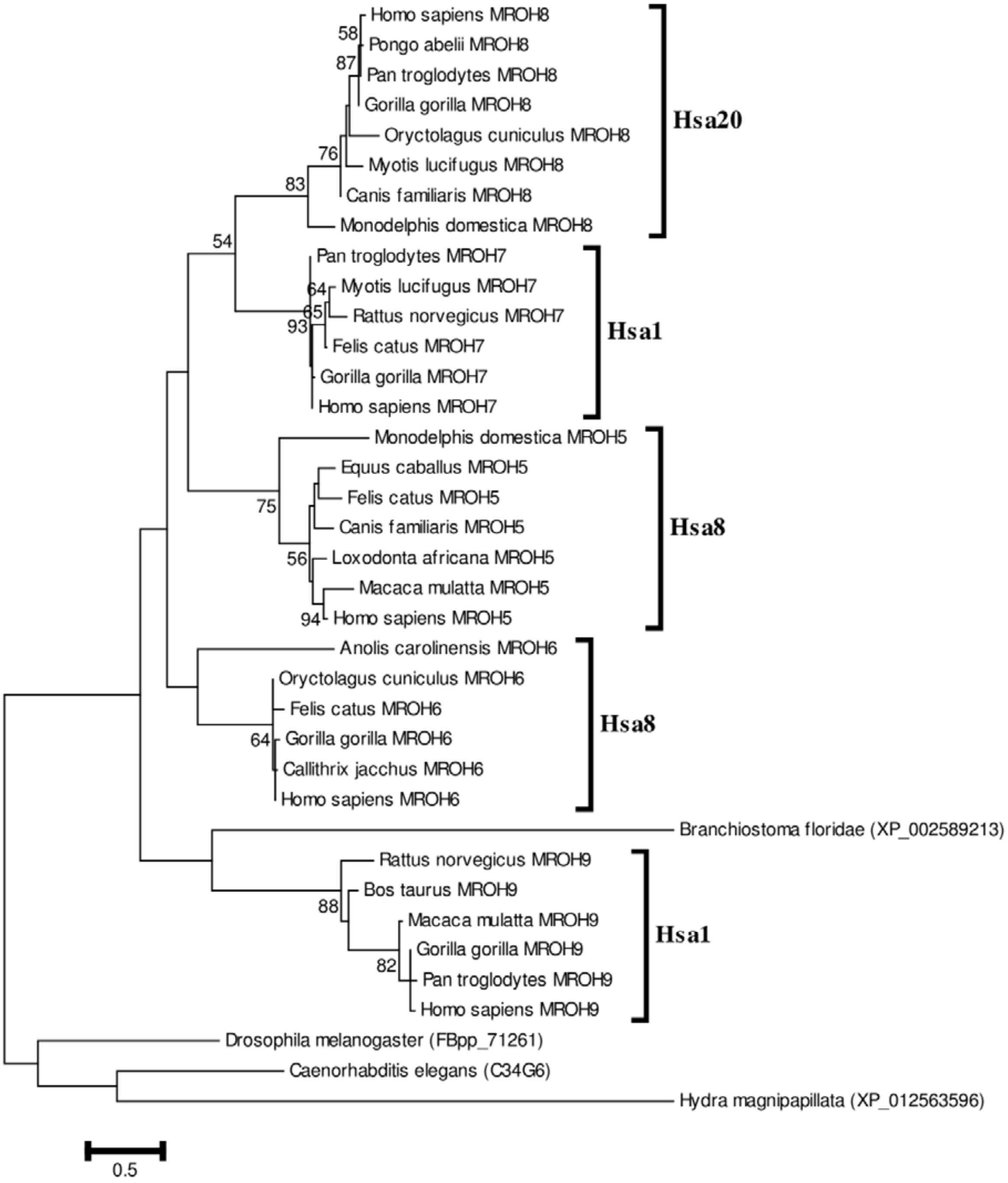
Additional file 4: Maximum Likelihood Trees of gene families (residing on human chromosomes 1/2/8/20) based on WAG model.

Co-duplicated group-1

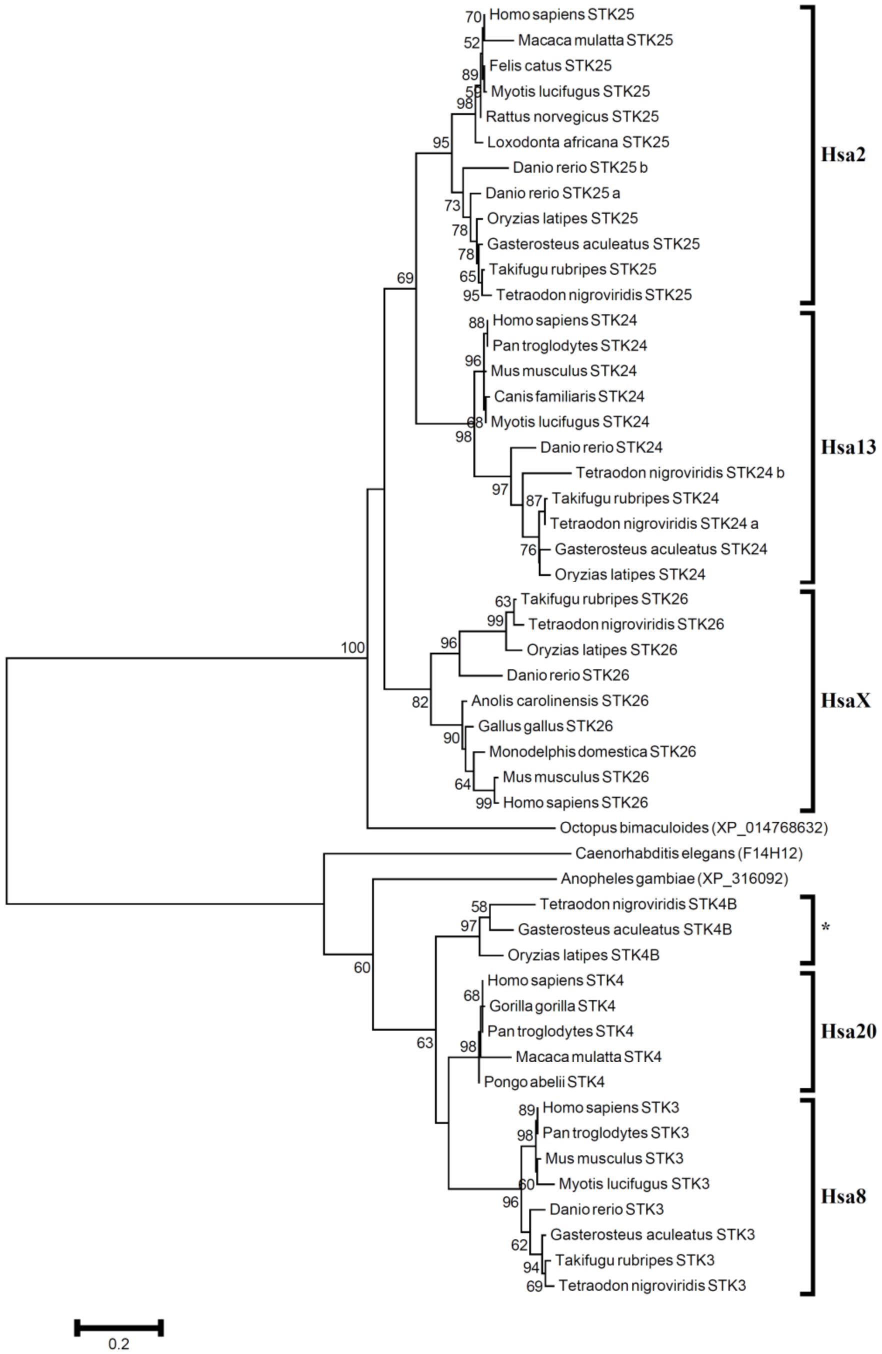
MROH8 and STK



Phylogenetic tree of MROH 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 (-3194.2605) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values ≥ 50% are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+*G*, parameter = 9.5137)). 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 80 positions in the final dataset.

Serine/Threonine-Protein Kinase-STK


70 Homo sapiens STK25
52 Macaca mulatta STK25
89 Felis catus STK25
59 Myotis lucifugus STK25
98 Rattus norvegicus STK25
95 Loxodonta africana STK25
Danio rerio STK25 b
73 Danio rerio STK25 a
78 Oryzias latipes STK25
78 Gasterosteus aculeatus STK25
65 Takifugu rubripes STK25
69
95 Tetraodon nigroviridis STK25
88 Homo sapiens STK24
Pan troglodytes STK24
96 Mus musculus STK24
Canis familiaris STK24
68 Myotis lucifugus STK24
98 Danio rerio STK24
Tetraodon nigroviridis STK24 b
97
87 Takifugu rubripes STK24
Tetraodon nigroviridis STK24 a
76 Gasterosteus aculeatus STK24
Oryzias latipes STK24
63 Takifugu rubripes STK26
99 Tetraodon nigroviridis STK26
96 Oryzias latipes STK26
100
Danio rerio STK26
82 Anolis carolinensis STK26
Gallus gallus STK26
90 Monodelphis domestica STK26
64 Mus musculus STK26
99 Homo sapiens STK26
Octopus bimaculoides (XP_014768632)
Caenorhabditis elegans (F14H12)
Anopheles gambiae (XP_316092)
58 Tetraodon nigroviridis STK4B
97 Gasterosteus aculeatus STK4B
60 Oryzias latipes STK4B
Homo sapiens STK4
68 Gorilla gorilla STK4
Pan troglodytes STK4
63
98 Macaca mulatta STK4
Pongo abelii STK4
89 Homo sapiens STK3
98 Pan troglodytes STK3
Mus musculus STK3
60 Myotis lucifugus STK3
96 Danio rerio STK3
62 Gasterosteus aculeatus STK3
94 Takifugu rubripes STK3
69 Tetraodon nigroviridis STK3
Hsa2
Hsa13
HsaX
*
Hsa20
Hsa8
0.2

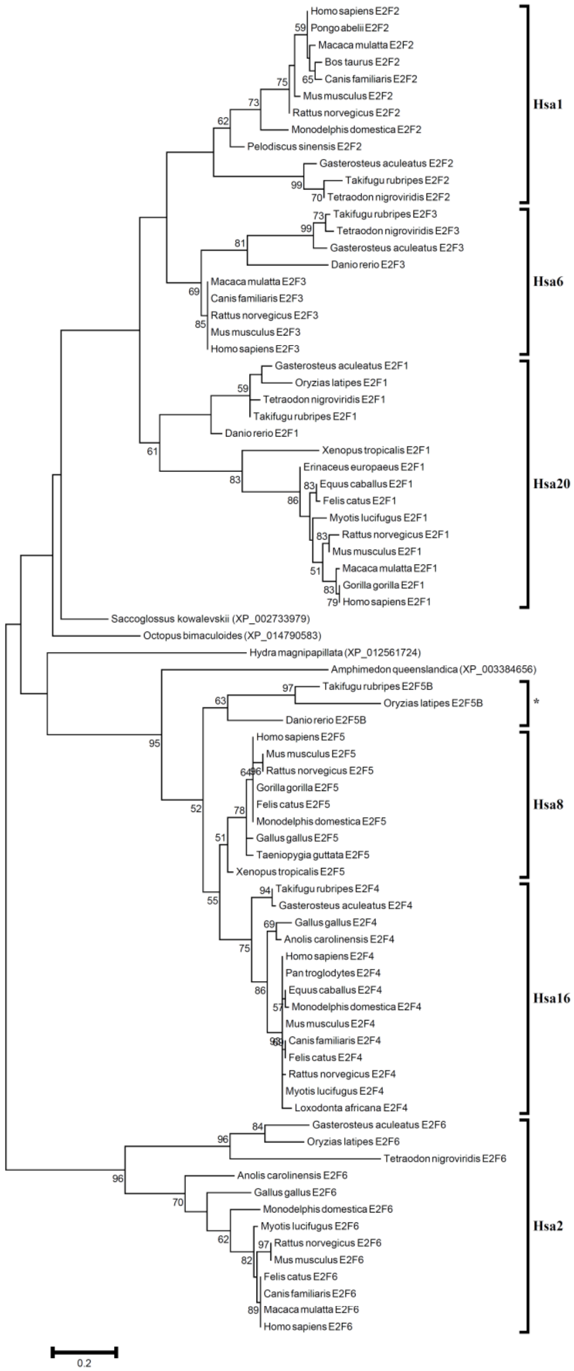
Phylogenetic tree of STK family.

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 (-5708.4638) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values ≥ 50% are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+*G*, parameter = 1.0610)). 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 252 positions in the final dataset.

