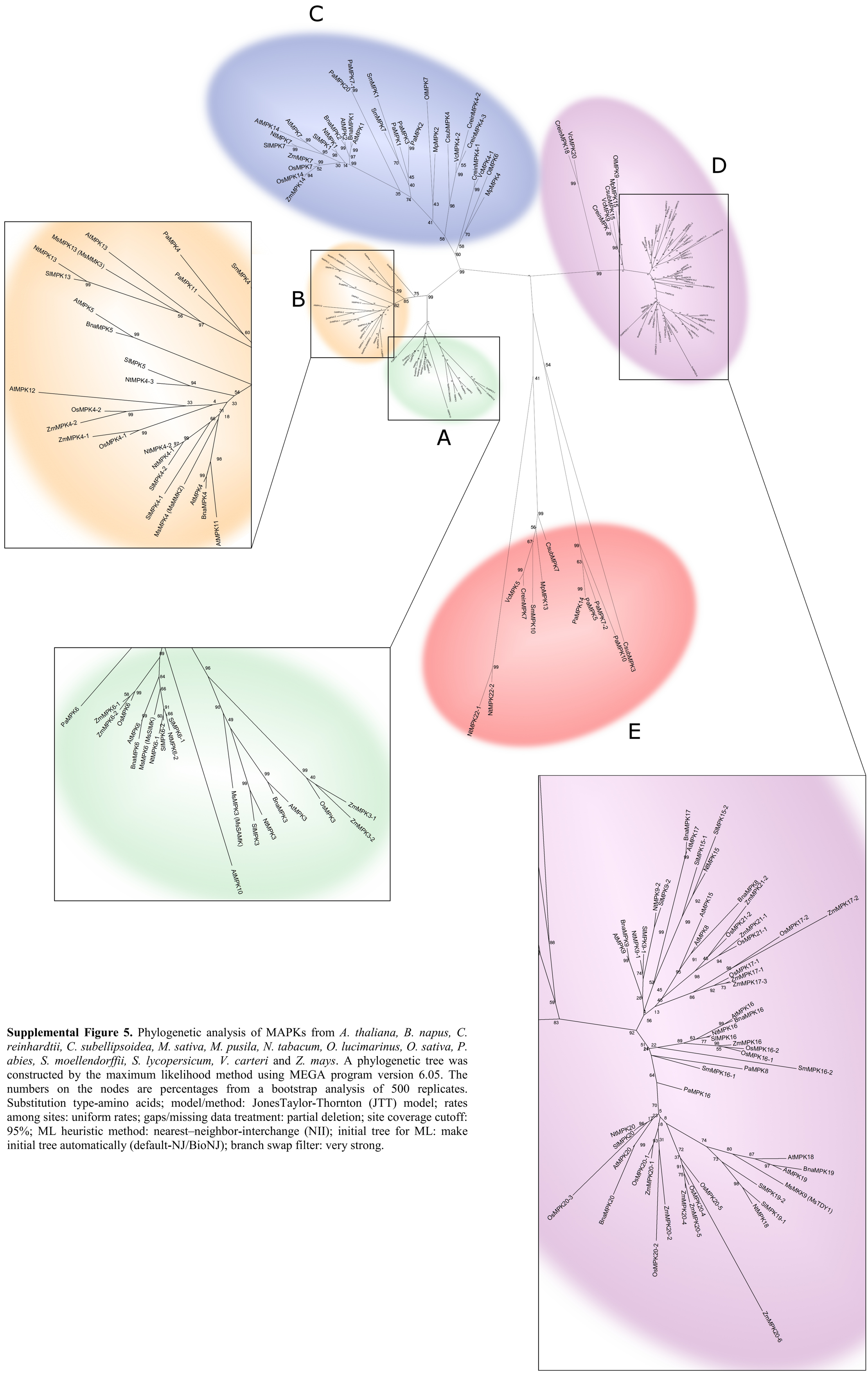

Supplemental Figure 5. Phylogenetic analysis of MAPKs from *A. thaliana, B. napus, C. reinhardtii, C. subellipsoidea, M. sativa, M. pusila, N. tabacum, O. lucimarinus, O. sativa, P. abies, S. moellendorffii, S. lycopersicum, V. carteri* and *Z. mays*. A phylogenetic tree was constructed by the maximum likelihood method using MEGA program version 6.05. The numbers on the nodes are percentages from a bootstrap analysis of 500 replicates. Substitution type-amino acids; model/method: JonesTaylor-Thornton (JTT) model; rates among sites: uniform rates; gaps/missing data treatment: partial deletion; site coverage cutoff: 95%; ML heuristic method: nearest–neighbor-interchange (NII); initial tree for ML: make initial tree automatically (default-NJ/BioNJ); branch swap filter: very strong.