SUPPLEMENTARY INFORMATION

Supplementary Figures

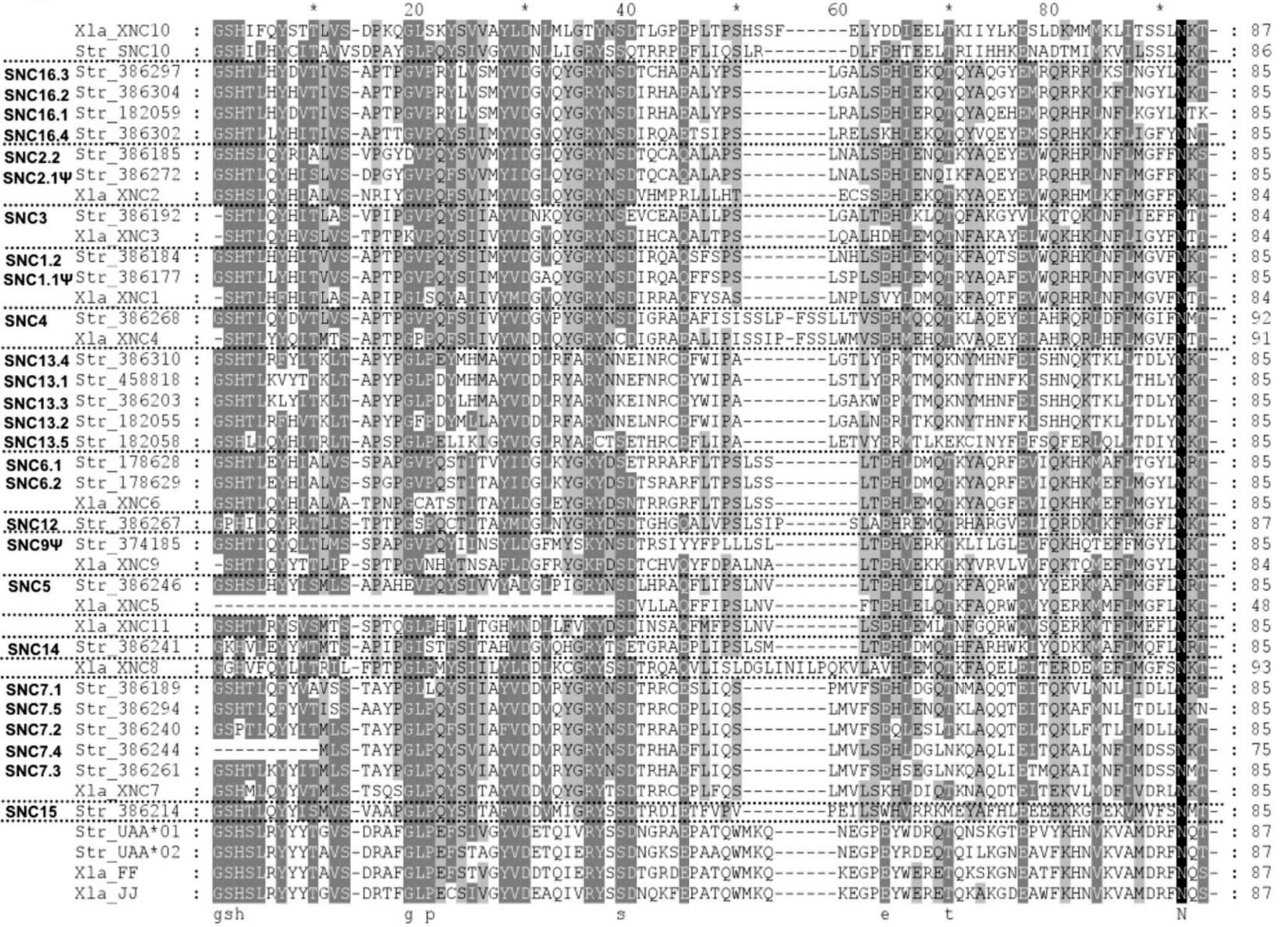
Figure S1: Multiple deduced amino acid alignment of α1 domains of *SNC* genes and *XNC* subfamilies. The alignment of *XNC* subfamilies and *SNC* genes with representative *X. laevis* and *S. tropicalis* class Ia was generated using ClustalX and manually adjusted with GeneDoc v2.5. Black shading indicates identical residues among all sequences. Gray shading indicates similar residues among most sequences. Dotted lines are used to depict the grouping of SNC genes into subfamilies and the gene name is illustrated next to the sequence.

Figure S2: Multiple deduced amino acid alignment of α2 domains of *SNC* genes and *XNC* subfamilies. Deduced amino acid sequence alignment of *XNC* subfamilies and *SNC* genes with representative *X. laevis* and *S. tropicalis* class Ia is generated using ClustalX. Alignment is viewed and manually adjusted with GeneDoc v2.5. Shading is as described in Figure S1.

Figure S3: Nucleotide alignment of α1 and α2 domains of *SNC10* RACE-PCR Products. Alignment of SNC10 RACE-PCR products was generated using ClustalX and manually adjusted with GeneDoc v2.5 from cDNA made from a pool of 20 *S. tropicalis* larval thymuses and spleen. The sequence labeled 'Genom' represents the original SNC10 sequence that came from the genome sequencing project. Shading of the alignment is as described in Figure S1.

