

Figure S1. Percent completeness of morphological data in fossil templates from each study. Horizontal lines represent median, boxes middle quartiles, and whiskers range.

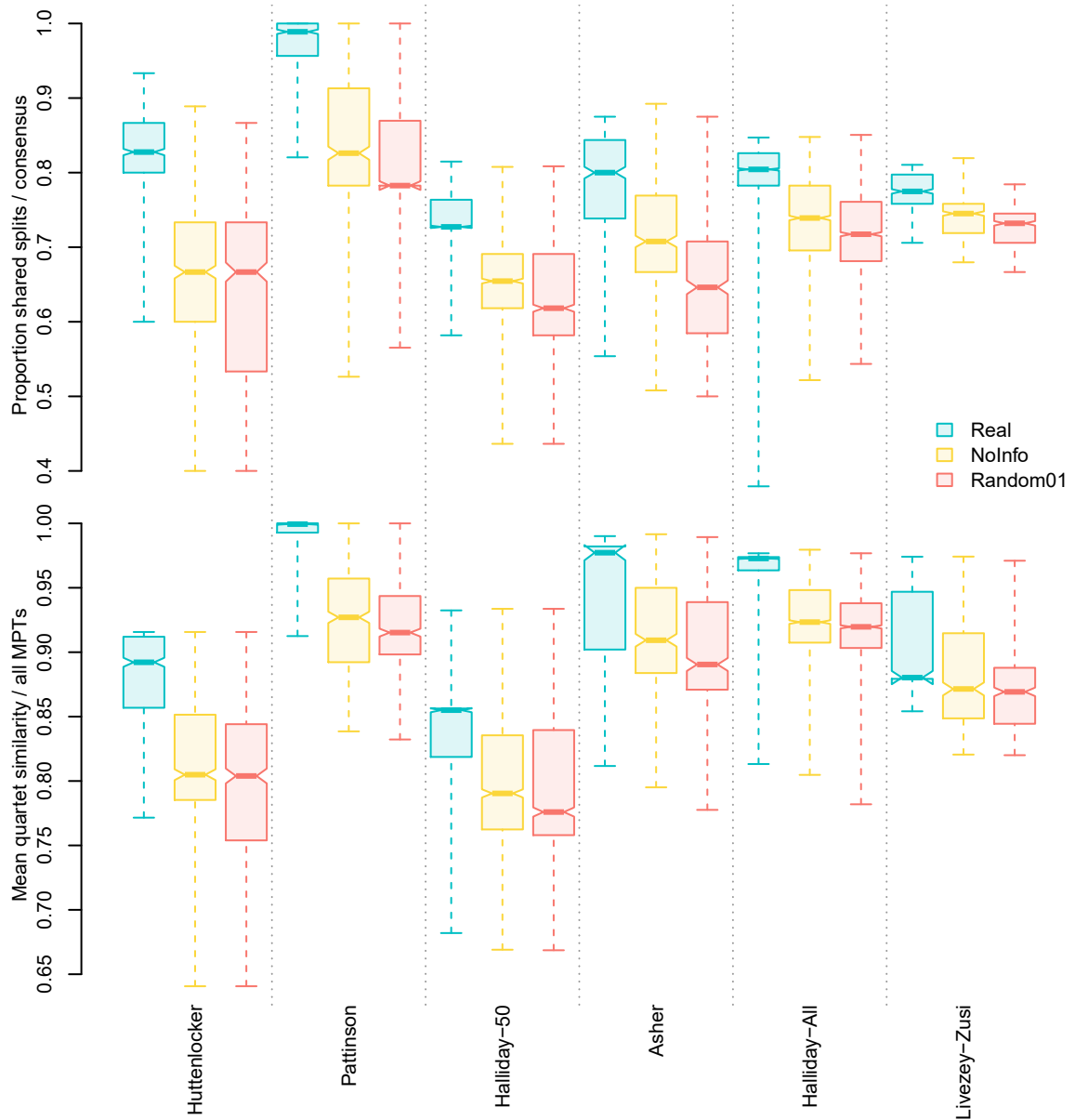


Figure S2. Congruence of artificial-extinction topologies with well-corroborated trees for each dataset, based on only templates of at least 53% complete (corresponding to the least complete template from Asher). Each horizontal bar shows the number of shared splits using strict consensus (top Y-axis) or quartet similarity averaged across all MPTs (bottom Y-axis), averaged across all extant subjects per fossil template. Datasets are ordered from largest (left) to smallest (right) difference in median shared splits obtained by real vs. 01-randomized character states (see Table 2). Boxes denote median and interquartile range, whiskers the range; non-overlapping notches represent a significant difference in medians (Chambers et al. 1983). Characters missing in a fossil template were coded as missing in each extant subject. Remaining characters were coded with the real states in each template (blue), randomized using states drawn from different extant taxa (yellow, "noInfo"), or randomized with states 0 or 1 (red, "random01").

