Supporting Information

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SI Text

Short descriptions of reasons for exclusions of families BAND 4.1 (EPB41). This is a large family with 13 members in humans. Only two of the genes in the family are located inside the investigated chromosomal regions; EPB41 on chromosome 1, 29.09 Mb and XP_932590.1 on chromosome 8, 49.99 Mb. However, these genes are very different and belong to different subfamilies.

SYNAPTOTAGAMIN-LIKE (SYTL). The two genes located within the selected chromosomal regions, SYTL1 on human chromosome 1 and SYTL3 on human chromosome 6, belong to different subfamilies according to the phylogenetic tree.

XP_945180.1/NP_067050.1/NP_660346.1. All proteins in this family are extremely conserved. Spotted green pufferfish, western clawed frog and mouse only have one gene in this family. Chicken has two genes, but they are very similar and cluster together in the tree. In humans and dogs there are three genes in the family but according to the topology in the tree they must have arisen by recent gene duplication events that occurred independently in the human and dog lineages. Therefore, there are no paralogous genes in this family that are the result of R1 or R2.

CONNECTOR ENHANCER OF KINASE SUPPRESSOR OF RAS (CNKSR). The proteins in this family have one or several of the following Pfam domains: PH, SAM_2, DUF1170, and PDZ. Unfortunately, none of the domains can be found in all (or most) of the proteins and they are therefore difficult to align.

HIGH-MOBILITY GROUP BOX (HMGB). There has been a large expansion of the HMGB family in human and mouse and many of the genes are retrotransposed copies. The numbers of genes are as follows: human, 19; mouse, 39, dog, 4; chicken, 3; frog, 3. It is difficult to determine which genes are orthologues and which are paralogues by only studying the tree topology. Three human genes in this family have four introns, HMGB3 on chromosome X, HMGB2 on chromosome 4 and HMGB1 on chromosome 13. The remaining human genes (including the genes on chromosomes 1 and 20) either lack introns completely or have only one intron, and are most likely retrotransposed copies.

PHOSPHATASE AND ACTIN REGULATOR (PHACTR). The sequences in this family align very poorly, making phylogenetic analysis unreliable. The genes contain a large number of introns and seem to be alternatively spliced. However, the transcripts of orthologous genes in different species are very different and we can not exclude the possibility that we are aligning different transcripts in all species.

Opioid receptors

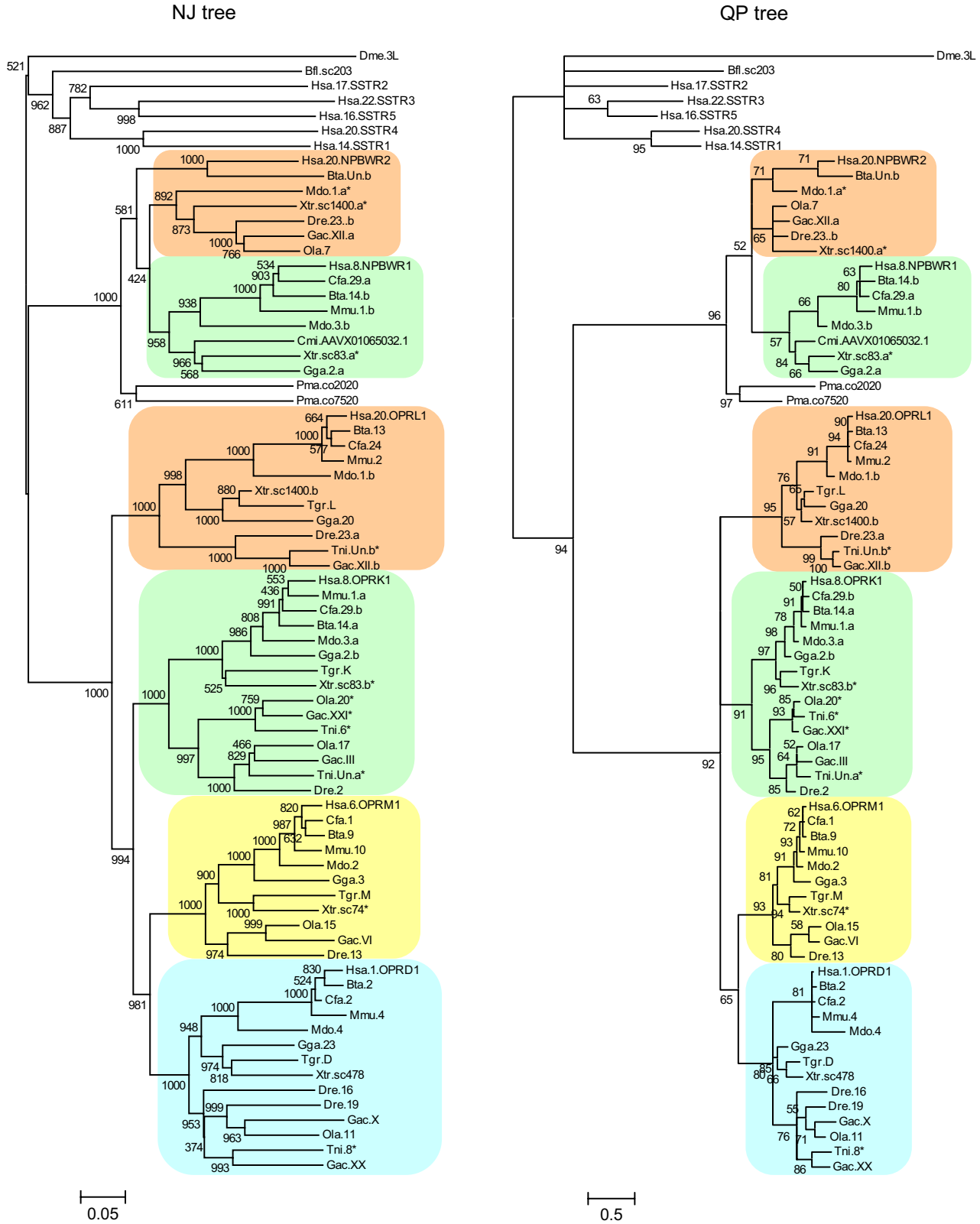

Fig. S1. Neighbor-joining and quartet-puzzling maximum likelihood trees for opioid receptors.

ARID1

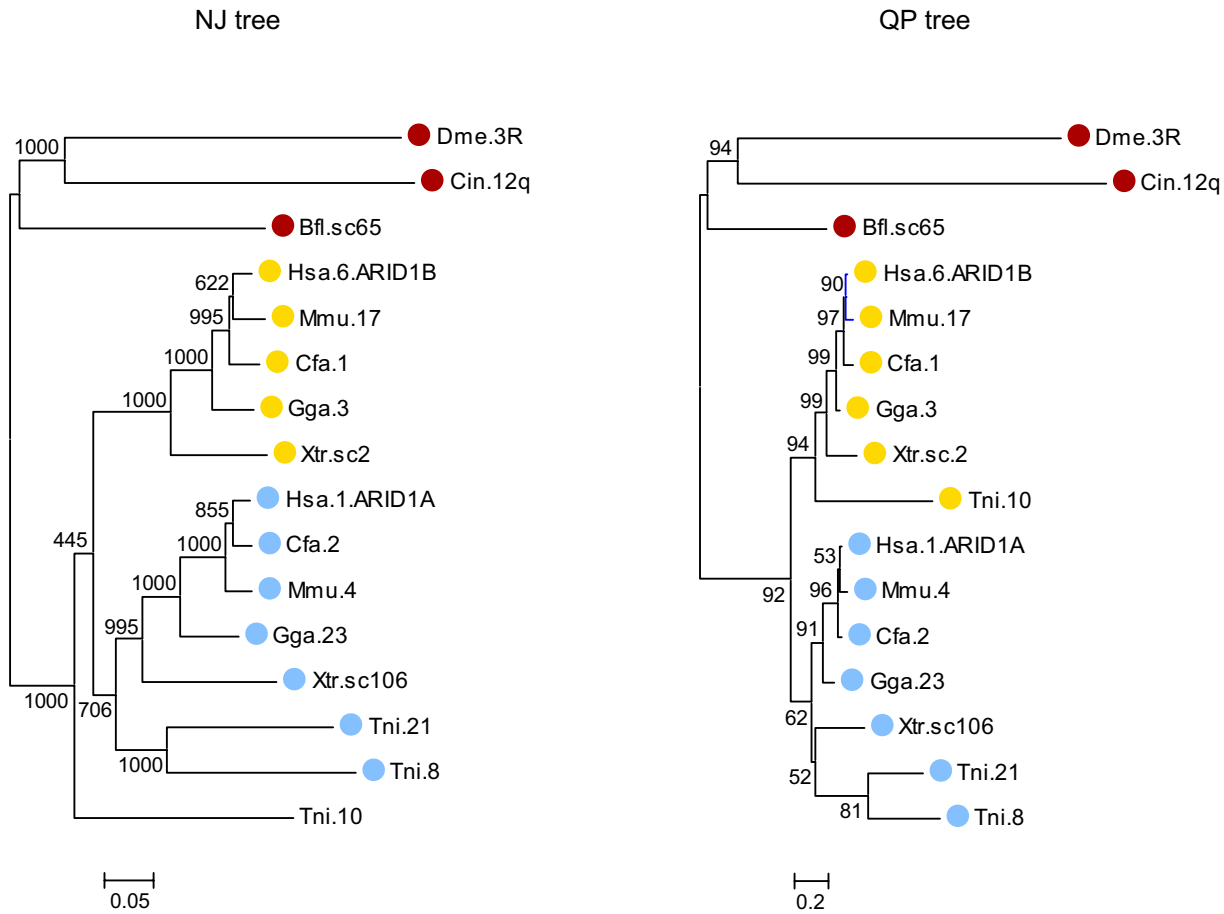

Fig. S2. Neighbor-joining and quartet-puzzling maximum likelihood trees for AT RICH INTERACTIVE DOMAIN 1 (ARID1). The ARID family consist of 15 genes in the human, mouse and dog genome. The proteins all contain the ARID domain, which has DNA-binding properties. The ARID family can be divided into 7 subfamilies., ARID1A and ARID1B belong to the ARID1 subfamily and show 80% sequence identity within the ARID domain and ≈50% identity across the full length amino acid sequence. ARID1A and ARID1B bind DNA with high affinity but without sequence specificity and they are alternative components of the SWI/SNF-related chromatin remodelling complexes (1, 2). Hsa, *Homo sapiens*; Mmu, *Mus musculus*; Cfa, *Canis familiaris*; Gga, *Gallus gallus*; Xtr, *Xenopus tropicalis*; Tni, *Tetraodon nigroviridis*; Bfl, *Branchiostoma floridae*; Dme, *Drosophila melanogaster*; Cin, *Ciona intestinalis*.

1. Patsialou A, Wilskerand D, Moran E (2005) DNA-binding properties of ARID family proteins. *Nucleic Acids Res* 33:66–80.
2. Wilsker D, Probst L, Wain HM, Maltais L, Tucker PW, Moran E (2005) Nomenclature of the ARID family of DNA-binding proteins. *Genomics* 86:242–251.

