

The evolution of vertebrate somatostatin receptors and their gene regions involves extensive chromosomal rearrangements

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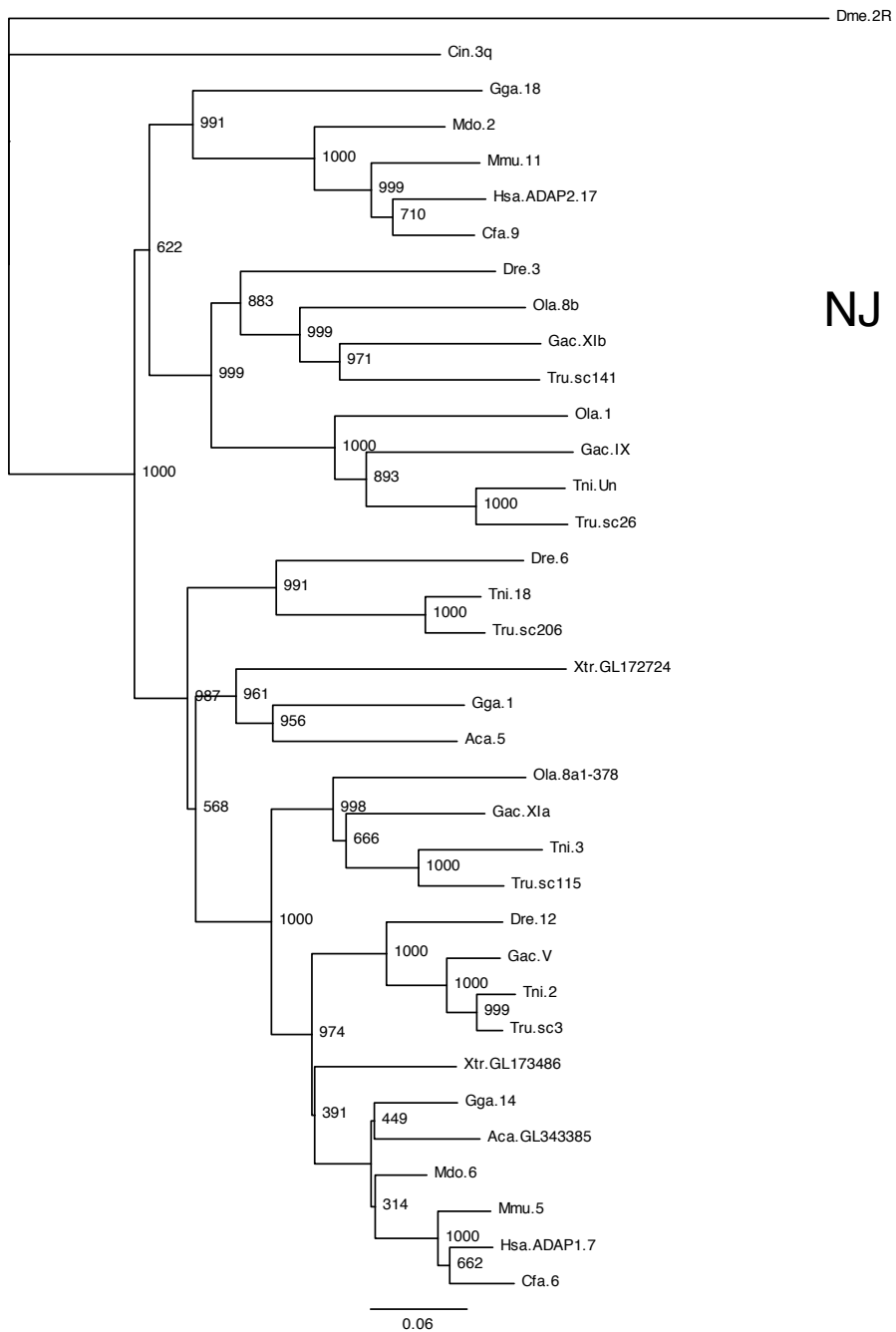
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Telephone: +46-18-4714173

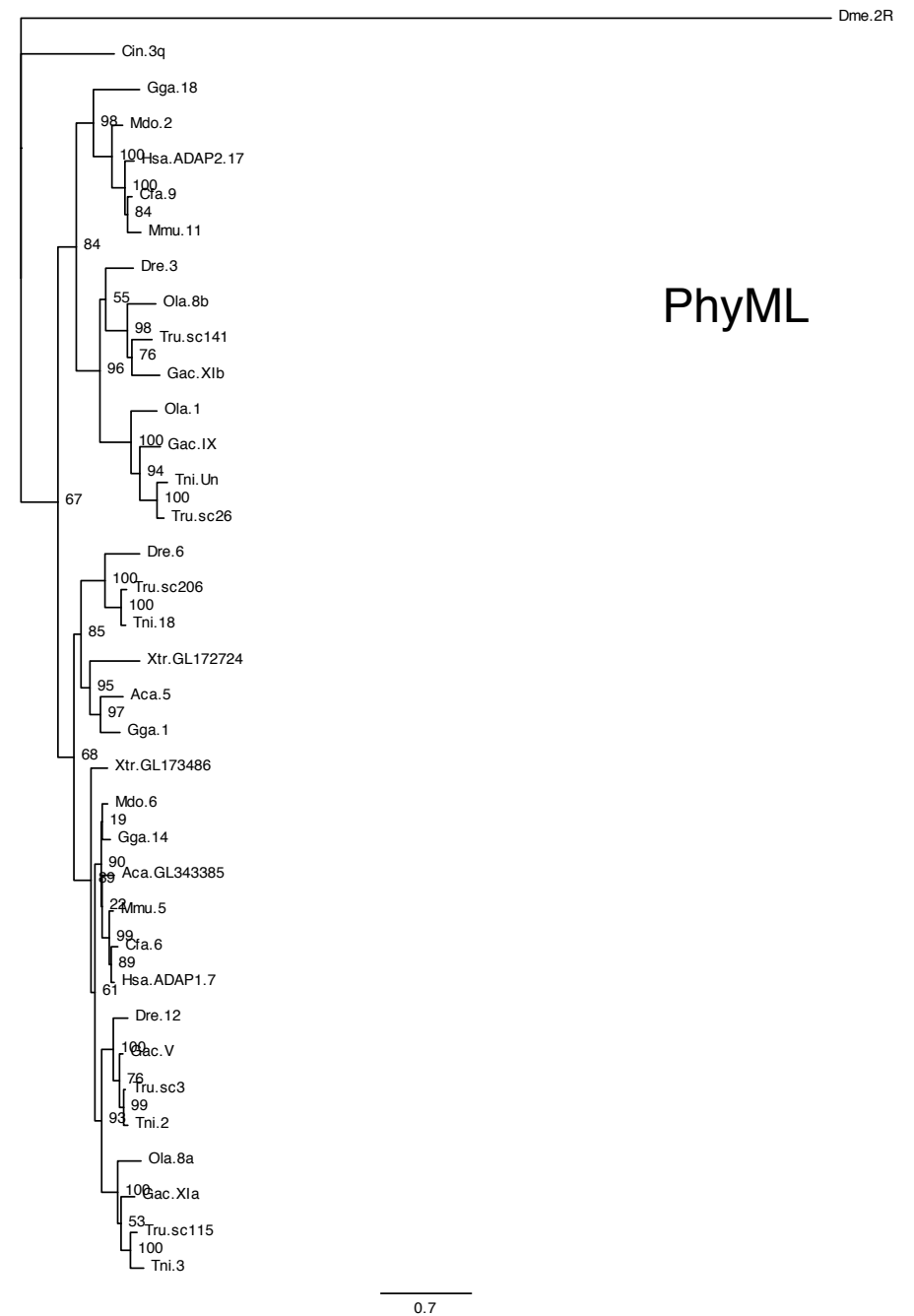
Fax: +46-18-511540

SUPPLEMENTAL FIGURES 21-50

Figures S21-50: Bootstrapped Neighbor Joining (NJ) and Phylogenetic Maximum Likelihood (PhyML) trees of the *SSTR2*, -3 and -5-neighboring gene families. The topologies are supported by non-parametric bootstrap analyses with 1000 (NJ) or 100 (PhyML) replicates (see Methods). Branch support is shown at the nodes. The trees are rooted with the identified fruit fly sequences, unless specified in Table 3. Species abbreviations are applied as follows: *Homo sapiens* (Hsa), *Mus musculus* (Mmu), *Canis familiaris* (Cfa), *Monodelphis domestica* (Mdo), *Macropus eugenii* (Meu), *Gallus gallus* (Gga), *Meleagris gallopavo* (Mga), *Taeniopygia guttata* (Tgu), *Anolis carolinensis* (Aca), *Silurana (Xenopus) tropicalis* (Xtr), *Danio rerio* (Dre), *Oryzias latipes* (Ola), *Gasterosteus aculeatus* (Gac), *Tetraodon nigroviridis* (Tni), *Takifugu rubripes* (Tru), *Ciona intestinalis* (Cin), *Ciona savignyi* (Csa), *Branchiostoma floridae* (Bfl), *Caenorhabditis elegans* (Cel) and *Drosophila melanogaster* (Dme). See Methods – “*Identification and analysis of neighboring gene families/Conserved syntenic analysis*” - for the choice of species representation. HGNC symbols are used for all human sequences. Other species' sequences are identified by chromosomal/genomic scaffold assignment. Lowercase a, b and c are used to distinguish sequences located on the same chromosomes. Comprehensive information about each sequence is available in Additional file 9, Table S3.



NJ



PhyML

Figure S21. ADAP

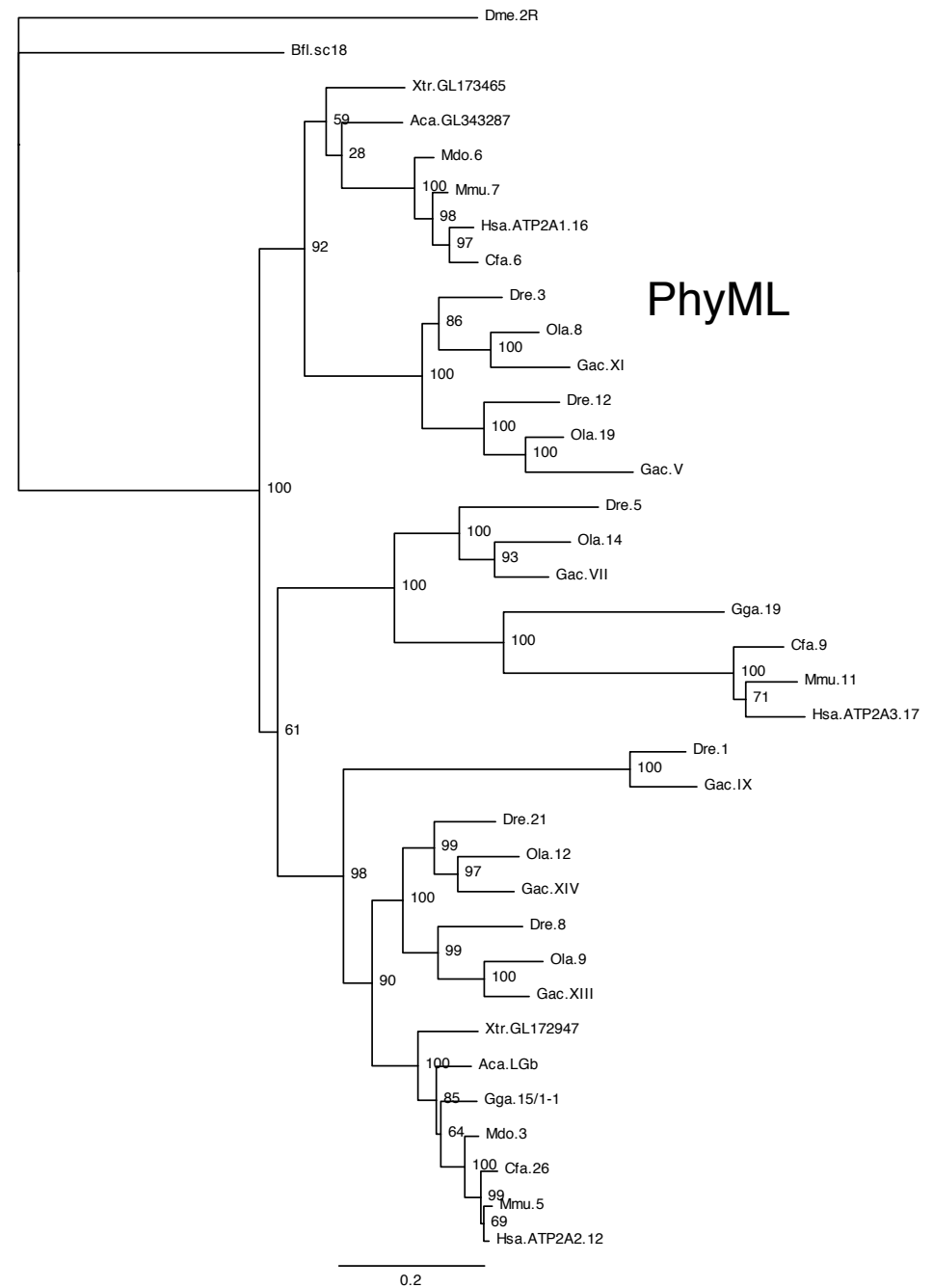
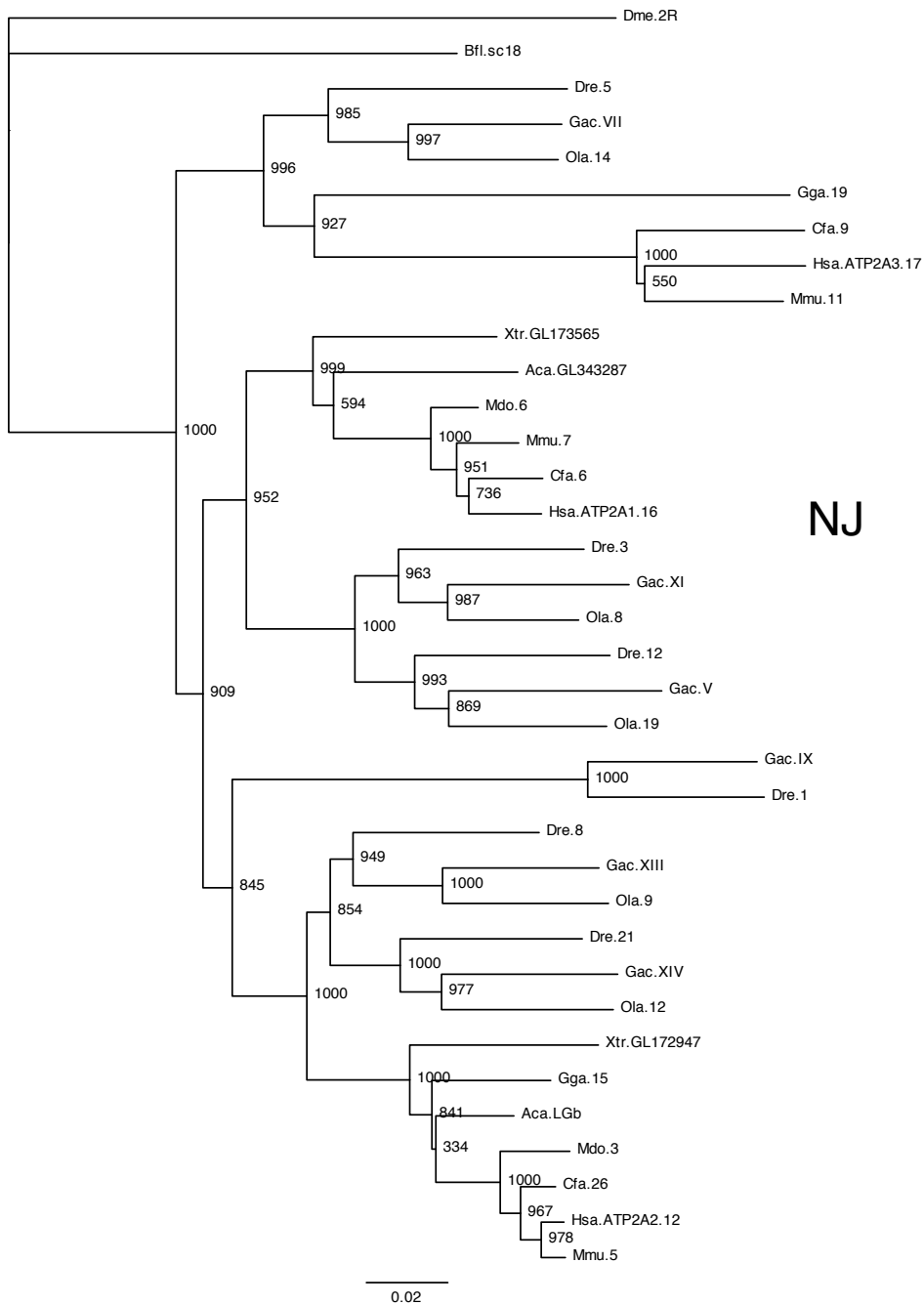


Figure S22. ATP2A

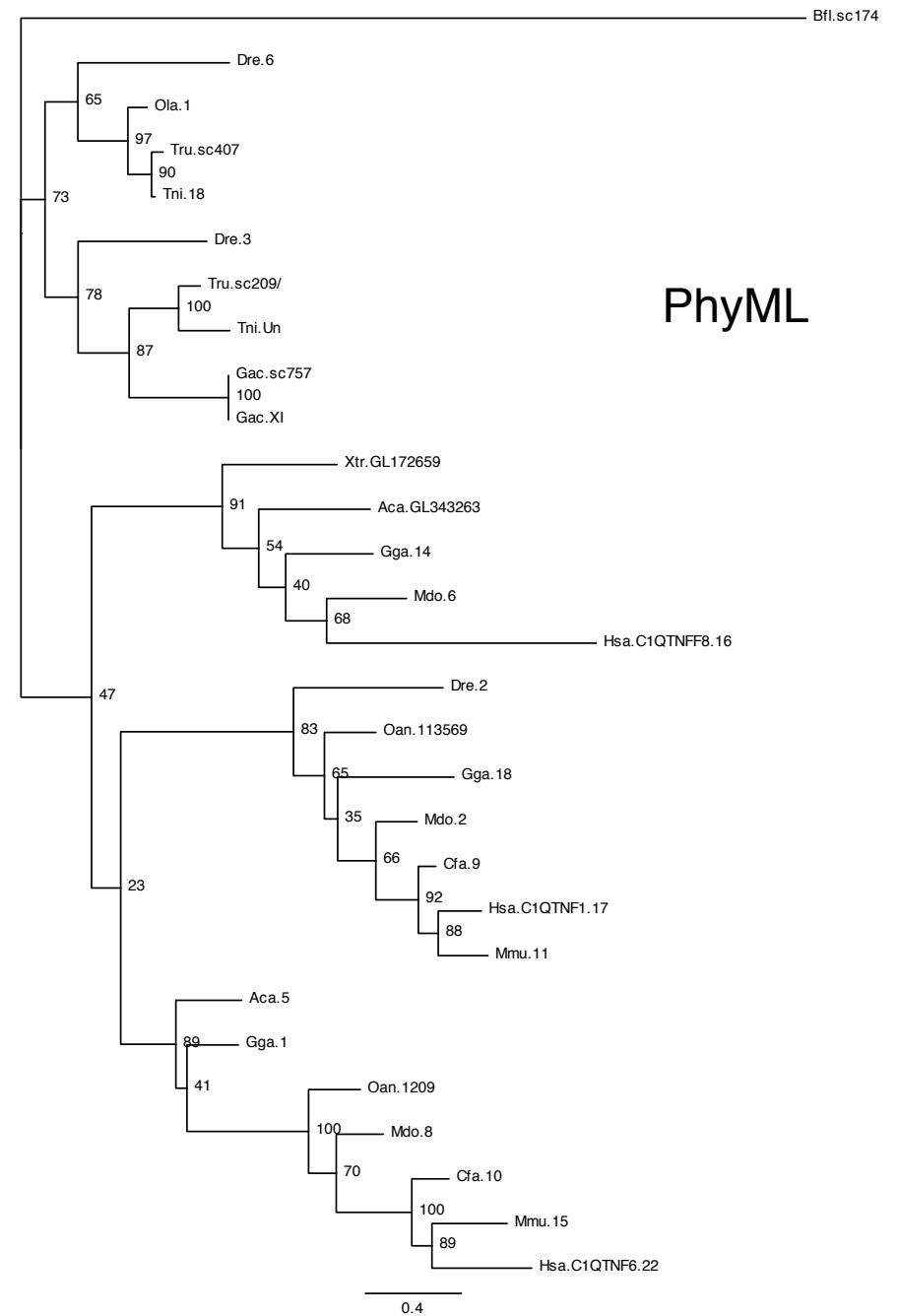
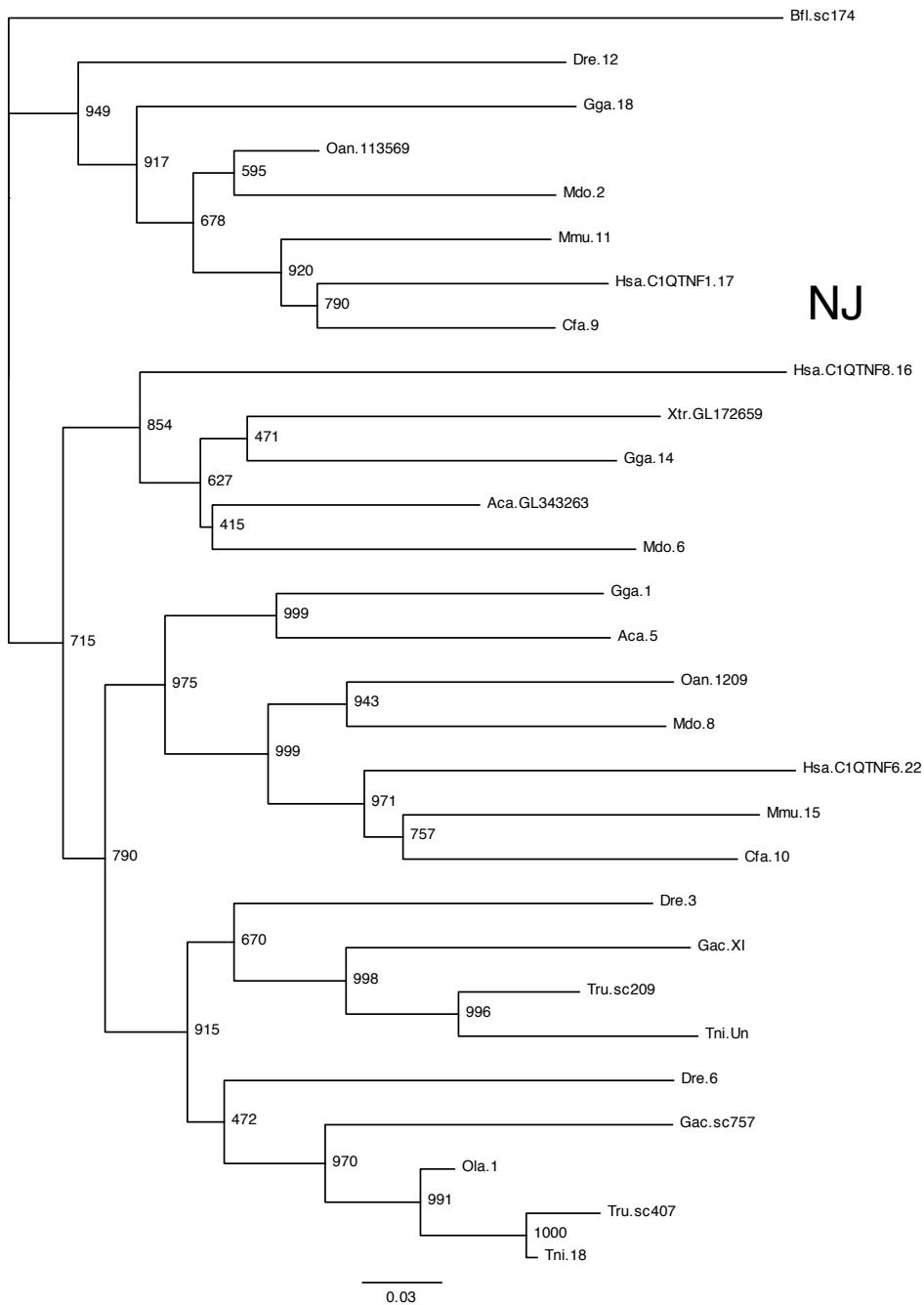


Figure S23. C1QTNF

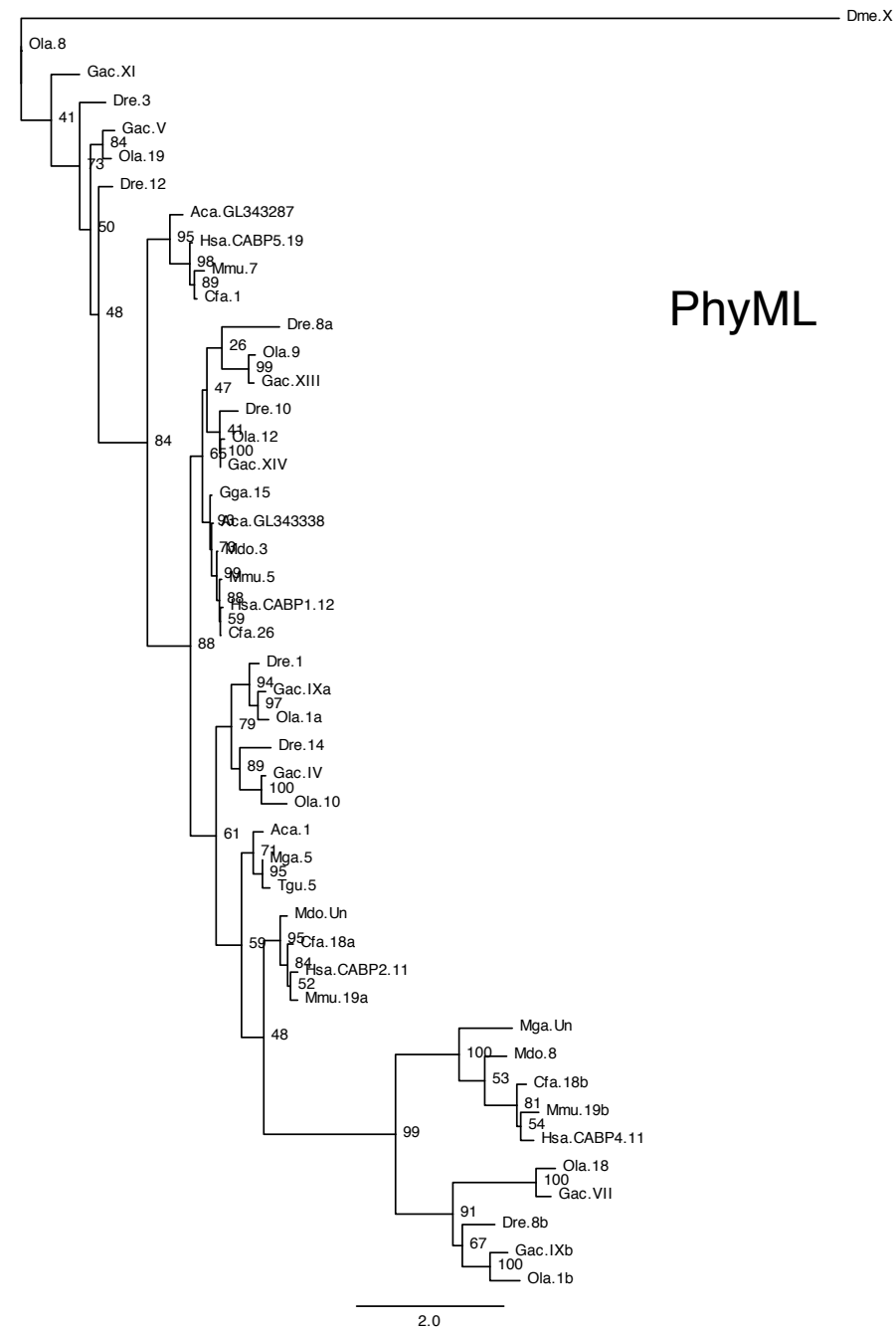
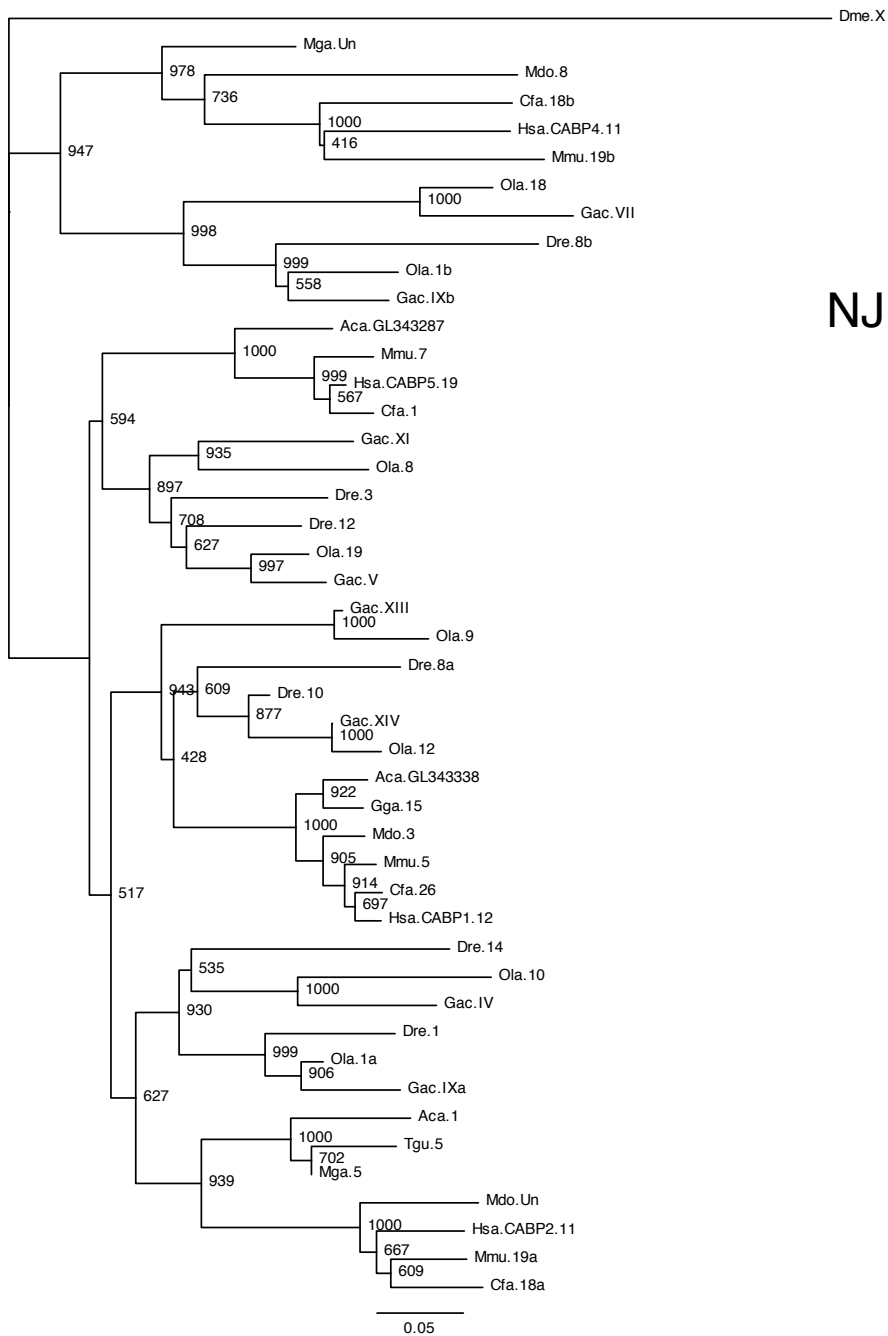


