

## Supplementary Material

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**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 (Heterokont algae)	Thiel, unpublished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 <b><u>FFKLLVALIVT</u></b> -----	15
OLPV2	-----MKNK <b><u>FIYLIVSTIFFSLVYSEIR</u></b>	23
AaV1	-----MKLLFGYN-----RFH <b><u>LLIYQIIFFSILYMELG</u></b>	28
TeV1	-----MSFVAK <b><u>VAVHIIIIITFFVINLTIN</u></b>	25
PBCV1	-----MLVFSKFL--TRTE <b><u>PFMIHLFILAMFVMIYKFFP</u></b>	32
OSyNE5	-----MFIIRKIL--TQSE <b><u>PFIHLLVLMFVMIYRFFP</u></b>	32
MT325	-----MS <b><u>ILGVHFALLLFAALYKFFP</u></b>	22
ATCV1	----- <b><u>MLLLIIHIIILIVFTAIYKMLP</u></b>	22
OtV6	-----MALT <b><u>KTLSLNFISILLFTLMYFTIS</u></b>	25
DishuiLV	-----MASTL <b><u>ARTVGLNLGAIFFAILYLALA</u></b>	27
EsV1	MSRR <b><u>LFATCGIAIALRGLVSGGV</u></b> KEIVSFRPLIDT <b><u>SLVGGILSNLILLVFAELYWQLD</u></b>	60
BpV1	-----MLNK <b><u>AVTIALIITLVYGYLY</u></b> ----	20
MpV1	-----MKTVLNIIIIITTLYGLLY----	18
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	:	
YSLV	----- <b><u>NLSFAGVMHSWV</u></b> TDSDM-----	32
OLPV2	PRNFHGFNKIQDKIQDVLVSEETDIIIEPFYAP-----YLDKKE--KEKEKEKEKD	71
AaV1	<b><u>SSHFSG</u></b> INTLEDILKNEIVSKQV--LDPIIEEKFTNASDPSKFISKDDIEVDKKEETEEIQ	86
TeV1	<b><u>ITNK</u></b> -----NAFS-----	33
PBCV1	<b><u>GGFE</u></b> -----NNFSVA-----	42
OSyNE5	<b><u>GGFE</u></b> -----NNFTVA-----	42
MT325	<b><u>GGFE</u></b> -----NNFKRG-----	32
ATCV1	<b><u>GGMF</u></b> -----SN-----	28
OtV6	KAGG-----EQFNGL-----	35
DishuiLV	RMGT-----EDFVGM-----	37
EsV1	QGDD-----HTHFGF-----	70
BpV1	<b><u>STMK</u></b> -----EDFGFS-----	30
MpV1	SKMK-----PEHFNF-----	28
YSLV	-----SGLRKGSTDRFVDLLYFSIV <b><u>SFSTTGYGD</u></b> IAPKSTRAK <b><u>MAVCLF</u></b>	76
OLPV2	EVKKEVKENVLEEKEKI-YNPSWWQHLYDSLYFSVI <b><u>TSCLLGYGD</u></b> IYPITNMSKIIIVSLQ	130
AaV1	EKAKEIKKEVKKELNILTDKDSFFDRFFLRFYFSFV <b><u>TSTTIGYGD</u></b> TTPSSISTRTLAMIQ	146
TeV1	-----KELTTLDVFFYYTVT <b><u>TWTTTGYGD</u></b> <b><u>IYPVITVSKMIAVTK</u></b>	71
PBCV1	-----NPD-KKASWIDCIYFGVT <b><u>THSTVGFGD</u></b> ILPK <b><u>TTGAKLCTIAH</u></b>	83

OSyNE5	-----NPD-KKASFVDCLYFGVT	<b>THSTVGFGD</b>	ILPK <b>TGAKLCTIAH</b>	83
MT325	-----DGSKEPVSWMDAIYVSAA	<b>THTTTGFGD</b>	IVADSRAAK <b>FAVTAH</b>	74
ATCV1	-----TDPTWVDCLYFSAS	<b>THTTVGYGD</b>	LTPKSP <b>VAKLTATAH</b>	66
OtV6	-----DKDSGFLDHLYFAFT	<b>VQSTVGFGD</b>	IYPISPMAKMIVMVQ	74
DishuiLV	-----DRMSSPLDALYLSMT	<b>VQSTIGFGD</b>	ITPKTTRAKLL <b>VMMQ</b>	76
EsV1	-----SSAIDAYYFSAVT	<b>TSSSVGYGD</b>	LLPKTPKAKLL <b>LTIAH</b>	106
BpV1	-----DDPLDPYYFSLMT	<b>TMSTVGYGD</b>	FSPKTRRAKALVMSH	66
MpV1	-----KSPLDPFYFSFT	<b>TMSSVGYGD</b>	FSPKTDAAKLVVMSQ	64

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YSLV	<b>LMFV--NI--AAIYGIYNALV</b> TSA-----	96
OLPV2	GFITLFLILS-----	140
AaV1	ACSTFYILMA-----	156
TeV1	<b>MLLFLVILMY</b> -----	81
PBCV1	<b>IVTVFFIVL</b> TL-----	94
OSyNE5	<b>IVVVFFIVL</b> TL-----	94
MT325	<b>MLIVFSIVVLGL</b> KPELITNLI-----	95
ATCV1	<b>MLIVFAIVISGFT</b> FPW-----	82
OtV6	QSVLILGILELISESKSVANVVPTVMKKMI-----	104
DishuiLV	<b>QFVVIVGIVNLLSGGGISL</b> KKNNAAMNTISNTISNVPAPA	116
EsV1	<b>ILAMFFVMLPVVA</b> 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	MATKKVNKVLIALHKYYTVLFAILALLSVALIVLDYMGRI SIDKSPYTEIDNGILVIFAI	60
Lactobacillus	MATKKVNKVLIALHKYYTVLFAILALLSVALIVLDYMGRI SIDKSPYTEIDNGILVIFAI	60
MpMyrna	-----	0
MpPhabba	-----	0
SpBillNye	-----	0
Acidobacterium	-----	0
Ptexasensis	-----	0
Rheinheimerera	-----	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	DYFSRMLHADSKWDFFKHNLIDLLAIIPFNAYAFSFFRFGRI FRLARLTRLMRLTRLARLA	120

