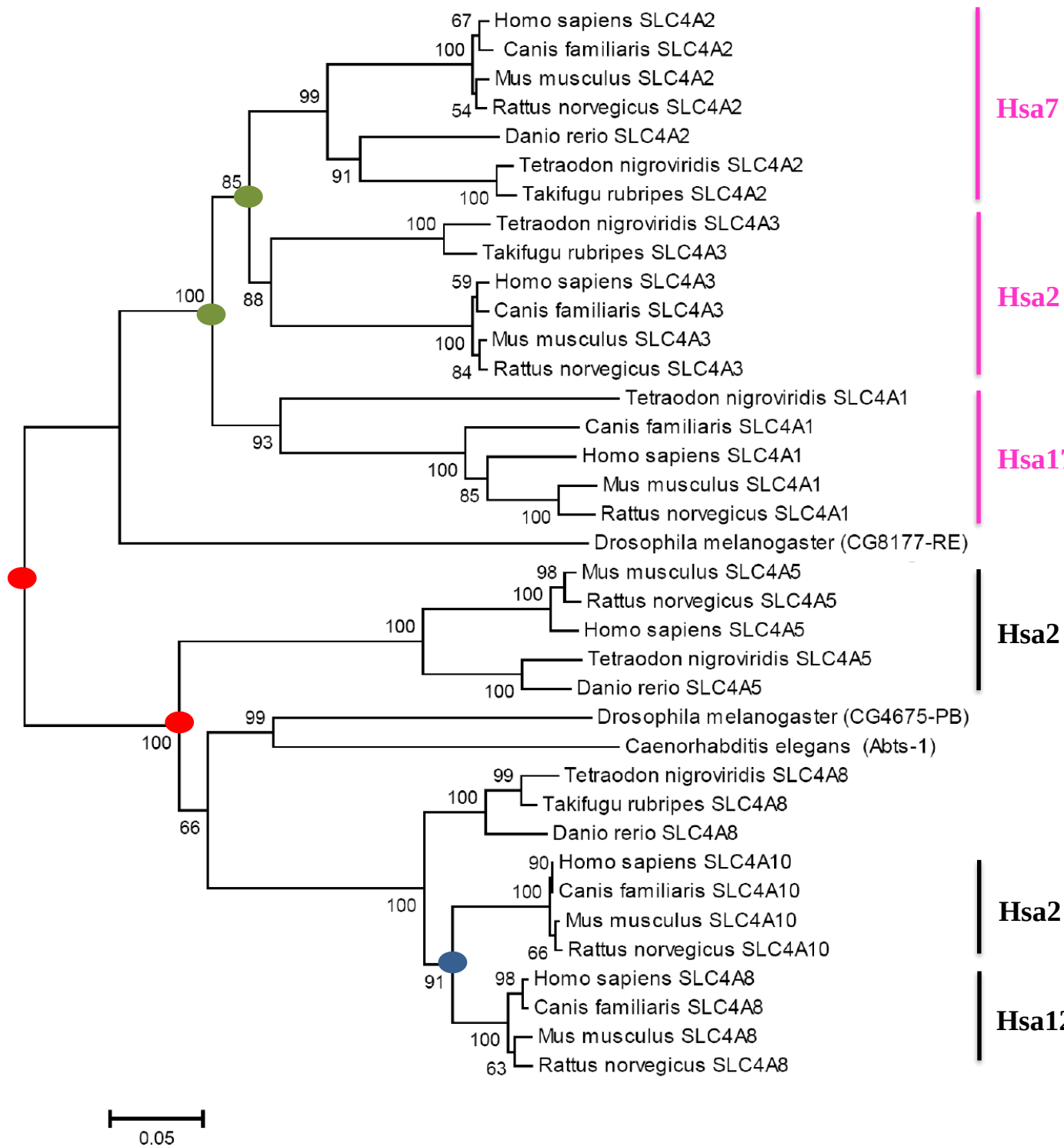


**Neighbor Joining Trees of gene families residing on
chromosomes 2, 7, 12 and 17.**

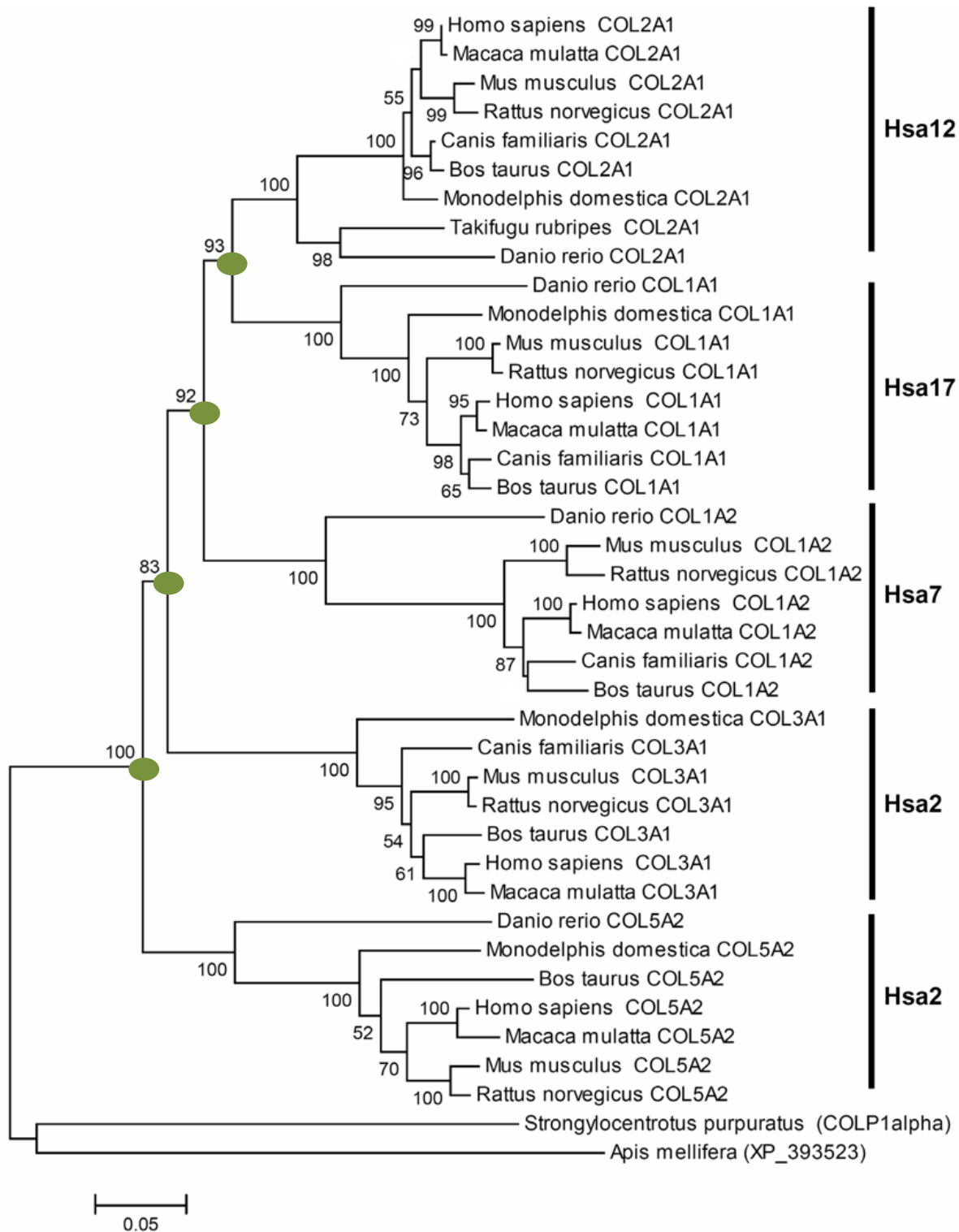
Anion exchanger family SLC4A (AE)-SLC4A



Phylogenetic tree of SLC4A family.

Neighbor-Joining tree of the SLC4A 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.

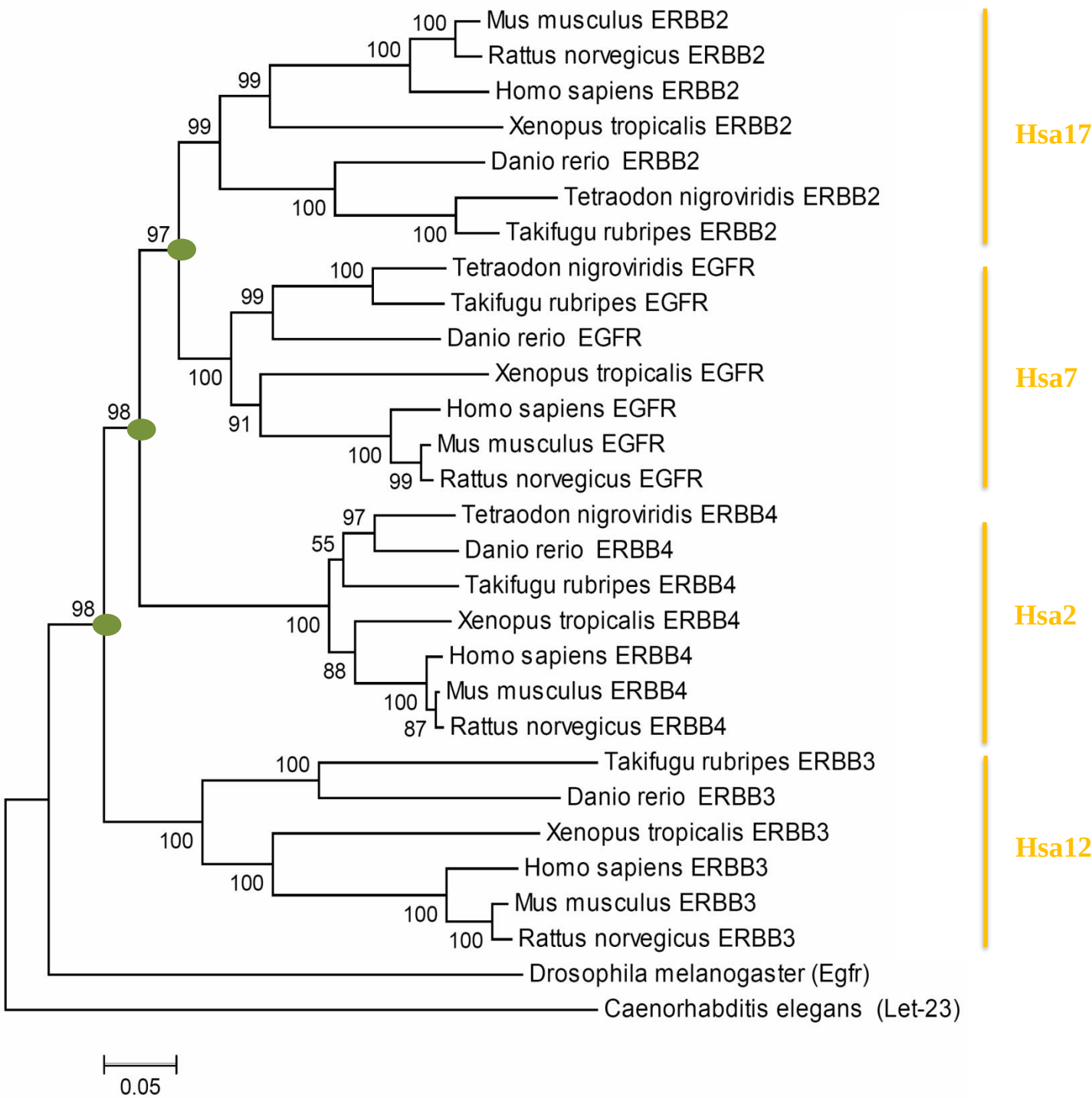
Fibrillar collagen family –COL



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.

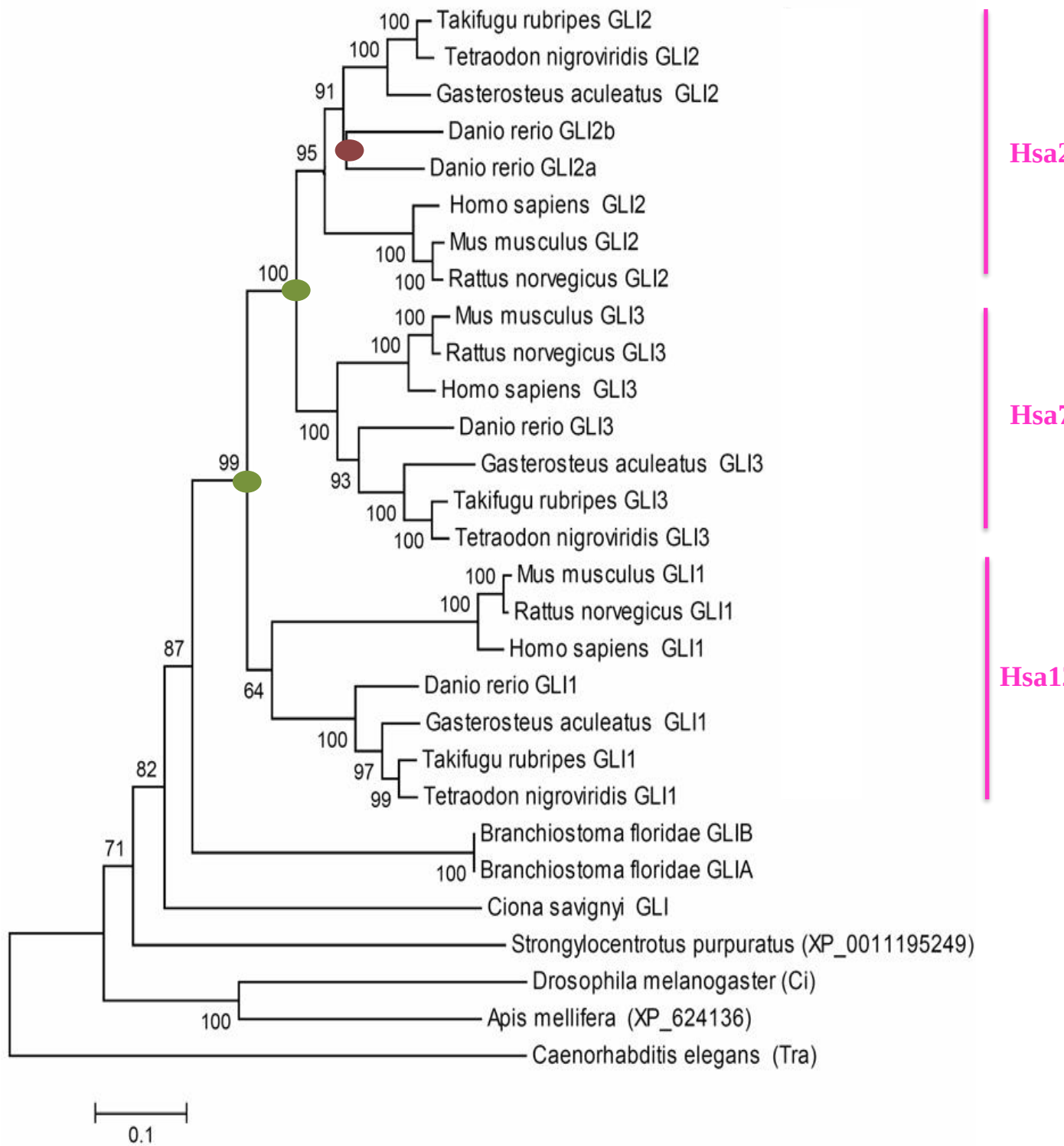
ERBB receptor protein-tyrosine kinase-ERBB



Phylogenetic tree of ERBB family.

Neighbor-Joining tree of the ERBB 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.

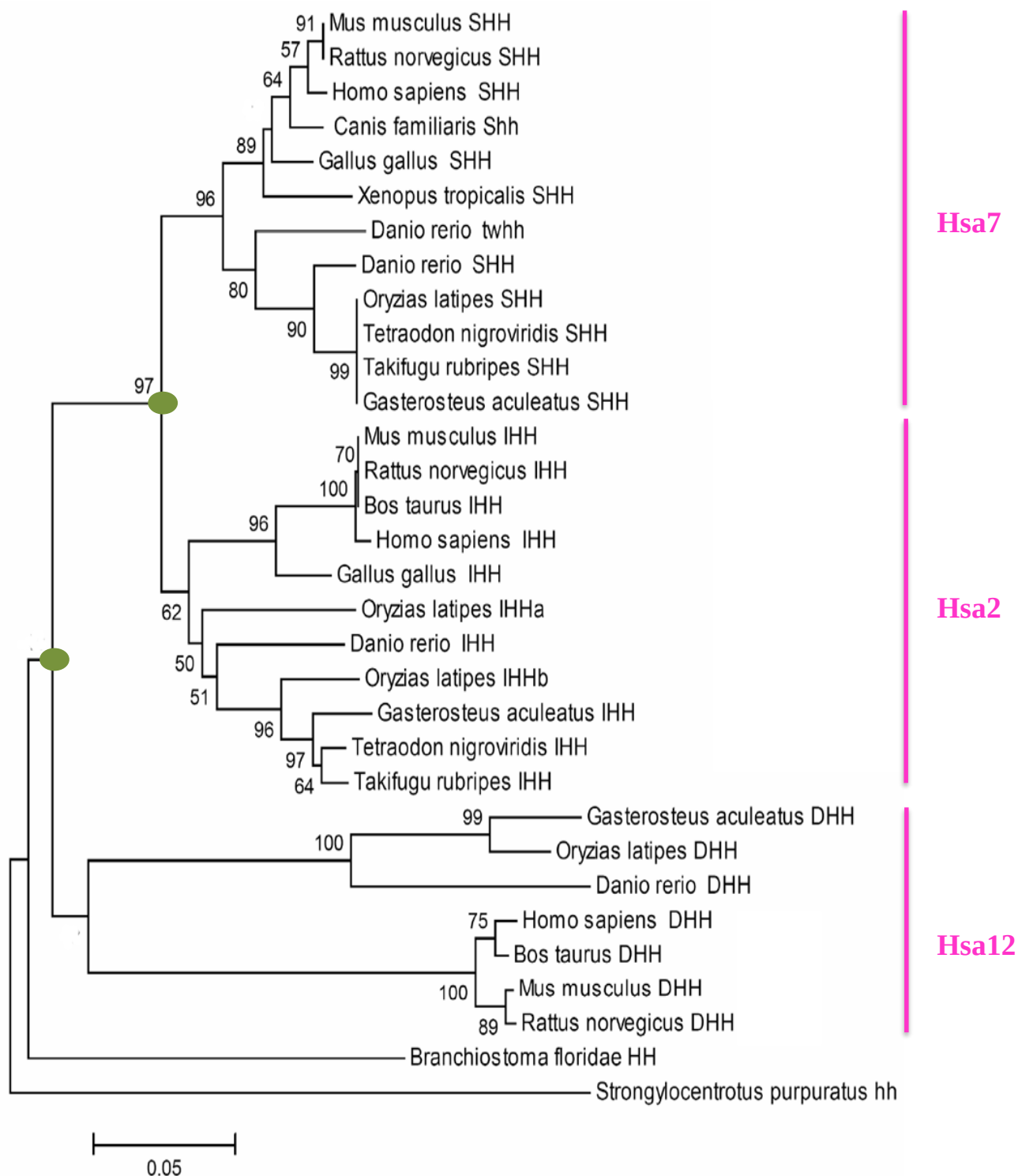
GLI zinc-finger protein family-GLI



Phylogenetic tree of GLI family.

Neighbor-Joining tree of the GLI 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.

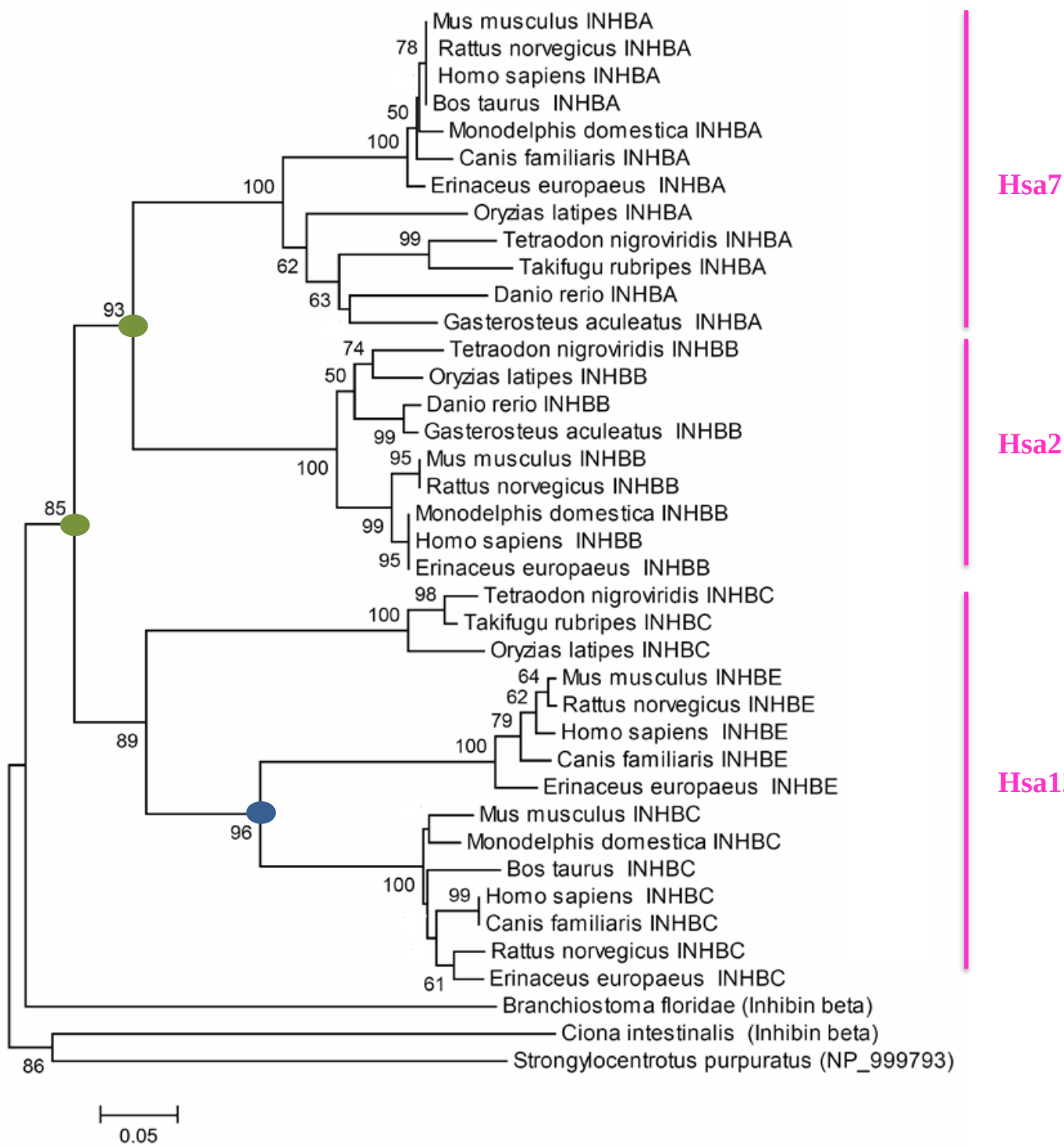
Hedgehog family -HH



Phylogenetic tree of HH family.

Neighbor-Joining tree of the HH 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.

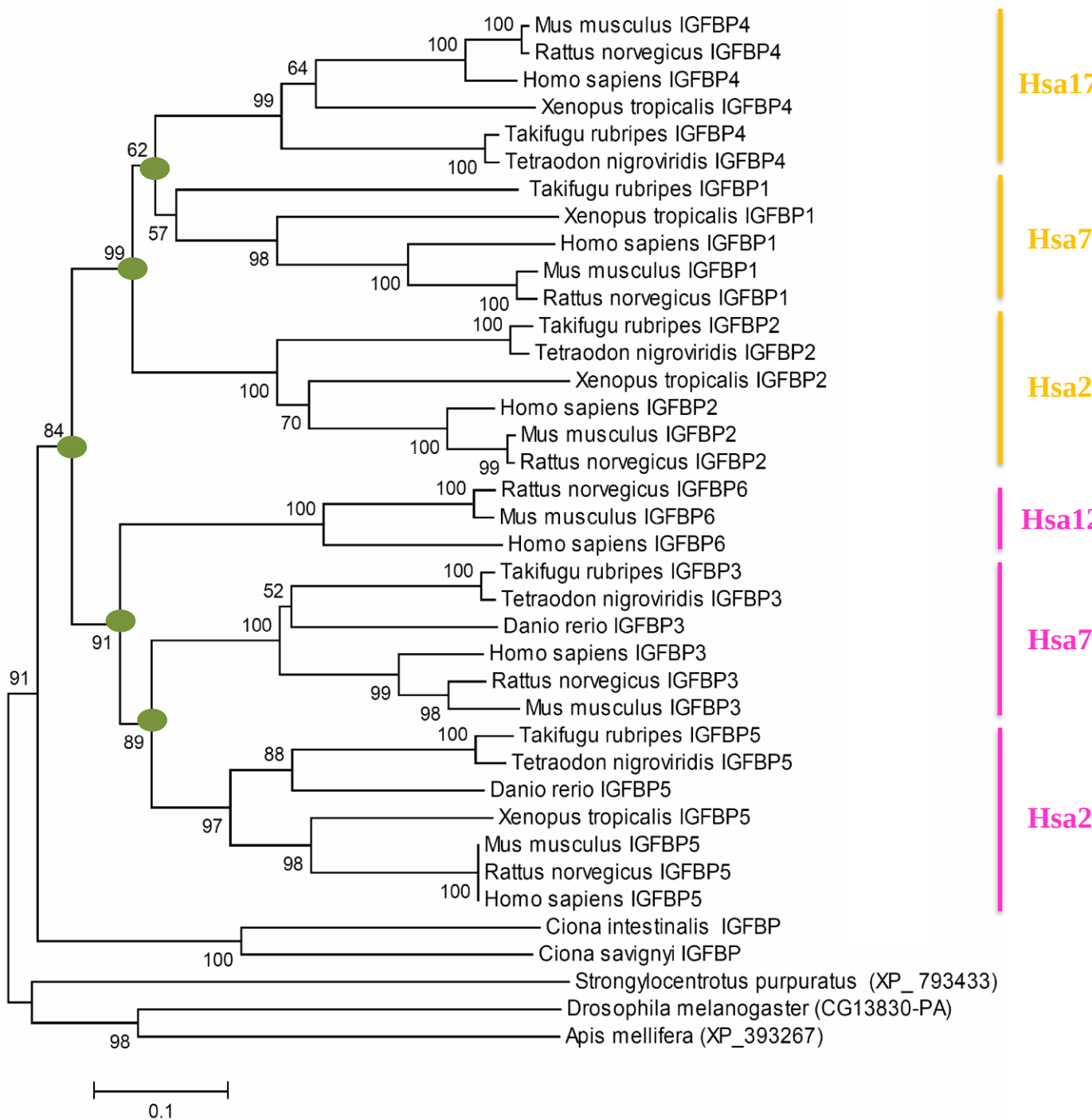
Inhibin -INHBA



Phylogenetic tree of INHB family.

Neighbor-Joining tree of the INHB 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.

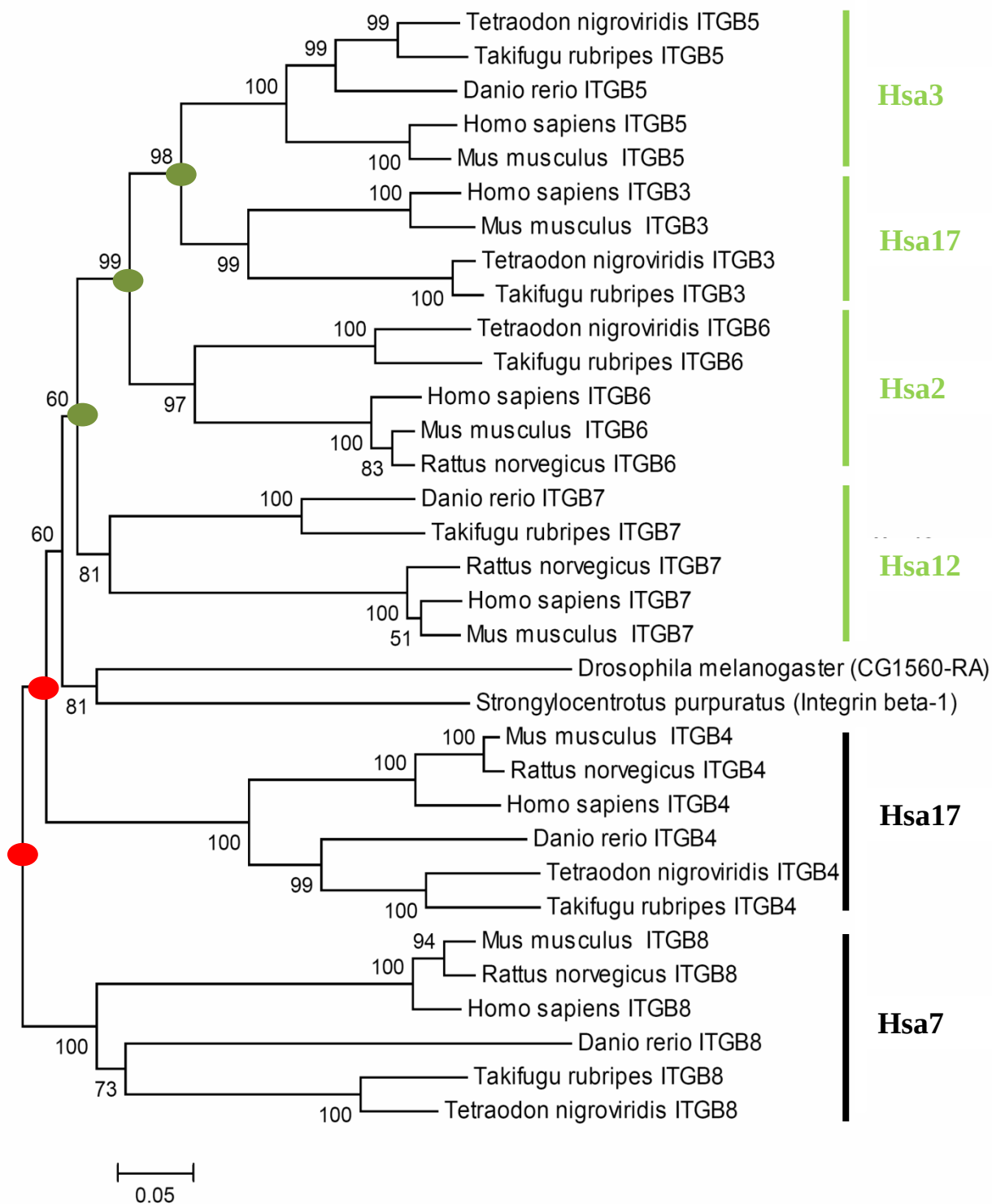
Insulin-like growth factor-binding protein-IGFBP



Phylogenetic tree of IGFBP family.

