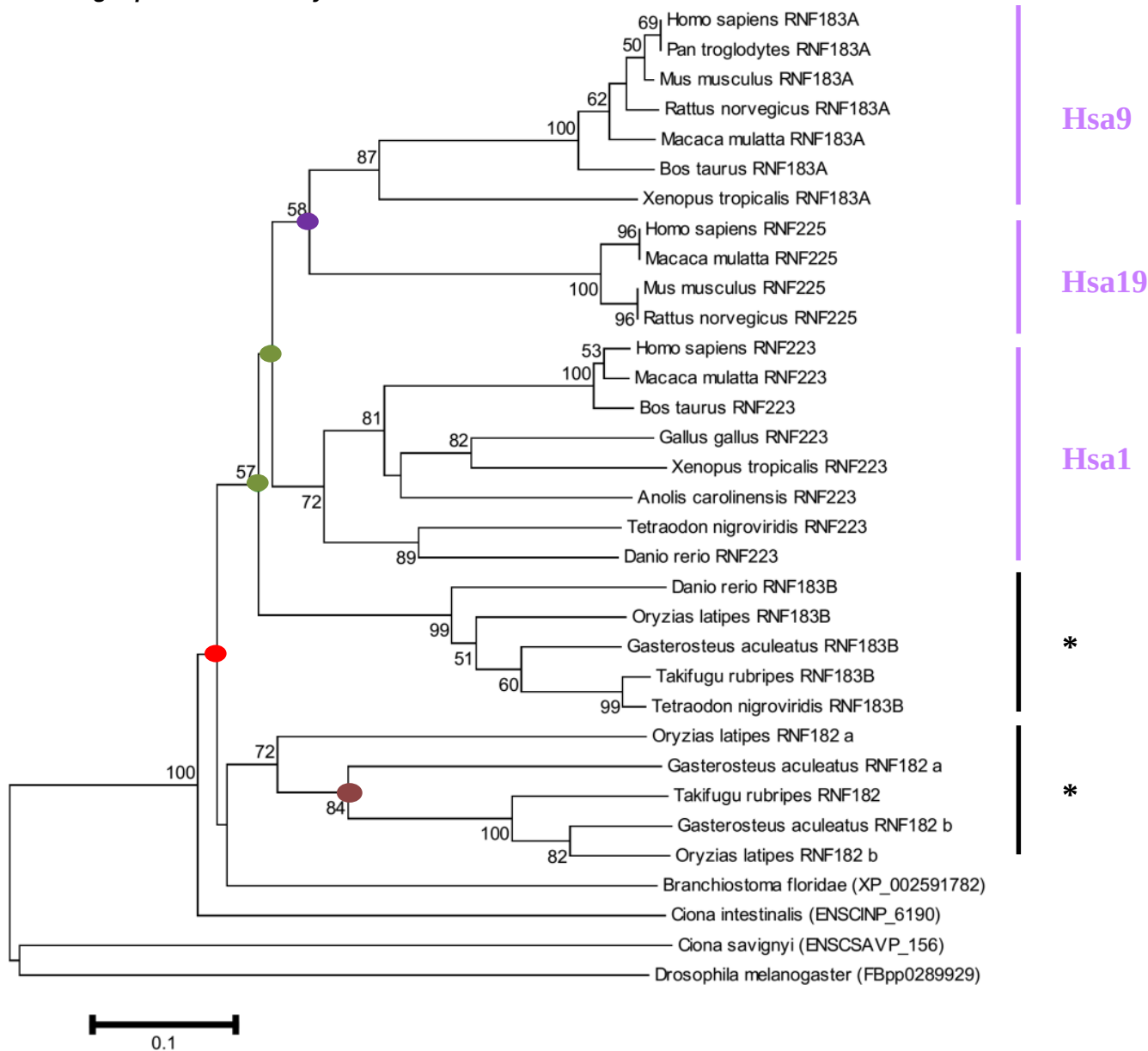


**Neighbor Joining Trees of gene families residing on
chromosomes 1, 6, 9 and 19.**

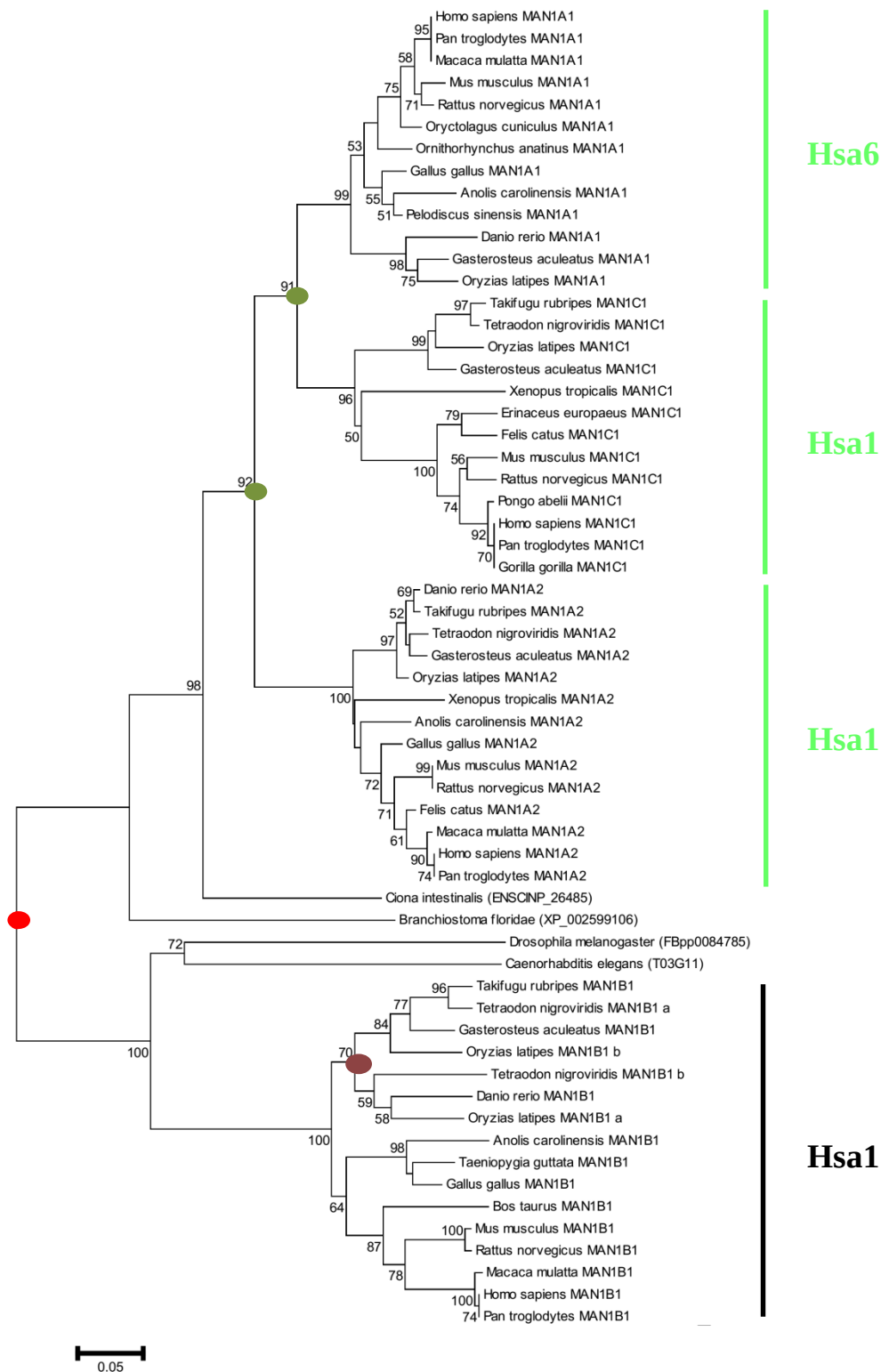
RING finger protein subfamily 2-RNF



Phylogenetic tree of RNF family.

Neighbor-Joining tree of the RNF 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 whose tetrapods are missing, named as RNF183B and RNF182 by our group.

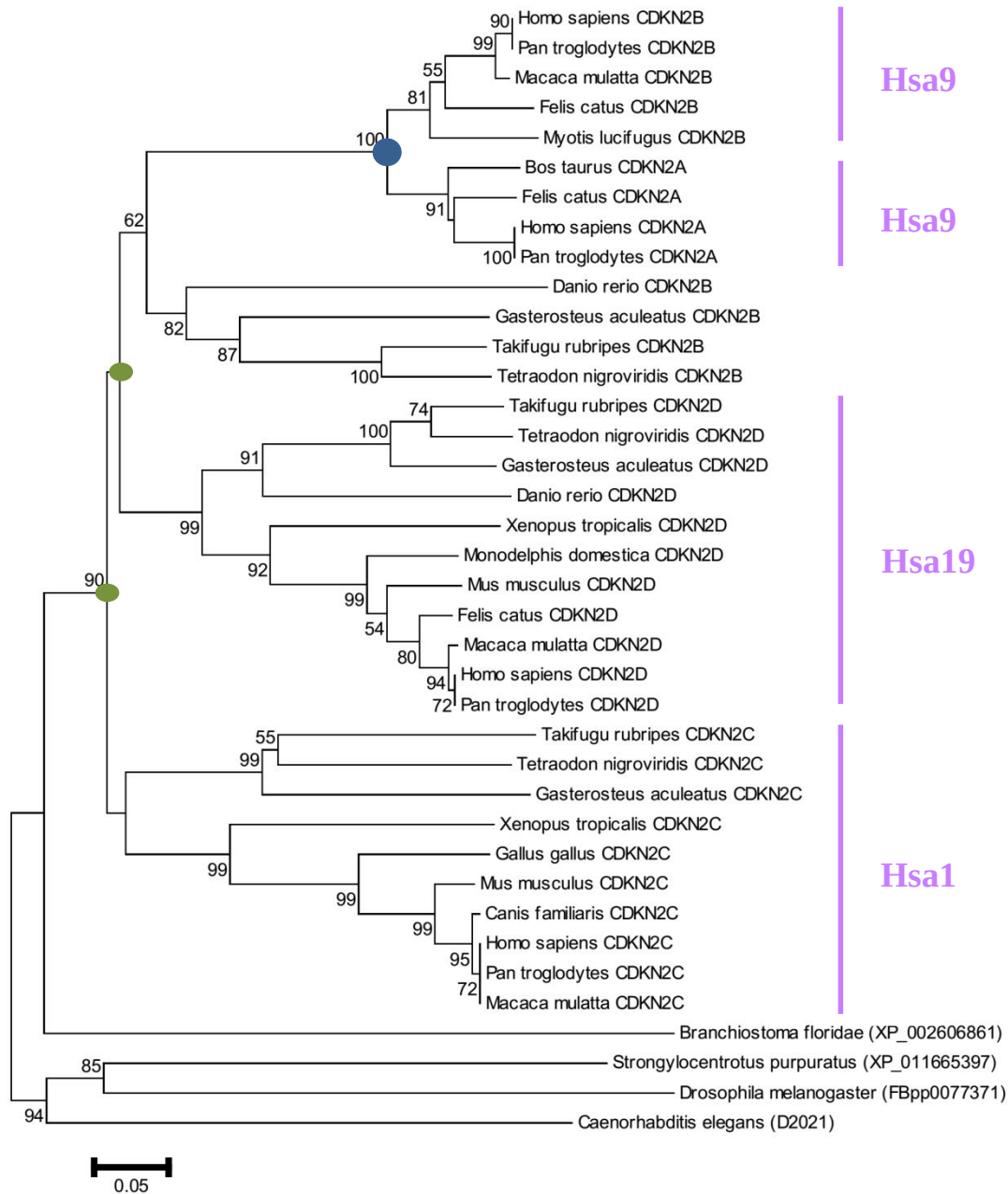
Mannosyl-oligosaccharide 1,2-alpha-mannosidase protein Family-MAN1



Phylogenetic tree of MAN1 family.

Neighbor-Joining tree of the MAN1 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.

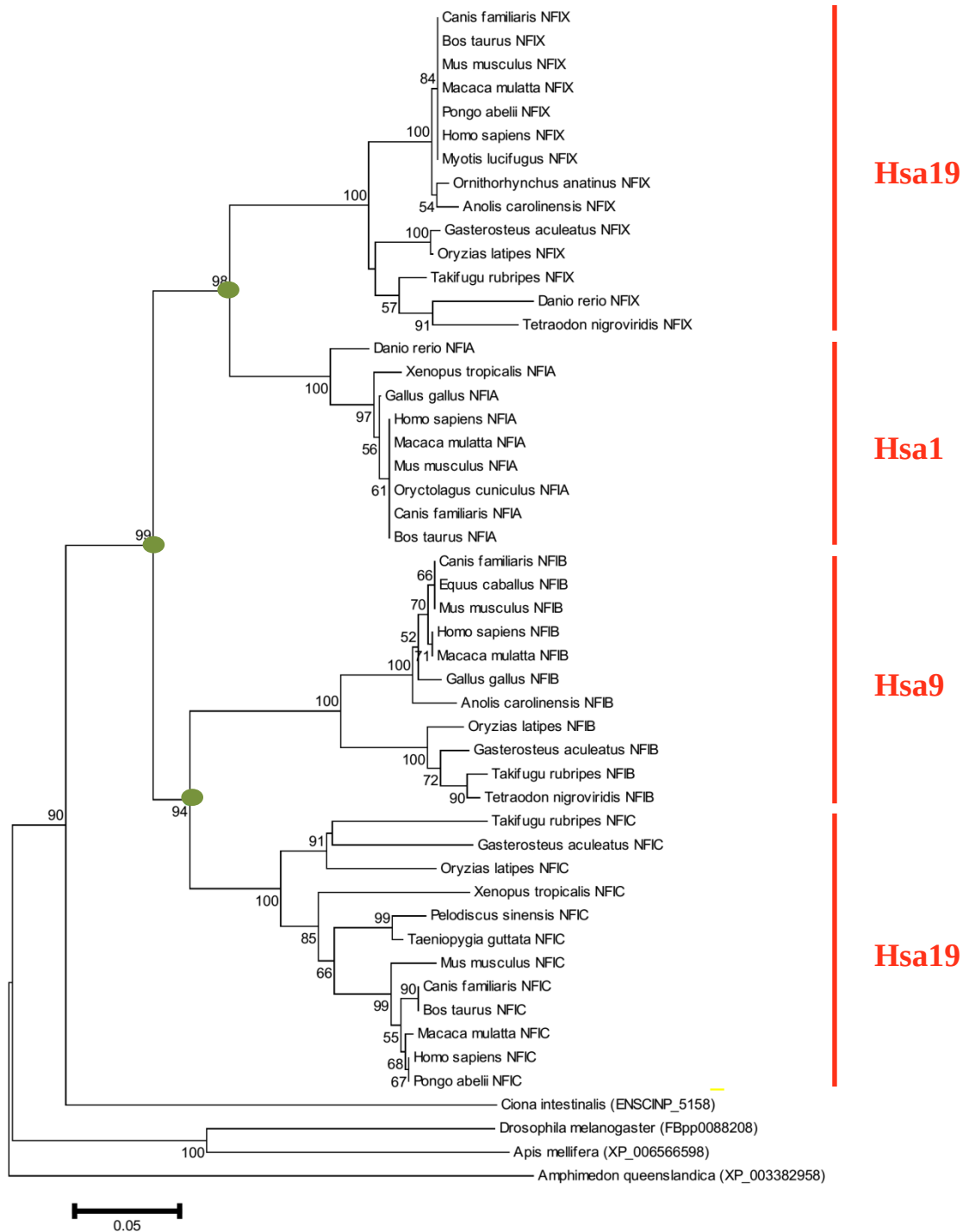
Cyclin-dependent kinase inhibitor Protein Family-CDKN2



Phylogenetic tree of CDKN2 family.

Neighbor-Joining tree of the CDKN2 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.

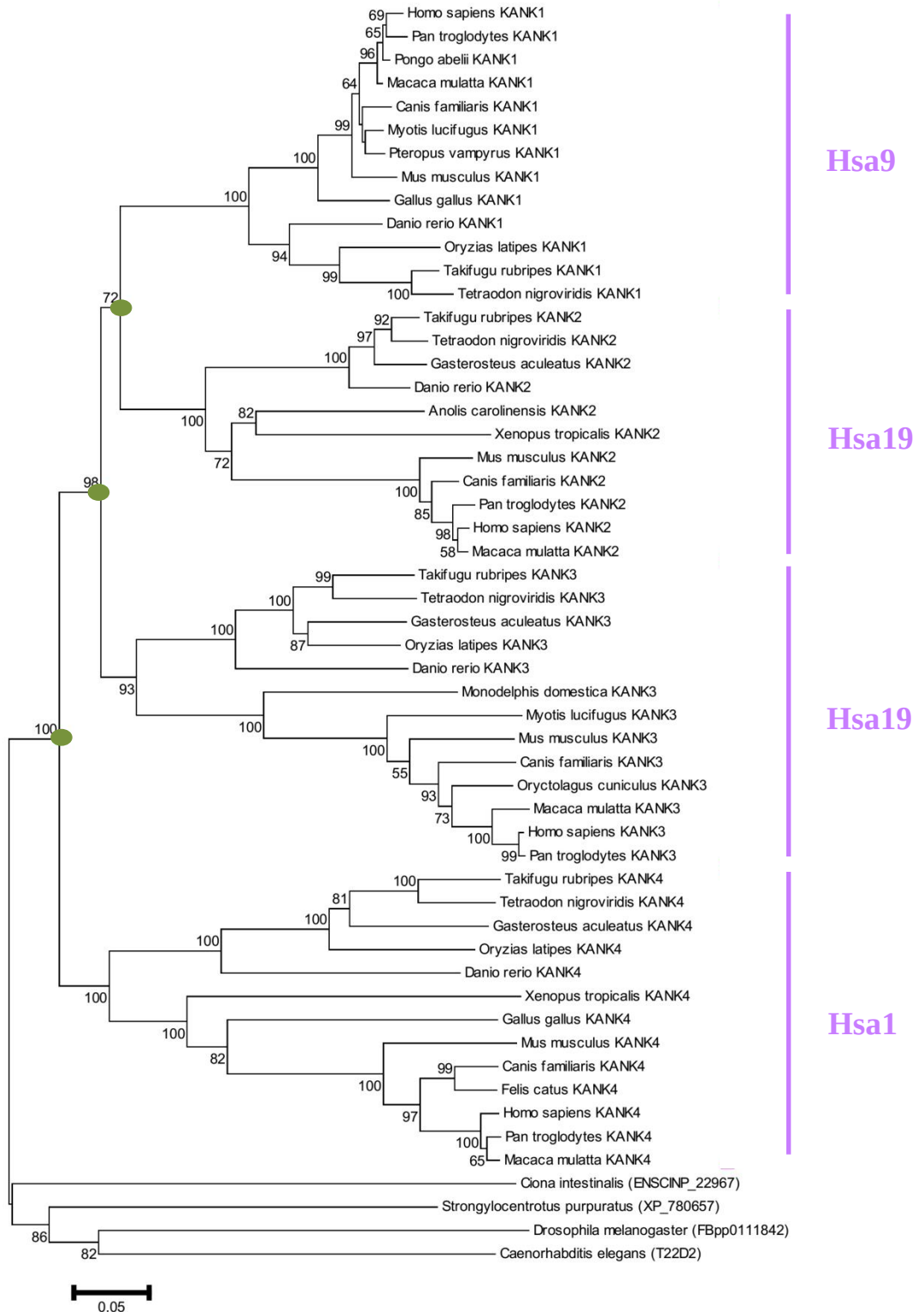
Nuclear factor 1 protein Family-NFI



Phylogenetic tree of NFI family.

