

# Morphological phylogenetics evaluated using novel evolutionary simulations

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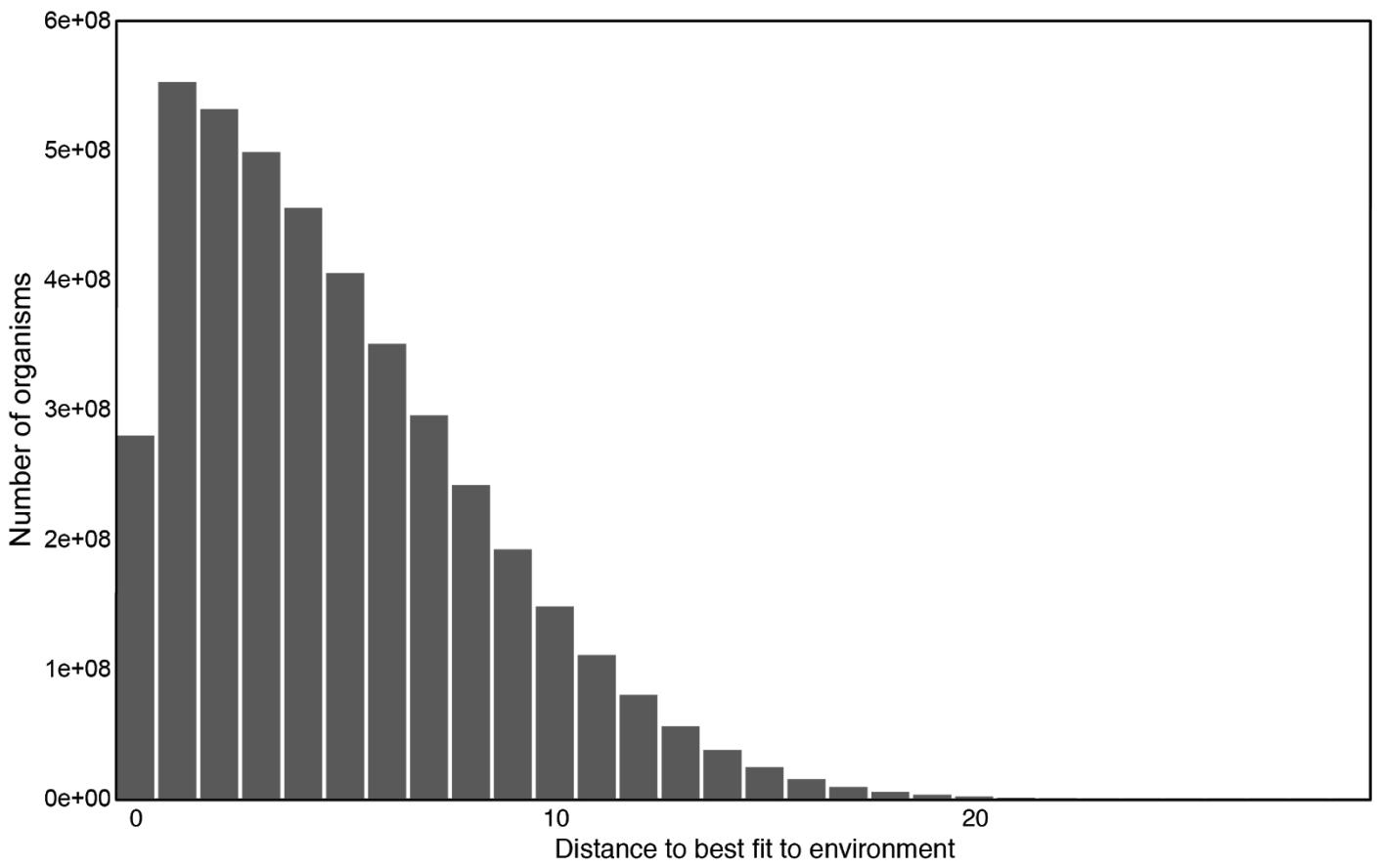
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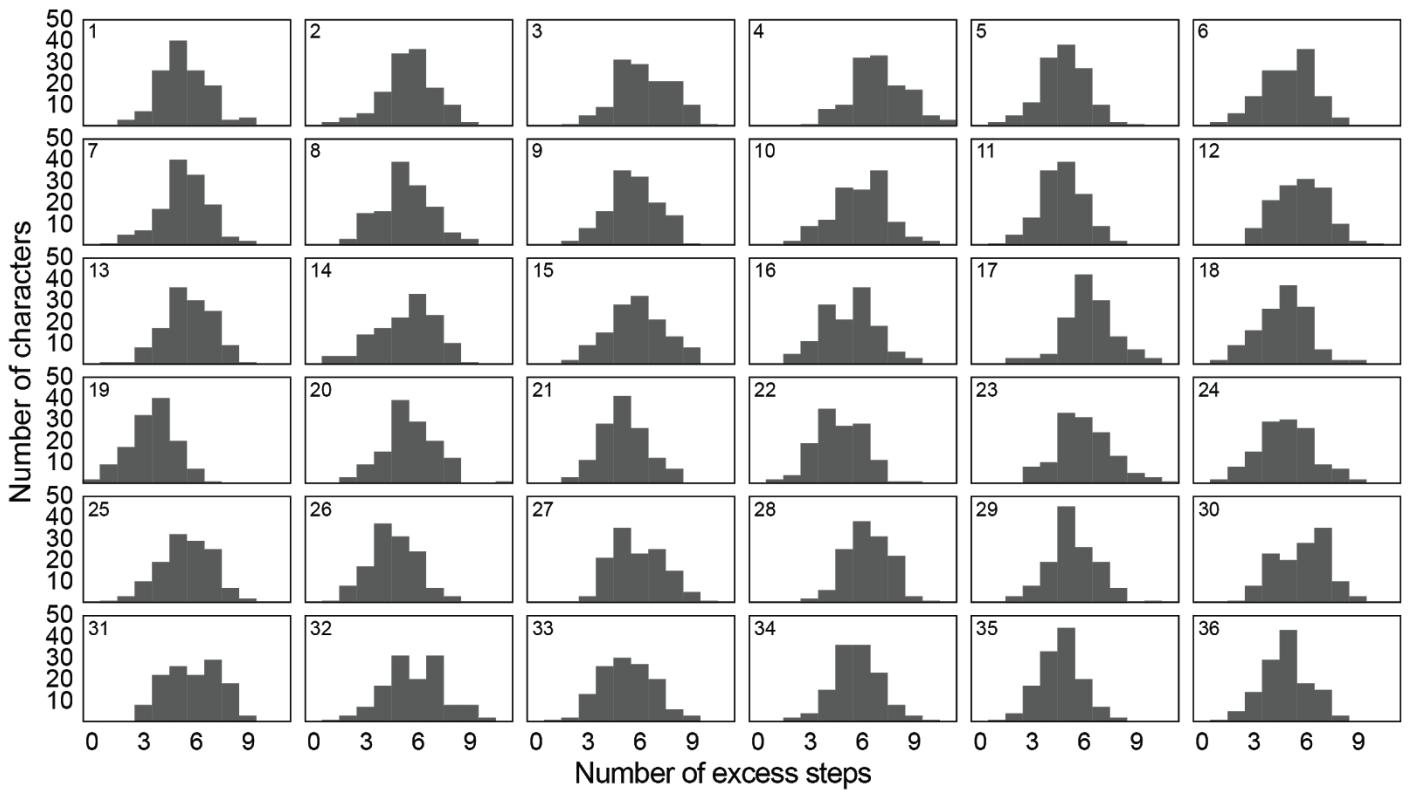
## Supplementary Information

