

Figures 3 Panels

Figure 3c

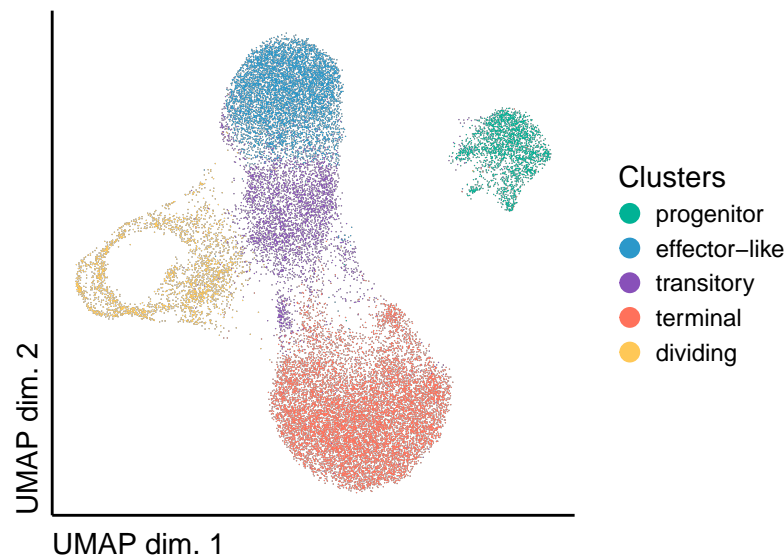


Figure 3d

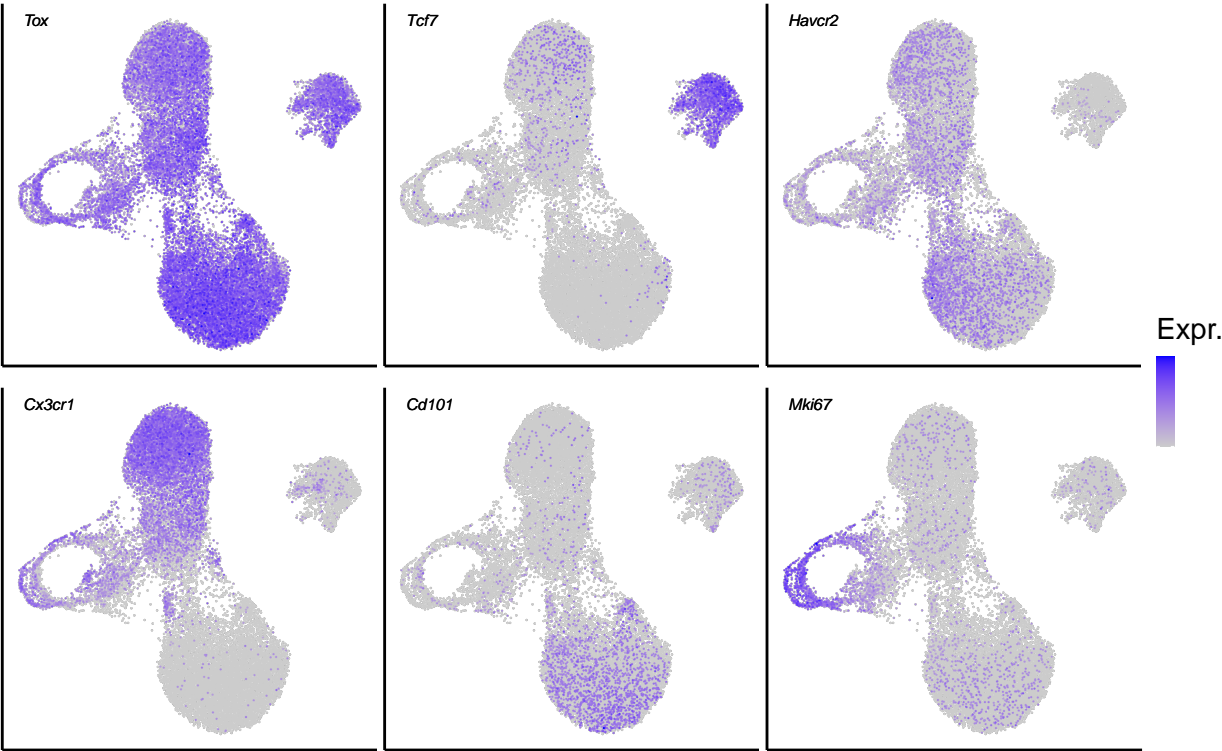