Neighbor-Joining tree of the NFI 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.

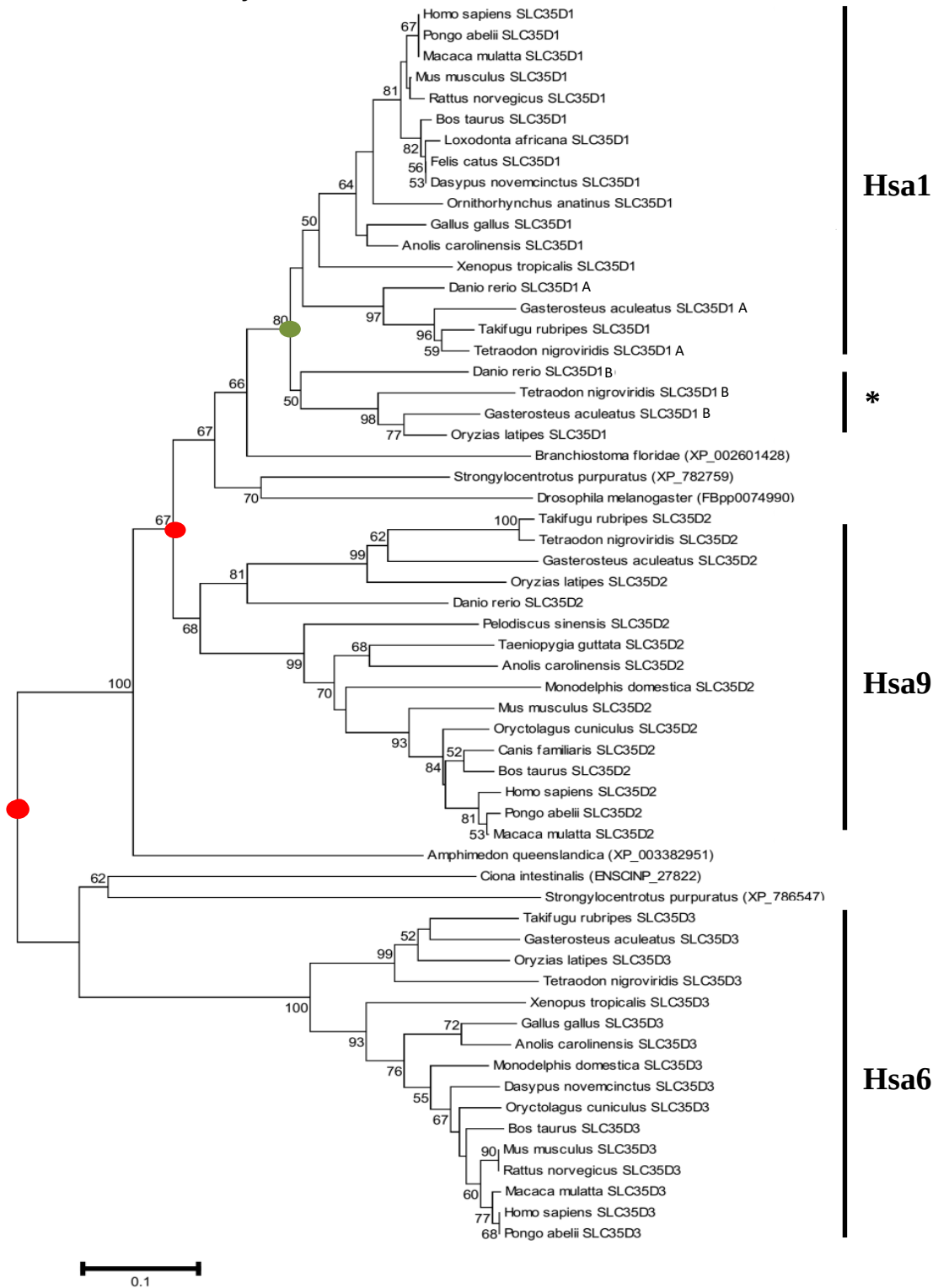
KN motif and ankyrin repeat domain Protein Family-KANK



Phylogenetic tree of KANK family.

Neighbor-Joining tree of the KANK 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.

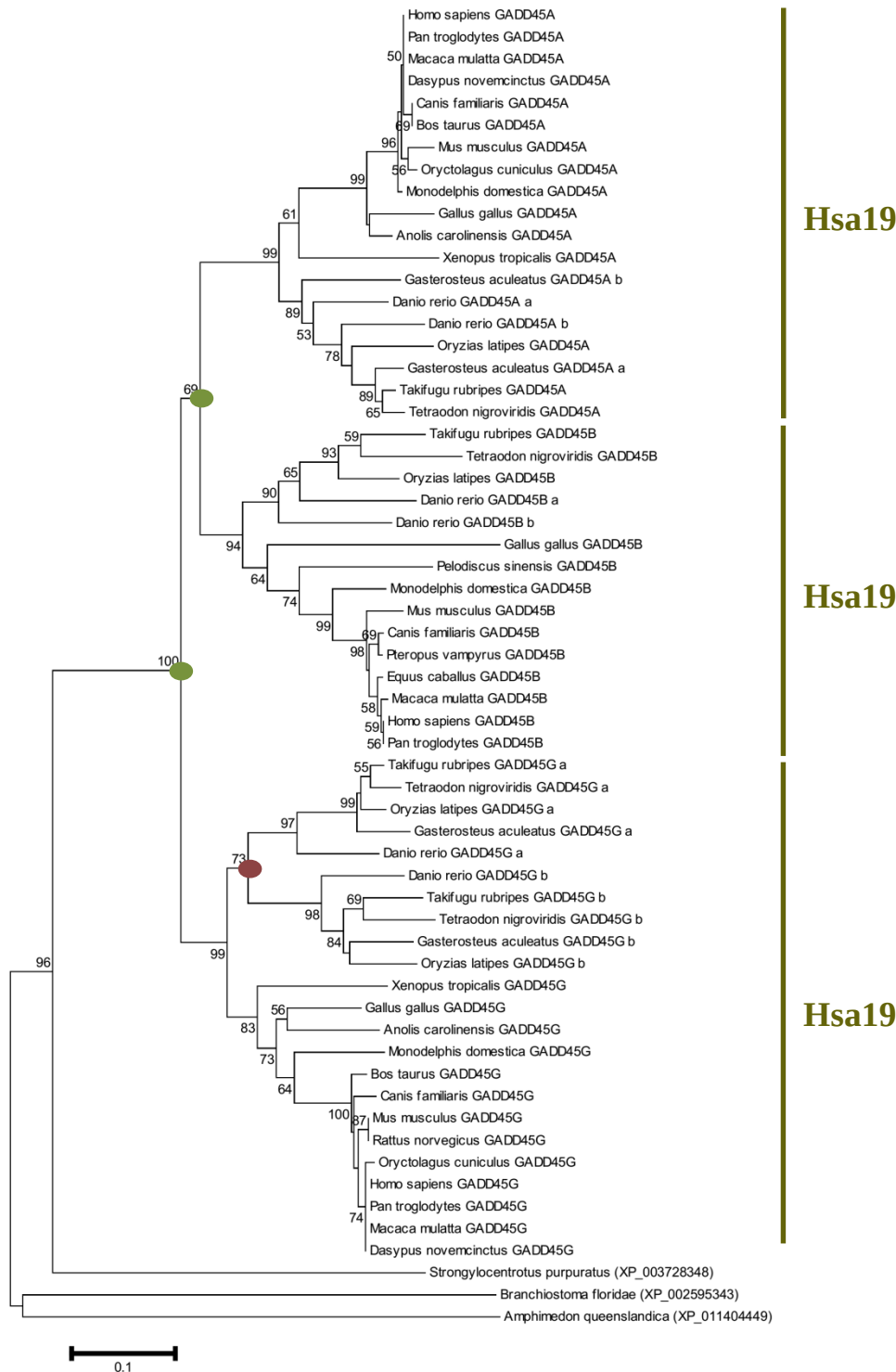
Solute Carrier Protein Family 35-SLC35



Phylogenetic tree of SLC35 family.

Neighbor-Joining tree of the SLC35 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 SLC35D1B by our group.

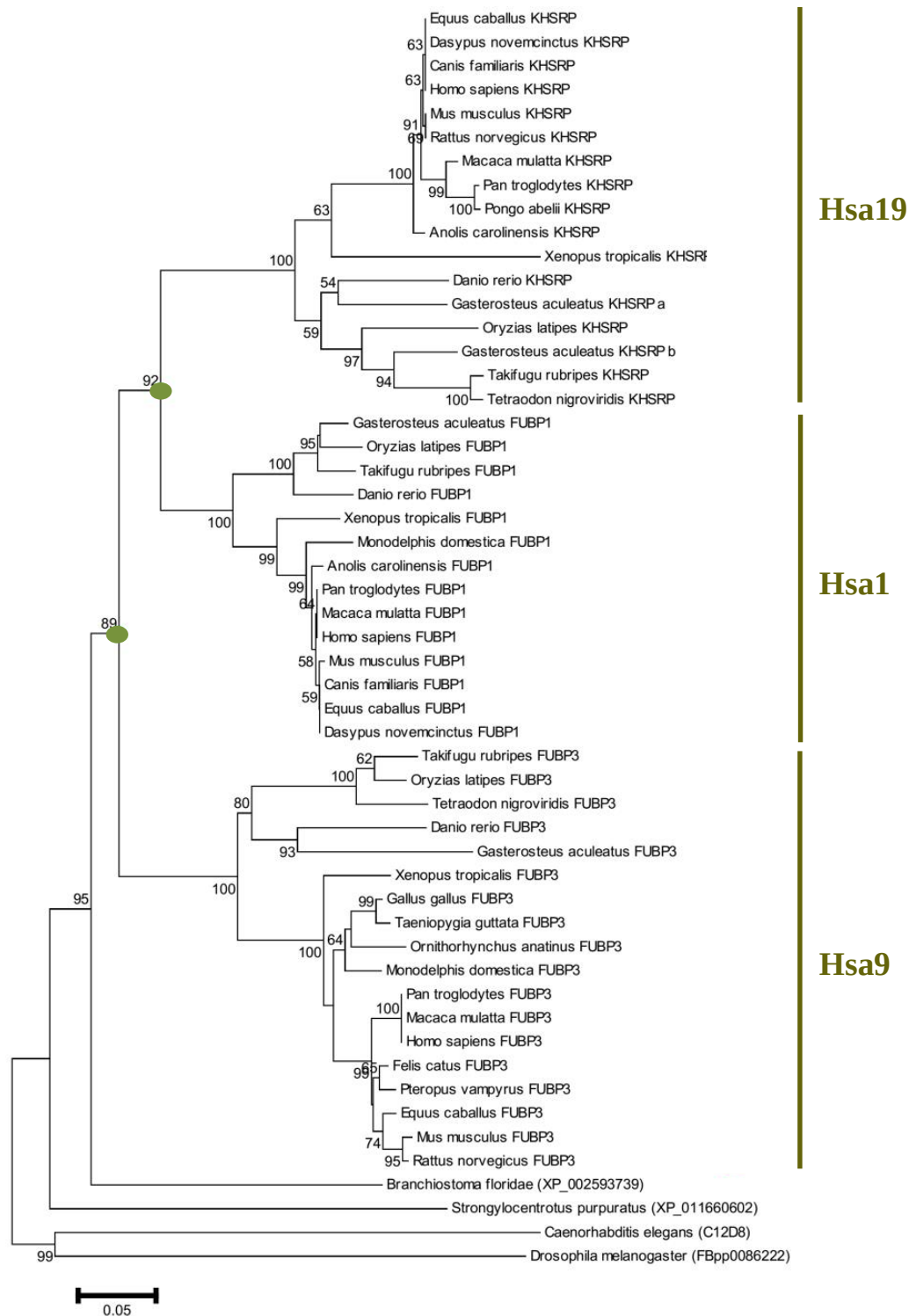
Growth arrest and DNA-damage-inducible 45 Protein Family-GADD45



Phylogenetic tree of GADD45 family.

Neighbor-Joining tree of the GADD45 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.

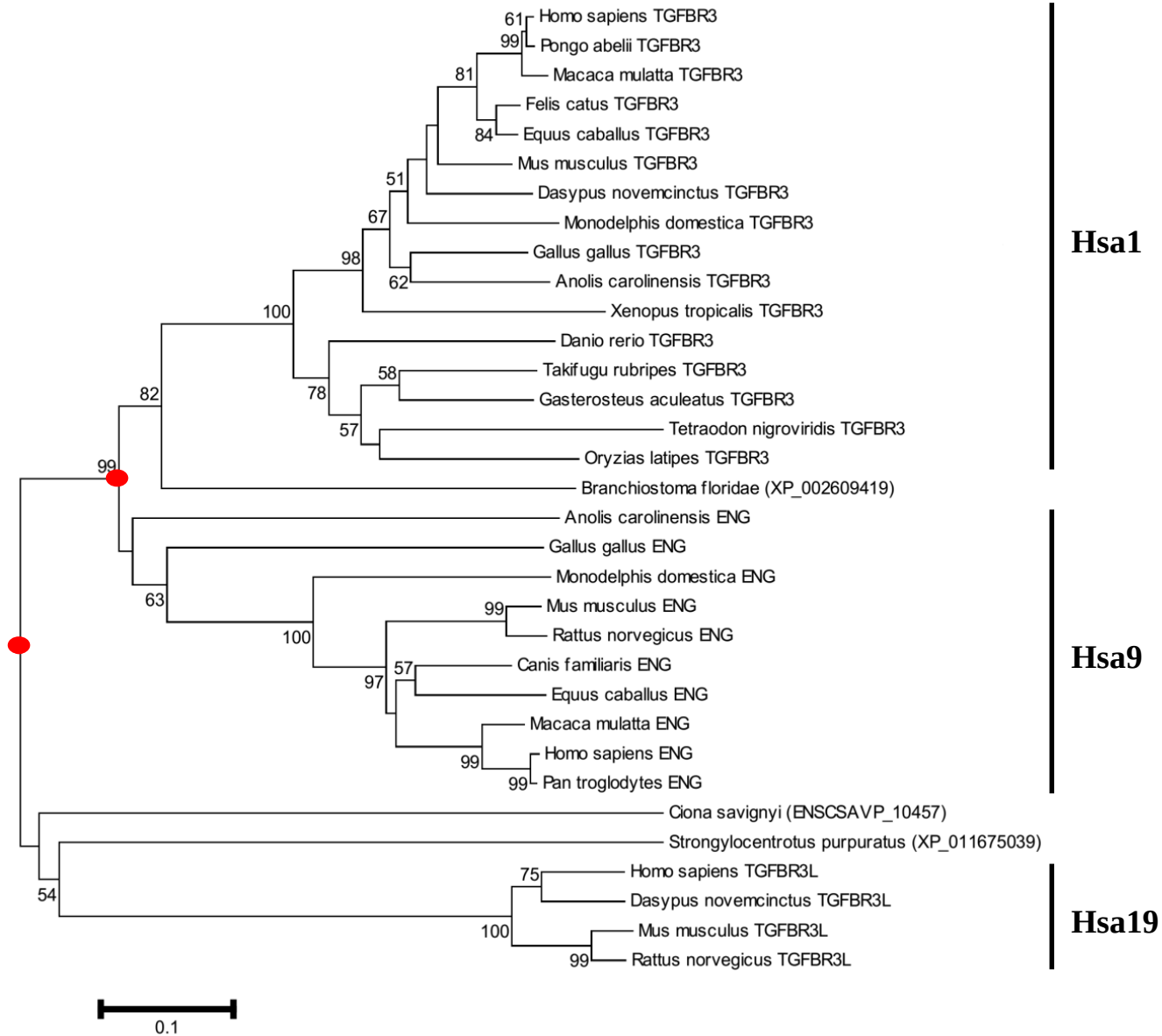
Far upstream element (FUSE) binding protein Family-FUBP



Phylogenetic tree of FUBP family.

Neighbor-Joining tree of the FUBP 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.

