

## Supplemental Figures for

### Genomic architecture constrained placental X Chromosome evolution

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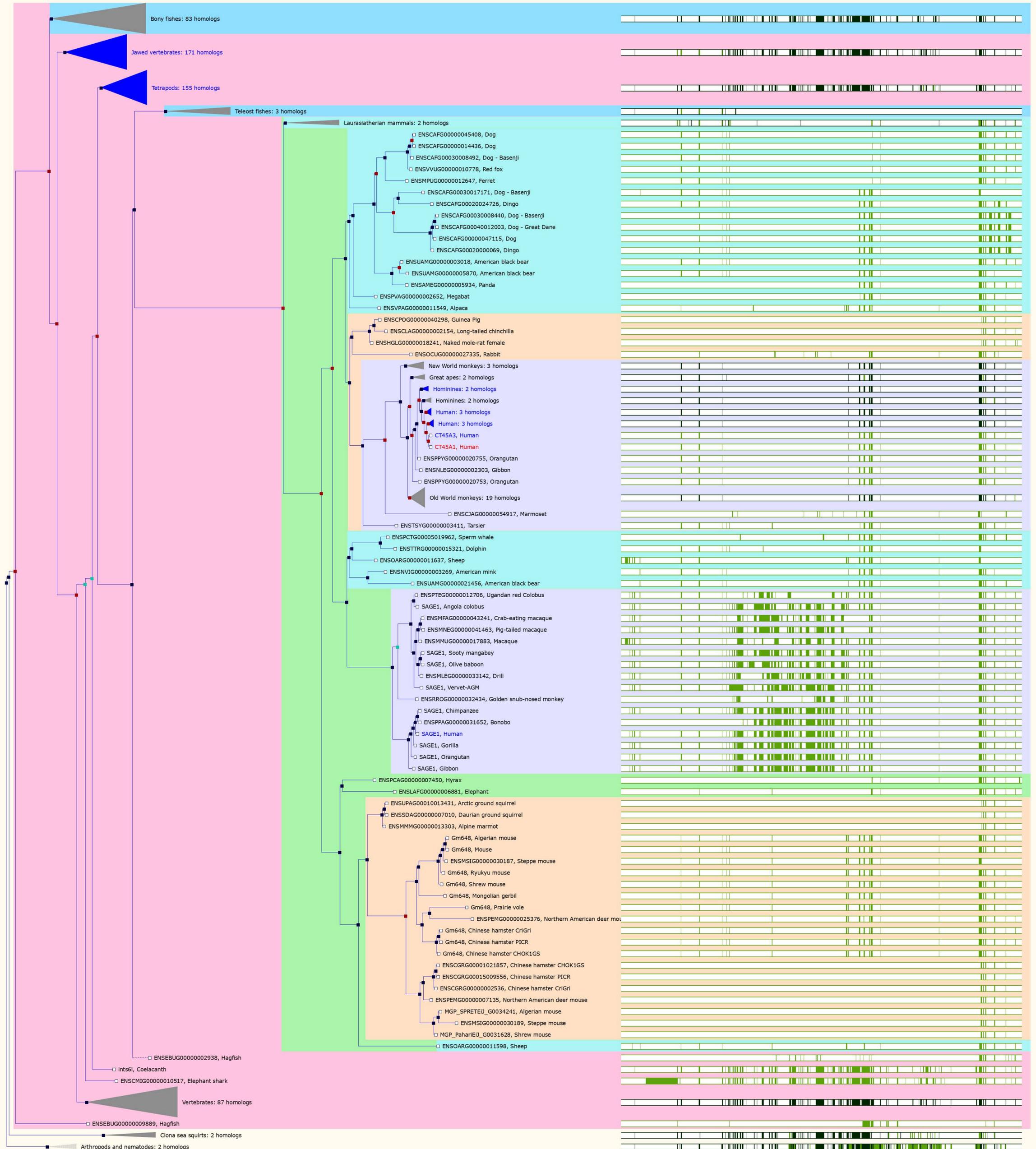
Reptiles and birds: 6 homologs



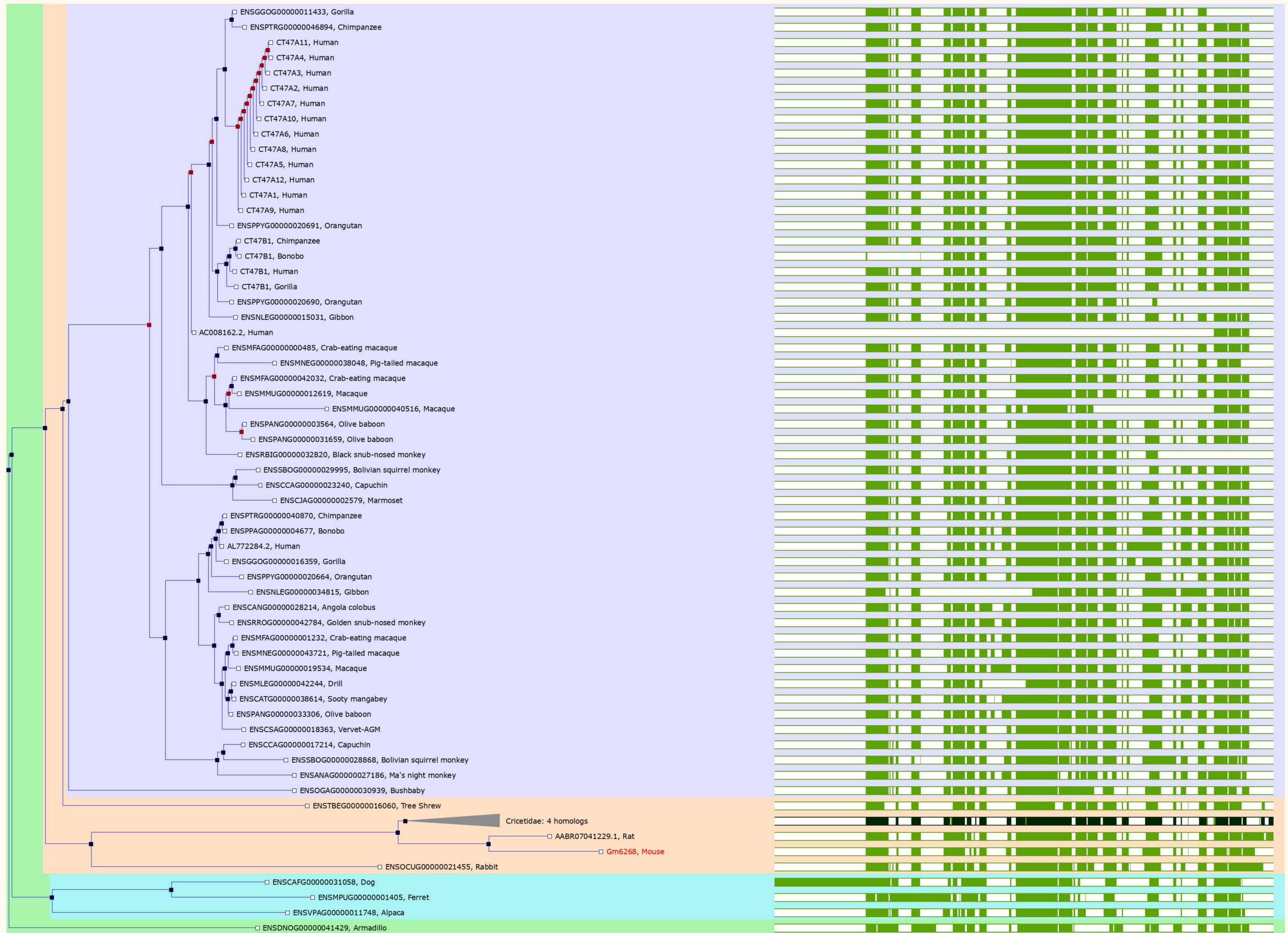
**LEGEND**

- Branch Length: x1 branch length, x10 branch length, x100 branch length
- Nodes: gene node, speciation node, duplication node, ambiguous node, gene split event
- Genes: Gene ID, gene of interest, Gene ID within-sp. paralog
- Collapsed nodes: collapsed sub-tree, collapsed (this gene), collapsed (paralog), (x10 branch length), (x100 branch length)
- Expanded Alignments: aligned seq
- Alignments: 0 - 33% aligned seq, 33 - 66% aligned seq, 66 - 100% aligned seq

