Survival Analysis with HGAT group and telomerase status

Run Jin

2/4/2022

This notebook will do the following survival analysis

1. Univariate analysis

- DMG H3K28 vs rest
- Telhunt score (separate into categories by 1.07)
- HGAT vs. non-HGAT for all samples
- ATRX (mut N/Y)
- ALT vs. non-ALT for all samples

2. Multivariate analysis

- DMG H3K28 vs rest + HGAT vs. non-HGAT + ALT vs. non-ALT + sex + ATRX (mut N/Y)
- DMG H3K28 vs rest + HGAT vs. non-HGAT + Telhunt score (categorical) + sex + ATRX (mut N/Y)
- DMG H3K28 vs rest + HGAT vs. non-HGAT + Telhunt score (continuous) + sex + ATRX (mut N/Y)

Packages and functions Read in set up script.

```
library(survival)
library(dplyr)
```

```
##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
##     filter, lag

## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
library(ggplot2)
library(ggpubr)
```

Set up directories

```
root_dir <- rprojroot::find_root(rprojroot::has_dir(".git"))
analysis_dir <- file.path(root_dir, "analyses", "survival-analysis")

plots_dir <- file.path(analysis_dir, "plots")
if (!dir.exists(plots_dir)) {
  dir.create(plots_dir)
}

output_dir <- file.path(analysis_dir, "output")
if (!dir.exists(output_dir)) {
  dir.create(plots_dir)
}
```

Read in files

```
# get the meta information
meta <- readr::read_tsv(file.path(root_dir,
                           "analyses/add-histologies/output/ALT PBTA oct 2021 (including all plates)-up
  # remove existing ones to get newer data
  dplyr::select(-c("OS_days", "OS_status"))
```

```
## Rows: 900 Columns: 115

## -- Column specification --------------------------------------------------------
## Delimiter: "\t"
## chr (56): Kids_First_Biospecimen_ID_DNA, Kids_First_Biospecimen_ID_RNA, Kids...
## dbl (52): TH T/TH N, UBTF Binary, ATRX Reverse Binary, ATRX IHC Binary, ATRX...
## lgl  (7): ATRX Stata, cell_line_composition, DAXX_fusion, ...34, NF...39, CC...

##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
# get survival information
survival_v21 <- readr::read_tsv(file.path(root_dir,
                                  "analyses/add-histologies/input-v21/pbta-histologies.tsv")) %>%
  dplyr::select("Kids_First_Participant_ID", "OS_days", "OS_status", "PFS_days") %>%
  distinct()
```

```
## Rows: 2840 Columns: 38

## -- Column specification --------------------------------------------------------
## Delimiter: "\t"
## chr (33): Kids_First_Biospecimen_ID, sample_id, aliquot_id, Kids_First_Parti...
## dbl  (5): OS_days, age_last_update_days, normal_fraction, tumor_fraction, tu...

##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

Organize data

```
# join with meta
meta <- meta %>%
  dplyr::left_join(survival_v21) %>%
  dplyr::distinct(Kids_First_Participant_ID, .keep_all = TRUE)
```

```
## Joining, by = "Kids_First_Participant_ID"
```

```
meta$PFS_days <- as.numeric(meta$PFS_days)
```

```
## Warning: NAs introduced by coercion
```

```
# recode for analysis
meta_formatted <- meta %>%
  # recode the categories -
  # DECEASED maps to a survival event status of 1, LIVING maps to a censored observation with value 0
  dplyr::mutate(OS_status_recoded = case_when(
    OS_status == "LIVING" ~ 0,
    OS_status == "DECEASED" ~1
 )) %>%
  # retain only ones with OS days
  dplyr::filter(!is.na(OS_days)) %>%
  # calculte the years
  dplyr::mutate(OS_years = OS_days / 365.25) %>%
  dplyr::mutate(PFS_years = PFS_days / 365.25) %>%
  dplyr::mutate(PFS_status = if_else(PFS_days < OS_days, 1, 0)) %>%
  # categorize by telhunt scores
  dplyr::mutate(telhunt_cat = case_when(
    `TH T/TH N` > 1.07 ~ "High",
    `TH T/TH N` < 1.07 ~ "Low"
  )) %>%
  # categorize by DMG, H3K28 or not
  dplyr::mutate(dmg_h3k28 = case_when(
    grepl("DMG, H3 K28", molecular_subtype) ~ "DMG",
    TRUE ~ "non-DMG"
  )) %>%
  # categorize ATRX
  dplyr::mutate(atrx_mut = case_when(
    !is.na(`ATRX Mutation`) ~ "ATRX_mut",
    TRUE ~ "non_ATRX_mut"
  )) %>%
  # rename telhunt score and CCA
  dplyr::mutate(telhunt_score = `TH T/TH N`,
                cca_telhunt = `CCA Sept 2021`)

# define as factor
meta_formatted$dmg_h3k28 <- factor(meta_formatted$dmg_h3k28, levels = c("non-DMG", "DMG"))
meta_formatted$telhunt_cat <- factor(meta_formatted$telhunt_cat, levels = c("Low", "High"))
meta_formatted$group <- factor(meta_formatted$group, levels = c("non-HGAT", "HGAT"))
meta_formatted$phenotype <- factor(meta_formatted$phenotype, levels = c("non-ALT", "ALT"))
```

```r
meta_formatted$atrx_mut <- factor(meta_formatted$atrx_mut, levels = c("non_ATRX_mut", "ATRX_mut"))


# define as numberic
meta_formatted$telhunt_score <- as.numeric(meta_formatted$telhunt_score)
meta_formatted_hgat <- meta_formatted %>%
  dplyr::filter(group == "HGAT")
```

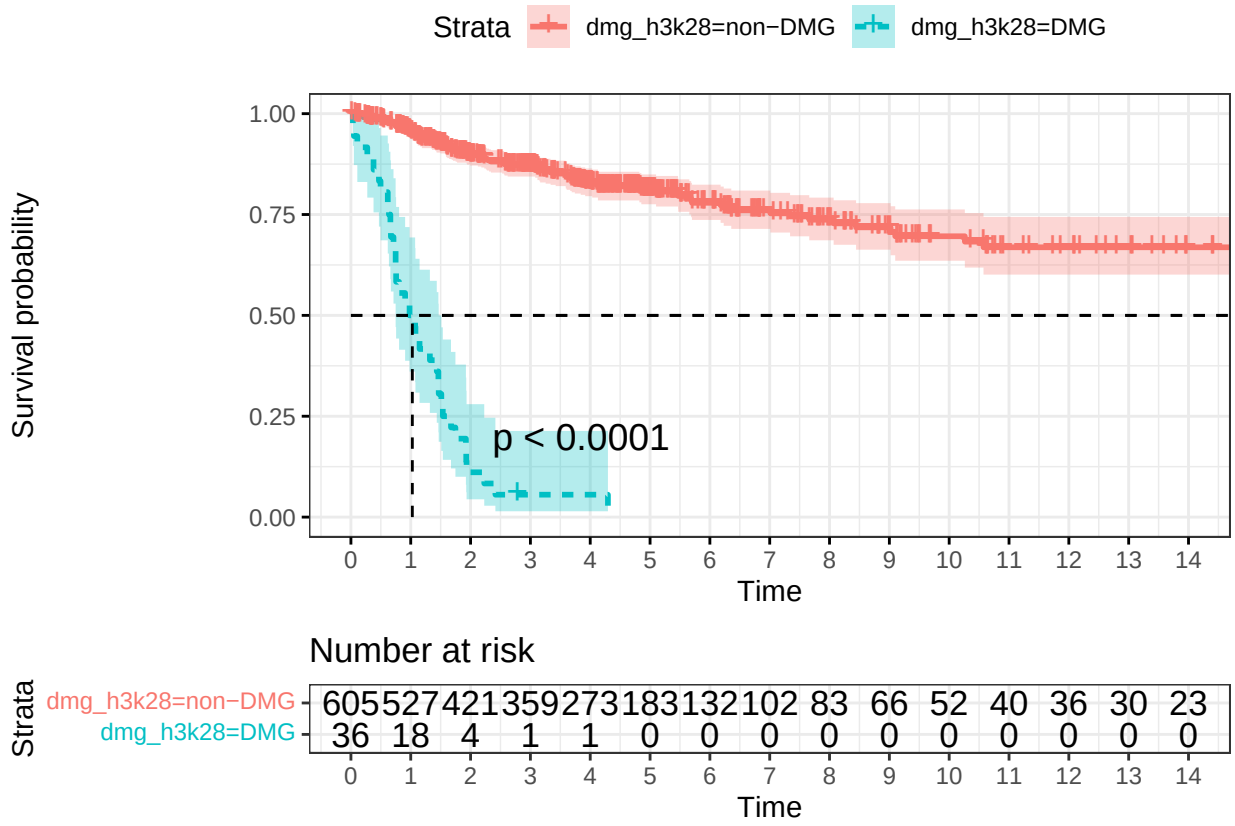
A Run for all samples

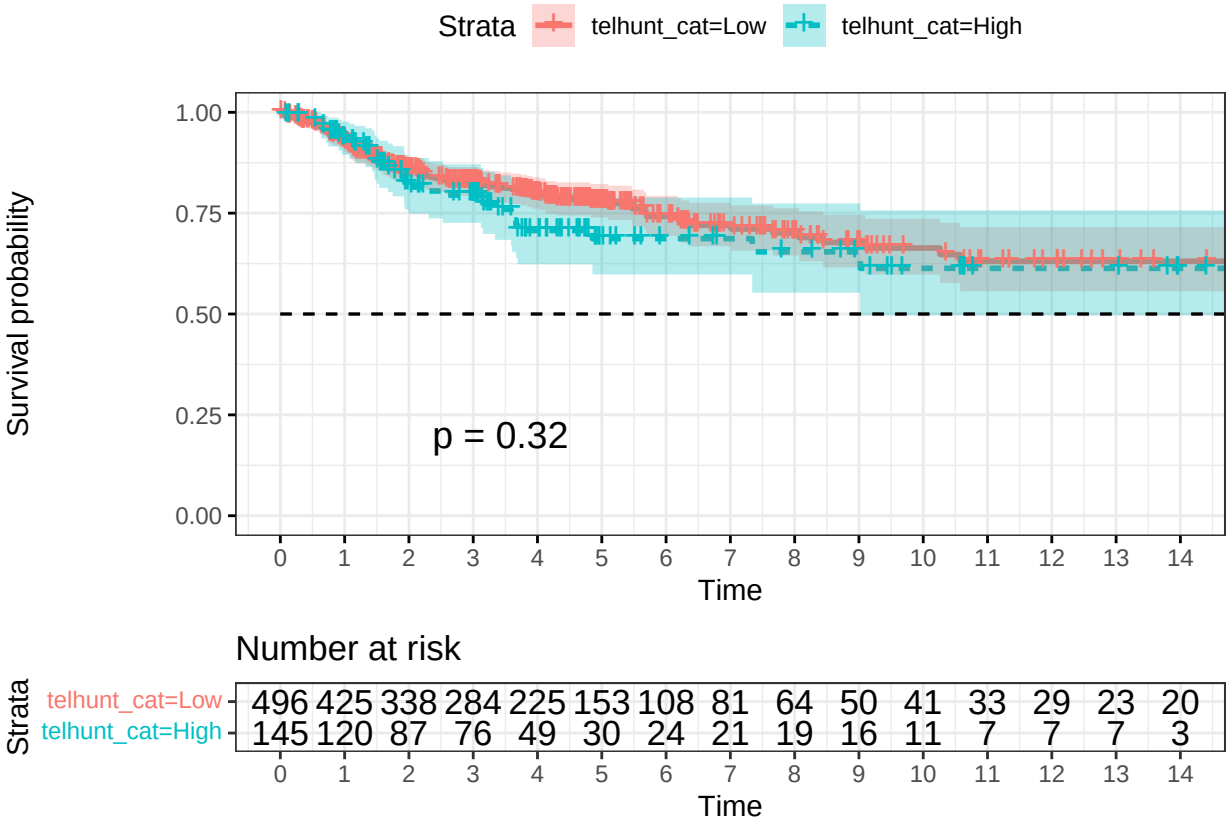
Log Rank analysis

Generate output for categorical files

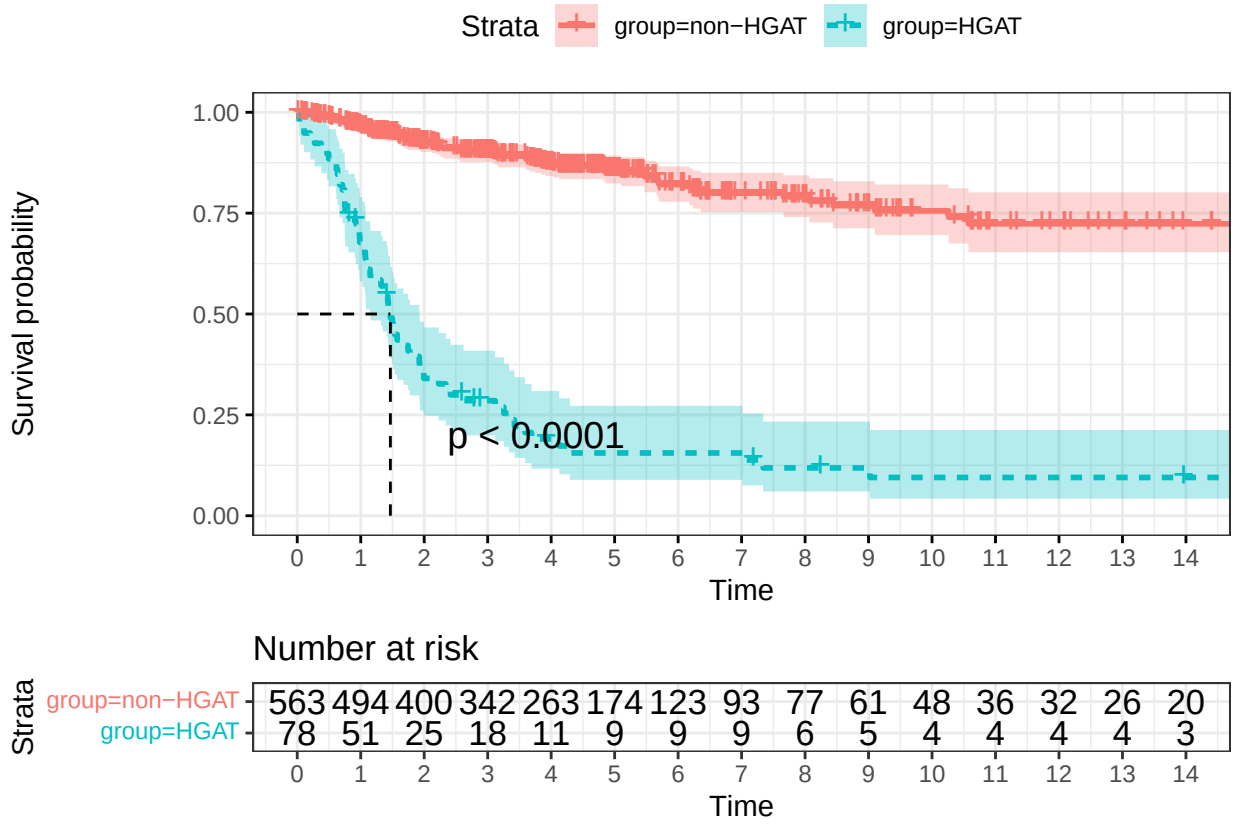
```r
for(ind_var in c("dmg_h3k28", "telhunt_cat", "group", "atrx_mut", "phenotype")){
  # define model
  model <- paste0("survival::Surv(time = OS_years, event = OS_status_recoded) ~ ", ind_var)

