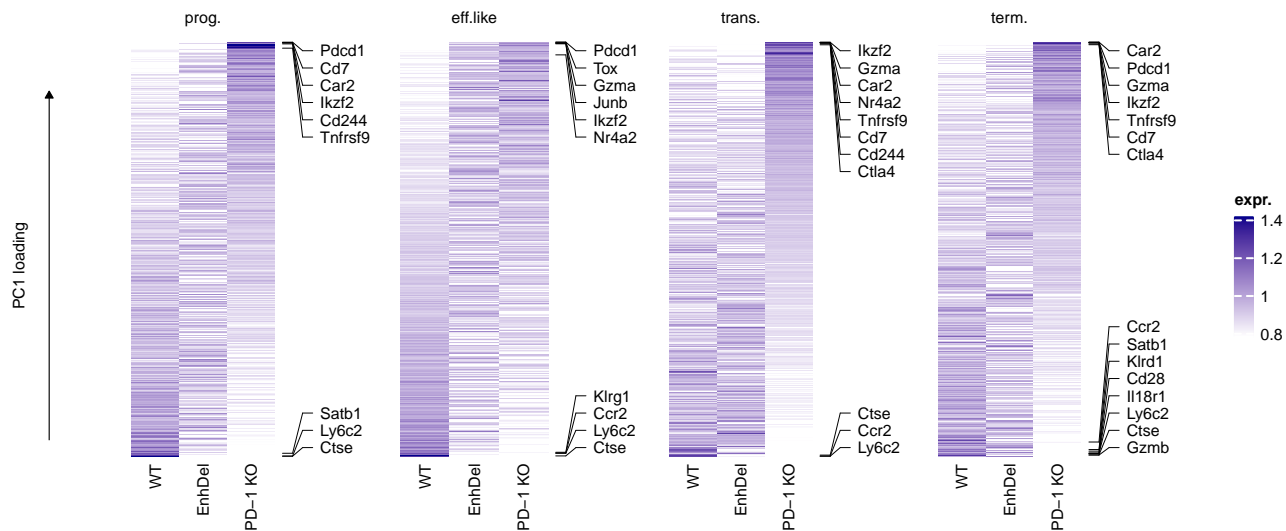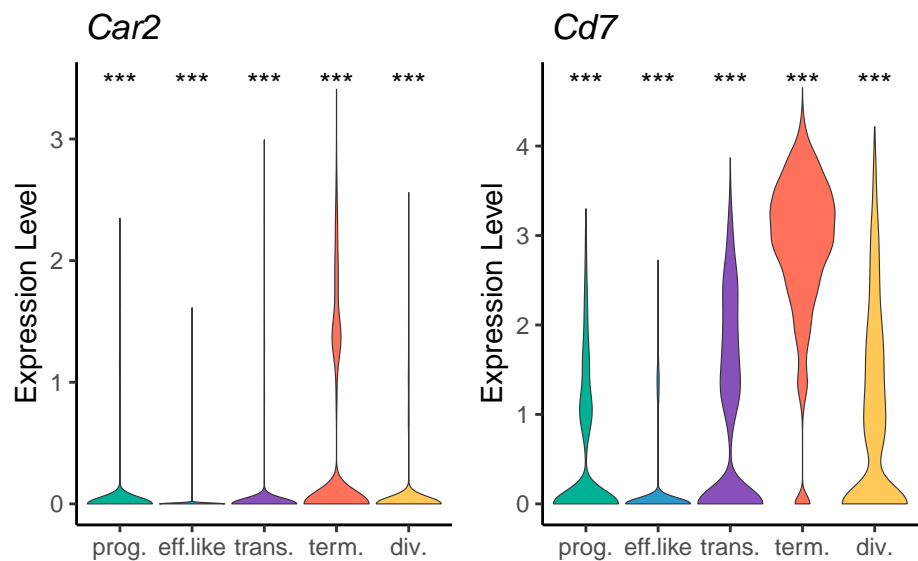# Supplementary Figures 4 Panels

