

**Table S1.** Percentage amino acid sequence divergence (p-distances) estimated from a CLUSTAL W alignment of perhabdovirus, cetarhavirus, siniperhavirus and scophrhavirus L proteins.

Species	Virus	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	
<i>Perhabdovirus perca*</i>	1 PRV_Dorson_JX679246																												
	2 PRV_16/065_MN964000	3.8																											
	3 PRV_P8350_MN963998	4.5	3.2																										
<i>Perhabdovirus leman</i>	4 LEMV_18/193_MN963996	14.8	13.4	13.1																									
<i>Perhabdovirus trutta*</i>	5 STRV_R6146_MN963999	19.8	18.8	18.5	18.3																								
	6 STRV_18/203_MN963997	20.0	19.1	18.7	18.4	5.2																							
	7 STRV_CH17_MN510774	20.0	19.0	18.6	18.3	5.0	0.9																						
<i>Perhabdovirus anguilla*</i>	8 EVA_J6B4_KC608038	29.4	28.6	28.2	27.6	28.1	27.7	27.7																					
	9 EVEX_CV1153311_FN557213	29.2	28.4	28.0	27.3	27.5	27.1	27.1	2.1																				
	10 EVEX_C30_JN639009	29.1	28.3	27.9	27.3	27.6	27.2	27.2	1.7	0.6																			
	11 EVEX_DF25/04_KC608037	29.2	28.4	28.0	27.4	27.7	27.2	27.2	2.1	0.9	0.4																		
	12 EVEX_DK3545_KC608034	29.2	28.3	28.0	27.3	27.7	27.2	27.2	1.8	0.9	0.3	0.7																	
	13 EVEX_DK3631_KC608035	29.3	28.5	28.1	27.5	27.8	27.3	27.3	2.2	1.1	0.6	1.0	0.8																
	14 EVEX_DK5743_KC608036	29.1	28.3	27.9	27.3	27.6	27.2	27.2	1.8	0.7	0.1	0.5	0.3	0.7															
	15 EVEX_GG129_JN639010	29.3	28.4	28.1	27.4	27.6	27.1	27.1	2.2	1.1	0.6	0.9	0.8	1.1	0.7														
	16 EVEX_GG184_KC608033	29.3	28.4	28.1	27.4	27.6	27.1	27.1	2.2	1.2	0.6	0.9	0.8	1.1	0.8	0.0													
17 EVEX_JP77_JX827265	70.9	28.3	27.9	27.3	27.6	27.2	27.2	1.7	0.6	0.0	0.4	0.3	0.6	0.1	0.6	0.6													
<i>Cetarhavirus lagalarhynchus</i>	18 DRV_KF958252	44.7	43.8	44.2	44.3	45.0	44.3	44.6	44.1	44.1	44.3	44.2	44.3	44.4	44.3	44.3	44.3	44.3	44.3										
<i>Cetarhavirus phocoena</i>	19 HPRV_MN103537	44.8	44.3	44.4	44.5	44.6	44.6	44.8	44.2	44.3	44.2	44.4	44.3	44.3	44.2	44.2	44.2	44.2	44.2	31.3									
<i>Siniperhavirus zoarcas</i>	20 EPRV_KR612230	48.2	47.7	47.9	47.4	47.8	47.5	47.7	48.5	48.0	48.1	48.1	48.2	48.3	48.1	48.2	48.2	48.1	46.1	47.5									
<i>Siniperhavirus chuatsi</i>	21 HSHV_C1207_KC519324	48.2	47.8	47.7	47.9	47.8	47.6	48.7	48.4	48.4	48.4	48.4	48.4	48.4	48.4	48.4	48.4	48.4	45.8	46.0	28.8								
	22 HSHV_SHVV19_MW291462	48.3	47.8	47.8	47.8	47.8	47.7	47.7	48.7	48.4	48.4	48.4	48.4	48.4	48.4	48.4	48.4	48.4	45.6	45.7	28.9	1.1							
	23 CRERV_MH319839	48.0	47.7	47.5	47.7	47.6	47.5	47.5	48.5	48.2	48.2	48.2	48.2	48.2	48.2	48.2	48.2	48.2	45.8	46.0	29.2	2.4	2.8						
	24 MSRV_MK397811	48.1	47.8	47.5	48.0	47.7	47.5	48.6	48.3	48.3	48.3	48.3	48.3	48.3	48.3	48.3	48.3	48.3	45.8	45.8	29.0	3.0	3.6	3.1					
	25 SCR_VDQ399789	48.4	48.0	47.8	48.3	48.1	47.9	47.9	48.9	48.6	48.6	48.6	48.6	48.6	48.6	48.6	48.6	48.6	46.1	46.1	29.3	2.4	2.9	2.6	2.1				
<i>Scophrhavirus maximus</i>	26 SMRV_HQ003891	53.4	52.8	53.1	53.4	52.9	53.1	53.2	53.8	53.7	53.6	53.6	53.6	53.7	53.6	53.5	53.5	53.6	53.2	53.3	54.0	53.5	53.6	53.4	53.4	53.5			
<i>Scophrhavirus chanodichthys</i>	27 WhRCDRV_MG600013	54.7	54.5	54.2	54.4	54.8	55.4	55.5	55.0	55.1	55.0	55.1	55.1	55.2	55.0	55.1	55.1	55.0	52.8	53.9	55.1	55.3	55.3	55.3	55.1	55.2	46.5		

