

6-Gene Ontology enrichment

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2021-09-30 16:11:46 +0200

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1 Description

The DE gene lists used for enrichment analyses were calculated using Seurat function FindMarkers[1] with default arguments except only.pos = TRUE in order to output only positively regulated genes and logfc.threshold of 0.2. KEGG and Gene Ontology enrichment analyses were made using enrichKEGG and enrichGO functions from package clusterProfiler package[2] with default arguments.

2 Load data and packages

```
library(Seurat)
library(ggplot2)
library(dplyr)
results <- readRDS(file = "../3-Merge and cell typing/so.merged_clusters.
  seuratObject.Rds")
```

3 DE genes and GO enrichment

3.1 Cluster 1 DE analysis and GO enrichment

The Cluster 1 mentioned in manuscript refers to cluster 0 in the codes following. The same for cluster 2-4 in manuscript, they are cluster 1-3 in the codes.

Calculate the DE genes.

```
de_ident0 <- FindMarkers(results, ident.1 = "0", only.pos = TRUE, logfc.
  threshold = 0.2)
head(de_ident0)
```

```
## # A tibble: 6 x 5
##   p_val avg_log2FC pct.1 pct.2 p_val_adj
##   <dbl>      <dbl> <dbl> <dbl>      <dbl>
## 1      0      0.689 1      0.935      0
## 2      0      0.682 0.994 0.892      0
## 3      0      0.622 0.998 0.912      0
## 4      0      0.379 0.993 0.941      0
## 5      0      0.733 0.477 0.107      0
## 6      0      0.670 0.994 0.955      0
```

Save data

```
write.csv(de_ident0, file = "../Results_lists/DE_cluster1.csv")
```

KEGG/GO enrichment:

```
library(clusterProfiler)

de_entrez.ident0 <- bitr( geneID = rownames(de_ident0), fromType = "SYMBOL",
  toType = "ENTREZID", OrgDb = "org.Hs.eg.db", drop = TRUE ) $ ENTREZID
result.enrichKEGG.de_ident0 <- enrichKEGG(de_entrez.ident0, organism = "hsa",
  keyType = "ncbi-geneid")
```

```
result.enrichKEGG.de_ident0@result
```

```
