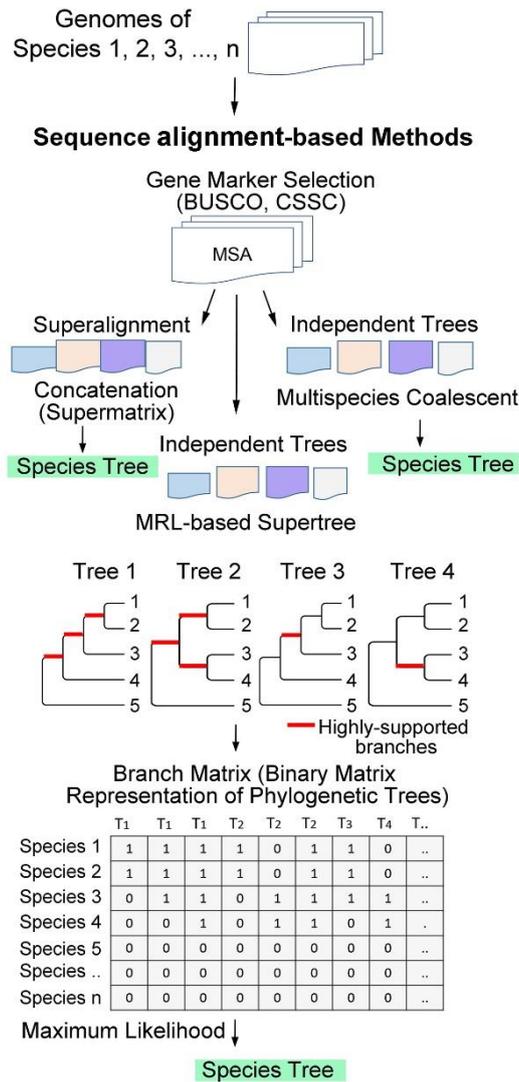
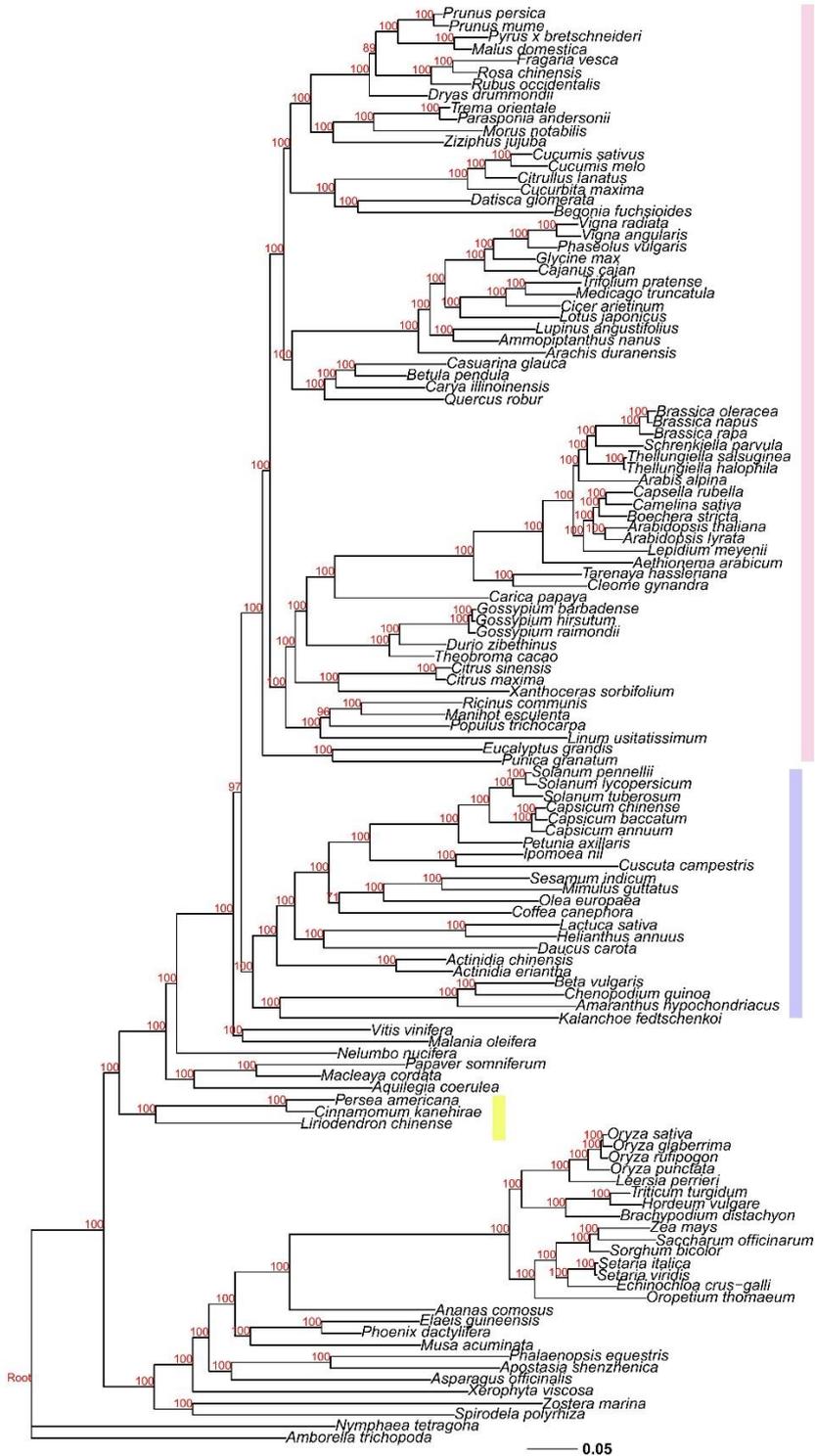


