

Figures 4 Panels

Figure 4a

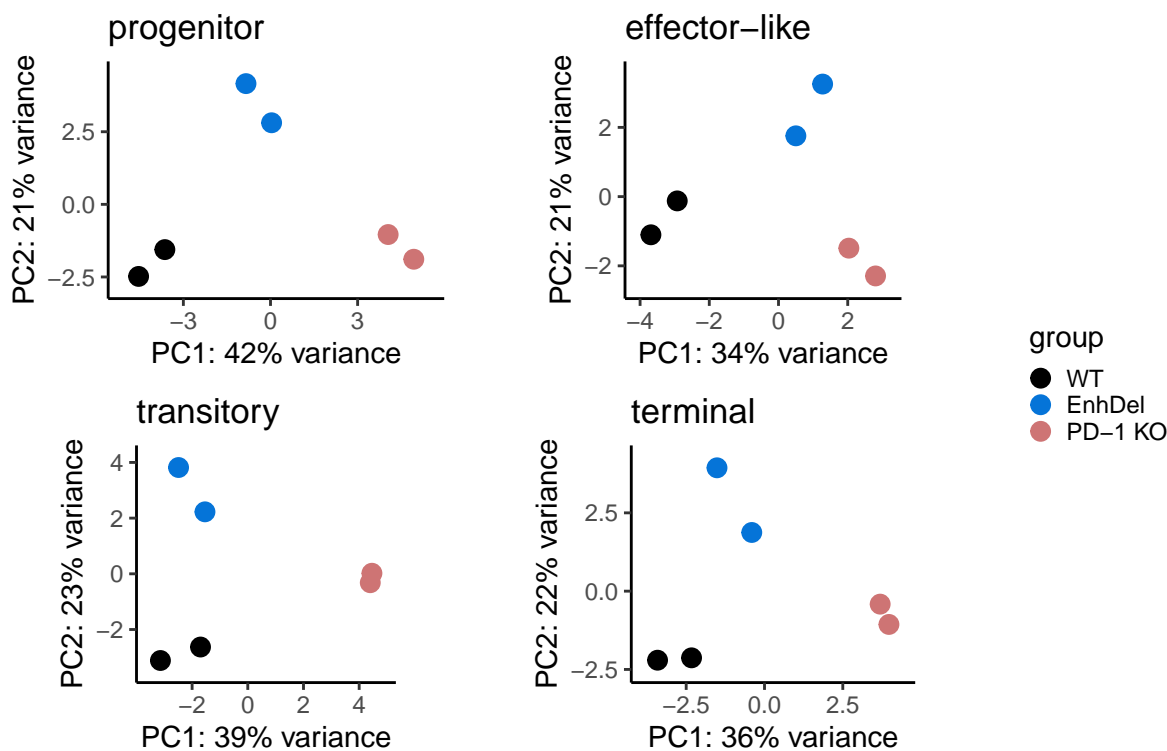


Figure 4b

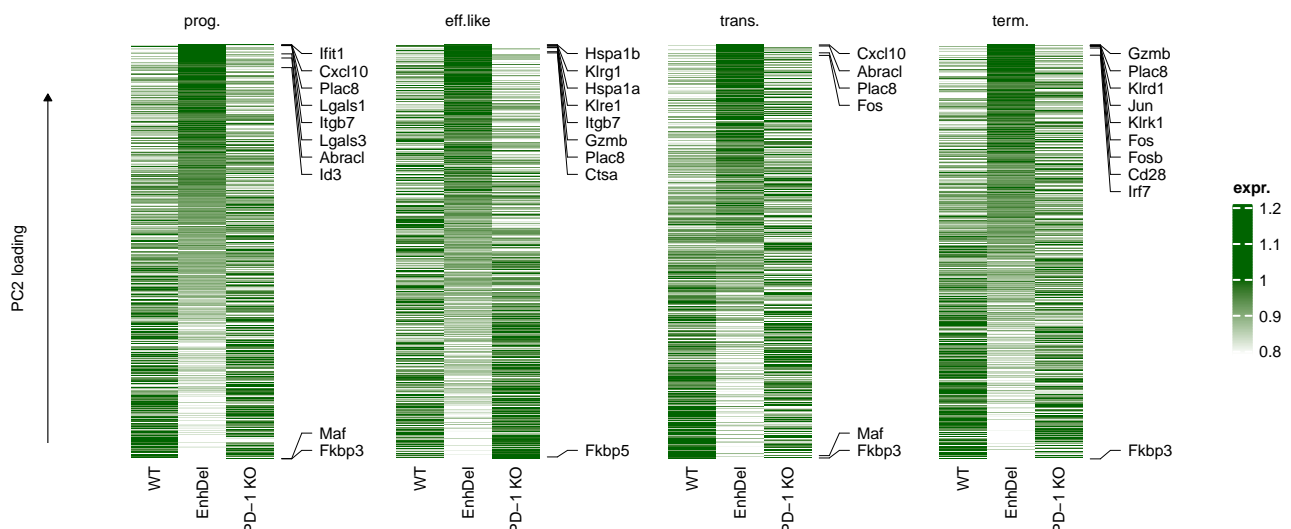


Figure 4c

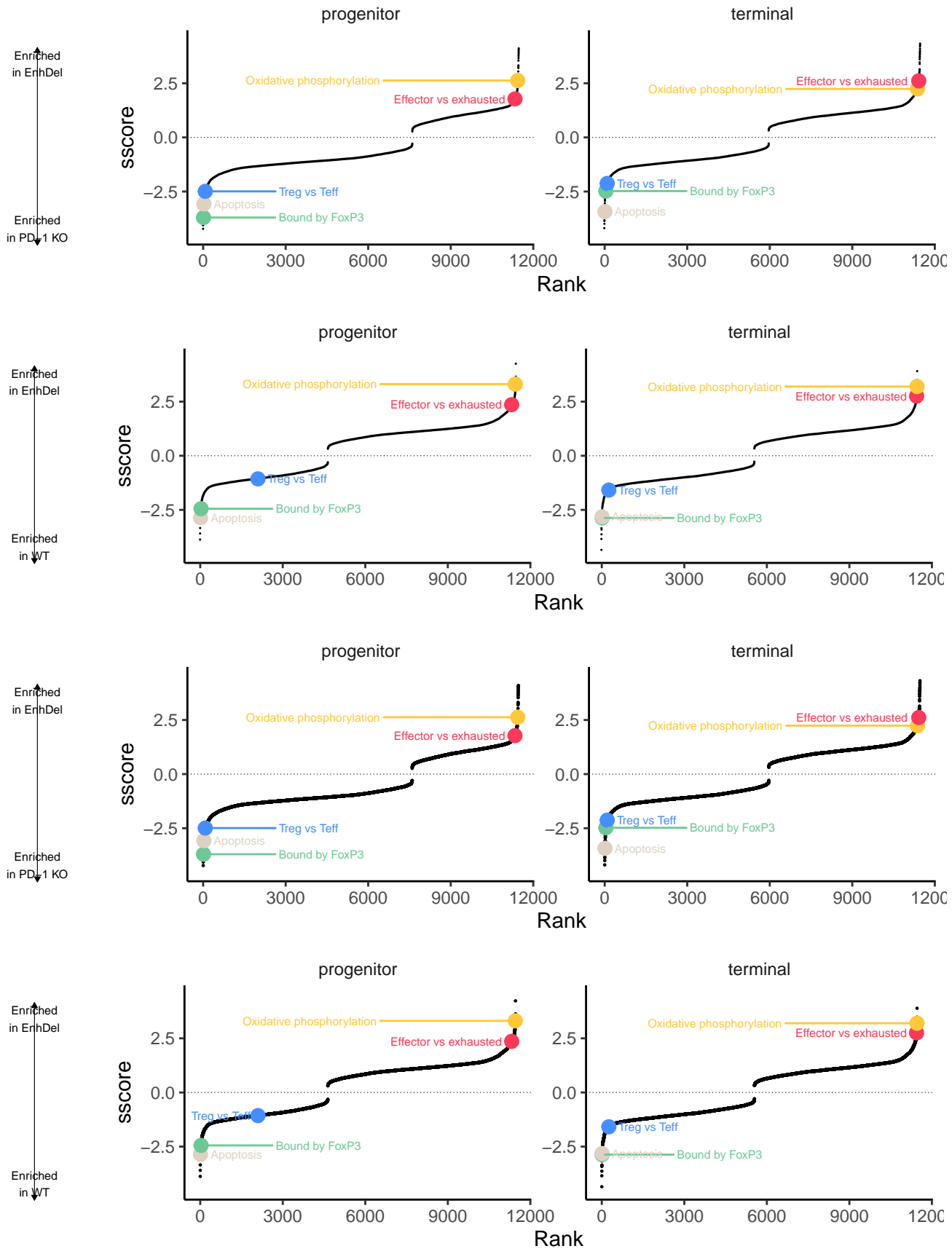