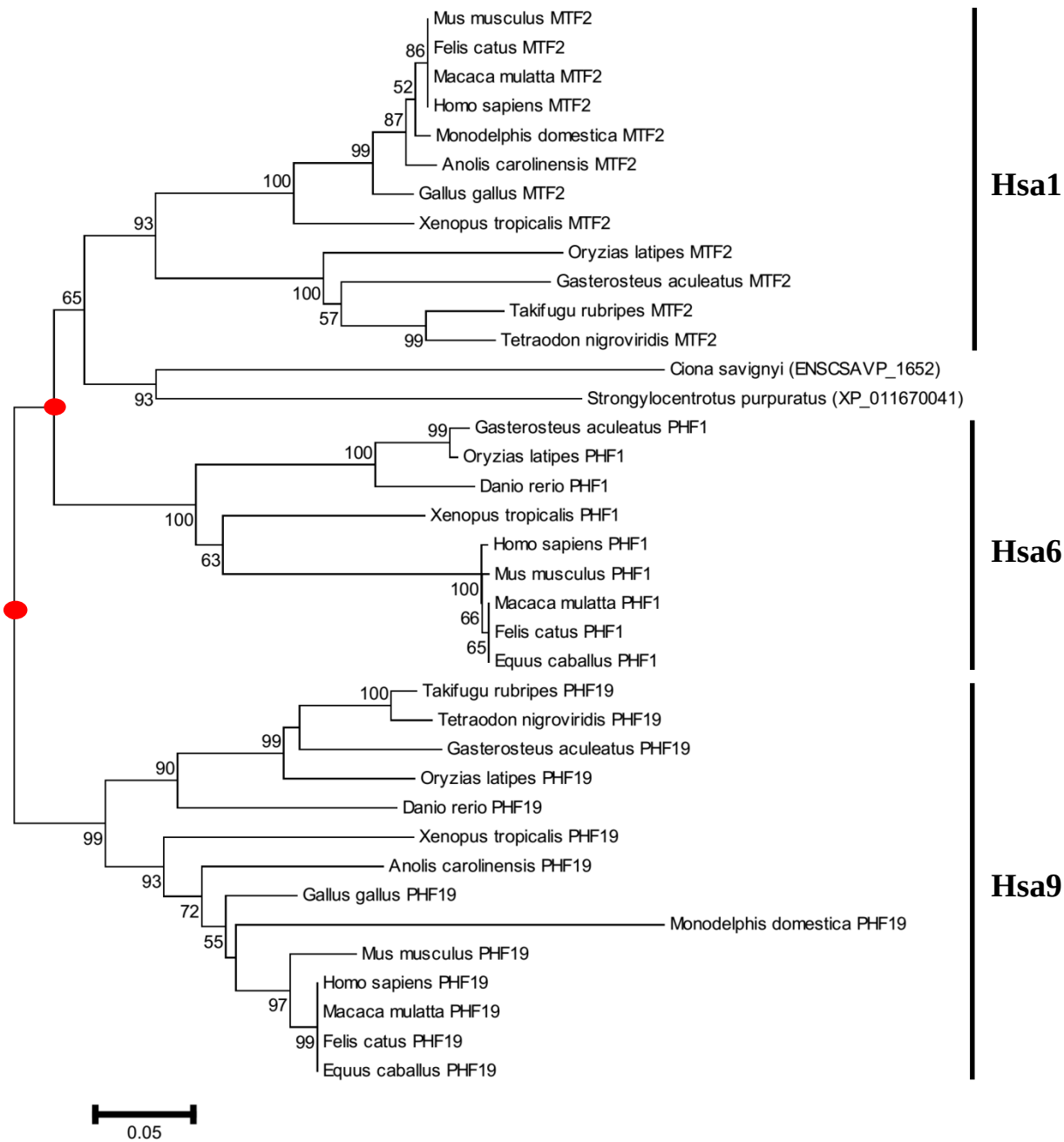
Transforming Growth Factor Beta Receptor Protein Family -TGFB β R



Phylogenetic tree of TGFBR family.

Neighbor-Joining tree of the TGFBR 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.

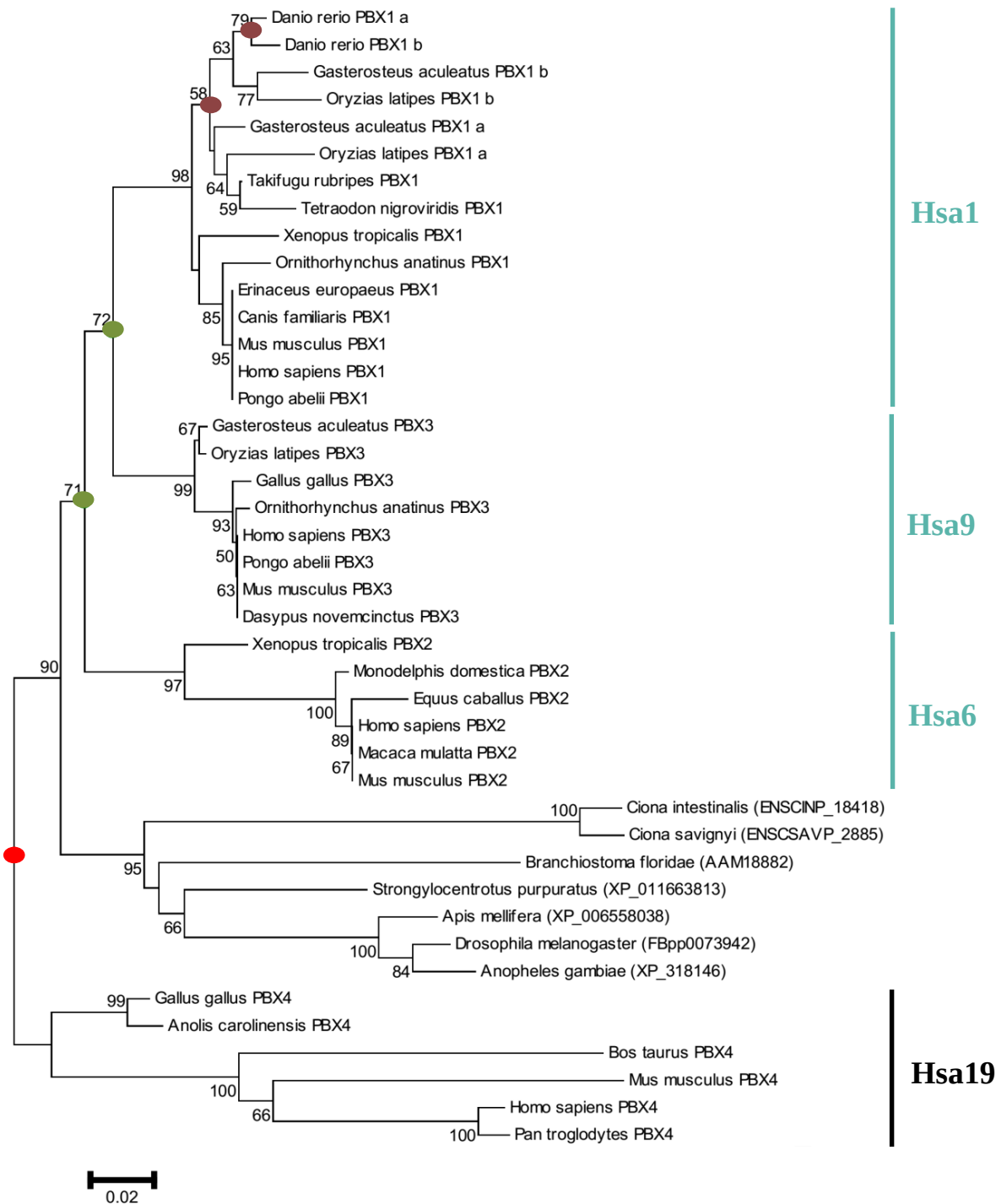
PHD finger protein Protein Family-PHF



Phylogenetic tree of PHF family.

Neighbor-Joining tree of the PHF 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.

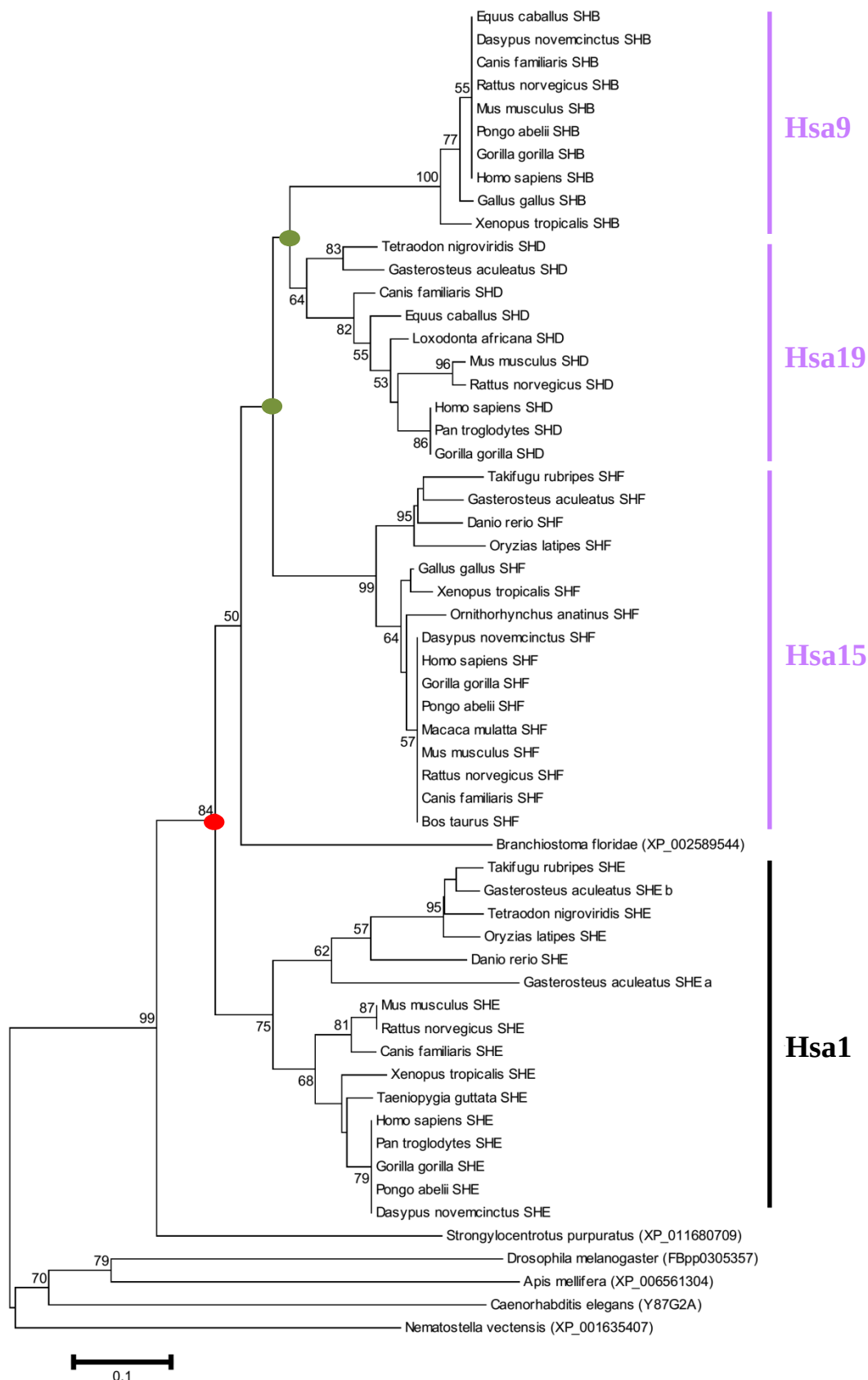
Pre-B-cell Leukemia Homeobox Protein Family-PBX



Phylogenetic tree of PBX family.

Neighbor-Joining tree of the PBX 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.

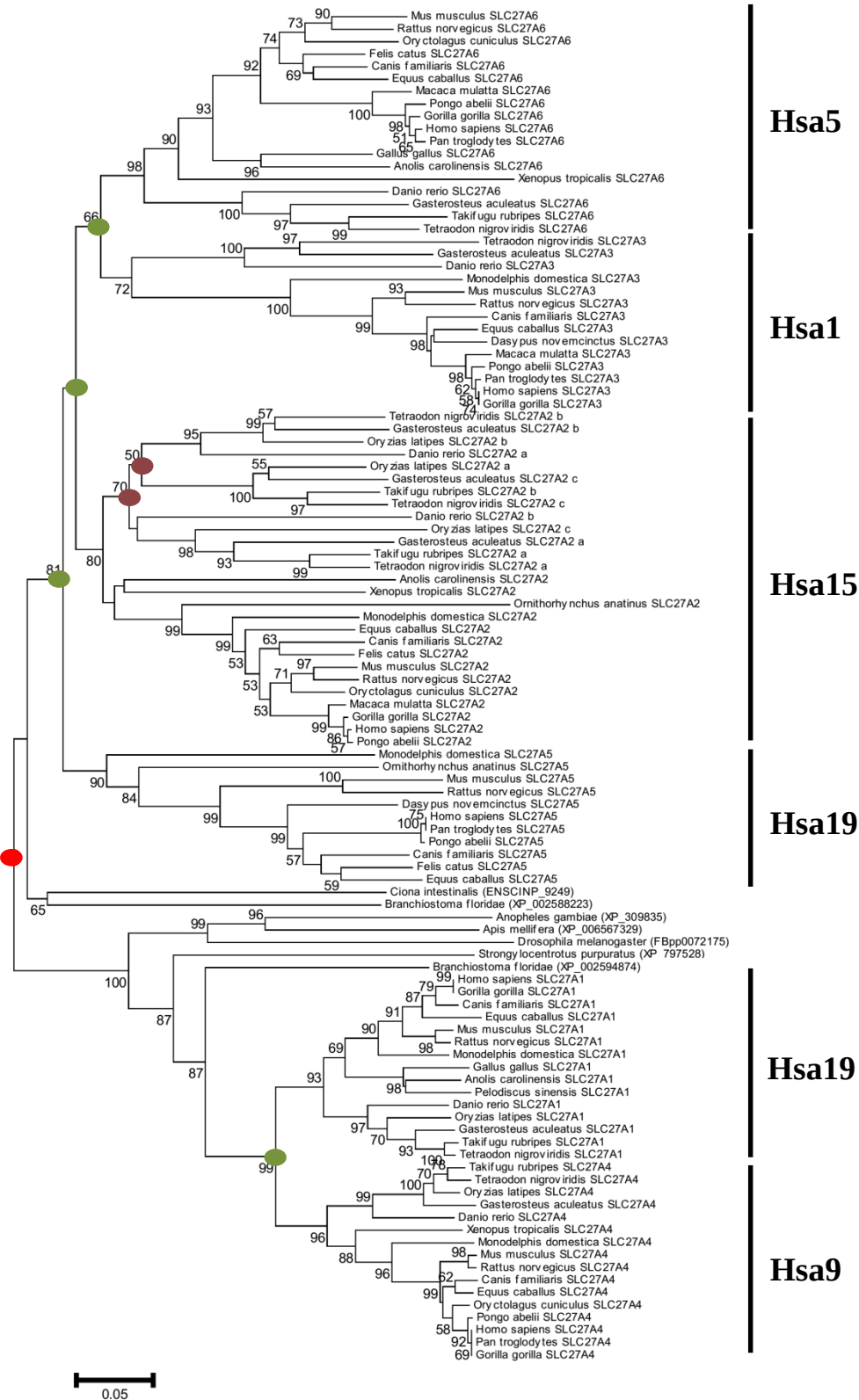
Src homology 2 domain containing adaptor protein - SH



Phylogenetic tree of SH family.

Neighbor-Joining tree of the SH 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 27 – SLC27A



Phylogenetic tree of SLC27A family.

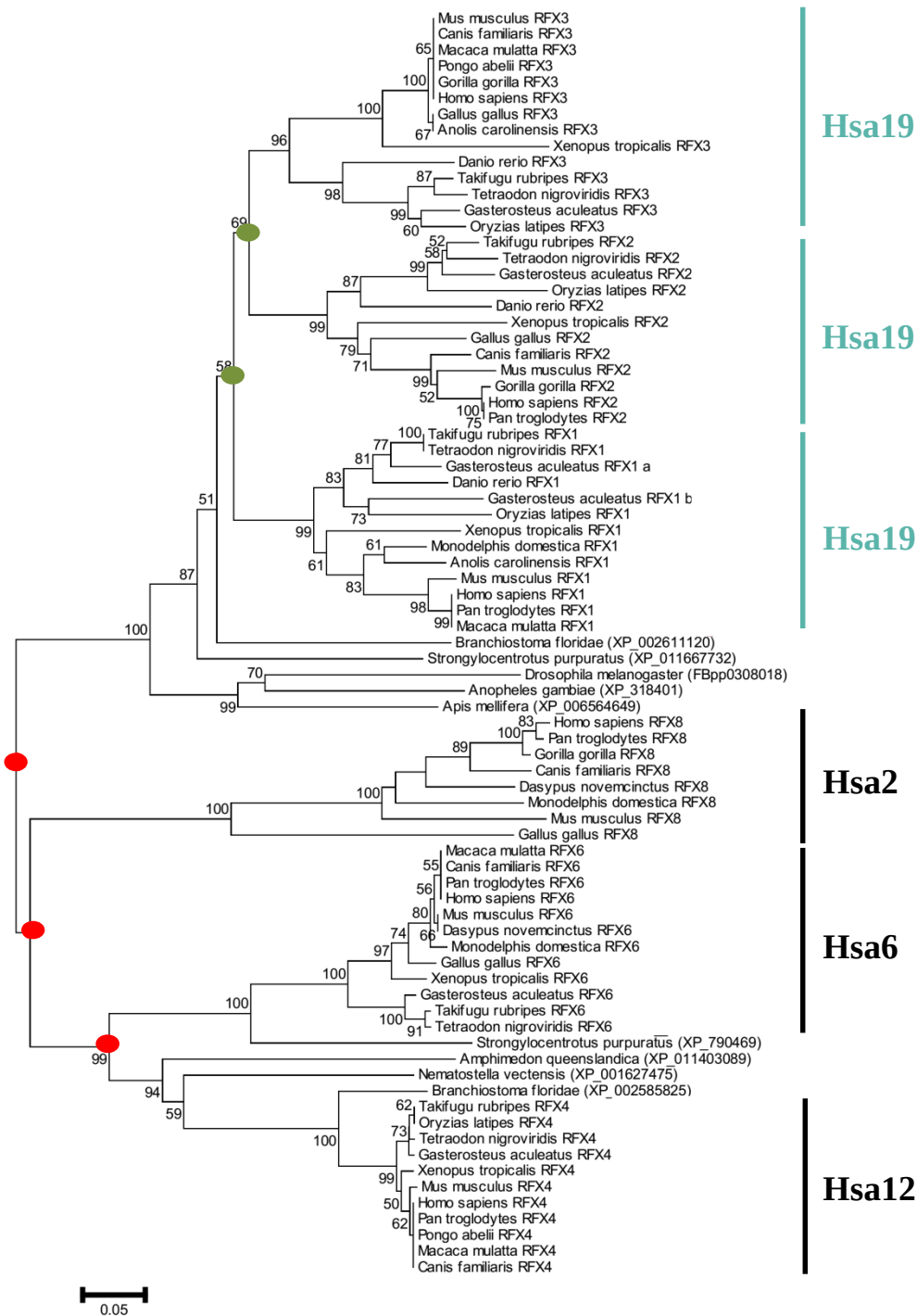
Neighbor-Joining tree of the SLC27A family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site.



