

Coral survivorship under nutrients and heat stress

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General project set-up

```
# Load all libraries and sources required to run the script
library(tidyverse)
library(ggthemes)
library(survival)
library(survminer)

# Default ggplot settings

Fill.colour<-c("black", "gray70", "gray35")

ggthe_bw<-theme(plot.background=element_blank(),
  panel.grid.major.y = element_blank(),
  panel.grid.major.x = element_blank(),
  panel.grid.minor.x = element_blank(),
  panel.grid.minor.y = element_blank(),
  legend.box.background = element_rect(),
  panel.background =element_rect(fill = NA, color = "black")
```

```
)+
theme_bw()
```

Acropora cervicornis

Import data

```
# Acer data
Survival.data<-read.csv("Data/Acer_Mortality.csv", header = TRUE)
summary(Survival.data)
```

```
##      Fragment      Treatment  Replicate      Date      Time_Point
## Ac_101 : 1    Ambient:39    R1:63      03/08/2018:37    T23      :37
## Ac_102 : 1      N      :41    R2:57      02/05/2018:25    T14      :25
## Ac_103 : 1    N_P      :40              03/05/2018:16    T22      :16
## Ac_104 : 1              02/19/2018:11    T18      :11
## Ac_105 : 1              03/01/2018: 9    T21      : 9
## Ac_106 : 1              02/15/2018: 8    T17      : 8
## (Other):114          (Other)  :14    (Other):14
##      Phase      Genotype      Gen_Treat  Days_Experiment
## Heat      :89    G_07:26    Ac_48_Ambient:10    Min.      : 65.00
## Nutrients:30    G_08: 8    Ac_62_N      :10    1st Qu.: 87.25
## Ramping   : 1    G_31:16    Ac_62_N_P    :10    Median   :106.00
##              G_48:28    Ac_07_Ambient: 9    Mean      : 99.90
##              G_50:13    Ac_07_N      : 9    3rd Qu.:113.00
##              G_62:29    Ac_48_N      : 9    Max.      :113.00
##              (Other)    :63
## Days_Survivor  Fu.time_tot  Fu.stat_tot  Fu.time_texp
## Min.      :179.0    Min.      :179.0    Min.      :0.0000    Min.      : 65.00
## 1st Qu.:201.2    1st Qu.:201.2    1st Qu.:0.0000    1st Qu.: 87.25
## Median :220.0    Median :220.0    Median :0.0000    Median :106.00
## Mean      :213.9    Mean      :213.9    Mean      :0.4833    Mean      : 99.90
## 3rd Qu.:227.0    3rd Qu.:227.0    3rd Qu.:1.0000    3rd Qu.:113.00
## Max.      :227.0    Max.      :227.0    Max.      :1.0000    Max.      :113.00
##
## Fu.stat_exp
## Min.      :0.0000
## 1st Qu.:0.0000
## Median :0.0000
## Mean      :0.4833
## 3rd Qu.:1.0000
## Max.      :1.0000
##
summary(Survival.data$Genotype)
```

```
## G_07 G_08 G_31 G_48 G_50 G_62
##   26   8   16   28   13   29

Survival.data$Genotype<-factor(Survival.data$Genotype,
                               levels=c("G_48", "G_62", "G_31", "G_08", "G_07", "G_50"))
summary(Survival.data$Genotype)
```

```
## G_48 G_62 G_31 G_08 G_07 G_50
## 28 29 16 8 26 13
```

Create survival object

```
## Add survival object (Fit survival data using the Kaplan-Meier method)
surv_object <- Surv(time = Survival.data$Fu.time_texp, event = Survival.data$Fu.stat_exp)
surv_object
```

```
## [1] 113+ 113+ 113+ 82+ 113+ 113+ 113+ 113+ 82+ 113+ 113+ 82+ 113+ 113+
## [15] 113+ 113+ 113+ 113+ 82+ 113+ 113+ 113+ 113+ 113+ 113+ 82+ 113+ 113+
## [29] 113+ 113+ 113+ 113+ 82+ 113+ 113+ 113+ 113+ 113+ 82+ 89 96 92
## [43] 82+ 92 71 96 82+ 96 92 92 82+ 99 82+ 103 99 82+
## [57] 103 110 82+ 110 110 110 82+ 110 106 106 92 76 71 71
## [71] 110 110 106 110 82+ 103 106 82+ 110 106 99 96 96 82+
## [85] 92 92 82+ 96 96 99 92 96 82+ 106 113+ 103 110 110
## [99] 106 82+ 106 82+ 113+ 110 113+ 96 96 65 96 82+ 106 110
## [113] 82+ 110 110 82+ 113+ 82+ 113+ 110
```

Nutrient treatment effect (A, N, N+P)

Figure 2 (1st panel)

```
# Only treatment model
# Kaplan-Meier estimator. The "log-log" confidence interval is preferred.
fit1 <- survfit(surv_object ~ Treatment, data = Survival.data)
summary(fit1)
```

```
## Call: survfit(formula = surv_object ~ Treatment, data = Survival.data)
```

```
##
```

```
## Treatment=Ambient
```

```
## time n.risk n.event survival std.err lower 95% CI upper 95% CI
```

```
##
```

```
## Treatment=N
```

```
## time n.risk n.event survival std.err lower 95% CI upper 95% CI
```

```
## 71 41 3 0.927 0.0407 0.850 1.000
```

```
## 76 38 1 0.902 0.0463 0.816 0.998
```

```
## 89 28 1 0.870 0.0548 0.769 0.984
```

```
## 92 27 5 0.709 0.0789 0.570 0.882
```

```
## 96 22 3 0.612 0.0856 0.466 0.805
```

```
## 99 19 2 0.548 0.0879 0.400 0.750
```

```
## 103 17 3 0.451 0.0884 0.307 0.662
```

```
## 106 14 5 0.290 0.0810 0.168 0.502
```

```
## 110 9 9 0.000 NaN NA NA
```

```
##
```

```
## Treatment=N_P
```

```
## time n.risk n.event survival std.err lower 95% CI upper 95% CI
```

```
## 65 40 1 0.975 0.0247 0.9278 1.000
```

```
## 92 30 3 0.877 0.0578 0.7712 0.999
```

```
## 96 27 8 0.617 0.0872 0.4682 0.814
```

```
## 99 19 2 0.552 0.0893 0.4025 0.758
```

