APPENDIX 1

Online supplementary information

This appendix contains the following supplemental materials:

Page

Table S1. Number of BEAST analyses of simulated alignments that failed to converge of in which any of the parameters failed to achieve a minimum effective sample size (ESS) of at least 200 after 200 million steps of the Markov chain Monte Carlo simulation. Numbers given are out of 100 replicates for each combination of tree prior, speciation scenario, and information level of the sequence alignment.

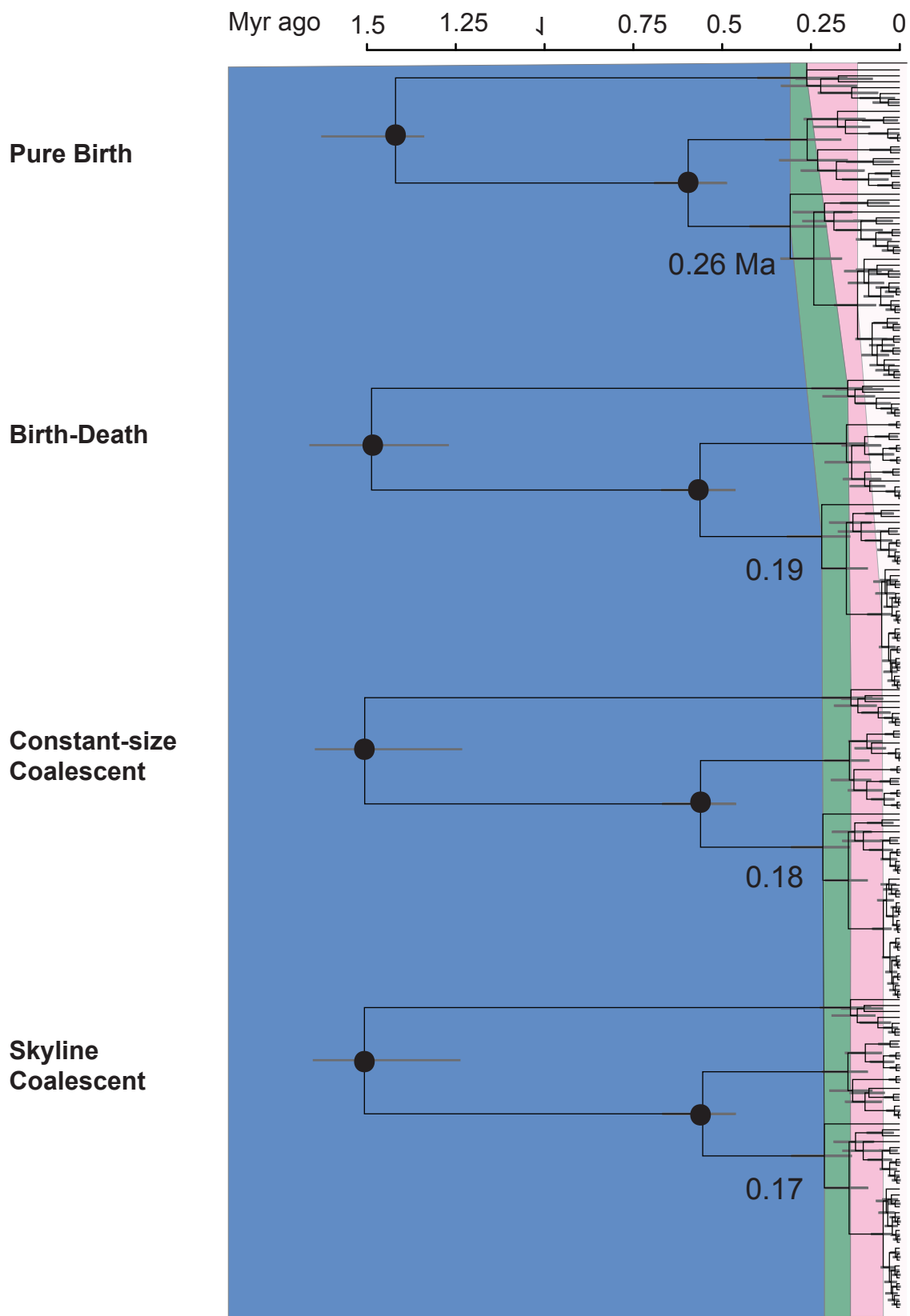|	LOW information					HIGH information				
Number of species	**1**	**2**	**5**	**25**	**50**	**1**	**2**	**5**	**25**	**50**
Pure birth	-	50	81	-	-	2	79	95	-	-
Birth-death	-	19	-	-	-	-	-	-	-	-
Constant-size coalescent	-	17	17	-	-	-	13	79	-	-
Skyline coalescent	-	9	-	-	-	16	1	-	-	-

