Figure A1.1. Phylogram depicting the relationship among selected angiosperm taxa and two gymnosperm outgroup taxa, as estimated using maximum-likelihood analysis of the first and second codon positions of 76 genes from 195 taxa in RAxML. The dataset was analysed using the optimal partitioning scheme of 28 partitions, as determined in PartitionFinder. Bootstrap support is indicated for each node.

Figure A1.2. Phylogram depicting the relationship among selected angiosperm taxa and two gymnosperm outgroup taxa, as estimated using maximum-likelihood analysis of the first and second codon positions of 76 genes from 195 taxa in RAxML. The dataset was partitioned by codon position. Bootstrap support is indicated for each node.

Figure A1.3. Phylogram depicting the relationship among selected angiosperm taxa and two gymnosperm outgroup taxa, as estimated using maximum-likelihood analysis of the first and second codon positions of 76 genes from 195 taxa in RAxML. The dataset was unpartitioned. Bootstrap support is indicated for each node.

Figure A1.4. Phylogram depicting the relationship among selected angiosperm taxa and two gymnosperm outgroup taxa, as estimated using maximum-likelihood analysis of all three codon positions of 76 genes from 195 taxa in RAxML. The dataset was partitioned by codon position. Bootstrap support is indicated for each node.

Figure A1.5. Phylogram depicting the relationship among selected angiosperm taxa and two gymnosperm outgroup taxa, as estimated using maximum-likelihood analysis of all three codon positions of 76 genes from 195 taxa in RAxML. The dataset was unpartitioned. Bootstrap support is indicated for each node.

Figure A1.6. Chronogram depicting the angiosperm evolutionary timescale, as estimated using Bayesian analysis of the first and second codon positions of 76 genes from 195 taxa, with 35 minimum and two maximum fossil constraints and an uncorrelated relaxed clock, in MCMCTREE. Mean ages (in millions of years) are indicated for nodes, with purple bars indicating the 95% credibility intervals for these nodes.

Figure A1.7. Chronogram depicting the angiosperm evolutionary timescale, as estimated using Bayesian analysis of the first and second codon positions of 76 genes from 195 taxa, with 35 minimum and two maximum fossil constraints and an uncorrelated relaxed clock, in MCMCTREE. In this analysis the mean of the gamma prior for the overall rate parameter was varied to be an order of magnitude faster than with the optimal settings ($\alpha =1$; $\beta = 1$). Mean ages (in millions of years) are indicated for nodes, with purple bars indicating the 95% credibility intervals for these nodes.

Figure A1.8. Chronogram depicting the angiosperm evolutionary timescale, as estimated using Bayesian analysis of the first and second codon positions of 76 genes from 195 taxa, with 35 minimum and two maximum fossil constraints and an uncorrelated relaxed clock, in MCMCTREE. In this analysis the mean of gamma prior for the overall rate parameter was varied to be an order of magnitude slower than the optimal settings ($\alpha =1$; $\beta = 100$). Mean ages (in millions of years) are indicated for nodes, with purple bars indicating the 95% credibility intervals for these nodes.

Figure A1.9. Chronogram depicting the angiosperm evolutionary timescale, as estimated using Bayesian analysis of the first and second codon positions of 76 genes from 195 taxa, with 35 minimum and two maximum fossil constraints and an uncorrelated relaxed clock, in MCMCTREE. In this analysis the mean of the gamma prior for rate variation across branches was varied by an order of magnitude from the optimal settings. Mean ages (in millions of years) are indicated for nodes, with purple bars indicating the 95% credibility intervals for these nodes.

Figure A1.10. Chronogram depicting the angiosperm evolutionary timescale, as estimated by sampling from the prior distribution of 35 minimum and two maximum fossil constraints using Bayesian analysis with an uncorrelated relaxed clock, in MCMCTREE. Mean ages (in millions of years) are indicated for nodes, with purple bars indicating the 95% credibility intervals for these nodes.

Figure A1.11. Chronogram depicting the angiosperm evolutionary timescale with *Amborella*+Nymphaeales constrained to be sister to all remaining angiosperms, as estimated using Bayesian analysis of the first and second codon positions of 76 genes from 195 taxa, with 35 minimum and two maximum fossil constraints and an uncorrelated relaxed clock, in MCMCTREE. Mean ages (in millions of years) are indicated for nodes, with purple bars indicating the 95% credibility intervals for these nodes.

Figure A1.12. Chronogram depicting the angiosperm evolutionary timescale, as estimated using Bayesian analysis of the first and second codon positions of 76 genes from 195 taxa, with 35 minimum and two maximum fossil constraints and an autocorrelated relaxed clock, in MCMCTREE. Mean ages (in millions of years) are indicated for nodes, with purple bars indicating the 95% credibility intervals for these nodes.

