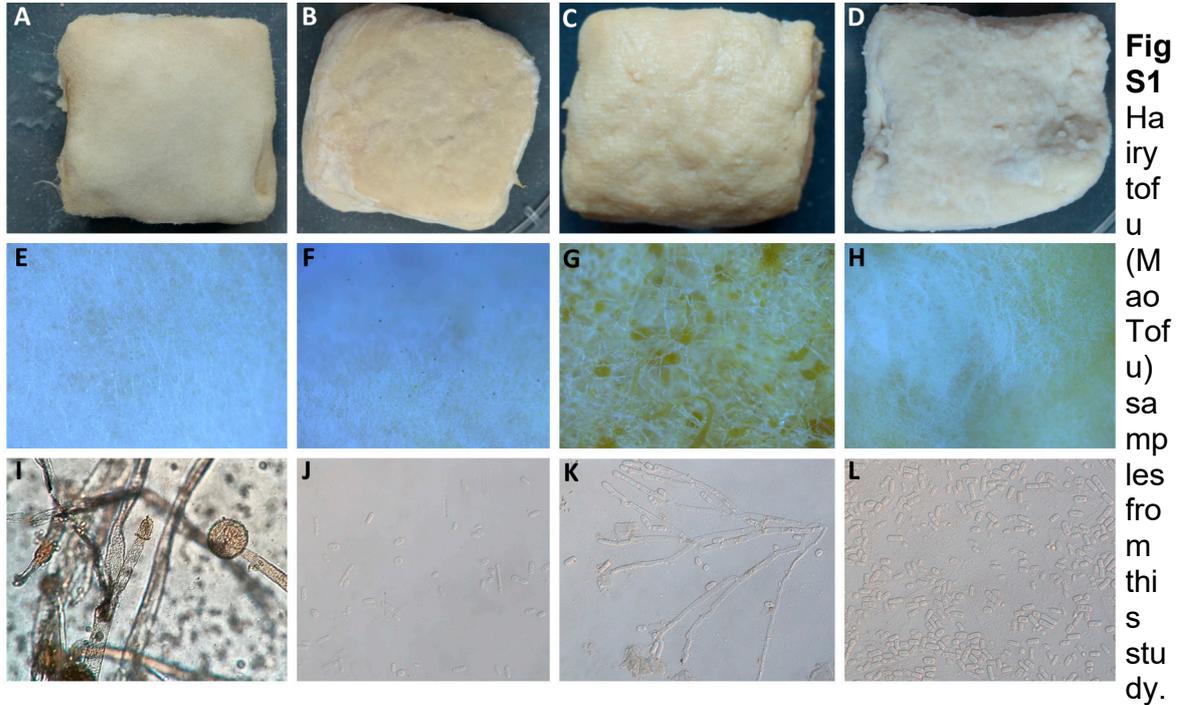
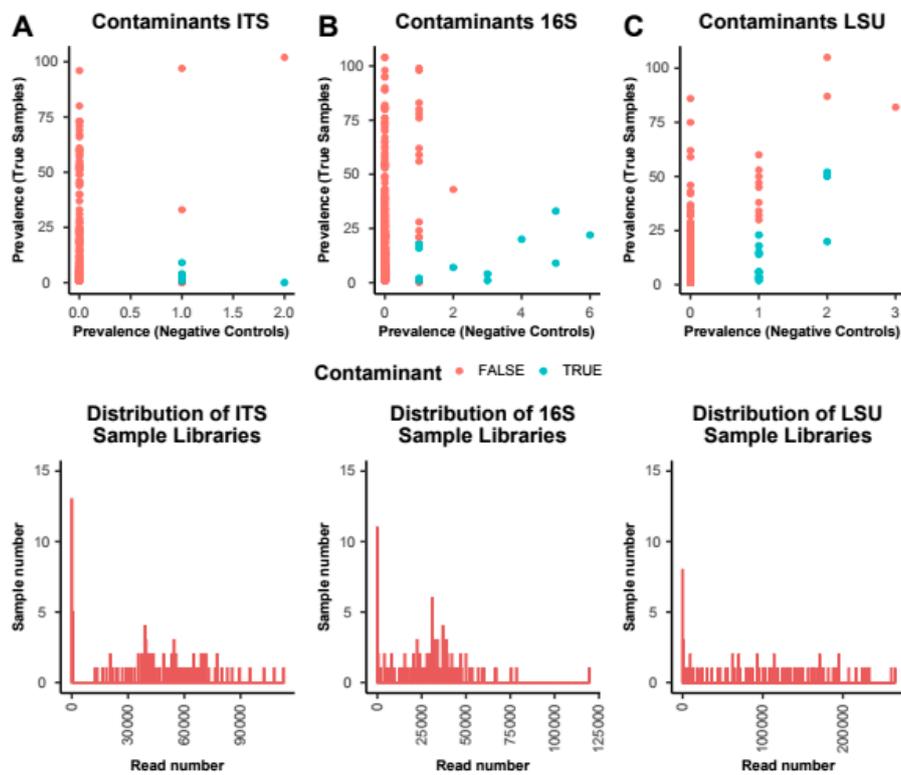


