

Functional and phylogenetic analyses of camel rumen microbiota associated to different lignocellulosic substrates

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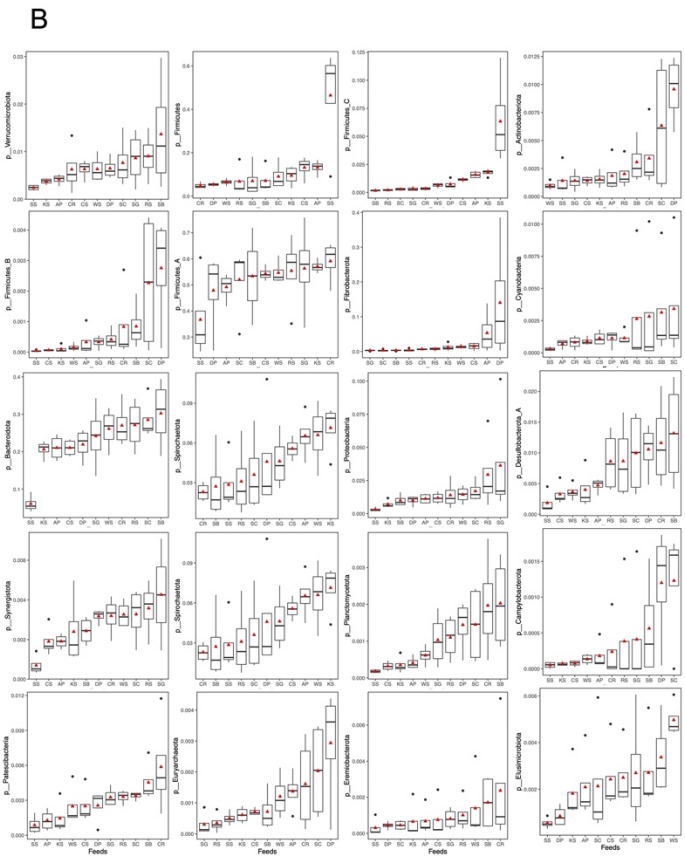
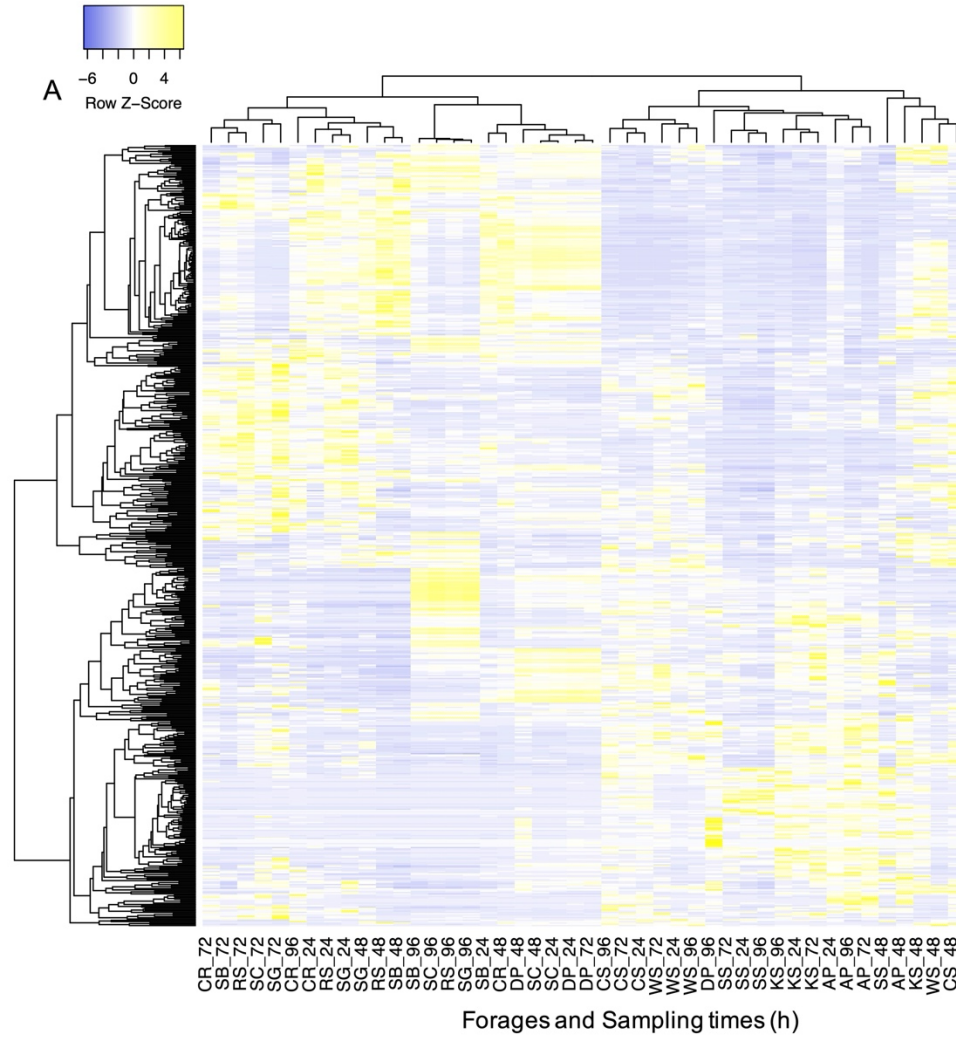