Figure S4: Multiple deduced amino acid alignment of α3 domains of *X. laevis* and *S. tropicalis* class Ia, *SNC* genes and *XNC* subfamilies. Alignment of α3 domains of *Xenopodinae* class Ia and class Ib sequences. Black triangles indicate putative β2m interaction sites and black circles represent putative CD8 interaction sites, modified from (12).

Fig. S1



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SNC16.4  Str_386302 : GSHTLLYHITIVS-APTTGVPQYSIIMYVDGVQYGRYNSDIRQAETSIPS--------LRELSKHIEKQTQYVQEYEMSQRHKLKFLIGFYNNT- : 85
SNC2.2   Str_386185 : GSHSLQYRIALVS-VPGYDVPQYSVVMYIDGLQYGRYNSDTQCAQALAPS--------LNALSEHIENQTKYAQEYEVWQRHRLNFLMGFFNKS- : 85
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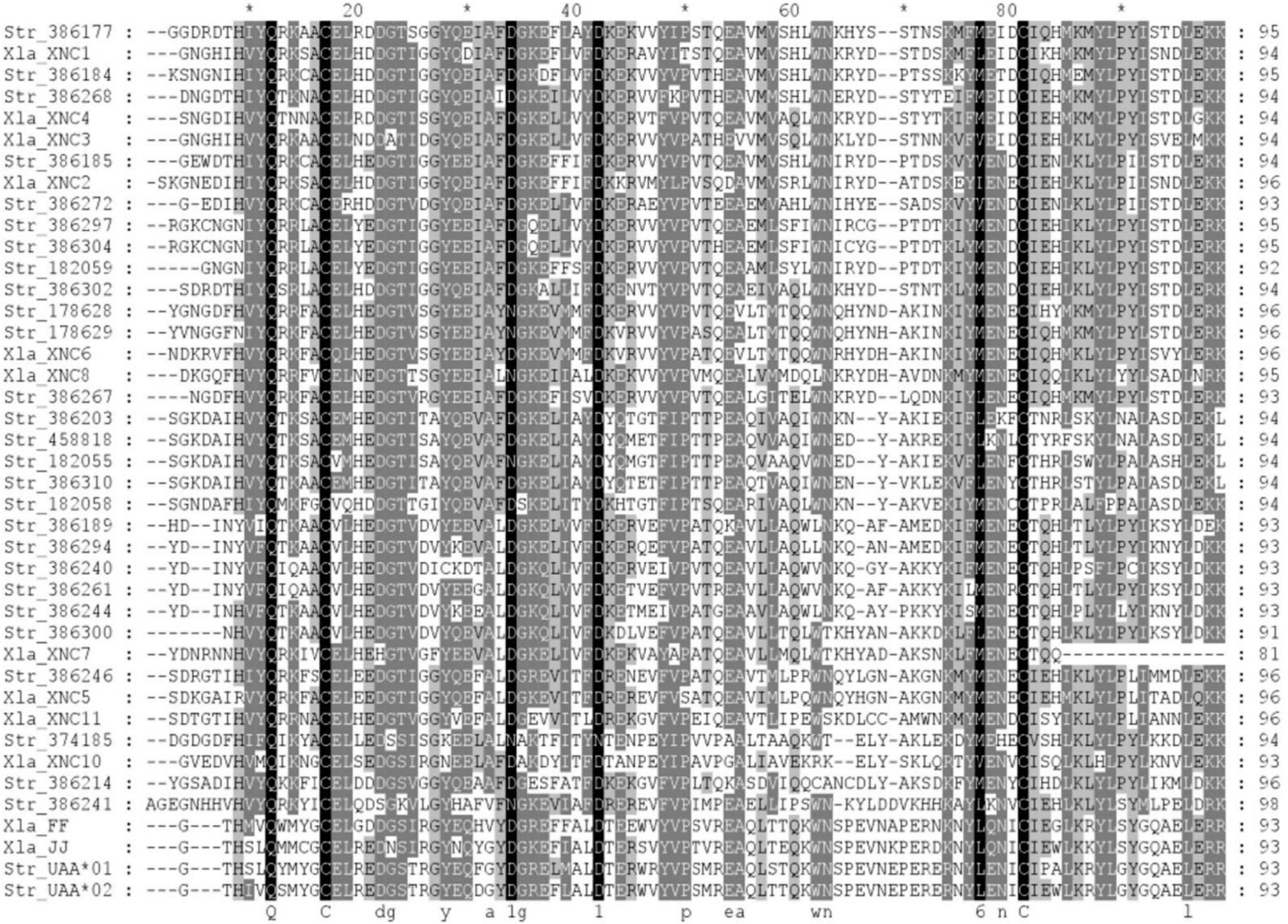
Fig. S2



