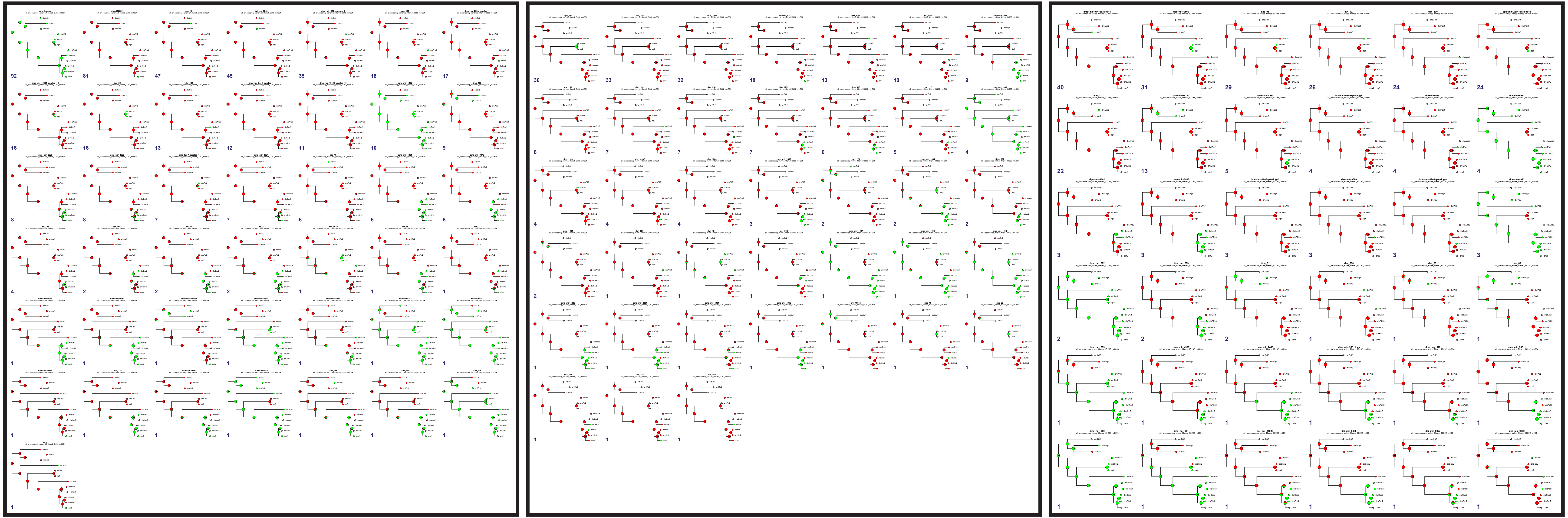

All Phylogenetic Tree Configurations (using Simple phylogenetic reconstruction model with universal parameters lambda = 0.292, mu = 0.694)

Canonical, non-testes-restricted miRNAs (497 alignments)

Mirtrons (234 alignments)

Testes-restricted, clustered, canonical miRNAs (265 alignments)

Supplementary Figure S17: All possible phylogenetic reconstruction of ancestral miRNA presence and absence for 3 miRNA classes using a phylogenetic probabilistic graphical model with universal parameters of λ = 0.292 and μ = 0.694. These parameters were computed by running the phylogenetic reconstruction algorithms on all mirtrons and miRNAs pooled together. These trees illustrate how the method's maximum likelihood reconstruction performs for all possible configurations of extant miRNAs presence and absence per alignment. Blue text indicates count of alignments with this particular configuration in each class. Summary of miRNA birth and death (Figure 6) are based upon these estimates of ancestral miRNA presence and absence.

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Supplementary Figure 17