GMEB

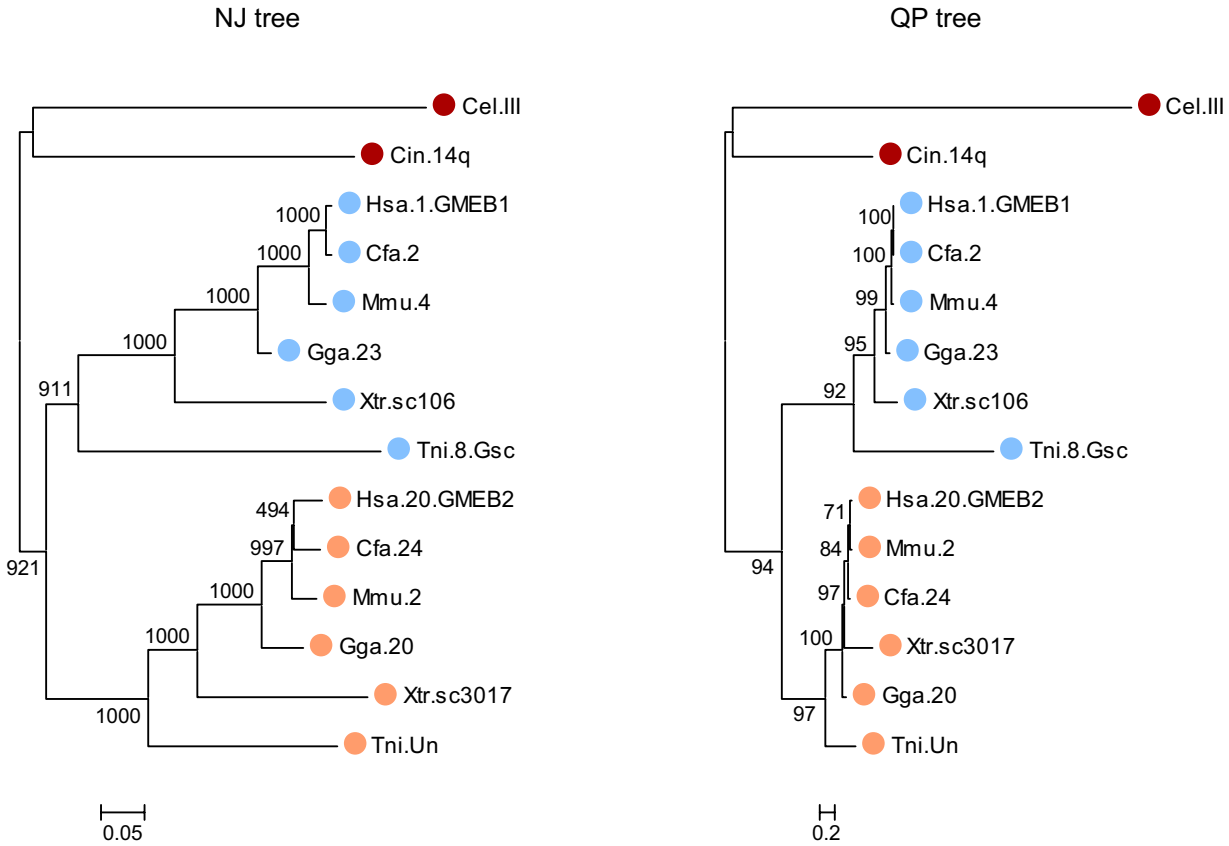

Fig. S3. Neighbor-joining and quartet-puzzling maximum likelihood trees for GLUCOCORTICOID MODULATORY ELEMENT BINDING PROTEIN (GMEB). The two proteins in this family, GMEB1 and GMEB2, contain a Pfam SAND domain, which has DNA binding activity. They are involved in regulation of the glucocorticoid receptors (GRs) sensitivity o steroid hormones. GMEB1 and GMEB2 form a heteromeric complex that binds to a cis-acting element called the glucocorticoid modulatory elment (GME) (1, 2). The GMEBs can also bind to the GR-ligand complex and thereby modify the GRs' induction properties (2). Hsa, *Homo sapiens*; Mmu, *Mus musculus*; Cfa, *Canis familiaris*; Gga, *Gallus gallus*; Xtr, *Xenopus tropicalis*; Tni, *Tetraodon nigroviridis*; Cin, *Ciona intestinalis;* Cel, *Caenorhabditis elegans.*

1. Kaul S, Blackford JA, Jr, Chen J, Ogryzko VV, S. Simons SS, Jr (2005) Properties of the glucocorticoid, modulatory element binding proteins GMEB-1 and -2: Potential receptor transactivationand members of the family of KDWK proteins. *Mol Endocrinol* 14:1010–1027.
2. Chen J, He Y, Simons SS, Jr (2004). Structure/activity relationships for GMEB-2: The second member of the glucocorticoid modulatory element-binding complex. *Biochemistry* 43:245–255.

LYPLA

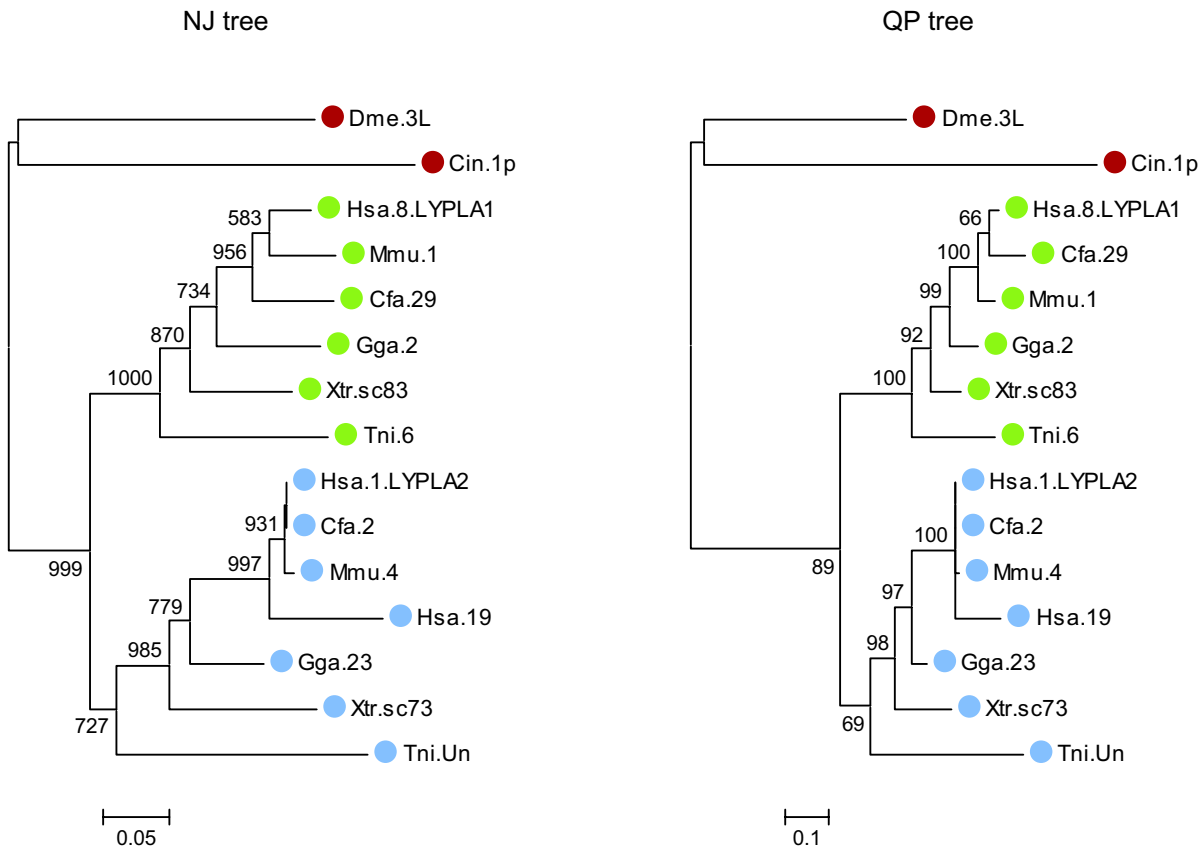

Fig. S4. Neighbor-joining and quartet-puzzling maximum likelihood trees for ACYL THIOESTERASE/LYSOPHOSPHOLIPASE (LYPLA). All proteins in this family contain the Pfam Abhydrolase_2 domain. The LYPLA family proteins are enzymes that hydrolyse the ester bond of lysophospholipds to produce a free fatty acid and a glycerolphosphate derivative. LYPLA1 and LYPLA2 have a catalytic triad composed of Ser-Asp-His and their catalytic mechanism resembles that of serine hydrolases. Lysophospholipds have many biological functions and can act as second messengers by transducing signals from membrane receptors. LYPLA1 and LYPLA2 are two of the many enzymes that control the lysophospholipds by regulating their levels [Wang A, Dennis EA (1999) Mamalian lysophospholipases. *Biochimicaet Biophysica Acta* 1439:1–16]. There are four human genes that belong to this Ensembl family and they are located on chromosme 1 (LYPLA2), 6 (LYPLA2P1), 8 (LYPLA1) and 19 (no HGNC name available). LYPLA2P1 and the gene on human chromosome 19 are also found in Chimpanzee but not in any of the other species. Because these two genes are very similar to LYPLA2 but lack introns they are probably retrotransposed copies specific to the human/chimpanzee line. Hsa, *Homo sapiens*; Mmu, *Mus musculus*; Cfa, *Canis familiaris*; Gga, *Gallus gallus*; Xtr, *Xenopus tropicalis*; Tni, *Tetraodon nigroviridis*; Dme, *Drosophila melanogaster*; Cin, *Ciona intestinalis*.

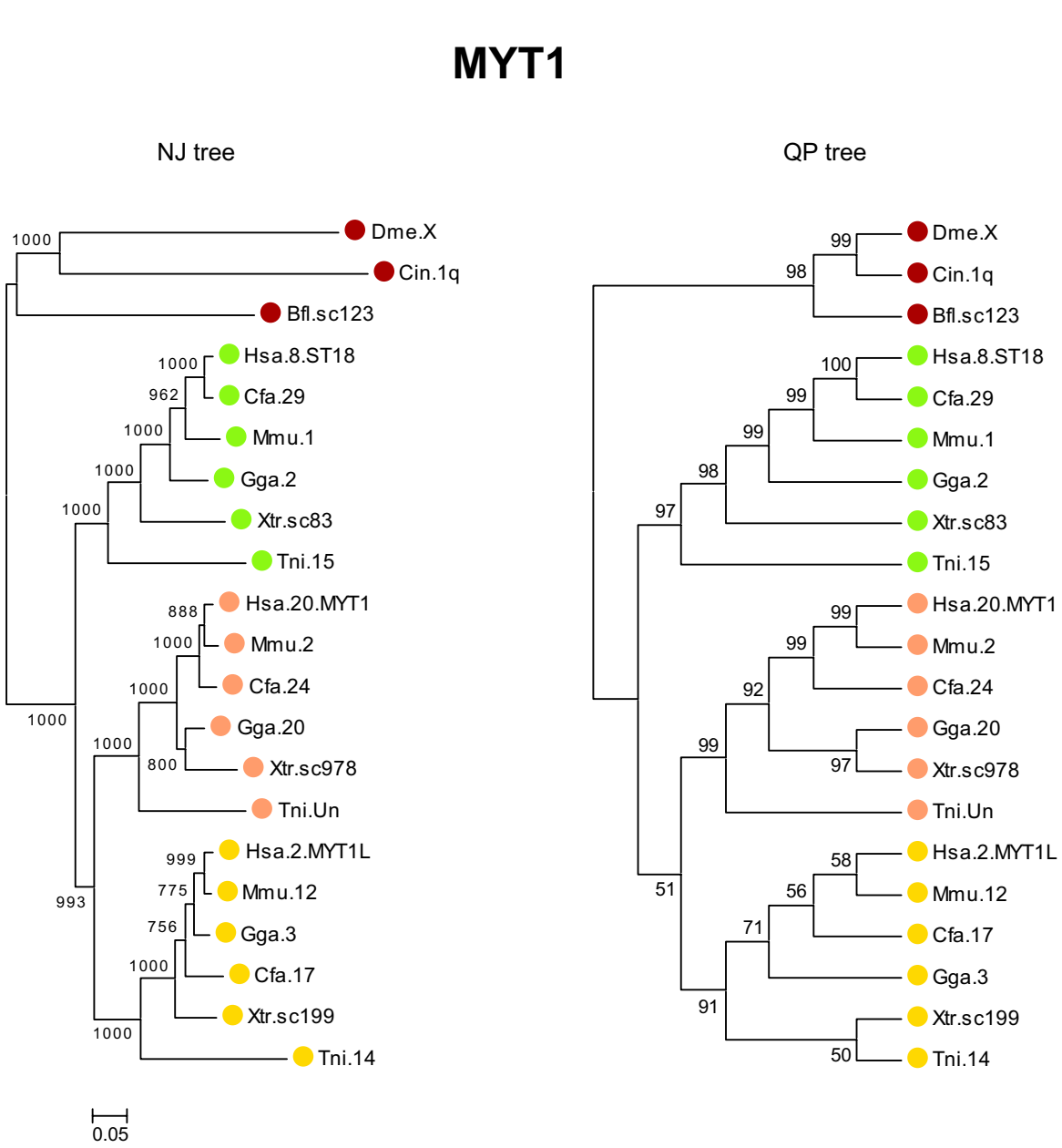

Fig. S5. Neighbor-joining and quartet-puzzling maximum likelihood trees for MYELIN TRANSCRIPTION FACTOR 1 (MYT1). The proteins that belong to this family are neural zinc fingers that act as transcription factors. The MYT1 family proteins bind to the transcriptional corepressor Sin3B while they also bind to promoters. Sin3B in turn binds histone deacetylase (HDAC), which modifies chromatin structure and thereby repress promoter activity [Rom E, Nielsen JA, Kim JG, Hudson LD (2005) Myt1 family recruits histone deacetylase to regulate neural transcription. *J Neurochem* 93:444–1453]. All members of this family contain several zf-C2HC domains and all except the Ciona intestinalis and *Drosophila* proteins have a PfamMYT1 domain. However, the MYT1 domain consist of zf-C2HC domains and the Ciona and *Drosophila* sequences align quite well with he other sequences. The human members are located on chromosome 2 (MYT1L), 8 (ST18), and 20 (MYT1). Hsa, *Homo sapiens*; Mmu, *Mus musculus*; Cfa, *Canis familiaris*; Gga, *Gallus gallus*; Xtr, *Xenopus tropicalis*; Tni, *Tetraodon nigroviridis*; Bfl, *Branchiostoma floridae*; Dme, *Drosophila melanogaster*; Cin, *Ciona intestinalis.*