Genetic perturbation of PD-1 expression does not alter formation of exhausted CD8+ T cell subsets.
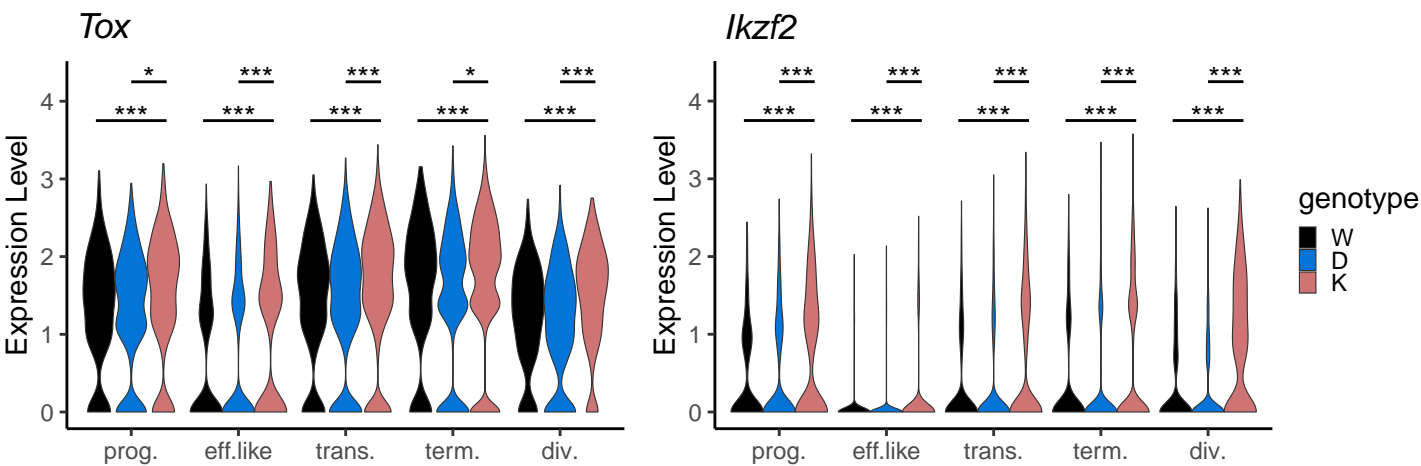