Lactobacillus	DYFSRMLHADSKWDFFKHNLIDLLAIIPFNAYAFSFFRFGRIFRLARLTRMLRLRLARLA	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----RTEPFMIHLFILAMFVMIYKFFPPGGFE-----	36
OSyNE5	RKIL----T----QSEPFIIHLLVLMFVMIYRFFPPGGFE-----	36
MT325	-----MSILGVHFALLLLFAALYKFFPPGGFE-----	26
ATCV1	-----MLLLIIHIIILIVFTAIYKMLPPGGMF-----	26
OtV6	----M--A----LTKTSLNLFISILLFTLMYFTISKAGG-----	29
DishuiLV	---MAS---T---LARTVGLNLGAIFFIFAILYLALARMGT-----	31
EsV1	RPLIDT---S---LVGGILSNLILLVVFAELYWQLDQGGD-----	64
BpV1	-----M----LNKAVTIALIITLVYGYLY----STMK-----	24
MpV1	-----MKTVLNIIITTLYGLLY----SKMK-----	22
Vp2	-----MLNCITVID----SHGRKEYKTSFLLLVN-IVTVLL	31
Vp3	-----MKKYLHWCISTSSKMYK----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----EHGVVQYNMLLI-FALI-ISISTS	34
LpPLE2	GIVGI----LTK---HAE-----RILKRTGLIYYI-----WLSAA	148
Lactobacillus	GIVGI----LTK---HAE-----RILKRTGLIYYI-----WLSAA	148

MpMyrna	-----MS-----LIHRATGSIKVV-----VGWAIG	20
MpPhabba	-----MS-----KIHDATGSVAKV-----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	--LDPIIEEKFTNASDPSKFIIS---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	NIYIGGLFLWHFEEGLQDSNINSLKEAMWAVFMTMTTIGFGDKYPITVEGYITTGVCFL	91
Vp3	NVIIGALFLYLFEHNVDNALINSYSSALWMNWMVATTVGFGDYYPITGGKIVTGSSAI	94
Moraxella	IAV-LAFLLLWAESGAQGANIETYGDAFWTLQMSASTIGFGDYYPVTLGGRTIVAAMFYI	96
Vp1	IALTAASLLYRFESGADGSNINSAGDALWTIWMSMSTIGFGDHYPVTVGGRVIVGSMFAV	89
VpVH7D	IALTAANILFSFEIQNPDANITTPGDSFWTVWMAMSTIGFGDKYPVTTGGRYVIGCMFVV	74
VpGrn1	IALTAANILFSFEIQNPDANITTPGDSFWTVWMAMSTIGFGDKYPVTTGGRYVIGCMFVV	67
VpValKK3	IALTAANILFSFEIQNPDANIKTPGDSFWTVWMAMSTIGFGDKYPVTTGGRYVIGCMFVV	94
VpST2	-----MAMSTIGFGDKYPVTTGGRYVIGCMFVV	28
Vpphipp2	IALVASNILFAFELSASNANIKTPGDAFWTVWMAMSTIGFGDHYPVTTGGRFVIGSMFVV	94
Vpnt1	IAFIAANFLFYFEVQDPNANIRTYGDAFWTVWMAMSTIGFGDHYPVTEGGRYTIGCMFVV	94
LpPLE2	LILIGASVYSVT-----ESVG-YGDSLWVAIVTATTVGYGDISPHTVLGRIA AVILMFN	201
Lactobacillus	LILIGASVYSVT-----ESVG-YGDSLWVAIVTATTVGYGDISPHTVLGRIA AVILMFN	201
MpMyrna	CTIAGAVAFCLF-----EGSTDGLAALYWAVVSGSSTGYGDIAPKTAAGRITTTIVYLIV	74

MpPhabba	FTVAGTLAYSLEF-----EHVT-PFESLYWAIVSGSSTGYGDYSPATVGGRVVTIVYLVI	73
SpBillNye	TILVSSVVFSLT-----EGVS-LFDGVYWSVVTMSTTGYGDLSPEIVGKAYTMLLMLW	74
Acidobacterium	TLTVSGVLFAYF-----EGKP-LFESFWWACVTGLTIGYGDMPVTVGGKIVAIVLMHV	77
Ptexasensis	SLIFGAISFAVI-----EQKS-LADGIWWATVTSLTIGYGDLPVTPIGRFVIGILFGHF	74
Rheinheimera	SLIFGAVSFAIL-----EQKS-LADGLWWATVTSLTIGYGDLPVTPAGRIVGILFGHF	74
Ap	SLVIASLLFSLT-----EGVS-YLDSLYWACVTSLTIGYGDYSPHTIAGKILAIVCGHF	73
Ppventosus	SVVLCALLFAWI-----ESKS-VLDSIWWACVTSLTIGYGDIAPVTTAGRALAVVFSHF	74
YSLV	-----SGLRK-----GSTDRFVDLLYFSIVSFSTTGYGDIAPKSTRAKMAVCLFLMF	79
OLPV2	K-----I-YNP-----SWWQHLYLDSLYFSVITSCLLGYGDIYPITNMSKIIVSLQGFI	133
AaV1	I-----LTDKD-----SFFDRFFLRFYFSEVTSSTTIGYGDTPSSIISTRTLAMIQACS	149
TeV1	-----KELTTLDFVYYTVTTWTTTGYGDIYPVITVSKMIAVTKMLL	74
PBCV1	-----NPD-----KKASWIDCIYFGVTTHTSTVGFVDILPKTTGAKLCTIAHIVT	86
OSyNE5	-----NPD-----KKASFVDCLYFGVTTHTSTVGFVDILPKTTGAKLCTIAHIVV	86
MT325	-----DGS-----KEPVSWMDAIYVSAATHTTTGFGDIVADSRAAKFAVTAHMLI	77
ATCV1	-----TDPTWVDCLYFSASTHTTVGYGDLPKSPVAKLTATAHMLI	69
OtV6	-----DKDSGFLDHLYFAFTVQSTVGFVDIYPISPMAKMIVMVQQSV	77
DishuiLV	-----DRMSSPLDALYLSMTVQSTIGFGDITPKTTRAKLLVMMQQQFV	79
EsV1	-----SSAIDAYYFSAVTSSSVGYGDLLPKTPKAKLLTIAHILA	109
BpV1	-----DDPLDPYYFSLMTMSTVGYGDFSPKTRRAKALVMSHHTV	69
MpV1	-----KSPLDPFYFSFTTMSSVGYGDFSPKTDAAKLVVMSQHLV	67

