



Maximum parsimony tree showing the results of all six analysis regimes on the R2 IBR data. Tip names are of the form R2 + analysis regime ("a", "aStr", etc) + accession + arbitrary cluster number + coverage (number of sequences in that cluster). The regimes labeled here as "a", "c", and "e" (as well as their Str equivalents) were referred to in the paper as regimes "a", "b", and "c", respectively. See Table 3 for more information about the regimes.