

SFigS5_GSEA_scatterplot.R

t

2024-11-13

```
# HEADER ####
#
# Version: 2024-11-13
#
# Figure S5:
#   Analysis of prognostic gene sets in pre-Tx biopsies
#   and post-Tx residual tumors.
#
#
#
# SETUP ####
```

```
Sys.setenv(lang = "en_US")
```

Install required packages if missing -----

```
# Package names from CRAN
packs <- c("tidyverse", "ggrepel")

# Install packages not yet installed
installed_packages <- packs %in% rownames(installed.packages())
if (any(installed_packages == FALSE)) {
  install.packages(packs[!installed_packages])
}
```

Load required packages -----

```
invisible(lapply(packs, library, character.only = TRUE))

## — Attaching core tidyverse packages ————— tidyverse 2.0.0 —
## ✓ dplyr      1.1.4      ✓ readr      2.1.5
## ✓ forcats    1.0.0      ✓ stringr    1.5.1
## ✓ ggplot2    3.5.1      ✓ tibble     3.2.1
## ✓ lubridate  1.9.3      ✓ tidyr      1.3.1
## ✓ purrr      1.0.2
## — Conflicts ————— tidyverse_conflicts() —
## ✗ dplyr::filter() masks stats::filter()
## ✗ dplyr::lag()    masks stats::lag()
## ⓘ Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts
to become errors
```

```

# FUNCTION Definitions #####
# *****
#
# The following functions shift_axis_y() and shift_axis_x()
# are applied to place x and y axes in the plots
# to hazard ratios = "1" (instead of "0")

shift_axis_y <- function(p, y=0){
  g <- ggplotGrob(p)
  dummy <- data.frame(y=y)
  ax <- g[["grobs"]][g$layout$name == "axis-b"][[1]]
  p + annotation_custom(grid::grobTree(ax,
                                         vp = grid::viewport(
                                           y=0, height=sum(ax$height))),
                        ymax=y, ymin=y) +
  geom_hline(aes(yintercept=y), data = dummy) +
  theme(axis.text.x = element_blank(),
        axis.ticks.x=element_blank())
}

shift_axis_x <- function(p, x=0){
  g <- ggplotGrob(p)
  dummy <- data.frame(x=x)
  ax <- g[["grobs"]][g$layout$name == "axis-l"][[1]]
  p + annotation_custom(grid::grobTree(ax,
                                         vp = grid::viewport(
                                           x=0, width = sum(ax$height))),
                        xmax=x, xmin=x) +
  geom_vline(aes(xintercept=x), data = dummy) +
  theme(axis.text.y = element_blank(),
        axis.ticks.y=element_blank(),
        legend.position = "none")
}

```

```

# IMPORT #####

# Normalized Enrichment Scores (NES) of pathways for iDFS prognosis
# from biopsy and resect samples

df <- read.table("biopsy_resect_HR_basedGSEA_20092024.txt", header=TRUE, sep='\t')

# Define four quadrants Q1-Q4 for coloring
df$quadrant <- dplyr::case_when(df$Resect > 0 & df$Biopsy > 0 ~ "Q1", #Q1... both x and
y are positive
                                df$Resect > 0 & df$Biopsy < 0 ~ "Q2",  #Q2... x is neg
and y is positive
                                df$Resect < 0 & df$Biopsy < 0 ~ "Q3",  #Q3... both x and
y are negative
                                df$Biopsy > 0 & df$Resect < 0 ~ "Q4") #Q4... x is pos
and y is negative

testplot<-ggplot(df, aes(x = Biopsy, y =Resect, color = quadrant), guides(fill = FALSE,
color = FALSE)) +

