

Description of Additional Supplementary Files

File name: Supplementary Data 1

Description: Relative abundances of fungal OTUs in different castes and degrading fungus comb obtained from Nanopore sequencing.

File name: Supplementary Data 2

Description: Relative abundances of the bacterial communities across degrading fungus comb obtained from Nanopore sequencing

File name: Supplementary Data 3

Description: Number of copies of Termitomyces and Pseudoxylaria with 95% Confidence intervals in different degrading stages of fungus comb using qPCR estimation (Figure 3c).

File name: Supplementary Data 4

Description: Inhibition of non-specific fungi by Termitomyces.(Figure 4)

File name: Supplementary Data 5

Description: Percentage of inhibition of the non-specific fungi by the 8 bacterial symbiotes(Figure 5).