  # depending on which variables are used, data used will be different
  data_used <- meta_formatted

  # run survival analysis
  fit <- survival::survdiff(formula(model),
                            data = data_used)
  # Obtain p value for Chi-Squared stat
  fit$p.value <- pchisq(fit$chisq, df = length(fit$n) - 1, lower = FALSE)

  # save the output
  saveRDS(fit, file.path(output_dir, paste0("log_rank_survival_per_", ind_var, ".RDS")))

  # generate plots fit
  fit_plot <- survfit(formula(model), data = data_used)

  # output the plot
  plot_logrank <- survminer::ggsurvplot(fit_plot,
                                        data=data_used,
                                        xlim = c(0, 14),
                                        break.time.by = 1,
                                        pval = TRUE,
                                        conf.int = TRUE,
                                        risk.table = TRUE, # Add risk table
                                        linetype = "strata", # Change line type by groups
                                        surv.median.line = "hv", # Specify median survival
                                        ggtheme = theme_bw())

  print(plot_logrank)
  # Make this plot a combined plot
  surv_plot_logrank <- cowplot::plot_grid(plot_logrank[[1]],
                                          plot_logrank[[2]],
                                          nrow = 2,
```

```
                                        rel_heights = c(2.5, 1))
  # Save the plot
  cowplot::save_plot(filename = file.path(plots_dir,
                                        paste0("logrank_survival_by_", ind_var, ".png")),
                     plot = surv_plot_logrank)

}
```

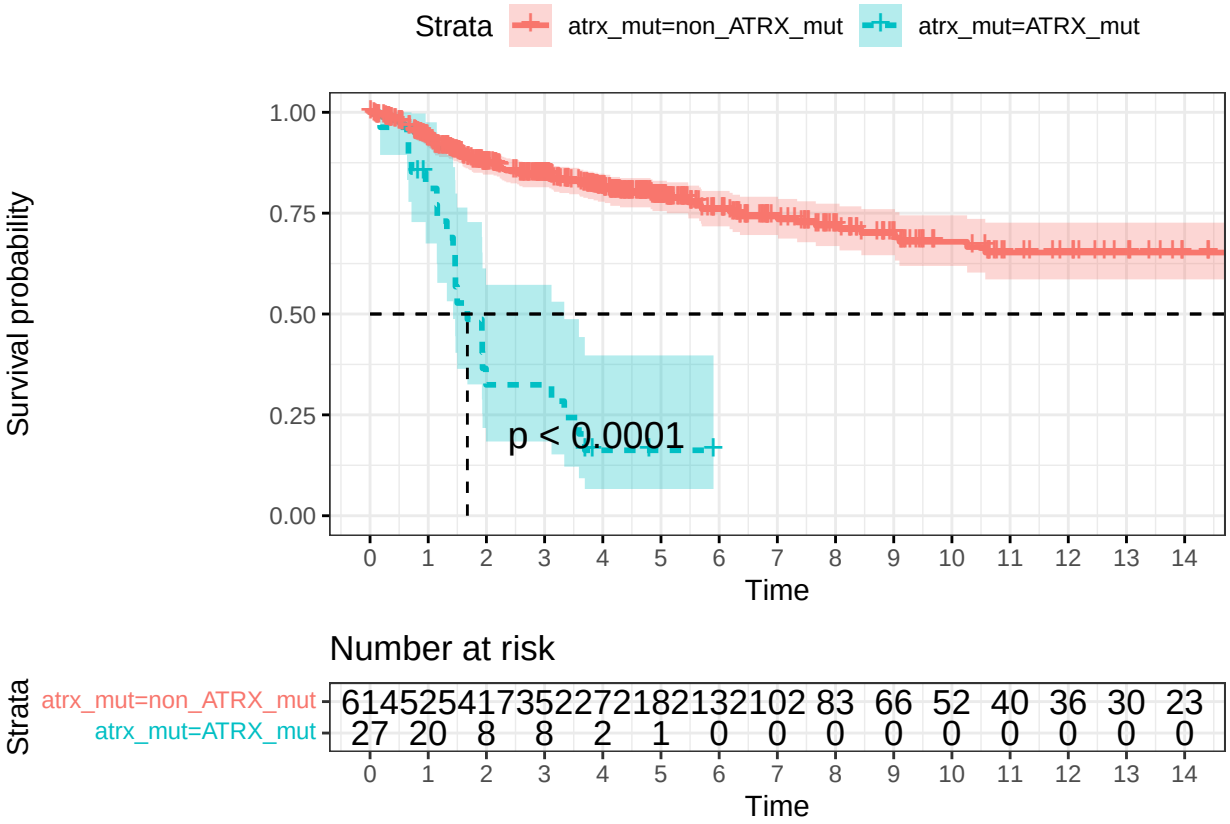


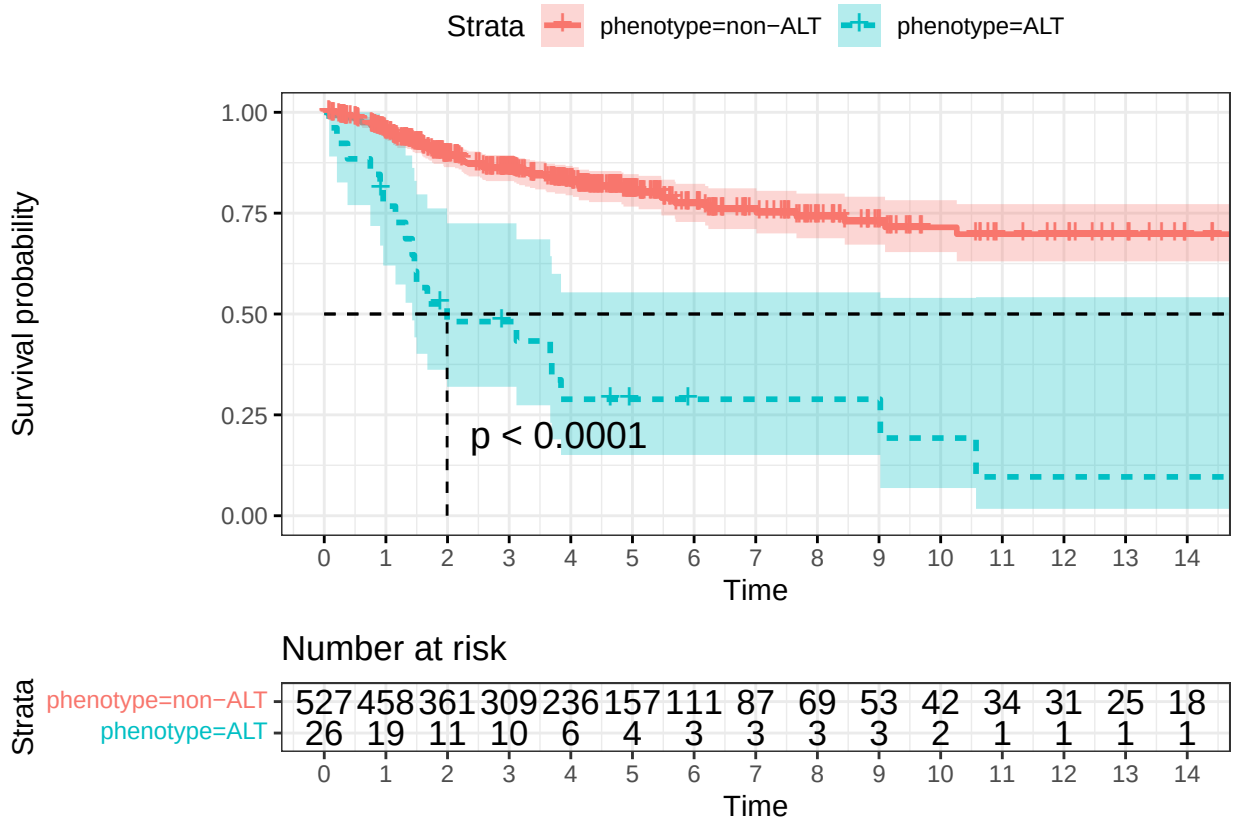

Strata
telhunt_cat=Low
telhunt_cat=High
Survival probability
1.00
0.75
0.50
0.25
0.00
p = 0.32
0
1
2
3
4
5
6
7
8
9
10
11
12
13
14
Time

Number at risk
Strata
telhunt_cat=Low
telhunt_cat=High
496 425 338 284 225 153 108 81 64 50 41 33 29 23 20
145 120 87 76 49 30 24 21 19 16 11 7 7 7 3
0
1
2
3
4
5
6
7
8
9
10
11
12
13
14
Time


Strata
group=non−HGAT
group=HGAT
Survival probability
1.00
0.75
0.50
0.25
0.00
p < 0.0001
0
1
2
3
4
5
6
7
8
9
10
11
12
13
14
Time

Number at risk
Strata
group=non−HGAT
group=HGAT
563 494 400 342 263 174 123 93 77 61 48 36 32 26 20
78 51 25 18 11 9 9 9 6 5 4 4 4 4 3
0
1
2
3
4
5
6
7
8
9
10
11
12
13
14
Time


Strata
atrx_mut=non_ATRX_mut
atrx_mut=ATRX_mut
Survival probability
1.00
0.75
0.50
0.25
0.00
p < 0.0001
0
1
2
3
4
5
6
7
8
9
10
11
12
13
14
Time
Number at risk
Strata
atrx_mut=non_ATRX_mut
atrx_mut=ATRX_mut
614 525 417 352 272 182 132 102 83 66 52 40 36 30 23
27 20 8 8 2 1 0 0 0 0 0 0 0 0 0
0
1
2
3
4
5
6
7
8
9
10
11
12
13
14
Time



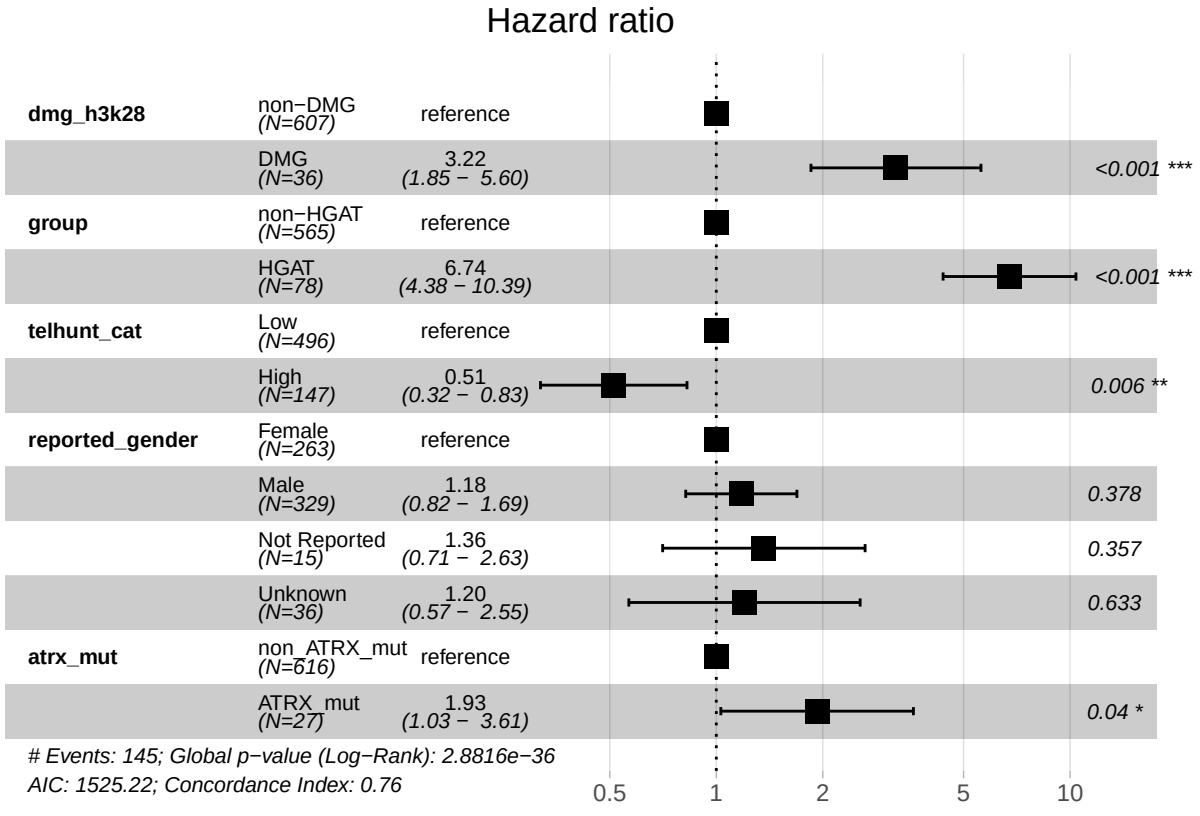
Multivariate analysis

Multivariate analysis - DMG H3K28 vs rest + HGAT vs. non-HGAT + ALT vs. non-ALT + sex + ATRX (mut N/Y) - DMG H3K28 vs rest + HGAT vs. non-HGAT + Telhunt score (categorical) + sex + ATRX (mut N/Y) - DMG H3K28 vs rest + HGAT vs. non-HGAT + Telhunt score (continuous) + sex + ATRX (mut N/Y)

