

Gene module analysis

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Introduction

This report is totally original without taking code from the github repo of the original paper. As this report also includes all the output for your references, we have also provided a table of content so that you might skip some of very tedious output and go straight to some code.

Data reading, normalizing, PCA, and clustring at different resolution.

The first part of the code did all the data reading, normalizing, PCA, and clustring at different resolution.

```
```r
library(Seurat)
library(Matrix)

List of patient IDs
patient_ids <- c("CID3586", "CID3838", "CID3921", "CID3941", "CID3946", "CID3948", "CID3963", "CID4040", "CID4066", "CID4067", "CID4290A", "CID4398", "CID4461", "CID4463", "CID4465", "CID4471", "CID4495", "CID4513", "CID4515", "CID4523", "CID4530N", "CID4535", "CID44041", "CID44971", "CID44991", "CID45171")

Initialize an empty list to store the Seurat objects
seurat_objects <- list()

Loop through each patient
for (patient_id in patient_ids) {
 # Define file paths for the patient's data
 count_matrix_barcode_path <- paste0("./GSE176078_RAW/", patient_id, "/count_matrix_barcode.tsv")
 count_matrix_genes_path <- paste0("./GSE176078_RAW/", patient_id, "/count_matrix_genes.tsv")
 count_matrix_sparse_path <- paste0("./GSE176078_RAW/", patient_id, "/count_matrix_sparse.mtx")
 metadata_path <- paste0("./GSE176078_RAW/", patient_id, "/metadata.csv")

 # Load count matrix and metadata
 count_matrix <- readMM(file = count_matrix_sparse_path)
 barcodes <- read.delim(count_matrix_barcode_path, header = FALSE, col.names = c("barcode"))
 genes <- read.delim(count_matrix_genes_path, header = FALSE, col.names = c("gene"))
 metadata <- read.csv(metadata_path, row.names = 1)

 # Set the colnames and rownames of the count matrix
 colnames(count_matrix) <- barcodes$barcode
 rownames(count_matrix) <- genes$gene

 # Create Seurat object
 seurat_obj <- CreateSeuratObject(counts = count_matrix, project = patient_id, assay = "RNA", meta.data = metadata)

 # Preprocessing, normalization, and scaling
 seurat_obj <- NormalizeData(seurat_obj, normalization.method = "LogNormaliz
```

```
e", scale.factor = 10000)
seurat_obj <- FindVariableFeatures(seurat_obj, selection.method = "vst", nfeatures = 2000)
seurat_obj <- ScaleData(seurat_obj, features = rownames(seurat_obj))

Run PCA on the scaled data
seurat_obj <- RunPCA(seurat_obj, features = VariableFeatures(object = seurat_obj))

Create a shared nearest neighbor graph
seurat_obj <- FindNeighbors(seurat_obj, reduction = "pca", dims = 1:20)

Find clusters at different resolutions
resolutions <- c(0.4, 0.8, 1.2, 1.6, 2.0)
for (res in resolutions) {
 seurat_obj <- FindClusters(seurat_obj, resolution = res, ident.1 = "neoplastic", algorithm = 3)
}

Add the processed Seurat object to the list
seurat_objects[[patient_id]] <- seurat_obj
}

Print the list of Seurat objects to check the results
seurat_objects
```

```
Warning: package 'Seurat' was built under R version 4.2.3Registered S3 method
overwritten by 'data.table':
 method from
 print.data.table
Registered S3 method overwritten by 'htmlwidgets':
 method from
 print.htmlwidget tools:rstudio
Attaching SeuratObject
Warning: package 'Matrix' was built under R version 4.2.3Performing log-normalization
0% 10 20 30 40 50 60 70 80 90 100%
[-----|-----|-----|-----|-----|-----|-----|
*****|*****|*****|*****|*****|*****|*****|
Calculating gene variances
0% 10 20 30 40 50 60 70 80 90 100%
[-----|-----|-----|-----|-----|-----|-----|
*****|*****|*****|*****|*****|*****|*****|
Calculating feature variances of standardized and clipped values
0% 10 20 30 40 50 60 70 80 90 100%
[-----|-----|-----|-----|-----|-----|-----|
*****|*****|*****|*****|*****|*****|*****|
Centering and scaling data matrix
|=====| 100%
PC_1
Positive: GPR183, NKG7, COTL1, ALOX5AP, RGS1, IFNG, KLRB1, CCL4, TIGIT, CD40LG
 GZMK, DUSP4, RGS2, XCL1, RP11-291B21.2, ZNF683, GZMA, KLRD1, TRGV10, TNF
 TRBV7-9, LDLRAD4, CTLA4, FOS, XCL2, PLAC8, BCL2A1, GNLY, TNFRSF4, LY9
Negative: TACSTD2, TM4SF1, CLDN4, MGP, KRT7, MDK, CLDN3, SLPI, LTF, KRT19
 KRT8, CD24, CLDN7, KRT18, FXVD3, MGST1, RARRES1, TPM1, S100A16, SFRP1
 CDC42EP1, GABRP, ELF3, CYR61, EPCAM, CLU, CRYAB, CXCL2, DSP, CX3CL1
PC_2
Positive: SLPI, CLDN4, KRT19, LTF, GABRP, CLDN3, CD24, RPS19, C2orf82, RPS7
 PIGR, RPS4X, KRT7, RPS6, RPL34, PDZK1IP1, CLDN7, AZGP1, RPL41, CCL28
 KRT15, KRT18, LCN2, RPL3, TACSTD2, EPCAM, KRT23, RPL12, ELF3, CALML5
Negative: IGFBP7, SPARCL1, IFI27, DCN, SERPING1, SPARC, CST3, IGFBP4, CXCL12, LUM
```

MMP2, APOD, CTSK, RARRES2, C1S, SERPINF1, COL6A2, GSN, TIMP3, BGN  
A2M, COL1A2, FN1, HSPG2, COL6A1, PTGDS, MFAP4, COL3A1, MXRA8, SFRP2

PC\_ 3  
Positive: DCN, C1S, SPARCL1, LUM, COL6A2, RARRES2, IGFBP4, APOD, CALD1, MXRA8  
SPARC, COL1A2, CTSK, BGN, COL3A1, MFAP4, COL6A1, FBLN1, C1R, COL1A1  
IGFBP7, SFRP2, TIMP3, COL6A3, CXCL12, MMP2, ISLR, AEBP1, MYL9, PLAC9  
Negative: C1QC, C1QB, C1QA, FCER1G, MS4A6A, CD68, TYROBP, LYZ, MS4A7, HLA-DQA1  
CYBB, HLA-DPA1, HLA-DRA, CSF1R, AIF1, SPI1, HLA-DRB5, HLA-DPB1, HLA-DQA2,  
IL1B  
CLEC7A, OLR1, HLA-DQB1, HLA-DRB1, CCL3L3, FCGR2A, PHACTR1, IL18, C5AR1,  
CXCL8  
PC\_ 4  
Positive: EGFL7, RAMP2, RNASE1, PLVAP, RAMP3, ADGRL4, ESAM, VWF, AQP1, PECAM1  
CRIP2, CALCRL, SLC9A3R2, GNG11, CLEC14A, EMCN, PTPRB, RBP7, CD93, HYAL2  
FABP4, THBD, CLDN5, HSPG2, CDH5, SOX18, ENG, CXorf36, CYR1, ACKR1  
Negative: DCN, LUM, C1S, CTSK, RARRES2, APOD, MXRA8, SFRP2, COL1A2, FBLN1  
SERPINF1, COL3A1, LRP1, MFAP4, COL1A1, COL6A3, TMEM176B, C1R, TMEM176A,  
ISLR  
C3, COL6A1, COL6A2, PCOLCE, AEBP1, CFD, MEG3, APOE, TNFAIP6, COL5A2  
PC\_ 5  
Positive: DCN, LUM, CTSK, CXCL12, C3, MFAP4, COL1A2, COL3A1, COL6A3, PTGDS  
MMP2, COL6A2, SFRP2, MGP, COL1A1, RARRES2, APOD, SLPI, ISLR, C2orf82  
LTF, GABRP, FN1, MFAP2, COL6A1, CFD, IFI27, LRP1, TMEM176B, TMEM176A  
Negative: KRT14, TAGLN, MYLK, KRT17, C2orf40, ACTA2, DST, SFN, CDH3, DKK3  
ACTG2, SEMA3C, COL17A1, CNN1, CALML3, TPM2, PDLIM4, MYL9, MAOB, TNS4  
TINAGL1, NNMT, PTN, LTBP2, PLAT, SERPINB5, MT1E, FHOD3, SYT8, LAMB3  
Computing nearest neighbor graph  
Computing SNN  
Warning: The following arguments are not used: ident.1warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo waltman and Nees Jan  
van Eck

Number of nodes: 6178  
Number of edges: 225911

Running smart local moving algorithm...  
0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|  
Maximum modularity in 10 random starts: 0.9006  
Number of communities: 13  
Elapsed time: 2 seconds  
warning: The following arguments are not used: ident.1warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo waltman and Nees Jan  
van Eck

Number of nodes: 6178  
Number of edges: 225911

Running smart local moving algorithm...  
0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|  
Maximum modularity in 10 random starts: 0.8503  
Number of communities: 16  
Elapsed time: 1 seconds  
warning: The following arguments are not used: ident.1warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo waltman and Nees Jan  
van Eck

Number of nodes: 6178  
Number of edges: 225911

Running smart local moving algorithm...  
0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|  
Maximum modularity in 10 random starts: 0.8159  
Number of communities: 18  
Elapsed time: 1 seconds

Warning: The following arguments are not used: ident.1  
Warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan van Eck

Number of nodes: 6178  
Number of edges: 225911

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.7870  
Number of communities: 23  
Elapsed time: 1 seconds

Warning: The following arguments are not used: ident.1  
Warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan van Eck

Number of nodes: 6178  
Number of edges: 225911

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.7628  
Number of communities: 24  
Elapsed time: 1 seconds

Performing log-normalization

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Calculating gene variances

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Calculating feature variances of standardized and clipped values

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Centering and scaling data matrix

|=====| 100%

PC\_1

Positive: LAPTM5, CD74, HLA-DRB1, HLA-DPA1, HLA-DPB1, HLA-DQA1, GPR183, HLA-DQB1, HLA-DRA, ALOX5AP

Negative: CTSC, CTSS, CD84, TYROBP, CCL4, HLA-DMB, C1orf162, LST1, GK, NCF1, GBP5, ACP5, AIF1, BCL2A1, FCER1G, CCL4L2, PLEK, CYBB, CCL3, TNFRSF18, SPARC, CALD1, BGN, COL6A2, PTRF, COL5A2, CNN3, COL3A1, NNMT, COL1A2, FSTL1, COL1A1, C1R, COL6A1, IGFBP7, PRRX1, MYL9, IGFBP4, THY1, TPM1, PRSS23, TPM2, TAGLN, PALLD, AEBP1, FBN1, TIMP3, COL12A1, PLS3, FKBP10

PC\_2

Positive: TNFRSF18, CTLA4, TNFRSF4, KLRB1, IFNG, INPP4B, NKG7, GZMK, HOPX, CCR7, CD40LG, FOXP3, LINC00152, CCR6, CD8A, TRGC2, PTTG1, GZMH, GZMB, RTKN2, IL2RA, TTN, CD8B, OASL, GNLY, CD70, ABLIM1, IRF4, FASLG, XCL2

Negative: C1QC, CD68, C1QB, C1QA, AIF1, MS4A7, CYBB, MSR1, SPI1, GRN, CTSS, SLC7A7, CTSZ, FPR3, FTL, FCGR3A, FCER1G, GPNMB, MS4A6A, PSAP, IGSF6, PLBD1, APOC1, CD14, MNDA, FCGR2A, TYROBP, FCGR1A, LYZ, FMNL2

PC\_3

Positive: COL10A1, COL11A1, SDC1, MFAP5, THBS2, SFRP2, LRRC15, DCN, LUM, GXYLT2, ITGBL1, COL8A1, ITGA11, FNDC1, FBLN1, CLMP, LOXL1, PLPP4, COL8A2, CTSC, PDGFR1, GAS1, FIBIN, RARRES2, OMD, CTHRC1, HSD17B6, SPON1, WNT2, PODNL1, SOX18, SHANK3, EMCN, RAMP3, AQP1, VWA1, CLEC14A, MMRN2, ADGRF5, CD93, CD34, VWF, ADAMTS9, PCDH17, PALMD, CXorf36, RAPGEF5, TIE1, FLT1, PTPRB

PC\_4

Positive: HSPG2, GJA1, S100A16, ADGRL4, TM4SF1, PLVAP, RAMP2, DPYSL3, ECSCR.1, MMP2, SULF2, CDH5, EGFL7, RAMP3, PODXL, SHANK3, CLEC14A, AQP1, VWF, EMCN, CD34, CXorf36, SOX18, TIE1, PTPRB, PCAT19, FAM198B, HYAL2, PECAM1, NPDC1, NDUFA4L2, TBX2, NOTCH3, SOD3, RGS5, HIGD1B, PPP1R14A, TPPP3, CCDC102B, RASL12

LG14, CDH6, ENPEP, COX4I2, SEPT4, GUCY1B3, HEYL, GUCY1A2, CSPG4, KCNJ8, EGFL6, FOXS1, LINGO1, AVPR1A, RNF152, PLEKHH3, ABCC9, CPE, KLHL23, EPS8

PC\_ 5

Positive: MKI67, TOP2A, TYMS, KIAA0101, RRM2, AURKB, NCAPG, TPX2, UBE2C, TK1  
BIRC5, ZWINT, KIF4A, SHCBP1, KIF15, CDCA5, HIST1H1B, GTSE1, CCNA2, ESCO2  
DLGAP5, HMMR, DIAPH3, ASPM, ANLN, KIF23, KIF11, MYBL2, SPC25, KIF2C  
Negative: GPR183, SLC40A1, TMEM37, CFD, SEPP1, FOLR2, IGSF21, GPR34, PILRA, FUCA1  
SLCO2B1, C3AR1, ME1, NCF1, LILRB5, IGHG3, TXNIP, MPEG1, ALDH1A1, MERTK  
C5AR1, MAFB, FCGR2A, IGHG1, RNASE6, SDC3, FTL, FTH1, SIGLEC1, IGLC3

Computing nearest neighbor graph

Computing SNN

Warning: The following arguments are not used: ident.1warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan  
van Eck

Number of nodes: 2353  
Number of edges: 86043

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.9211

Number of communities: 10

Elapsed time: 0 seconds

Warning: The following arguments are not used: ident.1warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan  
van Eck

Number of nodes: 2353  
Number of edges: 86043

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.8685

Number of communities: 12

Elapsed time: 0 seconds

Warning: The following arguments are not used: ident.1warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan  
van Eck

Number of nodes: 2353  
Number of edges: 86043

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.8261

Number of communities: 17

Elapsed time: 0 seconds

Warning: The following arguments are not used: ident.1warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan  
van Eck

Number of nodes: 2353  
Number of edges: 86043

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.7925

Number of communities: 19

Elapsed time: 0 seconds

Warning: The following arguments are not used: ident.1warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan  
van Eck

Number of nodes: 2353  
Number of edges: 86043

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.7629

Number of communities: 19

Elapsed time: 0 seconds

Performing log-normalization

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Calculating gene variances

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Calculating feature variances of standardized and clipped values

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Centering and scaling data matrix

|=====| 100%

PC\_ 1

Positive: CD74, HLA-DRB1, HLA-DPB1, HLA-DPA1, CTSS, HLA-DQA1, HLA-DQB1, CCL4, HLA-DQA2, HLA-DRA

Negative: TYROBP, ACP5, BCL2A1, FCER1G, LYZ, AIF1, SPI1, CD68, FCGR2B, NKG7  
FGL2, TNF, CYBB, MS4A6A, LAIR1, C1QA, FCGR2A, C1QB, CD40LG, IRF8  
ERBB2, KRT19, GRB7, CALML5, CLDN4, KRT7, S100A14, KRT8, KRT23, TACSTD2  
FXYP3, SLPI, AZGP1, CD24, MAL2, KRT18, CLDN3, SPDEF, MGST1, PSMD3  
ELF3, EPCAM, LRRC26, MIEN1, CASC3, RAB25, C17orf89, CLDN7, SERINC2, S100P

PC\_ 2

Positive: CCL4, TNF, AREG, NKG7, IFNG, CD40LG, CD8A, SPINT2, IRF4, GZMK  
CD79A, AQP3, CD8B, MZB1, GZMB, PTTG1, LY9, ZNF683, CD24, BCL2A1  
GNLY, ORMDL3, MAL, CXCL13, XCL2, GCHFR, GZMH, XCL1, IL2RA, CALML5  
Negative: IGFBP7, SPARC, CALD1, IGFBP4, TIMP3, NNMT, BGN, PRSS23, COL6A2, FSTL1  
PTRF, COL1A2, C1S, CTHRC1, CTGF, COL1A1, AEBP1, SERPING1, COL3A1, SPARCL1  
RARRES2, COL6A1, MYL9, IFI27, CAV1, LUM, MMP2, DCN, THY1, C1R

PC\_ 3

Positive: PLVAP, RAMP2, SPRY1, ADGRL4, VWF, ESAM, CALCRL, AQP1, SPARCL1, EMCN  
S1PR1, CD34, HSPG2, GNG11, CXorf36, EGFL7, BCAM, RAMP3, CD40LG, CLEC14A  
CAV1, CDH5, MMRN2, COL4A1, IFNG, CYR1, PALMD, ADAMTS1, TIE1, ADAMTS9  
Negative: CD68, LYZ, C1QA, C1QB, C1QC, FCER1G, SERPINA1, TYROBP, APOC1, FCGR3A  
AIF1, SPI1, APOE, FCGR2A, C15orf48, MS4A7, MS4A6A, IFI30, PILRA, TREM2  
CYBB, CSF1R, LILRB4, MSR1, FCGR1A, OLR1, CTSB, FPR3, CD14, C5AR1

PC\_ 4

Positive: PLVAP, PECAM1, RAMP2, VWF, ADGRL4, CD93, CALCRL, EMCN, AQP1, MCTP1  
CLEC14A, RAMP3, CXorf36, EGFL7, ESAM, CDH5, CD34, ENG, MMRN2, CYR1  
BCAM, PALMD, PTPRB, TIE1, CLDN5, RBP7, SOX17, HSPG2, MYCT1, GNG11  
Negative: LUM, DCN, RARRES2, COL1A2, SFRP2, COL1A1, MXRA8, COL3A1, CTSK, THBS2  
COL6A3, ISLR, FBLN1, C1S, AEBP1, PDGFRL, MXRA5, MFAP5, DPT, PRRX1  
HTRA3, CCDC80, PCOLCE, WISP2, PDPN, ASPN, COL5A2, SERPINF1, COL6A1, C1R

PC\_ 5

Positive: NDUFA4L2, RGS5, NOTCH3, HEYL, PPP1R14A, MYH11, SSTR2, MAP3K7CL, COX4I2,  
FRZB

Negative: NTRK2, HIGD1B, C1QTNF1, EDNRA, EFHD1, PLN, EGFLAM, SOD3, GJA4, ENPEP  
SEPT4, CCDC102B, KCNE4, ACTA2, FOXS1, CSRP2, KCNJ8, LGI4, TINAGL1,

C11orf96

Negative: CTHRC1, MMP2, SFRP2, DPT, FBLN1, MFAP5, MFAP2, PDPN, THBS2, PDGFRL  
LUM, VCAN, CCDC80, STEAP1, MDK, HTRA3, C3, DCN, SFRP4, WISP2  
CTSK, COL8A1, MXRA5, RARRES1, CXCL14, IGFBP6, FIBIN, DPYSL3, COL10A1, NOX4

Computing nearest neighbor graph

Computing SNN

Warning: The following arguments are not used: ident.1  
Warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan van Eck

Number of nodes: 3024

Number of edges: 111234

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.9235  
Number of communities: 13  
Elapsed time: 0 seconds  
warning: The following arguments are not used: ident.1warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan  
van Eck

Number of nodes: 3024  
Number of edges: 111234

Running smart local moving algorithm...  
0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.8770  
Number of communities: 17  
Elapsed time: 0 seconds  
warning: The following arguments are not used: ident.1warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan  
van Eck

Number of nodes: 3024  
Number of edges: 111234

Running smart local moving algorithm...  
0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.8446  
Number of communities: 18  
Elapsed time: 0 seconds  
warning: The following arguments are not used: ident.1warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan  
van Eck

Number of nodes: 3024  
Number of edges: 111234

Running smart local moving algorithm...  
0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.8145  
Number of communities: 19  
Elapsed time: 0 seconds  
warning: The following arguments are not used: ident.1warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan  
van Eck

Number of nodes: 3024  
Number of edges: 111234

Running smart local moving algorithm...  
0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.7852  
Number of communities: 21  
Elapsed time: 0 seconds  
Performing log-normalization  
0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|  
Calculating gene variances  
0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|  
Calculating feature variances of standardized and clipped values  
0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|  
Centering and scaling data matrix



```

|=====| 100%
PC_ 1
Positive: CD69, DUSP2, CCL5, IL7R, CCL4, TSTD1, RGS1, NKG7, GPR183, TUBA4A
 LTB, CST7, CD8B, CD8A, CCL4L2, SLA, UCP2, ALOX5AP, GZMK, GZMA
 AREG, SMIM22, SPINT2, AZGP1, IFNG, CCR7, KLRB1, ICOS, GATA3, CD24
Negative: SPARCL1, IGFBP7, SPARC, IFI27, COL4A2, A2M, COL4A1, ESAM, CAV1, CALCRL
 RAMP2, HSPG2, CALD1, GNG11, ENG, EPAS1, EMCN, PTRF, PLVAP, EGFL7
 AQP1, TM4SF1, RAMP3, NRP1, TCF4, EMP1, ADAMTS1, ADGRL4, VWF, CD93

PC_ 2
Positive: SMIM22, KRT8, KRT18, FXD3, AZGP1, KRT19, AGR3, S100A14, CLDN4, ANKRD30A
 SPINT2, CD24, S100A13, FASN, TFF3, HSPB1, CYB5A, XBP1, ELF3, PIP
 COX6C, MUC1, CRACR2B, UGDH, TRPS1, TSTD1, MIF, MYBPC1, CLDN7, TMC5
Negative: VIM, CD69, HLA-DRB5, HLA-DRB1, CCL4, CD74, RGS1, CCL5, DUSP2, HLA-DPB1
 IL7R, HLA-DPA1, HLA-DQA1, ANXA1, HLA-DRA, CCL4L2, GPR183, TUBA4A, ALOX5AP,
 NKG7
 HLA-DQB1, HLA-DQA2, SLA, LTB, CST7, CD8A, CD8B, S100A10, FABP5, GZMK