Neighbor-Joining tree of the IGFBP 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.

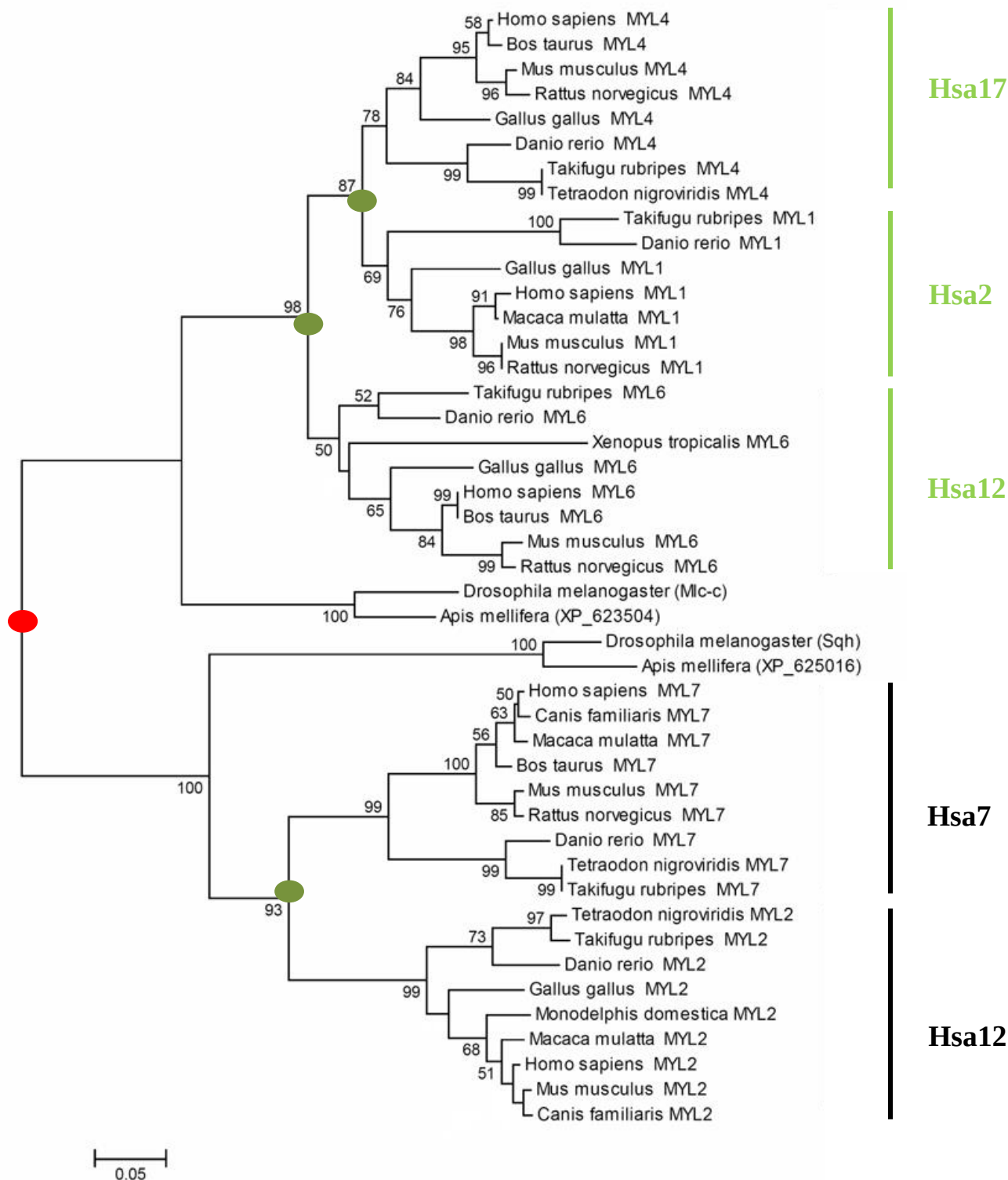
Integrin beta chain family-ITGB



Phylogenetic tree of ITGB family.

Neighbor-Joining tree of the ITGB 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.

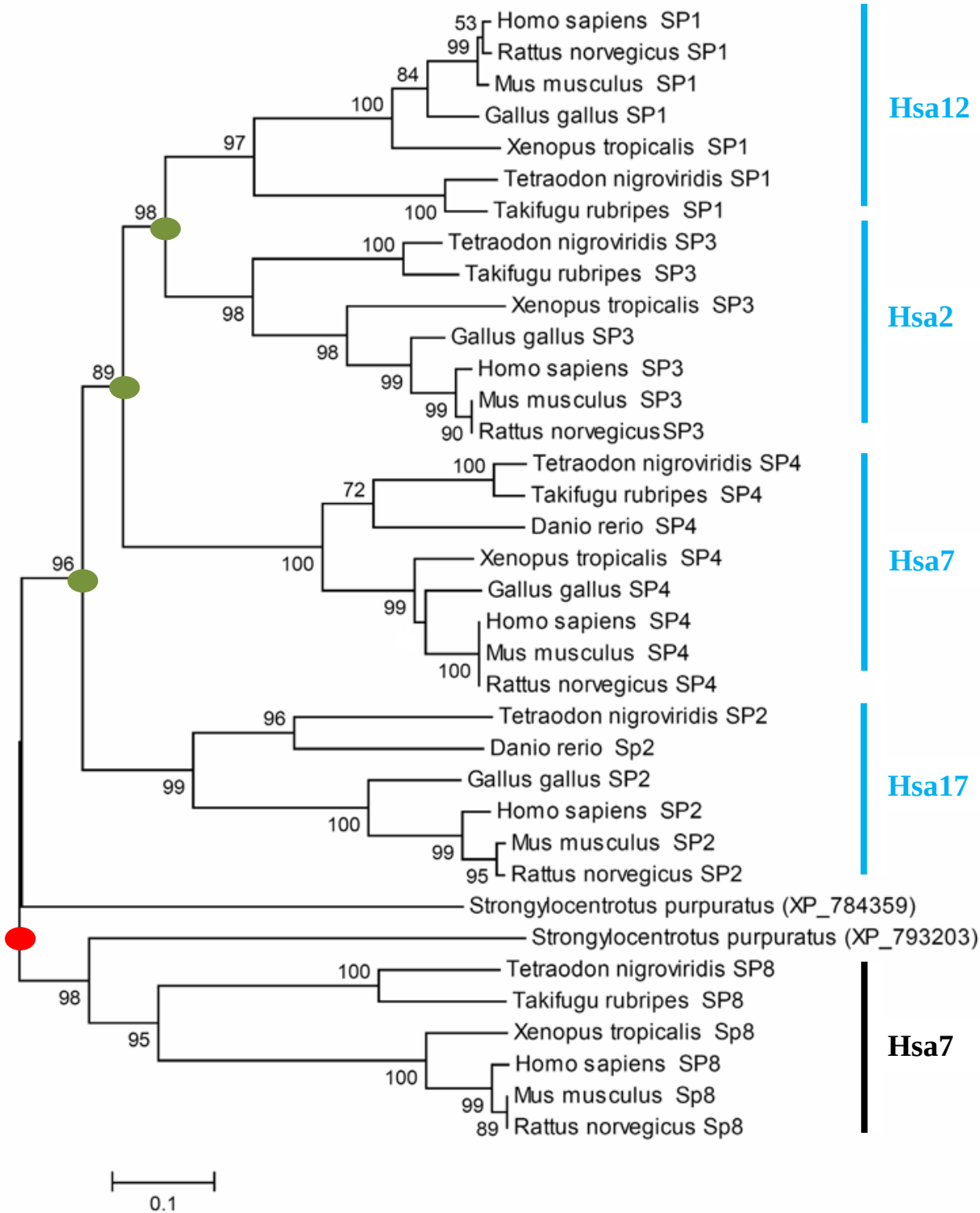
Myosin light chain-MYL



Phylogenetic tree of MYL family.

Neighbor-Joining tree of the MYL 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.

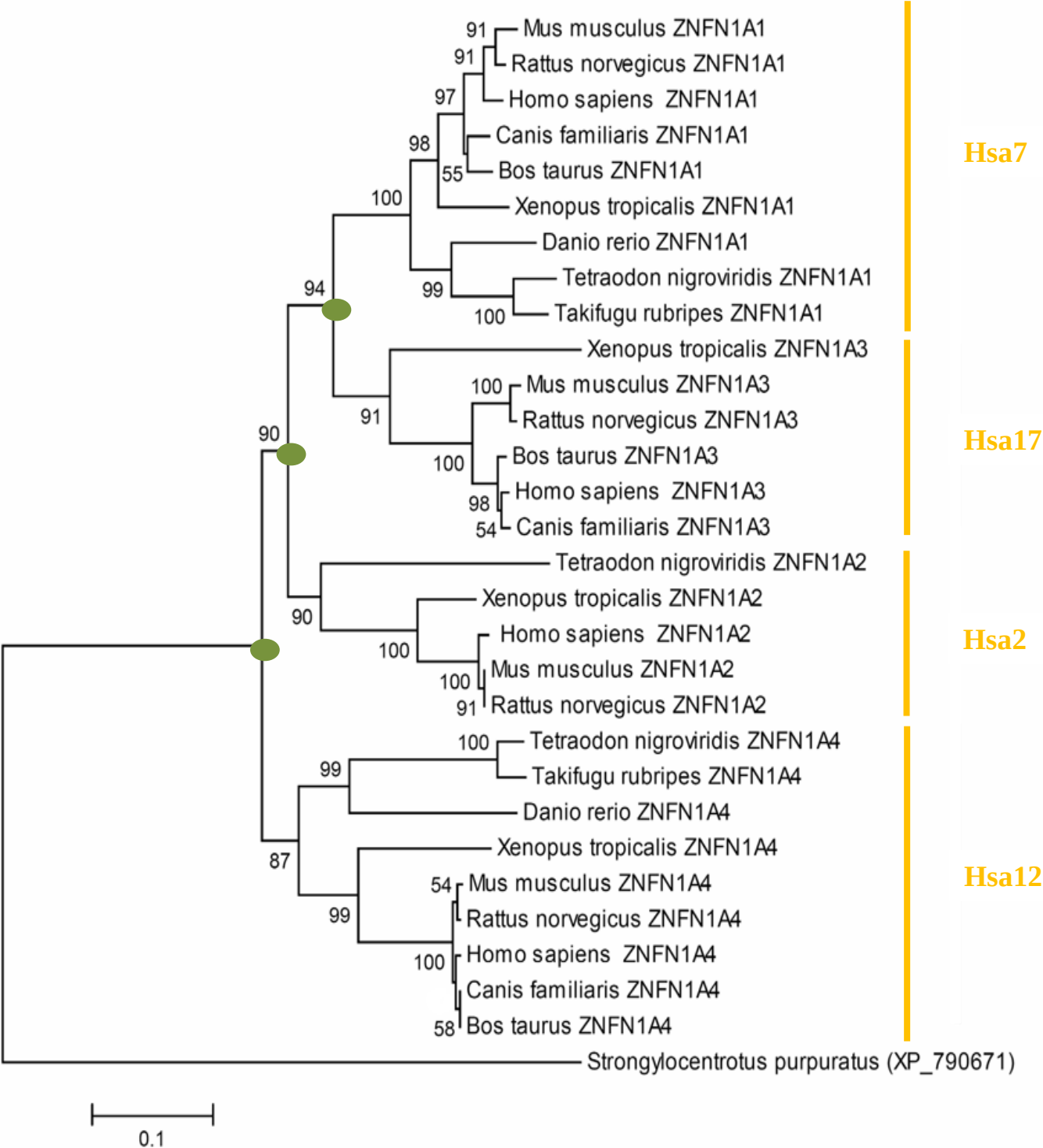
Sp1 c2h2-type zinc-finger protein family-SP



Phylogenetic tree of SP family.

Neighbor-Joining tree of the SP 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.

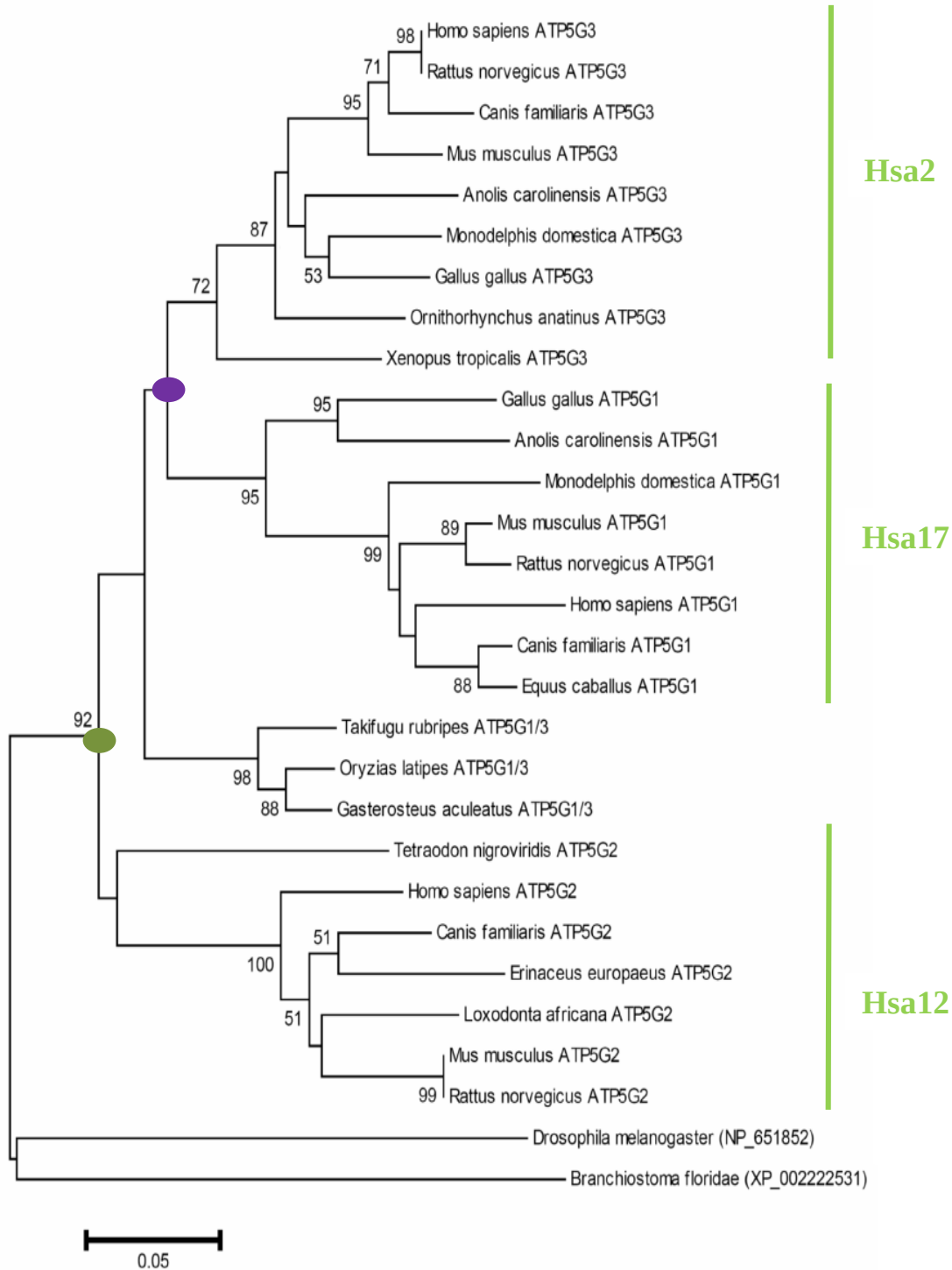
Zinc finger protein, subfamily 1A-ZNFN1A



Phylogenetic tree of ZNFN1A family.

Neighbor-Joining tree of the ZNFN1A 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.

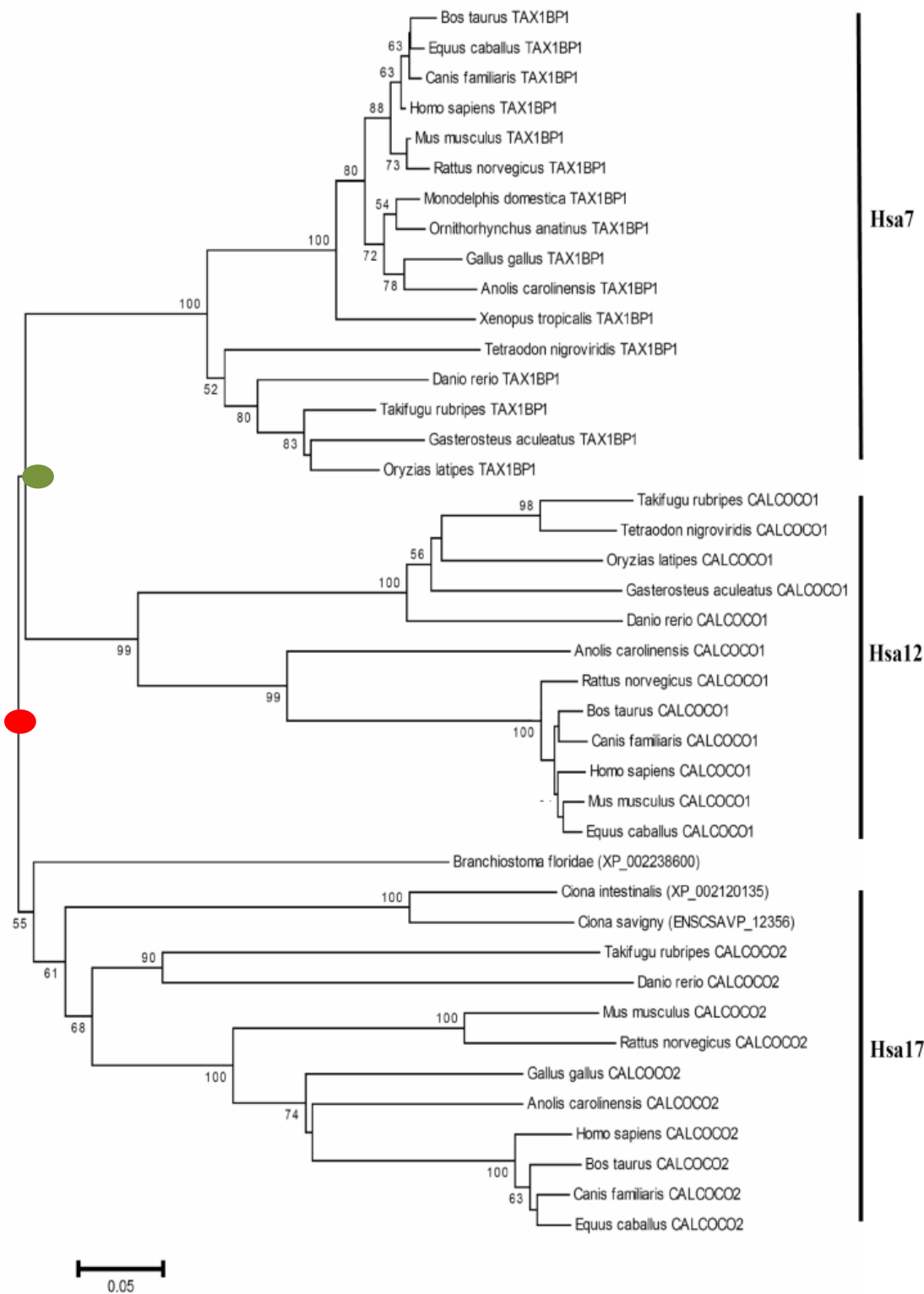
ATP synthase, H⁺ transporting, mitochondrial F0 complex –ATP5G



Phylogenetic tree of ATP5G family.

Neighbor-Joining tree of the ATP5G 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.

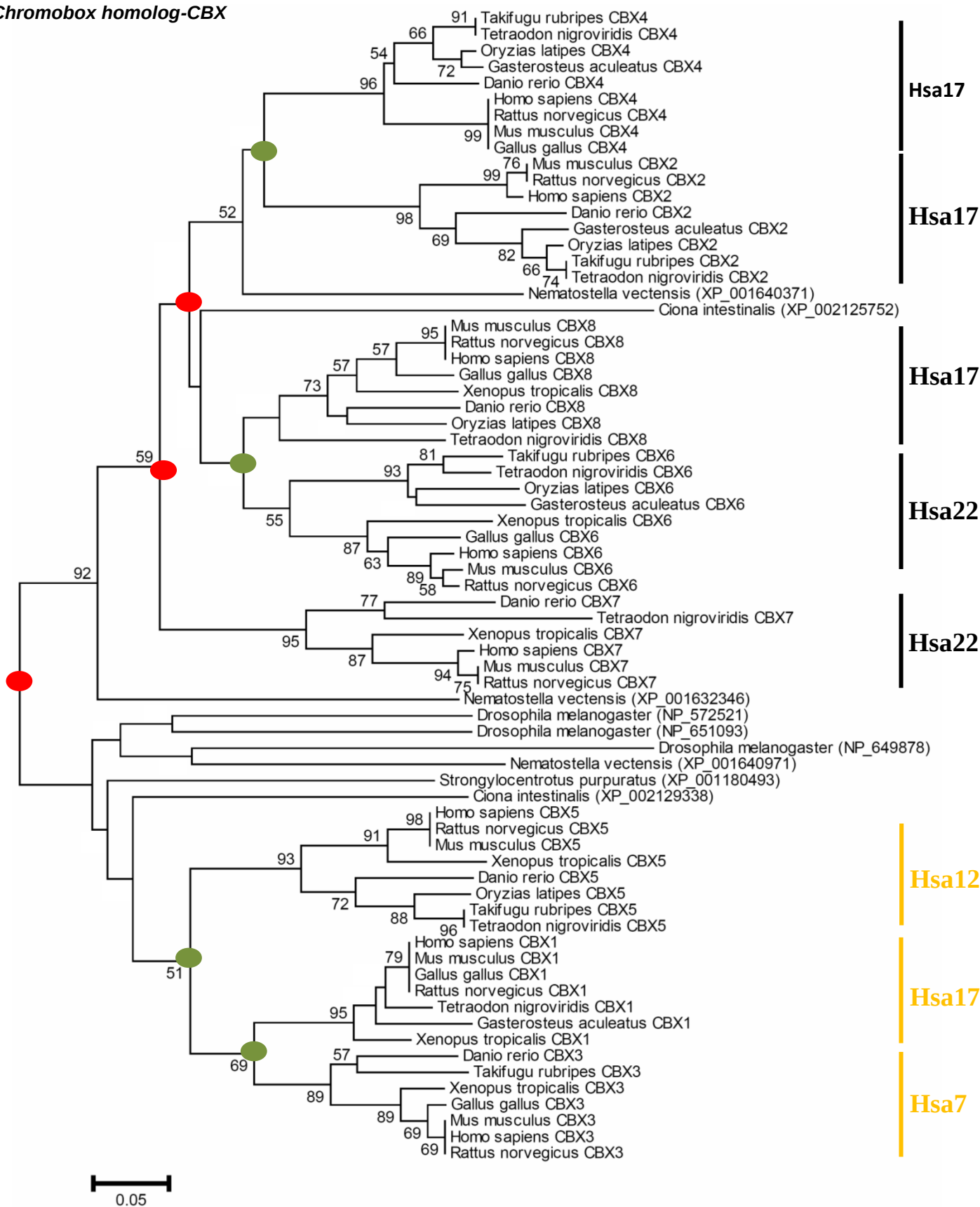
Calcium binding and coiled-coil domain-CALCOCO



Phylogenetic tree of CALCOCO family.

Neighbor-Joining tree of the CALCOCO 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.

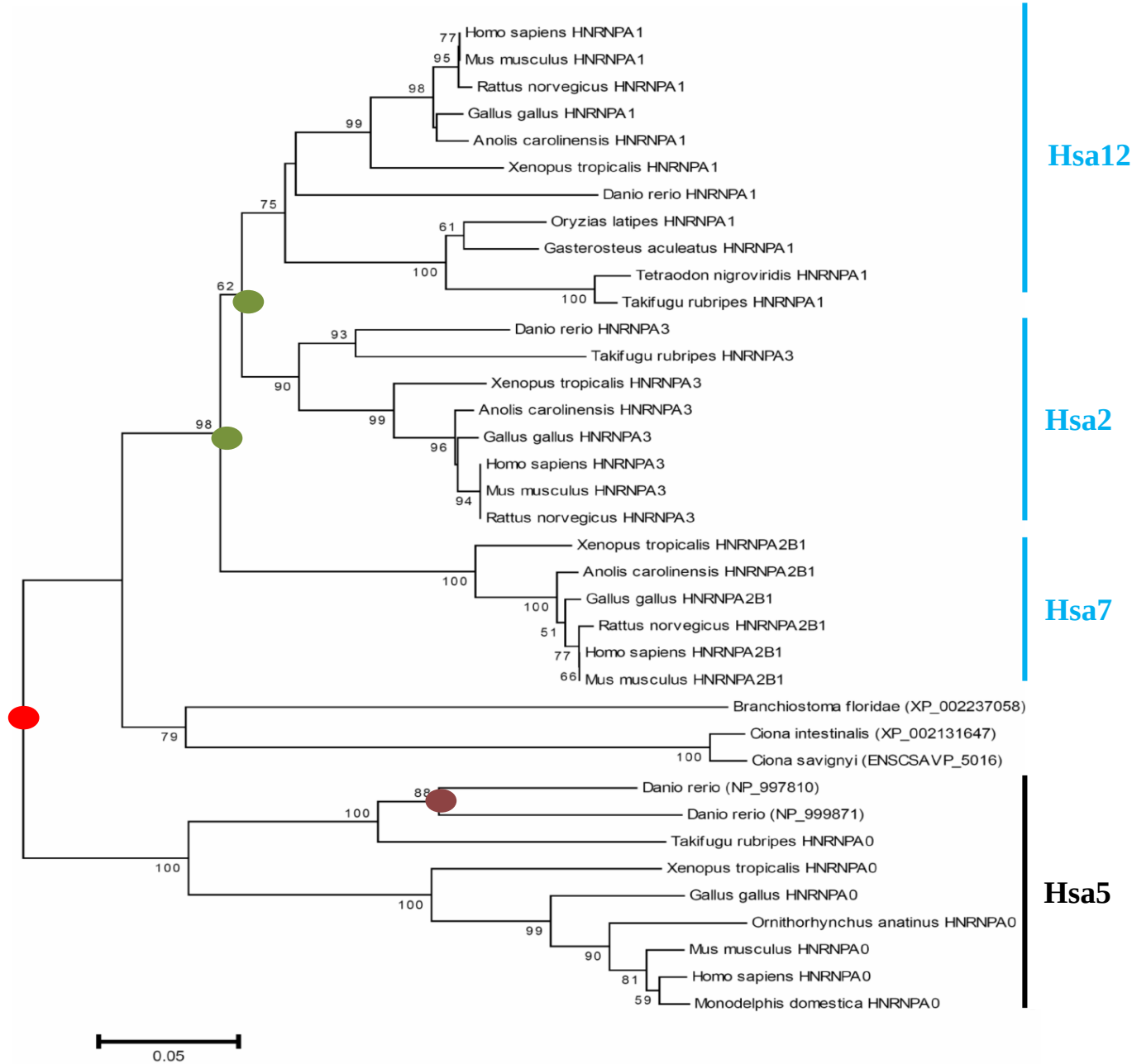
Chromobox homolog-CBX



Phylogenetic tree of CBX family.

Neighbor-Joining tree of the CBX 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.