**Supplemental Figure 1. LAGE/CTAG Gene Families Phylogeny**



**Supplemental Figure 2. CT45 Gene Family Phylogeny**



LEGEND

Branch Length

- x1 branch length
- ⋯ x10 branch length
- ⋯ x100 branch length

Nodes

- gene node
- speciation node
- duplication node
- ambiguous node
- gene split event

Genes

- Gene ID gene of interest
- Gene ID within-sp. paralog

Collapsed nodes

- ◀ collapsed sub-tree
- ▶ collapsed (this gene)
- ▶ collapsed (paralog)
- ▶ (x10 branch length)
- ▶ (x100 branch length)

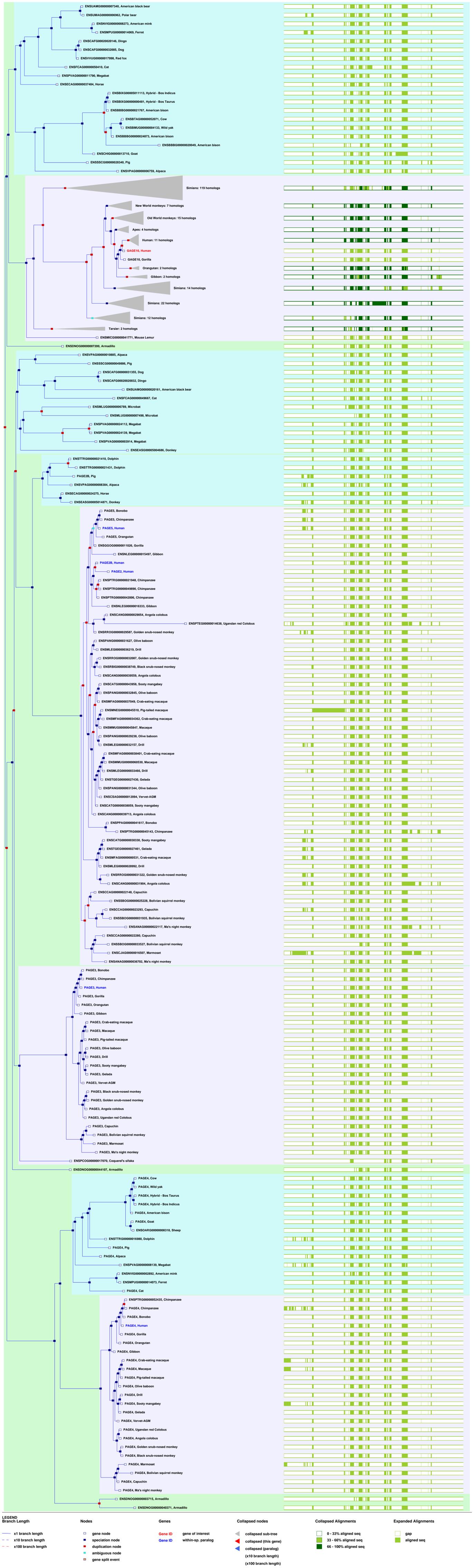
Collapsed Alignments

- 0 - 33% aligned seq
- 33 - 66% aligned seq
- 66 - 100% aligned seq

