

Supplementary Material

Table S1. Viral membrane transport proteins with homologs in living organisms. The shown proteins have been functionally characterized. Alga species are indicated by *.

Protein	NCBI Accession #	Length in aa, (Predicted TMs)	Virus	Virus family	Genome size in base pairs, (accession #)	Host (Phylum)	Reference
NC64A chlorovirus potassium channel Kcv	NP_048599.1	94 (2)	Paramecium bursaria chlorella virus-1 (PBCV-1)	Phycodnaviridae (Genus chlorellavirus)	330.661 (JF411744.1)	<i>Chlorella variabilis</i> NC64A* (formerly: <i>Chlorella</i> NC64A) (Green algae)	Plugge et al., 1999
Pbi chlorovirus potassium channel Kcv	ABA40764.1	95 (2)	Chlorella Pbi virus MT325	Phycodnaviridae (Genus chlorellavirus)	314.335 (DQ491001.1)	<i>Micractinium conductrix</i> * (formerly: <i>Chlorella</i> Pbi) (Green algae)	Gazzarrini et al., 2006
SAG chlorovirus potassium channel Kcv	YP_001427066.1	82 (2)	Acanthocystis turfacea chlorella virus-1 (ATCV-1)	Phycodnaviridae (Genus chlorellavirus)	288.047 (NC_008724.1)	<i>Chlorella heliozoae</i> * (formerly: <i>Chlorella</i> SAG3.83) (Green algae)	Gazzarrini et al., 2009
Prasinovirus potassium channel KBpV	YP_004061440.1	83 (2)	Bathycoccus sp. RCC1105 virus (BpV1)	Phycodnaviridae (Genus Prasinovirus)	198.519 (NC_014765.1)	<i>Bathycoccus</i> sp. RCC1105* (Green algae)	Siotto et al., 2014
Prasinovirus potassium channel KMpV	YP_004062056.1	79 (2)	Micromonas sp. RCC1109 virus (MpV1)	Phycodnaviridae (Genus Prasinovirus)	184.095 (NC_014767.1)	<i>Micromonas</i> sp. RC1109* (green algae)	Siotto et al., 2014
Prasinovirus potassium channel KotV	AFC34969.1	104 (2)	Ostreococcus tauri virus RT-2011 (OtV6)	Phycodnaviridae (Genus Prasinovirus)	189.567 (JN225873.1)	<i>Ostreococcus tauri</i> * (Green algae)	Siotto et al., 2014
Phycodnavirus potassium channel KOLPV	ADX06199.1	140 (2)	Organic Lake phycodna virus 2 (OLPV-2)	Phycodnaviridae (environmental sample)	282.077 (HQ704803.1)	Unknown alga*	Siotto et al., 2014

Aureococcus virus potassium channel KAaV	YP_009052228.1	156 (2)	Aureococcus anophagefferens virus isolate BtV-01 (AaV)	Phycodnaviridae	370.920 (NC_024697.1)	<i>Aureococcus anophagefferens*</i> (Heterokont algae)	Thiel, unpublished
Phaeovirus potassium channel KEsV	NP_077708.1	124 (3)	Ectocarpus siliculosus virus 1 (EsV-1)	Phycodnaviridae (Genus Phaeovirus)	355.593 (AF204951.1)	<i>Ectocarpus siliculosus*</i> (Brown algae)	Balss et al., 2008
Poxvirus GAAP	NP_570396.1	237 (7)	Camelpox virus	Poxviridae (Chordopoxvirinae, Orthopoxviruses)	205.719.1 (NC_003391.1)	<i>Camelus</i> sp. (Mammal)	Saraiva et al., 2013
Pbi chlorovirus aquaglyceroporin	ABT13584.1	270 (6)	Chlorella Pbi virus MT325	see above	see above	see above	Gazzarrini et al., 2006
Pbi chlorovirus potassium transporter HAKCV	ABT15395.1	660 (12)	Chlorella Pbi virus Fr483	unassigned, Phycodnaviridae (Genus chlorellavirus)	321.240 (NC_008603.1)	see above	Greiner et al., 2012
SAG chlorovirus potassium transporter HAKCV	YP_001427177.1	644 (12)	Acanthocystis turfacea chlorella virus-1 (ATCV-1)	see above	see above	see above	Greiner et al., 2012
Ostreococcus tauri ammonium transporter	AFC35023.1	439 (11)	Ostreococcus tauri virus RT-2011 (Otv6)	Phycodnaviridae	189.567 (JN225873.1)	see above	Monier et al., 2017
Chlorovirus Ca-ATPase	ABT14089.1	871 (10)	Chlorella Pbi virus MT325	see above	see above	see above	Bonza et al. 2010

Table S2. Viral membrane transport proteins found in the databases. Alga species are indicated by *.

Putative protein	Example protein NCBI Accession #	Virus (virus family)	Length in aa, (Predicted TMs)	Genome size in base pairs, (accession #)	Host (Phylum)
Potassium channel	YP_009325597.1	Chlorovirus OSy-NE5 (phycodnaviridae, chlorovirus)	94 (2)	327.147 (NC_032001)	<i>Chlorella variabilis</i> Syngen 2-3* (Green algae)
Potassium channel	AUT19143.1	Dishui lake phycodnavirus 1 (phycodnaviridae)	116 (2)	181.035 (NC_037057.1)	Unknown alga*
Potassium channel	YP_009174599.1	Yellowstone lake phycodnavirus (phycodnaviridae)	96 (2)	171.045 (NC_028110.1)	Unknown alga*
Potassium channel	AUF82121.1	Tetraselmis virus 1 (TeV-1) (Mimiviridae)	81 (2)	668.031 (KY322437.1)	<i>Tetraselmis</i> sp.* (Green alga)
Potassium channel	ACH62227.1	Mycobacterium phage Myrna (Caudovirales, myoviridae)	119 (2)	164.602 (NC_011273.1)	Mycobacterium (Actinobacteria)
Potassium channel	AFN37377.1	Vibrio phage phi-pp2 (Caudovirales, Myoviridae)	228 (2)	246.421 (JN849462)	<i>Vibrio parahaemolyticus</i> (Proteobacteria)
Potassium channel	AND75308.1	Acinetobacter phage vB_AbaM_ME3 (unclassified phage)	124 (2)	234.900 (KK935715)	<i>Acinetobacter baumannii</i> DSM 30007 (Proteobacteria)
Potassium channel	YP_009282368.1	Lactobacillus phage PLE2 (Caudovirales, Siphoviridae)	259 (4)	35.068 (NC_031036)	<i>Lactobacillus casei</i> BL23 (Firmicutes)
CLIC-like chloride channel	YP_003358251	Anguillid herpes virus 1 (Herpesvirales Alloherpesvirales, Cyprinivirus)	281 (2)	248.526 (NC_013668.3)	<i>Anguilla anguilla</i> (Fish)
MCLC-like chloride channel	YP_006908742	Abalone herpesvirus Victoria/AUS/2009 (Herpesvirales, unclassified)	333 (3)	211.518 (NC_018874.1)	<i>Haliotis rubra</i> (Molluscs)
Glutamate receptor	NP_048510.1	Paramecium bursaria chlorella virus-1 (Phycodnaviridae, chlorellavirus)	411 (3)	330.661 (JF411744)	<i>Chlorella variabilis</i> NC64A* (Green algae)
Ligand-gated ion channel	NP_048511.1	Paramecium bursaria chlorella virus-1 (Phycodnaviridae, chlorellavirus)	433 (5)	see above	see above
Aquaglyceroporin	YP_009325532.1	Chlorovirus OSy-NE5	269	see above	see above

		(phycodnaviridae, chlorovirus)	(6)		
Mechanosensitive channel	YP_009052121.1	Aureococcus anophagefferens virus isolate BtV-01 (Phycodnaviridae)	261 (3)	370.920 (NC_024697)	<i>Aureococcus anophagefferens</i> * (Heterokont algae)
Mechanosensitive channel	AUF82136.1	Tetraselmis virus 1 (TeV-1) (Mimiviridae)	101 (1-2)	668.031 (KY322437.1)	<i>Tetraselmis</i> sp.* (Green algae)
Mechanosensitive channel	YP_003969926.1	Cafeteria roenbergensis virus BV-PW-1 (Mimiviridae)	101 (2)	617.453 (NC_014637.1)	<i>Cafeteria roenbergensis</i> strain E4-10* (Heterokont algae)
Ammonium transporter	YP_009173407.1	Chrysochromulina ericina virus (Phycodnaviridae)	124 (2)	473.558 (NC_028094.1)	<i>Chrysochromulina ericina</i> * (Haptophyte algae)
Magnesium transporter	YP_009222254.1	Lactobacillus phage Lfelnf (Caudovirales, myoviridae)	322 (2/3)	106.071 (NC_029058.1)	<i>Lactobacillus fermentum</i> (Firmicutes)
Sodium calcium transporter	AUR86274.1	Vibrio phage 1.084.O. 10N.261.49.F5 (unclassified)	370 (9)	141.906 (MG592459.1; partial genome)	<i>Enterovibrio norvegicus</i> (Proteobacteria)
Sodium phosphate symporter	AEO97646.1	Emiliana huxleyi virus 84 (Phycodnaviridae, coccolithoviruses)	534 (10)	396.620 (JF974290.1)	<i>Emiliana huxleyi</i> 1516* (Heterokont algae)
Sodium glucose transporter	NP_932589.1	Aeromonas virus 44RR (Caudovirales, myoviridae)	507 (14)	173.591 (NC_005135.1)	<i>Aeromonas salmonicida</i> (Protobacteria)
short ATP-binding cassette transporter (ABC transporters)	BAV62853.1	Acanthamoeba castellanii mimivirus shirakomae (Mimiviridae)	532 (5)	1.182.849 (AP017645.1 (check))	<i>Acanthamoeba castellanii</i> (Amoebozoa)
large ATP-binding cassette transporter (ABC transporters)	YP_009001498.1	Anomala cuprea entomopoxvirus (Poxviridae entomopoxvirinae, Alphaentomopoxvirus)	1506 (14)	245.717 (NC_023426.1)	<i>Anomala cuprea</i> (Insect)
Nicotinamide mononucleotide transporter	AKJ73485.1	Salmonella phage 40 (unclassified bacterial virus)	239 (6)	63.263 (KR296694.1)	<i>Salmonella paratyphi</i> A (Proteobacteria)
Equilibrative nucleoside transporter	AJG42984.1	Harp seal herpesvirus (Herpesvirales, herpesviridae, gammaherpesviridae)	432 (11)	117.276 (partial) (KP136799.1)	<i>Pagophilus groenlandicus</i> (Mammal)
Amino acid transporter	BAZ95678.1	Red seabream iridovirus (Iridoviridae Alphairidovirinae; Megalocytivirus))	378 (11)	112.590 (AP017456.1)	<i>Pagrus major</i> (Fish)
Ca-ATPase	YP_009325865.1	Chlorovirus OSy-NE5	\$	see above	see above

Mg-ATPase	ARF11485.1	(Phycodnaviridae, chlorovirus) Klosneuvirus-1 (Mimiviridae, Klosneuvirinae)	922 (10)	451.653 (KY684108.1)	Unknown/Environmental sample
P-type ATPase	ARF08724.1	Catovirus CTV1 (Mimiviridae, Klosneuvirinae)	809 (6-7)	1.152.313 (KY684083.1)	Unknown/Environmental sample

Table S3. Putative potassium channel proteins from vibrio phages.

Phage	Length (aa)	TMs	Accession #
Vibrio phage phi-pp2	228	2	AFN37377.1
Vibrio phage nt-1	228	2	YP_008125342.1
Vibrio phage ValKK3	227	2	YP_009201217.1
Vibrio phage VH7D	207	2	YP_009006109.1
Vibrio phage phi-Grn1	200	2	ALP47069.1
Vibrio phage phi-ST2	161	1	ALP47495.1
Vibrio phage 1.081.O._10N.286.52.C2	219	2	AUR85893.1
Vibrio phage 1.084.O._10N.261.49.F5	219	2	AUR86273.1
Vibrio phage 2.275.O._10N.286.54.E11	149	2	AUS02797.1

Table S4. Putative potassium channel-like proteins from large DNA viruses.

Virus	Length (aa)	TMs	Accession #
Bandra mega virus	114	2	AUV58190.1
Megavirus courdo11	114	2	AFX92280.1
Megavirus courdo7	114	2	AEX61336.1
Powei lake megavirus	114	2	ANB50367.1
Moumouvirus Monve	113	2	AEX63115.1
Moumouvirus australiensis	113	2	AVL94583.1
Acanthamoeba polyphaga mimivirus	111	2	YP_003987221.1
	111	2	AKI80434.1
Hirudovirus strain Sangsue	127	2	AHA45141.1
Tupanvirus deep ocean	103	2	AUL80003.1

Table S5. Blastp search results of the MCLC-like protein from Abalone herpesvirus against sequences from cellular organisms; *partial sequence.