PC_ 3
Positive: EGFL7, RAMP2, PLVAP, EMCN, ADGRL4, HSPG2, CALCRL, VWF, COL15A1, RAMP3
 CXorf36, RNASE1, CLEC14A, PECAM1, CD93, HYAL2, CYR1, PODXL, TSPAN7, PTPRB
 FLT1, CDH5, MCTP1, ITGA6, CD34, AQP1, TM4SF1, INSR, ACKR1, SLC02A1
Negative: COL1A2, RGS5, NOTCH3, NDUFA4L2, COL3A1, HIGD1B, TPM2, COX4I2, ACTA2, COL5A2
 COL1A1, PDGFRB, CD248, PCOLCE, TAGLN, MFGE8, SEPT4, LHFP, PLAC9, CPE
 MYL9, HEYL, EDNRA, ENPEP, FAM162B, OLFML2B, FRZB, COL6A1, BGN, PRRX1

PC_ 4
Positive: S100A14, CYB5A, KRT18, AZGP1, S100A13, XBP1, KRT19, S100A16, MLPH, PDLIM1
 TFF3, TFF1, MYBPC1, FASN, COX6C, CRACR2B, ANKRD30A, MIF, MGST1, HSPB1
 NME4, SPDEF, SMIM22, MAPT, KRT8, SLC39A6, RP11-53019.1, CLDN4, CXCL13,

IER3
Negative: C20orf85, FAM183A, SNTN, C1orf194, ROPN1L, ENKUR, FAM166B, WDR49, CFAP73,
 CATSPERD
 CAPSL, TUBA4B, C5orf49, DRC1, FAM216B, MAP3K19, CFAP47, DYDC2, RP11-
 295M3.4, CDHR3
 SCGB2A1, EFHC2, CFAP77, EFCAB10, AGBL2, CFAP126, DNAH12, LRRIQ1, SRGAP3-
 AS2, PIFO

PC_ 5
Positive: FCER1G, TREM2, IGSF6, TYROBP, LYZ, FCGR2A, CSF2RA, TNFSF13, C3, PLD4
 C1QB, C1QA, SLC1A3, PLXDC2, CD68, C1QC, PTGS2, MS4A6A, HLA-DPA1, MS4A7
 AIF1, FCGR2B, CLEC7A, HLA-DQB1, APOE, FCGR3A, HLA-DMA, HLA-DRA, APOC1,
 RNASE6
Negative: IL7R, CD69, CCL5, NKG7, TUBA4A, CD8A, CD8B, GZMK, GZMA, CST7
 KLRB1, IFITM1, DUSP2, ITM2A, ICOS, IFNG, ATP2B4, ANXA1, XCL2, SPOCK2
 TRBC1, PCSK1N, XCL1, KLRD1, SPRY1, ZNF683, LTB, CDC42EP3, AIM1, CD40LG

Computing nearest neighbor graph
Computing SNN
Warning: The following arguments are not used: ident.1
Warning: The following arguments
are not used: ident.1
Modularity Optimizer version 1.3.0 by Ludo waltman and Nees Jan
van Eck

```

```

Number of nodes: 631
Number of edges: 19303

```

```

Running smart local moving algorithm...
0% 10 20 30 40 50 60 70 80 90 100%
[----|----|----|----|----|----|----|----|----|----|
*****|

```

```

Maximum modularity in 10 random starts: 0.8879
Number of communities: 7
Elapsed time: 0 seconds

```

```

Warning: The following arguments are not used: ident.1
Warning: The following arguments
are not used: ident.1
Modularity Optimizer version 1.3.0 by Ludo waltman and Nees Jan
van Eck

```

```

Number of nodes: 631
Number of edges: 19303

```

```

Running smart local moving algorithm...
0% 10 20 30 40 50 60 70 80 90 100%
[----|----|----|----|----|----|----|----|----|----|
*****|

```

```

Maximum modularity in 10 random starts: 0.8192
Number of communities: 8
Elapsed time: 0 seconds

```

Warning: The following arguments are not used: ident.1  
Warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan van Eck

Number of nodes: 631  
Number of edges: 19303

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.7594  
Number of communities: 9  
Elapsed time: 0 seconds

Warning: The following arguments are not used: ident.1  
Warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan van Eck

Number of nodes: 631  
Number of edges: 19303

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.7079  
Number of communities: 10  
Elapsed time: 0 seconds

Warning: The following arguments are not used: ident.1  
Warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan van Eck

Number of nodes: 631  
Number of edges: 19303

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.6635  
Number of communities: 12  
Elapsed time: 0 seconds

Performing log-normalization

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Calculating gene variances

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Calculating feature variances of standardized and clipped values

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Centering and scaling data matrix

|=====| 100%

PC\_1

Positive: IGFBP7, SPARC, CALD1, COL18A1, COL1A2, NDUFA4L2, COL6A2, BGN, RGS5, MGP  
COL1A1, LHFP, COL3A1, TIMP1, C11orf96, SPARCL1, COL4A2, C1R, COL6A1, MYL9  
COL4A1, CPE, NR2F2, NOTCH3, ADIRF, TPM2, MCAM, CHN1, SOD3, PDGFRB  
Negative: LAPTM5, TYROBP, ITGB2, APOC1, SPP1, CD68, CCL4, FCER1G, RNASE1, HCST  
CXCL8, CD14, C1QC, DUSP2, CXCR4, CD163, FCGR3A, C1QA, RGS1, RGS2  
CCL3, CD83, CD52, FCGR2A, CCL4L2, GPR183, PTPRC, GLUL, C1QB, S100A9

PC\_2

Positive: VWF, PECAM1, RAMP2, PLVAP, HSPG2, CLEC14A, CLDN5, VWA1, CD34, EMCN  
AQP1, ADGRL4, ECSCR.1, EGFL7, ACKR1, S100A16, SOX18, COL15A1, ZNF385D,  
NPDC1

Negative: TSPAN7, KDR, ICAM2, THSD7A, SH3BGRL2, PCAT19, CYYR1, TM4SF1, ITGA6, HVAL2  
COL6A2, COL1A2, NDUFA4L2, COL1A1, COL3A1, CALD1, TIMP1, APOE, COL6A1, TPM2  
RGS5, ACTA2, MYL9, POSTN, CPE, BGN, TAGLN, COL5A2, SOD3, C1R  
PDGFRB, MFGE8, NOTCH3, LHFP, C1S, COL18A1, FTL, GUCY1A3, C11orf96, MMP11

PC\_3

Positive: FTL, HSPA6, NEAT1, NR4A2, CCL3, LAPTM5, ITGB2, TYROBP, CTSD, FOSB  
DUSP2, CD68, DNAJB1, APOC1, PLIN2, HCST, PLD3, PLTP, RGS2, CD83  
IER5, CXCL8, CTSB, FCER1G, PPP1R15A, ZNF331, CCL4, APOE, NR4A3, CEBPB  
Negative: ACKR1, IGFBP7, PLVAP, VWF, CLDN5, SPARCL1, RAMP2, HSPG2, PECAM1, ADM5  
AQP1, ECSCR.1, CDKN3, COL15A1, CD34, ADIRF, ADGRL4, NPDC1, FABP4, MMRN2  
CYTL1, TSPAN7, CYR1, CADM3, CALCRL, IGFBP3, TM4SF1, RAMP3, HYAL2, EGFL7

PC\_4

Positive: APOC1, CTSB, SPP1, RNASE1, APOE, FTL, CD68, CTSD, TYROBP, PLD3  
PLTP, CD14, CTSB, CD163, GLUL, GPNMB, FCER1G, C1QC, FCGR3A, C1QA  
MMP9, FCGR2A, VSIG4, FN1, TMEM176B, C1QB, CD36, CXCL8, ITGB2, CXCL3  
Negative: CD7, TRAC, RGCC, LCK, CD3D, CCL5, CD2, CD3E, IL32, LTB  
TRBC1, TRBC2, RHOH, CD3G, SH2D2A, NKG7, CD69, GZMA, CST7, TBC1D10C  
CYTIP, RASGRP1, DUSP4, PTGER4, PTPN22, SAMS1, GNLY, TIGIT, CTLA4, ICOS

PC\_5

Positive: TAGLN, ACTA2, IGFBP5, JUNB, ADIRF, JUN, MYL9, RRAD, FOS, C11orf96  
EGR1, MYH11, TPM2, DSTN, RERGL, ZFP36, MYLK, CCL2, FRZB, TSC22D1  
ID3, PLAC9, DNAJB1, SOCS3, ATF3, H3F3B, FOSB, SLIT3, KLF2, MAP1B  
Negative: POSTN, COL3A1, COL1A1, COL6A1, COL4A1, COL5A2, COL1A2, COL6A2, COL4A2,  
MMP11

PRSS23, SPARC, CPXM1, DCN, TIMP1, CTSK, FN1, BMP1, NID1, ASPN  
CXCL9, KCNK17, LAMB1, C1R, BGN, AEBP1, PLXDC1, MXRA8, VCAN, FBLN2

Computing nearest neighbor graph

Computing SNN

Warning: The following arguments are not used: ident.1warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan  
van Eck

Number of nodes: 774  
Number of edges: 22226

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.9143

Number of communities: 7

Elapsed time: 0 seconds

Warning: The following arguments are not used: ident.1warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan  
van Eck

Number of nodes: 774  
Number of edges: 22226

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.8507

Number of communities: 9

Elapsed time: 0 seconds

Warning: The following arguments are not used: ident.1warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan  
van Eck

Number of nodes: 774  
Number of edges: 22226

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.8024

Number of communities: 11

Elapsed time: 0 seconds

Warning: The following arguments are not used: ident.1warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan  
van Eck

Number of nodes: 774  
Number of edges: 22226

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.7626

Number of communities: 14

Elapsed time: 0 seconds

Warning: The following arguments are not used: ident.1  
Warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan van Eck

Number of nodes: 774

Number of edges: 22226

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.7275

Number of communities: 14

Elapsed time: 0 seconds

Performing log-normalization

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Calculating gene variances

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Calculating feature variances of standardized and clipped values

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Centering and scaling data matrix

|=====| 100%

PC\_1

Positive: S100A4, CCL4, IGHG1, RGS2, IFNG, IGKC, XCL1, HLA-DRB5, XCL2, HLA-DPB1  
RP11-291B21.2, IGHG3, IGHV3-21, CCL4L2, IGLV2-8, GSTP1, TNF, CCR7, KLRB1,  
FABP5

ZNF683, HLA-DQA2, ITGB2, CD40LG, HLA-DQA1, HLA-DRB1, HLA-DPA1, IGKV3-11,  
GPR183, IGKV1-5

Negative: ELF3, KRT19, SMIM22, S100A14, KRT18, MGST1, CLDN4, KRT8, DSCAM-AS1, AGR3  
AZGP1, CRABP2, SLC39A6, CLDN3, RP11-53019.1, FXYD3, CA12, CLDN7, RAB25,  
ESR1

S100A13, TSPAN13, SPINT2, TNNT1, NME4, ZG16B, DSP, ADIRF, GDF15, FHL2

PC\_2

Positive: SLC9A3R1, TSTD1, ELF3, KRT19, TOB1, FXYD3, CLDN4, SMIM22, XBP1, DSCAM-AS1  
S100A14, KRT18, RP11-53019.1, AGR3, CLDN3, AZGP1, AC018816.3, DEGS2,  
SLC39A6, ESR1

Negative: GATA3, AGR2, DCXR, FSIP1, BTG2, RAB25, CA12, RARRES3, MGST1, CALML5  
IGFBP7, SPARC, GSN, FN1, A2M, COL4A2, SPARCL1, COL4A1, CALD1, CST3  
SERPING1, RNASE1, HSPG2, COL18A1, BGN, COL1A2, GNG11, COL6A2, ENG, FSTL1  
PRSS23, MMP2, COL6A1, NNMT, PTRF, CAV1, CALCRL, SERPINF1, ESAM, CCL2

PC\_3

Positive: CD68, TYROBP, FCER1G, C1QA, C1QB, C1QC, LYZ, AIF1, MS4A6A, APOE  
APOC1, MS4A7, CD14, TREM2, CYBB, LILRB4, IFI30, MSR1, HLA-DRA, FCGR3A  
SPI1, FPR3, PILRA, FCGR2A, IL18, C5AR1, CSF1R, PLTP, CLEC7A, TNFSF13

Negative: IGFBP7, SPARC, SPARCL1, COL4A2, COL4A1, CALD1, COL18A1, BGN, COL1A2, GNG11  
HSPG2, MYL9, CAV1, PRSS23, PTRF, ESAM, COL6A1, COL6A2, TIMP3, MCAM  
FSTL1, THY1, COL3A1, PRKCDP, NNMT, ADAMTS1, AQP1, RGS5, CALCRL, RAMP2

PC\_4

Positive: COL1A2, COL3A1, COL1A1, COL5A2, COL6A3, THY1, COL6A2, COL6A1, PRRX1, PDGFRB  
LUM, DCN, NOTCH3, C1S, CD248, ASPN, BGN, TAGLN, ISLR, MXRA5

Negative: CTSK, MXRA8, ADAM12, PCOLCE, COL5A1, TPM2, CTGF, COL12A1, TNFAIP6, RGS5  
CALCRL, PLVAP, AQP1, RAMP2, HYAL2, VWF, HSPG2, RNASE1, ADGRL4, EMCN  
EGFL7, RAMP3, CD93, SLC9A3R2, CXorf36, CDH5, RBP7, PODXL, SOX18, CYR1  
PECAM1, TM4SF1, CD34, TIE1, CLEC14A, PTPRB, VWA1, ESAM, FAM167B, MMRN2

PC\_5

Positive: CTHRC1, LUM, DCN, CILP, SFRP4, POSTN, ABI3BP, ISLR, COL8A1, SFRP2  
ELN, C1S, ADAM12, PDGFRA, TMEM119, CCL11, GXYLT2, OGN, EFEMP1, DPT  
THBS4, FRMD6, HAS2, LOX, MEG3, MFAP5, IGF1, MXRA5, CTGF, DPYSL3

Negative: RGS5, NDUFA4L2, COX4I2, NOTCH3, COL18A1, PPP1R14A, SEPT4, HIGD1B, TPM2, PDGFRB  
MYL9, LHFP, MCAM, PLXDC1, ACTA2, SPARCL1, CSPG4, SOD3, DKK3, GJA4  
C11orf96, MYLK, FRZB, IGFBP7, OLFML2A, TAGLN, HEYL, CD248, COL4A2, FAM162B

Computing nearest neighbor graph

Computing SNN

Warning: The following arguments are not used: ident.1  
Warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo waltman and Nees Jan van Eck

Number of nodes: 2327  
Number of edges: 88335

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.8941

Number of communities: 10

Elapsed time: 0 seconds

Warning: The following arguments are not used: ident.1  
Warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo waltman and Nees Jan van Eck

Number of nodes: 2327  
Number of edges: 88335

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.8333

Number of communities: 13

Elapsed time: 0 seconds

Warning: The following arguments are not used: ident.1  
Warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo waltman and Nees Jan van Eck

Number of nodes: 2327  
Number of edges: 88335

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.7823

Number of communities: 13

Elapsed time: 0 seconds

Warning: The following arguments are not used: ident.1  
Warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo waltman and Nees Jan van Eck

Number of nodes: 2327  
Number of edges: 88335

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.7389

Number of communities: 15

Elapsed time: 0 seconds

Warning: The following arguments are not used: ident.1  
Warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo waltman and Nees Jan van Eck

Number of nodes: 2327  
Number of edges: 88335

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|

```

*****|
Maximum modularity in 10 random starts: 0.7041
Number of communities: 18
Elapsed time: 0 seconds
Performing log-normalization
0% 10 20 30 40 50 60 70 80 90 100%
[----|----|----|----|----|----|----|----|----|----|
*****|
calculating gene variances
0% 10 20 30 40 50 60 70 80 90 100%
[----|----|----|----|----|----|----|----|----|----|
*****|
calculating feature variances of standardized and clipped values
0% 10 20 30 40 50 60 70 80 90 100%
[----|----|----|----|----|----|----|----|----|----|
*****|
Centering and scaling data matrix
|=====| 100%
PC_ 1
Positive: IFNG, GZMB, GNLY, LTB, XCL1, XCL2, CACYBP, RP11-291B21.2, BATF, TNFRSF18
 GZMK, C12orf75, CTLA4, RPL18A, PDCD1, CXCL13, CD40LG, HMGB2, KRT86, TRGV10
 RPL39, KLRC1, CSF1, CCR7, KLRC3, TRBV9, CRTAM, CD70, GPR25, TRDC
Negative: CST3, FN1, KLF4, GRN, PSAP, CD68, CTSZ, NPC2, GSN, CTSB
 C1QB, LYZ, C1QA, C1QC, MARCKS, SERPING1, C15orf48, TMEM176B, HLA-DRA,
 IFI27
 APOE, CTSH, IFNGR2, AIF1, GPX1, APOC1, SPI1, MS4A6A, LILRB4, TMEM176A
PC_ 2
Positive: MGP, KRT19, MGST1, WWTR1, CLDN4, C8orf4, KRT18, KRT8, S100A14, CD24
 KRT7, TACSTD2, CYR61, CP, PLPP2, ELF3, CLU, CRABP2, SMIM22, RARRES1
 EFEMP1, S100A16, TM4SF1, CNN3, RAB25, FXYD3, ASS1, PFN2, PDZK1IP1, C1S
Negative: C1QB, C1QC, LYZ, C1QA, CD68, AIF1, TYROBP, MS4A6A, APOE, SPI1
 CYBB, TMEM176B, APOC1, FCGR3A, LILRB4, FCER1G, FCGR2A, TMEM176A, LST1,
 CD14
 SERPINA1, CTSZ, CSF1R, S100A6, MS4A7, FPR3, GPNMB, MS4A4A, SLC02B1, CST3
PC_ 3
Positive: KRT19, MGST1, CLDN4, S100A14, SPINT2, CD24, RARRES1, ELF3, CP, TACSTD2
 KRT8, CLDN7, SMIM22, KRT7, RAB25, KRT18, PDZK1IP1, FXYD3, CRABP2, EFEMP1
 SERP1, RPL39, FTH1, SERINC2, CLU, RP11-206M11.7, PLPP2, CLDN3, MMP7, SOX9
Negative: COL4A2, COL4A1, SPARCL1, PLVAP, HSPG2, VWF, GNG11, CALCRL, EGFL7, RAMP2
 ESAM, SPARC, LAMA4, RAMP3, AQP1, COL15A1, ADGRL4, IGFBP7, ADGRF5, COL18A1
 CDH5, HTRA1, EMCN, TCF4, CD34, ENG, PODXL, BGN, A2M, CXorf36
PC_ 4
Positive: PLVAP, EGFL7, VWF, CALCRL, RAMP2, RAMP3, AQP1, HSPG2, ADGRL4, PODXL
 CDH5, FAM167B, CD34, SOX18, EMCN, CXorf36, VWA1, PECAM1, CLEC14A, PTPRB
 BCAM, EFNA1, DLL4, SLC9A3R2, INSR, FLT1, CD93, SLC02A1, KDR, PCDH17
Negative: COL1A2, COL1A1, COL3A1, TPM2, COL6A3, POSTN, PCOLCE, COL6A1, EDNRA, THY1
 COL5A2, PDGFRB, BGN, OLFML2B, PRRX1, CD248, NDUFA4L2, COL5A1, AEBP1,
 NOTCH3
 CCDC102B, TAGLN, MXRA8, LHFP, MYL9, KCNJ8, SOD3, PLAC9, LUM, PLXDC1
PC_ 5
Positive: UBE2C, MKI67, BIRC5, TOP2A, TROAP, ASPM, CDC20, RRM2, CDCA3, CCNA2
 TYMS, CDKN3, HMMR, PLK1, CDK1, CCNB2, STMN1, UBE2T, DLGAP5, TPX2
 KIFC1, AURKB, NUF2, CENPF, CKAP2L, CKS1B, NUSAP1, DEPDC1B, CENPE, PRC1
Negative: RPL39, CD55, GPR183, MT-ND3, CHMP1B, RPL36, MARCKSL1, RPL18A, FTH1, CCR7
 SLC25A37, MT-ND2, FOS, MT-CO3, RPS8, CP, MT-CYB, TIMP1, C8orf4, RPL8
 MT-ND4L, MT-CO2, GZMK, MT-ND1, TAF4B, LMNA, MYC, U47924.27, FTL, KLF4
Computing nearest neighbor graph
Computing SNN
Warning: The following arguments are not used: ident.1warning: The following arguments
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo waltman and Nees Jan
van Eck

