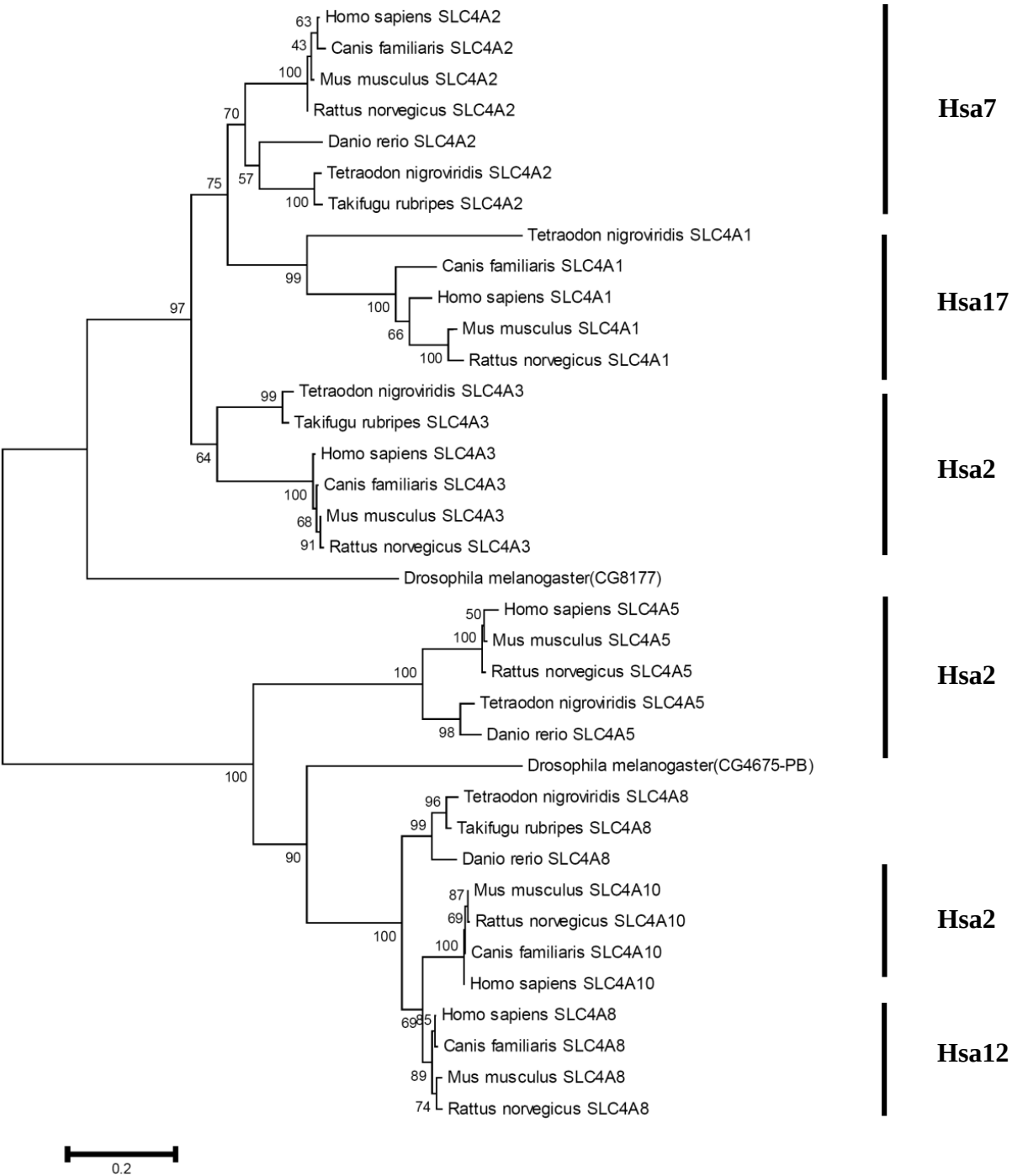


**Maximum Likelihood Trees of gene families residing on
chromosomes 2, 7, 12 and 17.**

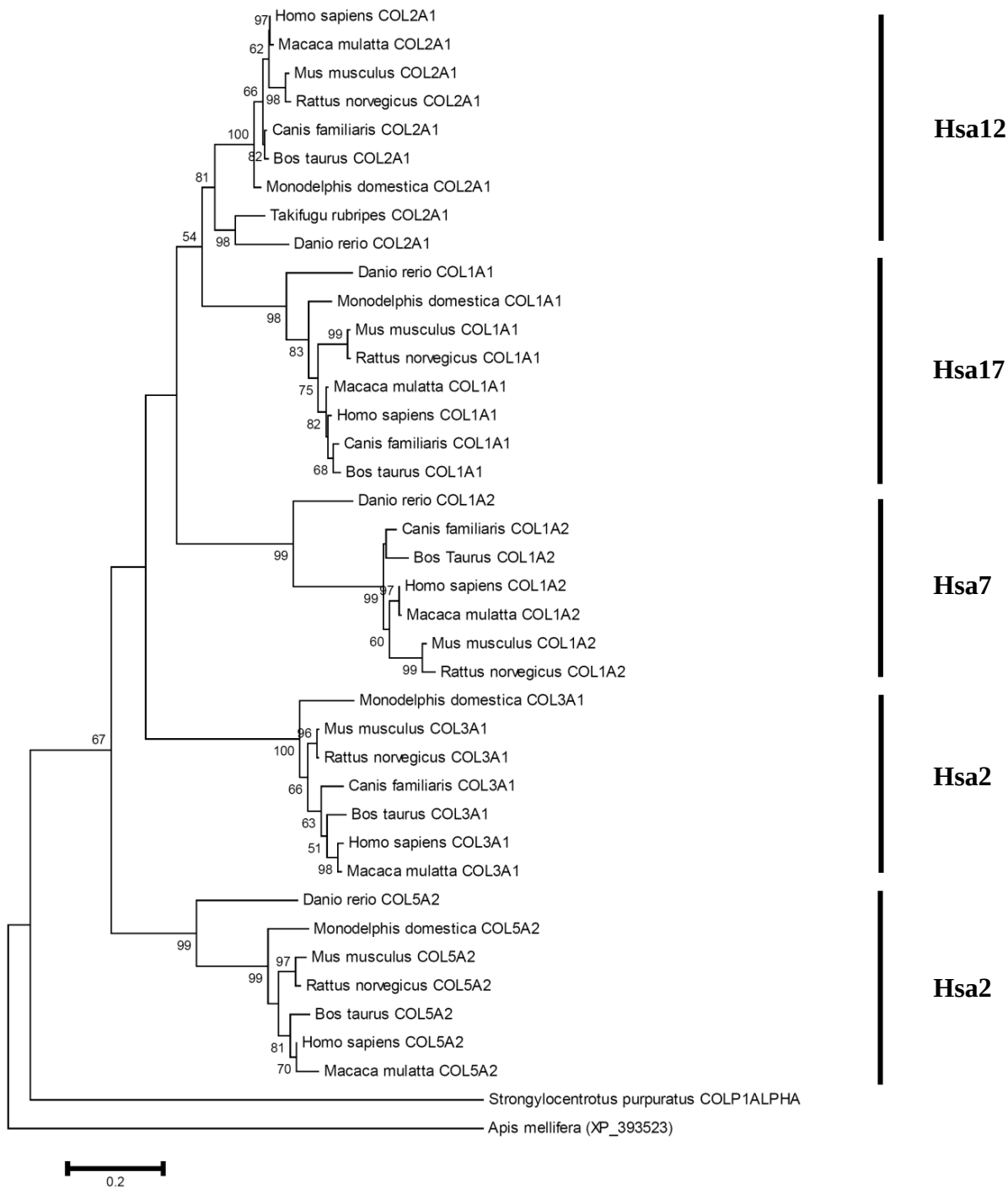
Anion exchanger family SLC4A (AE)-SLC4A



Phylogenetic tree of SLC4A family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the WAG model. The tree with the highest log likelihood (-8729.8710) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 1.6050)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 36 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 442 positions in the final dataset..

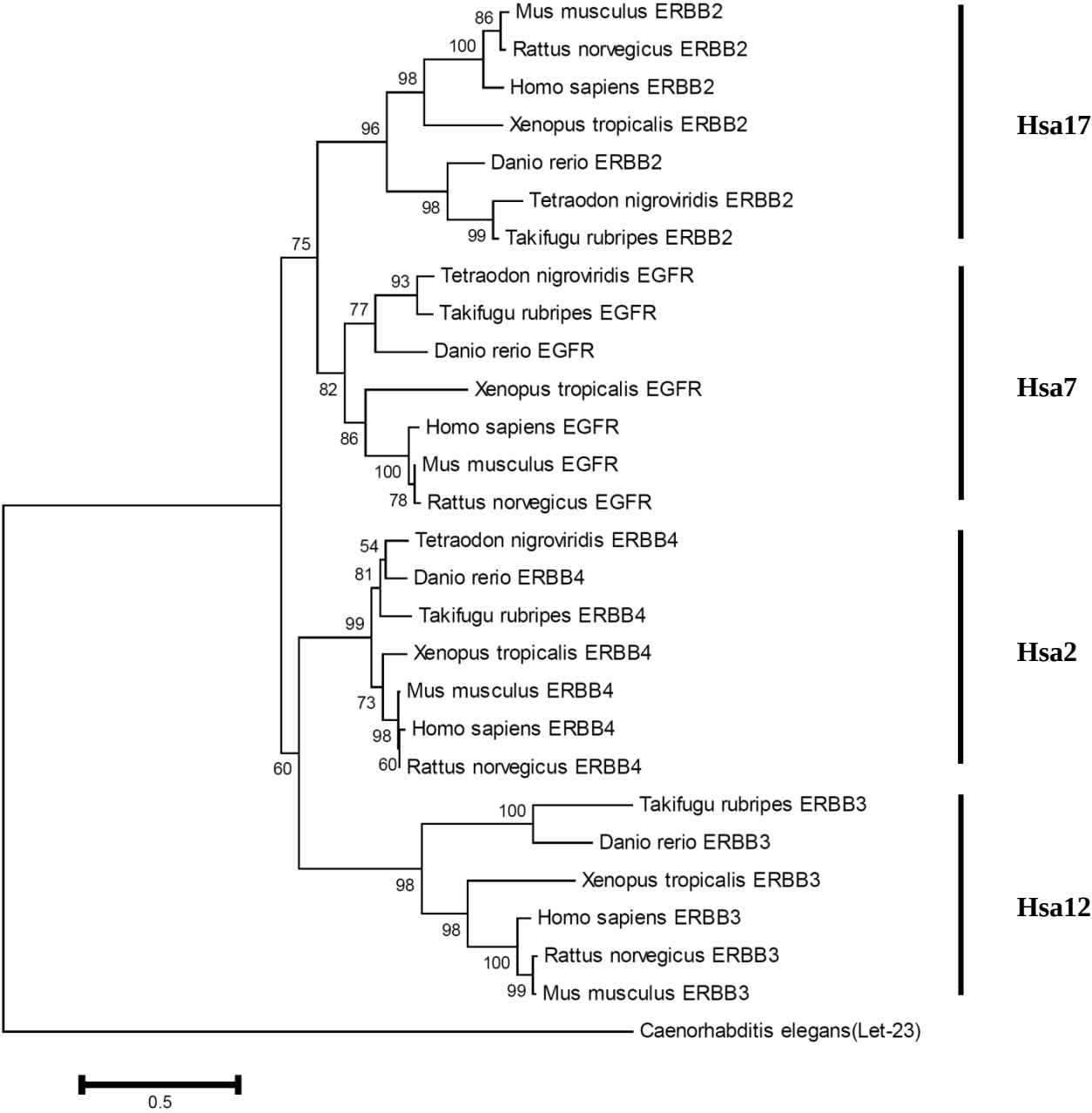
Fibrillar collagen family -COL



Phylogenetic tree of COL family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the WAG model. The tree with the highest log likelihood (-6504.3105) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 1.5379)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 40 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 303 positions in the final dataset.

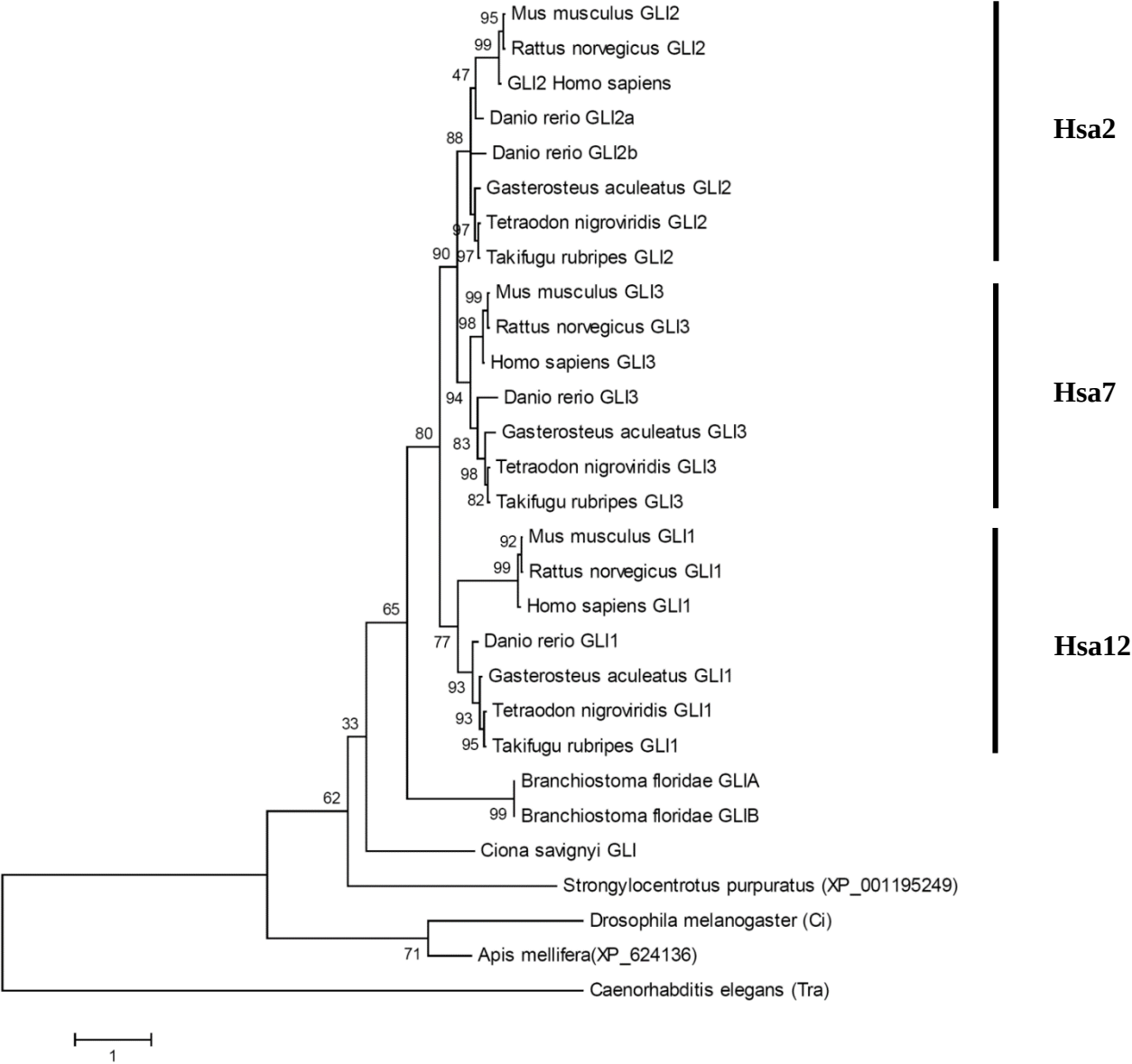
ERBB receptor protein-tyrosine kinase-ERBB



Phylogenetic tree of ERBB family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the WAG model. The tree with the highest log likelihood (-7989.1170) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 1.7171)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 28 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 311 positions in the final dataset.

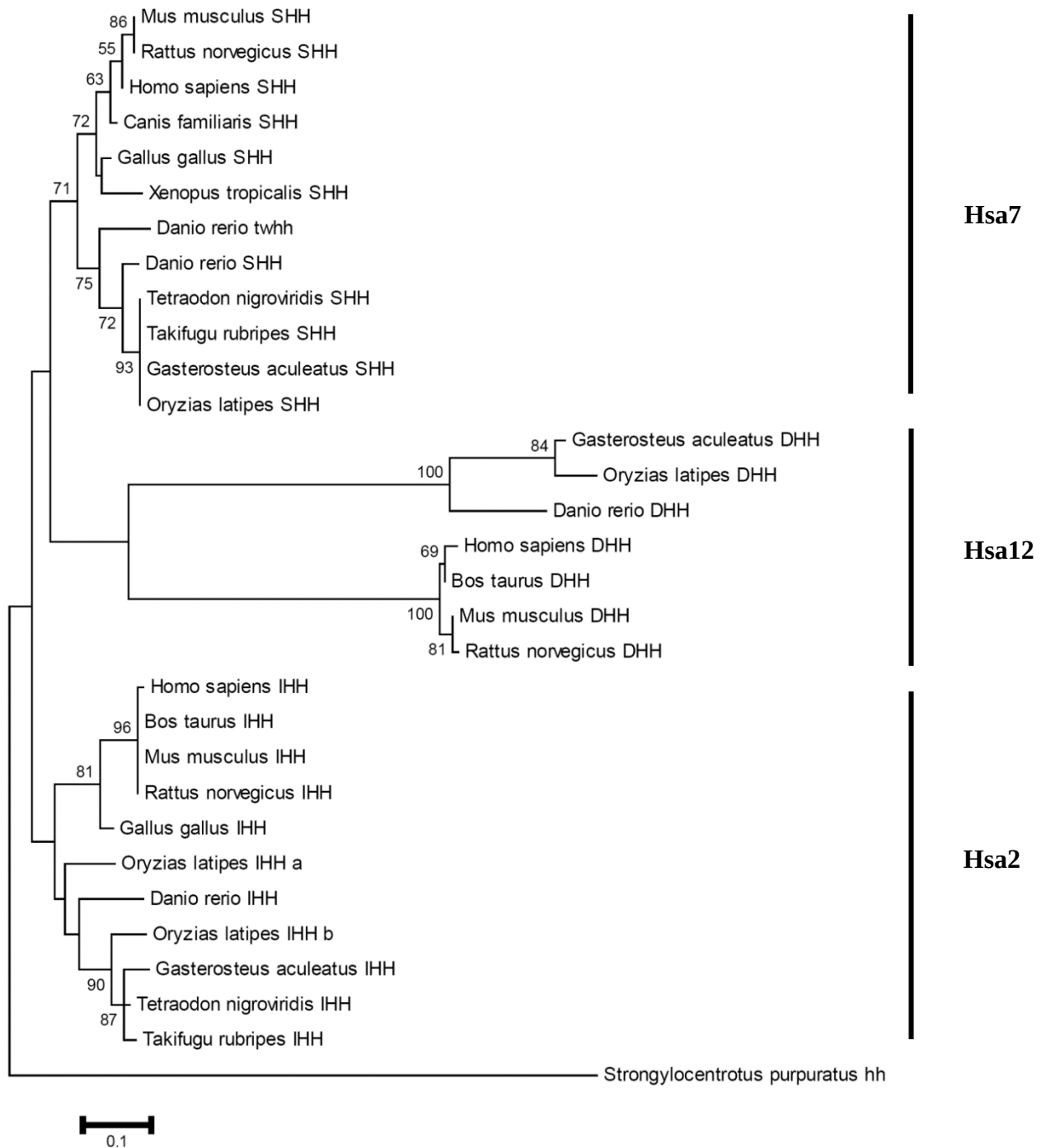
GLI zinc-finger protein family-GLI



Phylogenetic tree of GLI family.

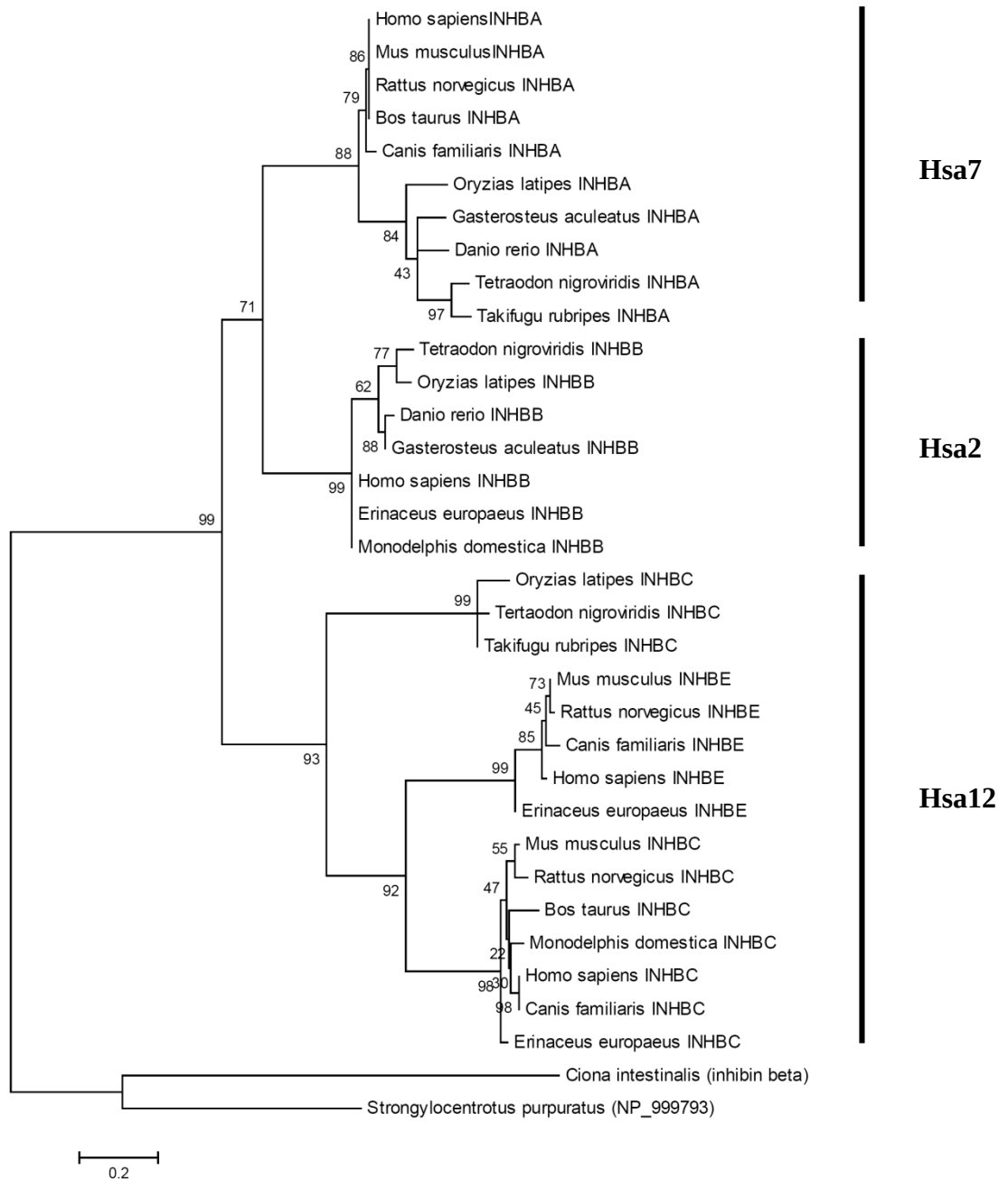
The evolutionary history was inferred by using the Maximum Likelihood method based on the WAG model. The tree with the highest log likelihood (-7926.3664) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 1.2112)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 29 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 307 positions in the final dataset.

Hedgehog family -HH



Phylogenetic tree of HH family.

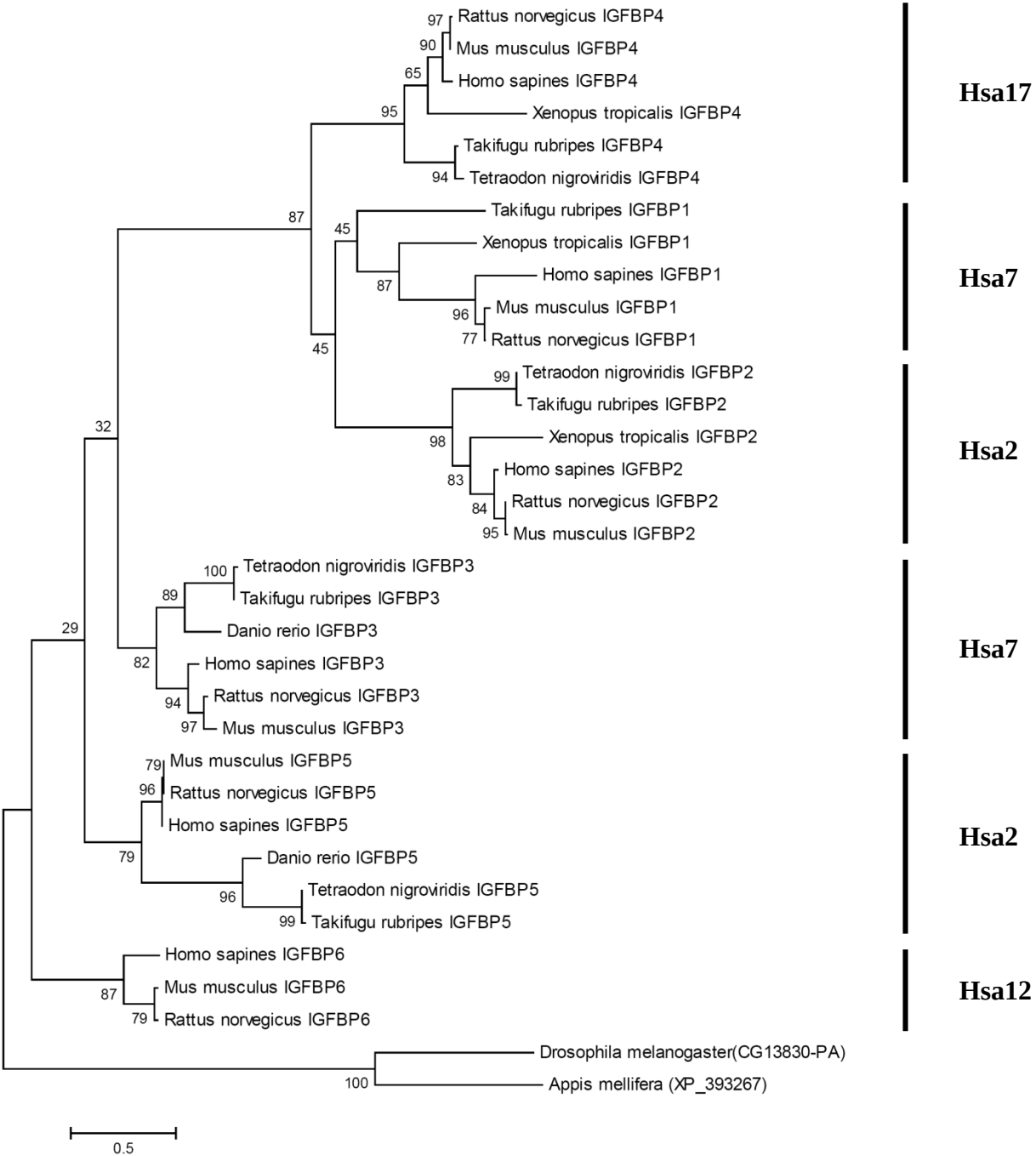
The evolutionary history was inferred by using the Maximum Likelihood method based on the WAG model. The tree with the highest log likelihood (-1931.6394) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 0.6190)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 31 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 168 positions in the final dataset.



Phylogenetic tree of INHB family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the WAG model. The tree with the highest log likelihood (-2051.7290) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 1.7184)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 34 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 105 positions in the final dataset.

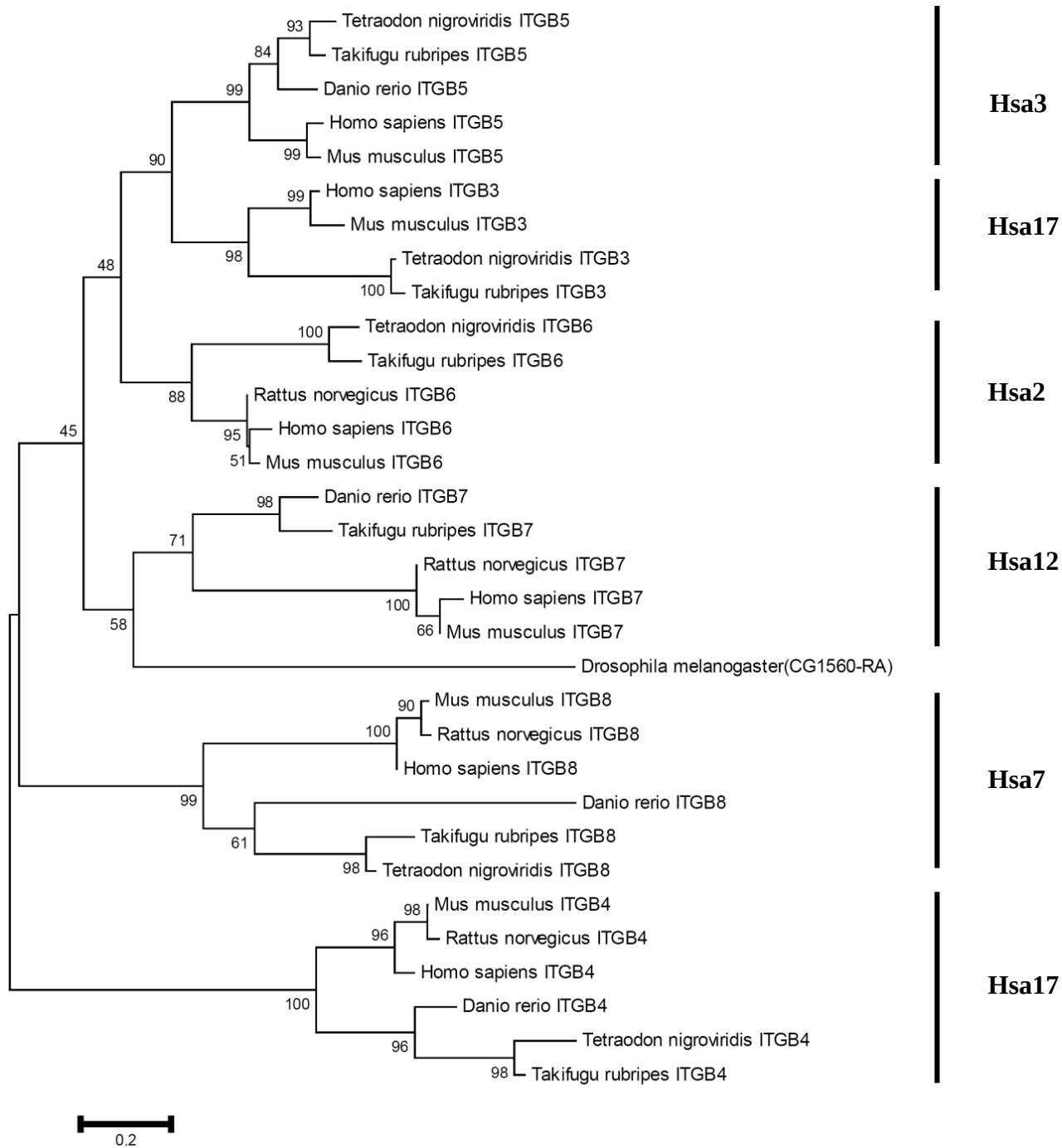
Insulin-like growth factor-binding protein-IGFBP



Phylogenetic tree of IGFBP family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the WAG model. The tree with the highest log likelihood (-4444.6045) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 2.8837)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 34 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 120 positions in the final dataset.

