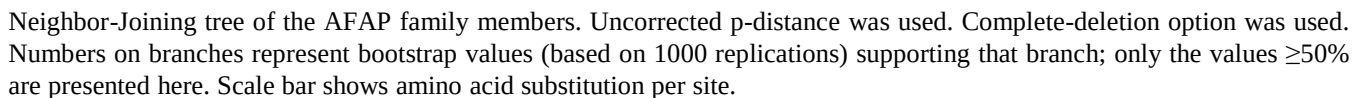
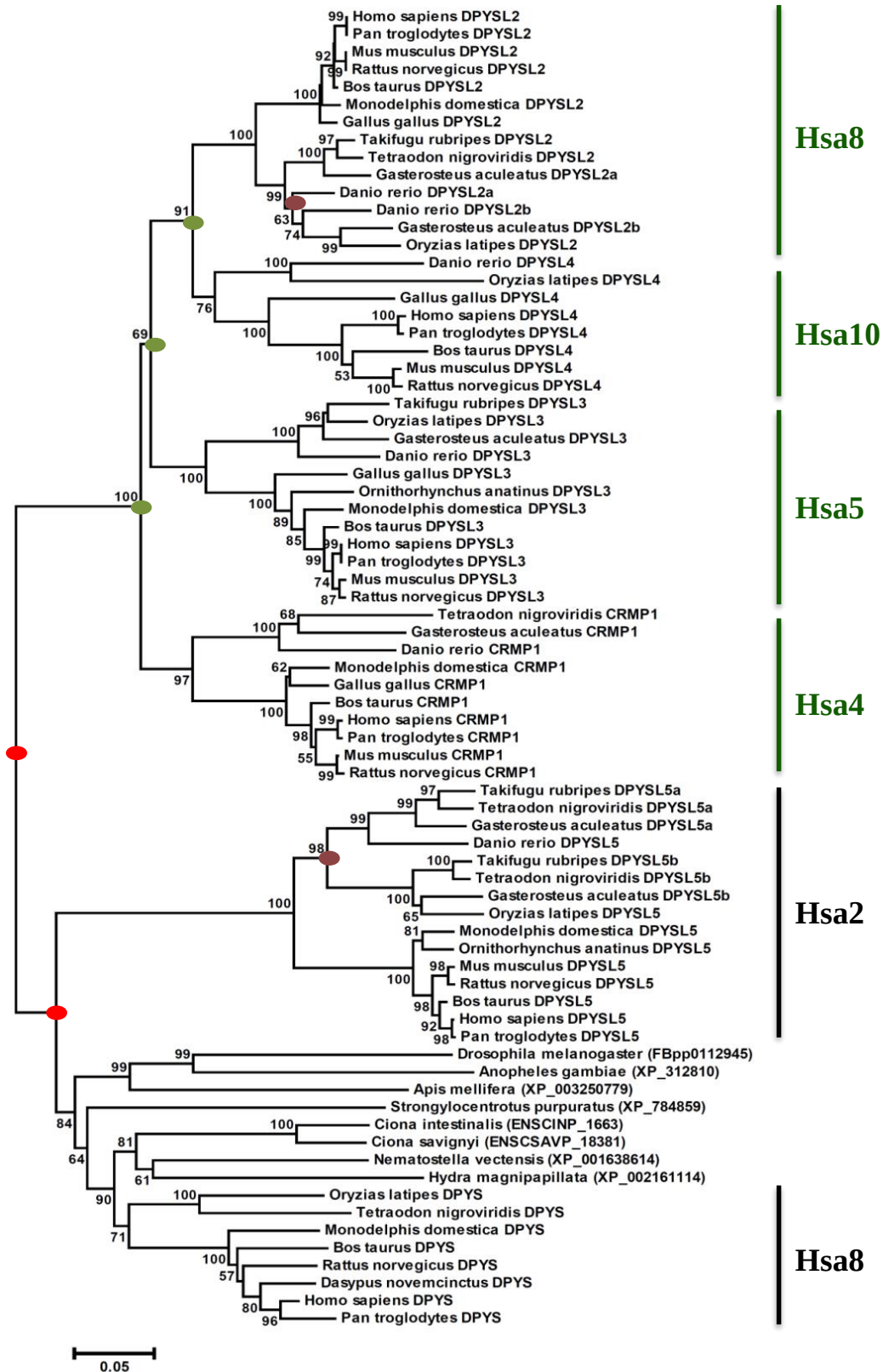


**Neighbor Joining Trees of gene families residing on
chromosomes 4, 5, 8 and 10.**

Phylogenetic tree of AFAP family.



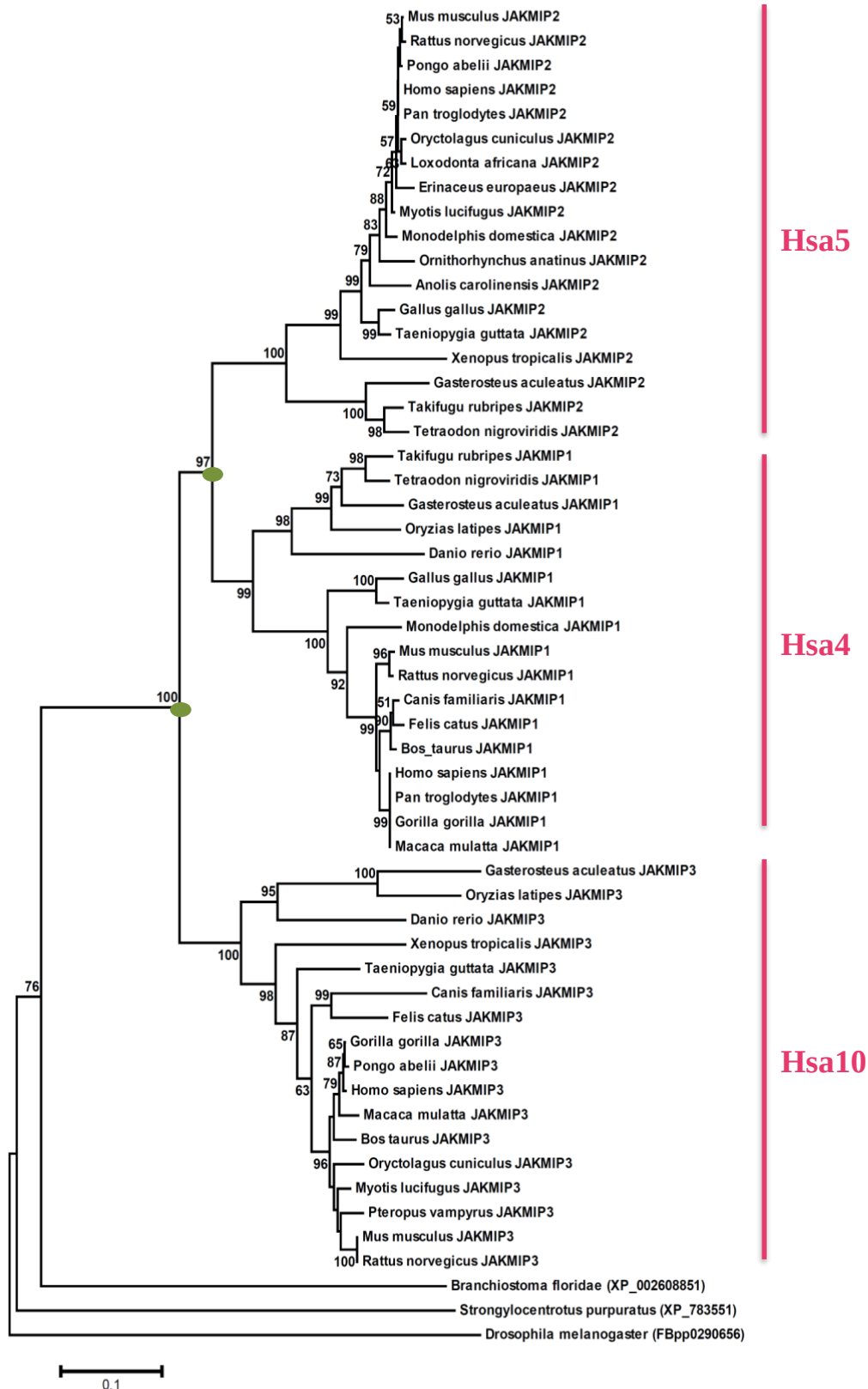
Dihydropyrimidinase-like – DPYSL



Phylogenetic tree of DPYSL family.

Neighbor-Joining tree of the DPYSL family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site.

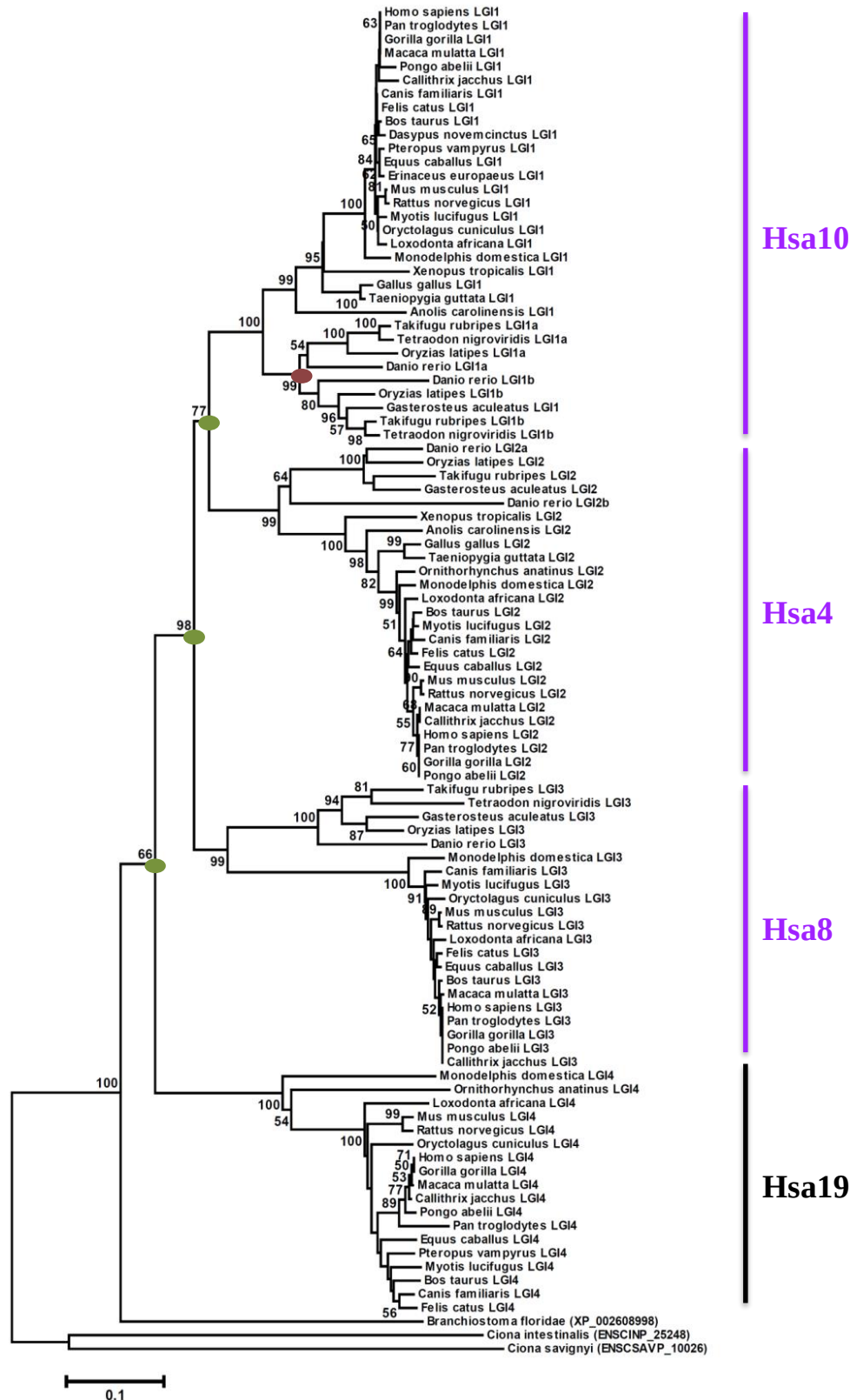
Janus kinase and microtubule interacting protein – JAKMIP



Phylogenetic tree of JAKMIP family.

Neighbor-Joining tree of the JAKMIP family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site.

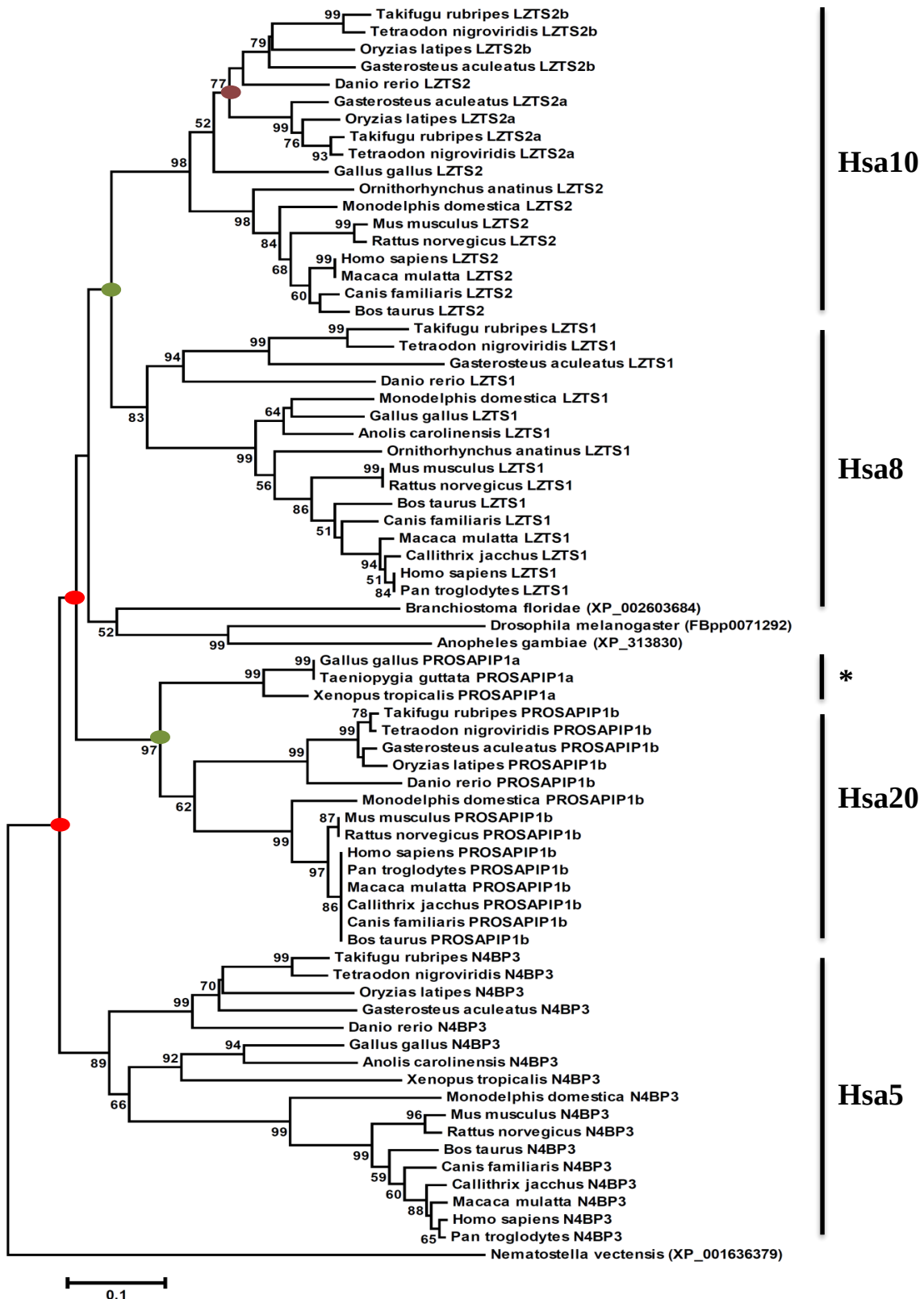
Leucine-rich, glioma inactivated – LGI



Phylogenetic tree of LGI family.

Neighbor-Joining tree of the LGI family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site.

Leucine zipper, putative tumor suppressor – LZTS



Phylogenetic tree of LZTS family.

Neighbor-Joining tree of the LZTS family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site. * shows another paralog which is missing in humans named as PROSAPIPa.

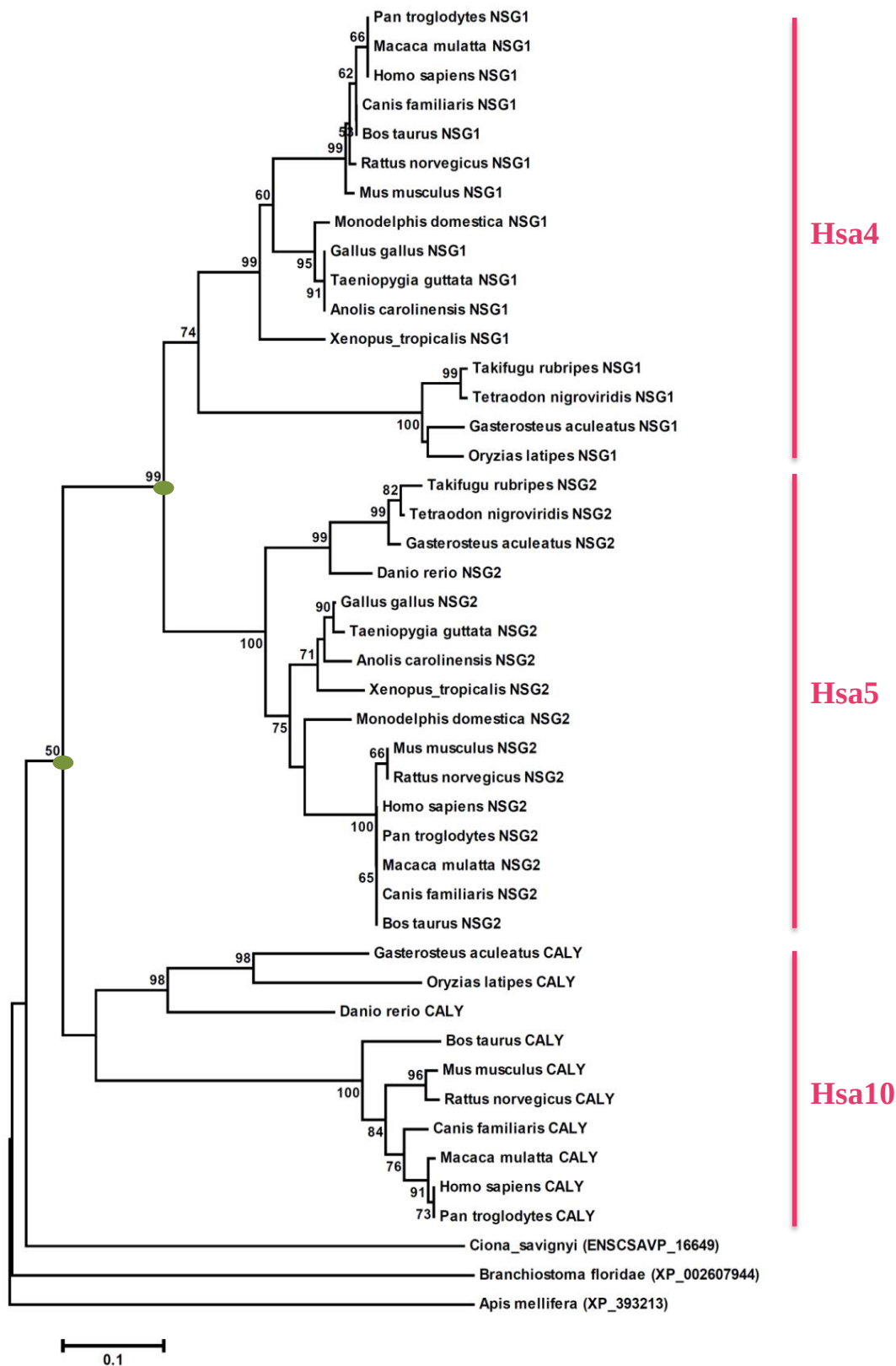
MAX dimerization protein – MXD



Phylogenetic tree of MXD family.

Neighbor-Joining tree of the MXD family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site. * shows another paralog which is missing in humans MXD4b.

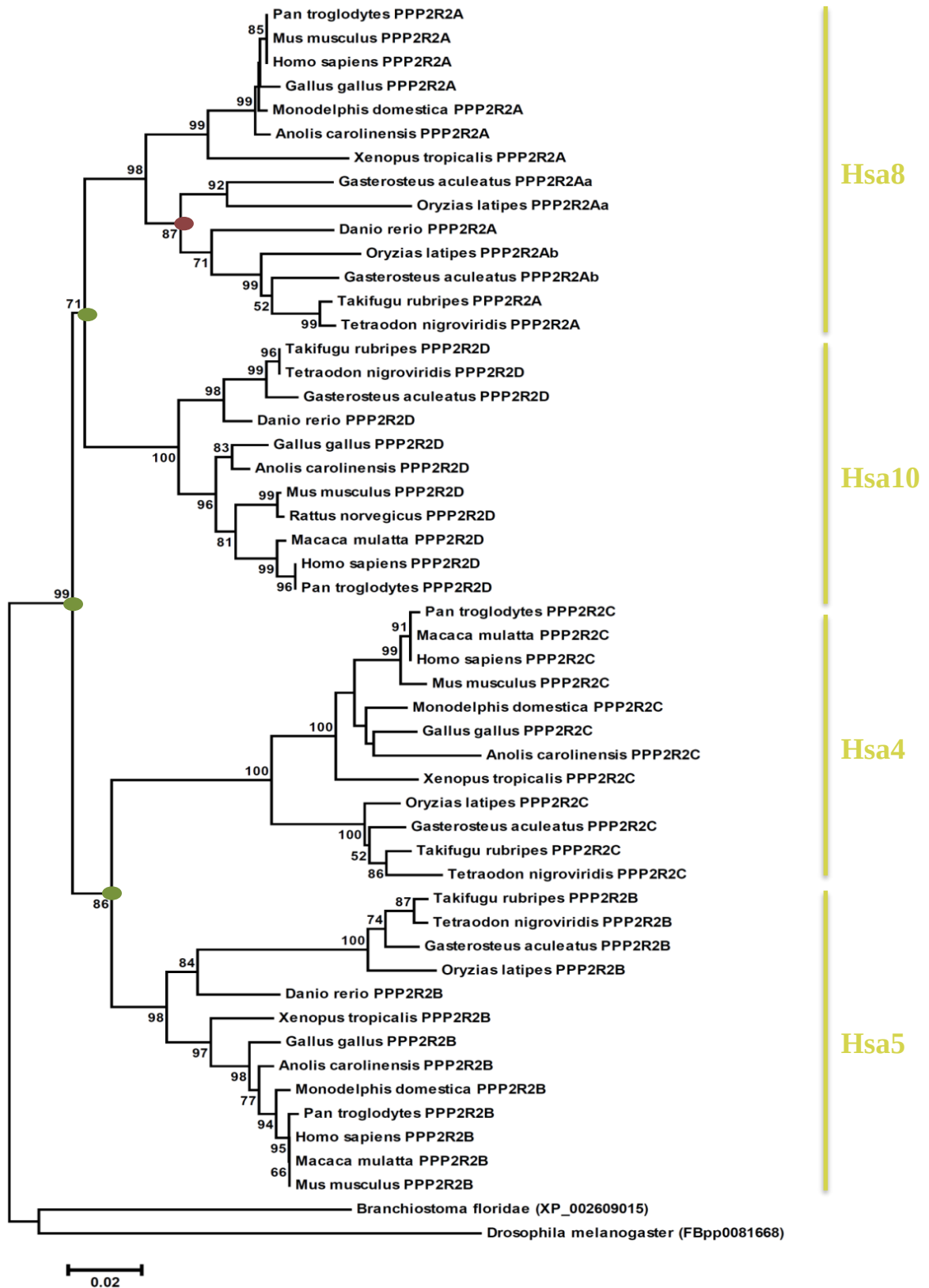
Neuron-specific protein family – NSG



Phylogenetic tree of NSG family.

Neighbor-Joining tree of the NSG family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site.

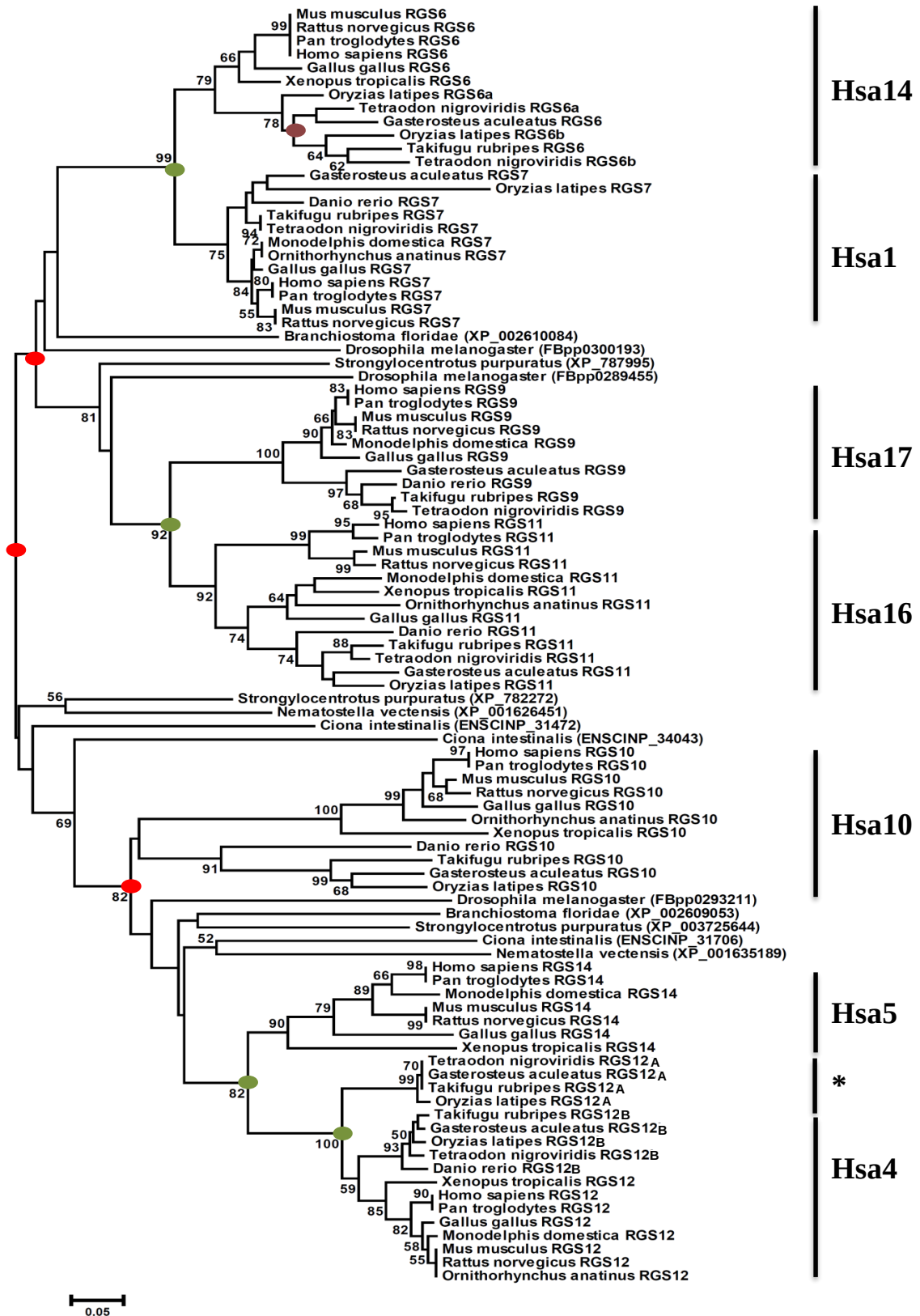
Protein phosphatase 2, regulatory subunit B – PPP2R2



Phylogenetic tree of PPP2R2 family.

Neighbor-Joining tree of the PPP2R2 family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site.

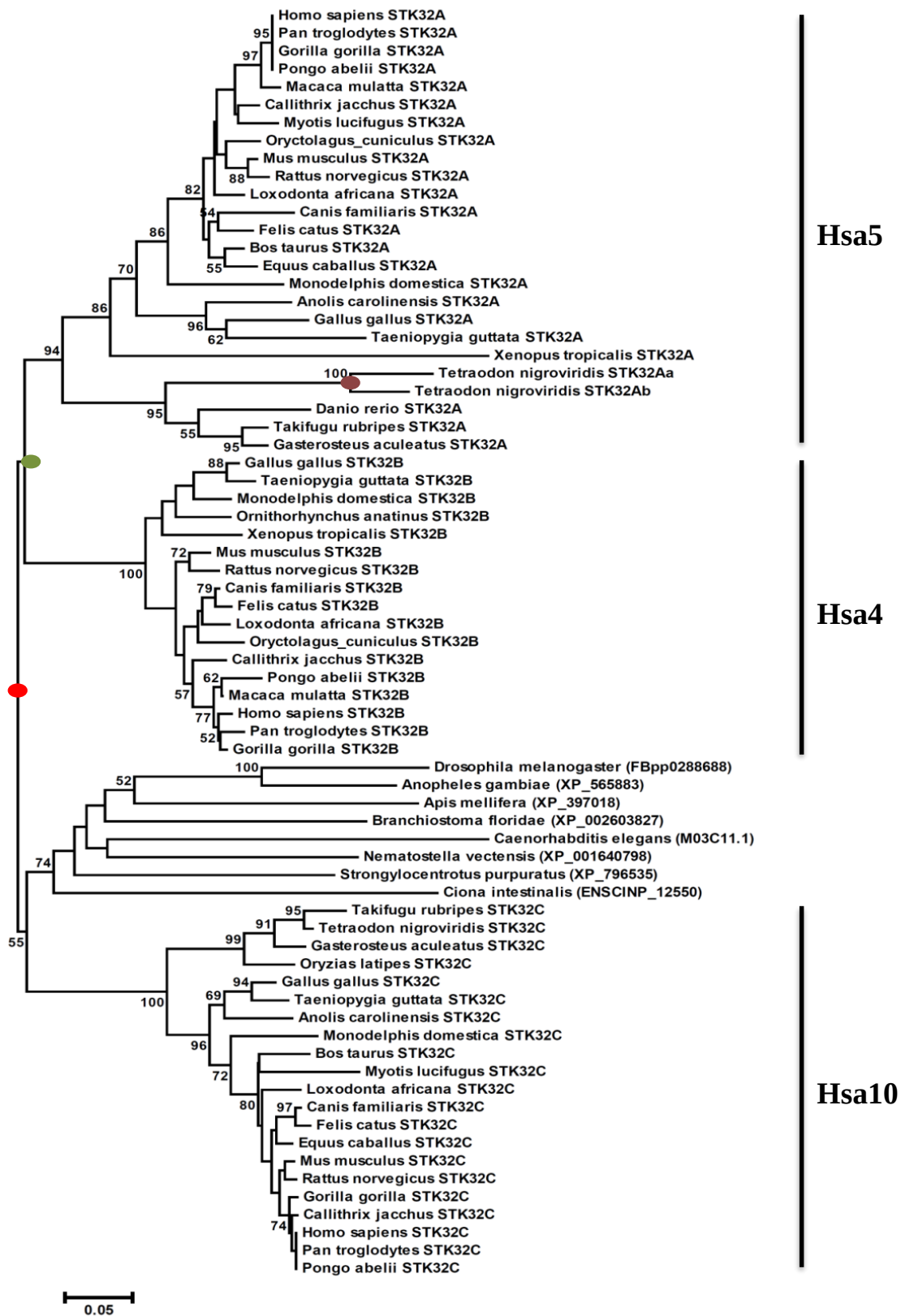
Regulator of G-protein signaling – RGS



Phylogenetic tree of RGS family.

Neighbor-Joining tree of the RGS family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site. * representing another paralog which is missing in tetrapods named as RGS12A by our group.

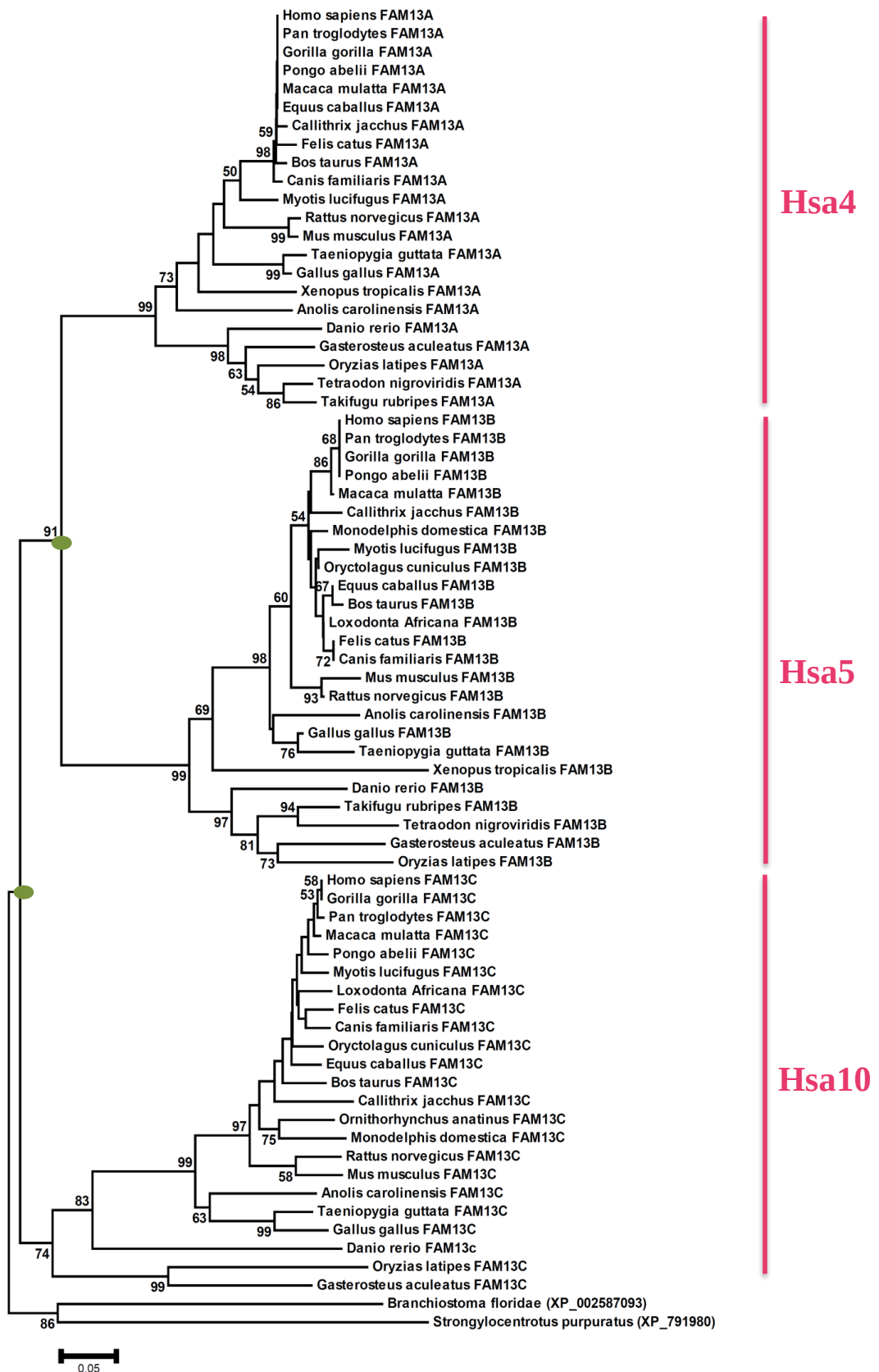
Serine/threonine kinase 32 – STK32



Phylogenetic tree of STK32 family.

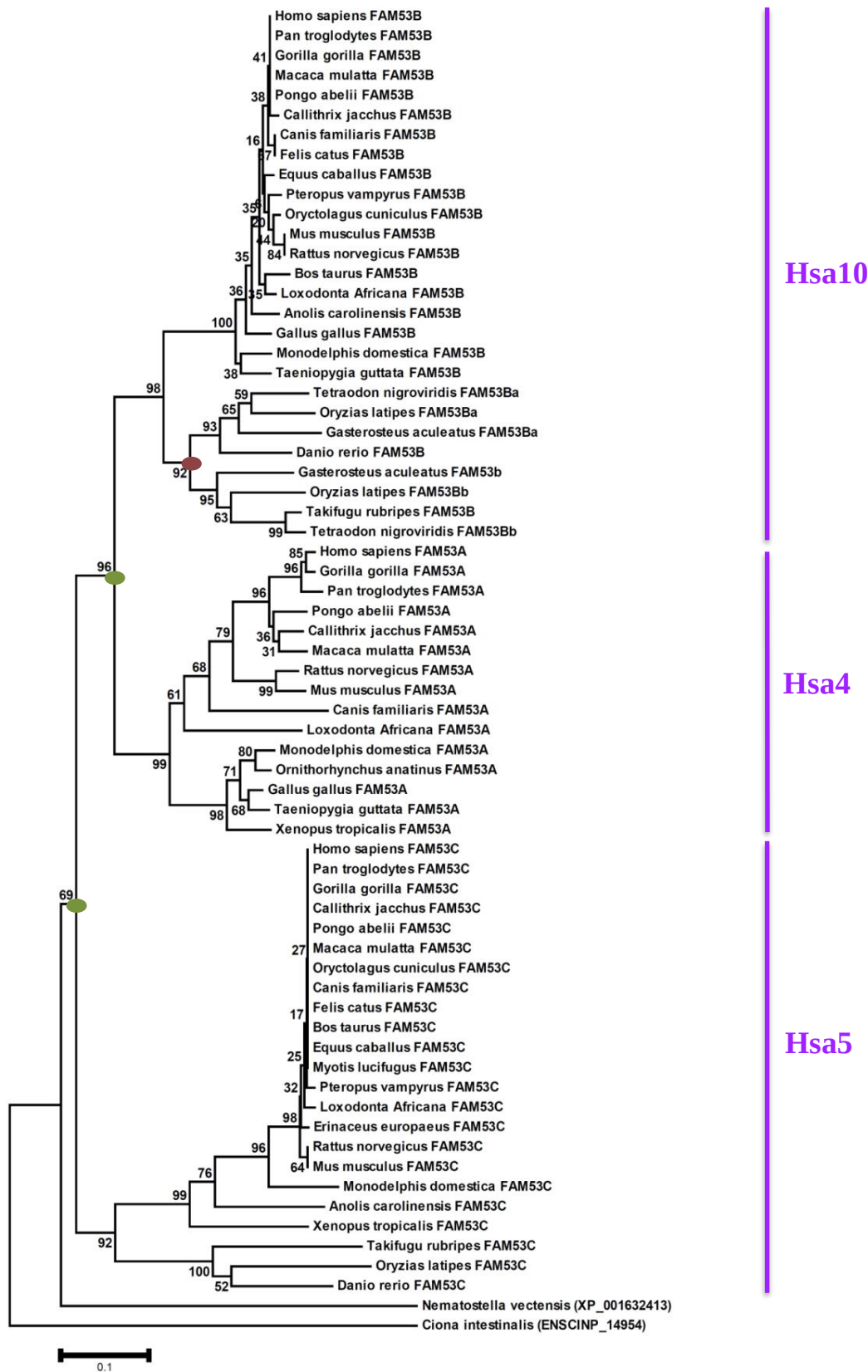
Neighbor-Joining tree of the STK32 family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site.

