Supplementary Figures

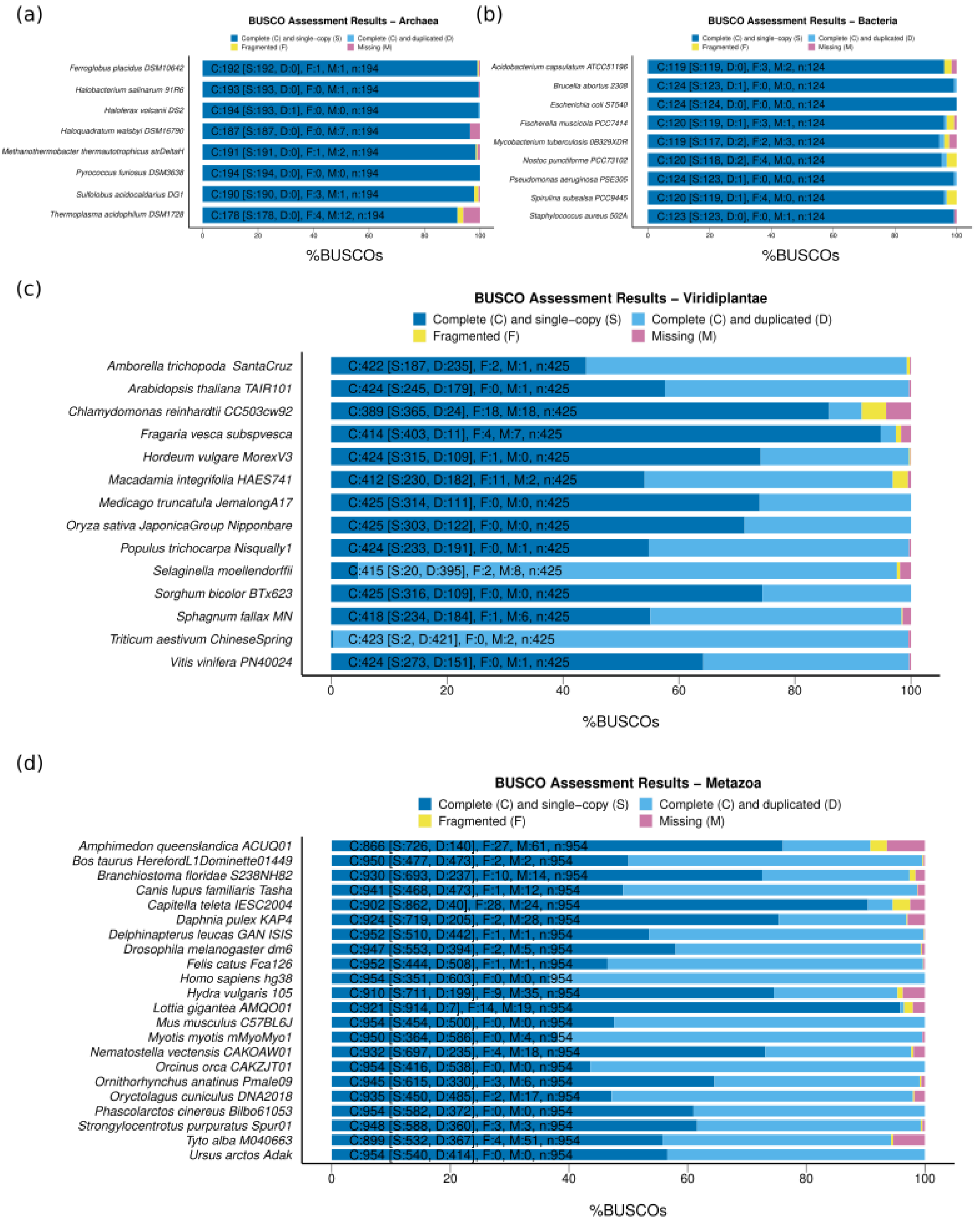


Fig S1. BUSCO assessment results of completeness for gene annotations for various taxa.
The taxa shown here are: (a) Archaea, (b) Bacteria, (c) Plants (Viridiplantae), and (d) Animals (Metazoa).

