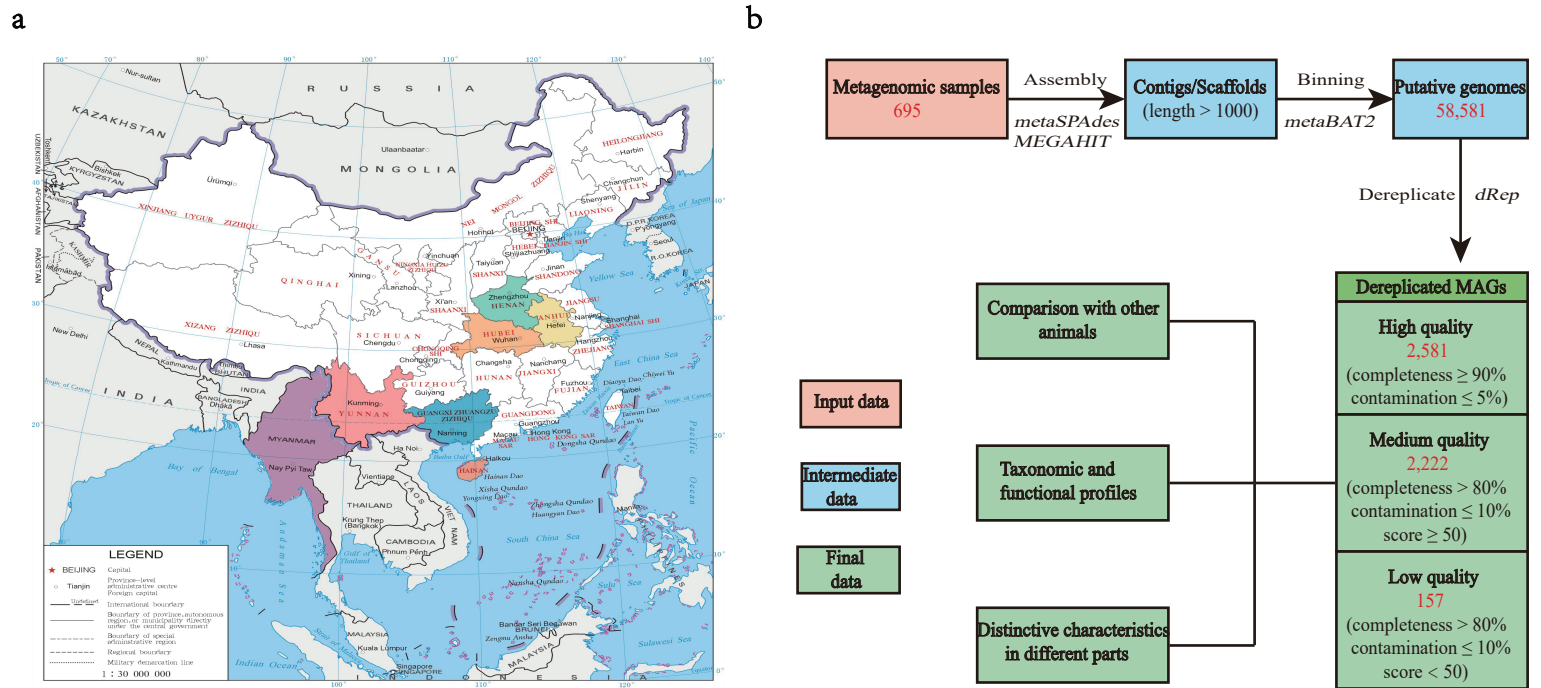
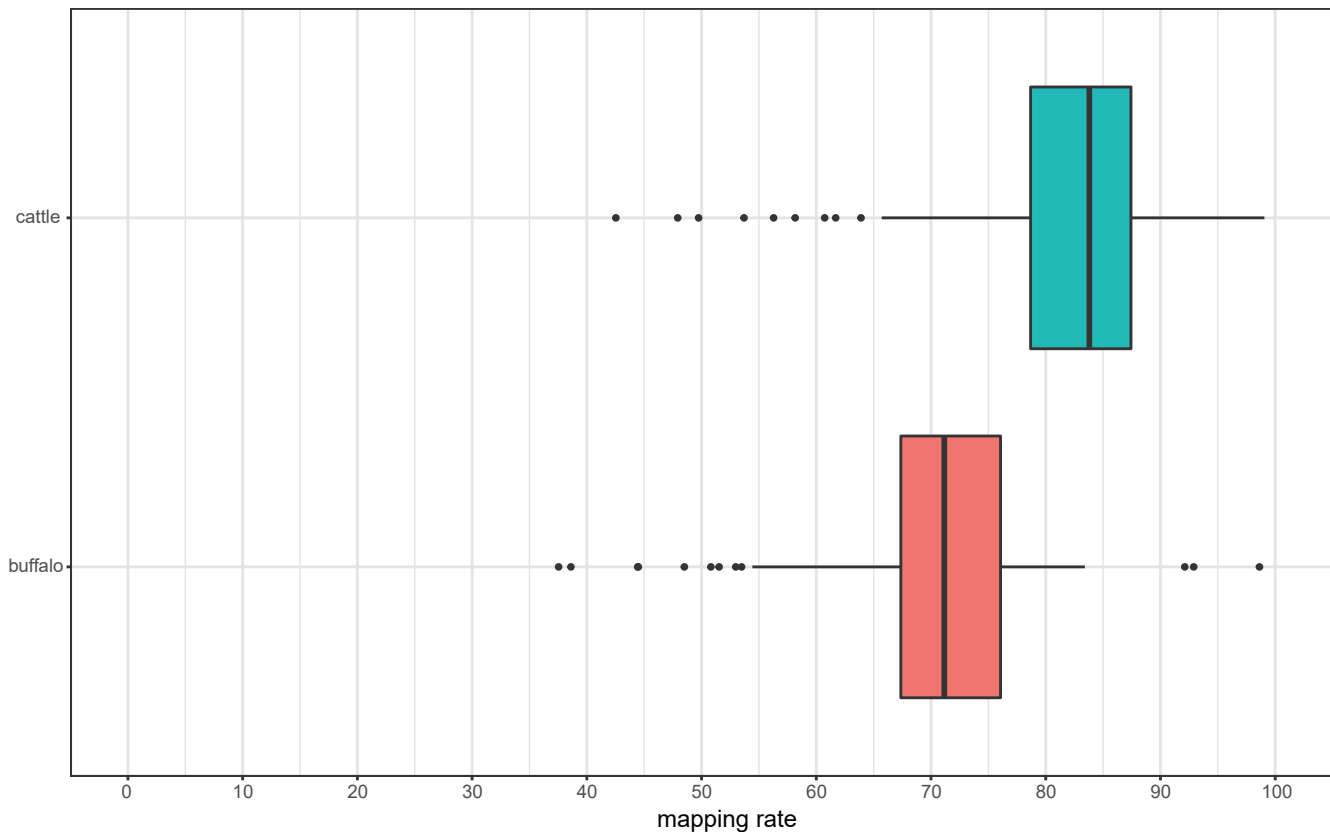
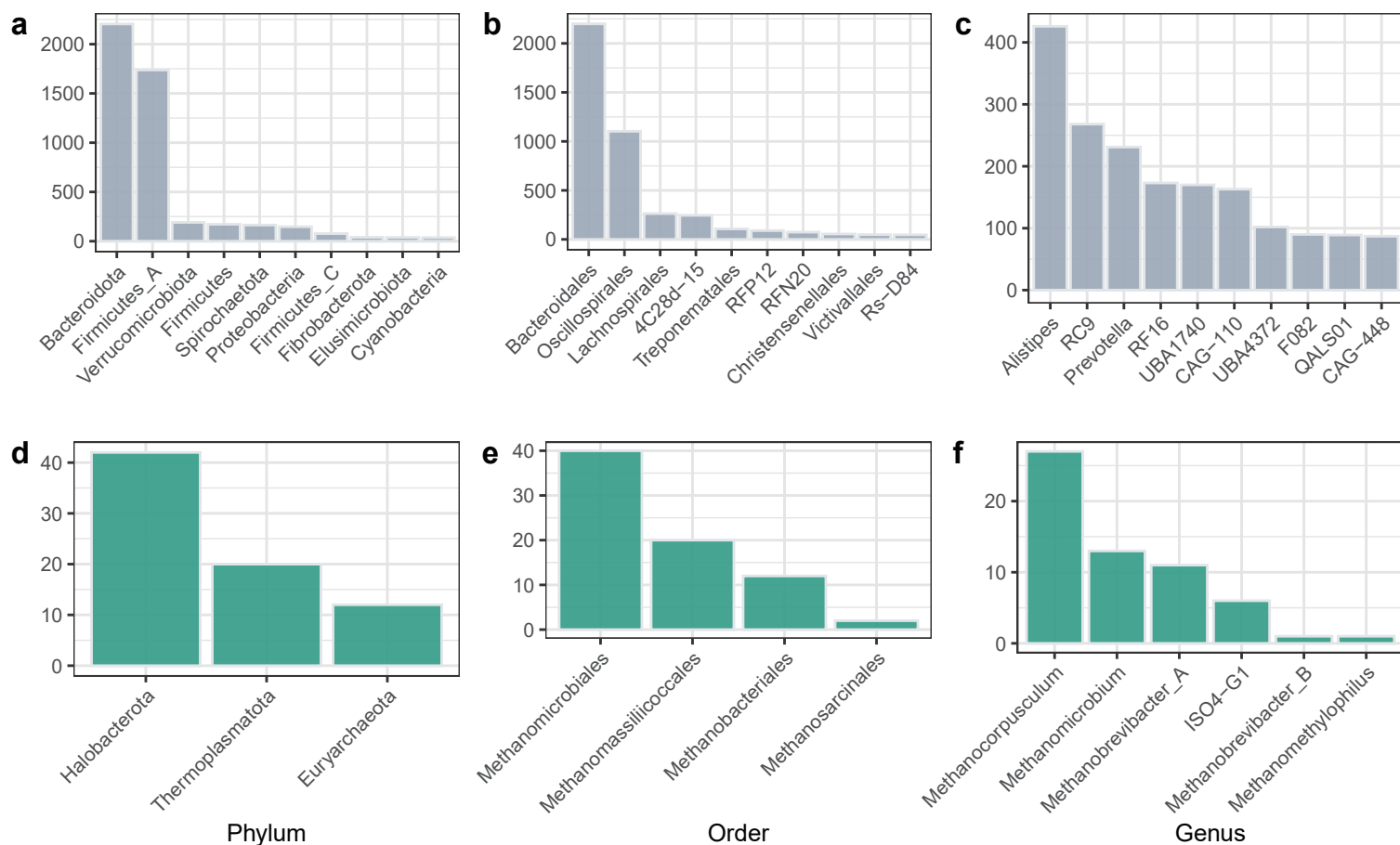




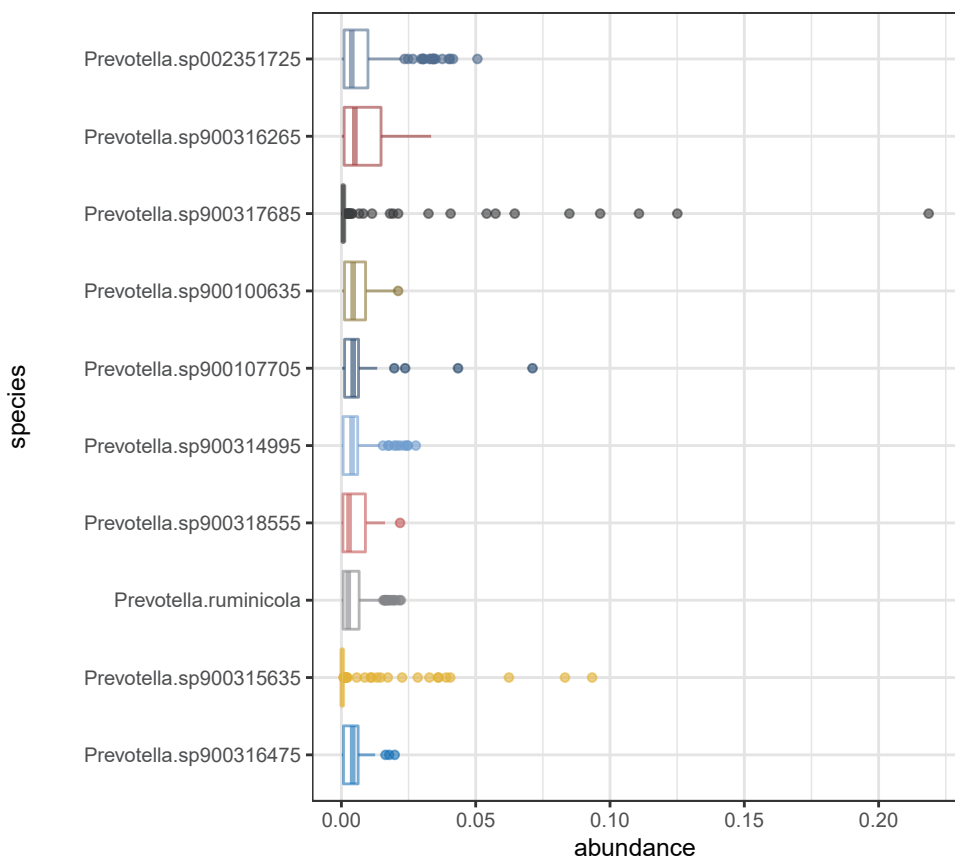
Supplementary Fig.1: Methodology overview