Co-duplicated group-2

E2F, STMN1, EYA*

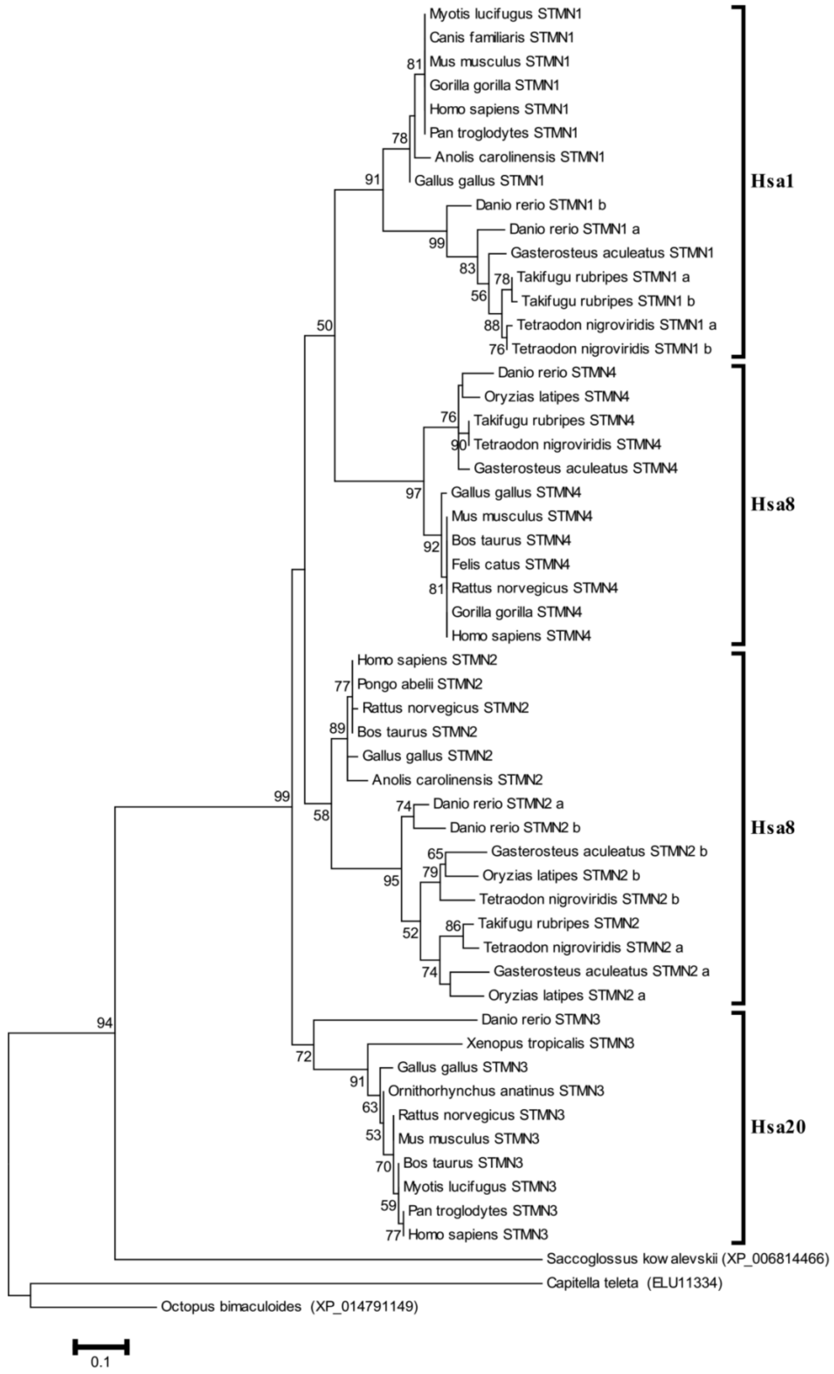
Asterisks (*) represent families published previously by our research group (for details see main text).



Phylogenetic tree of E2F 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 (-3603.2899) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values ≥ 50% are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+*G*, parameter = 1.4435)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 79 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 84 positions in the final dataset.

Stathmin-STMN



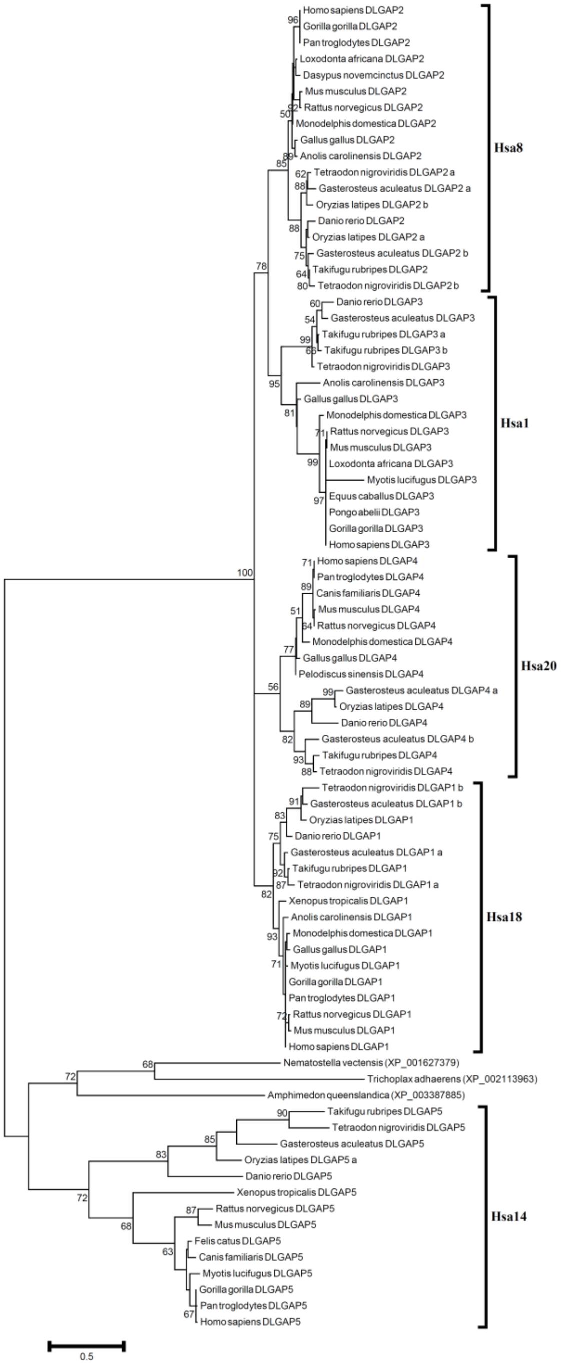
Phylogenetic tree of STMN family.

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 (-2434.5527) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values ≥ 50% are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+*G*, parameter = 1.7372)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 55 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 107 positions in the final dataset.

Co-duplicated group-3

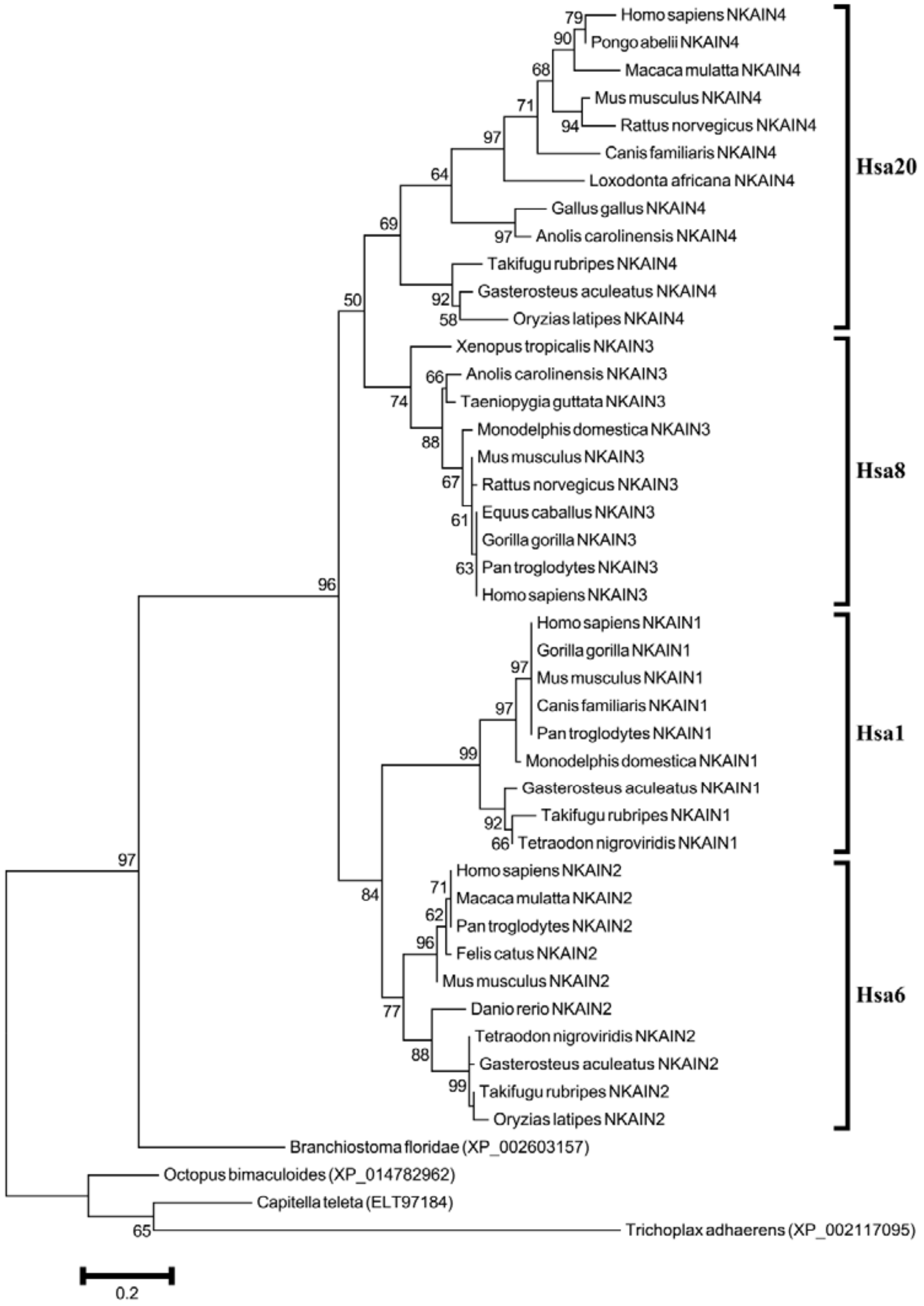
HCK*, DLGAP, NKAIN, KCNQ, MATN4*

Asterisks (*) represent families published previously by our research group (for details see main text).



Phylogenetic tree of DLGAP family.

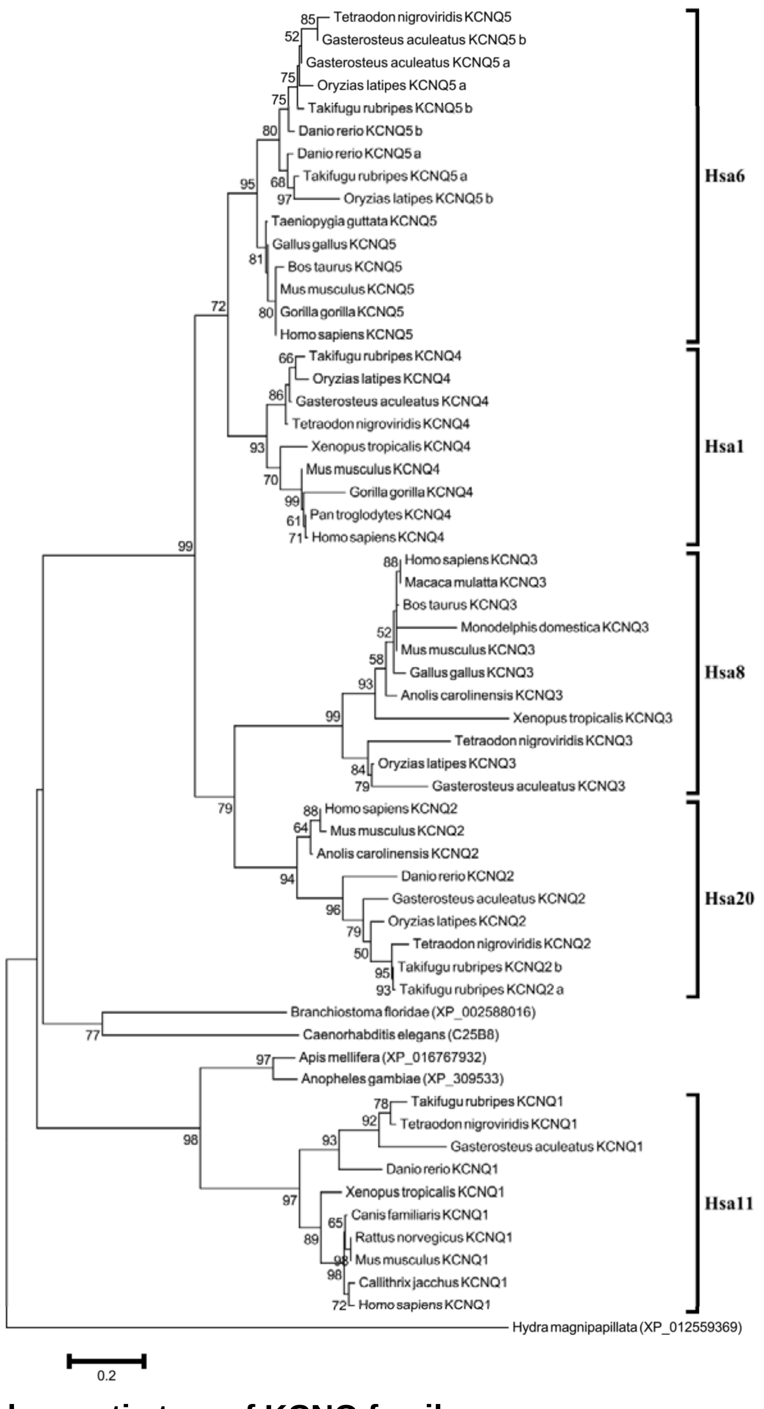
The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-7367.7106) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values ≥ 50% are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+*G*, parameter = 4.3659)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 82 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 146 positions in the final dataset.



