**Table 2**. Topological congruence between phylogenies inferred under different analytical approaches. The Robinson-Foulds distance is normalised so that “0.0” minimises distance (i.e., maximises congruence) and “1.0” maximises distance (i.e., minimises congruence). The proportion of common nodes is estimated relative to the maximum number of possible nodes for the smallest tree in each pairwise comparison. Pairwise comparisons against the reference topologies (under equal weighting and no dependencies; “ew-nondep”) entail topologies inferred with dependencies included under: equal weighting (“ew-dep”), extended implied weighting with concavity 5 (“k5-dep”), concavity 10 (“k10-dep”), concavity 15 (“k15-dep”) and concavity 20 (“k20-dep”).

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| **Comparison** | **RF distance** | **Proportion of common nodes** |
| ew-nondep vs ew-dep | 0.67 | 0.48 |
| ew-nondep vs k5-dep | 0.8 | 0.31 |
| ew-nondep vs k10-dep | 0.77 | 0.31 |
| ew-nondep vs k15-dep | 0.78 | 0.38 |
| ew-nondep vs k20-dep | 0.76 | 0.19 |