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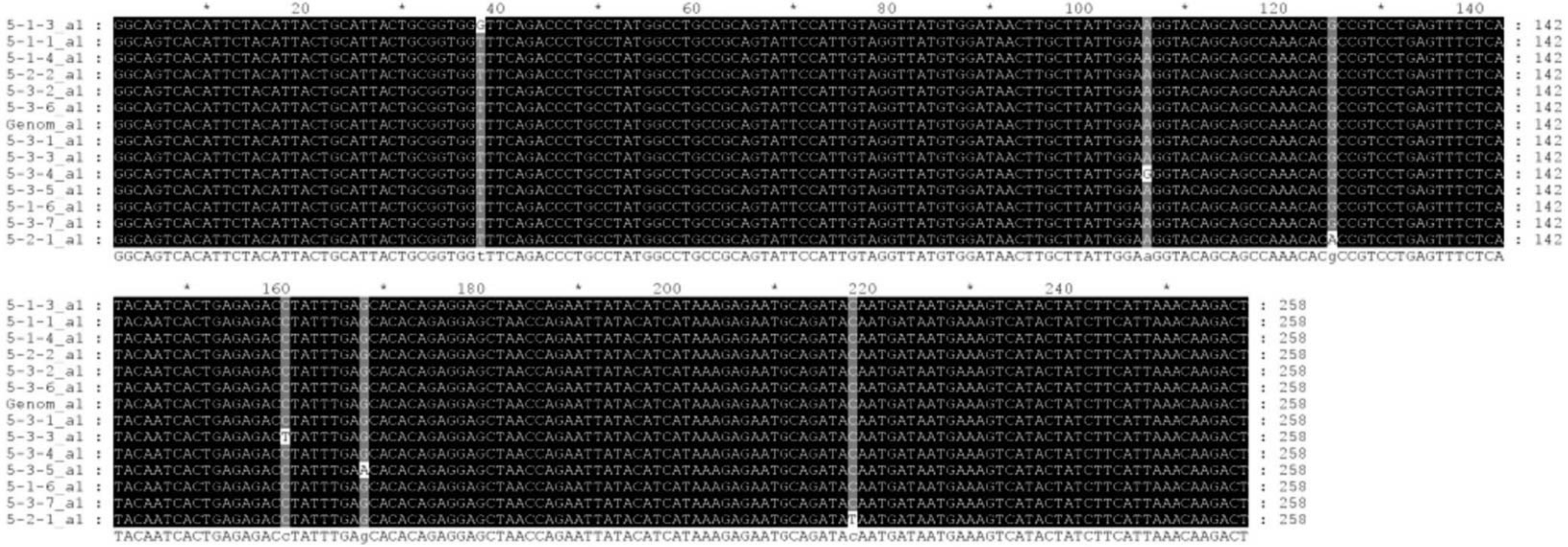
alpha 1 domain

Fig. S3



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Genom_a1 : TACAATCACTGAGAGACCTATTTGAGCACACAGAGGAGCTAACCAGAATTATACATCATAAAGAGAATGCAGATACAATGATAATGAAAGTCATACTATCTTCATTAAACAAGACT : 258
5-3-1_a1 : TACAATCACTGAGAGACCTATTTGAGCACACAGAGGAGCTAACCAGAATTATACATCATAAAGAGAATGCAGATACAATGATAATGAAAGTCATACTATCTTCATTAAACAAGACT : 258
5-3-3_a1 : TACAATCACTGAGAGACTTATTTGAGCACACAGAGGAGCTAACCAGAATTATACATCATAAAGAGAATGCAGATACAATGATAATGAAAGTCATACTATCTTCATTAAACAAGACT : 258
5-3-4_a1 : TACAATCACTGAGAGACCTATTTGAGCACACAGAGGAGCTAACCAGAATTATACATCATAAAGAGAATGCAGATACAATGATAATGAAAGTCATACTATCTTCATTAAACAAGACT : 258
5-3-5_a1 : TACAATCACTGAGAGACCTATTTGAACACACAGAGGAGCTAACCAGAATTATACATCATAAAGAGAATGCAGATACAATGATAATGAAAGTCATACTATCTTCATTAAACAAGACT : 258
5-1-6_a1 : TACAATCACTGAGAGACCTATTTGAGCACACAGAGGAGCTAACCAGAATTATACATCATAAAGAGAATGCAGATACAATGATAATGAAAGTCATACTATCTTCATTAAACAAGACT : 258
5-3-7_a1 : TACAATCACTGAGAGACCTATTTGAGCACACAGAGGAGCTAACCAGAATTATACATCATAAAGAGAATGCAGATACAATGATAATGAAAGTCATACTATCTTCATTAAACAAGACT : 258
5-2-1_a1 : TACAATCACTGAGAGACCTATTTGAGCACACAGAGGAGCTAACCAGAATTATACATCATAAAGAGAATGCAGATATAATGATAATGAAAGTCATACTATCTTCATTAAACAAGACT : 258
           TACAATCACTGAGAGACcTATTTGAgCACACAGAGGAGCTAACCAGAATTATACATCATAAAGAGAATGCAGATAcAATGATAATGAAAGTCATACTATCTTCATTAAACAAGACT
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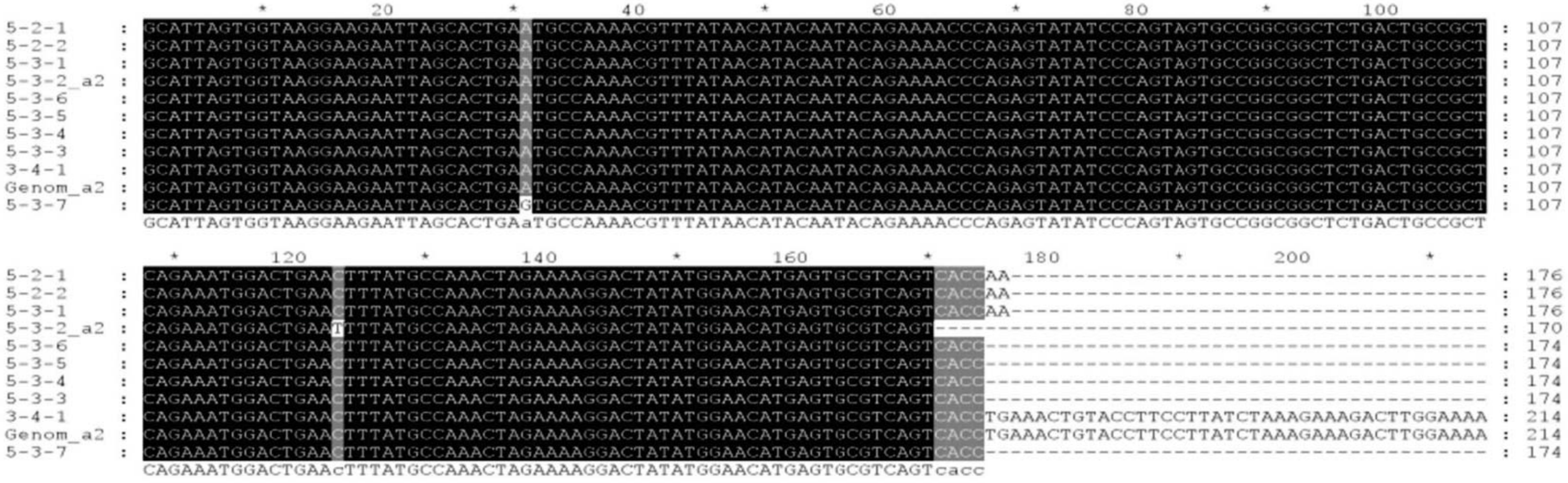
alpha 2 domain



