

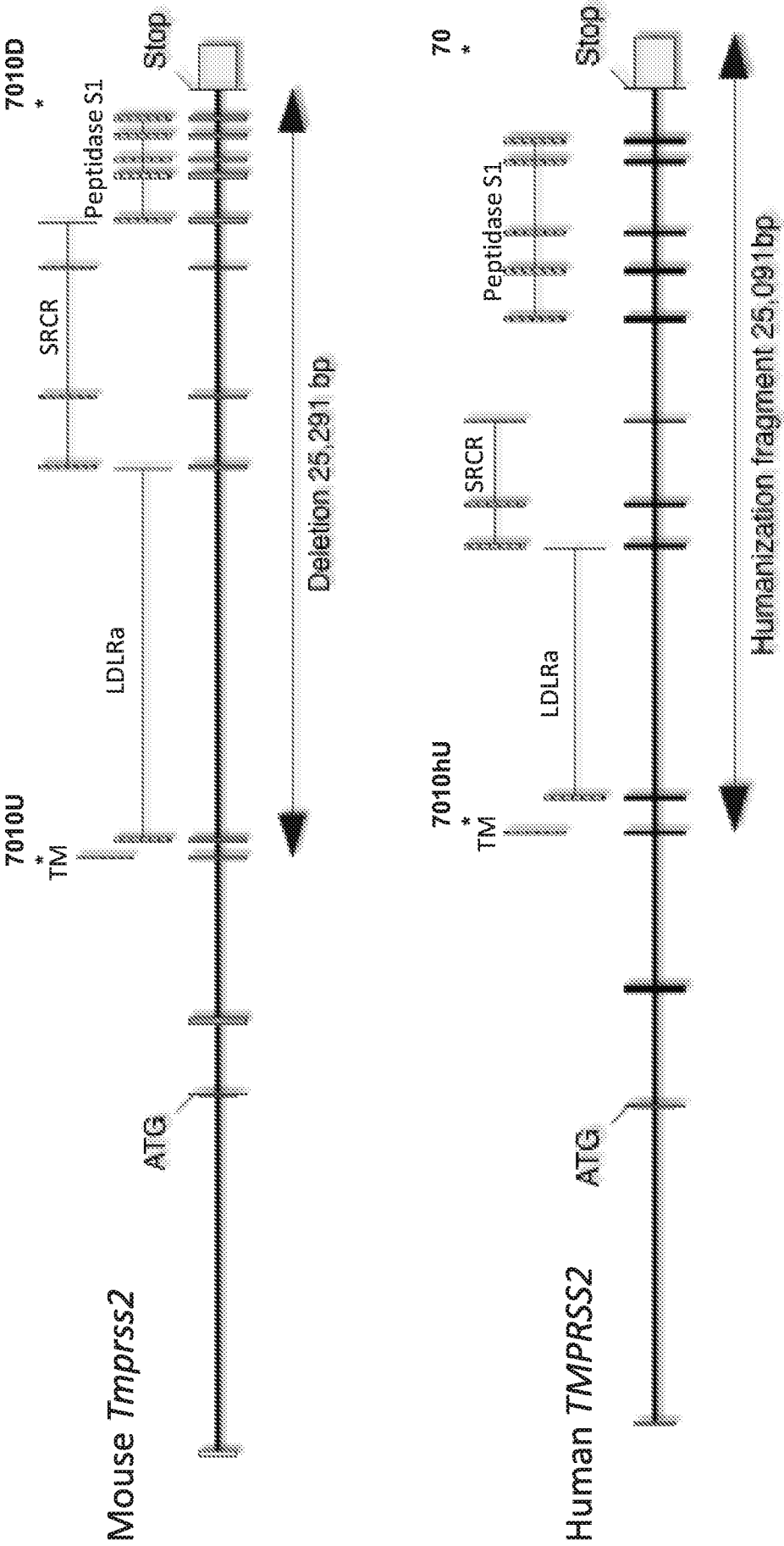


Figure 1A

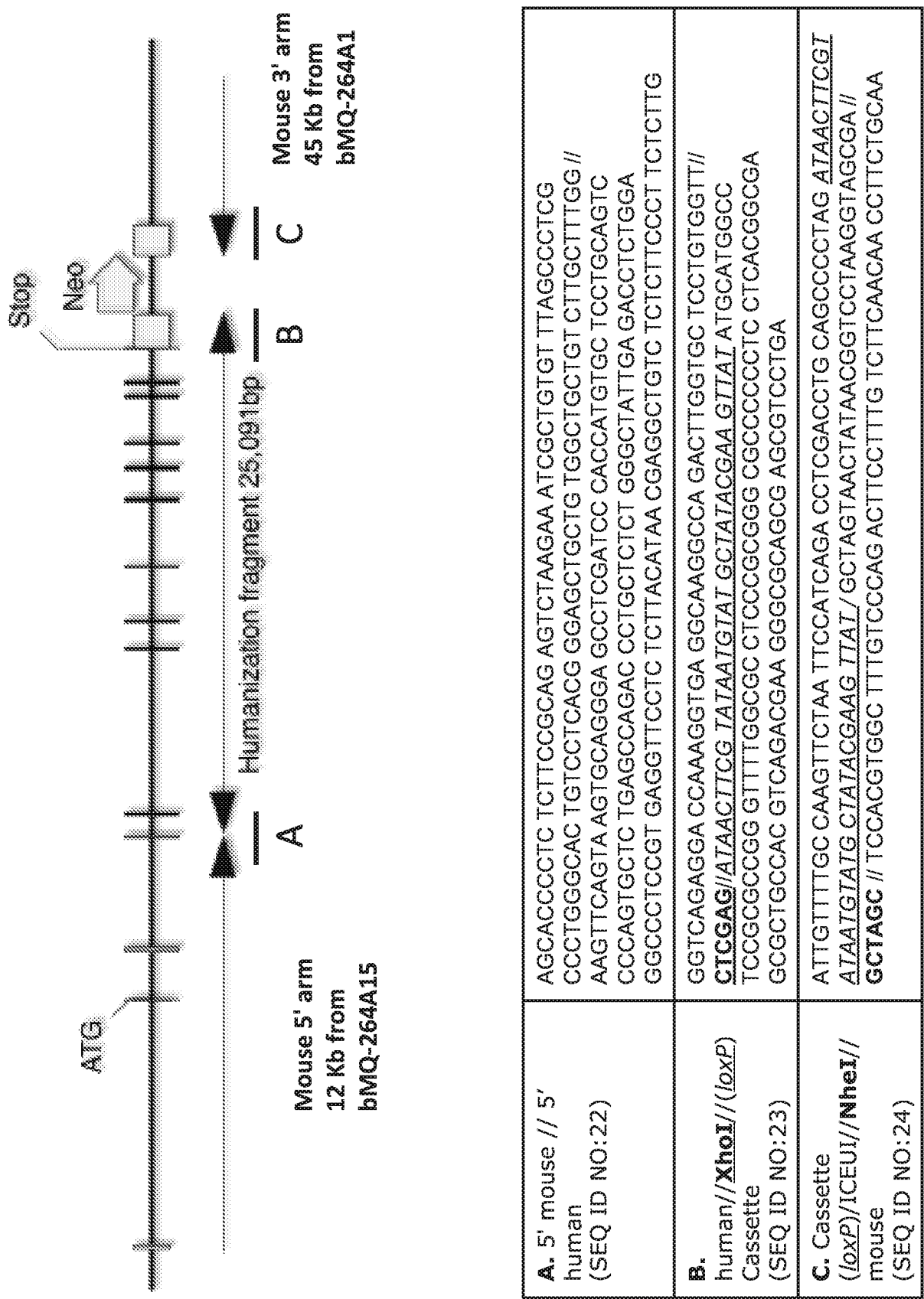
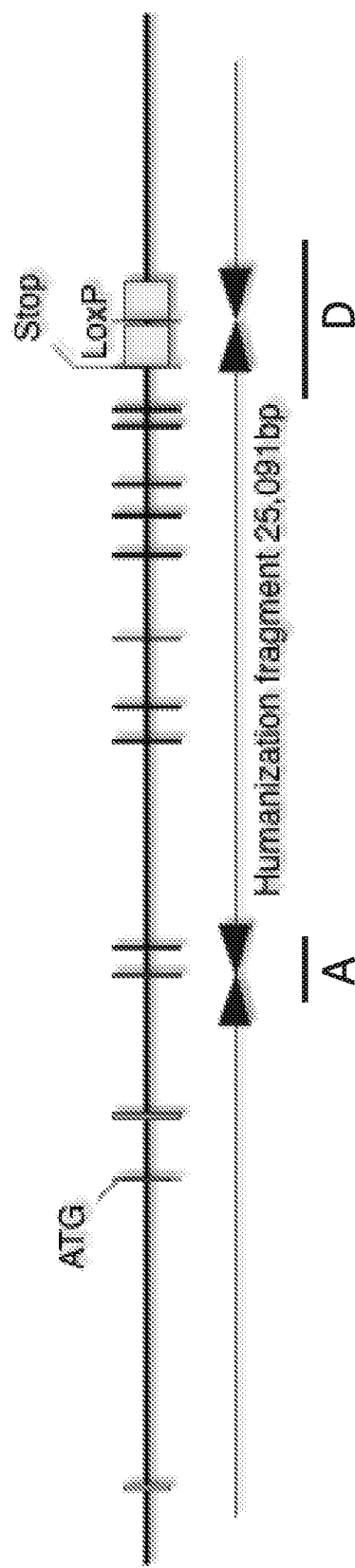


Figure 1B



A. 5' mouse // 5' human (SEQ ID NO:22)	AGCACCCCTC TCCTCCGAG AGCTAAGAA ATCGCTGTGT TTAGCCCTCG CCCTGGGCAC TGTCCTCACG GGAGCTGCTG TGGCTGCTGT CTTGCTTTGG // AAGTTCAGTA AGTGCAGGGA GCCTCGATCC CACCATGTGC TCCTGCAGTC CCCAGTGCTC TGAGCCAGAC CCTGCTCTCT GGGCTATTGA GACCTCTGGA GGCCCTCCGT GAGGTTCCCTC TCTTACATAA CGAGGCTGTC TCTCTCCCT TCTCTTG
D. human// <u>XhoI</u> //(<u>loxP</u>) /ICEUI// <u>NheI</u> // mouse (SEQ ID NO:25)	GGTCAGAGGA CCAAAGGTGA GGCAAGGCCA GACTTGGTGC TCCTGTGGTT// <u>CTCGAG</u> //ATAACTTCG TATAATGTAT GCTATACGAA GTTAT /GCTAGTAACATAACGGTCTAAGGTAGCGA // GCTAGC // TCCACGTGGC TTTGTCCCAG ACTTCCTTTG TCTTCAACAA CCTTCTGCAA