Number of nodes: 3527
Number of edges: 122425

Running smart local moving algorithm...
0% 10 20 30 40 50 60 70 80 90 100%
[----|----|----|----|----|----|----|----|----|----|
*****|
Maximum modularity in 10 random starts: 0.8908
Number of communities: 10
Elapsed time: 1 seconds

```

Warning: The following arguments are not used: ident.1  
Warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo waltman and Nees Jan van Eck

Number of nodes: 3527  
Number of edges: 122425

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.8359  
Number of communities: 14  
Elapsed time: 0 seconds

Warning: The following arguments are not used: ident.1  
Warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo waltman and Nees Jan van Eck

Number of nodes: 3527  
Number of edges: 122425

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.7926  
Number of communities: 15  
Elapsed time: 0 seconds

Warning: The following arguments are not used: ident.1  
Warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo waltman and Nees Jan van Eck

Number of nodes: 3527  
Number of edges: 122425

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.7577  
Number of communities: 18  
Elapsed time: 0 seconds

Warning: The following arguments are not used: ident.1  
Warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo waltman and Nees Jan van Eck

Number of nodes: 3527  
Number of edges: 122425

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.7295  
Number of communities: 21  
Elapsed time: 0 seconds

Performing log-normalization

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Calculating gene variances

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Calculating feature variances of standardized and clipped values

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Centering and scaling data matrix

|=====| 100%

PC\_1

Positive: LAPTM5, ITGB2, COTL1, NKG7, GZMA, BATF, GPR183, AREG, CCR7, CCL4



TRGC2, CD8A, KLRB1, KLRD1, HMGB2, TNFRSF18, CTLA4, IFNG, CD8B, NCF1  
 XCL2, HMGA1, CTSW, TNFRSF9, GNLY, CD40LG, XCL1, TNF, ADAM8, GZMB  
 Negative: IFITM3, IGFBP7, SPARCL1, SPARC, IGFBP4, CST3, IFI27, CALD1, PTRF, GSN  
 SERPING1, NNMT, A2M, CD59, CAV1, COL4A2, MGP, COL18A1, COL4A1, BGN  
 PRKDCBP, C1R, MYL9, CRIP2, PDLIM1, COL6A2, EPAS1, ACTN1, DSTN, RAB13  
 PC\_ 2  
 Positive: RAMP2, PECAM1, ADGRL4, CLEC14A, ECSCR.1, VWF, CDH5, EGFL7, CD34, RNASE1  
 EMCN, PTPRB, CD93, AQP1, CYR1, PLVAP, TMEM255B, HYAL2, SHANK3, TIE1  
 CXorf36, PALMD, PODXL, MMRN2, PCAT19, MYCT1, SOX18, MCTP1, HSPG2, JAM2  
 Negative: NOTCH3, SOD3, TPM2, PDGFRB, SERPINF1, ACTA2, COL1A2, PRRX1, PCOLCE,  
 NDUFA4L2  
 TAGLN, SMOC2, TBX2, SDC2, CPE, MFGE8, COL3A1, SEPT4, COL6A2, COL1A1  
 CRISPLD2, MYL9, DKK3, KCNE4, FRZB, OLFML2B, EDNRA, TGFBI, LGALS3BP, TPPP3  
 PC\_ 3  
 Positive: LUM, SFRP2, CTHRC1, THBS2, COL10A1, CTSK, WNT2, FBLN1, COL11A1, DCN  
 C3, PDPN, CLMP, COL8A2, FAP, MXRA5, LRRC15, HTRA3, PLPP4, DPT  
 STEAP1, MMP2, PLXDC2, RARRES1, GAS1, SDC1, LRP1, MFAP2, MFAP5, BICC1  
 Negative: MCAM, TINAGL1, NDUFA4L2, PTP4A3, ADIRF, PGF, TBX2, MYH11, BCAM, GJA4  
 WFDC1, GPRC5C, C1QTNF1, EFHD1, MAP3K7CL, PPP1R14A, ESAM, SEPT4, PTK2, LGI4  
 COX4I2, PDGFA, NOTCH3, LINGO1, PLN, TBX2-AS1, NTRK2, RASL12, SOD3, AOC3  
 PC\_ 4  
 Positive: LYZ, MS4A6A, C1QC, FCGR2A, C1QA, C1QB, LILRB4, FPR3, SPI1, IGSF6  
 PILRA, AIF1, CPVL, SERPINA1, OLR1, CSF1R, CD14, CD163, MS4A4A, CD68  
 MSR1, CYBB, RP11-1143G9.4, FCGR1A, C5AR1, APOC1, CLEC7A, MS4A7, SLC02B1,  
 FCGR3A  
 Negative: CTHRC1, SFRP2, LUM, THBS2, FAP, COL10A1, COL11A1, WNT2, DCN, HTRA3  
 FBLN1, MXRA5, MMP2, LRRC15, DPT, SDC1, PLPP4, GAS1, MMP11, MFAP2  
 COL8A1, MFAP5, STEAP1, COL6A3, GJB2, CREB3L1, PDGFRA, CLMP, RARRES2, PDPN  
 PC\_ 5  
 Positive: NOTCH4, HECW2, PODXL, DLL4, KDR, FLT1, SPRY4, PCDH12, SOX18, SLC9A3R2  
 NES, INSR, JAG2, ACE, SEMA3G, SEMA3F, ESM1, EXOC3L1, KCNN3, SOX17  
 KCNE3, IGFBP3, KIAA1462, ADGRF5, BCL6B, UNC5B, GABRD, COL4A1, MECOM, PLCB1  
 Negative: ACKR1, CCL14, C7, CLU, TSPAN7, LRRC1, SELP, RAB3C, PLCXD3, EPB41L3  
 AKR1C1, ZNF385D, AKR1C3, OLFML1, TLL1, CRTAC1, CADM3-AS1, TGFBR3, LIFR,  
 AKR1C2  
 CNTNAP3B, IL1R1, SYT15, LHX6, ELOVL7, MEOX2, CADM3, PTGS2, PDK4, CNKSR3  
 Computing nearest neighbor graph  
 Computing SNN  
 warning: The following arguments are not used: ident.1warning: The following arguments  
 are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo waltman and Nees Jan  
 van Eck

Number of nodes: 2531  
 Number of edges: 89321

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
 [----|----|----|----|----|----|----|----|----|----|  
 \*\*\*\*\*|

Maximum modularity in 10 random starts: 0.9145

Number of communities: 11

Elapsed time: 0 seconds

warning: The following arguments are not used: ident.1warning: The following arguments  
 are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo waltman and Nees Jan  
 van Eck

Number of nodes: 2531  
 Number of edges: 89321

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
 [----|----|----|----|----|----|----|----|----|----|  
 \*\*\*\*\*|

Maximum modularity in 10 random starts: 0.8652

Number of communities: 14

Elapsed time: 0 seconds

warning: The following arguments are not used: ident.1warning: The following arguments  
 are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo waltman and Nees Jan  
 van Eck

Number of nodes: 2531  
 Number of edges: 89321



Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.8212

Number of communities: 15

Elapsed time: 0 seconds

Warning: The following arguments are not used: ident.1  
Warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan van Eck

Number of nodes: 2531

Number of edges: 89321

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.7839

Number of communities: 19

Elapsed time: 0 seconds

Warning: The following arguments are not used: ident.1  
Warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan van Eck

Number of nodes: 2531

Number of edges: 89321

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.7567

Number of communities: 20

Elapsed time: 0 seconds

Performing log-normalization

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Calculating gene variances

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Calculating feature variances of standardized and clipped values

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Centering and scaling data matrix

|=====| 100%

PC\_1

Positive: LPTM5, CORO1A, LTB, RGS1, CD74, SPARC, NKG7, GPR183, ZNF683, KLRB1  
ALOX5AP, HLA-DPB1, BGN, ITM2A, ITGB2, LCP1, CCL4, RGS2, COL1A2, COL3A1  
HLA-DPA1, COL6A2, XCL1, HLA-DRB1, COL1A1, GZMK, THY1, DCN, FN1, TIMP1

Negative: KRT8, KRT18, KRT19, MGST1, GRB7, ERBB2, MAL2, CD24, S100A14, FXYD3  
AGR3, EPCAM, KRT7, AGR2, SPINT2, CLDN4, CLDN7, NQO1, ELF3, JUP  
TSPAN1, SPDEF, MIEN1, LRRC26, TFF3, CLDN3, SQLE, CEACAM6, GPR160, RAB25

PC\_2

Positive: CD74, LPTM5, RGS1, CORO1A, HLA-DRB1, COTL1, HLA-DPA1, LTB, HLA-DPB1, ITGB2  
ALOX5AP, HLA-DRA, UCP2, LCP1, VAMP8, HLA-DRB5, DUSP4, TYROBP, GPR183, CCL4  
HLA-DQA1, HLA-DMA, NKG7, HLA-DQB1, FCER1G, AREG, AIF1, CCL4L2, LYZ, MS4A6A

Negative: COL1A2, COL3A1, COL1A1, LUM, DCN, BGN, SFRP2, COL5A2, COL6A2, COL6A3  
CTSK, CTHRC1, COL6A1, SPARC, AEBP1, POSTN, FN1, MFAP2, CALD1, ISLR  
THY1, VCAN, COL5A1, RARRES2, MXRA5, FBLN2, THBS2, CCDC80, FBLN1, PALLD

PC\_3

Positive: RPL18A, RPL18, LTB, RPS5, KLRB1, ZNF683, NKG7, XCL1, DUSP4, RNF19A  
TC2N, GZMK, RP11-291B21.2, GNLY, SLC9A3R1, IFNG, CD40LG, TIGIT, SLC38A1,

XCL2

TNFRSF18, NDUFA4L2, TRGV10, PDCD4, PTP4A3, BATF, GATA3, RGS5, RARRES3,

CTLA4

Negative: C1QA, C1QC, C1QB, LYZ, AIF1, MS4A6A, FCER1G, CD68, SPI1, MS4A7  
CYBB, OLR1, TREM2, HLA-DQA1, FCGR2A, LY86, TYROBP, MND4, LILRB4, FCGR3A

TNFSF13, IGSF6, CSF1R, RNASE6, FCGR2B, HLA-DQB1, C5AR1, C15orf48, HLA-DRA,  
CD14  
PC\_4  
Positive: RAMP2, EGFL7, PLVAP, AQP1, RAMP3, RNASE1, EMCN, ADGRL4, CLEC14A, CALCRL  
PECAM1, VWF, ESAM, ENG, NPDC1, GNG11, CYR1, CD34, CXorf36, CLDN5  
TM4SF1, MCTP1, CD93, HSPG2, CDH5, FLT1, ACKR1, MMRN2, TMEM255B, SOX17  
Negative: CORO1A, RGS1, FTH1, LTB, LAPTM5, RPL18A, NKG7, LCP1, UCP2, ALOX5AP  
DUSP4, ITGB2, ZNF683, GPR183, CCL4, C12orf75, KLRB1, RARRES3, XCL1, RPL18  
SFRP2, LUM, AREG, RGS2, TSTD1, CTSK, RP11-291B21.2, DCN, THBS2, CAPG  
PC\_5  
Positive: CRYAB, WFDC2, KRT14, KRT5, KRT17, KRT6B, PTN, CHI3L1, SAA1, MYLK  
SLPI, SFRP1, PDZK1IP1, C2orf40, KRT15, GABRP, LTF, KRT23, KLK5, KRT81  
CALML3, MMP7, SYNM, ANXA3, DEFB1, SAA2, SFN, NDUFA4L2, PHLDA2, KLK8  
Negative: HSPG2, RAMP2, PLVAP, EGFL7, MMP2, CTHRC1, RAMP3, VWF, ENG, PECAM1  
ADGRL4, CLEC14A, AQP1, HOXB2, EMCN, COL15A1, VCAN, CXorf36, POSTN, CD34  
RNASE1, SQLE, FBLN2, STARD3, FAP, COL10A1, GOLM1, DIO2, CALCRL, CXCL14  
Computing nearest neighbor graph  
Computing SNN  
Warning: The following arguments are not used: ident.1  
Warning: The following arguments  
are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo waltman and Nees Jan  
van Eck

Number of nodes: 5309  
Number of edges: 186263

Running smart local moving algorithm...  
0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|  
Maximum modularity in 10 random starts: 0.9357  
Number of communities: 13  
Elapsed time: 1 seconds  
Warning: The following arguments are not used: ident.1  
Warning: The following arguments  
are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo waltman and Nees Jan  
van Eck

Number of nodes: 5309  
Number of edges: 186263

Running smart local moving algorithm...  
0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|  
Maximum modularity in 10 random starts: 0.8940  
Number of communities: 17  
Elapsed time: 1 seconds  
Warning: The following arguments are not used: ident.1  
Warning: The following arguments  
are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo waltman and Nees Jan  
van Eck

Number of nodes: 5309  
Number of edges: 186263

Running smart local moving algorithm...  
0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|  
Maximum modularity in 10 random starts: 0.8629  
Number of communities: 19  
Elapsed time: 1 seconds  
Warning: The following arguments are not used: ident.1  
Warning: The following arguments  
are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo waltman and Nees Jan  
van Eck

Number of nodes: 5309  
Number of edges: 186263

Running smart local moving algorithm...  
0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|  
Maximum modularity in 10 random starts: 0.8355

Number of communities: 21

Elapsed time: 1 seconds

Warning: The following arguments are not used: ident.1  
Warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan van Eck

Number of nodes: 5309

Number of edges: 186263

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%

[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.8097

Number of communities: 24

Elapsed time: 1 seconds

Performing log-normalization

0% 10 20 30 40 50 60 70 80 90 100%

[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Calculating gene variances

0% 10 20 30 40 50 60 70 80 90 100%

[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Calculating feature variances of standardized and clipped values

0% 10 20 30 40 50 60 70 80 90 100%

[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Centering and scaling data matrix

|=====| 100%

PC\_1

Positive: AZGP1, CD24, RP11-206M11.7, MGST1, KRT8, SLC39A6, MGP, AGR2, KRT18, SPINT2, KRT19, ELF3, PIP, S100A14, MUCL1, KRT7, CRABP2, SUSP3, WFDC2, SUB1, SCGB3A1, CLDN4, COX6C, SLC9A3R1, CA2, RARRES3, GSTM3, DEGS2, MS4A7, S100P

Negative: FN1, COL1A2, SPARC, COL3A1, COL1A1, COL6A1, CTHRC1, DCN, LUM, COL6A3, CALD1, POSTN, COL6A2, VIM, SFRP2, TIMP3, AEBP1, MMP2, VCAN, COL5A2, BGN, THBS2, RARRES2, SERPINF1, CTGF, MFAP2, ASPN, ISLR, CTSK, CDH11

PC\_2

Positive: MGP, COL1A2, COL1A1, COL3A1, DCN, LUM, COL6A1, COL6A3, IGFBP4, CTHRC1, COL5A2, SFRP2, THBS2, RARRES2, POSTN, AEBP1, ASPN, ISLR, CDH11, CTSK, MXRA8, COL6A2, MFAP2, MMP11, COL10A1, BGN, COL11A1, COL5A1, FBLN1, AZGP1

Negative: TYROBP, HLA-DPA1, HLA-DPB1, HLA-DQA1, AIF1, FCER1G, HLA-DQB1, HLA-DRB5, LAPTM5, HLA-DRA, HLA-DRB1, C1QB, C1QA, C1QC, CD68, RGS1, TREM2, CD83, CCL3, SRGN, MS4A6A, APOE, CD74, APOC1, SGK1, HLA-DMA, CCL4, MSR1, CCL3L3, HLA-DMB

PC\_3

Positive: CD3E, CD69, CCL5, CD52, SRGN, CD3D, IL7R, IL32, TNFAIP3, PTPRC, CST7, TRBC1, NKG7, RGCC, SLC2A3, CD2, GZMA, TMSB4X, TRBC2, DUSP2, TUBA4A, GNG2, KLRB1, CD7, ITM2A, STK17B, CXCR4, ANXA1, IFNG, LBH

Negative: CTSB, RHOB, IER3, GPX1, MS4A7, CFD, SPINT2, NPC2, PYCARD, CST3, KRT18, C1QB, C1QC, C1QA, ELF3, HSPB1, AIF1, APOE, TREM2, APOC1, CD68, MGST1, KRT8, S100A14, C15orf48, PSAP, KRT19, CD24, FCER1G, ATF3

PC\_4

Positive: EGFL7, RAMP2, PLVAP, CALCRL, EMCN, VWF, ESAM, AQP1, ACKR1, ADGRL4, GNG11, PECAM1, ENG, CLEC14A, TM4SF1, IFI27, CLDN5, CXorf36, IGFBP7, COL15A1

Negative: COL4A1, HSPG2, SPARCL1, A2M, RBP7, CD93, RAMP3, CAV1, SPRY1, MCTP1, CD69, DUSP2, S100A4, PTPRC, CXCR4, CD3E, CCL5, STK17B, TNFAIP3, CD52, RGCC, CST7, CD3D, IL7R, COL10A1, LUM, NKG7, THBS2, SFRP2, COL6A3, CTSK, COL11A1, DCN, SRGN, TRBC1, MMP11, COL1A1, CDH11, GZMA, COL1A2

PC\_5

Positive: GJA1, PIP, PSAP, MGP, SLC39A6, MUCL1, AZGP1, MS4A7, COX6C, CA2, ANPEP, APOE, APOC1, SCD, C1QC, TREM2, CYP4Z1, SUB1, C1QA, C1QB, PLAT, C3, CST3, TPSAB1, PDZK1, MSR1, SPPI1, RNASE1, NOTCH3, AIF1, DNAJB1, ZFP36, HSPH1, ATF3, DNAJA1, ZFAND2A, FOSB, PPP1R15A, BTG2, JUNB, JUN, HSP90AA1, TIPARP, NR4A1, DUSP1, FOS, MAFF, BAG3, MYC, DNAJB4, SERTAD1, KLF6, HSPB1, EGR1, CDKN1A, IRF1, MLF1, HSPD1, MRPL18, GADD45B

Computing nearest neighbor graph

Computing SNN

Warning: The following arguments are not used: ident.1  
Warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan van Eck

Number of nodes: 3764  
Number of edges: 119655

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.8923

Number of communities: 9

Elapsed time: 1 seconds

Warning: The following arguments are not used: ident.1  
Warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan van Eck

Number of nodes: 3764  
Number of edges: 119655

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.8378

Number of communities: 14

Elapsed time: 1 seconds

Warning: The following arguments are not used: ident.1  
Warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan van Eck

Number of nodes: 3764  
Number of edges: 119655

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.8028

Number of communities: 16

Elapsed time: 0 seconds

Warning: The following arguments are not used: ident.1  
Warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan van Eck

Number of nodes: 3764  
Number of edges: 119655

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.7742

Number of communities: 19

Elapsed time: 0 seconds

Warning: The following arguments are not used: ident.1  
Warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan van Eck

Number of nodes: 3764  
Number of edges: 119655

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.7500

Number of communities: 23

Elapsed time: 0 seconds

Performing log-normalization

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Calculating gene variances

```

0% 10 20 30 40 50 60 70 80 90 100%
[----|----|----|----|----|----|----|----|----|----|
*****|
Calculating feature variances of standardized and clipped values
0% 10 20 30 40 50 60 70 80 90 100%
[----|----|----|----|----|----|----|----|----|----|
*****|
Centering and scaling data matrix
|=====| 100%
PC_ 1
Positive: VIM, SPARC, IGFBP7, CALD1, COL6A2, SPARCL1, MMP2, BGN, IFI27, COL1A2
 COL3A1, TCF4, COL1A1, COL6A1, CTHRC1, HTRA1, B2M, THY1, PTRF, VCAN
 LUM, DCN, TIMP3, COL5A2, COL6A3, HLA-B, AEBP1, CTGF, FN1, SERPINF1
Negative: KRT19, CD24, S100A14, KRT18, KRT8, CLDN3, AZGP1, CLDN4, S100A1, CALML5
 ELF3, CRABP2, MGST1, PYCARD, CLDN7, PIP, KRT7, AGR2, SCGB1D2, CLU
 XBP1, PERP, TACSTD2, DSP, GATA3, SCGB2A1, EZR, DUSP4, DEGS2, CD9
PC_ 2
Positive: COL1A1, COL1A2, COL3A1, LUM, DCN, COL6A3, AEBP1, CTSK, COL6A1, RARRES2
 COL5A2, POSTN, SFRP2, CTHRC1, THBS2, FBLN1, MXRA8, ASPN, COL11A1, ISLR
 COL12A1, COL6A2, COL5A1, MMP11, C1S, BGN, IGFBP4, COL10A1, TIMP1, FBLN2
Negative: HLA-DRA, HLA-DPA1, HLA-DPB1, HLA-DRB5, HLA-DRB1, TYROBP, CD74, HLA-DQB1,
 C1QB, C1QA
 C1QC, CCL3, HLA-DQA1, LAPTM5, RGS1, AIF1, LYZ, CCL4, SRGN, FCER1G
 HLA-DMA, MS4A6A, CCL4L2, CCL3L3, CD68, HLA-DQA2, TREM2, CD83, OLR1, APOC1
PC_ 3
Positive: LUM, DCN, CTSK, SFRP2, COL1A1, COL6A3, COL1A2, SERPINF1, COL3A1, THBS2
 FBLN1, LRP1, COL11A1, ISLR, C1S, RARRES2, COL10A1, MMP11, AEBP1, POSTN
 ASPN, LRRC15, MXRA8, GPNMB, COL5A1, C3, COL8A1, MXRA5, CDH11, C1R
Negative: PLVAP, RAMP2, CALCRL, EMCN, RAMP3, EGFL7, VWF, CLEC14A, ADGRL4, ESAM
 CYYR1, AQP1, PODXL, PCDH17, FLT1, PECAM1, COL4A1, COL4A2, CD93, CD34
 GNG11, CDH5, CXorf36, PTPRB, ENG, INSR, NOTCH4, KDR, HSPG2, TIE1
PC_ 4
Positive: NEAT1, HSPB1, GPX1, KLF4, CD9, RHOB, CTSB, LGALS3, IER3, CST3
 S100A10, CTSD, C1QB, C1QA, C1QC, PYCARD, PSAP, CXCL8, ATF3, TM4SF1
 GSTP1, S100A6, CD68, LMNA, GAPDH, MS4A7, ZFP36L1, ALDOA, KRT18, APOE
Negative: CD69, IL7R, CD3E, CD7, CD52, KLRB1, CXCR4, LTB, CD3D, NKG7
 RHOH, CD2, CST7, PTPRC, CYTIP, DUSP2, B2M, ICOS, TNFAIP3, SRGN
 TRBC2, CTSW, HLA-B, GNLY, LIMD2, SLA, IL2RG, SLC2A3, CCL5, TRBC1
PC_ 5
Positive: MMP2, CTHRC1, COL10A1, COL11A1, LRRC15, MFAP2, COL8A1, COMP, SFRP2, HTRA1
 S100A10, MFAP5, FBLN1, ITGA11, LUM, THBS2, GJA1, FNDC1, FAP, ISLR
 WISP2, PDGFRL, SFRP4, SPON1, DPYSL3, POSTN, MMP11, ITGBL1, CTSK, ELN
Negative: NDUFA4L2, RGS5, PPP1R14A, ACTA2, NOTCH3, HIGD1B, COX4I2, MYH11, MCAM, SOD3
 MYLK, TPM2, LHFP, PDGFRB, EPS8, HEYL, COL18A1, GUCY1B3, TAGLN, ID4
 JAG1, ABCC9, ENPEP, GJA4, C11orf96, EBF1, PGF, NTRK2, MYL9, CRYAB
Computing nearest neighbor graph
Computing SNN
Warning: The following arguments are not used: ident.1warning: The following arguments
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo waltman and Nees Jan
van Eck

Number of nodes: 5789
Number of edges: 189547

Running smart local moving algorithm...
0% 10 20 30 40 50 60 70 80 90 100%
[----|----|----|----|----|----|----|----|----|----|
*****|
Maximum modularity in 10 random starts: 0.8902
Number of communities: 14
Elapsed time: 2 seconds
Warning: The following arguments are not used: ident.1warning: The following arguments
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo waltman and Nees Jan
van Eck

