**Supplementary Figures**

**Fig. S1.** (a) Schematic workflow for environmental *Dicranum scoparium* sampling and subsequent read mapping; (b) workflow for Fungal Nutrient Transporter Database (FNTD) construction; (c) workflow for assembling the Fungal CAZy Database (FCD); (d) workflow for Axenic *Dicranum scoparium* Transcriptome Database (ADTD) construction.

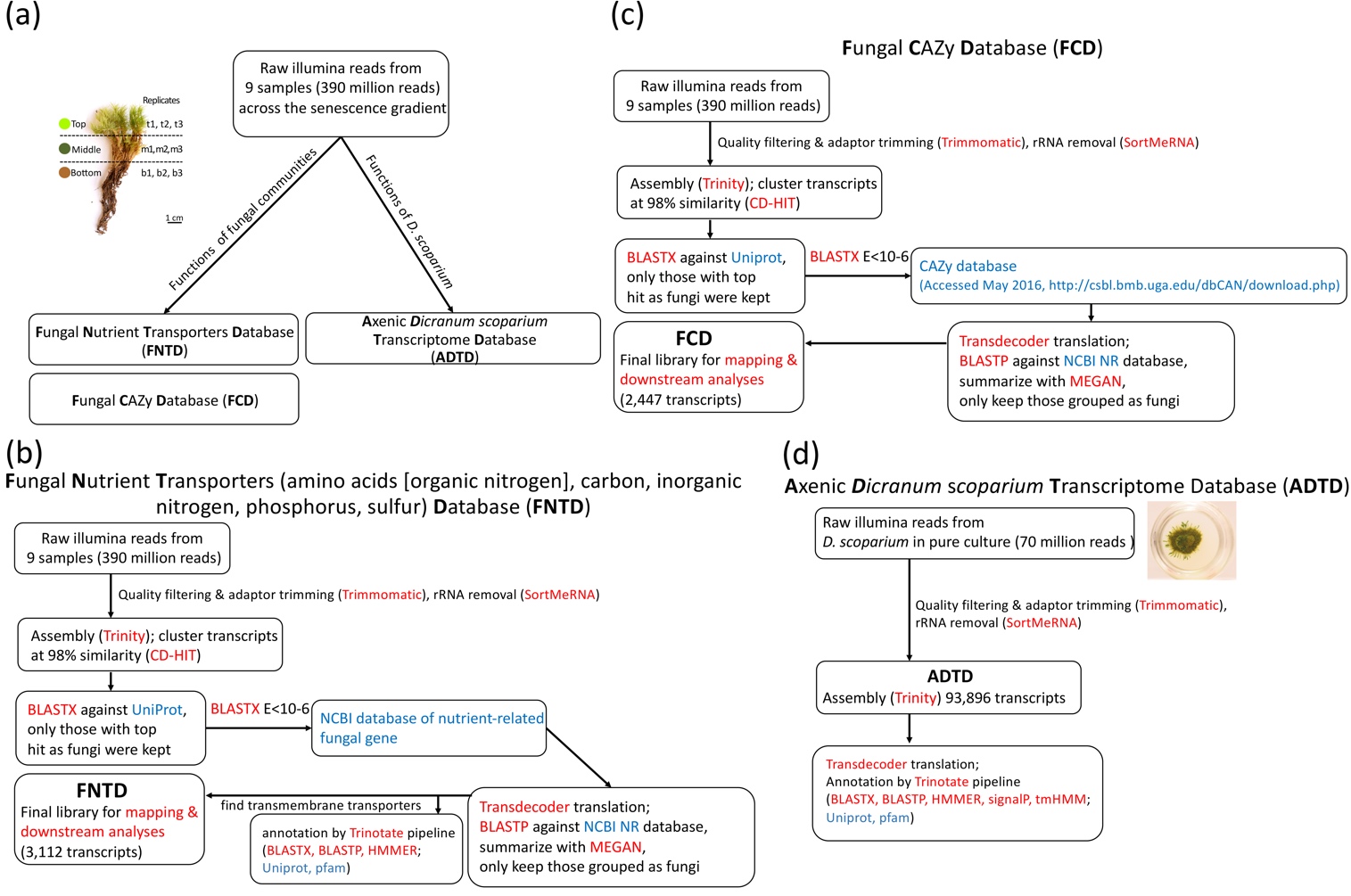
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Fig. S2. Percentage of reads mapped to assembled transcripts assigned to 10 taxonomic groups.

