

Merge RNA Data

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load function from local files

load data from local files

1. Read the QC Data

```
options(Seurat.object.assay.version = "v5")

# load data
sample_seurat_list <- readRDS(
  here::here("data", "synaptosomes_scRNA",
    "sample_seurat_RNA_list_2025-05-15.rds")
)

sample_meta <- readRDS(
  here::here("data", "synaptosomes_scRNA",
    "sample_meta_RNA_2025-05-15.rds")
)

# delete the Q3 and C3
# sample_seurat_list <- sample_seurat_list[!names(sample_seurat_list) %in% c("Q3", "C3")]
# sample_meta <- sample_meta[!sample_meta %in% c("Q3", "C3")]

for (samp in names(sample_seurat_list)) {
  cat("Sample:", samp, "\n")
  print(head(colnames(sample_seurat_list[[samp]]), 10))
  cat("\n")
}
```

```
## Sample: C1
## [1] "C1_AAACCCAAGACGGAAA-1" "C1_AAACCCAAGCAACAAT-1" "C1_AAACCCAAGCCAGAGT-1"
## [4] "C1_AAACCCAAGCCTGAGA-1" "C1_AAACCCAAGGGCGAGA-1" "C1_AAACCCAGTAGGACCA-1"
## [7] "C1_AAACCCAGTGCATTG-1" "C1_AAACCCAGTTCTCCTG-1" "C1_AAACCCAGTTGCTCAA-1"
## [10] "C1_AAACGAAAGAACAGGA-1"
##
## Sample: C2
## [1] "C2_AAACCCAAGTAATCCC-1" "C2_AAACCCACACGACTAT-1" "C2_AAACCCACACTTCTCG-1"
## [4] "C2_AAACCCACAGCACCCA-1" "C2_AAACCCAGTATCGAGG-1" "C2_AAACCCAGTATGCAAA-1"
## [7] "C2_AAACCCAGTGTCCATA-1" "C2_AAACCCATCATCGTAG-1" "C2_AAACCCATCTAGTTCT-1"
## [10] "C2_AAACGAAAGAACAGGA-1"
##
## Sample: C3
## [1] "C3_AAACCCAAGTAGAGTT-1" "C3_AAACCCAAGTATGAAC-1" "C3_AAACCCACAATGCAGG-1"
## [4] "C3_AAACCCACACAACCGC-1" "C3_AAACCCACATTACTCT-1" "C3_AAACCCAGTCAGTCCG-1"
## [7] "C3_AAACCCAGTCGGCCTA-1" "C3_AAACCCAGTGTCATCA-1" "C3_AAACCCAGTTCTCACC-1"
## [10] "C3_AAACCCATCAACTGAC-1"
##
## Sample: Q1
## [1] "Q1_AAACCCACAGAACTAA-1" "Q1_AAACCCACAGGTCCGT-1" "Q1_AAACCCAGTAGTCCTA-1"
## [4] "Q1_AAACCCAGTGTCTCTAA-1" "Q1_AAACCCATCAAACCCA-1" "Q1_AAACGAACACATAACC-1"
## [7] "Q1_AAACGAACATGACCCG-1" "Q1_AAACGAAGTAGTCCTA-1" "Q1_AAACGAAGTATAGCTC-1"
## [10] "Q1_AAACGAAGTATGAGAT-1"
##
## Sample: Q2
## [1] "Q2_AAACCCAAGGGACAGG-1" "Q2_AAACCCACAAGACGGT-1" "Q2_AAACCCACACCGTCGA-1"
## [4] "Q2_AAACCCACACGCACCA-1" "Q2_AAACCCACATAGAGGC-1" "Q2_AAACCCACATATGGCT-1"
## [7] "Q2_AAACCCACATCATTTC-1" "Q2_AAACCCAGTACAGGTG-1" "Q2_AAACGAAAGCGAACTG-1"
```

```
## [10] "Q2_AAACGAAAGGTAAAGG-1"
##
## Sample: Q3
## [1] "Q3_AAACCCAAGACCTCCG-1" "Q3_AAACCCAAGATAACGT-1" "Q3_AAACCCAAGATACCAA-1"
## [4] "Q3_AAACCCAAGCTCATAC-1" "Q3_AAACCCAAGGATTTGA-1" "Q3_AAACCCAAGGTGAGG-1"
## [7] "Q3_AAACCCACACAGAGAC-1" "Q3_AAACCCACACCCTCTA-1" "Q3_AAACCCACAGCTAACT-1"
## [10] "Q3_AAACCCAGTACAAAGT-1"
```

2. Merge the data

```
library(Seurat)
library(harmony)

## Warning: package 'harmony' was built under R version 4.4.1
## Loading required package: Rcpp
## Warning: package 'Rcpp' was built under R version 4.4.1
library(Signac)

## Warning: package 'Signac' was built under R version 4.4.1
library(GenomicRanges)

## Warning: package 'GenomicRanges' was built under R version 4.4.1
## Loading required package: stats4
## Loading required package: BiocGenerics
##
## Attaching package: 'BiocGenerics'
## The following object is masked from 'package:SeuratObject':
##
##     intersect
## The following objects are masked from 'package:lubridate':
##
##     intersect, setdiff, union
## The following objects are masked from 'package:dplyr':
##
##     combine, intersect, setdiff, union
## The following objects are masked from 'package:stats':
##
##     IQR, mad, sd, var, xtabs
## The following objects are masked from 'package:base':
##
##     anyDuplicated, aperm, append, as.data.frame, basename, cbind,
##     colnames, dirname, do.call, duplicated, eval, evalq, Filter, Find,
##     get, grep, grepl, intersect, is.unsorted, lapply, Map, mapply,
##     match, mget, order, paste, pmax, pmax.int, pmin, pmin.int,
##     Position, rank, rbind, Reduce, rownames, sapply, setdiff, table,
##     tapply, union, unique, unsplit, which.max, which.min
## Loading required package: S4Vectors
## Warning: package 'S4Vectors' was built under R version 4.4.1
##
## Attaching package: 'S4Vectors'
## The following objects are masked from 'package:lubridate':
##
##     second, second<-
```

```

## The following objects are masked from 'package:dplyr':
##
##   first, rename
## The following object is masked from 'package:tidyr':
##
##   expand
## The following object is masked from 'package:utils':
##
##   findMatches
## The following objects are masked from 'package:base':
##
##   expand.grid, I, unname
## Loading required package: IRanges
## Warning: package 'IRanges' was built under R version 4.4.1
##
## Attaching package: 'IRanges'
## The following object is masked from 'package:sp':
##
##   %over%
## The following object is masked from 'package:lubridate':
##
##   %within%
## The following objects are masked from 'package:dplyr':
##
##   collapse, desc, slice
## The following object is masked from 'package:purrr':
##
##   reduce
## Loading required package: GenomeInfoDb
library(dplyr)

names(sample_seurat_list) <- sample_meta

# 1) Pre-process each sample's RNA (normalize -> HVG -> scale -> PCA)

# sample_seurat_list <- lapply(sample_seurat_list, function(obj) {
#   DefaultAssay(obj) <- "RNA"
#   obj %>%
#     NormalizeData(assay = "RNA", layer = "counts.Gene Expression") %>%
#     FindVariableFeatures(assay = "RNA", layer = "counts.Gene Expression",
#                           nfeatures = 3000) %>%
#     ScaleData(assay = "RNA", layer = "counts.Gene Expression") %>%
#     RunPCA(assay = "RNA", reduction.name = "pca", npcs = 50)
# })
#
# print("PCA done")

# # 1. Compute the overlap of feature names across your list

