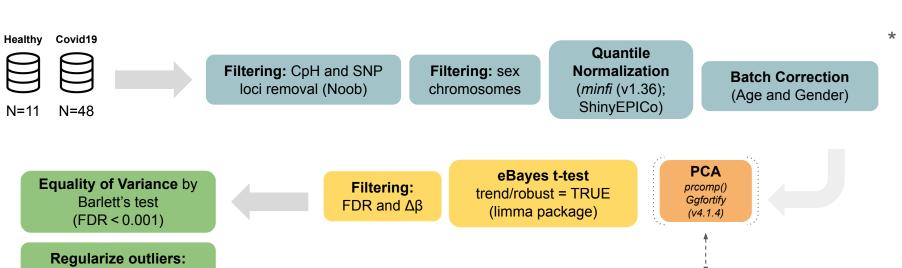# Methylation Pipeline

Link to dataset: https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE188573
Link to paper: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC9706884/

Healthy Covid19
N=11   N=48

Filtering: CpH and SNP loci removal (Noob)

Filtering: sex chromosomes

Quantile Normalization (*minfi* (v1.36); ShinyEPICo)

Batch Correction (Age and Gender)

*

PCA
prcomp()
Ggfortify
(v4.1.4)

eBayes t-test trend/robust = TRUE (limma package)

Filtering: FDR and Δβ

Equality of Variance by Barlett's test (FDR < 0.001)

Regularize outliers: t-test (pvalue<0.05)

SOFA Associations: Spearman corr. ρ

GO: GREAT (v3.0.0)

Clinical Variables (dexamethasone treatment, obesity, and hypertension)

Categorical variables: linear modeling

Numerical variables: Pearson corr.

Preprocessing +QC   DMR   DVPs   PCA   GO

*Repeat but with monocyte proportions for samples with information available