\*Existing species

**Table S2.** Percentage amino acid sequence divergence (p-distances) estimated from a CLUSTAL W alignment of perhabdovirus, cetarhavirus, siniperhavirus and scophrhavirus N proteins.

Species	Virus	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28			
<i>Perhabdovirus perca*</i>	1 PRV_Dorson_JX679246																															
	2 PRV_16/065_MN964000	2.7																														
	3 PRV_P8350_MN963998	2.0	2.4																													
<i>Perhabdovirus leman</i>	4 LEMV_18/193_MN963996	15.9	17.4	16.1																												
<i>Perhabdovirus trutta*</i>	5 LTRV_AF434991	24.9	25.9	25.2	27.1																											
	6 STRV_R6146_MN963999	24.9	25.9	25.2	27.4	0.5																										
	7 STRV_18/203_MN963997	25.9	26.9	26.2	27.9	5.9	5.9																									
	8 STRV_CH17_MN510774	26.2	26.9	26.4	28.1	6.1	6.1	1.5																								
	9 EVA_J6B4_KC608038	37.7	37.2	37.7	38.6	39.9	40.1	40.1	40.3																							
<i>Perhabdovirus anguilla*</i>	10 EVEX_CV1153311_FN557213	37.7	37.2	37.7	38.6	39.9	40.1	40.1	40.3	1.5																						
	11 EVEX_C30_JN639009	37.2	36.7	37.2	38.1	39.4	39.6	39.6	39.9	1.0	1.7																					
	12 EVEX_DF25/04_KC608037	37.4	36.9	37.4	38.4	39.6	39.9	39.9	40.1	0.7	1.0	1.0																				
	13 EVEX_DK3545_KC608034	37.2	36.7	37.2	38.1	39.1	39.4	39.4	39.6	1.2	1.7	0.7	1.0																			
	14 EVEX_DK3631_KC608035	37.2	36.7	37.2	38.1	39.1	39.4	39.4	39.6	1.0	1.5	0.5	0.7	0.2																		
	15 EVEX_DK5743_KC608036	37.2	36.7	37.2	38.1	39.1	39.4	39.4	39.6	1.2	1.7	0.7	1.0	0.0	0.2																	
	16 EVEX_GG129_JN639010	37.4	36.9	37.4	38.4	39.4	39.6	39.6	39.9	0.7	1.0	1.0	0.2	0.7	0.5	0.7																
	17 EVEX_GG184_KC608033	37.4	36.9	37.4	38.4	39.4	39.6	39.6	39.9	0.7	1.0	1.0	0.2	0.7	0.5	0.7	0.0															
	18 EVEX_JP77_JX827265	37.2	36.7	37.2	38.1	39.4	39.6	39.6	39.9	0.7	1.5	0.2	0.7	0.5	0.2	0.5	0.7	0.7														
	<i>Cetarhavirus legalothenchus</i>	19 DRV_KF958252	58.7	58.7	59.4	59.7	58.2	57.9	58.7	58.9	60.6	60.6	60.4	60.4	60.4	60.4	60.4	60.4	60.4	60.4												
<i>Cetarhavirus phocoena</i>	20 HPRV_MN103537	57.7	57.2	57.2	57.2	55.7	56.0	57.0	56.7	56.5	56.2	56.2	56.2	56.2	56.2	56.2	56.2	56.2	56.2	31.8												
<i>Siniperhavirus zoarces</i>	21 EPRV_KR612230	58.9	59.2	58.4	59.2	59.2	59.4	59.9	59.7	60.9	60.9	60.4	60.6	60.4	60.4	60.4	60.6	60.6	60.4	51.3	53.8											
<i>Siniperhavirus chuatsi</i>	22 HSHV_C1207_KC519324	55.5	55.5	56.2	58.4	56.5	56.2	57.0	56.7	58.2	58.2	58.2	57.7	58.2	58.2	58.2	57.9	57.9	58.2	51.6	53.3	34.2										
	23 HSHV_SHVV19_MW291462	55.5	55.5	56.2	58.4	56.7	56.5	57.2	57.0	58.2	58.2	58.2	57.7	58.2	58.2	58.2	57.9	57.1	58.2	51.8	53.5	34.0	0.7									
	24 CRERV_MH319839	56.2	56.2	56.7	57.7	56.7	56.5	57.2	57.0	57.5	57.5	57.5	57.3	57.5	57.5	57.5	57.2	57.2	57.5	57.2	53.5	33.7	3.7	4.4								
	25 MSRV_MK397811	56.7	56.2	56.7	58.2	57.0	56.7	57.2	57.0	58.2	58.2	57.9	58.2	58.2	58.2	58.2	57.9	57.9	58.2	52.8	53.0	35.7	5.6	6.4	6.8							
	26 SCRV_DQ399789	56.5	56.0	56.7	58.2	57.0	56.7	57.7	57.5	58.7	58.7	58.2	58.4	58.4	58.4	58.4	58.4	58.4	58.4	51.8	53.8	34.7	3.4	4.2	4.2	4.4						
	27 SMRV_HQ003891	68.9	68.7	69.2	69.4	71.6	71.6	71.4	71.4	69.9	69.9	69.4	69.7	69.4	69.4	69.4	69.7	69.7	69.4	68.9	68.7	72.9	72.6	72.6	72.1	72.9	72.6					
<i>Scophrhavirus chandocythys</i>	28 WnRCRV_MG600013	70.2	69.4	70.2	71.6	71.1	70.9	70.7	70.9	70.4	69.9	69.9	70.2	69.9	69.9	69.9	70.2	70.2	69.9	69.7	70.4	71.9	69.9	69.7	70.2	69.9	69.7	62.6				