Phylogenetic tree of SLC25A family.

Neighbor-Joining tree of the SLC25A 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 SLC25A42B.

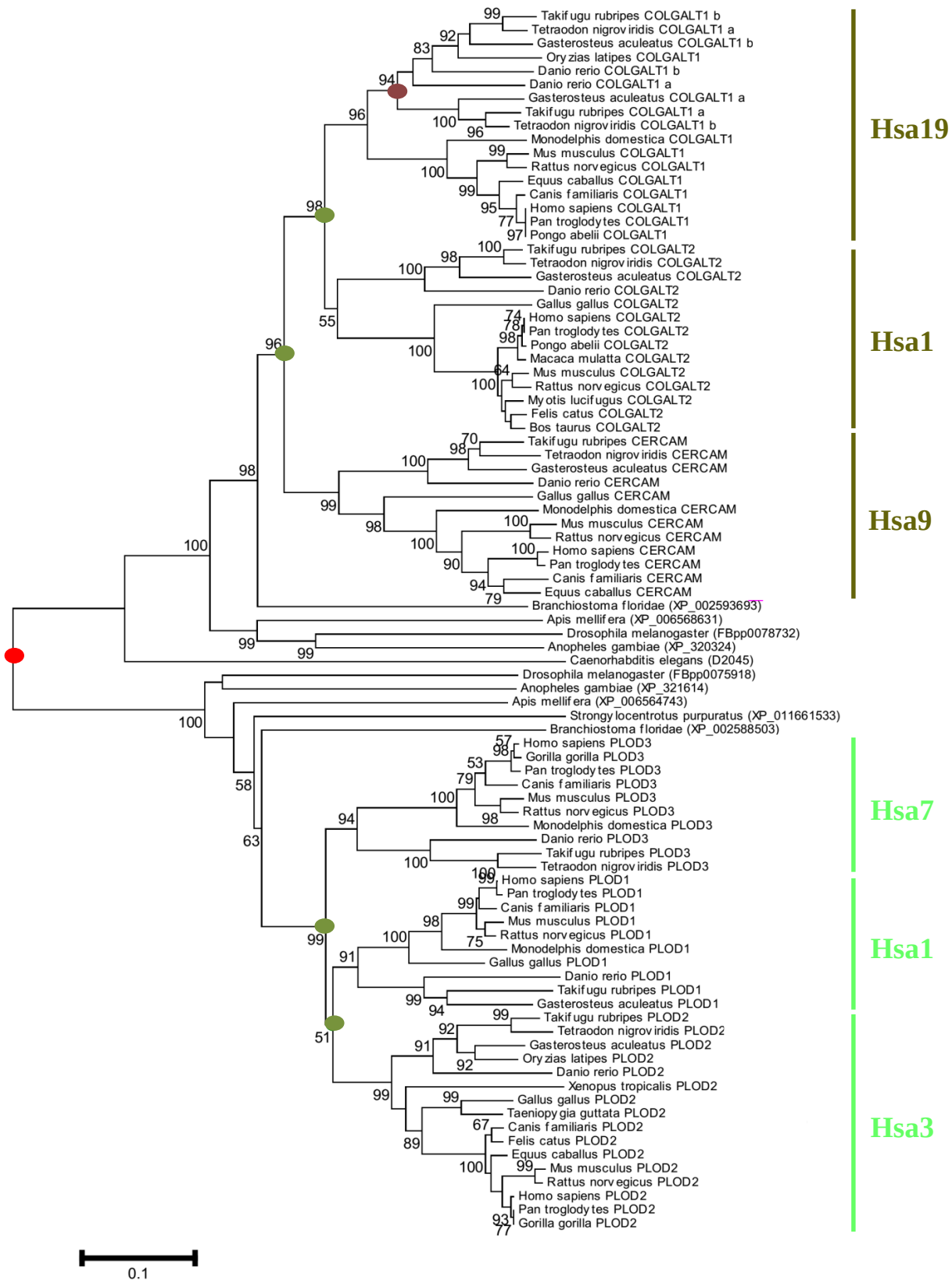
Regulatory factor X protein - RFX



Phylogenetic tree of RFX family.

Neighbor-Joining tree of the RFX 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.

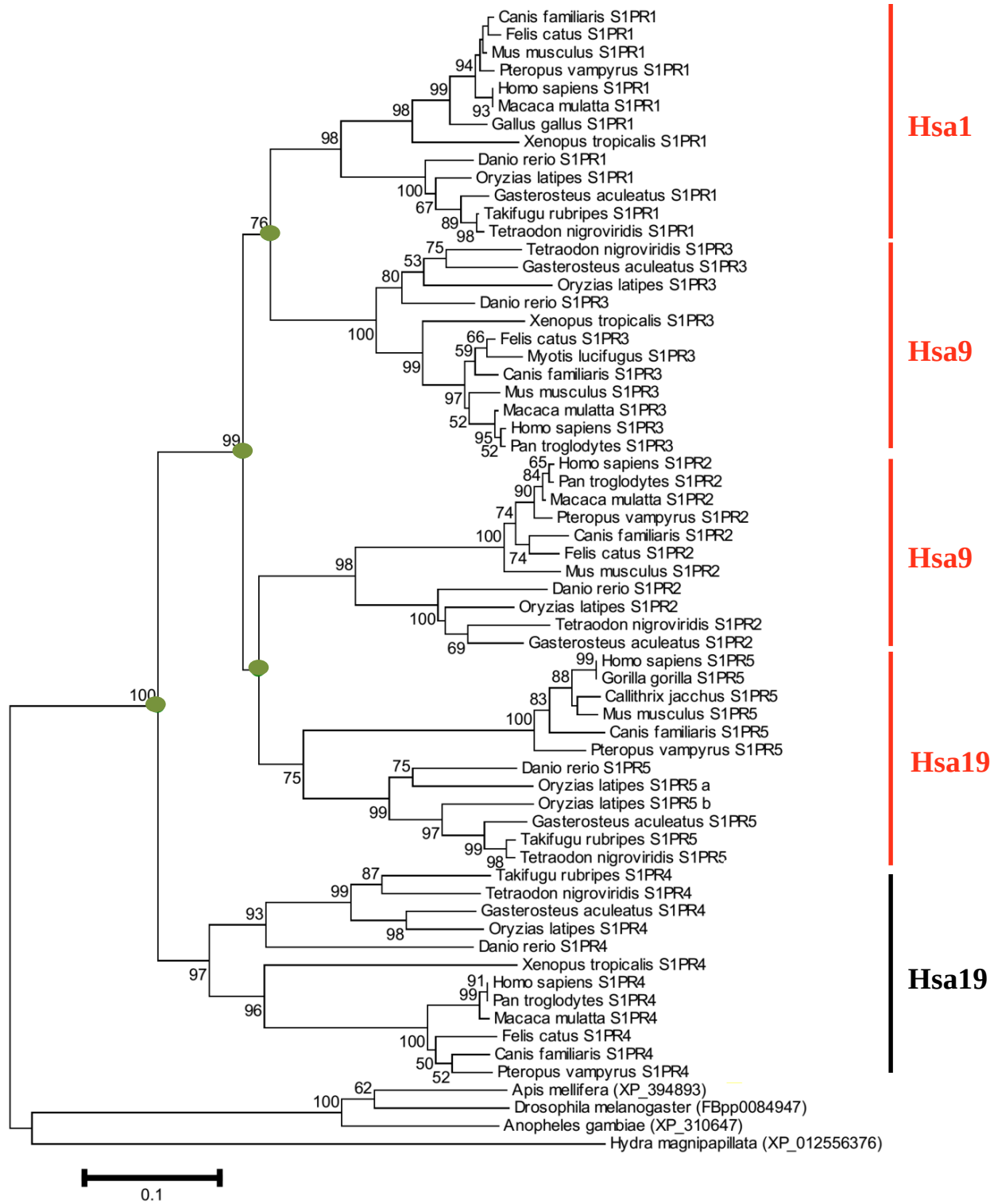
Hydroxylysine galactosyltransferase - COLGALT



Phylogenetic tree of COLGALT family.

Neighbor-Joining tree of the COLGALT 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.

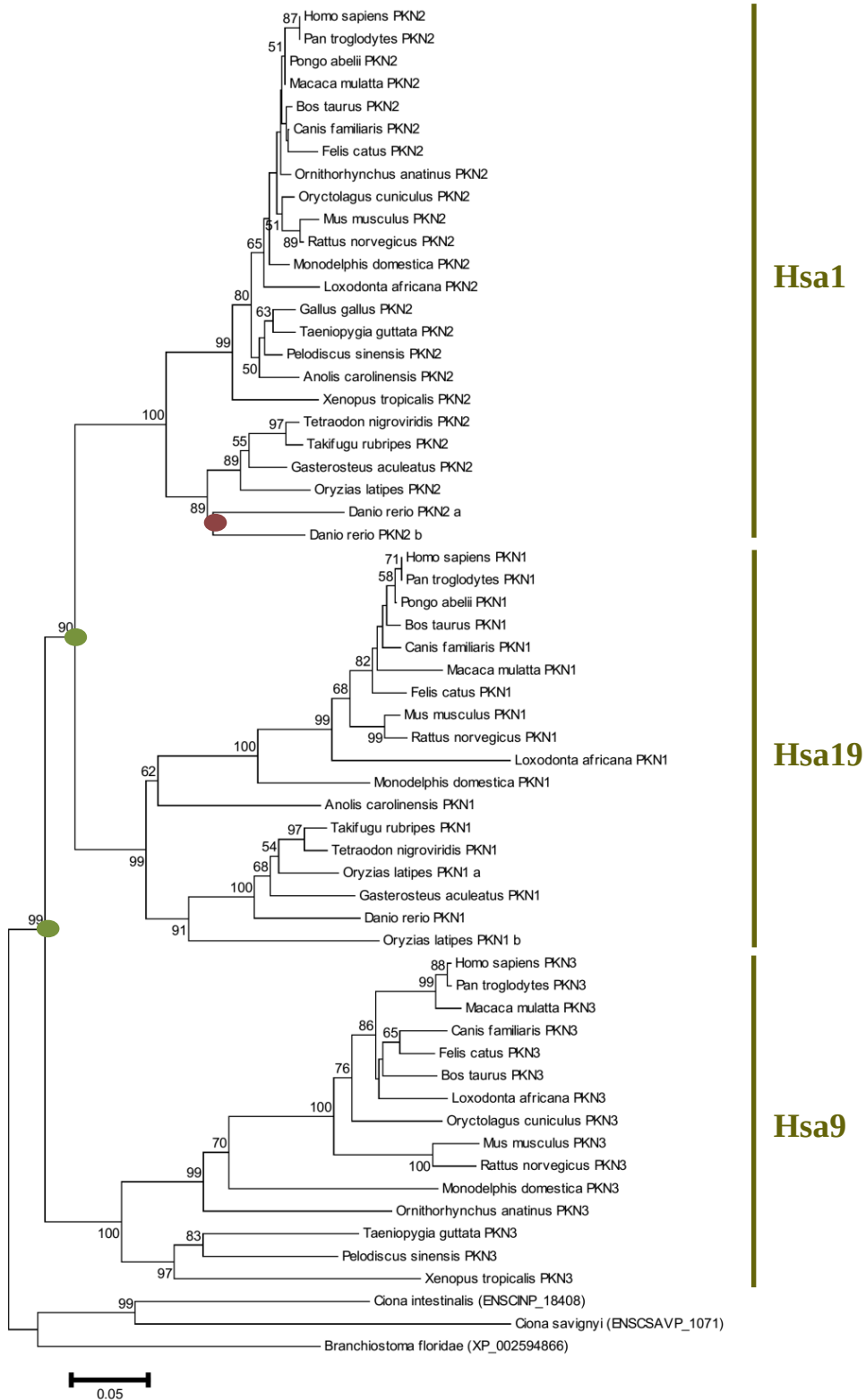
Sphingosine-1-phosphate receptor – S1PR



Phylogenetic tree of S1PR family.

Neighbor-Joining tree of the S1PR 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.

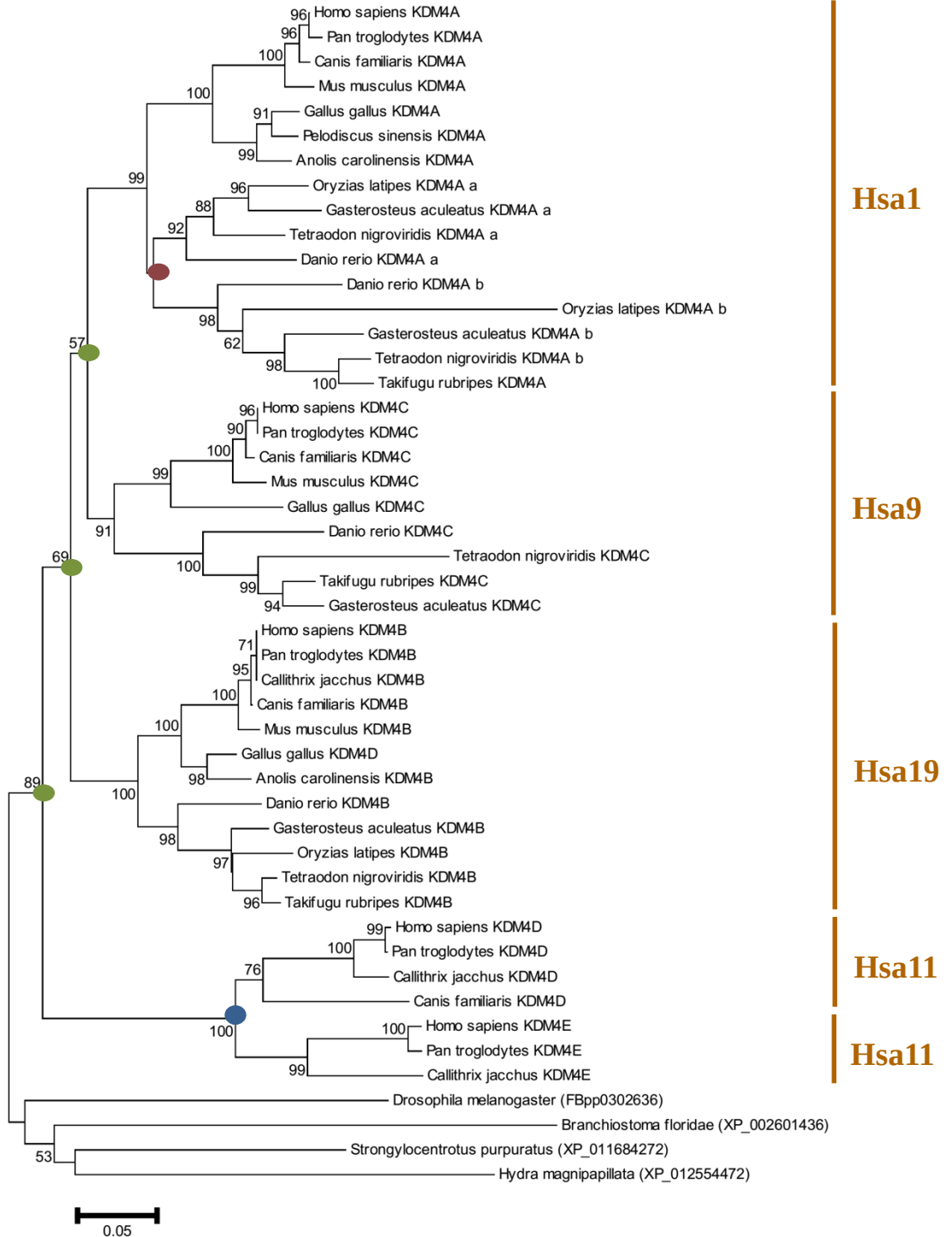
Protein-kinase C-related kinase - PKN



Phylogenetic tree of PKN family.

Neighbor-Joining tree of the PKN 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.

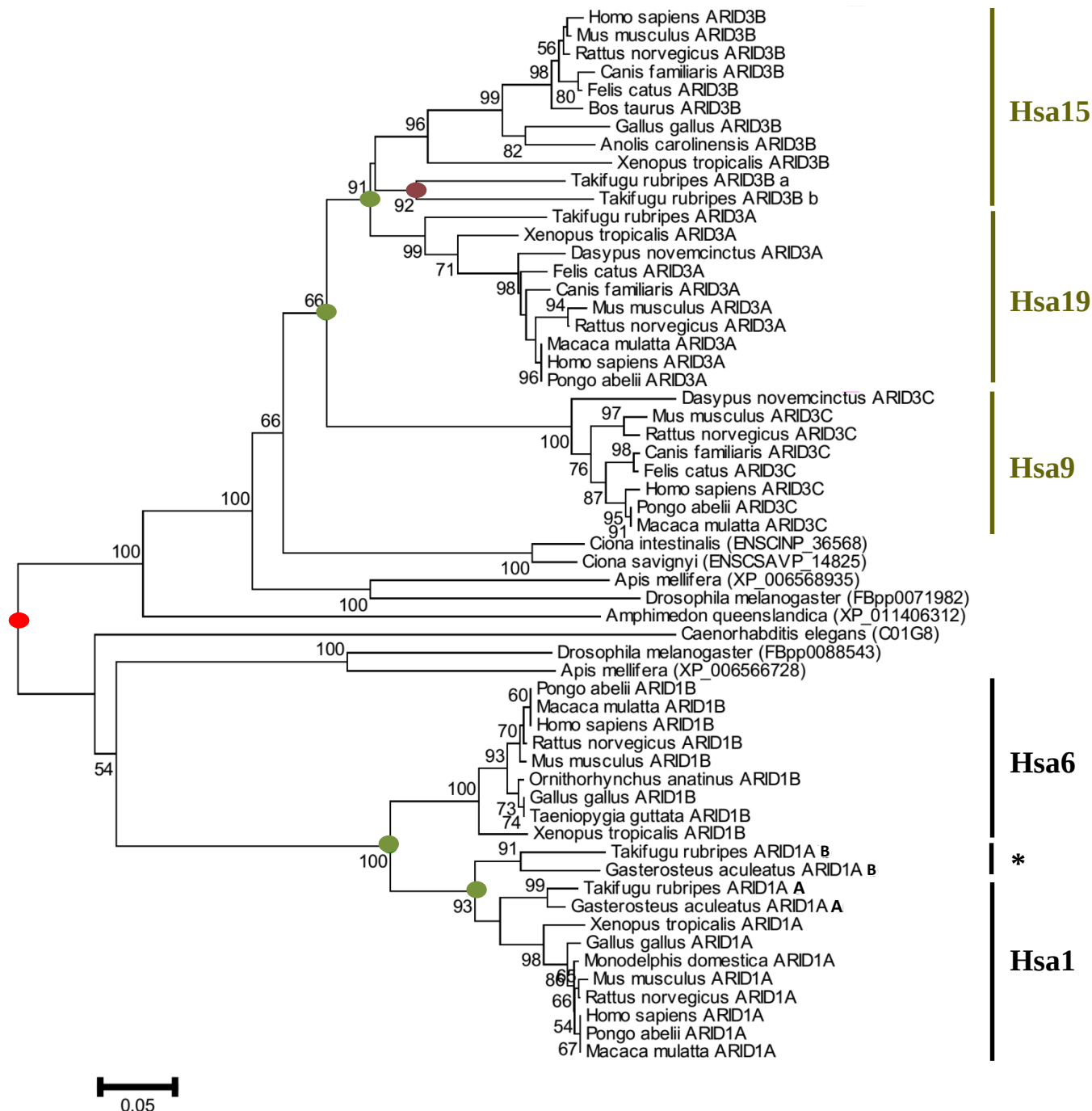
Lysine-specific demethylase - KDM



Phylogenetic tree of KDM family.

