

R Notebook

Code ▾

Test of pbmcs (this works)

Hide

```
library(scGSVA)
```

```
Registered S3 methods overwritten by 'htmltools':
  method          from
  print.html      tools:rstudio
  print.shiny.tag tools:rstudio
  print.shiny.tag.list tools:rstudio
Registered 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
```

Hide

```
data(pbmcs)
hsko <- buildAnnot(species="human",keytype="SYMBOL",anntype="KEGG")
```

```
'select()' returned 1:many mapping between keys and columns
```

Hide

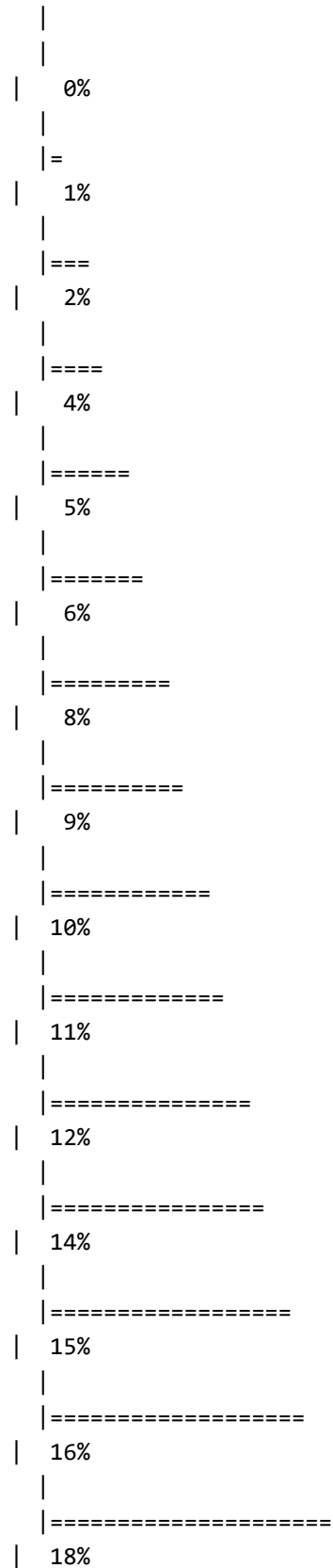
```
res <- scgsva(pbmcs, hsko, verbose = F)
```

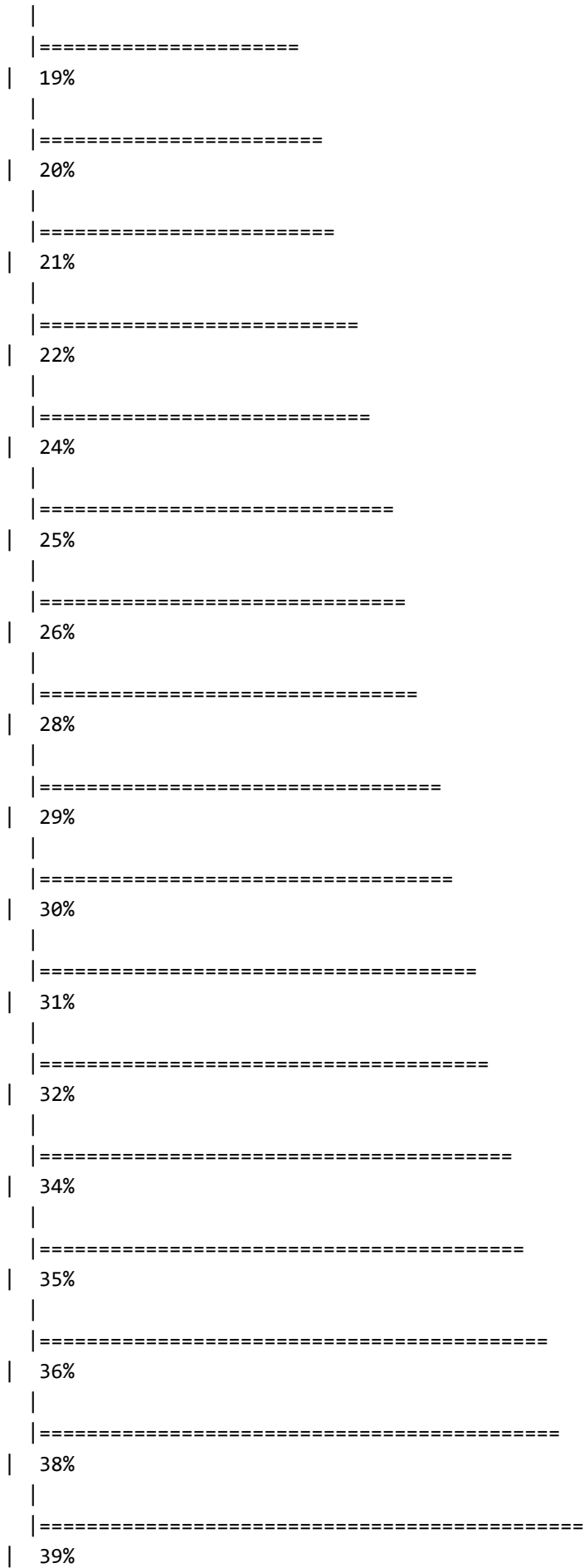
Setting parallel calculations through a MulticoreParam back-end
with workers=4 and tasks=100.

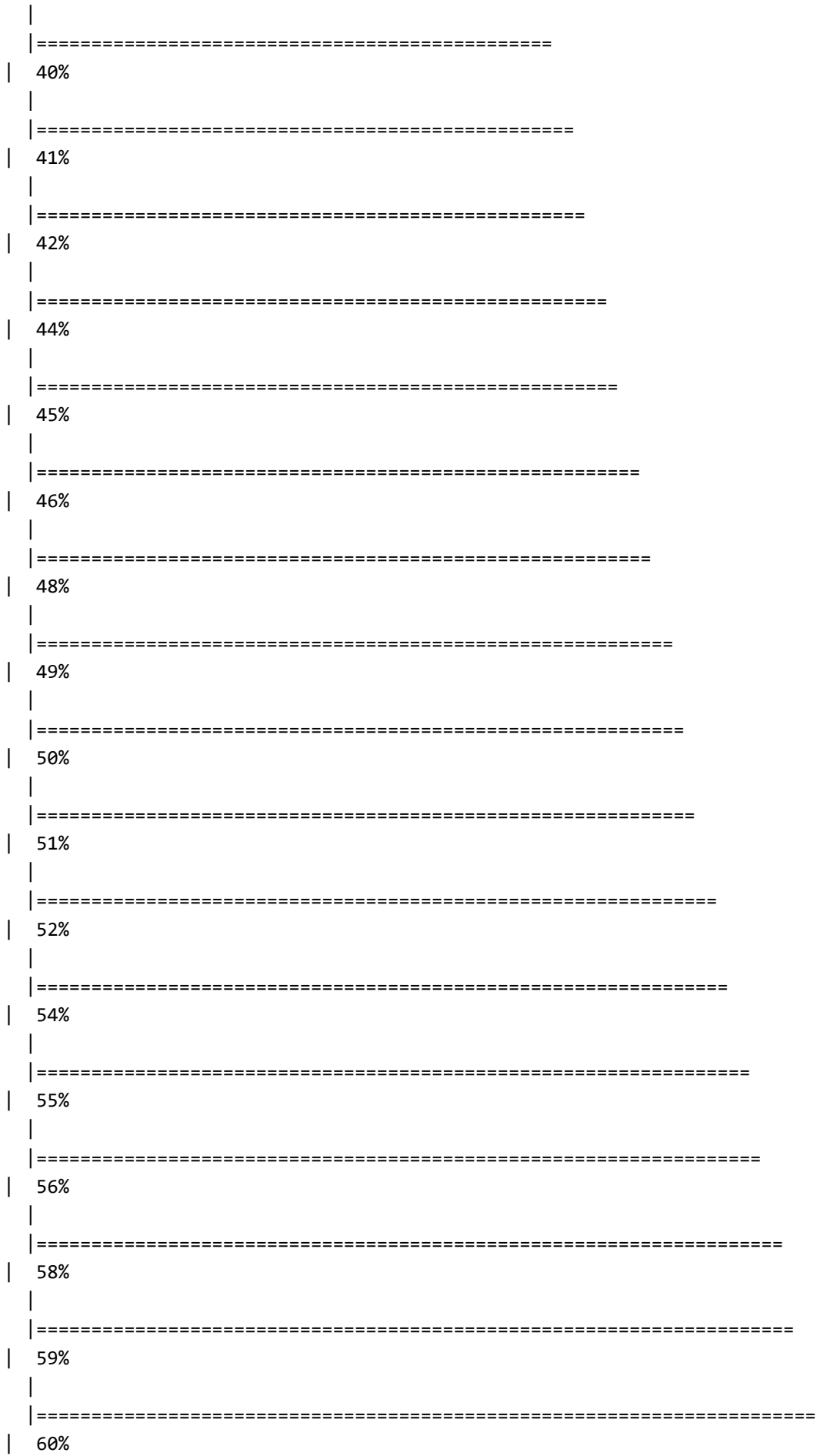
Estimating ssGSEA scores for 117 gene sets.