```
# define multi-variates that we are using for analyzing survival
list_of_variates <- c("dmg_h3k28+group+telhunt_cat+reported_gender+atrx_mut",
                      "dmg_h3k28+group+telhunt_score+reported_gender+atrx_mut",
                      "dmg_h3k28+group+phenotype+reported_gender+atrx_mut"
                      )

# define model
for (ind_var in list_of_variates){
  model <- paste0("survival::Surv(time = OS_years, event = OS_status_recoded) ~ ", ind_var)

  # depending on which variables are used, data used will be different
  data_used <- meta_formatted

  fit <- survival::coxph(
        formula(model),
        data = data_used
      )
  # generate output
```

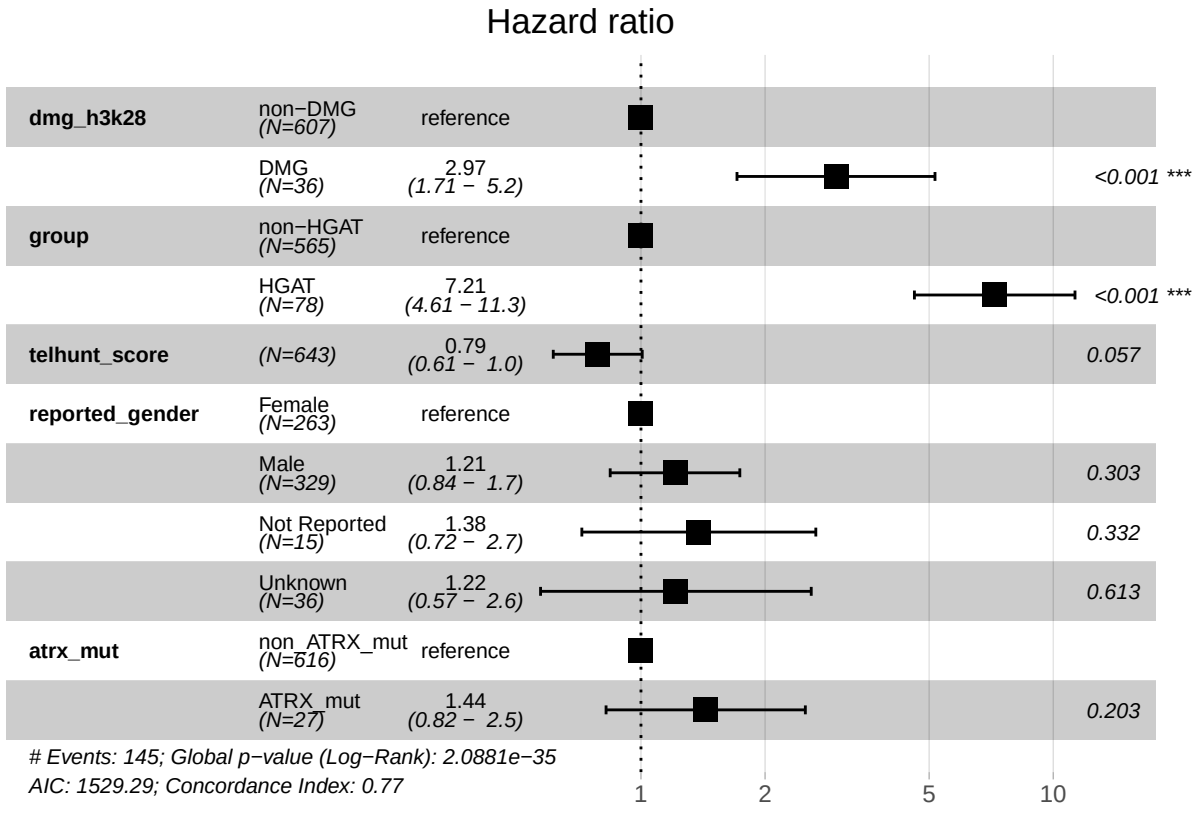
```
  table <- broom::tidy(fit)

  # Save the table data in a TSV
  readr::write_tsv(table, file.path(output_dir, paste0("cox_reg_results_per_", ind_var, ".tsv")))

  print(table)

  # printout the plot
  forest_coxph <- survminer::ggforest(fit, data = data_used)
  print(forest_coxph)

}
```

```
## # A tibble: 7 x 5
##   term                          estimate std.error statistic  p.value
##   <chr>                            <dbl>     <dbl>     <dbl>    <dbl>
## 1 dmg_h3k28DMG                      1.17     0.282      4.14  3.43e- 5
## 2 groupHGAT                         1.91     0.221      8.65  5.08e-18
## 3 telhunt_catHigh                  -0.668    0.243     -2.74  6.06e- 3
## 4 reported_genderMale               0.163    0.185      0.882 3.78e- 1
## 5 reported_genderNot Reported       0.310    0.336      0.921 3.57e- 1
## 6 reported_genderUnknown            0.184    0.384      0.478 6.33e- 1
## 7 atrx_mutATRX_mut                  0.656    0.320      2.05  4.01e- 2
```

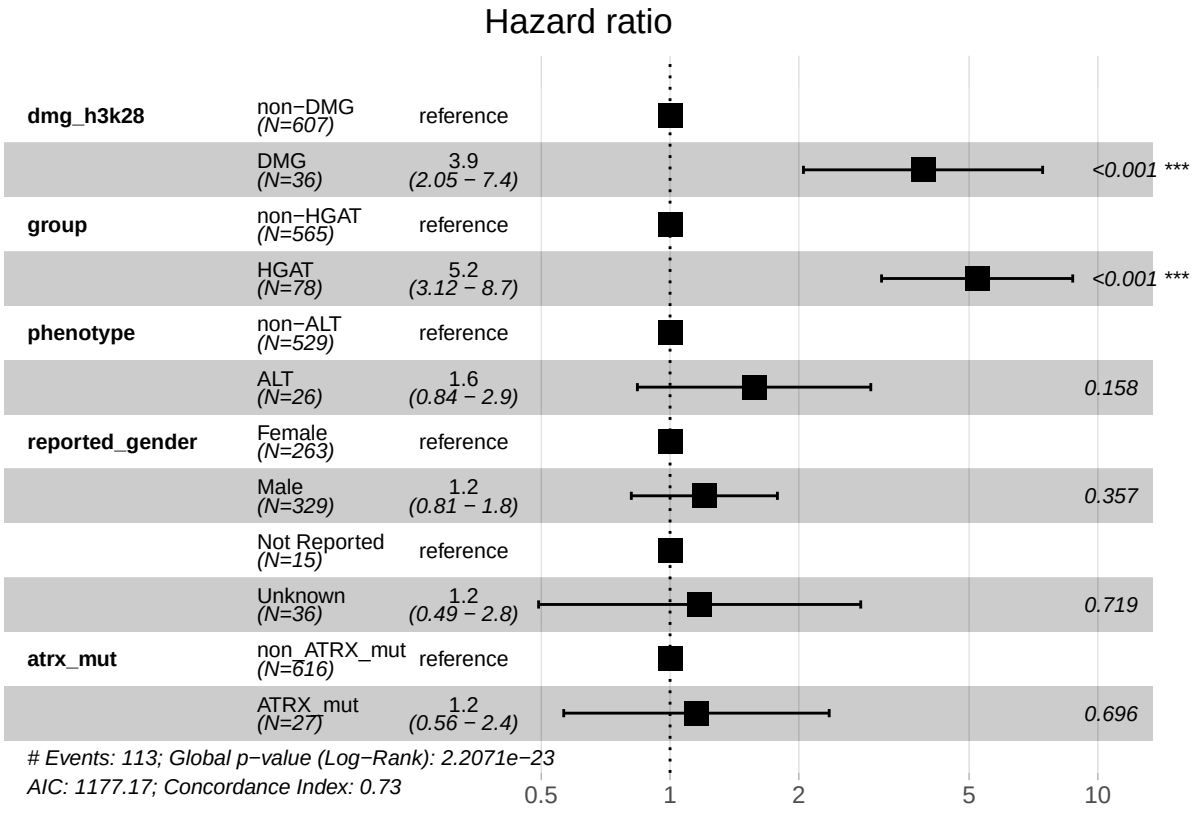