NKAIN

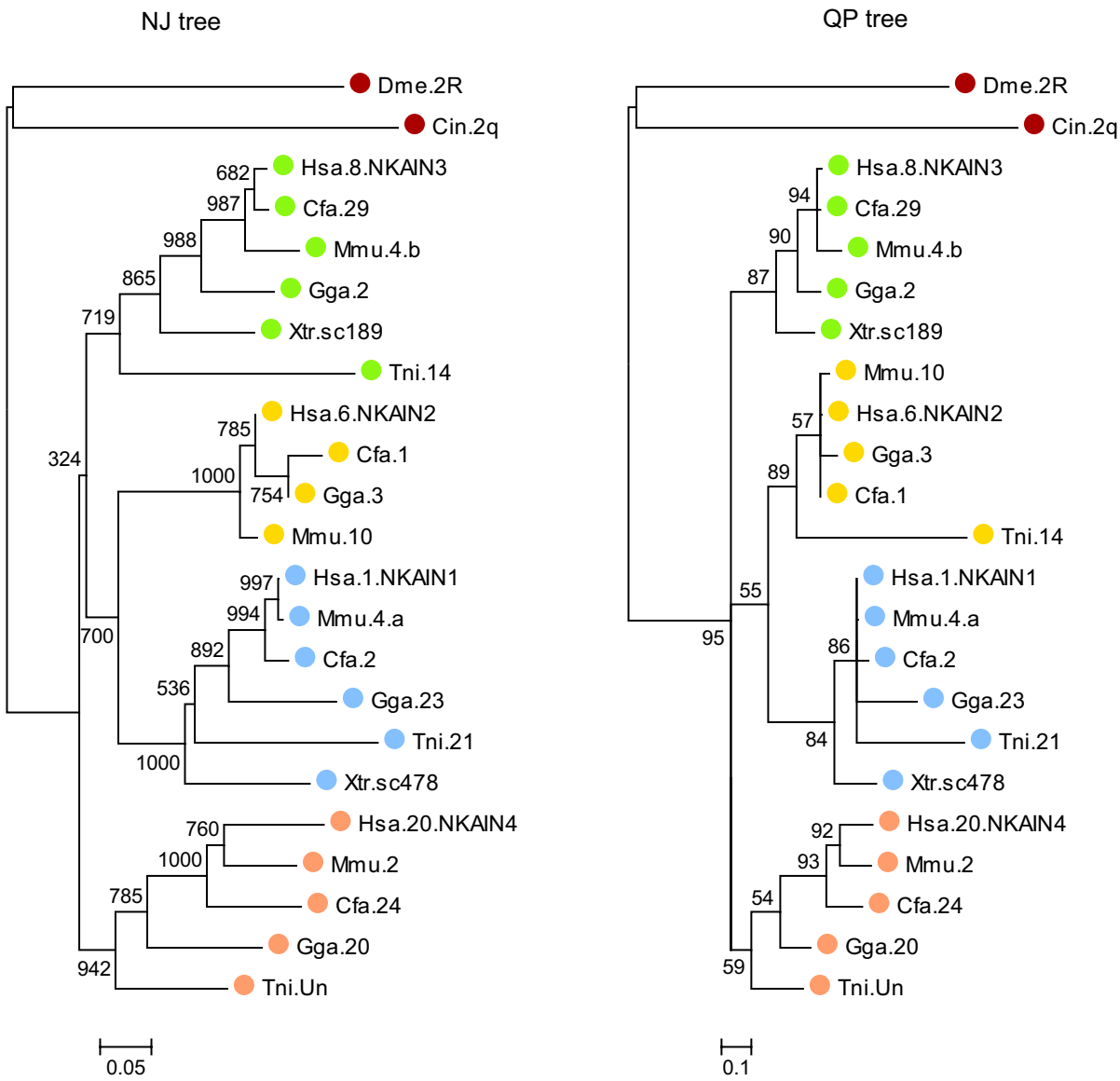

Fig. S6. Neighbor-joining and quartet-puzzling maximum likelihood trees for Na+/K+ transporting ATPase interacting (NKAIN). The proteins in this family are membrane proteins with three putative transmembrane domains. The NKAIN proteins are localized to neurons and interact with the β1subunitof the Na,K-ATPase [Gorokhova S, Bibert S, Geeringand K, Heintz N (2007) A novel family of transmembrane proteins interacting with β subunits of the Na,K-ATPase. *Human Mol Gen* 16:2394–2410]. Hsa, *Homo sapiens*; Mmu, *Mus musculus*; Cfa, *Canis familiaris*; Gga, *Gallus gallus*; Xtr, *Xenopus tropicalis*; Tni, *Tetraodon nigroviridis*; Dme, *Drosophila melanogaster*; Cin, *Ciona intestinalis.*

PCMTD

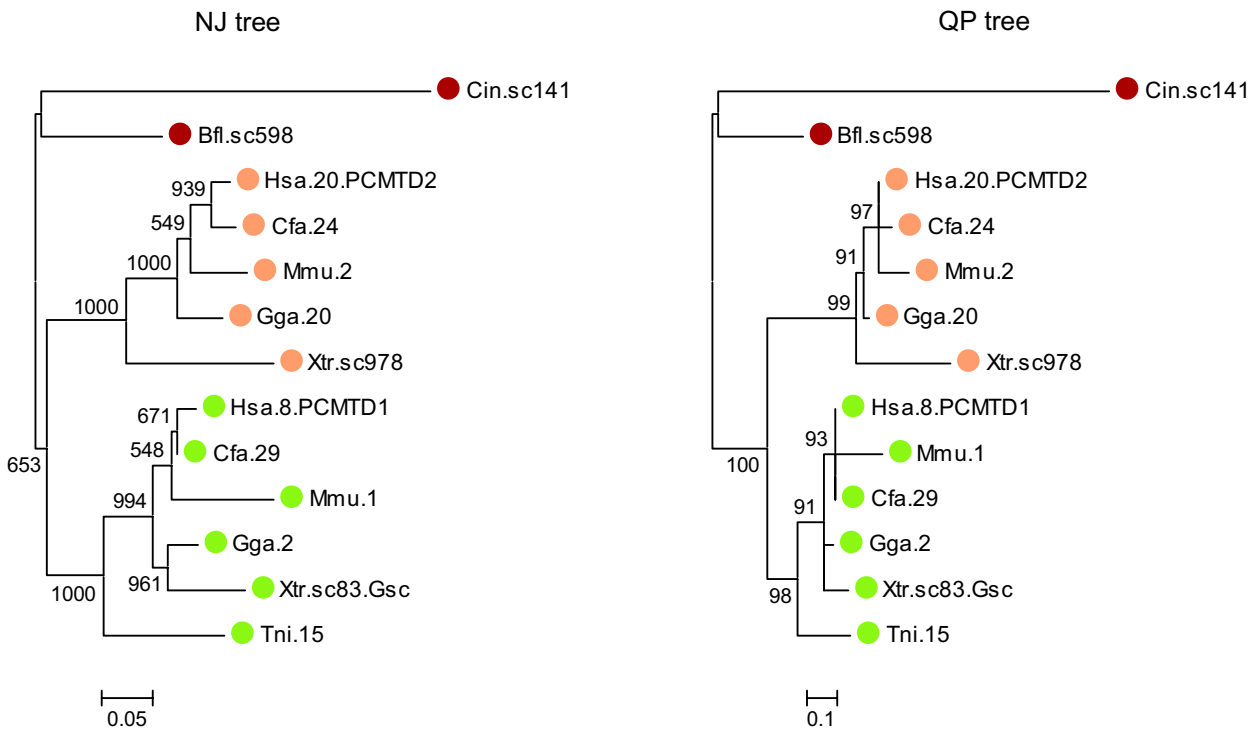

Fig. S7. Neighbor-joining and quartet-puzzling maximum likelihood trees for PROTEIN-L-ISOASPARTATE *O*-METHYLTRANSFERASE DOMAIN CONTAINING (PCMTD). The proteins in this family, PCMTD1 and PCMTD2, are enzymes and contain the catalytic PCMT domain. PCMTs methylate D-aspartyl and L-isoaspartyl residues in proteins and peptides. D-aspartyl and L-isoaspartyl are produced by spontaneous deamidation or racemization of normal asparagine residues and the PCMTs are thought to play a role in the repair and degradation of proteins with this type of damage (Boivin D, Bilodeau D, Béliveau R (1995) Immunochemical characterization of L-isoaspartyl-protein carboxyl methyltransferase from mammalian tissues. *Biochem J.* 309:993–998). Hsa, *Homo sapiens*; Mmu, *Mus musculus*; Cfa, *Canis familiaris*; Gga, *Gallus gallus*; Xtr, *Xenopus tropicalis*; Tni, *Tetraodon nigroviridis*; Bfl, *Branchiostoma floridae*; Cin, *Ciona intestinalis.*

RGS

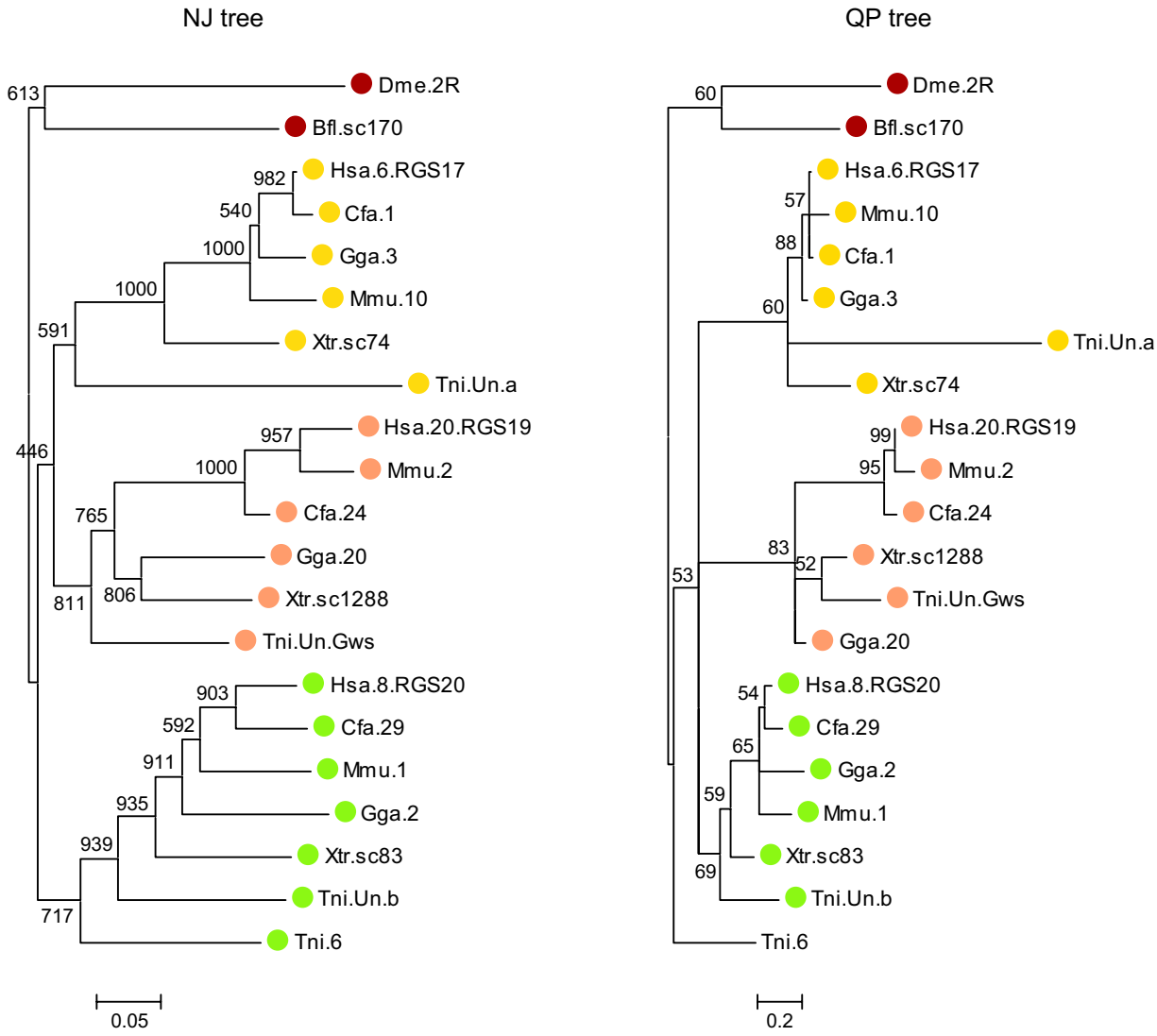

Fig. S8. Neighbor-joining and quartet-puzzling maximum likelihood trees for REGULATOR OF G-PROTEIN SIGNALING (RGS) subfamily RZ/A. RGS proteins activate the intrinsic GTPase activity of the Gα subunit of G proteins and thereby increase the hydrolysirate of the GTP bound to the Gα. The termination rate of G protein signaling can be increased by a 100-fold or more by the RGS-proteins. There are also indications that RGS proteins can have other functions such as interactions with receptors or intracellular signaling proteins [Nunn C, Mao H, Chidiac P, Albert PR (2006) RGS17/RGSZ2 and the RZ/A family of regulators of G protein signalling. *Seminars Cell Dev Biol* 17:390–399]. Hsa, *Homo sapiens*; Mmu, *Mus musculus*; Cfa, *Canis familiaris*; Gga, *Gallus gallus*; Xtr, *Xenopus tropicalis*; Tni, *Tetraodon nigroviridis*; Bfl, *Branchiostoma floridae*; Dme, *Drosophila melanogaster*.

