

Final Case Study

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Basic dependencies:

- R>=4.1 # <https://www.r-project.org/>
- RStudio>=1.4.1717 # <https://posit.co/download/rstudio-desktop/>

R Package Dependencies

```
options(warn=-1)
if (!require(pacman)) install.packages("pacman")

## Loading required package: pacman
pacman::p_load(tidyverse, glmnet, iregnet, penAFT,
               survival, mice, ggsurvfit, dplyr, xtable, ggplot2)

dir.create("plots", showWarnings = F)
theme_set(theme_classic(base_size = 12))
```

System Information

```
sessionInfo()

## R version 4.1.3 (2022-03-10)
## Platform: x86_64-redhat-linux-gnu (64-bit)
## Running under: Fedora Linux 36 (MATE-Compiz)
##
## Matrix products: default
## BLAS/LAPACK: /usr/lib64/libflexiblas.so.3.3
##
## locale:
##  [1] LC_CTYPE=en_US.UTF-8      LC_NUMERIC=C
##  [3] LC_TIME=en_US.UTF-8      LC_COLLATE=en_US.UTF-8
##  [5] LC_MONETARY=en_US.UTF-8  LC_MESSAGES=en_US.UTF-8
##  [7] LC_PAPER=en_US.UTF-8     LC_NAME=C
##  [9] LC_ADDRESS=C             LC_TELEPHONE=C
## [11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods    base
##
## other attached packages:
##  [1] xtable_1.8-4      ggsurvfit_0.3.0    mice_3.15.0        survival_3.5-5
##  [5] penAFT_0.3.0      iregnet_0.1.0.9000 glmnet_4.1-7        Matrix_1.5-4
```

```
## [9] lubridate_1.9.2    forcats_1.0.0      stringr_1.5.0      dplyr_1.1.2
## [13] purrr_1.0.1        readr_2.1.4        tidyr_1.3.0        tibble_3.2.1
## [17] ggplot2_3.4.2      tidyverse_2.0.0    pacman_0.5.1
##
## loaded via a namespace (and not attached):
## [1] shape_1.4.6         tidyselect_1.2.0    xfun_0.39
## [4] listenv_0.9.0       splines_4.1.3       lattice_0.21-8
## [7] colorspace_2.1-0    vctrs_0.6.2         generics_0.1.3
## [10] htmltools_0.5.5     yaml_2.3.7          utf8_1.2.3
## [13] rlang_1.1.0         pillar_1.9.0        glue_1.6.2
## [16] withr_2.5.0         foreach_1.5.2       lifecycle_1.0.3
## [19] munsell_0.5.0       gtable_0.3.3        future_1.32.0
## [22] codetools_0.2-19    evaluate_0.20        knitr_1.42
## [25] tzdb_0.3.0          fastmap_1.1.1       irlba_2.3.5.1
## [28] parallel_4.1.3      fansi_1.0.4         broom_1.0.4
## [31] Rcpp_1.0.10         backports_1.4.1     scales_1.2.1
## [34] parallelly_1.35.0   RhpcBLASctl_0.23-42 hms_1.1.3
## [37] digest_0.6.31       stringi_1.7.12      grid_4.1.3
## [40] cli_3.6.1           tools_4.1.3         magrittr_2.0.3
## [43] future.apply_1.10.0 pkgconfig_2.0.3     timechange_0.2.0
## [46] rmarkdown_2.21      rstudioapi_0.14     iterators_1.0.14
## [49] R6_2.5.1            globals_0.16.2      compiler_4.1.3
```

Load data

```
data = read.csv('METABRIC_RNA_Mutation.csv')
```

```
sum(is.na(data))
```

```
## [1] 638
```

```
# drop the patient with sarcoma
```

```
sum(data$cancer_type == "Breast Sarcoma")
```

```
## [1] 1
```

```
# only keep patients with Breast Invasive Ductal Carcinoma
```

```
data = data[data$cancer_type_detailed == 'Breast Invasive Ductal Carcinoma',]
```

```
# Drop the rare claudin low subtype
```

```
data = data[data$pam50_._claudin.low_subtype != 'NC',]
```

```
# drop: patient_id
```

```
data = data %>% select(-c('patient_id', 'cancer_type', 'cancer_type_detailed', 'cohort', 'overall_survival_months'))
```

```
sum(is.na(data))
```

```
## [1] 498
```

```
# select only the ones for which we know the surgery type
```

```
data_sel = data[data$type_of_breast_surgery != "",]
```

```
sum(is.na(data_sel$overall_survival_months))
```

```
## [1] 0
```

```
data_sel = Filter(function(x)(length(unique(x))>1), data_sel)
```

```
data_BIDC = data_sel
```

```

#print(names(data_BIDC))

#sum(is.na(data_sel))

num_cols = ncol(data_sel)
for (i in 1:num_cols)
{
  if (sum(is.na(data_sel[,i])) > 0)
  {
    print(i)
    print(colnames(data_sel[i]))
  }
}

## [1] 8
## [1] "neoplasm_histologic_grade"
## [1] 17
## [1] "mutation_count"
## [1] 23
## [1] "tumor_size"
## [1] 24
## [1] "tumor_stage"

# Recode the treatment prodecures: 0 - breast conserving, 1 - mastectomy
data_BIDC$treatment = 1*(data_BIDC$type_of_breast_surgery == "MASTECTOMY")
unique(data_BIDC$type_of_breast_surgery)

## [1] "MASTECTOMY"          "BREAST CONSERVING"

data_BIDC$primary_tumor_laterality[data_BIDC$primary_tumor_laterality == ""] = NA
data_BIDC$inferred_menopausal_state[data_BIDC$inferred_menopausal_state == ""] = NA
data_BIDC$er_status_measured_by_ihc[data_BIDC$er_status_measured_by_ihc == ""] = NA

sum(is.na(data_BIDC$primary_tumor_laterality))

## [1] 83
sum(is.na(data_BIDC$inferred_menopausal_state))

## [1] 0
sum(is.na(data_BIDC$er_status_measured_by_ihc))

## [1] 22
sum(is.na(data_BIDC[,26:514]))

## [1] 0

```

Data Imputation with MICE

```

# categorical_vars <- c("cellularity", "pam50_.claudin.low_subtype",
#                       "neoplasm_histologic_grade", "tumor_other_histologic_subtype",
#                       "integrative_cluster", "X3.gene_classifier_subtype")
#
# other_categorical = c("inferred_menopausal_state",

```

```

#           "primary_tumor_laterality",
#           "pr_status",
#           "tumor_stage",
#           "her2_status",
#           "er_status_measured_by_ihc",
#           "radio_therapy", "hormone_therapy", "chemotherapy")

categorical_vars <- c("cellularity", "pam50_.claudin.low_subtype",
                     "neoplasm_histologic_grade", "tumor_other_histologic_subtype",
                     "integrative_cluster", "X3.gene_classifier_subtype")

other_categorical = c("inferred_menopausal_state",
                     "primary_tumor_laterality",
                     "pr_status",
                     "tumor_stage",
                     "her2_status",
                     "er_status_measured_by_ihc",
                     "radio_therapy", "hormone_therapy", "chemotherapy")

data_mice <- data_BIDC %>% mutate(across(all_of(unlist(c(categorical_vars, other_categorical))), factor))

data_BIDC_2 = data_BIDC
data_BIDC_3 = data_BIDC
data_BIDC_4 = data_BIDC
data_BIDC_5 = data_BIDC

data_mice = data_mice[,1:24]
#sum(is.na(data_mice))
names(data_mice)

## [1] "age_at_diagnosis"           "type_of_breast_surgery"
## [3] "cellularity"                "chemotherapy"
## [5] "pam50_.claudin.low_subtype" "er_status_measured_by_ihc"
## [7] "er_status"                  "neoplasm_histologic_grade"
## [9] "her2_status_measured_by_snp6" "her2_status"
## [11] "tumor_other_histologic_subtype" "hormone_therapy"
## [13] "inferred_menopausal_state"    "integrative_cluster"
## [15] "primary_tumor_laterality"     "lymph_nodes_examined_positive"
## [17] "mutation_count"              "nottingham_prognostic_index"
## [19] "overall_survival_months"     "pr_status"
## [21] "radio_therapy"              "X3.gene_classifier_subtype"
## [23] "tumor_size"                 "tumor_stage"

set.seed(5)
mice_obj <- mice(data = data_mice, m = 5)

##
## iter imp variable
## 1 1 er_status_measured_by_ihc neoplasm_histologic_grade primary_tumor_laterality mutation_co
## 1 2 er_status_measured_by_ihc neoplasm_histologic_grade primary_tumor_laterality mutation_co
## 1 3 er_status_measured_by_ihc neoplasm_histologic_grade primary_tumor_laterality mutation_co
## 1 4 er_status_measured_by_ihc neoplasm_histologic_grade primary_tumor_laterality mutation_co
## 1 5 er_status_measured_by_ihc neoplasm_histologic_grade primary_tumor_laterality mutation_co

```

```
## 2 1 er_status_measured_by_ihc neoplasm_histologic_grade primary_tumor_laterality mutation_co
## 2 2 er_status_measured_by_ihc neoplasm_histologic_grade primary_tumor_laterality mutation_co
## 2 3 er_status_measured_by_ihc neoplasm_histologic_grade primary_tumor_laterality mutation_co
## 2 4 er_status_measured_by_ihc neoplasm_histologic_grade primary_tumor_laterality mutation_co
## 2 5 er_status_measured_by_ihc neoplasm_histologic_grade primary_tumor_laterality mutation_co
## 3 1 er_status_measured_by_ihc neoplasm_histologic_grade primary_tumor_laterality mutation_co
## 3 2 er_status_measured_by_ihc neoplasm_histologic_grade primary_tumor_laterality mutation_co
## 3 3 er_status_measured_by_ihc neoplasm_histologic_grade primary_tumor_laterality mutation_co
## 3 4 er_status_measured_by_ihc neoplasm_histologic_grade primary_tumor_laterality mutation_co
## 3 5 er_status_measured_by_ihc neoplasm_histologic_grade primary_tumor_laterality mutation_co
## 4 1 er_status_measured_by_ihc neoplasm_histologic_grade primary_tumor_laterality mutation_co
## 4 2 er_status_measured_by_ihc neoplasm_histologic_grade primary_tumor_laterality mutation_co
## 4 3 er_status_measured_by_ihc neoplasm_histologic_grade primary_tumor_laterality mutation_co
## 4 4 er_status_measured_by_ihc neoplasm_histologic_grade primary_tumor_laterality mutation_co
## 4 5 er_status_measured_by_ihc neoplasm_histologic_grade primary_tumor_laterality mutation_co
## 5 1 er_status_measured_by_ihc neoplasm_histologic_grade primary_tumor_laterality mutation_co
## 5 2 er_status_measured_by_ihc neoplasm_histologic_grade primary_tumor_laterality mutation_co
## 5 3 er_status_measured_by_ihc neoplasm_histologic_grade primary_tumor_laterality mutation_co
## 5 4 er_status_measured_by_ihc neoplasm_histologic_grade primary_tumor_laterality mutation_co
## 5 5 er_status_measured_by_ihc neoplasm_histologic_grade primary_tumor_laterality mutation_co
```

```
data_full <- complete(mice_obj,1)
data_full_2 <- complete(mice_obj,2)
data_full_3 <- complete(mice_obj,3)
data_full_4 <- complete(mice_obj,4)
data_full_5 <- complete(mice_obj,5)
```

```
data_BIDC[,1:24] = data_full
data_BIDC_2[,1:24] = data_full_2
data_BIDC_3[,1:24] = data_full_3
data_BIDC_4[,1:24] = data_full_4
data_BIDC_5[,1:24] = data_full_5
```

```
data_BIDC$tumor_stage = 0*(data_BIDC$tumor_stage == 0) + 1*(data_BIDC$tumor_stage == 1) + 2*(data_BIDC$tumor_stage == 2)
```

```
data_BIDC_2$tumor_stage = 0*(data_BIDC_2$tumor_stage == 0) + 1*(data_BIDC_2$tumor_stage == 1) + 2*(data_BIDC_2$tumor_stage == 2)
```

```
data_BIDC_3$tumor_stage = 0*(data_BIDC_3$tumor_stage == 0) + 1*(data_BIDC_3$tumor_stage == 1) + 2*(data_BIDC_3$tumor_stage == 2)
```

```
data_BIDC_4$tumor_stage = 0*(data_BIDC_4$tumor_stage == 0) + 1*(data_BIDC_4$tumor_stage == 1) + 2*(data_BIDC_4$tumor_stage == 2)
```

```
data_BIDC_5$tumor_stage = 0*(data_BIDC_5$tumor_stage == 0) + 1*(data_BIDC_5$tumor_stage == 1) + 2*(data_BIDC_5$tumor_stage == 2)
```

```
# sum(data_BIDC$tumor_stage == 0)
# sum(data$tumor_stage == 4, na.rm = TRUE)
```

```
# Drop patients with stage 0 or stage 4 tumor
# data_full_2 = data_full_2[data_BIDC$tumor_stage != 0 & data_BIDC$tumor_stage != 4,]
# data_full_3 = data_full_2[data_BIDC$tumor_stage != 0 & data_BIDC$tumor_stage != 4,]
# data_full_4 = data_full_2[data_BIDC$tumor_stage != 0 & data_BIDC$tumor_stage != 4,]
# data_full_5 = data_full_2[data_BIDC$tumor_stage != 0 & data_BIDC$tumor_stage != 4,]
```

```
# 0 - pre, 1 - post menopause
```

```

data_BIDC$menopause = 1*(data_BIDC$inferred_menopausal_state == "Post")

# 0 - left, 1 - right
data_BIDC$tumor_laterality = 1*(data_BIDC$primary_tumor_laterality == "Right")

# Recode more variables
data_BIDC$progesterone_status = 1*(data_BIDC$pr_status == "Positive")
data_BIDC$HER2_status = 1*(data_BIDC$her2_status == "Positive")
data_BIDC$er_status_ihc = 1*(data_BIDC$er_status_measured_by_ihc == "Positive")

#####
# 0 - pre, 1 - post menopause
data_BIDC_2$menopause = 1*(data_BIDC_2$inferred_menopausal_state == "Post")

# 0 - left, 1 - right
data_BIDC_2$tumor_laterality = 1*(data_BIDC_2$primary_tumor_laterality == "Right")

# Recode more variables
data_BIDC_2$progesterone_status = 1*(data_BIDC_2$pr_status == "Positive")
data_BIDC_2$HER2_status = 1*(data_BIDC_2$her2_status == "Positive")
data_BIDC_2$er_status_ihc = 1*(data_BIDC_2$er_status_measured_by_ihc == "Positive")
#####

#####
# 0 - pre, 1 - post menopause
data_BIDC_3$menopause = 1*(data_BIDC_3$inferred_menopausal_state == "Post")

# 0 - left, 1 - right
data_BIDC_3$tumor_laterality = 1*(data_BIDC_3$primary_tumor_laterality == "Right")

# Recode more variables
data_BIDC_3$progesterone_status = 1*(data_BIDC_3$pr_status == "Positive")
data_BIDC_3$HER2_status = 1*(data_BIDC_3$her2_status == "Positive")
data_BIDC_3$er_status_ihc = 1*(data_BIDC_3$er_status_measured_by_ihc == "Positive")
#####

#####
# 0 - pre, 1 - post menopause
data_BIDC_4$menopause = 1*(data_BIDC_4$inferred_menopausal_state == "Post")

# 0 - left, 1 - right
data_BIDC_4$tumor_laterality = 1*(data_BIDC_4$primary_tumor_laterality == "Right")

# Recode more variables
data_BIDC_4$progesterone_status = 1*(data_BIDC_4$pr_status == "Positive")
data_BIDC_4$HER2_status = 1*(data_BIDC_4$her2_status == "Positive")
data_BIDC_4$er_status_ihc = 1*(data_BIDC_4$er_status_measured_by_ihc == "Positive")
#####

#####
# 0 - pre, 1 - post menopause
data_BIDC_5$menopause = 1*(data_BIDC_5$inferred_menopausal_state == "Post")

