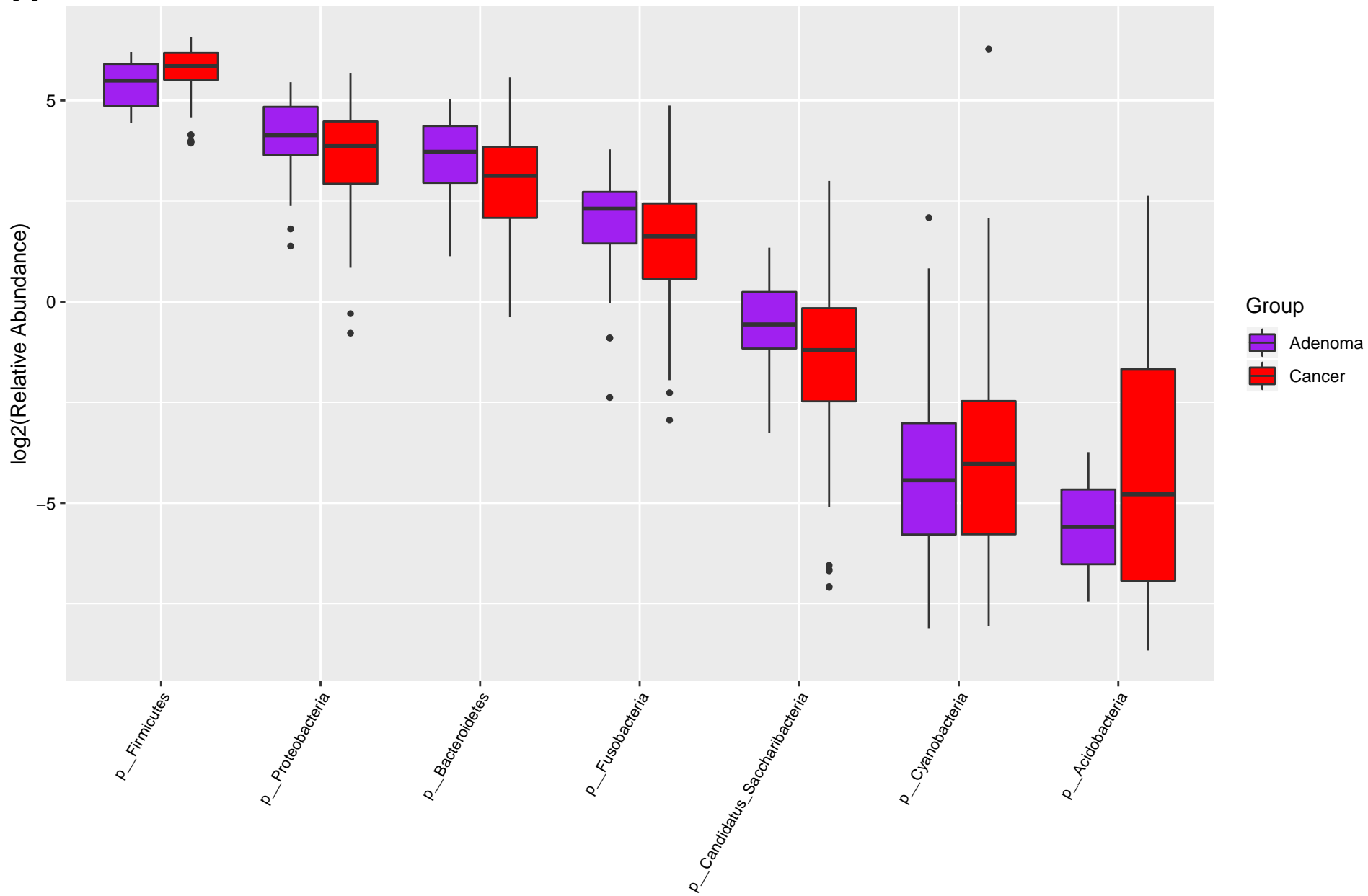


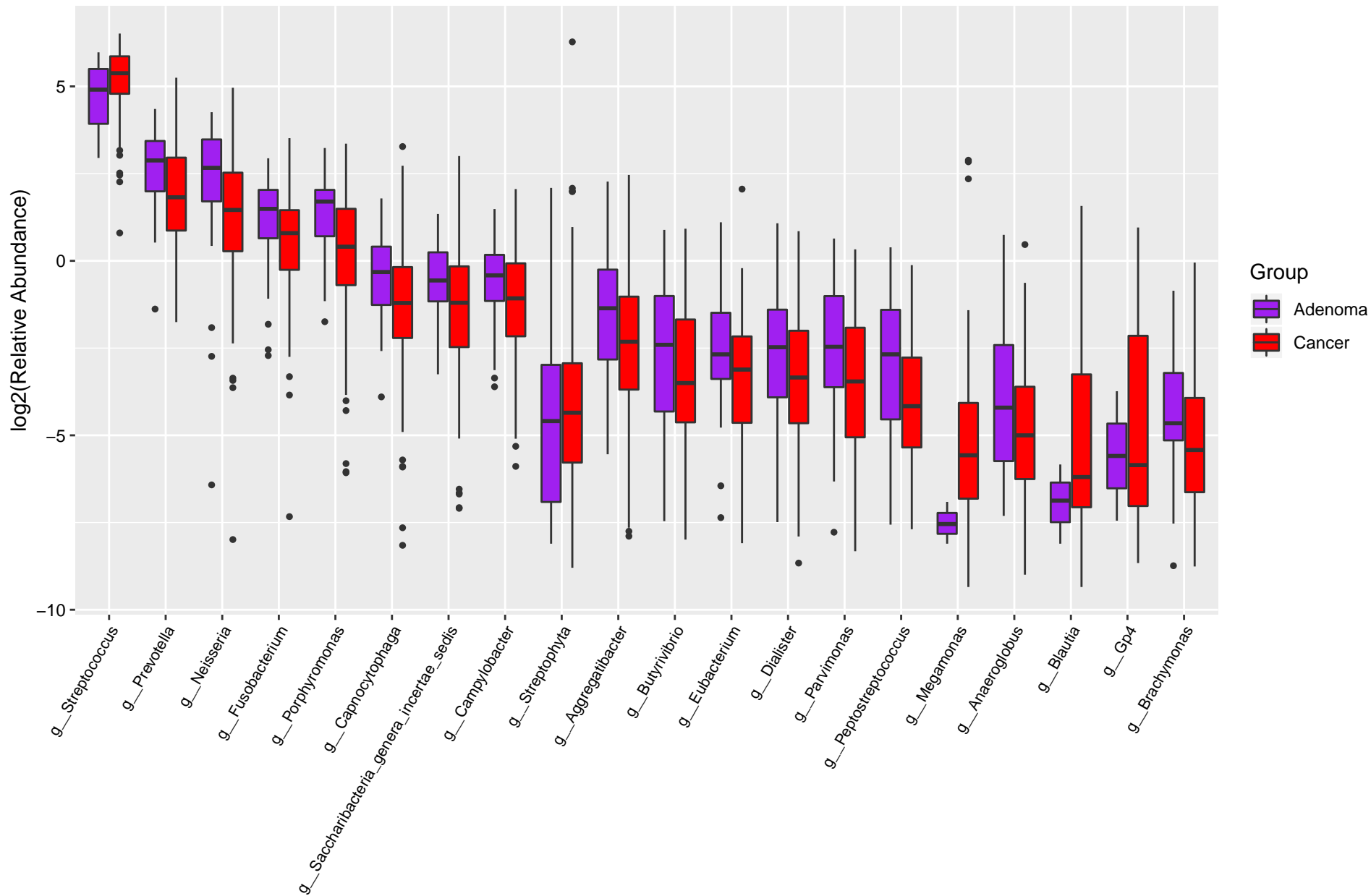
Supplementary figures and table legends

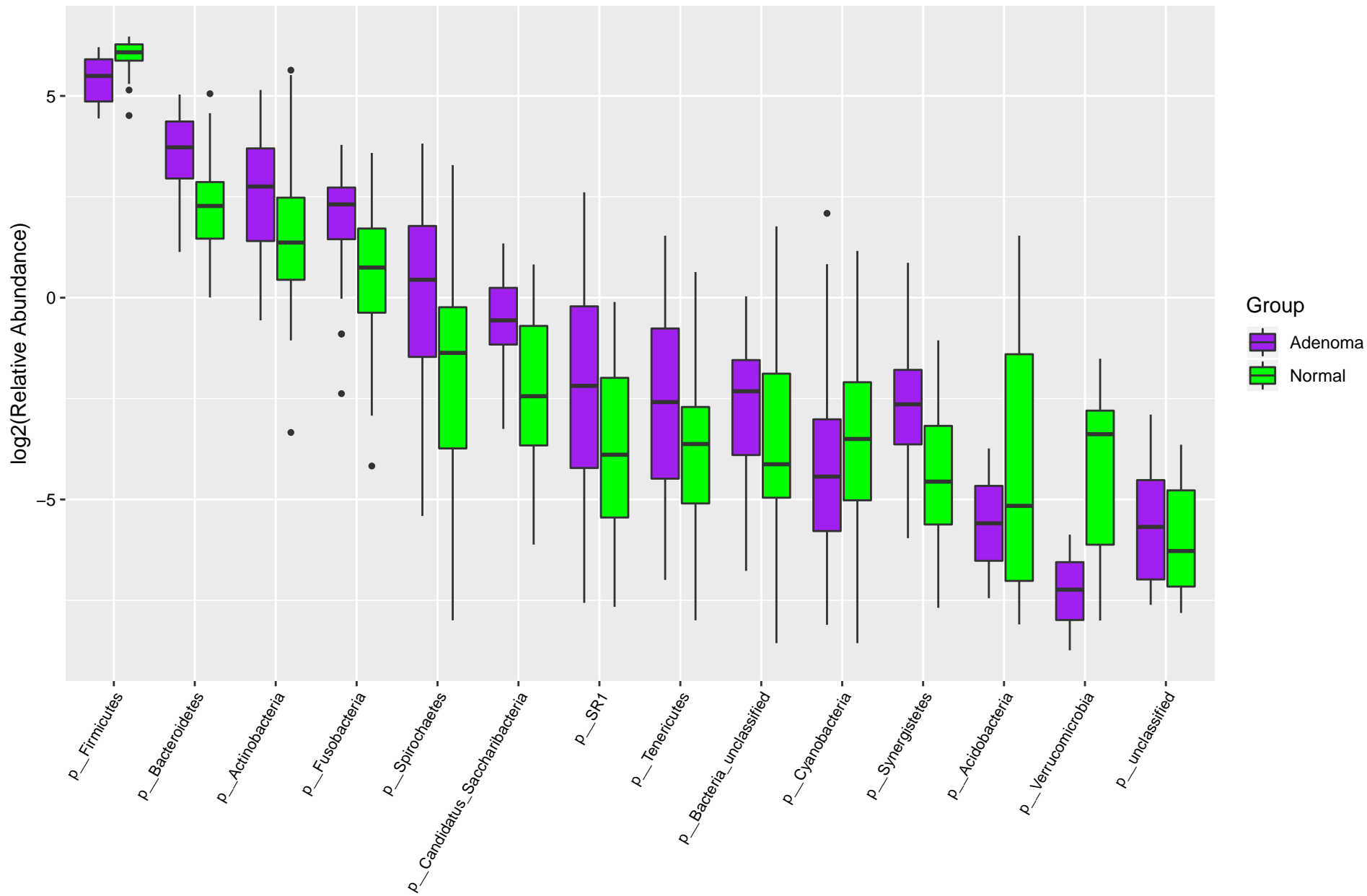
Figure S1. Phylogenetic profiles of oral microbes among patients with CRC (n = 161) and CRA (n = 34) and healthy controls (n = 58). The microbial communities at the phylum (A) and genus (B) levels in CRA versus CRC are represented. The microbial communities at the phylum (C) and genus (D) levels in CRA versus controls and in CRC versus controls (E and F, respectively) are also represented. CRA, colorectal adenoma; CRC, colorectal cancer.

