

# PAPER TITLE TO BE DEFINED (in common.yaml)

10-DE genes across pseudotime

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## Abstract

Lung interstitium macrophages (IMs) are non-alveolar resident tissue macrophages which contribute to the lung homeostasis. These cells were reported to be heterogeneous by our group and other teams, which contains two main distinct subpopulations: CD206+ IMs and CD206- IMs. However, the exact origin of IMs and the transcriptional programs that control IM differentiation remains unclear. In recent report, we analyzed the refilled IMs in the course of time after induced IM depletion with single-cell RNA sequencing (10X Genomics Chromium) and bulk RNA sequencing.

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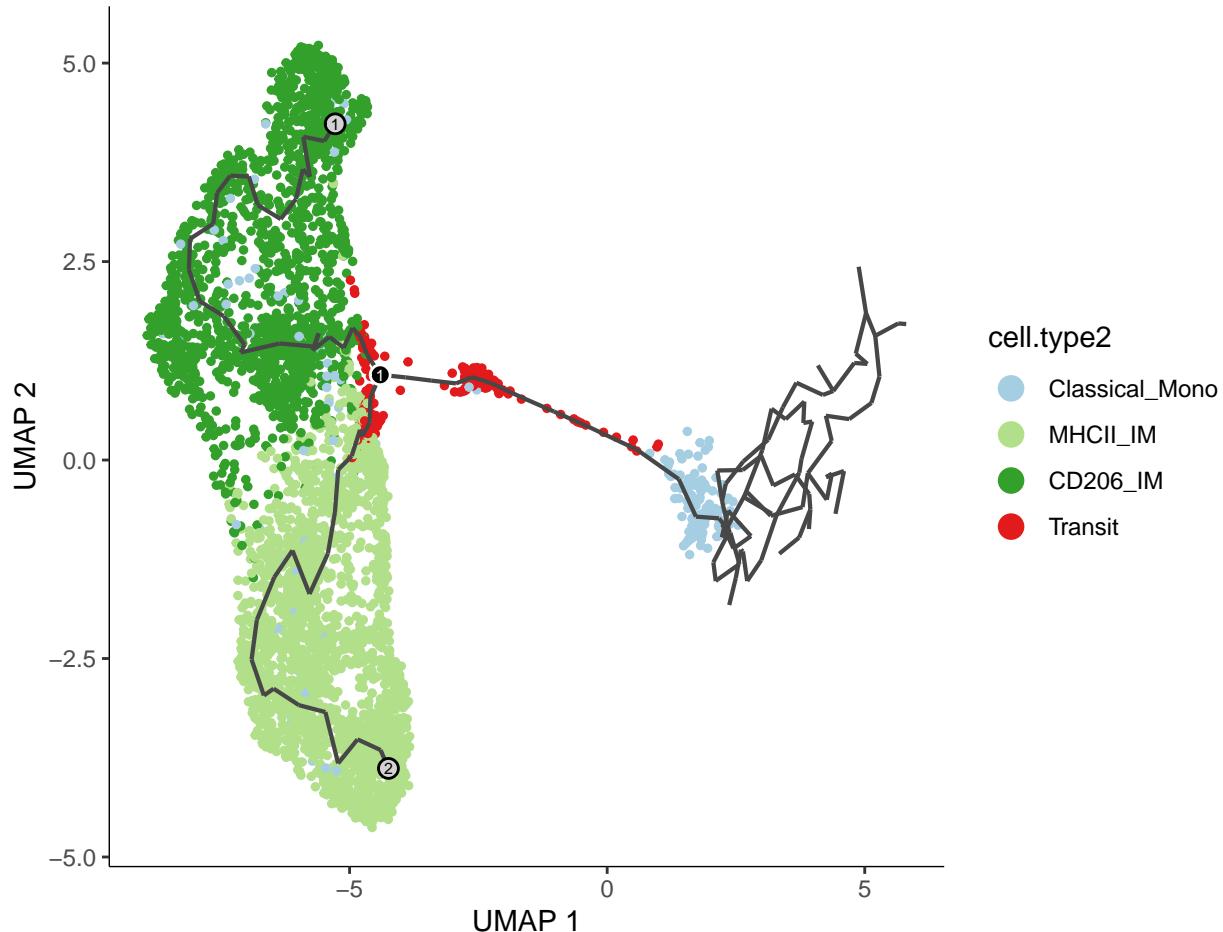
## 1 Description

## 2 Prepare data

```
suppressMessages(  
{  
library(Seurat)  
library(ComplexHeatmap)  
library(ggplot2)  
library(dplyr)  
library(RColorBrewer)  
library(circlize)  
library(monocle3)  
})  
  
mo <- readRDS(file = ".../9-Monocle_analysis_and_pseudotime_estimation/Mono_to_IM.cds")
```

Show trajectory in UMAP plot:

```
pal2 <- c(`Classical_Mono`="#A6CEE3",  
          `MHCII_IM`="#B2DF8A",  
          `CD206_IM`="#33A02C",  
          `Transit` = "#E31A1C")  
  
plot_cells(cds = mo, color_cells_by = "cell.type2",  
           cell_size = 1, label_cell_groups = FALSE,  
           label_branch_points = TRUE, label_leaves = TRUE,  
           label_roots = FALSE, alpha = 1) +  
           scale_color_manual(values = pal2)
```



```
ggsave(filename = ".../Figures/UMAPplot_trajectory.pdf", width = 6.5, height = 5)
```

### 3 DE gene expression across IM-differentiation

DE genes across pseudotime of IM differentiation ## Across pseudotime of IM differentiation

Prepare matrix with z-scores, smoothed and scaled data across pseudotime for heatmap.

```
pt.matrix <- exprs(mo)[match(genes, rownames(rowData(mo))), order(pseudotime(mo))]
cellnames <- colnames(pt.matrix)
#Can also use "normalized_counts" instead of "exprs" to use various normalization methods, for example:
#normalized_counts(cds, norm_method = "log")

pt.matrix <- t(apply(pt.matrix, 1, function(x){smooth.spline(x, df=3)$y}))
pt.matrix <- t(apply(pt.matrix, 1, function(x){(x-mean(x))/sd(x)}))
rownames(pt.matrix) <- genes
colnames(pt.matrix) <- cellnames
```

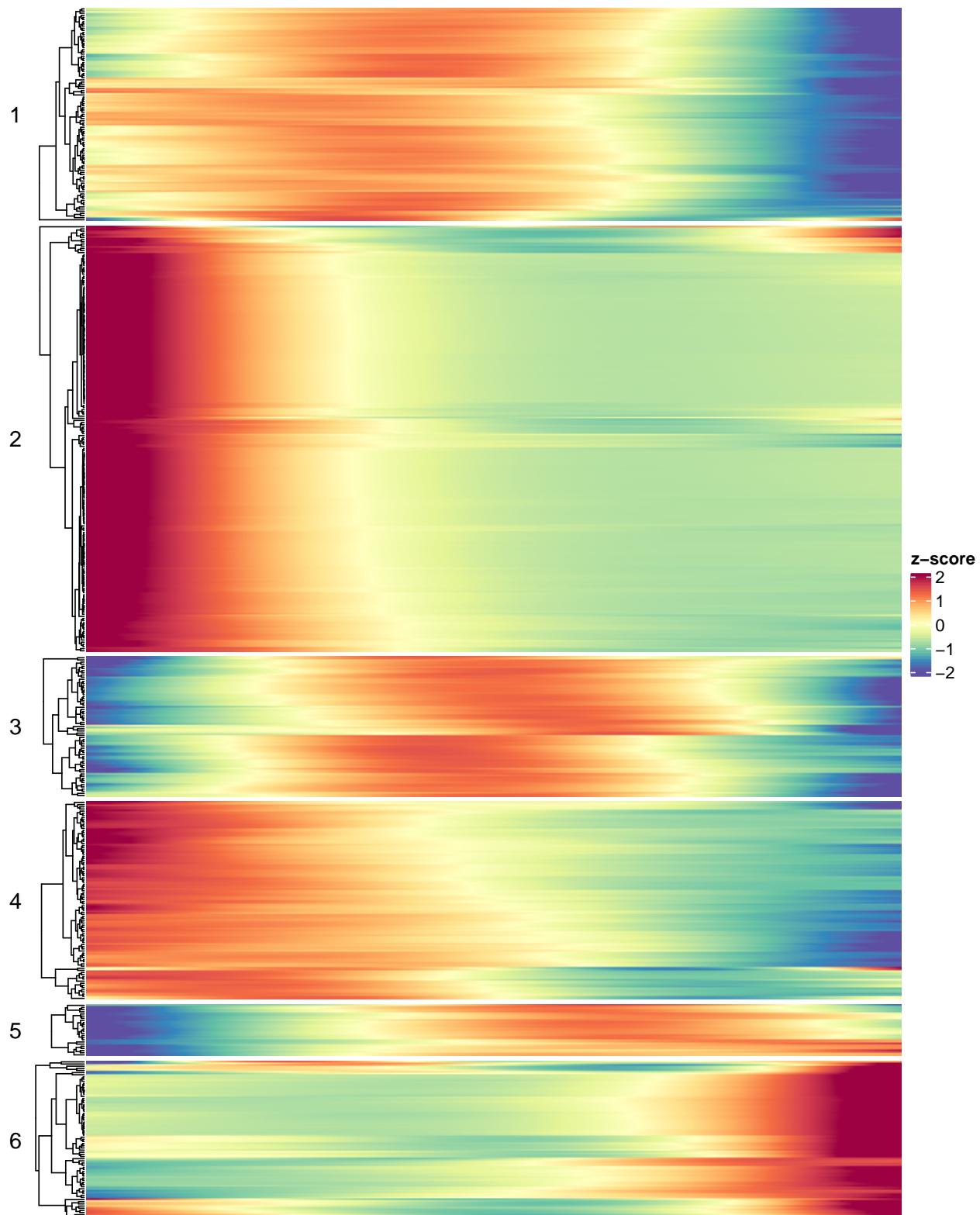
Show DE genes in unsupervised heatmap.

```
#K means with 6 groups
```

```

htkm <- Heatmap(
  pt.matrix,
  # use_raster = FALSE, # use FALSE to export to vector image.
  name                = "z-score",
  col                 = colorRamp2(seq(from=-2,to=2,length=11),
    rev(brewer.pal(11, "Spectral"))),
  show_row_names       = FALSE,
  show_column_names    = FALSE,
  row_names_gp         = gpar(fontsize = 3),
  row_km = 6,
  row_km_repeats = 31,
  row_dend_reorder = TRUE,
  row_title_rot        = 0,
  cluster_rows          = TRUE,
  cluster_row_slices    = FALSE,
  cluster_columns        = FALSE,
)
htkm <- draw(htkm)

```



In this heatmap, the x axis is pseudotime, which represents differentiation state from monocytes (left) to IMs (right).

### 3.1 Annotate the cells associated to either differentiation of CD206+ IMs or CD206- IMs

```

library(magrittr)                                     1
# Get the closest vertice for every cell           2
y_to_cells <- mo@principal_graph_aux$UMAP$pr_graph_cell_proj_closest_ 3
  vertex%>%as.data.frame()

y_to_cells$cells <- rownames(y_to_cells)           4
y_to_cells$Y <- y_to_cells$V1                      5

# Get the root vertices                           6
# It is the same node as above                  7
root <- mo@principal_graph_aux$UMAP$root_pr_nodes 8

principalgraph <- mo@principal_graph$UMAP          9

# Get the other endpoints                         10
endpoints <- names(which(igraph::degree(principalgraph) == 1))    11
endpoints <- endpoints[!endpoints %in% root]        12

# For each endpoint                            13
cellWeights <- lapply(endpoints, function(endpoint) { 14
  # We find the path between the endpoint and the root 15
  path <- igraph::shortest_paths(principalgraph, root, endpoint)$vpath 16
  [[1]]
  path <- as.character(path)                         17
  # We find the cells that map along that path      18
  df <- y_to_cells[y_to_cells$Y %in% path, ]         19
  df <- data.frame(weights = as.numeric(colnames(mo) %in% df$cells)) 20
  colnames(df) <- endpoint                         21
  return(df)
}) %>% do.call(what = 'cbind', args = .) %>%
  as.matrix()                                       22
rownames(cellWeights) <- colnames(mo)               23
colnames(cellWeights) <- c("CD206_IM_branch", "MHCII_IM_branch") 24
pseudotime <- matrix(mo@principal_graph_aux$UMAP$pseudotime, ncol = ncol( 25
  cellWeights),                                26
  nrow = ncol(mo), byrow = FALSE)                27
rownames(pseudotime) <- colnames(mo)               28

```

## 4 TradeSeq analysis for the differentiation of monocytes to either of IM subsets

### 4.1 Construct sce object for TradeSeq

```

suppressMessages(library(tradeSeq))                 1

# this step is VERY time consuming                2
sce <- fitGAM(counts = mo@assays$data$counts,      3
  pseudotime = pseudotime,
  cellWeights = cellWeights)                     4