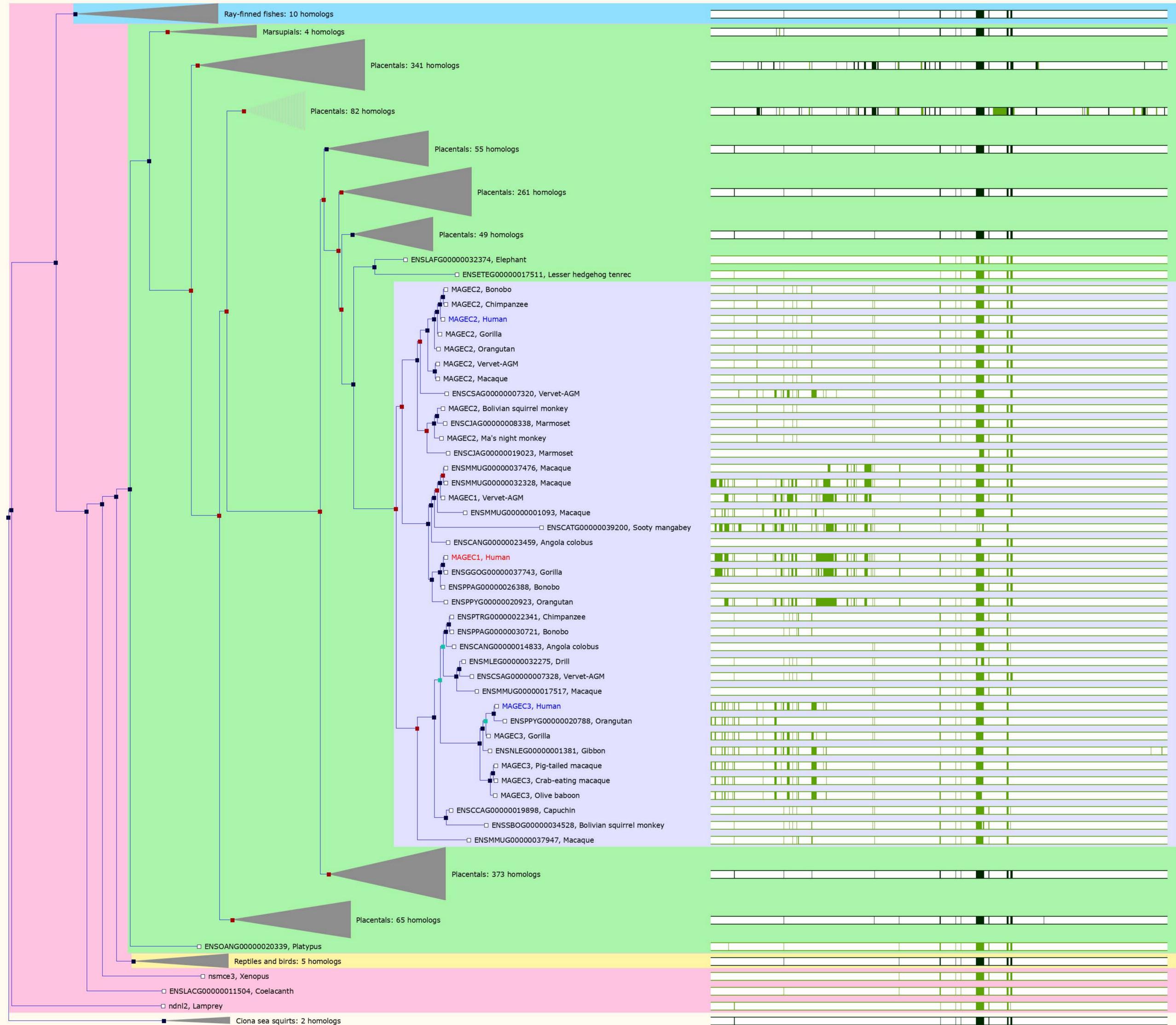
Expanded Alignments

- gap
- aligned seq

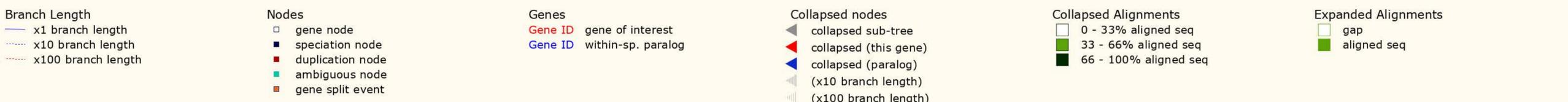
**Supplemental Figure 3. CT47 Gene Family Phylogeny**



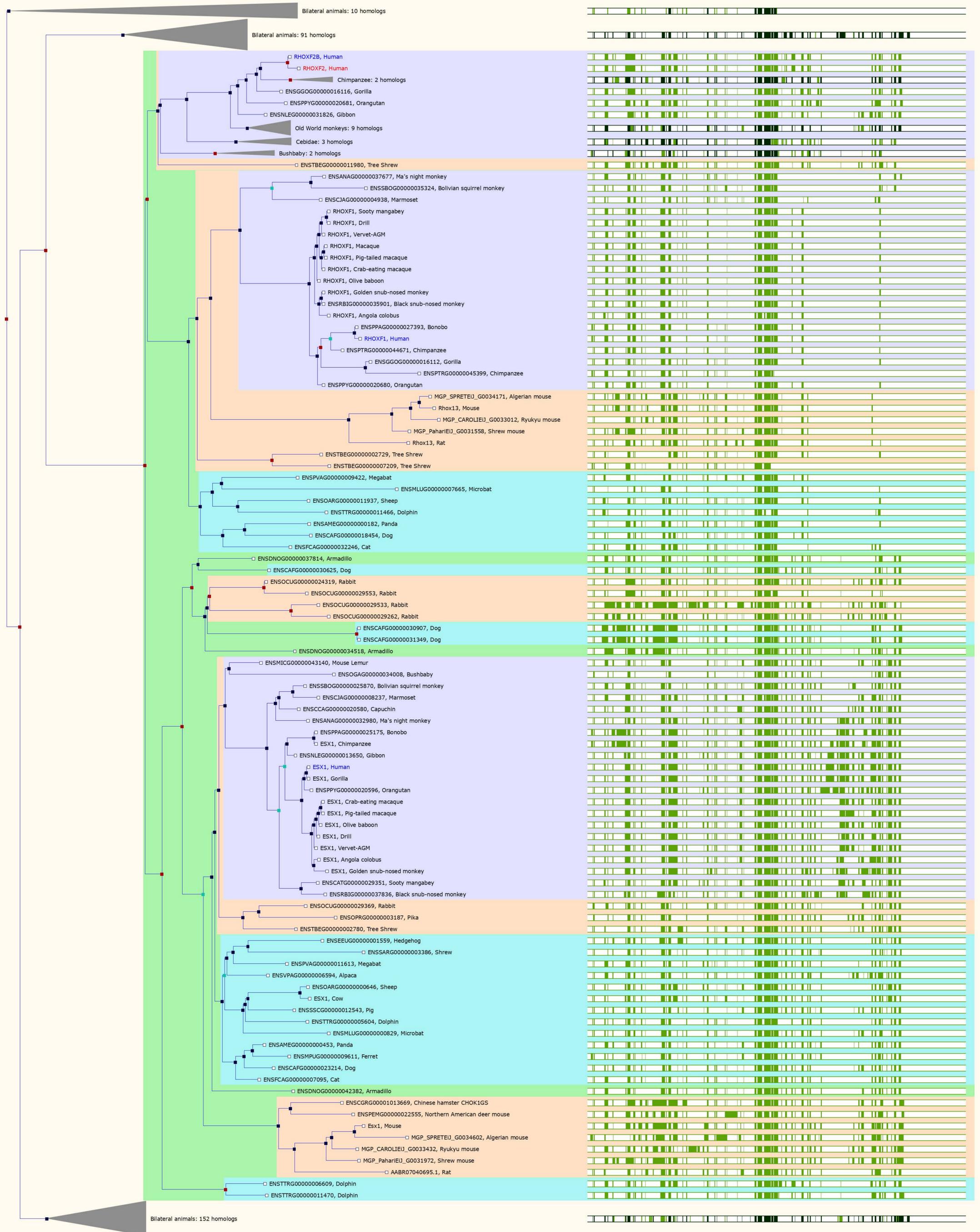
**Supplemental Figure 4. GAGE Gene Family Phylogeny**



LEGEND



**Supplemental Figure 5. MAGEC Gene Family Phylogeny**



**LEGEND**

Branch Length  
 x1 branch length  
 x10 branch length  
 x100 branch length

**Nodes**  
 gene node  
 speciation node  
 duplication node  
 ambiguous node  
 gene split event

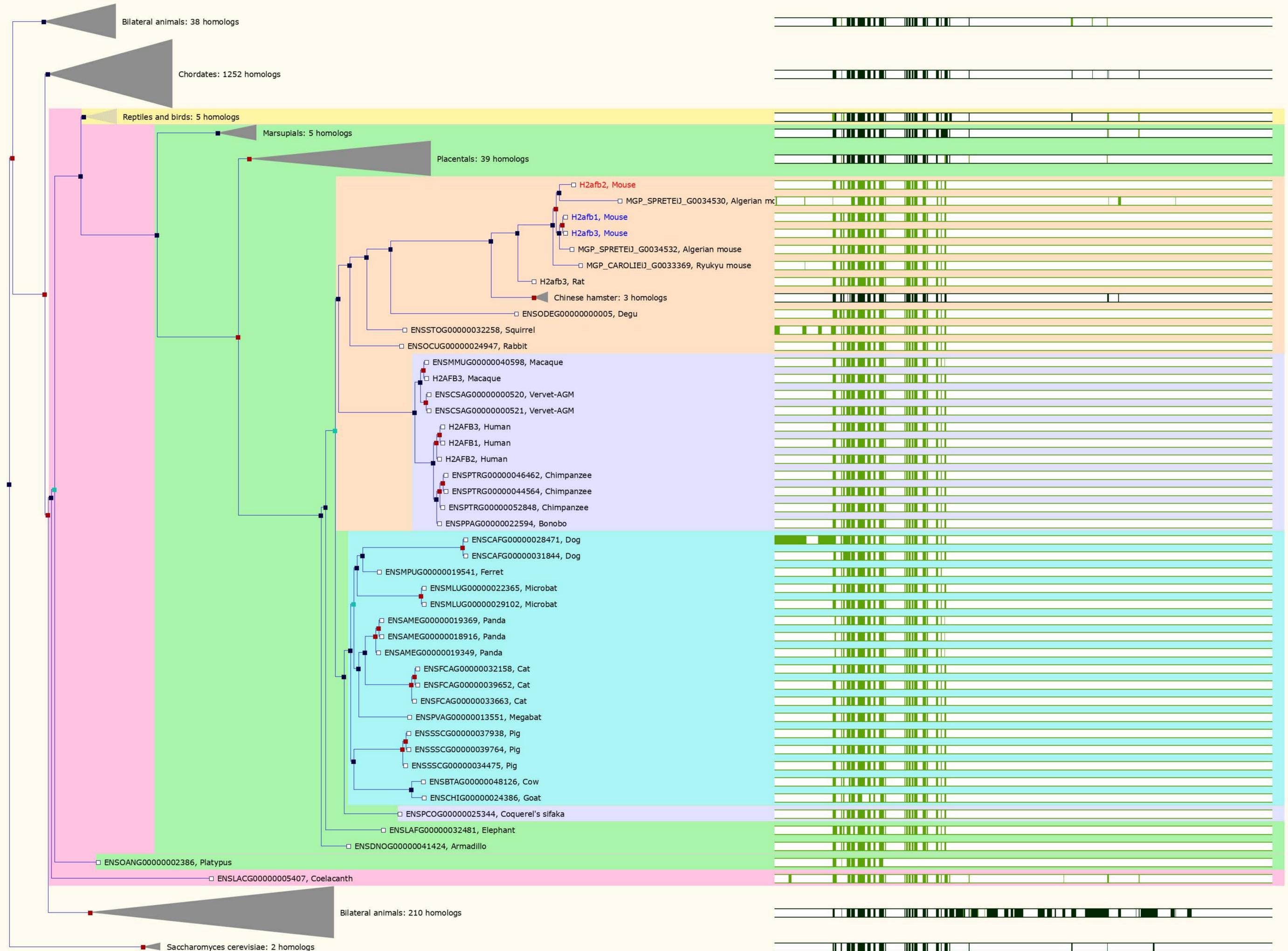
**Genes**  
 Gene ID gene of interest  
 Blue ID within-sp. paralog

