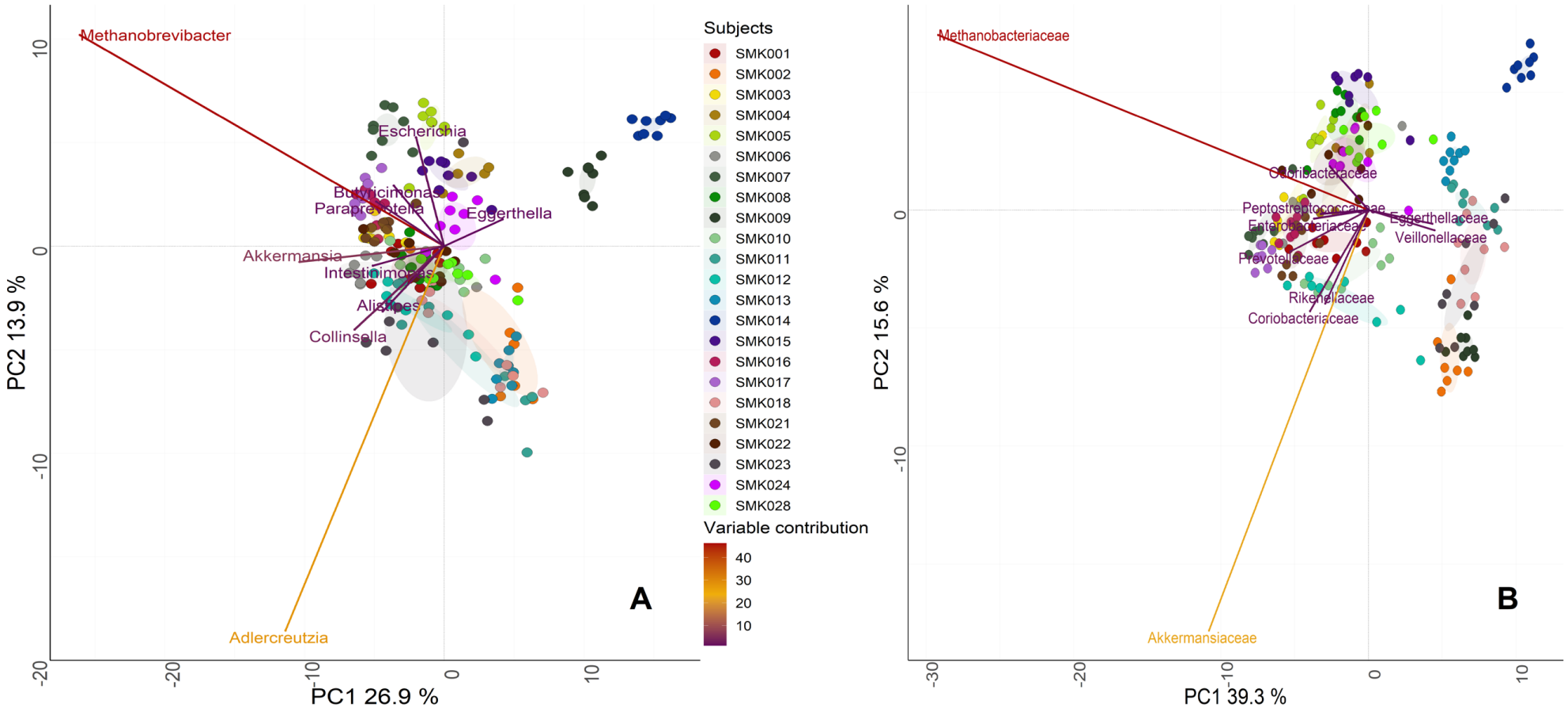


Figure S7. The PCA plot shows clustering patterns of samples based on microbiome composition. Sample distribution patterns **(A)** based on participant-specific gut microbiome profiles at the genus level and **(B)** based on participant-specific microbiome profiles at the family level. Arrows indicate the top ten contributing bacterial taxa. The arrows' colour corresponds to each variable's contribution to the principal axes. Ellipses show 95 % confidence intervals. Dots are coloured by the participant. The first two principal components, PC1 and PC2, explained the highest proportion of variation.