```
## # A tibble: 7 x 5
```

```
##   term                          estimate std.error statistic  p.value
##   <chr>                            <dbl>     <dbl>     <dbl>    <dbl>
## 1 dmg_h3k28DMG                      1.09      0.282     3.86  1.13e- 4
## 2 groupHGAT                         1.98      0.229     8.64  5.86e-18
## 3 telhunt_score                    -0.241     0.127    -1.90  5.68e- 2
## 4 reported_genderMale               0.190     0.185     1.03  3.03e- 1
## 5 reported_genderNot Reported       0.323     0.333     0.969 3.32e- 1
## 6 reported_genderUnknown            0.195     0.386     0.506 6.13e- 1
## 7 atrx_mutATRX_mut                  0.362     0.284     1.27  2.03e- 1
```




```
## # A tibble: 6 x 5
##   term                    estimate std.error statistic  p.value
##   <chr>                      <dbl>     <dbl>     <dbl>    <dbl>
## 1 dmg_h3k28DMG               1.36      0.328     4.15  3.38e- 5
## 2 groupHGAT                  1.65      0.262     6.30  3.04e-10
## 3 phenotypeALT               0.452     0.320     1.41  1.58e- 1
## 4 reported_genderMale        0.185     0.201     0.920 3.57e- 1
## 5 reported_genderUnknown     0.159     0.442     0.360 7.19e- 1
## 6 atrx_mutATRX_mut           0.142     0.364     0.390 6.96e- 1
```

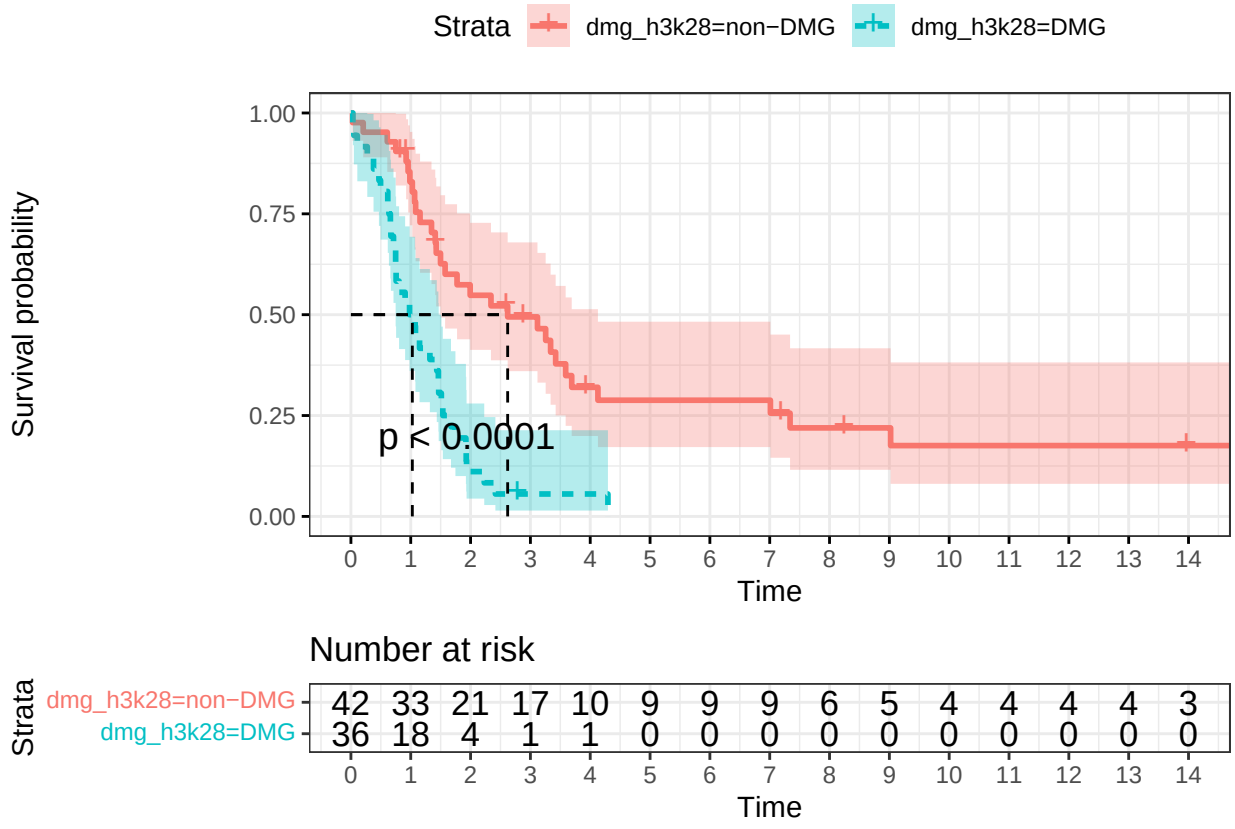


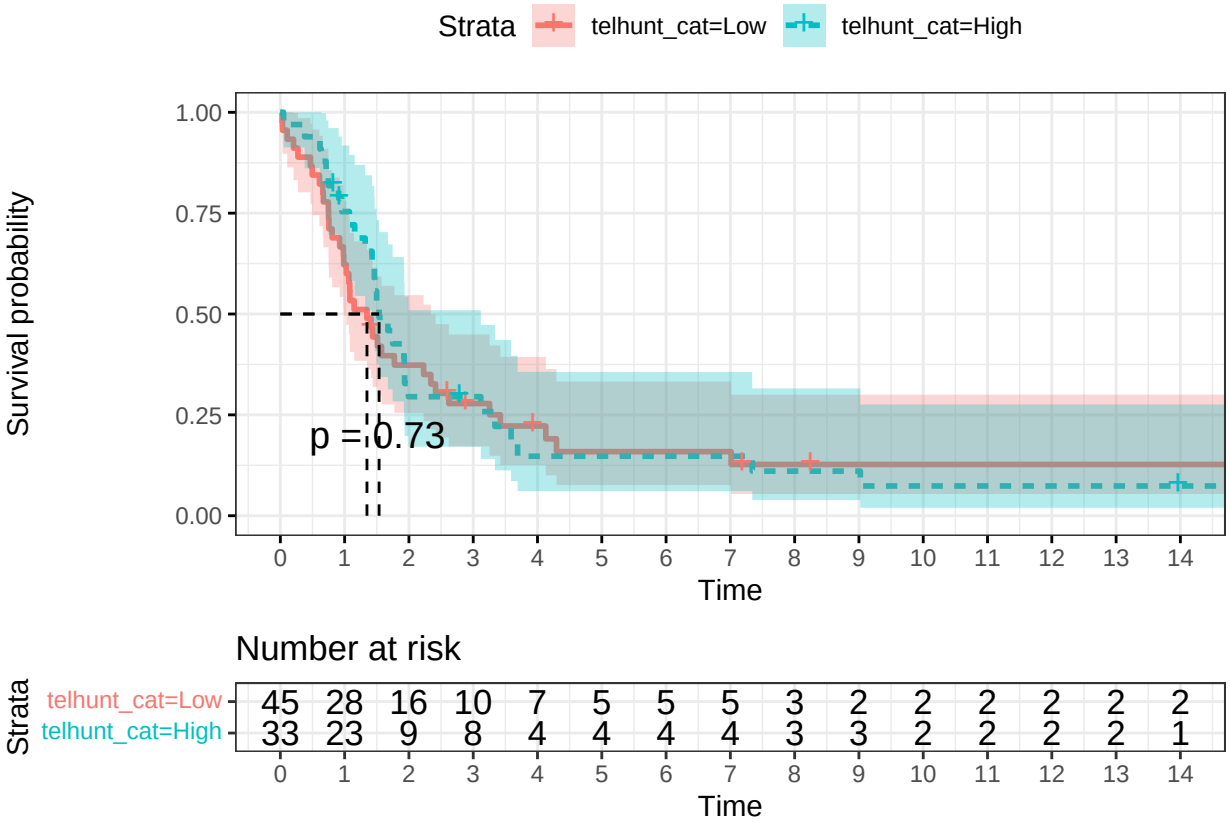
B run for HGAT only

Univariate analysis

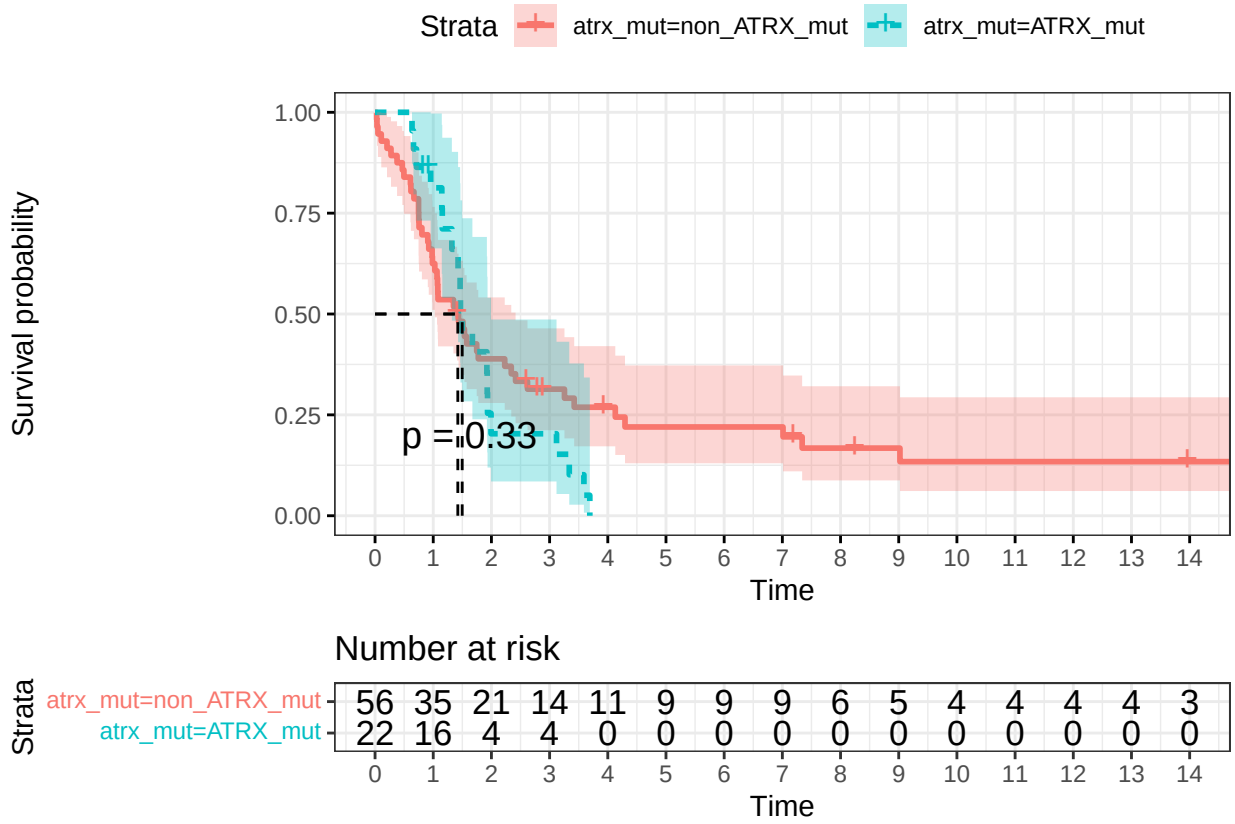
```
for(ind_var in c("dmg_h3k28", "telhunt_cat", "atrx_mut", "phenotype")){
  # define model
  model <- paste0("survival::Surv(time = OS_years, event = OS_status_recoded) ~ ", ind_var)

