

Figure S1. Relative abundance of bacterial taxa at genus level in treatment groups AE, AD, IE and ID.

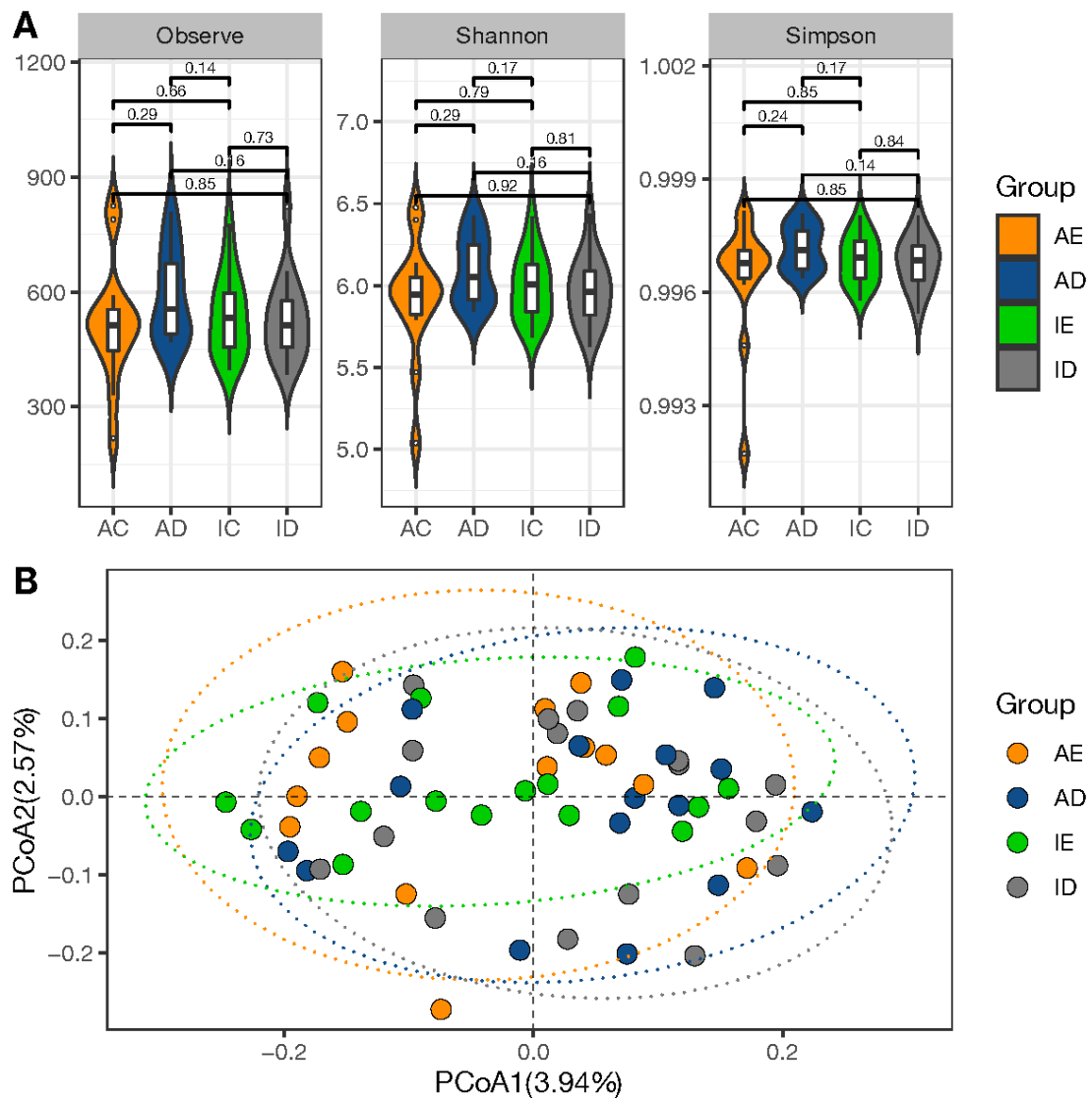


Figure S2. Bacterial alpha (**A**) and beta (**B**) diversity estimates based on treatment groups AE, AD, IE and ID.