```

```

# 0 - left, 1 - right
data_BIDC_5$tumor_laterality = 1*(data_BIDC_5$primary_tumor_laterality == "Right")

# Recode more variables
data_BIDC_5$progesterone_status = 1*(data_BIDC_5$pr_status == "Positive")
data_BIDC_5$HER2_status = 1*(data_BIDC_5$her2_status == "Positive")
data_BIDC_5$er_status_ihc = 1*(data_BIDC_5$er_status_measured_by_ihc == "Positive")
#####

data_BIDC_excl = data_BIDC[data_BIDC$tumor_stage != 0 & data_BIDC$tumor_stage != 4,]

data_BIDC_excl_2 = data_BIDC[data_BIDC_2$tumor_stage != 0 & data_BIDC_2$tumor_stage != 4,]
data_BIDC_excl_3 = data_BIDC[data_BIDC_3$tumor_stage != 0 & data_BIDC_3$tumor_stage != 4,]
data_BIDC_excl_4 = data_BIDC[data_BIDC_4$tumor_stage != 0 & data_BIDC_4$tumor_stage != 4,]
data_BIDC_excl_5 = data_BIDC[data_BIDC_5$tumor_stage != 0 & data_BIDC_5$tumor_stage != 4,]

# Mutation indicators
gene_expr_names = names(data_BIDC)[26:514]
mutation_names = names(data_BIDC)[515:687]

for (var in mutation_names) {
  data_BIDC[[var]] <- as.integer(data_BIDC[[var]] != 0)

  data_BIDC_2[[var]] <- as.integer(data_BIDC_2[[var]] != 0)
  data_BIDC_3[[var]] <- as.integer(data_BIDC_3[[var]] != 0)
  data_BIDC_4[[var]] <- as.integer(data_BIDC_4[[var]] != 0)
  data_BIDC_5[[var]] <- as.integer(data_BIDC_5[[var]] != 0)
}

# Exclude patients with rare mutations
p = ncol(data_BIDC)
n = nrow(data_BIDC)
include = rep(FALSE, n)

n_2 = nrow(data_BIDC_2)
n_3 = nrow(data_BIDC_3)
n_4 = nrow(data_BIDC_4)
n_5 = nrow(data_BIDC_5)

include_2 = rep(FALSE, nrow(data_BIDC_2))
include_3 = rep(FALSE, nrow(data_BIDC_3))
include_4 = rep(FALSE, nrow(data_BIDC_4))
include_5 = rep(FALSE, nrow(data_BIDC_5))

for (i in 1:n)
{
  if (sum(as.numeric(data_BIDC[i,c(608, 611:614, 616:687)])) == 0)
  {
    include[i] = TRUE
  }
}

```

```

# for (i in 1:n_2)
# {
#   print(i)
#   if (sum(as.numeric(data_BIDC_2[i,c(608, 611:614, 616:687)])) == 0)
#   {
#     include_2[i] = TRUE
#   }
# }
#
# for (i in 1:n_3)
# {
#   if (sum(as.numeric(data_BIDC_3[i,c(608, 611:614, 616:687)])) == 0)
#   {
#     include_3[i] = TRUE
#   }
# }
#
# for (i in 1:n_4)
# {
#   if (sum(as.numeric(data_BIDC_4[i,c(608, 611:614, 616:687)])) == 0)
#   {
#     include_4[i] = TRUE
#   }
# }
#
# for (i in 1:n_5)
# {
#   if (sum(as.numeric(data_BIDC_5[i,c(608, 611:614, 616:687)])) == 0)
#   {
#     include_5[i] = TRUE
#   }
# }

sum(include)

```

```
## [1] 889
```

```
data_BIDC_common = data_BIDC[data_BIDC$tumor_stage != 0 & data_BIDC$tumor_stage != 4 & include,]
```

```
data_BIDC_common_2 = data_BIDC_2[data_BIDC_2$tumor_stage != 0 & data_BIDC_2$tumor_stage != 4 & include,]
```

```
data_BIDC_common_3 = data_BIDC_3[data_BIDC_3$tumor_stage != 0 & data_BIDC_3$tumor_stage != 4 & include,]
```

```
data_BIDC_common_4 = data_BIDC_4[data_BIDC_4$tumor_stage != 0 & data_BIDC_4$tumor_stage != 4 & include,]
```

```
data_BIDC_common_5 = data_BIDC_5[data_BIDC_5$tumor_stage != 0 & data_BIDC_5$tumor_stage != 4 & include,]
```

```
nrow(data_BIDC_common)
```

```
## [1] 879
```

Sensitivity analysis data

```
# data_BIDC_2 = data_BIDC[include,]
```

```
# data_BIDC_3 = data_BIDC[include,]
```



```

# data_BIDC_4 = data_BIDC[include,]
# data_BIDC_5 = data_BIDC[include,]
#
# unique(data_BIDC_2$tumor_stage)

# data_BIDC_3 = data_BIDC[data_BIDC$tumor_stage != 0 & data_BIDC$tumor_stage != 4 & include,]
# data_BIDC_4 = data_BIDC[data_BIDC$tumor_stage != 0 & data_BIDC$tumor_stage != 4 & include,]
# data_BIDC_5 = data_BIDC[data_BIDC$tumor_stage != 0 & data_BIDC$tumor_stage != 4 & include,]

#colnames(data_BIDC)[1:24]
#colnames(x)[1:24]

# data_BIDC_2[,c(8,17,23,24)] = data_full_2[data_full_2$tumor_stage != 0 & data_full_2$tumor_stage != 4,]
#
# unique(data_BIDC_2$tumor_stage)
#
# data_BIDC_3[,c(8,17,23,24)] = data_full_2[data_BIDC$tumor_stage != 0 & data_BIDC$tumor_stage != 4 & include,]
#
# data_BIDC_4[,c(8,17,23,24)] = data_full_2[data_BIDC$tumor_stage != 0 & data_BIDC$tumor_stage != 4 & include,]
#
# data_BIDC_5[,c(8,17,23,24)] = data_full_2[data_BIDC$tumor_stage != 0 & data_BIDC$tumor_stage != 4 & include,]

# data_BIDC_common_2 = data_BIDC_2
# data_BIDC_common_3 = data_BIDC_3
# data_BIDC_common_4 = data_BIDC_4
# data_BIDC_common_5 = data_BIDC_5

# delete mutations which did not occur
mutation_names = setdiff(mutation_names, c("hras_mut", "siahl1_mut", "smarcb1_mut", "stmn2_mut", "foxo1_mut"))

# delete rare mutations
mutation_names = setdiff(mutation_names, names(data_BIDC)[c(608, 611:614, 616:685)])

```

Creating model matrix

```

# Convert the mutation variables, categorical variables, and treatment to factors

categorical_vars <- c("cellularity", "pam50_.claudin.low_subtype",
                     "neoplasm_histologic_grade", "tumor_other_histologic_subtype",
                     "integrative_cluster", "X3.gene_classifier_subtype", 'tumor_stage')

categorical_recoded <- c("menopause", "HER2_status", "progesterone_status", "tumor_laterality", "radiotherapy")
#data_BIDC_2 <- mutate_at(data_BIDC, vars(mutation_names, categorical_vars, "treatment"), as.factor)

data_BIDC_common <- data_BIDC_common %>% mutate(across(all_of(unlist(c(categorical_vars))), as.factor))

#####
data_BIDC_common_2 <- data_BIDC_common_2 %>% mutate(across(all_of(unlist(c(categorical_vars))), as.factor))
data_BIDC_common_3 <- data_BIDC_common_3 %>% mutate(across(all_of(unlist(c(categorical_vars))), as.factor))
data_BIDC_common_4 <- data_BIDC_common_4 %>% mutate(across(all_of(unlist(c(categorical_vars))), as.factor))
data_BIDC_common_5 <- data_BIDC_common_5 %>% mutate(across(all_of(unlist(c(categorical_vars))), as.factor))

```

```
#####
# sum(data_BIDC_common$pam50._claudin.low_subtype == 'NC')
# unique(data_BIDC_common$pam50._claudin.low_subtype)
#
# unique(data_BIDC$cellularity)
# unique(data_BIDC$pam50._claudin.low_subtype)
# unique(data_BIDC$neoplasm_histologic_grade)
# sum(is.na(data_BIDC$neoplasm_histologic_grade))
#
# unique(data_BIDC$tumor_other_histologic_subtype)
#
# unique(data_BIDC$integrative_cluster)
#
# unique(data_BIDC$X3.gene_classifier_subtype)

# Create the interaction terms
interaction_terms <- lapply(1:length(gene_expr_names), function(i) {
  if (paste0(gene_expr_names[i], "_mut") %in% mutation_names) {
    return(paste0(gene_expr_names[i], ":", gene_expr_names[i], "_mut"))
  }
})
interaction_terms <- unlist(interaction_terms)

# Define the main effects variables
main_effects <- c("age_at_diagnosis", "lymph_nodes_examined_positive", "tumor_size")

# Create the formula for the model matrix
# formula <- paste(" ~ ", paste(main_effects, collapse = " + "), " + ",
#                 paste(categorical_vars, collapse = " + "), " + ",
#                 paste(gene_expr_names, collapse = " + "), " + ",
#                 paste(interaction_terms, collapse = " + "), " + ",
#                 paste("treatment", "(", paste(main_effects, categorical_vars, gene_expr_names, collapse = " + "),
#                 "-1")

# Create the model matrix
#model_matrix <- model.matrix(as.formula(formula), data = data_BIDC)

#cat(formula, "\n")

vars1 = paste(main_effects, collapse = " + ")
vars2 = paste(categorical_vars, collapse = " + ")
vars3 = paste(categorical_recoded, collapse = " + ")
vars3 = paste(gene_expr_names, collapse = " + ")
vars4 = paste(interaction_terms, collapse = " + ")

vars_all = paste(vars1, vars2, vars3, vars4, sep = " + ")
form = paste(" ~ ", "treatment + ", vars_all, " + treatment:(", vars_all, ")")

# STANDARDIZE THE VARIABLES FOLLOWING GELMAN
data_BIDC_common_std = data_BIDC_common
```

```

data_BIDC_common_std_2 = data_BIDC_common_2
data_BIDC_common_std_3 = data_BIDC_common_3
data_BIDC_common_std_4 = data_BIDC_common_4
data_BIDC_common_std_5 = data_BIDC_common_5

cont.names = c(main_effects, gene_expr_names)

for (i in 1:ncol(data_BIDC_common))
{
  if (names(data_BIDC_common)[i] %in% cont.names)
  {
    data_BIDC_common_std[,i] = (data_BIDC_common[,i] - mean(data_BIDC_common[,i]))/ (2*sd(data_BIDC_com

    data_BIDC_common_std_2[,i] = (data_BIDC_common_2[,i] - mean(data_BIDC_common_2[,i]))/ (2*sd(data_BI

    data_BIDC_common_std_3[,i] = (data_BIDC_common_3[,i] - mean(data_BIDC_common_3[,i]))/ (2*sd(data_BI

    data_BIDC_common_std_4[,i] = (data_BIDC_common_4[,i] - mean(data_BIDC_common_4[,i]))/ (2*sd(dat

    data_BIDC_common_std_5[,i] = (data_BIDC_common_5[,i] - mean(data_BIDC_common_5[,i]))/ (2*sd

  }
}

model_matrix <- model.matrix(as.formula(form), data = data_BIDC_common_std)

model_matrix_2 <- model.matrix(as.formula(form), data = data_BIDC_common_std_2)
model_matrix_3 <- model.matrix(as.formula(form), data = data_BIDC_common_std_3)
model_matrix_4 <- model.matrix(as.formula(form), data = data_BIDC_common_std_4)
model_matrix_5 <- model.matrix(as.formula(form), data = data_BIDC_common_std_5)

delta_2 = 1*(data_BIDC_common_2$death_from_cancer == "Died of Disease")
delta_3 = 1*(data_BIDC_common_3$death_from_cancer == "Died of Disease")
delta_4 = 1*(data_BIDC_common_4$death_from_cancer == "Died of Disease")
delta_5 = 1*(data_BIDC_common_5$death_from_cancer == "Died of Disease")

y_2 = Surv(data_BIDC_common_2$overall_survival_months, delta_2)
y_3 = Surv(data_BIDC_common_3$overall_survival_months, delta_3)
y_4 = Surv(data_BIDC_common_4$overall_survival_months, delta_4)
y_5 = Surv(data_BIDC_common_5$overall_survival_months, delta_5)

treatment_2 = data_BIDC_common_2$treatment
treatment_3 = data_BIDC_common_3$treatment
treatment_4 = data_BIDC_common_4$treatment
treatment_5 = data_BIDC_common_5$treatment

dataX = model_matrix[,2:ncol(model_matrix)]
logY = log(data_BIDC_common$overall_survival_months)
delta = 1*(data_BIDC_common$death_from_cancer == "Died of Disease")

```

```

x = model_matrix
y = Surv(data_BIDC_common$overall_survival_months, delta)

p = ncol(dataX)

#weight.set <- list("w" = c(0, rep(1, p-1)))
set.seed(3)
fit.en.cv <- penAFT.cv(dataX, logY, delta, alpha = 0.5, nlambda = 30, nfolds = 5)

## CV through:  ###          20 %
## CV through:  ### ###      40 %
## CV through:  ### ### ###   60 %
## CV through:  ### ### ### ### 80 %
## CV through:  ### ### ### ### ### 100 %

```

Out-of-sample performance - concordance

```

#####
##### OUT OF SAMPLE PERFORMANCE #####
#####

get.concordance = function(pred_test, truth_test, death)
{
  nvalid = length(pred_test)
  agree.count = 0
  pair.count = 0
  for (i in 2:nvalid)
  {
    for (j in 1:(i-1))
    {
      pair.count = pair.count + death[j]
      agree.count = agree.count + death[j]*((pred_test[i] >= pred_test[j]) == (truth_test[i] >= truth_t
    }
  }

  concord = agree.count / pair.count
  return(concord)
}

ndata = nrow(data_BIDC_common)
nvalid = floor(0.3*nrow(data_BIDC_common))

#ndata = nrow(dataX)
#nvalid = floor(0.3*nrow(dataX))

#set.seed(4)

set.seed(4)
index = sample(1:ndata, size = nvalid, replace = FALSE)
test_data = data_BIDC_common[index,]
train_data = data_BIDC_common[-index,]

#en.gehan = penAFT(dataX[-index,], logY[-index], delta[-index], alpha = 0.6, lambda = c(lambda.gehan))

```

```

set.seed(8)
en.gehan.cv = penAFT.cv(dataX[-index,], logY[-index], delta[-index], alpha = 0.5, nlambda = 30, nfold =

## CV through: ###                20 %
## CV through: ### ###            40 %
## CV through: ### ### ###        60 %
## CV through: ### ### ### ###    80 %
## CV through: ### ### ### ### ### 100 %

#####
##### Change after fixing package #####

lambda = en.gehan.cv$full.fit$lambda
cv.err.linPred = en.gehan.cv$cv.err.linPred
lambda[which(cv.err.linPred == min(cv.err.linPred))]

## [1] 0.02274304

best.ind = which.min(cv.err.linPred)
lambda.min = lambda[which.min(cv.err.linPred)]
lambda.gehan = lambda.min

#beta.gehan = fit.en.cv$full.fit$beta[,best.ind]
#####

#saveRDS(en.gehan.cv, file = 'gehan_train.RDS')
#en.gehan = penAFT(dataX[-index,], logY[-index], delta[-index], alpha = 0.6, nlambda = 10)

x = model_matrix

set.seed(6)
p = ncol(x)
penalty = c(0, rep(1, p-1))
en.cox.cv = cv.glmnet(x[-index,], y[-index,], family = "cox", alpha = 0.5, nlambda = 30, nfold = 5)

en.cox.cv$index

##      Lambda
## min      6
## 1se      3

beta.cox = en.cox.cv$glmnet.fit$beta[,8]
lambda.cox = en.cox.cv$glmnet.fit$lambda[8]
preds.cox <- x[index,]%*%beta.cox

truth_test = logY[index]
death = delta[index]

preds.gehan <- penAFT.predict(en.gehan.cv, Xnew = dataX[index,], lambda = lambda.gehan)

get.concordance(-preds.cox, truth_test, death)

## [1] 0.677399

get.concordance(preds.gehan, truth_test, death)

```

```
## [1] 0.6635101
```

Causal Inference

Propensity Scores

```
x = model_matrix

delta = 1*(data_BIDC_common$death_from_cancer == "Died of Disease")
y = Surv(data_BIDC_common$overall_survival_months, delta)

# PROPENSITY SCORES

vars1 = paste(main_effects, collapse = " + ")
vars2 = paste(categorical_vars, collapse = " + ")
vars3 = paste(categorical_recoded, collapse = " + ")
vars3 = paste(gene_expr_names, collapse = " + ")
vars4 = paste(interaction_terms, collapse = " + ")

x = model_matrix

vars_all = paste(vars1, vars2, vars3, vars4, sep = " + ")
form_2 = paste("treatment ~ ", vars_all)

x_prop <- model.matrix(as.formula(form_2), data = data_BIDC_common_std)
treatment = data_BIDC_common$treatment

# ridge regression
set.seed(3)
prop.cv = cv.glmnet(x_prop, treatment, family = "binomial", alpha = 0, nlambda = 30, nfold = 5)
e.vec = predict(prop.cv, newx = x_prop, s = prop.cv$lambda.min, type = 'response')
omega = 1
W.vec = omega / (treatment*e.vec + (1-treatment)*e.vec)
W.vec = c(W.vec)
```