Whole-genome microsynteny-based phylogeny of angiosperms

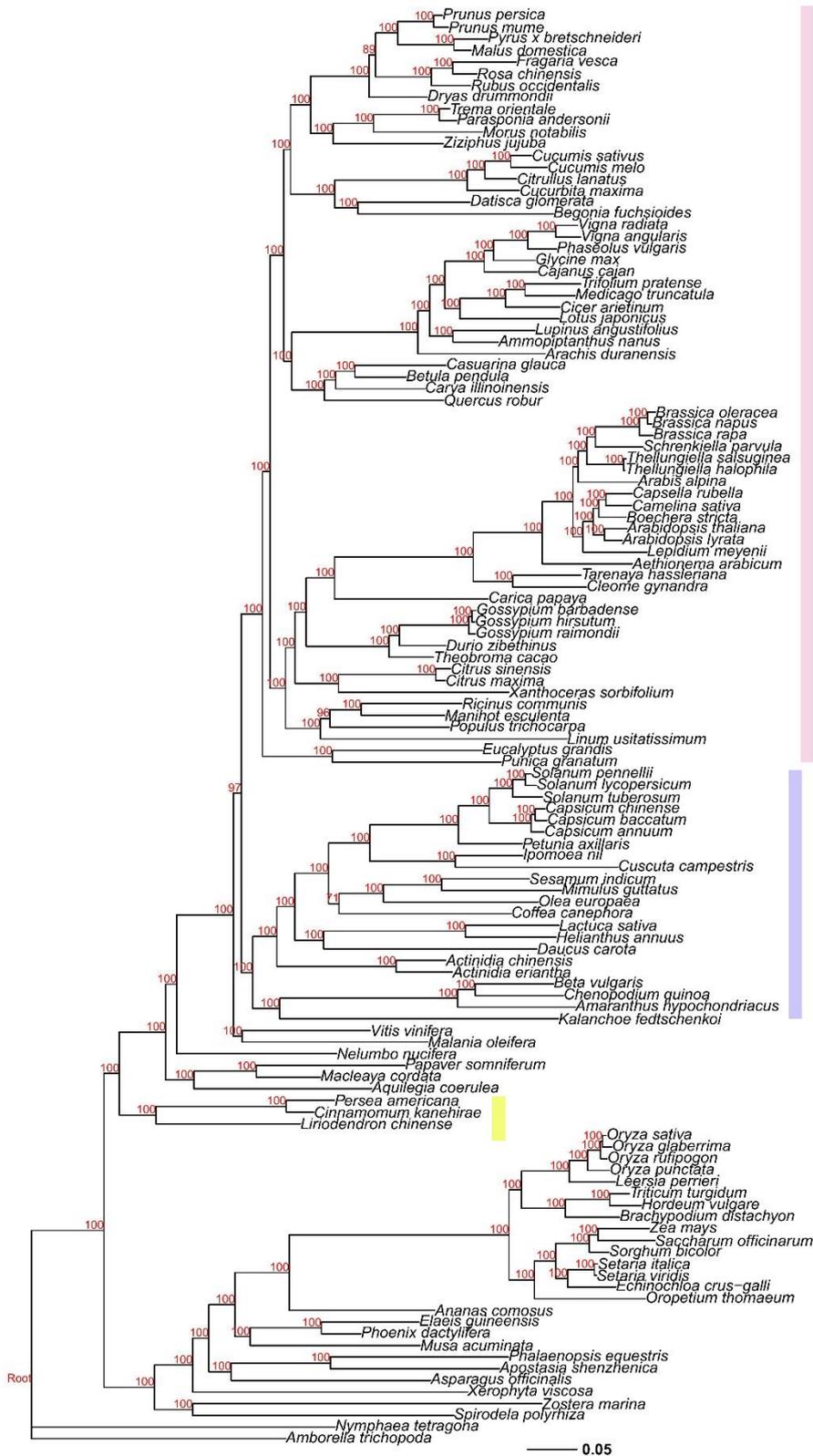
Zhao et al



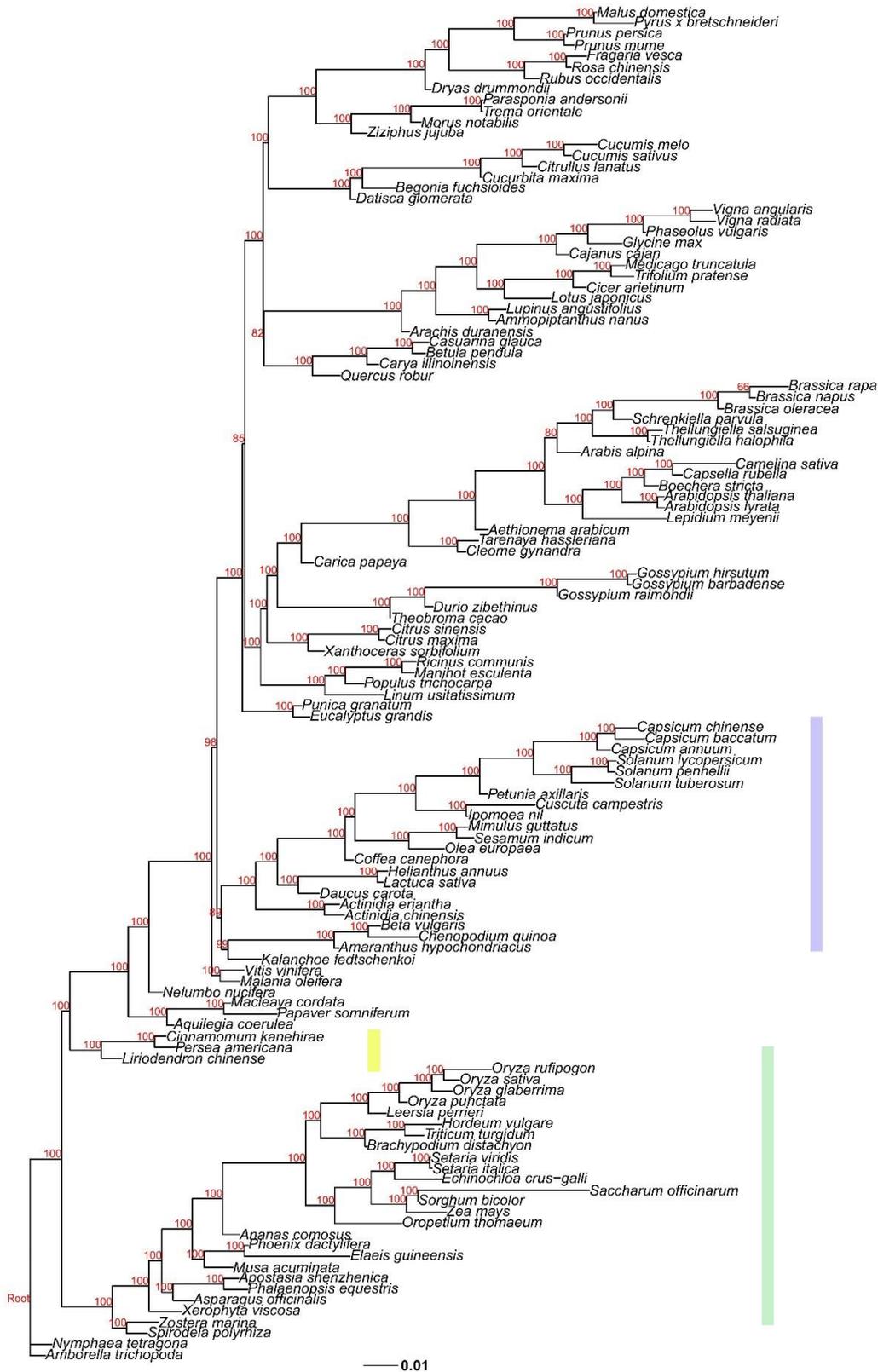
Supplementary Fig. 1 Representative sequence-based methods for reconstructing species trees used in this study, we used superalignment concatenation/supermatrix, multispecies coalescent, and MRL-based supertree methods for two sets of whole-genome-derived markers (BUSCO and CSSC) (see text for details). First, multiple sequence alignments (MSA) were first built for each of the whole-genome-derived markers (BUSCO and CSSC) and used as input for the Supermatrix method inferring species trees based on the concatenation of gene alignments. Second, independent gene trees can be inferred for each alignment, after which a species tree can be inferred from the set of obtained gene trees under the multispecies coalescent model, or by using a supertree method. In the latter case, we used a MRL-based method (see text for details). For example, Clade 1+2 is well-supported ($BS \geq 85\%$) in Tree 1, then this branching order (phylogenetic grouping) is coded as the first column of the matrix, similarly, Clade 1+2+3 of Tree 1 is coded as the second column. Leaves from well-supported nodes of all trees construct a binary branch matrix, which is then used for phylogenetic analysis by maximum likelihood.