Figure 1C

Tmprs2 protein alignment

	310	320	330	340	350	360
hTMPRSS2	PLNNPWHWTA	FAGILRQSF	MFYAGYQVE	KVISHPNYD	SKTKNNDI	ALMKLQPLTFNDL
mTmprss2	PLSSPRYWTA	FAGILRQSL	MFYGSRHQ	VEKVISHPNYD	SKTKNNDI	ALMKLQTPLAENDL
7010 mutant pro	PLNNPWHWTA	FAGILRQSF	MFYAGYQVE	KVISHPNYD	SKTKNNDI	ALMKLQPLTFNDL
	X	**X	*****X	*****X	*****X	*****X
	370	380	390	400	410	420
hTMPRSS2	VKPVCLPNP	GGMMLQPE	QLCWISGW	GATEEKGK	TSEVLNAA	KVLLIETQRCNSRYVVDNLI
mTmprss2	VKPVCLPNP	GGMMLDLD	QECWISGW	GATEYKGT	SDVLNAAM	VPLIEPSKCNISKYIYNNLI
7010 mutant pro	VKPVCLPNP	GGMMLQPE	QLCWISGW	GATEEKGK	TSEVLNAA	KVLLIETQRCNSRYVVDNLI
	*****X	*****X	*****X	*****X	*****X	*****X
	430	440	450	460	470	480
hTMPRSS2	TPAMICAGF	LQGNVDSC	QGDSCG	GPLVTSKNNI	WNLIGDTS	WGS GC AKAYRPGVYGNVMVF
mTmprss2	TPAMICAGF	LQGSVDSC	QGDSCG	GPLVTLKNGI	WNLIGDTS	WGS GC AKALRPGVYGNVTVE
7010 mutant pro	TPAMICAGF	LQGNVDSC	QGDSCG	GPLVTSKNNI	WNLIGDTS	WGS GC AKAYRPGVYGNVMVF
	*****	*****	*****	*****	*****	*****
	490					
hTMPRSS2	TDWIYRQMR	ADG				
mTmprss2	TDWIYQQMR	ANS				
7010 mutant pro	TDWIYRQMR	ADG				
	*****	*****				

solid line: TM
solid box: LDLRa
dotted box: SRCR domain
dotted line: peptidase S1

Figure 1D (Continued)