Family with sequence similarity 13-FAM13



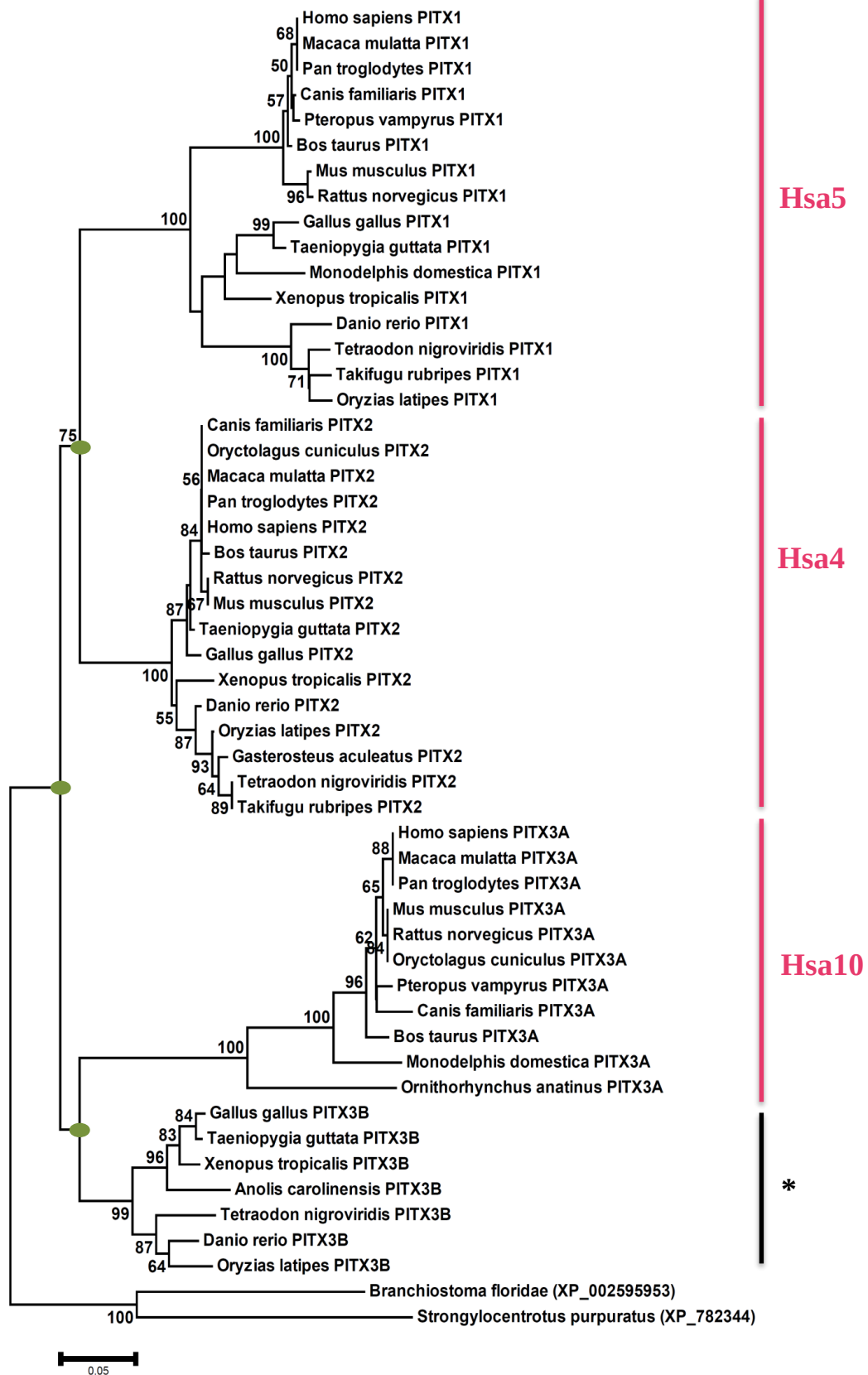
Phylogenetic tree of FAM13 family.

Neighbor-Joining tree of the FAM13 family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site.



Phylogenetic tree of FAM53 family.

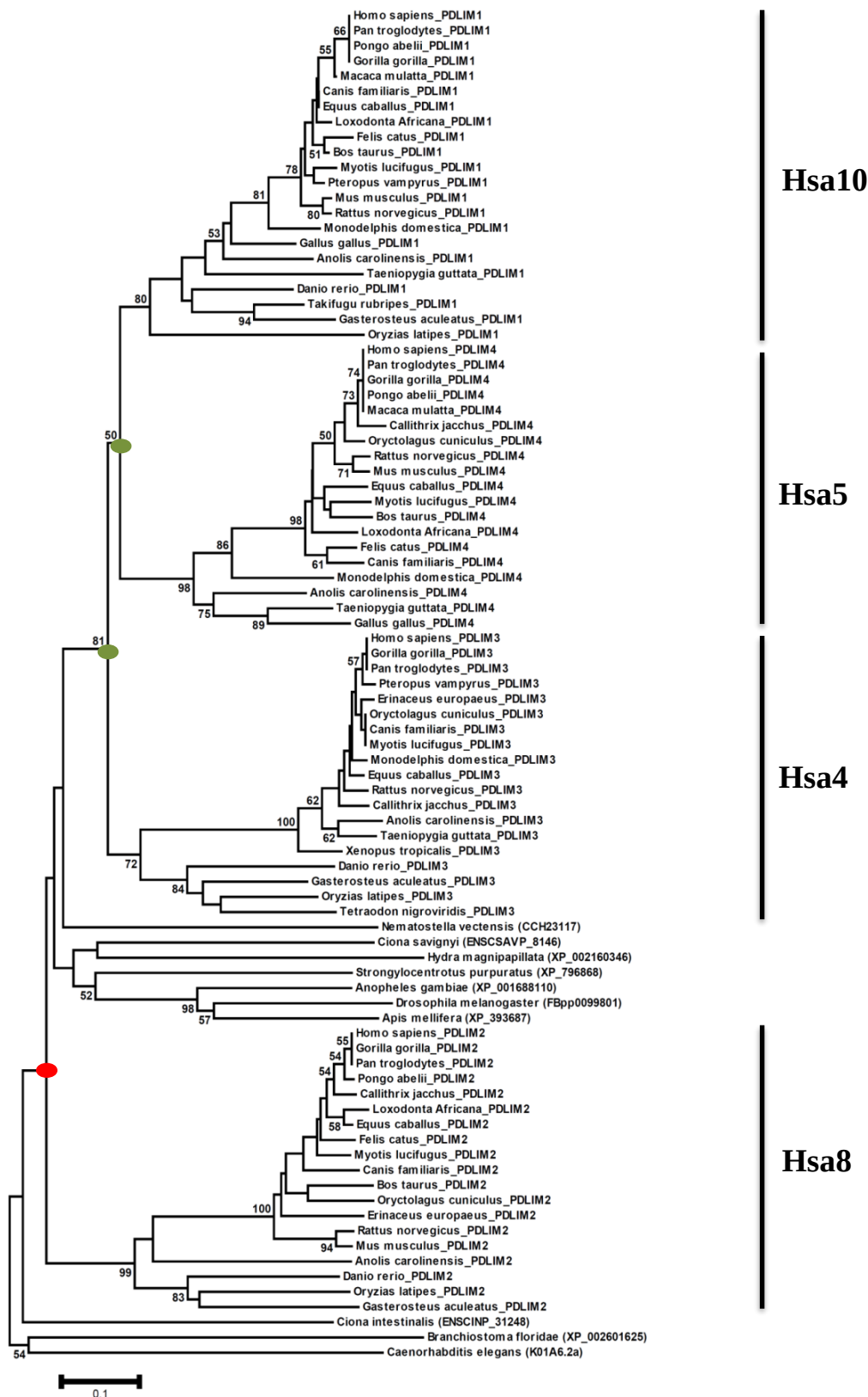
Neighbor-Joining tree of the FAM53 family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site.



Phylogenetic tree of PITX family.

Neighbor-Joining tree of the PITX family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site. * represents another paralog missing in mammals named as PITX3B

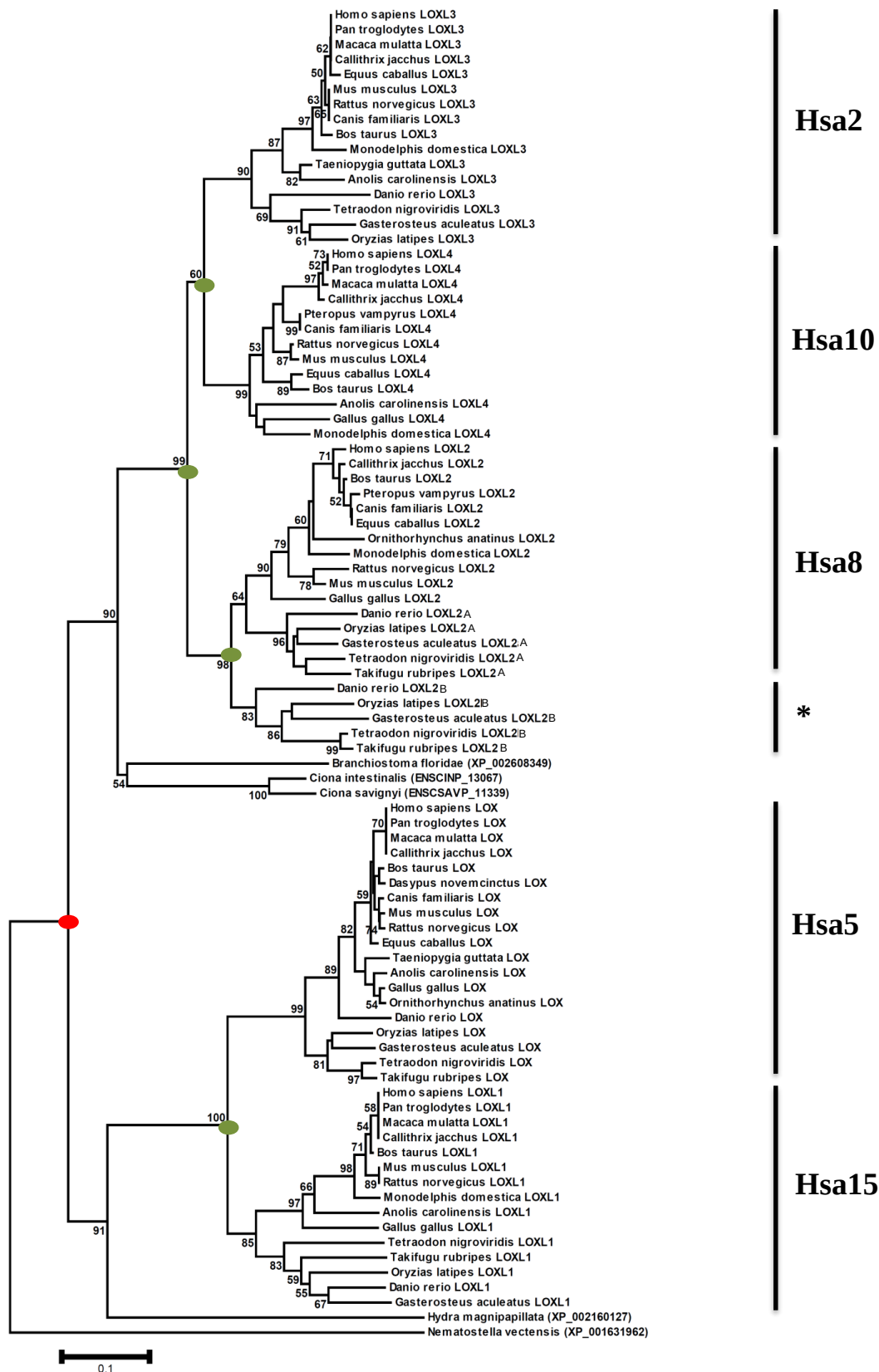
PDZ and LIM domain protein-PDLIM



Phylogenetic tree of PDLIM family.

Neighbor-Joining tree of the PDLIM family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site.

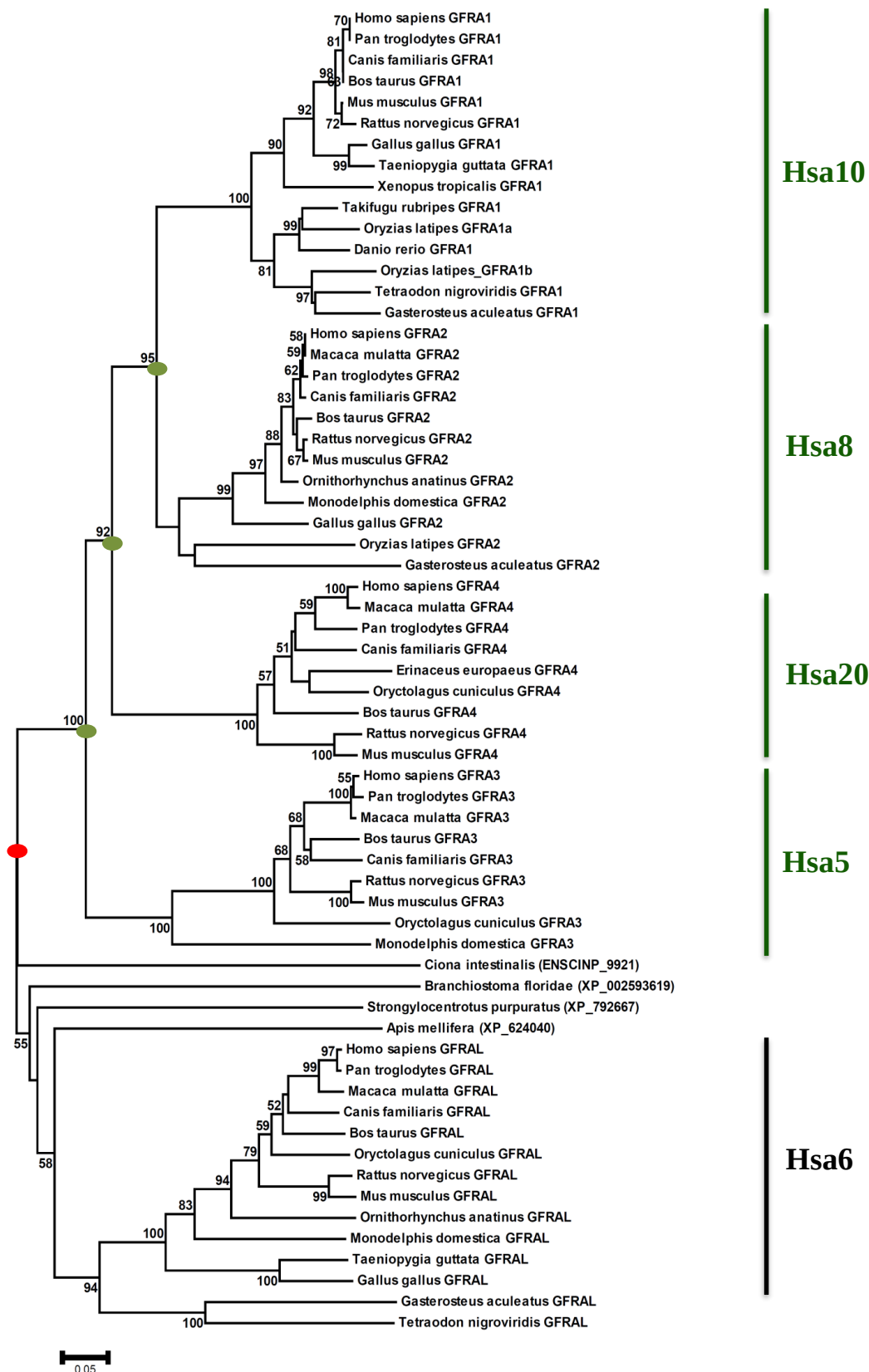
Lysyl oxidase homolog-LOXL



Phylogenetic tree of LOXL family.

Neighbor-Joining tree of the LOXL family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site. * representing another paralog named as LOXL2B by our group.

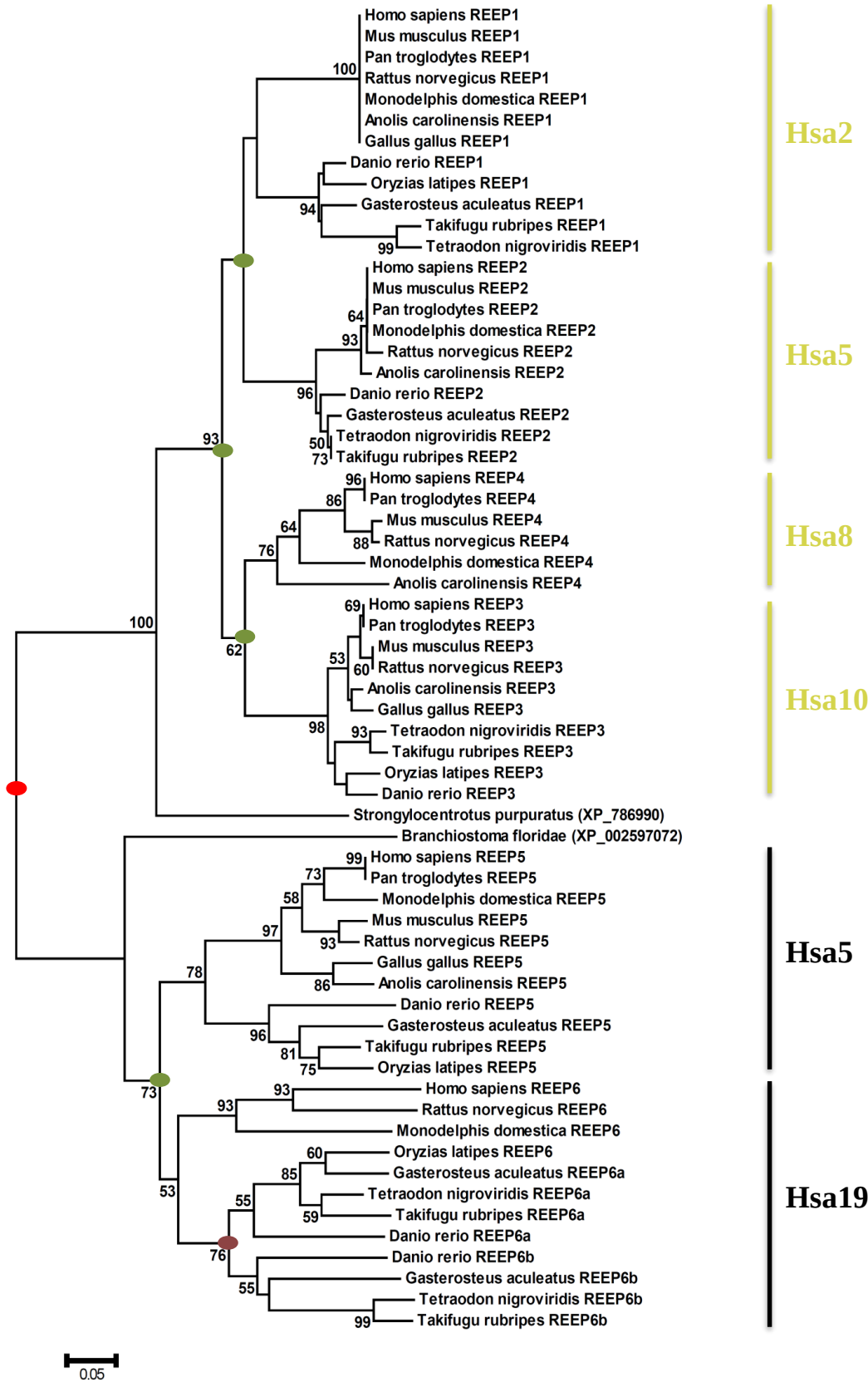
GDNF family receptor alpha-GFRA



Phylogenetic tree of GFRA family.

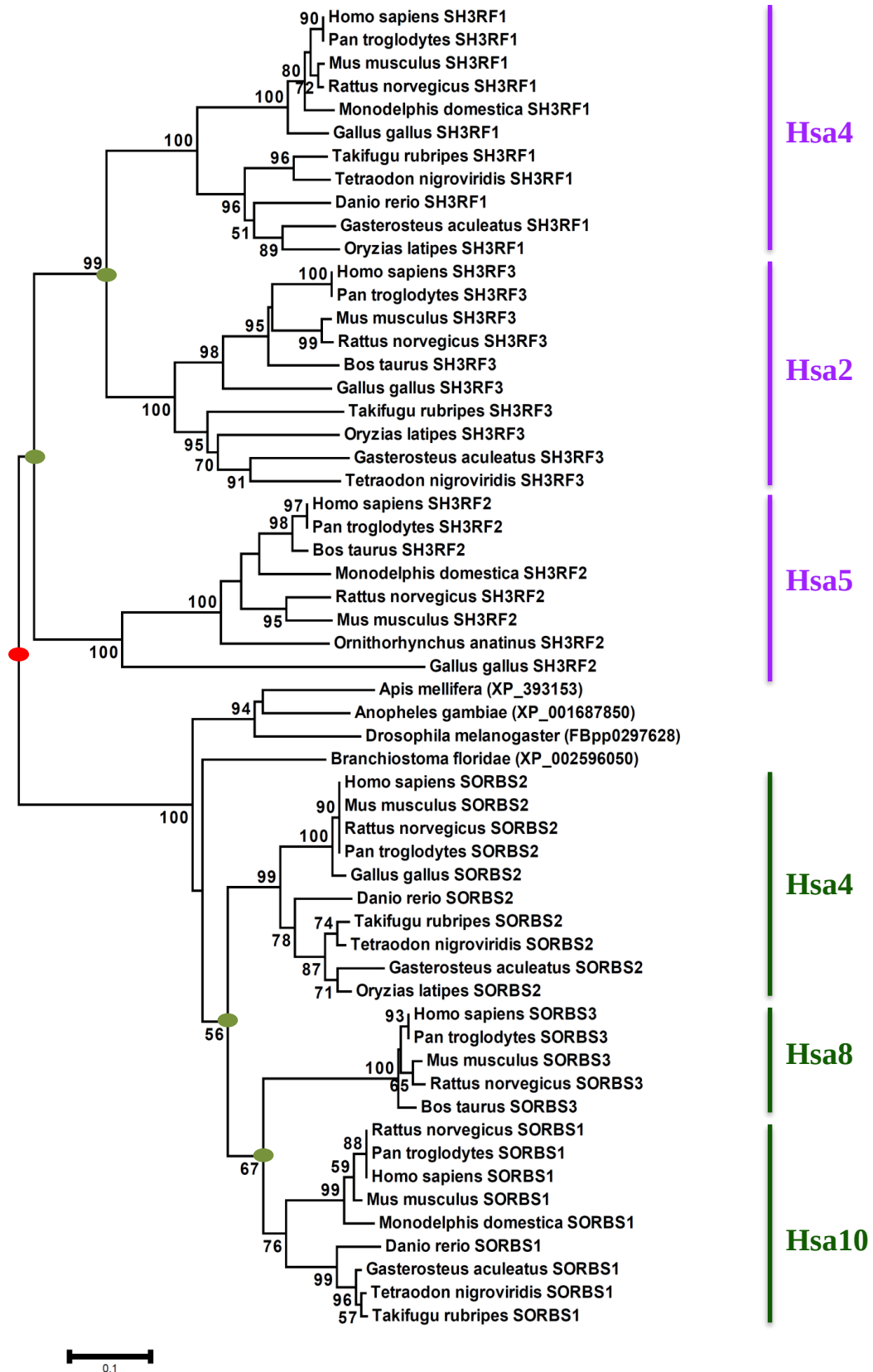
Neighbor-Joining tree of the GFRA family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site.

Receptor expression-enhancing protein-REEP



Phylogenetic tree of REEP family.

Neighbor-Joining tree of the REEP family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site.



Phylogenetic tree of SORBS family.

Neighbor-Joining tree of the SORBS family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site.

Phylogenetic tree showing the relationships between ANK domain proteins. The tree is rooted on the left and branches to the right. The proteins are grouped into three main clusters: ANK2 (top), ANK3 (middle), and ANK1 (bottom). Each cluster contains orthologs from various species, including Homo sapiens, Pan troglodytes, Macaca mulatta, Mus musculus, Rattus norvegicus, Monodelphis domestica, Gallus gallus, Ornithorhynchus anatinus, Tetraodon nigroviridis, Takifugu rubripes, Gasterosteus aculeatus, Danio rerio, Anolis carolinensis, Xenopus tropicalis, Strongylocentrotus purpuratus, and Drosophila melanogaster. Bootstrap values are indicated at the nodes. A scale bar of 0.1 is shown at the bottom left.

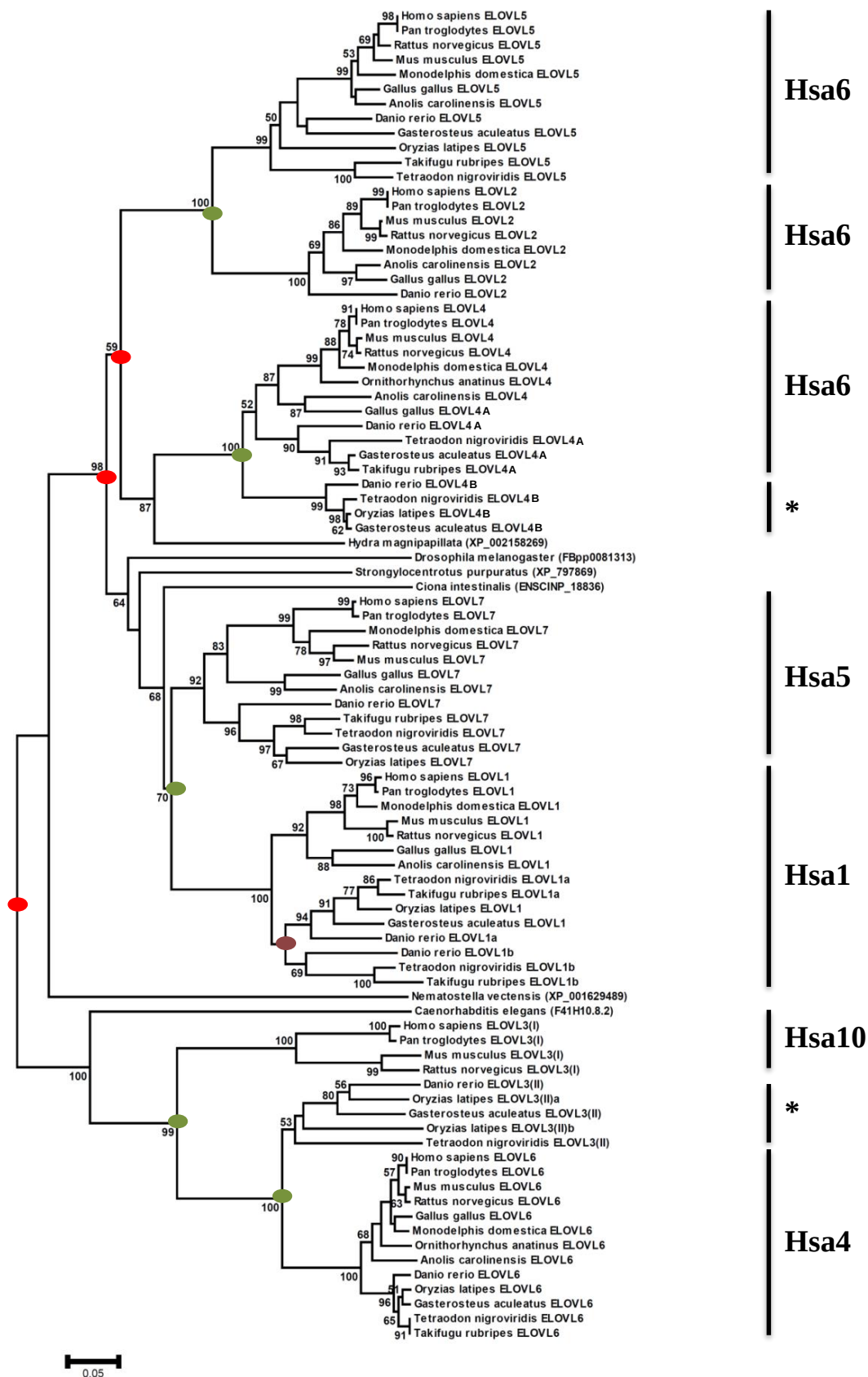
Species and protein names listed in the tree (from top to bottom):

- Homo sapiens ANK2
- Pan troglodytes ANK2
- Macaca mulatta ANK2
- Mus musculus ANK2
- Rattus norvegicus ANK2
- Monodelphis domestica ANK2
- Gallus gallus ANK2
- Ornithorhynchus anatinus ANK2
- Tetraodon nigroviridis ANK2
- Takifugu rubripes ANK2a
- Gasterosteus aculeatus ANK2
- Danio rerio ANK2a
- Takifugu rubripes ANK2b
- Danio rerio ANK2b
- Homo sapiens ANK3
- Pan troglodytes ANK3
- Macaca mulatta ANK3
- Rattus norvegicus ANK3
- Mus musculus ANK3
- Monodelphis domestica ANK3
- Anolis carolinensis ANK3
- Gallus gallus ANK3
- Gasterosteus aculeatus ANK3A
- Danio rerio ANK3A
- Danio rerio ANK3B
- Takifugu rubripes ANK3B
- Oryzias latipes ANK3B
- Gasterosteus aculeatus ANK3B
- Homo sapiens ANK1
- Pan troglodytes ANK1
- Macaca mulatta ANK1
- Rattus norvegicus ANK1
- Mus musculus ANK1
- Felis catus ANK1
- Anolis carolinensis ANK1
- Gallus gallus ANK1
- Xenopus tropicalis ANK1
- Takifugu rubripes ANK1
- Tetraodon nigroviridis ANK1a
- Gasterosteus aculeatus ANK1a
- Oryzias latipes ANK1
- Danio rerio ANK1
- Tetraodon nigroviridis ANK1b
- Gasterosteus aculeatus ANK1b
- Strongylocentrotus purpuratus (XP_003725772)
- Drosophila melanogaster (FBpp0088239)
- Homo sapiens ANKRD50
- Pan troglodytes ANKRD50
- Felis catus ANKRD50
- Mus musculus ANKRD50
- Rattus norvegicus ANKRD50
- Monodelphis domestica ANKRD50
- Gallus gallus ANKRD50
- Anolis carolinensis ANKRD50
- Danio rerio ANKRD50
- Caenorhabditis elegans (R11A8.7a)
- Hydra magnipapillata (XP_002157501)
- Drosophila melanogaster (FBpp0293580)
- Strongylocentrotus purpuratus (XP_001199736)
- Ciona savignyi (ENSCSAVP_6135)
- Homo sapiens ANKRD17
- Pan troglodytes ANKRD17
- Mus musculus ANKRD17
- Monodelphis domestica ANKRD17
- Anolis carolinensis ANKRD17
- Homo sapiens ANKHD1
- Felis catus ANKHD1
- Mus musculus ANKHD1
- Rattus norvegicus ANKHD1
- Gallus gallus ANKHD1
- Danio rerio ANKHD1
- Gasterosteus aculeatus ANKHD1
- Tetraodon nigroviridis ANKHD1
- Takifugu rubripes ANKHD1

Phylogenetic tree of ANK family.

Neighbor-Joining tree of the ANK family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site. * representing another paralog which is missing in tetrapods named as ANK3B by our group.

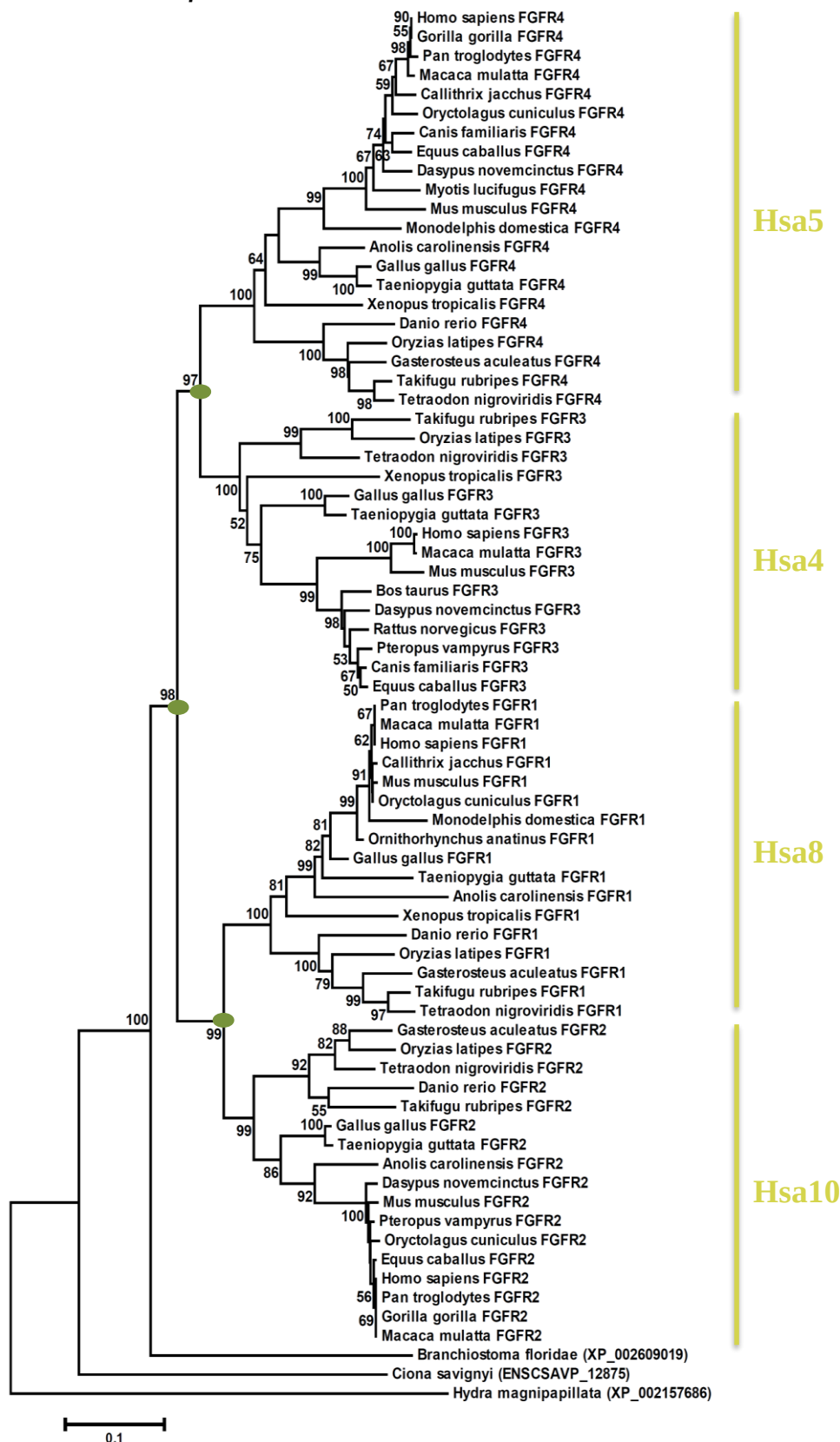
Elongation of very long chain fatty acids protein-ELOVL



Phylogenetic tree of ELOVL family.

Neighbor-Joining tree of the ELOVL family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site. * representing another paralogs which are missing in tetrapods named as ELOVL4B and ELOVL3(II) by our group.

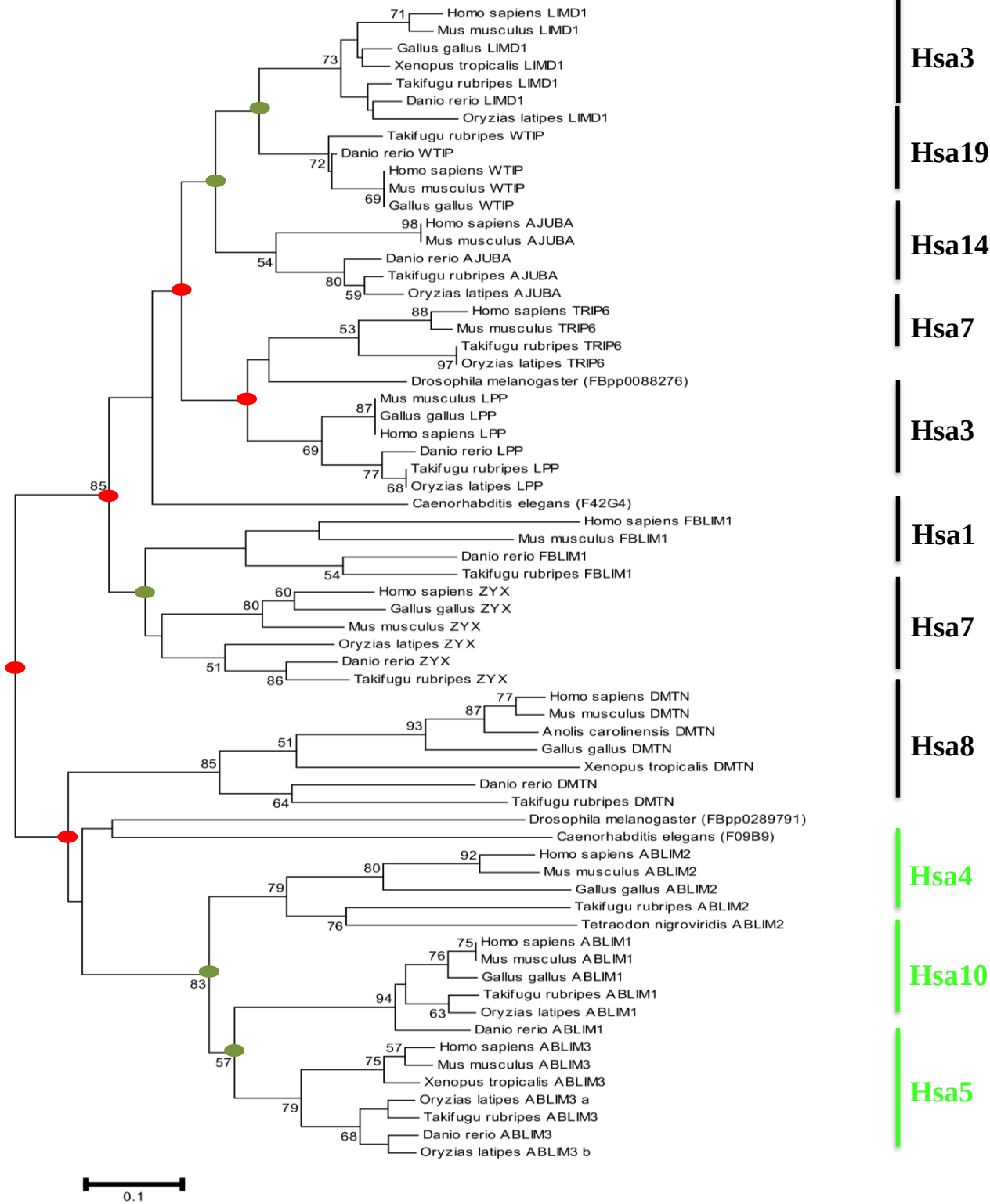
Fibroblast growth factor receptor-FGFR



Phylogenetic tree of FGFR family.