```

```
saveRDS(sce, file = "./sce.4339cells.newversion.Rds")
```

5  
6

Between-lineage comparisons (CD206+ IM vs CD206- IM differentiation) ## Between-lineage comparisons (CD206+ IM vs CD206- IM differentiation)

Association of gene expression with pseudotime (find significant DE genes along pseudotime).

```
assoRes <- associationTest(sce)
endRes <- diffEndTest(sce)
head(assoRes)
```

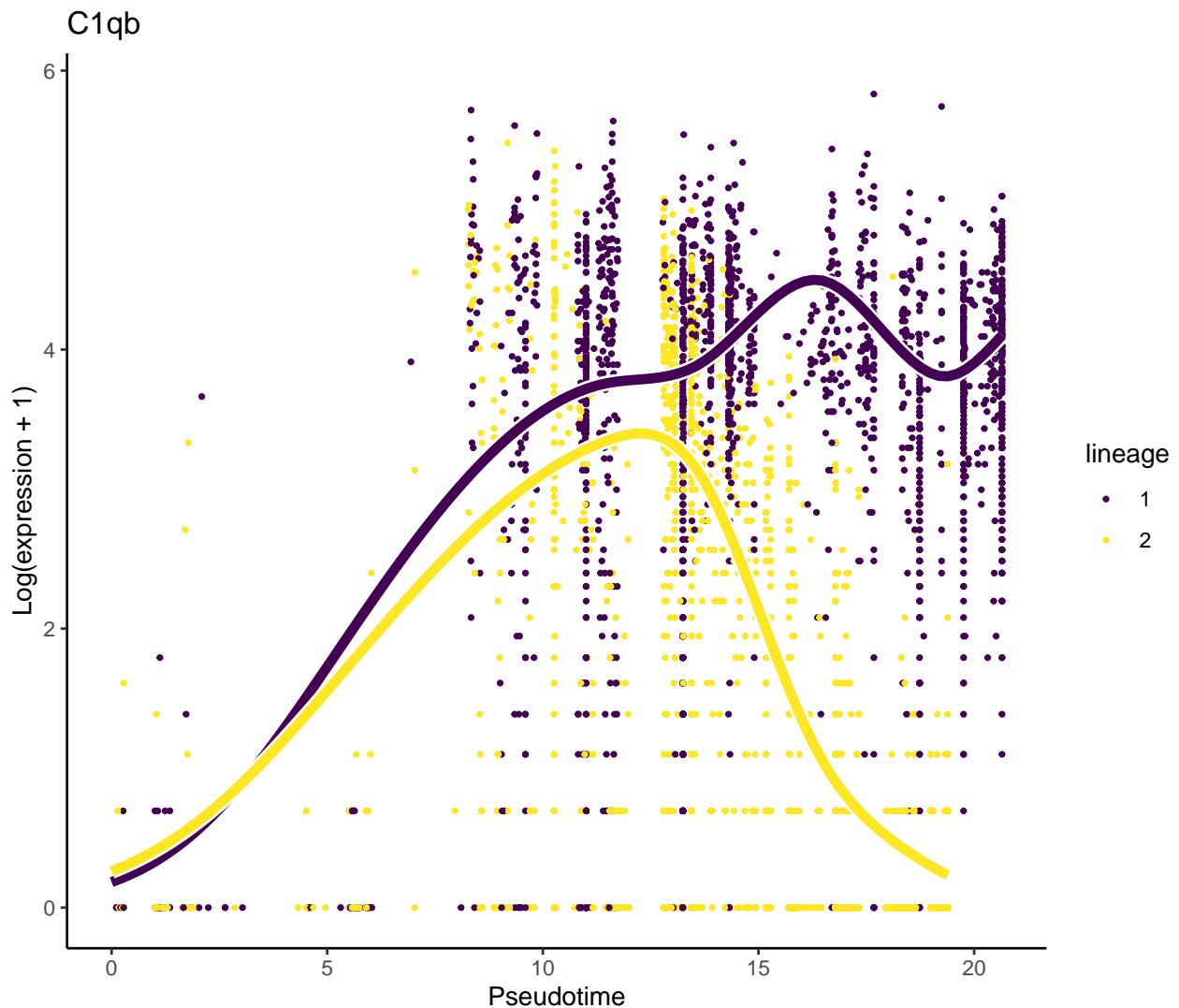
```
## # A tibble: 6 x 4
##   waldStat     df      pvalue  meanLogFC
##       <dbl>    <dbl>      <dbl>      <dbl>
## 1     210.      9     0.222
## 2     28.4      9    0.000815
## 3       NA      NA     NA     0.121
## 4     41.8      9    0.00000360
## 5     36.4      9    0.0000330
## 6     45.1      9    0.000000880
```

1  
2  
3  
4  
5  
6  
7  
8  
9

Plot the most sig gene:

```
library(ggplot2)
o <- order(endRes$waldStat, decreasing = TRUE)
sigGene <- names(sce)[o[1]]
plotSmoothers(sce, counts = counts(sce), gene = sigGene
               #, curvesCol = c("#33A02C", "#B2DF8A")
               ) + ggtitle(sigGene)
```

1  
2  
3  
4  
5  
6



What's the top genes?

```

names(sce)[o[1:20]]  

## [1] "C1qb"      "Ctsb"       "C1qa"       "Selenop"    "Csf1r"      "Timp2"      "Pf4"        1  

## [8] "C1qc"       "Serinc3"    "Cd209a"     "Lsp1"       "Lgmn"       "Apoe"       "Blvrb"     2  

## [15] "Olfm1"     "Tnip3"      "Rpl13"      "Ninj1"      "Rpl28"      "H2-DMb1"   3

```

## 4.2 Clustering using RSEC, clusterExperiment

tradeSeq provides the functionality to cluster genes according to their expression pattern along the lineages with the clusterExpressionPatterns function. A number of equally spaced points for every lineage are selected to perform the clustering, and the number of points can be selected with the nPoints argument. (from vignette("tradeSeq"))

```

library(clusterExperiment)
nPointsClus <- 20 # The number of points to use for clustering the  

# expression patterns..
clusPat <- clusterExpressionPatterns(sce ,  


```

```

nPoints = nPointsClus,
genes = genes,
random.seed = 43,
beta = 0.2
)

## 36 parameter combinations, 36 use sequential method, 36 use subsampling
## Running Clustering on Parameter Combinations...
## done.

clusterLabels <- primaryCluster(clusPat$rsec)

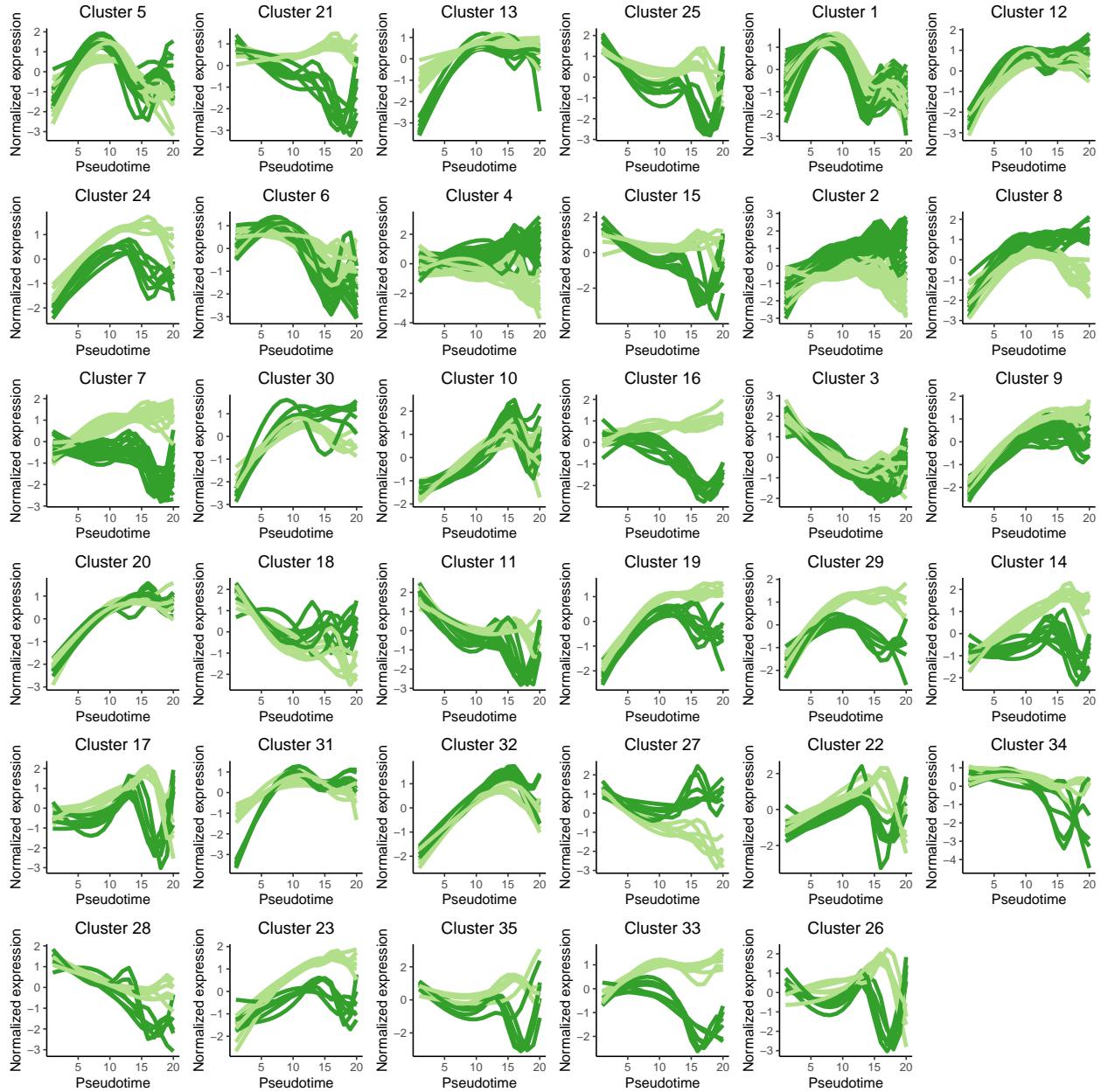
cUniq <- unique(clusterLabels) #
cUniq <- cUniq[!cUniq == -1] # remove unclustered genes

# cUniq <- cUniq[cUniq == -1]
#Any samples not found as part of a homogenous set of clusters at that
# point will be classified as unclustered (given a value of -1)

# beta: value between 0 and 1 to decide how stable cluster membership
# has to be before 'finding' and removing the cluster.
if (exists("p.total")) { rm(p.total)}

for (xx in cUniq) {
  cId <- which(clusterLabels == xx)
  p <- ggplot(data = data.frame(x = 1:nPointsClus,
                                 y = rep(range(clusPat$yhatScaled[cId, ]),
                                         nPointsClus / 2)),
               aes(x = x, y = y)) +
    geom_point(alpha = 0) +
    labs(title = paste0("Cluster", xx), x = "Pseudotime", y = "
Normalized expression") +
    theme_classic() +
    theme(plot.title = element_text(hjust = 0.5))
  for (ii in 1:length(cId)) {
    geneId <- rownames(clusPat$yhatScaled)[cId[ii]]
    p <- p +
      geom_line(data = data.frame(x = rep(1:nPointsClus, 2),
                                   y = clusPat$yhatScaled[geneId, ],
                                   lineage = rep(0:1, each = nPointsClus)),
                 aes(col = as.character(lineage), group = lineage), lwd =
                   1.5)
  }
  p <- p + guides(color = "none") +
    scale_color_manual(values = c("#33A02C", "#B2DF8A"),
                       breaks = c("0", "1"))
  if (exists("p.total")) { p.total <- p.total + p} else {p.total <- p}
}
print(p.total)

```



## 5 Show gene expression pattern calculated by TradeSeq in heatmap

### 5.1 Data preparation

Here we use the DE genes calculated in DE genes across pseudotime of IM differentiation.