**Collapsed nodes**  
 collapsed sub-tree  
 collapsed (this gene)  
 collapsed (paralog)  
 (x10 branch length)  
 (x100 branch length)

**Collapsed Alignments**  
 0 - 33% aligned seq  
 33 - 66% aligned seq  
 66 - 100% aligned seq

**Expanded Alignments**  
 gap  
 aligned seq

**Supplemental Figure 6. RHOXF Gene Family Phylogeny**



**LEGEND**

**Branch Length**

- x1 branch length
- ⋯ x10 branch length
- ⋯⋯ x100 branch length

**Nodes**

- gene node
- speciation node
- duplication node
- ambiguous node
- gene split event

**Genes**

- Gene ID gene of interest
- Gene ID within-sp. paralog

**Collapsed nodes**

- ◀ collapsed sub-tree
- ▶ collapsed (this gene)
- ▶ collapsed (paralog)
- ◀ (x10 branch length)
- ◀ (x100 branch length)

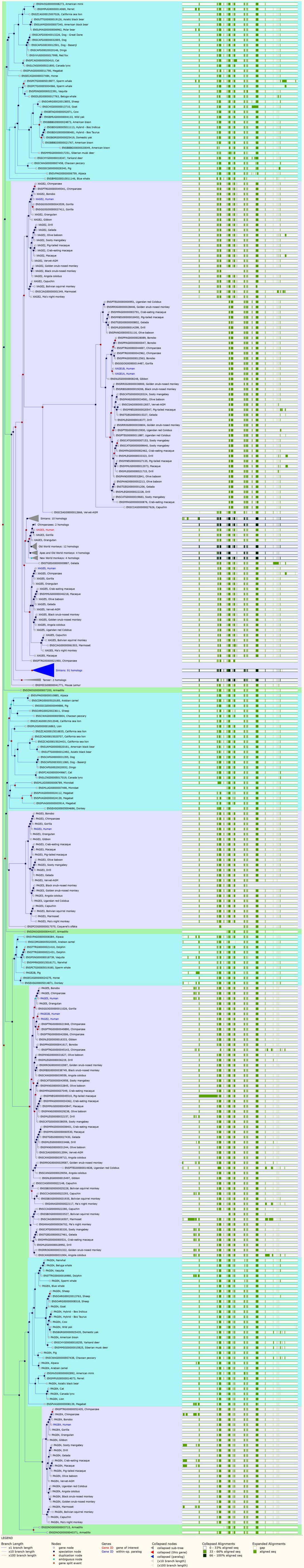
**Collapsed Alignments**

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- 33 - 66% aligned seq
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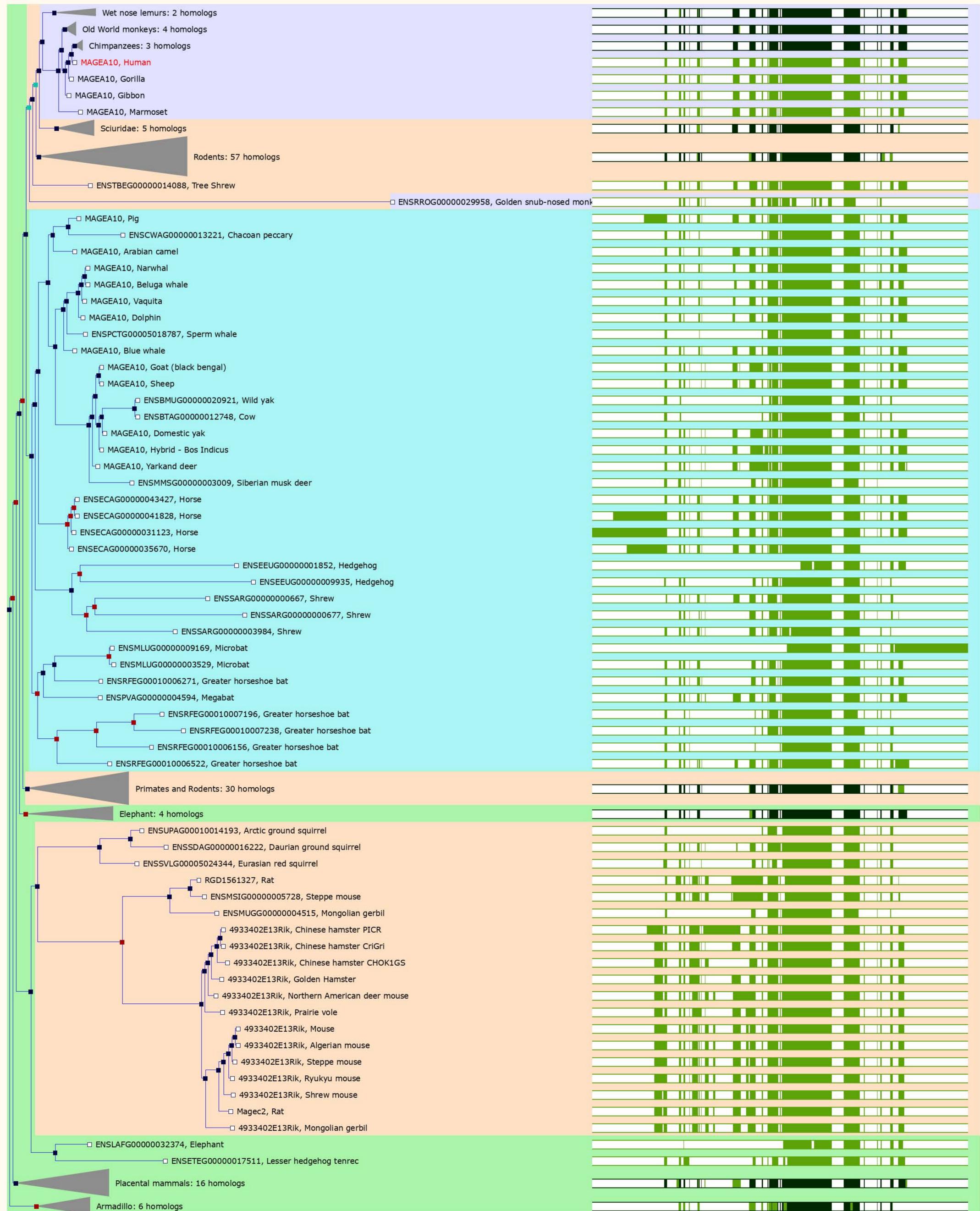
**Expanded Alignments**