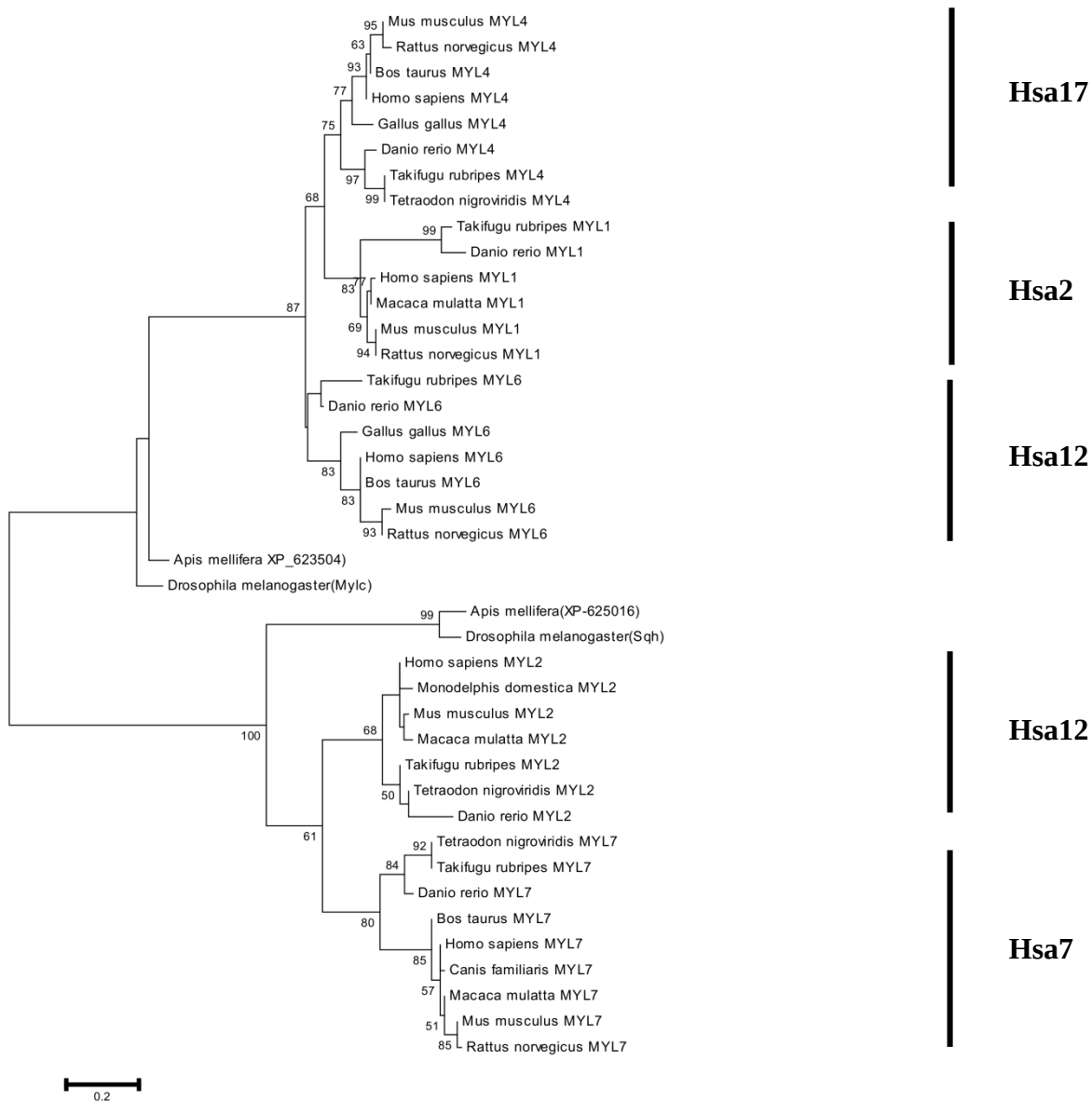
Integrin beta chain family-ITGB



Phylogenetic tree of ITGB family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the WAG model. The tree with the highest log likelihood (-5427.7026) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 1.6485)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 32 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 177 positions in the final dataset.

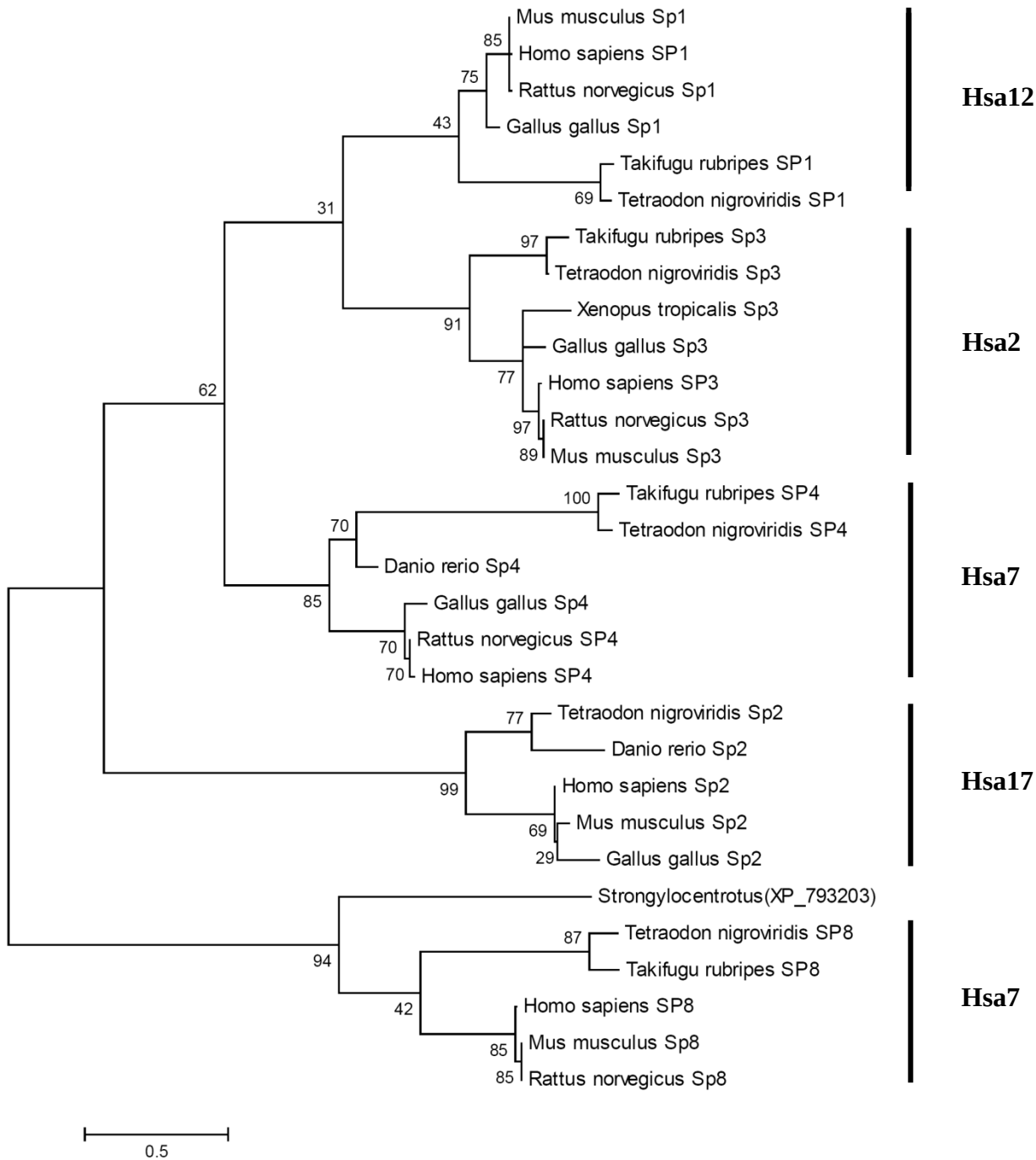
Myosin light chain-MYL



Phylogenetic tree of MYL family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the WAG model .The tree with the highest log likelihood (-1916.3575) is shown ; only the values $\geq 50\%$ are shown here. The percentage of trees in which the associated taxa clustered together is shown next to the branches A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 6.6982)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 41 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 85 positions in the final dataset.

Sp1 c2h2-type zinc-finger protein family-SP



Phylogenetic tree of SP family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the WAG model. The tree with the highest log likelihood (-3508.6500) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 4.8511)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 30 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 108 positions in the final dataset.

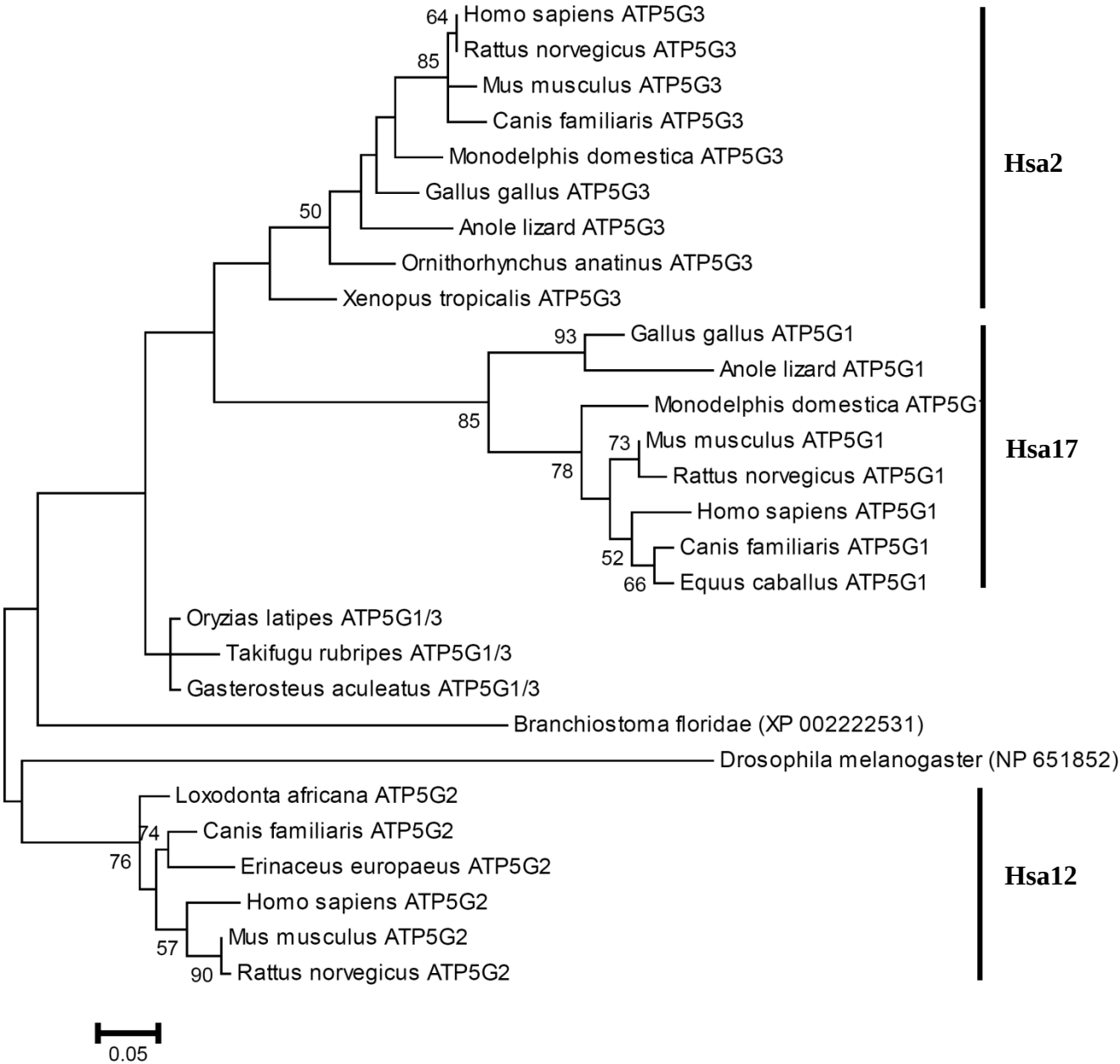
Zinc finger protein, subfamily 1A-ZNFN1A



Phylogenetic tree of ZNFN1A family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the WAG model. The tree with the highest log likelihood (-4473.4235) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 3.6164)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 20 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 313 positions in the final dataset..

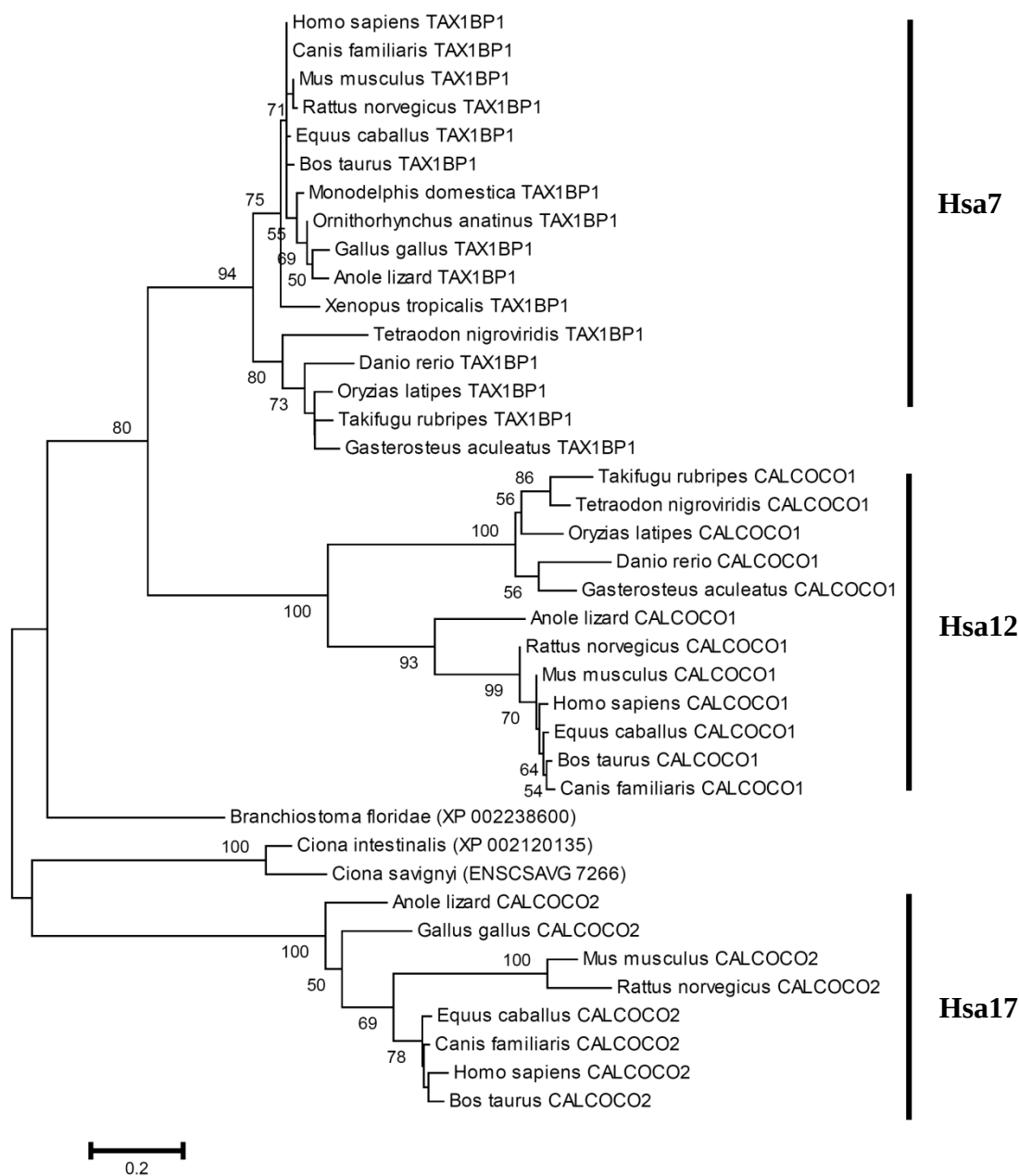
ATP synthase, H⁺ transporting, mitochondrial F0 complex-ATP5G



Phylogenetic tree of ATP5G family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the WAG model. The tree with the highest log likelihood (-1670.8340) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 0.3768)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 28 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 115 positions in the final dataset.

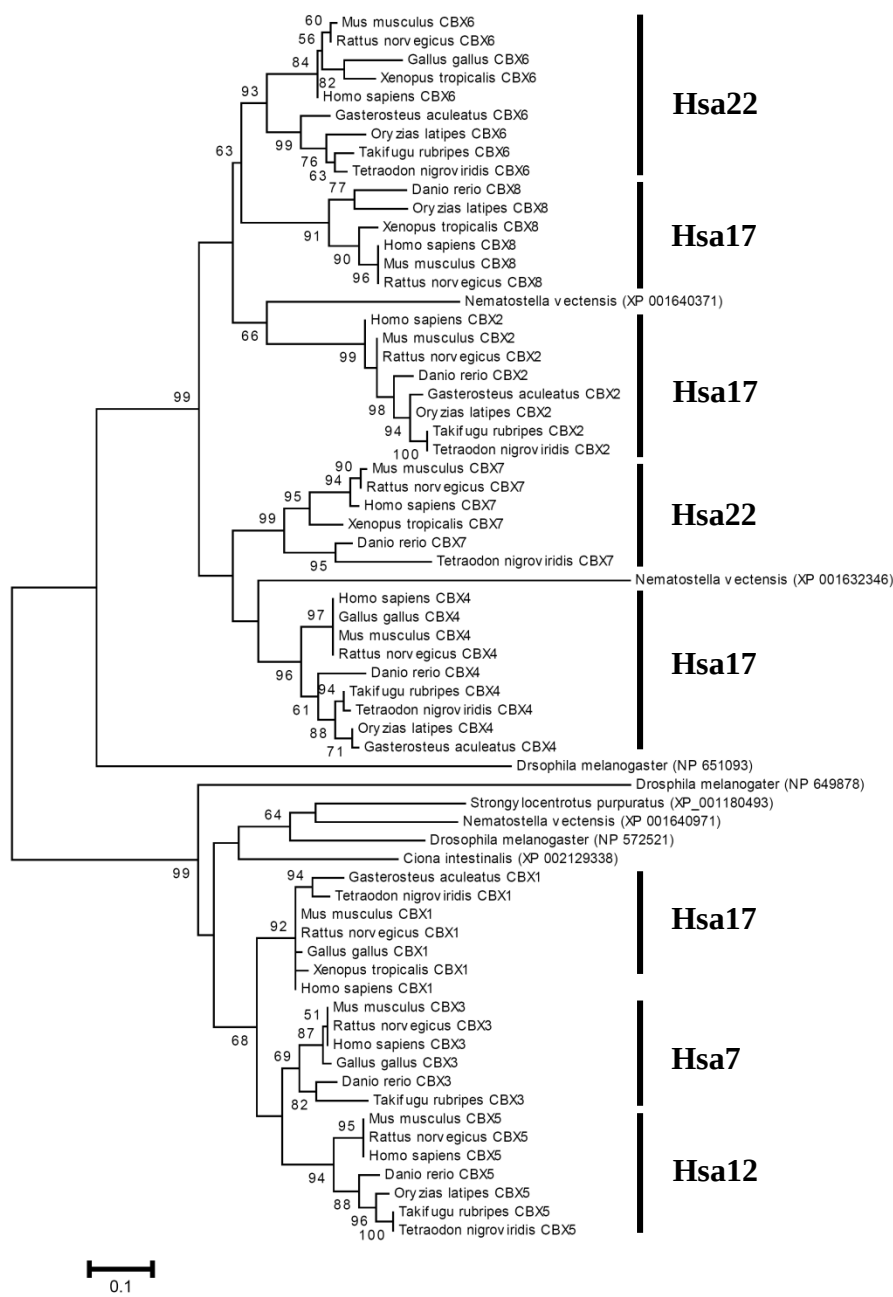
Calcium binding and coiled-coil domain-CALCOCO



Phylogenetic tree of CALCOCO family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the WAG model. The tree with the highest log likelihood (-3758.6399) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 1.6340)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 39 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 142 positions in the final dataset.

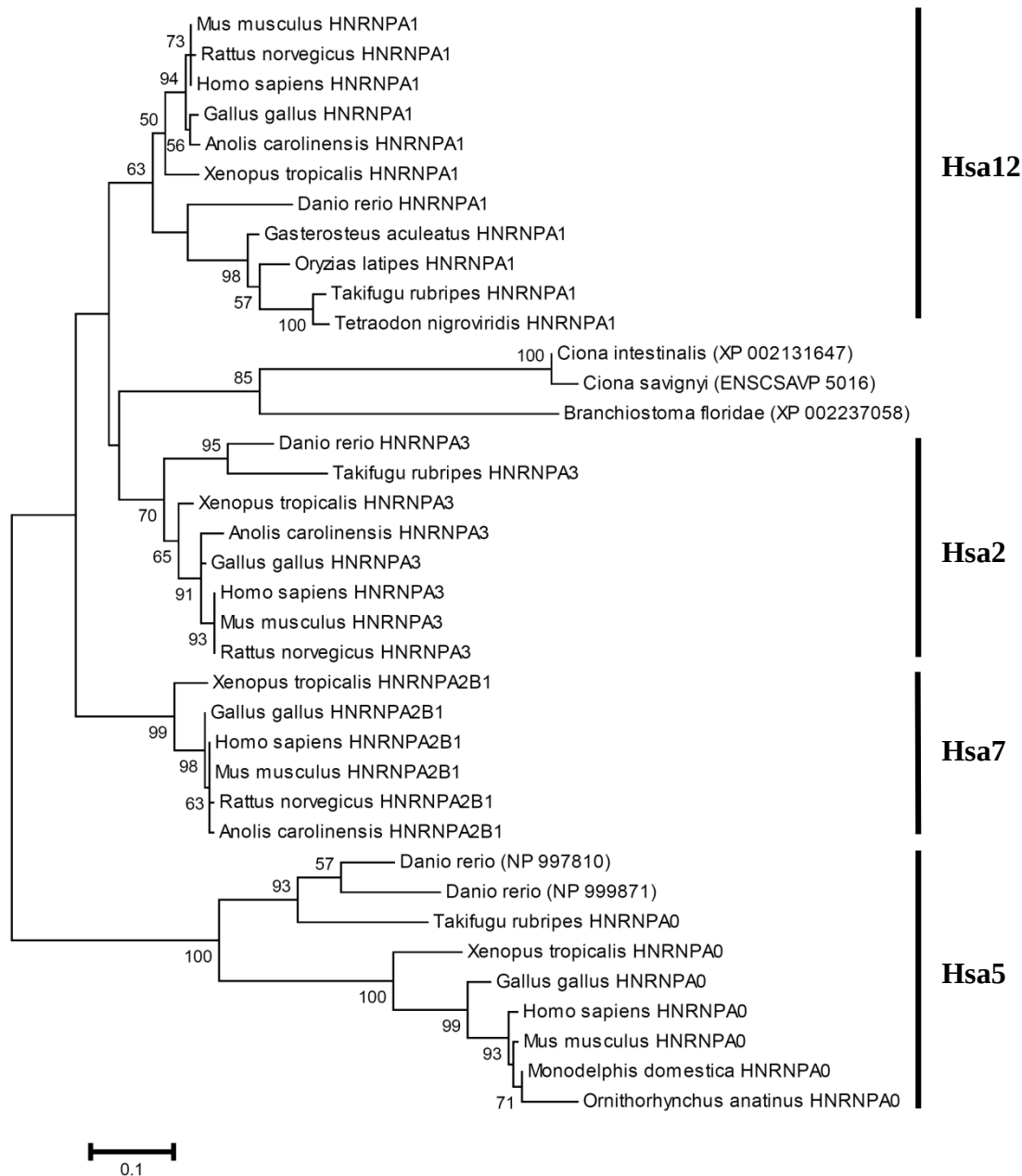
Chromobox homolog-CBX



Phylogenetic tree of CBX family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the WAG model. The tree with the highest log likelihood (-3016.0952) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 1.5451)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 66 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 74 positions in the final dataset.

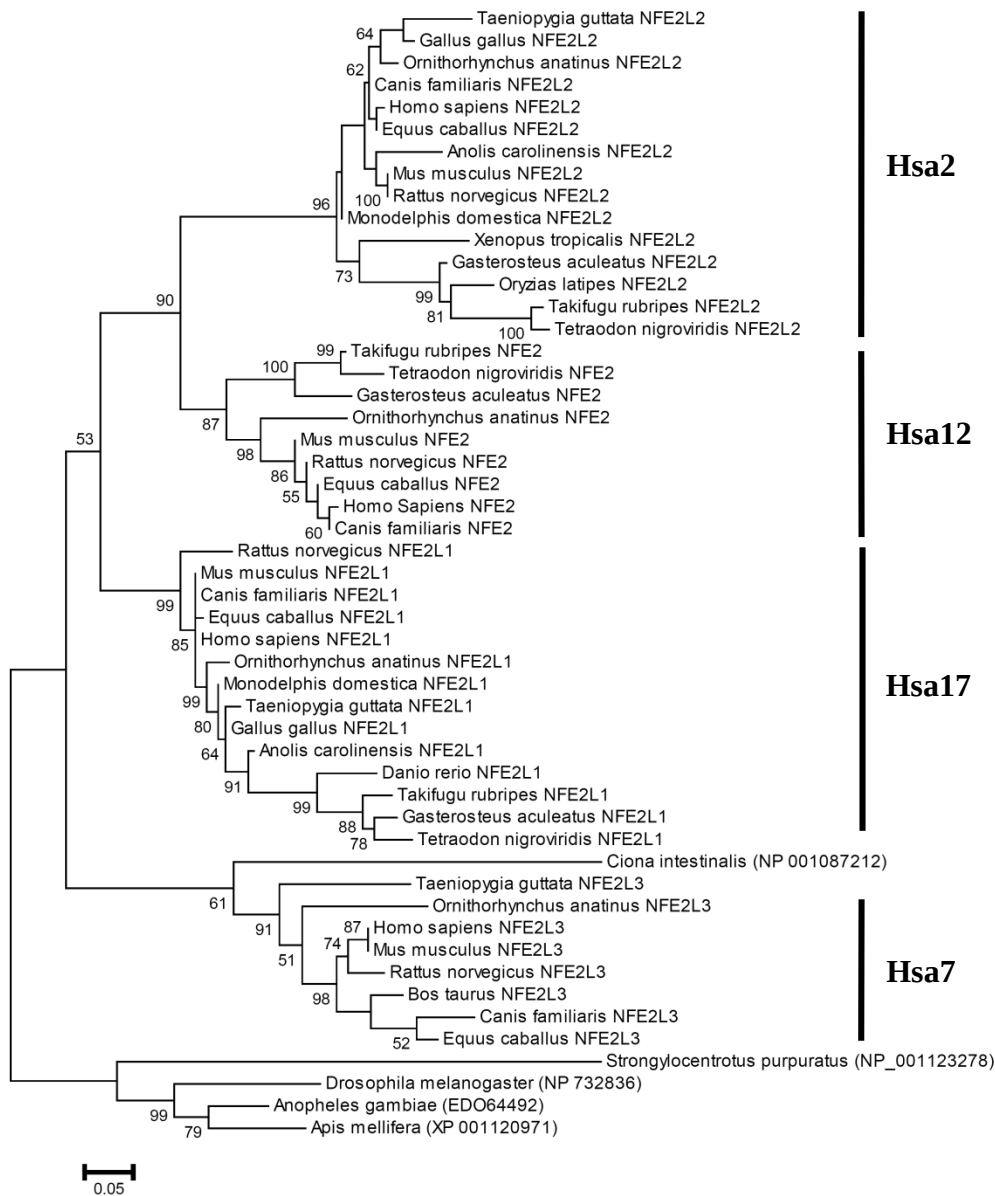
Heterogeneous nuclear ribonucleoprotein A-HNRNPA



Phylogenetic tree of HNRNPA family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the WAG model. The tree with the highest log likelihood (-3368.6875) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches; only the values $\geq 50\%$ are shown here.. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 0.7477)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 37 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 193 positions in the final dataset.