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5-2-1       : GCATTAGTGGTAAGGAAGAATTAGCACTGAATGCCAAAACGTTTATAACATACAATACAGAAAACCCAGAGTATATCCCAGTAGTGCCGGCGGCTCTGACTGCCGCT : 107
5-2-2       : GCATTAGTGGTAAGGAAGAATTAGCACTGAATGCCAAAACGTTTATAACATACAATACAGAAAACCCAGAGTATATCCCAGTAGTGCCGGCGGCTCTGACTGCCGCT : 107
5-3-1       : GCATTAGTGGTAAGGAAGAATTAGCACTGAATGCCAAAACGTTTATAACATACAATACAGAAAACCCAGAGTATATCCCAGTAGTGCCGGCGGCTCTGACTGCCGCT : 107
5-3-2_a2    : GCATTAGTGGTAAGGAAGAATTAGCACTGAATGCCAAAACGTTTATAACATACAATACAGAAAACCCAGAGTATATCCCAGTAGTGCCGGCGGCTCTGACTGCCGCT : 107
5-3-6       : GCATTAGTGGTAAGGAAGAATTAGCACTGAATGCCAAAACGTTTATAACATACAATACAGAAAACCCAGAGTATATCCCAGTAGTGCCGGCGGCTCTGACTGCCGCT : 107
5-3-5       : GCATTAGTGGTAAGGAAGAATTAGCACTGAATGCCAAAACGTTTATAACATACAATACAGAAAACCCAGAGTATATCCCAGTAGTGCCGGCGGCTCTGACTGCCGCT : 107
5-3-4       : GCATTAGTGGTAAGGAAGAATTAGCACTGAATGCCAAAACGTTTATAACATACAATACAGAAAACCCAGAGTATATCCCAGTAGTGCCGGCGGCTCTGACTGCCGCT : 107
5-3-3       : GCATTAGTGGTAAGGAAGAATTAGCACTGAATGCCAAAACGTTTATAACATACAATACAGAAAACCCAGAGTATATCCCAGTAGTGCCGGCGGCTCTGACTGCCGCT : 107
3-4-1       : GCATTAGTGGTAAGGAAGAATTAGCACTGAATGCCAAAACGTTTATAACATACAATACAGAAAACCCAGAGTATATCCCAGTAGTGCCGGCGGCTCTGACTGCCGCT : 107
Genom_a2    : GCATTAGTGGTAAGGAAGAATTAGCACTGAATGCCAAAACGTTTATAACATACAATACAGAAAACCCAGAGTATATCCCAGTAGTGCCGGCGGCTCTGACTGCCGCT : 107
5-3-7       : GCATTAGTGGTAAGGAAGAATTAGCACTGAGTGCCAAAACGTTTATAACATACAATACAGAAAACCCAGAGTATATCCCAGTAGTGCCGGCGGCTCTGACTGCCGCT : 107
              GCATTAGTGGTAAGGAAGAATTAGCACTGAaTGCCAAAACGTTTATAACATACAATACAGAAAACCCAGAGTATATCCCAGTAGTGCCGGCGGCTCTGACTGCCGCT