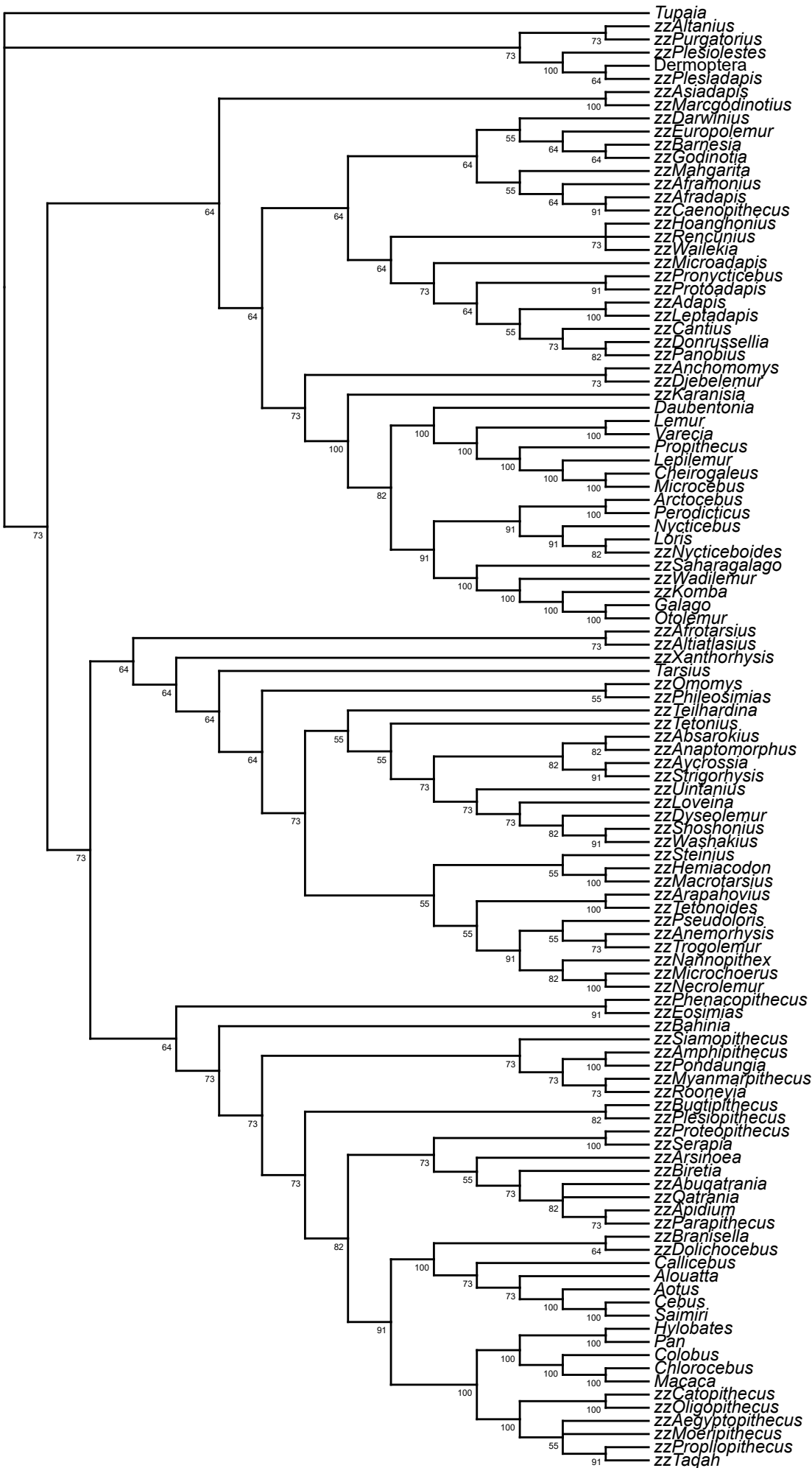


Figure S3. Majority Rule consensus (as shown by percentages adjacent to each node) of 11 topologies derived from the Pattinson dataset using equal and implied weighting values ($k = 2, 4, 8, 16, 32, 64, 128, 256, 512, 999$) that maximize quartet similarity with well-corroborated tree of living taxa (Table 3). Fossils shown with "zz".