Phylogenetic tree of NKAIN 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 (-2308.7286) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values ≥ 50% are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+*G*, parameter = 1.6036)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 45 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 94 positions in the final dataset.

Potassium Voltage-Gated Channel subfamily Q-KCNQ



Phylogenetic tree of KCNQ family.

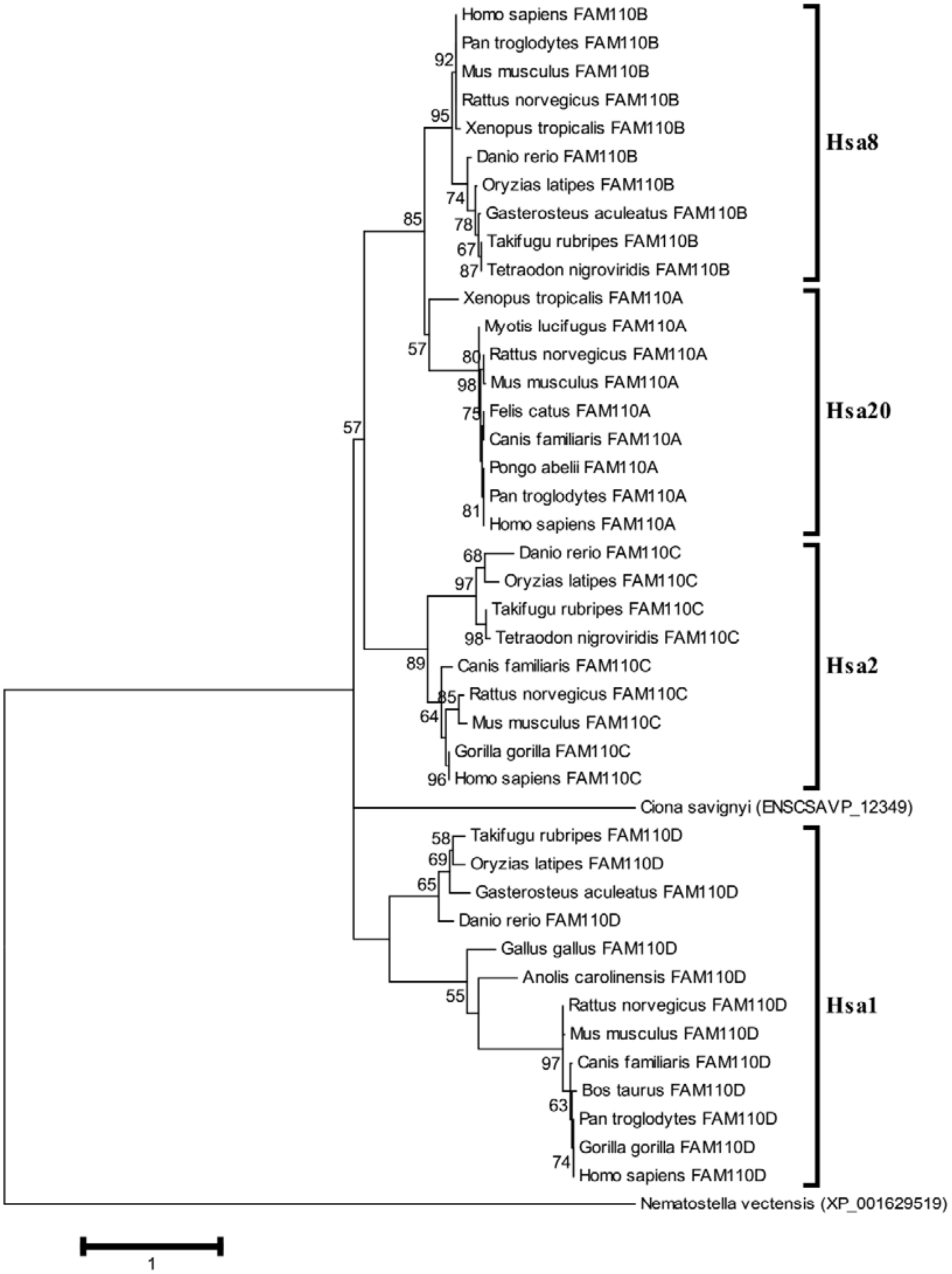
The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-6689.7208) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values ≥ 50% are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+*G*, parameter = 1.9925)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 59 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 206 positions in the final dataset.

Co-duplicated group-4

FAM110, NCOA, KCNS*, YTHDF, XKR, MYT

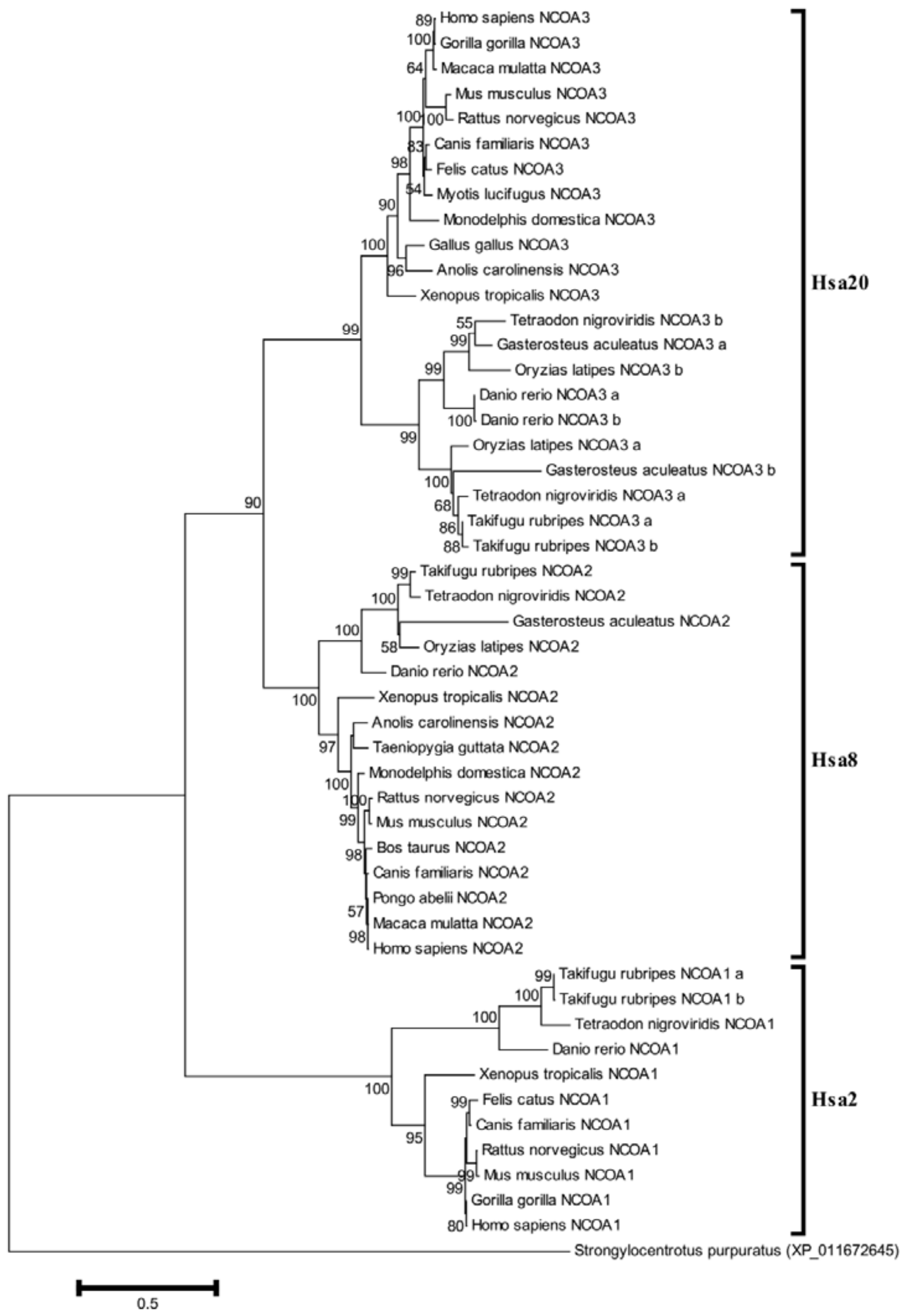
Asterisks (*) represent families published previously by our research group (for details see main text).

Family with Sequence Similarity 110-FAM110



Phylogenetic tree of FAM110 family.

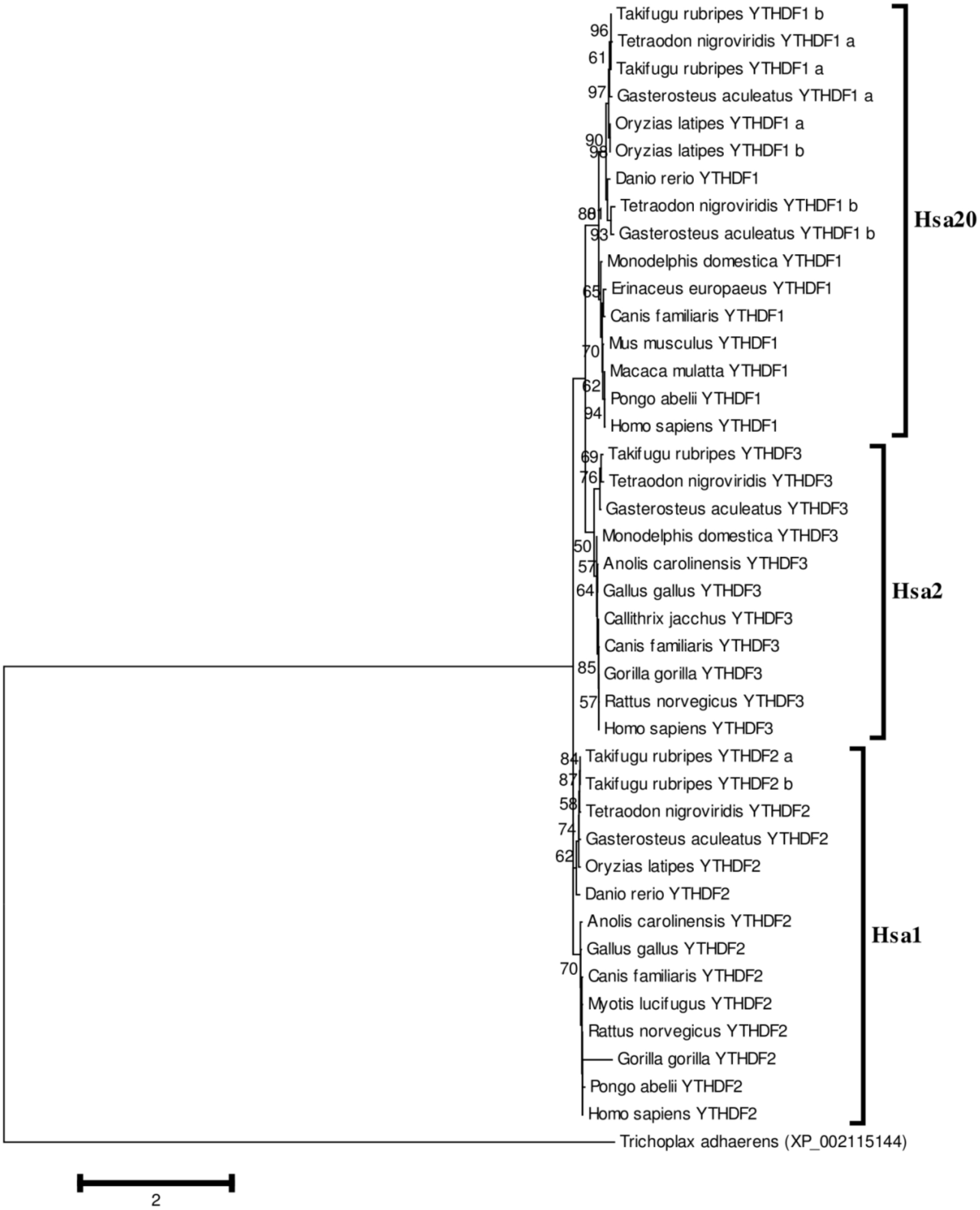
The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-2939.3885) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values ≥ 50% are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+*G*, parameter = 4.3955)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 43 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 95 positions in the final dataset.



Phylogenetic tree of NCOA family.

