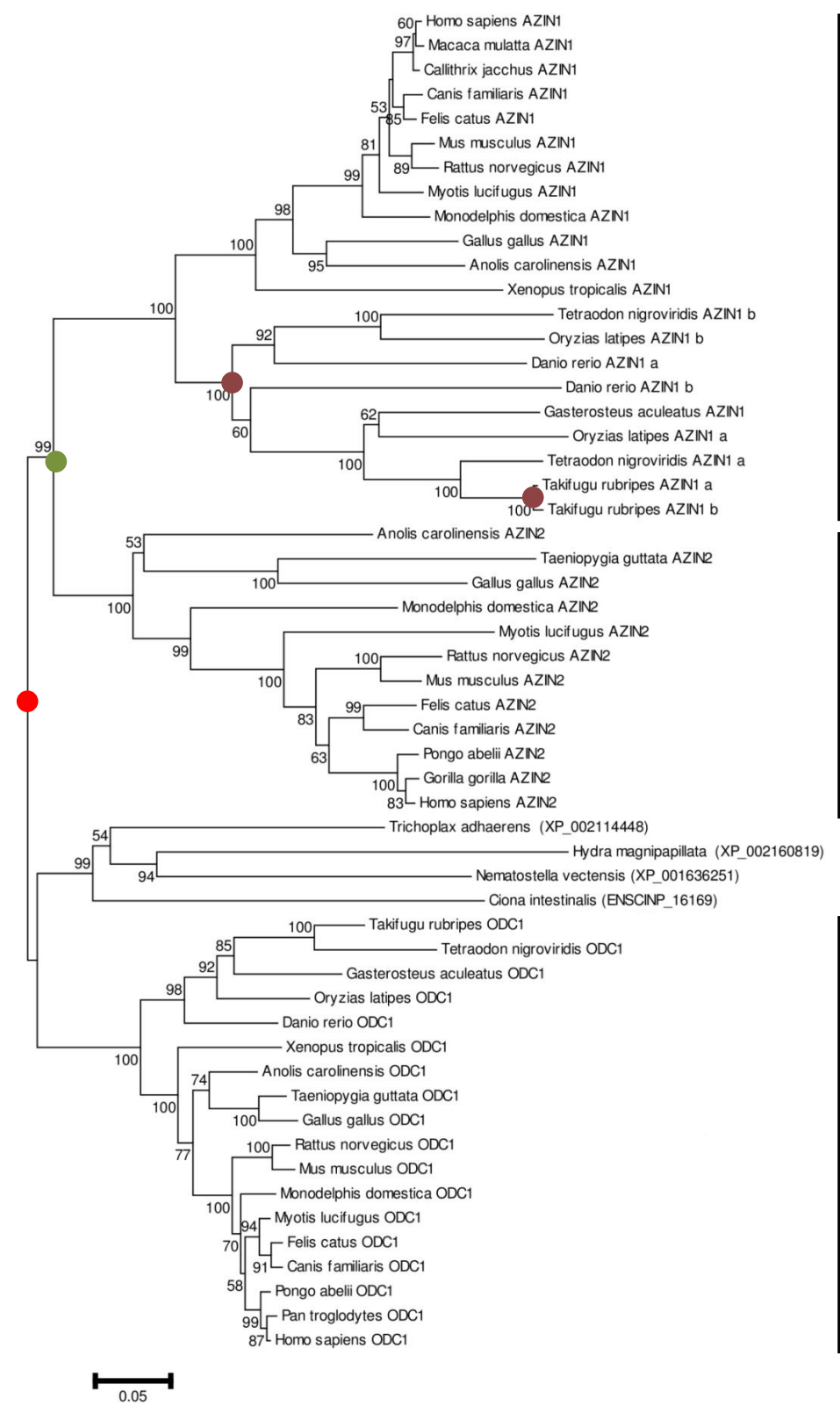


**Neighbor Joining Trees of gene families residing on
chromosomes 1, 2, 8 and 20.**

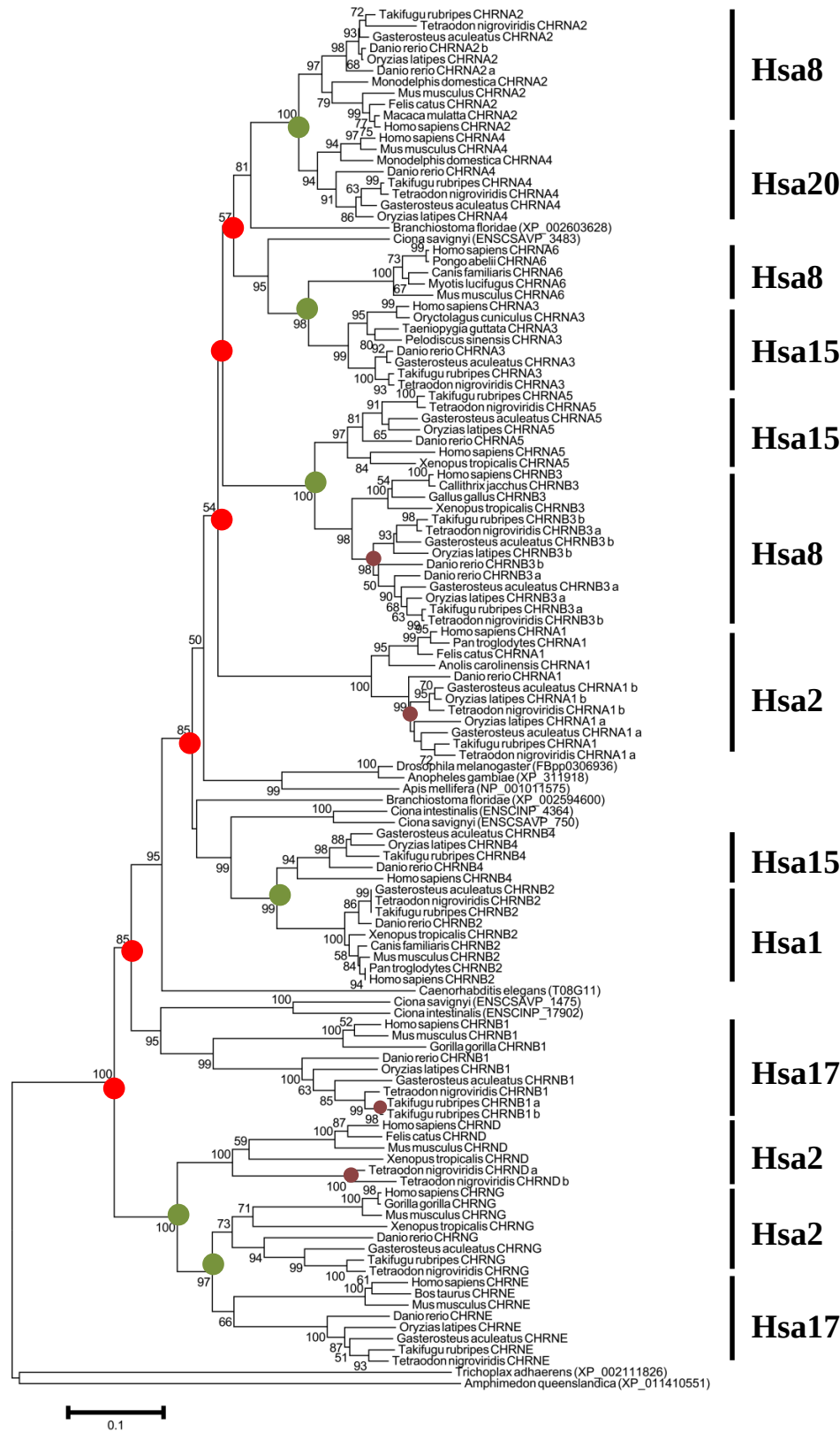
Antizyme Inhibitor-AZIN



Phylogenetic tree of AZIN family.

Neighbor-Joining tree of the AZIN 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.

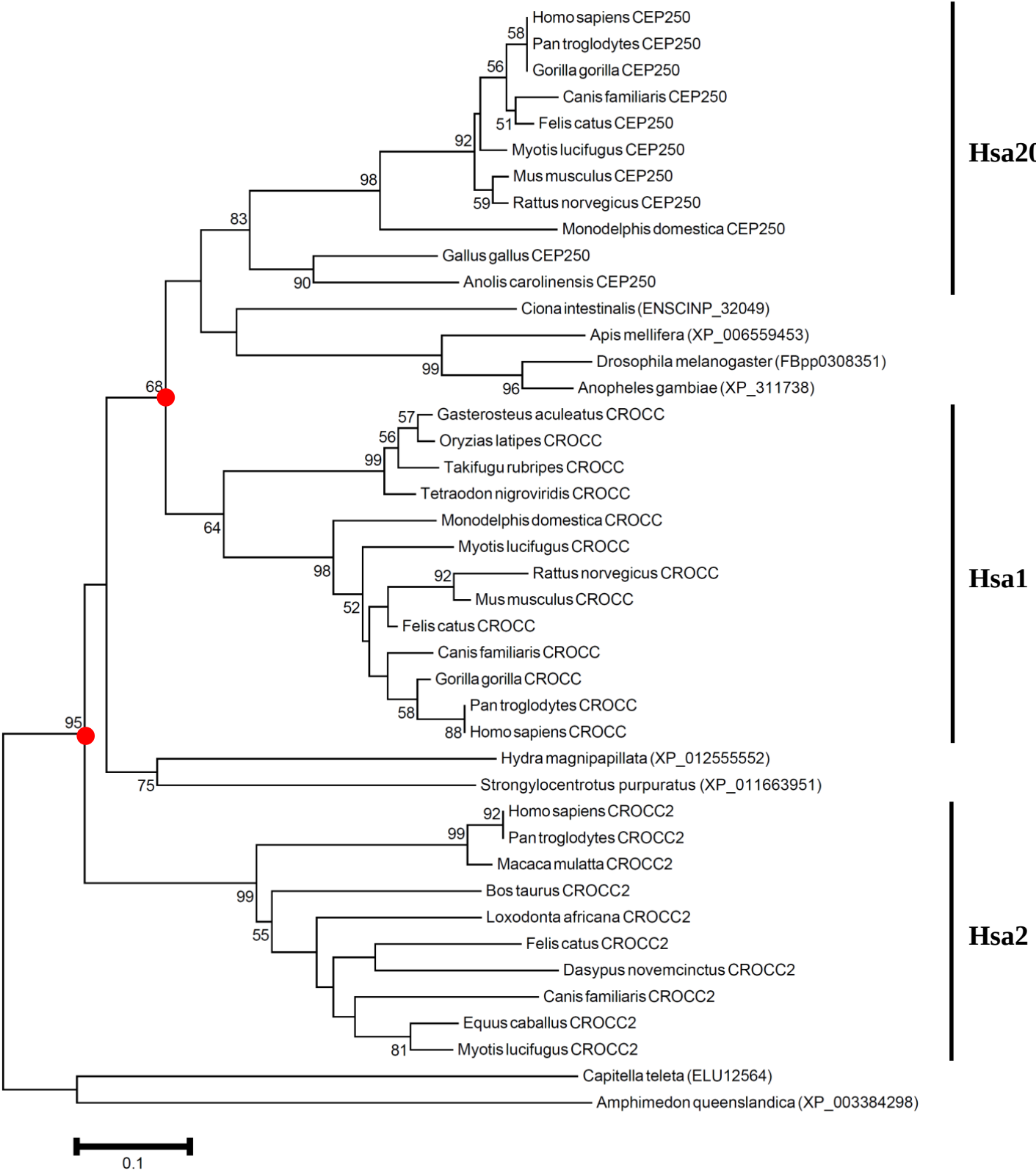
Cholinergic Receptor Nicotinic Subunits-CHRN



Phylogenetic tree of CHRN family.

Neighbor-Joining tree of the CHRN 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.

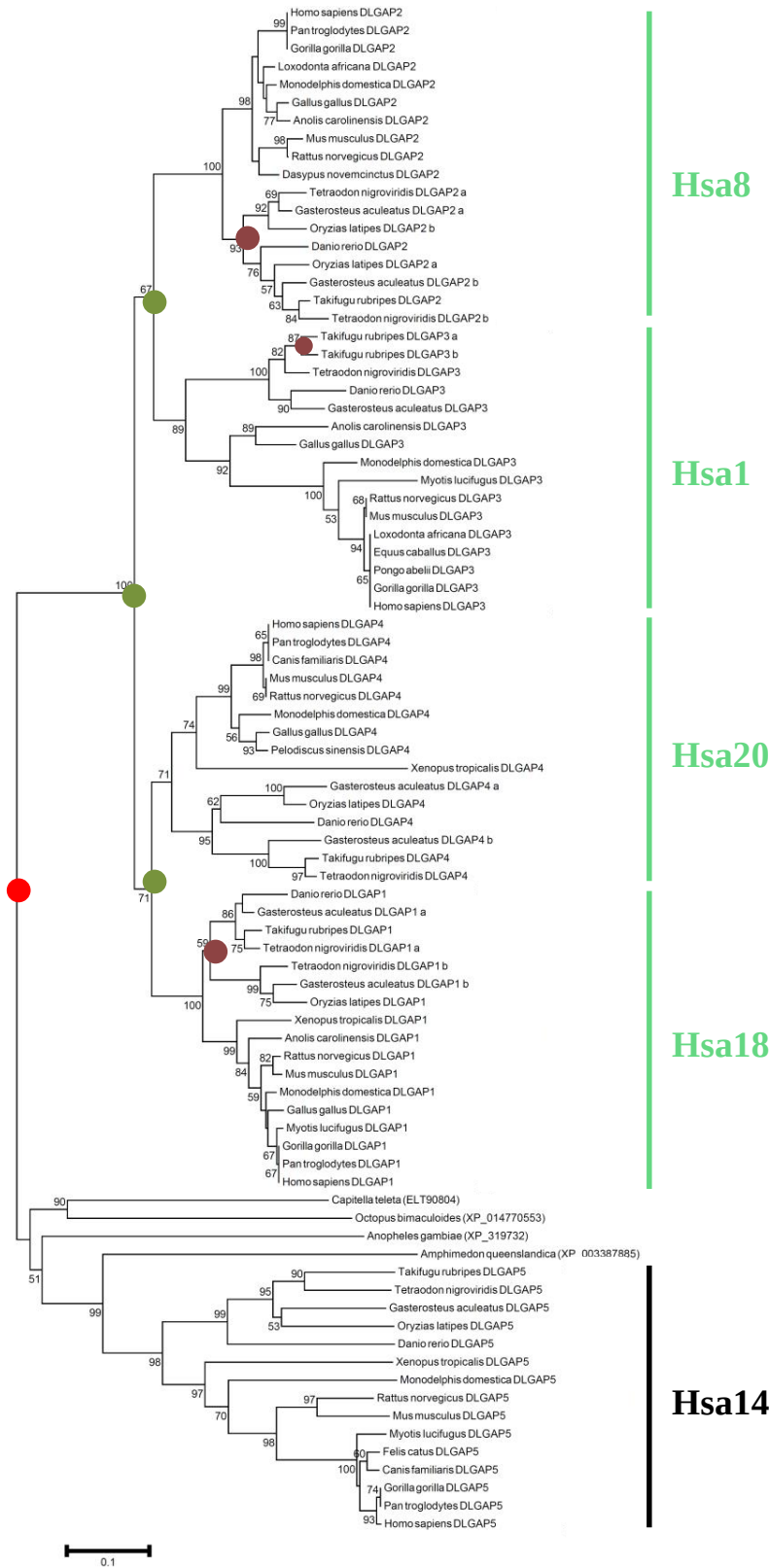
Ciliary Rootlet Coiled-Coil Protein-CROCC



Phylogenetic tree of CROCC family.

Neighbor-Joining tree of the CROCC 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.

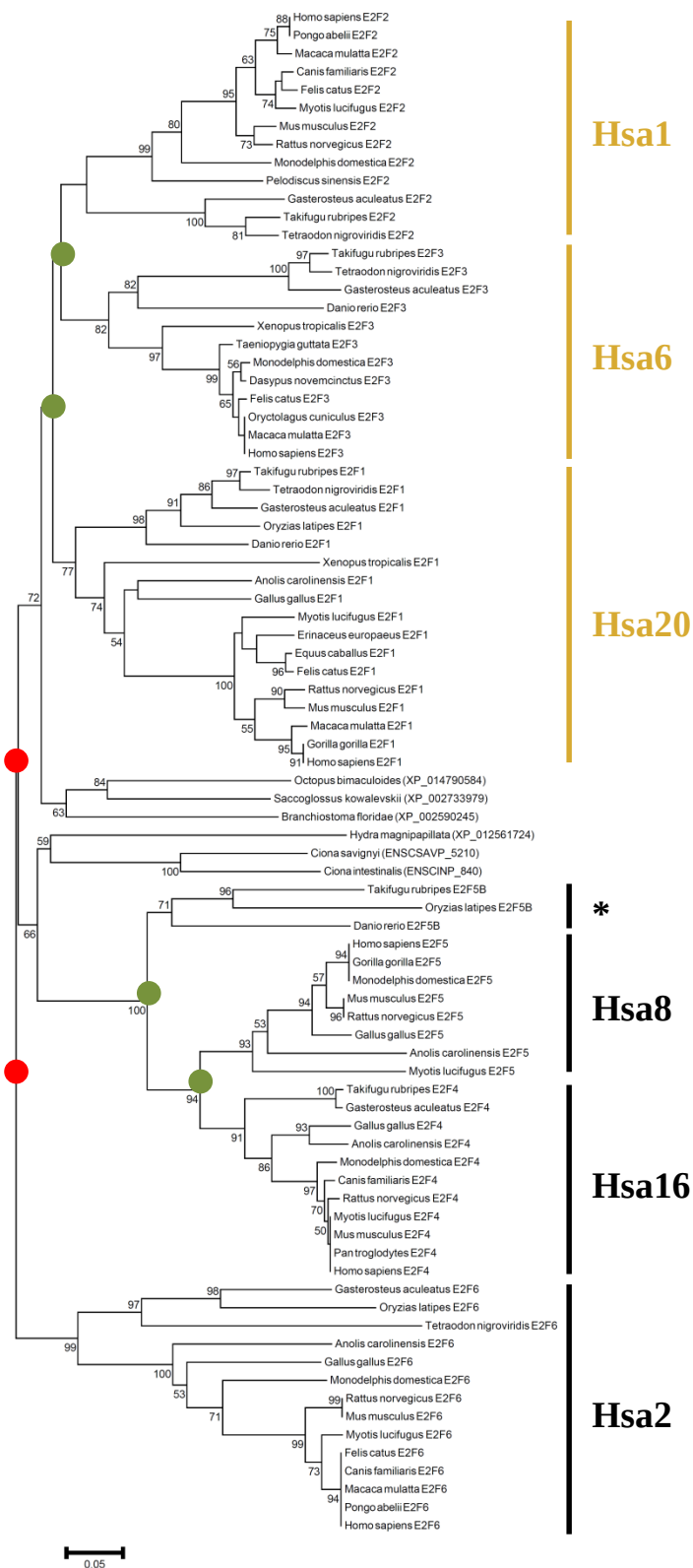
Discs, large Drosophila Homolog-associated Protein-DLGAP



Phylogenetic tree of DLGAP family.

