

Figure S1. The composition of the top 10 phyla and top 15 genera in bacteria (A and C) and eukaryota (B and D) of LFI and HFI cows were displayed in stacked bar plot. Data are presented as average relative abundances for all cows (n = 10). LFI: low feed intake, HFI: high feed intake.

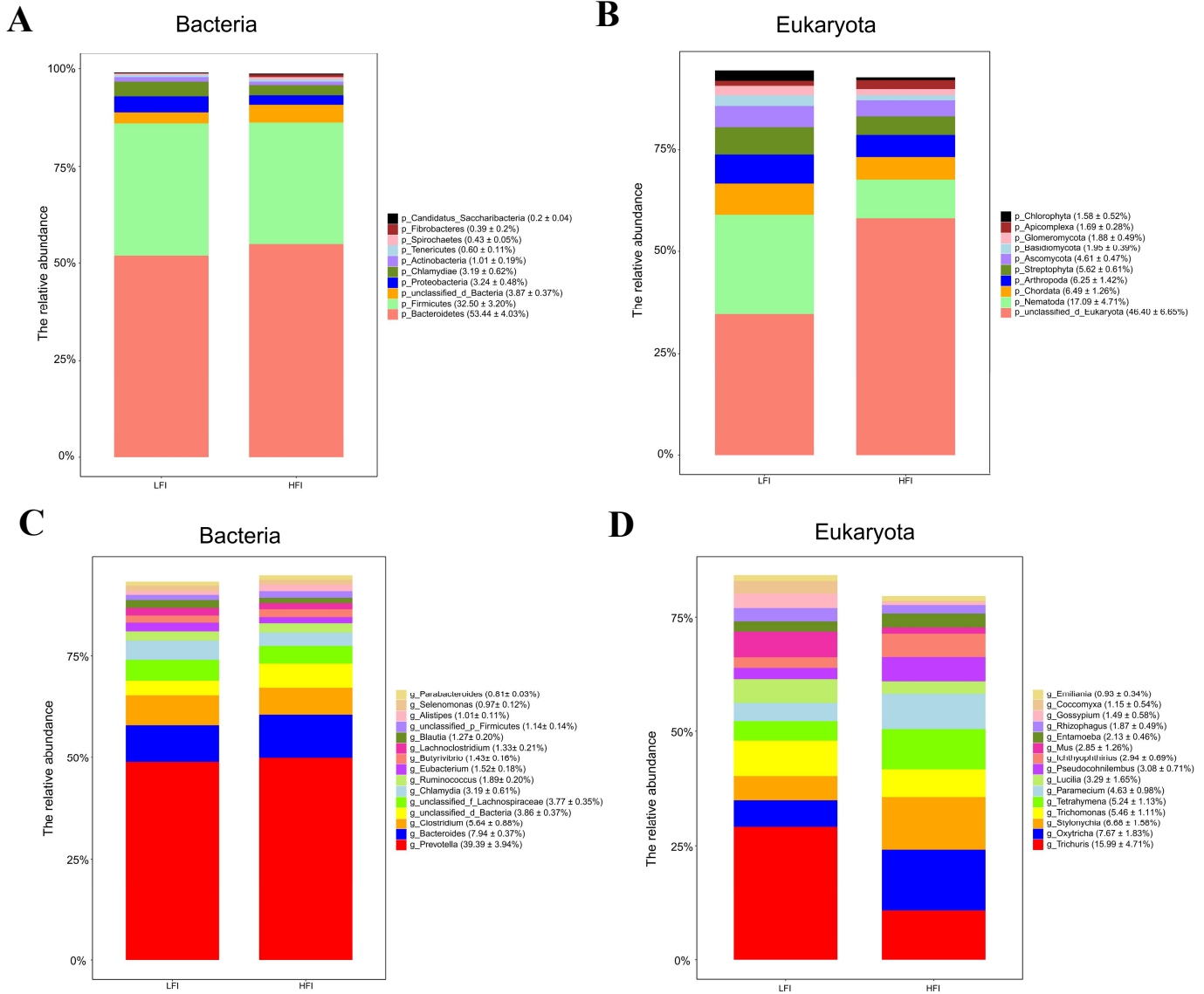


Figure S2. Microbial composition of archaeal (A) and viruses (B) was not influenced by feed intake using principal coordinate analysis (PCoA) based on the Bray Curtis matrices.

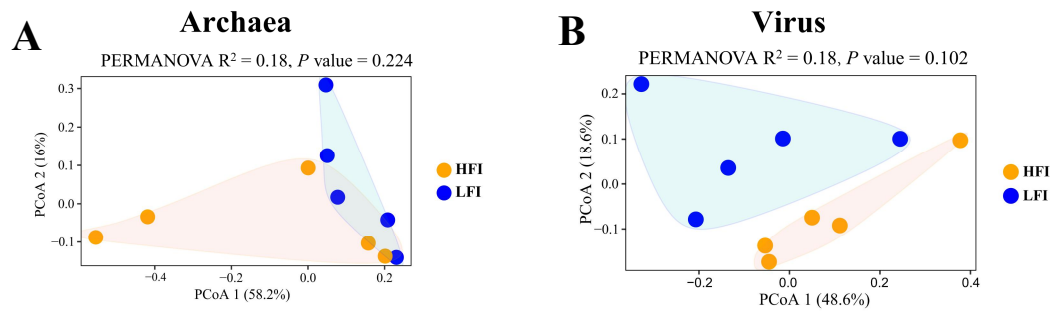


Figure S3. Constitution of CAZyme genes at the class (A) and family level (B) of dairy cow rumen microbiota. AAs: auxiliary activities; CBMs: carbohydrate-binding modules; PLs: polysaccharide lyases; CEs: carbohydrate esterases; GTs: glycosyltransferase; GHs: Glycoside Hydrolases.