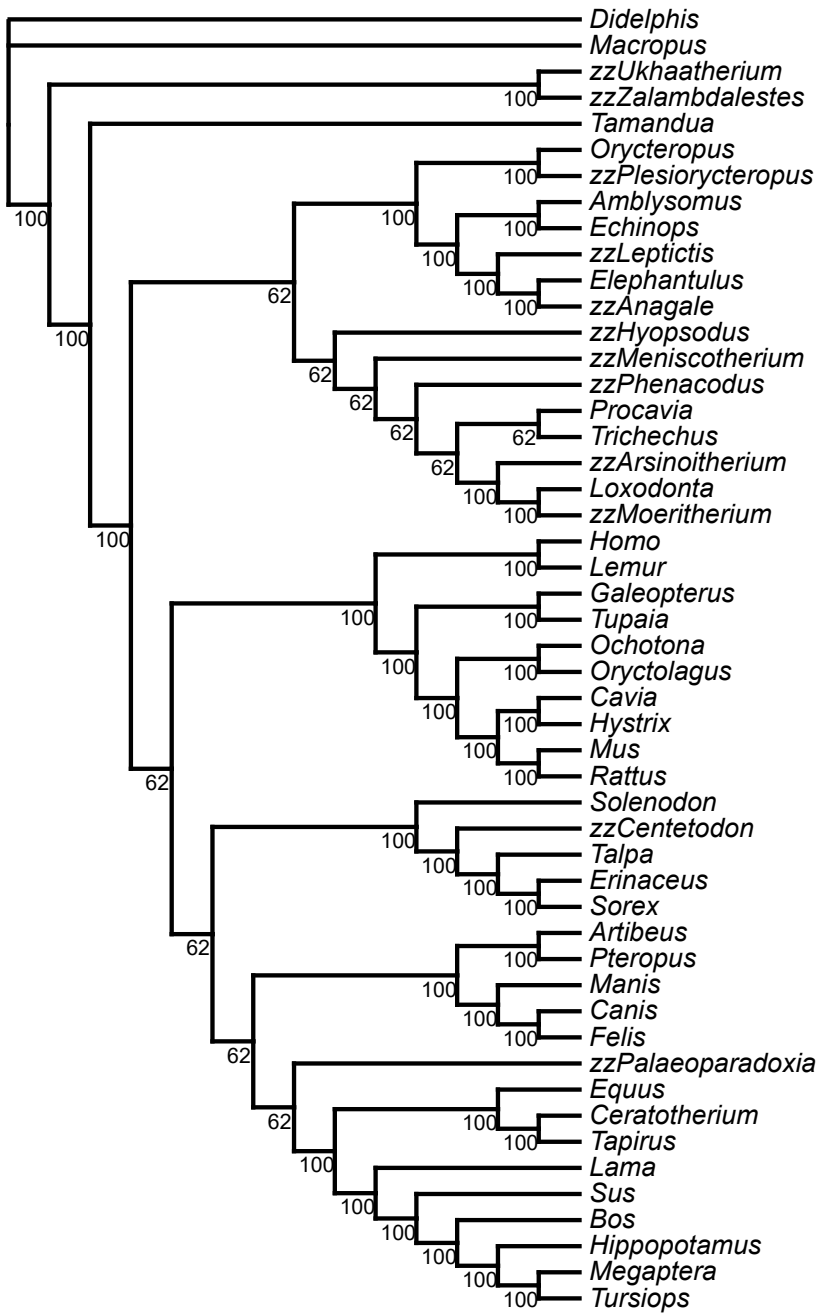


Figure S4. Majority Rule consensus (as shown by percentages adjacent to each node) of 7 topologies derived from the Asher dataset using implied weighting concavity values ($k = 8, 16, 32, 64, 128, 512, 999$) that maximize quartet similarity with well-corroborated tree of living taxa (Table 3). Fossils shown with "zz".