Neighbor-Joining tree of the DLGAP 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.

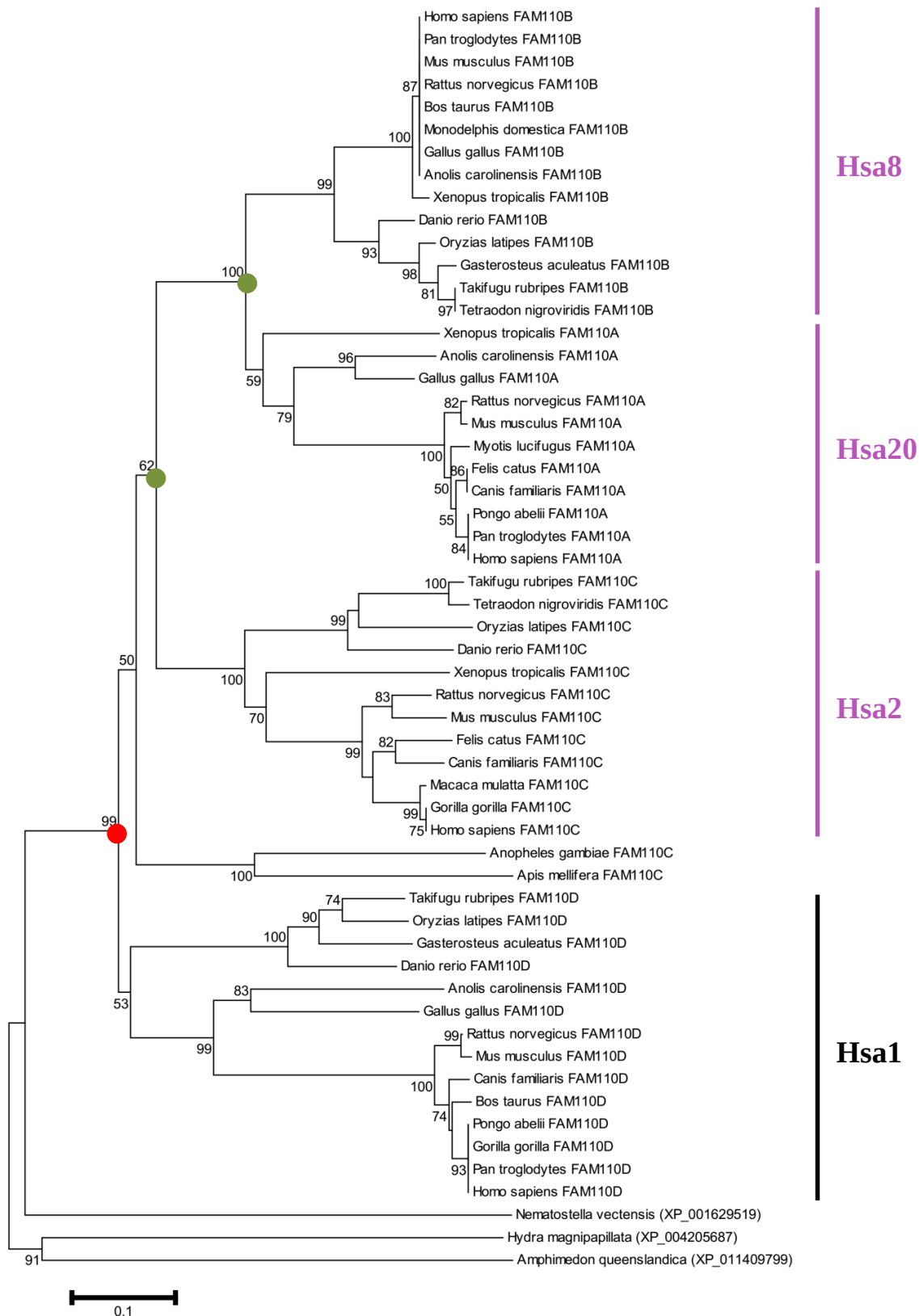
E2F Transcription Factor-E2F



Phylogenetic tree of E2F family.

Neighbor-Joining tree of the E2F 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.

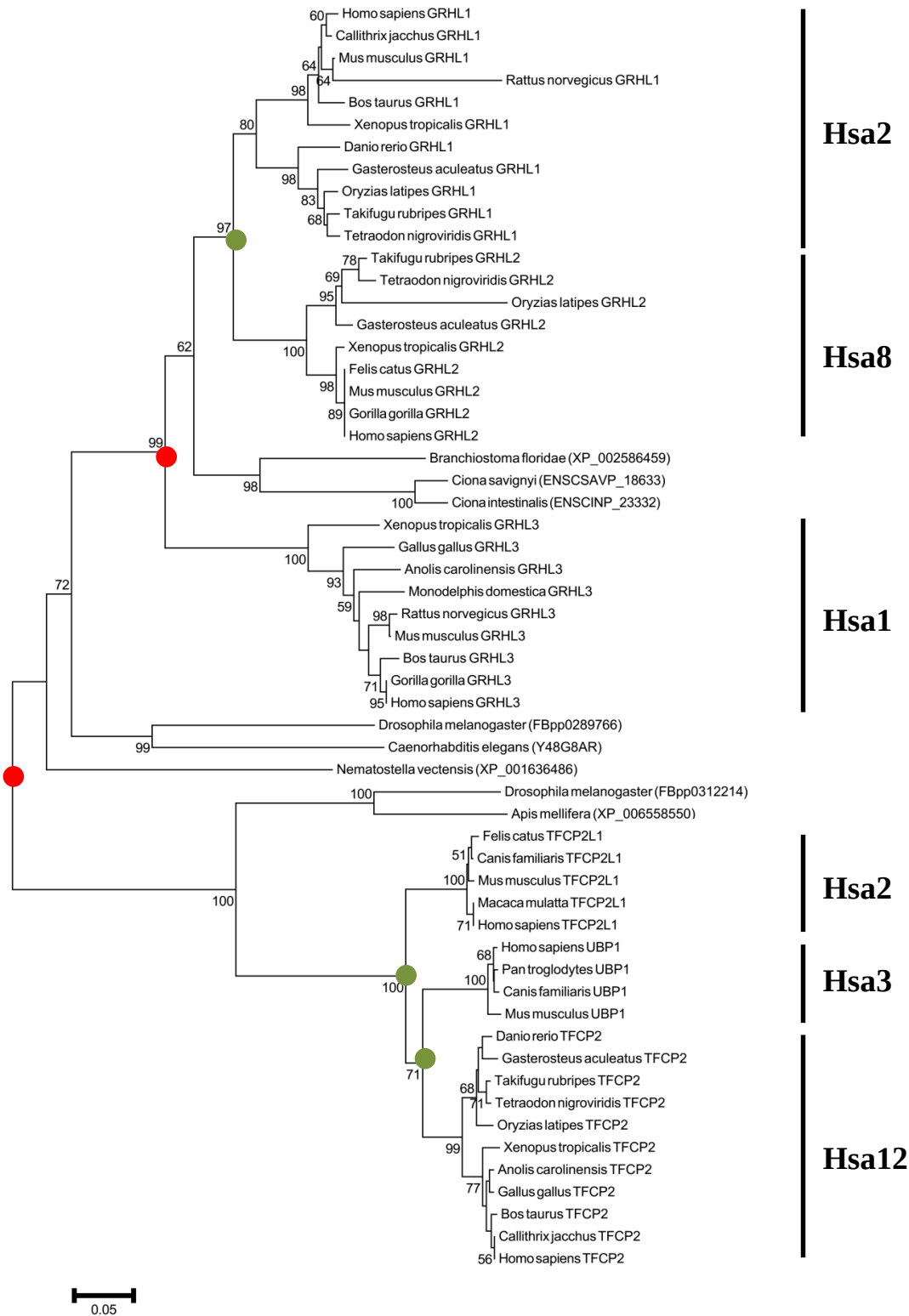
Family with Sequence Similarity 110-FAM110



Phylogenetic tree of FAM110 family.

Neighbor-Joining tree of the FAM110 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.

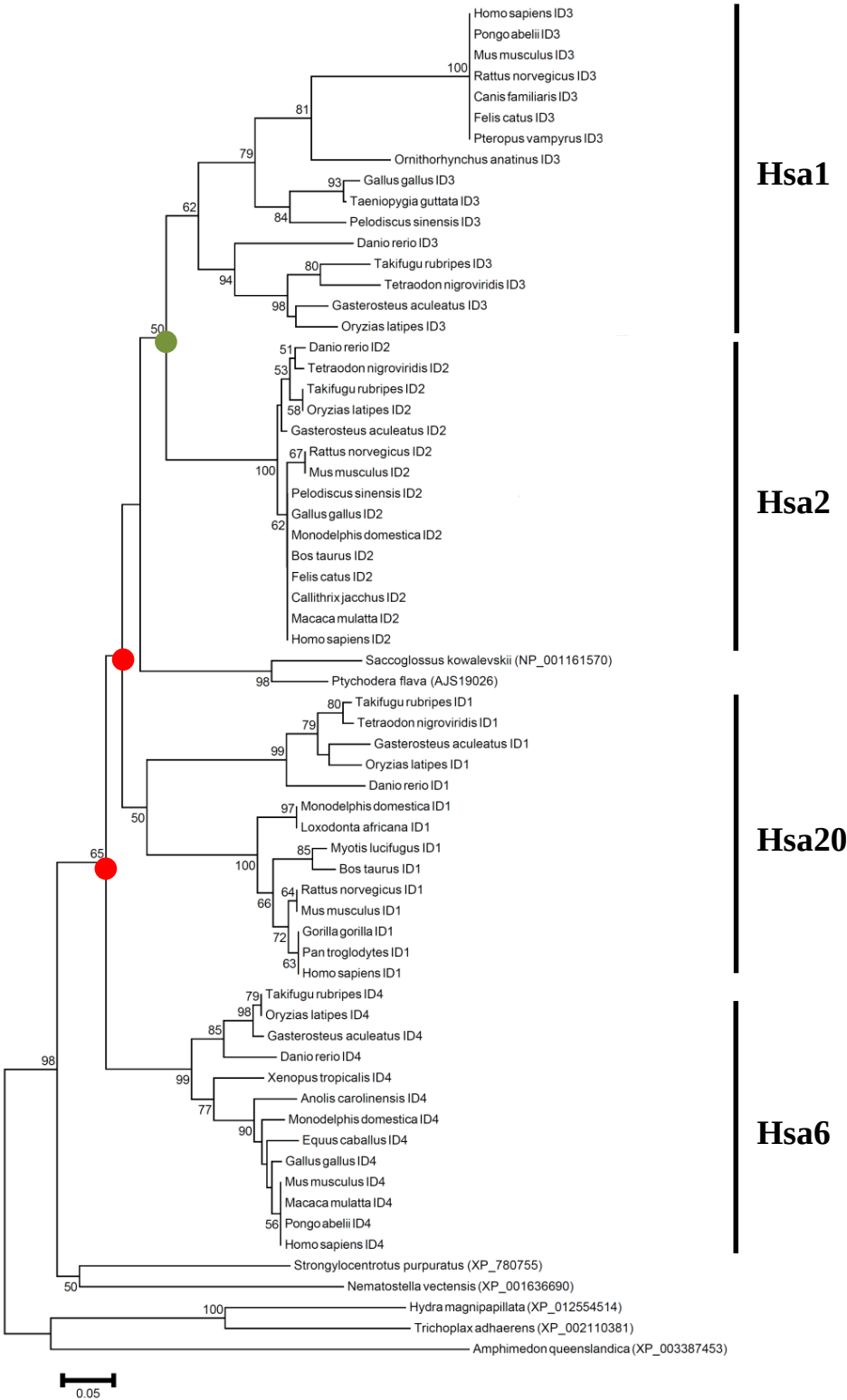
Grainyhead like Transcription factor-GRHL



Phylogenetic tree of GRHL family.

Neighbor-Joining tree of the GRHL 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.

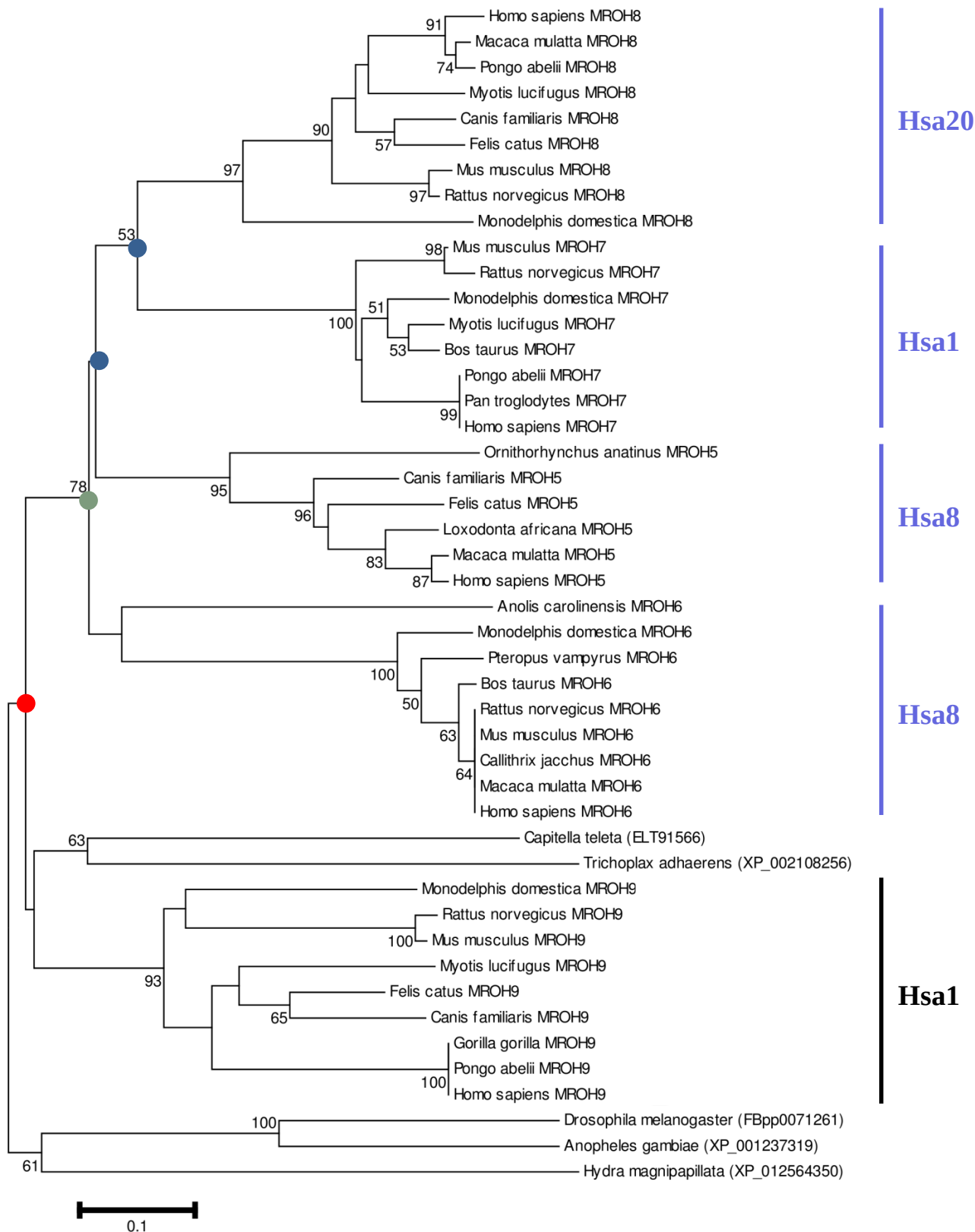
Inhibitor of DNA Binding protein-ID



Phylogenetic tree of ID family.

Neighbor-Joining tree of the ID 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.

