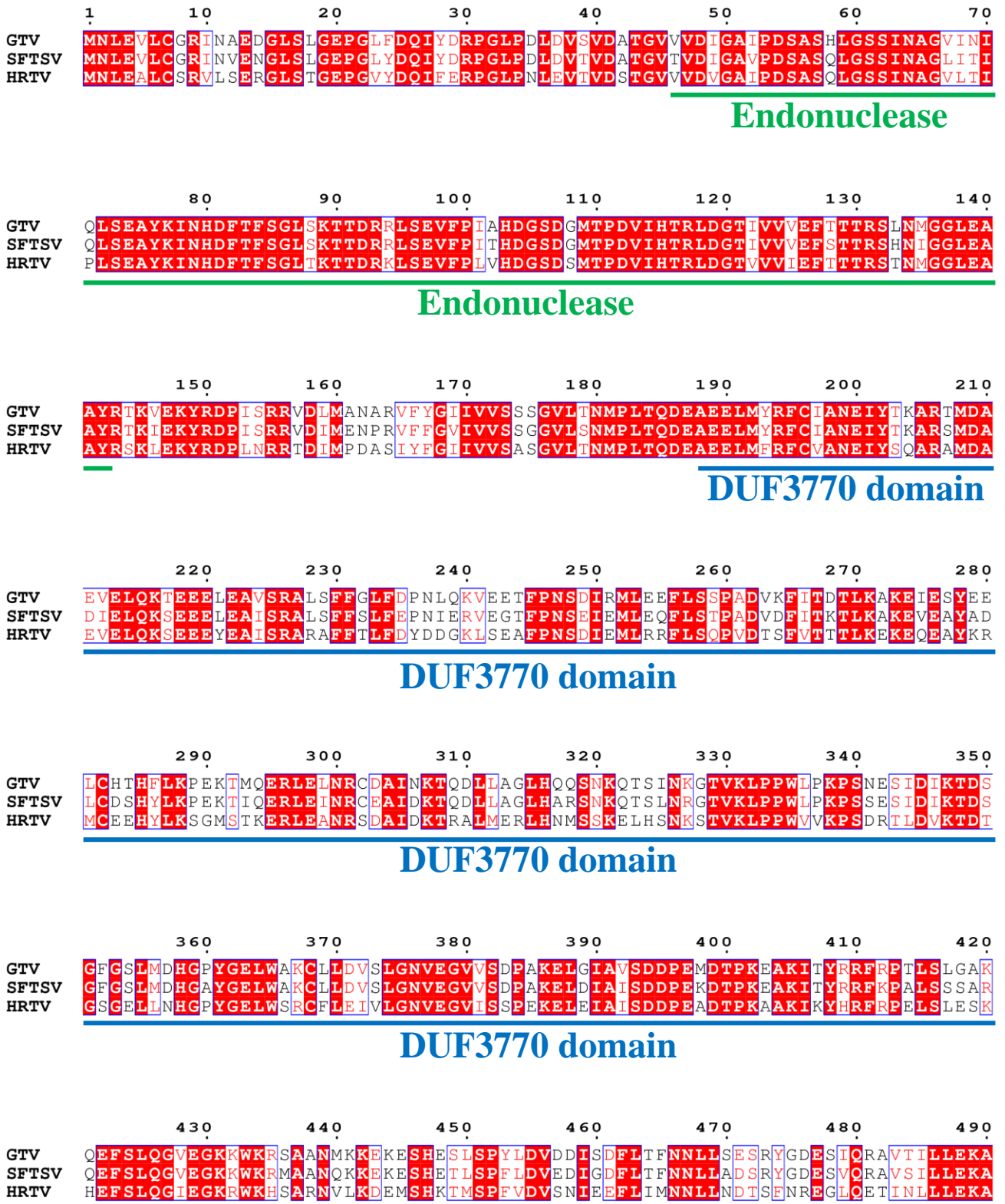


Figure S4 A



500 510 520 530 540 550 560

GTV S L M Q N T E L T N S L N D S F K R N L S S N V V Q W S L W V S C L A Q E L A S A L K Q H C R A G E F I I K K L K F W P I Y V I I K P T K S  
 SFTSV S A M Q D T E L T H A L N D S F K R N L S S N V V Q W S L W V S C L A Q E L A S A L K Q H C R A G E F I I K K L K F W P I Y V I I K P T K S  
 HRTV T E M H Q N G L S T A L N D S F K R N F N T N V V Q W S M W V S C L A Q E L A S A L K Q H C K P G E F I I K K L M H W P I F V I I K P T K S