Supplementary Figure 4a
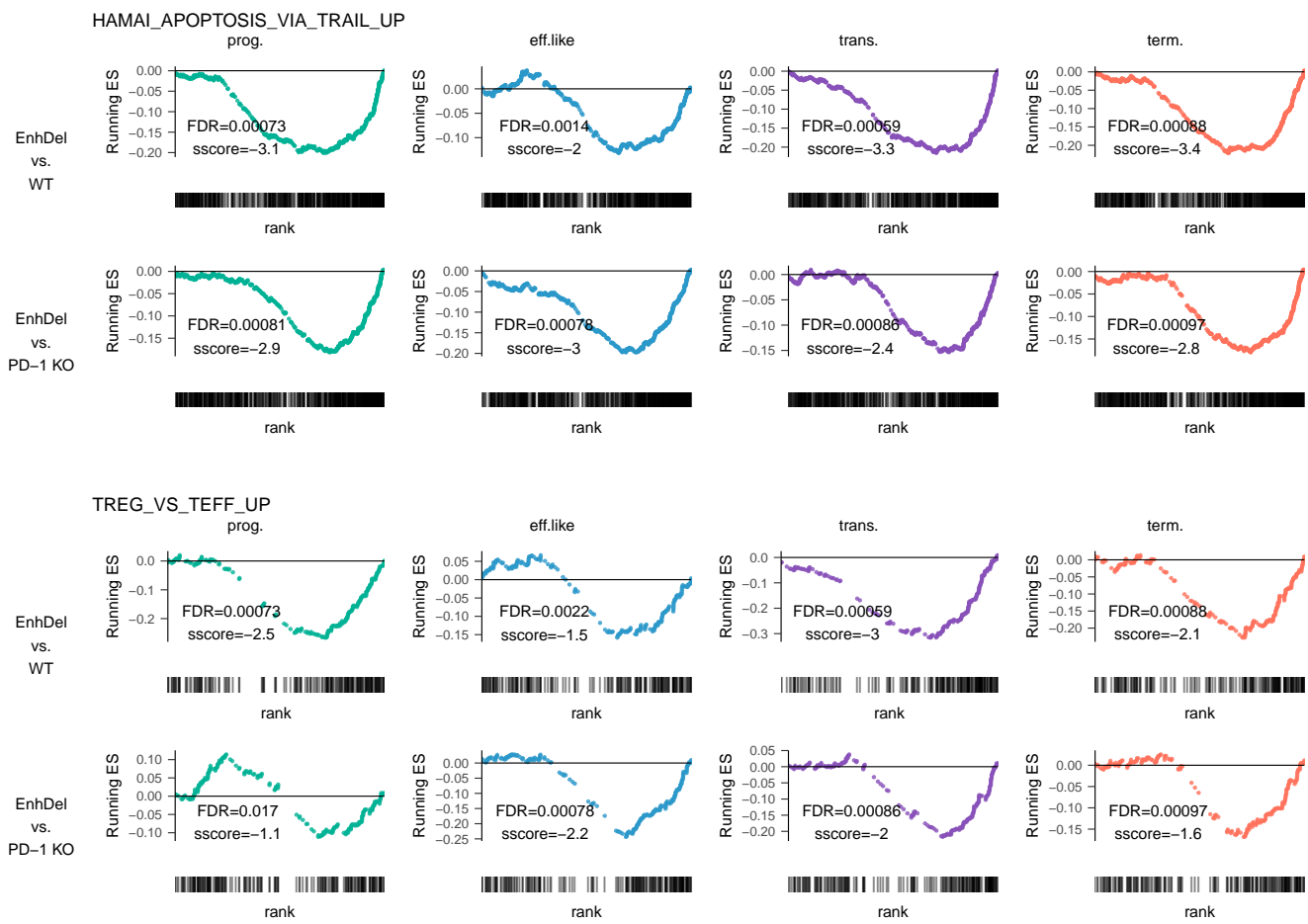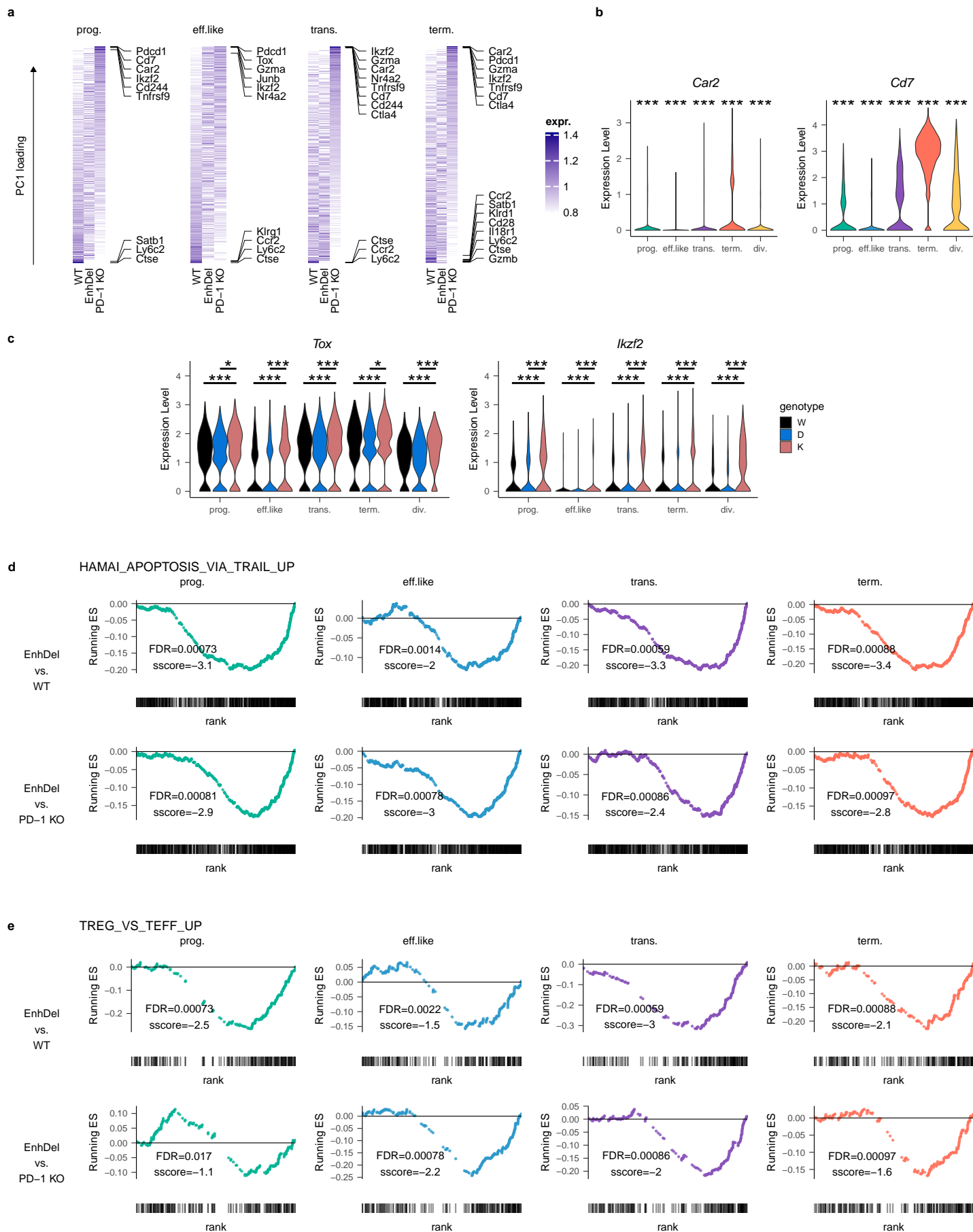