\*Existing species

**Table S3.** Percentage amino acid sequence divergence (p-distances) estimated from a CLUSTAL W alignment of perhabdovirus, cetarhavirus, siniperhavirus and scophrhavirus G proteins.

Species	Virus	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28		
<i>Perhabdovirus perca*</i>	1 PRV_Dorson_JX679246																														
	2 PRV_16/065_MN964000	3.3																													
	3 PRV_P8350_MN963998	1.8	3.1																												
<i>Perhabdovirus leman</i>	4 LEMV_18/193_MN963996	16.9	18.0	16.7																											
	5 LTRV_903/87_AF434991	30.4	31.0	30.8	32.4																										
<i>Perhabdovirus trutta*</i>	6 STRV_R6146_MN963999	30.2	31.0	30.6	32.0	4.3																									
	7 STRV_18/203_MN963997	32.0	32.2	32.0	31.8	10.4	11.6																								
	8 STRV_CH17_MN510774	32.0	32.7	32.0	31.8	9.6	11.0	2.7																							
	9 EVA_J6B4_KC608038	46.1	46.3	46.7	47.8	47.6	48.0	46.9	47.3																						
<i>Perhabdovirus anguilla*</i>	10 EVEX_CV1153311_FN557213	45.9	46.7	46.5	48.0	47.3	47.6	47.6	47.6	3.3																					
	11 EVEX_C30_JN639009	45.9	46.7	46.5	48.0	47.6	47.8	47.8	47.8	3.3	0.4																				
	12 EVEX_DF25/04_KC608037	46.1	46.7	46.7	48.0	47.3	47.6	47.3	47.3	3.5	1.0	1.0																			
	13 EVEX_DK3545_KC608034	45.5	46.3	46.1	47.6	47.1	47.3	47.1	47.1	3.5	0.8	0.8	1.2																		
	14 EVEX_DK3631_KC608035	45.5	46.3	46.1	47.8	47.6	47.8	47.8	47.8	3.9	2.2	2.2	2.7	1.8																	
	15 EVEX_DK5743_KC608036	46.5	47.3	47.1	48.6	48.2	48.4	48.4	48.4	4.1	1.2	0.8	1.8	1.6	3.1																
	16 EVEX_GG129_JN639010	46.1	46.9	46.7	48.0	47.6	47.8	47.8	47.8	3.7	0.8	0.8	1.4	1.2	2.7	1.6															
	17 EVEX_GG184_KC608033	46.1	46.9	46.7	48.0	47.6	47.8	47.8	47.8	3.5	0.6	0.6	1.2	1.0	2.4	1.4	0.2														
