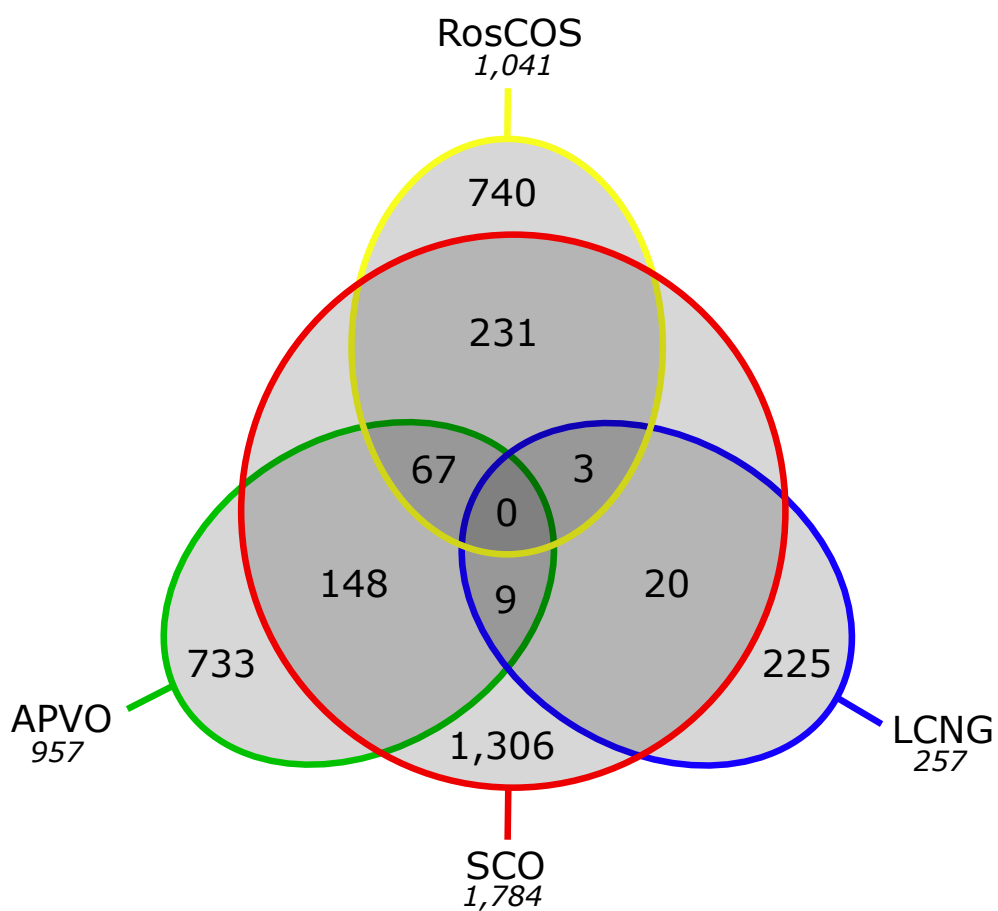
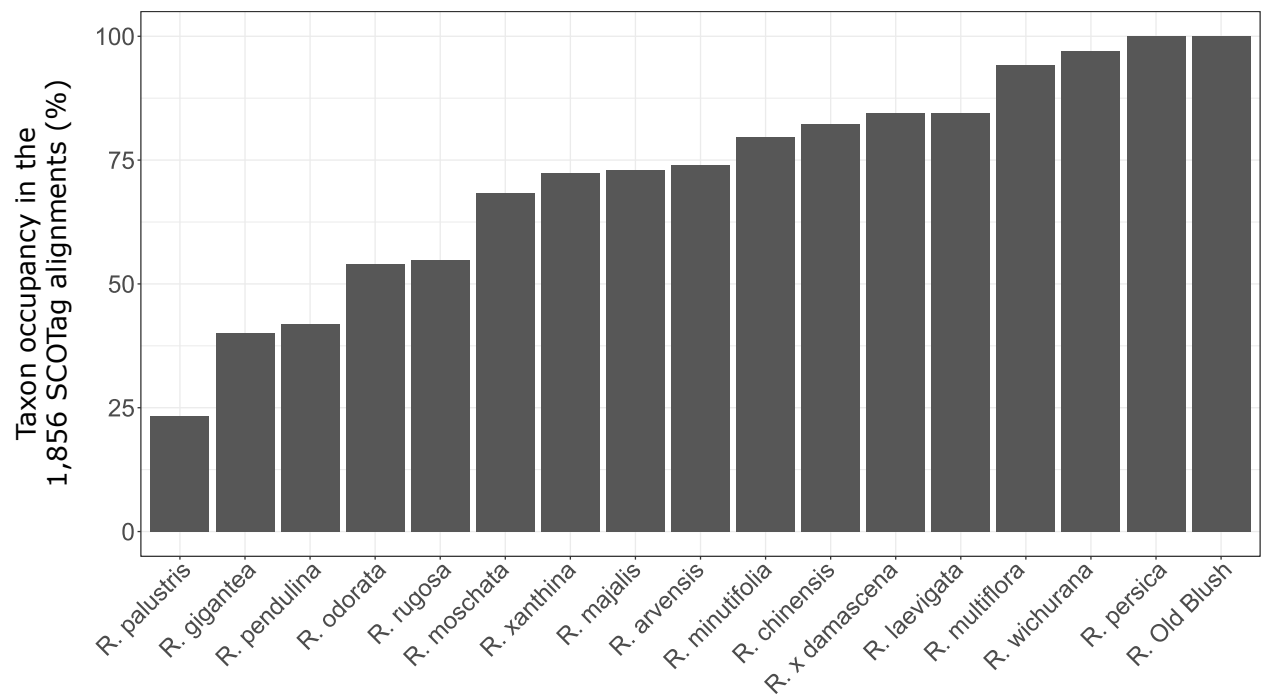


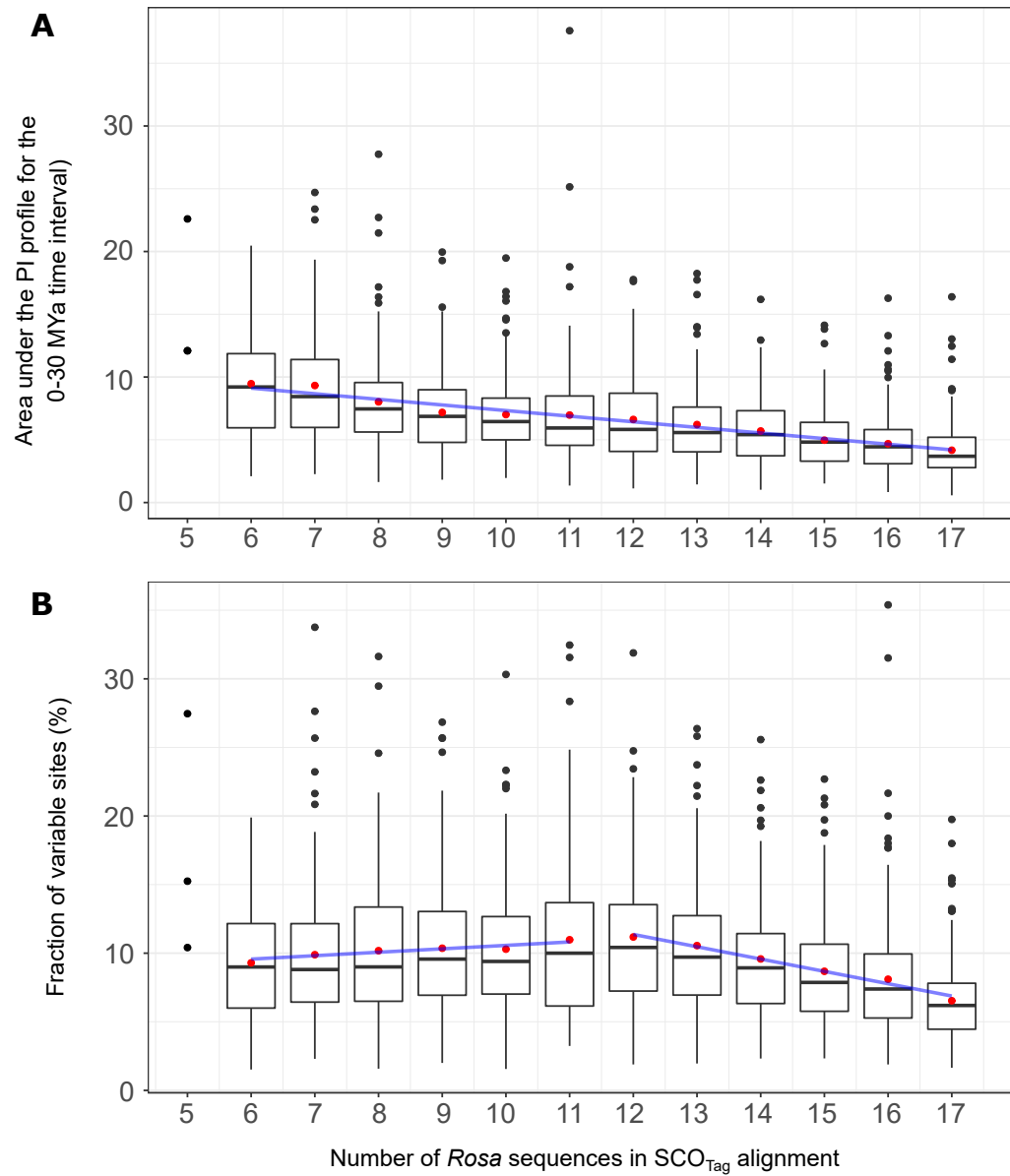
Supplementary Figure S1. Synteny analysis of the 1,784 Single-Copy Orthologs between the genome assemblies of *Fragaria vesca* and *R. 'Old Blush'*



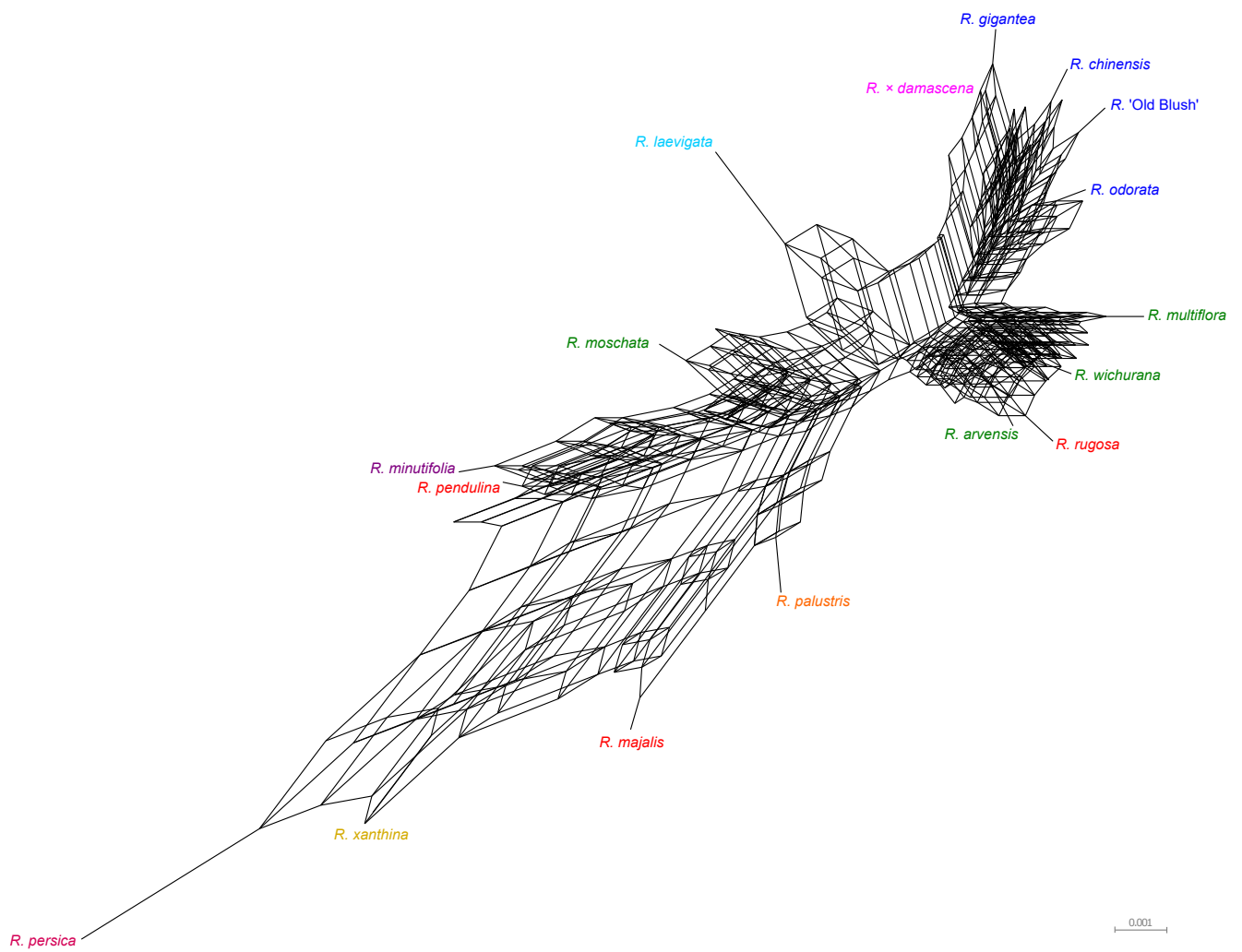
Supplementary Figure S2. Venn diagram showing the overlapping of the 1,784 Single-Copy Orthologs (SCO) with 3 already published datasets. APVO refers to the *Arabidopsis*, *Populus*, *Vitis*, *Oryza* dataset [23], LCNG refers to the Low-Copy Nuclear Genes found by [27] and RosCOS corresponds to the Rosaceae Conserved Ortholog Set of markers [26].



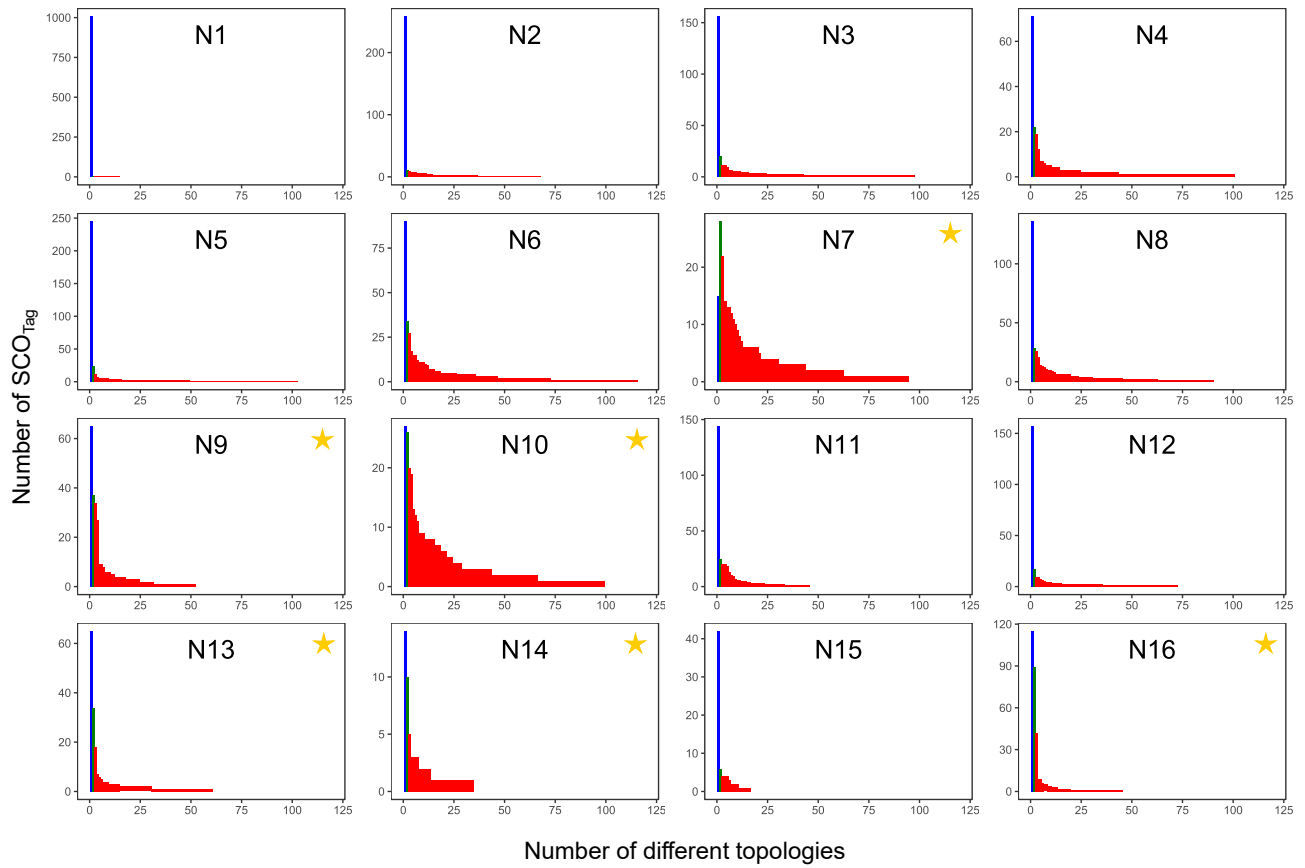
Supplementary Figure S3. Taxon occupancy of the *Rosa* ingroup for the 1,856 SCOTag_s.