Supplementary Figure 4b

Supplementary Figure 4c

Supplementary Figure 4d and 4e

Supplementary Figure 4 Layout

a

prog. | eff.like | trans. | term.

PC1 loading

prog.: Pdcd1, Cd7, Car2, Ikzf2, Cd244, Tnfrsf9 (top); Satb1, Ly6c2, Ctse (bottom)

eff.like: Pdcd1, Tox, Gzma, Junb, Ikzf2, Nr4a2 (top); Klrg1, Ccr2, Ly6c2, Ctse (bottom)

trans.: Ikzf2, Gzma, Car2, Nr4a2, Tnfrsf9, Cd7, Cd244, Ctla4 (top); Ctse, Ccr2, Ly6c2 (bottom)

term.: Car2, Pdcd1, Gzma, Ikzf2, Tnfrsf9, Cd7, Ctla4 (top); Ccr2, Satb1, Klrd1, Cd28, Il18r1, Ly6c2, Ctse, Gzmb (bottom)

WT / EnhDel / PD-1 KO

expr.: 1.4 / 1.2 / 1 / 0.8

b *Car2* *Cd7*

c *Tox* *Ikzf2*

genotype: W, D, K

d HAMAI_APOPTOSIS_VIA_TRAIL_UP

prog. | eff.like | trans. | term.

EnhDel vs. WT:
- prog.: FDR=0.00073, sscore=−3.1
- eff.like: FDR=0.0014, sscore=−2
- trans.: FDR=0.00059, sscore=−3.3
- term.: FDR=0.00088, sscore=−3.4

EnhDel vs. PD−1 KO:
- prog.: FDR=0.00081, sscore=−2.9
- eff.like: FDR=0.00078, sscore=−3
- trans.: FDR=0.00086, sscore=−2.4
- term.: FDR=0.00097, sscore=−2.8

e TREG_VS_TEFF_UP

prog. | eff.like | trans. | term.

EnhDel vs. WT:
- prog.: FDR=0.00073, sscore=−2.5
- eff.like: FDR=0.0022, sscore=−1.5
- trans.: FDR=0.00059, sscore=−3
- term.: FDR=0.00088, sscore=−2.1