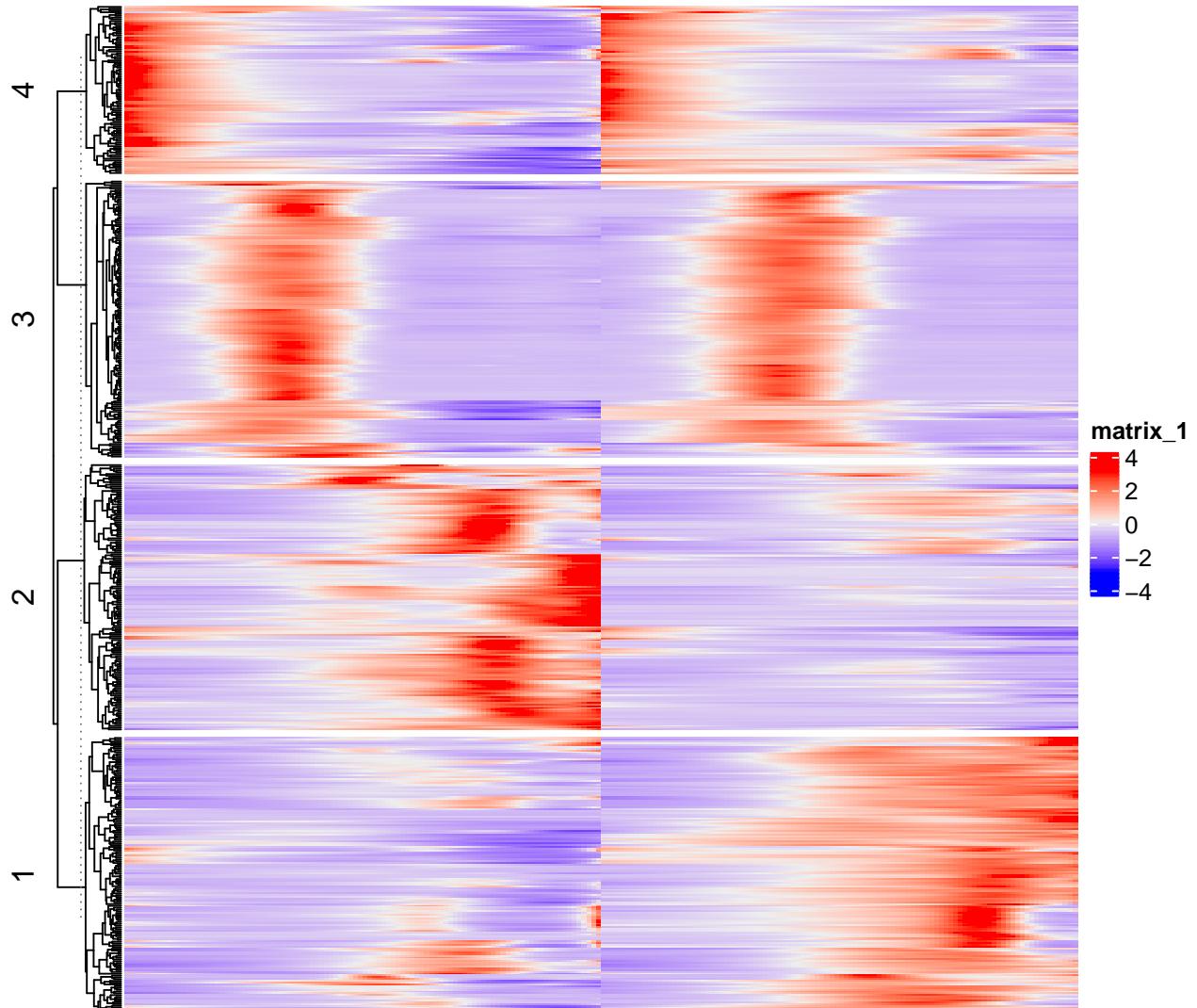
```
yhatSmooth <- predictSmooth(sce, gene = genes, nPoints = 100, tidy = FALSE) 1
      )
yhatSmoothScaled <- t(scale(t(yhatSmooth))) 2
```

### 5.2 Draw heatmap

```

heatSmooth <- Heatmap(yhatSmoothScaled, cluster_columns = FALSE, show_row_
  names = FALSE, show_column_names = FALSE, row_km = 4)
heatSmooth <- draw(heatSmooth)

```



Two IM differentiation show similar patterns but some genes (especially cluster 2 and 1) are different in CD206+ and CD206-.

### 5.3 Annotate DE genes as CD206+/CD206- IM differentiation specific or common genes

According to the heatmap above, some of DE genes should remain unchanged (common) and half of them are specific to one of two IM differentiation.

We use wald statistic calculated in diffEndTest to annotate the “common” genes and “specific” genes. (in Between-lineage comparisons (CD206+ IM vs CD206- IM differentiation))

```

endRes.DE <- endRes[rownames(yhatSmooth), ]
summary(endRes.DE$waldStat)

```

##	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	1
##	0.0027	3.8599	41.4571	123.7353	168.7434	1263.9587	2

Let's use waldStat > 40 and logFC > 2 as cut threshold.

```
genes.changed <- rownames(filter(endRes.DE, waldStat > 70 & (logFC1_2 > 2
| logFC1_2 < -2) ))
genes.noChange <- setdiff(rownames(endRes.DE), genes.changed)
```

Make heatmap with unchanged/common genes.

```
heatSmooth_cd206.unchanged <- Heatmap(yhatSmoothScaled[genes.noChange,
100:1], cluster_columns = FALSE, show_row_names = FALSE, show_column_
names = FALSE, column_title = "CD206+IM")  

1  

heatSmooth_mhcii.unchanged <- Heatmap(yhatSmoothScaled[genes.noChange,
101:200], cluster_columns = FALSE, show_row_names = TRUE, row_names_gp
= gpar(fontsize = 3), show_column_names = FALSE, column_title = "MHCII
+IM")  

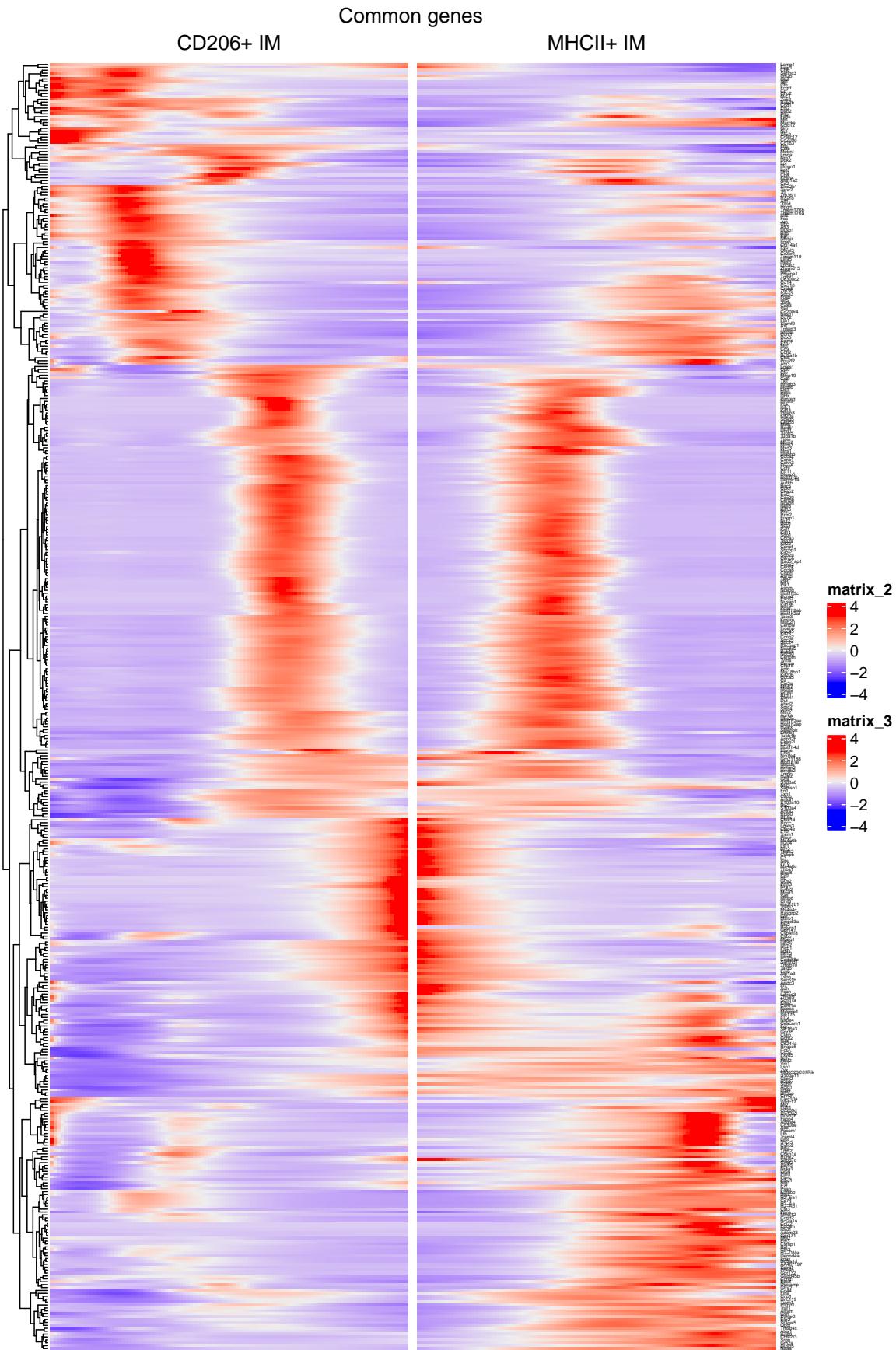
2  

heatSmooth_combined.unchanged <- draw (heatSmooth_cd206.unchanged +
heatSmooth_mhcii.unchanged, column_title = "Common genes", auto_adjust
= FALSE)  

3  

4  

5
```



## 5.4 Draw heatmap with expression patterns of unchanged/common genes in the order of pseudotime

Let's find the expression peak of each gene:

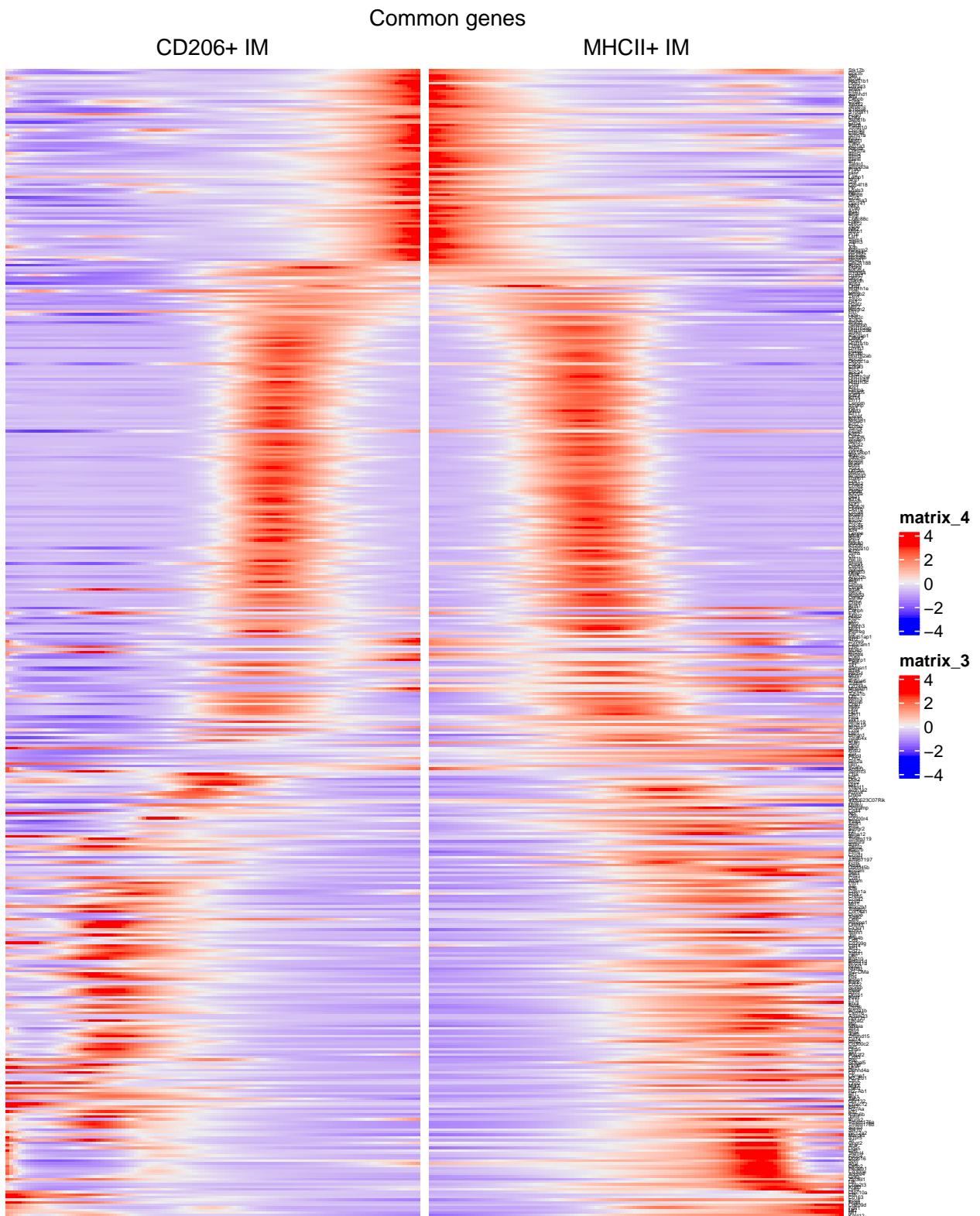
```

1  orderbyExpressionPeak <- function(x, # matrix
2      decreasing = FALSE,
3      output.position = FALSE # if true, give
4      relative position 0 - 1, or output
5      order.
6      )
7
8  indx.peak <- apply(x, 1 , which.max)
9
10 if(output.position) {
11   po <- indx.peak/nrow(x)
12   if (! length(rownames(x)) == 0) {names(po) <- rownames(x)}
13   return(po)
14 } else {
15   o <- order(indx.peak)
16   if (! length(rownames(x)) == 0) {names(o) <- rownames(x)[o]}
17   return (o)
18 }
```