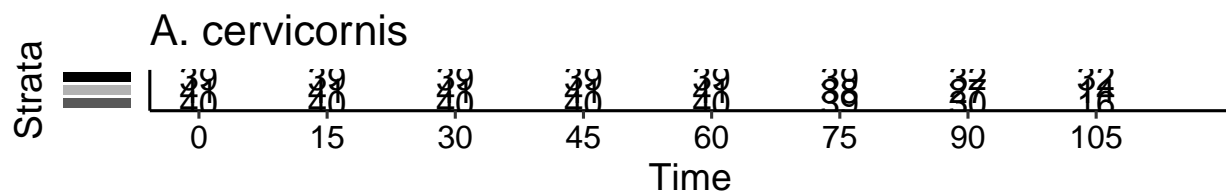
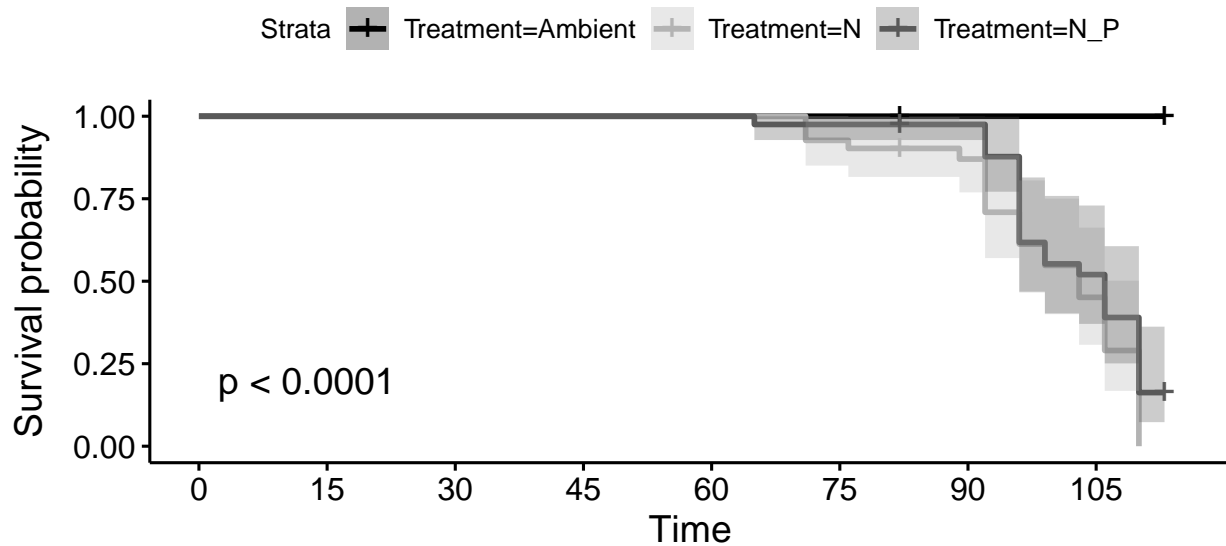
```
## 103 17 1 0.520 0.0898 0.3707 0.729
```

```
##      106      16      4      0.390 0.0878      0.2509      0.606
##      110      12      7      0.163 0.0665      0.0729      0.362
```

```
#coxfitAc <- coxph(surv_object ~ Treatment, data = Survival.data)
#summary(coxfitAc)

# Plot the survival model
Ac_Treatment_Only<-ggsurvplot(fit1, data = Survival.data, pval = TRUE,
                             conf.int = T, risk.table=T, palette=Fill.colour,
                             break.time.by=15, xlim=c(0,115), risk.table.y.text = FALSE,
                             risk.table.title="Number of fragments at risk") + ggtitle("A. cervicornis")
Ac_Treatment_Only
```

A. cervicornis



```
Acer.Probabilities<-Ac_Treatment_Only$data.survplot
```

Nutrient treatment effect (Compare N vs N+P)

```
# Data
Survival.data2<-Survival.data[(Survival.data$Treatment!="Ambient"),]
summary(Survival.data2)
```

```
##      Fragment      Treatment      Replicate      Date      Time_Point
## Ac_101 : 1      Ambient: 0      R1:42      02/05/2018:18      T14      :18
## Ac_103 : 1      N      :41      R2:39      03/05/2018:16      T22      :16
## Ac_104 : 1      N_P      :40      02/19/2018:11      T18      :11
## Ac_106 : 1      03/01/2018: 9      T21      : 9
## Ac_107 : 1      02/15/2018: 8      T17      : 8
```

```
## Ac_109 : 1                                03/08/2018: 5   T23      : 5
## (Other):75                                (Other)   :14   (Other):14
##      Phase      Genotype      Gen_Treat  Days_Experiment  Days_Survivor
## Heat      :57    G_48:18    Ac_62_N :10    Min.      : 65.00    Min.      :179.0
## Nutrients:23    G_62:20    Ac_62_N_P:10    1st Qu.: 82.00    1st Qu.:196.0
## Ramping   : 1    G_31:11    Ac_07_N : 9    Median : 96.00    Median :210.0
##           G_08: 6    Ac_48_N : 9    Mean   : 96.27    Mean   :210.3
##           G_07:17    Ac_48_N_P: 9    3rd Qu.:110.00    3rd Qu.:224.0
##           G_50: 9    Ac_07_N_P: 8    Max.   :113.00    Max.   :227.0
##           (Other) :26
## Fu.time_tot  Fu.stat_tot  Fu.time_texp  Fu.stat_exp
## Min.      :179.0    Min.      :0.000    Min.      : 65.00    Min.      :0.000
## 1st Qu.:196.0    1st Qu.:0.000    1st Qu.: 82.00    1st Qu.:0.000
## Median :210.0    Median :1.000    Median : 96.00    Median :1.000
## Mean   :210.3    Mean   :0.716    Mean   : 96.27    Mean   :0.716
## 3rd Qu.:224.0    3rd Qu.:1.000    3rd Qu.:110.00    3rd Qu.:1.000
## Max.   :227.0    Max.   :1.000    Max.   :113.00    Max.   :1.000
##
```

```
summary(Survival.data2$Genotype)
```

```
## G_48 G_62 G_31 G_08 G_07 G_50
##   18  20  11   6  17   9
```

```
Survival.data2$Genotype<-factor(Survival.data2$Genotype,
                                levels=c("G_48", "G_62", "G_31", "G_08", "G_07", "G_50"))
summary(Survival.data2$Genotype)
```

```
## G_48 G_62 G_31 G_08 G_07 G_50
##   18  20  11   6  17   9
```

```
summary(Survival.data2$Treatment)
```

```
## Ambient      N      N_P
##         0     41     40
```

```
Survival.data2$Treatment<-factor(Survival.data2$Treatment,
                                  levels=c("N", "N_P"))
```

```
## Add survival object (Fit survival data using the Kaplan-Meier method)
surv_object2 <- Surv(time = Survival.data2$Fu.time_texp,
                     event = Survival.data2$Fu.stat_exp)

surv_object2
```

```
## [1] 89 96 92 82+ 92 71 96 82+ 96 92 92 82+ 99 82+
## [15] 103 99 82+ 103 110 82+ 110 110 110 82+ 110 106 106 92
## [29] 76 71 71 110 110 106 110 82+ 103 106 82+ 110 106 99
## [43] 96 96 82+ 92 92 82+ 96 96 99 92 96 82+ 106 113+
## [57] 103 110 110 106 82+ 106 82+ 113+ 110 113+ 96 96 65 96
## [71] 82+ 106 110 82+ 110 110 82+ 113+ 82+ 113+ 110
```

```
# Only treatment model
# Kaplan-Meier estimator. The "log-log" confidence interval is preferred.
fit1_2 <- survfit(surv_object2 ~ Treatment, data = Survival.data2)
summary(fit1_2)
```

```
## Call: survfit(formula = surv_object2 ~ Treatment, data = Survival.data2)
##
```