	Characters		
Model	128	512	1024
MBL2017	2,000,000	2,000,000	2,000,000
TREvoSim	2,000,000	10,000,000	25,000,000

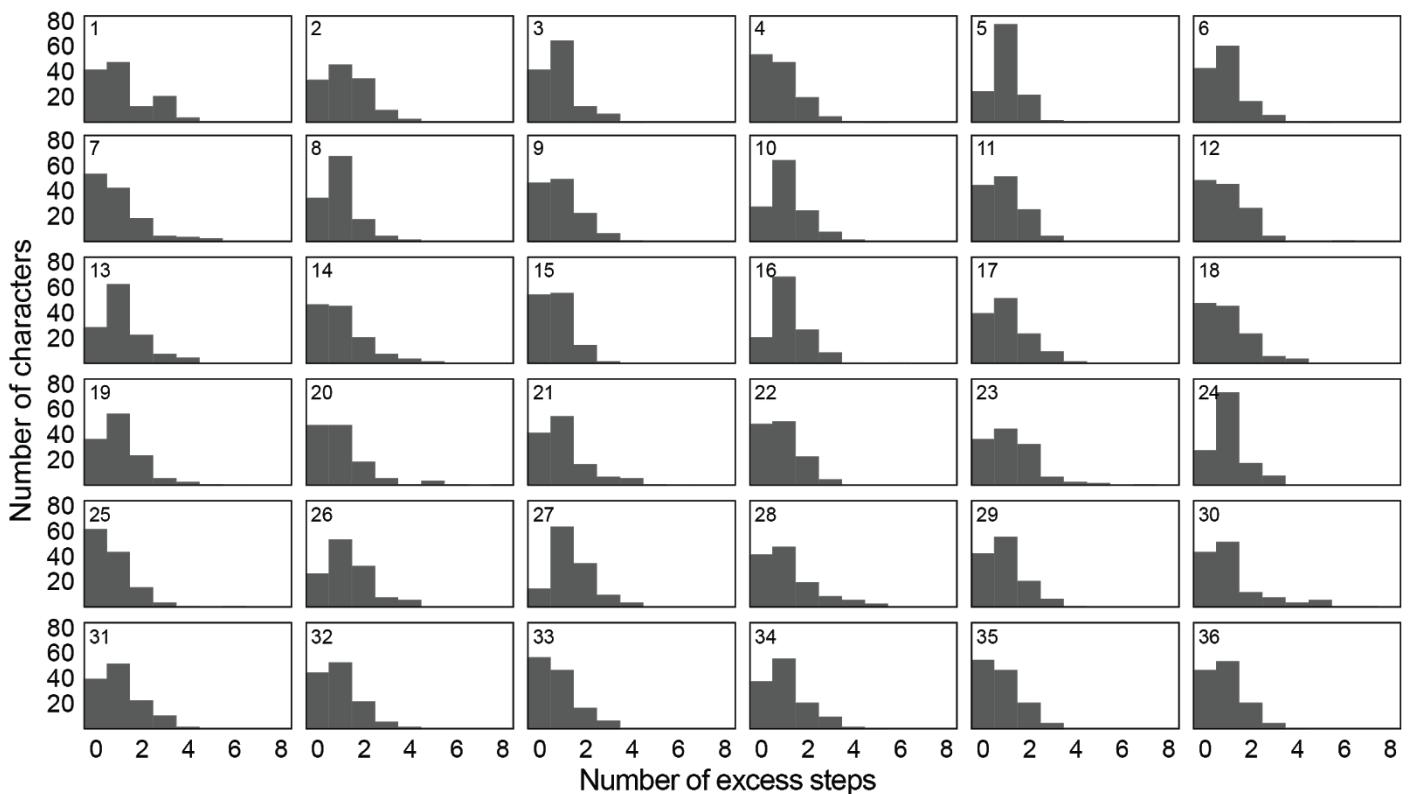
Supplementary table 1. Number of generations used in MrBayes analysis per character number and model.



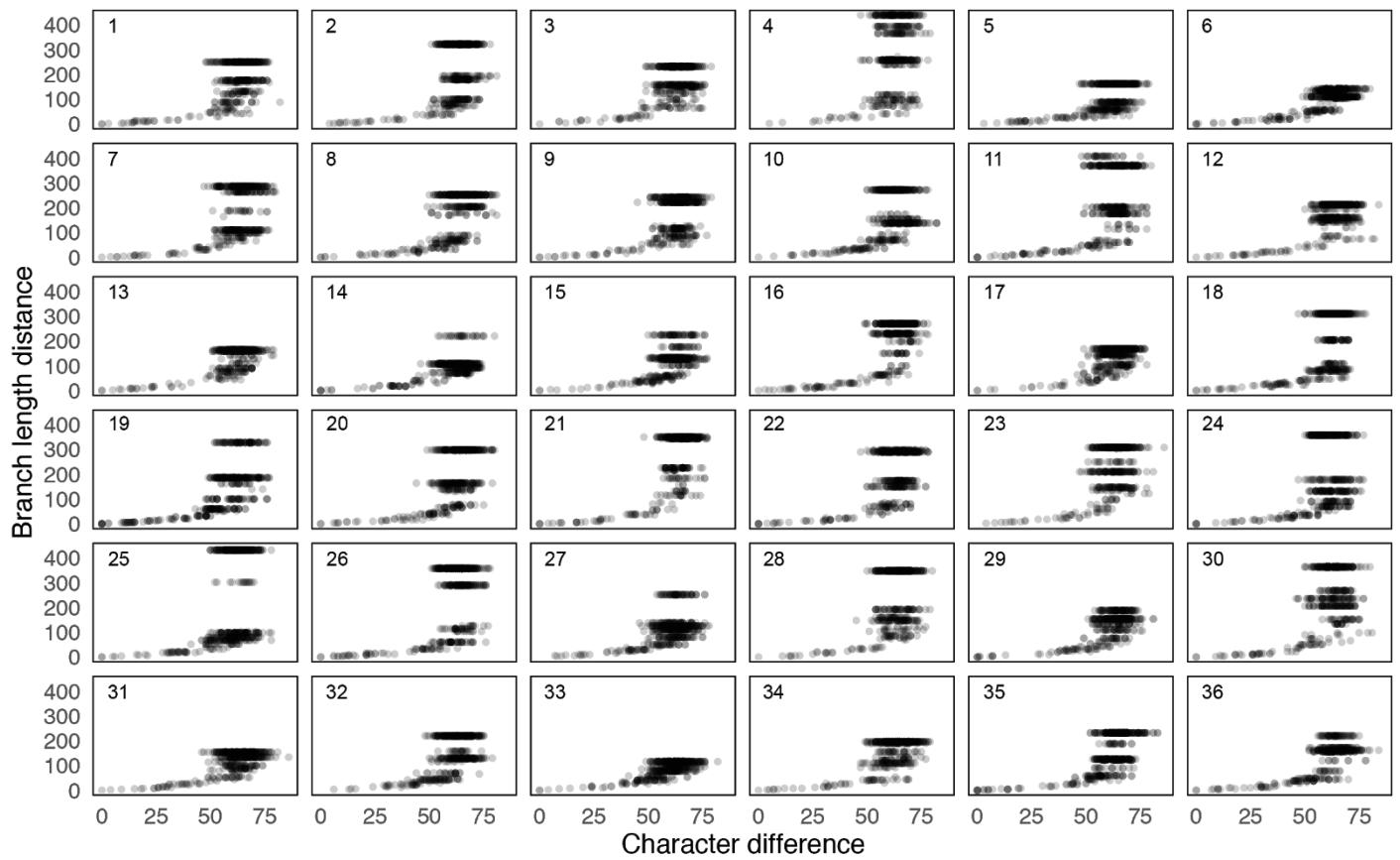
*Supplementary Figure 1. A histogram showing the distance to best fit to environment (=0) computed for all possible 32-bit organisms, using five masks.*



