Data Overview

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Generate dendrogram

mf1.dendro.gen.v3.R
It also requires subtype markers, as calculated in this script: mar.calc.R; zfun.wilcox.R

Do circular plot

mf1.plot.v8.R
It also requires subtype average expression, as calculated in this script: avg.calc.R

Plot data quality

- nGenes, nUMIs, percent.mito, etc:
  sf1.quality.v3.R

- Sample contribution:
  sf1.sample.contribution.R

Calculate cluster robustness

- Source functions:
  robust.fun.R

- Randomly remove one sample and integrate the rest three samples
  inte.3donor.exn.R
  inte.3donor.inn.R
  inte.3donor.nnc.R

- Then, Calculate AUC scores evaluating cluster separability followed by visualization
  calc.robust.auc.R
  plot.robust.auc.R

- Also checked the # markers per subtype
  plot.robust.mar.R

Alternative integration methods

- Harmony
  harmony.ctp.all.R

- MNN
  mnn.ctp.all.R

- Seurat
  seurat.ctp.all.R

Robustness to different gene annotation models

- Extract count data
  extract_sp.R

- Cluster in each species and visualize
  cluster.insp.R
  cluster.insp.vis.R

- Visualize species-specific subtypes
  subcluster.insp.R
  subcluster.insp.cbn.vis.R

- Visualize species-specific expression
  plot.dem.exn.R
  plot.dem.inn.R
  plot.dem.nnc.R
  plot.th.umap.R
  plot.foxp2.R