Number of nodes: 5789
Number of edges: 189547

Running smart local moving algorithm...
0% 10 20 30 40 50 60 70 80 90 100%
[----|----|----|----|----|----|----|----|----|----|
*****|

```

Maximum modularity in 10 random starts: 0.8467

Number of communities: 15

Elapsed time: 1 seconds

Warning: The following arguments are not used: ident.1  
Warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan van Eck

Number of nodes: 5789

Number of edges: 189547

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.8142

Number of communities: 20

Elapsed time: 1 seconds

Warning: The following arguments are not used: ident.1  
Warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan van Eck

Number of nodes: 5789

Number of edges: 189547

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.7868

Number of communities: 23

Elapsed time: 1 seconds

Warning: The following arguments are not used: ident.1  
Warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan van Eck

Number of nodes: 5789

Number of edges: 189547

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.7651

Number of communities: 25

Elapsed time: 1 seconds

Performing log-normalization

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Calculating gene variances

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Calculating feature variances of standardized and clipped values

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Centering and scaling data matrix

|=====| 100%

PC\_1

Positive: SPARC, CALD1, NNMT, IFITM3, SERPING1, C1R, C1S, VCAN, S100A13, COL1A2, IGFBP4, CCDC80, FSTL1, IGFBP7, SPARCL1, CTSK, PMP22, LUM, EMP1, WBP5, DCN, IFI27, FN1, TCF4, COL6A3, TIMP2, COL3A1, SERPINF1, TIMP3, CTGF

Negative: BIRC3, TMSB4X, KLRB1, GZMA, NKG7, CCR7, GPR183, HMGB2, KLRD1, TIGIT, CCL4, GZMH, GZMB, PLAC8, GNLY, CRTAM, CTLA4, TRGC2, XCL2, XCL1, TNFRSF9, TRDC, KLRC1, IGKC, RP11-291B21.2, CMC1, AREG, IFNG, RTKN2, RP11-1399P15.1

PC\_2

Positive: COL1A2, C1R, DCN, C1S, COL3A1, CCDC80, LUM, CTSK, COL6A3, COL1A1, DPT, FBLN1, FSTL1, COL14A1, SFRP2, MEG3, COL5A2, BGN, THBS2, THY1, EFEMP1, CALD1, AEBP1, COL6A1, MFAP5, MFAP4, PRRX1, FGF7, COL6A2, FAP

Negative: LYZ, MS4A7, AIF1, C1QB, CD68, IGSF6, FCGR2A, MS4A6A, LILRB4, OLR1

CD86 SERPINA1, CYBB, MNDA, HLA-DMB, PHACTR1, CD163, C1QA, C15orf48, MS4A4A,  
SLC7A7, LGALS2, CLEC7A, APOC1, C5AR1, CSTA, FPR3, HLA-DRA, C1QC, FCER1G

PC\_3  
Positive: C3, CTSK, LUM, DCN, COL6A3, FBLN1, DPT, SFRP2, CCDC80, COL1A2  
C1S, SERPINF1, COL3A1, MEG3, THBS2, COL1A1, C1R, OLFML3, MFAP4, MXRA5  
IGF1, EFEMP1, MFAP5, GPNMB, TMEM176B, OGN, COL6A1, PDGFR, LRP1, BICC1  
Negative: ECSCR.1, VWF, AQP1, PALMD, EMCN, CD93, ADGRL4, TM4SF1, PECAM1, PTPRB  
SDPR, CDH5, ACKR1, CLEC14A, TSPAN7, PLVAP, EPAS1, MYCT1, CALCRL, ADAMTS9  
MCTP1, ERG, MTUS1, PODXL, THSD7A, PCAT19, CNKSR3, GNG11, RAMP2, FABP4

PC\_4  
Positive: MMP2, SFRP2, S100A16, FBLN1, C3, CYP1B1, VCAN, DPT, VWF, ECSCR.1  
MFAP5, AQP1, MXRA5, GJA1, CTHRC1, EFEMP1, GAS1, IL33, FAP, COL15A1  
LUM, CCDC80, THBS2, CXCL14, IGF1, SFRP4, CTSK, CTGF, POSTN, EMCN  
Negative: ACTA2, NOTCH3, RGS5, MAP3K7CL, MYH11, PLN, ADIRF, MYL9, TAGLN, SEPT4  
CSRP2, LMOD1, MT1M, MYLK, C11orf96, PTK2, RERGL, HIGD1B, MT1A, TPM2  
COX4I2, ADAMTS4, CRYAB, ACTG2, MRV11, SLIT3, ADAMTS1, STEAP4, ENPEP, FRZB

PC\_5  
Positive: KIAA0101, MKI67, TYMS, RRM2, ZWINT, TOP2A, CDK1, SPC25, AURKB, CLSPN  
STMN1, BIRC5, NUSAP1, CENPW, CENPF, CKS1B, RAD51AP1, ASPM, TK1, SMC2  
DLGAP5, CKAP2L, KIF15, UBE2T, TUBB, GTSE1, MAD2L1, ESCO2, PBK, HMGB3  
Negative: FOS, PDK4, CD163, SEPP1, C1QB, APOE, C1QA, FCGR2A, SLC02B1, APOC1  
MAFB, MS4A4A, MS4A7, MSR1, CD68, C1QC, C5AR1, SLC40A1, SERPING1, CYBB  
A2M, MT1M, GPNMB, FTL, RNASE1, GPR183, TMEM176B, RHOB, SLC7A7, ADAMDEC1

Computing nearest neighbor graph

Computing SNN

Warning: The following arguments are not used: ident.1warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo waltman and Nees Jan  
van Eck

Number of nodes: 4451  
Number of edges: 173111

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.8876

Number of communities: 12

Elapsed time: 1 seconds

Warning: The following arguments are not used: ident.1warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo waltman and Nees Jan  
van Eck

Number of nodes: 4451  
Number of edges: 173111

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.8242

Number of communities: 16

Elapsed time: 1 seconds

Warning: The following arguments are not used: ident.1warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo waltman and Nees Jan  
van Eck

Number of nodes: 4451  
Number of edges: 173111

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.7829

Number of communities: 17

Elapsed time: 1 seconds

Warning: The following arguments are not used: ident.1warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo waltman and Nees Jan  
van Eck



Number of nodes: 4451  
Number of edges: 173111

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.7487

Number of communities: 19

Elapsed time: 1 seconds

Warning: The following arguments are not used: ident.1  
Warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan van Eck

Number of nodes: 4451  
Number of edges: 173111

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.7184

Number of communities: 22

Elapsed time: 1 seconds

Performing log-normalization

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Calculating gene variances

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Warning: pseudoinverse used at -2.499  
Warning: neighborhood radius 0.30103  
Warning: reciprocal condition number 2.0259e-15  
Calculating feature variances of standardized and clipped values

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Centering and scaling data matrix

|=====| 100%

PC\_1

Positive: KRT19, KRT18, SPINT2, SLC9A3R1, KRT8, ADIRF, TFPI, SNCG, BAMBI, PDPDF  
MGST1, TSPAN13, CLDN3, RBP1, COX6C, APOD, DCXR, MDK, MAGED2, STARD10  
NDUFB11, CLDN4, ARMT1, EFHD1, MYEOV2, GATA3, C19orf33, CXorf40A, LAGE3,

AZGP1

Negative: IGFBP7, A2M, SPARC, CD74, VWF, PLVAP, SPRY1, HLA-DRB1, HLA-DRB5, GSTP1  
IFITM1, PLPP1, SERPING1, RNASE1, ACKR1, MEF2C, HYAL2, AQP1, C1orf54, PRCP  
MMP2, HLA-DRA, CALD1, ENG, COL15A1, RAMP3, ADAMTS1, FN1, COL1A2, TSPAN7

PC\_2

Positive: CD74, HLA-DRA, HLA-DRB1, IGSF6, AIF1, HLA-DQA1, FCER1G, MS4A6A, LYZ, TYROBP  
HLA-DPA1, HLA-DRB5, LGALS2, IFI30, HLA-DPB1, CD68, MNDA, C1QA, HLA-DQB1,

HLA-DMA

SERPINA1, C15orf48, CCL3L3, FAM26F, HLA-DQA2, LST1, RNASE6, C1QB, C1QC,

FABP5

Negative: COL1A1, COL1A2, LUM, SFRP2, C1S, DCN, C1R, COL3A1, MFAP4, COL6A3  
SFRP4, CTSK, CTHRC1, SERPINF1, AEBP1, CCDC80, CXCL14, EFEMP1, MMP2, HTRA3  
MFAP5, MEG3, SPON2, ASPN, MXRA8, C3, CYR61, POSTN, SERPING1, CTGF

PC\_3

Positive: IGSF6, TYROBP, LYZ, CD68, FCER1G, IFI30, MS4A6A, AIF1, C1QA, HLA-DQA1  
HLA-DRA, SERPINA1, LGALS2, C15orf48, MNDA, HLA-DPA1, PLA2G7, PLAUR, CCL3L3,  
FAM26F

Negative: C1QC, C1QB, CXCL10, FTL, HLA-DPB1, RNASE6, SDS, TNFSF13B, CD86, HLA-DQA2  
PLVAP, VWF, HYAL2, A2M, IGFBP7, AQP1, ACKR1, RNASE1, RAMP3, SPRY1  
TM4SF1, IFITM1, CLDN5, PLPP1, SPARC, RAMP2, GNG11, PTP4A3, TSPAN7, THBD  
ENG, CYR1, PRCP, RBP7, NDUFA4L2, SELE, IFI27, INSR, ADAMTS1, APLNR

PC\_4

Positive: TOP2A, NUSAP1, HMGB2, PBK, PTTG1, PLK1, UBE2C, NUF2, SPC25, CDC20  
CDK1, CENPF, BIRC5, CCNB1, HMGN2, HIST1H4C, KIAA0101, MAD2L1, SMC4, CDKN3  
RAD51AP1, UBE2T, CENPU, PRC1, KIF22, GGH, TK1, CKS1B, CCNB2, KNSTRN

Negative: IFI27, PLVAP, VWF, HYAL2, A2M, BST2, IGFBP7, RAMP2, AQP1, RNASE1  
TM4SF1, SPRY1, ACKR1, PRCP, ARL4A, SPARC, ENG, GNG11, TSPAN7, CXCL2  
IFITM1, NRP1, RAMP3, CYR1, HES1, CLU, CLDN5, SELE, C1orf54, MAGED2



PC\_ 5

Positive: TOP2A, HYAL2, STMN1, NUSAP1, RNASE1, VWF, CDKN3, CENPF, TUBA1B, PRCP  
MAD2L1, RAD51AP1, PLVAP, RAMP2, PBK, SMC4, AQP1, ACKR1, CDK1, ARL4A  
IFI27, TM4SF1, RAMP3, SPC25, CD74, BIRC5, TUBB, HIST1H4C, GGH, GNG11  
Negative: IGHGP, IGHG4, NDUFA4L2, IGHG3, IGHG2, IGLC7, IGLL1, MAP3K7CL, IGLC6, ITM2C  
DERL3, IGHG1, CPE, ACTA2, SSR4, JCHAIN, KCNK15, MT1M, RASD1, MYLK  
IGLC3, MAGED2, MYL9, SOD3, RGS5, DNAAF1, IGLV3-1, IGLC5, IGKV1-12, MZB1

Computing nearest neighbor graph

Computing SNN

Warning: The following arguments are not used: ident.1warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan  
van Eck

Number of nodes: 631  
Number of edges: 22898

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.9029

Number of communities: 7

Elapsed time: 0 seconds

Warning: The following arguments are not used: ident.1warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan  
van Eck

Number of nodes: 631  
Number of edges: 22898

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.8157

Number of communities: 7

Elapsed time: 0 seconds

Warning: The following arguments are not used: ident.1warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan  
van Eck

Number of nodes: 631  
Number of edges: 22898

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.7364

Number of communities: 8

Elapsed time: 0 seconds

Warning: The following arguments are not used: ident.1warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan  
van Eck

Number of nodes: 631  
Number of edges: 22898

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.6682

Number of communities: 9

Elapsed time: 0 seconds

Warning: The following arguments are not used: ident.1warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan  
van Eck

Number of nodes: 631  
Number of edges: 22898

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.6139

Number of communities: 10

Elapsed time: 0 seconds

Performing log-normalization

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Calculating gene variances

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Calculating feature variances of standardized and clipped values

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Centering and scaling data matrix

|=====| 100%

PC\_1

Positive: VIM, CD74, HLA-DRB1, HLA-DRB5, GSTP1, HLA-DRA, HLA-DPA1, HLA-DPB1, S100A6, RNASE1

HLA-DQB1, LGALS1, TYROBP, HLA-DMA, CD68, GSN, HLA-DQA1, C1QC, A2M, FCER1G  
SRGN, FABP5, HLA-DQA2, APOE, C1QB, SERPING1, AIF1, C1QA, CTSS, ANXA1  
Negative: KRT19, KRT18, AZGP1, KRT8, SLC39A6, ELF3, CLDN4, COX6C, H2AFJ, CCND1  
STARD10, WFDC2, FAM3B, CD24, DCXR, PDZK1, CRABP2, SLC9A3R1, ESR1, TACSTD2  
CCDC74A, SPDEF, GSTM3, SCGB2A2, LRRC26, GPRC5A, NUCB2, PEG10, PKIB, STC2

PC\_2

Positive: TYROBP, CD68, FCER1G, C1QB, C1QC, AIF1, C1QA, MS4A6A, TREM2, ITGB2  
APOC1, IFI30, LILRB4, MS4A7, SPI1, IGSF6, C5AR1, CTSS, LAPTM5, CAPG  
MS4A4A, PLEK, FCGR3A, HLA-DQA1, LYZ, LY86, MSR1, FCGR1A, CCL3, HLA-DQA2  
Negative: IGFBP7, SPARC, NNMT, SPARCL1, CALD1, CAV1, GNG11, PTRF, BGN, CTGF  
POSTN, FBLN2, PLPP1, ELN, PLAC9, EMP1, PRKCSBP, CYR61, COL6A2, CNND3  
TAGLN, HSPG2, LMCD1, ID3, RAMP2, CTHRC1, CLEC14A, FSTL1, MYL9, ESAM

PC\_3

Positive: CST3, GPX1, PSAP, NPC2, CTSB, FTL, CTSD, TUBA1B, TUBB, ANAPC11  
LGMN, TMEM176B, MDK, TMEM176A, HMG2, H2AFJ, COX6C, TCEAL4, HSPB1, COA3  
NUPR1, DBI, KRT8, SEPP1, AZGP1, KRT19, KRT18, GPNMB, CFD, C1QC  
Negative: CD3E, IL32, CD3D, CCL5, PTPRCAP, IL2RG, CTSW, IL7R, PTPRC, CST7  
CD2, TRBC2, CD7, DUSP2, GZMK, NKG7, CORO1A, GIMAP7, HCST, CD8A  
SH2D2A, CD3G, CD8B, TRBC1, LTB, SH3BGL3, CD69, ITM2A, SOCS1, GZMA

PC\_4

Positive: ADGRL4, RAMP2, PLVAP, VWF, PECAM1, CLEC14A, EMCN, SDPR, EGFL7, ESAM  
FABP4, TSPAN7, HYAL2, CD93, CLEC3B, RNASE1, ACKR1, THBD, SPRY1, MMRN2  
CXorf36, CD34, CALCRL, TIE1, CYR1, CDH5, ENG, HSPG2, TM4SF1, TMEM255B  
Negative: SFRP2, LUM, COL1A1, COL1A2, CTSK, DCN, COL3A1, SFRP4, AEBP1, ASPN  
C1S, MXRA8, DPT, CTHRC1, MFAP4, THBS2, COL14A1, SERPINF1, COL6A3, RARRES2  
COL6A1, COL8A1, CILP, PDGFRL, ISLR, ITGBL1, THBS4, PCOLCE, CCDC80, COL6A2

PC\_5

Positive: FTL, BTG2, CEBPD, CLDN4, SAT1, FOSB, ELF3, C5AR1, CST3, GPRC5A  
GADD45B, PDK4, MS4A7, TRIB1, EGR1, TACSTD2, EFNA1, ATF3, C15orf48, PSAP  
CPVL, MAFF, PILRA, CD163, MS4A6A, KRT19, CXCL8, CD68, TSC22D1, SLC02B1  
Negative: UBE2C, TOP2A, TPX2, NUSAP1, BIRC5, CDCA3, CDK1, KIF23, CENPF, MKI67  
PBK, CDKN3, CCNA2, SPC25, PLK1, PKMYT1, CDC20, KIFC1, DEPDC1, CCNB2  
RRM2, GTSE1, NUF2, TYMS, PTTG1, PRC1, DLGAP5, CDC25C, HMMR, HJURP

Computing nearest neighbor graph

Computing SNN

Warning: The following arguments are not used: ident.1  
Warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan van Eck

Number of nodes: 1138

Number of edges: 31527

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.8908

Number of communities: 9

Elapsed time: 0 seconds  
Warning: The following arguments are not used: ident.1Warning: The following arguments are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan van Eck

Number of nodes: 1138  
Number of edges: 31527

Running smart local moving algorithm...  
0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.8289  
Number of communities: 12  
Elapsed time: 0 seconds

Warning: The following arguments are not used: ident.1Warning: The following arguments are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan van Eck

Number of nodes: 1138  
Number of edges: 31527

Running smart local moving algorithm...  
0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.7874  
Number of communities: 16  
Elapsed time: 0 seconds

Warning: The following arguments are not used: ident.1Warning: The following arguments are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan van Eck

Number of nodes: 1138  
Number of edges: 31527

Running smart local moving algorithm...  
0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.7576  
Number of communities: 18  
Elapsed time: 0 seconds

Warning: The following arguments are not used: ident.1Warning: The following arguments are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan van Eck

Number of nodes: 1138  
Number of edges: 31527

Running smart local moving algorithm...  
0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.7301  
Number of communities: 19  
Elapsed time: 0 seconds

Performing log-normalization  
0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Calculating gene variances  
0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Calculating feature variances of standardized and clipped values  
0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Centering and scaling data matrix  
|=====| 100%  
PC\_ 1

Positive: SPARCL1, DCN, COL1A1, ACTA2, LUM, TIMP1, IFI27, NDUFA4L2, ASPN, SFRP4, DERL3, PTP4A3, POSTN, RGS5, IGHGP, SFRP2, MMP11, MZB1, ENPEP, CTHRC1, THBS2, MFAP4, IGLL1, CCDC80, IGLC7, CRYAB, OR51E1, HIGD1B, MT1M, GPX3

Negative: CD24, FABP7, RP11-10A14.5, SMIM22, EPCAM, KRT19, CENPW, CSN3, ODAM, MAGEA4, CDKN2A, PRR27, DCXR, FDCSP, MAGEA3, SPINT2, BIRC5, ANAPC11, GABRP, TSTD1, SPTSSA, ATP1B1, CKS1B, TSPAN13, GGCT, SGOL1, CRISP3, CDK1, ENSA, SUMO2

PC\_2

Positive: COL1A1, LUM, DCN, SFRP2, DERL3, MFAP2, IGHG4, IGHGP, ACTA2, IGHG3, MMP11, RARRES1, POSTN, TSTD1, IGHG2, SFRP4, THBS2, CDKN2A, IGLL1, ASPN, CD79A, IGHG1, SMIM22, CTHRC1, CD24, IGLC7, MDK, NUSAP1, MZB1, FABP7

Negative: PLVAP, VWF, ACKR1, ADGRL4, TSPAN7, RAMP2, PCAT19, RAMP3, CLEC14A, HYAL2, AQP1, EMCN, FKBP1A, SDPR, PECAM1, FABP4, EGFL7, CD93, ECSCR.1, HSPG2, PRCP, CLDN5, TM4SF1, SPRY1, RNASE1, TGM2, TMEM255B, SLC02A1, EDN1, GNG11

PC\_3

Positive: FCER1G, LYZ, C1QA, AIF1, MS4A6A, TYROBP, C1QB, IGSF6, HLA-DRA, HLA-DQB1, C1QC, MNDA, HLA-DRB1, CD68, HLA-DRB5, HLA-DQA1, HLA-DPB1, C15orf48, HLA-DPA1, CAPG

Negative: HLA-DQA2, FCGR3A, APOC1, LAPTM5, CCL3, SPI1, LST1, PLEK, C3AR1, FAM26F, SPARCL1, LUM, COL1A1, DCN, CTHRC1, SFRP2, ACTA2, POSTN, MDK, CYR61, MFAP2, CD59, TIMP3, MGP, HSPB1, TIMP1, IFI27, CTGF, HES1, ASPN, CCDC80, SFRP4, SOX4, EFEMP1, ADIRF, MFAP5, MFAP4, COL4A1, TFPI, THBS2

PC\_4

Positive: LUM, SFRP2, DCN, CTHRC1, COL1A1, POSTN, MFAP2, FN1, SFRP4, MFAP5, THBS2, CCDC80, CXCL14, TIMP3, FBLN1, MMP11, IFI27, ISLR, TIMP1, MXRA5, MFAP4, MDK, EFEMP1, CYR61, SULF1, C1QTNF3, RARRES1, C3, CTGF, COL12A1

Negative: IGHGP, IGHG4, IGHG1, IGLL1, MZB1, IGHG3, IGLC7, IGHG2, CD79A, JCHAIN, DERL3, CD2, ISG20, TNFRSF17, TRAC, OCIAD2, LTB, IGLC3, IGHA2, CD3E, TPD52, IGLC6, IGLC2, GZMB, PTTG1, BIRC3, NUSAP1, PLVAP, LINC01480, DUSP4

PC\_5

Positive: IGHG1, IGHGP, IGHG3, IGHG4, IGHG2, IGLL1, DERL3, IGLC7, MZB1, SSR4, JCHAIN, IGLC3, IGLC2, CD79A, TNFRSF17, IGLC6, CTHRC1, XBP1, IGHA1, SFRP2, ISG20, DCN, IGLV3-1, FAM46C, LUM, LINC01480, IGLV6-57, MFAP2, RGCC, IGHM

Negative: NDUFA4L2, PTP4A3, ACTA2, ADIRF, SPARCL1, RGS5, PPP1R14A, OR51E1, MAP3K7CL, MYLK

GPX3, RERGL, CRYAB, ENPEP, WFDC1, HIGD1B, SORBS2, HSPB1, PLN, MT-CO2, CNN1, TPPP3, ACTG2, MCAM, PHLDA2, HSPB6, CASQ2, MT-CO1, GJA4, TFPI

Computing nearest neighbor graph

Computing SNN

Warning: The following arguments are not used: ident.1warning: The following arguments are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo waltman and Nees Jan van Eck

Number of nodes: 1564  
Number of edges: 55844

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.9252

Number of communities: 7

Elapsed time: 0 seconds

Warning: The following arguments are not used: ident.1warning: The following arguments are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo waltman and Nees Jan van Eck

Number of nodes: 1564  
Number of edges: 55844

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.8693

Number of communities: 8

Elapsed time: 0 seconds

Warning: The following arguments are not used: ident.1warning: The following arguments are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo waltman and Nees Jan van Eck

Number of nodes: 1564  
Number of edges: 55844

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.8225

Number of communities: 11

Elapsed time: 0 seconds

Warning: The following arguments are not used: ident.1  
Warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan van Eck

Number of nodes: 1564

Number of edges: 55844

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.7819

Number of communities: 11

Elapsed time: 0 seconds

Warning: The following arguments are not used: ident.1  
Warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan van Eck

Number of nodes: 1564

Number of edges: 55844

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.7490

Number of communities: 14

Elapsed time: 0 seconds

Performing log-normalization

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Calculating gene variances

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Calculating feature variances of standardized and clipped values

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Centering and scaling data matrix

|=====| 100%

PC\_1

Positive: SPINT2, KRT18, AZGP1, CLDN4, ELF3, CLDN7, KRT8, CD24, KRT19, WFDC2  
TSTD1, TACSTD2, KRT7, CLDN3, FXYD3, MGST1, ATP1B1, SPDEF, KIAA1324, ERBB3  
EPCAM, ZG16B, RAB25, SMIM22, TRPS1, DSP, CRACR2B, RASEF, SERINC2, SPINT1

Negative: SPARC, TIMP3, COL1A2, SERPINF1, DCN, C1S, AEBP1, CCDC80, COL6A2, BGN  
IFI27, LUM, VCAN, COL6A3, COL1A1, CTGF, PCOLCE, RARRES2, SFRP2, COL3A1  
COL6A1, COL14A1, CTSK, MFAP4, MMP2, C1R, FN1, FBLN1, FSTL1, CTHRC1

PC\_2

Positive: CD74, HLA-DRB1, HLA-DRA, HLA-DPA1, HLA-DPB1, HLA-DRB5, PLVAP, RNASE1, SRGN,  
VWF

AQP1, EMCN, HLA-DQB1, HLA-DMA, ACKR1, RAMP2, ADGRL4, GIMAP7, CLDN5, RAMP3  
CLEC14A, MCTP1, EGFL7, CD93, SDPR, ZNF385D, RBP7, HLA-DQA1, FABP5, CCL14  
Negative: COL6A2, COL1A2, LUM, SFRP2, CCDC80, DCN, COL6A3, FBLN1, AEBP1, COL1A1  
C1S, COL6A1, MXRA8, CTSK, SERPINF1, COL14A1, COL3A1, RARRES2, MFAP4, ISLR  
LRP1, PCOLCE, MMP2, SPON2, PODN, THBS2, BGN, MGP, COL5A2, C1R

PC\_3

Positive: RAMP2, TM4SF1, IFI27, VWF, CAV1, EMCN, AQP1, PLVAP, ADGRL4, CLEC14A  
SPRY1, RAMP3, CLDN5, SDPR, ACKR1, ZNF385D, EGFL7, RBP7, CLU, FABP4  
CALCRL, ADAMTS9, NRN1, TSPAN7, FLT1, LIFR, SPARC, CD93, CCL14, COL15A1  
Negative: TYROBP, FCER1G, AIF1, MS4A7, C1QA, LAPTM5, C1QC, RGS1, C1QB, MS4A6A  
SPI1, C1orf162, CSF1R, IGSF6, GPR183, ITGB2, FYB, LYZ, C5AR1, CXCR4  
TREM2, CYBA, CD68, MSR1, CD37, CD83, FCGR3A, LST1, RNASE6, PTPRC

PC\_4  
Positive: PRSS23, VCAN, IFI27, SOCS2, RAMP2, FBLN2, MLPH, HLA-DRB1, SPRY1, HLA-DRA  
HLA-DPA1, CTHRC1, RNASE1, HLA-DRB5, SPDEF, VWF, PLVAP, TSPAN13, FBP1, HLA-  
DMA  
Negative: HLA-DQB1, HLA-DPB1, XBP1, STC2, ANKRD30A, ACKR1, EMCN, MARCKS, RAMP3, CTSB  
CRYAB, ACTA2, TPM2, MYH11, TAGLN, NTRK2, PPP1R14A, C2orf40, CNN1, MYL9  
ACTG2, MYLK, KRT14, SYNM, KRT5, FBXO32, LMOD1, MT1E, KRT17, RERGL  
MT1X, PLN, MT1M, KCNMB1, DKK3, SORBS2, S100A4, SAA1, TRIM29, TNS4

PC\_5  
Positive: PTN, KRT15, SFRP1, CCL28, SAA1, GABRP, KLK5, STAC2, SLPI, ANXA1  
KRT14, KRT5, LTF, DSC2, KIT, RARRES1, MMP7, KRT6B, KRT16, FOLR1  
SAA2, PDLIM4, PLEKHS1, SGK1, CHI3L1, BBOX1, LCN2, C2orf82, KRT23, TPT1-AS1  
Negative: S100A4, EFHD1, CD3E, BATF, CD52, SPDEF, RERGL, IL7R, CD3D, SOD3  
NDUFA4L2, RAC2, PLN, NOTCH3, ANKRD30A, IGFBP5, ACAP1, CD7, AR, CRIP1  
LTB, CD2, C1orf64, CD69, CCL5, GJA4, CYTIP, TRBC2, AGR2, RBPMS2

Computing nearest neighbor graph

Computing SNN

Warning: The following arguments are not used: ident.1warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan  
van Eck

Number of nodes: 8609  
Number of edges: 312111

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.9503

Number of communities: 16

Elapsed time: 3 seconds

Warning: The following arguments are not used: ident.1warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan  
van Eck

Number of nodes: 8609  
Number of edges: 312111

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.9168

Number of communities: 19

Elapsed time: 2 seconds

Warning: The following arguments are not used: ident.1warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan  
van Eck

Number of nodes: 8609  
Number of edges: 312111

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.8917

Number of communities: 23

Elapsed time: 2 seconds

Warning: The following arguments are not used: ident.1warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan  
van Eck

Number of nodes: 8609  
Number of edges: 312111

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.8697

Number of communities: 28

Elapsed time: 2 seconds

Warning: The following arguments are not used: ident.1  
Warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan van Eck

Number of nodes: 8609

Number of edges: 312111

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.8502

Number of communities: 31

Elapsed time: 2 seconds

Performing log-normalization

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Calculating gene variances

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Calculating feature variances of standardized and clipped values

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Centering and scaling data matrix

|=====| 100%

PC\_ 1

Positive: SPARC, IGFBP7, SERPING1, NNMT, COL6A2, SPARCL1, PRSS23, COL6A1, IFITM3, GSN  
COL1A2, C1R, COL3A1, PLPP3, PTRF, IGFBP4, C1S, FSTL1, TIMP1, BGN  
COL4A2, CALD1, THY1, EFEMP2, COL5A2, SERPINF1, MMP2, CTSK, A2M, COL1A1

Negative: CD79A, MZB1, IGKV1-5, JCHAIN, DERL3, IGKV3-20, POU2AF1, IGKV3-11, IGLL5,  
IGLV3-1

GZMK, IGLV3-25, IGKV1-9, IGHG1, IGKC, IGLV1-51, TNFRSF17, IGLV2-14, IGKV3-  
15, IGHG4

IGLV1-40, IGKV4-1, AREG, RP11-290F5.1, IGHG3, IGLC2, IGHV3-30, PTTG1,  
HIST1H4C, IGLV6-57

PC\_ 2

Positive: TYROBP, FCER1G, AIF1, SERPINA1, MS4A6A, CD68, LILRB4, LYZ, SPI1, C1QA  
FCGR3A, C1QB, C1QC, PILRA, IGSF6, C15orf48, CD14, FPR3, FCGR1A, APOC1  
CYBB, CSF1R, MS4A7, LILRB2, IL4I1, FCGR2A, FGL2, LST1, CLEC7A, SLAMF8

Negative: MGP, CALD1, MGST1, KRT7, TM4SF1, CSRP2, KRT18, CDKN2A, CNN3, CD24  
EPCAM, CKB, FDCSP, GAL, MDK, CLDN3, KRT8, MEST, MARCKSL1, TPM2  
PFN2, AZGP1, TUSC3, RBPMS, NFIB, EFHD1, PFDN2, PTRF, TSTD1, CDC42EP1

PC\_ 3

Positive: SELM, IGFBP4, CD79A, NNMT, PRSS23, SPARCL1, MZB1, COL1A2, COL3A1, BGN  
SPARC, ID3, JCHAIN, COL1A1, COL5A2, PCOLCE, THY1, EFEMP2, CTSK, CCDC80  
IGKV1-5, CD248, C1R, AEBP1, COL6A2, FBN1, COL6A1, DCN, COL6A3, DERL3

Negative: MGST1, CD24, KRT7, FDCSP, PFDN2, CKB, KRT18, EPCAM, CLDN3, KRT8  
GAL, AZGP1, MARCKSL1, LTBR, NME4, CDKN2A, CDC42EP1, MARCO, MTCH2, CLDN7  
MEST, TSTD1, FKBP4, TM4SF1, LINC01315, BZW2, CSRP2, GABRP, CLDN4, GCAT

PC\_ 4

Positive: VWF, ADGRL4, CLEC14A, PLVAP, EGFL7, RAMP2, EMCN, ESAM, CDH5, CD93  
KDR, CXorf36, RAMP3, CYR1, CD34, CALCRL, BCAM, FLT1, SLC9A3R2, INSR  
PTPRB, PALMD, TIE1, VWA1, SOX18, PODXL, PCDH17, MMRN2, ERG, NOTCH4

Negative: DCN, LUM, COL3A1, COL1A2, COL6A3, COL1A1, CTSK, RARRES2, SFRP2, MXRA8  
ISLR, CCDC80, MXRA5, CYP1B1, POSTN, DPT, COL6A1, THBS2, MFAP4, COL5A2  
PRRX1, AEBP1, C1S, VCAN, PODN, EMILIN1, LOXL1, PCOLCE, TMEM119, OLFML3

PC\_ 5

Positive: MMP2, DCN, SFRP2, LUM, CTHRC1, FBLN2, DPT, MFAP4, CYP1B1, DPYSL3  
CXCL12, PODN, MFAP2, S100A16, POSTN, CILP, HTRA3, PDGFRA, EFEMP1, VCAN  
THBS2, MFAP5, C3, TMEM119, IGF1, PDPN, HTRA1, APOD, MEG3, LTBP2

Negative: NDUFA4L2, RGS5, COX4I2, NOTCH3, KCNJ8, EDNRA, C1QTNF1, HIGD1B, FRZB, SEPT4  
FAM162B, SMOC2, STEAP4, ADIRF, CPE, TDO2, PGF, GUCY1B3, REM1, TBX2  
FOXS1, ANGPT2, RP11-598F7.6, PLXDC1, ABCC9, SOD3, FAM13C, PDGFRB, OR51E1,

NEURL1B

Computing nearest neighbor graph

Computing SNN



Warning: The following arguments are not used: ident.1  
Warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan van Eck

Number of nodes: 7985  
Number of edges: 286925

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.9401  
Number of communities: 15  
Elapsed time: 2 seconds

Warning: The following arguments are not used: ident.1  
Warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan van Eck

Number of nodes: 7985  
Number of edges: 286925

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.9042  
Number of communities: 16  
Elapsed time: 2 seconds

Warning: The following arguments are not used: ident.1  
Warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan van Eck

Number of nodes: 7985  
Number of edges: 286925

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.8749  
Number of communities: 20  
Elapsed time: 2 seconds

Warning: The following arguments are not used: ident.1  
Warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan van Eck

Number of nodes: 7985  
Number of edges: 286925

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.8515  
Number of communities: 25  
Elapsed time: 2 seconds

Warning: The following arguments are not used: ident.1  
Warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan van Eck

Number of nodes: 7985  
Number of edges: 286925

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.8297  
Number of communities: 27  
Elapsed time: 2 seconds

Performing log-normalization

0% 10 20 30 40 50 60 70 80 90 100%