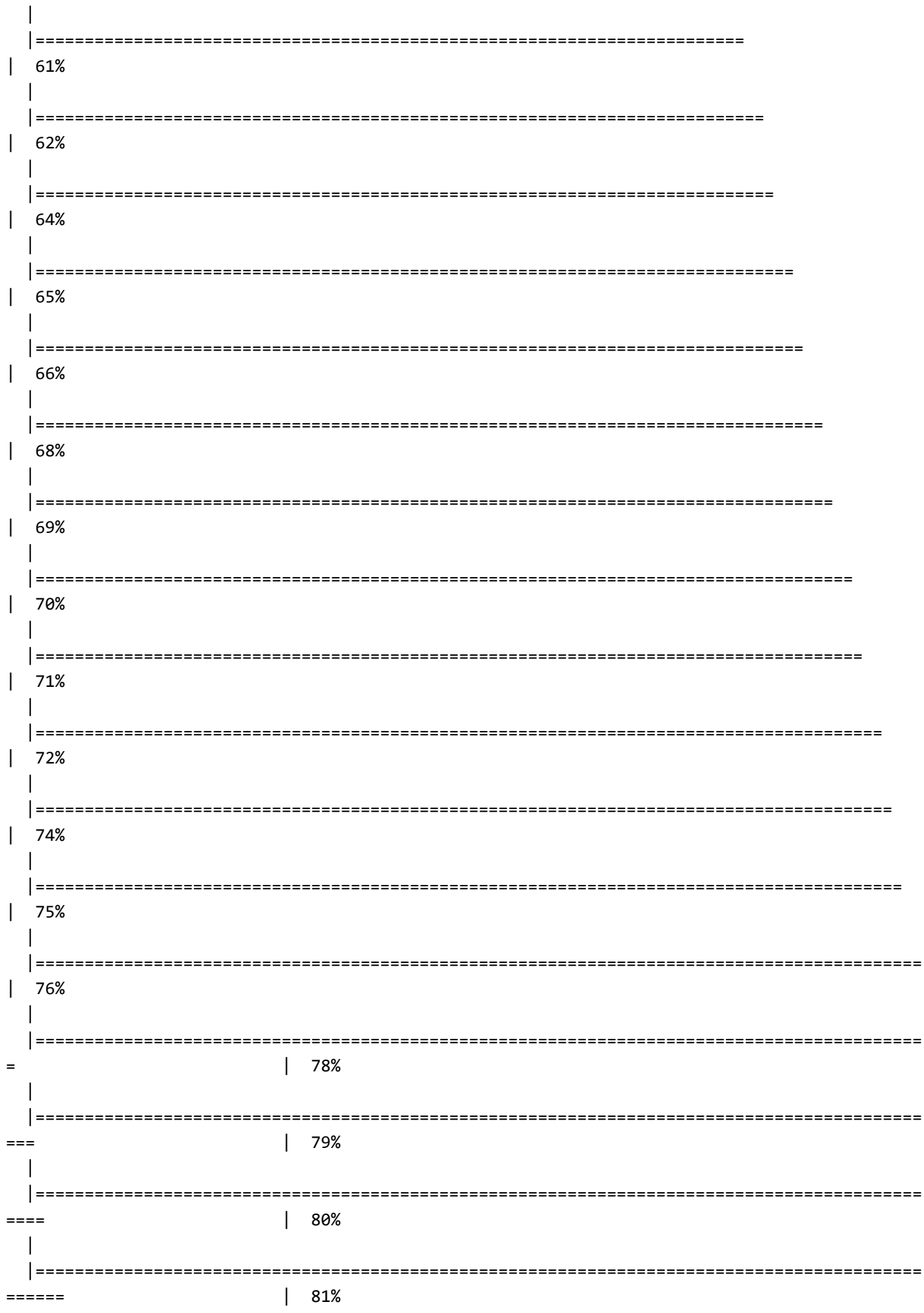
[1] "Calculating ranks..."

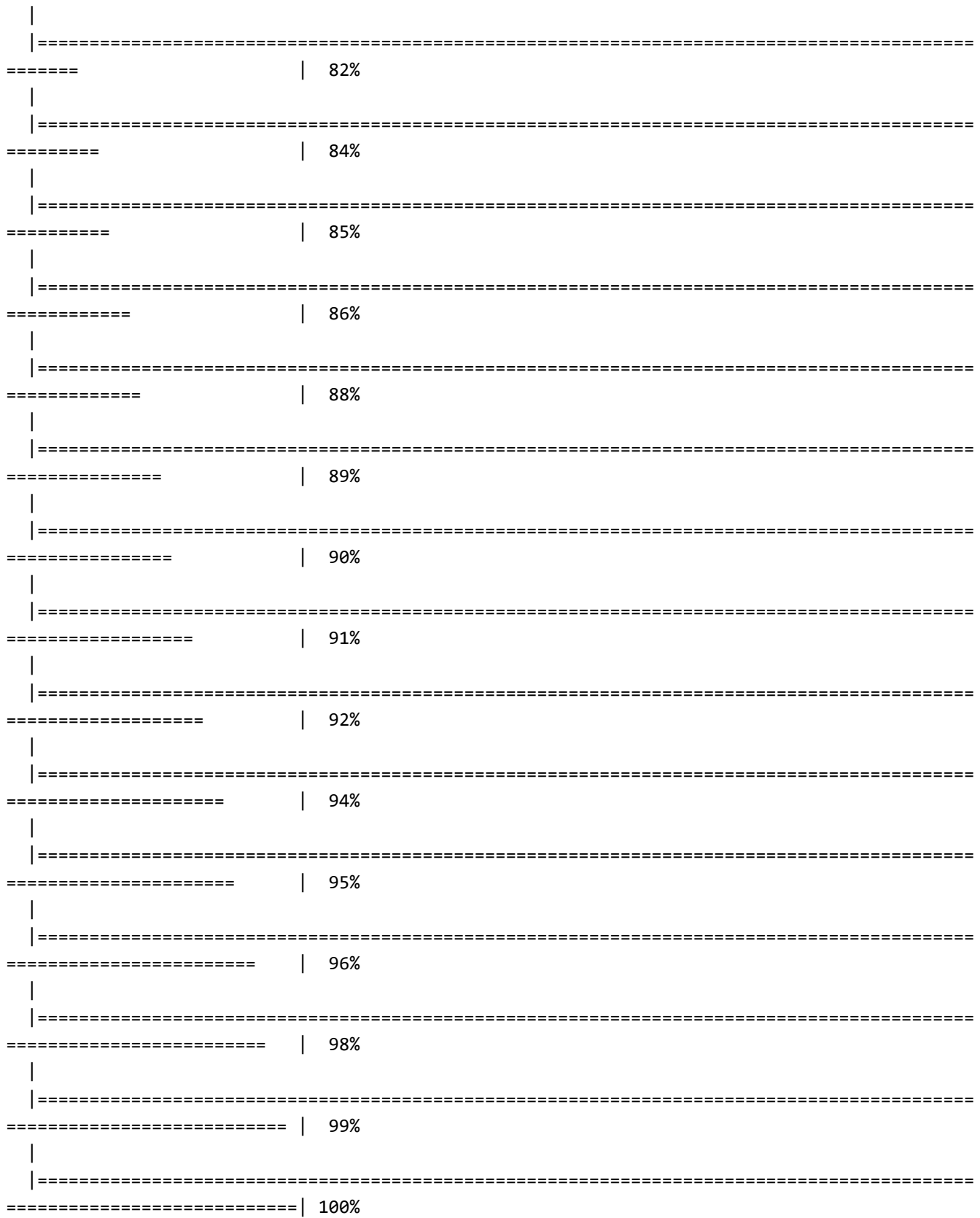
[1] "Calculating absolute values from ranks..."







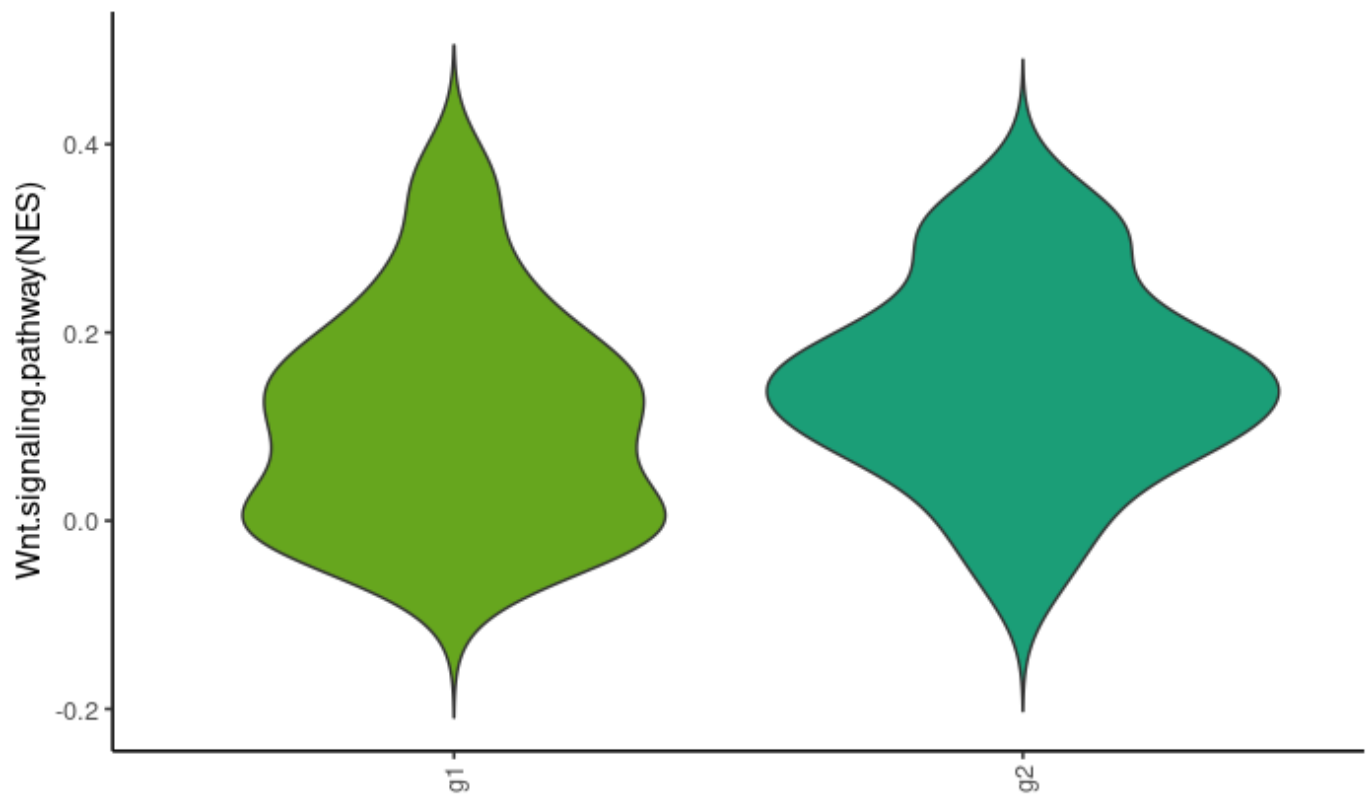




[1] "Normalizing..."