Figure 3e

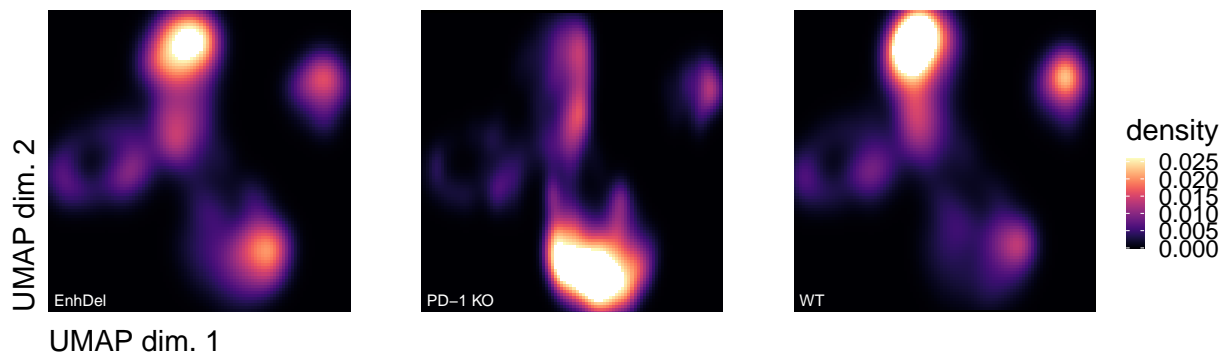


Figure 3f

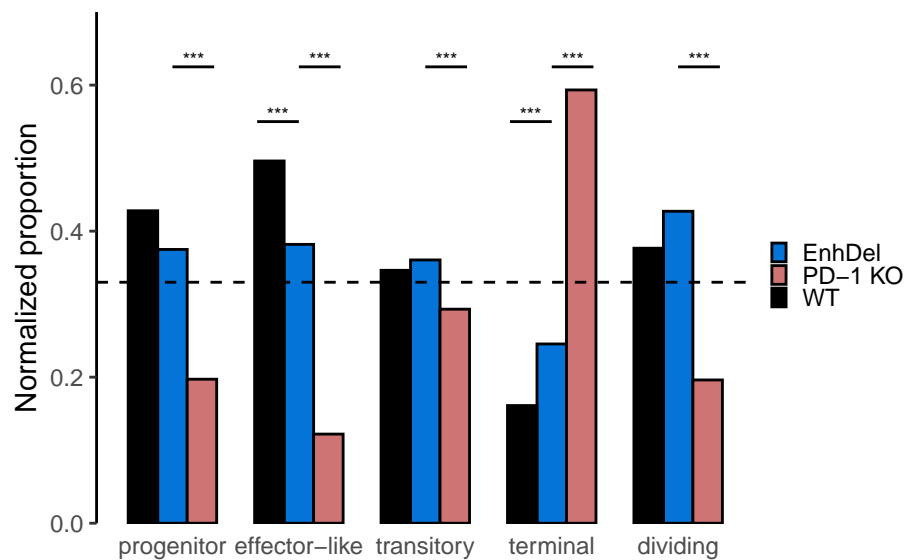


Figure 3i