Make average peak pseudotime peak for each gene:

```

1  po.cd206 <- orderbyExpressionPeak(yhatSmoothScaled[genes.noChange , 1:100] ,
2      output.position = TRUE)
3  po.mhcii <- orderbyExpressionPeak(yhatSmoothScaled[genes.noChange ,
4      101:200] , output.position = TRUE)
5  order.mean <- order ( ( po.cd206 + po.mhcii ) /2)
6
7  heatSmooth_cd206.unchanged.ordered <- Heatmap(yhatSmoothScaled[genes.
8      noChange , 100:1] , cluster_columns = FALSE, show_row_names = FALSE,
9      show_column_names = FALSE, row_order = order.mean, column_title =
10      "CD206+IM")
11
12  heatSmooth_combined.unchanged.ordered <- draw ( heatSmooth_cd206.unchanged
13      .ordered + heatSmooth_mhcii.unchanged, column_title = "Common genes",
14      auto_adjust = FALSE)
```



```

pdf(file = ".../Figures/Heatmap_common_genes_IMs_diff_across_pseudotime.pdf" 1
  , width = 8, height = 10)
heatSmooth_combined.unchanged.ordered
dev.off() 2
 3

```

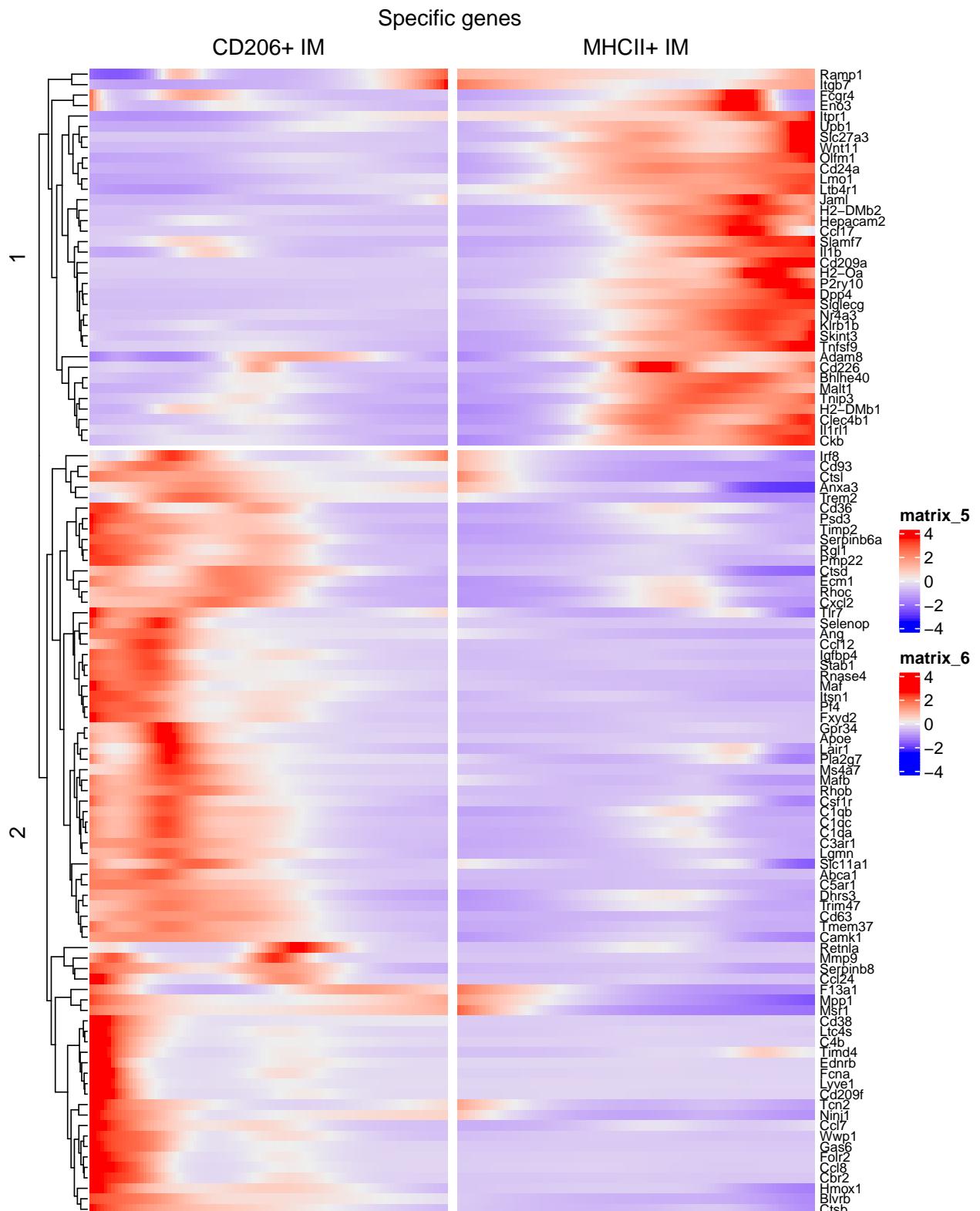
```
## pdf  
## 2
```

1  
2

## 5.5 Make with changed/specific genes

```
heatSmooth_cd206.changed <- Heatmap(yhatSmoothScaled[genes.changed,  
100:1], cluster_columns = FALSE, show_row_names = FALSE, cluster_rows  
= hclust(dist(yhatSmoothScaled[genes.changed, ])), show_column_names =  
FALSE, column_title = "CD206+IM")  
  
heatSmooth_mhcii.changed <- Heatmap(yhatSmoothScaled[genes.changed,  
101:200], cluster_columns = FALSE, show_row_names = TRUE, row_names_gp  
= gpar(fontsize = 8), show_column_names = FALSE, column_title = "MHCII+  
IM")  
  
heatSmooth_combined.changed <- draw ( heatSmooth_cd206.changed +  
heatSmooth_mhcii.changed, column_title = "Specific genes", split = 2)
```

1  
2  
3  
4  
5



```

geneSymbol.changed.mhcii <- read.csv("./geneSymbol_changed_mhcii_IM.csv",
  col.names = FALSE)[[1]]
geneSymbol.changed.cd206 <- read.csv("./geneSymbol_changed_cd206_IM.csv",
  col.names = FALSE)[[1]]

```

MHCII IM high genes:

```
geneSymbol.changed.mhcii
## [1] "Ramp1"      "Itgb7"       "Fcgr4"       "Eno3"        "Itpr1"       "Upb1"        1
## [7] "Slc27a3"    "Wnt11"       "Olfm1"       "Cd24a"       "Lmo1"        "Ltb4r1"      2
## [13] "Jaml"        "H2-DMb2"     "Hepacam2"   "Ccl17"       "Slamf7"      "Il1b"        3
## [19] "Cd209a"      "H2-0a"        "P2ry10"      "Dpp4"        "Siglecg"    "Nr4a3"      4
## [25] "Klrb1b"      "Skint3"      "Tnfsf9"      "Adam8"       "Cd226"       "Bhlhe40"    5
## [31] "Malt1"        "Tnip3"       "H2-DMb1"     "Clec4b1"    "Il1rl1"      "Ckb"        6

geneSymbol.changed.cd206
## [1] "Irf8"        "Cd93"        "Ctsl"        "Anxa3"       "Trem2"       "Cd36"        1
## [7] "Psd3"        "Timp2"       "Serpina6a"   "Rgl1"        "Pmp22"       "Ctsd"        2
## [13] "Ecm1"        "Rhoc"        "Cxcl2"       "Tlr7"        "Selenop"    "Ang"         3
## [19] "Ccl12"       "Igfbp4"      "Stab1"       "Rnase4"     "Maf"        "Itsn1"      4
##
## [25] "Pf4"         "Fxyd2"       "Gpr34"       "Apoe"        "Lair1"       ""           5
"Pla2g7"
## [31] "Ms4a7"       "Mafb"        "Rhob"        "Csf1r"       "C1qb"       "C1qc"      6
## [37] "C1qa"        "C3ar1"      "Lgmn"        "Slc11a1"    "Abca1"      "C5ar1"     7
##
## [43] "Dhrs3"       "Trim47"      "Cd63"        "Tmem37"     "Camk1"       ""           8
"Retnla"
## [49] "Mmp9"        "Serpina8"   "Ccl24"       "F13a1"       "Mpp1"        "Msrl"      9
## [55] "Cd38"        "Ltc4s"       "C4b"         "Timd4"       "Ednrb"      "Fcna"     10
## [61] "Lyve1"       "Cd209f"     "Tcn2"        "Ninj1"       "Ccl7"        "Wwp1"     11
## [67] "Gas6"        "Folr2"       "Ccl8"        "Cbr2"        "Hmox1"      "Blvrb"    12
##
## [73] "Ctsb"        ""           ""           ""           ""           ""           13

write.csv(geneSymbol.changed.cd206, file = "./geneSymbol_changed_cd206_IM.csv",
          quote = FALSE, row.names = FALSE)
write.csv(geneSymbol.changed.mhcii, file = "./geneSymbol_changed_mhcii_IM.csv",
          quote = FALSE, row.names = FALSE)
```

## 5.6 GO enrichment on the changed/specific genes

```
suppressMessages(library(clusterProfiler))
source("../R/entrez2symbol.R")
source("../R/replaceEntrezID.R")
```

### 5.6.1 GO enrichment on MHCII IM

```
symb <- geneSymbol.changed.mhcii
de_entrez <- bitr( geneID = symb, fromType = "SYMBOL", toType = "ENTREZID"
  , OrgDb = "org.Mm.eg.db", drop = TRUE ) $ ENTREZID
result.enrichGO <- enrichGO(de_entrez, OrgDb = "org.Mm.eg.db", ont = "BP")
result.enrichGO <- replaceEntrezID(result.enrichGO, organism = "mmu")
write.csv(result.enrichGO@result, file = "../Results_enrichment/enrichGO_MHCII_IM_specific_genes.csv")
result.enrichGO@result
```

```

## # A tibble: 1,257 x 9
##   ID      Description  GeneRatio  BgRatio    pvalue  p.adjust    qvalue
##   <chr>    <chr>        <chr>      <chr>      <dbl>      <dbl>      <dbl> <chr>
##   >   <int>
## 1 GO:00~ regulation o~ 9/36       321/23~ 1.07e-9  1.35e-6 8.17e-7
##   Cd24a/~/ 9
## 2 GO:00~ positive reg~ 9/36       479/23~ 3.46e-8  1.17e-5 7.11e-6
##   Cd24a/~/ 9
## 3 GO:19~ positive reg~ 7/36       221/23~ 4.12e-8  1.17e-5 7.11e-6
##   Cd24a/~/ 7
## 4 GO:00~ leukocyte ce~ 8/36       345/23~ 4.45e-8  1.17e-5 7.11e-6
##   Itgb7/~/ 8
## 5 GO:00~ positive reg~ 9/36       496/23~ 4.67e-8  1.17e-5 7.11e-6
##   Cd24a/~/ 9
## 6 GO:00~ positive reg~ 7/36       265/23~ 1.42e-7  2.98e-5 1.80e-5
##   Cd24a/~/ 7
## 7 GO:00~ regulation o~ 8/36       440/23~ 2.86e-7  4.76e-5 2.88e-5
##   Cd24a/~/ 8
## 8 GO:00~ positive reg~ 8/36       449/23~ 3.34e-7  4.76e-5 2.88e-5
##   Wnt11/~/ 8
## 9 GO:19~ regulation o~ 7/36       309/23~ 4.01e-7  4.76e-5 2.88e-5
##   Cd24a/~/ 7
## 10 GO:00~ regulation o~ 6/36      192/23~ 4.56e-7  4.76e-5 2.88e-5
##   Cd24a/~/ 6
## # ... with 1,247 more rows

```

### 5.6.2 GO enrichment on CD206+ IM

```

symb <- geneSymbol.changed.cd206
de_entrez <- bitr( geneID = symb, fromType = "SYMBOL", toType = "ENTREZID"
  , OrgDb = "org.Mm.eg.db", drop = TRUE ) $ ENTREZID
result.enrichGO <- enrichGO(de_entrez, OrgDb = "org.Mm.eg.db", ont = "BP")
result.enrichGO <- replaceEntrezID(result.enrichGO, organism = "mmu")
write.csv(result.enrichGO@result, file = "./Results_enrichment/enrichGO_
  CD206_IM_specific_genes.csv")
result.enrichGO@result

```

```

## # A tibble: 1,842 x 9
##   ID      Description  GeneRatio  BgRatio    pvalue  p.adjust    qvalue
##   <chr>    <chr>        <chr>      <chr>      <dbl>      <dbl>      <dbl> <chr>
##   >   <int>
## 1 GO:00~ leukocyte ~ 17/70       360/23~ 4.11e-16 7.56e-13 4.90e-13
##   Trem2/~/ 17
## 2 GO:00~ leukocyte ~ 14/70       219/23~ 3.30e-15 2.03e-12 1.31e-12
##   Cxcl2/~/ 14
## 3 GO:00~ myeloid le~ 14/70       219/23~ 3.30e-15 2.03e-12 1.31e-12
##   Trem2/~/ 14
## 4 GO:00~ cell chemo~ 14/70       303/23~ 2.90e-13 1.34e-10 8.65e-11
##   Cxcl2/~/ 14
## 5 GO:00~ regulation~ 12/70       217/23~ 2.05e-12 7.55e-10 4.89e-10
##   Trem2/~/ 12