	18 EVEX_JP77_JX827265	45.9	46.7	46.5	48.0	47.3	47.6	47.3	47.3	3.3	0.2	0.4	1.0	0.8	2.2	1.2	0.8	0.6													
<i>Cetarhavirus legalathynchus</i>	19 DRV_KF958252	67.3	67.1	67.3	66.7	68.8	69.2	67.1	67.3	68.2	68.6	68.6	68.4	68.4	68.4	69.0	69.0	68.8	68.6												
<i>Cetarhavirus phocena</i>	20 HPRV_MN103537	66.5	66.3	66.7	66.3	68.4	68.4	68.0	68.0	66.9	67.3	67.3	67.1	67.3	67.6	67.8	67.6	67.6	67.3	56.1											
<i>Siniperhavirus zoarces</i>	21 EPRV_KR612230	72.9	72.7	73.1	73.3	75.5	74.9	75.3	74.9	71.4	71.4	71.4	71.2	71.4	71.2	71.6	71.8	71.6	71.2	71.2	73.7										
<i>Siniperhavirus chuatsi</i>	22 HSHV_C1207_KC519324	73.1	73.1	73.3	72.7	73.1	72.7	73.5	73.7	72.7	72.4	72.4	72.2	72.2	72.0	72.7	72.4	72.4	69.4	70.4	50.4										
	23 HSHV_SHVV19_MW291462	73.1	73.1	73.3	73.1	73.1	72.7	73.9	74.1	73.3	73.1	73.1	72.9	72.9	72.7	73.7	73.3	73.1	73.1	69.8	71.2	50.0	3.9								
	24 CRERV_MH319839	72.7	72.7	72.9	72.4	73.7	73.5	74.3	74.5	72.9	72.7	72.7	72.4	72.2	72.9	72.9	72.7	72.7	70.0	71.2	50.0	8.6	10.6								
	25 MSRV_MK397811	72.9	72.7	73.1	72.9	74.1	73.9	74.9	75.3	73.3	73.3	73.3	73.3	73.1	73.1	73.9	73.5	73.5	73.3	73.3	69.6	71.6	51.8	8.6	10.6	8.6					
	26 SCR_V_DQ399789	72.2	72.2	72.4	72.4	73.9	73.7	74.9	75.1	73.3	73.1	73.1	72.9	72.9	72.7	73.3	73.3	73.1	73.1	69.2	72.0	51.2	6.3	8.4	6.7	3.1					
<i>Scophrhavirus maximus</i>	27 SMRV_HQ003891	78.0	78.2	78.4	77.6	78.8	78.6	77.8	77.8	76.1	76.3	76.3	76.1	76.3	76.9	76.5	76.3	76.3	76.3	78.2	77.8	79.8	80.0	80.8	78.8	81.0	80.6				
<i>Scophrhavirus chandoychthys</i>	28 WnRCDRV_MG600013	74.4	73.9	74.7	75.1	75.1	75.5	75.5	75.3	74.9	74.5	74.5	74.3	74.3	74.3	75.1	74.7	74.7	74.5	76.7	77.8	79.0	79.0	78.8	78.6	78.8	79.4	71.0			

\*Existing species