

[illegible]

10 20 30 40 50 60 70
 HAELO_68264899 MRTSLLVFVICYISYGTGSLPIECQQRKFRTATGNCNNEGPSVRVGYDKEKGDVRYYYNSCRGNKNNFASRSECL

85 95 105 115 125 135 145
 HAELO_68264899 NRCNPESRCLLFTYENEGNWRLFKSYYYNATLDECRLTKTYTYHSTSEKYNRFANMKDCEKACRRNDTEDVYSSG

10 20 30 40 50 60 70 80 90 100
 AMBVA_325302602 MNCLRIGLLFMAIFLAEARTATRNQCSYIERRSTWPRYDQFCKPNTLPRWELYKPRLCCLKQGYIRNSWGHCIKRQECNSCRHVRKKDFKQCSSACPLVCGK
 113 123 133 143 153 163 173 183 193 203
 AMBVA_325302602 RVPQVCTEQC VVGCCACPPGYVIHPSNQKSCVPVSHCPPRCPRHSTFQLCSSTCAPSCDSPRPKRC EIRCHEGECVCHPW FATALVKGDDKCVPRNRCPTRGE

Figure 1-S – metastrongylid – KGD (midgut serine proteinase)

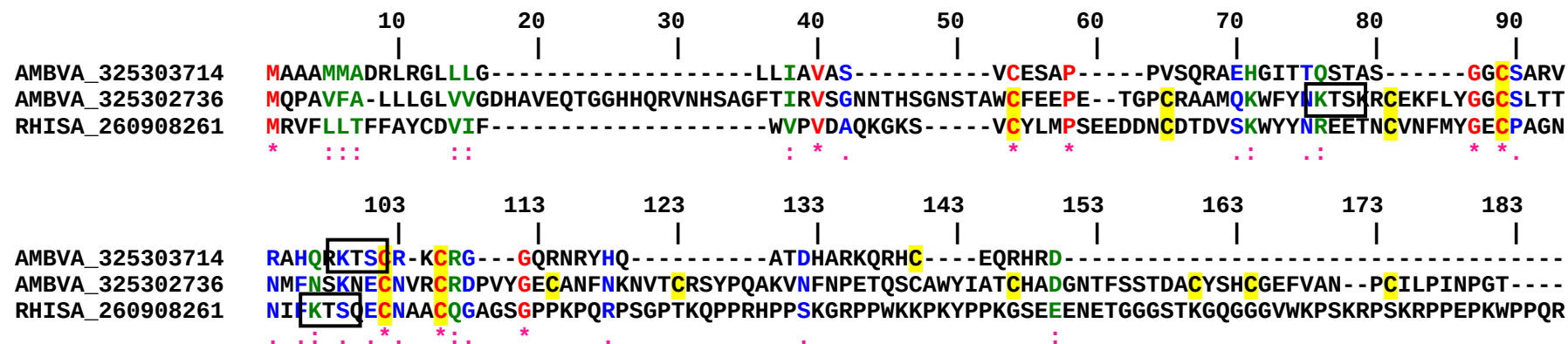


Figure 2-S – metastriate - KTS

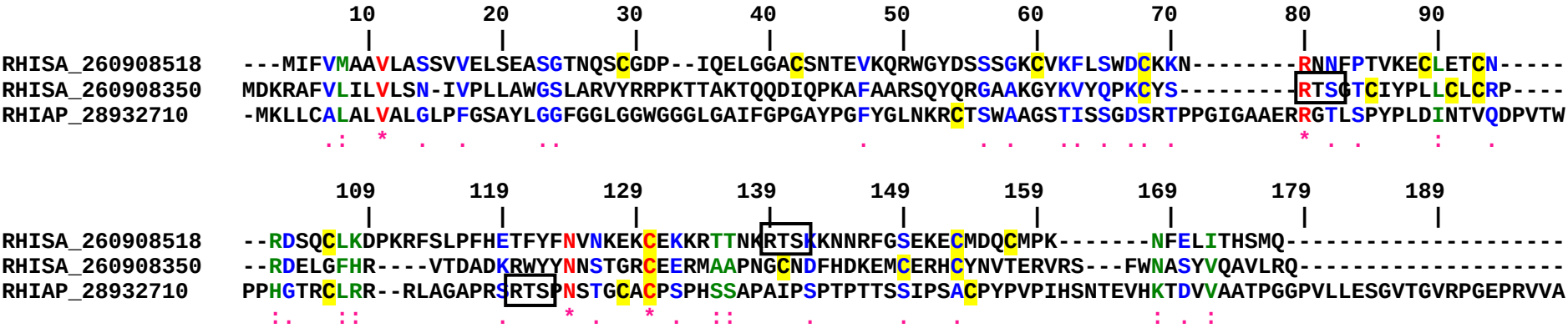


Figure 3-S – metastriate – RTS

	10	20	30	40	50	60	70