SOX

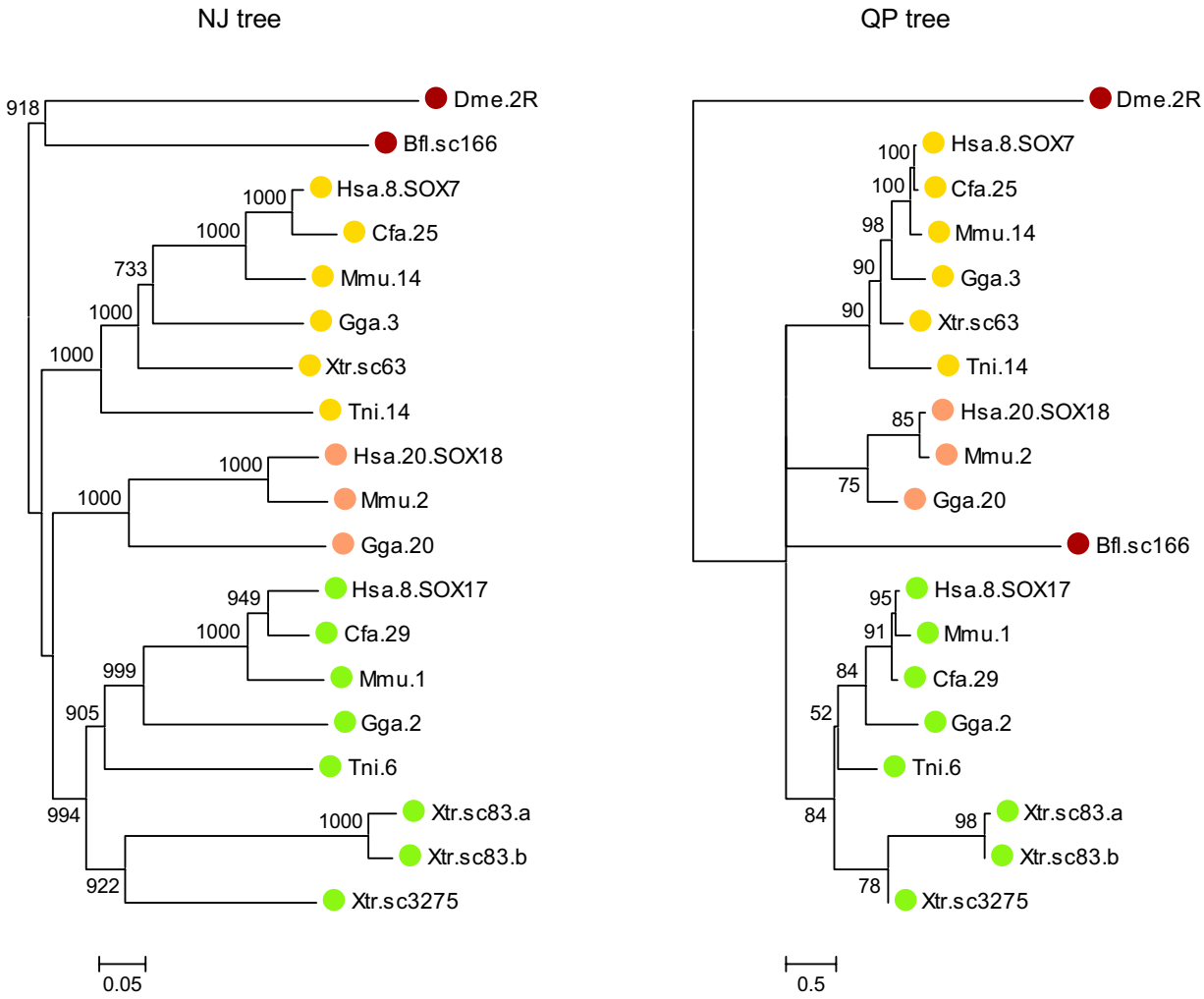

Fig. S9. Neighbor-joining and quartet-puzzling maximum likelihood trees for TRANSCRIPTION FACTOR SOX (SOX). The SOX proteins are transcription factors that contain the DNA binding HMG-box domain. The SOX HMG-domains are well preserved and bind the DNA target sequence, AACAA(A/T)G (1). This Ensembl family of transcription factors has 11 members in humans but can be divided further into subfamilies. The genes located close to OPRK1 and OPRL1, SOX17 and SOX18 respectively, belong to subfamily F together with SOX7 (2). Hsa, *Homo sapiens*; Mmu, *Mus musculus*; Cfa, *Canis familiaris*; Gga, *Gallus gallus*; Xtr, *Xenopus tropicalis*; Tni, *Tetraodon nigroviridis*; Bfl, *Branchiostoma floridae*; Dme, *Drosophila melanogaster*.

1. Koopman P, Schepers G, Brenner S, Venkatesh B (2004). Origin and diversity of the *Sox* transcription factor gene family: Genome-wide analysis in Fugu rubripes. *Gene* 328:177–186.
2. Bowles J, Schepers G, Koopman P (2000) Phylogeny of the SOX family of developmental transcription factors based on sequence and structural indicators. *Dev Biol* 227:239–255.

SRC-B

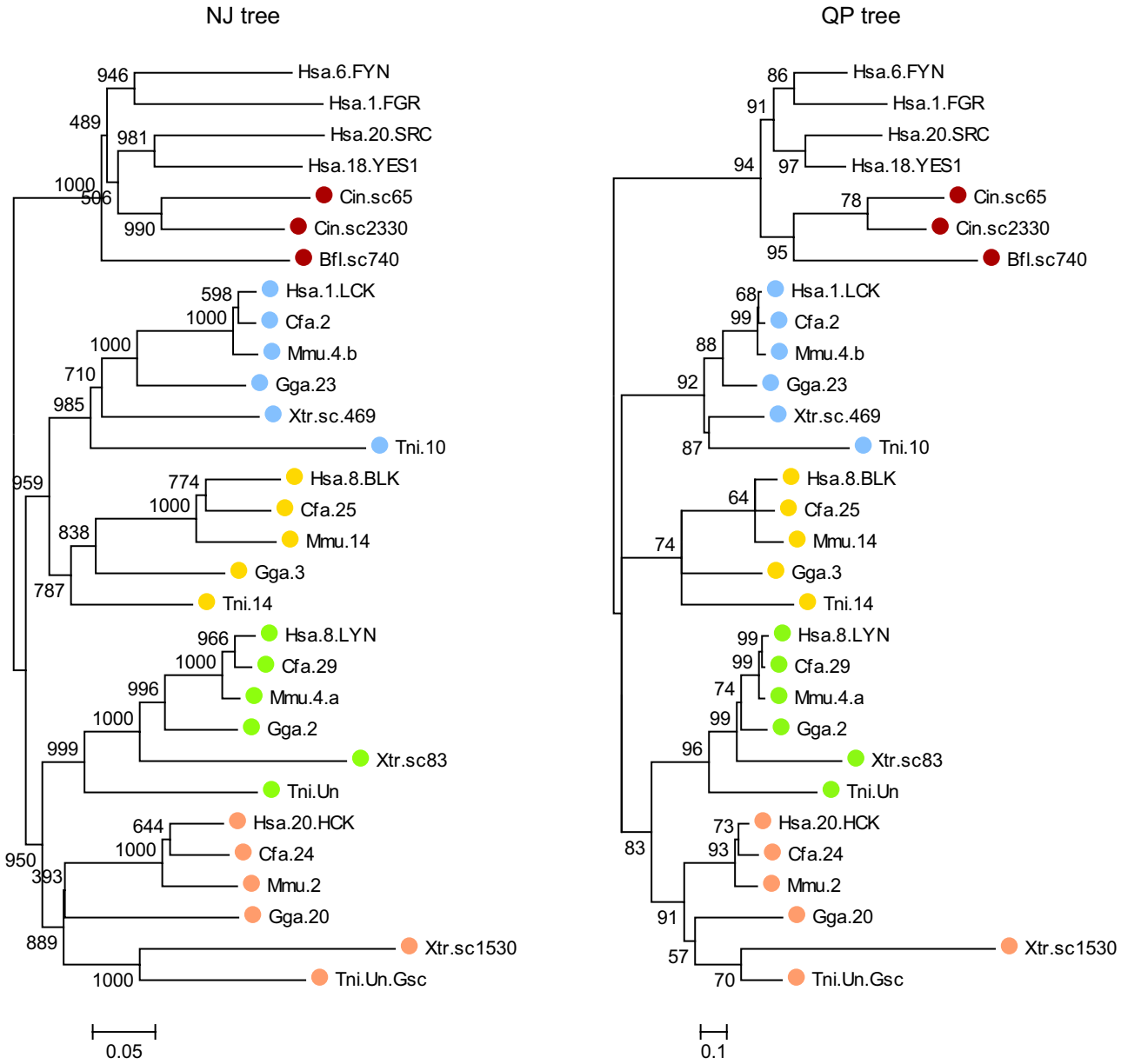

Fig. S10. Neighbor-joining and quartet-puzzling maximum likelihood trees for TYROSINE KINASE. The nonreceptor tyrosine kinases can be divided into 11 sub-families (1) and this Ensembl family consists of five of them. However, only one of these subfamilies, the SRC-B family, has more than one gene in the chromosome location of interest. Therefore, only the SRC-B subfamily was investigated further. *SRC-B family*SRC-B is a subfamily of the nonreceptor protein-tyrosine kinases. They have one Srchomology 2 domain (SH2), one Srchomology 3 domain (SH3), and a Kinase domain (1). The SRC-B protein-tyrosine kinases are attached to the inside of the cytoplasmic membranes by their N-amino termini and are expressed in specific cells of hematopoietic origin. They are coupled to cytokine receptors and are important for the receptor signaling. (2). The genes included in the SRC-B family are BLK, LYN, HCK and LCK (Robinson *et al.*). Hsa, *Homo sapiens*; Mmu, *Mus musculus*; Cfa, *Canis familiaris*; Gga, *Gallus gallus*; Xtr, *Xenopus tropicalis*; Tni, *Tetraodon nigroviridis*; Bfl, *Branchiostoma floridae*; Cin, *Ciona intestinalis.*

1. Robinson DR, Wu Y-M, Lin S-F (2000) The protein tyrosine kinase family of the human genome. *Oncogene* 19:5548–55572.
2. Neet K, Hunter T (1996). Vertebrate non-receptor protein-tyrosine kinase families. *Genes Cells* 1:147–169.

