

Supplementary figures:

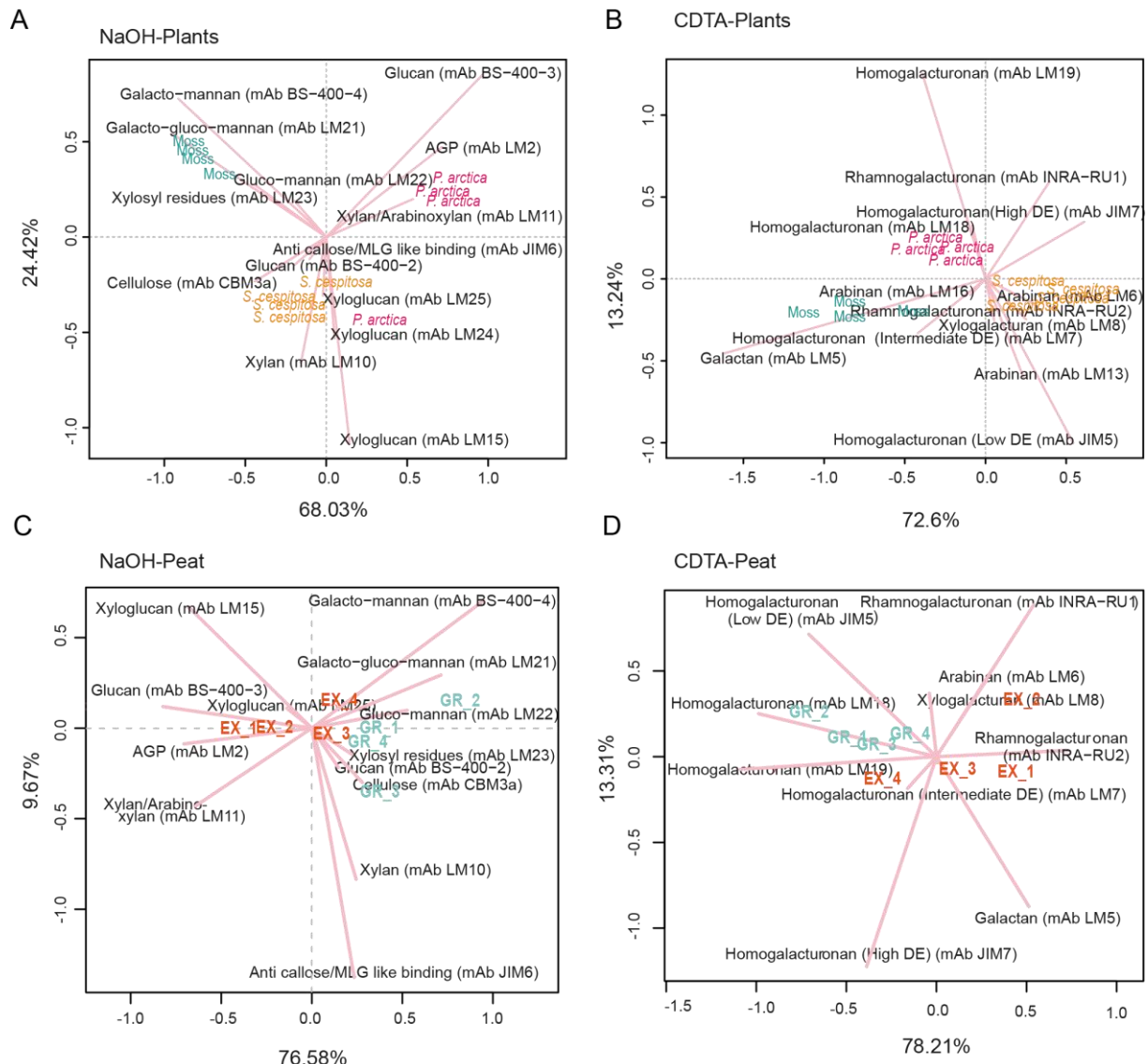
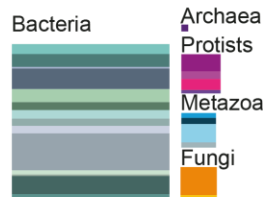


Figure S1: Correspondence Analysis of polysaccharide binding signals in *Poa arctica*, *Saxifraga cespitosa* and a moss mix. A) NaOH extraction (cellulose, hemicelluloses and glycoproteins) of the three plants. B) CDTA extraction (pectins) of the three plants. **Correspondence Analysis of polysaccharide binding signals in exclosed and grazed sites.** C) NaOH extraction (cellulose, hemicelluloses and glycoproteins) of the two sites. D) CDTA extraction (pectins) of the two sites.