                *       120         *       140         *       160         *       180         *       200         *
5-2-1       : CAGAAATGGACTGAACTTTATGCCAAACTAGAAAAGGACTATATGGAACATGAGTGCGTCAGTCACCAA-------------------------------------- : 176
5-2-2       : CAGAAATGGACTGAACTTTATGCCAAACTAGAAAAGGACTATATGGAACATGAGTGCGTCAGTCACCAA-------------------------------------- : 176
5-3-1       : CAGAAATGGACTGAACTTTATGCCAAACTAGAAAAGGACTATATGGAACATGAGTGCGTCAGTCACCAA-------------------------------------- : 176
5-3-2_a2    : CAGAAATGGACTGAATTTTATGCCAAACTAGAAAAGGACTATATGGAACATGAGTGCGTCAGT-------------------------------------------- : 170
5-3-6       : CAGAAATGGACTGAACTTTATGCCAAACTAGAAAAGGACTATATGGAACATGAGTGCGTCAGTCACC---------------------------------------- : 174
5-3-5       : CAGAAATGGACTGAACTTTATGCCAAACTAGAAAAGGACTATATGGAACATGAGTGCGTCAGTCACC---------------------------------------- : 174
5-3-4       : CAGAAATGGACTGAACTTTATGCCAAACTAGAAAAGGACTATATGGAACATGAGTGCGTCAGTCACC---------------------------------------- : 174
5-3-3       : CAGAAATGGACTGAACTTTATGCCAAACTAGAAAAGGACTATATGGAACATGAGTGCGTCAGTCACC---------------------------------------- : 174
3-4-1       : CAGAAATGGACTGAACTTTATGCCAAACTAGAAAAGGACTATATGGAACATGAGTGCGTCAGTCACCTGAAACTGTACCTTCCTTATCTAAAGAAAGACTTGGAAAA : 214
Genom_a2    : CAGAAATGGACTGAACTTTATGCCAAACTAGAAAAGGACTATATGGAACATGAGTGCGTCAGTCACCTGAAACTGTACCTTCCTTATCTAAAGAAAGACTTGGAAAA : 214
5-3-7       : CAGAAATGGACTGAACTTTATGCCAAACTAGAAAAGGACTATATGGAACATGAGTGCGTCAGTCACC---------------------------------------- : 174
              CAGAAATGGACTGAAcTTTATGCCAAACTAGAAAAGGACTATATGGAACATGAGTGCGTCAGTcacc
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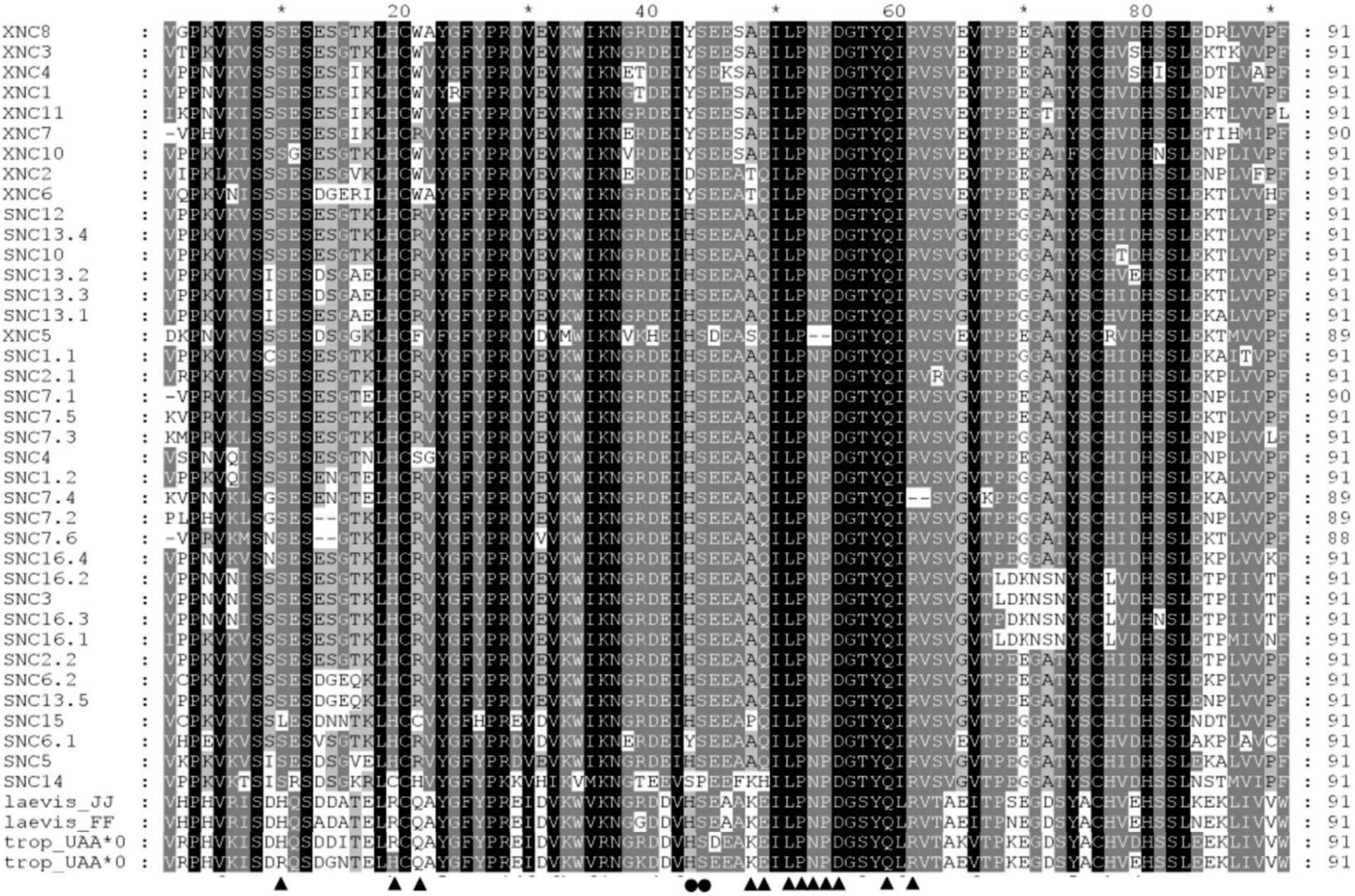