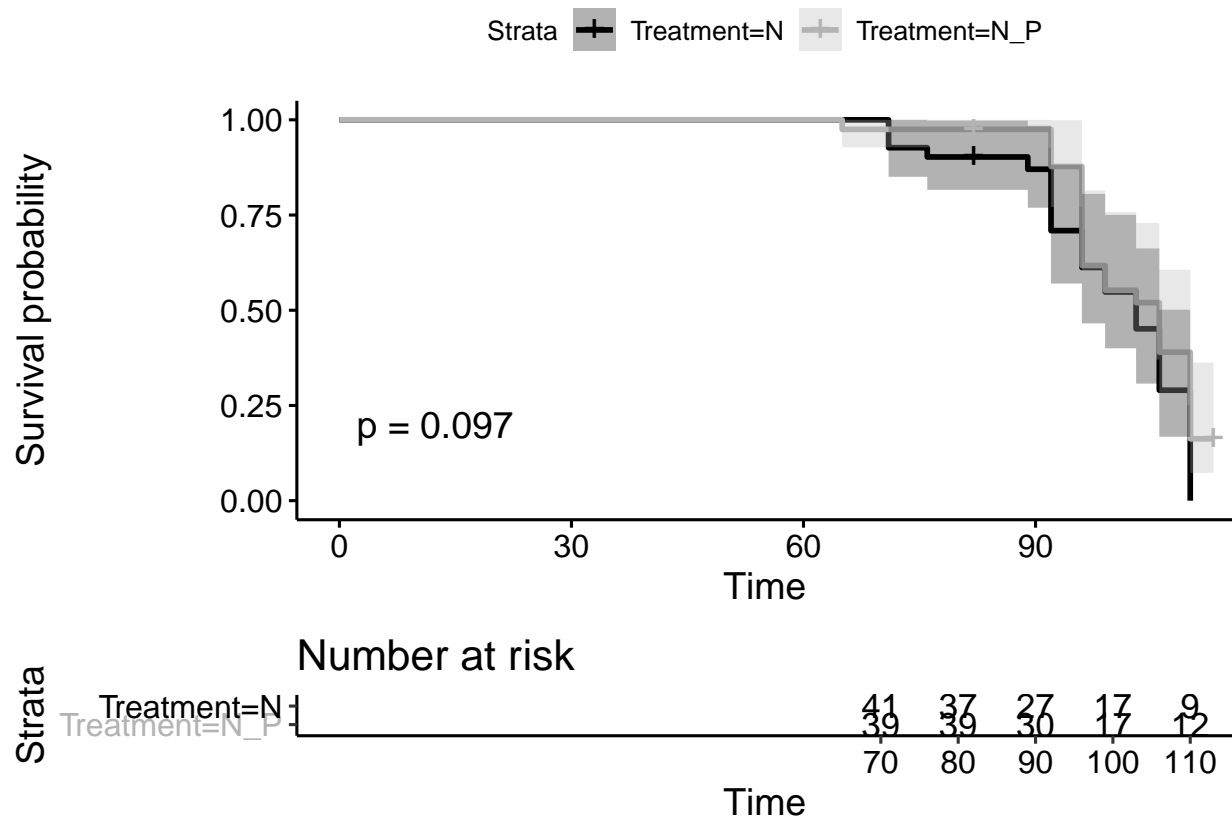
```
##           Treatment=N
##  time n.risk n.event survival std.err lower 95% CI upper 95% CI
##    71    41      3   0.927  0.0407    0.850    1.000
##    76    38      1   0.902  0.0463    0.816    0.998
##    89    28      1   0.870  0.0548    0.769    0.984
##    92    27      5   0.709  0.0789    0.570    0.882
##    96    22      3   0.612  0.0856    0.466    0.805
##    99    19      2   0.548  0.0879    0.400    0.750
##   103    17      3   0.451  0.0884    0.307    0.662
##   106    14      5   0.290  0.0810    0.168    0.502
##   110     9      9   0.000    NaN      NA      NA
##
##           Treatment=N_P
##  time n.risk n.event survival std.err lower 95% CI upper 95% CI
##    65    40      1   0.975  0.0247    0.9278    1.000
##    92    30      3   0.877  0.0578    0.7712    0.999
##    96    27      8   0.617  0.0872    0.4682    0.814
##    99    19      2   0.552  0.0893    0.4025    0.758
##   103    17      1   0.520  0.0898    0.3707    0.729
##   106    16      4   0.390  0.0878    0.2509    0.606
##   110    12      7   0.163  0.0665    0.0729    0.362
```

```
surv_pvalue(fit1_2)
```

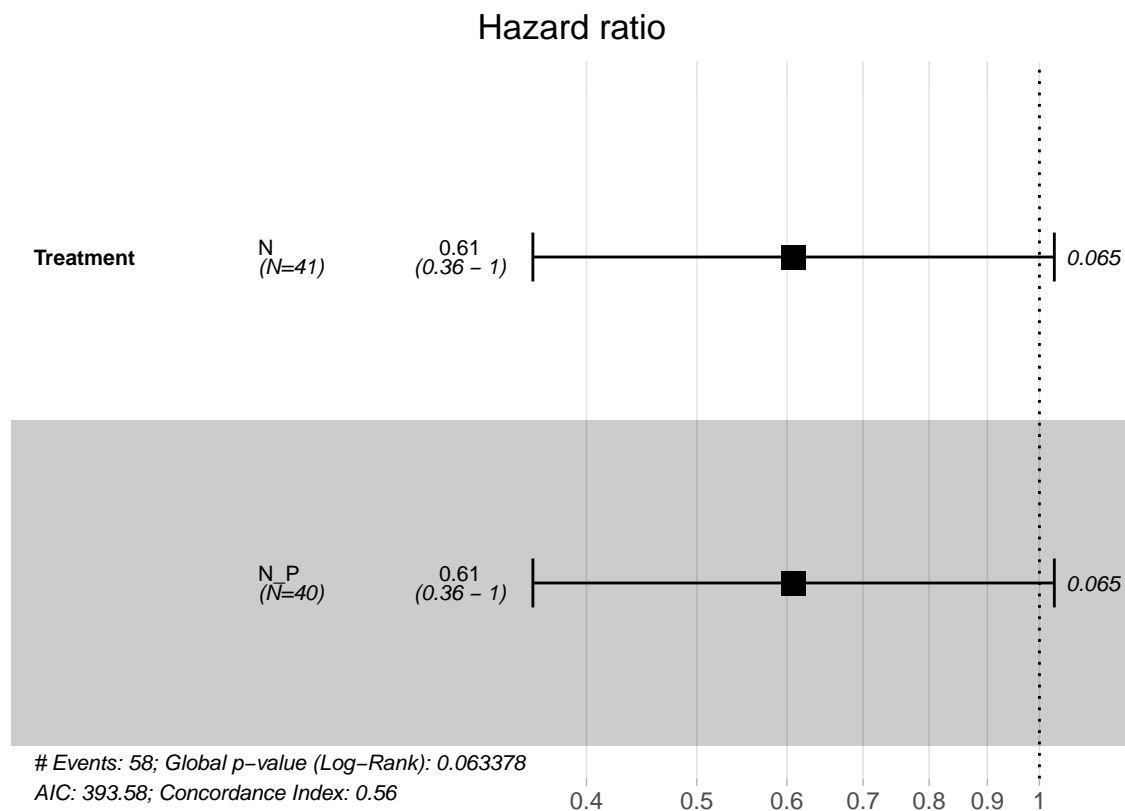
```
##      variable      pval  method  pval.txt
## 1 Treatment 0.09720048 Log-rank p = 0.097
```

```
# Plot the survival model
```

```
N_NP_Only<-ggsurvplot(fit1_2, data = Survival.data2, pval = TRUE,
  conf.int = T, risk.table=T, palette=Fill.colour)
N_NP_Only
```



```
# Hazard ratio
fit.coxph1_2 <- coxph(surv_object2 ~ Treatment, data = Survival.data2)
ggforest(fit.coxph1_2, data = Survival.data2)
```



```
fit.coxph1_2
```

```
## Call:
## coxph(formula = surv_object2 ~ Treatment, data = Survival.data2)
##
##               coef exp(coef) se(coef)      z      p
## TreatmentN_P -0.4973    0.6082   0.2691 -1.848 0.0646
##
## Likelihood ratio test=3.45  on 1 df, p=0.06338
## n= 81, number of events= 58
```

Orbicella faveolata

Import data

```
# Data
Survival.Of.data<-read.csv("Data/Ofav_Mortality.csv", header = TRUE)

summary(Survival.Of.data)
```

