

Figure S1

hHv1	MAT-----WDEKAVTRR-AKVA-----	16
mHv1	MTS-----HDPKAVTRR-TKVA-----	16
DrHv1	M-----	1
CiHv1	MEGDNCNKSRRHKSHNMI-----NPNYASVRC TQPLPSVIQLRSRNMIGITEDPSSDSEPVSSNQ-----PLLLTNLS	68
SpHv1	MKPD-LKQTEEVVSQGLLEQGDGGSSSHGNKVGEK-SGDGQFAEQGGVCETSEDKNDGCETHSGAKTDKHKTKLEGETAP	78
NpHv1	MWL-----	3
LpHv1	MAG-----	3
kHv1	M-----	1

hHv1	--PAERMSKFLRHFTVVGDDYHAWNINYKKWENEEEEEEEEQPPPTPVSGEEGRAA-APDVAPAPGPAPRAPLD	93
mHv1	--PTKRMSRFLKHFTVVGDDYHTWNVNYKKWENEEEEEEE--PAP TSAEG-EGNAE-GPDAEAGSASTPRQSLD	89
DrHv1	-----SRYLKHFTAVGDNKNA-----VPTWHEEDTSHH-----V TTLHD-APDGLVSTGQHLGQLS	58
CiHv1	YEVHTFNDNNNHERPAPQEQTQ--NTMISMQSEQKSDR--FTASNLGMFQYMKFEIGEDGDDHEEE---AILT	141
SpHv1	ADAEMFGFRRLSDTTKPSEGNDQ---QRVIVKDDSSDS-----VVSD-SHDGHPARTE---PLS	136
NpHv1	---KMDAHKRLSE-----DLEKVMKEDGNSS-----IMTEPDHNIQPSK-----TVRERLR	47
LpHv1	-----HH-----GAPS-KHEEHAATAPH-----GIKHGL-	26
kHv1	-----DRILHH-----AVHT-VHTSKSARDAE--GHGT	32

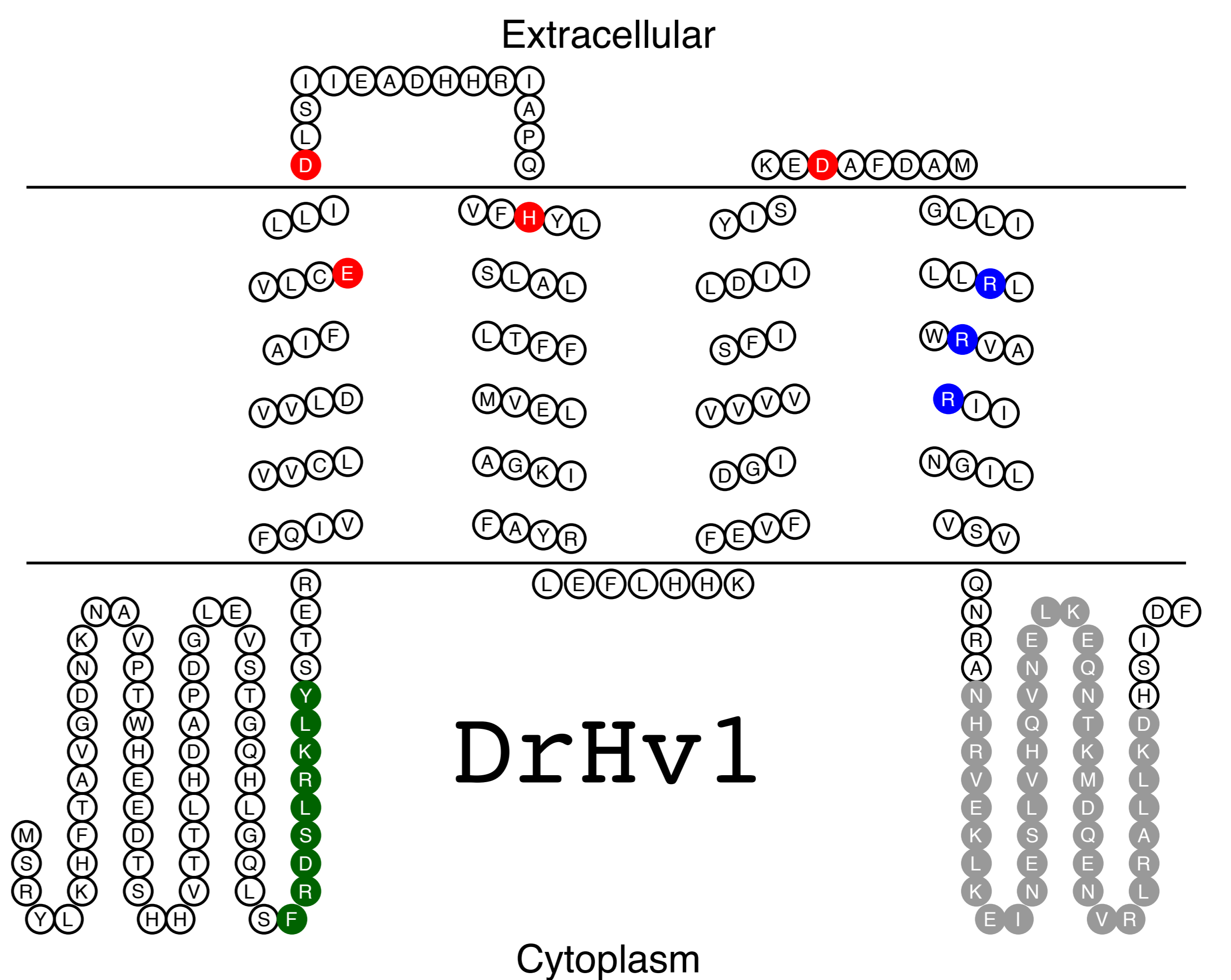
hHv1	KLFSSHRFQVVIICLVVLDALLVLAELILD	128
mHv1	KLFSSHRFQVVIICLVVLDALLVLAELLLD	124
DrHv1	KLYSTERFQIVVVCLVVLDAIFVLCCELLI	93
CiHv1	HILHSKPIHVAIIVLVVLD SFLVVGELLI	176
SpHv1	EIMETQKFHIAILVVLVIDCIVVIVELVI	183
NpHv1	KLLHSHKFFQISVITLVIIDCLLVITELLI	80
LpHv1	QLYNSKACLVLVFFLLILDVCIVVASGVLE	106
kHv1	EALNSSSKVHTILNVLLICDLMTVIIIGMLLE	90