IXOSC_241690880	MEMKTLGAAL	ALTFAAASL	VAFVGA	QPVNDDNFK---	EV	PVGYDEV	TPTPREVGQSCNAYS
IXOSC_67083399	--MNTFIVV	LVSSLALTM	FEVFAD	PDQQPDVTY---	SV	PSG-----	ICSKNSECGPNLCCRETHKGDIA
IXOSC_241250787	MALYGATPS	VCTMALLLL	LGLSAV	PGGHGDDAFFRRRL	VP	ES-----	LQTLGGDGSTQVLGRPEFFKAPREDQAEA
IXOSC_241859419	-MAFSLAGS	LGLATTSA	LRR TSA	AIRC	CLATSTENIADL	VKG-----	DKVVVFMKGVPESPRCGFSNAVVQVLRMHGV
	:	:	.	:	.		

	88	98	108	118	128	138	148
IXOSC_241690880	ITTCQPRSAPG-----	QRCTGVQVESPFYLDY	CPCL	KGD	---RLF	SPHC	-----
IXOSC_67083399	VVTCAPLAKSG-----	VPCSNSETGDEPYKTY	CSC	ETG	---LEC	INNVCTALPAPVPVE	-----
IXOSC_241250787	VADLPSLMDESQL-----	QDCHIEVQVTERLRGH	CSTLELM	---GKN	FPVCR	KGD	HLSVNHHECSHA-----
IXOSC_241859419	QYKAHDVME	ENLRQGIKAYS	NWPTIPQVYIDGQFVGG	CDILLQMHQNGEL	IDE	LAKVGIKSLLVDAAPASEQETTKK	
			*		:		