Fragment	Colony	Treatment	Replicate	Tre_Gen	Date
Of_20-11: 1	Of_20:18	A :24	R1:36	A_Of_20: 6	2018-02-05:24
Of_20-14: 1	Of_31:18	N :24	R2:36	A_Of_31: 6	2018-04-20:18
Of_20-17: 1	Of_34:18	N+P:24		A_Of_34: 6	2018-03-27:16
Of_20-19: 1	Of_6 :18			A_Of_6 : 6	2018-02-15: 3
Of_20-2 : 1				N_Of_20: 6	2018-02-22: 3
Of_20-21: 1				N_Of_31: 6	2018-03-05: 3


```
## (Other) :66 (Other):36 (Other) : 5
## Days_Experiment Fu.stat_exp Fu.time_texp
## Min. : 82.0 Min. :0.0000 Min. : 82.0
## 1st Qu.: 82.0 1st Qu.:0.0000 1st Qu.: 82.0
## Median :110.0 Median :0.0000 Median :110.0
## Mean :115.3 Mean :0.1806 Mean :100.3
## 3rd Qu.:138.0 3rd Qu.:0.0000 3rd Qu.:113.0
## Max. :156.0 Max. :1.0000 Max. :113.0
##
Survival.Of.data$Genotype<-factor(Survival.Of.data$Colony,
                                  levels = c("Of_34", "Of_20", "Of_6", "Of_31"))
summary(Survival.Of.data$Genotype)

## Of_34 Of_20 Of_6 Of_31
## 18 18 18 18
```

Create survival object

```
## Add survival object (Fit survival data using the Kaplan-Meier method)
surv_object_Of <- Surv(time = Survival.Of.data$Fu.time_texp,
                      event = Survival.Of.data$Fu.stat_exp)
surv_object_Of

## [1] 82+ 113+ 113+ 82+ 113+ 113+ 82+ 110 106 113+ 82+ 113+ 113+ 82+
## [15] 113+ 113+ 82+ 113+ 92 82+ 106 113+ 82+ 113+ 113+ 82+ 113+ 113+
## [29] 113+ 82+ 99 99 82+ 82+ 113+ 113+ 82+ 113+ 113+ 113+ 113+ 82+
## [43] 92 82+ 110 113+ 82+ 113+ 113+ 113+ 82+ 113+ 113+ 82+ 89 82+
## [57] 110 82+ 113+ 113+ 99 113+ 82+ 113+ 82+ 113+ 82+ 92 96 82+
## [71] 113+ 113+
```

Nutrient treatment effect (A, N, N+P)

Figure 2 (2nd panel)

```
# Only treatment model
# Kaplan-Meier estimator. The "log-log" confidence interval is preferred.
fit2_Of <- survfit(surv_object_Of ~ Treatment, data = Survival.Of.data)
summary(fit2_Of)

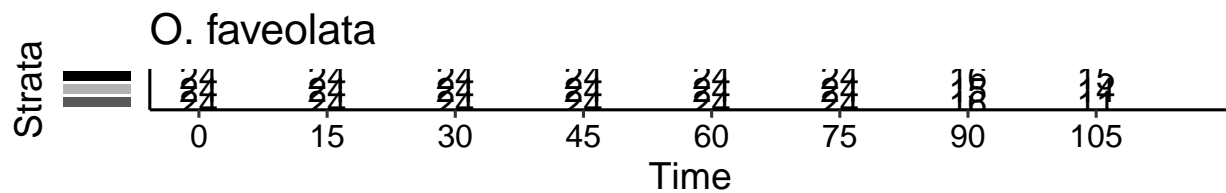
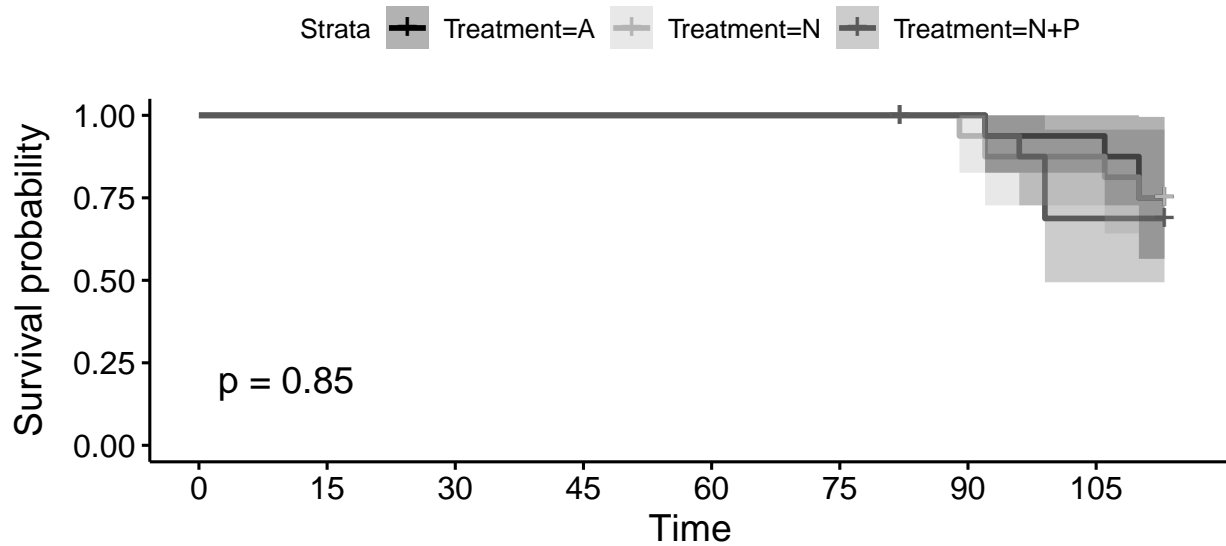
## Call: survfit(formula = surv_object_Of ~ Treatment, data = Survival.Of.data)
##
## Treatment=A
## time n.risk n.event survival std.err lower 95% CI upper 95% CI
## 92 16 1 0.938 0.0605 0.826 1.000
## 106 15 1 0.875 0.0827 0.727 1.000
## 110 14 2 0.750 0.1083 0.565 0.995
##
## Treatment=N
## time n.risk n.event survival std.err lower 95% CI upper 95% CI
## 89 16 1 0.938 0.0605 0.826 1.000
## 92 15 1 0.875 0.0827 0.727 1.000
```

```
##      106      14      1      0.812 0.0976      0.642      1.000
##      110      13      1      0.750 0.1083      0.565      0.995
##
##
##              Treatment=N+P
## time n.risk n.event survival std.err lower 95% CI upper 95% CI
##      92      16      1      0.938 0.0605      0.826      1.000
##      96      15      1      0.875 0.0827      0.727      1.000
##      99      14      3      0.688 0.1159      0.494      0.957
```

```
# Plot the survival model
```

```
Of_Treatment_Only<-ggsurvplot(fit2_Of, data = Survival.Of.data, pval = TRUE,
                              conf.int = T, risk.table=T, palette=Fill.colour,
                              break.time.by=15, xlim=c(0,115), risk.table.y.text = FALSE,
                              risk.table.title="Number of fragments at risk") + ggtitle("O. faveolata")
Of_Treatment_Only
```