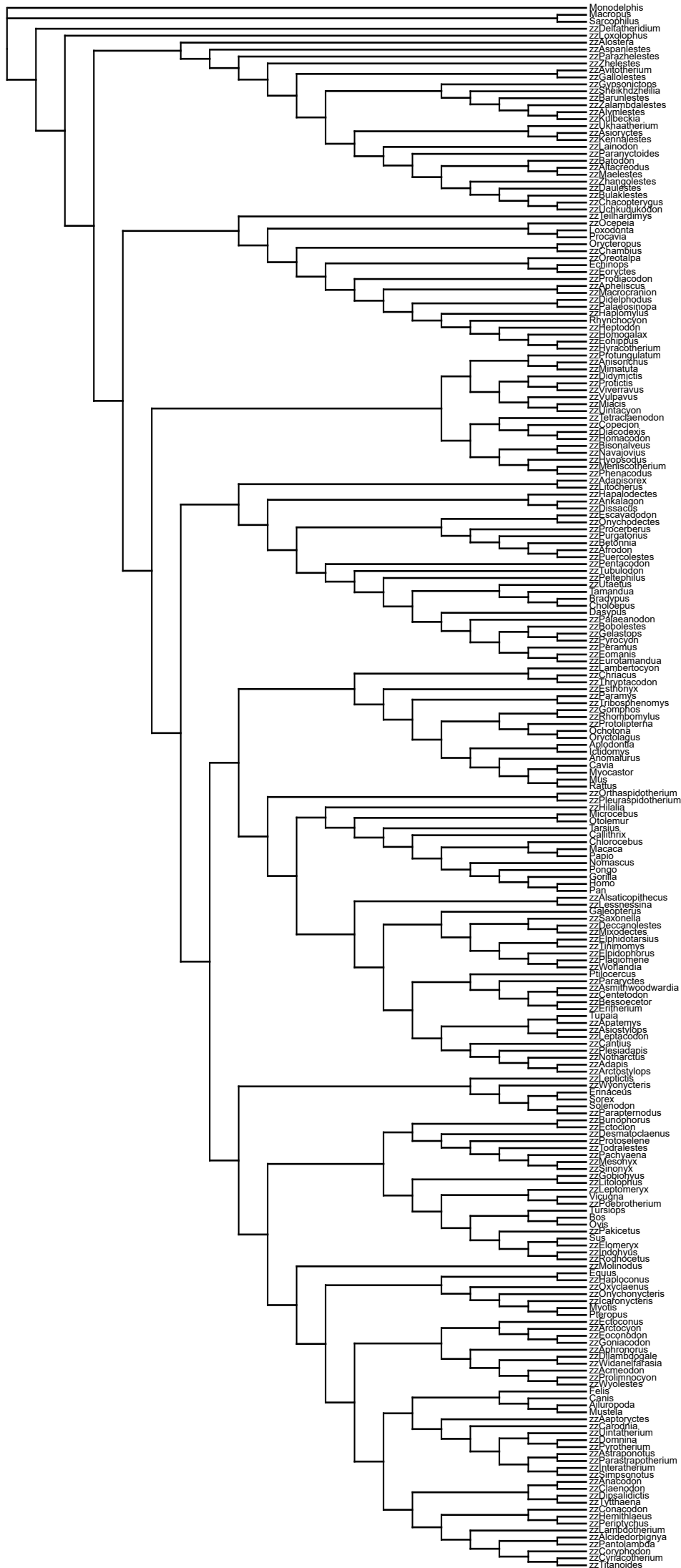


Figure S5. Single MPT derived from Halliday-All dataset using implied weighting value ($k = 2$, 11026.82414 steps) that maximizes quartet similarity with well-corroborated tree of living taxa (Table 3). Fossils shown with "zz".