Figure A1.13. Chronogram depicting the angiosperm evolutionary timescale, as estimated using Bayesian analysis of the first and second codon positions of 76 genes from 195 taxa, with 35 minimum and two maximum fossil constraints and a strict clock, in MCMCTREE. Mean ages (in millions of years) are indicated for nodes, with purple bars indicating the 95% credibility intervals for these nodes.

Figure A1.14. Chronogram depicting the angiosperm evolutionary timescale, as estimated using Bayesian analysis of all three codon positions of 76 genes from 195 taxa, with 35 minimum and two maximum fossil constraints and an uncorrelated relaxed clock, in MCMCTREE. Mean ages (in millions of years) are indicated for nodes, with purple bars indicating the 95% credibility intervals for these nodes.

Figure A1.15. Corrected (GTR) vs uncorrected pairwise differences for (a) first and second codon positions, and (b) third codon positions for the 76-gene dataset. The dashed line represents equal corrected and uncorrected pair wise differences. The plot for third codon positions diverges rapidly and substantially from a linear relationship with increasing genetic distance, indicating strong saturation.

Figure A1.16. Chronogram depicting the angiosperm evolutionary timescale, as estimated

using Bayesian analysis of the third codon position of 76 genes from 195 taxa, with 35 minimum and two maximum fossil constraints and an uncorrelated relaxed clock, in MCMCTREE. Mean ages (in millions of years) are indicated for nodes, with purple bars indicating the 95% credibility intervals for these nodes.

Figure A1.17. Chronogram depicting the angiosperm evolutionary timescale, as estimated using Bayesian analysis of the first and second codon positions of three genes from 195 taxa, with 35 minimum and two maximum fossil constraints and an uncorrelated relaxed clock, in MCMCTREE. Mean ages (in millions of years) are indicated for nodes, with purple bars indicating the 95% credibility intervals for these nodes.

Figure A1.18. Chronogram depicting the angiosperm evolutionary timescale, as estimated using Bayesian analysis of the first and second codon positions of 11 genes from 195 taxa, with 35 minimum and two maximum fossil constraints and an uncorrelated relaxed clock, in MCMCTREE. Mean ages (in millions of years) are indicated for nodes, with purple bars indicating the 95% credibility intervals for these nodes.

Figure A1.19. Chronogram depicting the angiosperm evolutionary timescale, as estimated using Bayesian analysis of the first and second codon positions of 20 genes from 195 taxa, with 35 minimum and two maximum fossil constraints and an uncorrelated relaxed clock, in MCMCTREE. Mean ages (in millions of years) are indicated for nodes, with purple bars indicating the 95% credibility intervals for these nodes.

Figure A1.20. Chronogram depicting the angiosperm evolutionary timescale, as estimated using Bayesian analysis of the first and second codon positions of 30 genes from 195 taxa, with 35 minimum and two maximum fossil constraints and an uncorrelated relaxed clock, in MCMCTREE. Mean ages (in millions of years) are indicated for nodes, with purple bars indicating the 95% credibility intervals for these nodes.

Figure A1.21. Chronogram depicting the angiosperm evolutionary timescale, as estimated using Bayesian analysis of the first and second codon positions of 40 genes from 195 taxa, with 35 minimum and two maximum fossil constraints and an uncorrelated relaxed clock, in MCMCTREE. Mean ages (in millions of years) are indicated for nodes, with purple bars indicating the 95% credibility intervals for these nodes.

Figure A1.22. Chronogram depicting the angiosperm evolutionary timescale, as estimated using Bayesian analysis of the first and second codon positions of 50 genes from 195 taxa, with 35 minimum and two maximum fossil constraints and an uncorrelated relaxed clock, in MCMCTREE. Mean ages (in millions of years) are indicated for nodes, with purple bars indicating the 95% credibility intervals for these nodes.

Figure A1.23. Chronogram depicting the angiosperm evolutionary timescale, as estimated using Bayesian analysis of the first and second codon positions of 60 genes from 195 taxa, with 35 minimum and two maximum fossil constraints and an uncorrelated relaxed clock, in MCMCTREE. Mean ages (in millions of years) are indicated for nodes, with purple bars indicating the 95% credibility intervals for these nodes.

Figure A1.24. Chronogram depicting the angiosperm evolutionary timescale, as estimated using Bayesian analysis of the first and second codon positions of 70 genes from 195 taxa, with 35 minimum and two maximum fossil constraints and an uncorrelated relaxed clock, in MCMCTREE. Mean ages (in millions of years) are indicated for nodes, with purple bars indicating the 95% credibility intervals for these nodes.