```

```

# common_genes <- Reduce(
#   intersect,
#   lapply(sample_seurat_list, function(obj) {
#     rownames(obj[["RNA"]])
#   })
# )
#
# # 2. Subset each Seurat object to only those shared genes
# sample_seurat_list <- lapply(sample_seurat_list, function(obj) {
#   subset(obj, features = common_genes)
# })
#

# normalize data, find variable genes, scale data, run PCA
sample_seurat_list %>%
  lapply(., function(obj) {
    obj %>%
      NormalizeData() %>%
      FindVariableFeatures(nfeatures = 3000) %>%
      ScaleData() %>%
      RunPCA()
  }) -> sample_seurat_list

## Normalizing layer: counts

## Finding variable features for layer counts

## Centering and scaling data matrix

## PC_ 1
## Positive: VIM, SOX2, HMGB2, SLC1A3, GLI3, PHGDH, NUSAP1, DBI, PTN, ANP32E
##           FBXL7, ZFP36L1, TTYH1, HES1, QKI, SMC4, SFRP1, TOP2A, HSPB1, HMGN2
##           CD99, B2M, H2AX, CENPF, SOX6, MIR9-1HG, CLU, ADGRV1, PTTG1, PBK
## Negative: STMN2, MYT1L, LRRC7, GRIA2, SYT1, CTNNA2, ANK3, CCSE1, PPFIA2, CNTNAP2
##           GAP43, SNHG14, NSG2, RUNX1T1, NRXN1, RTN1, LINC01122, NBEA, NALF1, PTPRD
##           DOK6, NELL2, GABRB3, UNC79, OPCML, ERC2, DCX, INA, XKR4, PAK5
## PC_ 2
## Positive: TOP2A, NUSAP1, CENPF, H3C2, MKI67, H1-5, UBE2C, SMC4, SPC25, PBK
##           SYNE2, ASPM, UBE2T, H3C4, H2BC9, CDK1, KNL1, TPX2, AURKB, PIMREG
##           H2AC11, BIRC5, GTSE1, PRC1, DLGAP5, RRM2, NDC80, H2AC16, H4C4, KIF11
## Negative: EDNRB, NTRK2, CLU, SPARCL1, GLIS3, FAM89A, SERPINE2, BCAN, PI15, LRRC4C
##           GRID2, LRP2, PSAP, PTN, S100A13, PTGDS, SPATS2L, MT3, METRN, S100B
##           S100A16, TTYH1, MGST1, RMST, SPARC, DIPK1C, PAX3, GRM1, PCDH10, GREB1L
## PC_ 3
## Positive: NRG3, TOP2A, NUSAP1, DIAPH3, CDK1, TPX2, MKI67, ASPM, CENPF, PBK
##           KIF11, PDE4B, AURKB, NDC80, SPC25, LSAMP, DLGAP5, NEGR1, GTSE1, UBE2C
##           SGO1, UBE2T, CENPE, H3C2, NLGN1, KNL1, SMC2, KIF4A, BUB1B, MIS18BP1
## Negative: FTL, TPT1, CDKN1A, CRYAB, GAS5, EIF1, GADD45A, DLX6-AS1, FTH1, DDIT3
##           GDF15, GPX1, PPP1R15A, TRMT112, DLX5, TAC3, NUPR1, GADD45G, SNHG21, MAP1LC3B
##           ENSG00000289413, SNHG8, TOMM6, TBC1D22A-DT, ENSG00000241231, ATF5, MDM2, PURPL, SCGN, ARF4
## PC_ 4
## Positive: PTPRZ1, SOX5, FABP7, NFIB, NFIA, NEUROD6, PDE1A, ZBTB18, CSRP2, NEUROD2
##           SLA, OPCML, GAREM1, SLC44A5, NLGN1, BHLHE22, MIR9-1HG, SEMA3C, ARPP21, PDGFC