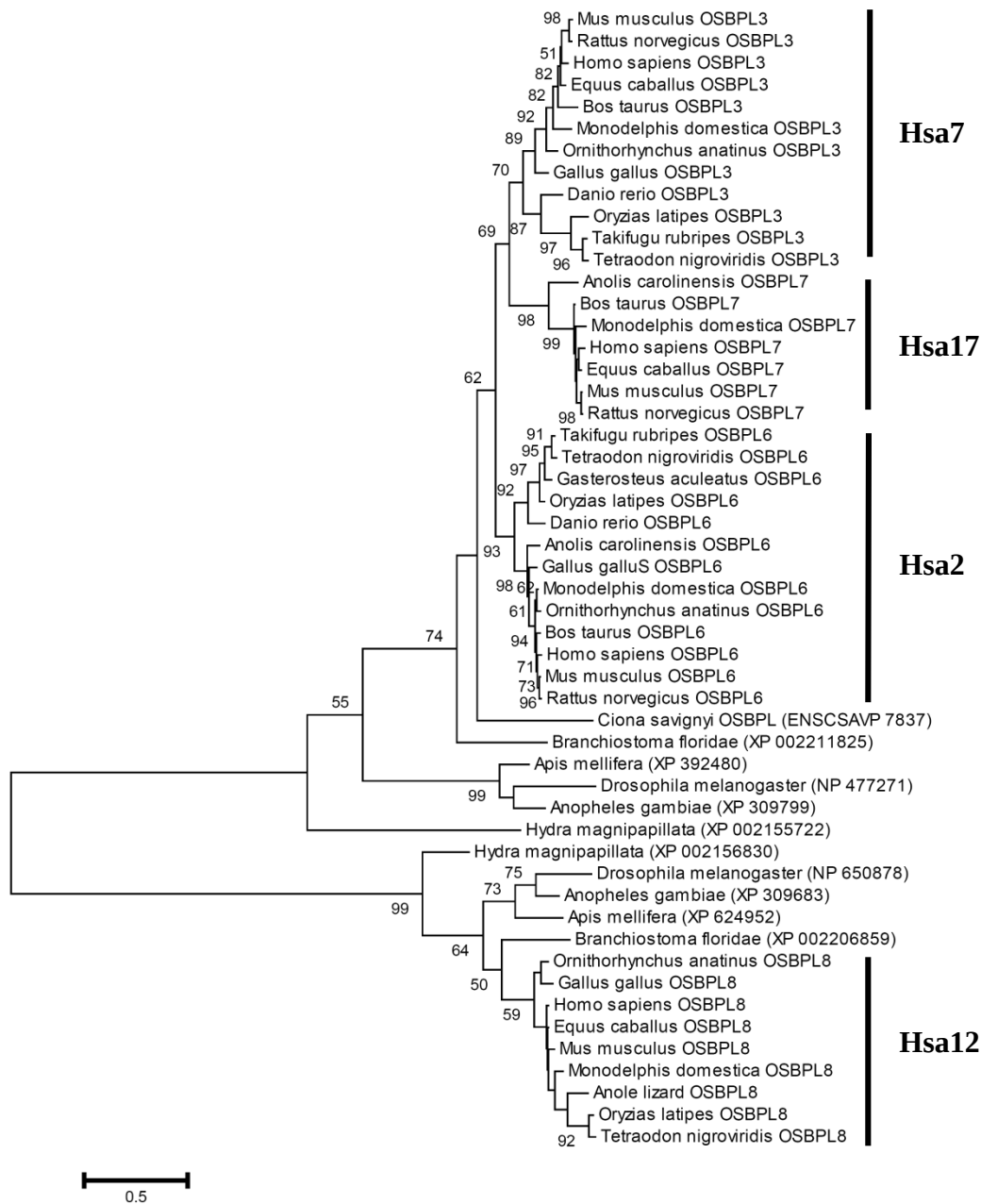
Nuclear Factor (erythroid derived 2)-NFE2



Phylogenetic tree of NFE2 family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model (WAG). The tree with the highest log likelihood (-2574.3850) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 0.9121)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 51 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 85 positions in the final dataset.

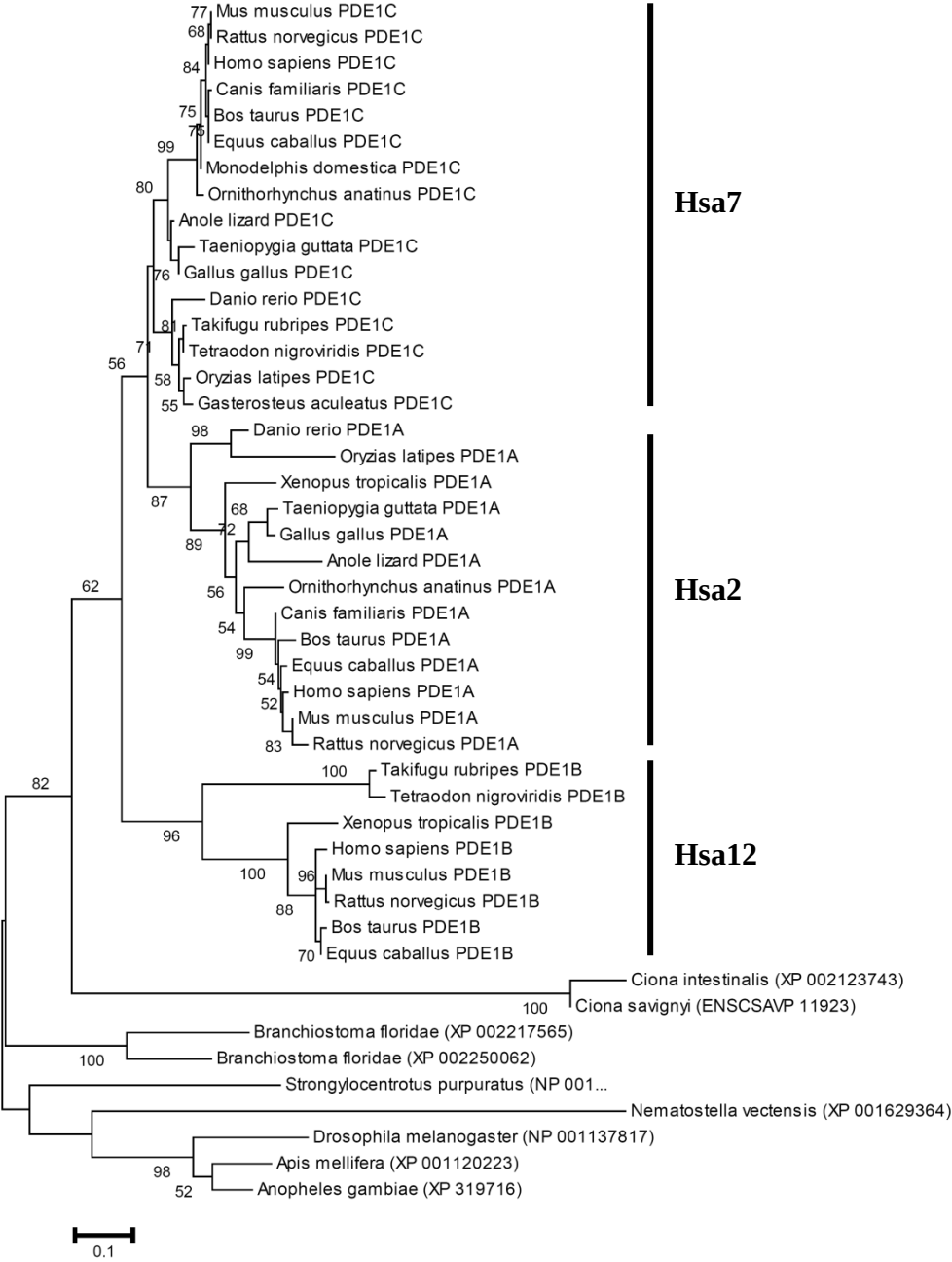
Oxysterol binding protein like-OSBPL



Phylogenetic tree of OSBPL family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the WAG model. The tree with the highest log likelihood (-13471.2479) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 1.6112)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 52 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 357 positions in the final dataset.

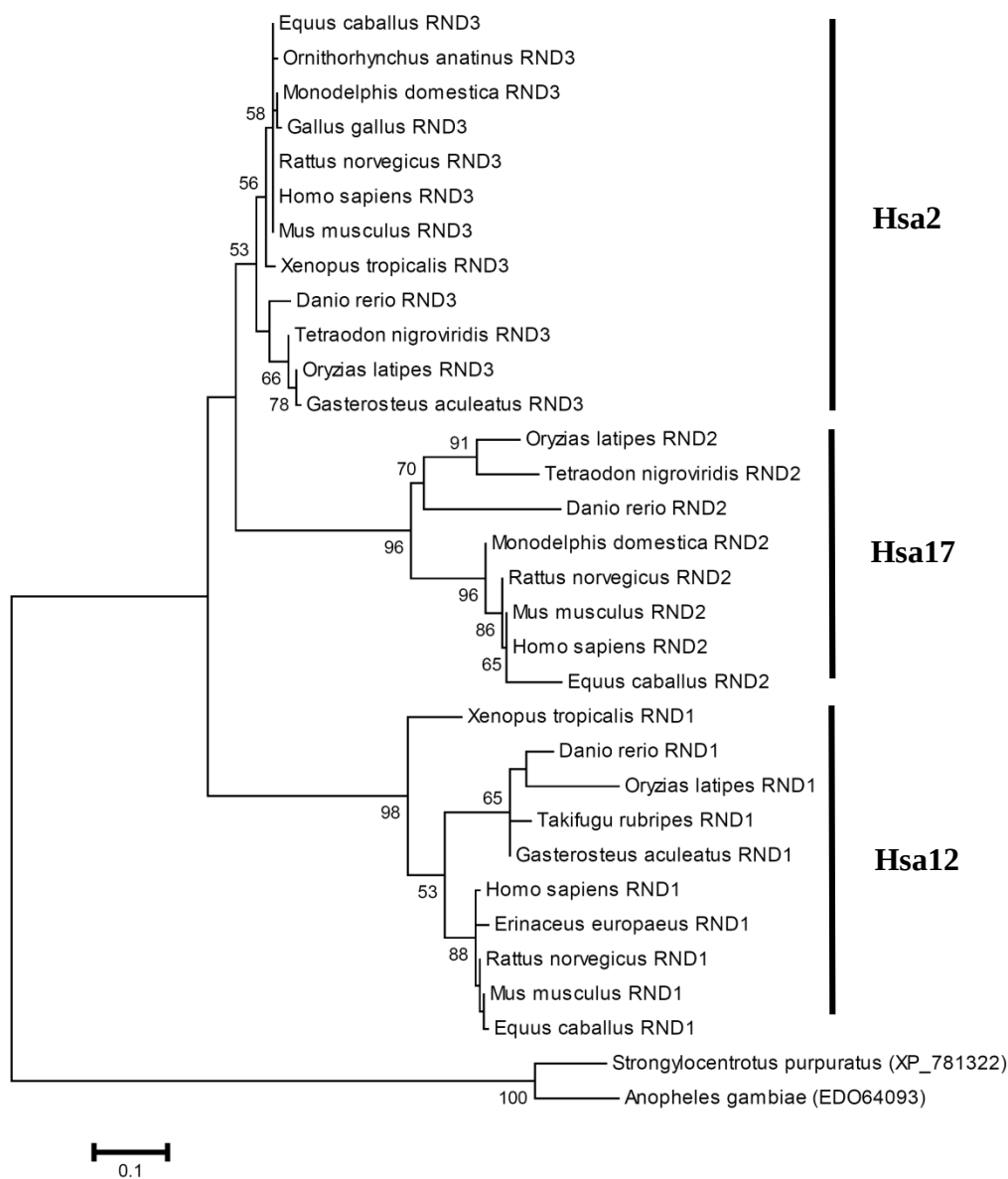
Phosphodiesterase 1, Clamodulin-dependent-PDE1



Phylogenetic tree of PDE1 family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the WAG model. The tree with the highest log likelihood (-5324.9973) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 0.9309)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 46 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 232 positions in the final dataset.

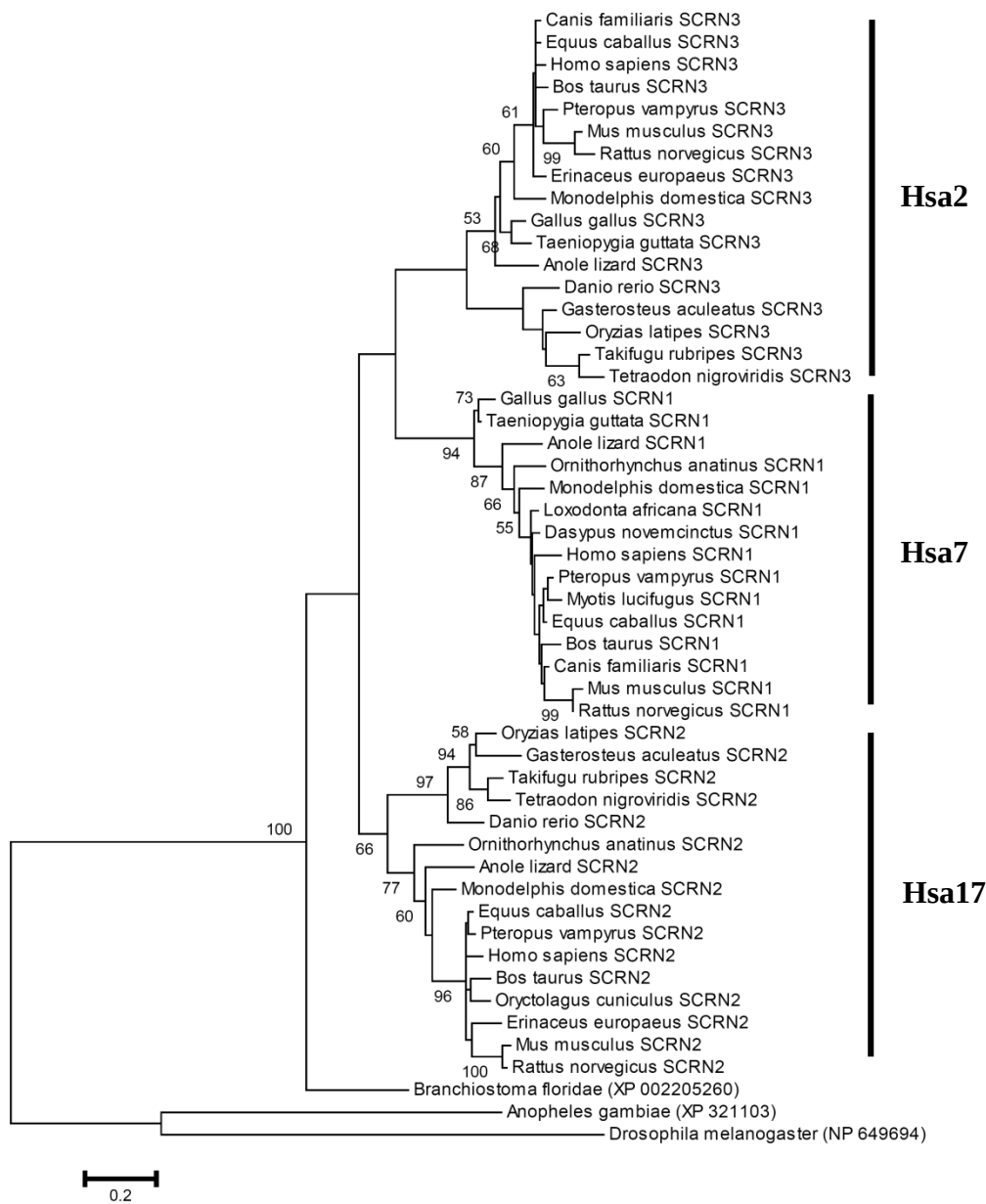
Rho family GTPase-RND



Phylogenetic tree of RND family.

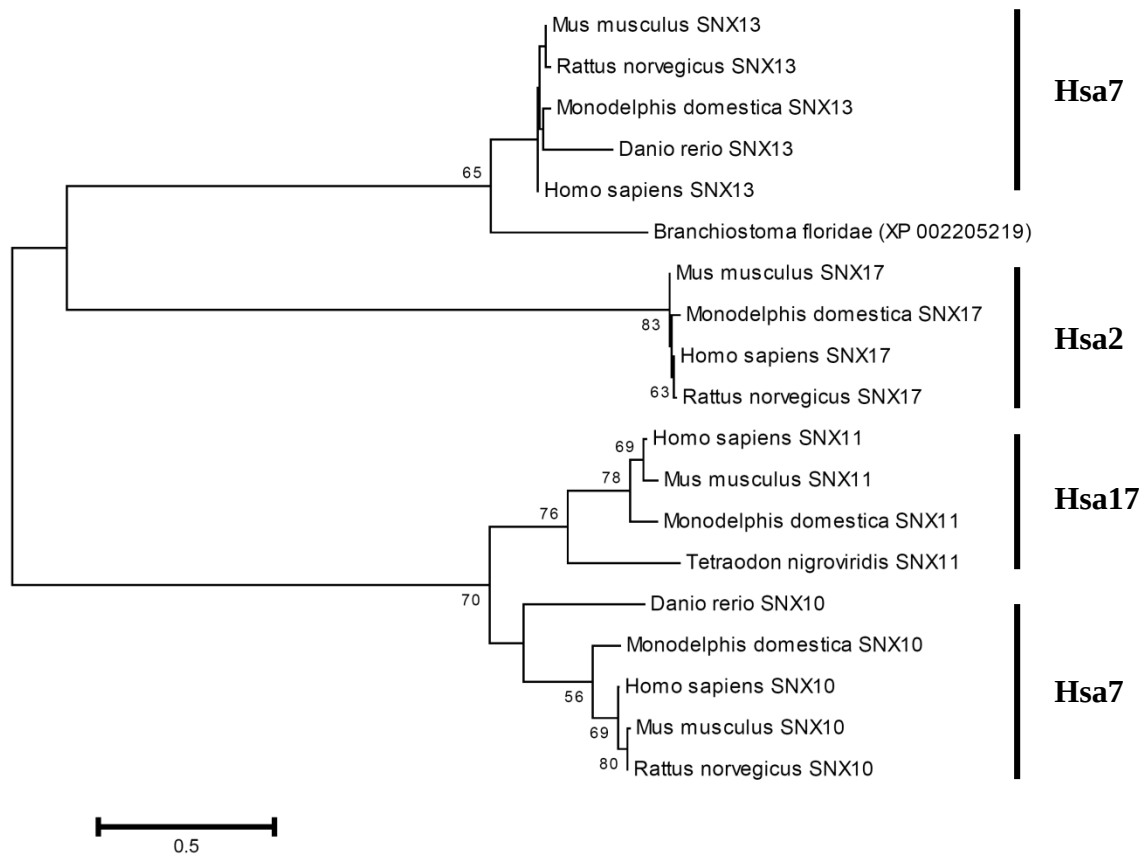
The evolutionary history was inferred by using the Maximum Likelihood method based on the WAG model. The tree with the highest log likelihood (-2533.8139) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 0.8158). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 32 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 186 positions in the final dataset.

Secernin-SCRN



Phylogenetic tree of SCR family.

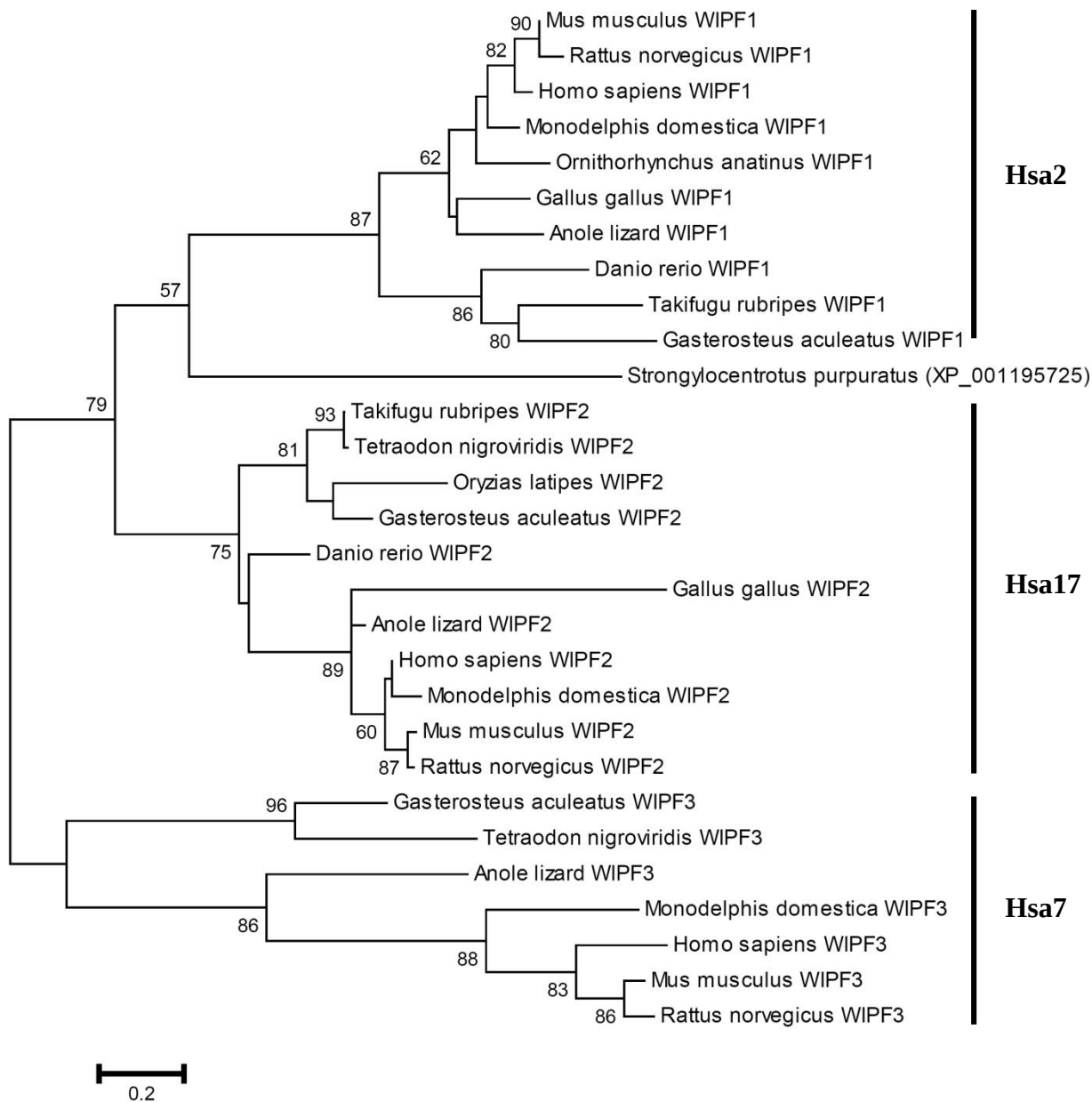
The evolutionary history was inferred by using the Maximum Likelihood method based on the WAG model. The tree with the highest log likelihood (-4877.1740) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 1.1168)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 51 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 160 positions in the final dataset.



Phylogenetic tree of SNX family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the WAG model. The tree with the highest log likelihood (-3180.7915) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 3.9690)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 19 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 170 positions in the final dataset.

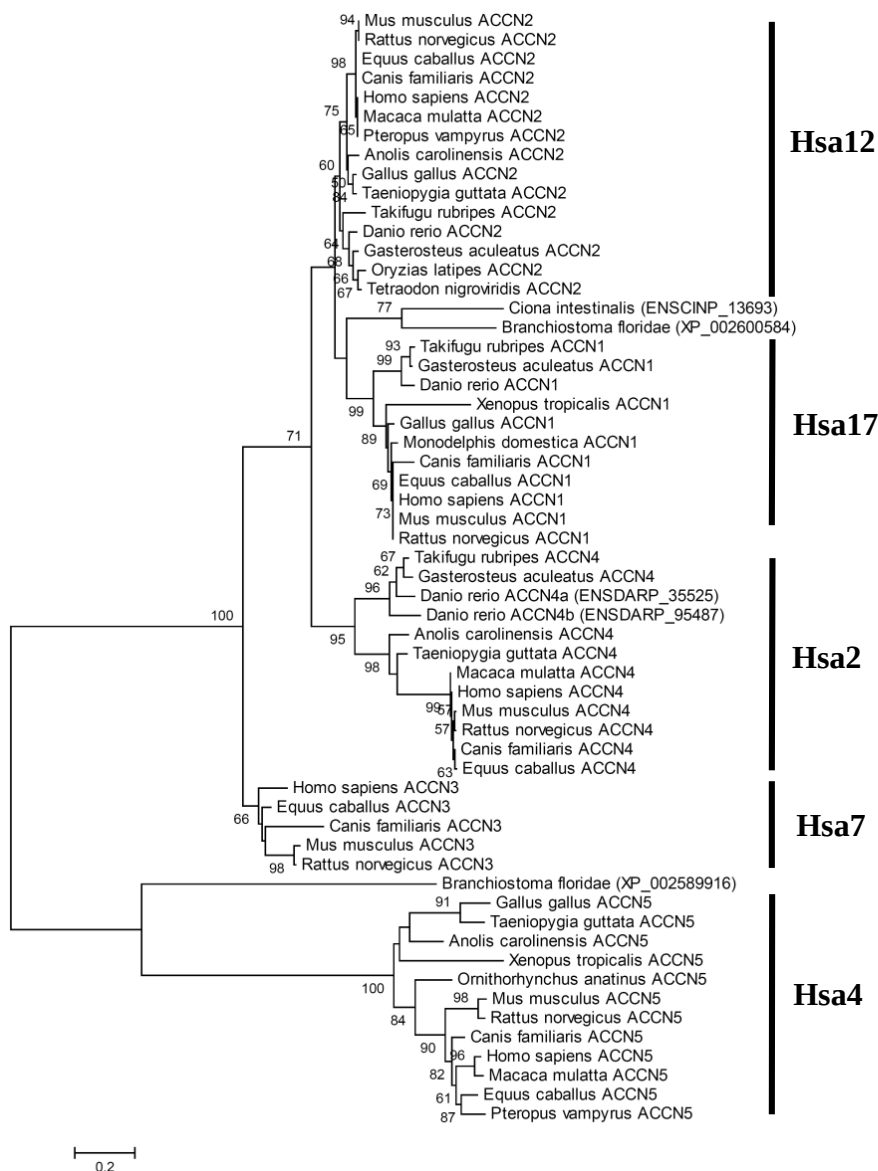
WAS/WASL interacting protein family-WIPF



Phylogenetic tree of WIPF family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the WAG model. The tree with the highest log likelihood (-3581.1795) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 3.1761). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 29 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 105 positions in the final dataset.

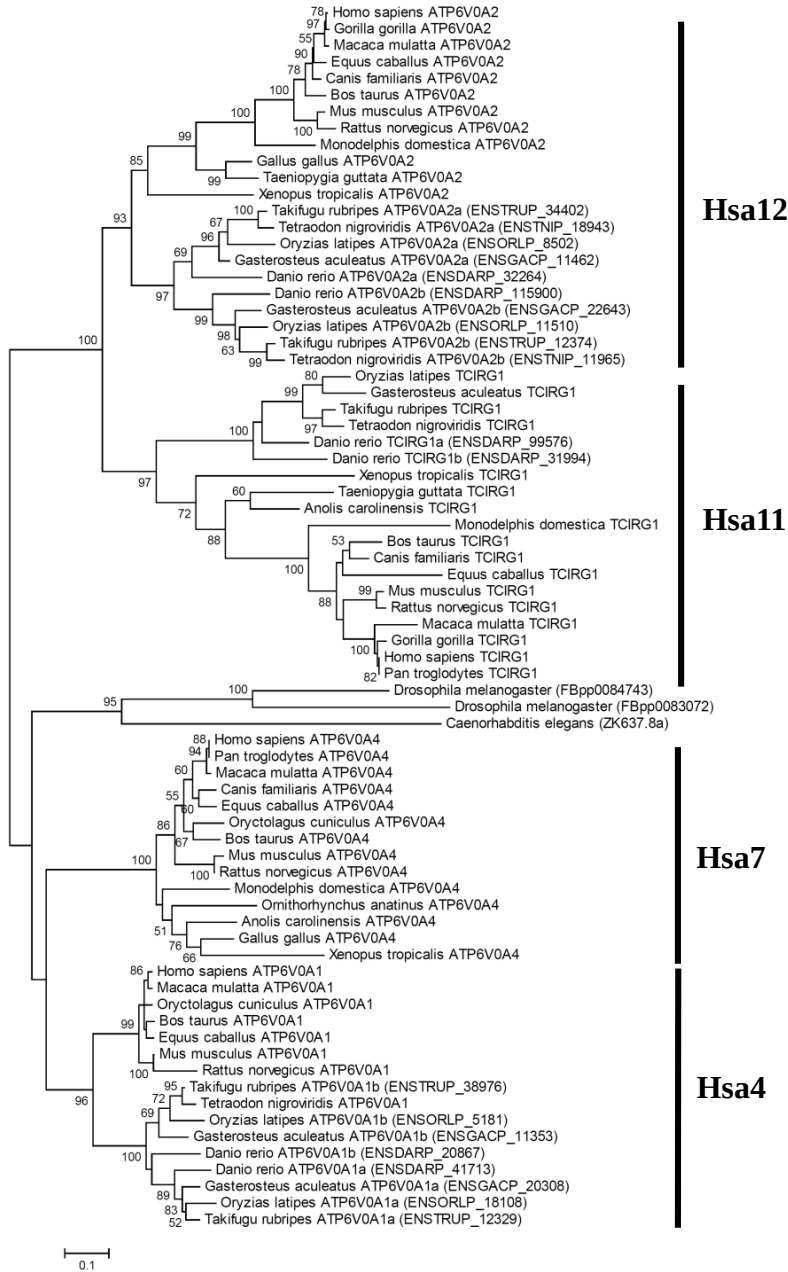
Amiloride-sensitive cation channel neuronal-ACCN



Phylogenetic tree of ACCN family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model (WAG). The tree with the highest log likelihood (-2574.3850) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 0.9121)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 51 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 85 positions in the final dataset.