EDA

```
data_EDA = data_BIDC_common
data_EDA$prop_score = e.vec

data_EDA$death = ifelse(delta, "Yes", "No")

print(nrow(data_EDA))

## [1] 879

print(sum(delta))

## [1] 303

data_EDA$treatment_name = data_EDA$type_of_breast_surgery

g1 <- ggplot(data_EDA, aes(x = treatment_name, fill = death)) +
```

```

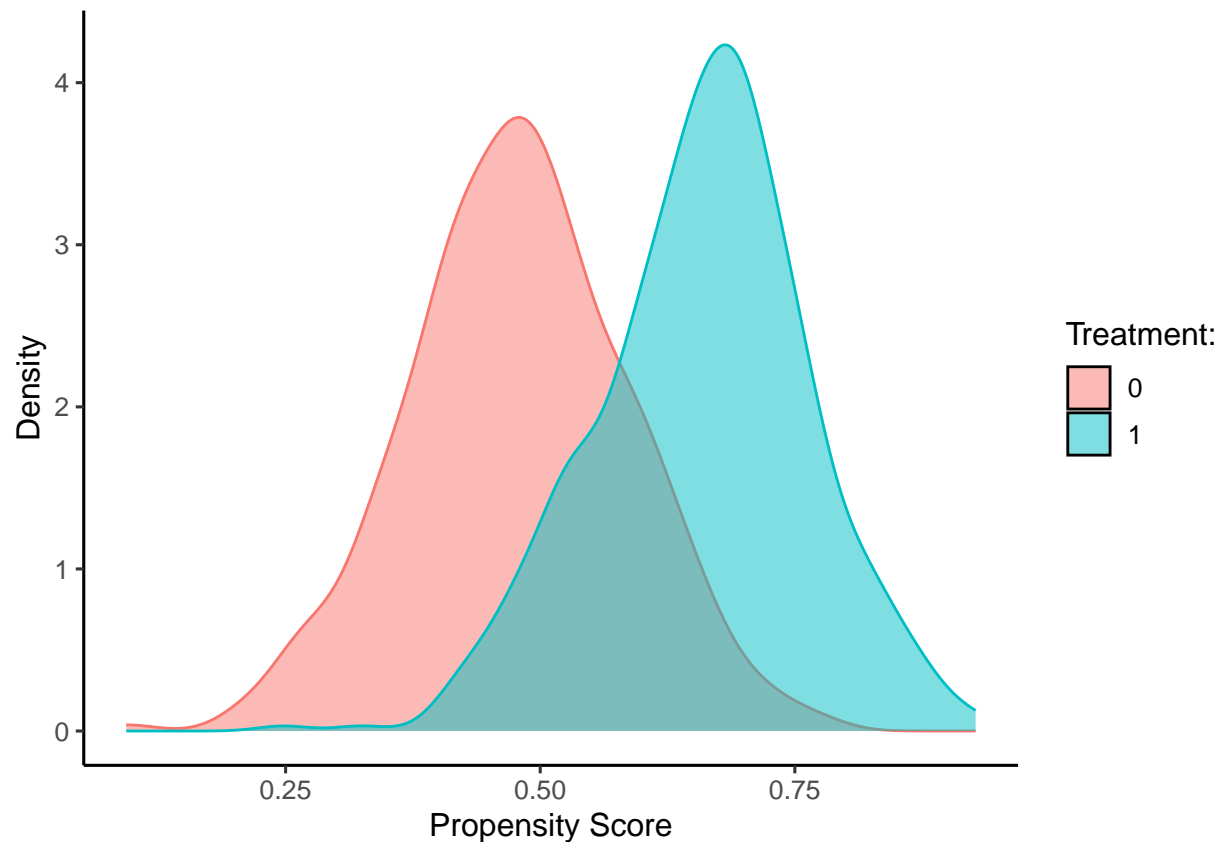
geom_bar(position = "fill") +
ggtitle("Censoring by Treatment") +
theme(axis.title.x = element_blank()) +
labs(fill = "Death Observed", y = "Proportion")

pdf("plots/censoring_by_trt.pdf", height = 3.5, width = 6)
g1
dev.off()

## pdf
## 2
data_EDA = data_BIDC_common
data_EDA$prop_score = e.vec
data_EDA$Mastectomy = as.factor(data_EDA$treatment)

p_prop_score <- ggplot(data_EDA, aes(x = prop_score, fill = Mastectomy,
                                     color = Mastectomy)) +
  geom_density(alpha = 0.5) +
  labs(x = "Propensity Score",
       y = "Density",
       fill = "Treatment:") +
  scale_color_discrete(guide = "none")
p_prop_score

```



```

PlotKMCurve <- function(group_var, var_name = NULL, data, y) {
  if (is.null(var_name)) var_name <- group_var

```

```

survfit2(y ~ get(group_var), data = data) %>%
  ggsurvfit() +
  add_confidence_interval() +
  labs(
    x = "Days",
    y = "Survival probability",
    fill = element_blank(), color = element_blank()
  )
}

fig1 <- PlotKMCurve("Mastectomy", var_name = NULL, data_EDA, y) +
  labs(subtitle = "") +
  scale_color_manual(values = c("purple", "orange"), labels = c("BCS", "Mastectomy")) +
  scale_fill_manual(values = c("purple", "orange"), labels = c("BCS", "Mastectomy"))

pdf("plots/surv_curve.pdf", height = 3.5, width = 6)
fig1
dev.off()

## pdf
## 2

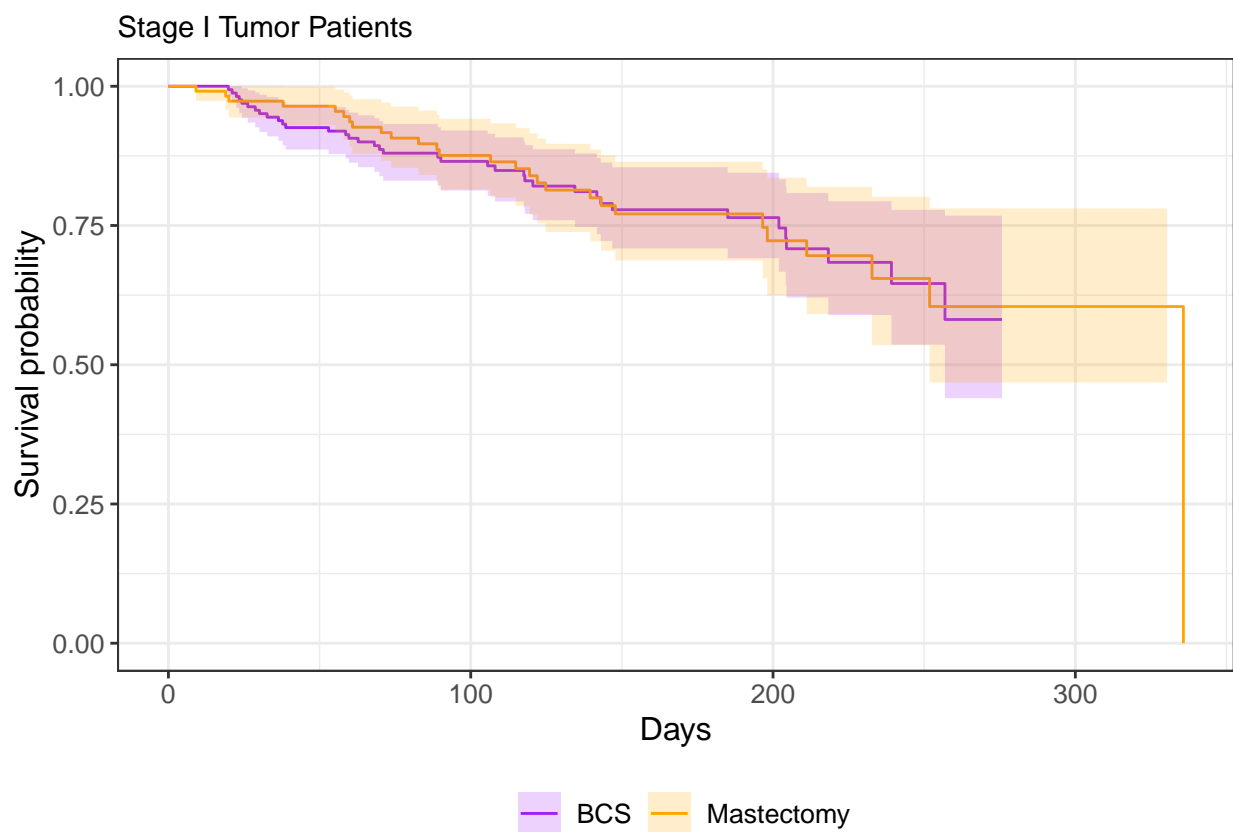
fig_stage1 <- PlotKMCurve("Mastectomy", var_name = NULL, data_EDA[data_EDA$tumor_stage == 1,], y[data_EDA$tumor_stage == 1,]) +
  labs(subtitle = "Stage I Tumor Patients") +
  scale_color_manual(values = c("purple", "orange"), labels = c("BCS", "Mastectomy")) +
  scale_fill_manual(values = c("purple", "orange"), labels = c("BCS", "Mastectomy"))

fig_stage2 <- PlotKMCurve("Mastectomy", var_name = NULL, data_EDA[data_EDA$tumor_stage == 2,], y[data_EDA$tumor_stage == 2,]) +
  labs(subtitle = "Stage II Tumor Patients") +
  scale_color_manual(values = c("purple", "orange"), labels = c("BCS", "Mastectomy")) +
  scale_fill_manual(values = c("purple", "orange"), labels = c("BCS", "Mastectomy"))

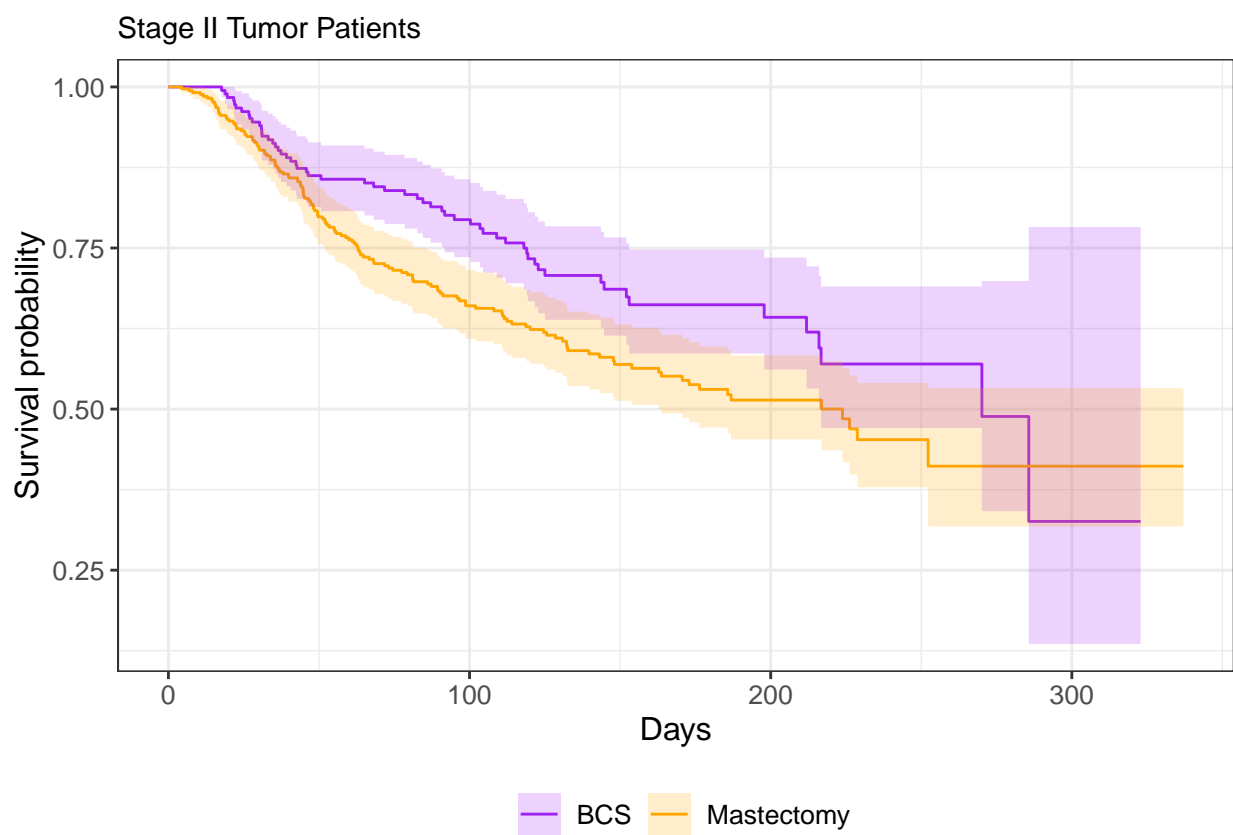
fig_stage3 <- PlotKMCurve("Mastectomy", var_name = NULL, data_EDA[data_EDA$tumor_stage == 3,], y[data_EDA$tumor_stage == 3,]) +
  labs(subtitle = "Stage III Tumor Patients") +
  scale_color_manual(values = c("purple", "orange"), labels = c("BCS", "Mastectomy")) +
  scale_fill_manual(values = c("purple", "orange"), labels = c("BCS", "Mastectomy"))

fig_stage1

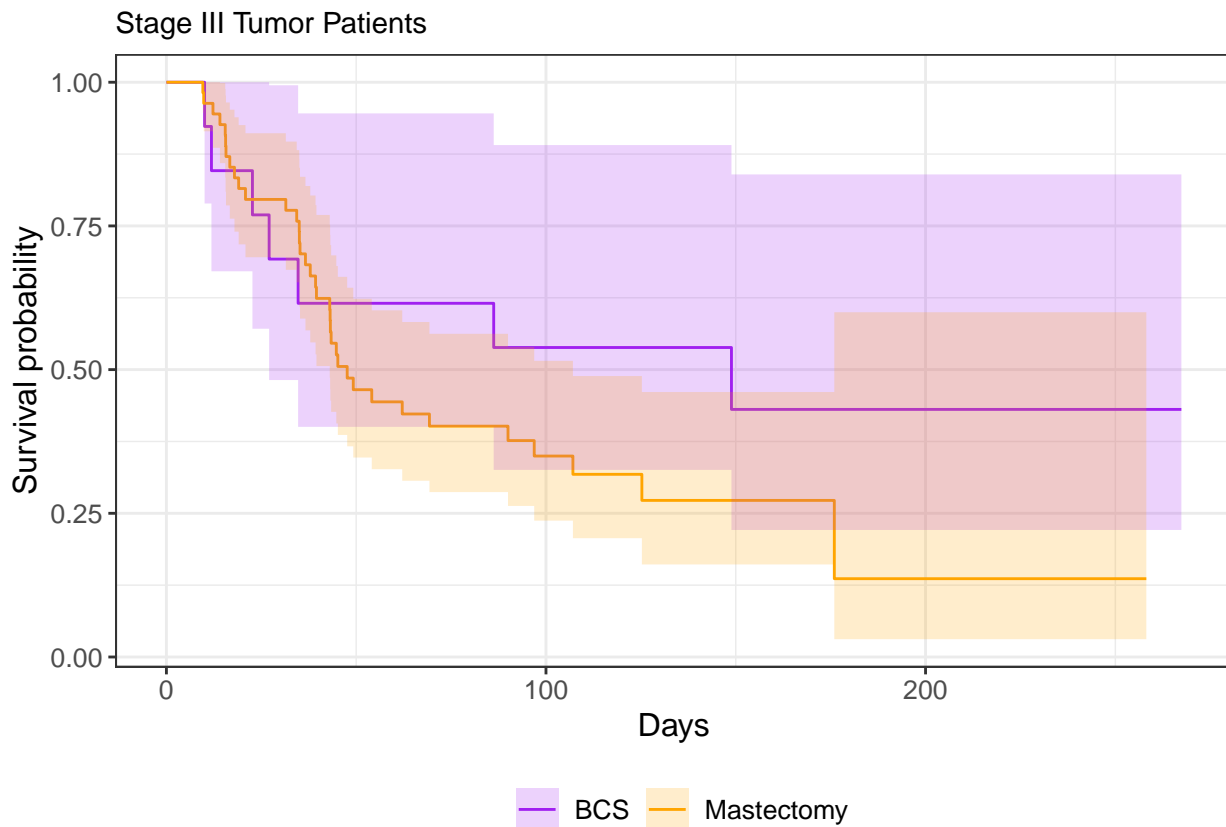
```

fig_stage2



```
fig_stage3
```



```
pdf("plots/stage1_diff.pdf", height = 3.5, width = 6)
fig_stage1
dev.off()
```

```
## pdf
## 2

pdf("plots/stage2_diff.pdf", height = 3.5, width = 6)
fig_stage2
dev.off()
```

```
## pdf
## 2

pdf("plots/stage3_diff.pdf", height = 3.5, width = 6)
fig_stage3
dev.off()
```

```
## pdf
## 2

data_EDA$hormone_therapy
```

```
## [1] 1 1 1 1 1 0 1 1 1 1 0 1 1 1 1 0 1 1 1 1 1 1 1 1 1 0 1 1 1 1 1 1 1 1 0
## [38] 1 1 1 0 0 1 1 1 1 1 1 1 0 1 1 1 0 1 1 0 0 1 1 1 0 0 1 1 1 0 1 0 0 0 1 1 1 1
## [75] 0 1 0 0 1 1 0 1 1 1 1 1 1 1 0 0 0 1 1 1 0 0 1 1 0 1 1 1 1 1 1 1 1 1 1 0 1 0
## [112] 1 1 1 1 1 1 1 0 0 1 1 1 1 1 1 1 1 0 1 1 1 1 1 1 1 1 0 1 0 1 1 0 0 0 1 1 1
## [149] 1 1 0 1 0 1 1 1 0 0 1 1 1 1 1 1 1 1 1 0 1 1 0 1 0 1 1 0 1 1 0 1 1 0 1 1
```



```

# Exclude treatment from the penalized predictors
p = ncol(x)
penalty = c(0, 0, rep(1, p-2))

set.seed(4)
cox.cv = cv.glmnet(x, y, weights = W.vec, penalty.factor = penalty, family = "cox", alpha = 0.5, nlambdas = 100)
lambda.cox = cox.cv$lambda.min

cox.fit = glmnet(x, y, weights = W.vec, family = "cox", alpha = 0.5, penalty.factor = penalty, lambda = lambda.cox)

cox.fit$beta[,1]['treatment']

## treatment
## 0.3477823

cox.en.beta = cox.fit$beta[,1]
cox.en.beta.nonzero = cox.fit$beta[,1][abs(cox.fit$beta[,1]) > 1e-10][order(cox.fit$beta[,1][abs(cox.fit$beta[,1]) > 1e-10])]

