Gene module analysis

Mikayla, Mustafa, Yibo

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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 clusetring at different resolution.

# The first part of the code did all the data reading, normalizing, PCA, and clusetring 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\_barcodes\_path <- paste0("./GSE176078\_RAW/", patient\_id, "/count\_matrix\_barcodes.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\_barcodes\_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 = "LogNormalize", 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%

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

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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, FXYD3, 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, CYYR1, 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%

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

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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%

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

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Maximum modularity in 10 random starts: 0.8159

Number of communities: 18

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%

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

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Maximum modularity in 10 random starts: 0.7870

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: 6178

Number of edges: 225911

Running smart local moving algorithm...

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

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

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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

CTSC, CTSS, CD84, TYROBP, CCL4, HLA-DMB, C1orf162, LST1, GK, NCF1

GBP5, ACP5, AIF1, BCL2A1, FCER1G, CCL4L2, PLEK, CYBB, CCL3, TNFRSF18

Negative: 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

CTSB, 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, CTSK

PDGFRL, GAS1, FIBIN, RARRES2, OMD, CTHRC1, HSD17B6, SPON1, WNT2, PODNL1

Negative: PLVAP, CALCRL, ESAM, ARHGAP29, RAMP2, ADGRL4, ECSCR.1, EGFL7, CDH5, PODXL

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

Negative: NDUFA4L2, TBX2, NOTCH3, SOD3, RGS5, HIGD1B, PPP1R14A, TPPP3, CCDC102B, RASL12

LGI4, 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%

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

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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%

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

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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%

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

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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

TYROBP, ACP5, BCL2A1, FCER1G, LYZ, AIF1, SPI1, CD68, FCGR2B, NKG7

FGL2, TNF, CYBB, MS4A6A, LAIR1, C1QA, FCGR2A, C1QB, CD40LG, IRF8

Negative: ERBB2, KRT19, GRB7, CALML5, CLDN4, KRT7, S100A14, KRT8, KRT23, TACSTD2

FXYD3, 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, CYYR1, 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, CYYR1

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

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.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: 0.9235

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, FXYD3, 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, CYYR1, PODXL, TSPAN7, PTPRB

FLT1, CDH5, MCTP1, ITGA6, CD34, AQP1, TM4SF1, INSR, ACKR1, SLCO2A1

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, RP11-53O19.1, 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.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: 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.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: 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.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: 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.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: 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.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: 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

TSPAN7, KDR, ICAM2, THSD7A, SH3BGRL2, PCAT19, CYYR1, TM4SF1, ITGA6, HYAL2

Negative: 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, CYYR1, CADM3, CALCRL, IGFBP3, TM4SF1, RAMP3, HYAL2, EGFL7

PC\_ 4

Positive: APOC1, CTSB, SPP1, RNASE1, APOE, FTL, CD68, CTSD, TYROBP, PLD3

PLTP, CD14, CTSL, 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, SAMSN1, 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.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: 0.7275

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, RP11-53O19.1, 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, RP11-53O19.1, AGR3, CLDN3, AZGP1, AC018816.3, DEGS2, SLC39A6, ESR1

GATA3, AGR2, DCXR, FSIP1, BTG2, RAB25, CA12, RARRES3, MGST1, CALML5

Negative: 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, PRKCDBP, 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

CTSK, MXRA8, ADAM12, PCOLCE, COL5A1, TPM2, CTGF, COL12A1, TNFAIP6, RGS5

Negative: CALCRL, PLVAP, AQP1, RAMP2, HYAL2, VWF, HSPG2, RNASE1, ADGRL4, EMCN

EGFL7, RAMP3, CD93, SLC9A3R2, CXorf36, CDH5, RBP7, PODXL, SOX18, CYYR1

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.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: 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.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: 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.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: 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.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: 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.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: 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, SLCO2B1, 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, SLCO2A1, 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.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%

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

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Maximum modularity in 10 random starts: 0.8359

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: 3527

Number of edges: 122425

Running smart local moving algorithm...

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

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

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Maximum modularity in 10 random starts: 0.7926

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: 3527

Number of edges: 122425

Running smart local moving algorithm...