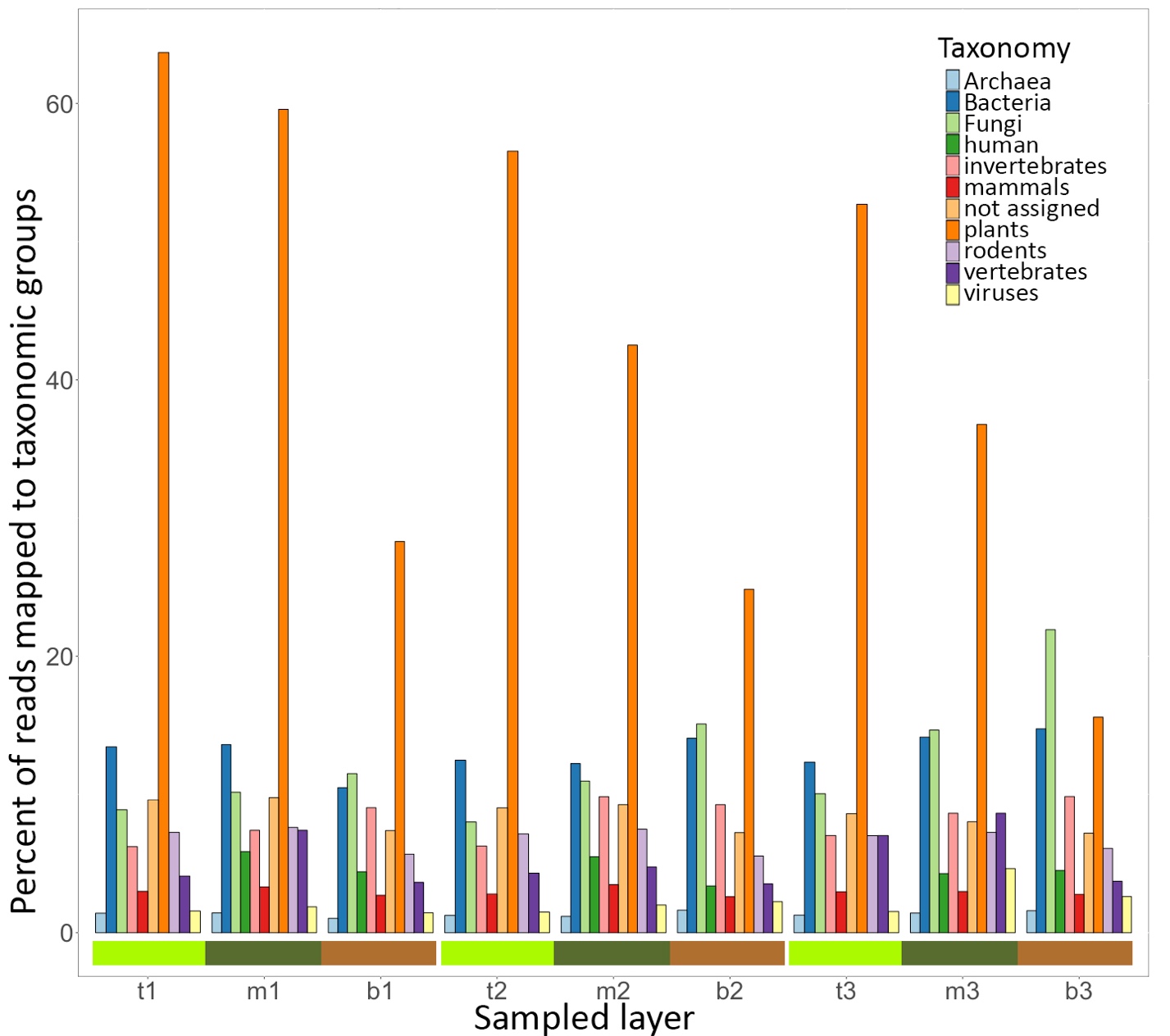


Fig. S3. Principal coordinate analyses of (a) Fungal Nutrient Transporters (FNTD), (b) fungal CAZy *(*FCD), and (c) axenic *Dicranum scoparium* (ADTD) expression levels across replicates and senescence layers of *D. scoparium*.