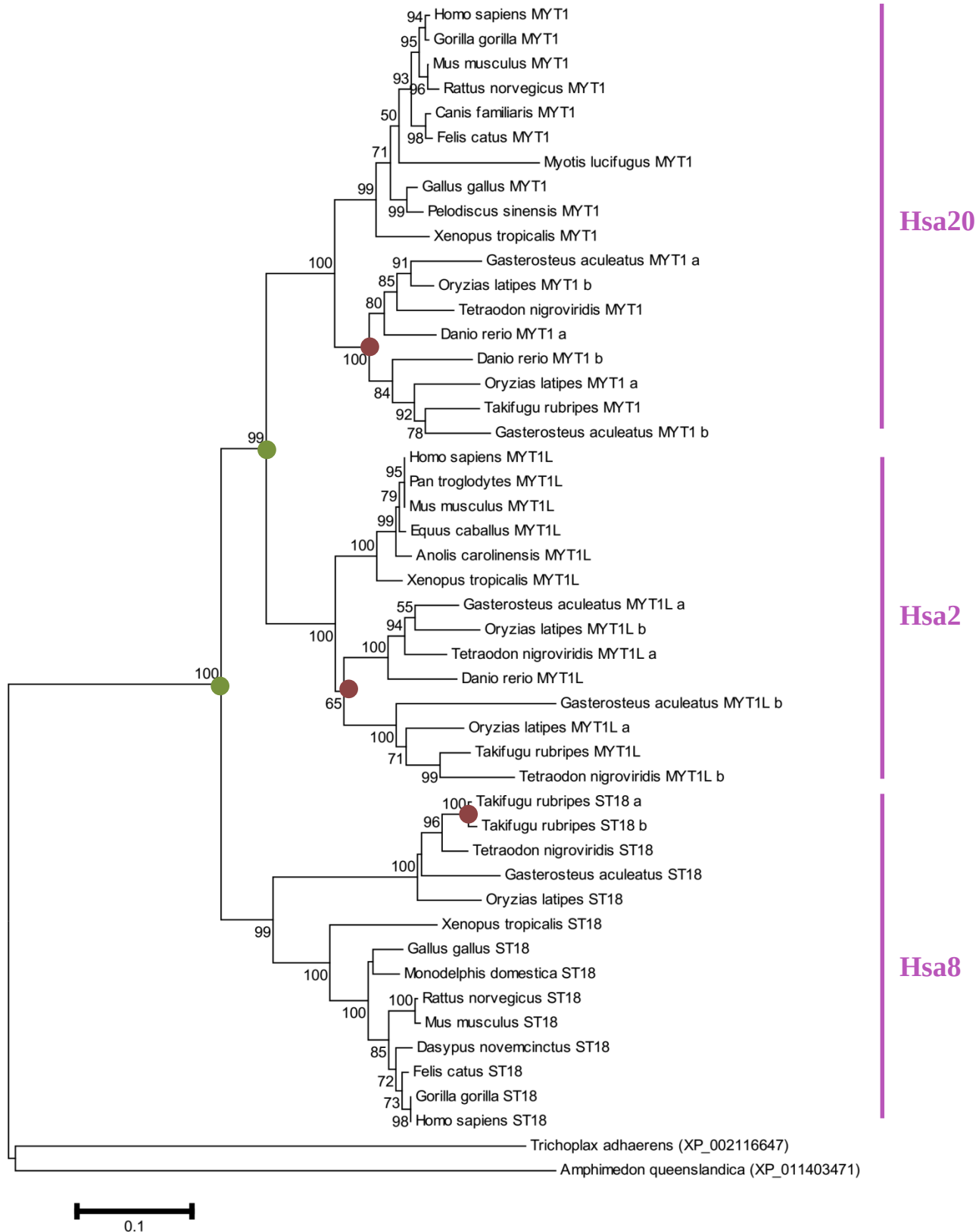
Maestro Heat-like Repeat-containing Protein Family -MROH



Phylogenetic tree of MROH family.

Neighbor-Joining tree of the MROH 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.

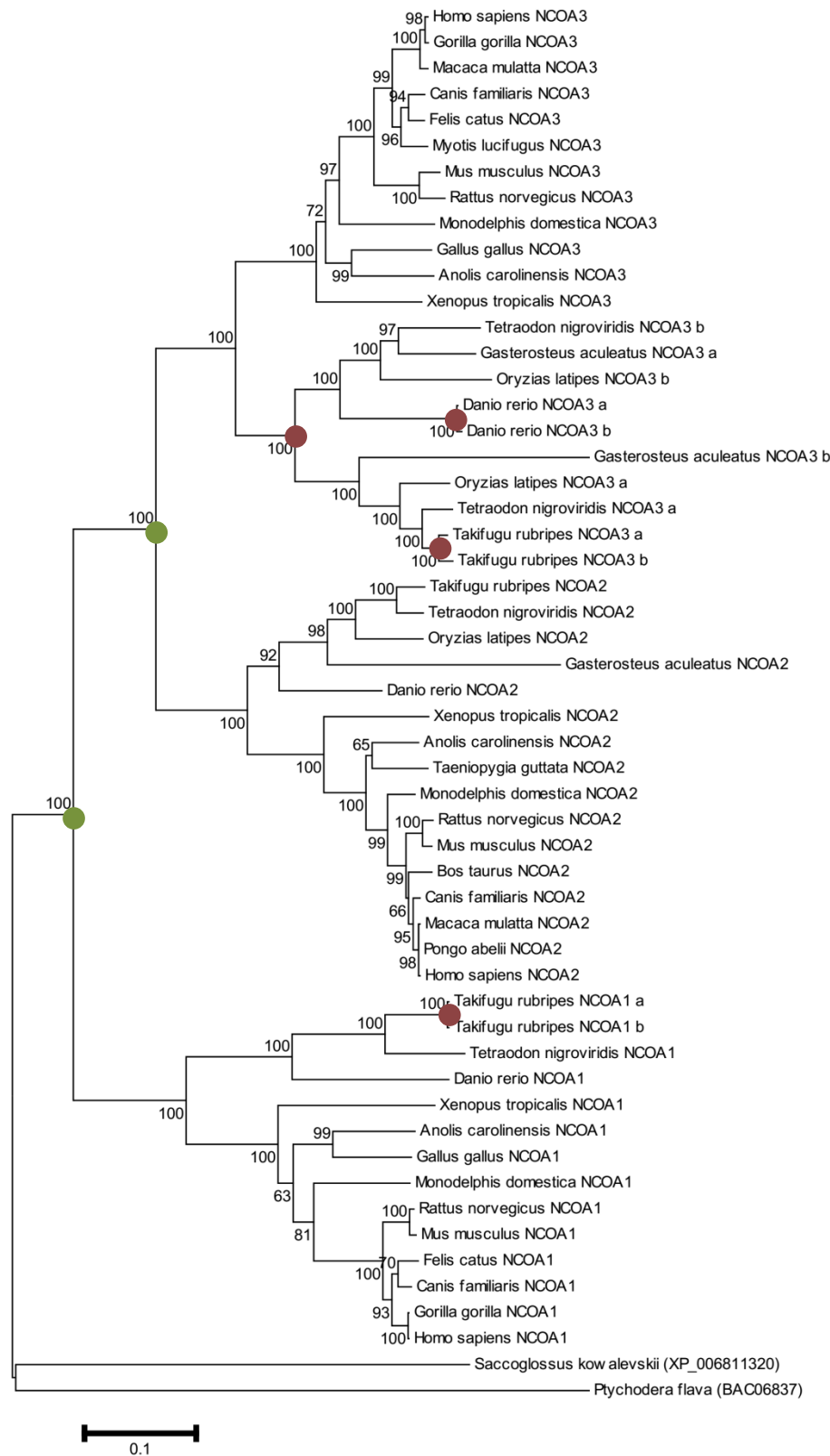
Myelin Transcription Factor-MYT



Phylogenetic tree of MYT family.

Neighbor-Joining tree of the MYT 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 Coactivator-NCOA



Hsa20

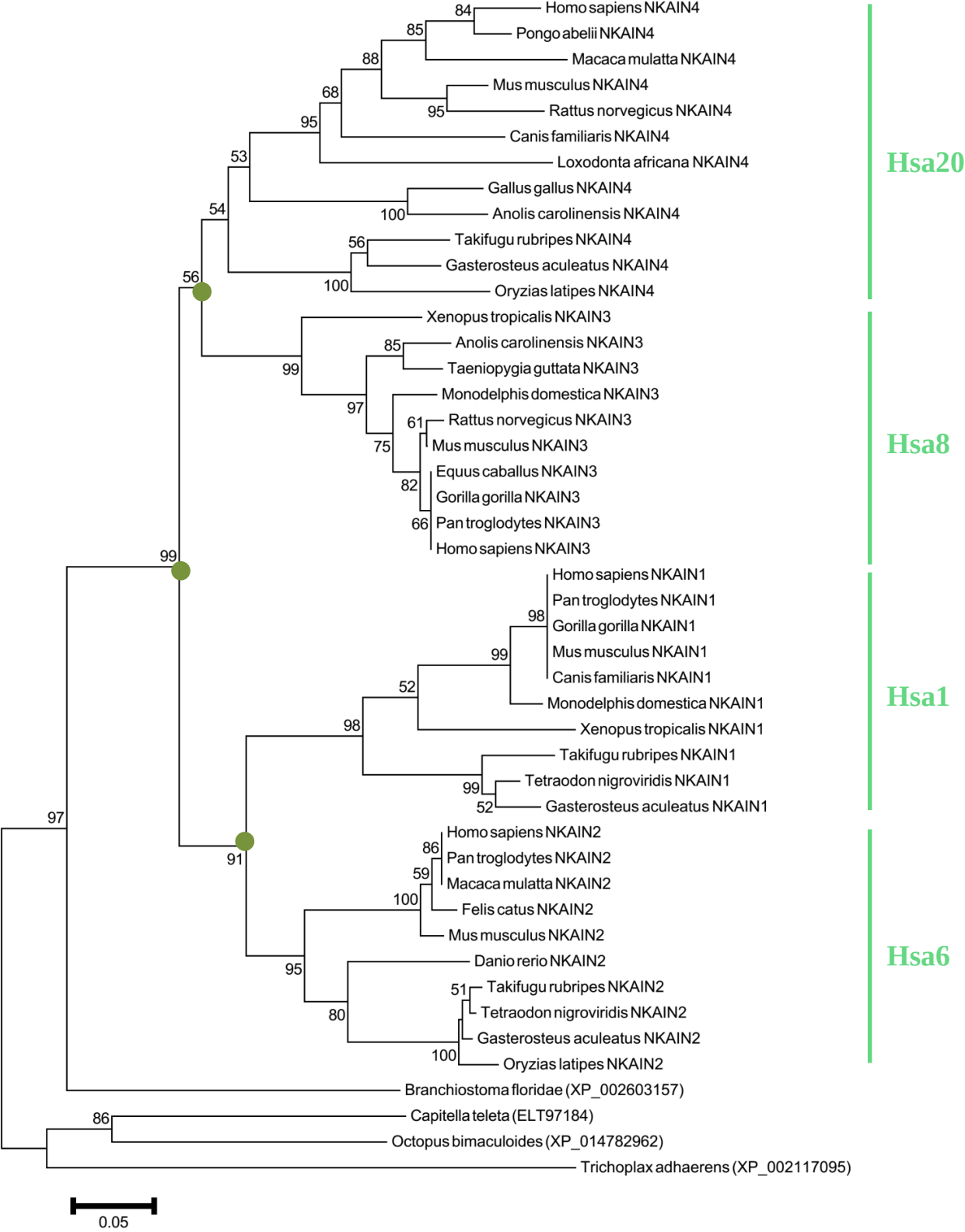
Hsa8

Hsa2

Phylogenetic tree of NCOA family.

Neighbor-Joining tree of the NCOA 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.

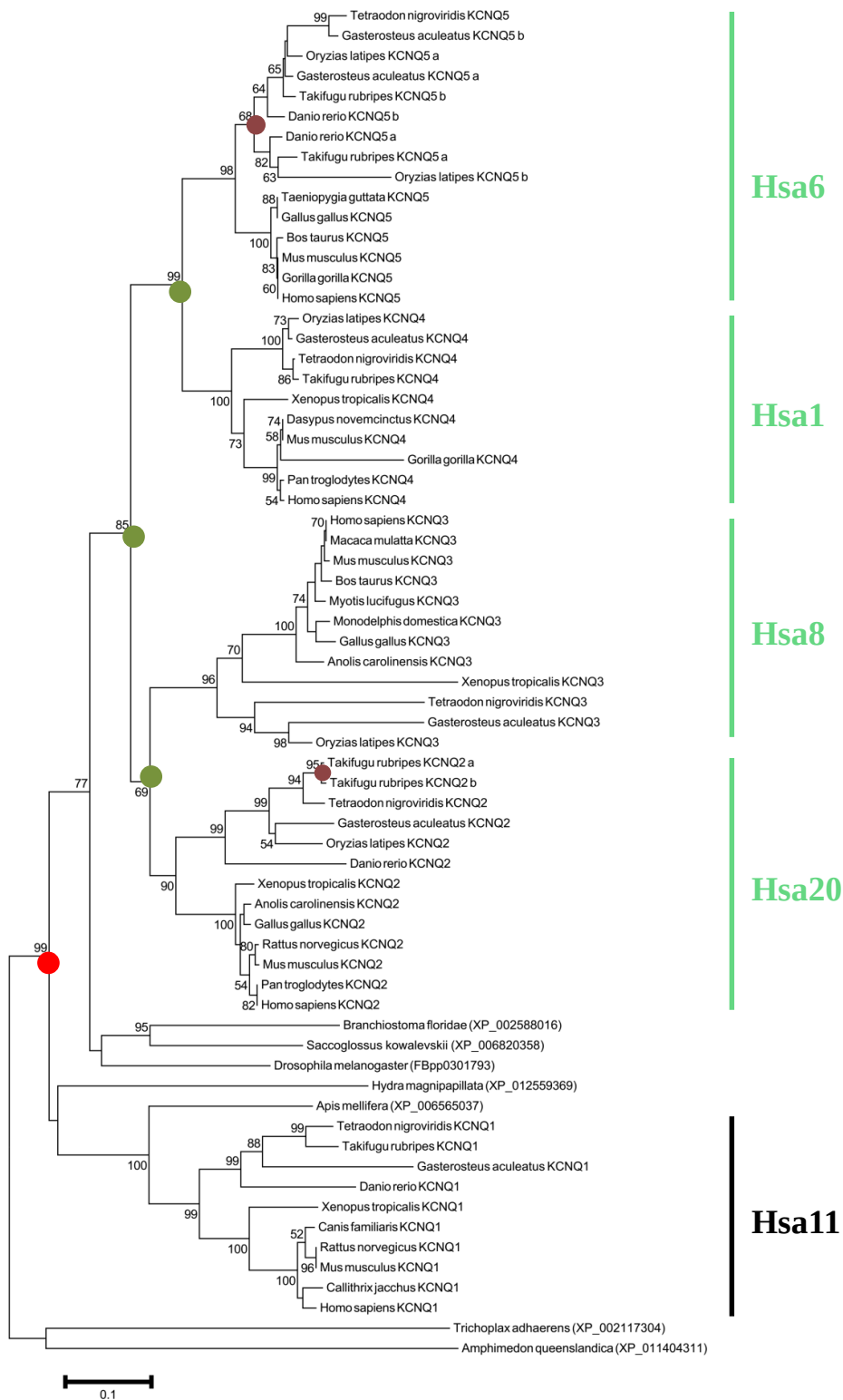
Na⁺/K⁺ Transporting ATPase Interacting Protein-NKAIN



Phylogenetic tree of NKAIN family.

Neighbor-Joining tree of the NKAIN 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.

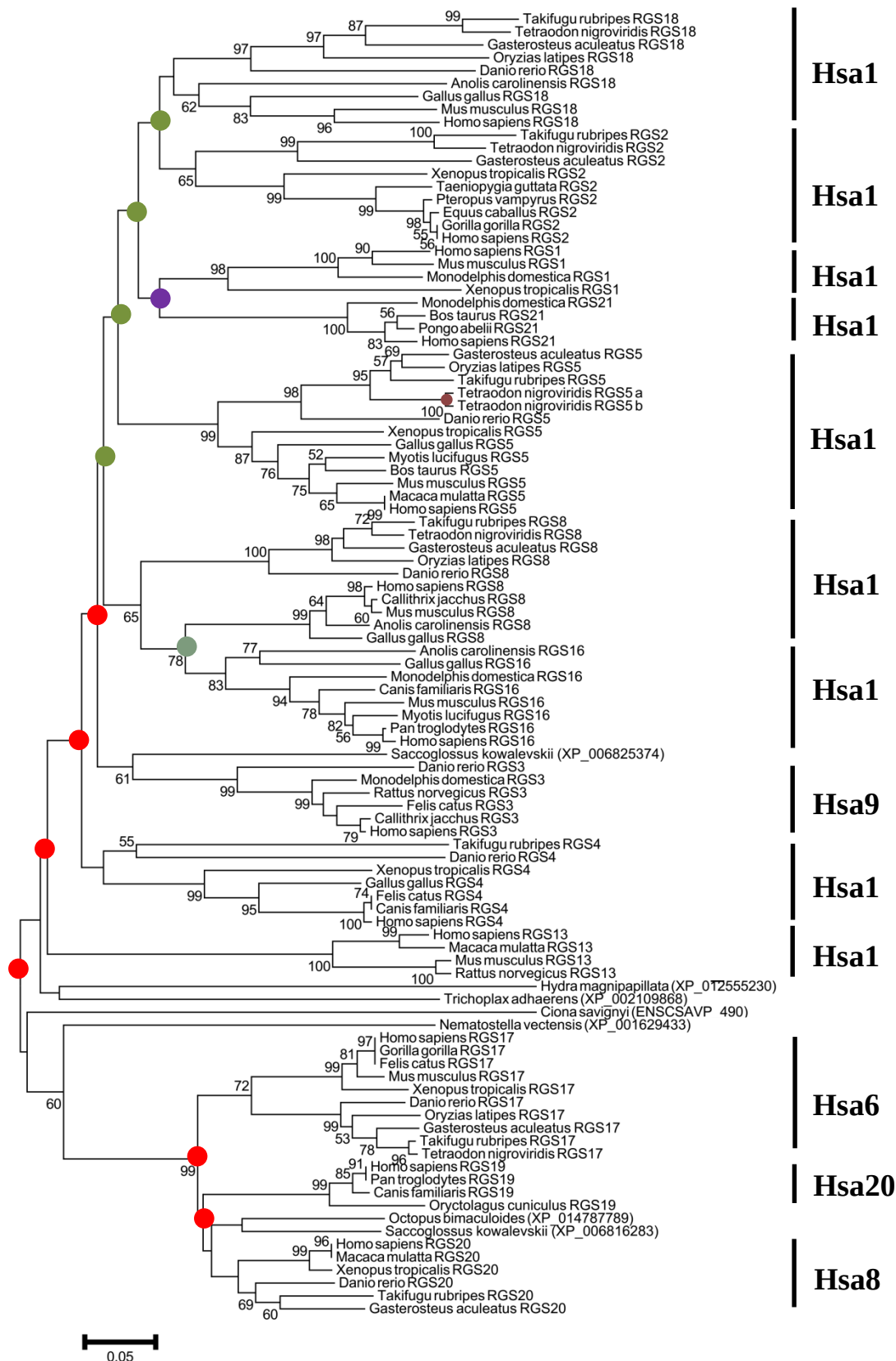
Potassium Voltage-Gated Channel subfamily KCNQ



Phylogenetic tree of KCNQ family.