Hide

```
vlnPlot(res, features="Wnt.signaling.pathway", group_by="groups")
```



Hide

```
pbmcs
```

```
An object of class Seurat  
230 features across 80 samples within 1 assay  
Active assay: RNA (230 features, 20 variable features)  
2 dimensional reductions calculated: pca, tsne
```

Hide

```
library(Seurat)  
  
pbmcs.sce <- as.SingleCellExperiment(pbmcs)  
  
pbmcs.sce
```

```
class: SingleCellExperiment
dim: 230 80
metadata(0):
assays(2): counts logcounts
rownames(230): MS4A1 CD79B ... SPON2 S100B
rowData names(0):
colnames(80): ATGCCAGAACGACT CATGGCCTGTGCAT ... GGAACACTTCAGAC CTTGATTGATCTTC
colData names(8): orig.ident nCount_RNA ... seurat_clusters ident
reducedDimNames(2): PCA TSNE
mainExpName: RNA
altExpNames(0):
```

Hide

```
suppressMessages(library(scran))
head(logcounts(pbmcs.sce))
```

6 x 80 sparse Matrix of class "dgCMatrix"

```
[[ suppressing 80 column names 'ATGCCAGAACGACT', 'CATGGCCTGTGCAT', 'GAACCTGATGAACC' ... ]]
```


MS4A1	5.779448	4.660719	5.98
4036	6.666083	5.313305	5.190573							
CD79B	4.968821	4.615121	5.779448	5.349125	5.69
7193	6.378826	5.313305	5.190573							
CD79A	5.571318	5.29	
3404	5.974209	6.226636	6.167916							
HLA-DRA	.	4.776153	.	4.074201	4.968821	4.940848	.	7.722706	7.290953	7.48
6153	7.225153	7.323931	7.419181							
TCL1A	6.183883	.	5.29
3404	6.666083	.	.							
HLA-DQB1	4.968821	5.089387	5.753005	5.29
3404	5.974209	5.313305	6.167916							
MS4A1	6.106491	5.694729	5.537982	5.621232	3.117873	.
.
CD79B	5.012325	5.004940	5.537982	6.130608
.	.	3.378564
CD79A	5.012325	5.917200	6.451909	7.004807	.	.	3.870125	.	.	.
3.820847
HLA-DRA	6.952515	7.563681	7.144267	7.292262	5.463405	6.296873	.	6.072815	4.872060	.
4.814816	4.904746	5.272516	5.911533							
TCL1A	6.106491	5.408168	5.942135	5.217575
.
HLA-DQB1	5.702139	5.004940	4.848761	5.217575	.	4.316042
3.452557	.	3.356926
MS4A1
.
CD79B	3.729311	.	4.671146
.	.	3.330567
CD79A
.
HLA-DRA	.	4.476843	.	4.175964	3.834037	4.208048	.	4.576296	4.3	
8658	4.676402	5.600427								
TCL1A
.
HLA-DQB1
.
MS4A1
.
CD79B	.	4.289671	4.625072	3.831826	3.891037	.	.	4.641885	.	.
.	.	4.472554
CD79A
.	.	5.159975
HLA-DRA	5.558363	5.665630	4.625072	4.915886	6.510947	5.299333	5.997035	5.148847	5.201734	7.2
24972	7.326865	7.268618	6.813544							
TCL1A
.	.	4.472554
HLA-DQB1	3.289886	4.289671	.	3.831826	.	.	3.461483	3.562368	.	5.5

```
90375 5.841041 4.662449 4.693411
```

```
MS4A1 . . . 3.449600 . . . . .  
. . . .  
CD79B 2.523157 . . . . .  
. . . .  
CD79A . . . 3.284923 . . . . .  
. . . .  
HLA-DRA 7.367436 6.991211 6.928669 6.127561 6.193245 7.230064 3.874733 . . . 4.485477 2.9944  
98 3.922071 . 4.900324 5.708535  
TCL1A . . . . .  
. . . .  
HLA-DQB1 4.845342 5.050805 4.906964 3.449600 3.959171 4.989674 . . . . .  
. . . 3.782335
```

Hide

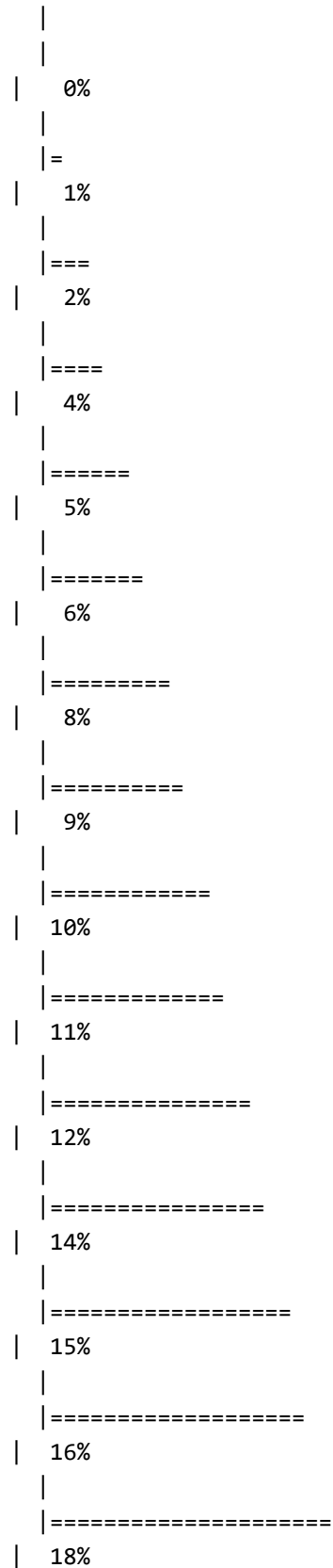
```
res2 <- scgsva(pbmcs.sce, hsko, verbose = F)
```

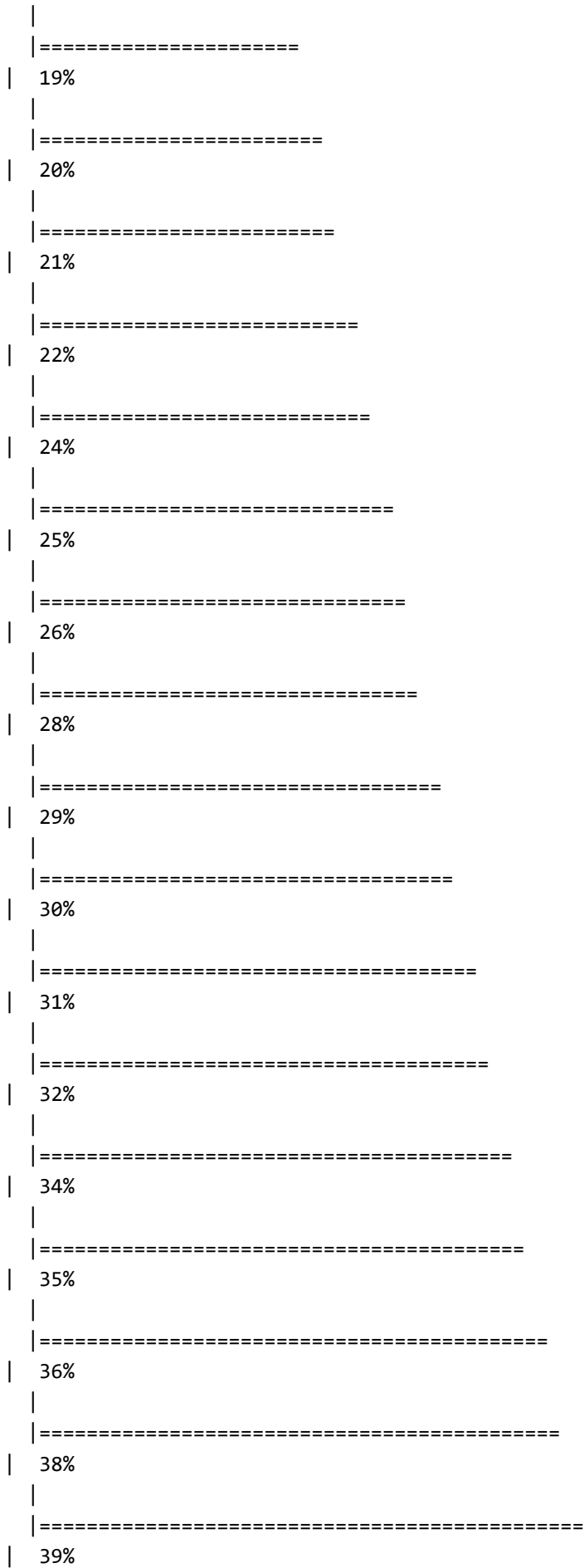
Setting parallel calculations through a MulticoreParam back-end
with workers=4 and tasks=100.