```

Sensitivity Analysis - different MICE imputations

```

x_2 = model_matrix_2
x_3 = model_matrix_3
x_4 = model_matrix_4
x_5 = model_matrix_5

x_prop_2 <- model.matrix(as.formula(form_2), data = data_BIDC_common_std_2)
x_prop_3 <- model.matrix(as.formula(form_2), data = data_BIDC_common_std_3)
x_prop_4 <- model.matrix(as.formula(form_2), data = data_BIDC_common_std_4)
x_prop_5 <- model.matrix(as.formula(form_2), data = data_BIDC_common_std_5)

# ridge regression
set.seed(3)
prop.cv_2 = cv.glmnet(x_prop_2, treatment_2, family = "binomial", alpha = 0, nlambda = 30, nfold = 5)
e.vec_2 = predict(prop.cv_2, newx = x_prop_2, s = prop.cv_2$lambda.min, type = 'response')
omega = 1
W.vec_2 = omega / (treatment_2*e.vec_2 + (1-treatment_2)*e.vec_2)

set.seed(3)
prop.cv_3 = cv.glmnet(x_prop_3, treatment_3, family = "binomial", alpha = 0, nlambda = 30, nfold = 5)
e.vec_3 = predict(prop.cv_3, newx = x_prop_3, s = prop.cv_3$lambda.min, type = 'response')
omega = 1
W.vec_3 = omega / (treatment_3*e.vec_3 + (1-treatment_3)*e.vec_3)

set.seed(3)
prop.cv_4 = cv.glmnet(x_prop_4, treatment_4, family = "binomial", alpha = 0, nlambda = 30, nfold = 5)
e.vec_4 = predict(prop.cv_4, newx = x_prop_4, s = prop.cv_4$lambda.min, type = 'response')
omega = 1
W.vec_4 = omega / (treatment_4*e.vec_4 + (1-treatment_4)*e.vec_4)

set.seed(3)
prop.cv_5 = cv.glmnet(x_prop_5, treatment_5, family = "binomial", alpha = 0, nlambda = 30, nfold = 5)
e.vec_5 = predict(prop.cv_5, newx = x_prop_5, s = prop.cv_5$lambda.min, type = 'response')
omega = 1

```

```
W.vec_5 = omega / (treatment_5*e.vec_5 + (1-treatment_5)*e.vec_5)
```

```
set.seed(4)
```

```
cox.cv_2 = cv.glmnet(x_2, y_2, weights = W.vec_2, penalty.factor = penalty, family = "cox", alpha = 0.5)
lambda.cox_2 = cox.cv_2$lambda.min
```

```
cox.fit_2 = glmnet(x_2, y_2, weights = W.vec_2, family = "cox", alpha = 0.5, penalty.factor = penalty,
```

```
set.seed(4)
```

```
cox.cv_3 = cv.glmnet(x_3, y_3, weights = W.vec_3, penalty.factor = penalty, family = "cox", alpha = 0.5)
lambda.cox_3 = cox.cv_3$lambda.min
```

```
cox.fit_3 = glmnet(x_3, y_3, weights = W.vec_3, family = "cox", alpha = 0.5, penalty.factor = penalty,
```

```
set.seed(4)
```

```
cox.cv_4 = cv.glmnet(x_4, y_4, weights = W.vec_4, penalty.factor = penalty, family = "cox", alpha = 0.5)
lambda.cox_4 = cox.cv_4$lambda.min
```

```
cox.fit_4 = glmnet(x_4, y_4, weights = W.vec_4, family = "cox", alpha = 0.5, penalty.factor = penalty,
```

```
set.seed(4)
```

```
cox.cv_5 = cv.glmnet(x_5, y_5, weights = W.vec_5, penalty.factor = penalty, family = "cox", alpha = 0.5)
lambda.cox_5 = cox.cv_5$lambda.min
```

```
cox.fit_5 = glmnet(x_5, y_5, weights = W.vec_5, family = "cox", alpha = 0.5, penalty.factor = penalty,
```

```
cox.en.beta
```

```
##                                (Intercept)
##                                0.000000000
##                                treatment
##                                0.347782309
##                                age_at_diagnosis
##                                0.000000000
##                                lymph_nodes_examined_positive
##                                0.429991335
##                                tumor_size
##                                0.039285186
##                                cellularityHigh
##                                0.000000000
##                                cellularityLow
##                                0.000000000
##                                cellularityModerate
##                                0.000000000
##                                pam50_.claudin.low_subtypeclaudin-low
##                                0.000000000
##                                pam50_.claudin.low_subtypeHer2
##                                0.000000000
##                                pam50_.claudin.low_subtypeLumA
##                                -0.152032481
##                                pam50_.claudin.low_subtypeLumB
##                                0.000000000
```

```

##          pam50_._claudin.low_subtypeNormal
##          0.000000000
##          neoplasm_histologic_grade2
##          0.000000000
##          neoplasm_histologic_grade3
##          0.000000000
##          tumor_other_histologic_subtypeMedullary
##          0.000000000
##          tumor_other_histologic_subtypeTubular/ cribriform
##          0.000000000
##          integrative_cluster10
##          0.000000000
##          integrative_cluster2
##          0.000000000
##          integrative_cluster3
##          -0.036916691
##          integrative_cluster4ER-
##          0.000000000
##          integrative_cluster4ER+
##          0.000000000
##          integrative_cluster5
##          0.261403318
##          integrative_cluster6
##          0.000000000
##          integrative_cluster7
##          0.000000000
##          integrative_cluster8
##          0.000000000
##          integrative_cluster9
##          0.000000000
##          X3.gene_classifier_subtypeER-/HER2-
##          0.000000000
##          X3.gene_classifier_subtypeER+/HER2- High Prolif
##          0.000000000
##          X3.gene_classifier_subtypeER+/HER2- Low Prolif
##          0.000000000
##          X3.gene_classifier_subtypeHER2+
##          0.000000000
##          tumor_stage2
##          0.000000000
##          tumor_stage3
##          0.000000000
##          brca1
##          0.000000000
##          brca2
##          -0.042959447
##          palb2
##          0.000000000
##          pten
##          0.000000000
##          tp53
##          0.000000000
##          atm
##          0.000000000

```

##	cdh1
##	0.000000000
##	chek2
##	0.000000000
##	nbn
##	0.000000000
##	nf1
##	0.000000000
##	stk11
##	0.000000000
##	bard1
##	0.000000000
##	mlh1
##	0.000000000
##	msh2
##	0.000000000
##	msh6
##	0.000000000
##	pms2
##	0.000000000
##	epcam
##	0.000000000
##	rad51c
##	0.000000000
##	rad51d
##	0.000000000
##	rad50
##	0.000000000
##	rb1
##	0.000000000
##	rb11
##	0.000000000
##	rb12
##	0.000000000
##	ccna1
##	0.000000000
##	ccnb1
##	0.000000000
##	cdk1
##	0.000000000
##	ccne1
##	0.000000000
##	cdk2
##	0.000000000
##	cdc25a
##	0.000000000
##	ccnd1
##	0.000000000
##	cdk4
##	0.000000000
##	cdk6
##	0.000000000
##	ccnd2
##	0.000000000

##	cdkn2a
##	0.000000000
##	cdkn2b
##	0.000000000
##	myc
##	0.000000000
##	cdkn1a
##	0.000000000
##	cdkn1b
##	0.000000000
##	e2f1
##	-0.057084879
##	e2f2
##	0.000000000
##	e2f3
##	0.000000000
##	e2f4
##	0.000000000
##	e2f5
##	0.000000000
##	e2f6
##	0.000000000
##	e2f7
##	0.060377905
##	e2f8
##	0.000000000
##	src
##	0.000000000
##	jak1
##	0.000000000
##	jak2
##	0.000000000
##	stat1
##	0.000000000
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##	0.000000000
##	l1cam:l1cam_mut
##	0.000000000
##	lama2:lama2_mut
##	0.000000000
##	lamb3:lamb3_mut
##	0.000000000
##	lifr:lifr_mut
##	0.000000000
##	muc16:muc16_mut
##	0.000000000
##	myo1a:myo1a_mut
##	0.000000000
##	myo3a:myo3a_mut
##	0.000000000
##	ncoa3:ncoa3_mut
##	0.000000000
##	pbrm1:pbrm1_mut
##	0.000000000
##	ptprm:ptprm_mut
##	0.000000000
##	ryr2:ryr2_mut
##	0.000000000
##	sbno1:sbno1_mut
##	0.000000000
##	setd1a:setd1a_mut
##	0.000000000
##	setd2:setd2_mut
##	0.000000000
##	setdb1:setdb1_mut
##	0.000000000
##	sf3b1:sf3b1_mut
##	0.000000000
##	shank2:shank2_mut
##	0.000000000

```

##          smarcc2:smarcc2_mut
##          0.000000000
##          stab2:stab2_mut
##          0.000000000
##          syne1:syne1_mut
##          0.000000000
##          taf1:taf1_mut
##          0.000000000
##          tg:tg_mut
##          0.000000000
##          thada:thada_mut
##          0.000000000
##          thsd7a:thsd7a_mut
##          0.000000000
##          ubr5:ubr5_mut
##          0.000000000
##          ush2a:ush2a_mut
##          0.000000000
##          usp9x:usp9x_mut
##          0.000000000
##          utrnl:utrnl_mut
##          0.000000000
##          treatment:age_at_diagnosis
##          0.000000000
##          treatment:lymph_nodes_examined_positive
##          0.000000000
##          treatment:tumor_size
##          0.189831732
##          treatment:cellularityHigh
##          0.000000000
##          treatment:cellularityLow
##          0.000000000
##          treatment:cellularityModerate
##          0.000000000
##          treatment:pam50_._claudin.low_subtypeclaudin-low
##          0.000000000
##          treatment:pam50_._claudin.low_subtypeHer2
##          0.000000000
##          treatment:pam50_._claudin.low_subtypeLumA
##          0.000000000
##          treatment:pam50_._claudin.low_subtypeLumB
##          0.000000000
##          treatment:pam50_._claudin.low_subtypeNormal
##          0.000000000
##          treatment:neoplasm_histologic_grade2
##          0.000000000
##          treatment:neoplasm_histologic_grade3
##          0.000000000
##          treatment:tumor_other_histologic_subtypeMedullary
##          0.000000000
##          treatment:tumor_other_histologic_subtypeTubular/ cribriform
##          0.000000000
##          treatment:integrative_cluster10
##          0.000000000

```

```

##                treatment:integrative_cluster2
##                0.000000000
##                treatment:integrative_cluster3
##                0.000000000
##                treatment:integrative_cluster4ER-
##                0.000000000
##                treatment:integrative_cluster4ER+
##                0.000000000
##                treatment:integrative_cluster5
##                0.000000000
##                treatment:integrative_cluster6
##                0.000000000
##                treatment:integrative_cluster7
##                0.000000000
##                treatment:integrative_cluster8
##                0.000000000
##                treatment:integrative_cluster9
##                0.000000000
##                treatment:X3.gene_classifier_subtypeER-/HER2-
##                0.000000000
##                treatment:X3.gene_classifier_subtypeER+/HER2- High Prolif
##                0.000000000
##                treatment:X3.gene_classifier_subtypeER+/HER2- Low Prolif
##                0.000000000
##                treatment:X3.gene_classifier_subtypeHER2+
##                0.000000000
##                treatment:tumor_stage2
##                0.000000000
##                treatment:tumor_stage3
##                0.000000000
##                treatment:brca1
##                0.000000000
##                treatment:brca2
##                0.000000000
##                treatment:palb2
##                0.000000000
##                treatment:pten
##                0.000000000
##                treatment:tp53
##                0.000000000
##                treatment:atm
##                0.000000000
##                treatment:cdh1
##                0.000000000
##                treatment:chek2
##                0.000000000
##                treatment:nbn
##                0.000000000
##                treatment:nf1
##                0.000000000
##                treatment:stk11
##                0.000000000
##                treatment:bard1
##                0.000000000

```

##	treatment:mlh1
##	0.000000000
##	treatment:msh2
##	0.000000000
##	treatment:msh6
##	0.000000000
##	treatment:pms2
##	0.000000000
##	treatment:epcam
##	0.000000000
##	treatment:rad51c
##	0.000000000
##	treatment:rad51d
##	0.000000000
##	treatment:rad50
##	0.000000000
##	treatment:rb1
##	0.000000000
##	treatment:rb11
##	0.000000000
##	treatment:rb12
##	0.000000000
##	treatment:ccna1
##	0.000000000
##	treatment:ccnb1
##	0.000000000
##	treatment:cdk1
##	0.000000000
##	treatment:ccne1
##	0.000000000
##	treatment:cdk2
##	0.000000000
##	treatment:cdc25a
##	0.000000000
##	treatment:ccnd1
##	0.000000000
##	treatment:cdk4
##	0.000000000
##	treatment:cdk6
##	0.000000000
##	treatment:ccnd2
##	0.000000000
##	treatment:cdkn2a
##	0.000000000
##	treatment:cdkn2b
##	0.000000000
##	treatment:myc
##	0.000000000
##	treatment:cdkn1a
##	0.000000000
##	treatment:cdkn1b
##	0.000000000
##	treatment:e2f1
##	0.000000000

##	treatment:e2f2
##	0.000000000
##	treatment:e2f3
##	0.000000000
##	treatment:e2f4
##	0.000000000
##	treatment:e2f5
##	0.000000000
##	treatment:e2f6
##	0.000000000
##	treatment:e2f7
##	0.040005288
##	treatment:e2f8
##	0.219624668
##	treatment:src
##	0.000000000
##	treatment:jak1
##	0.000000000
##	treatment:jak2
##	0.000000000
##	treatment:stat1
##	0.000000000
##	treatment:stat2
##	0.000000000
##	treatment:stat3
##	0.000000000
##	treatment:stat5a
##	0.000000000
##	treatment:stat5b
##	0.000000000
##	treatment:mdm2
##	0.000000000
##	treatment:tp53bp1
##	0.000000000
##	treatment:adam10
##	0.000000000
##	treatment:adam17
##	0.000000000
##	treatment:aph1a
##	0.000000000
##	treatment:aph1b
##	0.000000000
##	treatment:arrdc1
##	0.000000000
##	treatment:cir1
##	0.000000000
##	treatment:ctbp1
##	0.000000000
##	treatment:ctbp2
##	0.000000000
##	treatment:cul1
##	-0.145590316
##	treatment:dll1
##	0.000000000

##	treatment:dll3
##	0.000000000
##	treatment:dll4
##	0.000000000
##	treatment:dtx1
##	0.000000000
##	treatment:dtx2
##	0.000000000
##	treatment:dtx3
##	0.000000000
##	treatment:dtx4
##	0.000000000
##	treatment:ep300
##	0.000000000
##	treatment:fbxw7
##	0.000000000
##	treatment:hdac1
##	0.000000000
##	treatment:hdac2
##	0.000000000
##	treatment:hes1
##	0.000000000
##	treatment:hes5
##	0.000000000
##	treatment:hey1
##	0.000000000
##	treatment:itch
##	0.000000000
##	treatment:jag1
##	0.000000000
##	treatment:jag2
##	0.000000000
##	treatment:kdm5a
##	0.000000000
##	treatment:lfng
##	0.000000000
##	treatment:maml1
##	0.000000000
##	treatment:maml2
##	0.000000000
##	treatment:maml3
##	0.000000000
##	treatment:ncor2
##	0.000000000
##	treatment:ncstn
##	0.000000000
##	treatment:notch1
##	0.000000000
##	treatment:notch2
##	0.000000000
##	treatment:notch3
##	0.000000000
##	treatment:nrarp
##	0.031220094


```

##          treatment:numb
##          0.000000000
##          treatment:numbl
##          0.000000000
##          treatment:psen1
##          0.000000000
##          treatment:psen2
##          0.000000000
##          treatment:psenen
##          0.000000000
##          treatment:rbpj
##          0.000000000
##          treatment:rbpj1
##          0.000000000
##          treatment:rfng
##          0.000000000
##          treatment:snw1
##          0.000000000
##          treatment:spen
##          0.000000000
##          treatment:hes2
##          0.000000000
##          treatment:hes4
##          0.000000000
##          treatment:hes7
##          0.000000000
##          treatment:hey1
##          0.000000000
##          treatment:hey2
##          0.000000000
##          treatment:acvr1
##          0.000000000
##          treatment:acvr1b
##          0.000000000
##          treatment:acvr1c
##          -0.014745488
##          treatment:acvr2a
##          0.000000000
##          treatment:acvr2b
##          0.000000000
##          treatment:acvr11
##          0.000000000
##          treatment:akt1
##          0.000000000
##          treatment:akt1s1
##          0.000000000
##          treatment:akt2
##          0.000000000
##          treatment:apaf1
##          0.000000000
##          treatment:arl11
##          0.000000000
##          treatment:atr
##          0.000000000