Supplemental Information for:

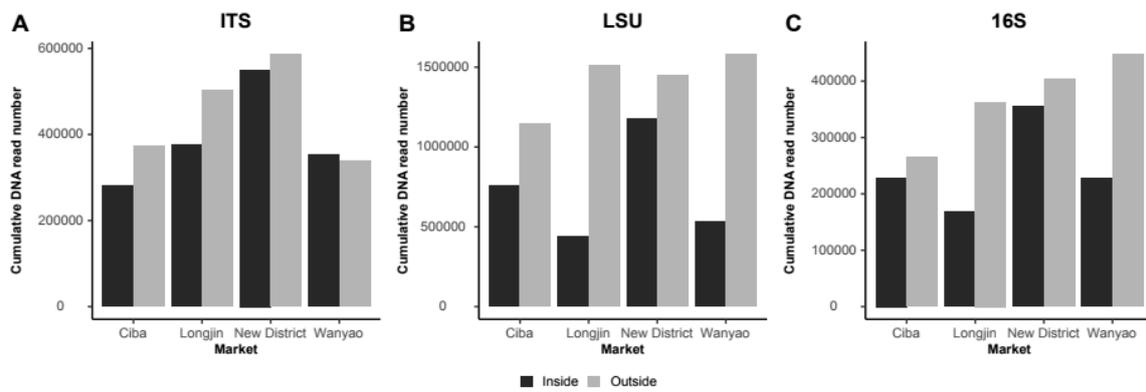
Yeast and lactic acid bacteria dominate the core microbiome of fermented 'hairy' tofu (Mao tofu)



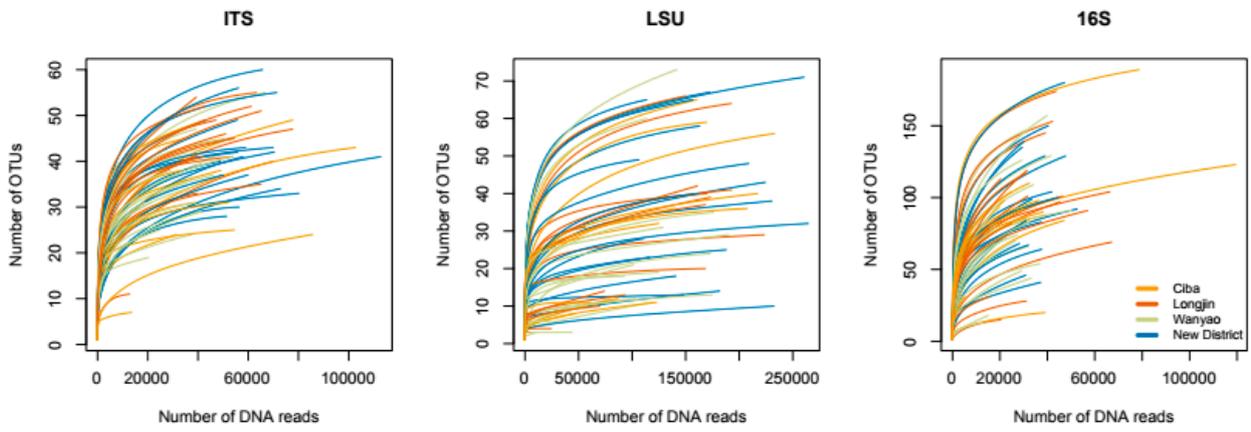
Representative images of fermented tofu from Ciba (A), Longjin (B), Wanyao (C), New District (D). Micrographs of tofu surface as visualized with a stereo microscope at 60X for Ciba (E), Longjin (F), Wanyao (G), New District (H). Micrographs of tofu surface as visualized with a compound microscope at 1000X for Ciba (I), Longjin (J), Wanyao (K), New District (L).



