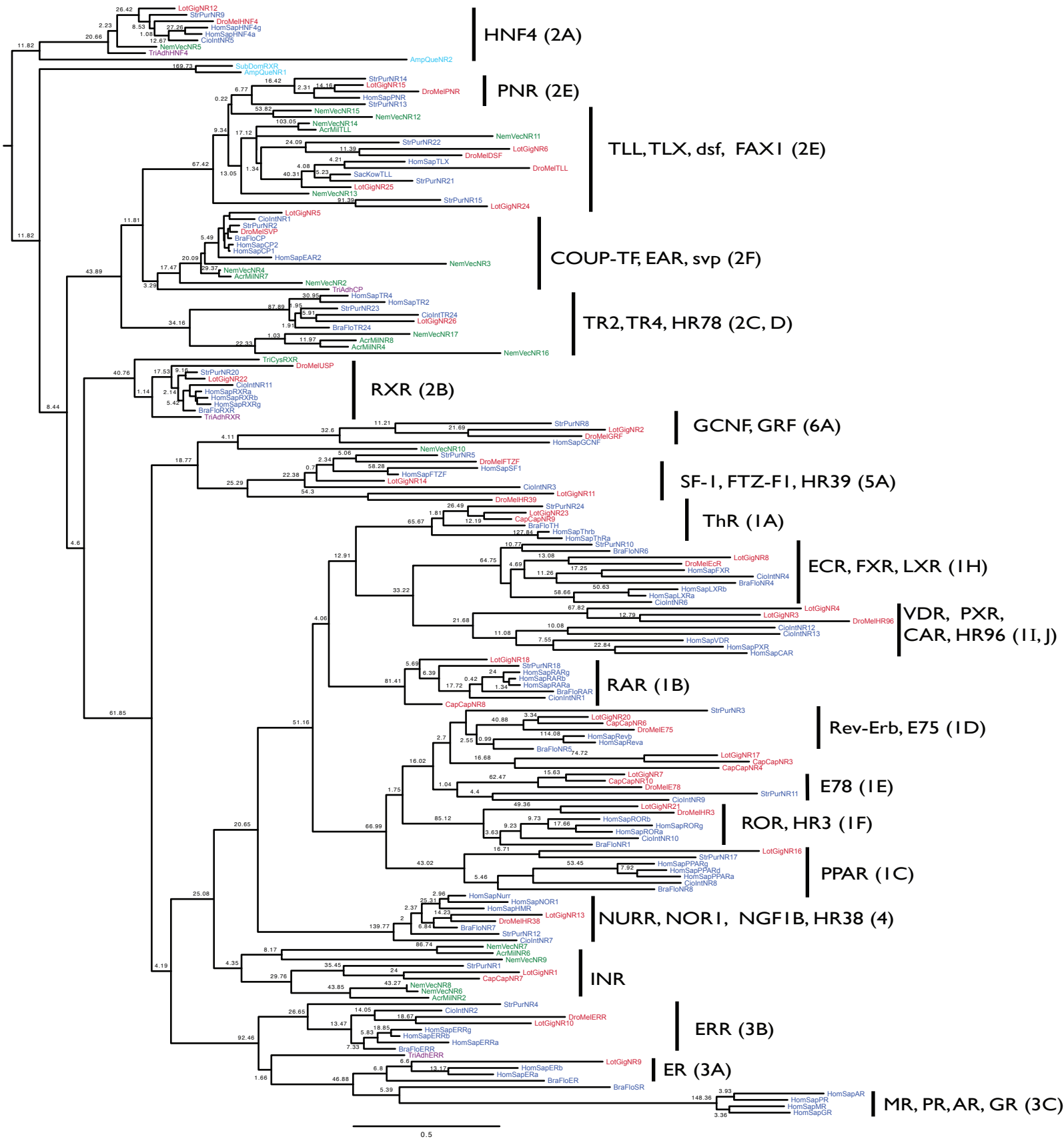Fig. S5. Maximum likelihood NR phylogeny on a reduced dataset. We used maximum likelihood to analyze the same 174-sequence dataset used for Bayesian MCMC analysis, which excludes the taxa at the end of the longest branches in the 275-sequence dataset. Branch labels show approximate likelihood ratios. Sequence names are colored as in Fig. S2.