

Demo

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```

library(tidyverse)
library(survival)
library(survminer)

by_celltype <- veteran %>%
  nest_by(celltype) %>%
  mutate(model = list(survfit(Surv(time, status) ~ trt, data = data)),
         name = str_glue("Survival curve by treatmeant for celltype: {celltype}"),
         plot = list(ggsurvplot(model, data)))

all_plots <- as.list(by_celltype$plot)
names(all_plots) <- by_celltype$name

for(plot in names(all_plots)){
  print(all_plots[[plot]])
  cat('\n\n')
}

```

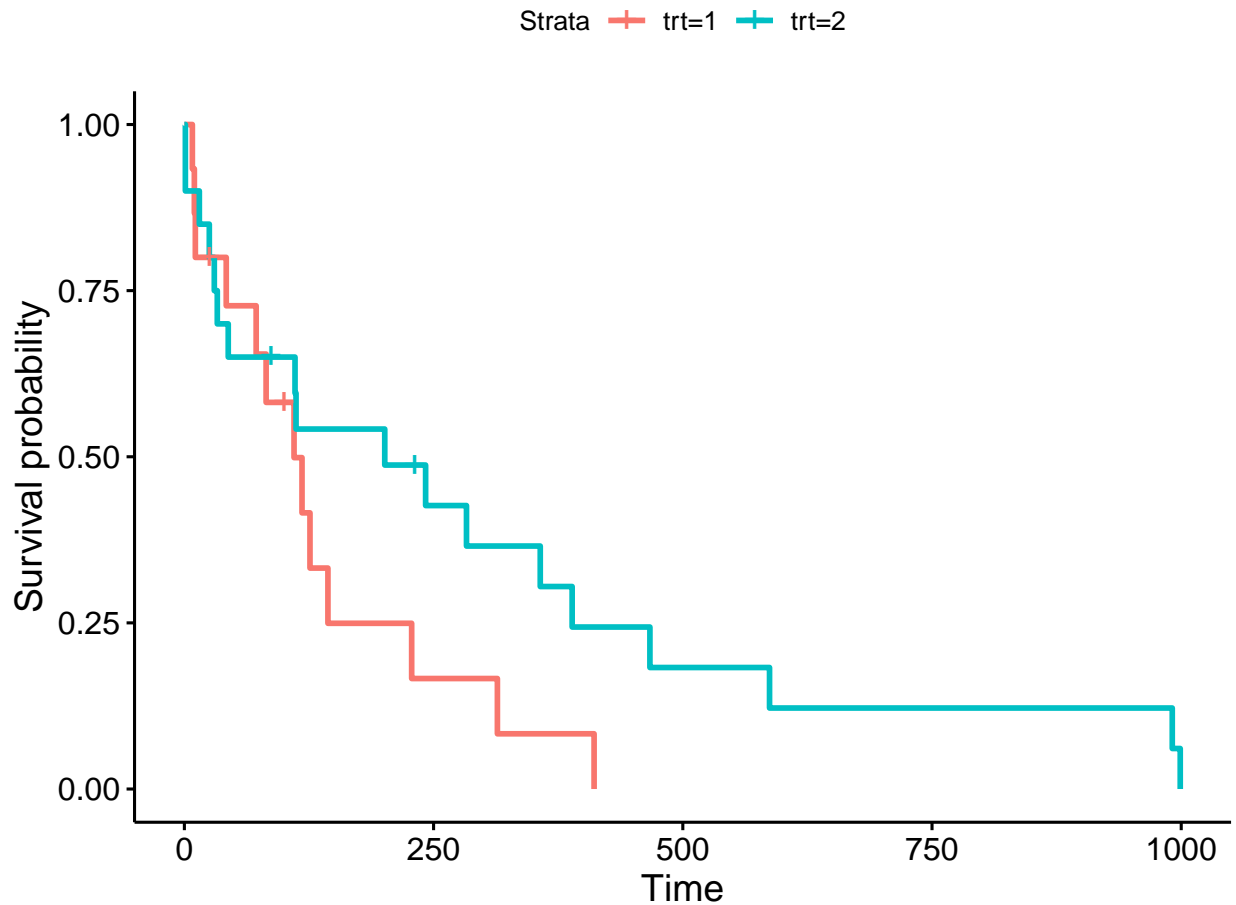


Figure 1: Survival curve by treatmeant for celltype: squamous

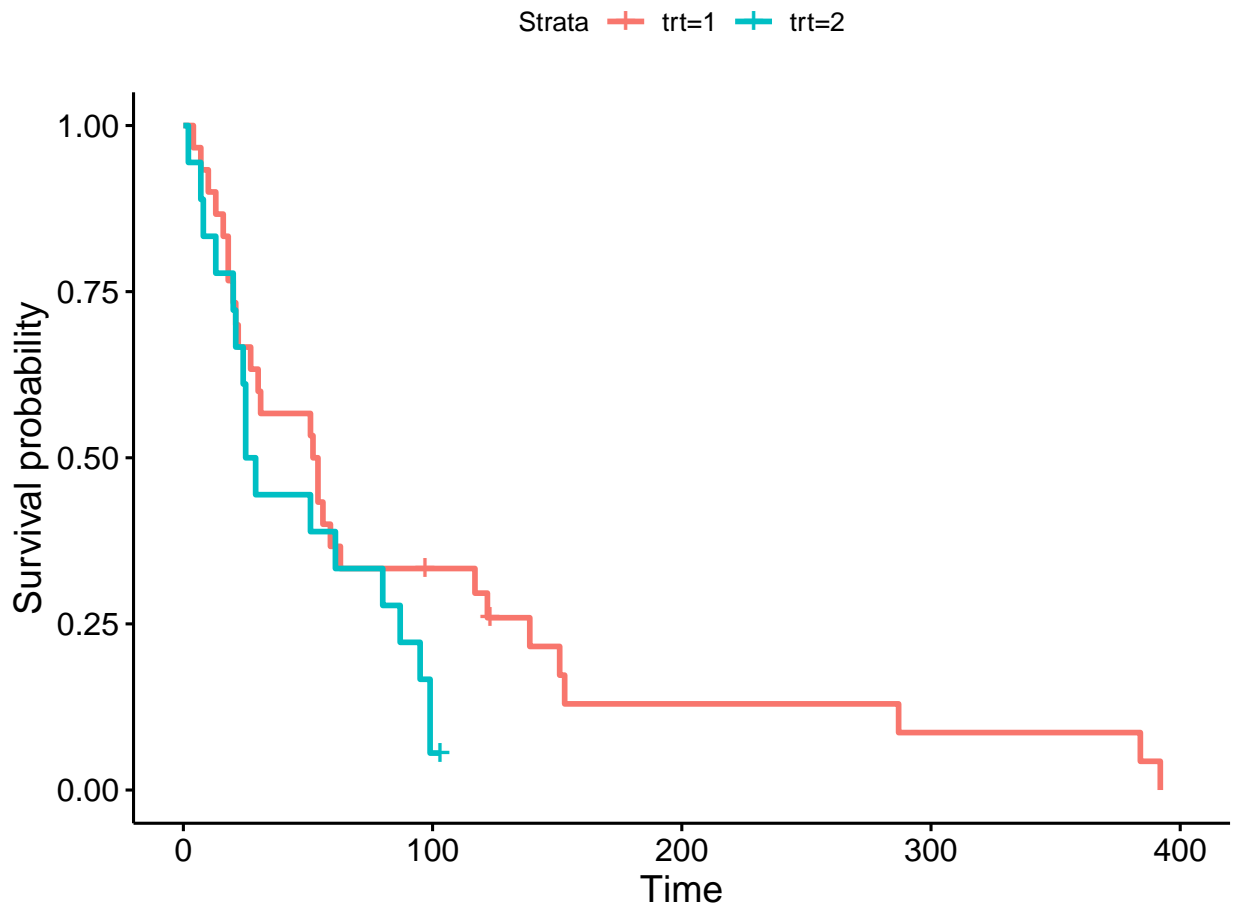