```

```

## HYCC1, CELF2, SLC24A2, NELL2, FEZF2, NCKAP5, TMEM108, SLC4A10, EPHA4, CYRIA
## Negative: RIMS2, PBX3, LINGO2, NEFL, MIR325HG, ADGRL3, NRXN3, RBMS3, GAD2, EBF3
## EBF1, LHX1, RCAN2, KCNIP4, NEFM, TFAP2A, LRFN5, CNTNAP4, UNC5C, SCG5
## VAV3, GAD1, TFAP2B, SPOCK3, TMEFF2, CNTNAP5, LINC01414, LHX1-DT, SCG2, GRIA4
## PC_ 5
## Positive: DDIT3, CYCS, CRYAB, MPC1, EIF1, NEUROD6, MAP1LC3B, CCN3, SLC3A2, CSRP2
## FTH1, FTL, ARPP21, GADD45A, HRK, ARF4, PDE1A, CEBPB, SNCA, TRMT112
## SELENOM, SLC24A2, CAV1, SQSTM1, KRT10, GDF15, OPCML, UPP1, NEUROD2, P4HB
## Negative: NRXN3, DLX6-AS1, SOX2-OT, ENSG00000239381, GAD2, ENSG00000258637, SNTG1, PDZRN3, ENSG00000
## NNAT, DLX5, DNAH11, ROBO2, MT-ND3, NPAS3, SOX6, MT-CYB, MIR99AHG, MT-CO3
## PBX3, ENSG00000289413, MT-ATP6, DLX2, SCGN, MT-CO1, MIR9-1HG, GAD1, CALB2, MIR325HG

## Normalizing layer: counts

## Finding variable features for layer counts

## Centering and scaling data matrix

## PC_ 1
## Positive: LRRC7, STMN2, MYT1L, SYT1, GRIA2, CTNNA2, NRXN1, RBFOX1, CNTNAP2, CCSER1
## PTPRO, CTTNBP2, PTPRD, MAPT, OPCML, NSG2, NELL2, PPFA2, TNIK, NBEA
## PCSK1N, GAP43, ARPP21, ANK3, NEUROD2, NEUROD6, SNHG14, RTN1, ANKS1B, SRGAP1
## Negative: HMGB2, VIM, GLI3, SOX2, SFRP1, HMGN2, SLC1A3, NUSAP1, DACH1, SMC4
## ANP32E, FBXL7, LINC01965, PHGDH, H2AX, TOP2A, HES1, PCLAF, SHROOM3, RPS27L
## CENPF, TUBA1B, PTTG1, QKI, CDK1, LHX2, PBK, MKI67, HSPB1, CKS1B
## PC_ 2
## Positive: NTRK2, EDNRB, CLU, BCAN, PMP2, RMST, LRRC4C, FAM89A, ERBB4, GRID2
## GLIS3, GREB1L, PCDH10, PAX3, LRP2, ALCAM, S100A16, PI15, S100B, PTN
## LINC03000, MAML2, TENM2, SPARC, IRX1, C1orf54, NEAT1, LGR4, NR2F2-AS1, SPATA6
## Negative: BCL11A, NFIB, IGFBPL1, TOP2A, UBE2T, LINC01572, NUSAP1, CENPF, SPC25, MKI67
## UBE2C, NEUROD6, TPX2, CDK1, AURKB, PIMREG, UBE2S, CSRP2, SMC4, H3C2
## CACNA2D1, PBK, ASPM, HMGB1, SOX5, ZBTB18, H2BC9, H3C4, H1-5, NEUROD2
## PC_ 3
## Positive: TOP2A, DIAPH3, NRG3, NUSAP1, CDK1, TPX2, NDC80, SPC25, ADGRB3, KIF11
## ASPM, PBK, NEGR1, AURKB, CENPF, GTSE1, MKI67, KNL1, CENPE, SCLT1
## SGO2, NUF2, BUB1B, ENSG00000290886, UBE2C, MXD3, KIF4A, KIF15, RTKN2, KIFC1
## Negative: FTL, TAC3, H3-3B, NHLH1, EIF1, FTH1, CDKN1A, GAS5, GADD45G, EPHA3
## GNG8, GADD45A, IGFBPL1, CRYAB, RPS27L, PURPL, CRABP1, NUPR1, ENSG00000285755, TRMT112
## GDF15, EOMES, DDIT4, DDIT3, GAPDH, ADM, BBC3, NNAT, TUBA4A, MDM2
## PC_ 4
## Positive: PBX3, MIR325HG, EBF1, RIMS2, TFAP2B, TENM2, LHX1, LRFN5, LINGO2, CNTN5
## RBMS3, LINC01414, EBF3, RCAN2, LHX1-DT, TMEFF2, NEFL, RBMS1, DIRAS2, SPOCK3
## GALNTL6, NXPH1, UNCX, TENM3-AS1, GAD2, CNTNAP4, SCG2, KCNIP4, NRXN3, VAV3
## Negative: PTPRZ1, SOX5, NFIB, GAREM1, NCKAP5, NFIA, MIR9-1HG, SLC1A3, ADGRB3, FAT3
## PDGFC, FABP7, LIMCH1, GPM6B, KAZN, CTNND2, TTYH1, ENSG00000274441, SHROOM3, EEPD1
## LRRC3B, TNC, PDE1A, SPARC, PLPP3, QKI, PON2, DELEC1, PTN, IQGAP2
## PC_ 5
## Positive: FTH1, CCNB1, ARL6IP1, CDC20, PLK1, UBE2C, CDKN3, DLGAP5, SGO2, KNSTRN
## EIF1, AURKA, MPC1, NEK2, PSRC1, PIMREG, CCNB2, TUBB4B, CENPE, DDIT3
## CDCA3, FAM89A, KPNA2, CKS2, BUB1, TPX2, PTTG1, PIF1, CDCA8, BIRC5
## Negative: DACH1, ZBTB20, MIR99AHG, ZNF804A, ENSG00000271860, ROBO2, SYNE2, ZFHX4, KCNH7, NRG1
## HDAC9, ZFPM2, GPC6, FOXP2, TENM4, ENSG00000231252, CASC15, LINC01748, ZFPM2-AS1, MAGI1
## PLCB1, NKAIN3, CDON, LINC01965, DGKB, ZNF536, NFIA-AS2, SHROOM3, PTPRG, COL4A5

## Normalizing layer: counts

## Finding variable features for layer counts

```

```

## Centering and scaling data matrix

## PC_ 1
## Positive: NRXN1, CNTNAP2, STMN2, NRG1, PPFIA2, CCSER1, MYT1L, ANK3, ENSG00000258162, RTN1
##          CTNNA2, CELF4, DSCAM, GRIA2, NSG2, DCX, TENM1, XKR4, KLHL1, CNTN1
##          NALF1, TRPM3, SYN3, GRIA4, SYT1, RIMS1, SEZ6L2, CACNA2D1, SLC8A1, LRRTM4
## Negative: VIM, GNG5, SOX2, CLU, TTYH1, PTN, MIR9-1HG, METRN, EDNRB, CD99
##          FAM89A, GPM6B, SLC1A3, PON2, GSTP1, RPS27L, PLPP3, MGST1, QKI, B2M
##          PTPRZ1, CLIC1, NPC2, HES1, FABP7, FAM181B, NKAIN4, SAT1, CST3, PMP2
## PC_ 2
## Positive: FTL, DDIT3, FTH1, GADD45A, CRYAB, ATF3, PPP1R15A, YBX3, CDKN1A, GDF15
##          HRK, GAS5, LGALS3, CYTOR, CEBPB, ATF5, CALCB, CCN3, GPNMB, TRMT112
##          EIF1, CAV1, TPT1, TRIB3, UPP1, NUPR1, SNHG25, CALCA, SNHG8, MAP1LC3B
## Negative: ANKS1B, CSMD3, ENSG00000257458, LRRC4C, NKAIN3, PDE4D, PPP2R2B, LSAMP, CADM2, GRID2
##          GABBR2, ERBB4, TENM2, DMD, SNCAIP, CACHD1, MAML2, OPHN1, NBEA, SCN1A-AS1
##          SOX2-OT, KIRREL3, NCKAP5, SEZ6L, KAZN, RBMS3, PCDH7, SOX5, MEF2C-AS2, DCC
## PC_ 3
## Positive: TOP2A, PBK, NUSAP1, CENPF, MKI67, CDK1, UBE2C, SPC25, GTSE1, ASPM
##          BIRC5, TPX2, NDC80, PIMREG, DLGAP5, KIFC1, PTTG1, MAD2L1, PRC1, CDKN3
##          PCLAF, AURKB, CDC20, CCNB1, ESCO2, TTK, KNL1, SMC4, KIF4A, ECT2
## Negative: PI15, PARD3B, LRRC4C, ENSG00000271904, ADGRV1, ENSG00000231114, ENSG00000274441, NTRK2, E
##          SOX5, SLC1A3, KAZN, ANOS1, NCKAP5, PTPRZ1, ENSG00000257458, MEGF10, PLPP3, QKI
##          PPP2R2B, BCAN, SOX6, GLIS3, LRP2, PDE3A, FAT4, ANKS1B, CSMD3, ADAMTS3
## PC_ 4
## Positive: MT-CO1, CYP26B1, RGCC, FABP7, S100B, TFPI, TOP2A, SLC1A3, LAMA4, EDNRB
##          PBK, CST3, PMP2, PCLAF, ANOS1, MIR9-1HG, NUSAP1, MKI67, CDK1, SPON1
##          BIRC5, CENPF, FAM181B, BCAN, PTN, GRAMD1B, WDR49, PI15, PCDH9, UBE2C
## Negative: DDIT3, MAP1LC3B, EIF1, GADD45A, PPP1R15A, ATF3, ENSG00000223786, SQSTM1, BNIP3, CEBPB
##          CCPG1, TRMT112, FTL, SGCG, HERPUD1, DDIT4, PGK1, MPC1, ENO1, SLC3A2
##          GAS5, ATF5, CYCS, KRT10, YBX3, SLFN5, ZFAS1, HRK, ODC1, ARF4
## PC_ 5
## Positive: TCF4, ST18, NFIB, GAD2, NHLH1, CBLB, EBF3, NEUROD2, BHLHE22, GAD1
##          EBF2, LHX5-AS1, ROBO3, CECR2, NEUROD1, CHD7, TFAP2A, DCC, NRXN3, INSM1
##          PAX2, SGCD, CRYBG3, CACNG3, SV2B, NEUROD6, NFIA-AS2, DPF3, HS6ST3, KLHL35
## Negative: CDH9, SEMA5A, SLC17A6, ENSG00000289612, ZNF804B, BRINP1, TENM3-AS1, NRN1, SCN9A, PDE7B
##          ARHGAP24, SNCA, LINC00290, PTPRR, ADCYAP1, CALCRL, CALY, NTNG1, SCG2, GLRA3
##          SCN1A-AS1, RELN, ENSG00000249883, STXBP5-AS1, ENSG00000286648, ENSG00000287775, ADAMTSL1, LINC02
## Normalizing layer: counts

## Finding variable features for layer counts

## Centering and scaling data matrix

## PC_ 1
## Positive: VIM, GSTP1, NUSAP1, HMGB2, TOP2A, TYMS, CENPF, SMC4, CKS1B, PCLAF
##          GLI3, UBE2C, MKI67, ZFP36L1, NES, METRN, TTYH1, CDK1, DIAPH3, TUBA1B
##          TPX2, SPC25, BIRC5, PBK, QKI, RPS18, PTTG1, ASPM, RRM2, IGFBP2
## Negative: STMN2, ANK3, NRXN1, GAP43, GRIA2, RTN1, XKR4, CTNNA2, NALF1, CCSER1
##          RUNX1T1, MYT1L, DSCAM, CELF4, NAV3, CDH18, GRIA4, NEGR1, MGAT4C, SLC8A1
##          CNTNAP2, ZFH3, POU2F2, ZFH3, TANC2, KLHL1, NRG1, PHACTR1, NKAIN2, SYN3
## PC_ 2
## Positive: FTL, CLU, RPS18, GAS5, CD63, TPT1, VIM, IFITM3, SPARC, ENSG00000223786
##          TIMP1, RHOC, DDIT3, HSPB1, DDIT4, PLTP, SAT1, SNHG8, HLA-C, PARD3B
##          NPC2, BLVRB, GSN, CD99, CHCHD10, SGCG, MAP1LC3B, CDKN1A, YBX3, EDNRB
## Negative: TOP2A, NUSAP1, CENPF, UBE2C, TPX2, MKI67, CDK1, PBK, SPC25, DLGAP5