Organism (Phylum)	length (aa)	max score/total score/query cover (%) /E-value/identity (%) / accession #
Lingula anatina (Brachiopoda) isoform X2	441	92.8/92.8/47/2e-17/32/XP_13403059.1
Lingula anatina	467	93.2/93.2/47/2e-17/32/XP_013416639.1
Lingula anatina isoform X1	467	92.8/92.8/47/2e-17/32/XP_013403058.1
Branchiostoma floridae (Chordata)	685	87.0/87.0/51/3e-15/26/XP_002610653.1
Saccoglossus kowalevskii (Hemichordata)	196*	78.2/78.2/45/2e-13/33/XP_006819247.1
Branchiostoma belcheri (Chordata)	573	72.4/72.4/50/2e-10/24/XP_019625644.1
Acropora digitifera (Cnidaria)	441	68.9/68.9/81/2e-9/22/XP_015775446.1
Orbicella faveolata (Cnidaria)	523	66.6/66.6/50/2e-8/25/XP_020611811.1
Hydra vulgaris (Cnidaria)	576	60.8/60.8/47/1e-6/26/XP_002154667.2
Lingua anatina (Brachiopoda)	475	60.1/60.1/49/2e-6/28/XP_013385450.1
Lingua anatina	366	59.3/59.3/49/3e-6/28/XP_013408110.1
Intoshia linei (Orthonectida)	389	56.6/56.6/30/2e-5/24/OAF71881.1
Crassostrea gigas (Mollusca)	265	55.1/55.1/35/5e-5/23/EKC19861.1
Crassostrea gigas	354	55.5/55.5/39/5e-5/24/XP_011419399.1
Lottia gigantea (Mollusca)	616	53.9/53.9/39/2e-4/22/XP_009044054.1
Strongylocentrotus purpuratus (Echinodermata)	347*	53.1/53.1/37/3e-4/28/XP_011676168.1
Diachasma alloeum (Arthropoda)	501	52.4/52.4/68/6e-4/23/XP_015115510.1

Table S6. Results of blastp search of camel pox virus GAAP against viral protein sequences.

Virus	length (aa)	TMs	E value	aa identity	Accession #
Camelpox virus	237	7	-	-	NP_570396.1
	237	7	2e-175	99%	AAG37461.1
Cowpox virus	237	7	1e-169	97%	ADZ29755.1
	237	7	7e-169	96%	SNB58186.1
	237	7	1e-168	96%	SNB53700.1
	237	7	3e-168	96%	ADZ30397.1
	237	7	1e-160	96%	ADZ30183.1
	237	7	2e-160	96%	CRL86727.1
	237	7	2e-158	95%	AQQ13071.1
	237	7	5e-158	95%	ADZ24213.1
	210	6	1e-142	95%	CAD90752.1
	199	5	5e-129	95%	CRL87022.1
	197	5	2e-127	95%	SNB49536.1
	114	3	1e-77	96%	ABD97561.1
	79	2	2e-41	94%	ABD97560.1
Vaccinia virus	237	7	1e-158	95%	AAV98625.1
	237	7	6e-158	95%	Q49P94.1
	237	7	4e-157	94%	AAW21699.1
Scale drop disease virus	236	7	1e-80	47%	YP_009163856.1
Monkeypox virus	121	4	6e-64	80%	AAV96807.1
	105	3	3e-55	80%	AKG51345.1
	105	3	1e-54	81%	AGR36454.1
	105	3	6e-54	80%	NP_536611.1
	105	3	9e-54	80%	AAV97191.1
Harp seal herpesvirus	244	6	4e-61	48%	AJG42933.1
uncultured Caudovirales phage)	233	7	5e-15	30%	ASN71498.1
Panine betaherpesvirus 2	254	7	1e-10	27%	NP_612793.1

Table S7. Blastp results of camel poxvirus GAAP versus living organisms.

Hit	Max score/Total score/Query cover/E value/Ident/Accession
protein lifeguard 4 (<i>Castor canadensis</i>)	353/353/100%/2e-121/75%/XP_020024307.1
protein lifeguard 4 isoform X1 (<i>Odocoileus virginianus texanus</i>)	350/350/97%/7e-120/76%/XP_020738958.1
protein lifeguard 4 isoform X1 (<i>Condylura cristata</i>)	349/349/100%/2e-119/74%/XP_012576116.1
protein lifeguard 4 (<i>Ovis aries musimon</i>)	348/348/97%/4e-119/76%/XP_011995634.1
protein lifeguard 4 (<i>Capra hircus</i>)	347/347/97%/7e-119/76%/XP_017903468.1
protein lifeguard 4 (<i>Bos taurus</i>)	347/347/97%/1e-118/76%/NP_001014914.1
protein lifeguard 4 (<i>Physeter catodon</i>)	346/346/100%/2e-118/74%/XP_007126330.1
protein lifeguard 4 isoform X1 (<i>Desmodus rotundus</i>)	346/346/97%/2e-118/74%/XP_024431972.1
protein lifeguard 4 (<i>Ovis aries</i>)	345/345/96%/4e-118/76%/XP_014950252.1
protein lifeguard 4 (<i>Bison bison bison</i>)	345/345/97%/4e-118/76%/XP_010839876.1

Table S8. ABC transporter diversity among large DNA viruses. Shown are the results of a blastp search of the mimivirus ABC transporter (YP_003987262.1) against virus sequences.

Virus (genome size; accession #)	length (aa)	TMs	E value	aa identity	Accession #
Acanthamoeba polyphaga mimivirus (1.181.404; AY653733.1)	532	5	0.0	100%	YP_003987262.1
	532	5	0.0	99%	AKI79520.1
	532	5	0.0	98%	AKI81410.1
	532	5	0.0	93%	AKI80473.1
	532	5	0.0	98%	AEJ34979.1
	532	5	4e-122	100%	AEJ34978.1
	532	5	4e-87	36%	AVG45935.1
	532	5	3e-86	35%	AVG47038.1
Acanthamoeba castellanii mamavirus (1.191.693 bp; JF801956.1)	532	5	0.0	99%	AEQ60944.1
Acanthamoeba polyphaga moumouvirus (1.021.348 bp; NC_020104.1)	535	5	1e-91	37%	YP_007354121.1
Moumouvirus Monve (no full genome sequence)	492	1-4	1e-90	36%	AEX63154.1
Megavirus courdo11 (1.246.126 bp; JX975216.1)	542	4	2e-88	35%	AFX92233.1
Powei lake megavirus (1.208.707 bp; KU877344.1)	526	3-4	7e-88	35%	ANB50323.1
Megavirus courdo7 (no full genome sequence)	526	3-4	3e-87	35%	AEX61283.1
Megavirus lba (1.230.522 bp; JX885207.1)	599	3-4	3e-86	35%	AGD92104.1
Megavirus chiliensis (1.259.197 bp; NC_016072.1)	605	3	4e-86	35%	YP_004894252.1
Megavirus vitis (1.242.360 bp; MG807319.1)	484	1-2	2e-84	36%	AVL93548.1

Bandra megavirus (73.092 bp (partial); MG779341.1)	535	3-4	3e-82	36%	AUV58153.1
Moumouvirus australiensis (1.098.002 bp; MG807320.1)	534	5	7e-82	36%	AVL94552.1
Moumouvirus goulette (1.016.844 bp; KC008572.1)	535	5	9e-76	34%	AGF85616.1
Tupanvirus deep ocean (1.516.267 bp; MF405918.1)	572 545	4-5 3	5e-16 2.9	32% 31%	AUL79468.1 AUL79194.1
Catovirus CTV1 (1.152.313 bp; KY684083.1)	545	5	4e-7	24%	ARF09084.1
Indivirus ILV1 (267.262; KY684085.1)	547	5	0.008	31%	ARF09888.1
Hokovirus HKV1 (450.695 bp; KY684103.1)	551	5	0.012	23%	ARF10734.1
Bodo saltans virus (1.385.869 bp; MF782455.1)	452	4	0.029	24%	ATZ80684.1
Tupanvirus soda lake (1.439.508 bp; KY523204.1)	545	3	2.4	29%	AUL77901.1

Table S9. Putative sodium phosphate transporters from viruses that infect marine picoplankton; *possibly partial sequence.

Virus	Length (aa)	TMs	Accession #
Emiliana huxleyi virus 86	534	10	YP_293871.1
Emiliana huxleyi virus 203	534	10	AEO98102.1
Emiliana huxleyi virus 86	508*	9	YP_002296186.1
Emiliana huxleyi virus 202	534	10	AET42514.1
Bathycoccus sp. RCC1105 virus BpV1	503	9	YP_004061633.1
Ostreococcus lucimarinus virus 2	459	9	YP_009172747.1
Ostreococcus tauri virus 2	459	9	YP_004063655.1
Ostreococcus lucimarinus virus OIV4	290*	5	AET84692.1
Ostreococcus lucimarinus virus 1	459	9	YP_004061866.1
Ostreococcus lucimarinus virus OIV4	176*	3-5	AET84699.1

Table S10. Phage nicotinamide mononucleotide transporter variety. Blastp comparison of Salmonella phage 40 protein against viral sequences.

Phage	Length (aa)	TMs	blastp E value (compared to the protein from Salmonella phage 40)	aa identity	Accession #
Salmonella phage 40	239	6-7		100%	AKJ73485.1
Salmonella phage PVO-SE1	242	6-7	1e-157	94%	YP_004893838.1
Klebsiella phage vB KpnM KB57	240	7	4e-154	89%	YP_009187643.1
Klebsiella phage vB KpnM BIS47	240	7	6e-154	89%	ARB12513.1
Salmonella phage SSE121	237	8	7e-152	89%	YP_009148852.1
Raultella phage Ro1	233	6-7	1e-138	83%	AUE23444.1
Cronobacter phage vB CsaM GAP31	235	6-7	4e-137	82%	YP_006987079.1
Escherichia phage 4MG	240	6-7	1e-131	77%	YP_008857242.1
Yersinia phage fHe-Yen9-03	267	8	6e-89	60%	SOK59171.1
Yersinia phage fHe-Yen9-04	267	8	4e-88	60%	SOK58638.1
Serratia phage BF	267	7-8	2e-86	60%	AQW88885.1
Pectobacterium phage CBB	267	7	7e-86	61%	AMM43925.1
Cronobacter phage vB CsaM GAP 32	267	7	2e-85	60%	YP_006987459.1
Bacillus phage PBC2	228	8	5e-44	38%	AKQ08367.1
Salmonella phage 100268_sal2	225	7	2e-40	39%	YP_009320809.1
Escherichia virus EPS7	225	7	3e-40	39%	YP_001837008.1
Salmonella virus Stitch	225	7	3e-40	39%	YP_009146019.1
Salmonella phage BSP22A	225	7	1e-39	39%	ARM69751.1
Bacteriophage T5-like chee130_1	225	7	1e-39	39%	ASU02438.1
Bacillus phage vB BanS-Tsamsa	228	8	2e-38	35%	YP_008873313.1
Yersinia phage phiR201	225	7	2e-38	38%	YP_007237046.1
Vibrio phage 11895-B1	231	8	8e-38	36%	YP_007673552.1
Vibrio phage S4-7	234	7	1e-36	39%	AOQ26732.1
Lactobacillus phage Bacchae	256	6-7	2e-17	31%	AUV59971.1
Lactobacillus phage Semele	256	6-8	8e-17	32%	AUV60242.1
Lactobacillus phage LpeD	256	8	1e-16	30%	ATG86388.1
Lactobacillus virus LP65	256	6-8	2e-15	30%	YP_164718.1

Cronobacter phage vB CsaP GAP52	207	7-8	6e-13	27%	YP_006987679.1
Vibrio virus Thalassa	208	8	8e-13	29%	AUG85311.1
Vibrio phage 2.275.O._10N.286.54.E11	246	7-8	2e-11	24%	AUS02861.1
Vibrio virus Ceto	208	7-8	3e-11	26%	AUG85113.1
Vibrio phage pVp-1	210	6	5e-11	27%	YP_007007886.1
Enterococcus phage EFDG1	263	7-8	3e-5	23%	YP_009218286.1
Enterococcus phage EFP01	254	7-8	3e-5	24%	APZ82054.1
Enterococcus phage EF1	256	8	2e-4	24%	ASZ76735.1

Table S11. Phage channels and transporters that are identical to a protein from a bacterium.

