# Install R package devtools

if (!requireNamespace("BiocManager", quietly=TRUE))

install.packages("BiocManager")

suppressWarnings(suppressMessages(library(BiocManager)))

if (!requireNamespace("phyloseq", quietly=TRUE))

BiocManager::install("phyloseq")

library(phyloseq)

result=BetaDiv(otu=otutab\_rare, map=metadata, group="Group",

dist="bray", method="NMDS", Micromet="adonis")

# Install R package devtools

if (!requireNamespace("devtools", quietly=TRUE))

install.packages("devtools")

library(devtools)

if (!requireNamespace("amplicon", quietly=TRUE))

install\_github("microbiota/amplicon")

suppressWarnings(suppressMessages(library(amplicon)))

# Principal coordinate analysis, PCoA

(p=beta\_pcoa(beta\_bray\_curtis, metadata, "Group"))

ggsave(paste0("p1.PCoA.bray.pdf"), p, width=89, height=56, units="mm")