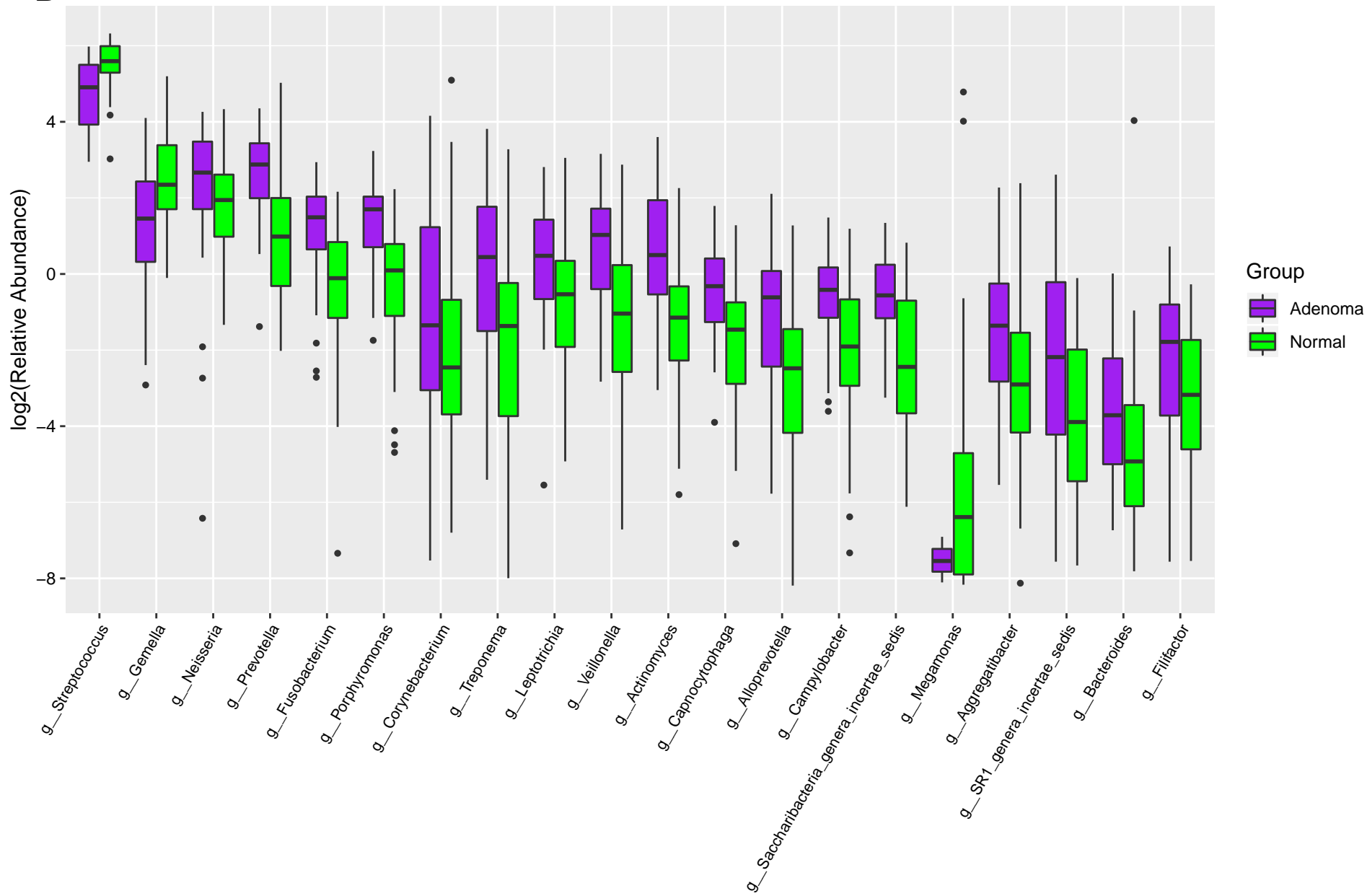
Figure S2. Associations of oral microbiota with inferred functions. The heatmaps show partial Spearman correlation coefficients between 32 genera and differential KEGG pathways in CRC versus controls (A), between 9 genera and differential KEGG pathways in CRA versus controls (B), and between 4 genera and differential KEGG pathways in CRC versus CRA (C). CRA, colorectal adenoma; CRC, colorectal cancer; KEGG, Kyoto encyclopedia of genes and genomes.