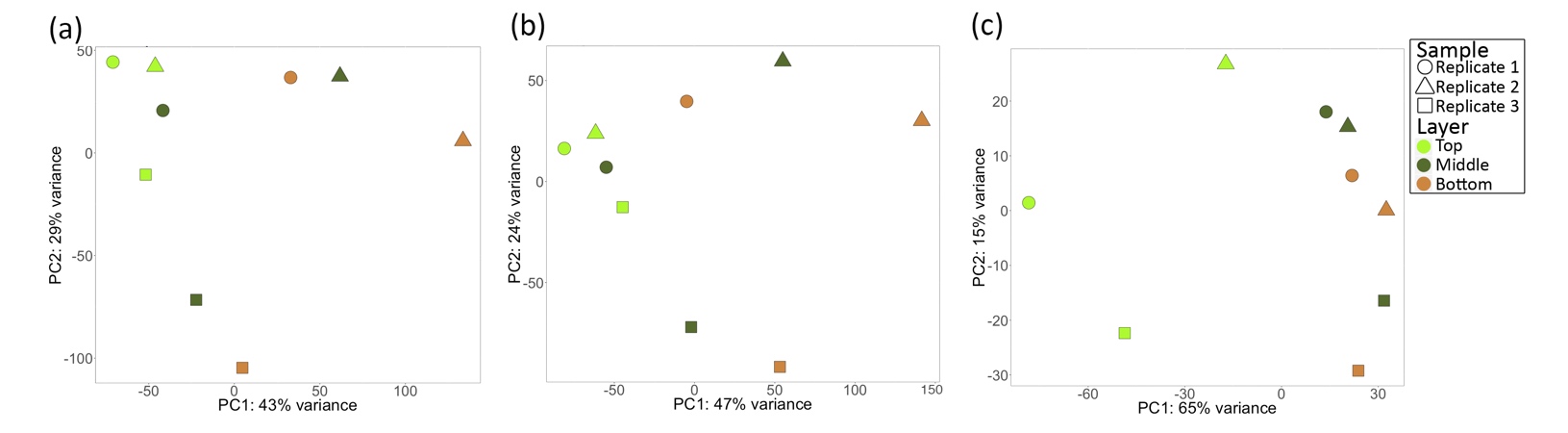


Fig. S4. Taxonomic distribution of 3,112 fungal nutrient transporter genes (amino acids [organic nitrogen], carbon, inorganic nitrogen, phosphorus and sulfur) found in fungal communities associated with *Dicranum scoparium*.

