McKeeley Stansberry

Project Assignment 4: ASV table

1. For your assignment submit table.qzv, rep-seqs.qzv and stats-dada2.qzv.

Text

Description automatically generated

Graphical user interface

Description automatically generated with medium confidence

Chart, histogram

Description automatically generated

Graphical user interface, application

Description automatically generated

Graphical user interface, text, application, email

Description automatically generated

1. What is an appropriate value for subsampling? Justify your answer.

The appropriate subsampling depth is 2629 that way the retained percent is lower and that you still have majority of your samples with the percent samples is high. This choice for the p-sampling depth excludes 8 samples. We will now be retaining 233,464 (20.50%) features in 88 (91.67%) samples at the specified sampling depth. The core-metrics-phylogenetic command will read the 88 samples sequences and the 8 samples that did not meet the minimum number will be dropped from this command.