



Supplemental Figure S4. Phylogenetic trees for five YX gametologs. (A,D,G,J,M) Bayesian phylogenetic tree using MetaPIGA with GTR model but without invariable sites, 110 replicates with 200 iterations each, trees sampled every 5 generations. (B,E,H,K,N) Bayesian phylogenetic tree using MrBayes with GTR model, gamma distribution and invariable sites. 1,000,000 generations, sampled every 1000 generations until the average standard deviation of split frequencies converged and was below 0.01 and PSRF was close to 1 for all parameters. (C,F,I,L,O) Maximum likelihood phylogenetic using PhyML with estimated site variation, gamma distribution and 1000 bootstrap replicates. All trees are based on coding nucleotide sequences of XY gametologs from *Anolis* and 1:1 orthologous genes. Key nodes with statistical support (red arrows) are indicative of XY gametolog divergences relative to specific speciation/lineage divergence events.