Neighbor-Joining tree of the FGFR family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site.

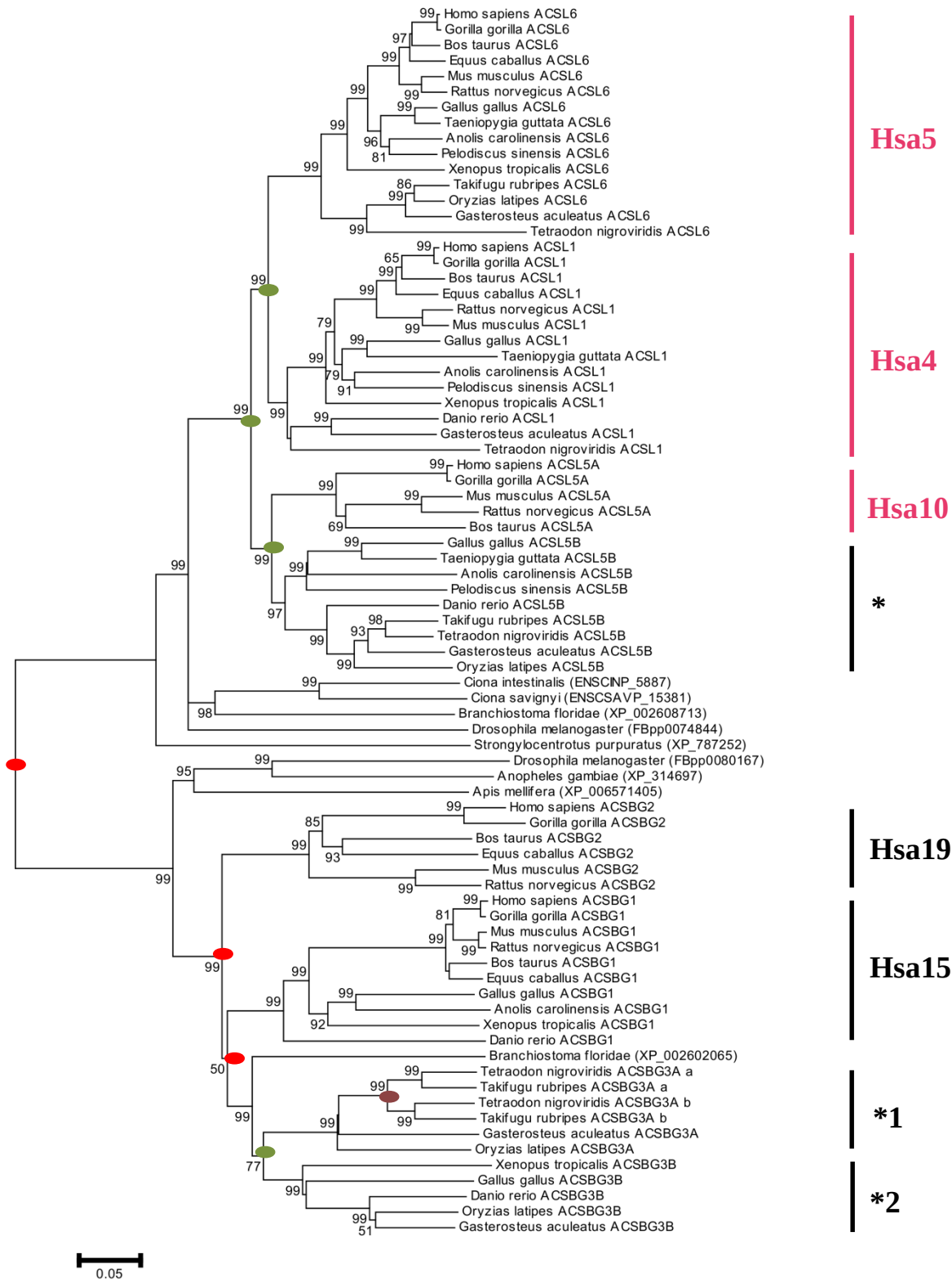
Actin Binding LIM protein-ABLIM



Phylogenetic tree of ABLIM family.

Neighbor-Joining tree of the ABLIM family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site.

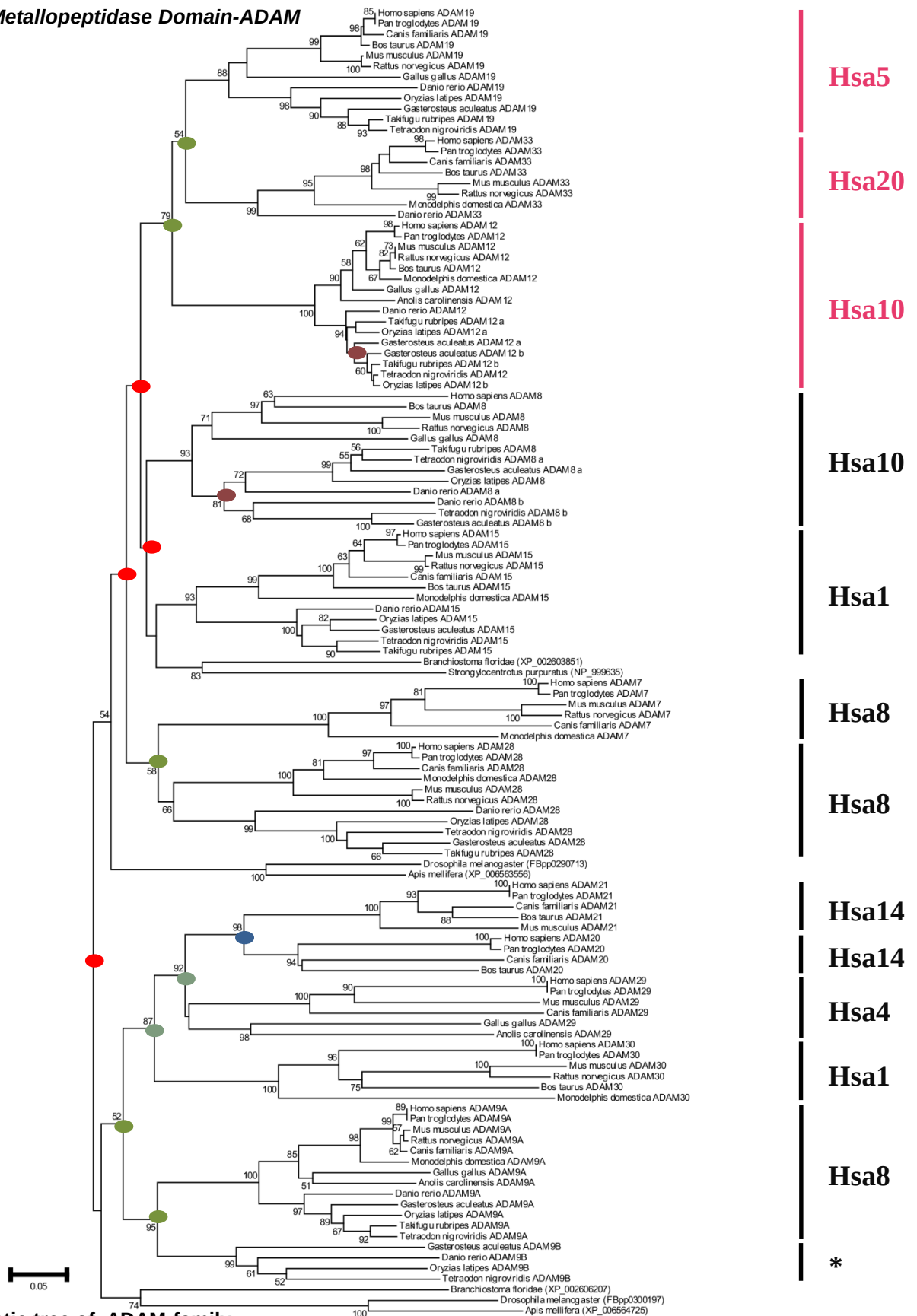
Acyl-CoA Synthetase Family-ACSL



Phylogenetic tree of ACSL family.

Neighbor-Joining tree of the ACSL family members. Uncorrected p-distance was used. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site. * and *2 shows another paralog with deleted mammals, *1 represents another paralog which is missing in tetrapods. These are named as ACSL5B, ACSBG3B and ACSBG3A by our group.

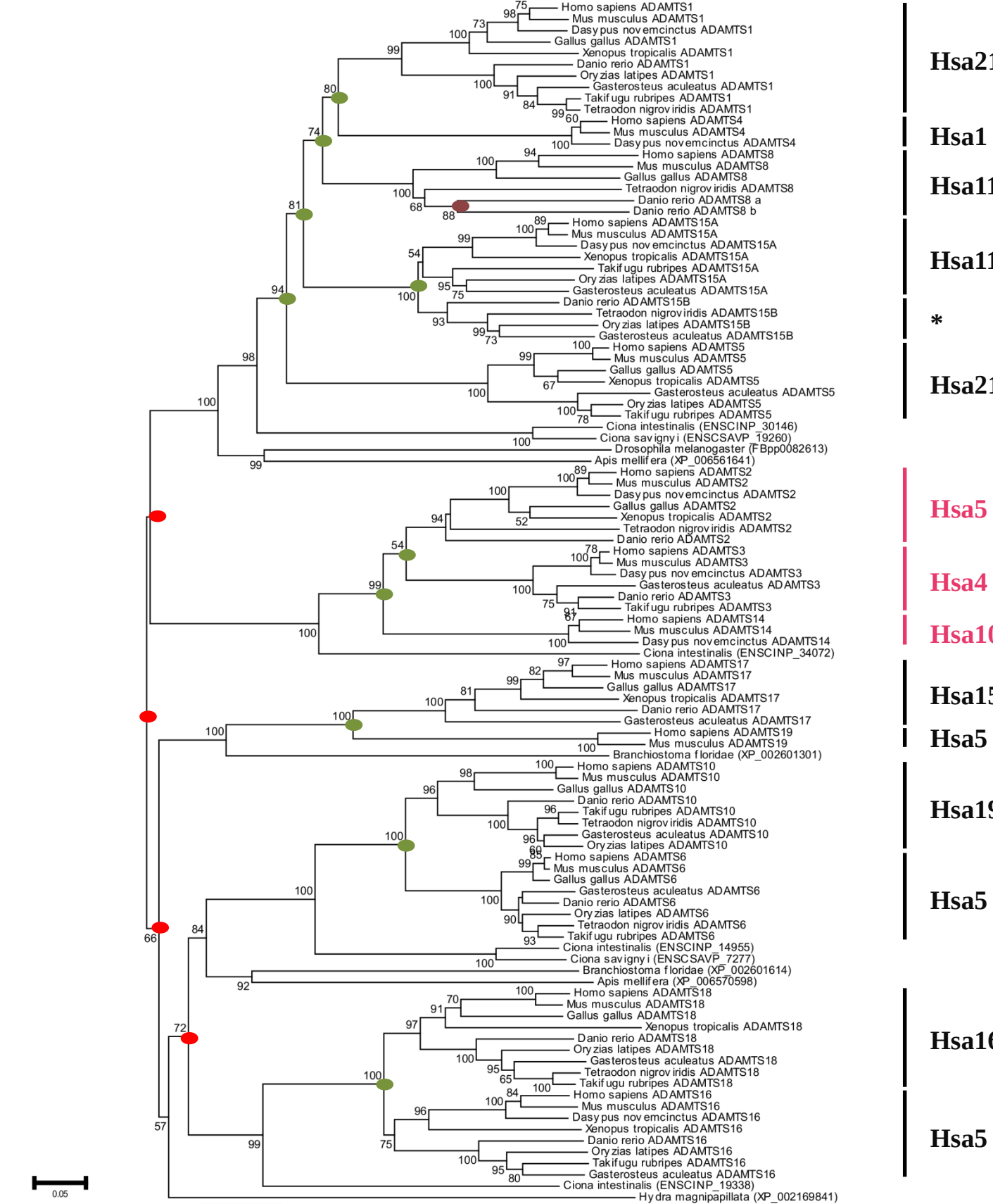
ADAM Metallopeptidase Domain-ADAM



Phylogenetic tree of ADAM family.

Neighbor-Joining tree of the ADAM family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site. * is another paralog which is missing in tetrapods, named as ADAM9B by our group.

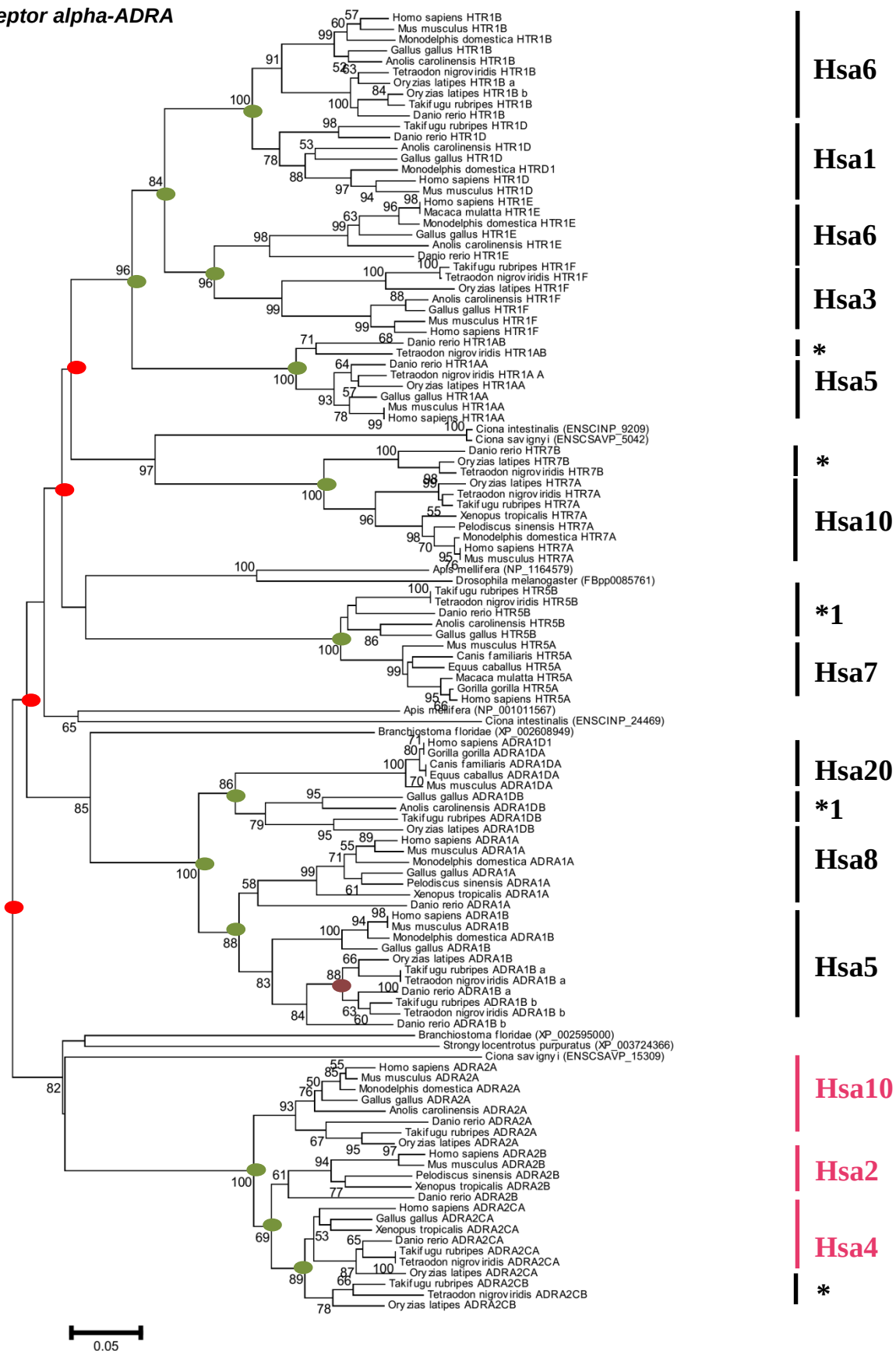
ADAM Metallopeptidase with Thrombospondin Type 1 Motif-ADAMTS



Phylogenetic tree of ADAMTS family.

Neighbor-Joining tree of the ADAMTS family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site. * representing another paralog which is missing in tetrapods, named as ADAMTS15B by our group.

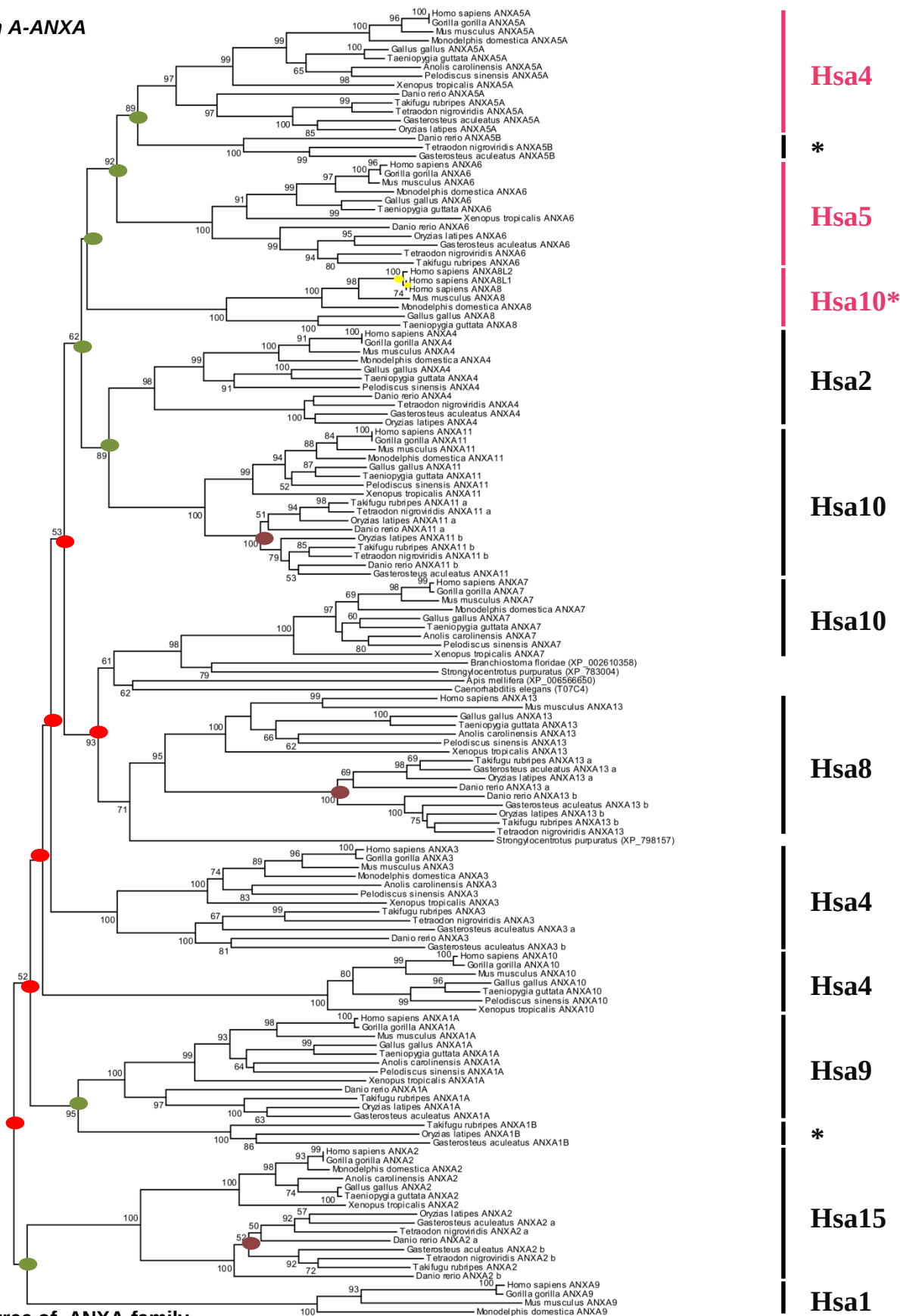
Adrenoceptor α -ADRA



Phylogenetic tree of ADRA family.

Neighbor-Joining tree of the ADRA family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site. * show another paralogs which are missing in tetrapods named as HTR1AB, HTR7B and ADRA2CB while *1 show another paralogs which are missing in mammals named as HTR5B and ADRA1D.

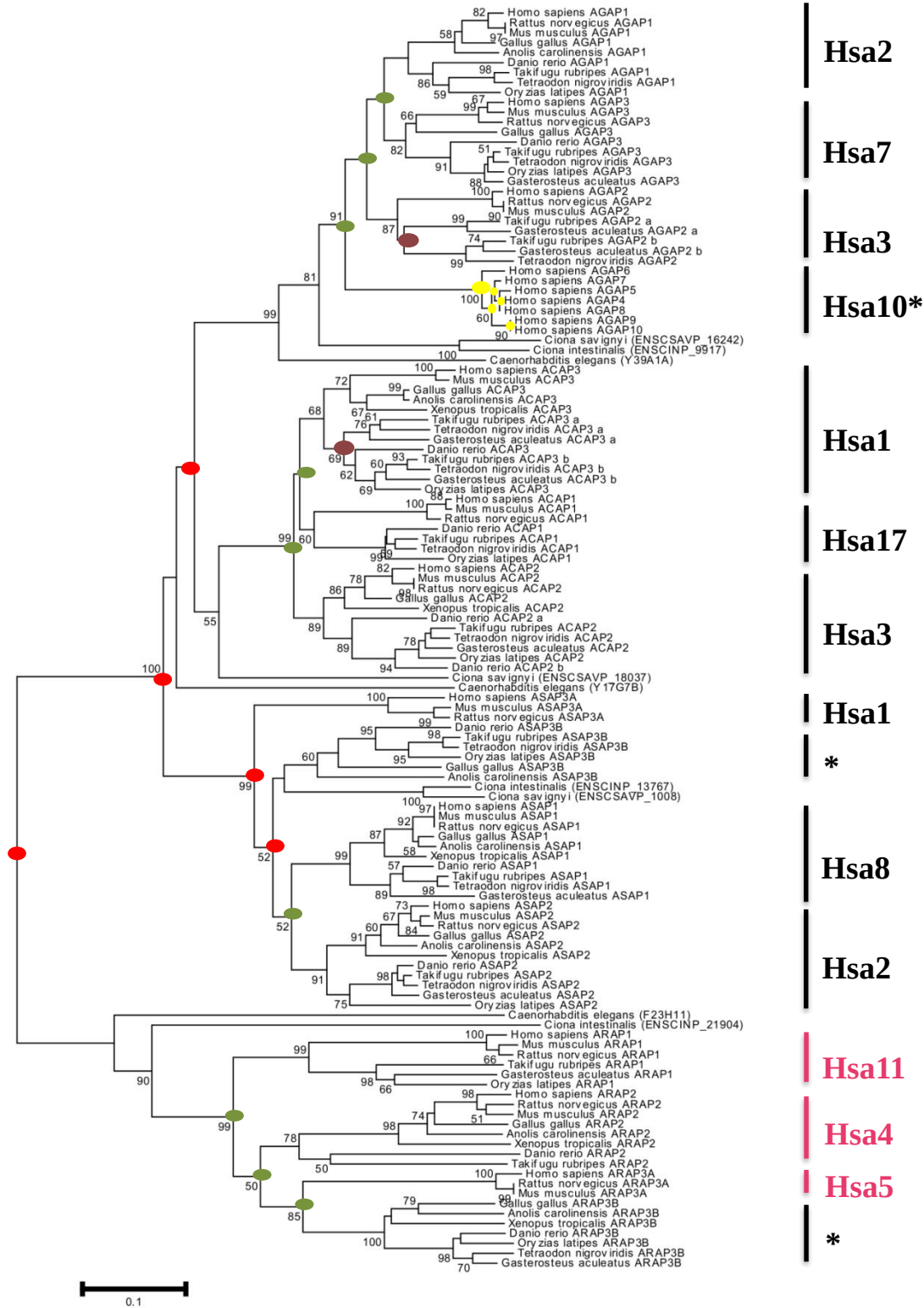
Annexin A-ANXA



Phylogenetic tree of ANXA family.

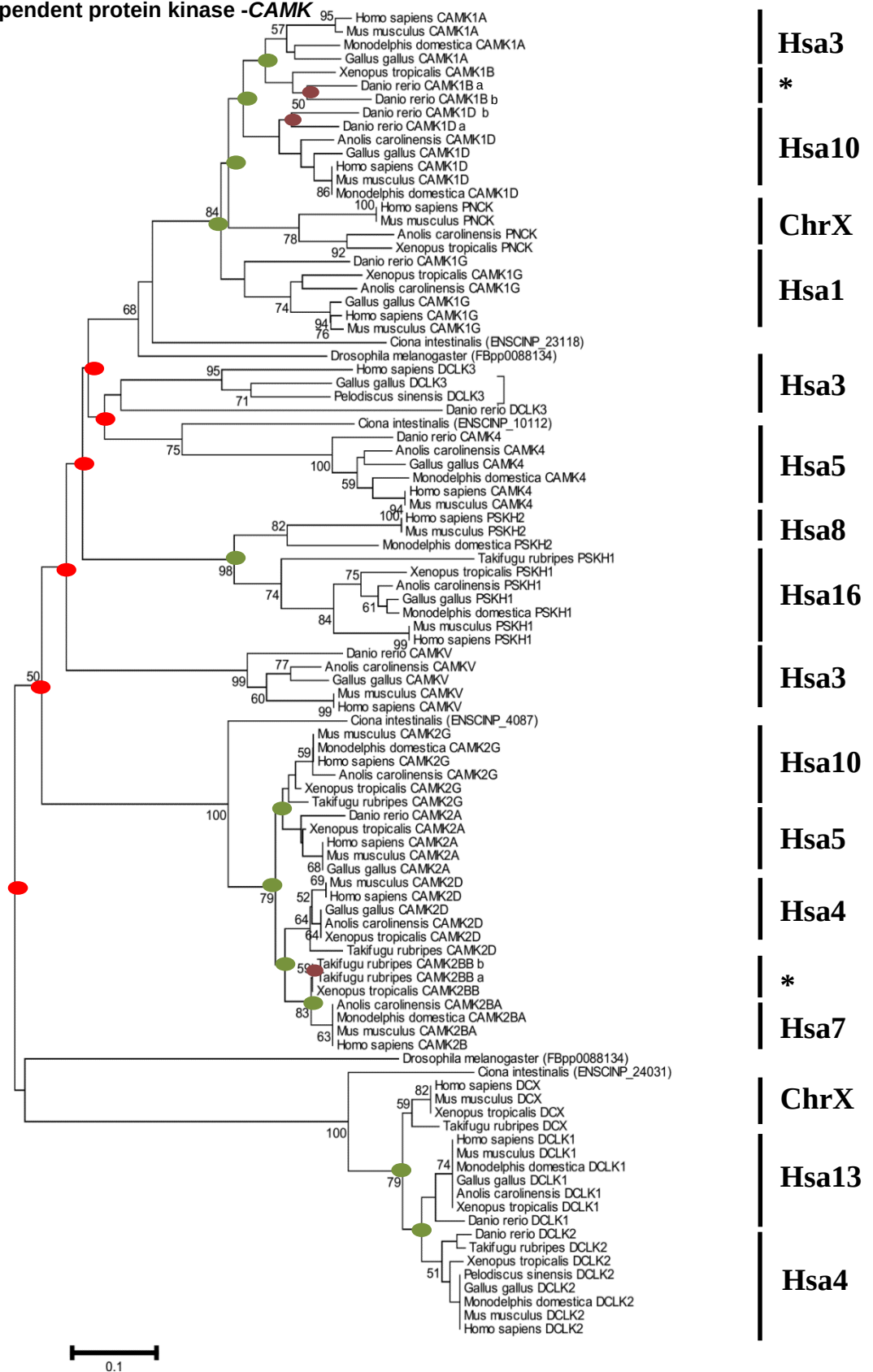
Neighbor-Joining tree of the ANXA family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site. 10* shows two human specific duplication on chromosome 10. * represents another paralogs which are missing in tetrapods. These are named as ANXA5B and ANXA1B, respectively by our group.

ArfGAP(Ankyrin Repeat and PH Domain)-ARAP



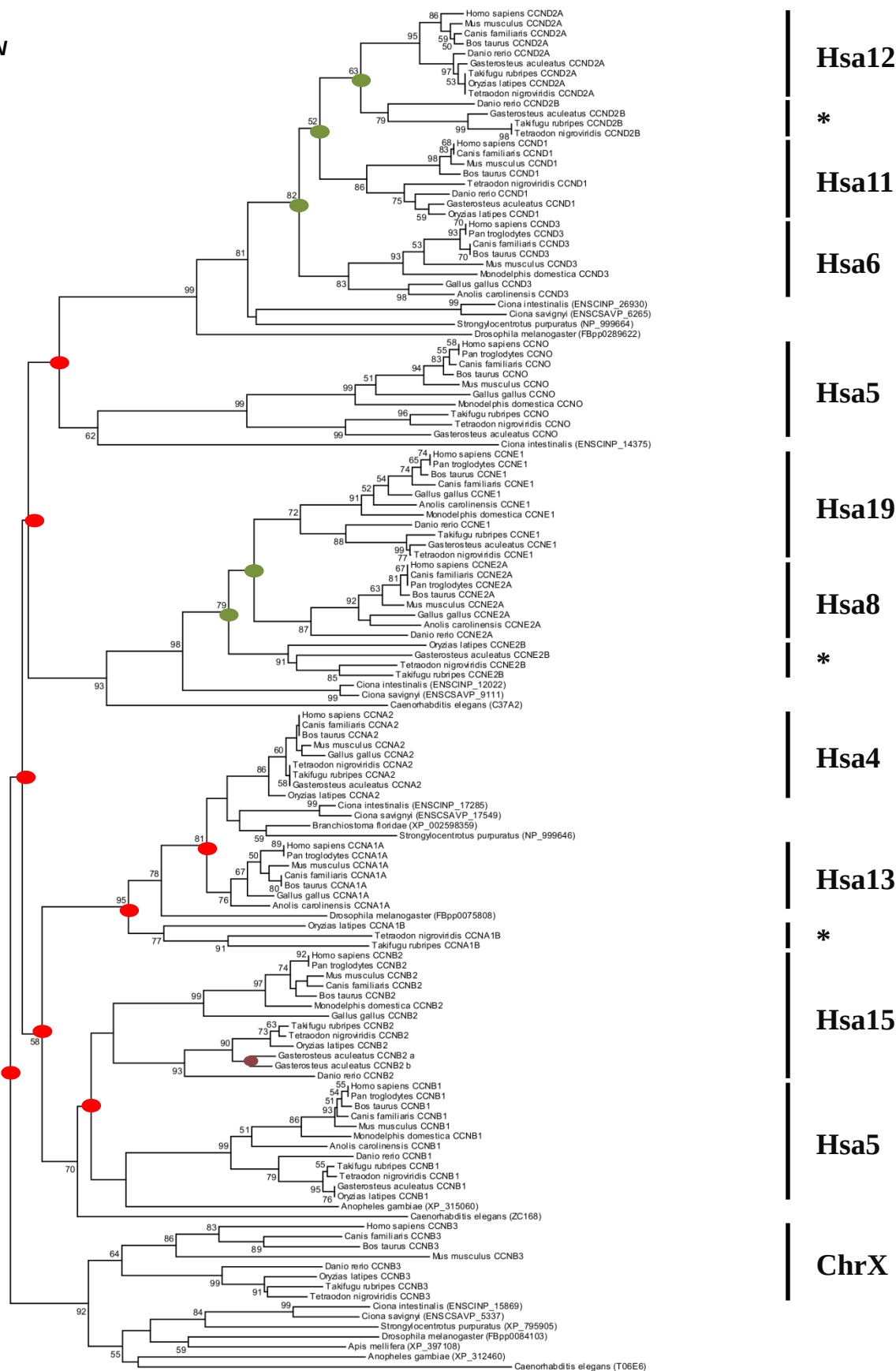
Phylogenetic tree of ARAP family.

Neighbor-Joining tree of the ARAP family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site. * shows another paralog whose mammals are missing. 10* shows 6 human specific duplication on chromosome 10.



Phylogenetic tree of CAMK family.

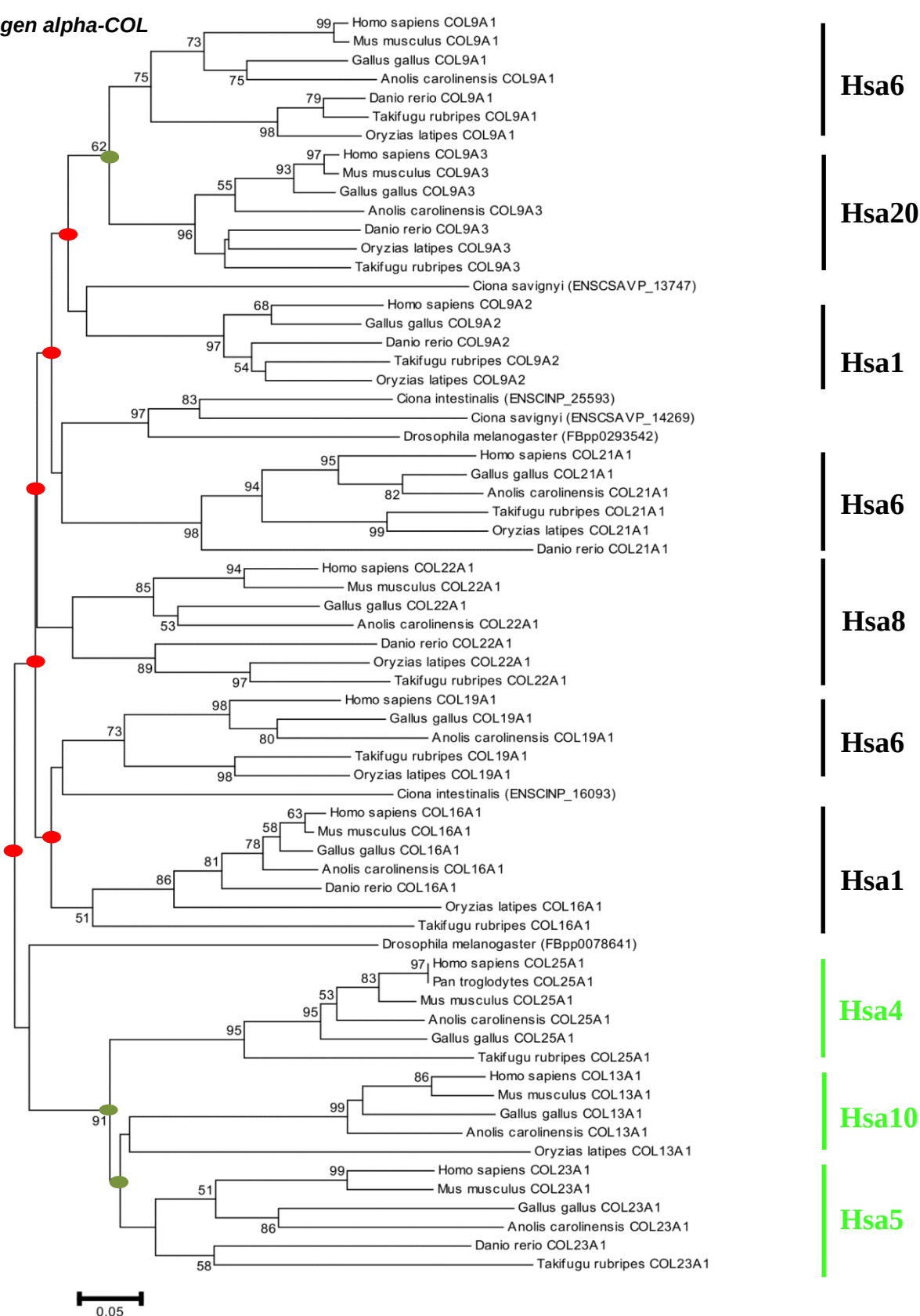
Neighbor-Joining tree of the CAMK family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site. * shows another paralogs which are missing in amniotes named as CAMK1B and CAMK2BB.



Phylogenetic tree of CCN family.

Neighbor-Joining tree of the CCN family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site. * shows another paralogs which are missing in tetrapods. These are named as CCND2B, CCNE2B and CCNA1B, respectively by our group.

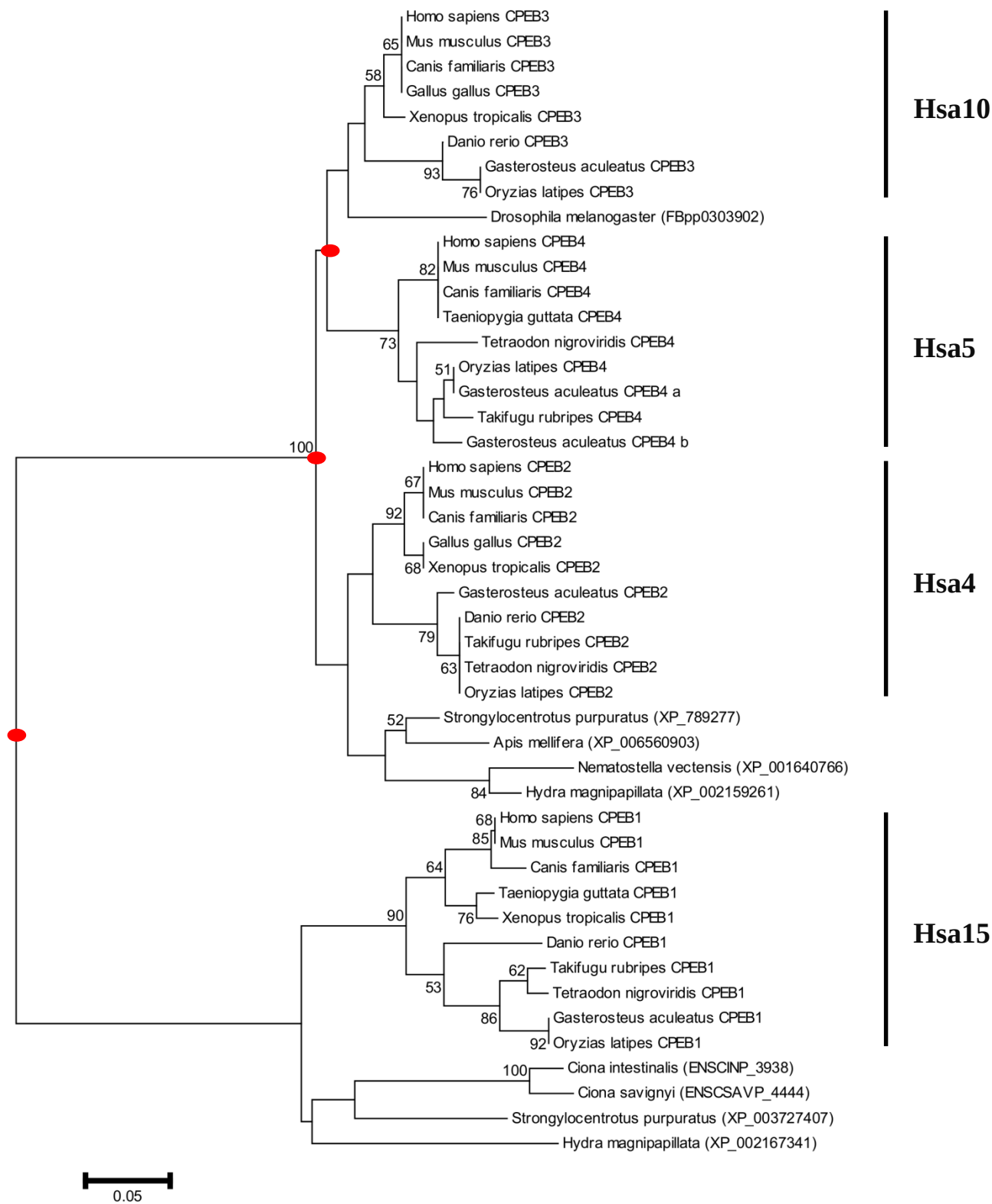
Collagen alpha-COL



Phylogenetic tree of COL family.