Neighbor-Joining tree of the KCNQ 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.

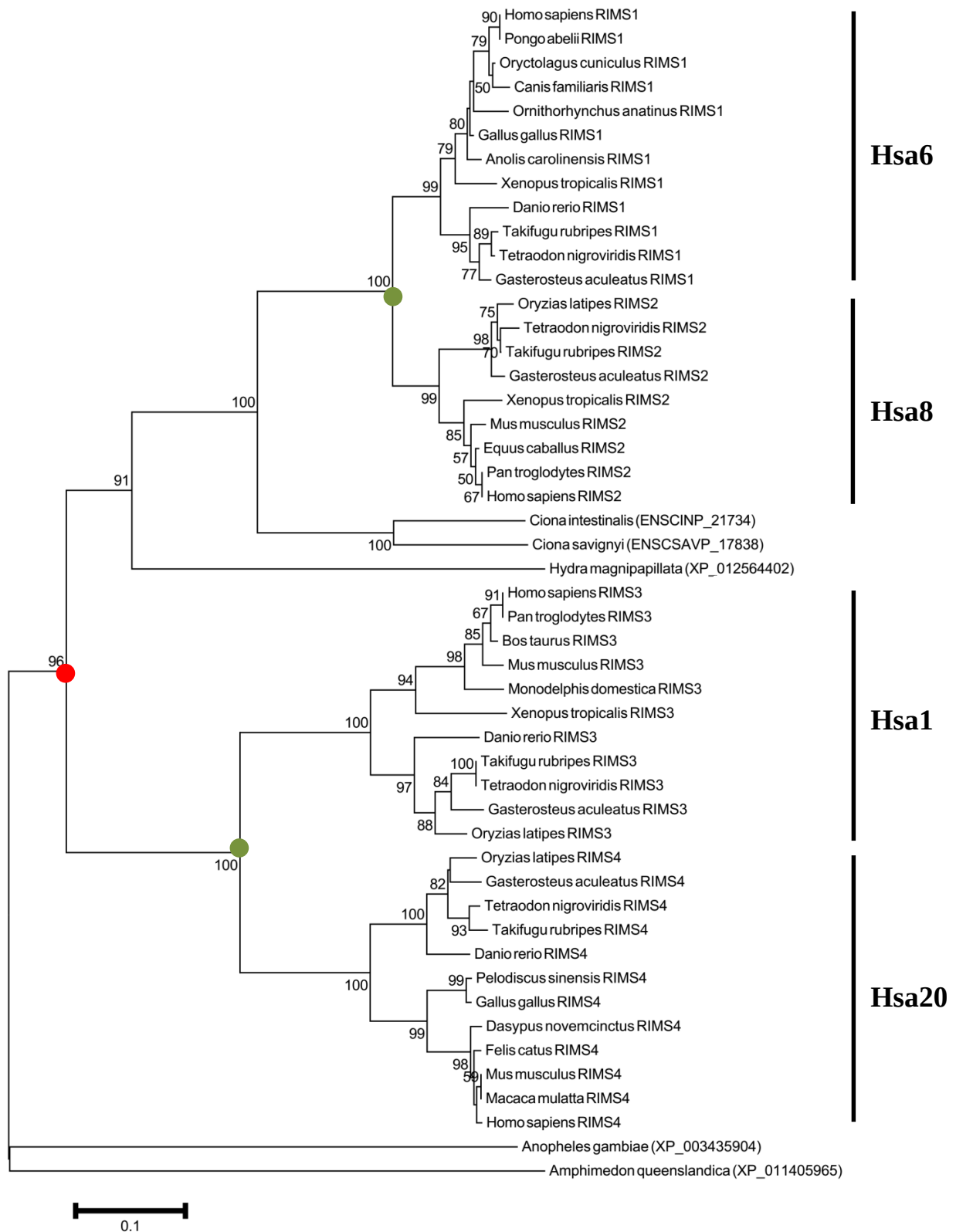
Regulator of G-protein Signaling-RGS



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.

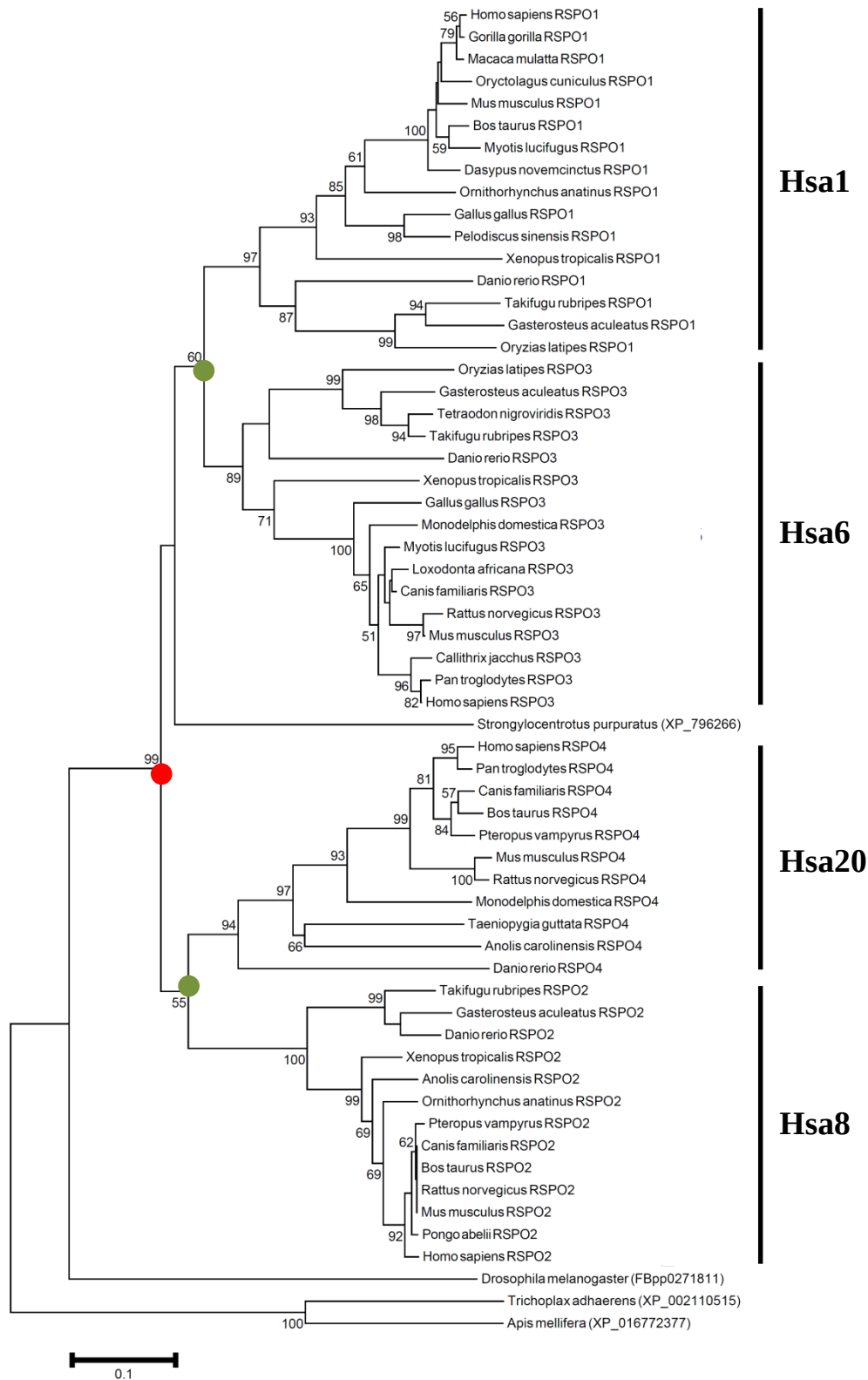
Regulating Synaptic Membrane Exocytosis Protein -RIMS



Phylogenetic tree of RIMS family.

Neighbor-Joining tree of the RIMS 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.

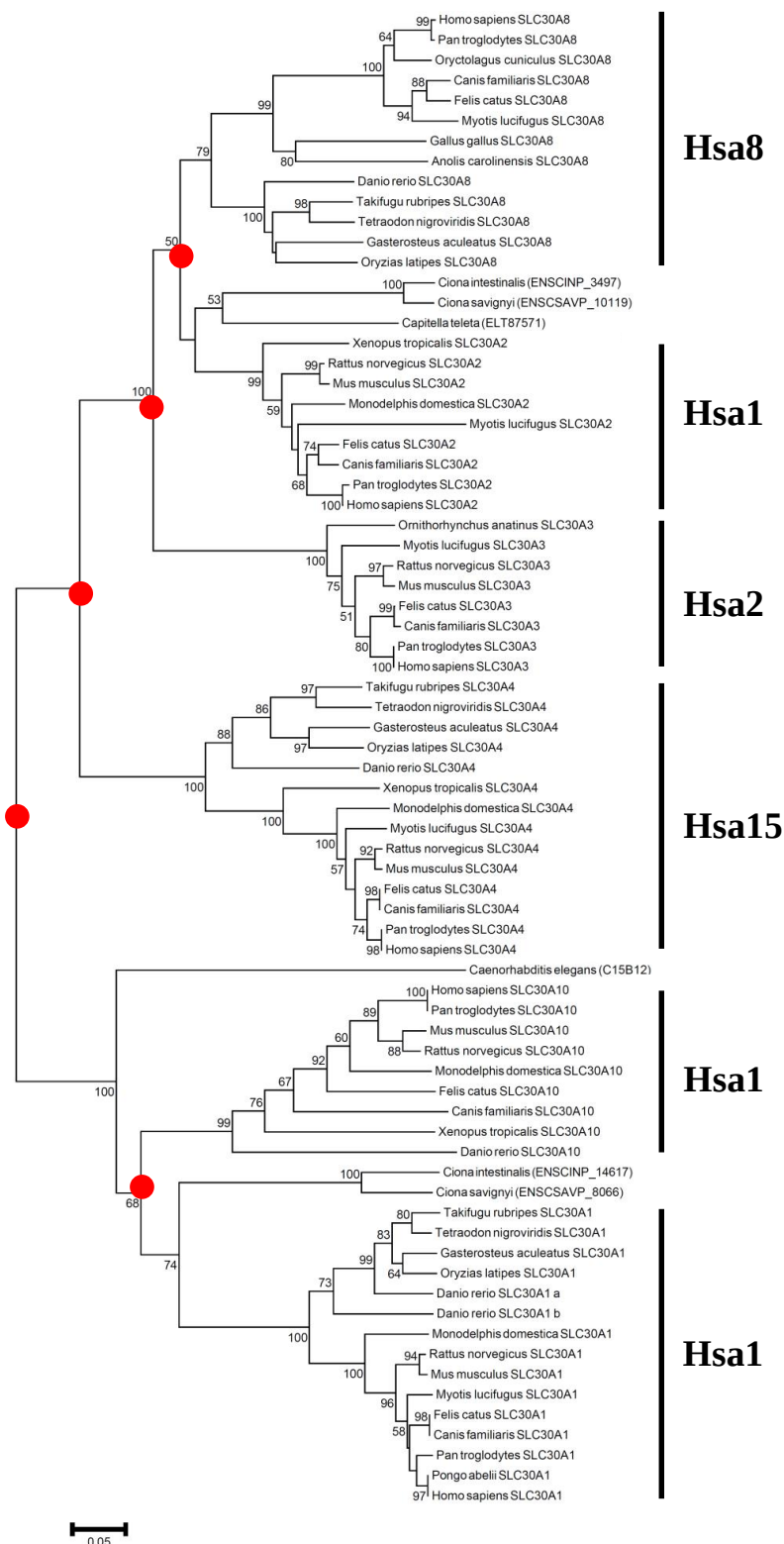
R-Spondin Homolog-RSPO



Phylogenetic tree of RSPO family.

Neighbor-Joining tree of the RSPO 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.

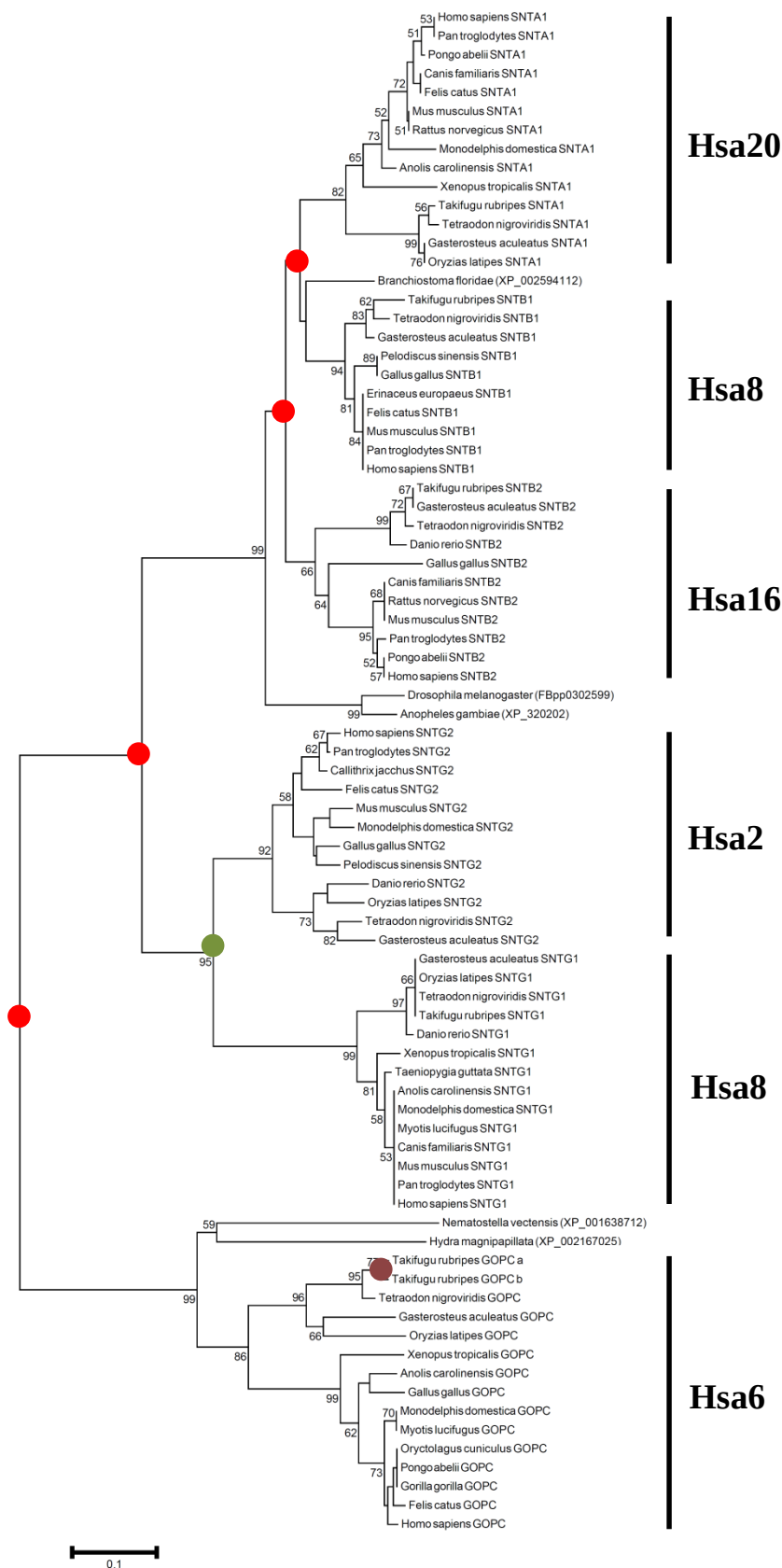
Solute Carrier Family-SLC30A



Phylogenetic tree of SLC30A family.

Neighbor-Joining tree of the SLC30A 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.