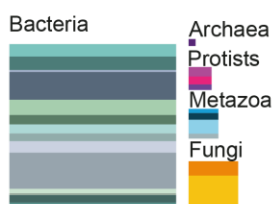
A) mRNA

Exclosed

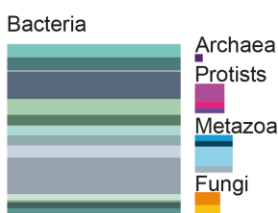
EX1



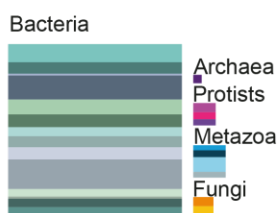
EX2



EX3

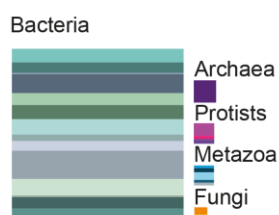


EX4

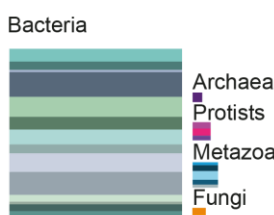


Grazed

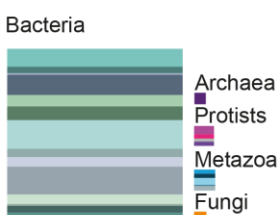
GR1



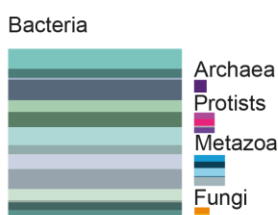
GR2



GR3



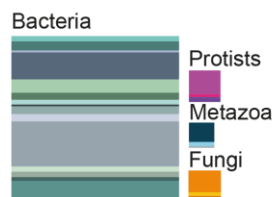
GR4



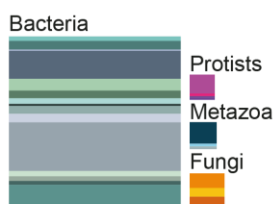
B) SSU rRNA gene

Exclosed

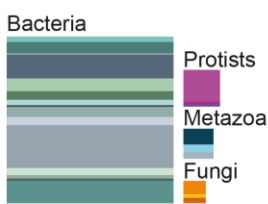
EX1



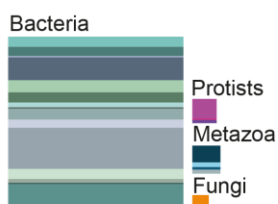
EX2



EX3

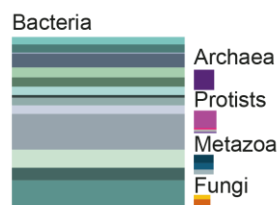


EX4

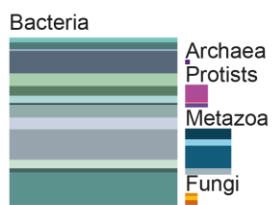


Grazed

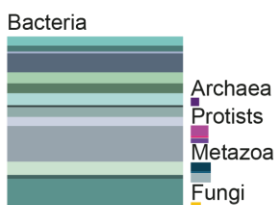
GR1



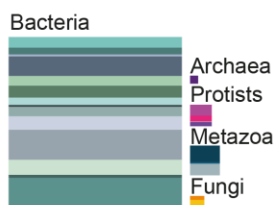
GR2



GR3



GR4



Legend



Figure S2: Microbial community composition A) based on mRNA sequences and therefore representing the transcriptionally active microbial community. B) based on SSU rRNA gene sequences reflecting the potential microbial community in peat soil from exclosures and grazed sites. The size of the boxes reflect the relative abundances of taxa. Taxonomy profiles are displayed at phylum-level (class-level for *Proteobacteria*) and show each replicate separately.