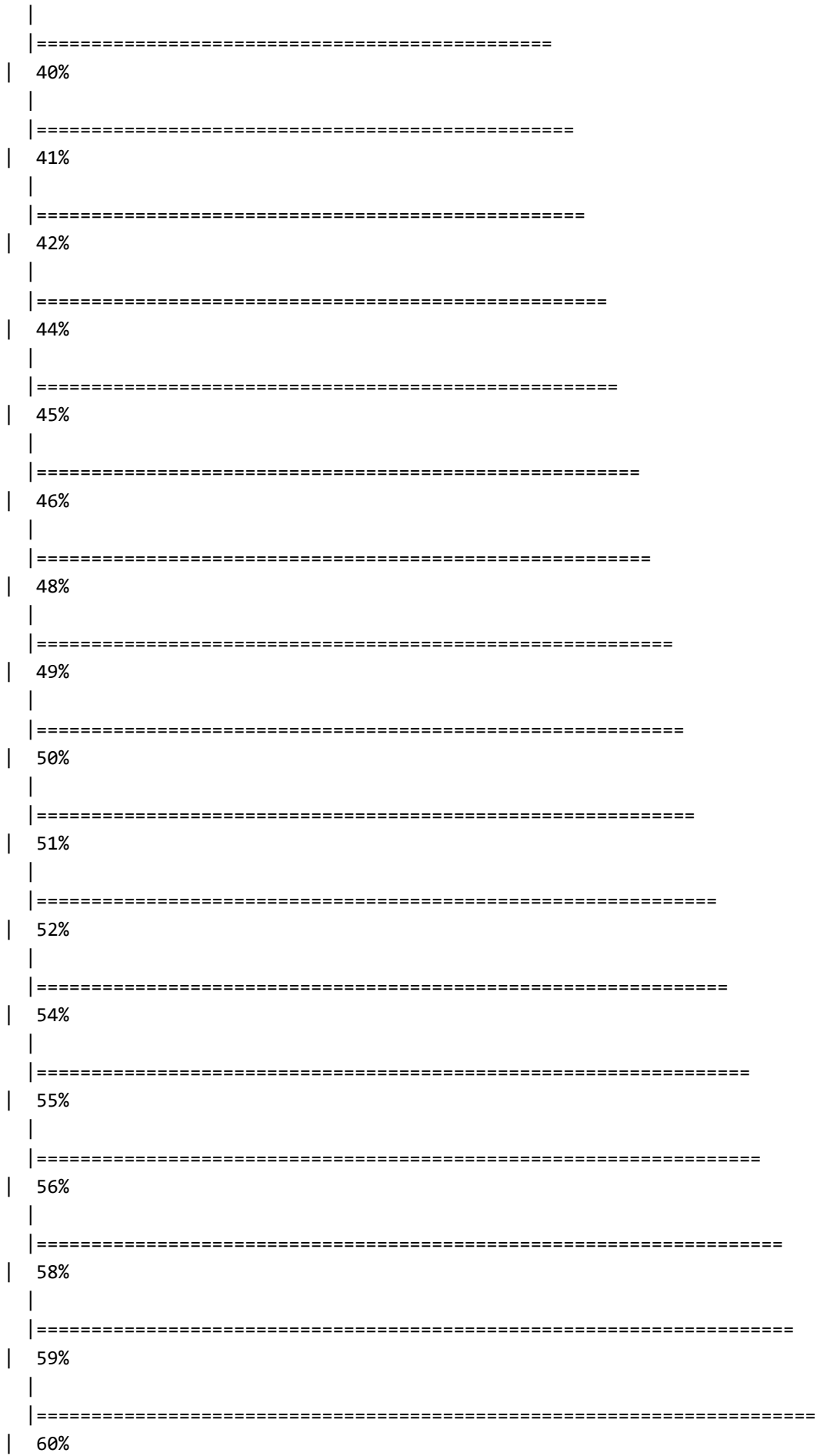
Estimating ssGSEA scores for 117 gene sets.

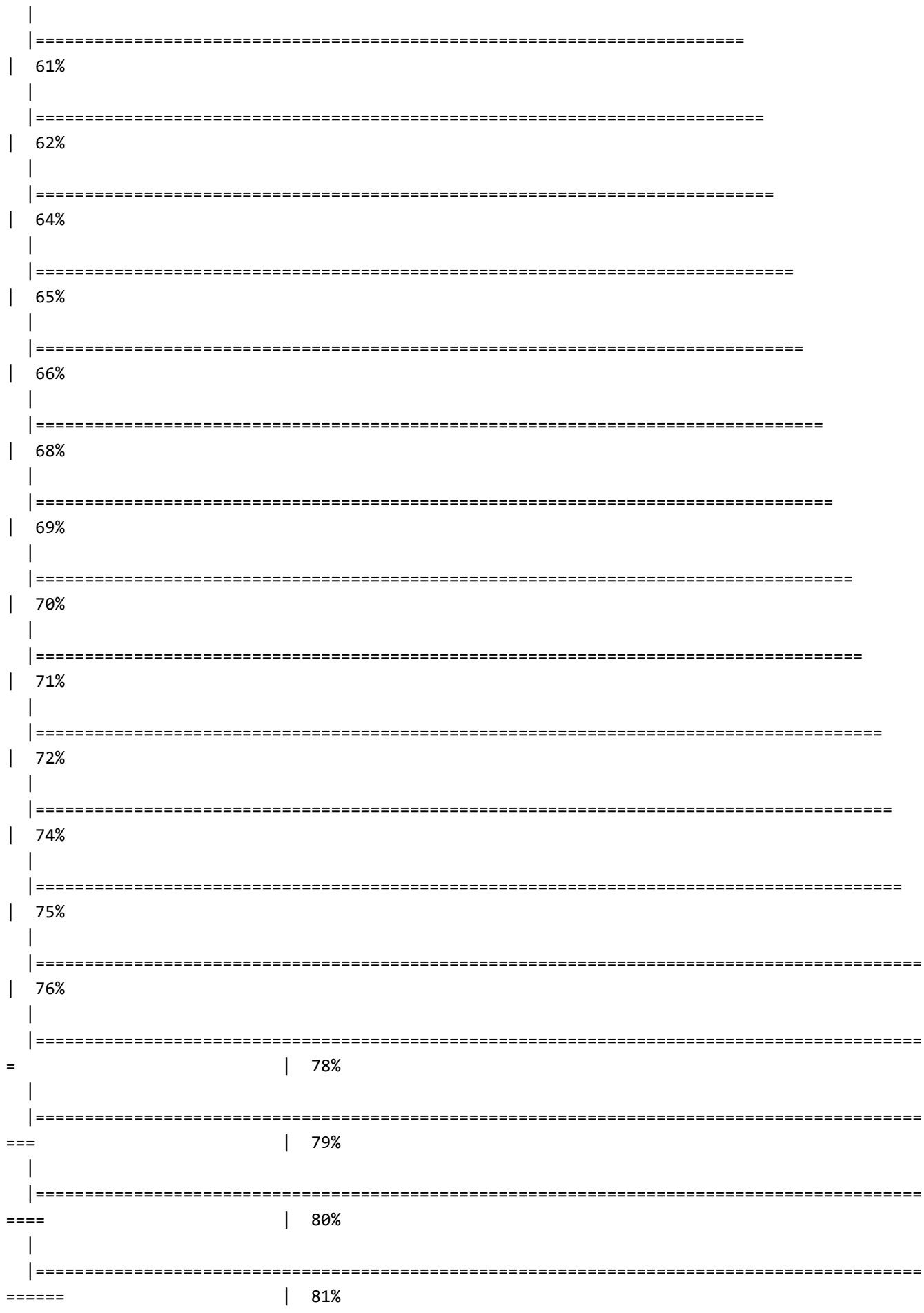
[1] "Calculating ranks..."

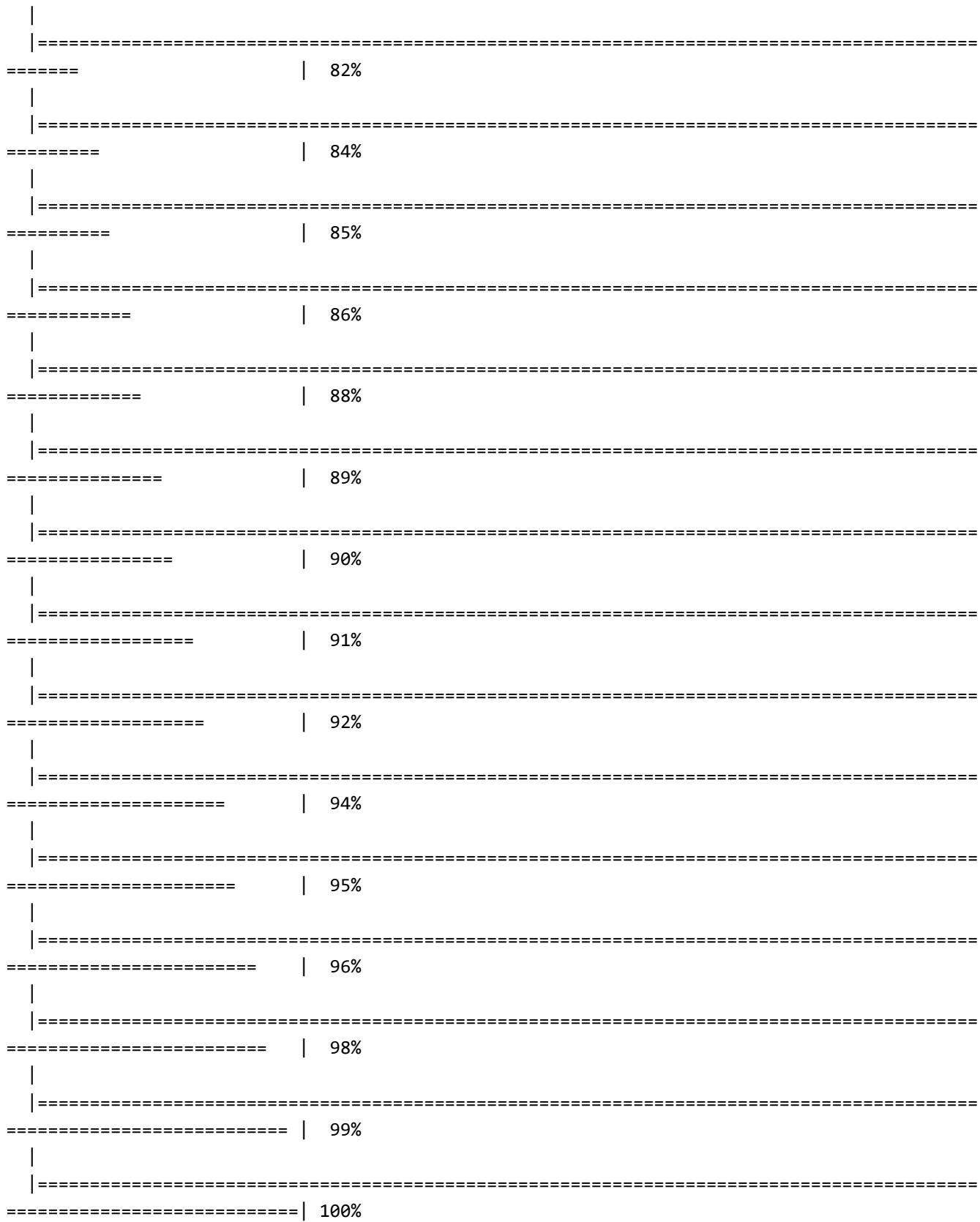
[1] "Calculating absolute values from ranks..."