## # A tibble: 199 x 9
##   ID      Description  GeneRatio BgRatio  pvalue p.adjust  qvalue geneID
##   <chr>    <chr>        <chr>    <chr>    <dbl>  <dbl>    <dbl> <chr>
##   <int>
## 1 hsa05150 Staphylococ~ 12/99      96/8095 1.52e-9 3.02e-7 2.61e-7 712/7~
##    12
## 2 hsa04940 Type I diab~ 8/99      43/8095 3.83e-8 3.81e-6 3.29e-6 1363/~
##    8
## 3 hsa05330 Allograft r~ 7/99      38/8095 3.06e-7 1.91e-5 1.65e-5 3107/~
##    7
## 4 hsa04612 Antigen pro~ 9/99      78/8095 3.85e-7 1.91e-5 1.65e-5 972/3~
##    9
## 5 hsa05332 Graft-versu~ 7/99      42/8095 6.28e-7 2.50e-5 2.16e-5 3107/~
##    7
## 6 hsa04610 Complement ~ 9/99      85/8095 8.10e-7 2.69e-5 2.32e-5 712/7~
##    9
## 7 hsa05320 Autoimmune ~ 7/99      53/8095 3.22e-6 9.14e-5 7.88e-5 3107/~
##    7
## 8 hsa05416 Viral myoca~ 7/99      60/8095 7.51e-6 1.87e-4 1.61e-4 3107/~
##    7
## 9 hsa04514 Cell adhesi~ 10/99     149/80~ 1.27e-5 2.80e-4 2.41e-4 3107/~
##   10
## 10 hsa04145 Phagosome   10/99     152/80~ 1.51e-5 3.00e-4 2.59e-4 8685/~
##   10
## # ... with 189 more rows
```

```
write.csv(result.enrichKEGG.de_ident0, file = "./Results_lists/enrichKEGG_DE_
cluster1.csv")
```

```
result.enrichGO.de_ident0 <- enrichGO(gene = de_entrez.ident0, OrgDb = "org.Hs
.eg.db")
result.enrichGO.de_ident0@result
```

```
## # A tibble: 459 x 9
##   ID      Description  GeneRatio BgRatio  pvalue p.adjust  qvalue geneID
##   Count
##   <chr>    <chr>        <chr>    <chr>    <dbl>  <dbl>    <dbl> <chr>
##   <int>
## 1 GO:00~ peptide bin~ 19/166     308/18~ 4.99e-11 2.29e-8 1.88e-8 712/86~
##    19
## 2 GO:00~ amide bindi~ 20/166     381/18~ 2.67e-10 6.13e-8 5.01e-8 712/86~
##    20
## 3 GO:00~ peptide ant~ 6/166      31/183~ 3.05e- 7 4.67e-5 3.83e-5 3107/3~
##    6
## 4 GO:00~ MHC class I~ 4/166      10/183~ 1.30e- 6 1.49e-4 1.22e-4 3122/3~
##    4
## 5 GO:00~ peptidase r~ 11/166     229/18~ 7.77e- 6 7.13e-4 5.84e-4 26577/~
##   11
## 6 GO:00~ MHC class I~ 4/166      16/183~ 1.08e- 5 8.26e-4 6.76e-4 972/97~
##    4
## 7 GO:00~ antioxidant~ 7/166      86/183~ 1.29e- 5 8.44e-4 6.91e-4 4259/8~
##    7
```

```
## 8 GO:00~ enzyme inhi~ 13/166 383/18~ 4.71e- 5 2.70e-3 2.21e-3 10628/~ 11
13
## 9 GO:00~ amyloid-bet~ 6/166 77/183~ 6.98e- 5 3.23e-3 2.65e-3 712/86~ 12
6
## 10 GO:00~ MHC protein~ 4/166 25/183~ 7.04e- 5 3.23e-3 2.65e-3 972/97~ 13
4
## # ... with 449 more rows 14
```

```
write.csv(result.enrichGO.de_ident0, file = "./Results_lists/enrichGO_DE_ 1
cluster1.csv")
```