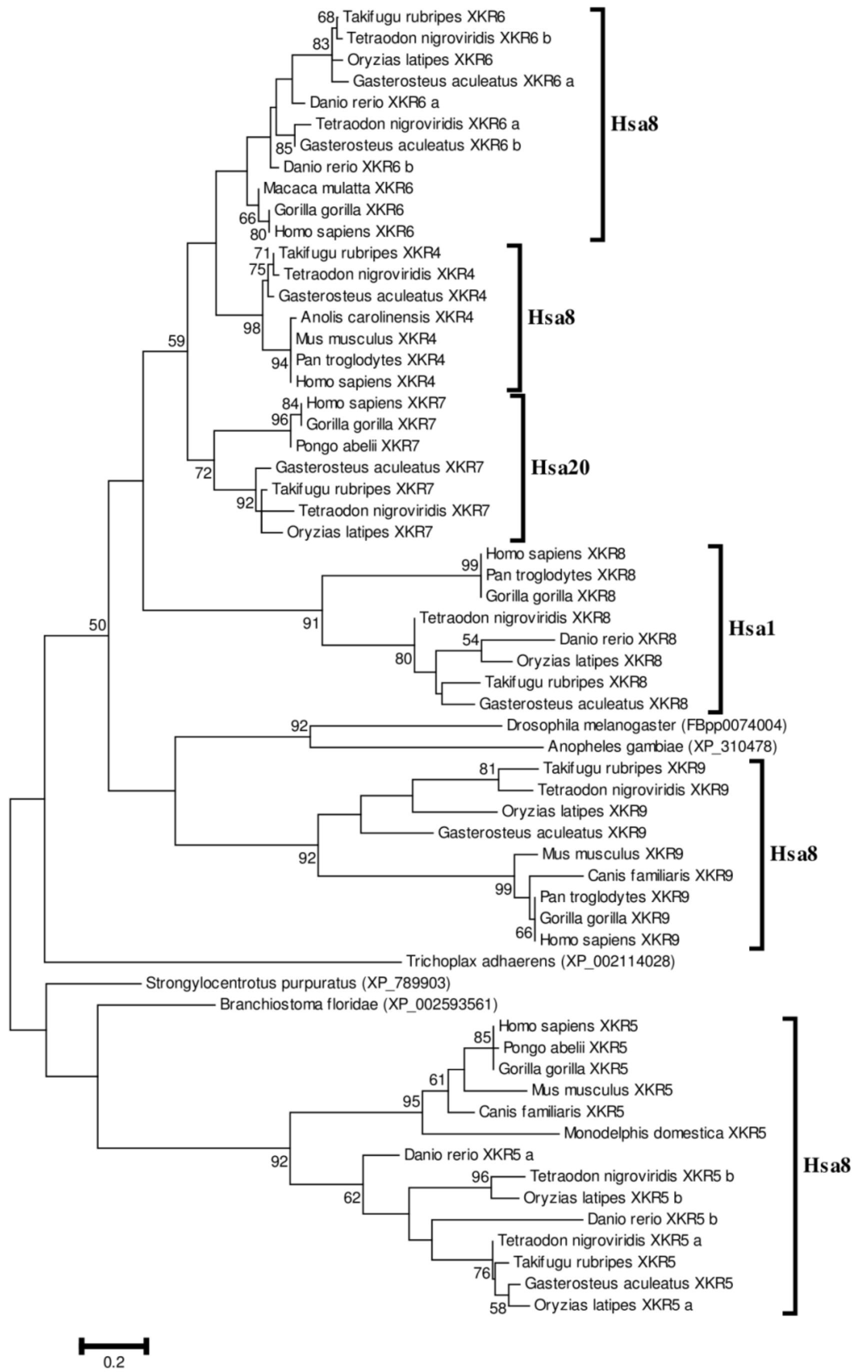
The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-24506.3558) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values ≥ 50% are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+*G*, parameter = 2.7804)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 50 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 747 positions in the final dataset.

YTH Domain-Containing Family Protein-YTHDF



Phylogenetic tree of YTHDF family.

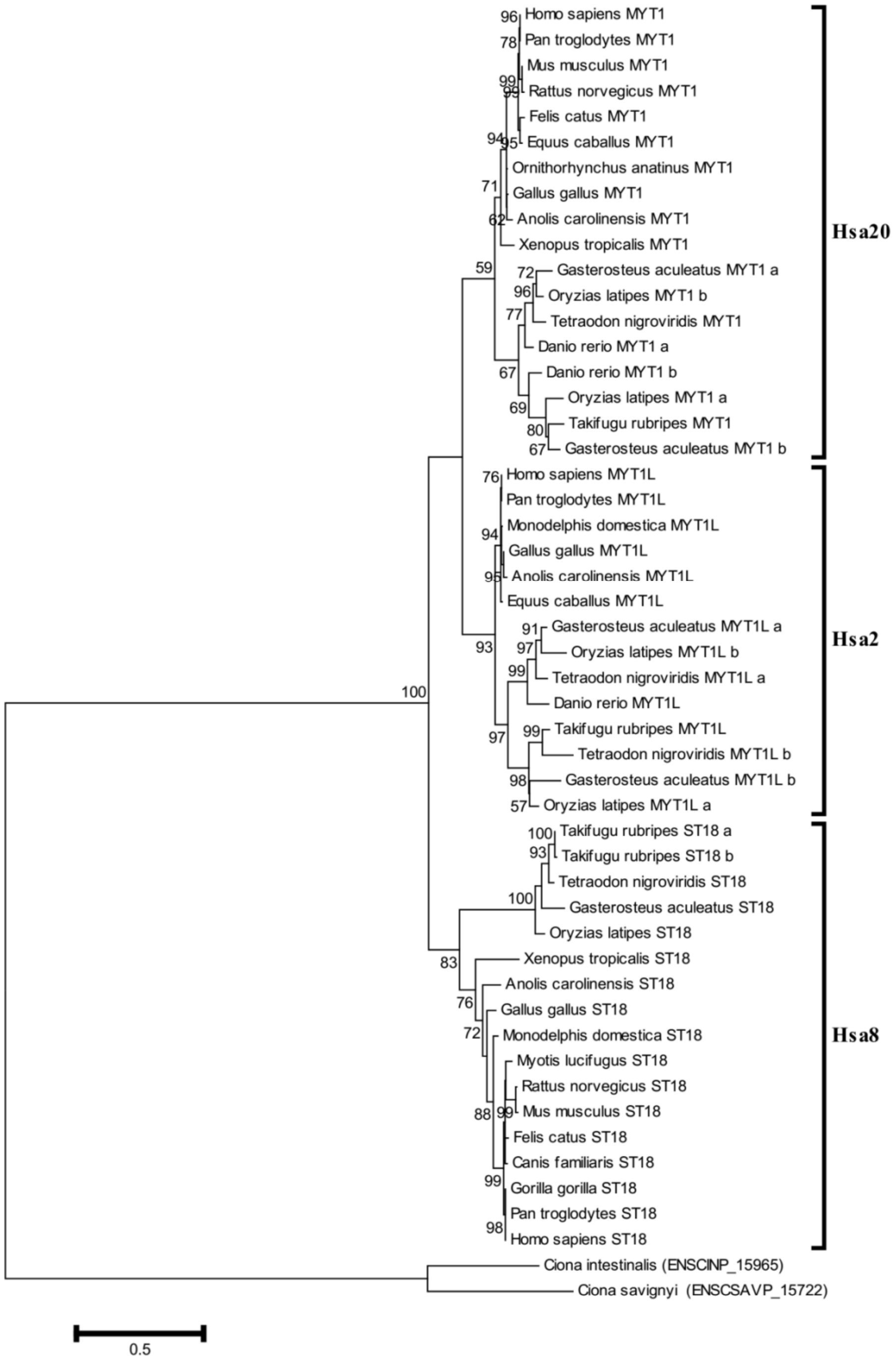
The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-4540.4192) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values ≥ 50% are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+*G*, parameter = 3.5033)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 42 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 293 positions in the final dataset.


68 Takifugu rubripes XKR6
83 Tetraodon nigroviridis XKR6 b
Oryzias latipes XKR6
Gasterosteus aculeatus XKR6 a
Danio rerio XKR6 a
Tetraodon nigroviridis XKR6 a
85 Gasterosteus aculeatus XKR6 b
Danio rerio XKR6 b
Macaca mulatta XKR6
66 Gorilla gorilla XKR6
80 Homo sapiens XKR6
Hsa8
71 Takifugu rubripes XKR4
75 Tetraodon nigroviridis XKR4
Gasterosteus aculeatus XKR4
Anolis carolinensis XKR4
98 Mus musculus XKR4
94 Pan troglodytes XKR4
Homo sapiens XKR4
Hsa8
59
84 Homo sapiens XKR7
96 Gorilla gorilla XKR7
Pongo abelii XKR7
72 Gasterosteus aculeatus XKR7
Takifugu rubripes XKR7
92 Tetraodon nigroviridis XKR7
Oryzias latipes XKR7
Hsa20
99 Homo sapiens XKR8
Pan troglodytes XKR8
Gorilla gorilla XKR8
91 Tetraodon nigroviridis XKR8
54 Danio rerio XKR8
80 Oryzias latipes XKR8
Takifugu rubripes XKR8
Gasterosteus aculeatus XKR8
Hsa1
50
92 Drosophila melanogaster (FBpp0074004)
Anopheles gambiae (XP_310478)
81 Takifugu rubripes XKR9
Tetraodon nigroviridis XKR9
Oryzias latipes XKR9
Gasterosteus aculeatus XKR9
92 Mus musculus XKR9
Canis familiaris XKR9
99 Pan troglodytes XKR9
Gorilla gorilla XKR9
66 Homo sapiens XKR9
Hsa8
Trichoplax adhaerens (XP_002114028)
Strongylocentrotus purpuratus (XP_789903)
Branchiostoma floridae (XP_002593561)
85 Homo sapiens XKR5
Pongo abelii XKR5
Gorilla gorilla XKR5
61 Mus musculus XKR5
95 Canis familiaris XKR5
Monodelphis domestica XKR5
92 Danio rerio XKR5 a
96 Tetraodon nigroviridis XKR5 b
62 Oryzias latipes XKR5 b
Danio rerio XKR5 b
Tetraodon nigroviridis XKR5 a
Takifugu rubripes XKR5
76 Gasterosteus aculeatus XKR5
58 Oryzias latipes XKR5 a
Hsa8
0.2

Phylogenetic tree of XKR 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 (-3313.2103) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values ≥ 50% are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+*G*, parameter = 3.1313)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 61 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 67 positions in the final dataset.