Figure S24. CABP

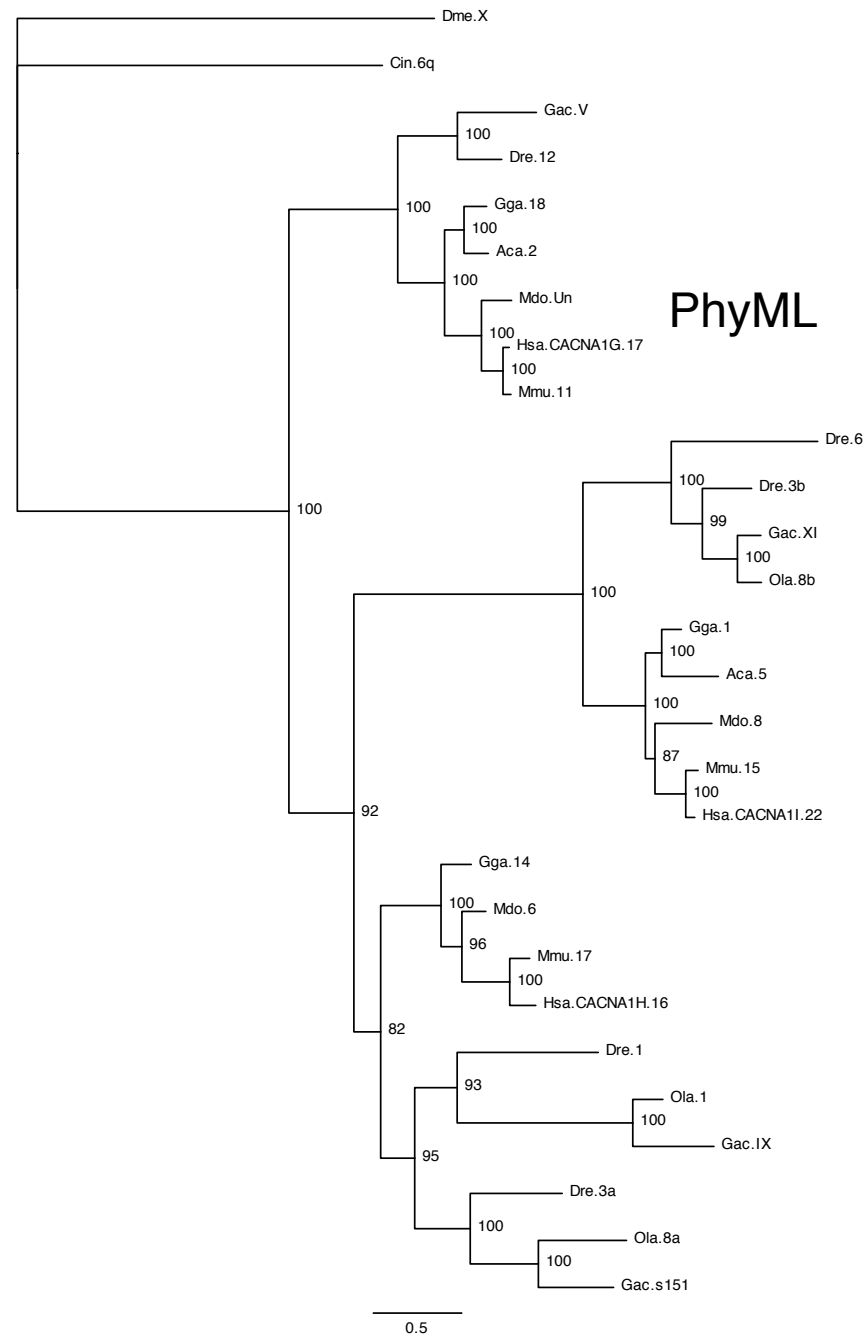
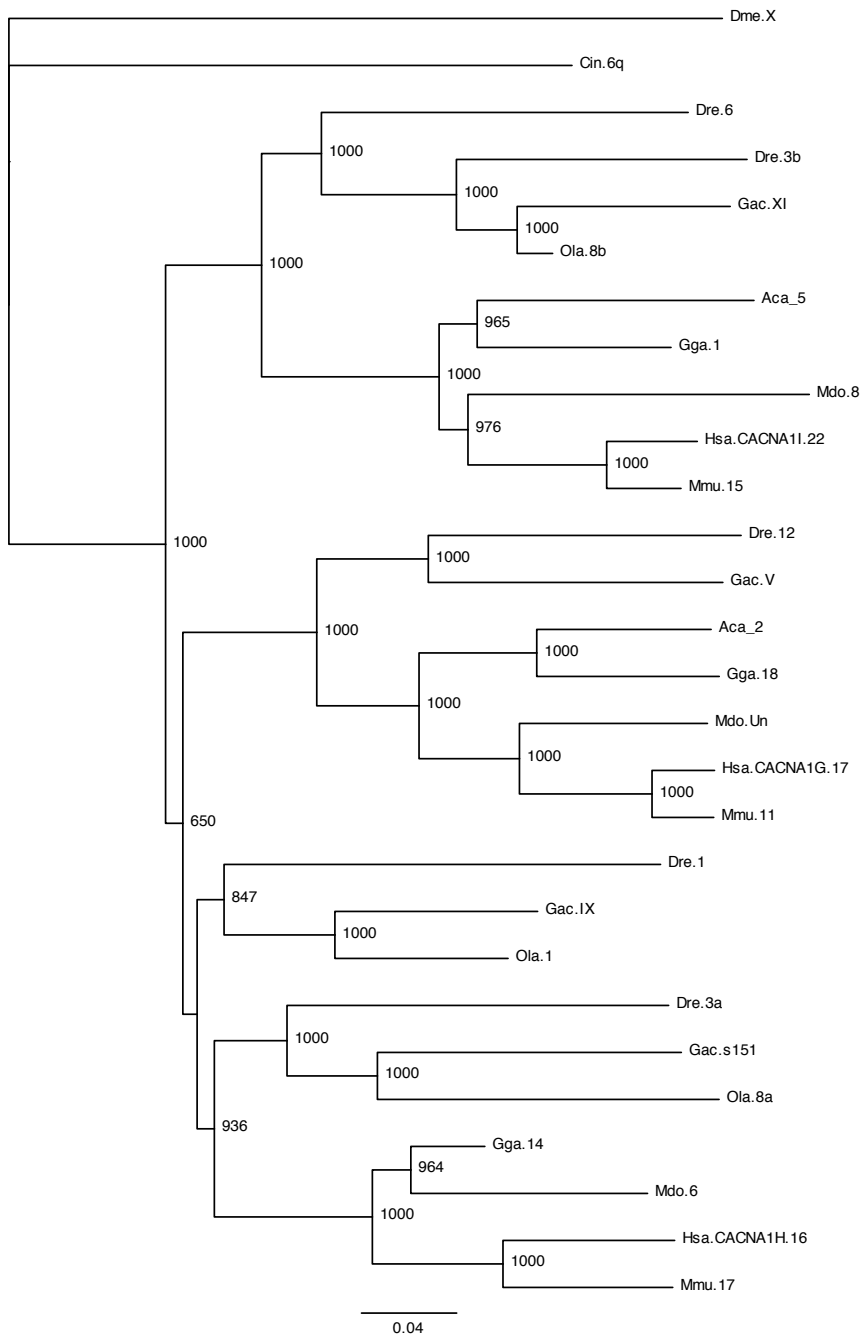


Figure S25. CACNA1

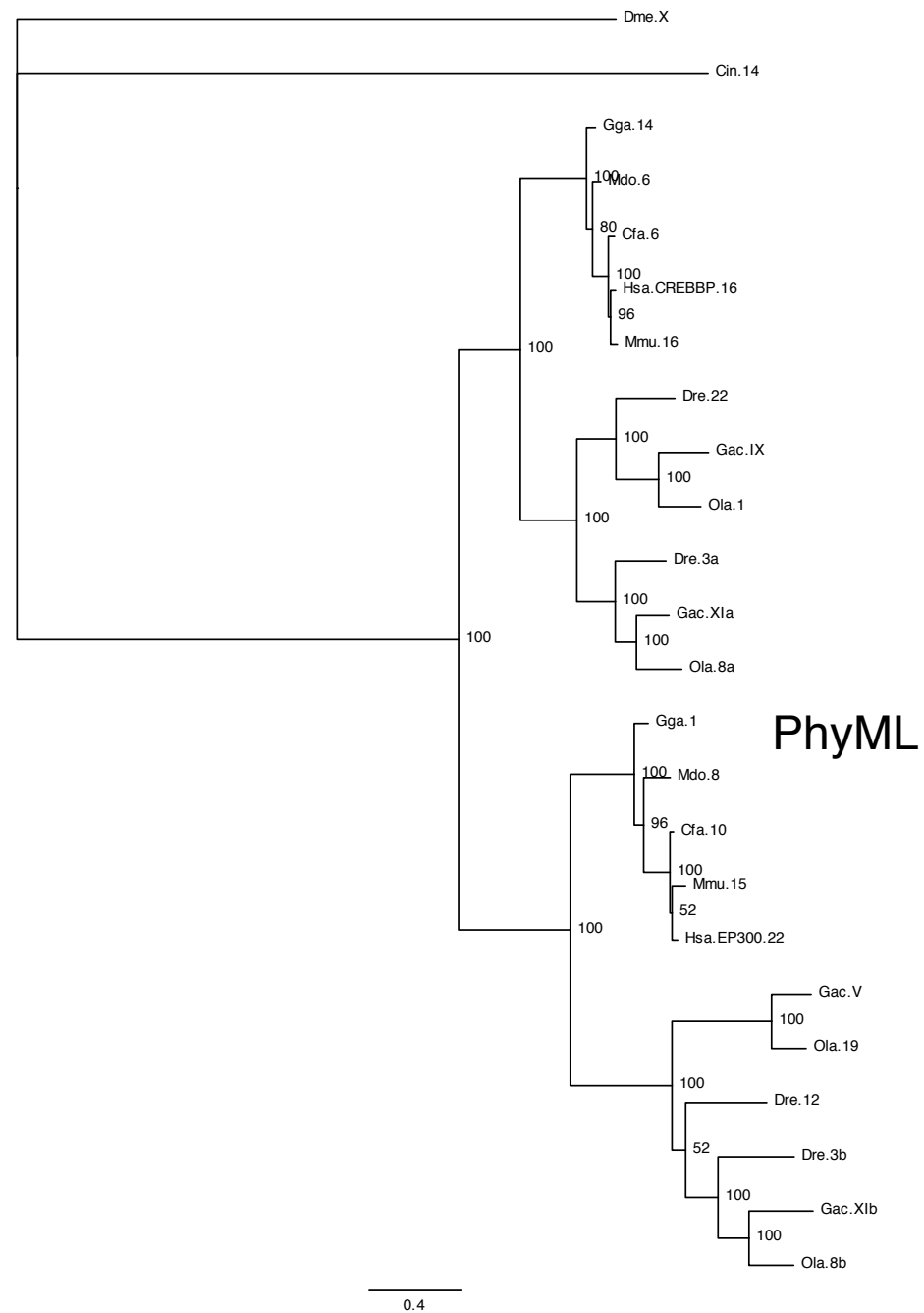
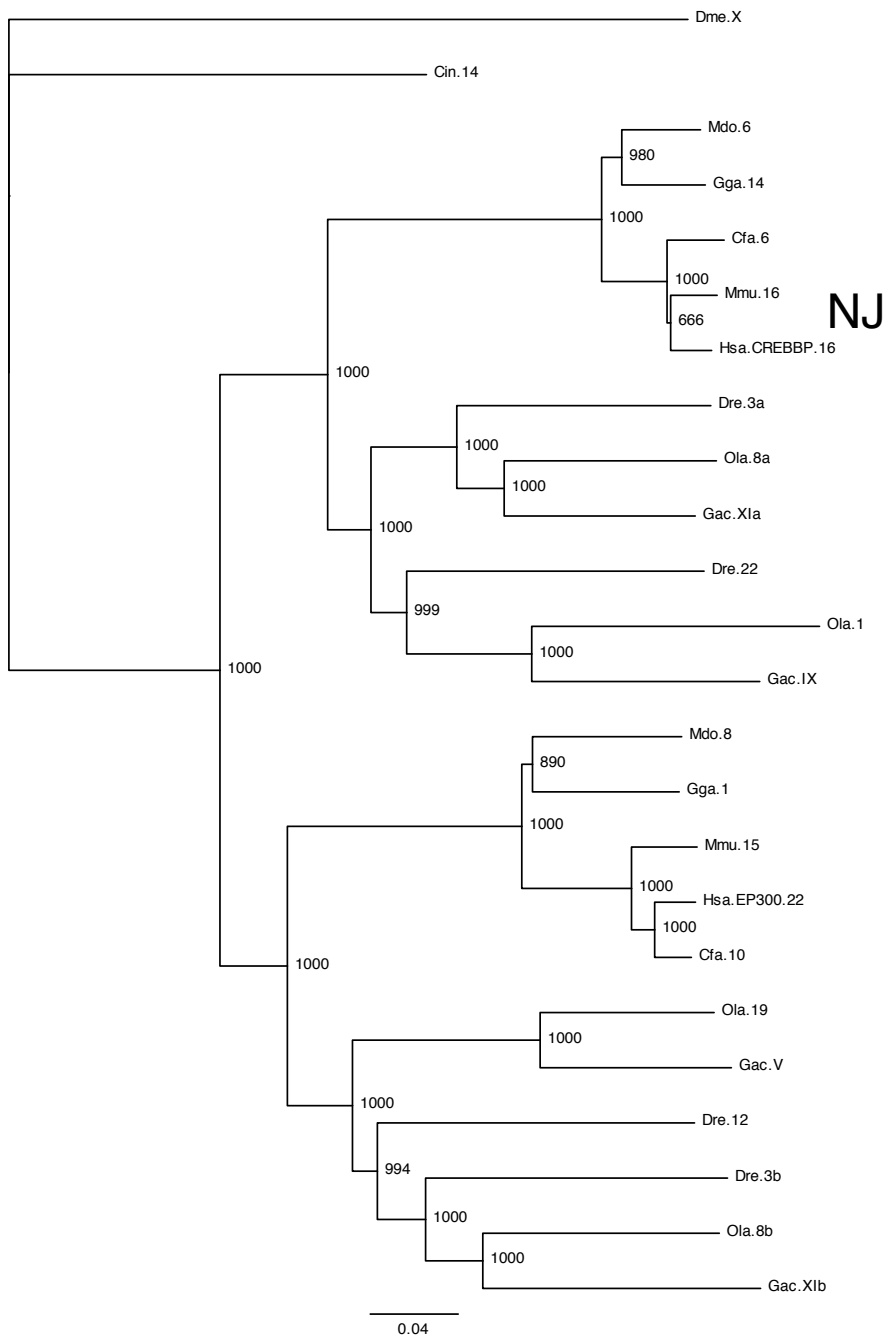


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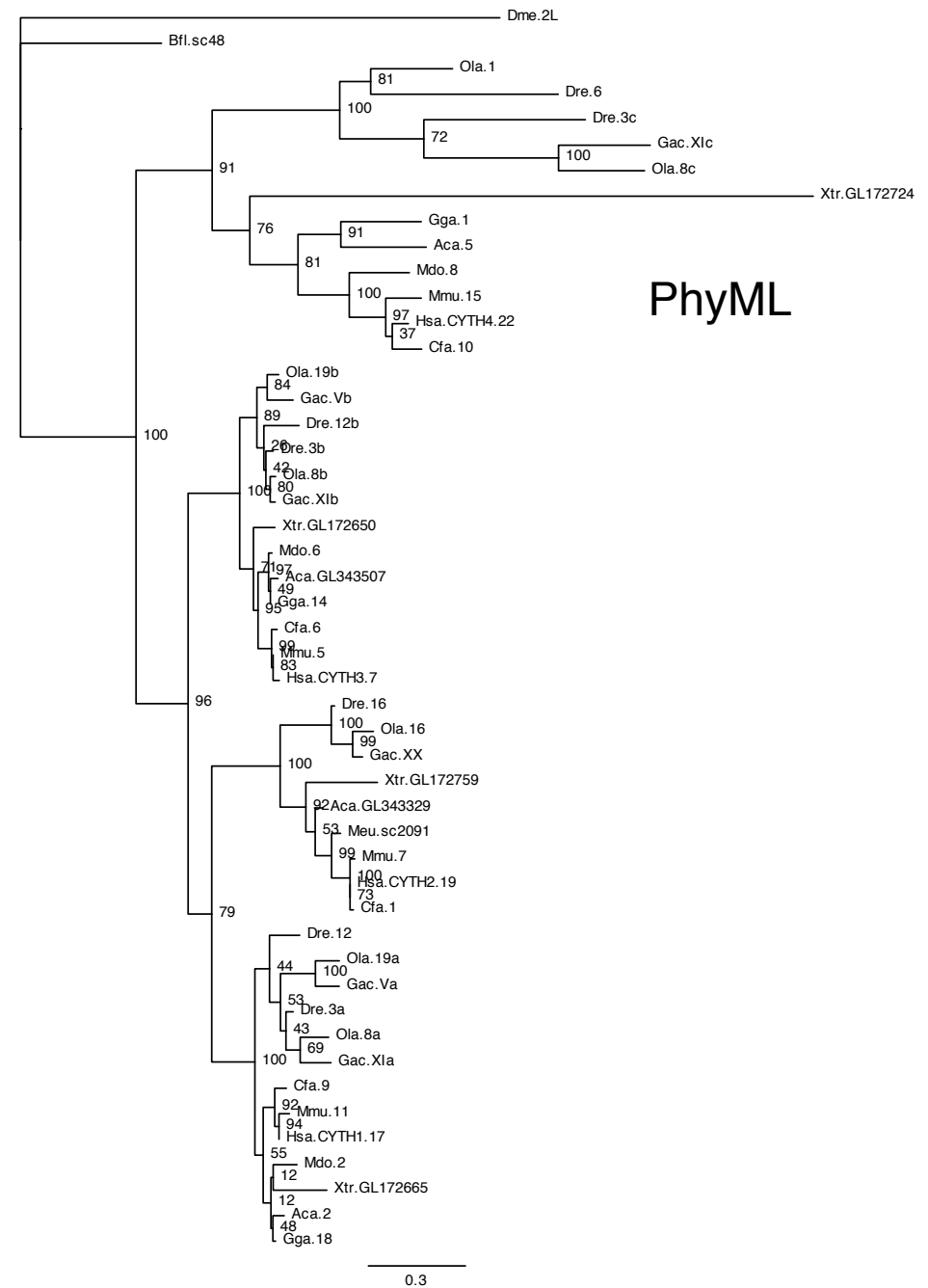
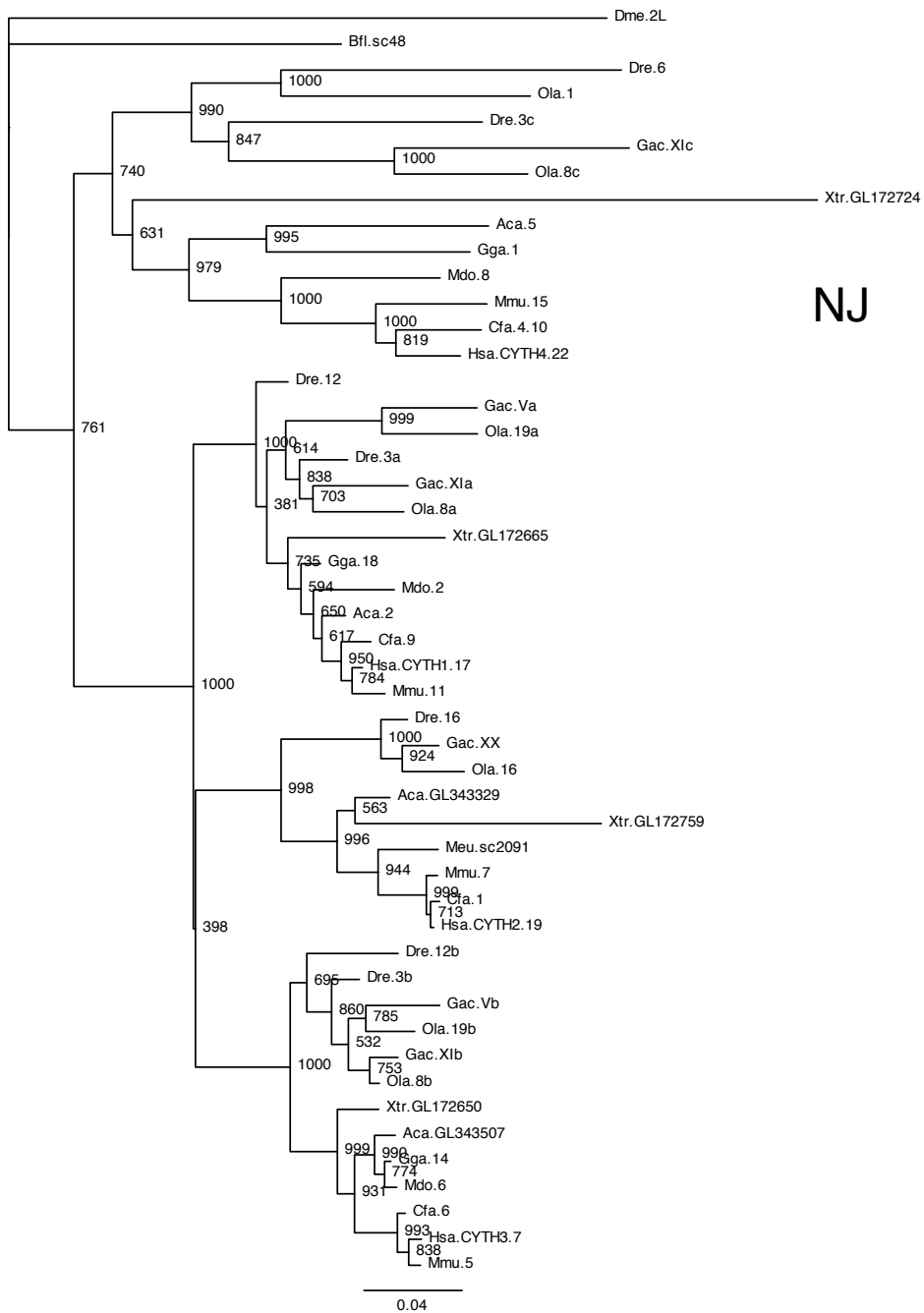