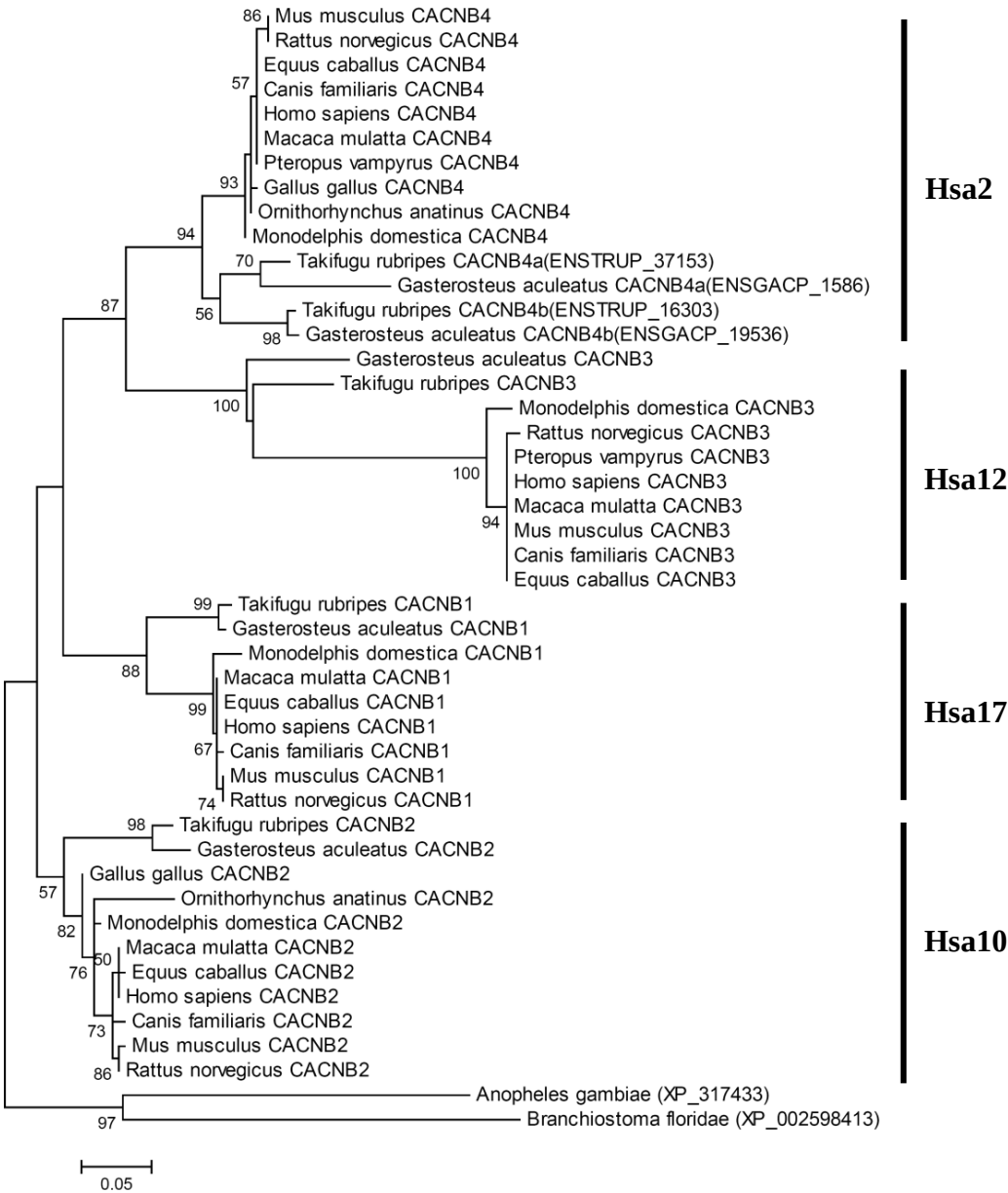
ATPase, H⁺ transporting, lysosomal V0-ATP6V0A



Phylogenetic tree of ATP6V0A family.

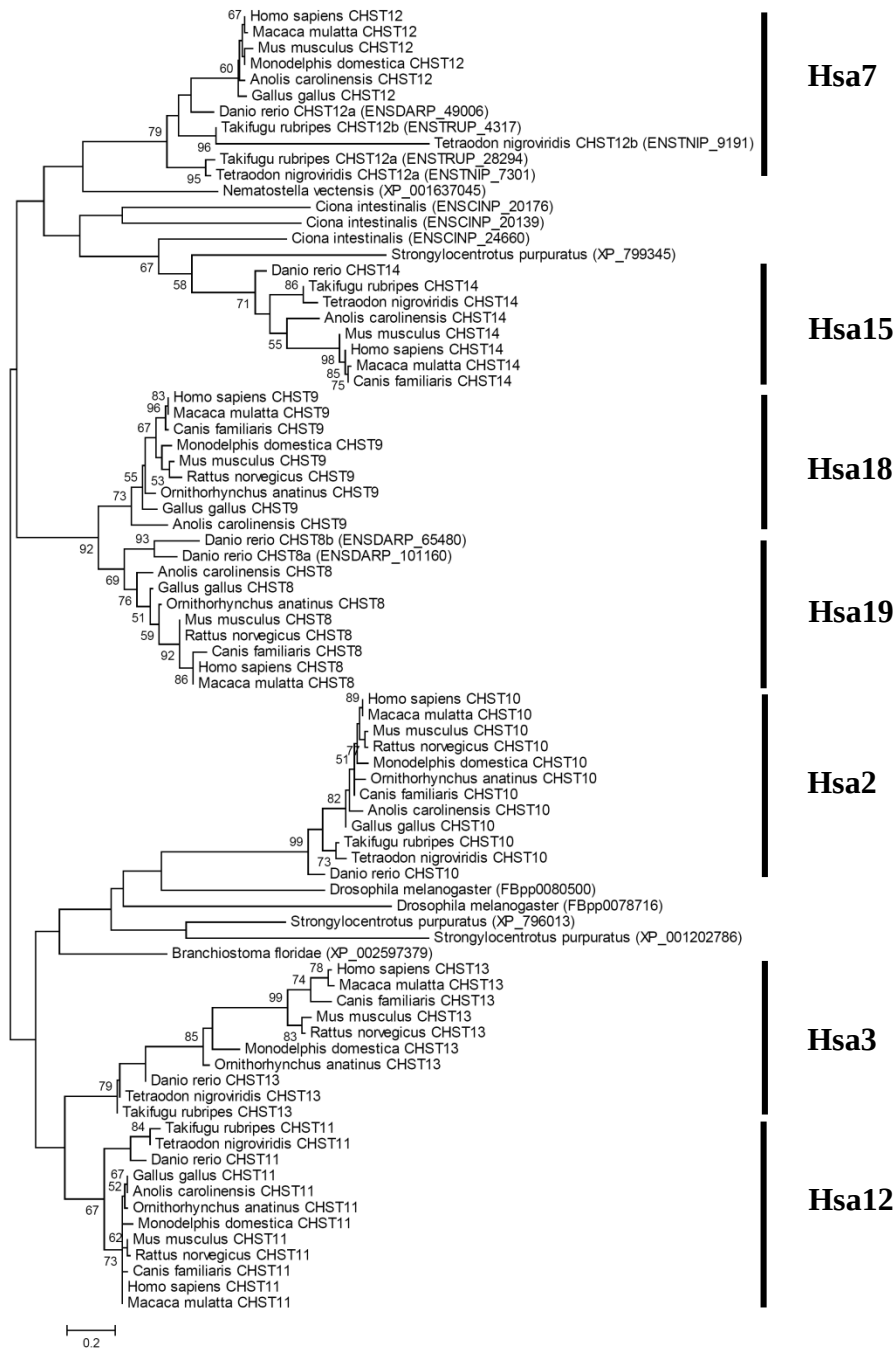
The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model (WAG). The tree with the highest log likelihood (-2574.3850) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 0.9121). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 51 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 85 positions in the final dataset.

Calcium channel voltage-dependent beta-CACNB



Phylogenetic tree of CACNB family.

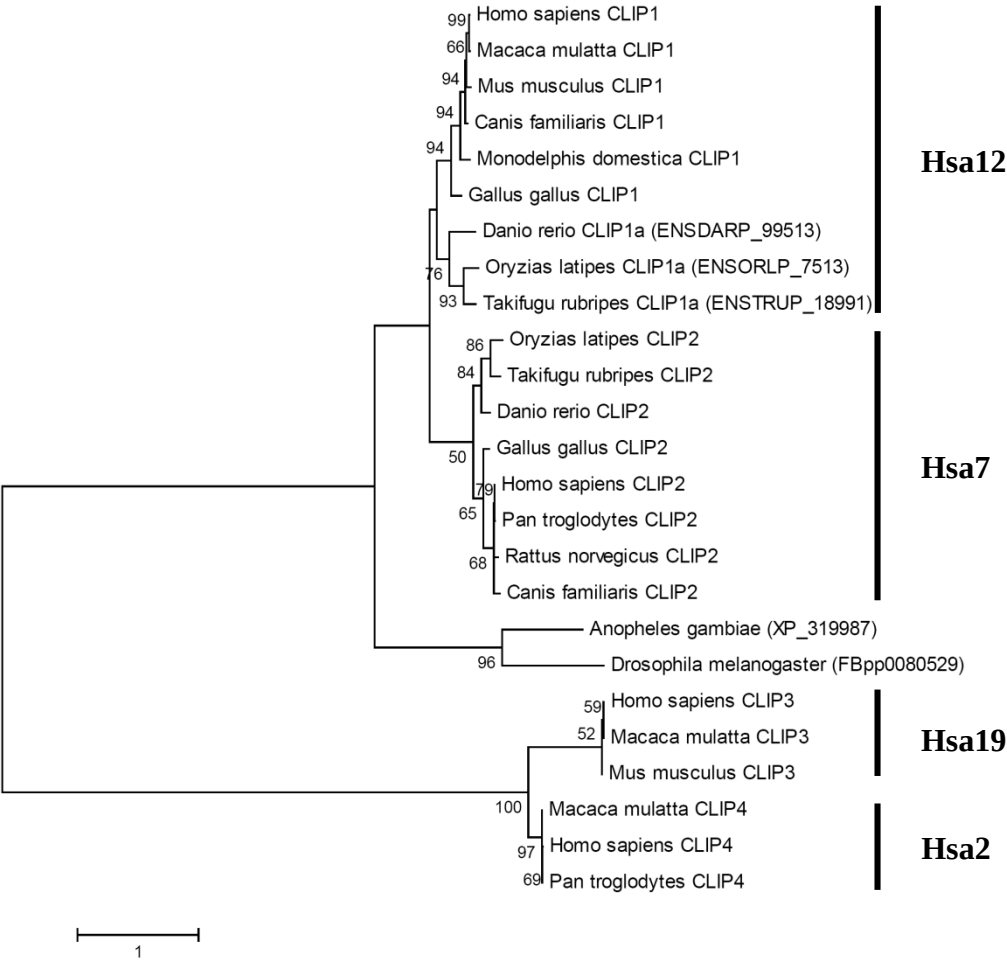
The evolutionary history was inferred by using the Maximum Likelihood method based on the WAG model. The tree with the highest log likelihood (-13471.2479) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 1.6112). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 52 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 357 positions in the final dataset.



Phylogenetic tree of CHST family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the WAG model. The tree with the highest log likelihood (-13471.2479) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 1.6112)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 52 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 357 positions in the final dataset.

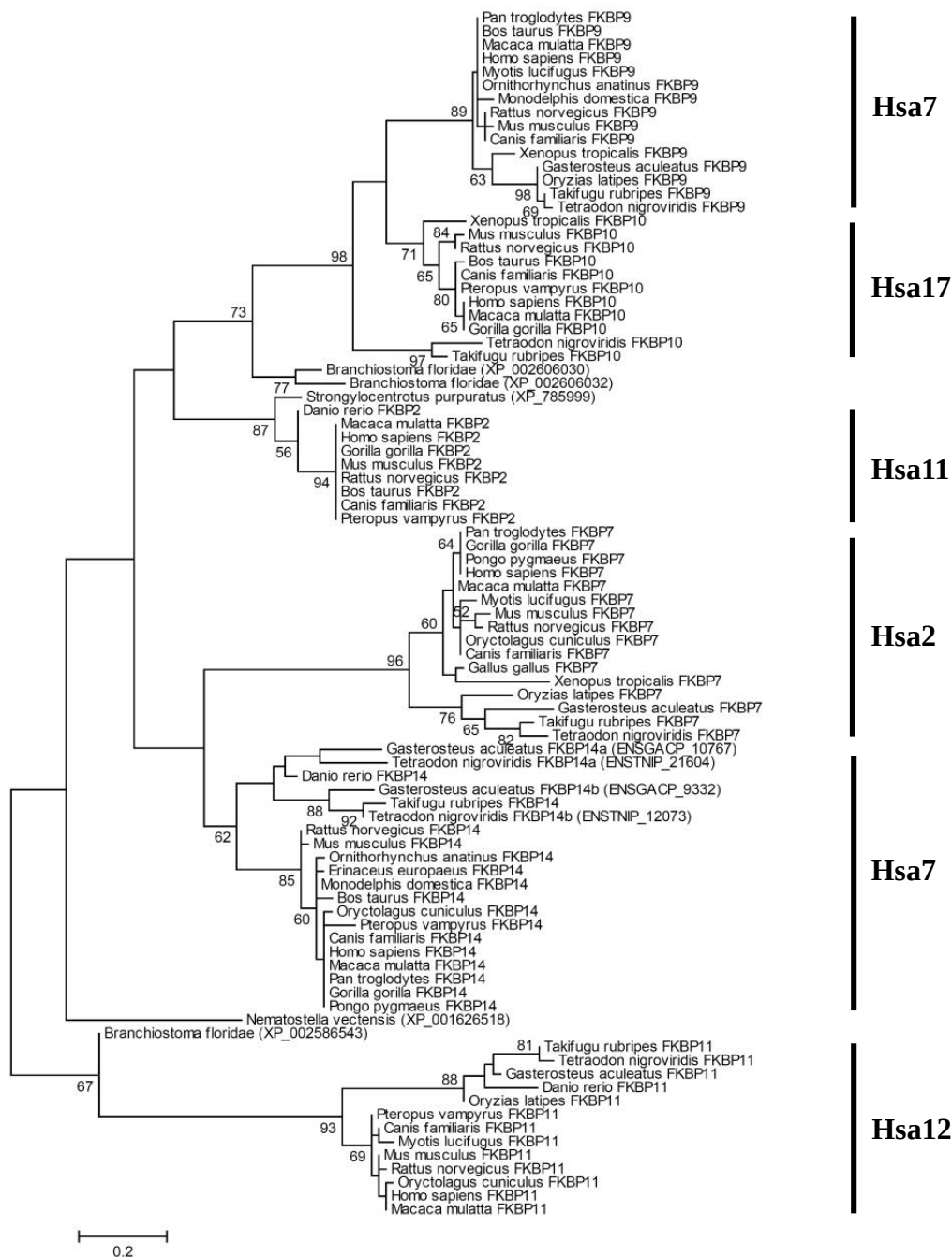
CAP-GLY domain containing linker protein-CLIP



Phylogenetic tree of CLIP family.

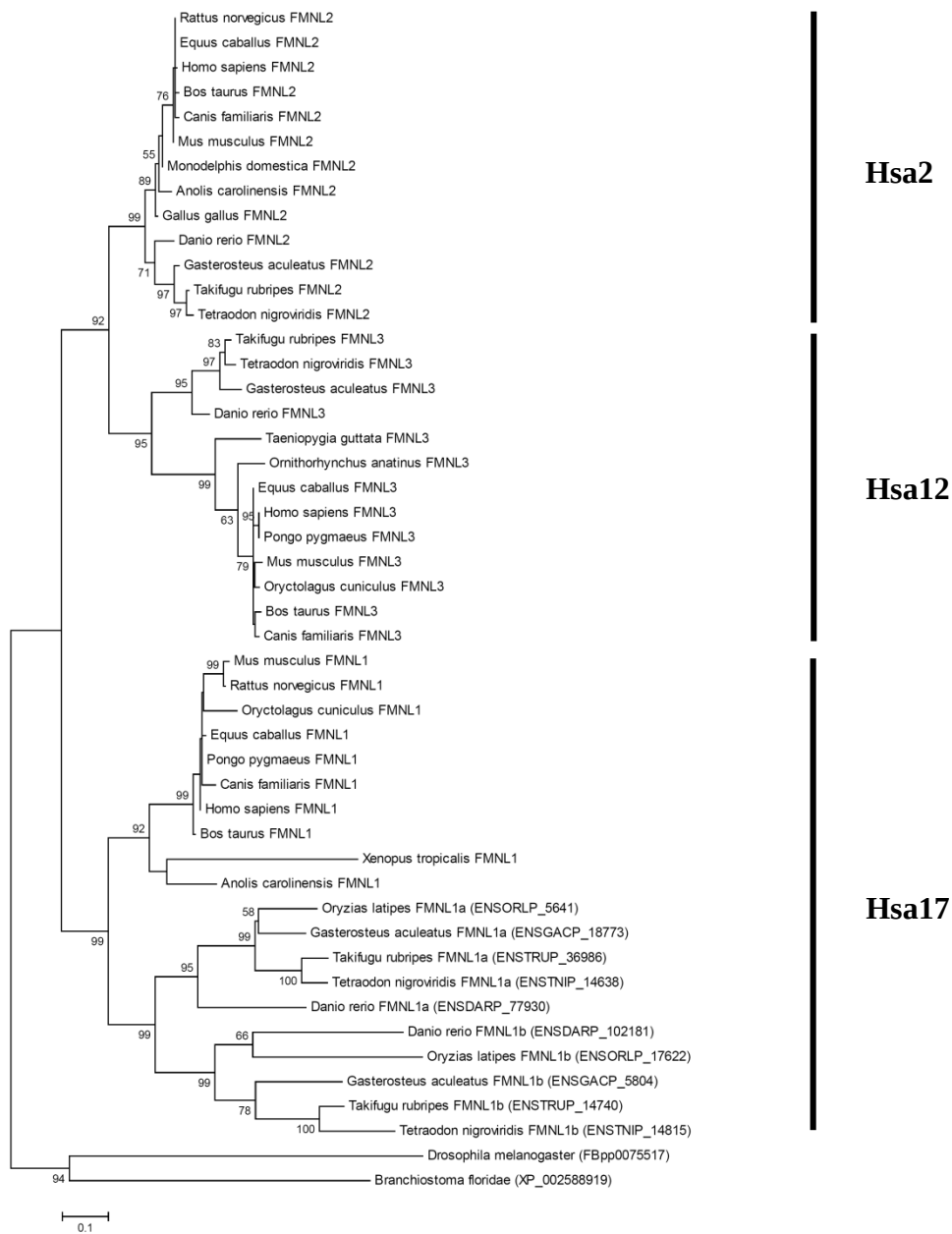
The evolutionary history was inferred by using the Maximum Likelihood method based on the WAG model. The tree with the highest log likelihood (-3016.0952) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 1.5451)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 66 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 74 positions in the final dataset.

FK506 binding protein precursor-FKBP



Phylogenetic tree of FKBP family.

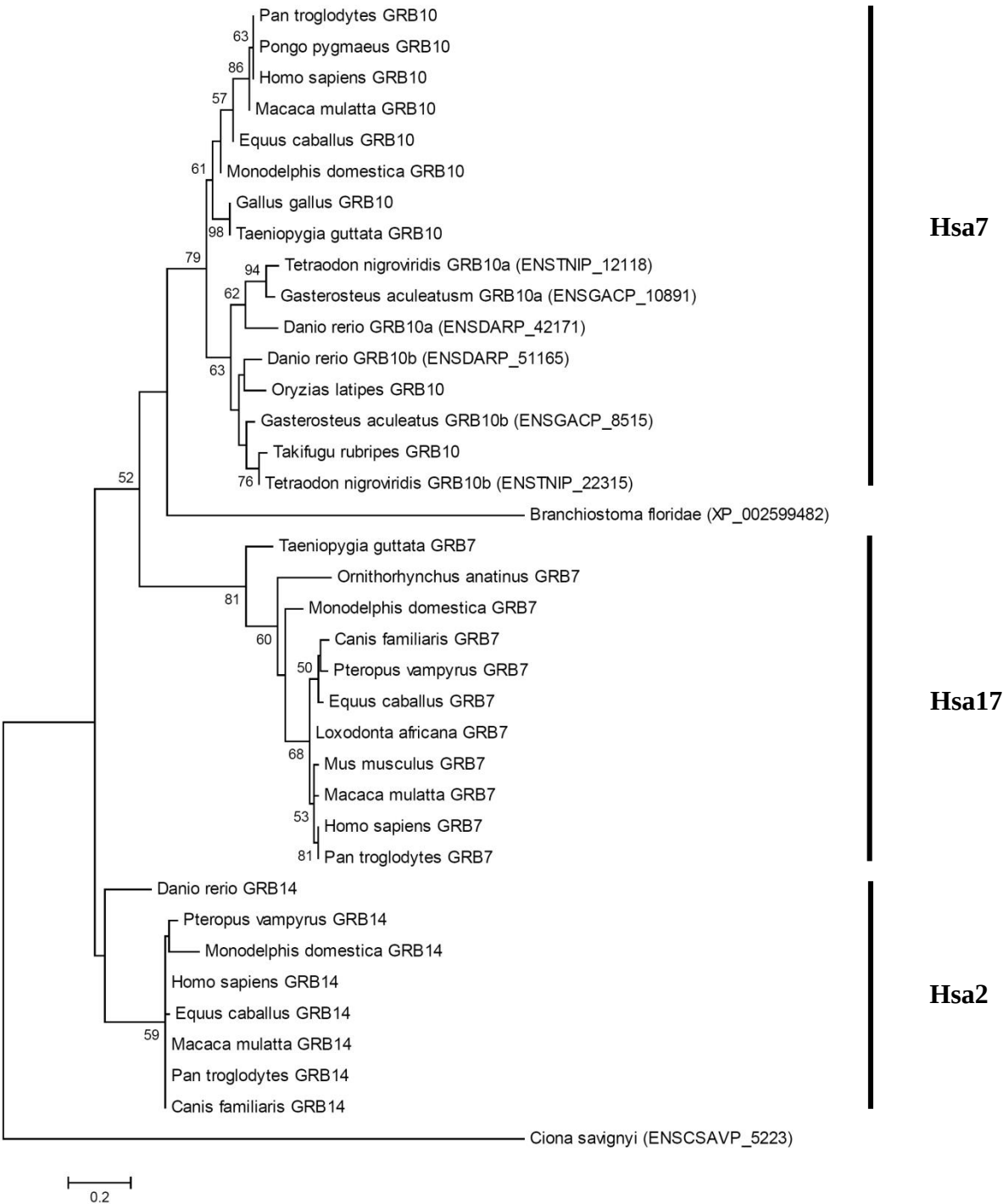
The evolutionary history was inferred by using the Maximum Likelihood method based on the WAG model. The tree with the highest log likelihood (-3016.0952) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 1.5451)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 66 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 74 positions in the final dataset.



Phylogenetic tree of FMNL family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the WAG model. The tree with the highest log likelihood (-4877.1740) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 1.1168)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 51 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 160 positions in the final dataset.

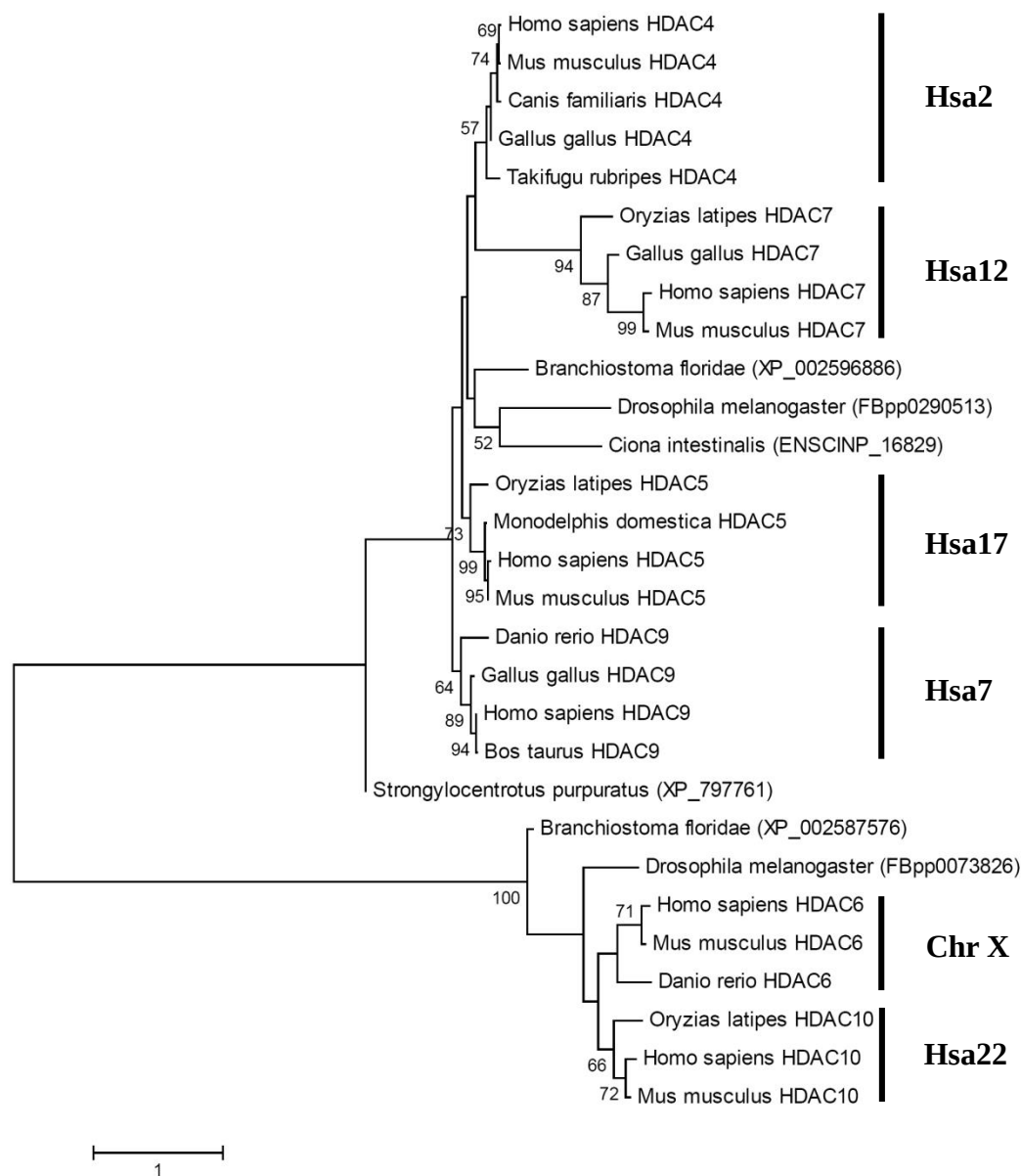
Growth factor receptor-bound protein-GRB



Phylogenetic tree of GRB family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the WAG model. The tree with the highest log likelihood (-1670.8340) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 0.3768)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 28 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 115 positions in the final dataset.

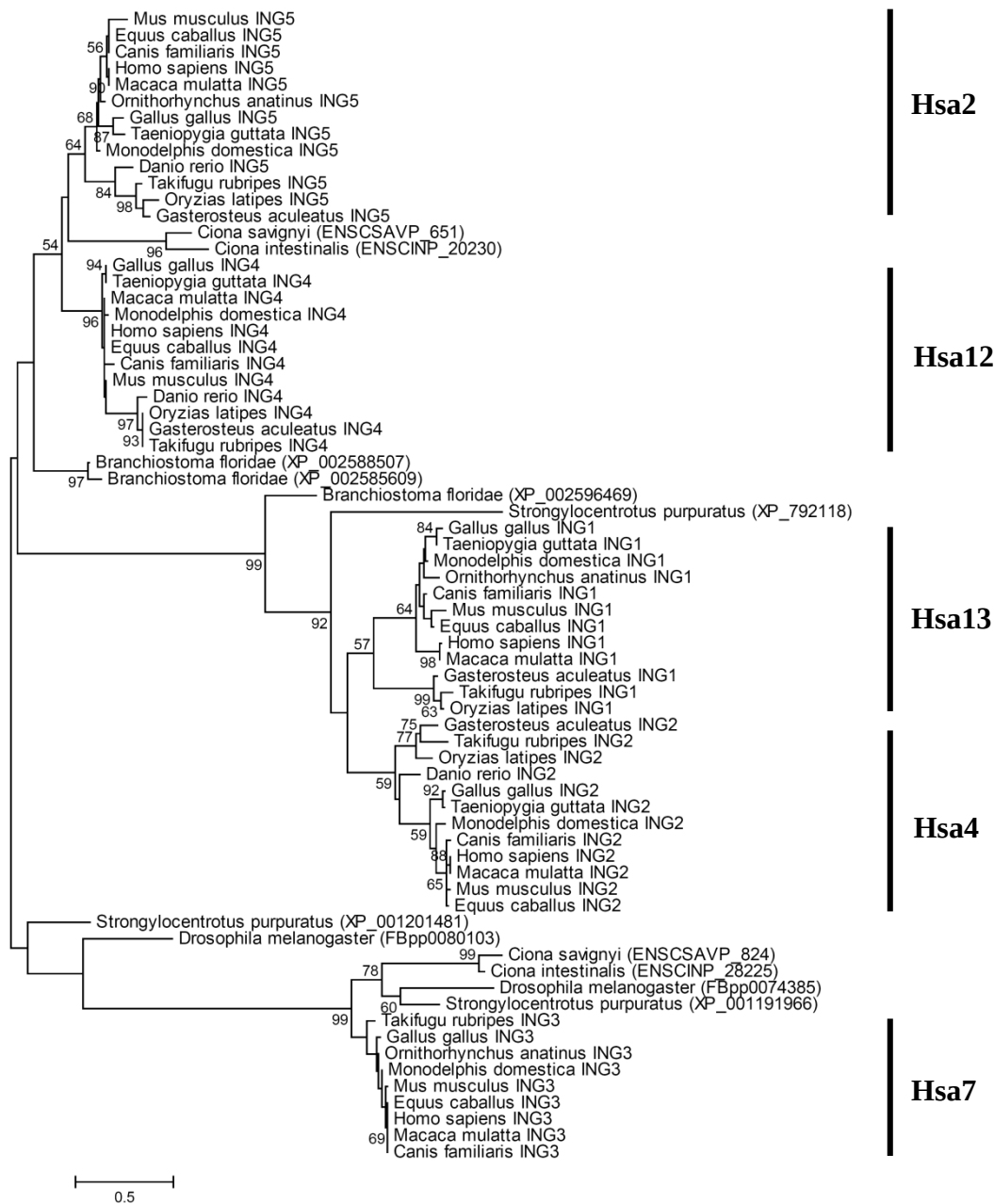
Histone deacetylase-HDAC



Phylogenetic tree of HDAC family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the WAG model. The tree with the highest log likelihood (-2533.8139) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 0.8158)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 32 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 186 positions in the final dataset.