```

```

geom_point(size=2) +
geom_text_repel(aes(label = Pathway),size=3.5, box.padding = 0.5, max.overlaps=Inf) +
theme(panel.background = element_rect(fill="white"),
      plot.margin = margin(1, 1, 1, 1, "cm"),
      axis.title=element_blank(),
      axis.ticks.length=unit(.2, "cm"))+
scale_x_continuous(limits = c(-3, 3), n.breaks=7) +
scale_y_continuous(limits = c(-3, 3),n.breaks=7)+
labs(title = "paired 540 samples",
      caption = "NES: normalized enrichment score \n(pos. NES: genes set enriched in
tumors from patients with good prognosis; neg. NES = gene set enriched in tumors from
patients with poor prognosis)") +
  theme(plot.title = element_text(hjust = 0, vjust = 10, margin = margin(t = 10)),
        plot.caption = element_text(hjust = 0))

# Add central axes and axis labels

p1 <- testplot +
  annotate("segment", x = -Inf, xend = Inf, y = 0, linewidth=1.5, yend = 0, color =
"purple") +
  annotate("segment", x = 0, xend = 0, y = -Inf, linewidth=1.5, yend = Inf, color =
"blue") +

  annotate("text", x = -Inf, y = 1, label = "NES for iDFS in post.Tx \u2192 improved
survival", angle = 90,size=4, hjust=1.0, vjust=-2.0, color = "red") +
  annotate("text", x = -1, y = Inf, label = "NES for iDFS in pre.Tx \u2192 improved
survival", hjust=0,vjust=30, size=4, color = "blue") +

  annotate("text", x = -Inf, y = Inf, label = "good iDFS in post.Tx &\npoor iDFS in
pre.Tx", vjust = 1, hjust=0, size=3.5)+
  annotate("text", x = -Inf, y = -Inf, label = "poor iDFS in post.Tx & pre.Tx", vjust =
0, hjust=0, size=3.5)+
  annotate("text", x = Inf, y = Inf, label = "good iDFS in post.Tx & pre.Tx", vjust = 1,
hjust=1, size=3.5)+
  annotate("text", x = Inf, y = -Inf, label = "good iDFS in pre.Tx &\npoor iDFS in
post.Tx", vjust = 0, hjust=1, size=3.5)+

  coord_cartesian(clip = "off") # Allow annotations to be outside the plot area

# Shift axis labels

p1<-shift_axis_y(p1, y=0)
p1<-shift_axis_x(p1, x=0)
p1

```

[illegible]

```
ggsave(file="SFig5.svg", plot=p1, width=10, height=8)
dev.off()

## null device
##      1
```

SESSION INFO

sessionInfo()

```
## R version 4.4.1 (2024-06-14 ucrt)
## Platform: x86_64-w64-mingw32/x64
## Running under: Windows 11 x64 (build 22631)
##
## Matrix products: default
##
## locale:
## [1] LC_COLLATE=German_Germany.utf8  LC_CTYPE=German_Germany.utf8
## [3] LC_MONETARY=German_Germany.utf8 LC_NUMERIC=C
## [5] LC_TIME=German_Germany.utf8
##
## time zone: Europe/Berlin
## tzcode source: internal
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods   base
##
## other attached packages:
## [1] ggrepel_0.9.6    lubridate_1.9.3 forcats_1.0.0    stringr_1.5.1
## [5] dplyr_1.1.4      purrr_1.0.2     readr_2.1.5      tidyr_1.3.1
## [9] tibble_3.2.1     ggplot2_3.5.1   tidyverse_2.0.0
##
## loaded via a namespace (and not attached):
## [1] gtable_0.3.5      highr_0.11        compiler_4.4.1    Rcpp_1.0.13
## [5] tidyselect_1.2.1  textshaping_0.4.0 systemfonts_1.1.0 scales_1.3.0
## [9] yaml_2.3.10       fastmap_1.2.0     R6_2.5.1          labeling_0.4.3
## [13] generics_0.1.3    knitr_1.48        munsell_0.5.1     svglite_2.1.3
## [17] pillar_1.9.0      tzdb_0.4.0        rlang_1.1.4       utf8_1.2.4
## [21] stringi_1.8.4     xfun_0.47         timechange_0.3.0  cli_3.6.3
## [25] withr_3.0.1       magrittr_2.0.3    digest_0.6.37     grid_4.4.1
## [29] rstudioapi_0.16.0 hms_1.1.3         lifecycle_1.0.4   vctrs_0.6.5
## [33] evaluate_1.0.0    glue_1.7.0        farver_2.1.2      ragg_1.3.2
## [37] fansi_1.0.6       colorspace_2.1-1  rmarkdown_2.28    tools_4.4.1
## [41] pkgconfig_2.0.3   htmltools_0.5.8.1
```