Figure S27. CYTH

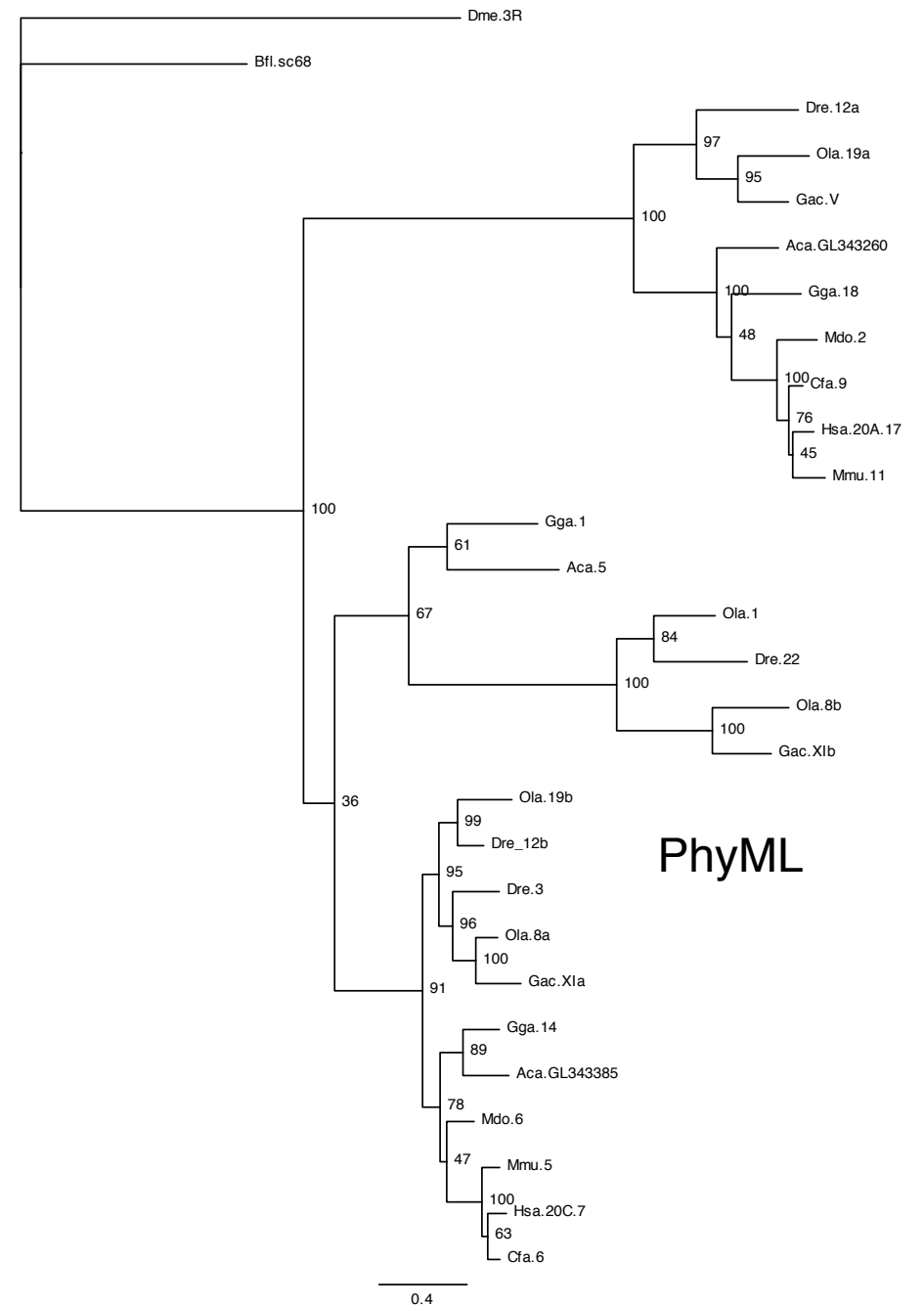
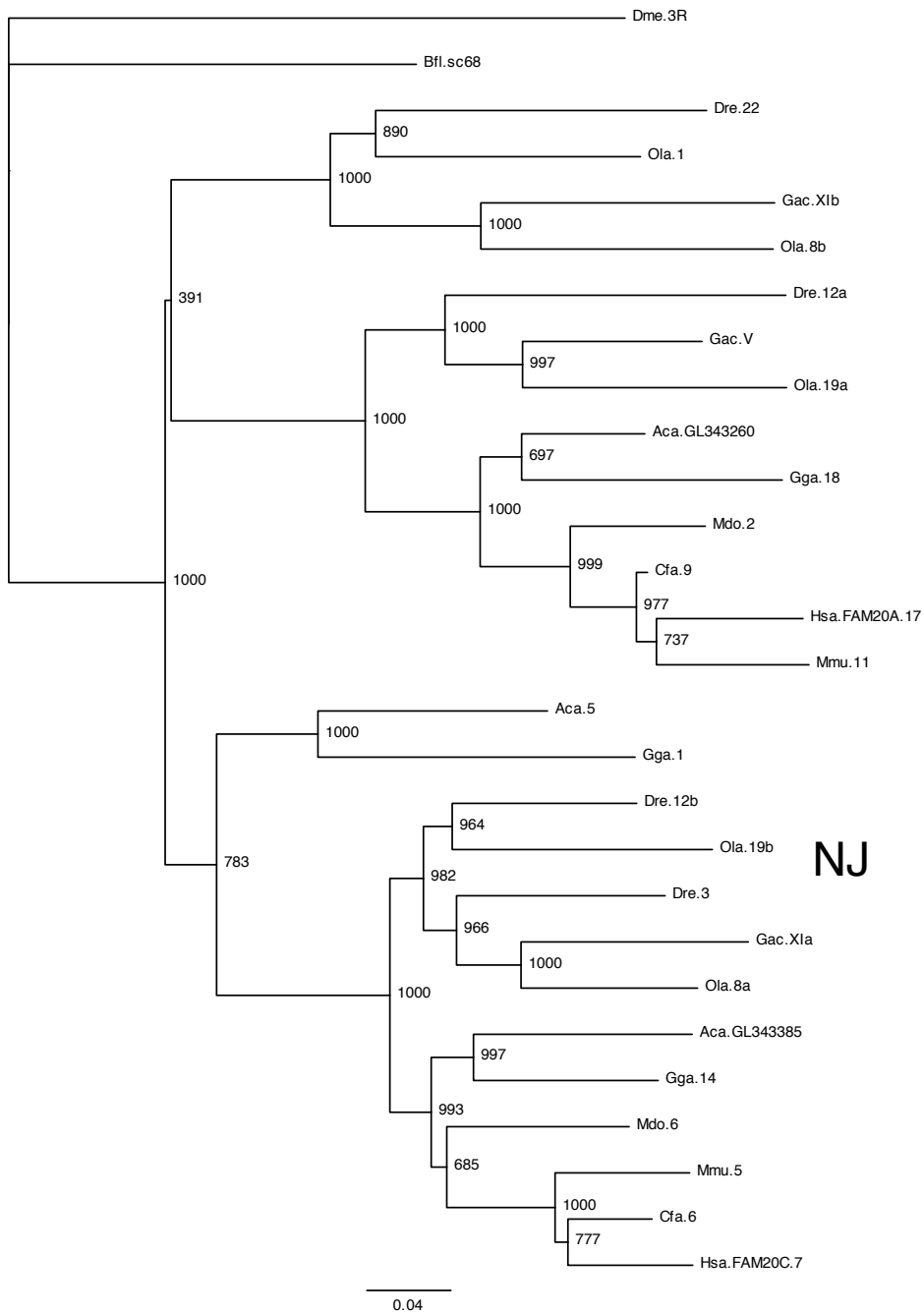


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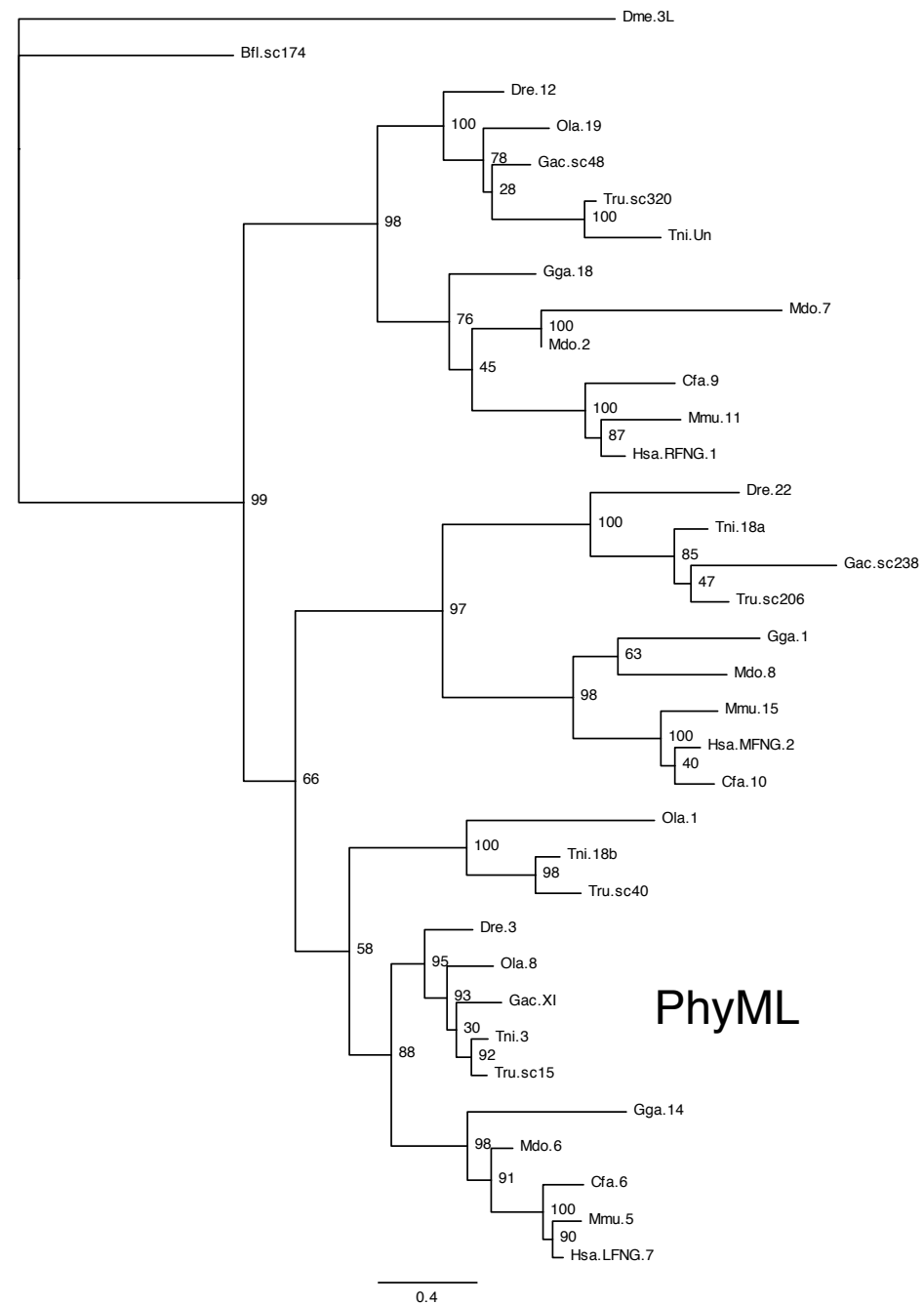
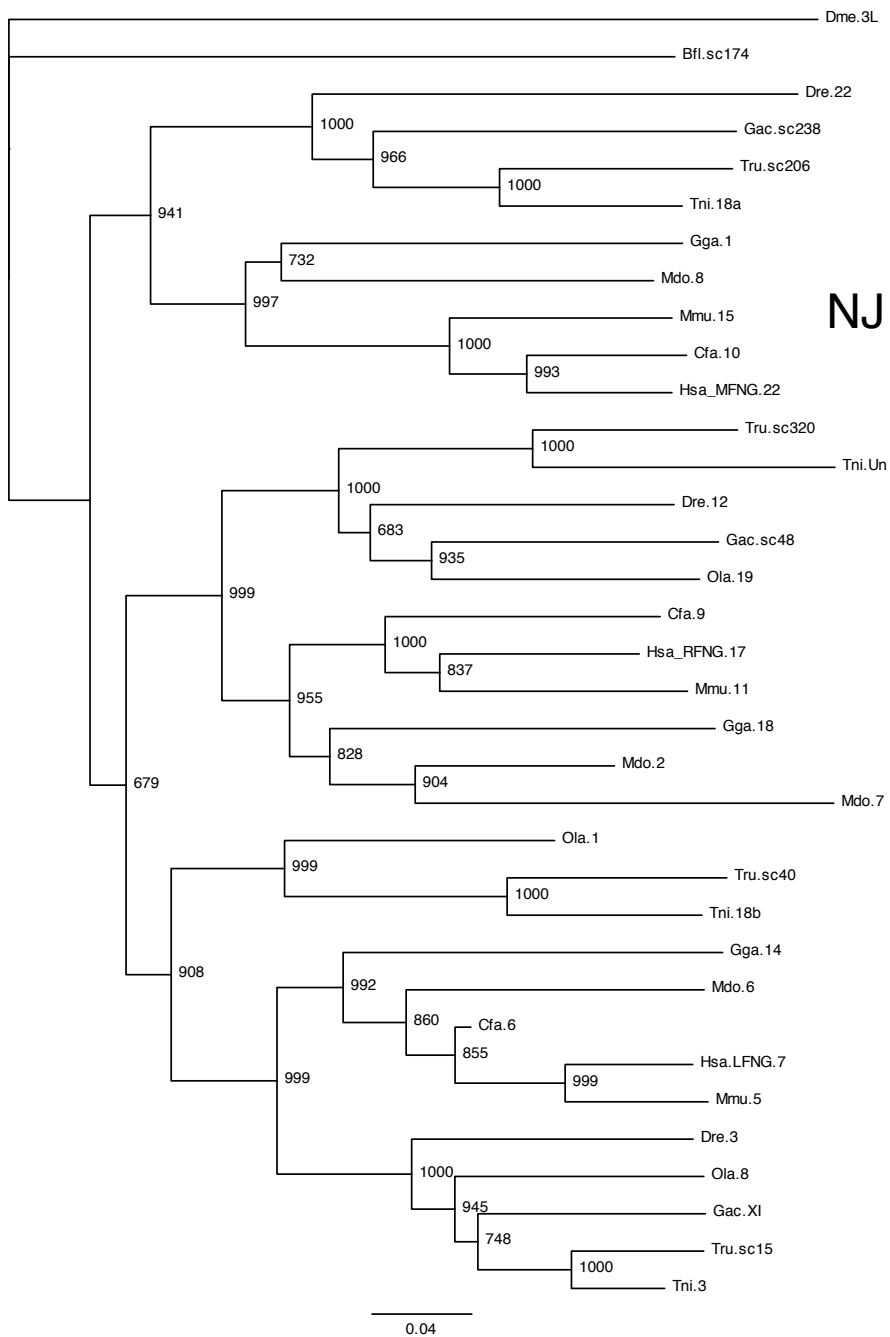


Figure S29. FNG

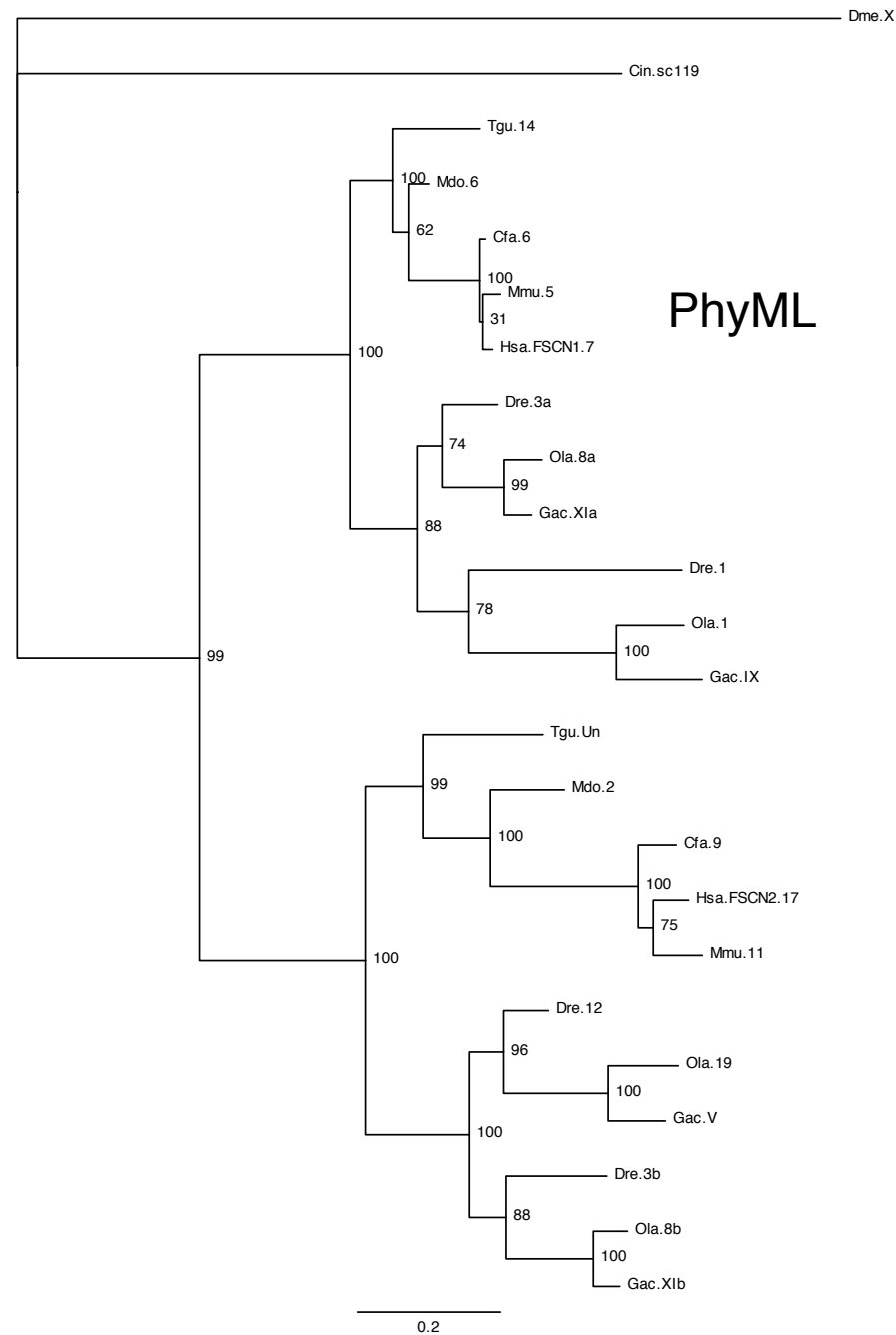
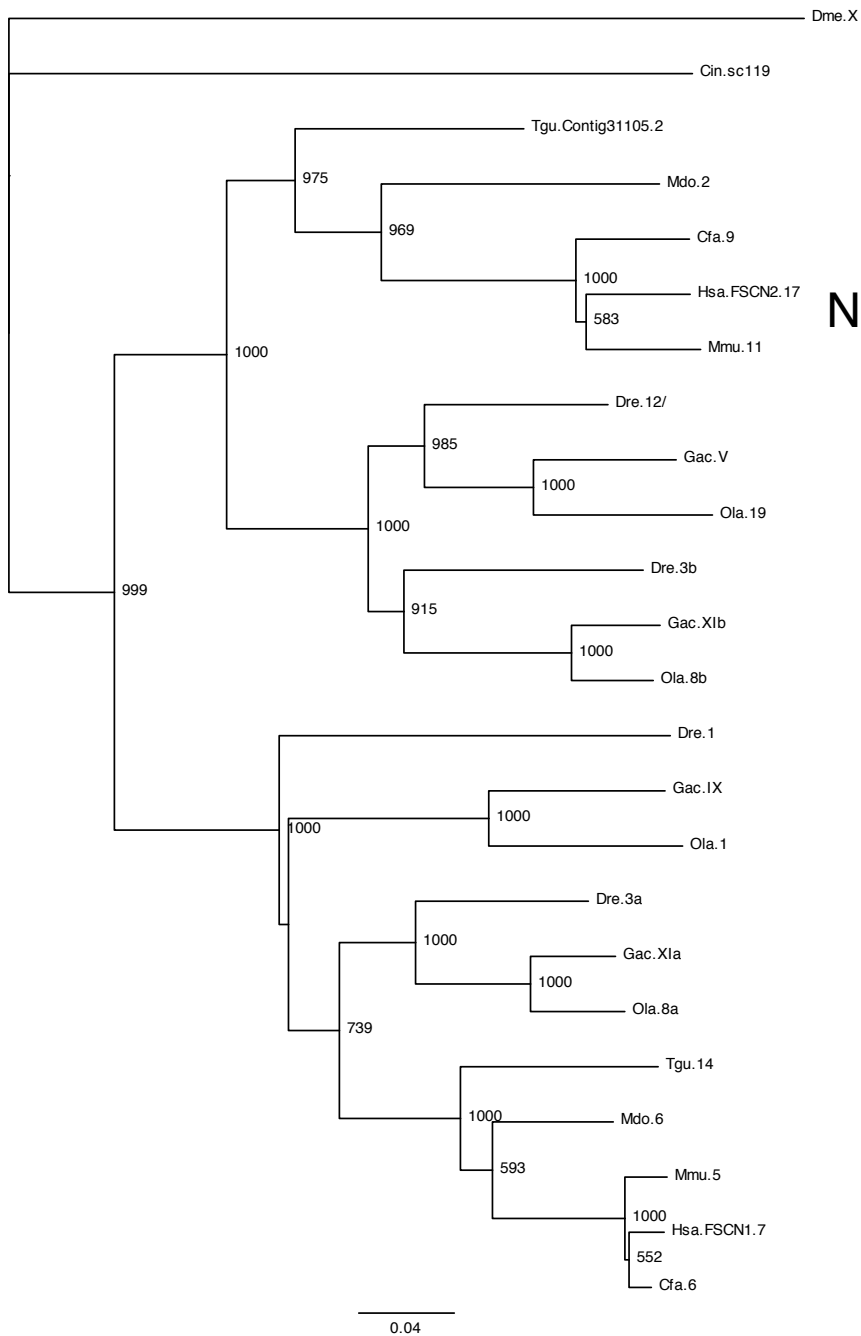


Figure S30. FSCN

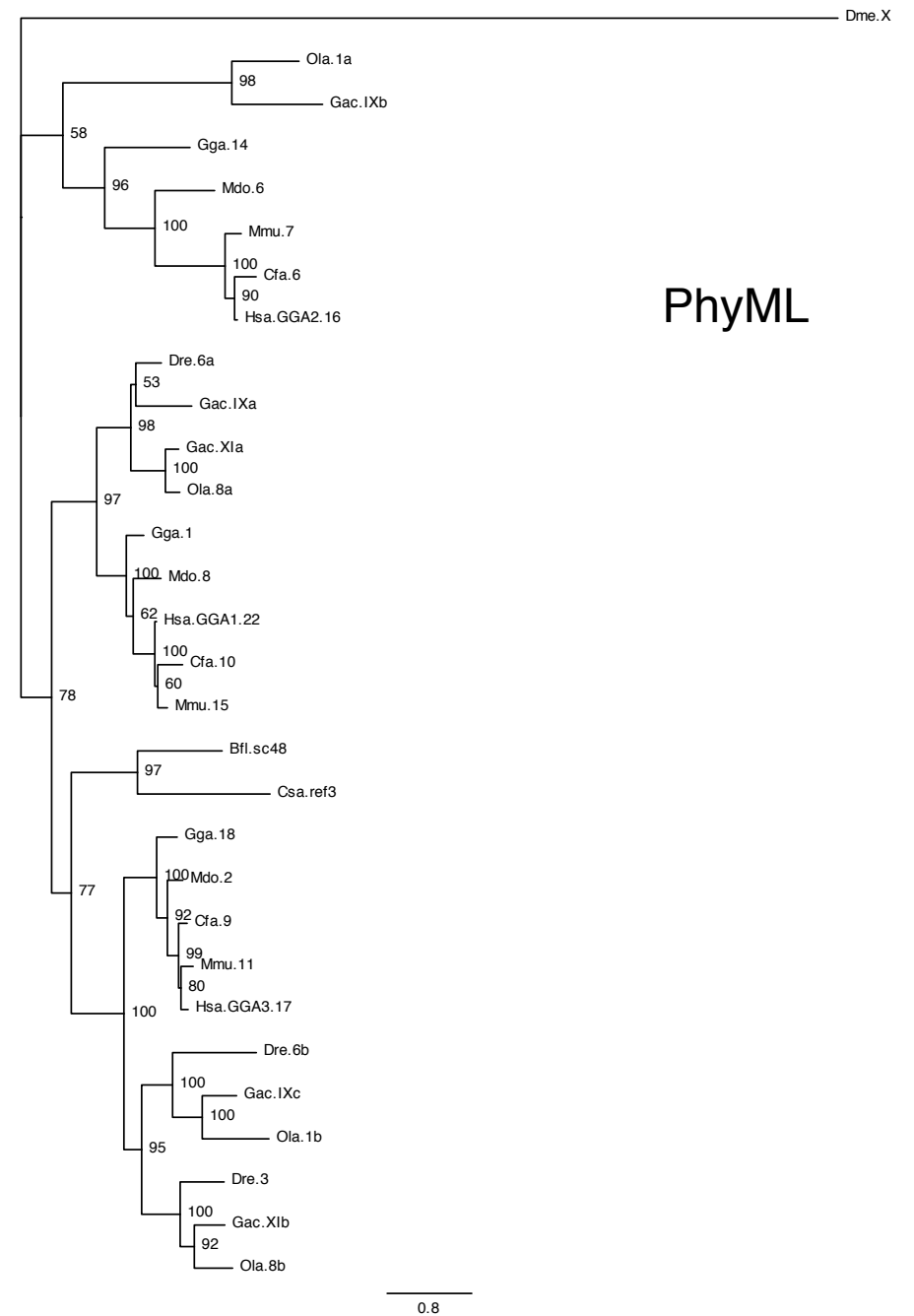
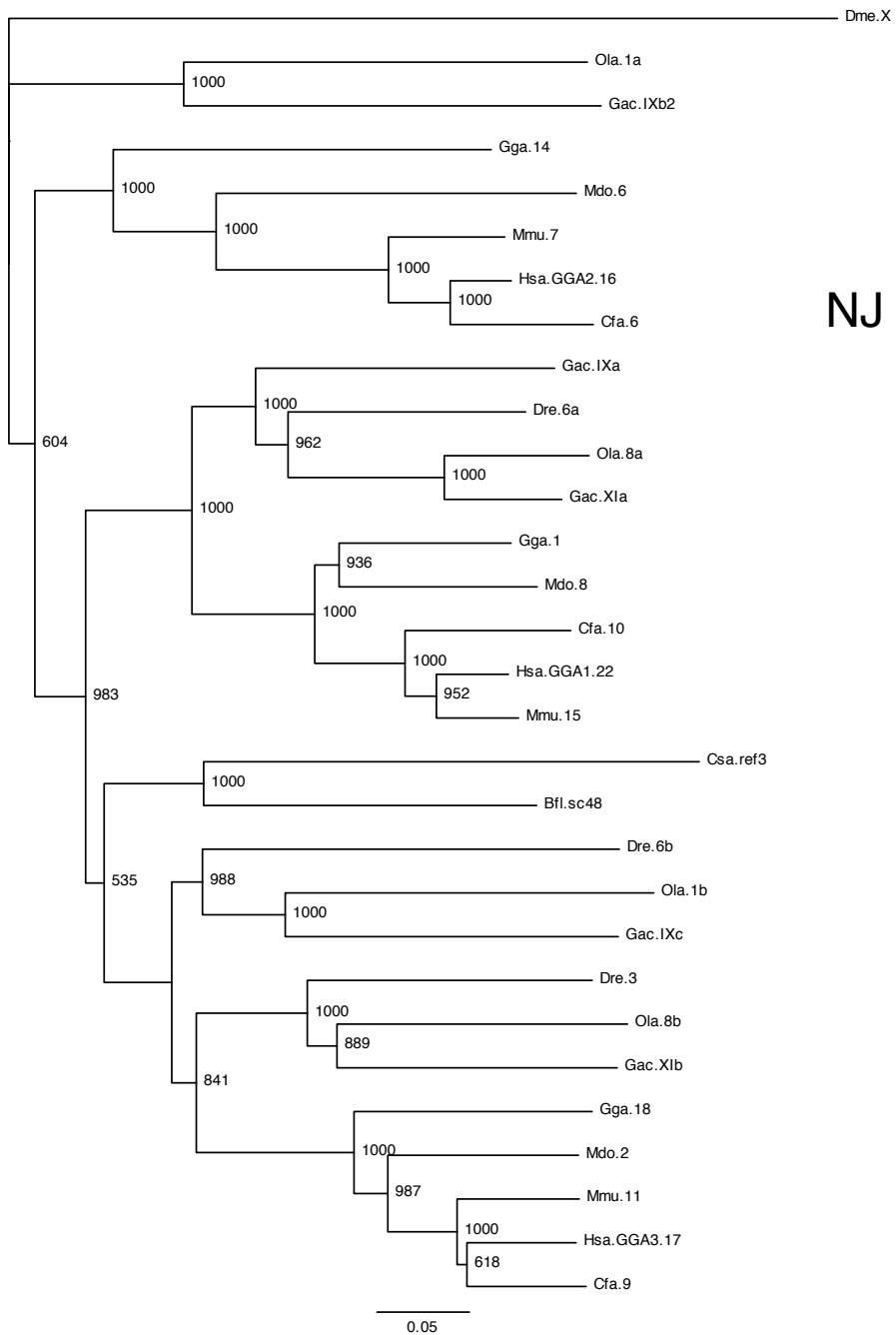