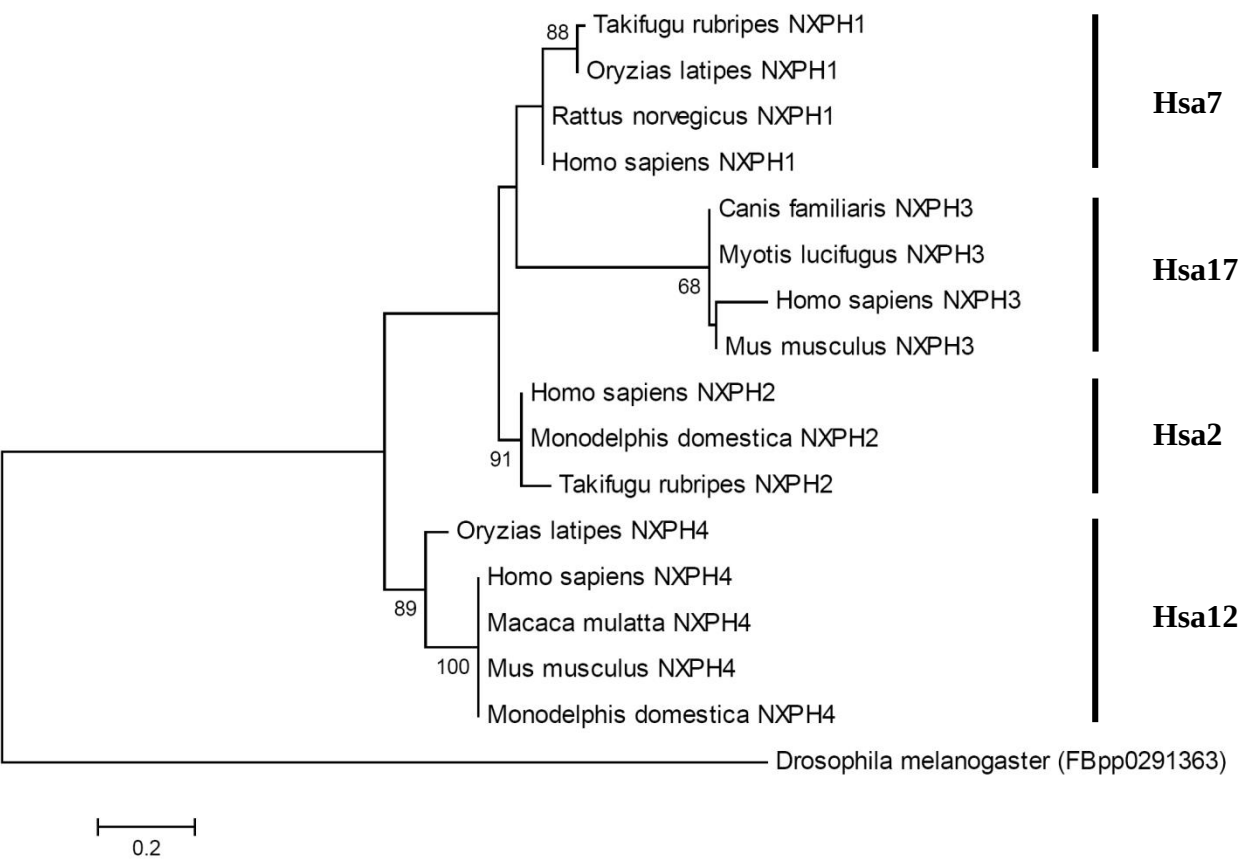
Inhibitor of growth family-ING



Phylogenetic tree of ING family.

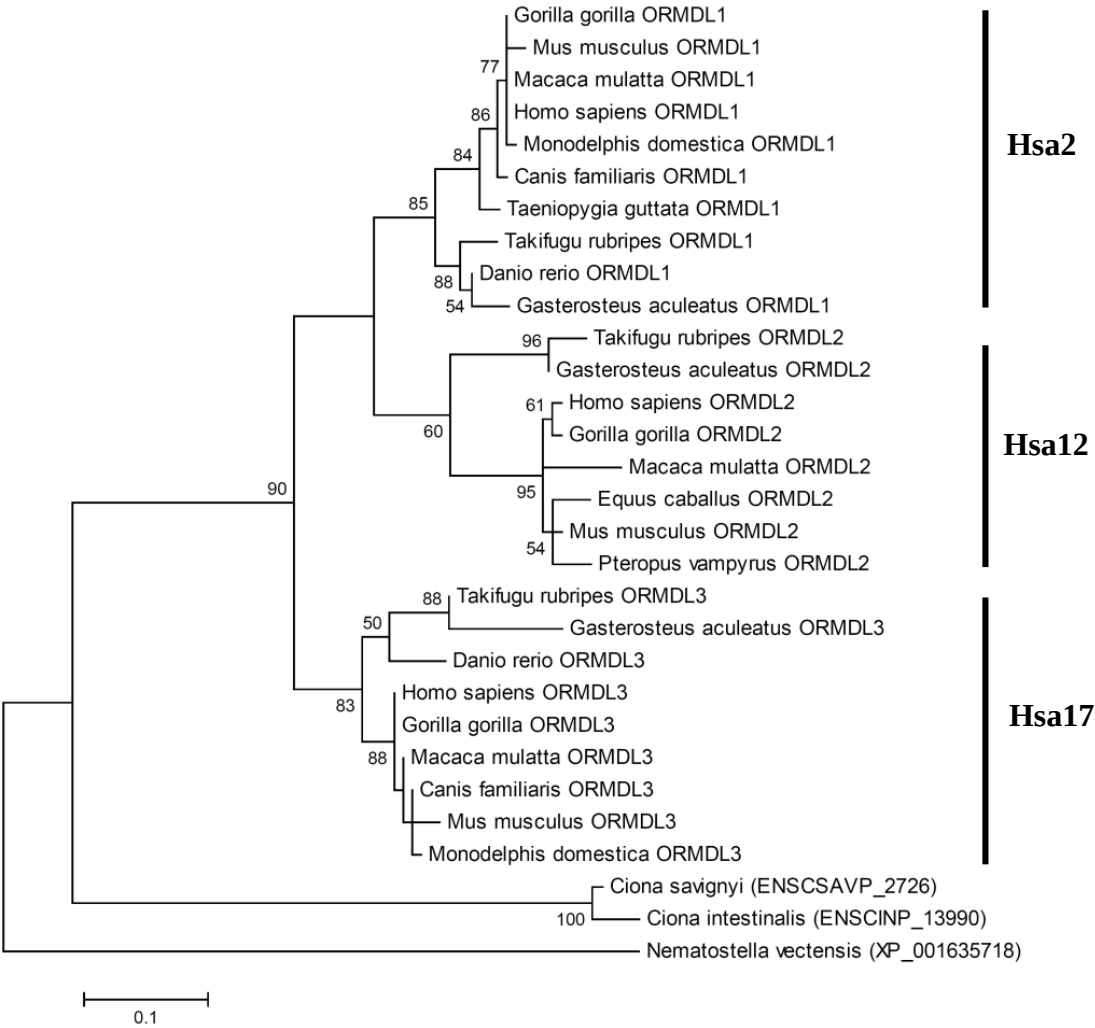
The evolutionary history was inferred by using the Maximum Likelihood method based on the WAG model. The tree with the highest log likelihood (-1670.8340) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 0.3768)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 28 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 115 positions in the final dataset.

Neurexophilin-NXPH



Phylogenetic tree of NXPH family.

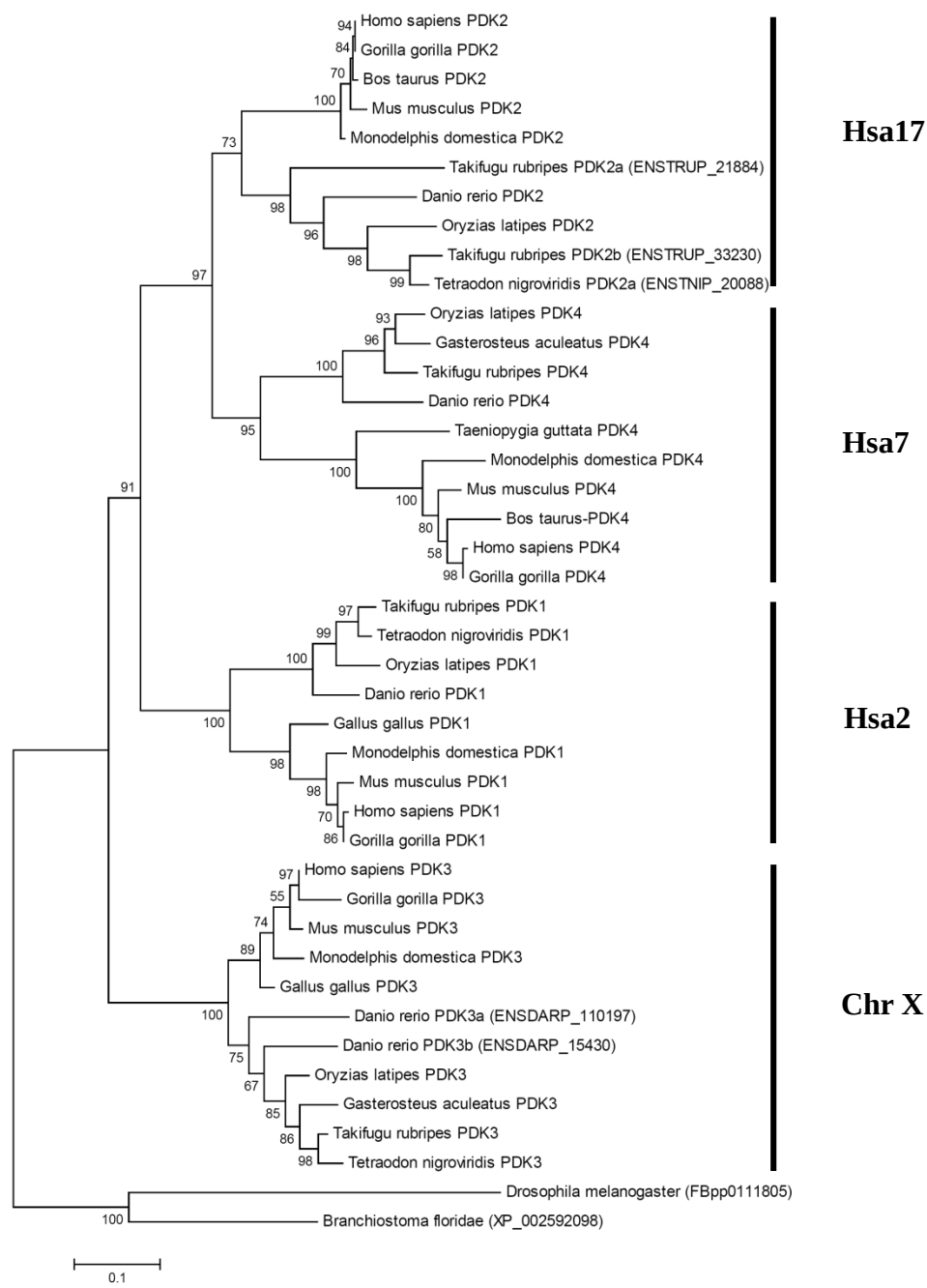
The evolutionary history was inferred by using the Maximum Likelihood method based on the WAG model. The tree with the highest log likelihood (-3581.1795) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 3.1761)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 29 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 105 positions in the final dataset.



Phylogenetic tree of ORMDL family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the WAG model. The tree with the highest log likelihood (-4877.1740) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 1.1168)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 51 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 160 positions in the final dataset.

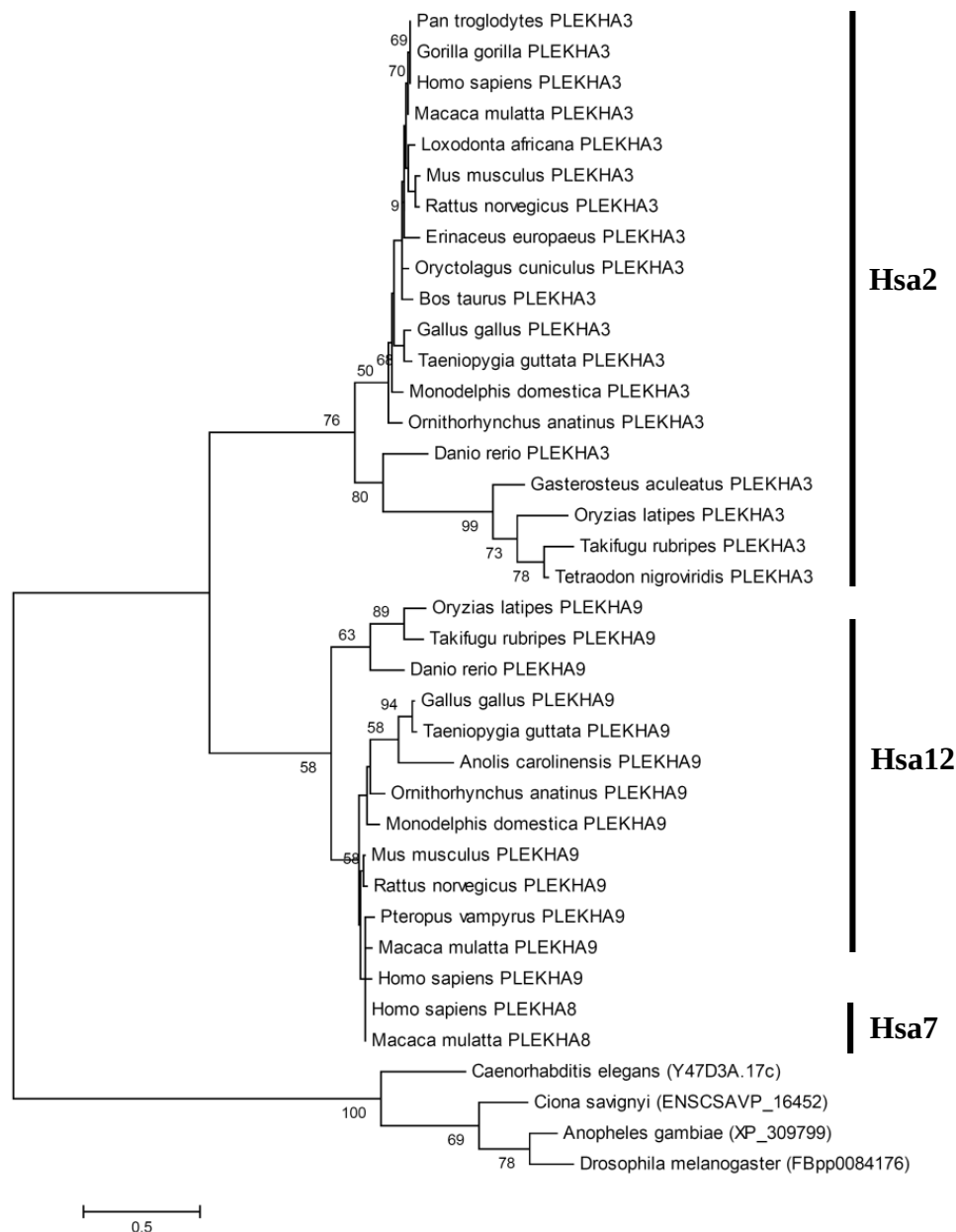
Pyruvate dehydrogenase kinase-PDK



Phylogenetic tree of PDK family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the WAG model. The tree with the highest log likelihood (-3758.6399) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 1.6340)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 39 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 142 positions in the final dataset.

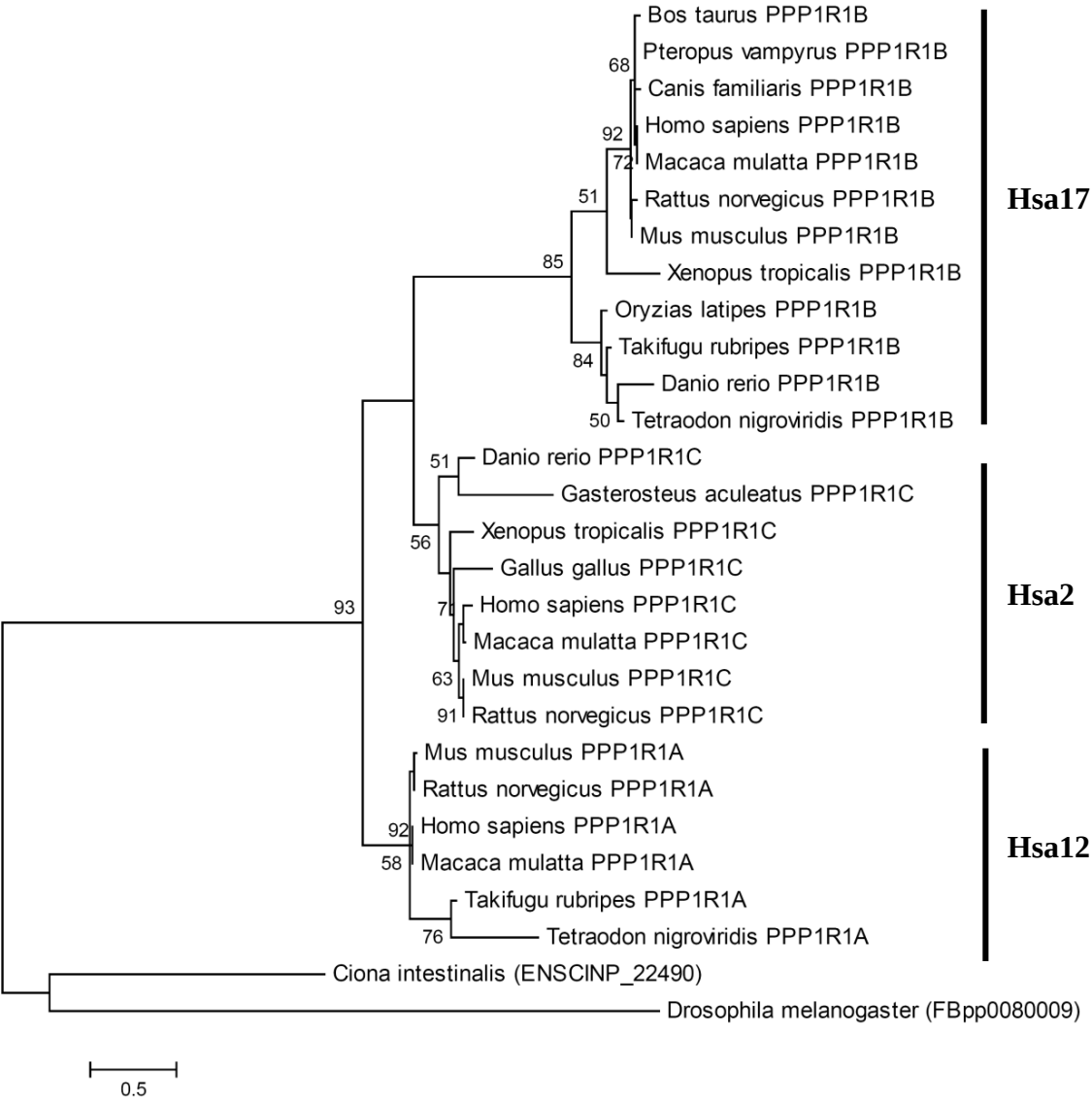
Pleckstrin homology domain containing family A-*PLEKHA*



Phylogenetic tree of PLEKHA family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the WAG model. The tree with the highest log likelihood (-2533.8139) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 0.8158)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 32 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 186 positions in the final dataset.

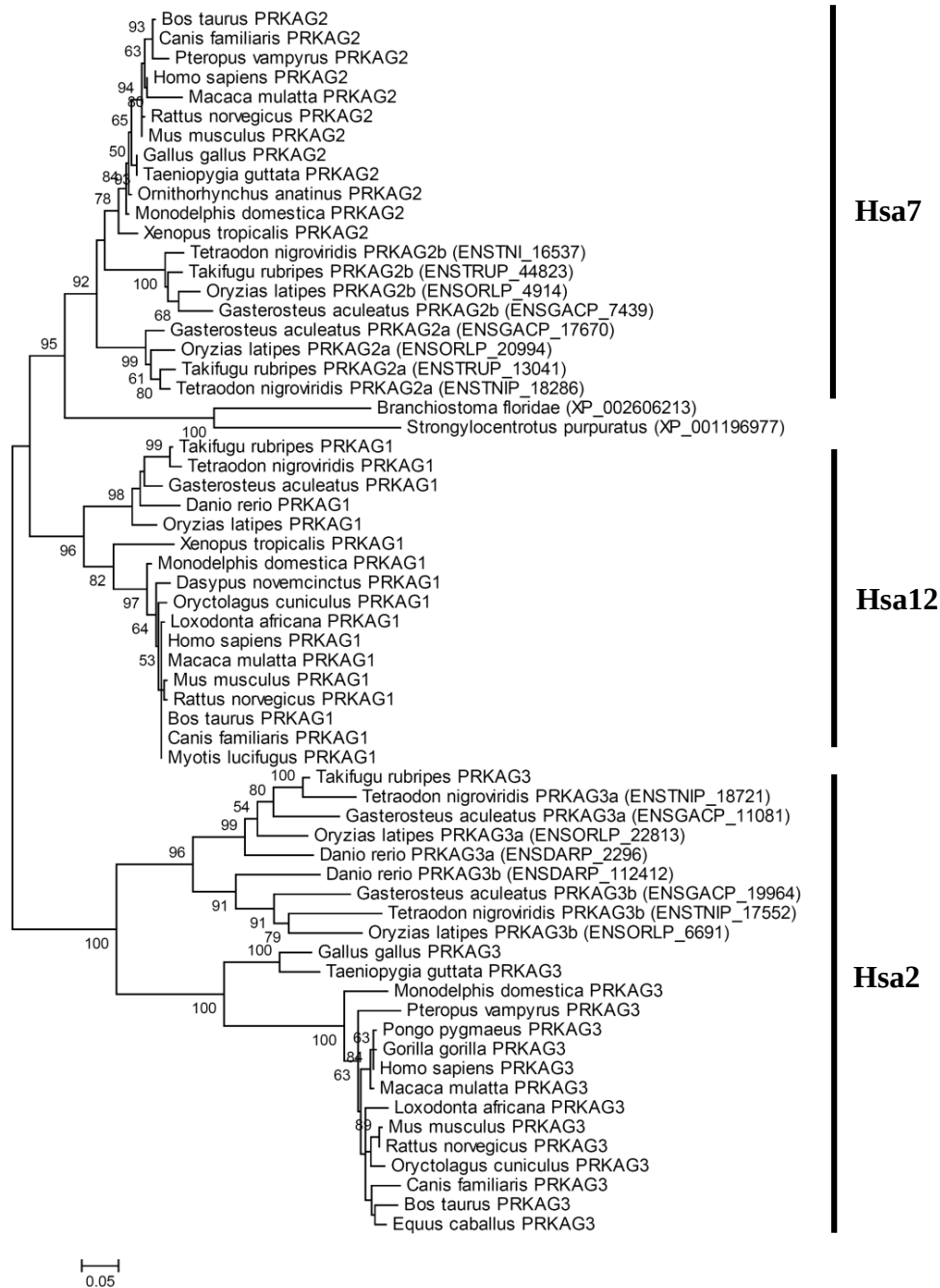
Protein phosphatase 1 regulatory (inhibitor)-PPP1R1



Phylogenetic tree of PPP1R1 family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the WAG model. The tree with the highest log likelihood (-3581.1795) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 3.1761)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 29 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 105 positions in the final dataset.

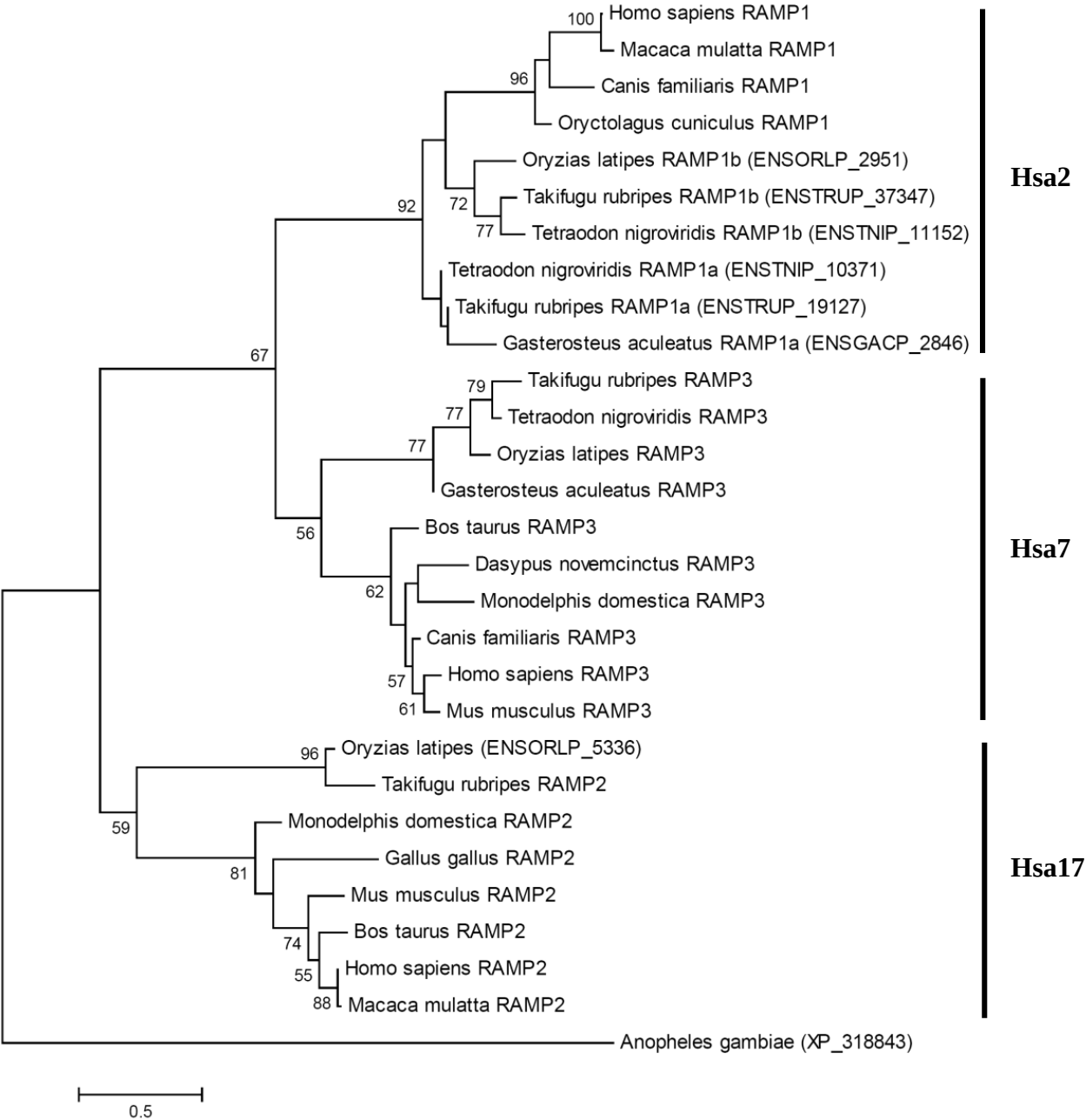
Protein kinase gamma subunit -PRKAG



Phylogenetic tree of PRKAG family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the WAG model. The tree with the highest log likelihood (-3758.6399) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 1.6340)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 39 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 142 positions in the final dataset.

