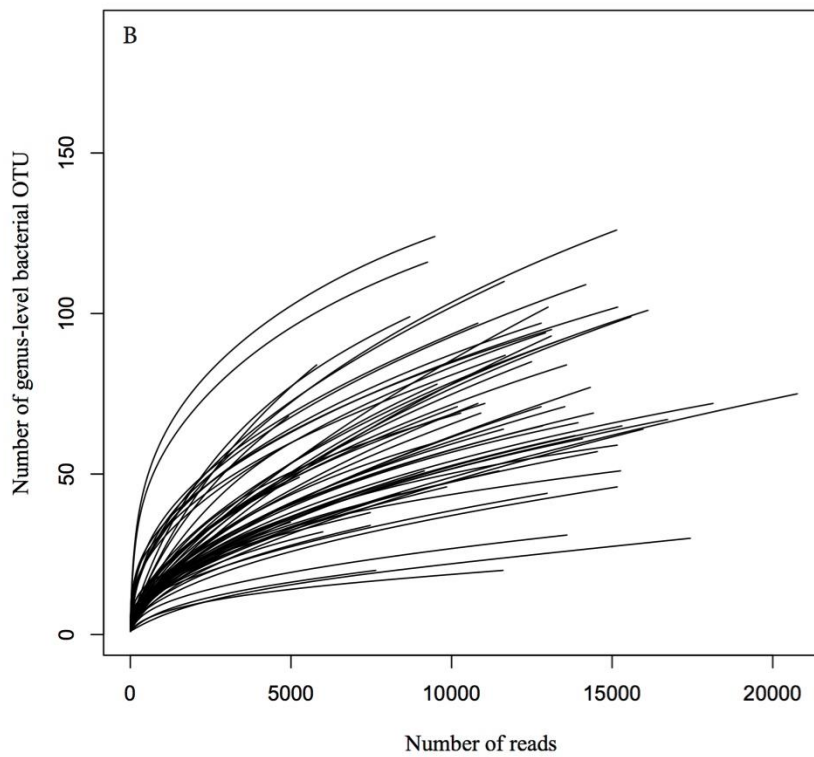
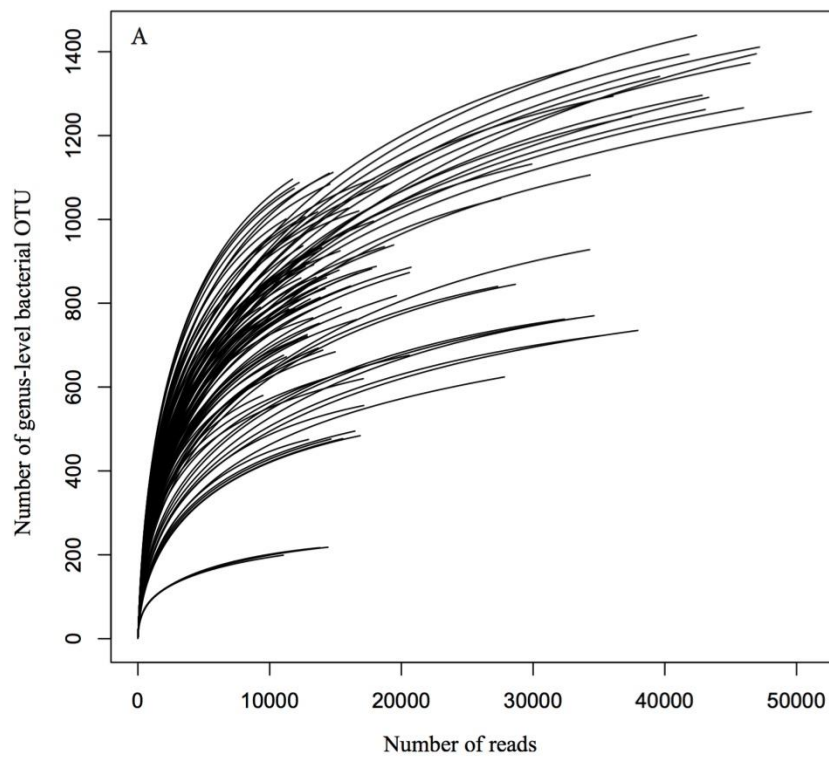