Neighbor-Joining tree of the KDM 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.

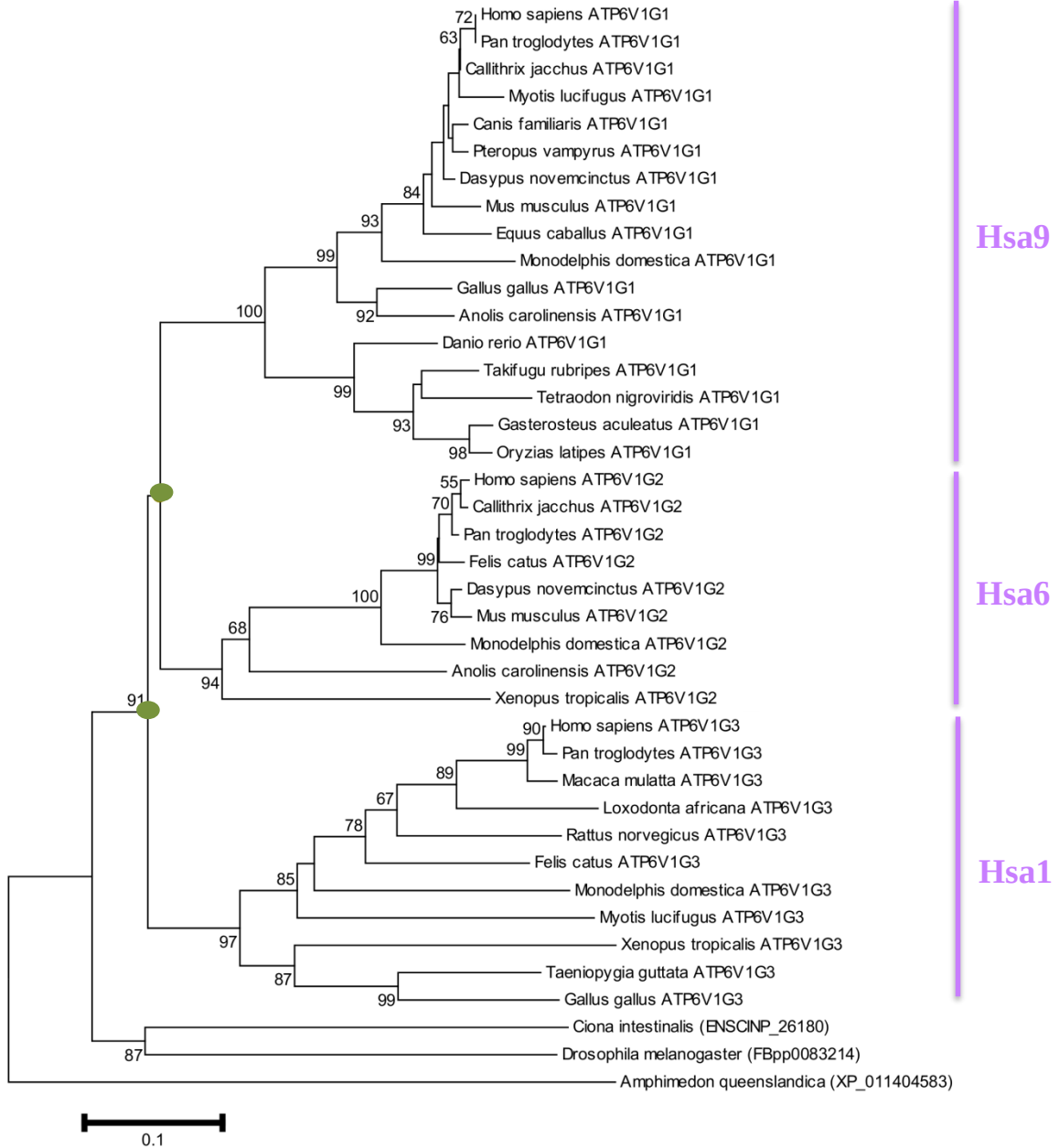
AT-rich interactive domain-containing protein - ARID



Phylogenetic tree of ARID family.

Neighbor-Joining tree of the ARID 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 ARID1AB.

ATPase, H⁺ transporting subunits – ATP6V1G



Phylogenetic tree of ATP6V1G family.

Neighbor- Joining tree of the ATP6V1G 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.

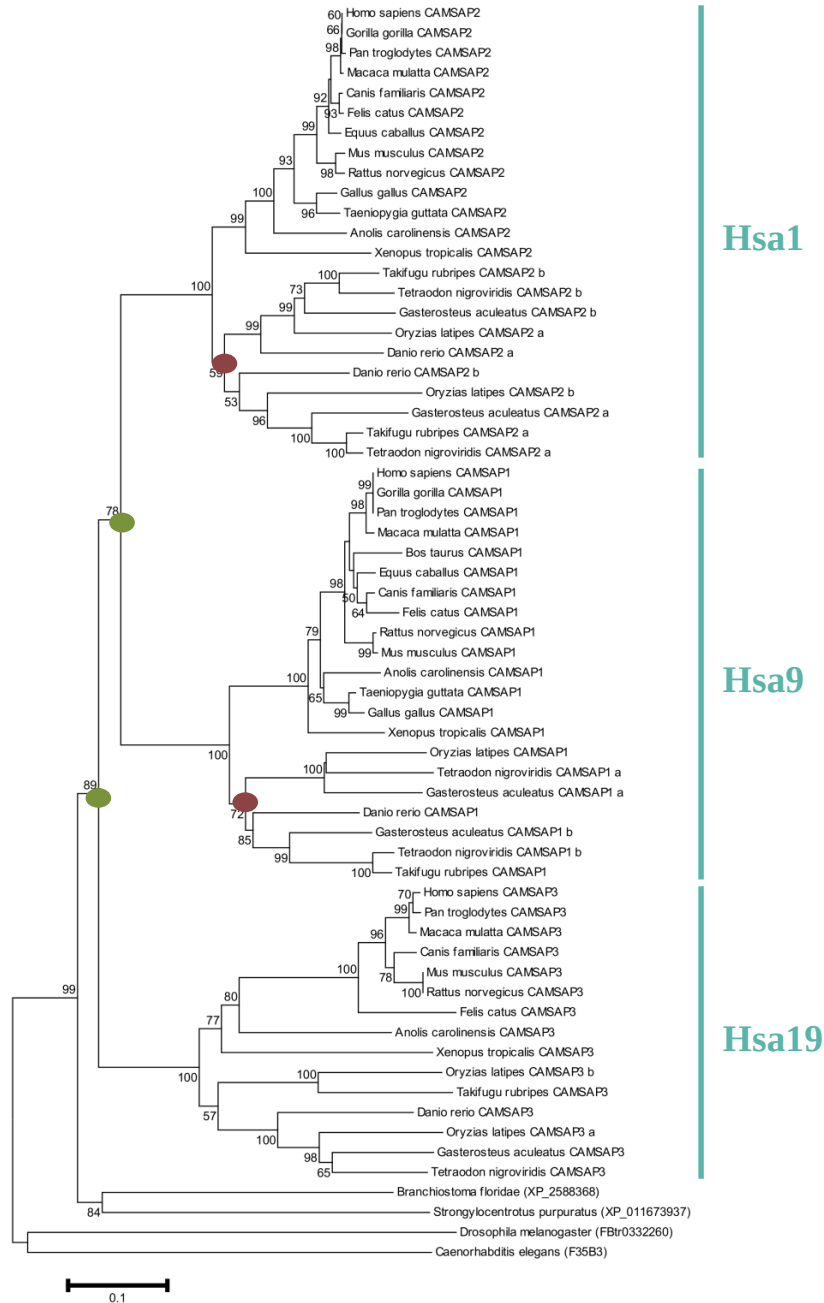
Bromodomain containing family - BRD



Phylogenetic tree of BRD family.

Neighbor- Joining tree of the BRD 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.

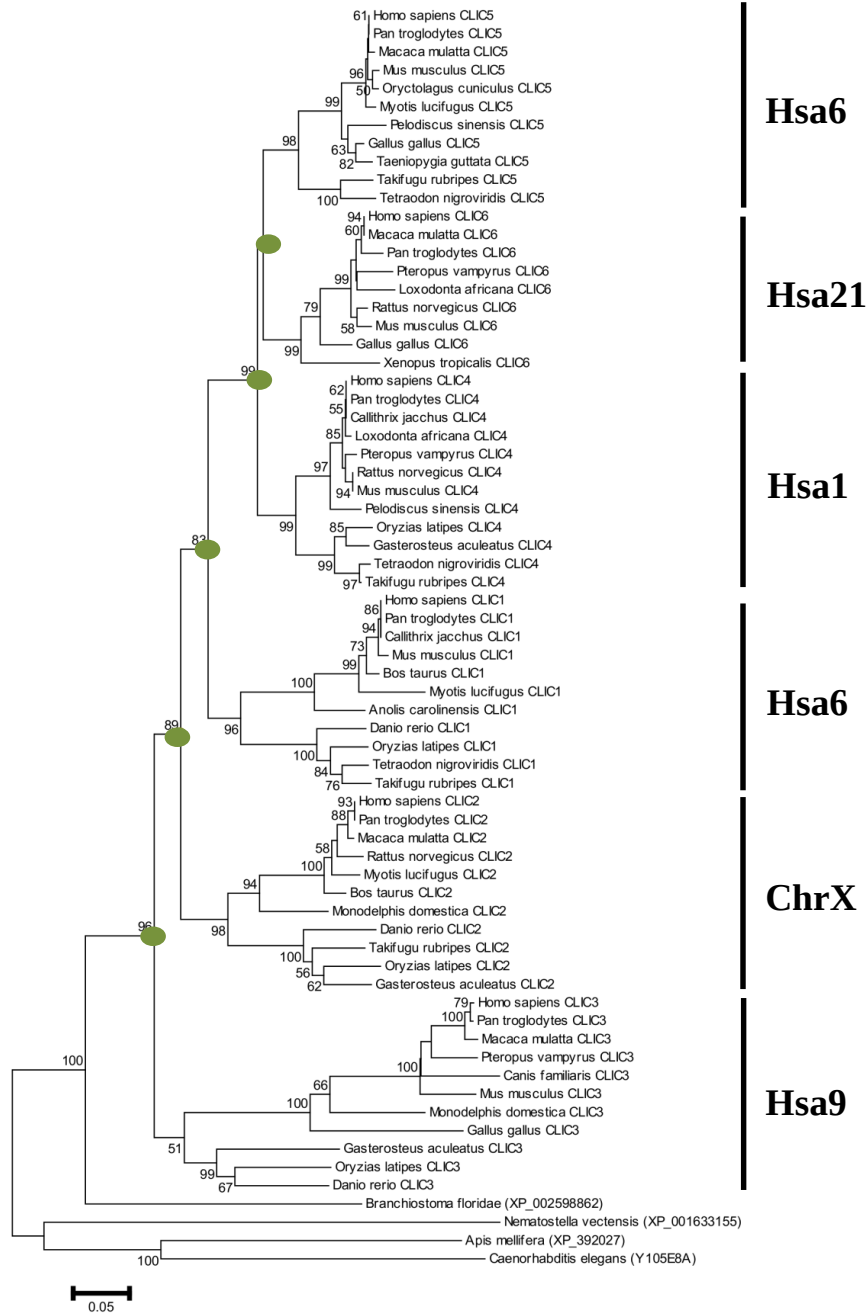
Calmodulin regulated spectrin associated protein family - CAMSAP



Phylogenetic tree of CAMSAP family.

Neighbor- Joining tree of the CAMSAP 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.

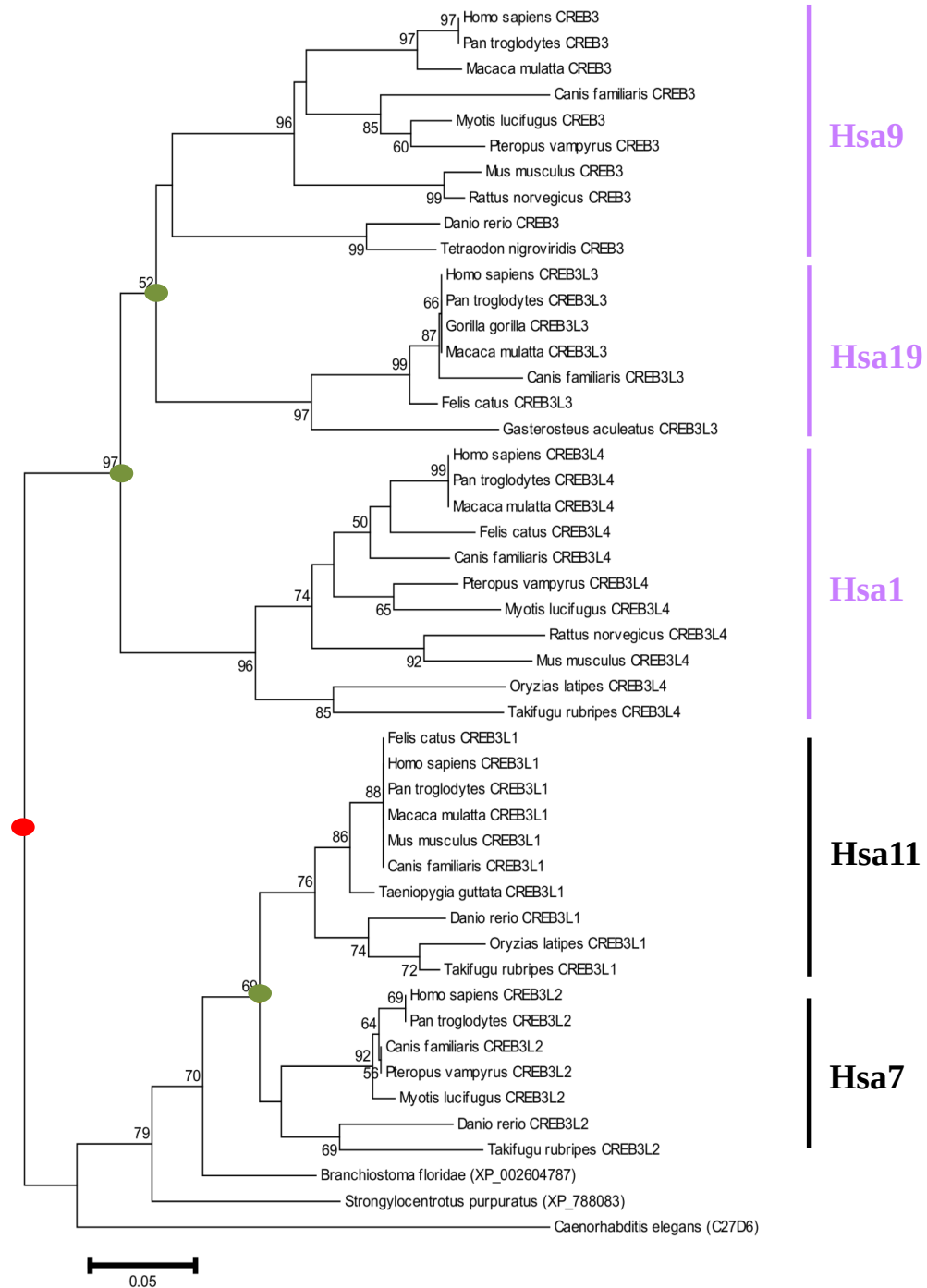
Chloride intracellular channel family - CLIC



Phylogenetic tree of CLIC family.

Neighbor- Joining tree of the CLIC 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.