STMN

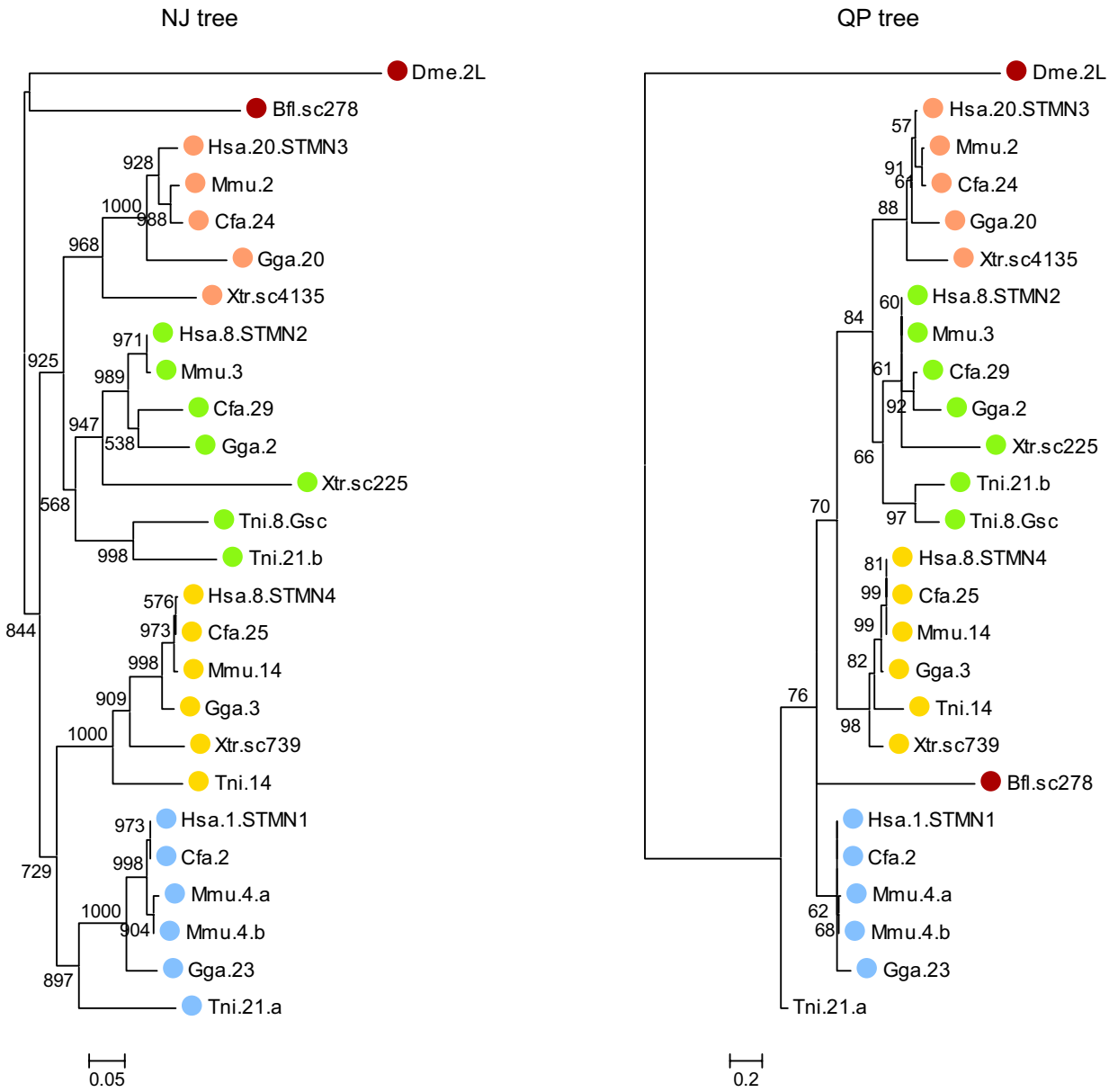

Fig. S11. Neighbor-joining and quartet-puzzling maximum likelihood trees for STATHMIN (STMN). The proteins in this family all have a Pfam Stahtmin domain. Four human genes belong to this family. The Stathmin family proteins play important roles in cell proliferation by regulating microtubule growth and shrinkage, important in mitosis. Stathmin can bind free tubulin and thereby prevent microtubule growth but can also bind to the end of microtubules and depolymerize them. Sthathmin has four phosphorylation sites and is totally inactivated by phosphorylation of all sites. However, its activity can be regulated and finely tuned by phosphorylating some but not all of the sites to partially inactivated or down regulate its activity (1, 2). Hsa, *Homo sapiens*; Mmu, *Mus musculus*; Cfa, *Canis familiaris*; Gga, *Gallus gallus*; Xtr, *Xenopus tropicalis*; Tni, *Tetraodon nigroviridis*; Bfl, *Branchiostoma floridae*; Dme, *Drosophila melanogaster*.

1. Curmi PA, *et al.* (1999). Stathmin and its phosphoprotein family: General properties, biochemical and functional interaction with tubulin. *Cell Structure Function* 24:345–357.
2. Rubin CI, Atweh GF (2004) The role of Stathmin in the regulation of the cell cycle. *J Cell Biochem* 93:242–250.

TCEA

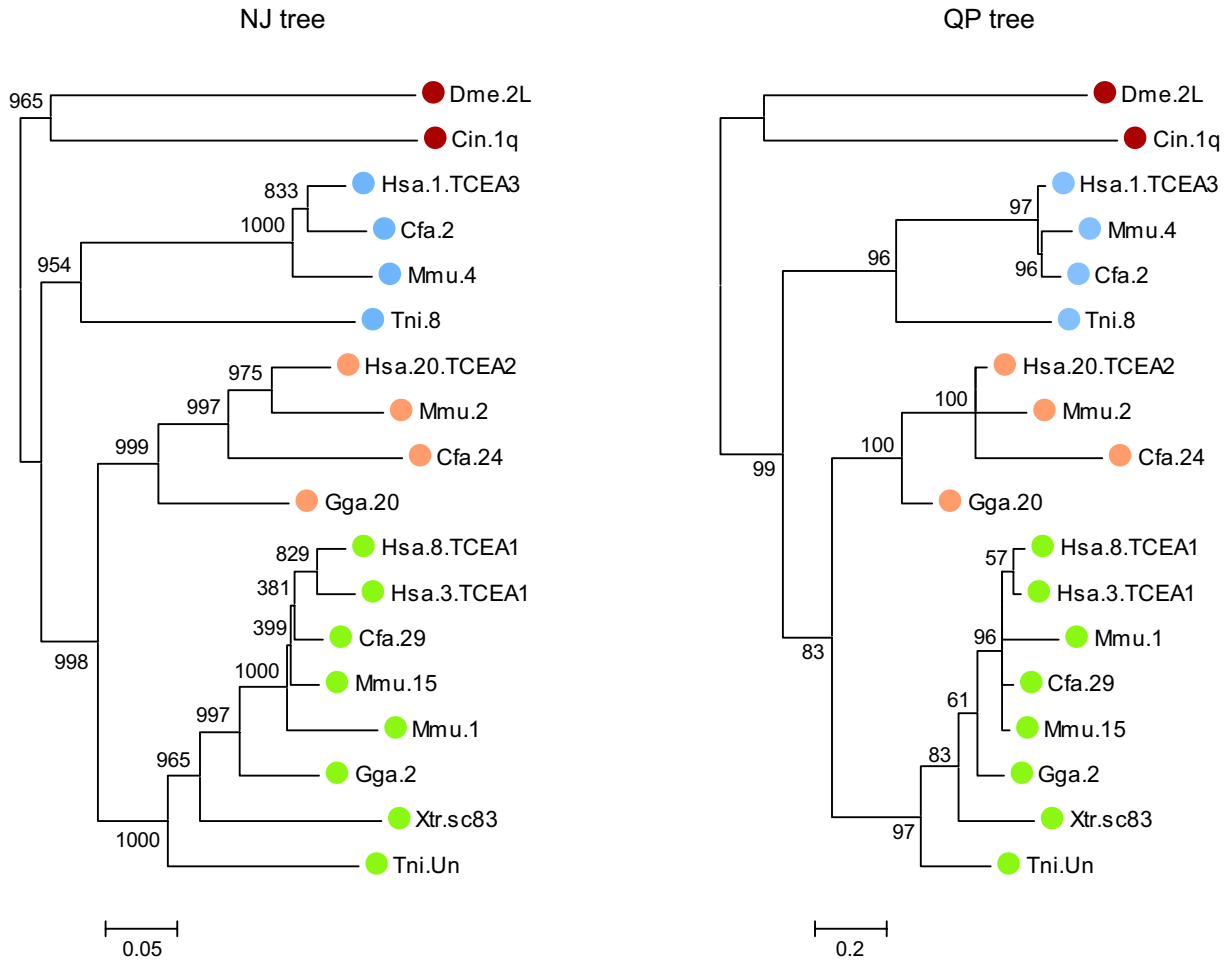

Fig. S12. Neighbor-joining and quartet-puzzling maximum likelihood trees for TRANSCRIPTION ELONGATION FACTOR A (SII) (TCEA). The proteins of this family play an important role in transcription. They bind to polII and when transcription is stalled they restart the arrested polII by stimulating an intrinsic nuclease activity of the polymerase. PolII then cleaves the RNA and thereby makes a fresh 3′-hydroxyl group available to the catalytic site and transcriptioncan continue (Wind M, Reines D (2000) Transcription elongation factor SII. *BioEssays* 22:327–336). Hsa, *Homo sapiens*; Mmu, *Mus musculus*; Cfa, *Canis familiaris*; Gga, *Gallus gallus*; Xtr, *Xenopus tropicalis*; Tni, *Tetraodon nigroviridis*; Dme, *Drosophila melanogaster*; Cin, *Ciona intestinalis*.

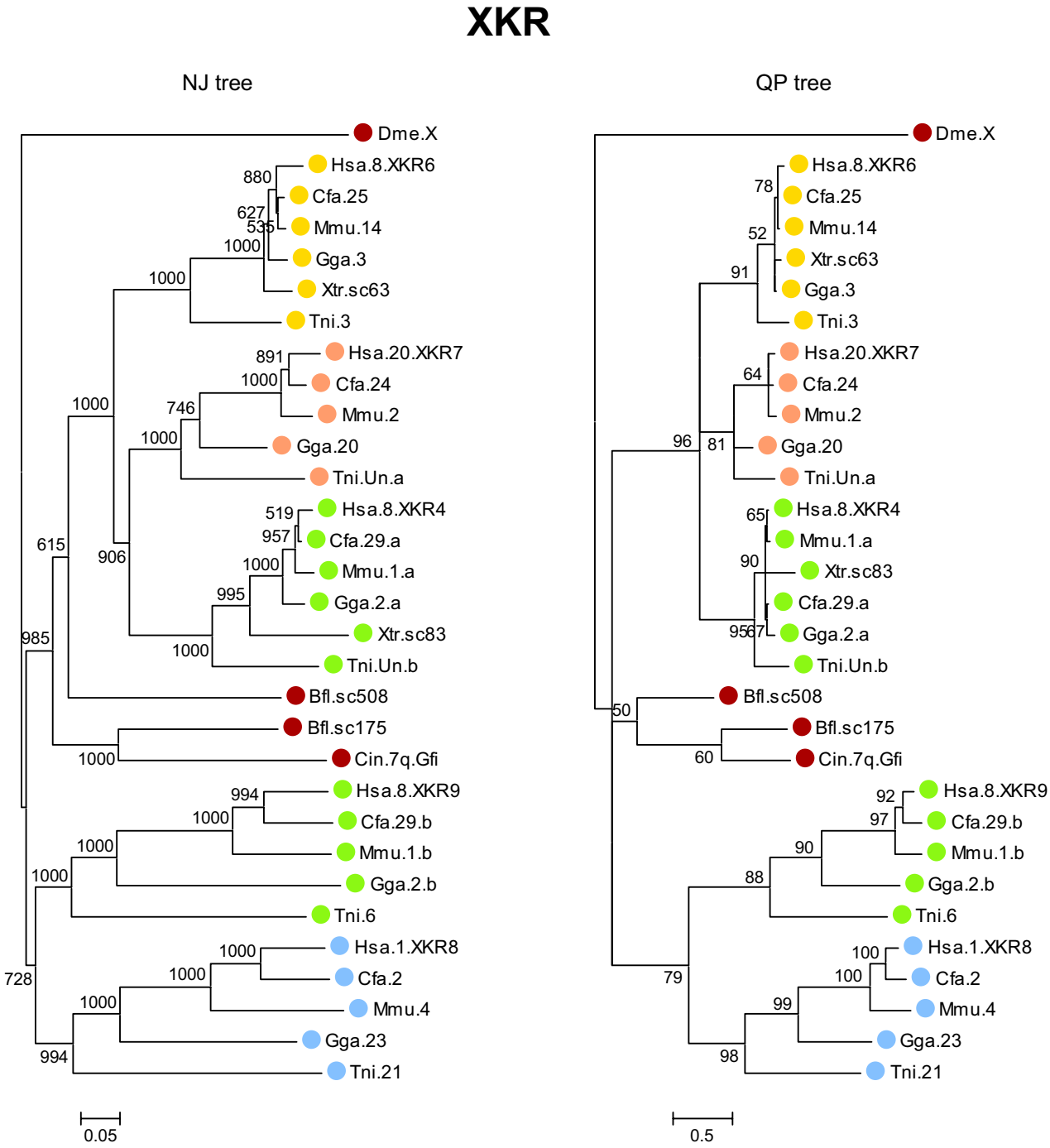

Fig. S13. Neighbor-joining and quartet-puzzling maximum likelihood trees for XK RELATED (XKR). This is a subfamily of the XK (Kell blood group complex) family. Five genes are included in this Ensembl family but our analysis shows that they can be divided into two distinct subfamiles. The proteins have the structural characteristics of membrane transport proteins but the substrate/substrates are not known [Calenda G, *et al.* (2006). Identification of two new members, XPLAC and XTES, of the XK family. *Gene* 370:6–16.]. In humans, the proteins of this family have 6–10 predicted transmembraneregions. However, some of the proteins from other species have as few as two or three transmembrane regions. The varying number of TMs and the different length of the proteins make them difficult to align. Hsa, *Homo sapiens*; Mmu, *Mus musculus*; Cfa, *Canis familiaris*; Gga, *Gallus gallus*; Xtr, *Xenopus tropicalis*; Tni, *Tetraodon nigroviridis*; Bfl, *Branchiostoma floridae*; Dme, *Drosophila melanogaster*; Cin, *Ciona intestinalis.*

