

Scoring cell Epithelial

Abinet Joan

2023-09-28 13:30:59 +0200

Contents

Loading package	1
Loading the normalised count matrix	1
Get score AT2	1
Get score PrimedAT2	2
Get score DATP	2
Get score AT1	2
Write csv file for singscore	3
plotting score in pheatmap	3

Loading package

```
suppressMessages(library(dplyr))
suppressMessages(library(patchwork))
suppressMessages(library(ggplot2))
suppressMessages(library(readxl))
suppressMessages(library(singscore))
suppressMessages(library(pheatmap))
```

Loading the normalised count matrix

```
Norm_exprMat <- read_excel("../Data_Thomas/Q3 - publication - V2.xlsx", sheet =
"TargetCountMatrix")
Norm_exprMat <- as.data.frame(Norm_exprMat)
rownames(Norm_exprMat) <- Norm_exprMat$TargetName
Norm_exprMat$TargetName <- NULL
```

Get score AT2

```
markers_AT2 <- read_csv("Signature/Markers_AT2.csv")

markers_AT2 <- markers_AT2$X[1:20]

rankData <- rankGenes(Norm_exprMat)
```

```
scoredf <- simpleScore(rankData, upSet = markers_AT2)

## Warning in checkGenes(upSet, rownames(rankData)): 2 genes missing: Sdpr, Malat1
AT2 <- scoredf$TotalScore
```

Get score PrimedAT2

```
markers.PrimedAT2 <- read.csv("Signature/Markers_PrimedAT2.csv")
markers.PrimedAT2 <- markers.PrimedAT2$X[1:20]

rankData <- rankGenes(Norm_exprMat)

scoredf <- simpleScore(rankData, upSet = markers.PrimedAT2)

## Warning in checkGenes(upSet, rownames(rankData)): 3 genes missing: Atp5f1,
## Wbp5, Ngfrap1
PrimedAT2 <- scoredf$TotalScore

cell_singscore <- data.frame(AT2, PrimedAT2)
```

Get score DATP

```
markers.DATP <- read.csv("Signature/Markers_DATP.csv")
markers.DATP <- markers.DATP$X[1:20]

rankData <- rankGenes(Norm_exprMat)

scoredf <- simpleScore(rankData, upSet = markers.DATP)

## Warning in checkGenes(upSet, rownames(rankData)): 2 genes missing: Gm26870,
## Hist1h2bc
cell_singscore <- cbind(cell_singscore, DATP = scoredf$TotalScore)
```

Get score AT1

```
markers.AT1 <- read.csv("Signature/Markers_AT1.csv")
markers.AT1 <- markers.AT1$X[1:20]

rankData <- rankGenes(Norm_exprMat)
scoredf <- simpleScore(rankData, upSet = markers.AT1)

## Warning in checkGenes(upSet, rownames(rankData)): 2 genes missing: Ly6i, mt-Nd2
cell_singscore <- cbind(cell_singscore, AT1 = scoredf$TotalScore)
```

Write csv file for singscore

```
rownames(cell_singscore) <- colnames(Norm_exprMat)

#write.csv(cell_singscore, "Score_Epithelial.csv")
```

plotting score in pheatmap

```
annotation_sample <- read_excel("../Data_Thomas/Q3 - publication - V2.xlsx", sheet =
"SegmentProperties")
singscores <- cell_singscore
singscores <- merge(singscores, annotation_sample[,c(5,25)], by.x = "row.names", by.y =
"SegmentDisplayName")
singscores <- singscores[order(singscores$Group),]
singscores$Group<- NULL

rownames(singscores) <- singscores$Row.names
singscores$Row.names <- NULL

df <- as.data.frame(annotation_sample[,c(5,25)])
df$Group <- as.factor(df$Group)
levels(df$Group) <- c( "Extraleisional", "Intraleisional", "Perileisional", "Control")
rownames(df)<-df$SegmentDisplayName
df$SegmentDisplayName <- NULL

pheatmap_singscore<- pheatmap(t(singscores), cluster_rows=FALSE, show_rownames=T,
cluster_cols=F, scale = "row", annotation_col=df, main = "Singscores",
labels_row = c("AT2", "Primed AT2", "DATP", "AT1"), color =
colorRampPalette(c("blue", "white", "red"))(100))
```


## [1] KEGGREST_1.40.0	SummarizedExperiment_1.30.2
## [3] gtable_0.3.3	xfun_0.39
## [5] lattice_0.21-8	Biobase_2.60.0
## [7] vctrs_0.6.3	tools_4.3.1
## [9] bitops_1.0-7	generics_0.1.3
## [11] stats4_4.3.1	tibble_3.2.1
## [13] fansi_1.0.4	AnnotationDbi_1.62.1
## [15] RSQLite_2.3.1	highr_0.10
## [17] blob_1.2.4	pkgconfig_2.0.3
## [19] Matrix_1.6-0	RColorBrewer_1.1-3
## [21] S4Vectors_0.38.1	graph_1.78.0
## [23] lifecycle_1.0.3	GenomeInfoDbData_1.2.10
## [25] farver_2.1.1	stringr_1.5.0
## [27] compiler_4.3.1	Biostrings_2.68.1
## [29] munsell_0.5.0	GenomeInfoDb_1.36.0
## [31] htmltools_0.5.5	RCurl_1.98-1.12
## [33] yaml_2.3.7	tidyr_1.3.0
## [35] pillar_1.9.0	crayon_1.5.2
## [37] limma_3.56.2	DelayedArray_0.26.3
## [39] cachem_1.0.8	locfit_1.5-9.8
## [41] tidyselect_1.2.0	digest_0.6.33
## [43] stringi_1.7.12	reshape2_1.4.4
## [45] purrr_1.0.1	fastmap_1.1.1
## [47] grid_4.3.1	colorspace_2.1-0
## [49] cli_3.6.1	magrittr_2.0.3
## [51] S4Arrays_1.0.4	XML_3.99-0.14
## [53] utf8_1.2.3	GSEABase_1.62.0
## [55] edgeR_3.42.4	withr_2.5.0
## [57] scales_1.2.1	bit64_4.0.5
## [59] rmarkdown_2.23	XVector_0.40.0
## [61] httr_1.4.6	matrixStats_1.0.0
## [63] bit_4.0.5	cellranger_1.1.0
## [65] png_0.1-8	memoise_2.0.1
## [67] evaluate_0.21	knitr_1.43
## [69] GenomicRanges_1.52.0	IRanges_2.34.0
## [71] rlang_1.1.1	Rcpp_1.0.11
## [73] xtable_1.8-4	glue_1.6.2
## [75] DBI_1.1.3	BiocGenerics_0.46.0
## [77] rstudioapi_0.14	annotate_1.78.0
## [79] plyr_1.8.8	R6_2.5.1
## [81] MatrixGenerics_1.12.2	zlibbioc_1.46.0