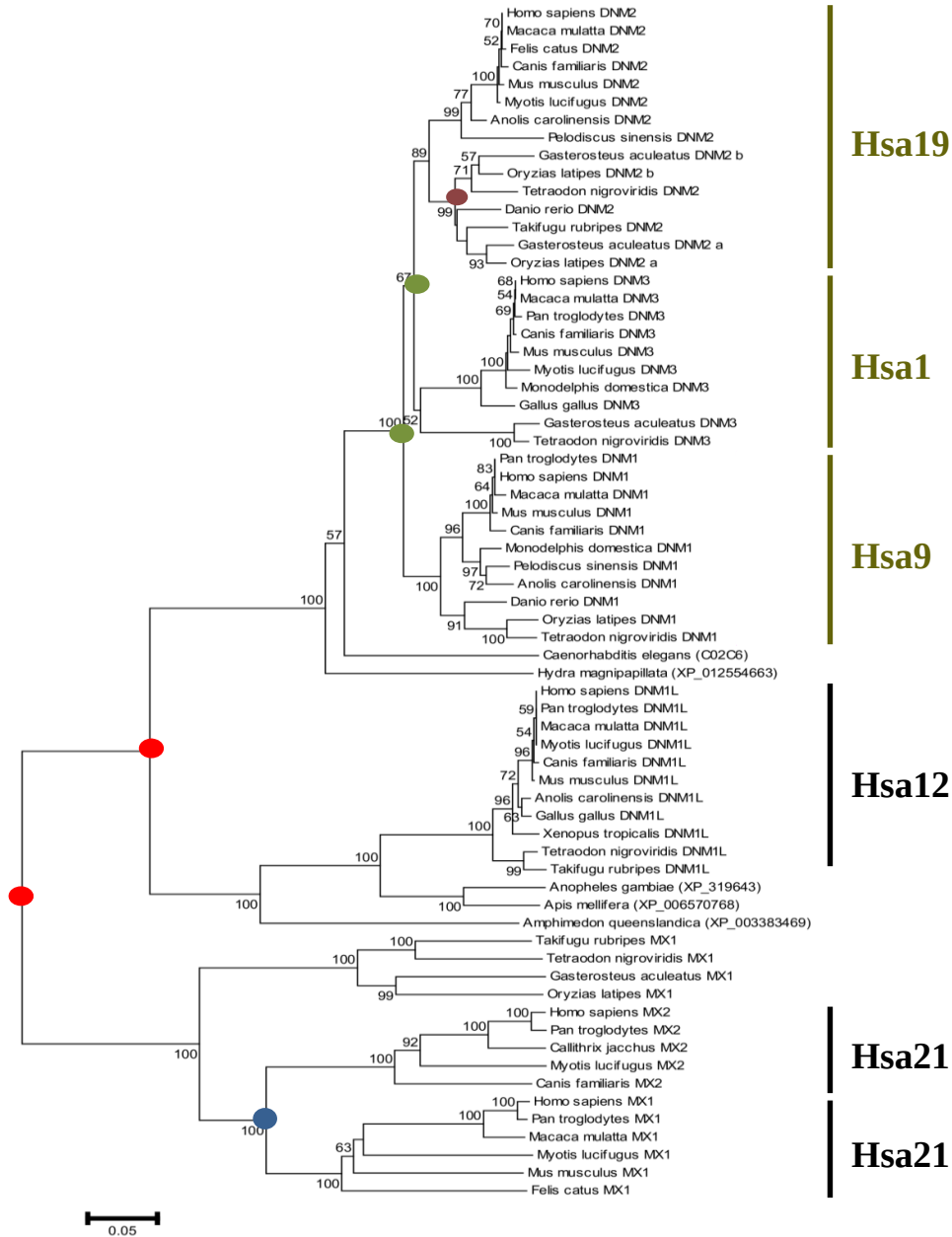
cAMP responsive element binding protein family - CREB



Phylogenetic tree of CREB family.

Neighbor- Joining tree of the CREB 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.

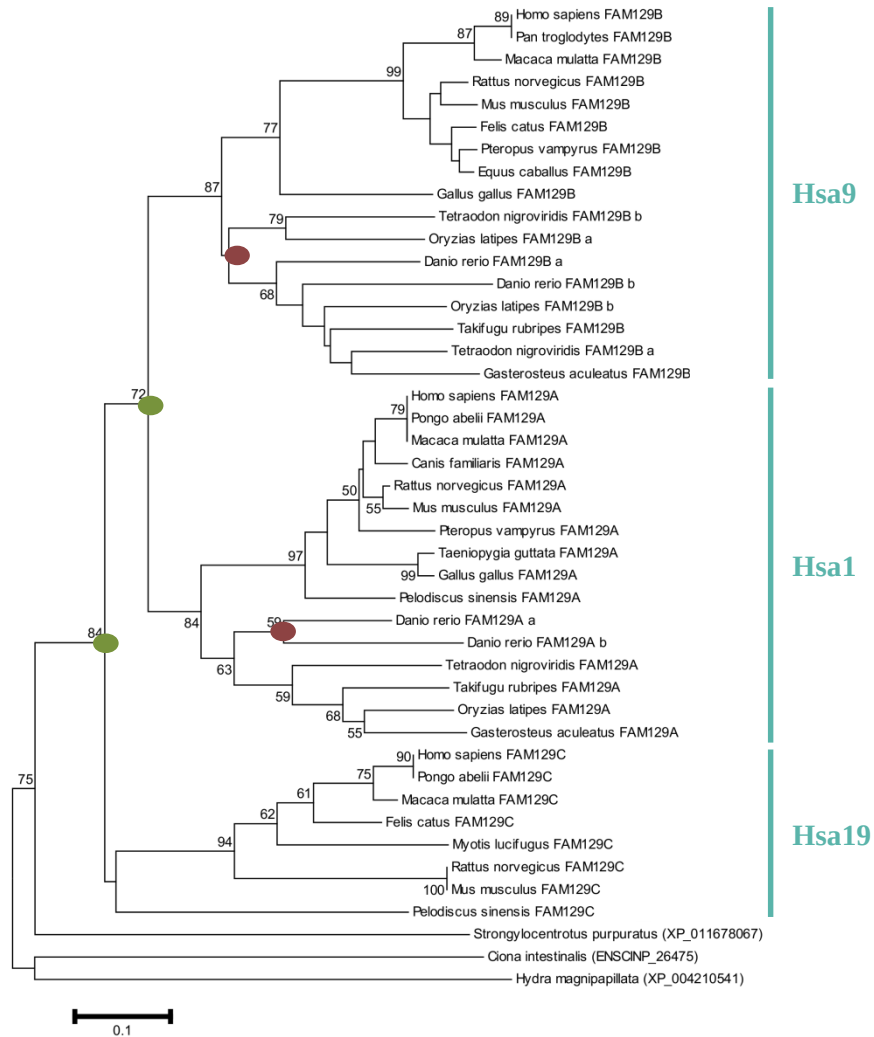
Dynamin family - DNM



Phylogenetic tree of DNM family.

Neighbor- Joining tree of the DNM 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.

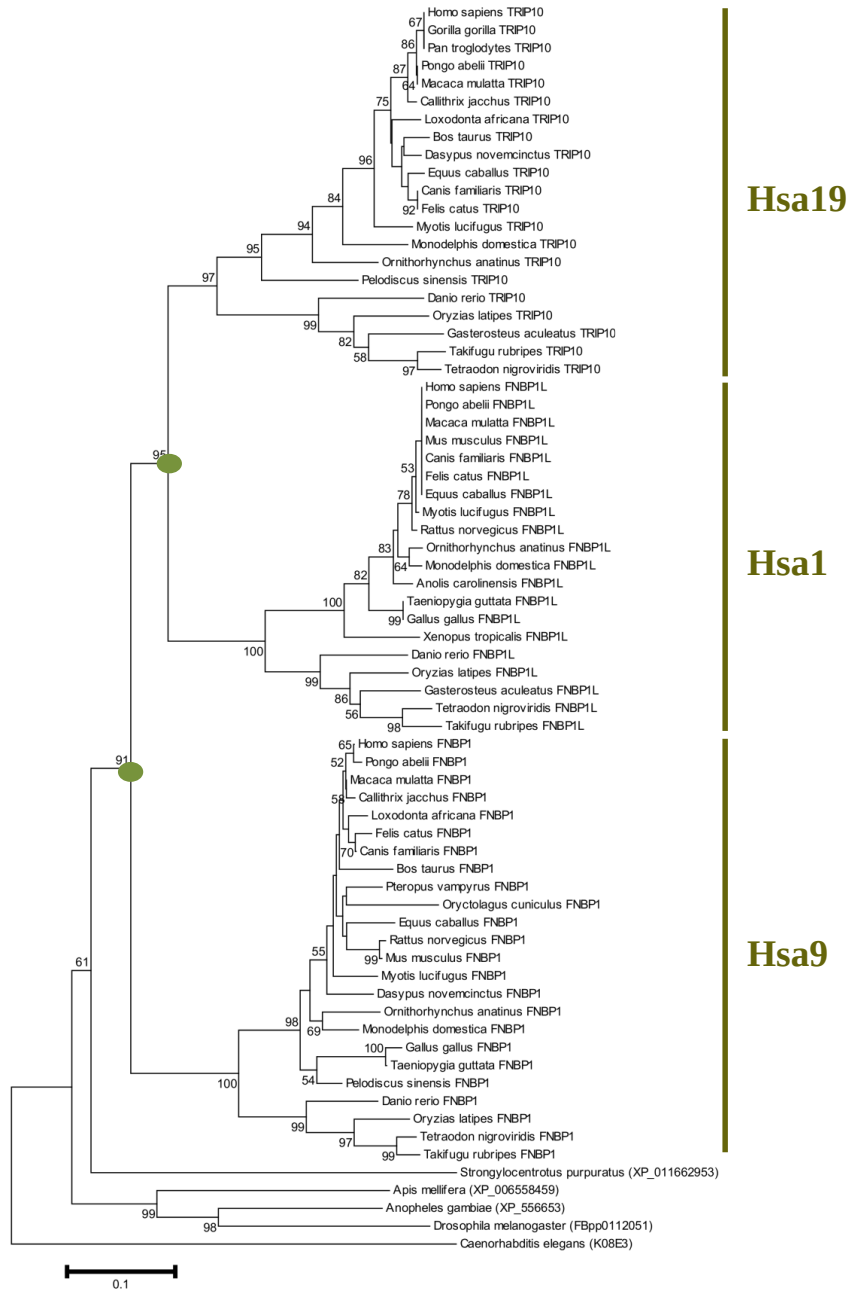
Family with sequence similarity 129 - FAM129



Phylogenetic tree of FAM129 family.

Neighbor- Joining tree of the FAM129 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.

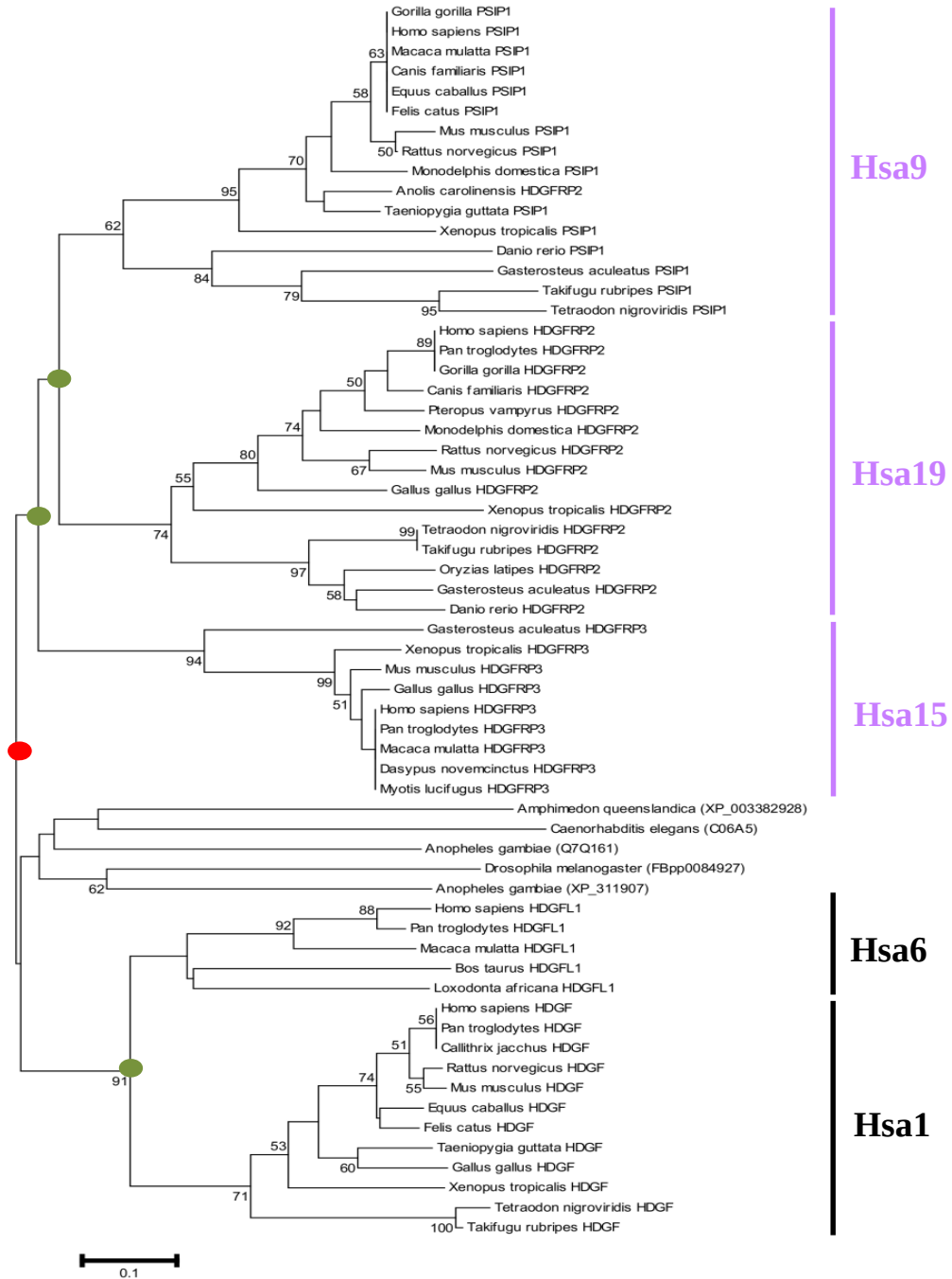
Formin binding protein Family - FBNP



Phylogenetic tree of FBNP family.

Neighbor- Joining tree of the FBNP 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.

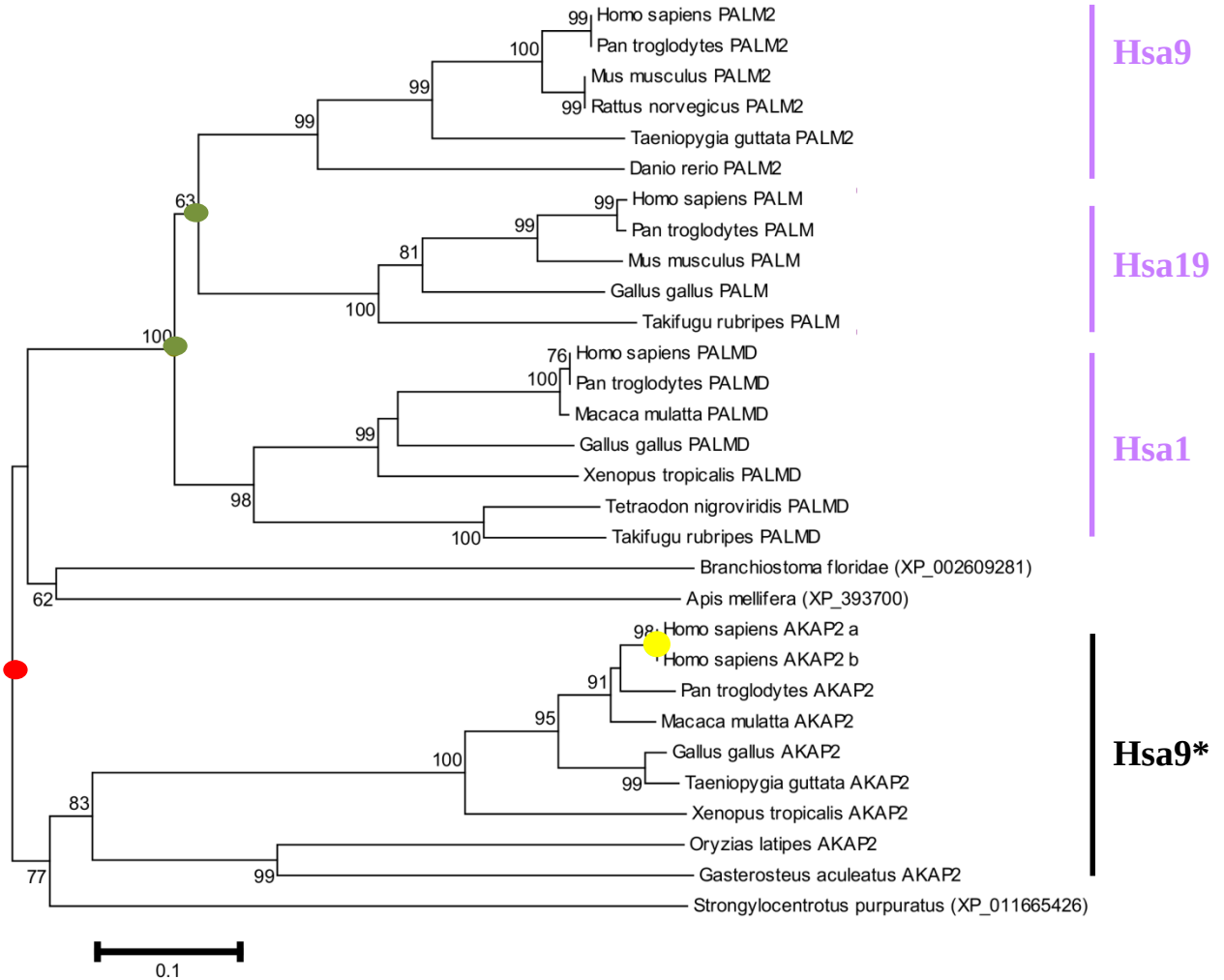
Hepatoma derived growth factor family - HDGF



Phylogenetic tree of HDGF family.

Neighbor- Joining tree of the HDGF 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.