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

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

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Maximum modularity in 10 random starts: 0.7577

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: 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%

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

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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

PRKCDBP, 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, CYYR1, 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, SLCO2B1, 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, OLFM1, 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%

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

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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%

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

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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.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%

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

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Maximum modularity in 10 random starts: 0.7839

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: 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: LAPTM5, 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, LAPTM5, 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, MNDA, 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, CYYR1, 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.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: 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.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: 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.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: 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.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: 5309

Number of edges: 186263

Running smart local moving algorithm...

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

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

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Maximum modularity in 10 random starts: 0.8355

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: 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, SUSD3, 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

COL4A1, HSPG2, SPARCL1, A2M, RBP7, CD93, RAMP3, CAV1, SPRY1, MCTP1

Negative: 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, SPP1, RNASE1, NOTCH3, AIF1

Negative: 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.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: 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.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: 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.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: 3764

Number of edges: 119655

Running smart local moving algorithm...

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

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

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Maximum modularity in 10 random starts: 0.8028

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: 3764

Number of edges: 119655

Running smart local moving algorithm...

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

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

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Maximum modularity in 10 random starts: 0.7742

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: 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%

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

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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%

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

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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.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%

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

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Maximum modularity in 10 random starts: 0.8142

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: 5789

Number of edges: 189547

Running smart local moving algorithm...

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

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

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Maximum modularity in 10 random starts: 0.7868

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: 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%

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

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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

SERPINA1, CYBB, MNDA, HLA-DMB, PHACTR1, CD163, C1QA, C15orf48, MS4A4A, CD86

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, PDGFRL, 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, MRVI1, 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, SLCO2B1, 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%

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

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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%

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

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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%

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

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Maximum modularity in 10 random starts: 0.7487

Number of communities: 19

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: 0.7184

Number of communities: 22

Elapsed time: 1 seconds

Performing log-normalization

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

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

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Calculating gene variances

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

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

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*|

Warning: pseudoinverse used at -2.499Warning: neighborhood radius 0.30103Warning: reciprocal condition number 2.0259e-15Calculating 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, PPDPF

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

C1QC, C1QB, CXCL10, FTL, HLA-DPB1, RNASE6, SDS, TNFSF13B, CD86, HLA-DQA2

Negative: PLVAP, VWF, HYAL2, A2M, IGFBP7, AQP1, ACKR1, RNASE1, RAMP3, SPRY1

TM4SF1, IFITM1, CLDN5, PLPP1, SPARC, RAMP2, GNG11, PTP4A3, TSPAN7, THBD

ENG, CYYR1, 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, CYYR1, 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, PRKCDBP, CYR61, COL6A2, CNN3

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, HMGN2, 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, SH3BGRL3, 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, CYYR1, 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, SLCO2B1

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.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: 0.8908

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, SLCO2A1, 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

HLA-DQA2, FCGR3A, APOC1, LAPTM5, CCL3, SPI1, LST1, PLEK, C3AR1, FAM26F

Negative: 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.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: 0.7819

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: 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%

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

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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

HLA-DQB1, HLA-DPB1, XBP1, STC2, ANKRD30A, ACKR1, EMCN, MARCKS, RAMP3, CTSB

Negative: 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.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: 0.8502

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, CYYR1, 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.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: 7985

Number of edges: 286925

Running smart local moving algorithm...

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

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

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Maximum modularity in 10 random starts: 0.9401

Number of communities: 15

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: 7985

Number of edges: 286925

Running smart local moving algorithm...

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

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Maximum modularity in 10 random starts: 0.9042

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: 7985

Number of edges: 286925

Running smart local moving algorithm...

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

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Maximum modularity in 10 random starts: 0.8749

Number of communities: 20

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: 7985

Number of edges: 286925

Running smart local moving algorithm...

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

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Maximum modularity in 10 random starts: 0.8515

Number of communities: 25

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: 7985

Number of edges: 286925

Running smart local moving algorithm...

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

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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%

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

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Calculating gene variances

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

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

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Calculating feature variances of standardized and clipped values

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

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

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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, CYYR1, 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

CYYR1, 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%

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

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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%

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

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Maximum modularity in 10 random starts: 0.8705

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: 5619

Number of edges: 199185

Running smart local moving algorithm...

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

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Maximum modularity in 10 random starts: 0.8390

Number of communities: 18

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: 5619

Number of edges: 199185

Running smart local moving algorithm...

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

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

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Maximum modularity in 10 random starts: 0.8118

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: 5619

Number of edges: 199185

Running smart local moving algorithm...