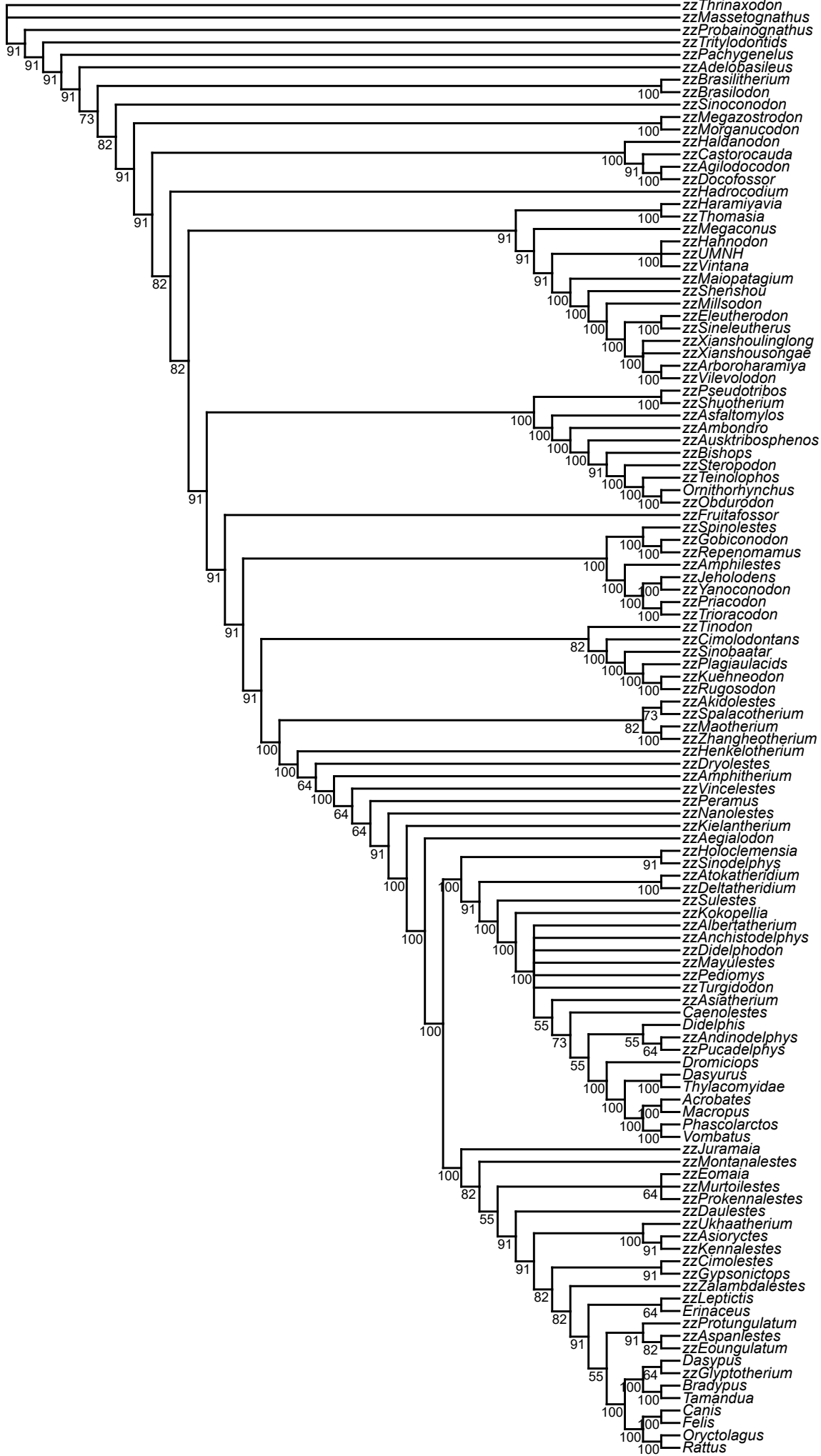


Figure S6. Majority Rule consensus (as shown by numbers adjacent to each node) of 11 topologies derived from the Huttenlocker dataset using equal and implied weighting values ($k = 2, 4, 8, 16, 32, 64, 128, 256, 512, 999$) that maximize quartet similarity with well-corroborated tree of living taxa (Table 3). Fossils shown with "zz".