hHv1	-----PDKNNYAAMVFHYMSITILVFFMMEIIFKLFVFRLEF	165
mHv1	-----PDEQDYAVTAFHYMSFAILVFFMLEIFFKIFVFRLEF	161
DrHv1	-----ADHHRIAPQVFHYLSLALLTFFMVELAGKIFAYRLEF	130
CiHv1	-----VPHGNPAPEILHGFSLSILSIFMVEIALKIIADHRHF	213
SpHv1	-----KEEKEVTAANVLHYISIGILSIFMIELLIKIPVFRMEF	221
NpHv1	-----HEESLAQHVLYHCSITILSIFIVEIFLKLYAFRQEF	117
LpHv1	DGLDAADAEASSGGGLFLAGHDAGRQLSSSDGDQIDCHHPHFGNHS LHDAEKILAYISIGILVIFIIEQLLLIAAMRGAY	186
kHv1	-----SHLAHYGNHDLHEWAERMEYASLAILLIFLLENMLLVLANGCRF	134

hHv1	FHHKFEILDVVVVVVSFILDIV--LLFQEHQFEAL	241
mHv1	FHHKFEILDVAVVVVVSFVLDLV--LLFKSHHFEAL	237
DrHv1	LHHKFEVFDGIVVVVVSFILDII--YISKEDAFDAM	206
CiHv1	IHHKVEVLDAVVVVVISFGVDIALIFVGESEALAAI	291
SpHv1	FRSKLEVFDGIIIIVISFVLDV--SLIYEEQFAVL	297
NpHv1	FKHRLEVFDALIVIVSFALDIA--FRNSRDALSGV	193
LpHv1	FREKLMVLDGFVITLSLLEILV----TNLPLG	253
kHv1	FANPFHILDIVVVVVSVGFELQ--GILGEGHDAGI	212

hHv1	IQH-LEFSCSEKEQEIERLNKLLRQHGLL-----	269
mHv1	IQH-LEFSCSEKEQEIERLNKLLKQNGLL-----	265
DrHv1	VNE-LKEQNTKMDQENVRLRALLKDHSIDF-----	235
CiHv1	IHN-LEEKLSQKEQDMSRLHEILRCNNIDIPPTVPLTTSVQIHSTTTASADV-----	342
SpHv1	MEK-FRRYCAAQEKEIEVLRNTLNQHG IQIDDDYVAKKPQFSLNQLNVVEMNSADKH-DTGEDEGE GEEGGDGNTRRH	375
NpHv1	LSR-CRQVCAAQQRELDVLRVLAHQHG LD-----QQLPDGNRVDVVADVEKR-----	239
LpHv1	LSEQVWAHMSGEKWEAMLLRNGTEKLEMDVAKEEQRIAAQIAQAHPSVVLRALAAERQRQAAREQLQAQESKASG-----	328
kHv1	LQK-----GSFEQHAAG-----TSGVHHARSQASSNREGRE-----G-----	244