Figure S1. Visual comparison of median age estimates for divergences

in a whitefish (*Coregonus*) dataset under four different tree priors. Selected nodes are

joined to their equivalents in other trees by the colored contour lines. Gray bars indicate

95% highest posterior density intervals. Black circles indicate calibrated nodes. Ages are

given in text for nodes on the first contour. Estimates of node times under the pure-birth tree

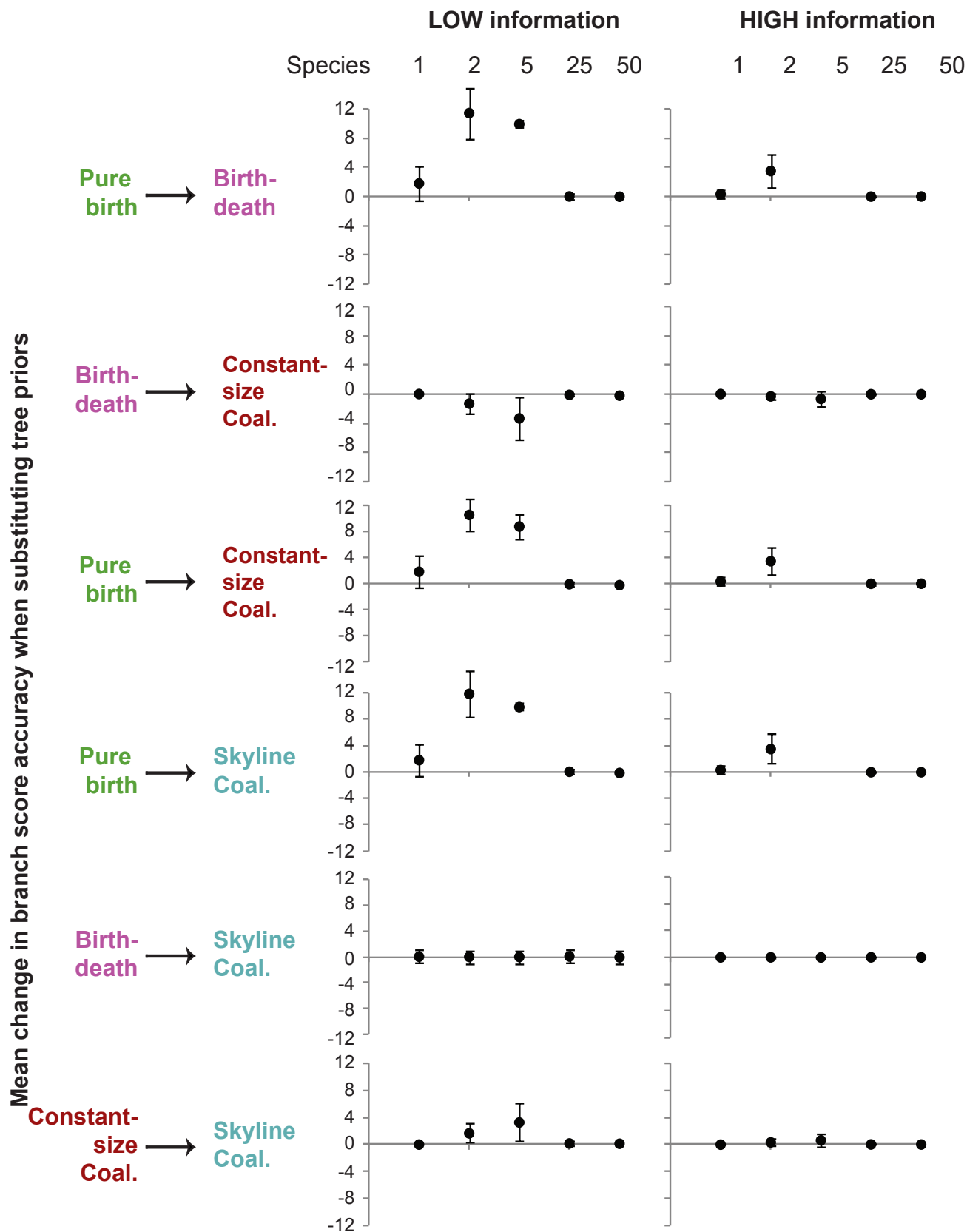prior are seen to be older than those inferred under the other priors.