Neighbor-Joining tree of the COL family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site.

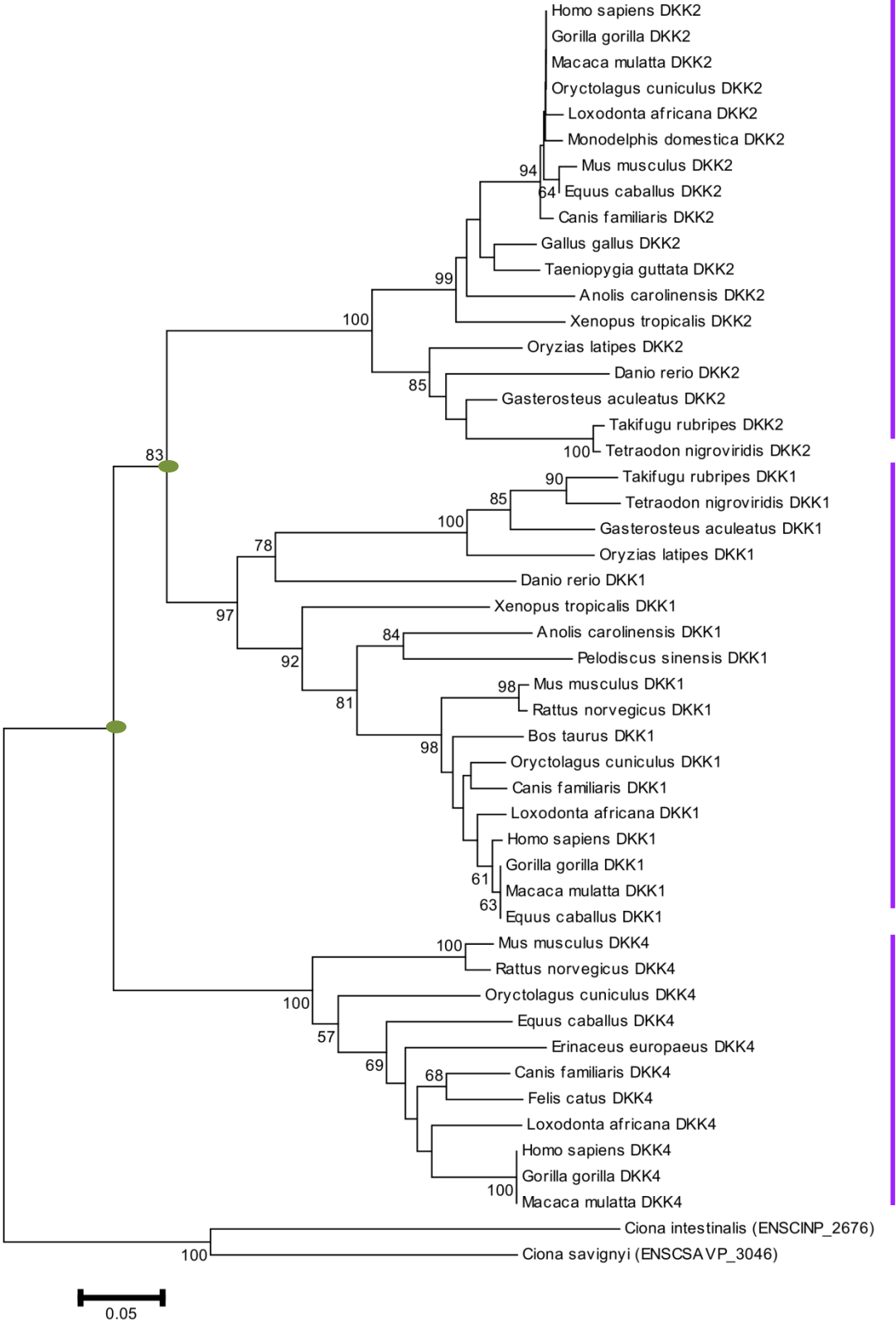
Cytoplasmic Polyadenylation Element Binding Protein-CPEB



Phylogenetic tree of CPEB family.

Neighbor-Joining tree of the CPEB family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site.

Dickkopf WNT Signaling Pathway Inhibitor -DKK



Hsa4

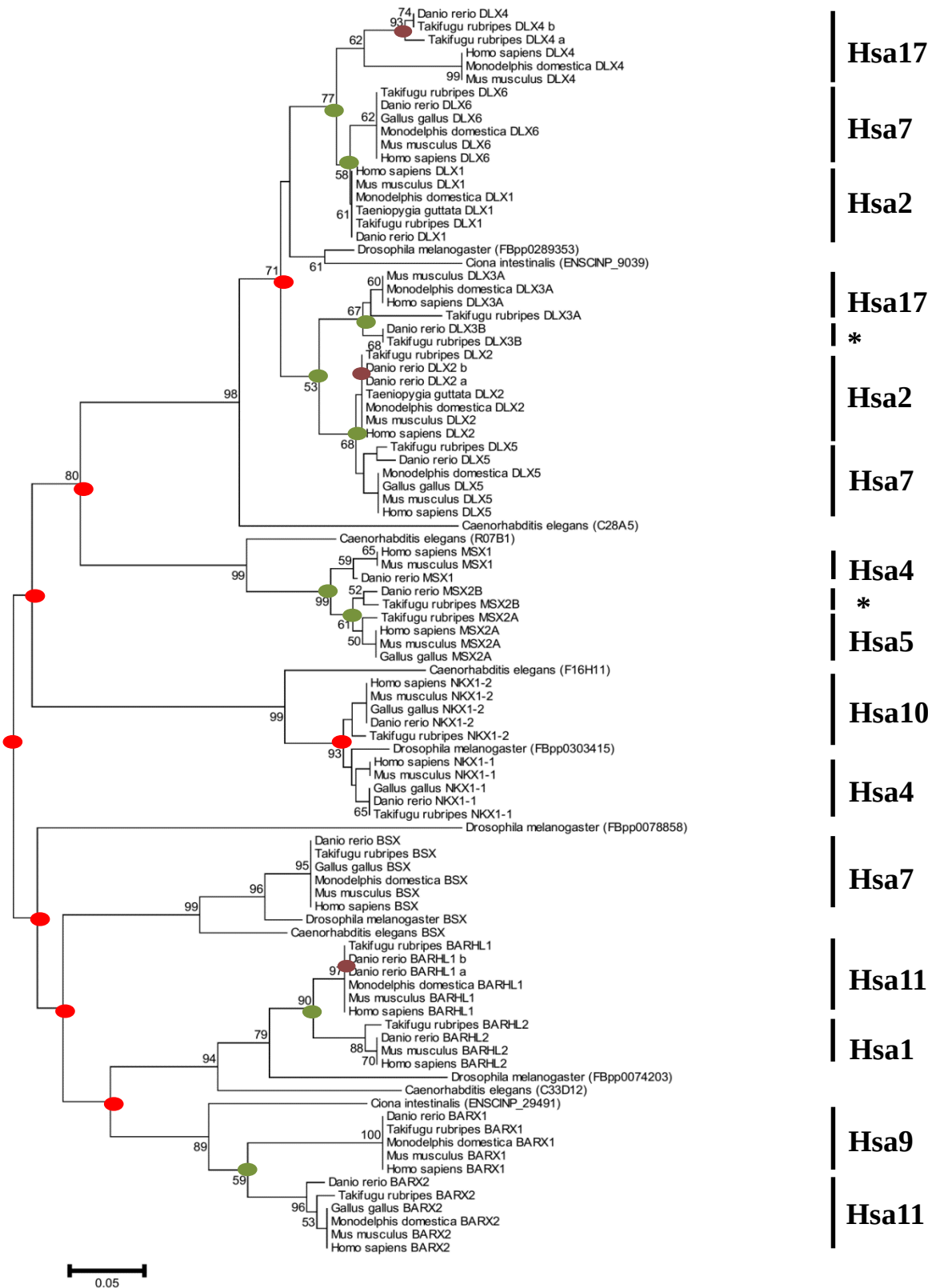
Hsa10

Hsa8

Phylogenetic tree of DKK family.

Neighbor-Joining tree of the DKK family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site.

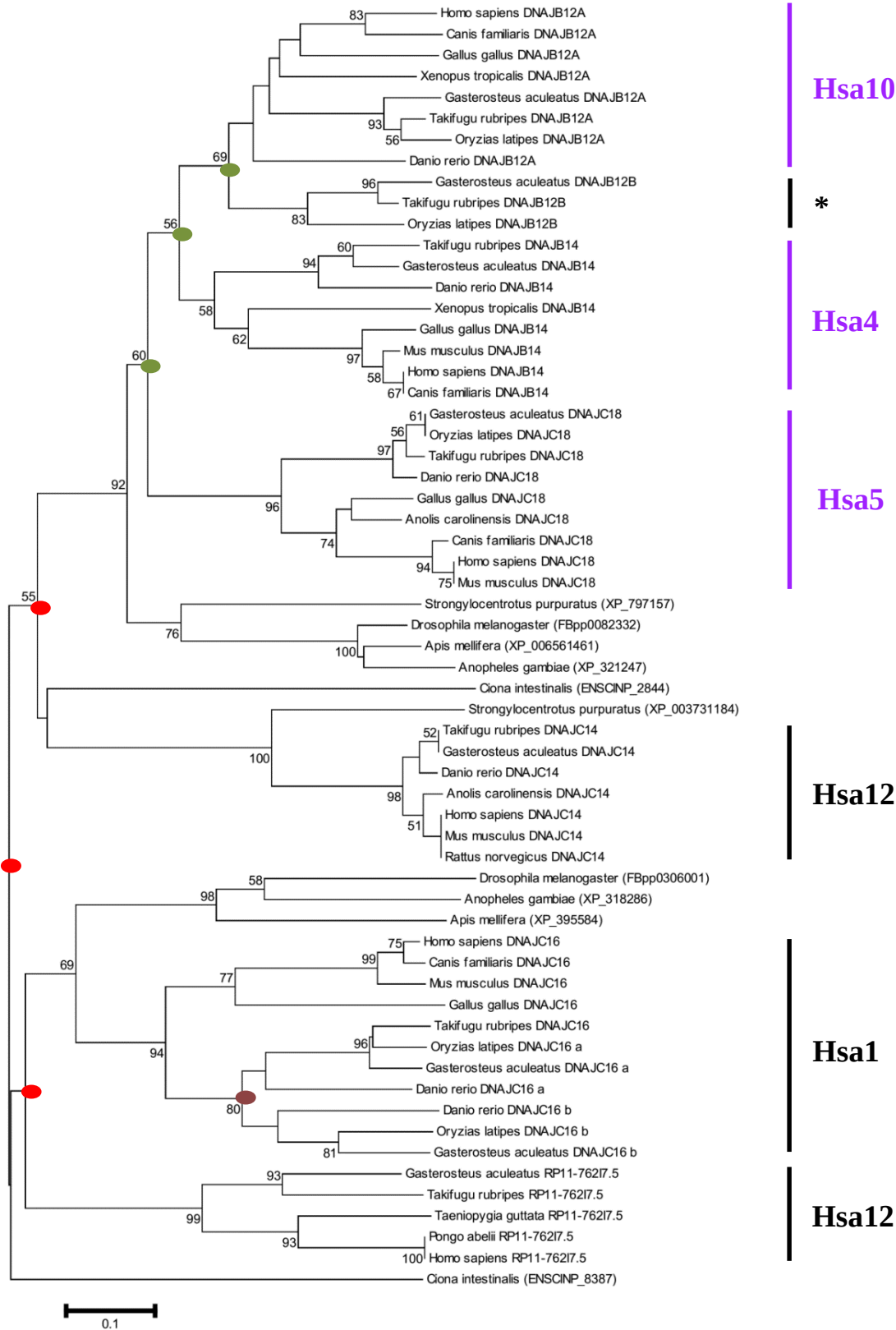
Distal-less homeobox -DLX



Phylogenetic tree of DLX family.

Neighbor-Joining tree of the DLX family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site. * represent paralogs which are missing in tetrapods named as DLX3B and MSX2B by our group.

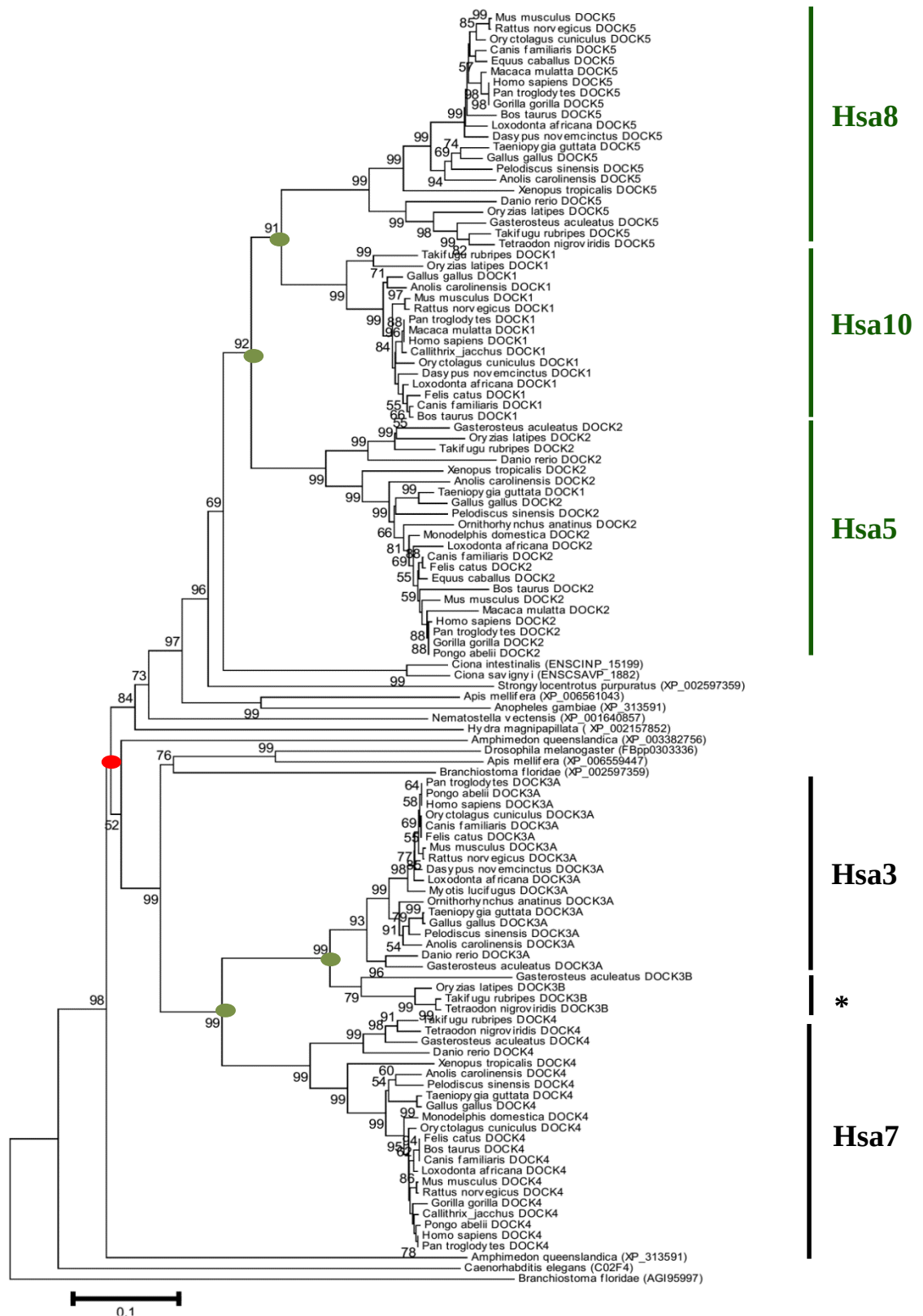
DNAJ (Hsp40) homolog -DNAJ



Phylogenetic tree of DNAJ family.

Neighbor-Joining tree of the DNAJ family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site. * shows another paralogs which is missing in tetrapods. * represents paralog which is missing in tetrapods named as DNAJB12B by our group.

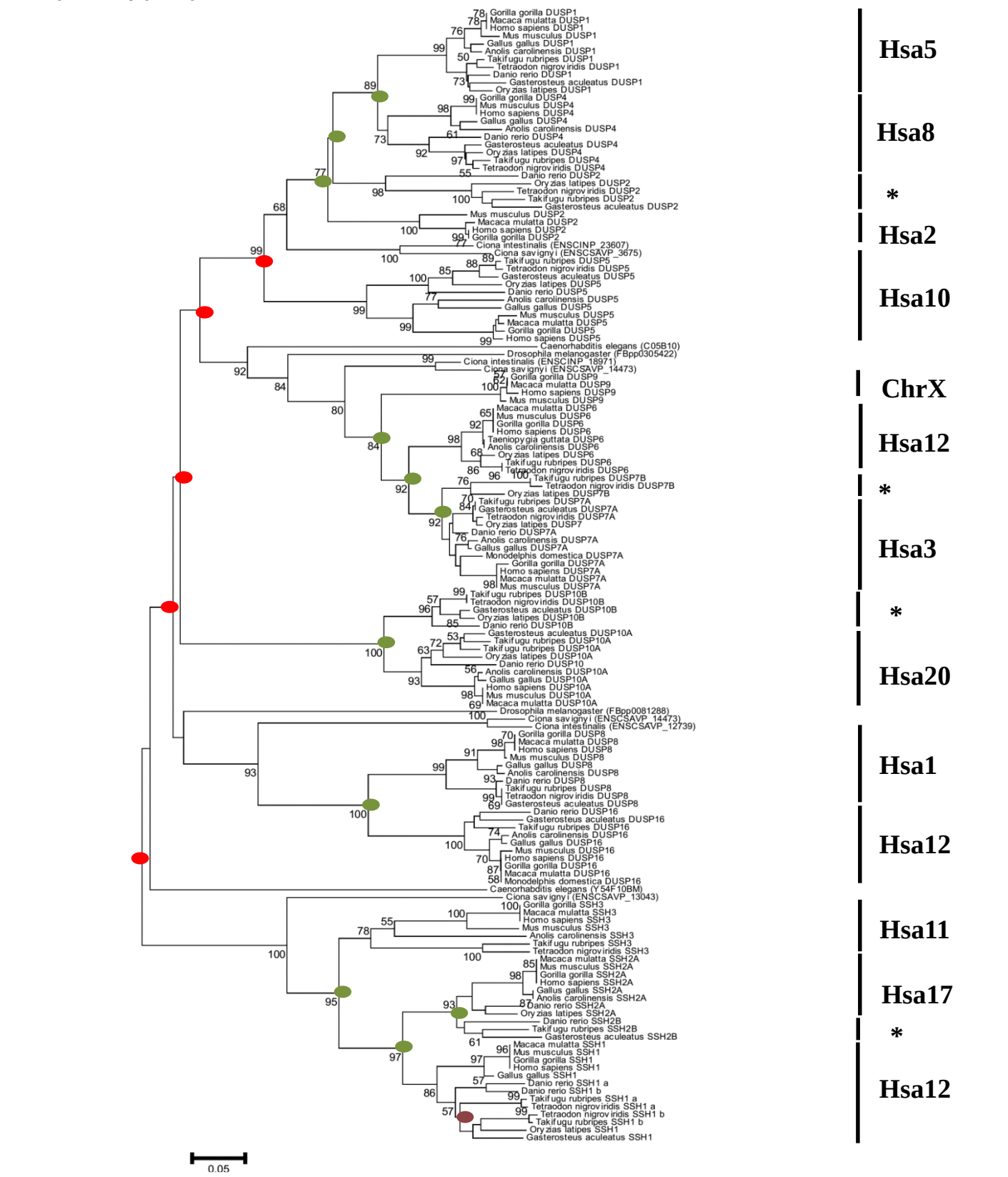
Dedicator of cytokinesis DOCK



Phylogenetic tree of DOCK family.

Neighbor-Joining tree of the DOCK family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site. * shows another paralog which is missing in tetrapods named as DOCK3B by our group.

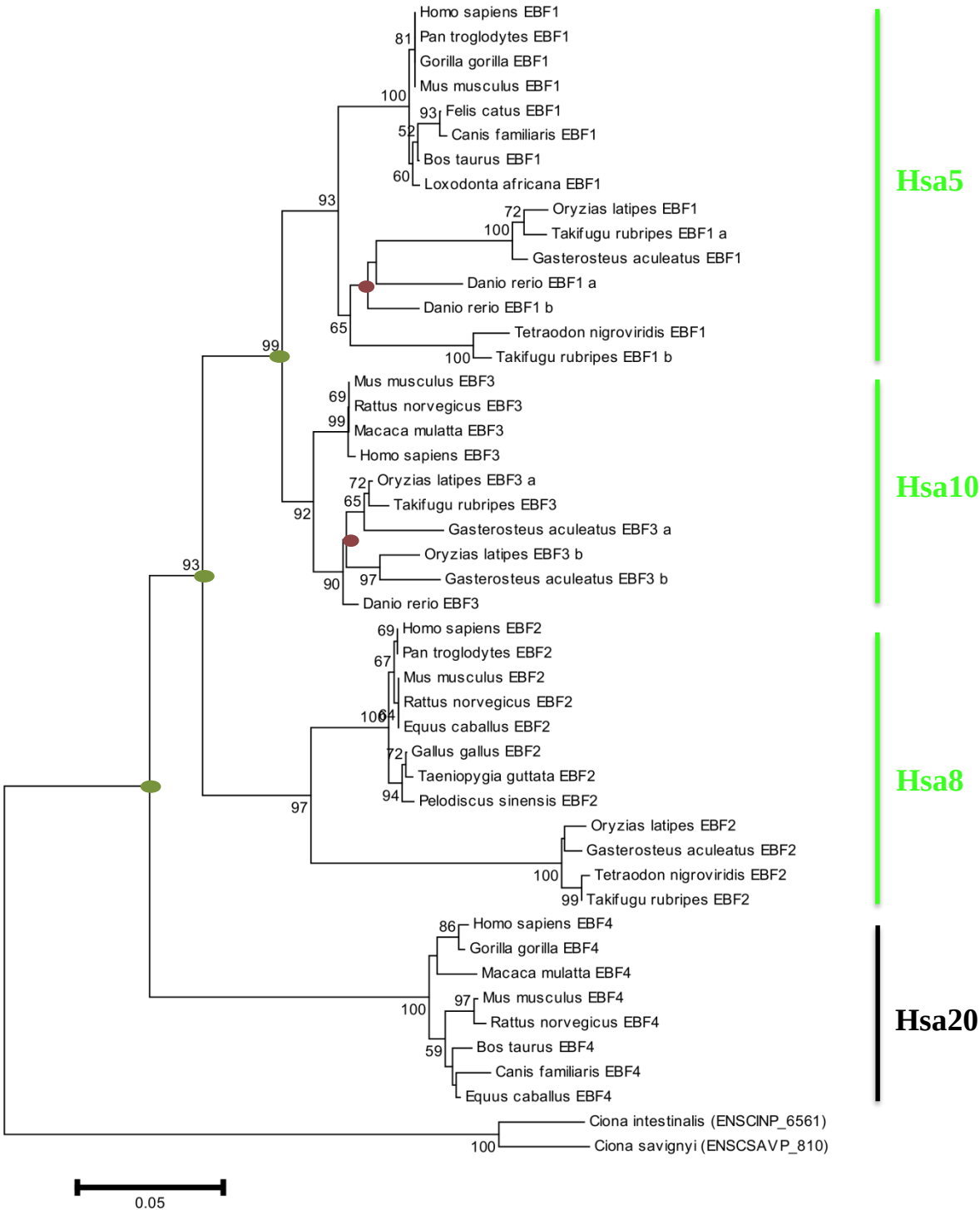
Dual specificity phosphatase -DUSP



Phylogenetic tree of DUSP family.

Neighbor-Joining tree of the DUSP family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site. * shows another paralogs which is missing in tetrapods named as DUSP2, DUSP7B, DUSP10B, SSH2B by our group.

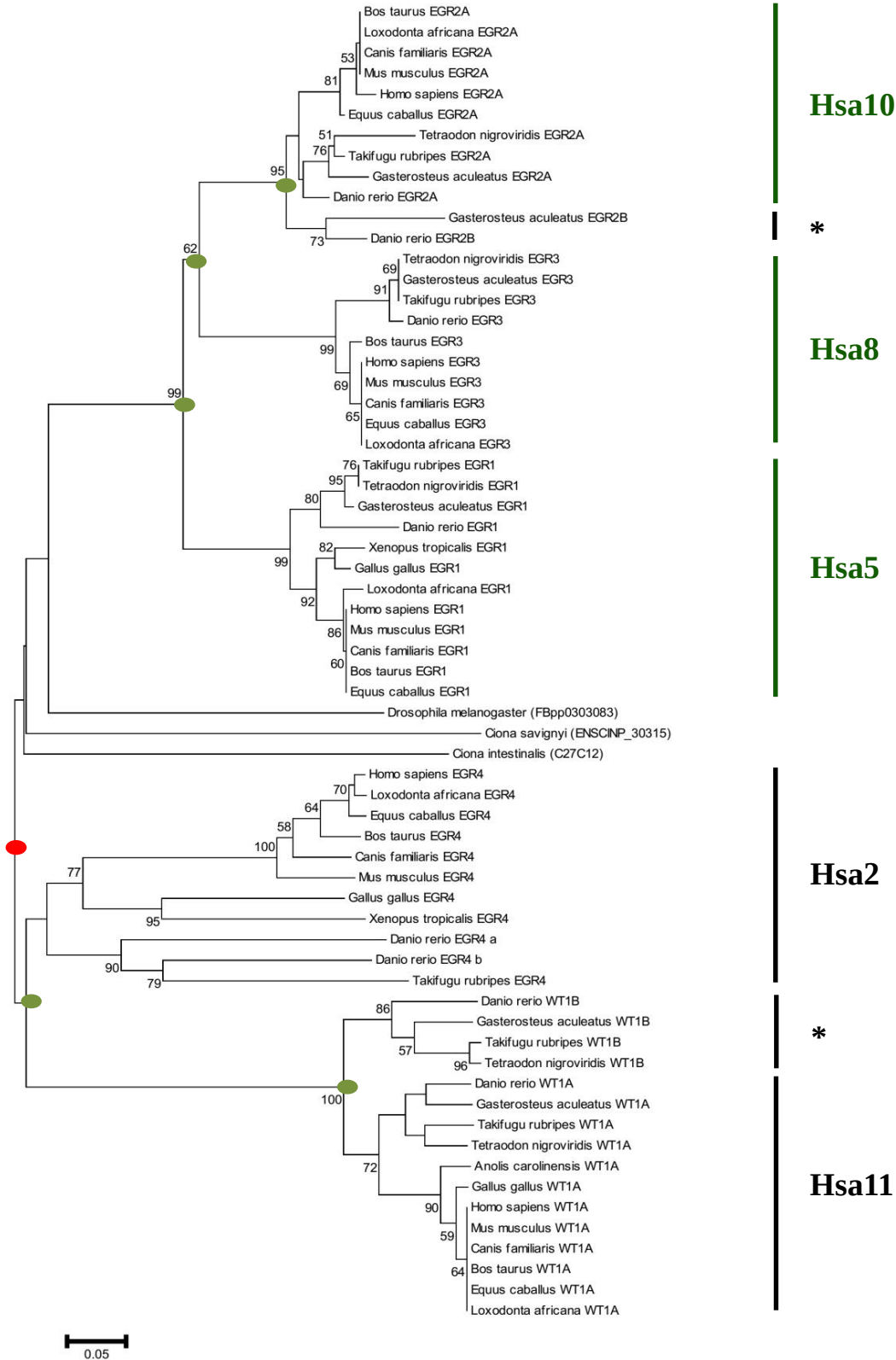
Early B-cell Factor-EBF



Phylogenetic tree of EBF family.

Neighbor-Joining tree of the EBF family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site.

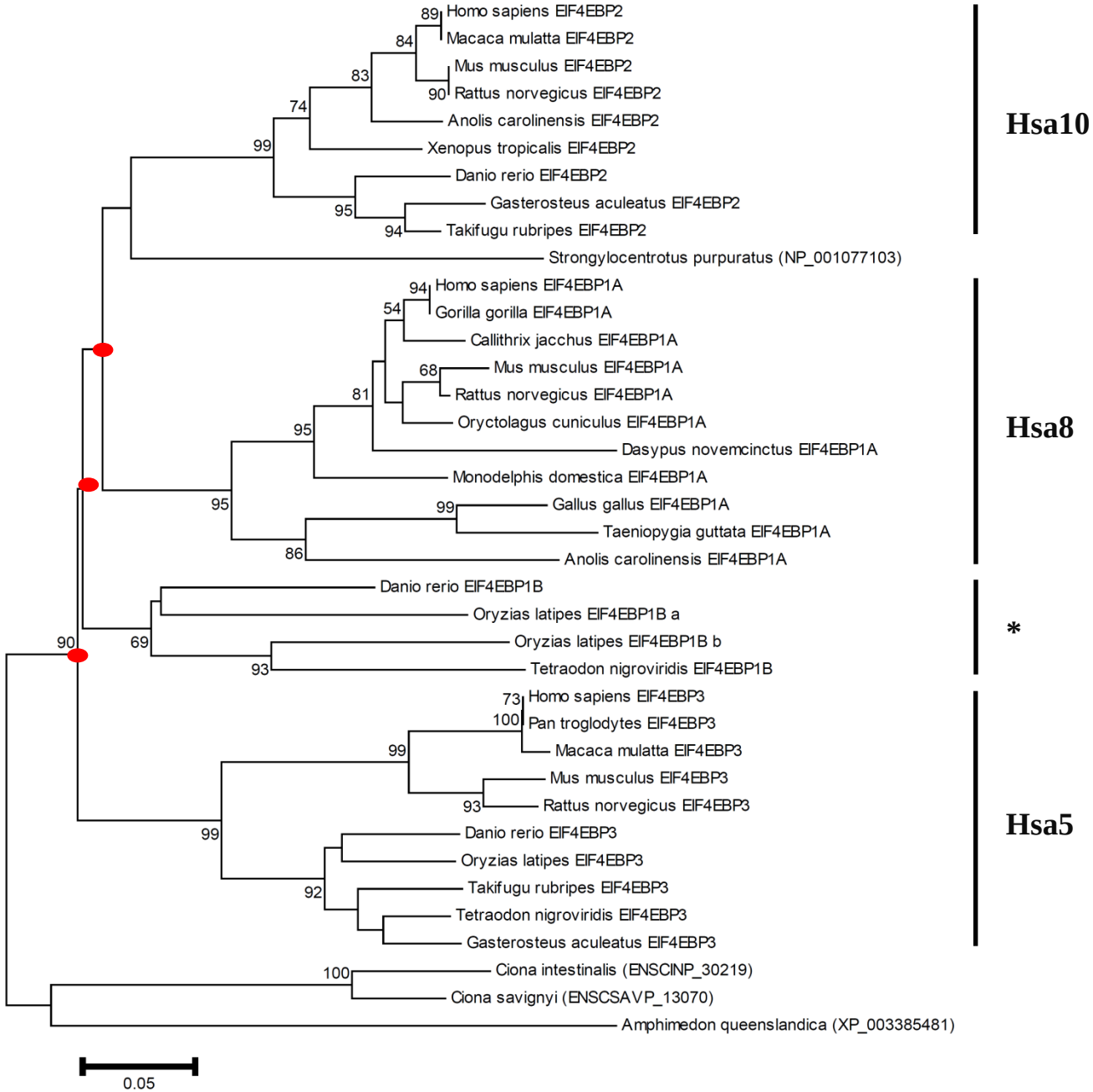
Early Growth Response-EGR



Phylogenetic tree of EGR family.

Neighbor-Joining tree of the EGR family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site. * represent paralogs which are missing tetrapods named as EGR2B and WT1B by our group.

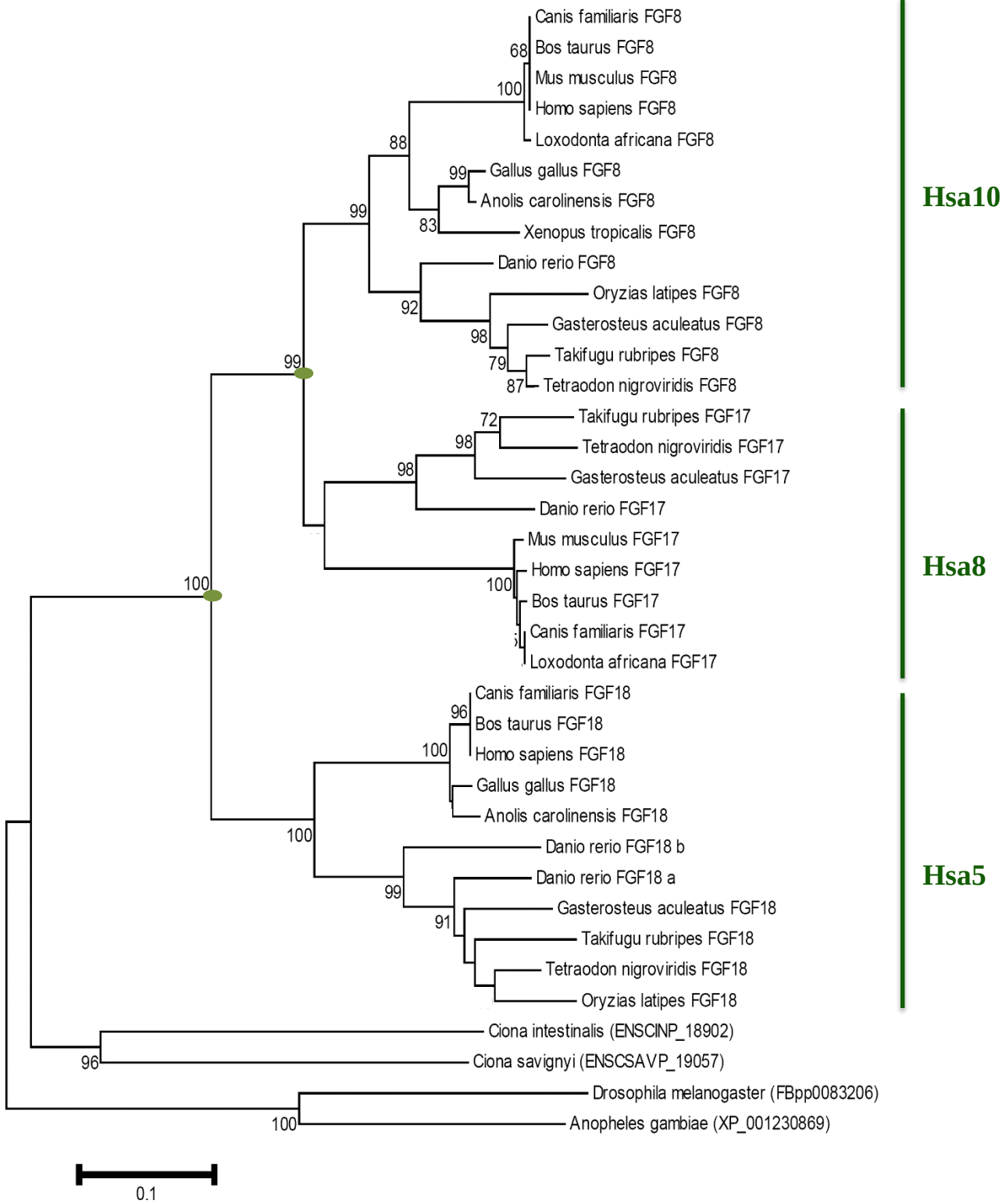
Eukaryotic Translation Initiation Factor 4E Binding Protein-EIF4EBP



Phylogenetic tree of EIF4EBP family.

Neighbor-Joining tree of the EIF4EBP family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site. * shows another paralogs which is missing in tetrapods, named as EIF4EBP1B by our group.