- gap
- aligned seq

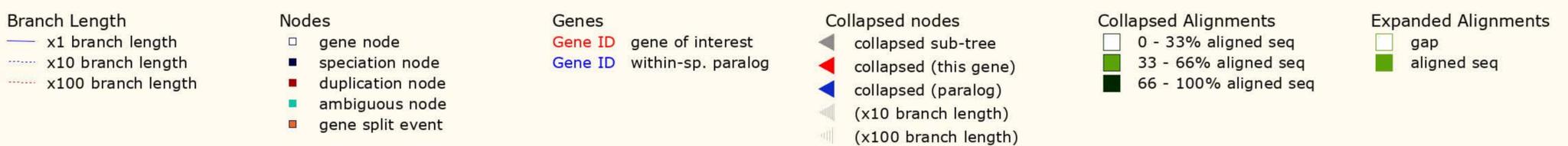
**Supplemental Figure 7. H2AFB Gene Family Phylogeny**



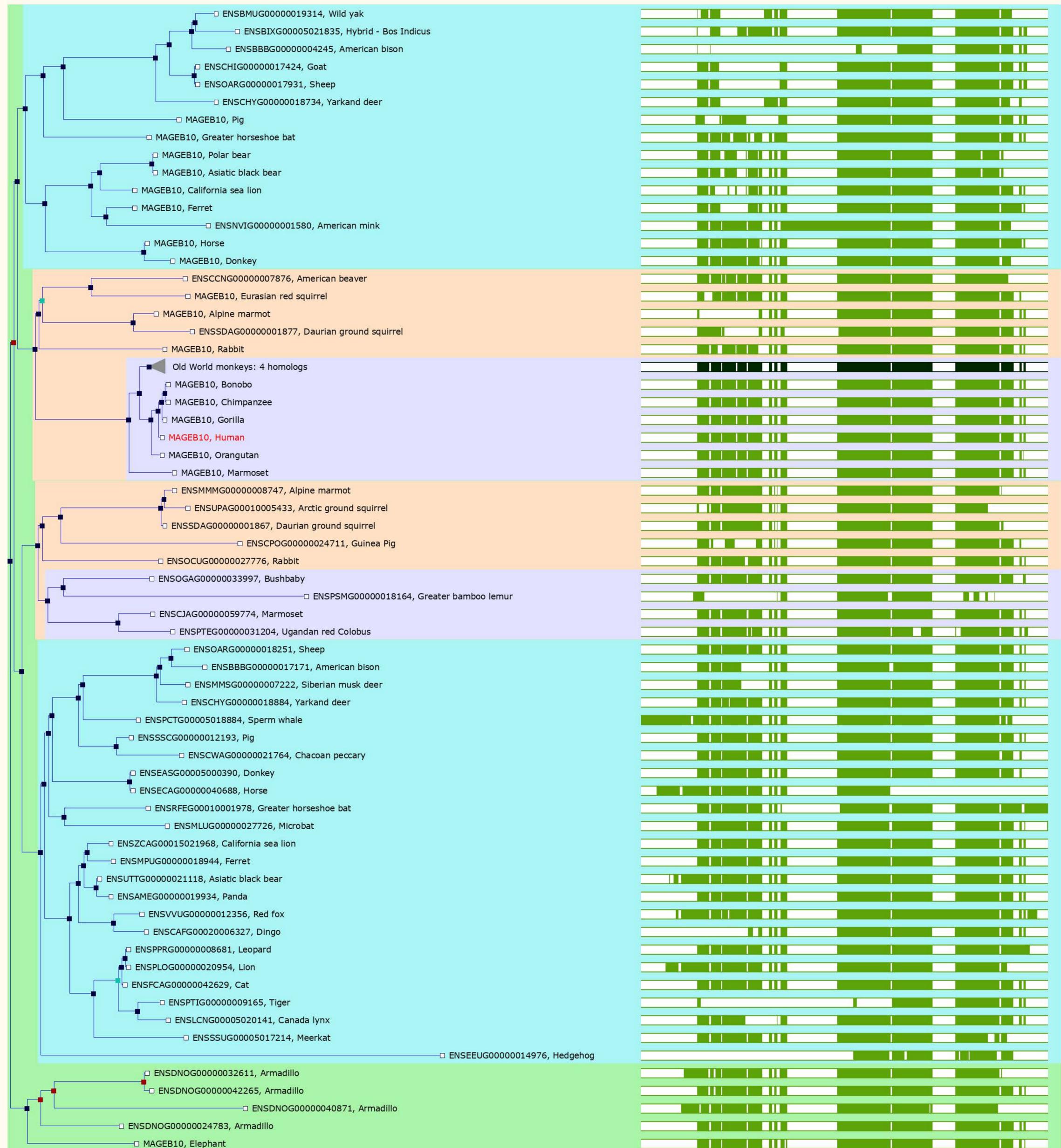
**Supplemental Figure 8. XAGE/PAGE Gene Families Phylogeny**