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Vp2	GAVNLGTLIKTASNLVKD--KNEVDNRQIYSIITEL--LR--SNQHIEQELNLTQEV--T	143
Vp3	GIGMFGLFTSVVSGILMEHTDDSI RNRELKEQNARI--EI--ELNEVKKIL-----VSFT	145
Moraxella	GVGIVGFIGAQVADRFLGFADTNVKNRELKRQNEQI--LE--HNKVLEKKLKDILLS----	148
Vp1	GATLIGLNIGIASAWVTSKFDKSVQNRVLKLSQDNL--IQ--KIDRLETFLNVDQTVYFG	145
VpVH7D	GTSLGGLTIGI INSWVSKFDKSIQNRVLKLSQNDAL--LH--KDRLETHLGLDQEVRFD	130
VpGrn1	GTSLGGLTIGI INSWVSKFDKSIQNRVLKLSQNDAL--LH--KDRLETHLGLDQEVRFD	123
VpValKK3	GTSLGGLTIGI INSWVSKFDKSIQNRVLKLSQNDAL--LH--KDRLETHLGLDQEVRFD	150
VpST2	GTSLGGLTIGI INSWVSKFDKSIQNRVLKLSQNDAL--LH--KDRLETHLGLDQEVRFD	84
Vpphipp2	GASLIGLNIGIANAWITSKFDKSIQNRVLKLSQNDAL--LQ--KDRLETHLGLDQEVFLS	150
Vpnt1	GASLIGLNIGIVNGWISSKFDKSIQNRVLKLSQNDAL--LQ--KDRLETFLGQVNEVFLFD	150
LpPLE2	GI---GLISALTSAVT----AYLSGTNSDSSQSPTDEIKKLYDLKQIGAITQSEYDAK--	252
Lactobacillus	GI---GLISALTSAVT----AYLSGTNSDSSQSPTDEIKKLYDLKQIGAITQSEYDAK--	252
MpMyrna	ML--WVITPVLTARIA----AYMIVNNDAWTDSEQESLKG--DIAAIKRKLGA-----	119
MpPhabba	ML--WVITPVLTARIA----AYMIVNNDAWTDNEQETLQK--DIADIKRKLGA-----	118

SpBillNye	SV--FFLVPSAVAQII----MKFIHNRNEFTHEEQEKIMQ--QQKRIELLEGGKSE---	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----NITLEDRLNLFTHHEEQEEMKT--LLRKLAEKA-----	117
YSLV	V----NI---AAIYGI----YNALV TSA-----	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	QNSHGLDKVFEQNRYSVDNFADGWITRGEDSSGLLIISLEAYCKETGKSTKRWIPTDTLK	203
Vp3	KDKK-----	149
Moraxella	----AMEPF-----SDKKD-----	158
Vp1	PDAHGIDETLKQK-QFDVSOQKAIIVTLGRDDGGRFIVATNTQT-DSGRNKLKWISYLKFD	203
VpVH7D	KDAHGIDTIIIDQY-FDSNDKADRFVTLGQDDSGRYVVAINQLIVETQHTSMKWHTFINEK	189
VpGrn1	KDAHGIDTIIIDQY-FDSNEKADRIVTLGQDDSGRYVVAINQLMVETQHTSMKWHTFINEK	182
VpValKK3	KDAHGIDTIIIDQY-FDSNEKADRIVTLGQDDSGRYVVAINQLMVETQHTSMKWHTFINEK	209
VpST2	KDAHGIDTIIIDQY-FDSNEKADRFVTLGQDDSGRYVVAINQLMVETQHTSMKWHTFINEK	143
Vpphipp2	KDAHGIDTMIIDQY-FDSNDKAERFVTLGQDDSGRYVVAINQQI IETQKTSWKWHTFIKED	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<sup>+</sup> 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<sub>MpV1</sub>). **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>VEYNIGMIFAGLMALSFTIALTAAS</u> LLYRFESGADGSNINSAGD	55
VpVH7D	----- <u>MLMIFGLMIVIALSIALTAANIL</u> FSFEIQNPDANITTPGD	40
VpValKK3	MKRFFKHIRKYDEHGVAQYN <u>MLMIFGLMIVIALSIALTAANIL</u> FSFEIQNPDANIKTPGD	60
VpGrn1	----- <u>MIVIALSIALTAANILFSFEI</u> QNPANITTPGD	33
Vphipp2	MKRFFKHIKKYDEHGVVQYN <u>MLMIFALIVTISMSIALVASNIL</u> FAFELSASNANIKTPGD	60
Vnt1	MKRLKHIRKYDEHGVVQYN <u>MLLIFALIISISTSIAFIAANFL</u> FYFEVQDPNANIRTYGD	60
	.. :*: ** .: * : .	
V2	AMWAVFMTMT <u>TTIGFGD</u> KYPI <u>TVEGYITTGVCFLLGAVNLGTLI</u> KTASNLVKDK--NEVDN	115
V3	ALWMNWMVATTVGFGDYYPISGGKIVT <u>GISSAIGIGMFGLFTSVVSGILM</u> EHTDDSI RN	120
V1	ALWTIWMSM <u>STIGFGD</u> HYPVTVGGRV <u>IVGSMFAVGATLIGLNIGIASAW</u> VTSKFDKSVQN	115
VpVH7D	SFWTVWMAM <u>STIGFGD</u> KYPVTTGGRYV <u>IGCMFVVGTSLLGLTIGIINSWV</u> VSKFDKSIQN	100
VpValKK3	SFWTVWMAM <u>STIGFGD</u> KYPVTTGGRYVI <u>IGCMFVVGTSLLGLTIGIINSWV</u> VSKFDKSIQN	120
VpGrn1	SFWTVWMAM <u>STIGFGD</u> KYPVTTGGRYVI <u>IGCMFVVGTSLLGLTIGIINSWV</u> VSKFDKSIQN	93
Vpphipp2	AFWTVWMAM <u>STIGFGD</u> HYPVTTGGRFVI <u>GSMFVVGASLIGLNIGIANAWI</u> TSKFDKSIQN	120
Vpnt1	AFWTVWMAM <u>STIGFGD</u> HYPVTEGGRYT <u>IGCMFVVGASLIGLNIGIVNGWI</u> SSKFDKSIQN	120
	* :* :*:***** **: : * * :* :* . : .: .: : *	
V2	RQIYSIITELLRSNQHIEQELNLTQEV--TQNSHGLDKVFEQNRYVSDNFADGWITRGED	173
V3	RELKEQNARIEIELNEVKKIL-----VSFTKDKK-----	149
V1	RVLKLSQSDTLIQKIDRLETFLNVDQTVYFGPDAHGIDETLKQK-QFDVSQGKAIIVTLGRD	174
VpVH7D	RVLKSQNDALLHKLDRLETHLGDQEVRFDKDAHGIDTIIIDQY-FDSNDKADRIVTLGQD	159
VpValKK3	RVLKSQNDALLHKLDRLETHLGDQEVRFDKDAHGIDTIIIDQY-FDSNEKADRIVTLGQD	179
VpGrn1	RVLKSQNDALLHKLDRLETHLGDQEVRFDKDAHGIDTIIIDQY-FDSNEKADRIVTLGQD	152
Vphipp2	RVLKSQNDALLQKLDRETHLGDQEVLFSDAHGIDTMIDQY-FDSNDKAERFVTLGQD	179
Vpnt1	RVLKSQNDALLQKLDRETHLGVNQEVLFDKDAHGVDTFIDQY-YDSNDSADRIVTLGQD	179
	: : . :.: * *	

