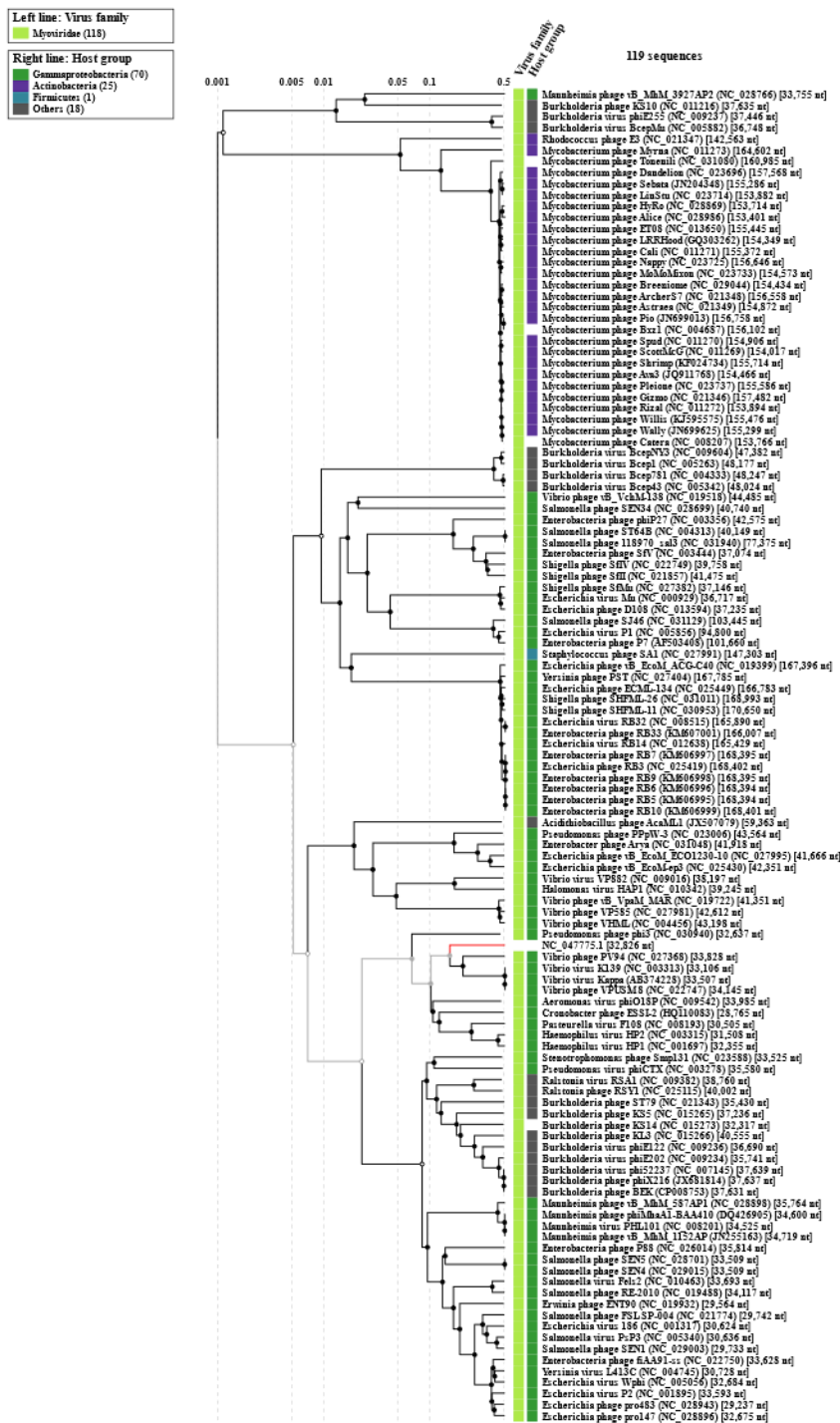


## SUPPLEMENTARY DATA



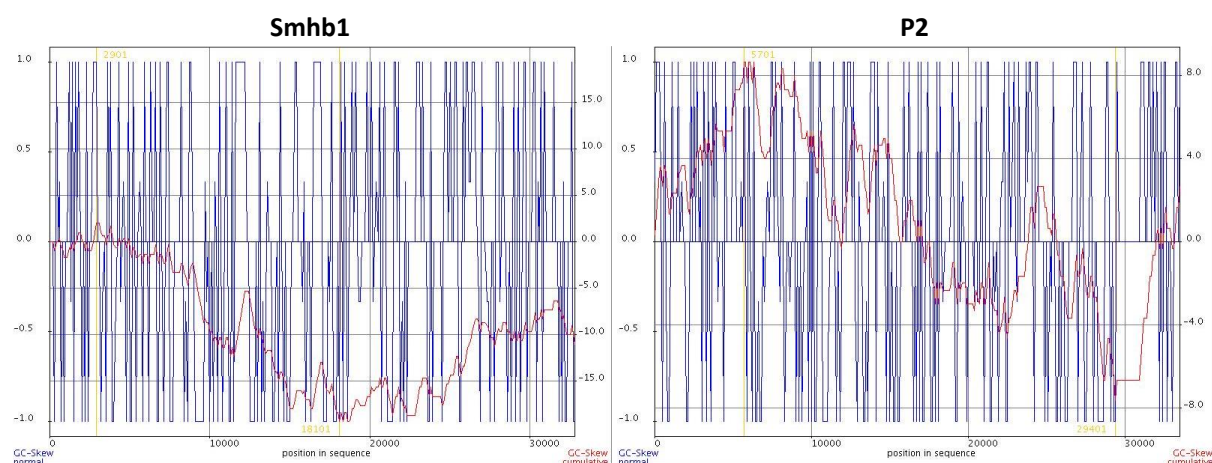
**Figure S1.** Agarose gel electrophoresis of digested phage DNA. Lane one phage Lambda DNA cut with PstI used as a molecular marker.



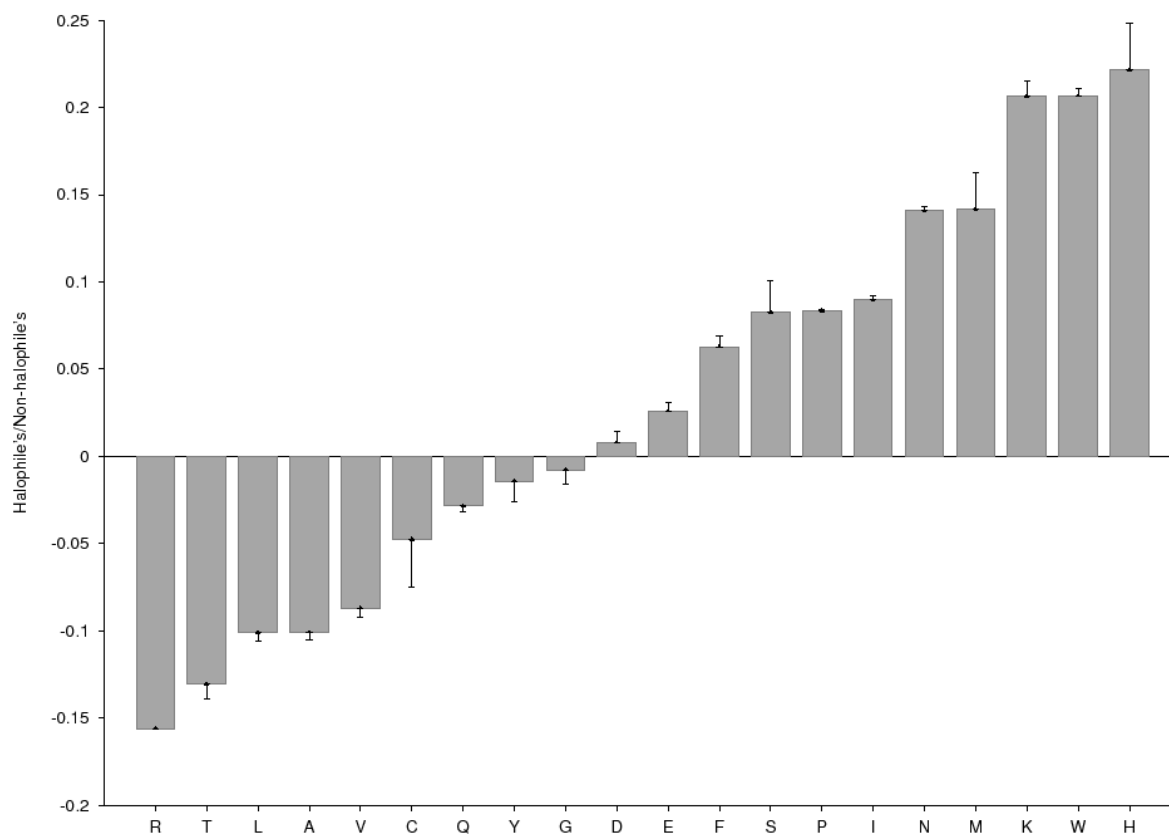
**Figure S2.** ViPTree analysis of Smhb1 encoded proteins compared with those of other *Peduovirinae* phages present on the Virus-Host DB: RefSeq release 93. The branch that Smhb1 (NC\_047775.1) is on, is highlighted in red.