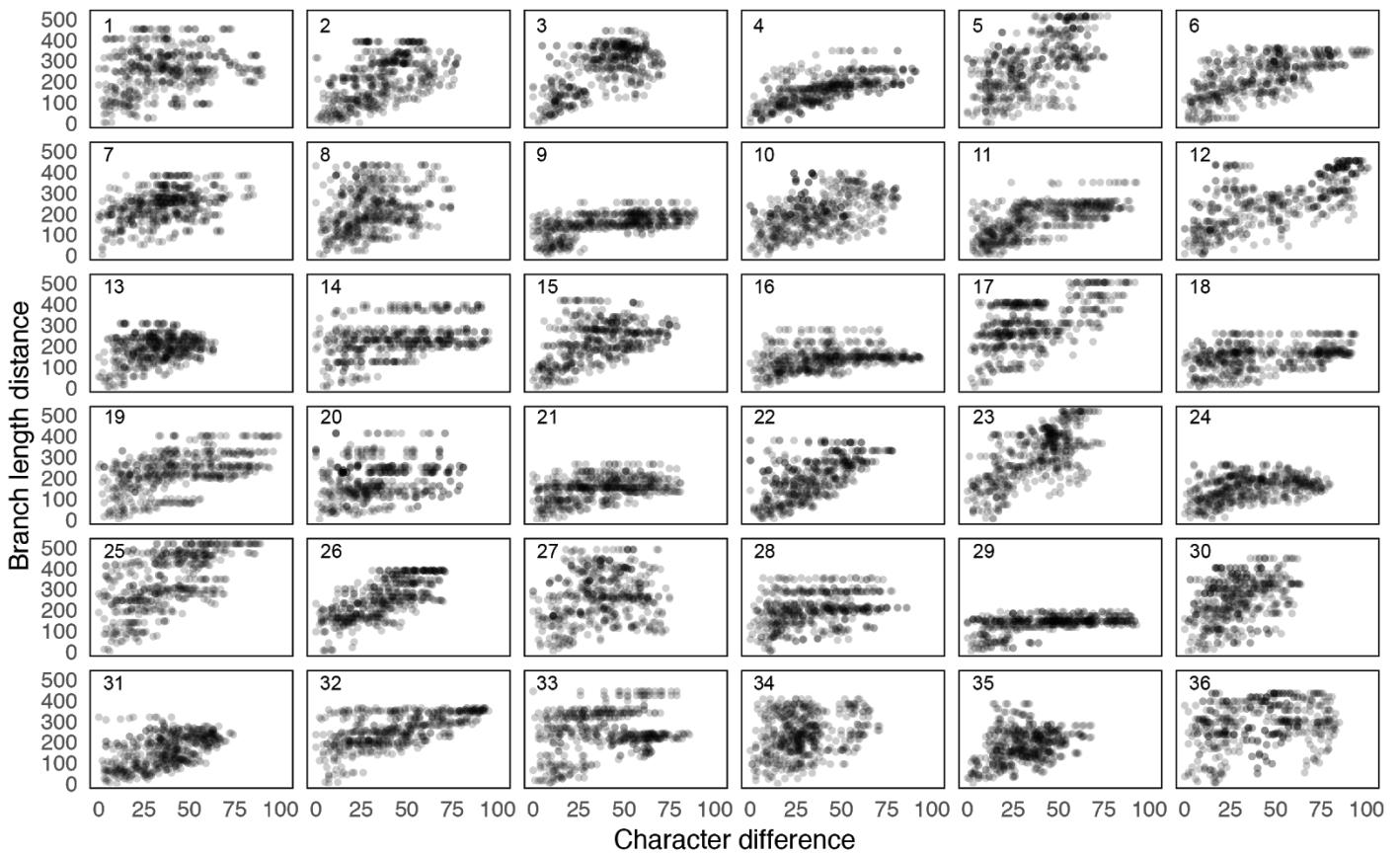
*Supplementary Figure 2. Histograms showing the distribution of characters for additional parsimony steps (above the minimum number of steps (=1)) calculated using the true tree for 36 datasets simulated using MBL2017, 128 characters.*



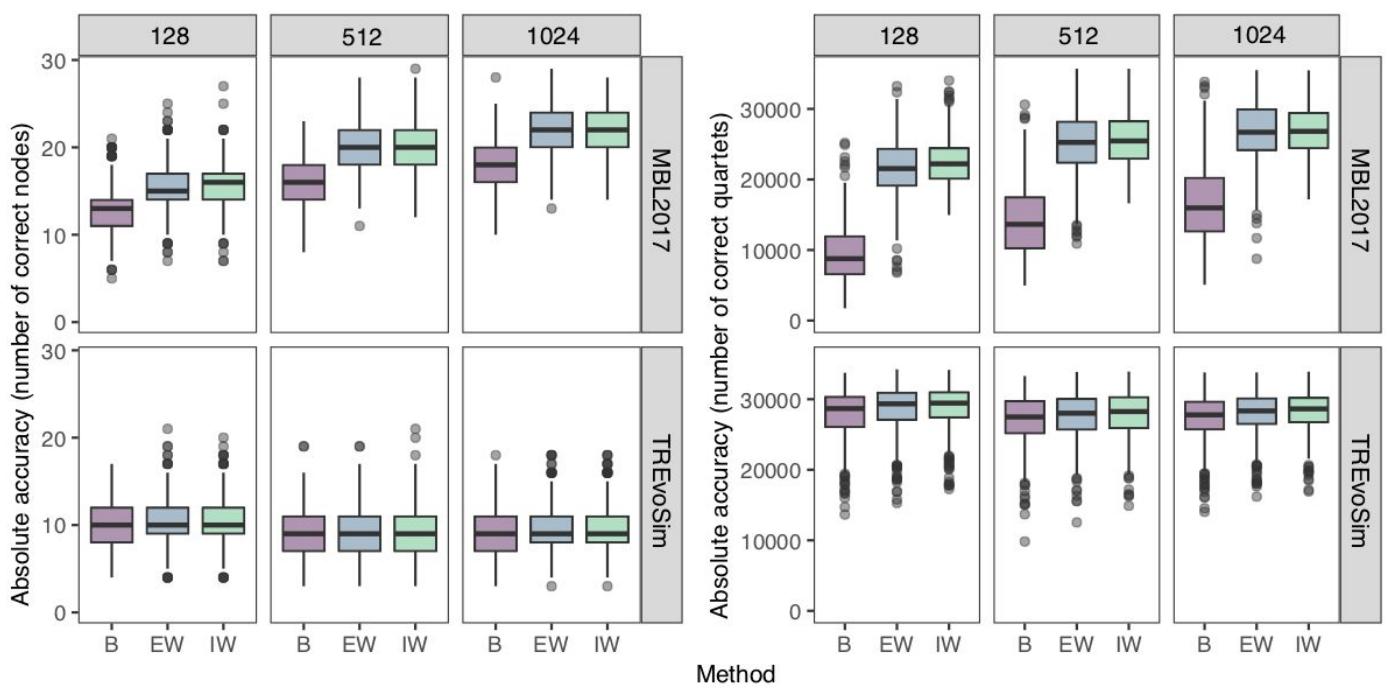
*Supplementary Figure 3. Histograms showing the distribution of characters for additional parsimony steps (above the minimum number of steps (=1)) calculated using the true tree for 36 datasets simulated using TREvSim, 128 characters.*