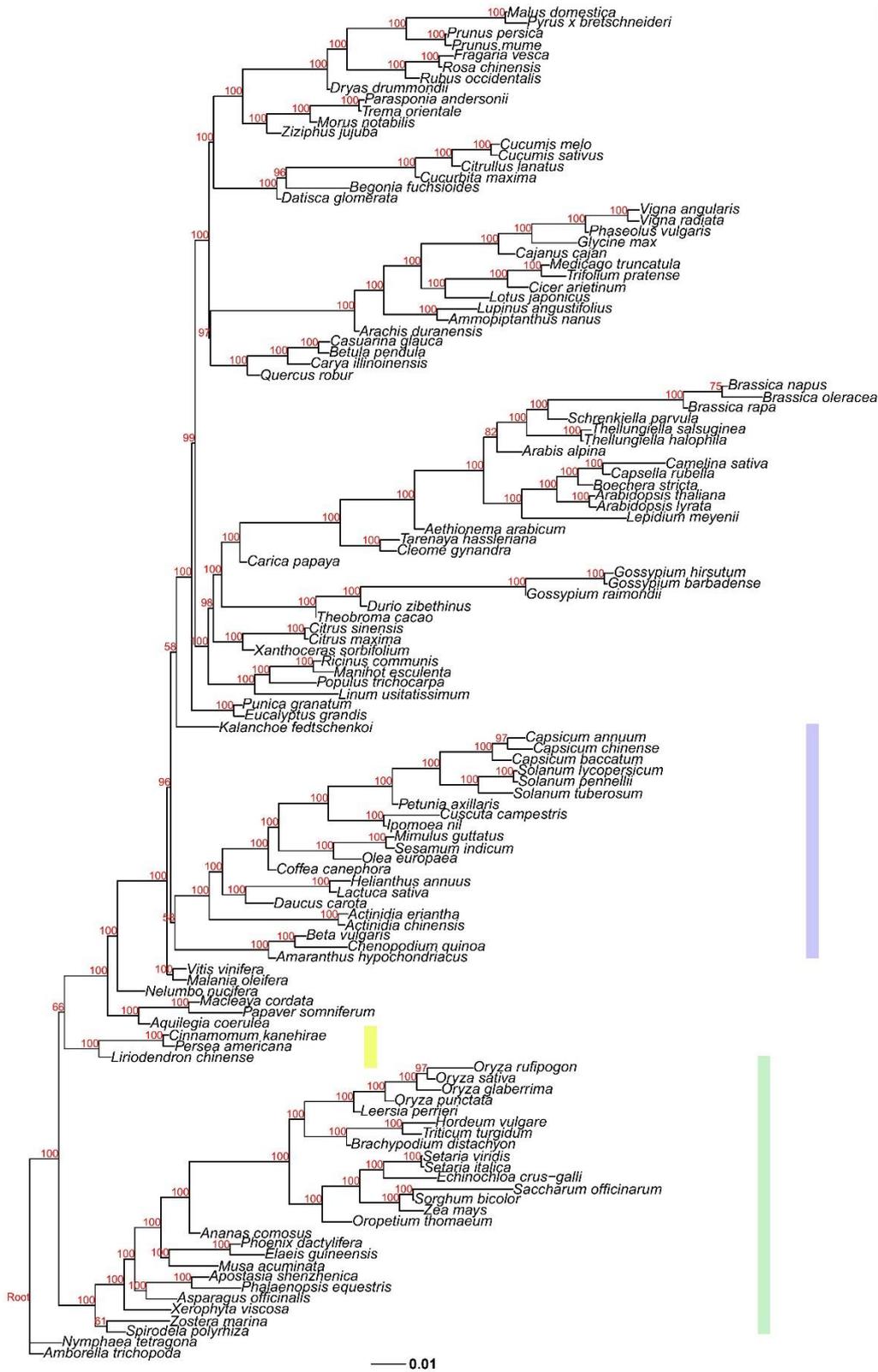
Supplementary Fig. 2 Maximum likelihood concatenation-BUSCO tree. The tree is rooted by *Amborella*, and four main clades, i.e. superrosids, superasterids, monocots, and magnoliids are shaded in light-red, light-purple, light-green, and light-yellow, respectively. This applies to all other phylogenetic trees.



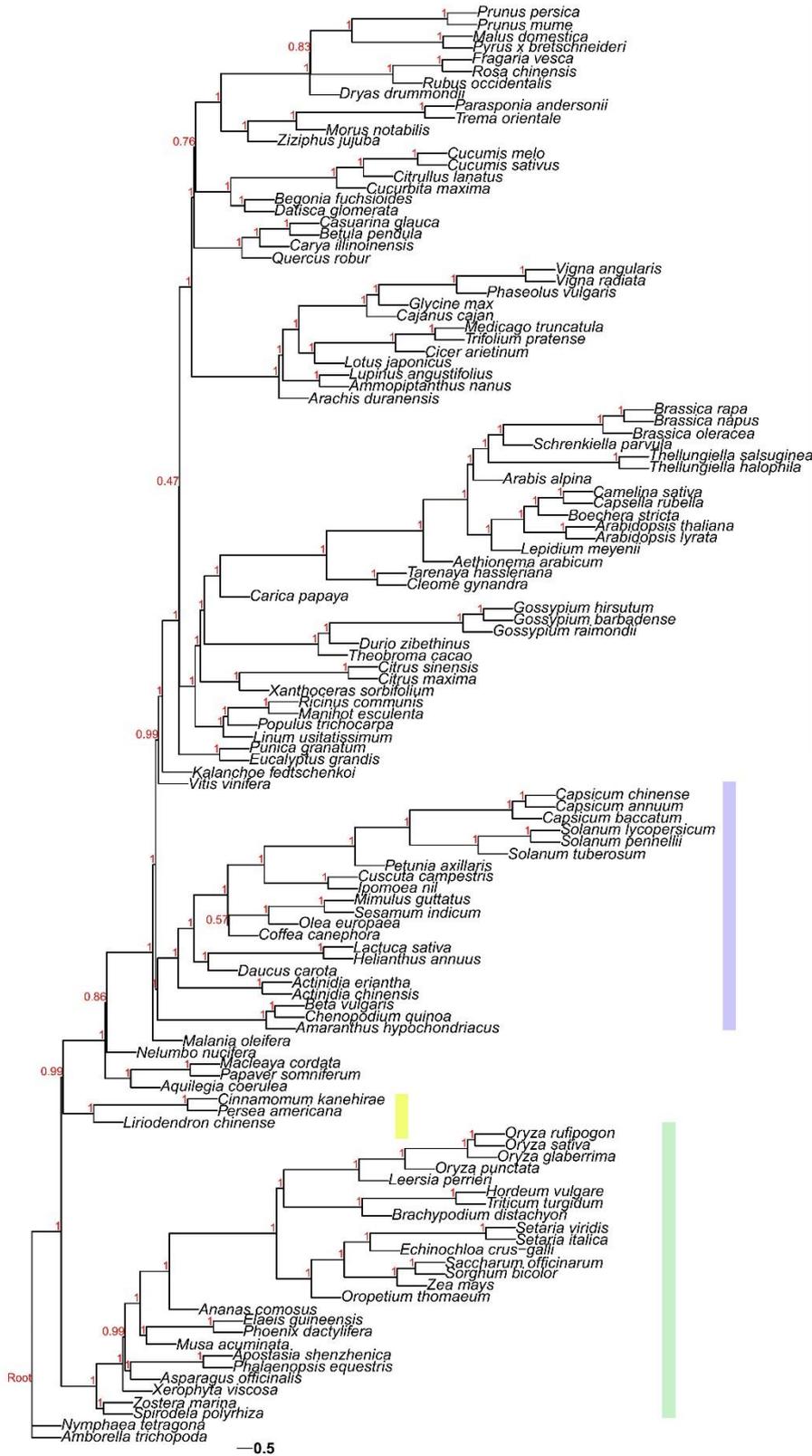
Supplementary Fig. 3 Maximum likelihood concatenation-CSSC tree.