570 580 590 600 610 620 630

GTV S S H I F Y S L A I K K S D I S K R L M G R V F S D T V D A G D W E L M E F K S L K T C K L T N L V N L P C T M L N S I A F W R E K L G V A  
 SFTSV S S H I F F S L G I R K A D V T R R L T G R V F S D T I D A G E W E L T E F K S L K T C K L T N L V N L P C T M L N S I A F W R E K L G V A  
 HRTV S S H I F Y S L A I K K A N I K R R L I G D V F T D T I D A G E W E F S E F K S L K T C K L T N L I N L P C T M L N S I A F W R E K M G V A

## BUNV\_Polymerase domain

640 650 660 670 680 690 700

GTV P W L V R K P C A E L R E Q V S L T F L V S L E D K A K T E E I I T L T R Y T Q M E G F V S A P M L P K P Q K M I S K L E G P L R T K L Q V  
 SFTSV P W L V R K P C S E L R E Q V G L T F L V S L E D K S K T E E I I T L T R Y T Q M E G F V S P P M L P K P Q K M I G K L D G P L R T K L Q V  
 HRTV P W I S R K A C S E L R E Q V A I T F L M S L E D K S T T E E L V T L T R Y S Q M E G F V S P P L L P K P Q K M V E K L E V P L R T K L Q V

## BUNV\_Polymerase domain

710 720 730 740 750 760 770

GTV F L L R K H L D C M V R V A S O P F T L I P R E G R I E W G G T F H A I S G R S T N L E N M V N S W Y I G Y Y K N K E E S T E V N A L G E M  
 SFTSV Y L L R K H L D C M V R I A S O P F N L I P R E G R V E W G G T F H A I S G R S T N L E N M V N S W Y I G Y Y K N K E E S T E L N A L G E M  
 HRTV F L F R R H L D A I V R V A A S P F P I V A R D G R V E W T G T F N A I T G R S T G L E N M V N N W Y I G Y Y K N K E E S T E L N A L G E M

## BUNV\_Polymerase domain

780 790 800 810 820 830 840

GTV Y K K I V E M E E D K P D D P T F L G W G D T S S P K R H E F S R S F L R A A C S S L E K E I T Q R H G R S W K Q N L E E R V L K E I G S K  
 SFTSV Y K K I V E M E E D K P S S P E F L G W G D T D S P K R H E F S R S F L R A A C S S L E R E I A Q R H G R Q W K Q N L E E R V L K E I G T K  
 HRTV Y K K I V E I E A E K P T S S E Y L G W G D T S S P K R H E F S R S F L K S A C I S L E K E I E M R H G K S W K Q S L E E R V L K E L G S K

## BUNV\_Polymerase domain

850 860 870 880 890 900 910

GTV N I L D L A S M K A T S N F S K E W E I F S E V Q T K E Y H R S K L L E K M A G L I E R G F M W Y I D A V G Q A W K A V L E D G C M R I C L  
 SFTSV N I L D L A S M K A T S N F S K D W E L Y S E V Q T K E Y H R S K L L E K M A T L I E K G V M W Y I D A V G Q A W K A V L D D G C M R I C L  
 HRTV N L L D L A T M K A T S N F S K E W E A F S E V R T K E Y H R S K L L E K M A E L I E H G L M W Y V D A A G H A W K A V L D D K C M R I C L

## BUNV\_Polymerase domain

920 930 940 950 960 970 980

GTV F K K N Q H G G L R E I Y V M D V N A R L V Q F G V E T M A R C V C E L S P H E T V A N P R L K S S I I E N H G L K S A R S L G P G S I N I  
 SFTSV F K K N Q H G G L R E I Y V M D A N A R L V Q F G V E T M A R C V C E L S P H E T V A N P R L K N S I I E N H G L K S A R S L G P G S I N I  
 HRTV F K K N Q H G G L R E I Y V T N A N A R L V Q F G V E T M A R C V C E L S P H E T I A N P R L K S S I I E N H G L K S A R O L G Q G T I N V

## BUNV\_Polymerase domain

	990	1000	1010	1020	1030	1040	1050	
GTV	NSSNDAKKWN	QGHYTTKLAL	VLCWFMP	SKFHKFIW	SAISMFR	RKKMMIDLRF	LTHLSKSD	SKSSDAFRE
SFTSV	NSSNDAKKWN	QGHYTTKLAL	VLCWFMP	AKFHRFIW	AAISMFR	RKKMMVDLRF	LATHLSK	SESRSDPFR
HRTV	NSSNDAKKWS	QGHYTTKLAM	VLCWFMP	AKFHRFIW	AGISMFR	CKKMMIDLRF	LEKLS	TKANQKTD