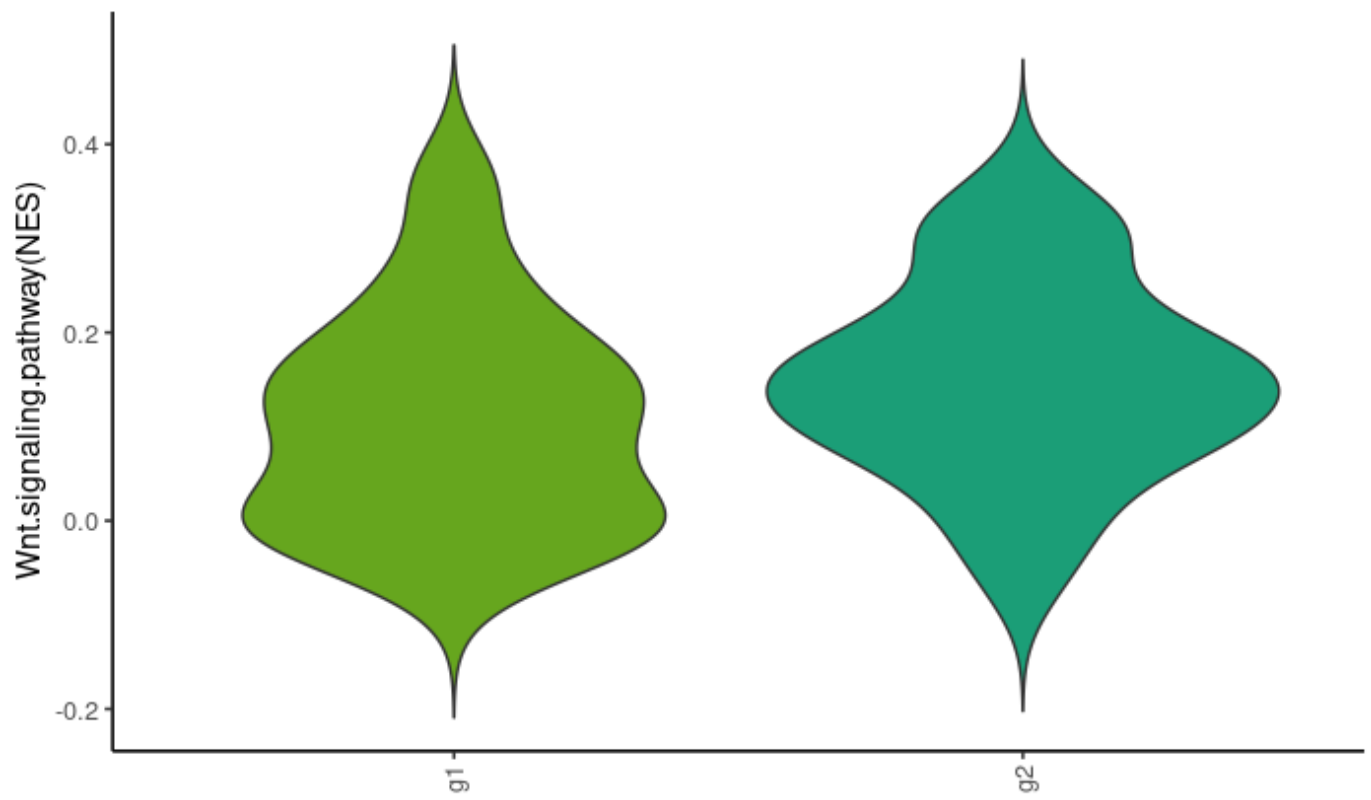




[1] "Normalizing..."

Hide

```
vlnPlot(res2, features="Wnt.signaling.pathway", group_by="groups")
```



Hide

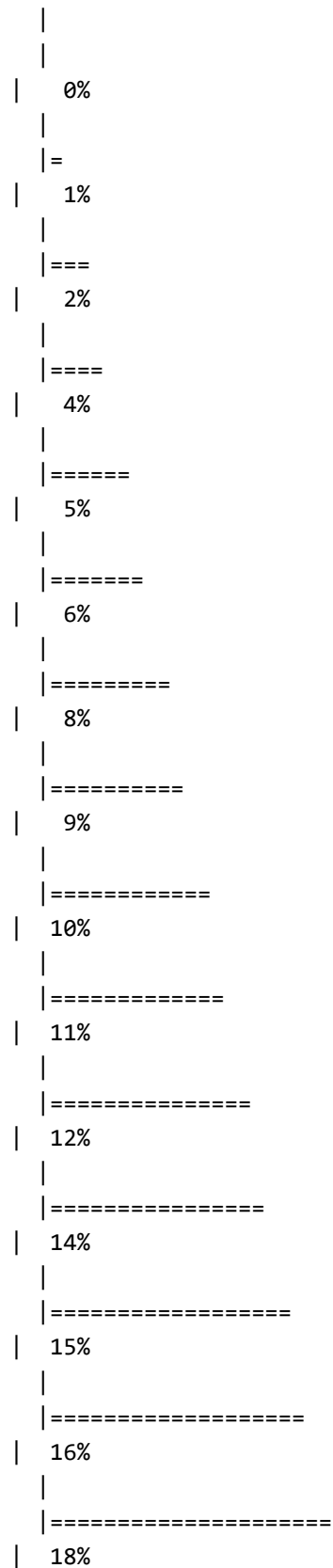
```
pbmcs.mat <- as.matrix(logcounts(pbmcs.sce))  
res3 <- scgsva(pbmcs.mat, hsko)
```

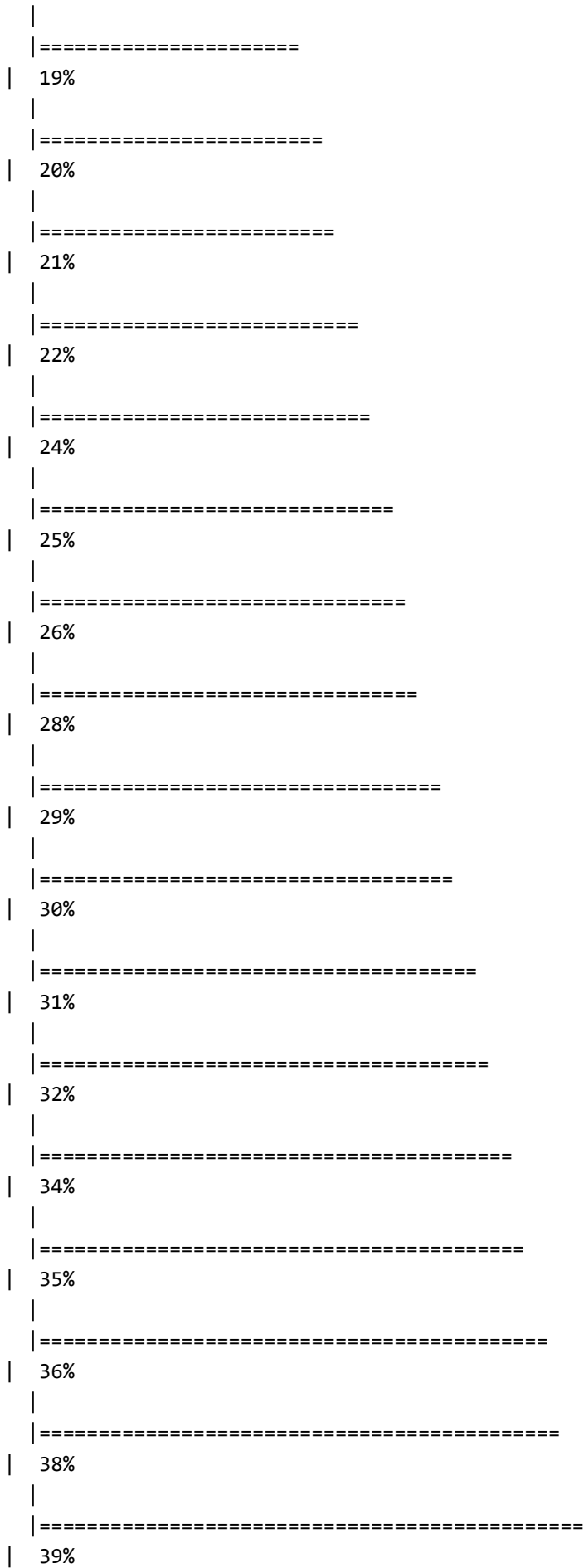

Setting parallel calculations through a MulticoreParam back-end
with workers=4 and tasks=100.