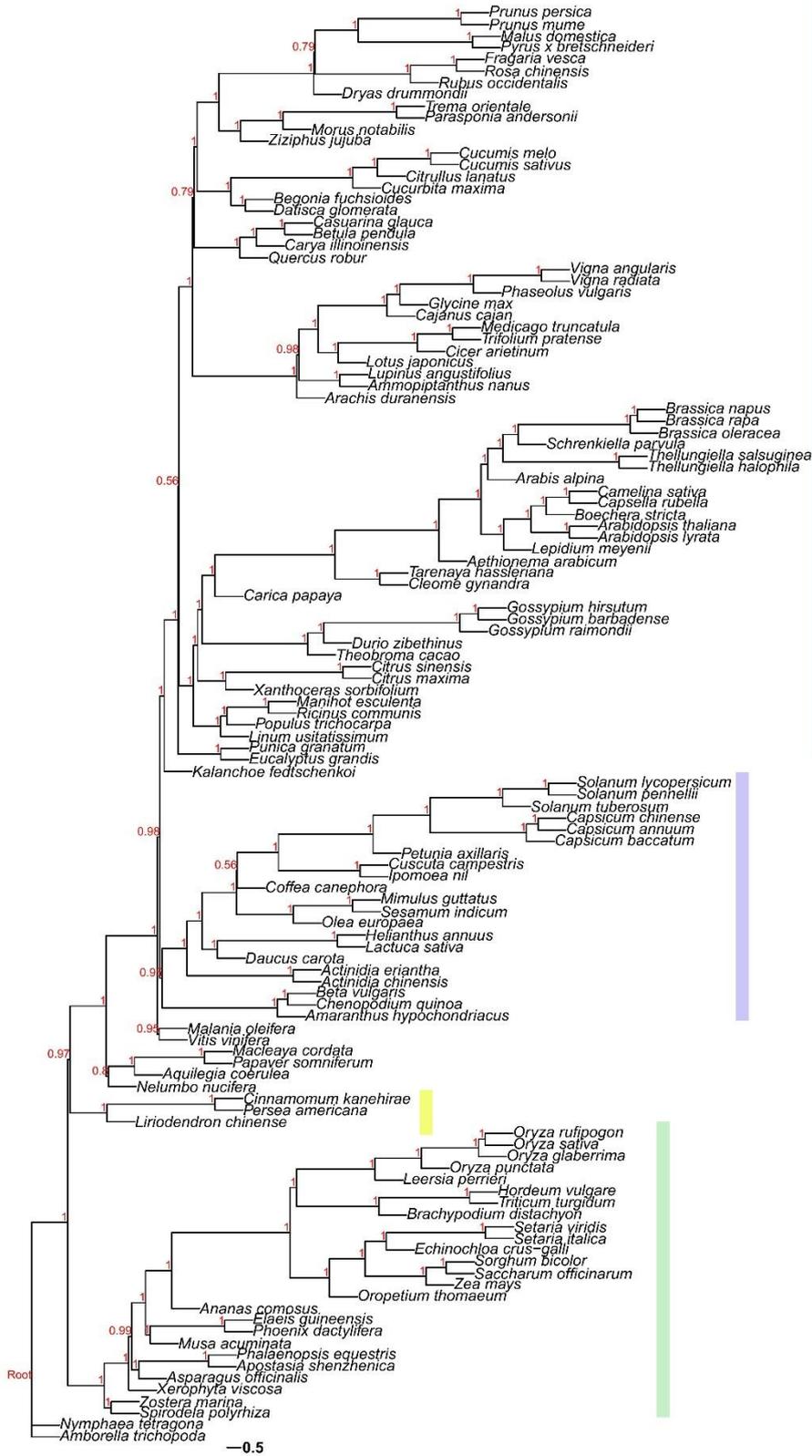
Supplementary Fig. 4 MRL-BUSCO tree.



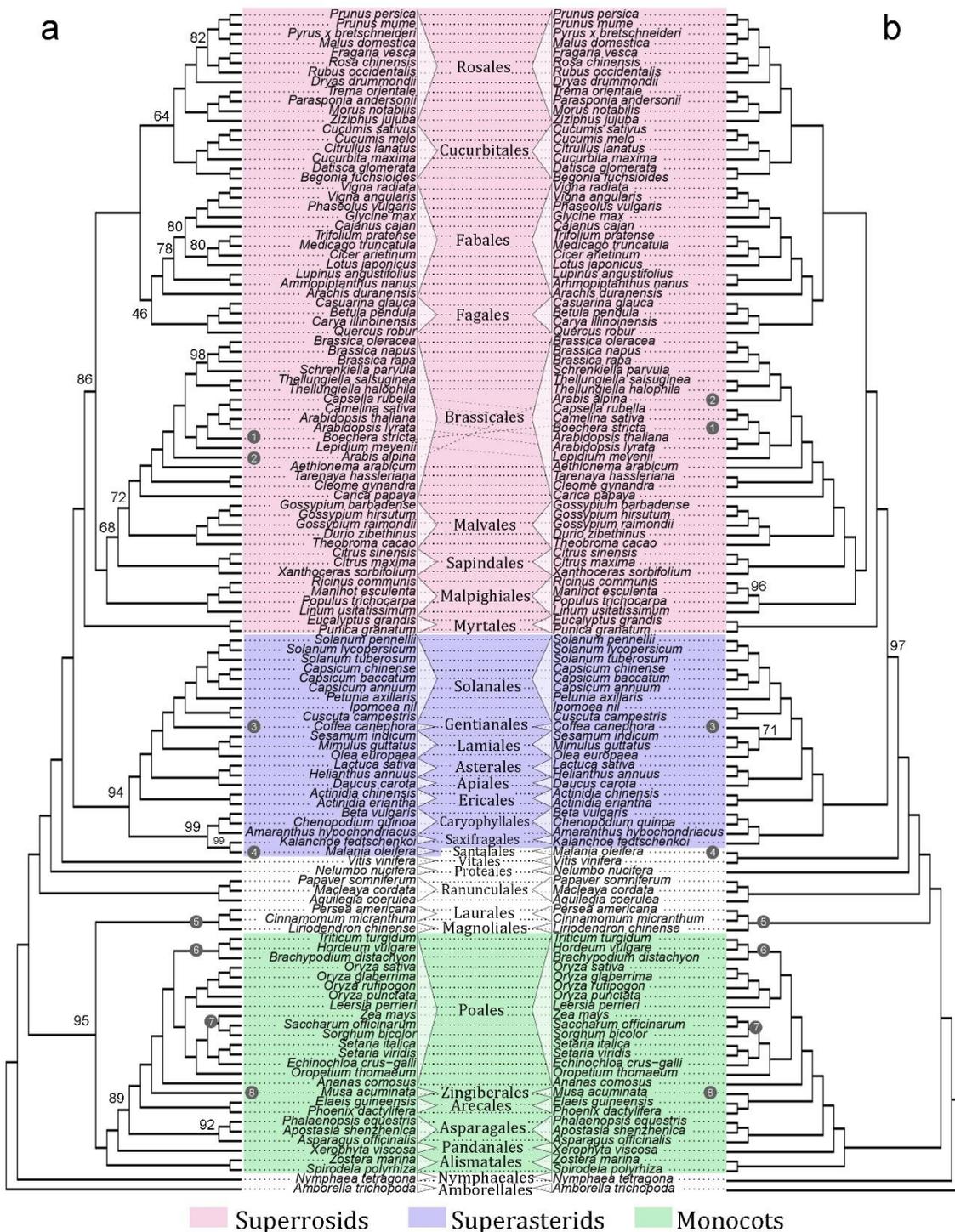
Supplementary Fig. 5 MRL-CSSC tree.