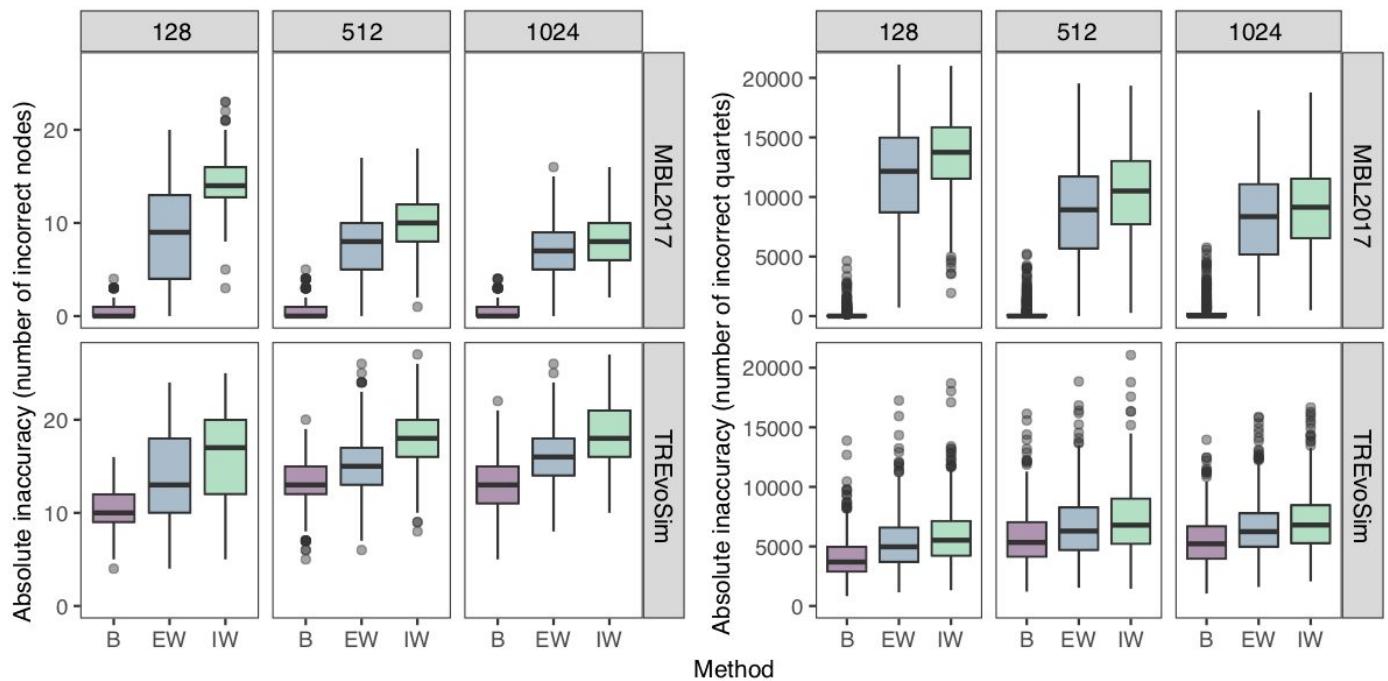
*Supplementary Figure 4. Visualization of morphological coherence. Scatter plot of branch length distance against character difference of taxon pairs for 36 MBL2017 datasets of 128 characters.*



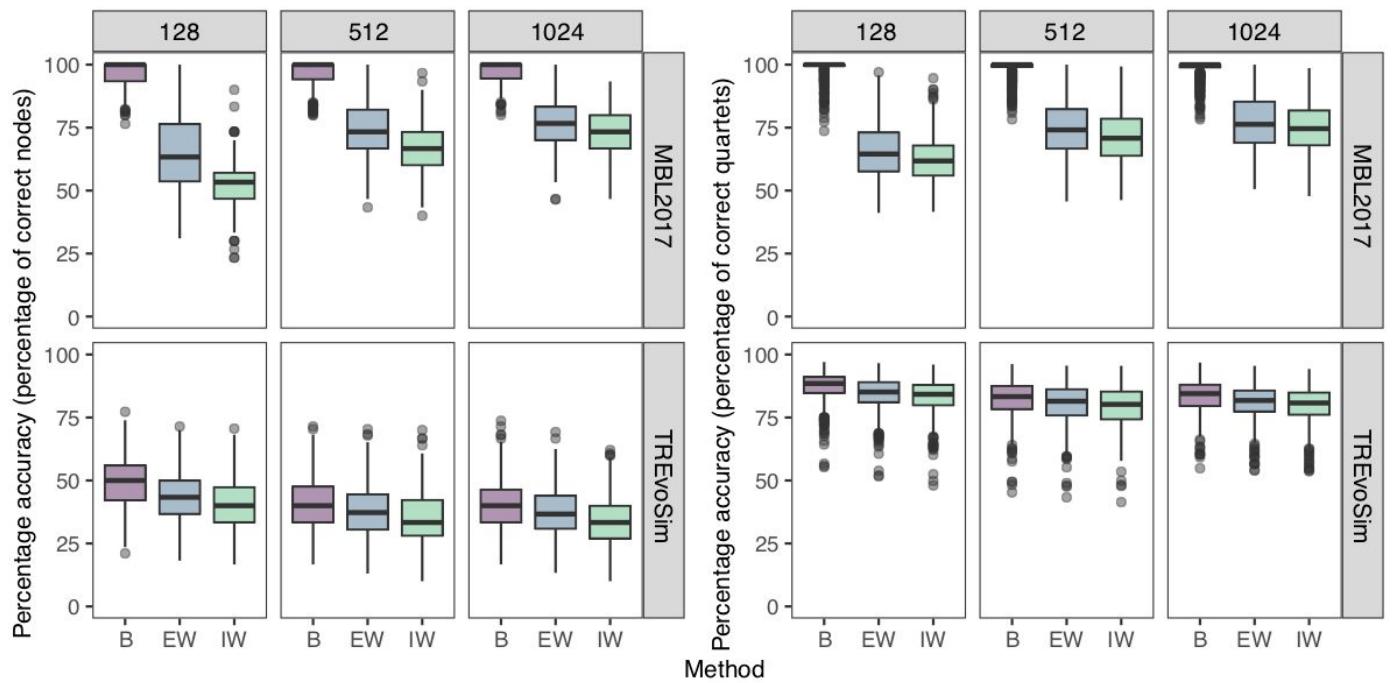
*Supplementary Figure 5. Visualization of morphological coherence. Scatter plot of branch length distance against character difference of taxon pairs for 36 TREvoSim datasets of 128 characters.*