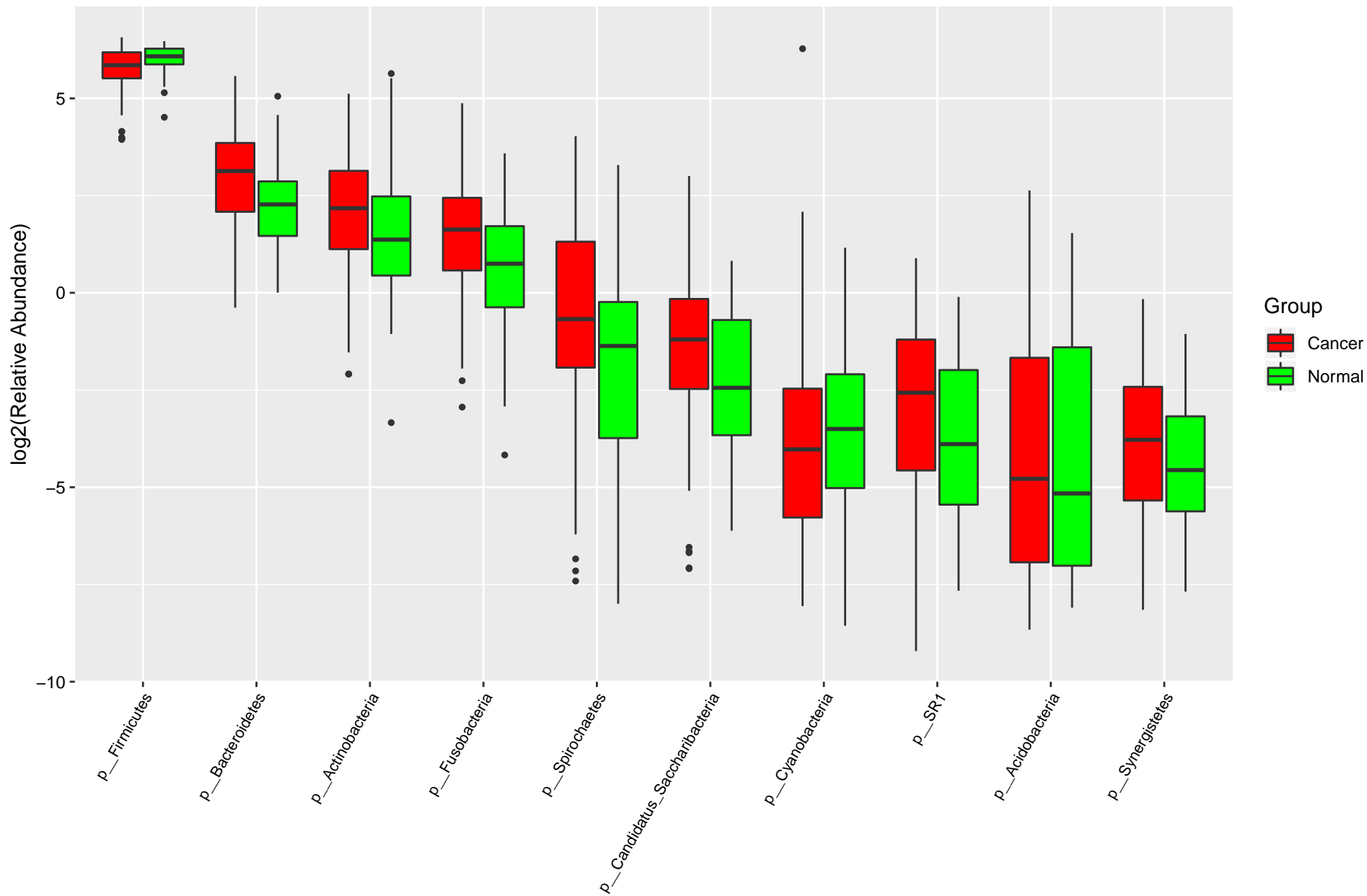
Figure S3. Relative abundance of two CAGs in oral samples of each group. (A). Relative abundance of pathogen CAG. (B) Relative abundance of biofilm CAG. n (control) = 58, n (CRC) = 161, n (CRA) = 34. CRA, colorectal adenoma; CRC, colorectal cancer; CAGs, co-abundance groups.