```

[----|----|----|----|----|----|----|----|----|----|
*****|
calculating gene variances
0% 10 20 30 40 50 60 70 80 90 100%
[----|----|----|----|----|----|----|----|----|----|
*****|
calculating feature variances of standardized and clipped values
0% 10 20 30 40 50 60 70 80 90 100%
[----|----|----|----|----|----|----|----|----|----|
*****|
Centering and scaling data matrix
|=====| 100%
PC_ 1
Positive: CAV1, COL6A2, MAP1B, COL6A1, PTRF, CNN3, TUSC3, PRSS23, S100A16, FKBP10
 COL6A3, SPARC, MDK, CALD1, COL1A2, PLOD2, TIMP3, FBLIM1, TPM2, FN1
 TM4SF1, MAP1A, PFN2, CRIP2, NGFRAP1, PCOLCE, LOXL1, SDC1, ASPH, CKAP4
Negative: CD74, HLA-DPA1, HLA-DPB1, HLA-DRB1, HLA-DRA, HLA-DRB5, HLA-DQB1, C1QA, C1QB,
 C1QC
 CD14, LYZ, S100A9, HLA-DQA1, CFD, FOLR2, MS4A4A, CCL3, SEPP1, CCL4
 BCL2A1, MAFB, CD69, CD52, LGMN, APOC1, CST7, IL1B, ACP5, RNASE1
PC_ 2
Positive: ESAM, RAMP2, CDH5, PLVAP, ADGRL4, CD34, CLEC14A, AQP1, SPARCL1, VWF
 ADGRF5, COL4A2, COL4A1, CYR1, CXorf36, KDR, PCDH17, TIE1, FAM167B, RAMP3
 COL15A1, PODXL, EMCN, PALMD, CALCRL, FZD4, HSPG2, FLT1, LINC01235, INSR
Negative: HMGA1, MGST1, EMP3, PFN2, TNFRSF12A, HMGA2, SDC1, LOXL1, FGF5, CD82
 HGF, CA12, STEAP1, CLMP, PERP, SPHK1, LINC01605, SFN, RPL22L1, IGF2BP3
 SLC7A11, SERPINE1, TUBA1C, DSG2, MAP1A, TFPI2, MME, PGD, PDLIM4, ARHGAP22
PC_ 3
Positive: PDGFRB, CD248, NOTCH3, SMOC2, NDUFA4L2, RGS5, SERPINF1, SEPT4, COX4I2,
 GUCY1B3
 EDNRA, CPE, SOD3, HIGD1B, MXRA8, PLAC9, CRISPLD2, PLXDC1, HEYL, CCDC102B
 COL3A1, FRZB, MFGE8, C1QTNF1, SLIT3, THY1, PPP1R14A, ACTA2, EFHD1, SDC2
Negative: STMN1, CDH5, CLEC14A, PLVAP, CD34, ADGRL4, RAMP2, VWF, AQP1, KDR
 CYR1, TIE1, CXorf36, PODXL, RAMP3, MKI67, EMCN, RRM2, FAM167B, H2AFZ
 PCDH17, FLT1, TM4SF1, HMGB2, MYCT1, UBE2C, ROBO4, ITGA6, CDKN3, PTTG1
PC_ 4
Positive: CST7, GZMA, CCL5, CD7, CD69, NKG7, CD52, HOPX, IFITM1, CD3D
 XCL1, LTB, GZMK, CTSW, IFNG, PRF1, TRBC2, TUBA4A, TRBC1, STK17A
 C12orf75, DUSP4, IL2RB, KLRD1, SPOCK2, XCL2, SH2D1A, MATK, GNLY, GZMB
Negative: C1QA, C1QC, C1QB, CD14, PLTP, HLA-DRA, RNASE1, SEPP1, FOLR2, LGMN
 MS4A4A, MAFB, S100A9, CTSL, HLA-DRB5, LYZ, CFD, APOC1, HLA-DQB1, HLA-DPB1
 HMOX1, HLA-DPA1, HLA-DRB1, CTSD, HLA-DQA1, APOE, SLC40A1, CPVL, CXCL2,
 CD74
PC_ 5
Positive: MKI67, RRM2, UBE2C, TOP2A, TPX2, CCNA2, CENPF, CDK1, TYMS, TUBA1B
 STMN1, CKS1B, BIRC5, GTSE1, ASPM, CDCA5, NUSAP1, ASF1B, ZWINT, CDCA8
 HMMR, PKMYT1, CDCA3, CDKN3, NCAPH, CDC20, CENPM, CKAP2L, AURKB, CLSPN
Negative: POSTN, CTHRC1, TMEM119, FIBIN, CST7, LTB, CCL5, CD7, MFAP4, CD69
 PTGDS, MMP2, STK17A, CD52, CD3D, RP11-865I6.2, COL5A1, GZMA, CRABP2,
 CERCAM
 CLIC3, CHPF, NKG7, COL3A1, KIF26B, LRRC17, COL8A1, ZMAT3, FAP, MFAP2
Computing nearest neighbor graph
Computing SNN
Warning: The following arguments are not used: ident.1warning: The following arguments
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan
van Eck

Number of nodes: 5619
Number of edges: 199185

Running smart local moving algorithm...
0% 10 20 30 40 50 60 70 80 90 100%
[----|----|----|----|----|----|----|----|----|----|
*****|
Maximum modularity in 10 random starts: 0.9180
Number of communities: 12
Elapsed time: 2 seconds
Warning: The following arguments are not used: ident.1warning: The following arguments
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan
van Eck

Number of nodes: 5619

```

Number of edges: 199185

Running smart local moving algorithm...

```
0% 10 20 30 40 50 60 70 80 90 100%
[----|----|----|----|----|----|----|----|----|----|
*****|
```

Maximum modularity in 10 random starts: 0.8705

Number of communities: 17

Elapsed time: 1 seconds

Warning: The following arguments are not used: ident.1  
Warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan van Eck

Number of nodes: 5619

Number of edges: 199185

Running smart local moving algorithm...

```
0% 10 20 30 40 50 60 70 80 90 100%
[----|----|----|----|----|----|----|----|----|----|
*****|
```

Maximum modularity in 10 random starts: 0.8390

Number of communities: 18

Elapsed time: 1 seconds

Warning: The following arguments are not used: ident.1  
Warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan van Eck

Number of nodes: 5619

Number of edges: 199185

Running smart local moving algorithm...

```
0% 10 20 30 40 50 60 70 80 90 100%
[----|----|----|----|----|----|----|----|----|----|
*****|
```

Maximum modularity in 10 random starts: 0.8118

Number of communities: 21

Elapsed time: 1 seconds

Warning: The following arguments are not used: ident.1  
Warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan van Eck

Number of nodes: 5619

Number of edges: 199185

Running smart local moving algorithm...

```
0% 10 20 30 40 50 60 70 80 90 100%
[----|----|----|----|----|----|----|----|----|----|
*****|
```

Maximum modularity in 10 random starts: 0.7874

Number of communities: 24

Elapsed time: 1 seconds

Performing log-normalization

```
0% 10 20 30 40 50 60 70 80 90 100%
[----|----|----|----|----|----|----|----|----|----|
*****|
```

Calculating gene variances

```
0% 10 20 30 40 50 60 70 80 90 100%
[----|----|----|----|----|----|----|----|----|----|
*****|
```

Calculating feature variances of standardized and clipped values