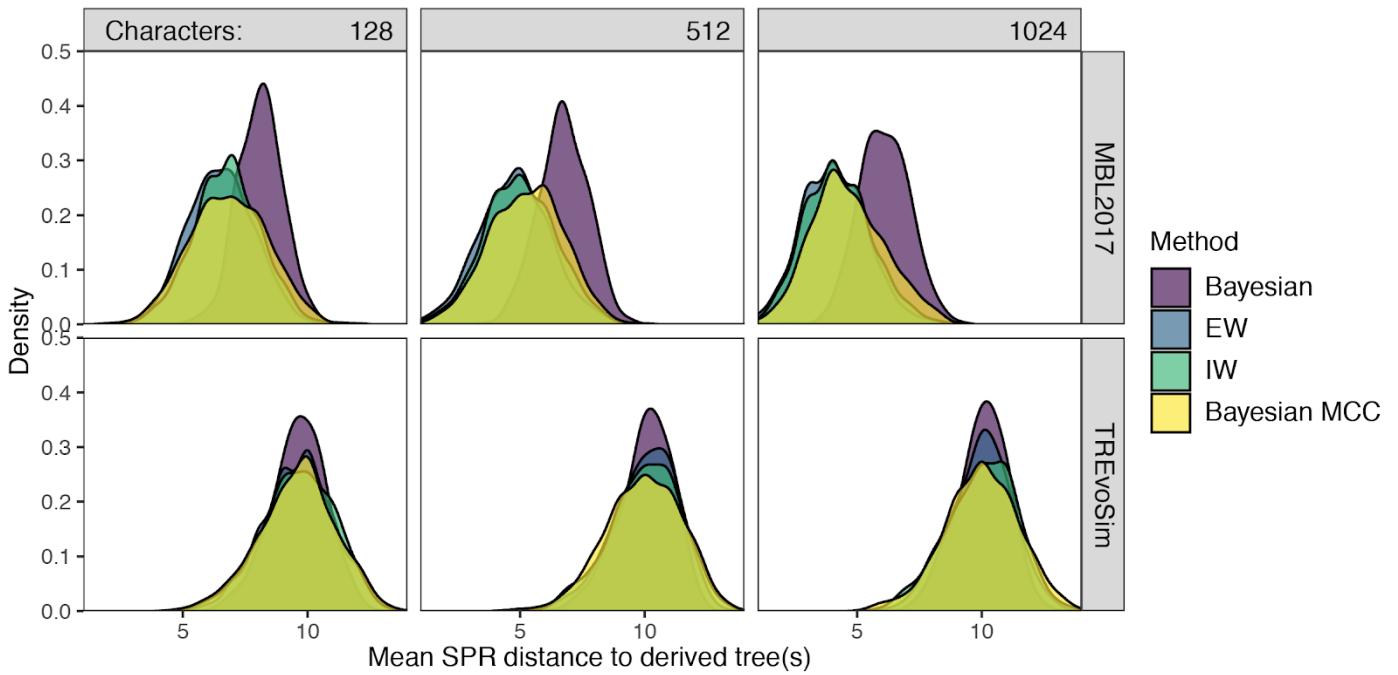
*Supplementary Figure 6. Box plots showing the absolute accuracy (in number of correct nodes and number of correct quartets) of the standard consensus trees for Bayesian inference (B), equal weighting parsimony (EW) and implied weighting parsimony (IW). 500 replicates; 128, 512, and 1024 characters.*



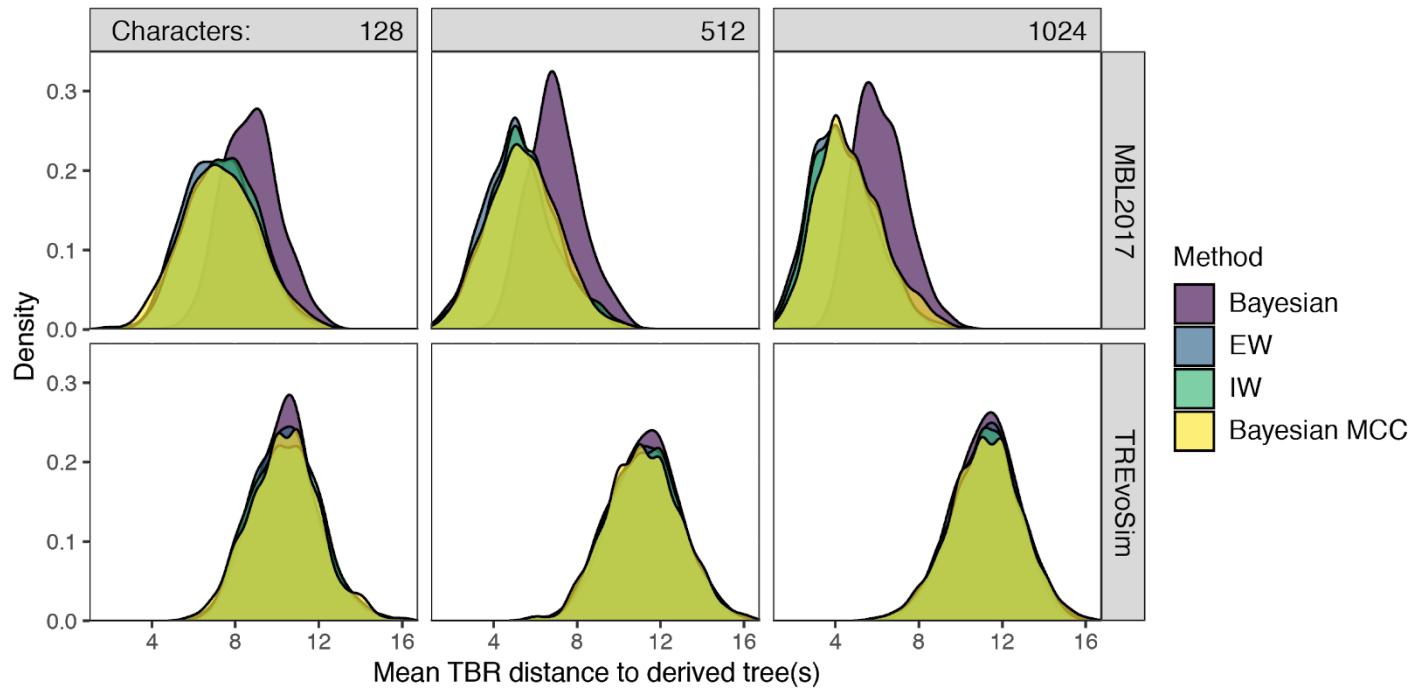
*Supplementary Figure 7.* Box plots showing the absolute inaccuracy (in number of incorrect nodes and number of incorrect quartets) of the standard consensus trees for Bayesian inference (B), equal weighting parsimony (EW) and implied weighting parsimony (IW). 500 replicates; 128, 512, and 1024 characters.