Phage	Protein type	Accession # (phage protein)	Organism	Accession # (bacterial protein)
Lactobacillus phage PLE2	Potassium channel	YP_009282368.1	<i>Lactobacillus casei</i>	WP_012491300.1
Streptococcus phage phiZJ20091101-4	CLC-like chloride channel	ANM47568.1	<i>Streptococcus suis</i>	WP_024390438.1
Streptococcus phage phi-SsuD.1	Cu-translocating P-type ATPase	CBR26873.1	<i>Streptococcus sp.</i>	WP_000086363.1
Dickeya phage phiDP10.3	Malate/Na symporter	AIM51479.1	<i>Dickeya solani</i>	WP_02263587.1
Burkholderia virus phi1026b	MFS transporter	AAR23210.1	<i>Burkholderia pseudomallei</i>	WP_004552955.1
Flavobacterium phage 6H	Cytochrome c oxidase	YP_008320461.1	<i>Flavobacterium psychrophilum</i>	WP_034099077.1
Staphylococcus phage UPMK_1	Arsenical pump	ATW68282.1	<i>Staphylococcus aureus</i>	WP_000989117.1
Leptospira phage vB_LinZ_10-LE1	RND transporter, Heavy Metal Efflux (HME) family	AGS80748.1	<i>Leptospira inadai</i>	WP_010420104.1

Figure S1

A

YSLV	-----MFHN FFKLLVALIVT -----	15
OLPV2	-----MKNK FIYLIVSTIFFSLVYSEIR	23
AaV1	-----MKLLFGYN-----RFH LLIYQIIFFSILYMELG	28
TeV1	-----MSFVAK VAVHIILLITFFVINLTIN	25
PBCV1	-----MLVFSKFL--TRTE PFMIHLFILAMFVMIYKFFP	32
OSyNE5	-----MFIIRKIL--TQSE PFIIHLLVLMFVMIYRFFP	32
MT325	-----MS ILGVHFALLLFAALYKFFP	22
ATCV1	----- MLLLIIHIIILIVFTAIYKMLP	22
OtV6	-----MAL TKTLNLNFISILLFTLMYFTIS	25
DishuiLV	-----MAST LARTVGLNLGAIFIFAILYLALA	27
EsV1	MSRR LFATCGIAIALRGLVSGGV KEIVSFRPLIDT SIVGGILSNLILLVFAELYWQLD	60
BpV1	-----MLNK AVTIALIITLVYGYLY ----	20
MpV1	-----MKTVLNIIITTLYGLLY----	18
	. :	
YSLV	----- NLSFAGVMHSWV TDSDM-----	32
OLPV2	PRNFHGFNKIQDKIQDVLVSEETDIEPFYAP-----YLDKKE--KEKEKEKEKD	71
AaV1	SSHFSG INTLEDILKNEIVSKQV--LDPIIEEKFTNASDPSKFISKDDIEVDKKETEEIQ	86
TeV1	ITNK -----NAFS-----	33
PBCV1	GGFE -----NNFSVA-----	42
OSyNE5	GGFE -----NNFTVA-----	42
MT325	GGFE -----NNFKRG-----	32
ATCV1	GGMF -----SN-----	28
OtV6	KAGG-----EQFNGL-----	35
DishuiLV	RMGT-----EDFVGM-----	37
EsV1	QGDD-----HTHFGF-----	70
BpV1	STMK -----EDFGFS-----	30
MpV1	SKMK-----PEHFNF-----	28
YSLV	-----SGLRKGSTDRFVDLLYFSIV SFSTTGYGD IAPKSTRAK MAVCLF	76
OLPV2	EVKKEVKENVLEEKEKI-YNPSWWQHYLDSLYFSVI TSCLLGYGD IYPITNMSKIIVSLQ	130
AaV1	EKAKEIKKEVKKELNILTDKDSFFDRFFLRFYFSFV TSTTIGYGD TTPSSISTRTLAMIQ	146
TeV1	-----KELTTLDVFYYTVT TWTTTGYGD IYPVITVSKMIAVTK	71
PBCV1	-----NPD-KKASWIDCIYFGVT THSTVGFGD ILPK TTGAKLCTIAH	83

OSyNE5	-----NPD-KKASFVDCLYFGVT	THSTVGFGD	ILPK TTGAKLCTIAH	83
MT325	-----DGSKEPVSWMDAIYVSAA	THTTTGFGD	IVADSRAAK FAVTAH	74
ATCV1	-----TDPTWVDCLYFSAS	THTTVGYGD	LTPKSP VAKLTATAH	66
OtV6	-----DKDSGFLDHLYFAFT	VQSTVGFGD	IYPISPMAKMIVMVQ	74
DishuiLV	-----DRMSSPLDALYLSMT	VQSTIGFGD	ITPKTTRAKLL VMMQ	76
EsV1	-----SSAIDAYYFSAV	TSSSVGYGD	LLPKTPKAKLL LTIAH	106
BpV1	-----DDPLDPYYFSLM	TMSTVGYGD	FSPKTRRAKALVMSH	66
MpV1	-----KSPLDPFYFSFT	TMSSVGYGD	FSPKTDAAKLVVMSQ	64
	.	*	*: **	:: .

YSLV	<u>LMFV</u> -- <u>NI</u> --- <u>AAIYGIYNALV</u> TSA-----	96
OLPV2	GFITLFLILS-----	140
AaV1	ACSTFYILMA-----	156
TeV1	<u>MLLFLVILMY</u> -----	81
PBCV1	<u>IVTVFFIVL</u> TL-----	94
OSyNE5	<u>IVVVFFIVL</u> TL-----	94
MT325	<u>MLIVFSIVVLGL</u> KPELITNLI-----	95
ATCV1	<u>MLIVFAIVISGFT</u> FPW-----	82
OtV6	QSVLILGILELISESKSVANVVPTVMKKMI-----	104
DishuiLV	<u>QFVVIVGIVNLLSGGGISL</u> KKNNAAMNTISNTISNVPAPA	116
EsV1	<u>ILAMFFVMLPVVA</u> KALEK-----	124
BpV1	HTVILVELATILSKMTK-----	83
MpV1	HLVMIGELAKILKIF-----	79

B

Vp2	-----	0
Vp3	-----	0
Moraxella	-----	0
Vp1	-----	0
VpVH7D	-----	0
VpGrn1	-----	0
VpValKK3	-----	0
VpST2	-----	0
Vpphipp2	-----	0
Vpnt1	-----	0

LpPLE2	MATKKVNKVLIALHKYYTVLFAILALLSVALIVLDYMGRISIDKSPYTEIDNGILVIFAI	60
Lactobacillus	MATKKVNKVLIALHKYYTVLFAILALLSVALIVLDYMGRISIDKSPYTEIDNGILVIFAI	60
MpMyrna	-----	0
MpPhabba	-----	0
SpBillNye	-----	0
Acidobacterium	-----	0
Ptexasensis	-----	0
Rheinheimera	-----	0
Ap	-----	0
Ppventosus	-----	0
YSLV	-----	0
OLPV2	-----	0
AaV1	-----MKLLFGY	7
TeV1	-----	0
PBCV1	-----MLVF	4
OSyNE5	-----MFII	4
MT325	-----	0
ATCV1	-----	0
OtV6	-----	0
DishuiLV	-----	0
EsV1	-----MSRRLFATC---G---IAIALRG-----LVVSGGVKEIVSF	30
BpV1	-----	0
MpV1	-----	0
Vp2	-----	0
Vp3	-----	0
Moraxella	-----	0
Vp1	-----	0
VpVH7D	-----	0
VpGrn1	-----	0
VpValKK3	-----	0
VpST2	-----	0
Vpphipp2	-----	0
Vpnt1	-----	0
LpPLE2	DYFSRMLHADSKWDFFKHNLIDLLAIIPFNAYAFSFFRFGRIFRLARLTRLMRLTRLARLA	120

Lactobacillus	DYFSRMLHADSKWDFFKHNLIDLLAIIPFNAYFSFFRFGRIFRLARLTRLMRLTRLARLA	120
MpMyrna	-----	0
MpPhabba	-----	0
SpBillNye	-----	0
Acidobacterium	-----	0
Ptexasensis	-----	0
Rheinheimera	-----	0
Ap	-----	0
Ppventosus	-----	0
YSLV	-----MFHNFFKLLVALIVT-----	15
OLPV2	-----MKNKFIYLIVSTIFFSLVYSFIRPRNFHGFNKIQDKIQDVLVSEET	46
AaV1	N-----RFHLLIYQIIFFSILYMFLGSSHSFGINTLEDILKNEIVSKQV	51
TeV1	----M---S----FVAKVAVHIILIIITFFVINLTINITNK-----	29
PBCV1	SKFL----T---RTEPFMIHLFILAMFVMIYKFFPGGFE-----	36
OSyNE5	RKIL----T---QSEPFIIHLLVLMFMVMIYRFFPGGFE-----	36
MT325	-----MSILGVHFAILLLLFAALYKFFPGGFE-----	26
ATCV1	-----MLLLIIHIIILIVFTAIYKMLPGGMF-----	26
OtV6	----M---A----LTKTSLNFIISILLFTLMYFTISKAGG-----	29
DishuiLV	---MAS---T---LARTVGLNLGAIFIFAILYLALARMGT-----	31
EsV1	RPLIDT---S---LVGGILSNLILLVVFVFAELYWQLDQGDD-----	64
BpV1	-----M---LNKAVTIALIITLVYGYLY----STMK-----	24
MpV1	-----MKTVLNIIIIITTLYGLLY----SKMK-----	22
Vp2	-----MLNCITVID----SHGRKEYKTSFLLLLVN-IVTVLL	31
Vp3	-----MKKYLHCWISTSSKMYK----KYGT-----KYILILT-GSITGL	34
Moraxella	-----MSRF---TLSKRIYRTD---EFEVRNYNMLFLTFFVAVVILYLS	37
Vp1	-----MKFKSYD----SFGVVEYNIGMIFAGL-MALSFT	29
VpVH7D	-----MLMIFGLM-IVIALS	14
VpGrn1	-----M-IVIALS	7
VpValKK3	-----MKRF-----KKHIRKYD----EHGVAQYNMLMIFGLM-IVIALS	34
VpST2	-----	0
Vpphipp2	-----MKRF-----KKHIKKYD----EHGVVQYNMLMIFALI-VTISMS	34
Vpnt1	-----MKRL-----KKHIRKYD----EHGVVQYNMLLIFALI-ISISTS	34
LpPLE2	GIVGI----LTK---HAE-----RILKRTGLIYYI-----WLSAA	148
Lactobacillus	GIVGI----LTK---HAE-----RILKRTGLIYYI-----WLSAA	148

MpMyrna	-----MS-----LIHRATGSIKVV-----VGWAIG	20
MpPhabba	-----MS-----KIHDATGSAKV-----GLWAVG	20
SpBillNye	-----MKR-----VFFRLANTTHML-----VLTIIIG	21
Acidobacterium	-----MSN---INK-----LIARATDSFPEI-----IAYYLA	24
Ptexasensis	-----MKK-----LLIYIANRLWLI-----LAIYAG	21
Rheinheimera	-----MKK-----LLIYIANRLWLI-----IALYAA	21
Ap	-----MA-----YFLLIANNIRYV-----FLAYLL	20
Ppventosus	-----MKR-----SILWLSNSIWRV-----FGLYLI	21
YSLV	-----NLSFAGVMHSWVT---DSDM-----	32
OLPV2	DIIEPFYAP-----YLD---KKE--KEKEKEKEKDEVKKEVKEN-----VLEEKE	86
AaV1	--LDPIIEEKFTNASDPSKFIS---KDDIEVDKKETEEIQEKAKEIKKE-----VKKELN	101
TeV1	-----NAFS-----	33
PBCV1	-----NNFSVA-----	42
OSyNE5	-----NNFTVA-----	42
MT325	-----NNFKRG-----	32
ATCV1	-----SN-----	28
Otv6	-----EQFNGL-----	35
DishuiLV	-----EDFVGM-----	37
EsV1	-----HTHFGF-----	70
BpV1	-----EDFGFS-----	30
MpV1	-----PEHFNF-----	28
Vp2	NIYIGGLFLWHFEEGLQDSNINSLKEAMWAVFMTMTTIGFGDKYPITVEGYITTGVCFLL	91
Vp3	NVIIGALFLYLFEBNVDNALINSYSSALWMNWMVATTVGFGDYYPITGGKIVTGISSAI	94
Moraxella	IAV-LAFLLLWAESGAQGANIETYGDAFWTLQMSASTIGFGDYYPVTLGGRTIVAAMFYI	96
Vp1	IALTAASLLYRFESGADGSNINSAGDALWTIWMSMSTIGFGDHYPVTVGGRVIVGSMFAV	89
VpVH7D	IALTAANILFSFEIQNPANITTPGDSFWTVWMAMSTIGFGDKYPVTTGGRYVIGCMFVV	74
VpGrn1	IALTAANILFSFEIQNPANITTPGDSFWTVWMAMSTIGFGDKYPVTTGGRYVIGCMFVV	67
VpValKK3	IALTAANILFSFEIQNPANIKTPGDSFWTVWMAMSTIGFGDKYPVTTGGRYVIGCMFVV	94
VpST2	-----MAMSTIGFGDKYPVTTGGRYVIGCMFVV	28
Vpphipp2	IALVASNILFAFELSASNANIKTPGDAFWTVWMAMSTIGFGDHYPVTTGGRFVIGSMFVV	94
Vpnt1	IAFIAANFLFYFEVQDPNANIRTYGDAFWTVWMAMSTIGFGDHYPVTEGGRYTIGCMFVV	94
LpPLE2	LILIGASVYSVT-----ESVG-YGDSLWVAIVTATTVGYGDISPHTVLGRIAAVILMFN	201
Lactobacillus	LILIGASVYSVT-----ESVG-YGDSLWVAIVTATTVGYGDISPHTVLGRIAAVILMFN	201
MpMyrna	CTIAGAVAFCLF-----EGSTDGLAALYWAVVSGSSTGYGDIAPKTAAGRITIVYLIV	74