  # depending on which variables are used, data used will be different
  data_used <- meta_formatted_hgat

  # run survival analysis
  fit <- survival::survdiff(formula(model),
                            data = data_used)
  # Obtain p value for Chi-Squared stat
  fit$p.value <- pchisq(fit$chisq, df = length(fit$n) - 1, lower = FALSE)

  # save the output
  saveRDS(fit, file.path(output_dir, paste0("log_rank_survival_per_", ind_var, "_os_only_hgat.RDS")))

  # generate plots fit
  fit_plot <- survfit(formula(model), data = data_used)
```

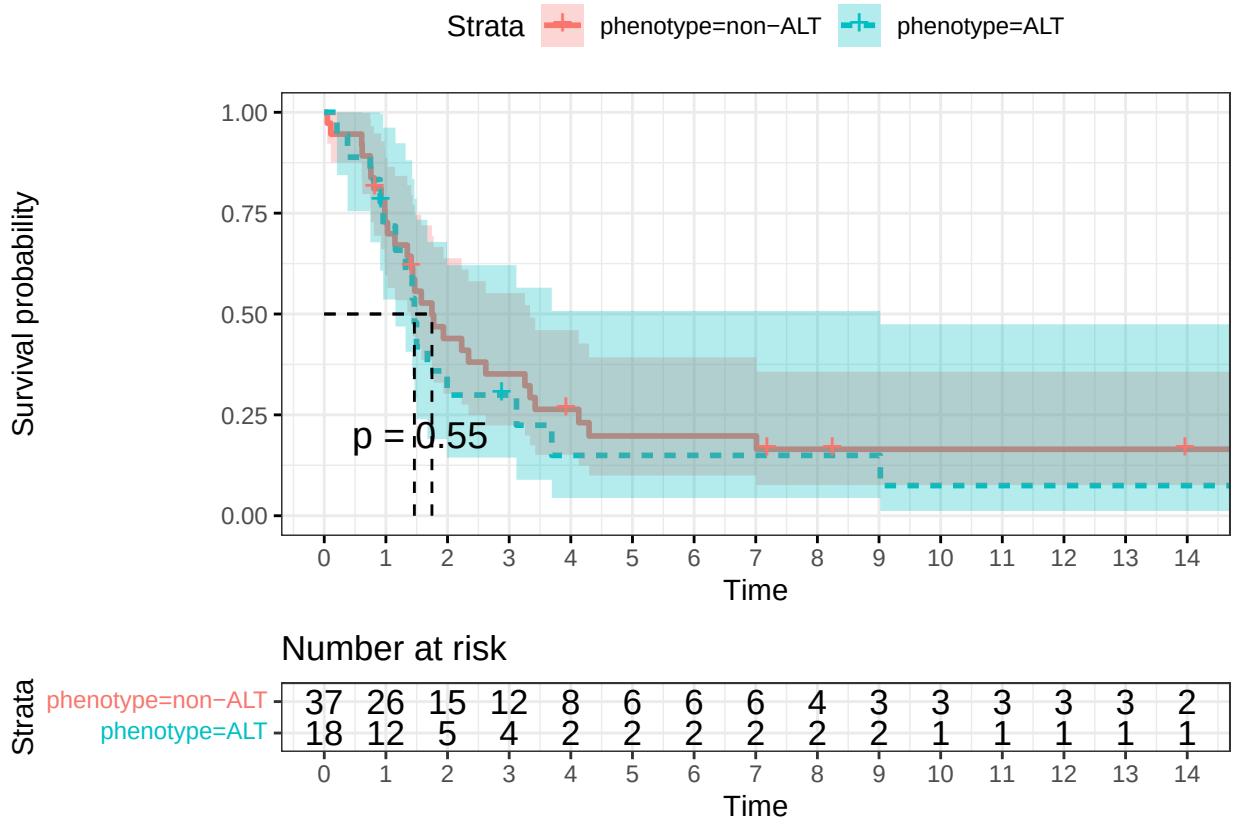
```r
  # output the plot
  plot_logrank <- survminer::ggsurvplot(fit_plot,
                                        data=data_used,
                                        xlim = c(0, 14),
                                        break.time.by = 1,
                                        pval = TRUE,
                                        conf.int = TRUE,
                                        risk.table = TRUE, # Add risk table
                                        linetype = "strata", # Change line type by groups
                                        surv.median.line = "hv", # Specify median survival
                                        ggtheme = theme_bw())

  print(plot_logrank)
  # Make this plot a combined plot
  surv_plot_logrank <- cowplot::plot_grid(plot_logrank[[1]],
                                          plot_logrank[[2]],
                                          nrow = 2,
                                          rel_heights = c(2.5, 1))
  # Save the plot
  cowplot::save_plot(filename = file.path(plots_dir,
                                          paste0("logrank_survival_by_", ind_var, "_os_only_hgat.png")),
                     plot = surv_plot_logrank)


}
```




Strata
telhunt_cat=Low
telhunt_cat=High
Survival probability
1.00
0.75
0.50
0.25
0.00
p = 0.73
0
1
2
3
4
5
6
7
8
9
10
11
12
13
14
Time

Number at risk
Strata
telhunt_cat=Low
telhunt_cat=High
45 28 16 10 7 5 5 5 3 2 2 2 2 2 2
33 23 9 8 4 4 4 4 3 3 2 2 2 2 1
0
1
2
3
4
5
6
7
8
9
10
11
12
13
14
Time


Strata
atrx_mut=non_ATRX_mut
atrx_mut=ATRX_mut
Survival probability
1.00
0.75
0.50
0.25
0.00
p = 0.33
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14
Time
Number at risk
Strata
atrx_mut=non_ATRX_mut
atrx_mut=ATRX_mut
56 35 21 14 11 9 9 9 6 5 4 4 4 4 3
22 16 4 4 0 0 0 0 0 0 0 0 0 0 0
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14
Time



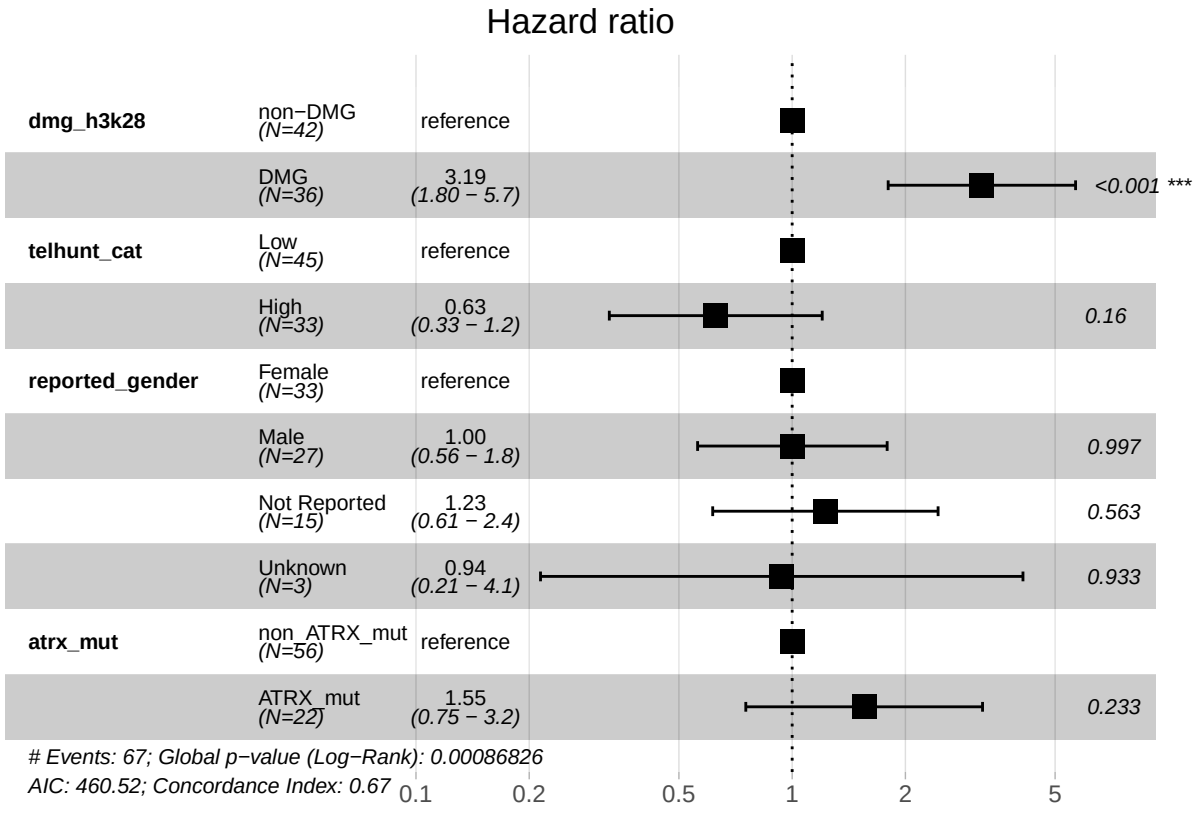
Multivariate analysis

Multivariate analysis for HGAT samples only - DMG H3K28 vs rest + ALT vs. non-ALT + sex + ATRX (mut N/Y) - DMG H3K28 vs rest + Telhunt score (categorical) + sex + ATRX (mut N/Y) - DMG H3K28 vs rest + Telhunt score (continuous) + sex + ATRX (mut N/Y)

```
# define multi-variates that we are using for analyzing survival
list_of_variates <- c("dmg_h3k28+telhunt_cat+reported_gender+atrx_mut",
                      "dmg_h3k28+telhunt_score+reported_gender+atrx_mut",
                      "dmg_h3k28+phenotype+reported_gender+atrx_mut"
                      )

# define model
for (ind_var in list_of_variates){
  model <- paste0("survival::Surv(time = OS_years, event = OS_status_recoded) ~ ", ind_var)