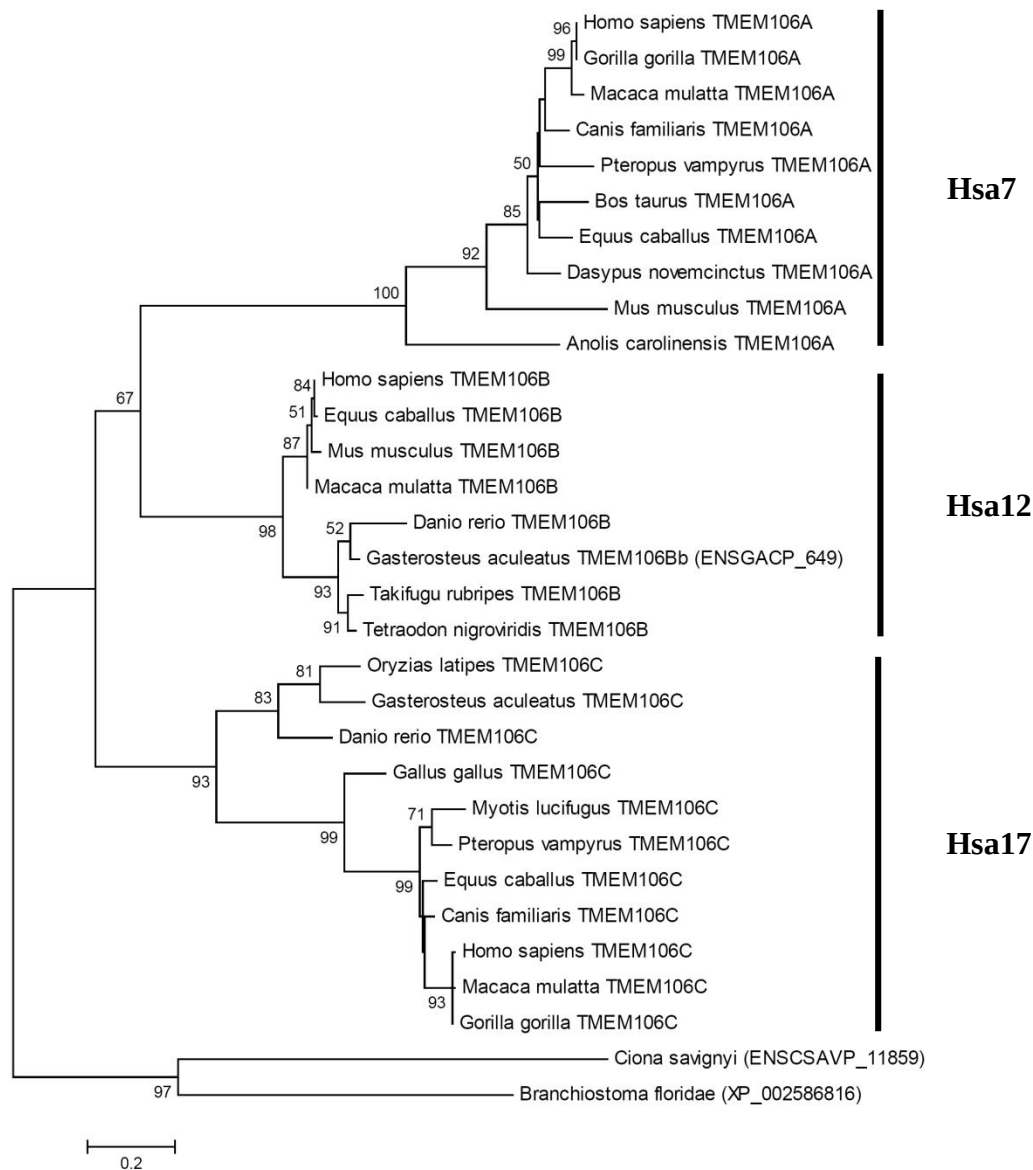
Receptor activity modifying protein-RAMP



Phylogenetic tree of RAMP family.

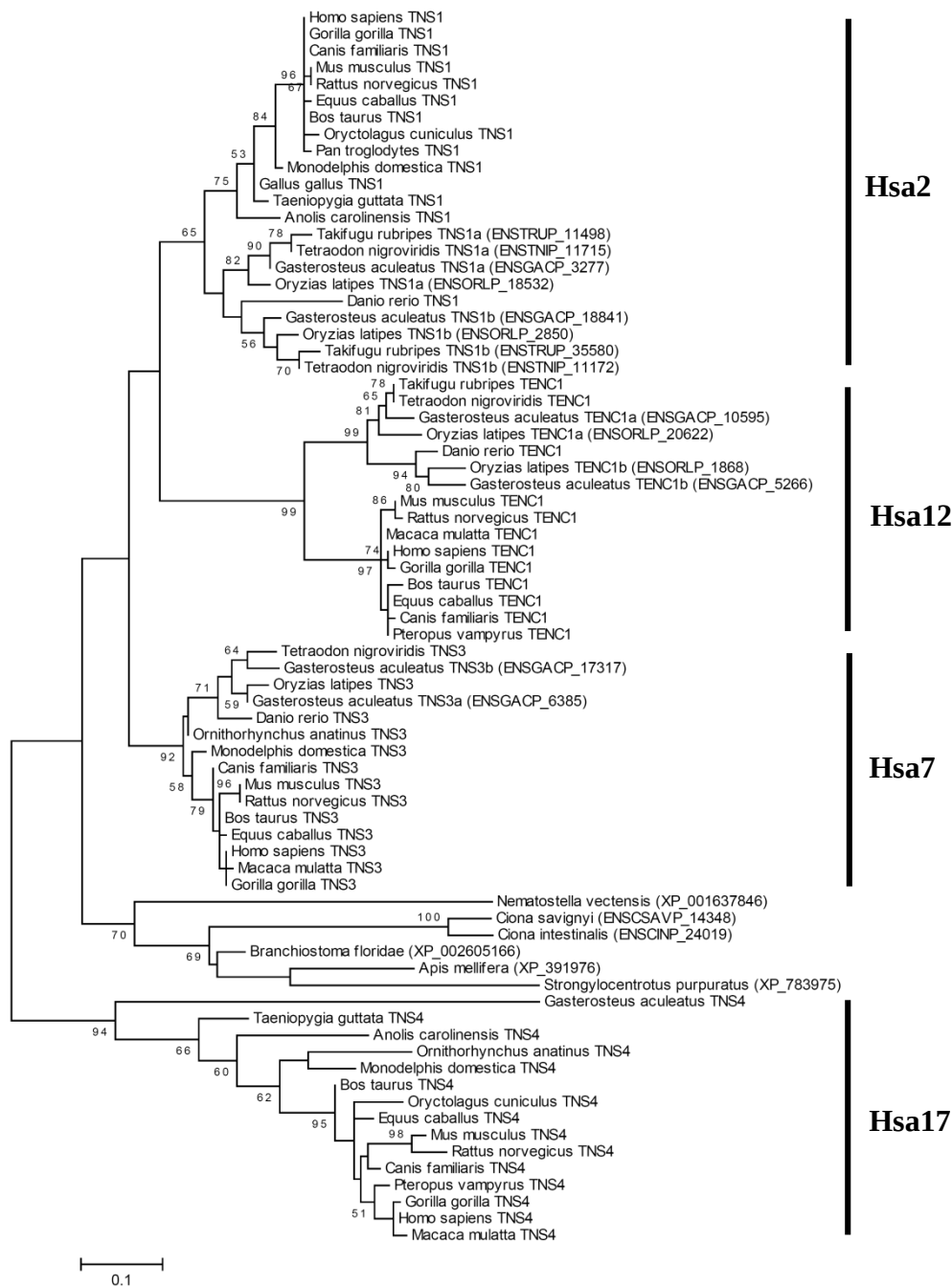
The evolutionary history was inferred by using the Maximum Likelihood method based on the WAG model. The tree with the highest log likelihood (-3368.6875) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches; only the values $\geq 50\%$ are shown here.. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 0.7477)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 37 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 193 positions in the final dataset.

Transmembrane protein 106-TMEM106



Phylogenetic tree of TMEM106 family.

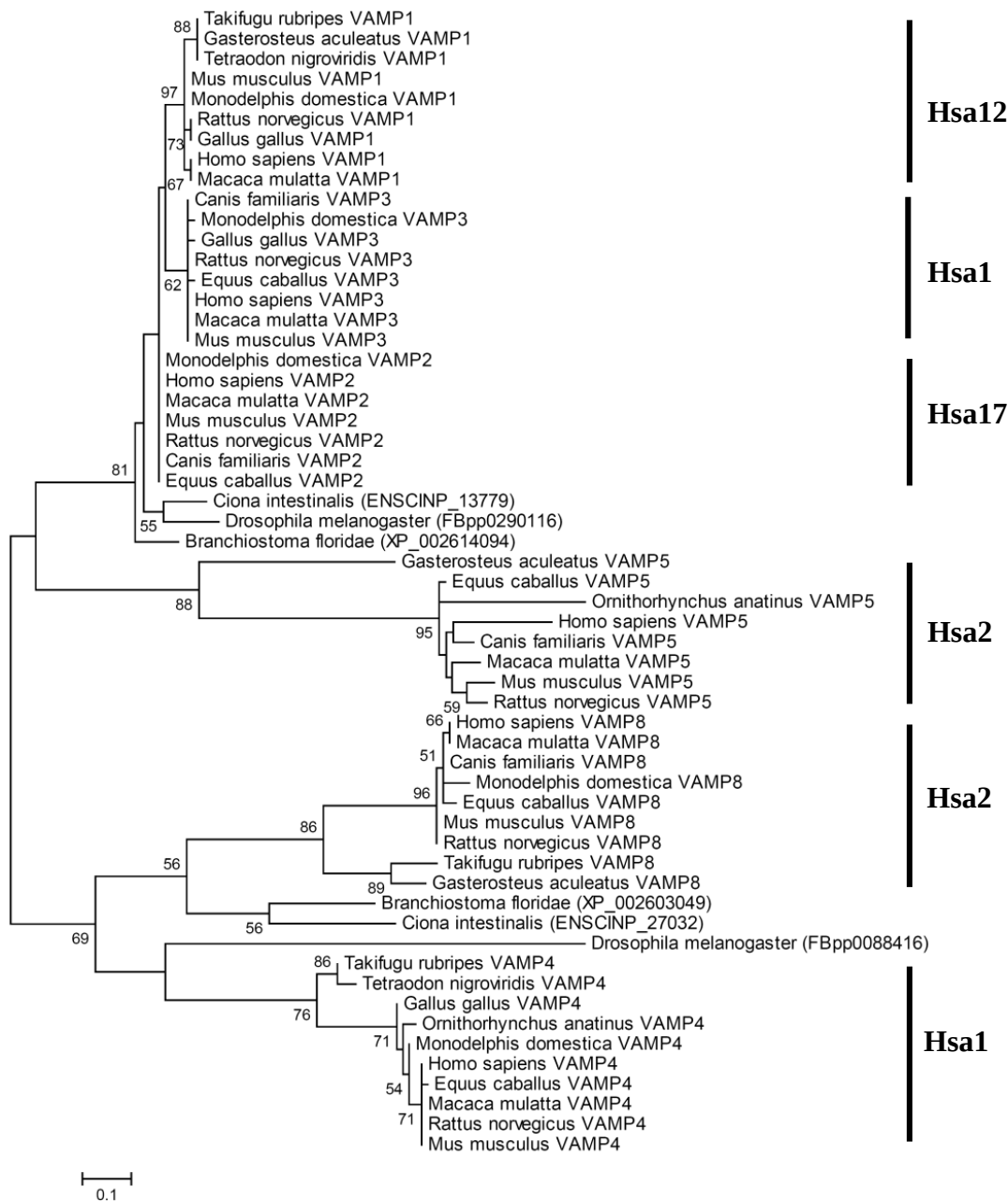
The evolutionary history was inferred by using the Maximum Likelihood method based on the WAG model. The tree with the highest log likelihood (-3180.7915) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 3.9690)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 19 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 170 positions in the final dataset.



Phylogenetic tree of TNS family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the WAG model. The tree with the highest log likelihood (-3368.6875) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches; only the values $\geq 50\%$ are shown here.. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 0.7477)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 37 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 193 positions in the final dataset.

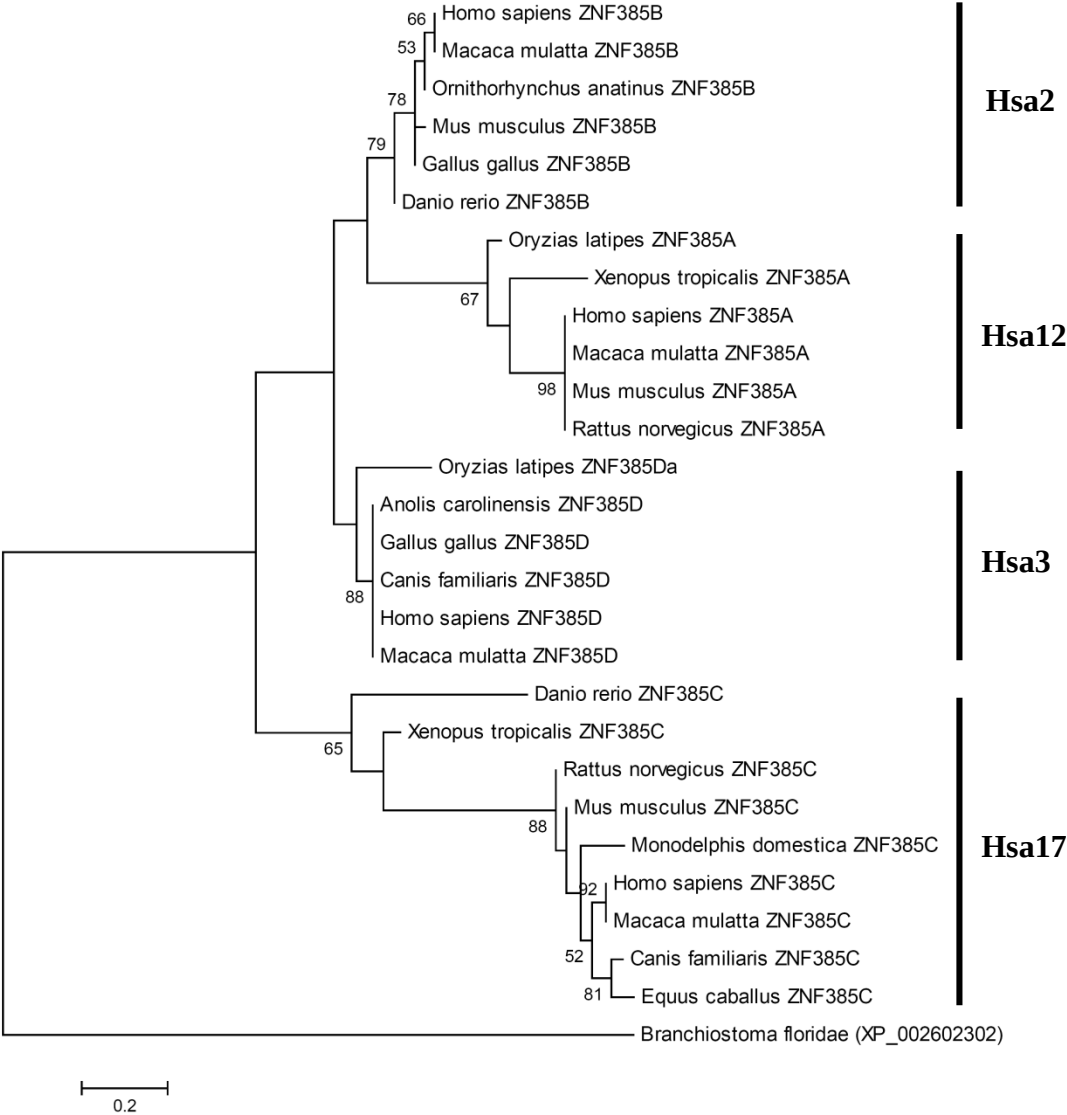
Vesicle-associated membrane protein-VAMP



Phylogenetic tree of VAMP family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the WAG model. The tree with the highest log likelihood (-5324.9973) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 0.9309)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 46 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 232 positions in the final dataset.

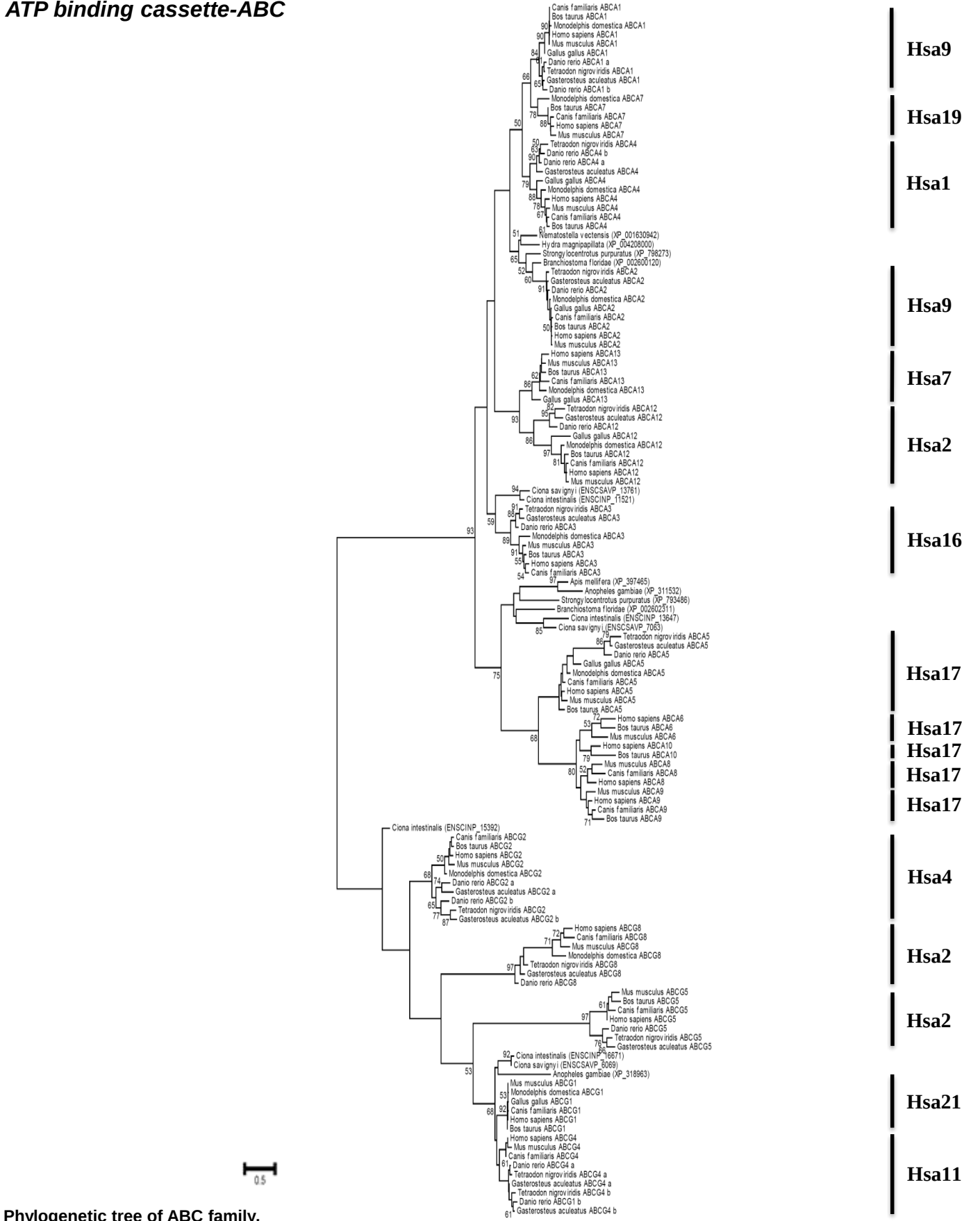
Zinc finger protein 385-ZNF385



Phylogenetic tree of ZNF385 family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the WAG model. The tree with the highest log likelihood (-3180.7915) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 3.9690)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 19 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 170 positions in the final dataset.

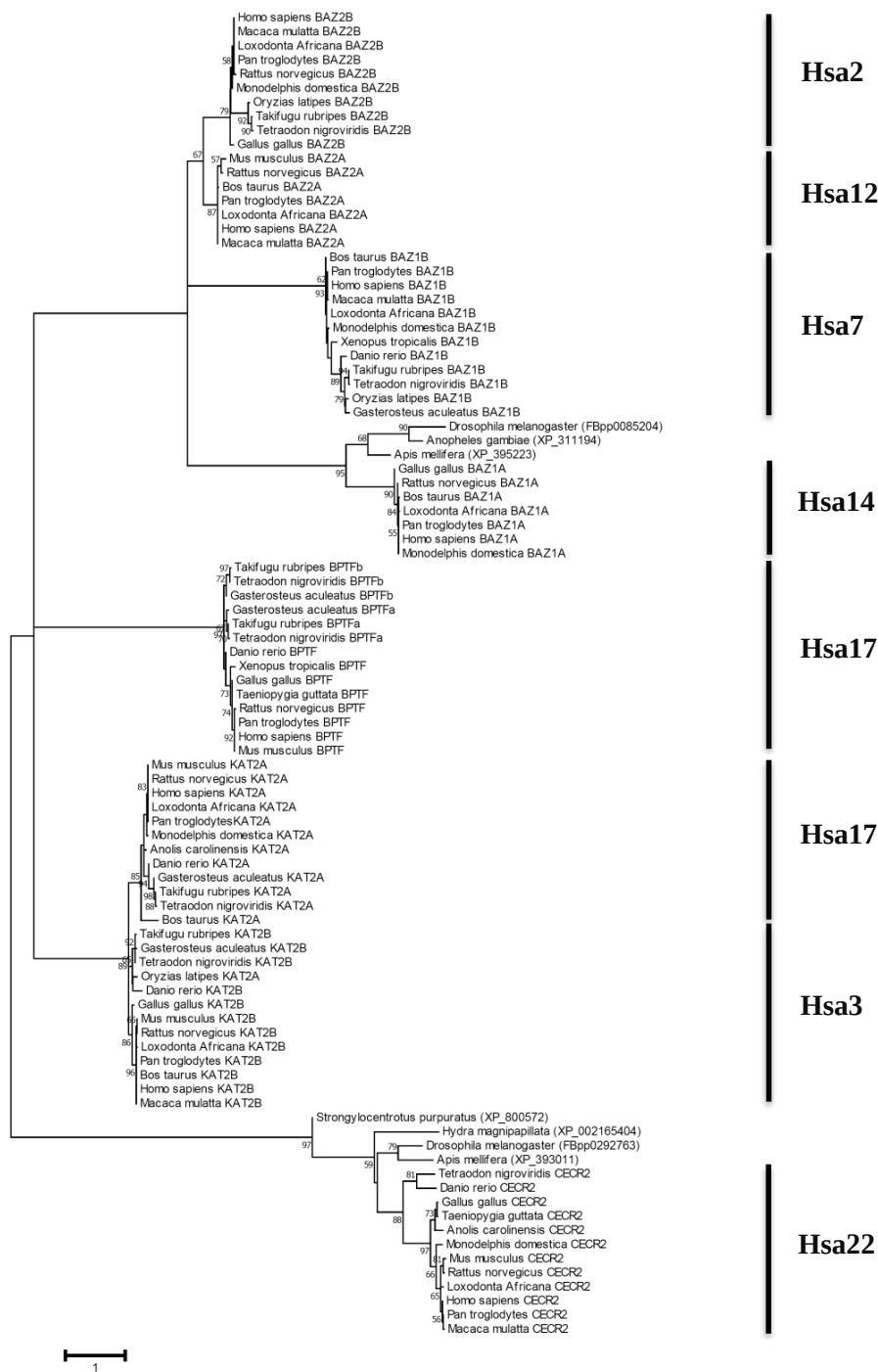
ATP binding cassette-ABC



Phylogenetic tree of ABC family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model (WAG) . The tree with the highest log likelihood (-12875.7865) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 6.5279)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 133 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 106 positions in the final dataset.

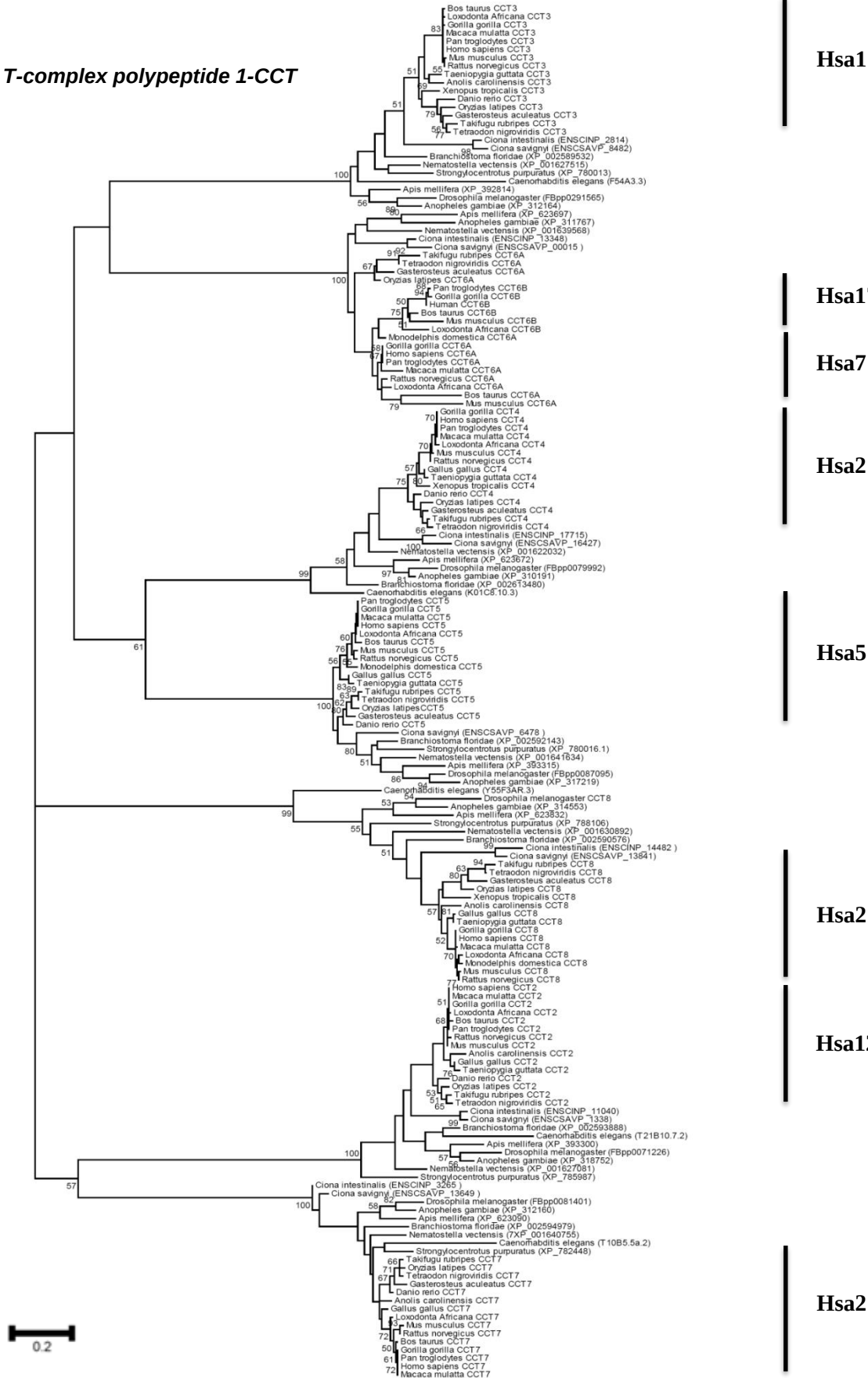
Bromodomain adjacent to zinc finger domain-BAZ



Phylogenetic tree of BAZ family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model (WAG). The tree with the highest log likelihood (-4470.3882) is shown. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 15.7989)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 94 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 74 positions in the final dataset.

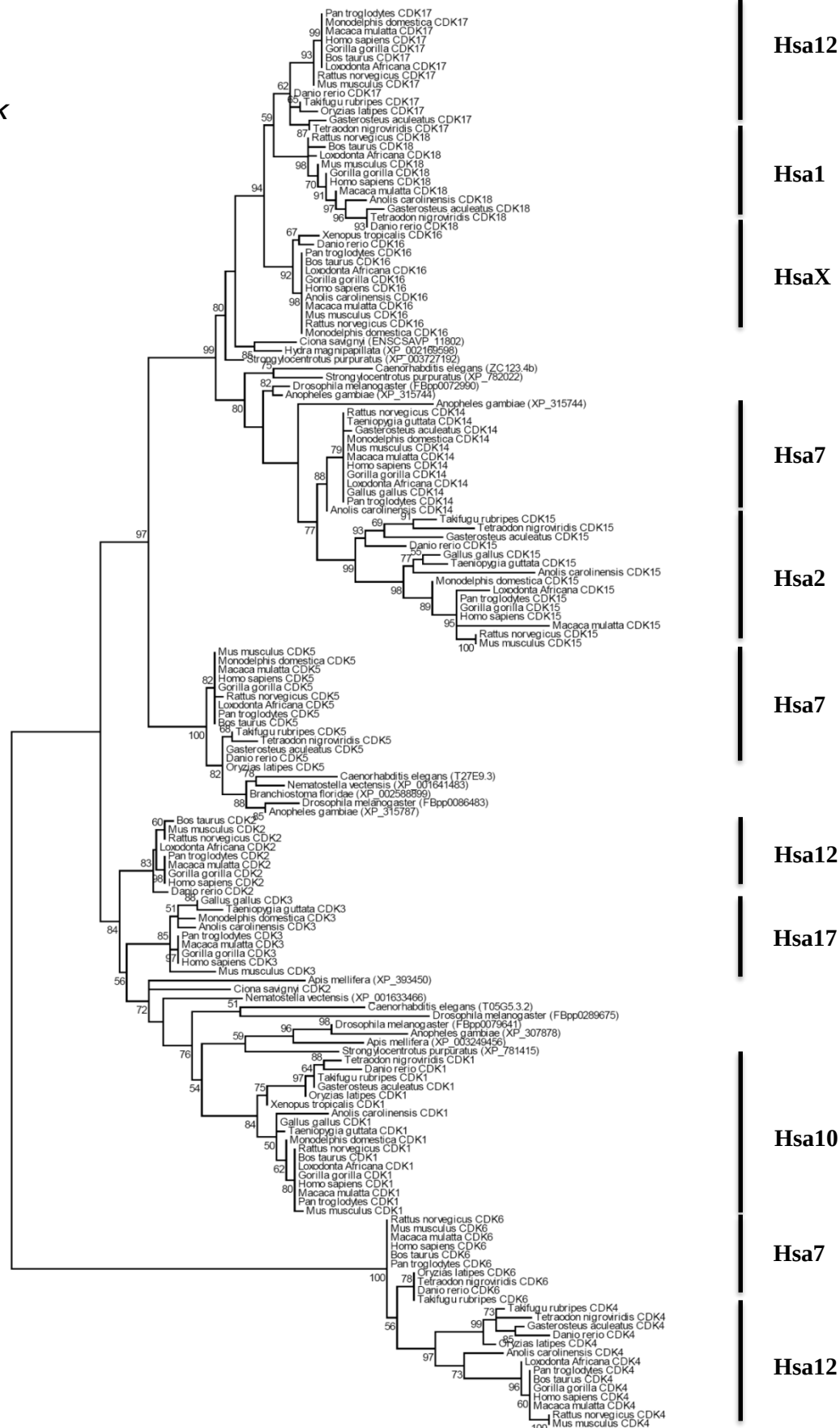
Chaperonin containing T-complex polypeptide 1-CCT



Phylogenetic tree of CCT family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model (WAG). The tree with the highest log likelihood (-15044.2076) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 2.8325)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 167 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 181 positions in the final dataset.