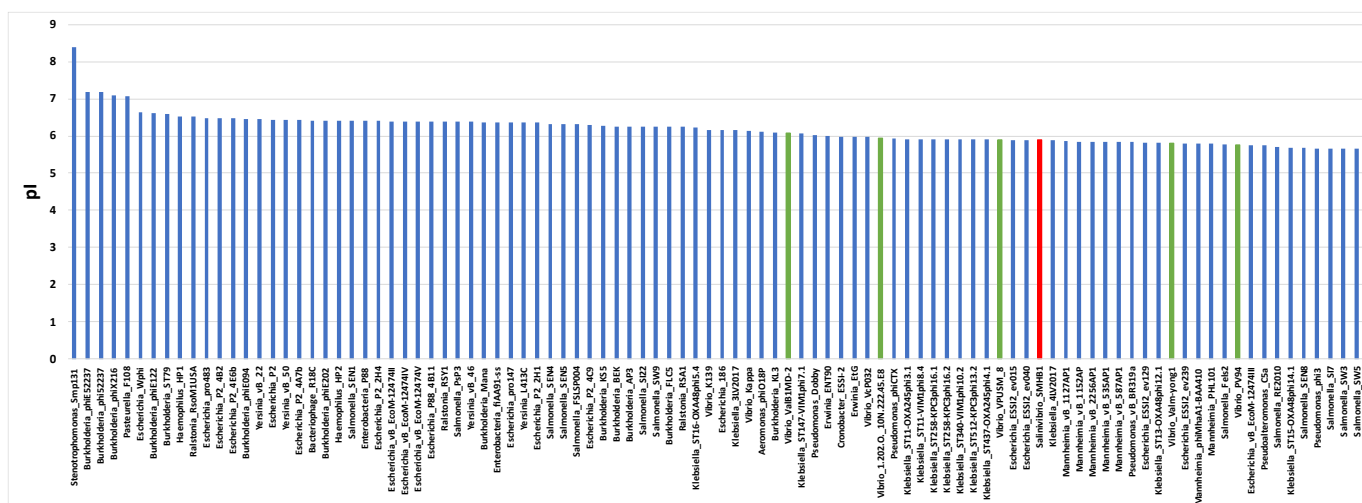
**Figure S3.** Alignment of origin of replication (*ori*) sequences from Smhb1 and related *Peduoviruses*. Only differences from the reference (Smhb1) are shown.