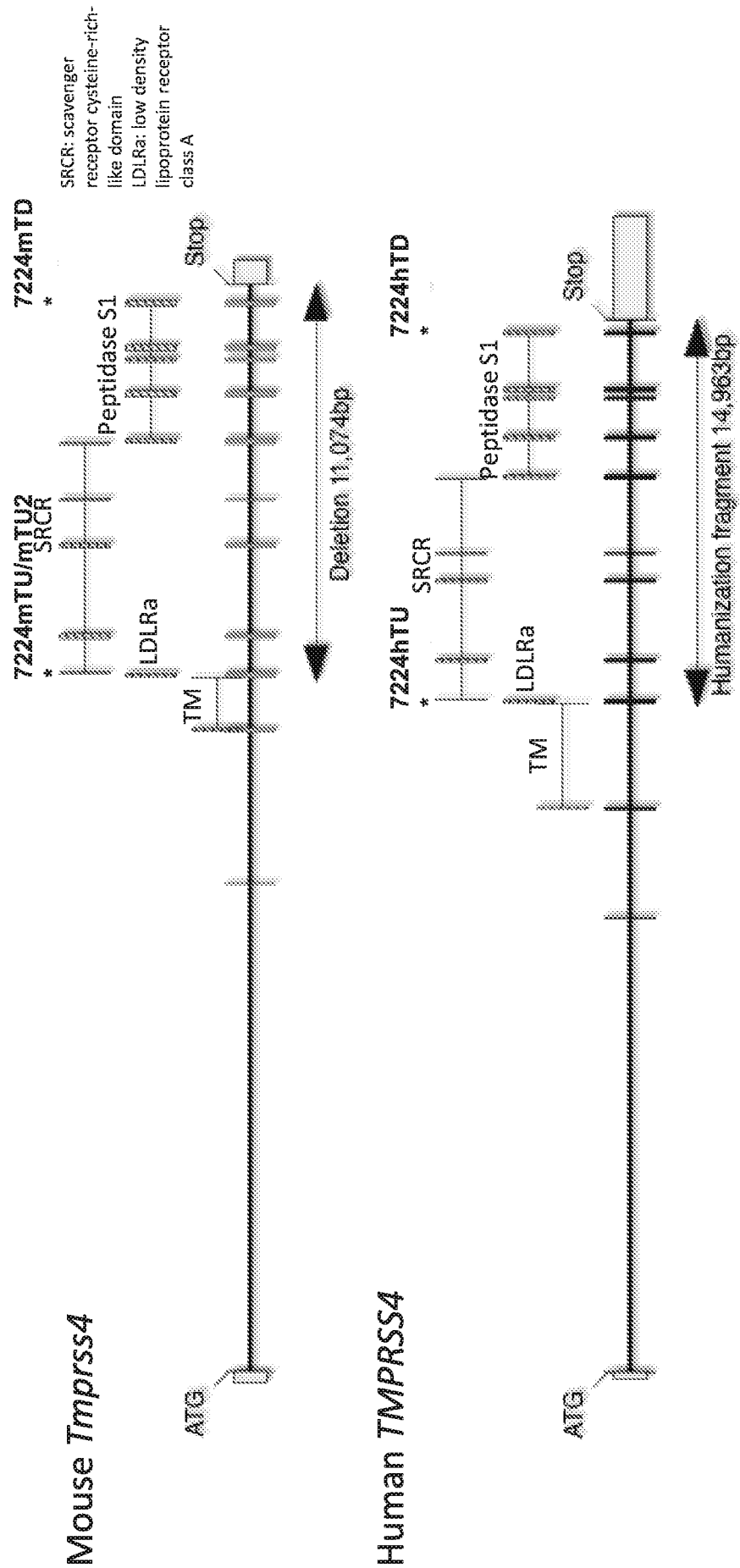


Figure 2A

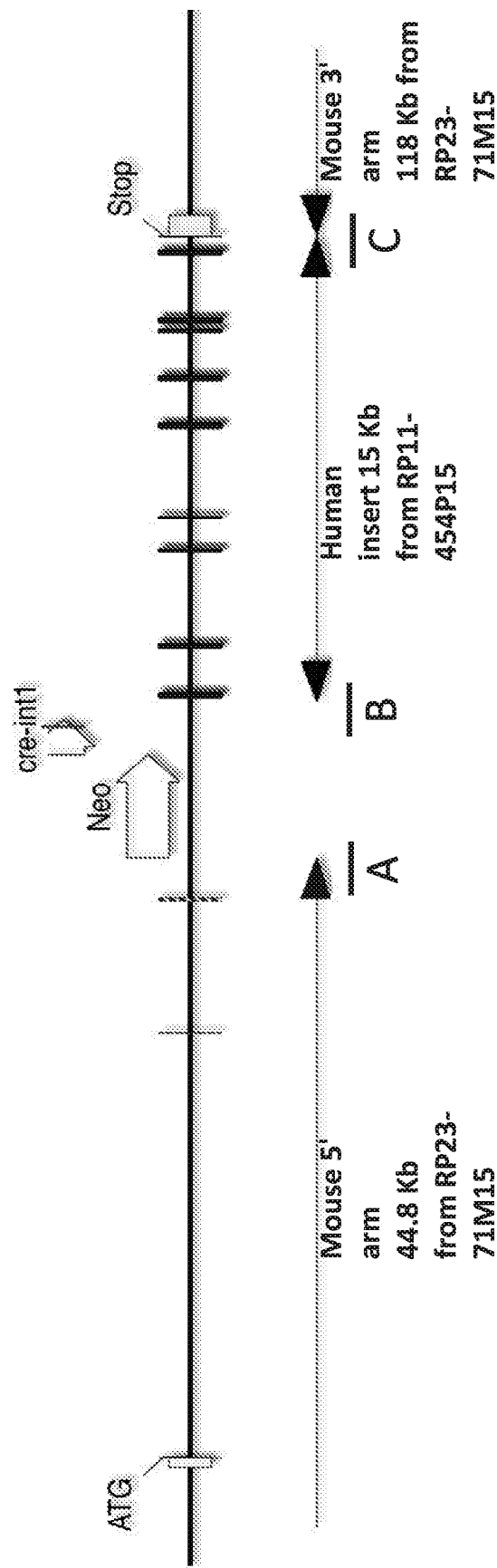
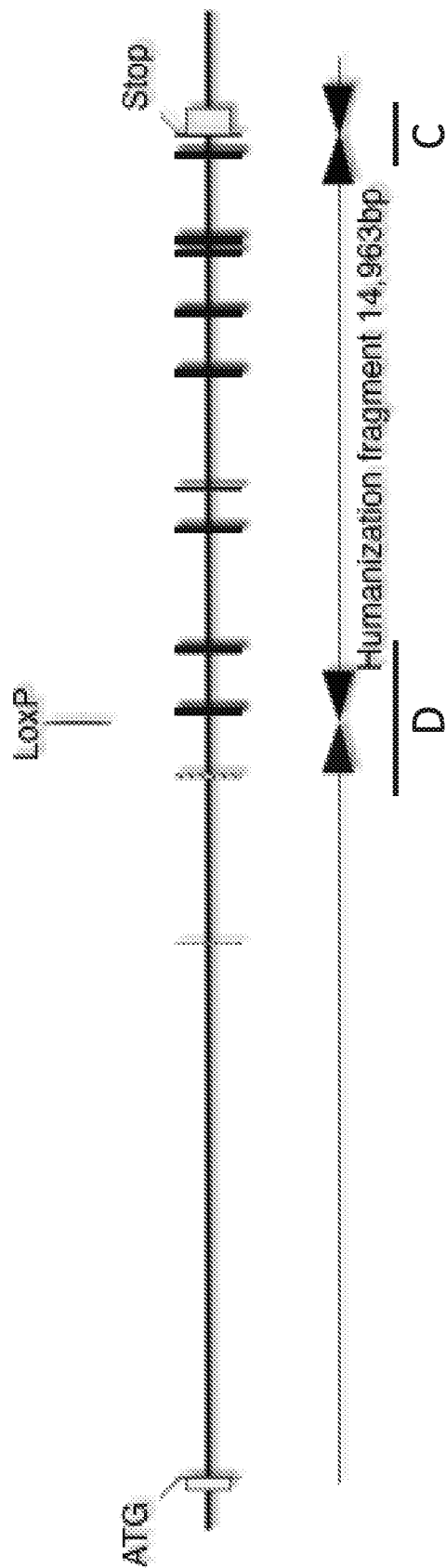