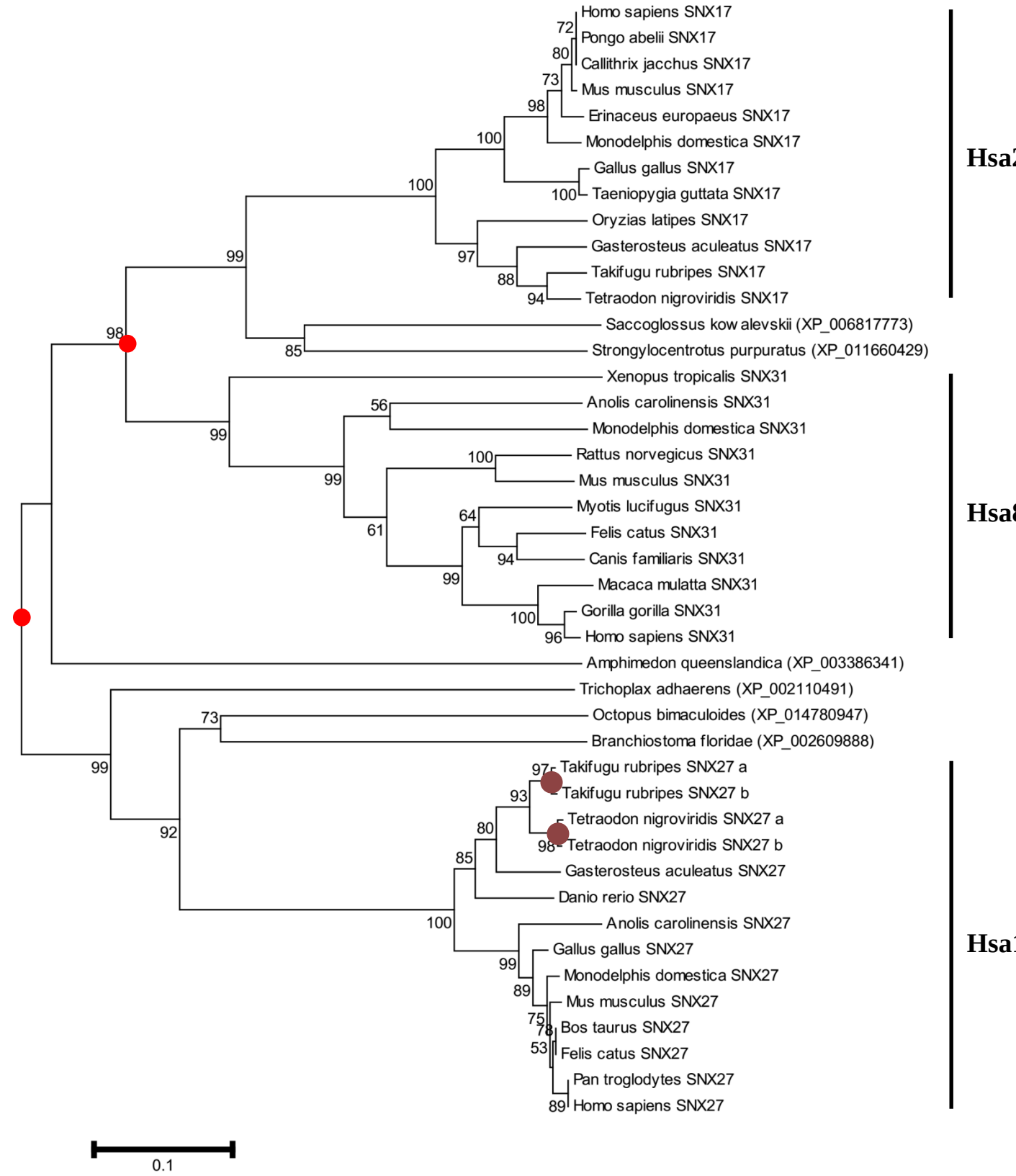
Syntrophin, Gamma-SNT



Phylogenetic tree of SNT family.

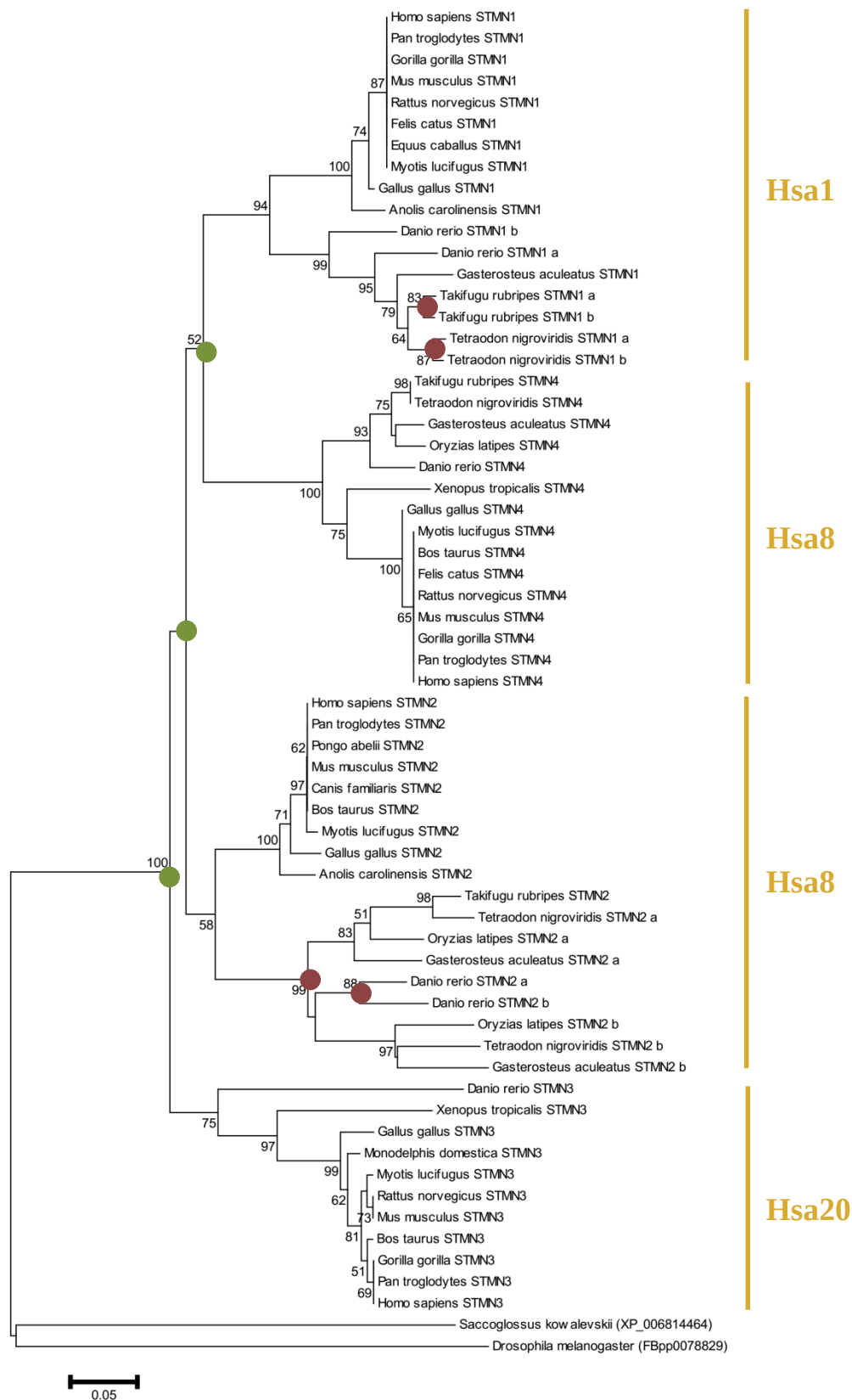
Neighbor-Joining tree of the SNT family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution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

Sorting Nexin Family-SNX



Phylogenetic tree of SNX family.

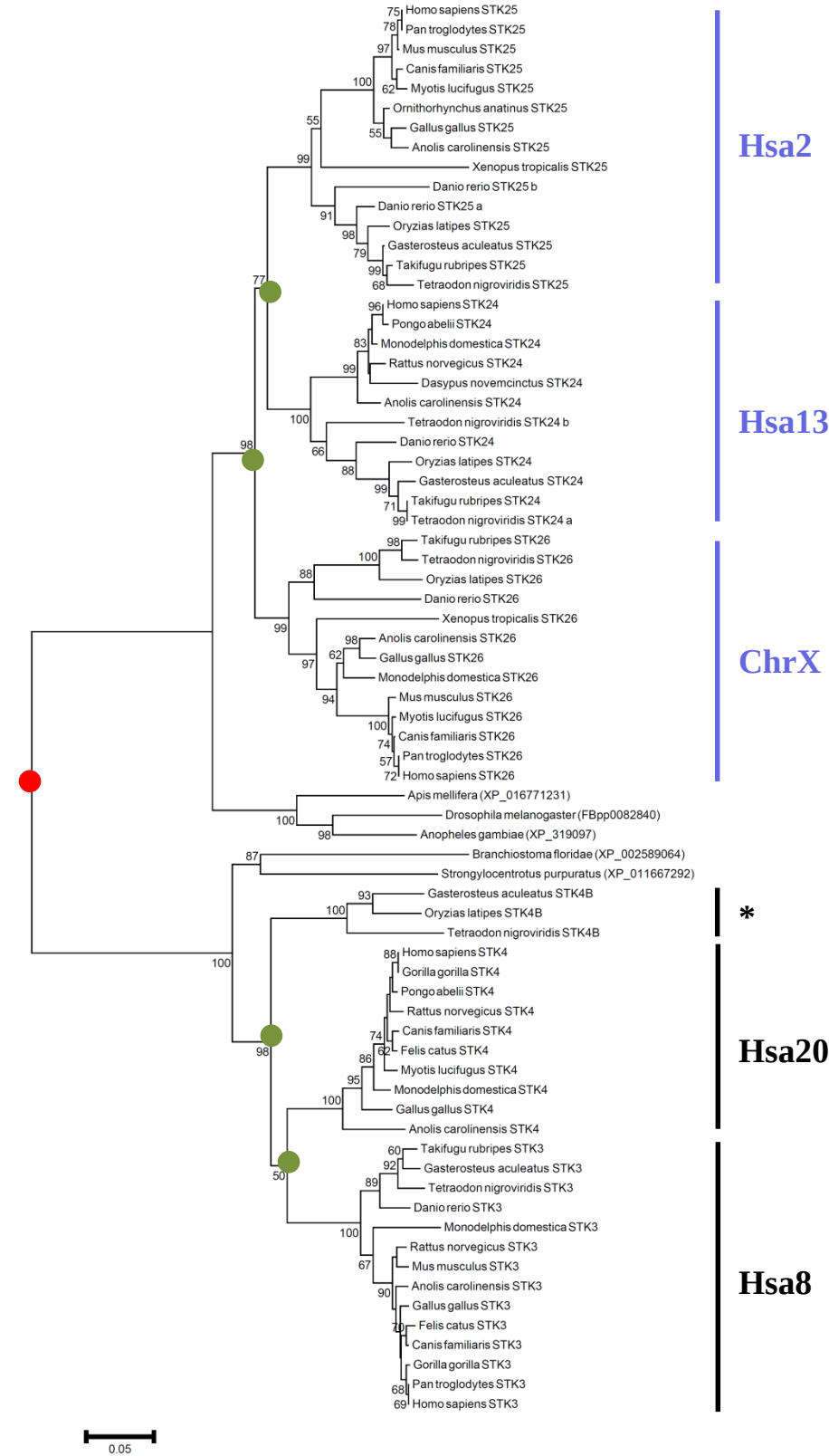
Neighbor-Joining tree of the SNX family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution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



Phylogenetic tree of STMN family.

Neighbor-Joining tree of the STMN 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.

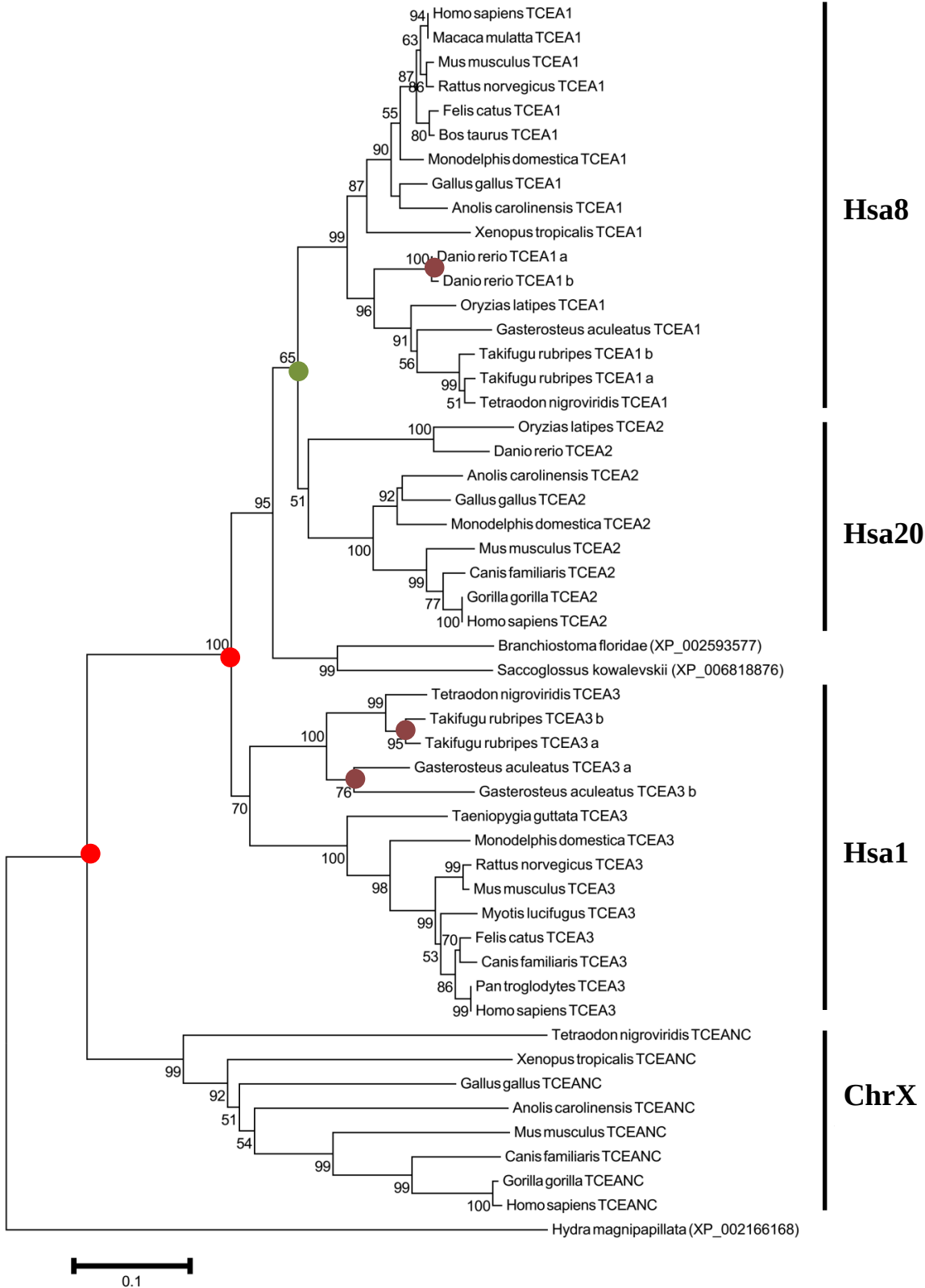
Serine/Threonine-Protein Kinase-*STK*



Phylogenetic tree of STK family.

Neighbor-Joining tree of the STK 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.

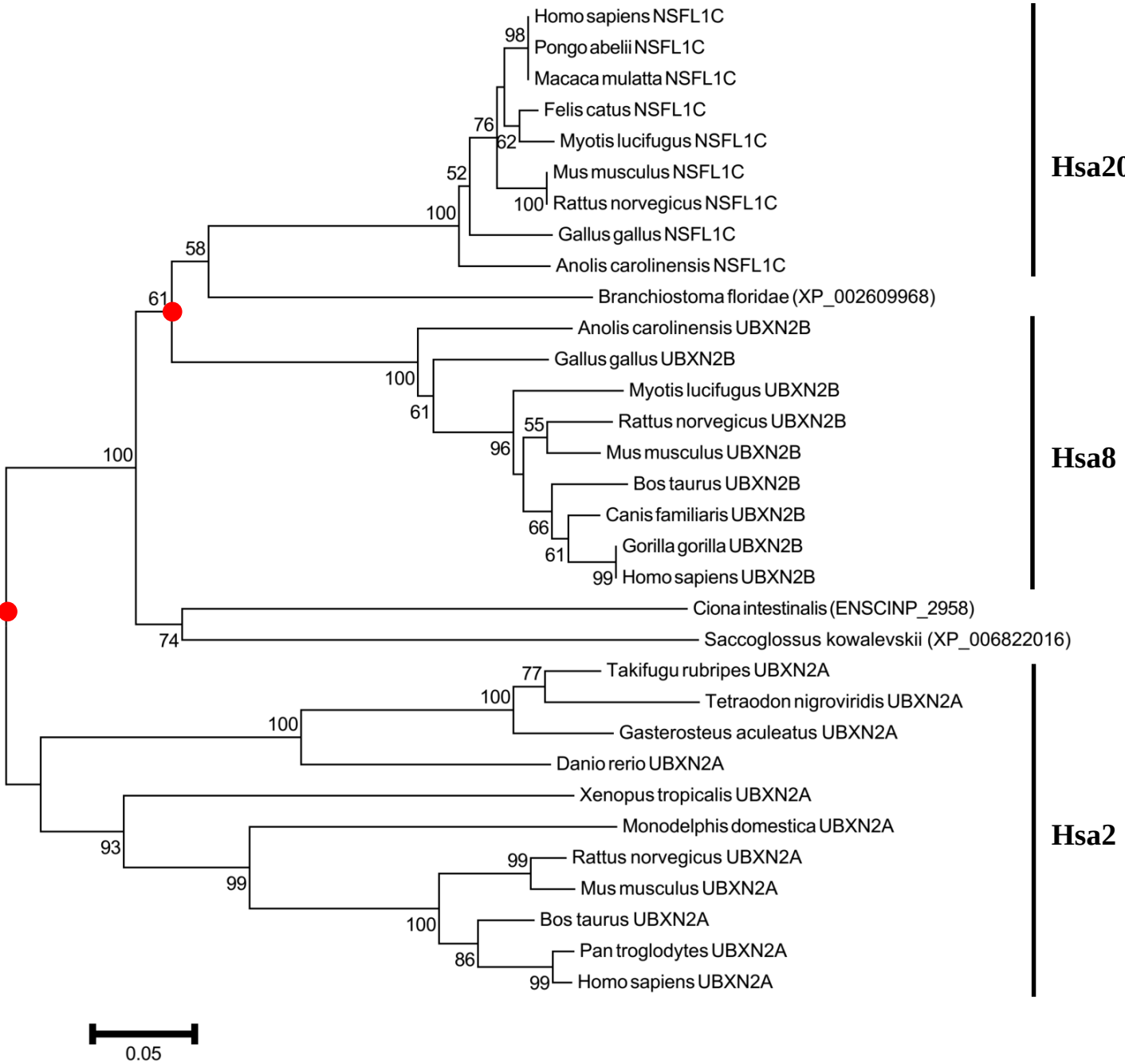
Transcription Elongation factor A (SII) Protein-TCEA



Phylogenetic tree of TCEA family.