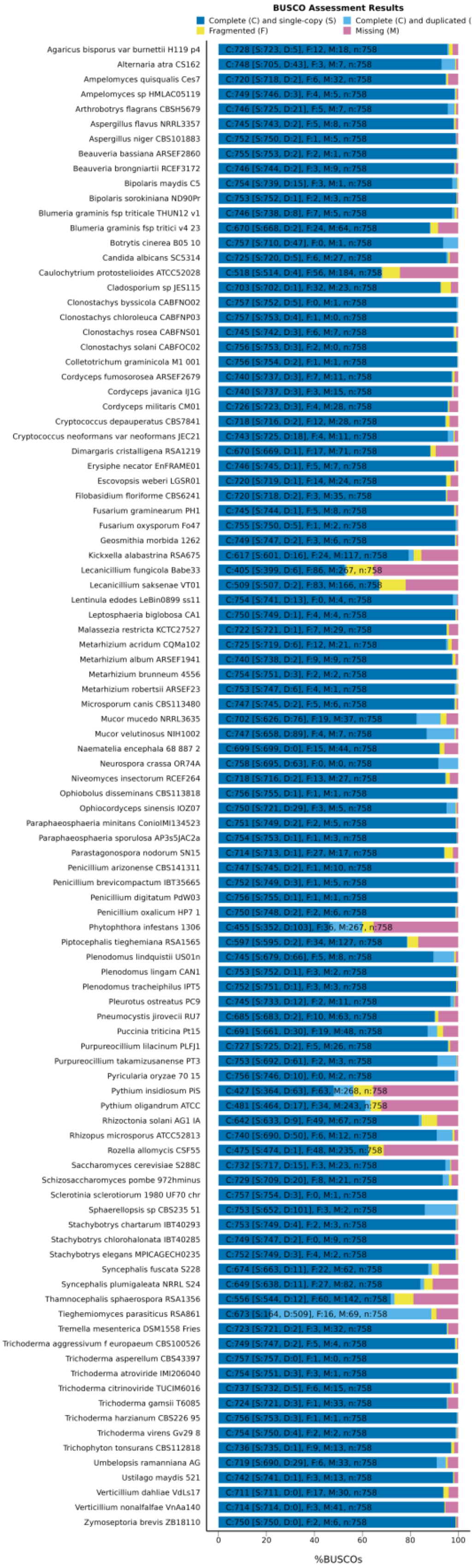
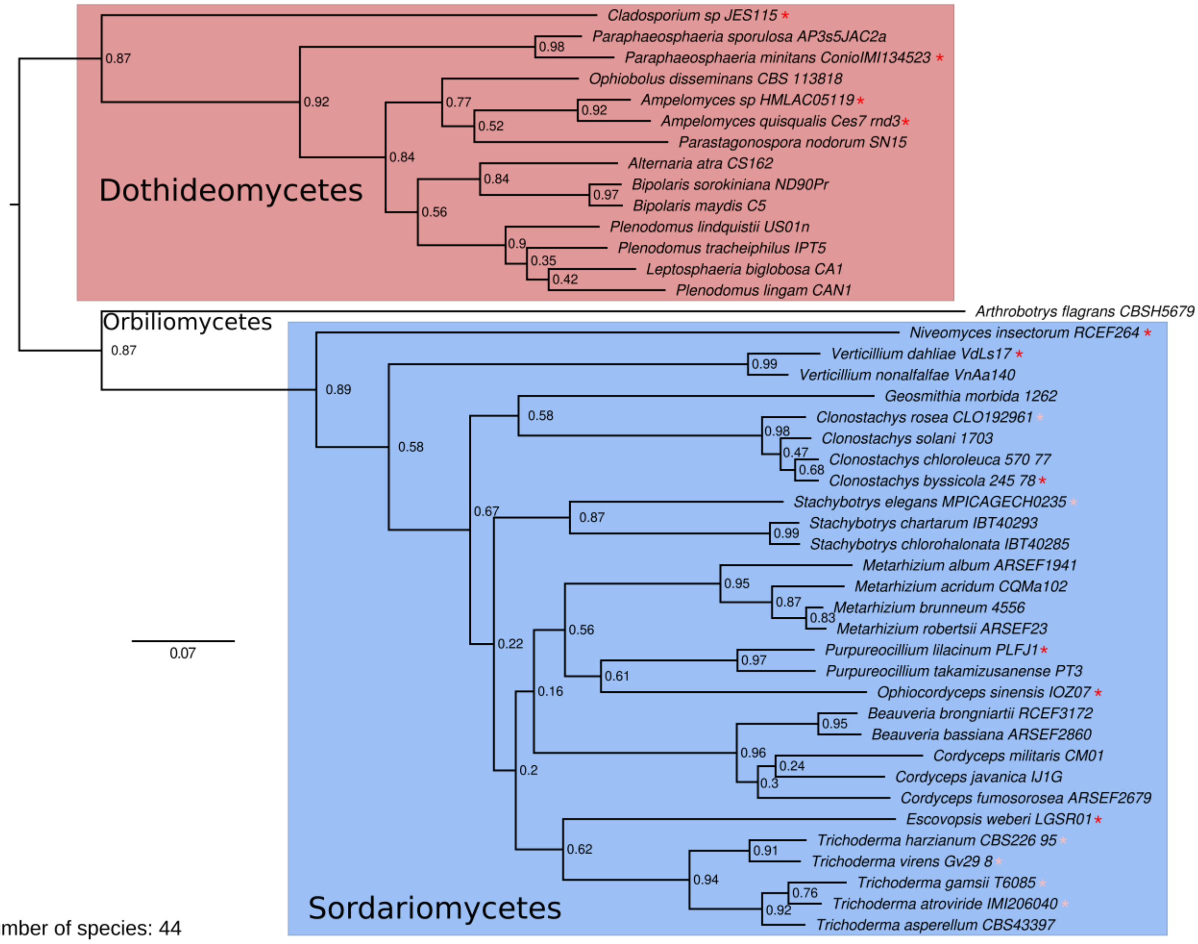