```
0% 10 20 30 40 50 60 70 80 90 100%
[----|----|----|----|----|----|----|----|----|----|
*****|
```

Centering and scaling data matrix

|=====| 100%

PC\_1

Positive: CST3, IFITM2, SPARC, ISG15, SAT1, HINT1, SERPING1, CTSL, IFITM3, SERPINF1  
IFI6, DCN, CCDC80, COL5A2, COL1A1, LUM, EMP3, COL6A3, THY1, COL3A1  
CTSK, IGFBP7, HIF1A, TIMP2, IGFBP4, SRGN, RARRES2, FILIP1L, PCOLCE, COL1A2  
Negative: EPCAM, KRT19, RPS3, KRT7, TACSTD2, KRT18, CD24, MAL2, SAA1, KRT8  
STRA13, CALML5, KLK6, CCND1, S100A14, KRT6B, LEMD1, WFDC2, C6orf15, PRDX2  
TK1, MGP, RARRES1, FBXO2, KRT5, NQO1, LY6D, AARD, KRT14, KLK5

PC\_ 2  
Positive: SRGN, LAPTM5, PTPRC, CD53, TYROBP, RGS1, CD52, CORO1A, FCER1G, CD48  
LCP1, SAMS1, HCST, FYB, GPR183, GMFG, AIF1, LYZ, Clorf162, RAC2  
LST1, CTSS, SLA, ALOX5AP, CD69, ZNF331, MNDA, PLAC8, RNASE6, PLEK  
Negative: CALD1, C1S, C1R, PRRX1, COL1A2, CTHRC1, NNMT, CCDC80, COL6A1, SERPINH1  
PPIC, FSTL1, COL6A2, MMP2, LUM, DCN, SPARC, COL6A3, TPM2, COL1A1  
COL5A2, RARRES2, COL3A1, THY1, PCOLCE, CAV1, FBLN1, CTSK, TIMP3, IFI27

PC\_ 3  
Positive: AIF1, FCER1G, TYROBP, FTL, C1QB, C1QA, C1QC, PLAUR, CTSZ, CTSB  
LYZ, C15orf48, CD68, FCGR2A, LST1, MSR1, MS4A6A, TNFSF13B, MS4A4A, CTSB  
FPR3, CTSD, SPP1, SPI1, C5AR1, IL4I1, IL1RN, CD14, CD163, PILRA  
Negative: ITM2A, CD79A, S100A1, MS4A1, SPARCL1, FAM3D, AZGP1, AQP1, CEACAM6, GLYATL2  
CD69, LTB, PALMD, PPP1R1B, SCGB2A1, ZG16B, SYNM, SCGB1D2, FAM84A, PDLIM1  
IGFBP7, KIAA1324, RHCG, COL4A1, SPRY1, ECSCR.1, ADAMTS9, ADGRL4, RAMP2,

CCL28

PC\_ 4  
Positive: DCN, SFRP2, LUM, CTSK, CCDC80, THBS2, FBLN1, COL6A3, DPT, FGF7  
IGF1, COL1A1, MXRA5, PLA2G2A, TWIST2, CLMP, MEG3, COL1A2, COL3A1, WISP2  
PDGFR, PDPN, IGFBP6, OLFML3, ABI3BP, COL6A1, RARRES2, PTN, CXCL14, SPON2  
Negative: ECSCR.1, RAMP2, CLEC14A, VWF, PLVAP, ADGRL4, RAMP3, EGFL7, EMCN, CDH5  
PCAT19, PECAM1, CALCRL, ESAM, ACKR1, MMRN2, ADAMTS9, HYAL2, CXorf36, MYCT1  
HSPG2, ENG, CLDN5, CD93, TSPAN7, PTPRB, GNG11, PREX2, RHOJ, APOLD1

PC\_ 5  
Positive: CD7, GZMA, HMGB2, GZMB, NKG7, NUSAP1, CENPF, MKI67, BIRC5, CD69  
TOP2A, CD247, CD52, UBE2C, KLRD1, CCL5, KLRB1, CST7, PRF1, CTSW  
CORO1A, CENPA, AURKB, ASPM, IL32, PTPRC, GTSE1, HMGB1, TPX2, TRBC2  
Negative: S100A1, AZGP1, ZG16B, SLPI, CEACAM6, NDRG2, FAM3D, GLYATL2, PPP1R1B, SEPP1  
CALML5, SCGB2A1, TM4SF1, CD24, RHCG, SCGB1D2, SELENBP1, KIAA1324, CRABP2,  
MFGE8

CLDN4, PRSS21, NUPR1, FAM84A, CLDN3, SYNM, ROPN1B, PDZK1IP1, AHNAK2,

SCGB2A2

Computing nearest neighbor graph

Computing SNN

Warning: The following arguments are not used: ident.1warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan  
van Eck

Number of nodes: 4149  
Number of edges: 134090

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.9438

Number of communities: 18

Elapsed time: 0 seconds

Warning: The following arguments are not used: ident.1warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan  
van Eck

Number of nodes: 4149  
Number of edges: 134090

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.9105

Number of communities: 23

Elapsed time: 0 seconds

Warning: The following arguments are not used: ident.1warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan  
van Eck

Number of nodes: 4149  
Number of edges: 134090

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.8862  
Number of communities: 25  
Elapsed time: 0 seconds  
Warning: The following arguments are not used: ident.1  
Warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan van Eck

Number of nodes: 4149  
Number of edges: 134090

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.8634  
Number of communities: 26  
Elapsed time: 0 seconds

Warning: The following arguments are not used: ident.1  
Warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan van Eck

Number of nodes: 4149  
Number of edges: 134090

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.8421  
Number of communities: 27  
Elapsed time: 0 seconds

Performing log-normalization

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Calculating gene variances

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Calculating feature variances of standardized and clipped values

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Centering and scaling data matrix

|=====| 100%

PC\_1

Positive: COL1A2, COL3A1, PRRX1, COL6A3, COL5A2, BGN, COL6A2, COL6A1, AEBP1, RARRES2  
COL1A1, DCN, LUM, SPARC, FSTL1, SERPINF1, CTGF, PCOLCE, MXRA8, MYL9  
COL5A1, COL12A1, FN1, CTSK, FKBP10, SULF1, CDH11, IGFBP4, POSTN, EMILIN1  
Negative: S100A9, KRT18, CD24, S100P, KRT19, HMGB3, S100A8, KRT17, AQP3, PERP  
SERPINB3, EPCAM, KRT6A, AKR1C2, FABP5, DEFB1, KIAA0101, PITX1, SFN,

TACSTD2

LAD1, DSP, TM4SF1, STMN1, CKS1B, S100A7, TUBA1C, SERPINB4, SLPI, NQO1

PC\_2

Positive: SRGN, TYROBP, FCER1G, HCST, CXCR4, VIM, ALOX5AP, RGS1, CD52, FTH1  
PTPRC, LSP1, LYZ, COTL1, CORO1A, AIF1, CLEC2B, CYTIP, HLA-B, HLA-DPB1  
CCL4, HLA-DPA1, BCL2A1, CCL3, G0S2, DUSP2, LST1, SLC2A3, CCL5, AREG

Negative: KRT18, CD24, AQP3, HMGB3, PERP, KRT19, S100P, EPCAM, TACSTD2, PITX1  
DSP, TM4SF1, FURIN, CD59, LGALS3BP, KRT17, MUC1, AGR2, FDPS, CPS1  
PRSS23, DEFB1, TUBB, RDH10, IGSF8, ATP1B1, PDZK1IP1, LAPTM4B, C8orf4, NMB

PC\_3

Positive: CD7, CCL5, GZMA, GZMB, NKG7, CTSW, CD2, APOBEC3G, TRAC, PRF1  
KLRD1, TRBC2, HOPX, KLRC1, TNFRSF18, LCK, CD69, GNLY, CD247, AC092580.4  
KRT86, ZNF683, KLRC2, TIGIT, CD96, TRBC1, CCL4, CD3D, KLRB1, CD3E

Negative: SOD2, LYZ, C15orf48, G0S2, AIF1, BCL2A1, CXCL8, CD14, LST1, TREM1  
MS4A7, IL1B, VCAN, PLIN2, FTH1, RNASE6, TIMP1, FCGR2A, SPP1, SPI1  
HBEGF, THBD, C1orf162, CTSB, CYBB, RNASE1, CXCL3, CST3, OLR1, FCN1

PC\_4

Positive: MT-ND1, MT-ND4, MT-CO2, MT-ND2, MT-CO3, MT-CYB, MT-ND5, CP, MUC1, CFD  
CD74, SLC16A3, ATP1B1, CPS1, HSP90B1, HLA-C, FGA, CEBPD, RDH10, MSLN  
MT-ND4L, HLA-DRB1, CHML, HLA-DRA, HSPA5, CTSZ, MUC5B, FURIN, AZGP1, HLA-B

Negative: FABP5, SFN, S100A8, S100A9, KRT17, S100A2, KRT6A, SERPINB3, KRT16, TUBB

AKR1B10, TUBA1C, S100A7, RAB38, SERPINB4, KIAA0101, TUBA1B, KRT6B, LAD1,  
MYC  
PTTG1, RRM2, ID1, ZWINT, IRF6, CDK1, LY6D, PCNA, SERPINB5, UBE2T  
PC\_5  
Positive: CCNB1, CDC20, UBE2C, NUSAP1, CKS2, MKI67, CCNB2, CENPF, PLK1, TOP2A  
PRC1, BIRC5, ASPM, AURKA, CKS1B, HMMR, PTTG1, DEPDC1, CENPA, TPX2  
AURKB, DLGAP5, CENPE, KNSTRN, HMGB2, NUF2, CDK1, CENPW, CDKN3, NEK2  
Negative: S100P, C8orf4, FGG, AGR2, SLC34A2, TMC5, FGA, CP, KRT81, KRT19  
AZGP1, ZG16B, MDK, MSLN, MUC5B, MUC5AC, HGD, ATP1B1, LCN2, CXCL17  
HSD17B2, SLPI, ERFFI1, FBXO32, TFF3, RDH10, NDUFA4L2, GPRC5A, ELF3, EGLN3  
Computing nearest neighbor graph  
Computing SNN  
Warning: The following arguments are not used: ident.1warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo waltman and Nees Jan  
van Eck

Number of nodes: 1754  
Number of edges: 54420

Running smart local moving algorithm...  
0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|  
Maximum modularity in 10 random starts: 0.9043  
Number of communities: 9  
Elapsed time: 0 seconds  
Warning: The following arguments are not used: ident.1warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo waltman and Nees Jan  
van Eck

Number of nodes: 1754  
Number of edges: 54420

Running smart local moving algorithm...  
0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|  
Maximum modularity in 10 random starts: 0.8590  
Number of communities: 11  
Elapsed time: 0 seconds  
Warning: The following arguments are not used: ident.1warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo waltman and Nees Jan  
van Eck

Number of nodes: 1754  
Number of edges: 54420

Running smart local moving algorithm...  
0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|  
Maximum modularity in 10 random starts: 0.8256  
Number of communities: 15  
Elapsed time: 0 seconds  
Warning: The following arguments are not used: ident.1warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo waltman and Nees Jan  
van Eck

Number of nodes: 1754  
Number of edges: 54420

Running smart local moving algorithm...  
0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|  
Maximum modularity in 10 random starts: 0.7960  
Number of communities: 16  
Elapsed time: 0 seconds  
Warning: The following arguments are not used: ident.1warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo waltman and Nees Jan  
van Eck

Number of nodes: 1754  
Number of edges: 54420

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.7674

Number of communities: 17

Elapsed time: 0 seconds

Performing log-normalization

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Calculating gene variances

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Calculating feature variances of standardized and clipped values

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Centering and scaling data matrix

|=====| 100%

PC\_1

Positive: VIM, SPARCL1, IGFBP7, A2M, GNG11, PTRF, IGFBP4, TCF4, PECAM1, EMCN  
CAV1, RNASE1, GSN, ECSCR.1, ADGRL4, ESAM, CLEC14A, RAMP2, VAMP5, HSPG2  
SPARC, ID1, AQP1, ENG, CD93, TGFB2, JAM2, ID3, PLVAP, VWF  
Negative: KRT19, GATA3, TACSTD2, AGR2, PIP, CLDN3, SLPI, WFDC2, PHGR1, KRT8  
KCNK6, TFPI2, ATP1B1, GPRC5A, S100P, MUC1, CA12, MYBPC1, AQP3, SDC4  
CRABP2, KRT7, ERBB3, FASN, SCGB1B2P, CHPT1, PKIB, TFF3, HMGA1, CRISP3

PC\_2

Positive: EGFL7, CD74, PECAM1, TM4SF1, RNASE1, ECSCR.1, ADGRL4, RAMP2, EMCN, VWF  
HLA-DRB1, PLVAP, CLEC14A, HLA-DRA, CD93, TSPAN7, CXorf36, CYR1, MMRN2,  
HYAL2  
Negative: RAMP3, PALMD, ETS2, CLDN5, HLA-DPA1, AQP1, ITGA6, GIMAP7, CDH5, ACKR1  
COL1A2, COL1A1, LUM, DCN, COL3A1, COL6A2, COL6A3, SFRP2, C1S, COL6A1  
CTSK, CCDC80, MFAP4, MXRA8, FBLN1, AEBP1, BGN, PCOLCE, ASPN, COL5A2  
MEG3, LOXL1, SERPINF1, RARRES2, COL14A1, C1R, ISLR, LRP1, IGF1, LGALS1

PC\_3

Positive: TACSTD2, EFNA1, KRT19, MYC, KRT7, PRSS23, CLDN3, WFDC2, KRT8, SLPI  
CRABP2, EFHD1, HEBP2, HES4, CEBPD, GPRC5A, CD24, TM4SF1, SH3YL1, CCND1  
AGR2, CRACR2B, MUC1, PIP, SDC4, SLC9A3R2, CRNDE, GATA3, PHGR1, DSP  
Negative: TYROBP, PTPRC, ITGB2, CORO1A, LAPTM5, RGS1, CD53, FCER1G, CD48, AIF1  
CXCR4, DUSP2, CD37, GPR183, CD52, MS4A6A, LST1, CCL4, HCST, ALOX5AP  
FYB, EVI2B, SRGN, PLEK, SPI1, SAMS1, IL1B, C1QB, COTL1, LCPI

PC\_4

Positive: NDUFA4L2, ACTA2, MYH11, NTRK2, PPP1R14A, TPM2, NOTCH3, COX4I2, RERGL, SOD3  
WFDC1, MFGE8, MYL9, PLN, CASQ2, SEPT4, MAP3K7CL, MCAM, TAGLN, PGF  
C2orf40, PHLDA2, TBX2-AS1, RGS5, TBX2, IGFBP5, GJA4, S100A4, CRYAB, MYLK  
Negative: VCAN, CTHRC1, POSTN, SFRP2, LUM, MMP2, FBLN2, COL6A3, IGF1, CILP  
MXRA5, CTSK, MFAP2, MEG3, LOXL1, FBLN1, ADAM12, COL10A1, CDH11, THBS2  
HTRA1, FAP, COL5A2, COL5A1, COL3A1, FSTL1, PRSS23, MRC2, FN1, CXCL14

PC\_5

Positive: KRT15, GABRP, SFRP1, CCL28, MMP7, KRT5, KRT23, RARRES1, AC005152.3, CLDN8  
KIT, CXCL17, PROM1, KRT6B, RP11-817J15.2, CXCL2, TPT1-AS1, KRT17, BBOX1,  
ROPN1

Negative: FOLR1, C2orf82, KRT14, CXADR, SLC34A2, ELF5, KRT16, CXCL3, TTYH1, KLF5  
PRSS23, PHGR1, AGR2, PIP, CRISP3, S100P, ISG15, TFPI2, SCGB1B2P, HOXA9  
IFI6, TFF3, KCNK6, IFI27, PTP4A3, CLGN, CXCL13, AQP3, NDUFA4L2, HOPX  
SCGB2A1, IGFBP7, PSCA, STEAP4, MYBPC1, SOD3, RGS5, PLAC9, PRKAA2, COX4I2

Computing nearest neighbor graph

Computing SNN

Warning: The following arguments are not used: ident.1  
Warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan van Eck

Number of nodes: 4409  
Number of edges: 141560

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%

```
[----|----|----|----|----|----|----|----|----|----|
*****|
Maximum modularity in 10 random starts: 0.9369
Number of communities: 16
Elapsed time: 1 seconds
Warning: The following arguments are not used: ident.1Warning: The following arguments
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan
van Eck
```

Number of nodes: 4409  
Number of edges: 141560

```
Running smart local moving algorithm...
0% 10 20 30 40 50 60 70 80 90 100%
[----|----|----|----|----|----|----|----|----|----|
*****|
```

Maximum modularity in 10 random starts: 0.9032  
Number of communities: 21  
Elapsed time: 1 seconds  
Warning: The following arguments are not used: ident.1Warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan  
van Eck

Number of nodes: 4409  
Number of edges: 141560

```
Running smart local moving algorithm...
0% 10 20 30 40 50 60 70 80 90 100%
[----|----|----|----|----|----|----|----|----|----|
*****|
```

Maximum modularity in 10 random starts: 0.8754  
Number of communities: 23  
Elapsed time: 0 seconds  
Warning: The following arguments are not used: ident.1Warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan  
van Eck

Number of nodes: 4409  
Number of edges: 141560

```
Running smart local moving algorithm...
0% 10 20 30 40 50 60 70 80 90 100%
[----|----|----|----|----|----|----|----|----|----|
*****|
```

Maximum modularity in 10 random starts: 0.8502  
Number of communities: 24  
Elapsed time: 0 seconds  
Warning: The following arguments are not used: ident.1Warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan  
van Eck

Number of nodes: 4409  
Number of edges: 141560

```
Running smart local moving algorithm...
0% 10 20 30 40 50 60 70 80 90 100%
[----|----|----|----|----|----|----|----|----|----|
*****|
```

Maximum modularity in 10 random starts: 0.8281  
Number of communities: 26  
Elapsed time: 0 seconds

```
Performing log-normalization
0% 10 20 30 40 50 60 70 80 90 100%
[----|----|----|----|----|----|----|----|----|----|
*****|
```

```
Calculating gene variances
0% 10 20 30 40 50 60 70 80 90 100%
[----|----|----|----|----|----|----|----|----|----|
*****|
```

```
Calculating feature variances of standardized and clipped values
0% 10 20 30 40 50 60 70 80 90 100%
[----|----|----|----|----|----|----|----|----|----|
```



\*\*\*\*\*|

Centering and scaling data matrix

|=====| 100%

PC\_ 1

Positive: VIM, TMSB4X, GSTP1, IFITM2, ARHGDIB, GSN, BST2, SERPING1, IFITM3, IFI16  
ANXA5, SPARCL1, LGALS3, ACTB, A2M, IGFBP7, CAV1, CALD1, ID3, SPARC  
TIMP1, PTRF, VAMP5, S100A4, MEF2C, TCF4, LDHB, PRKCDP, MYL9, ANXA1

Negative: SLC39A6, DHRS2, TSPAN13, STARD10, CRABP2, SLC9A3R1, ARMT1, AZGP1, COX6C,  
DNAJC12

ELF3, ANKRD30A, MRPS30, BMPR1B, CCND1, AGR2, STC2, GPRC5A, CHPT1, CLDN4  
RP11-53019.1, SDC4, ISOC1, CD24, C1orf64, MAGED2, GJA1, BUB3, RAB11FIP1,

TRH

PC\_ 2

Positive: TYROBP, FCER1G, HLA-DQA1, AIF1, LYZ, IGSF6, MS4A6A, HLA-DQB1, CYBB, HLA-DMB  
CPVL, CTSS, SPI1, ITGB2, LST1, HLA-DPA1, FAM26F, LAPTM5, CD68, HLA-DPB1  
LILRB4, HLA-DRA, HLA-DMA, HLA-DRB5, C1orf162, C1QA, C3AR1, C1QB, FGL2,

C1QC

Negative: CALD1, SPARCL1, IGFBP7, MYL9, TPM1, SOD3, ADIRF, TAGLN, NDUFA4L2, BGN  
MFGE8, SPARC, CAV1, PLAC9, ACTA2, TPM2, PTRF, CPE, LHFP, COL18A1  
MYLK, RGS5, FRZB, TINAGL1, MCAM, MAP1B, SEPT4, TGFB1I1, PGF, PRKCDP

PC\_ 3

Positive: CLEC14A, RAMP2, ADGRL4, EMCN, ECSCR.1, PECAM1, CLDN5, SLC9A3R2, TM4SF1,  
RNASE1

CYYR1, JAM2, CD34, PALMD, NOTCH4, S100A16, SOX17, PCAT19, CDH5, PTPRB  
HYAL2, IGFBP3, EGFL7, MECOM, ENG, RBP7, AQP1, MYCT1, PLPP1, MALL

Negative: NDUFA4L2, TPM2, SOD3, ACTA2, TAGLN, RGS5, CPE, FRZB, TGFB1, SDC2  
TPPP3, MFGE8, SERPINF1, PLAC9, PGF, SMOG2, COX4I2, PCOLCE, MAP3K7CL, MYL9  
COL6A2, CRYAB, BGN, SEPT4, PDGFRB, CRISPLD2, OLFML2B, LGI4, PLN, MYLK

PC\_ 4

Positive: CD69, CD7, CD2, CD3D, RAC2, TRAC, CXCR4, CYTIP, CD52, TRBC1

CD3E, IL7R, CCL5, NKG7, CORO1A, CTSW, CST7, IL2RG, DUSP2, KLRD1  
LTB, LCK, TRBC2, CD27, STK17A, XCL1, PTPRC, CD247, ZFP36L2, CD96

Negative: TUBA1B, GRN, SEPP1, TUBB, PSAP, TMEM176B, FEN1, IFI27, CDK1, CFD  
PCNA, CKS1B, TK1, PLD3, UBE2T, TOP2A, GGCT, FAM111B, PKMYT1, CCND1  
UBE2C, ARL6IP1, CTSL, DHFR, MAD2L1, KIAA0101, RNASEH2A, STRA13, NUSAP1,

BIRC5

PC\_ 5

Positive: CDK1, NUSAP1, TOP2A, UBE2C, MKI67, BIRC5, UBE2T, NUF2, TPX2, TYMS  
AURKB, KIAA0101, TK1, MELK, PKMYT1, CENPM, CDKN3, PBK, CDCA5, SPC25  
PTTG1, RRM2, PRC1, CENPK, FAM111B, MAD2L1, CDCA3, CKAP2L, MXD3, GTSE1

Negative: HIST1H2BD, STC2, MAGED2, HIST1H2AC, CCND1, SEPP1, RP11-53019.1, GJA1,  
TMEM176B, C1QA

TNFSF10, C1QC, CD14, HIST2H2BE, PSAP, LYZ, DNAJC12, AIF1, C1QB, STARD10  
PLD3, FAM84A, CTSL, CLU, PDK4, C1orf64, SDC4, CFD, IGSF6, SLC39A6

Computing nearest neighbor graph

Computing SNN

Warning: The following arguments are not used: ident.1  
Warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo waltman and Nees Jan van Eck

Number of nodes: 3961

Number of edges: 128137

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%

[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.9135

Number of communities: 14

Elapsed time: 1 seconds

Warning: The following arguments are not used: ident.1  
Warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo waltman and Nees Jan van Eck

Number of nodes: 3961

Number of edges: 128137

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%

[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.8659



Number of communities: 19  
Elapsed time: 0 seconds  
warning: The following arguments are not used: ident.1warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo waltman and Nees Jan  
van Eck

Number of nodes: 3961  
Number of edges: 128137

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.8354

Number of communities: 24

Elapsed time: 0 seconds

warning: The following arguments are not used: ident.1warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo waltman and Nees Jan  
van Eck

Number of nodes: 3961  
Number of edges: 128137

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.8119

Number of communities: 28

Elapsed time: 0 seconds

warning: The following arguments are not used: ident.1warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo waltman and Nees Jan  
van Eck

Number of nodes: 3961  
Number of edges: 128137

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.7932

Number of communities: 34

Elapsed time: 0 seconds

Performing log-normalization

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Calculating gene variances

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Calculating feature variances of standardized and clipped values

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Centering and scaling data matrix

|=====| 100%

PC\_1

Positive: CD52, CXCR4, SRGN, CD69, LAPTM5, TRAC, CD37, IL32, TRBC2, NR4A2  
RGS1, RPS19, CD2, CD74, CCL5, TNFAIP3, KLF6, VAMP8, ALOX5AP, HLA-DPA1  
SAMS1, GPR183, BIRC3, CD7, HLA-DRA, LT8, IL7R, RASGEF1B, HLA-DRB5, UCP2  
Negative: COL1A2, LUM, DCN, MEG3, COL3A1, CALD1, CXCL12, COL6A2, AP0D, COL1A1  
IGF1, TIMP1, CTSK, PCOLCE, C1S, COL6A1, LGALS1, SEPP1, ISLR, SPARC  
SRPX, COL6A3, VCAN, SERPINF1, C1R, FSTL1, GSN, TMEM176B, LRP1, ITM2A

PC\_2

Positive: CD52, CXCR4, CD69, SRGN, TRAC, LAPTM5, TRBC2, CD37, CCL5, NR4A2  
IL32, CD2, TNFAIP3, RGS1, CD7, IL7R, SAMS1, CST7, KLRB1, ALOX5AP  
LT8, BIRC3, GPR183, CCL4, TAGAP, GPR65, PRMT9, RGS2, RASGEF1B, RUNX3  
Negative: AZGP1, KRT8, KRT18, KRT19, FXYD3, SMIM22, WFDC2, CLDN4, ANKRD30A, ELF3  
AGR2, AGR3, STC2, S100A14, CLDN7, TFF3, SPINT2, TFF1, TACSTD2, MGST1  
PTHLH, KIAA1324, DSP, ZG16B, MUC1, VTCN1, CDH1, MLPH, MAL2, SPDEF

```

PC_ 3
Positive: TRAC, IL32, TRBC2, CD2, CCL5, CD52, CD7, CD69, IL7R, CXCR4
 KLRB1, CST7, RPS18, RPS4X, TRBC1, MT1X, RPL3, ICOS, TRGC2, MT2A
 TUBA4A, RPL36, AC092580.4, KLRC1, ZNF683, CD8B, GZMA, CD8A, RPS6, AREG
Negative: MS4A6A, FCER1G, TYROBP, MS4A7, C1QA, C1QC, C1QB, CSF1R, LYZ, AIF1
 IL1B, HLA-DRB1, CLEC7A, HLA-DRB5, CCL3L3, HLA-DPA1, HLA-DRA, CD14, CD68,
LST1
 HLA-DMA, MSR1, CCL3, IFI30, CXCL8, HLA-DQB1, P2RY13, HLA-DQA2, CSF2RA,
FCGR2A
PC_ 4
Positive: EMCN, FABP4, ADGRL4, AQP1, ECSCR.1, VWF, PALMD, RAMP2, PLVAP, TSPAN7
 CAV1, CD36, EGFL7, PECAM1, RBP7, CLDN5, ACKR1, CCL14, CRIP2, LMCD1
 RAMP3, NRN1, GNG11, SDPR, ESAM, NOSTRIN, EPAS1, SPARCL1, BCAM, SNCG
Negative: TYROBP, MS4A6A, FCER1G, AIF1, MS4A7, LYZ, TMEM176B, CD68, C1QA, LST1
 C1QC, IL1B, C1QB, CSF1R, CCL3, CRABP2, IGF1, IFI30, CCL3L3, MEG3
 CLEC7A, RNASE6, PLAUR, FTL, IER3, CSF2RA, CTSB, NR4A2, FCGR2A, CAPG
PC_ 5
Positive: AQP1, ADGRL4, RAMP2, PLVAP, ECSCR.1, VWF, EMCN, TSPAN7, EGFL7, PECAM1
 ACKR1, ITM2A, RAMP3, CCL14, NOSTRIN, GIMAP7, CLDN5, PALMD, TM4SF18, PRSS23
 ANKRD30A, RBP7, JAM2, PCAT19, S100A16, CD34, AGR3, PLAT, CXorf36, STC2
Negative: TAGLN, ACTA2, NTRK2, RERGL, PLN, IGFBP5, MYH11, LMOD1, CRYAB, MYL9
 CASQ2, PPP1R14A, NOTCH3, TPM2, SORBS2, TPM1, RGS5, NDRG2, CARMN, MAP3K7CL
 C2orf40, MCAM, MYLK, FHL5, NDUFA4L2, GUCY1A3, SEPT4, COX4I2, PPP1R12B,
MFGE8
Computing nearest neighbor graph
Computing SNN
warning: The following arguments are not used: ident.1warning: The following arguments
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo waltman and Nees Jan
van Eck

