

1 **Table A1:** Metadata of the analyzed 198 unique VHSV isolates including information on overall
2 genotype- (GT) based on the G gene, sublineage- (SL) and clade (CL) affiliation, as well as the isolate
3 name, host origin, environment of isolation (Env), country of isolation (C), year of isolation (Year),
4 official NCBI accession number (Acc No.), the six amino acid sites detected under positive selection
5 (aa6, aa212, aa258, aa259, aa505, aa506), and the associated positive selection site restricted
6 haplotype (Haplo) that was generated based on the amino acid combinations at sites that undergo
7 positive selection. Amino acids identified under positive selection are listed using standard one letter
8 abbreviations and are color coded according to chemical characteristics: light grey) neutral, nonpolar
9 amino acids; dark grey) neutral, polar amino acids; orange) acidic amino acids; and blue) basic amino
10 acids. Dotted horizontal lines separate the different phylogenetic groups.

GT	SL	CL	Isolate	Host ^a	Env ^b	C ^c	Year	Acc No.	Sites under positive selection ^d						
									6	212	258	259	505	506	Haplo
I	n.a.	n.a.	DK-F1	RT	FW	DK	1962	AF345857.1	F	T	T	E	Q	T	H39
I	n.a.	n.a.	DK-Hededam	RT	FW	DK	1970	U28798.1	F	K	T	D	Q	T	H26
I	Ia	n.a.	FR-0284	RT	FW	FR	1984	U28800	F	K	T	E	Q	T	H27
I	Ia	Ia-1	Dau170-04	RT	FW	DE	2004	EU708742.1	F	E	E	K	Q	M	H2
I	Ia	Ia-1	Dau42-99	RT	FW	DE	1999	EU708739.1	F	N	A	D	Q	T	H28
I	Ia	Ia-1	Dfr195-05	RT	FW	DE	2005	EU708760.1	F	K	A	D	Q	T	H6
I	Ia	Ia-1	DK-200027-3	RT	FW	DK	2000	AY546609.1	F	K	E	D	Q	M	H10
I	Ia	Ia-1	DK-200079-1	RT	FW	DK	2000	AY546613.1	F	K	E	D	Q	T	H11
I	Ia	Ia-1	DK-204022	RT	FW	DK	2004	JF681347.1	F	K	E	D	Q	M	H10
I	Ia	Ia-1	DK-204038	RT	FW	DK	2004	JF681342.1	F	K	K	D	Q	M	H23
I	Ia	Ia-1	DK-204062	RT	FW	DK	2004	JF681314.1	F	K	E	D	Q	M	H10
I	Ia	Ia-1	DK-204070	RT	FW	DK	2004	JF681334.1	F	K	G	D	Q	M	H19
I	Ia	Ia-1	DK-204129	RT	FW	DK	2004	JF681340.1	F	K	G	D	Q	M	H19
I	Ia	Ia-1	DK-204249	RT	FW	DK	2004	JF681348.1	F	K	K	D	Q	M	H23
I	Ia	Ia-1	DK-204408-1	RT	FW	DK	2004	JF681338.1	F	K	E	D	Q	M	H10
I	Ia	Ia-1	DK-205001	RT	FW	DK	2005	JF681308.1	F	K	E	D	Q	M	H10
I	Ia	Ia-1	DK-205061	RT	FW	DK	2005	JF681345	F	K	G	D	Q	M	H19
I	Ia	Ia-1	DK-205070	RT	FW	DK	2005	JF681328.1	F	K	G	D	Q	M	H19
I	Ia	Ia-1	DK-205090	RT	FW	DK	2005	JF681333.1	F	K	G	D	Q	M	H19
I	Ia	Ia-1	DK-205107	RT	FW	DK	2005	JF681354.1	F	K	G	D	Q	M	H19
I	Ia	Ia-1	DK-205297-1	RT	FW	DK	2005	JF681332.1	F	K	G	D	Q	M	H19
I	Ia	Ia-1	DK-205363	RT	FW	DK	2005	JF681339.1	F	K	K	D	Q	M	H23
I	Ia	Ia-1	DK-205416	RT	FW	DK	2005	JF681346.1	F	K	E	D	Q	M	H10
I	Ia	Ia-1	DK-206130	RT	FW	DK	2006	JF681329.1	F	K	G	D	Q	M	H19
I	Ia	Ia-1	DK-206262	RT	FW	DK	2006	JF681313.1	F	K	G	D	Q	M	H19