hHv1	-----GEVN	273
mHv1	-----GDVN	269
DrHv1	-----	235
CiHv1	-----	342
SpHv1	EKEREALGEHTITLTTDDNVNTIQADYHPQDTTFT	410
NpHv1	-----	239
LpHv1	-----RPAV	332
kHv1	-----CCVQ	248



Histidine-binding residue

Figure S2

hHv1	MATWDEKAVTRRAKVAPAERMSKFLRHFTVVGDDYHAWNINYKKWENEEEEEEEQ-PPPTPVS GEEGRAAAPDVAPAPG	79
mHv1	MTSHDPKAVTRRTKVAPT KRMSRFLKHFTVVGDDYHTWNVNYKKWENEEEEEE-----PAP TSAEGE-GNAEGPDAEAGSA	75
XlHv1	-----MAGCLRHFSTVGD DTK-----KREWKQED-----VEVAYEEPLKNT P	37
OlHv1	-----MSRYLKHFTVGD KH-----HTVWEDEE-----LHAVSED-LSPAS	35
TnHv1	-----MSRYLRFVTTVGD DQ-----PAQWDEEE-----LHVNSEE-LSSAT	35
OnHv1	-----MSRYLKHFTA VGDQH-----VVHSDEEE-----LHVSSEE-LSSAT	35
DrHv1	-----MSRYLKHFTA VGDNKNA-----VPTWHEEDTSHH-----VTTLHDAPDG-LEVST	44
IpHv1	-----MVRFLRFFTVVG DDDHQA-----ASRWHEED-----LHKVSED-LEAAK	37