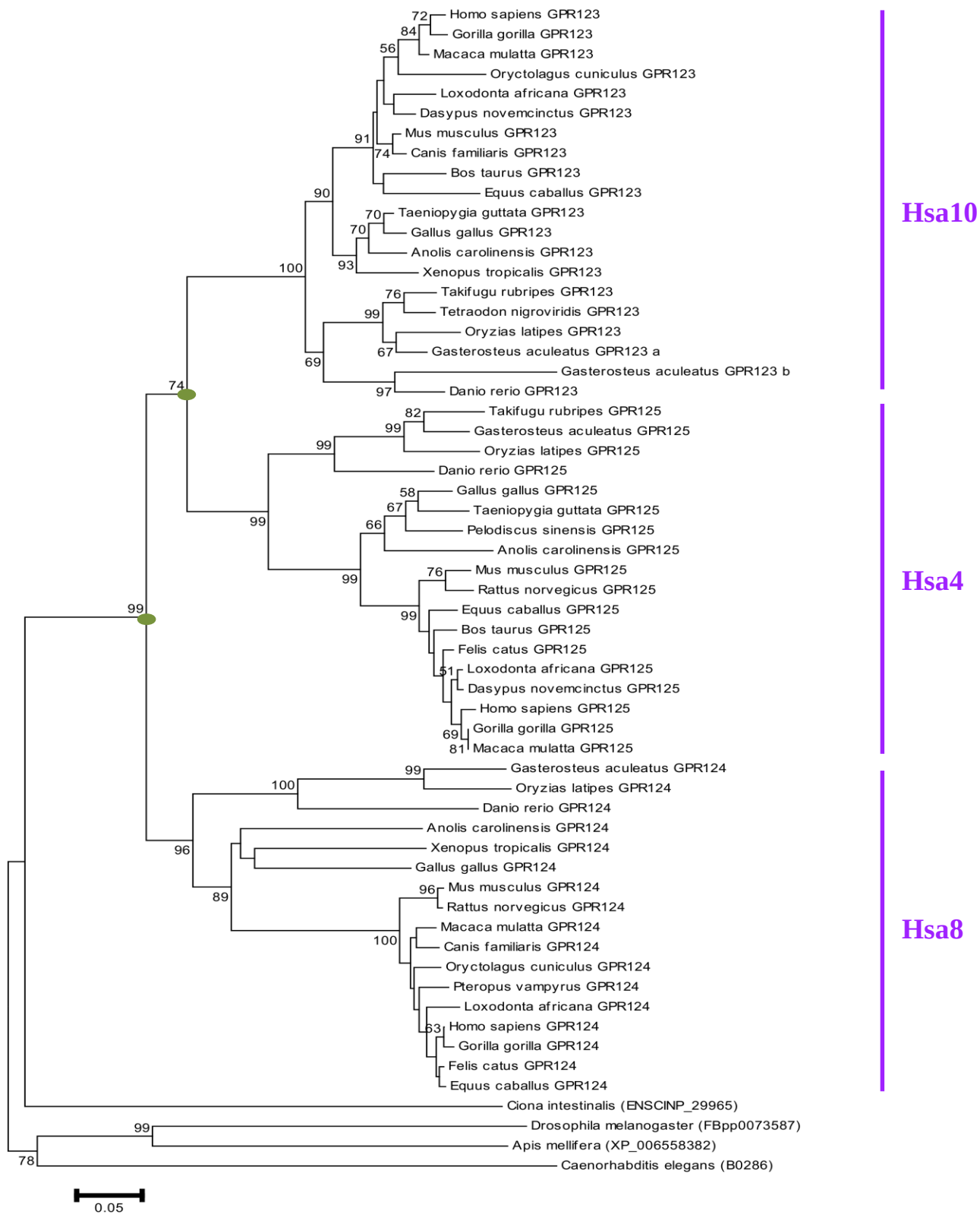
Fibroblast Growth Factor-FGF



Phylogenetic tree of FGF family.

Neighbor-Joining tree of the FGF family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site.

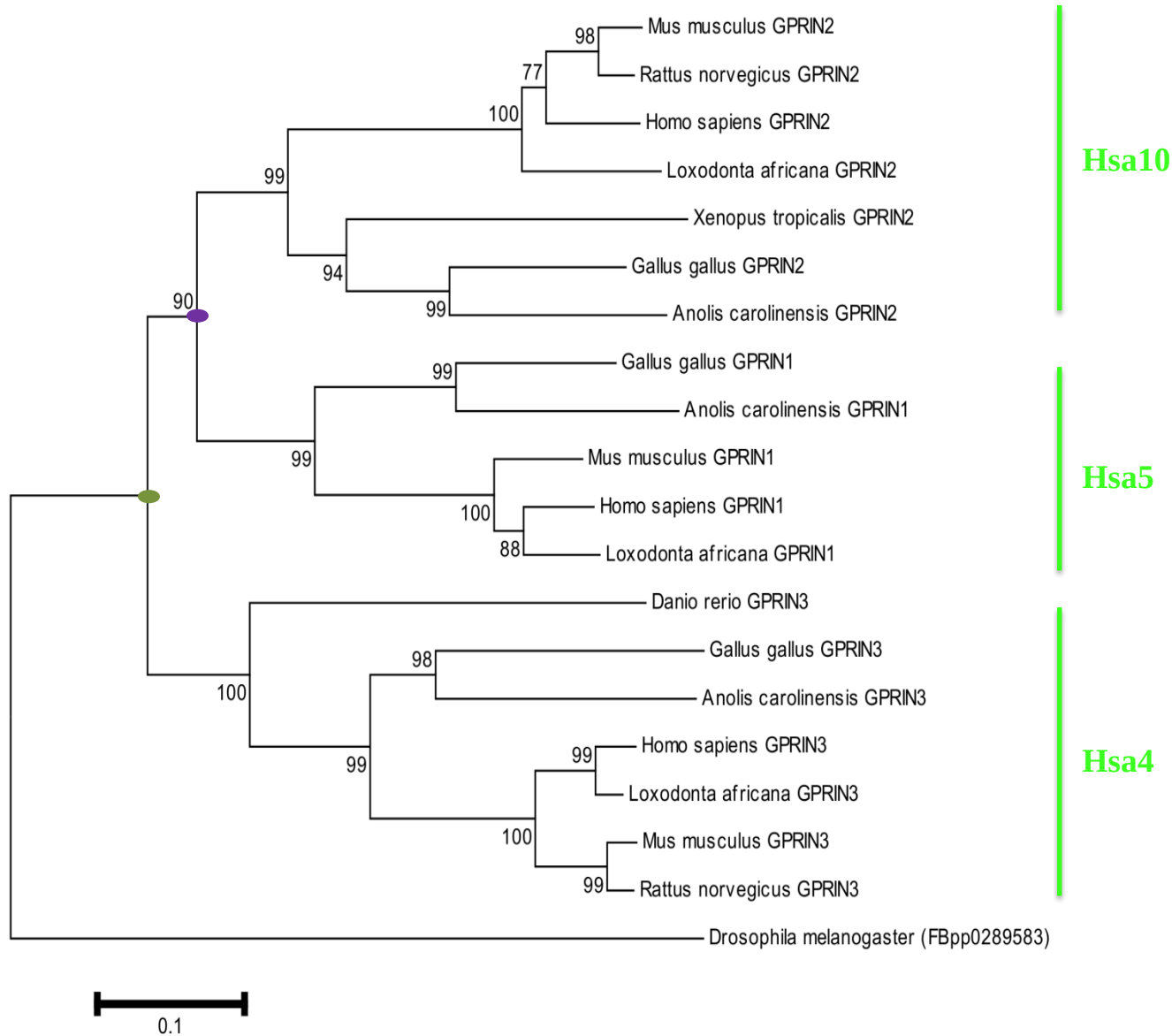
G Protein-Coupled Receptor-GPR



Phylogenetic tree of GPR family.

Neighbor-Joining tree of the GPR family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site.

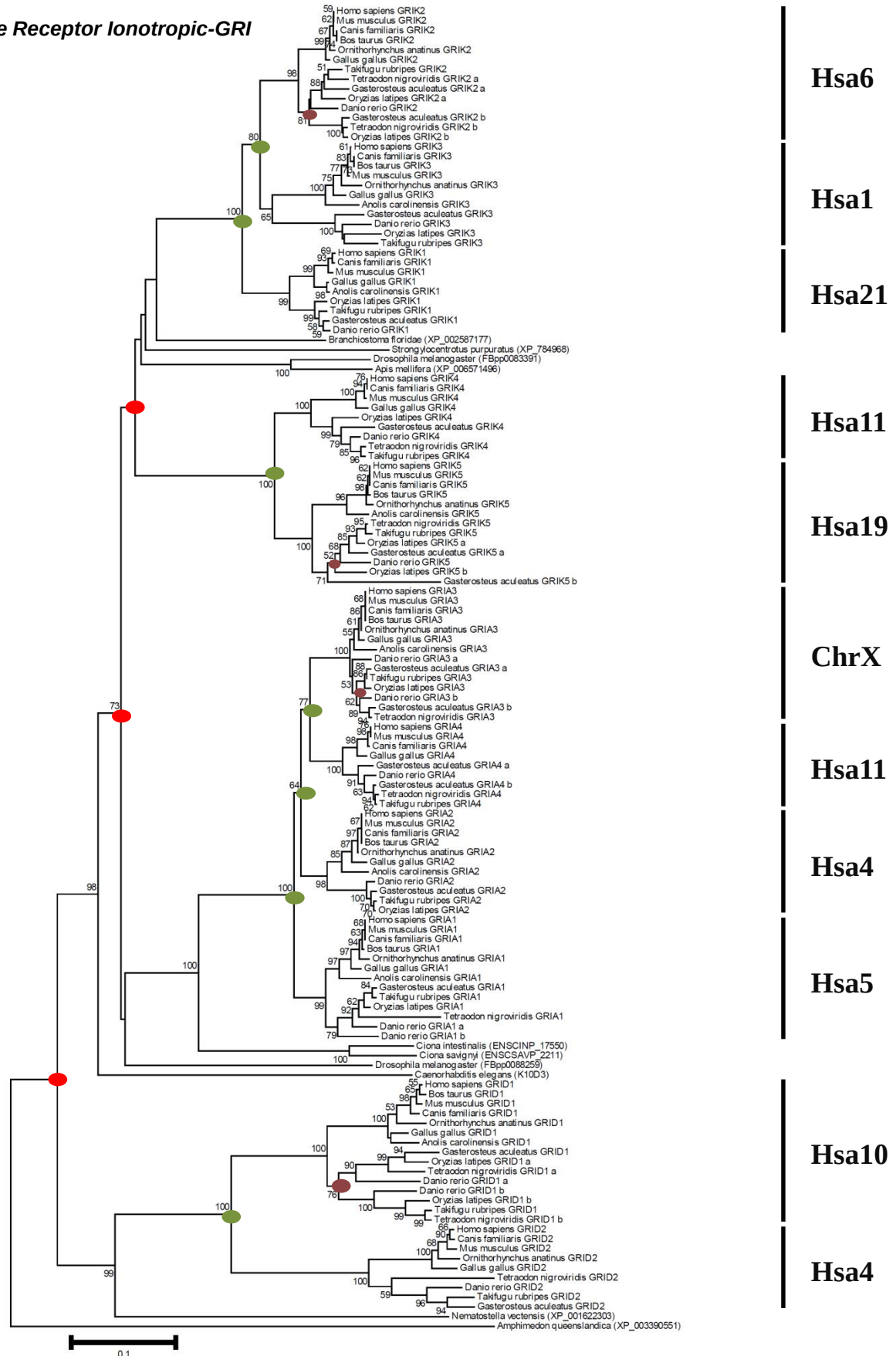
G Protein Regulated Inducer of Neurite Outgrowth-GPRIN



Phylogenetic tree of GPRIN family.

Neighbor-Joining tree of the GPRIN family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site.

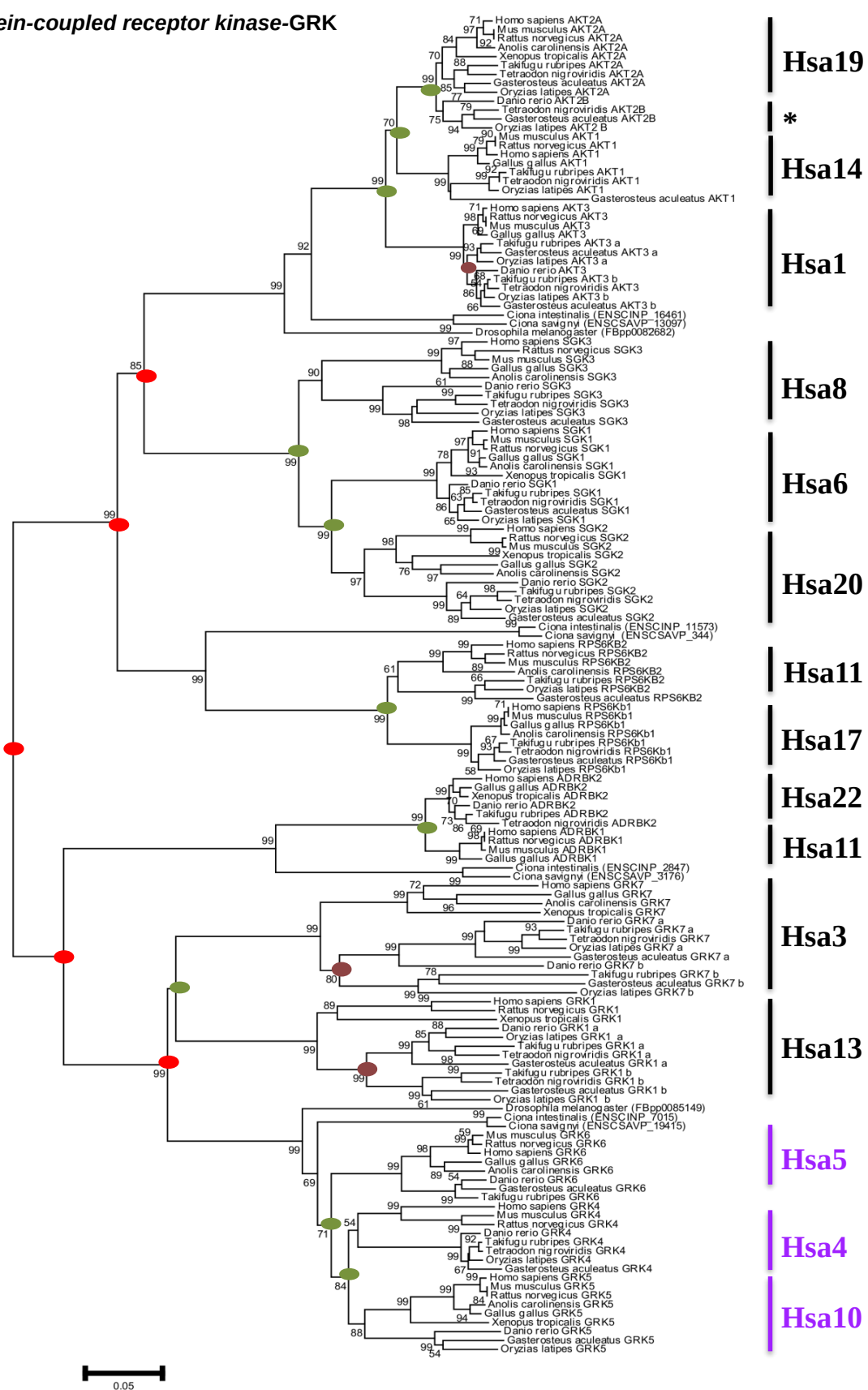
Glutamate Receptor Ionotropic-GRI



Phylogenetic tree of GRI family.

Neighbor-Joining tree of the GRI family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site.

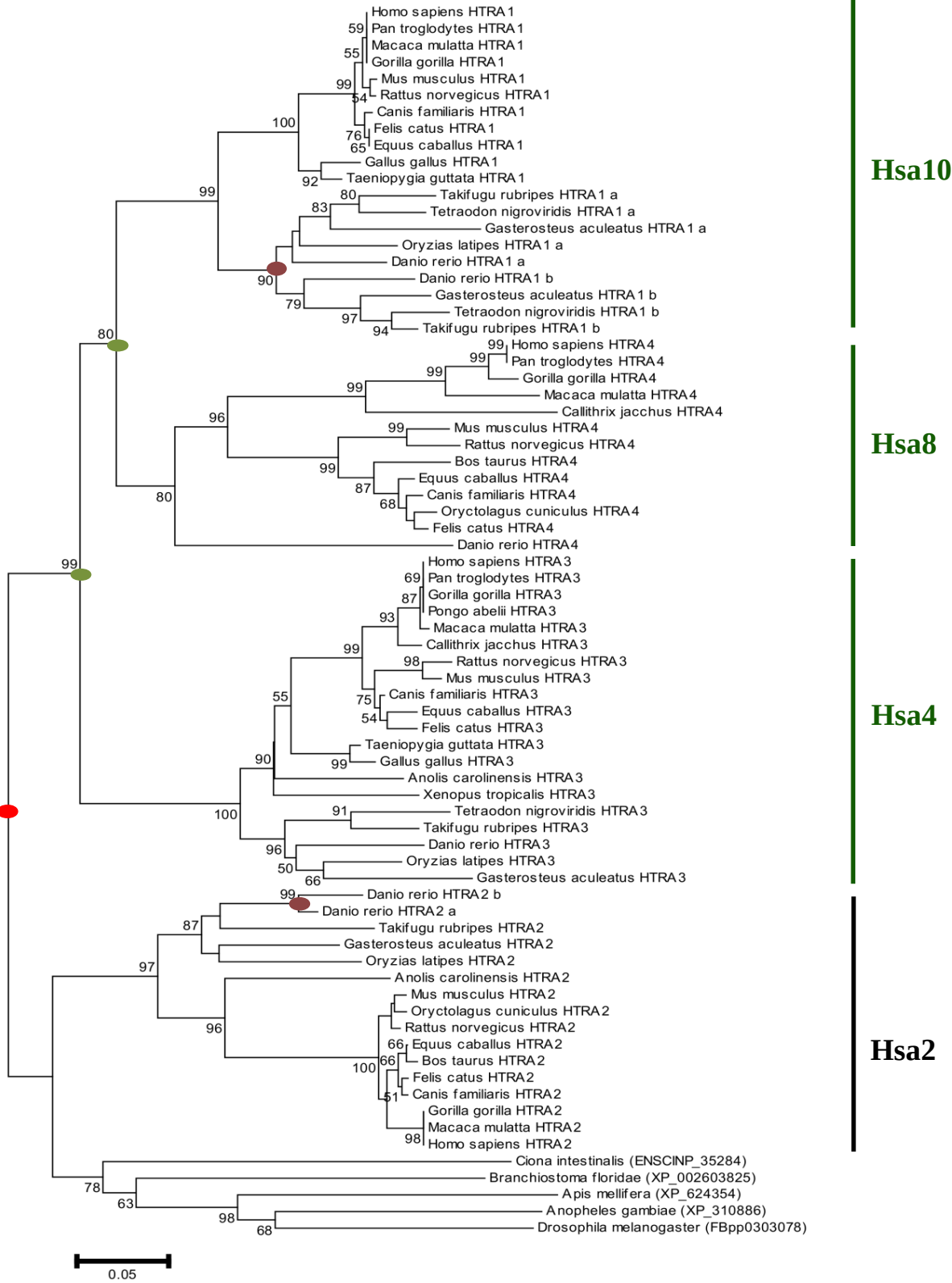
G protein-coupled receptor kinase-GRK



Phylogenetic tree of GRK family.

Neighbor-Joining tree of the GRK family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site. * shows another paralog which is missing in tetrapods named as AKT2B by our group.

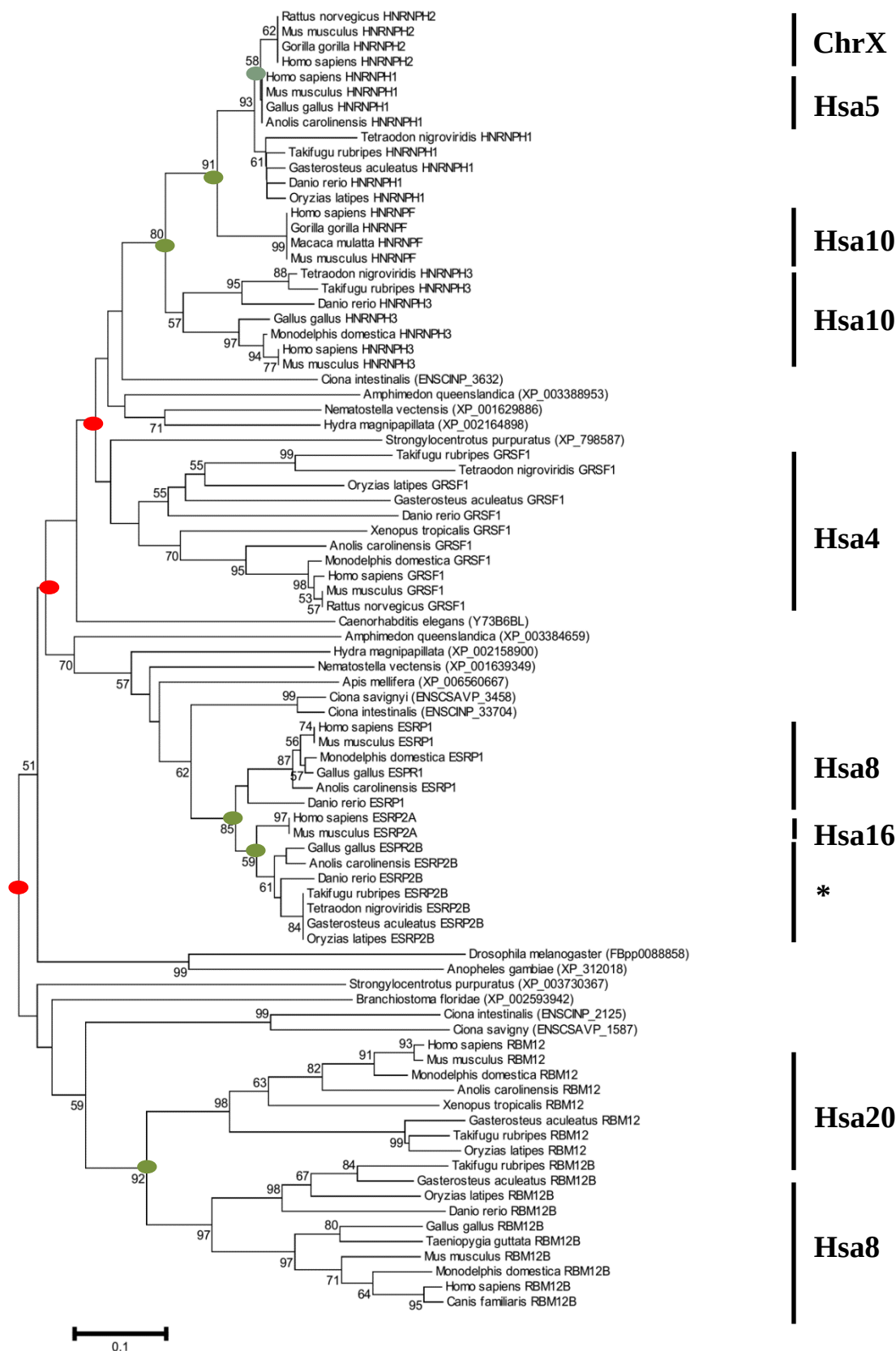
HtrA Serine Peptidase-HTRA



Phylogenetic tree of HTRA family.

Neighbor-Joining tree of the HTRA family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site.

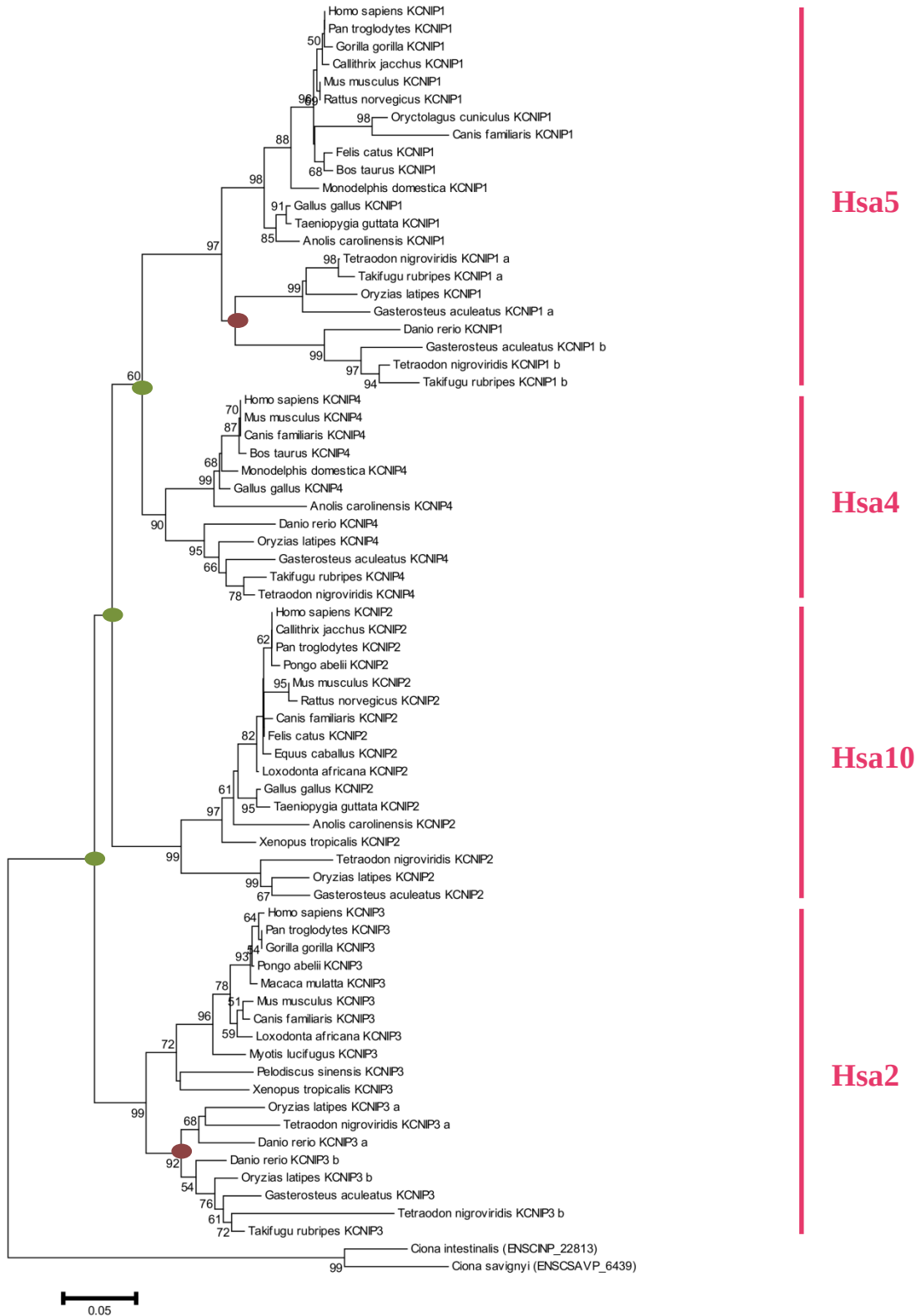
Heterogeneous ribonucleoprotein- HNRNP



Phylogenetic tree of HNRNP family.

Neighbor-Joining tree of the HNRNP family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site. * representing another paralog which is missing in mammals named as ESRP2B by our group.

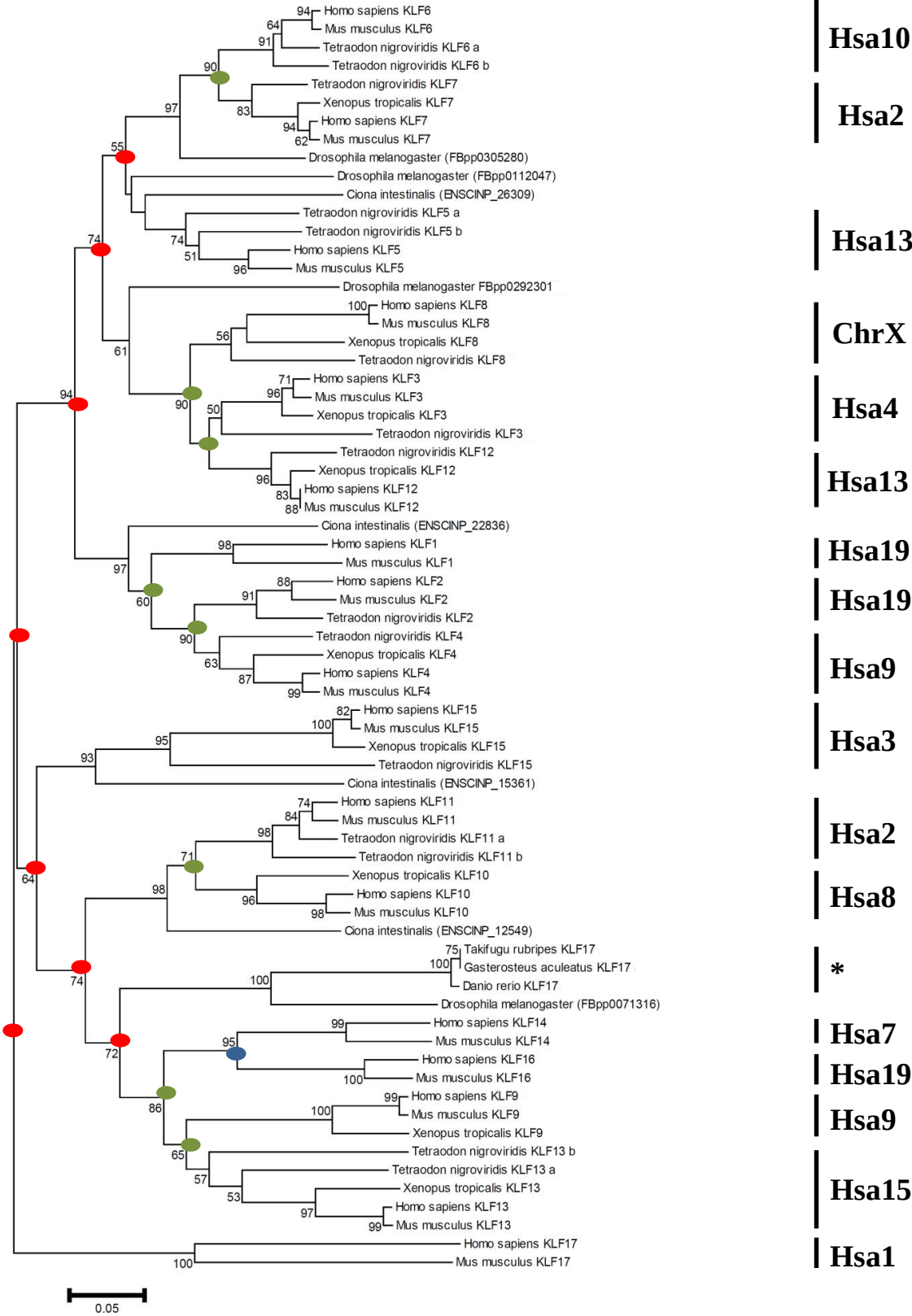
Kv Channel Interacting Protein-KCNIP



Phylogenetic tree of KCNIP family.

Neighbor-Joining tree of the KCNIP family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site.

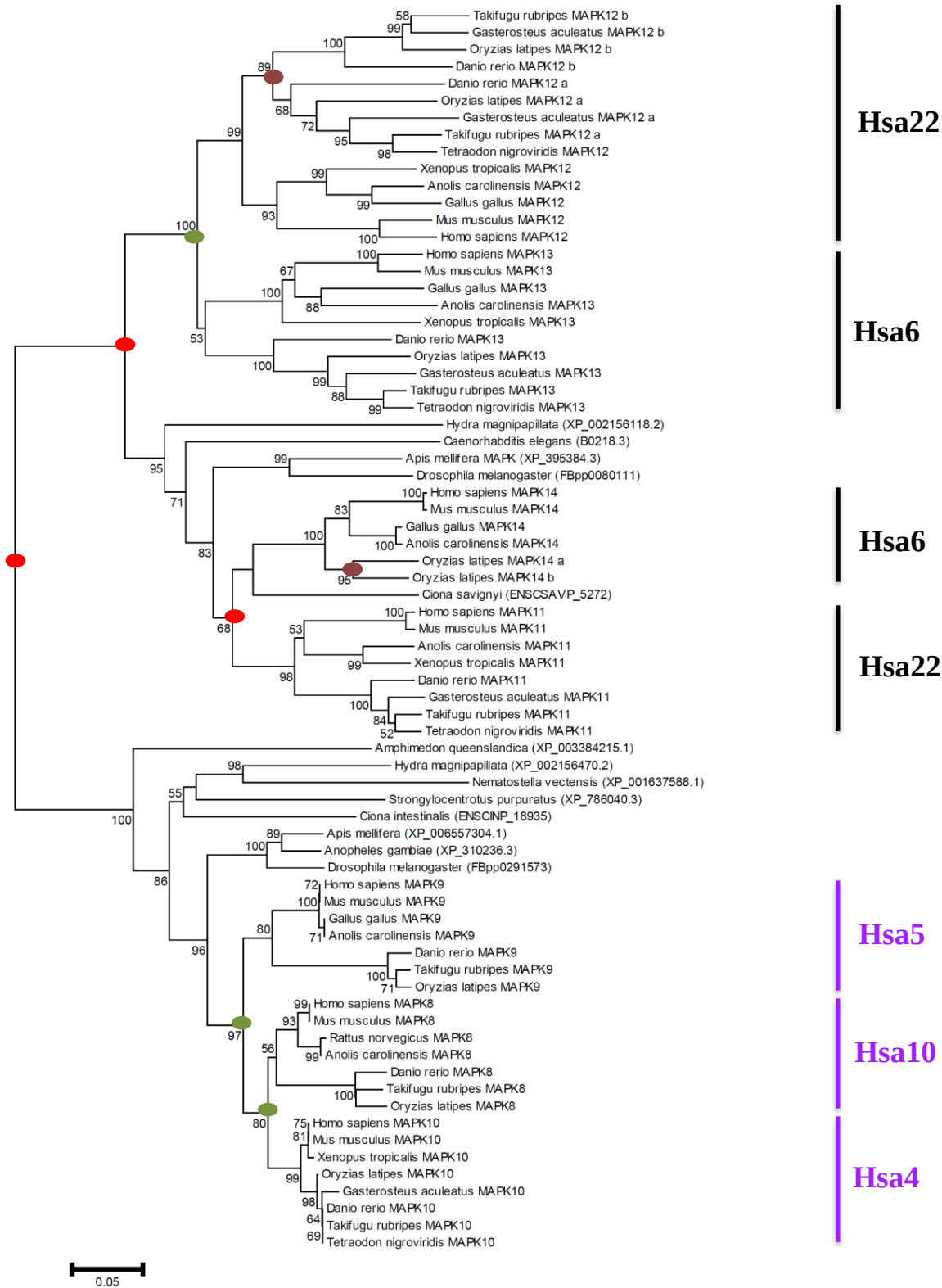
Kruppel-like factor-KLF



Phylogenetic tree of KLF family.

Neighbor-Joining tree of the KLF family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site. * represent paralog which is missing in tetrapods named as KLF17 by our group.

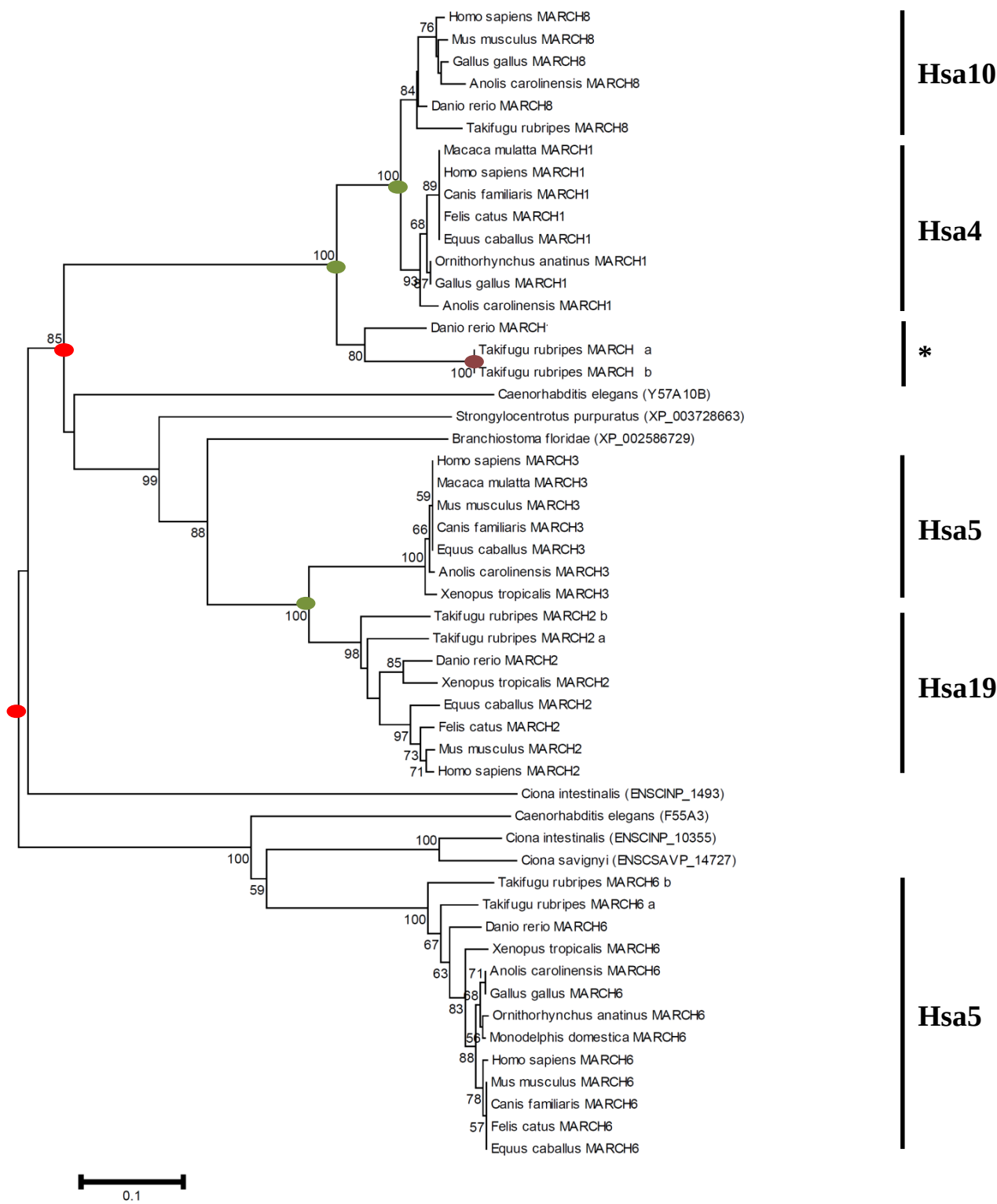
Mitogen-activated protein kinase-MAPK



Phylogenetic tree of MAPK family.