MpPhabba	FTVAGTLAYSLEF-----EHVT-PFESLYWAIIVSGSSTGYGDYSPATVGGRVVTIVYLV	73
SpBillNye	TILVSSVVFSLT-----EGVS-LFDGVYWSVVTMSTTGYGDLSPESIVGKAYTMLLMW	74
Acidobacterium	TLTVSGVLFAYF-----EGKP-LFESFWWACVTGLTIGYGDMPVTVGGKIVAIVLMHV	77
Ptexasensis	SLIFGAISFAVI-----EQKS-LADGIWWATVTSLTIGYGDLPVTPIGRFVGILFGHF	74
Rheinheimera	SLIFGAVSFALL-----EQKS-LADGLWWATVTSLTIGYGDLPVTPAGRIVGILFGHF	74
Ap	SLVIASLLFSLT-----EGVS-YLDSLYWACVTSLTIGYGDYSPHTIAGKILAIVCGHF	73
Ppventosus	SVVLCALLFAWI-----ESKS-VLDSIWWACVTSLTIGYGDIAPVTTAGRALAVVFSHF	74
YSLV	-----SGLRK-----GSTDRFVDLLYFSIVSFSTTGYGDIAPKSTRAKMAVCLFLMF	79
OLPV2	K-----I-YNP-----SWWQHYLDSLYFSVITSCLLYGDIYPITNMSKIIVSLQGFI	133
AaV1	I-----LTDKD-----SFFDRFFLRFYFSFVTSTTIGYGDTPSSISTRTLAMIQACS	149
TeV1	-----KELTTLDFVYYTVTTWTTTGYGDIYPVITVSKMIAVTKMLL	74
PBCV1	-----NPD-----KKASWIDCIYFGVTTHSTVGFGDILPKTTGAKLCTIAHIVT	86
OSyNE5	-----NPD-----KKASFVDCLYFGVTTHSTVGFGDILPKTTGAKLCTIAHIVV	86
MT325	-----DGS-----KEPVSWMDAIYVSAATHTTTGFGDIVADSRAAKFAVTAHMLI	77
ATCV1	-----TDPTWVDCLYFSASTHTTVGYGDLPKSPVAKLTATAHMLI	69
OtV6	-----DKDSGFLDHLFYFAFTVQSTVGFGDIYPISPMAKMIVMVQQSV	77
DishuiLV	-----DRMSSPLDALYLSMTVQSTIGFGDITPKTTTRAKLLVMMQQFV	79
EsV1	-----SSAIDAYYFSAVTSSSVGYGDLLPKTPKAKLLTIAHILA	109
BpV1	-----DDPLDPYYFSLMTMSTVGYGDFSPKTRRAKALVMSHHTV	69
MpV1	-----KSPLDPFYFSFTTMSSVGYGDFSPKTDAAKLVMVMSQHLV	67

* : **

Vp2	GAVNLGTLIK TASNLVKD--KNEVDNRQIYSIITEL--LR--SNQHIEQEELNLTQEV--T	143
Vp3	GIGMFGLFTSVVSGILMEHTDDSI RNRELKEQNARI--EI--ELNEVKKIL-----VSFT	145
Moraxella	GVGIVGFIGAQVADRFLGFADTNVKNRELKRQNEQI--LE--HNKVLEKKLKD KLLS----	148
Vp1	GATLIGLNIGIASAWVTSKFDKSVQNRVLKLQSDTL--IQ--KIDRLETFLNVDQTVYFG	145
VpVH7D	GTSLLGLTIGI INSWVVS KFDKSIQNRVLK SQNDAL--LH--KLDRL ETLH LGIDQEVRFD	130
VpGrn1	GTSLLGLTIGI INSWVVS KFDKSIQNRVLK SQNDAL--LH--KLDRL ETLH LGIEQEVRFD	123
VpValKK3	GTSLLGLTIGI INSWVVS KFDKSIQNRVLK SQNDAL--LH--KLDRL ETLH LGIDQEVRFD	150
VpST2	GTSLLGLTIGI INSWVVS KFDKSIQNRVLK SQNDAL--LH--KLDRL ETLH LGIDQEVRFD	84
Vpphipp2	GASLIGLNIGIANAWITSKFDKSIQNRVLK SQNDAL--LQ--KLDRL ETLH LGIDQEV LFS	150
Vpnt1	GASLIGLNIGIVNGWISSKFDKSIQNRVLK SQNDAL--LQ--KLDRL ETLFLGVNQEV LFD	150
LpPLE2	GI---GLISALTS AVT---AYLSGTNSDSSQSPTDEIKKLYDLKQIGAITQSEYDAK--	252
Lactobacillus	GI---GLISALTS AVT---AYLSGTNSDSSQSPTDEIKKLYDLKQIGAITQSEYDAK--	252
MpMyrna	ML--WVITPVLTARIA---AYMIVNNDAWTDSEQESLKG--DIAAIKRKLGA-----	119
MpPhabba	ML--WVVTPVLTARIA---AYMIVNNDAWTDNEQETLQK--DIADIKRKLGA-----	118

SpBillNye	SV--FFLVPSAVAQII---MKFIHNRNEFTHEEQEKIMQ--QQKRIIEELLEGGKSE---	123
Acidobacterium	VP--LIIIPLIVARLL---STVIEDKNVFSDAEQEALKS--DIAAIKKALKIEKAKE--	127
Ptexasensis	WI--FVVIPMIVANII---MHLVEDKHLFSDEEQRELMQ--RLKRIEARLEQSKD----	122
Rheinheimera	WI--FIVIPMIVANII---MHLVEDKHLFSDEEQRELMQ--RLKRIESRLTQQEQDN--	124
Ap	WI--FFIIPSVISHIL---AALIKNRNEFTHEEQEDIKE--SLSQIKCHLLKNQDDL--	123
Ppventosus	WI--FGVAPLVISNML---NITLEDRLNLFTHREEQEEMKT--LLRKLAEKA-----	117
YSLV	V---NI---AAIYGI---YNALVTSA-----	96
OLPV2	TL--FLILS-----	140
AaV1	TF--YILMA-----	156
TeV1	FL--VILMY-----	81
PBCV1	VF--FIVLTL-----	94
OSyNE5	VF--FIVLTL-----	94
MT325	VF--SIVVLGLKPELI---TNLI-----	95
ATCV1	VF--AIVISGFTFPW-----	82
OtV6	LI--LGILELISESKS---VANVVPTVMKK-----MI-----	104
DishuiLV	VI--VGIVNLLSGGGI---SLKKNNAAMNT-----ISN--TISNVPAPA-----	116
EsV1	MF--FVMLPVVAKALE---K-----	124
BpV1	IL--VELATILSKMTK-----	83
MpV1	MI--GELAKILKIF-----	79
Vp2	QNSHGLDKVFEQNRYVSDNFADGWITRGEDSSGLLIISLEAYCKETGKSTKRWIPTDTLK	203
Vp3	KDKK-----	149
Moraxella	---AMEPF-----SDKKD-----	158
Vp1	PDAHGIDETLKQK-QFDVSQGKAIVTLGRDDGGRFIVATNTQT-DSGRNKLKWISYLKFD	203
VpVH7D	KDAHGIDTIIDQY-FDSNDKADRFVTLGQDDSGRYVVAINQLIVETQHTSMKWHTFINEK	189
VpGrn1	KDAHGIDTIIDQY-FDSNEKADRIVTLGQDDSGRYVVAINQLMVETQHTSMKWHTFINEK	182
VpValKK3	KDAHGIDTIIDQY-FDSNEKADRIVTLGQDDSGRYVVAINQLMVETQHTSMKWHTFINEK	209
VpST2	KDAHGIDTIIDQY-FDSNEKADRFVTLGQDDSGRYVVAINQLMVETQHTSMKWHTFINEK	143
Vpphipp2	KDAHGIDTMIDQY-FDSNDKAERFVTLGQDDSGRYVVAINQQIIETQKTSLKWHTFIKED	209
Vpnt1	KDAHGVDTFIDQY-YDSNDSADRIVTLGQDDSGRYVVAINQQMRDTQKTSMKWHTFILES	209
LpPLE2	--KRQLLRL-----	259
Lactobacillus	--KRQLLRL-----	259
MpMyrna	-----	119
MpPhabba	-----	118
SpBillNye	-----	123

Acidobacterium	--E-----	128
Ptexasensis	-----	122
Rheinheimera	--IRS-----	127
Ap	--K-----	124
Ppventosus	-----	117
YSLV	-----	96
OLPV2	-----	140
AaV1	-----	156
TeV1	-----	81
PBCV1	-----	94
OSyNE5	-----	94
MT325	-----	95
ATCV1	-----	82
OtV6	-----	104
DishuiLV	-----	116
EsV1	-----	124
BpV1	-----	83
MpV1	-----	79

Vp2	DQKYTYNRFINNMNEL---	219
Vp3	-----	149
Moraxella	-----	158
Vp1	DALDFYNDVAVELDAV---	219
VpVH7D	DAVKFFEETSELFHTELL-	207
VpGrn1	DAVKFFEETSELFHTELL-	200
VpValKK3	DAVKFFEETSELFHTELL-	227
VpST2	DAVKFFEETSELFHTELL-	161
Vpphipp2	D-----	210
Vpnt1	DALKFYKDTSELFHTEIFS	228
LpPLE2	-----	259
Lactobacillus	-----	259
MpMyrna	-----	119
MpPhabba	-----	118
SpBillNye	-----	123
Acidobacterium	-----	128

Ptexasensis	-----	122
Rheinheimera	-----	127
Ap	-----	124
Ppventosus	-----	117
YSLV	-----	96
OLPV2	-----	140
AaV1	-----	156
TeV1	-----	81
PBCV1	-----	94
OSyNE5	-----	94
MT325	-----	95
ATCV1	-----	82
OtV6	-----	104
DishuiLV	-----	116
EsV1	-----	124
BpV1	-----	83
MpV1	-----	79

Figure S1. Alignments of virus potassium channels. **A:** Alignment of known alga virus K⁺ channels from the following viruses: *Paramecium bursaria chlorella virus-1* (PBCV-1), *Only Syngen chlorella virus* (OSy-NE5), *Ectocarpus siliculosus virus-1* (EsV-1), *Chlorella Pbi virus MT325* (MT325), *Acanthocystis turfacea virus-1* (ATCV-1), *Bathycoccus sp. RCC1105 virus* (BpV1), *Micromonas sp. RCC1109 virus* (MpV1), *Ostreococcus tauri virus RT-2011* (OtV6), *Dishui lake phycodnavirus 1* (DishuiLV), *Yellowstone Lake phycodnavirus* (YSLV), *Aureococcus anophagefferens virus-1* (AaV1), *Tetraselmis virus-1* (TeV-1), *Organic Lake Phycodnavirus-2* (OLPV2). The conserved filter region is highlighted in yellow. Predicted TMs are underlined. Note that not all TMs were recognized by the algorithm even though the functionality of some of the channels was confirmed in experiments (e.g. K_{MpV1}). **B:** Alignment of all known viral potassium channel and closely related bacterial proteins. The alignment corresponds to the phylogenetic tree in Figure 2. Sequences were abbreviated as follows: *Vibrio* phage phi-pp2 (Vpphipp2), *Vibrio* phage nt-1 (Vpnt1), *Vibrio* phage ValKK3 (VpValKK3), *Vibrio* phage VH7D (VpVH7D), *Vibrio* phage phi-Grn1 (VpGrn1), *Vibrio* phage phi-ST2 (VpST2), *Vibrio* phage 1.081.O._10N.286.52.C2 (Vp1), *Vibrio* phage 1.084.O._10N.261.49.F5 (Vp2), *Vibrio* phage 2.275.O._10N.286.54.E11 (Vp3), *Pararheinheimera texasensis* (Ptexasensis), *Rheinheimera sp. F8* (Rheinheimera), *Acinetobacter* phage (Ap), *Pseudomonas* phage ventosus (Ppventosus), *Mycobacterium* phage Myrna (MpMyrna), *Mycobacterium* phage Phabba (MpPhabba), *Lactobacillus* phage PLE2 (LpPLE2), *Streptomyces* phage BillNye (SpBillNye), *Moraxella* bacterium (Moraxella). In the alignment, identical amino acids are indicated by "*", conserved and semi-conserved amino acids are indicated by ":" and ".", respectively.