```

```

## 6 GO:00~ granulocyt~ 10/70      126/23~ 4.44e-12 1.36e- 9 8.82e-10 9
Cxcl2/~          10
## 7 GO:00~ mononuclea~ 9/70       89/233~ 6.08e-12 1.60e- 9 1.04e- 9 10
Ccl12/~          9
## 8 GO:00~ neutrophil~ 9/70       99/233~ 1.62e-11 3.72e- 9 2.41e- 9 11
Cxcl2/~          9
## 9 GO:00~ granulocyt~ 10/70      155/23~ 3.53e-11 6.93e- 9 4.48e- 9 12
Cxcl2/~          10
## 10 GO:00~ positive r~ 10/70     156/23~ 3.76e-11 6.93e- 9 4.48e- 9 13
Trem2/~          10
## # ... with 1,832 more rows      14

```

## 6 Functionality analysis of DE genes across pseudotime (common genes)

```

common.genes <- heatSmooth_cd206.unchanged.ordered@row_names_param$labels[ 1
heatSmooth_cd206.unchanged.ordered@row_order] 2

```

### 6.1 Manually classify genes by expression timing peak

Class-1 genes are the genes expressed in monocytes but turned off in the very early phase:

```

genes.class1 <- common.genes[1:which(common.genes == "Gm21188")]
length(genes.class1) 1
## [1] 75 2

```

Class-2 genes are the genes up-regulated in early phase of differentiation and turned off during transit phase.

```

genes.class2 <- common.genes[(which(common.genes == "Gm21188") + 1) : which(
  common.genes == "Diaph3")]
length(genes.class2) 1
## [1] 140 2

```

Class-3 genes are the late upregulated genes during IM differentiation.

```

genes.class3 <- common.genes[(which(common.genes == "Diaph3") + 1) : length(
  common.genes)]
length(genes.class3) 1
## [1] 228 2

```

Save gene lists:

```

write.csv(genes.class1, file = "./common_genes_class1.csv", quote = FALSE) 1
write.csv(genes.class2, file = "./common_genes_class2.csv", quote = FALSE) 2
write.csv(genes.class3, file = "./common_genes_class3.csv", quote = FALSE) 3

```

## 6.2 GO/KEGG enrichment analysis with 3 classes of common genes

### 6.2.1 KEGG enrichment for common genes class 1

```

symb <- genes.class1
1
de_entrez <- bitr( geneID = symb, fromType = "SYMBOL", toType = "ENTREZID"
2
  , OrgDb = "org.Mm.eg.db", drop = TRUE ) $ ENTREZID
result.enrichKEGG <- enrichKEGG(de_entrez, organism = "mmu", keyType = "
3
  ncbi-geneid")
result.enrichKEGG <- replaceEntrezID(result.enrichKEGG, organism = "mmu")
4
write.csv(result.enrichKEGG@result, file = "./Results_enrichment/
5
  enrichKEGG_common_genes_class1.csv")
result.enrichKEGG@result
6

```

	ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	
	geneID	Count	<chr>	<chr>	<chr>	<dbl>	<dbl>	<dbl> <
			chr>	chr>	chr>	<dbl>	<dbl>	<dbl> <
##	1 mmu04145	Phagosome	7/36	182/89~	6.53e-6	0.000974	9.01e-4	1
	Thbs1~	7						2
##	2 mmu05152	Tuberculosis	6/36	180/89~	7.22e-5	0.00538	4.98e-3	3
	Cebpb~	6						4
##	3 mmu05140	Leishmanias~	3/36	70/8942	2.73e-3	0.119	1.10e-1	5
	Cybb/~	3						6
##	4 mmu04918	Thyroid hor~	3/36	74/8942	3.19e-3	0.119	1.10e-1	7
	Plcb1~	3						8
##	5 mmu04970	Salivary se~	3/36	86/8942	4.88e-3	0.145	1.35e-1	9
	Plcb1~	3						10
##	6 mmu04610	Complement ~	3/36	93/8942	6.07e-3	0.151	1.39e-1	11
	Plaur~	3						12
##	7 mmu04613	Neutrophil ~	4/36	207/89~	9.20e-3	0.167	1.55e-1	13
	Plcb1~	4						14
##	8 mmu04621	NOD-like re~	4/36	211/89~	9.83e-3	0.167	1.55e-1	1
	Ifi20~	4						2
##	9 mmu04960	Aldosterone~	2/36	38/8942	1.01e-2	0.167	1.55e-1	3
	Scnn1~	2						4
##	10 mmu04973	Carbohydrat~	2/36	48/8942	1.58e-2	0.236	2.18e-1	1
	Plcb1~	2						2
## # ... with 139 more rows								3

### 6.2.2 GO enrichment for common genes class 1

```

result.enrichGO <- enrichGO(de_entrez, OrgDb = "org.Mm.eg.db", ont = "BP")
1
result.enrichGO <- replaceEntrezID(result.enrichGO, organism = "mmu")
2
write.csv(result.enrichGO@result, file = "./Results_enrichment/enrichGO_
3
  common_genes_class1.csv")
result.enrichGO@result
4

```

	ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	
	geneID	Count	<chr>	<chr>	<chr>	<dbl>	<dbl>	<dbl> <chr>
			<int>					
##	## # A tibble: 1,740 x 9							1
##	ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	2
	geneID	Count	<chr>	<chr>	<chr>	<dbl>	<dbl>	<dbl> <chr>
##	<chr>	<int>						3

## 1 GO:00~ myeloid leu~ 10/72	219/23~ 1.40e-9	2.16e-6 1.65e-6 Gpr35	4
/S~ 10			
## 2 GO:00~ cellular ex~ 7/72	72/233~ 2.48e-9	2.16e-6 1.65e-6 Sell/	5
P1~ 7			
## 3 GO:00~ leukocyte m~ 11/72	360/23~ 1.32e-8	7.68e-6 5.86e-6 Gpr35	6
/S~ 11			
## 4 GO:00~ leukocyte c~ 9/72	219/23~ 2.45e-8	1.07e-5 8.14e-6 Gpr35	7
/S~ 9			
## 5 GO:00~ positive re~ 11/72	418/23~ 6.08e-8	2.12e-5 1.61e-5 Sell/	8
If~ 11			
## 6 GO:00~ type I inte~ 5/72	40/233~ 1.47e-7	3.64e-5 2.78e-5	9
Samhd1/~ 5			
## 7 GO:00~ cellular re~ 5/72	40/233~ 1.47e-7	3.64e-5 2.78e-5	10
Samhd1/~ 5			
## 8 GO:00~ defense res~ 11/72	464/23~ 1.74e-7	3.64e-5 2.78e-5 Slpi/	11
Ce~ 11			
## 9 GO:00~ positive re~ 9/72	278/23~ 1.88e-7	3.64e-5 2.78e-5	12
Ifi204/~ 9			
## 10 GO:00~ response to~ 5/72	45/233~ 2.70e-7	4.70e-5 3.59e-5	13
Samhd1/~ 5			
## # ... with 1,730 more rows			14

### 6.2.3 KEGG enrichment for common genes class 2

```

symb <- genes.class2
de_entrez <- bitr( geneID = symb, fromType = "SYMBOL", toType = "ENTREZID"
  , OrgDb = "org.Mm.eg.db", drop = TRUE ) $ ENTREZID
result.enrichKEGG <- enrichKEGG(de_entrez, organism = "mmu", keyType = "
  ncbi-geneid")
result.enrichKEGG <- replaceEntrezID(result.enrichKEGG, organism = "mmu")
write.csv(result.enrichKEGG@result, file = "./Results_enrichment/
  enrichKEGG_common_genes_class2.csv")
result.enrichKEGG@result

```

## # A tibble: 88 x 9	1
##   ID      Description GeneRatio BgRatio    pvalue p.adjust    qvalue	2
##   geneID Count	3
##   <chr>  <chr>     <chr>     <chr>     <dbl>    <dbl>    <dbl> <	3
##   chr>  <int>	
## 1 mmu04114 Oocyte mei~ 11/50	4
Aurka~ 11	
## 2 mmu04110 Cell cycle 11/50	5
Ccnb1~ 11	
## 3 mmu04914 Progestero~ 9/50	6
Aurka~ 9	
## 4 mmu04115 p53 signal~ 5/50	7
Ccnb1~ 5	
## 5 mmu00240 Pyrimidine~ 4/50	8
Rrm2/~ 4	
## 6 mmu04218 Cellular s~ 6/50	9
Ccnb1~ 6	
## 7 mmu05222 Small cell~ 4/50	10
/C~ 4	

```

## 8 mmu05166 Human T-ce~ 6/50      250/89~ 2.55e- 3  2.65e-2 2.28e-2 11
Bub1b~       6
## 9 mmu05132 Salmonella~ 6/50      253/89~ 2.71e- 3  2.65e-2 2.28e-2 12
Gapdh~       6
## 10 mmu04512 ECM-recept~ 3/50     88/8942 1.29e- 2  1.14e-1 9.81e-2 Fn1 13
/H~          3
## # ... with 78 more rows           14

```

#### 6.2.4 GO enrichment for common genes class 2

```

result.enrichGO <- enrichGO(de_entrez, OrgDb = "org.Mm.eg.db", ont = "BP") 1
result.enrichGO <- replaceEntrezID(result.enrichGO, organism = "mmu") 2
write.csv(result.enrichGO@result, file = "./Results_enrichment/enrichGO_ 3
  common_genes_class2.csv")
result.enrichGO@result 4

```

```

## # A tibble: 1,780 x 9
##   ID      Description GeneRatio BgRatio    pvalue p.adjust    qvalue
##   <chr>  <chr>        <chr>      <chr>      <dbl>    <dbl>    <dbl> <chr>
##   >      <int>
##   1 GO:00~ chromosome~ 50/127    324/23~ 7.39e-60 1.32e-56 1.08e-56 1
Ube2c/~      50
##   2 GO:00~ nuclear ch~ 43/127    262/23~ 2.75e-52 1.75e-49 1.44e-49 2
Ube2c/~      43
##   3 GO:00~ sister chr~ 39/127    181/23~ 2.95e-52 1.75e-49 1.44e-49 3
Ube2c/~      39
##   4 GO:01~ mitotic nu~ 43/127    268/23~ 7.78e-52 2.91e-49 2.39e-49 4
Ube2c/~      43
##   5 GO:00~ mitotic si~ 37/127    151/23~ 8.18e-52 2.91e-49 2.39e-49 5
Ube2c/~      37
##   6 GO:00~ nuclear di~ 46/127    418/23~ 9.43e-48 2.80e-45 2.30e-45 6
Ube2c/~      46
##   7 GO:00~ organelle ~ 47/127    472/23~ 9.12e-47 2.32e-44 1.91e-44 7
Mtfr2/~      47
##   8 GO:00~ spindle or~ 27/127    179/23~ 1.59e-31 3.54e-29 2.91e-29 8
Aurka/~      27
##   9 GO:19~ microtubul~ 24/127    142/23~ 2.56e-29 5.06e-27 4.16e-27 9
Aurka/~      24
##  10 GO:00~ regulation~ 21/127    103/23~ 1.42e-27 2.53e-25 2.08e-25 10
Ube2c/~      21
## # ... with 1,770 more rows 11-14

```

#### 6.2.5 KEGG enrichment for common genes class 3

```

symb <- genes.class3
de_entrez <- bitr( geneID = symb, fromType = "SYMBOL", toType = "ENTREZID" 1
  , OrgDb = "org.Mm.eg.db", drop = TRUE ) $ ENTREZID 2
result.enrichKEGG <- enrichKEGG(de_entrez, organism = "mmu", keyType = " 3
  ncbi-geneid")
result.enrichKEGG <- replaceEntrezID(result.enrichKEGG, organism = "mmu") 4
write.csv(result.enrichKEGG@result, file = "./Results_enrichment/ 5
  enrichKEGG_common_genes_class3.csv")