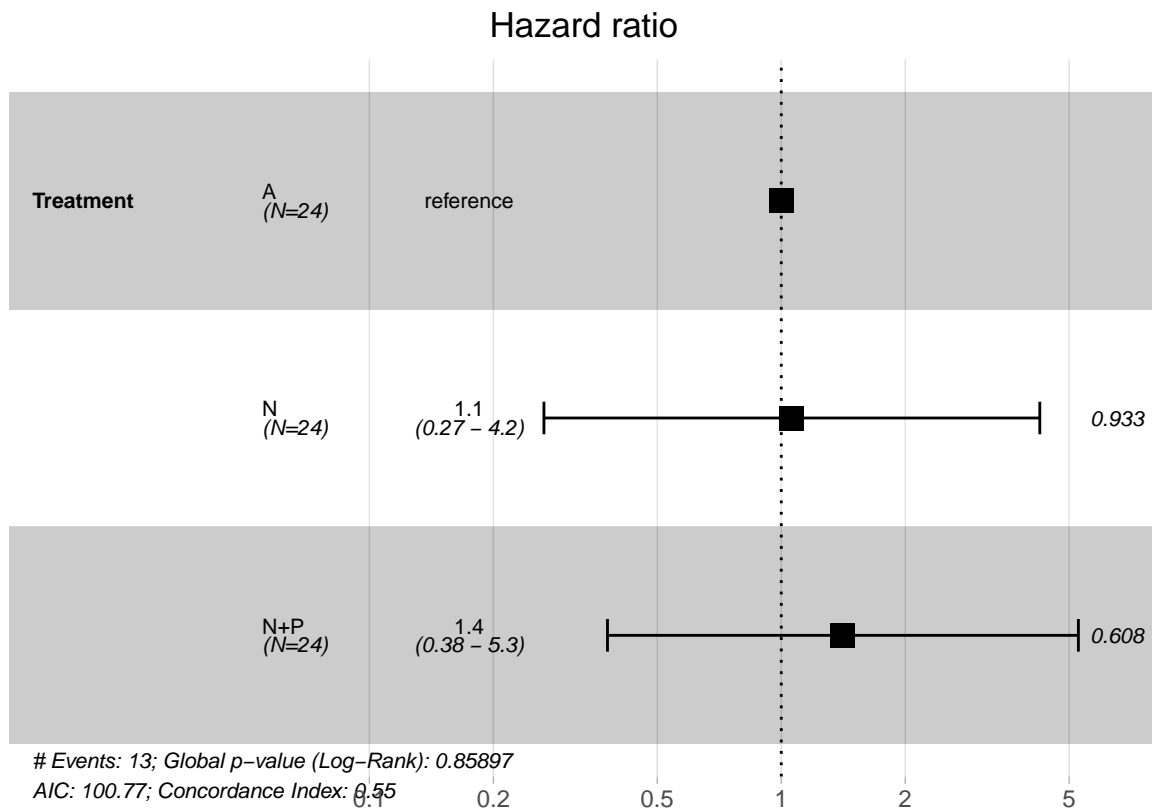
O. faveolata



```
#ggsave("Outputs/Ofav_Surv_Treatment_Of.svg",
#        Of_Treatment_Only$plot, width=4, height=3.5,dpi = 300)
#ggsave("Outputs/Fig_SX4_Surv_Treatment_Of.pdf", print(Treatment_Only),
#        #width=5, height=6,dpi = 300)
```

```
# Hazard ratio
```

```
fit.coxph1_3 <- coxph(surv_object_Of ~ Treatment, data = Survival.Of.data)
ggforest(fit.coxph1_3, data = Survival.Of.data)
```



```
fit.coxph1_3
```

```
## Call:
## coxph(formula = surv_object_Of ~ Treatment, data = Survival.Of.data)
##
##               coef exp(coef) se(coef)      z      p
## TreatmentN  0.05912  1.06091  0.70713  0.084  0.933
## TreatmentN+P 0.34464  1.41148  0.67155  0.513  0.608
##
## Likelihood ratio test=0.3  on 2 df, p=0.859
## n= 72, number of events= 13
```

```
summary(fit.coxph1_3)
```

```
## Call:
## coxph(formula = surv_object_Of ~ Treatment, data = Survival.Of.data)
##
##      n= 72, number of events= 13
##
##               coef exp(coef) se(coef)      z Pr(>|z|)
## TreatmentN  0.05912  1.06091  0.70713  0.084    0.933
## TreatmentN+P 0.34464  1.41148  0.67155  0.513    0.608
##
##               exp(coef) exp(-coef) lower .95 upper .95
## TreatmentN      1.061      0.9426    0.2653    4.242
## TreatmentN+P      1.411      0.7085    0.3785    5.264
##
## Concordance= 0.548  (se = 0.076 )
## Likelihood ratio test= 0.3  on 2 df,  p=0.9
```

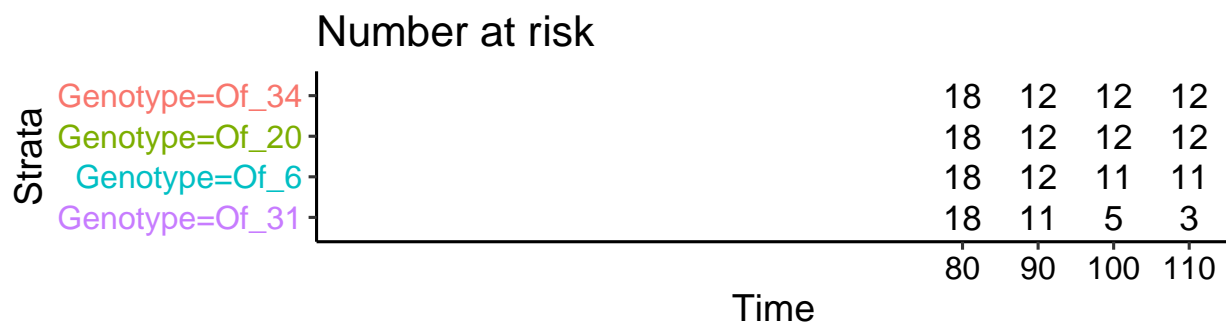
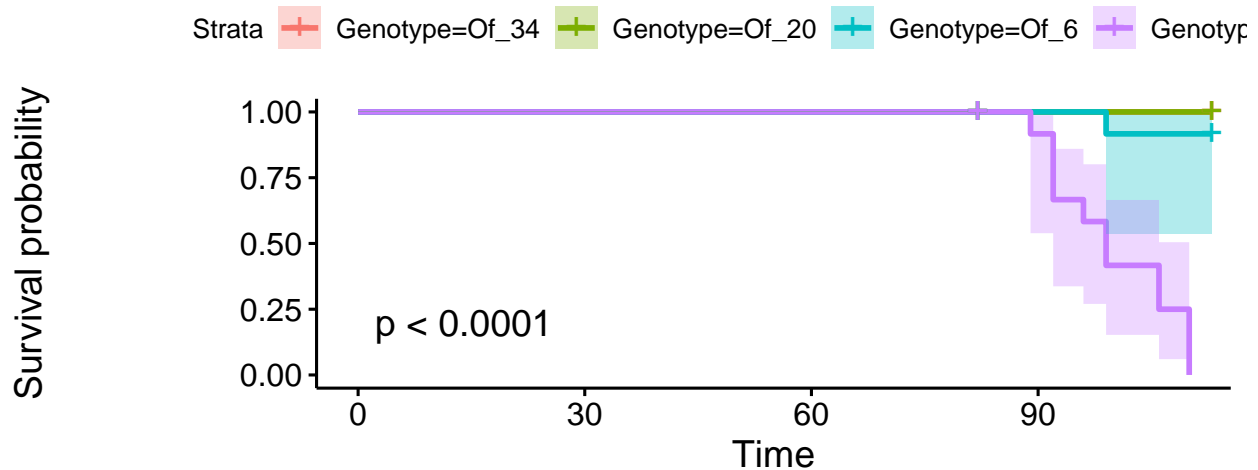
```
## Wald test          = 0.31  on 2 df,   p=0.9
## Score (logrank) test = 0.31  on 2 df,   p=0.9
```