3.2 Cluster 2 DE analysis and GO enrichment

The Cluster 2 mentioned in manuscript refers to cluster 1 in the codes following.

Calculate the DE genes.

```
de_ident1 <- FindMarkers(results, ident.1 = "1", only.pos = TRUE, logfc. 1
threshold = 0.2)
head(de_ident1) 2
```

```
## # A tibble: 6 x 5 1
## p_val avg_log2FC pct.1 pct.2 p_val_adj 2
## <dbl> <dbl> <dbl> <dbl> <dbl> 3
## 1 0 0.421 0.848 0.69 0 4
## 2 0 0.400 0.776 0.555 0 5
## 3 0 0.387 0.274 0.097 0 6
## 4 0 0.345 0.976 0.977 0 7
## 5 0 0.369 0.272 0.094 0 8
## 6 0 0.556 0.416 0.133 0 9
```

Save data

```
write.csv(de_ident1, file = "./Results_lists/DE_cluster2.csv") 1
```

KEGG/GO enrichment:

```
de_entrez.ident1 <- bitr( geneID = rownames(de_ident1), fromType = "SYMBOL", 1
toType = "ENTREZID", OrgDb = "org.Hs.eg.db", drop = TRUE ) $ ENTREZID
result.enrichKEGG.de_ident1 <- enrichKEGG(de_entrez.ident1, organism = "hsa", 2
keyType = "ncbi-geneid")
```

```
result.enrichKEGG.de_ident1@result 1
```

```
## # A tibble: 200 x 9 1
## ID Description GeneRatio BgRatio pvalue p.adjust qvalue geneID 2
Count
## <chr> <chr> <chr> <chr> <dbl> <dbl> <dbl> <chr> 3
<int>
## 1 hsa04142 Lysosome 11/93 128/80~ 2.04e-7 4.08e-5 3.75e-5 58511~ 4
11
## 2 hsa04145 Phagosome 9/93 152/80~ 5.74e-5 5.74e-3 5.29e-3 65336~ 5
9
```

```
## 3 hsa04966 Collecting ~ 4/93 27/8095 2.34e-4 1.19e-2 1.09e-2 24597~ 6
4
## 4 hsa05110 Vibrio chol~ 5/93 50/8095 2.53e-4 1.19e-2 1.09e-2 537/2~ 7
5
## 5 hsa05171 Coronavirus~ 10/93 232/80~ 3.09e-4 1.19e-2 1.09e-2 1536/~ 8
10
## 6 hsa00030 Pentose pho~ 4/93 30/8095 3.56e-4 1.19e-2 1.09e-2 5226/~ 9
4
## 7 hsa03010 Ribosome 8/93 158/80~ 4.41e-4 1.26e-2 1.16e-2 6170/~ 10
8
## 8 hsa05323 Rheumatoid ~ 6/93 93/8095 6.68e-4 1.67e-2 1.54e-2 1435/~ 11
6
## 9 hsa05120 Epithelial ~ 5/93 70/8095 1.21e-3 2.68e-2 2.47e-2 537/2~ 12
5
## 10 hsa04979 Cholesterol~ 4/93 50/8095 2.51e-3 5.02e-2 4.63e-2 3988/~ 13
4
## # ... with 190 more rows 14
```

```
write.csv(result.enrichKEGG.de_ident1, file = "./Results_lists/enrichKEGG_DE_ 1
cluster2.csv")
```

```
result.enrichGO.de_ident1 <- enrichGO(gene = de_entrez.ident1, OrgDb = "org.Hs 1
.eg.db")
result.enrichGO.de_ident1@result 2
```

```
## # A tibble: 379 x 9 1
## ID Description GeneRatio BgRatio pvalue p.adjust qvalue geneID 2
Count
## <chr> <chr> <chr> <chr> <dbl> <dbl> <dbl> <chr> 3
<int>
## 1 GO:0003735 structural~ 8/129 202/18~ 9.16e-5 0.0224 0.0189 6170/~ 4
8
## 2 GO:0009055 electron t~ 6/129 111/18~ 1.33e-4 0.0224 0.0189 65336~ 5
6
## 3 GO:0016209 antioxidan~ 5/129 86/183~ 3.51e-4 0.0224 0.0189 5052/~ 6
5
## 4 GO:0044769 ATPase act~ 3/129 20/183~ 3.54e-4 0.0224 0.0189 24597~ 7
3
## 5 GO:0046961 proton-tra~ 3/129 20/183~ 3.54e-4 0.0224 0.0189 24597~ 8
3
## 6 GO:0043021 ribonucleo~ 6/129 133/18~ 3.55e-4 0.0224 0.0189 4193/~ 9
6
## 7 GO:0015035 protein di~ 3/129 22/183~ 4.74e-4 0.0236 0.0200 7295/~ 10
3
## 8 GO:0052689 carboxylic~ 6/129 143/18~ 5.22e-4 0.0236 0.0200 3988/~ 11
6
## 9 GO:0019829 ATPase-cou~ 4/129 54/183~ 5.61e-4 0.0236 0.0200 24597~ 12
4
## 10 GO:0042625 ATPase-cou~ 4/129 58/183~ 7.37e-4 0.0271 0.0229 24597~ 13
4
## # ... with 369 more rows 14
```

```
write.csv(result.enrichGO.de_ident1, file = "./Results_lists/enrichGO_DE_
cluster2.csv")
```

3.3 Cluster 3 DE analysis

The Cluster 3 mentioned in manuscript refers to cluster 2 in the codes following.

Calculate the DE genes.

```
de_ident2 <- FindMarkers(results, ident.1 = "2", only.pos = TRUE, logfc.
threshold = 0.2)
nrow(de_ident2)
```

```
## [1] 660
```

Save data

```
write.csv(de_ident2, file = "./Results_lists/DE_cluster3.csv")
```

3.4 Cluster 4 DE analysis

The Cluster 4 mentioned in manuscript refers to cluster 3 in the codes following.

