Figures 4 Panels

Figure 4a
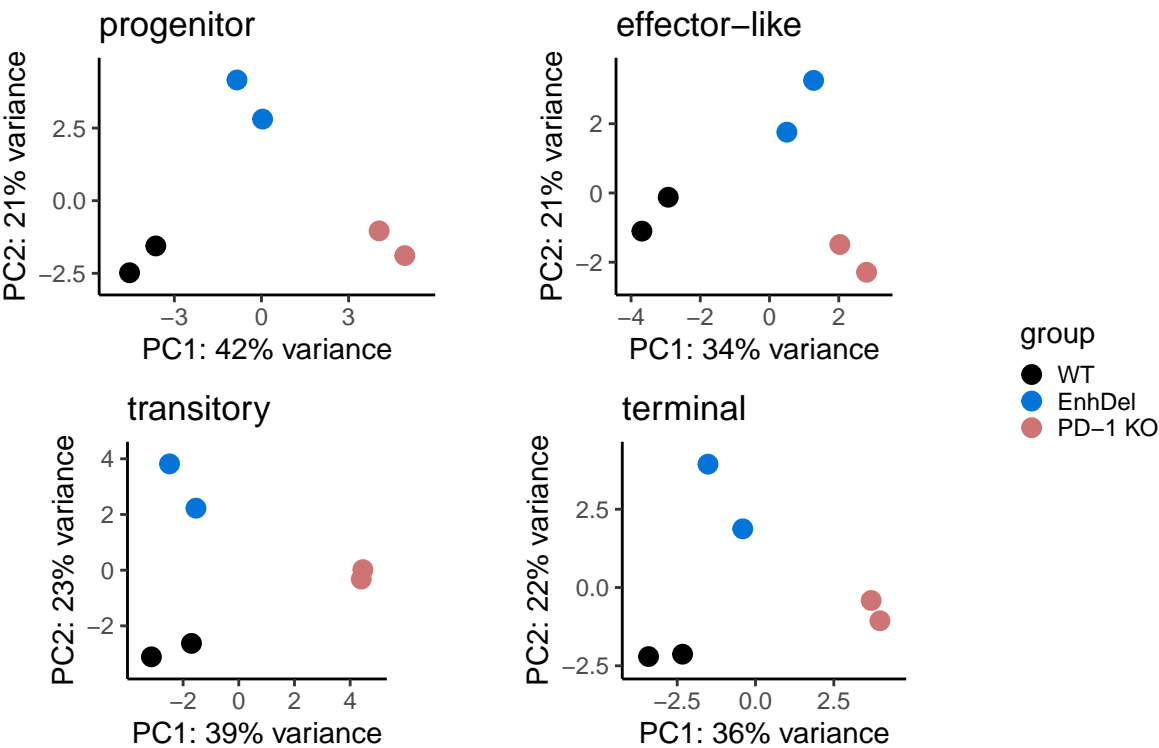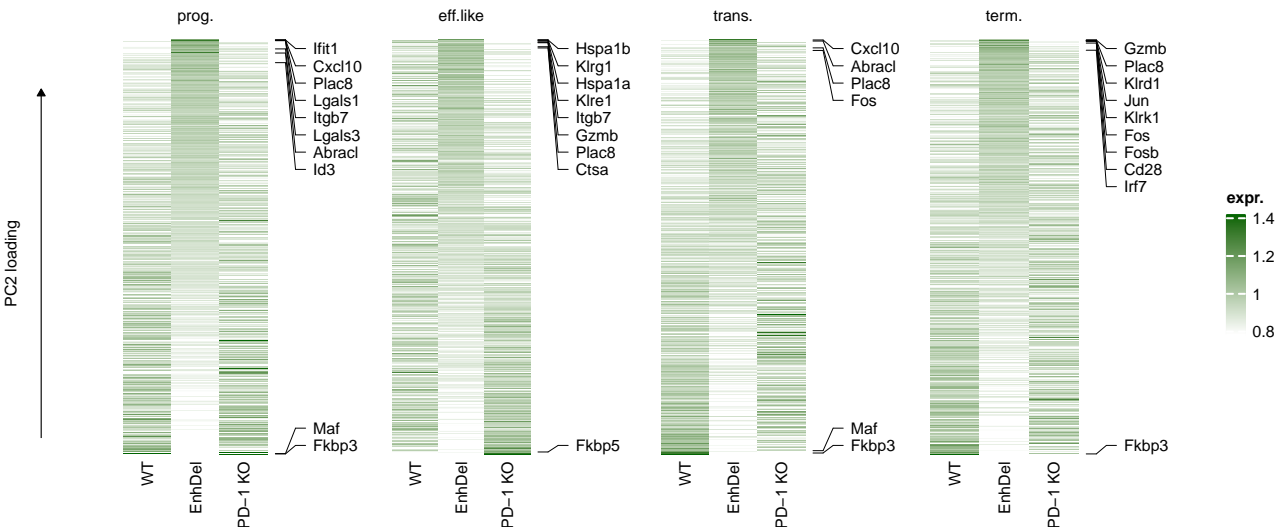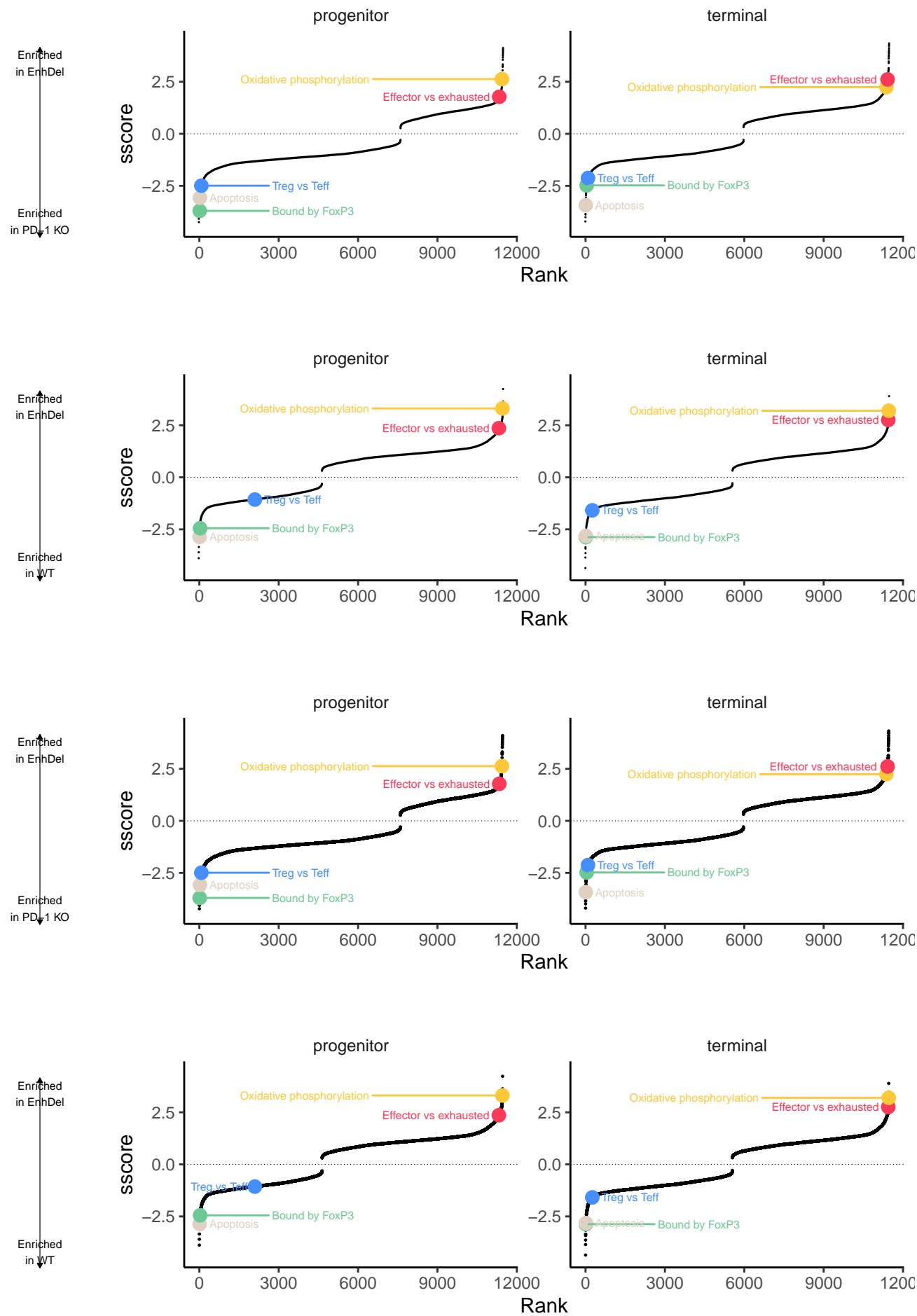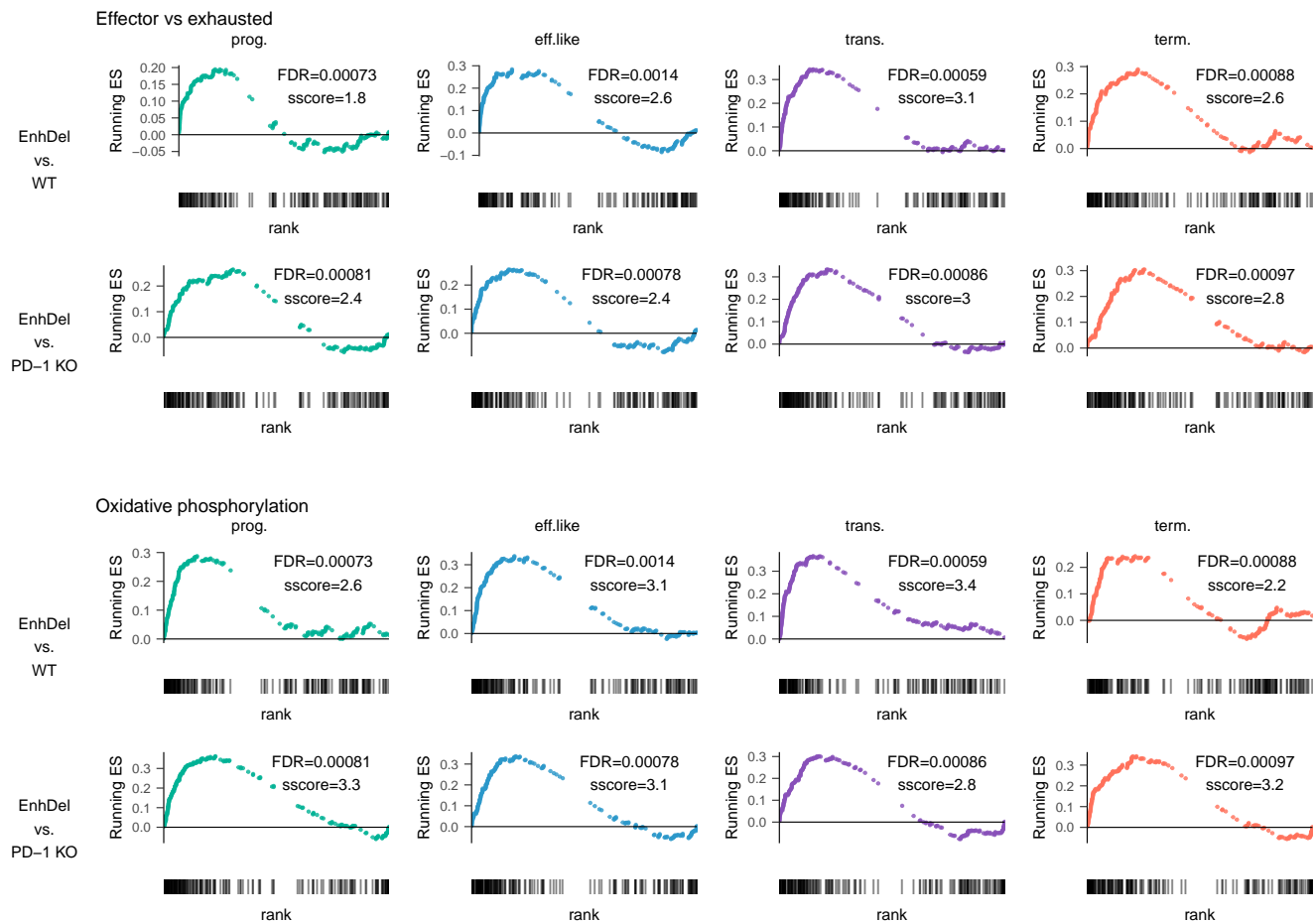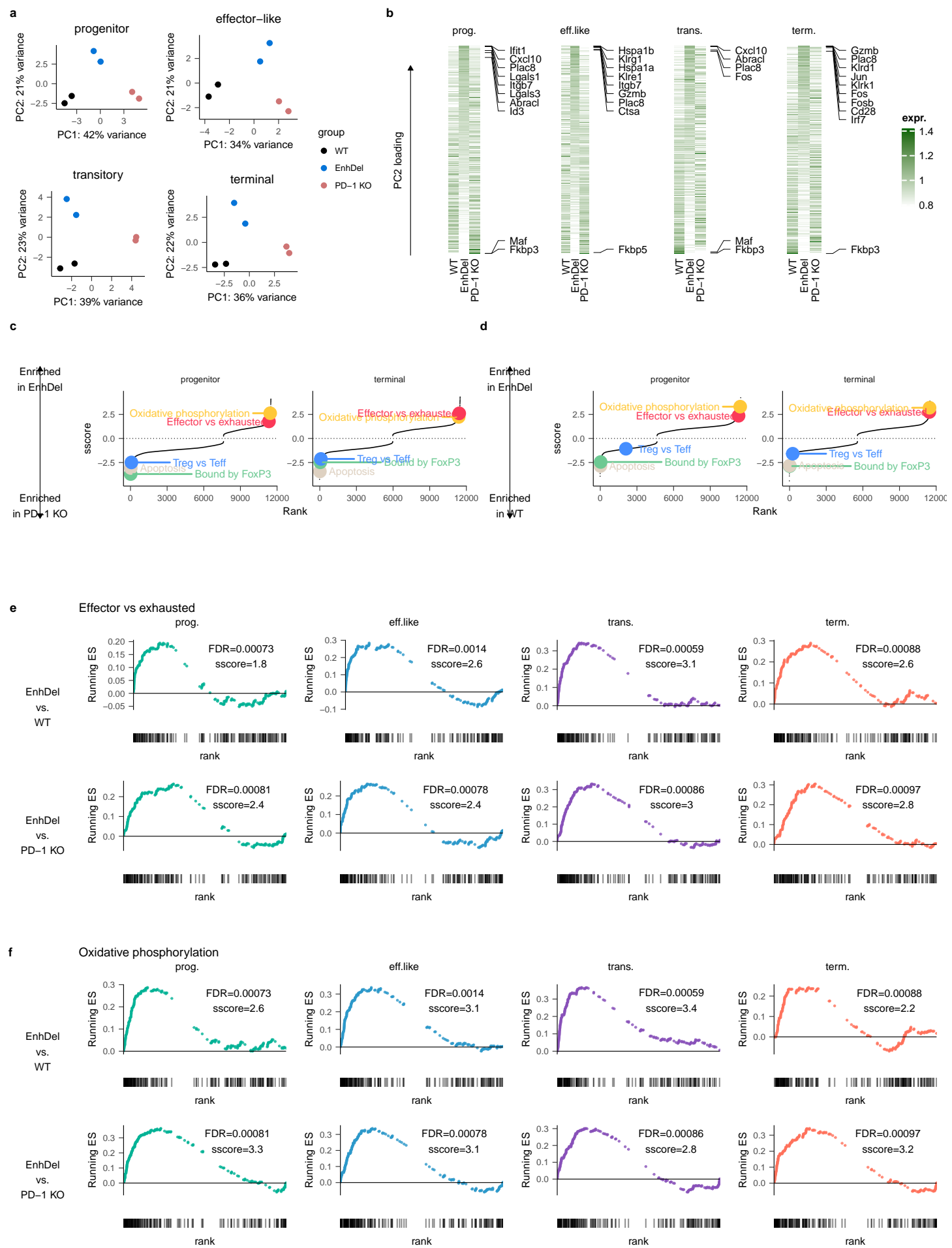

Figure 4b

Figure 4c

Figure 4e and 4f

Figure 4 Panel Layout

Figure 4. Enhancer deletion confers unique transcriptional programs in exhausted CD8+ T cells, distinct from PD-1 KO and WT

```
## 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] Seurat_3.1.1              ggrastr_1.0.1
##  [3] scattermore_0.8           ggforce_0.3.3
##  [5] ggrepel_0.9.1             circlize_0.4.14
##  [7] ComplexHeatmap_2.4.3      ggridges_0.5.3
##  [9] gridExtra_2.3             viridis_0.6.2
## [11] viridisLite_0.4.0         ggpubr_0.4.0
## [13] cowplot_1.1.1             readr_2.1.2
## [15] tibble_3.1.6              purrr_0.3.4
## [17] tidyr_1.2.0               stringr_1.4.0