V2	SSGLLIISLEAYCKETGKSTKRWIPTDTLKDQKYTYNRFINNMNEL---	219
V3	-----	149
V1	DGGRFIVATNTQT-DSGRNKLKWI SYLKFD DALDFYNDVAVELDAV---	219
VpVH7D	DSGRYVVAINQLIVETQHTSMKWHTFINEKDAVKFFEETSELFHTELL-	207
VpValKK3	DSGRYVVAINQLMVETQHTSMKWHTFINEKDAVKFFEETSELFHTELL-	227
VpGrn1	DSGRYVVAINQLMVETQHTSMKWHTFINEKDAVKFFEETSELFHTELL-	200
Vpphipp2	DSGRYVVAINQQIIETQKTSLKWHTFIKEDDATKFKYKDTSELFHTELF	228
Vpnt1	DSGRYVVAINQQMRDTQKTSMKWHTFILES DALKFKYKDTSELFHTEIFS	228

**B**

Vpphipp2	MKRFK--KHIKKYDEHGVVQYN <u>MLMIFAL-IVTISMSIALVASNIL</u> FAFELSASNANIKT	57
Moraxella	MSRFTLSKRIYRTDEFEVRN <u>YNMFLTFVAVVILYLSIAVLAF</u> -LLLWAESGAQGANIET	59
	*.*.*. *: * : *. * :*****: : : * : :*****:* :*: * .*.***:*	
Vpphipp2	PGDAFWTVWMAMSTIGFGDHYPVTTGGRFVI <u>GSMFVVGASLIGLNIGIANAW</u> ITSKFDKS	117
Moraxella	YGDAFWTLQMSASTIGFGDYYPVTL <u>GGRTIVAAMFYIGVGIVGFIGAQ</u> VADRFLGFADTN	119
	*****: *: *****:***** *** ::::* :*...:*: . . : . *..	
Vpphipp2	IQNRVLKSQNDALLQKLDRLLETHLGIDQEVLF SKDAHGIDT MIDQYFDSNDKAERFVTLG	177
Moraxella	VKNRELKQNEQILEHNKVLEKKLDKL-----LSAMEPFSDKKD-----	158
	::** *:.**: :*: . **.*. : : : *.*:	
Vpphipp2	QDDSGRYVVAINQQIIETQKTSLKWHTFIKEDDATKFKYKDTSELFHTELF	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.





AngHV-1 -----  
*Pundamilia nyererei* RPPAAKDNSVGENKAKSEPKAARSDSSESKNKTSKGNENLSQDQPDRDVALLRPELDPST

**B**

AngHV-1 -----  
*Homo sapiens* MLCSLLLCECLLLVAGYAHDDDWIDPTDMLNYDAASGTMRKSQAKYGISGEKDVSPDLSC

AngHV-1 -----MKMNRILVLLL-LFWGTRAEWDV-----TSYTAKLGLVKGCKCR  
*Homo sapiens* ADEISECYHKLDSLTYKIDECEKKKREYESQSNPVFRRYLNKILIEAGKLGFLHD----  
\*:: : : . \* :: : : . \* \* \* \* . : .

AngHV-1 PEEVKEVKKVWRFE~~DTF~~GVEIDTVLQICSCVLVIVMIVCGELWSTVSWFLQLERAFIICL  
*Homo sapiens* ----FETWKWRFE~~DSFGVDP~~YNVLMVLLCLLCIVVLVATELWTYVRWYTQLRRVLIISF  
. \* \* \* \* : \* \* \* : . \* \* : \* : \* \* \* : \* . \* \* \* : \* \* : \* \* . \* : \* \* : .

AngHV-1 FVSFIWNWIYLYKAAYAEHQANMIKLDGVAKRCAN-ADFMSTLKDWRSTWTLQDDPCKK  
*Homo sapiens* LFSLGWNWMYLYKLAFAHQAEVAKMEPLNNVCAKKMDWTGSIWEWFRSSWTYKDDPCQK  
: . \* : \* \* \* : \* \* \* \* \* \* : \* : \* \* \* : : \* \* : \* : . : : \* \* \* \* : \* \* : \* \* \* \* : \*

AngHV-1 YHEVLIINPVLIVPPTKAISVTFVTFVTEPLKHFGHGIGEFIKALLKDLPTLQVPVWGD  
*Homo sapiens* YYELLVNPIWLVVPPPTKALAVTFTTFVTEPLKHIGKGTGEFIKALMKEIPALLHLPVLI  
\* : \* : \* : \* : \* : \* \* \* \* \* : \* \* \* \* \* \* \* \* \* \* \* : \* \* \* \* \* \* \* : \* : \* \*

AngHV-1 HFSSRCRVYVRNLF CGGW--PLISLRTHHTH-----TTHE~~DRRWKH~~-----FWK  
*Homo sapiens* MALA-----ILSFCYGAGKSVHVLRHIGGPESEPPQALRPRDRRRQEEIDYRPDGGAGD  
: \* \* \* : \* \* . \* \* \* : .