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XNC3        : VTPKVKVSSSESESGTKLHCWVYGFYPRDVEVKWIKNGRDEIYSEESAEILPNPDGTYQIRVSVEVTPEEGATYSCHVSHSSLEKTKVVPF : 91
XNC4        : VPPNVKVSSSESESGIKLHCWVYGFYPRDVEVKWIKNETDEIYSEKSAEILPNPDGTYQIRVSVEVTPEEGATYSCHVSHISLEDTLVAPF : 91
XNC1        : VPPNVKISSSESESGIKLHCWVYRFYPRDVEVKWIKNGTDEIYSEESAEILPNPDGTYQIRVSVEVTPEEGATYSCHVDHSSLENPLVVPF : 91
XNC11       : IKPNVKISSSESESGIKLHCWVYGFYPRDVEVKWIKNGRDEIYSEESAEILPNPDGTYQIRVSVEVTPEEGTTYSCHVDHSSLEKTLVVPL : 91
XNC7        : -VPHVKISSSESESGIKLHCRVYGFYPRDVEVKWIKNERDEIYSEESAEILPDPDGTYQIRVSVEVTPEEGATYSCHVDHSSLETIHMIPF : 90
XNC10       : VPPKVKISSSGSESGTKLHCWVYGFYPRDVEVKWIKNVRDEIYSEESAEILPNPDGTYQIRVSVEVTPEEGATFSCHVDHNSLENPLIVPF : 91
XNC2        : VIPKLKVSSSESESGVKLHCWVYGFYPRDVEVKWIKNERDEIDSEEATQILPNPDGTYQIRVSVEVTPEEGATYSCHVDHSSLENPLVFPF : 91
XNC6        : VQPKVNISSSESDGERILHCWAYGFYPRDVEVKWIKNGRDEIYSEEATQILPNPDGTYQIRVSVEVTPEEGATYSCHVDHSSLEKTLVVHF : 91
SNC12       : VPPKVKVSSSESESGTKLHCRVYGFYPRDVEVKWIKNGRDEIHSEEAAQILPNPDGTYQIRVSVGVTPEGGATYSCHIDHSSLEKTLVIPF : 91
SNC13.4     : VPPKVKVSSSESESGTKLHCRVYGFYPRDVEVKWIKNGRDEIHSEEAAQILPNPDGTYQIRVSVGVTPEGGATYSCHIDHSSLEKTLVVPF : 91
SNC10       : VPPKVKVSSSESESGTKLHCRVYGFYPRDVEVKWIKNGRDEIHSEEAAQILPNPDGTYQIRVSVGVTPEGGATYSCHTDHSSLEKTLVVPF : 91
SNC13.2     : VPPKVKVSISESDSGAELHCRVYGFYPRDVEVKWIKNGRDEIHSEEAAQILPNPDGTYQIRVSVGVTPEGGATYSCHVEHSSLEKTLVVPF : 91
SNC13.3     : VPPKVKVSISESDSGAELHCRVYGFYPRDVEVKWIKNGRDEIHSEEAAQILPNPDGTYQIRVSVGVTPEGGATYSCHIDHSSLEKTLVVPF : 91
SNC13.1     : VPPKVKVSISESESGAELHCRVYGFYPRDVEVKWIKNGRDEIHSEEAAQILPNPDGTYQIRVSVGVTPEGGATYSCHVDHSSLEKALVVPF : 91
XNC5        : DKPNVKVSSSESDSGGKLHCFVFGFYPRDVDVMWIKNVKHEIHSDEASQILP--DGTYQIRVSVEVTPEEGATYSCRVDHSSLEKTMVVPF : 89
SNC1.1      : VPPKVKVSCSESESGTKLHCRVYGFYPRDVEVKWIKNGRDEIHSEEAAQILPNPDGTYQIRVSVGVTPEGGATYSCHIDHSSLEKAITVPF : 91
SNC2.1      : VRPKVKVSSSESESGTKLHCRVYGFYPRDVEVKWIKNGRDEIHSEEAAQILPNPDGTYQIRVRVGVTPEGGATYSCHIDHSSLEKPLVVPF : 91
SNC7.1      : -VPRVKLSSSESESGTELHCRVYGFYPRDVEVKWIKNGRDEIHSEEAAQILPNPDGTYQIRVSVGVTPEEGATYSCHIDHSSLENPLIVPF : 90
SNC7.5      : KVPRVKLSSSESESGTKLHCRVYGFYPRDVEVKWIKNGRDEIHSEEAAQILPNPDGTYQIRVSVGVTPEEGATYSCHIDHSSLEKTLVVPF : 91
SNC7.3      : KMPRVKLSSSESESGTKLHCRVYGFYPRDVEVKWIKNGRDEIHSEEAAQILPNPDGTYQIRVSVGVTPEGGATYSCHIDHSSLENPLVVLF : 91
SNC4        : VSPNVQISSSESESGTNLHCSGYGFYPRDVEVKWIKNGRDEIHSEEAAQILPNPDGTYQIRVSVGVTPEEGATYSCHIDHSSLENPLVVPF : 91