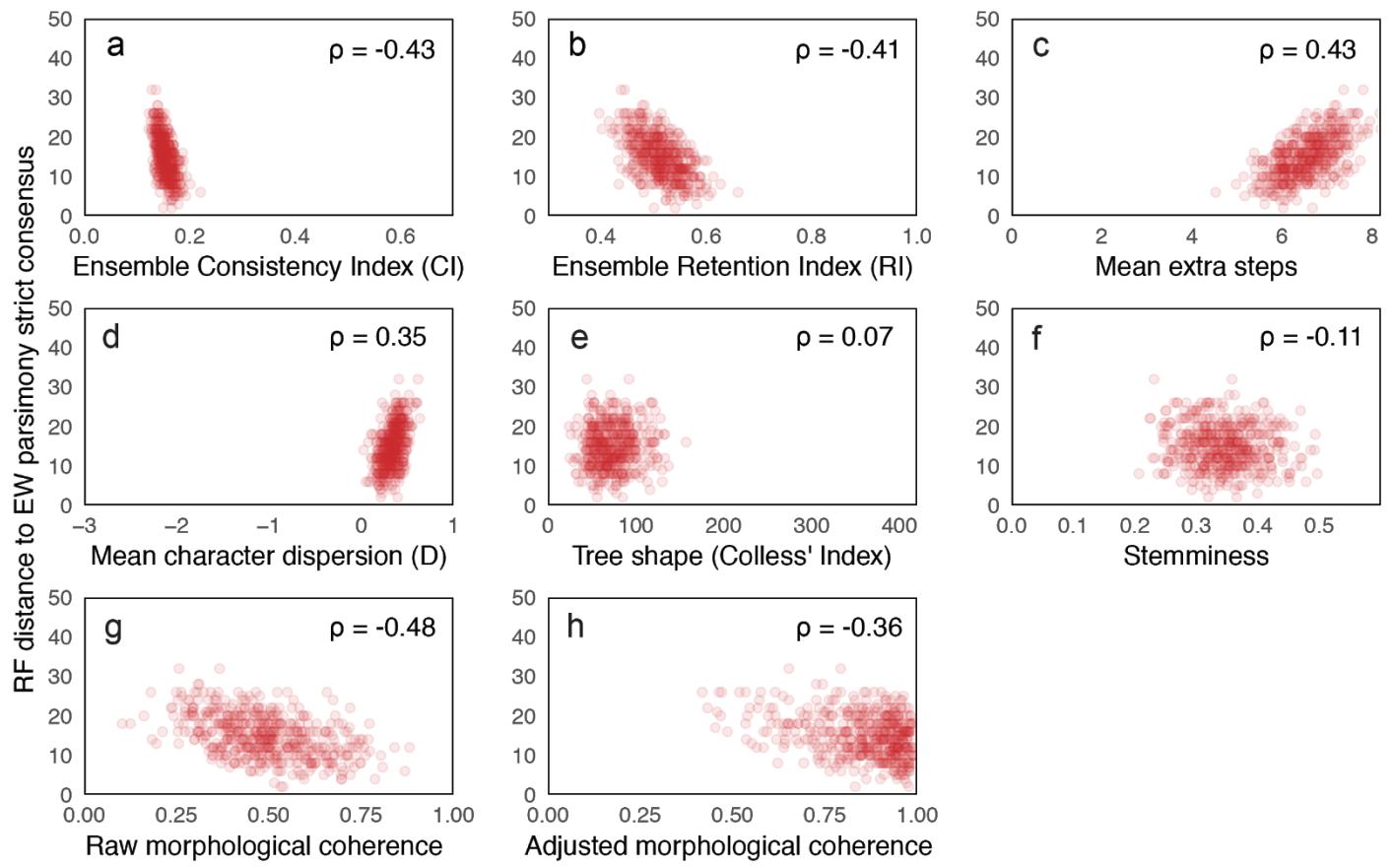
*Supplementary Figure 8.* Box plots showing percentage accuracy (in percentage correct nodes and percentage correct quartets) of the standard consensus trees for Bayesian inference (B), equal weighting parsimony (EW) and implied weighting parsimony (IW). 500 replicates; 128, 512, and 1024 characters.



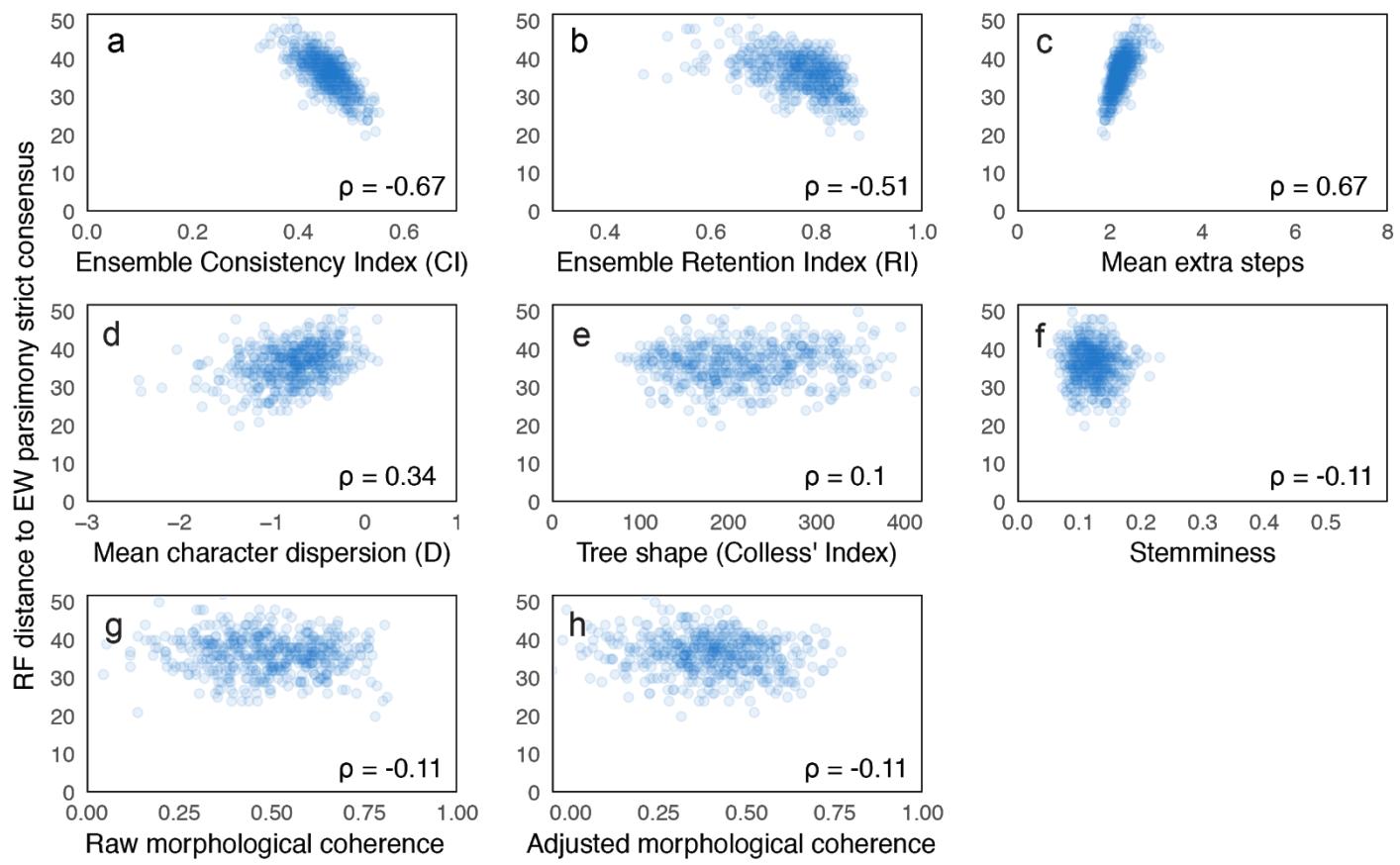
*Supplementary Figure 9. Density plot of mean Subtree Prune and Regraft (SPR) distance between derived tree(s) and true tree generated using TREvoSim and MBL2017 simulated data (500 replicates).*