AngHV-1 CGLDFRGYLNRAEFPAARE-----  
*Homo sapiens* ADFHYRGQMGPTEQGPYAKTYEGRREILRERDVDLRFQTGNKSPEVLRAFDVPDAEAREH  
. . . . \* \* : . . : \* \* :

AngHV-1 -----  
*Homo sapiens*      PTVVPSHKSPVLDTKPKETGGILGEGTPKESSTESSQSAKPVSGQDTSGNTEGSPAAEKA

AngHV-1 -----  
*Homo sapiens*      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.





B

PBCV-1 <i>Cricetulus griseus</i>	-----MEDID-----NIYDCTPSTLTNL----- MCPETEEQEDDHLSIVTLEEAPFVIVESVDPLSGTCMRNTVPCQKRIISENKTDEEPGYI :*.*                  *     *      :::	18 60
PBCV-1 <i>Cricetulus griseus</i>	TAC-----FI-----PSSEAWCNIGDTCVSNIRYDPKCN KKCCKGFCIDILKKISKSVKFTYDLYLVTNGKHGKCKINGTWNMIGEV---VMKRAPLCY . *                                  ::                  . :* .: .          :: * *	48 117
PBCV-1 <i>Cricetulus griseus</i>	FFGY--ADQYLTHIIPRTFKCFNVIRQCVTSYTD AERQGC DILYGE PNPLAYTN-KSNYW NVLTVASYCFLQVVMKRAP <u>ACYNILTVASYCFLOVVM</u> KRAYMAVG---SLTINEERSEVV .      :  :*  ::  *:  **::  .  .:  .:  :  .:  *     *  .:  ::  **:	105 174
PBCV-1 <i>Cricetulus griseus</i>	AESV-LYDVDS PAILFNPKSYIPWDFLKP <u>SWELWAMLIIVMCIITPLVTSLEI</u> YDTGE DFSVPF IETGISVMVSRNGTVSPSAFLEPFSAD <u>VWVMMFVMLLIVSAVAVFVFEYF</u> SPV **  :  ...  .:  .  :  :  *  **:*  **  :  :*  *  .:  .:  *  .:  *  *  :	164 234
PBCV-1 <i>Cricetulus griseus</i>	TVVGNFIKYL PDSIH--AHLGIDLISSESMT---NNTSYTLA <u>VFINIFAIIMLALYSSNL</u> G----YNRCLADG <u>RAIWLLWGLVFNNSVPVQ</u> NPKGTTSKIM <u>MVSVWAFFAVIFLASYTANL</u> :  :  *  *  .                  *:  :  .*  :          ..**  :.  .  :*  *:  **  *  *  **	219 290
PBCV-1 <i>Cricetulus griseus</i>	<u>VAYVL</u> YKNYSLSSL-----PYSYKPTWDI-----FIDNTISNSFSELPNDLLYIDSS <u>AAF</u> MIQEEYVDQVSGLSDKKRPNDPFPFRFGTVPNGSTERNIRNRYAEMHAYMGKFNQR .  *  .:  .:  *  .                  *  ...  *  :  :                  ...  *  *  .:  *  :  :  .:  .	266 350
PBCV-1 <i>Cricetulus griseus</i>	KIPE---IIDSSEFDAIIGQRTFLQIF-----KDCSSELTIIHGPGI GVDDALLSLKTGKLDAFIYDAAVLNYMAGRDEGCKLVTIGSGKVFASSTGYGIAIQKDSGW :  :          .:  .:  .:  **:*  :  .:  *  :  :                  .  .  :*  :.  *	305 410
PBCV-1 <i>Cricetulus griseus</i>	YKYVNLATKAGMLNIRRLIAQIQMASVNRQFTSPTCTEQ-----PQSINLNSMYG <u>VFLLF</u> KRQVD-----LAILQLFGDGEMEELEALWLTGICHNEKNEVMSSQLDIDNMA <u>GVFYML</u> :  *:                  *  *  *:  .:  :*  .:  :  :  *  .:          ...  .:  *  **  *  *  *  :	360 463