I	Ia	Ia-1	DK-207017	RT	FW	DK	2007	JF681321	F	K	E	D	Q	M	H10
I	Ia	Ia-1	DK-207023	RT	FW	DK	2007	JF681355.1	F	K	E	D	Q	M	H10
I	Ia	Ia-1	DK-207048	RT	FW	DK	2007	JF681356.1	F	K	E	D	Q	M	H10
I	Ia	Ia-1	DK-207057	RT	FW	DK	2007	JF681322.1	F	K	E	D	Q	M	H10
I	Ia	Ia-1	DK-207076-2	RT	FW	DK	2007	JF681344.1	F	K	E	D	Q	M	H10
I	Ia	Ia-1	DK-207081	RT	FW	DK	2007	JF681316.1	F	K	E	D	Q	M	H10
I	Ia	Ia-1	DK-207085	RT	FW	DK	2007	JF681350.1	F	K	E	D	Q	M	H10
I	Ia	Ia-1	DK-207193	RT	FW	DK	2007	JF681337.1	F	K	E	D	Q	M	H10
I	Ia	Ia-1	DK-207227	RT	FW	DK	2007	JF681318.1	F	K	E	D	Q	M	H10
I	Ia	Ia-1	DK-208048	RT	FW	DK	2008	JF681336.1	F	K	K	D	Q	M	H23
I	Ia	Ia-1	DK-208195-2	RT	FW	DK	2008	JF681353.1	F	K	E	N	Q	M	H15
I	Ia	Ia-1	DK-209005-1	RT	FW	DK	2008	JF681352.1	F	K	E	D	Q	M	H10
I	Ia	Ia-1	DK-5151	RT	FW	DK	1988	AF345859.1	F	N	A	D	Q	T	H28
I	Ia	Ia-1	DK-6045	RT	FW	DK	1991	AY546592.1	F	N	A	D	Q	T	H28
I	Ia	Ia-1	DK-6137	RT	FW	DK	1991	AY546593.1	F	K	A	D	Q	T	H6
I	Ia	Ia-1	DK-7380	RT	FW	DK	1994	AY546594.1	F	N	K	D	Q	T	H31
I	Ia	Ia-1	DK-7974	RT	FW	DK	1994	AY546595.1	F	N	A	D	Q	T	H28
I	Ia	Ia-1	DK-9595168	RT	FW	DK	1995	AY546596.1	F	N	E	D	Q	T	H29
I	Ia	Ia-1	DK-9795568	RT	FW	DK	1997	AY546598.1	F	K	K	D	Q	T	H24
I	Ia	Ia-1	DK-9895093	RT	FW	DK	1998	AY546600.1	F	N	K	D	Q	T	H31
I	Ia	Ia-1	DK-9995007	RT	FW	DK	1999	AY546601.1	F	K	K	D	Q	T	H24
I	Ia	Ia-1	Dns46-07	RT	FW	DE	2007	EU708769.1	F	K	G	D	Q	M	H19
I	Ia	Ia-1	Dns6-07	RT	FW	DE	2007	EU708767.1	F	K	G	D	Q	M	H19
I	Ia	Ia-1	Dri01-06	G	FW	DE	2006	EU708772.1	F	K	E	D	L	M	H9
I	Ia	Ia-1	Dsteinbutt	T	M	DE	1991	EU708793.1	F	N	A	D	Q	T	H28
I	Ia	Ia-1	Dstg22-03	RT	FW	DE	2003	EU708794.1	F	K	E	D	Q	M	H10
I	Ia	Ia-1	UK-J167	RT	FW	UK	2001	JN180851.1	F	K	E	D	Q	M	H10
I	Ia	Ia-2	Au28-95	RT	FW	AT	1995	EU708729.1	F	E	A	D	Q	T	H1
I	Ia	Ia-2	Au299-94	RT	FW	AT	1994	EU708732.1	F	K	E	E	Q	T	H1
I	Ia	Ia-2	Au77-99	RT	FW	AT	1999	EU708731.1	F	K	E	E	Q	T	H13
I	Ia	Ia-2	AU-8-95	RT	FW	AT	1995	AY546570.1	F	E	A	D	Q	T	H13
I	Ia	Ia-2	Au917-04	RT	FW	AT	2004	EU708733.1	F	K	G	E	Q	T	H21
I	Ia	Ia-2	CH-FI262BFH	RT	FW	CH	1999	AY546571.1	F	K	G	E	Q	M	H20
I	Ia	Ia-2	Dau1124-00	RT	FW	DE	2000	EU708749.1	F	K	E	E	Q	T	H13
I	Ia	Ia-2	Dau1402-97	RT	FW	DE	1997	EU708750.1	F	E	T	D	Q	T	H5
I	Ia	Ia-2	Dau1556-98	RT	FW	DE	1998	EU708752.1	F	K	E	E	Q	T	H13
I	Ia	Ia-2	Dau201-05	RT	FW	DE	2005	EU708743.1	F	K	G	A	Q	M	H17
I	Ia	Ia-2	Dau24-02	RT	FW	DE	2002	EU708737.1	F	K	G	A	Q	M	H17
I	Ia	Ia-2	Dau412-02	RT	FW	DE	2002	EU708744.1	F	K	G	E	Q	T	H21
I	Ia	Ia-2	Dau52-98	RT	FW	DE	1998	EU708740.1	F	K	E	E	Q	T	H13
I	Ia	Ia-2	Dau543-03	RT	FW	DE	2003	EU708747.1	F	K	G	A	Q	M	H17
I	Ia	Ia-2	Dau56-02	RT	FW	DE	2002	EU708741.1	F	E	T	D	Q	T	H5
I	Ia	Ia-2	Dau686-97	RT	FW	DE	1997	EU708748.1	F	E	T	D	Q	T	H5
I	Ia	Ia-2	Db359-92	RT	FW	DE	1992	EU708755.1	P	E	T	D	Q	T	H44
I	Ia	Ia-2	Db416-92	RT	FW	DE	1992	EU708756.1	P	E	T	D	Q	T	H44
I	Ia	Ia-2	Db493-08	RT	FW	DE	2008	EU708757.1	F	K	G	A	Q	T	H18