Figure S2

A

Vp2	---MLNCITVIDSHGRKEYKTSFL <u>LLVNIIVTVLLNIYIGGLFLWHFE</u> EGLQDSNINSLKE	57
Vp3	MKKYLHWCISTSSKMYKKYGTK <u>YILILTGSITGLNVIIGALFLYL</u> FEHNVDNALINSYSS	60
V1	-----MKFKSYDSFGV <u>VEYNIGMIFAGLMALSFTTIALTA</u> ASLLYRFESGADGSNINSAGD	55
VpVH7D	----- <u>MLMIFGLMIVIALSIALTAANIL</u> FSFEIQNPDPANITTPGD	40
VpValKK3	MKRFFKKHIRKYDEHGVAQYN <u>MLMIFGLMIVIALSIALTAANIL</u> FSFEIQNPDPANIKTPGD	60
VpGrn1	----- <u>MIVIALSIALTAANILFSFEI</u> QNPDPANITTPGD	33
Vphipp2	MKRFFKKHIKKYDEHGVVQYN <u>MLMIFALIVTISMSIALVASNIL</u> FAFELSASNANIKTPGD	60
Vnt1	MKRLKKHIRKYDEHGVVQYN <u>MLLIFALIISISTSIAFIAANFL</u> FYFEVQDPNANIRTYGD	60
	.. :*: ** .: * : .	
V2	AMWAVFMTMTTIGFGDKYPI <u>TVEGYITTGVCFLLGAVNLGTLI</u> KTASNLVKDK--NEVDN	115
V3	ALWMNWMVATTVGFGDYYP ISTGGKIVT <u>GISSAIGIGMFGLFTSVVSGILME</u> HTDDSI RN	120
V1	ALWTIWMSMSTIGFGDHYPVTVGGRV <u>IVGSMFAVGATLIGLNIGIASAW</u> VTSKFDKSVQN	115
VpVH7D	SFWTVWMAMSTIGFGDKYPVTTGGRYV <u>IGCMFVVGTSLLGLTIGIINSWV</u> VSKFDKSIQN	100
VpValKK3	SFWTVWMAMSTIGFGDKYPVTTGGRYVI <u>IGCMFVVGTSLLGLTIGIINSWV</u> VSKFDKSIQN	120
VpGrn1	SFWTVWMAMSTIGFGDKYPVTTGGRYVI <u>IGCMFVVGTSLLGLTIGIINSWV</u> VSKFDKSIQN	93
Vpphipp2	AFWTVWMAMSTIGFGDHYPVTTGGRFVI <u>GSMFVVGASLIGLNIGIANAWI</u> TSKFDKSIQN	120
Vpnt1	AFWTVWMAMSTIGFGDHYPVTEGGRYT <u>IGCMFVVGASLIGLNIGIVNGWI</u> SSKFDKSIQN	120
	* :* :*:***** **: : * * :* :* . : .: .: : *	
V2	RQIYSIITELLRSNQHIEQELNLTQEV--TQNSHGLDKVFEQNRYVSDNFADGWITRGED	173
V3	RELKEQNARIEIELNEVKKIL-----VSFTKDKK-----	149
V1	RVLKLQSDTLIQKIDRLETFLNVDQTVYFGPDAHGIDETLKQK-QFDVSQGKAIVTLGRD	174
VpVH7D	RVLKSQNDALLHKLDRLETHLGIDQEVRFDKDAHGIDTIIIDQY-FDSNDKADRFTVLGQD	159
VpValKK3	RVLKSQNDALLHKLDRLETHLGIDQEVRFDKDAHGIDTIIIDQY-FDSNEKADRIVTLGQD	179
VpGrn1	RVLKSQNDALLHKLDRLETHLGIEQEVRFDKDAHGIDTIIIDQY-FDSNEKADRIVTLGQD	152
Vphipp2	RVLKSQNDALLQKLDRLLETHLGIDQEVLFSDAHGIDTMIDQY-FDSNDKAERFVTGQD	179
Vpnt1	RVLKSQNDALLQKLDRLLETHLGIVNQEVLFDKDAHGVDTFIDQY-YDSNDSADRIVTLGQD	179
	: : . :.: * *	

V2	SSGLLIISLEAYCKETGKSTKRWIPTDTLKDQKYTYNRFINNMNEL---	219
V3	-----	149
V1	DGGRFIVATNTQT-DSGRNKLKWISYLFDDALDFYNDVAVELDAV---	219
VpVH7D	DSGRYVVAINQLIVETQHTSMKWHTFINEKDAVKFFEETSELFHTELL-	207
VpValKK3	DSGRYVVAINQLMVETQHTSMKWHTFINEKDAVKFFEETSELFHTELL-	227
VpGrn1	DSGRYVVAINQLMVETQHTSMKWHTFINEKDAVKFFEETSELFHTELL-	200
Vpphipp2	DSGRYVVAINQQIIETQKTSCLKWHTFIKEDDATKFYKDTSELFHTELF	228
Vpnt1	DSGRYVVAINQQMRDTQKTSCLKWHTFILESALKFYKDTSELFHTEIFS	228

B

Vpphipp2	MKRFK--KHKKYDEHGVVQYN <u>MLMIFAL-IVTISMSIALVASNIL</u> FAFELSASNANIKT	57
Moraxella	MSRFTLSKRIYRTDEFEVRN <u>YNMFLTFVAVVILYLSIAVLAF</u> -LLLWAESGAQGANIET	59
	..*. *: * : *. * :*****: : : * : :*****: * : * : * .*.*****: *	
Vpphipp2	PGDAFWTVWMAMSTIGFGDHYPVTTGGRFVI <u>GSMFVVGASLIGLNIGIANAW</u> ITSKFDS	117
Moraxella	YGDAFWTLQMSASTIGFGDYYPVTL <u>GGRTIVAAMFYIGVGIVGFIGAQ</u> VADRFLGFADTN	119
	*****: *: *****:***** *** :.:*** :*.:***: . . : . *..	
Vpphipp2	IQNRVLKSQNDALLQKLDRLLETHLGIDQEVLFSDKDAHGIDTMIDQYFDSNDKAERFVTLG	177
Moraxella	VKNRELKQNEQILEHNKVLEKKLDKL-----LSAMEPFSDKKD-----	158
	:.*** *:.*.*: :*.: . **.*.*. : : : *.*.*	
Vpphipp2	QDDSGRYVVAINQQIIETQKTSCLKWHTFIKEDDATKFYKDTSELFHTELF	228
Moraxella	-----	158

Figure S2. Putative potassium channels from vibrio phage. **A:** Alignment of vibrio phage potassium channel sequences. The conserved signature motif (T/S)T(I/V)GFGD is highlighted in yellow. The TM domains as predicted by TMHMM are underlined. **B:** Alignment of the vibrio phage potassium channel versus the most similar protein from a bacterium of the Moraxellaceae family. Viruses: Vibrio phage phi-pp2 (Vpphipp2), Vibrio phage nt-1 (Vpnt1), Vibrio phage ValKK3 (VpValKK3), Vibrio phage VH7D (VpVH7D), Vibrio phage phi-Grn1 (VpGrn1), Vibrio phage phi-ST2 (VpST2), Vibrio phage 1.081.O_10N.286.52.C2 (Vp1), Vibrio phage 1.084.O_10N.261.49.F5 (Vp2), and Vibrio phage 2.275.O_10N.286.54.E11 (Vp3). In the alignment, identical amino acids are indicated by "*", conserved and semi-conserved amino acids are indicated by ":" and ".", respectively.

A

AngHV-1	-----
<i>Pundamilia nyererei</i>	MFFIALLWSLSLTAVGQQEDNEWLDPYDMLNYDASTKTMRKPTPEASYDNVGTKRREYNQ
AngHV-1	-----
<i>Pundamilia nyererei</i>	DSSQTELTSCKEQVEDLQKQNEQKKTIKLISQQPTCSPVFKRFLSRLLKEIQRVGVPSD
AngHV-1	-----MKMNR-ILVLLLLFWGTRAEDVTSYTAKLGLVKGCKCRPEEVKEVKKVWR
<i>Pundamilia nyererei</i>	STDVFFDAKVKLSKQAMTEIQTLLEGEDRWRTGALDNAISQIL-VDLKPH--DYEAWKWR : * : : : : . * . : : : . : * *
AngHV-1	FEDTF <u>GVEIDTVLQICSCVLVIVMIVC</u> GELWSTVSWFLQLER <u>RAFIICLFVSFIWNWIYLY</u>
<i>Pundamilia nyererei</i>	FEDTFGVELDTVLKI <u>GSFVLIIVAIISTELWTTISWFFVQ</u> FRRL <u>LEAVCFFVSIWNWFYLY</u> ***** : ***** : * * ** : ** * : . *** : * : * : * : * : * * : * : * : * : *
AngHV-1	<u>KAAY</u> AEHQANMIKLDGVAKRCA--ADFMSTLKDWFIRSTWTTLQDDPCKKYHEVLIINPV
<i>Pundamilia nyererei</i>	<u>KIAFA</u> AEHQNNIVKMEGFNAKCTGVKKIDWSDSLKEWFIRSTWTTLQDDPCKRYEVLNPNPI * * : ***** * : * : * : . : * : . * : . : ** : ***** : * : * : * : * :
AngHV-1	LLV <u>PPTKAISVT</u> FVTFVTEPLKHFGHGIGEFIKALLKDLPTTLQVPVWGDHFSSRCRVYV
<i>Pundamilia nyererei</i>	LLV <u>PPTKAISVT</u> ITTFITEPLKHFGQGISSEFLRALLKDL <u>PVTLQIPVLLTIVIAVVVFMY</u> ***** : * : ***** : * . * : : ***** : * : * : * : . : .
AngHV-1	---RNLFCGGWPLISLRTTHTTHTTHE-----DR-----RWKHFWK-----CGLDFR
<i>Pundamilia nyererei</i>	<u>GSVQAA</u> FQHGIM-APLRRPRRDPPELEQPPQAQPRRLRIEDRNHFAGGDAPQQQHALRYR : * * ** : * : : * * . * :
AngHV-1	GYLN-----RVA-----EFPAARE-----
<i>Pundamilia nyererei</i>	ADEARLNRNDLHQRRPNRQRVETLGTAEDEPDRAKEVPEADQNLSVEPDSENQRGAEE * * . * ***

AngHV-1 -----
Pundamilia nyererei RPPAAKDNSVGENKAKSEPKAARSDSSESKNKTSKGNENLSQDQPDRDVALLRPELPDST

B
AngHV-1 -----
Homo sapiens MLCSLLLCECLLLVAGYAHDDDWIDPTDMLNYDAASGTMRKSQAKYGISGEKDVSPDLSC

AngHV-1 -----MKMNRILVLLL-LFWGTRAEDV-----TSYTAKLGLVKGCKCR
Homo sapiens ADEISECYHKLDSTLYKIDECEKKKREDYESQSNPVFRRYLNKILIEAGKLGLFHD----
*:: : : . * :: : : *****::

AngHV-1 PEEVKEVKKVWRFEDTFGVEIDTVLQICSCVLVIVMIVCGELWSTVSWFLQLERAFIICL
Homo sapiens ----FETWKWRFEDSFGVDPYNVLMVLLCLLCIVVLVATELWTYVRWYTQLRRVLIISF
. *****:***: . ** : *: * **::*. ***: * *: **. *:***:.

AngHV-1 FVSFIWNWIYLYKAAYAEHQANMIKLDGVAKRCAN-ADFMSTLKDWFIRSTWTQLQDDPCKK
Homo sapiens LFSLGWNWMYLYKLAFAQHQAEVAKMEPLNNVCAKKMDWTGSIWEWFRSSWTYKDDPCQK
:. *: ***:***** *:***:***: :*: : : *: *: .: : *****:*** :*****:*

AngHV-1 YHEVLIINPVLIVPPTKAISVTFVTFVTEPLKHFGHGIGEFIKALLKDLPTLQVPVWGD
Homo sapiens YYELLVNPIWLVPPPTKALAVTFTTFVTEPLKHIGKGTGEFIKALMKEIPALLHLPVLI
*:***:***: *****:***.*****:***: *****:***: * *:***

AngHV-1 HFSSRCRVYVRNLF CGGW--PLISLRTHHTH-----TTHEDRRWKH-----FWK
Homo sapiens MALA-----ILSFCYGAGKSVHVL RHIGGPESEPPQALRPRDRRRQEEIDYRPDGGAGD
: ** * : ** . *** :.

AngHV-1 CGLDFRGYLN RVAEFPAARE-----
Homo sapiens ADFHYRGQMGPTEQGPYAKTYEGRREILRERDVDLRFQTGNKSPEVLRAFDVPDAEAREH
...:*** :. . : * *:

AngHV-1	-----
<i>Homo sapiens</i>	PTVVP SHKSPVLDTKPKETGGILGEGTPKESSTESSQSAKPVSGQDTSGNTEGSPAAEKA

AngHV-1	-----
<i>Homo sapiens</i>	QLKSEAAGSPDQGSTYSPARGVAGPRGQDPVSSPCG

Figure S3. Putative CLIC-like chloride channels from AngHV-1. Alignments of the CLIC-like chloride channel from Anguillid herpesvirus-1 (AngHV-1) versus the chloride channel from the fish *Pundamilia nyererei* (**A**) versus the human homolog (**B**). Predicted TM domains are underlined; conserved regions are shown in yellow. In the alignment, identical amino acids are indicated by "*", conserved and semi-conserved amino acids are indicated by ":" and ".", respectively.

