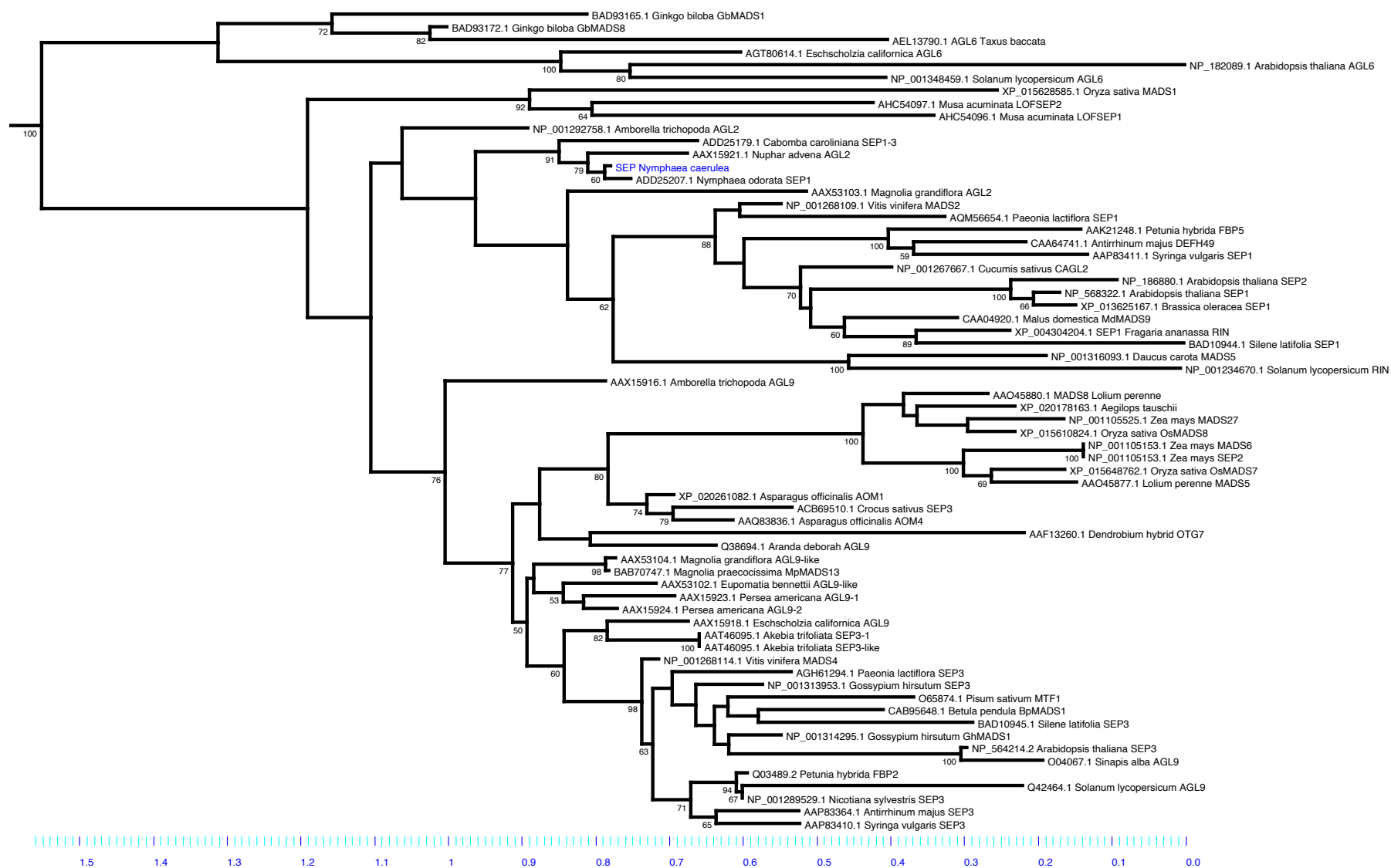




Supplementary Figure 5. Maximum-likelihood tree of 58 representatives of E lineage protein sequences plus the NycSEP protein. The tree has been generated using the PhyML package included in the software Seaview v. 4.7. The analysis was performed applying 5 random starts and 100 bootstrap replicates. The evolutionary distances were computed using the JTT matrix-based method and are in the units of the number of amino acid substitutions per site. *N. caerulea* sequence is evidenced in blue. The tree has been rooted using AGL6 protein sequences.