Figure 5-S – prostriates - KGD

	10	20	30	40	50	60	70	80
IXOSC_67083629	----	MSGIEL	LILL----	LFHICIVYGAETTKCNLT	KTS	CPGLKEK-WHFNGLIG-----	RCERSTPSF	CGGKDN
IXOSC_67083208	----	MSGIKL	LILL----	LFHICIVCGVETTQCNLT	KTS	CPRRKQN-WHFNYLIG-----	RCERSTTSF	CGGKDI
IXOSC_241802506	----	MNHSTL	LLLLGAAAF	ACTIGLCRAGVYKD	LAECTTENVEK	CGVDFVPYFGGNTL----	AVNAADLEKQ	C TEYLTQLK C
IXOSC_241998684	---	MLRTIA	VACL----	LLGLFEYTAAGPTTKTPAG	CGTESFEK	CGTDLIIFAGGPVI----	PVSKEELVTT	CPKE KTS EC
IXOSC_241165998	--	MKIPGAI	IGLAAFVVC	AFVLRQGSAA	SAKCAFPR	TSCFKSHLNDLTGNLTDL	TRKQGAALDAAL	TNYTRRFSAA FQC
IXOSC_242002184	MPSTV	HYPAILL	CTLSLLAV	FLVADSKTLKEGD	CEVCVGAL	KKLHDLRLEVEERS-----	NEGSVEAGFLEF	QKTS KG
IXOSC_241250792	----	LCLGLL	LLASSVSA	ARAGTRPHPGGNQRTLL	RPLPSHDL	PVIDLVEPAGHVYDP--	GPEDLDITRLQRT	LAGHFDP
IXOSC_241159543	-----	MSIVK	TALLVVLG	VVCVSSAF	PGVWRKHHPD	VDPTRYKEWAHFAIS-----	SQVEDRTNFD	TLMTL
IXOSC_332691297	-MLTV	SLLT	LSLAAY-	ASAVATVTDANN	FMDAVLHTRIPALIT	SEILFPFATIP-----	PFNFTVAGTNIL	TNREL
	:							
	90	100	110	120	130	140	150	160
IXOSC_67083629	TFPDFKE	C QRT	CENAEIITAED	CRMALNKGIC	EHKKKGRPKK	P-----	ITRWYFNSTDSN	CH KFMWQ R CSGNR
IXOSC_67083208	TFSSFEE	C QRT	CEKEEIVSPQD	CRMNFNRGT	CEEKRKGRPKK	W-----	VYRWYFNSTDSQ	CH RFQWY R CSANR
IXOSC_241802506	SDDFSVK	C LDGLPKGT	ILLMLRAARDEYDAI	CNVTS	SPRHQ E KTS	VL----	TVCS-LKPF	C SFSGSYADFAN C ATSGLK
IXOSC_241998684	ARAYAQK	C LARFPRGMV	MLLLD	GIRTEVNAK	CND	SGAGHQG-----		
IXOSC_241165998	FVESEK	R CANSQETQYIGRVQ	STDLLVREL	TNKTALTAIVTAYK	C ----	HDVERFTP	C MSKAIRDFLSEPI	KTS KADAK
IXOSC_242002184	PEHRF	C YYVGGLEESATKIVNEL	TKPFSWGM	PALKV C EKL	VAK-----		DSQ C DLKYPKVIDLK	
IXOSC_241250792	KFMAVHR	PKESFLHPNGSLQPGFRL	KKGRLVPAR	MPRDLQRIRL	KGLDFPGGI	KVRLDLGRKLRRKL	RQLLW	TYTY C PL
IXOSC_241159543	ISVESQ	VIAGVDYKLKMKVAESN	CVIGVDSYSRER	CHLKVDAP-----			YMI C TALVNYPWEH	KTS .K
IXOSC_332691297	QVNVSRGEIRGFSTEVKRVGD	C MPPVLREG	KTS	R CTLNFTGIN----	ATFDTHTRGDNIVASD	KNIWVRASVIDTTG	QF	
	170	180	190	200	210	220	230	
IXOSC_67083629	NNFPTKQD	C MVC	QRAIPTTP-----	TTSTTPATSTTPATPATPA	APAQT--	TPPA-----		
IXOSC_67083208	NNFPTKED	C QIC	QKAMP	TTTP-----	TTSTTPATSTTPATPATPA	APAET--	TPP EC	
IXOSC_241802506	TK C GDKEAE	AFD	TIQHVFGEVLDL-----	ACGKYRAGSE	A CKSLT	PLPTVDDARAKDKGFIEPL	TVIASKLG----	
IXOSC_241998684	-----							
IXOSC_241165998	TL C SNVDDASKT	C L	VARN C TPAAE-----	PGKKAVRKLFTSFRTI	WGCKGSG	GAPAATSVLP	TVSVMLALIARKML	
IXOSC_242002184	TVNLKKLKV	DKLKKILSDWD-----		ER- C EG C VEK	TD	FVKRIEELKTVHMREEL-----		
IXOSC_241250792	VYRWKDLGLRF	WPRWIREGR	CYNSRR C SFP	PGMT C RE KTS	A EKTVLRWH	CRDWTQRRQ C RWIPATLSVL	VE C C C	
IXOSC_241159543	SYN C SDRVYGV	KAAE-----						
IXOSC_332691297	EAVAERGKQGNVHTFLVDKIHVKV	KNDKALSLNDRK	KKKFRQHFEDKVL	TVLPQIFYGAYLHLLGA	AVSSVPF	PHV--		