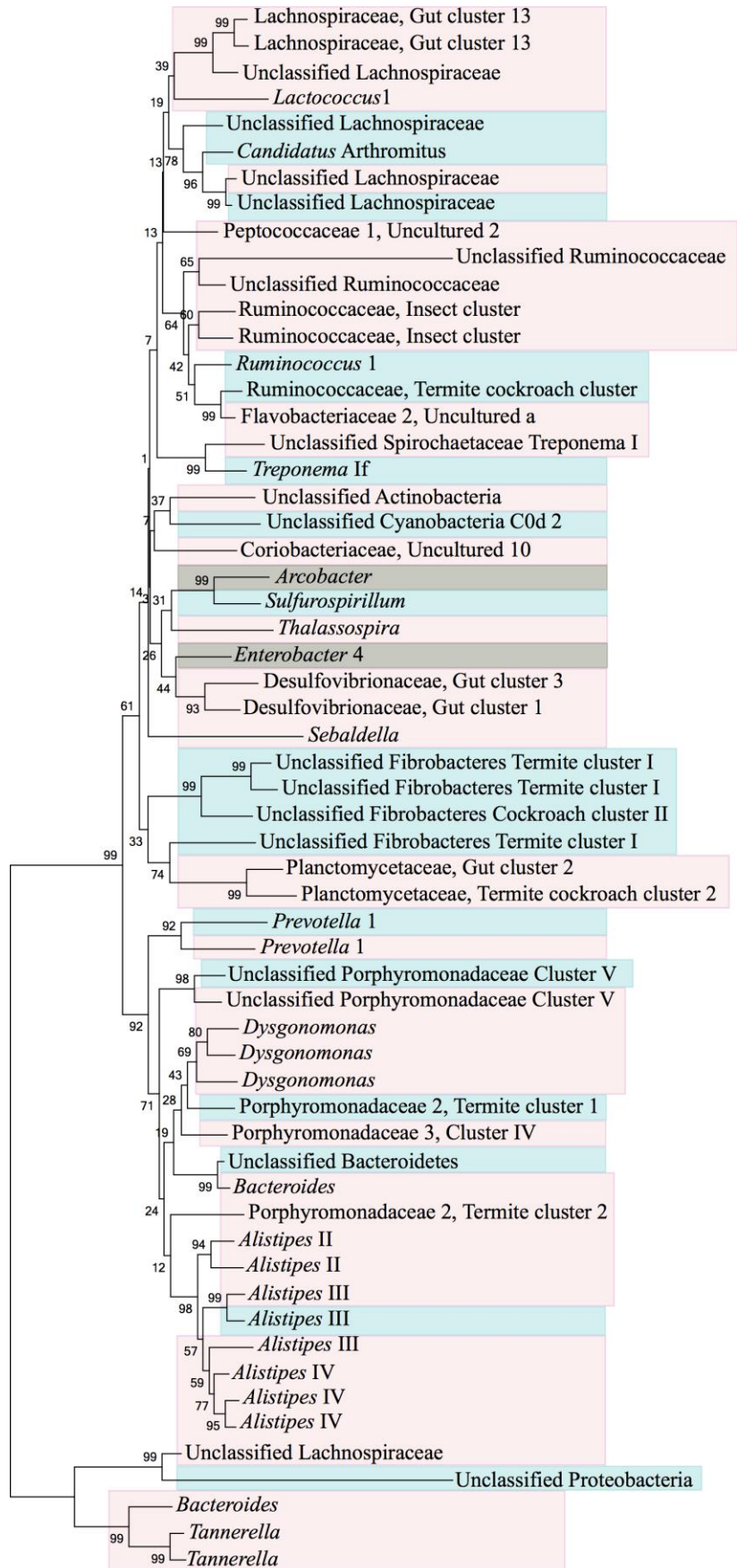
**Supplementary Figure S1.** A) Rarefaction curves for sterile castes. B) Rarefaction curves for reproductive castes.