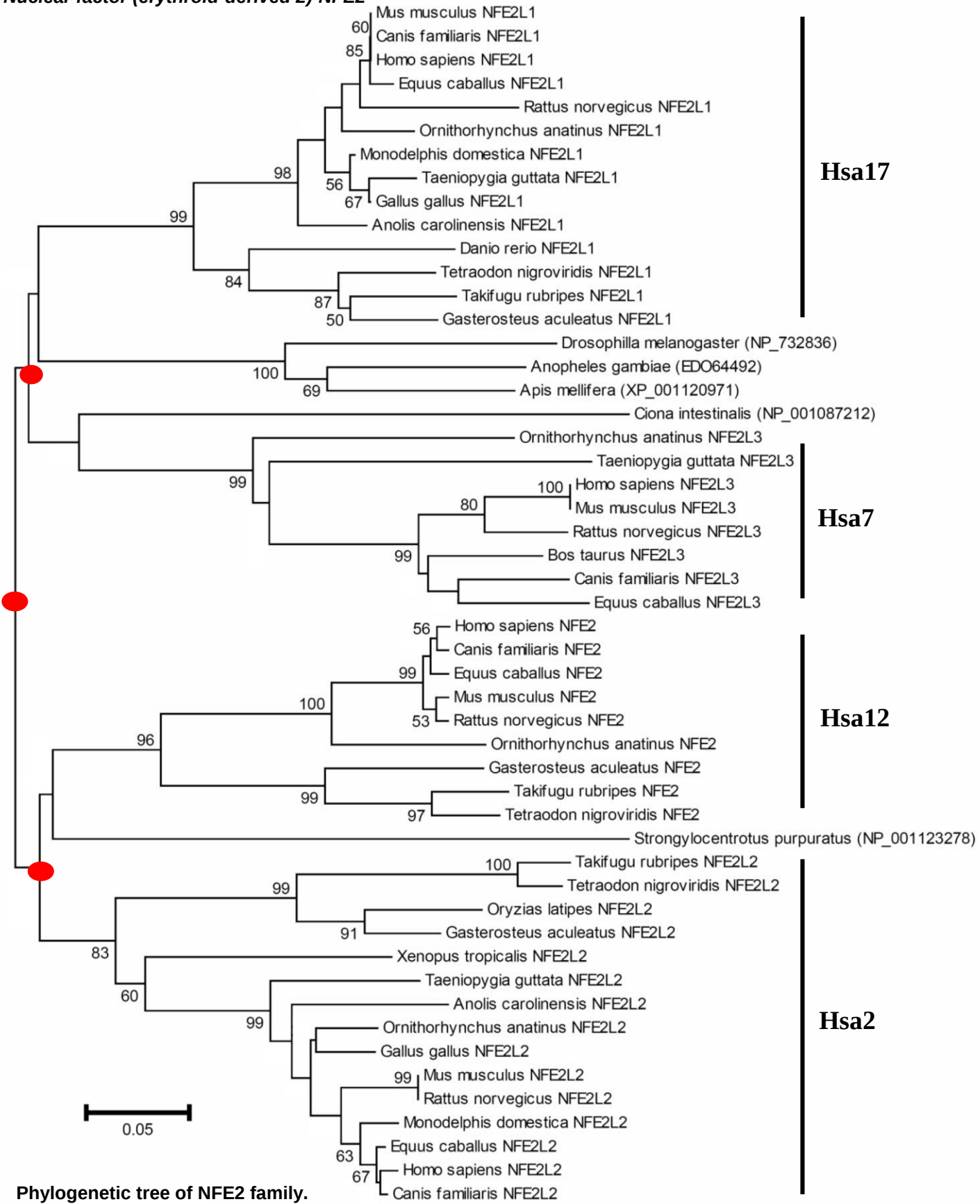
Heterogeneous nuclear ribonucleoprotein A-HNRNPA



Phylogenetic tree of HNRNPA family.

Neighbor-Joining tree of the HNRNPA 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.

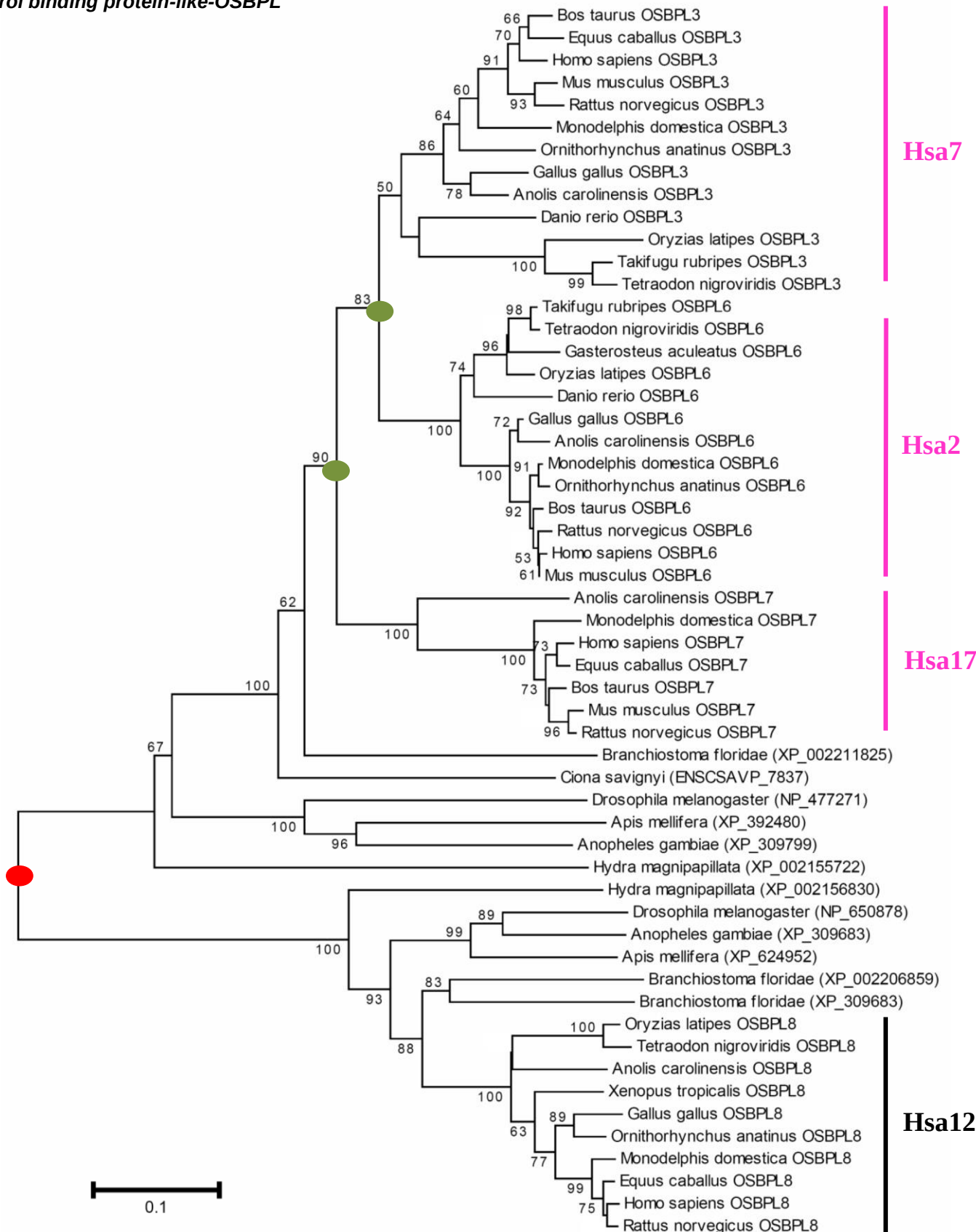
Nuclear factor (erythroid-derived 2)-NFE2



Phylogenetic tree of NFE2 family.

Neighbor-Joining tree of the NFE2 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.

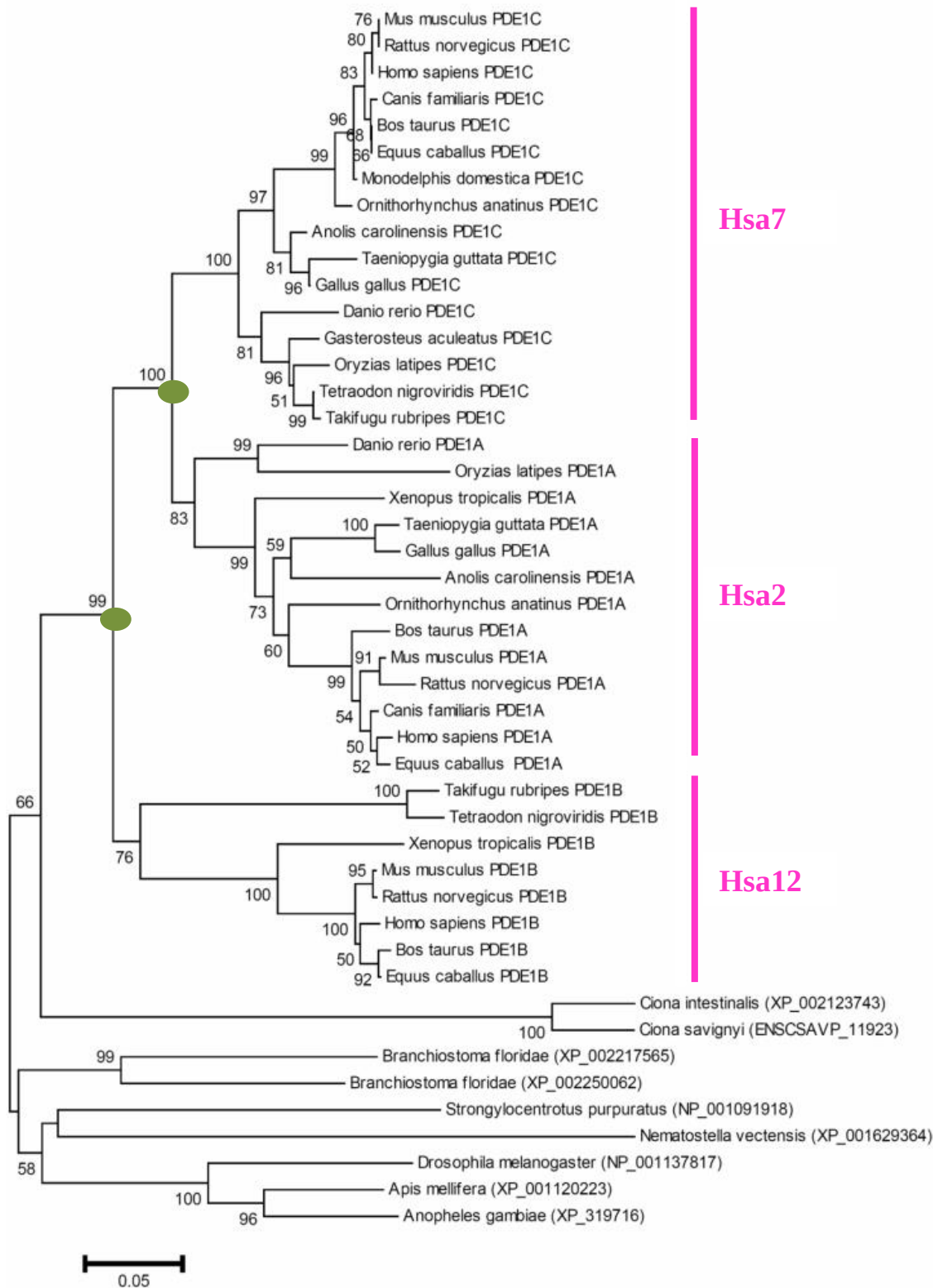
Oxysterol binding protein-like-OSBPL



Phylogenetic tree of OSBPL family.

Neighbor-Joining tree of the OSBPL 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.

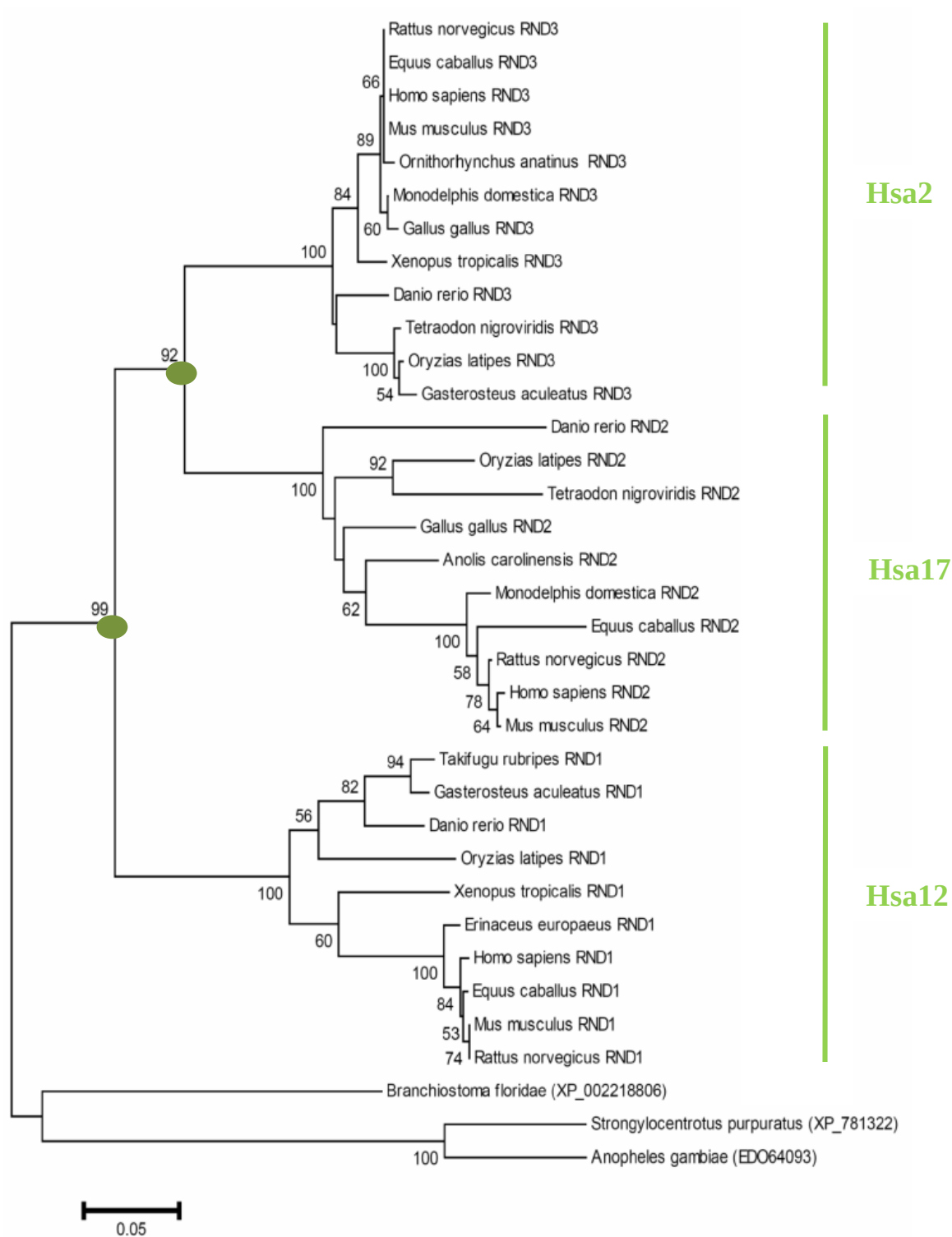
Phosphodiesterase 1, Calmodulin-dependent-PDE1



Phylogenetic tree of PDE1 family.

Neighbor-Joining tree of the PDE1 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.

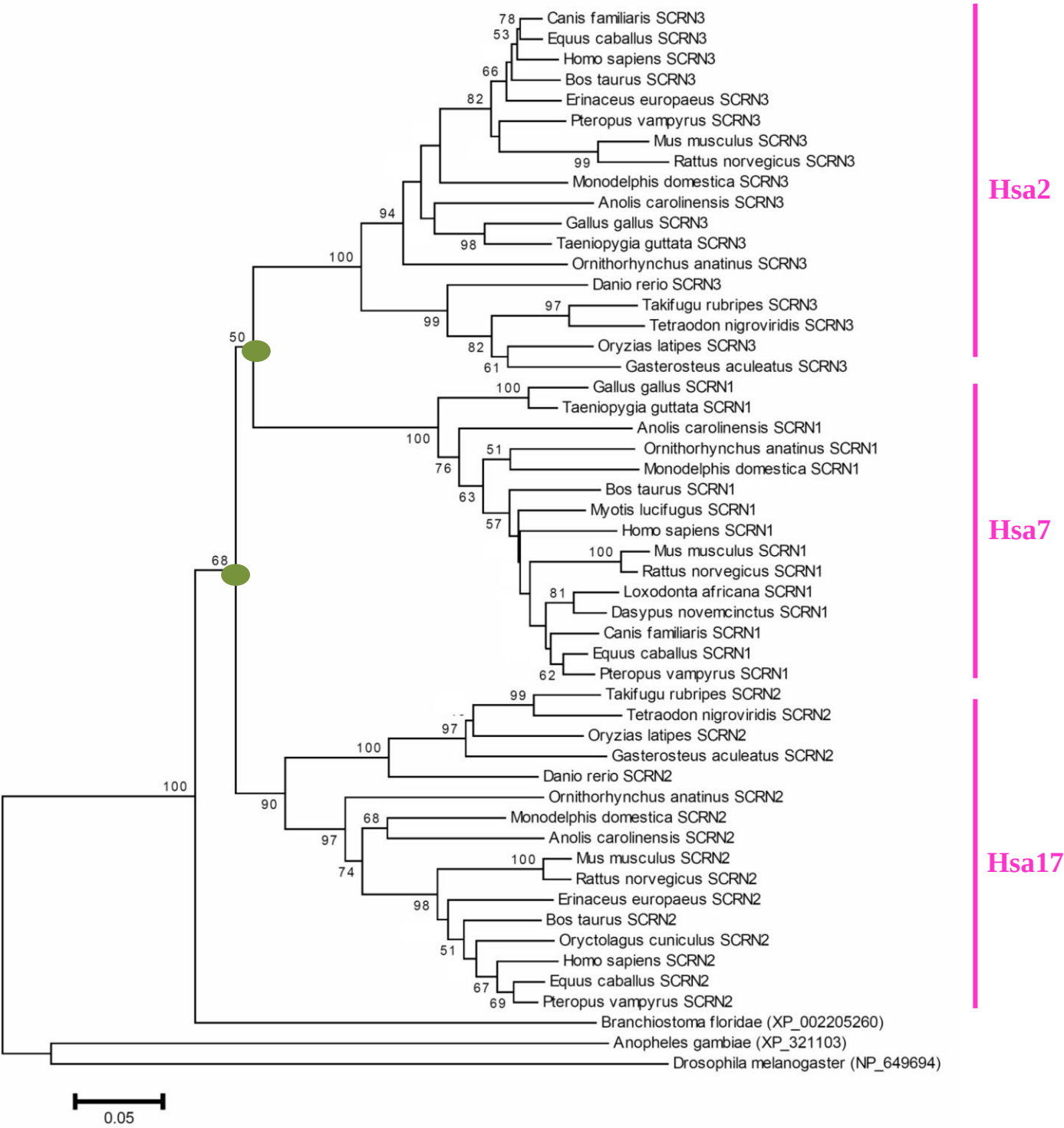
Rho family GTPase-RND



Phylogenetic tree of RND family.

Neighbor-Joining tree of the RND 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.

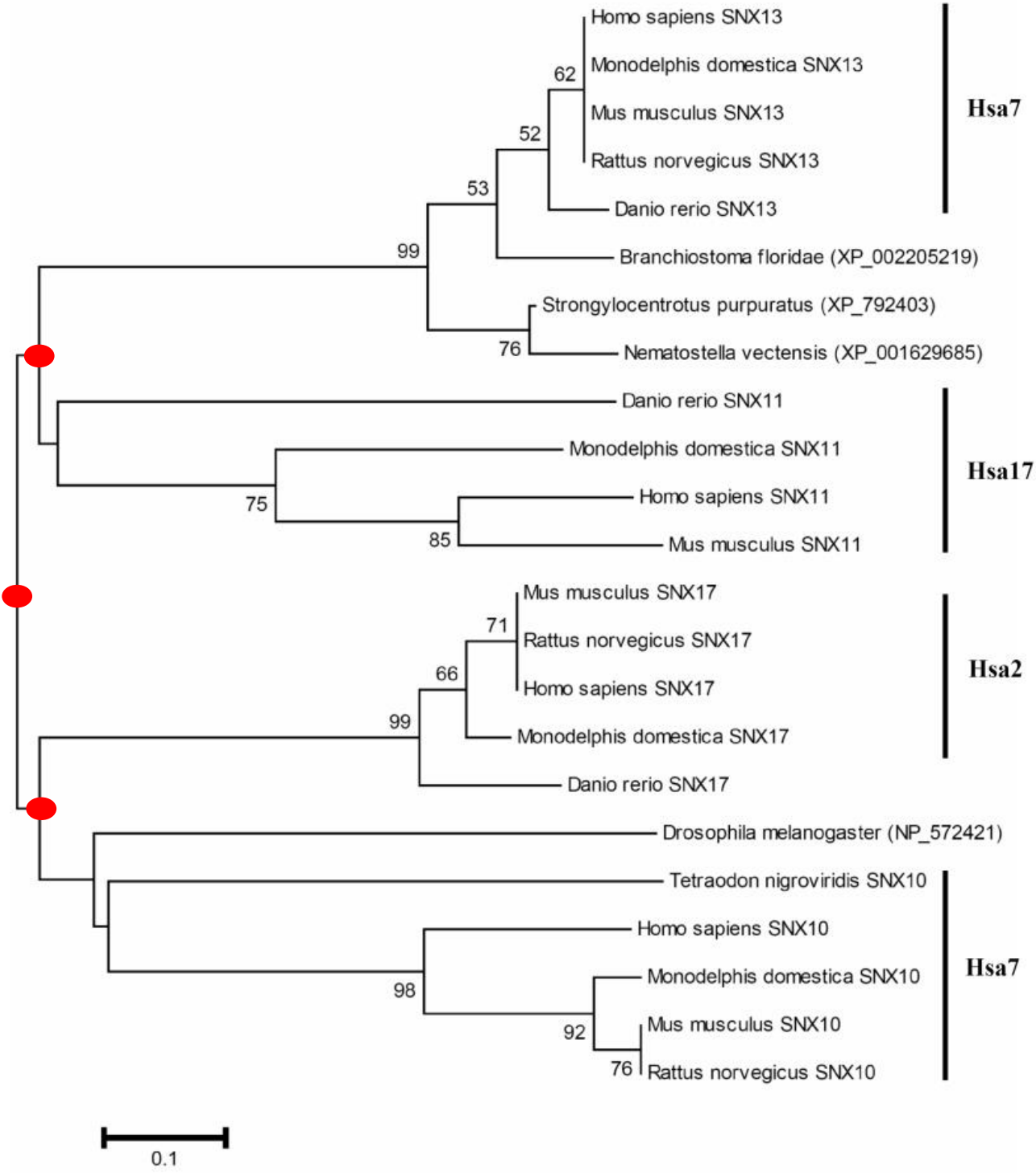
Secernin-SCRN



Phylogenetic tree of SCR family.

Neighbor-Joining tree of the SCR 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.

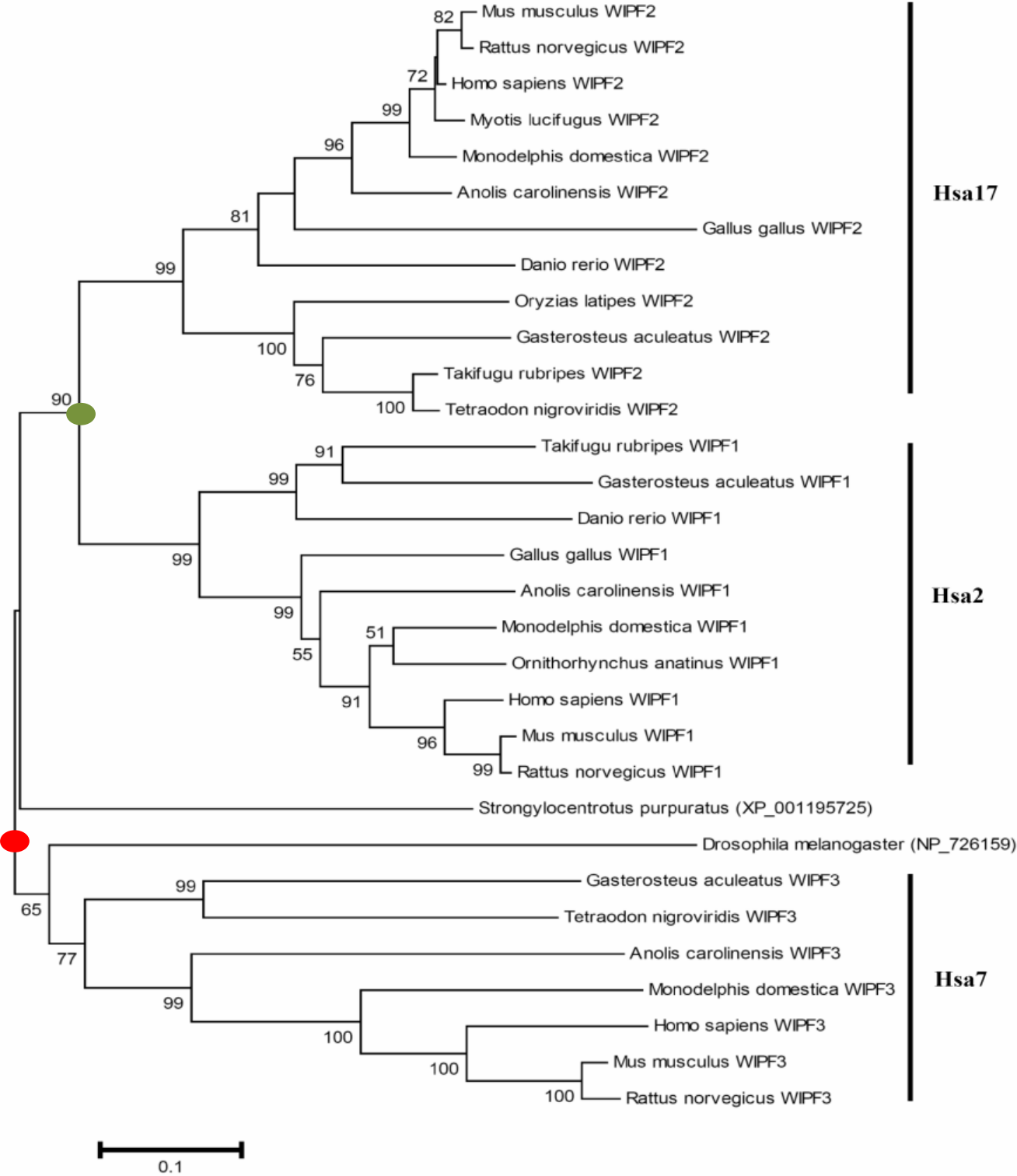
Sorting nexin -SNX



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 $\geq 50\%$ are presented here. Scale bar shows amino acid substitution per site.

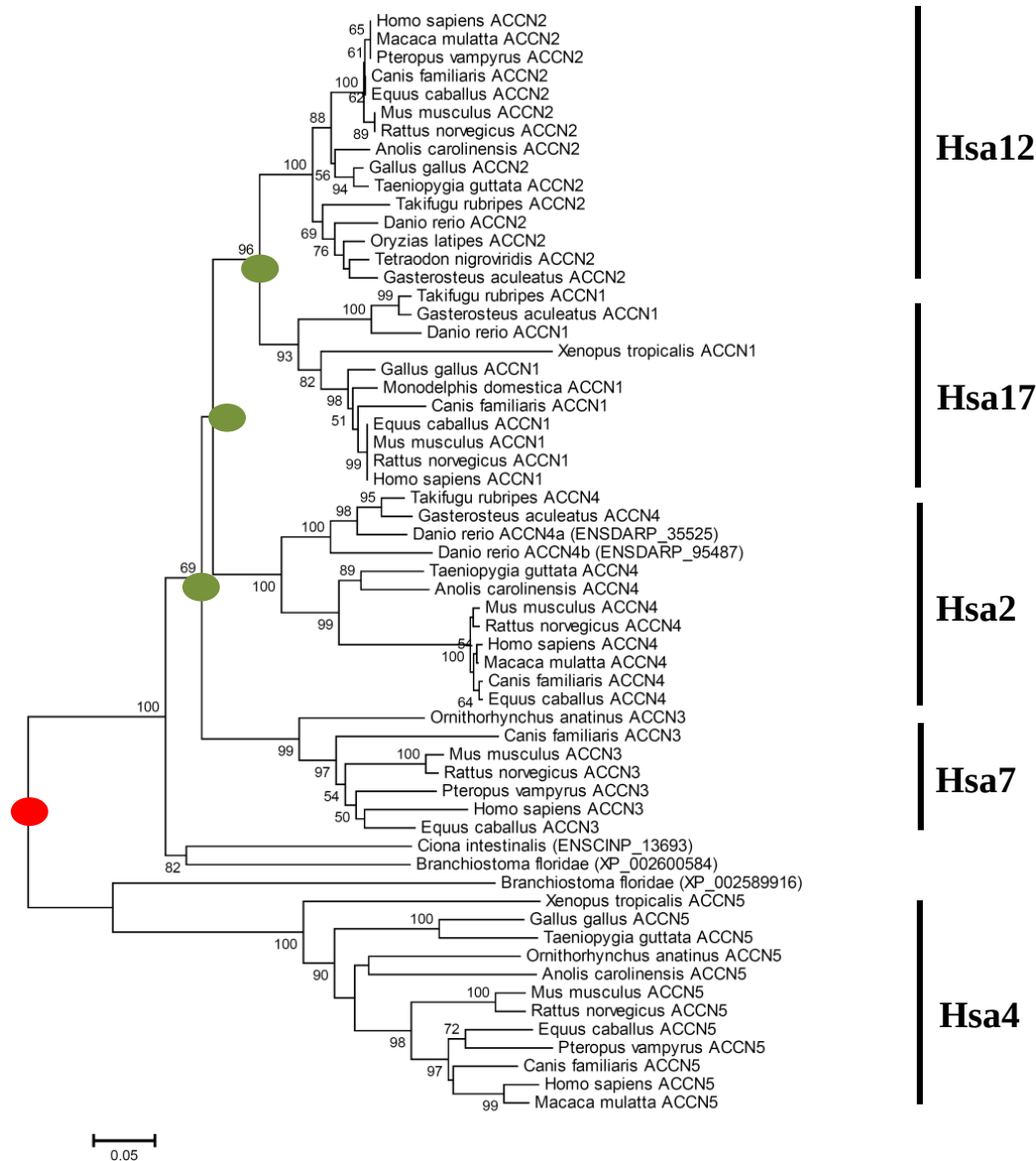
WAS/WASL interacting protein family-WIPF



Phylogenetic tree of WIPF family.

Neighbor-Joining tree of the WIPF 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.