Number of nodes: 2131
Number of edges: 73734

Running smart local moving algorithm...
0% 10 20 30 40 50 60 70 80 90 100%
[----|----|----|----|----|----|----|----|----|----|
*****|
Maximum modularity in 10 random starts: 0.9274
Number of communities: 11
Elapsed time: 0 seconds
warning: The following arguments are not used: ident.1warning: The following arguments
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo waltman and Nees Jan
van Eck

Number of nodes: 2131
Number of edges: 73734

Running smart local moving algorithm...
0% 10 20 30 40 50 60 70 80 90 100%
[----|----|----|----|----|----|----|----|----|----|
*****|
Maximum modularity in 10 random starts: 0.8834
Number of communities: 11
Elapsed time: 0 seconds
warning: The following arguments are not used: ident.1warning: The following arguments
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo waltman and Nees Jan
van Eck

Number of nodes: 2131
Number of edges: 73734

Running smart local moving algorithm...
0% 10 20 30 40 50 60 70 80 90 100%
[----|----|----|----|----|----|----|----|----|----|
*****|
Maximum modularity in 10 random starts: 0.8435
Number of communities: 15
Elapsed time: 0 seconds
warning: The following arguments are not used: ident.1warning: The following arguments
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo waltman and Nees Jan
van Eck

```

Number of nodes: 2131  
Number of edges: 73734

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.8108

Number of communities: 17

Elapsed time: 0 seconds

Warning: The following arguments are not used: ident.1  
Warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan van Eck

Number of nodes: 2131  
Number of edges: 73734

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.7840

Number of communities: 18

Elapsed time: 0 seconds

Performing log-normalization

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Calculating gene variances

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Calculating feature variances of standardized and clipped values

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Centering and scaling data matrix

|=====| 100%

PC\_1

Positive: CALD1, IGFBP4, CYR61, SPARC, GSN, SERPING1, SEPP1, C1S, CNN3, COL6A2, RARRES2, PLPP3, MXRA8, CTGF, PTRF, NNMT, ISLR, LUM, COL1A2, COL6A1, DCN, S100A13, COL3A1, TIMP3, CXCL12, CTSK, COL1A1, PPIC, CPE, SFRP2

Negative: CD74, HLA-DPA1, HLA-DPB1, HLA-DRB1, HLA-DRB5, HLA-DQA2, HLA-DQA1, HLA-DQB1, CCL4, HLA-DRA

CCR7, GZMB, HLA-DMA, NCF1, BATF, GZMK, CXCL13, ZNF683, TNFRSF18, GPR183, CCL4L2, CTSS, RP11-291B21.2, TNFRSF9, CCL3, CD79A, KRT86, MIR155HG,

Clorf162, PTTG1

PC\_2

Positive: CD24, EPCAM, CLDN3, MGST1, CLDN4, TPD52L1, DSC2, PERP, KRT8, KRT7, PLPP2, PRSS8, KRT18, KRT19, ELF3, RAB25, CRABP1, DSP, FKBP4, TFAP2A, ACTR3B, GABRP, ELF5, UCHL1, TTYH1, MARCKSL1, CRNDE, CRACR2B, PVRL4, STAP2

Negative: DCN, LUM, COL1A2, COL3A1, CXCL12, SERPING1, COL1A1, SERPINF1, CTSK, SFRP2, OLFML3, RARRES2, APOD, COL6A2, MFAP4, PCOLCE, TCF4, IGF1, MXRA8, ISLR, COL6A3, COL6A1, CPE, CCDC80, MMP2, IFI27, CD248, SRPX, AEBP1, MEG3

PC\_3

Positive: TYROBP, FCER1G, SPI1, IGSF6, AIF1, CD68, C1QA, C1QB, C1QC, MS4A7, GRN, TREM2, FCGR2A, MS4A6A, FPR1, LYZ, ADAP2, MNDA, LILRB4, PILRA, FCGR3A, CXCL16, SERPINA1, HCK, CSF1R, FCGR1A, MSR1, CST3, CYBB, CPVL, RPS12, DCN, COL1A2, LUM, COL3A1, COL1A1, CXCL13, LDHB, SFRP2, MFAP4, CTSK, COL6A3, APOD, RARRES2, COL6A2, GZMK, CCR7, MXRA8, FBLN5, PCOLCE, ISLR, COL6A1, C1S, SPON2, COL5A2, FXDY1, FBLN1, CPE, MEG3, SRPX

PC\_4

Positive: APOE, UCHL1, CENPW, LUM, OLFML3, CYP1B1, MFAP2, SFRP2, DCN, COL3A1, CTSK, FRZB, COL1A1, COL1A2, C1S, LGALS1, MFAP4, CKS1B, FBLN1, FTL, TUBB, IGF1, MDK, SERPINF1, PLTP, CRABP1, COL6A3, RBP1, STMN1, APOC1

Negative: ADGRL4, EMCN, PLVAP, VWF, ESAM, BCAM, SDPR, CLEC14A, RAMP2, RBP7, AQP1, EGFL7, CXorf36, PALMD, EPAS1, RAMP3, FLT1, CRIP2, SOX17, NOSTRIN, PTPRB, RNASE1, MMRN2, CDH5, CLDN5, TMEM88, BTNL9, APOLD1, ROBO4, ADGRF5

PC\_5

Positive: CLDN7, AZGP1, FXDY3, CXCL2, WFDC2, TACSTD2, MLPH, TFF3, FAM3B, AREG, ZG16B, AGR2, ANKRD30A, AGR3, MUC1, SLPI, CA12, SERPINA3.1, TFF1, S100A1, KRT18, PRSS22, CCL28, PDZK1IP1, PPP1R1B, MAFF, LTF, PIGR, TNFRSF12A, DCDC2

Negative: ADGRL4, PLVAP, EMCN, VWF, ESAM, CLEC14A, AQP1, EGFL7, RAMP2, SDPR  
CXorf36, RAMP3, FLT1, GNG11, APOLD1, RNASE1, STMN1, CD34, SOX17, PTPRB  
RBP7, MMRN2, CYR1, CDH5, PECAM1, BTNL9, CD93, UBE2C, ADGRF5, ROBO4

Computing nearest neighbor graph

Computing SNN

Warning: The following arguments are not used: ident.1warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan  
van Eck

Number of nodes: 7986  
Number of edges: 290437

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.9411

Number of communities: 16

Elapsed time: 2 seconds

Warning: The following arguments are not used: ident.1warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan  
van Eck

Number of nodes: 7986  
Number of edges: 290437

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.9072

Number of communities: 22

Elapsed time: 2 seconds

Warning: The following arguments are not used: ident.1warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan  
van Eck

Number of nodes: 7986  
Number of edges: 290437

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.8794

Number of communities: 24

Elapsed time: 2 seconds

Warning: The following arguments are not used: ident.1warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan  
van Eck

Number of nodes: 7986  
Number of edges: 290437

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.8559

Number of communities: 30

Elapsed time: 2 seconds

Warning: The following arguments are not used: ident.1warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan  
van Eck

Number of nodes: 7986  
Number of edges: 290437

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.8348

Number of communities: 33

Elapsed time: 2 seconds

Performing log-normalization

0% 10 20 30 40 50 60 70 80 90 100%

[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

\*\*\*\*\*|

Calculating gene variances

0% 10 20 30 40 50 60 70 80 90 100%

[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

\*\*\*\*\*|

Calculating feature variances of standardized and clipped values

0% 10 20 30 40 50 60 70 80 90 100%

[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

\*\*\*\*\*|

Centering and scaling data matrix

|=====| 100%

PC\_ 1

Positive: SPARC, FN1, COL3A1, COL1A2, SERPING1, BGN, LUM, DCN, AEBP1, SERPINF1  
TPM2, THY1, TMEM176A, COL1A1, RARRES2, VCAN, COL5A2, TMEM176B, IGFBP7,

CTSK

Negative: C1S, TAGLN, SFRP2, MMP2, CTHRC1, COL6A3, COL6A2, POSTN, TIMP2, MXRA8

MUCL1, AZGP1, CKB, SLPI, HEBP2, TFF3, TMSB15A, SFN, TM7SF2, FDPS  
BAMBI, LINC01285, FABP7, MESP1, LINC01133, CTAG2, CLCA2, NUDT8, SCD, IMPA2  
TK1, ZG16B, RHOV, PDZK1P1, LGALS12, HIST1H1C, APOD, EFNA1, HMGC1S, GMNN

PC\_ 2

Positive: COL3A1, CALD1, COL1A1, COL1A2, SERPINH1, AEBP1, LUM, CTHRC1, BGN, DCN

THY1, COL5A2, SFRP2, TAGLN, COL6A2, MYL9, TPM2, COL6A1, COL6A3, AZGP1  
RARRES2, TNFRSF12A, MUCL1, CCDC80, COL5A1, POSTN, MDK, MXRA8, THBS2, MFAP2  
Negative: CD74, C1QA, FCER1G, C1QB, C1QC, TYROBP, LYZ, LILRB4, AIF1, HLA-DQA1

HLA-DPA1, IGSF6, HLA-DRB5, FCGR1A, HLA-DQA2, CYBB, FCGR3A, CD14, HLA-DQB1,

HLA-DRB1

APOC1, MS4A6A, SPI1, HLA-DPB1, HLA-DRA, RASSF4, CTSS, SRGN, CD68, FCGR2A

PC\_ 3

Positive: IGHG1, MZB1, IGHG4, CD79A, IGKC, FKBP11, DERL3, IGKV3-15, ITM2C, IGKV1-9

IGHKV3-11, IGHKV3-20, JCHAIN, IGKV1-5, IGLL5, IGKV4-1, JSRP1, IGKV1-27,  
IGHKV1-12, IGKV1-8  
PIM2, CD27, IGKV3D-11, IGLV3-1, CYBA, IGKV1-17, IGKV1D-39, IGHG3, TNFRSF17,

ZBP1

Negative: AZGP1, SLPI, MUCL1, CKB, HEBP2, TFF3, CAPG, SFN, TUBA1B, S100A9

EGLN3, SCD, TK1, FDPS, TNFSF10, CTSD, HSPB1, HES4, CCND1, CTSZ  
APOE, TMSB15A, C1QC, CST3, PDZK1P1, SERPINA1, C1QA, C1QB, LINC01133,

IMPA2

PC\_ 4

Positive: CD3E, CORO1A, CD52, IL32, CD3D, CD2, S100A4, CD7, LCK, RAC2

HMGB2, COTL1, CCL5, LAT, ARHGDIB, MKI67, GZMA, FYB, CST7, CD3G  
NKG7, PTPRC, PTTG1, IL2RG, UBE2C, TRBC2, CENPF, CD8A, NUSAP1, CXCL13

Negative: FTL, IGHG4, IGHG1, DERL3, MZB1, IGKC, PSAP, CD79A, FKBP11, JSRP1  
JCHAIN, IGLL5, GRN, ITM2C, IGKV1-12, IGKV1-27, IGKV1D-39, IGHG3, RP11-  
160E2.6, IGKV1-17

TNFRSF17, CD59, IGKV1-8, IGKV1-39, RP11-16E12.2, IGKV1-16, LMTK3, APOE,  
IGHKV1D-8, IGKV1-5

PC\_ 5

Positive: CD3E, CD52, CD7, IL32, CD2, CD3D, LTB, CST7, LCK, S100A4

RARRES3, CCL5, LAT, S100A6, CORO1A, GZMA, CD3G, FYB, ARHGDIB, IFITM2  
TRBC2, NKG7, IFITM1, COTL1, SPOCK2, CD69, KLRB1, TNFRSF18, HCST, ALOX5AP

Negative: UBE2C, MKI67, NUSAP1, TPX2, CENPF, CDK1, RRM2, BIRC5, PRC1, PLK1  
CDC20, CCNB2, CENPA, CDCA8, KIF23, KIFC1, MZB1, ASPM, IGHG4, DERL3  
HIST1H4C, IGHG1, CENPW, TYMS, NUF2, ZWINT, DLGAP5, IGKC, GTSE1, TOP2A

Computing nearest neighbor graph

Computing SNN

Warning: The following arguments are not used: ident.1  
warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan van Eck

Number of nodes: 7023

Number of edges: 233391

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%

[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.9324  
Number of communities: 17  
Elapsed time: 2 seconds  
warning: The following arguments are not used: ident.1warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan  
van Eck

Number of nodes: 7023  
Number of edges: 233391

Running smart local moving algorithm...  
0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.9014  
Number of communities: 20  
Elapsed time: 1 seconds  
warning: The following arguments are not used: ident.1warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan  
van Eck

Number of nodes: 7023  
Number of edges: 233391

Running smart local moving algorithm...  
0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.8778  
Number of communities: 23  
Elapsed time: 1 seconds  
warning: The following arguments are not used: ident.1warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan  
van Eck

Number of nodes: 7023  
Number of edges: 233391

Running smart local moving algorithm...  
0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.8579  
Number of communities: 28  
Elapsed time: 1 seconds  
warning: The following arguments are not used: ident.1warning: The following arguments  
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan  
van Eck

Number of nodes: 7023  
Number of edges: 233391

Running smart local moving algorithm...  
0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.8411  
Number of communities: 34  
Elapsed time: 1 seconds

Performing log-normalization

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Calculating gene variances

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Calculating feature variances of standardized and clipped values

0% 10 20 30 40 50 60 70 80 90 100%  
[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
\*\*\*\*\*|

Centering and scaling data matrix

```

|=====| 100%
PC_ 1
Positive: KRT18, CD24, KRT7, SPINT2, KRT8, FXYD3, NUPR1, MGST1, TACSTD2, CD9
 CALML5, EPCAM, PDLIM3, TSC22D1, TM7SF2, SCGB1B2P, HSPB1, ADAM15, GGCT,
 CLDN4
Negative: NFIB, LMTK3, TM4SF1, SEPP1, MAL2, DBI, TFAP2B, PLPP2, NFIX, ERBB2
 VIM, CD74, LGALS1, BIRC3, HLA-DPB1, CCL4, NKG7, HLA-DRB1, HLA-DPA1, TYROBP
 HLA-DRA, FCER1G, CTSS, GZMB, GNLY, KLRD1, GZMH, ISG15, HLA-DQA1, TRDC
 FCGR3A, TIMP1, CCL4L2, FGFBP2, PLEK, XCL2, RARRES3, HLA-DQB1, AP1S2, MT2A

PC_ 2
Positive: SCGB2B2, MUCL1, SCGB1B2P, ACADM, HPD, DBI, AZGP1, EBP, PHGDH, SLPI
 MGST1, CKS2, NUDT8, TM7SF2, FXYD3, FGG, HMGCS2, GGCT, PAFAH1B3, ISOC1
 SPINK8, CENPM, IDH2, CDK1, CD24, SPINT2, KRT7, FOLR1, CALML5, HMGA1
Negative: COL1A2, COL3A1, SPARC, COL1A1, LUM, SFRP2, C1S, COL6A3, COL6A2, BGN
 AEBP1, DCN, RARRES2, SERPING1, PRRX1, FN1, COL6A1, FSTL1, COL5A2, C1R
 CTHRC1, CDH11, CTSK, SERPINF1, TIMP3, CCDC80, SPARCL1, PRKCDBP, MMP14,

CXCL12
PC_ 3
Positive: COL1A2, COL3A1, LUM, SFRP2, COL1A1, AEBP1, BGN, COL6A3, C1S, PRRX1
 COL5A2, CTHRC1, DCN, NKG7, CDH11, COL6A2, RARRES2, FSTL1, SPARC, NBL1
 C1R, TIMP3, CCDC80, COL12A1, PCOLCE, MGP, SMOC2, POSTN, THY1, COL6A1
Negative: IL1B, AIF1, FCN1, LYZ, PLAUR, S100A9, LST1, SPI1, G0S2, S100A8
 CST3, CXCL8, SERPINA1, C5AR1, CD14, CD68, RP11-1143G9.4, CXCL2, MNDA,

LGALS2
 HBEGF, CTSS, SOD2, EREG, IFI30, IER3, MS4A7, S100A12, HCK, MS4A6A

PC_ 4
Positive: MT-CO1, MT-ND4, MT-CYB, MT-CO3, MT-CO2, MT-ATP6, MT-ND2, MT-ND3, MT-ND1,
 INHBB
Negative: NEAT1, AARD, PCAT1, MT-ND5, KRT15, PTPRF, ITGB6, SREBF1, FAT1, GPRC5A
 TRPS1, ENAH, EMP1, FBXO32, ARFGF3, RND3, FLNB, SOX9, KIAA1522, ZFP36L1
 CDK1, ZWINT, UBE2C, NUSAP1, BIRC5, UBE2T, KIAA0101, PHGDH, MUCL1, CENPW
 SCGB2B2, CCNB2, TK1, BLVRB, CDC20, CKS1B, RAD51AP1, MAD2L1, NUF2, STMN1
 RRM2, CCNB1, SPC25, AURKB, ACADM, TPX2, FAM111B, GGCT, HPD, TMSB15A

PC_ 5
Positive: HMGCS2, SEPP1, ALDH3B2, MUCL1, S100P, CXCL17, SERHL2, PIP, KYNU, CYB5A
 FGG, AZGP1, MGST1, SULT2B1, TM7SF2, CALML5, NUPR1, KRT7, PERP, BLVRB
 DKK1, XBP1, PKIB, PRRT3-AS1, LGALS3, RP11-462G2.1, FBP2, HOXA7, DIO1,

ALDH2
Negative: NUSAP1, TOP2A, KIAA0101, UBE2C, BIRC5, ZWINT, MKI67, TPX2, CDK1, RRM2
 AURKB, STMN1, NT5DC2, AARD, NUF2, CDKN3, PLK1, RAD51AP1, CDC20, GTSE1
 SREBF1, SGOL1, NEK2, LY6D, HMMR, CCNB2, HMGB2, PCAT1, CENPA, TYMS

Computing nearest neighbor graph
Computing SNN
Warning: The following arguments are not used: ident.1warning: The following arguments
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan
van Eck

Number of nodes: 2447
Number of edges: 93937

Running smart local moving algorithm...
0% 10 20 30 40 50 60 70 80 90 100%
[----|----|----|----|----|----|----|----|----|----|
*****|
Maximum modularity in 10 random starts: 0.9085
Number of communities: 12
Elapsed time: 0 seconds
Warning: The following arguments are not used: ident.1warning: The following arguments
are not used: ident.1Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan
van Eck

Number of nodes: 2447
Number of edges: 93937

Running smart local moving algorithm...
0% 10 20 30 40 50 60 70 80 90 100%
[----|----|----|----|----|----|----|----|----|----|
*****|
Maximum modularity in 10 random starts: 0.8524
Number of communities: 13
Elapsed time: 0 seconds

```



Warning: The following arguments are not used: ident.1  
Warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan van Eck

Number of nodes: 2447  
Number of edges: 93937

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.8077  
Number of communities: 15  
Elapsed time: 0 seconds

Warning: The following arguments are not used: ident.1  
Warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan van Eck

Number of nodes: 2447  
Number of edges: 93937

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.7693  
Number of communities: 18  
Elapsed time: 0 seconds

Warning: The following arguments are not used: ident.1  
Warning: The following arguments are not used: ident.1  
Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan van Eck

Number of nodes: 2447  
Number of edges: 93937

Running smart local moving algorithm...

0% 10 20 30 40 50 60 70 80 90 100%  
[----|----|----|----|----|----|----|----|----|----|  
\*\*\*\*\*|

Maximum modularity in 10 random starts: 0.7367  
Number of communities: 19  
Elapsed time: 0 seconds

\$CID3586  
An object of class Seurat  
29733 features across 6178 samples within 1 assay  
Active assay: RNA (29733 features, 2000 variable features)  
1 dimensional reduction calculated: pca

\$CID3838  
An object of class Seurat  
29733 features across 2353 samples within 1 assay  
Active assay: RNA (29733 features, 2000 variable features)  
1 dimensional reduction calculated: pca

\$CID3921  
An object of class Seurat  
29733 features across 3024 samples within 1 assay  
Active assay: RNA (29733 features, 2000 variable features)  
1 dimensional reduction calculated: pca

\$CID3941  
An object of class Seurat  
29733 features across 631 samples within 1 assay  
Active assay: RNA (29733 features, 2000 variable features)  
1 dimensional reduction calculated: pca

\$CID3946  
An object of class Seurat  
29733 features across 774 samples within 1 assay  
Active assay: RNA (29733 features, 2000 variable features)  
1 dimensional reduction calculated: pca



\$CID3948  
An object of class Seurat  
29733 features across 2327 samples within 1 assay  
Active assay: RNA (29733 features, 2000 variable features)  
1 dimensional reduction calculated: pca

\$CID3963  
An object of class Seurat  
29733 features across 3527 samples within 1 assay  
Active assay: RNA (29733 features, 2000 variable features)  
1 dimensional reduction calculated: pca

\$CID4040  
An object of class Seurat  
29733 features across 2531 samples within 1 assay  
Active assay: RNA (29733 features, 2000 variable features)  
1 dimensional reduction calculated: pca

\$CID4066  
An object of class Seurat  
29733 features across 5309 samples within 1 assay  
Active assay: RNA (29733 features, 2000 variable features)  
1 dimensional reduction calculated: pca

\$CID4067  
An object of class Seurat  
29733 features across 3764 samples within 1 assay  
Active assay: RNA (29733 features, 2000 variable features)  
1 dimensional reduction calculated: pca

\$CID4290A  
An object of class Seurat  
29733 features across 5789 samples within 1 assay  
Active assay: RNA (29733 features, 2000 variable features)  
1 dimensional reduction calculated: pca

\$CID4398  
An object of class Seurat  
29733 features across 4451 samples within 1 assay  
Active assay: RNA (29733 features, 2000 variable features)  
1 dimensional reduction calculated: pca

\$CID4461  
An object of class Seurat  
29733 features across 631 samples within 1 assay  
Active assay: RNA (29733 features, 2000 variable features)  
1 dimensional reduction calculated: pca

\$CID4463  
An object of class Seurat  
29733 features across 1138 samples within 1 assay  
Active assay: RNA (29733 features, 2000 variable features)  
1 dimensional reduction calculated: pca

\$CID4465  
An object of class Seurat  
29733 features across 1564 samples within 1 assay  
Active assay: RNA (29733 features, 2000 variable features)  
1 dimensional reduction calculated: pca

\$CID4471  
An object of class Seurat  
29733 features across 8609 samples within 1 assay  
Active assay: RNA (29733 features, 2000 variable features)  
1 dimensional reduction calculated: pca

\$CID4495  
An object of class Seurat  
29733 features across 7985 samples within 1 assay  
Active assay: RNA (29733 features, 2000 variable features)  
1 dimensional reduction calculated: pca