```



```

## ASPM, AURKB, GTSE1, H4C3, H3C2, UBE2T, CCNA2, RRM2, CENPE, PIMREG
## H1-5, MAD2L1, HMGB1, DIAPH3, BIRC5, NDC80, KNL1, MXD3, PRC1, KIF4A
## PC_ 3
## Positive: ADGRV1, NPAS3, CKB, PAX3, TTYH1, NCKAP5, PTPRZ1, FGFBP3, ERBB4, BOC
## IGDCC3, SMOC1, HES5, ARL4A, MIR9-1HG, ITGB8, GPM6B, SOX2-OT, SOX5, LUCAT1
## MUSTN1, EPHA4, CXCR4, CCND1, LINC01414, MAPK10, GLI3, SHROOM3, ID4, HES4
## Negative: LGALS1, IGF2, TPM2, S100A11, DCN, SGCA, PITX2, COL3A1, EYA4, KLHL41
## RYR1, COL1A1, COL5A1, GXYLT2, NEB, PDLIM4, EMP3, PRRX1, SGCD, TNNT2
## TNNT1, IFITM2, MSC-AS1, SIX1, COL1A2, MRLN, TNNT1, MIR503HG, COL6A3, MYL4
## PC_ 4
## Positive: TPM2, ST18, SGCA, NHLH1, MYL11, CRABP1, ROBO3, KLHL41, TNNT2, TPT1
## TNNT2, RBP1, CDH15, RPS3, UBE2S, KLHL35, GADD45G, TNNT1, PDLIM4, DES
## HES6, MYL4, MRLN, FITM1, MYOG, SIX1, ACTC1, FNDC5, RPS18, MYL1
## Negative: NTRK2, KAZN, GRID2, PARD3B, FAT3, PTN, LSAMP, SDK1, QKI, PTPRZ1
## LIMCH1, THSD4, DPP6, LRRC4C, PDE1A, CADM2, ADAMTSL1, NPAS3, GPM6B, NCKAP5
## NOS1AP, GALNT17, KCNH8, MAPK10, ANKS1B, ZC3H12B, ITGB8, GLIS3, CRISPLD1, LIFR
## PC_ 5
## Positive: COL3A1, FTL, FTH1, APOE, LUM, COL1A1, IFITM1, BST2, NUPR1, COL5A1
## DCN, COL6A2, COL6A3, ANXA1, TIMP1, IFITM2, S100A10, SERPINE1, MFAP4, DDIT3
## IGFBP3, EMP3, FXYD5, MGP, MME, DLC1, S100A11, FAM114A1, SELENOP, COL5A2
## Negative: MYL11, KLHL41, MYL4, TNNT2, ACTC1, TNNT1, TNNT2, TNNT1, MRLN, TRIM55
## MYH3, DES, ENO3, MYOG, MYL1, TTN, CKM, TNNT3, MYOZ2, SMPX
## SMYD1, MYO18B, UNC45B, CASQ2, HSPB3, NEB, HSPB2, FITM1, RYR1, MYPN
## Normalizing layer: counts
## Finding variable features for layer counts
## Centering and scaling data matrix
## PC_ 1
## Positive: VIM, SOX2, TTYH1, SLC1A3, PTN, QKI, CLU, HES1, PON2, MIR9-1HG
## METRN, CD99, GPM6B, RPS27L, PLPP3, ZFP36L1, ANXA5, B2M, DBI, CLIC1
## PHGDH, ADGRV1, MGST1, GLI3, PMP2, EDNRB, FAM181B, HSPB1, CD63, MYO10
## Negative: STMN2, PPFIA2, SYT1, CCSER1, CNTNAP2, MYT1L, NRXN1, SNHG14, CTNNA2, RTN1
## ANK3, NSG2, GRIA2, SEZ6L2, INA, DCX, NALF1, XKR4, ENSG00000258162, LINC01122
## HECW1, DAB1, LRRC7, SRRM4, RUNX1T1, ERC2, TENM2, HS6ST3, SHTN1, NSG1
## PC_ 2
## Positive: LHX2, LINC01551, TOP2A, NUSAP1, LINC01965, CENPF, MPPED2, SMC4, H3C2, MKI67
## SFRP1, CDK1, FOXG1, MEIS2, SPC25, RRM2, SYNE2, PBK, BIRC5, H1-5
## UBE2C, PCLAF, DIAPH3, H2BC9, NDC80, H3C4, AURKB, TPX2, H2AC14, ASPM
## Negative: NTRK2, LRRC4C, GRID2, EDNRB, GREB1L, FAM89A, NR2F2, BCAN, ERBB4, RMST
## MAML2, PI15, SPATS2L, PMP2, GLIS3, SERPINE2, CLU, MGST1, GABBR2, PAX3
## NR2F2-AS1, PTN, PCDH10, LRP2, CSMD3, NRG3, ADGRL3, SPON1, CST3, LGR4
## PC_ 3
## Positive: TOP2A, DIAPH3, NUSAP1, GRID2, PBX3, CENPF, CDK1, RBMS3, MIR325HG, CSMD3
## NPAS3, MKI67, TPX2, PBK, ADGRL3, NDC80, AURKB, RORA, KIF11, ASPM
## TENM2, SPC25, UBE2C, NEGR1, DACH1, LRFN5, SGO1, PTPRM, NRG3, H3C2
## Negative: NEUROD6, SEMA3C, SLA, NEUROD2, BHLHE22, PALMD, CSRP2, FTH1, ARPP21, BCL11B
## HYCC1, FTL, TG, ZBTB18, SATB2, EPHA3, TBR1, GAS5, IGFBPL1, SATB2-AS1
## PLXNA2, FOXG1, SSTR2, LINC01551, TPT1, EIF4EBP1, TAC3, GADD45A, GNG8, GADD45G
## PC_ 4
## Positive: NFIB, SOX5, PTPRZ1, ARPP21, ENSG00000260664, LINC01572, NEUROD6, ZBTB18, PDE1A, TCF4
## NEUROD2, SATB2, SLA, BHLHE22, CSRP2, ZEB2, TMEM108, SEMA3C, FABP7, SLC44A5
## PLXNA2, AFF3, OPCML, LRRC7, PBX1, HYCC1, GAREM1, NFIA, NELL2, CTNND2
## Negative: CA8, LHX1, ZNF385D, SKOR2, DIRAS2, RBMS1, PCP4, TMEFF2, CNTNAP4, LHX1-DT