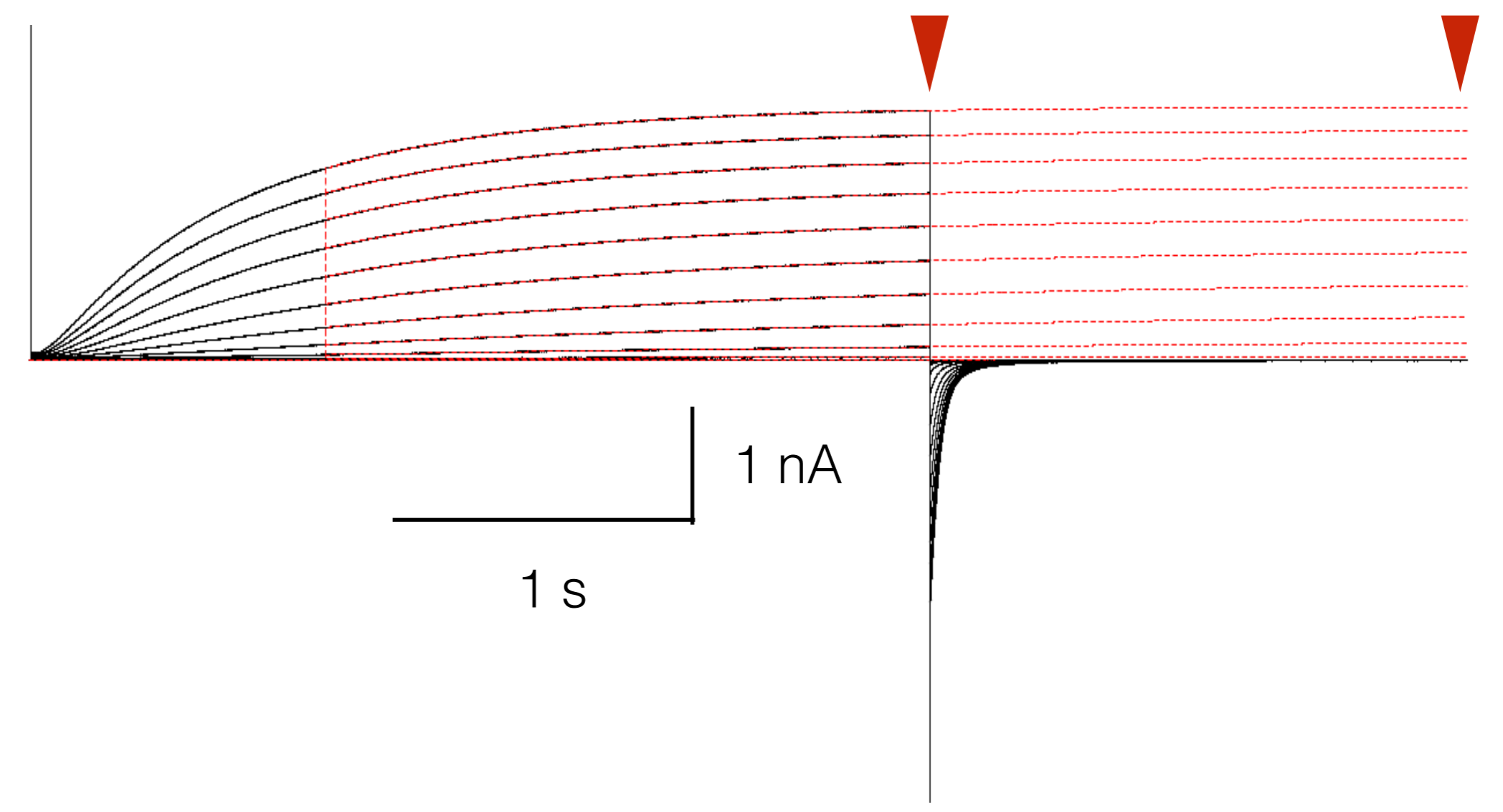
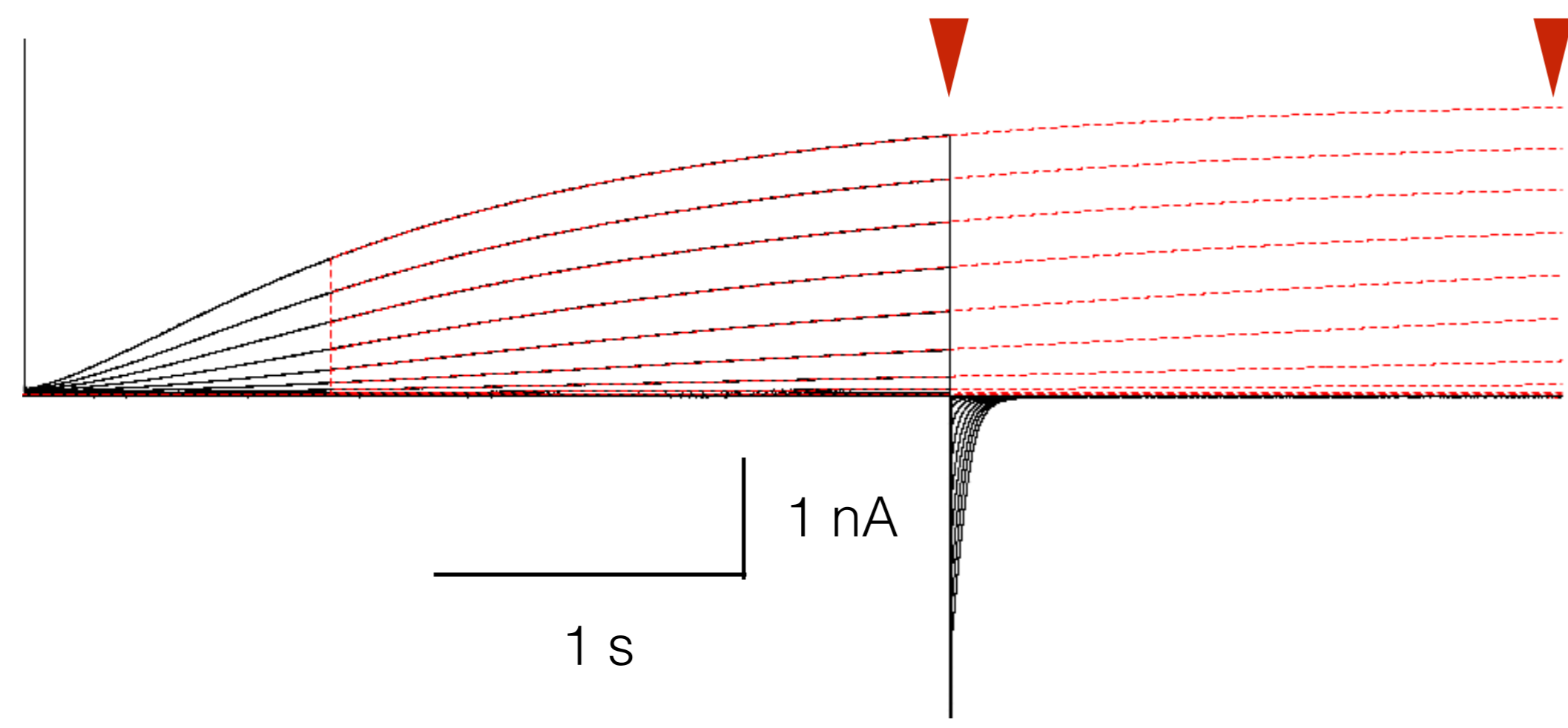
	S0	S1	S2		
hHv1	PAPRAPLD	FRGMLRKLFS	SSHRFQVIIICLVVLDALLVLAELIID	DLKIIQPDKNNYAAMVFHYMSITILVFFMMEIIFKLF	159
mHv1	STPRQSLD	FRSRLRKLFS	SSHRFQVIIICLVVLDALLVLAELLLD	DLKIIIEPDEQDYAVTAFHYMSFAILVFFMLEIFFKIF	155
XlHv1	HPFIASYS	FRGALKWLL	SSHKFQIVIIICLVILDALFVLVEVLLD	LELLAEKVDHIPEIFHYLSISVLTFFILEIAGKLY	117
OlHv1	GLFPTSLS	FRALKRLYV	SERFQVAVVCLVILDACFVLAELIID	DLSVIKLDHGHIAPFVHYLSLAVLTFMMELAGKLF	115
TnHv1	GQYPTTLT	VRERLQMYC	SERFQILVVCLVILD AIFVLVELLD	DLSIIKLDHG SVAPEVHFHLSLGLVFFLLELAGKLF	115
OnHv1	GQLPATLT	FRDSFKRLY	SSERFQVLVVCLVILD AIFVLAELIID	DLAVIKLEHGHIAPFVHYLSLAILTFFMLELAGKLF	115
DrHv1	GQHLGQLS	FRDSLRLKLY	STERFQIVVVCLV VLD AIFVLC ELLID	DLSII EADHHRIAPQVHFHYLSLALLTFFMVELAGKIF	124
IpHv1	PPAT-QLT	FRDGLKNLF	SSQR FQIAVVCLVIMDALFVLC ELLID	DLSII EVDEHHIAPQVHFHYLSLALLTFFIVELAFKLY	116