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Figure S2. Impact of changing tree priors on the accuracy of simulated alignments with 50 taxa divided into 1, 2, 5, 25, or 50 species and generated with HIGH and LOW numbers of informative sites. The vertical axis shows the average change in branch score accuracy when substituting priors as indicated. The branch score accuracy is the negative of the branch score distance between the true tree and the median-node-height estimate. For trees with identical topologies, the branch score distance is the square root of the sum of squared differences in lengths of equivalent branches between two trees. Dashed lines indicate missing results.
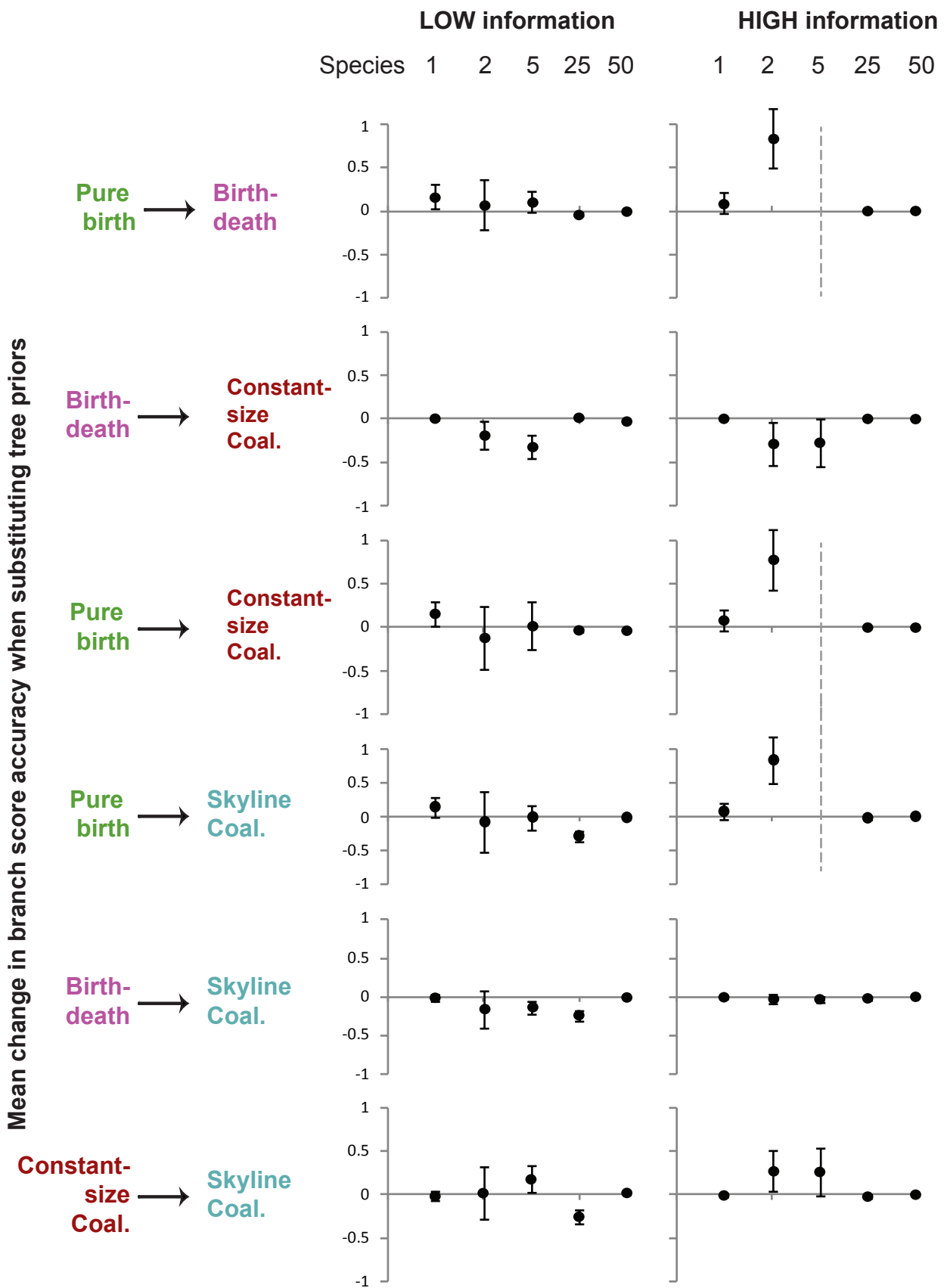
Figure S3. Impact of changing tree priors on the normalised highest posterior density (HPD) precision of simulated alignments with 50 taxa divided into 1, 2, 5, 25 or 50 species and generated on HIGH and LOW numbers