```

```
result.enrichKEGG@result
```

1  
2  
3  
4  
5  
6  
7  
8  
9  
10  
11  
12  
13  
14

```
## # A tibble: 228 x 9
##   ID      Description  GeneRatio BgRatio    pvalue p.adjust    qvalue
##   <chr>    <chr>       <chr>     <dbl>    <dbl>    <dbl>    <dbl>    <
##   geneID Count
##   <chr>  <int>
##   chr>  <int>
##   1 mmu04210 Apoptosis  15/141    136/89~  2.97e-9  6.78e-7  4.73e-7
##   Ctsc/~    15
##   2 mmu04145 Phagosome  15/141    182/89~  1.56e-7  1.78e-5  1.24e-5
##   Tubb5/~    15
##   3 mmu05166 Human T-cel~ 17/141    250/89~  3.62e-7  2.27e-5  1.58e-5
##   Il1r2~    17
##   4 mmu05202 Transcripti~ 16/141    223/89~  3.98e-7  2.27e-5  1.58e-5
##   Il1r2~    16
##   5 mmu04640 Hematopoiet~ 10/141    94/8942  2.02e-6  9.21e-5  6.42e-5
##   Il1r2~    10
##   6 mmu04380 Osteoclast ~ 11/141    128/89~  5.11e-6  1.94e-4  1.35e-4
##   Fosl2~    11
##   7 mmu05323 Rheumatoid ~ 9/141     87/8942  8.43e-6  2.75e-4  1.91e-4
##   Ctsk/~    9
##   8 mmu05140 Leishmanias~ 8/141     70/8942  1.30e-5  3.70e-4  2.58e-4
##   Itga4~    8
##   9 mmu05152 Tuberculosis 12/141    180/89~  2.55e-5  6.47e-4  4.51e-4
##   Lsp1/~    12
##   10 mmu04064 NF-kappa B ~ 9/141    105/89~  3.89e-5  8.86e-4  6.18e-4
##   Gadd4~    9
##   # ... with 218 more rows
```

### 6.2.6 GO enrichment for common genes class 3

```
result.enrichGO <- enrichGO(de_entrez, OrgDb = "org.Mm.eg.db", ont = "BP")
result.enrichGO <- replaceEntrezID(result.enrichGO, organism = "mmu")
write.csv(result.enrichGO@result, file = "./Results_enrichment/enrichGO_
common_genes_class3.csv")
result.enrichGO@result
```

```
## # A tibble: 3,419 x 9
##   ID      Description  GeneRatio BgRatio    pvalue p.adjust    qvalue
##   <chr>    <chr>       <chr>     <dbl>    <dbl>    <dbl>    <dbl>    <
##   geneID Count
##   <chr>  <int>
##   >  <int>
##   1 GO:00~ regulation ~ 23/224    372/23~  1.72e-12  5.89e-9  4.30e-9
##   Il1r2/~    23
##   2 GO:00~ negative re~ 22/224    462/23~  8.04e-10  7.67e-7  5.61e-7
##   Ce~    22
##   3 GO:00~ positive re~ 17/224    265/23~  8.72e-10  7.67e-7  5.61e-7
##   Ceacam~    17
##   4 GO:19~ regulation ~ 21/224    424/23~  9.85e-10  7.67e-7  5.61e-7
##   Ceacam~    21
##   5 GO:00~ leukocyte c~ 19/224    345/23~  1.12e- 9  7.67e-7  5.61e-7
##   Ceacam~    19
```

```

## 6 GO:00~ leukocyte m~ 19/224      360/23~ 2.27e- 9  1.29e-6 9.44e-7 9
  Itga4/~   19
## 7 GO:00~ regulation ~ 19/224     372/23~ 3.88e- 9  1.75e-6 1.28e-6 10
  Ceacam~   19
## 8 GO:19~ positive re~ 15/224     221/23~ 4.10e- 9  1.75e-6 1.28e-6 11
  Ceacam~   15
## 9 GO:00~ lymphocyte ~ 11/224     103/23~ 4.60e- 9  1.75e-6 1.28e-6 12
  Itga4/~   11
## 10 GO:00~ antigen pro~ 6/224    16/233~ 5.42e- 9  1.85e-6 1.35e-6 Ctss 13
   /H~       6
## # ... with 3,409 more rows        14

```

### 6.2.7 GO enrichment for MHCII IM specific genes + common genes class 3

As the specific genes have limited number. We try add the class 3 genes, which are also terminated differentiation genes. But we have to pay attention that the class 3 gene number is huge compare to the specific genes, so enrichment results will be diluted.

```

symb <- c(geneSymbol.changed.mhcii, genes.class3)                                1
de_entrez <- bitr( geneID = symb, fromType = "SYMBOL", toType = "ENTREZID"          2
                  , OrgDb = "org.Mm.eg.db", drop = TRUE ) $ ENTREZID
result.enrichGO <- enrichGO(de_entrez, OrgDb = "org.Mm.eg.db", ont = "BP")        3
result.enrichGO <- replaceEntrezID(result.enrichGO, organism = "mmu")             4
write.csv(result.enrichGO@result, file = "./Results_enrichment/enrichGO_        5
  MHCIIISpecific_plus_Class3_common.csv")
result.enrichGO@result                                         6

```

```

## # A tibble: 3,607 x 9
##   ID      Description  GeneRatio BgRatio      pvalue p.adjust      qvalue
##   <chr>    <chr>      <chr>      <chr>      <dbl>      <dbl>      <dbl> <
##   chr>    <int>
##   1 GO:00~ regulation ~ 28/260      372/23~ 1.81e-15 4.10e-12 2.84e-12 1
  Cd24a~   28
##   2 GO:00~ leukocyte c~ 27/260      345/23~ 2.28e-15 4.10e-12 2.84e-12 2
  Itgb7~   27
##   3 GO:00~ positive re~ 24/260      265/23~ 3.41e-15 4.10e-12 2.84e-12 3
  Cd24a~   24
##   4 GO:19~ positive re~ 22/260      221/23~ 7.08e-15 6.38e-12 4.41e-12 4
  Cd24a~   22
##   5 GO:00~ antigen pro~ 9/260       16/233~ 2.47e-14 1.78e-11 1.23e-11 H2- 5
  DM~      9
##   6 GO:00~ leukocyte m~ 26/260      360/23~ 5.13e-14 3.08e-11 2.13e-11 6
  Itgb7~   26
##   7 GO:00~ positive re~ 28/260      449/23~ 1.99e-13 1.03e-10 7.09e-11 7
  Wnt11~   28
##   8 GO:00~ regulation ~ 24/260      321/23~ 2.38e-13 1.07e-10 7.40e-11 8
  Cd24a~   24
##   9 GO:19~ regulation ~ 27/260      424/23~ 3.35e-13 1.20e-10 8.30e-11 9
  Cd24a~   27
##  10 GO:00~ positive re~ 29/260     496/23~ 3.65e-13 1.20e-10 8.30e-11 10
   Cd24a~  29
## # ... with 3,597 more rows        11

```

### 6.2.8 GO enrichment for CD206 IM specific genes + common genes class 3

```

symb <- c(geneSymbol.changed.cd206, genes.class3) 1
de_entrez <- bitr( geneID = symb, fromType = "SYMBOL", toType = "ENTREZID" 2
  , OrgDb = "org.Mm.eg.db", drop = TRUE ) $ ENTREZID
result.enrichGO <- enrichGO(de_entrez, OrgDb = "org.Mm.eg.db", ont = "BP") 3
result.enrichGO <- replaceEntrezID(result.enrichGO, organism = "mmu") 4
write.csv(result.enrichGO@result, file = "./Results_enrichment/enrichGO_ 5
  CD206Specific_plus_Class3_common.csv")
result.enrichGO@result 6

```

	## # A tibble: 3,810 x 9	1
	## ID Description GeneRatio BgRatio pvalue p.adjust qvalue	2
	geneID Count	3
	<chr> <chr> <chr> <chr> <dbl> <dbl> <dbl> <chr>	4
>	<int>	5
## 1	GO:00~ leukocyte ~ 36/294 360/23~ 6.24e-22 2.38e-18 1.60e-18 Trem2/~/ 36	6
## 2	GO:00~ myeloid le~ 25/294 219/23~ 6.62e-17 1.26e-13 8.50e-14 Trem2/~/ 25	7
## 3	GO:00~ cell chemo~ 28/294 303/23~ 2.25e-16 2.86e-13 1.93e-13 Cxcl2/~/ 28	8
## 4	GO:00~ leukocyte ~ 24/294 219/23~ 7.21e-16 6.87e-13 4.63e-13 Cxcl2/~/ 24	9
## 5	GO:00~ lymphocyte~ 17/294 103/23~ 1.39e-14 1.06e-11 7.16e-12 Ecm1 /C~/ 17	10
## 6	GO:00~ regulation~ 28/294 372/23~ 4.15e-14 2.26e-11 1.52e-11 Ctsl /E~/ 28	11
## 7	GO:00~ regulation~ 28/294 372/23~ 4.15e-14 2.26e-11 1.52e-11 Trem2/~/ 28	12
## 8	GO:00~ regulation~ 22/294 217/23~ 6.10e-14 2.91e-11 1.96e-11 Trem2/~/ 22	13
## 9	GO:00~ ERK1 and E~ 26/294 325/23~ 8.50e-14 3.60e-11 2.42e-11 Trem2/~/ 26	14
## 10	GO:00~ response t~ 18/294 137/23~ 1.40e-13 5.32e-11 3.58e-11 Irf8 /C~/ 18	
## # ... with 3,800 more rows		

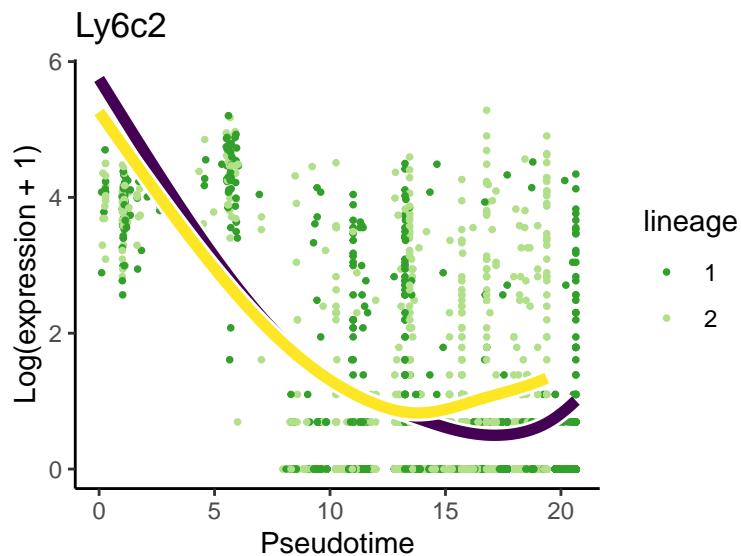
## 7 Show gene expression pattern with TradeSeq results

### 7.1 Class 1 common genes

```

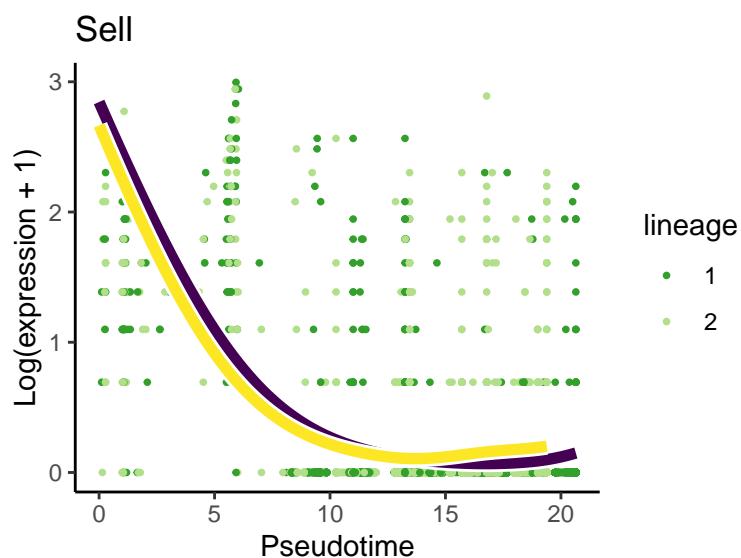
require(ggplot2)
sigGene <- "Ly6c2"
plotSmothers(sce, counts = counts(sce), gene = sigGene) + ggtitle(sigGene 1
  ) + scale_color_manual(values =c("#33A02C", "#B2DF8A")) 2
  3

```

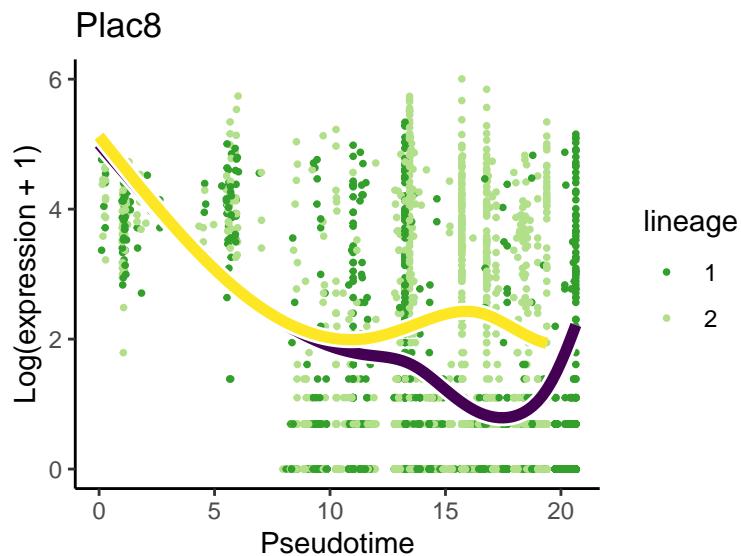


```
ggsave(filename = paste("../Figures/TradeSeq_plot_IM_lineages_",
  ".pdf"),
  width = 4, height = 3) 1
2
```

```
sigGene <- "Sell"
plotSmothers(sce, counts = counts(sce), gene = sigGene) + ggtitle(sigGene 1
  ) + scale_color_manual(values =c("#33A02C", "#B2DF8A")) 2
```