Fig S2. BUSCO assessment results of completeness for gene annotations for Fungi and Oomycetes.



Number of species: 44
Number of orthogroups with all species present: 2589
Number of single-copy orthogroups: 993

Fig S3. Cladogram using orthogroups with a subset of Ascomycete fungi.

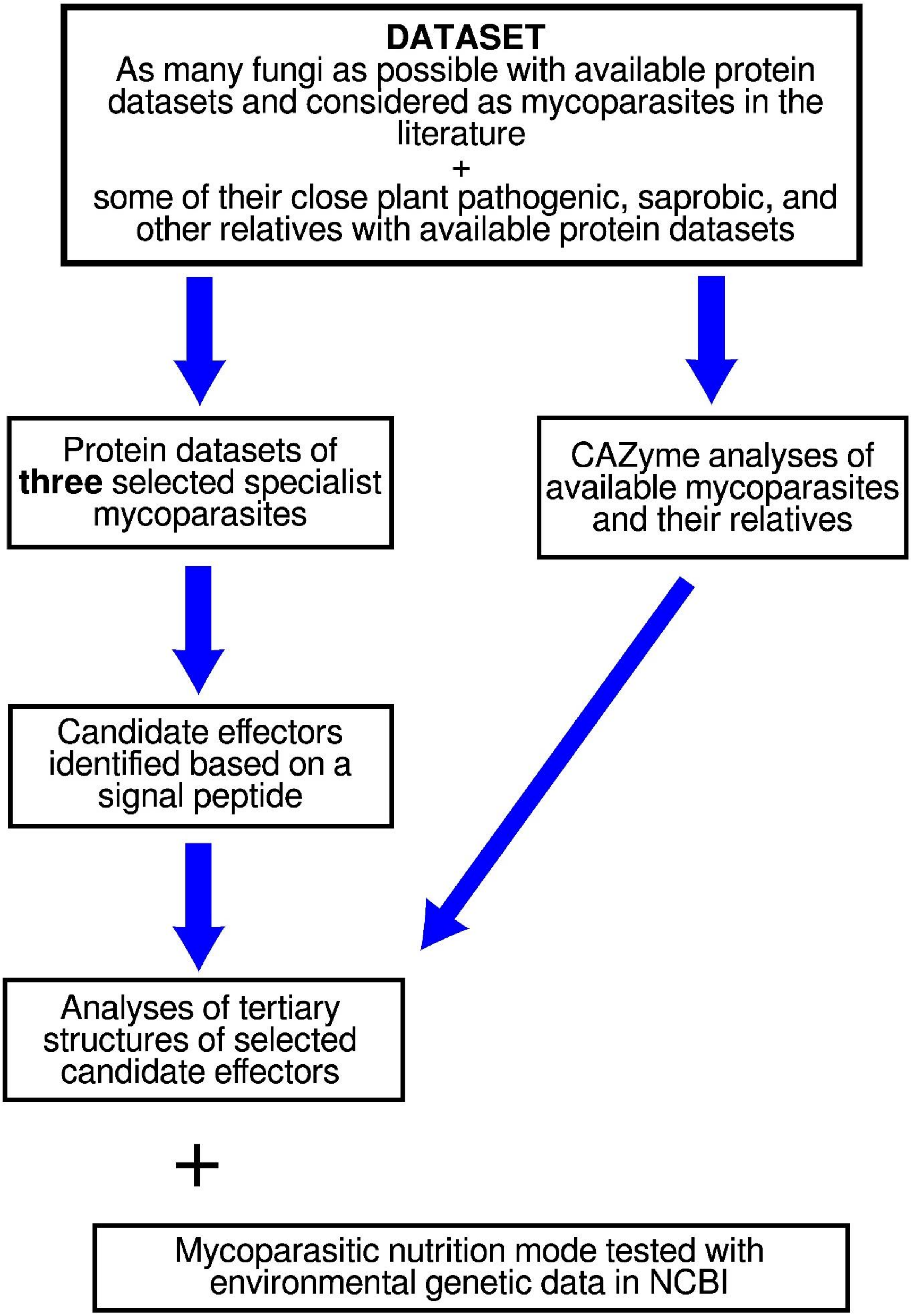


Fig S4. Diagram of the workflow for the main analyses used in this study.

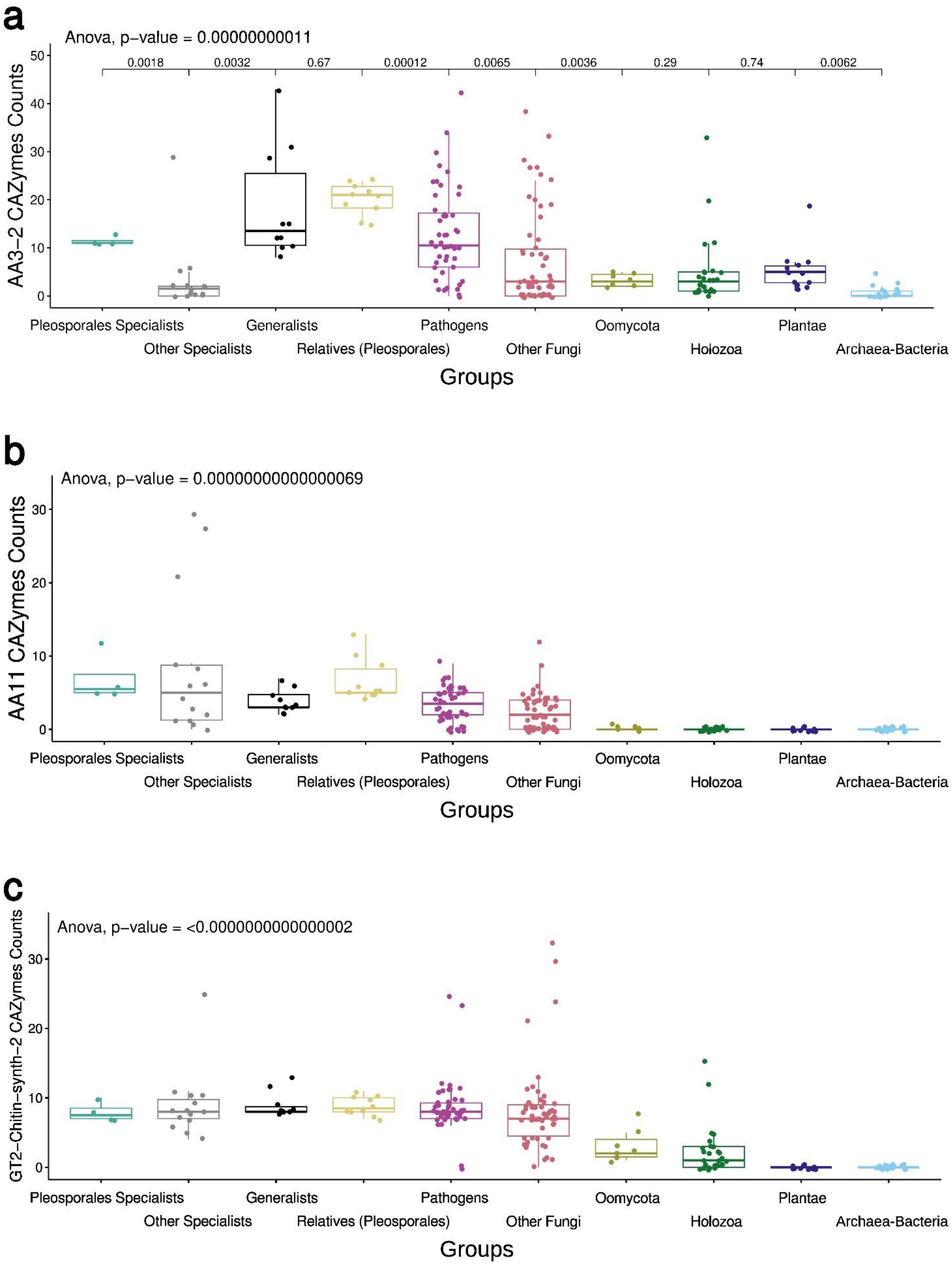


Fig S5. Counts of enzymes per species for three CAZyme families: (a) AA3-2, (b) AA11, and (c) GT2-Chitin.