A

[illegible]

B

PBCV-1	-----MEDID-----NIYDCTPSTLTNL-----	18
<i>Cricetulus griseus</i>	MCPETEEQEDDHLSIVTLEEAPFVIVESVDPLSGTCMRNTVPCQKRIISENKTDEEPGYI *:.* * * :::	60
PBCV-1	TAC-----FI-----PSSEAWCNIGDTCVSNIRYDPKCN	48
<i>Cricetulus griseus</i>	KKCKGFCIDILKKISKSVKFTYDLYLVTNGKHGKKINGTWNGMIGEV---VMKRAPLCY * :: . :* .:. :: * *	117
PBCV-1	FFGY--ADQYLTHIIPRTFKCFNVIRQCVTSYTD AERQGC DILYGE PNPLAYTN-KSNYW	105
<i>Cricetulus griseus</i>	NVLTVAS YCFLQVVMKRAP <u>ACYNILTVASYCFLQVVM</u> KRAYMAVG---SLTINEERSEVV : :* :: *: *:*: . .: .: : .: * *: .: *::	174
PBCV-1	AESV-LYDV DSPAILFNPD KSYIPWDF LKPF <u>SWELWAMLIIVMCIITPLVTS</u> LI EYDTGE	164
<i>Cricetulus griseus</i>	DFSVPFIETGISVMVSRNGTVSPSAFLEPFSAD <u>VWVMFVMLLIVSAVAVFVFEYF</u> SPV ** : : . : : * **:*:* : *.*: .: *: .: *: :	234
PBCV-1	TVVGNFIKYL PDSIH--AHLGIDLISSESMT---NNTSYTLA <u>VFINIFAIIMLALYSSNL</u>	219
<i>Cricetulus griseus</i>	G---YNRCLADG <u>RAIWLLWGLVFNNSVPVQ</u> NPKGTTSKIM <u>MVSVWAFFAVIFLAS</u> YTANL : : * * . *: : .* : ..** :. . : *: *: * *: *: *	290
PBCV-1	<u>VAYVL</u> YKNYSLSSL-----PYSYKPTWDI-----FIDNTISNSFSELPNDLLYIDSS	266
<i>Cricetulus griseus</i>	<u>AAF</u> MIQE EYVDQVSGLSDKKRPND FSP PFRFGTVPNGSTERNIRN NYAEMHAYMGKFNQR .*: .: :* . * ...* : : ...* *.: *: : .: :	350
PBCV-1	KIPE---IIDSSEFDAIIGQRTFLQIF-----KDCSSELTIIHGPGI	305
<i>Cricetulus griseus</i>	GVDDALLSLKTGKLDAFIYDAAVLNYMAGRDEGCKLVTIGSGKVFASTGYGIAIQKDSGW : : .: .: *: * : .: *: : . . : *: .. *	410
PBCV-1	YKYVNLATKAGMLNIRRLIAQIQMASVNRQFTSPTCTEQ-----PQSINLNSMYG <u>VFLLF</u>	360
<i>Cricetulus griseus</i>	KRQVD-----LAILQLFGDGEMEELEALWLTGICHNEKNEVMSSQLDIDNMA <u>GVFYML</u> *: * * *: .: :* .: : : * : .: .: * *** : :	463

PBCV-1	<u>FIPMTLLFLITIIRF</u> ---- <u>TLKRKF</u> ----SADNSMVI PKTHS-----	394
<i>Cricetulus griseus</i>	<u>GAAMALSLITFICEHLFY</u> WQFRHCFMGVCSGKPGMVFSISRGIYSCIHGVAIEERQSVMN *:* :: * .. ::: * *.. .** : ::.	523
PBCV-1	-PD-----DLEKY-EAEGSSESVV-----	411
<i>Cricetulus griseus</i>	SPTATMNNTHSNILRLLRTAKNMANLSGVNGSPQSALDFIRRESSVYDISEHRRSFTHSD * :: : .:** :*.:	583
PBCV-1	-----	411
<i>Cricetulus griseus</i>	CKSYNNPPCEENLFSDYISEVERTFGNLQLKDSNVYQDHYHHHHRPHSIGSTSSIDGLYD	643
PBCV-1	-----	411
<i>Cricetulus griseus</i>	CDNPPFTTQPRSISKKPLDIGLPSSKHSQLSDLYGKFSFKSDRYSGHDDLIRSDVSDIST	703
PBCV-1	-----	411
<i>Cricetulus griseus</i>	HTVTYGNIEGNAAKRRKQQYKDSLKKRPASAKSRREFDEIELAYRRRPPRSPDHKRYFRD	763
PBCV-1	-----	411
<i>Cricetulus griseus</i>	KEGLRDFYLDQFRTKENS PHWEHVDLTDIYKERSDDFKRDSVSGGGPCTNRSHLKHGSGD	823
PBCV-1	-----	411
<i>Cricetulus griseus</i>	KHGVVGGVPAPWEKNLTNVDWEDRSGGNFCRSCPSKLHNYSSTVAGQNSGRQACIRCEAC	883
PBCV-1	-----	411
<i>Cricetulus griseus</i>	KKAGNLYDISEDNSLQELDQPAAPVAVTSNASTTKYPQSPTNSKAQKKNRNKLRRQHSYD	943

PBCV-1	-----	411
<i>Cricetulus griseus</i>	TFVDLQKEEAALAPRSVSLKDKGRFLDGSPYAHMFEMPAGESSFANNKSSVPTAGHHNN	1003
PBCV-1	-----	411
<i>Cricetulus griseus</i>	PGGGYMLSKSLYPDRVTONPFIPTFGDDQCLLHGSKSYFFRQPTVAGASKTRPDFRALVT	1063
PBCV-1	-----	411
<i>Cricetulus griseus</i>	NKPVVSALHGAVPGRFQKDICIGNQSNPCVPNNKNPRAFNGSSNGHVYEKLSSIESDV	1121

Figure S4. Putative glutamate receptor-like channels from Phycodnaviridae. **A:** Alignment of the putative glutamate receptors-like channels from viruses PBCV-1 and OSy-NE5. **B:** Alignment of the putative glutamate receptor from chlorovirus PBCV-1 versus the homologous protein from *Cricetulus griseus* (chinese hamster). Predicted TM domains are underlined. In the alignment, identical amino acids are indicated by "*", conserved and semi-conserved amino acids are indicated by ":" and ".", respectively.

Figure S5

AaV	---MRET---FTDLYNSPN <u>FIYIR</u> ----- <u>YISAIIVLLTFPISSIL</u> TQKLQDTD	44
TeV1	MGAKKPKYKNFVHWLDEKSVISVAVAFSVSMVNRFMQTLIDNLVIAIISKTTGAE----	56
CroV	---MSQIYVDFKDFLKDND <u>IIVTIIATIVSSNISMLS</u> SKSFMKNLVMPIINIDLNNDGIPD	57
	* . . . * : :: *. : *	
AaV	YKNEFDKFFQT <u>GLSIL</u> ---- <u>LIRFATMFVLILIALKVA</u> NVNNLVIASYAGILL <u>IAVPAA</u>	100
TeV1	---DLEWEI-TKELSIKYGKI <u>IVESINLMIILYLSYLI</u> IK-----	92
CroV	RQNLDNWVIHMKGVLD <u>LKIGQFLLTFIEFFLILIIY</u> LINK-----	97
	: . :: :: : : :	
AaV	<u>MSTQISNYISGLLLIA</u> FDRITLNDYIIIDDFEGRIKKLNLFSIEVKDEFTHKTRFIPNAD	160
TeV1	-----	92
CroV	-----	97
AaV	FWTKSFINVSKNTTAVAKIEITVASDNDFDEIEDKILNIIDNNFEGIDASKTRIRYDHSI	220
TeV1	-----	92
CroV	-----	97
AaV	WGVKLSIAVEVPSKKYFEYKMLLLRVIRKKISEDEDINFVM	261
TeV1	-----ASNRYLGWT-----	101
CroV	-----LSKI-----	101
	* :	

Figure S5. Putative mechanosensitive-like channels from large DNA viruses. Alignment of putative mechanosensitive ion channels from Aureococcus anophagefferens virus (AaV), Tetraselmis virus-1 (TeV1), and Cafeteria roenbergensis virus (CroV). Predicted TM domains are underlined. In the alignment, identical amino acids are indicated by "*", conserved and semi-conserved amino acids are indicated by ":" and ".", respectively.

Figure S6

KNV1	MLEVLFGISNTNFSNNEVKRTKHSIFWIPLLLTIYKY <u>FFWNYENIYFLFLSLFQLSTLYFL</u>	60
CTV1	----MEGDNSI--YLTRFKFSGLLILYVCH <u>IIYGYINYFFEDFINIFCLLISFF</u> QIYDY---	51
	: ** : : : : * :*: :*: *:*:*:	
KNV1	PKEWSPTGPy <u>STAIPLGICILAEIITHMITWY</u> NDWITDYKENNKEYECLDHSYQLIKKN	120
CTV1	----R---DFRSFIPLSIFS--TLY---SVYYTYTVSKLI---REQNSI-NSEMFMRKPI	95
	: : ***.* : :*. :. :* :. :*	
KNV1	RNIYPGDIIHLEKEDICPIDGILIDTTNNEKYSKISLALLTGESNINYVIKPAKLFLQD	180
CTV1	NQIKRGDILELSYQDKIPADILILTDDFHVSTNELE---LSGE---NIVLNKKALF--ED	147
	.* ***:.* :* * * : : : . :. :*: * *: : ** :*	
KNV1	YKDYKIN-----ISNYHQNNFNIEGKLLNGKEEHNIQGENFVVGSSIISDDIYLWVIG	235
CTV1	YDNNQLLKSINICINQKKNNGFIEYDNKK-----YKYDENNIVFRGTKMLDGKLKGLVVE	201
	*. : : *.: :*. * : :.* : : :*: * *: : . : : *	
KNV1	CGRDKKSYLKKS-VKNDRKKNRIDTFVGNyMINVNAILLILLI-- <u>LITTTIKLVNSFSFG</u>	292
CTV1	IGNDCMIYNIDNRVLKD--KTWLYKKVNN-- <u>ITFNNLYYLLIISAFIAGAL</u> K--YVYPQR	255
	. * .. * :* *. : . *. * *. : :*: * *: :*: :*	
KNV1	NIIFYM <u>IQNWILFNGIMPFSVKIFLL</u> ----- <u>LARN</u> LQTGIHNYHKSITINNSLLIDDIG	347
CTV1	KF <u>IFLVKTTVLLLNTVVPLSLQSFY</u> NACTWILSRKIQTEN-----NVTINSHGINCFEN	309
	:*: : . :*: * :*:*: : * *:*:*: .:***. :	
KNV1	KINKILTDKTGTLTKNELEFSKLLESW-KNDIIDVET-----YQQNYDIDLNFHKCIGL	401
CTV1	NPKYVVTDKTGTITKNQLKLIQVINISKNKNIIEKNDITNSSNINFFDI---MSCTLI	365
	: : :*:****:****: : : : *:*: : :*: * *	
KNV1	CIHQTEENYSTPED-KTLRYRYQYLNNRINQTSQI-ITLTINNNNYDYKY-----I	450
CTV1	NTHSTTKQLLKNDEMEYLLLEWCCKNNKIKIMNNNYNEINKNLSFYKYKFNNKEEKINKI	425
	. : : . : : * .: *:*: : : . * . *.**:	
KNV1	EIGGLDFTFERRLSSKIVKDISTDSYIIYCKGAMDVIGKKIKTDYKTE-LKRLDQMVSQK	509

CTV1	IYKGFYKLGIK---YCITEKDDIYTLNIQGTPEMINLYTNKNLINEGEKLLDEVSNNS	481
	::*:* : . * * : :* : :*. :. : . * * * : : .	
KNV1	YPELRLACAFRKIDKNELDMALHESTNKSQIVTLLENDLHLLGIIGIKDNLQEGVKETI	569
CTV1	Y---RRIICYAKKNITSPTYLDIKNNCN---IN-EYLKDFEYANIYVFEDQVMDDLANHF	534
	* * : * :* . : : : : * * :* : . * :* : : : : :	
KNV1	EQFNHYGLFSCLLTGDRKITALAIAKEAGIIDHENTICDFTQEMLDKDITNLHKK-TILF	628
CTV1	DKLMKNGKHITILTGDRHSSSVGVKILGMCDDMVLID-KK-----EDMNNIDKTVSLSV	588
	: : : * . :***** : : : . * * : * . * . :* : . * . : : .	
KNV1	GGALFDIVSQNVKYESFYDKLALSRNFIGYNLIPEHKKKLTNILE--NKNIKTLTVGDG	686
CTV1	NGKIFNELIREEK---FKNIILNTNKIIVYRATPEIKEKYIQYLFKFADEKNQVMIGDG	644
	. * :* : : : * * : : : : * * . * * * : * : : : : : * * *	
KNV1	FNDIGMFHTSSMSIAIKNGFVESN-ADFTIKEFKQLKHLFD---MSLKYYSKNAQLVNL	742
CTV1	SNDISAIMRADVGVAVKGESNQIQNISDVVIDSWCKIPELLKNFSYKKEIIIEHNVKWVLT	704
	***. : : : : :* :* : . * :* . * . : : . * : . : : * : *	
KNV1	<u>TFLRASAVIMSIMTYSLIYY</u> NQ---TTSLFNG <u>FVIQAFNFAWTILGVGYITL</u> KQRNLPHQ	799
CTV1	<u>KHIMTATILMTMLLI</u> --SNYKEIRDPTNPFH <u>MLILNCLLFVCMSEFNNNLRI</u> INNPIIN	762
	. : : : : :* : : * : : * . * : : : : : * . : . * : * * :	
KNV1	DQDYYQNKHLVLTNYKN <u>TSIWNGAGIIFGIVLTLMNYYWF</u> RESKY <u>YFGDICGLMLVMILNG</u>	859
CTV1	EKDYKTHI-----HKGIIV <u>GMIIGTIVFTIFSV</u> ----- <u>NIGIIIAI</u> -----	798
	: : * * : * * . * : : : : : * : : : : :	
KNV1	<u>KLILNNKLDLWGIGLSLMGIVNFMGYMMYMG</u> SLYDVIIIT <u>LLTTSKYYWLGVF</u> GMYFGINL	919
CTV1	-----I-----AKFIYLSLIL-----	809
	* . :* : : :	
KNV1	FIF 922	
CTV1	--- 809	

Figure S6. Giant virus ATPases. Alignment of Klosneuvirus-1 ATPase vs. Catovirus-1 ATPase. Predicted TMs are underlined. In the alignment, identical amino acids are indicated by "*", conserved and semi-conserved amino acids are indicated by ":" and ".", respectively.