of metagenomic analysis. a) The geographical distribution of metagenomics sampling, including Anhui, Hubei, Yunnan, Henan, Hainan, and Guangxi. The original map was come from National Standard Map Service of China (<http://bzdt.ch.mnr.gov.cn/browse.html?picId=%224o28b0625501ad13015501ad2bfc0275%22>). b) The flow diagram of metagenomic analysis.



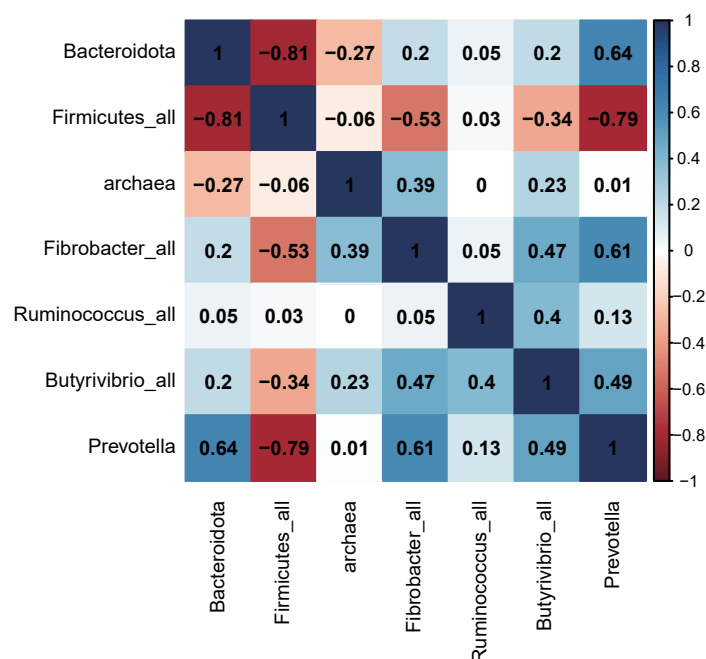
Supplementary Fig.2: Mapping rate for our MAGs and RUGs against the reads of Stewart et al. Red box and cyan box indicate the percentages of metagenomics reads from Stewart et al with MAGs of buffalo and RUGs of cattle, respectively.



