1. Edit Metadata file. E.g. should contain header for sample and treatment and list of root names for ViReMa output folders, followed by conditions. Example:

#sample treatment

FHV-R1\_ViReMa FHV

FHV-R2\_ViReMa FHV

FHV-R4\_ViReMa FHV

S2-FHV-R1\_ViReMa S2-FHV

S2-FHV-R2\_ViReMa S2-FHV

S2-FHV-R4\_ViReMa S2-FHV

1. Put metadata file in same folder at ViReMa analysis, or you an add paths to metadata file: e.g.

#sample treatment

/data/andrew/FHVEXP/FHV-R1\_ViReMa FHV

/data/andrew/FHVEXP/FHV-R2\_ViReMa FHV

/data/andrew/FHVEXP/FHV-R4\_ViReMa FHV

/data/andrew/FHVEXP/S2-FHV-R1\_ViReMa S2-FHV

/data/andrew/FHVEXP/S2-FHV-R2\_ViReMa S2-FHV

/data/andrew/FHVEXP/S2-FHV-R4\_ViReMa S2-FHV

1. Run: *python3 Make\_Count\_table.py Metadata.txt*

Only required argument is name/path of metadata file

Output is ‘*Rec\_Counts.txt*’

1. Run: *Rscript R.virema.txt Rec\_Counts.txt [cond1] [cond2] [reps]*

Requires DESeq2 installed

Output is DESeq2 analysis csv file and PCA plot in pdf