Calculate the DE genes.

```
de_ident3 <- FindMarkers(results, ident.1 = "3", only.pos = TRUE, logfc.
threshold = 0.2)
head(de_ident3)
```

```
## # A tibble: 6 x 5
##   p_val avg_log2FC pct.1 pct.2 p_val_adj
##   <dbl>      <dbl> <dbl> <dbl>      <dbl>
## 1     0      0.244 0.274 0.028         0
## 2     0      0.208 0.175 0.002         0
## 3     0      2.34  0.983 0.684         0
## 4     0      0.770 0.473 0.014         0
## 5     0      0.319 0.225 0.009         0
## 6     0      0.885 0.352 0.003         0
```

Save data

```
write.csv(de_ident3, file = "./Results_lists/DE_cluster4.csv")
```

3.5 GO/KEGG enrichment and DE analysis in subpopulations of Cluster 3 after re-clustering

Load Cluster 3 object:

```
results.c2 <- readRDS("../4-Functional characterization of clustered
populations/cluster2_clustered.seuratObject.Rds")
```

REMIND: the subpopulations cluster 1-4 (after reclustering the cluster 3) in the manuscript refer to the cluster 0-3 in the following codes.

Calculate the DE genes.

DE genes for each subpopulations:

```
de_subpop0.c2 <- FindMarkers(object = results.c2, ident.1 = "0", only.pos = 1
  TRUE, logfc.threshold = 0.2, verbose = FALSE)
de_subpop1.c2 <- FindMarkers(object = results.c2, ident.1 = "1", only.pos = 2
  TRUE, logfc.threshold = 0.2, verbose = FALSE)
de_subpop2.c2 <- FindMarkers(object = results.c2, ident.1 = "2", only.pos = 3
  TRUE, logfc.threshold = 0.2, verbose = FALSE)
de_subpop3.c2 <- FindMarkers(object = results.c2, ident.1 = "3", only.pos = 4
  TRUE, logfc.threshold = 0.2, verbose = FALSE)
```

Save data

```
write.csv(de_subpop0.c2, file = "./Results_lists/DE_subpop1_c3.csv") 1
write.csv(de_subpop1.c2, file = "./Results_lists/DE_subpop2_c3.csv") 2
write.csv(de_subpop2.c2, file = "./Results_lists/DE_subpop3_c3.csv") 3
write.csv(de_subpop3.c2, file = "./Results_lists/DE_subpop4_c3.csv") 4
```

Since the subpopulations 2 and 3 are very similar. We would like also to have the DE genes in both subpopulations 2 and 3.

```
de_subpop1_2.c2 <- FindMarkers(object = results.c2, ident.1 = c("1", "2"), 1
  only.pos = TRUE, logfc.threshold = 0.2, verbose = FALSE)
write.csv(de_subpop1_2.c2, file = "./Results_lists/DE_subpop2_and_3_of_c3.csv" 2
  )
```