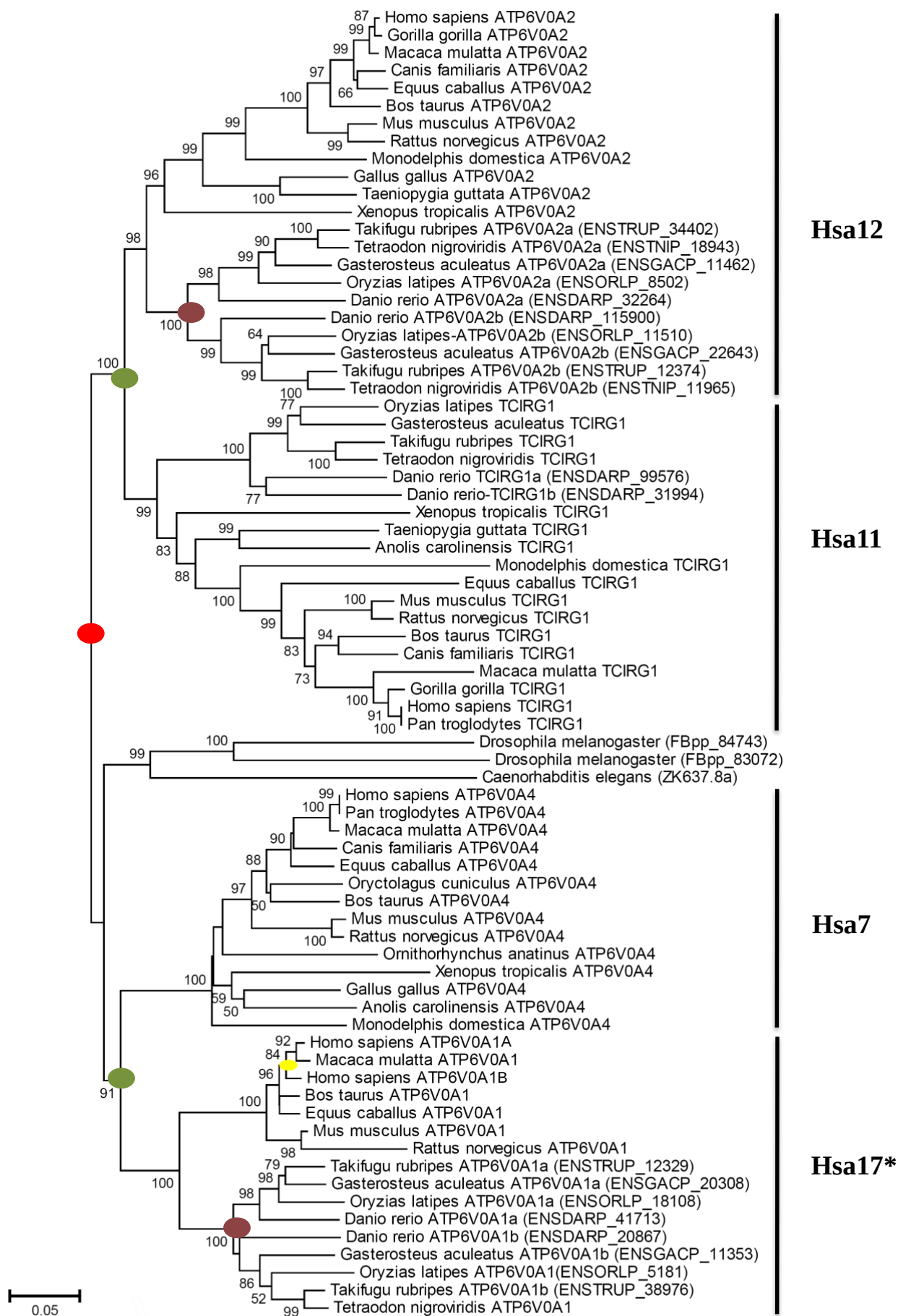
Amiloride-sensitive cation channel neuronal-ACCN



Phylogenetic tree of ACCN family.

Neighbor-Joining tree of the ACCN 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.

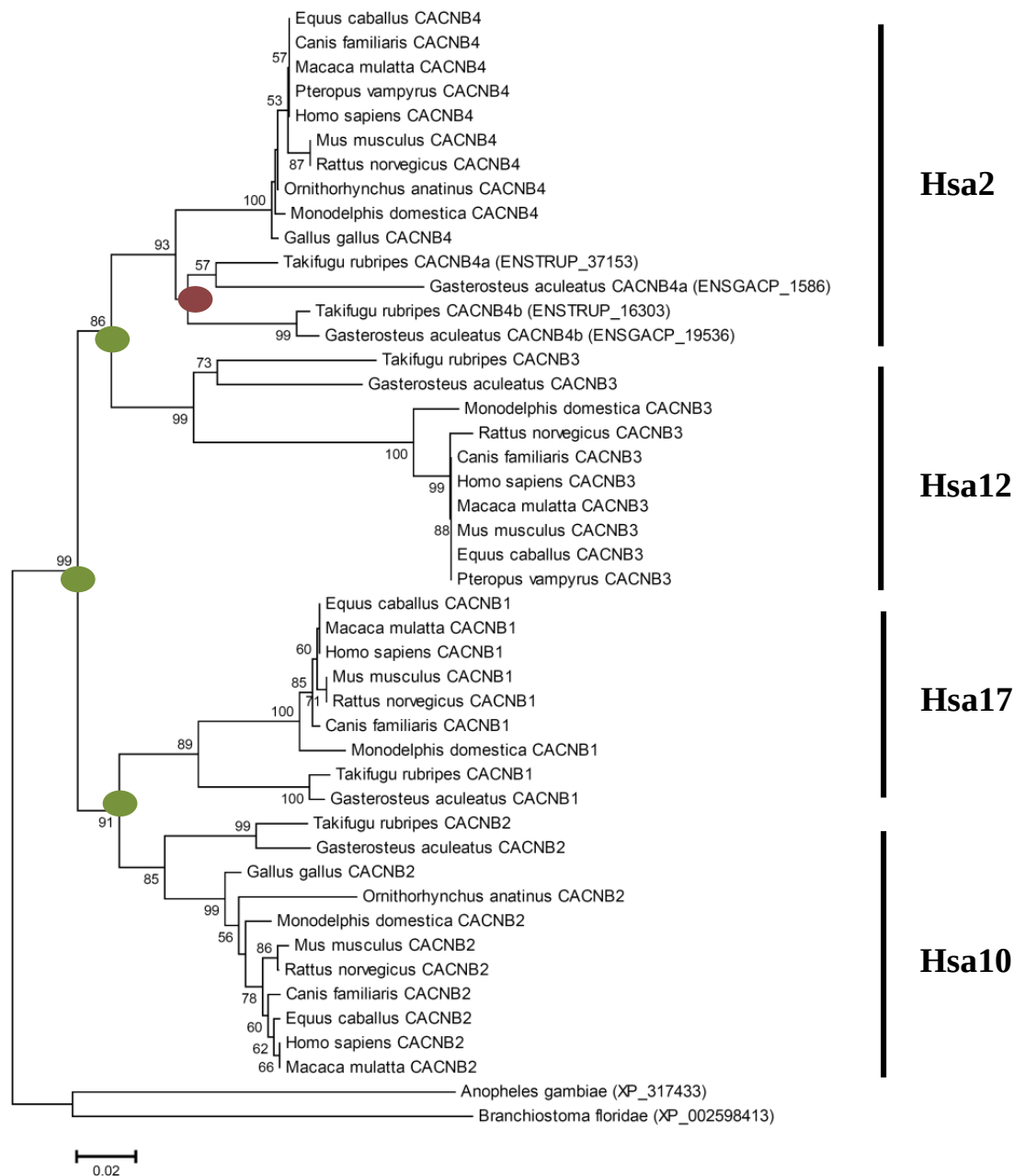
ATPase, H⁺ transporting, lysosomal V0 Subunit A –ATP6V0A



Phylogenetic tree of ATP6V0A family.

Neighbor-Joining tree of the ATP6V0A 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. 17* shows human specific duplication on chromosome 17.

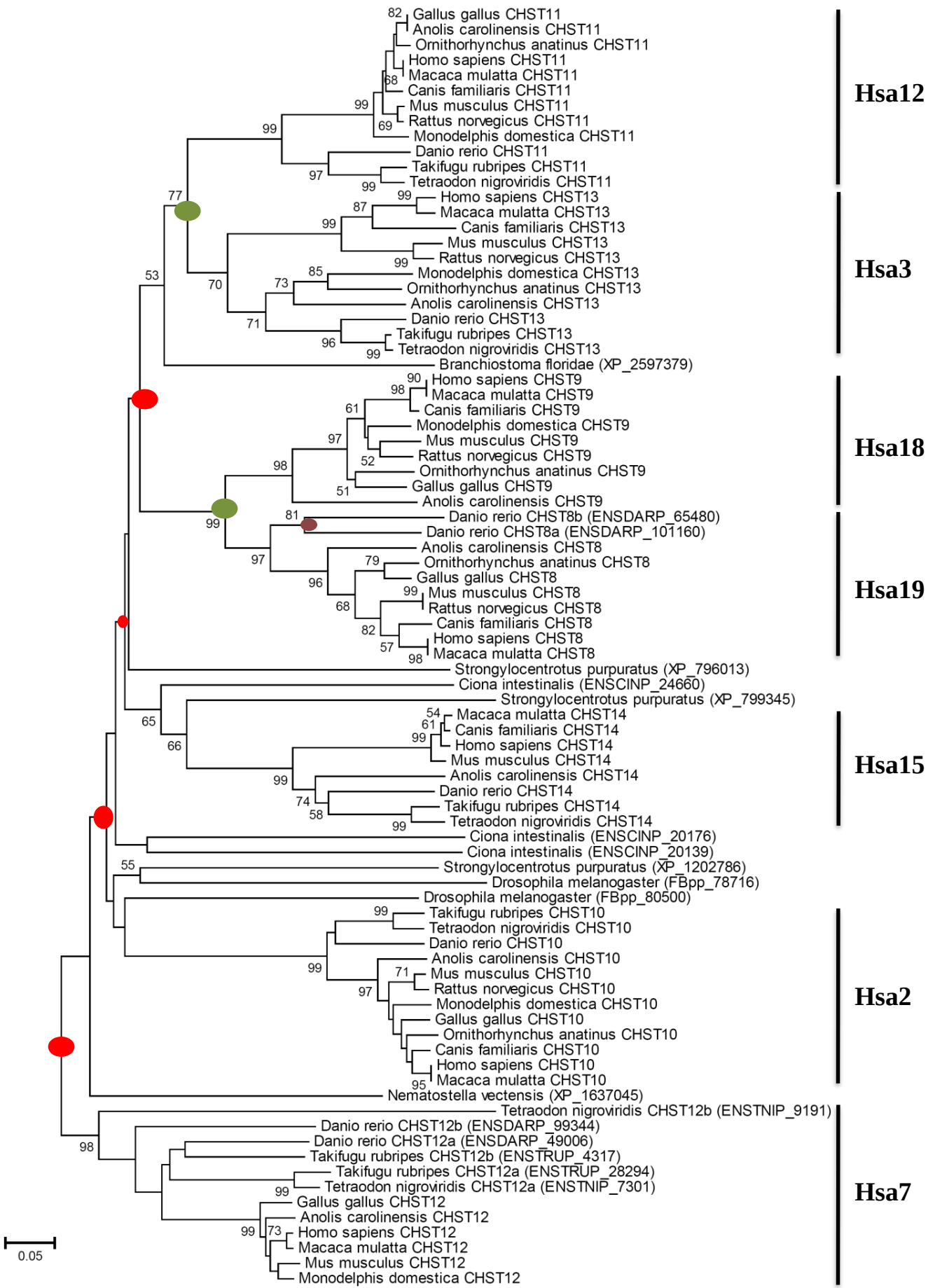
Calcium channel voltage-dependent beta-CACNB



Phylogenetic tree of CACNB family.

Neighbor-Joining tree of the CACNB 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.

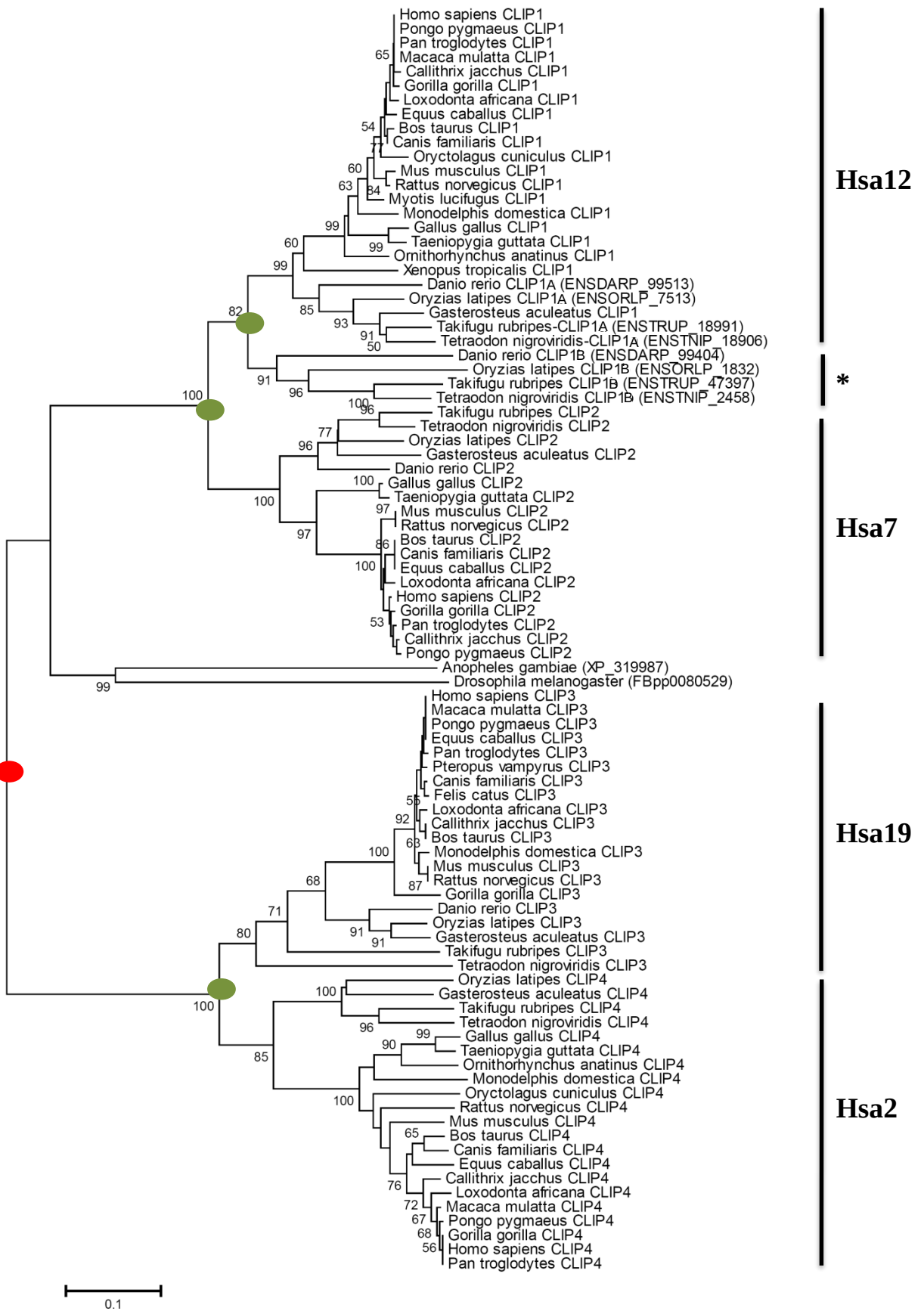
Carbohydrate sulfotransferase-CHST



Phylogenetic tree of CHST family.

Neighbor-Joining tree of the CHST 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.

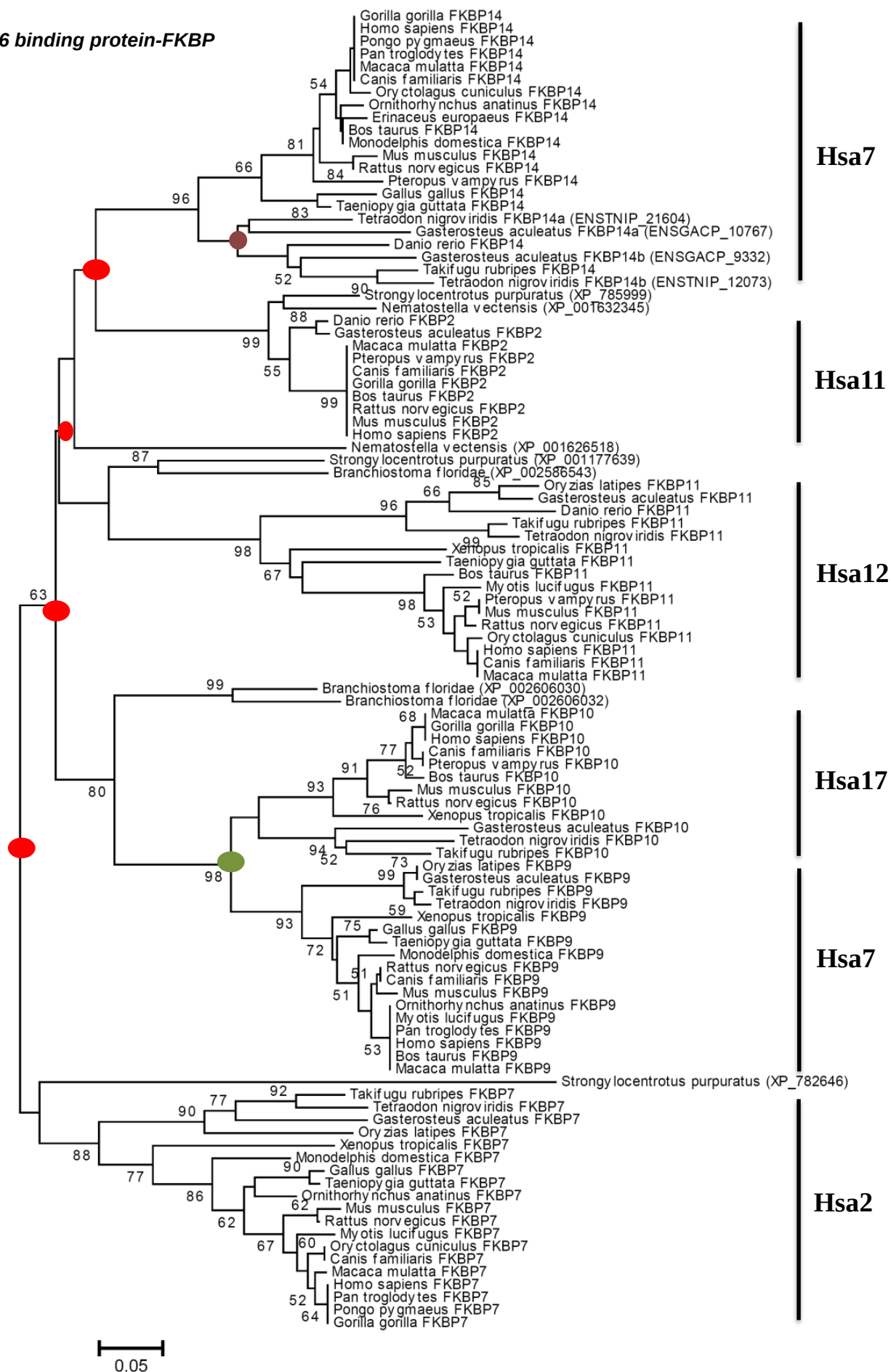
CAP-GLY domain containing linker protein-CLIP



Phylogenetic tree of CLIP family.

Neighbor-Joining tree of the CLIP 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 with missing tetrapods named as CLIP1B by our group.

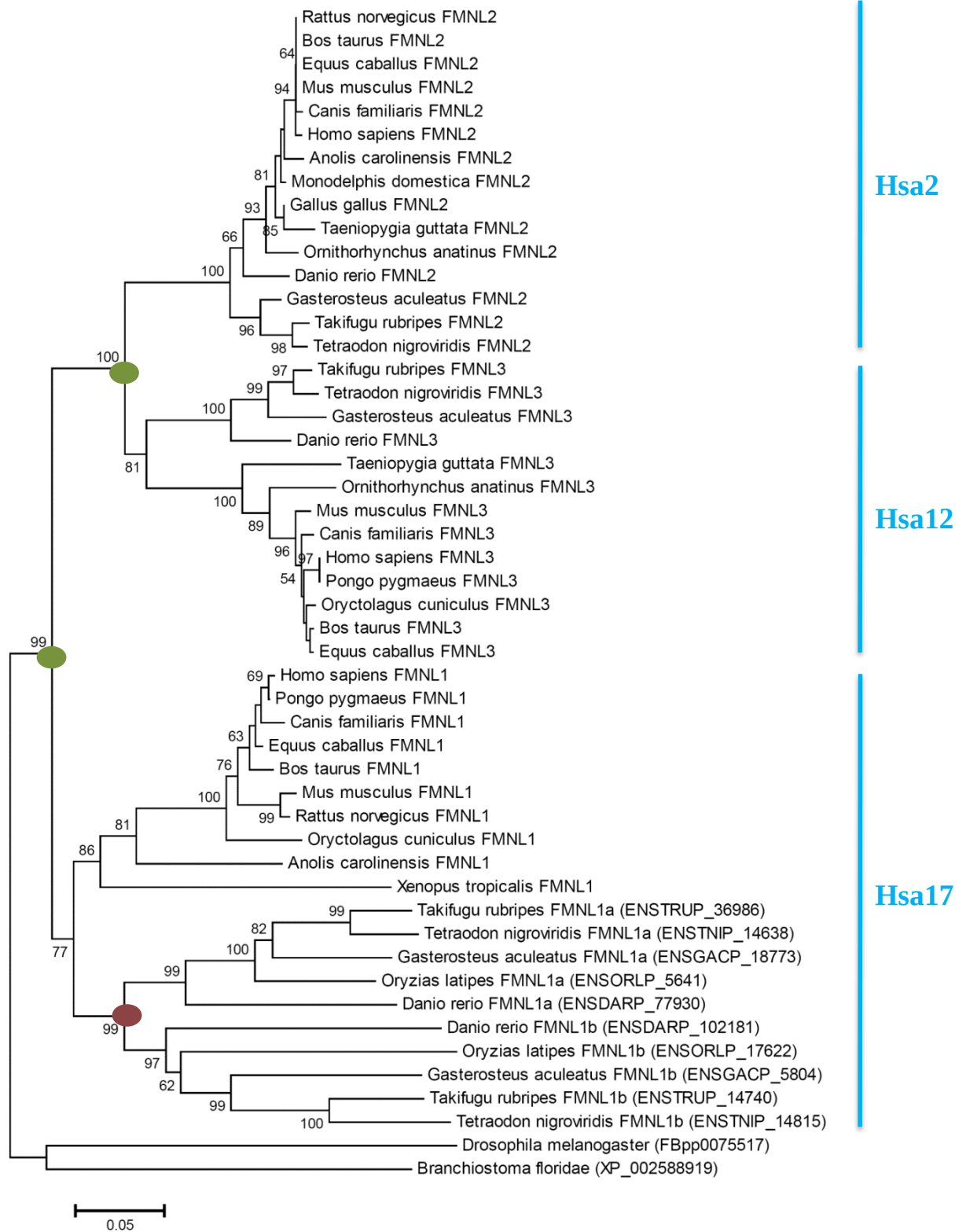
FK506 binding protein-FKBP



Phylogenetic tree of FKBP family.

Neighbor-Joining tree of the FKBP 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.

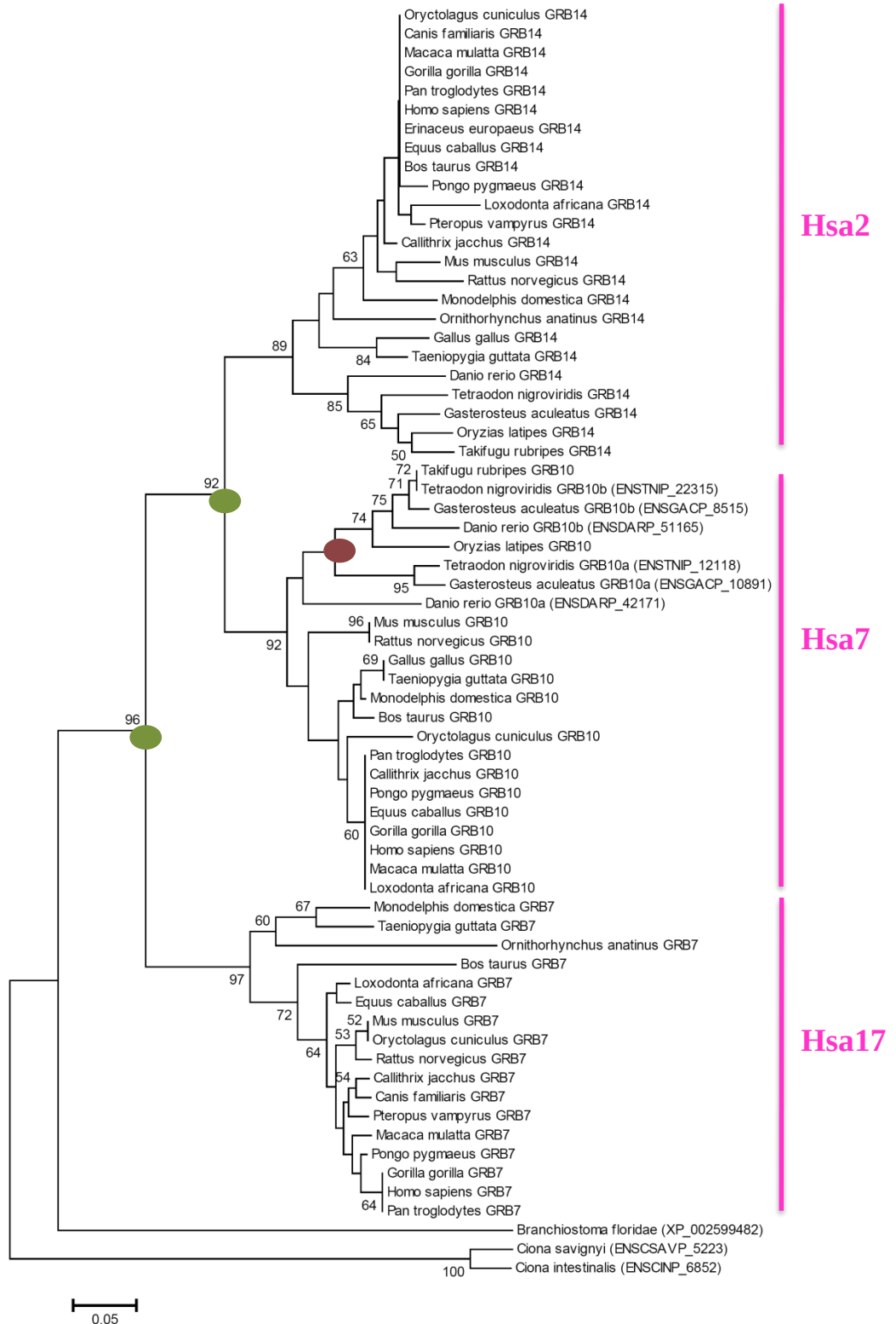
Formin-like-FMNL



Phylogenetic tree of FMNL family.

Neighbor-Joining tree of the FMNL 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.

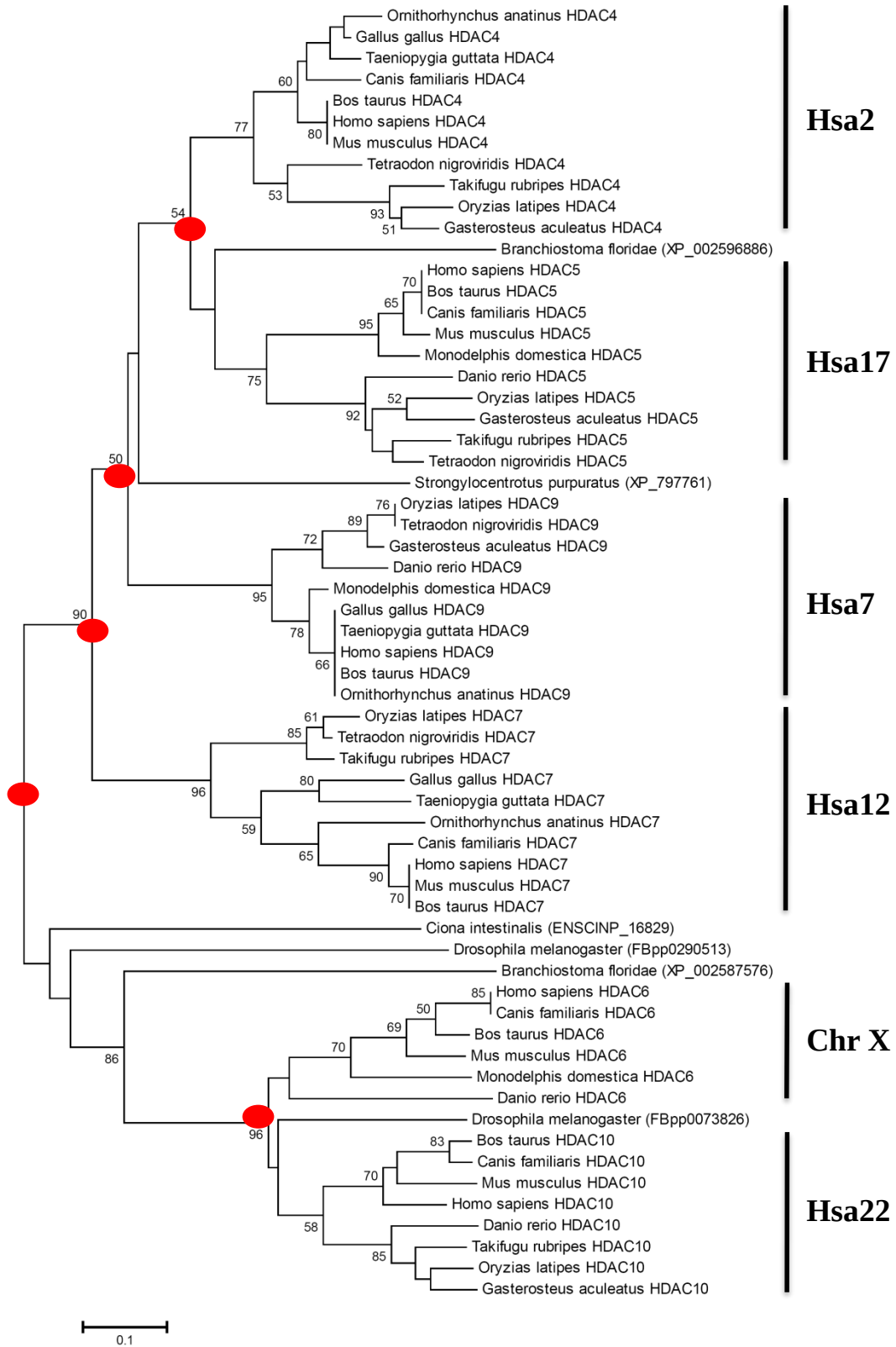
Growth factor receptor-bound protein-GRB



Phylogenetic tree of GRB family.