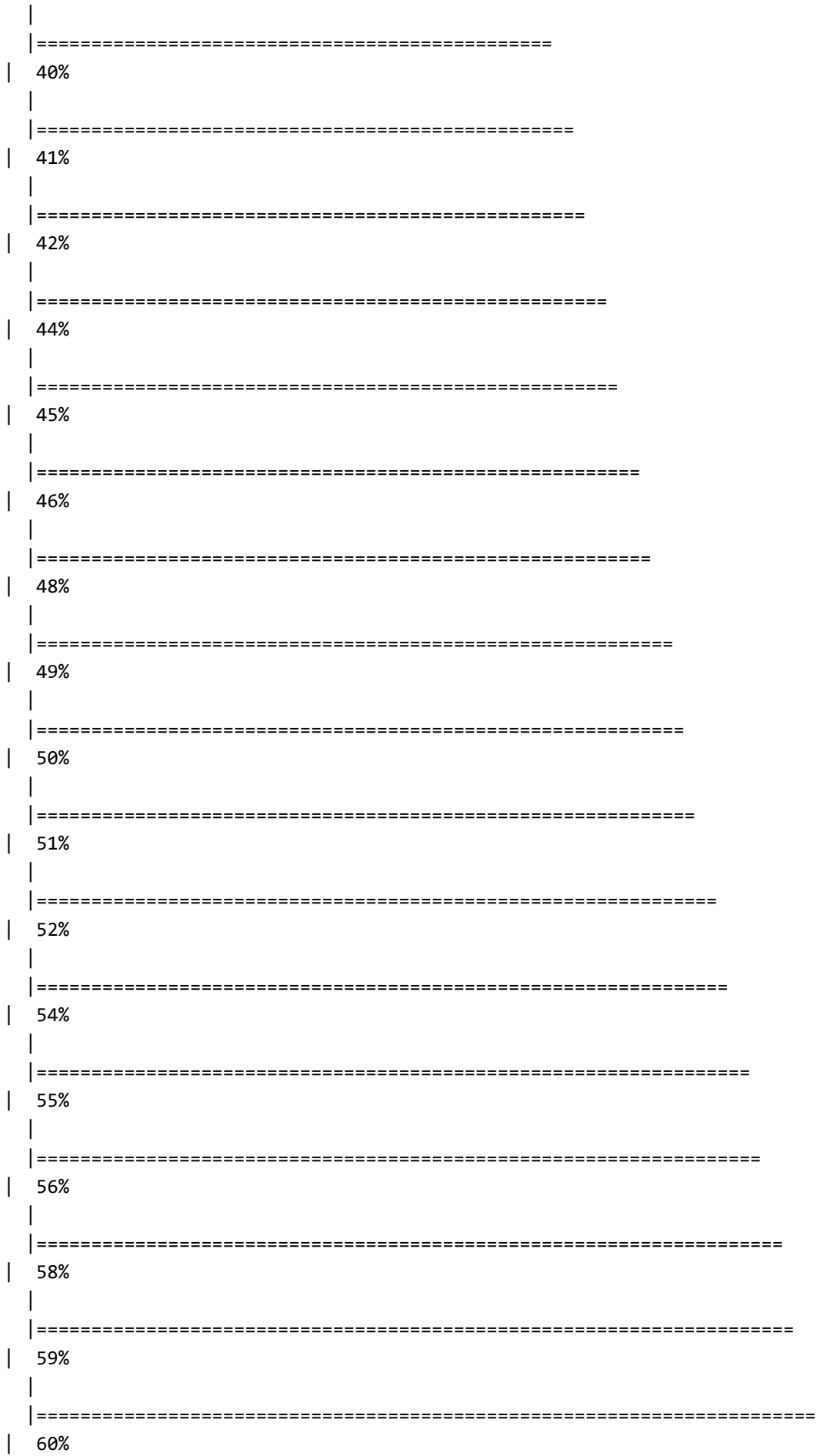
Estimating ssGSEA scores for 117 gene sets.

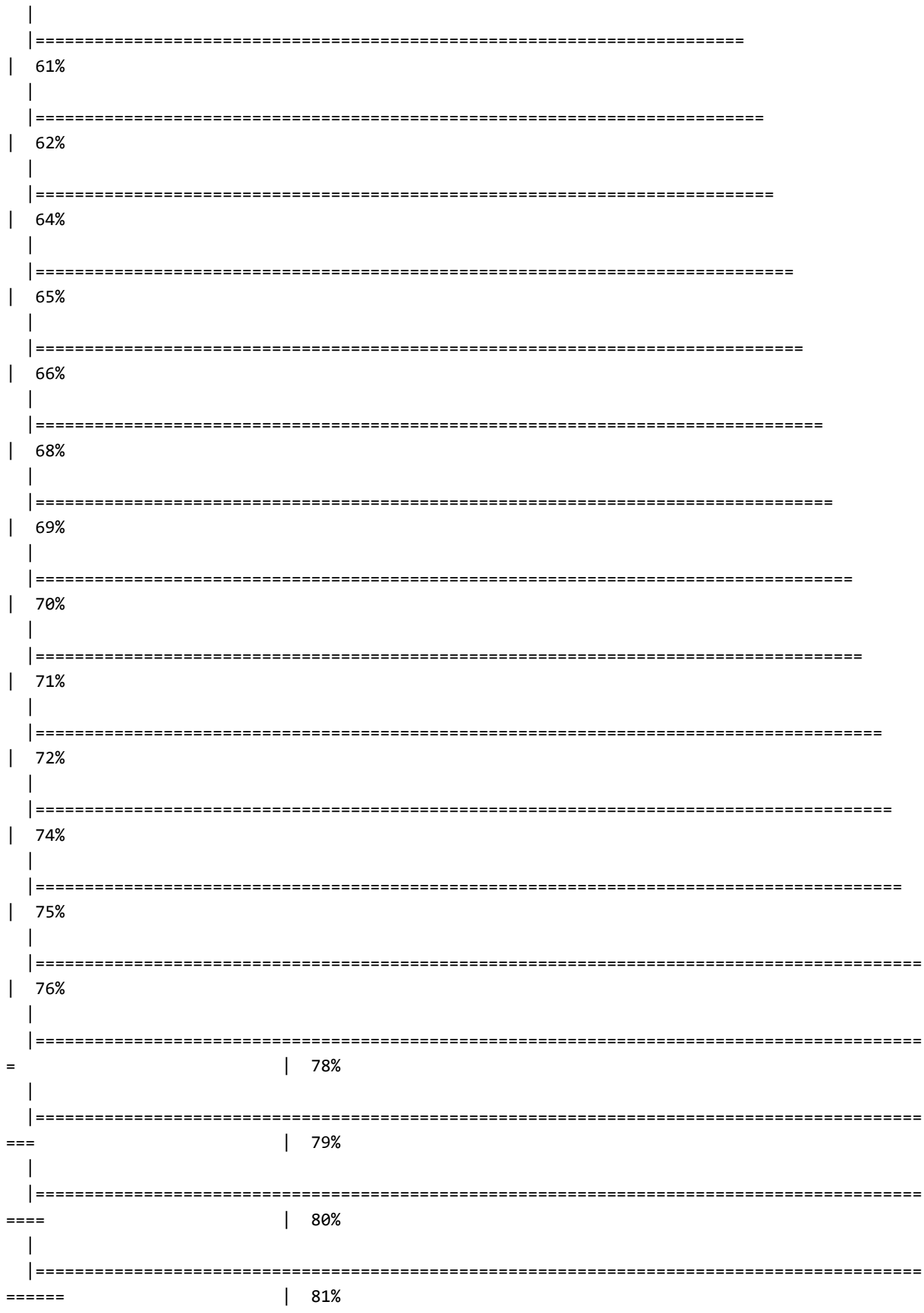
[1] "Calculating ranks..."

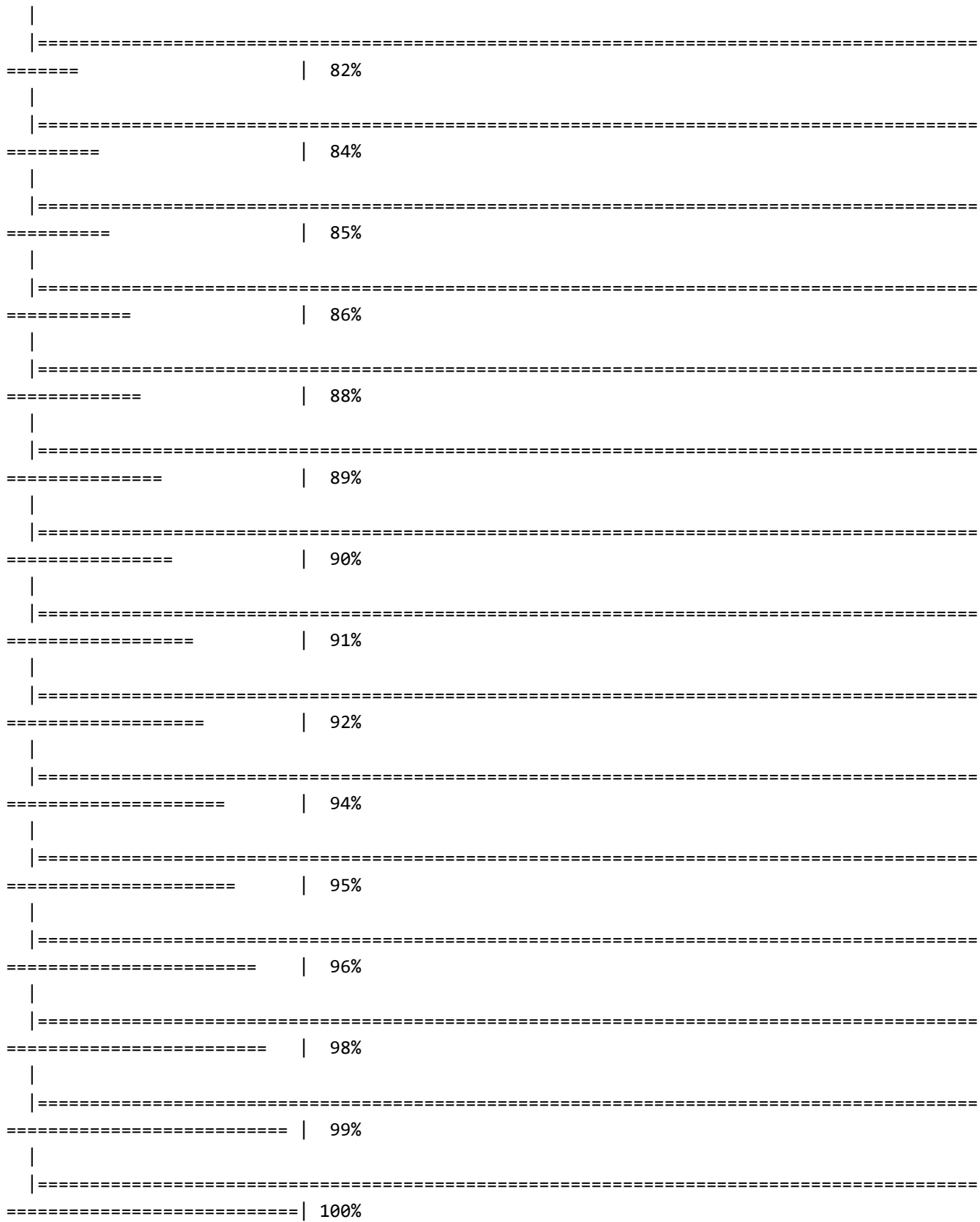
[1] "Calculating absolute values from ranks..."











[1] "Normalizing..."