KEGG enrichment:

```
de_entrez.subpop0.c2 <- bitr( geneID = rownames(de_subpop0.c2), fromType = " 1
  SYMBOL", toType = "ENTREZID", OrgDb = "org.Hs.eg.db", drop = TRUE ) $
  ENTREZID
de_entrez.subpop1.c2 <- bitr( geneID = rownames(de_subpop1.c2), fromType = " 2
  SYMBOL", toType = "ENTREZID", OrgDb = "org.Hs.eg.db", drop = TRUE ) $
  ENTREZID
de_entrez.subpop2.c2 <- bitr( geneID = rownames(de_subpop2.c2), fromType = " 3
  SYMBOL", toType = "ENTREZID", OrgDb = "org.Hs.eg.db", drop = TRUE ) $
  ENTREZID
de_entrez.subpop3.c2 <- bitr( geneID = rownames(de_subpop3.c2), fromType = " 4
  SYMBOL", toType = "ENTREZID", OrgDb = "org.Hs.eg.db", drop = TRUE ) $
  ENTREZID
result.enrichKEGG.de_entrez.subpop0.c2 <- enrichKEGG(de_entrez.subpop0.c2, 5
  organism = "hsa", keyType = "ncbi-geneid") 6
result.enrichKEGG.de_entrez.subpop1.c2 <- enrichKEGG(de_entrez.subpop1.c2, 7
  organism = "hsa", keyType = "ncbi-geneid")
result.enrichKEGG.de_entrez.subpop2.c2 <- enrichKEGG(de_entrez.subpop2.c2, 8
  organism = "hsa", keyType = "ncbi-geneid")
result.enrichKEGG.de_entrez.subpop3.c2 <- enrichKEGG(de_entrez.subpop3.c2, 9
  organism = "hsa", keyType = "ncbi-geneid")
result.enrichG0.de_entrez.subpop0.c2 <- enrichG0(gene = de_entrez.subpop0.c2, 10
  OrgDb = "org.Hs.eg.db") 11
result.enrichG0.de_entrez.subpop1.c2 <- enrichG0(gene = de_entrez.subpop1.c2, 12
  OrgDb = "org.Hs.eg.db")
```

```

result.enrichGO.de_entrez.subpop2.c2 <- enrichGO(gene = de_entrez.subpop2.c2, 13
  OrgDb = "org.Hs.eg.db")
result.enrichGO.de_entrez.subpop3.c2 <- enrichGO(gene = de_entrez.subpop3.c2, 14
  OrgDb = "org.Hs.eg.db")

```

```

write.csv(result.enrichKEGG.de_entrez.subpop0.c2, file = "./Results_lists/ 1
  enrichKEGG_DE_subpop1_c3.csv")
write.csv(result.enrichKEGG.de_entrez.subpop1.c2, file = "./Results_lists/ 2
  enrichKEGG_DE_subpop2_c3.csv")
write.csv(result.enrichKEGG.de_entrez.subpop2.c2, file = "./Results_lists/ 3
  enrichKEGG_DE_subpop3_c3.csv")
write.csv(result.enrichKEGG.de_entrez.subpop3.c2, file = "./Results_lists/ 4
  enrichKEGG_DE_subpop4_c3.csv")

write.csv(result.enrichGO.de_entrez.subpop0.c2, file = "./Results_lists/ 5
  enrichGO_DE_subpop1_c3.csv")
write.csv(result.enrichGO.de_entrez.subpop1.c2, file = "./Results_lists/ 6
  enrichGO_DE_subpop2_c3.csv")
write.csv(result.enrichGO.de_entrez.subpop2.c2, file = "./Results_lists/ 7
  enrichGO_DE_subpop3_c3.csv")
write.csv(result.enrichGO.de_entrez.subpop3.c2, file = "./Results_lists/ 8
  enrichGO_DE_subpop4_c3.csv")

```

Head 10 lines in GO:

For subpop 1:

```

head(result.enrichGO.de_entrez.subpop0.c2@result, 10) 1

```

```

## # A tibble: 10 x 9 1
##   ID      Description GeneRatio BgRatio   pvalue p.adjust   qvalue geneID 2
##   <chr> <chr>      <chr>    <chr>    <dbl>   <dbl>   <dbl> <chr> 3
##   <int> 4
## 1 G0:00~ electron t~ 28/756    111/18~ 5.76e-15 5.00e-12 4.25e-12 1536/8~ 4
##    28
## 2 G0:00~ proton tra~ 25/756    127/18~ 6.00e-11 2.60e- 8 2.21e- 8 6556/9~ 5
##    25
## 3 G0:00~ proton-tra~ 10/756    19/183~ 8.75e-10 2.53e- 7 2.15e- 7 506/51~ 6
##    10
## 4 G0:00~ cadherin b~ 40/756    332/18~ 1.19e- 9 2.59e- 7 2.20e- 7 6282/7~ 7
##    40
## 5 G0:00~ actin bind~ 46/756    437/18~ 5.55e- 9 9.63e- 7 8.19e- 7 6275/1~ 8
##    46
## 6 G0:00~ oxidoreduc~ 20/756    109/18~ 1.75e- 8 2.53e- 6 2.15e- 6 1536/4~ 9
##    20
## 7 G0:00~ proton cha~ 10/756    26/183~ 3.87e- 8 4.80e- 6 4.08e- 6 506/51~ 10
##    10
## 8 G0:00~ actin fila~ 27/756    206/18~ 1.07e- 7 1.16e- 5 9.88e- 6 10109/~ 11
##    27
## 9 G0:00~ oxidoreduc~ 10/756    29/183~ 1.30e- 7 1.26e- 5 1.07e- 5 5447/1~ 12
##    10
## 10 G0:00~ cytochrome~ 9/756     28/183~ 1.11e- 6 8.04e- 5 6.83e- 5 1349/1~ 13
##     9