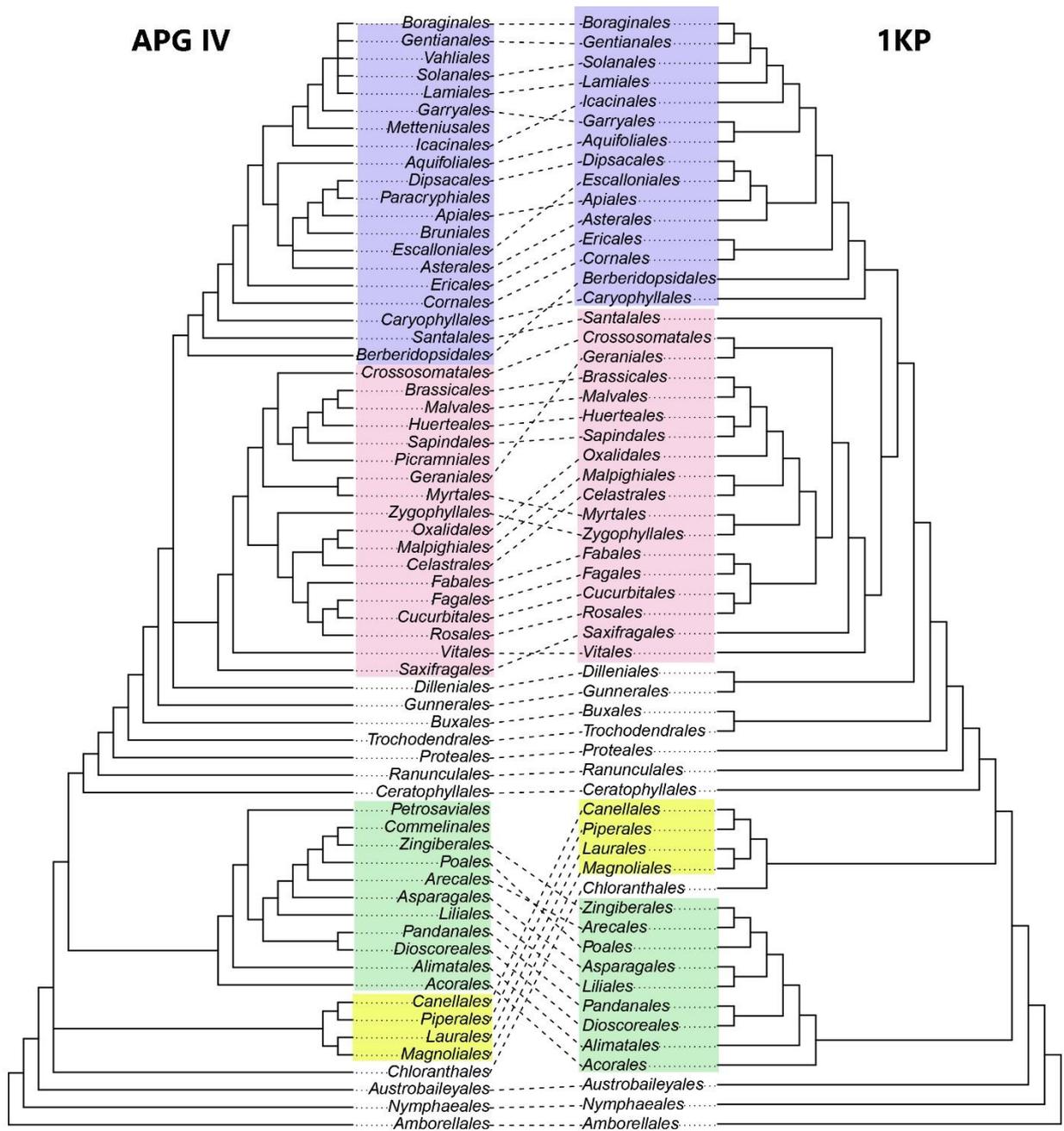
Supplementary Fig. 6 ASTRAL-BUSCO tree.



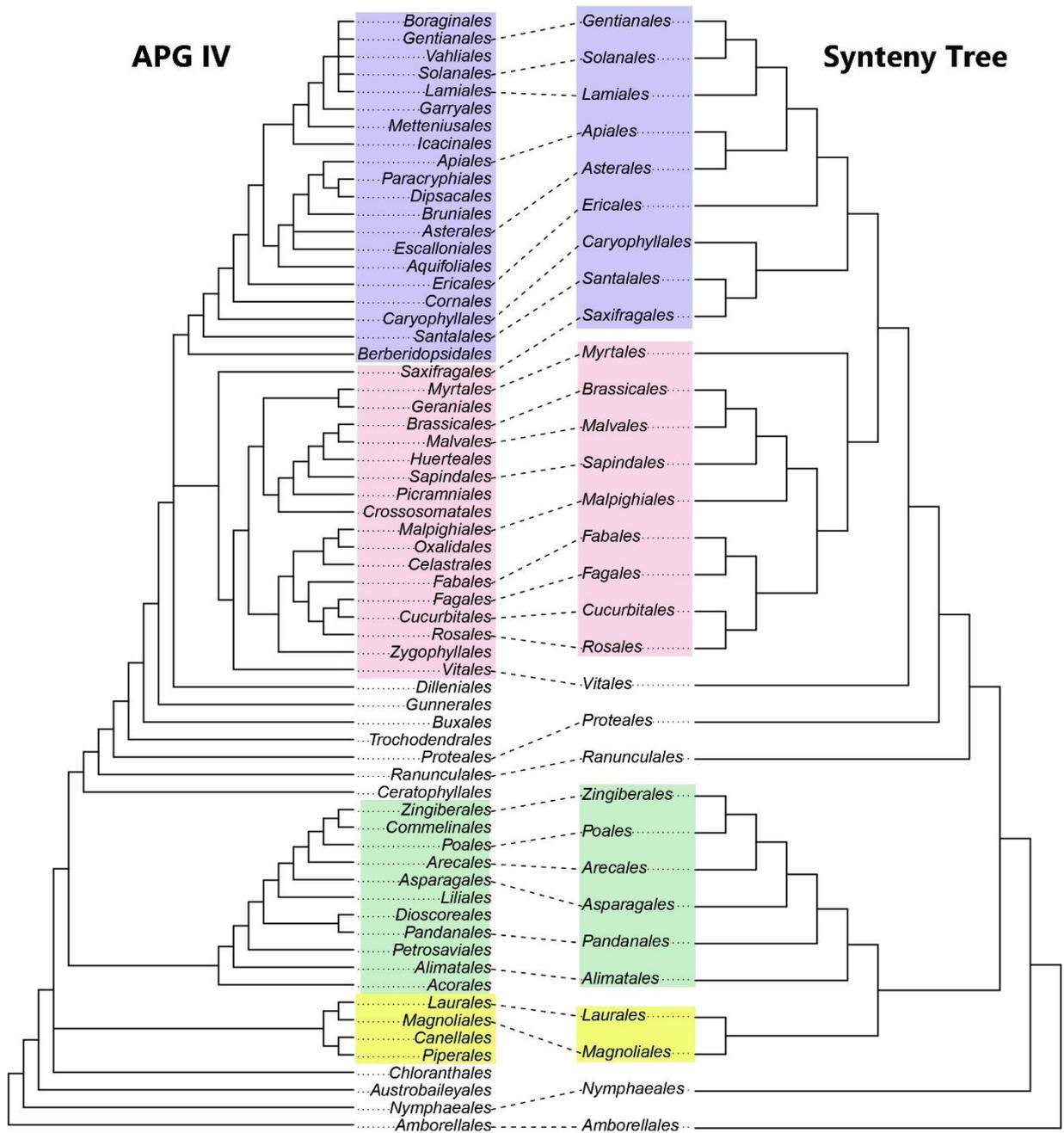
Supplementary Fig. 7 ASTRAL-CSSC tree.