Figure 6-S – prostriates – KTS

	10	20	30	40	50	60	70	80	90	100												
IXOSC_67083443	-----	MEIWW	CRLFVLV	IVAAMQAR	--	GDPGVPDTP	CE	DRLPNVAT	CSEGA	SEAWYFDLE	EKVC	RSIIG	CNYSTNY	FENSTEC	ESV	CSPDKYC	LLLEKPQE					
IXOSC_242000850	MGPCYRR	SGALFAPLL	WLLVGV	GSRR	RD	CGDPVVRT	AE	ARLTSPNY	PLAYPAG	VRCSYR	VLPSWPGV	CAVLLS	FEDMD	IEG	--	TPPNC	ERGD	--VLRVP-S				
IXOSC_241719667	-----	MFWLL	SQTL	LFI	LDVH	GNGV	R	-----	SPL	CGGALIT	PQHVLT	AAHCT	FNGN	KS	SLTPDA	FVARLGE	HDYLSN	-----DD-----				
		.	:	:	:	.	*		:	:	:	:	:	:	:	:	:	*				
	112	122	132	142	152	162	172	182	192	202												
IXOSC_67083443	PVDAC	VDQEK	KTEPN	LDNQ	KNSLWY	FDK	KLRC	CVETDE	LSRNT	FPSQ	RHCQAS	CAKY	SVCYAQ	ESAWN	QRR	CNPEL	VWYFD	PIRKDC	FYGKRC	GNSTNR	FA	
IXOSC_242000850	TGDSFC	GVTPPE	SLVLP	PLPG	GLTLE	FSSD	TERSGV	GFALRL	AQV	PN	SCPTD	VTSP	CGGR	FSEQEF	RIEGPS	ARSAG	CLYL	VTKFR	DDV	QQLR	--YDRFS	
IXOSC_241719667	-----	GANPV	DEPV	VQI	HRHS	---	D	FNSR	TYLND	VAVL	KLRRP	V	PLNK	DIALI	C	LPY	GPLQ	TD	TYEG	KMANI	AGWGE	LYYGGPSSASLQDTRIP--IQSLD
		.	:	:	:	.	*	.	:	:	:	:	:	:	:	:	:	:	:	:	:	
	214	224	234	244	254	264	274	284	294	304												
IXOSC_67083443	TRED	CLRE	CPYAGE	IPE	CHLEK	DYGSS	CPPA	----	ESGR	EWGS	WKAFL	PLARAS	LRWYYD	VDGE	CRS	FIYQC	CGGN	ENNFPT	KRTC	CNAIC	RHRTSY	ITGTA
IXOSC_242000850	-----	VGD	IAS	CTHGRRL	I	AGTP	----	ECGR	KPP	GKVD	VEFP	SRTL	-----	T	LLYL	GGDS	AH	DSFV	LDFF	QEE	CPDTR	-----
IXOSC_241719667	T-----	CKESF	KRTS	ITFTD	NYLC	AGSL	KGDKDA	RGDS	GGPL	MLLD	Q	QERFT	-----	IIG	ITS	FRR	CAEP	GYPG	VYTR	VAKYL	DWIA	QRLN--
		.	:	:	:	.	*	:	:	:	:	:	:	:	:	:	:	:	:	:	:	