Neighbor-Joining tree of the GRB 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.

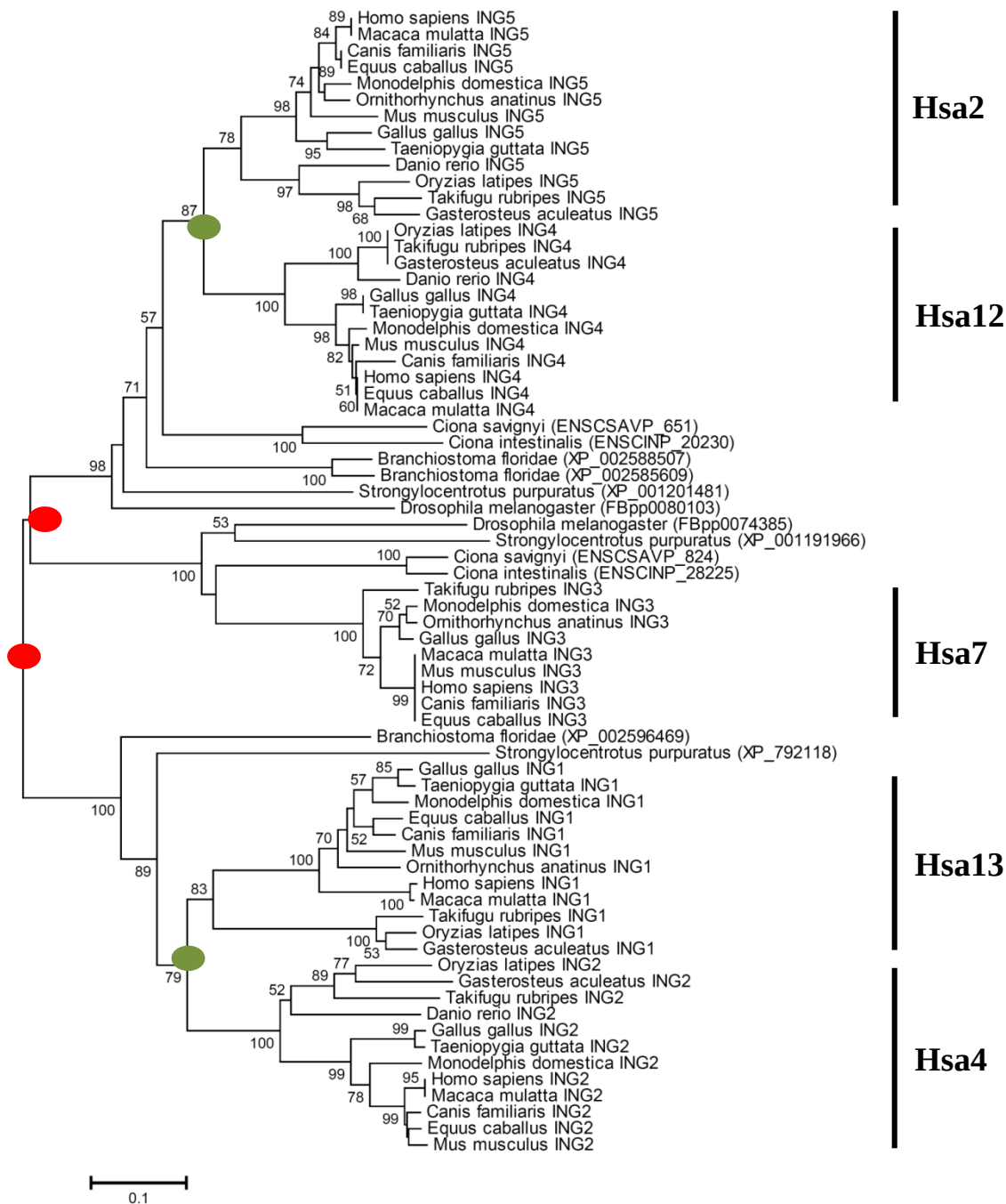
Histone deacetylase-HDAC



Phylogenetic tree of HDAC family.

Neighbor-Joining tree of the HDAC 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.

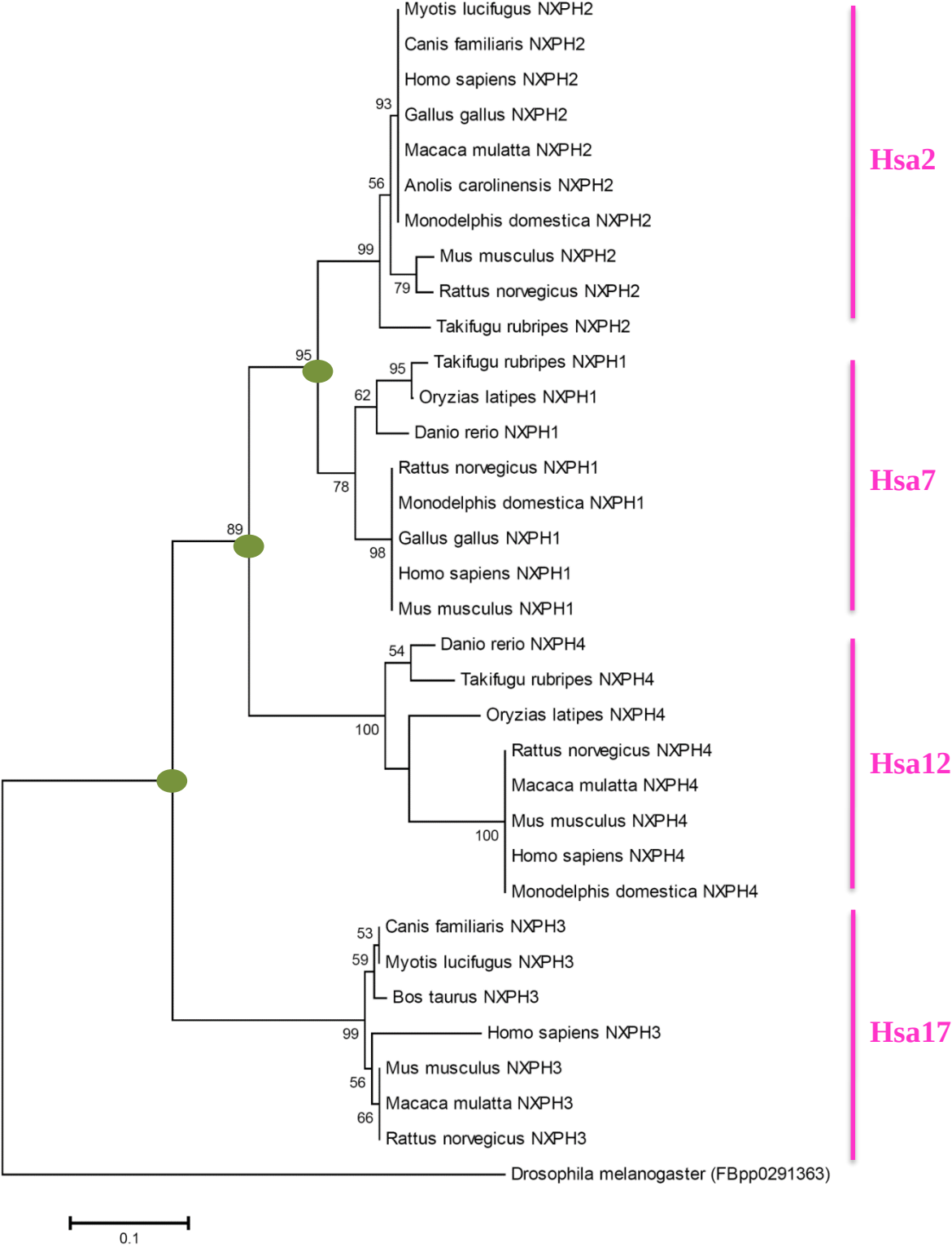
Inhibitor of growth family-ING



Phylogenetic tree of ING family.

Neighbor-Joining tree of the ING 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.

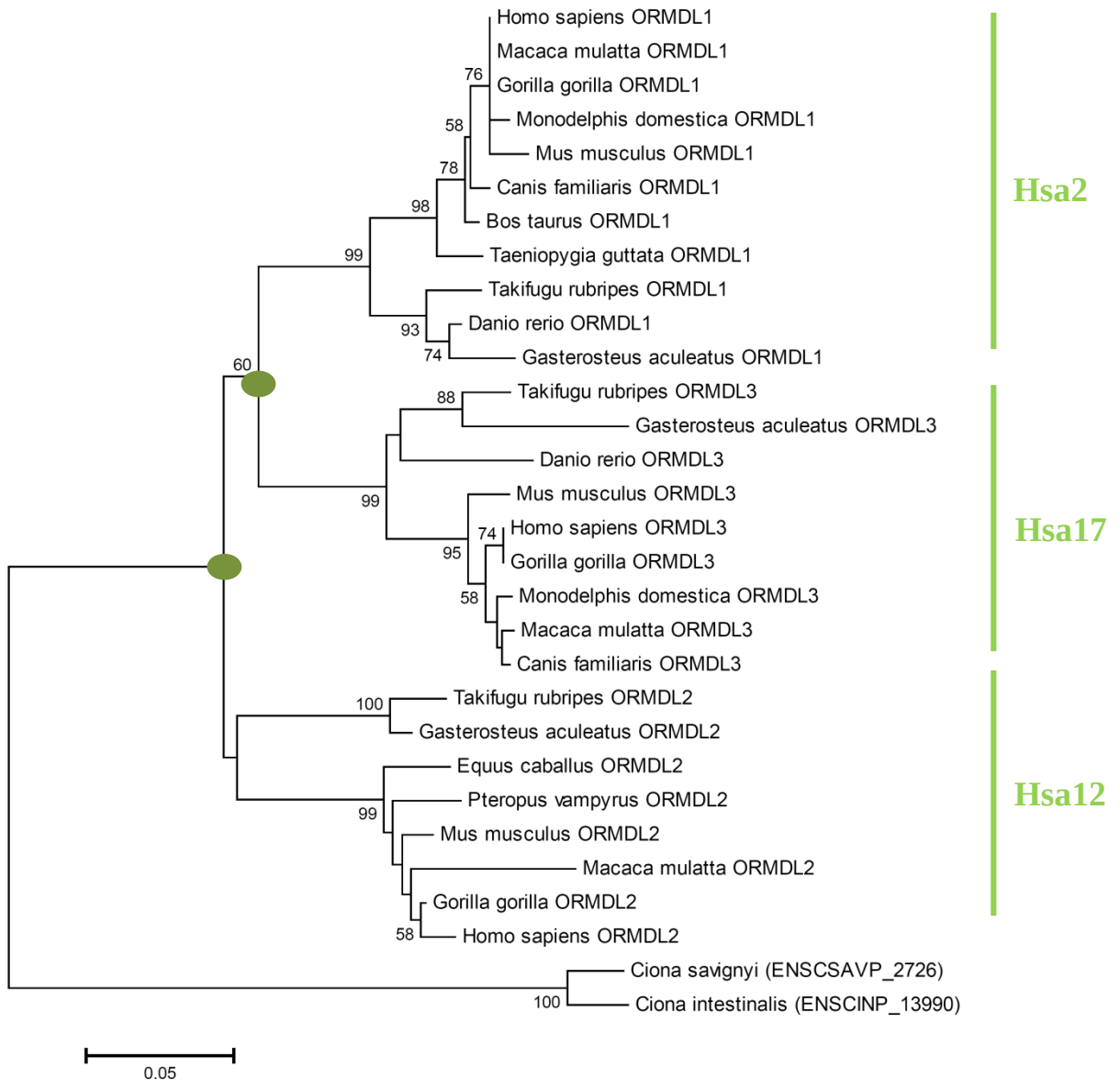
Neurexophilin-NXPH



Phylogenetic tree of NXPH family.

Neighbor-Joining tree of the NXPH 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.

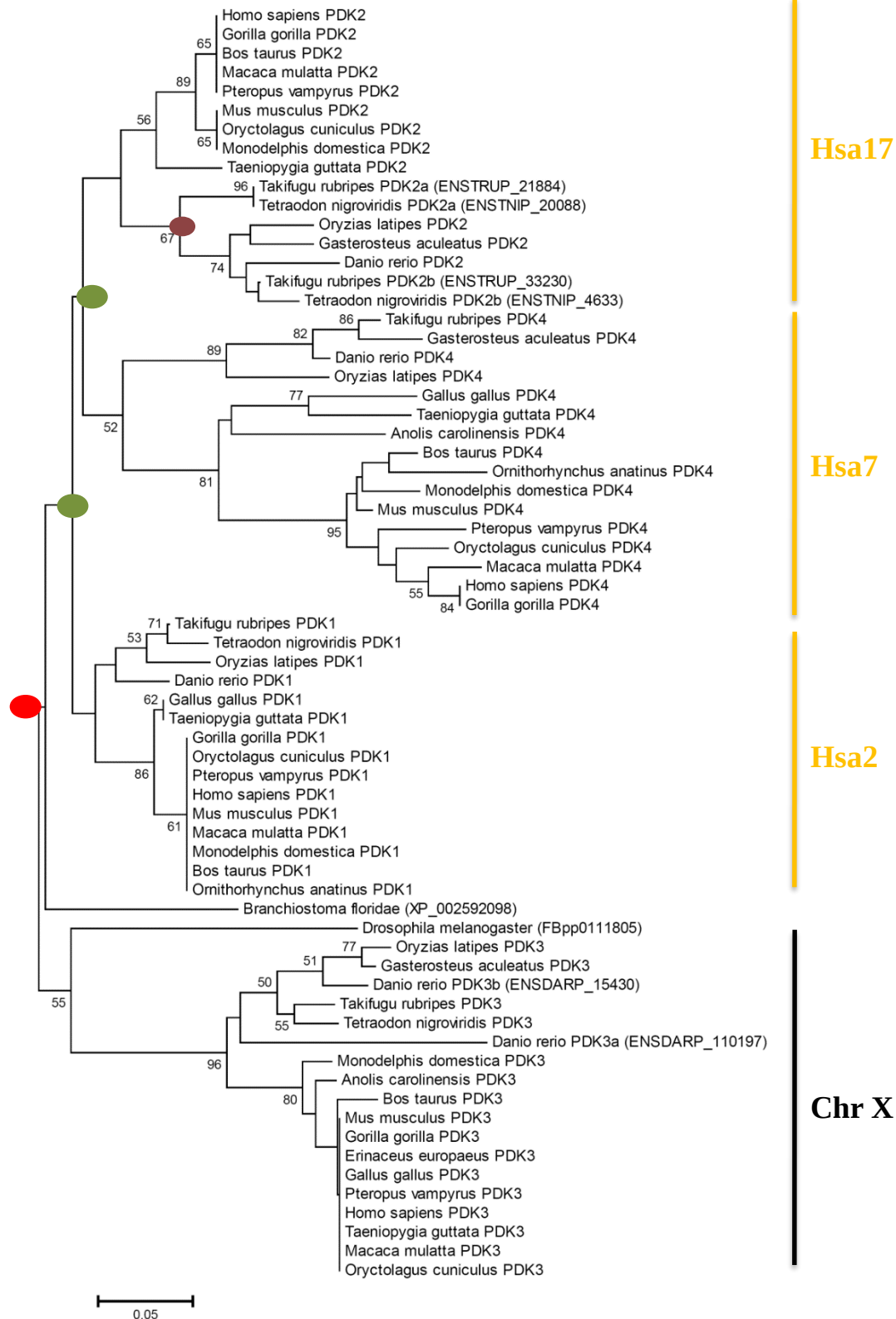
ORM1-like-ORMDL



Phylogenetic tree of ORMDL family.

Neighbor-Joining tree of the ORMDL 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.

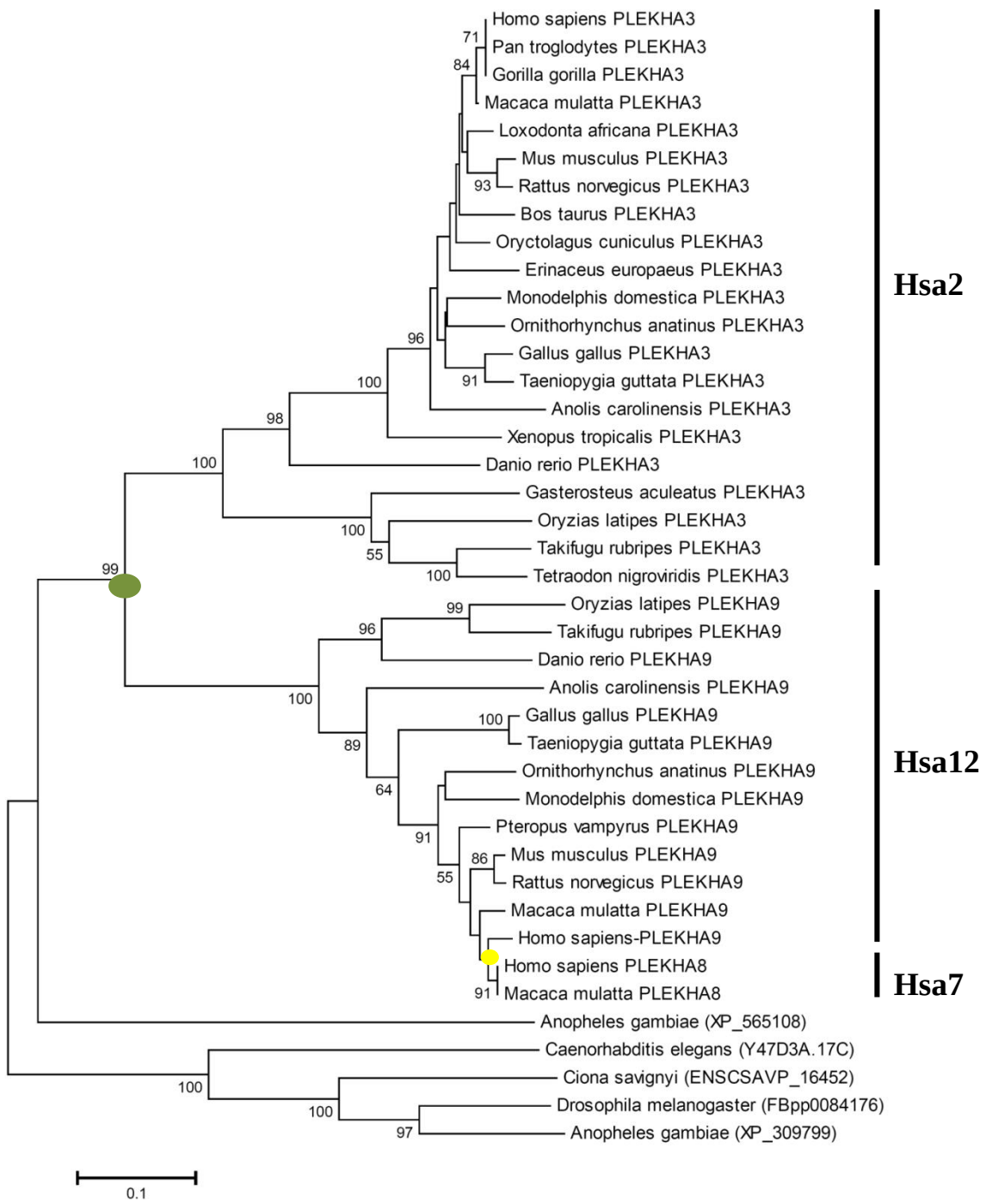
Pyruvate dehydrogenase kinase-PDK



Phylogenetic tree of PDK family.

Neighbor-Joining tree of the PDK 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.

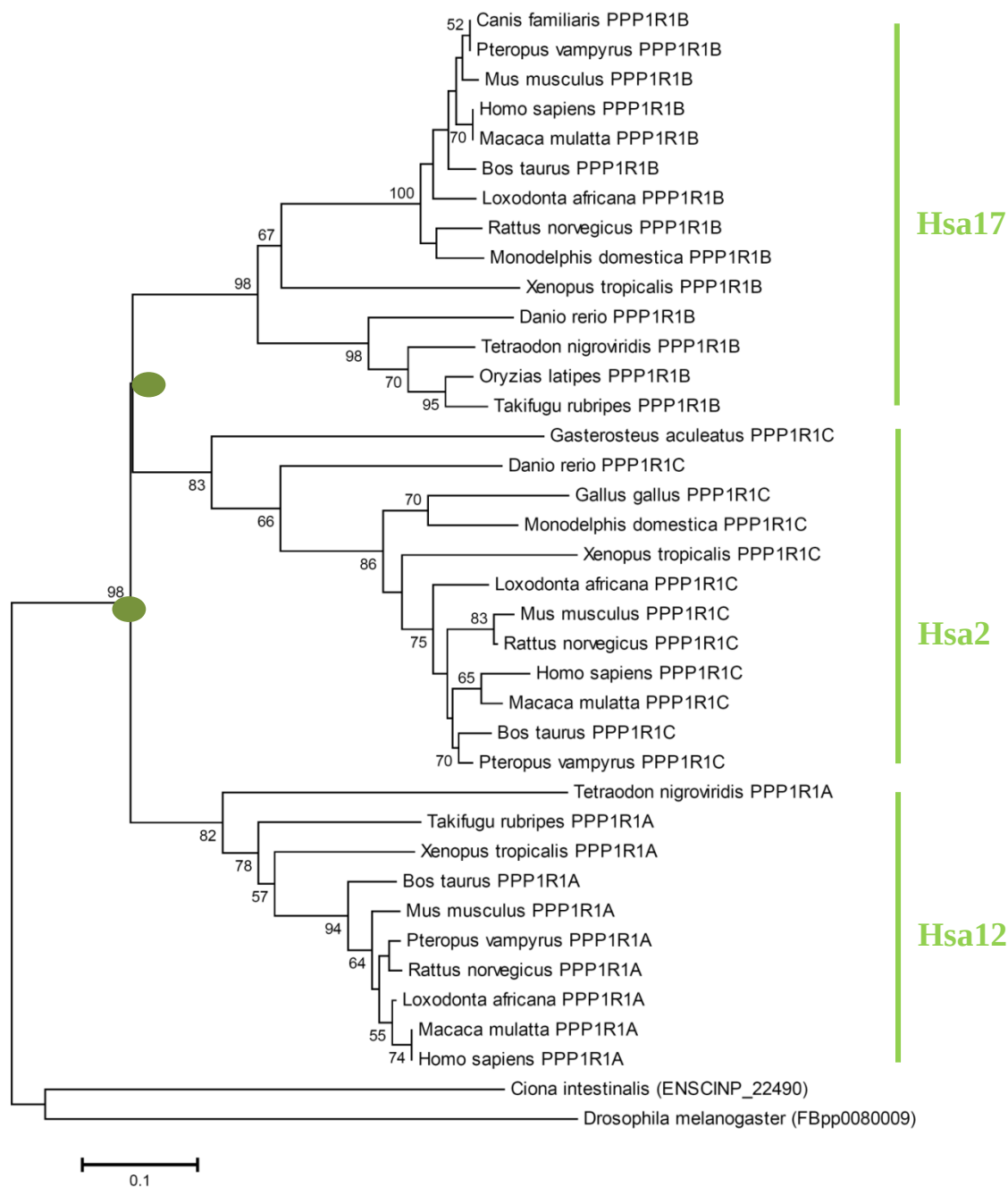
Pleckstrin homology domain containing family A-*PLEKHA*



Phylogenetic tree of PLEKHA family.

Neighbor-Joining tree of the PLEKHA 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.

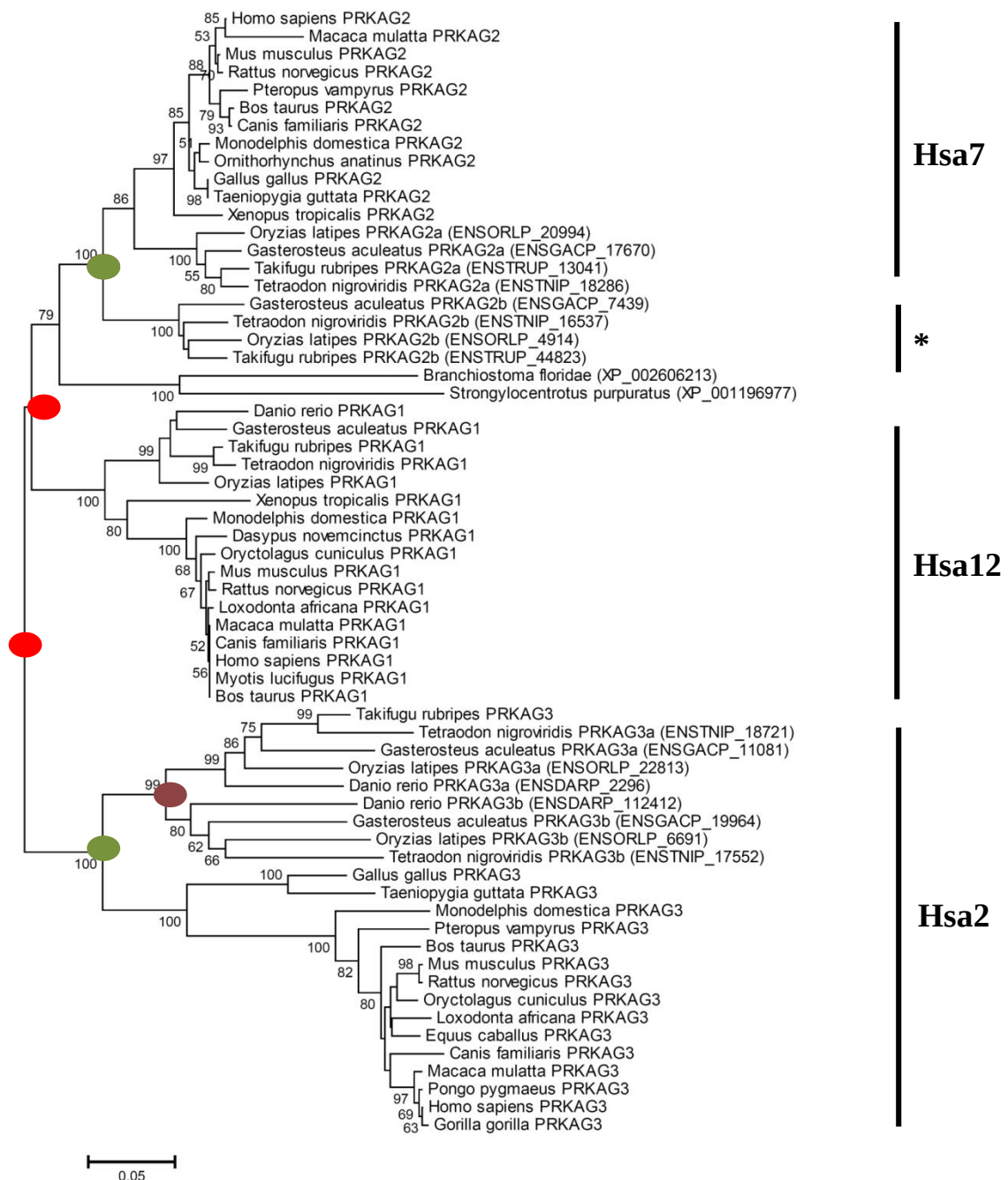
Protein phosphatase 1 regulatory (inhibitor)-PPP1R1



Phylogenetic tree of PPP1R1 family.

Neighbor-Joining tree of the PPP1R1 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.

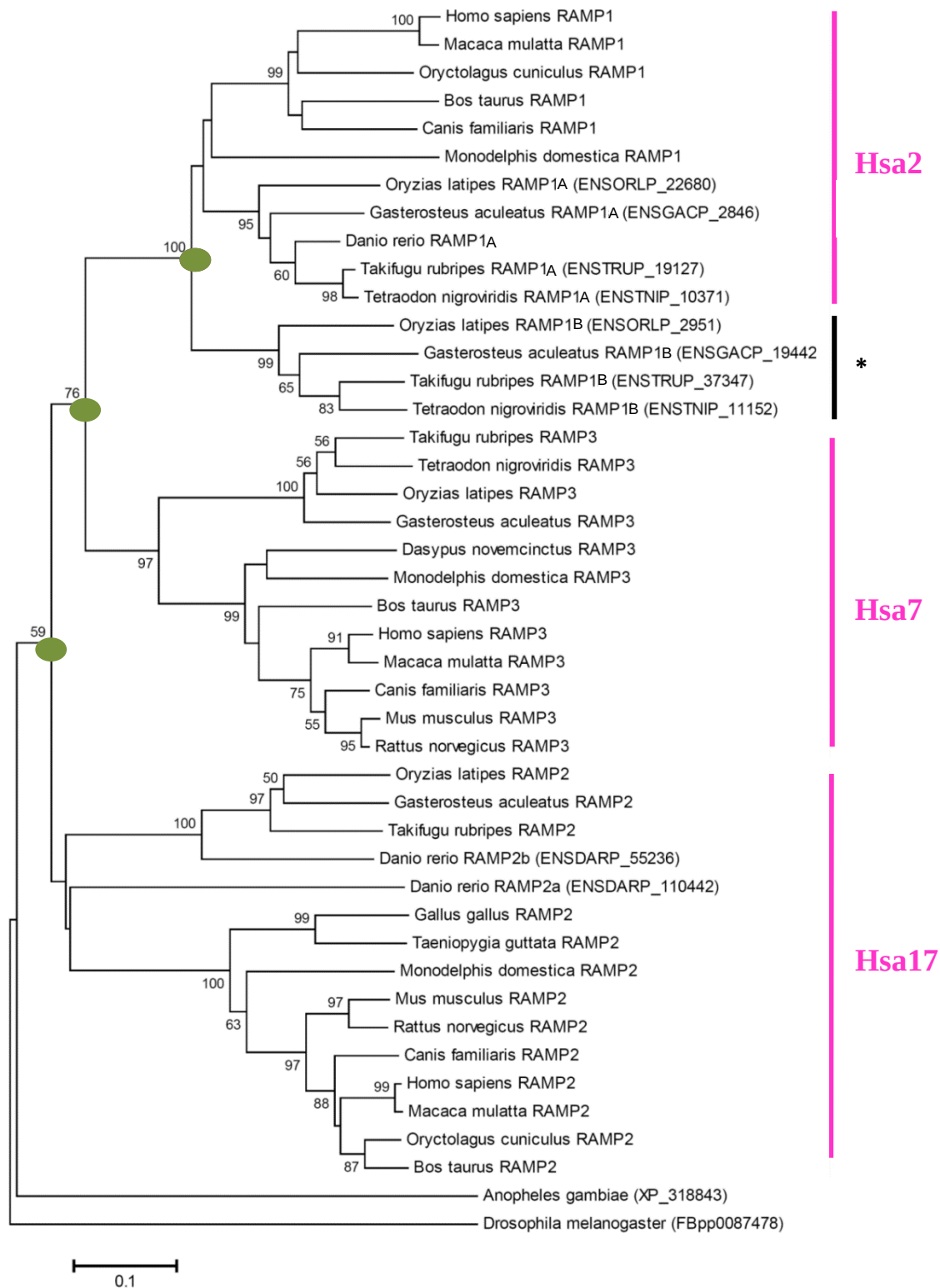
Protein kinase gamma subunit -PRKAG



Phylogenetic tree of PRKAG family.