**Figure S4.** GC skew analysis of the genome of phage Smhb1 and P2 to predict the putative replication origin (*ori*) and termination sites (*ter*) calculated using a window size of 1000 bp and a step size of 100 bp



**Figure S5.** Amino acid composition profiles comparing moderately halophilic *Peduovirinae* proteins to non-halophilic *Peduovirinae* encoded proteins ordered by observed difference



**Figure S6.** Predicted protein isoelectric point (pI) of selected *Peduovirinae* encoded proteins ranked from highest to lowest. Smhb1 predicted protein pI indicated in red and those of *Vibrio* infecting phages in green

**Table S1:** Sequencing analysis report for the assembly of phage Smhb1 and the genomes of DV and BNH

Attribute	<i>S. proteolyticus</i> DV	<i>S. kushneri</i> BNH	Smhb1
Total number of reads	1,681,207	2,029,522	543,053
Avg. Read length (bp)	273	279	288

Genome size (bp)	3,710,861	3,482,133	32826
DNA G+C (%)	49.8	50.5	50.8
Number of contigs >500bp	145	45	-
Largest contig (bp)	184,643	399,209	-
N50 (bp)	51,625	187,815	-
Avg. coverage	124x	211x	1991x
Number of proteins	3242	3051	49
Accession number	MEBP00000000	MEBQ00000000	NC_047775

Table S2:

ORF number / direction	ORF start – end position (bp)	Accession Number	Closest phage BLASTp hit(s)	Identities	Positives	E-value
gp01 / +	450-1514	YP_009786943.1	Integrase <i>Pseudoalteromonas</i> phage C5a	204/279 (73%)	244/279 (87%)	2e-157
gp02 / +	1617-2105	YP_009786944.1	Hypothetical protein	-	-	-
gp03 / -	2154-2663	YP_009786945.1	Hypothetical protein Lv-1_gp24 <i>Lactobacillus</i> phage Lv-1	31/88 (35%)	48/88 (54%)	0.001
gp04 / -	2715-3167	YP_009786946.1	Hypothetical protein	-	-	-
gp05 / -	3213-3812	YP_009786947.1	CI repressor <i>Vibrio</i> phage 1.202.O._10N.222.45.E8	83/199 (42%)	121/199 (60%)	9e-47
gp06 / +	3905-4105	YP_009786948.1	Regulatory protein <i>Vibrio</i> phage Valm-yong1 Cox <i>Pasteurella</i> virus F108	45/65 (69%) 21/53 (40%)	55/65 (84%) 34/53 (64%)	9e-28 2e-10
gp07 / +	4108-4266	YP_009786949.1	Hypothetical protein	-	-	-
gp08 / +	4294-4815	YP_009786950.1	Regulatory protein CII <i>Vibrio</i> phage 1.202.O._10N.222.45.E8	85/173 (49%)	118/173 (68%)	2e-53
gp09 / +	4829-5092	YP_009786951.1	Pyocin activator PrtN family protein <i>Pseudoalteromonas</i> phage C5a	49/84 (58%)	65/84 (77%)	6e-33
gp10 / +	5102-5506	YP_009786952.1	Protein of unknown function DUF5347 <i>Vibrio</i> phage Valm-yong1	37/99 (37%)	49/99 (49%)	2e-12
gp11 / +	5571-5780	YP_009786953.1	Hypothetical protein	-	-	-
gp12 / +	5790-5906	YP_009786954.1	Hypothetical protein	-	-	-
gp13 / +	5911-6372	YP_009786955.1	Hypothetical protein	-	-	-
gp14 / +	6381-6617	YP_009786956.1	Hypothetical protein K139p11 <i>Vibrio</i> virus K139	36/72 (50%)	51/72 (70%)	3e-20
gp15 / +	6614-9046	YP_009786957.1	Replication endonuclease <i>Vibrio</i> phage PV94	390/772(51%)	520/772(67%)	0.0
gp16 / +	9056-9610	YP_009786958.1	Putative exonuclease <i>Vibrio</i> phage vB_VpaM_MAR	147/182 (81%)	170/182 (93%)	1e-109
gp17 / +	9621-9965	YP_009786959.1	Hypothetical protein	-	-	-
gp18 / -	9998-10333	YP_009786960.1	Putative transposon-related DNA-binding protein <i>Vibrio</i> phage Valm-yong1 Helix-turn-helix transcriptional regulator <i>Vibrio</i> phage PV94	30/93 (32%) 39/103 (38%)	55/93 (59%) 59/103 (57%)	4e-12 3e-11
gp19 / +	10314-10439	YP_009786961.1	Hypothetical protein	-	-	-
gp20 / +	10563-10724	YP_009786962.1	Hypothetical protein	-	-	-
gp21 / +	10880-11275	YP_009786963.1	Hypothetical protein	-	-	-
gp22 / +	11340-11474	YP_009786964.1	Hypothetical protein Her_0050 <i>Vibrio</i> phage Her	23/34 (68%)	28/34 (82%)	2e-10
gp23 / +	11492-11941	YP_009786965.1	Hypothetical protein	-	-	-
gp24 / +	11938-12252	YP_009786966.1	Hypothetical protein	-	-	-
gp25 / -	12234-12671	YP_009786967.1	ogr/Delta-like zinc finger family protein <i>Vibrio</i> phage 1.202.O._10N.222.45.E8	77/150 (51%)	103/150 (68%)	8e-47