Figure S31. GGA

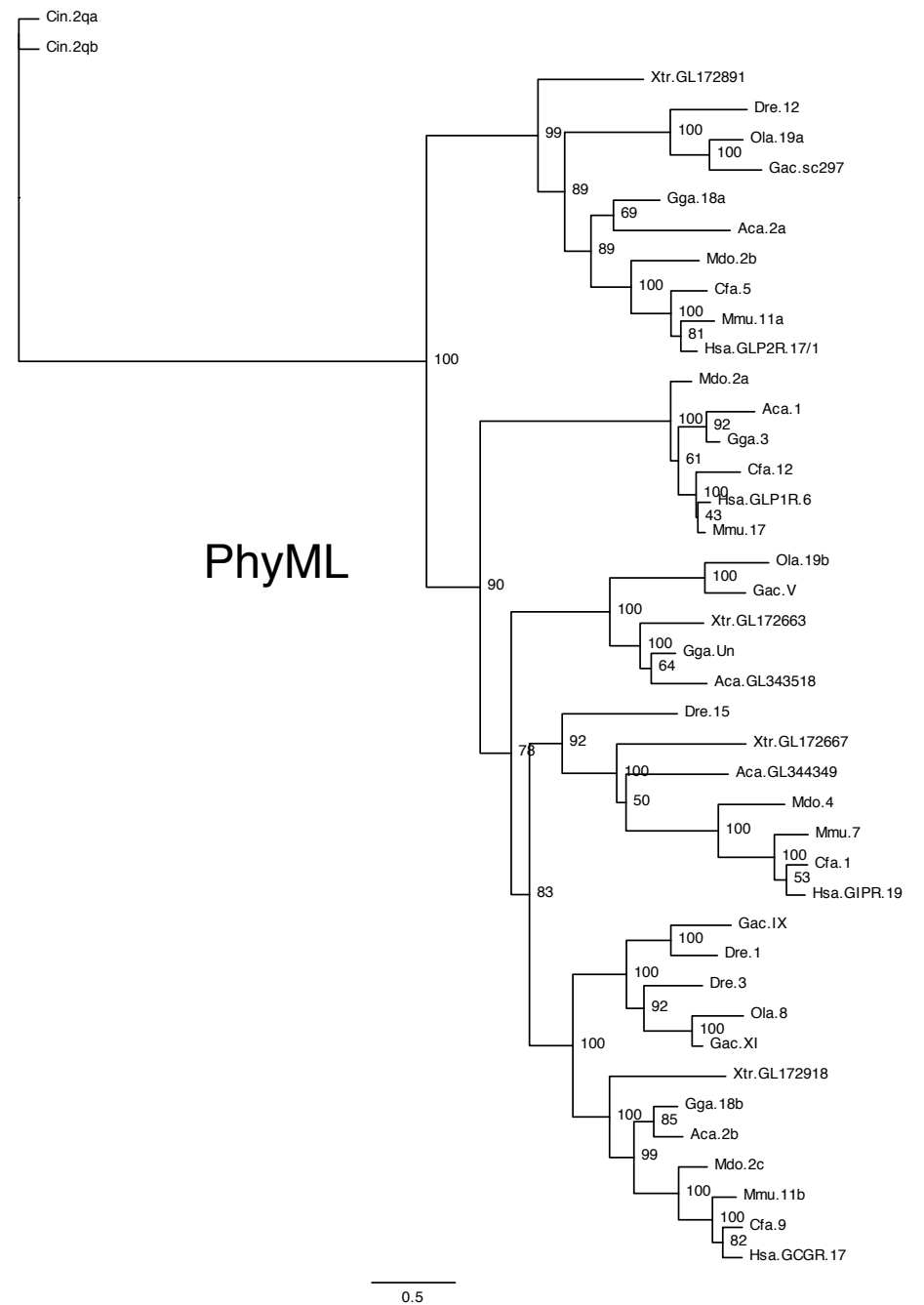
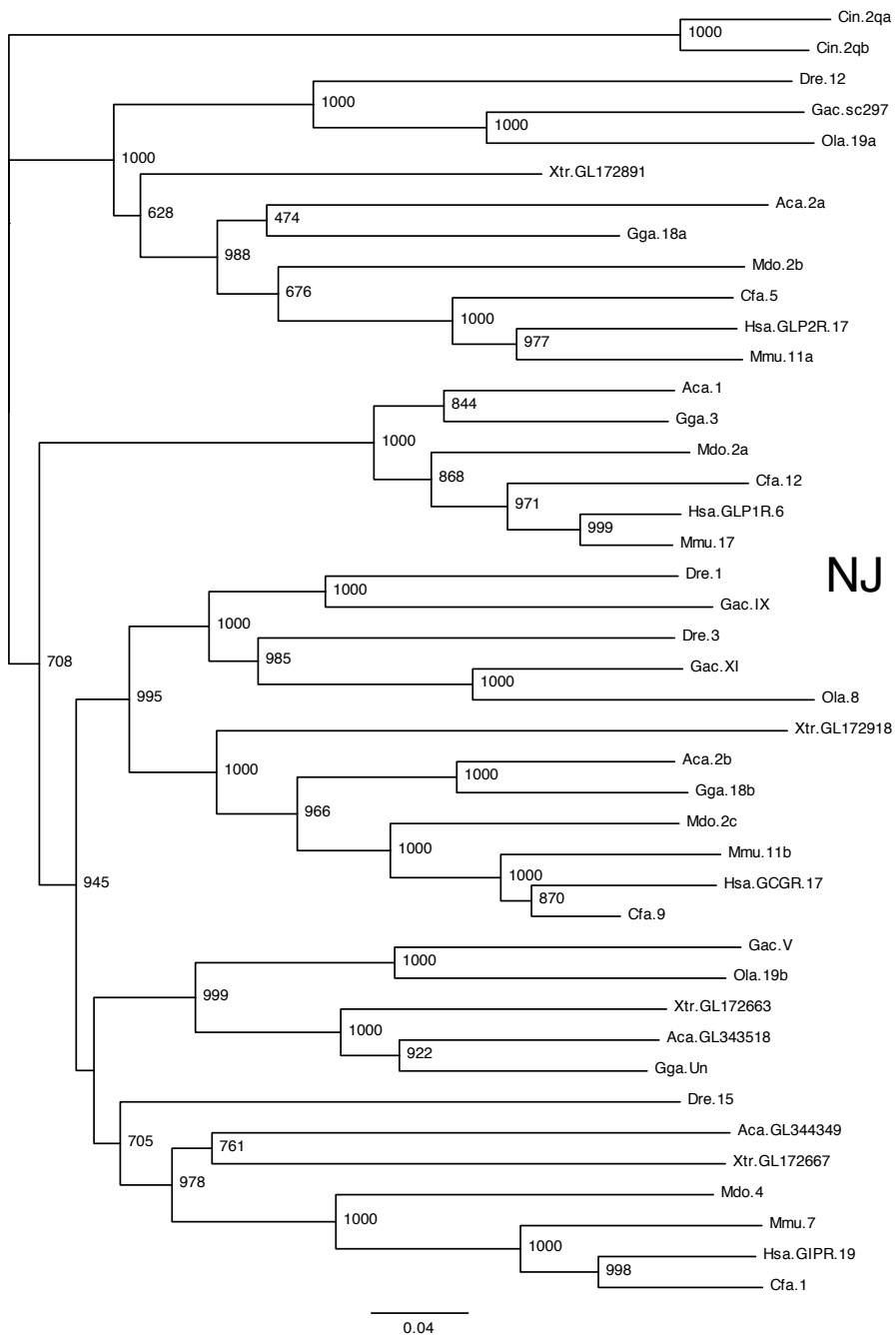


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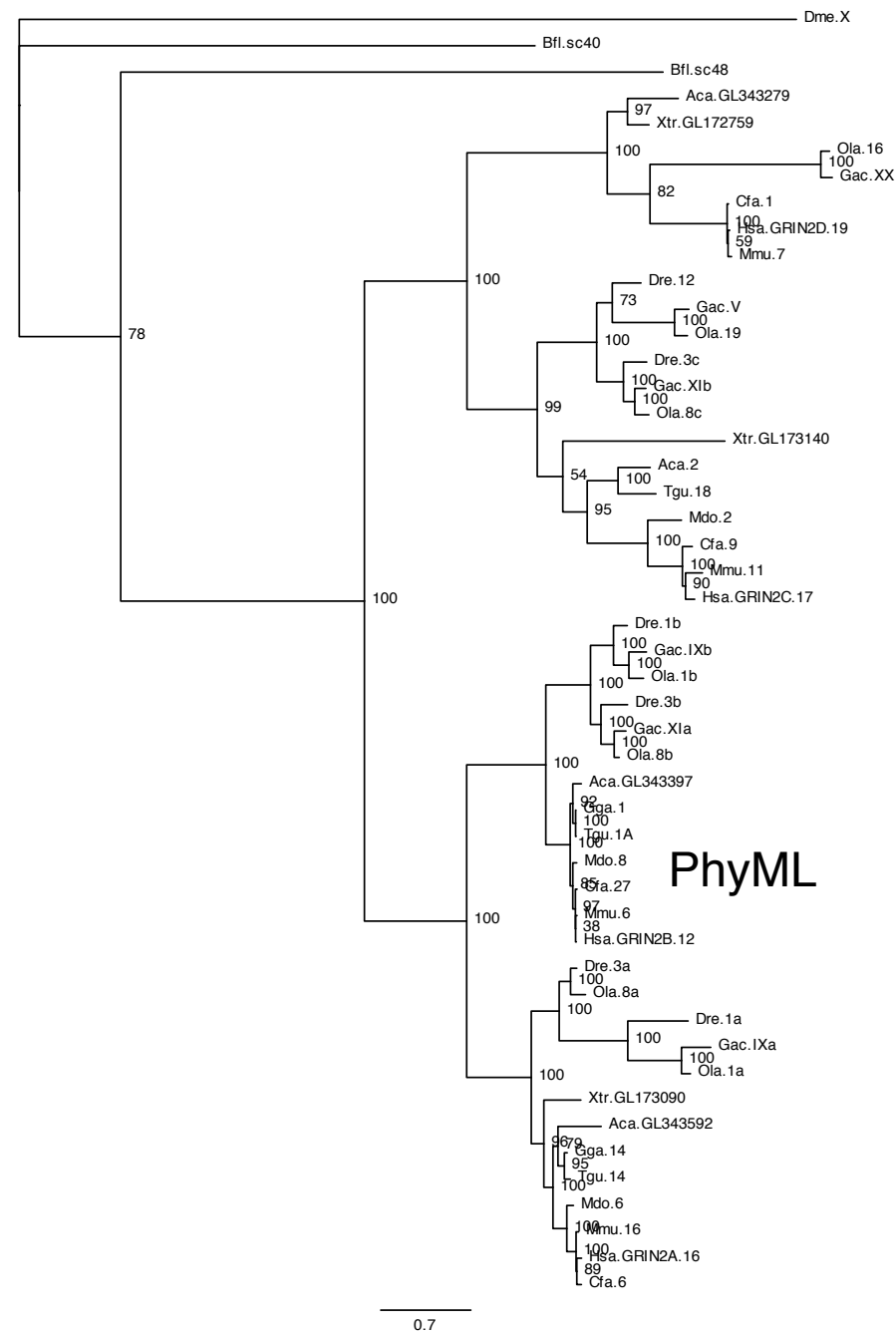
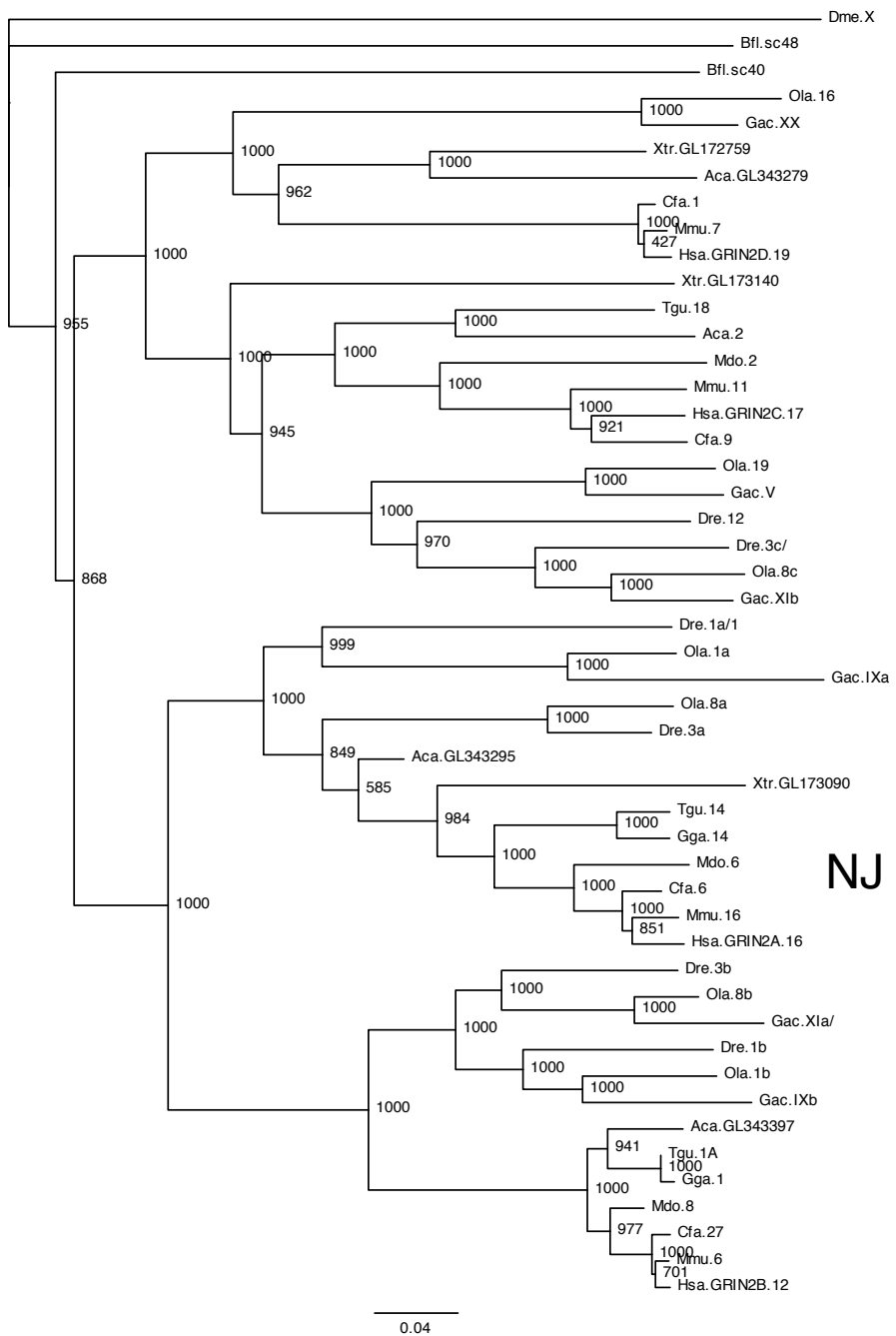


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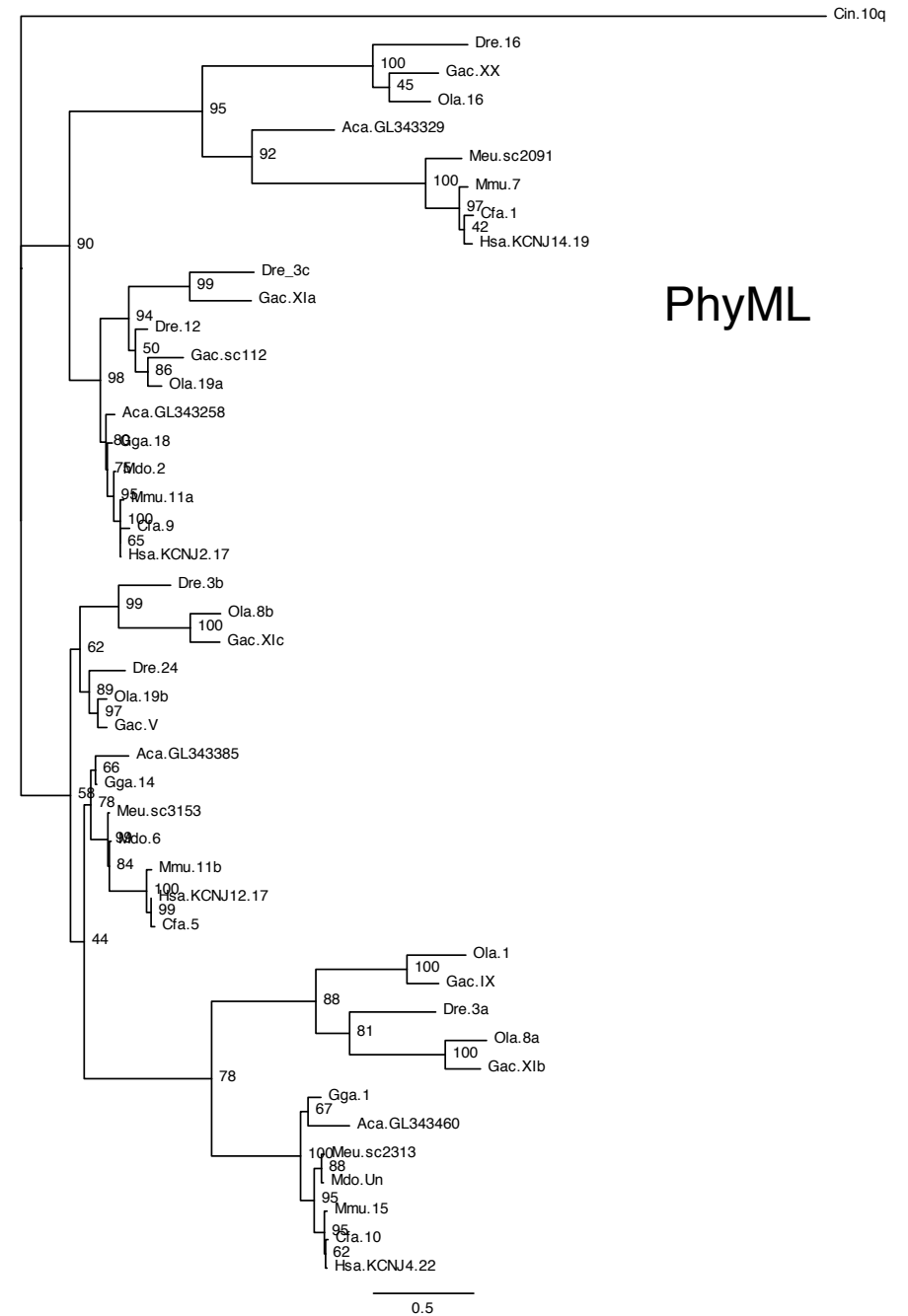
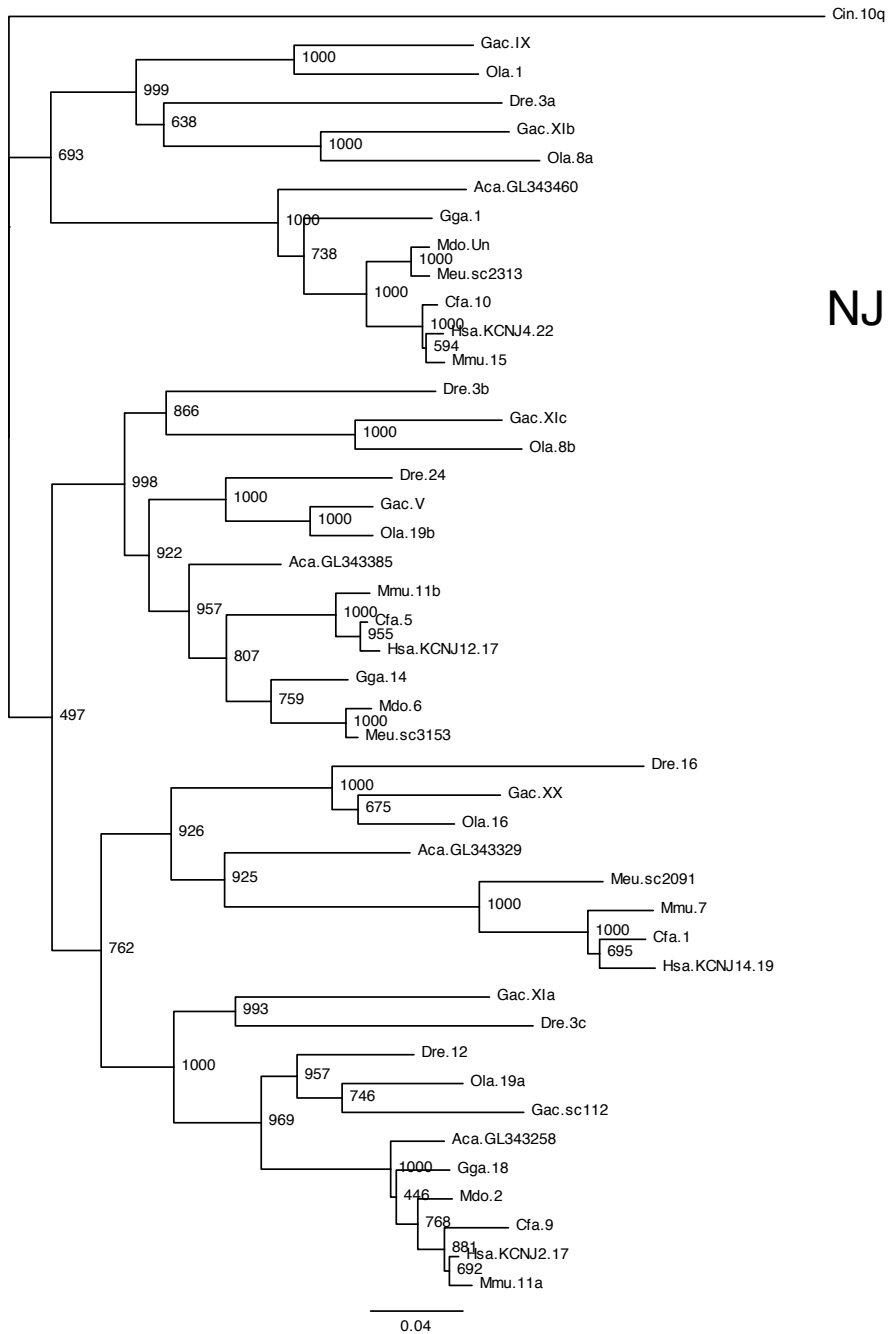


Figure S34. KCNJ

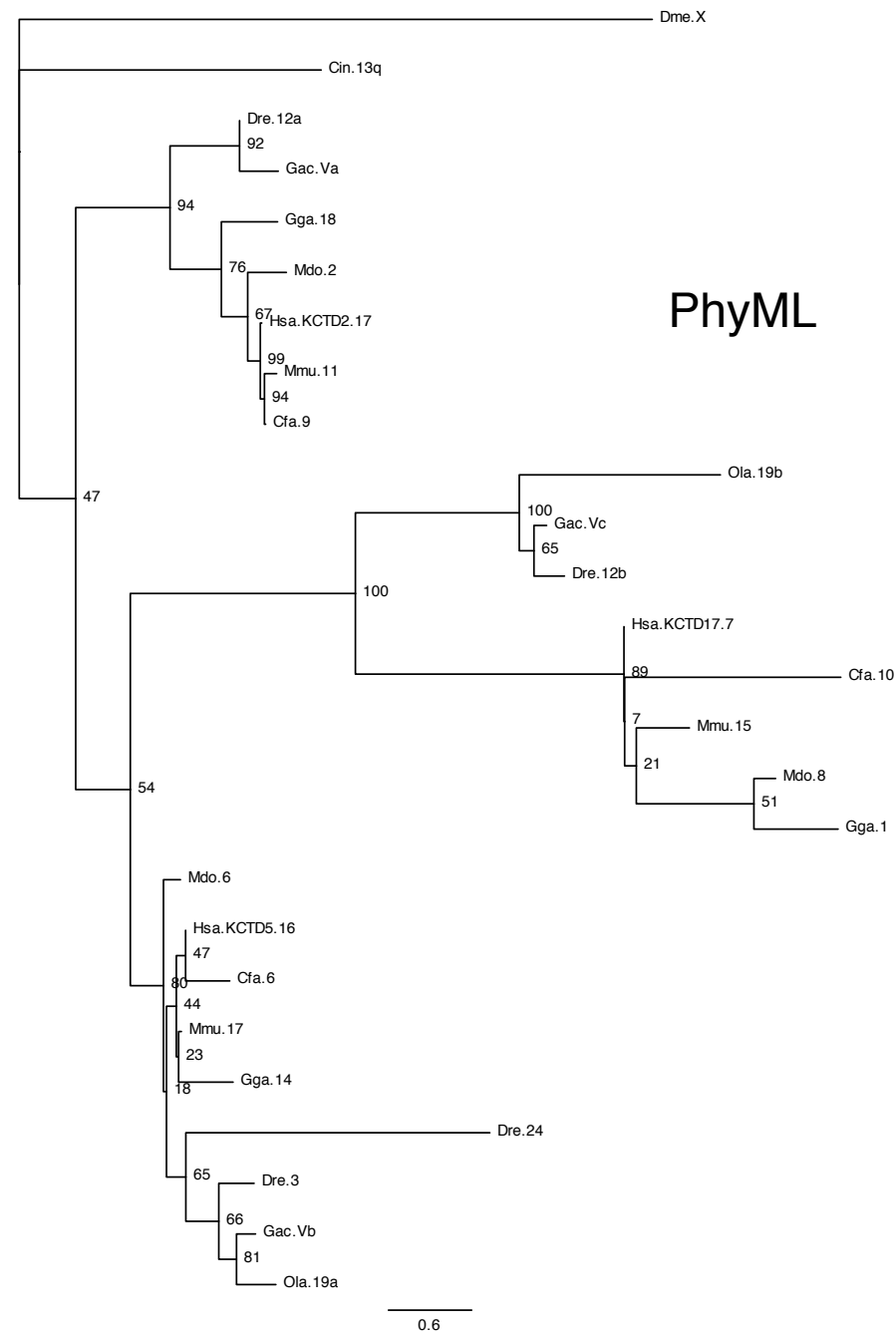
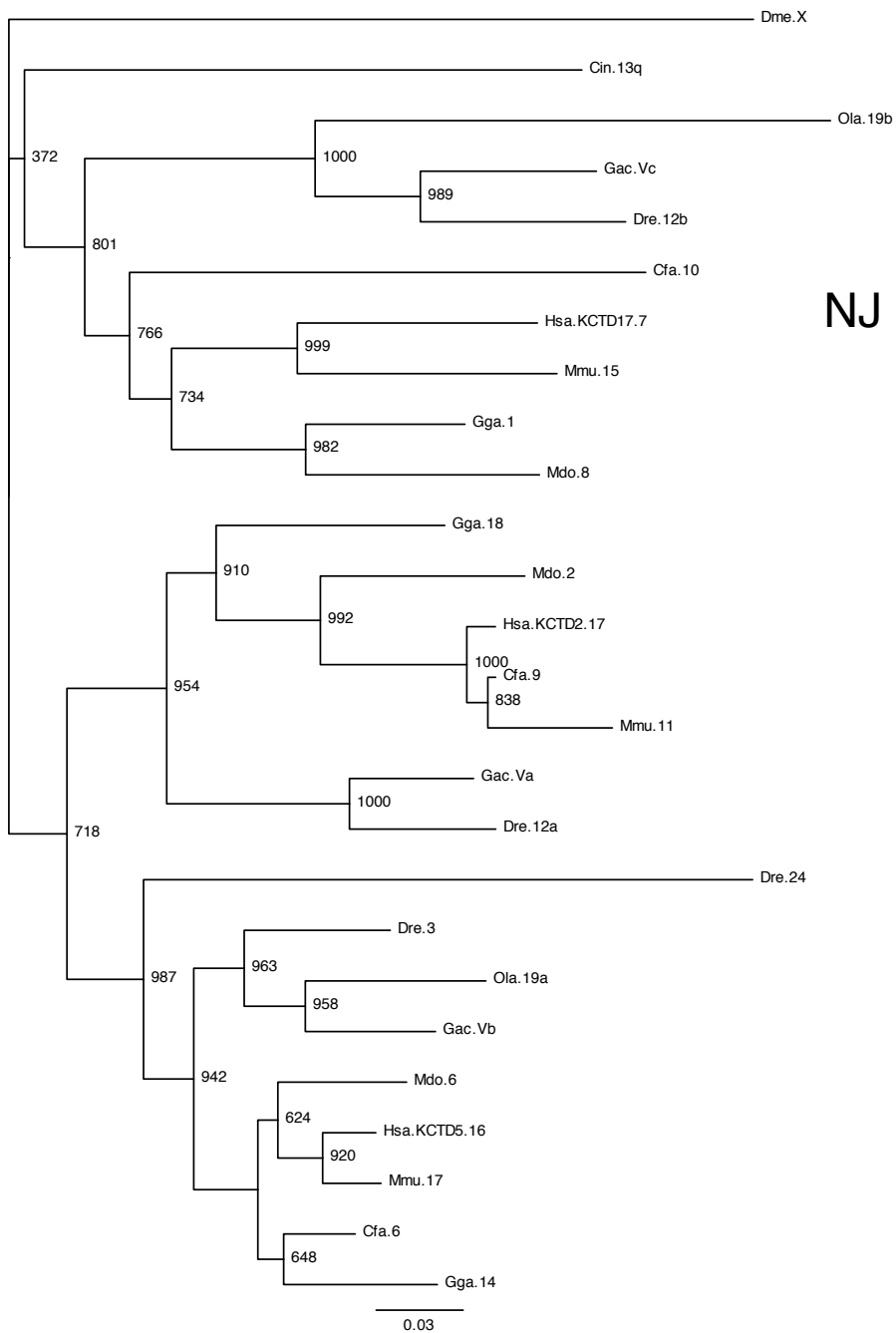