I	Ia	Ia-2	Db905-03	RT	FW	DE	2003	EU708758.1	F	K	G	A	Q	T	H18
I	Ia	Ia-2	Dfr148-07	RT	FW	DE	2007	EU708762.1	F	K	G	A	Q	M	H17
I	Ia	Ia-2	Dfr2247-06	RT	FW	DE	2006	EU708764	F	K	G	A	Q	M	H17
I	Ia	Ia-2	Dfr2868-06	RT	FW	DE	2006	EU708765.1	F	K	G	A	Q	M	H17
I	Ia	Ia-2	Dfr378-07	RT	FW	DE	2007	EU708763.1	F	K	G	A	Q	M	H17
I	Ia	Ia-2	Dfr404-05	RT	FW	DE	2005	EU708761.1	F	K	E	E	Q	T	H13
I	Ia	Ia-2	DK-200098	RT	FW	DK	2000	AY546605.1	F	K	K	E	Q	T	H25
I	Ia	Ia-2	DK-204157	RT	FW	DK	2004	JF681357.1	F	K	E	K	Q	T	H14
I	Ia	Ia-2	DK-208037-1	RT	FW	DK	2008	JF681359.1	F	K	E	K	Q	T	H14
I	Ia	Ia-2	DK-208308-1	RT	FW	DK	2008	JF681358.1	F	K	E	K	Q	T	H14
I	Ia	Ia-2	DK-9995144	RT	FW	DK	1999	AY546602.1	F	K	K	E	Q	T	H25
I	Ia	Ia-2	Dns13462-03	RT	FW	DE	2003	EU708771.1	F	K	G	A	L	T	H16
I	Ia	Ia-2	Dns166-06	RT	FW	DE	2006	EU708770.1	F	K	G	A	Q	T	H18
I	Ia	Ia-2	Dri04-08	RT	FW	DE	2008	EU708775.1	F	K	G	A	Q	M	H17
I	Ia	Ia-2	Dri07-05	RT	FW	DE	2005	EU708773.1	F	K	T	D	Q	T	H26
I	Ia	Ia-2	Dri47-06	RT	FW	DE	2006	EU708776.1	F	K	T	D	Q	T	H26
I	Ia	Ia-2	Dsa05-00	RT	FW	DE	2000	EU708777.1	F	E	T	D	L	T	H4
I	Ia	Ia-2	Dsa12-99	RT	FW	DE	1999	EU708779.1	F	K	E	E	Q	T	H13
I	Ia	Ia-2	Dsa141-7-94	RT	FW	DE	1994	EU708784.1	F	K	E	E	L	T	H12
I	Ia	Ia-2	Dsa142-96	RT	FW	DE	1996	EU708785.1	F	K	A	D	Q	T	H6
I	Ia	Ia-2	Dsa14893-05	RT	FW	DE	2005	EU708787.1	F	K	T	D	Q	T	H26
I	Ia	Ia-2	Dsa14894-05	RT	FW	DE	2005	EU708788.1	F	N	G	A	Q	M	H30
I	Ia	Ia-2	Dsa19-7-93	RT	FW	DE	1993	EU708780.1	F	K	K	D	Q	T	H24
I	Ia	Ia-2	Dsa21583-03	RT	FW	DE	2003	EU708790.1	F	K	T	D	Q	T	H26
I	Ia	Ia-2	Dsa67-01	RT	FW	DE	2001	EU708781.1	F	E	S	D	Q	T	H3
I	Ia	Ia-2	Dsa6915-02	RT	FW	DE	2002	EU708786.1	F	E	T	D	Q	T	H5
I	Ia	Ia-2	Dsa82-99	RT	FW	DE	1999	EU708782.1	F	E	T	D	Q	T	H5
I	Ia	Ia-2	Dsa90-98	RT	FW	DE	1998	EU708783.1	F	K	E	E	Q	T	H13
I	Ia	Ia-2	Dstg21-07	RT	FW	DE	2007	EU708804.1	F	K	G	A	Q	M	H17
I	Ia	Ia-2	Dstg28-06	RT	FW	DE	2006	EU708805.1	F	K	G	A	Q	M	H17
I	Ia	Ia-2	Dstg31-07	RT	FW	DE	2007	EU708806.1	F	K	G	A	Q	M	H17
I	Ia	Ia-2	Dstg36-06	RT	FW	DE	2006	EU708807.1	F	K	G	T	Q	M	H22
I	Ia	Ia-2	Dstg42-06	RT	FW	DE	2006	EU708808.1	F	K	G	A	Q	M	H17
I	Ia	Ia-2	Dstg44-04	RT	FW	DE	2004	EU708798.1	F	K	G	A	Q	M	H17
I	Ia	Ia-2	Dstg50-2-04	RT	FW	DE	2004	EU708800.1	F	K	G	T	Q	M	H22
I	Ia	Ia-2	Dstg54-1-07	RT	FW	DE	2007	EU708809.1	F	K	G	A	Q	T	H18
I	Ia	Ia-2	Dstg74-03	RT	FW	DE	2003	EU708801.1	F	K	G	A	Q	M	H17
I	Ia	Ia-2	Dstg8-06	RT	FW	DE	2006	EU708803.1	F	K	G	A	Q	M	H17
I	Ia	Ia-2	Dstg82-1-07	RT	FW	DE	2007	EU708810.1	F	K	T	D	Q	T	H26
I	Ia	Ia-2	Dstg89-1-07	RT	FW	DE	2007	EU708811.1	F	K	T	D	Q	T	H26
I	Ia	Ia-2	Dvgeig	RT	FW	DE	2007	EU708812.1	F	K	T	E	Q	T	H27
I	Ia	Ia-2	Dwb86-04	RT	FW	DE	2004	EU708814.1	F	K	G	A	Q	M	H17
I	Ia	Ia-2	Dwb88-04	RT	FW	DE	2004	EU708815.1	F	K	G	A	Q	M	H17
I	Ia	Ia-2	FR-0771	RT	FW	FR	1971	AY546616.1	F	K	T	E	Q	T	H27
I	Ia	Ia-2	Slo1455-07	RT	FW	SI	2007	GQ292534.1	F	K	G	A	Q	M	H17
I	Ia	Ia-3	Dfi13-83	RT	FW	DE	1983	EU708759.1	F	K	A	E	L	T	H7