gp26 / -	12730-13788	YP_009786968.1	Portal protein <i>Vibrio</i> phage Valm-yong1	248/346 (72%)	288/346 (83%)	0.0
gp27 / -	13770-15563	YP_009786969.1	Terminase <i>Vibrio</i> phage ValB1MD-2	465/596 (78%)	514/596 (86%)	0.0
gp28 / +	15745-16704	YP_009786970.1	Capsid scaffolding protein <i>Vibrio</i> phage VD1	153/323 (47%)	188/323 (58%)	2e-80
gp29 / +	16704-17756	YP_009786971.1	Major capsid protein <i>Vibrio</i> phage VD1	209/346 (60%)	259/346 (74%)	2e-151
gp30 / +	17759-18475	YP_009786972.1	Terminase small subunit <i>Vibrio</i> phage Valm-yong1	138/239 (58%)	187/239 (78%)	1e-100
gp31 / +	18574-18981	YP_009786973.1	Head completion/stabilization protein <i>Vibrio</i> phage PV94	77/139 (55%)	93/139 (66%)	2e-43
gp32 / +	18981-19457	YP_009786974.1	Tail completion protein R <i>Vibrio</i> phage Valm-yong1	93/155 (60%)	121/155 (78%)	4e-66
gp33 / +	19441-20097	YP_009786975.1	Virion morphogenesis protein <i>Vibrio</i> phage 1.202.O._10N.222.45.E8	152/219 (69%)	178/219 (81%)	3e-103
gp34 / +	20100-21221	YP_009786976.1	DUF2586 family protein <i>Vibrio</i> phage PV94 Tail fibers protein <i>Vibrio</i> phage Valm-yong1	264/373(71%) 264/376(70%)	308/373(82%) 305/376(81%)	0.0 0.0
gp35 / +	21221-21676	YP_009786977.1	Tail tube protein <i>Vibrio</i> phage Valm-yong1	111/151 (74%)	130/151 (86%)	2e-77
gp36 / +	21695-21901	YP_009786978.1	Hypothetical protein	-	-	-
gp37 / +	21906-22319	YP_009786979.1	Peptidase M15A uncultured Mediterranean phage uvMED	75/128 (59%)	96/128 (75%)	2e-50
gp38 / +	22322-22906	YP_009786980.1	Hypothetical protein VP3213_05 <i>Vibrio</i> phage vB_VchM_VP-3213	78/183 (43%)	112/183 (61%)	6e-35
gp39 / +	22907-23155	YP_009786981.1	Hypothetical protein HYQ07_gp37 <i>Vibrio</i> phage Valm-yong1	32/75 (43%)	56/75 (74%)	7e-16
gp40 / +	23152-23418	YP_009786982.1	Tail assembly chaperone <i>Vibrio</i> phage PV94	43/85 (51%)	60/85 (70%)	9e-25
gp41 / +	23607-25733	YP_009786983.1	Tail tape measure protein <i>Vibrio</i> phage PV94	423/707 (60%)	518/707 (73%)	0.0
gp42 / +	25730-26059	YP_009786984.1	DUF2590 family protein <i>Vibrio</i> phage PV94	74/107 (69%)	94/107 (87%)	1e-49
gp43 / +	26052-27239	YP_009786985.1	Baseplate J/gp47 family protein <i>Vibrio</i> phage PV94	248/392 (63%)	311/392 (79%)	0.0
gp44 / +	27226-27840	YP_009786986.1	Hemolysin <i>Vibrio</i> phage PV94	89/162 (55%)	119/162 (73%)	3e-61
gp45 / +	27837-30023	YP_009786987.1	ORF35 <i>Vibrio</i> phage O395 Putative tail fiber protein <i>Vibrio</i> phage VPUSM 8	175/273 (64%) 175/273 (64%)	213/273 (78%) 213/273 (78%)	2e-119 4e-117
gp46 / +	30023-30481	YP_009786988.1	Hypothetical protein ICP12011A_066 <i>Vibrio</i> phage ICP1_2011_A	45/81 (56%)	60/81 (74%)	5e-24
gp47 / +	30485-31030	YP_009786989.1	Tail-collar fiber protein <i>Vibrio</i> phage Valm-yong1	107/181 (59%)	135/181 (74%)	6e-73
gp48 / +	31027-31713	YP_009786990.1	Hypothetical protein HOU21_gp40 <i>Vibrio</i> phage 1.202.O._10N.222.45.E8	131/226 (58%)	172/226 (76%)	9e-103
gp49 / +	31704-32435	YP_009786991.1	Tail spike <i>Pseudoalteromonas</i> phage C5a	152/254 (60%)	182/254 (71%)	9e-102