Figure S35. KCTD

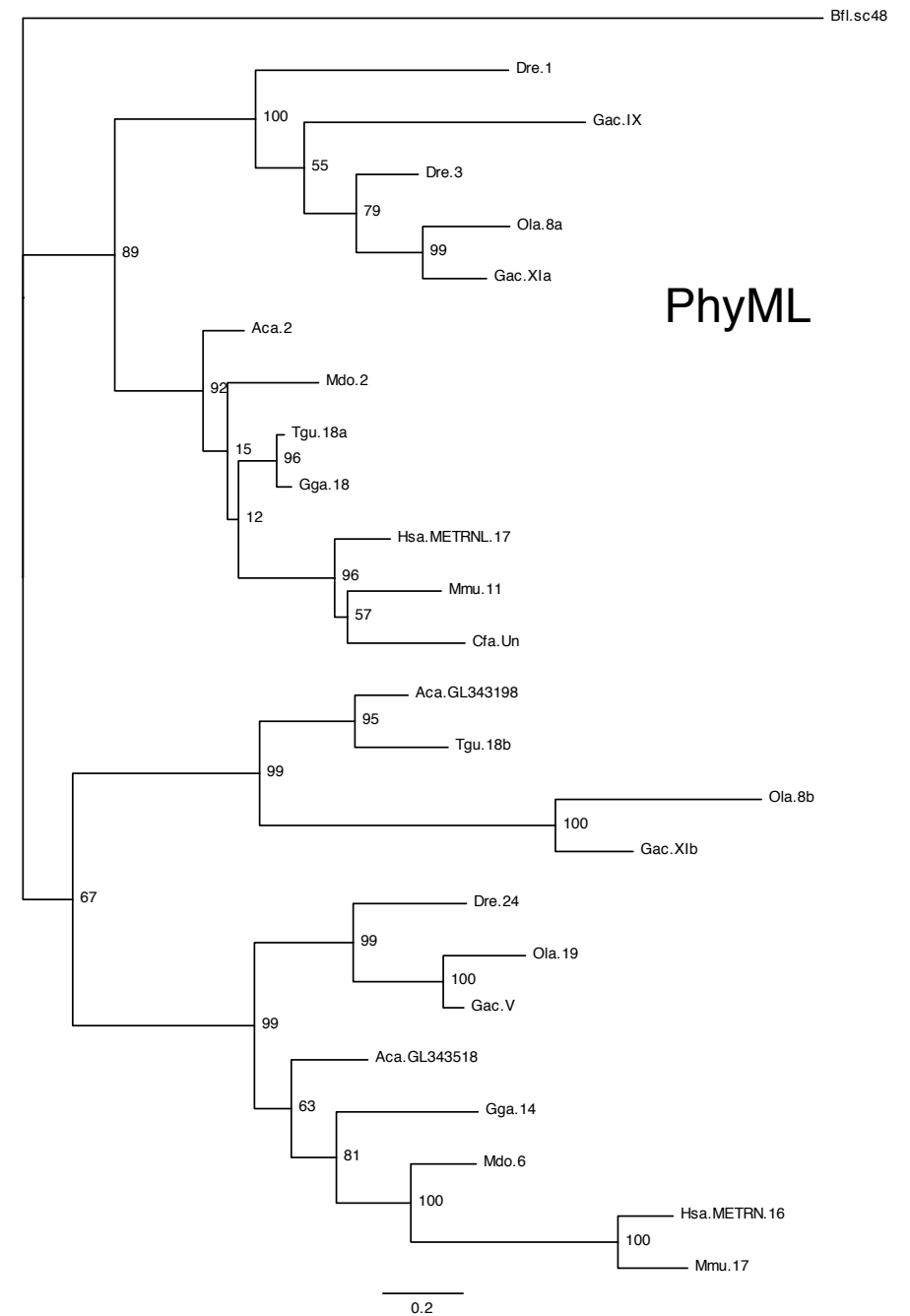
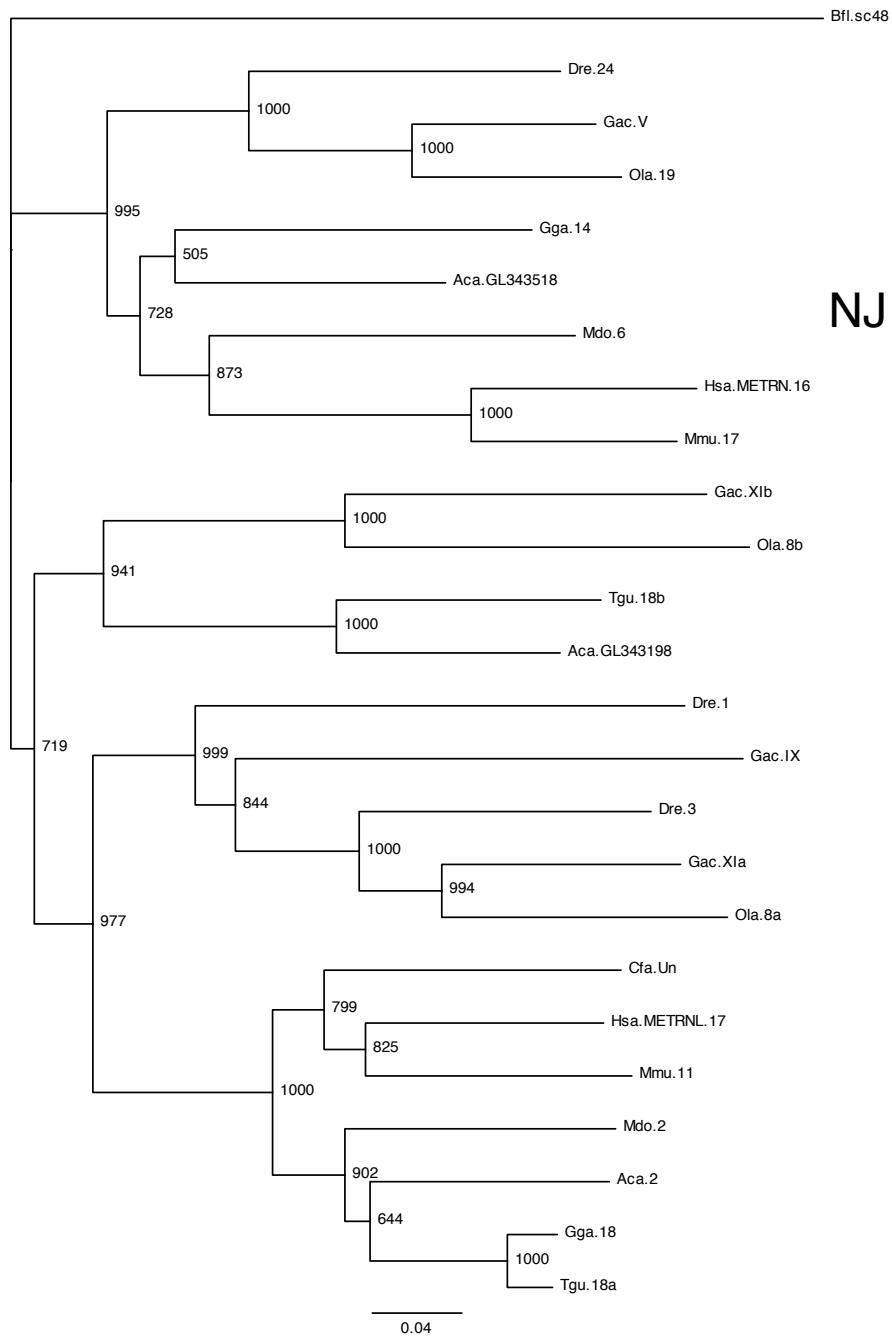


Figure S36. METRN

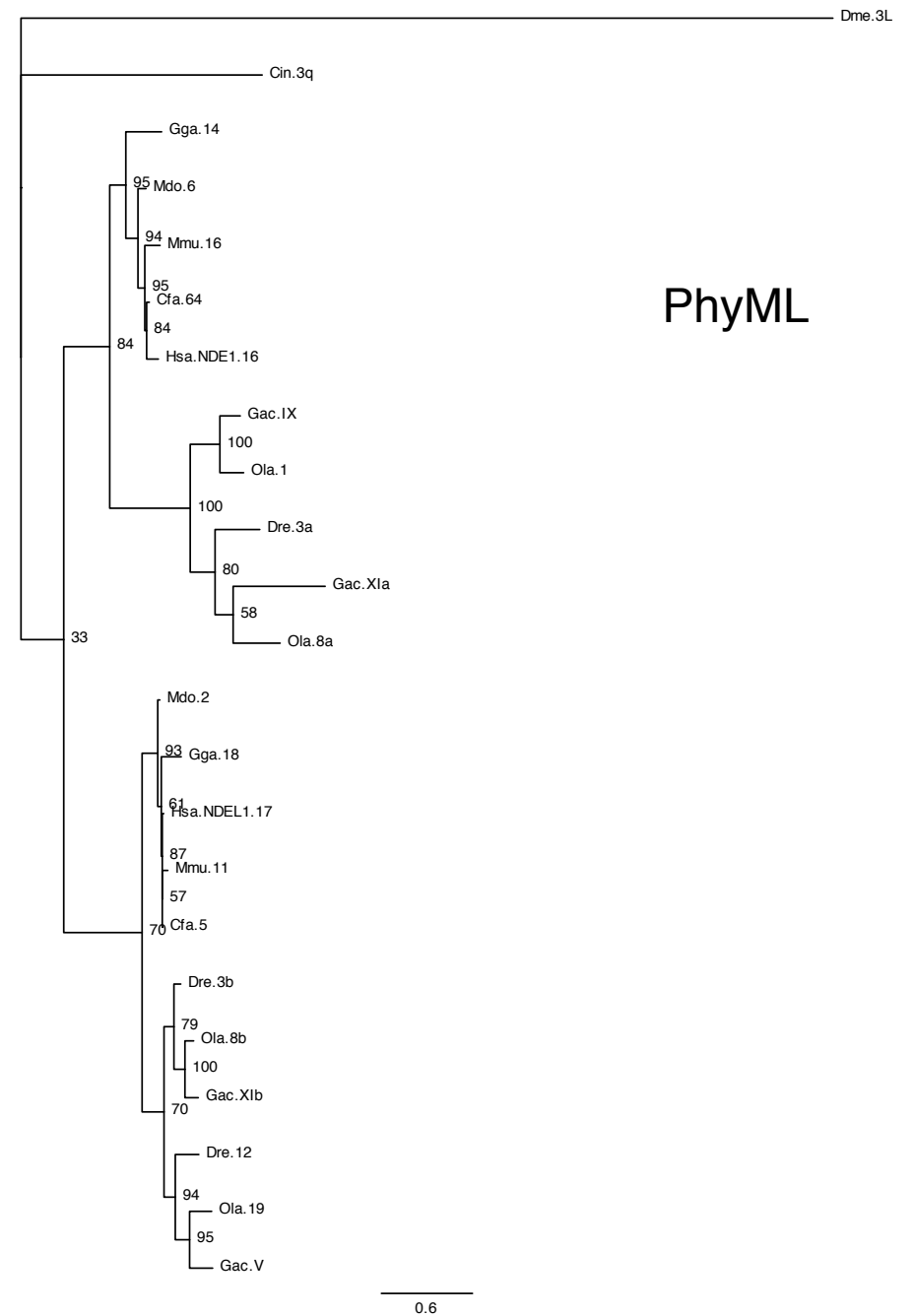
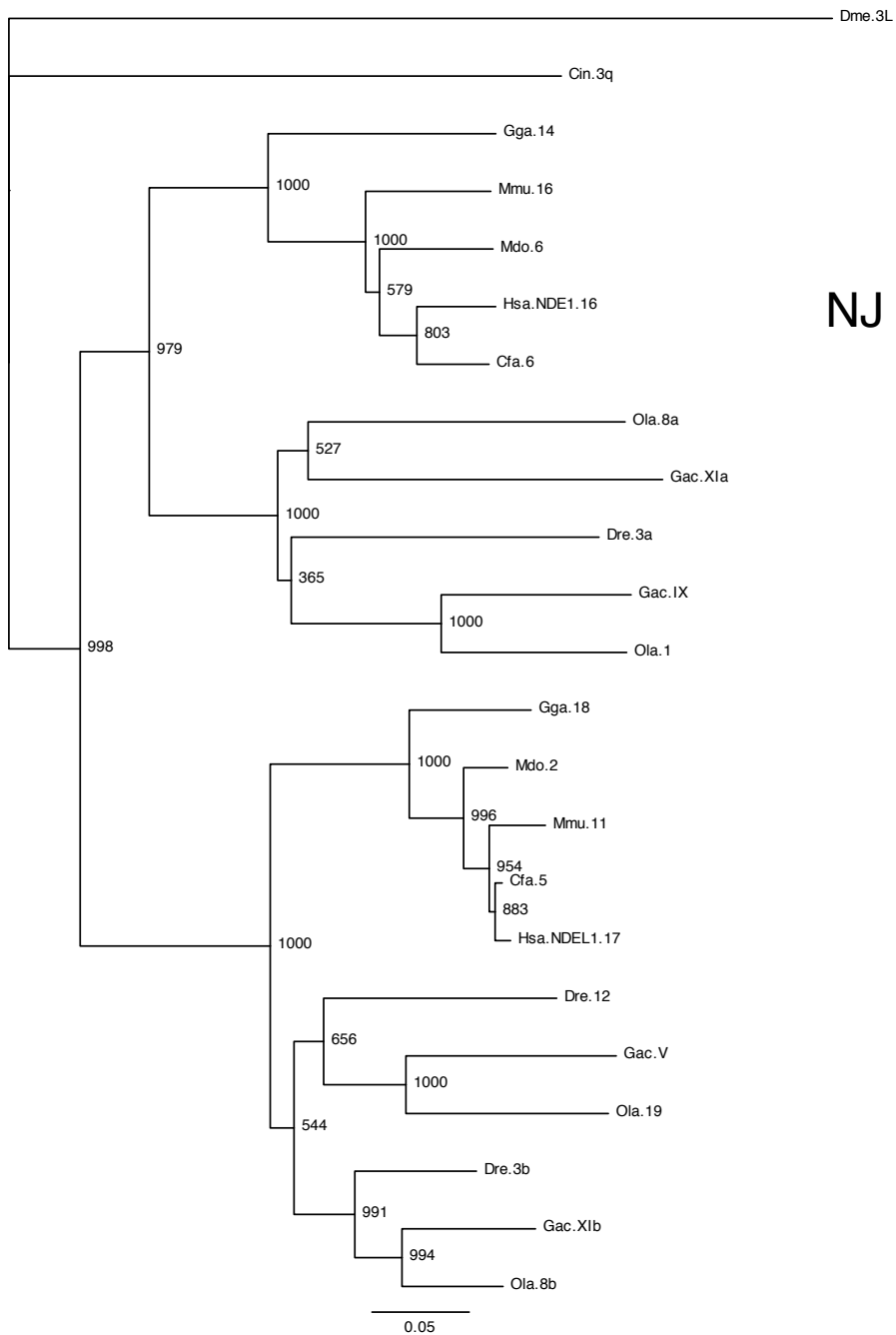


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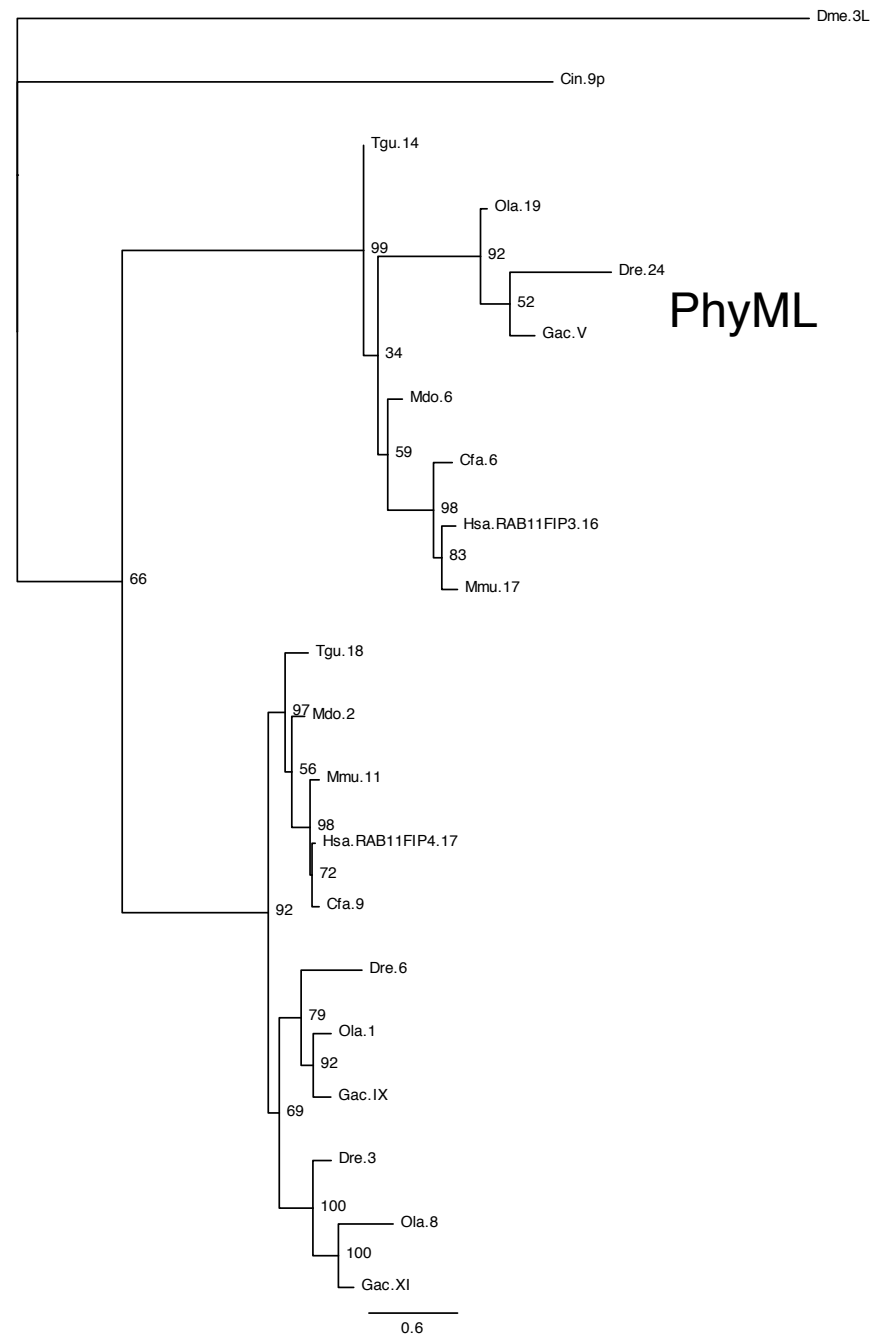
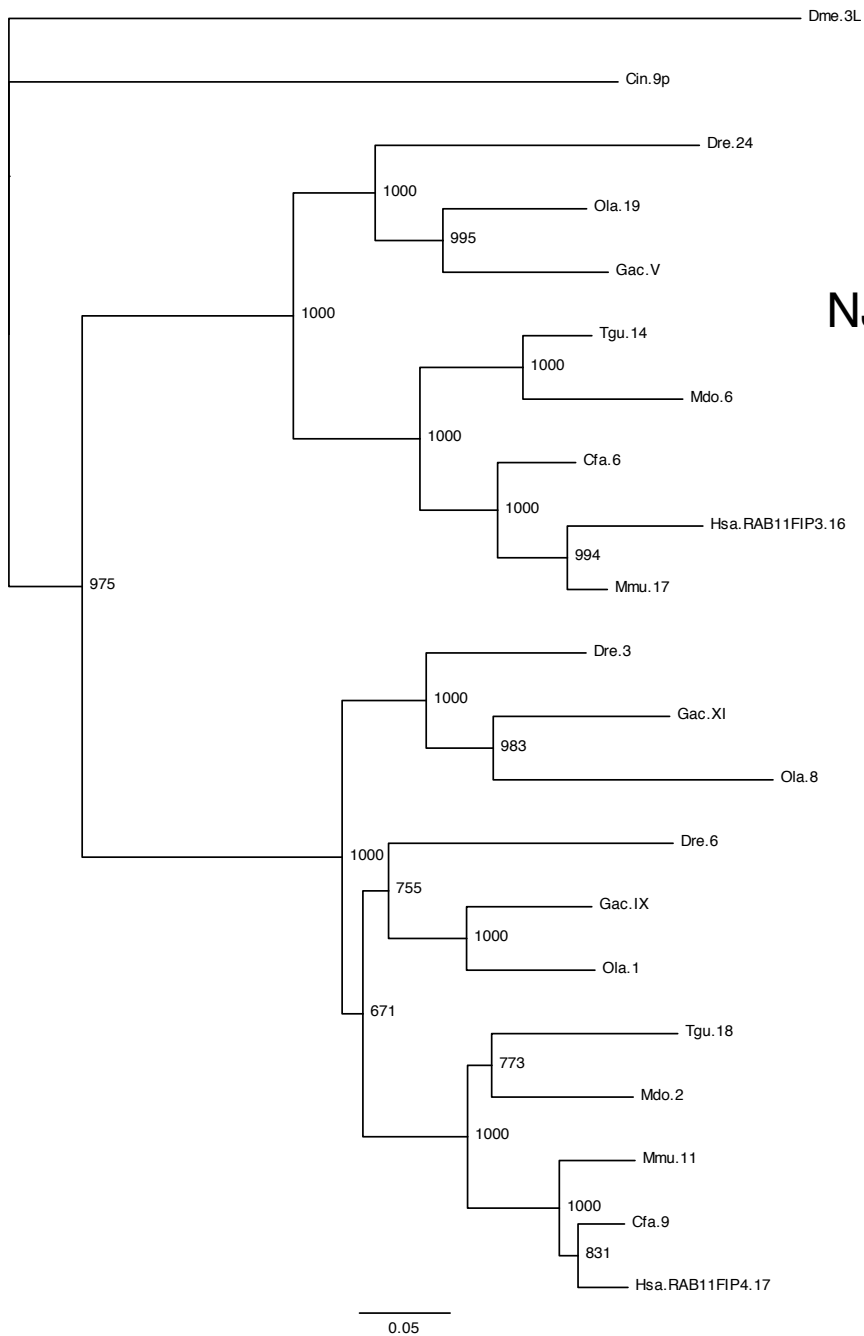


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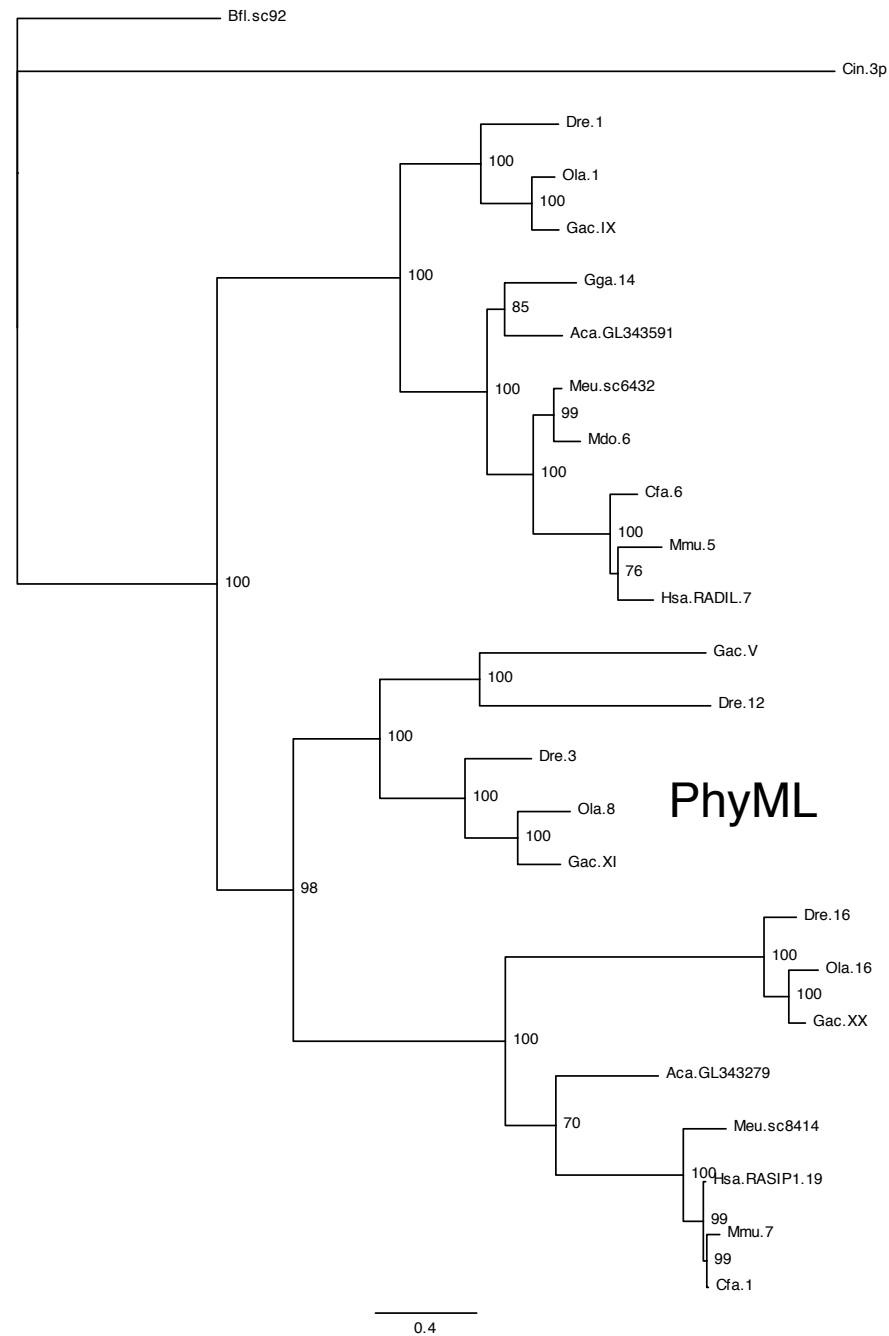
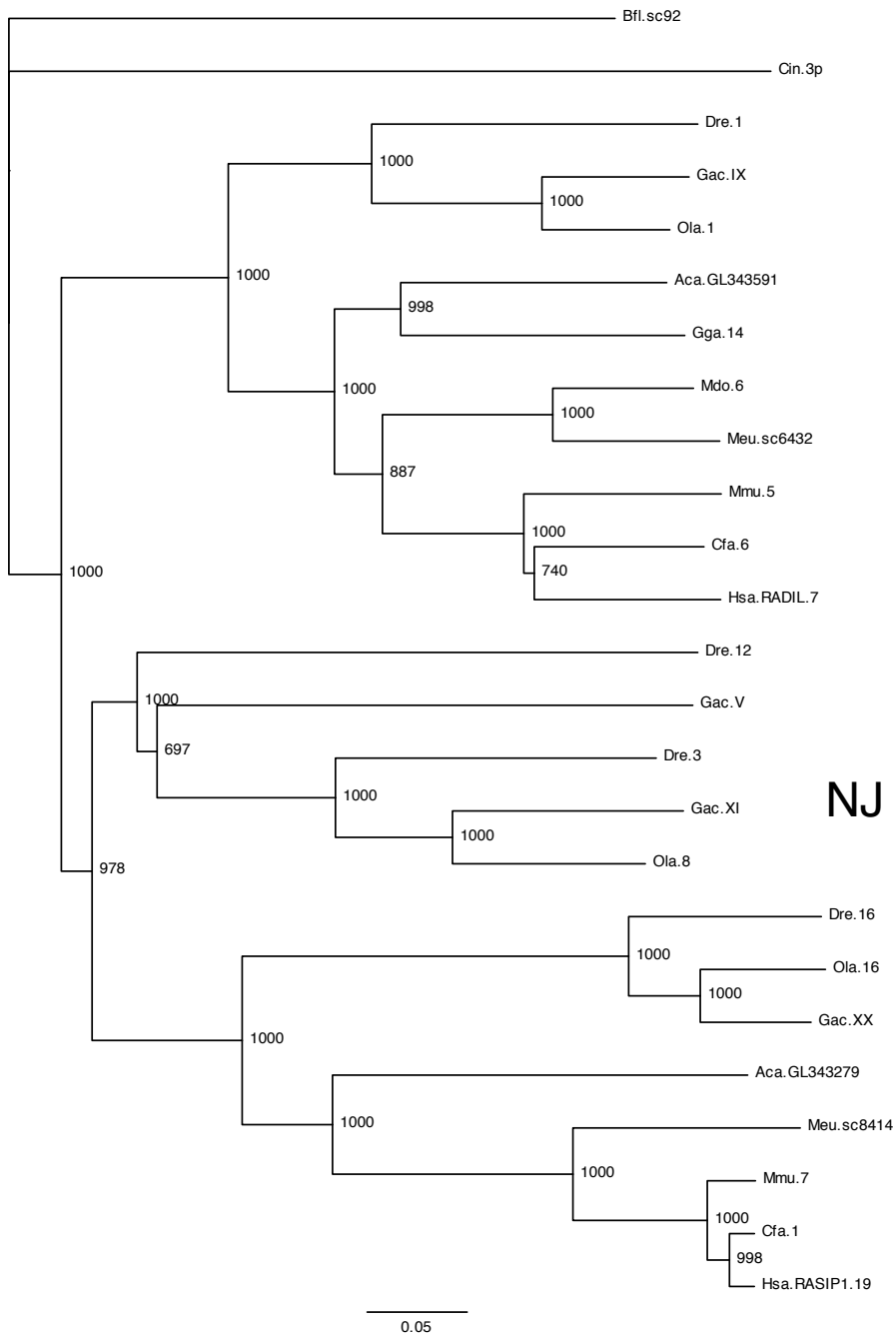