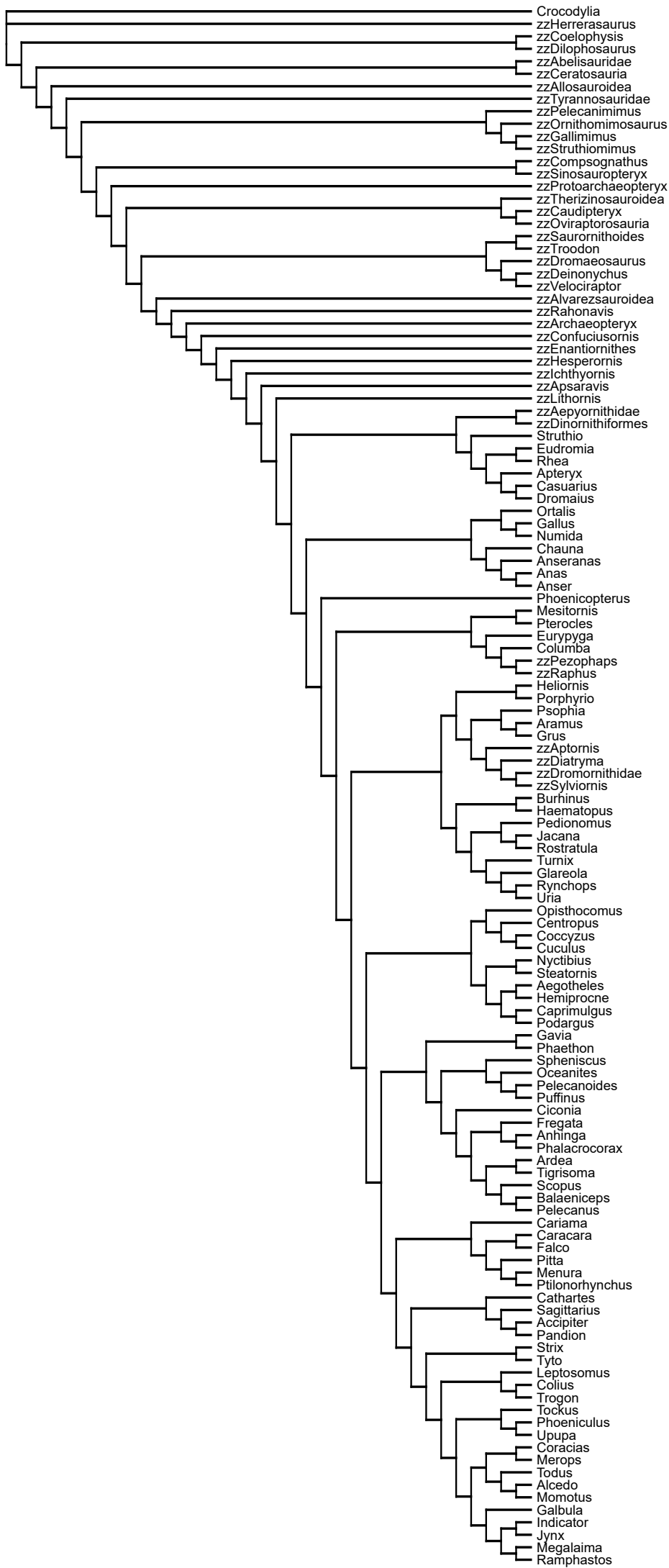


Figure S7. Single MPT derived from Livezey-Zusi dataset using implied weighting value ($k = 4$, 65443.9752 steps) that maximizes quartet similarity with well-corroborated tree of living taxa (Table 3). Fossils shown with "zz".