  # depending on which variables are used, data used will be different
  data_used <- meta_formatted_hgat

  fit <- survival::coxph(
        formula(model),
        data = data_used
      )
  # generate output
  table <- broom::tidy(fit)
```

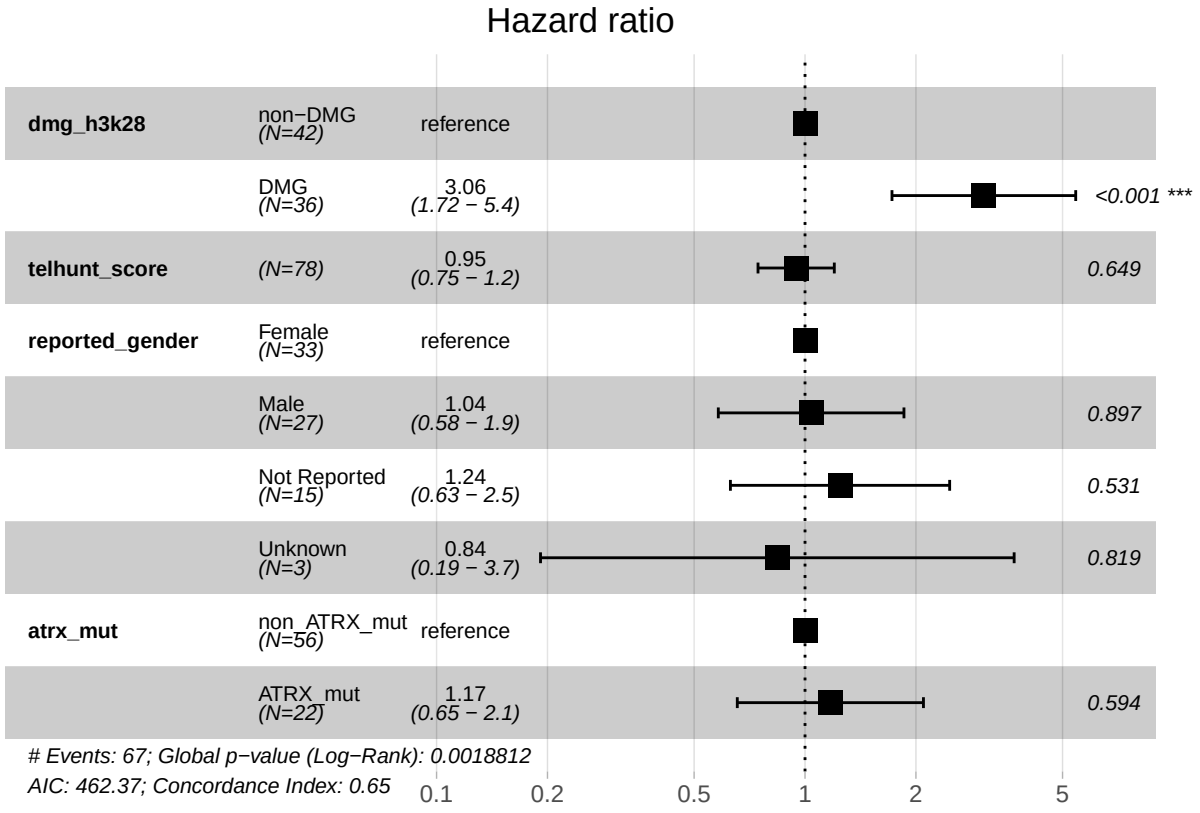
```
  # Save the table data in a TSV
  readr::write_tsv(table, file.path(output_dir, paste0("cox_reg_results_per_", ind_var, "_os_only_hgat.t

  print(table)

  # printout the plot
  forest_coxph <- survminer::ggforest(fit, data = data_used)
  print(forest_coxph)

}
```

```
## # A tibble: 6 x 5
##   term                          estimate std.error statistic   p.value
##   <chr>                            <dbl>     <dbl>     <dbl>     <dbl>
## 1 dmg_h3k28DMG                   1.16        0.293   3.97    0.0000724
## 2 telhunt_catHigh               -0.468       0.332  -1.41    0.160
## 3 reported_genderMale            0.00129     0.296   0.00437 0.997
## 4 reported_genderNot Reported    0.203       0.352   0.578   0.563
## 5 reported_genderUnknown        -0.0638      0.753  -0.0846  0.933
## 6 atrx_mutATRX_mut               0.441       0.370   1.19    0.233
```

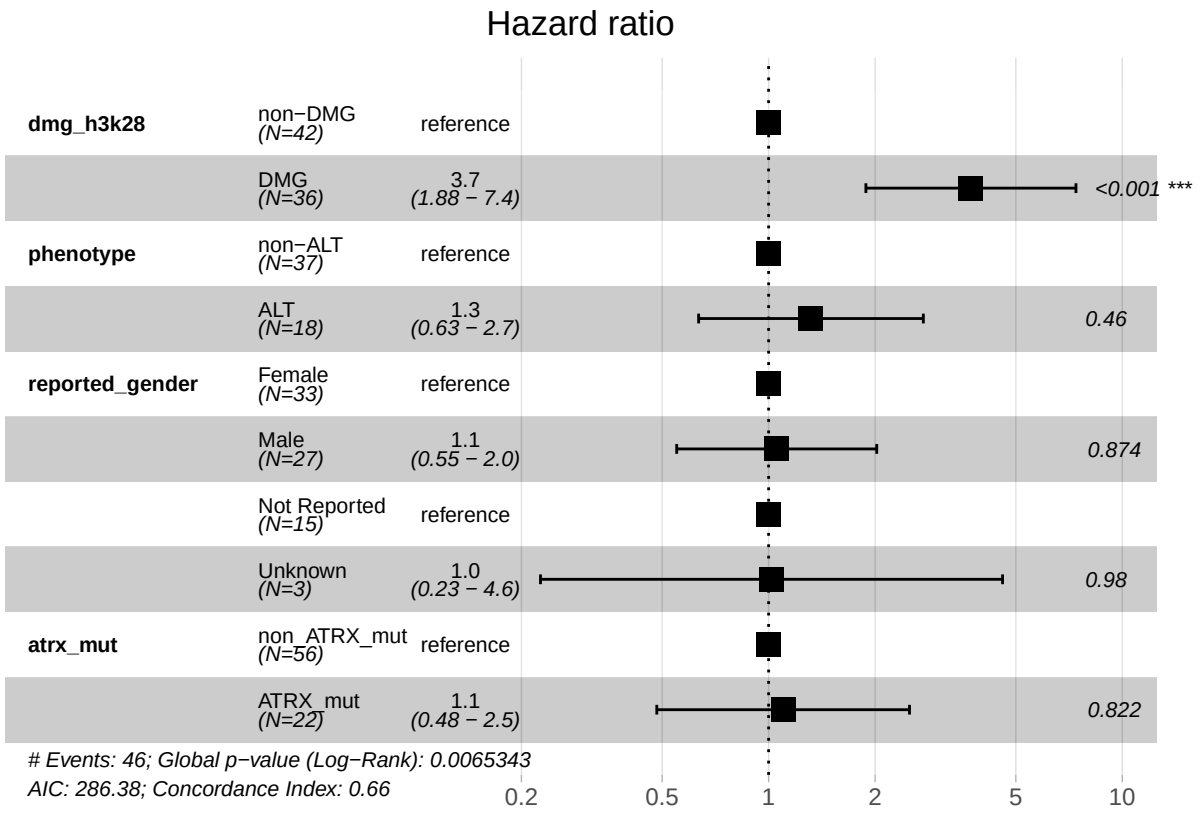



```
## # A tibble: 6 x 5
##   term                          estimate std.error statistic  p.value
##   <chr>                            <dbl>     <dbl>     <dbl>    <dbl>
```

```
## 1 dmg_h3k28DMG                  1.12       0.293     3.82  0.000136
## 2 telhunt_score                -0.0554     0.122    -0.455 0.649
## 3 reported_genderMale           0.0382     0.296     0.129 0.897
## 4 reported_genderNot Reported   0.219      0.350     0.626 0.531
## 5 reported_genderUnknown       -0.173      0.755    -0.229 0.819
## 6 atrx_mutATRX_mut              0.158      0.297     0.534 0.594
```



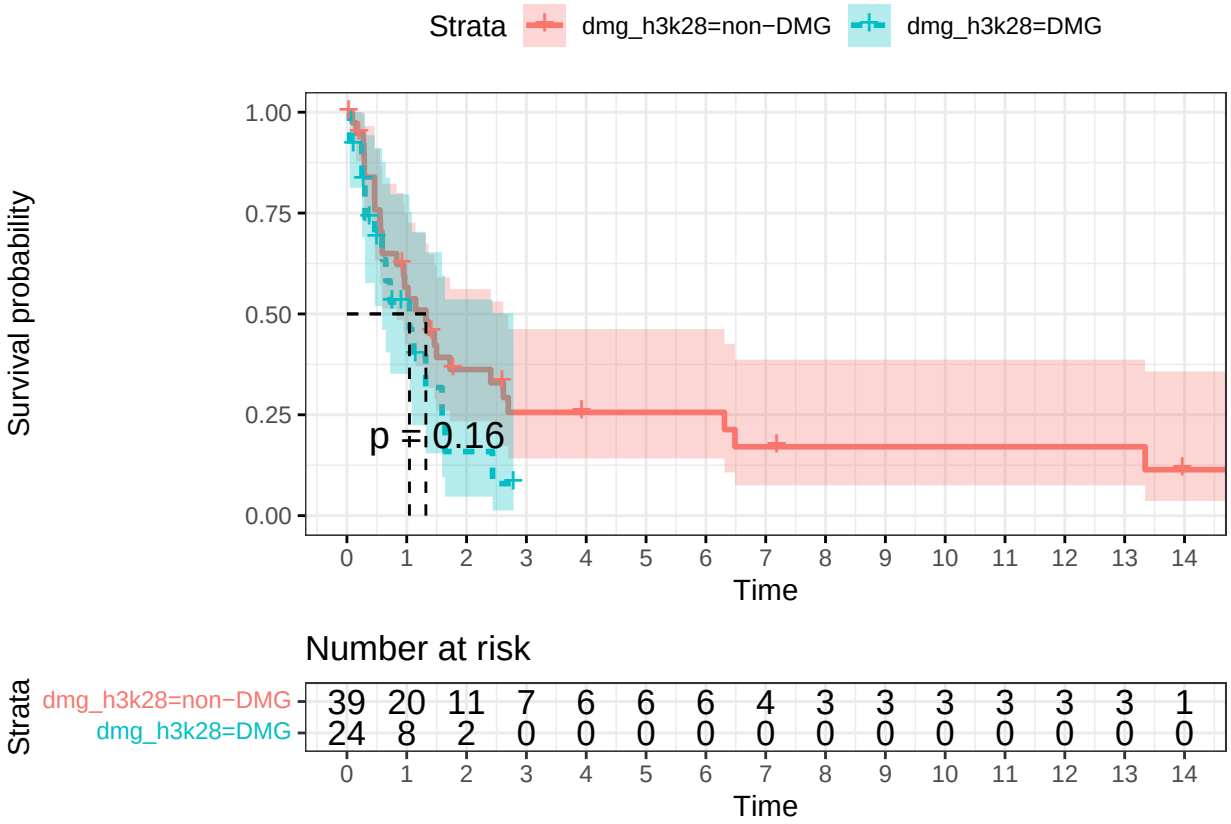