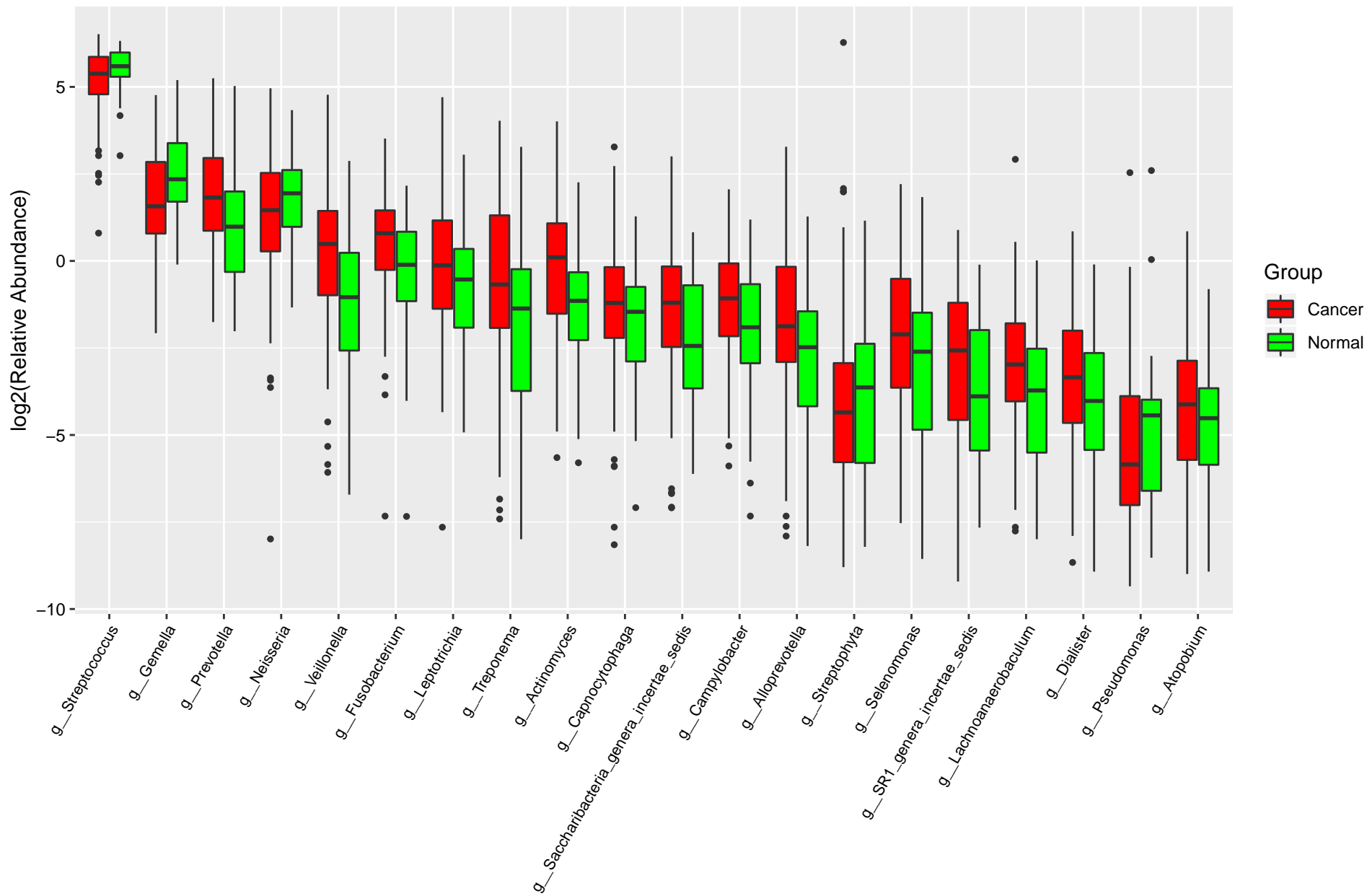
A

B

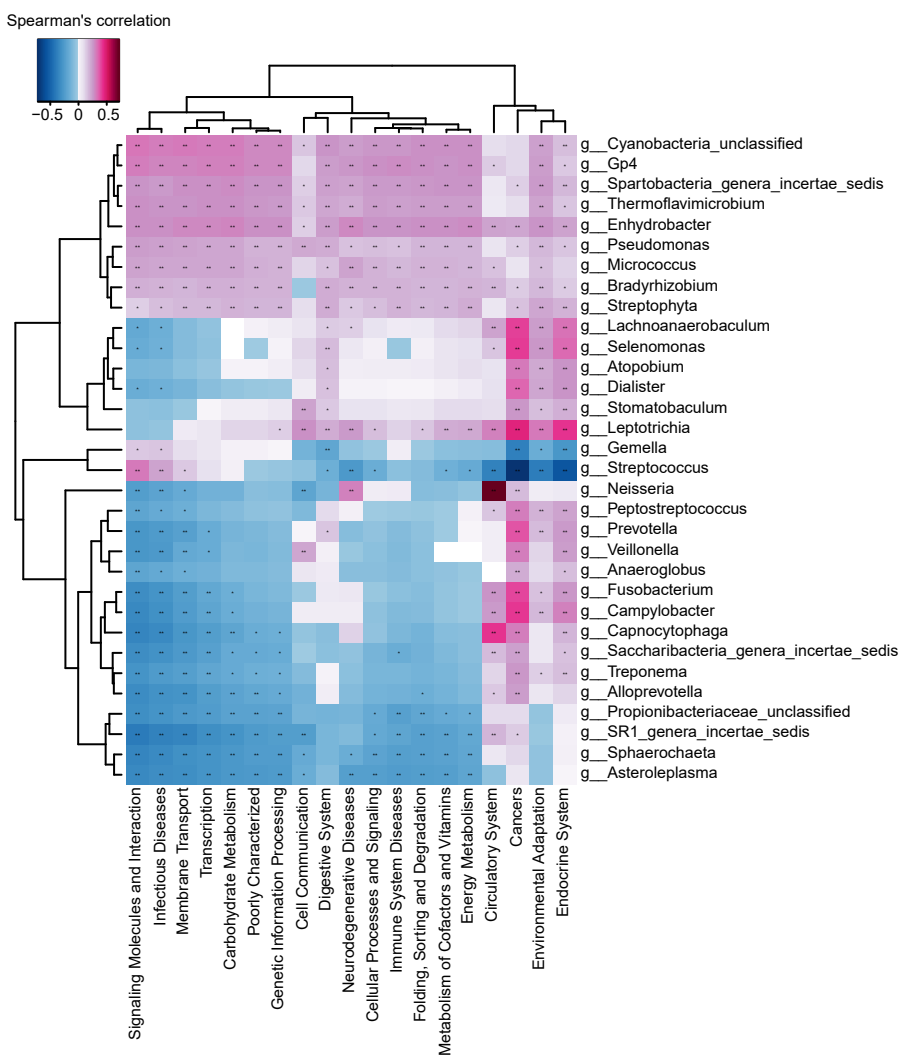
C