```

$CID4513
An object of class Seurat
29733 features across 5619 samples within 1 assay
Active assay: RNA (29733 features, 2000 variable features)
 1 dimensional reduction calculated: pca

$CID4515
An object of class Seurat
29733 features across 4149 samples within 1 assay
Active assay: RNA (29733 features, 2000 variable features)
 1 dimensional reduction calculated: pca

$CID4523
An object of class Seurat
29733 features across 1754 samples within 1 assay
Active assay: RNA (29733 features, 2000 variable features)
 1 dimensional reduction calculated: pca

$CID4530N
An object of class Seurat
29733 features across 4409 samples within 1 assay
Active assay: RNA (29733 features, 2000 variable features)
 1 dimensional reduction calculated: pca

$CID4535
An object of class Seurat
29733 features across 3961 samples within 1 assay
Active assay: RNA (29733 features, 2000 variable features)
 1 dimensional reduction calculated: pca

$CID44041
An object of class Seurat
29733 features across 2131 samples within 1 assay
Active assay: RNA (29733 features, 2000 variable features)
 1 dimensional reduction calculated: pca

$CID44971
An object of class Seurat
29733 features across 7986 samples within 1 assay
Active assay: RNA (29733 features, 2000 variable features)
 1 dimensional reduction calculated: pca

$CID44991
An object of class Seurat
29733 features across 7023 samples within 1 assay
Active assay: RNA (29733 features, 2000 variable features)
 1 dimensional reduction calculated: pca

$CID45171
An object of class Seurat
29733 features across 2447 samples within 1 assay
Active assay: RNA (29733 features, 2000 variable features)
 1 dimensional reduction calculated: pca

```

## Identify all DEGs

```

Initialize an empty list to store the differentially expressed genes (DEGs)
for each patient at different resolutions
patient_DEGs <- list()

Loop through each patient
for (patient_id in patient_ids) {
 # Get the Seurat object for the patient
 seurat_obj <- seurat_objects[[patient_id]]

```

```

Initialize an empty list to store the DEGs for each resolution
resolution_DEGs <- list()

Loop through each resolution
for (res in resolutions) {
 # Update the active identity to the one corresponding to the current resolution
 Idents(seurat_obj) <- paste0("RNA_snn_res.", res)

 # Find the top 200 differentially expressed genes for each cluster
 DEGs <- FindAllMarkers(seurat_obj, only.pos = TRUE, min.pct = 0.25, logfc.threshold = 0.25, test.use = "wilcox", max.cells.per.ident = Inf, min.cells.group = 5, max.features = 200)

 # Add the DEGs to the list
 resolution_DEGs[[as.character(res)]] <- DEGs
}

Add the DEGs at different resolutions to the list
patient_DEGs[[patient_id]] <- resolution_DEGs
}

```

## Check data structure

```
#str(patient_DEGs)
```

## Filter to preserve only top 200 DEGs

```

Initialize an empty list to store the differentially expressed genes (DEGs) for each patient at different resolutions
patient_DEGs_top200 <- list()

Loop through each patient
for (patient_id in patient_ids) {
 # Get the DEGs for the patient at different resolutions
 patient_res_DEGs <- patient_DEGs[[patient_id]]

 # Initialize an empty list to store the top 200 DEGs for each resolution
 resolution_DEGs_top200 <- list()

 # Loop through each resolution
 for (res in names(patient_res_DEGs)) {
 # Get the DEGs for the current resolution
 res_DEGs <- patient_res_DEGs[[res]]

 # Initialize an empty list to store the top 200 DEGs for each cluster
 cluster_DEGs_top200 <- list()
 }
}

```

```

Get unique cluster IDs
unique_clusters <- unique(res_DEGs$cluster)

Loop through each cluster
for (cluster_id in unique_clusters) {
 # Filter the DEGs for the current cluster
 cluster_DEGs <- res_DEGs[res_DEGs$cluster == cluster_id,]

 # Get the top 200 DEGs for the current cluster
 top200_DEGs <- head(cluster_DEGs, n = min(200, nrow(cluster_DEGs)))

 # Add the top 200 DEGs for the current cluster to the list
 cluster_DEGs_top200[[cluster_id]] <- top200_DEGs
}

Add the top 200 DEGs for each cluster at the current resolution to the list
resolution_DEGs_top200[[res]] <- cluster_DEGs_top200
}

Add the top 200 DEGs at different resolutions for the current patient to the list
patient_DEGs_top200[[patient_id]] <- resolution_DEGs_top200
}

```

## Check the result

```
str(patient_DEGs_top200)
```

## Filter to keep n.gene>5 and n.cell>5

## Check how to find cell number

```

Initialize an empty list to store the filtered DEGs for each patient at different resolutions
patient_DEGs_filtered <- list()

Loop through each patient
for (patient_id in patient_ids) {
 cat("Patient:", patient_id, "\n")

 # Get the top 200 DEGs for the patient at different resolutions
 patient_res_DEGs_top200 <- patient_DEGs_top200[[patient_id]]

 # Get the metadata of the Seurat object for the current patient
 metadata <- seurat_objects[[patient_id]]@meta.data
}

```

```

Initialize an empty list to store the filtered DEGs for each resolution
resolution_DEGs_filtered <- list()

Loop through each resolution
for (res in names(patient_res_DEGs_top200)) {
 cat(" Resolution:", res, "\n")

 # Get the top 200 DEGs for the current resolution
 res_cluster_DEGs_top200 <- patient_res_DEGs_top200[[res]]

 # Get the cluster column name for the current resolution
 cluster_col_name <- paste0("RNA_snn_res.", res)

 # Calculate the number of cells in each cluster at the current resolution
 cluster_counts <- table(metadata[[cluster_col_name]])
 cat(" Cluster cell counts:", cluster_counts, "\n")

 # Initialize an empty list to store the filtered DEGs for each cluster
 cluster_DEGs_filtered <- list()

 # Loop through each cluster
 for (cluster_id in names(res_cluster_DEGs_top200)) {
 # Get the top 200 DEGs for the current cluster
 cluster_top200_DEGs <- res_cluster_DEGs_top200[[cluster_id]]

 # Get the number of cells in the current cluster
 cluster_cell_count <- cluster_counts[[cluster_id]]

 # Check if the gene set contains more than 5 genes and originates from
a cluster with more than 5 cells
 if (nrow(cluster_top200_DEGs) > 5 && cluster_cell_count > 5) {
 # Add the filtered DEGs for the current cluster to the list
 cluster_DEGs_filtered[[cluster_id]] <- cluster_top200_DEGs
 }
 }

 # Add the filtered DEGs for each cluster at the current resolution to the
list
 resolution_DEGs_filtered[[res]] <- cluster_DEGs_filtered
 cat(" Number of filtered clusters:", length(cluster_DEGs_filtered), "\n")
}

Add the filtered DEGs at different resolutions for the current patient to
the list
patient_DEGs_filtered[[patient_id]] <- resolution_DEGs_filtered
}

```

## Compare the filtered result with the original result to ensure the filter process is okay

```
Count the number of clusters in patient_DEGs_filtered
total_clusters_filtered <- sum(sapply(patient_DEGs_filtered, function(x) sum(
sapply(x, length))))

Count the number of clusters in patient_DEGs_top200
total_clusters_top200 <- sum(sapply(patient_DEGs_top200, function(x) sum(sapp
ly(x, length))))

cat("Total number of clusters in patient_DEGs_filtered:", total_clusters_filt
ered, "\n")
cat("Total number of clusters in patient_DEGs_top200:", total_clusters_top200
, "\n")
```

## Remove redundancy within one sample according to jaccard index > 0.75

```
Function to compute the Jaccard index
jaccard <- function(set1, set2) {
 intersect_size <- length(intersect(set1, set2))
 union_size <- length(union(set1, set2))
 return(intersect_size / union_size)
}

Loop through each patient
for (patient_id in patient_ids) {
 patient_res_DEGs_filtered <- patient_DEGs_filtered[[patient_id]]

 # Loop through each resolution
 for (res in names(patient_res_DEGs_filtered)) {
 res_cluster_DEGs_filtered <- patient_res_DEGs_filtered[[res]]

 # Calculate Jaccard index for all pairs of gene sets
 jaccard_values <- matrix(0, nrow = length(res_cluster_DEGs_filtered), nco
l = length(res_cluster_DEGs_filtered))
 for (i in 1:(length(res_cluster_DEGs_filtered) - 1)) {
 for (j in (i + 1):length(res_cluster_DEGs_filtered)) {
 set1 <- rownames(res_cluster_DEGs_filtered[[i]])
 set2 <- rownames(res_cluster_DEGs_filtered[[j]])
 jaccard_values[i, j] <- jaccard(set1, set2)
 }
 }

 cat("Number of gene set pairs with Jaccard index greater than 0.75 in pat
ient", patient_id, "resolution", res, ":", sum(jaccard_values > 0.75), "\n")
 }
}
```

```

 # Find pairs with Jaccard index greater than 0.75 and remove the one with
 # fewer genes
 to_remove <- c()
 for (i in 1:(length(res_cluster_DEGs_filtered) - 1)) {
 for (j in (i + 1):length(res_cluster_DEGs_filtered)) {
 if (jaccard_values[i, j] > 0.75) {
 if (length(rownames(res_cluster_DEGs_filtered[[i]])) < length(rowna
mes(res_cluster_DEGs_filtered[[j]]))) {
 to_remove <- c(to_remove, i)
 } else {
 to_remove <- c(to_remove, j)
 }
 }
 }
 }

 cat("Number of gene sets removed in patient", patient_id, "resolution", r
es, ":", length(to_remove), "\n")

 # Remove the gene sets identified above if to_remove is not empty
 if (length(to_remove) > 0) {
 res_cluster_DEGs_filtered <- res_cluster_DEGs_filtered[-to_remove]
 }

 # Update patient_DEGs_filtered
 patient_res_DEGs_filtered[[res]] <- res_cluster_DEGs_filtered
 }

 # Update patient_DEGs_filtered
 patient_DEGs_filtered[[patient_id]] <- patient_res_DEGs_filtered
}

```

## Identify gene modules

```

library(cola)

Combine all gene signatures from patient_DEGs_filtered
all_gene_signatures <- list()
for (patient_id in patient_ids) {
 for (res in names(patient_DEGs_filtered[[patient_id]])) {
 all_gene_signatures <- c(all_gene_signatures, patient_DEGs_filtered[[pati
ent_id]][[res]])
 }
}

Calculate Jaccard similarity matrix
jaccard_similarity_matrix <- matrix(0, nrow = length(all_gene_signatures), nc
ol = length(all_gene_signatures))
for (i in 1:(length(all_gene_signatures) - 1)) {

```

```

for (j in (i + 1):length(all_gene_signatures)) {
 set1 <- rownames(all_gene_signatures[[i]])
 set2 <- rownames(all_gene_signatures[[j]])
 jaccard_similarity_matrix[i, j] <- jaccard(set1, set2)
 jaccard_similarity_matrix[j, i] <- jaccard_similarity_matrix[i, j]
}
}

```

## Find the optimal K value based on the elbow method

```

library(cola)

r1 = run_all_consensus_partition_methods(jaccard_similarity_matrix, top_value
_method = c("SD", "MAD"), partition_method = c("skmeans", "kmeans"), max_k = 1
0)

cola_report(r1, output_dir = "C:/yc/cb_project/scRNASeq_analysis/")

```

## The code below use optimized parameters as found in the cola\_report for consensus clustering

```

Perform consensus clustering using skmeans from cola package

set.seed(42) # Set seed for reproducibility

k <- 10 # Number of gene modules

consensus_clustering <- consensus_partition(jaccard_similarity_matrix, partit
ion_method = "skmeans", top_value_method = "SD", max_k = k)

```

## Find the 10 gene modules

```

library(dplyr)

Get the class labels for each gene signature
class_labels <- consensus_clustering@object_list[["10"]][["class_df"]][["clas
s"]]

Assign class labels to each gene signature in all_gene_signatures
labeled_gene_signatures <- lapply(seq_along(all_gene_signatures), function(i)
{
 gene_signature <- all_gene_signatures[[i]]
 gene_signature$module <- class_labels[i]
 return(gene_signature)
})

Combine all labeled gene signatures into one data frame
combined_gene_signatures <- do.call(rbind, labeled_gene_signatures)

```



```
Identify the top 200 most commonly expressed genes for each clustered gene module
```

```
top_200_genes_per_module <- combined_gene_signatures %>%
 group_by(module, gene) %>%
 summarise(count = n()) %>%
 arrange(module, desc(count)) %>%
 group_by(module) %>%
 slice_max(count, n = 200)
```

```
Split the top 200 genes per module into a list of data frames
```

```
top_200_genes_list <- split(top_200_genes_per_module, top_200_genes_per_module$module)
```

## Calculate gene module scores based on the module above and AUCell

```
library(Matrix)
library(AUCell)
```

```
patient_ids <- c("CID3586", "CID3838", "CID3921", "CID3941", "CID3946", "CID3948", "CID3963", "CID4040", "CID4066", "CID4067", "CID4290A", "CID4398", "CID4461", "CID4463", "CID4465", "CID4471", "CID4495", "CID4513", "CID4515", "CID4523", "CID4530N", "CID4535", "CID44041", "CID44971", "CID44991", "CID45171")
```

```
aucell_scores_all_patients <- list()
```

```
for (i in 1:length(patient_ids)) {
 patient_id <- patient_ids[i]
 cat("Dealing with", i, "of", length(patient_ids), "patients:", patient_id,
 "\n")

 count_matrix_barcode_path <- paste0("./GSE176078_RAW/", patient_id, "/count_matrix_barcode.tsv")
 count_matrix_genes_path <- paste0("./GSE176078_RAW/", patient_id, "/count_matrix_genes.tsv")
 count_matrix_sparse_path <- paste0("./GSE176078_RAW/", patient_id, "/count_matrix_sparse.mtx")

 count_matrix <- readMM(file = count_matrix_sparse_path)
 barcodes <- read.delim(count_matrix_barcode_path, header = FALSE, col.names = c("barcode"))
 genes <- read.delim(count_matrix_genes_path, header = FALSE, col.names = c("gene"))

 colnames(count_matrix) <- barcodes$barcode
 rownames(count_matrix) <- genes$gene

 exprMatrix <- as.matrix(count_matrix) # Convert the dgTMatrix to a regular matrix
```

```

Calculate enrichment scores for the top 200 genes of each module
aucell_scores_list <- list()
for (j in 1:length(top_200_genes_list)) {
 geneSet <- top_200_genes_list[[j]]$gene
 aucell_scores <- AUCell_run(exprMatrix, list(geneSet=geneSet), aucMaxRank
=nrow(exprMatrix)*0.05)
 aucell_scores_list[[paste0("GM", j)]] <- aucell_scores

 # Calculate percentage of cells processed
 percentage_processed <- (j / length(top_200_genes_list)) * 100
 cat("Processed", round(percentage_processed, 2), "% cells of patient", pa
tient_id, "\n")
}

aucell_scores_all_patients[[patient_id]] <- aucell_scores_list
}

Print the list of AUCell scores for each patient
aucell_scores_all_patients

```

## Assign a gene module to each cell based on the highest AUCell score

```

library(SummarizedExperiment)

assign_gene_module <- function(patient_id) {
 cell_ids <- colnames(aucell_scores_all_patients[[patient_id]][["GM1"]])

 cell_module_assignments <- sapply(cell_ids, function(cell_id) {
 # Get the scores for the selected cell in each gene module
 cell_scores <- sapply(names(aucell_scores_all_patients[[patient_id]]), fu
nction(module) {
 as.numeric(assays(aucell_scores_all_patients[[patient_id]][[module]])$A
UC[, cell_id])
 })

 # Find the gene module with the highest score
 max_module <- names(cell_scores)[which.max(unlist(cell_scores))]

 return(max_module)
 }, simplify = FALSE)

 names(cell_module_assignments) <- cell_ids
 return(cell_module_assignments)
}

cell_gene_module_assignments <- lapply(names(aucell_scores_all_patients), ass
ign_gene_module)
names(cell_gene_module_assignments) <- names(aucell_scores_all_patients)

```

```
Loading required package: MatrixGenerics
Loading required package: matrixStats
Warning: package 'matrixStats' was built under R version 4.2.3
Attaching package: 'matrixStats'
```

```
The following object is masked from 'package:dplyr':
```

```
count
```

```
The following objects are masked from 'package:genefilter':
```

```
rowSds, rowVars
```

```
Attaching package: 'MatrixGenerics'
```

```
The following objects are masked from 'package:matrixStats':
```

```
colAlls, colAnyNAs, colAnys, colAvgPerRowSet,
colCollapse, colCounts, colCummaxs, colCummins,
colCumprods, colCumsums, colDiffs, colIQRDiffs,
colIQRs, colLogSumExps, colMadDiffs, colMads,
colMaxs, colMeans2, colMedians, colMins,
colOrderStats, colProds, colQuantiles, colRanges,
colRanks, colSdDiffs, colSds, colSums2,
colTabulates, colVarDiffs, colVars,
colweightedMads, colweightedMeans,
colweightedMedians, colweightedSds,
colweightedVars, rowAlls, rowAnyNAs, rowAnys,
rowAvgPerColSet, rowCollapse, rowCounts,
rowCummaxs, rowCummins, rowCumprods, rowCumsums,
rowDiffs, rowIQRDiffs, rowIQRs, rowLogSumExps,
rowMadDiffs, rowMads, rowMaxs, rowMeans2,
rowMedians, rowMins, rowOrderStats, rowProds,
rowQuantiles, rowRanges, rowRanks, rowSdDiffs,
rowSds, rowSums2, rowTabulates, rowVarDiffs,
rowVars, rowweightedMads, rowweightedMeans,
rowweightedMedians, rowweightedSds, rowweightedVars
```

```
The following objects are masked from 'package:genefilter':
```

```
rowSds, rowVars
```

```
Loading required package: GenomicRanges
Loading required package: stats4
Loading required package: BiocGenerics
```

```
Attaching package: 'BiocGenerics'
```

```
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, sort, table, tapply, union,
unique, unsplit, which.max, which.min
```

```
Loading required package: S4Vectors
```

```
Attaching package: 'S4Vectors'
```

The following objects are masked from ‘package:dplyr’:

first, rename

The following objects are masked from ‘package:Matrix’:

expand, unname

The following objects are masked from ‘package:base’:

expand.grid, I, unname

Loading required package: IRanges

Attaching package: ‘IRanges’

The following objects are masked from ‘package:dplyr’:

collapse, desc, slice

The following object is masked from ‘package:grDevices’:

windows

Loading required package: GenomeInfoDb

Loading required package: Biobase

Welcome to Bioconductor

Vignettes contain introductory material; view with  
'browseVignettes()'. To cite Bioconductor, see  
'citation("Biobase")', and for packages  
'citation("pkgname")'.

Attaching package: ‘Biobase’

The following object is masked from ‘package:MatrixGenerics’:

rowMedians

The following objects are masked from ‘package:matrixStats’:

anyMissing, rowMedians

Attaching package: ‘SummarizedExperiment’

The following object is masked from ‘package:SeuratObject’:

Assays

The following object is masked from ‘package:Seurat’:

Assays

## Calculate gini simpson index, entropy, and CV for each patient.

```
Function to calculate Gini-Simpson index
```

```
gini_simpson <- function(counts) {
 total_counts <- sum(counts)
 proportions <- counts / total_counts
 return(1 - sum(proportions^2))
}
```

```
Function to calculate entropy
```

```
entropy <- function(counts) {
```

```

 total_counts <- sum(counts)
 proportions <- counts / total_counts
 return(-sum(proportions * log2(proportions)))
}

Function to calculate coefficient of variation (CV)
cv <- function(counts) {
 total_counts <- sum(counts)
 proportions <- counts / total_counts
 mean_proportions <- mean(proportions)
 sd_proportions <- sd(proportions)
 return(sd_proportions / mean_proportions)
}

Calculate Gini-Simpson index, entropy, and CV for each patient
gini_simpson_list <- list()
entropy_list <- list()
cv_list <- list()

for (patient_id in names(cell_gene_module_assignments)) {
 gene_module_assignments <- unlist(cell_gene_module_assignments[[patient_id]
])
 gene_module_counts <- table(gene_module_assignments)
 gini_simpson_list[[patient_id]] <- gini_simpson(gene_module_counts)
 entropy_list[[patient_id]] <- entropy(gene_module_counts)
 cv_list[[patient_id]] <- cv(gene_module_counts)
}

Combine results into a data frame
result <- data.frame(
 Patient_ID = names(cell_gene_module_assignments),
 Gini_Simpson = unlist(gini_simpson_list),
 Entropy = unlist(entropy_list),
 CV = unlist(cv_list)
)

print(result)

write.csv(result, file = "gene_module_ok.csv", row.names = FALSE)

```

## Result Visualization

```

library(ggplot2)
library(reshape2)

```

```

Replace Patient_ID with numbers 1 to 26

```

```
result$Patient_ID <- as.factor(seq(1, nrow(result)))
```

```
Melt the data frame for ggplot
```

```
melted_result <- melt(result, id.vars = "Patient_ID", variable.name = "Metric", value.name =
"Value")
```

```
Create the bar plot
```

```
p <- ggplot(melted_result, aes(x = Patient_ID, y = Value, fill = Metric)) +
 geom_bar(stat = "identity", position = "dodge") +
 theme(axis.text.x = element_text(angle = 90, hjust = 1, size = 8)) +
 labs(x = "Patient Number", y = "Value", title = "Metrics for Patients") +
 facet_wrap(~Metric, scales = "free_y")
```

```
print(p)
```