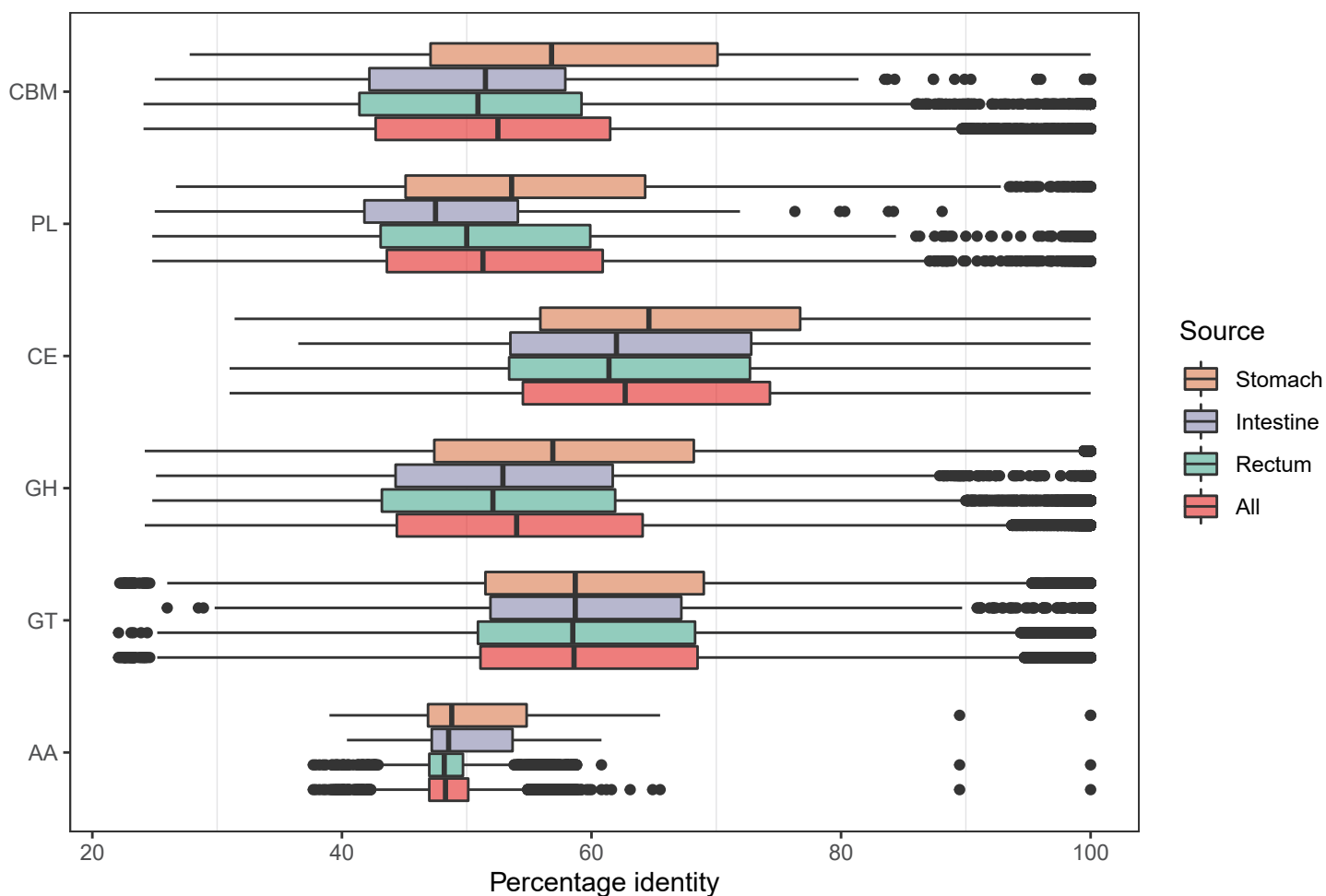
Supplementary Fig.3: Taxonomy assignments of 4,960 MAGs. X-axis indicate bacteria and archaea classified to phylum (a, d), order (b, e), and genus (c, f) level, respectively. Y-axis indicate the number of MAGs.