```

```

##      SLIT2, LINGO2, EBF1, ZNF385D-AS2, DDIT3, GADD45A, NELL1, TAF4B, FOXP2, KCTD8
##      VAV3, LINC01414, UNC5C, CNTN5, NEFL, TRPC3, POSTN, SLC1A6, PCP4L1, PPP1R1A
## PC_ 5
## Positive: CA8, ITPR1, SKOR2, PCP4, EPHA5, ZNF385D-AS2, POSTN, LRRC3B, TRPC3, KITLG
##      SLC1A6, RBMS1, PRKG1, MIR4500HG, ADGRL2, ENSG00000235978, CHST11, TAF4B, NELL1, DAB1
##      SLIT2, SIAH3, CDH11, SLITRK5, ZNF385D, ISLR2, ENSG00000289368, ENSG00000236676, TMEFF2, ATP2B2
## Negative: TFAP2B, ADARB2, NXPH1, EBF2, ERBB4, RMST, NEUROD1, CDH7, PAX2, TSHZ2
##      CACNG3, ZNF385B, GRIA4, SV2B, ROBO3, PCDH15, RYR3, CBLB, PRKCB, ENSG00000271774
##      SGCD, ELAVL4, KLHL13, NOVA1, HS3ST5, LHX5-AS1, GLRA2, ROBO1, GAD1, TENM1

## Normalizing layer: counts

## Finding variable features for layer counts

## Centering and scaling data matrix

## PC_ 1
## Positive: GNG5, SOX2, VIM, TTYH1, PTN, CLU, MIR9-1HG, SLC1A3, PTPRZ1, FAM89A
##      GPM6B, METRN, EDNRB, CLIC1, PON2, NFIA, QKI, FABP7, CD99, PARD3B
##      B2M, GSTP1, PLPP3, RPS27L, MGST1, S100A13, SAT1, NPC2, NKAIN4, ATP6V0E1
## Negative: STMN2, NRG1, CNTNAP2, RTN1, CELF4, GAP43, CNTNAP5, SYN3, GRIN2B, NEGR1
##      LINGO2, TENM1, GALNTL6, CNTN1, CNTN5, KLHL1, KCNB2, LINC01414, CDH18, ZFH3
##      RBFOX1, TRPM3, NLGN1, RUNX1T1, LHFPL3, EPHA5, TMEFF2, PGM2L1, GRIA4, FGF14
## PC_ 2
## Positive: GADD45A, DDIT3, CYTOR, HRK, FTH1, FTL, ATF3, CDKN1A, ATF5, ADM
##      DHRS2, ENSG00000288758, S100A10, PPP1R15A, GADD45G, DDIT4, TNFRSF12A, GDF15, BBC3, VIM
##      TSPAN19, RPS27L, YBX3, SLC3A2, STC2, CSRP1, HSPB1, LDHA, GPNMB, CEBPB
## Negative: ANKS1B, CSMD3, PTPRD, LSAMP, PPP2R2B, KAZN, SCN1A-AS1, TENM2, NEGR1, TRPM3
##      LRRC4C, GRID2, CSMD1, KHDRBS2, RBMS3, NLGN1, ENSG00000257458, MAGI3, KCNH7, TENM1
##      LHFPL3, NCAM2, DMD, NPAS3, PHLPP1, KCND2, GRIK1, DOK6, GALNT13, PCDH9
## PC_ 3
## Positive: MT-ATP6, MT-CO3, MT-CYB, MT-ND3, MT-CO1, MT-ND2, ENSG00000243620, SLC1A3, MT-ND1, CYP26B1
##      PTN, ATP1A2, MEGF10, MT-ND5, MIR9-1HG, NFIA, NFIB, CDH20, VGLL3, FABP7
##      BOC, CDK6-AS1, PTPRZ1, ADAMTS6, PARD3B, ENSG00000274441, PREX1, ENSG00000231114, NPY, CDK6
## Negative: PGK1, BNIP3, PPP1R15A, ENO1, H4C3, MAP1LC3B, LDHA, H2AZ1, CYTOR, S100A10
##      FTL, HRK, CD163L1, DDIT3, GAPDH, ATF3, GAS5, HERPUD1, GADD45A, ADM
##      FAM162A, ENSG00000288758, SNHG8, SLC16A3, JUN, SQSTM1, ATF5, DHRS2, SLC3A2, DDIT4
## PC_ 4
## Positive: TOP2A, NUSAP1, CENPF, CDK1, BIRC5, SPC25, MKI67, PBK, UBE2C, NDC80
##      PCLAF, ASPM, GTSE1, TPX2, CCNB2, RRM2, PIMREG, KIFC1, DLGAP5, ESCO2
##      KIF11, SG01, CCNB1, HJURP, SMC4, AURKB, ZWINT, SKA3, CDC20, CDCA3
## Negative: PMP2, BCAN, PI15, FAM181B, ANOS1, CLU, EDNRB, SERPINE2, ANKFN1, WNT7B
##      PON2, MLC1, S100B, S100A16, SAT1, F3, LIX1, GABBR2, FAM89A, LINC01896
##      CPLX1, AKR1C3, RAMP1, IFI27L2, HLA-C, TTYH1, FAM107A, TM7SF2, LRRC10B, EEPD1
## PC_ 5
## Positive: UNC5C, MARCHF1, CASC15, ENSG00000243620, NEAT1, ENSG00000223786, RORA-AS1, ZBTB20, ZIC1,
##      GNG12-AS1, ZEB2, CHD7, DLGAP1, KITLG, PSD3, EPHA3, FOXP1, VGLL3, ENSG00000272243
##      FOXP2, CDK6, LINC00472, ENSG00000286757, KCNH8, EBF3, PVT1, CECR2, ENSG00000287069, GAD2
## Negative: TUBB2A, PEG10, TUBA1B, MT-CO3, CAMK2N1, RPRM, TOP2A, MT-CO1, MT3, MT-CYB
##      CDK1, CALY, NUSAP1, PBK, MT-ATP6, S100B, DBI, MT-ND3, BIRC5, NRN1
##      PCLAF, MSMO1, CENPF, LY6H, UBE2C, RGCC, MKI67, TLX3, FAM181B, C1QTNF4

# select integration features (genes)
# integration_features <- SelectIntegrationFeatures(sample_seurat_list,
#
#                                     nfeatures = 2000
# )