EnhDel vs. PD−1 KO:
- prog.: FDR=0.017, sscore=−1.1
- eff.like: FDR=0.00078, sscore=−2.2
- trans.: FDR=0.00086, sscore=−2
- term.: FDR=0.00097, sscore=−1.6

```
## R version 4.0.3 (2020-10-10)
## Platform: x86_64-apple-darwin17.0 (64-bit)
## Running under: macOS Big Sur 10.16
##
## Matrix products: default
## BLAS:   /Library/Frameworks/R.framework/Versions/4.0/Resources/lib/libRblas.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/4.0/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] grid      parallel  stats4    stats     graphics  grDevices utils
##  [8] datasets  methods   base
##
## other attached packages:
##  [1] Rsc_0.0.0.9000             Seurat_3.1.1
##  [3] ggrepel_0.9.1             circlize_0.4.14
##  [5] ComplexHeatmap_2.4.3      ggridges_0.5.3
##  [7] gridExtra_2.3             viridis_0.6.2
##  [9] viridisLite_0.4.0         ggpubr_0.4.0
## [11] cowplot_1.1.1             readr_2.1.2
## [13] tibble_3.1.6              purrr_0.3.4
## [15] tidyr_1.2.0               stringr_1.4.0
## [17] ggplot2_3.3.6             dplyr_1.0.9
## [19] DESeq2_1.28.1             SummarizedExperiment_1.18.2
## [21] DelayedArray_0.14.1       matrixStats_0.61.0
## [23] Biobase_2.48.0            GenomicRanges_1.40.0
## [25] GenomeInfoDb_1.24.2       IRanges_2.22.2
## [27] S4Vectors_0.26.1          BiocGenerics_0.34.0
## [29] here_1.0.1
##
## loaded via a namespace (and not attached):
##   [1] backports_1.4.1     sn_2.0.2            plyr_1.8.7
##   [4] igraph_1.3.0        lazyeval_0.2.2     splines_4.0.3
##   [7] BiocParallel_1.22.0 listenv_0.8.0      qqconf_1.2.3
##  [10] TH.data_1.1-1       digest_0.6.29      htmltools_0.5.2
##  [13] fansi_1.0.3         magrittr_2.0.3     memoise_2.0.1
##  [16] cluster_2.1.3       ROCR_1.0-11        tzdb_0.3.0
##  [19] globals_0.14.0      annotate_1.66.0    vroom_1.5.7
##  [22] R.utils_2.11.0      sandwich_3.0-1     colorspace_2.0-3
##  [25] blob_1.2.3          rbibutils_2.2.7    xfun_0.30
##  [28] crayon_1.5.1        RCurl_1.98-1.6     jsonlite_1.8.0
##  [31] genefilter_1.70.0   survival_3.3-1     zoo_1.8-9
##  [34] ape_5.6-2           glue_1.6.2         gtable_0.3.0
##  [37] zlibbioc_1.34.0     XVector_0.28.0     leiden_0.3.10
##  [40] GetoptLong_1.0.5    car_3.0-13         future.apply_1.9.0
##  [43] shape_1.4.6         abind_1.4-5        scales_1.2.0
##  [46] mvtnorm_1.1-3       DBI_1.1.2          rstatix_0.7.0
##  [49] Rcpp_1.0.9          plotrix_3.8-2      metap_1.8
##  [52] xtable_1.8-4        tmvnsim_1.0-2      clue_0.3-60
##  [55] reticulate_1.24     rsvd_1.0.5         bit_4.0.4
##  [58] SDMTools_1.1-221    tsne_0.1-3.1       htmlwidgets_1.5.4
##  [61] httr_1.4.2          RColorBrewer_1.1-3 TFisher_0.2.0
##  [64] ellipsis_0.3.2      ica_1.0-2          farver_2.1.0
##  [67] pkgconfig_2.0.3     XML_3.99-0.9       R.methodsS3_1.8.1
##  [70] uwot_0.1.11         locfit_1.5-9.4     utf8_1.2.2
##  [73] labeling_0.4.2      reshape2_1.4.4     tidyselect_1.1.2
##  [76] rlang_1.0.2         AnnotationDbi_1.50.3 munsell_0.5.0
##  [79] tools_4.0.3         cachem_1.0.6       cli_3.2.0
##  [82] generics_0.1.2      RSQLite_2.2.12     mathjaxr_1.6-0
##  [85] broom_0.8.0         evaluate_0.15      fastmap_1.1.0
##  [88] yaml_2.3.5          knitr_1.39         bit64_4.0.5
```

```
##   [91] fitdistrplus_1.1-8     RANN_2.6.1            pbapply_1.5-0
##   [94] future_1.25.0          nlme_3.1-157         R.oo_1.24.0
##   [97] compiler_4.0.3         rstudioapi_0.13      plotly_4.10.0
##  [100] png_0.1-7              ggsignif_0.6.3       geneplotter_1.66.0
##  [103] stringi_1.7.6          lattice_0.20-45      Matrix_1.4-1
##  [106] multtest_2.44.0        vctrs_0.4.1          mutoss_0.1-12
##  [109] pillar_1.7.0           lifecycle_1.0.1      Rdpack_2.3
##  [112] lmtest_0.9-40          GlobalOptions_0.1.2  RcppAnnoy_0.0.19
##  [115] data.table_1.14.2      bitops_1.0-7         irlba_2.3.5
##  [118] R6_2.5.1               KernSmooth_2.23-20   parallelly_1.31.1
##  [121] codetools_0.2-18       MASS_7.3-56          assertthat_0.2.1
##  [124] rprojroot_2.0.3        rjson_0.2.21         withr_2.5.0
##  [127] sctransform_0.3.3      mnormt_2.0.2         multcomp_1.4-19
##  [130] GenomeInfoDbData_1.2.3 hms_1.1.1            rmarkdown_2.14
##  [133] carData_3.0-5          Rtsne_0.15           numDeriv_2016.8-1.1
```