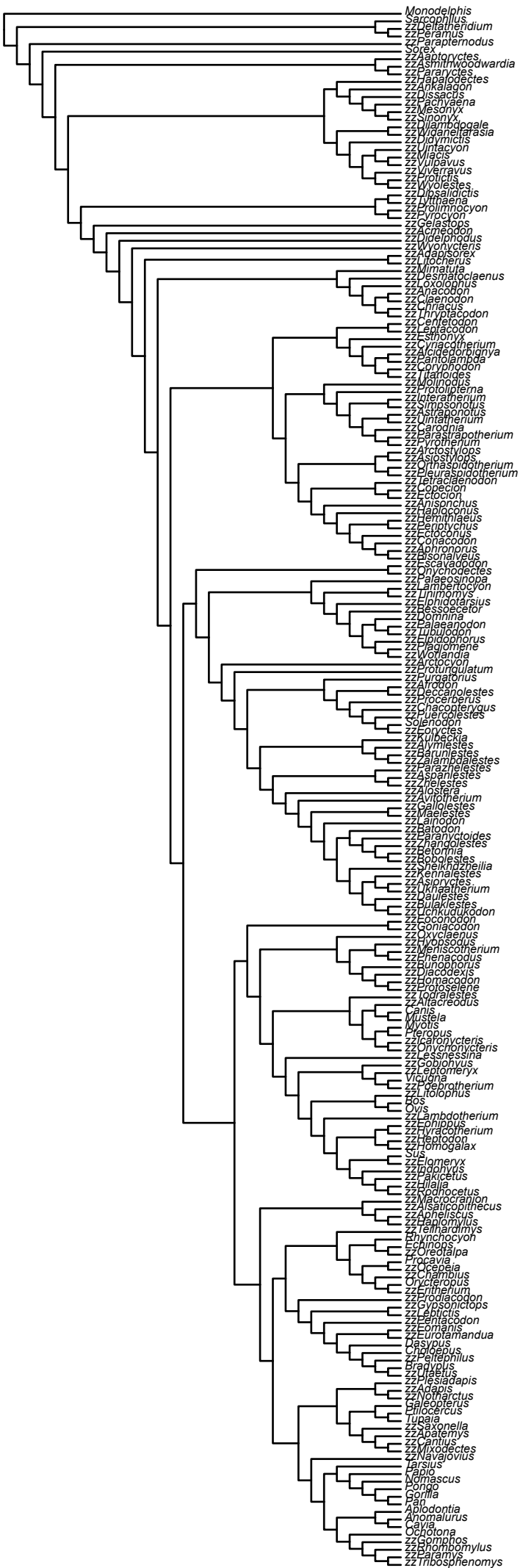


Figure S8. Single MPT derived from Halliday-50 dataset using implied weighting concavity value ($k = 999$, 46.99872 steps) that maximizes quartet similarity with well-corroborated tree of living taxa (Table 3). Fossils shown with "zz".