Figure 7-S – prostriates – RGD and KGD – 2 domains

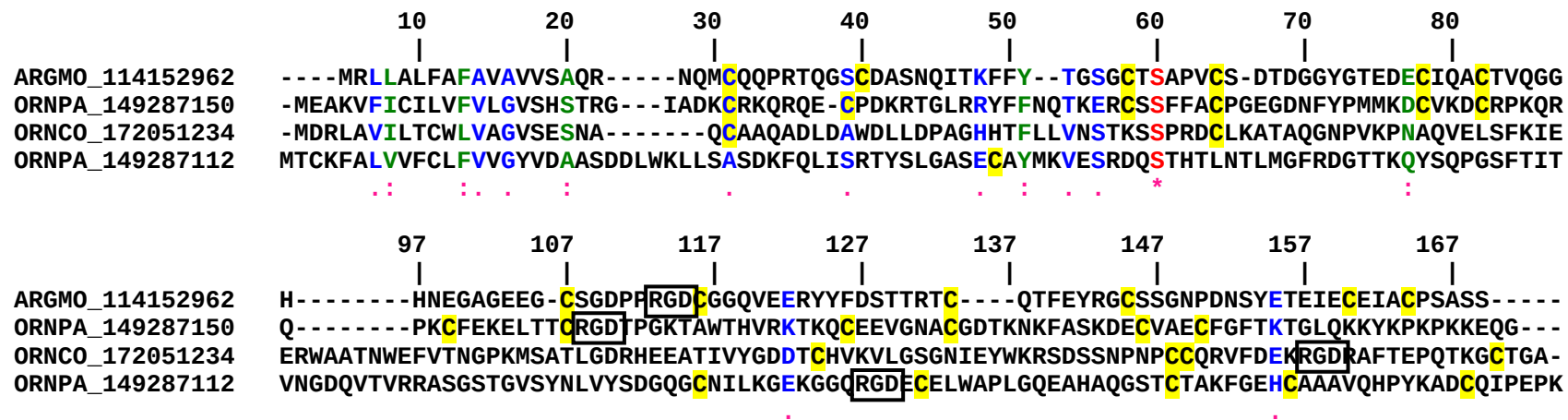


Figure 8-S – Soft ticks – RGD long

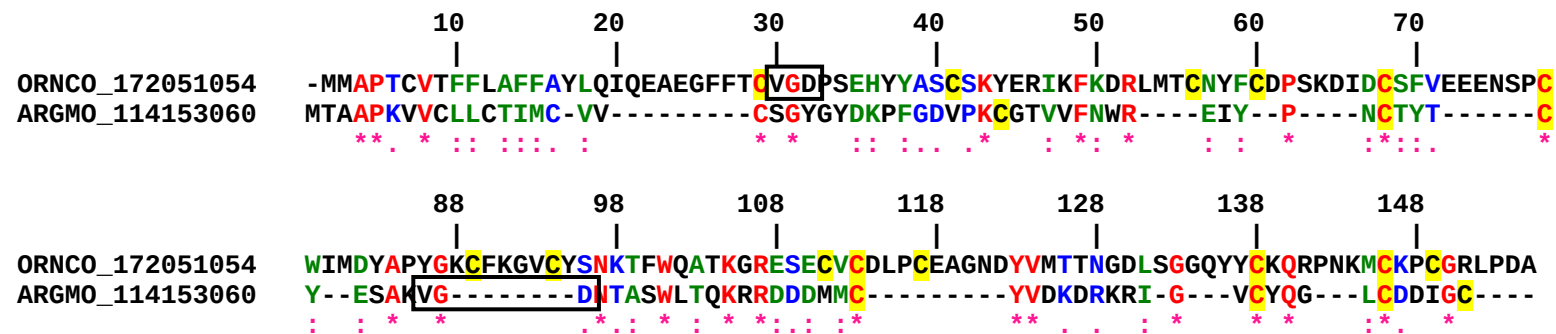


Figure 11-S – Soft tick – VGD

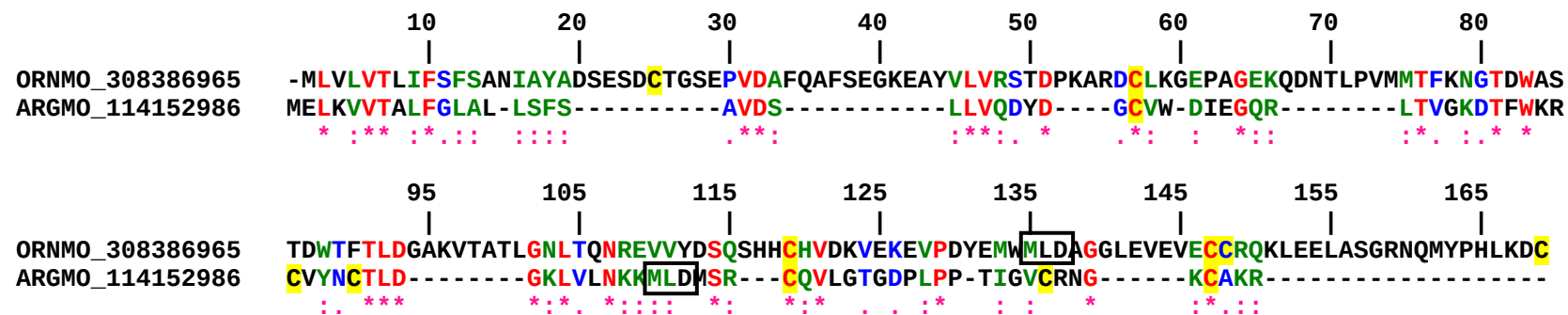


Figure 12-S – Soft tick - MLD