HIV\_multiomics

Files verified =

SNF\_cross\_validation.Rmd

Produced files

"processing/cluster\_SNF\_3\_omics\_3\_clusters.csv"

“cluster\_SNF\_3\_omics\_3\_clusters\_plusHC.csv”

Missing files

"processing/table\_clinical\_data.csv"

"processing/relative\_abundance\_table.csv"

Changes

Data → change “Original\_Scale\_Data\_CLP.xlsx” no IDs → right file : clp\_lipidomics\_data.csv

Data → change “Supplementary Data 1.xlsx” no IDs → right file : cocomo\_norm\_data\_filt.csv

Data → add clp\_um\_new\_data.csv