```

```

##      treatment:aurka
##      0.000000000
##      treatment:bad
##      0.000000000
##      treatment:bcl2
##      0.000000000
##      treatment:bcl2l1
##      0.000000000
##      treatment:bmp10
##      0.000000000
##      treatment:bmp15
##      0.000000000
##      treatment:bmp2
##      0.000000000
##      treatment:bmp3
##      0.000000000
##      treatment:bmp4
##      0.000000000
##      treatment:bmp5
##      0.000000000
##      treatment:bmp6
##      0.000000000
##      treatment:bmp7
##      0.000000000
##      treatment:bmpr1a
##      0.000000000
##      treatment:bmpr1b
##      0.000000000
##      treatment:bmpr2
##      0.000000000
##      treatment:braf
##      0.000000000
##      treatment:casp10
##      0.000000000
##      treatment:casp3
##      0.000000000
##      treatment:casp6
##      0.000000000
##      treatment:casp7
##      0.000000000
##      treatment:casp8
##      0.000000000
##      treatment:casp9
##      0.000000000
##      treatment:chek1
##      0.000000000
##      treatment:csf1
##      0.000000000
##      treatment:csf1r
##      0.000000000
##      treatment:cxcl8
##      0.000000000
##      treatment:cxcr1
##      0.000000000

```

```

##          treatment:cxcr2
##          0.000000000
##          treatment:dab2
##          0.000000000
##          treatment:diras3
##          0.000000000
##          treatment:dlec1
##          0.000000000
##          treatment:dph1
##          0.000000000
##          treatment:egfr
##          0.000000000
##          treatment:EIF4E
##          0.000000000
##          treatment:EIF4EBP1
##          0.000000000
##          treatment:EIF5A2
##          0.000000000
##          treatment:ERBB2
##          0.000000000
##          treatment:ERBB3
##          0.000000000
##          treatment:ERBB4
##          0.000000000
##          treatment:FAS
##          0.000000000
##          treatment:FGF1
##          0.000000000
##          treatment:FGFR1
##          0.000000000
##          treatment:FOLR1
##          0.000000000
##          treatment:FOLR2
##          0.000000000
##          treatment:FOLR3
##          0.000000000
##          treatment:FOXO1
##          0.000000000
##          treatment:FOXO3
##          0.000000000
##          treatment:GDF11
##          0.000000000
##          treatment:GDF2
##          0.000000000
##          treatment:GSK3B
##          0.000000000
##          treatment:HIF1A
##          0.000000000
##          treatment:HLA.G
##          0.000000000
##          treatment:HRAS
##          0.000000000
##          treatment:IGF1
##          0.000000000

```

```

##      treatment:igf1r
##      0.000000000
##      treatment:inha
##      -0.052234841
##      treatment:inhba
##      0.000000000
##      treatment:inhbc
##      0.000000000
##      treatment:itgav
##      0.000000000
##      treatment:itgb3
##      0.000000000
##      treatment:izumolr
##      0.000000000
##      treatment:kdr
##      0.000000000
##      treatment:kit
##      0.000000000
##      treatment:kras
##      0.000000000
##      treatment:map2k1
##      0.000000000
##      treatment:map2k2
##      0.000000000
##      treatment:map2k3
##      0.000000000
##      treatment:map2k4
##      0.000000000
##      treatment:map2k5
##      0.000000000
##      treatment:map3k1
##      0.000000000
##      treatment:map3k3
##      0.000000000
##      treatment:map3k4
##      0.000000000
##      treatment:map3k5
##      0.000000000
##      treatment:mapk1
##      0.000000000
##      treatment:mapk12
##      0.000000000
##      treatment:mapk14
##      0.000000000
##      treatment:mapk3
##      0.000000000
##      treatment:mapk4
##      0.000000000
##      treatment:mapk6
##      0.000000000
##      treatment:mapk7
##      0.000000000
##      treatment:mapk8
##      0.000000000

```

##	treatment:mapk9
##	0.000000000
##	treatment:mdc1
##	0.000000000
##	treatment:mlst8
##	0.000000000
##	treatment:mmp1
##	0.000000000
##	treatment:mmp10
##	0.000000000
##	treatment:mmp11
##	0.000000000
##	treatment:mmp12
##	0.000000000
##	treatment:mmp13
##	0.000000000
##	treatment:mmp14
##	0.000000000
##	treatment:mmp15
##	0.000000000
##	treatment:mmp16
##	0.000000000
##	treatment:mmp17
##	0.000000000
##	treatment:mmp19
##	0.000000000
##	treatment:mmp2
##	0.000000000
##	treatment:mmp21
##	0.000000000
##	treatment:mmp23b
##	0.000000000
##	treatment:mmp24
##	0.000000000
##	treatment:mmp25
##	0.000000000
##	treatment:mmp26
##	0.000000000
##	treatment:mmp27
##	0.000000000
##	treatment:mmp28
##	0.000000000
##	treatment:mmp3
##	0.000000000
##	treatment:mmp7
##	0.000000000
##	treatment:mmp9
##	0.000000000
##	treatment:mtor
##	0.000000000
##	treatment:nfkb1
##	0.000000000
##	treatment:nfkb2
##	0.000000000

```

##          treatment:opcml
##          0.000000000
##          treatment:pdgfa
##          0.000000000
##          treatment:pdgfb
##          0.000000000
##          treatment:pdgfra
##          0.000000000
##          treatment:pdgfrb
##          0.000000000
##          treatment:pdpk1
##          0.000000000
##          treatment:peg3
##          0.000000000
##          treatment:pik3ca
##          0.000000000
##          treatment:pik3r1
##          0.000000000
##          treatment:pik3r2
##          0.000000000
##          treatment:plagl1
##          0.000000000
##          treatment:ptk2
##          0.000000000
##          treatment:rab25
##          0.000000000
##          treatment:rad51
##          0.000000000
##          treatment:raf1
##          0.000000000
##          treatment:rassf1
##          0.000000000
##          treatment:rheb
##          0.000000000
##          treatment:riCTOR
##          0.000000000
##          treatment:rps6
##          0.000000000
##          treatment:rps6ka1
##          0.000000000
##          treatment:rps6ka2
##          0.000000000
##          treatment:rps6kb1
##          0.000000000
##          treatment:rps6kb2
##          0.000000000
##          treatment:rptor
##          0.000000000
##          treatment:slc19a1
##          0.000000000
##          treatment:smad1
##          0.000000000
##          treatment:smad2
##          0.000000000

```

##	treatment:smad3
##	0.000000000
##	treatment:smad4
##	0.000000000
##	treatment:smad5
##	0.000000000
##	treatment:smad6
##	0.000000000
##	treatment:smad7
##	0.000000000
##	treatment:smad9
##	0.000000000
##	treatment:sptbn1
##	0.000000000
##	treatment:terc
##	0.000000000
##	treatment:tert
##	0.000000000
##	treatment:tgfb1
##	0.000000000
##	treatment:tgfb2
##	0.000000000
##	treatment:tgfb3
##	0.000000000
##	treatment:tgfbr1
##	0.000000000
##	treatment:tgfbr2
##	0.000000000
##	treatment:tgfbr3
##	0.000000000
##	treatment:tsc1
##	0.000000000
##	treatment:tsc2
##	0.000000000
##	treatment:vegfa
##	0.000000000
##	treatment:vegfb
##	0.000000000
##	treatment:wfdc2
##	0.000000000
##	treatment:wwox
##	0.000000000
##	treatment:zfyve9
##	0.084331358
##	treatment:arid1a
##	0.000000000
##	treatment:arid1b
##	0.000000000
##	treatment:cbfb
##	0.000000000
##	treatment:gata3
##	0.000000000
##	treatment:kmt2c
##	0.000000000

```

##          treatment:kmt2d
##          0.000000000
##          treatment:myh9
##          0.000000000
##          treatment:ncor1
##          0.000000000
##          treatment:pde4dip
##          0.000000000
##          treatment:ptprd
##          0.000000000
##          treatment:ros1
##          0.000000000
##          treatment:runx1
##          0.000000000
##          treatment:tbx3
##          0.000000000
##          treatment:abcb1
##          0.000000000
##          treatment:abcb11
##          0.000000000
##          treatment:abcc1
##          0.000000000
##          treatment:abcc10
##          0.000000000
##          treatment:bbc3
##          0.000000000
##          treatment:bmf
##          0.000000000
##          treatment:cyp2c8
##          0.000000000
##          treatment:cyp3a4
##          0.000000000
##          treatment:fgf2
##          0.000000000
##          treatment:fn1
##          0.000000000
##          treatment:map2
##          0.000000000
##          treatment:map4
##          0.000000000
##          treatment:mapt
##          -0.317144317
##          treatment:nr1i2
##          0.000000000
##          treatment:slco1b3
##          0.000000000
##          treatment:tubb1
##          0.000000000
##          treatment:tubb4a
##          0.000000000
##          treatment:tubb4b
##          0.000000000
##          treatment:twist1
##          0.000000000

```


##	treatment:adgra2
##	0.000000000
##	treatment:afdn
##	0.000000000
##	treatment:aff2
##	0.000000000
##	treatment:agmo
##	0.000000000
##	treatment:agtr2
##	0.000000000
##	treatment:ahnak
##	0.000000000
##	treatment:ahnak2
##	0.000000000
##	treatment:akap9
##	0.000000000
##	treatment:alk
##	0.000000000
##	treatment:apc
##	0.000000000
##	treatment:arid2
##	0.000000000
##	treatment:arid5b
##	0.000000000
##	treatment:asx11
##	0.000000000
##	treatment:asx12
##	0.000000000
##	treatment:bap1
##	0.000000000
##	treatment:bcas3
##	0.000000000
##	treatment:birc6
##	0.000000000
##	treatment:cacna2d3
##	0.000000000
##	treatment:ccnd3
##	0.000000000
##	treatment:chd1
##	0.000000000
##	treatment:clk3
##	0.000000000
##	treatment:clrn2
##	0.000000000
##	treatment:col12a1
##	0.000000000
##	treatment:col22a1
##	0.000000000
##	treatment:col6a3
##	0.000000000
##	treatment:ctcf
##	0.000000000
##	treatment:ctnna1
##	0.000000000

```

##          treatment:ctnna3
##          0.000000000
##          treatment:dnah11
##          0.000000000
##          treatment:dnah2
##          0.000000000
##          treatment:dnah5
##          0.000000000
##          treatment:dtwd2
##          0.000000000
##          treatment:fam20c
##          0.000000000
##          treatment:fanca
##          0.000000000
##          treatment:fancd2
##          0.000000000
##          treatment:flt3
##          0.000000000
##          treatment:foxp1
##          0.000000000
##          treatment:frmd3
##          0.000000000
##          treatment:gh1
##          0.000000000
##          treatment:gldc
##          0.000000000
##          treatment:gpr32
##          0.000000000
##          treatment:gps2
##          0.000000000
##          treatment:hdac9
##          0.000000000
##          treatment:herc2
##          0.000000000
##          treatment:hist1h2bc
##          0.000000000
##          treatment:kdm3a
##          0.000000000
##          treatment:kdm6a
##          0.000000000
##          treatment:klrg1
##          0.000000000
##          treatment:llcam
##          0.000000000
##          treatment:lama2
##          0.000000000
##          treatment:lamb3
##          0.000000000
##          treatment:large1
##          0.000000000
##          treatment:ldlrp1
##          0.000000000
##          treatment:lifr
##          0.000000000

```

```

##          treatment:lipi
##          0.000000000
##          treatment:magea8
##          0.000000000
##          treatment:map3k10
##          0.000000000
##          treatment:map3k13
##          0.000000000
##          treatment:men1
##          0.000000000
##          treatment:mtap
##          0.000000000
##          treatment:muc16
##          0.000000000
##          treatment:myo1a
##          0.000000000
##          treatment:myo3a
##          0.000000000
##          treatment:ncoa3
##          0.000000000
##          treatment:nek1
##          0.000000000
##          treatment:nf2
##          0.000000000
##          treatment:npnt
##          0.000000000
##          treatment:nr2f1
##          0.000000000
##          treatment:nr3c1
##          0.000000000
##          treatment:nras
##          0.000000000
##          treatment:nrg3
##          -0.008037592
##          treatment:nt5e
##          0.000000000
##          treatment:or6a2
##          0.000000000
##          treatment:palld
##          0.000000000
##          treatment:pbrm1
##          0.000000000
##          treatment:ppp2cb
##          0.000000000
##          treatment:ppp2r2a
##          0.000000000
##          treatment:prkacg
##          0.000000000
##          treatment:prkce
##          0.000000000
##          treatment:prkcq
##          0.000000000
##          treatment:prkcz
##          0.000000000

```

```

##          treatment:prkg1
##          0.000000000
##          treatment:prps2
##          0.000000000
##          treatment:prr16
##          0.000000000
##          treatment:ptpn22
##          0.000000000
##          treatment:ptprm
##          0.000000000
##          treatment:rasgef1b
##          0.000000000
##          treatment:rpgr
##          -0.031102534
##          treatment:ryr2
##          0.000000000
##          treatment:sbno1
##          0.000000000
##          treatment:setd1a
##          0.000000000
##          treatment:setd2
##          0.000000000
##          treatment:setdb1
##          0.000000000
##          treatment:sf3b1
##          0.000000000
##          treatment:sgcd
##          0.000000000
##          treatment:shank2
##          0.000000000
##          treatment:siah1
##          0.000000000
##          treatment:sik1
##          0.000000000
##          treatment:sik2
##          0.000000000
##          treatment:smarcb1
##          0.000000000
##          treatment:smarcc1
##          0.000000000
##          treatment:smarcc2
##          0.000000000
##          treatment:smarcd1
##          0.000000000
##          treatment:spaca1
##          0.000000000
##          treatment:stab2
##          0.000000000
##          treatment:stmn2
##          0.000000000
##          treatment:syne1
##          0.000000000
##          treatment:taf1
##          0.000000000

```

```

##          treatment:taf4b
##          0.000000000
## treatment:tbl1xr1
##          0.000000000
##          treatment:tg
##          0.000000000
##          treatment:thada
##          0.000000000
##          treatment:thsd7a
##          0.000000000
##          treatment:ttyh1
##          0.000000000
##          treatment:ubr5
##          0.000000000
##          treatment:ush2a
##          0.013131015
##          treatment:usp9x
##          0.000000000
##          treatment:utrnl
##          0.000000000
## treatment:zfp36l1
##          0.000000000
##          treatment:ackr3
##          0.000000000
##          treatment:akr1c1
##          0.000000000
##          treatment:akr1c2
##          0.000000000
##          treatment:akr1c3
##          0.000000000
##          treatment:akr1c4
##          0.000000000
##          treatment:akt3
##          0.000000000
##          treatment:ar
##          0.000000000
##          treatment:bche
##          0.000000000
##          treatment:cdk8
##          0.000000000
##          treatment:cdkn2c
##          0.000000000
##          treatment:cyb5a
##          0.000000000
##          treatment:cyp11a1
##          -0.154061815
##          treatment:cyp11b2
##          0.000000000
##          treatment:cyp17a1
##          0.000000000
##          treatment:cyp19a1
##          0.000000000
##          treatment:cyp21a2
##          0.000000000

```

```

##      treatment:cyp3a43
##      0.000000000
##      treatment:cyp3a5
##      0.000000000
##      treatment:cyp3a7
##      0.000000000
##      treatment:ddc
##      0.000000000
##      treatment:hes6
##      0.000000000
##      treatment:hsd17b1
##      0.000000000
##      treatment:hsd17b10
##      0.000000000
##      treatment:hsd17b11
##      0.000000000
##      treatment:hsd17b12
##      0.000000000
##      treatment:hsd17b13
##      0.000000000
##      treatment:hsd17b14
##      0.000000000
##      treatment:hsd17b2
##      0.000000000
##      treatment:hsd17b3
##      0.000000000
##      treatment:hsd17b4
##      0.000000000
##      treatment:hsd17b6
##      0.000000000
##      treatment:hsd17b7
##      -0.003366814
##      treatment:hsd17b8
##      0.000000000
##      treatment:hsd3b1
##      0.000000000
##      treatment:hsd3b2
##      0.000000000
##      treatment:hsd3b7
##      0.000000000
##      treatment:mecom
##      0.000000000
##      treatment:met
##      0.000000000
##      treatment:ncoa2
##      0.000000000
##      treatment:nrip1
##      0.000000000
##      treatment:pik3r3
##      0.000000000
##      treatment:prkci
##      0.000000000
##      treatment:prkd1
##      0.000000000

```

```

##          treatment:ran
##          0.000000000
##          treatment:rdh5
##          0.000000000
##          treatment:sd4
##          0.000000000
##          treatment:serpini1
##          0.000000000
##          treatment:shbg
##          0.000000000
##          treatment:slc29a1
##          0.000000000
##          treatment:sox9
##          0.000000000
##          treatment:spry2
##          0.000000000
##          treatment:srd5a1
##          0.000000000
##          treatment:srd5a2
##          0.000000000
##          treatment:srd5a3
##          -0.002806890
##          treatment:st7
##          0.000000000
##          treatment:star
##          0.000000000
##          treatment:tnk2
##          0.000000000
##          treatment:tulp4
##          0.000000000
##          treatment:ugt2b15
##          0.000000000
##          treatment:ugt2b17
##          -0.041345522
##          treatment:ugt2b7
##          0.000000000
##          treatment:brca1:brca1_mut
##          0.000000000
##          treatment:brca2:brca2_mut
##          0.000000000
##          treatment:pten:pten_mut
##          0.000000000
##          treatment:tp53:tp53_mut
##          0.000000000
##          treatment:cdh1:cdh1_mut
##          0.000000000
##          treatment:nf1:nf1_mut
##          0.000000000
##          treatment:rb1:rb1_mut
##          0.000000000
##          treatment:jak1:jak1_mut
##          0.000000000
##          treatment:ep300:ep300_mut
##          0.000000000