Neighbor-Joining tree of the TCEA 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.

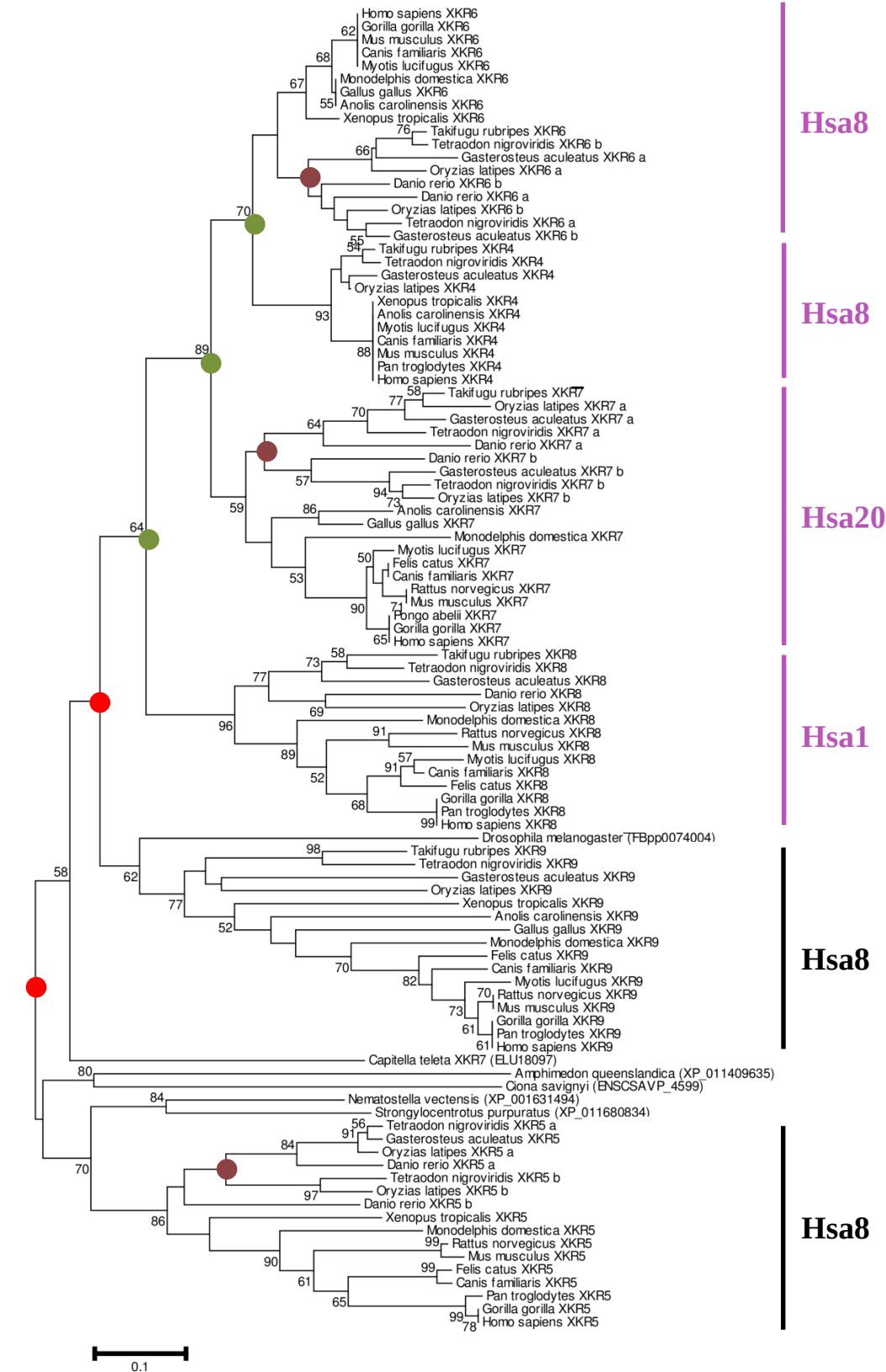
UBX Domain-Containing Protein-UBXN



Phylogenetic tree of UBXN family.

Neighbor-Joining tree of the UBXN 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.

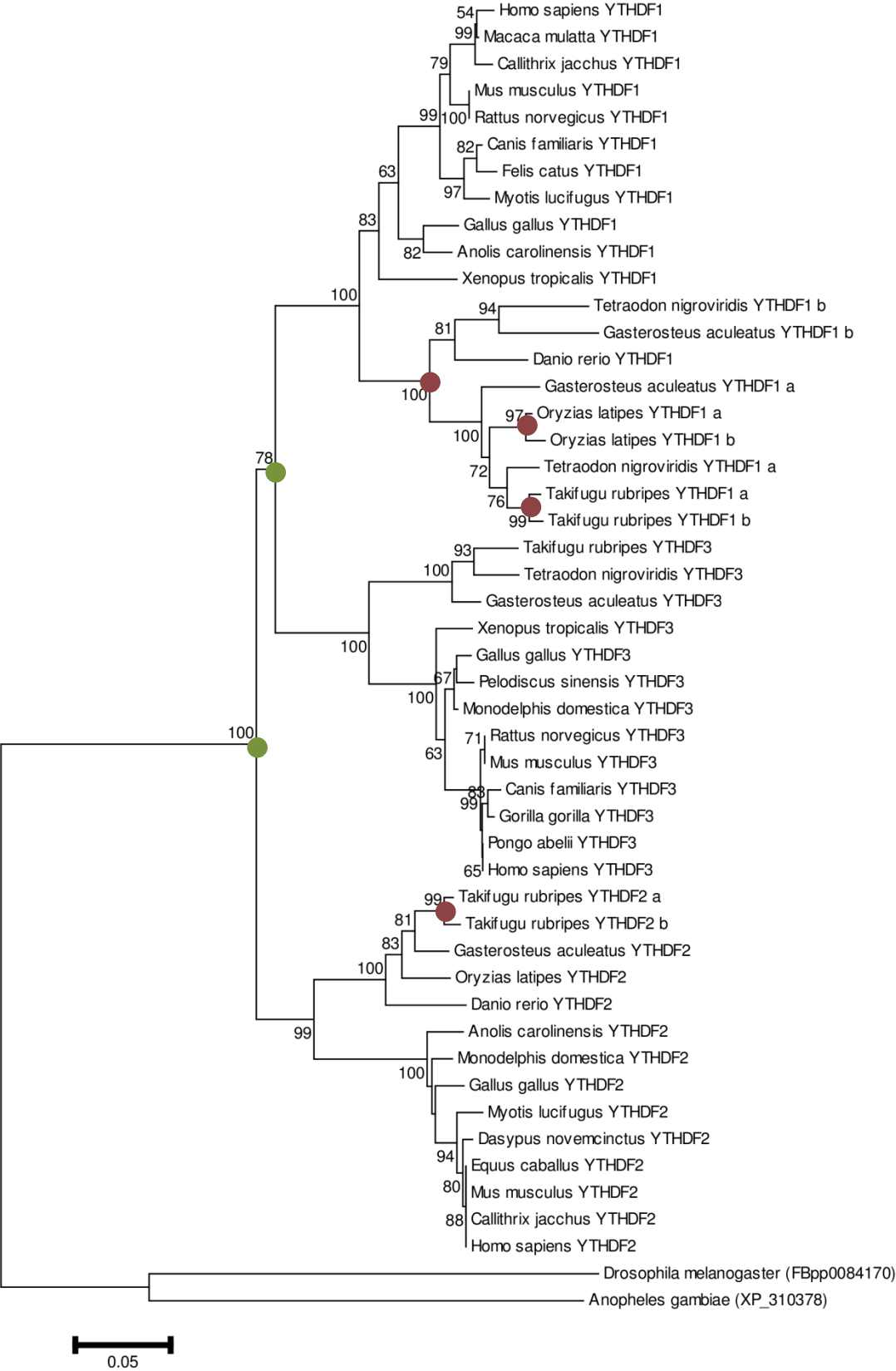
X Kell Blood Group Precursor-related Family-XKR



Phylogenetic tree of XKR family.

Neighbor-Joining tree of the XKR 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.

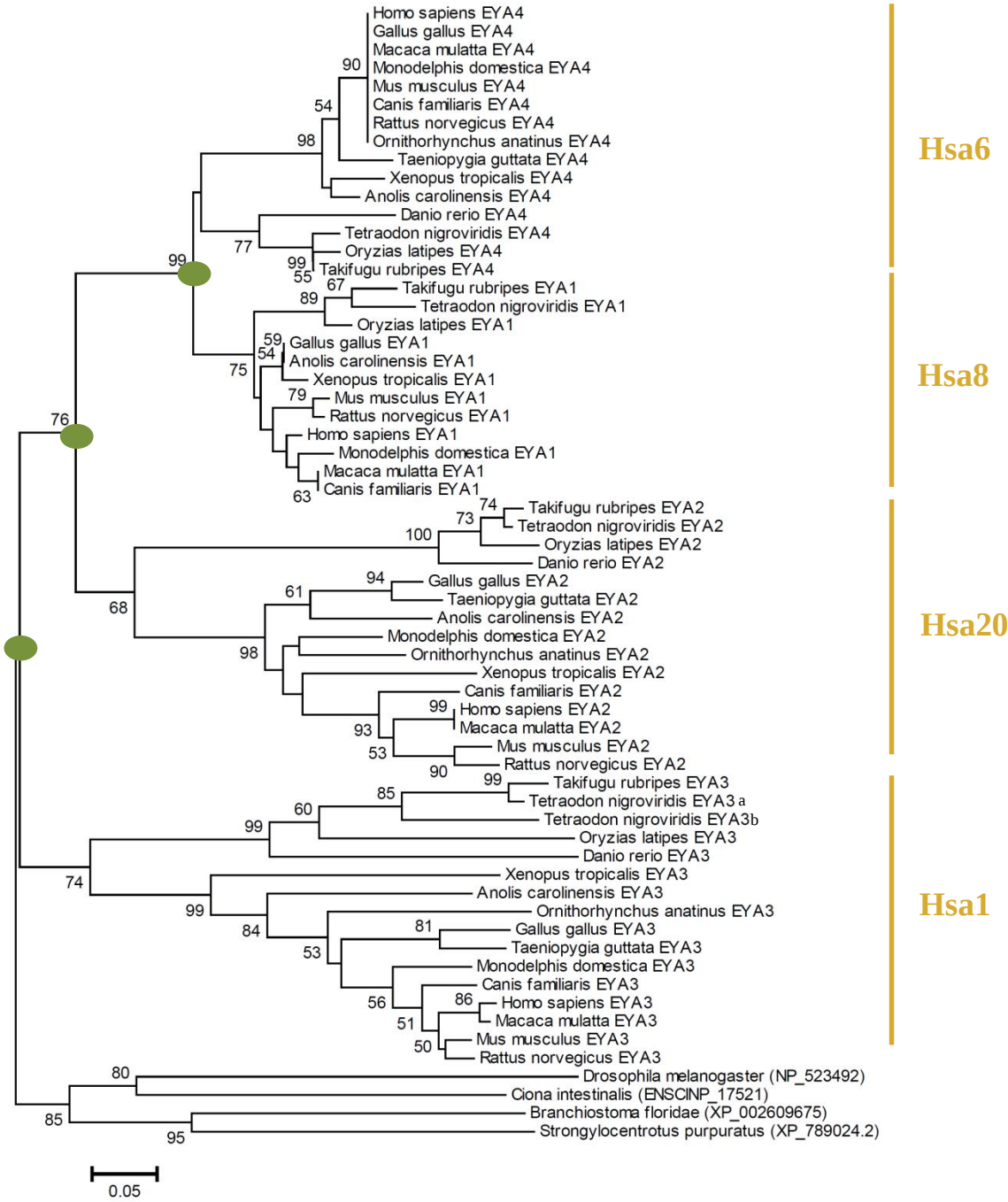
YTH Domain-Containing Family Protein-YTHDF



Phylogenetic tree of YTHDF family.

Neighbor-Joining tree of the YTHDF 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.

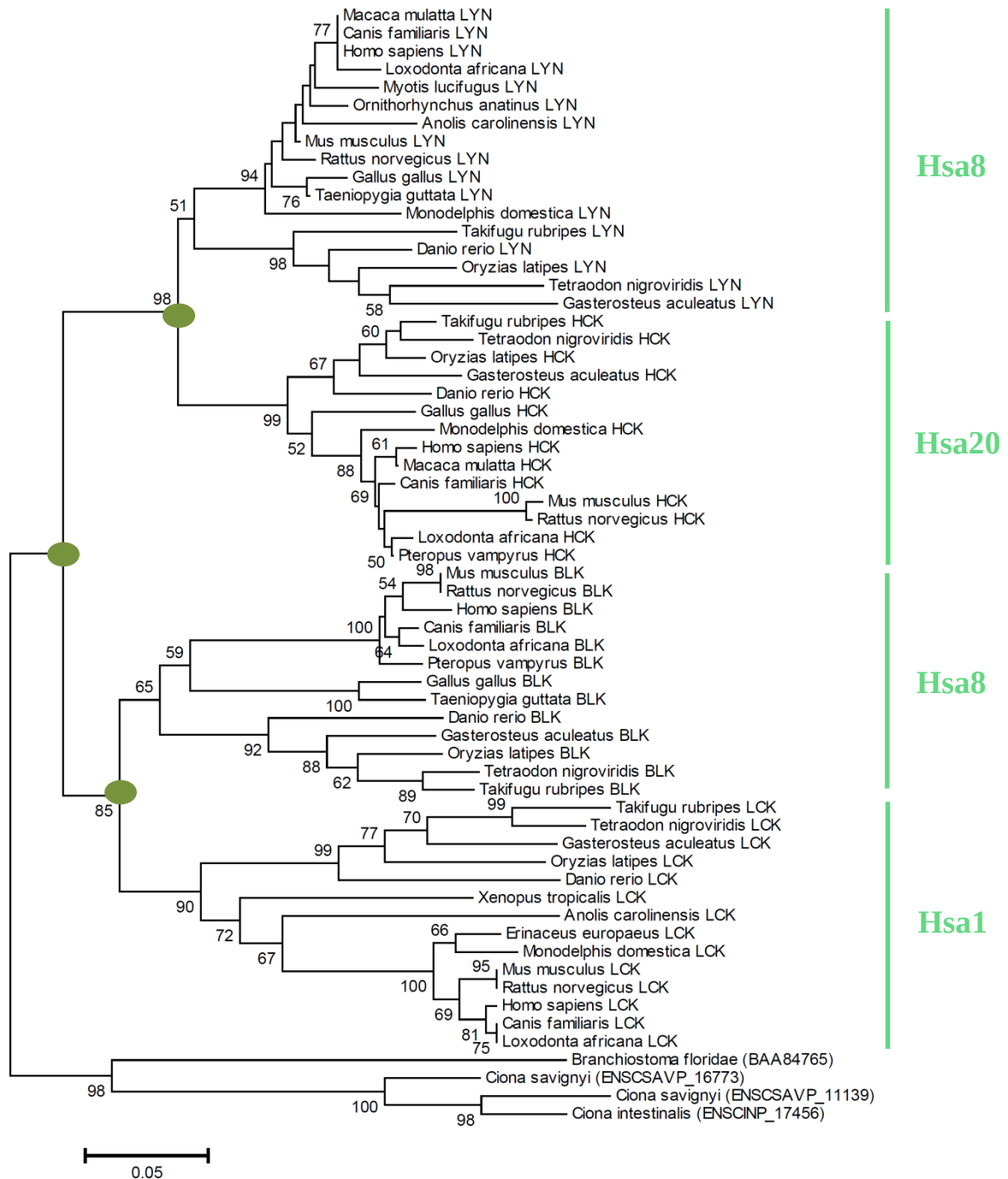
Eyes absent (EYA) family -EYA



Phylogenetic tree of EYA family.

Neighbor-Joining tree of the EYA 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.