**Supplementary Figure S2.**

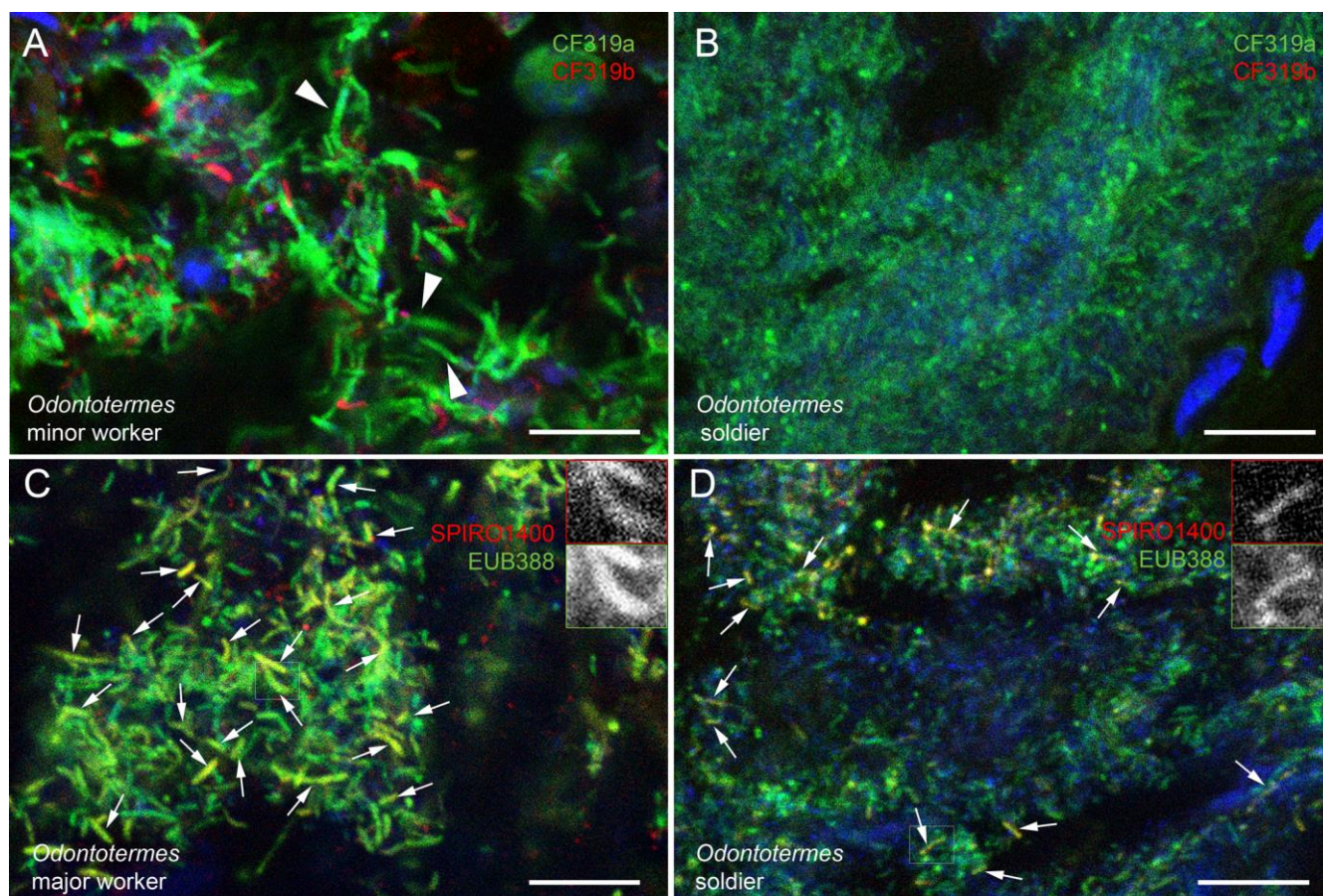
Maximum Likelihood phylogeny of differentially abundant OTUs between sterile castes.

Differentially abundant OTUs between *Odontotermes* workers and soldiers highlighted in pink boxes, between *M. natalensis* workers and soldiers in blue boxes, and between workers and soldiers in both termite genera in grey boxes.