Colony effect (Figure S4)

```
# Only genotype model
# Kaplan-Meier estimator. The "log-log" confidence interval is preferred.
fit3_Of <- survfit(surv_object_Of ~ Genotype, conf.type = "log-log",
                  data = Survival.Of.data)
summary(fit3_Of)

## Call: survfit(formula = surv_object_Of ~ Genotype, data = Survival.Of.data,
##               conf.type = "log-log")
##
##               Genotype=Of_34
##      time n.risk n.event survival std.err lower 95% CI upper 95% CI
##
##               Genotype=Of_20
##      time n.risk n.event survival std.err lower 95% CI upper 95% CI
##
##               Genotype=Of_6
##      time      n.risk      n.event      survival      std.err
##      99.0000      12.0000       1.0000       0.9167       0.0798
## lower 95% CI upper 95% CI
##      0.5390       0.9878
##
##               Genotype=Of_31
##      time n.risk n.event survival std.err lower 95% CI upper 95% CI
##      89    12     1    0.917  0.0798     0.5390     0.988
##      92    11     3    0.667  0.1361     0.3370     0.860
##      96     8     1    0.583  0.1423     0.2701     0.801
##      99     7     2    0.417  0.1423     0.1525     0.665
##     106     5     2    0.250  0.1250     0.0601     0.505
##     110     3     3    0.000    NaN         NA         NA

# Plot the survival model
Genotype_only_OF<-ggsurvplot(fit3_Of, data = Survival.Of.data, pval = TRUE,
                             risk.table=T, tables.height=0.4, conf.int = T, n.risk = TRUE )
Genotype_only_OF
```



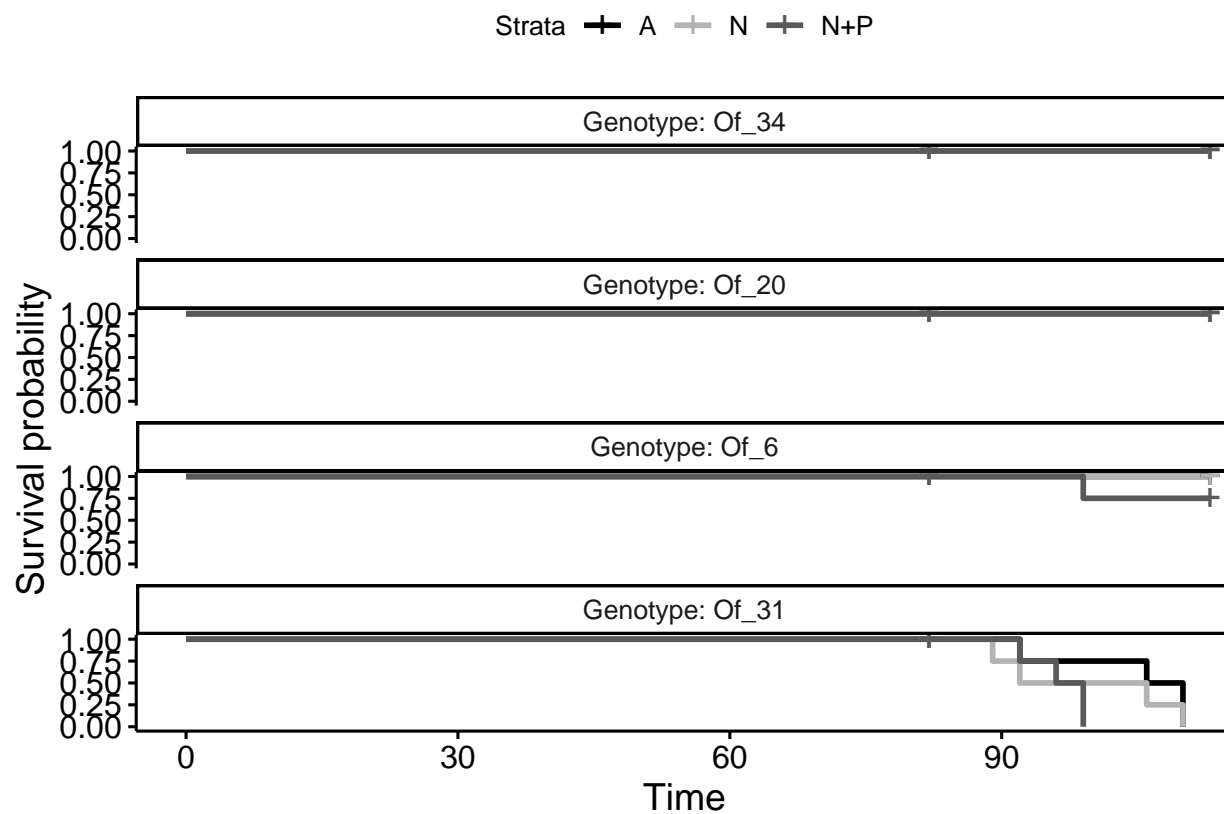
```
Ofav.Probabilities<-Genotype_only_OF$data.survplot
```

```
# Treatment and genotype model 1
# Kaplan-Meier estimator. The "log-log" confidence interval is preferred.
fit4_Of <- survfit(surv_object_Of ~ Genotype + Treatment, data = Survival.Of.data)
summary(fit4_Of)
```

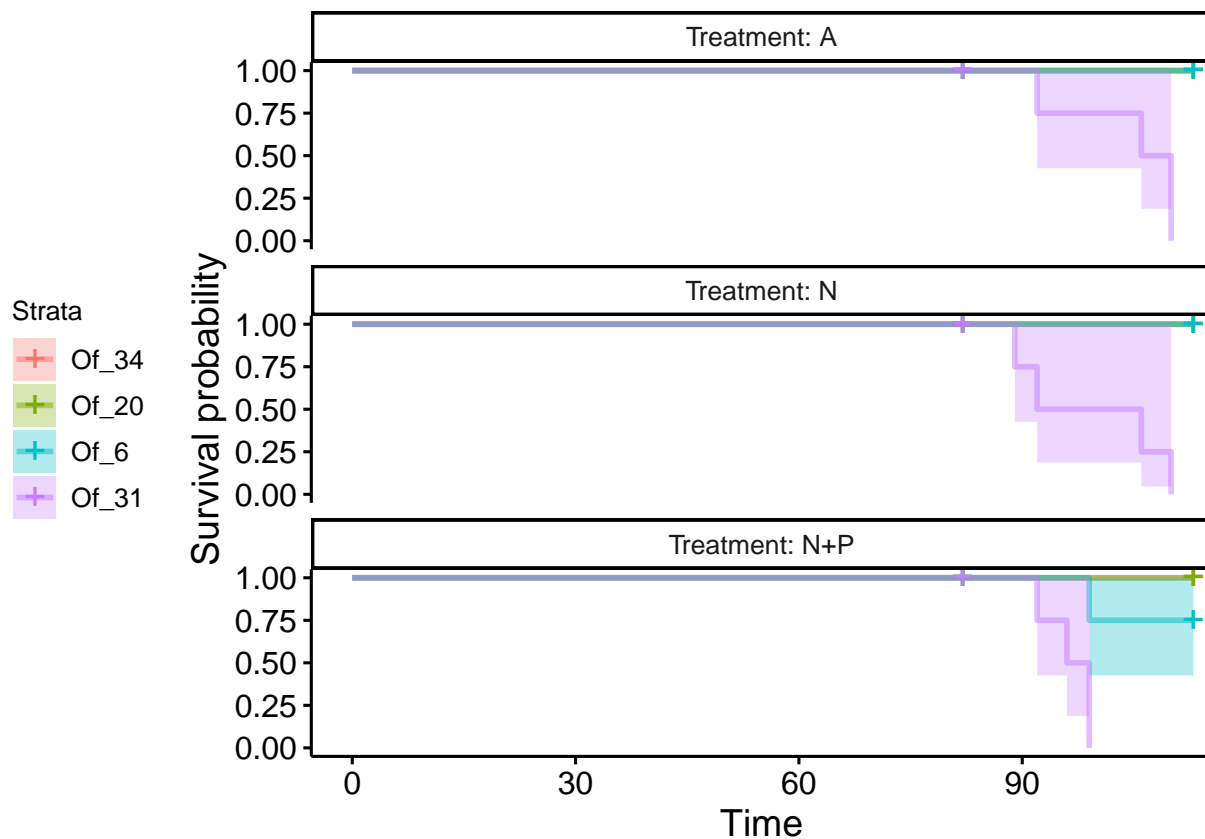
```
## Call: survfit(formula = surv_object_Of ~ Genotype + Treatment, data = Survival.Of.data)
##
##           Genotype=Of_34, Treatment=A
##   time n.risk n.event survival std.err lower 95% CI upper 95% CI
##
##           Genotype=Of_34, Treatment=N
##   time n.risk n.event survival std.err lower 95% CI upper 95% CI
##
##           Genotype=Of_34, Treatment=N+P
##   time n.risk n.event survival std.err lower 95% CI upper 95% CI
##
##           Genotype=Of_20, Treatment=A
##   time n.risk n.event survival std.err lower 95% CI upper 95% CI
##
##           Genotype=Of_20, Treatment=N
##   time n.risk n.event survival std.err lower 95% CI upper 95% CI
##
##           Genotype=Of_20, Treatment=N+P
##   time n.risk n.event survival std.err lower 95% CI upper 95% CI
##
##           Genotype=Of_6, Treatment=A
```

```
##      time n.risk n.event survival std.err lower 95% CI upper 95% CI
##
##      Genotype=Of_6, Treatment=N
##      time n.risk n.event survival std.err lower 95% CI upper 95% CI
##
##      Genotype=Of_6, Treatment=N+P
##      time      n.risk      n.event      survival      std.err
##      99.000      4.000      1.000      0.750      0.217
## lower 95% CI upper 95% CI
##      0.426      1.000
##
##      Genotype=Of_31, Treatment=A
## time n.risk n.event survival std.err lower 95% CI upper 95% CI
##   92     4     1     0.75  0.217     0.426     1
##  106     3     1     0.50  0.250     0.188     1
##  110     2     2     0.00   NaN      NA      NA
##
##      Genotype=Of_31, Treatment=N
## time n.risk n.event survival std.err lower 95% CI upper 95% CI
##   89     4     1     0.75  0.217     0.4259     1
##   92     3     1     0.50  0.250     0.1877     1
##  106     2     1     0.25  0.217     0.0458     1
##  110     1     1     0.00   NaN      NA      NA
##
##      Genotype=Of_31, Treatment=N+P
## time n.risk n.event survival std.err lower 95% CI upper 95% CI
##   92     4     1     0.75  0.217     0.426     1
##   96     3     1     0.50  0.250     0.188     1
##   99     2     2     0.00   NaN      NA      NA
```

```
ggsurvplot_facet(fit4_Of, data = Survival.Of.data, facet.by="Genotype",
                  #risk.table=T, tables.height=0.5,
                  nrow = 4, alpha=1,
                  palette=Fill.colour, linetype=1)
```



```
Ofav_Plot<- ggsurvplot_facet(fit4_Of, data = Survival.Of.data,
  facet.by="Treatment",
  # risk.table=T, tables.height=0.5,
  nrow = 3, alpha=0.5, conf.int = T,
  linetype=1)+theme(legend.position = "left")
Ofav_Plot
```