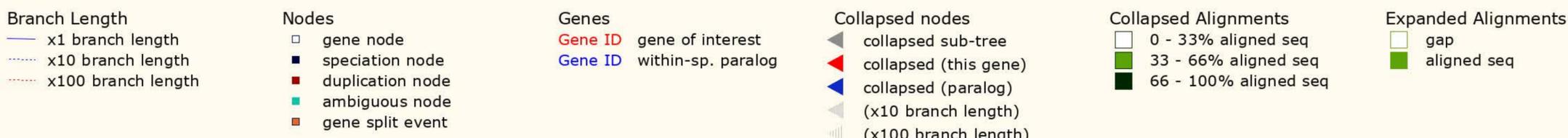
**LEGEND**



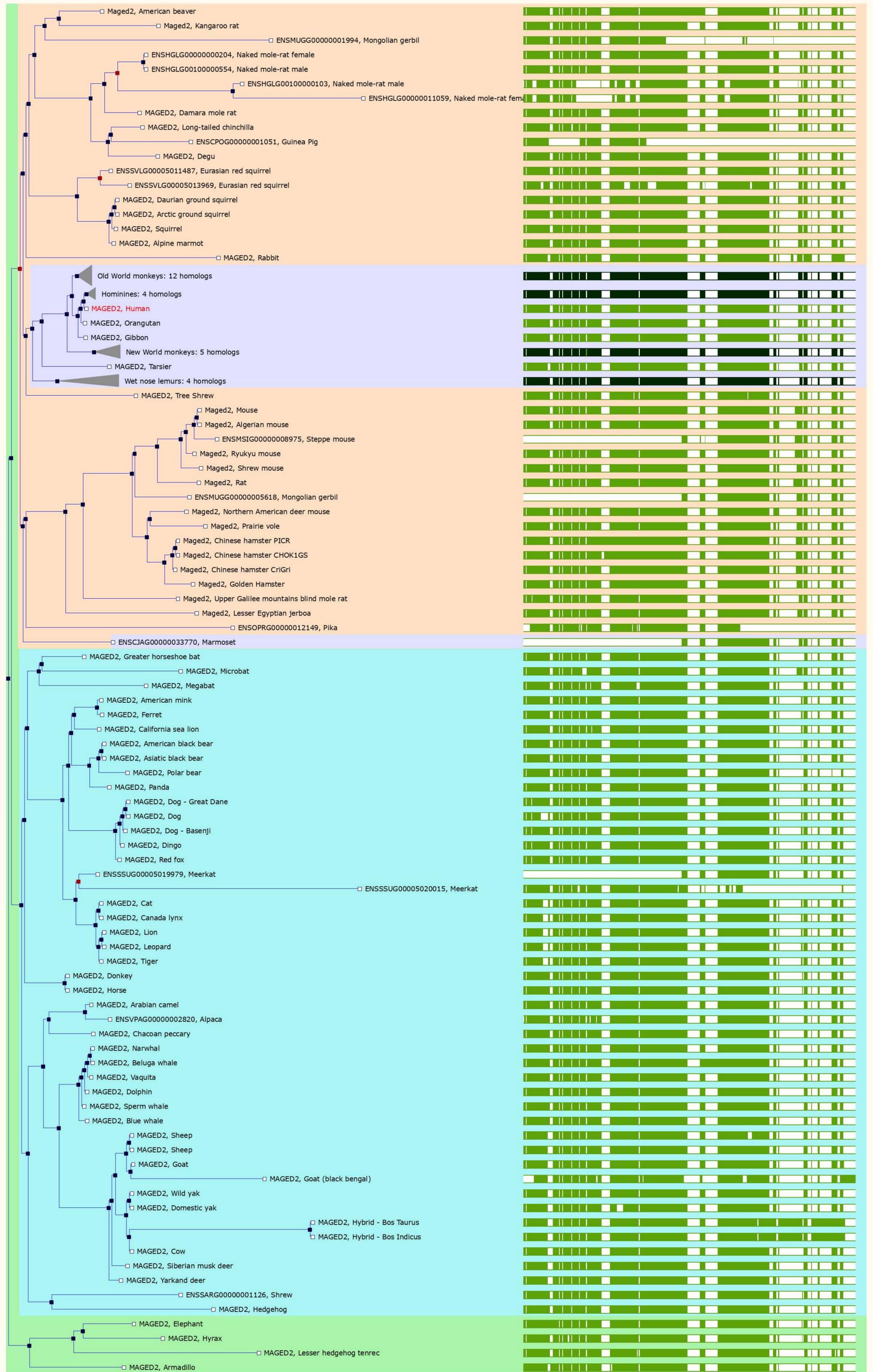
**Supplemental Figure 9. MAGEA Gene Family Phylogeny**



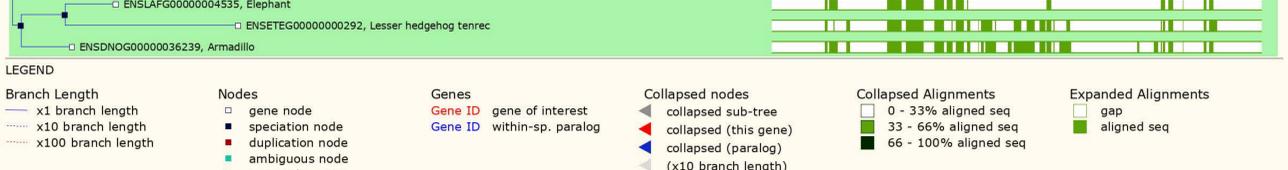
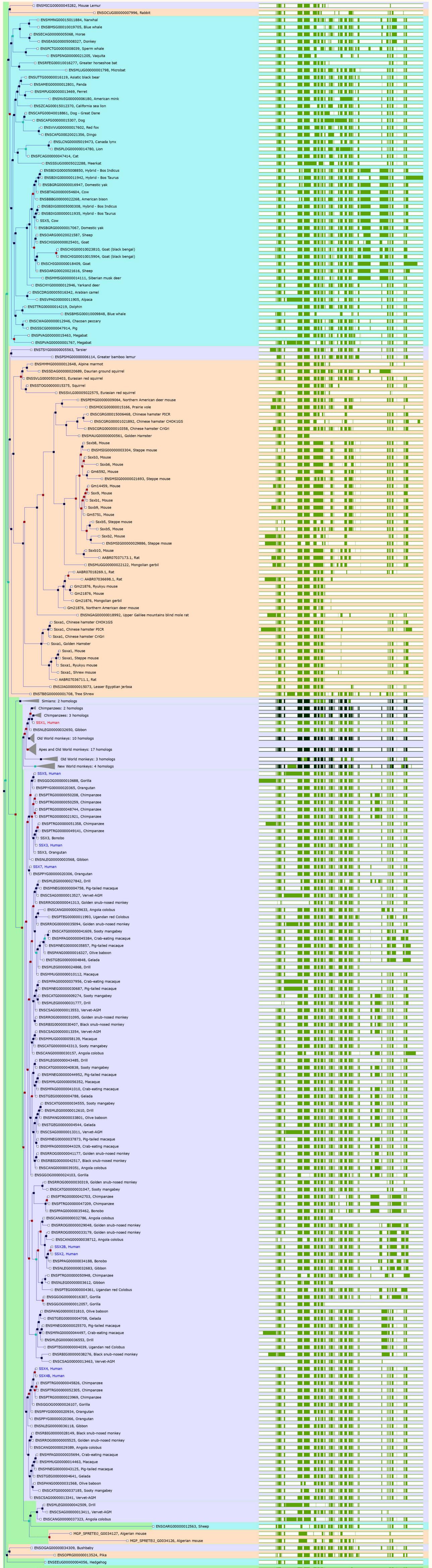
LEGEND



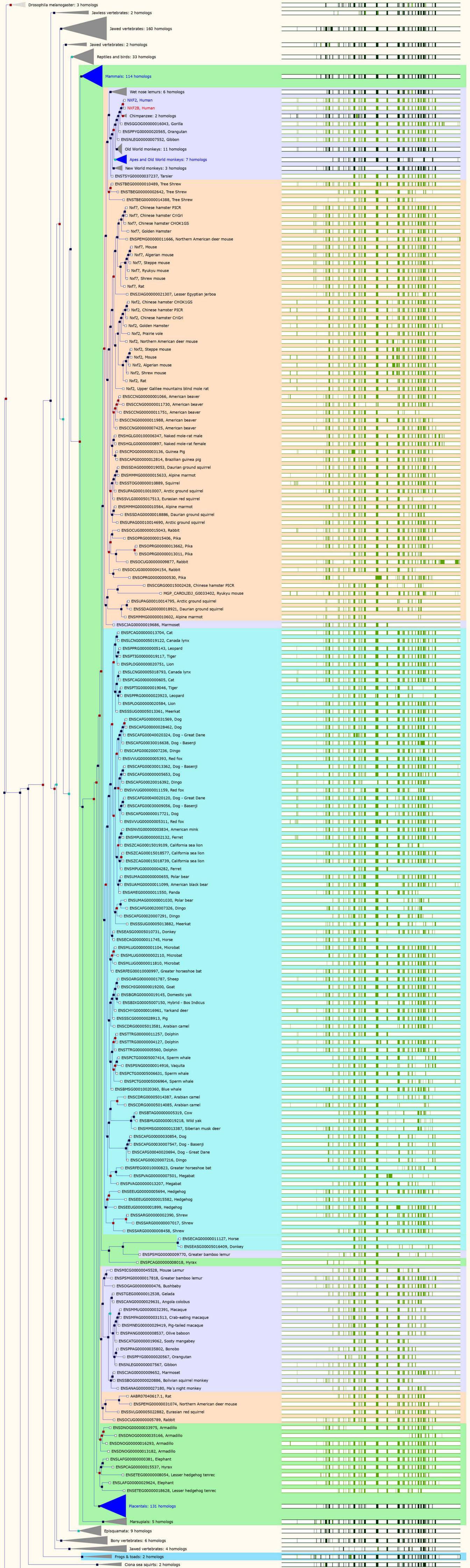
**Supplemental Figure 10. MAGEB Gene Family Phylogeny**