Figure 2B



D. mouse// <u>Sall</u> /Xh <u>oI</u> //(loxP) /ICEUI// <u>NheI</u> // human (SEQ ID NO:41)	CCAGTCAGGG ACACACATGC TCACACGCCG GCCACCCGC ACACACTACA // GTCGAG //ATAACTTCG TATAATGIAT GCTATACGAA GTTAT /GCTAGTAACTATAACGGTCCTAAGGTAGCGA// GCTAGC // CAAGTCTGTG TGCTACCAAG TAGCAAAACT GAGCCTGGAA CTCACACATG
C. human//mouse (SEQ ID NO:40)	TAATCTGACT TTCTCTTCAT CCGTCTCTCT TATTCTAGGC TGAGCTGTAA // CGCTGCCGTC CCCCACATCC AGAAGCTGCT TCCCTTCAGA CCTACCTACG

Figure 2C

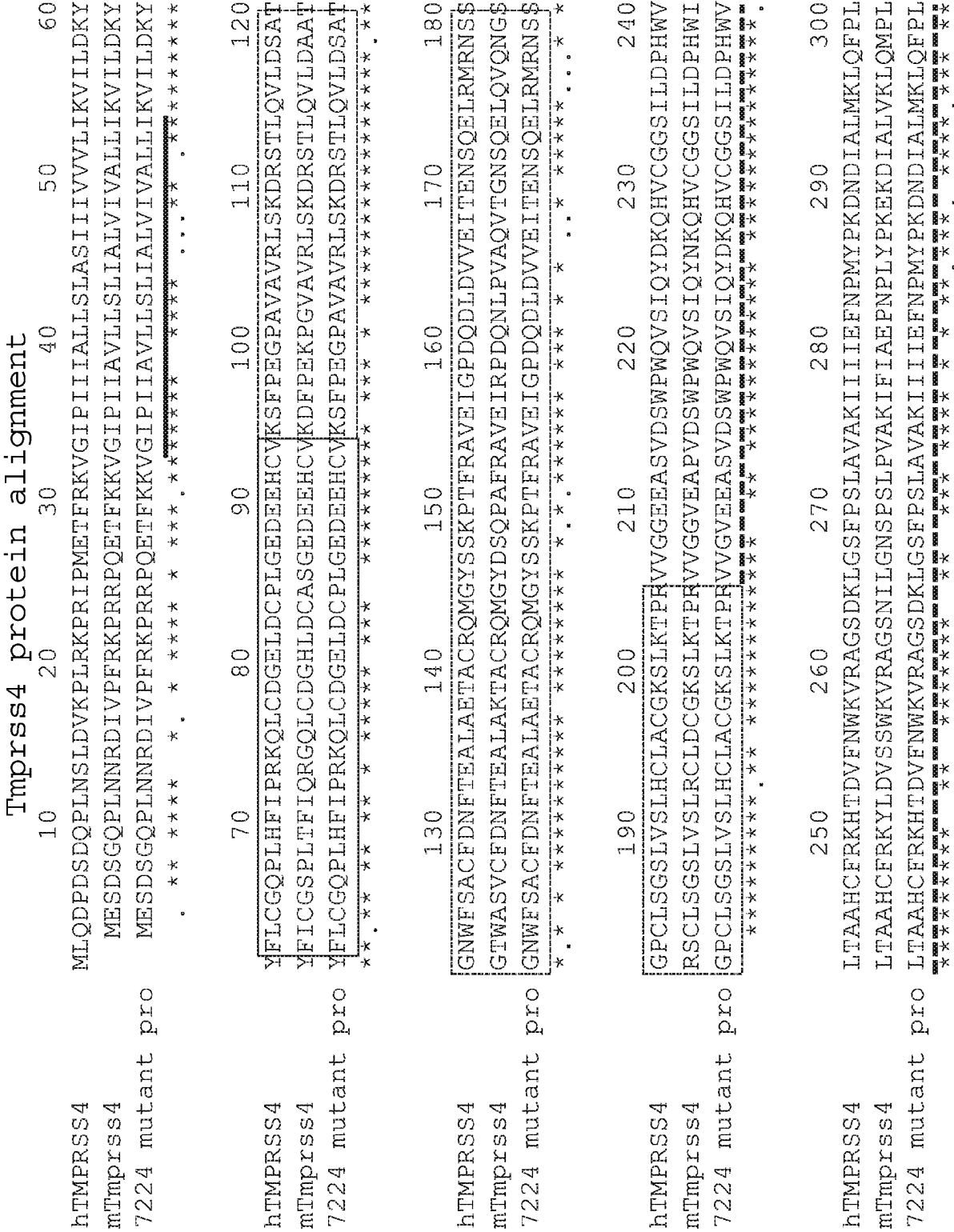


Figure 2D

Figure 2D (Continued)