YTHDF

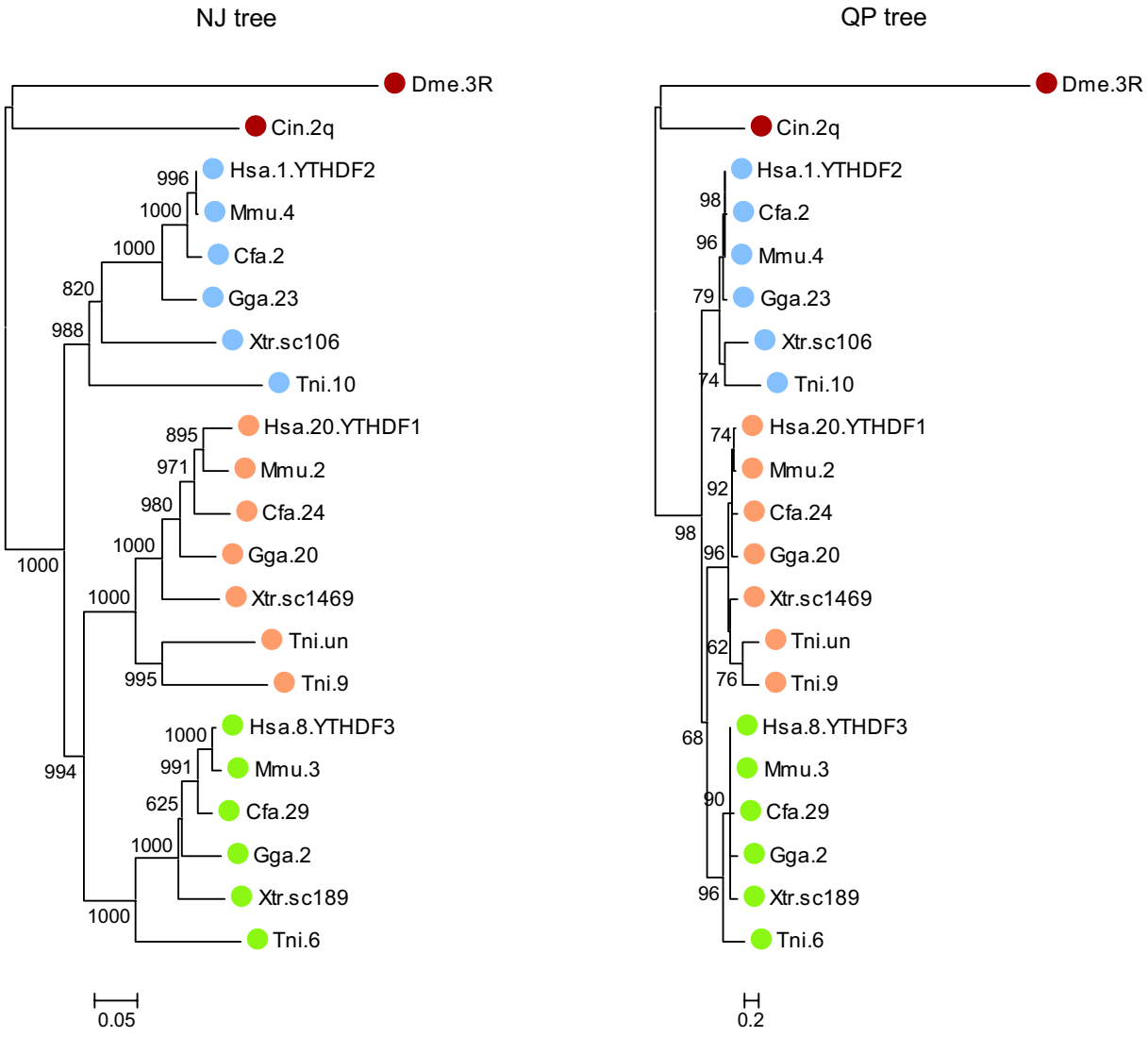

Fig. S14. Neighbor-joining and quartet-puzzling maximum likelihood trees for YTH DOMAIN PROTEIN (YTHDF). The proteins of this family are not characterized but they have a Pfam YTH (YT521-B homology) domain. The YTH domain contains conserved aromatic residues that are similar to aromatic residues in the RNA recognition motif (RRM) domain. The aromatic residues in the RRM domain are crucial for RNA binding it is therefore likely that the YTH domain also binds RNA (1). (The YT521-B protein is not a member of this family but it also contains the YTH domain and can alter splice site selection of the pre-mRNA (1, 2). Hsa, *Homo sapiens*; Mmu, *Mus musculus*; Cfa, *Canis familiaris*; Gga, *Gallus gallus*; Xtr, *Xenopus tropicalis*; Tni, *Tetraodon nigroviridis;* Dme, *Drosophila melanogaster*; Cin, *Ciona intestinalis.*

1. Stoilov P, Rafalska I, Stamm S (2002) YTH: A new domain in nuclear proteins. *Trends Biochem Sci* 27:495–497.
2. Rafalska I, *et al.* (2004) The intranuclear localization and function of YT521-B is regulated by tyrosine phosphorylation. *Human Mol Gen* 13:1535–1549.

ZDHHC

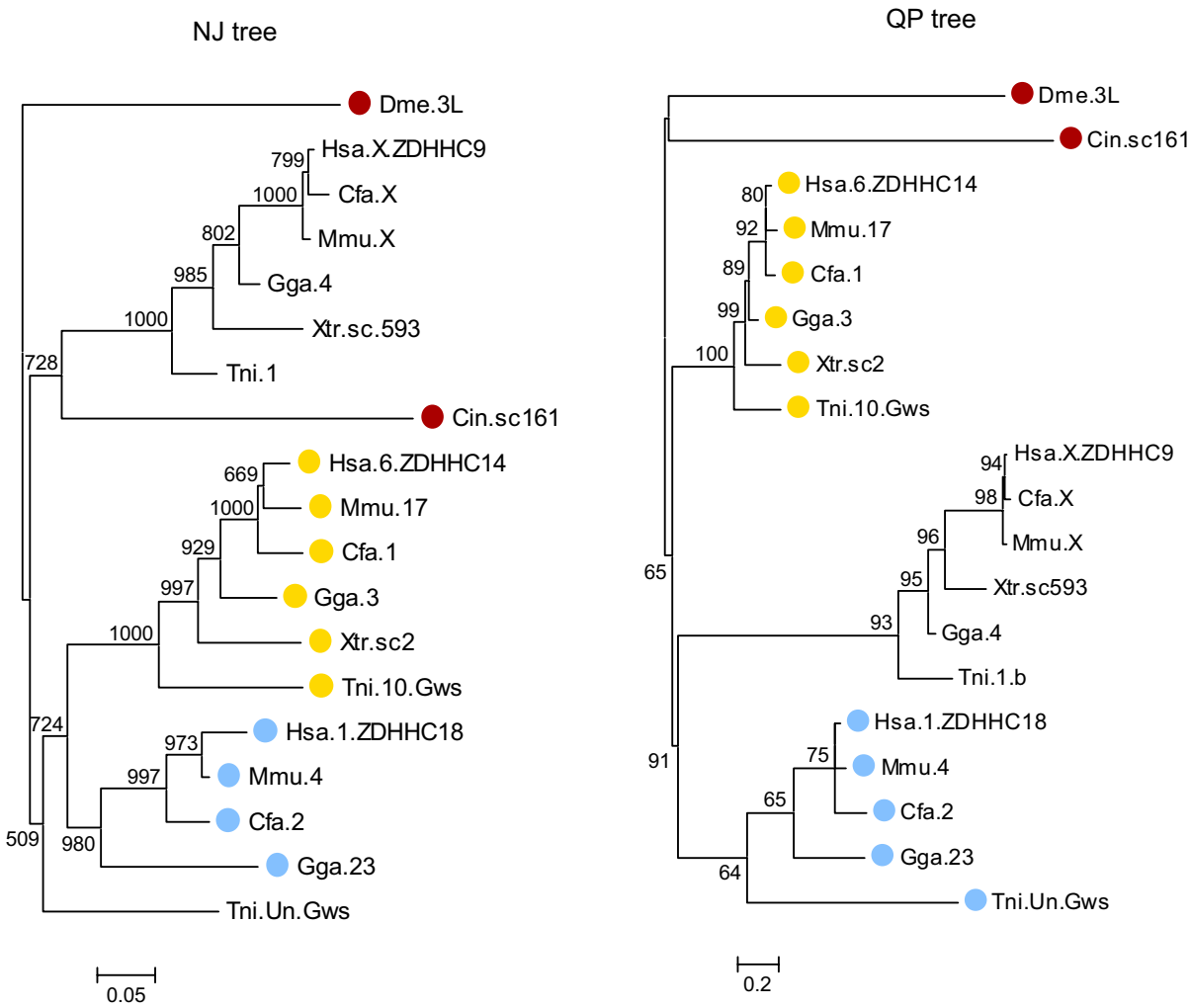

Fig. S15. Neighbor-joining and quartet-puzzling maximum likelihood trees for PALMITOYLTRANSFERASE–ZINC FINGER DHHC DOMAIN CONTAINING (ZDHHC). All proteins in this family have a Pfam zf-DHHC domain, although the domain can also be found in proteins belonging to other families. The proteins of this family are thought to act as palmitoyltransferases, linking long fatty acids (usually palmitoyl) by thioester bonds to the side chains of cystein (Mitchell DA, Vasudevan A, Linder ME, Deschens RJ (2006) Protein palmitoylationby a family of DHHC protein S-acyltransferases. *J Lipid Res* 47:1118–1127). The Pfam zf-DHHC domain is also predicted to be zinc binding (Pfam). After a phylogenetic analysis, a subfamily to this Ensembl family was found consisting of ZDHHC18, ZDHHC14 and ZDHHC9 in humans. Hsa, *Homo sapiens*; Mmu, *Mus musculus*; Cfa, *Canis familiaris*; Gga, *Gallus gallus*; Xtr, *Xenopus tropicalis*; Tni, *Tetraodon nigroviridis*; Dme, *Drosophila melanogaster*; Cin, *Ciona intestinalis.*

Family	Opossum chromosome 3		Opossum chromosome 1		Opossum chromosome 4		Opossum chromosome 2		Opossum chromosome 1		Other chromosomes		
ARID1					ARID1A	353.98 Mb	ARID1B	438.80 Mb					
GMEB			GMEB2	473.44 Mb	GMEB1	361.10 Mb					GMEB1	Chr 8	243.62 Mb
LYPLA	LYPLA1	186.54 Mb			LYPLA2	358.16 Mb							
MYT1	ST18	188.74 Mb	MYT1	471.86 Mb					MYT1L	542.21 Mb			
NKAIN	NKAIN3	175.79 Mb	NKAIN4	474.56 Mb	NKAIN1	425.86 Mb	NKAIN2	395.46 Mb					
NPBWR	NPBWR1	187.78 Mb	NPBWR2	472.32 Mb									
OPR	OPRK1	187.42 Mb	OPRL1	472.36 Mb	OPRD1	361.30 Mb	OPRM1	434.89 Mb					
PCMTD	PCMTD1	189.15 Mb	PCMTD2	471.60 Mb									
RGS	RGS20	186.66 Mb	RGS19	472.46 Mb			RGS17	433.18 Mb					
SOX*	SOX17	186.03 Mb	SOX18	472.54 Mb					SOX7	586.79 Mb			
SRC-B	LYN	184.10 Mb	HCK	423.26 Mb	LCK	420.63 Mb			BLK	560.17 Mb			
STMN*	STMN2	154.64 Mb	STMN3	473.39 Mb	STMN1	355.21 Mb			STMN4	504.67 Mb			
TCEA	TCEA1	186.60 Mb	TCEA2	472.47 Mb	TCEA3	347.57 Mb							
XKR*	XKR9	166.14 Mb			XKR8	360.40 Mb							
	XKR4	184.60 Mb	XKR7	423.17 Mb					XKR6	586.56 Mb			
YTHDF	YTHDF3	175.41 Mb	YTHDF1	474.76 Mb	YTHDF2	361.17 Mb							
ZDHHC*					ZDHHC18	353.90 Mb	ZDHHC14	439.24 Mb			ZDHHC9*	Chr X	31.28 Mb

