Supplemental Table S2. Session info describing fGSEA gene set enrichment analysis using the Hallmark database

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> sessionInfo()
R version 4.2.2 (2022-10-31)
Platform: x86_64-apple-darwin17.0 (64-bit)
Running under: macOS Monterey 12.3

Matrix products: default
LAPACK: /Library/Frameworks/R.framework/Versions/4.2/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       stats4    stats     graphics  grDevices utils
datasets   methods    base

other attached packages:
 [1] factoextra_1.0.7          UCell_2.2.0
biomaRt_2.54.0            Matrix_1.5-3
 [5] hdf5r_1.3.7               SeuratObject_4.1.3
Seurat_4.3.0              VennDiagram_1.7.3
 [9] futile.logger_1.4.3       gdata_2.18.0.1
colorRamps_2.3.1         fgsea_1.24.0
[13] msigdbr_7.5.1             forcats_0.5.2
stringr_1.5.0           purrr_0.3.5
[17] readr_2.1.3               tidyr_1.2.1
tidyverse_1.3.2         tibble_3.1.8
[21] RColorBrewer_1.1-3        gplots_3.1.3
EnhancedVolcano_1.16.0   ggrepel_0.9.2
[25] ggplot2_3.4.0            dplyr_1.0.10
msImpute_1.8.0          reticulate_1.26
[29] proDA_1.12.0             limma_3.54.0
DEP_1.20.0              SummarizedExperiment_1.28.0
[33] Biobase_2.58.0           GenomicRanges_1.50.1
GenomeInfoDb_1.34.4     IRanges_2.32.0
[37] S4Vectors_0.36.1         BiocGenerics_0.44.0
MatrixGenerics_1.10.0   matrixStats_0.63.0

loaded via a namespace (and not attached):
  [1] rappdirs_0.3.3           scattermore_0.8
bit64_4.0.5             irlba_2.3.5.1
  [5] DelayedArray_0.24.0       data.table_1.14.6
KEGGREST_1.38.0         RCurl_1.98-1.9
  [9] doParallel_1.0.17         generics_0.1.3
preprocessCore_1.60.0   ScaledMatrix_1.6.0
 [13] cowplot_1.1.1             lambda.r_1.2.4
RSQLite_2.2.19         RANN_2.6.1
 [17] future_1.29.0             bit_4.0.5
tzdb_0.3.0             spatstat.data_3.0-0
 [21] xml2_1.3.3                lubridate_1.9.0
httpuv_1.6.6           assertthat_0.2.1
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 [25] gargle_1.2.1                    hms_1.1.2
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 [29] progress_1.2.2                 fansi_1.0.3
caTools_1.18.2                 dbplyr_2.2.1
 [33] readxl_1.4.1                   igraph_1.3.5
DBI_1.1.3                      htmlwidgets_1.5.4
 [37] spatstat.geom_3.0-3           googledrive_2.0.0
ellipsis_0.3.2                 ggpubr_0.5.0
 [41] backports_1.4.1               deldir_1.0-6
sparseMatrixStats_1.10.0       vctrs_0.5.1
 [45] SingleCellExperiment_1.20.0 imputeLCMD_2.1
ROCR_1.0-11                    abind_1.4-5
 [49] cachem_1.0.6                  withr_2.5.0
progressr_0.11.0               sctransform_0.3.5
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crayon_1.5.2                   spatstat.explore_3.0-5
 [61] edgeR_3.40.0                  pkgconfig_2.0.3
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 [65] ProtGenerics_1.30.0          rlang_1.0.6
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 [69] miniUI_0.1.1.1               sandwich_3.0-2
filelock_1.0.2                 affyio_1.68.0
 [73] BiocFileCache_2.6.0          modelr_0.1.10
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 [77] cellranger_1.1.0             lmtest_0.9-40
carData_3.0-5                  zoo_1.8-11
 [81] reprex_2.0.2                  ggridges_0.5.4
GlobalOptions_0.1.2            googlesheets4_1.0.1
 [85] viridisLite_0.4.1            png_0.1-8
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 [89] bitops_1.0-7                  shinydashboard_0.7.2
KernSmooth_2.23-20             Biostrings_2.66.0
 [93] blob_1.2.3                    DelayedMatrixStats_1.20.0
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 [97] parallelly_1.32.1            rstatix_0.7.1
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[105] plyr_1.8.8                    ica_1.0-3
zlibbioc_1.44.0                compiler_4.2.2
[109] dqrng_0.3.0                   pcaMethods_1.90.0
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[113] cli_3.4.1                     affy_1.76.0
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[117] pbapply_1.6-0                 patchwork_1.1.2
formatR_1.12                   MASS_7.3-58.1
[121] tidyselect_1.2.0             vsn_3.66.0
stringi_1.7.8                  BiocSingular_1.14.0
[125] locfit_1.5-9.6               norm_1.0-10.0
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[129] tools_4.2.2                   timechange_0.1.1
future.apply_1.10.0            parallel_4.2.2
```

[133] circlize_0.4.15   rstudioapi_0.14
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[137] foreach_1.5.2   gridExtra_2.3
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[141] mzID_1.36.0   Rtsne_0.16
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Rcpp_1.0.9   car_3.1-1
[149] broom_1.0.1   scuttle_1.8.1
later_1.3.0   RcppAnnoy_0.0.20
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[165] statmod_1.4.37   spatstat.utils_3.0-1
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jsonlite_1.8.4   futile.options_1.0.1
[173] R6_2.5.1   pillar_1.8.1
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curl_4.3.3   leiden_0.4.3
[189] gtools_3.9.4   survival_3.4-0
munsell_0.5.0   GetoptLong_1.0.5
[193] GenomeInfoDbData_1.2.9   iterators_1.0.14
impute_1.72.1   reshape2_1.4.4
[197] haven_2.5.1   gtable_0.3.1