Table S3:

Bacterium (Strain)
<i>Salinivibrio costicola</i> (LMG11651)
<i>Vibrio casei</i> (LMG25240)
<i>Vibrio splendidus</i> (LMG19031)
<i>Vibrio chagasii</i> (LMG21353)
<i>Vibrio atlanticus</i> (LMG24300)
<i>Vibrio aestuarianus</i> (LMG7909)
<i>Vibrio harveyi</i> (LMG4044)
<i>Vibrio neocistes</i> (NRRL B-1037)

Table S4:

DV		BNH	
CRISPR repeat consensus	Number of Spacers	CRISPR repeat consensus	Number of Spacers
GAAGCGAAAGCTAAGCGTGAAGC (23 bp)	5	TTTCTAAGCTGCCTGTGCGGCAGTGAAC (28 bp)	36
TGTTCACTGCCGCACAGGCAGCTTAGAAA (29bp)	3	TTTCTAAGCTGCCTGTGCGGCAGTGAAC (28 bp)	41
GTTCACTGCCGCACAGGCAGCTTAGAAA (28bp)	9	GTGTTCCCCGTGCCACGGGGATGAACCG (29 bp)	47
GTTCACTGCCGCATAGGCAGCTTAGAAA (28bp)	35		
TTTCTAAGCTGCCTGTGCGGCAGTGAAC (28 bp)	24		
CGGTTCATCCCCGTGGGCACGGGGAACAC (29 bp)	42		
GTGCGCCTCCCCCAGGCGCGTGGATTGAAAC (32bp)	178		

Table S5:

Spacer	Smhb1 genome coordinates	Smhb1 gene recognized
TTAGCTTCTGCGGGGTGGTTCGCGCAGCGGTAGC	22081-22114	Hypothetical protein
ACATCAACGGCGTGCCCTATCTGCGTGAAGACGAG	21621-21655	Putative tail tube protein
ATTGTTGCCTGCTGATCAGGTCAAAGGGCAAGTTA	16871-16905	Capsid protein
CGGTGTATATGCCATATGCGGCAATAGTACGCC	15540-15572	Terminase large subunit
GATGGTGTCGTTGCCGACACCGATTTTTTGTC	8883-8914	Replication protein
AGCGGCCCCACGTATTCGCGTGTTTTGGTTTT	8000-8031	Replication protein
GAATGCGGCGTTGTAGTTCACCACCCATTCGA	6922-6953	Replication protein