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

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

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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%

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

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Calculating gene variances

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

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

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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, SAMSN1, HCST, FYB, GPR183, GMFG, AIF1, LYZ, C1orf162, 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, CTSL

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

PDGFRL, 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%

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

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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%

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

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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%

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

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Maximum modularity in 10 random starts: 0.8862

Number of communities: 25

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%

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

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Maximum modularity in 10 random starts: 0.8634

Number of communities: 26

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%

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

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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%

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

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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, ERRFI1, 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%

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

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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%

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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%

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

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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%

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\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*|

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%

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

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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, TGFBR2, 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, CYYR1, MMRN2, HYAL2

RAMP3, PALMD, ETS2, CLDN5, HLA-DPA1, AQP1, ITGA6, GIMAP7, CDH5, ACKR1

Negative: 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, SAMSN1, IL1B, C1QB, COTL1, LCP1

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

FOLR1, C2orf82, KRT14, CXADR, SLC34A2, ELF5, KRT16, CXCL3, TTYH1, KLF5

Negative: 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.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%

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

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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%

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

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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%

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

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Calculating gene variances

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

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

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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, PRKCDBP, MYL9, ANXA1

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

ELF3, ANKRD30A, MRPS30, BMPR1B, CCND1, AGR2, STC2, GPRC5A, CHPT1, CLDN4

RP11-53O19.1, 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, PRKCDBP

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, TGFBI, SDC2

TPPP3, MFGE8, SERPINF1, PLAC9, PGF, SMOC2, 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, RP11-53O19.1, 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.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: 0.9135

Number of communities: 14

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: 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%

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

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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%

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

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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%

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

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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

SAMSN1, GPR183, BIRC3, CD7, HLA-DRA, LTB, IL7R, RASGEF1B, HLA-DRB5, UCP2

Negative: COL1A2, LUM, DCN, MEG3, COL3A1, CALD1, CXCL12, COL6A2, APOD, 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, SAMSN1, CST7, KLRB1, ALOX5AP

LTB, 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.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: 0.7840

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, C1orf162, 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

Negative: 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, FXYD1, 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, FXYD3, 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, CYYR1, 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

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

Negative: MUCL1, AZGP1, CKB, SLPI, HEBP2, TFF3, TMSB15A, SFN, TM7SF2, FDPS

BAMBI, LINC01285, FABP7, MESP1, LINC01133, CTAG2, CLCA2, NUDT8, SCD, IMPA2

TK1, ZG16B, RHOV, PDZK1IP1, LGALS12, HIST1H1C, APOD, EFNA1, HMGCS1, 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

IGKV3-11, IGKV3-20, JCHAIN, IGKV1-5, IGLL5, IGKV4-1, JSRP1, IGKV1-27, IGKV1-12, 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, PDZK1IP1, 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, IGKV1D-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.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: 0.9324

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

NFIB, LMTK3, TM4SF1, SEPP1, MAL2, DBI, TFAP2B, PLPP2, NFIX, ERBB2

Negative: 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

NEAT1, AARD, PCAT1, MT-ND5, KRT15, PTPRF, ITGB6, SREBF1, FAT1, GPRC5A

TRPS1, ENAH, EMP1, FBXO32, ARFGEF3, RND3, FLNB, SOX9, KIAA1522, ZFP36L1

Negative: 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.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: 0.8077

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: 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.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: 0.7367

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(sapply(x, length))))  
  
cat("Total number of clusters in patient\_DEGs\_filtered:", total\_clusters\_filtered, "\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), ncol = 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 patient", 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(rownames(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", res, ":", 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[[patient\_id]][[res]])  
 }  
}  
  
# Calculate Jaccard similarity matrix  
jaccard\_similarity\_matrix <- matrix(0, nrow = length(all\_gene\_signatures), ncol = 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 = 10)  
  
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, partition\_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"]][["class"]]  
  
# 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\_barcodes\_path <- paste0("./GSE176078\_RAW/", patient\_id, "/count\_matrix\_barcodes.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\_barcodes\_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", patient\_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]]), function(module) {  
 as.numeric(assays(aucell\_scores\_all\_patients[[patient\_id]][[module]])$AUC[, 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), assign\_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, colAvgsPerRowSet,

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,

rowAvgsPerColSet, 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)