```

```

integration_features <- SelectIntegrationFeatures(
  object.list = sample_seurat_list,
  nfeatures   = 1000
)

# sample_seurat_list <- lapply(sample_seurat_list, function(obj) {
#   obj <- ScaleData(obj, features = integration_features, verbose = FALSE)
#   obj <- RunPCA(obj,      features = integration_features, verbose = FALSE)
#   obj
# })

# integrate data
integration_anchors <-
  FindIntegrationAnchors(sample_seurat_list,
                        anchor.features = integration_features,
                        reduction = "rpca"
  )

## Scaling features for provided objects

## Warning: Different features in new layer data than already exists for
## scale.data

## Warning: Different features in new layer data than already exists for
## scale.data

## Warning: Different features in new layer data than already exists for
## scale.data

## Warning: Different features in new layer data than already exists for
## scale.data

## Warning: Different features in new layer data than already exists for
## scale.data

## Warning: Different features in new layer data than already exists for
## scale.data

## Computing within dataset neighborhoods

## Warning: package 'future' was built under R version 4.4.1

## Finding all pairwise anchors

## Warning: The `slot` argument of `GetAssayData()` is deprecated as of SeuratObject 5.0.0.
## i Please use the `layer` argument instead.
## i The deprecated feature was likely used in the Seurat package.
## Please report the issue at <https://github.com/satijalab/seurat/issues>.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.

## Projecting new data onto SVD

## Projecting new data onto SVD

## Finding neighborhoods

## Finding anchors

## Found 3968 anchors

```

```
## Projecting new data onto SVD
## Projecting new data onto SVD

## Finding neighborhoods

## Finding anchors

## Found 1773 anchors

## Projecting new data onto SVD
## Projecting new data onto SVD

## Finding neighborhoods

## Finding anchors

## Found 1384 anchors

## Projecting new data onto SVD
## Projecting new data onto SVD

## Finding neighborhoods

## Finding anchors

## Found 1419 anchors

## Projecting new data onto SVD
## Projecting new data onto SVD

## Finding neighborhoods

## Finding anchors

## Found 1269 anchors

## Projecting new data onto SVD
## Projecting new data onto SVD

## Finding neighborhoods

## Finding anchors

## Found 1694 anchors

## Projecting new data onto SVD
## Projecting new data onto SVD

## Finding neighborhoods

## Finding anchors

## Found 3390 anchors

## Projecting new data onto SVD
## Projecting new data onto SVD

## Finding neighborhoods

## Finding anchors

## Found 2918 anchors

## Projecting new data onto SVD
## Projecting new data onto SVD

## Finding neighborhoods

## Finding anchors
```

```

## Found 2873 anchors
## Projecting new data onto SVD
## Projecting new data onto SVD
## Finding neighborhoods
## Finding anchors
## Found 1428 anchors
## Projecting new data onto SVD
## Projecting new data onto SVD
## Finding neighborhoods
## Finding anchors
## Found 1587 anchors
## Projecting new data onto SVD
## Projecting new data onto SVD
## Finding neighborhoods
## Finding anchors
## Found 1296 anchors
## Projecting new data onto SVD
## Projecting new data onto SVD
## Finding neighborhoods
## Finding anchors
## Found 3543 anchors
## Projecting new data onto SVD
## Projecting new data onto SVD
## Finding neighborhoods
## Finding anchors
## Found 2065 anchors
## Projecting new data onto SVD
## Projecting new data onto SVD
## Finding neighborhoods
## Finding anchors
## Found 2263 anchors
# clean up the memory with merged and sample_seurat_list
rm(sample_seurat_list)
rm(merged)

## Warning in rm(merged): object 'merged' not found
merged <- IntegrateData(integration_anchors)

## Merging dataset 2 into 1
## Extracting anchors for merged samples

```

```

## Finding integration vectors
## Finding integration vector weights
## Integrating data
## Warning: Layer counts isn't present in the assay object; returning NULL
## Merging dataset 3 into 6
## Extracting anchors for merged samples
## Finding integration vectors
## Finding integration vector weights
## Integrating data
## Warning: Layer counts isn't present in the assay object; returning NULL
## Merging dataset 5 into 1 2
## Extracting anchors for merged samples
## Finding integration vectors
## Warning: Different cells in new layer data than already exists for scale.data
## Finding integration vector weights
## Integrating data
## Warning: Layer counts isn't present in the assay object; returning NULL
## Merging dataset 4 into 6 3
## Extracting anchors for merged samples
## Finding integration vectors
## Warning: Different cells in new layer data than already exists for scale.data
## Finding integration vector weights
## Integrating data
## Warning: Layer counts isn't present in the assay object; returning NULL
## Merging dataset 1 2 5 into 6 3 4
## Extracting anchors for merged samples
## Finding integration vectors
## Warning: The `slot` argument of `SetAssayData()` is deprecated as of SeuratObject 5.0.0.
## i Please use the `layer` argument instead.
## i The deprecated feature was likely used in the Seurat package.
##   Please report the issue at <https://github.com/satijalab/seurat/issues>.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
## Finding integration vector weights
## Integrating data
## Warning: Layer counts isn't present in the assay object; returning NULL