PBCV-1	<b>FIPMTLLFLITIIIRF</b> ----TLKRKF----SADNSMVI PKTHS-----	394
<i>Cricetulus griseus</i>	<b>GAAMALSLITFICEHLFY</b> WQFRHCFMGVCSGKPGMVFSISRGIYSCIHGVAIEERQSVMN	523
	*:* :: * .. ::: * *.. .** : ::.	
PBCV-1	-PD-----DLEKY-EAEGSSESVV-----	411
<i>Cricetulus griseus</i>	SPTATMNNTHSNILRLLRTAKNMANLSGVNGSPQSALDFIRRESSVYDI SEHRRSFTHSD	583
	* :: : .:** :*.:	
PBCV-1	-----	411
<i>Cricetulus griseus</i>	CKSYNNPPCEENLFSYDISEVERTFGNLQLKDSNVYQDHYHHHRPHSIGSTSSIDGLYD	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>	KHGVVGGVPAPWEKNLTNVDWEDRSGGNFCRSCPSKLNYSSTVAGQNSGRQACIRCEAC	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>	PGGGYMLSLSLYPDRVTQNPFIPTFGDDQCLLHGSKSYFFRQPTVAGASKTRPDFRALVT	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	YKNEDFDKFFQT <u>GLSIL</u> --- <u>LIRFATMFVLILIALKVA</u> NVNNLVIASYAGILL <u>IAVPAA</u>	100
TeV1	---DLEWEI-TKELSIKYGKI <u>IVESINLMIILYLSYLII</u> K-----	92
CroV	RQNLDNWVIHMKGVD <u>LKIGQFLTFIEFFLILIIYLINK</u> -----	97
	: . : : : : : : : :	
AaV	<u>MSTQISNYISGLLLIA</u> FDRIITLNDYIIIDDFEGRIKKNLFSIEVKDEFTHKTRFIPNAD	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	MLEVLFGISNTNFSNNEVKRTRKHSIFWIPLLLTIYKY <u>FFWNYENIYFLFLSLFQLSTLYFL</u>	60
CTV1	----MEGDNSI--YLTRFKFSGLILYVCH <u>IYGYINYFFDFINIFCLLISFF</u> QIYDY---	51
	: * .. ...* : : : : * :*:: ** : *::**:	
KNV1	PKEWSPTGPy <u>STAIPLGICILAEIITHMITWY</u> NDWITDYKENNKEYECLDHSYQLIKKKN	120
CTV1	----R---DFRSFIPLSIFS--TLY---SVYYTYTVSKLI---REQNSI-NSEMFMRKPI	95
	: : ***.* : :*. :. :* :. :*	
KNV1	RNIYPGDI IHLEKEDICPIDGILIDTTNNEKYSKISLALLTGESNINIVIKPAKLFKLQD	180
CTV1	NQIKRGDILELSYQDKIPADILILTDDFHVSTNELE---LSGE---NIVLNKKALF--ED	147
	.* ***:.* :* * * : : : . :. : *:* * * : : ** :*	
KNV1	YKDYKIN-----ISNYHQNNFNIEGKLLNGKEEHNIQGENFVVGSI IKSDDIYLWVIG	235
CTV1	YDNNQLLKSNICINQKKNNGFIEYDNKK-----YKYDENNIVFRGTKMLDGKLGKLVVE	201
	*. : : * . : :*. * : :.* : : : *:* . * : : . . . : *	
KNV1	CGRDKKSYLKKS-VKNDRKKNRIDTF <u>VGNYMINVNAILLLLLI</u> -- <u>LITTTI</u> KLVNSFSFG	292
CTV1	IGNDCMIYNIDNRVLKD--KTWLYKKVNN-- <u>ITFNNLYYLLIISAFIAGAL</u> K--YVYPQR	255
	*.* * .. * :* * . : . *.* *..* : **:* :* : :*	
KNV1	NIIFYM <u>IQNWILFNGIMPFSVKIFLL</u> ----- <u>LARN</u> LQGTGIHNYHKSITINNSLLIDDIG	347
CTV1	KF <u>IFLVKTTVLLLNTVVPLSLQSFY</u> NACTWILSRKIQTEN-----NVTINSHGINCFEN	309
	::** : . :*: * :*:** : * *:*::** .:*** . :	
KNV1	KINKILTDKTGTLTKNELEFSKLLSW-KNDIIDVET-----YQQNYDIDLNFHKCIGL	401
CTV1	NPKYVVTDKTGTITKNQLKLIQVINISNKNNIEKNDITNSSNINFFDI---MSCTLI	365
	: : :*:*:*:*:*:* : : : *:*:* : :*:*:* . * :	
KNV1	CIHQTEENYSTPED-KTLRYRYQYLNNRINQTSQI-ITLTINNNNYDYKY-----I	450
CTV1	NTHSTTKQLLKNDEMEYLLLEWCCKNNKIKIMNNNYNEINKNLSFYKYKFNKKEEKINKI	425
	*.* : : . : : * . : *:*:* : . : . * . *.* : *	
KNV1	EIGGLDFTFERRLSSKIVKDISTDSYIYCKGAMDVIGKIKTDYKTE-LKRLDQMVSQK	509

CTV1	IYKGFYKLGIK----YCITEKDDIYTLNIQGTPEMINLYTNKNLINEGEKLLDEVSNNS	481
	*:*:*:* : . * * : :* : :*. :. : . * * ** : . . .	
KNV1	YPELRLACAFRKIDKNELDMALHESTNKSQIVTLLLENDLHLLGIIGIKDNLQEGVKETI	569
CTV1	Y---RRIICYAKKNITSPTYLDIKNNCN---IN-EYLNKDFEYANIYVFEDQVMDDLANHF	534
	* * : * :* . . : : : . * * : * : . * : * : : : : :	
KNV1	EQFNHYGLFSCLLTGDRKITALAIAKEAGIIDHENTICDFTQEMLDKIDITNLHKK-TILF	628
CTV1	DKLMKNGKHITILTGDRHSSSVEVGKILGMCDDMVLID-KK-----EDMNNIDKTVSLSV	588
	: : : : * . : * * * * : : : . * * : * . * . : * : * : * . : : .	
KNV1	GGALFDIVSQNVKYSESFYDKLALSRNFIGYNLIPEHKKKLTNILE--NKNIKTLTVGDG	686
CTV1	NGKIFNELIREEK----FKNIILNTNKIIVYRATPEIKEKYIQYLKFADEKNQVMMIGDG	644
	. * : * : : : * * : : : : * * . ** * : * : * : : : : : * * *	
KNV1	FNDIGMFHTSSMSIAIKNGFVESN-ADFTIKEFKQLKHLFD---MSLKYYSKNAQLVNL	742
CTV1	SNDISAIMRADVGVAVKGESNQIQNISDVVIDSWCKIPELLKNFSYKKEIIEHNVK <u>WVLT</u>	704
	* * * . : : : : * : * * . . * : * . * . . : : . * : . : : * : * *	
KNV1	<u>TFLRASAVIMSIMTYSLIYY</u> NQ---TTSLEFNG <u>FVIQAFNFAWTILGVGYITL</u> KQRNLPHQ	799
CTV1	<u>KHIMTATILMTMLLI</u> --SNYKEIRDPTNPFH <u>MLILNCLLFVCMSEFNNLRI</u> INNPIN	762
	. . : : : : * : : : * : : * . * : : : : : * . : . * : * * :	
KNV1	DQDYQNKHLVLTNYKN <u>TSIWNAGAGIIFGIVLTLMNYYWF</u> RESKY <u>YFGDICGLMLVMILNG</u>	859
CTV1	EKDYKTHI-----HKGIIIV <u>GMIIGTIVFTIFSV</u> ----- <u>NIGIIIAI</u> -----	798
	: : * * : : * * * . * : : : : * : : * : : : :	
KNV1	<u>KLILNNKLDLWGIGLSLMGIVNFMGYMMY</u> MSLYDVIIT <u>LLTTSKYYWLGVFGMYFGINL</u>	919
CTV1	----- <u>I</u> -----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.