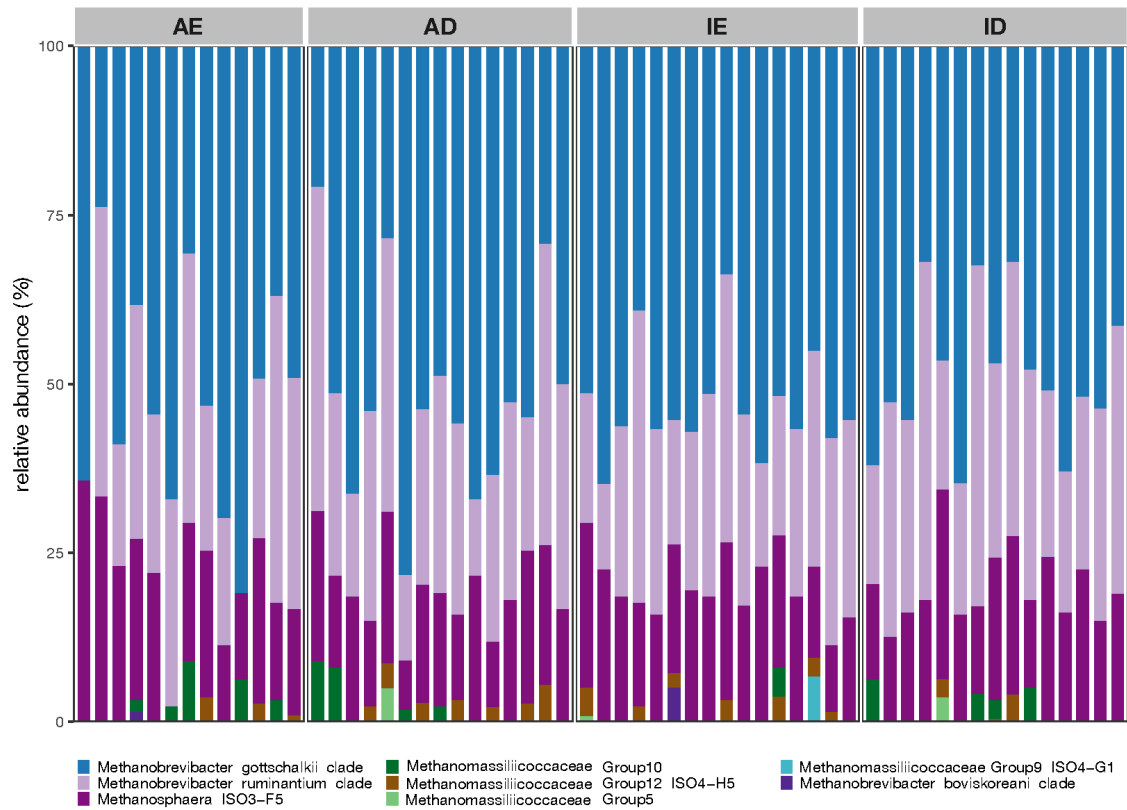


Figure S3. Relative abundance of archaea at species level in treatment groups AE, AD, IE and ID.

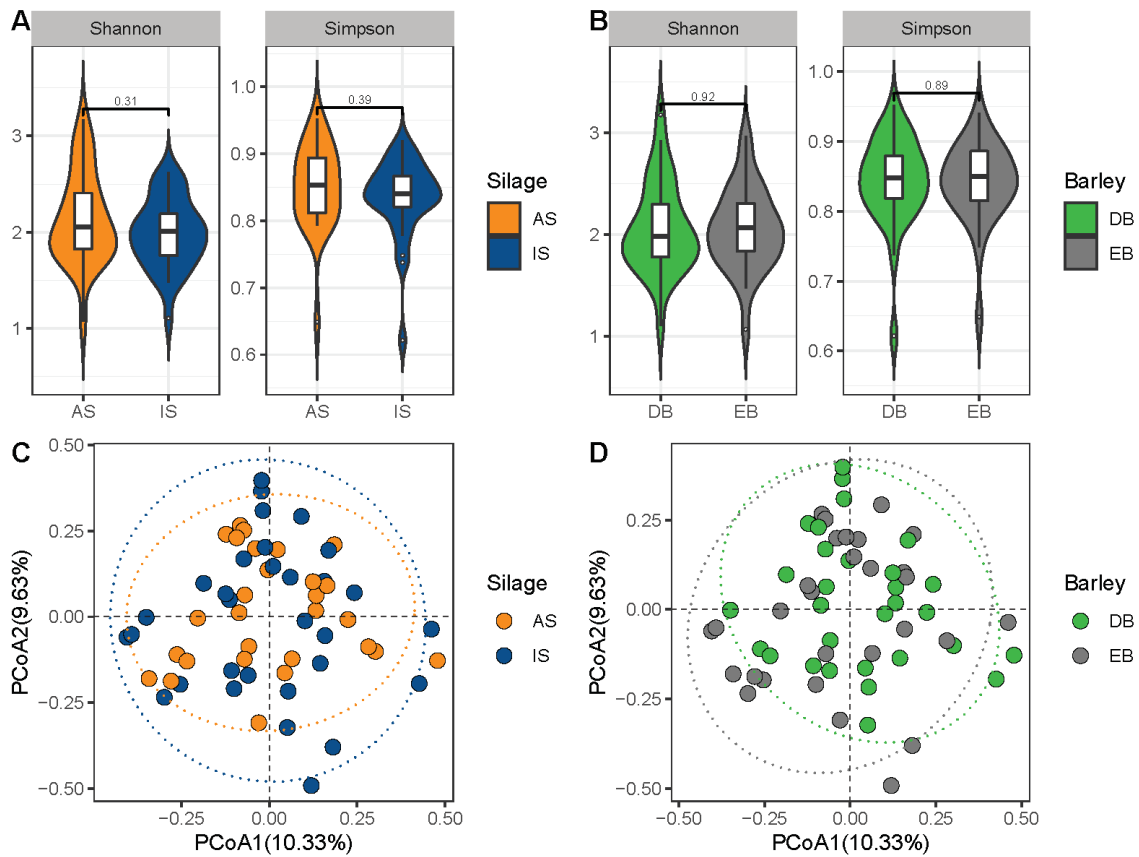


Figure S4. Archaeal alpha and beta diversity estimates for groups based on silage (A and C) and barley (B and D) preparation methods.