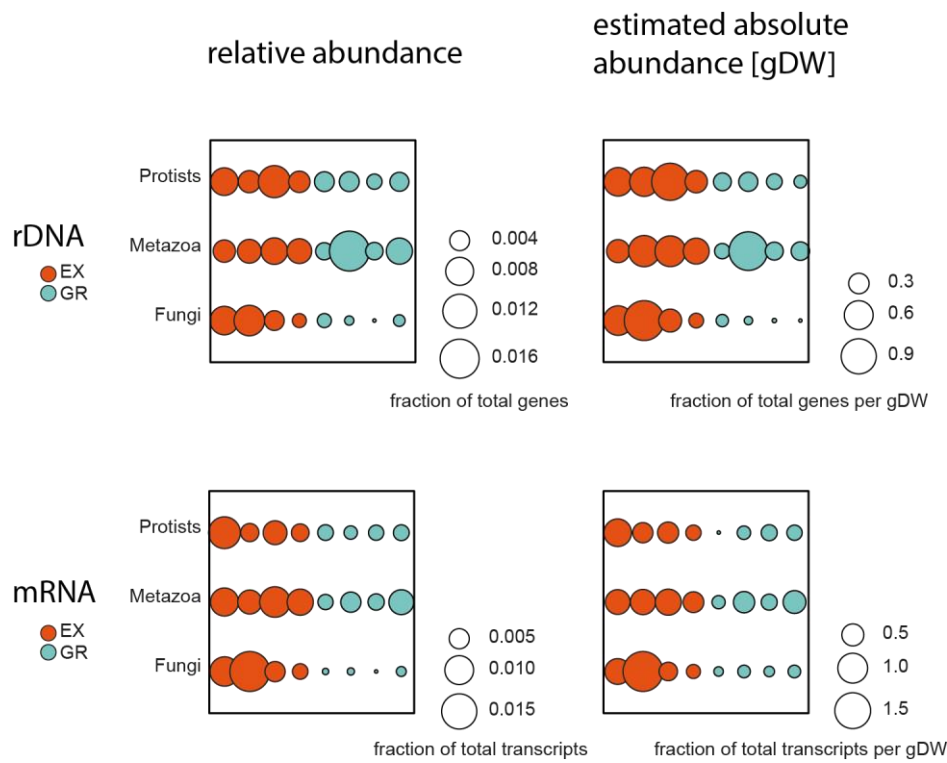
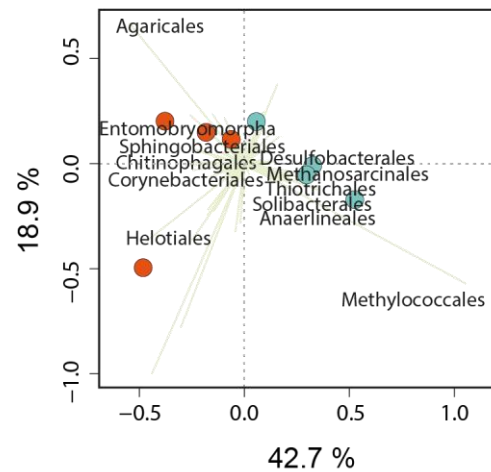


Figure S3: Abundances of eukaryotic kingdoms in the grazed sites and exclosures. Fraction of eukaryotic reads belonging to fungi, Protista and Metazoa for the mRNA and SSU rRNA gene datasets as relative abundances and relative abundances normalized by DNA and RNA masses per gram of dry soil (gDW). The size of each circle represents the fraction of reads in the total number of genes or transcripts.

A



B



Figure S4: Extraction of the microbial orders that have the largest differences in transcriptional activity between the exclosures and grazed sites. A) Correspondence analysis based on mRNA counts at order level taxonomy. B) Number of mRNA transcripts and rRNA genes assigned to the 20 taxa with the largest differences in transcriptional activity between exclosures and grazed sites along the first axis in both directions from A).