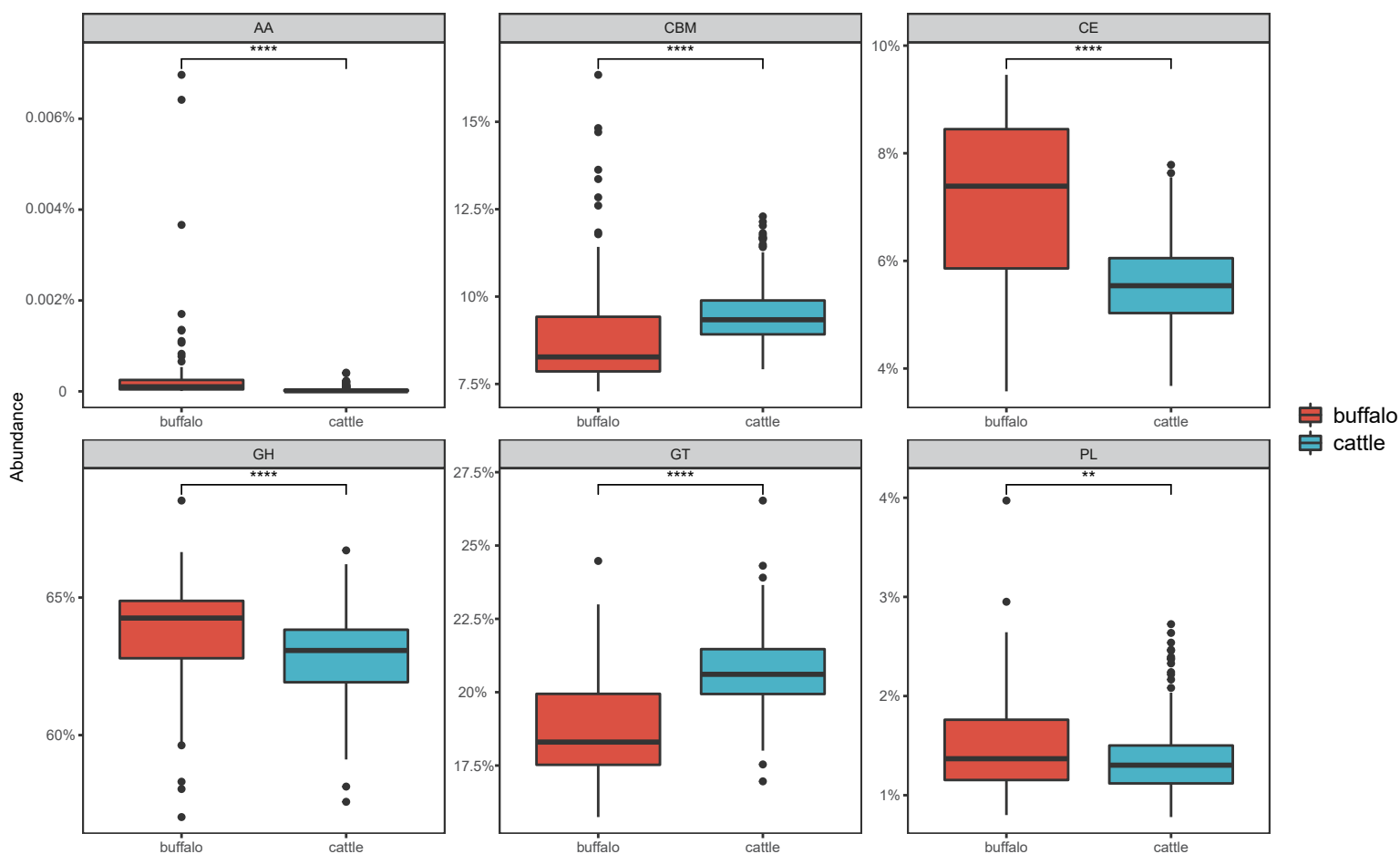
Supplementary Fig.4: Boxplot of the *Prevotella* species with top abundance in rumen. X-axis indicate the relative abundance, and y-axis indicate top 10 abundances of *Prevotella* species.