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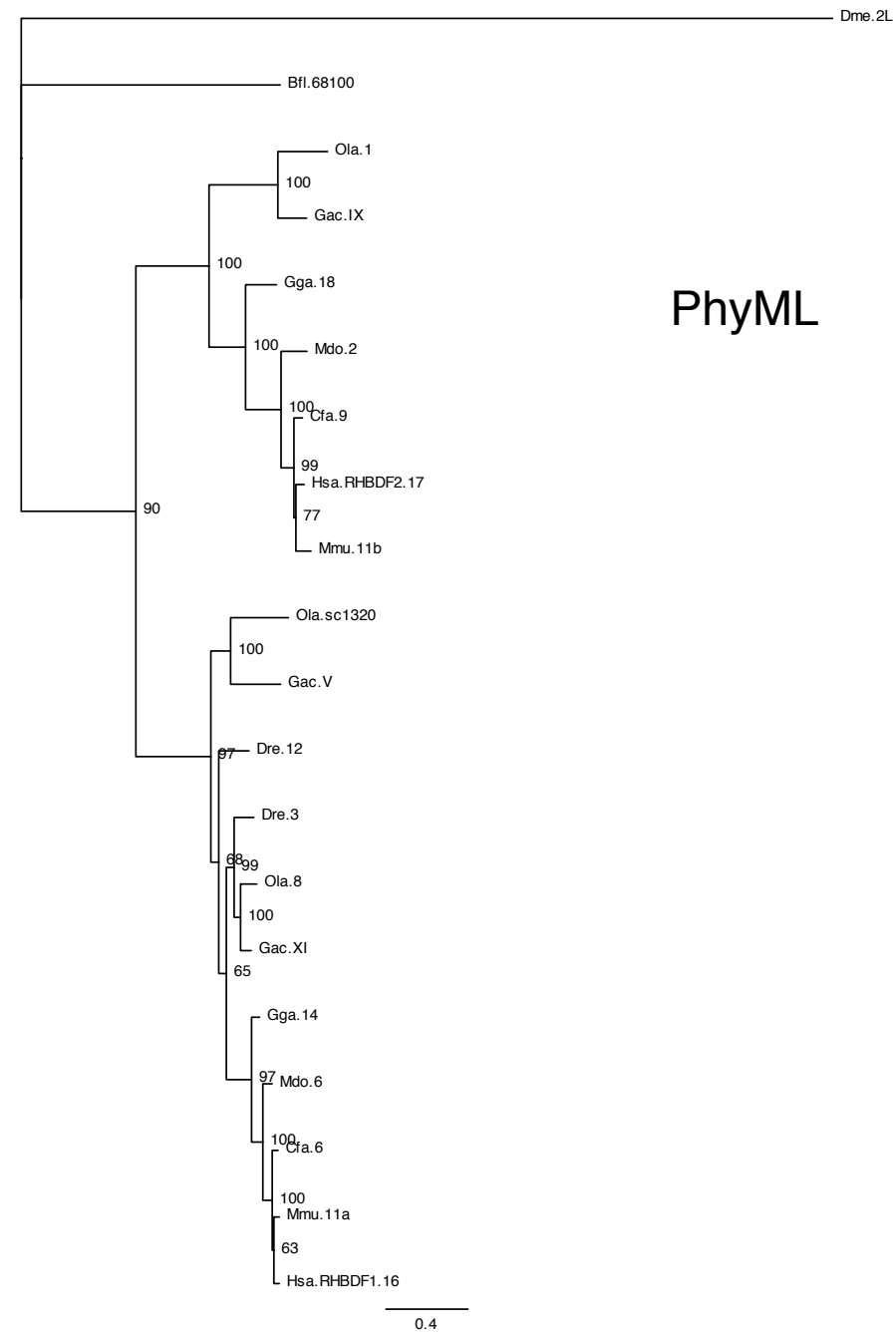
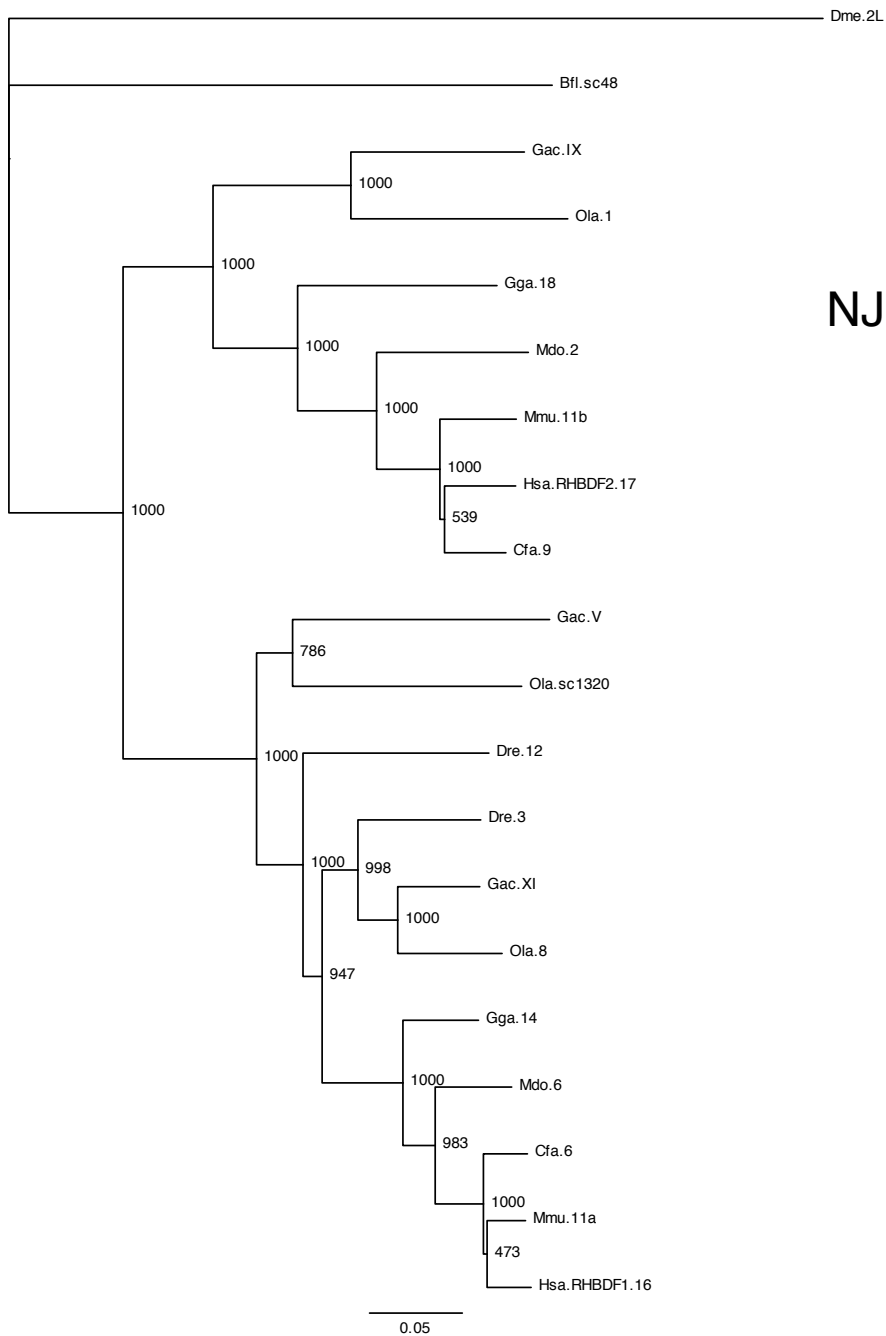


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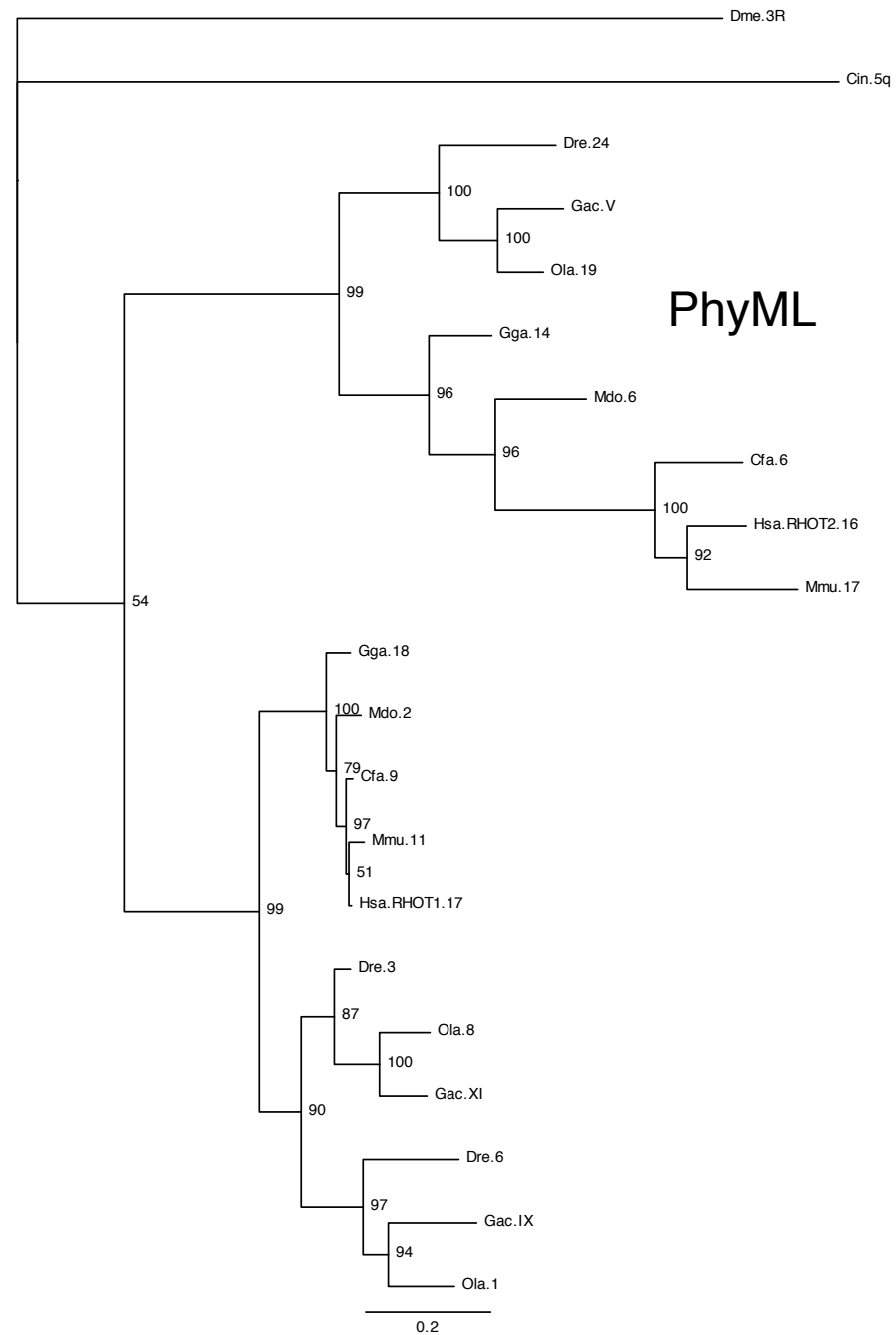
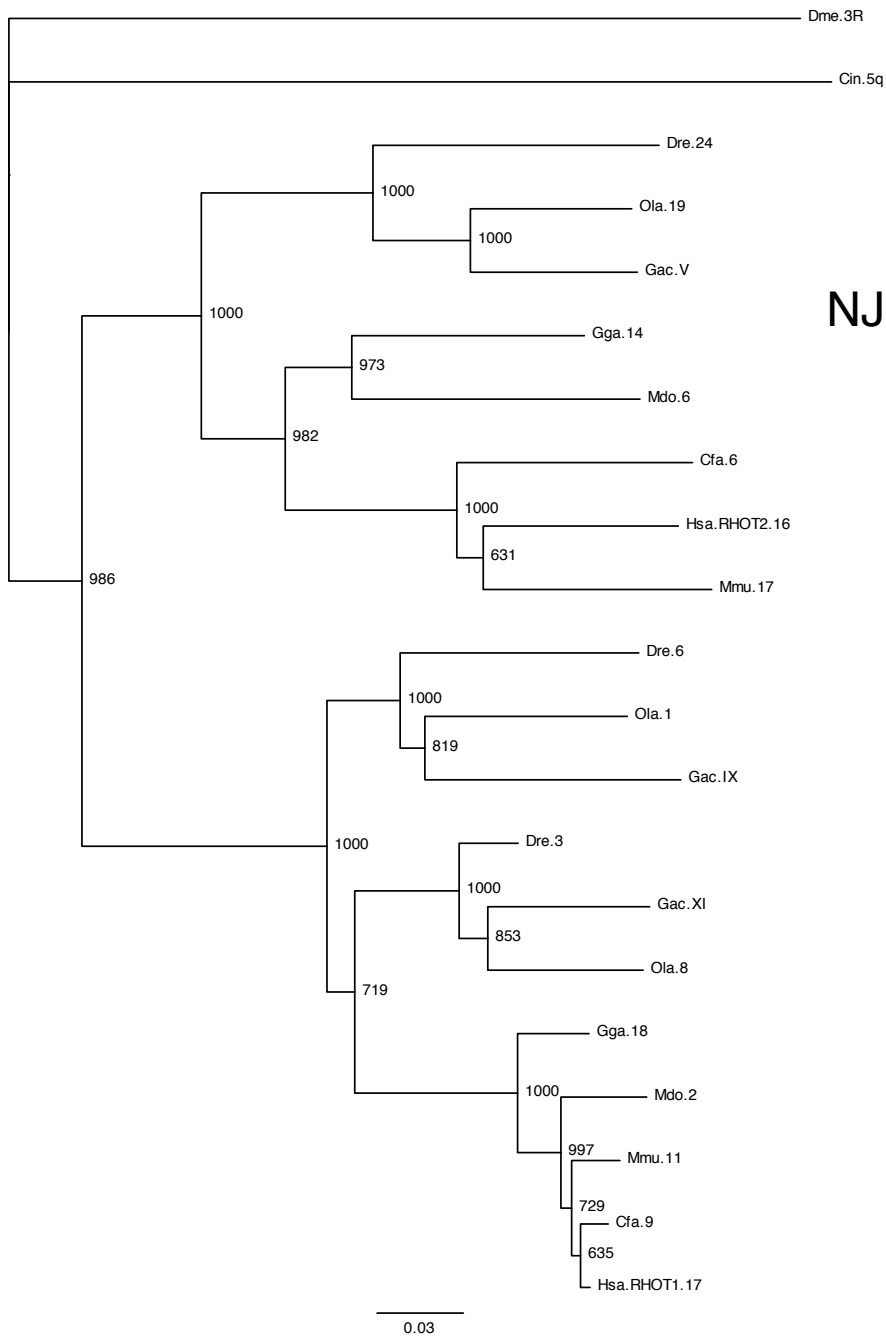
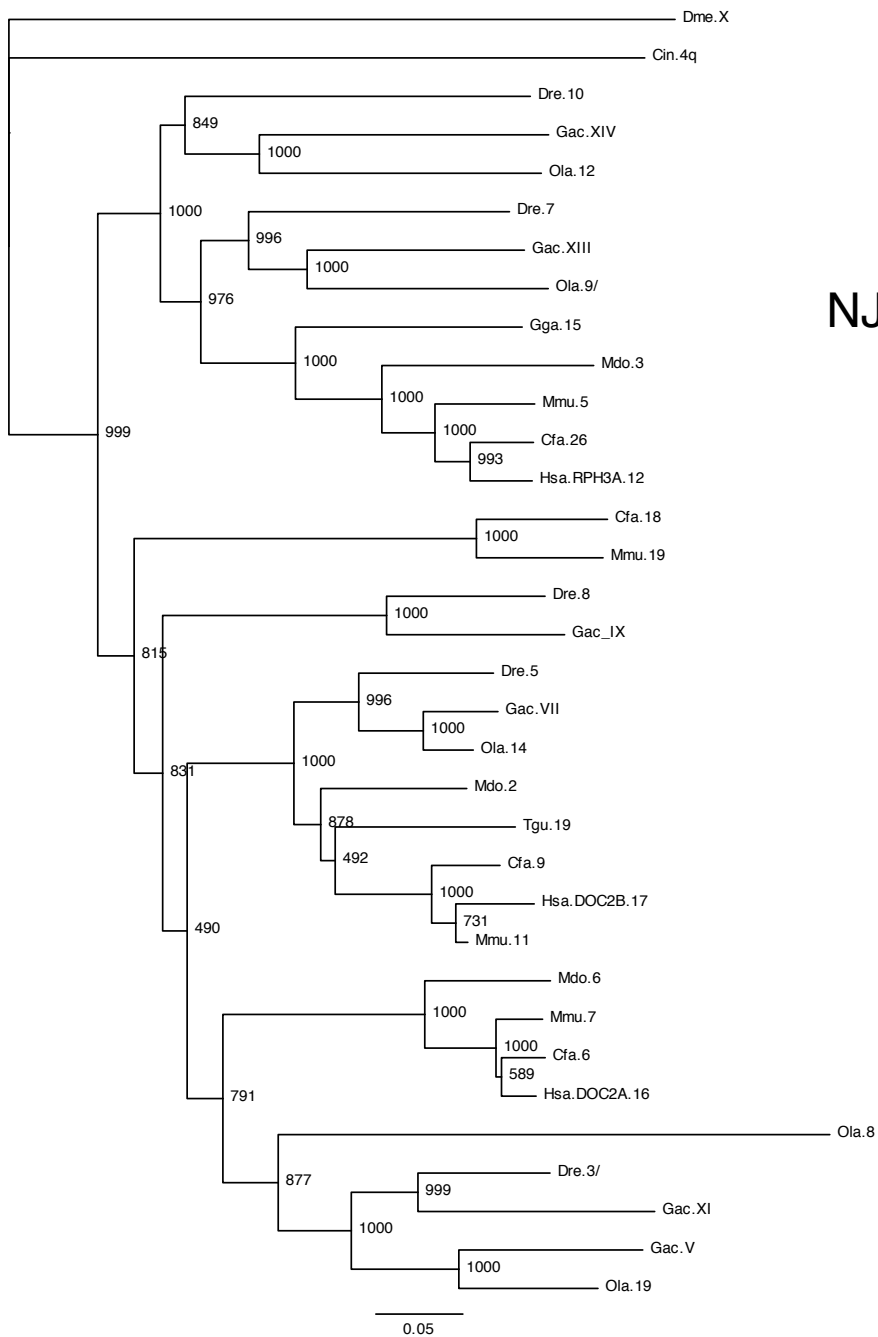
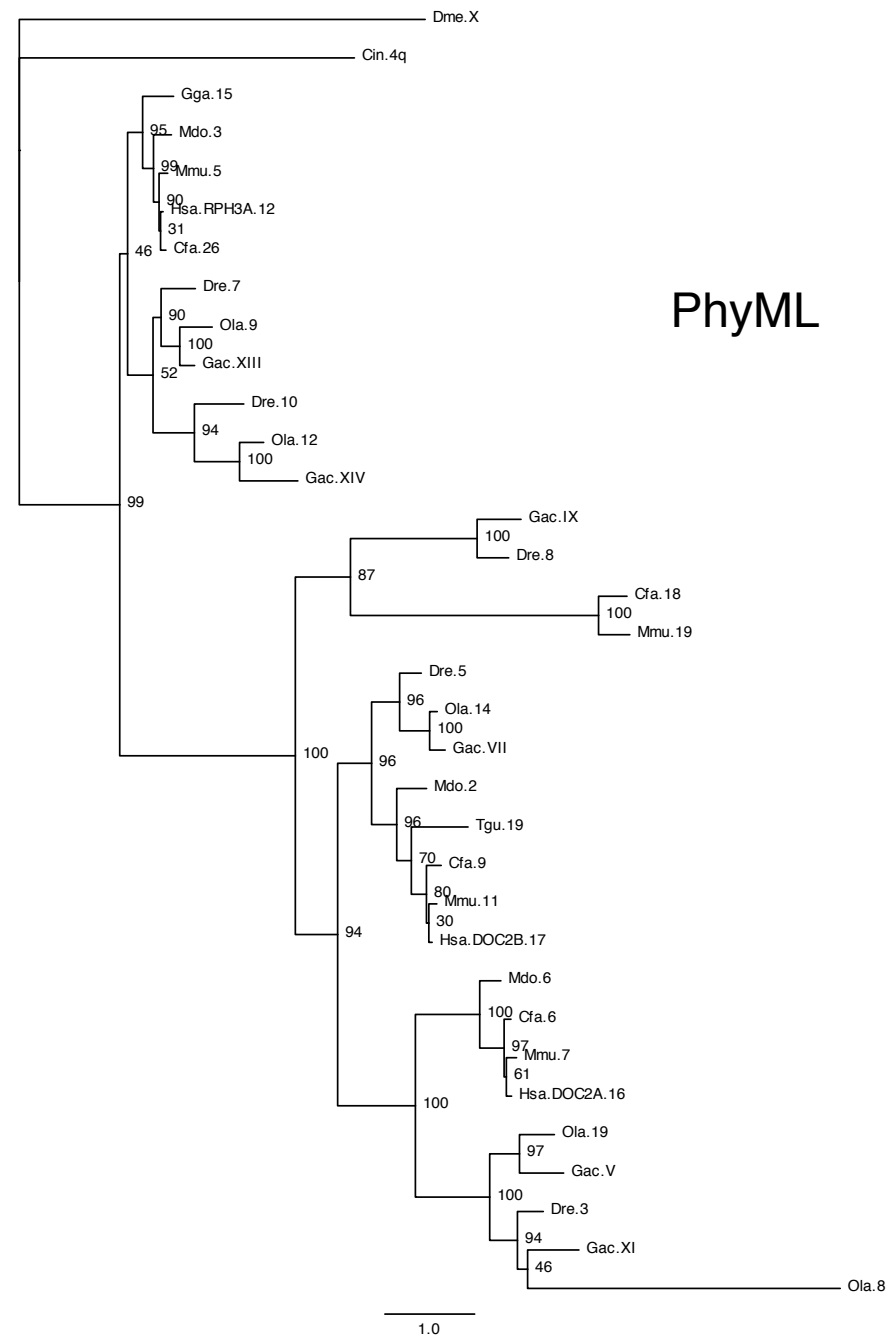