## BUNV\_Polymerase domain

	1060	1070	1080	1090	1100	1110	1120	
GTV	AMTN	AFHGNSEAS	WMEK	GKTYIQ	TETGMMQ	GILHFTSS	LLHSCVQ	SFYKTYFV
SFTSV	AMTD	AFHGNREVS	WMDK	GRTYIK	TETGMMQ	GILHFTSS	LLHSCVQ	SFYKSYFV
HRTV	DLAG	AFHGNVEVP	WMTQ	GATYIQ	TETGMMQ	GILHFTSS	LLHSCVQ	SFYKAYFL

## BUNV\_Polymerase domain

	1130	1140	1150	1160	1170	1180	1190
GTV	VVEGSDDSA	IMISIRPK	SDMDEV	RSRFFV	ANLLH	SVKYL	LNPLFG
SFTSV	VIEGSDDSA	IMISIRPK	SDMDEV	RSRFFV	ANLLH	SVKYL	LNPLFG
HRTV	VLEGSDDSA	IMISLKP	ASDN	EEAMARE	LTANLL	YSVRV	LNPLFG

## BUNV\_Polymerase domain

	1200	1210	1220	1230	1240	1250	1260
GTV	LVRPTIRW	VAAASHQ	ISETEAL	ASRQEDY	SNNLLTQ	CLEGGAS	SFSLTYL
SFTSV	LVRPTIRW	VAAASHQ	ISETEAL	ASRQEDY	SNNLLTQ	CLEGGAS	SFSLTYL
HRTV	LVRPTIRW	VAAASHQ	ISESEAL	ASRQEDY	ANLLTQ	CLEGGSS	SFSLTYL

## BUNV\_Polymerase domain

	1270	1280	1290	1300	1310	1320	1330
GTV	FMGMILS	DPDPALG	FFLMDN	PAFAGG	AGFRNL	WRACKT	TDLGR
SFTSV	FMGMILS	DPDPALG	FFLMDN	PAFAGG	AGFRNL	WRACKT	TDLGR
HRTV	FVGMILS	DPDPALG	FFLMDN	PAFAGG	AGFRNL	WRACKF	TNLGR

## BUNV\_Polymerase domain

	1340	1350	1360	1370	1380	1390	1400
GTV	GGTLSHSV	MYWGD	RKKYQS	LLERM	GLPSD	WVEQID	ENPGT
SFTSV	GGTLSHSV	MYWGD	RKKYQ	ALLNR	MGLP	EDWVE	QIDENP
HRTV	GGTLSHSV	MYWGD	RKKYQ	HLLDR	MGLP	KDWVE	RIDENP

	1410	1420	1430	1440	1450	1460	1470
GTV	KGHVVPRV	VAAAGV	LLSRHC	FRFS	ASIHG	KGPS	OKASLI
SFTSV	KGHVVPRV	VAAAGV	LLSRHC	FRFS	SSIHG	RGS	OKASLI
HRTV	KGHVVPRV	VAAAGV	LLSRHC	FRYTA	ASIHG	RGS	OKASLI

1480 1490 1500 1510 1520 1530 1540  
GTV YERVCTLLLEVENLTGKFVVRERNIVRSRIDLFQDPVDLRCKAEDLVSEVWFGLKRTKLGPRLLKEEWDK  
SFTSV YDRVCTLLLEVEHELTGKFVVRERNIVRSRIDLFQEPVDLRCKAEDLVSEVWFGLKRTKLGPRLLKEEWDK  
HRTV YERVL TLLDEVTA LTGKFVVRERNIVRSRVELFQEPVDLRCKAENLIAEMWFG LKRTKLGPRLLKEEWDK

1550 1560 1570 1580 1590 1600 1610  
GTV LRASF AWLSTD PAETL RDGPFMSHVQFRNFIAHVDAKRSVRLLGAPVKKSGGVTTINQVVRM NFFPGF C  
SFTSV LRASF AWLSTD PS ETL RDGPF LSHVQFRNFIAHVDAKRSVRLLGAPVKKSGGVTTISQVVRM NFFPGF S  
HRTV LRASF SWLSTD HK ETL DVGPF LSHVQFRNFIAHVDAKRSVRLLGAPVKKSGGVTTV SQVVK S NFFPGF I