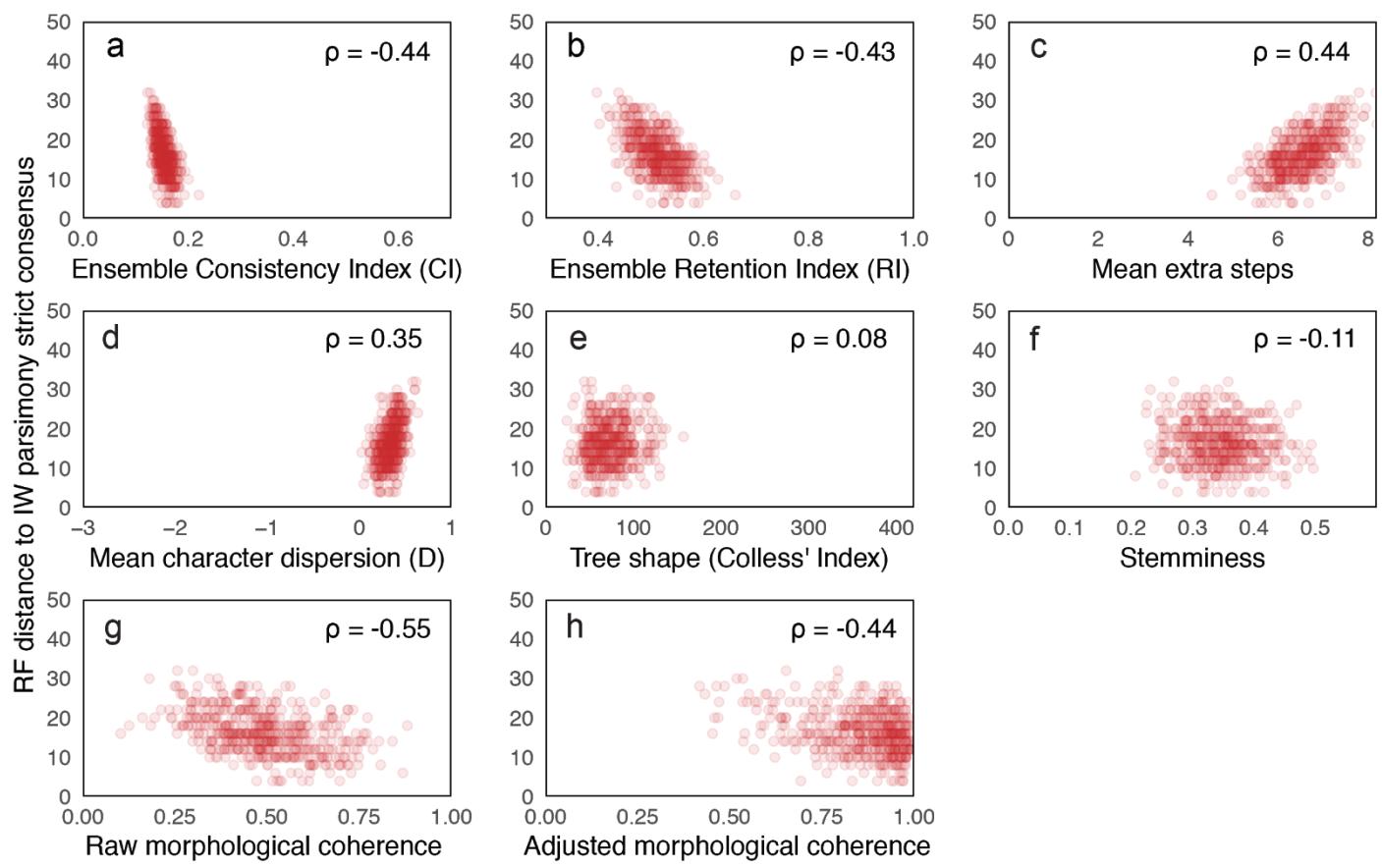
*Supplementary Figure 10.* Density plot of mean Tree Bisection and Reconnection (TBR) distance between derived tree(s) and true tree generated using TREvoSim and MBL2017 simulated data (500 replicates).



