Figure S1: A maximum-likelihood tree (iML), generated using the 5S rRNA alignment under an independent sites model. The iML topology is used when conditioning upon a fixed topology.
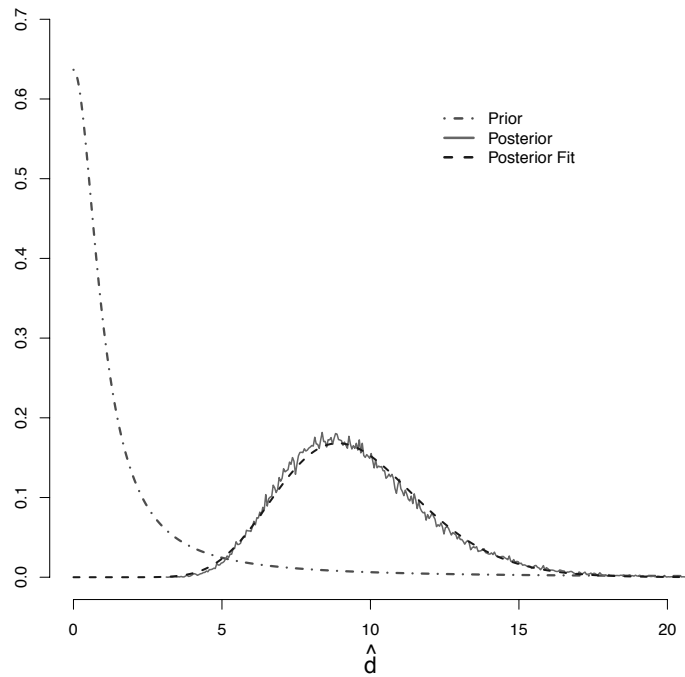
Figure S2: Savage-Dickey approach to calculating Bayes factors for nested models. The marginal posterior distribution of d (solid line) is fit to a gamma distribution (dashed line). The analytical prior density (dot-dashed line) and fitted posterior density are evaluated at $d = 0$ to calculate the Bayes factors comparing the general model to the specific case.