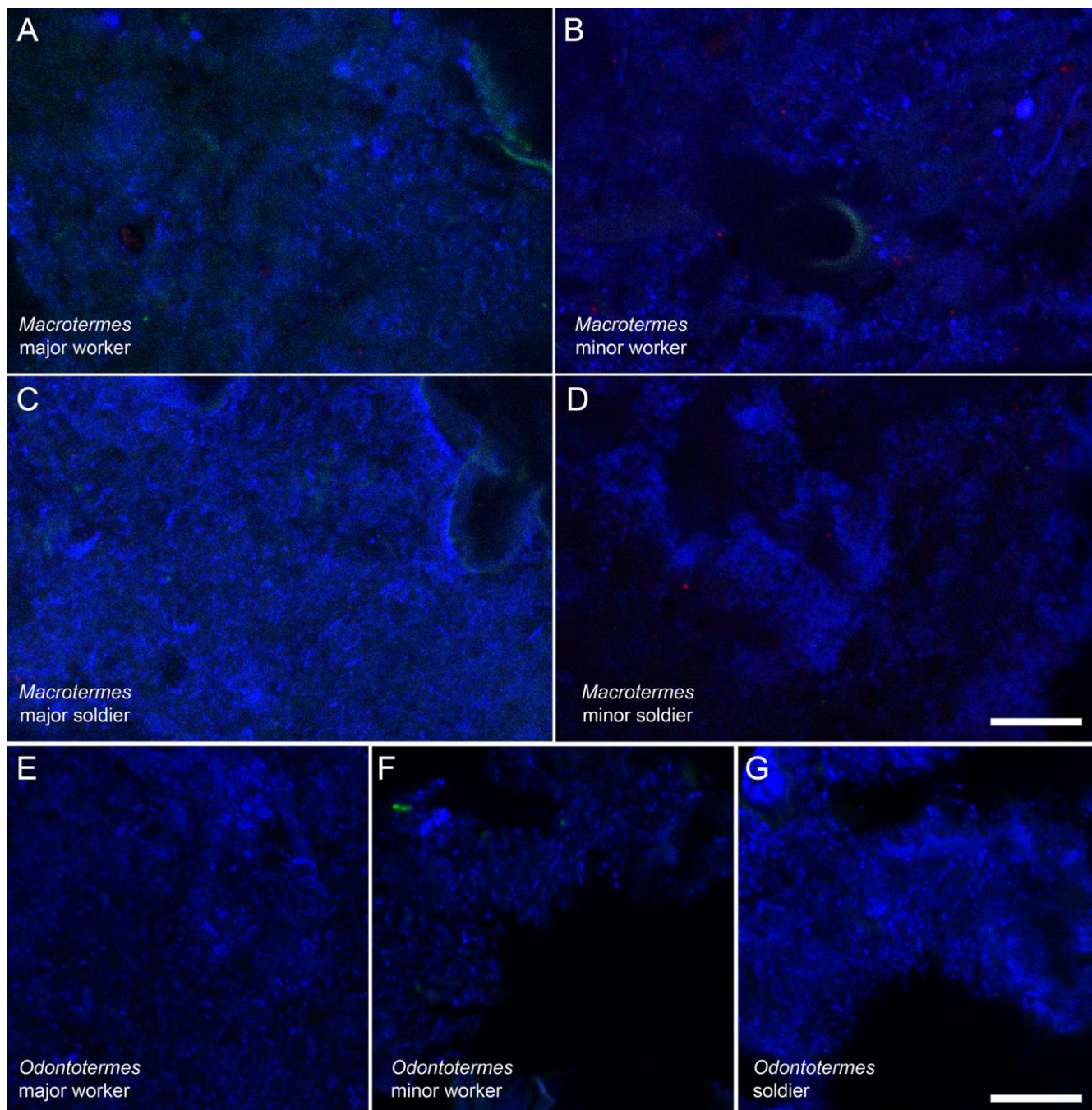


0,05

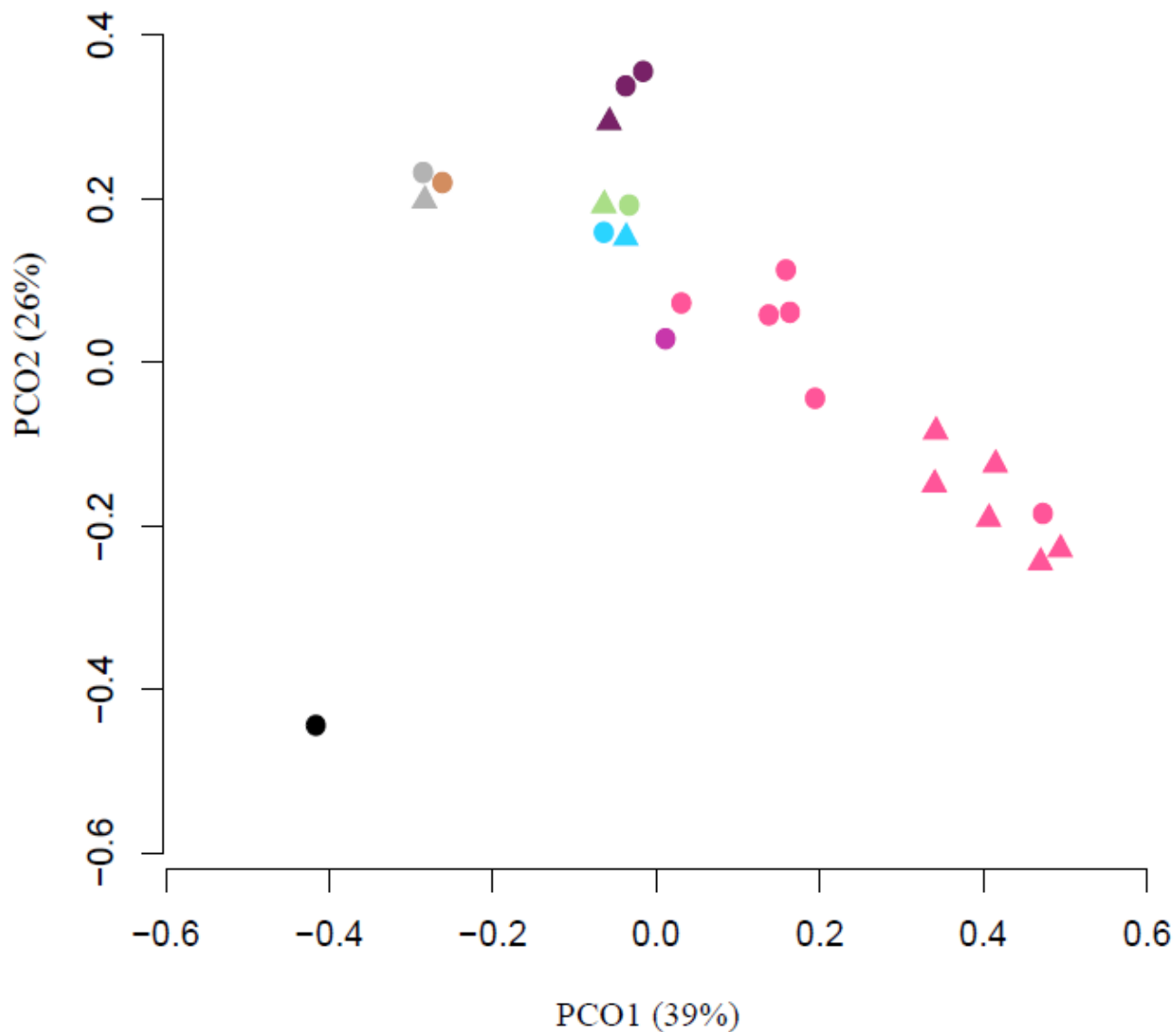
**Supplementary Figure S3.** Representative images of fluorescent *in situ* hybridization (FISH) of the remaining three probes (two bacterial taxa) not included in Figure 2G-J. A, B) FISH with two probes (CF319a, green and CF319b, red) targeting members of Bacteroidetes in sterile castes of *Odontotermes* cf. *badius*. Note that bacteria stained with CF319a appear larger in minor workers (arrowheads). C, D) FISH with a probe targeting members of the family Spirochaetaceae in sterile castes of *Odontotermes* cf. *badius*. Scale bars are 10  $\mu$ m.



**Supplementary Figure S4.** Negative controls of fluorescent *in situ* hybridization using nonEUB388 probe in *M. natalensis* guts (A-D) and *O. badius* guts (E-G). Note the absence of signal. All images are combining three channels: blue (DNA), green (probe staining and autofluorescence), red (autofluorescence). Scale bars are 10  $\mu$ m.



**Supplementary Figure S5.** Queen and king gut microbiota similarity analysis (Bray-Curtis) visualised by principal coordinate analysis (PCoA) in R (R core team, 2013). The symbols indicate a royal pair (circle=queen, triangle=king) and colours represents different termite taxa (grey=*Ancistrotermes guineensis*, brown=*Ancistrotermes cavithorax*, green=*Pseudacanthotermes*, blue=*Odontotermes*, light pink=*Macrotermes natalensis*, dark pink=*Macrotermes bellicosus* and purple=*Macrotermes* sp.).



**Supplementary Figure S6.** Diversity and evenness indices in gut microbiota from sterile and reproductive castes. A) Shannon diversity indices of sterile and reproductive caste gut communities calculated with an R-implemented script in Mothur and visualised by a violin plot in R. B) Evenness index of termite sterile and reproductive caste gut bacterial communities calculated with an R-implemented script in Mothur and visualised by a violin plot in R. \*  $p < 0.00001$  ( $p$ -values are from Mann–Whitney–Wilcoxon tests in R, Table S5).