SNC1.2      : VPPKVQISSSESENGTELHCRVYGFYPRDVEVKWIKNGRDEIHSEEAAQILPNPDGTYQIRVSVGVTPEGGATYSCHIDHSSLEKALVVPF : 91
SNC7.4      : KVPNVKLSGSESENGTELHCRVYGFYPRDVEVKWIKNGRDEIHSEEAAQILPNPDGTYQI--SVGVKPEGGATYSCHIDHSSLEKALVVPF : 89
SNC7.2      : PLPHVKLSGSES--GTKLHCRVYGFYPRDVEVKWIKNGRDEIHSEEAAQILPNPDGTYQIRVSVGVTPEGGATYSCHIDHSSLENPLVVPF : 89
SNC7.6      : -VPRVKMSNSES--GTKLHCRVYGFYPRDVVVKWIKNGRDEIHSEEAAQILPNPDGTYQIRVSVGVTPEGGATYSCHIDHSSLEKTLVVPF : 88
SNC16.4     : VPPNVKVSNSESESGTKLHCRVYGFYPRDVEVKWIKNGRDEIHSEEAAQILPNPDGTYQIRVSVGVTPEGGATYSCHIDHSSLEKPLVVKF : 91
SNC16.2     : VPPNVNISSSESESGTKLHCRVYGFYPRDVEVKWIKNGRDEIHSEEAAQILPNPDGTYQIRVSVGVTLDKNSNYSCLVDHSSLETPIIVTF : 91
SNC3        : VPPNVNISSSESESGTKLHCRVYGFYPRDVEVKWIKNGRDEIHSEEAAQILPNPDGTYQIRVSVGVTLDKNSNYSCLVDHSSLETPIIVTF : 91
SNC16.3     : VPPNVNISSSESESGTKLHCRVYGFYPRDVEVKWIKNGRDEIHSEEAAQILPNPDGTYQIRVSVGVTPDKNSNYSCLVDHNSLETPIIVTF : 91
SNC16.1     : IPPKVKVSSSESESGTKLHCRVYGFYPRDVEVKWIKNGRDEIHSEEAAQILPNPDGTYQIRVSVGVTLDKNSNYSCLVDHSSLETPMIVNF : 91
SNC2.2      : VPPKVKVSSSESESGTKLHCRVYGFYPRDVEVKWIKNGRDEIHSEEAAQILPNPDGTYQIRVSVGVTPEEGATYSCHIDHSSLETPLVVPF : 91
SNC6.2      : VCPKVKVSSSESDGEQKLHCRVYGFYPRDVEVKWIKNGRDEIHSEEAAQILPNPDGTYQIRVSVGVTPEEGATYSCHIDHSSLEKPLVVPF : 91
SNC13.5     : VPPKVKVSSSESDGEQKLHCRVYGFYPRDVEVKWIKNGRDEIHSEEAAQILPNPDGTYQIRVSVGVTPEEGATYSCHIDHSSLENPLVVPF : 91
SNC15       : VCPKVKISSLESDNNTKLHCCVYGFHPREVDVKWIKNGRDEIHSEEAPQILPNPDGTYQIRVSVGVTPEGGATYSCHIDHSSLNDTLVVPF : 91
SNC6.1      : VHPEVKVSSSESVSGTKLHCRVYGFYPRDVDVKWIKNERDEIYSEEAAQILPNPDGTYQIRVSVEVTPEEGATYSCHVDHSSLAKPLAVCF : 91
SNC5        : VKPKVKVSISESDSGVELHCRVYGFYPRDVEVKWIKNGRDEIHSEEAAQILPNPDGTYQIRVSVGVTPEGGATYSCHIDHSSLEKALVVPF : 91
SNC14       : VPPKVKTSISRSDSGKRLCCHVYGFYPKKVHIKVMKNGTEEVSPEEFKHILPNPDGTYQIRVSVGVTPEGGATYSCHVDHSSLNSTMVIPF : 91
laevis_JJ   : VHPHVRISDHQSDDATELRCQAYGFYPREIDVKWVKNGRDDVHSEAAKEILPNPDGSYQLRVTAEITPSEGDSYACHVEHSSLKEKLIVVW : 91
laevis_FF   : VHPHVRISDHQSADATELRCQAYGFYPREIDVKWVKNGGDDVHSEAAKEILPNPDGSYQLRVTAEITPNEGDSYACHVEHSSLNEKLIVVW : 91
trop_UAA*0  : VRPHVKISDHQSDDITELRCQAYGFYPREIDVKWVRNGRDDVHSDEAKEILPNPDGSYQLRVTAKVTPKEGDSYACHVDHSSLEEKLIVVW : 91
trop_UAA*0  : VRPHVKISDRQSDGNTELHCQAYGFYPREIDVKWVRNGKDDVHSEEAKEILPNPDGSYQLRVTAEVTPKEGDSYACHVEHSSLEEKLIVVW : 91
                       ▲        ▲ ▲                     ●●   ▲▲ ▲▲▲▲▲   ▲ ▲
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Fig. S4