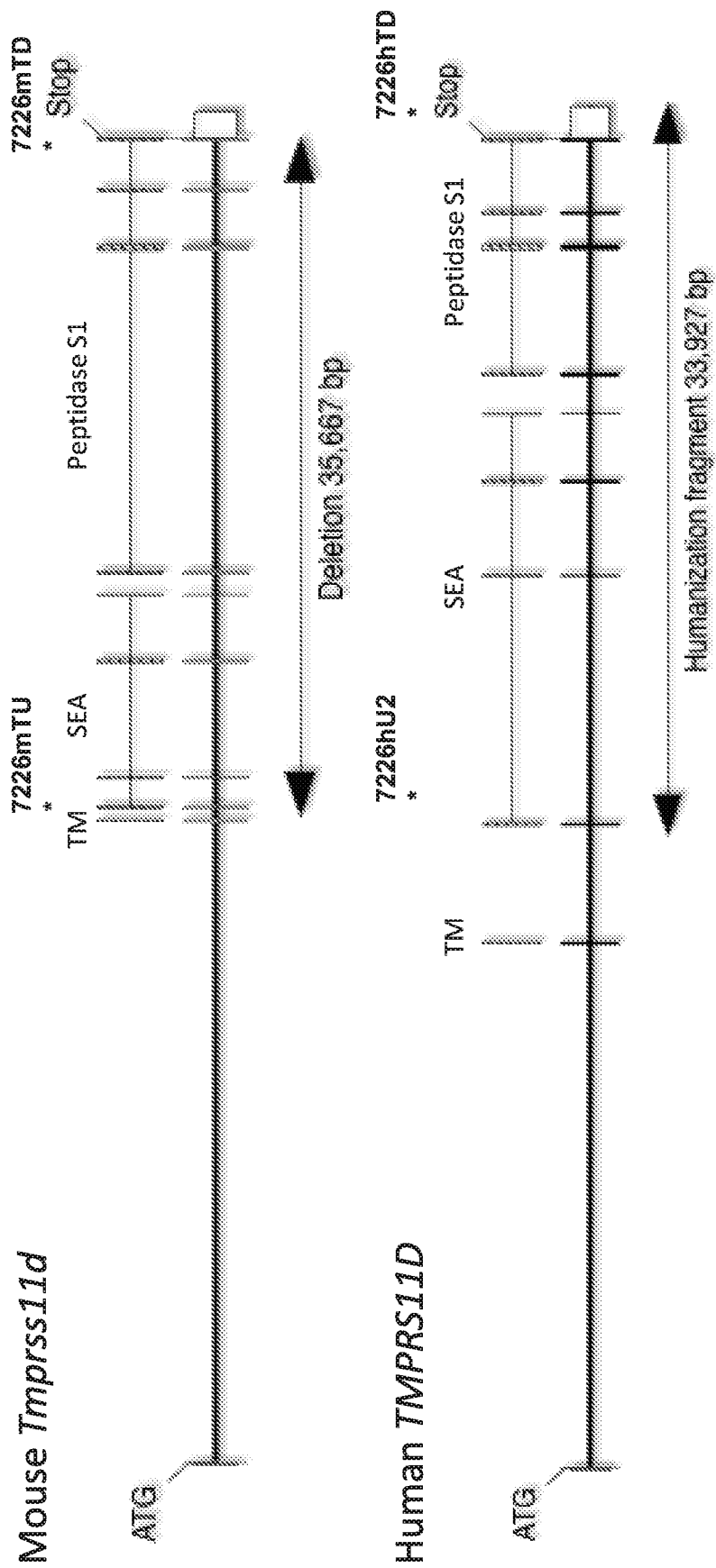
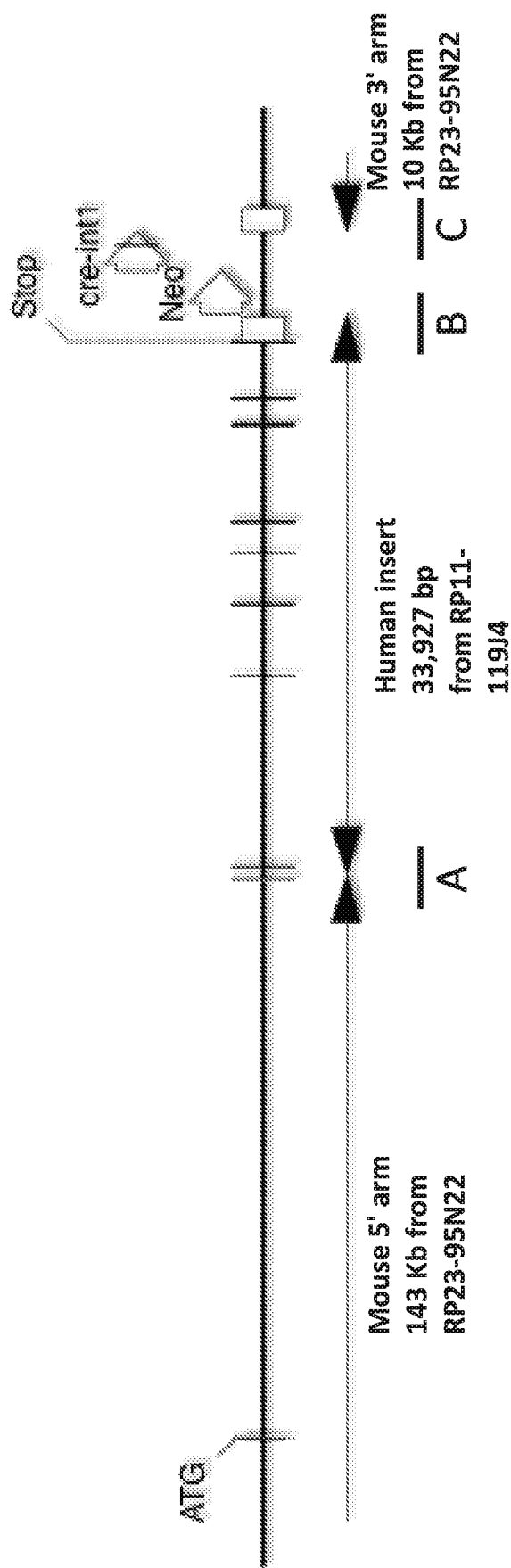
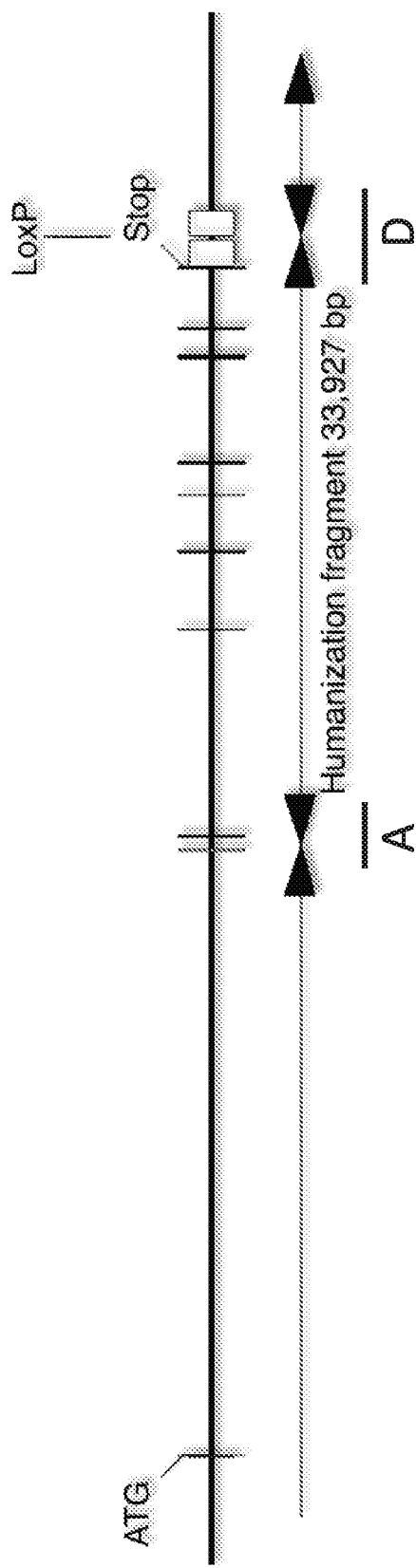