```

```

##          treatment:ncor2:ncor2_mut
##          0.000000000
## treatment:notch1:notch1_mut
##          0.000000000
##          treatment:akt1:akt1_mut
##          0.000000000
##          treatment:atr:atr_mut
##          0.000000000
##          treatment:egfr:egfr_mut
##          0.000000000
## treatment:erbb2:erbb2_mut
##          -0.030886788
## treatment:erbb3:erbb3_mut
##          0.000000000
## treatment:erbb4:erbb4_mut
##          0.000000000
## treatment:foxo3:foxo3_mut
##          0.000000000
## treatment:map2k4:map2k4_mut
##          0.000000000
## treatment:map3k1:map3k1_mut
##          0.000000000
## treatment:pik3ca:pik3ca_mut
##          0.000000000
## treatment:pik3r1:pik3r1_mut
##          0.000000000
##          treatment:smad4:smad4_mut
##          0.000000000
## treatment:arid1a:arid1a_mut
##          0.000000000
## treatment:arid1b:arid1b_mut
##          0.000000000
##          treatment:cbfb:cbfb_mut
##          0.000000000
##          treatment:gata3:gata3_mut
##          0.000000000
## treatment:kmt2c:kmt2c_mut
##          0.000000000
## treatment:kmt2d:kmt2d_mut
##          0.000000000
##          treatment:myh9:myh9_mut
##          0.000000000
##          treatment:ncor1:ncor1_mut
##          0.000000000
## treatment:pde4dip:pde4dip_mut
##          0.000000000
##          treatment:ptprd:ptprd_mut
##          0.000000000
##          treatment:ros1:ros1_mut
##          0.000000000
## treatment:runx1:runx1_mut
##          0.000000000
##          treatment:tbx3:tbx3_mut
##          0.000000000

```



```

##          treatment:adgra2:adgra2_mut
##          0.000000000
##          treatment:afdn:afdn_mut
##          0.000000000
##          treatment:aff2:aff2_mut
##          0.000000000
##          treatment:ahnak:ahnak_mut
##          0.000000000
##          treatment:ahnak2:ahnak2_mut
##          0.000000000
##          treatment:akap9:akap9_mut
##          0.000000000
##          treatment:alk:alk_mut
##          0.000000000
##          treatment:apc:apc_mut
##          0.000000000
##          treatment:arid2:arid2_mut
##          0.000000000
##          treatment:arid5b:arid5b_mut
##          0.000000000
##          treatment:asx11:asx11_mut
##          0.000000000
##          treatment:asx12:asx12_mut
##          0.000000000
##          treatment:bap1:bap1_mut
##          0.000000000
##          treatment:birc6:birc6_mut
##          0.000000000
##          treatment:cacna2d3:cacna2d3_mut
##          0.000000000
##          treatment:chd1:chd1_mut
##          -0.059168382
##          treatment:col12a1:col12a1_mut
##          0.000000000
##          treatment:col22a1:col22a1_mut
##          0.000000000
##          treatment:col6a3:col6a3_mut
##          0.000000000
##          treatment:ctcf:ctcf_mut
##          0.000000000
##          treatment:ctnna3:ctnna3_mut
##          0.000000000
##          treatment:dnah11:dnah11_mut
##          0.000000000
##          treatment:dnah2:dnah2_mut
##          0.000000000
##          treatment:dnah5:dnah5_mut
##          0.000000000
##          treatment:fam20c:fam20c_mut
##          0.000000000
##          treatment:fanca:fanca_mut
##          0.000000000
##          treatment:fancd2:fancd2_mut
##          0.000000000

```

```

##          treatment:gldc:gldc_mut
##          0.000000000
##          treatment:herc2:herc2_mut
##          0.000000000
##          treatment:kdm3a:kdm3a_mut
##          0.000000000
##          treatment:kdm6a:kdm6a_mut
##          0.000000000
##          treatment:l1cam:l1cam_mut
##          0.000000000
##          treatment:lama2:lama2_mut
##          0.000000000
##          treatment:lamb3:lamb3_mut
##          0.000000000
##          treatment:lifr:lifr_mut
##          0.000000000
##          treatment:muc16:muc16_mut
##          0.000000000
##          treatment:myo1a:myo1a_mut
##          0.000000000
##          treatment:myo3a:myo3a_mut
##          0.000000000
##          treatment:ncoa3:ncoa3_mut
##          0.000000000
##          treatment:pbrm1:pbrm1_mut
##          0.000000000
##          treatment:ptprm:ptprm_mut
##          0.000000000
##          treatment:ryr2:ryr2_mut
##          0.000000000
##          treatment:sbno1:sbno1_mut
##          0.000000000
##          treatment:setd1a:setd1a_mut
##          0.000000000
##          treatment:setd2:setd2_mut
##          0.000000000
##          treatment:setdb1:setdb1_mut
##          0.000000000
##          treatment:sf3b1:sf3b1_mut
##          0.000000000
##          treatment:shank2:shank2_mut
##          0.000000000
##          treatment:smarcc2:smarcc2_mut
##          0.000000000
##          treatment:stab2:stab2_mut
##          0.000000000
##          treatment:syne1:syne1_mut
##          0.000000000
##          treatment:taf1:taf1_mut
##          0.000000000
##          treatment:tg:tg_mut
##          0.000000000
##          treatment:thada:thada_mut
##          0.000000000

```

```
##          treatment:thsd7a:thsd7a_mut
##                      0.000000000
##          treatment:ubr5:ubr5_mut
##                      0.000000000
##          treatment:ush2a:ush2a_mut
##                      0.000000000
##          treatment:usp9x:usp9x_mut
##                      0.000000000
##          treatment:utrnr:utrnr_mut
##                      0.000000000
```

```
cox.en.beta.nonzero
```

```
## lymph_nodes_examined_positive          kdm3a:kdm3a_mut
##          0.429991335                      0.369957710
##          treatment          integrative_cluster5
##          0.347782309                      0.261403318
##          gsk3b          treatment:e2f8
##          0.239318961                      0.219624668
##          prkg1          treatment:tumor_size
##          0.199972830                      0.189831732
##          eif4ebp1          treatment:zfyve9
##          0.129527071                      0.084331358
##          e2f7          dll13
##          0.060377905                      0.054955479
##          treatment:e2f7          tumor_size
##          0.040005288                      0.039285186
##          smad7          treatment:nrarp
##          0.031579997                      0.031220094
##          prkacg          pdgfb
##          0.026250727                      0.015773806
##          treatment:ush2a          akt3
##          0.013131015                      0.007516268
##          men1          smad6
##          0.006066667                      0.003035938
##          treatment:srd5a3          treatment:hsd17b7
##          -0.002806890                      -0.003366814
##          treatment:nrg3          map3k1
##          -0.008037592                      -0.011575291
##          casp7          mmp25
##          -0.012710693                      -0.014298532
##          treatment:acvr1c          igf1
##          -0.014745488                      -0.015017205
##          treatment:erbb2:erbb2_mut          treatment:rpgr
##          -0.030886788                      -0.031102534
##          integrative_cluster3          treatment:ugt2b17
##          -0.036916691                      -0.041345522
##          brca2          ugt2b17
##          -0.042959447                      -0.043295059
##          treatment:inha          mapt
##          -0.052234841                      -0.055817428
##          e2f1          treatment:chd1:chd1_mut
##          -0.057084879                      -0.059168382
##          diras3          tbx3:tbx3_mut
##          -0.078511004                      -0.079733374
```

```
##          acvr1c          cul1
##          -0.105162501          -0.106889044
##          stat5a          tp53:tp53_mut
##          -0.111515329          -0.121472412
##          gata3:gata3_mut          treatment:cul1
##          -0.138823153          -0.145590316
## pam50_._claudin.low_subtypeLumA          treatment:cyp11a1
##          -0.152032481          -0.154061815
##          treatment:mapt
##          -0.317144317
```

```
cox.en.beta_2 = cox.fit_2$beta[,1]
cox.en.beta.nonzero_2 = cox.fit_2$beta[,1][abs(cox.fit_2$beta[,1]) > 1e-10][order(cox.fit_2$beta[,1][abs(cox.fit_2$beta[,1]) > 1e-10])

cox.en.beta_3 = cox.fit_3$beta[,1]
cox.en.beta.nonzero_3 = cox.fit_3$beta[,1][abs(cox.fit_3$beta[,1]) > 1e-10][order(cox.fit_3$beta[,1][abs(cox.fit_3$beta[,1]) > 1e-10])

cox.en.beta_2 = cox.fit_2$beta[,1]
cox.en.beta.nonzero_2 = cox.fit_2$beta[,1][abs(cox.fit_2$beta[,1]) > 1e-10][order(cox.fit_2$beta[,1][abs(cox.fit_2$beta[,1]) > 1e-10])

cox.en.beta.nonzero_2
```

```
## lymph_nodes_examined_positive          treatment
##          0.3962247677          0.3643216028
##          kdm3a:kdm3a_mut          integrative_cluster5
##          0.3415824700          0.2874316842
##          gsk3b          treatment:tumor_size
##          0.2434052539          0.2022740288
##          treatment:e2f8          prkg1
##          0.1786587844          0.1395393081
##          eif4ebp1          tumor_stage3
##          0.1299748576          0.1213385278
##          treatment:zfyve9          treatment:nrarp
##          0.1081327068          0.0703986734
##          treatment:prkc2          tumor_stage2
##          0.0565429854          0.0500720413
##          tumor_size          treatment:e2f7
##          0.0357496013          0.0321913606
##          e2f7          dll3
##          0.0280666054          0.0266294111
##          treatment:ush2a          treatment:cxcl8
##          0.0240795448          0.0103307838
##          pdgfb          treatment:eif4ebp1
##          0.0094421874          0.0080216058
##          men1          treatment:terc
##          0.0077136094          0.0076179627
##          smad7          shank2:shank2_mut
##          0.0025447624          -0.0001583666
##          treatment:pbrm1          nr3c1
##          -0.0011144275          -0.0034206502
##          birc6:birc6_mut          treatment:srd5a3
##          -0.0042340371          -0.0080621912
##          casp7          treatment:acvr1c
##          -0.0114110918          -0.0166340409
##          igf1          integrative_cluster3
```

##	-0.0196002170	-0.0197492308
##	brca2	e2f1
##	-0.0318839150	-0.0329041489
##	map3k1	mapt
##	-0.0350371329	-0.0382757821
##	treatment:nrg3	gata3:gata3_mut
##	-0.0468981186	-0.0539752577
##	treatment:inha	ugt2b17
##	-0.0581064544	-0.0653846921
##	treatment:hsd17b7	treatment:chd1:chd1_mut
##	-0.0665996709	-0.0768081300
##	diras3	tp53:tp53_mut
##	-0.0804763607	-0.0813106049
##	treatment:cyp11a1	atr:atr_mut
##	-0.0860935572	-0.0878894843
##	cul1	acvr1c
##	-0.0944239601	-0.0997078098
##	tbx3:tbx3_mut	treatment:cul1
##	-0.1021060807	-0.1254065359
##	stat5a pam50_._claudin.low_subtypeLumA	
##	-0.1442501922	-0.1679222503
##	treatment:mapt	
##	-0.3331440694	

cox.en.beta.nonzero_3

##	lymph_nodes_examined_positive	treatment
##	0.3841860734	0.3476927998
##	integrative_cluster5	gsk3b
##	0.2384409930	0.2284688367
##	tumor_stage3	treatment:e2f8
##	0.2141502347	0.1785825332
##	treatment:tumor_size	eif4ebp1
##	0.1514550933	0.1186634378
##	prkg1	e2f7
##	0.1026237250	0.0375293907
##	aurka	d1l3
##	0.0241813119	0.0221239338
##	treatment:zfyve9	treatment:e2f7
##	0.0100678051	0.0090238419
##	smad7	pdgfb
##	0.0069072699	0.0009589283
##	brca2	treatment:rpgr
##	-0.0016476231	-0.0058930115
##	e2f1	mapt
##	-0.0065817850	-0.0207472337
##	ugt2b17	tp53:tp53_mut
##	-0.0228313861	-0.0299565115
##	gata3:gata3_mut	map3k1
##	-0.0303628989	-0.0335650384
##	cul1	treatment:hsd17b7
##	-0.0352237413	-0.0394587768
##	diras3	acvr1c
##	-0.0605019989	-0.0774130175
##	stat5a	treatment:cyp11a1

```
##          -0.1088171940          -0.1148574350
##          treatment:cul1 pam50_._claudin.low_subtypeLumA
##          -0.1158318310          -0.1289206891
##          treatment:mapt
##          -0.2602185733

nonzero_2 = as.numeric(which(abs(cox.fit_2$beta[,1]) > 1e-10))
nonzero_3 = as.numeric(which(abs(cox.fit_3$beta[,1]) > 1e-10))
nonzero_4 = as.numeric(which(abs(cox.fit_4$beta[,1]) > 1e-10))
nonzero_5 = as.numeric(which(abs(cox.fit_5$beta[,1]) > 1e-10))

common = intersect(nonzero_2, intersect(nonzero_3, intersect(nonzero_4, nonzero_5)))

cox.fit_2$beta[common,1]
```

```
##          treatment lymph_nodes_examined_positive
##          0.364321603          0.396224768
## pam50_._claudin.low_subtypeLumA integrative_cluster5
##          -0.167922250          0.287431684
##          e2f7          stat5a
##          0.028066605          -0.144250192
##          cul1          acvr1c
##          -0.094423960          -0.099707810
##          diras3          eif4ebp1
##          -0.080476361          0.129974858
##          gsk3b          map3k1
##          0.243405254          -0.035037133
##          pdgfb          mapt
##          0.009442187          -0.038275782
##          prkg1          ugt2b17
##          0.139539308          -0.065384692
##          tp53:tp53_mut          gata3:gata3_mut
##          -0.081310605          -0.053975258
##          treatment:tumor_size          treatment:e2f8
##          0.202274029          0.178658784
##          treatment:cul1          treatment:zfyve9
##          -0.125406536          0.108132707
##          treatment:mapt          treatment:cyp11a1
##          -0.333144069          -0.086093557
##          treatment:hsd17b7
##          -0.066599671
```

```
cox.fit_2$beta[common]
```

```
## [1] 0.364321603 0.396224768 -0.167922250 0.287431684 0.028066605
## [6] -0.144250192 -0.094423960 -0.099707810 -0.080476361 0.129974858
## [11] 0.243405254 -0.035037133 0.009442187 -0.038275782 0.139539308
## [16] -0.065384692 -0.081310605 -0.053975258 0.202274029 0.178658784
## [21] -0.125406536 0.108132707 -0.333144069 -0.086093557 -0.066599671
```

```
cox.fit_3$beta[common]
```

```
## [1] 0.3476927998 0.3841860734 -0.1289206891 0.2384409930 0.0375293907
## [6] -0.1088171940 -0.0352237413 -0.0774130175 -0.0605019989 0.1186634378
## [11] 0.2284688367 -0.0335650384 0.0009589283 -0.0207472337 0.1026237250
## [16] -0.0228313861 -0.0299565115 -0.0303628989 0.1514550933 0.1785825332
```

```
## [21] -0.1158318310 0.0100678051 -0.2602185733 -0.1148574350 -0.0394587768
cox.fit_4$beta[common]

## [1] 0.34996087 0.37844573 -0.13994924 0.31536490 0.05016256 -0.10684454
## [7] -0.05271470 -0.07773049 -0.07644247 0.10434735 0.20454000 -0.03935772
## [13] 0.01722024 -0.03311242 0.12420754 -0.02813309 -0.07297772 -0.03921558
## [19] 0.23477622 0.17115736 -0.13667896 0.08778544 -0.25136692 -0.11628356
## [25] -0.02933571
cox.fit_5$beta[common]

## [1] 0.331994022 0.396280534 -0.144294892 0.240822534 0.029789071
## [6] -0.132510561 -0.100009043 -0.102728346 -0.078702380 0.122959331
## [11] 0.243855479 -0.022577776 0.001276889 -0.033054844 0.146136591
## [16] -0.070581607 -0.061837565 -0.093933651 0.122027642 0.196330185
## [21] -0.148044856 0.100526881 -0.309994398 -0.165852232 -0.058253673
sum((cox.fit$beta[common] > 0 & cox.fit_2$beta[common] <= 0) | (cox.fit$beta[common] <= 0 & cox.fit_2$beta[common] > 0))

## [1] 0
sum((cox.fit_2$beta[common] > 0 & cox.fit_3$beta[common] <= 0) | (cox.fit_2$beta[common] <= 0 & cox.fit_3$beta[common] > 0))

## [1] 0
sum((cox.fit_2$beta[common] > 0 & cox.fit_4$beta[common] <= 0) | (cox.fit_2$beta[common] <= 0 & cox.fit_4$beta[common] > 0))

## [1] 0
sum((cox.fit_2$beta[common] > 0 & cox.fit_5$beta[common] <= 0) | (cox.fit_2$beta[common] <= 0 & cox.fit_5$beta[common] > 0))

## [1] 0
get.race.unpenalized = function(x, model, weights)
{
  n = nrow(x)
  ind = which(names(x) == 'treatment')
  x0 = x
  x1 = x
  x0[,ind] = 0
  x1[,ind] = 1

  scurve0 = survfit(model, newdata = x0, weights = W.vec)
  scurve1 = survfit(model, newdata = x1, weights = W.vec)

  AUC0 = sum(rowMeans(scurve0$surv) * c(scurve0$time[1], diff(scurve0$time)))
  AUC1 = sum(rowMeans(scurve1$surv) * c(scurve1$time[1], diff(scurve1$time)))

  RACE = AUC1 - AUC0
  return(RACE)
}
```