[illegible]

	:::***::**:	**:	:	***	:	.	.	:	::*.....	:	::						
ACEV	D--LNSVIQLKNVSKIYNKKIKVIDDISFDIKKNIKISILLGNNGAGKSTLMSTMIMRMTSI	518															
<i>Onthophagus taurus</i>	DPNDEVLLLEIKNLTKKYNDL-VAVNKLNMKIYKDNLTVILGHNGAGKTTTLSILAGLEKE	534															
	* : ::::**:* **.	.::::..*	* :::::***:*****:* :	: .													
ACEV	TSGHITG-----IERNKIAYCPQDNLLYKELTVIQHLILCGLLHGLNKNESKQKGEY	570															
<i>Onthophagus taurus</i>	TSGELTIAEIEENVNLKDRQLVSICPQENMLFTELTVEEHLVLFGKLKGLSDEDIKQNVKN	594															
	.:*	:	**:	::	***::.*****	::**:* *	*:**.*:::	**:	:								
ACEV	LLKNVLNMIDKKNLYPNELSGGMKRKLSLGIALMTPDVLILDEPTSSIDIEGRQEIYNL	630															
<i>Onthophagus taurus</i>	LLENKLNLANKKDDLVKNLSGGMKRKLSIGIAIMGTPKVVLDEPTAGIDPEGREIWDL	654															
	:* **:	:::	:	*****:***:*	.*.**:*****:	.** ***:***::~*											
ACEV	I LSLNK--TVLISTHLL EEA EYLADYII I INSGKLLYYGNIIDLKNKYDIGYICTIKNKS	688															
<i>Onthophagus taurus</i>	ILECKKDSNIILSTHLMEEAEELADRVAAILGNGLTERYGKPMDLKQKLGVGYRIQLFYED	714															
	.	:*	.:::**:*****	***	:	*:..*.*	**:	:***:*	.:**	:	::						
ACEV	IDENKI-KEIV----GHIKIKDDNIICNI--DKTNKNKVPLLLKYLD----EL-NIEYL	735															
<i>Onthophagus taurus</i>	PTKEKVIKTFVEENIDAKINPDNNKLVLEFCITPEKKCMIPKFKEVLNSRKGELS IKDYK	774															
	::*:	*	:	*	.:::		::	:	*	:	*	:	*	:	**	:	*
ACEV	FSSISLNDLYIKVQNKE---II-NNNNQYYINH I --NQSLRIKINY YFNK-----RKLF	783															
<i>Onthophagus taurus</i>	IRSVTLEDVFLRSLENHDREIRLTINRQESINSQGTHKNLTCFPNNLWHKFVLIAEKMK	834															
	:	*	::*:*:*:::	::.	*	.	*.*	**	::.*	*	::*	:	*				
ACEV	FIRKIK-QYLYIYIISLCIIGLSIYLSNFGYVNLIDDGNKIKLDDLVDVYGHTDIYYSLVGQ	842															
<i>Onthophagus taurus</i>	ILR <u>AMPIPWITMIALFYSLFALS FAM</u> NDSGHKHTDRDGKTLQLNLDSYGCTKV FYEMKND	894															
	::* :	:	:	:	**:	:::	*:	:	**:::***:**	** *	.::*:.	:	:				
ACEV	DS-----INIITHTSNSLIKVDNVNKS IIDVGINNIVHYIYKLIIAFEFNFNTN--NSIN	894															
<i>Onthophagus taurus</i>	DANLERIFVDLIDSTISNSHKVDDISEAVISVGENNIVKYRQKLIVGAKMNFDESSREIT	954															
	*	:	:	::* *	.	***:.....*	** ******	***:	:	**	:	:	*	:	*		

ACEV	IMYSNKAYHSMPIAINVFSNTLLNYYTNDNYSIYLTHTPLHSNNKQIEKIQIGEYSNL FI	954
<i>Onthophagus taurus</i>	VFYGSQPIHGAPISFNLLSNVLAKYLVGENHEIIASHTPLRSVKSTTRQTNVYVAD YIIS	1014
	:.*.: * . **::*:**.* :* ...*:.* :****:* .. .: :. . :.	
ACEV	WSILLPIGPLILISTSLLLPA IDYVKNIKTLERLCNIKAYQ YWLFNYVFDITCYIASISI	1014
<i>Onthophagus taurus</i>	WMILLSNACLFVIMFSAL PTLEKNSFIKTLRSRIYNLNSICYWLH NYITDVIIYLVMIIP	1074
	* *** . *: : **::: . ****.*: *::: ***.**: *: *:. *	
ACEV	ILII IYIMPIH--YLDVYTI IQLGGLFILYGVIFIPQSYIFTY MSTVENT TYFNFLIV-H	1070
<i>Onthophagus taurus</i>	PIAVLYVV SKLDWALLQID GYCYLVIILIWYGITMIPHTYLS SFYSSVSNA AIALLLIPN	1134
	: :*: : **:	
ACEV	IFCSPLISVILII -----IDKEY IIILILLSPHTSLCYLLASISI IKLIRYHNWNINKSYE	1125
<i>Onthophagus taurus</i>	MLSSIPVGVIL SLQSSGSVAPQ IFLYLFALLDPHIILTYTLSIFC DKMIKNHNWDMKTPS	1194
	:.* :.*** : : : : * : **.* * * * : . *: : ***::: .	
ACEV	HKKAICSITDHVCCNLNSLECNDFKIFIDYKL IFCS-IISLCISIFILLSMNYITRNISK	1184
<i>Onthophagus taurus</i>	QKEYICNETPLPCCDPDSVECA AEDRAYIQYPIYLMISVVSALIVMFIIV --- WLDK ----	1247
	:* : * . * ** : :*: : : : * : : : * * :*: : : :	
ACEV	LLLYKQFNKTNTQSTSNNNILYINNVSKEYWKWPCNVLKVINDITIVINNNICFGLL GTN	1244
<i>Onthophagus taurus</i>	EKSYKKNHEEGVTIG--AKEVQKHYNIRTLRSFKKTTVKAVDDLSTVSKGECYGLLGVN	1305
	** : : . : : : : . : * :*: :*: :*: :* :*	
ACEV	GAGKT TMFKMMTNEIEPTIGKIK--INGTIGYCPQQDSLIDEFTGKELLYLYGKLRGITN	1302
<i>Onthophagus taurus</i>	GAGKSTSFKILTQVRPDKGEIFRRQNSLIGYCPQEHALLNFFTGRELLKYFGKLRNPSI	1365
	****.* **:*:*:*. *:* *. *****:*: : ***:*** :****. :	
ACEV	INHVVNKLKIKFDLCNIANQICGTYSGGNKRKLSTCLSLIGYPNCVLLDEPTNGIDPITR	1362
<i>Onthophagus taurus</i>	QEDEIDDLLNKCGLNEYSNKPCGTYSGGNKRKLNTCIALIGHPDIIITLDEPTTGVDPQNR	1425
	:. :*: * . * : * : *****.***:***: : *****.*:* *	

ACEV	NELWDVIEY--IKKKSIVILSSHNVDCEKLC DNLCILHKGIVKEQ--TSIKKLKNKYCI	1418
<i>Onthophagus taurus</i>	RKIKELINETKLNKKS AII FTSHSMDECELLCDKLSIMKAGKLET DANLSVP ELKEKYNI	1485
	.:: :*: :*: :*: :*: :*: :*: :*: :*: :*: :*	
ACEV	GHILKLKFDNKH I KI-EHQLHSNFDTKN I KILSNHDYMITVRILNYNWITIFDI I ERIK	1477
<i>Onthophagus taurus</i>	GHIIQMVKVKS PQQIDTILEALRESFNNV I IEKIAARNNLLTVSIKNSNWGSIISGMESMK	1545
	:. . :*: . . *:.*: . *: : : : :*: * * ** :*. :* :*	
ACEV	NDTENNIEDYWIMESTLDEALIEIANNKL	1506
<i>Onthophagus taurus</i>	TH-RNEIVDYMVKES SLEEVFLK VAKG--	1571
	. . .*: * ** : ***:*. :*:*:*	

Figure S7. Comparison of the ABC-transporter protein from virus ACEV and the most similar protein from beetles. Alignment of insectvirus *Anomala cuprea* entomopoxvirus (ACEV) versus the homologous protein from the beetle *Onthophagus taurus*. The highly conserved Walker A motif is shown in grey. Predicted TM domains are underlined. In the alignment, identical amino acids are indicated by "*", conserved and semi-conserved amino acids are indicated by ":" and ".", respectively.

Figure S8

Fr483	MSETGV-----VTIEQEEKILELGRKNIRGWSL <u>VILSLASLGVFGDIGTSPLYVL</u> PA	53
<i>Micractinium conductrix</i>	MPGVSVSALWARDADLSAKIEAQEHRRNASGLRL <u>LALAVSTLGVVYGDIGTSPLYVY</u> GS	60
	* ..* . : : * *:* * *:* *:::*****:*****:	
Fr483	IFGELRHQPTEN <u>FILGVFSTIFWTITLMVLVKYVW</u> FTLAIDDHGEGGVFALYSIIRRAIT	113
<i>Micractinium conductrix</i>	VFPDGAP-ADANR <u>VLGVASTIFWTITSIVLVKYVVF</u> TMQADDNGEGGIFALYALICRSCN	119
	:* : * :*** ***** :***** **: **:*****:*****:* * : .	
Fr483	SKPSDFGV-----DTQEEKIPSKTKDFLENNKWARK <u>VIMGIVITCASLTMAD</u>	160
<i>Micractinium conductrix</i>	IRSGTRMTEADLTLSQYQGGQTRGRSRVAARLRGAQERSATLQTL <u>LLVVVLLASNMIISD</u>	179
	: . . : : : : *.. :::: *: : : : : *	
Fr483	<u>GILTPSISVISATEGIQFHTGISHDTVIFITIGILVGLFSIQFL</u> GTGKVG <u>VIFGPTMLVW</u>	220
<i>Micractinium conductrix</i>	<u>GVLTPAISVVSIAIEGIQFQTGISQGAVTGISVGILVALFALQSV</u> GTQQRVS <u>FLFAPIMVLW</u>	239
	*:***:***:* *****:*****:::* *:*****.*:::* :** :*...*.* *::*	
Fr483	<u>FVENLSVGVYNVT</u> KM--PGVFRAFSPHYMYFWEEF <u>GSWEAFKLLGEVFLAITGVEALYA</u>	278
<i>Micractinium conductrix</i>	<u>FICNATLGIYNIC</u> RFGGPSIFRALSPHYMYFWSGDA-HAAWRALGNIMLCVTGAELYA	298
	*: * :*:***: : *.:***:*****. . *: : **::*:*.*****	
Fr483	DMGHLNAMSIR <u>ISFSAIVPSLVMNVLGQTAVVL</u> LDYNTSSSLYWSSIPAKLAW <u>WPSLAIA</u>	338
<i>Micractinium conductrix</i>	DMGHFNAQSIR <u>VSFLAVVFPSLTTLTYLGQTAMILQ</u> EPAKAAAFWESVPTPVLWP <u>VVLA</u>	358
	****:* * :*: * *:*:***.:.*****:* : : : : : *:*:*: : ** : : *	
Fr483	<u>ASAAVIASQALITGTF</u> TIVQQAMHANVFPRVAI <u>FQTNKKHAGQIYIPVVNFALLVGSISV</u>	398
<i>Micractinium conductrix</i>	<u>TGAIIASQALITGAFSIV</u> QQAMAMNAFPRVTLRHTSKHN <u>NIGQVYIPEINWLLMVGALIV</u>	418
	:.**:*****:*:***** *.*****: :*.*: : **:* * : *:**: : *	
Fr483	<u>VLIFQSSSKIVSAYGFAVSIVVVLTHIFFCIVL</u> LHIQGR-NKLFSEVFSFFGVISIAFAA	457
<i>Micractinium conductrix</i>	<u>VVVFKTSASIGNAYGLAVITVMLLDTSLFALVAL</u> TAWEWHV <u>AAVGAFWLFFTFVTGTFLS</u>	478
	.::*:*. * ***** *.:* :*:* : : : * ** : : : *	