Myelin Transcription Factor-MYT

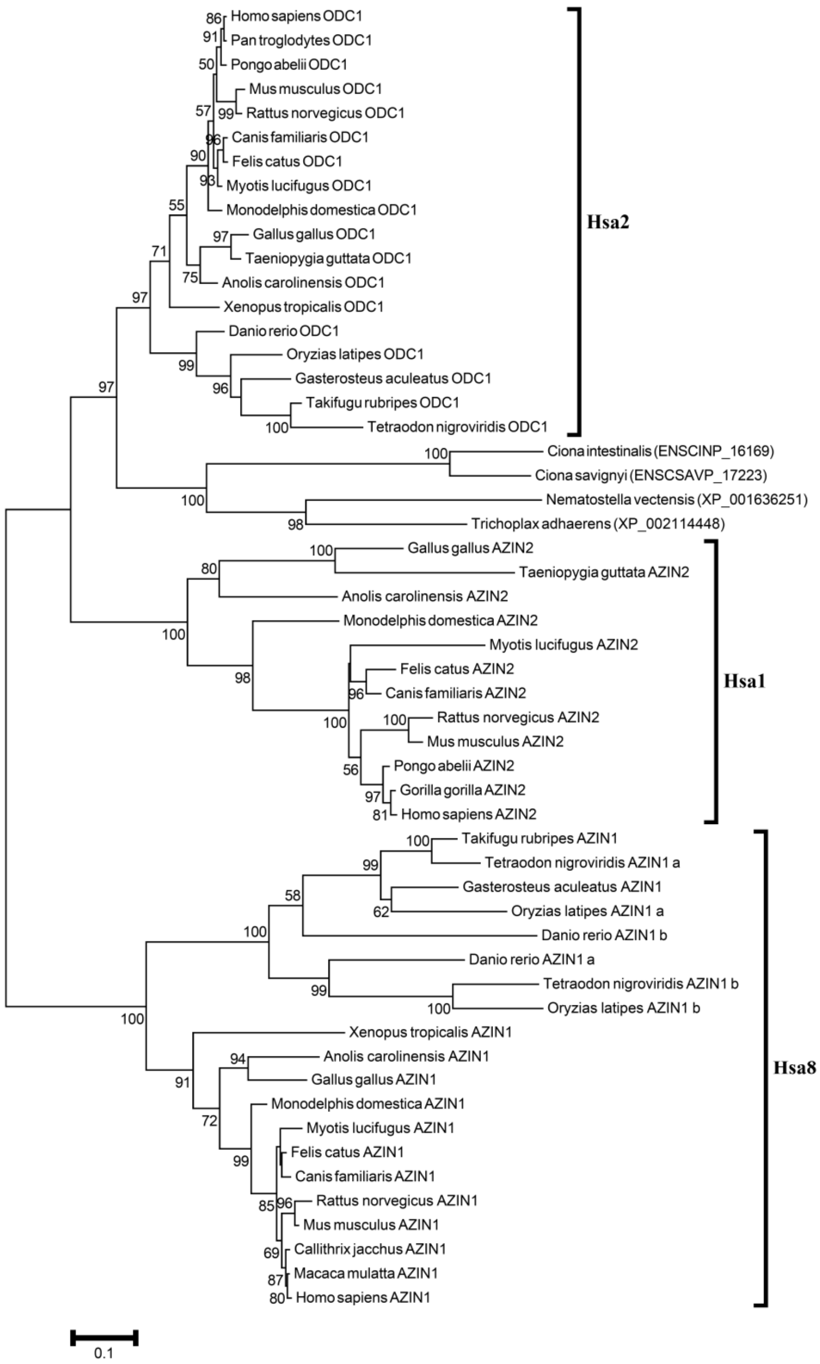

96 Homo sapiens MYT1
78 Pan troglodytes MYT1
Mus musculus MYT1
99
99 Rattus norvegicus MYT1
Felis catus MYT1
94
95 Equus caballus MYT1
Ornithorhynchus anatinus MYT1
71 Gallus gallus MYT1
62 Anolis carolinensis MYT1
Xenopus tropicalis MYT1
59
72 Gasterosteus aculeatus MYT1 a
96 Oryzias latipes MYT1 b
77 Tetraodon nigroviridis MYT1
Danio rerio MYT1 a
67 Danio rerio MYT1 b
69 Oryzias latipes MYT1 a
80 Takifugu rubripes MYT1
67 Gasterosteus aculeatus MYT1 b
76 Homo sapiens MYT1L
Pan troglodytes MYT1L
Monodelphis domestica MYT1L
94 Gallus gallus MYT1L
95 Anolis carolinensis MYT1L
Equus caballus MYT1L
91 Gasterosteus aculeatus MYT1L a
93
97 Oryzias latipes MYT1L b
99 Tetraodon nigroviridis MYT1L a
100
Danio rerio MYT1L
97
99 Takifugu rubripes MYT1L
Tetraodon nigroviridis MYT1L b
98 Gasterosteus aculeatus MYT1L b
57 Oryzias latipes MYT1L a
100 Takifugu rubripes ST18 a
93 Takifugu rubripes ST18 b
Tetraodon nigroviridis ST18
100 Gasterosteus aculeatus ST18
Oryzias latipes ST18
83 Xenopus tropicalis ST18
Anolis carolinensis ST18
76 Gallus gallus ST18
72 Monodelphis domestica ST18
Myotis lucifugus ST18
Rattus norvegicus ST18
88 99 Mus musculus ST18
Felis catus ST18
Canis familiaris ST18
99 Gorilla gorilla ST18
Pan troglodytes ST18
98 Homo sapiens ST18
Ciona intestinalis (ENSCINP_15965)
Ciona savignyi (ENSCSAVP_15722)
Hsa20
Hsa2
Hsa8
0.5

Phylogenetic tree of MYT 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 (-11734.7917) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values ≥ 50% are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+*G*, parameter = 2.3022)). 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 469 positions in the final dataset.

Other gene families analyzed in the present study

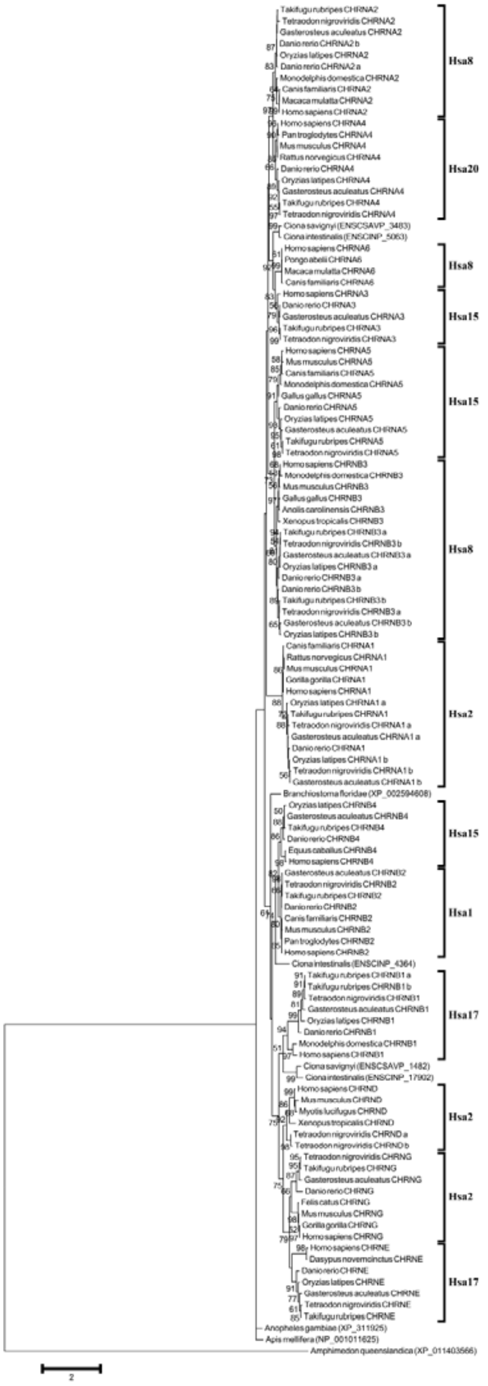
Antizyme Inhibitor-AZIN



Phylogenetic tree of AZIN 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 (-11900.2271) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches; only the values ≥ 50% are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+*G*, parameter = 2.2632)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 54 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 327 positions in the final dataset.

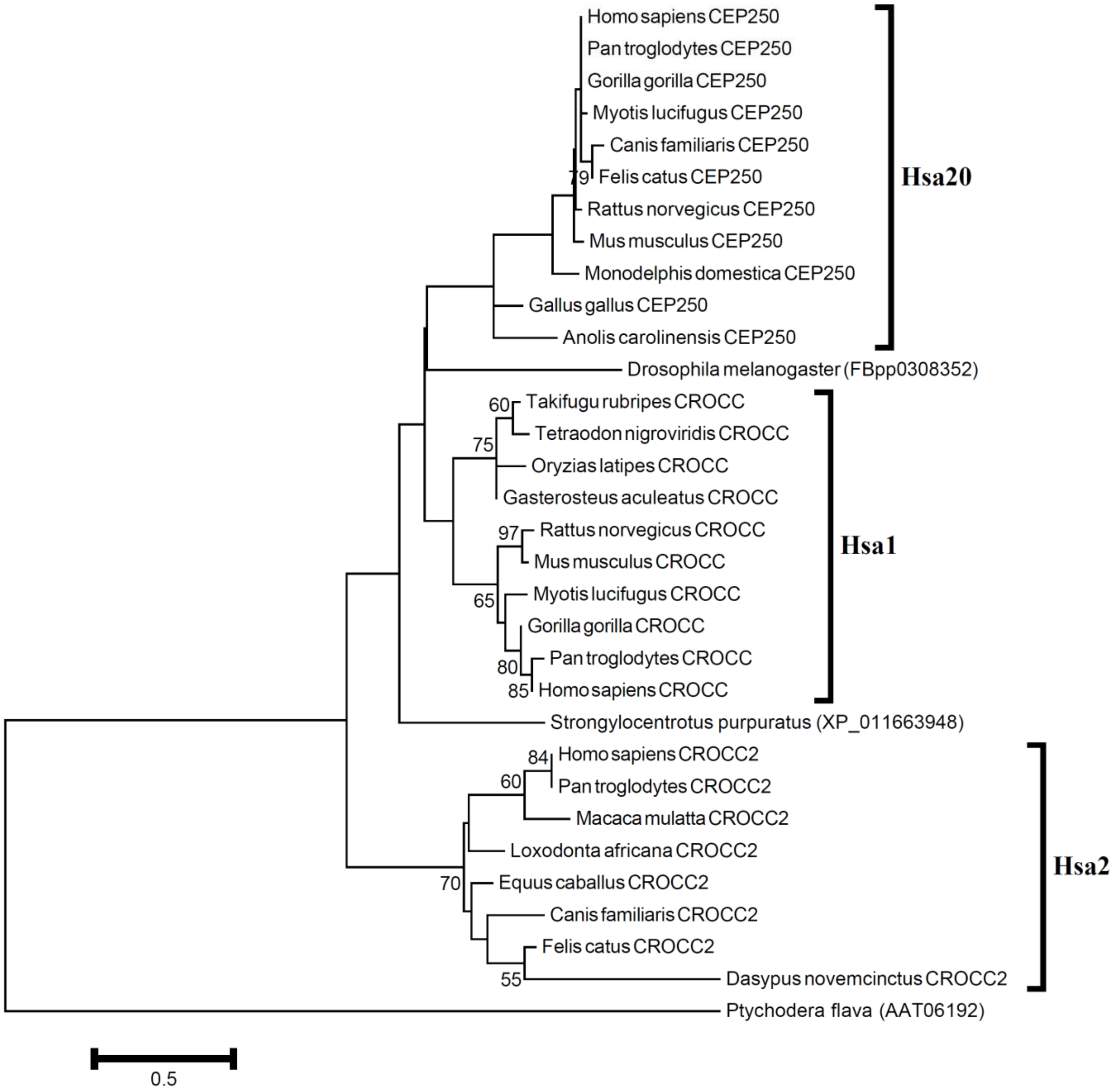
Cholinergic Receptor Nicotinic Subunits-CHRN



Phylogenetic tree of CHRN 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 (-10408.3266) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values ≥ 50% are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+*G*, parameter = 1.2835)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 119 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 182 positions in the final dataset.

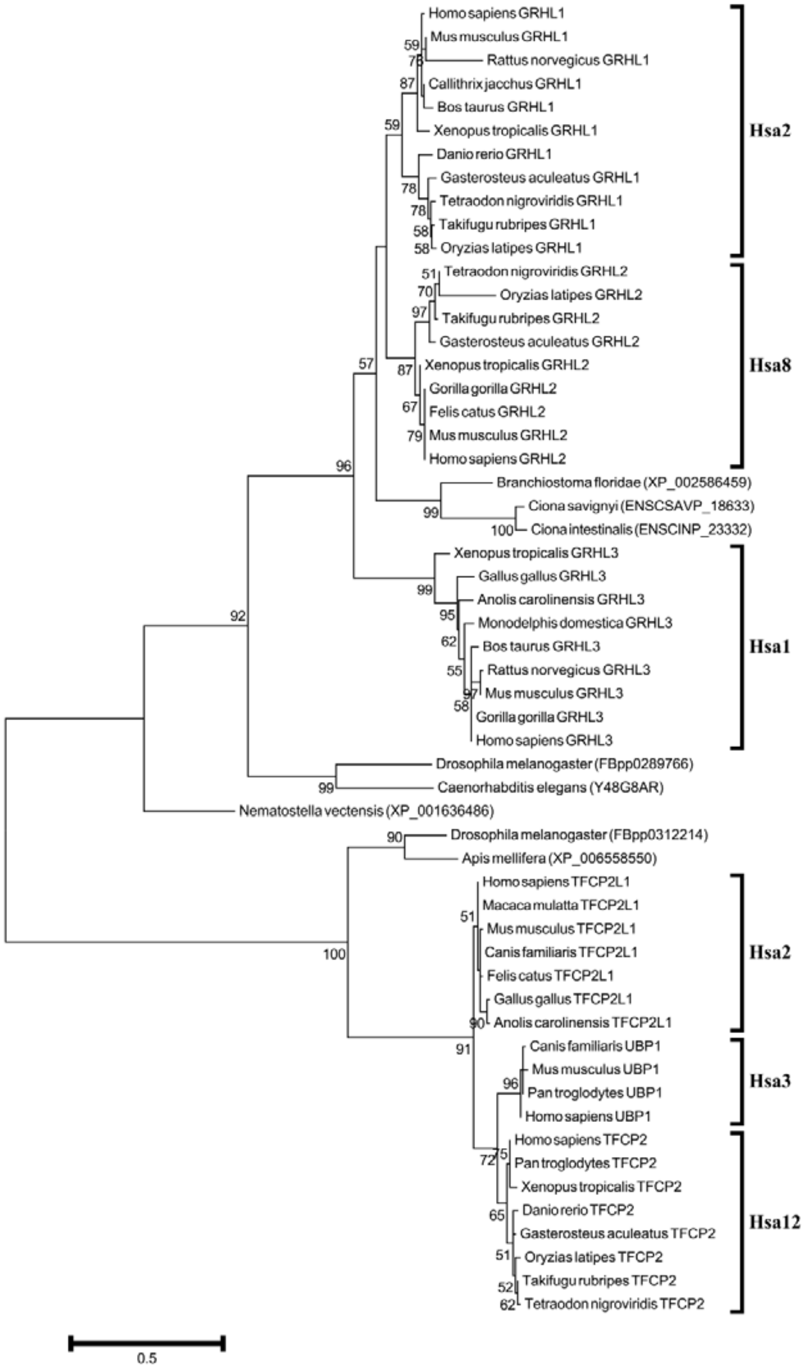
Ciliary Rootlet Coiled-Coil Protein-CRO



Phylogenetic tree of CRO 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 (-1419.2573) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values ≥ 50% are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+*G*, parameter = 7.5189)). 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 49 positions in the final dataset.

