



Supplemental Figure S2. Individual phylogenetic trees of *RPL6* and *PPP1CC* (stratum 1) YX gametologs. (A-C) Phylogenetic trees for *RPL6*. (D-F) Phylogenetic trees for *PPP1CC*. (A,D) Bayesian phylogenetic tree reconstructed using MetaPIGA with GTR model but without invariable sites, 110 replicates with 200 iterations each, trees sampled every 5 generations. (B,E) Bayesian phylogenetic tree reconstructed 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) Maximum likelihood phylogenetic tree reconstructed 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* (*RPL6* or *PPP1CC*) and 1:1 orthologous genes. Probabilities at key nodes support the sex chromosome origin (red arrows) prior to the divergence of pleurodonts (*Anolis* / iguana) and acrodonts (*Pogona*; agamids).