Family	Dog chromosome 29		Dog chromosome 24		Dog chromosome 2		Dog chromosome 1		Dog chromosome 17		Dog chromosome 25		Other chromosomes		
ARID1					ARID1A	76.22 Mb	ARID1B	49.42 Mb							
GMEB			GMEB2	50.22 Mb	GMEB1	74.70 Mb									
LYPLA	LYPLA1	8.67 Mb			LYPLA2	78.60 Mb									
MYT1	ST18	6.98 Mb	MYT1	50.67 Mb					MYT1L	3.96 Mb					
NKAIN	NKAIN3	15.71 Mb	NKAIN4	50.00 Mb	NKAIN1	72.70 Mb	NKAIN2	66.28 Mb							
NPBWR	NPBWR1	7.78 Mb													
OPR	OPRK1	8.03 Mb	OPRL1	50.59 Mb	OPRD1	74.58 Mb	OPRM1	47.02 Mb							
PCMTD	PCMTD1	6.72 Mb	PCMTD2	50.72 Mb											
RGS	RGS20	8.53 Mb	RGS19	50.56 Mb			RGS17	46.22 Mb							
SOX*	SOX17	8.99 Mb	SOX18	50.54 Mb							SOX7	30.20 Mb			
SRC-B	LYN	10.39 Mb	HCK	24.44 Mb	LCK	71.83 Mb					BLK	29.32 Mb			
STMN*	STMN2	30.05 Mb	STMN3	50.26 Mb	STMN1	76.93 Mb					STMN4	33.34 Mb			
TCEA	TCEA1	8.62 Mb	TCEA2	50.56 Mb	TCEA3	78.89 Mb									
XKR*	XKR9	22.77 Mb			XKR8	75.31 Mb									
	XKR4	9.65 Mb	XKR7	24.37 Mb							XKR6	29.98 Mb			
YTHDF	YTHDF3	16.24 Mb	YTHDF1	49.97 Mb	YTHDF2	74.68 Mb									
ZDHHC*					ZDHHC18	76.17 Mb	ZDHHC14	50.15 Mb					ZDHHC9*	Chr X	104.07 Mb

Fig. S16. The figure shows the analyzed gene families and the chromosomal location of the genes they contain for gray short-tailed opossum and dog. All genes have been given the name of their human orthologs and the tables are color-coded based on the chicken chromosomes (chromosome 2, green; chromosome 20, orange; chromosome 23, blue and chromosome 3, yellow). Note that, except for the opioid receptors, the opossum sequences have not been analyzed phylogenetically in this study, but are instead predicted by Ensembl as orthologs of the human genes.

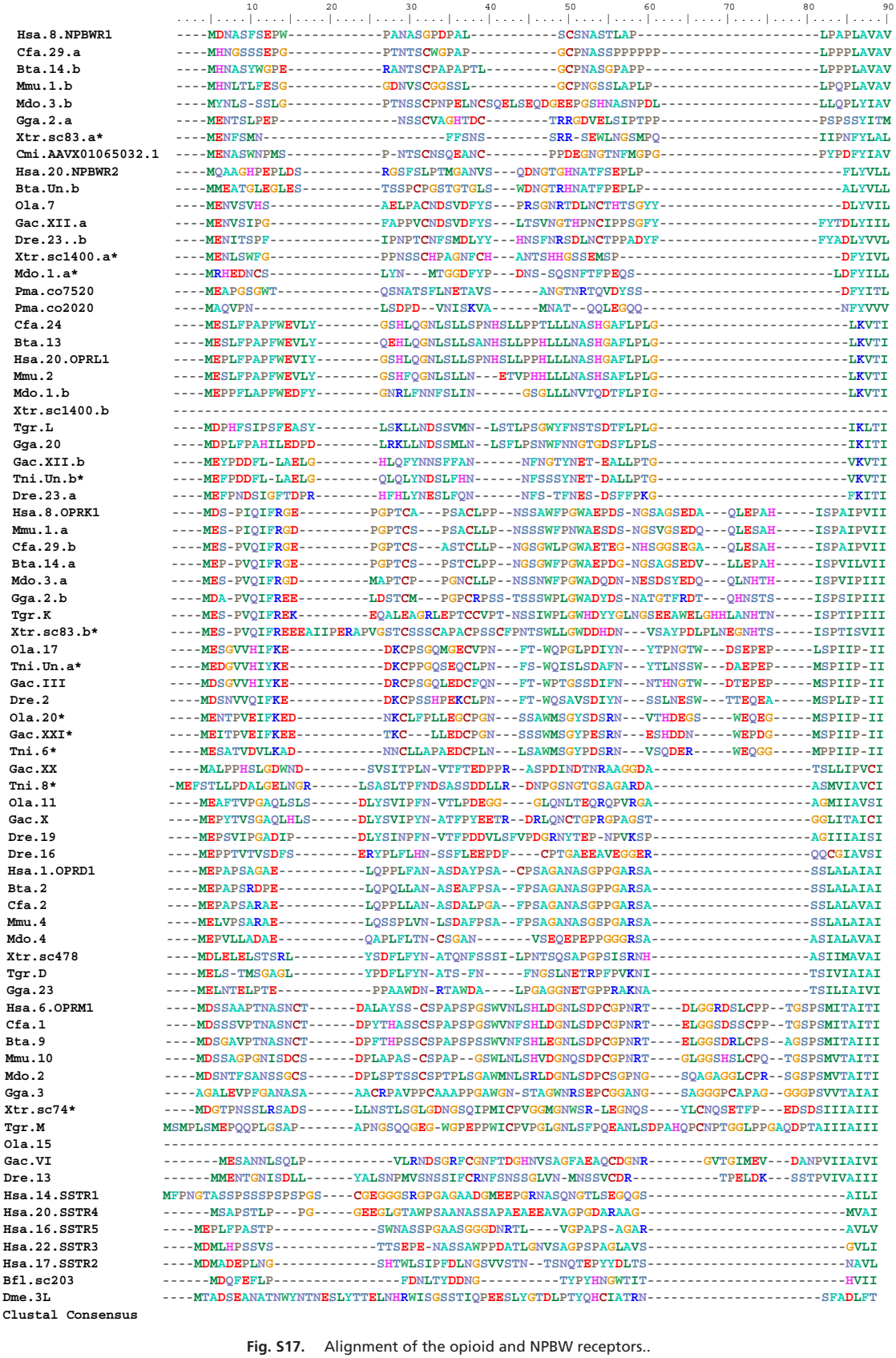

Fig. S17. Alignment of the opioid and NPBW receptors..

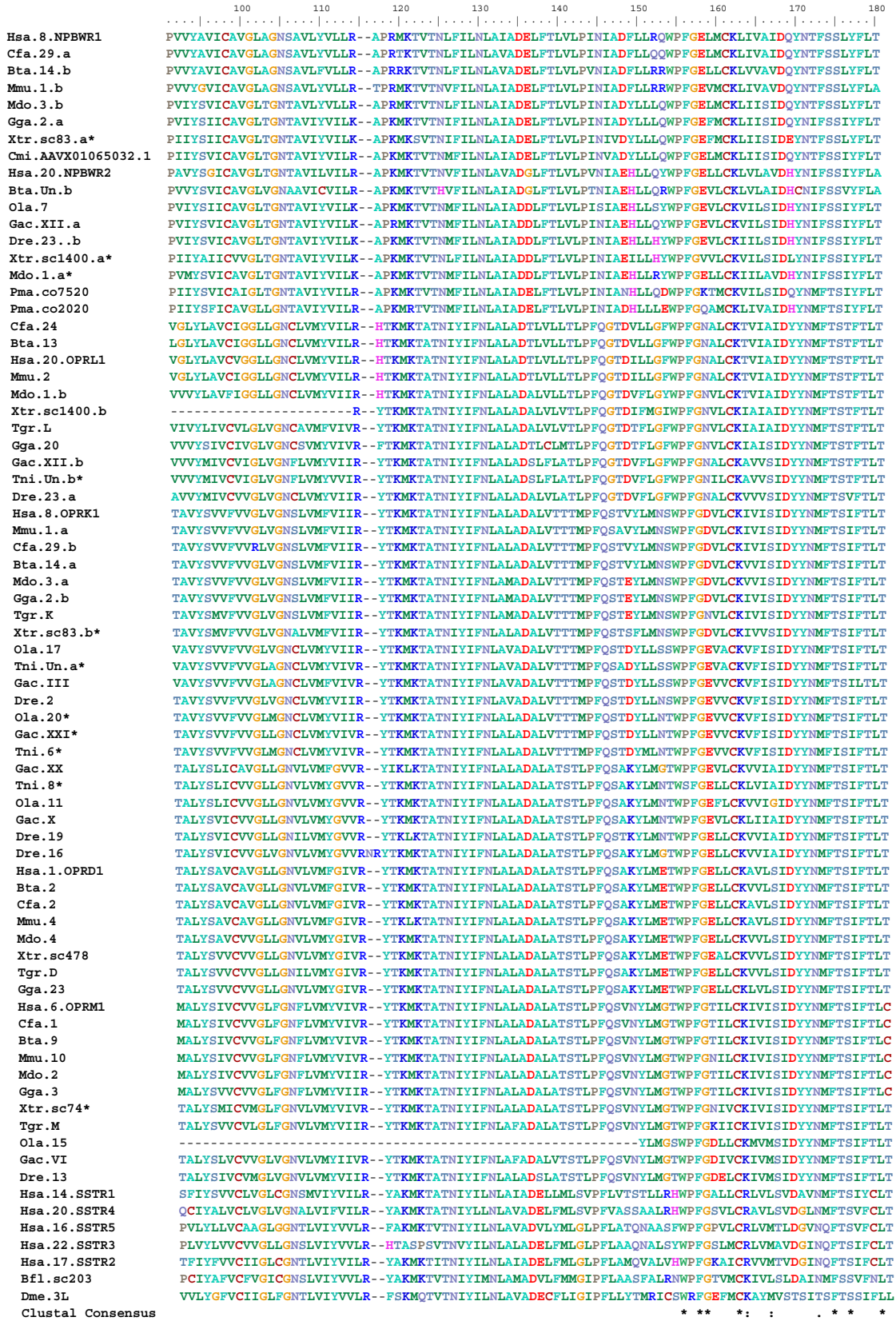

Fig. S17 (continued).

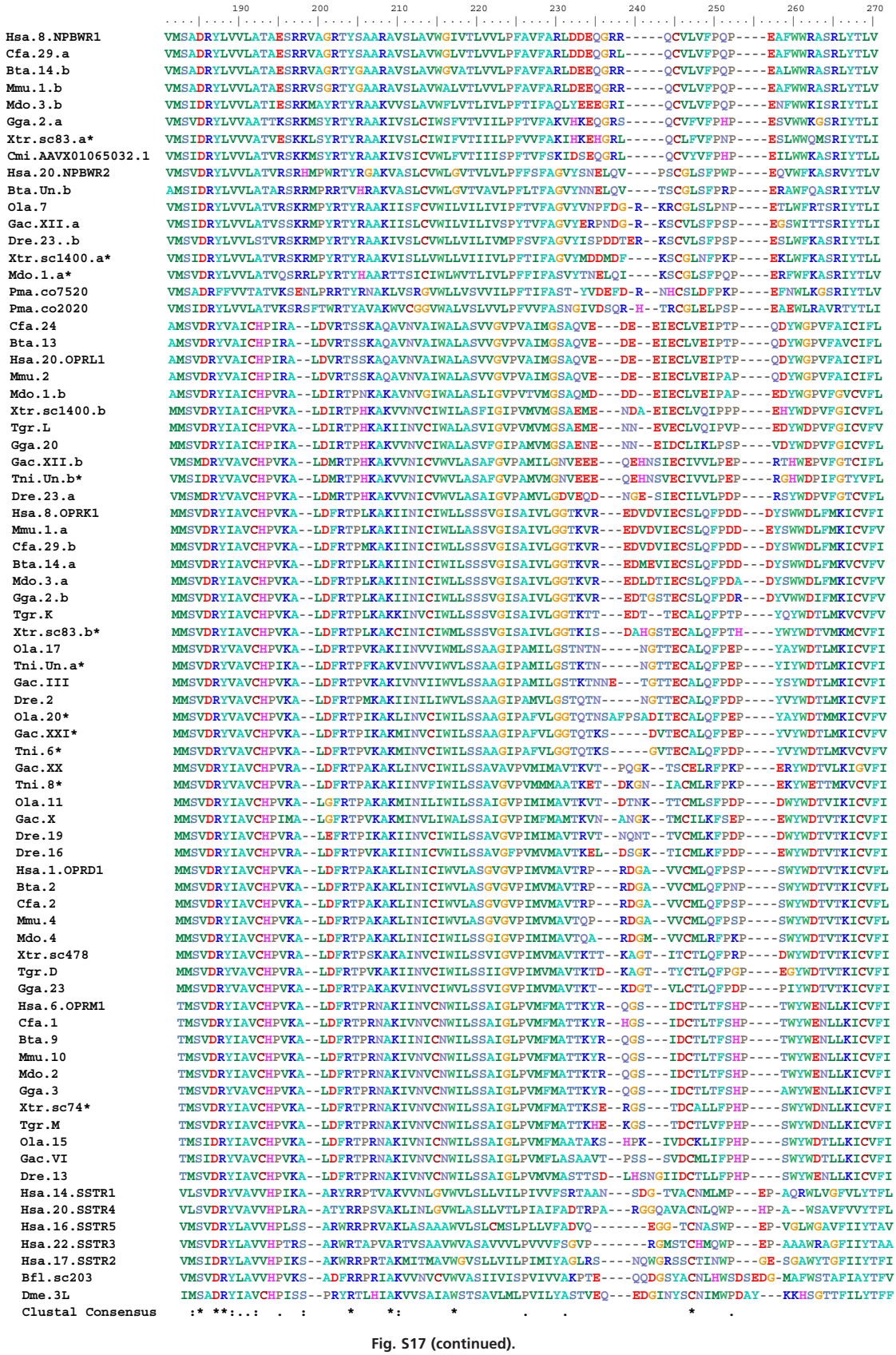

Fig. S17 (continued).