```

```
DefaultAssay(merged) <- "integrated"
```

```
merged %>%  
  ScaleData() %>%  
  RunPCA(npcs = 50) %>%  
  RunUMAP(reduction = "pca", dims = 1:50) -> merged
```

```
## Centering and scaling data matrix
```

```
## PC_ 1
```

```
## Positive: VIM, PTN, METRN, CLU, SLC1A3, TTYH1, EDNRB, MT2A, S100A13, GPM6B  
##           QKI, B2M, MIR9-1HG, FABP7, PON2, PLPP3, SPARC, HMGB2, ZFP36L1, NES  
##           S100A16, SPARCL1, NPC2, PARD3B, GLIS3, BCAN, HES1, PTPRZ1, HES4, MGST1  
## Negative: STMN2, CNTNAP2, RTN1, CELF4, NRG1, GRIN2B, TENM1, RALYL, KLHL1, LINGO2  
##           TMEFF2, FGF14, RBFOX1, GAP43, PTPRO, PTPRD, CNTN5, CDH18, CNTN1, LINC01122  
##           GALNTL6, DPP10, SYN3, TRPM3, EPHA6, KCNB2, FGF12, KCNIP4, RUNX1T1, KCND2
```

```
## PC_ 2
```

```
## Positive: DDIT3, DDIT4, ENSG00000223786, PLTP, CDKN1A, HSPA5, CEBPB, FTL, SLFN5, CLU  
##           ENSG00000272243, TTYH1, PON2, GADD45A, HLA-C, BCAN, SQSTM1, ATF3, SGCG, GSN  
##           FTH1, TNC, DELEC1, MAP1LC3B, NEAT1, YBX3, TRIB3, CD63, SNTB1, UNC5B  
## Negative: TOP2A, NUSAP1, CENPF, MKI67, CDK1, DLGAP5, TPX2, UBE2C, ASPM, BIRC5  
##           PRC1, SPC25, KIF4A, CCNB1, TTK, PBK, KIF11, CCNA2, KIF23, NDC80  
##           CENPE, CDCA3, SG02, PTTG1, ECT2, SG01, GTSE1, SMC4, CDKN3, KNL1
```

```
## PC_ 3
```

```
## Positive: ANKS1B, GABBR2, PPP2R2B, LRRC4C, LSAMP, PTPRZ1, GRID2, CSMD3, SLC1A3, KAZN  
##           NCAM2, FAT3, NTRK2, ENSG00000257458, SOX5, ANKFN1, NCKAP5, DMD, PARD3B, BCAN  
##           HS6ST2, GLIS3, QKI, ADAMTS3, LRP1B, CADM2, CYP26B1, ANOS1, PCDH7, SLC4A4  
## Negative: GADD45A, FTL, DDIT3, ATF3, HRK, DHRS2, GDF15, GAS5, CYTOR, ATF5  
##           GADD45G, TUBA4A, FTH1, GPNMB, UBE2S, SNHG8, CDKN1A, CRYAB, LINC02154, S100A10  
##           ENSG00000287097, RGS16, NEFL, NEFM, SERPINE1, SERPINB9, CALCB, ENSG00000288758, CEBPB, GADD45B
```

```
## PC_ 4
```

```
## Positive: ZFH3, LINC01414, MAB21L1, ERBB4, NTNG1, FSTL4, CNTNAP5, TENM2, ZNF804B, ENSG00000258081  
##           TENM3-AS1, ZFH4-AS1, NRG1, GALNTL6, LINGO2, ZFH4, LINC00290, RBMS3, MAST4, RBMS1  
##           ARHGAP24, SCN9A, NEFL, CSMD3, STXBP5-AS1, SYN3, LINC02223, LINC01568, CA10, RIT2  
## Negative: NFIB, NEUROD2, NEUROD6, SOX5, BCL11B, NFIA, ZEB2, OPCML, TFAP2A, BHLHE22  
##           LMO3, CACNA1A, GRIA3, NFIA-AS2, DLGAP1, GABRG3, SSTR2, EPHA4, CDH13, NDST4  
##           ARPP21, TLL1, SLC24A2, MCTP1, PTPRZ1, CSRP2, KLHL29, NNAT, EBF3, EBF2
```

```
## PC_ 5
```

```
## Positive: SFRP1, CA8, NNAT, NKAIN3, SKOR2, LHX1, LHX1-DT, FABP7, CYP26B1, GAD2  
##           LINC01965, LRRC3B, NRXN3, MIR9-1HG, FAM181B, PDGFD, S100B, UNC5C, ENSG00000241231, SLC1A3  
##           DCC, RGCC, TIMP4, FAM111B, PCP4, FOXP2, HS6ST3, SYNE2, SLC4A4, ENSG00000289368  
## Negative: ENSG00000223786, ENSG00000272243, SGCG, DDIT3, SQSTM1, SLFN5, ATF3, NEBL, CEBPB, UNC5B  
##           MAP1LC3B, ATF5, FTL, DDIT4, STRIT1, CHRM3, NIBAN1, TRIB3, CALCB, HRK  
##           UPP1, DLGAP1, GAS5, HSPA5, GADD45A, FTH1, STC2, MPC1, YBX3, TNFRSF12A
```

```
## Warning: The default method for RunUMAP has changed from calling Python UMAP via reticulate to the R  
## To use Python UMAP via reticulate, set umap.method to 'umap-learn' and metric to 'correlation'  
## This message will be shown once per session
```

```
## 16:39:28 UMAP embedding parameters a = 0.9922 b = 1.112
```

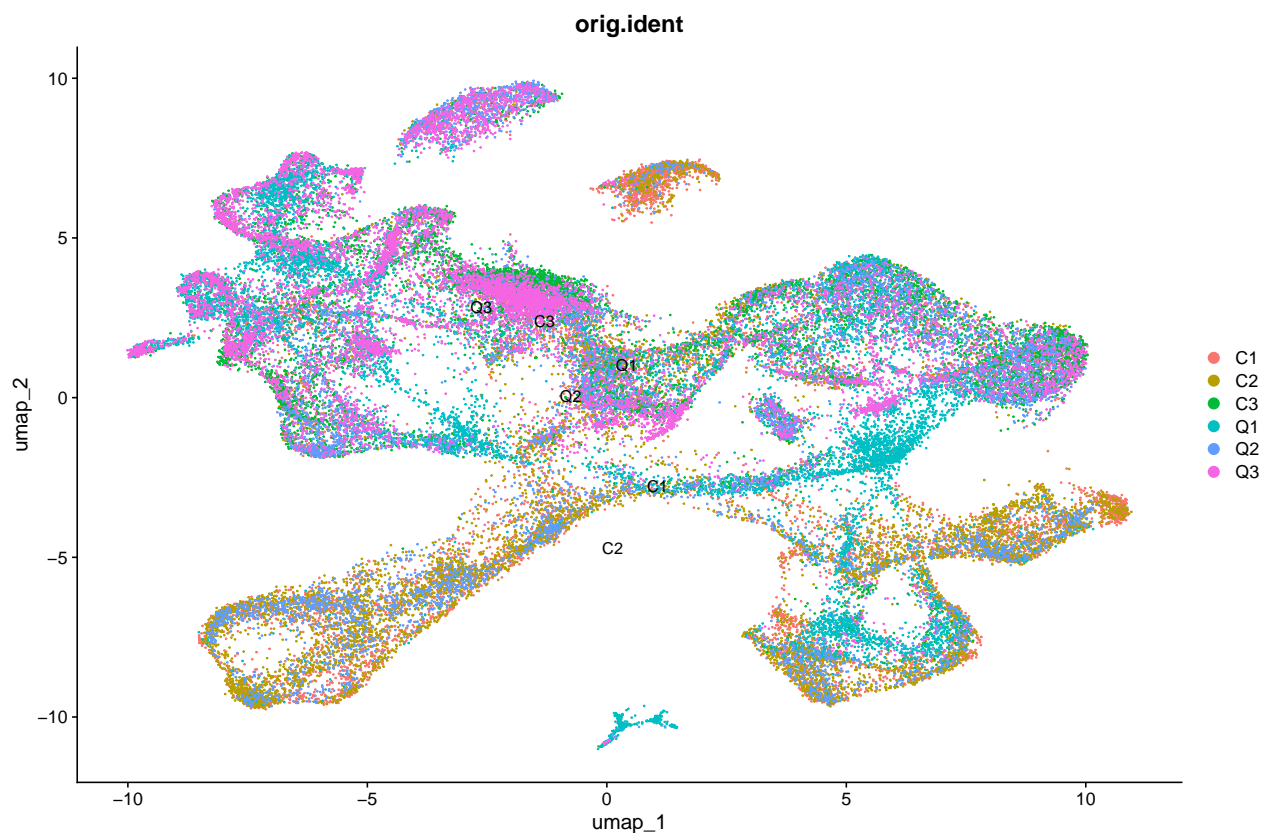
```
## 16:39:28 Read 53211 rows and found 50 numeric columns
```

```
## 16:39:28 Using Annoy for neighbor search, n_neighbors = 30
```

```
## 16:39:28 Building Annoy index with metric = cosine, n_trees = 50
```

```
## 0% 10 20 30 40 50 60 70 80 90 100%
## [----|----|----|----|----|----|----|----|----|----|
## *****|
## 16:39:31 Writing NN index file to temp file /var/folders/62/9y36k0q92vv6hckwc077f_1r0000gn/T//RtmpyX
## 16:39:31 Searching Annoy index using 1 thread, search_k = 3000
## 16:39:41 Annoy recall = 100%
## 16:39:41 Commencing smooth kNN distance calibration using 1 thread with target n_neighbors = 30
## 16:39:42 Initializing from normalized Laplacian + noise (using RSpectra)
## 16:39:43 Commencing optimization for 200 epochs, with 2457504 positive edges
## 16:39:43 Using rng type: pcg
## 16:39:57 Optimization finished
```

```
DimPlot(merged,
  group.by = "orig.ident", label = T)
```



```
# save the data
saveRDS(merged, here::here("data", "synaptosomes_scRNA", "merged_RNA_2025-05-15.rds"),
  compress = FALSE)
```


