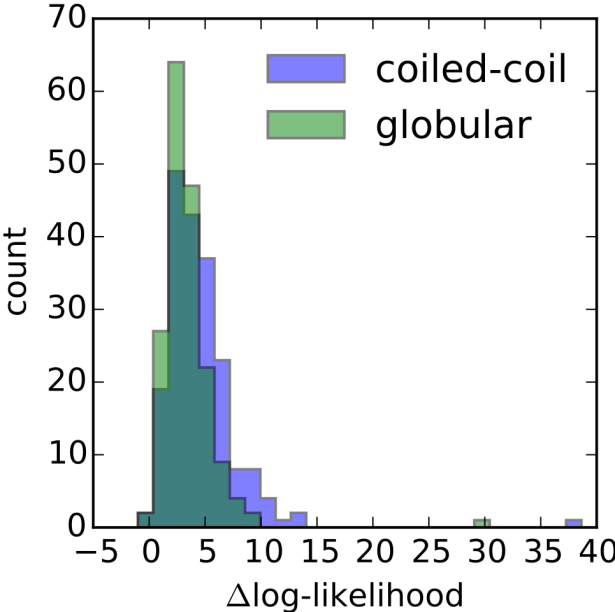# Supplementary material

Fig. S1. Per site log-likelihood difference between a random and the best (maximum likelihood) guess of the evolutionary relationship between sequences.
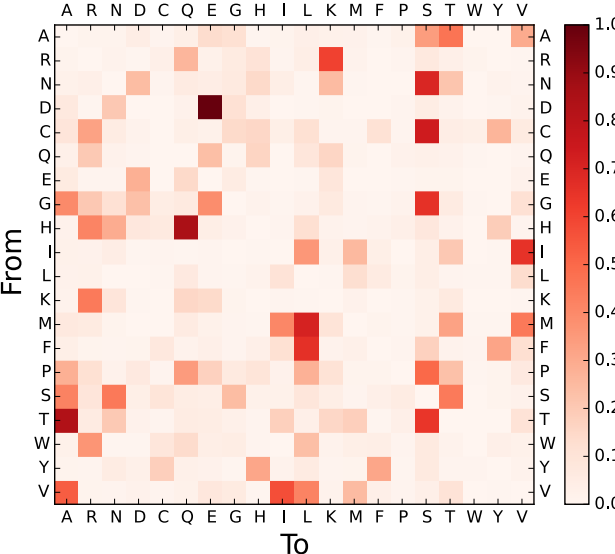

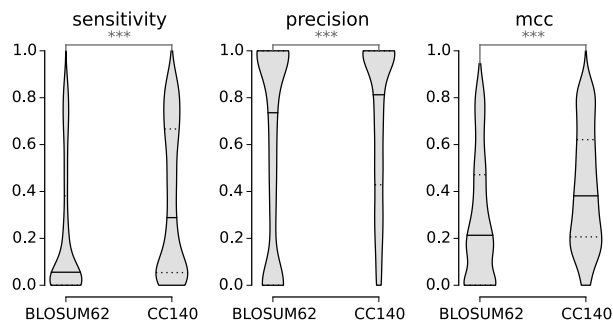**Fig. S2.** Amino acid substitution rates (q_{ij}) in the CC model.

Fig. S3. Homology search improvement under the CC model in plants (Ensembl Plants). Homology search comparison between CC140 and BLOSUM62 scoring matrix at the e-value threshold of 1e-08. Statistical significance between samples was estimated with the Mann-Whitney U test (*** p-value < 0.001).