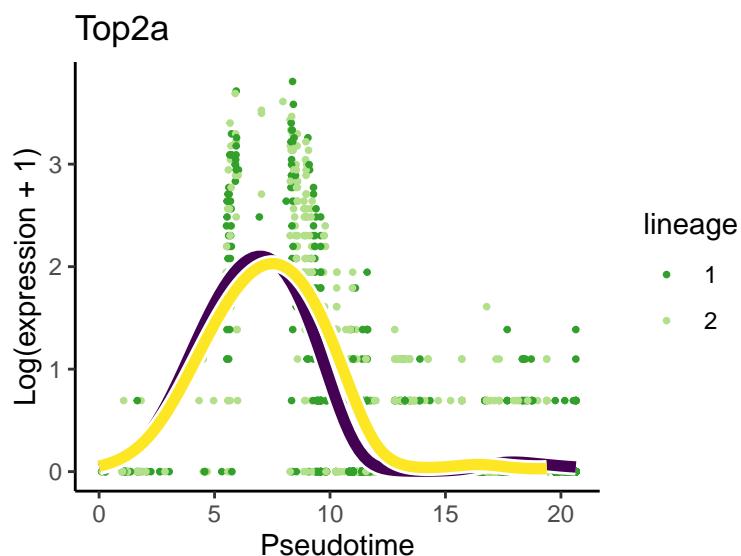
```
sigGene <- "Plac8"
plotSmothers(sce, counts = counts(sce), gene = sigGene) + ggtitle(sigGene 1
  ) + scale_color_manual(values =c("#33A02C", "#B2DF8A")) 2
```



```
ggsave(filename = paste("../Figures/TradeSeq_plot_IM_lineages_",
  sigGene,
  ".pdf"),
  width = 4, height = 3)
```

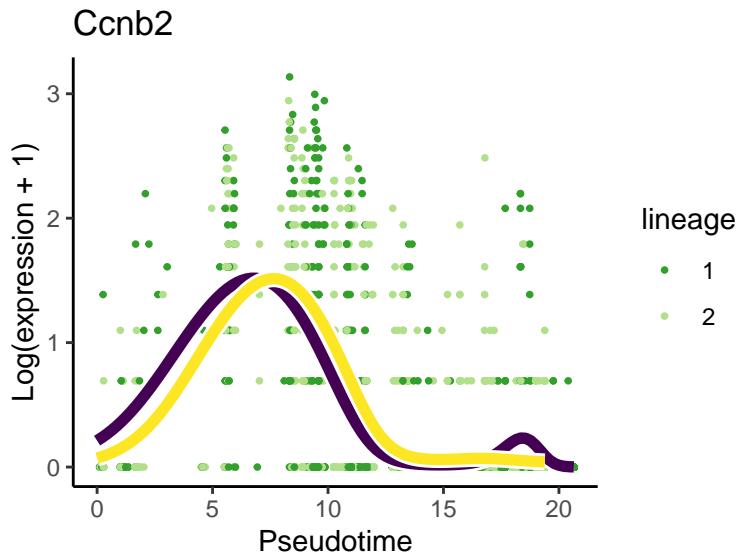
## 7.2 Class 2 common genes

```
sigGene <- "Top2a"
plotSmothers(sce, counts = counts(sce), gene = sigGene) + ggtitle(sigGene)
  + scale_color_manual(values =c("#33A02C", "#B2DF8A"))
```



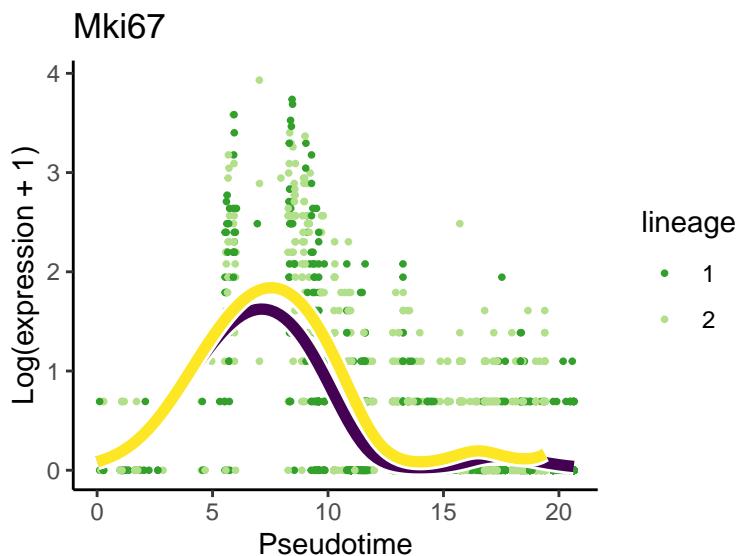
```
ggsave(filename = paste("../Figures/TradeSeq_plot_IM_lineages_",
  sigGene,
  ".pdf"),
  width = 4, height = 3)
```

```
sigGene <- "Ccnb2"
plotSmothers(sce, counts = counts(sce), gene = sigGene) + ggtitle(sigGene)
  + scale_color_manual(values =c("#33A02C", "#B2DF8A"))
```



```
ggsave(filename = paste("../Figures/TradeSeq_plot_IM_lineages_", sigGene,
  ".pdf"),
  width = 4, height = 3) 1
2
```

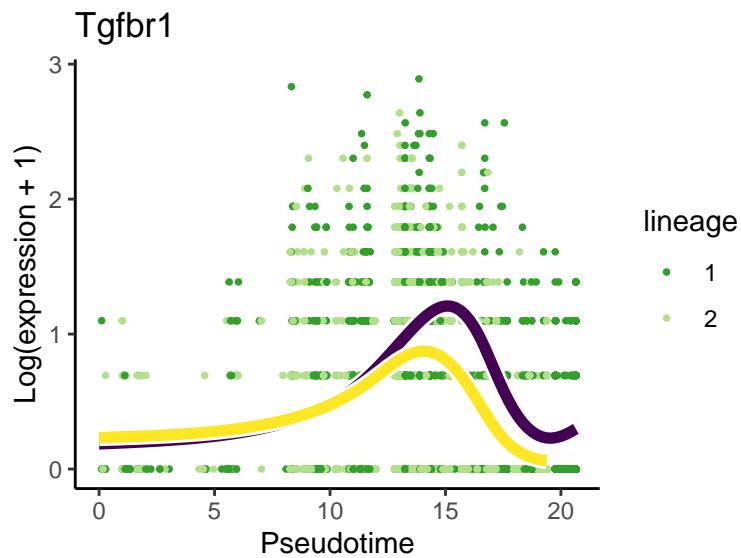
```
sigGene <- "Mki67"
plotSmothers(sce, counts = counts(sce), gene = sigGene) + ggtitle(sigGene)
  + scale_color_manual(values = c("#33A02C", "#B2DF8A")) 1
2
```



```
ggsave(filename = paste("../Figures/TradeSeq_plot_IM_lineages_", sigGene,
  ".pdf"),
  width = 4, height = 3) 1
2
```

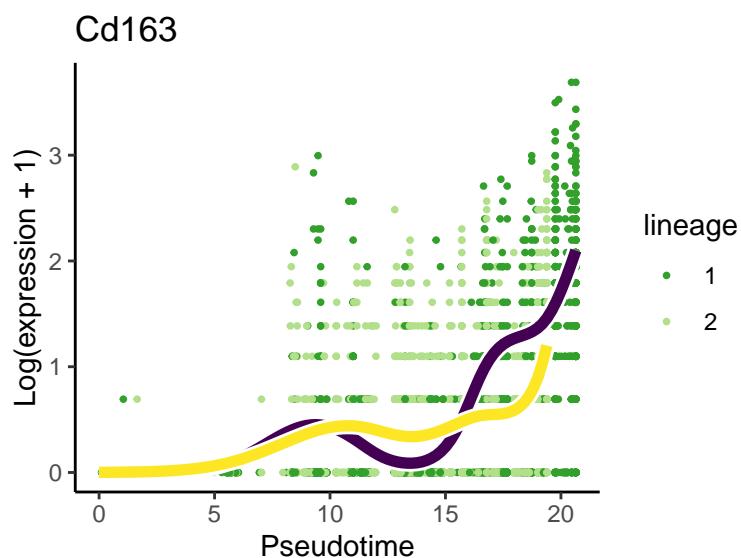
### 7.3 Class 3 common genes

```
sigGene <- "Tgfbri1"
plotSmothers(sce, counts = counts(sce), gene = sigGene) + ggtitle(sigGene)
  + scale_color_manual(values = c("#33A02C", "#B2DF8A")) 1
2
```



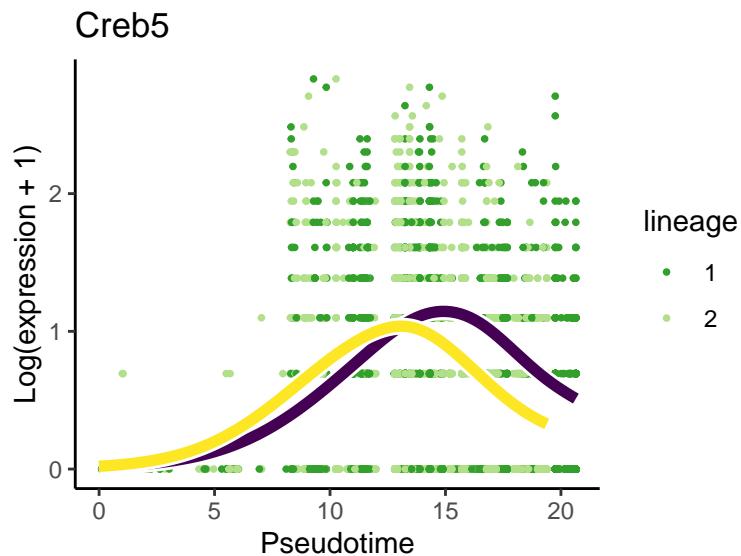
```
1 ggsave(filename = paste("../Figures/TradeSeq_plot_IM_lineages_", sigGene,
2   ".pdf"),
  width = 4, height = 3)
```

```
1 sigGene <- "Cd163"
2 plotSmothers(sce, counts = counts(sce), gene = sigGene) + ggtitle(sigGene)
  + scale_color_manual(values =c("#33A02C", "#B2DF8A"))
```



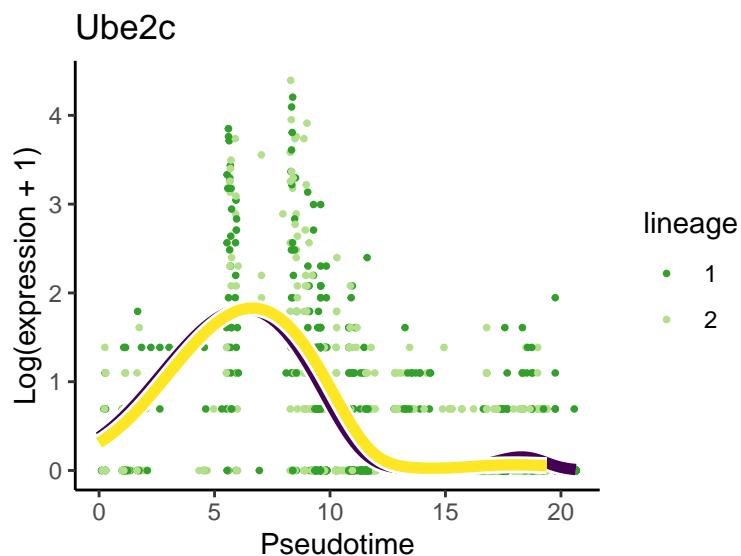
```
1 ggsave(filename = paste("../Figures/TradeSeq_plot_IM_lineages_", sigGene,
2   ".pdf"),
  width = 4, height = 3)
```

```
1 sigGene <- "Creb5"
2 plotSmothers(sce, counts = counts(sce), gene = sigGene) + ggtitle(sigGene)
  + scale_color_manual(values =c("#33A02C", "#B2DF8A"))
```