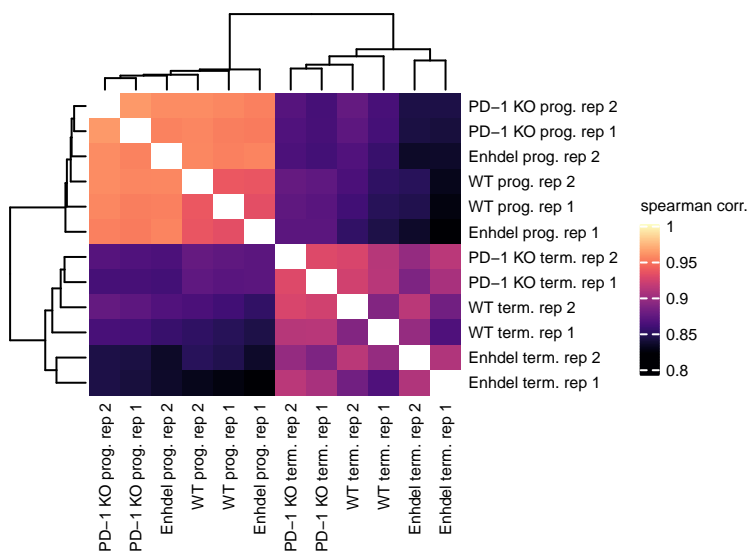


Figure 3j

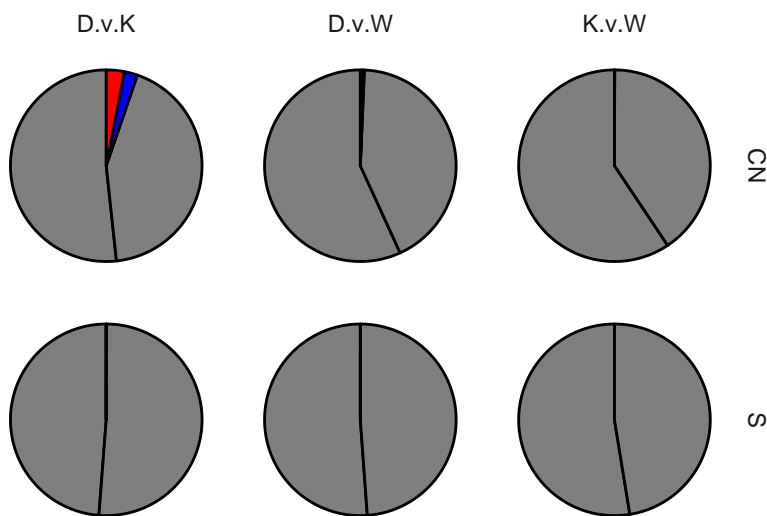
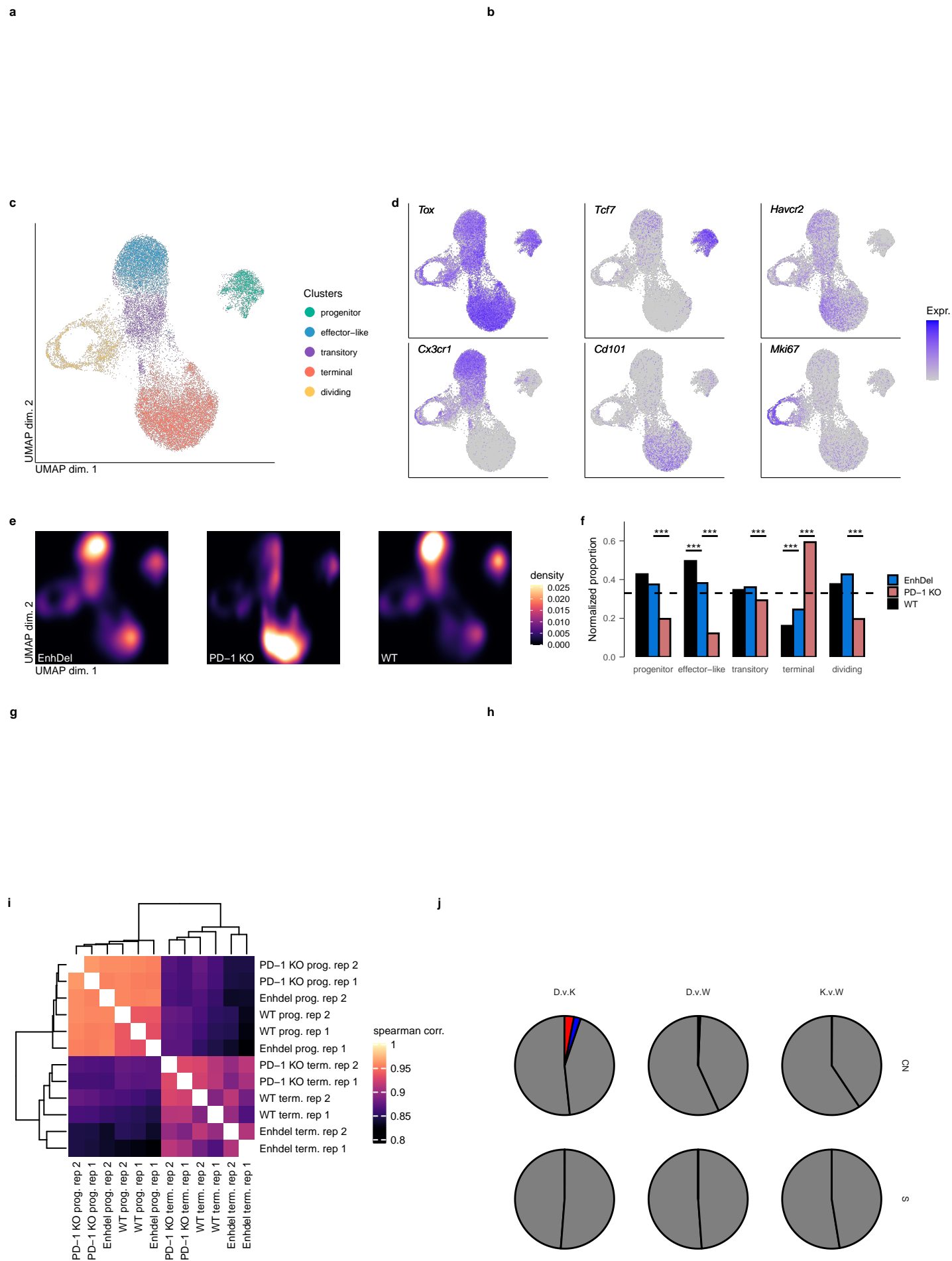