Figure 4e and 4f

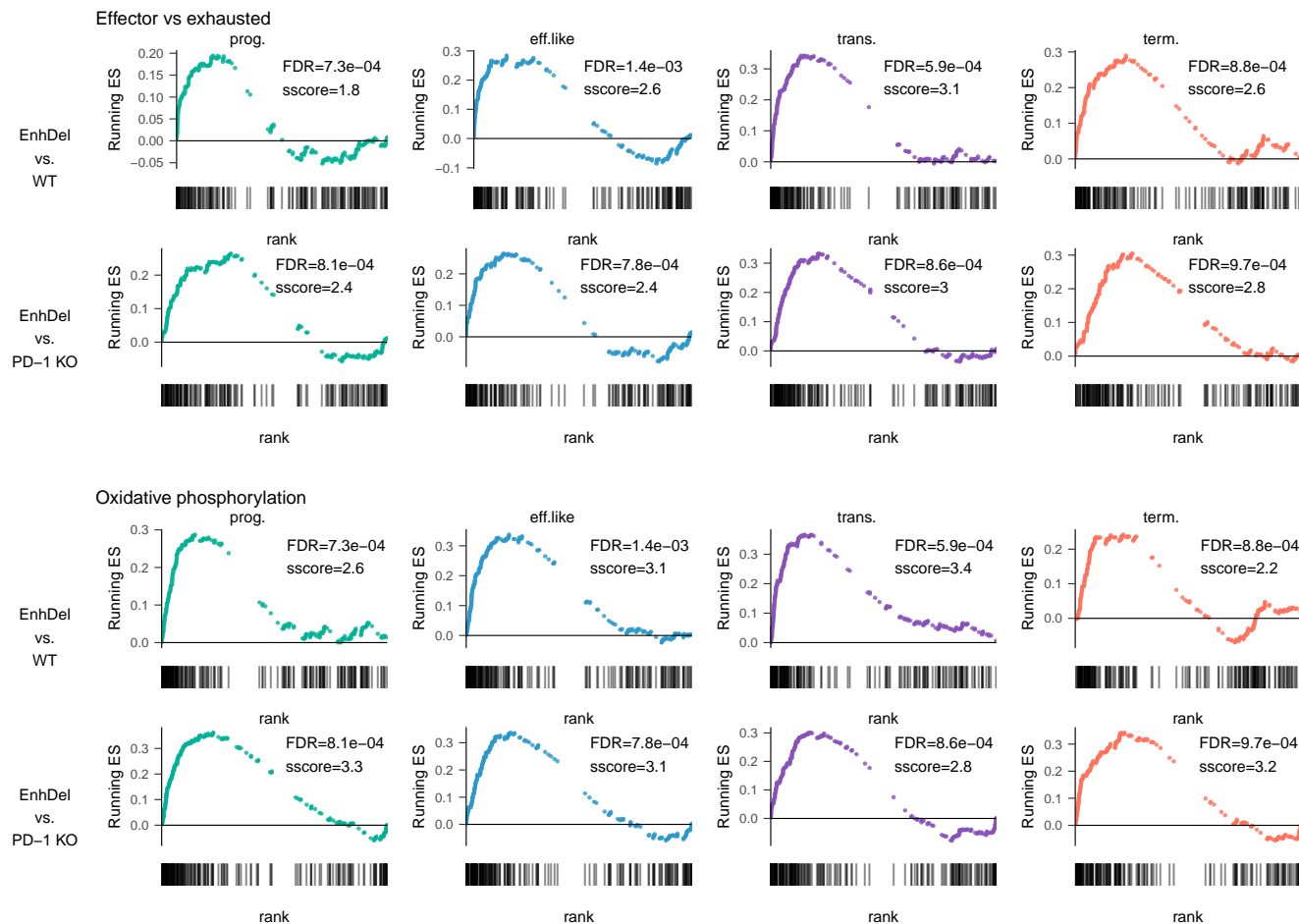
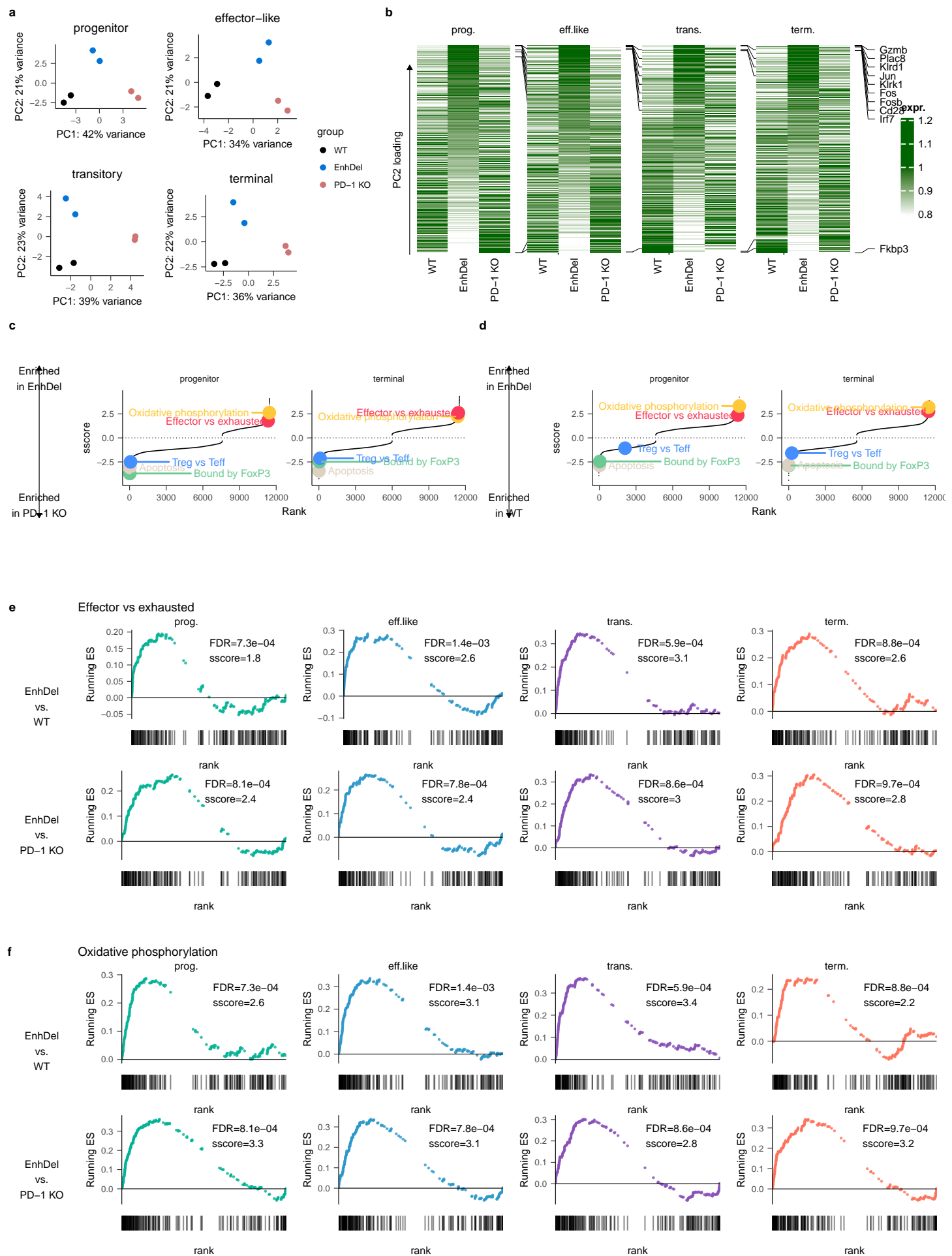


Figure 4 Panel Layout

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 ggirdges_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] vctr_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 SDMTTools_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 TFSher_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] lmttest_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	