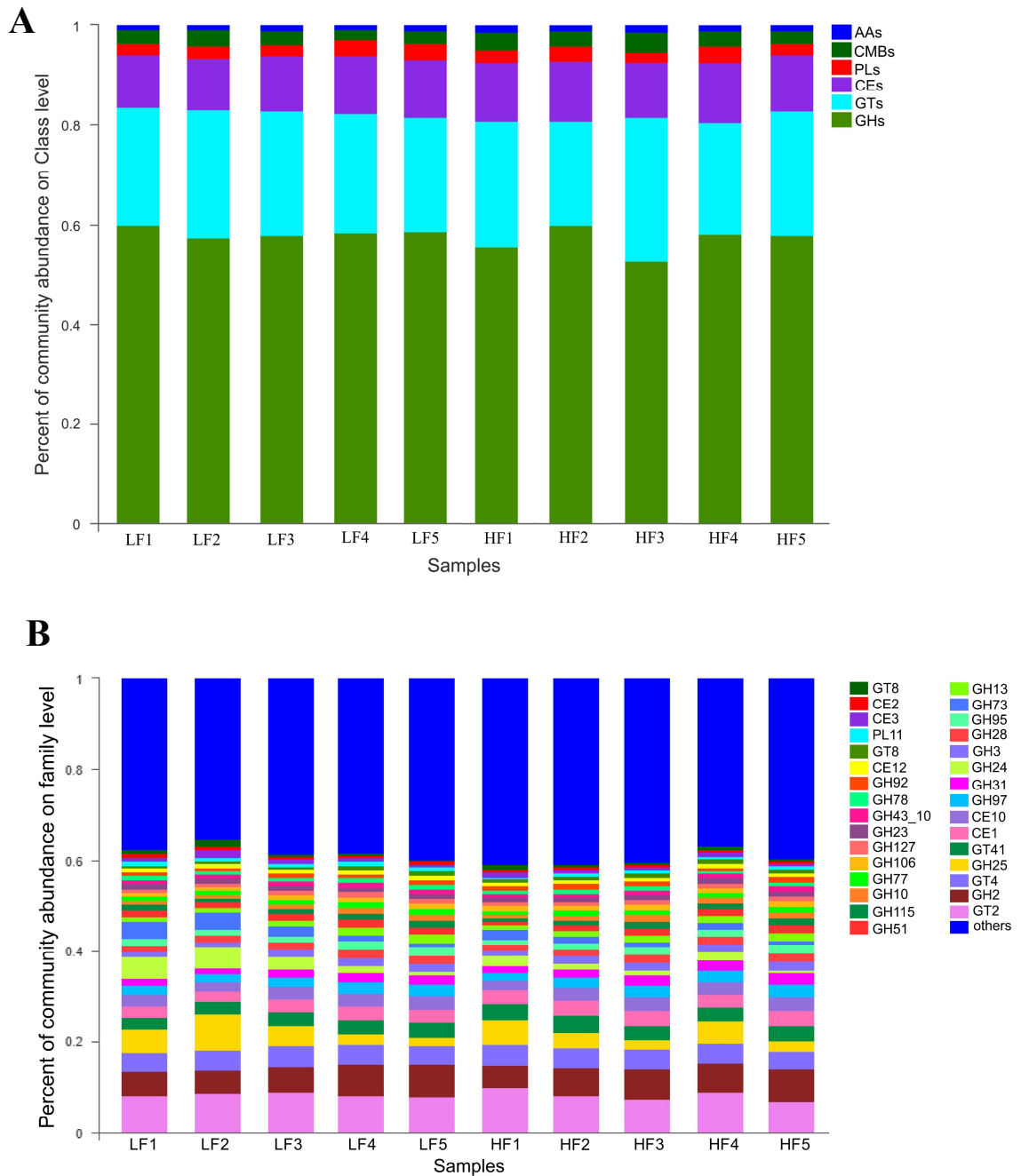


Figure S4. Distribution of COG genes at function level from dairy cow rumen microbiota. S: function unknown; L: replication, recombination, and repair; M: cell wall/membrane/envelope biogenesis; G: carbohydrate transport and metabolism; E: amino acid transport and metabolism; T: signal transduction mechanisms; J: translation, ribosomal structure and biogenesis; P: inorganic ion transport and metabolism; O: posttranslational modification, protein turnover, chaperones; K: transcription; F: nucleotide transport and metabolism; C: energy production and conversion; V: defense mechanisms; H: coenzyme transport and metabolism; I: lipid transport and metabolism; U: intracellular trafficking, secretion, and vesicular transport; D: cell cycle control, cell division, chromosome partitioning.