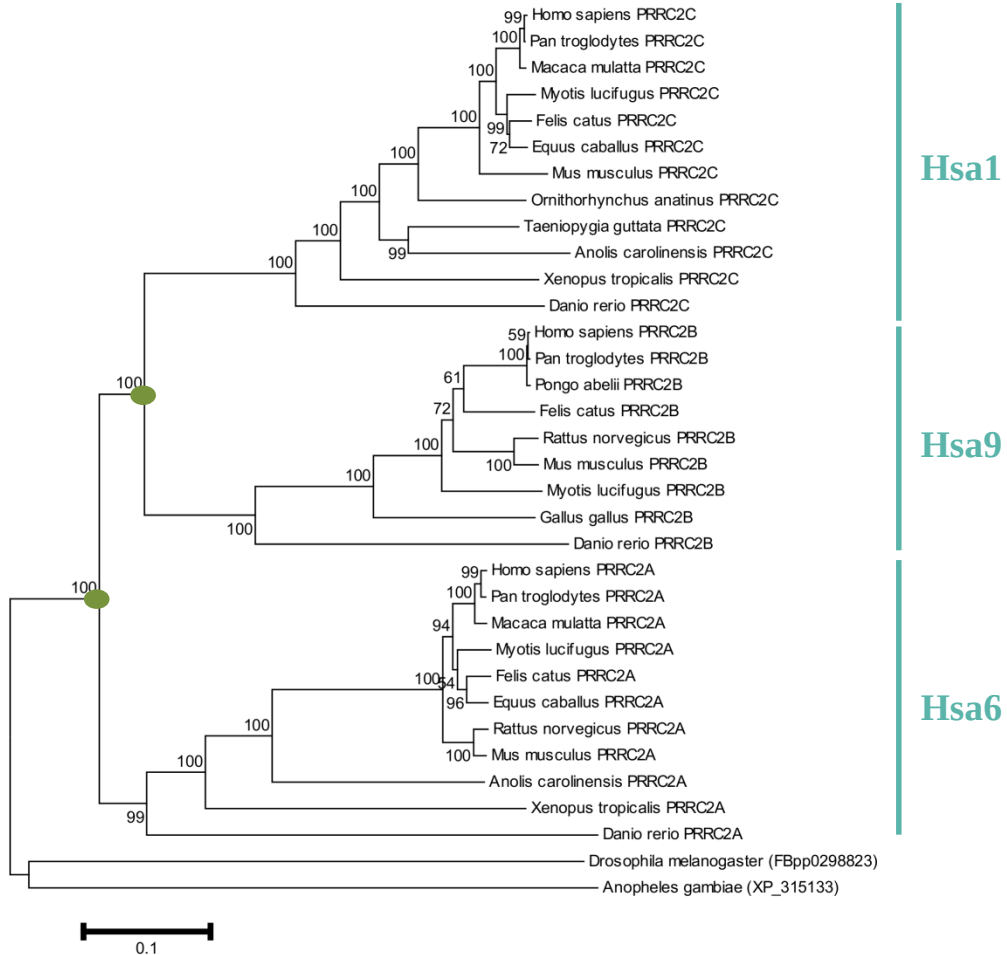
Palmdephin - PALM



Phylogenetic tree of PALM family.

Neighbor- Joining tree of the PALM 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. 9* shows human specific duplication on chromosome 9.

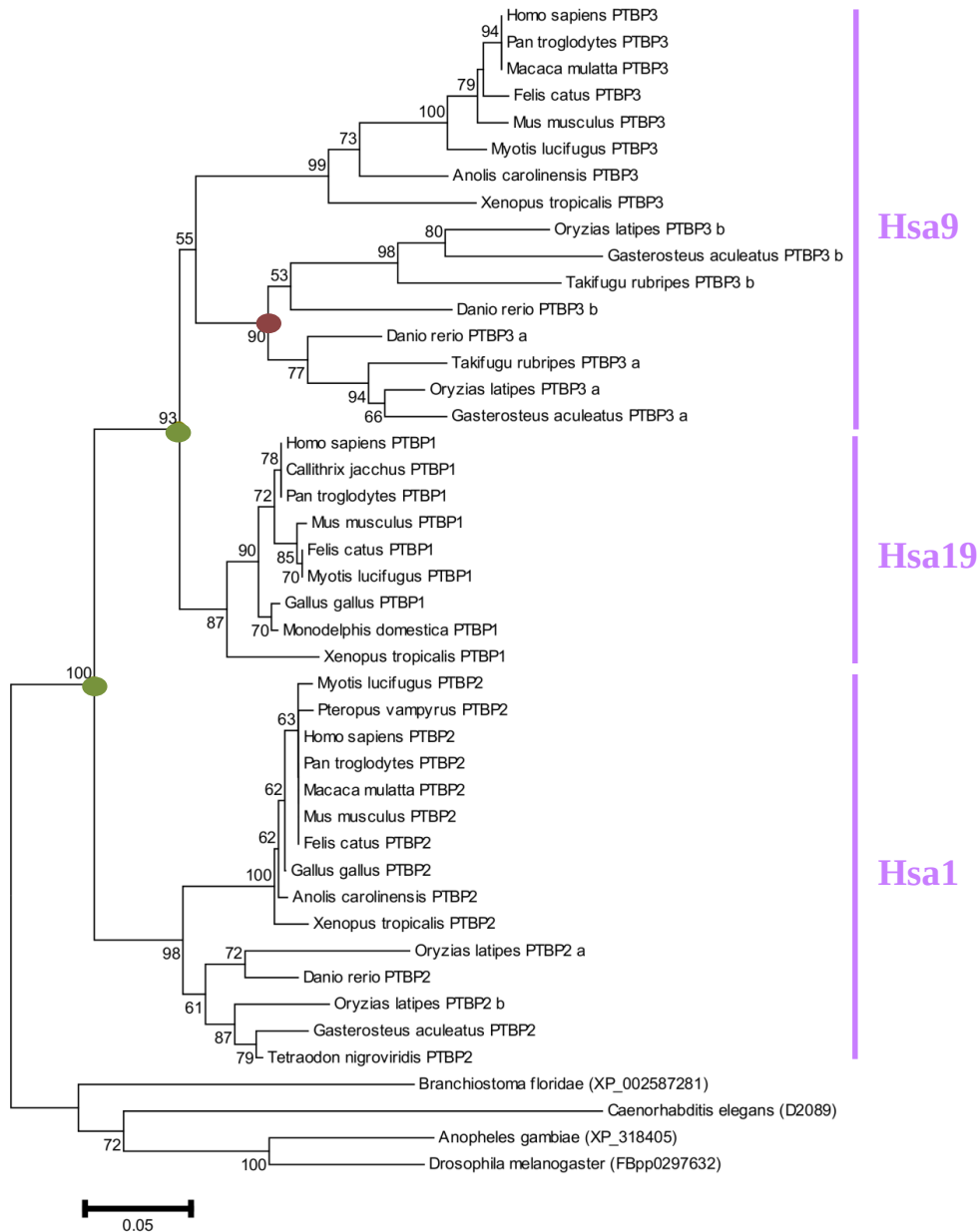
Proline rich coiled coil - PRRC2



Phylogenetic tree of PRRC2 family.

Neighbor- Joining tree of the PRRC2 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.

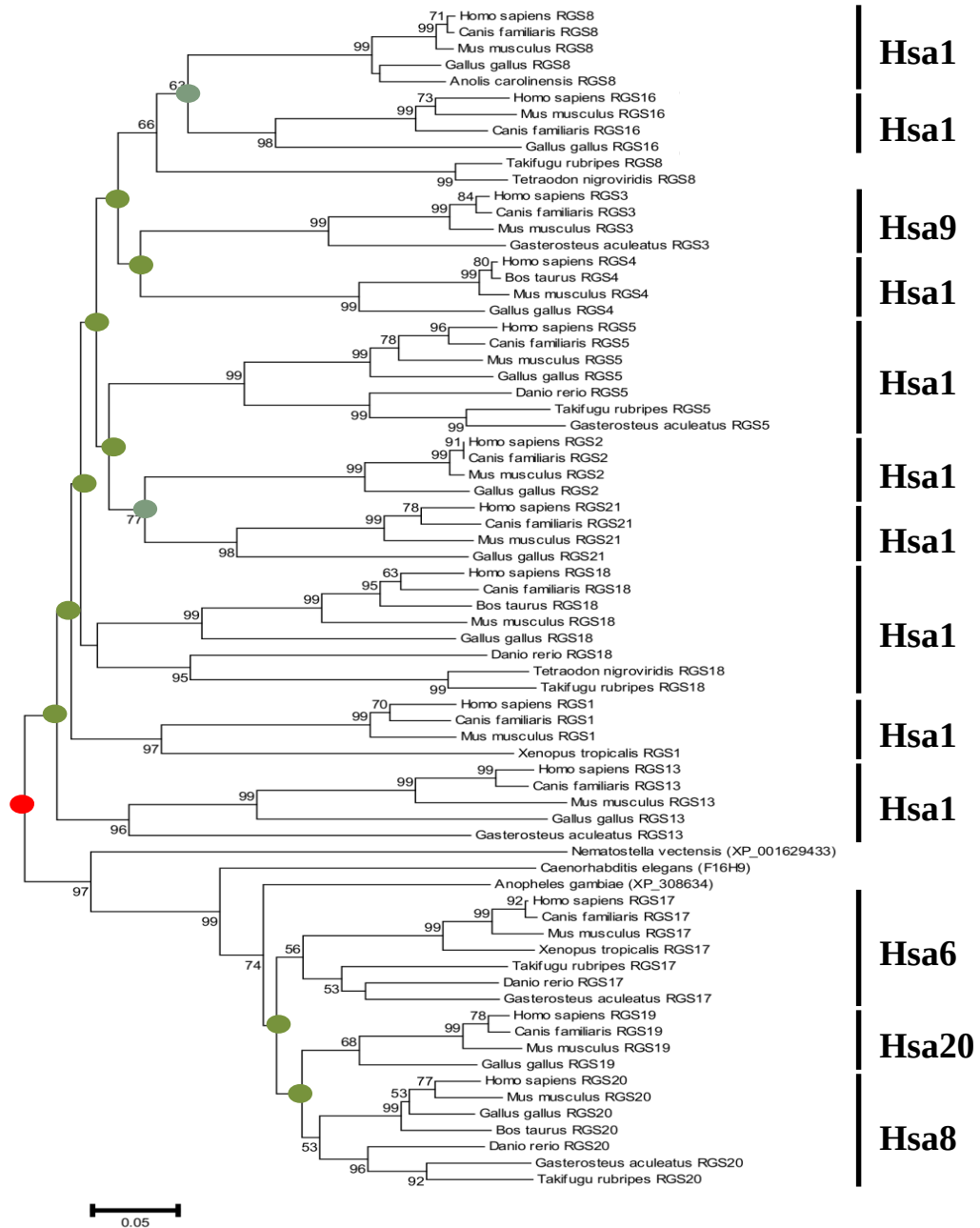
Polypyrimidine tract binding protein family - PTBP



Phylogenetic tree of PTBP family.

Neighbor- Joining tree of the PTBP 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.

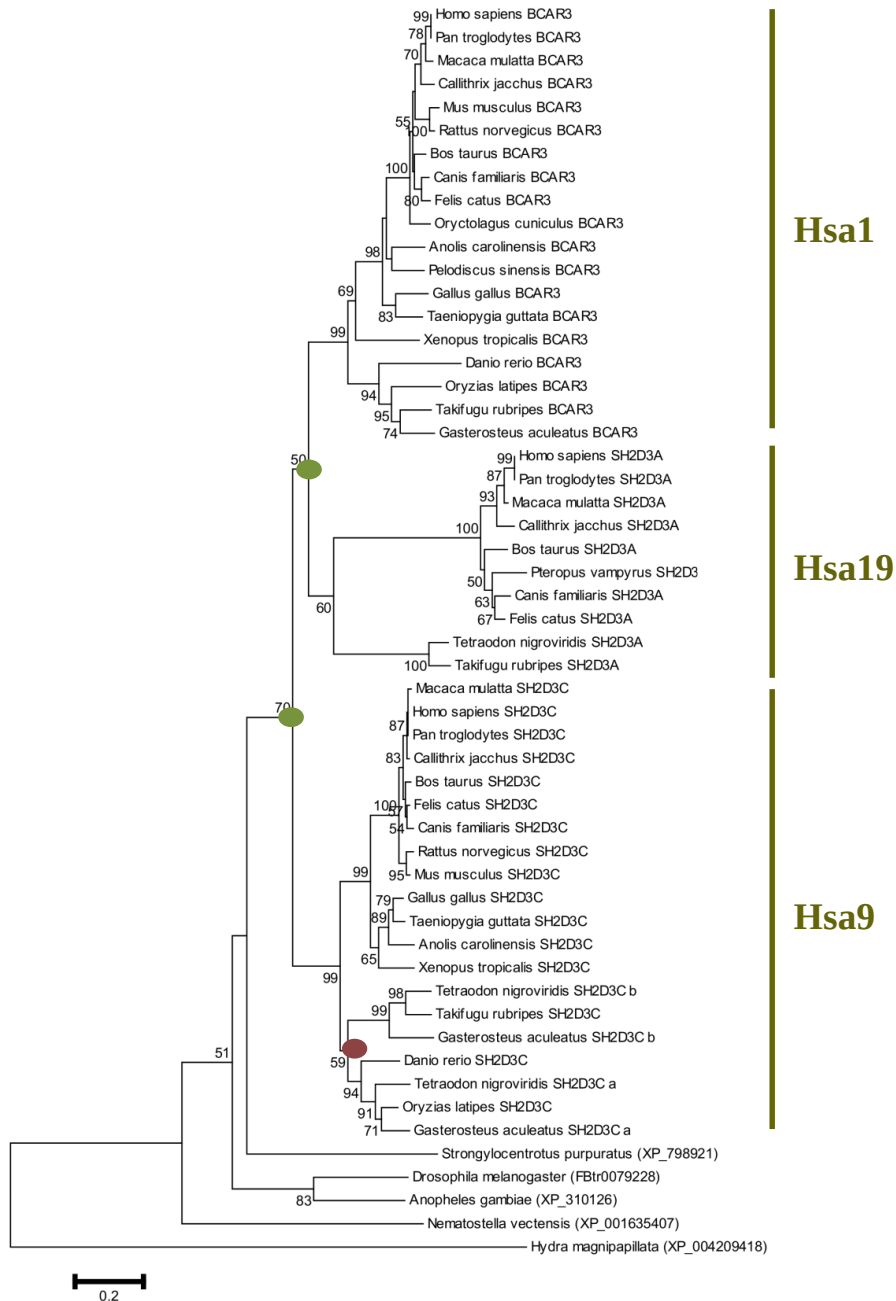
Regulator of G-protein signaling family - RGS



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.

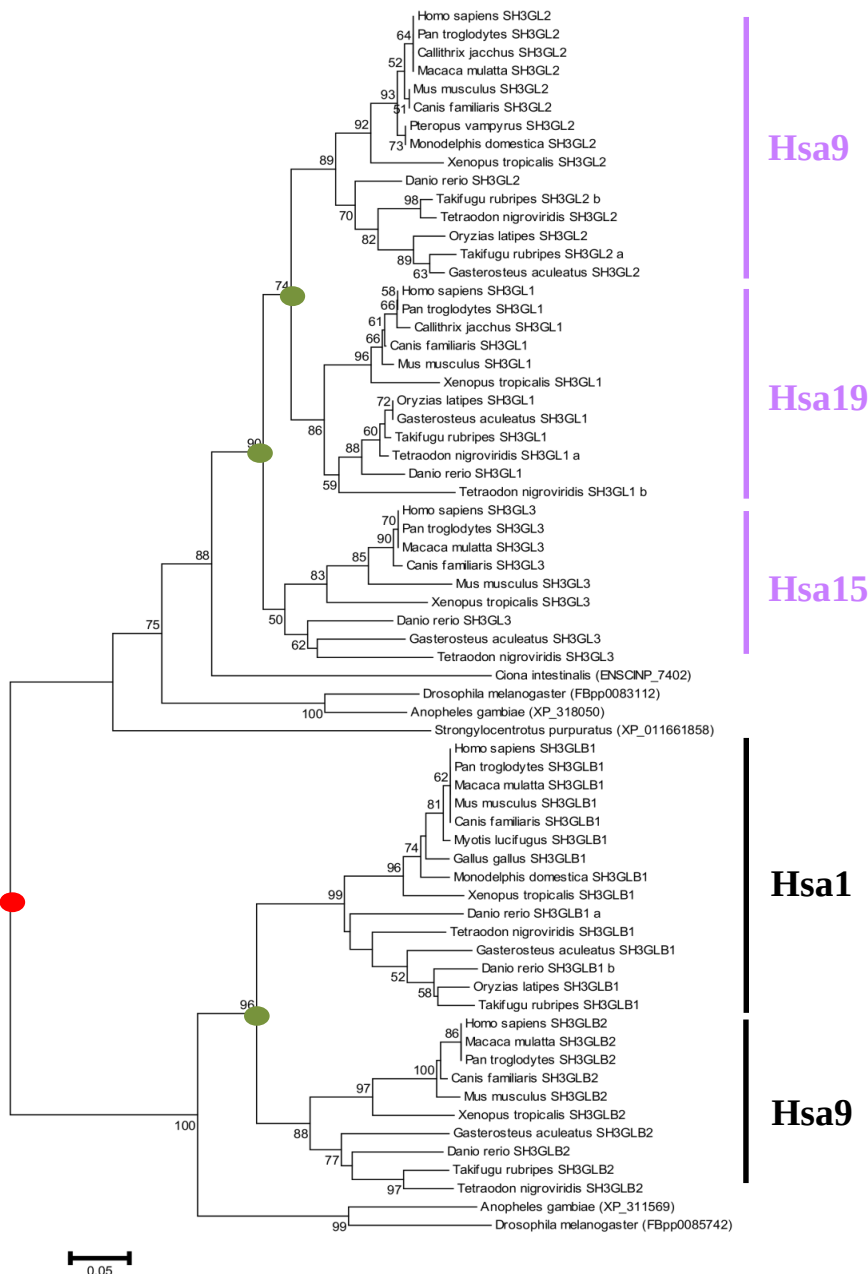
SH2 domain containing protein - SH2D



Phylogenetic tree of SH2D family.

Neighbor- Joining tree of the SH2D 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.