Table SI: List of accession numbers for MHC class I sequences used in Figure 4

Sequence Name	**Accession Number**
***Xenopus laevis* (African clawed frog)**	
GG (class Ia – *g* haplotype)	AF185579
RR (class Ia – *r* haplotype)	AF185582
FF (class Ia – *f* haplotype)	AAF03402
JJ (class Ia – *j* haplotype)	AF185586
XNC1	M58019
XNC2	L20725
XNC3	L20726
XNC4	L20727
XNC5	L20728
XNC6	L20729
XNC7	L20730
XNC8	L20731
XNC9	L20732
XNC10	FJ589642
XNC11	FJ589643
***Xenopus laevis* x *Xenopus gilli* (hybrid clone)**	
LG-ac-1	AF185583
LG-ac-2	AF185585
LG-bd-1	AF185581
LG-bd-2	AF185584
***Homo sapiens* (human)**	
HLA-A2	Z30341
HLA-B	U11265
HLA-C	X58536
HLA-E	NM_005516
HLA-F	NM_001098479
HLA-G	NM_002127
HLA-H	U60319
hum_CD1a	NM_001763
hum_CD1b	NM_001764
hum_CD1c	CR457080
hum CD1e	X14975
hum_CD1d	NM_001766
hum_MICA	AJ563426
hum_MR1	AJ249778
hum_FcRn	AF220542
***Pan troglodytes* (chimpanzee)**	
Patr-MICA/B	NM_001045494
***Pongo pygmaeus* (Bornean orangutan)**	
Popy-BAB	M30681
***Macaca fascicularis* (crab-eating macaque)**	
Mafa_E1	U02976
Mafa_E2	U02977
***Macaca fascicularis* (cattle)**	
Bota-BL3-6	M21044
***Ovis aries* (sheep)**	
Ovar-E	M34676
***Macropus rufogriseus* (red-necked wallaby)**	
Maru-UA1	L04950
Maru-UB1	L04952
***Monodelphis domestica* (gray short-tailed opossum)**	
Modo-UA1	NM_001044223
Modo-UG	DQ138606
Modo-3	AF125540
***Mus musculus* (house mouse)**	
H2-K	X01815
mus_H-2Dd	U47326
mus_TL	D14027
mus_MR1	NM_008209
mus_H2-M3	U18797
mus_Qa-2	D90146
mus_Q4	M18837
mus_Q10k	X16426
mus_T23	Y00629
mus_CD1d	NM_007639
***Mus spretus* (western wild mouse)**	
mussp_H2-M3	L36072
***Rattus rattus* (black rat)**	
rat_FcRn	X14323
***Gallus gallus* (chicken)**	
ch_BF19	M84766
ch_BFw-02	AB178043
ch_RfpY	AF218783
ch_CD1.2	NM_001024582
ch_CD1.1	AY849319
***Coturnix japonica* (Japanese quail)**	
quail_QF41	
***Ameiva ameiva* (lizard)**	
Amam-LCI	M81094
***Rana pipiens* (northern leopard frog)**	
Rapi-R6	AF185587
Rapi-R9	AF185588
***Ambystoma mexicanum* (axolotl)**	

Amme_Ia3	U83137
Amme_Ia4	U83138
***Latimeria chalumnae* (coelacanth)**	
Lach_UB1	U08034
***Cyprinus carpio* (common carp)**	
Cyca-UA1*01	X91015
Cyca-UAW1	X91022
Cyca-ZE	AJ420957
Cyca-NEW	AB018581
Cyca-ZA1	M37107
Cyca-ZB1	L10420
Cyca-ZC1	L10421
***Oncorhynchus mykiss* (rainbow trout)**	
Onmy_UAA	L63541
Onmy_UBA	AF091785
Onmy-UCA	AY523659
Onmy-UDA	AY523666
Onmy-C32	U55380
***Carassius auratus* (goldfish)**	
Caau-ZA1	L10418
***Danio rerio* (zebrafish)**	
Dare-UAA01	Z46776
Dare-UBA01	Z46777
***Takifugu rubripes* (Fugu rubripes)**	
Furu-I2	AF001216
***Salmo salar* (Atlantic salmon)**	
Sasa-UBA101	AF504019
***Ginglymostoma cirratum* (nurse shark)**	
Gici_UAA*01	AF220063
Gici-11	AF028557
Gici-NC1	AF357923
***Heterodontus francisci* (horn shark)**	
Hefr-19	AF028558
Hefr-20	AF028559
***Triakis scyllium* (banded houndshark)**	
Trsc-UAA*101	AF034316
Trsc-UBA*201	AF034345