I	Ia	Ia-3	DK-3592b	RT	FW	DK	1986	X66134	F	K	A	E	Q	T	H8
I	Ia	Ia-3	DK-3946	RT	FW	DK	1987	AY546586.1	F	K	A	E	Q	T	H8
I	Ia	Ia-3	DK-3971	RT	FW	DK	1987	AY546587.1	F	K	A	E	Q	T	H8
I	Ia	Ia-3	Fil3	RT	FW	DE	1983	Y18263.1	F	K	A	E	Q	T	H8
I	Ia	Ia-4	DK-5741	RT	FW	DK	1990	AY546591.1	F	K	T	E	Q	T	H27
I	Ia	Ia-4	DK-9695377	RT	FW	DK	1996	AY546597.1	F	K	T	E	Q	T	H27
I	Ia	Ia-4	DK-9895024	RT	FW	DK	1998	AY546599.1	F	K	T	E	Q	T	H27
I	Ia	Ia-4	DK-9895174	RT	FW	DK	1998	AY546603.1	F	K	T	E	Q	T	H27
I	Ia	Ia-4	Dsan152	RT	FW	DE	2001	EU708791.1	F	K	T	E	Q	T	H27
I	Ib	n.a.	CH150208	H	M	NO	2008	FJ384761.1	F	T	A	E	Q	M	H35
I	Ib	n.a.	Dglaaal	Eel	M	DE	1999	EU708766.1	F	T	T	E	Q	M	H38
I	Ib	n.a.	DK-1p40	R	M	DK	1996	AY546575.1	F	T	T	E	Q	M	H38
I	Ib	n.a.	DK-1p8	AH	M	DK	1996	AY546573.1	F	T	T	E	Q	M	H38
I	Ib	n.a.	DK-1p86	S	M	DK	1996	AY546579.1	F	T	T	E	Q	M	H38
I	Ib	n.a.	DK-4p37	BW	M	DK	1997	FJ460590.1	F	T	T	E	Q	M	H38
I	Ib	n.a.	DK-5e59	Dab	M	DK	1998	AY546583.1	F	T	T	E	Q	M	H38
I	Ib	n.a.	DK-6p403	AH	M	DK	1999	AY546584.1	F	T	T	E	Q	M	H38
I	Ib	n.a.	DK-M.rhabdo	Cod	M	DK	1979	Z93414	F	T	T	E	Q	M	H38
I	Ib	n.a.	KRRV9601	JF	M	JP	1996	AB672614.1	F	T	T	E	Q	M	H38
I	Ib	n.a.	NO-R-190310-174	AH	M	NO	2010	JQ755260.1	F	T	A	E	Q	M	H35
I	Ib	n.a.	NO-R-220410-239	AH	M	NO	2010	JQ755265.1	F	T	T	E	Q	M	H38
I	Ib	n.a.	SE-SVA-1033	RT	M	SE	2000	FJ460591.1	F	T	T	E	Q	M	H38
I	Ib	n.a.	SE-SVA14	RT	M	SE	1998	AY546622.1	F	T	T	E	Q	M	H38
I	Ib	n.a.	SE-SVA31	AH	M	SE	2000	AY546626.1	F	T	T	E	Q	M	H38
I	Ib	n.a.	SE-SVA32	PG	M	SE	2000	AY546627.1	F	T	T	E	Q	M	H38
I	Ib	n.a.	UK-9643	AH	M	UK	1996	AF143862	F	T	T	E	Q	M	H38
I	Ib	n.a.	UK-MLA98-6HE1	H	M	UK	1998	AY546631.1	F	T	T	E	Q	M	H38
I	Ic	n.a.	Au62-96	RT	FW	AT	1996	EU708730.1	L	T	T	D	Q	T	H42
I	Ic	n.a.	Dau10-97	RT	FW	DE	1997	EU708736.1	F	T	T	D	Q	T	H37
I	Ic	n.a.	Dau9-97	RT	FW	DE	1997	EU708735.1	F	T	T	D	Q	T	H37
I	Ic	n.a.	DK-2835	RT	FW	DK	1982	AY546585.1	L	T	T	D	Q	T	H42
I	Ic	n.a.	DK-5123	RT	FW	DK	1988	AY546588.1	F	T	T	D	Q	T	H37
I	Ic	n.a.	DK-5131	RT	FW	DK	1988	AF345858.1	P	T	T	D	Q	T	H45
I	Ic	n.a.	Dri12-95	RT	FW	DE	1995	EU708774.1	F	T	T	D	Q	T	H37
I	Id	n.a.	FI-ka422	RT	M	FI	2000	AY546615.1	L	T	T	E	Q	T	H43
I	Id	n.a.	FI-ka66	RT	M	FI	2000	AY546614.1	F	T	T	E	Q	T	H39
I	Id	n.a.	NO-A16368G	RT	M	NO	1968	AY546621.1	F	T	V	E	Q	T	H41
I	Ie	n.a.	GE-1.2	RT	FW	GE	1981	AY546619.1	F	T	T	D	Q	M	H36
I	If	n.a.	Datt107	RT	FW	DE	n.a.	EU708734.1	S	A	T	D	Q	T	H46
I	If	n.a.	Dau1503-01	RT	FW	DE	2001	EU708751.1	F	T	T	D	Q	T	H37
I	If	n.a.	Daulab	RT	FW	DE	2001	EU708753.1	F	T	T	D	Q	T	H37
I	If	n.a.	FR-1458	RT	FW	FR	1990	AF143863	F	T	T	D	Q	T	H37
I	If	n.a.	FR-2375	RT	FW	FR	1975	AY546617.1	F	T	T	D	Q	T	H37
II	n.a.	n.a.	DK-1p53	AH	M	DK	1996	AY546577.1	F	T	T	E	Q	M	H38
II	n.a.	n.a.	DK-1p55	S	M	DK	1996	AY546578.1	F	T	T	E	Q	M	H38
II	n.a.	n.a.	FI-ka350_06	BH	M	FI	2006	HQ112233.1	F	T	T	E	Q	M	H38