```
## # A tibble: 5 x 5
##   term                   estimate std.error statistic  p.value
##   <chr>                     <dbl>     <dbl>     <dbl>    <dbl>
## 1 dmg_h3k28DMG              1.32      0.349     3.78   0.000160
## 2 phenotypeALT              0.276     0.373     0.739  0.460
## 3 reported_genderMale       0.0527    0.332     0.159  0.874
## 4 reported_genderUnknown    0.0189    0.767     0.0246 0.980
## 5 atrx_mutATRX_mut          0.0946    0.420     0.225  0.822
```

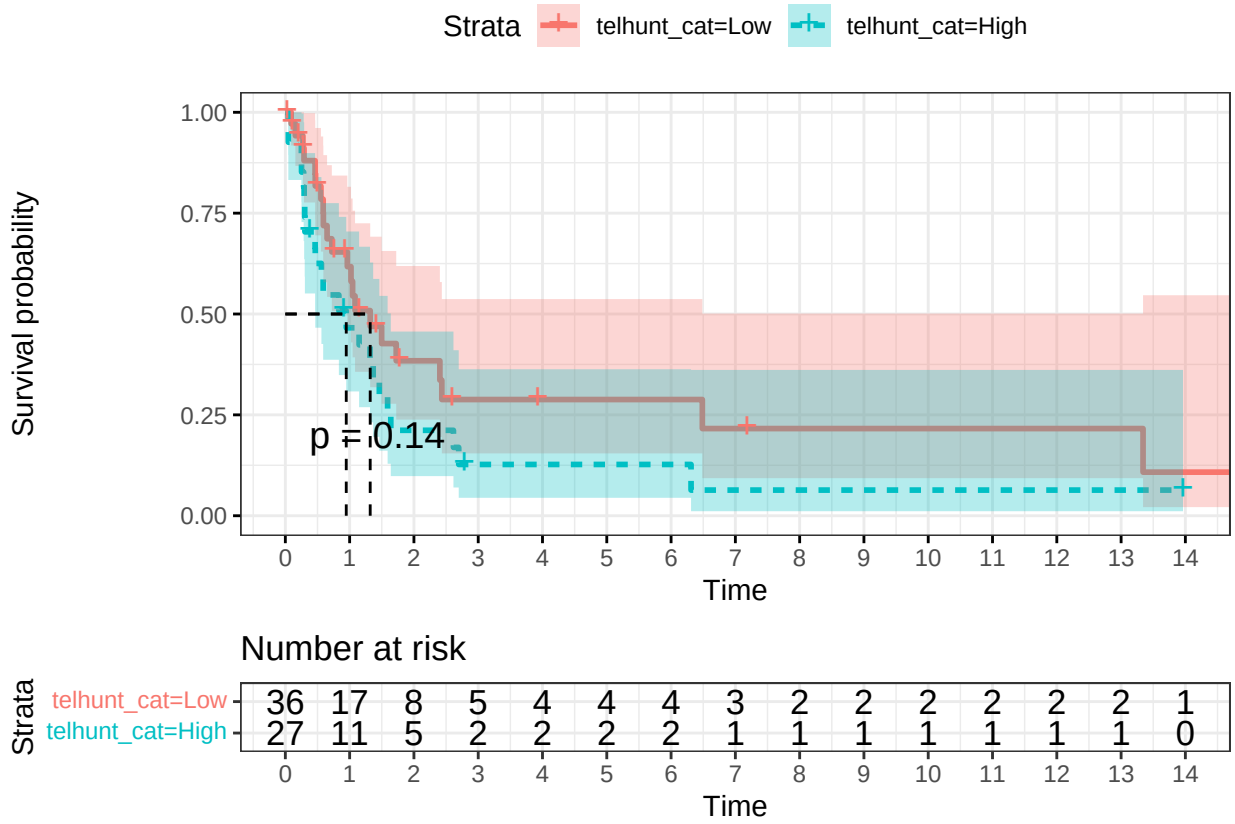


C run for HGAT only but use PFS

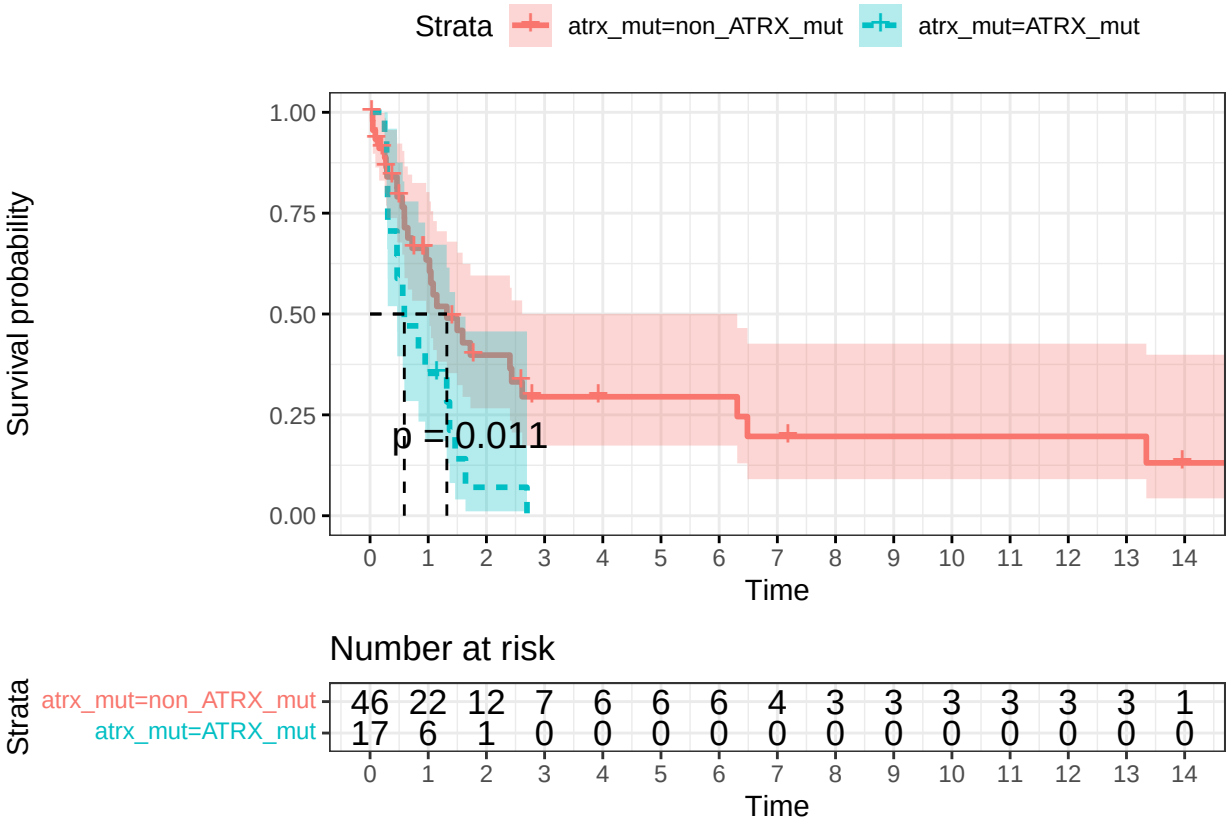
```
for(ind_var in c("dmg_h3k28", "telhunt_cat", "atrx_mut", "phenotype")){
  # define model
  model <- paste0("survival::Surv(time = PFS_years, event = PFS_status) ~ ", ind_var)

  # depending on which variables are used, data used will be different
  data_used <- meta_formatted_hgat

  # run survival analysis
  fit <- survival::survdiff(formula(model),
                            data = data_used)
  # Obtain p value for Chi-Squared stat
  fit$p.value <- pchisq(fit$chisq, df = length(fit$n) - 1, lower = FALSE)

  # save the output
  saveRDS(fit, file.path(output_dir, paste0("log_rank_survival_per_", ind_var, "_pfs_only_hgat.RDS")))

  # generate plots fit
  fit_plot <- survfit(formula(model), data = data_used)

  # output the plot
  plot_logrank <- survminer::ggsurvplot(fit_plot,
```

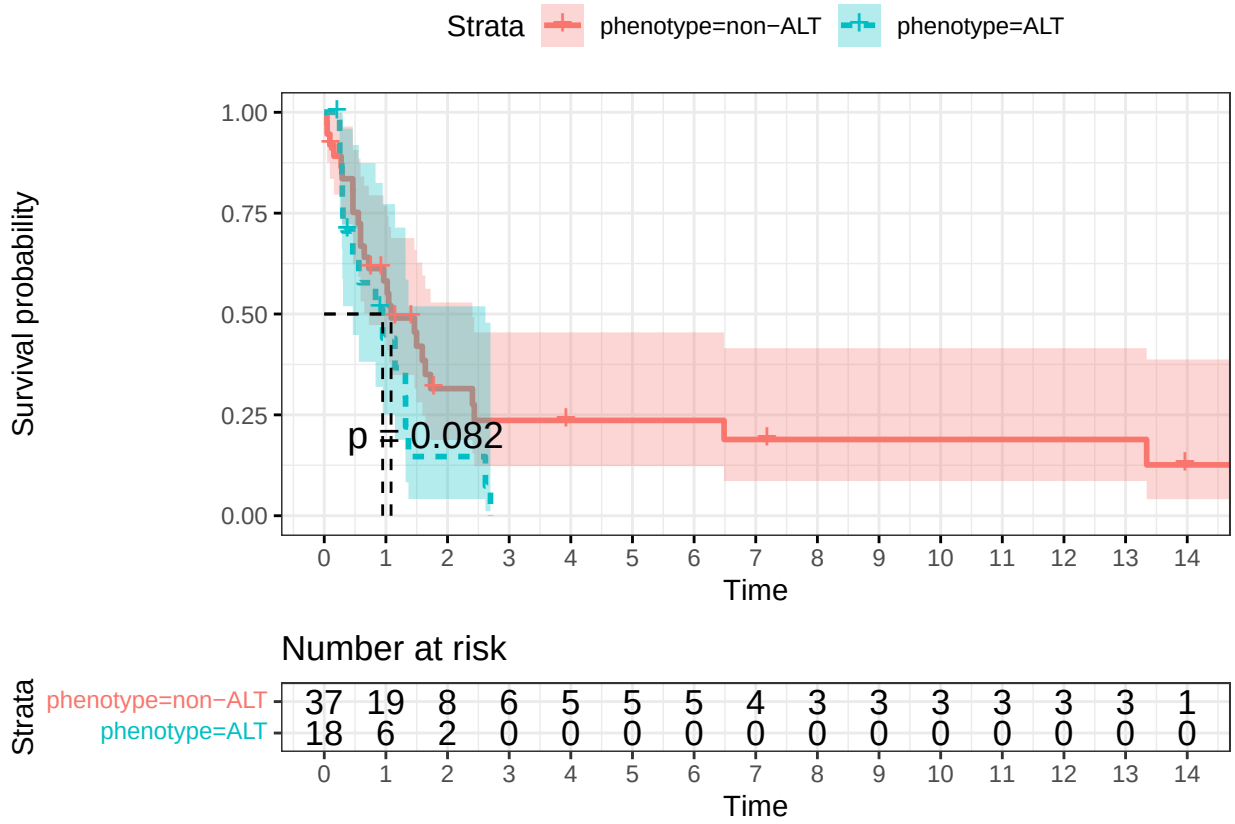
```
                                        data=data_used,
                                        xlim = c(0, 14),
                                        break.time.by = 1,
                                        pval = TRUE,
                                        conf.int = TRUE,
                                        risk.table = TRUE, # Add risk table
                                        linetype = "strata", # Change line type by groups
                                        surv.median.line = "hv", # Specify median survival
                                        ggtheme = theme_bw())

  print(plot_logrank)
  # Make this plot a combined plot
  surv_plot_logrank <- cowplot::plot_grid(plot_logrank[[1]],
                                          plot_logrank[[2]],
                                          nrow = 2,
                                          rel_heights = c(2.5, 1))
  # Save the plot
  cowplot::save_plot(filename = file.path(plots_dir,
                                          paste0("logrank_survival_by_", ind_var, "_pfs_only_hgat.png")),
                     plot = surv_plot_logrank)