Neighbor-Joining tree of the PRKAG 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 with missing tetrapods named as PRKAG2 by our group.

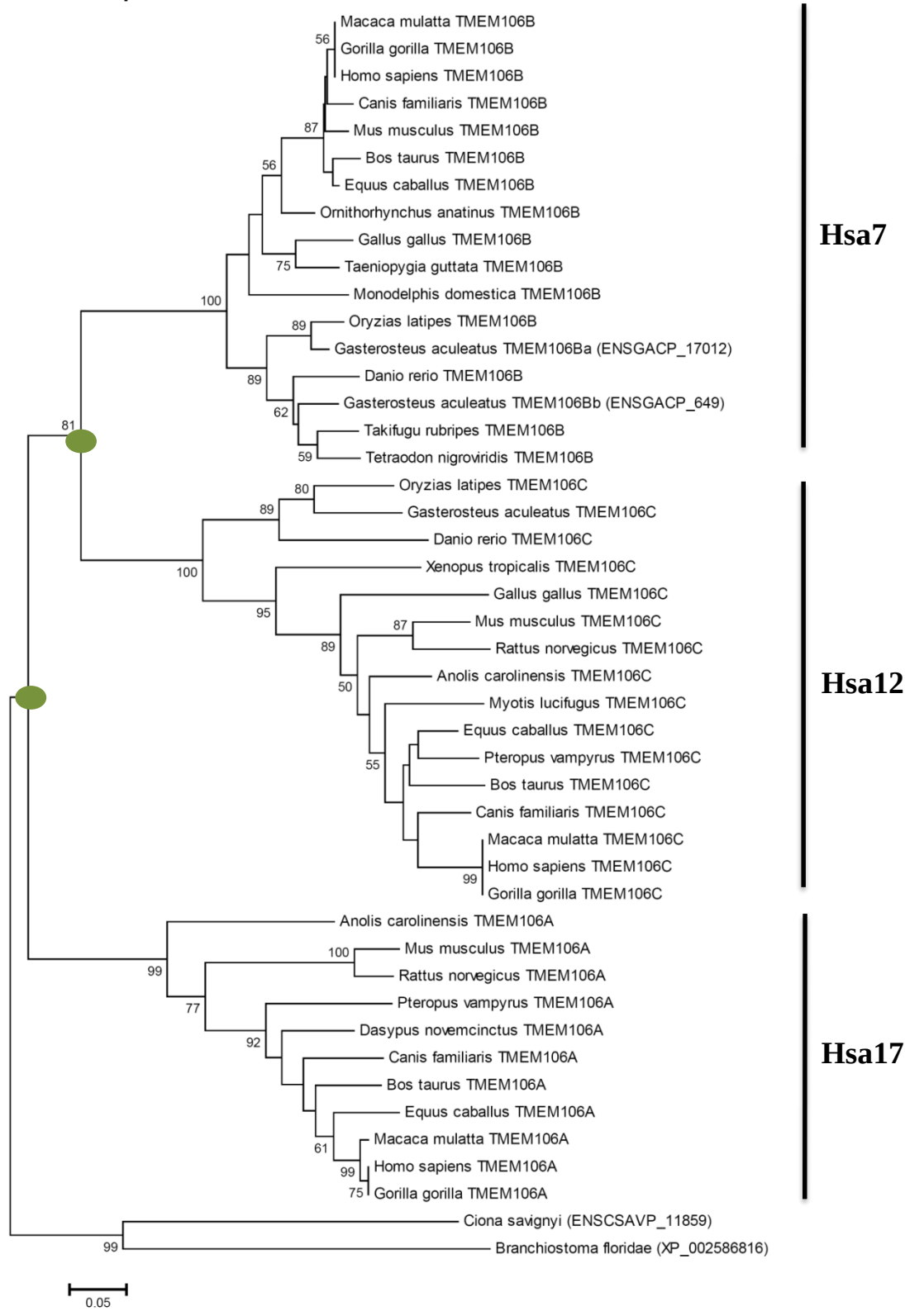
Receptor activity modifying protein-RAMP



Phylogenetic tree of RAMP family.

Neighbor-Joining tree of the RAMP 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 RAMP1B by our group.

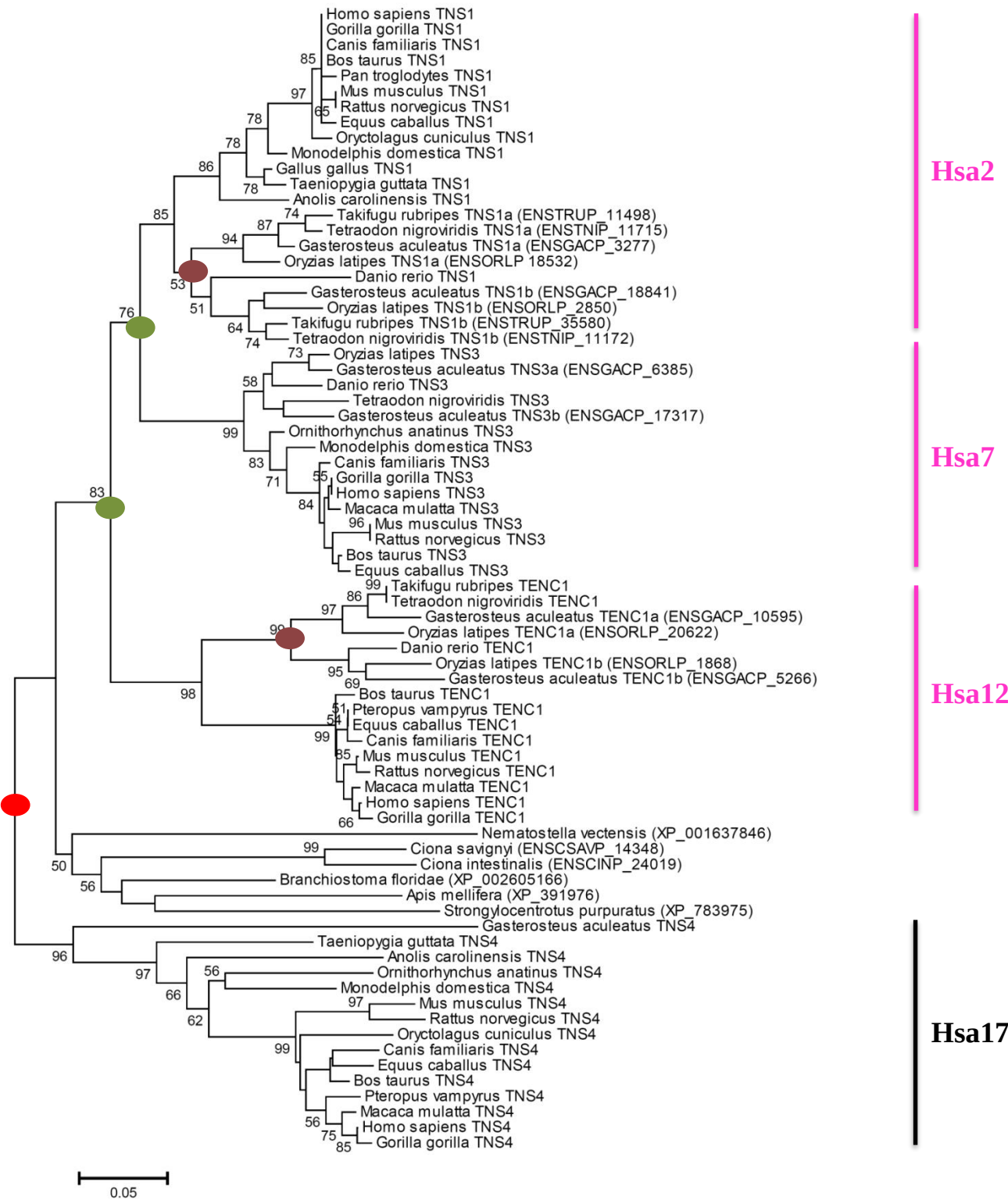
Transmembrane protein 106-TMEM106



Phylogenetic tree of TMEM106 family.

Neighbor-Joining tree of the TMEM106 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.

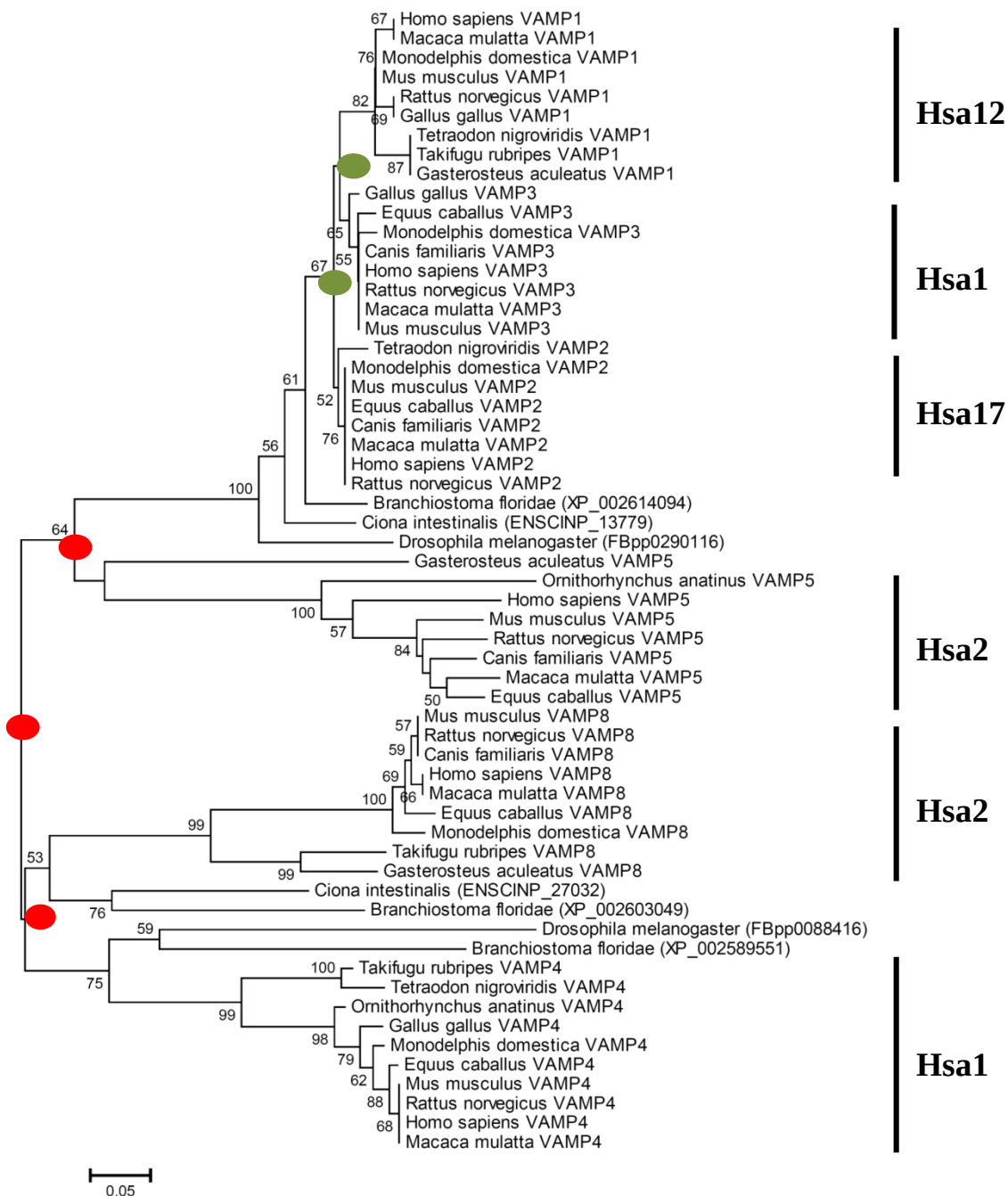
Tensin -TNS



Phylogenetic tree of TNS family.

Neighbor-Joining tree of the TNS 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.

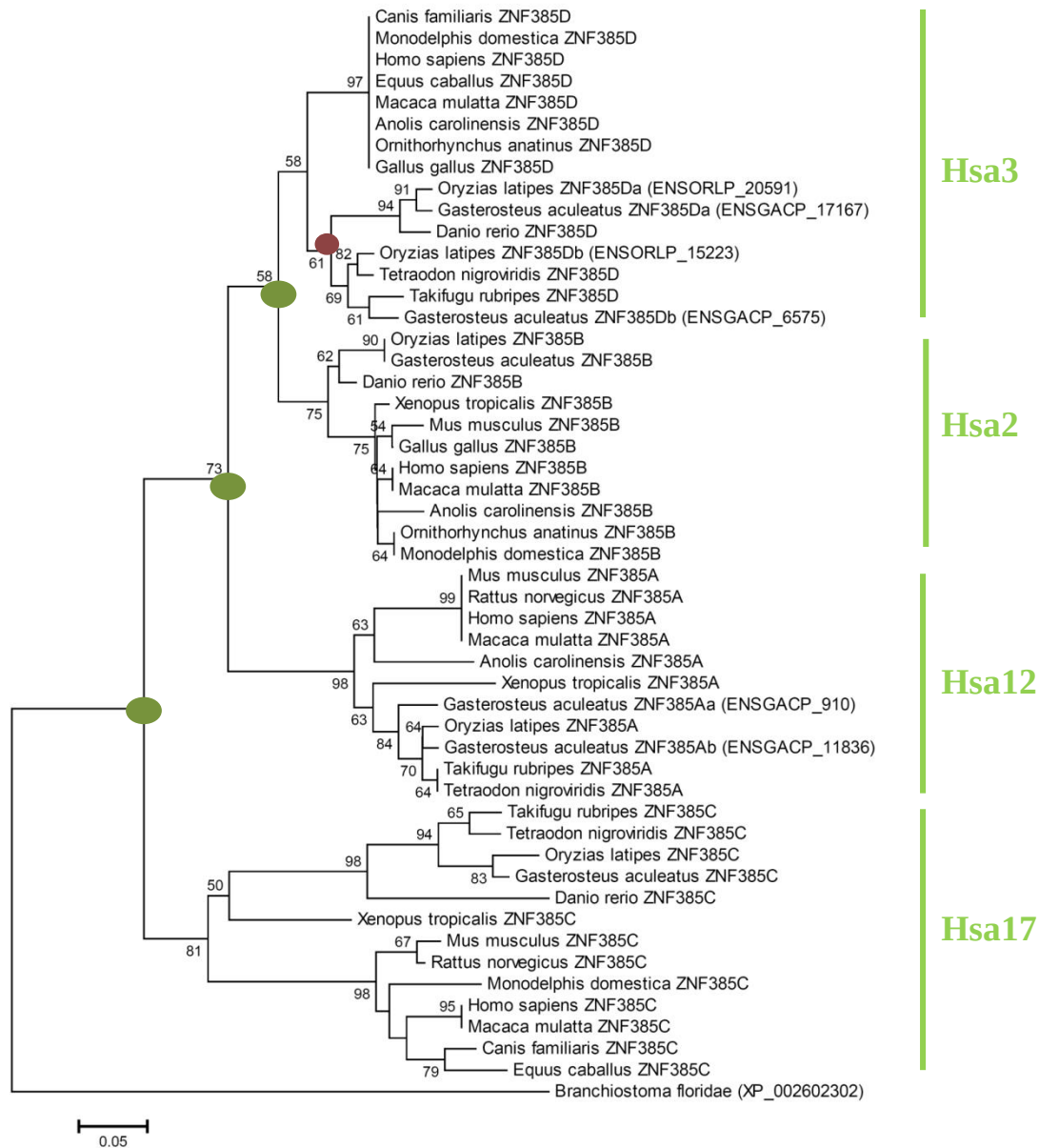
Vesicle-associated membrane protein-VAMP



Phylogenetic tree of VAMP family.

Neighbor-Joining tree of the VAMP 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.

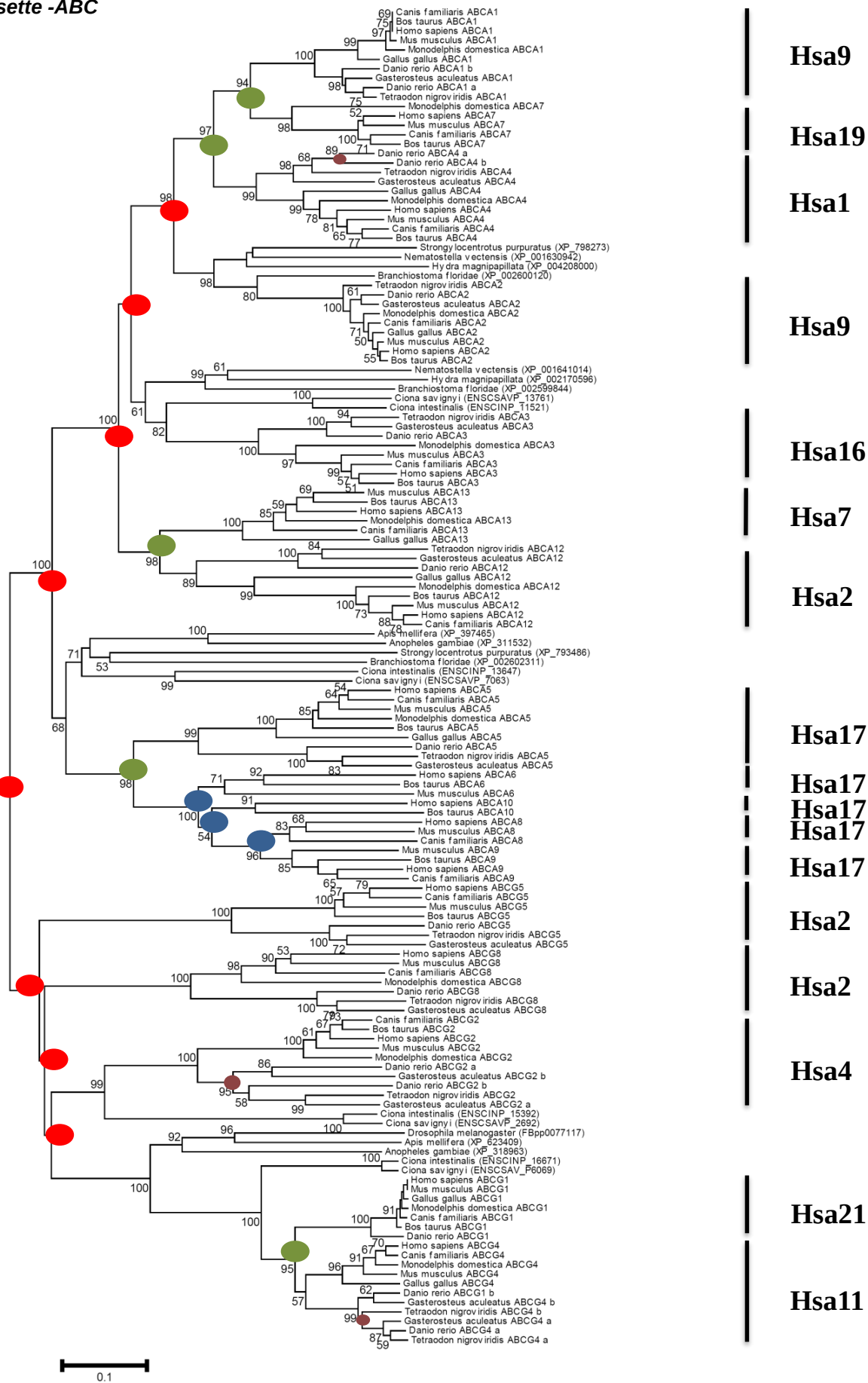
Zinc finger protein 385-ZNF385



Phylogenetic tree of ZNF385 family.

Neighbor-Joining tree of the ZNF385 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.

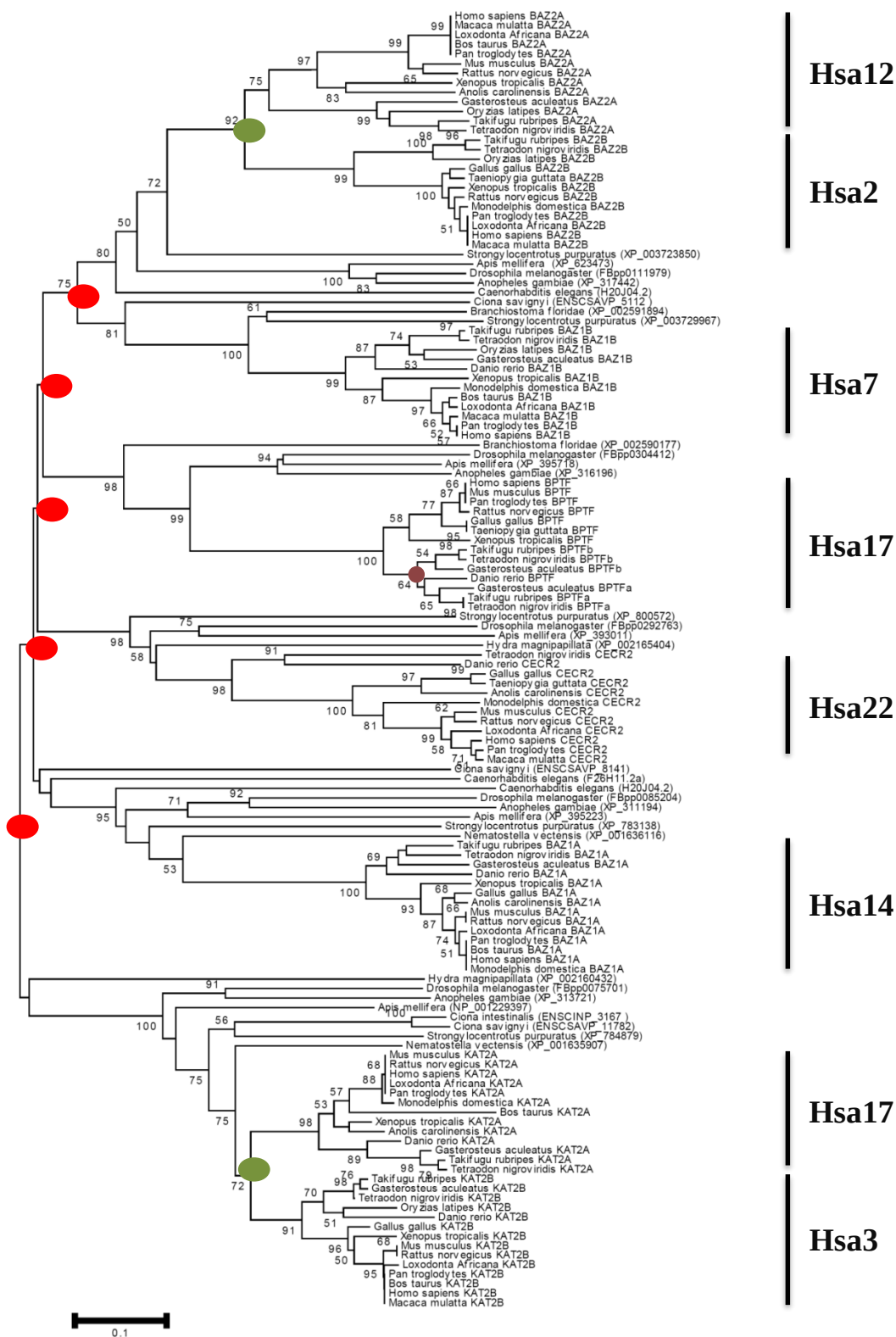
ATP binding cassette -ABC



Phylogenetic tree of ABC family.

Neighbor-Joining tree of the ABC 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.

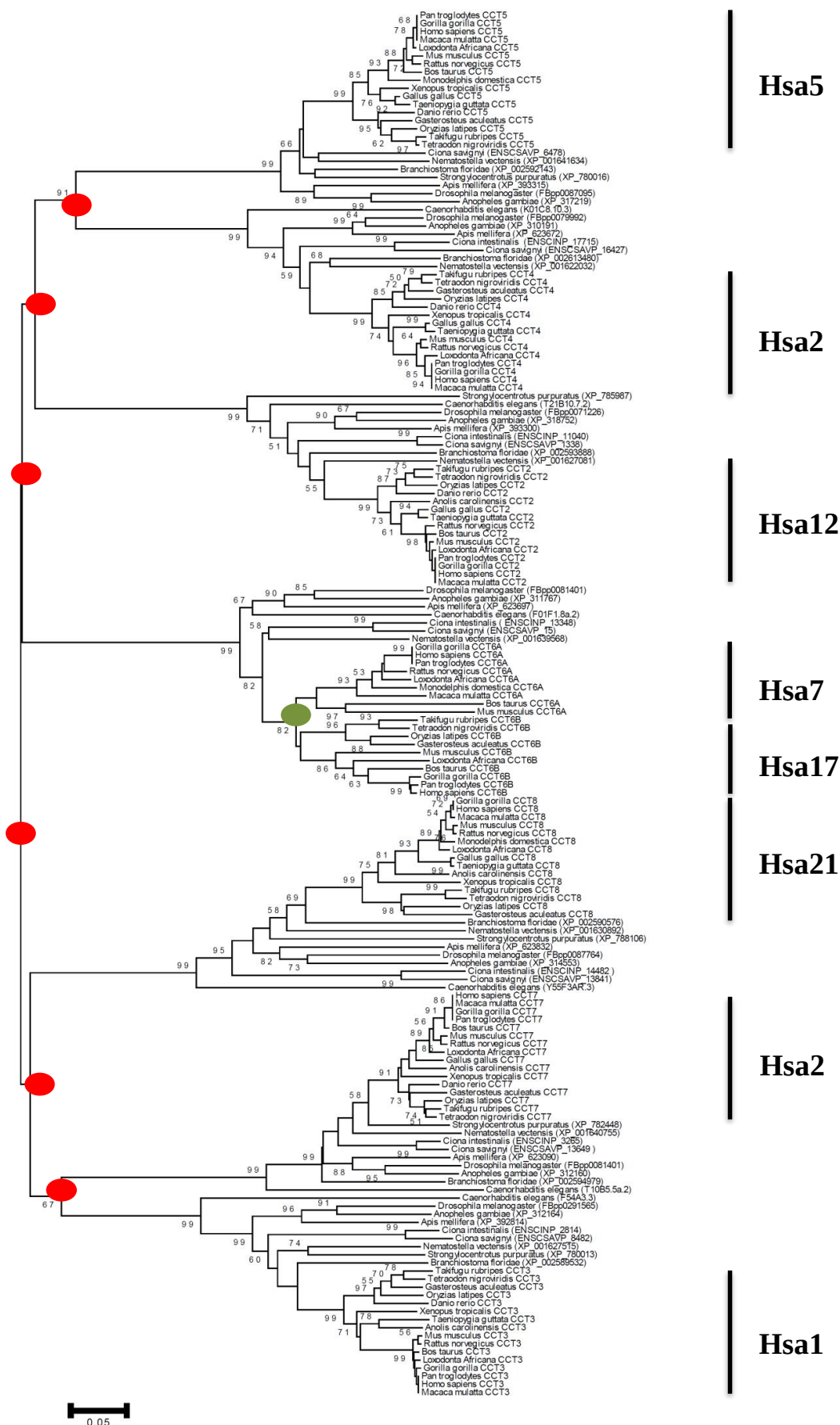
Bromodomain adjacent to zinc finger domain-BAZ



Phylogenetic tree of BAZ family.

Neighbor-Joining tree of the BAZ 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.