Figure A1.25. Branch-specific substitution rates plotted against the midpoint ages of these branches, for a) first codon positions, and b) second codon positions. Both the rates and ages were estimated using Bayesian analysis of the first and second codon positions of 76 genes from 195 taxa, with 35 minimum and two maximum fossil constraints and an uncorrelated relaxed clock, in MCMCTREE.

Figure A1.26. Rategram, in which each branch length is proportional to the corresponding branch rate, as obtained through our main analysis of dataset CP12. This rategram is for locus 1, corresponding to 1st codon positions.

Figure A1.27. Rategram, in which each branch length is proportional to the corresponding branch rate, as obtained through our main analysis of dataset CP12. This rategram is for locus 2, corresponding to 2nd codon positions.

Figure A1.28. Chronogram depicting the angiosperm evolutionary timescale, as estimated using Bayesian analysis of the first and second codon positions of 76 genes from 74 taxa, with 26 minimum and two maximum fossil constraints and an uncorrelated relaxed clock, in MCMCTREE. Prior to this analysis, all current or ancestrally herbaceous taxa, as inferred through ancestral state reconstruction, were removed from the data set. Mean ages (in millions of years) are indicated for nodes, with purple bars indicating the 95% credibility intervals for these nodes.

Figure A1.29. Chronogram depicting the angiosperm evolutionary timescale, as estimated using Bayesian analysis of the first and second codon positions of 76 genes from 195 taxa, with 35 minimum and two maximum fossil constraints and an uncorrelated relaxed clock, in MCMCTREE. In this analysis the sampling proportion (s) parameter for the birth-death-process tree prior was set to 0.001. Mean ages (in millions of years) are indicated for nodes, with purple bars indicating the 95% credibility intervals for these nodes.

Figure A1.30. Chronogram depicting the angiosperm evolutionary timescale, as estimated using Bayesian analysis of the first and second codon positions of 76 genes from 195 taxa, with 35 minimum and two maximum fossil constraints and an uncorrelated relaxed clock, in MCMCTREE. In this analysis the sampling proportion (s) parameter for the birth-death-process tree prior was set to 0.01. Mean ages (in millions of years) are indicated for nodes, with purple bars indicating the 95% credibility intervals for these nodes.

Figure A1.31. Chronogram depicting the angiosperm evolutionary timescale, as estimated using Bayesian analysis of the first and second codon positions of 76 genes from 195 taxa, with 35 minimum and two maximum fossil constraints and an uncorrelated relaxed clock, in MCMCTREE. In this analysis the sampling proportion (s) parameter for the birth-death-process tree prior was set to 0.1. Mean ages (in millions of years) are indicated for nodes,

with purple bars indicating the 95% credibility intervals for these nodes.

Figure A1.32. Chronogram depicting the angiosperm evolutionary timescale, as estimated using Bayesian analysis of the first and second codon positions of 76 genes from 195 taxa, with 35 minimum and two maximum fossil constraints and an uncorrelated relaxed clock, in MCMCTREE. In this analysis the sampling proportion (s) parameter for the birth-death-process tree prior was set to 1. Mean ages (in millions of years) are indicated for nodes, with purple bars indicating the 95% credibility intervals for these nodes.

Figure A1.33. Chronogram depicting the angiosperm evolutionary timescale, as estimated using Bayesian analysis of the first and second codon positions of 76 genes from 195 taxa, with 35 minimum and two maximum fossil constraints and an uncorrelated relaxed clock, in MCMCTREE. In this analysis the birth rate (λ) parameter of the birth-death-process tree prior was set to 1, and the death rate parameter (μ) was set to 0, to represent zero extinction. Mean ages (in millions of years) are indicated for nodes, with purple bars indicating the 95% credibility intervals for these nodes.

Figure A1.34. Chronogram depicting the angiosperm evolutionary timescale, as estimated using Bayesian analysis of the first and second codon positions of 76 genes from 195 taxa, with 35 minimum and two maximum fossil constraints and an uncorrelated relaxed clock, in MCMCTREE. In this analysis the birth rate (λ) parameter of the birth-death-process tree prior was set to 1, and the death rate parameter (μ) was set to 0.5, to represent medium extinction. Mean ages (in millions of years) are indicated for nodes, with purple bars indicating the 95% credibility intervals for these nodes.