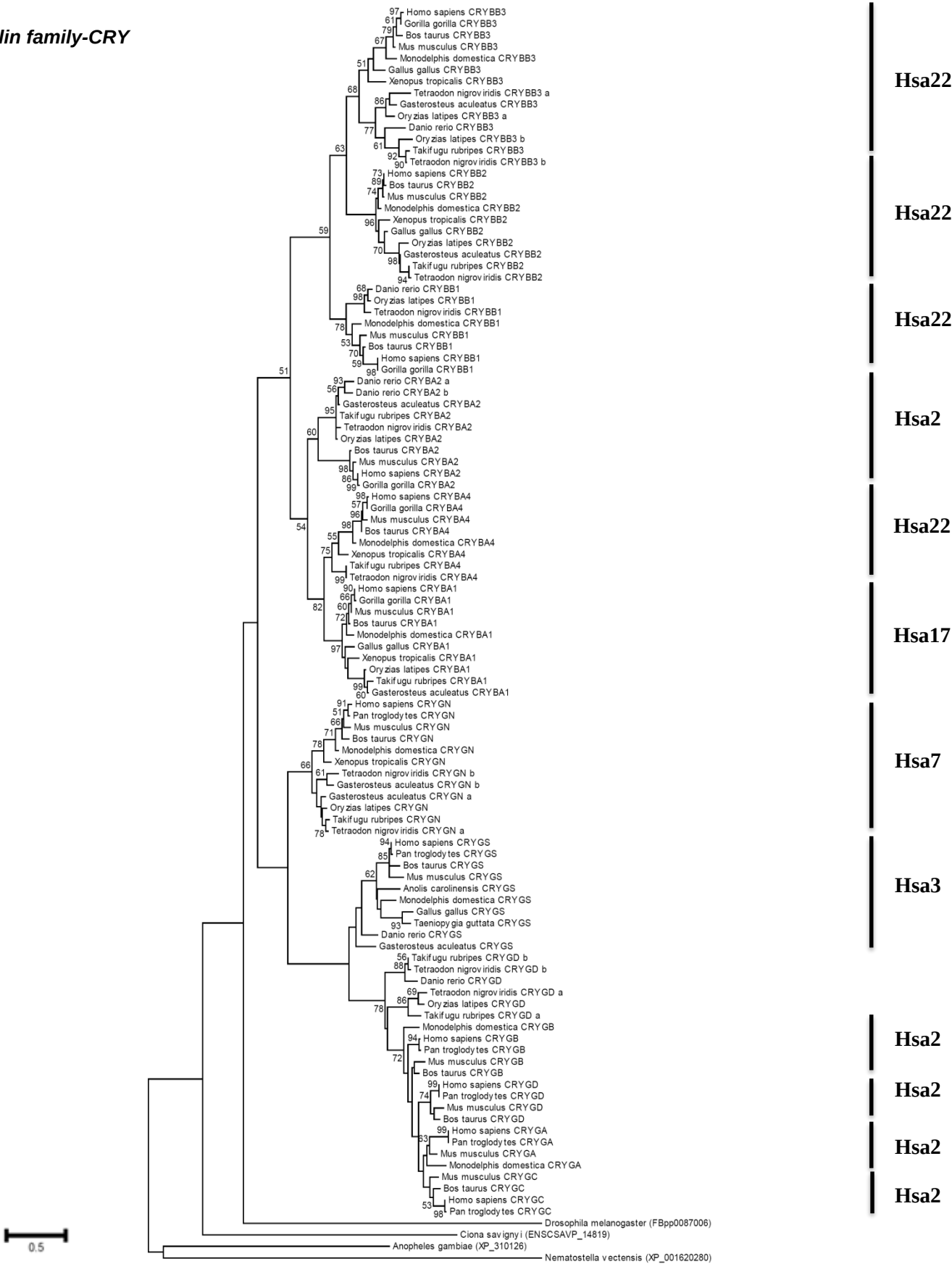
Cyclin-dependent kinases-CDK



Phylogenetic tree of CDK family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model (WAG). The tree with the highest log likelihood (-3143.8460) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 0.7603)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 160 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 89 positions in the final dataset.

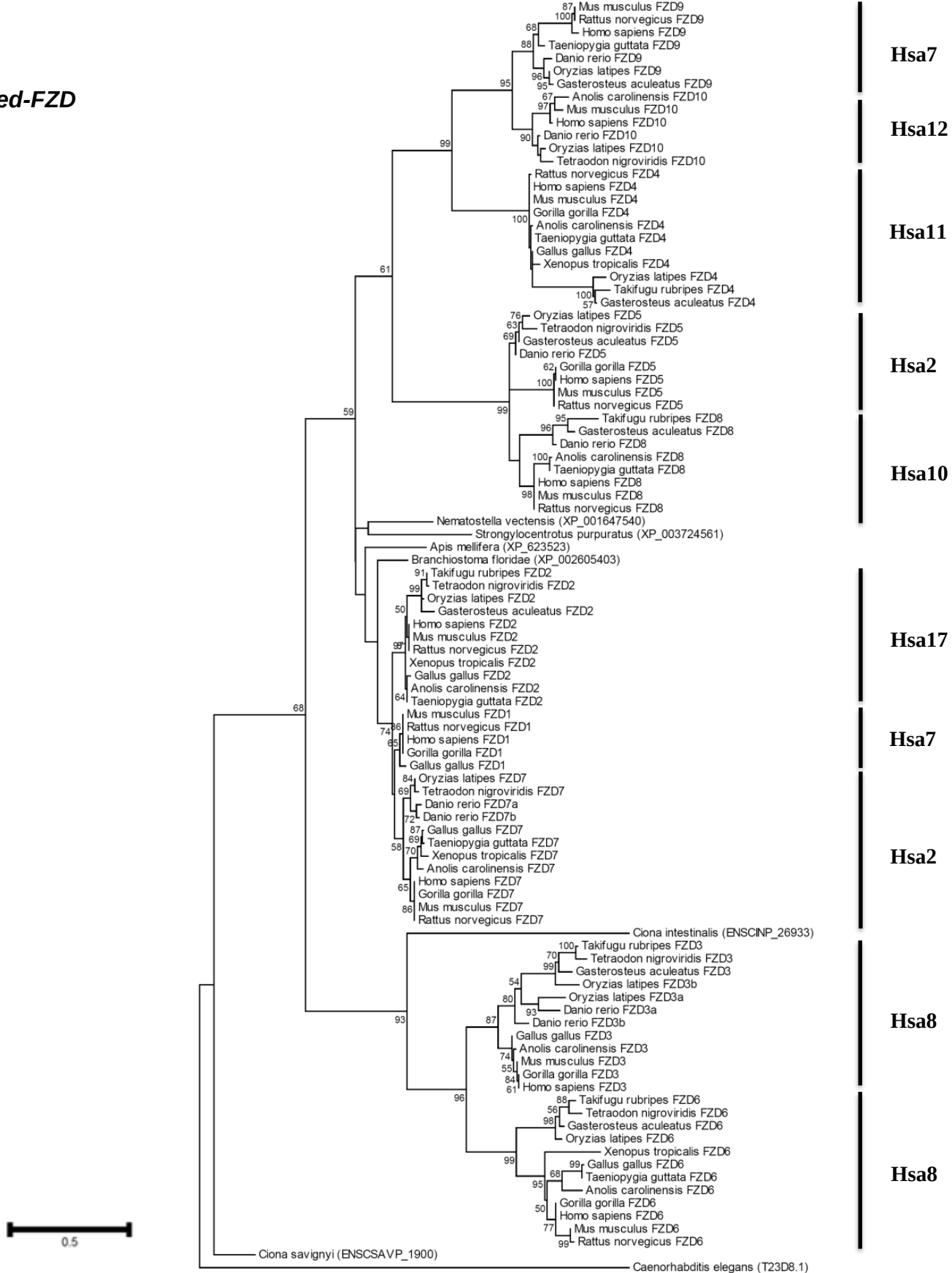
Crystallin family-CRY



Phylogenetic tree of CRY family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model (WAG) . The tree with the highest log likelihood (-8187.3532) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 4.1151)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 109 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 110 positions in the final dataset.

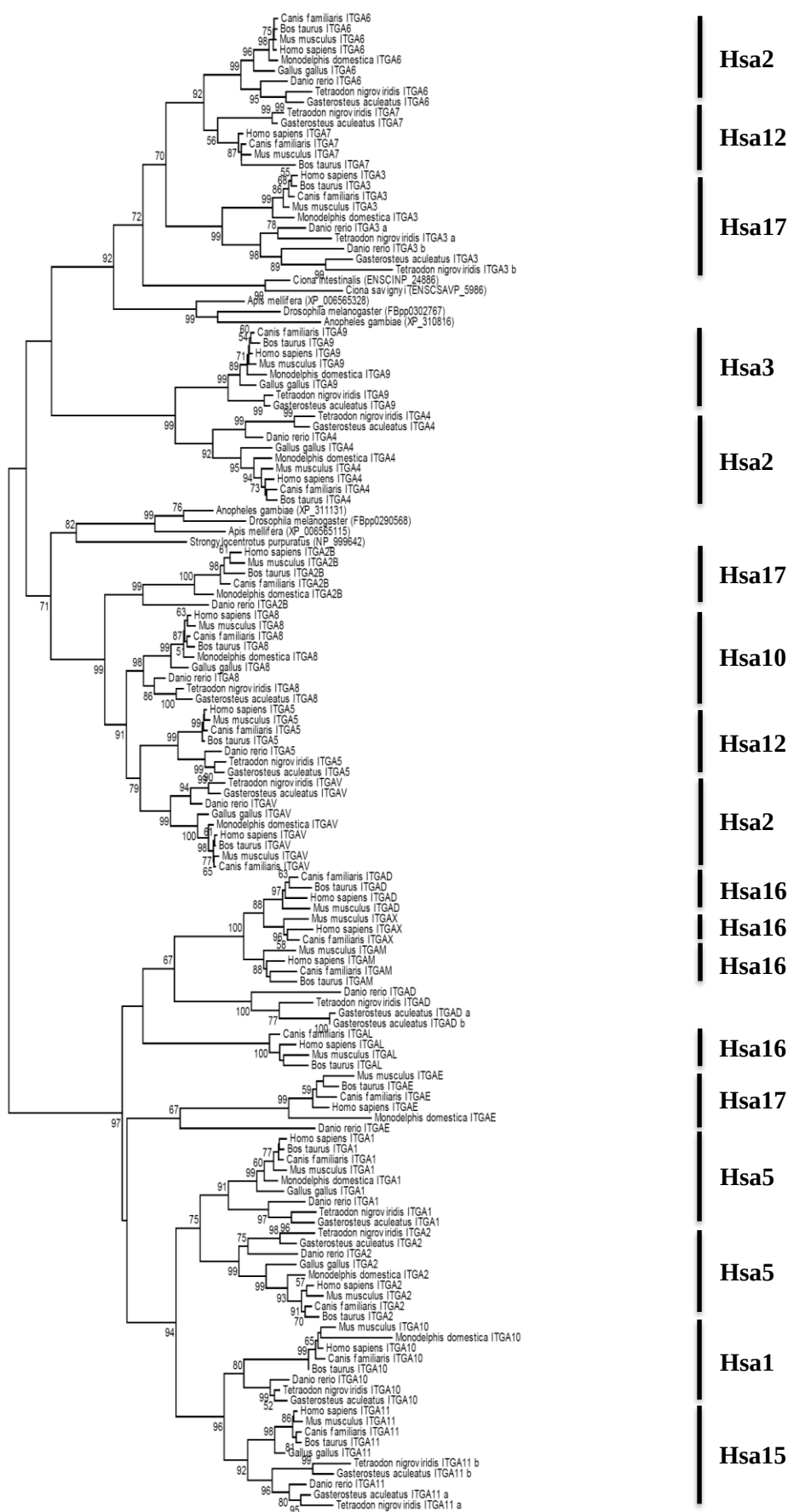
Frizzled-FZD



Phylogenetic tree of FZD family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model (WAG). The tree with the highest log likelihood (-6464.5208) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 1.0348)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 99 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 187 positions in the final dataset.

Integrin alpha family –ITGA

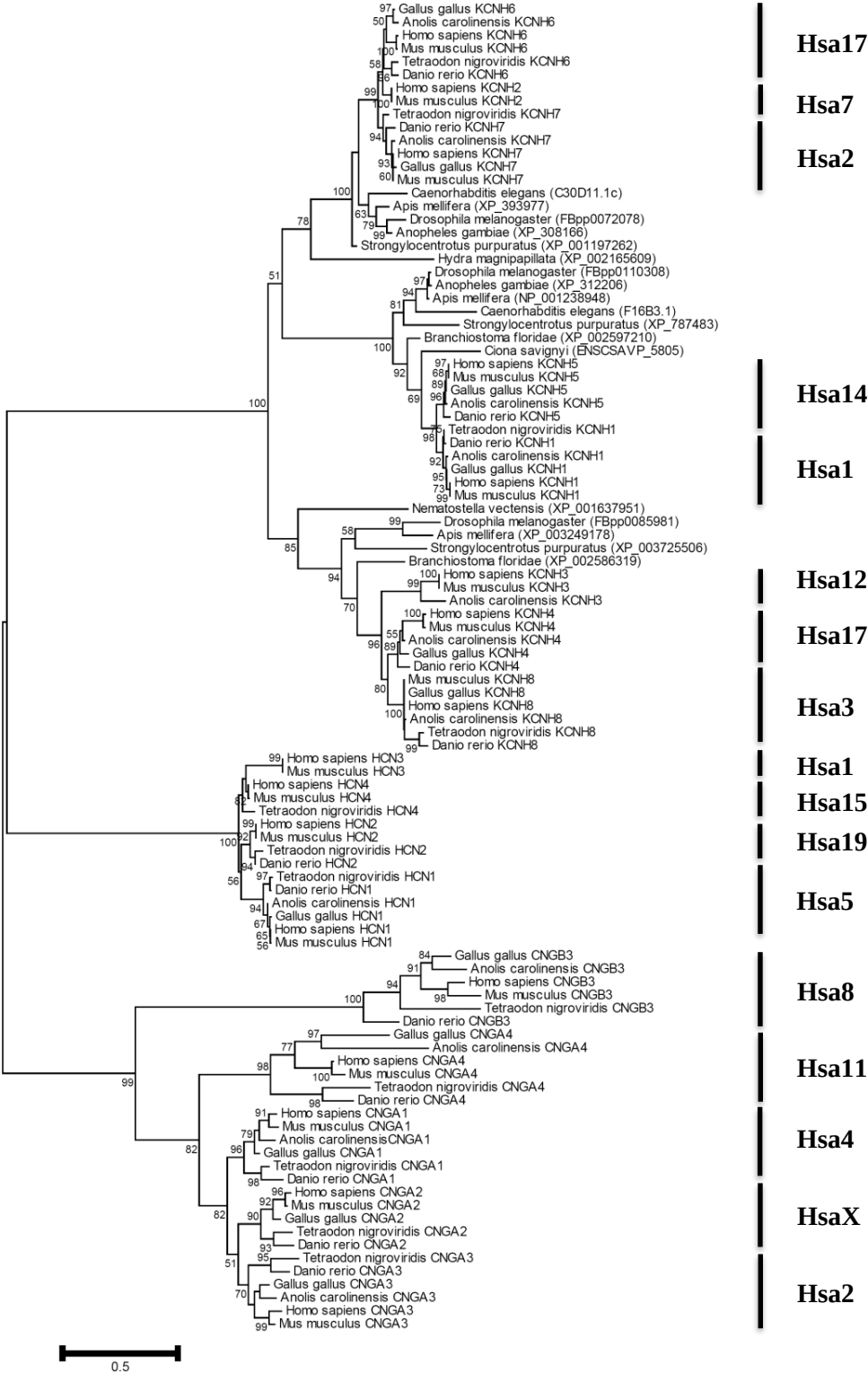


0.2

Phylogenetic tree of ITGA family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model (WAG) . The tree with the highest log likelihood (-31941.7119) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 2.6582)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 143 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 241 positions in the final dataset.

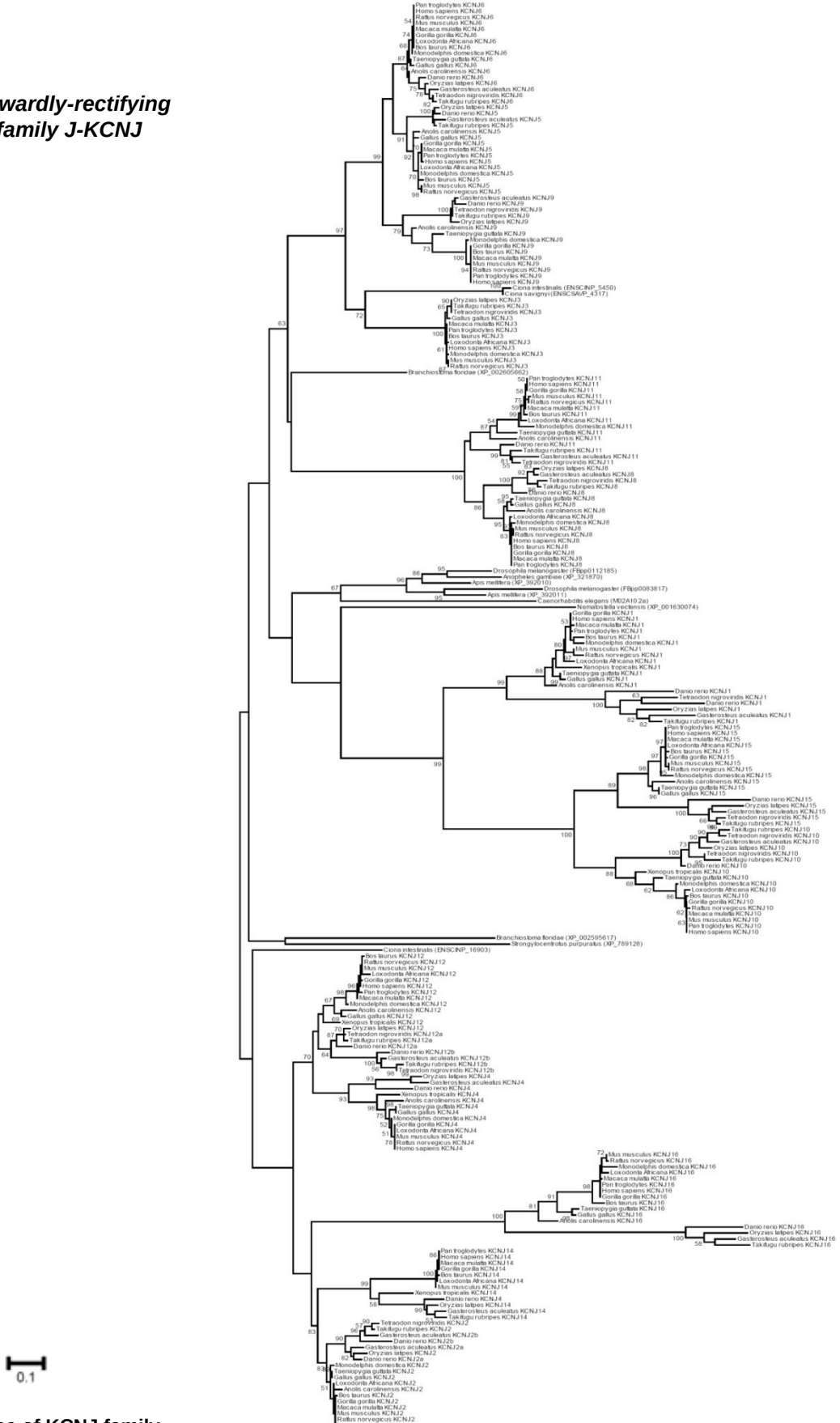
Potassium voltage-gated channel, subfamily H-KCNH



Phylogenetic tree of KCN family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model (WAG). The tree with the highest log likelihood (-18772.7372) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 2.2870)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 101 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 331 positions in the final dataset.

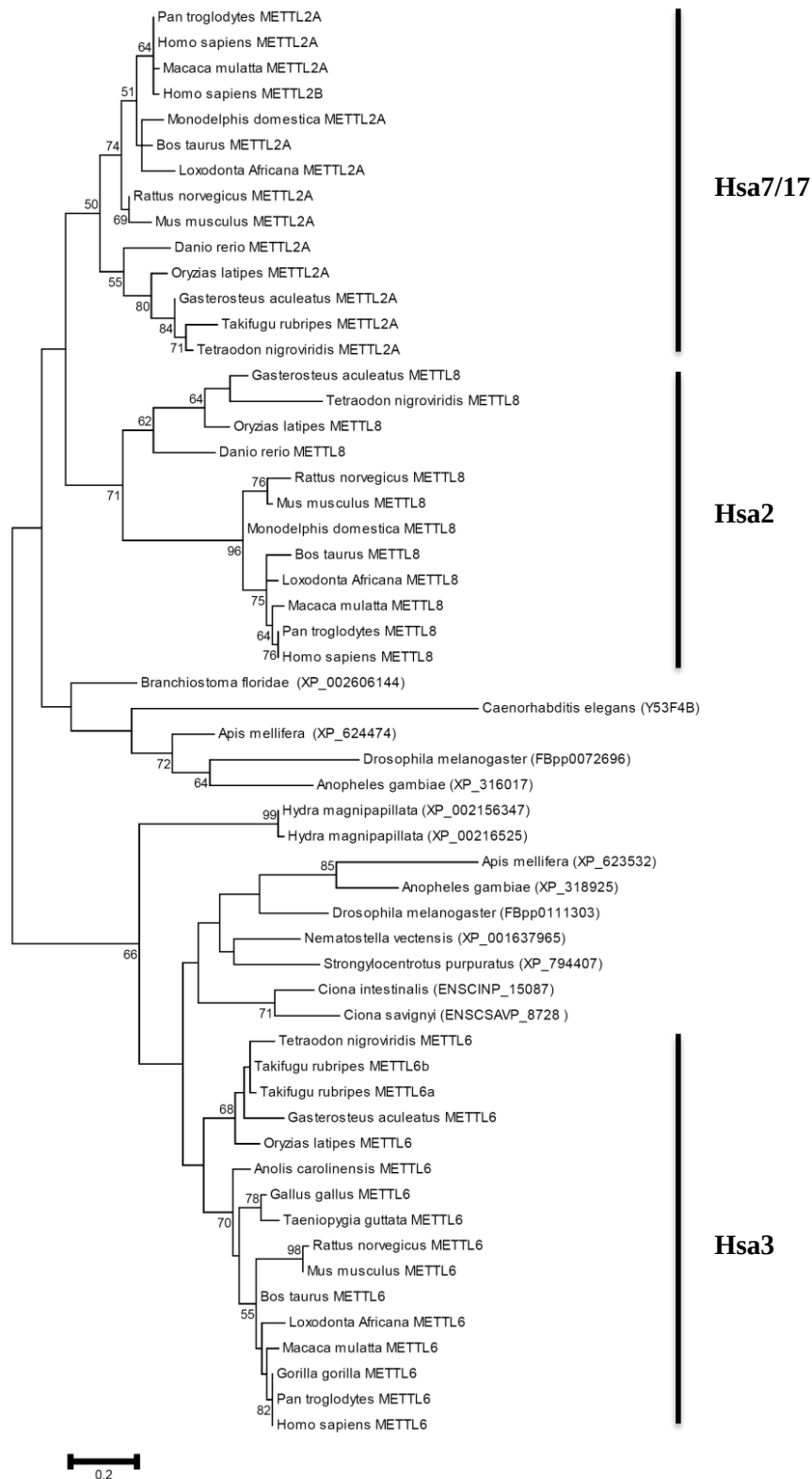
Hsa21
Hsa11
Hsa1
Hsa2
Hsa11
Hsa12
Hsa11
Hsa21
Hsa1
Hsa17
Hsa22
Hsa17
Hsa19
Hsa17



Phylogenetic tree of KCNJ family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-16545.8773) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 1.3860)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 238 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 226 positions in the final dataset.

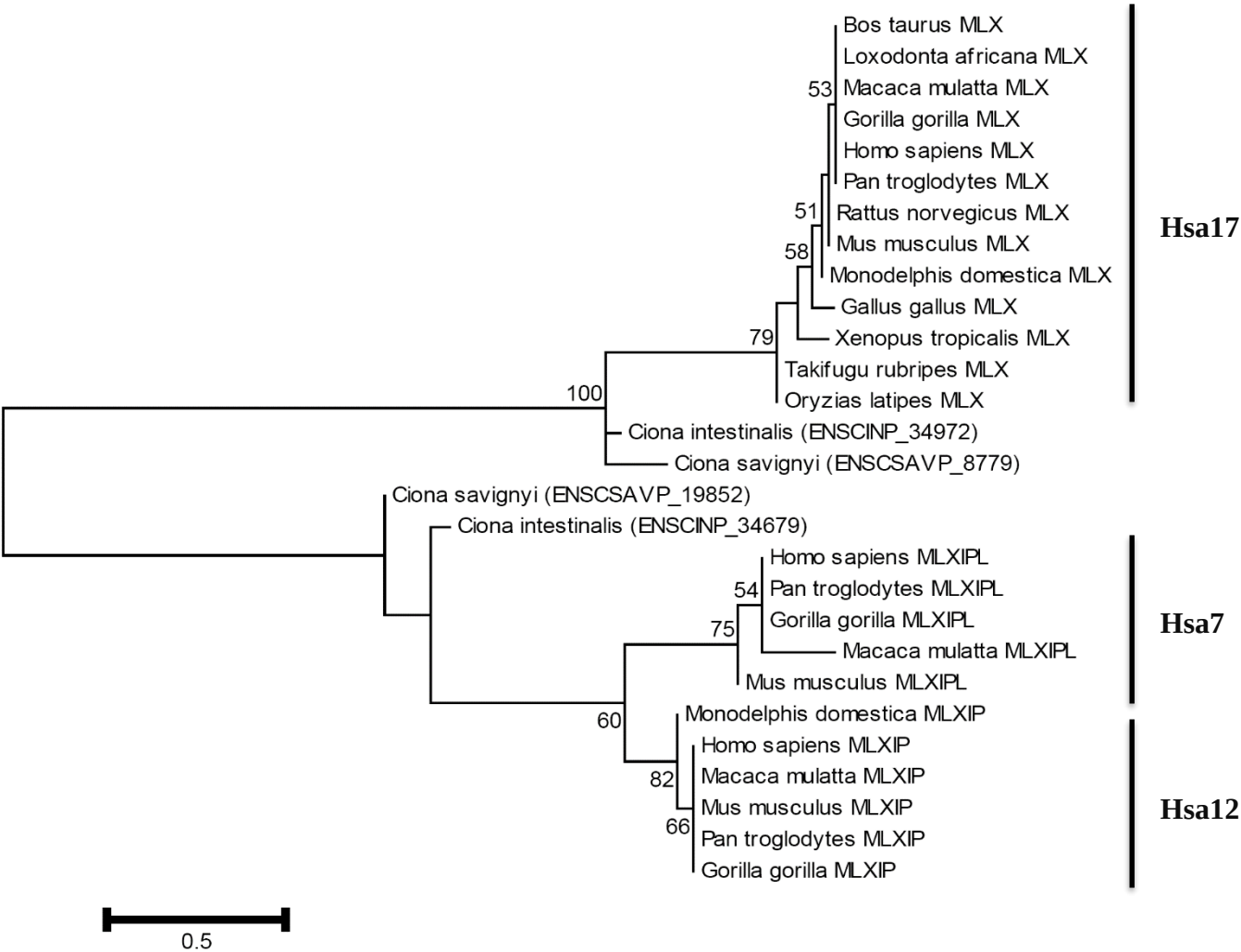
Methyltransferase-METTL



Phylogenetic tree of METTL family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model (WAG).The tree with the highest log likelihood (-2411.5458) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 1.9442)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 56 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 59 positions in the final dataset

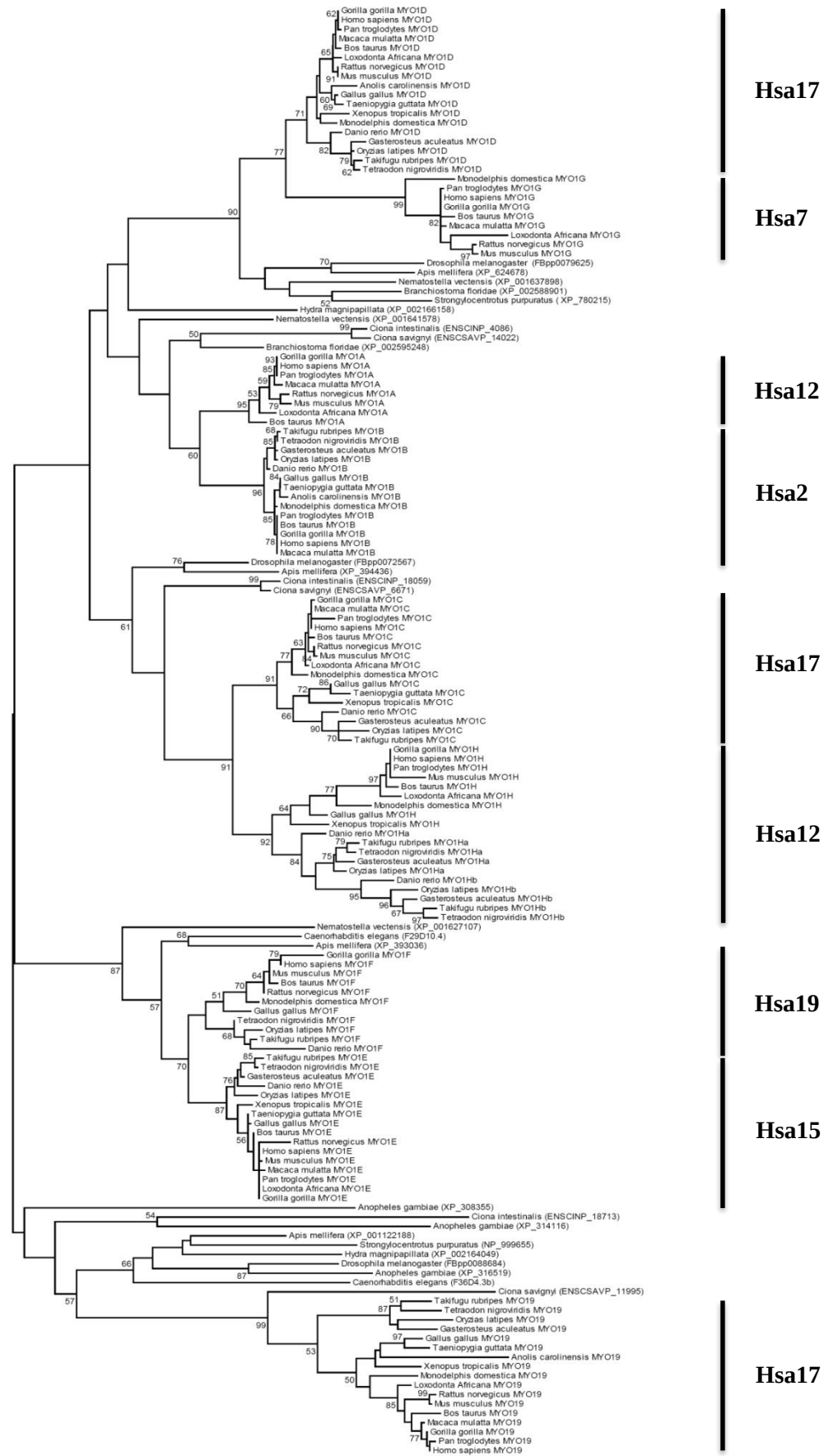
MLX interacting protein-MLX



Phylogenetic tree of MLX family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model (WAG). The tree with the highest log likelihood (-729.9093) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 3.7464)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 28 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 48 positions in the final dataset.