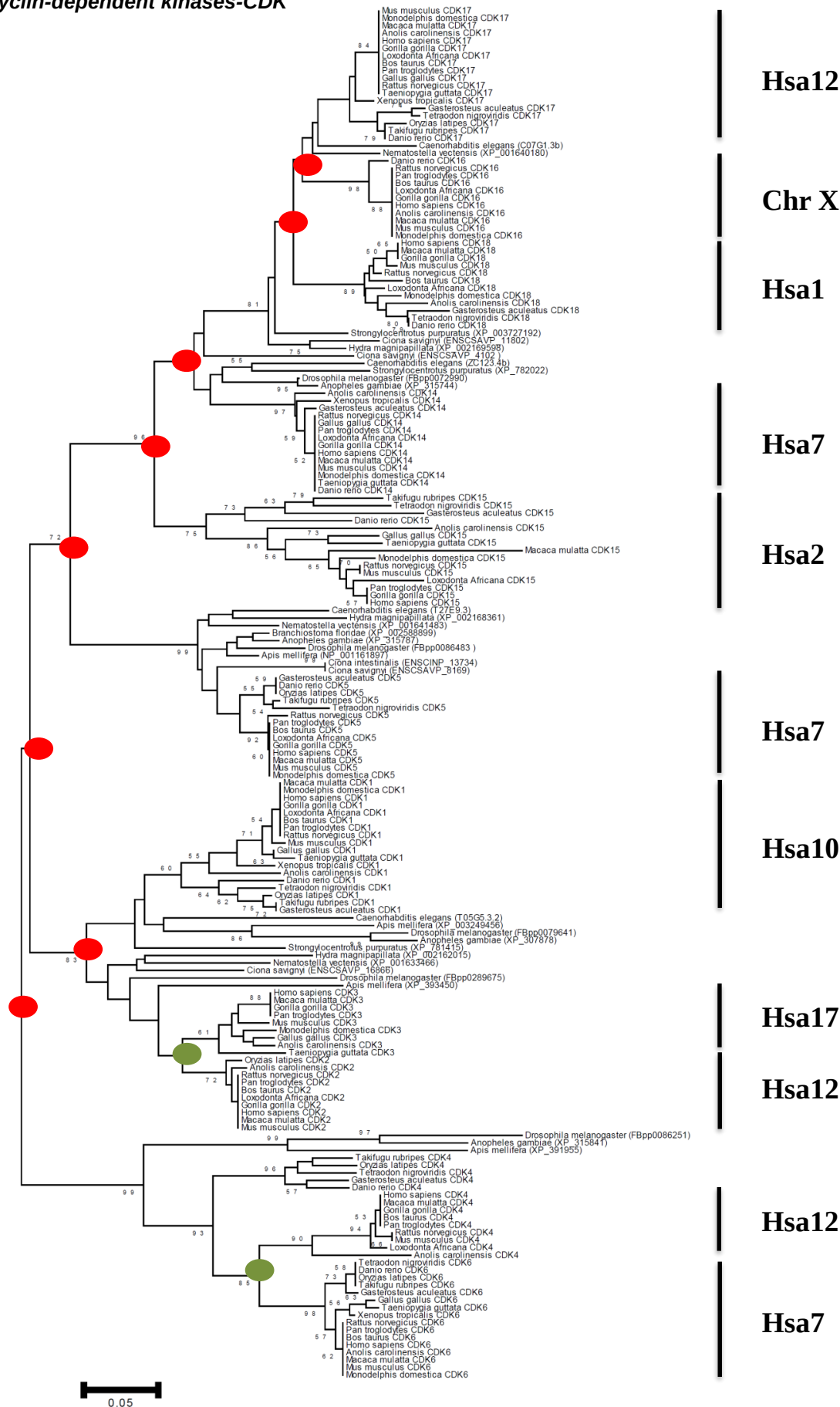
Chaperonin containing T-complex polypeptide 1-CCT



Phylogenetic tree of CCT family.

Neighbor-Joining tree of the CCT 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.

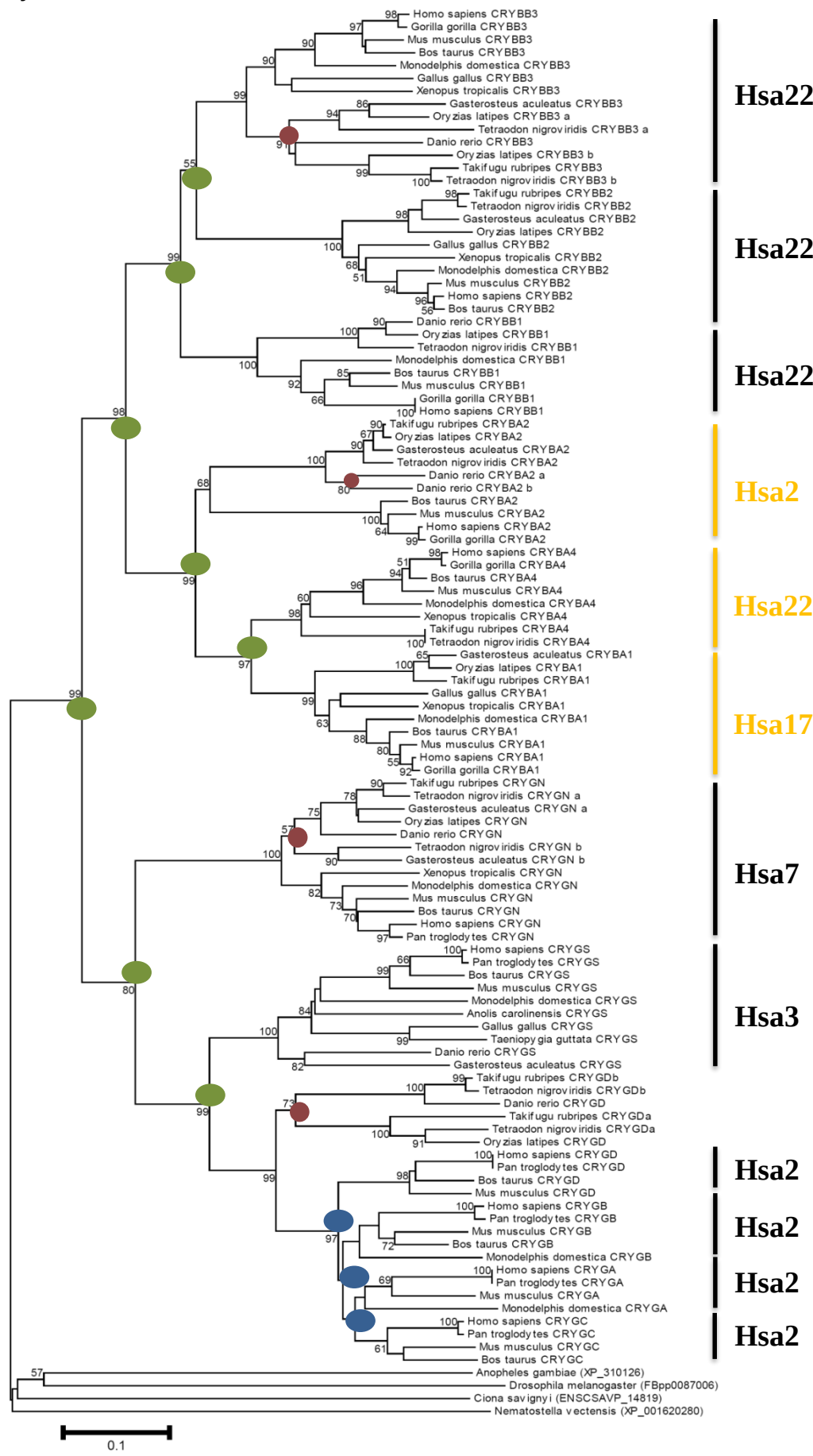
Cyclin-dependent kinases-CDK



Phylogenetic tree of CDK family.

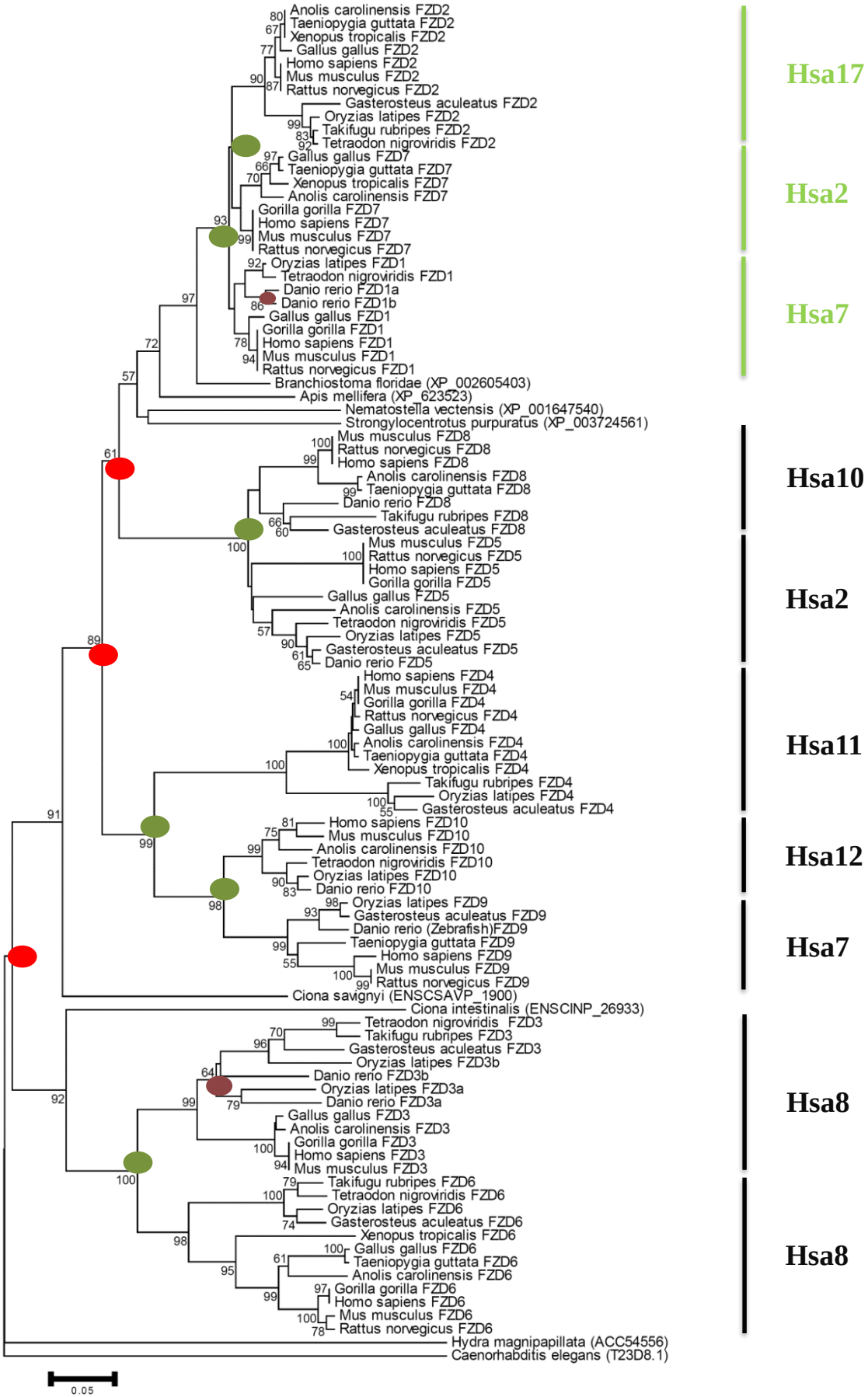
Neighbor-Joining tree of the CDK family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution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

Crystallin family-CRY



Phylogenetic tree of CRY family.

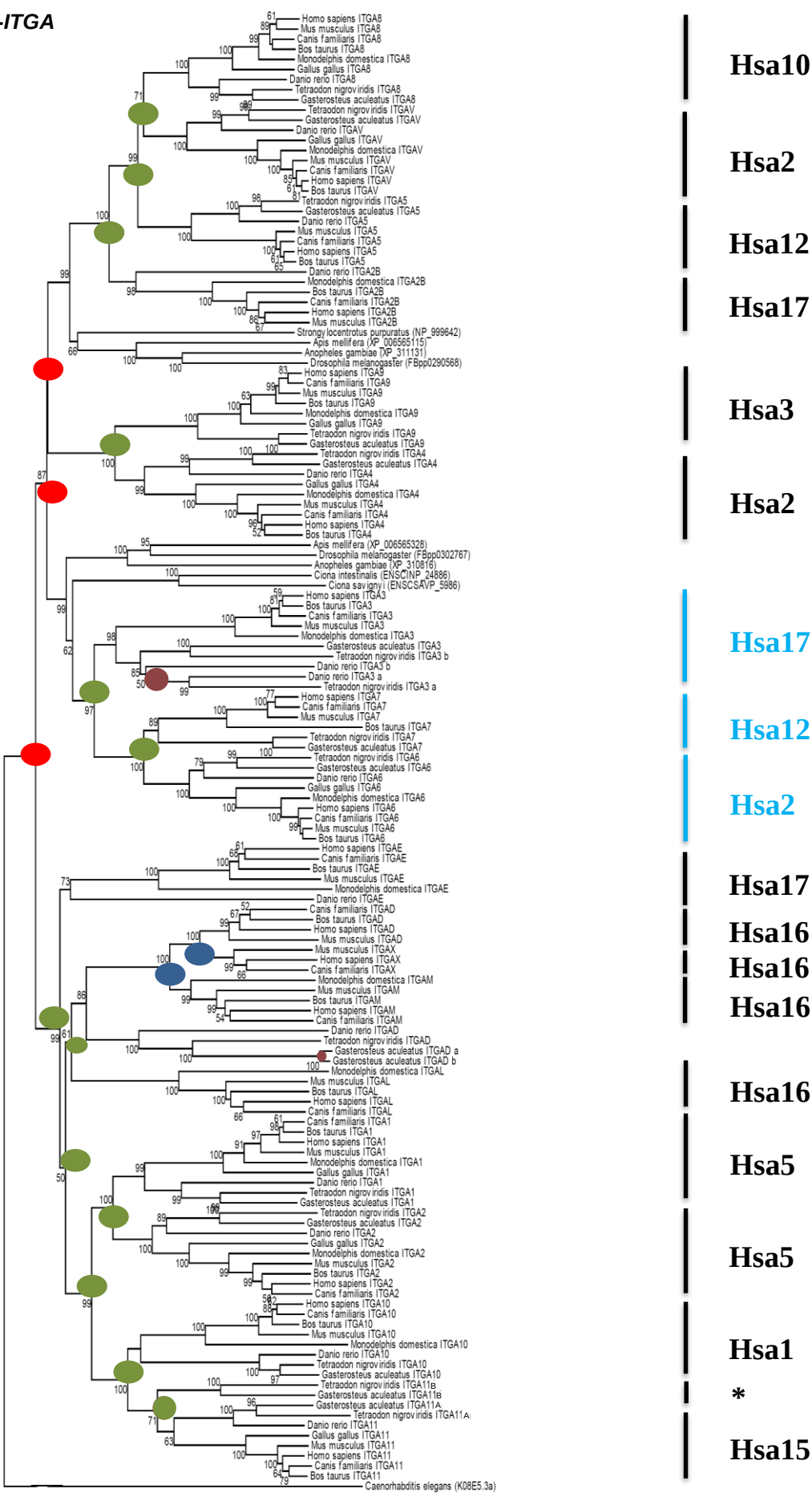
Neighbor-Joining tree of the CRY family members. Uncorrected p-distance was used. Complete-deletion option was used. Numbers on branches represent bootstrap values (based on 1000 replications) supporting that branch; only the values $\geq 50\%$ are presented here. Scale bar shows amino acid substitution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



Phylogenetic tree of FZD family.

Neighbor-Joining tree of the FZD 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.

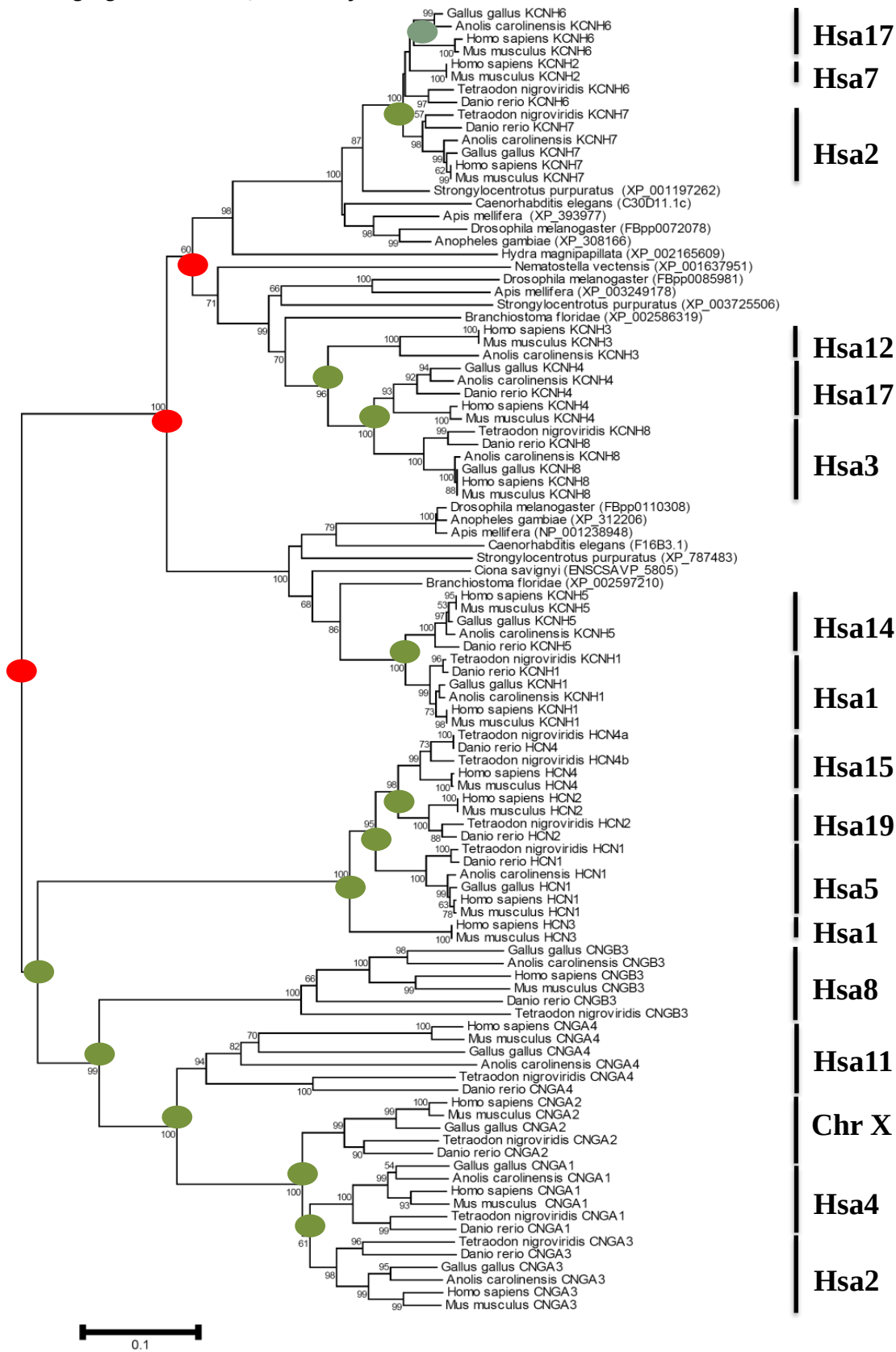
Integrin alpha family-ITGA



Phylogenetic tree of ITGA family.

Neighbor-Joining tree of the ITGA 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 ITGA11B by our group.

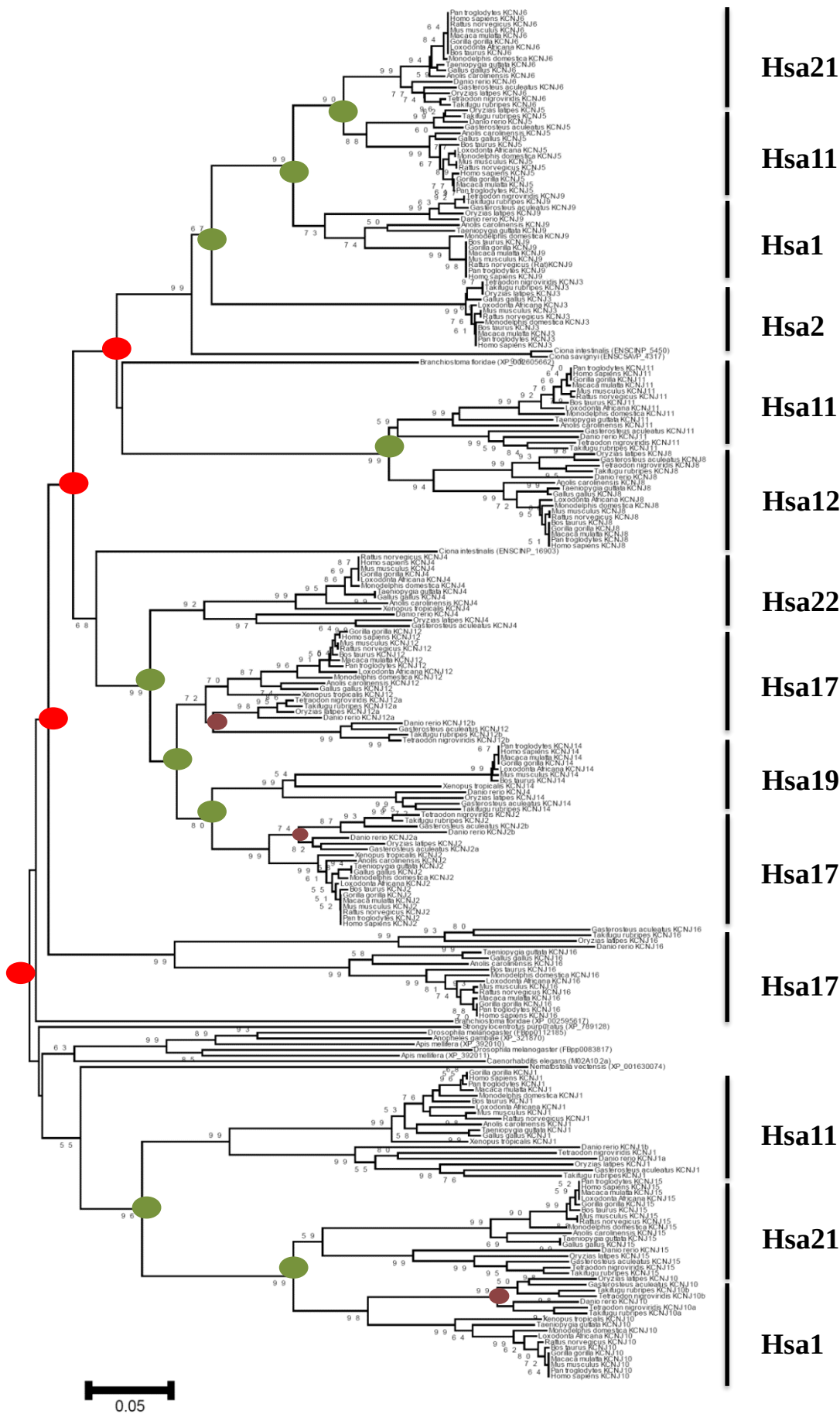
Potassium voltage-gated channel, subfamily H-KCNH



Phylogenetic tree of KCNH family.

Neighbor-Joining tree of the KCNH 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.

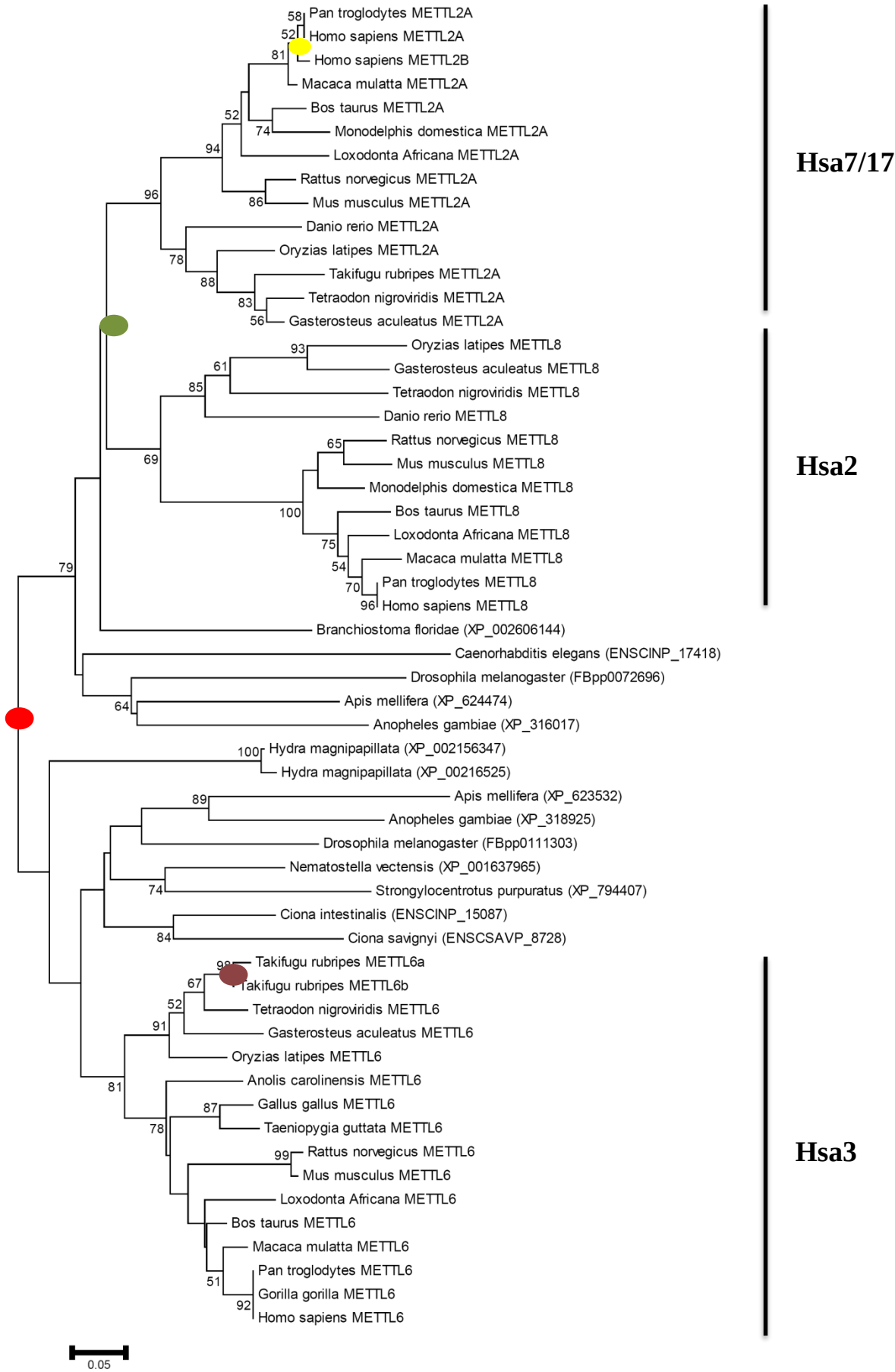
Potassium inwardly-rectifying channel, subfamily J-KCNJ



Phylogenetic tree of KCNJ family.

Neighbor-Joining tree of the KCNJ 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.

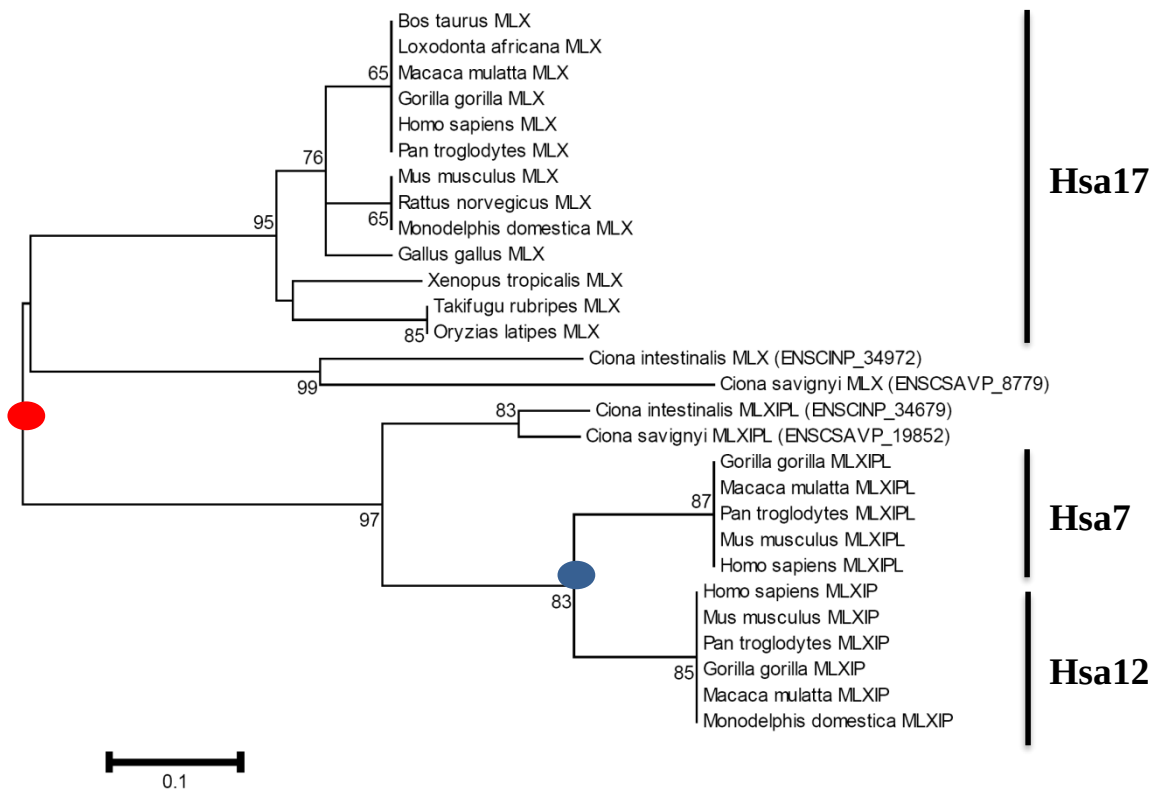
Methyltransferase -METTL



Phylogenetic tree of METTL family.

Neighbor-Joining tree of the METTL 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.