II	n.a.	n.a.	FI-ka383_04	BH	M	FI	2004	HQ112236.1	F	T	T	E	Q	M	H38
II	n.a.	n.a.	FI-ka427_04	BH	M	FI	2004	HQ112240.1	F	T	T	E	Q	M	H38
II	n.a.	n.a.	FI-ka436_04	BH	M	FI	2004	HQ112241.1	F	T	T	E	Q	M	H38
II	n.a.	n.a.	FI-ka494_05	BH	M	FI	2005	HQ112242.1	F	T	T	E	Q	M	H38
II	n.a.	n.a.	FI-ka560_04	BH	M	FI	2004	HQ112243.1	F	T	T	E	Q	M	H38
II	n.a.	n.a.	FI-ka564_04	BH	M	FI	2004	HQ112244.1	F	T	T	E	Q	M	H38
II	n.a.	n.a.	FI-ka646_04	BH	M	FI	2004	HQ112246.1	F	T	T	E	Q	M	H38
II	n.a.	n.a.	FI-ka663_06	BH	M	FI	2006	HQ112247.1	F	T	T	E	Q	M	H38
II	n.a.	n.a.	FI-ka664_04	BH	M	FI	2004	HQ112248.1	F	T	T	E	Q	M	H38
II	n.a.	n.a.	FI-lamprey-739.03	L	FW	FI	2003	GQ504014.1	F	T	T	E	Q	M	H38
III	n.a.	n.a.	DK-4p101	W	M	DK	1997	AY546581.1	F	T	T	D	Q	M	H36
III	n.a.	n.a.	DK-4p168	AH	M	DK	1997	AY546582.1	F	T	T	D	Q	M	H36
III	n.a.	n.a.	FA280208-VG	RT	M	NO	2008	GU121101.1	F	T	T	D	Q	M	H36
III	n.a.	n.a.	FR-L59X	Eel	F	FR	1987	AY546618.1	F	T	T	D	Q	T	H37
III	n.a.	n.a.	IR-F13.02.97	T	M	IE	1997	AY546620.1	F	T	T	D	Q	M	H36
III	n.a.	n.a.	UK-860-94	T	M	UK	1994	AY546628.1	F	T	T	E	Q	V	H40
III	n.a.	n.a.	UK-H17-2-95	Ha	M	UK	1995	AY546629.1	F	T	T	D	Q	M	H36
III	n.a.	n.a.	UK-H17-5-93	Cod	M	UK	1993	AY546630.1	F	T	T	D	Q	M	H36
III	n.a.	n.a.	UK-MLA98-6PT11	NP	M	UK	1998	AY546632.1	F	T	T	D	Q	M	H36
IV	IVa	n.a.	AY167587	OF	M	KR	n.a.	AY167587.1	F	Q	T	E	Q	M	H34
IV	IVa	n.a.	BC93-372	PH	M	CA	1993	DQ401186.1	F	Q	T	E	Q	M	H34
IV	IVa	n.a.	BC98-250	AS	M	CA	1998	DQ401187.1	F	Q	T	D	Q	M	H33
IV	IVa	n.a.	BC99-001	PS	M	CA	1999	DQ401195.1	F	Q	T	E	Q	M	H34
IV	IVa	n.a.	BC99-010	PH	M	CA	1999	DQ401194.1	F	Q	T	E	Q	M	H34
IV	IVa	n.a.	BC99-292	AS	M	CA	1999	DQ401188.1	F	Q	T	D	Q	M	H33
IV	IVa	n.a.	JF00Ehi1	JF	M	JP	2000	AB490792.1	F	Q	T	E	Q	M	H34
IV	IVa	n.a.	JP99Obama25	JF	M	JP	1999	DQ401191.1	F	Q	T	E	Q	M	H34
IV	IVa	n.a.	KJ2008	OF	M	KR	2008	JF792424.1	F	Q	T	E	Q	M	H34
IV	IVa	n.a.	KR-CJA	OF	M	KR	2010	JQ651388.1	F	Q	T	E	Q	M	H34
IV	IVa	n.a.	KRRV9822	JF	M	JP	1998	AB179621.1	F	Q	T	E	Q	M	H34
IV	IVa	n.a.	US-Makah	CS	FW	US	1988	U28747.1	F	Q	T	E	Q	M	H34
IV	IVa	n.a.	WA91Clearwater	CS	M	US	1991	DQ401189.1	F	Q	T	D	Q	M	H33
IV	IVa	n.a.	ME03	AH	M	US	2003	DQ401192.1	F	Q	T	E	Q	M	H34
IV	IVb	n.a.	Goby1-5	RG	FW	US	2006	AB672615.1	F	Q	A	E	P	M	H32
IV	IVb	n.a.	MI03GL	M	FW	US	2003	GQ385941.1	F	Q	A	E	P	M	H32