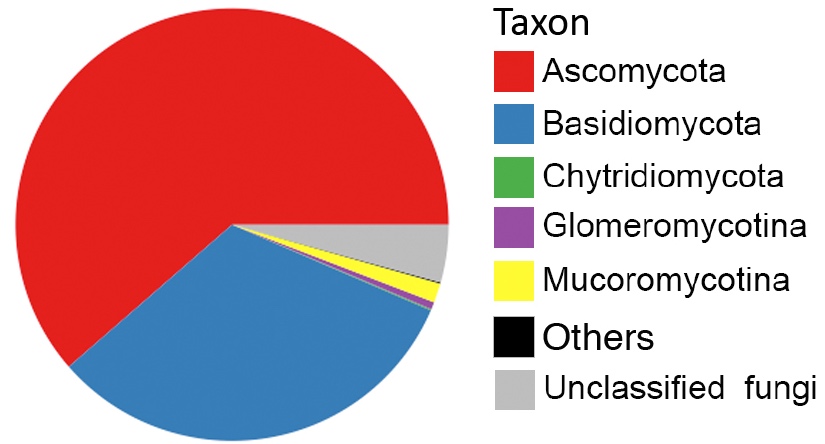
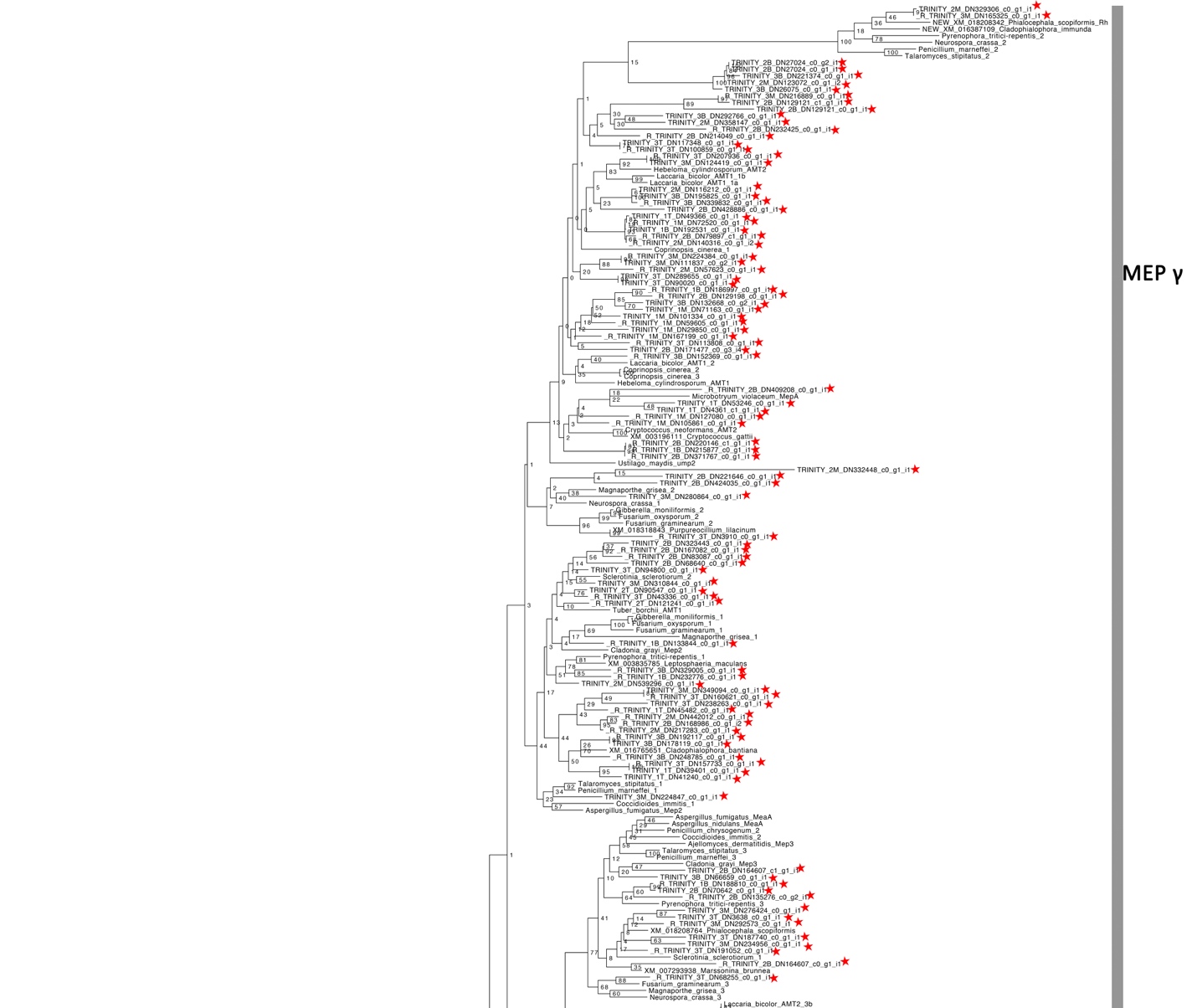
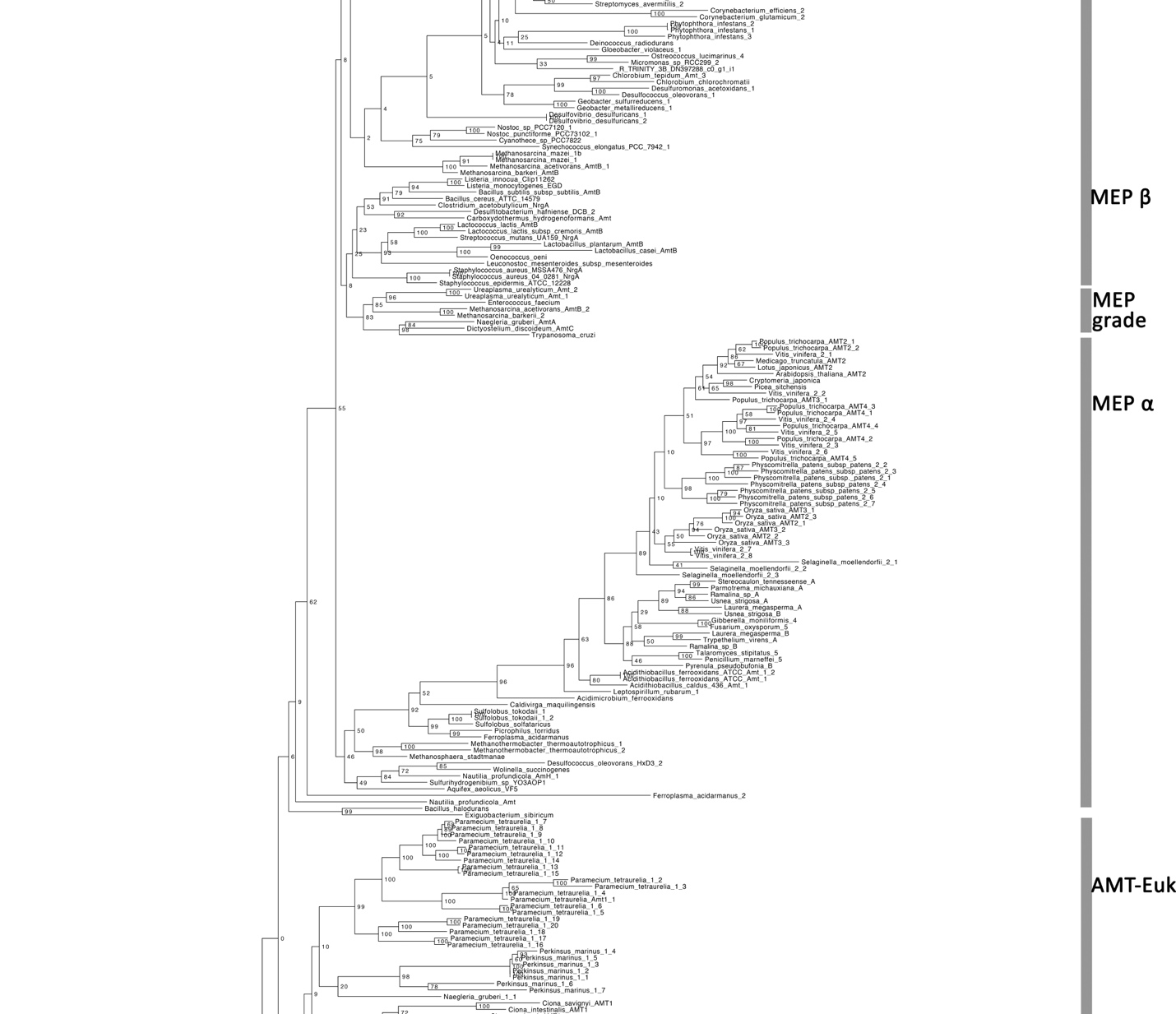


Fig. S5. Ammonium transporter/methylammonium permease/Rhesus factor (AMT/MEP/Rh) gene family ML tree. Nomenclature of the gene clades follows Mcdonald *et al.* (2012). Red asterisks show phylogenetic placement of ammonium transporters we detected from fungi associated with *Dicranum scoparium*.