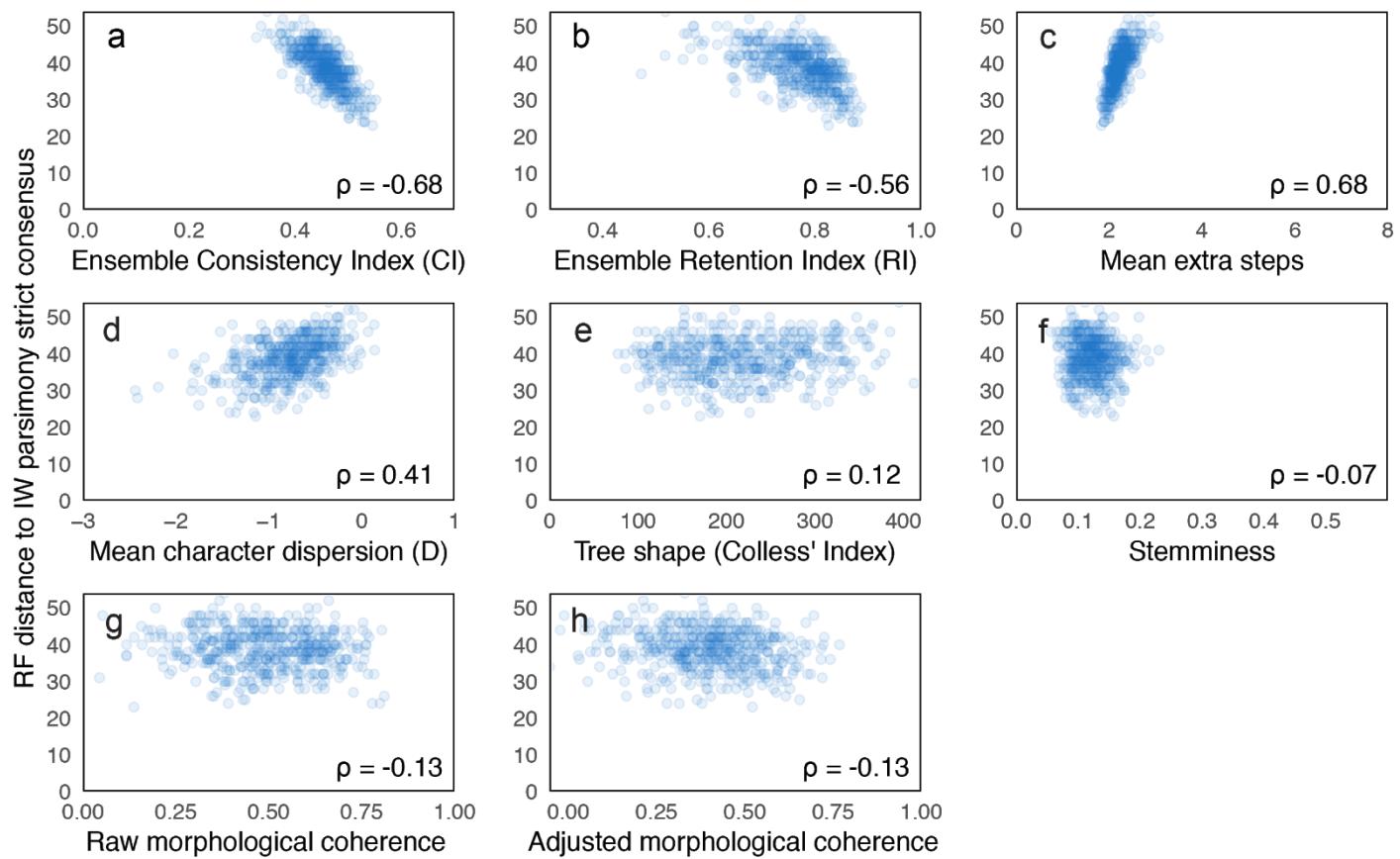
*Supplementary Figure 11. Scatter plots of correlation of 8 measured tree and data attributes against RF distance between the true tree and the equal weighting parsimony strict consensus tree for MBL2017 datasets of 128, 512 and 1024 simulated characters (500 replicates).  $\rho$  = Spearman's Rank correlation.*



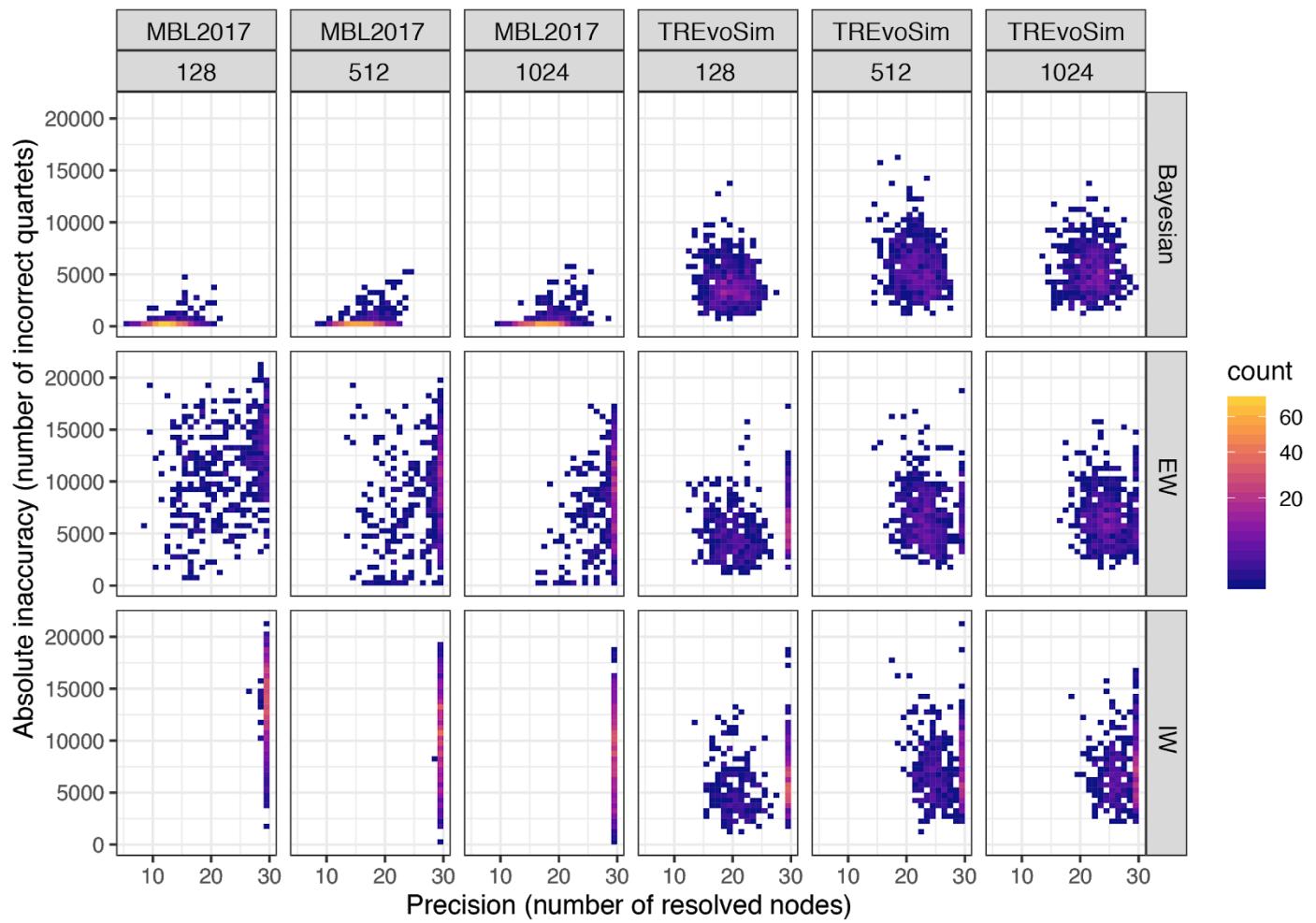
*Supplementary Figure 12. Scatter plots of correlation of 8 measured tree and data attributes against RF distance between the true tree and the equal weighting parsimony strict consensus tree for TREvoSim datasets of 128, 512 and 1024 simulated characters (500 replicates).  $\rho$  = Spearman's Rank correlation.*



*Supplementary Figure 13. Scatter plots of correlation of 8 measured tree and data attributes against RF distance between the true tree and the implied weighting parsimony strict consensus tree for MBL2017 datasets of 128, 512 and 1024 simulated characters (500 replicates).  $\rho$  = Spearman's Rank correlation.*



*Supplementary Figure 14. Scatter plots of correlation of 8 measured tree and data attributes against RF distance between the true tree and the implied weighting parsimony strict consensus tree for TREvoSim datasets of 128, 512 and 1024 simulated characters (500 replicates).  $\rho$  = Spearman's Rank correlation.*



*Supplementary Figure 15.* Heatmap of the number of resolved nodes against the number of incorrect quartets for each standard consensus tree for 128, 512 and 1024 character datasets (500 replicates). Bayesian estimates are generally less inaccurate and less precise than EW or IW parsimony estimates.