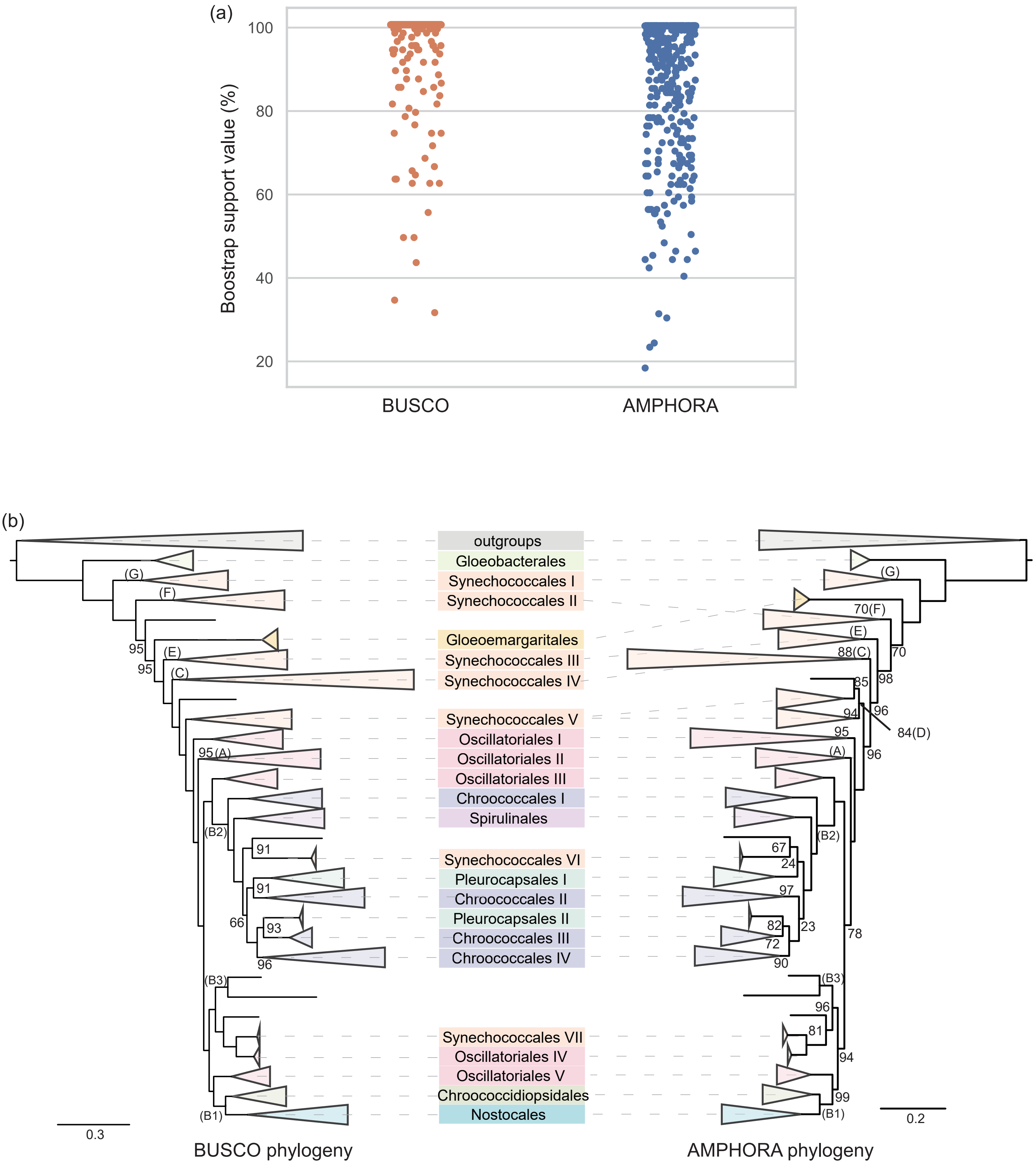

Fig. S2. Comparison of phylogenetic tree inferred from BUSCO and AMPHORA data sets. a, Bootstrap support values across all branches of phylogenetic trees from BUSCO and AMPHORA data sets. b, Comparision of backbone phylogenies from two data sets. Internodes without numeral label denote maximal support. Letters in parentheses next to internodes represent clades found in Shih et al., (2008). Scale bar is in substitutions per amino acid position.