Figure S41. RHOT



NJ



PhyML

Figure S42. RPH3A

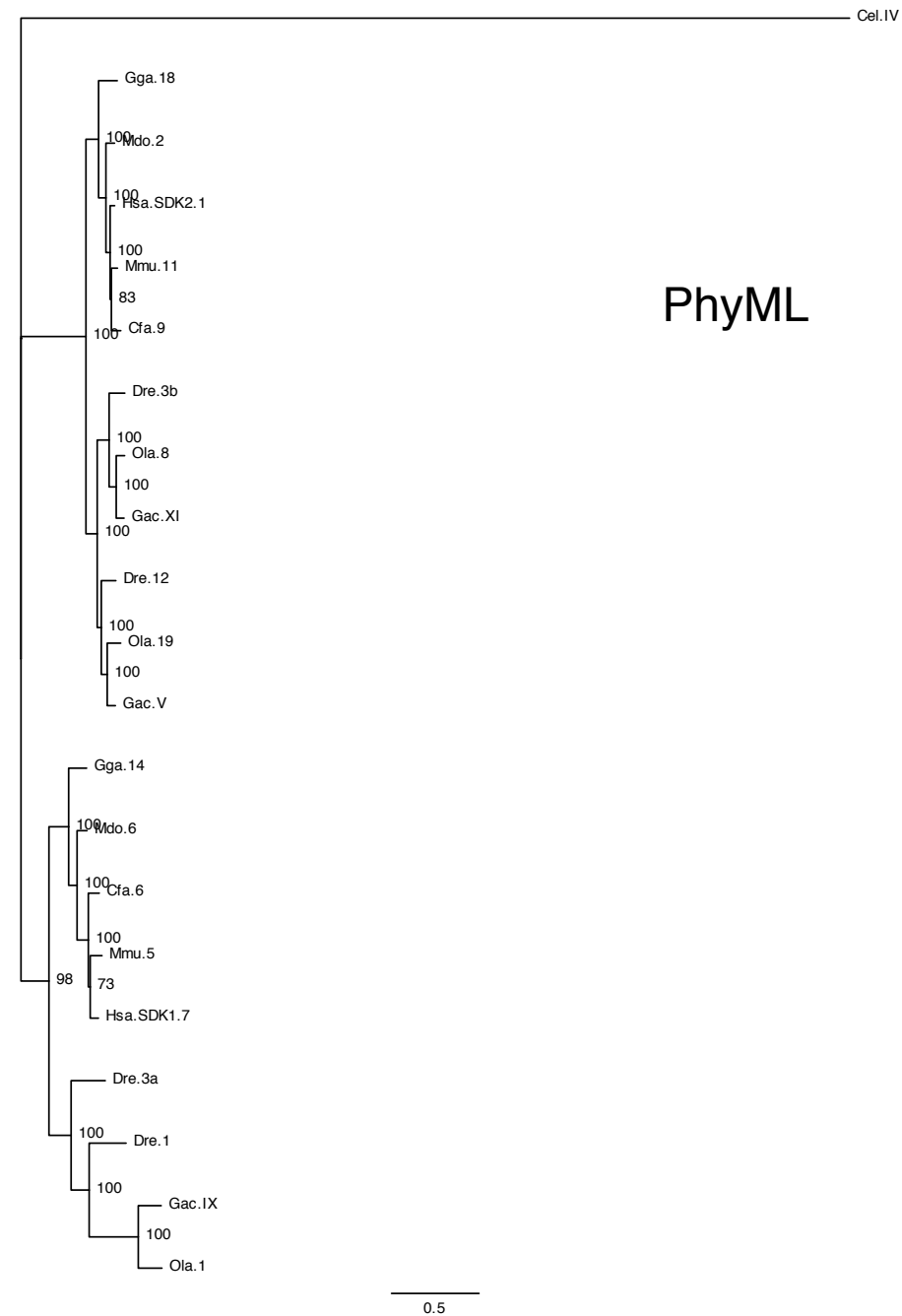
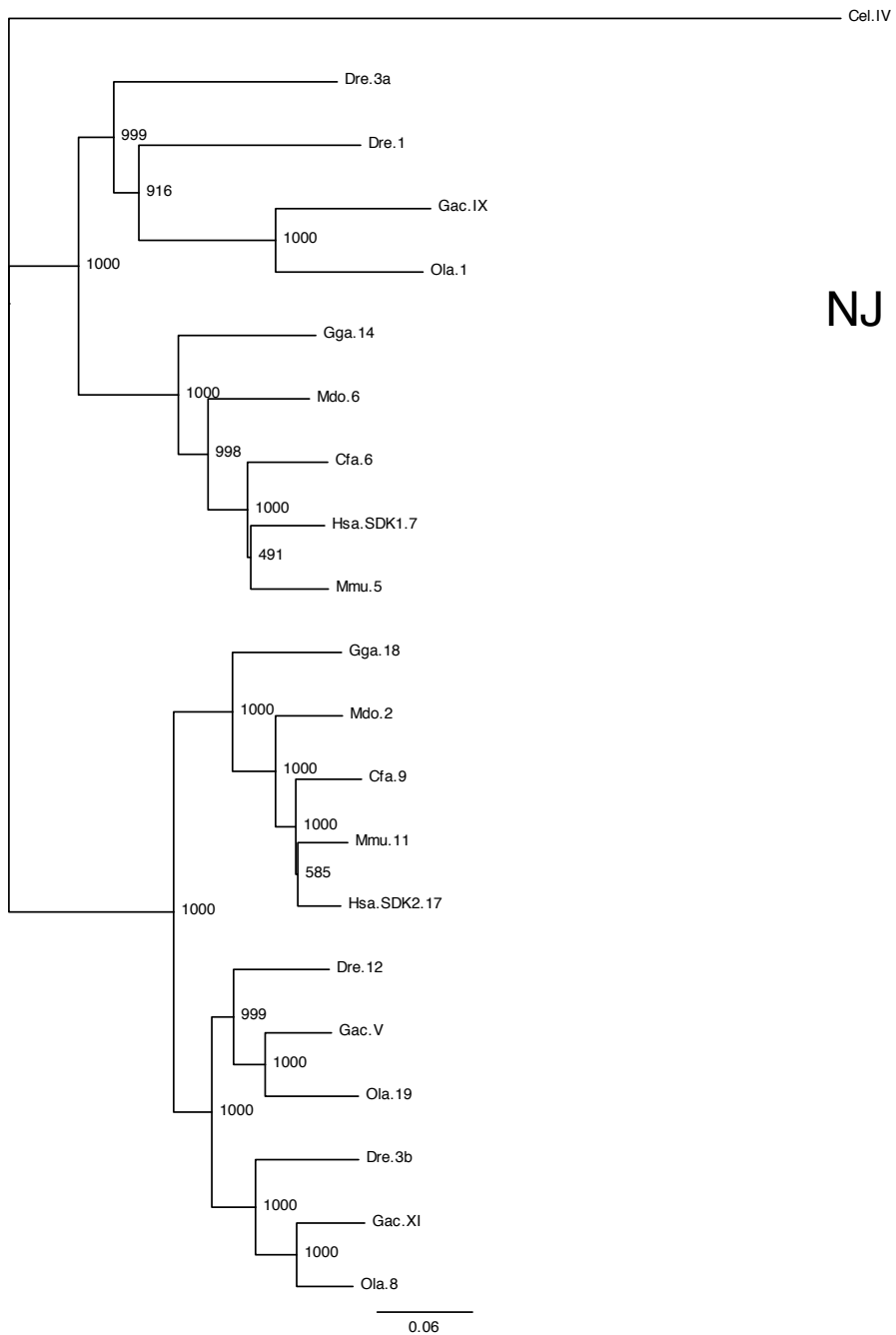


Figure S43. SDK

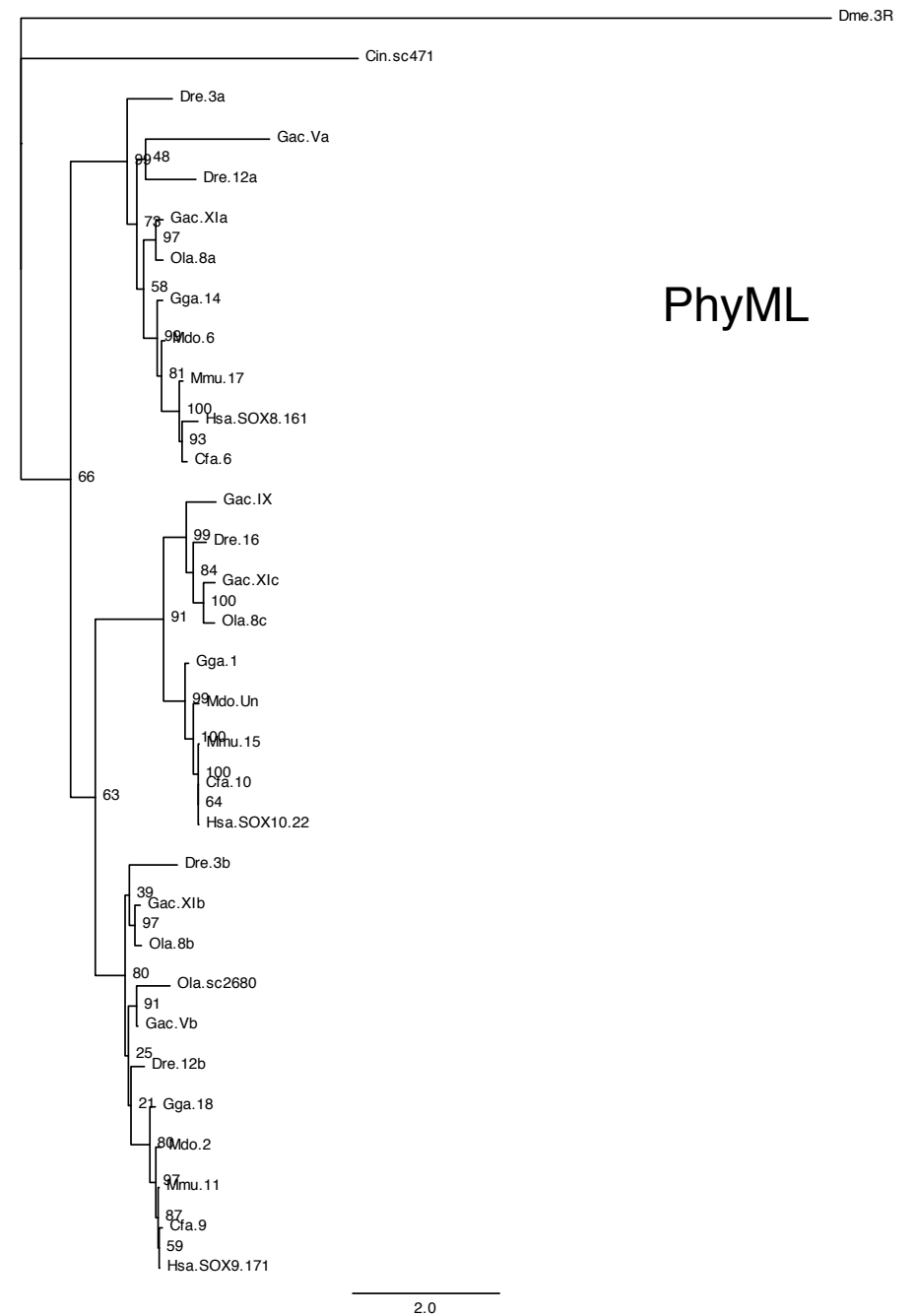
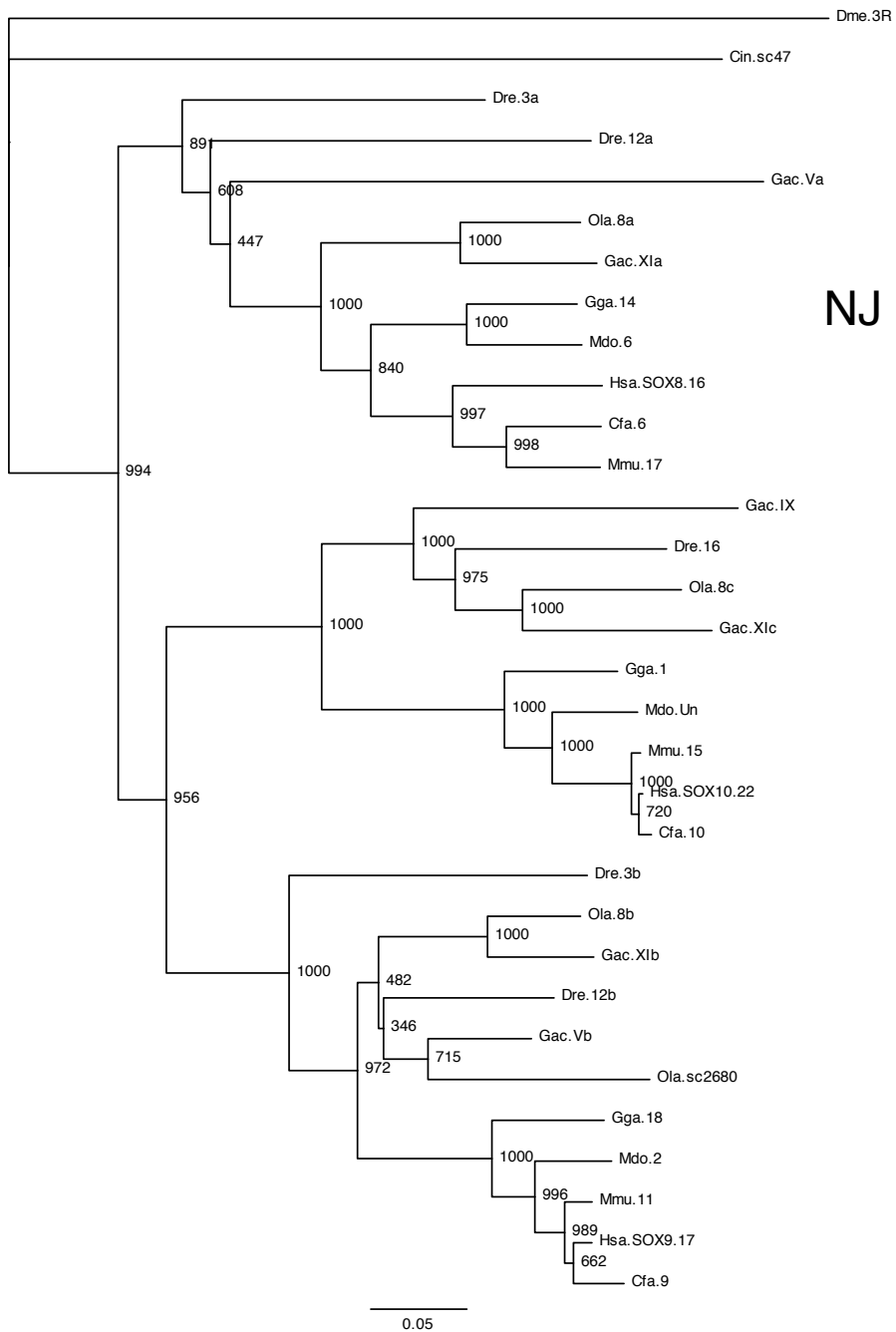


Figure S44. SOX

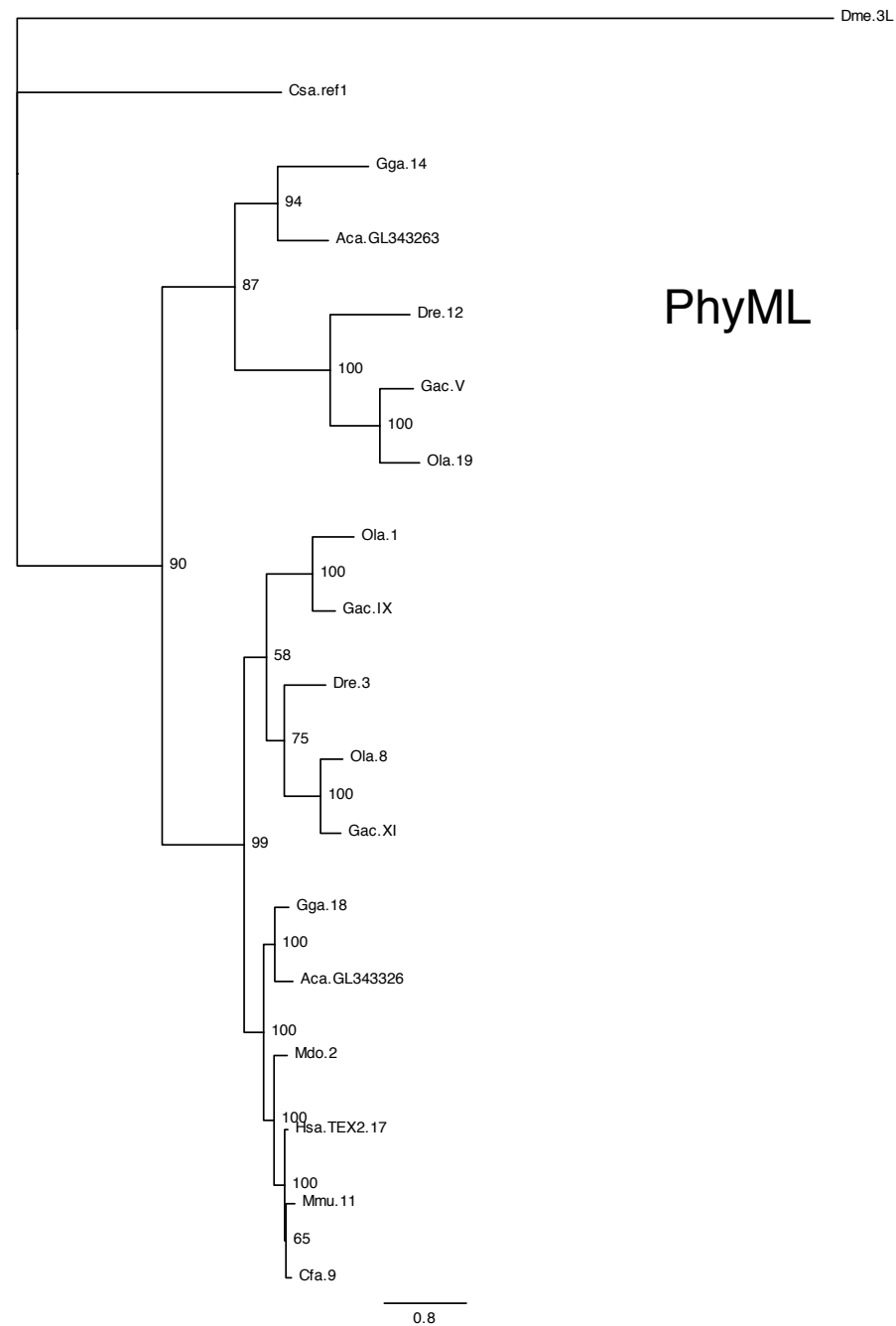
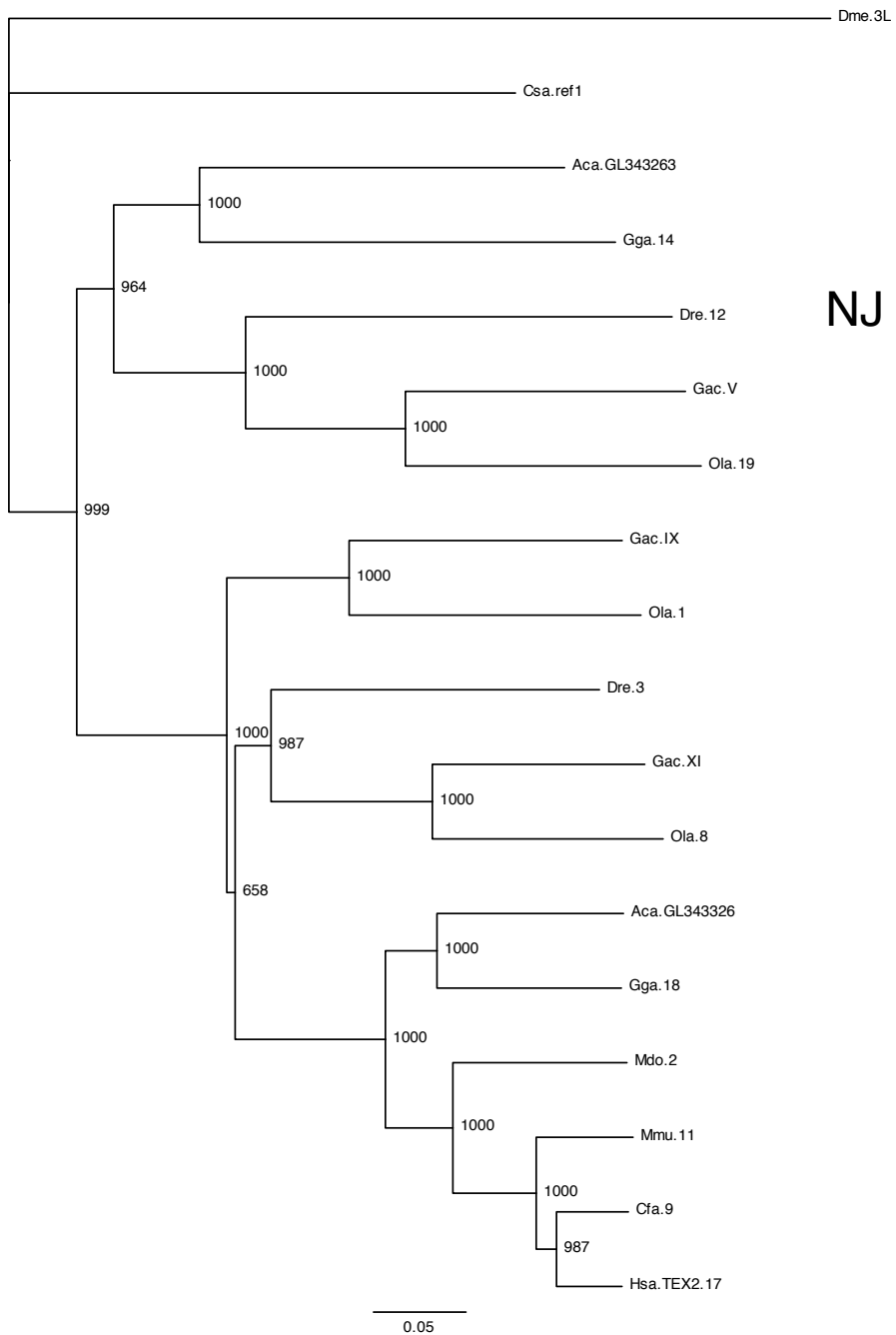


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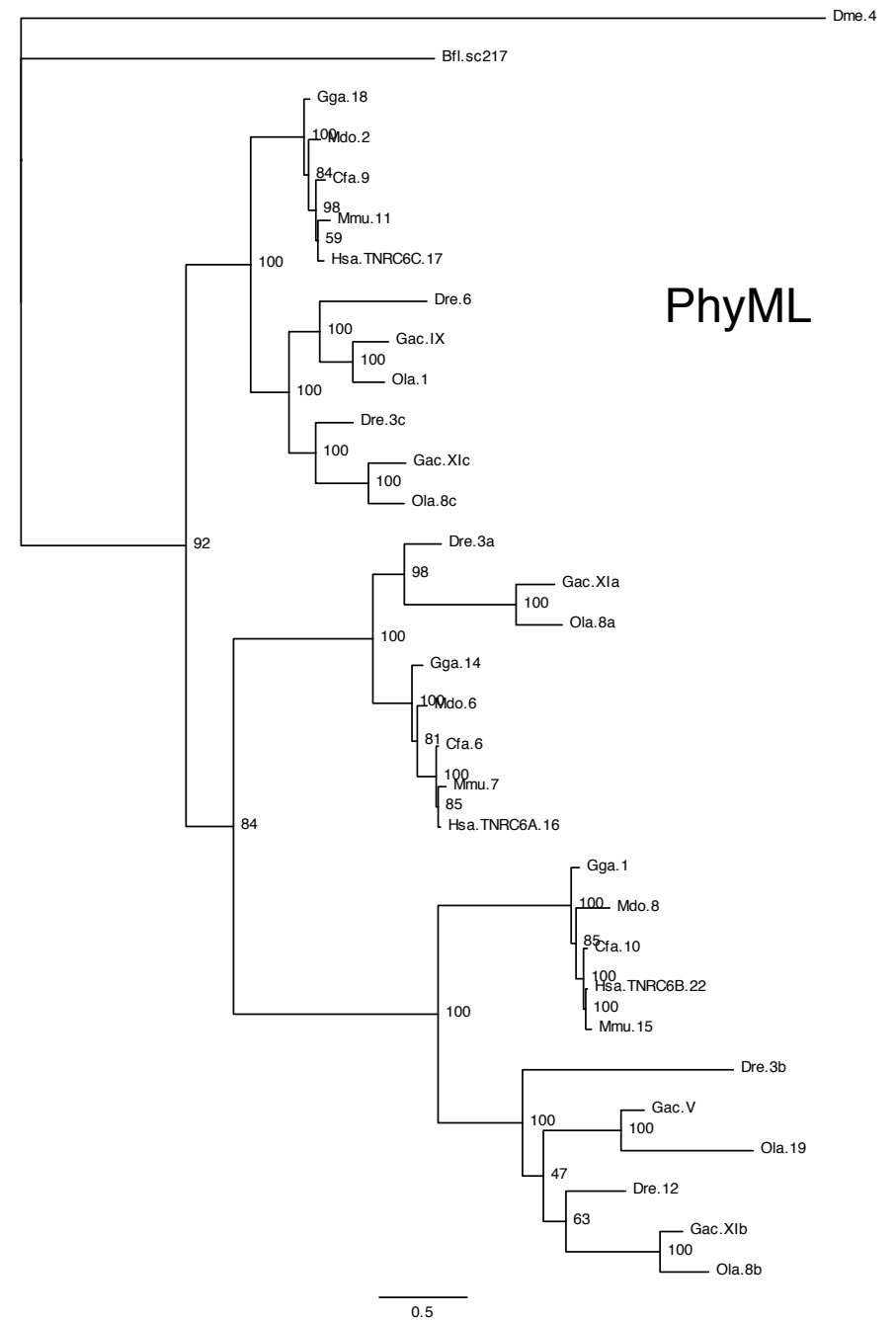
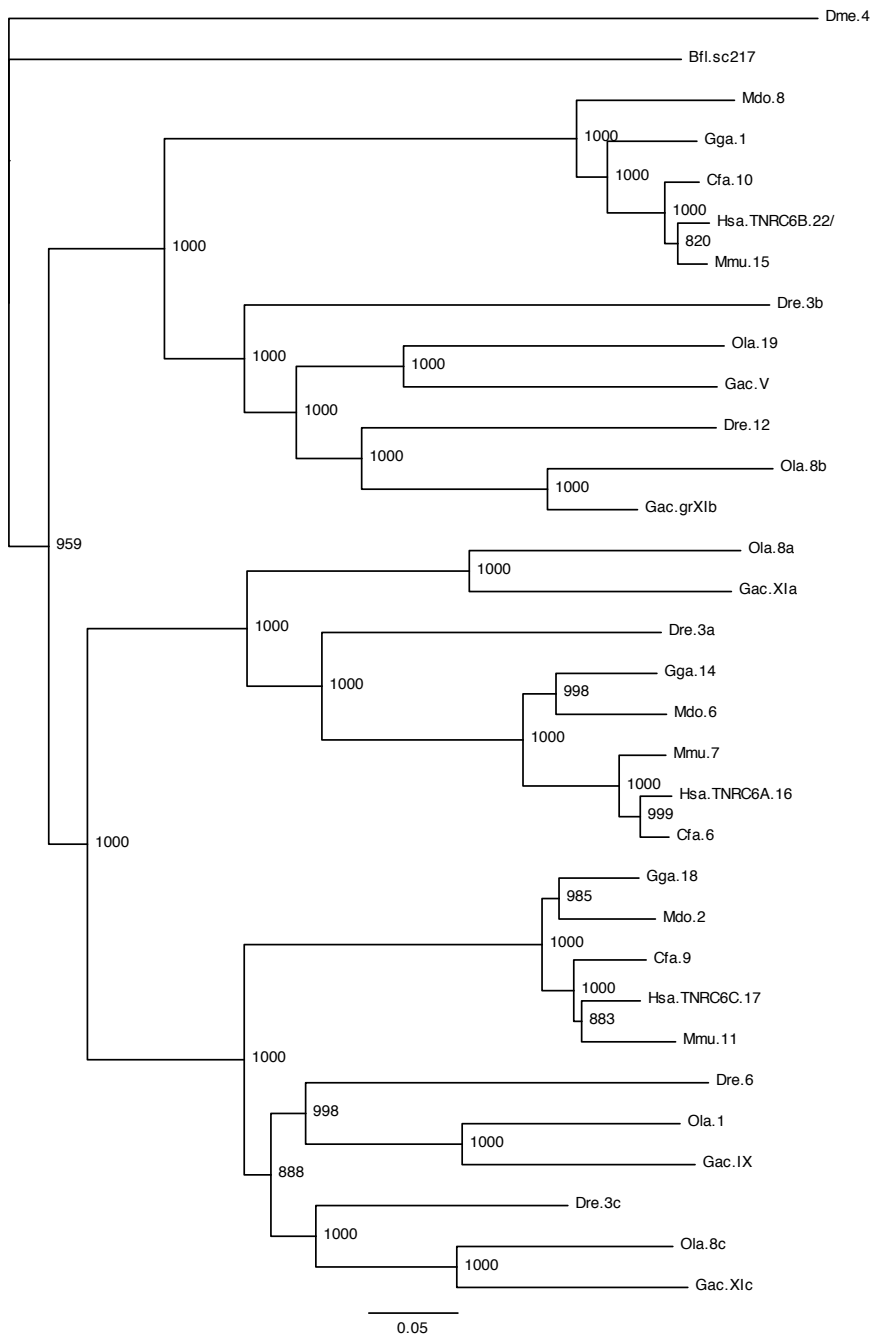