Fr483		SLTIKIPKGAWFSAAGSALIFVSLVWHRGHRMKVRYIKINRLSARQVFSPSNNS----	513
Micractinium conductrix		SNMSKIPEGAWFSLALSAVLSCITYLWHWGQRKKLDYVRDNKILLRELYEPDPSQADTAG	538
		* ***:***** *:.:.* :: : ** *: * *: *:: *: : *:::: .::	
Fr483		-----KNIVFYNE	521
Micractinium conductrix		GSGAAAAAHGLLRPSGVSLARSSDSGRGAEEVQPLQLQLVGSCLPVARVPGIGIYYNE	598
		: : ***	
Fr483		LTDGIVPAYNQLENLITISGTNNIVLSVRKMTIPRVREDQRFLI--TGYDGVYHVVARYG	579
Micractinium conductrix		LLLGVPVPLERFMSLVPALHEVVIFLTVRVVPVPCVLPQERLLVRQLRFGAMYHVVARYG	658
		* *: *. ::: .*: *.*:** : :* * ::*:*: :..:*****	
Fr483		YAEI IDHGNCFAKLCQAVNAESSDVVFVMGRTKLLTTNTSFYNKA--VIAMYSLLVKLS	637
Micractinium conductrix		YMDAIDHGEEFVDSILQEIH EYLHPATGI---ADLSA-EAAAANA AHGKLASEDLEKGLD	714
		* : ****: *. .: * :: .. : :.* : ::: * * :* . * *	
Fr483		SWTTDTFNTPTSKLIIFEASYEI-----	660
Micractinium conductrix		HHGDNEGSVHRGAIVRVDAAESLTSATGAQVSSSLALQLLSLR RFSSAPQPRSTGSAGDS	774
		: .. . : : .:*: .:	
Fr483		-----	660
Micractinium conductrix		GMQASGATQRQASGAAGPSLARASTSTLAVPLVGDEGSMHSGKGEAADDGPSPWQMPSQ	834
Fr483		-----	660
Micractinium conductrix		VRRVRTHLLGLPEGAPAALDDGLHSLPLPESTQRPPLLPLL RGDSTKSLPLPPAGGSARR	894
Fr483		-----	660
Micractinium conductrix		TPLYRVQRAMSAASGAQEQQGGGQQAQQAQAQQPQPSP LATPTSTLTPAARARLGQQLWQ	954

Fr483	-----	660
<i>Micractinium conductrix</i>	RLQMGRLLHRTSAASAMPTLAEGEQAQPADSDARSSLDGRVAATVRTEDILGSAAPEGEE	1014
Fr483	-----	660
<i>Micractinium conductrix</i>	ALDTDAARRRLFALQGHAGDAGTPLEDGLAAERLLLLAARQRGVVYLVGKSALCAEPGSS	1074
Fr483	-----	660
<i>Micractinium conductrix</i>	WLKTFLLESAYAALVANCRIPTTALYRVPRQGLLAESCRPAAGALVQLAFSCKGMLTAAEA	1134
Fr483	-----	660
<i>Micractinium conductrix</i>	AEPMWRMQCQRLGWSLDWLDTLPPGTSTWRYFCARMHARHHLRLLRSLSRAADPSAWEV	1194
Fr483	-----	660
<i>Micractinium conductrix</i>	FELYRVVDGQDRERGGIQFFHEARLLSLREAVAAAQERHGPLRLARAFALAVQRSNGSQ	1254
Fr483	-----	660
<i>Micractinium conductrix</i>	AAGSGGGDSSSVPPPDQPSSSSCALPLDDRPKSEDTEQEPVLLPLSEEMRGRRRFCAD	1314
Fr483	-----	660
<i>Micractinium conductrix</i>	LRGLIWLASGFHTRCAADSLAVLLQSILT	1343

Figure S8. Comparison of viral K⁺ transporter from virus and its host. Alignment of the Pbi chlorella virus Fr483 potassium transporter versus a homologous protein from the host *Micractinium conductrix* (Chlorella Pbi). The algal protein exhibits a much longer C-terminus (the same is true for other alga potassium transporters). Predicted TM domains are underlined. In the alignment, identical amino acids are indicated by "*", conserved and semi-conserved amino acids are indicated by ":" and ".", respectively.

Figure S9

MQQLYKIRSTHEIENIKGGDYDWLEITKPDDSDLSLVQKRTGLEISTSKLILSSHESHIEGLTEPDKPLMIVLQYPKMVESNLGDFKE
YATSPIILILSNDGDNNDLITISNHEPSFIAKIQEDSKSLKVPITNKKDIMLLVIYYMSQEYRSILRSLNKDANSLEQSLKTATNNIIF
YHVMSIQKTVSSFLDSLANNQNICKEIENDANYFASEKYTELARSASLAEETSEAAARHLDYILDKYTSLVSSIVGNNQLVTINKFTEW
GIVLSFLSASFGALGMNYLPGESSHVTTILVFATIFASSIWLSKYIRKLLKGKK

Figure S9. Sequence and topology of Lactobacillus phage magnesium transporter. Shown is the amino acid sequence of the putative magnesium transporter from *Lactobacillus* phage Lfelnf. Predicted transmembrane domains are underlined; however, experimental data indicate 3 TM domains (Smith et al., 1993). The highly conserved GMN motif is shown in yellow.

Figure S10

MQLLDMVIFAGYIGCIVMAGLVIGWKKSGTTKSYFMADRSLPWWILGCAILAANISAEHLIGTTGSAYAMGIAIGAFELTGALALVVAA
WLAIPYFVKNQITTMPQFLAMKYDNRVRSMFATFWIVVYTLVNLTAVSYMGALAFTSIGIPLEVGWVALIGFAVLYSAVGGLSSLVWTD
FIQVGILLTAGIACTWFTLDAYGVHVGSTSIAGSMVSLYKELPNHFQLVLEPGHPAYENIPGILGVGVFLGSLSYFAFNQFIVQGALA
AKSVKEAQKGMVFAAFLKLLMPLVVIIPGIMAYSMTNGSLTPSDKAYPWLIDNFMPAGFHGLVMAALFAAIISTLAAILNSISTMFTLD
IVKVHKPELSDKTLMKVARTVVVVCGAIGASLAIPFLGNLDQAYHFIQEFVGFVTPAMLVIFFAALYWKTNSNAAIAVTVFSVAANAIV
KFTVPELAWLDRFLMVLVGCGLVLSLFSGKQVEDAHIAPSKTLVIGGSIVAIFFATYITFA

Figure S10. Sequence and topology of the Aeromonas virus 44RR2 sodium/glucose transporter. Predicted TMs are underlined.

Figure S11

Vibrio phage	-MELMTG <u>LVMMASASLFIMYACNSLEQ</u> TLDYLGRNMKAGAK <u>GALLMAVASSLPEIMVAFA</u>	59
<i>Vibrio jasicida</i>	MLET <u>IFPFLLIILACYLLKYSCD</u> TFEQAAGYLGRNFPAGVK <u>GATVNAIGSSMP</u> EMCVVIA	60
	:* : :::: *. :: *:*:*:*:*. :*****: **.*** : *:*.***:*. :*.:*	
Vibrio phage	<u>FL-FS</u> GKPE <u>ELVLAGVFV</u> TAGSAIFNILLIPAVSILYAGDGQGNKVDSFQLDRKVLSDTF	118
<i>Vibrio jasicida</i>	<u>CLFWF</u> NDPQ <u>LVIVALGVTAGSAIFNGCVIPAL</u> SIIVAKDDEGNSVDQIELNK <u>SALLRDVF</u>	120
	* : ..*:*.:.: ***** :***:*. : * *.***.***:..* **.*	
Vibrio phage	WLLTVEA <u>IFIYFLGLNVFTTIGMAATLIILY</u> ALYVSHVIHDSNKAGEQPEGFEFEELDHTF	178
<i>Vibrio jasicida</i>	<u>WVLTAEIALIVCLGFSEFSIWMALLLNVIYLG</u> YAIHLYFDAKKHGGDDDEYEEYEEIDDRG	180
	:. * :* **:. *: * * * ::* *. *: .*: * * : : :*:***:.	
Vibrio phage	TPKFIAWIGYV--LDFNKHLEFKNKAYTTKTA <u>SIVCALSCTIIAVACHYLAVSTEIVSAAL</u>	236
<i>Vibrio jasicida</i>	-----FIGNLLTFNFNAILFSNKTFTLTRA <u>LIVLALAI</u> AVISGSSHILVEGVLGSA <u>AAVL</u>	234
	:** : ::** **.**:*: * * * *: :*: :.* *. .. :*. *	
Vibrio phage	<u>GIPVLIGA</u> AAVF <u>AAAATS</u> LPDITILSKSASENGEGDDAVANAVGSNIFD <u>TSFAIGLPLLIAL</u>	296
<i>Vibrio jasicida</i>	<u>GVPEFFSGLVFGAAASSIP</u> DLILSVKDAQKGEYEDAIAN <u>PLASNTFDTTVA</u> FALPLFVWF	294
	: :... **.***:*.*** *** . :*: * :*: * :..* ***:.*:***: : :	
Vibrio phage	<u>TPLGEWLF</u> GINLKEGIPLVQGDSE <u>MDTVRYFVIGTSALAAAGLWVQA</u> KNVTKK <u>TAYYLLT</u>	356
<i>Vibrio jasicida</i>	<u>I-----</u> LNGVDSLPM AQD-NN <u>LTILRWSIIGITA</u> AVACSLFNYKKVTKS <u>VAYFLLA</u>	345
	:* :.:*:*. . : :*: **: * *.*** : :*:***..***:***:	
Vibrio phage	<u>LYGTWIA</u> YLIYHVS	370
<i>Vibrio jasicida</i>	<u>MF</u> AIWATSMYFVIQ	359
	:.. * : : : .	

Figure S11. Comparison of viral sodium/calcium symporter with most similar protein from a *Vibrio* bacterium. Alignment of vibrio phage 1.084.O_10N.261.49.F5 sodium/calcium symporter versus the most similar protein from *Vibrio jasicida*. Predicted TMs are underlined. In the alignment, identical amino acids are indicated by "*", conserved and semi-conserved amino acids are indicated by ":" and ".", respectively.

Figure S12

RSIV -----
Pagrus major MSSAEMGKFNISPDEDSSSYSSNSNDFSYPYPTKPAAMKSHYADIDPENQNFLLDSNLGK

RSIV -----MAPCVLQCGVTDVFLHTLNCMIGIGLLALPHAVAVVGPVVFVGVLLFVAVAAIV
Pagrus major KKYETQYHPGTTSFGM--SVFNLSNAIVGSGILGLSEFAMANTGIALFVILLLEVSIFSLY
* . . *: .:: *::* *:*. * .*: * . * .: ** :****:: ::

RSIV STHMLTACLRTHRG-NLEDICAAMFGRGGYWIMCAVIILENLGSVCSYMHMLMSVLAVLV
Pagrus major SVHLLLKTANEGGSLLYEQLGMKAFGMAGKLAASGSITMQNIGAMSSYLFIVKYELPLVI
:.: . . *: * . * .: ** :****:: * ::

RSIV P-----DISMYAVG-----MLILLVLFFPVSLPKSSRCLMIISGPALMCVLAFVVYTI
Pagrus major KTFMNIEETTGEWYLNGDYLVLLVSVILILPLSLLKNLGYLGYTSGFSLLCMVFFLIVVI
. : * * : : : : : * * . * * : * : : * : *

RSIV YYCVHA-----TVPGPAWPLFDDRMVRDQC-----LSIITFAFVC
Pagrus major WKMFQIPCPMDSVVMNVTFNATVAPLVDENITIDMCKPKYFIFNSQTVYAVPILTFSEVC
: .: * . . *.*:.: : * * : * : * : *

RSIV QPTIVTTANL-HGDKASGAAAAAMCAMSVGTVLYAVIALCGWLPMGPETPDNIVLAYMAT
Pagrus major HPAILPIYEELKGRSRKRMMNVSYVSFFAMFLMYLLAALFGYLTFYGKVEPELLHTYSAY
:.: : : * . . : : . : * : * * * : : : : * *

RSIV LDGKIVAGVM----CVSVVLTVPALLLPVVHMMAPI--DRSPMQWMSTL----GMYACMY
Pagrus major LGADVLLLIVRLAVLTAVTLTPVVIFPIRSSITQLLWAGKEFSWLRHCSITVALLAFTN
...: : :.*****.:*: : : . :.*: .: *

RSIV VLVIMIPSEFKIGVVVVGVAGVTVLVFALPALMYTWLFYRRRVVLAWMV--VVLYTTIGIAV
Pagrus major VLVIFVPTIRDIFGFIGASAAAMLIFILPSAFYIKLVKKEPMKSVQKIGASFFFLSGILV

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          ***** . .: ** * .: *: * **: :* *. . . : : . : : ** *
RSIV      S-----VMAIYDIKIQLQGY
Pagrus major MTGCMTLIILDWTQNVTSGDH
          :: : :: :*:

```

Figure S12. Comparison of viral amino acid transporter with most similar protein from a fish. Alignment of red seabream iridovirus (RSIV) amino acid transporter versus the most similar protein from *Pagrus major* (red seabream). Predicted TMs are underlined. In the alignment, identical amino acids are indicated by "*", conserved and semi-conserved amino acids are indicated by ":" and ".", respectively.