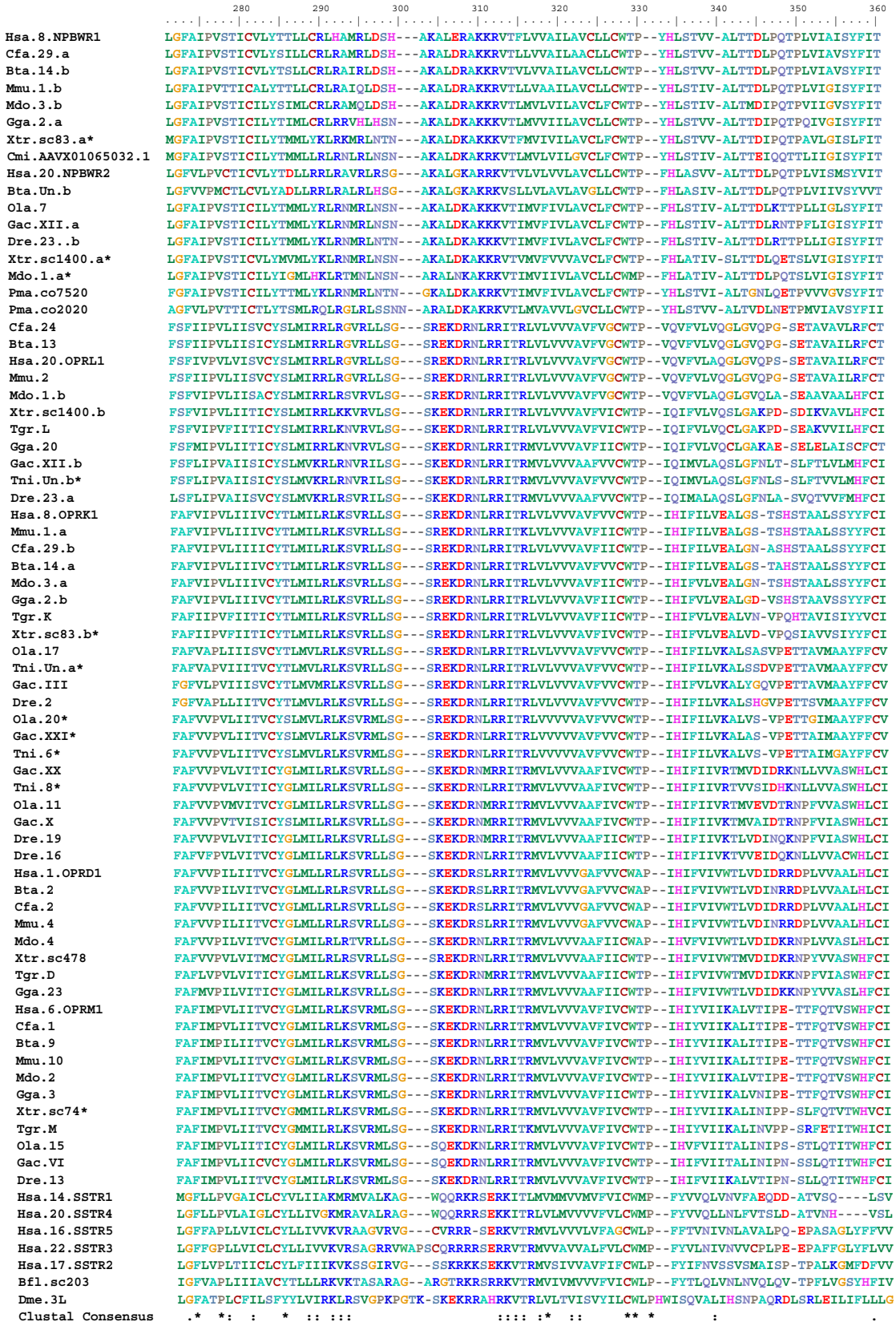

Fig. S17 (continued).

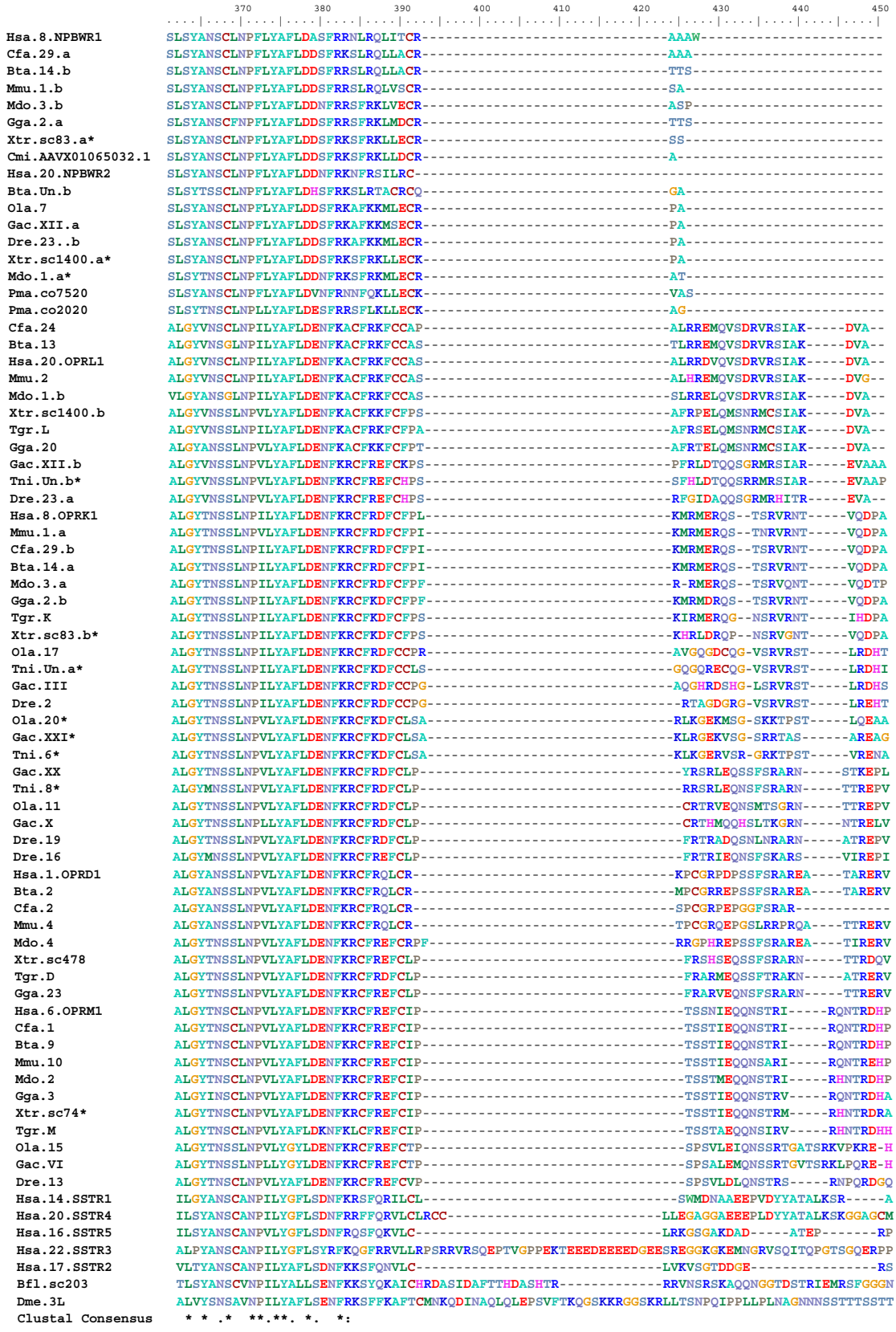

Fig. S17 (continued).

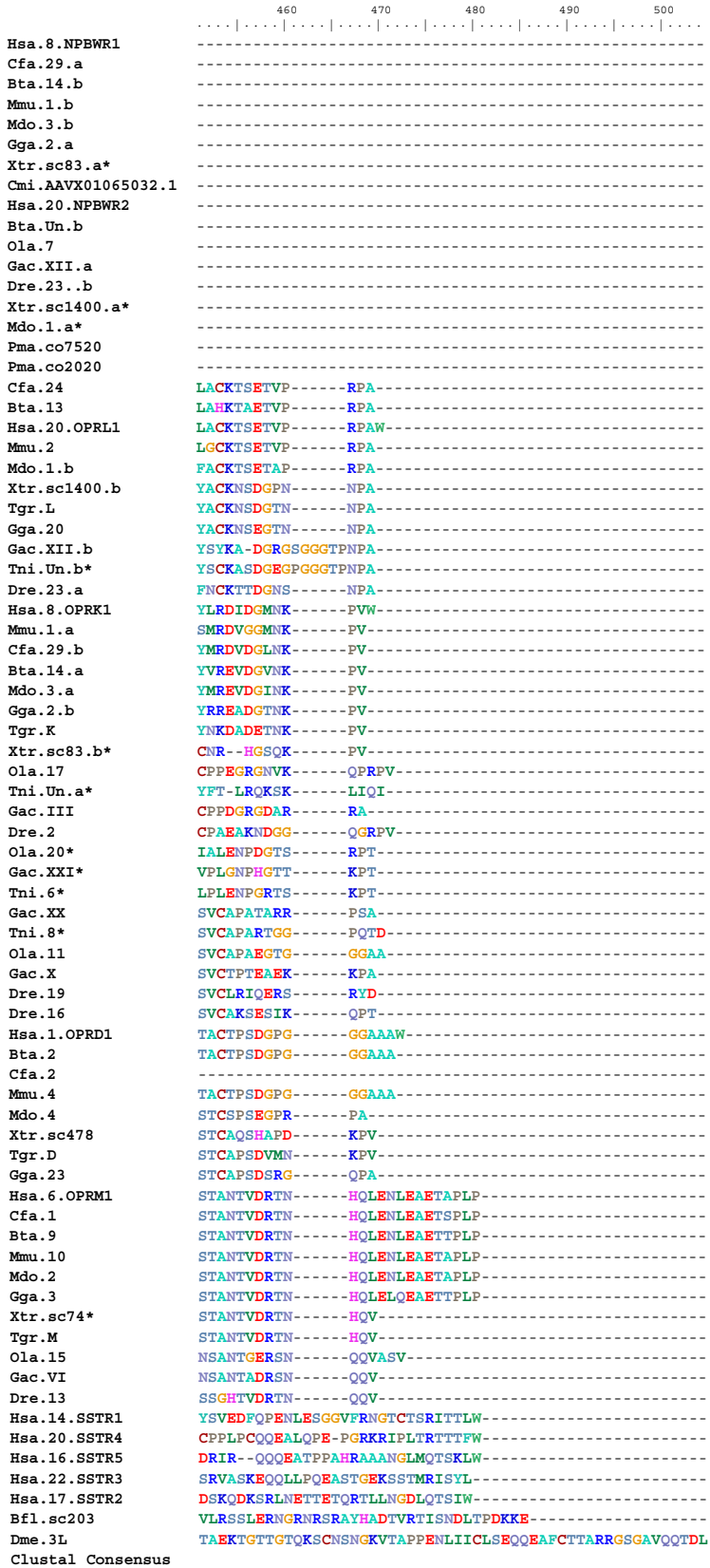

Fig. S17 (continued).

Other Supporting Information Files

Table S1