11 ^aHost species abbreviations: AH) Atlantic herring; AS) Atlantic salmon; BH) Baltic herring; BW) blue whiting; CS) coho
12 salmon; G) grayling; H) herring; Ha) Haddock; JF) Japanese flounder; L) lamprey; M) muskellung; NP) Norway pout;
13 OF) olive flounder; PG) rock gunnel; PH) Pacific herring; PS) Pacific sadine; R) rockling; RG) round goby; RT) rainbow
14 trout; S) sprat; T) turbot;

15 ^b Environmental abbreviations: M) marine or brackish water; FW) freshwater;

16 ^c Geographic abbreviation: AT) Austria, CA) Canada; CH) Switzerland; DE) Germany; DK) Denmark; FI) Finland; FR)
17 France; GE) Georgia; IE) Ireland; JP) Japan; KR) Korea; NO) Norway; SE) Sweden; SI) Slovenia; UK) United Kingdom;
18 US) United States;

19 ^d Amino acid abbreviations: N) Asparagine; L) Leucine; P) Proline; D) Aspartate; E) Glutamate; Q) Glutamine; K)
20 Lysine; T) Threonine, A) Alanine; V) Valine; S) Serine; F) Phenylalanine; G) Glycine; M) Methionine;
21 Applied abbreviation: n.a. ~ no affiliation

22 **Table A2:** Parameters of codon substitution models used for detection of positive selection
 23 pressures.