**Supplemental Figure 11. MAGED Gene Family Phylogeny**

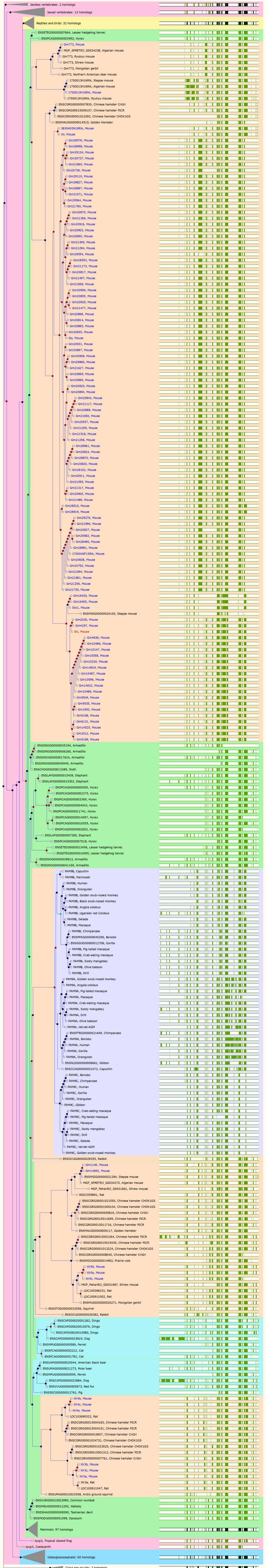


**Supplemental Figure 12. SSX Gene Family Phylogeny**



MEX67, Saccharomyces cerevisiae  
**LEGEND**  
**Branch Length**  
 — x1 branch length  
 — x10 branch length  
 — x100 branch length  
**Nodes**  
 ■ speciation  
 ■ gene node  
 ■ duplication node  
 ■ ambiguous node  
 ■ gene split event  
**Genes**  
 Gene ID  
 ■ within-sp. paralog  
**Collapsed nodes**  
 ◀ collapsed sub-tree  
 ◀ collapsed (this gene)  
 ◀ collapsed (paralog)  
 ◀ (x10 branch length)  
 ◀ (x100 branch length)  
**Collapsed Alignments**  
 ■ 0 - 33% aligned seq  
 ■ 33 - 66% aligned seq  
 ■ 66 - 100% aligned seq  
**Expanded Alignments**  
 ■ gap  
 ■ aligned seq

**Supplemental Figure 13. NXF2 Gene Family Phylogeny**



**LEGEND**

**Branch Length**

- x1 branch length
- x10 branch length
- x100 branch length

**Nodes**

- gene node
- speciation node
- duplication node
- ambiguous node
- gene split event

**Genes**

- Gene ID
- gene in-sp.
- gene in-sep. paral.

**Collapsed nodes**

- ◻ collapsed sub-tree
- ◻ collapsed (paralog)
- ◻ (x10 branch length)
- ◻ (x100 branch length)

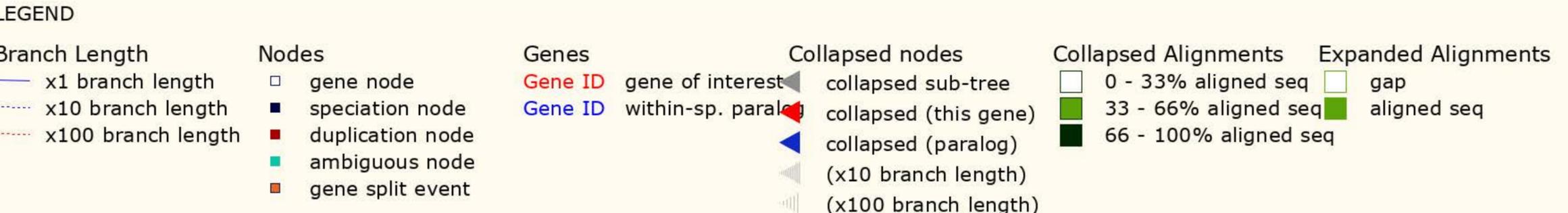
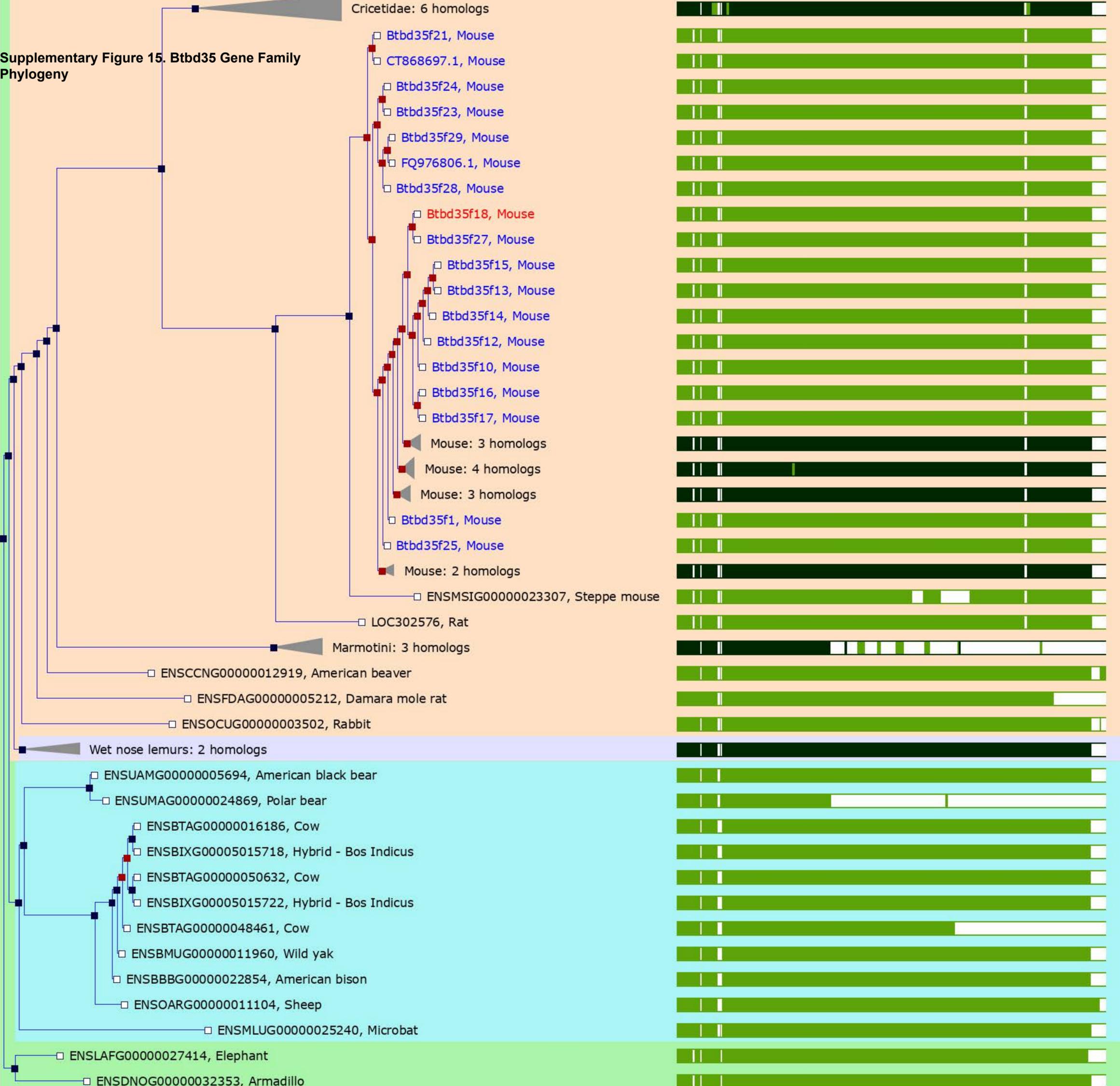
**Collapsed Alignments**