Figure 3 Panel Layout

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



```

## 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      stats      graphics  grDevices  utils      datasets  methods
## [8] base
##
## other attached packages:
## [1] Rsc_0.0.0.9000      SeuratObject_4.0.4  Seurat_3.1.1
## [4] gggrastr_1.0.1      scattermore_0.8      ggforce_0.3.3
## [7] ggrepel_0.9.1       circlize_0.4.14     ComplexHeatmap_2.4.3
## [10] gggridges_0.5.3     gridExtra_2.3       viridis_0.6.2
## [13] viridisLite_0.4.0   ggpubr_0.4.0        cowplot_1.1.1
## [16] readr_2.1.2         tibble_3.1.6        purrr_0.3.4
## [19] tidyr_1.2.0         stringr_1.4.0       ggplot2_3.3.6
## [22] dplyr_1.0.9         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] listenv_0.8.0        qqconf_1.2.3         TH.data_1.1-1
## [10] digest_0.6.29        htmltools_0.5.2     fansi_1.0.3
## [13] magrittr_2.0.3       cluster_2.1.3        ROCR_1.0-11
## [16] tzdb_0.3.0           globals_0.14.0      matrixStats_0.61.0
## [19] vroom_1.5.7          R.utils_2.11.0      sandwich_3.0-1
## [22] colorspace_2.0-3     rbibutils_2.2.7      xfun_0.30
## [25] crayon_1.5.1         jsonlite_1.8.0       survival_3.3-1
## [28] zoo_1.8-9            ape_5.6-2            glue_1.6.2
## [31] polyclip_1.10-0      gtable_0.3.0         leiden_0.3.10
## [34] GetoptLong_1.0.5     car_3.0-13           future.apply_1.9.0
## [37] shape_1.4.6          BiocGenerics_0.34.0  abind_1.4-5
## [40] scales_1.2.0         mvtnorm_1.1-3        DBI_1.1.2
## [43] rstatix_0.7.0        Rcpp_1.0.9           metap_1.8
## [46] plotrix_3.8-2        tmvnsim_1.0-2        clue_0.3-60
## [49] reticulate_1.24      bit_4.0.4            rsvd_1.0.5
## [52] SDMTools_1.1-221     tsne_0.1-3.1         stats4_4.0.3
## [55] htmlwidgets_1.5.4    httr_1.4.2           RColorBrewer_1.1-3
## [58] TFiisher_0.2.0       ellipsis_0.3.2       ica_1.0-2
## [61] pkgconfig_2.0.3      R.methodsS3_1.8.1    farver_2.1.0
## [64] uwot_0.1.11          utf8_1.2.2           labeling_0.4.2
## [67] reshape2_1.4.4       tidyselect_1.1.2     rlang_1.0.2
## [70] munsell_0.5.0        tools_4.0.3          cli_3.2.0
## [73] generics_0.1.2       broom_0.8.0          mathjaxr_1.6-0
## [76] evaluate_0.15        fastmap_1.1.0        yaml_2.3.5
## [79] bit64_4.0.5          knitr_1.39           fitdistrplus_1.1-8
## [82] RANN_2.6.1           pbapply_1.5-0        future_1.25.0
## [85] nlme_3.1-157         R.oo_1.24.0          compiler_4.0.3
## [88] rstudioapi_0.13      beeswarm_0.4.0       plotly_4.10.0
## [91] png_0.1-7            ggsignif_0.6.3       tweenr_1.0.2
## [94] stringi_1.7.6        lattice_0.20-45      Matrix_1.4-1
## [97] multtest_2.44.0      vctr_0.4.1           mutoss_0.1-12
## [100] pillar_1.7.0         lifecycle_1.0.1      Rdpack_2.3
## [103] lmtest_0.9-40        GlobalOptions_0.1.2  RcppAnnoy_0.0.19
## [106] data.table_1.14.2    irlba_2.3.5          R6_2.5.1
## [109] KernSmooth_2.23-20   vipor_0.4.5          parallelly_1.31.1

```

## [112]	codetools_0.2-18	MASS_7.3-56	assertthat_0.2.1
## [115]	rprojroot_2.0.3	rjson_0.2.21	withr_2.5.0
## [118]	sctransform_0.3.3	mnormt_2.0.2	multcomp_1.4-19
## [121]	parallel_4.0.3	hms_1.1.1	rmarkdown_2.14
## [124]	carData_3.0-5	Rtsne_0.15	numDeriv_2016.8-1.1
## [127]	Biobase_2.48.0	ggbeeswarm_0.6.0	