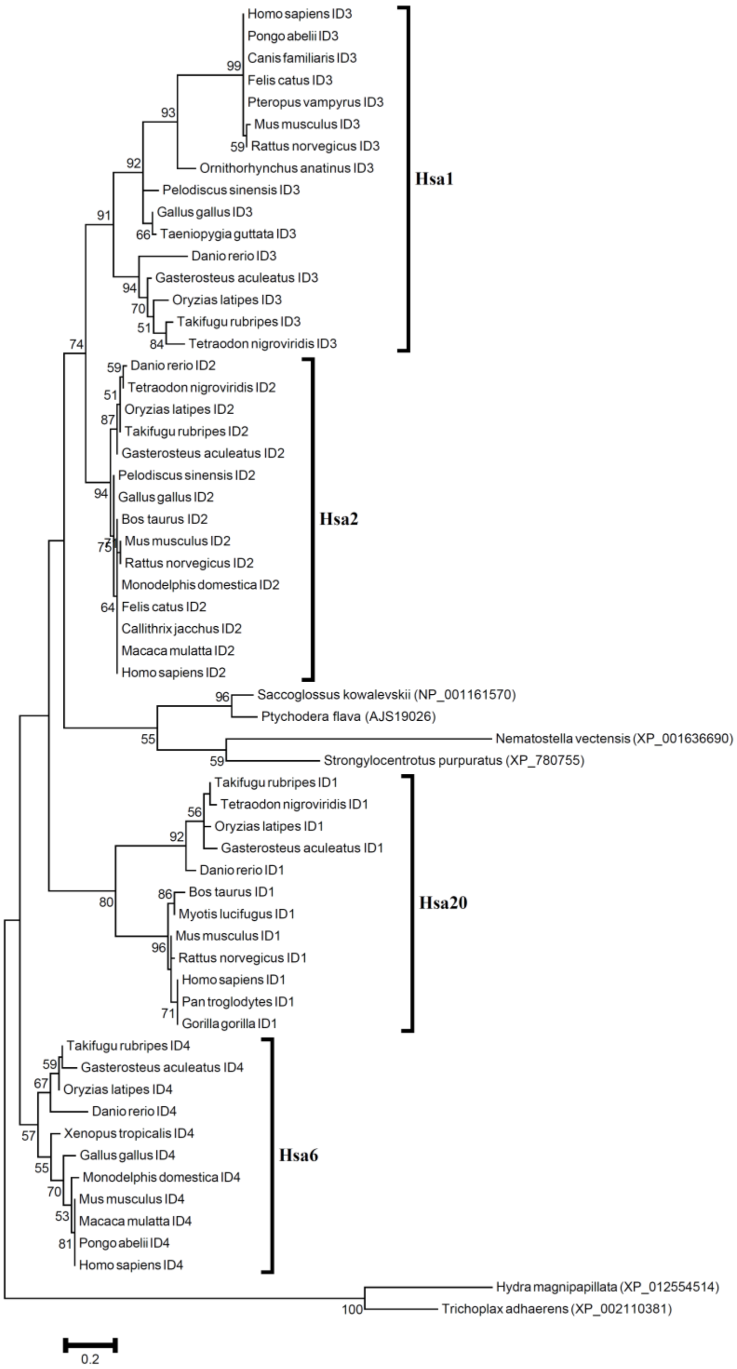
Grainyhead like Transcription factor-GRHL



Phylogenetic tree of GRHL 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 (-3783.1102) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values ≥ 50% are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+*G*, parameter = 2.6106)). 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 146 positions in the final dataset.

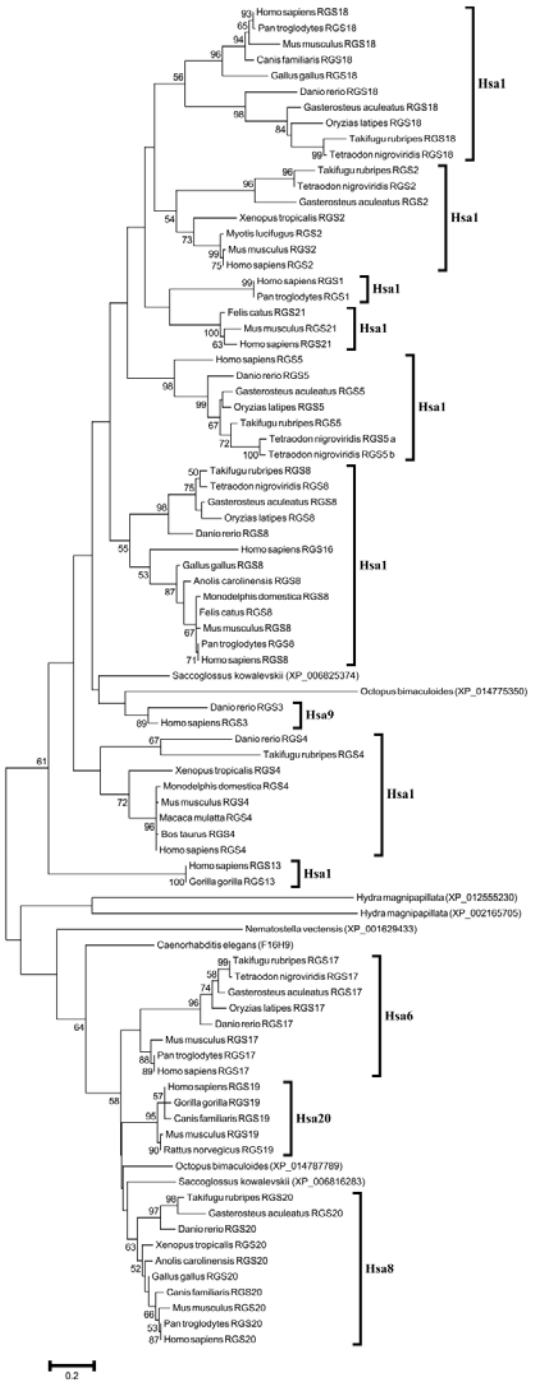
Inhibitor of DNA Binding protein-ID



Phylogenetic tree of ID family.

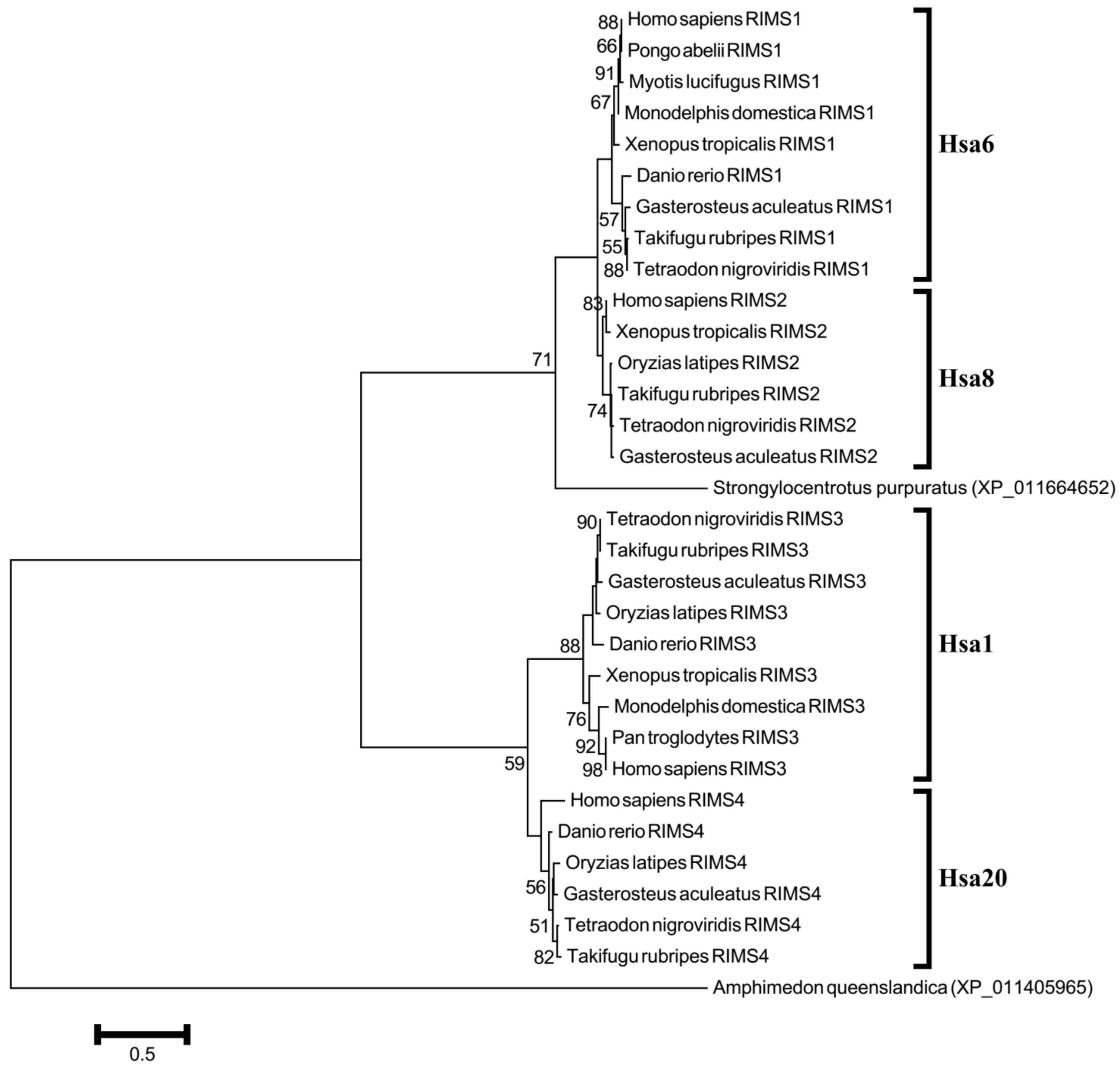
The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-2160.3041) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values ≥ 50% are shown here . A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+*G*, parameter = 2.0164)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 60 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 71 positions in the final dataset.

Regulator of G-protein Signaling-RGS



Phylogenetic tree of RGS family.

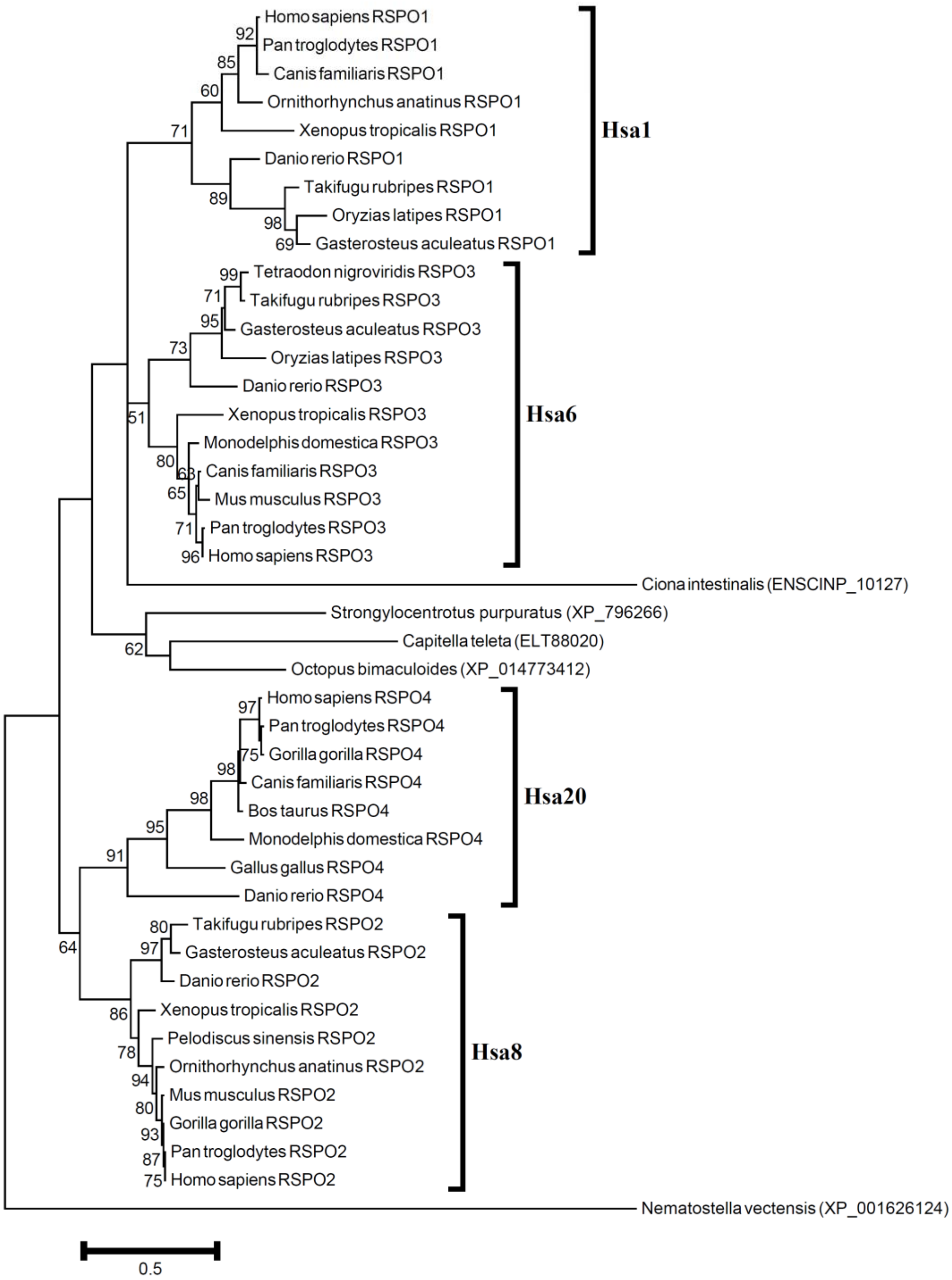
The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-7082.8656) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values ≥ 50% are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+*G*, parameter = 1.9111)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 85 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 115 positions in the final dataset.