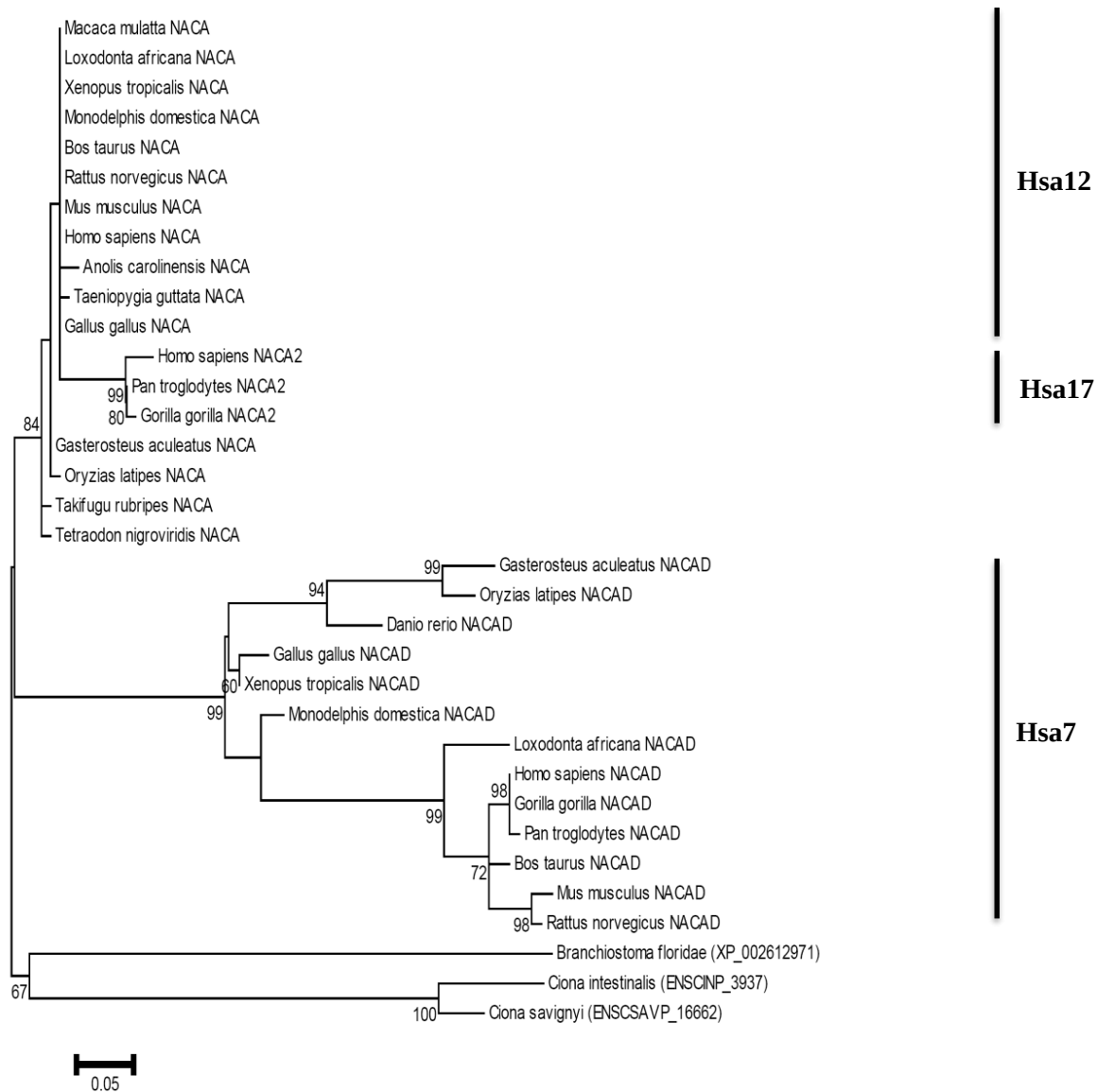
Myosin 1-MYO1



Phylogenetic tree of MYO1 family.

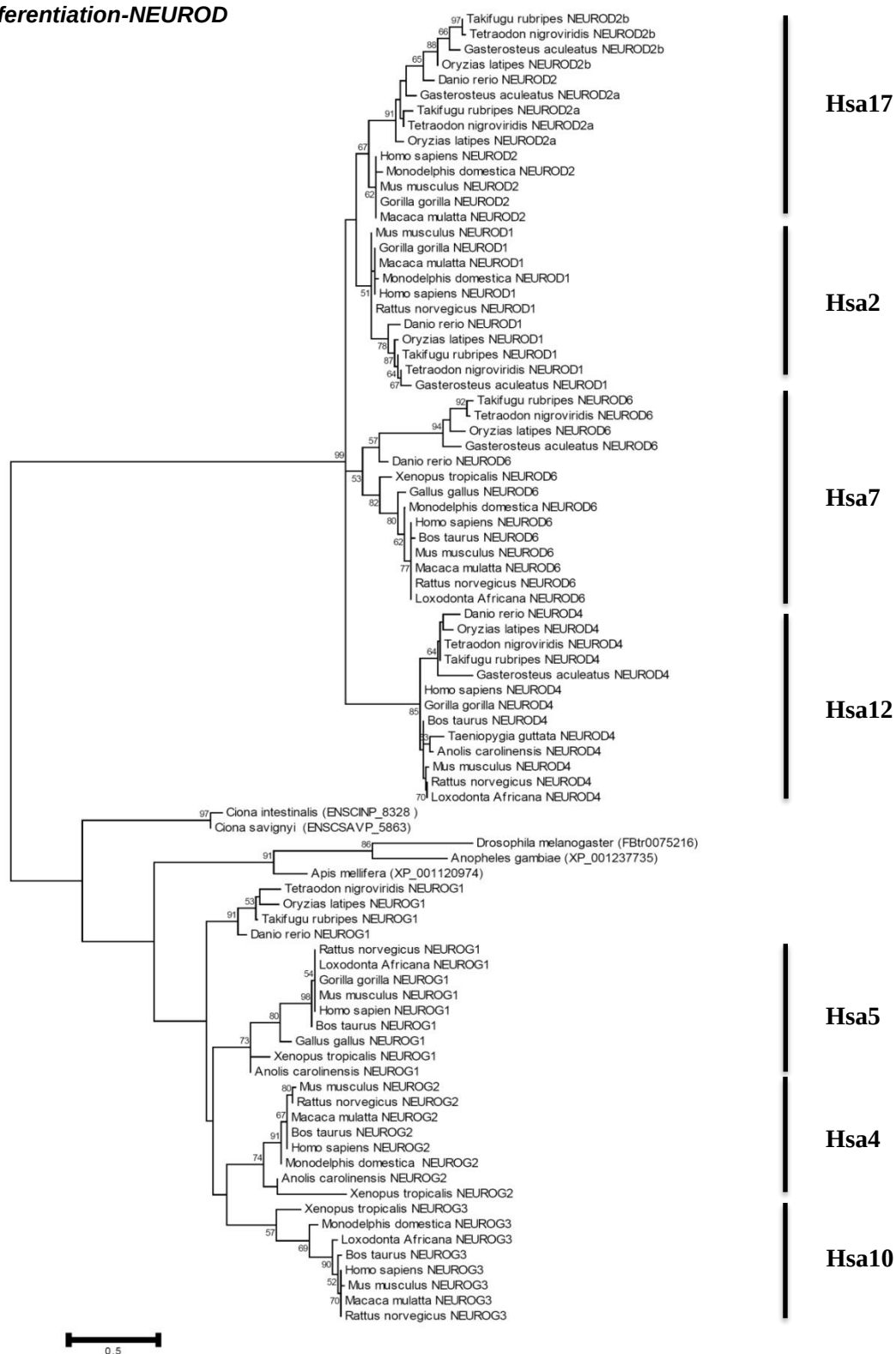
The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model (WAG). The tree with the highest log likelihood (-10608.9913) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 1.4415)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 155 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 113 positions in the final dataset.

NAC alpha domain proteins-NACA



Phylogenetic tree of NACA family.

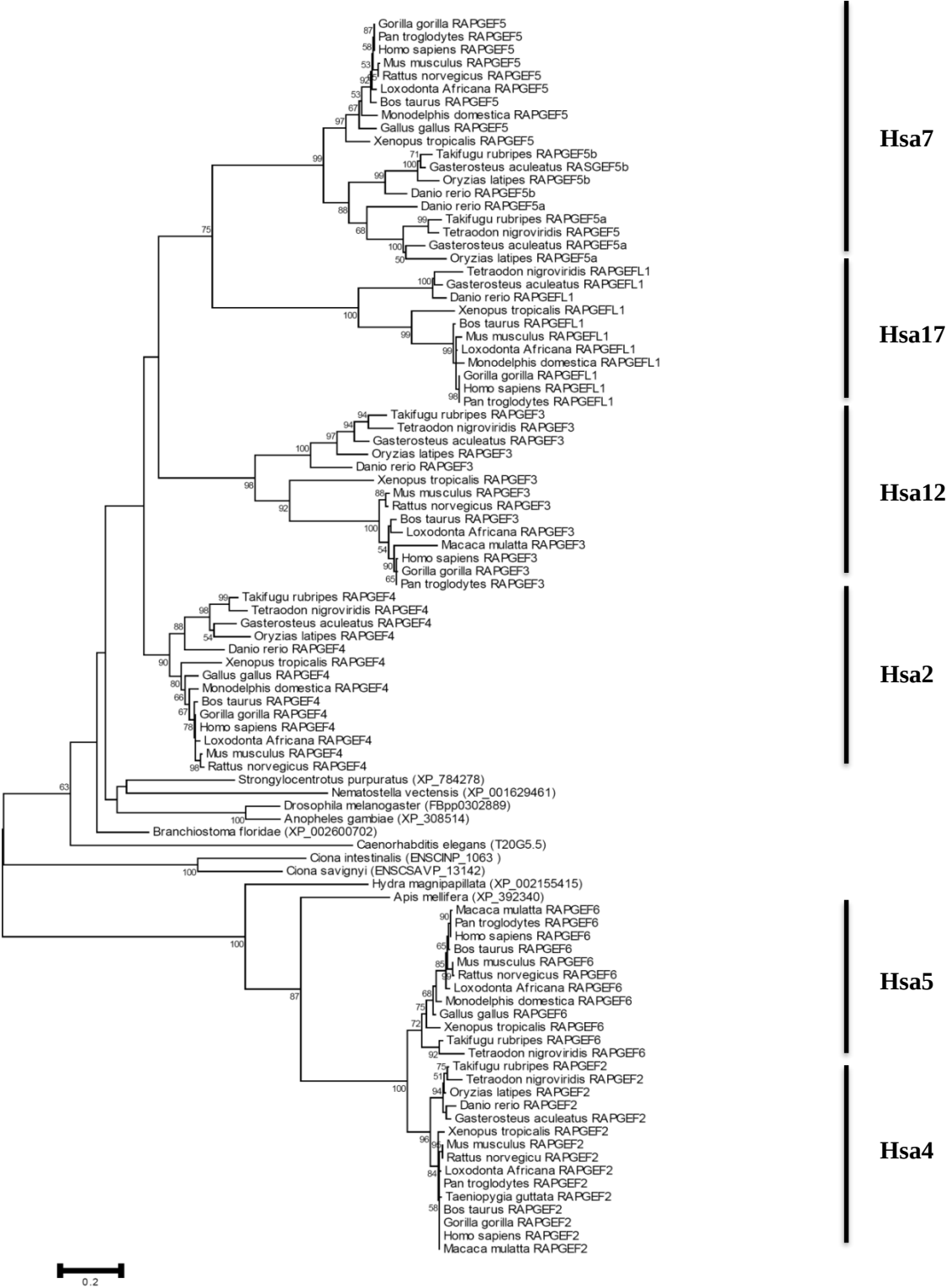
The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model (WAG). The tree with the highest log likelihood (-1422.3537) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 0.8852)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 34 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 123 positions in the final dataset.



Phylogenetic tree of NEUROD family.

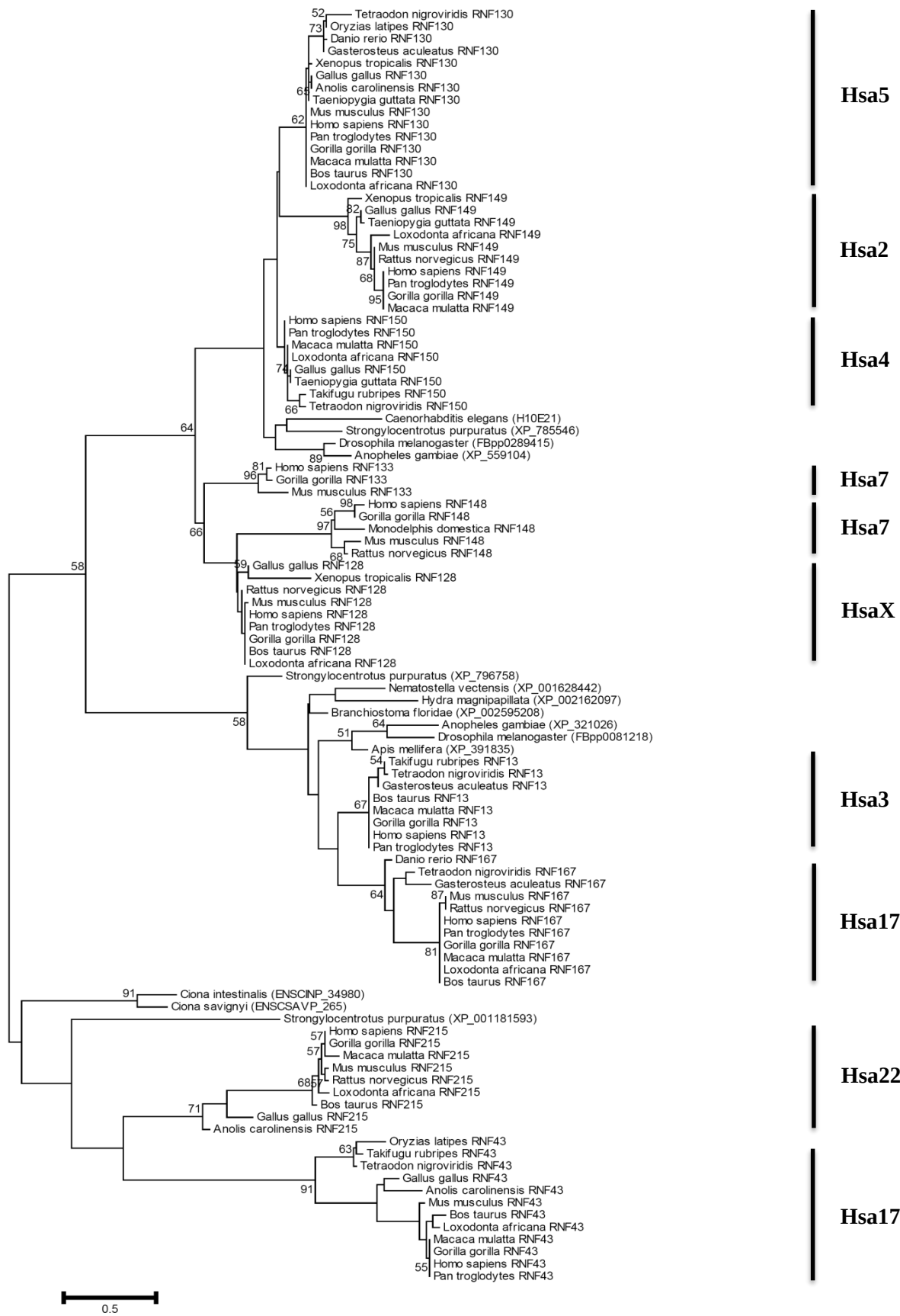
The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model (WAG). The tree with the highest log likelihood (-2687.5484) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 0.8219)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 86 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 84 positions in the final dataset.

Rap guanine nucleotide exchange factor-RAPGEF



Phylogenetic tree of RAPGEF family.

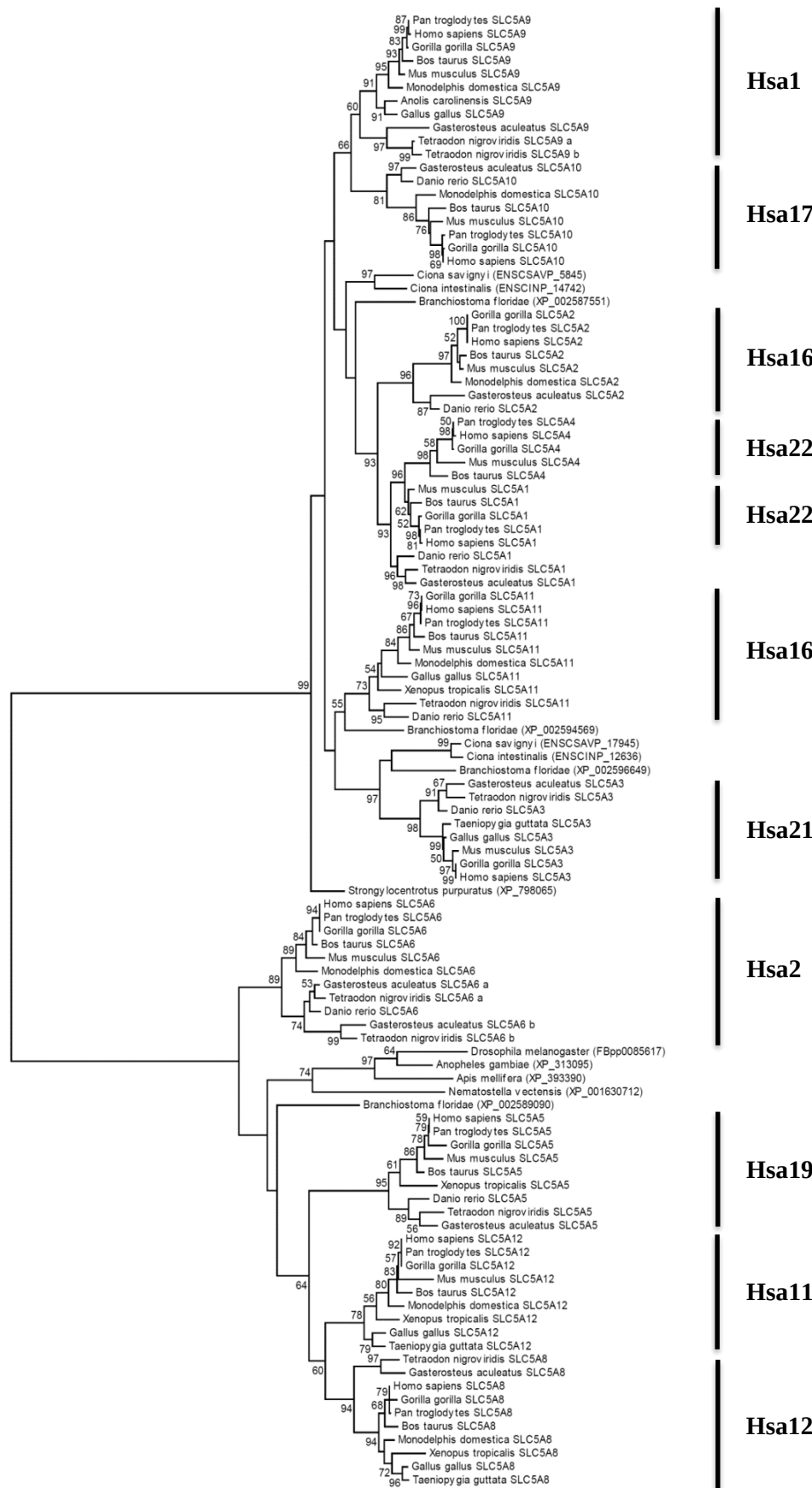
The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model (WAG.)The tree with the highest log likelihood (-14824.4970) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 2.7948)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 95 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 263 positions in the final dataset.



Phylogenetic tree of RNF family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model (WAG). The tree with the highest log likelihood (-3788.2676) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values $\geq 50\%$ are shown here . A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 6.2230)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 104 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 58 positions in the final dataset.

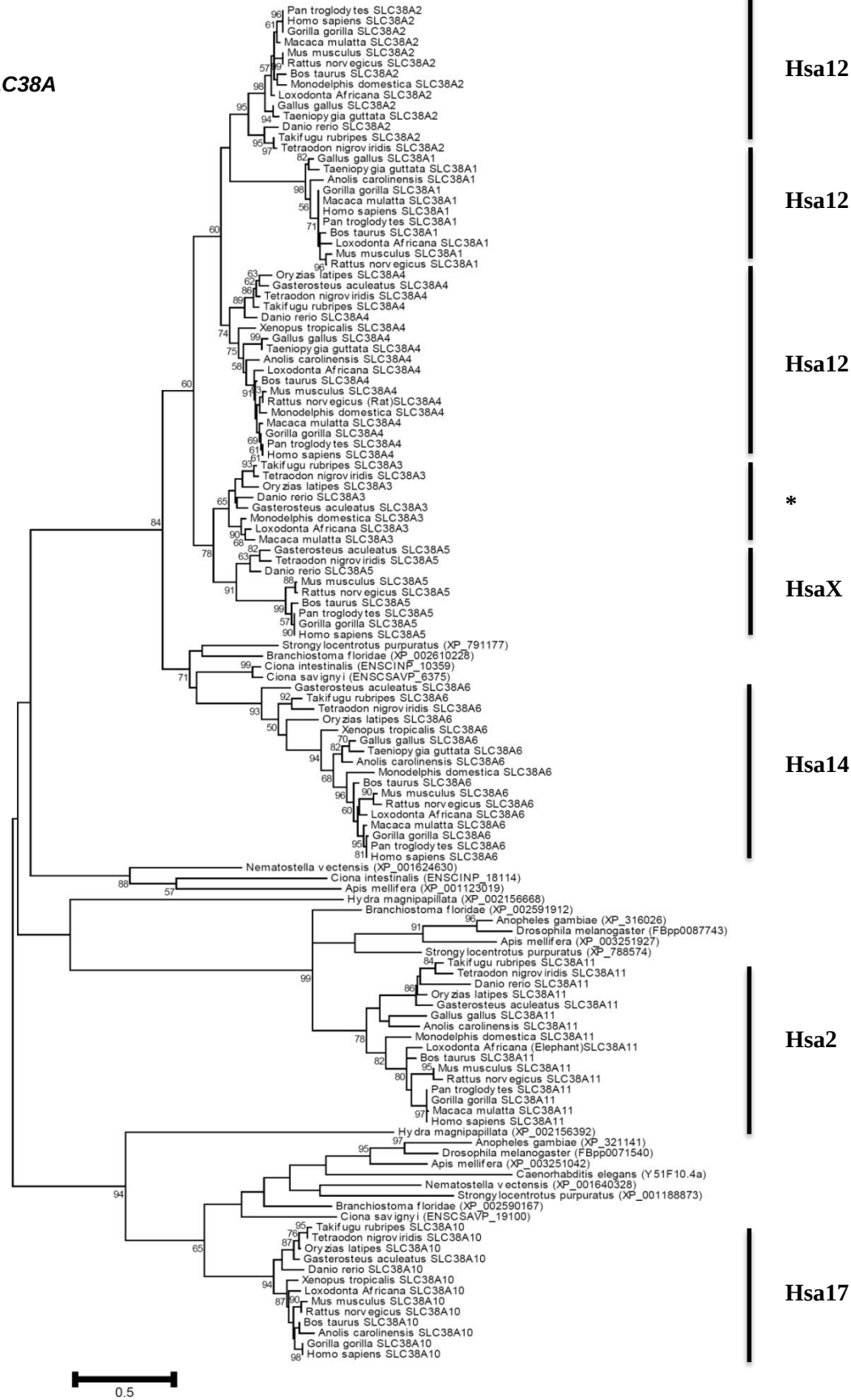
Solute carrier family 5 A-SLC5A



Phylogenetic tree of SLC5A family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model (WAG). The tree with the highest log likelihood (-18874.9381) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values $\geq 50\%$ are shown here . A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 1.7805)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 110 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 278 positions in the final dataset.

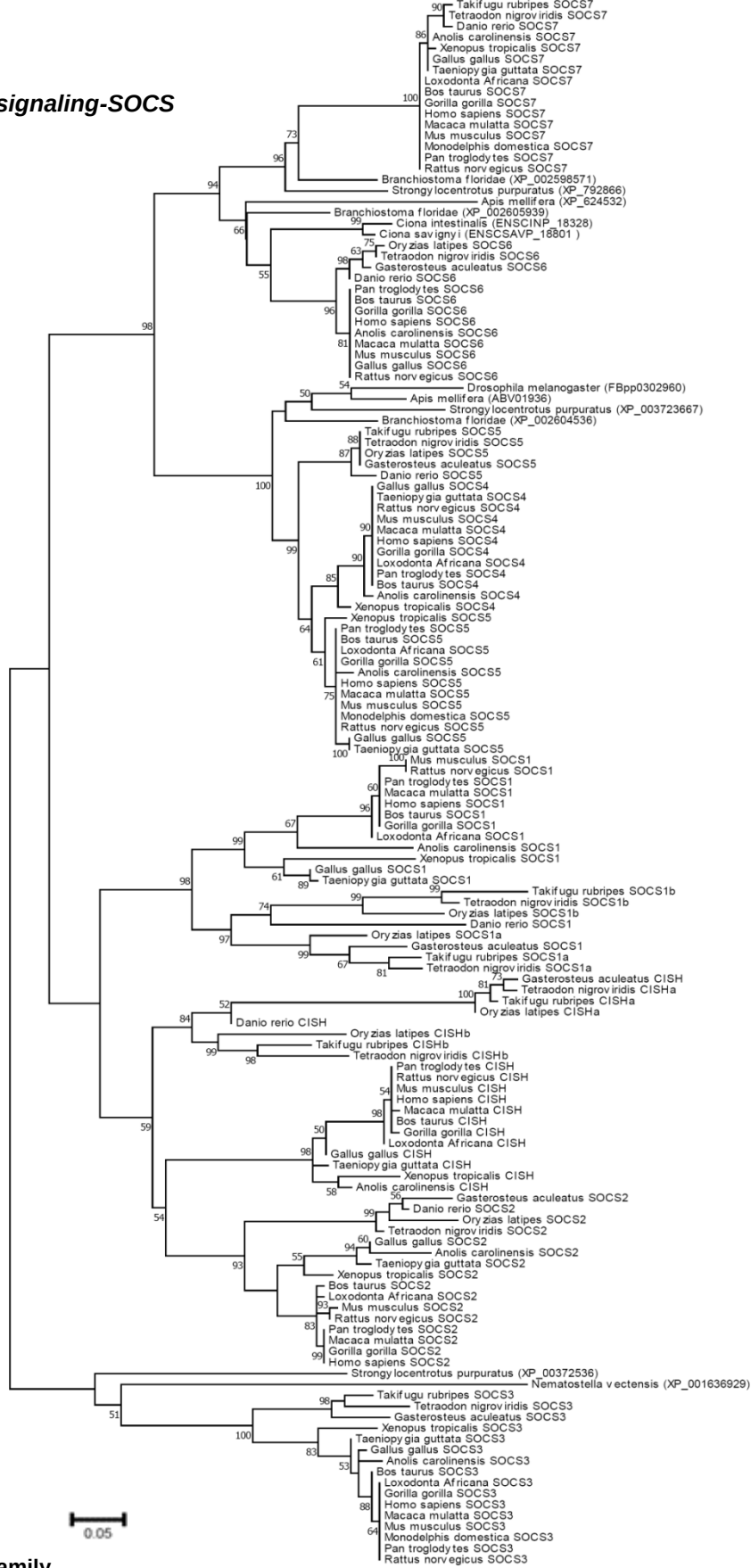
Solute carrier family 38 A-SLC38A



Phylogenetic tree of SLC38A family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-13076.0884) is shown. The percentage in which the associated taxa clustered together is shown next to the branches; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 2.8208)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 128 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 160 positions in the final dataset.

Suppressor of cytokine signaling-SOCS



Phylogenetic tree of SOCS family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model (WAG). The tree with the highest log likelihood (-4508.8205) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches; only the values $\geq 50\%$ are shown here.. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 1.5753)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 143 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 77 positions in the final dataset.