

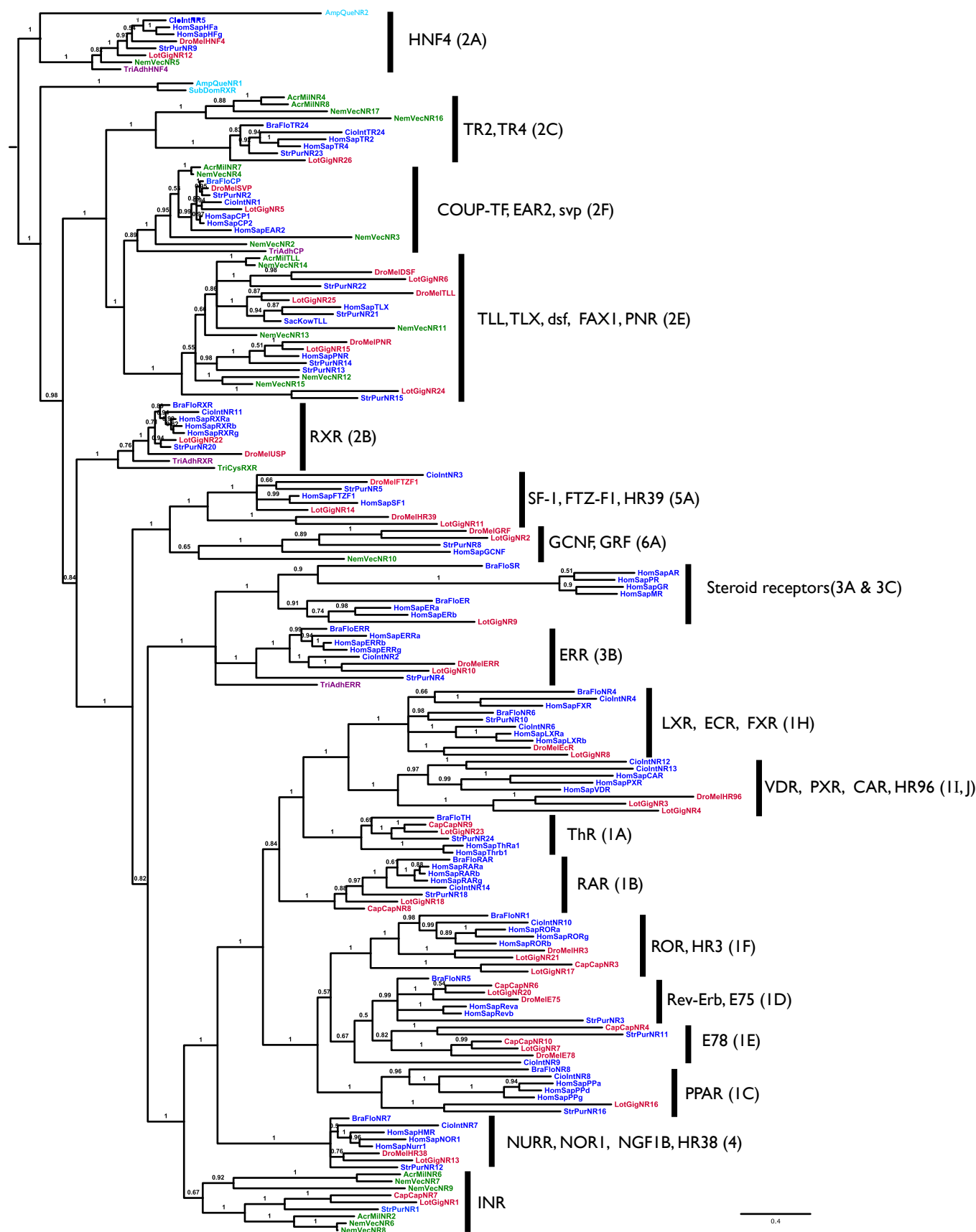


Fig. S3. Bayesian phylogeny of the nuclear receptor family inferred using Bayesian MCMC. Node labels indicate Bayesian posterior probabilities > 50%. Sequence names are colored as in Fig. S2.