## [19] ggplot2_3.3.6             dplyr_1.0.9
## [21] DESeq2_1.28.1             SummarizedExperiment_1.18.2
## [23] DelayedArray_0.14.1       matrixStats_0.61.0
## [25] Biobase_2.48.0            GenomicRanges_1.40.0
## [27] GenomeInfoDb_1.24.2       IRanges_2.22.2
## [29] S4Vectors_0.26.1          BiocGenerics_0.34.0
## [31] here_1.0.1
##
## loaded via a namespace (and not attached):
##   [1] utf8_1.2.2             reticulate_1.24       R.utils_2.11.0
##   [4] tidyselect_1.1.2       RSQLite_2.2.12        AnnotationDbi_1.50.3
##   [7] htmlwidgets_1.5.4      BiocParallel_1.22.0   Rtsne_0.15
##  [10] munsell_0.5.0          codetools_0.2-18      mutoss_0.1-12
##  [13] ica_1.0-2              future_1.25.0         withr_2.5.0
##  [16] colorspace_2.0-3       knitr_1.39            rstudioapi_0.13
##  [19] ROCR_1.0-11            ggsignif_0.6.3        listenv_0.8.0
##  [22] labeling_0.4.2         Rdpack_2.3            GenomeInfoDbData_1.2.3
##  [25] mnormt_2.0.2           polyclip_1.10-0       bit64_4.0.5
##  [28] farver_2.1.0           rprojroot_2.0.3       parallelly_1.31.1
##  [31] vctrs_0.4.1            generics_0.1.2        TH.data_1.1-1
##  [34] xfun_0.30              R6_2.5.1              ggbeeswarm_0.6.0
##  [37] clue_0.3-60            rsvd_1.0.5            locfit_1.5-9.4
##  [40] bitops_1.0-7           cachem_1.0.6          assertthat_0.2.1
##  [43] vroom_1.5.7            SDMTools_1.1-221      scales_1.2.0
##  [46] multcomp_1.4-19        beeswarm_0.4.0        gtable_0.3.0
##  [49] globals_0.14.0         sandwich_3.0-1        rlang_1.0.6
##  [52] genefilter_1.70.0      GlobalOptions_0.1.2   splines_4.0.3
##  [55] rstatix_0.7.0          lazyeval_0.2.2        broom_0.8.0
##  [58] reshape2_1.4.4         yaml_2.3.5            abind_1.4-5
##  [61] backports_1.4.1        