Figure 2: Survival curve by treatment for celltype: smallcell

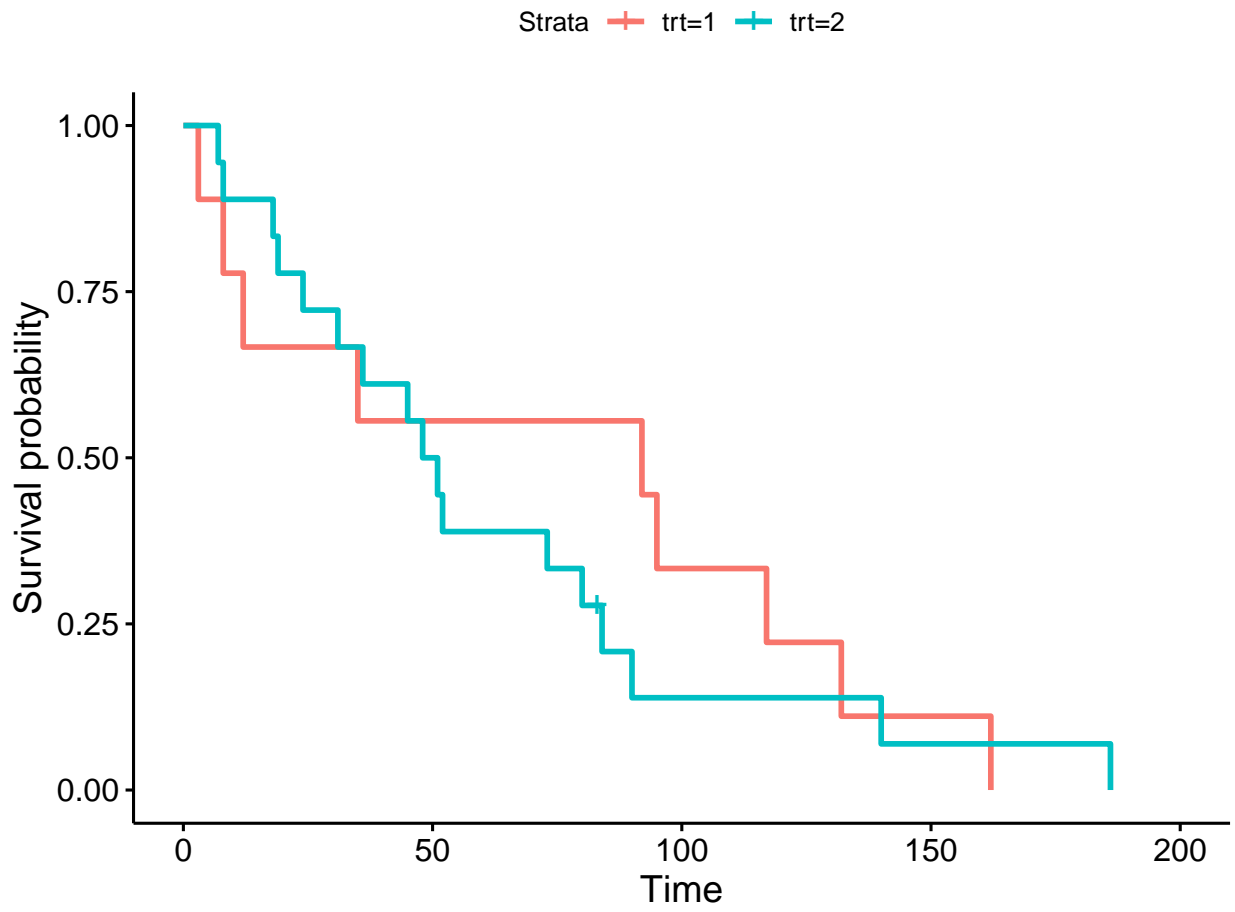


Figure 3: Survival curve by treatment for celltype: adeno

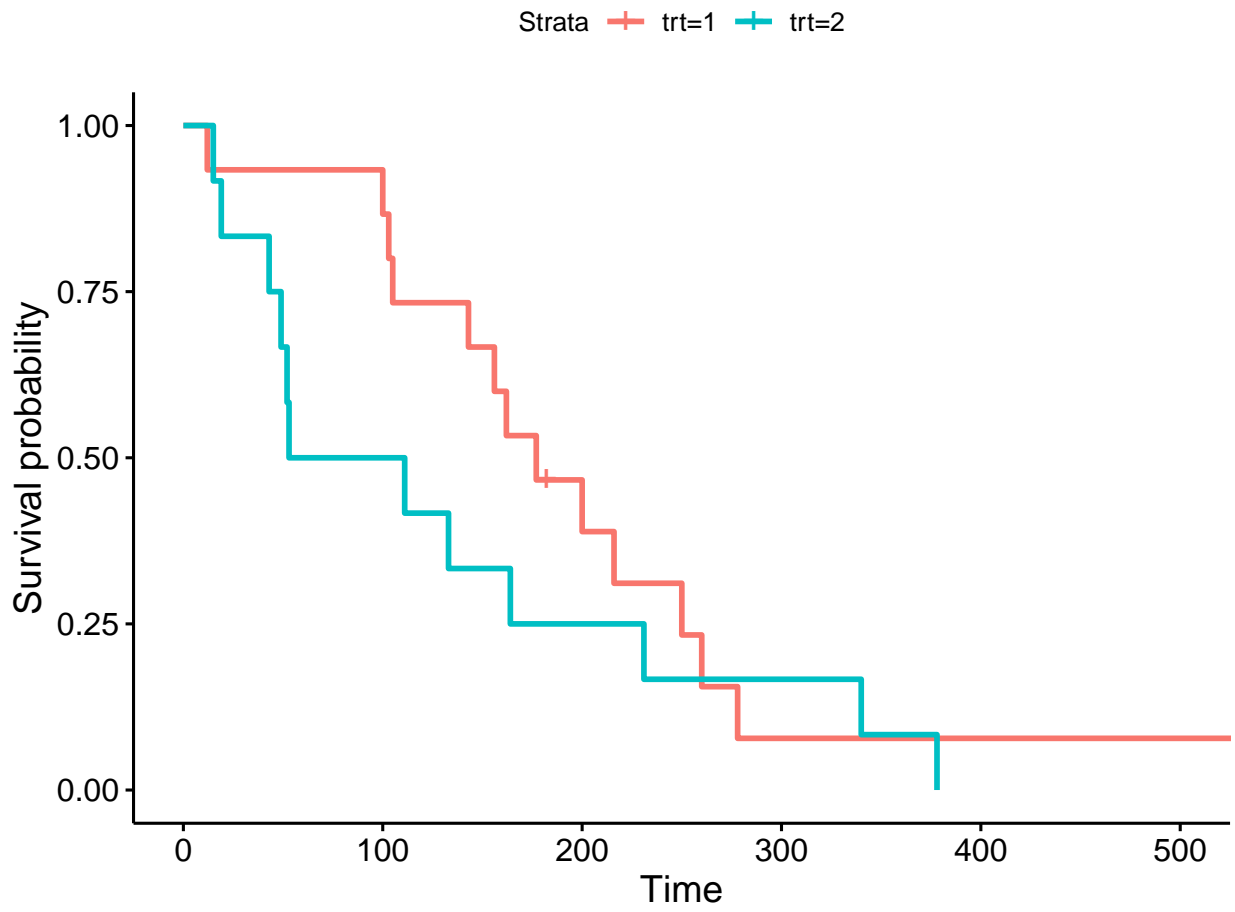


Figure 4: Survival curve by treatment for celltype: large