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Import data

```
# Data
Survival.Ss.data<-read.csv("Data/Ssid_Mortality.csv", header = TRUE)
summary(Survival.Ss.data)
```

```
##      Fragment      Colony      Treatment  Replicate Days_Experiment
## Ss_20-1 : 1      Ss_20:24  Control:54    R1 :79      Min. : 63.0
## Ss_20-11: 1      Ss_22:24  N :55        R2 :82      1st Qu.: 82.0
## Ss_20-13: 1      Ss_23:24  NP :52        NA's: 1      Median :113.0
## Ss_20-15: 1      Ss_24:22  NA's : 1      Mean :104.8
## Ss_20-17: 1      Ss_27:24      3rd Qu.:113.0
## Ss_20-19: 1      Ss_28:20      Max. :113.0
## (Other) :156      Ss_30:24
## Fu.stat_exp      Fu.time_texp
## Min. :0.000000    Min. : 63.0
## 1st Qu.:0.000000    1st Qu.: 82.0
## Median :0.000000    Median :113.0
## Mean :0.006173      Mean :104.8
## 3rd Qu.:0.000000    3rd Qu.:113.0
## Max. :1.000000      Max. :113.0
##
```



```
Survival.Ss.data$Genotype<-factor(Survival.Ss.data$Colony, levels = c(
  "Ss_22", "Ss_23", "Ss_27", "Ss_28", "Ss_24", "Ss_30", "Ss_20"))
summary(Survival.Ss.data$Genotype)
```

```
## Ss_22 Ss_23 Ss_27 Ss_28 Ss_24 Ss_30 Ss_20
##      24      24      24      20      22      24      24
```

Create survival object

```
## Add survival object (Fit survival data using the Kaplan-Meier method)
surv_object_SS <- Surv(time = Survival.Ss.data$Fu.time_texp,
  event = Survival.Ss.data$Fu.stat_exp)
surv_object_SS
```

```
##      [1] 82+ 113+ 113+ 113+ 113+ 82+ 113+ 113+ 82+ 113+ 113+ 113+ 113+ 113+
##      [15] 113+ 82+ 113+ 113+ 82+ 113+ 113+ 113+ 82+ 82+ 113+ 113+ 113+ 82+
##      [29] 113+ 113+ 113+ 113+ 113+ 113+ 82+ 82+ 113+ 113+ 113+ 113+ 113+ 113+
##      [43] 82+ 113+ 82+ 113+ 113+ 113+ 82+ 113+ 82+ 113+ 113+ 113+ 113+ 113+
##      [57] 113+ 82+ 82+ 113+ 113+ 113+ 113+ 82+ 113+ 113+ 113+ 82+ 113+ 113+
##      [71] 113+ 82+ 113+ 82+ 113+ 113+ 113+ 113+ 82+ 113+ 113+ 113+ 113+ 82+
##      [85] 63 113+ 113+ 82+ 113+ 113+ 113+ 82+ 113+ 113+ 82+ 113+ 113+ 113+
##      [99] 82+ 113+ 113+ 82+ 113+ 113+ 113+ 82+ 113+ 113+ 113+ 82+ 113+ 113+
##     [113] 113+ 82+ 113+ 82+ 113+ 113+ 113+ 113+ 113+ 82+ 113+ 113+ 113+
##     [127] 82+ 113+ 113+ 113+ 82+ 113+ 113+ 82+ 113+ 113+ 82+ 113+ 113+ 113+
##     [141] 113+ 113+ 82+ 82+ 113+ 113+ 113+ 113+ 113+ 82+ 113+ 82+ 113+
##     [155] 113+ 113+ 113+ 113+ 113+ 113+ 82+ 113+
```

Nutrient treatment effect (A, N, N+P)

Figure 2 (3rd panel)