Matrix loses the group information

Hide

```
vlnPlot(res3, features="Wnt.signaling.pathway", group_by="groups")
```

```
Error in vlnPlot(res3, features = "Wnt.signaling.pathway", group_by = "groups") :  
trying to get slot "meta.data" from an object of a basic class ("matrix") with no slots
```

Test of 5k PBMC (this doesn't)

Load processed B-cell subset from a 5k PBMC dataset (10X)

Hide

```
sce <- HDF5Array::loadHDF5SummarizedExperiment(  
  dir = "/home/data/NGS/scRNAseq/bioc/output/total/N_N_PBMC/",  
  prefix = "N_N_PBMC_Bcells_"  
)  
sce
```

```
class: SingleCellExperiment  
dim: 36601 417  
metadata(1): Samples  
assays(2): counts logcounts  
rownames(36601): MIR1302-2HG FAM138A ... AC007325.4 AC007325.2  
rowData names(3): ID Symbol Type  
colnames(417): AAACGAATCCGAGGCT-1 AAACGAATCGCCTTGT-1 ... TTTGGTTCAACTCGAT-1 TTTGTTGGTCGTTGGC-  
1  
colData names(18): Sample Barcode ... phases_seurat phases_cyclone  
reducedDimNames(3): PCA TSNE UMAP  
mainExpName: NULL  
altExpNames(0):
```

Hide

```
head(logcounts(sce))
```

```
<6 x 417> sparse matrix of class DelayedMatrix and type "double":
      AACGAATCCGAGGCT-1 AACGAATCGCCTTGT-1 AAACGCTCAGTAGAAT-1 ... TTTGGTTCAACTCGAT-1 T
TTGTTGGTCGTTGGC-1
MIR1302-2HG          0          0          0 .          0
0
FAM138A              0          0          0 .          0
0
OR4F5                0          0          0 .          0
0
AL627309.1          0          0          0 .          0
0
AL627309.3          0          0          0 .          0
0
AL627309.2          0          0          0 .          0
0
```

Hide

```
res4 <- scgsva(sce, hsko)
```

```
Error in h(simpleError(msg, call)) :
  error in evaluating the argument 'i' in selecting a method for function '[': $ operator is
invalid for atomic vectors
```

```
Error in h(simpleError(msg, call)) :
  error in evaluating the argument 'i' in selecting a method for function '[': $ operator is
invalid for atomic vectors
```

```
5. h(simpleError(msg, call))
4. .handleSimpleError(function (cond)
  .Internal(C_tryCatchHelper(addr, 1L, cond)), "$ operator is invalid for atomic vectors",
  base::quote(summary(input)$i))
3. tabulate(summary(input)$i)
2. input[tabulate(summary(input)$i) != 0, , drop = FALSE]
1. scgsva(sce, hsko)
```

Trying to switch the type of matrix to dgCMatrix

Hide

```
counts(sce) <- as(counts(sce), "dgCMatrix")
counts(sce)
```

```
36601 x 417 sparse Matrix of class "dgCMatrix"
```

```
[[ suppressing 56 column names 'AAACGAATCCGAGGCT-1', 'AAACGAATCGCCTTGT-1', 'AAACGCTCAGTAGAA
T-1' ... ]]
[[ suppressing 56 column names 'AAACGAATCCGAGGCT-1', 'AAACGAATCGCCTTGT-1', 'AAACGCTCAGTAGAA
T-1' ... ]]
```

```
MIR1302-2HG . . . . .
. . . . .
FAM138A . . . . .
. . . . .
OR4F5 . . . . .
. . . . .
AL627309.1 . . . . .
. . . . .
AL627309.3 . . . . .
. . . . .
AL627309.2 . . . . .
. . . . .
AL627309.5 . . . . .
. . . . .
AL627309.4 . . . . .
. . . . .
AP006222.2 . . . . .
. . . . .

.....
.....suppressing 361 columns and 36584 rows in show(); maybe adjust 'options(max.print=
*, width = *)'
.....
```

```
[[ suppressing 56 column names 'AAACGAATCCGAGGCT-1', 'AAACGAATCGCCTTGT-1', 'AAACGCTCAGTAGAA
T-1' ... ]]
```



```
AC136616.1 . . . . .
. . . . .
AC136616.3 . . . . .
. . . . .
AC136616.2 . . . . .
. . . . .
AC141272.1 . . . . .
. . . . .
AC023491.2 . . . . .
. . . . .
AC007325.1 . . . . .
. . . . .
AC007325.4 . . . . .
. . . . .
AC007325.2 . . . . .
. . . . .
```

Hide

```
logcounts(sce) <- as(logcounts(sce), "dgCMatrx")
logcounts(sce)
```

36601 x 417 sparse Matrix of class "dgCMatrx"

```
[[ suppressing 56 column names 'AAACGAATCCGAGGCT-1', 'AAACGAATCGCCTTGT-1', 'AAACGCTCAGTAGAA
T-1' ... ]]
[[ suppressing 56 column names 'AAACGAATCCGAGGCT-1', 'AAACGAATCGCCTTGT-1', 'AAACGCTCAGTAGAA
T-1' ... ]]
```

```
MIR1302-2HG . . . . .
. . . . .
FAM138A . . . . .
. . . . .
OR4F5 . . . . .
. . . . .
AL627309.1 . . . . .
. . . . .
AL627309.3 . . . . .
. . . . .
AL627309.2 . . . . .
. . . . .
AL627309.5 . . . . .
. . . . .
AL627309.4 . . . . .
. . . . .
AP006222.2 . . . . .
. . . . .

.....
.....suppressing 361 columns and 36584 rows in show(); maybe adjust 'options(max.print=
*, width = *)'
.....
```

```
[[ suppressing 56 column names 'AAACGAATCCGAGGCT-1', 'AAACGAATCGCCTTGT-1', 'AAACGCTCAGTAGAA
T-1' ... ]]
```

```
AC136616.1 . . . . .
. . . . .
AC136616.3 . . . . .
. . . . .
AC136616.2 . . . . .
. . . . .
AC141272.1 . . . . .
. . . . .
AC023491.2 . . . . .
. . . . .
AC007325.1 . . . . .
. . . . .
AC007325.4 . . . . .
. . . . .
AC007325.2 . . . . .
. . . . .
```

Hide

```
res3 <- scgsva(sce, hsko)
```

```
Warning: Non-unique features (rownames) present in the input matrix, making uniqueError: Attempting to add a different number of cells and/or features
```

```
Error: Attempting to add a different number of cells and/or features
```

```
6. stop("Attempting to add a different number of cells and/or features",
      call. = FALSE)
5. SetAssayData.Assay(object = a, slot = "data", new.data = mats$data)
4. SetAssayData(object = a, slot = "data", new.data = mats$data)
3. as.Seurat.SingleCellExperiment(obj)
2. as.Seurat(obj)
1. scgsva(sce, hsko)
```

The problem is with conversion to Seurat:

Hide

```
as.Seurat(sce)
```

```
Warning: Non-unique features (rownames) present in the input matrix, making uniqueError: Attempting to add a different number of cells and/or features
```

Loading the dataset from source

Hide

```
sce.unprocessed <-
  DropletUtils::read10xCounts(
    "/home/data/NGS/scRNAseq/bioc/samples/N_N_PBMC/filtered_feature_bc_matrix/",
    sample.names = "N_N_PBMC",
    col.names = TRUE
  )
```

```
Warning: 'as(<dgTMatrix>, "dgCMatrix")' is deprecated.
Use 'as(., "CsparseMatrix")' instead.
See help("Deprecated") and help("Matrix-deprecated").
```

Hide

```
sce.unprocessed
```

```
class: SingleCellExperiment
dim: 36601 5140
metadata(1): Samples
assays(1): counts
rownames(36601): ENSG00000243485 ENSG00000237613 ... ENSG00000278817 ENSG00000277196
rowData names(3): ID Symbol Type
colnames(5140): AAACCCAGTCGGCCTA-1 AAACCCATCAGATGCT-1 ... TTTGTTGTCGAAGTGG-1 TTTGTTGTCGCATAGT
-1
colData names(2): Sample Barcode
reducedDimNames(0):
mainExpName: NULL
altExpNames(0):
```

Hide

```
sce.lc <- logNormCounts(sce.unprocessed)
sce.lc
```

```
class: SingleCellExperiment
dim: 36601 5140
metadata(1): Samples
assays(2): counts logcounts
rownames(36601): ENSG00000243485 ENSG00000237613 ... ENSG00000278817 ENSG00000277196
rowData names(3): ID Symbol Type
colnames(5140): AAACCCAGTCGGCCTA-1 AAACCCATCAGATGCT-1 ... TTTGTTGTCGAAGTGG-1 TTTGTTGTCGCATAGT
-1
colData names(3): Sample Barcode sizeFactor
reducedDimNames(0):
mainExpName: NULL
altExpNames(0):
```

Hide

```
head(counts(sce.lc))
```

```
6 x 5140 sparse Matrix of class "dgCMatrix"
```

```
[[ suppressing 58 column names 'AAACCCAGTCGGCCTA-1', 'AAACCCATCAGATGCT-1', 'AAACGAAAGATTAGC
A-1' ... ]]
```

```

ENSG00000243485 . . . . .
. . . . .
ENSG00000237613 . . . . .
. . . . .
ENSG00000186092 . . . . .
. . . . .
ENSG00000238009 . . . . .
. . . . . 1 . . .
ENSG00000239945 . . . . .
. . . . .
ENSG00000239906 . . . . .
. . . . .

ENSG00000243485 . . . . .
ENSG00000237613 . . . . .
ENSG00000186092 . . . . .
ENSG00000238009 . . . . .
ENSG00000239945 . . . . .
ENSG00000239906 . . . . .

```

```

.....suppressing 5082 columns in show(); maybe adjust 'options(max.print= *, width = *)'
.....

```

Hide

```
head(logcounts(sce.lc))
```

```
6 x 5140 sparse Matrix of class "dgMatrix"
```

```
[[ suppressing 58 column names 'AAACCCAGTCGGCCTA-1', 'AAACCCATCAGATGCT-1', 'AAACGAAAGATTAGC
A-1' ... ]]
```

```

ENSG00000243485 . . . . .
. . . . .
ENSG00000237613 . . . . .
. . . . .
ENSG00000186092 . . . . .
. . . . .
ENSG00000238009 . . . . .
. . . . .
ENSG00000239945 . . . . .
. . . . .
ENSG00000239906 . . . . .
. . . . .

ENSG00000243485 . . . . .
ENSG00000237613 . . . . .
ENSG00000186092 . . . . .
ENSG00000238009 1.120681 . . . . .
ENSG00000239945 . . . . .
ENSG00000239906 . . . . .

.....suppressing 5082 columns in show(); maybe adjust 'options(max.print= *, width = *)'
.....