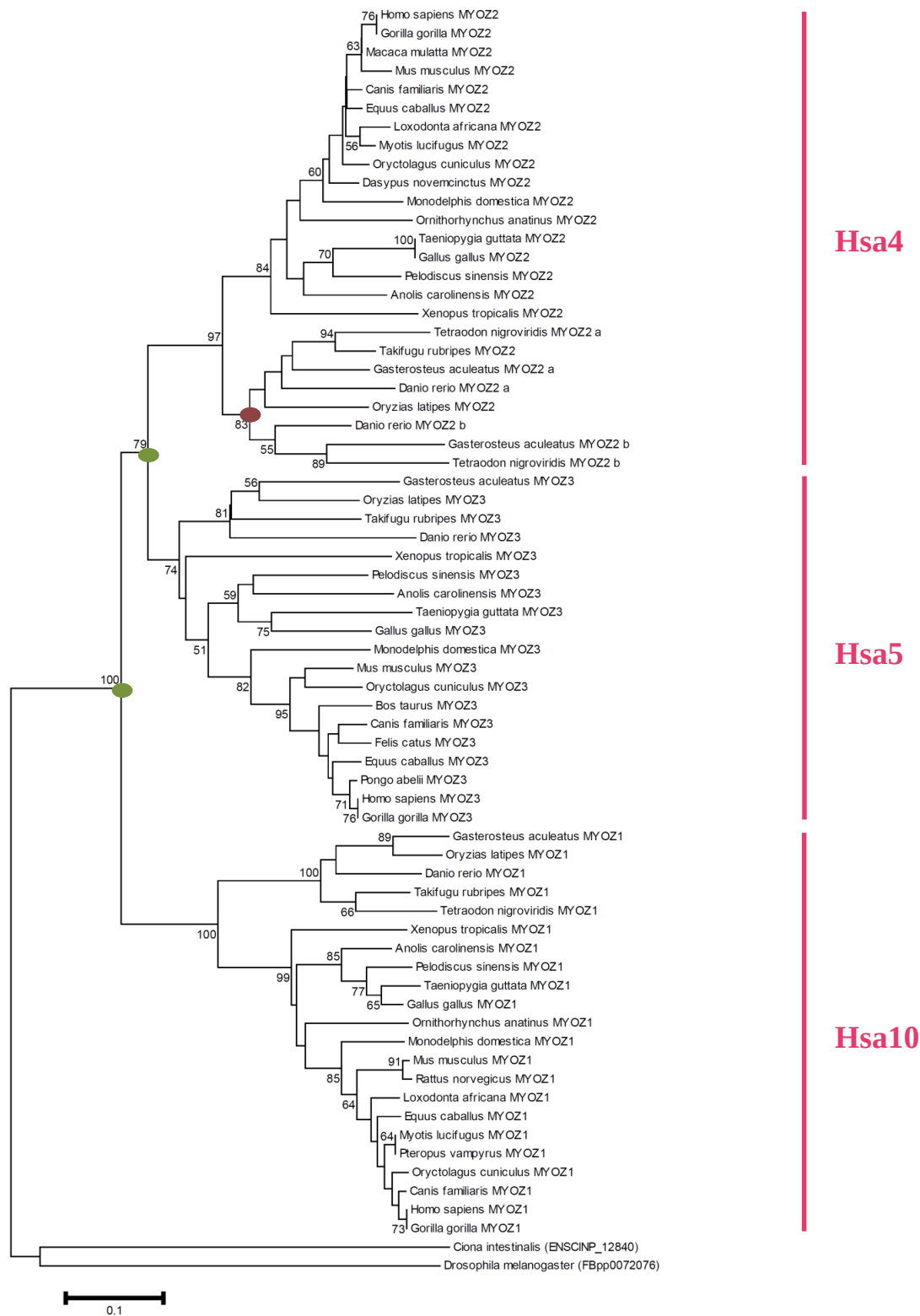
Neighbor-Joining tree of the MAPK family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site.

Membrane-associated ring finger (C3HC4)-MARCH



Phylogenetic tree of MARCH family.

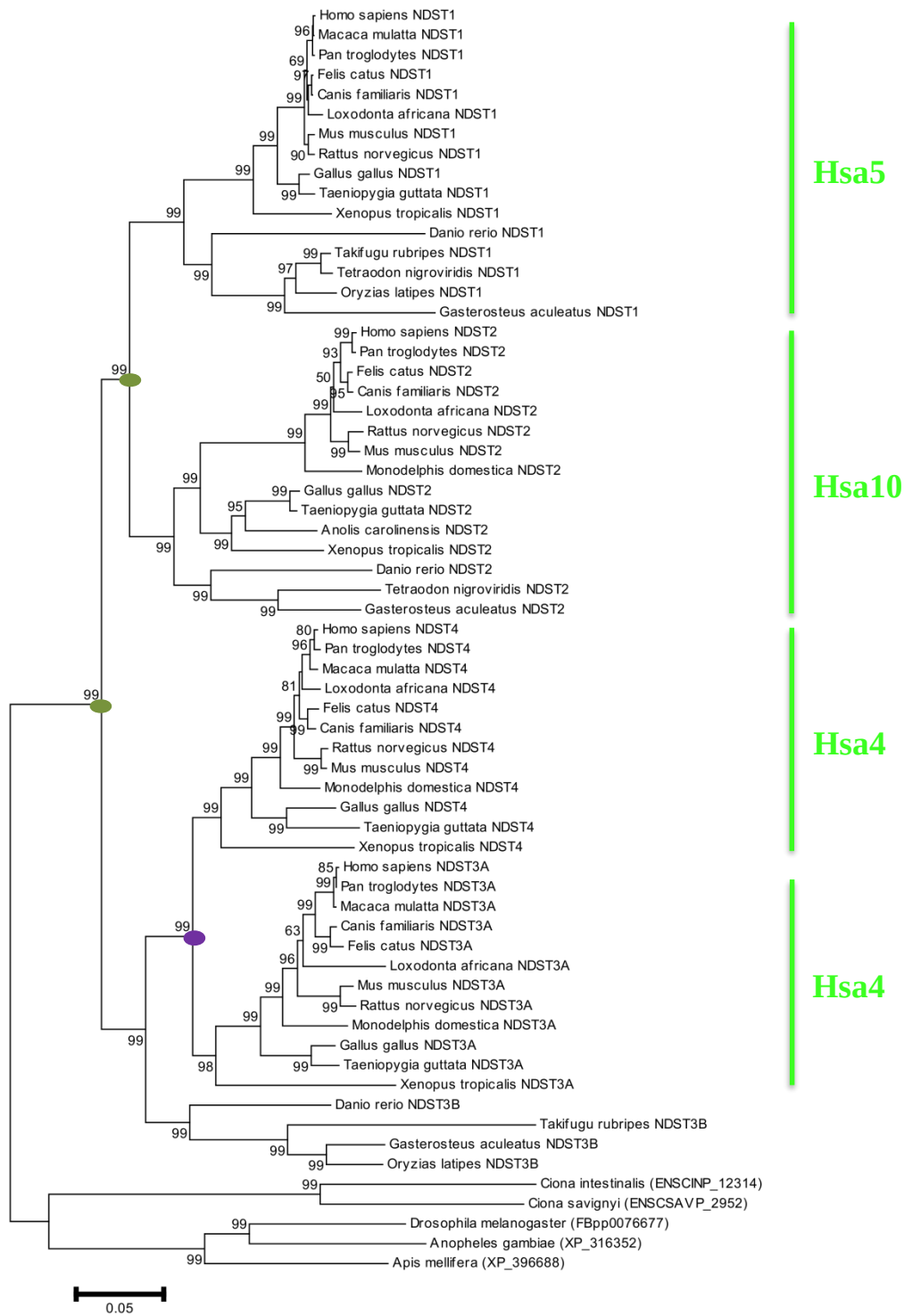
Neighbor-Joining tree of the MARCH family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site. * representing paralog which is missing in tetrapods named as MARCH by our group.



Phylogenetic tree of MYOZ family.

Neighbor-Joining tree of the MYOZ family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site.

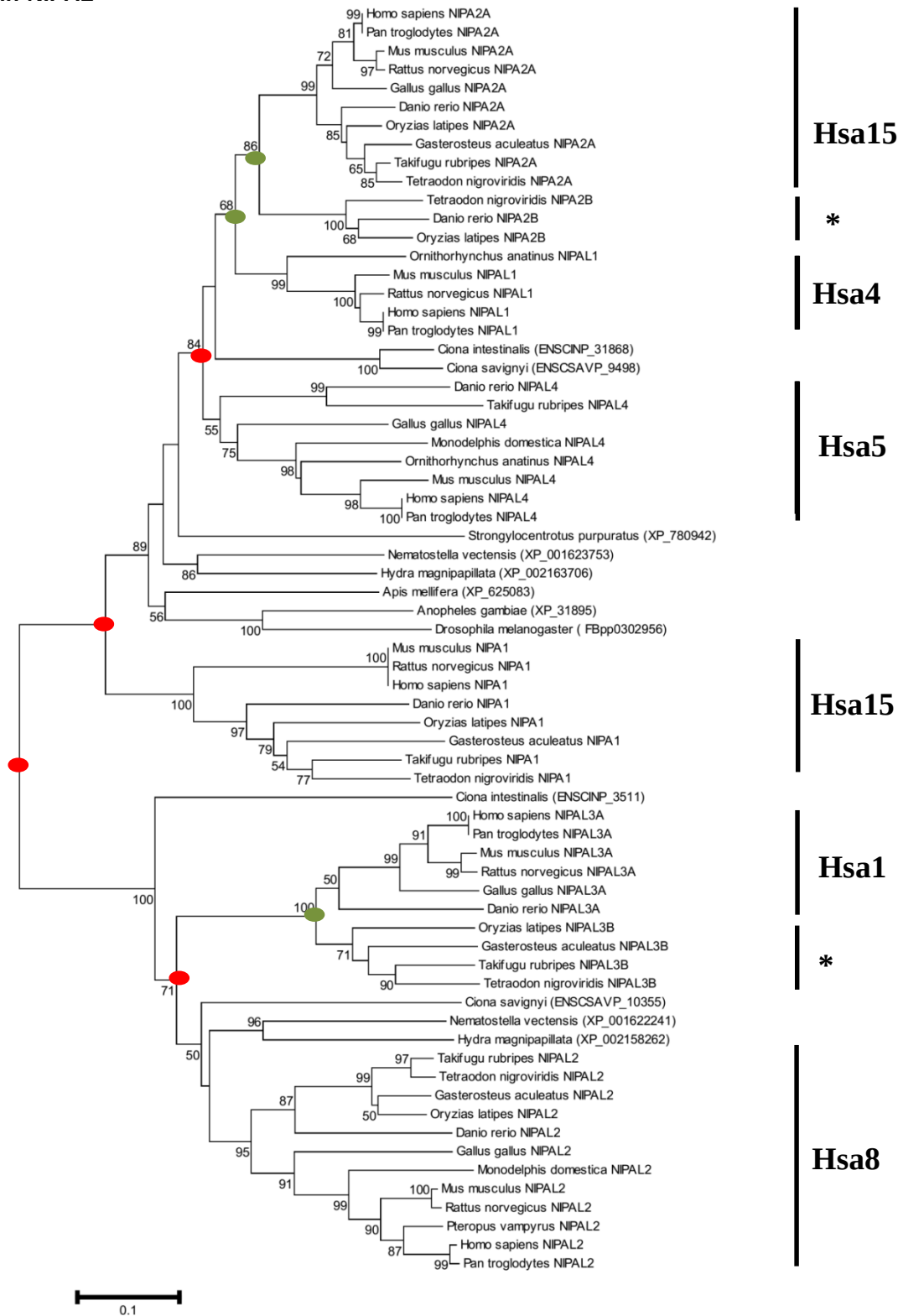
N-deacetylase/*N*-sulfotransferase-NDST



Phylogenetic tree of NDST family.

Neighbor-Joining tree of the NDST family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site.

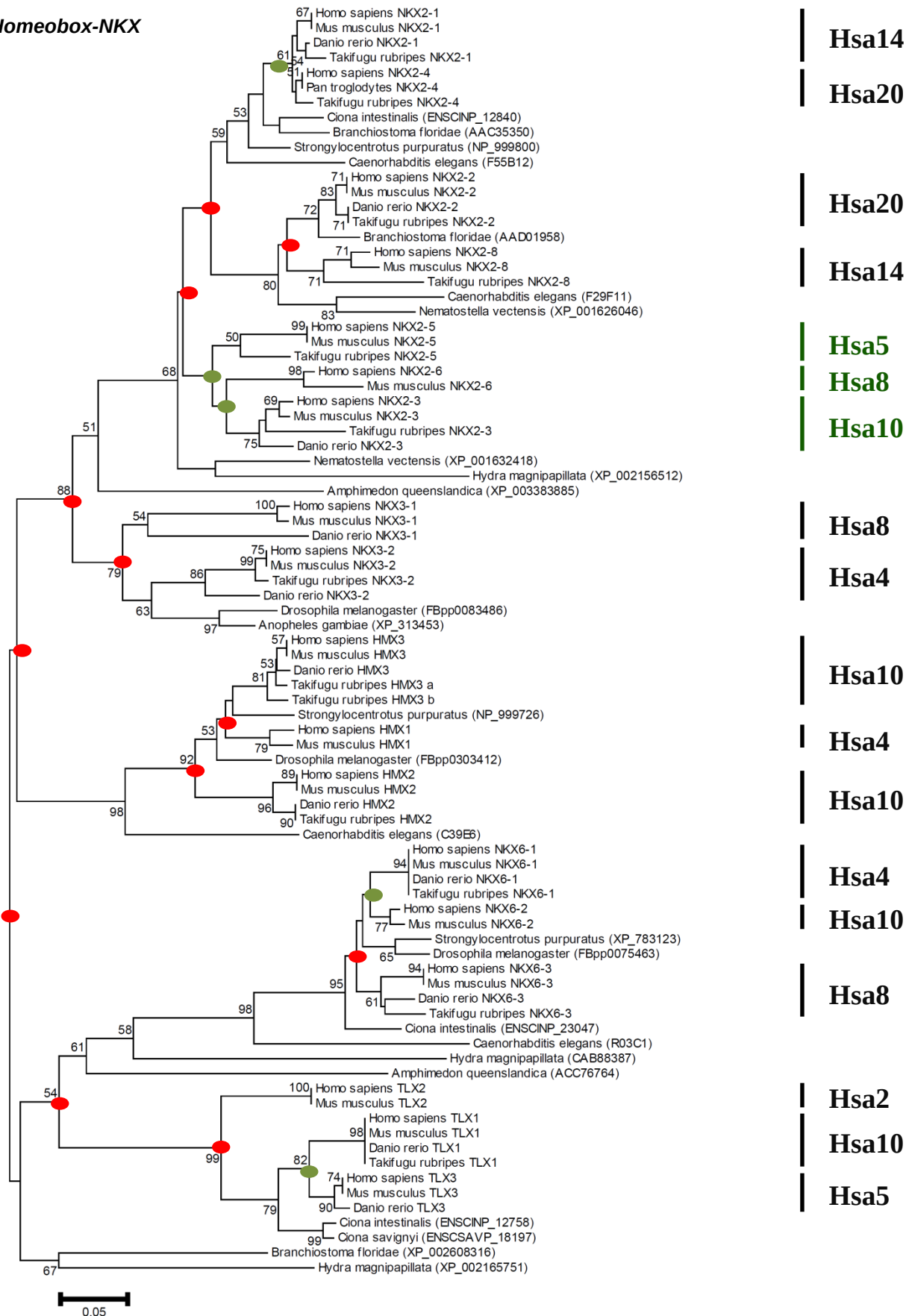
NIPA-like domain-NIPAL



Phylogenetic tree of NIPAL family.

Neighbor-Joining tree of the NIPAL family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site. * shows paralog with missing tetrapods named as NPA2B and NPAL3B by our group.

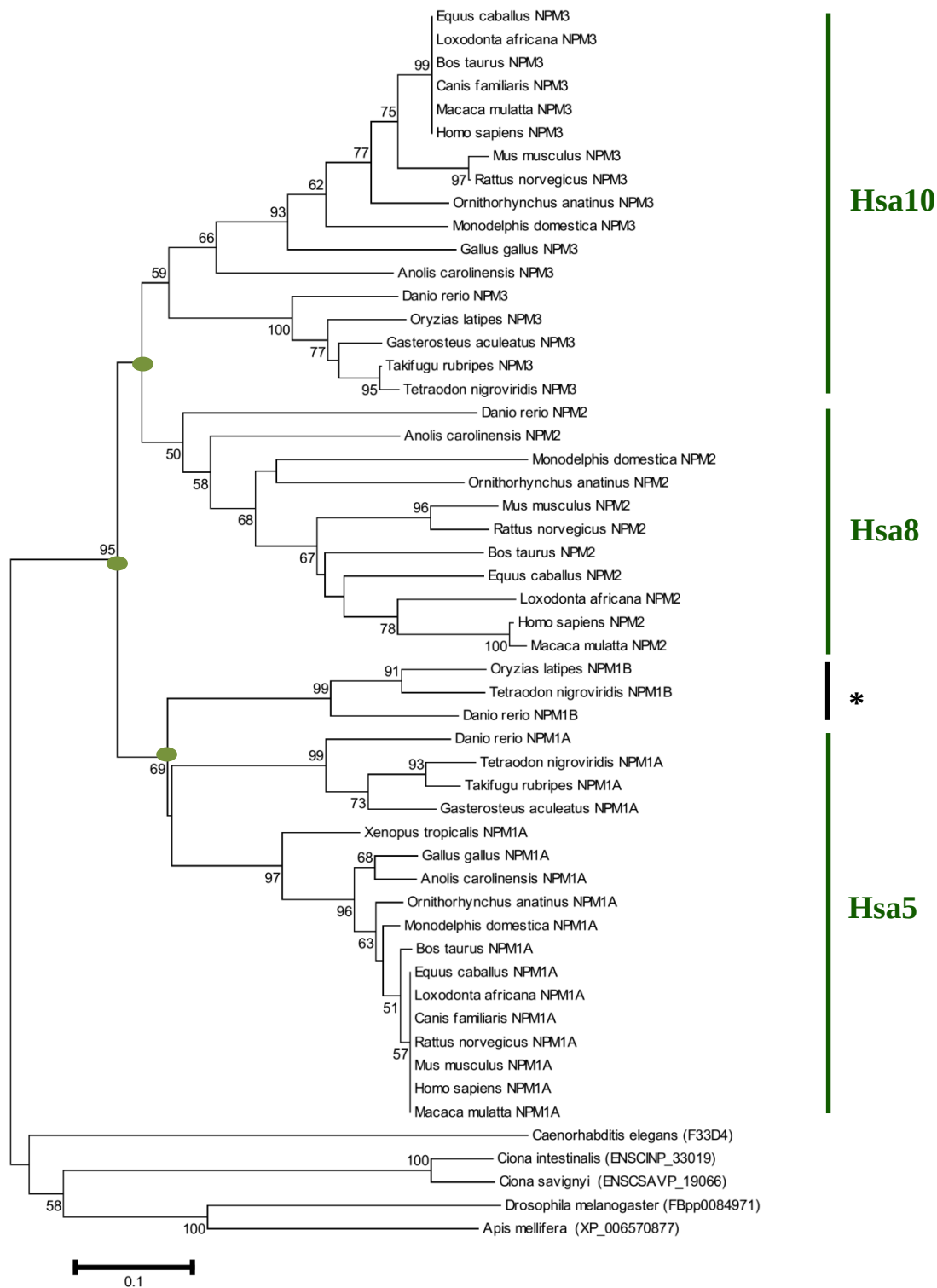
NK Homeobox-NKX



Phylogenetic tree of NKX family.

Neighbor-Joining tree of the NKX family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values ≥ 50 are presented here. Scale bar shows amino acid substitution per site.

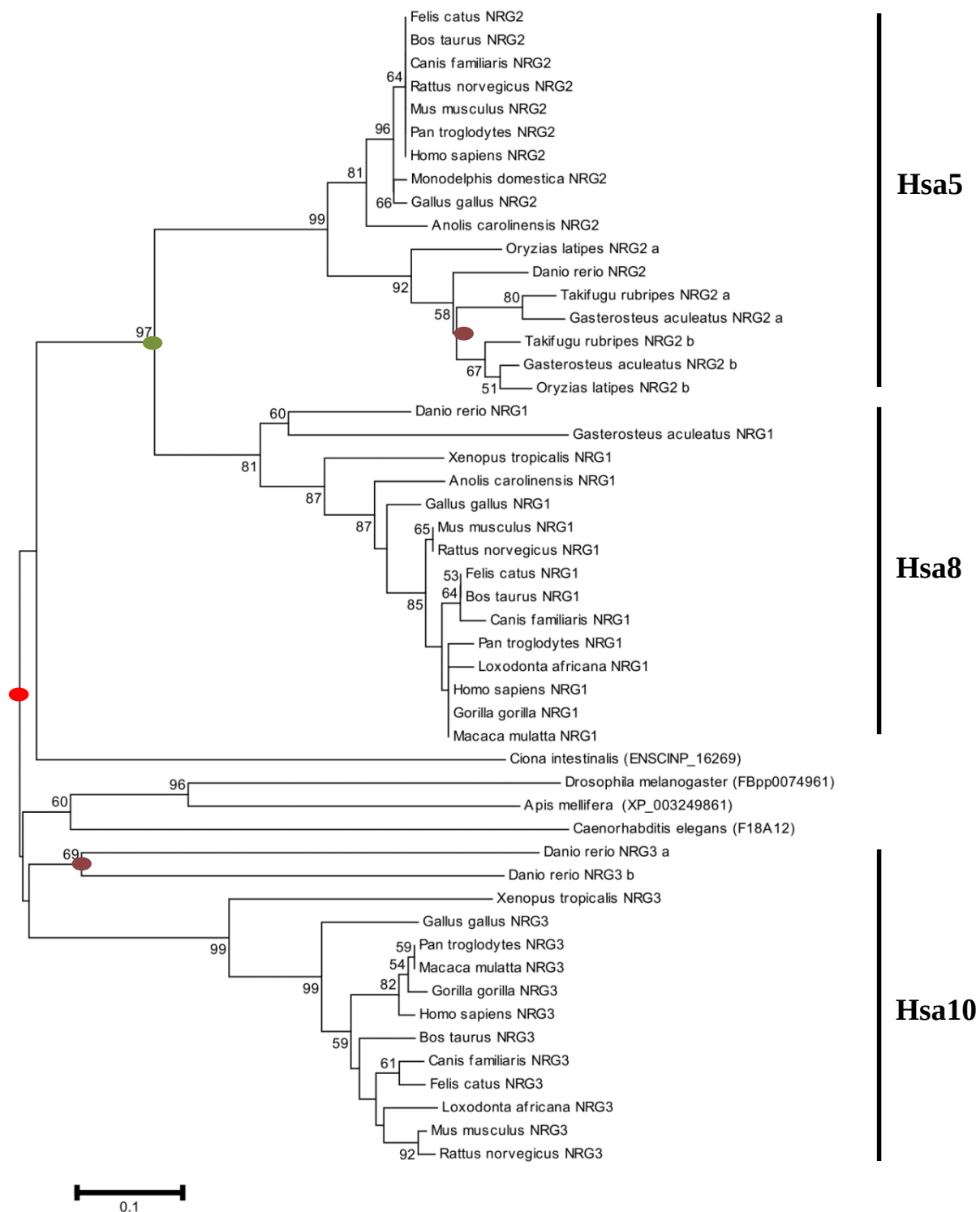
Nucleophosmin-NPM



Phylogenetic tree of NPM family.

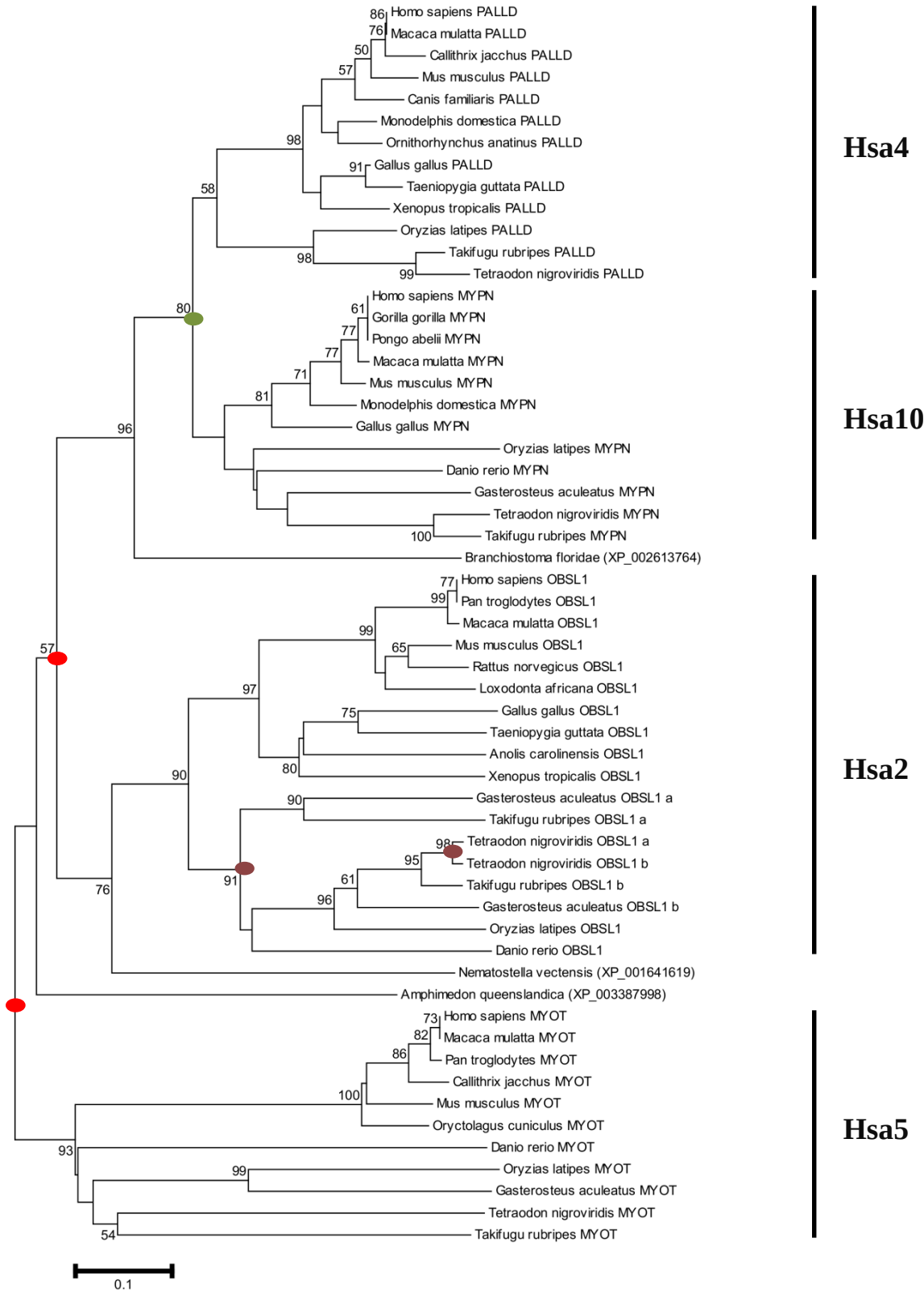
Neighbor-Joining tree of the NPM family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site. * shows paralog with missing tetrapods named as NPM1B by our group.

Neuregulin-NRG



Phylogenetic tree of NRG family.

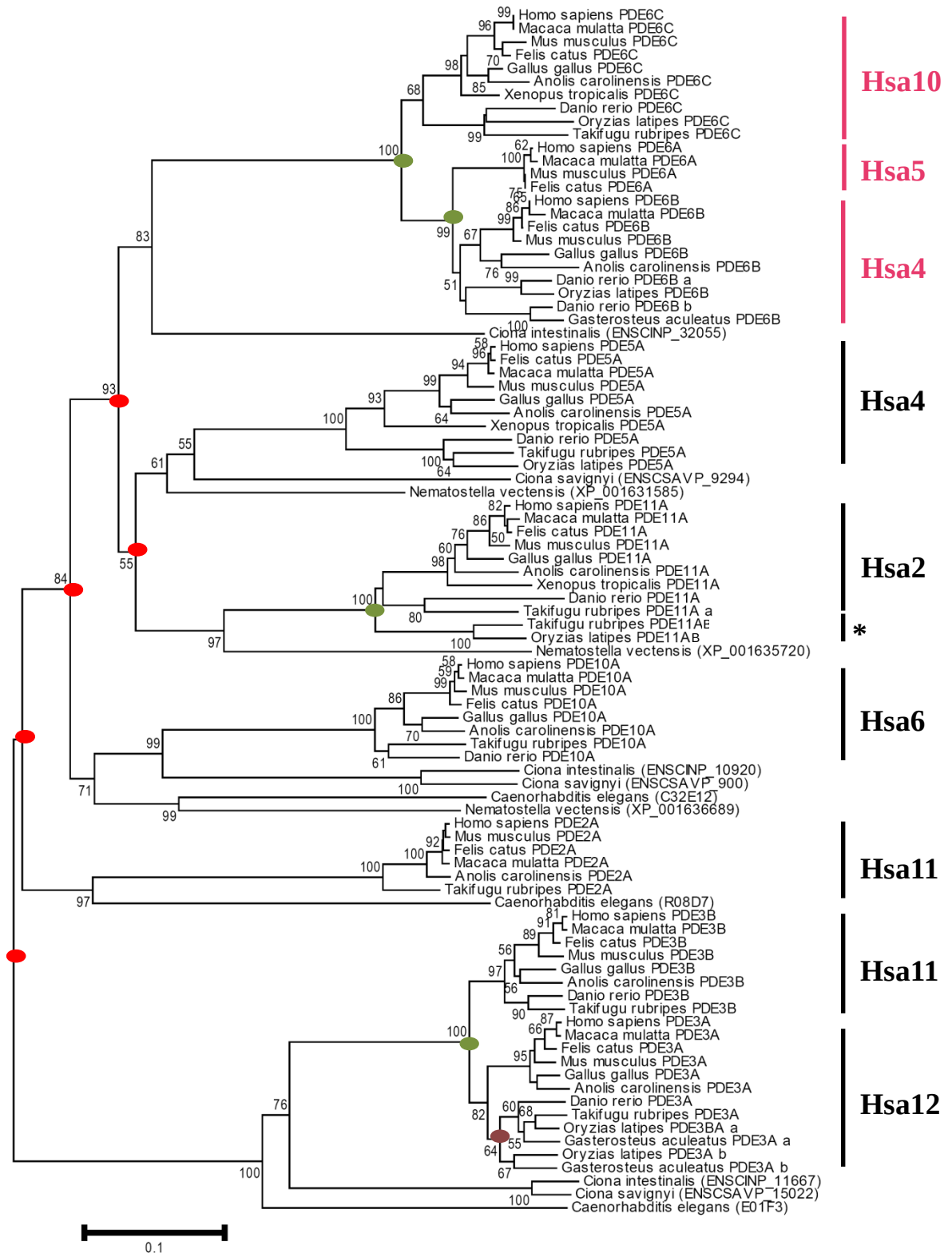
Neighbor-Joining tree of the NRG family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site.



Phylogenetic tree of PALLD family.

Neighbor-Joining tree of the PALLD family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site.

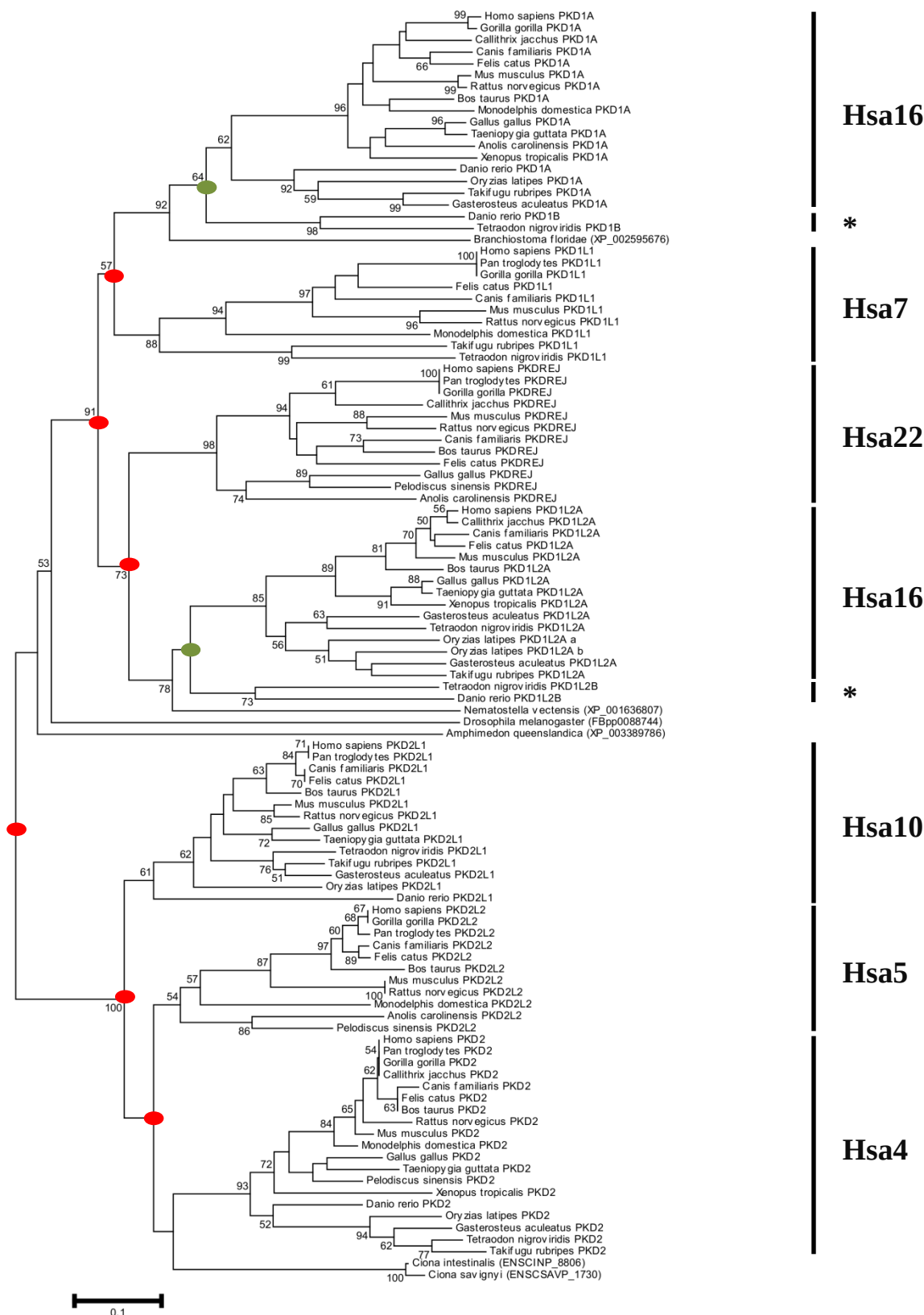
Phosphodiesterase-PDE



Phylogenetic tree of PDE family.

Neighbor-Joining tree of the PDE family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site. * is showing another paralog which is missing in tetrapods named as PDE11AB by our group.

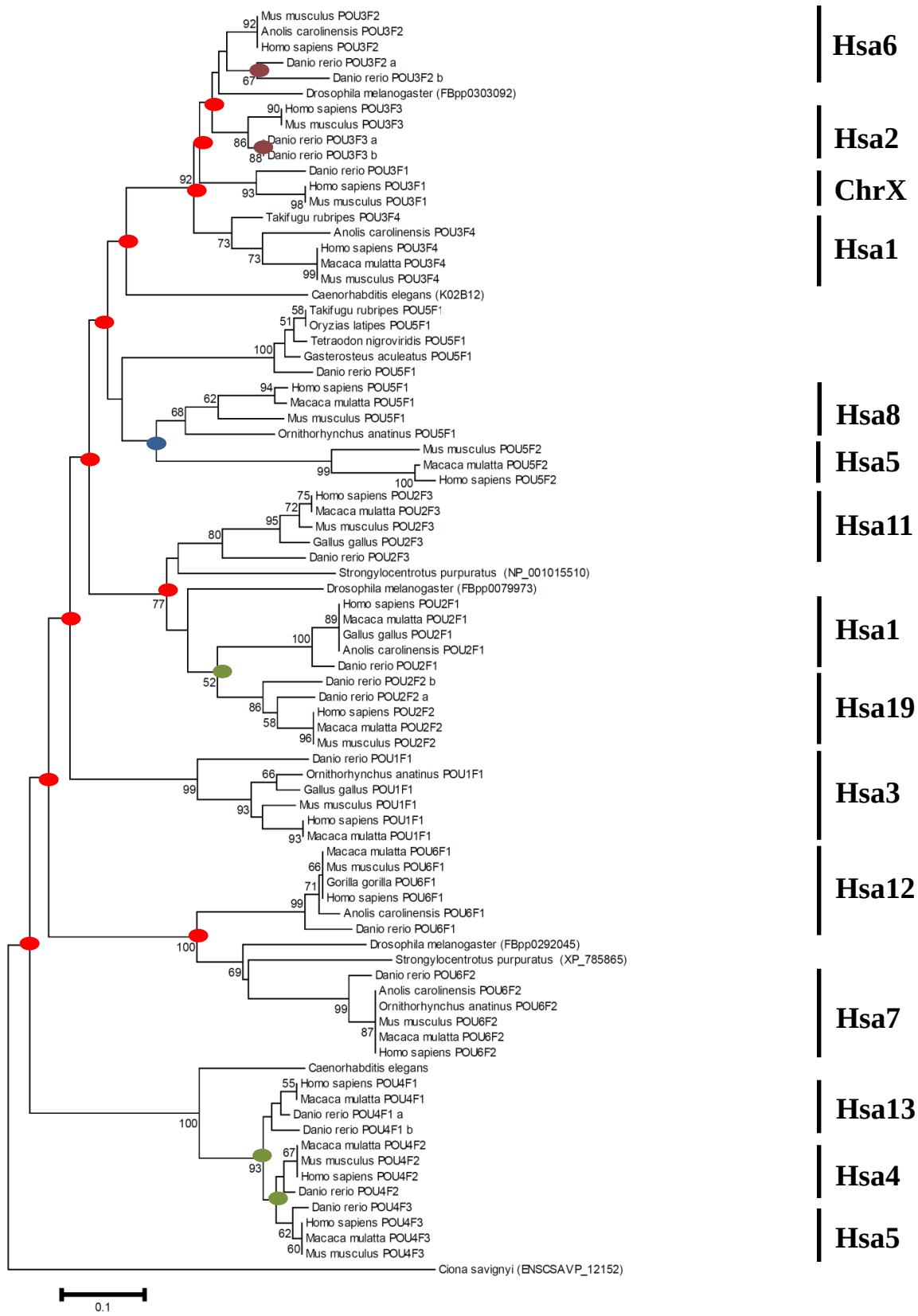
Polycystic Kidney Disease-PKD



Phylogenetic tree of PKD family.

Neighbor-Joining tree of the PKD family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site. * shows another paralogs which are missing in tetrapods, named as PKD1B and PKD1L2B, respectively by our group.