Model	P	Parameter	Notes
M0 (one ratio) ^a	1	ω	One ω ratio for all sites
M1 (neutral) ^a	1	p_0	Accounting for sites under purifying and neutral selection. $p_1 = 1 - p_0, 0 < \omega_0 < 1, \omega_1 = 1,$
M2 (positive selection) ^a	3	p_0, p_1, ω	Expansion of M1, with an additional site class accounting for positive selection. $p_2 = 1 - p_0 - p_1, 0 < \omega_0 < 1, \omega_1 = 1$
M7 (beta) ^b	2	p, q	ω is described by a beta distribution (B(p,q)), with p and q describing the shape of the distribution.
M8 (beta& ω) ^b	4	p_0, p, q, ω	Expansion to M7 with an additional discrete site class accounting for positive selection. p_0 drawn from B(p,q), $p_1 = 1 - p_0$ with ω_1

24 ^a Discret model

25 ^b Continuous model

26 Applied abbreviations: P ~ number of free parameters in the ω distribution

27

28 **Table A3:** Parameter estimates retrieved from evolutionary molecular analysis of VHSV G protein
 29 sequences (complete coding region) employing substitution model M8. Sequences were divided into
 30 sub-datasets based on phylogenetic reconstruction.

Dataset	Tree length	p	q	ω_1	p_0	p_1	Mean ω
Genotype							
I	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
II	0.089	26.772	99.000	3.754	1.000	0.000	0.269
III	0.210	9.403	99.000	2.944	0.951	0.049	0.244
IV	0.252	0.005	3.039	1.351	0.778	0.222	0.320
Sublineage							
Ia*	1.158	0.157	0.755	7.305	0.991	0.009	0.236
Ib	0.114	19.735	99.000	9.420	0.987	0.013	0.305
Ic*	0.151	16.932	99.000	26.336	0.994	0.006	0.263
Id	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
Ie	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
If	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
IVa	0.131	27.458	99.000	7.314	0.982	0.018	0.360
IVb	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
IVc	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
Clade							
Ia-1*	0.323	0.013	0.076	19.503	0.996	0.004	0.238
Ia-2*	0.689	0.263	1.219	5.427	0.989	0.011	0.240

31 * datasets detected for positive selection;

32 p and q represent parameters of beta distribution indicating the shape of the distribution;

33 ω_1 : strength of positive selection;

34 p_0 : proportion of amino acid sites under neutral or purifying selection;

35 p_1 : proportion of amino acid sites under positive selection

36

37

38 **Table A4:** Inferring gene-wide selection pressure along phylogenetic branches using the **Branch-Site**
39 **Unrestricted Statistical Test for Episodic Diversification (BUSTED)** algorithm implemented in the
40 HyPhy software package. BUSTED fits a codon model with three rate classes, constraining the dN/dS
41 ratios as $\omega_1 \leq \omega_2 \leq 1 \leq \omega_3$ (allowing positive selection) in the Alternative Model and comparing the
42 model fit to the Null Model where $\omega_3 = 1$ (disallowing positive selection) on the defined test/
43 foreground branches. Model fit was tested using likelihood ratio test statistics (LRT), comparing
44 twice the log-likelihood (logL) difference to a χ^2 distribution (df = 2). Significant LRT demonstrate
45 evidence of positive selection.