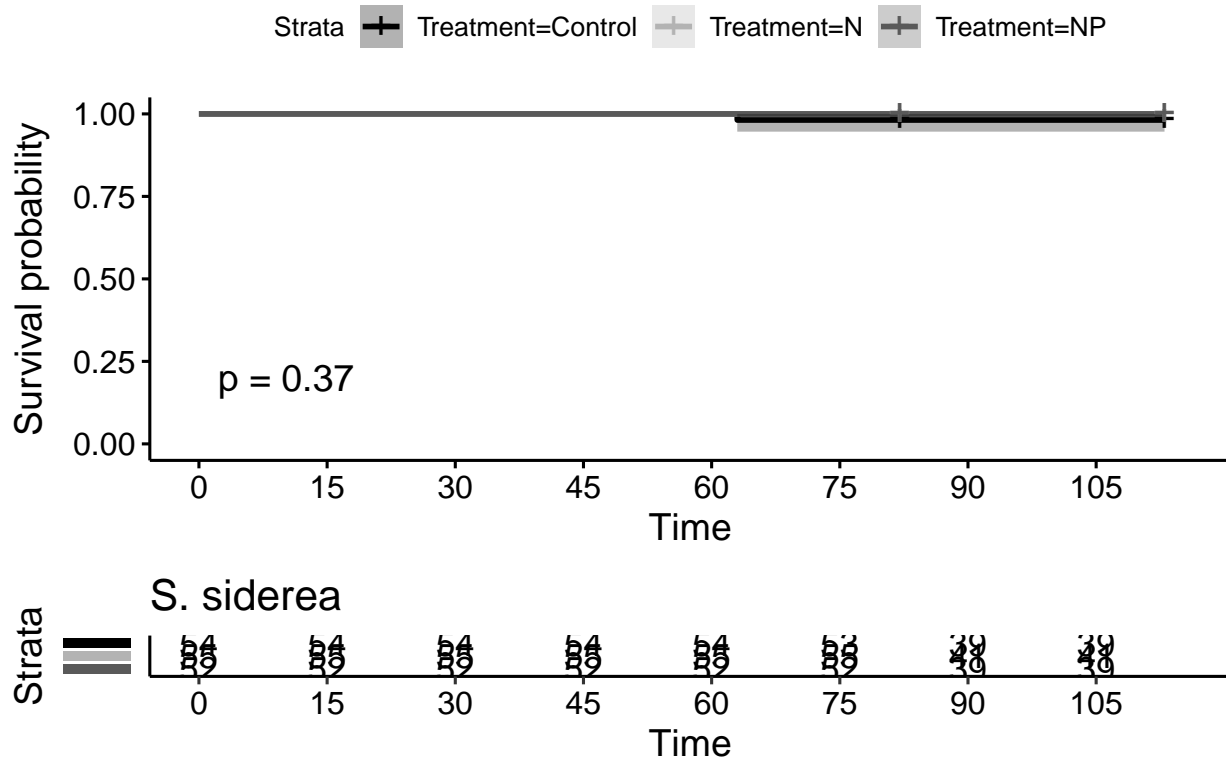
```
# Only treatment model
# Kaplan-Meier estimator. The "log-log" confidence interval is preferred.
fit5Ss <- survfit(surv_object_SS ~ Treatment, data = Survival.Ss.data)
summary(fit5Ss)
```

```
## Call: survfit(formula = surv_object_SS ~ Treatment, data = Survival.Ss.data)
##
## 1 observation deleted due to missingness
##
##           Treatment=Control
##           time      n.risk      n.event      survival      std.err
##           63.0000      54.0000      1.0000      0.9815      0.0183
## lower 95% CI upper 95% CI
##           0.9462      1.0000
##
##           Treatment=N
##           time n.risk n.event survival std.err lower 95% CI upper 95% CI
##
##           Treatment=NP
##           time n.risk n.event survival std.err lower 95% CI upper 95% CI
```

```
coxfitSs <- coxph(surv_object_SS ~ Treatment, data = Survival.Ss.data)
summary(coxfitsSs)
```

```
## Call:
## coxph(formula = surv_object_SS ~ Treatment, data = Survival.Ss.data)
##
##      n= 161, number of events= 1
##      (1 observation deleted due to missingness)
##
##              coef exp(coef)    se(coef)      z Pr(>|z|)
## TreatmentN -2.113e+01  6.631e-10  3.848e+04 -0.001      1
## TreatmentNP -2.113e+01  6.631e-10  3.957e+04 -0.001      1
##
##              exp(coef) exp(-coef) lower .95 upper .95
## TreatmentN  6.631e-10  1.508e+09      0      Inf
## TreatmentNP  6.631e-10  1.508e+09      0      Inf
##
## Concordance= 0.834 (se = 0.019 )
## Likelihood ratio test= 2.18 on 2 df,  p=0.3
## Wald test              = 0 on 2 df,  p=1
## Score (logrank) test = 1.98 on 2 df,  p=0.4
##
## # Plot the survival model
Ss_Treatment_Only<-ggsurvplot(fit5Ss, data = Survival.Ss.data, pval = TRUE,
                              conf.int = T, risk.table=T, palette=Fill.colour,
                              break.time.by=15, xlim=c(0,115), risk.table.y.text = FALSE,
                              risk.table.title="Number of fragments at risk") + ggtitle("S. siderea")
Ss_Treatment_Only
```

S. siderea



```
#ggsave("Outputs/Fig_Ssid_Surv_Treatment.svg",
#Ss_Treatment_Only$plot, width=4, height=3.5, dpi = 300)
```

Colony effect

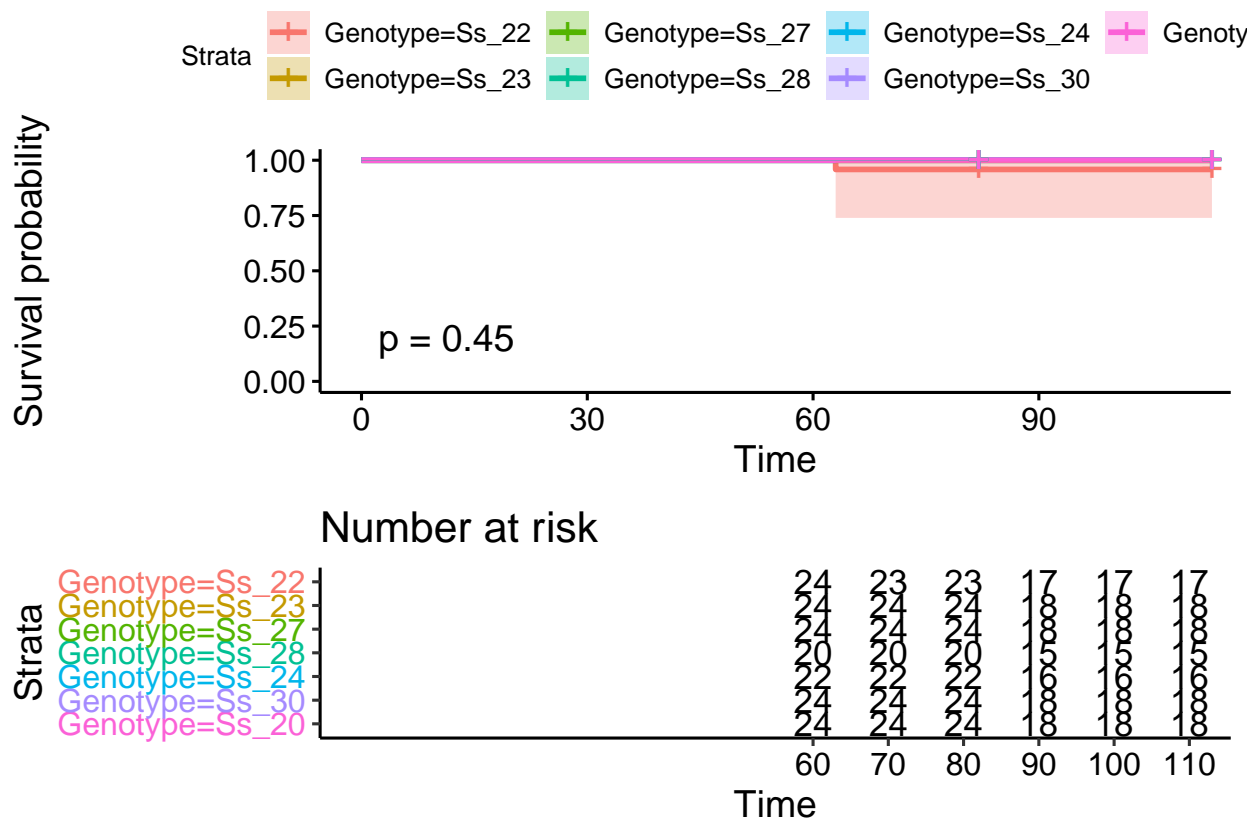
```
# Only genotype model
# Kaplan-Meier estimator. The "log-log" confidence interval is preferred.
fit6Ss <- survfit(surv_object_SS ~ Genotype, conf.type = "log-log",
data = