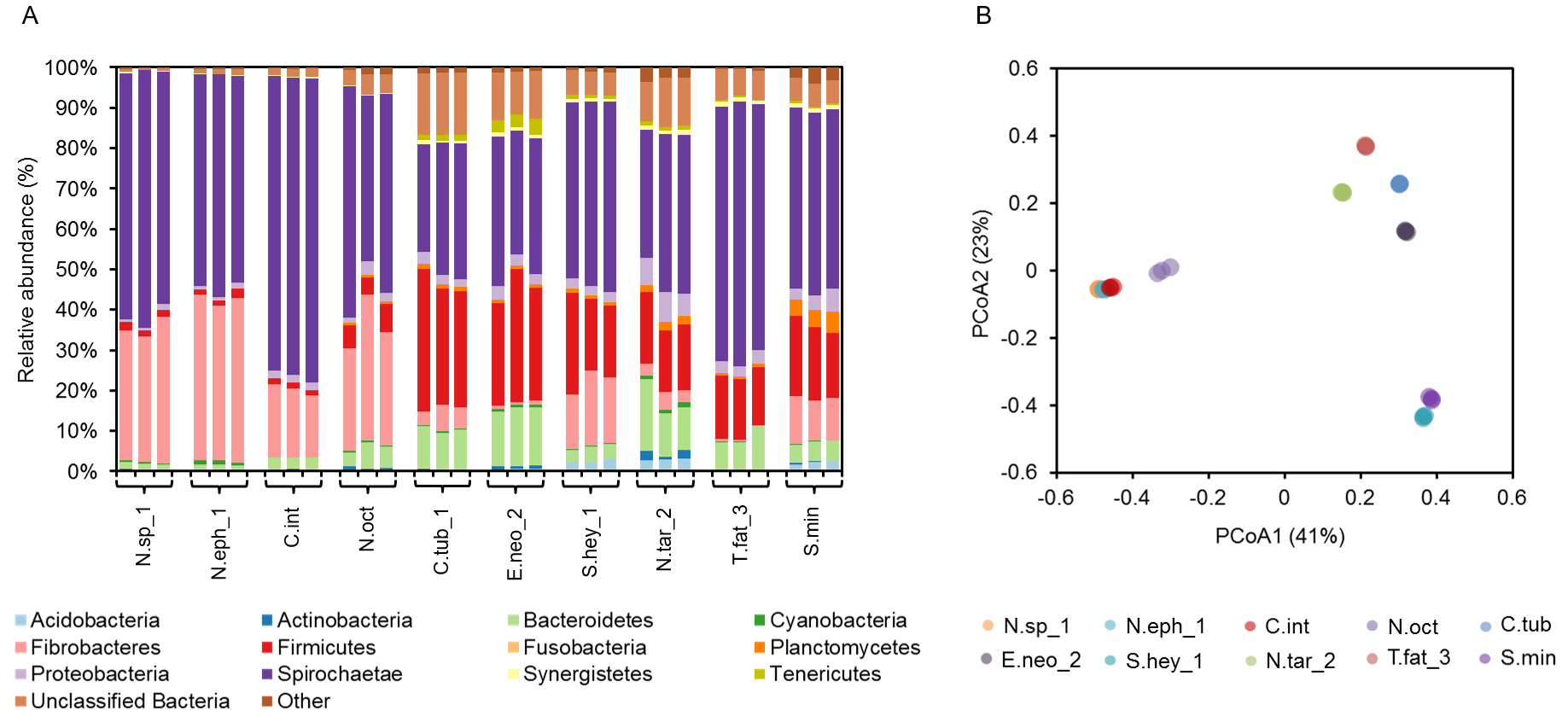
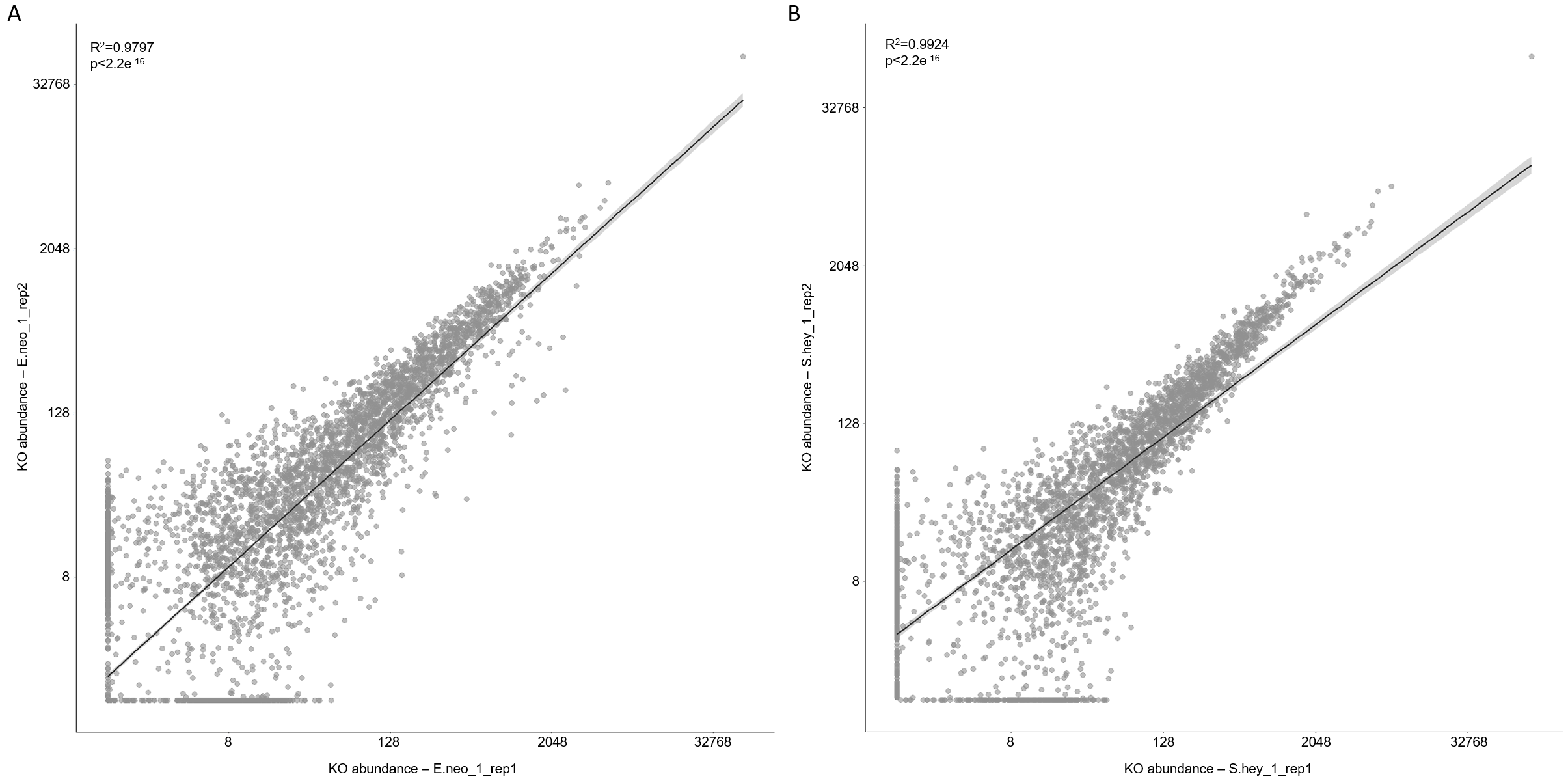
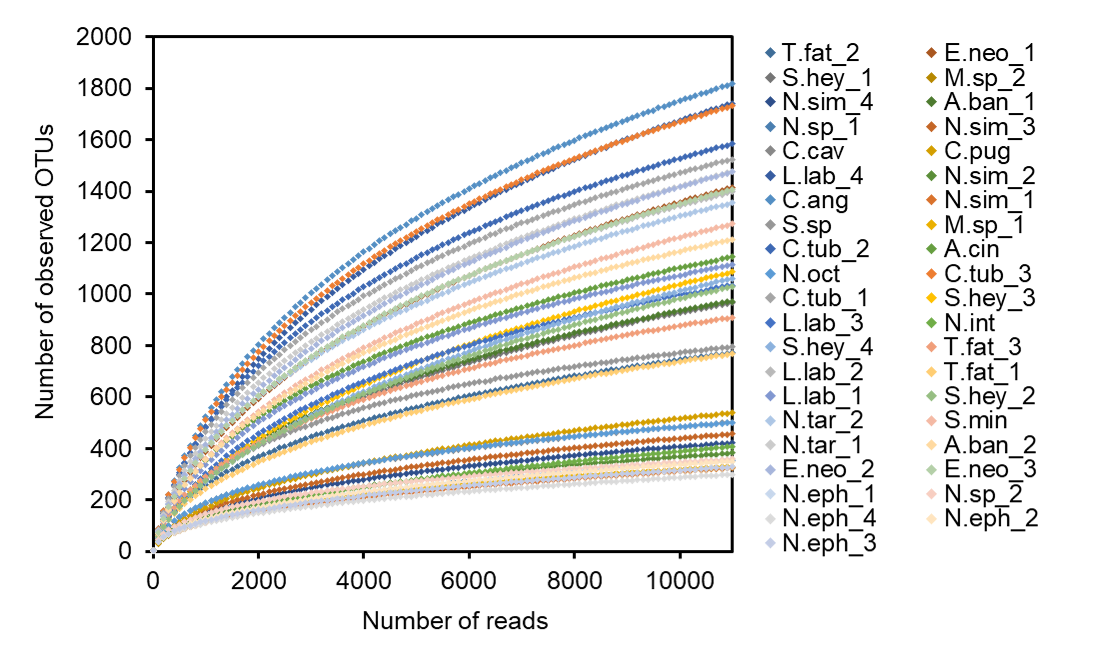
**Additional file 1**



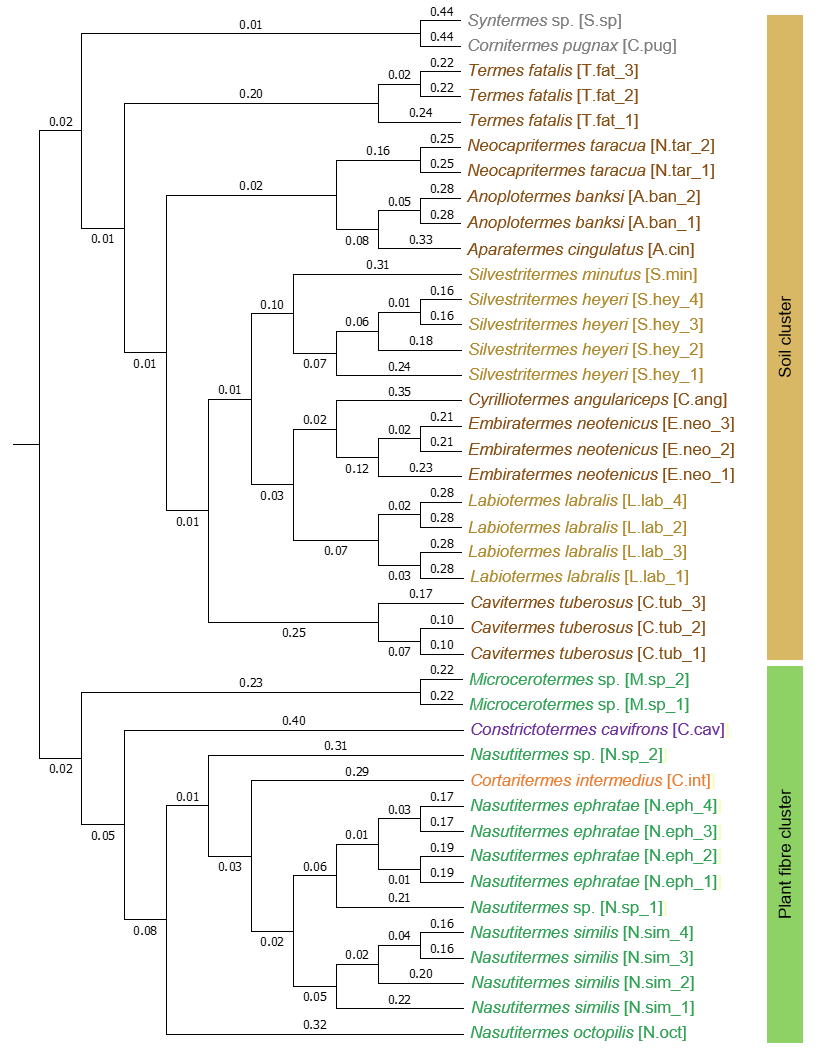
**Fig. S1** 16S rRNA gene amplicon sequencing results for triplicates, presented for 10 selected samples. PCoA ordination of the calculated Bray-Curtis dissimilarities in bacterial community structures at the OTU level showed close grouping of triplicates.



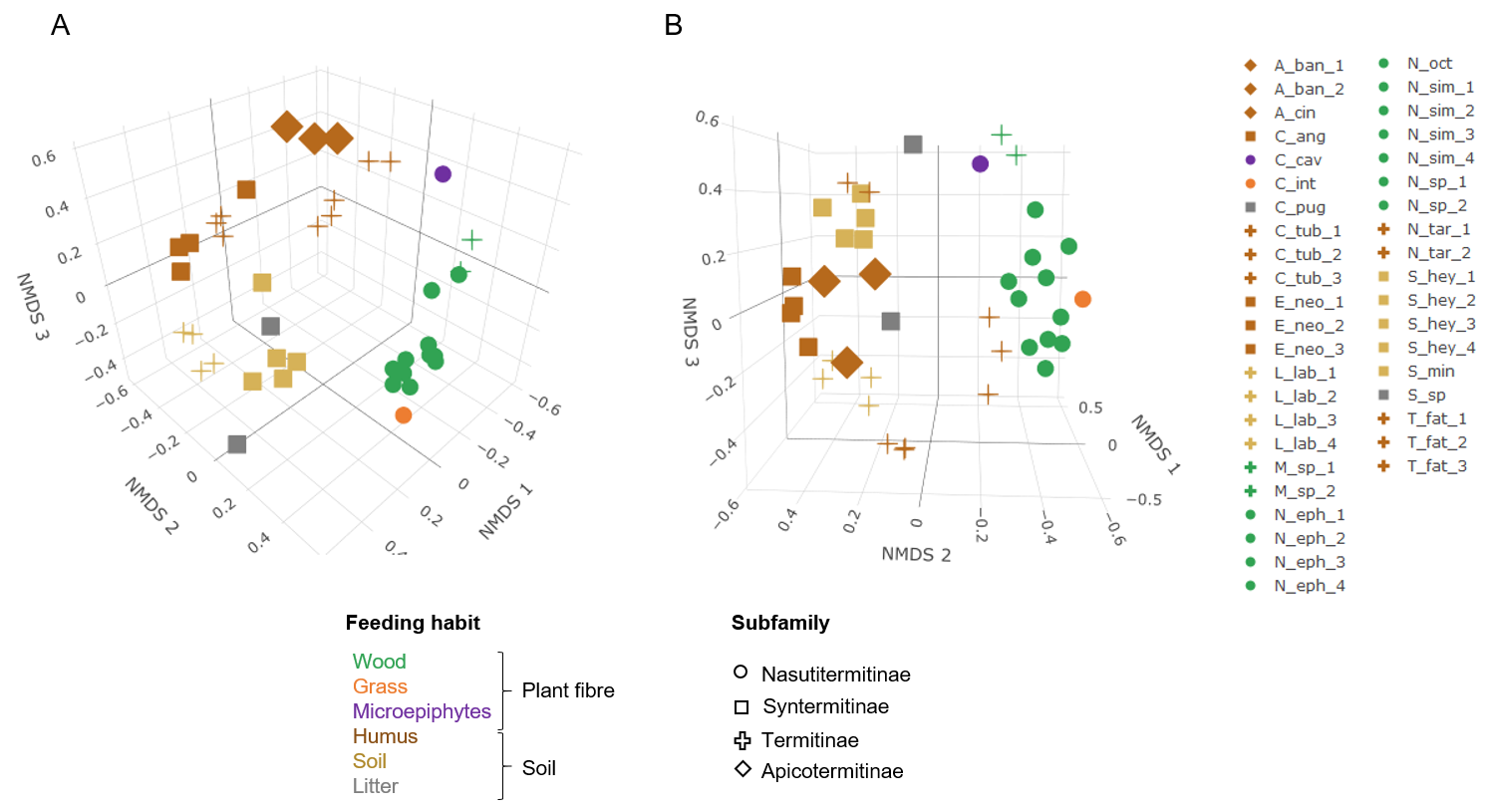
**Fig. S2** Duplicates (biological replicates) of metatranscriptomic libraries for two selected colonies (E.neo\_1, S.hey\_1). **A.** Cumulative abundance of all transcripts annotated to KEGG Ontology categories (KO abundance), for E.neo\_1\_rep1 *versus* E.neo\_1\_rep2 (R2=0.9797, p-value< 2.2e-16). **B.** Cumulative abundance of all transcripts annotated to KEGG Ontology categories (KO abundance), for S.hey\_1\_rep1 *versus* S.hey\_1\_rep2 (R2=0.9797, p-value< 2.2e-16).



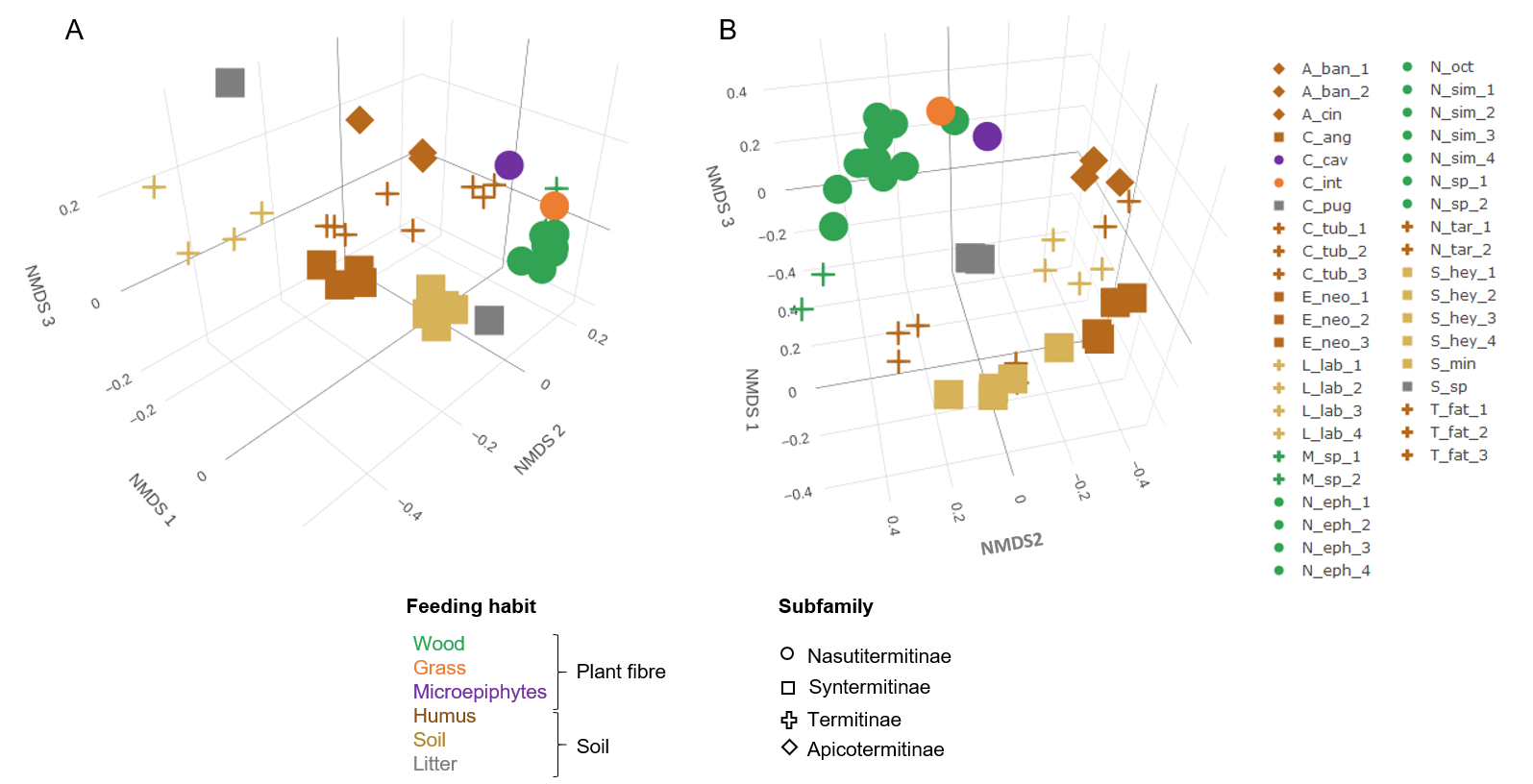
**Fig. S3** The observed richness estimator rarefaction curves based on high-throughput amplicon sequencing of 16S rRNA gene for 41 tested samples of termite gut bacteria.



