

```
head(assoc4Knots, 10)
```

```
##           waldStat df      pvalue medianLogFC
## Gene5    0.091605606 2 0.95523031 0.04845875
## Gene22   6.149435030 2 0.04620268 0.50949594
## Gene34   0.008029220 2 0.99599344 0.01573701
## Gene35   4.223127054 2 0.12104856 1.22182621
## Gene36   5.061733018 2 0.07959002 1.27113707
## Gene46   0.345851194 2 0.84120020 0.11943466
## Gene48   0.475783171 2 0.78828815 0.14861999
## Gene55   3.661519181 2 0.16029177 0.21214087
## Gene73   0.003576864 2 0.99821317 0.01175880
## Gene78   0.181962090 2 0.91303502 0.08062226
```

```
head(assoc5Knots, 10)
```

```
##           waldStat df      pvalue medianLogFC
## Gene5   12178.86204 3 0.0000000000 0.06053789
## Gene22   115.26501 3 0.0000000000 0.36642098
## Gene34   1578.57183 3 0.0000000000 0.01959401
## Gene35    14.38982 3 0.0024198155 0.15603398
## Gene36    16.30827 3 0.0009803366 0.17331498
## Gene46   9466.75842 3 0.0000000000 0.14823778
## Gene48   123.53952 3 0.0000000000 0.11650725
## Gene55   650.20350 3 0.0000000000 0.56791925
## Gene73   493.40762 3 0.0000000000 0.01454362
## Gene78  40028.24544 3 0.0000000000 0.10034468
```

```
summary(assoc4Knots$waldStat)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
## 0.0000  0.3148  1.2643  2.6132  3.4004 48.4780
```

```
summary(assoc5Knots$waldStat)
```

```
##      Min.  1st Qu.   Median     Mean  3rd Qu.    Max.
##      0.0    139.7    5505.4 102064.4 103524.7 2305836.0
```

```
sessionInfo()
```

```
## R version 3.6.0 (2019-04-26)
## Platform: x86_64-apple-darwin15.6.0 (64-bit)
## Running under: macOS Mojave 10.14.6
##
## Matrix products: default
## BLAS:   /Library/Frameworks/R.framework/Versions/3.6/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/3.6/Resources/lib/libRlapack.dylib
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## attached base packages:
## [1] parallel stats4      stats      graphics  grDevices  utils      datasets
## [8] methods   base
##
## other attached packages:
## [1] slingshot_1.4.0          princurve_2.1.4
```

```

## [3] tradeSeq_1.1.17          splatter_1.10.0
## [5] SingleCellExperiment_1.8.0 SummarizedExperiment_1.16.0
## [7] DelayedArray_0.12.0       BiocParallel_1.20.0
## [9] matrixStats_0.55.0        Biobase_2.46.0
## [11] GenomicRanges_1.38.0      GenomeInfoDb_1.22.0
## [13] IRanges_2.20.0            S4Vectors_0.24.0
## [15] BiocGenerics_0.32.0
##
## loaded via a namespace (and not attached):
## [1] Rtsne_0.15                 VGAM_1.1-2                 colorspace_1.4-1
## [4] XVector_0.26.0             bit64_0.9-7                ggrepel_0.8.1
## [7] AnnotationDbi_1.48.0       RSpecra_0.16-0            xml2_1.2.2
## [10] codetools_0.2-16          splines_3.6.0              docopt_0.6.1
## [13] doParallel_1.0.15         knitr_1.26                 zeallot_0.1.0
## [16] ade4_1.7-13                locfdr_1.1-8               annotate_1.64.0
## [19] phylobase_0.8.6           gridBase_0.4-7            kernlab_0.9-29
## [22] cluster_2.0.8              pheatmap_1.0.12           HDF5Array_1.14.1
## [25] compiler_3.6.0            httr_1.4.1                 backports_1.1.5
## [28] assertthat_0.2.1          Matrix_1.2-17              lazyeval_0.2.2
## [31] limma_3.42.0              htmltools_0.4.0           prettyunits_1.0.2
## [34] tools_3.6.0                igraph_1.2.4.2             gtable_0.3.0
## [37] glue_1.3.1                 GenomeInfoDbData_1.2.2    RANN_2.6.1
## [40] reshape2_1.4.3            dplyr_0.8.3                Rcpp_1.0.3
## [43] softImpute_1.4            zinbwave_1.8.0             slam_0.1-47
## [46] DDRTree_0.1.5             NMF_0.21.0                 vctrs_0.2.0
## [49] ape_5.3                    nlme_3.1-139               iterators_1.0.12
## [52] xfun_0.11                  stringr_1.4.0              lifecycle_0.1.0
## [55] irlba_2.3.3                rngtools_1.5                XML_3.98-1.20
## [58] edgeR_3.28.0               zlibbioc_1.32.0           MASS_7.3-51.4
## [61] scales_1.1.0              hms_0.5.2                  rhdf5_2.30.1
## [64] monocle_2.12.0            RColorBrewer_1.1-2        yaml_2.2.0
## [67] pbapply_1.4-2              memoise_1.1.0              gridExtra_2.3
## [70] ggplot2_3.2.1             pkgmaker_0.31              RSQLite_2.1.2
## [73] fastICA_1.2-2             stringi_1.4.3              genefilter_1.68.0
## [76] foreach_1.4.7             clusterExperiment_2.6.1    checkmate_1.9.4
## [79] densityClust_0.3          bibtex_0.4.2.2            rlang_0.4.1
## [82] pkgconfig_2.0.3          bitops_1.0-6               qlcMatrix_0.9.7
## [85] rnc1_0.8.3                 evaluate_0.14              lattice_0.20-38
## [88] Rhdf5lib_1.8.0            purrr_0.3.3                bit_1.1-14
## [91] tidyselect_0.2.5         plyr_1.8.4                 magrittr_1.5
## [94] R6_2.4.1                   combinat_0.0-8             DBI_1.0.0
## [97] pillar_1.4.2              withr_2.1.2                mgcv_1.8-28
## [100] survival_2.44-1.1         RCurl_1.95-4.12           tibble_2.1.3
## [103] crayon_1.3.4              uuid_0.1-2                 howmany_0.3-1
## [106] rmarkdown_2.1             viridis_0.5.1              progress_1.2.2
## [109] RNeXML_2.4.0              locfit_1.5-9.1            grid_3.6.0
## [112] blob_1.2.0                 FNN_1.1.3                  HSMMSingleCell_1.4.0
## [115] sparsesvd_0.2            digest_0.6.22              xtable_1.8-4
## [118] tidyr_1.0.0               munsell_0.5.0             registry_0.5-1
## [121] viridisLite_0.3.0

```