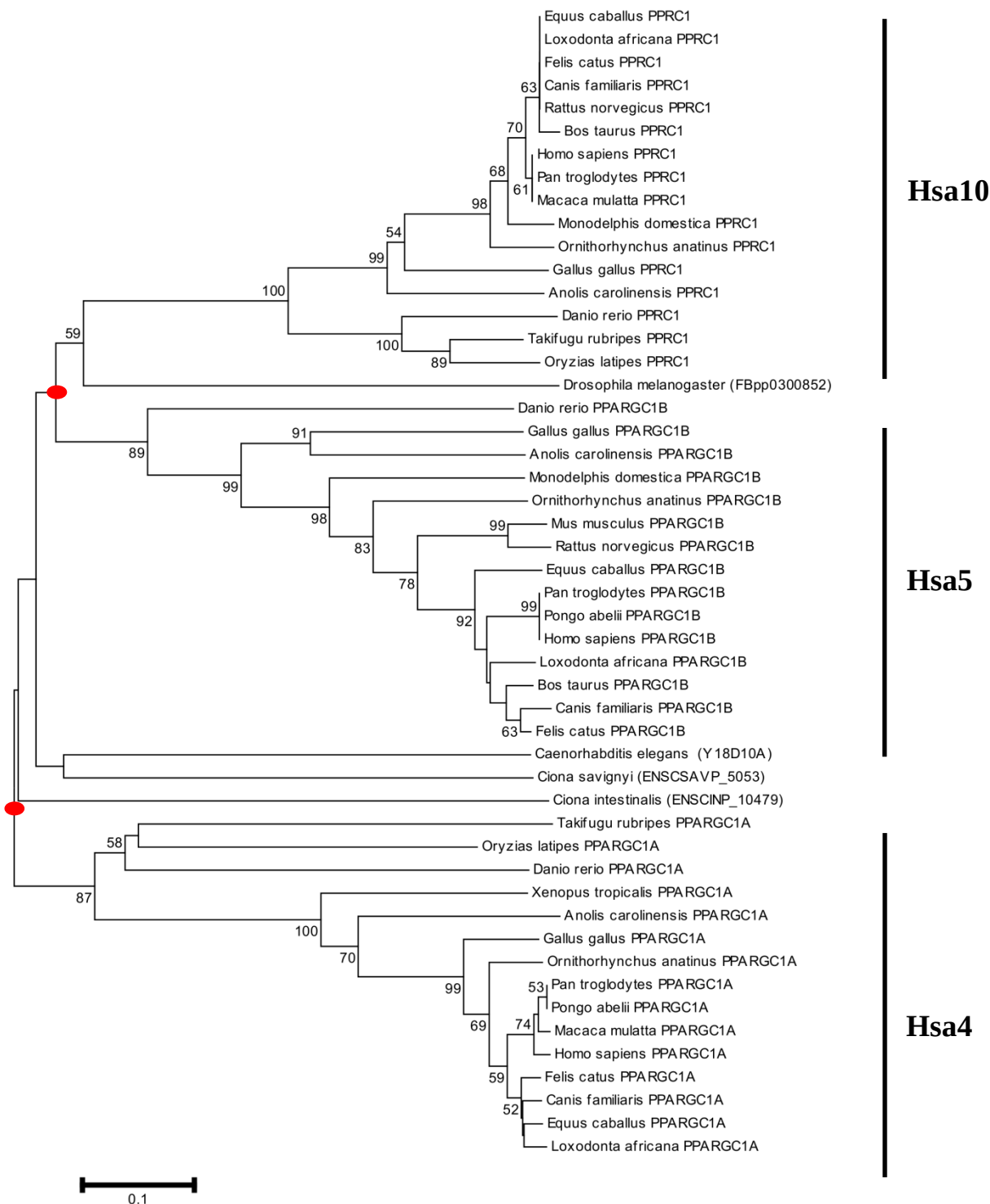
POU Family



Phylogenetic tree of POU family.

Neighbor-Joining tree of the POU family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site.

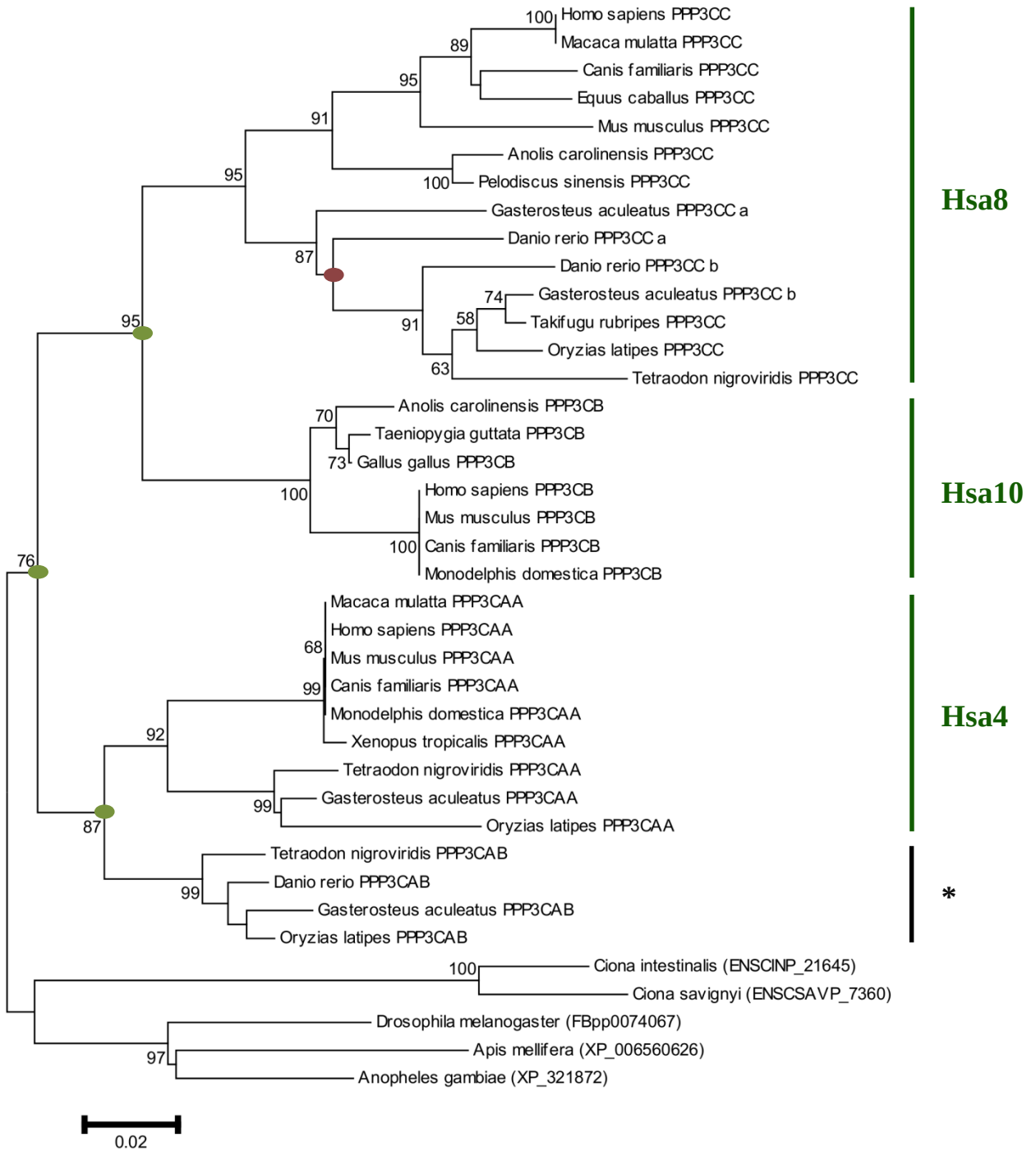
Peroxisome Proliferator-Activated Receptor Gamma, Coactivator -PPARGC



Phylogenetic tree of PPARGC family.

Neighbor-Joining tree of the PPARGC family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site.

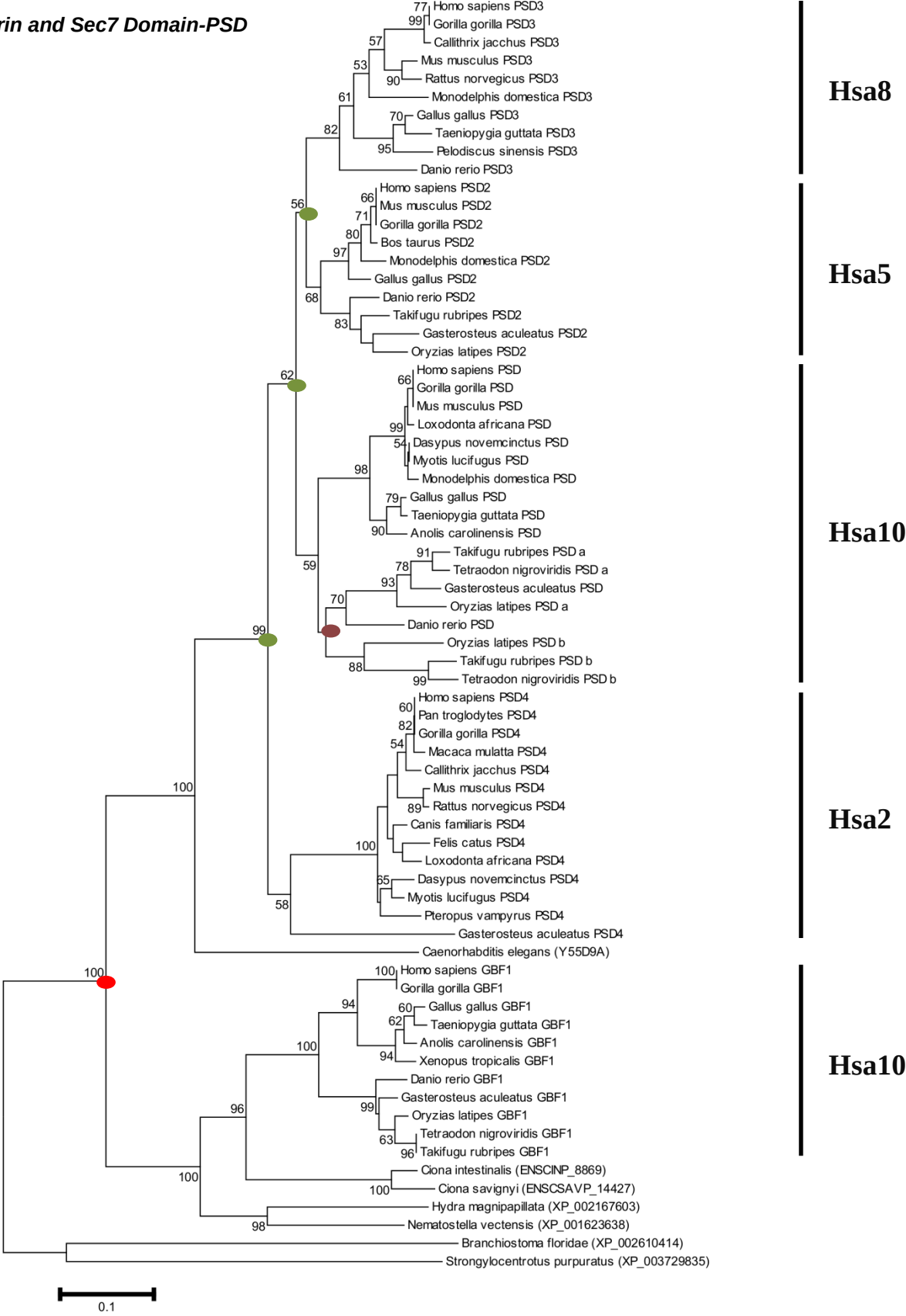
Protein Phosphate 3 Catalytic Subunit-PPP3C



Phylogenetic tree of PPP3C family.

Neighbor-Joining tree of the PPP3C family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site. * shows another paralog which is missing in tetrapods, named as PPP3CAB by our group.

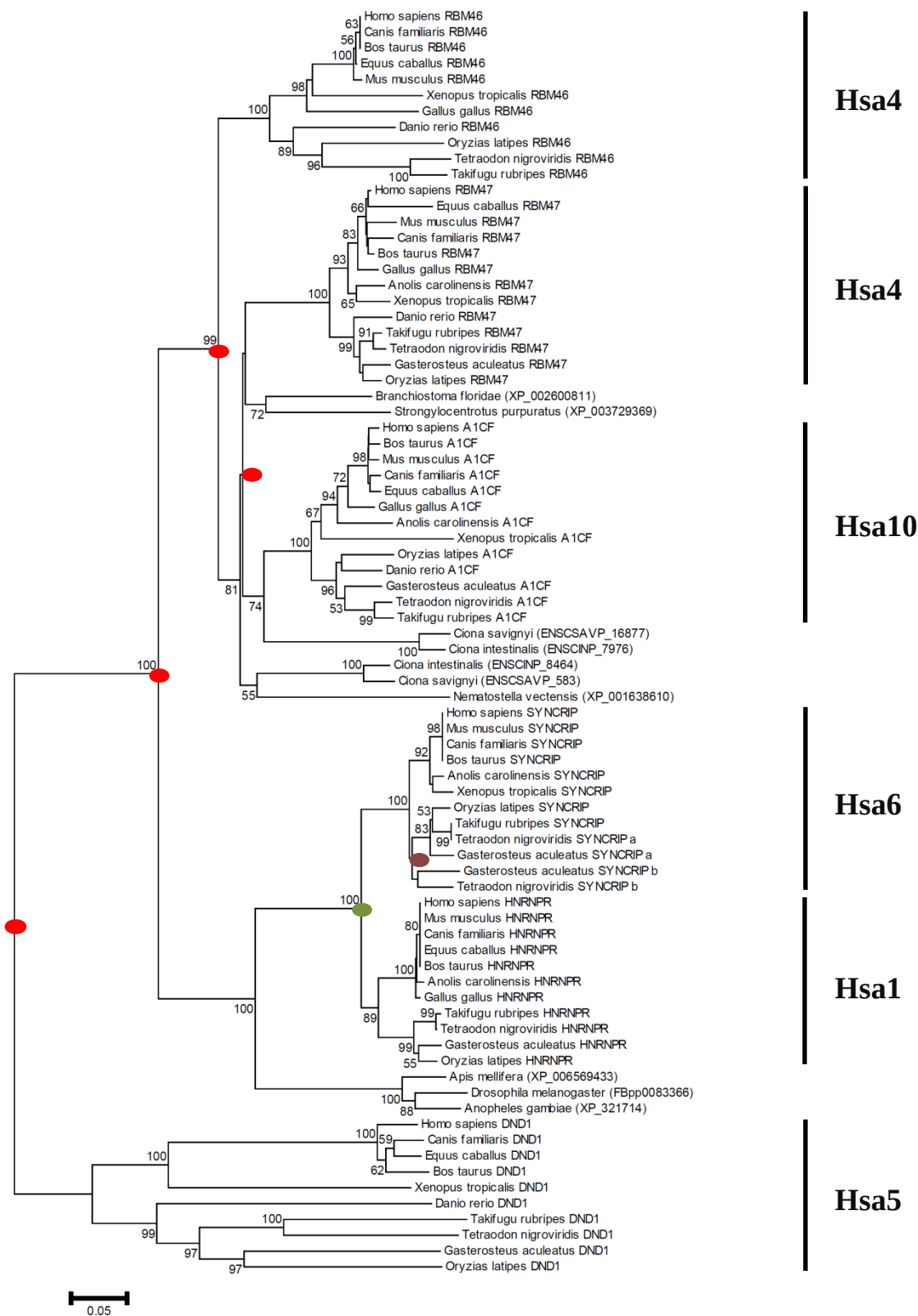
Pleckstrin and Sec7 Domain-PSD



Phylogenetic tree of PSD family.

Neighbor-Joining tree of the PSD family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site.

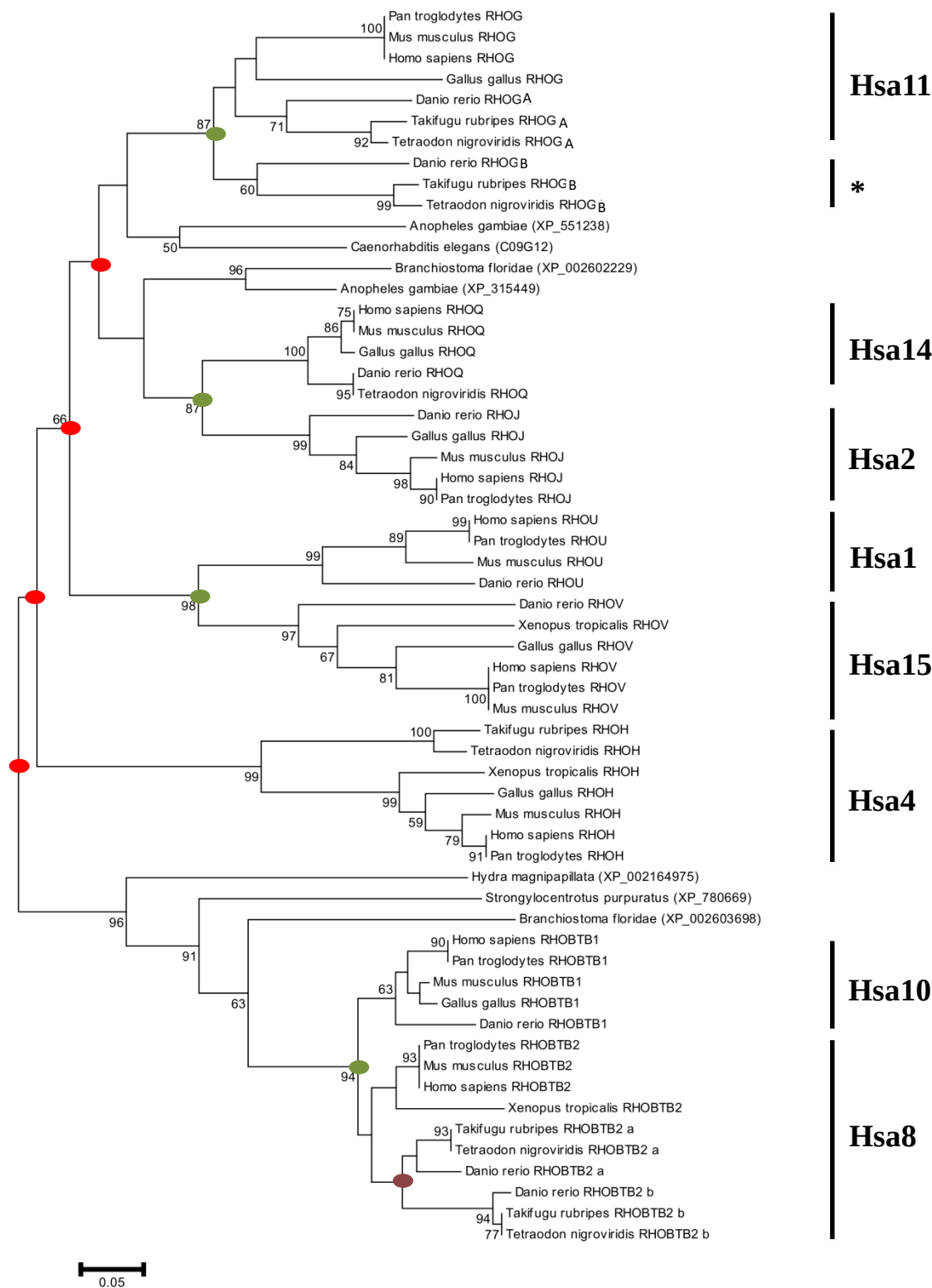
RNA Binding Motif-RBM



Phylogenetic tree of RBM family.

Neighbor-Joining tree of the RBM family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site.

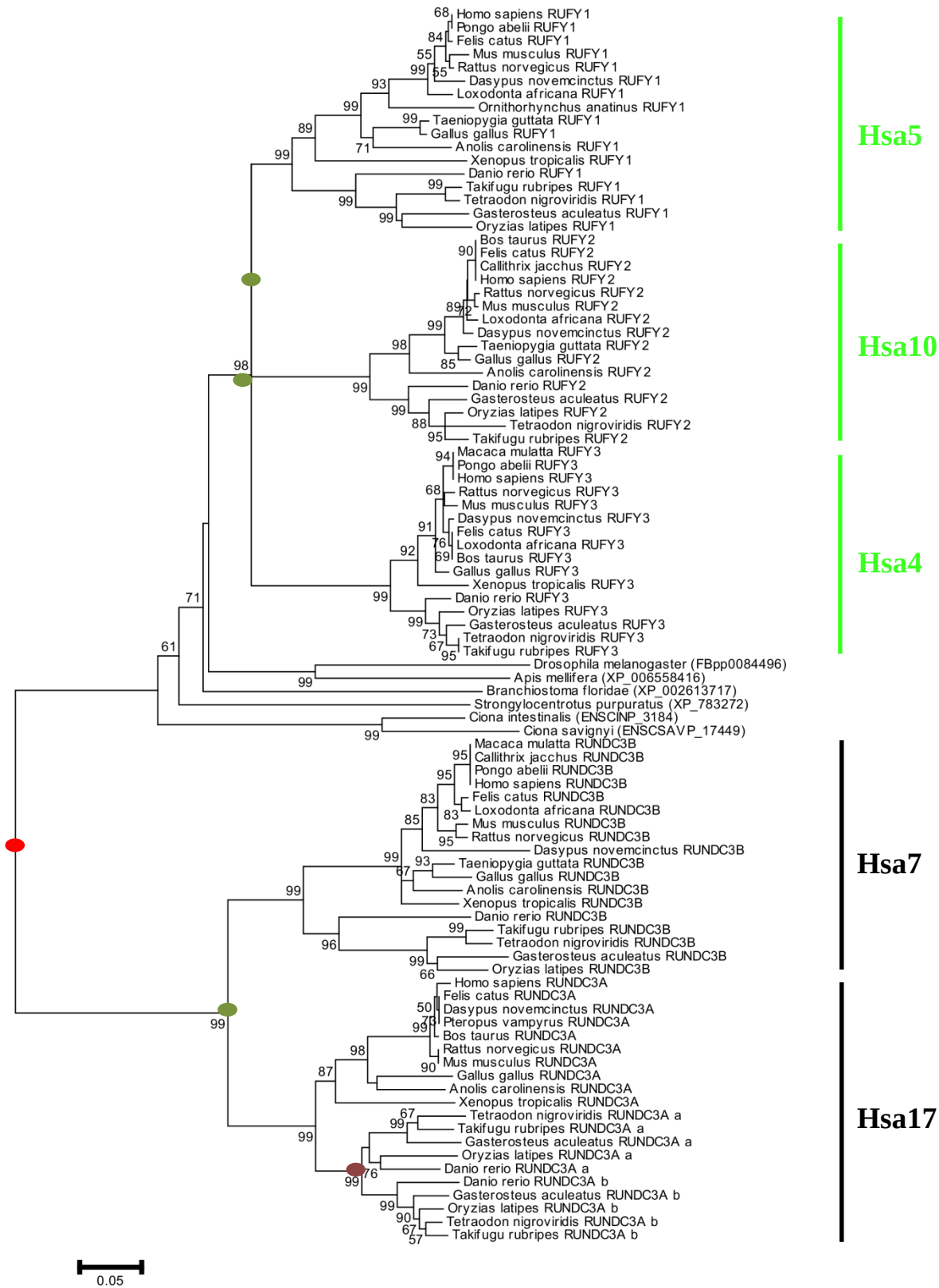
Ras Homolog Family-RHOH



Phylogenetic tree of RHOH family.

Neighbor-Joining tree of the RHOH family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site. * shows another paralog which is missing in tetrapods named as RHOGB by our group.

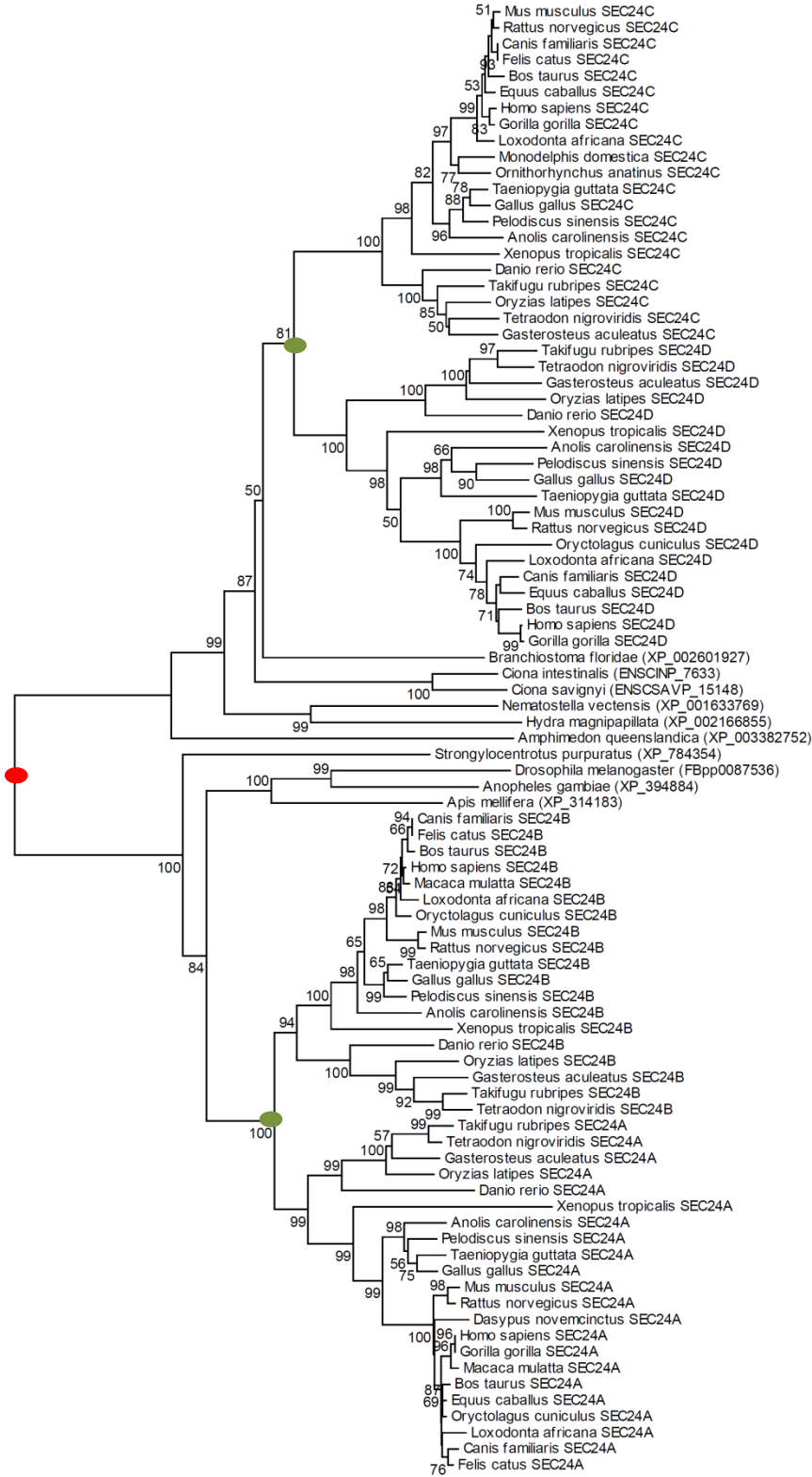
RUN and FYVE domain containing-RUFY



Phylogenetic tree of RUFY family.

Neighbor-Joining tree of the RUFY family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site.

Protein transport protein SEC24



Hsa10

Hsa4

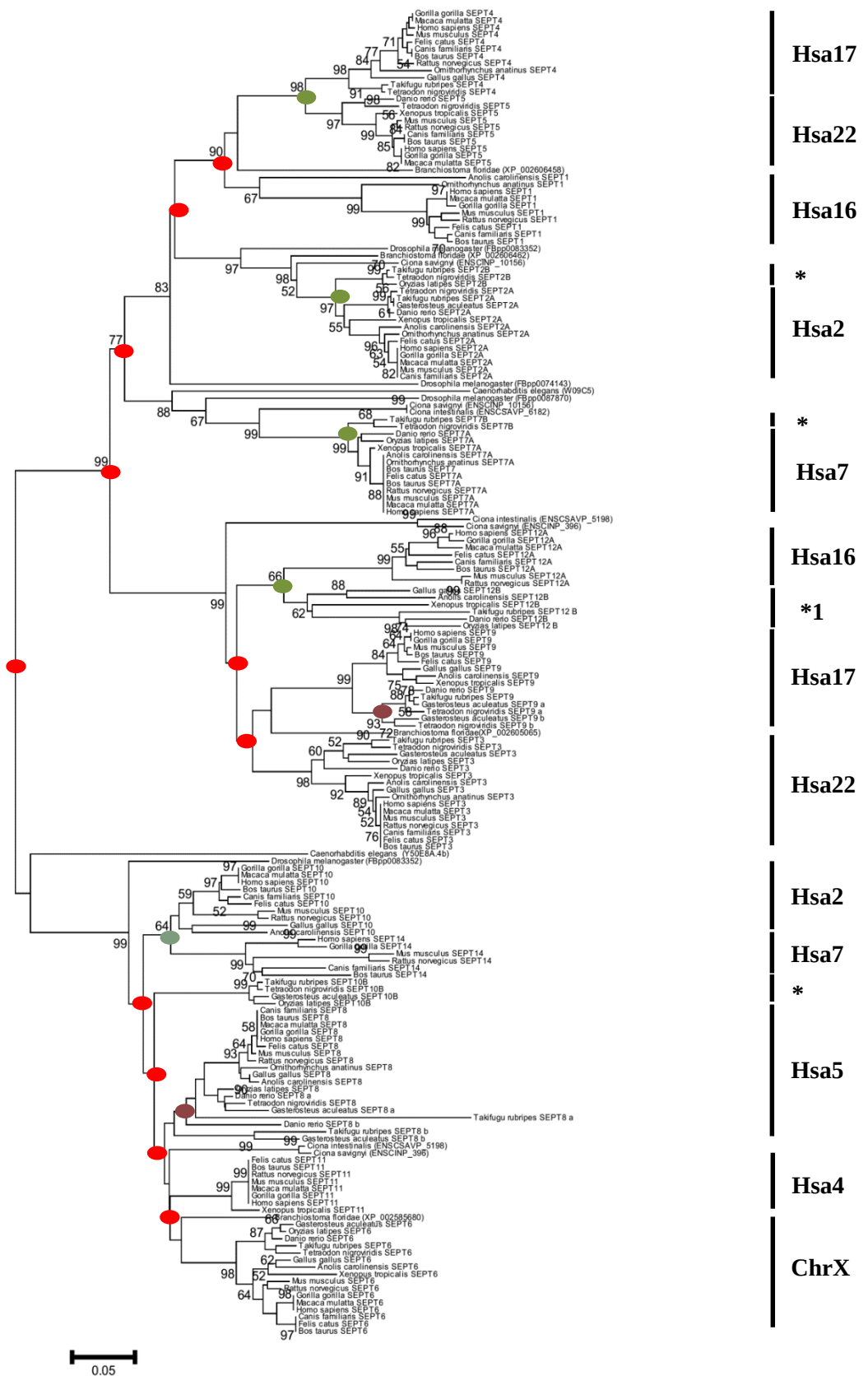
Hsa4

Hsa5

Phylogenetic tree of SEC24 family.

Neighbor-Joining tree of the SEC24 family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site.

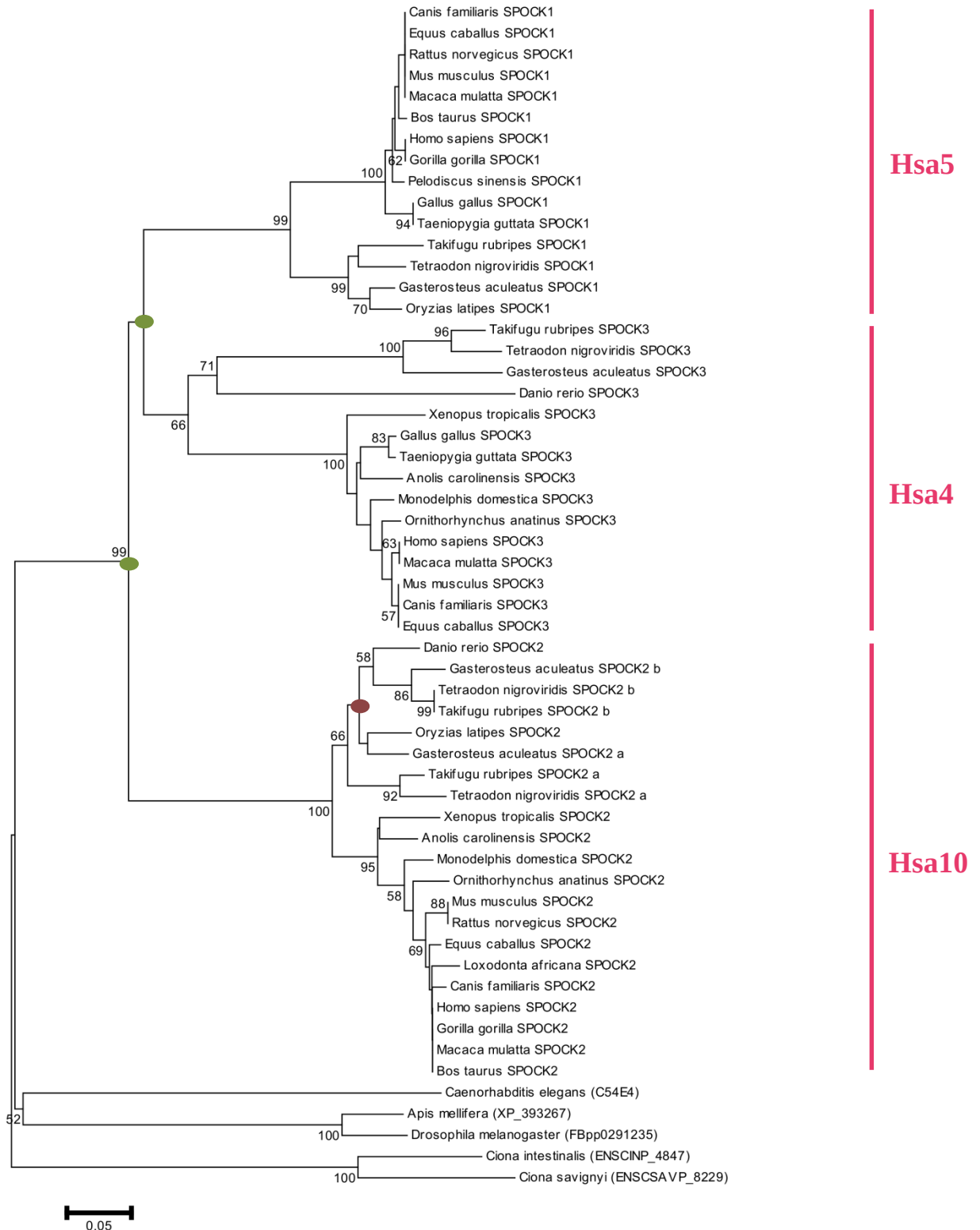
Septin-SEPT



Phylogenetic tree of SEPT family.

Neighbor-Joining tree of the SEPT family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site. * represent paralogs which is missing in tetrapods. SEPT7B, SEPT2B and SEPT10B. *1 represents paralog which is missing in mammals named as SEPT12B by our group.

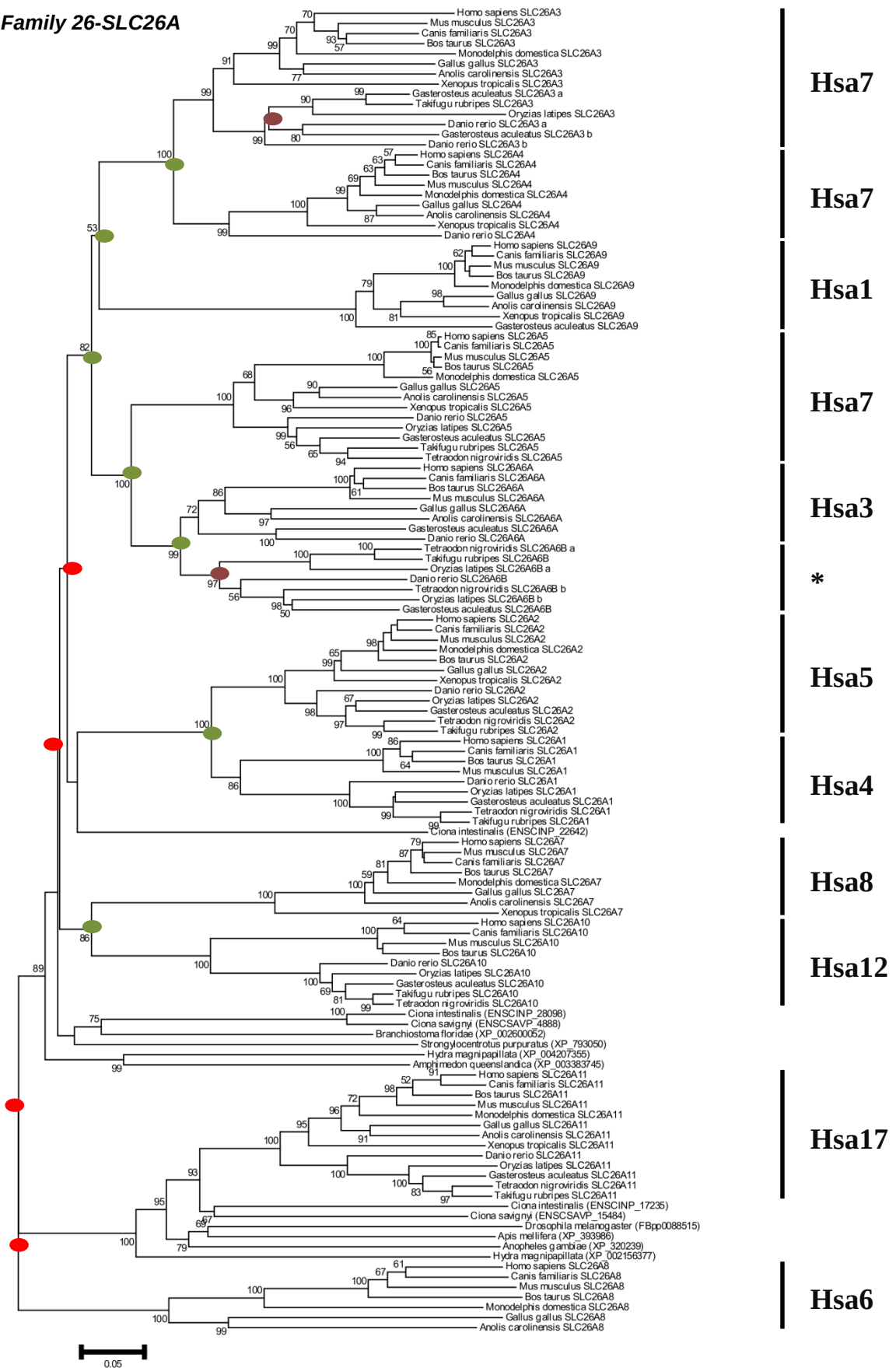
Sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) - SPOCK



Phylogenetic tree of SPOCK family.

Neighbor-Joining tree of the SPOCK family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site.