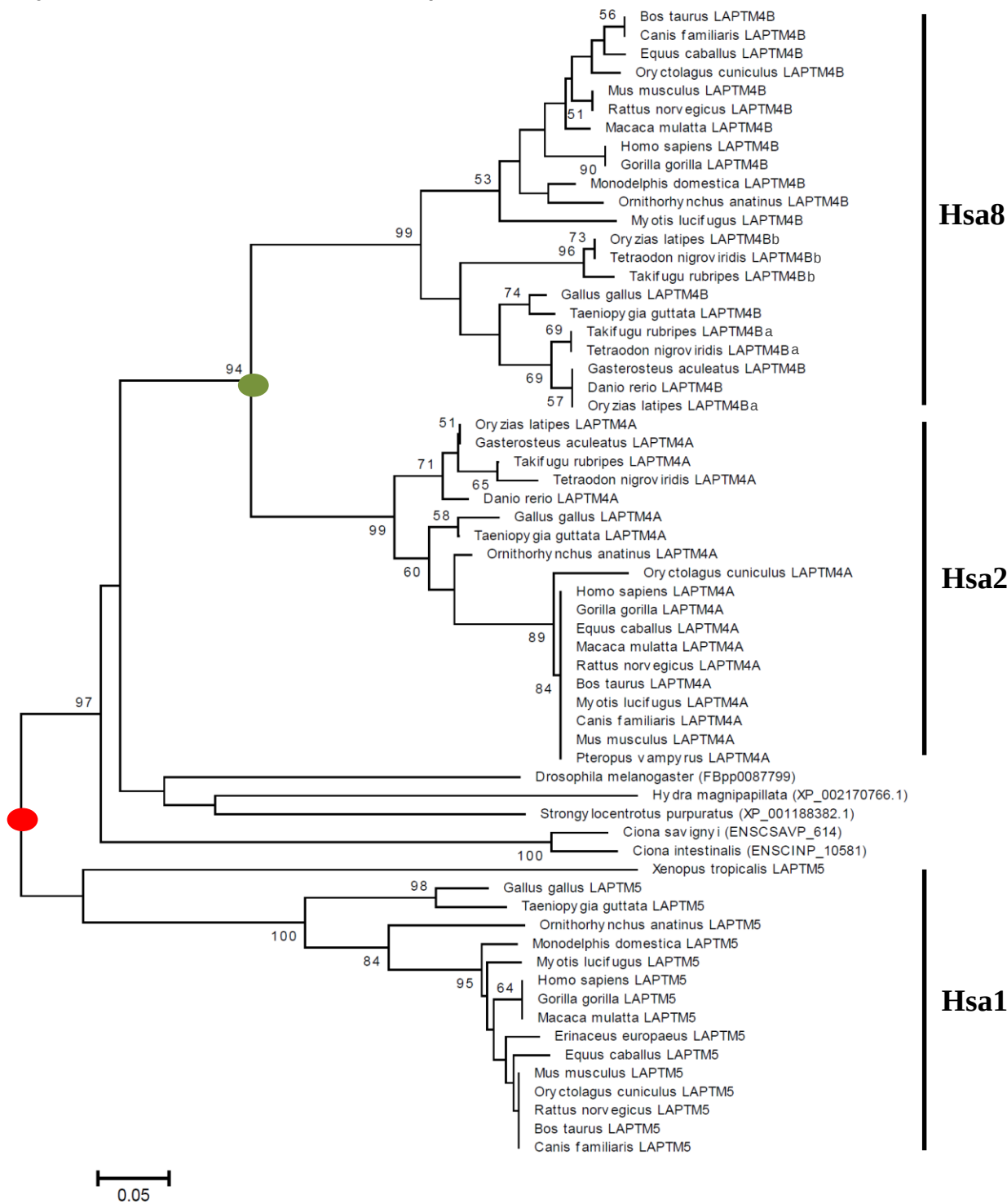
HCK-related tyrosine kinases family - HCK Kinases



Phylogenetic tree of HCK-kinases family.

Neighbor-Joining tree of the HCK Kinases 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.

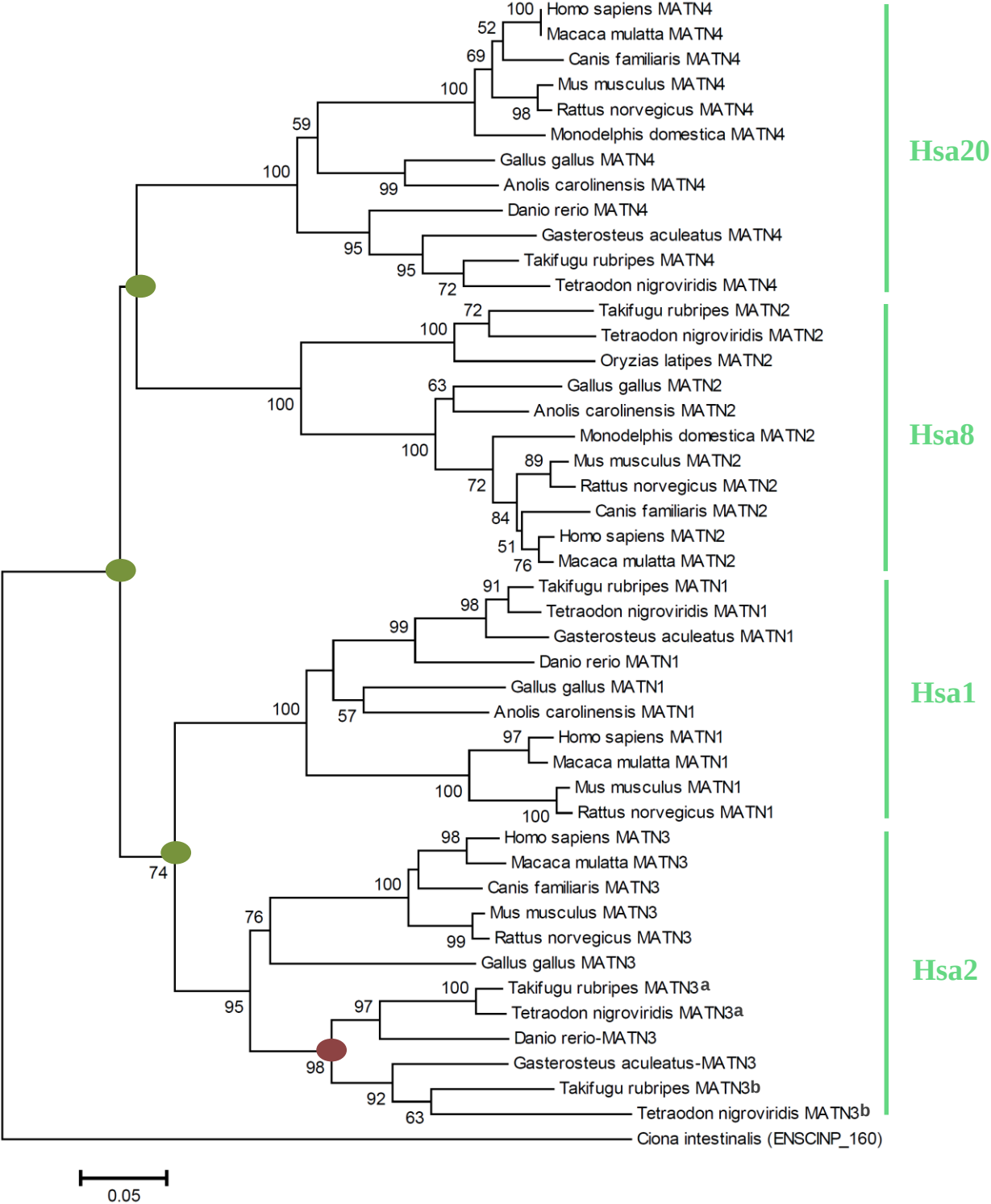
Lysosomal associated transmembrane protein-LPTM



Phylogenetic tree of LPTM family.

Neighbor-Joining tree of the LPTM 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.

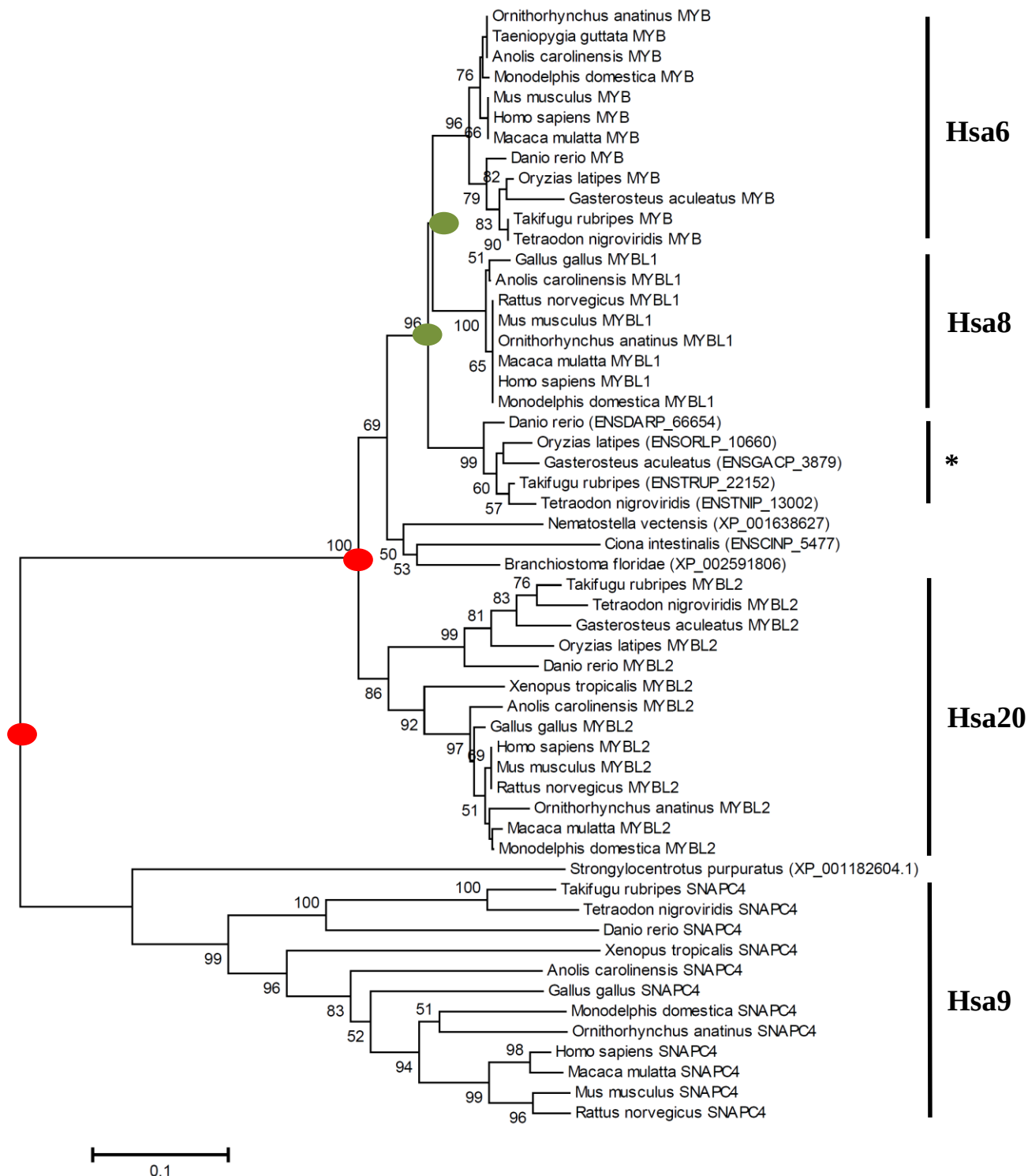
Matrilin-cartilage matrix protein precursor-MATN



Phylogenetic tree of MATN family.

Neighbor-Joining tree of the MATN 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.

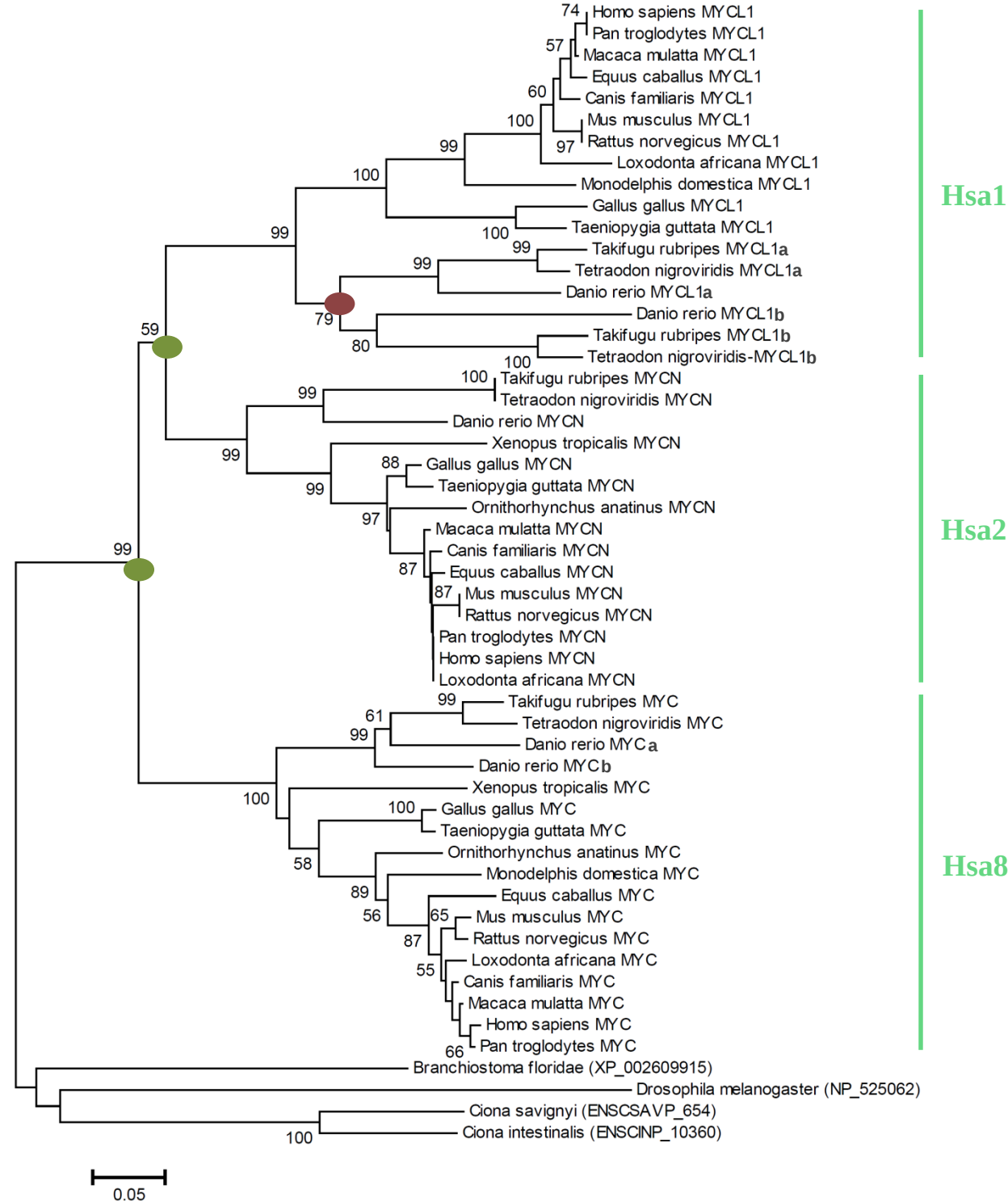
MYB family of transcription factor genes-MYB



Phylogenetic tree of MYB family.

Neighbor-Joining tree of the MYB 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.

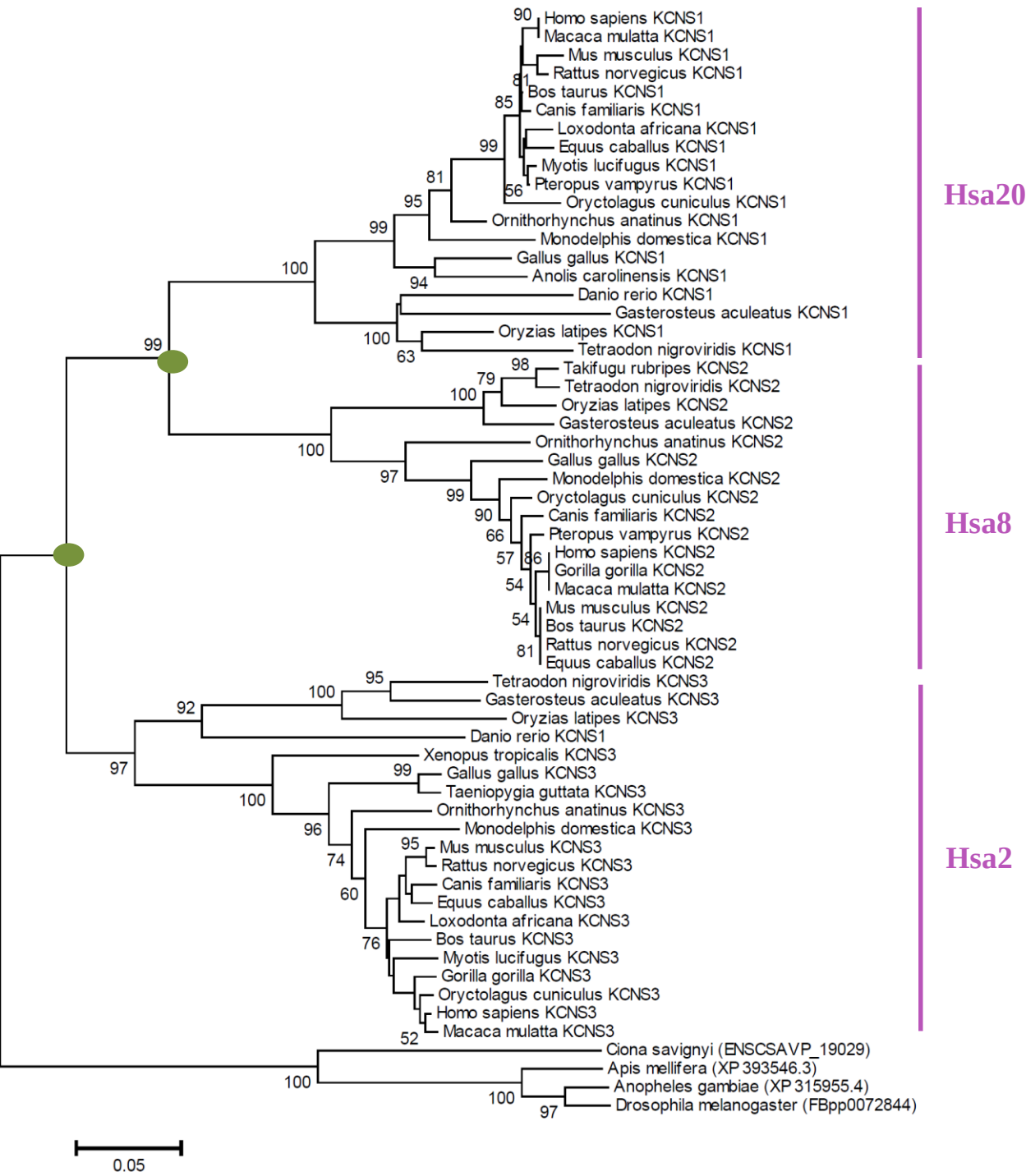
Myc proto-oncogene protein -MYC



Phylogenetic tree of MYC family.