```


For subpop 2:

```
head(result.enrichGO.de_entrez.subpop1.c2@result, 10)
```

```
## # A tibble: 10 x 9
##   ID      Description  GeneRatio BgRatio  pvalue p.adjust  qvalue geneID
##   <chr>  <chr>          <chr>     <chr>    <dbl>   <dbl>    <dbl> <chr>
##   <int>
## 1 G0:00~ antioxidant~ 13/305    86/183~ 1.68e-9  1.05e-6  8.56e-7 6648/34~
##    13
## 2 G0:00~ chemokine a~ 9/305    49/183~ 9.86e-8  3.08e-5  2.51e-5 6362/63~
##    9
## 3 G0:00~ chemokine r~ 10/305   70/183~ 2.28e-7  4.74e-5  3.87e-5 6362/63~
##   10
## 4 G0:00~ amide bindi~ 21/305   381/18~ 1.75e-6  2.73e-4  2.23e-4 4311/53~
##   21
## 5 G0:00~ peptide bin~ 18/305   308/18~ 4.34e-6  5.42e-4  4.42e-4 4311/54~
##   18
## 6 G0:00~ peptidase r~ 15/305   229/18~ 7.10e-6  7.39e-4  6.03e-4 710/265~
##   15
## 7 G0:00~ oxidoreduct~ 11/305   130/18~ 1.12e-5  1.00e-3  8.17e-4 231/864~
##   11
## 8 G0:00~ proteoglyca~ 6/305    36/183~ 2.57e-5  2.00e-3  1.64e-3 1514/34~
##    6
## 9 G0:00~ carboxylic ~ 13/305   212/18~ 5.75e-5  3.99e-3  3.26e-3 2167/34~
##   13
## 10 G0:00~ endopeptida~ 12/305   192/18~ 9.22e-5  5.71e-3  4.66e-3 710/591~
##   12
```

For subpop 3:

```
head(result.enrichGO.de_entrez.subpop2.c2@result, 10)
```

```
## # A tibble: 10 x 9
##   ID      Description  GeneRatio BgRatio  pvalue p.adjust  qvalue geneID
##   <chr>  <chr>          <chr>     <chr>    <dbl>   <dbl>    <dbl> <chr>
##   <int>
## 1 G0:00~ virus recep~ 14/531    74/183~ 2.25e-8  8.75e-6  6.91e-6 7852/39~
##   14
## 2 G0:01~ exogenous p~ 14/531    74/183~ 2.25e-8  8.75e-6  6.91e-6 7852/39~
##   14
## 3 G0:00~ cytokine bi~ 18/531   135/18~ 6.99e-8  1.36e-5  1.07e-5 7852/88~
##   18
## 4 G0:01~ immune rece~ 18/531   135/18~ 6.99e-8  1.36e-5  1.07e-5 7852/12~
##   18
## 5 G0:00~ proteoglyca~ 9/531    36/183~ 6.23e-7  9.68e-5  7.65e-5 1508/15~
##    9
## 6 G0:00~ integrin bi~ 17/531   144/18~ 9.40e-7  1.22e-4  9.62e-5 6696/10~
##   17
## 7 G0:00~ phospholipi~ 32/531   454/18~ 3.59e-6  3.99e-4  3.15e-4 19/5360~
##   32
```

```
## 8 GO:00~ extracellul~ 10/531 57/183~ 4.81e-6 4.67e-4 3.69e-4 6696/39~ 11
10
## 9 GO:00~ complement ~ 6/531 21/183~ 2.14e-5 1.84e-3 1.46e-3 966/137~ 12
6
## 10 GO:00~ phosphatidy~ 21/531 262/18~ 2.68e-5 2.08e-3 1.64e-3 1687/85~ 13
21
```