Figure A1.35. Chronogram depicting the angiosperm evolutionary timescale, as estimated using Bayesian analysis of the first and second codon positions of 76 genes from 195 taxa, with 35 minimum and two maximum fossil constraints and an uncorrelated relaxed clock, in MCMCTREE. In this analysis the birth rate (λ) parameter of the birth-death-process tree prior was set to 1, and the death rate parameter (μ) was set to 0.9, to represent high extinction. Mean ages (in millions of years) are indicated for nodes, with purple bars indicating the 95% credibility intervals for these nodes.

Figure A1.36. Chronogram depicting the angiosperm evolutionary timescale, as estimated using Bayesian analysis of the first and second codon positions of 76 genes from 195 taxa, with 35 minimum and two maximum fossil constraints and an uncorrelated relaxed clock, in MCMCTREE. In this analysis, we used a published estimate of the angiosperm diversification rate assuming a relaxed crown age with a low relative death rate (ε) (derived from Magallón S., Castillo A. 2009. Angiosperm diversification through time. Am. J. Bot. 96:349–365) to obtain values for the birth- (λ) and death-rate (μ) parameters of the birth-death-process tree prior. This led to values of $\lambda=0.0489$ and $\mu=0$ when assuming a relative death rate of 0. Mean ages (in millions of years) are indicated for nodes, with purple bars indicating the 95% credibility intervals for these nodes.

Figure A1.37. Chronogram depicting the angiosperm evolutionary timescale, as estimated using Bayesian analysis of the first and second codon positions of 76 genes from 195 taxa, with 35 minimum and two maximum fossil constraints and an uncorrelated relaxed clock, in

MCMCTREE. In this analysis, we used a published estimate of the angiosperm diversification rate assuming a relaxed crown age with a high relative death rate (ε) (derived from Magallón S., Castillo A. 2009. Angiosperm diversification through time. Am. J. Bot. 96:349–365) to obtain values for the birth- (λ) and death-rate (μ) parameters of the birth-death-process tree prior. This led to values of $\lambda=0.42$ and $\mu=0.378$ when assuming a relative death rate of 0.9. Mean ages (in millions of years) are indicated for nodes, with purple bars indicating the 95% credibility intervals for these nodes.

Figure A1.38. Chronogram depicting the angiosperm evolutionary timescale, as estimated using penalized-likelihood analysis of 76 genes from 195 taxa with 35 minimum and two maximum fossil constraints in r8s. Median ages (in millions of years) are indicated for nodes, with purple bars indicating the 95% bootstrap confidence intervals for these nodes.

Figure A1.39. Chronogram depicting the angiosperm evolutionary timescale, as estimated using Bayesian analysis of the first and second codon positions of 76 genes from 195 taxa, with 35 minimum and two maximum fossil constraints and an uncorrelated relaxed clock, in MCMCTREE. In this analysis, all calibrations were implemented as gamma priors. Mean ages (in millions of years) are indicated for nodes, with purple bars indicating the 95% credibility intervals for these nodes.

Figure A1.40. Chronogram depicting the angiosperm evolutionary timescale, as estimated using Bayesian analysis of the first and second codon positions of 76 genes from 195 taxa, with 35 minimum and two maximum fossil constraints and an uncorrelated relaxed clock, in MCMCTREE. In this analysis, all calibrations were implemented as gamma priors, but without any direct constraint on the angiosperm maximum age. Mean ages (in millions of years) are indicated for nodes, with purple bars indicating the 95% credibility intervals for these nodes.

Figure A1.41. Chronogram depicting the angiosperm evolutionary timescale, as estimated using Bayesian analysis of 76 genes from 195 taxa with 35 minimum and two maximum fossil constraints in MCMCTREE. Mean ages (in millions of years) are indicated for nodes, with purple bars indicating the 95% credibility intervals for these nodes. A strong maximum age constraint of 139.35–138.7 Ma for crown-group angiosperms was used in this analysis as a means of comparison with Magallón S., Gómez-Acevedo S., Sánchez-Reyes L.L. & Hernández-Hernández T. 2015. A metacalibrated time-tree documents the early rise of flowering plant phylogenetic diversity. New Phytol. 207:437–453. Mean ages (in millions of years) are indicated for nodes, with purple bars indicating the 95% credibility intervals for these nodes.

Figure A1.42. A comparison of the ages inferred in this study for important angiosperm nodes, using a maximum of 139.35 Ma on the angiosperm crown node, with those inferred by Magallón S., Gómez-Acevedo S., Sánchez-Reyes L.L. & Hernández-Hernández T. 2015. A metacalibrated timetree documents the early rise of flowering plant phylogenetic diversity. New Phytol. 207:437–453. We used an uncorrelated relaxed clock with uniform calibration priors.

