

Supplementary Figure 1: Robinson-Foulds distances between trees differing due to ILS and due to paralogy (8 taxa). Trees A and B differ by ILS (yellow and light blue lines represent new polymorphisms that become fixed) resulting in a Robinson-Foulds distance of 4. Tree C originates in a duplication event in one clade (red and light blue lines) with loss of one gene copy in each terminal (dashed red and light blue lines). Tree C differs from trees A and B by a Robinson-Foulds distance of 8.

Supplementary Figure 2: Idealised illustration of the one-tailed test based on Robinson-Foulds (RF) distances. Coalescent distances are the RF distances between an observed gene tree (represented by a sample of trees drawn from the Bayesian posterior distribution) and the simulated 'gene trees' under the multispecies coalescent, where the observed gene tree is used as a surrogate species tree. The gene tree distances are the RF distances between one observed gene tree (the posterior sample, as before) and another observed gene tree (the posterior sample, as before). As the posterior samples of the observed gene trees include inference uncertainty, we considered the resulting distribution of RF distances to also include this uncertainty. We therefore used only the lower value of the 95% highest posterior density of the observed gene tree comparison to compare to the critical value of the coalescent distances to determine acceptance or rejection of the null hypothesis.

Supplementary Figure 3: Sequence simulation scheme for one replicate, from coalescent tree simulations to nucleotide data. The two principal trees (PT1, PT2) that describe the species network and one Paralogous Tree (PT1 affected by paralogy) were the basis of the gene tree simulations. Gene trees simulated under the multispecies coalescent (using Mesquite) were simulated from each of Principal Tree 1 (PT1) and Principal Tree 2 (PT2) as well as from the Paralogous Tree. Sequence data were then generated under the model described in the text from each gene tree.

Supplementary Figure 4: Paralogy test for bin RF=8 at different critical values (cv), for blocks with paralogous genes.

Supplementary Figure 5: Hybridisation test for bin RF=8 at different critical values.

Supplementary Figure 6: Grouping of blocks test for bin RF=8 at different critical values.

Supplementary Figure 7: Species trees inferred using *BEAST for: grouped blocks as indicated by the paralogy and hybridisation tests; grouped blocks ignoring the paralogy test; block A with putative paralogue removed; all 12 genes. Species tree inferred using BEAST for a concatenated dataset of 12 genes.