DS ^a	Alternative Model							Null Model							LRT (p-value)
	logL	Foreground Branches			Background Branches			logL	Foreground Branches			Background Branches			
		ω_1 (%)	ω_2 (%)	ω_3 (%)	ω_1 (%)	ω_2 (%)	ω_3 (%)		ω_1 (%)	ω_2 (%)	ω_3^b (%)	ω_1 (%)	ω_2 (%)	ω_3 (%)	
Genotype															
I	See sublinages														
II	-10,579.70	0.05	0.61	2.55	0.03	0.08	7.76	-10,579.70	0.03	0.72	1.00	0.03	0.08	7.76	1.00
		(81.47)	(14.95)	(3.59)	(82.84)	(14.35)	(2.81)		(73.34)	(22.00)	(4.66)	(82.85)	(14.35)	(2.80)	
III	-10,577.70	0.24	0.26	1.01	0.02	0.12	8.72	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	1.00
		(94.41)	(5.59)	(0.00)	(79.09)	(18.45)	(2.46)								
IV	-10,573.90	0.33	0.33	1.46	0.03	0.17	9.20	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	1.00
		(90.60)	(9.40)	(0.00)	(90.10)	(7.60)	(2.29)								
Sublinage															
Ia	-10,578.30	0.00	0.14	3.60	0.03	0.20	10.32	-10,579.90	0.00	0.00	1.00	0.03	0.14	10.28	0.204
		(77.84)	(16.02)	(6.14)	(89.70)	(8.14)	(2.17)		(22.82)	(53.64)	(23.54)	(89.70)	(8.13)	(2.18)	
Ib	-10,579.60	0.09	0.26	2.37	0.03	0.08	7.78	-10,579.60	0.09	0.45	1.00	0.03	0.07	7.78	1.00
		(65.34)	(28.63)	(6.03)	(87.46)	(9.79)	(2.76)		(59.53)	(33.89)	(6.58)	(87.46)	(9.78)	(2.76)	
Ic	-10,578.10	0.15	0.17	266.70	0.02	0.08	7.12	-10,582.20	0.00	0.17	1.00	0.03	0.07	7.14	0.02
		(8.20)	(91.69)	(0.11)	(82.67)	(14.29)	(3.05)		(80.07)	(0.00)	(19.93)	(83.70)	(14.27)	(3.02)	
Id	-10,575.40	0.40	0.44	1.00	0.03	0.10	8.18	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	1.00
		(99.91)	(0.09)	(0.00)	(83.29)	(14.14)	(2.57)								
Ie	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
If	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
IVa	-10,577.30	0.32	0.51	1.00	0.03	0.07	7.86	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	1.00
		(93.90)	(0.00)	(6.10)	(89.09)	(8.25)	(2.66)								
IVb	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
Clade															
Ia-1	-10,579.20	0.01	0.12	3.48	0.03	0.11	8.42	-10,579.40	0.00	0.00	1.00	0.03	0.05	8.48	0.79
		(82.41)	(12.27)	(5.32)	(88.70)	(8.64)	(2.67)		(15.70)	(63.89)	(20.46)	(88.77)	(8.58)	(2.64)	
Ia-2	-10,579.80	0.00	0.00	5.95	0.03	0.10	7.82	-10,582.70	0.00	0.00	1.00	0.03	0.07	7.88	0.05
		(10.01)	(85.87)	(4.12)	(86.67)	(10.54)	(2.87)		(3.78)	(73.48)	(22.75)	(86.66)	(10.59)	(2.75)	
Ia-3	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
Ia-4	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
Rainbow trout vs. non-rainbow trout															
RT	-10,576.90	0.00	0.01	4.61	0.03	0.23	8.36	-10,582.90	0.00	0.00	1.00	0.03	0.20	8.37	0.002
		(79.43)	(14.78)	(5.78)	(90.36)	(7.58)	(2.06)		(20.04)	(55.01)	(24.95)	(90.36)	(7.58)	(2.06)	

46 ^a Datasets (DS) in bold were submitted to molecular evolutionary analysis using BUSTED. Datasets are defined as
47 described in Table 1 and Table 2.

48 ^b ω_3 constrained to 1 (neutral), disallowing positive selection in the test branches.

49 Applied abbreviations: n.a. ~ not analysed

50 **Table A5:** Inferring amino acid (aa) sites under positive selection pressure in the VHSV G protein
51 using the **F**ast, **U**nconstraint **B**ayesian **A**ppRoXimation (FUBAR) algorithm implemented in the
52 HyPhy software package with associated posterior probability estimates and potential functional
53 relevance. FUBAR analysis was conducted using the online version implemented at datamonkey.org
54 and applying default settings: 5 MCMC chains conducted, chain length set to 2,000,000, burn-in of
55 1,000,000 samples, 100 samples drawn from each chain, and Dirichlet prior set to 0.5.

aa Site	Probability of positive selection ^a				Function
	Ia	Ia-1	Ia-2	Ic	
8 ^b	-	-	-	0.896	Signal peptide
212	0.925	0.975	0.788	-	Proximity of Cys215
214	-	-	-	0.938	Proximity of Cys215
229	0.956	-	0.949	-	unk.
258	0.999	0.998	0.952	-	Conformation-dependent neutralizing epitope; Proximity of Cys256
283	0.823	-	-	-	Conformation-dependent neutralizing epitope; Proximity of Cys285
284	0.915	0.841	-	-	Conformation-dependent neutralizing epitope; Proximity of Cys285
290	0.916	-	0.964	-	unk.
371	0.790	-	0.847	-	unk.
459	0.804	-	-	-	unk.
476	0.782	0.811	-	-	Proximity of membrane, extracellular side
486		0.854	-	-	
505	0.987	-	0.940	-	Proximity of membrane, intracellular side
506	0.997	0.753	0.953	-	Proximity of membrane, intracellular side

56 ^a Values in bold indicate posterior probability above 95%, missing values indicate a posterior probability below 70%.

57 ^b Amino acids belonging to the signal peptide, which is removed at the endoplasmic reticulum during protein synthesis;

58 Applied abbreviations: unk. ~ unknown