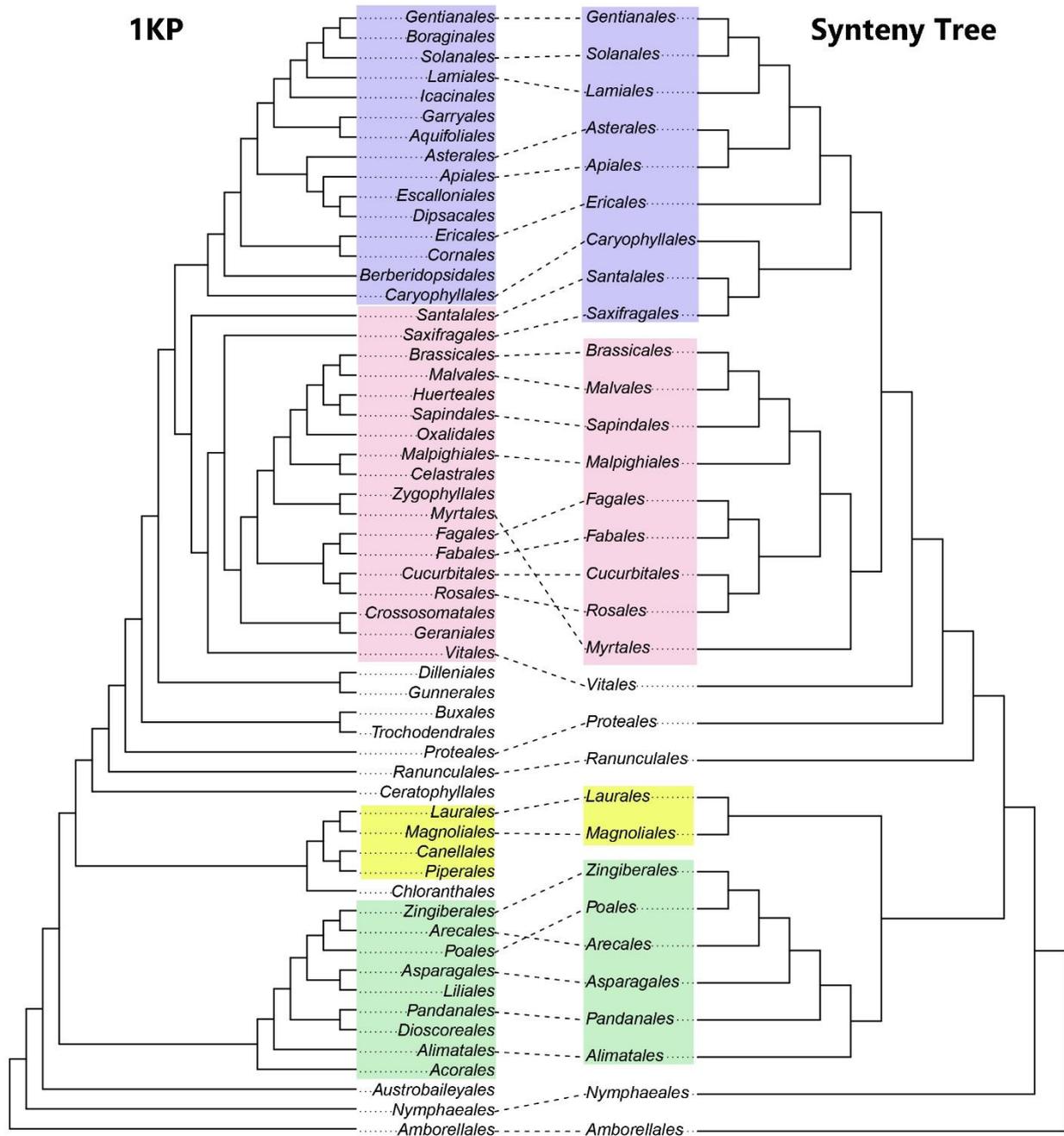
Supplementary Fig. 8 Comparison of synteny tree and the SA tree. Both trees are rooted by *Amborella*, and three main clades, i.e. superrosids, superasterids, and monocots are shaded in light-red, light-purple, and light-green, respectively. Eight differences are indicated by indexed black dots. Branches are not drawn to scale. Ultrafast bootstrapping values (see text for details) were marked for nodes with less than 100% support.



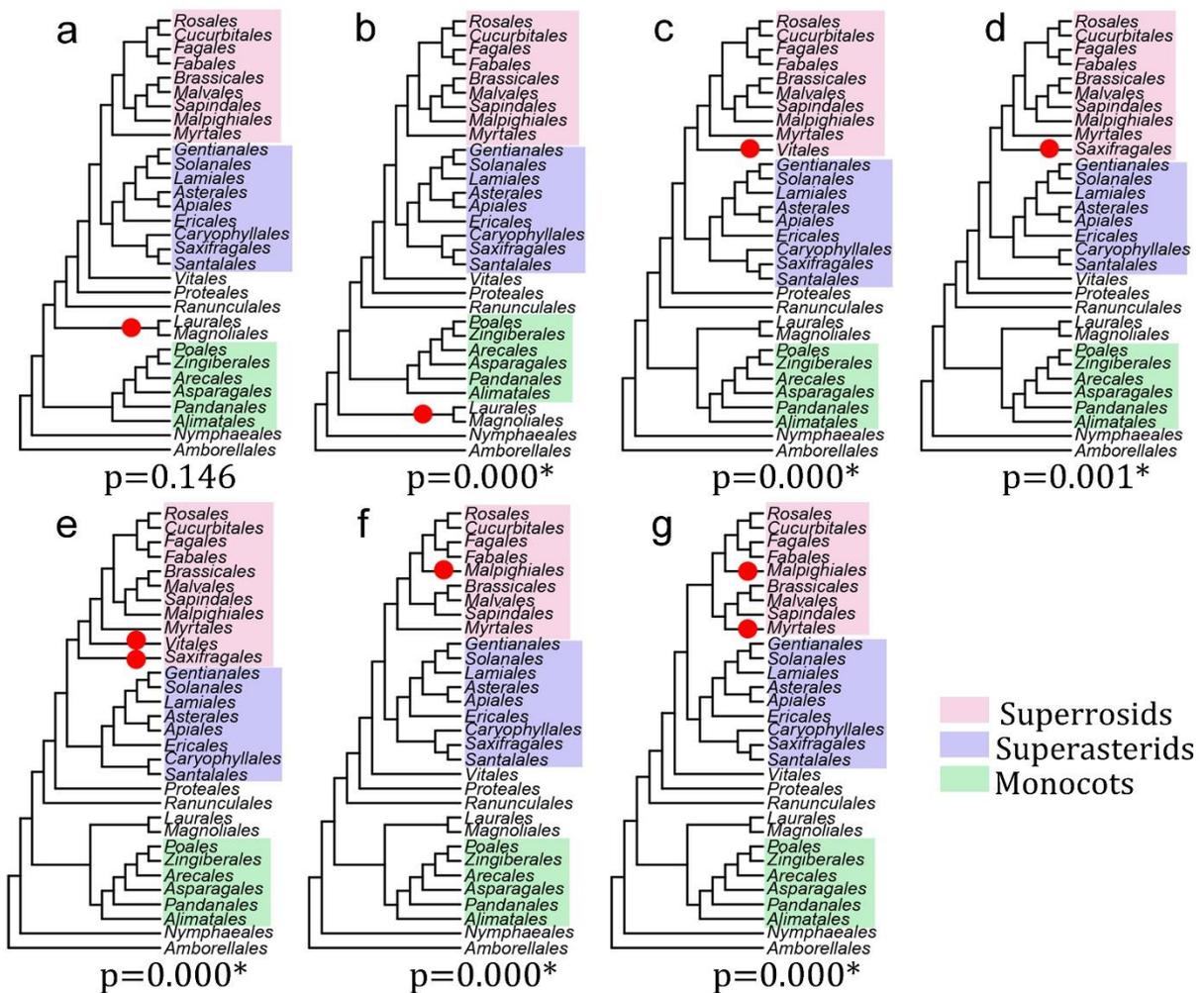
Supplementary Fig. 9 Comparison of phylogenetic relationships between the phylogeny of Angiosperm Phylogeny Group IV and 1KP.