D

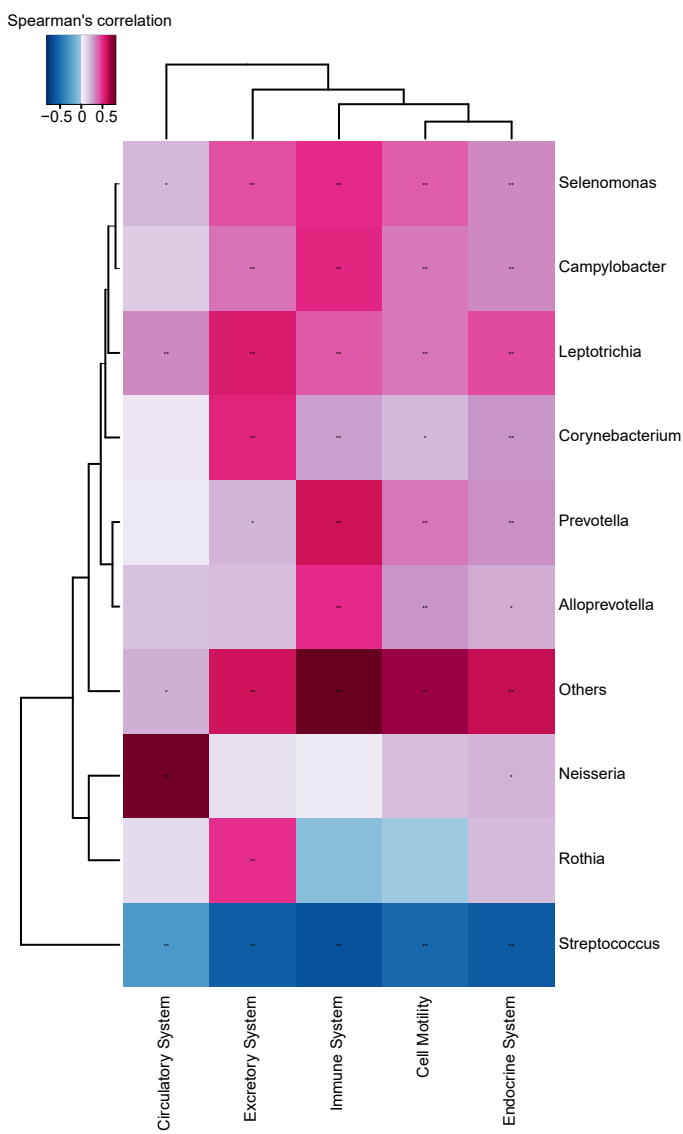
E

F

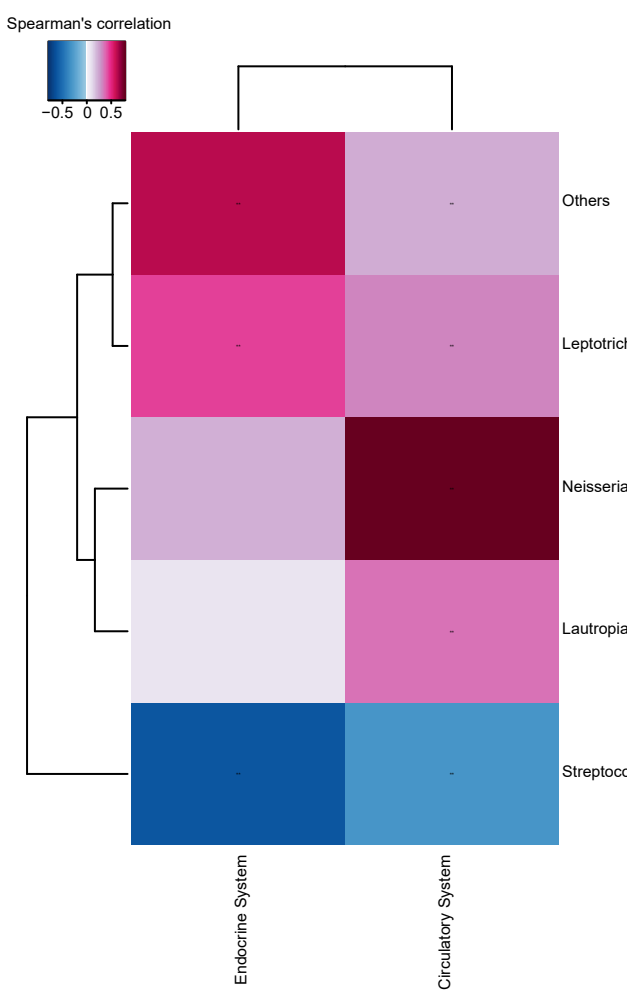