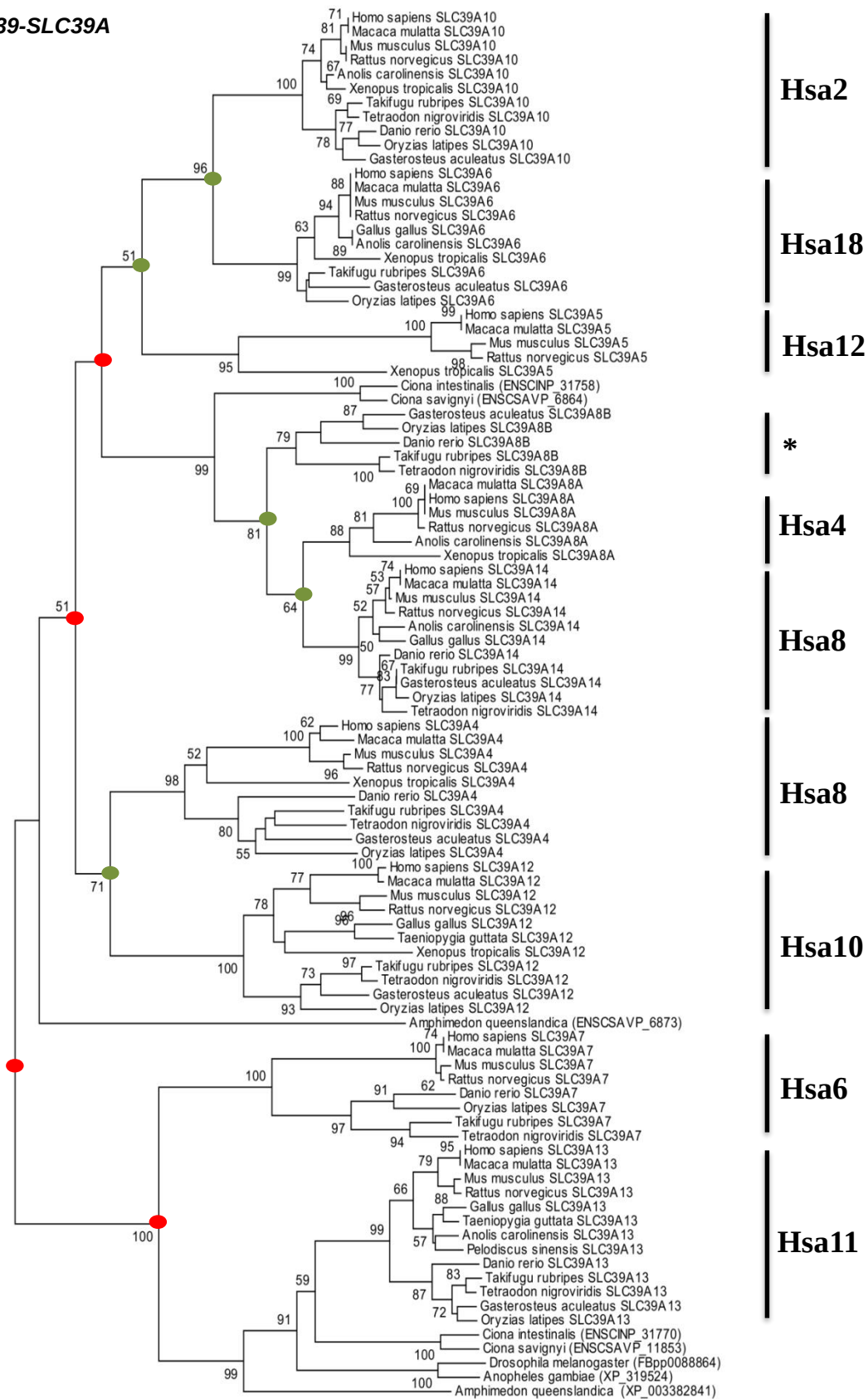
Solute Carrier Family 26-**SLC26A**



Phylogenetic tree of **SLC26A** family.

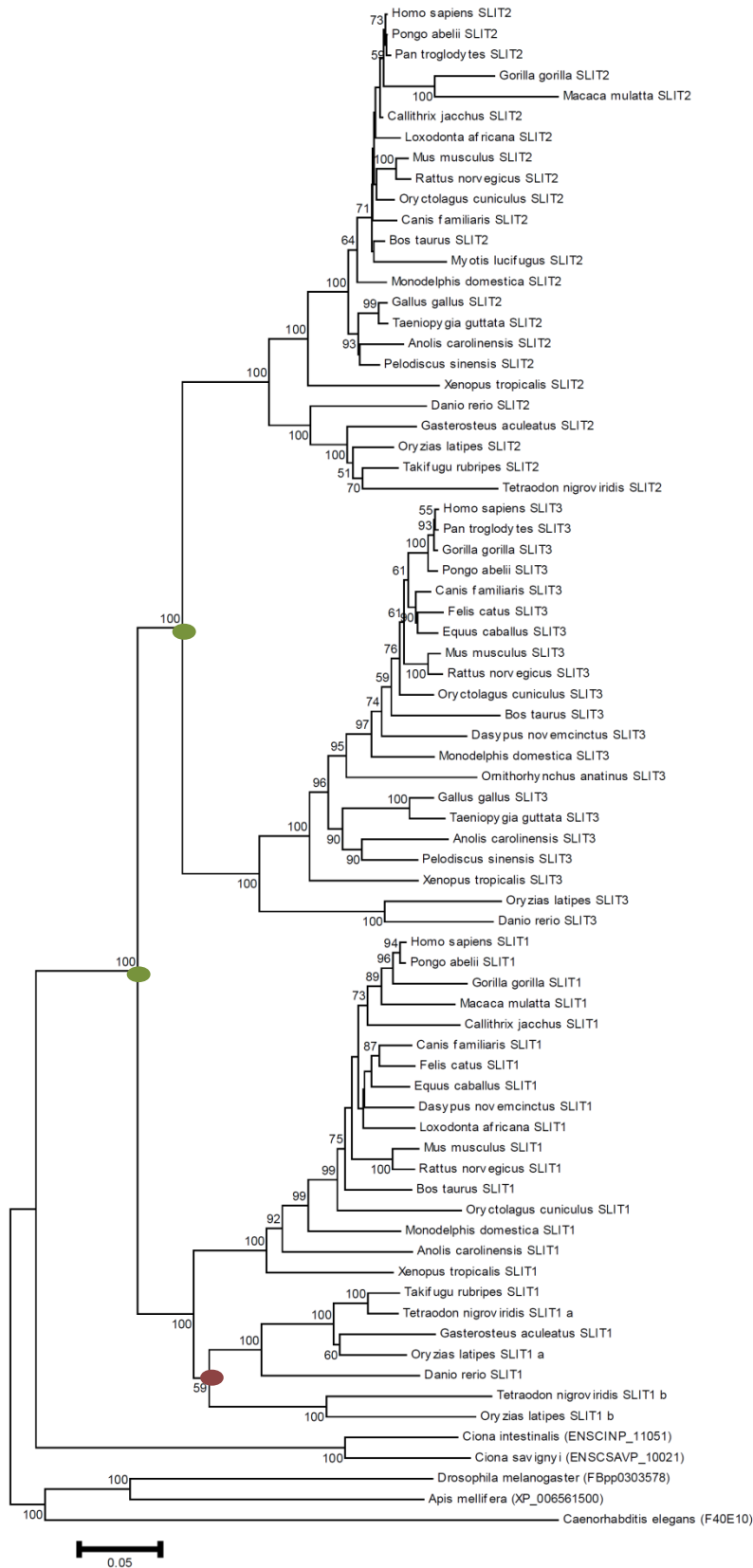
Neighbor-Joining tree of the SLC26A family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site. * shows another paralog which is missing in tetrapods, named as SLC26A6B by our group.

Solute Carrier Family 39-**SLC39A**



Phylogenetic tree of SLC39A family.

Neighbor-Joining tree of the SLC39A family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site. * shows another paralog which is missing in tetrapods named as SLC39A8B by our group.



Hsa4

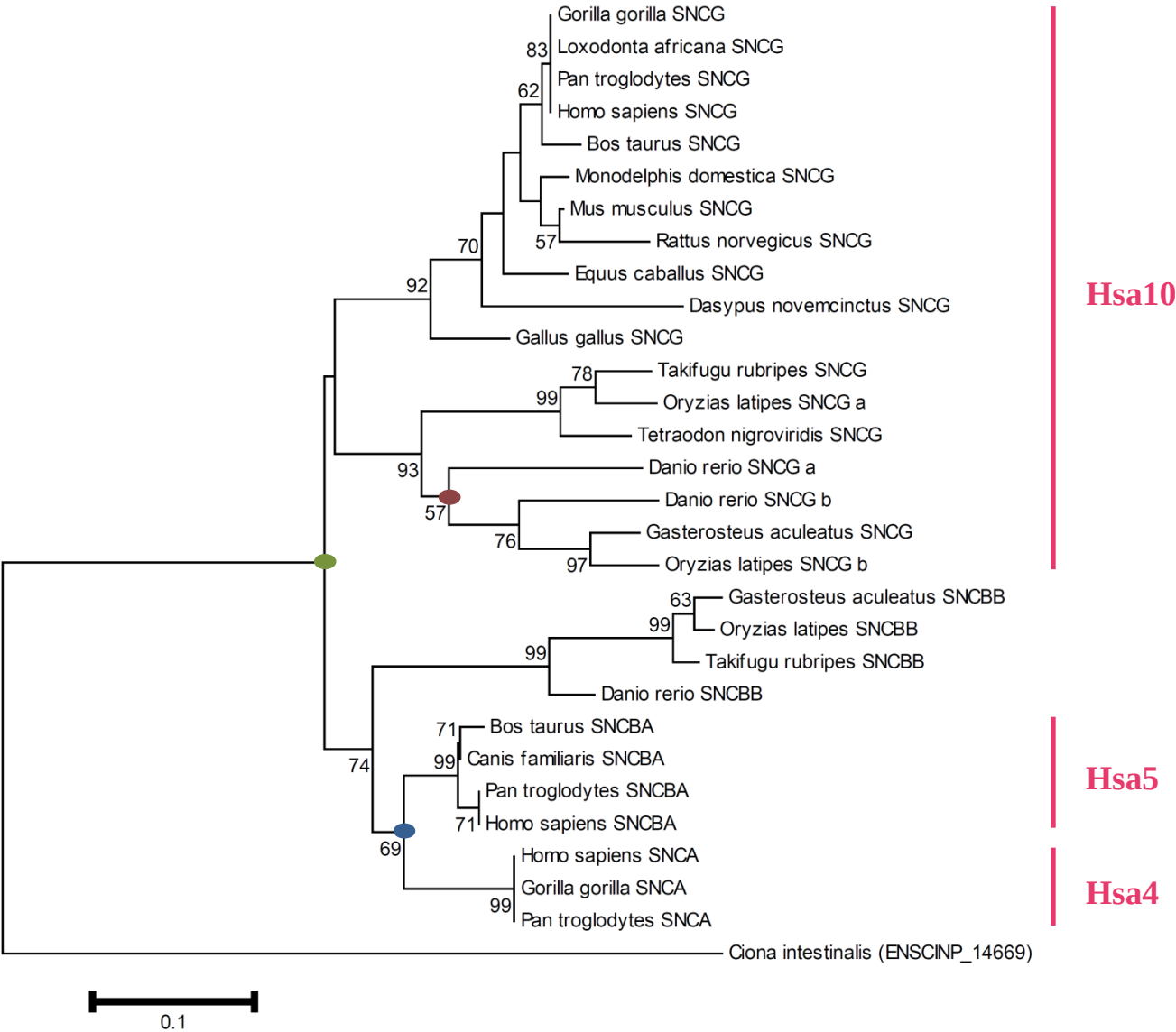
Hsa5

Hsa10

Phylogenetic tree of SLIT family.

Neighbor-Joining tree of the SLIT family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site.

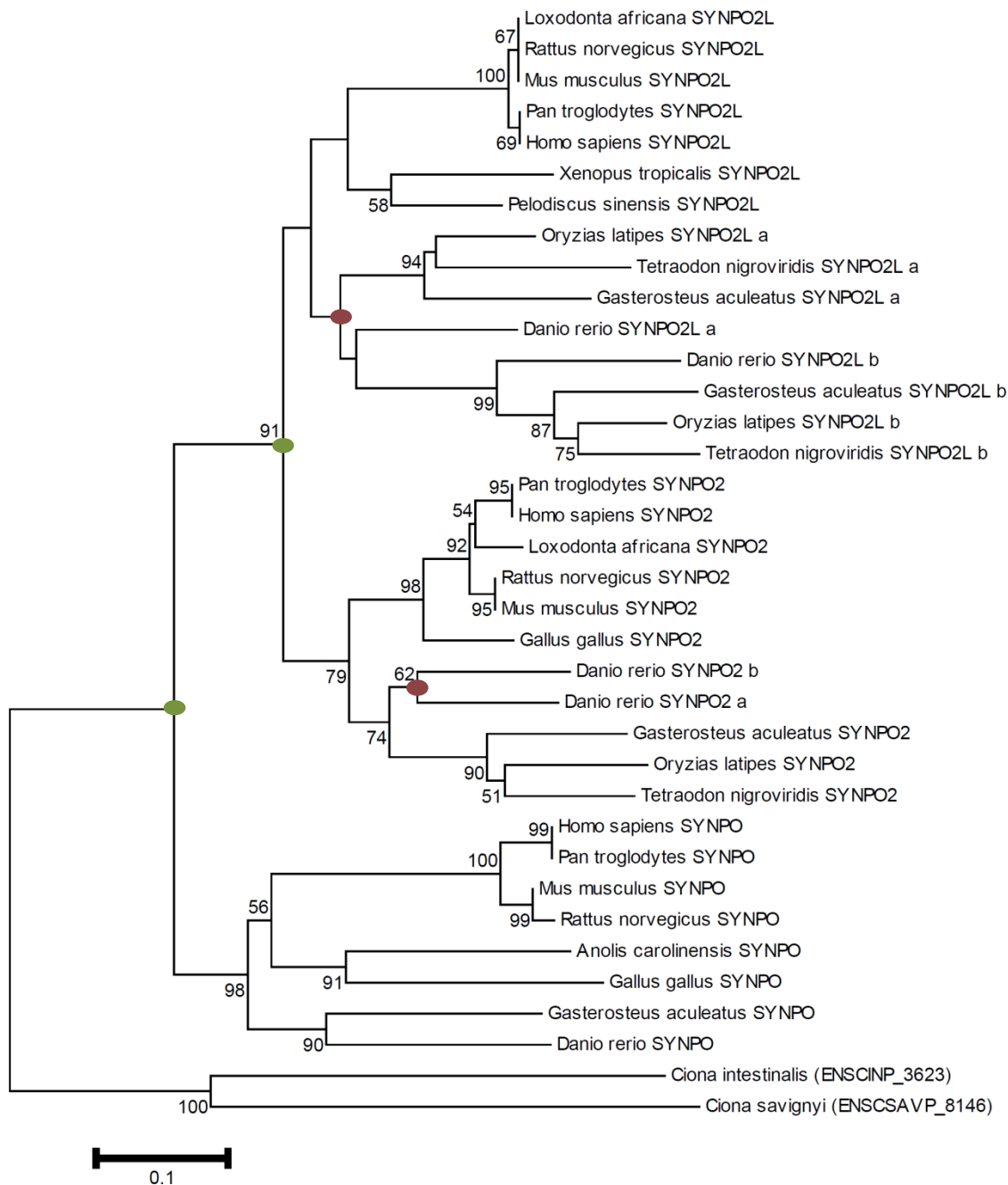
Synuclein-SNC



Phylogenetic tree of SNC family.

Neighbor-Joining tree of the SNC family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site.

Synaptopodin-SYNPO



Hsa10

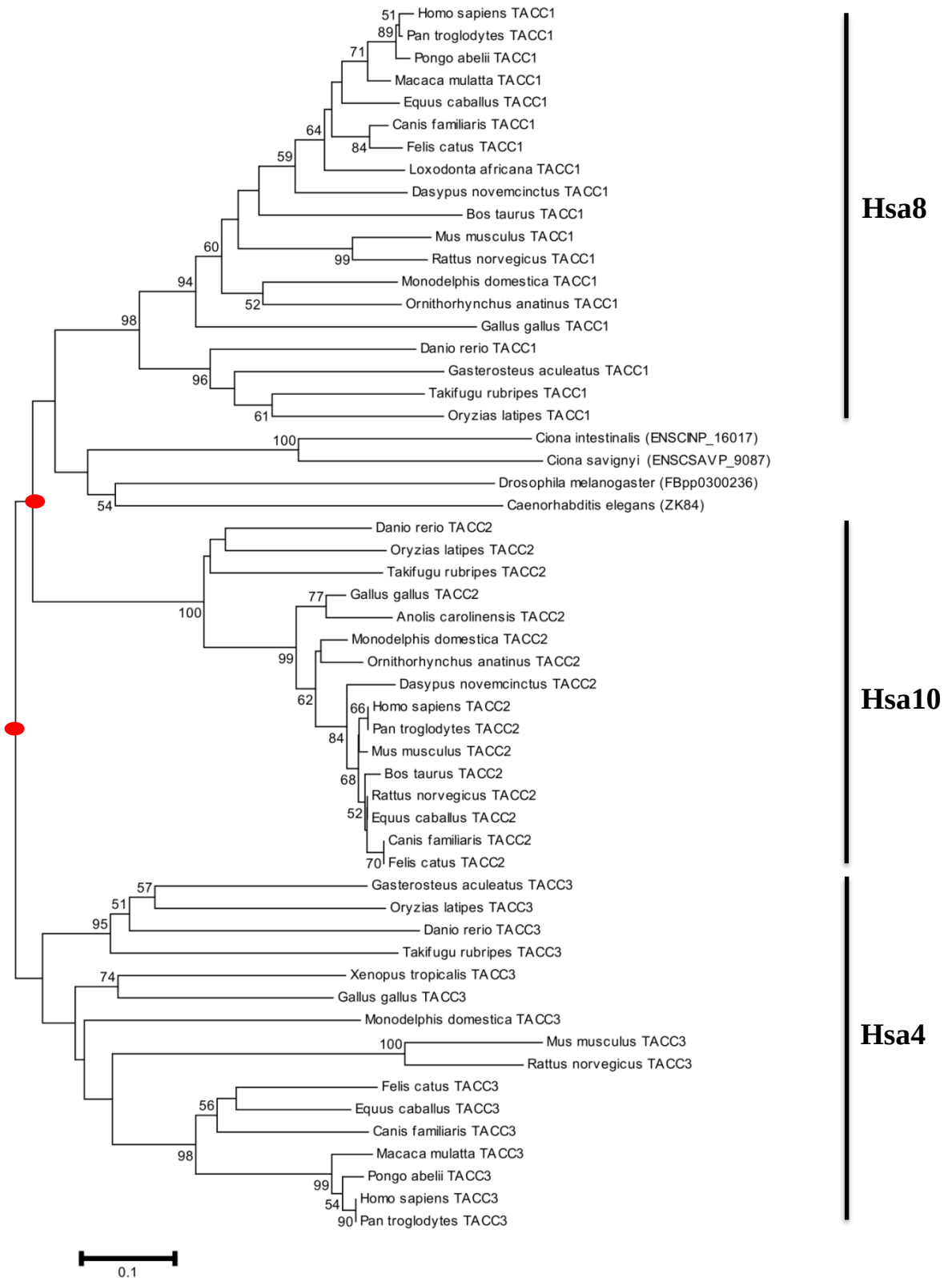
Hsa4

Hsa5

Phylogenetic tree of SYNPO family.

Neighbor-Joining tree of the SYNPO family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site.

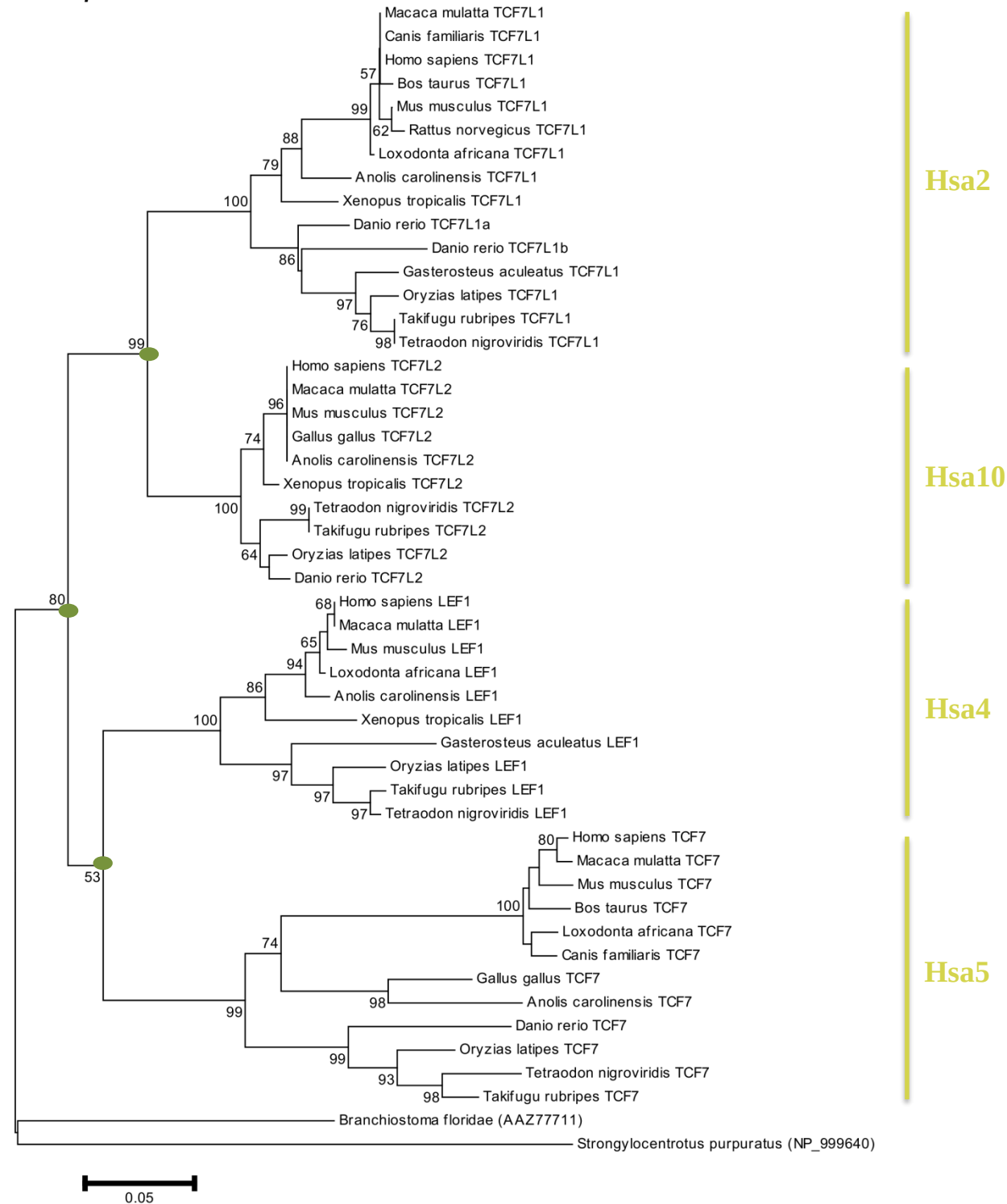
Transforming, acidic coiled-coil containing protein-TACC



Phylogenetic tree of TACC family.

Neighbor-Joining tree of the TACC family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site.

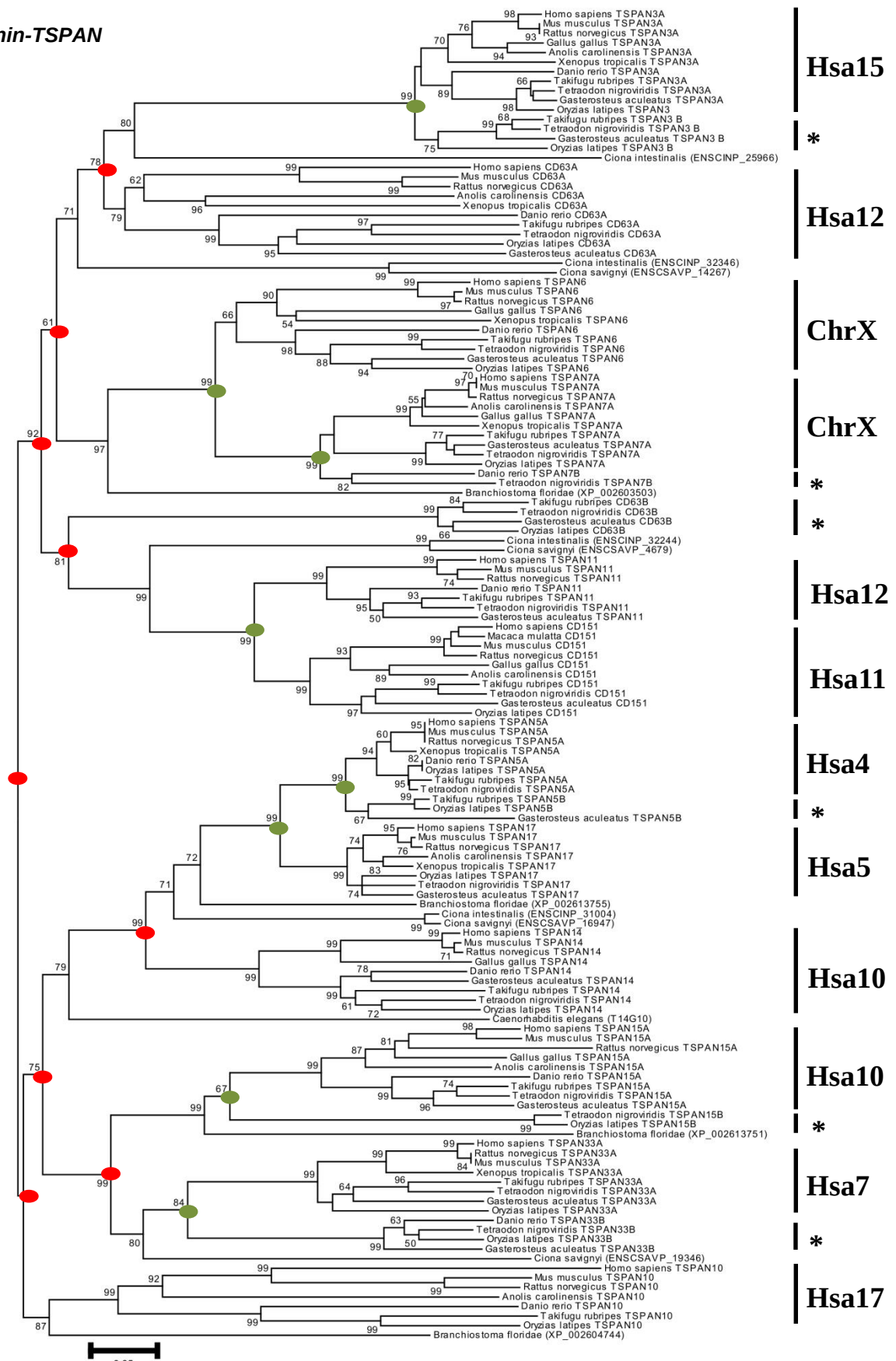
Transcription Factor 7-TCF7



Phylogenetic tree of TCF family.

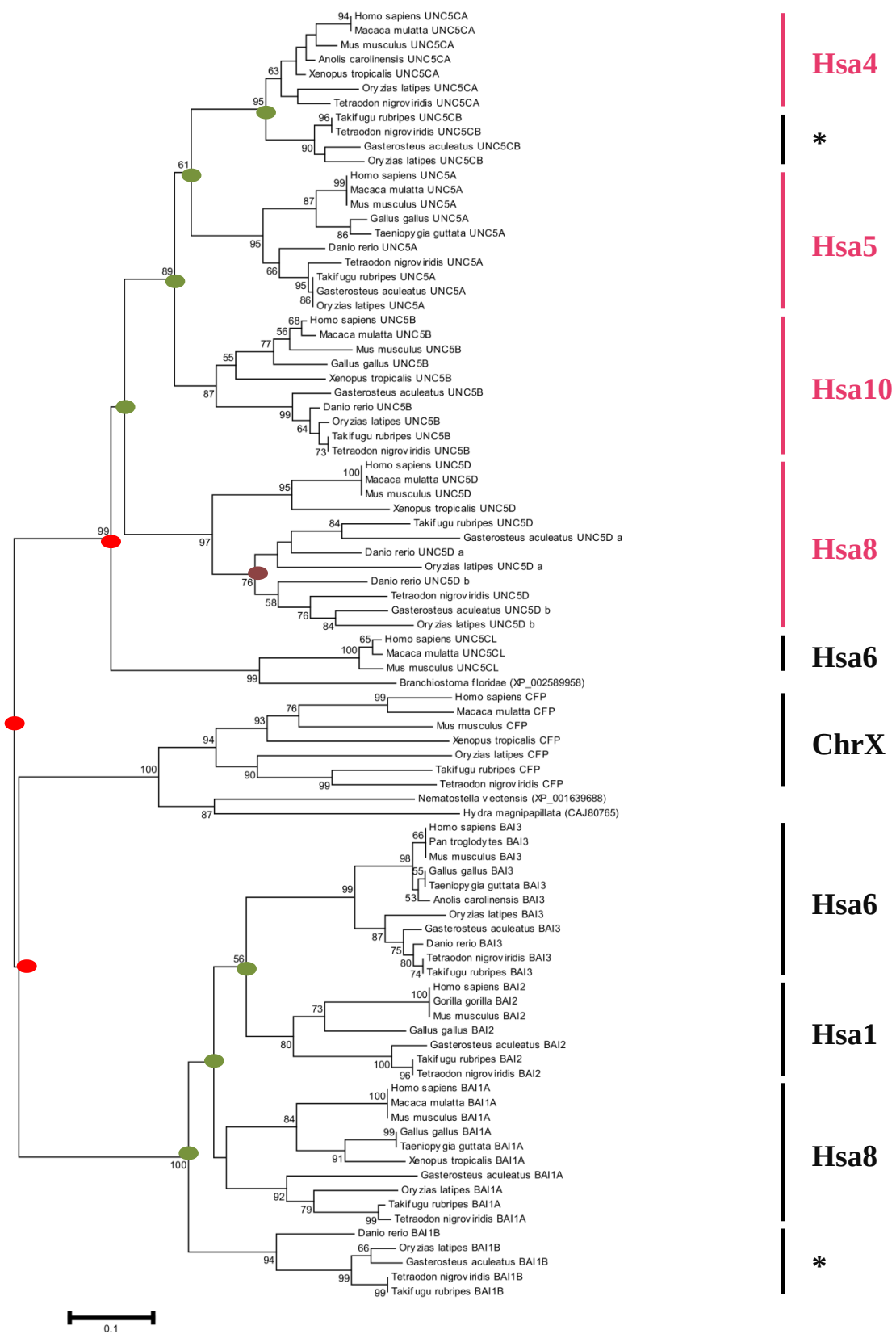
Neighbor-Joining tree of the TCF family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site.

Tetraspanin-TSPAN



Phylogenetic tree of TSPAN family.

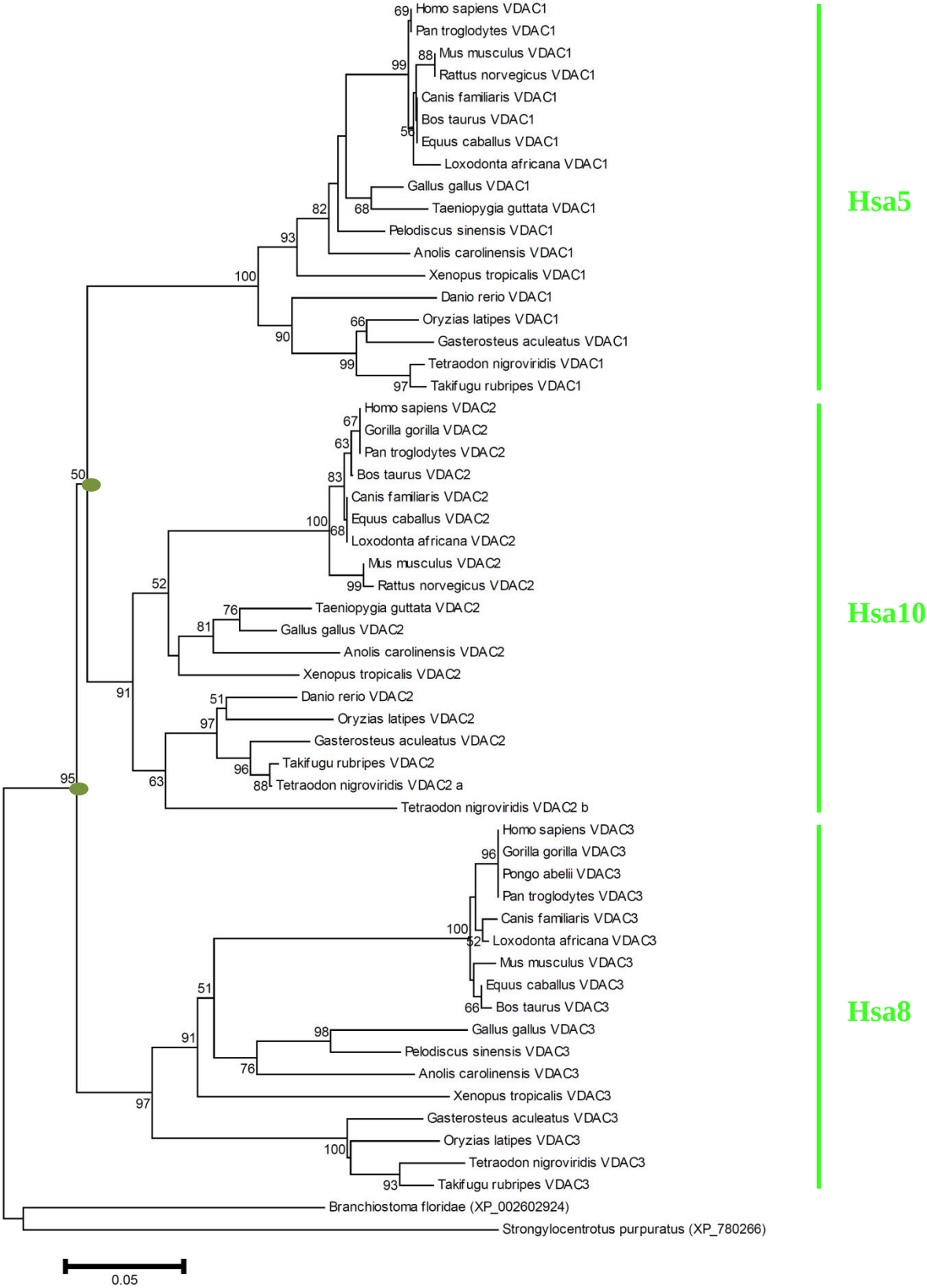
Neighbor-Joining tree of the TSPAN family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site. * shows another paralog which are missing in tetrapods TSPAN3B, TSPAN7B, CD63B, TSPAN5B, TSPAN15B and TSPAN33B by our group.



Phylogenetic tree of UNC5 family.

Neighbor-Joining tree of the UNC5 family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site. * shows another paralogs which are missing in tetrapods, named as UNC5CB and BAI1B, respectively by our group.

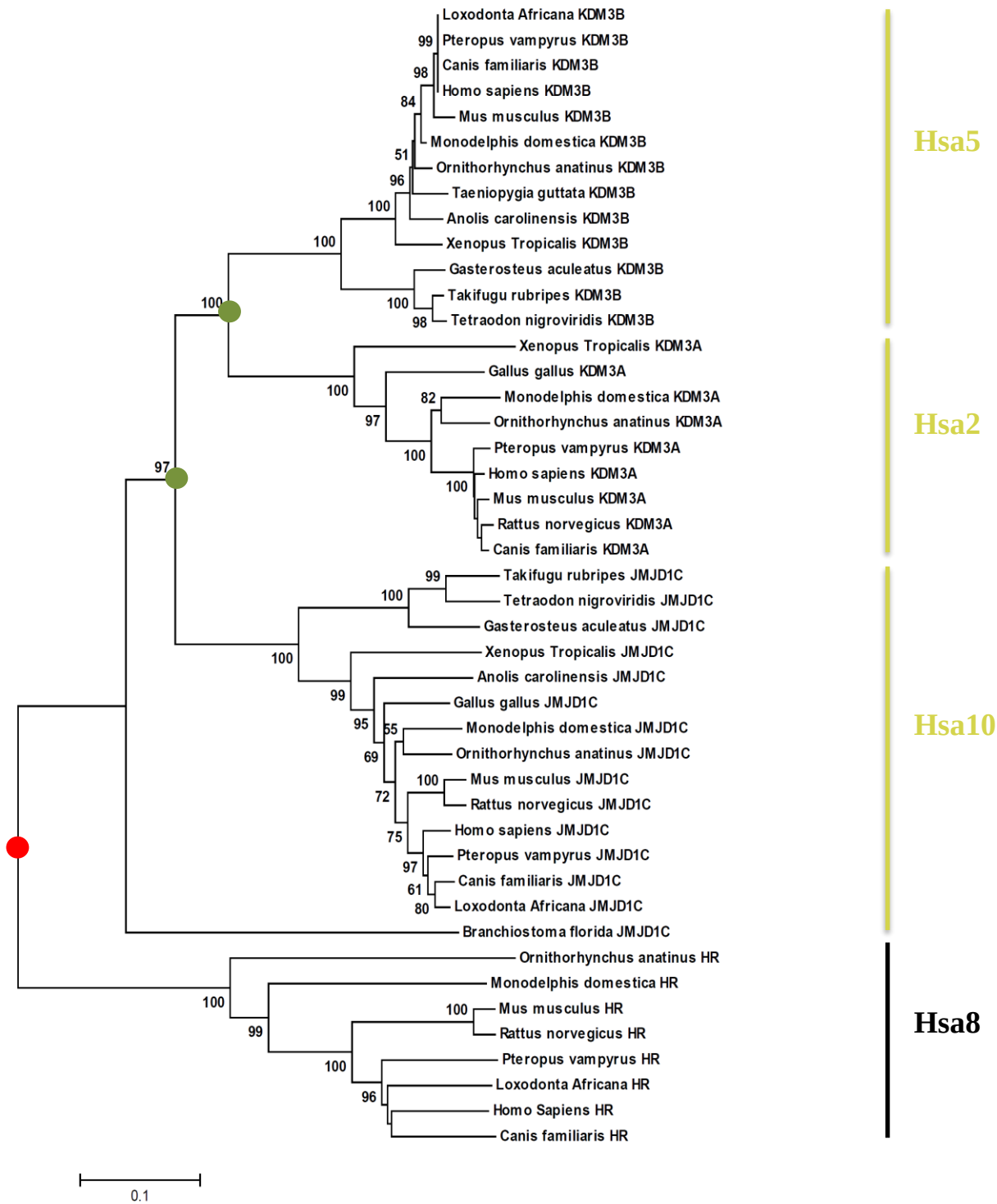
Voltage-dependent anion channel-VDAC



Phylogenetic tree of VDAC family.

Neighbor-Joining tree of the VDAC family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site.

HR lysine demethylase and nuclear receptor corepressor (HR)



Phylogenetic tree of HR family:

Neighbor-Joining tree of the HR family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site.

Nuclear Receptor Binding SET domain protein-NSD



Phylogenetic tree of NSD family:

Neighbor-Joining tree of the NSD family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site.