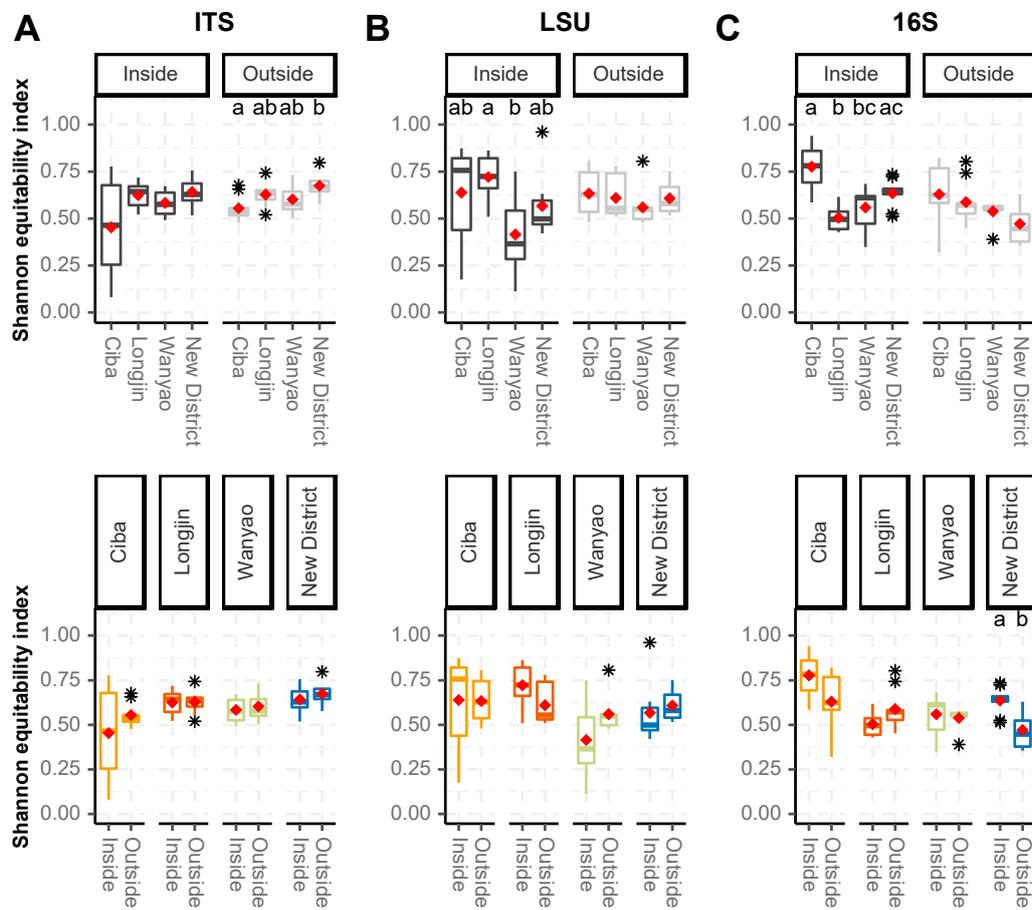
**Fig S2** Graphical view of decontamination analysis using the R package *decontam* and distribution of sample libraries for A) ITS, B) LSU, and C) 16S datasets. OTUs that were detected as TRUE contaminants on the base of their prevalence were removed from the datasets.