Supplementary Figure S4. Impact of taxon occupancy on A) the area under PI profiles for the 0-30 MYa time interval ([6-17]: $y=11.8-0.45x$, $R^2=0.18$) and B) the fraction of variable sites in SCO_{Tag} alignment ([6-11]: $y=8.1+0.25x$, $R^2=0.004$; [12-17]: $y=22.1-0.90x$, $R^2=0.11$). Red dots indicate the mean values. Situations with less than 30 points were plotted but not used in the calculation of correlations.



Supplementary Figure S6. Network representing the conflict between the 1,856 SCOTag trees for the *Rosa* ingroup. Species colors follow Figure 3.



Supplementary Figure S5. Number of SCO_{Tag}s supporting each bipartition. Each plot title indicates the node name as shown in Figure 4. Blue represents the SCO_{Tag}s that support the species-tree bipartition (ie. concordant SCO_{Tag}s), green indicates the SCO_{Tag}s that agree with the main alternative bipartition (ie. main conflicting SCO_{Tag}s) and red corresponds to SCO_{Tag}s that support other alternative bipartitions (ie. other conflicting SCO_{Tag}s). Stars indicate nodes with significant conflicts, ie the proportion of SCO_{Tag}s supporting the main alternative bipartition is greater than 50% of the proportion of SCO_{Tag}s supporting the species-tree bipartition.