Figure 3A



A. mouse // human (SEQ ID NO:57)	GACCATTTTA AGGTTTGTGCT TGGTTGTTTT GGAGGGAGGG TGGTGCTTTG // CTAATGGTGA ATTACTAACT CCTCAATAAA GAATATTATT TGAATAAATT
B. human// <u>XhoI</u> // (<u>loxP</u>) Cassette (SEQ ID NO:58)	GCTGCTTTT AATCCAGCGC TATAATTGAG GCAAGCGTCC AGCTTGACAC// <u>CTCGAG</u> // <u>ATAACITTCG TATAATGTA</u> <u>T GCTATACGAA GTTA</u> <u>T</u> ATGCATGGCC TCCGCGCCGG GTTTTGGCGC CTCGCGCGG CGCCCCCTC CTCACGGCGA GCGCTGCCAC GTCAGACGAA GGCGCAGCG AGCGTCCTGA
C. Cassette (<u>loxP</u>)/ICEUI// <u>N</u> <u>heI</u> //mouse (SEQ ID NO:59)	ATTGTTTTGC CAAGTTCTAA TTCCATCAGA CCTCGACCTG CAGCCCCCTAG <u>ATAACITTCGT</u> <u>ATAATGTATG CTATACGAAG TTA</u> <u>T</u> /GCTAGTACTATAACGGTCCTAAGGTAGCGA // <u>GCTAGC</u> //TGCAACCGAG GAAAAACGT GCCATGAGGT CTCTGTATCC AAGTGTGACT

Figure 3B



A. mouse // human (SEQ ID NO:57)	GACCAATTTTA AGGTTTTTGCT TGGTTGTTTT GGAGGGAGGG TGGTGCTTTG // CTAATGGTGA ATTACTAACT CCTCAATAAA GAATATTATT TGAATAATT
D. human// <u>XhoI</u> //(<i>loxP</i>) /ICEUI// <u>NheI</u> //mouse (SEQ ID NO:60)	CCAGTCAGGG ACACACATGC TCACACGCCC GCCACCCGC ACACACTACA //CTCGAG//ATAACTTCG TATAATGTAT GCTATACGAA GTTAT /GCTAGTAACTATAACGGTCCCTAAGGTAGCGA // GCTAGC // TGCAACCCGAG GAAAAAACGT GCCATGAGGT CTCTGTATCC AAGTGTGACT