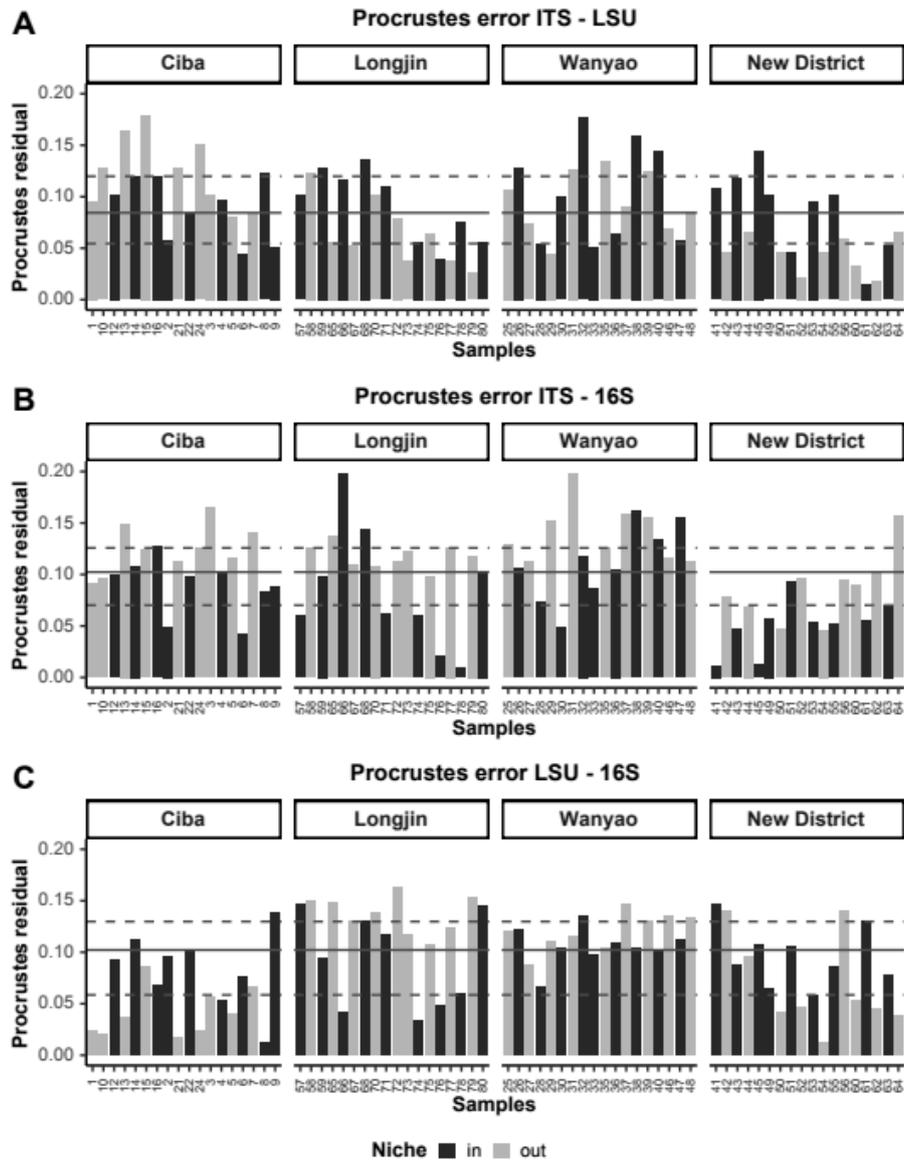
**Fig S3** Amount of sequence reads obtained for each market in the inside and outside niche.



**Fig S4** Rarefaction curves highlighting samples of different Markets for the A) ITS, B) LSU, and C) 16S datasets.



**Fig S5.** Boxplot of samples distribution of Shannon equitability (diversity) index. Red diamonds represent the mean of the distribution. Letters, when present, represent pairwise Wilcoxon tests among groups after Kruskal-Wallis test ( $p \leq 0.05$  after Bonferroni adjustment).



**Fig S6** Procrustes error plots. Each bar represents the residuals for each sample between two community matrices. The horizontal lines, from bottom to top, are the 25% (dashed), 50% (solid), and 75% (dashed) quantiles of the residuals.