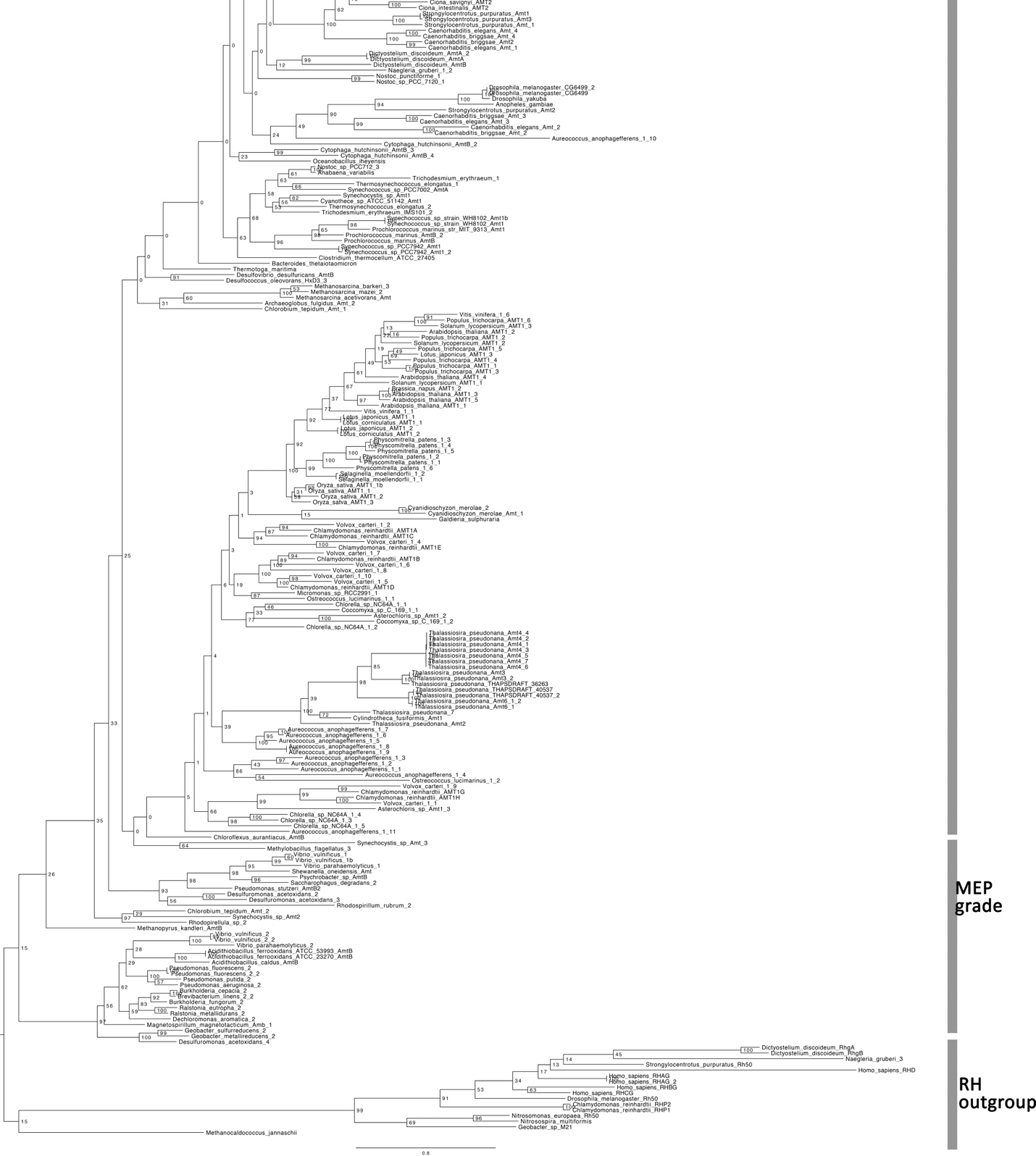


Fig. S6. Expression levels of commonly expressed LRR/defense/symbiosis related genes of *D. scoparium* in the top and bottom layers.