ACEV	NELWDVIEY--IKKKSIVILSSHNVDCEKLCNLCILHKGIVKEQ--TSIKKLNKNCYCI	1418
<i>Onthophagus taurus</i>	RKIKELINETKLNKKSIAIIFTSHSMDECELLCDKLSIMKAGKLETDANLSVPELKEKYNI	1485
	.:: :*: :*:** :*::** .::** ***:*.*: : * : : * : :*:** *	
ACEV	GHILKLFYDNKHIKI-EHQLHSNFDTKNIKILSNHDYMITVRILNYNWITIFDIIERIK	1477
<i>Onthophagus taurus</i>	GHIIQMKVKSPQQIDTILEALRESFNNVIEKIAARNLLTWSIKNSNWGSIISGMESMK	1545
	***:***. . :*: . *:.*. . * : : : : :** * * ** :*:. :* :*	
ACEV	NDTENNIEDYWIMESTLDEALIEIANNKL	1506
<i>Onthophagus taurus</i>	TH-RNEIVDYMVKESSELEEVFLKVAKG--	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>VILSLASLGVVFGDIGTSPLYVLP</u> PA	53
<i>Micractinium conductrix</i>	MPGVSVSALWARDADLSAKIEAQEHRRNASGLRL <u>LALAVSTLGVVYGDIGTSPLYVYGS</u>	60
	* ..* . :. : : * *:* * * : * : : : * : * : * : * : * : * : * : * : * : * : *	
Fr483	IFGELRHQPTEN <u>FILGVFSTIFWTITLMVLVKYVW</u> FTLAIDDDHGEVVGFALYSIIRRAIT	113
<i>Micractinium conductrix</i>	VFPDGAP-ADANR <u>VLGVASTIFWTITSIVLVKYVVF</u> TMQADDNNGEGGIFALYALICRSCN	119
	:* : * :*** ***** :***** ** : ** :***** :***** : : * * : .	
Fr483	SKPSDFGV-----DTQEEKIPSKTKDFLENNKWARD <u>VIMGIVITCASLTMAD</u>	160
<i>Micractinium conductrix</i>	IRSGTRMTEADLTLSQYQGGQTRRGRSVAARLRGAQERSATLQTL <u>LLVVVLLASNMIISD</u>	179
	: . . : : : : : : * . . : : : : * : . : : : * *	
Fr483	<u>GILTPSISVISATEGIQFHTGISHDTVIFITIGILVGLFSIQFLGTGKVGVI</u> FGPTMLW	220
<i>Micractinium conductrix</i>	<u>GVLTPAISVVSIAIEGIQFQTGISQGAVTGISVGLVALFALQSVGTQRVS</u> FLFAPIMVLW	239
	* : * * : * * : * * * * * * * : * : * * * * * * * : * * : * . . : * . * * : * *	
Fr483	<u>FVFNLSVGVYNVT</u> KM--PGVFRAFSPHYMYFWEEF <u>GSWEAFKLLGEVFLAITGVEALYA</u>	278
<i>Micractinium conductrix</i>	<u>FICNATLGIYNIC</u> RFGGPSIFRALSPHYMYFWSGDÄ-HA <u>AWRALGNIMLCVTGAEALYA</u>	298
	* : * : * : * * : : * . : * * * : * * * * * * . . * : : * * : : * : * . * * * *	
Fr483	DMGHLNAMSIR <u>ISFSAIVYPSLVMNYLGQTAVVLL</u> LDYNTSSSLYWSSIPAKLAW <u>WPSLAIA</u>	338
<i>Micractinium conductrix</i>	DMGHFNAQSIR <u>VSFLAVVFPSTLTLTYLGQTAMIL</u> QEPAKAAAFWESVPTPVLWP <u>VVVLA</u>	358
	*** : * * * * : * * * : * : * * * * * : * : . : : : * . * : * : * * : . : *	
Fr483	<u>ASAAVIASQALITGTF</u> TIVQQAMHANVFPRVAI <u>FQTNKKHAGQIYIPVNVFALLVGSISV</u>	398
<i>Micractinium conductrix</i>	<u>TGAAIIASQALITGAFSIV</u> QQAMAMNAFPRVTLRHTSKHN <u>IGQVYIPEINWLLMVGALIV</u>	418
	: . * * : * * * * * * * : * : * * * * * * * . * . * * * : : * . * : : * * : * : * * : *	
Fr483	<u>VLIFQSSSKI</u> VSAYGFAVSIVVVLTHIFFCIVLHIQGR-N <u>KLFSFVFSFFGVISIAFAA</u>	457
<i>Micractinium conductrix</i>	<u>VVVFKTSASIG</u> NAYGLAVITVMLLDTSLFALVALTAWEWHV <u>AAVGAFWLFVTFVTGTFLS</u>	478
	* : * : * : * : * . * * * : * * * : * : * * : * : * . : . * * * . : : * * : *	



Fr483	-----	660
<i>Micractinium conductrix</i>	RLQMGRL LHRTSAASAMPTLAEGEQAQPADSDARSSLDGRVAATVRTEDILGSAAPEGEE	1014
Fr483	-----	660
<i>Micractinium conductrix</i>	ALDTDAARRRLFALQGHAGDAGTPLEDGLAAERLLLLAARQRGVVYLVGKSALCAEPGSS	1074
Fr483	-----	660
<i>Micractinium conductrix</i>	WLKTFLLSAYAALVANCRPTTALYRVPRQGLLAESCRPAAGALVQLAFSCKGMLTAAEA	1134
Fr483	-----	660
<i>Micractinium conductrix</i>	AEPMWRMQCQRLGWSLDWLDTLPPGTSTWRYFCARMHARHHLRLLRSLSRADPSAWEV	1194
Fr483	-----	660
<i>Micractinium conductrix</i>	FELYRVVDGQDRERGGIQFFHEARLLSLREAVAAAQERHGPLRLARAFALAVQRSNGSQ	1254
Fr483	-----	660
<i>Micractinium conductrix</i>	AAGSGGGDSSSVPPPDDQPSSSSCALPLDDRPKSEDTEQEPVLLPLSEEMRGRRRFCAD	1314
Fr483	-----	660
<i>Micractinium conductrix</i>	LRGLIWLASGFHTRCAADSLAVLLQSILT	1343

**Figure S8.** Comparison of viral K<sup>+</sup> 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**

MQQLYKIRSTHEIENIKGGDYDWLEITKPDDSDLSLVQKRTGLEISTSKLILSSHESHIEGLTEPKPLMIVLQYPKMVESNLGDFKE  
YATSPIILILSNLDGDNNDLITISNHEPSFIAKIQEDSKSLKVPITNKKDIMLLVIYYMSQEYRSILRSLNKDANSLEQSLKTATNNIIF  
YHVMSIQKTVSSFLDSLANNQNICEKIENDANYFASEKYTELARSASLAEETSEAARHLDYILDKYTSLVSSIVGNNQLVTINKFTEW  
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 Lfellnf. 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**