	S3	S4	Coiled-coil domain			
hHv1	VFRLEFFHHK	FEILD AVVVVS FILDIVLLF	QEHQFEAL	GLLILLRLWRVARIINGIISV	KTRSERQLLRLKQMNVQLA	239
mHv1	VFRLEFFHHK	FEILDAFVVVVS FVLDLVLLF	KSHHFEAL	GLLILLRLWRVARIINGIISV	KTRSERQILRLKQINIQLA	235
XlHv1	AFRLEFFHHK	FEVFDAAIVVIS FII DIVYIS	REDIFNAV	GLLILLRLWRVARI VNGVIVSV	KTRAE EKMKHLKEQKGSLL	197
OlHv1	AFRLEFFHHK	FEMFDGLVVVVS FILDIVFIF	HEDAFDGM	GLLILLRLWRVARIINGIVVSV	KNRADQRIHKLKESYDHVV	195
TnHv1	AFRKEFFDHK	FEVFDGLVVTVS FVLDVAFIF	HEDAFDGI	GLLILLRLWRVARIINGILVSV	KTREQQKLHKLKESYDHLV	195
OnHv1	AYHLEFFLHK	FEVFDGFVVIVS FILDIVFIF	HEDAFDGI	GLLILLRLWRVARIINGILVSV	KTRADQKIHKLKESYDHLV	195
DrHv1	AYRLEFLHHK	FEVFDGIVVVVS FILDIIYIS	KE DAFDAM	GLLILLRLWRVARIINGILVSV	QNRA NHRVEKLKEINESLV	204
IpHv1	AFRLEFFHHR	FEVFD AIVVIVS FILDIVYIS	KENAFDGM	GLLILLRLWRVARIINGILLSV	KSQANHRVQKLKEENDRLH	196