Fitting the Cox model with selected variables

```
data_matrix = data.frame(model_matrix)

coxmodel <- coxph(y ~ kdm3a.kdm3a_mut + lymph_nodes_examined_positive +
                  treatment + as.factor(integrative_cluster5) +
```

```

        as.factor(integrative_cluster3) +
        gsk3b + treatment.tumor_size +
        prkg1 + treatment.e2f8 +
        eif4ebp1 + treatment.zfyve9 +
        treatment.ush2a + dll3 +
        treatment.nrarp + tumor_size +
        treatment.e2f7 + e2f7 +
        smad7 + men1 +
        prkacg + treatment.notch1 +
        pdgfb + as.factor(tumor_stage2) +
        mmp25 + treatment.acvr1c +
        treatment.srd5a3 + treatment.hsd17b7 +
        mlh1 + casp7 +
        brca2 + treatment.rpgr +
        treatment.ugt2b17 + igf1 +
        treatment.nrg3 + map3k1 +
        mapt + e2f1 +
        ugt2b17 +
        treatment.inha + diras3 +
        tp53.tp53_mut + atr.atr_mut +
        gata3.gata3_mut + acvr1c +
        cul1 + stat5a +
        treatment.cul1 + as.factor(pam50._claudin.low_subtypeLumA) +
        birc6.birc6_mut + treatment.cyp11a1 +
        tbx3.tbx3_mut + treatment.mapt, weights = c(W.vec), data = data_matrix)

```

```
summary(coxmodel)
```

```

## Call:
## coxph(formula = y ~ kdm3a.kdm3a_mut + lymph_nodes_examined_positive +
##   treatment + as.factor(integrative_cluster5) + as.factor(integrative_cluster3) +
##   gsk3b + treatment.tumor_size + prkg1 + treatment.e2f8 + eif4ebp1 +
##   treatment.zfyve9 + treatment.ush2a + dll3 + treatment.nrarp +
##   tumor_size + treatment.e2f7 + e2f7 + smad7 + men1 + prkacg +
##   treatment.notch1 + pdgfb + as.factor(tumor_stage2) + mmp25 +
##   treatment.acvr1c + treatment.srd5a3 + treatment.hsd17b7 +
##   mlh1 + casp7 + brca2 + treatment.rpgr + treatment.ugt2b17 +
##   igf1 + treatment.nrg3 + map3k1 + mapt + e2f1 + ugt2b17 +
##   treatment.inha + diras3 + tp53.tp53_mut + atr.atr_mut + gata3.gata3_mut +
##   acvr1c + cul1 + stat5a + treatment.cul1 + as.factor(pam50._claudin.low_subtypeLumA) +
##   birc6.birc6_mut + treatment.cyp11a1 + tbx3.tbx3_mut + treatment.mapt,
##   data = data_matrix, weights = c(W.vec))
##
##   n= 879, number of events= 303
##
##
##               coef exp(coef) se(coef)
## kdm3a.kdm3a_mut      3.43128  30.91621  0.87534
## lymph_nodes_examined_positive 0.72412   2.06292  0.07472
## treatment            0.26090   1.29810  0.11607
## as.factor(integrative_cluster5)1 0.40535   1.49983  0.13883
## as.factor(integrative_cluster3)1 -0.32163   0.72497  0.21011
## gsk3b                0.15196   1.16411  0.11760
## treatment.tumor_size  0.71672   2.04770  0.26737
## prkg1                0.56714   1.76322  0.09176

```


## treatment.e2f8	0.34472	1.41159	0.13453
## eif4ebp1	0.16990	1.18518	0.10304
## treatment.zfyve9	0.16526	1.17970	0.12904
## treatment.ush2a	0.46345	1.58955	0.15592
## dll3	0.14217	1.15278	0.09442
## treatment.nrarp	0.32735	1.38729	0.13669
## tumor_size	-0.20912	0.81129	0.24517
## treatment.e2f7	-0.05427	0.94718	0.18771
## e2f7	0.09505	1.09971	0.14381
## smad7	0.18508	1.20331	0.10507
## men1	0.14010	1.15039	0.10113
## prkacg	0.28760	1.33322	0.09446
## treatment.notch1	0.22936	1.25780	0.16225
## pdgfb	0.07733	1.08040	0.10269
## as.factor(tumor_stage2)1	0.22849	1.25670	0.10079
## mmp25	-0.26227	0.76930	0.10686
## treatment.acvr1c	-0.09333	0.91089	0.20565
## treatment.srd5a3	-0.28892	0.74907	0.12379
## treatment.hsd17b7	0.07064	1.07319	0.15018
## mlh1	-0.16297	0.84962	0.10250
## casp7	-0.21199	0.80898	0.10512
## brca2	-0.27453	0.75993	0.09850
## treatment.rpgr	-0.06215	0.93974	0.15395
## treatment.ugt2b17	0.10298	1.10847	0.28363
## igf1	-0.11583	0.89063	0.13754
## treatment.nrg3	-0.52297	0.59276	0.18325
## map3k1	0.07408	1.07690	0.11572
## mapt	-0.10249	0.90258	0.16762
## e2f1	-0.27502	0.75956	0.09713
## ugt2b17	-0.73711	0.47849	0.21794
## treatment.inha	-0.41856	0.65799	0.13396
## diras3	-0.31422	0.73036	0.13913
## tp53.tp53_mut	-0.44054	0.64369	0.10476
## atr.atr_mut	-0.80931	0.44517	0.51444
## gata3.gata3_mut	-0.93305	0.39335	0.37258
## acvr1c	-0.36373	0.69508	0.14311
## cul1	-0.51979	0.59465	0.15983
## stat5a	-0.20024	0.81854	0.10493
## treatment.cul1	-0.07283	0.92976	0.19944
## as.factor(pam50._.claudin.low_subtypeLumA)1	-0.21972	0.80274	0.13744
## birc6.birc6_mut	-0.75198	0.47143	0.49710
## treatment.cyp11a1	-0.46299	0.62940	0.15905
## tbx3.tbx3_mut	-1.80113	0.16511	0.49935
## treatment.mapt	-0.64863	0.52276	0.23365
##	robust se	z Pr(> z)	
## kdm3a.kdm3a_mut	0.87844	3.906	9.38e-05 ***
## lymph_nodes_examined_positive	0.09717	7.452	9.21e-14 ***
## treatment	0.15719	1.660	0.09695 .
## as.factor(integrative_cluster5)1	0.18966	2.137	0.03257 *
## as.factor(integrative_cluster3)1	0.25933	-1.240	0.21488
## gsk3b	0.16454	0.923	0.35575
## treatment.tumor_size	0.39037	1.836	0.06636 .
## prkg1	0.12583	4.507	6.56e-06 ***
## treatment.e2f8	0.19751	1.745	0.08093 .

```

## eif4ebp1 0.14410 1.179 0.23839
## treatment.zfyve9 0.17868 0.925 0.35503
## treatment.ush2a 0.21685 2.137 0.03258 *
## dll3 0.13962 1.018 0.30854
## treatment.nrap 0.17981 1.820 0.06868 .
## tumor_size 0.36376 -0.575 0.56537
## treatment.e2f7 0.25431 -0.213 0.83103
## e2f7 0.19582 0.485 0.62741
## smad7 0.16864 1.097 0.27244
## men1 0.14157 0.990 0.32236
## prkacg 0.12491 2.302 0.02131 *
## treatment.notch1 0.23105 0.993 0.32085
## pdgfb 0.15567 0.497 0.61934
## as.factor(tumor_stage2)1 0.13628 1.677 0.09363 .
## mmp25 0.14638 -1.792 0.07317 .
## treatment.acvr1c 0.28847 -0.324 0.74628
## treatment.srd5a3 0.16516 -1.749 0.08023 .
## treatment.hsd17b7 0.19819 0.356 0.72154
## mlh1 0.15217 -1.071 0.28417
## casp7 0.13960 -1.519 0.12887
## brca2 0.13500 -2.033 0.04200 *
## treatment.rpgr 0.20772 -0.299 0.76477
## treatment.ugt2b17 0.41469 0.248 0.80387
## igf1 0.18137 -0.639 0.52307
## treatment.nrg3 0.28169 -1.857 0.06338 .
## map3k1 0.15638 0.474 0.63569
## mapt 0.23227 -0.441 0.65902
## e2f1 0.13588 -2.024 0.04298 *
## ugt2b17 0.32051 -2.300 0.02146 *
## treatment.inha 0.15524 -2.696 0.00701 **
## diras3 0.18277 -1.719 0.08558 .
## tp53.tp53_mut 0.16012 -2.751 0.00594 **
## atr.atr_mut 0.46068 -1.757 0.07896 .
## gata3.gata3_mut 0.42745 -2.183 0.02905 *
## acvr1c 0.21455 -1.695 0.09001 .
## cul1 0.25120 -2.069 0.03853 *
## stat5a 0.16514 -1.213 0.22530
## treatment.cul1 0.28862 -0.252 0.80078
## as.factor(pam50._.claudin.low_subtypeLumA)1 0.18119 -1.213 0.22525
## birc6.birc6_mut 0.76160 -0.987 0.32346
## treatment.cyp11a1 0.19968 -2.319 0.02042 *
## tbx3.tbx3_mut 0.80544 -2.236 0.02534 *
## treatment.mapt 0.32369 -2.004 0.04508 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##
## exp(coef) exp(-coef) lower .95
## kdm3a.kdm3a_mut 30.9162 0.03235 5.52654
## lymph_nodes_examined_positive 2.0629 0.48475 1.70517
## treatment 1.2981 0.77036 0.95392
## as.factor(integrative_cluster5)1 1.4998 0.66674 1.03420
## as.factor(integrative_cluster3)1 0.7250 1.37938 0.43609
## gsk3b 1.1641 0.85903 0.84321
## treatment.tumor_size 2.0477 0.48835 0.95275

```

## prkg1	1.7632	0.56714	1.37786
## treatment.e2f8	1.4116	0.70842	0.95849
## eif4ebp1	1.1852	0.84375	0.89357
## treatment.zfyve9	1.1797	0.84767	0.83115
## treatment.ush2a	1.5895	0.62911	1.03918
## dll3	1.1528	0.86747	0.87680
## treatment.nrarp	1.3873	0.72083	0.97523
## tumor_size	0.8113	1.23260	0.39769
## treatment.e2f7	0.9472	1.05576	0.57539
## e2f7	1.0997	0.90933	0.74919
## smad7	1.2033	0.83104	0.86463
## men1	1.1504	0.86927	0.87164
## prkacg	1.3332	0.75006	1.04370
## treatment.notch1	1.2578	0.79504	0.79973
## pdgfb	1.0804	0.92558	0.79631
## as.factor(tumor_stage2)1	1.2567	0.79574	0.96211
## mmp25	0.7693	1.29988	0.57743
## treatment.acvr1c	0.9109	1.09783	0.51752
## treatment.srd5a3	0.7491	1.33499	0.54192
## treatment.hsd17b7	1.0732	0.93180	0.72774
## mlh1	0.8496	1.17700	0.63052
## casp7	0.8090	1.23613	0.61534
## brca2	0.7599	1.31591	0.58326
## treatment.rpgr	0.9397	1.06413	0.62545
## treatment.ugt2b17	1.1085	0.90214	0.49174
## igf1	0.8906	1.12280	0.62419
## treatment.nrg3	0.5928	1.68703	0.34127
## map3k1	1.0769	0.92859	0.79261
## mapt	0.9026	1.10793	0.57250
## e2f1	0.7596	1.31655	0.58197
## ugt2b17	0.4785	2.08989	0.25531
## treatment.inha	0.6580	1.51977	0.48538
## diras3	0.7304	1.36919	0.51046
## tp53.tp53_mut	0.6437	1.55355	0.47031
## atr.atr_mut	0.4452	2.24636	0.18046
## gata3.gata3_mut	0.3934	2.54225	0.17019
## acvr1c	0.6951	1.43869	0.45647
## cul1	0.5946	1.68167	0.36344
## stat5a	0.8185	1.22169	0.59221
## treatment.cul1	0.9298	1.07555	0.52808
## as.factor(pam50_._claudin.low_subtypeLumA)1	0.8027	1.24573	0.56279
## birc6.birc6_mut	0.4714	2.12120	0.10596
## treatment.cyp11a1	0.6294	1.58882	0.42556
## tbx3.tbx3_mut	0.1651	6.05646	0.03406
## treatment.mapt	0.5228	1.91293	0.27719
##	upper .95		
## kdm3a.kdm3a_mut	172.9494		
## lymph_nodes_examined_positive	2.4957		
## treatment	1.7665		
## as.factor(integrative_cluster5)1	2.1751		
## as.factor(integrative_cluster3)1	1.2052		
## gsk3b	1.6071		
## treatment.tumor_size	4.4010		
## prkg1	2.2564		

```

## treatment.e2f8                2.0789
## eif4ebp1                      1.5720
## treatment.zfyve9              1.6744
## treatment.ush2a               2.4314
## dll3                          1.5156
## treatment.nrarp               1.9734
## tumor_size                    1.6551
## treatment.e2f7                1.5592
## e2f7                          1.6142
## smad7                        1.6747
## men1                         1.5183
## prkacg                       1.7030
## treatment.notch1              1.9782
## pdgfb                        1.4658
## as.factor(tumor_stage2)1      1.6415
## mmp25                        1.0249
## treatment.acvr1c              1.6033
## treatment.srd5a3              1.0354
## treatment.hsd17b7             1.5826
## mlh1                         1.1448
## casp7                        1.0636
## brca2                        0.9901
## treatment.rpgr                1.4119
## treatment.ugt2b17             2.4987
## igf1                         1.2708
## treatment.nrg3                1.0296
## map3k1                       1.4631
## mapt                         1.4230
## e2f1                         0.9913
## ugt2b17                      0.8968
## treatment.inha                0.8920
## diras3                       1.0450
## tp53.tp53_mut                 0.8810
## atr.atr_mut                   1.0981
## gata3.gata3_mut               0.9091
## acvr1c                       1.0584
## cul1                         0.9729
## stat5a                       1.1314
## treatment.cul1                1.6370
## as.factor(pam50._.claudin.low_subtypeLumA)1 1.1450
## birc6.birc6_mut               2.0975
## treatment.cyp11a1             0.9309
## tbx3.tbx3_mut                 0.8005
## treatment.mapt                0.9859
##
## Concordance= 0.808 (se = 0.013 )
## Likelihood ratio test= 694.6 on 52 df, p=<2e-16
## Wald test = 502.7 on 52 df, p=<2e-16
## Score (logrank) test = 834.7 on 52 df, p=<2e-16, Robust = 214.2 p=<2e-16
##
## (Note: the likelihood ratio and score tests assume independence of
## observations within a cluster, the Wald and robust score tests do not).