Neighbor-Joining tree of the MYC 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.

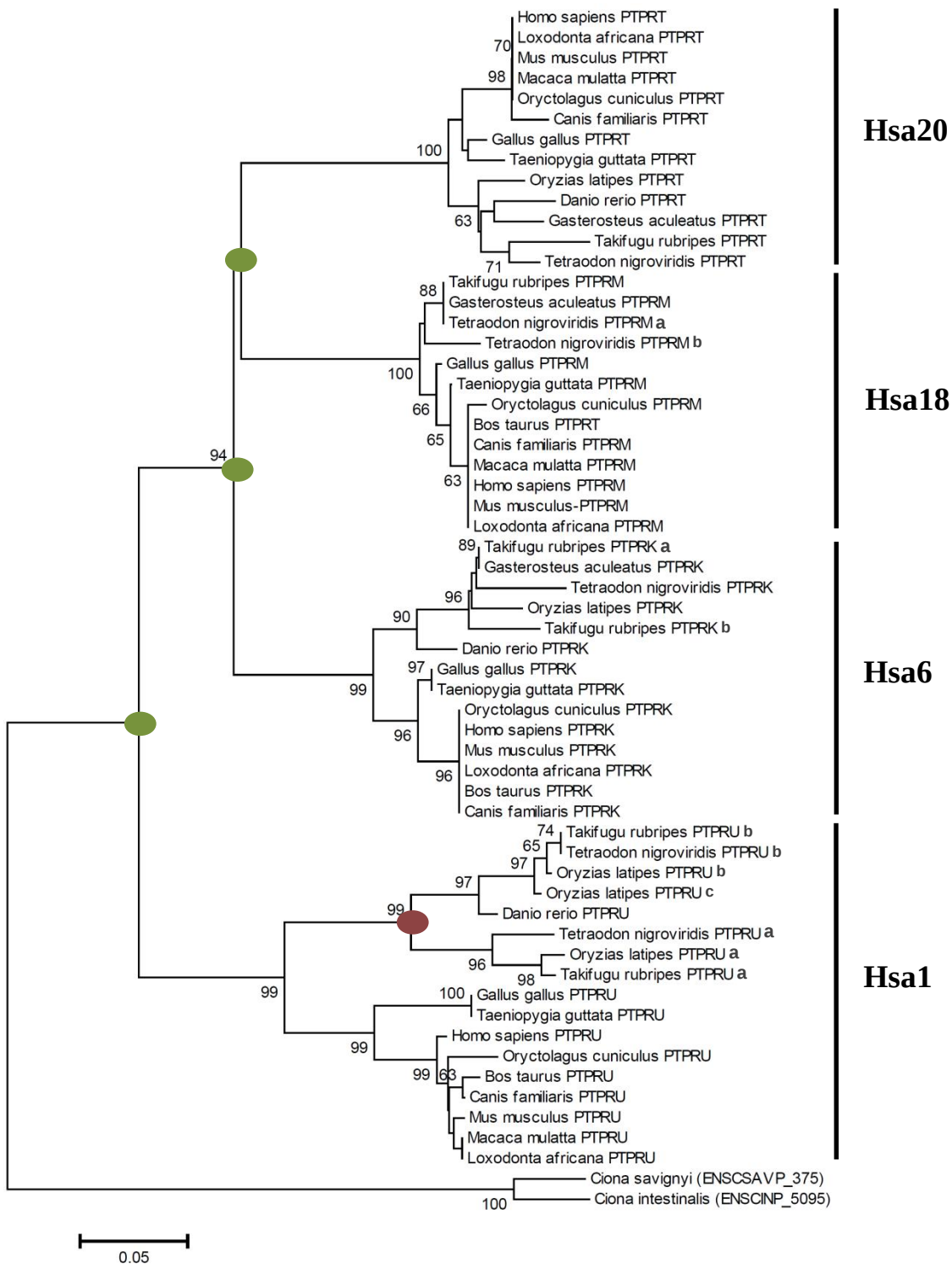
Potassium voltage-gated channel delayed-rectifier, subfamily S - KCNS



Phylogenetic tree of KCNS family.

Neighbor-Joining tree of the KCNS 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.

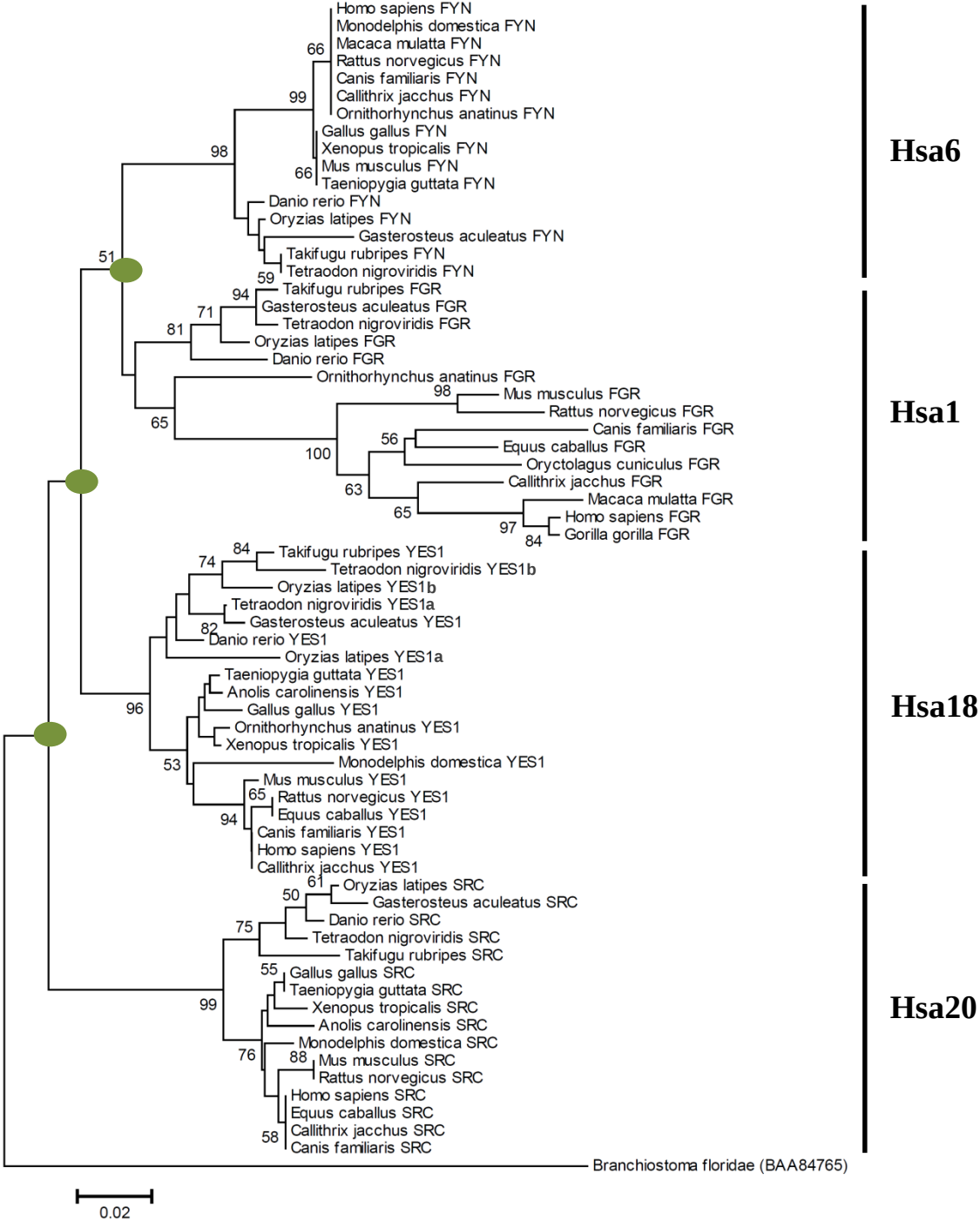
Protein tyrosine phosphatase, receptor-PTPR



Phylogenetic tree of PTPR family.

Neighbor-Joining tree of the PTPR 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.

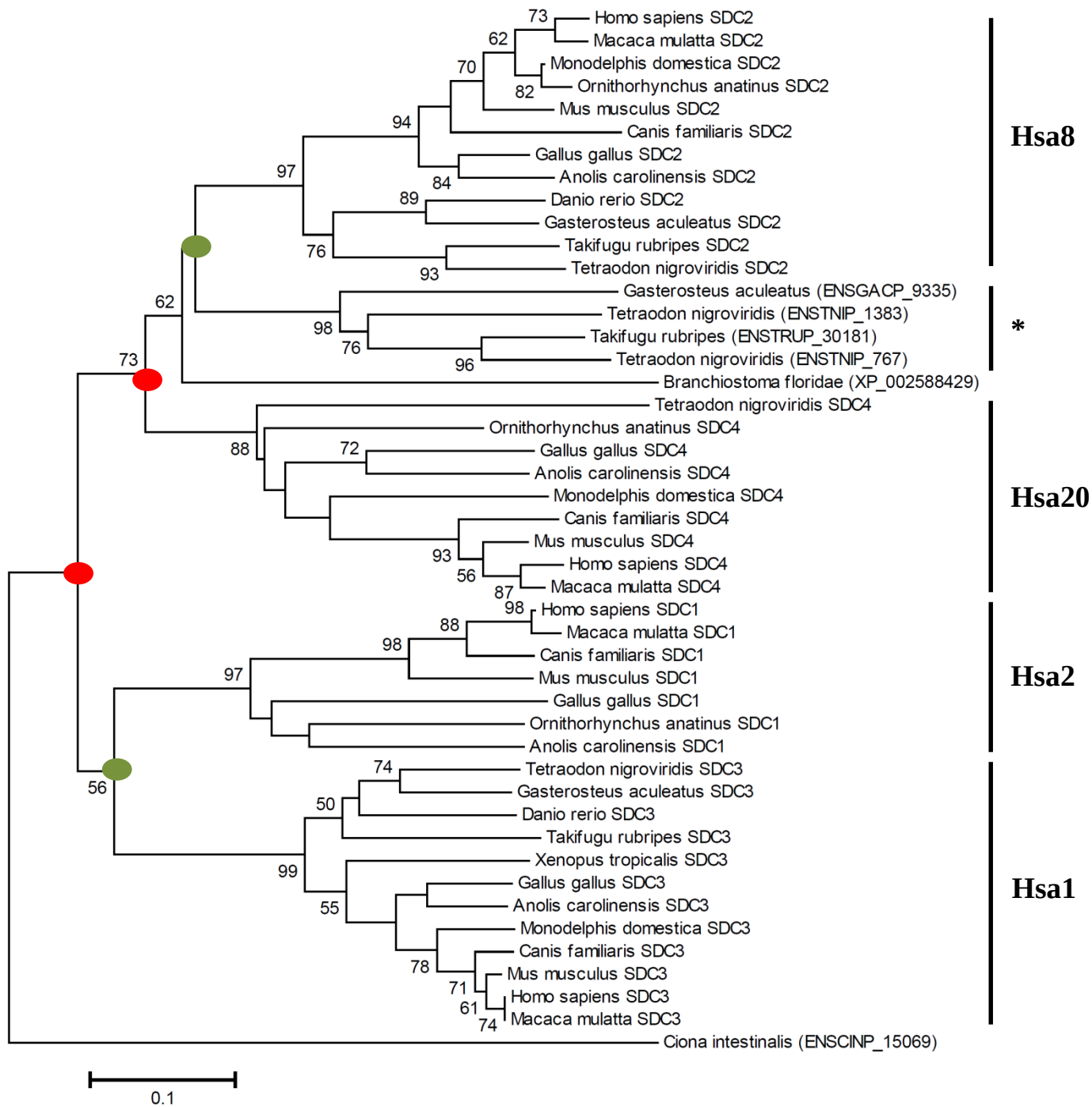
SRC-related tyrosine kinase family-SRC kinases



Phylogenetic tree of SRC kinases family.

Neighbor-Joining tree of the SRC Kinases 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.

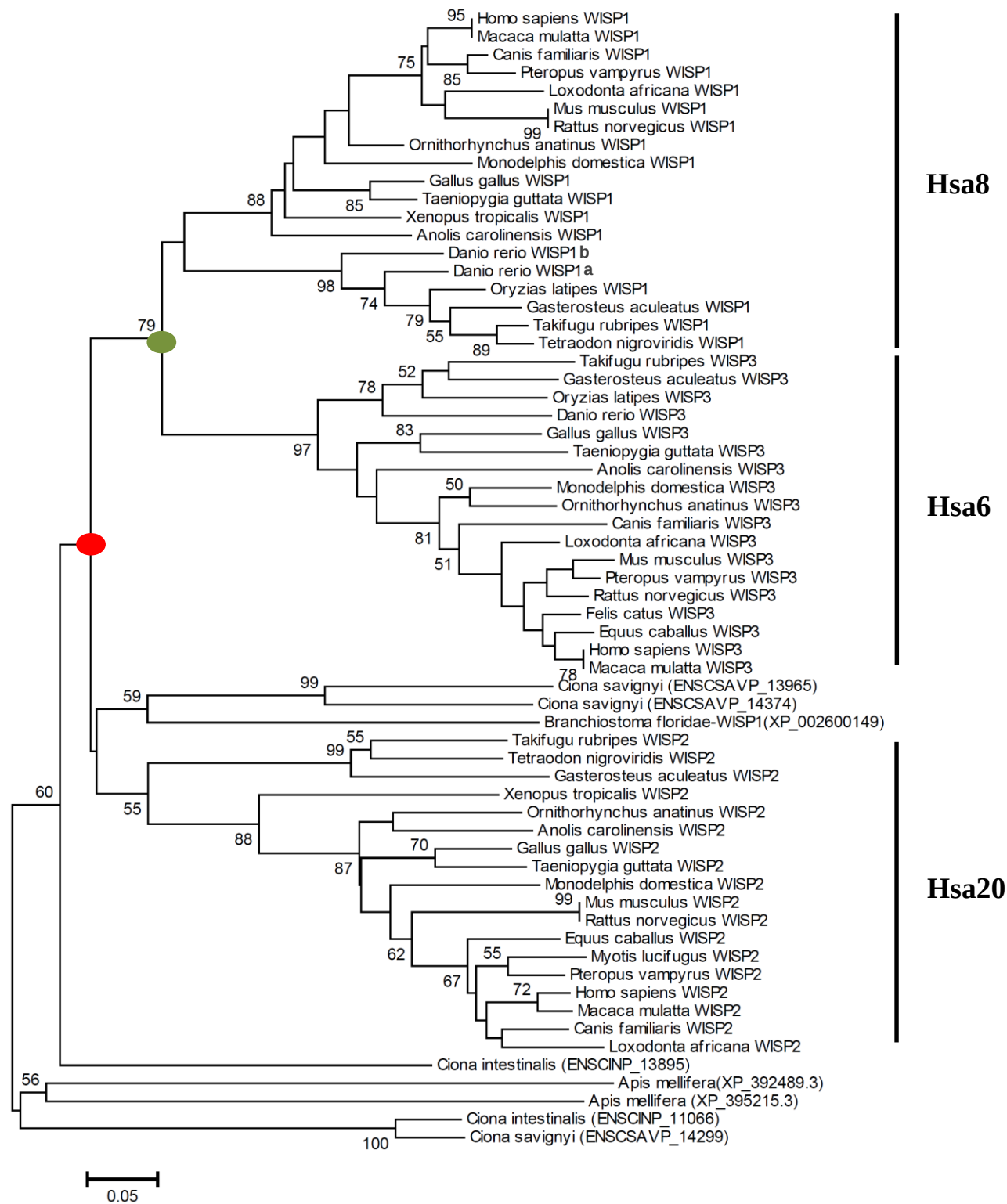
Syndecan proteoglycan family–SDC



Phylogenetic tree of SDC family.

Neighbor-Joining tree of the SDC 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 missing in tetrapods.

WNT1 inducible signaling pathway (WISP) protein-WISP



Phylogenetic tree of WISP family.

Neighbor-Joining tree of the WISP 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.