of informative sites. The vertical axis shows the average change in normalised HPD precision when substituting priors as indicated. Normalised HPD precision is the negative of the average size of 95% HPD intervals across the tree, where HPD range is expressed as a proportion of the median node height estimate. Dashed lines indicate results omitted due to high failure rates.
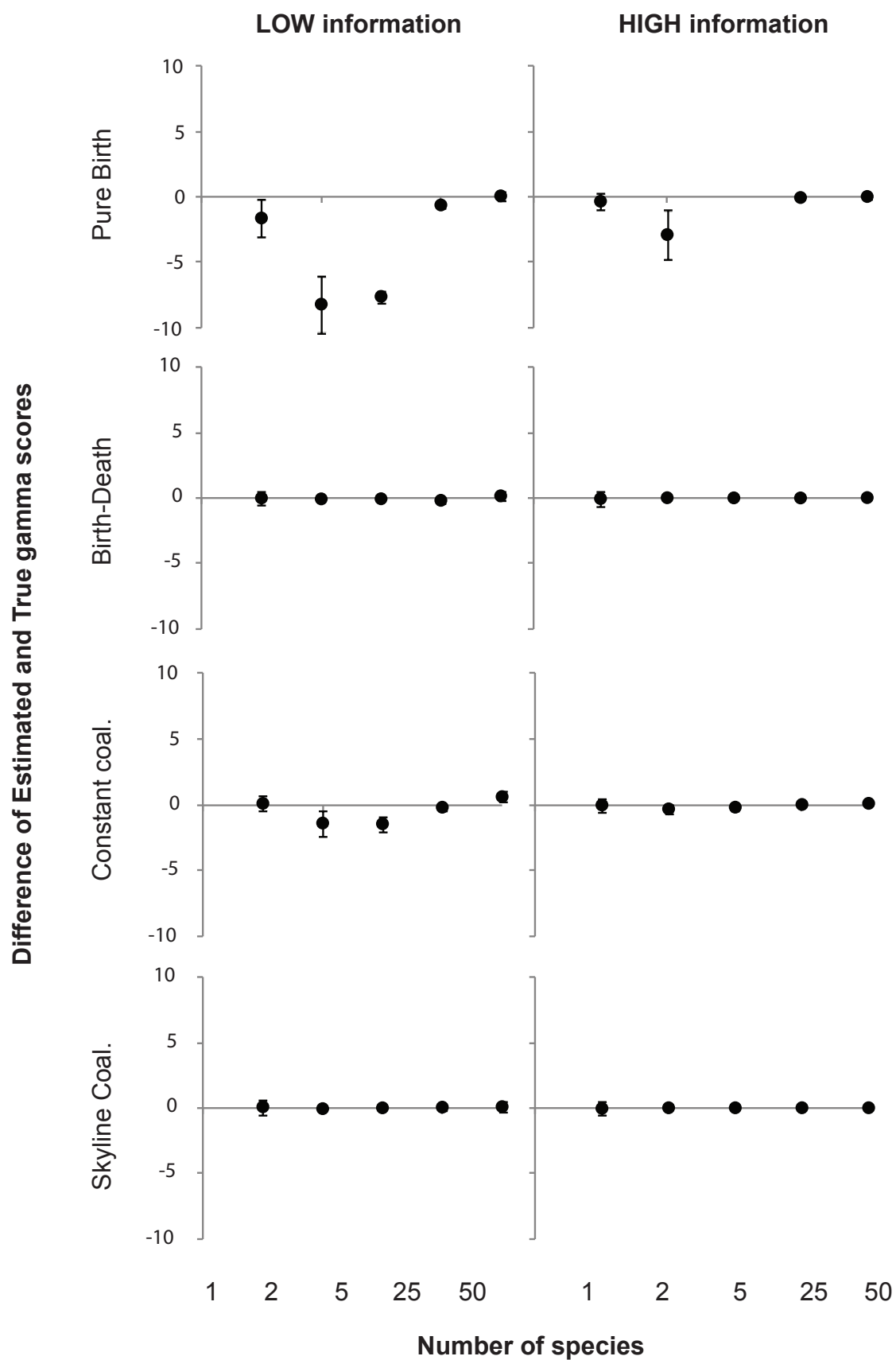
Figure S4. Mean differences between gamma statistics for simulated trees and estimates of the same trees under various tree priors. Trees were simulated with 50 taxa divided into 1, 2, 5 and 50 species. Separate sets of alignments were generated conditional on HIGH and LOW numbers of informative sites. A value of zero indicates that gamma values were similar to those for the true trees. Negative values indicate that the distribution of estimated node times is more consistent with a pure birth process than the true distribution.