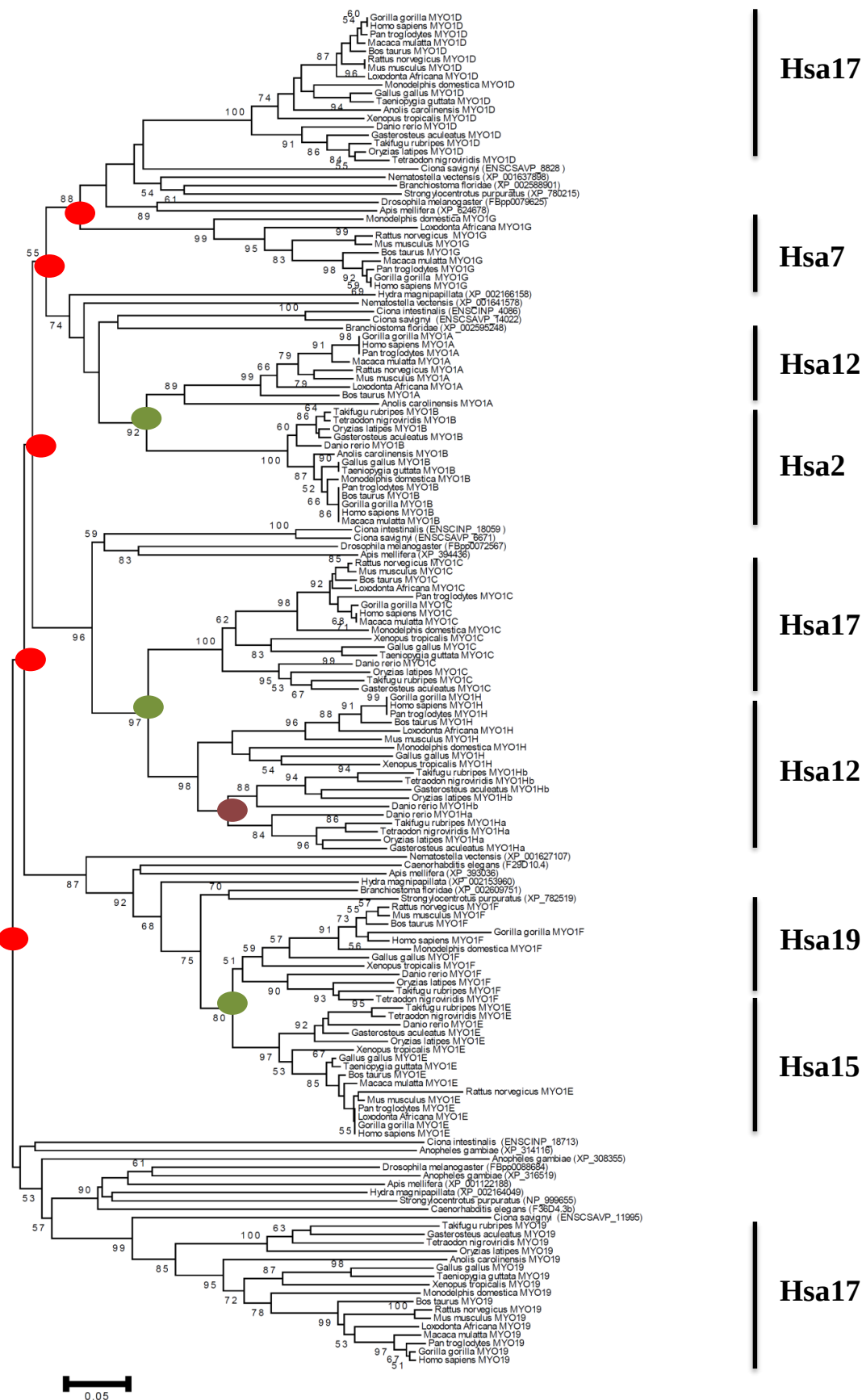
MLX interacting protein-MLX



Phylogenetic tree of MLX family.

Neighbor-Joining tree of the MLX 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.

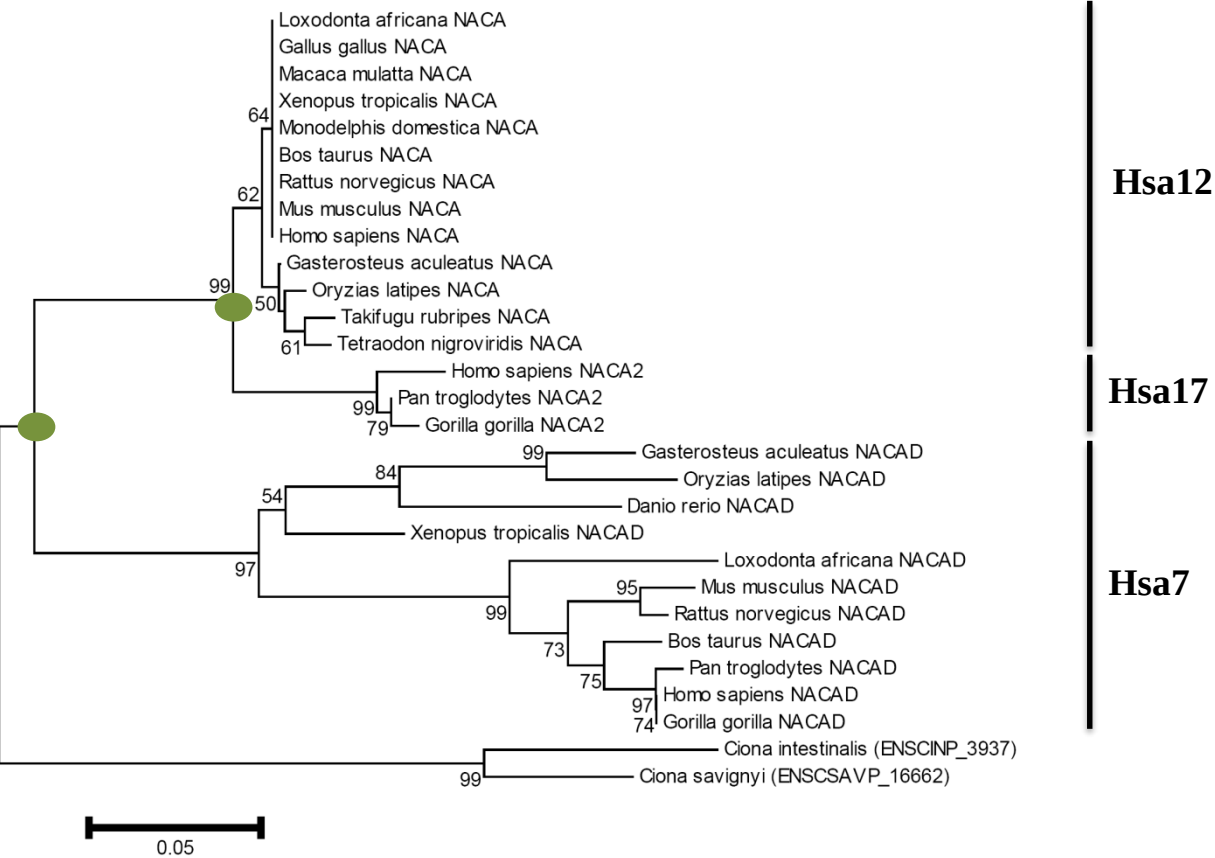
Myosin 1-MYO1



Phylogenetic tree of MYO1 family.

Neighbor-Joining tree of the MYO1 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.

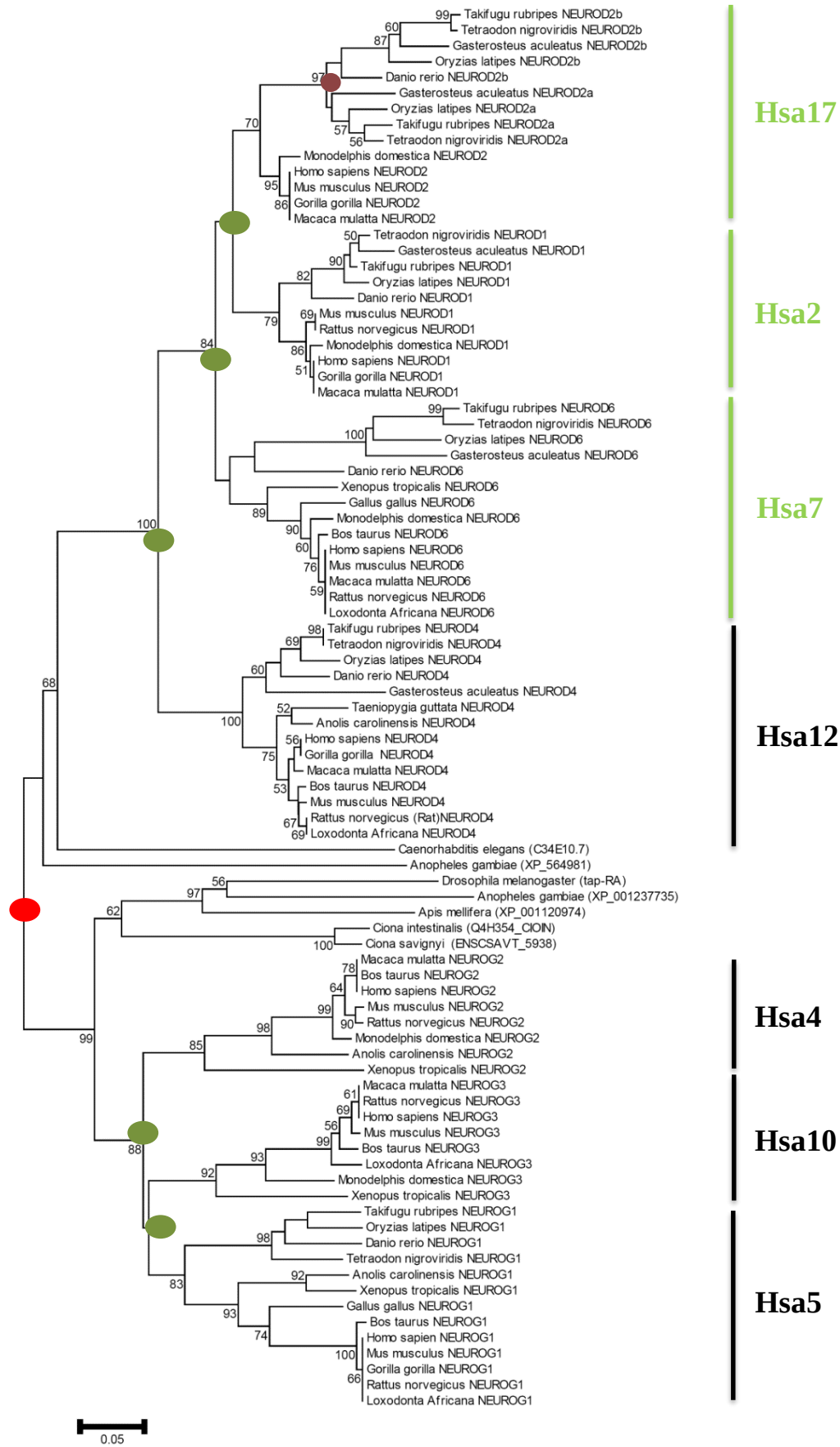
NAC alpha domain proteins-NACA



Phylogenetic tree of NACA family.

Neighbor-Joining tree of the NACA 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.

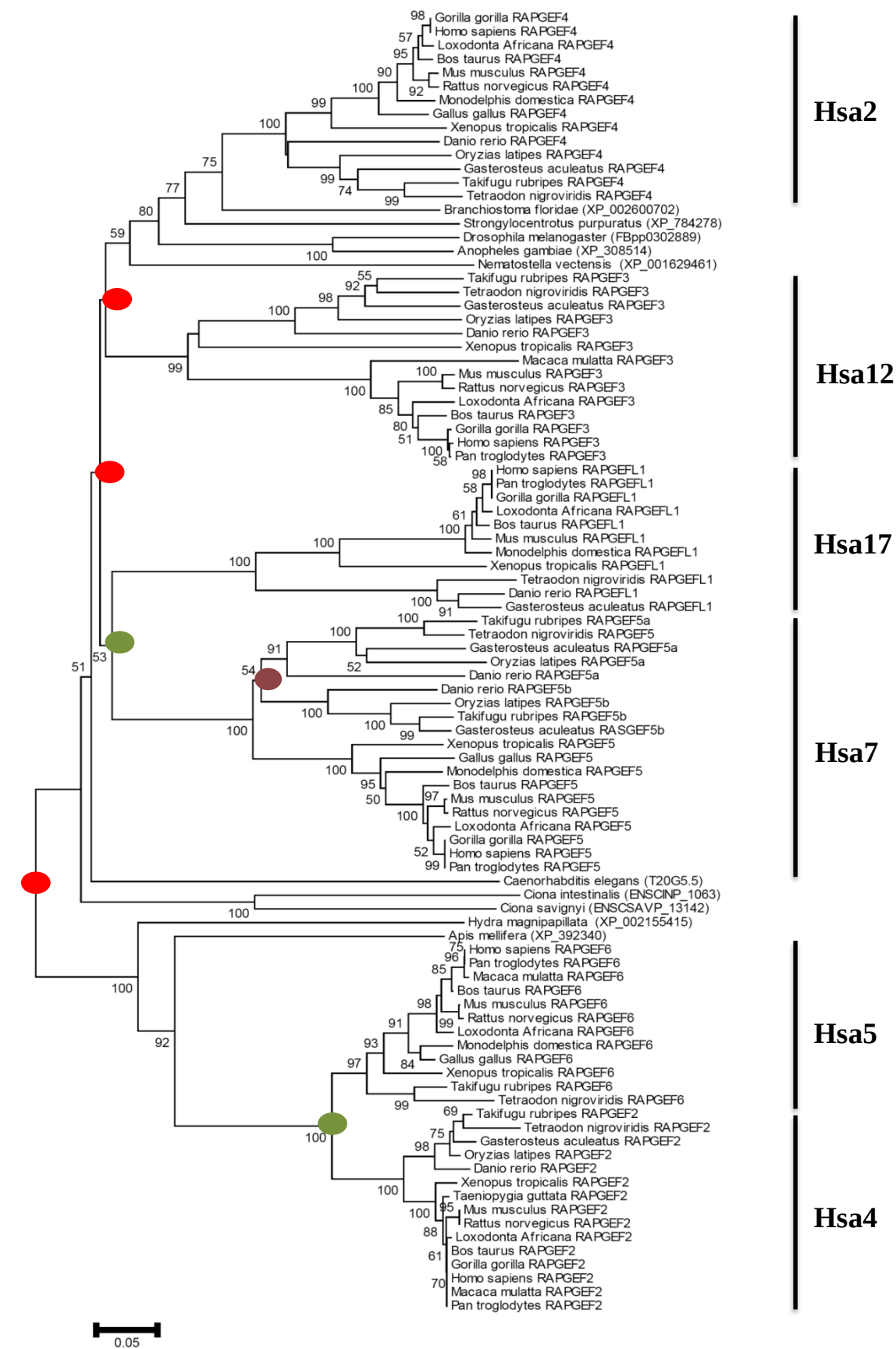
Neurogenic differentiation- NEUROD



Phylogenetic tree of NEUROD family.

Neighbor-Joining tree of the NEUROD 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.

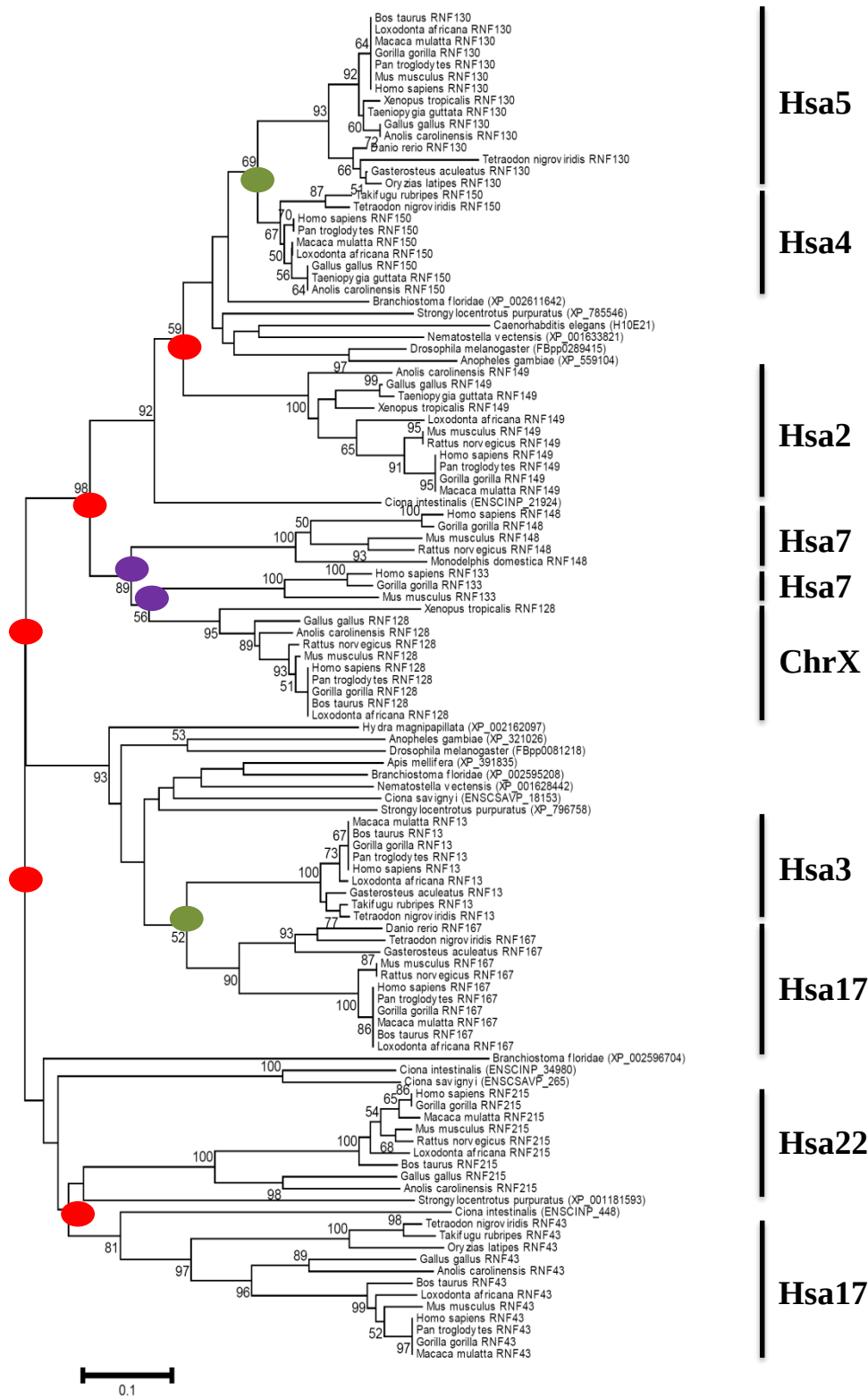
Rap guanine nucleotide exchange factor-RAPGEF



Phylogenetic tree of RAPGEF family.

Neighbor-Joining tree of the RAPGEF 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.

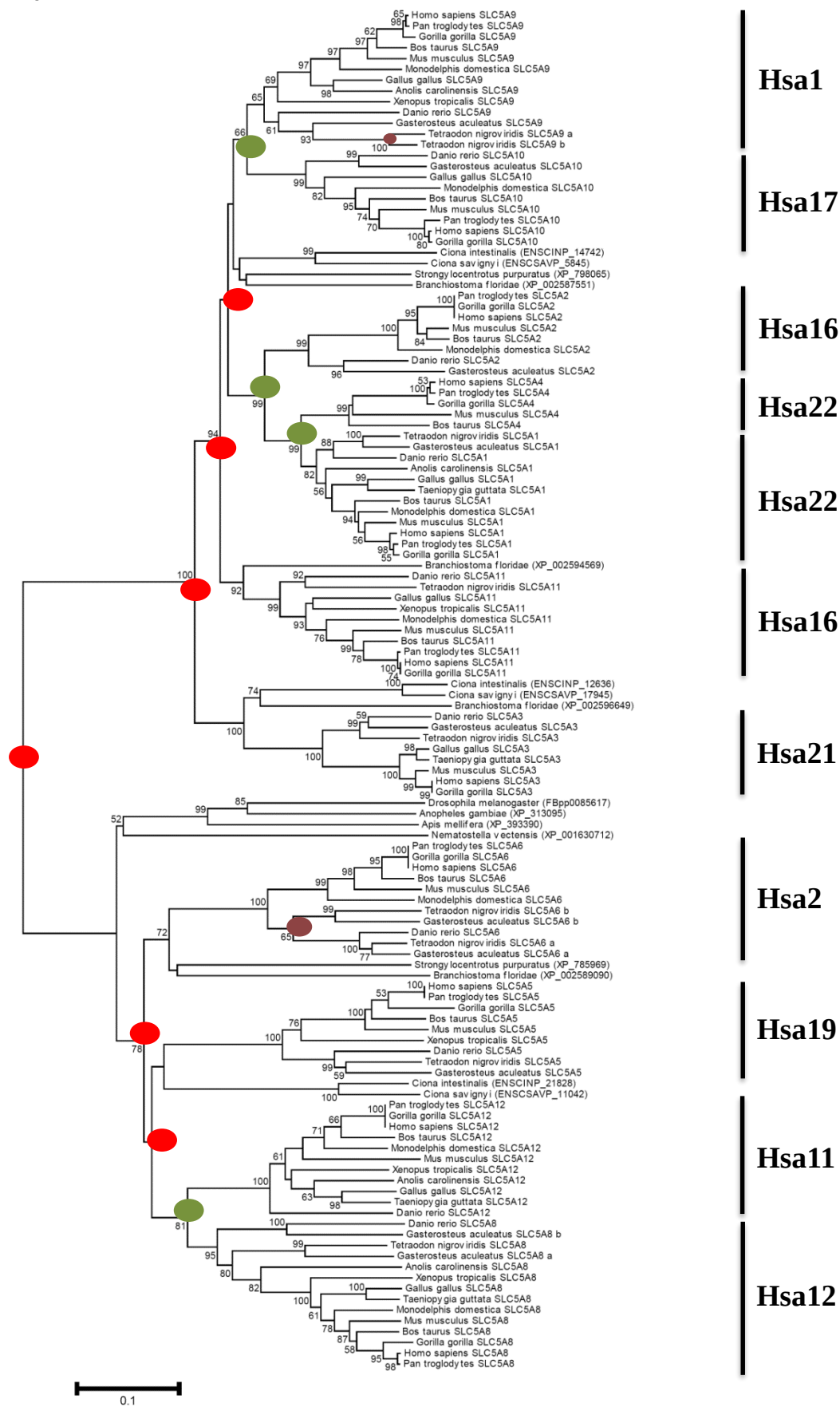
Ring finger protein family-RNF



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.

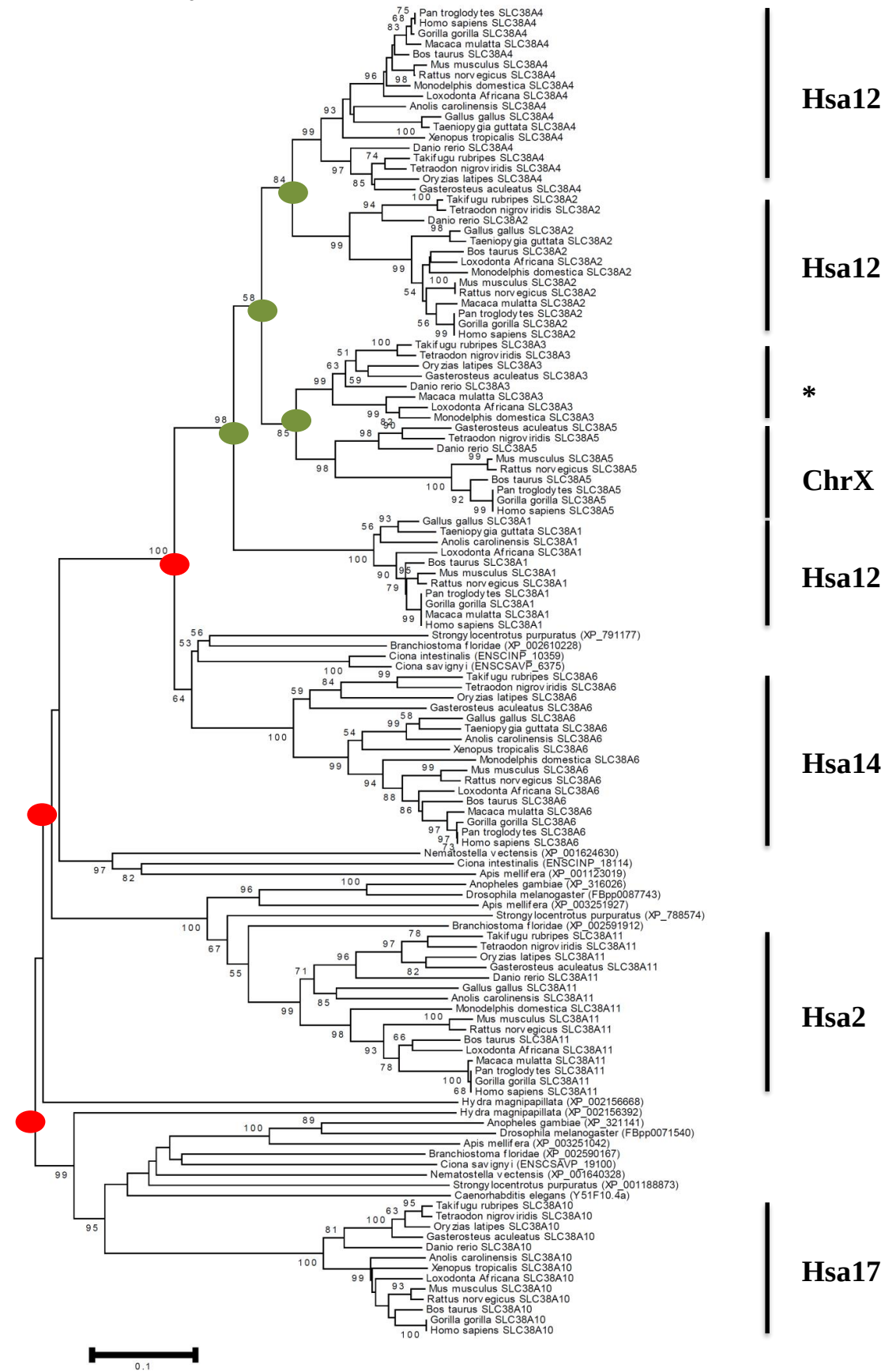
Solute carrier family 5 A-SLC5A



Phylogenetic tree of SLC5A family.

Neighbor-Joining tree of the SLC5A 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.

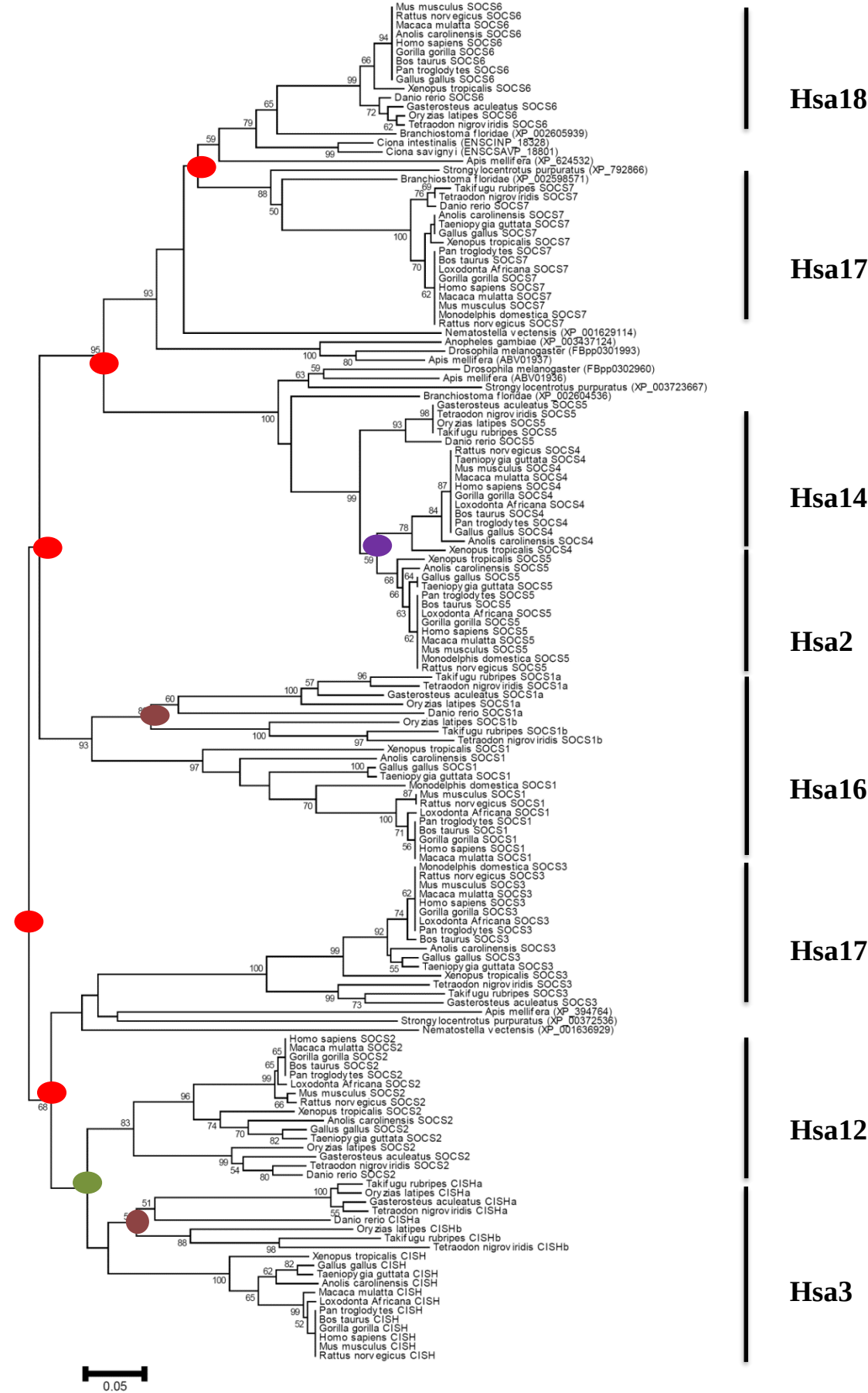
Solute carrier family 38 A-**SLC38A**



Phylogenetic tree of SLC38A family.

Neighbor-Joining tree of the SLC38A 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 which is missing in humans named as SLC38A3 by our group.

Suppressor of cytokine signaling-SOCS



Phylogenetic tree of SCOS family.

Neighbor-Joining tree of the SCOS 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.