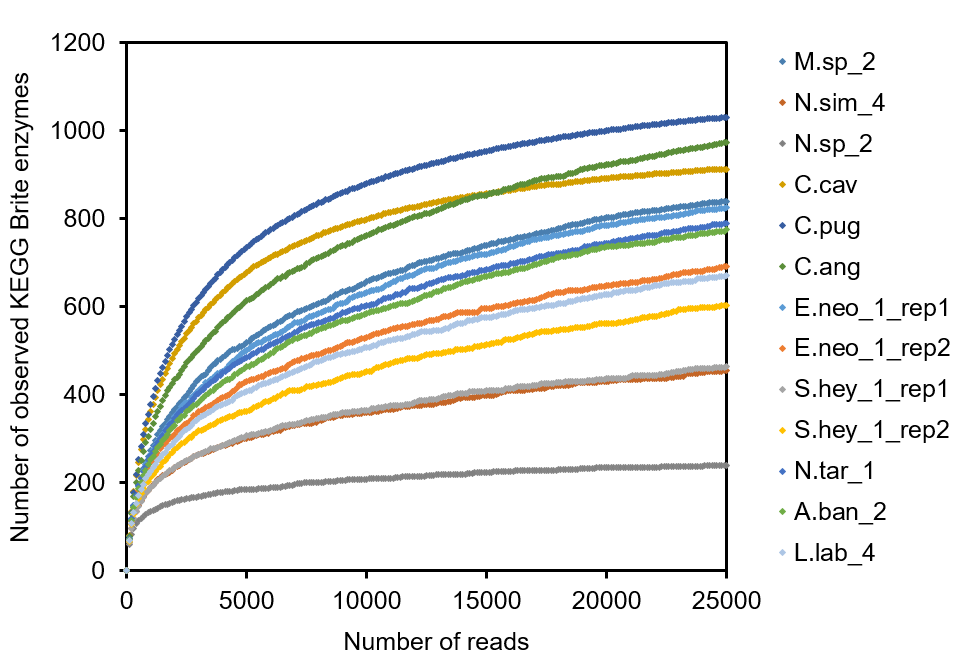
**Fig. S4** Tree based on the calculated Jaccard similarity in bacterial community membership, based on 16S rRNA gene amplicon sequencing; ANOSIM R for the two clusters was equal to 0.98 with p < 0.001.



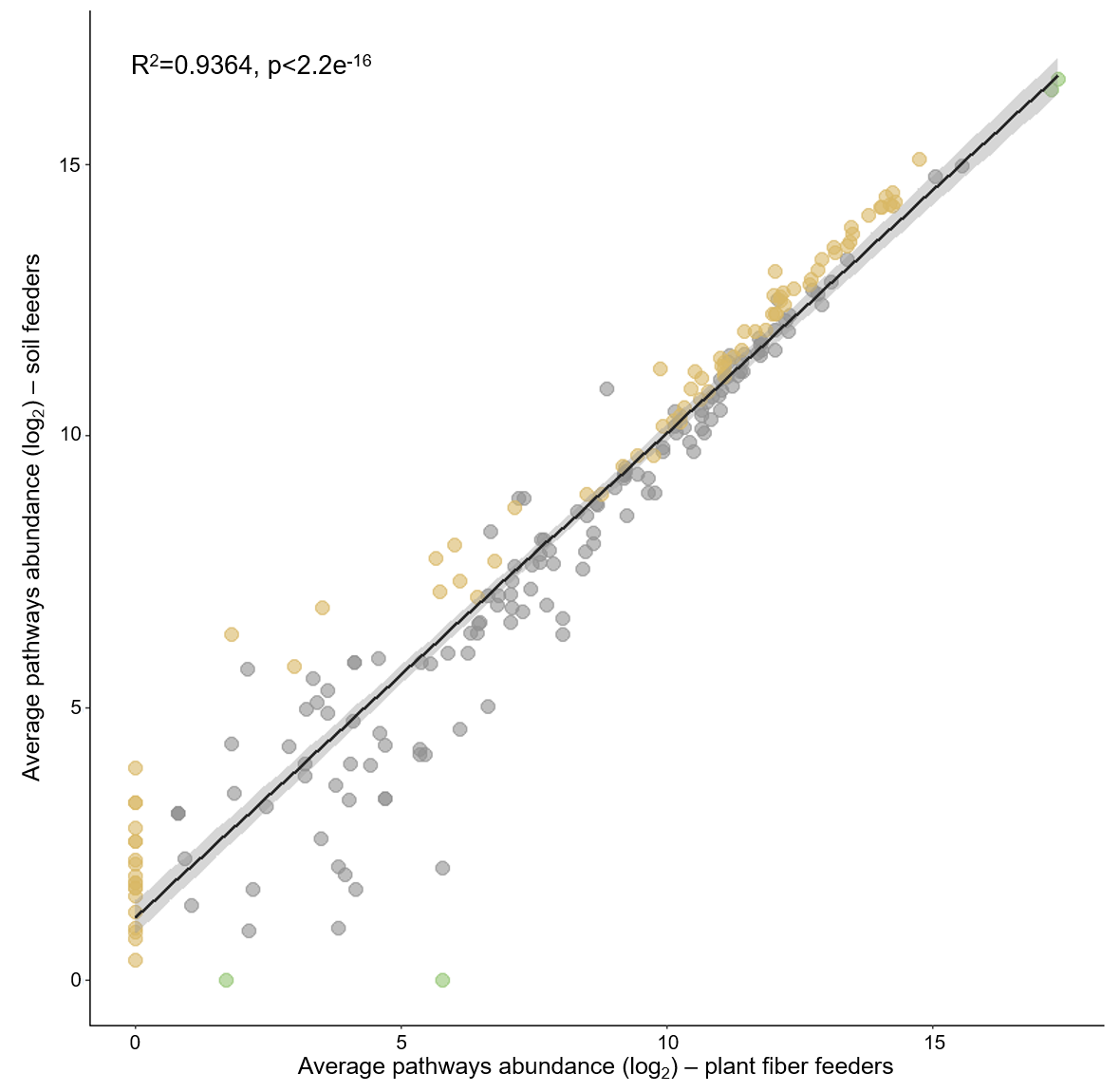
**Fig. S5** 3D-NMDS ordination of the calculated Bray-Curtis (A) and Jaccard (B) dissimilarities in bacterial community structures at the OTU level. Stress values: 0.21, R2=0.66 (Bray-Curtis) and 0.23, R2=0.63 (Jaccard).



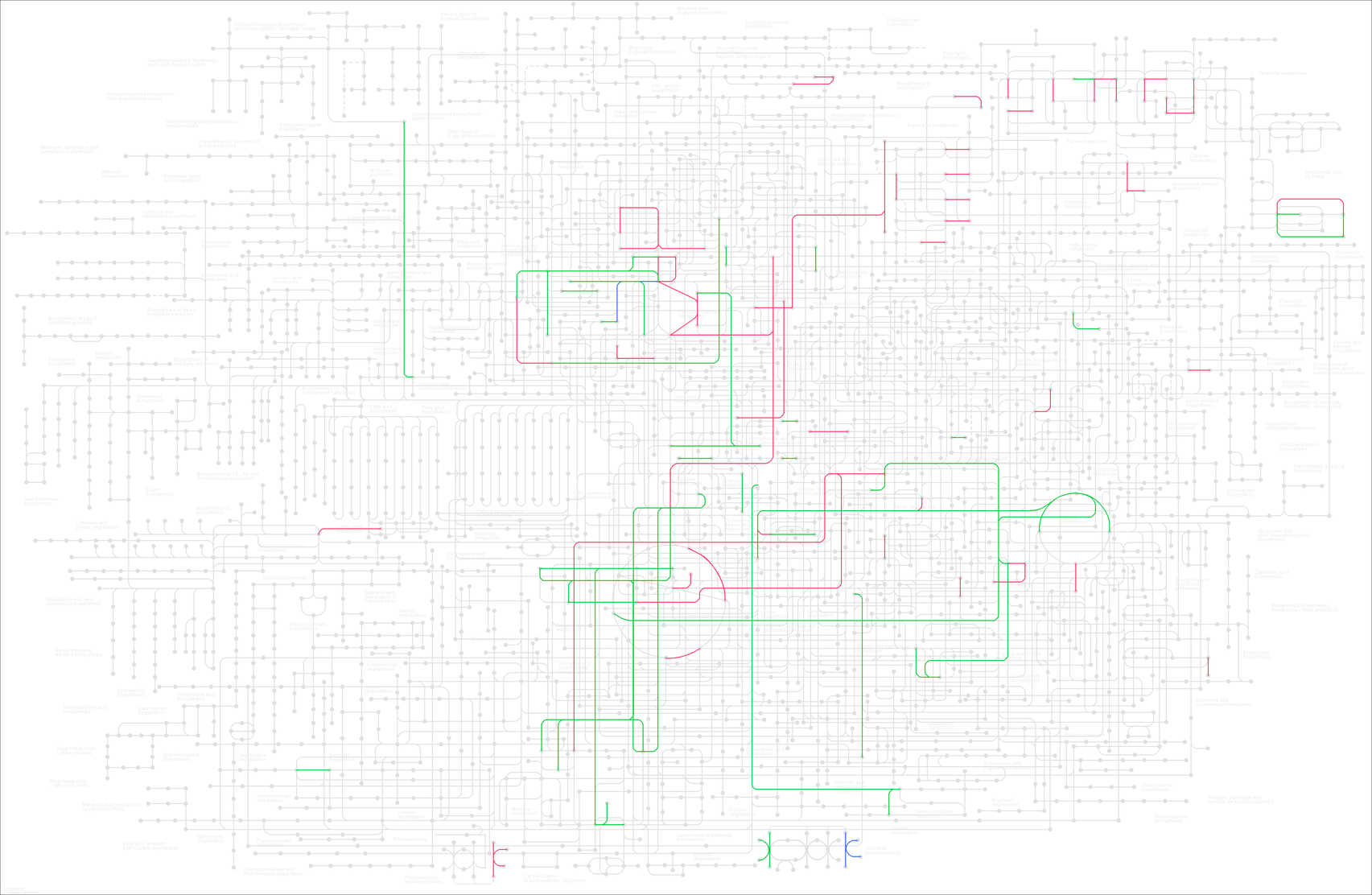
**Fig. S6** 3D-NMDS ordination of the weighted (A) and unweighted (B) UniFrac-calculated pairwise distance across all samples. Stress values: 0.09, R2=0,96 (weighted) and 0.21, R2=0.73 (unweighted).



