Supplementary material

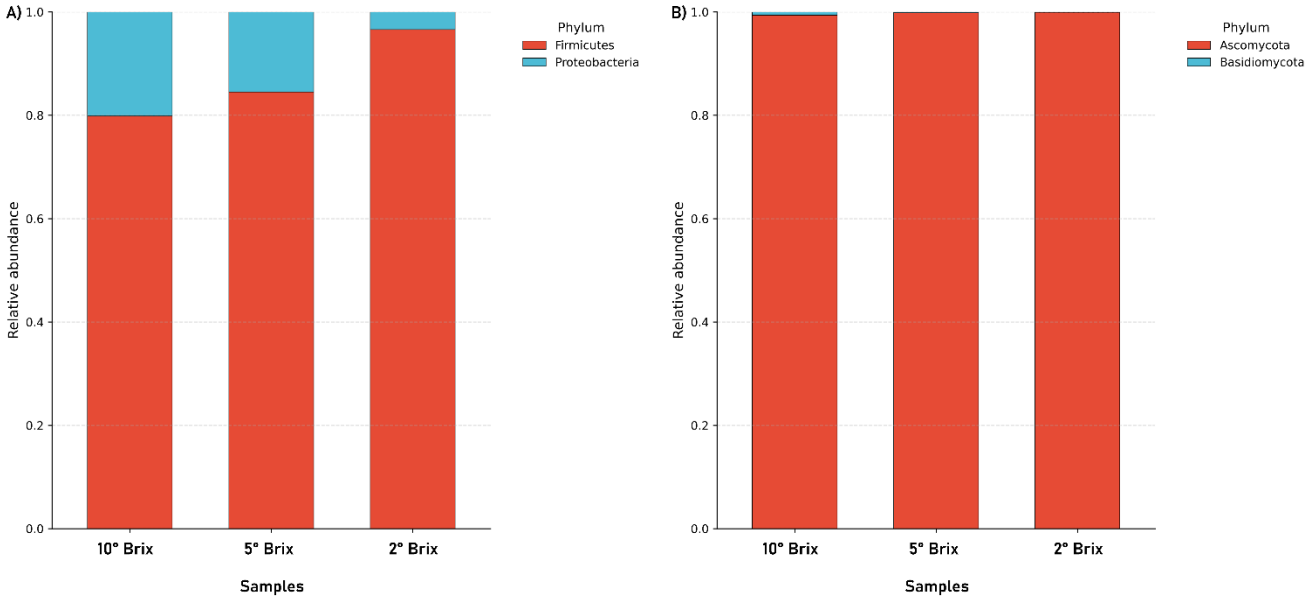


Figure S1. Relative abundance of bacterial and fungal communities at the phylum level during spontaneous *A. cupreata* must fermentation. (A) Bacterial phyla detected using 16S rRNA gene amplicon sequencing; (B) fungal phyla detected using ITS1 amplicon sequencing. One pooled composite sample was analyzed at each fermentation stage; therefore, the displayed values are descriptive.