}
```




Strata
telhunt_cat=Low
telhunt_cat=High
Survival probability
1.00
0.75
0.50
0.25
0.00
p = 0.14
0
1
2
3
4
5
6
7
8
9
10
11
12
13
14
Time

Number at risk
Strata
telhunt_cat=Low
telhunt_cat=High
36 17 8 5 4 4 4 3 2 2 2 2 2 2 1
27 11 5 2 2 2 2 1 1 1 1 1 1 1 0
0
1
2
3
4
5
6
7
8
9
10
11
12
13
14
Time


Strata
atrx_mut=non_ATRX_mut
atrx_mut=ATRX_mut
Survival probability
1.00
0.75
0.50
0.25
0.00
p = 0.011
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14
Time
Number at risk
Strata
atrx_mut=non_ATRX_mut
atrx_mut=ATRX_mut
46 22 12 7 6 6 6 4 3 3 3 3 3 3 1
17 6 1 0 0 0 0 0 0 0 0 0 0 0 0
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14
Time

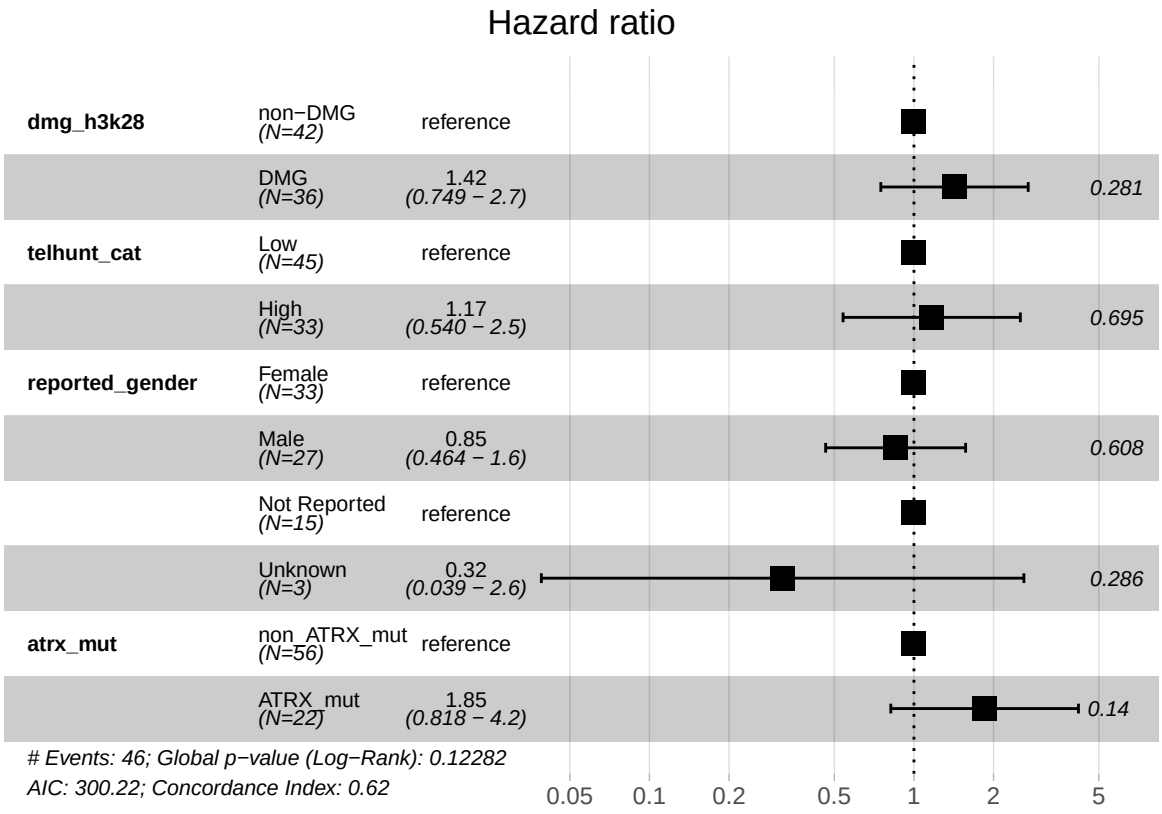


Multivariate analysis

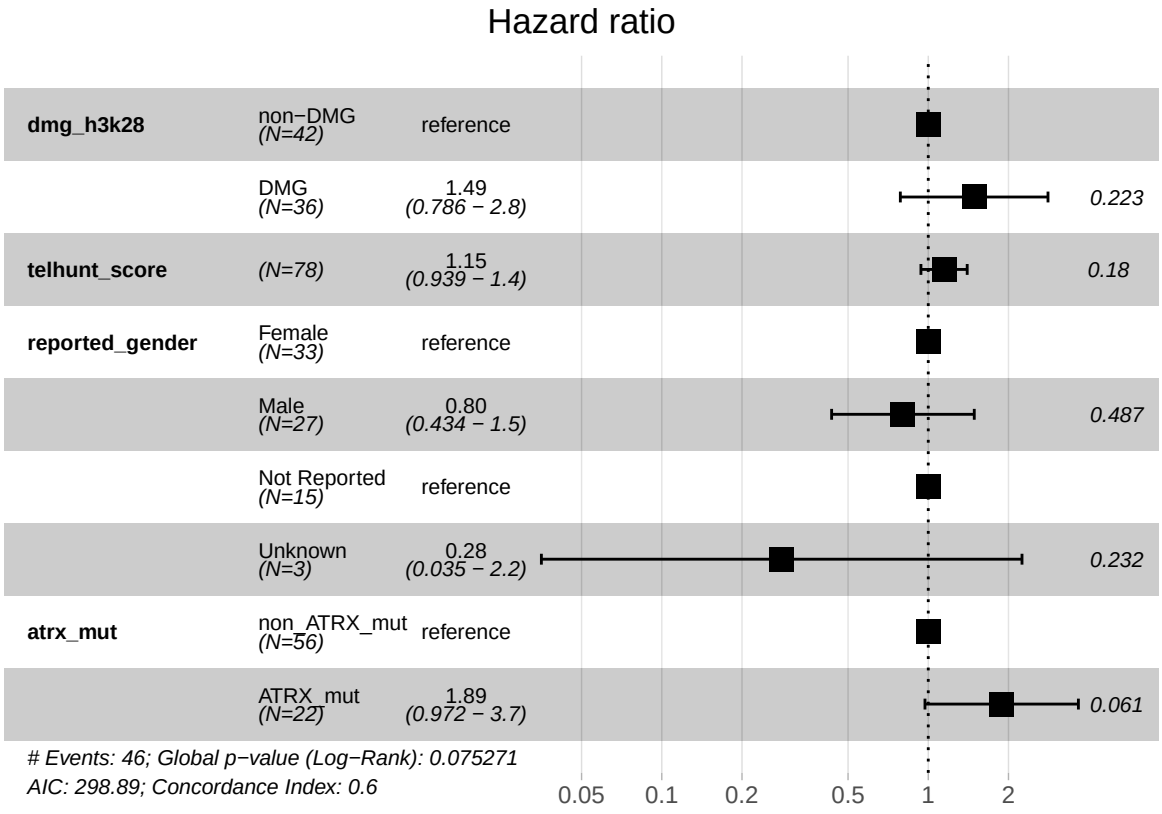
```
# define multi-variates that we are using for analyzing survival
list_of_variates <- c("dmg_h3k28+telhunt_cat+reported_gender+atrx_mut",
                      "dmg_h3k28+telhunt_score+reported_gender+atrx_mut",
                      "dmg_h3k28+phenotype+reported_gender+atrx_mut")

# define model
for (ind_var in list_of_variates){
  model <- paste0("survival::Surv(time = PFS_years, event = PFS_status) ~ ", ind_var)

  # depending on which variables are used, data used will be different
  data_used <- meta_formatted_hgat

  fit <- survival::coxph(
        formula(model),
        data = data_used
      )
  # generate output
  table <- broom::tidy(fit)

  # Save the table data in a TSV
  readr::write_tsv(table, file.path(output_dir, paste0("cox_reg_results_per_", ind_var, "_pfs_only_hgat
```

```
  print(table)

  # printout the plot
  forest_coxph <- survminer::ggforest(fit, data = data_used)
  print(forest_coxph)

}
```

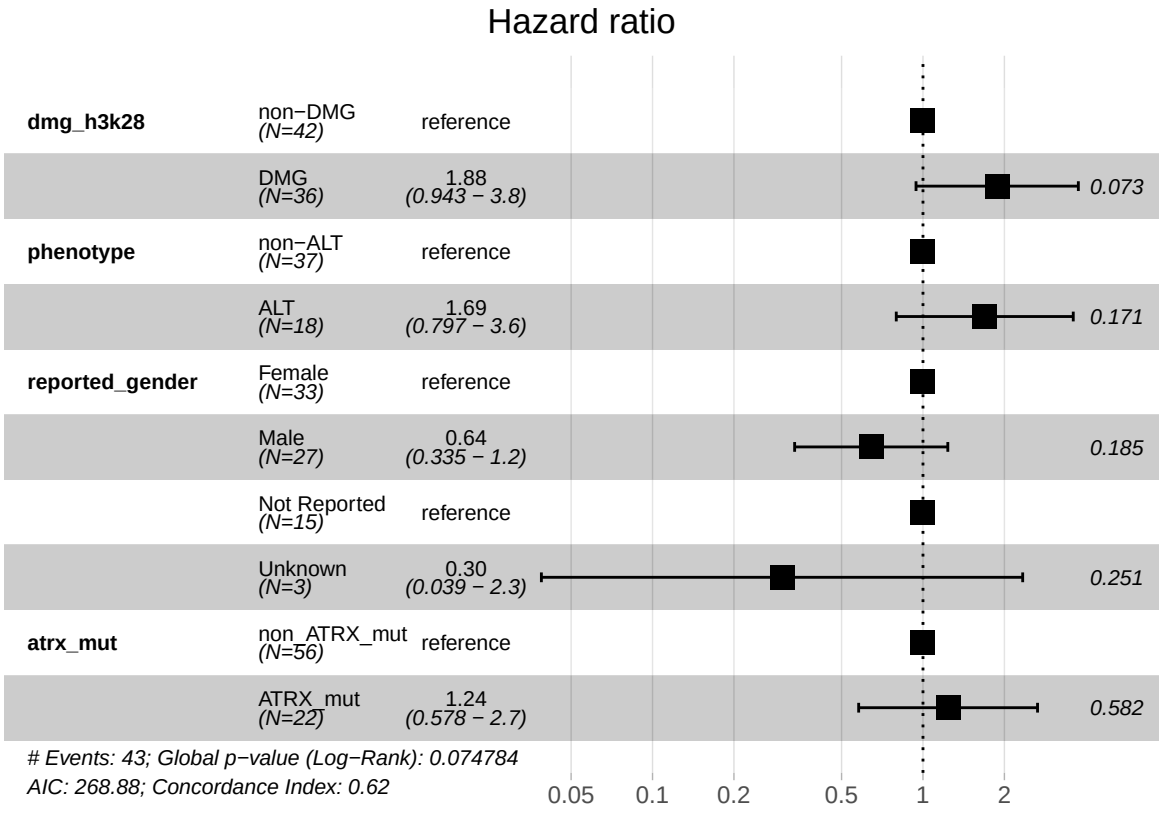
```
## # A tibble: 5 x 5
##   term                    estimate std.error statistic p.value
##   <chr>                      <dbl>     <dbl>     <dbl>   <dbl>
## 1 dmg_h3k28DMG               0.353     0.327     1.08    0.281
## 2 telhunt_catHigh            0.155     0.394     0.393   0.695
## 3 reported_genderMale       -0.159     0.311    -0.513   0.608
## 4 reported_genderUnknown    -1.14      1.07     -1.07    0.286
## 5 atrx_mutATRX_mut           0.615     0.417     1.48    0.140
```




```
## # A tibble: 5 x 5
##   term                    estimate std.error statistic p.value
##   <chr>                      <dbl>     <dbl>     <dbl>   <dbl>
## 1 dmg_h3k28DMG               0.397     0.325     1.22    0.223
## 2 telhunt_score              0.137     0.102     1.34    0.180
## 3 reported_genderMale       -0.219     0.314    -0.696   0.487
## 4 reported_genderUnknown    -1.27      1.06     -1.20    0.232
## 5 atrx_mutATRX_mut           0.635     0.338     1.88    0.0606
```




```
## # A tibble: 5 x 5
##   term                    estimate std.error statistic p.value
##   <chr>                      <dbl>     <dbl>     <dbl>   <dbl>
## 1 dmg_h3k28DMG               0.632     0.353     1.79   0.0731
## 2 phenotypeALT               0.526     0.384     1.37   0.171
## 3 reported_genderMale       -0.441     0.333    -1.32   0.185
## 4 reported_genderUnknown    -1.20      1.05     -1.15   0.251
## 5 atrx_mutATRX_mut           0.214     0.389     0.551  0.582
```


Hazard ratio
dmg_h3k28
non−DMG (N=42) reference
DMG (N=36) 1.88 (0.943 − 3.8) 0.073
phenotype
non−ALT (N=37) reference
ALT (N=18) 1.69 (0.797 − 3.6) 0.171
reported_gender
Female (N=33) reference
Male (N=27) 0.64 (0.335 − 1.2) 0.185
Not Reported (N=15) reference
Unknown (N=3) 0.30 (0.039 − 2.3) 0.251
atrx_mut
non_ATRX_mut (N=56) reference
ATRX_mut (N=22) 1.24 (0.578 − 2.7) 0.582
Events: 43; Global p−value (Log−Rank): 0.074784
AIC: 268.88; Concordance Index: 0.62
0.05
0.1
0.2
0.5
1
2