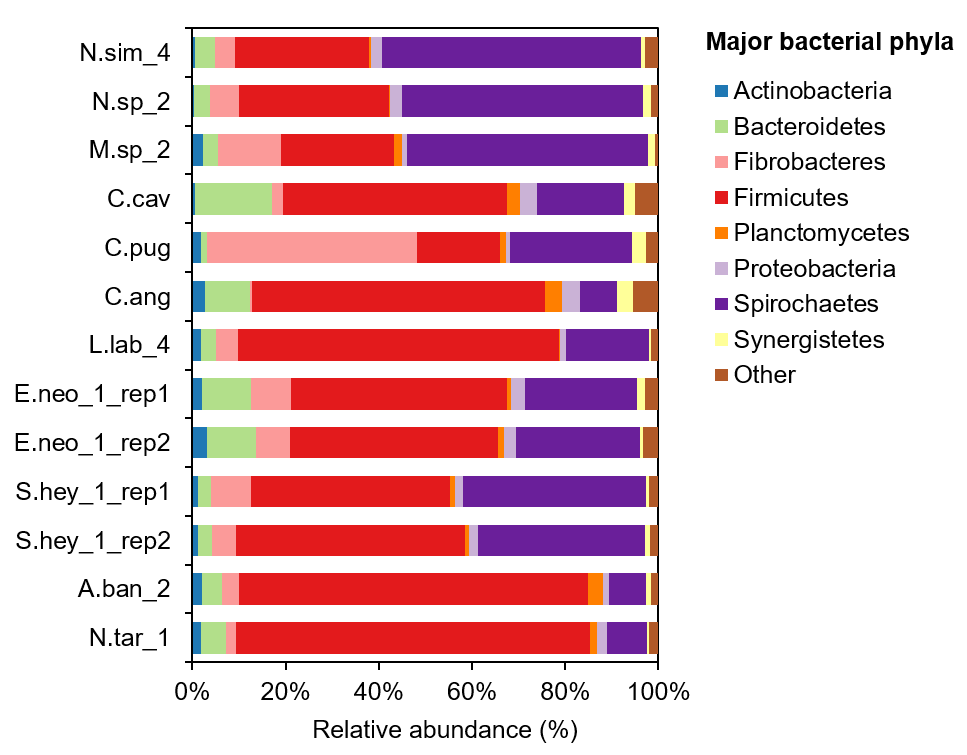
**Fig. S7** The calculated rarefaction curves of all the captured enzymatic annotations (reflected by the assigned KEGG BTITE enzyme numbers).



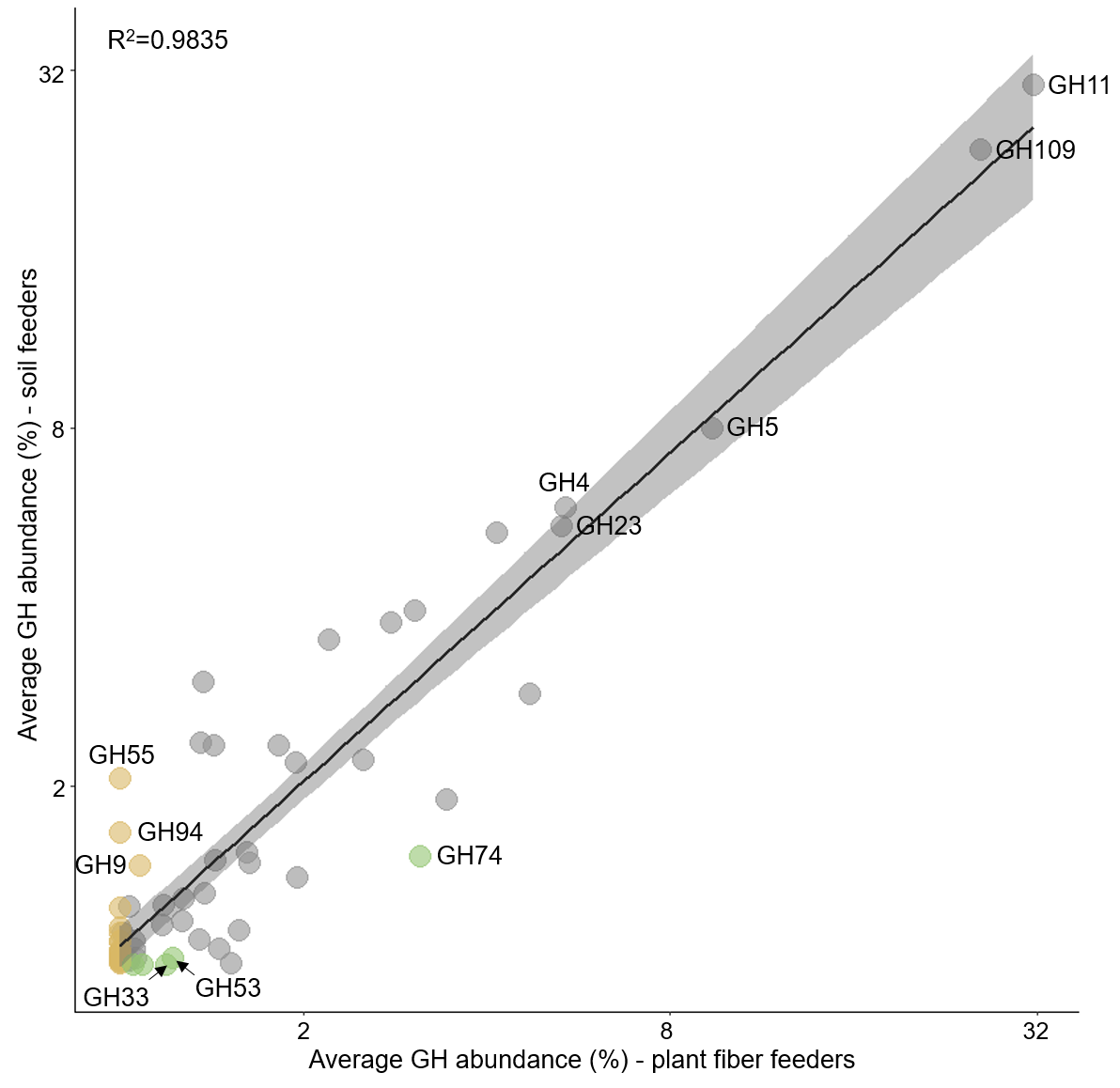
**Fig. S8** Average expression of pathways (cumulative abundance of transcripts assigned to given pathway) across prokaryotic microbiomes of plant fibre- and soil-feeding termites. Pathways enriched (LEfSE analysis) or present exclusively in plant fibre- or soil feeders are marked in green and brown colour, respectively. R2=0.9364; p-value <2.2e-16



**Fig. S9** Illustration of the overrepresented KEGG Ontology categories showing low metabolic overlap between the two clusters in terms of cluster-specific functionalities. Functionalities specific to plant fibre- or soil-feeding termite cluster are marked in green and red, respectively. Overlapping functions are marked with blue.



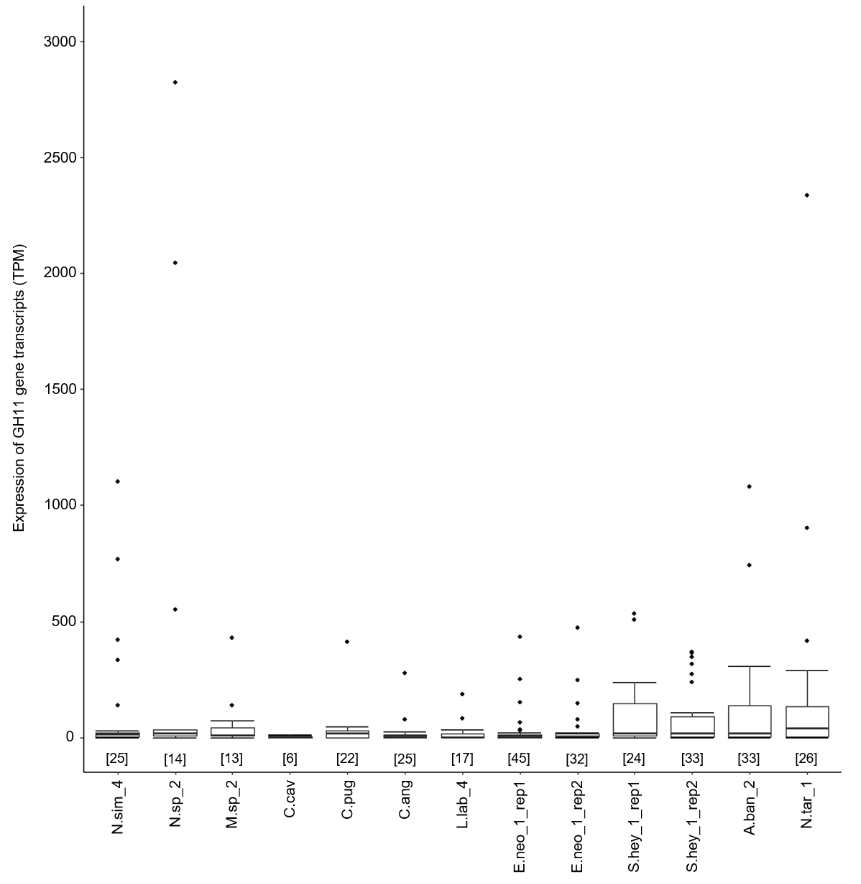
**Fig. S10** Taxonomic prediction of prokaryotic groups contributing the putative CAZymes expression in plant fibre- and soil-feeding termites.



**Fig. S11** Average GH expression in prokaryotic gut microbiomes of plant fibre- and soil-feeding termites (results without application of the dbCAN tool threshold of e-value <10−18 and coverage >0.35); GHs enriched (LEfSE analysis) or present exclusively in plant fibre- or soil-feeding termite cluster are marked in green and brown colour, respectively.



**Fig. S12** Correlation between the number of gene transcripts assigned to a gene category and its cumulative expression per sample.

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**Fig. S13** Expression of the gene transcripts assigned to GH11 CAZy family across all prokaryotic microbiomes. Number in the square bracket corresponds to the number of gene transcripts per each sample.