1620 1630 1640 1650 1660 1670 1680  
GTV LDAEK SLDNQERLESISILKHL LFM TLNGPYTEEYK LDMIMEAFESLALPQPT EVIRKSR TMTLCLISNY  
SFTSV LEAEK SLDNQERLESISILKHV LFM TLNGPYTEEYK LEMIEAFSTLVIPQPS EVIRKSR TMTLCLISNY  
HRTV LD SSE SLD DQERVE GVSILKHL LFM TLNGPYTDEQK KAMVLETE QYFALPHAAEVVKRSRSL TLCLMKNF

1690 1700 1710 1720 1730 1740 1750  
GTV FS QKGG SILDQIEK AQSGLGGFSKPKRTFIRPGGS IGYKKG VWTGV MEDTHVQLLIDGDGT SNWLEEI  
SFTSV LS SKGG SILDQIERAQSGLGGFSKPKRTFIRPGGVGYKKG VWTGV MEDTHVQLLIDGDGT SNWLEEI  
HRTV IE ORGG SILDQIEK AQSGLVGGFSKPKP YRKQSG IGYKKG VWSGIME NTNVQLLIDGDGS SNWLEEI

1760 1770 1780 1790 1800 1810 1820  
GTV RLSS E ARLYDVIES IRRLCD D LGI NN RVAS SFRGHCMVRLS GFKTKPASRT DGCPIRV L ERGFW IRELQN  
SFTSV RLSS D ARLYDVIES IRRLCD D LGI NN RVAS AYRGHCMVRLS GFKTKPASRT DGCPIRIM ERGFRIRELQN  
HRTV RLSS E SRLFDVIES VRRLCD D I NVN RVTS SFRGHCMVRLS NFKV KPASRV EGCPIR LMPSSFR IRELQN

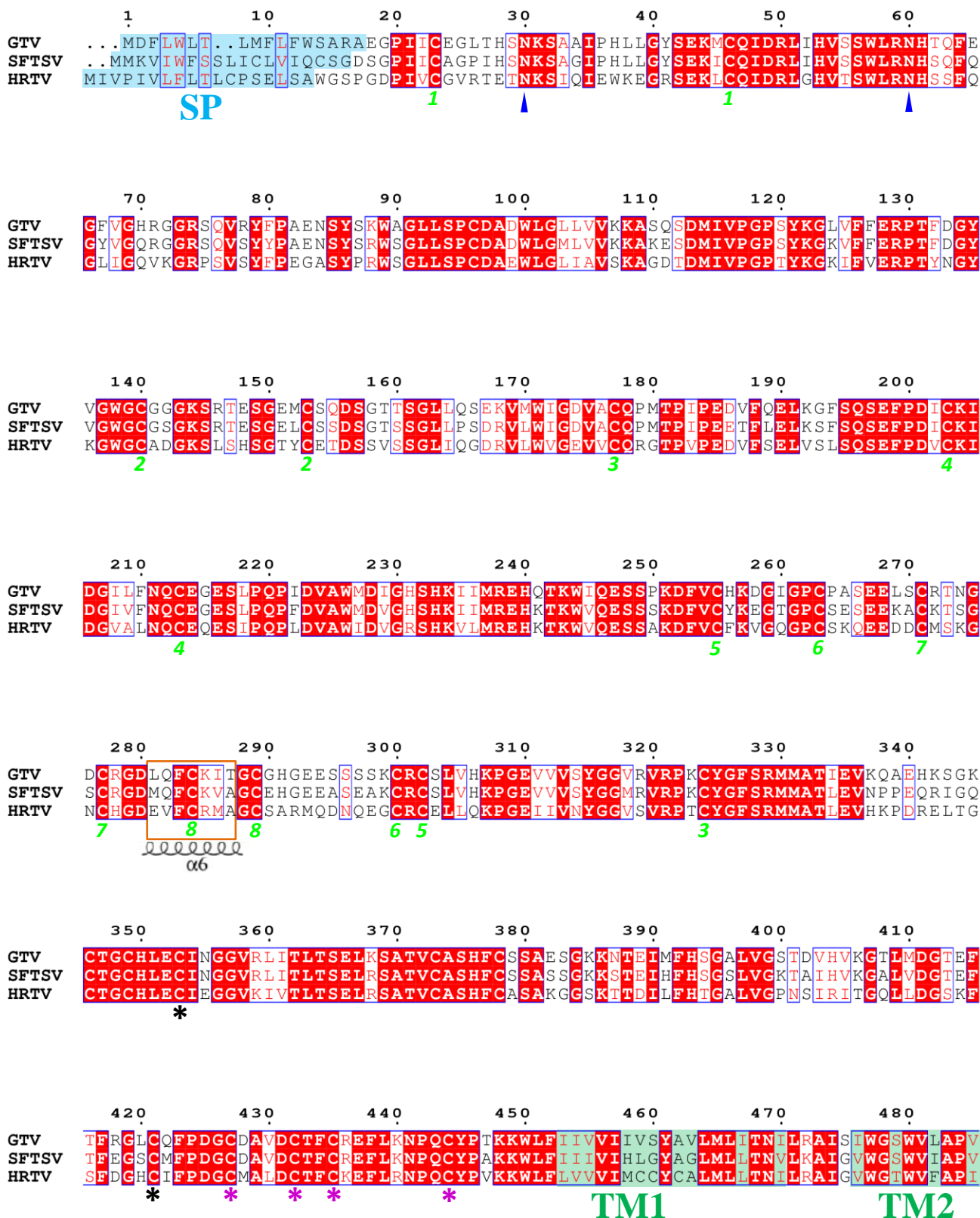
1830 1840 1850 1860 1870 1880 1890  
GTV PDEV F MRVRGDILNLSV RIQEG RIMN ILSYR PRD TDISESAA AFLWSNK D SFSFGKKEPSCSWI CLKTL D  
SFTSV PDEV K MRVRGDILNLSV TIQEG RVMN ILSYR PRD TDISESAA YLWSNRDL SFSFGKKEPSCSWI CLKTL D  
HRTV PDEV F LRVRGDILNLSI ILQED RVMN ILSYR ARD TDISESAA SYLWMNR TD SFSFGKKEPSCSWM CLKTL D