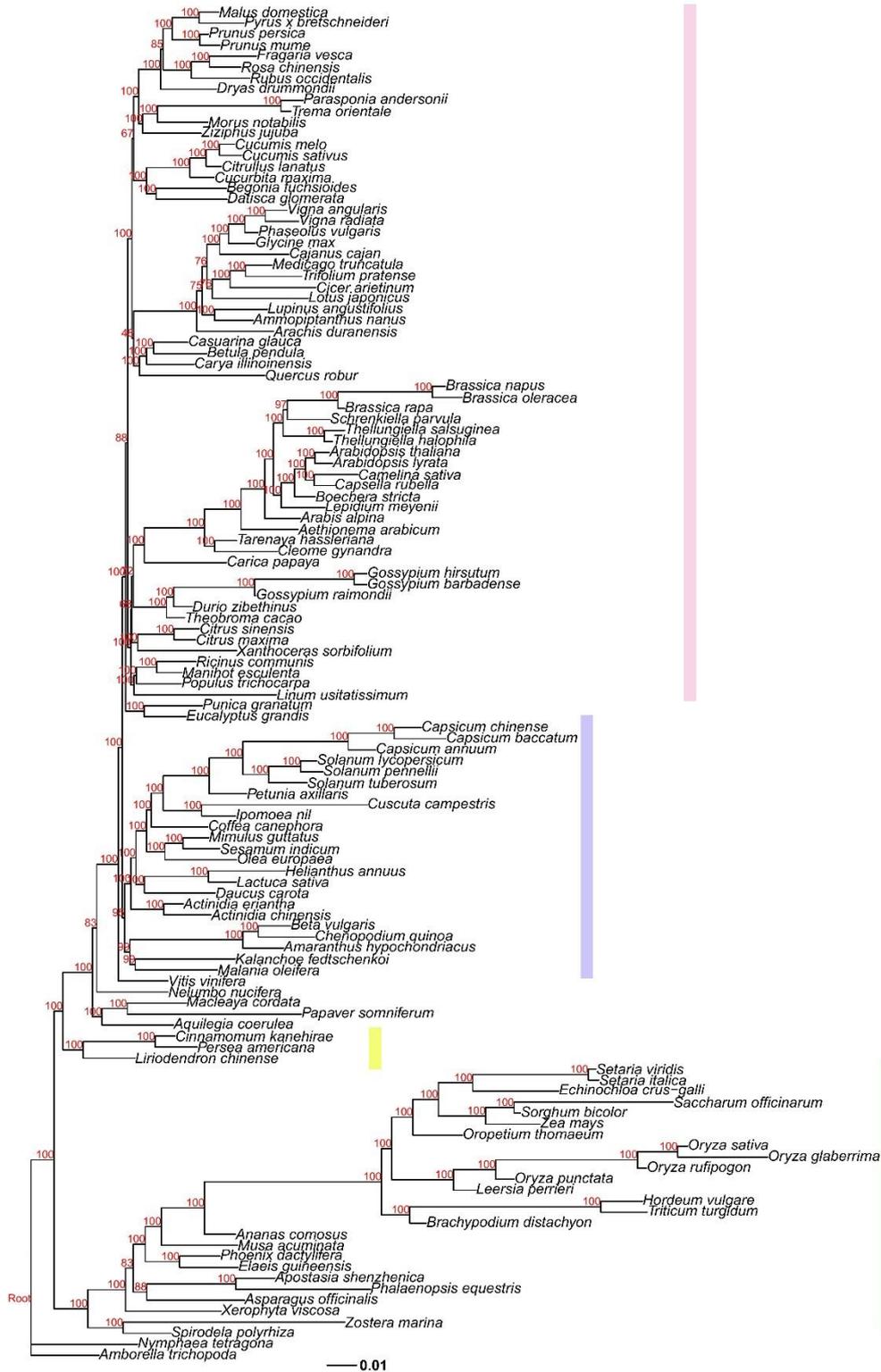
Supplementary Fig. 10 Comparison of phylogenetic relationships between APG IV and the synteny tree.



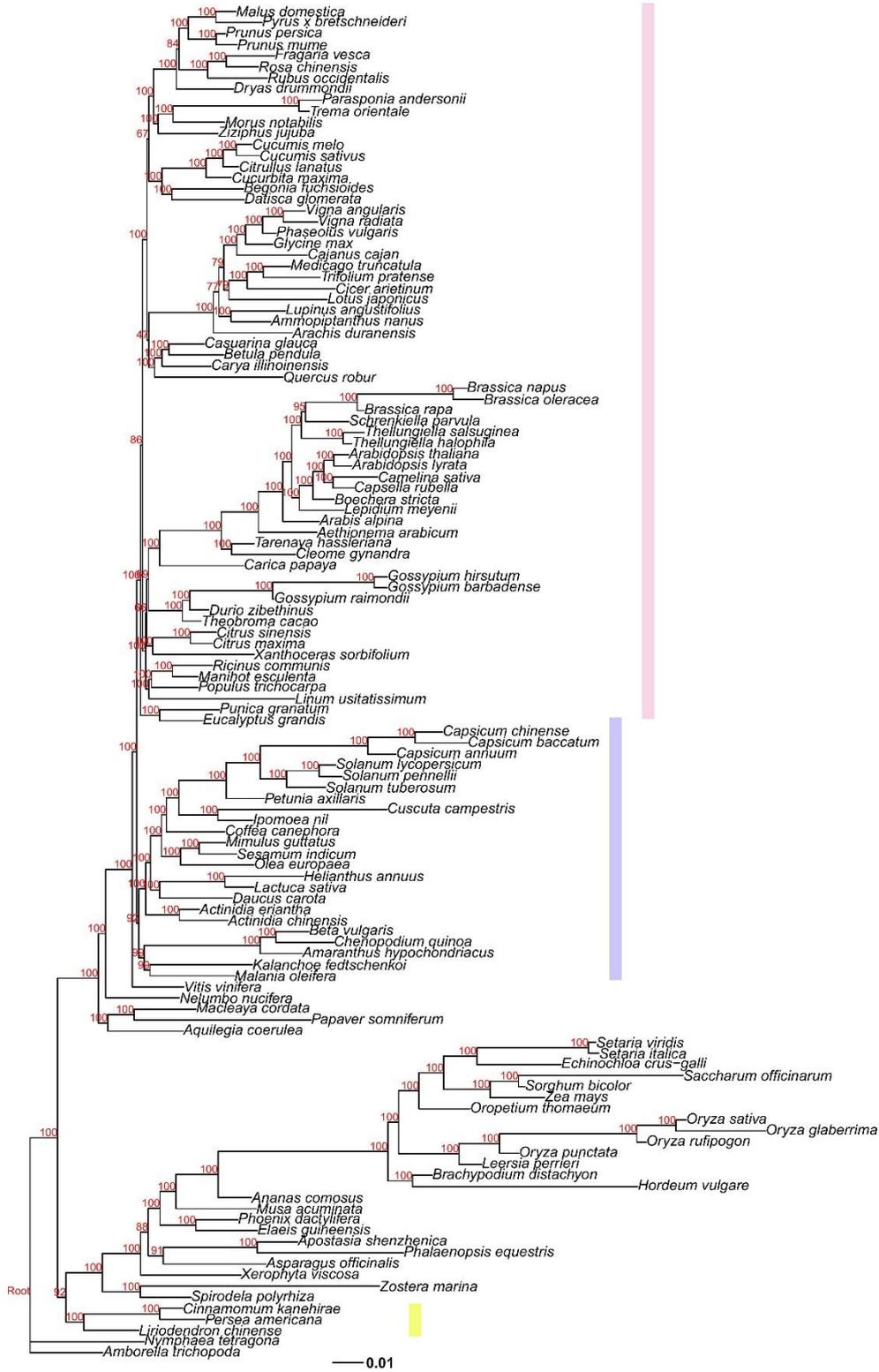
Supplementary Fig. 11 Comparison of phylogenetic relationships between the phylogeny of 1KP study (angiosperms part) and the synteny tree.