Figure S46. TNRC6

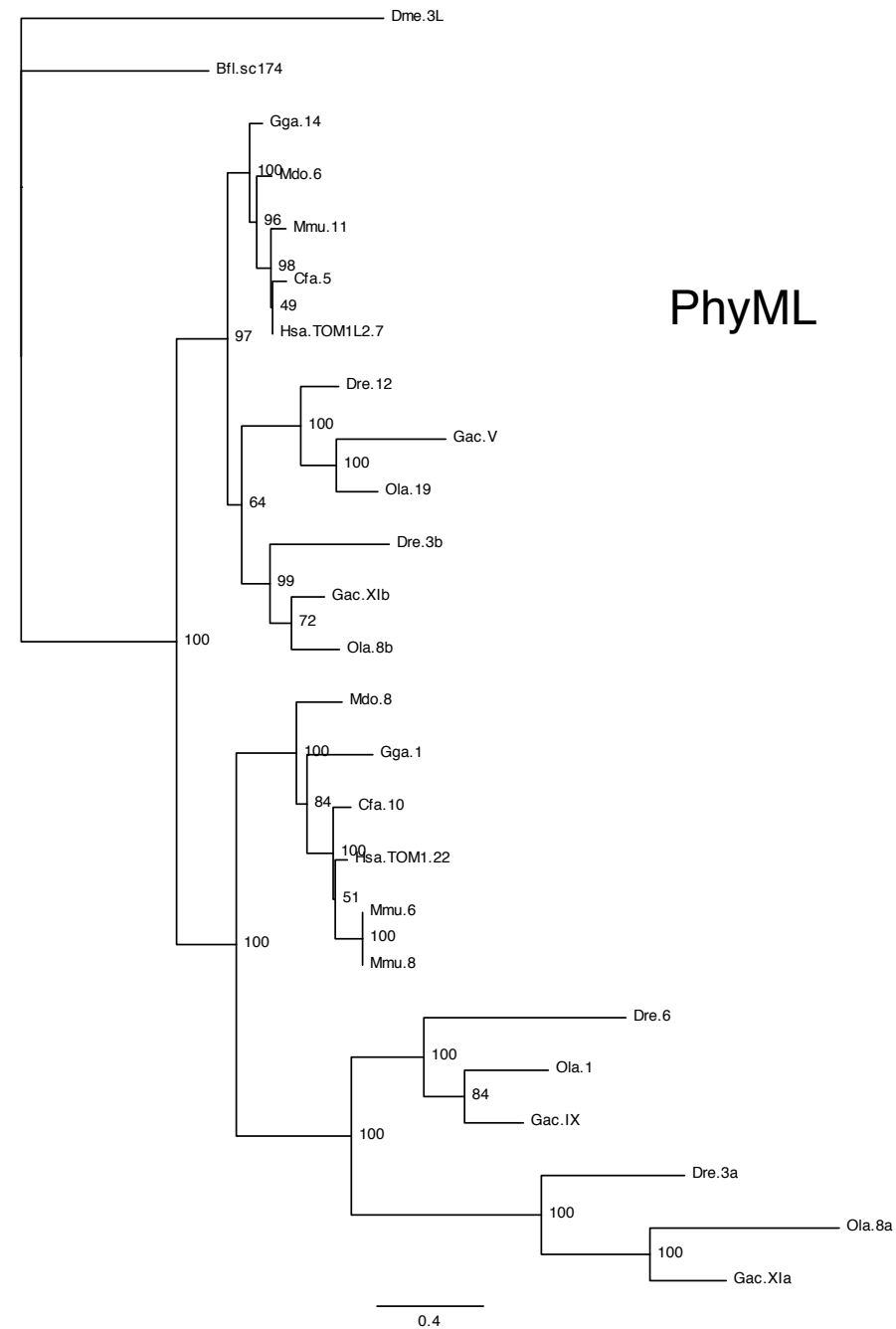
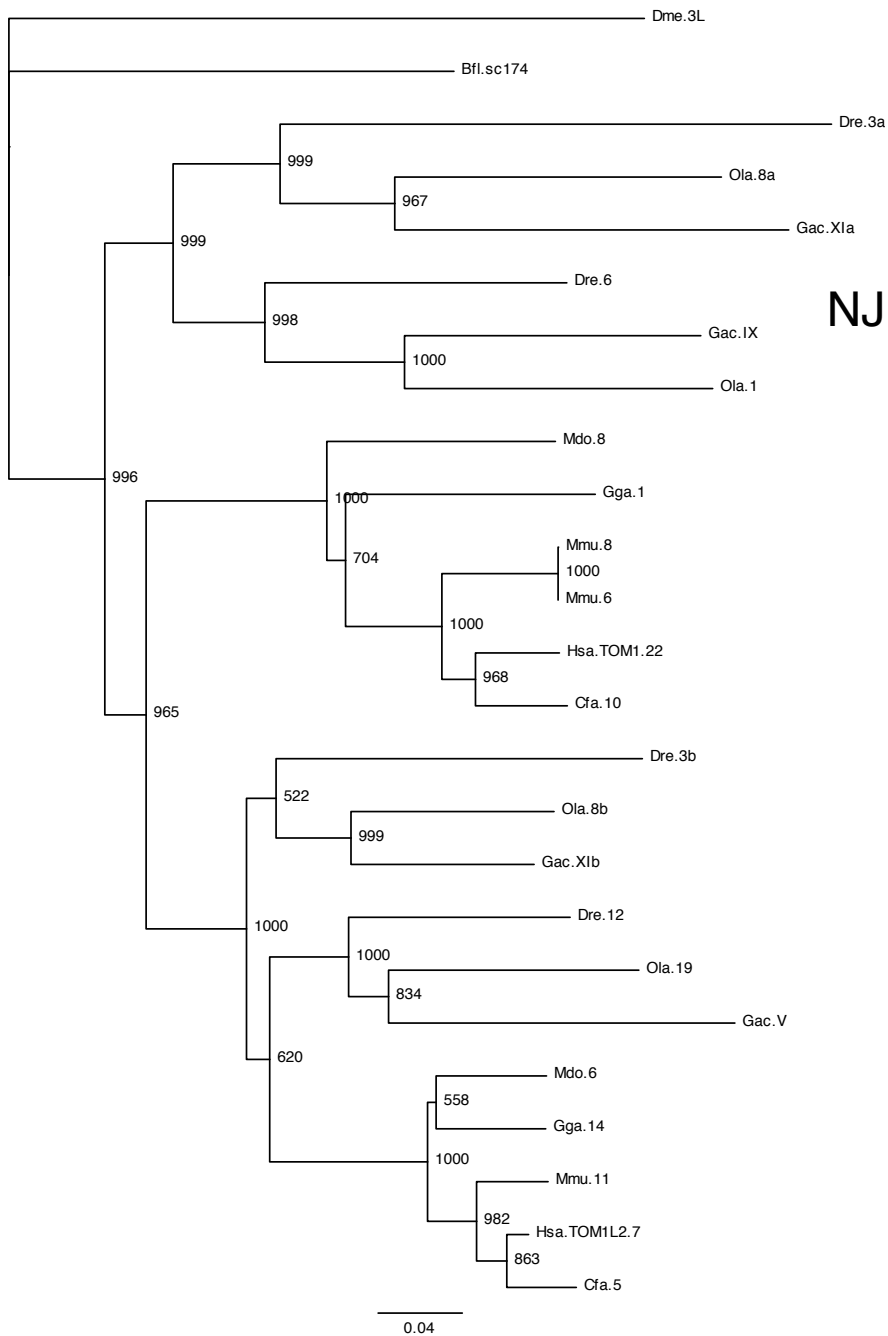
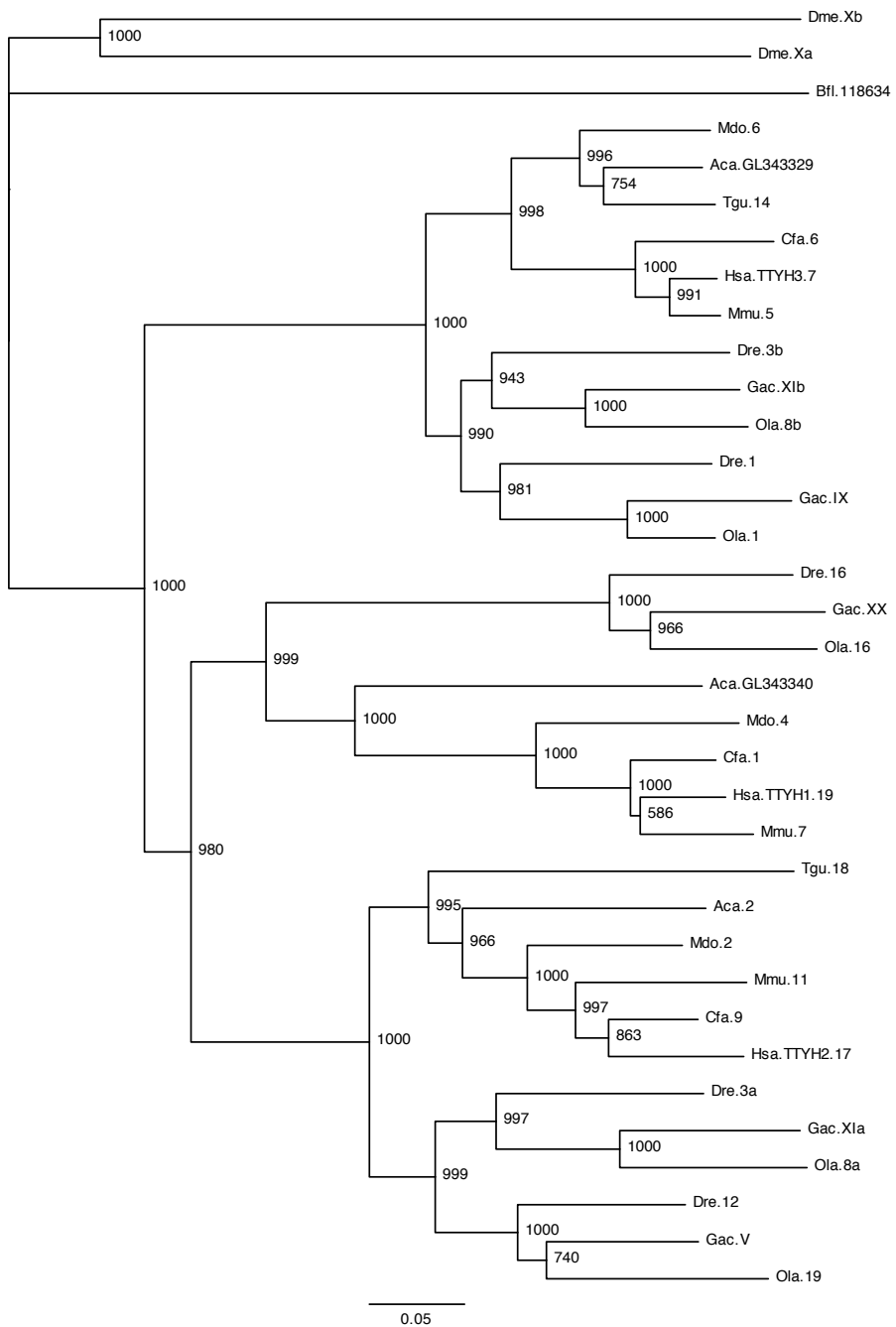
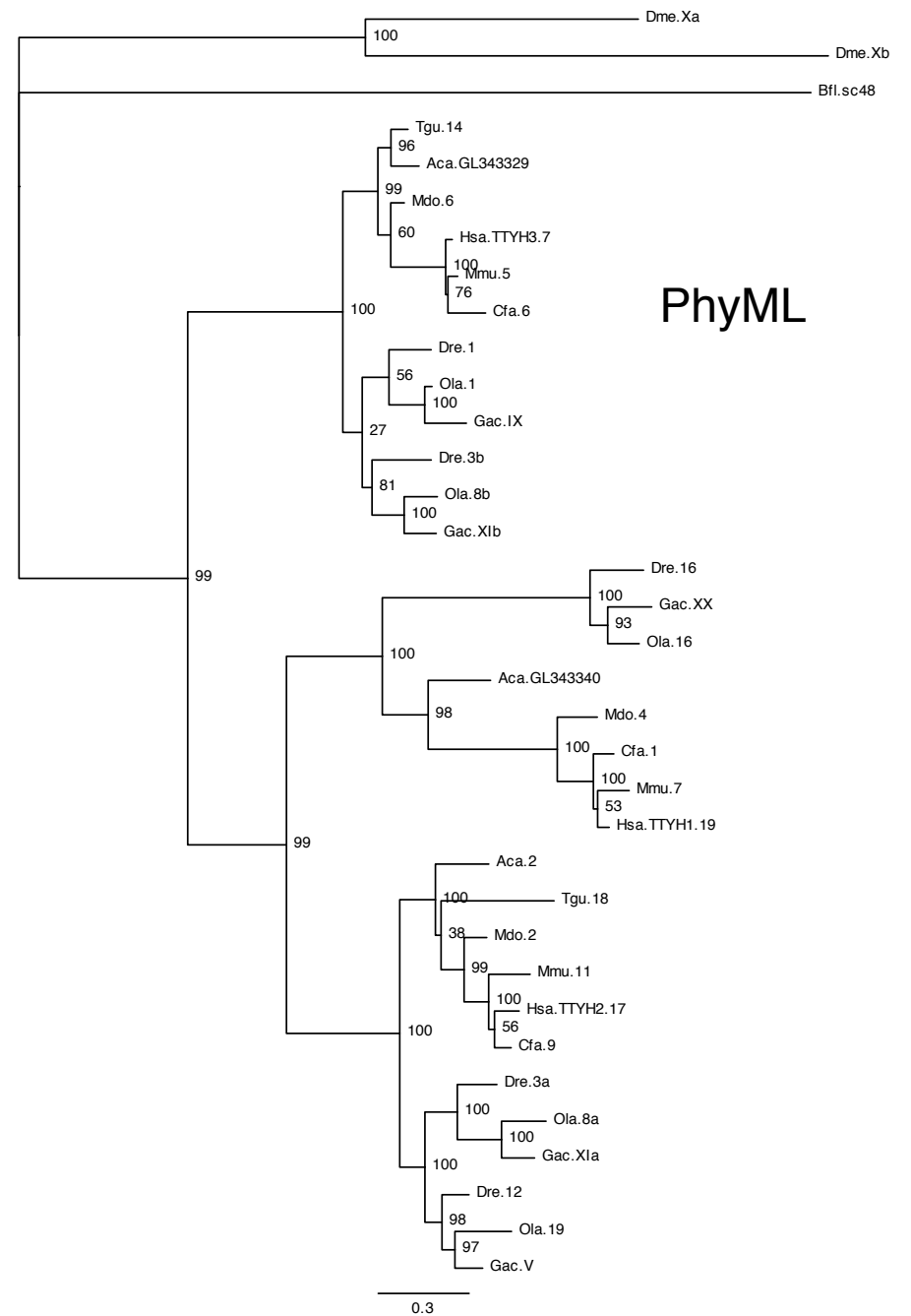


Figure S47. TOM1



NJ



PhyML

Figure S48. TTYH

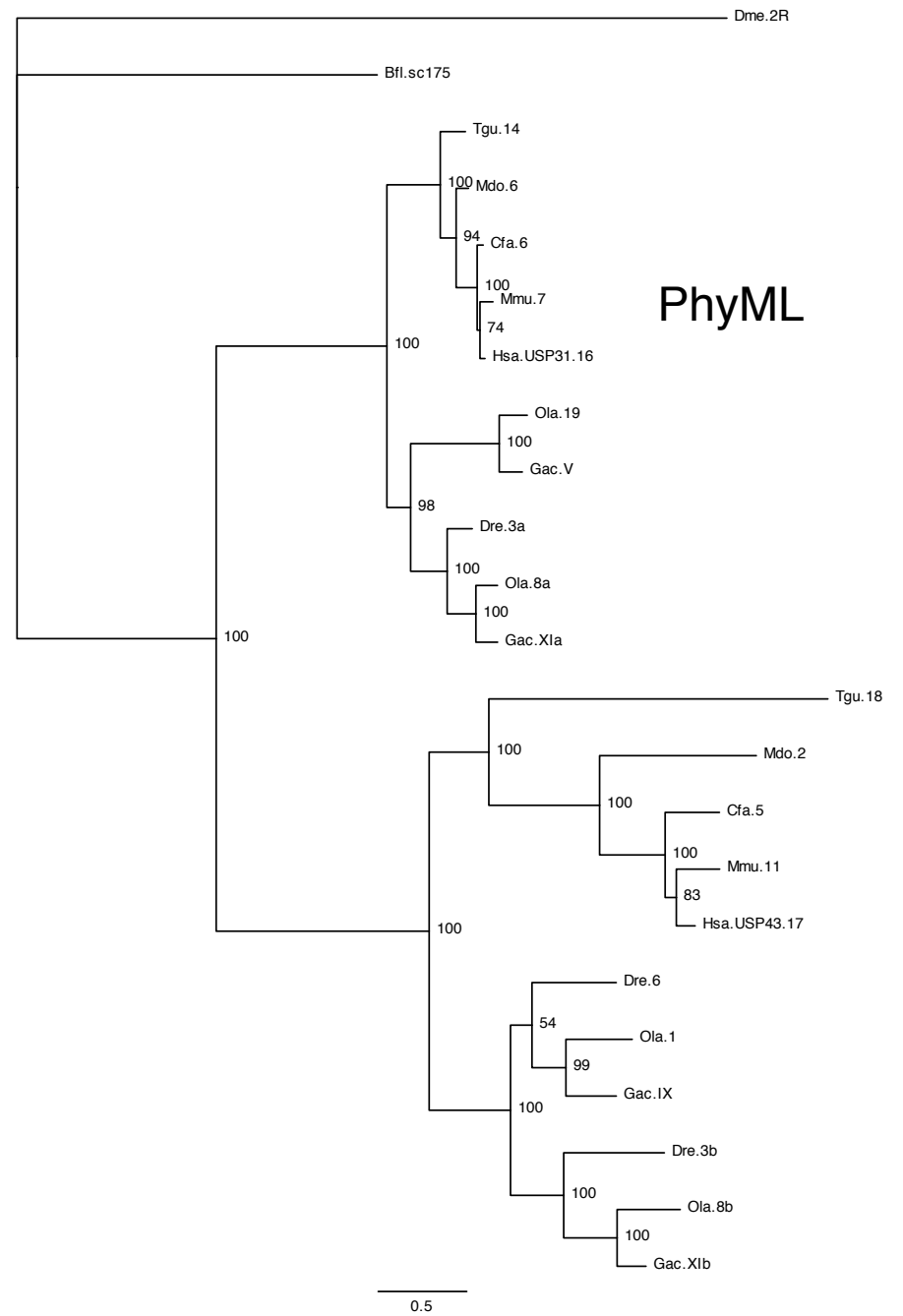
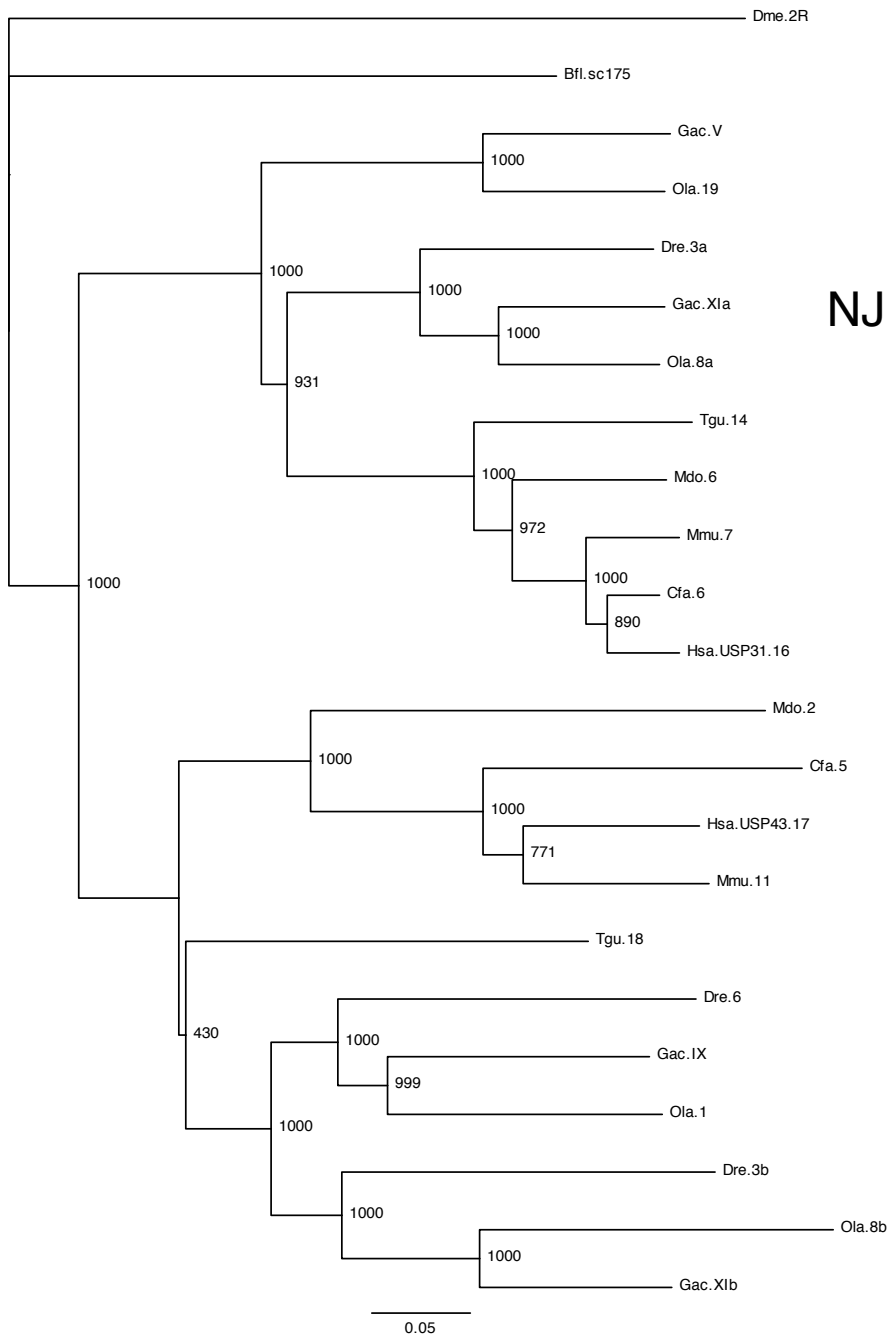


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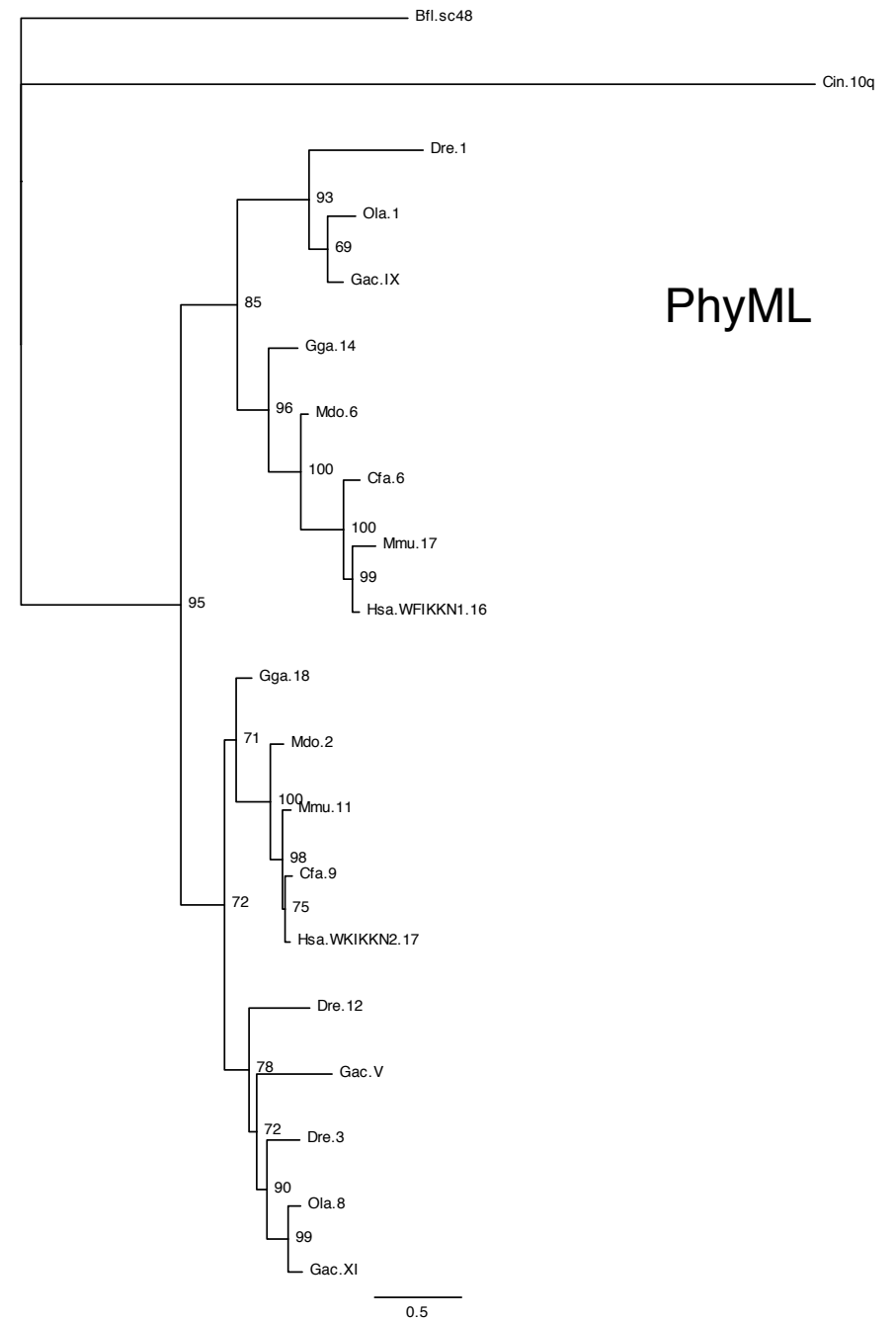
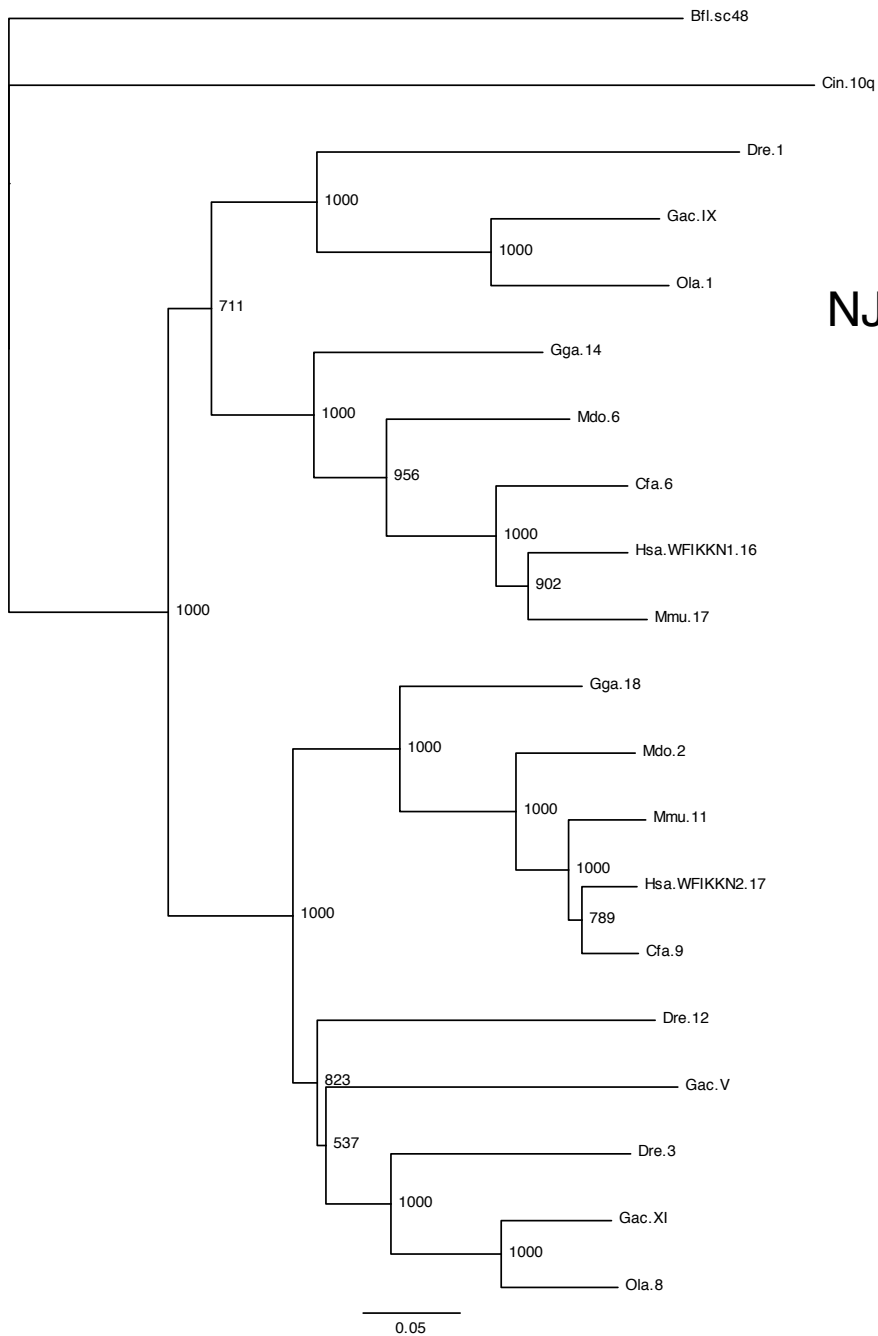


Figure S50. WFIKKN