Phylogenetic tree of RIMS family.

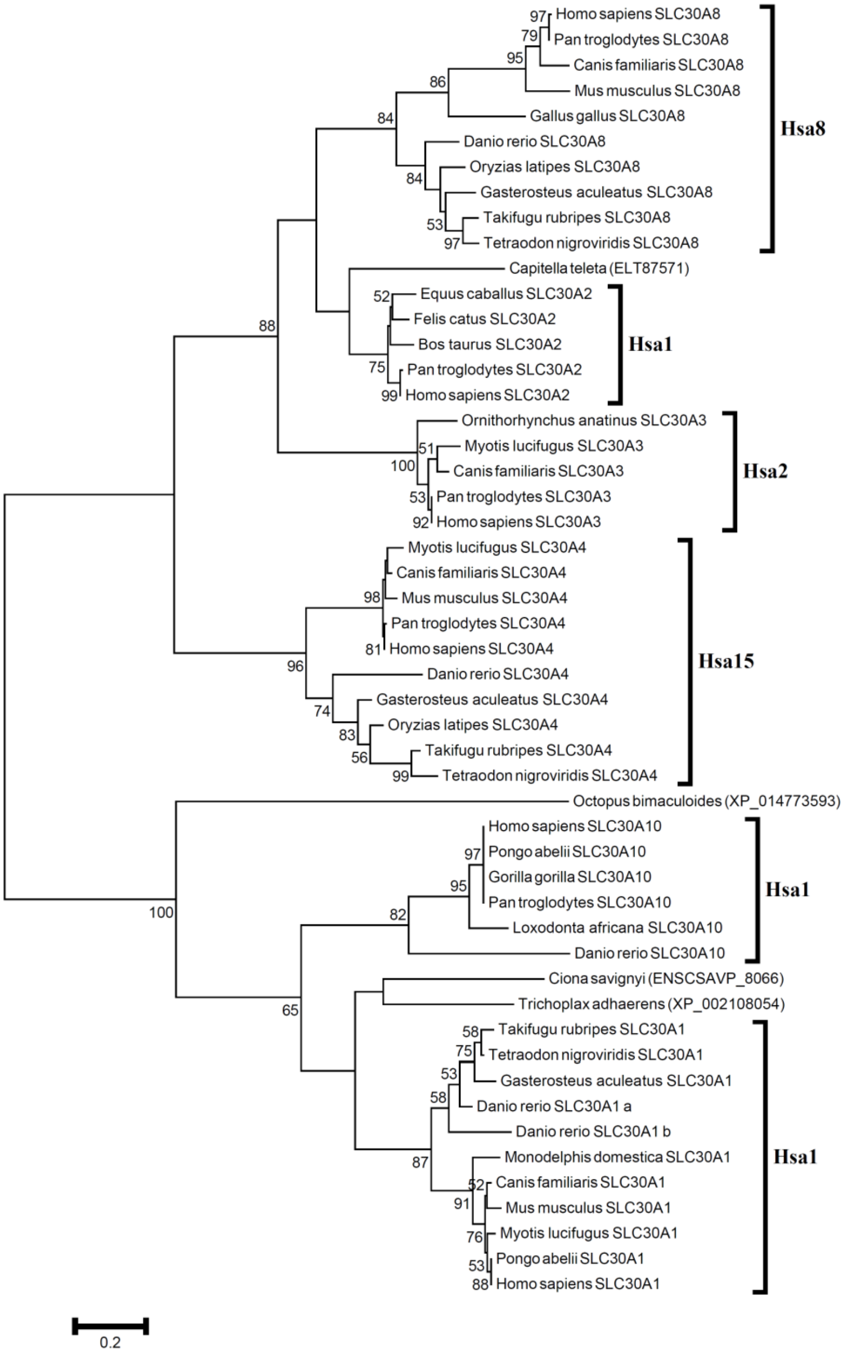
The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-3878.5361) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values ≥ 50% are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+*G*, parameter = 8.5411)). 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 211 positions in the final dataset.

R-Spondin Homolog-RSPO



Phylogenetic tree of RSPO family.

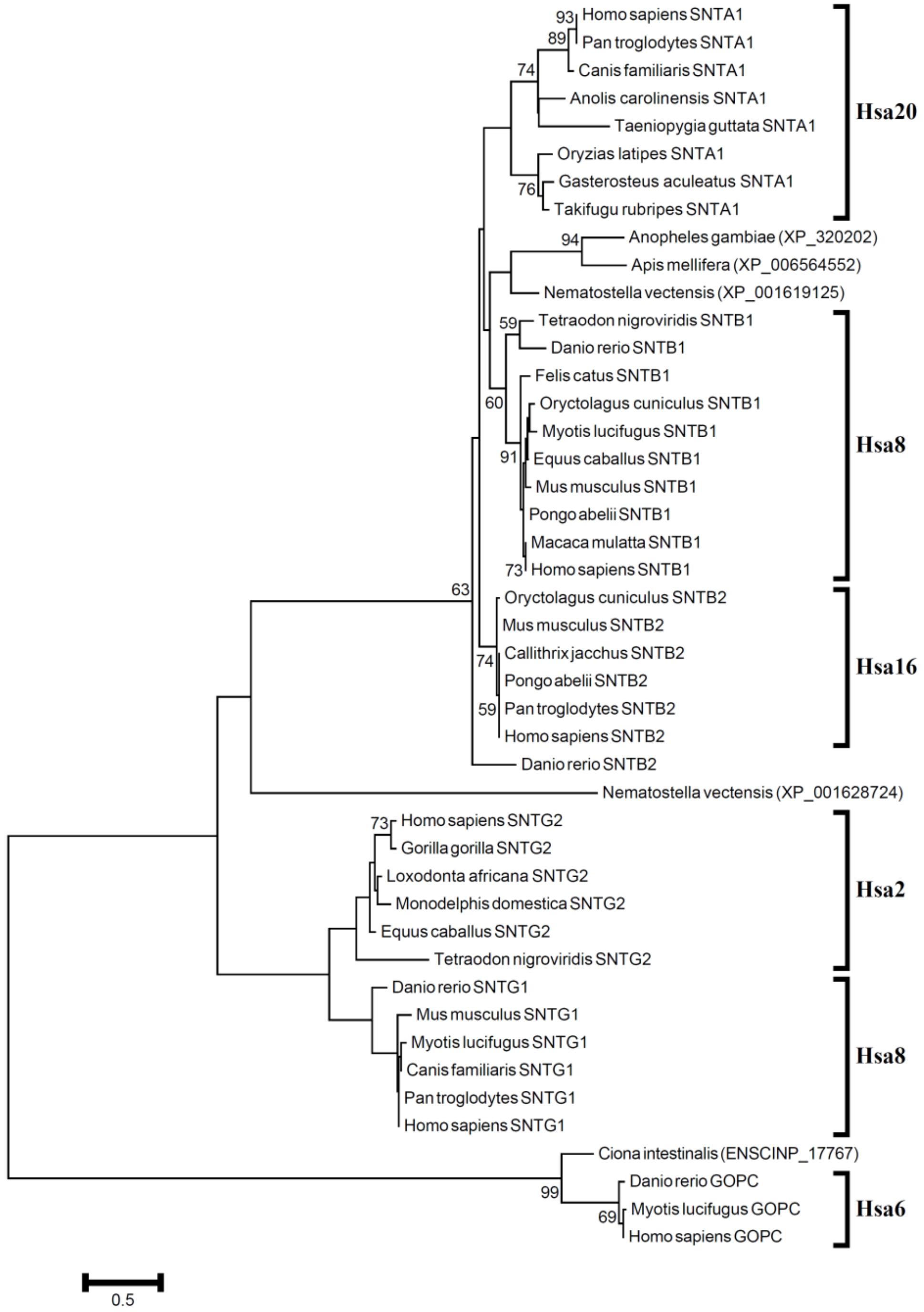
The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-5260.9960) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values ≥ 50% are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+*G*, parameter = 2.6368)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 43 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 141 positions in the final dataset.


97 Homo sapiens SLC30A8
79 Pan troglodytes SLC30A8
95 Canis familiaris SLC30A8
86 Mus musculus SLC30A8
Gallus gallus SLC30A8
84 Danio rerio SLC30A8
Oryzias latipes SLC30A8
84 Gasterosteus aculeatus SLC30A8
53 Takifugu rubripes SLC30A8
97 Tetraodon nigroviridis SLC30A8
Hsa8
Capitella teleta (ELT87571)
88
52 Equus caballus SLC30A2
Felis catus SLC30A2
Bos taurus SLC30A2
75 Pan troglodytes SLC30A2
99 Homo sapiens SLC30A2
Hsa1
Ornithorhynchus anatinus SLC30A3
51 Myotis lucifugus SLC30A3
100 Canis familiaris SLC30A3
53 Pan troglodytes SLC30A3
92 Homo sapiens SLC30A3
Hsa2
Myotis lucifugus SLC30A4
Canis familiaris SLC30A4
98 Mus musculus SLC30A4
Pan troglodytes SLC30A4
81 Homo sapiens SLC30A4
96 Danio rerio SLC30A4
74 Gasterosteus aculeatus SLC30A4
83 Oryzias latipes SLC30A4
56 Takifugu rubripes SLC30A4
99 Tetraodon nigroviridis SLC30A4
Hsa15
Octopus bimaculoides (XP_014773593)
Homo sapiens SLC30A10
97 Pongo abelii SLC30A10
95 Gorilla gorilla SLC30A10
Pan troglodytes SLC30A10
100
82 Loxodonta africana SLC30A10
Danio rerio SLC30A10
Hsa1
Ciona savignyi (ENSCSAVP_8066)
65 Trichoplax adhaerens (XP_002108054)
58 Takifugu rubripes SLC30A1
75 Tetraodon nigroviridis SLC30A1
53 Gasterosteus aculeatus SLC30A1
58 Danio rerio SLC30A1 a
Danio rerio SLC30A1 b
87 Monodelphis domestica SLC30A1
52 Canis familiaris SLC30A1
91 Mus musculus SLC30A1
76 Myotis lucifugus SLC30A1
53 Pongo abelii SLC30A1
88 Homo sapiens SLC30A1
Hsa1
0.2

Phylogenetic tree of SLC 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 (-4999.4232) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values ≥ 50% are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+*G*, parameter = 2.3472)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 68 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 131 positions in the final dataset.