Fig. S1: The abundance distribution and composition of RUIs attached to the 11 substrates incubated for 24, 48, 72 and 96 h in the camel rumen. (A) Heatmap illustrates the abundance profile of 591 RUIs across 44 samples. The RUIs were hierarchically clustered based on their abundances estimated by mapping reads to the contigs larger than 2 Kbp using an average linkage method and Spearman-rank correlation distance measurement implemented in Heatmapper ¹⁰⁴. (B) box plots show the abundance profile of the major phyla in the incubated feeds. The relative abundances of RUIs were summarized at phylum level according to the taxonomies inferred by GTDB-Tk. The boxes represent the median (center line) and interquartile ranges, red triangle represents mean and whiskers extend to one and a half times of the interquartile range.

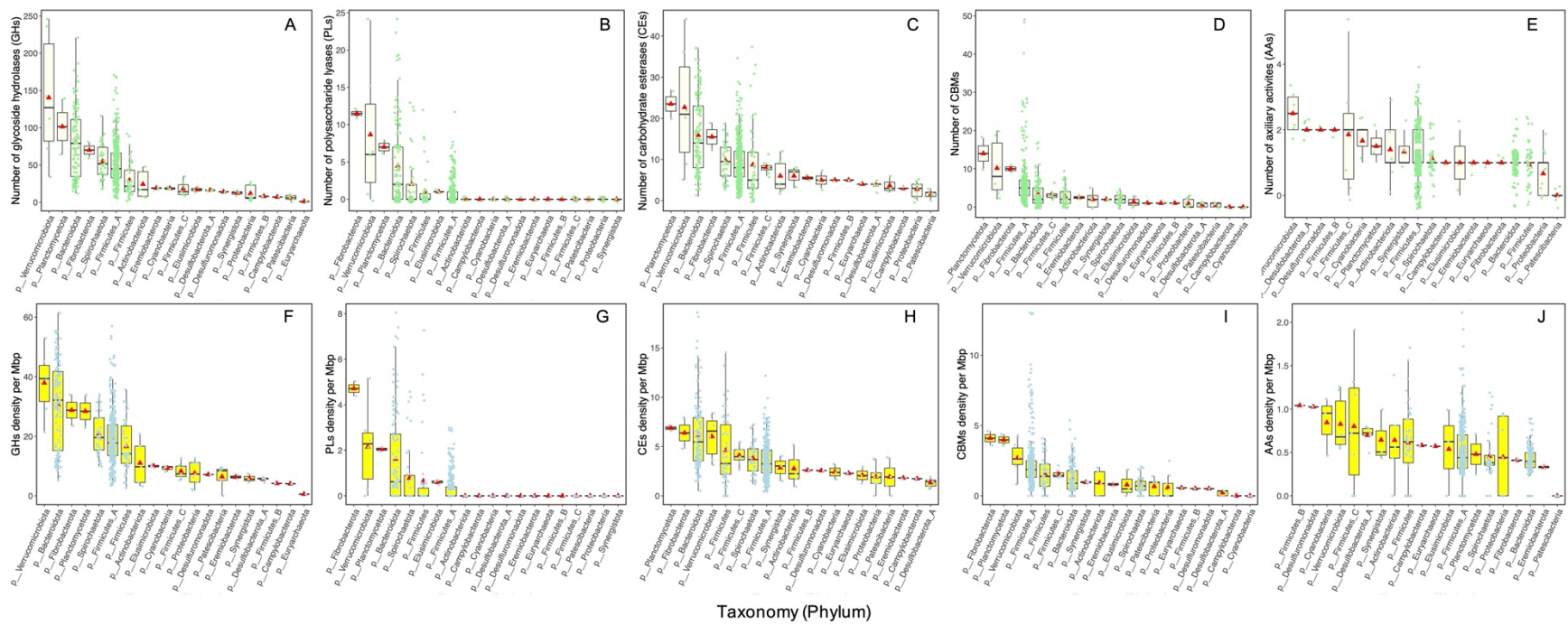


Fig. S2: Number of CAZymes (A-E) and their average densities per Mb of genome size (F-J) in RUIs. The RUIs were classified at phylum level based on taxonomies inferred by GTDB-Tk. Taxa were sorted according to their average CAZyme count or CAZyme density. The boxes represent the median (center line) and interquartile ranges, red triangle represents mean and whiskers extend to one and a half times of the interquartile range.