tools_4.0.3           ellipsis_0.3.2
##  [64] RColorBrewer_1.1-3     TFisher_0.2.0         Rcpp_1.0.9
##  [67] plyr_1.8.7             zlibbioc_1.34.0       RCurl_1.98-1.6
##  [70] pbapply_1.5-0          GetoptLong_1.0.5      zoo_1.8-9
##  [73] cluster_2.1.3          magrittr_2.0.3        data.table_1.14.2
##  [76] lmtest_0.9-40          RANN_2.6.1            tmvnsim_1.0-2
##  [79] mvtnorm_1.1-3          fitdistrplus_1.1-8    hms_1.1.1
##  [82] evaluate_0.15          xtable_1.8-4          XML_3.99-0.9
##  [85] shape_1.4.6            compiler_4.0.3        KernSmooth_2.23-20
```

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##   [88] crayon_1.5.1          R.oo_1.24.0          htmltools_0.5.2
##   [91] tzdb_0.3.0            geneplotter_1.66.0   DBI_1.1.2
##   [94] tweenr_1.0.2          MASS_7.3-56          Matrix_1.4-1
##   [97] car_3.0-13            cli_3.4.1            R.methodsS3_1.8.1
##  [100] rbibutils_2.2.7       metap_1.8           qqconf_1.2.3
##  [103] igraph_1.3.0          pkgconfig_2.0.3     sn_2.0.2
##  [106] numDeriv_2016.8-1.1   plotly_4.10.0       annotate_1.66.0
##  [109] vipor_0.4.5           multtest_2.44.0     XVector_0.28.0
##  [112] digest_0.6.29         tsne_0.1-3.1        sctransform_0.3.3
##  [115] RcppAnnoy_0.0.19      rmarkdown_2.14      leiden_0.3.10
##  [118] uwot_0.1.11           rjson_0.2.21        lifecycle_1.0.1
##  [121] nlme_3.1-157          jsonlite_1.8.0      carData_3.0-5
##  [124] fansi_1.0.3           pillar_1.7.0        lattice_0.20-45
##  [127] fastmap_1.1.0         httr_1.4.2          plotrix_3.8-2
##  [130] survival_3.3-1        glue_1.6.2          png_0.1-7
##  [133] bit_4.0.4             stringi_1.7.6       blob_1.2.3
##  [136] memoise_2.0.1         mathjaxr_1.6-0      irlba_2.3.5
##  [139] future.apply_1.9.0    ape_5.6-2
```