Figure 3C

Tmprssl1d protein alignment

	10	20	30	40	50	60
hTMPRSS11D	MYRPARVTSTSRFLNPYVVC	FI	VAGV	ILAV	TIALLVYFLAFDQ	KSYFYRSSFQLLNVE
mTmprssl1d	MYRPRPMLSPSRFFTPFA	VA	FVVI	ITVGLLAMAGLI	IHF	LAFDKKAIFYHSSFQILLNVE
7226 mutant	MYRPRPMLSPSRFFTPFA	VA	FVVI	ITVGLLAMAGLI	IHF	LAFDQKSYFYRSSFQLLNVE

	70	80	90	100	110	120
hTMPRSS11D	YNSQLNSPATQ	EYRTL	SGRIE	SLITK	TFKES	NLRNQFIRAHVAKLRQD
mTmprssl1d	YTEALNSPATHE	YRTL	SERIE	AMITD	EFRGSS	LKSEFIRTHVVKLRKEGTGVVADVVMKE
7226 mutant	YNSQLNSPATQ	EYRTL	SGRIE	SLITK	TFKES	NLRNQFIRAHVAKLRQD

	130	140	150	160	170	180
hTMPRSS11D	QFTRNNNGAS	MKSRIE	SVLRQ	MLN	SGN	LEINPSTEITSLTDQ
mTmprssl1d	RSSKRN	NRKVMK	TRIQSV	LRRLSS	SGN	LEIAPSNEITSLTDQ
7226 mutant	QFTRNNNGAS	MKSRIE	SVLRQ	MLN	SGN	LEINPSTEITSLTDQ

	190	200	210	220	230	240
hTMPRSS11D	TLSEQRILG	GTEAEE	GSWP	QVSL	RNLN	NAHHC
mTmprssl1d	TLSEERI	IGGMQ	AE	PGD	WPQV	SLQLNNVH
7226 mutant	TLSEQRILG	GTEAEE	GSWP	QVSL	RNLN	NAHHC

	250	260	270	280	290	300
hTMPRSS11D	TSGISTTF	PKLR	MRV	NRN	ILIH	NNYKS
mTmprssl1d	TFGVST	MS	PR	LR	VR	RAIL
7226 mutant	TSGISTTF	PKLR	MRV	NRN	ILIH	NNYKS

Figure 3D

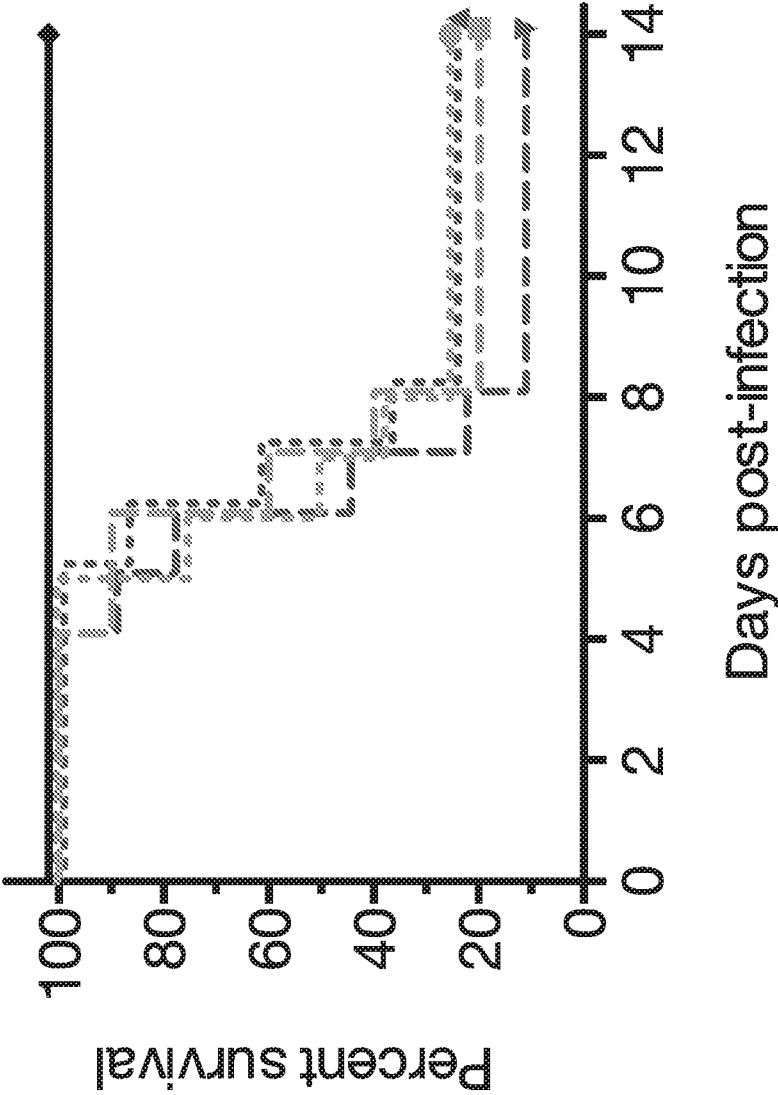


Figure 4