For subpop 4:

```
head(result.enrichGO.de_entrez.subpop3.c2@result, 10) 1

## # A tibble: 10 x 9 1
## ID Description GeneRatio BgRatio pvalue p.adjust qvalue geneID 2
## Count
## <chr> <chr> <chr> <chr> <dbl> <dbl> <dbl> <chr> 3
## <int>
## 1 GO:00~ structural~ 82/934 202/18~ 9.37e-53 7.83e-50 6.95e-50 6141/6~ 4
82
## 2 GO:00~ rRNA bindi~ 25/934 64/183~ 2.04e-16 8.51e-14 7.56e-14 6208/6~ 5
25
## 3 GO:00~ MHC class ~ 9/934 10/183~ 2.11e-11 5.87e- 9 5.21e- 9 3112/3~ 6
9
## 4 GO:01~ immune rec~ 24/934 135/18~ 7.57e- 8 1.58e- 5 1.40e- 5 1235/1~ 7
24
## 5 GO:00~ translatio~ 24/934 139/18~ 1.34e- 7 2.24e- 5 1.99e- 5 6208/6~ 8
24
## 6 GO:00~ 5S rRNA bi~ 7/934 11/183~ 2.38e- 7 3.32e- 5 2.95e- 5 6125/6~ 9
7
## 7 GO:00~ translatio~ 17/934 84/183~ 9.08e- 7 1.08e- 4 9.62e- 5 1915/1~ 10
17
## 8 GO:00~ translatio~ 19/934 109/18~ 2.30e- 6 2.41e- 4 2.14e- 4 1915/1~ 11
19
## 9 GO:00~ kinase reg~ 28/934 216/18~ 5.24e- 6 4.83e- 4 4.29e- 4 5570/5~ 12
28
## 10 GO:00~ enzyme inh~ 41/934 383/18~ 5.82e- 6 4.83e- 4 4.29e- 4 8530/9~ 13
41
```