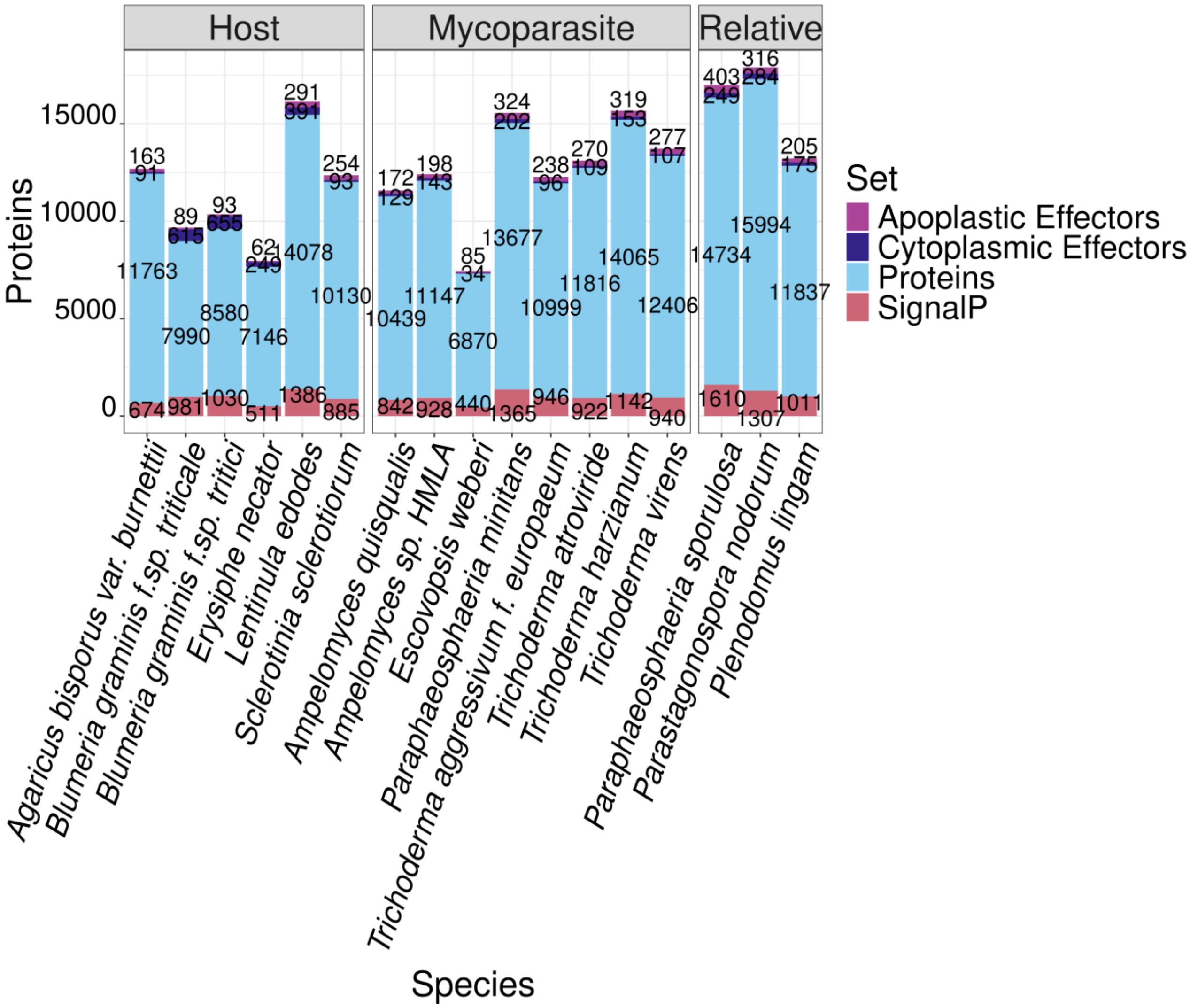


Fig S6. Number of proteins per genome annotation with different characteristics such as: proteins with signal peptide, and candidate effectors (apoplastic and cytoplasmic ones).