1900 1910 1920 1930 1940 1950 1960  
GTV NWAWS HASTL LATKR KTPG I NNE LMGNIFRDCLEG SLRKQGLMRSKLS ELVEKNV IPLT TQELVDILEED  
SFTSV NWAWS HASVLL ANDRK TPQGI DN RAMGNIFRDCLEG SLRKQGLMRSKLS TEMVEKNV V IPLT TQELVDILEED  
HRTV SWAWN QAARV LERNI KTPG I DNT AMGNIFRDCLES SLRKQGLMRSRI AEMVERHVI IPLT S QELVDILEED

	1970	1980	1990	2000	2010	2020	2030									
GTV	IDFS	DVIATELS	EGSLDIE	SIFDGA	PMLWS	AEVEE	FGE	GMVAIS	YS	SKYYHL	T	LMDQAA	A	TMCA	IMGKE	G
SFTSV	IDFS	DVIATELS	EGSLDIE	SIFDGA	PMLWS	AEVEE	FGE	GVVAVS	YS	SKYYHL	T	LMDQAA	A	TMCA	IMGKE	G
HRTV	VDFSE	EMMQSDI	MEGLDID	ILMEG	SPMLWA	AEVEE	MGE	AMVILS	QS	GKYYHL	K	LMDQAA	T	LS	ILGKD	G

	2040	2050	2060	2070	2080								
GTV	CRS	LLTEKRCMSA	IREQVKPFL	IFLQI	PEDS	ITWV	C	QIA	ESRGL	D	EES	AI	MWG
SFTSV	CRG	LLTEKRCMAA	IREQVRPFL	IFLQI	PEDS	ISWV	S	DQFC	DSRGL	N	EES	TI	MWG
HRTV	CRL	LLGRPTGRSN	LREQVKPYL	TLLQI	REGD	VNWV	S	EYKD	DRGL	D	EDS	AE	MWG