A



B

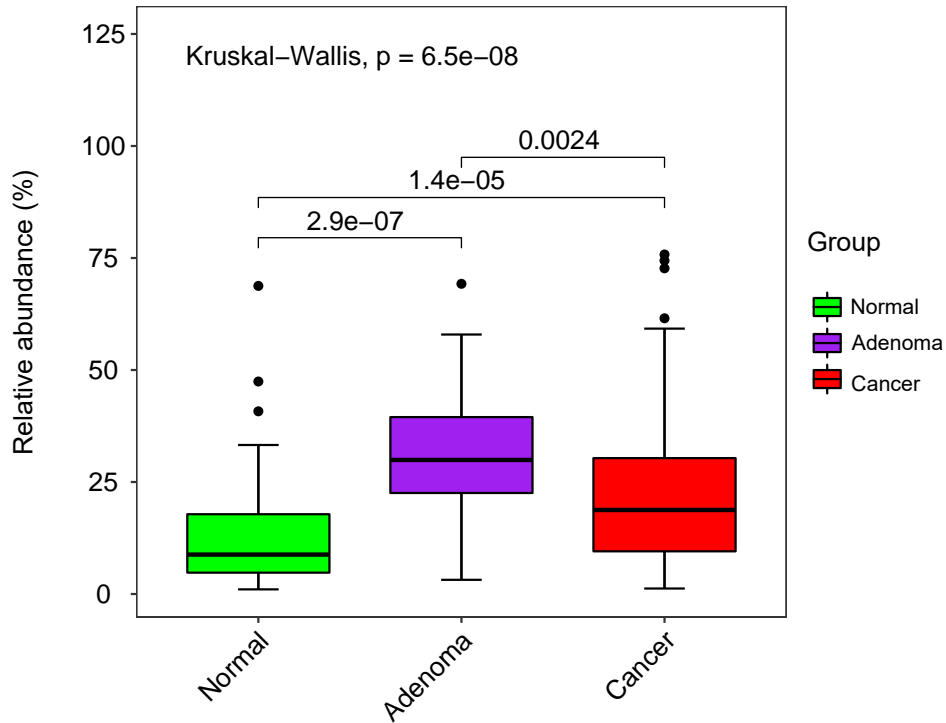


C



A

Pathogen CAG



B

Biofilm CAG