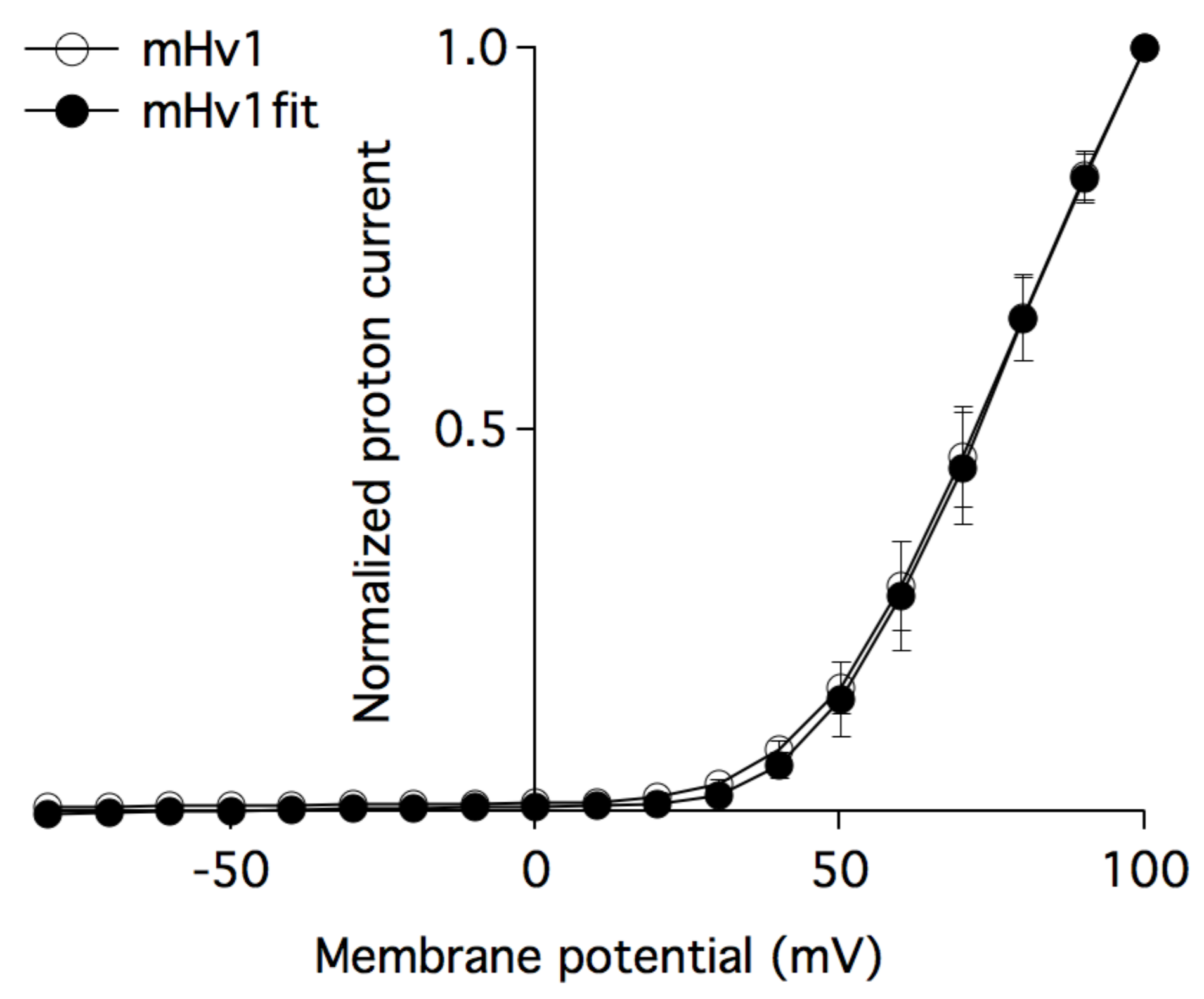
	Coiled-coil domain		
hHv1	AKIQHLEFSCSEKEQEIERLNKLLRQ	HGLLGEVN	273
mHv1	TKIQHLEFSCSEKEQEIERLNKLLKQ	NGLLGDVN	269
XlHv1	EKVAQLEQQCAQQEQEIGRLHKLLQE	HNVFPAS-	230
OlHv1	QRVTELQKSCDDL TQENHRLKAILKE	NQIDF---	226
TnHv1	QRVTELQQLTDKLEKEKQRLQALLKK	HDIEF---	226
OnHv1	QRVTELQERNDKLAQENDNLKALLKK	HGIDI---	226
DrHv1	HQVNELKEQNTKMDQENVRLRALLKD	HSIDF---	235
IpHv1	HQIGELKEHKTAMEQEVSKLRAVLAK	HSIQY---	227

Figure S3

A



B



C