```

```
mod = coxmodel
sum.cox = summary(coxmodel)

sum.cox$coefficients
```

	coef	exp(coef)	se(coef)
##			
## kdm3a.kdm3a_mut	3.43128063	30.9162096	0.87533658
## lymph_nodes_examined_positive	0.72412208	2.0629192	0.07471657
## treatment	0.26090224	1.2981008	0.11606538
## as.factor(integrative_cluster5)1	0.40535206	1.4998304	0.13883499
## as.factor(integrative_cluster3)1	-0.32163112	0.7249656	0.21011256
## gsk3b	0.15195506	1.1641079	0.11760331
## treatment.tumor_size	0.71671626	2.0476980	0.26737407
## prkg1	0.56714275	1.7632219	0.09176190
## treatment.e2f8	0.34471991	1.4115945	0.13452821
## eif4ebp1	0.16989771	1.1851836	0.10304041
## treatment.zfyve9	0.16525917	1.1796988	0.12904053
## treatment.ush2a	0.46344797	1.5895453	0.15591579
## dll3	0.14217304	1.1527761	0.09442464
## treatment.nrarp	0.32735148	1.3872890	0.13669412
## tumor_size	-0.20912356	0.8112950	0.24516521
## treatment.e2f7	-0.05426543	0.9471807	0.18770652
## e2f7	0.09504816	1.0997118	0.14380892
## smad7	0.18507795	1.2033122	0.10506580
## men1	0.14010413	1.1503936	0.10112524
## prkacg	0.28759578	1.3332183	0.09446375
## treatment.notch1	0.22936329	1.2577989	0.16225380
## pdgfb	0.07733314	1.0804019	0.10268740
## as.factor(tumor_stage2)1	0.22848613	1.2566961	0.10079390
## mmp25	-0.26226930	0.7693038	0.10686085
## treatment.acvr1c	-0.09333213	0.9108909	0.20564650
## treatment.srd5a3	-0.28892172	0.7490708	0.12379355
## treatment.hsd17b7	0.07063676	1.0731913	0.15017965
## mlh1	-0.16297151	0.8496154	0.10250335
## casp7	-0.21198567	0.8089763	0.10511610
## brca2	-0.27452524	0.7599328	0.09850426
## treatment.rpgr	-0.06215372	0.9397384	0.15394690
## treatment.ugt2b17	0.10298370	1.1084733	0.28363251
## igf1	-0.11582710	0.8906292	0.13753803
## treatment.nrg3	-0.52297085	0.5927569	0.18324556
## map3k1	0.07408287	1.0768960	0.11571953
## mapt	-0.10249324	0.9025842	0.16761950
## e2f1	-0.27501543	0.7595604	0.09712506
## ugt2b17	-0.73710986	0.4784948	0.21794217
## treatment.inha	-0.41856185	0.6579924	0.13396076
## diras3	-0.31421748	0.7303602	0.13912730
## tp53.tp53_mut	-0.44053949	0.6436891	0.10475601
## atr.atr_mut	-0.80931011	0.4451651	0.51443996
## gata3.gata3_mut	-0.93305056	0.3933519	0.37257845
## acvr1c	-0.36373322	0.6950766	0.14311082
## cul1	-0.51978521	0.5946483	0.15982677
## stat5a	-0.20023811	0.8185358	0.10493288
## treatment.cul1	-0.07282955	0.9297593	0.19943786
## as.factor(pam50_._claudin.low_subtypeLumA)1	-0.21972172	0.8027422	0.13744390

## birc6.birc6_mut	-0.75198266	0.4714309	0.49710438
## treatment.cyp11a1	-0.46298904	0.6293995	0.15905476
## tbx3.tbx3_mut	-1.80112564	0.1651129	0.49934880
## treatment.mapt	-0.64863482	0.5227589	0.23364665
##	robust se	z	Pr(> z)
## kdm3a.kdm3a_mut	0.87844389	3.9060897	9.380171e-05
## lymph_nodes_examined_positive	0.09717444	7.4517750	9.209268e-14
## treatment	0.15718601	1.6598312	9.694842e-02
## as.factor(integrative_cluster5)1	0.18965755	2.1372841	3.257489e-02
## as.factor(integrative_cluster3)1	0.25932535	-1.2402610	2.148789e-01
## gsk3b	0.16454298	0.9234977	3.557479e-01
## treatment.tumor_size	0.39037447	1.8359711	6.636193e-02
## prkg1	0.12582532	4.5073818	6.563246e-06
## treatment.e2f8	0.19751076	1.7453222	8.092880e-02
## eif4ebp1	0.14409919	1.1790330	2.383850e-01
## treatment.zfyve9	0.17868104	0.9248836	3.550264e-01
## treatment.ush2a	0.21684668	2.1372150	3.258051e-02
## dll3	0.13961913	1.0182920	3.085392e-01
## treatment.nrarp	0.17981464	1.8204940	6.868381e-02
## tumor_size	0.36376281	-0.5748899	5.653658e-01
## treatment.e2f7	0.25431345	-0.2133801	8.310305e-01
## e2f7	0.19582417	0.4853750	6.274103e-01
## smad7	0.16864305	1.0974538	2.724431e-01
## men1	0.14157371	0.9896197	3.223601e-01
## prkacg	0.12491001	2.3024237	2.131129e-02
## treatment.notch1	0.23104541	0.9927195	3.208466e-01
## pdgfb	0.15566633	0.4967878	6.193387e-01
## as.factor(tumor_stage2)1	0.13628255	1.6765619	9.362819e-02
## mmp25	0.14637605	-1.7917501	7.317300e-02
## treatment.acvr1c	0.28846578	-0.3235466	7.462813e-01
## treatment.srd5a3	0.16516027	-1.7493415	8.023200e-02
## treatment.hsd17b7	0.19819419	0.3564018	7.215397e-01
## mlh1	0.15216652	-1.0710076	2.841660e-01
## casp7	0.13959532	-1.5185730	1.288700e-01
## brca2	0.13500276	-2.0334786	4.200419e-02
## treatment.rpgr	0.20772003	-0.2992187	7.647732e-01
## treatment.ugt2b17	0.41469452	0.2483363	8.038742e-01
## igf1	0.18137107	-0.6386195	5.230705e-01
## treatment.nrg3	0.28169400	-1.8565211	6.337933e-02
## map3k1	0.15638240	0.4737290	6.356932e-01
## mapt	0.23227235	-0.4412632	6.590225e-01
## e2f1	0.13588075	-2.0239470	4.297560e-02
## ugt2b17	0.32050869	-2.2998124	2.145885e-02
## treatment.inha	0.15523830	-2.6962538	7.012422e-03
## diras3	0.18277159	-1.7191812	8.558139e-02
## tp53.tp53_mut	0.16012105	-2.7512903	5.936102e-03
## atr.atr_mut	0.46068497	-1.7567539	7.895976e-02
## gata3.gata3_mut	0.42744665	-2.1828468	2.904709e-02
## acvr1c	0.21454785	-1.6953478	9.000947e-02
## cul1	0.25120008	-2.0692080	3.852658e-02
## stat5a	0.16513718	-1.2125562	2.252995e-01
## treatment.cul1	0.28861813	-0.2523388	8.007792e-01
## as.factor(pam50_._claudin.low_subtypeLumA)1	0.18118632	-1.2126838	2.252507e-01
## birc6.birc6_mut	0.76160103	-0.9873709	3.234609e-01

```

## treatment.cyp11a1          0.19968264 -2.3186244 2.041541e-02
## tbx3.tbx3_mut             0.80544247 -2.2361940 2.533906e-02
## treatment.mapt            0.32369130 -2.0038686 4.508414e-02

coefs = tibble(coef = rownames(sum.cox$coefficients), estimate = unname(sum.cox$coefficients[,1]), exp_
               robust_se = unname(sum.cox$coefficients[,4]), pval = unname(sum.cox$coefficients[,6]))

xtable(coefs, caption = "...", digits = 3, display = c('g','g', 'g', 'g', 'g', 'g'))

## % latex table generated in R 4.1.3 by xtable 1.8-4 package
## % Wed Apr 26 17:00:18 2023
## \begin{table}[ht]
## \centering
## \begin{tabular}{rlrrrr}
## \hline
## & coef & estimate & exp\_estimate & robust\_se & pval \\
## \hline
## 1 & kdm3a.kdm3a\_mut & 3.43 & 30.9 & 0.878 & 9.38e-05 \\
## 2 & lymph\_nodes\_examined\_positive & 0.724 & 2.06 & 0.0972 & 9.21e-14 \\
## 3 & treatment & 0.261 & 1.3 & 0.157 & 0.0969 \\
## 4 & as.factor(integrative\_cluster5)1 & 0.405 & 1.5 & 0.19 & 0.0326 \\
## 5 & as.factor(integrative\_cluster3)1 & -0.322 & 0.725 & 0.259 & 0.215 \\
## 6 & gsk3b & 0.152 & 1.16 & 0.165 & 0.356 \\
## 7 & treatment.tumor\_size & 0.717 & 2.05 & 0.39 & 0.0664 \\
## 8 & prkg1 & 0.567 & 1.76 & 0.126 & 6.56e-06 \\
## 9 & treatment.e2f8 & 0.345 & 1.41 & 0.198 & 0.0809 \\
## 10 & eif4ebp1 & 0.17 & 1.19 & 0.144 & 0.238 \\
## 11 & treatment.zfyve9 & 0.165 & 1.18 & 0.179 & 0.355 \\
## 12 & treatment.ush2a & 0.463 & 1.59 & 0.217 & 0.0326 \\
## 13 & dll3 & 0.142 & 1.15 & 0.14 & 0.309 \\
## 14 & treatment.nrarp & 0.327 & 1.39 & 0.18 & 0.0687 \\
## 15 & tumor\_size & -0.209 & 0.811 & 0.364 & 0.565 \\
## 16 & treatment.e2f7 & -0.0543 & 0.947 & 0.254 & 0.831 \\
## 17 & e2f7 & 0.095 & 1.1 & 0.196 & 0.627 \\
## 18 & smad7 & 0.185 & 1.2 & 0.169 & 0.272 \\
## 19 & men1 & 0.14 & 1.15 & 0.142 & 0.322 \\
## 20 & prkacg & 0.288 & 1.33 & 0.125 & 0.0213 \\
## 21 & treatment.notch1 & 0.229 & 1.26 & 0.231 & 0.321 \\
## 22 & pdgfb & 0.0773 & 1.08 & 0.156 & 0.619 \\
## 23 & as.factor(tumor\_stage2)1 & 0.228 & 1.26 & 0.136 & 0.0936 \\
## 24 & mmp25 & -0.262 & 0.769 & 0.146 & 0.0732 \\
## 25 & treatment.acvr1c & -0.0933 & 0.911 & 0.288 & 0.746 \\
## 26 & treatment.srd5a3 & -0.289 & 0.749 & 0.165 & 0.0802 \\
## 27 & treatment.hsd17b7 & 0.0706 & 1.07 & 0.198 & 0.722 \\
## 28 & mlh1 & -0.163 & 0.85 & 0.152 & 0.284 \\
## 29 & casp7 & -0.212 & 0.809 & 0.14 & 0.129 \\
## 30 & brca2 & -0.275 & 0.76 & 0.135 & 0.042 \\
## 31 & treatment.rpgr & -0.0622 & 0.94 & 0.208 & 0.765 \\
## 32 & treatment.ugt2b17 & 0.103 & 1.11 & 0.415 & 0.804 \\
## 33 & igf1 & -0.116 & 0.891 & 0.181 & 0.523 \\
## 34 & treatment.nrg3 & -0.523 & 0.593 & 0.282 & 0.0634 \\
## 35 & map3k1 & 0.0741 & 1.08 & 0.156 & 0.636 \\
## 36 & mapt & -0.102 & 0.903 & 0.232 & 0.659 \\
## 37 & e2f1 & -0.275 & 0.76 & 0.136 & 0.043 \\
## 38 & ugt2b17 & -0.737 & 0.478 & 0.321 & 0.0215

```

```
## 39 & treatment.inha & -0.419 & 0.658 & 0.155 & 0.00701 \\
## 40 & diras3 & -0.314 & 0.73 & 0.183 & 0.0856 \\
## 41 & tp53.tp53\_mut & -0.441 & 0.644 & 0.16 & 0.00594 \\
## 42 & atr.atr\_mut & -0.809 & 0.445 & 0.461 & 0.079 \\
## 43 & gata3.gata3\_mut & -0.933 & 0.393 & 0.427 & 0.029 \\
## 44 & acvr1c & -0.364 & 0.695 & 0.215 & 0.09 \\
## 45 & cul1 & -0.52 & 0.595 & 0.251 & 0.0385 \\
## 46 & stat5a & -0.2 & 0.819 & 0.165 & 0.225 \\
## 47 & treatment.cul1 & -0.0728 & 0.93 & 0.289 & 0.801 \\
## 48 & as.factor(pam50\_.\_claudin.low\_subtypeLumA)1 & -0.22 & 0.803 & 0.181 & 0.225 \\
## 49 & birc6.birc6\_mut & -0.752 & 0.471 & 0.762 & 0.323 \\
## 50 & treatment.cyp11a1 & -0.463 & 0.629 & 0.2 & 0.0204 \\
## 51 & tbx3.tbx3\_mut & -1.8 & 0.165 & 0.805 & 0.0253 \\
## 52 & treatment.mapt & -0.649 & 0.523 & 0.324 & 0.0451 \\
## \hline
## \end{tabular}
## \caption{...}
## \end{table}
```

```
#coefs
```

```
#survfit(formula = coxmodel, newdata = data_matrix)
```

```
get.race.unpenalized(data_matrix, coxmodel, W.vec)
```

```
## [1] -15.73215
```

Sensitivity Analysis - Propensity Scores

```
coxmodel_overlap <- coxph(y[e.vec > 0.35 & e.vec < 0.8] ~ kdm3a.kdm3a_mut + lymph_nodes_examined_posit.
      treatment + as.factor(integrative_cluster5) +
      as.factor(integrative_cluster3) +
      gsk3b + treatment.tumor_size +
      prkg1 + treatment.e2f8 +
      eif4ebp1 + treatment.zfyve9 +
      treatment.ush2a + dll3 +
      treatment.nrarp + tumor_size +
      treatment.e2f7 + e2f7 +
      smad7 + men1 +
      prkacg + treatment.notch1 +
      pdgfb + as.factor(tumor_stage2) +
      mmp25 + treatment.acvr1c +
      treatment.srd5a3 + treatment.hsd17b7 +
      mlh1 + casp7 +
      brca2 + treatment.rpgr +
      treatment.ugt2b17 + igf1 +
      treatment.nrg3 + map3k1 +
      mapt + e2f1 +
      ugt2b17 +
      treatment.inha + diras3 +
      tp53.tp53_mut + atr.atr_mut +
      gata3.gata3_mut + acvr1c +
      cul1 + stat5a +
      treatment.cul1 + as.factor(pam50\_.\_claudin.low_subtypeLumA) +
      birc6.birc6_mut + treatment.cyp11a1 +
```



```

tbx3.tbx3_mut + treatment.mapt, weights = W.vec[e.vec > 0.35 & e.vec < 0.8,]
get.race.unpenalized(data_matrix[e.vec > 0.35 & e.vec < 0.8,], coxmodel_overlap, W.vec[e.vec > 0.35 & e.vec < 0.8,])

## [1] -20.6392

# BOOTSTARP
n = nrow(data_matrix)
S = 1000
boot.RACE.unpenalized = vector(length = S)
ind_matrix = array(rep(NA, n*S), c(S,n))

# set.seed(4)
# for (i in 1:S)
# {
#   cat('Progress: ', i/S, '\n')
#   boot_ind = sample(1:n, size = n, replace = TRUE)
#   data_matrix_boot = x[boot_ind,]
#   y_boot = y[boot_ind,]
#   W_boot = W.vec[boot_ind]
#
#   ind_matrix[i,] = boot_ind
#
#   coxmodel.boot <- coxph(y_boot ~ kdm3a.kdm3a_mut + lymph_nodes_examined_positive +
#     treatment + as.factor(integrative_cluster5) +
#     as.factor(integrative_cluster3) +
#     gsk3b + treatment.tumor_size +
#     prkg1 + treatment.e2f8 +
#     eif4ebp1 + treatment.zfyve9 +
#     treatment.ush2a + dll3 +
#     treatment.nrarp + tumor_size +
#     treatment.e2f7 + e2f7 +
#     smad7 + men1 +
#     prkacg + treatment.notch1 +
#     pdgfb + as.factor(tumor_stage2) +
#     mmp25 + treatment.acvr1c +
#     treatment.srd5a3 + treatment.hsd17b7 +
#     mlh1 + casp7 +
#     brca2 + treatment.rpgr +
#     treatment.ugt2b17 + igf1 +
#     treatment.nrg3 + map3k1 +
#     mapt + e2f1 +
#     ugt2b17 +
#     treatment.inha + diras3 +
#     tp53.tp53_mut + atr.atr_mut +
#     gata3.gata3_mut + acvr1c +
#     cul1 + stat5a +
#     treatment.cul1 + as.factor(pam50_.claudin.low_subtypeLumA) +
#     birc6.birc6_mut + treatment.cyp11a1 +
#     tbx3.tbx3_mut + treatment.mapt, weights = W_boot, data = data_matrix_boot)
#   boot.RACE.unpenalized[i] = get.race.unpenalized(data_matrix_boot, coxmodel.boot, W_boot)
# }

```

```

#saveRDS(boot.RACE.unpenalized, file = 'boot_RACE_unpenalized.RDS')

boot.RACE.unpenalized = readRDS(file = 'boot_RACE_unpenalized.RDS')

#boot.RACE.unpenalized

#boot.RACE.unpenalized
quantile(boot.RACE.unpenalized, c(0.025, 0.975))

##          2.5%          97.5%
## -35.055441    3.424606

```

Diagnostics

Cox-Snell Residuals

```

source("http://myweb.uiowa.edu/pbreheny/7210/f18/notes/fun.R")
sfit <- survfit(coxmodel)
H0 <- -log(sfit$surv)
H <- approxfun(c(0, sfit$time), c(0, H0), method='constant')
e1 <- H(coxmodel$y[,1])*exp(coxmodel$linear.predictors)
e2 <- coxmodel$y[,2]-residuals(coxmodel)
head(e1)

## [1] 2.342085e-01 4.409510e-02 8.648566e-02 2.494864e-02 8.578785e-05
## [6] 2.084147e-01

head(e2)

##          1          2          3          7          12          13
## 2.342085e-01 4.409510e-02 8.648566e-02 2.494864e-02 8.578785e-05 2.084147e-01

efit <- survfit(Surv(e1, coxmodel$y[,2])~1)
lim <- c(0,5)
pdf("plots/cox_snell_resid.pdf", height = 3.5, width = 6)
plot(efit, fun='cumhaz', mark.time=FALSE, bty='n', conf.int=FALSE, lwd=1, las=1,
     xlab='Residual', ylab='Cumulative hazard', xlim=lim, ylim=lim)
ciband(efit, fun=function(x) -log(x))
lines(lim, lim, col='red', lwd=1)
dev.off()

## pdf
## 2

```