Session Info

```
sessionInfo()
```

```
## R version 4.4.0 (2024-04-24)
## Platform: aarch64-apple-darwin20
## Running under: macOS 15.4
##
## Matrix products: default
## BLAS:   /Library/Frameworks/R.framework/Versions/4.4-arm64/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/4.4-arm64/Resources/lib/libRlapack.dylib; LAPACK v
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## time zone: America/New_York
## tzcode source: internal
##
## attached base packages:
## [1] stats4      stats      graphics  grDevices  utils      datasets  methods
## [8] base
##
## other attached packages:
## [1] future_1.49.0      GenomicRanges_1.56.2 GenomeInfoDb_1.40.1
## [4] IRanges_2.38.1     S4Vectors_0.42.1     BiocGenerics_0.50.0
## [7] Signac_1.14.0      harmony_1.2.3         Rcpp_1.0.14
## [10] Seurat_5.3.0       SeuratObject_5.1.0    sp_2.2-0
## [13] knitr_1.50         lubridate_1.9.4       forcats_1.0.0
## [16] stringr_1.5.1      dplyr_1.1.4           purrr_1.0.4
## [19] readr_2.1.5        tidyr_1.3.1           tibble_3.2.1
## [22] ggplot2_3.5.2      tidyverse_2.0.0
##
## loaded via a namespace (and not attached):
## [1] RColorBrewer_1.1-3      rstudioapi_0.17.1      jsonlite_2.0.0
## [4] magrittr_2.0.3          spatstat.utils_3.1-3    farver_2.1.2
## [7] rmarkdown_2.29          zlibbioc_1.50.0         vctrs_0.6.5
## [10] ROCR_1.0-11             Rsamtools_2.20.0        spatstat.explore_3.4-2
## [13] tinytex_0.57            RcppRoll_0.3.1          htmltools_0.5.8.1
## [16] sctransform_0.4.2       parallelly_1.44.0       KernSmooth_2.23-26
## [19] htmlwidgets_1.6.4       ica_1.0-3               plyr_1.8.9
## [22] plotly_4.10.4           zoo_1.8-14              igraph_2.1.4
## [25] mime_0.13               lifecycle_1.0.4         pkgconfig_2.0.3
## [28] Matrix_1.7-3            R6_2.6.1                fastmap_1.2.0
## [31] GenomeInfoDbData_1.2.12 fitdistrplus_1.2-2      shiny_1.10.0
## [34] digest_0.6.37           colorspace_2.1-1        patchwork_1.3.0
## [37] rprojroot_2.0.4         tensor_1.5              RSpectra_0.16-2
## [40] irlba_2.3.5.1           labeling_0.4.3          progressr_0.15.1
## [43] spatstat.sparse_3.1-0    timechange_0.3.0        httr_1.4.7
## [46] polyclip_1.10-7         abind_1.4-8             compiler_4.4.0
## [49] here_1.0.1              withr_3.0.2             BiocParallel_1.38.0
## [52] fastDummies_1.7.5       MASS_7.3-65            tools_4.4.0
## [55] lmtest_0.9-40           httpuv_1.6.16           future.apply_1.11.3
## [58] goftest_1.2-3           glue_1.8.0              nlme_3.1-168
## [61] promises_1.3.2          grid_4.4.0              Rtsne_0.17
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## [64] cluster_2.1.8.1	reshape2_1.4.4	generics_0.1.4
## [67] gtable_0.3.6	spatstat.data_3.1-6	tzdb_0.5.0
## [70] data.table_1.17.2	hms_1.1.3	XVector_0.44.0
## [73] spatstat.geom_3.3-6	RcppAnnoy_0.0.22	ggrepel_0.9.6
## [76] RANN_2.6.2	pillar_1.10.2	spam_2.11-1
## [79] RcppHNSW_0.6.0	later_1.4.2	splines_4.4.0
## [82] lattice_0.22-7	survival_3.8-3	deldir_2.0-4
## [85] tidysselect_1.2.1	Biostrings_2.72.1	miniUI_0.1.2
## [88] pbapply_1.7-2	gridExtra_2.3	scattermore_1.2
## [91] xfun_0.52	matrixStats_1.5.0	stringi_1.8.7
## [94] UCSC.utils_1.0.0	lazyeval_0.2.2	yaml_2.3.10
## [97] evaluate_1.0.3	codetools_0.2-20	cli_3.6.5
## [100] uwot_0.2.3	xtable_1.8-4	reticulate_1.42.0
## [103] dichromat_2.0-0.1	globals_0.18.0	spatstat.random_3.3-3
## [106] png_0.1-8	spatstat.univar_3.1-3	parallel_4.4.0
## [109] dotCall64_1.2	bitops_1.0-9	listenv_0.9.1
## [112] viridisLite_0.4.2	scales_1.4.0	ggribes_0.5.6
## [115] crayon_1.5.3	rlang_1.1.6	fastmatch_1.1-6
## [118] cowplot_1.1.3		