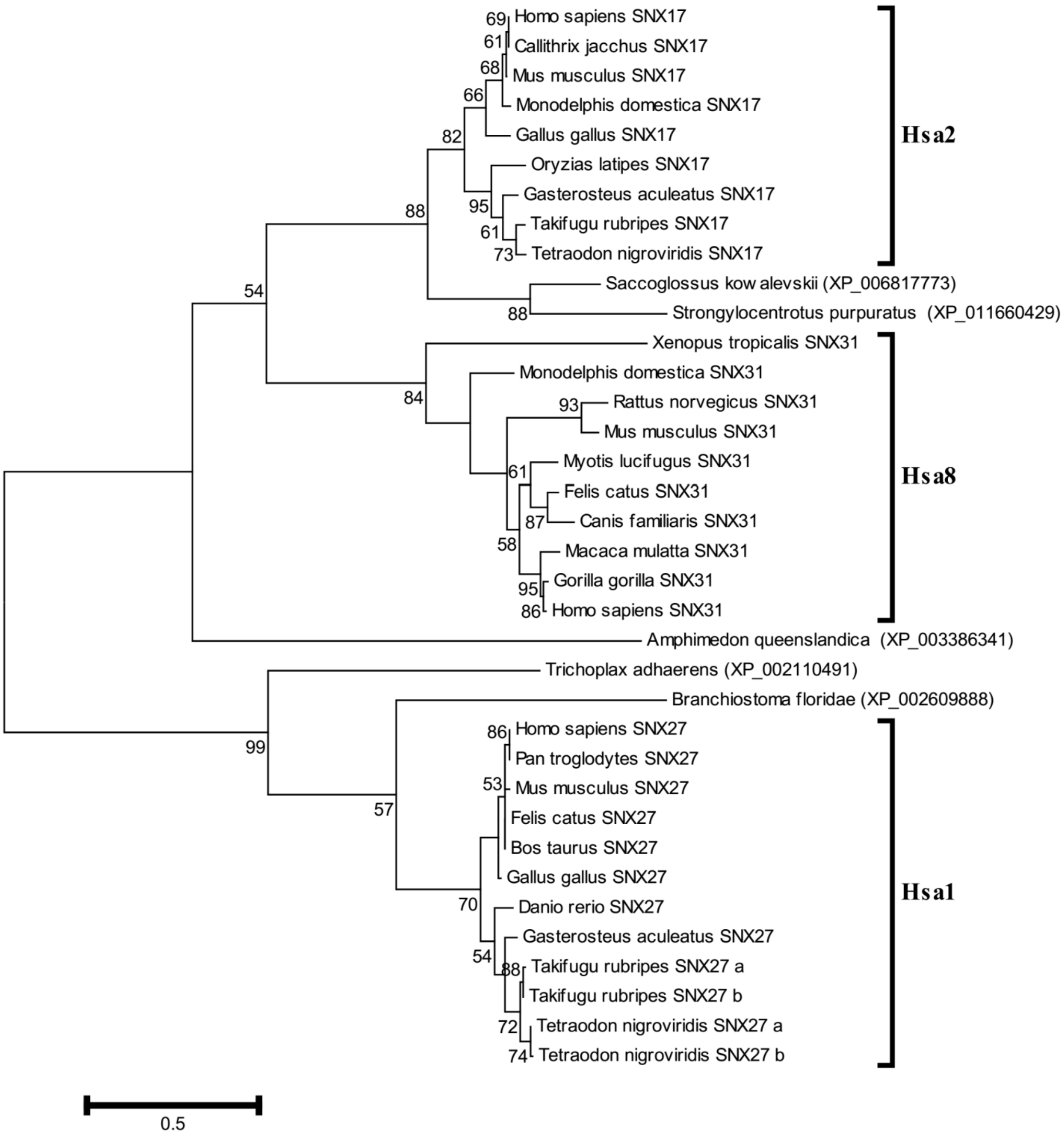
Syntrophin, Gamma-SNT



Phylogenetic tree of SNT 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 (-2524.4722) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values ≥ 50% are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+*G*, parameter = 5.9303)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 45 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 67 positions in the final dataset.

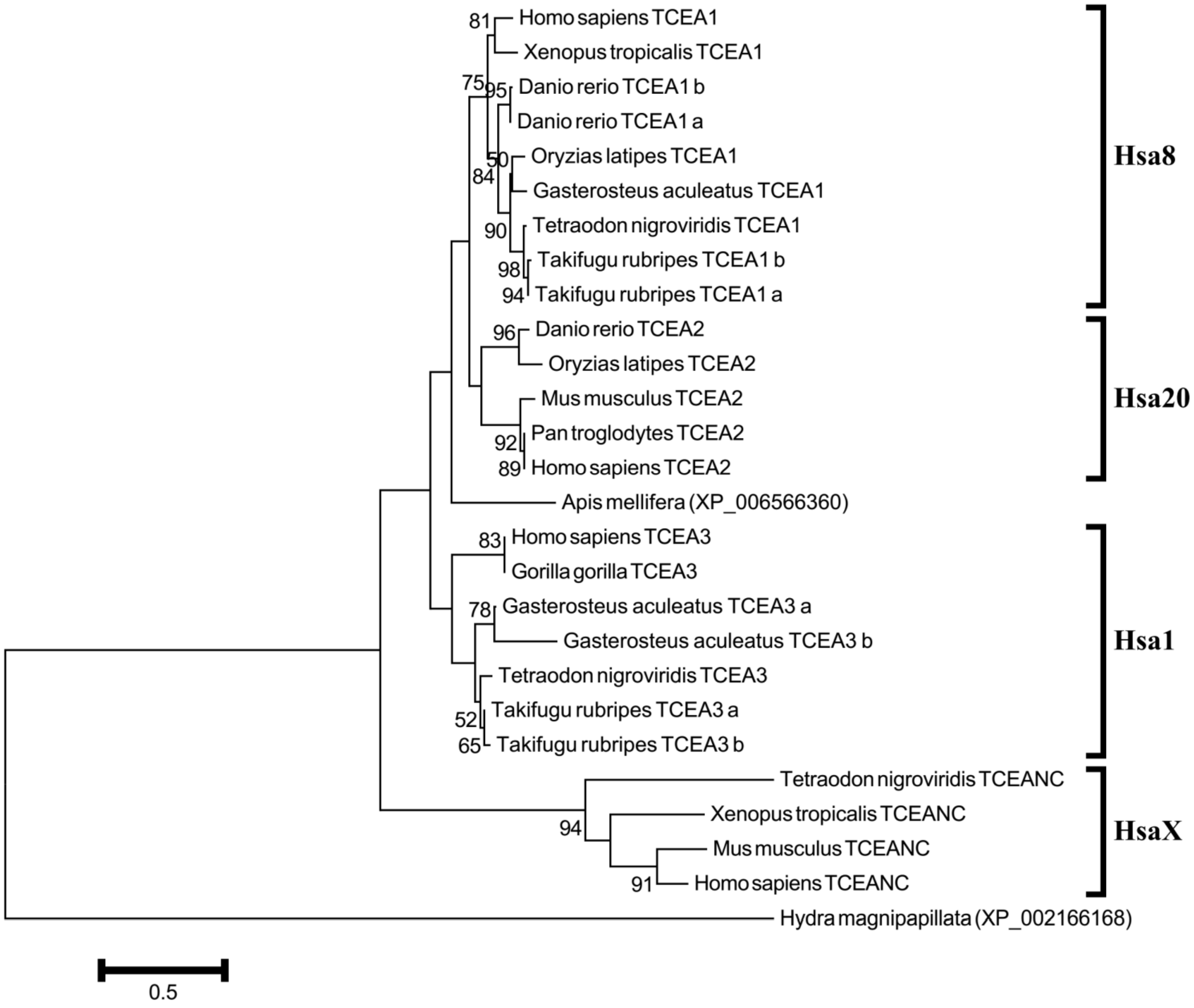
Sorting Nexin Family-SNX


69 Homo sapiens SNX17
61 Callithrix jacchus SNX17
68 Mus musculus SNX17
66 Monodelphis domestica SNX17
Gallus gallus SNX17
82 Oryzias latipes SNX17
Gasterosteus aculeatus SNX17
88
95 Takifugu rubripes SNX17
61
73 Tetraodon nigroviridis SNX17
Saccoglossus kowalevskii (XP_006817773)
54
88 Strongylocentrotus purpuratus (XP_011660429)
Xenopus tropicalis SNX31
Monodelphis domestica SNX31
84
93 Rattus norvegicus SNX31
Mus musculus SNX31
Myotis lucifugus SNX31
61 Felis catus SNX31
87 Canis familiaris SNX31
58 Macaca mulatta SNX31
95 Gorilla gorilla SNX31
86 Homo sapiens SNX31
Amphimedon queenslandica (XP_003386341)
Trichoplax adhaerens (XP_002110491)
Branchiostoma floridae (XP_002609888)
99
86 Homo sapiens SNX27
Pan troglodytes SNX27
57
53 Mus musculus SNX27
Felis catus SNX27
Bos taurus SNX27
Gallus gallus SNX27
70 Danio rerio SNX27
Gasterosteus aculeatus SNX27
54
88 Takifugu rubripes SNX27 a
Takifugu rubripes SNX27 b
72 Tetraodon nigroviridis SNX27 a
74 Tetraodon nigroviridis SNX27 b
Hsa2
Hsa8
Hsa1
0.5

Phylogenetic tree of SNX family.

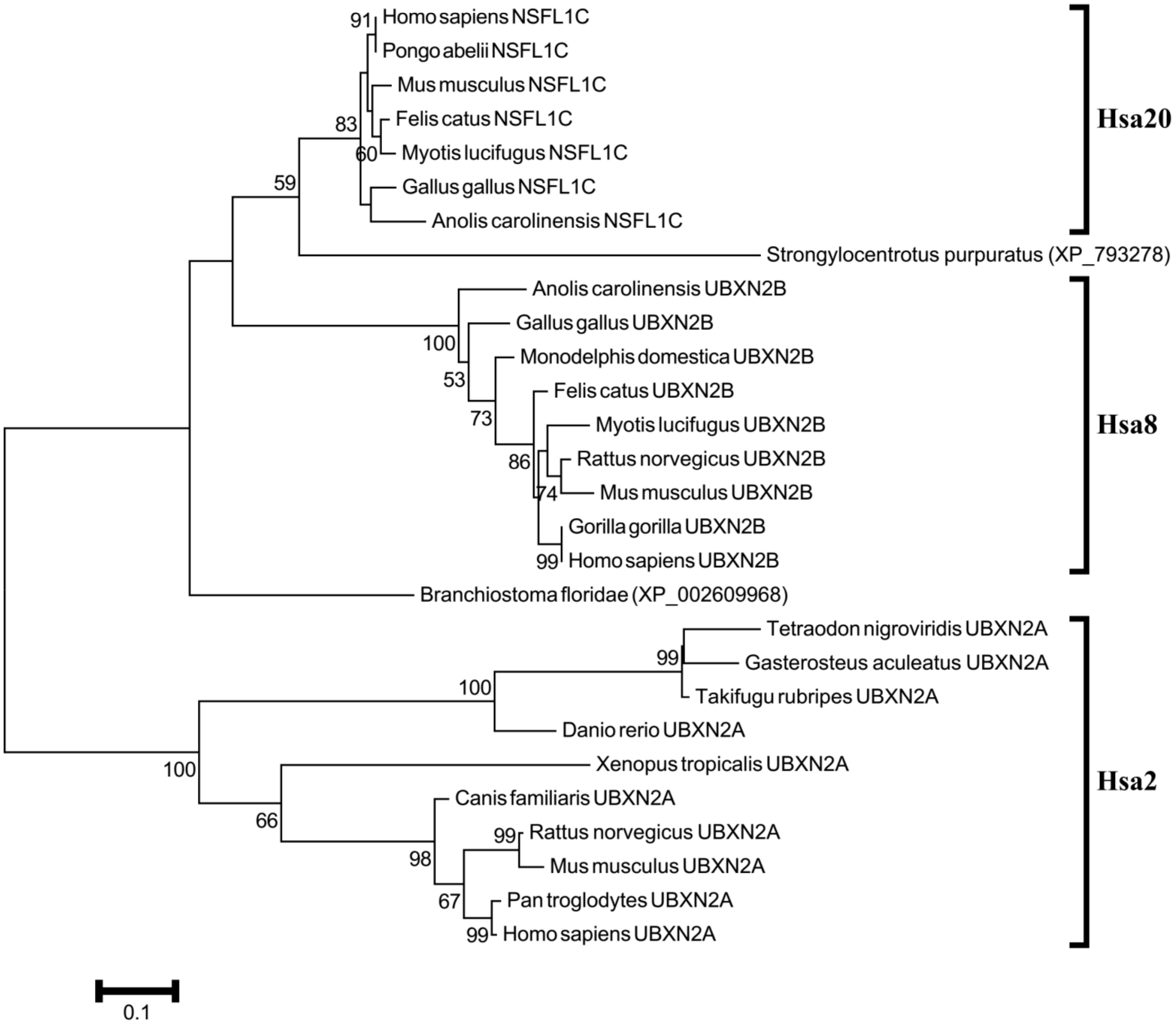
The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-4476.6316) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values ≥ 50% are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+*G*, parameter = 5.5801)). 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 153 positions in the final dataset.

Transcription Elongation factor A (SII) Protein-TCEA


81
Homo sapiens TCEA1
Xenopus tropicalis TCEA1
75
95
Danio rerio TCEA1 b
Danio rerio TCEA1 a
50
Oryzias latipes TCEA1
84
Gasterosteus aculeatus TCEA1
90
Tetraodon nigroviridis TCEA1
98
Takifugu rubripes TCEA1 b
94
Takifugu rubripes TCEA1 a
96
Danio rerio TCEA2
Oryzias latipes TCEA2
Mus musculus TCEA2
92
Pan troglodytes TCEA2
89
Homo sapiens TCEA2
Apis mellifera (XP_006566360)
83
Homo sapiens TCEA3
Gorilla gorilla TCEA3
78
Gasterosteus aculeatus TCEA3 a
Gasterosteus aculeatus TCEA3 b
Tetraodon nigroviridis TCEA3
52
Takifugu rubripes TCEA3 a
65
Takifugu rubripes TCEA3 b
Tetraodon nigroviridis TCEANC
94
Xenopus tropicalis TCEANC
Mus musculus TCEANC
91
Homo sapiens TCEANC
Hydra magnipapillata (XP_002166168)
Hsa8
Hsa20
Hsa1
HsaX
0.5

Phylogenetic tree of TCEA 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 (-4688.8104) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values ≥ 50% are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+*G*, parameter = 2.5721)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 27 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 197 positions in the final dataset.



Phylogenetic tree of UBXN 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 (-3195.4561) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values ≥ 50% are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+*G*, parameter = 2.3205)). 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 163 positions in the final dataset.