

**Supplementary Figure 3.** Phylogenetic tree of *Qs*HMTs and their orthologous sequences. Three well individualized clusters are defined with *Q. suber* proteins grouping with its orthologous sequences (arrows). Tree was constructed on MEGA 7 software, using the maximum likelihood method and a bootstrap of 1000. All protein sequences were aligned with MUSCLE and the alignment was trimmed with GBLOCKS. The protein sequences of angiosperms used in the analysis are listed in Supplementary Table 1.