```

Hide

```
res4 <- scgsva(sce.lc, hsko)
```

```

Warning: sparse->dense coercion: allocating vector of size 1.4 GiBWarning: sparse->dense coercion: allocating vector of size 1.1 GiBError in .mapGeneSetsToFeatures(gset.idx.list, rownames(expr)) :
  No identifiers in the gene sets could be matched to the identifiers in the expression data.

```

The problem is with genesymbols:

Hide

```
rownames(sce.lc) <- rowData(sce.lc)[["Symbol"]]
head(counts(sce.lc))
```

```
6 x 5140 sparse Matrix of class "dgCMatrix"
```

```
[[ suppressing 58 column names 'AAACCCAGTCGGCCTA-1', 'AAACCCATCAGATGCT-1', 'AAACGAAAGATTAGCA-1' ... ]]
```

```

MIR1302-2HG . . . . .
. . . . .
FAM138A . . . . .
. . . . .
OR4F5 . . . . .
. . . . .
AL627309.1 . . . . .
. . . . . 1 . . . . .
AL627309.3 . . . . .
. . . . .
AL627309.2 . . . . .
. . . . .

MIR1302-2HG .....
FAM138A .....
OR4F5 .....
AL627309.1 .....
AL627309.3 .....
AL627309.2 .....

```

```

.....suppressing 5082 columns in show(); maybe adjust 'options(max.print= *, width = *)'
.....

```

Hide

```
head(logcounts(sce.lc))
```

```
6 x 5140 sparse Matrix of class "dgCMatrix"
```

```
[[ suppressing 58 column names 'AAACCCAGTCGGCCTA-1', 'AAACCCATCAGATGCT-1', 'AAACGAAAGATTAGC
A-1' ... ]]
```

```

MIR1302-2HG . . . . .
. . . . .
FAM138A . . . . .
. . . . .
OR4F5 . . . . .
. . . . .
AL627309.1 . . . . .
. . . . . 1.120681 .
AL627309.3 . . . . .
. . . . .
AL627309.2 . . . . .
. . . . .

MIR1302-2HG . . . . .
FAM138A . . . . .
OR4F5 . . . . .
AL627309.1 . . . . .
AL627309.3 . . . . .
AL627309.2 . . . . .

.....suppressing 5082 columns in show(); maybe adjust 'options(max.print= *, width = *)'
.....

```

But then we have the same Seurat conversion issue:

Hide

```
res5 <- scgsva(sce.lc, hsko)
```

```

Warning: sparse->dense coercion: allocating vector of size 1.4 GiBWarning: sparse->dense coercion: allocating vector of size 1.1 GiBWarning: Non-unique features (rownames) present in the input matrix, making uniqueError: Attempting to add a different number of cells and/or features

```

```
Error: Attempting to add a different number of cells and/or features
```

```

6. stop("Attempting to add a different number of cells and/or features", call. = FALSE)
5. SetAssayData.Assay(object = a, slot = "data", new.data = mats$data)
4. SetAssayData(object = a, slot = "data", new.data = mats$data)
3. as.Seurat.SingleCellExperiment(obj)
2. as.Seurat(obj)
1. scgsva(sce.lc, hsko)

```

Note that conversion of a SingleCellExperiment with geneIDs in rownames works:

Hide


```
rownames(sce.lc) <- rowData(sce.lc)[["ID"]]
sce.lc.seu <- SeuratObject::as.Seurat(sce.lc, counts = "counts", data = "logcounts")
sce.lc.seu
```

An object of class Seurat
36601 features across 5140 samples within 1 assay
Active assay: originalexp (36601 features, 0 variable features)

But this converted Seurat object is somehow botched:

Hide

```
res6 <- scgsva(sce.lc.seu, hsko)
```

```
Error in scgsva(sce.lc.seu, hsko) :  
trying to get slot "counts" from an object of a basic class ("NULL") with no slots
```

Hide

```
sessionInfo()
```

R version 4.2.3 (2023-03-15)
Platform: x86_64-pc-linux-gnu (64-bit)
Running under: Ubuntu 22.04.2 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/libopenblas-p-r0.3.20.so

locale:
[1] LC_CTYPE=en_US.UTF-8 LC_NUMERIC=C LC_TIME=en_US.UTF-8 LC_COLLATE=en_US.UTF-8
[5] LC_MONETARY=en_US.UTF-8 LC_MESSAGES=en_US.UTF-8 LC_PAPER=en_US.UTF-8 LC_NAME=C
[9] LC_ADDRESS=C LC_TELEPHONE=C LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C

attached base packages:
[1] stats4 stats graphics grDevices utils datasets methods base

other attached packages:
[1] scanr_1.26.2 scuttle_1.8.4 SingleCellExperiment_1.20.1 SummarizedExperiment_1.28.0
[5] GenomicRanges_1.50.2 GenomeInfoDb_1.34.9 MatrixGenerics_1.10.0 matrixStats_0.63.0
[9] Seurat_4.3.0 org.Hs.eg.db_3.16.0 AnnotationDbi_1.60.2 IRanges_2.32.0
[13] S4Vectors_0.36.2 Biobase_2.58.0 BiocGenerics_0.44.0 Seurat_4.1.3
[17] scGSVA_0.0.14

loaded via a namespace (and not attached):
[1] utf8_1.2.3 spatstat.explore_3.1-0 reticulate_1.28 R.utils_2.12.2
[5] tidyselect_1.2.0 RSQLite_2.3.1 htmlwidgets_1.6.2 grid_4.2.3
[9] BiocParallel_1.32.6 Rtsne_0.16 DropletUtils_1.18.1 munsell_0.5.0
[13] ScaledMatrix_1.6.0 codetools_0.2-19 ica_1.0-3 statmod_1.5.0
[17] future_1.32.0 miniUI_0.1.1.1 withr_2.5.0 spatstat.random_3.1-4
[21] colorspace_2.1-0 progressr_0.13.0 knitr_1.42 rstudioapi_0.14
[25] ROCR_1.0-11 tensor_1.5 listenv_0.9.0 labeling_0.4.2
[29] GenomeInfoDbData_1.2.9 polyclip_1.10-4 farver_2.1.1 bit64_4.0.5
[33] pheatmap_1.0.12 rhdf5_2.42.1 parallelly_1.35.0 vctrs_0.6.1
[37] generics_0.1.3 xfun_0.38 R6_2.5.1 rsvd_1.0.5

[41] locfit_1.5-9.7 ers_1.10.1	msigdbr_7.5.1	bitops_1.0-7	rhdf5filt
[45] spatstat.utils_3.0-2 1.2.0.1	cachem_1.0.7	DelayedArray_0.24.0	promises_
[49] scales_1.2.1 0.16.2	gtable_0.3.3	beachmat_2.14.2	globals_
[53] goftest_1.2-3 0.7.2	rlang_1.1.0	splines_4.2.3	rstatix_
[57] lazyeval_0.2.2 1.4.4	spatstat.geom_3.1-0	broom_1.0.4	reshape2_
[61] abind_1.4-5 2.3	backports_1.4.1	httpuv_1.6.9	tools_4.
[65] ggplot2_3.4.2 0.5.4	ellipsis_0.3.2	RColorBrewer_1.1-3	ggribbles_
[69] Rcpp_1.0.10 1.44.0	plyr_1.8.8	sparseMatrixStats_1.10.0	zlibbioc_
[73] purrr_1.0.1 1.7-0	RCurl_1.98-1.12	deldir_1.0-6	pbapply_
[77] viridis_0.6.2 0.9.3	cowplot_1.1.1	zoo_1.8-11	ggrepel_
[81] cluster_2.1.4 re_0.8	magrittr_2.0.3	data.table_1.14.8	scattermo
[85] lmtest_0.9-40 _1.1.2	RANN_2.6.1	fitdistrplus_1.1-8	patchwork
[89] mime_0.12 0.14	GSVA_1.46.0	xtable_1.8-4	XML_3.99-
[93] gridExtra_2.3 h_2.23-20	compiler_4.2.3	tibble_3.2.1	KernSmooth
[97] crayon_1.5.2 3.0	R.oo_1.25.0	htmltools_0.5.5	later_1.
[101] tidyr_1.3.0 _22.9	DBI_1.1.3	MASS_7.3-58.3	babelgene
[105] Matrix_1.5-4 S3_1.8.2	car_3.1-2	cli_3.6.1	R.methods
[109] metapod_1.6.0 _2.0.3	parallel_4.2.3	igraph_1.4.2	pkgconfig
[113] sp_1.6-0 1.76.0	plotly_4.10.1	spatstat.sparse_3.0-1	annotate_
[117] dqrng_0.3.0 6.31	XVector_0.38.0	stringr_1.5.0	digest_0.
[121] sctransform_0.3.5 data_3.0-1	RcppAnnoy_0.0.20	graph_1.76.0	spatstat.
[125] Biostrings_2.66.0 0.2	leiden_0.4.3	uwot_0.1.14	edgeR_3.4
[129] DelayedMatrixStats_1.20.0 _1.0.3	GSEABase_1.60.0	shiny_1.7.4	lifecycle
[133] nlme_3.1-162 bors_1.16.0	jsonlite_1.8.4	Rhdf5lib_1.20.0	BiocNeigh
[137] carData_3.0-5 0.4	viridisLite_0.4.1	limma_3.54.2	fansi_1.
[141] pillar_1.9.0	lattice_0.21-8	KEGGREST_1.38.0	fastmap_

1.1.1

[145] httr_1.4.5

[149] bluster_1.8.0
_1.26.0

[153] blob_1.2.4

1.1

[157] irlba_2.3.5.1

survival_3.5-5

bit_4.0.5

BiocSingular_1.14.0

future.apply_1.10.0

glue_1.6.2

stringi_1.7.12

memoise_2.0.1

png_0.1-8

HDF5Array

dplyr_1.