- ◻ 0 - 33% aligned seq
- ◻ 33 - 66% aligned seq
- ◻ 66 - 100% aligned seq
- ◻ gap
- ◻ aligned seq

**Expanded Alignments**

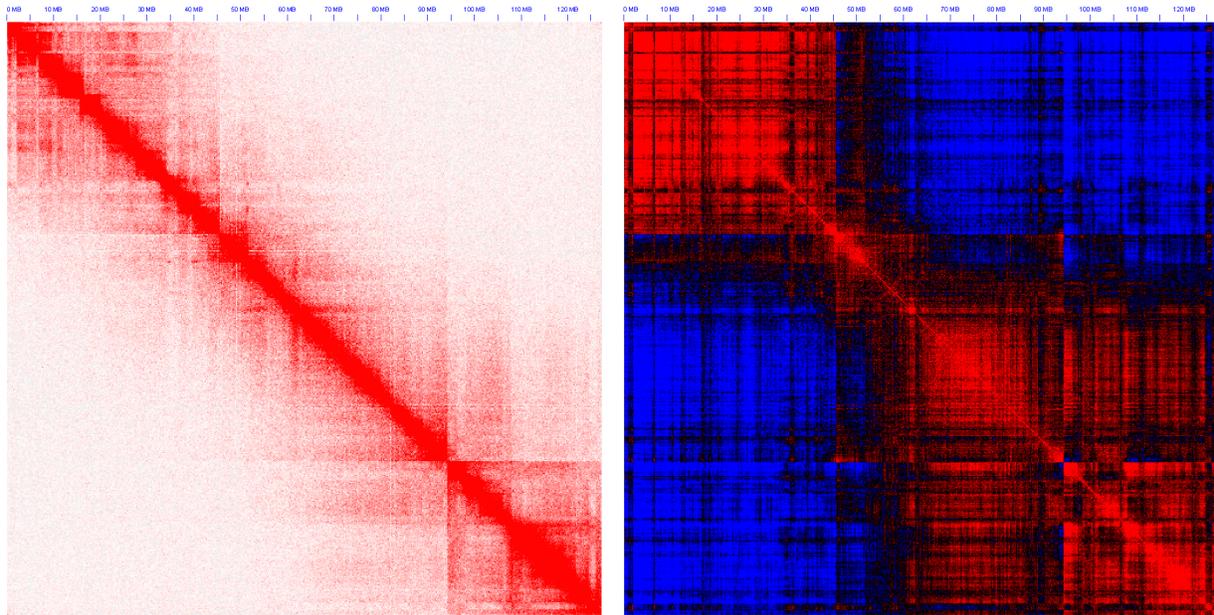
**Supplemental Figure 14. FAM9/Slx/Sly/Xlr Gene Families Phylogeny**

Supplementary Figure 15. Btbd35 Gene Family Phylogeny

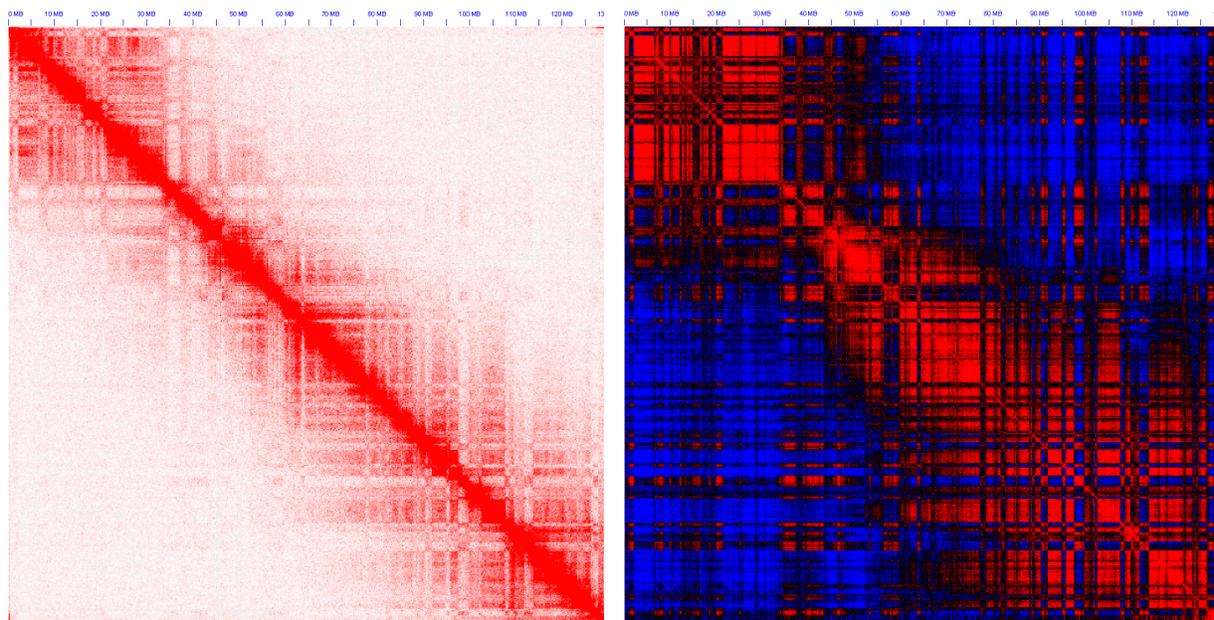


**Supplemental Figure 15. Btbd35 Gene Family Phylogeny**

F1 Phased Female Fibroblasts: Domestic Cat/Xi



F1 Phased Female Fibroblasts: Asian Leopard Cat/Xa



**Supplemental Figure 16. Hi-C contact maps (left) and Pearson's correlation maps (right) (both maps calculated at 250 kb resolution) generated from the phased domestic cat (top) and Asian leopard cat (bottom) Hi-C reads**