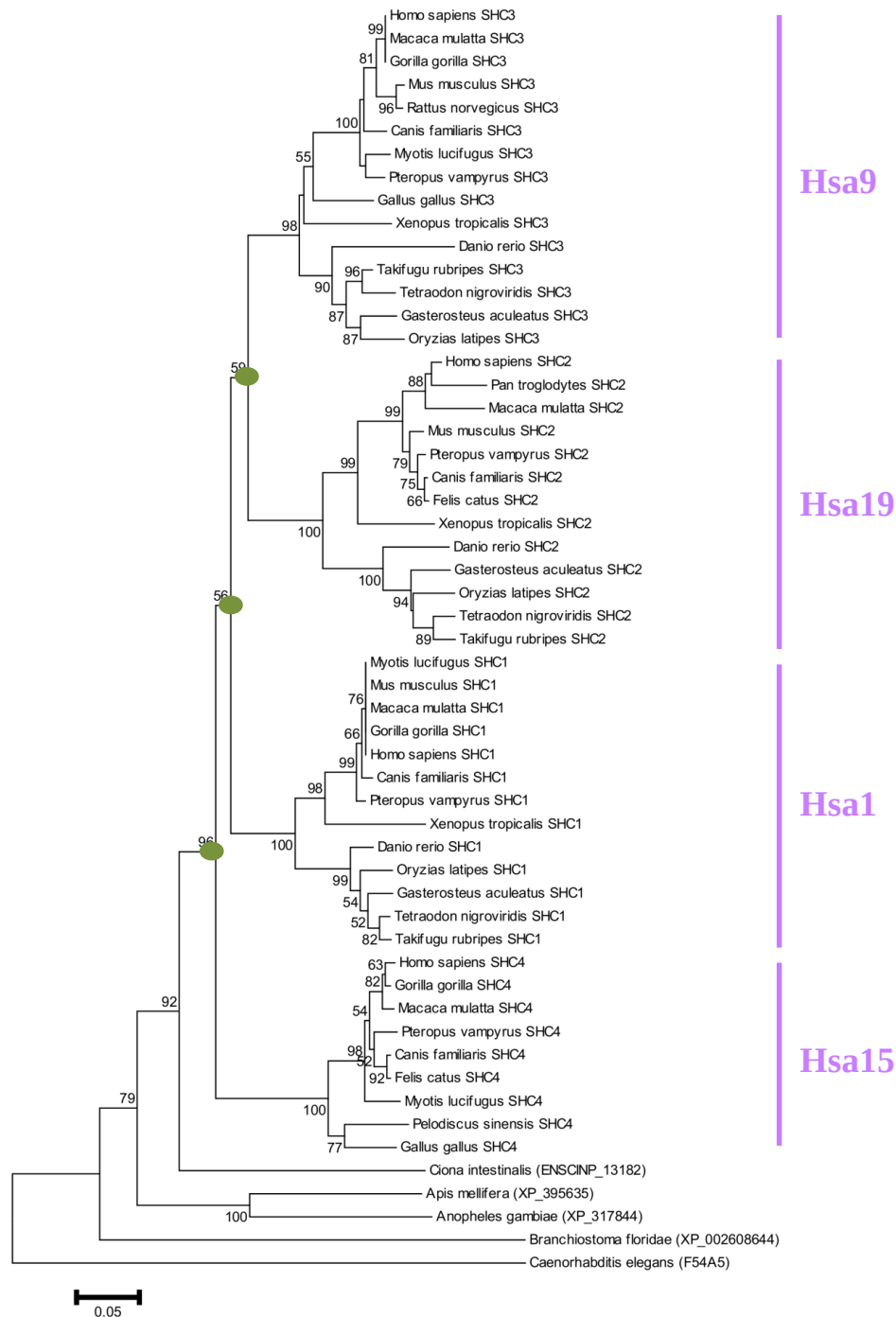
SH3 domain GRB2 like endophilin family - SH3GL



Phylogenetic tree of SH3GL family.

Neighbor- Joining tree of the SH3GL 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.

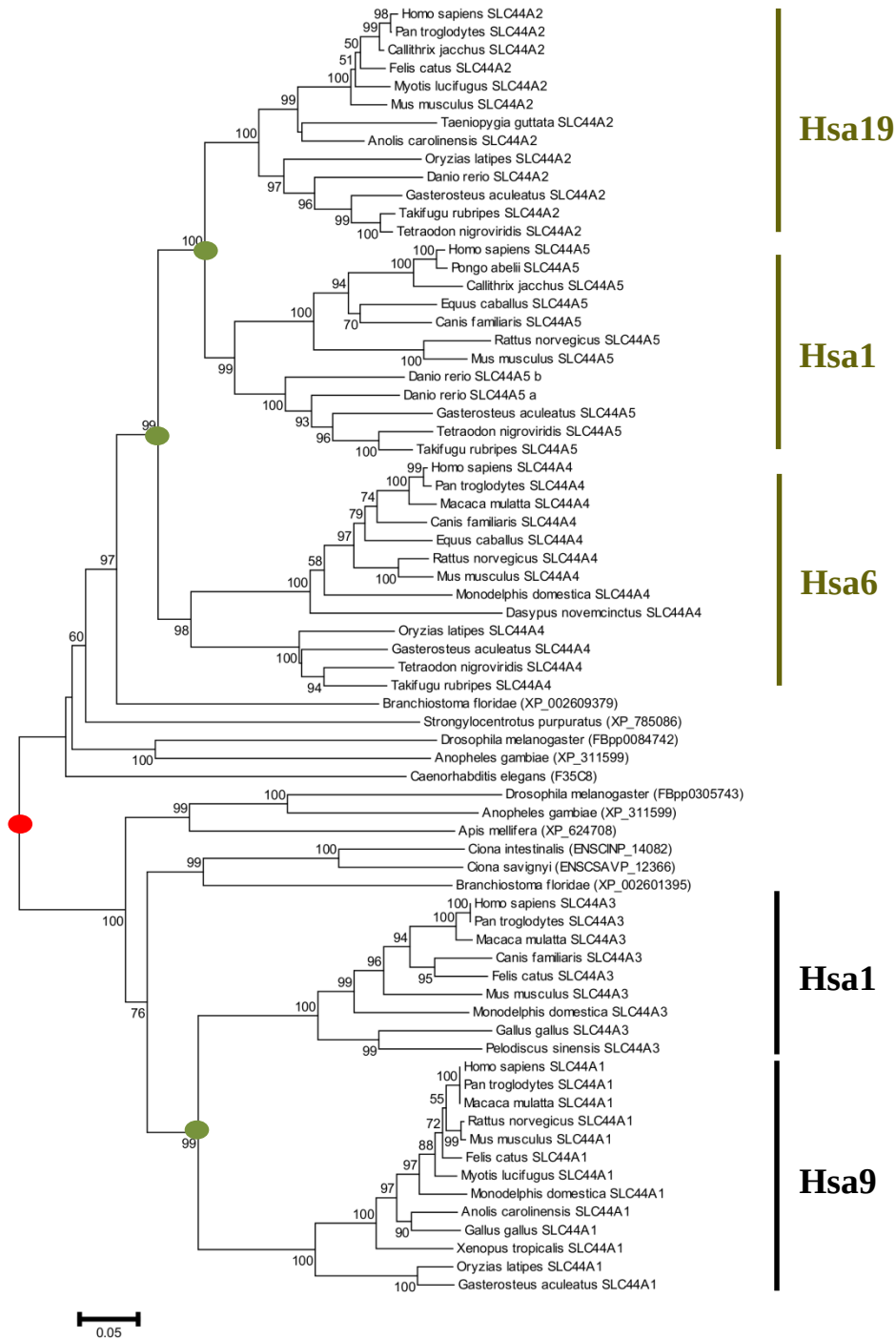
Src homology 2 domain containing) transforming protein family - SHC



Phylogenetic tree of SHC family.

Neighbor- Joining tree of the SHC 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.

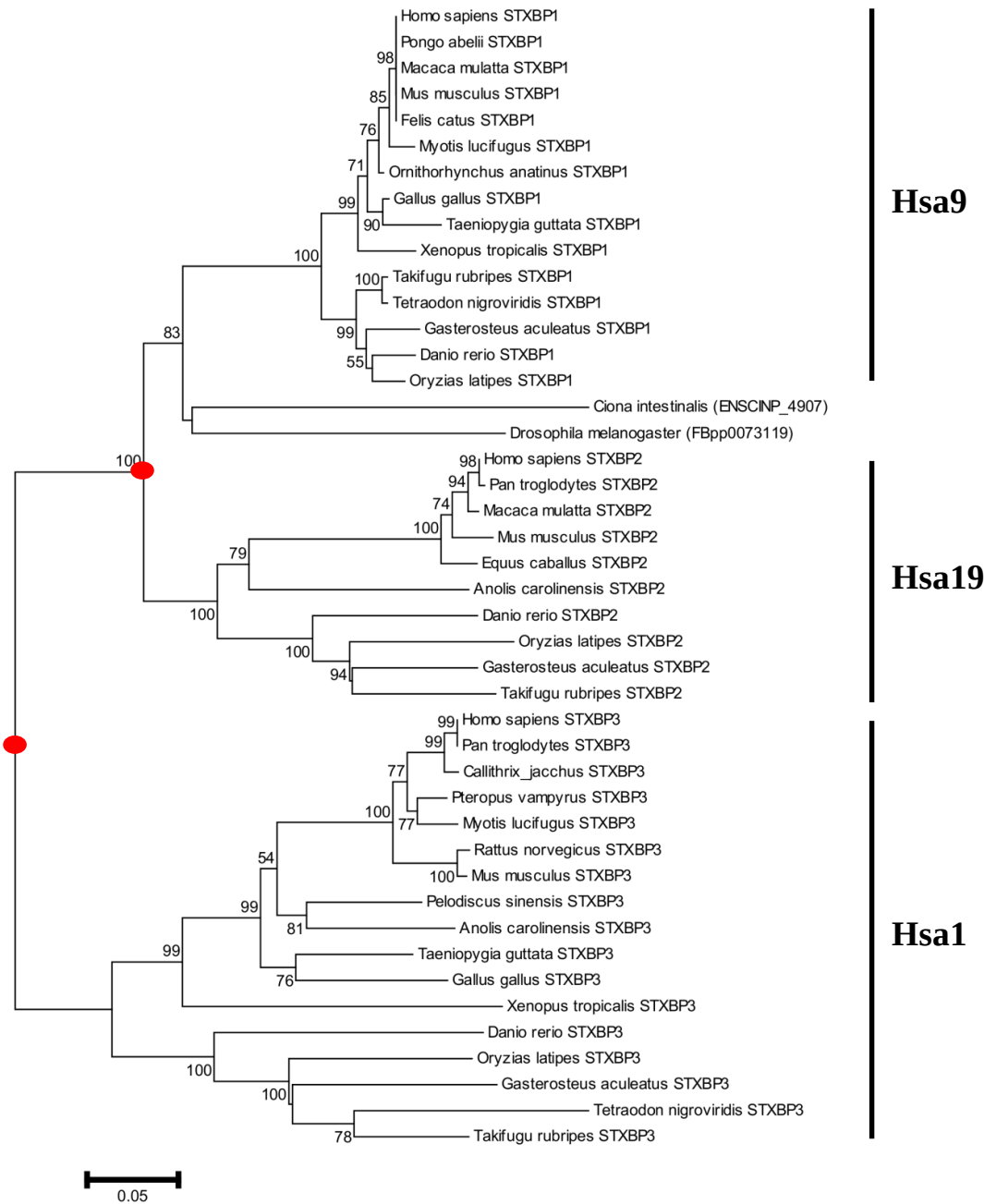
Solute carrier family 44 - SLC44



Phylogenetic tree of SLC44 family.

Neighbor- Joining tree of the SLC44 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.

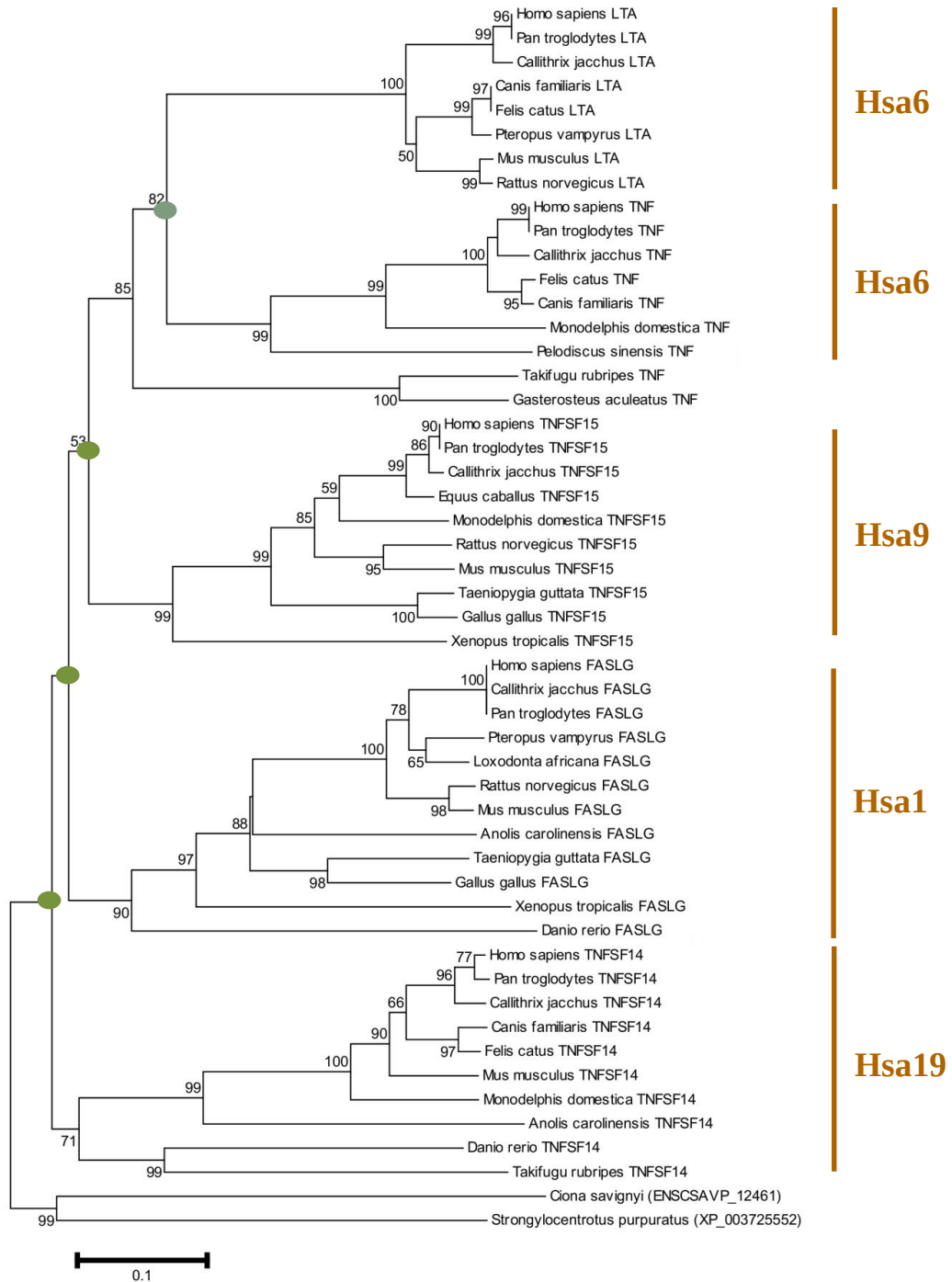
Syntaxin binding protein - STXBP



Phylogenetic tree of STXBP family.

Neighbor- Joining tree of the STXBP 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.

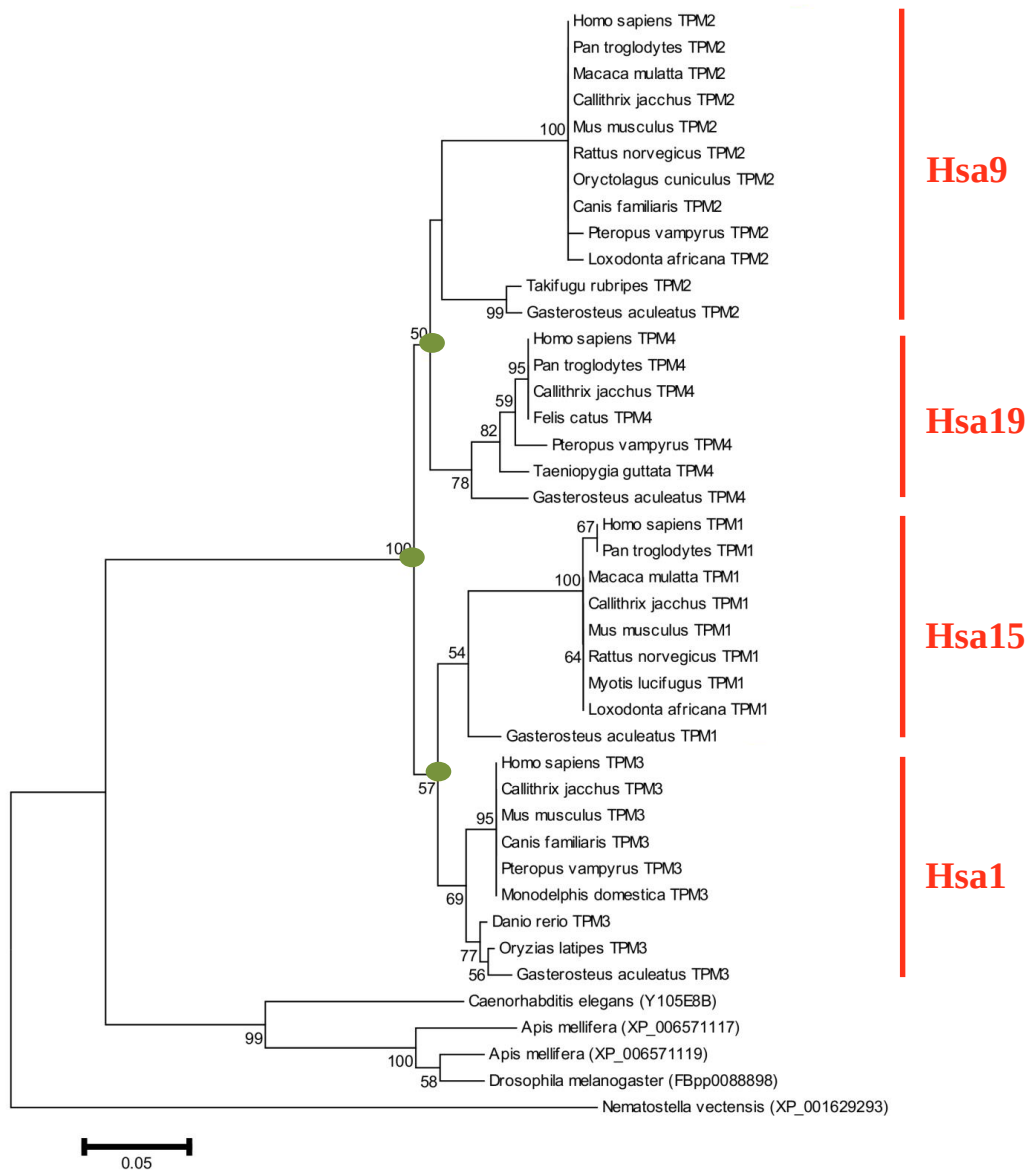
Fas ligand (TNF superfamily) - TNF



Phylogenetic tree of TNF family.

Neighbor- Joining tree of the TNF 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.

Tropomyosin family - TPM



Phylogenetic tree of TPM family.

Neighbor- Joining tree of the TPM 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.