4 Session information

R session:

```
sessionInfo() 1

## R version 4.0.3 (2020-10-10) 1
## Platform: x86_64-pc-linux-gnu (64-bit) 2
## Running under: Ubuntu 20.04.3 LTS 3
## 4
## Matrix products: default 5
## BLAS: /usr/lib/x86_64-linux-gnu/openblas-pthread/libblas.so.3 6
## LAPACK: /usr/lib/x86_64-linux-gnu/openblas-pthread/liblapack.so.3 7
## 8
## locale: 9
## [1] LC_CTYPE=en_US.UTF-8 LC_NUMERIC=C 10
```

```

## [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] parallel stats4      stats      graphics  grDevices utils      datasets
## [8] methods  base
##
## other attached packages:
## [1] org.Hs.eg.db_3.12.0      AnnotationDbi_1.52.0     IRanges_2.24.1
## [4] S4Vectors_0.28.1        Biobase_2.50.0           BiocGenerics_0.36.1
## [7] clusterProfiler_3.18.1  dplyr_1.0.7              ggplot2_3.3.5
## [10] SeuratObject_4.0.2      Seurat_4.0.3
##
## loaded via a namespace (and not attached):
## [1] shadowtext_0.0.8        fastmatch_1.1-3         plyr_1.8.6
## [4] igraph_1.2.6            lazyeval_0.2.2          splines_4.0.3
## [7] BiocParallel_1.24.1     listenv_0.8.0           scattermore_0.7
## [10] digest_0.6.27           htmltools_0.5.1.1       GOsemSim_2.16.1
## [13] viridis_0.6.1           GO.db_3.12.1            fansi_0.5.0
## [16] magrittr_2.0.1          memoise_2.0.0           tensor_1.5
## [19] cluster_2.1.0           ROCR_1.0-11             limma_3.46.0
## [22] graphlayouts_0.7.1      globals_0.14.0          matrixStats_0.60.0
## [25] spatstat.sparse_2.0-0   enrichplot_1.10.2       colorspace_2.0-2
## [28] blob_1.2.2              ggrepel_0.9.1           xfun_0.24
## [31] crayon_1.4.1            jsonlite_1.7.2          scatterpie_0.1.6
## [34] spatstat.data_2.1-0     survival_3.2-7          zoo_1.8-9
## [37] glue_1.4.2              polyclip_1.10-0         gtable_0.3.0
## [40] leiden_0.3.9            future.apply_1.7.0      abind_1.4-5
## [43] scales_1.1.1           DOSE_3.16.0            DBI_1.1.1
## [46] miniUI_0.1.1.1         Rcpp_1.0.7              viridisLite_0.4.0
## [49] xtable_1.8-4           reticulate_1.20         spatstat.core_2.3-0
## [52] bit_4.0.4              htmlwidgets_1.5.3       httr_1.4.2
## [55] fgsea_1.16.0           RColorBrewer_1.1-2     ellipsis_0.3.2
## [58] ica_1.0-2              farver_2.1.0            pkgconfig_2.0.3
## [61] uwot_0.1.10.9000       deldir_0.2-10          utf8_1.2.2
## [64] tidyselect_1.1.1       rlang_0.4.11           reshape2_1.4.4
## [67] later_1.2.0            munsell_0.5.0          tools_4.0.3
## [70] cachem_1.0.5           downloader_0.4          cli_3.0.1
## [73] generics_0.1.0         RSQlite_2.2.7           ggridges_0.5.3
## [76] evaluate_0.14          stringr_1.4.0          fastmap_1.1.0
## [79] yaml_2.2.1             goftest_1.2-2          knitr_1.33
## [82] bit64_4.0.5           fitdistrplus_1.1-5     tidygraph_1.2.0
## [85] purrr_0.3.4           RANN_2.6.1             ggraph_2.0.5
## [88] pbapply_1.4-3          future_1.21.0          nlme_3.1-152
## [91] mime_0.11             DO.db_2.9              compiler_4.0.3
## [94] rstudioapi_0.13        plotly_4.9.4.1         png_0.1-7
## [97] spatstat.utils_2.2-0   tibble_3.1.3          tweenr_1.0.2
## [100] stringi_1.7.3         lattice_0.20-41        Matrix_1.3-4
## [103] vctrs_0.3.8           pillar_1.6.2           lifecycle_1.0.0
## [106] BiocManager_1.30.16    spatstat.geom_2.2-2    lmtest_0.9-38
## [109] RcppAnnoy_0.0.19      data.table_1.14.0      cowplot_1.1.1

```

## [112]	irlba_2.3.3	httpuv_1.6.1	patchwork_1.1.1	65
## [115]	qvalue_2.22.0	R6_2.5.0	promises_1.2.0.1	66
## [118]	KernSmooth_2.23-20	gridExtra_2.3	parallelly_1.27.0	67
## [121]	codetools_0.2-18	MASS_7.3-53	assertthat_0.2.1	68
## [124]	withr_2.4.2	sctransform_0.3.2	mgcv_1.8-33	69
## [127]	grid_4.0.3	rpart_4.1-15	tidyr_1.1.3	70
## [130]	rvcheck_0.1.8	rmarkdown_2.9	Rtsne_0.15	71
## [133]	ggforce_0.3.3	shiny_1.6.0		72

References

1. Hao Y, Hao S, Andersen-Nissen E, Mauck III WM, Zheng S, Butler A, Lee MJ, Wilk AJ, Darby C, Zagar M, Hoffman P, Stoeckius M, Papalexi E, Mimitou EP, Jain J, Srivastava A, Stuart T, Fleming LB, Yeung B, Rogers AJ, McElrath JM, Blish CA, Gottardo R, Smibert P, Satija R. Integrated analysis of multimodal single-cell data. *Cell* [Internet] 2021; Available from: <https://doi.org/10.1016/j.cell.2021.04.048>.
2. Yu G, Wang L-G, Han Y, He Q-Y. clusterProfiler: An r package for comparing biological themes among gene clusters. *OMICS: A Journal of Integrative Biology* 2012; 16: 284–287.