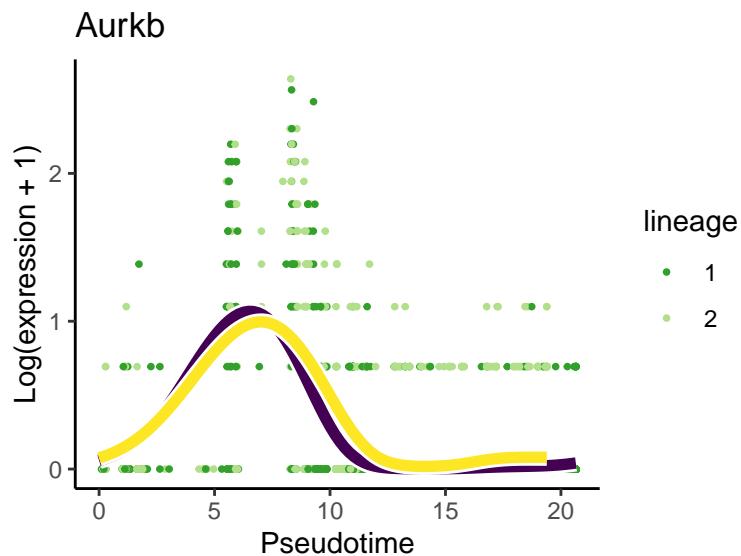
```
ggsave(filename = paste("../Figures/TradeSeq_plot_IM_lineages_", sigGene, ".pdf"),
       width = 4, height = 3) 1
2
```

```
sigGene <- "Ube2c"
plotSmothers(sce, counts = counts(sce), gene = sigGene) + ggtitle(sigGene) 1
  + scale_color_manual(values = c("#33A02C", "#B2DF8A")) 2
```



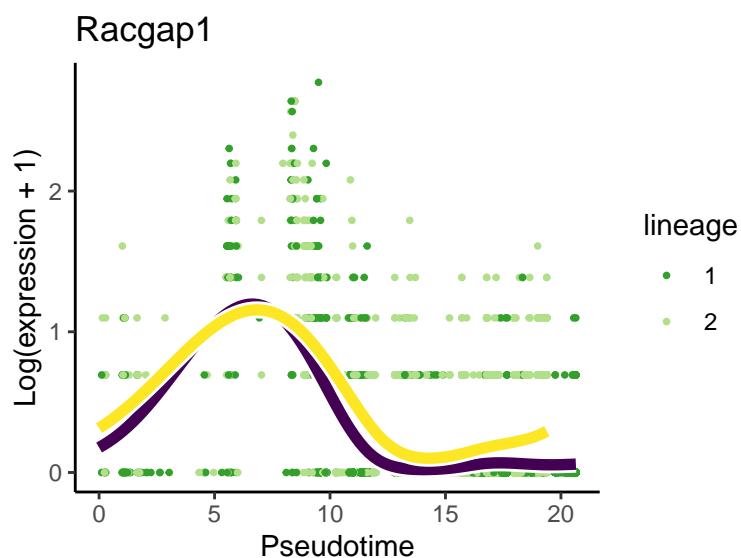
```
ggsave(filename = paste("../Figures/TradeSeq_plot_IM_lineages_", sigGene, ".pdf"),
       width = 4, height = 3) 1
2
```

```
sigGene <- "Aurkb"
plotSmothers(sce, counts = counts(sce), gene = sigGene) + ggtitle(sigGene) 1
  + scale_color_manual(values = c("#33A02C", "#B2DF8A")) 2
```



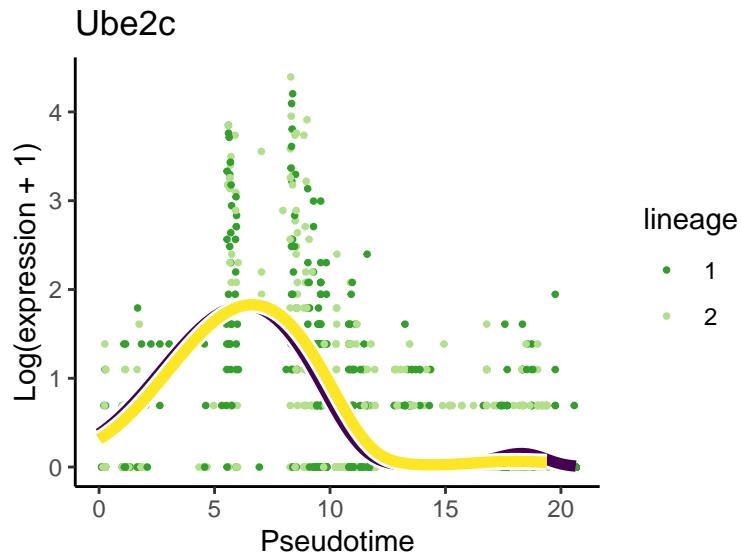
```
ggsave(filename = paste("../Figures/TradeSeq_plot_IM_lineages_", sigGene, ".pdf"),
       width = 4, height = 3) 1
2
```

```
sigGene <- "Racgap1"
plotSmothers(sce, counts = counts(sce), gene = sigGene) + ggtitle(sigGene) 1
) + scale_color_manual(values =c("#33A02C", "#B2DF8A")) 2
```



```
ggsave(filename = paste("../Figures/TradeSeq_plot_IM_lineages_", sigGene, ".pdf"),
       width = 4, height = 3) 1
2
```

```
sigGene <- "Ube2c"
plotSmothers(sce, counts = counts(sce), gene = sigGene) + ggtitle(sigGene) 1
) + scale_color_manual(values =c("#33A02C", "#B2DF8A")) 2
```



```

ggsave(filename = paste("../Figures/TradeSeq_plot_IM_lineages_",
  ".pdf"),
  width = 4, height = 3)
  
```

## 8 Session information

R session:

```

sessionInfo()
  
```

---

```

## R version 4.0.3 (2020-10-10)
## Platform: x86_64-pc-linux-gnu (64-bit)
## Running under: Ubuntu 20.04.3 LTS
##
## Matrix products: default
## BLAS:    /usr/lib/x86_64-linux-gnu/openblas-pthread/libblas.so.3
## LAPACK:  /usr/lib/x86_64-linux-gnu/openblas-pthread/liblapack.so.3
##
## locale:
##   [1] LC_CTYPE=en_US.UTF-8          LC_NUMERIC=C
##   [3] LC_TIME=en_GB.UTF-8          LC_COLLATE=en_US.UTF-8
##   [5] LC_MONETARY=en_GB.UTF-8      LC_MESSAGES=en_US.UTF-8
##   [7] LC_PAPER=en_GB.UTF-8         LC_NAME=C
##   [9] LC_ADDRESS=C                 LC_TELEPHONE=C
##  [11] LC_MEASUREMENT=en_GB.UTF-8   LC_IDENTIFICATION=C
##
## attached base packages:
##   [1] stats4     parallel   grid       stats      graphics   grDevices utils
##   [8] datasets   methods    base
##
## other attached packages:
##   [1] org.Mm.eg.db_3.12.0        AnnotationDbi_1.52.0
##   [3] clusterProfiler_3.18.1     clusterExperiment_2.11.2
##   [5] tradeSeq_1.4.0             magrittr_2.0.1
##   [7] monocle3_1.0.0            SingleCellExperiment_1.12.0
  
```

## [9] SummarizedExperiment_1.20.0	GenomicRanges_1.42.0	26
## [11] GenomeInfoDb_1.26.7	IRanges_2.24.1	27
## [13] S4Vectors_0.28.1	MatrixGenerics_1.2.1	28
## [15] matrixStats_0.61.0	Biobase_2.50.0	29
## [17] BiocGenerics_0.36.1	circlize_0.4.13	30
## [19] RColorBrewer_1.1-2	dplyr_1.0.7	31
## [21] ggplot2_3.3.5	ComplexHeatmap_2.6.2	32
## [23] SeuratObject_4.0.4	Seurat_4.0.5	33
##		34
## loaded via a namespace (and not attached):		35
## [1] rsvd_1.0.5	ica_1.0-2	36
## [4] class_7.3-17	foreach_1.5.1	37
## [7] crayon_1.4.2	spatstat.core_2.3-2	38
## [10] rhdf5filters_1.2.1	nlme_3.1-153	39
## [13] GOSemSim_2.16.1	rlang_0.4.12	40
## [16] ROCR_1.0-11	irlba_2.3.5	41
## [19] phylobase_0.8.10	BiocParallel_1.24.1	42
## [22] bit64_4.0.5	glue_1.5.1	43
## [25] rngtools_1.5.2	sctransform_0.3.2	44
.0-0		
## [28] classInt_0.4-3	DOSE_3.16.0	45
## [31] VGAM_1.1-5	tidyselect_1.1.1	46
## [34] XML_3.99-0.8	tidyrr_1.1.4	47
## [37] sf_1.0-4	xtable_1.8-4	48
## [40] evaluate_0.14	cli_3.1.0	49
## [43] rstudioapi_0.13	miniUI_0.1.1.1	50
## [46] rpart_4.1-15	fastmatch_1.1-3	51
## [49] locfdr_1.1-8	shiny_1.7.1	52
## [52] xfun_0.28	clue_0.3-60	53
## [55] tidygraph_1.2.0	tibble_3.1.6	54
## [58] ggrepel_0.9.1	ape_5.5	55
## [61] png_0.1-7	future_1.23.0	56
## [64] bitops_1.0-7	slam_0.1-49	57
## [67] plyr_1.8.6	sparsesvd_0.2	58
## [70] coda_0.19-4	pillar_1.6.4	59
## [73] cachem_1.0.6	kernlab_0.9-29	60
## [76] GetoptLong_1.0.5	gmodels_2.18.1	61
## [79] ellipsis_0.3.2	generics_0.1.1	62
## [82] tools_4.0.3	rnc1_0.8.4	63
## [85] tweenr_1.0.2	fgsea_1.16.0	64
## [88] DelayedArray_0.16.3	fastmap_1.1.0	65
.10.0		
## [91] compiler_4.0.3	abind_1.4-5	66
## [94] pkgmaker_0.32.2	plotly_4.10.0	67
.2.4		
## [97] gridExtra_2.3	edgeR_3.32.1	68
## [100] deldir_1.0-6	utf8_1.2.2	69
## [103] wk_0.5.0	jsonlite_1.7.2	70
## [106] prcurve_2.1.6	docopt_0.7.1	71
## [109] genefilter_1.72.1	lazyeval_0.2.2	72
## [112] promises_1.2.0.1	doParallel_1.0.16	73
## [115] spatstat.utils_2.2-0	reticulate_1.22	74
## [118] cowplot_1.1.1	textshaping_0.3.6	75
## [121] downloader_0.4	softImpute_1.4-1	76

## [124] igraph_1.2.9	HDF5Array_1.18.1	survival_3.2-7	77
## [127] yaml_2.2.1	systemfonts_1.0.3	DDRTree_0.1.5	78
## [130] htmltools_0.5.2	memoise_2.0.1	locfit_1.5-9.4	79
## [133] graphlayouts_0.7.2	viridisLite_0.4.0	digest_0.6.29	80
## [136] assertthat_0.2.1	mime_0.12	densityClust_0.3	81
## [139] registry_0.5-1	units_0.7-2	RSSQLite_2.2.9	82
## [142] yulab.utils_0.0.4	future.apply_1.8.1	data.table_1.14.2	83
## [145] blob_1.2.2	RNeXML_2.4.5	ragg_1.2.1	84
## [148] fastICA_1.2-3	splines_4.0.3	labeling_0.4.2	85
## [151] Rhdf5lib_1.12.1	Cairo_1.5-12.2	RCurl_1.98-1.5	86
## [154] monocle_2.18.0	hms_1.1.1	r hdf5_2.34.0	87
## [157] colorspace_2.0-2	BiocManager_1.30.16	shape_1.4.6	88
## [160] Rcpp_1.0.7	RANN_2.6.1	enrichplot_1.10.2	89
## [163] fansi_0.5.0	parallelly_1.29.0	R6_2.5.1	90
## [166] ggridges_0.5.3	lifecycle_1.0.1	gdata_2.18.0	91
## [169] leiden_0.3.9	D0.db_2.9	Matrix_1.3-4	92
## [172] howmany_0.3-1	qvalue_2.22.0	RcppAnnoy_0.0.19	93
## [175] iterators_1.0.13	stringr_1.4.0	htmlwidgets_1.5.4	94
## [178] beachmat_2.6.4	polyclip_1.10-0	purrr_0.3.4	95
## [181] shadowtext_0.0.9	terra_1.4-22	mgcv_1.8-33	96
## [184] globals_0.14.0	patchwork_1.1.1	slingshot_1.8.0	97
## [187] codetools_0.2-18	G0.db_3.12.1	FNN_1.1.3	98
## [190] gtools_3.9.2	prettyunits_1.1.1	gridBase_0.4-7	99
## [193] gtable_0.3.0	DBI_1.1.1	ggfun_0.0.4	100
## [196] tensor_1.5	httr_1.4.2	highr_0.9	101
## [199] KernSmooth_2.23-20	stringi_1.7.6	progress_1.2.2	102
## [202] reshape2_1.4.4	farver_2.1.0	uuid_1.0-3	103
## [205] spdep_1.1-12	annotate_1.68.0	viridis_0.6.2	104
## [208] magick_2.7.3	xml2_1.3.3	combinat_0.0-8	105
## [211] rvcheck_0.2.1	boot_1.3-25	s2_1.0.7	106
## [214] ade4_1.7-18	scattermore_0.7	bit_4.0.4	107
## [217] scatterpie_0.1.7	spatstat.data_2.1-0	ggraph_2.0.5	108
## [220] pkgconfig_2.0.3	knitr_1.36		109

## 9 References