**MQLLDMVIFAGYIGCIVMAGLVIGWKKSGTTKSYFMADRSLPWWILGCAILANISAEHLIGTTGSAYAMGIAIGAFELTGALALVVAA  
WLAIPYFVKNQITTMPQFLAMKYDNRVRSMFATFWIVVYTLVNLTAVSYMGALAFTSIGIPLEVGVWALIGFAVLYSAVGGLSSLVWTD  
FIQVGILLTAGIACTWFTLDAYGVHVGSTS IAGSMVSLYKELPNHFQLVLEPGHPAYENIPGILGVGVFLGSLSYFAFNQFIVQALA  
AKSVKEAQKGMVFAAFLKLLMPLVVIIPGIMAYSMTNGSLTPSDKAYPWLIDNFMPAGFHGLVMAALFAAIISTLAAILNSISTMFTLD  
IVKVHKPELSDKTLMKVARTVVVVCGAIGASLAIPFLGNLDQAYHFIQEFVGFVTPAMLVIFFAALYWKTNSNAAIAVTVFSVAANAIV  
KFTVPELAWLDRFLMVLVGCGVLYSLFSGKQVEDAHIAPSKTLVIGGSIVAIIFFATYITFA**

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

**Figure S11**

Vibrio phage	-MELMT <u>GLVMMASASLFI</u> <u>MYACNSLEQ</u> TLDYLG RNMKAGAK <u>GALLMAVASSLPEIMVAFA</u>	59
<i>Vibrio jasicida</i>	MLET <u>IFPFLLIILACYLLKYS</u> CDTFEQAAGYLGRNFPAGVK <u>GATVNAIGSSMPEMCVVIA</u>	60
	:* : :::: *. :: *:*::** : .*****: **.*** : *:.**:*: *:.*	
Vibrio phage	<u>FL-FS</u> GKPE <u>LVLAGVFTAGSAIFNILLIPA</u> VSILYAGDGQGNKVDSFQLDRKVLSDTF	118
<i>Vibrio jasicida</i>	<u>CLFWF</u> NDPQ <u>LVIVALGVTAGSAIFNGCVIPAL</u> SIIVAKDDEGNSVDQIELNK <u>SALLRDVF</u>	120
	* : ..*:*:..: ***** :***:*: * *:.**.*.:::..* **.*	
Vibrio phage	WLLTVEA <u>IFIYFLGLNVFTIGMAATLIILY</u> ALYVSHVIHDSNKAGEQPEGFEFEELDHTF	178
<i>Vibrio jasicida</i>	<u>WLTAEIALIVCLGFSEFSIWMALLNVIYLYG</u> YAIHLYFDAKKHGGDDDEYEEIDDRG	180
	*:.**.* :* **:. *:* ** * ::* *. *: .*:.* * : : :*:.**:*.	
Vibrio phage	TPKFIAWIGYV--LDFNKHLFKNKAYTTKT <u>ASIVCALSCTIIAVACHYLAVSTEIVSAAL</u>	236
<i>Vibrio jasicida</i>	-----FIGNLLTFNFNAILFSNKTFTL <u>TRALIVLALAIAVISGSSHILVEGVLGSAAVL</u>	234
	:** : ::** **.*:*: * . * ** ** : :*: :.* * . . :*.*	
Vibrio phage	<u>GIPVLIGAAVFAAAATS</u> LPDTILSKSASENGEGDDAVANAVGSNIFD <u>TSFAIGLPLLI</u> AL	296
<i>Vibrio jasicida</i>	<u>GVPEFFSGLVFGAAASSIP</u> DLILSVKDAQKGEYEDAIAN <u>PLASNTFDTTVAFALPLFVWF</u>	294
	*:* :... **.***:*:* ** . ::* ** :**:* :.* ***:.*:.**:*: :	
Vibrio phage	<u>TPLGEWLFGINLKEGIPLVQGDSFMDTVRYFVIGTSALAAAGLWVQA</u> KNVTKK <u>TAYYLLT</u>	356
<i>Vibrio jasicida</i>	<u>I-----L</u> NGVDSLPM AQD-NN <u>LTILRWSIIGITAAVACSLLF</u> NYKKVTKS <u>VAYFLLA</u>	345
	:* :.***.* . . : :*: ** :* .**.* : : *:*..**:*:	
Vibrio phage	<u>LYGTWIA</u> YLIYHVS	370
<i>Vibrio jasicida</i>	<u>MFAIWATS</u> MYFVIQ	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--SVFNLSNAIVGSGILGLSEFAMANTGIALEFVILLLEFVSIFSLY  
\* . . \* : . : : \* . : : \* \* : \* . \* : \* . \* : : \* \* : \* \* \* : : : :

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

RSIV P-----DISMYAVG-----MLILLVLFFPVSLPKSSRCLMIISGPALMCVLAFFVYTI  
*Pagrus major* KTFMNIEETTGEWYLNGDYLVLLVSUILILPLSLLKNLGYLGYTSGFSLLCMVFFLIVVI  
. : \* \* : : : : : \* \* \* . \* \* \* : \* \* : : \* : : . \*

RSIV YCVHA-----TVPGPAWPLFDDRMVVDQC-----LSIITFAFVC  
*Pagrus major* WKMFQIPCPMDSVVMNVTFNATVAPLVDENITIDMCKPKYFIFNSQTVYAVPILTFSEFVC  
: . : \* . . \* \* . \* : : : \* \* : : \* \* : \* \* : \* \* :

RSIV QPTIVTTANL-HGDKASGAAAAAMCAMSVGTVLYAVIALCGWLPMPETPDNIVLAYMAT  
*Pagrus major* HPAILPIYEELKGRSRKRMMNVSYVSEFFAMFLMYLLAALFGYLTFYGKVEPELLHTYSAY  
: \* \* : : : \* . . : : : : \* : \* \* \* \* : : : : \* \*

RSIV LDGKIVAGVM----CVSVVLTVPALLLPVVHMMAPI--DRSPMQWMSTL----GMYACMY  
*Pagrus major* LGADVLLLIVRLAVLTAVTLTVPVVIFPIRSSITQLLWAGKEFSWLRHCSITVALLAFTN  
\* . . . : : . : \* . \* \* \* . : : : \* : : : . : \* : : \* :

RSIV VLVIMIPSFKIGVVVVGAVAGTVLVFALPALMYTWLFYRRRVLAWMV--VVLYTTIGIAV  
*Pagrus major* VLVIFVPTIRDIGFIGASAAAMLIFILPSAFYIKLVKKEPMKSVQKIGASFFLSGILV

```

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

```

**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.