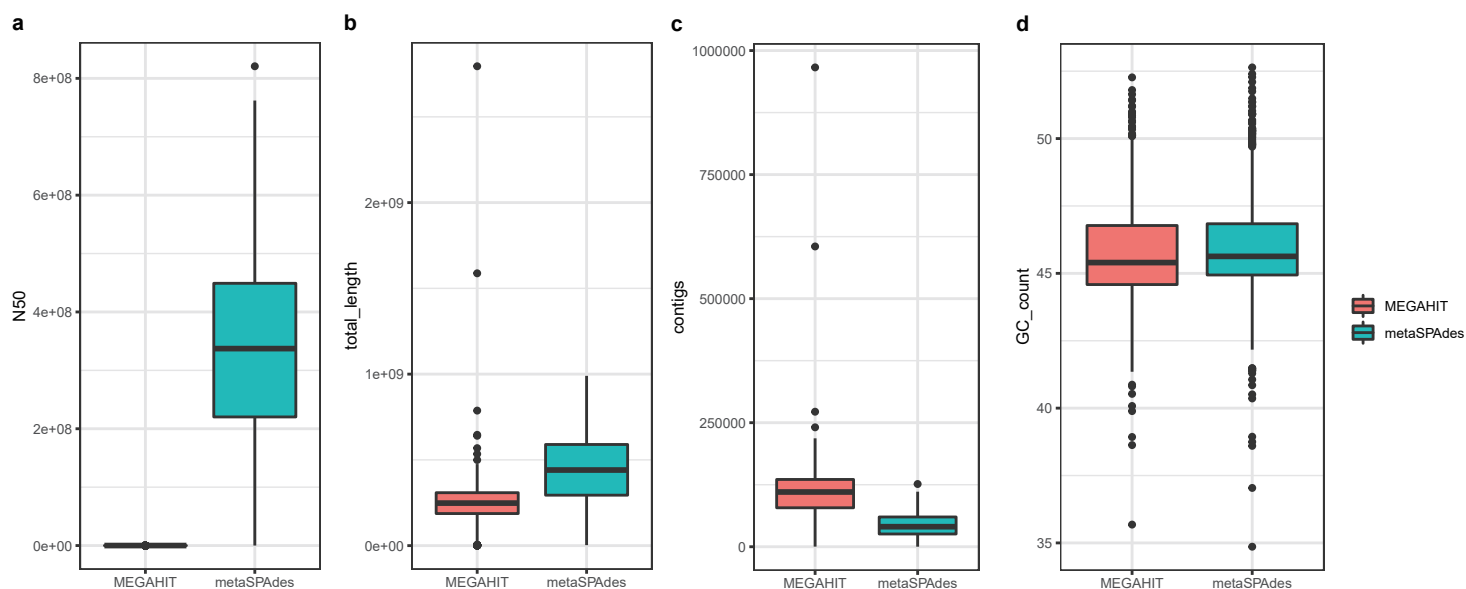
Supplementary Fig.5: Heatmap of the correlation among microbes that play important roles in the DT. Correlation of three phyla (Bacteroidota, Firmicutes_all, and Archaea) and four genera (Fibrobacter_all, Ruminococcus_all, Butyrivibrio_all, and Prevotella) were calculated. Red indicate negative correlation, and blue indicate positive correlation. The number in each square showed the correlation coefficient of them.



Supplementary Fig.6: Maximum percentage identity between predicted proteins from the MAGs and CAZy database. X-axis indicate the percentage identity. Y-axis indicate six enzyme classes in CAZy database, glycoside hydrolases (GH, n = 76,224), glycosyl transferases (GT, n = 21,402), carbohydrate-binding modules (CBM, n = 11,645), carbohydrate esterases (CE, n = 3,804), polysaccharide lyases (PL, n = 1,879) and auxiliary activities (AA, n = 35).



Supplementary Fig.7: Comparison of six CAZy families' relative abundance between buffalo and cattle based on all CAZy protein abundances. X-axis indicate proteins belong to buffalo (red) and cattle (blue). Y-axis shows the relative abundances of protein families; GH, glycoside hydrolase; GT, glycosyl transferase; PL, polysaccharide lyase; CE, carbohydrate esterase; AA, auxiliary activities; CBM, carbohydrate-binding module. * P < 0.05, ** P < 0.01, *** P < 0.001, **** P < 0.0001.



Supplementary Fig.8: Boxplot comparison of the assembly results between metaSPAdes (blue) and MEGAHIT (red). The comparison of metaSPAdes and MEGAHIT at a) N50, b) total length, c) contigs numbers, and d) GC counts level.