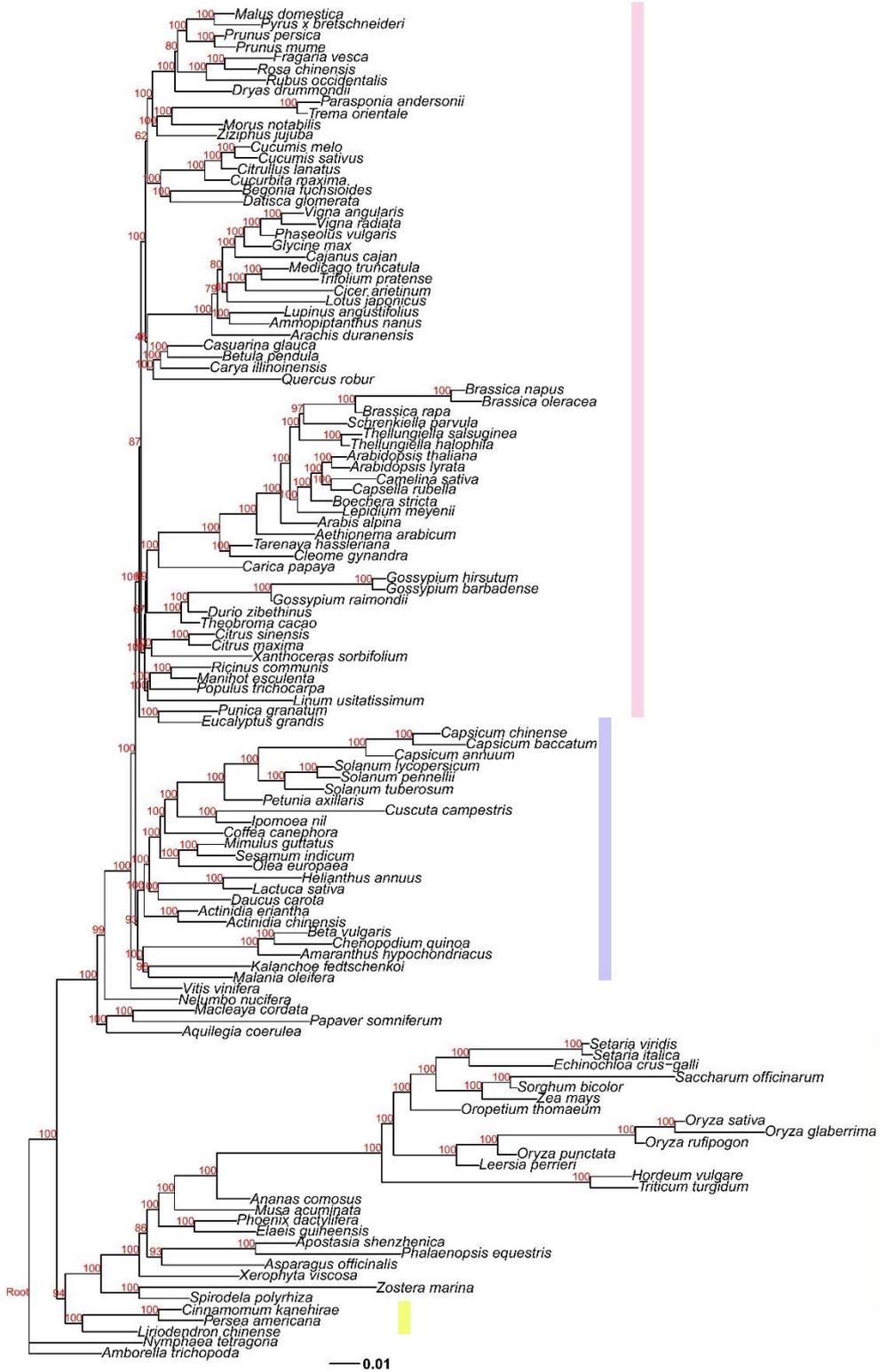
Supplementary Fig. 12 Approximate unbiased (AU) test for alternative topologies, with resulting p values indicated under the trees. Alternative (tested) topologies include (a) magnoliids as sister to eudicots, which is the only scenario tested that cannot be significantly rejected (see text for details). (b) magnoliids as sister to both monocots and eudicots, (c) Vitales as early-diverging rosids, (d) Saxifragales as early-diverging rosids, (e) Vitales and Saxifragales as early-diverging rosids, (f) Malpighiales as early-diverging Fabids, and (g) Malpighiales as early-diverging Fabids plus Myrtales as early-diverging Malvids.



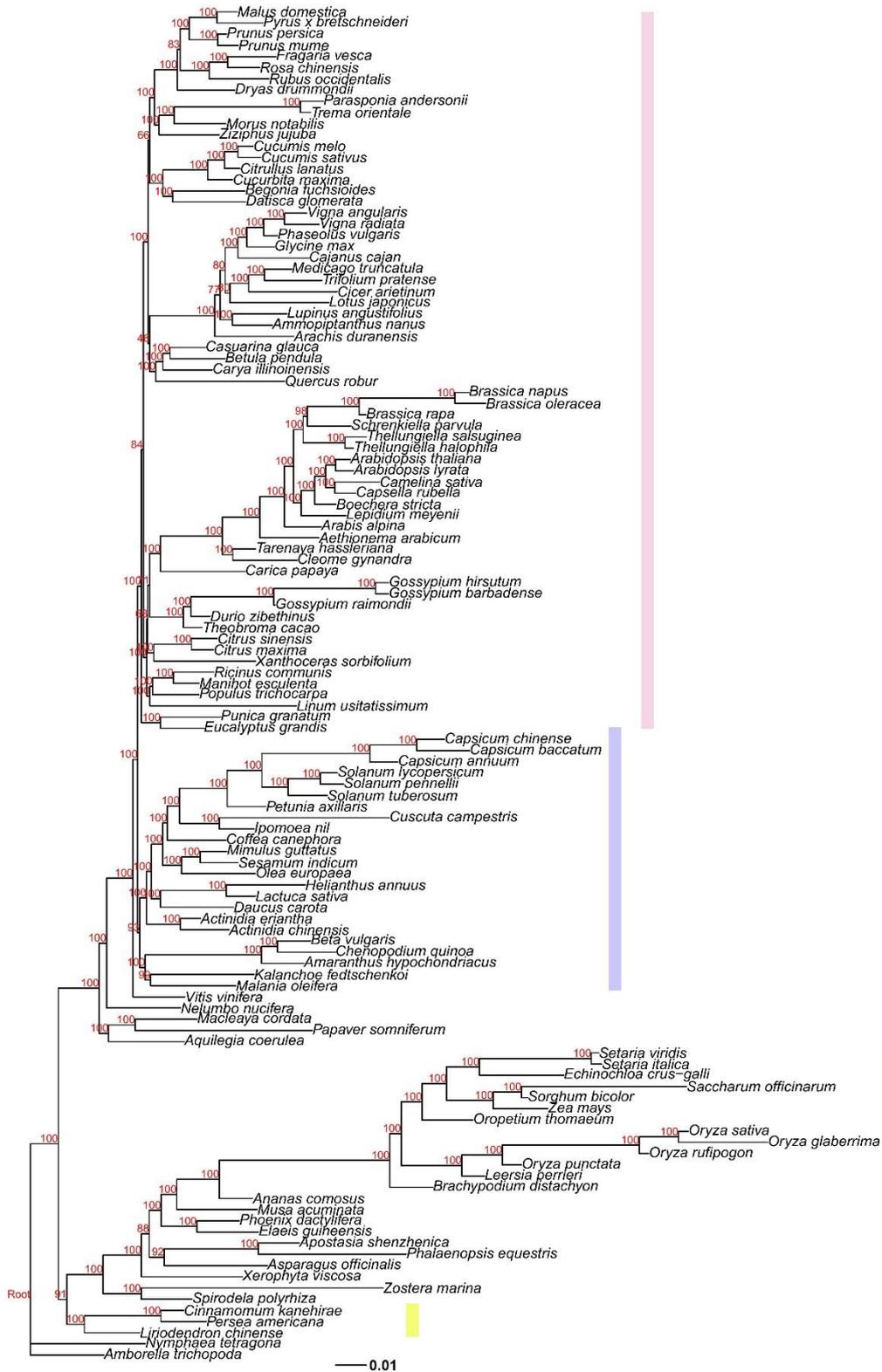
Supplementary Fig. 13 Syn-MRL tree based on the synteny matrix without 1107 (Figure 4a) specific signals.



Supplementary Fig. 14 Syn-MRL tree based on the synteny matrix without *Triticum turgidum* (wheat).



Supplementary Fig. 16 Syn-MRL tree based on the synteny matrix without *Brachypodium distachyon* (*Brachypodium*).



Supplementary Fig. 17 Syn-MRL tree based on the synteny matrix without *Triticum turgidum*(wheat) and *Hordeum vulgare* (barley).