# Supplementary Figure Legends

**Figure A3.1.** Phylogram depicting the relationship among 52 angiosperm taxa and two gymnosperm outgroup taxa, as estimated using maximum-likelihood analysis of 79 genes from 54 taxa in IQ-TREE. The dataset was partitioned by codon position. Ultrafast bootstrap support is indicated for each node.

**Figure A3.2.** Mean age inferences and associated 95% credibility intervals for six nodes in the angiosperm phylogeny with increasing numbers of clock-subsets ($k$), as inferred using an autocorrelated lognormal relaxed clock, clock-partitioning according to the optimal schemes identified in ClockstaR, and uniform calibration priors.

**Figure A3.3.** Mean age inferences and associated 95% credibility intervals for six nodes in the angiosperm phylogeny with increasing numbers of clock-subsets ($k$), as inferred using an autocorrelated lognormal relaxed clock, clock-partitioning according to relative rates of substitution, and uniform calibration priors.

**Figure A3.4.** Mean age inferences and associated 95% credibility intervals for six nodes in the angiosperm phylogeny with increasing numbers of clock-subsets ($k$), as inferred using an autocorrelated lognormal relaxed clock, clock-partitioning according to random assignment of genes to clock subsets, and uniform calibration priors. The estimates presented here are the averages of three random assignments of genes to clock-subsets for each value of $k$.

**Figure A3.5.** Mean age inferences and associated 95% credibility intervals for six nodes in the angiosperm phylogeny with increasing numbers of clock-subsets ($k$), as inferred using an uncorrelated lognormal relaxed clock, clock-partitioning according to the optimal schemes identified in ClockstaR, and gamma calibration priors.

**Figure A3.6.** Comparison of the posterior and prior distributions for six nodes of interest in the angiosperm phylogeny with increasing numbers of clock-subsets ($k$), as inferred using an uncorrelated lognormal relaxed clock with uniform calibration priors.

**Figure A3.7.** Comparison of the posterior and prior distributions for six nodes of interest in the angiosperm phylogeny with increasing numbers of clock-subsets ($k$), as inferred using an autocorrelated lognormal relaxed clock with uniform calibration priors.

**Figure A3.8.** Comparison of the posterior and prior distributions for six nodes of interest in the angiosperm phylogeny with increasing numbers of clock-subsets ($k$), as inferred using an uncorrelated lognormal relaxed clock with gamma calibration priors.