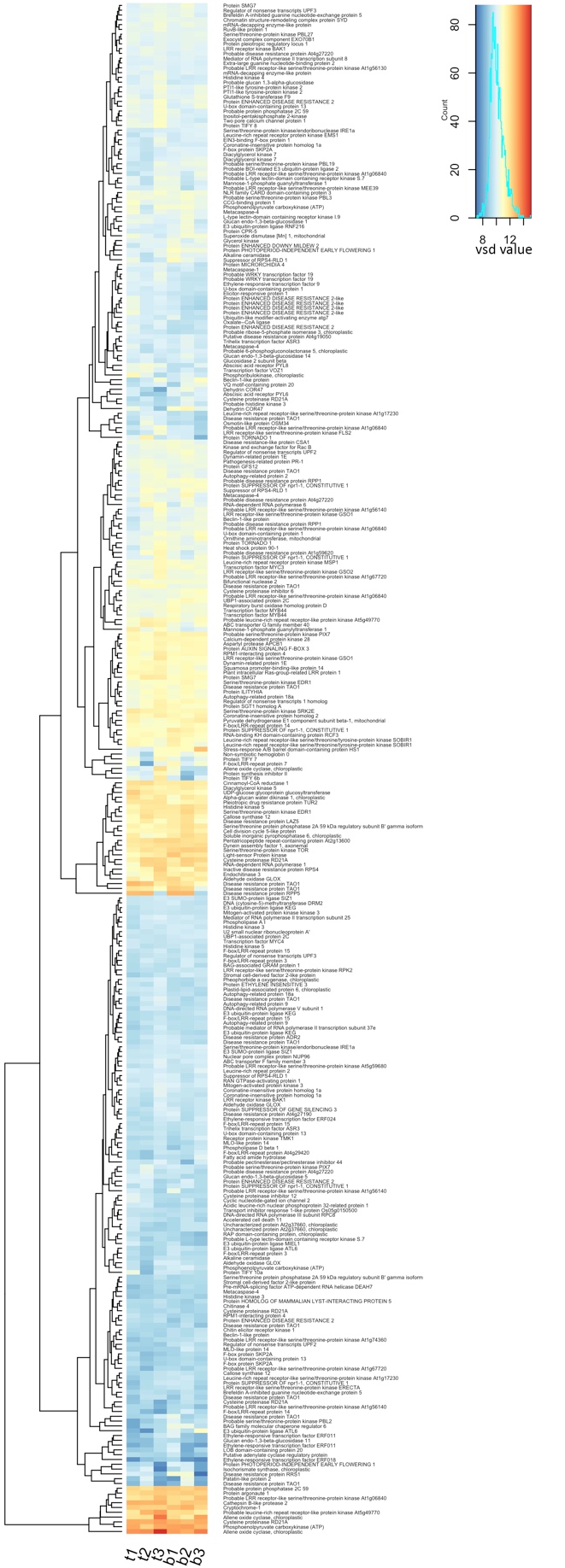


Fig. S7. Differentially expressed genes of *D. scoparium* associated with enriched catabolic processes (GO term enriched, P < 0.05).