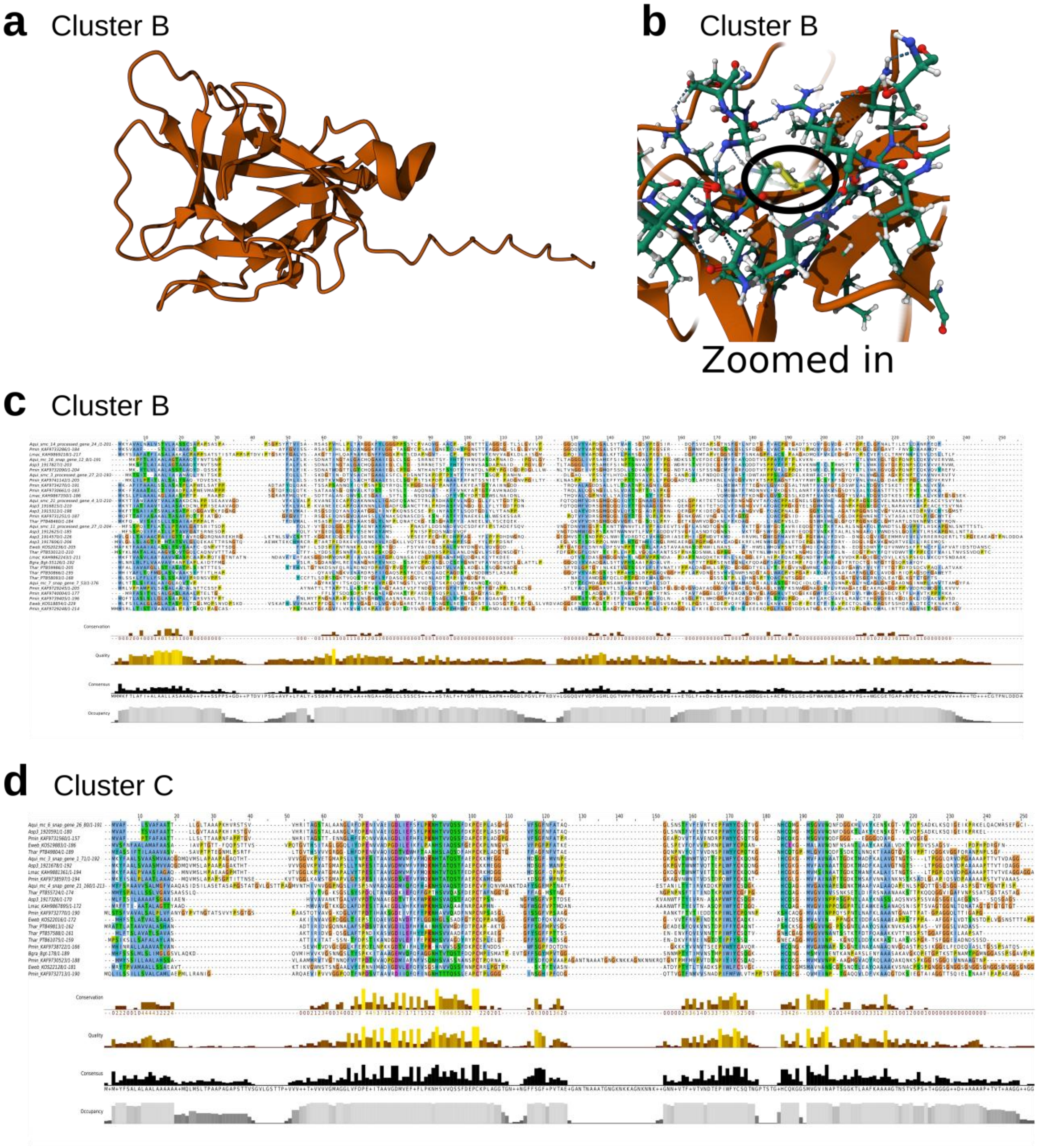


Fig S7. Alignments and structures of proteins of interest. (a) Protein structure of a Cluster B protein (from Fig. 4), (b) Zoomed in version of the protein from (a) with a cysteine bridge circle in yellow, (c) A protein alignment with ClustalW of all the proteins of Cluster B (from Fig. 4), and (d) A protein alignment with ClustalW of all the proteins of Cluster C (from Fig. 4).