Figure A1.43. Branch-specific substitution rates plotted against the midpoint ages of these

branches, for a) first codon positions, and b) second codon positions. Both the rates and ages were estimated using Bayesian analysis of the first and second codon positions of 76 genes from 195 taxa, with 35 minimum and two maximum fossil constraints and an uncorrelated relaxed clock, in MCMCTREE.

Figure A1.44. Rategram, in which each branch length is proportional to the corresponding branch rate, as obtained through our analysis of dataset CP12 with a maximum constraint for the angiosperm crown node of 139.35 Ma. This rategram is for locus 1, corresponding to 1st codon positions.

Figure A1.45. Rategram, in which each branch length is proportional to the corresponding branch rate, as obtained through our analysis of dataset CP12 with a maximum constraint for the angiosperm crown node of 139.35 Ma. This rategram is for locus 2, corresponding to 2nd codon positions.

Figure A1.46. Chronogram depicting the angiosperm evolutionary timescale, as estimated using Bayesian analysis of 76 genes from 195 taxa with 35 minimum and two maximum fossil constraints in MCMCTREE. Mean ages (in millions of years) are indicated for nodes, with purple bars indicating the 95% credibility intervals for these nodes. A maximum age constraint of 248 Ma for crown-group angiosperms was used in this analysis. Mean ages (in millions of years) are indicated for nodes, with purple bars indicating the 95% credibility intervals for these nodes.

Figure A1.47. Chronogram depicting the angiosperm evolutionary timescale, as estimated using Bayesian analysis of 76 genes from 195 taxa with 35 minimum and two maximum fossil constraints in MCMCTREE. Mean ages (in millions of years) are indicated for nodes, with purple bars indicating the 95% credibility intervals for these nodes. A maximum age constraint of 300 Ma for the divergence between angiosperms and gymnosperms was used in this analysis. Mean ages (in millions of years) are indicated for nodes, with purple bars indicating the 95% credibility intervals for these nodes.

Figure A1.48. Chronogram depicting the angiosperm evolutionary timescale, as estimated using Bayesian analysis of 76 genes from 195 taxa with 35 minimum and two maximum fossil constraints in MCMCTREE. Mean ages (in millions of years) are indicated for nodes, with purple bars indicating the 95% credibility intervals for these nodes. A maximum age constraint of 330 Ma for the divergence between angiosperms and gymnosperms was used in this analysis. Mean ages (in millions of years) are indicated for nodes, with purple bars indicating the 95% credibility intervals for these nodes.

Figure A1.49. Chronogram depicting the angiosperm evolutionary timescale, as estimated using Bayesian analysis of 76 genes from 195 taxa with 35 minimum and two maximum fossil constraints in MCMCTREE. Mean ages (in millions of years) are indicated for nodes, with purple bars indicating the 95% credibility intervals for these nodes. A maximum age constraint of 366 Ma for the divergence between angiosperms and gymnosperms was used in this analysis. Mean ages (in millions of years) are indicated for nodes, with purple bars indicating the 95% credibility intervals for these nodes.

Figure A1.50. Chronogram depicting the angiosperm evolutionary timescale, as estimated using Bayesian analysis of 76 genes from 195 taxa with 35 minimum and two maximum fossil constraints in MCMCTREE. Mean ages (in millions of years) are indicated for nodes, with purple bars indicating the 95% credibility intervals for these nodes. A maximum age constraint of 454 Ma for the divergence between angiosperms and gymnosperms was used in this analysis. Mean ages (in millions of years) are indicated for nodes, with purple bars indicating the 95% credibility intervals for these nodes.

Figure A1.51. Chronogram depicting the angiosperm evolutionary timescale, as estimated using Bayesian analysis of 76 genes from 195 taxa with 35 minimum and two maximum fossil constraints in MCMCTREE. Mean ages (in millions of years) are indicated for nodes, with purple bars indicating the 95% credibility intervals for these nodes. A maximum age constraint of 1024 Ma for the divergence between angiosperms and gymnosperms was used in this analysis. Mean ages (in millions of years) are indicated for nodes, with purple bars indicating the 95% credibility intervals for these nodes.

Figure A1.52. Chronogram depicting the angiosperm evolutionary timescale, as estimated using Bayesian analysis of the first and second codon positions of 76 genes from 195 taxa, with 35 minimum and two maximum fossil constraints and an uncorrelated relaxed clock, in MCMCTREE.In this analysis, all calibrations were implemented with hard bounds. Mean ages (in millions of years) are indicated for nodes, with purple bars indicating the 95% credibility intervals for these nodes.