# Figure S4 B





490 500 510 520 530 540 550

GTV KLTIAIMRKLVRLLTLKA LNQAADRGRRVIYEMDGA..QRVHEEGA RVEIARPRR VRHWMYSPVILGITL

SFTSV KLMFAITKKLMR TVSCLV GKLMDRGRQVIHEEIGEN..GEGNQDDVRIEMARPRR VRHWMYSPVILTILA

HRTV KLALALGLRLAKLSKKG LVAVVT RGMIVNDELHQVRRVERGEQNEG RQGYGPRGP I RHWLYSPALITILT

TM2

560 570 580 590 600 610 620

GTV AGSAN GCDELVHADSKL I SCCKQGGNNKVKCAT TGRALLPAVNPQT ACLHFSAPGSPDSKCLKIKVKIN

SFTSV IGLAE GCDELVHADSKL V SCCKQGGNNKVKCAT TGRALLPAVNPQT ACLHFTAPGSPDSKCLKIKVKRIN

HRTV TSICS GCDELVHAESKLS ITCKSASGNKVKCAT TGRALLPAVNPQT ACLHFSVPGSPDSKCLKIKVKSIN

1 2 2 1

630 640 650 660 670 680 690

GTV LRCKKKA SSYVVPDARS RCTSVRRRCRWAGDCQSGCPSHFTSNSFSDDWAGKMDRAGLGFSGCSDGCGGAAC

SFTSV LRCKKKS SSYVVPDARS RCTSVRRRCRWAGDCQSGCPSHFTSNSFSDDWAGKMDRAGLGFSGCSDGCGGAAC

HRTV LRCKQA SSYVVPDARS RCTSVRRRCRWAGDCQSGCPSHFTSNSFSDDWAGKMDRAGLGM SGCSDGCGGAAC

3 4 5 6 7 8

Loop 1

Loop 2

700 710 720 730 740 750 760

GTV GCFNAAPSCIFWRKQVENPHGVIWKVSPCAAWVPSAEVEVTIPSGKSKVVFHPMSGVPTQAFKGVSTITYLG

SFTSV GCFNAAPSCIFWRKQVENPHGVIWKVSPCAAWVPSAEVEVTIPSGKSKVVFHPMSGVPTQAFKGVSTITYLG

HRTV GCFNAAPSCIFWRKQVENPHSNRVIWKVSPCAAWVPSAEVEVTIPSGKSKVVFHPMSGVPTQAFKGVSTITYLG

5 6 3

Loop 2

770 780 790 800 810 820 830

GTV SELEVSGITELCEIEELKSGR LALAPCNQAGMGVVGK IGEIQCSS EESARTIKK DGCIWN S DLVGIELRV

SFTSV SDMEVSGITDLCEIEELKSKK LALAPCNQAGMGVVGK VGEIQCSS EESARTIKK DGCIWN A DLVGIELRV

HRTV SSELIVGMITRLCEMKEMGTGIMALAPCNDP GHAIMGNVGEIQCSS IESAKHIRS DGCIWN A DLVGIELRV

9 9 10 10

840 850 860 870 880 890 900

GTV DDAVCFESKITSVEAVANYS AIP TITIGGLRFE RSHDSQGGKIS GSPLDITAIRGE FSVSYRGLRLS LSEITA

SFTSV DDAVCFESKITSVEAVANYS AIP TITIGGLRFE RSHDSQGGKIS GSPLDITAIRGE FSVNYRGLRLS LSEITA

HRTV DDAVCFESKITSVEAVANYS AIP TITIGGLRFE RSHDSQGGKIS GSPLDITAIRGE FSVSFRGMRLK LSEISA

4

910 920 930 940 950 960 970

GTV TCTGEVNTISGCYSCMMGAKVSIIRLHNSKNST AHLKCS S DETAFSVSEGVHSYTVSLSYDHA VVDETC IIL

SFTSV TCTGEVNTVSGCYSCMTGAKVSIKRLHNSKNNT AHVRC KGG DETAFSVLEGVHSYIVSLSFDH AVVDETC QL

HRTV SCTGEITNTVSGCYSCMTGASVSIKRLHNSKNNT TGH LKCS D S DETAFSVMEGHTYRPHMS EDKAVI DEECVL

11 12 12 13 13

	980	990	1000	1010	1020	1030	1040					
GTV	NCGGHE	SQVNVKGNL	VFLDIPRF	FVDGSYV	QTYHST	VP	TGASIPSP	TDWLNALFG	NGITRW	ILGAAGVLL	T	
SFTSV	NCGGHE	SQVTLKGNL	IFLDVPK	FVDGSYM	QTYHST	VP	TGANIPSP	TDWLNALFG	NGLSRW	ILGVIGVLL	G	
HRTV	NCGGHS	SKLLKGS	LVFMDVPR	FVDGSYV	QTYHST	KVP	AGGRV	PNP	V	DWLNALFG	DGITRW	ILGIIGVLLA

11 TM3

	1050	1060	
GTV	GFAVIHL	DCVSPEIWN	KEVD.....
SFTSV	GLALFFL	IMFLLKLGT	KQVFRSRTKLA
HRTV	CVMLFVV	VVAITRRLI	KGLT.QRAKVA

TM3



# Figure S4 C