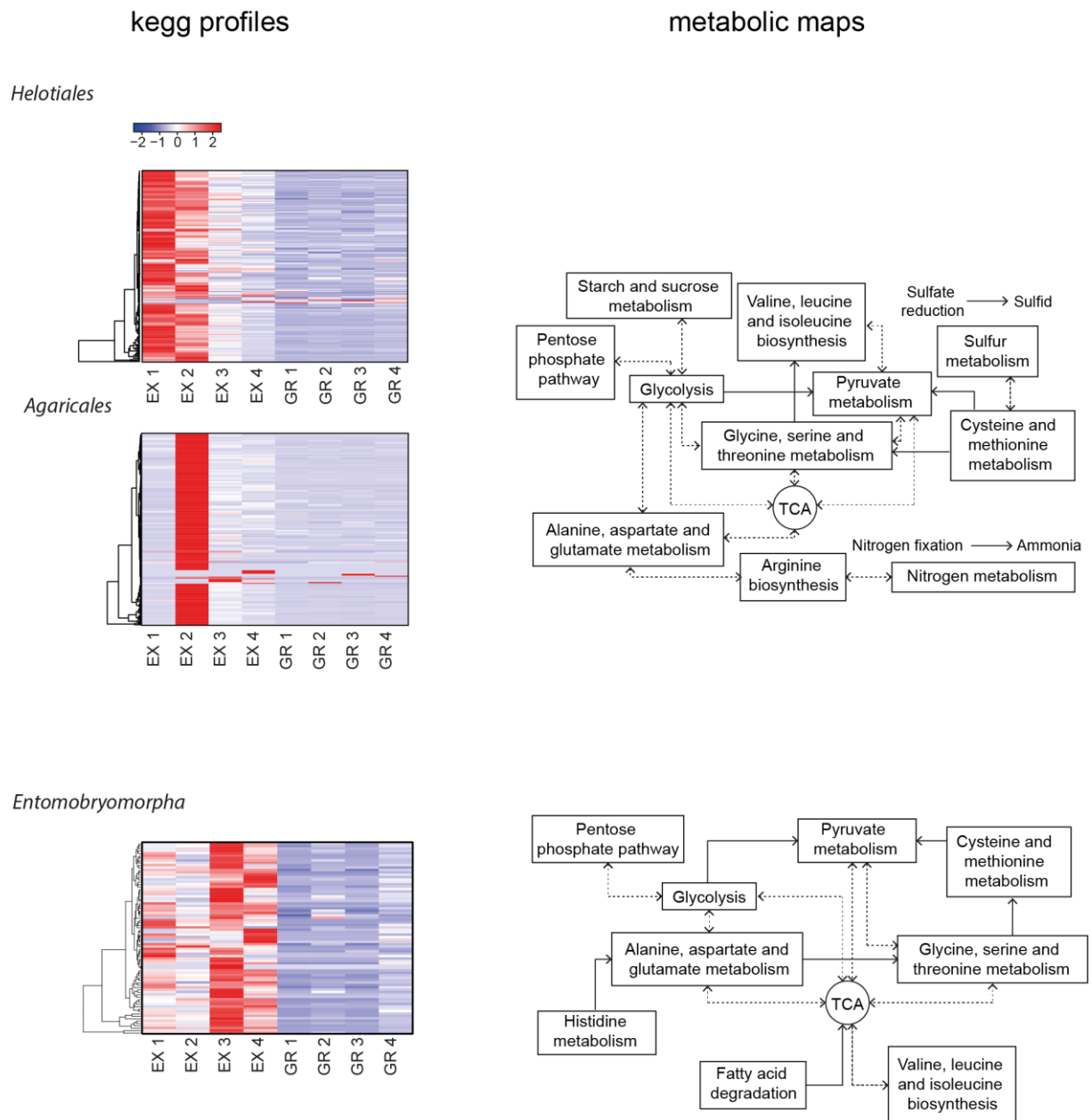


Figure S5: Kegg profiles of the central metabolism in the eukaryotic orders *Helotiales*, *Agaricales* and *Entomobryomorpha*. Each line in the heatmap corresponds to a k number, which represents one molecular function. The central metabolism map to the right of each heatmap show the categories of central metabolism functions included in the heatmap. Overall, the figure shows that the transcription of genes for the central metabolism enzymes is higher for all three taxa in the exclusions.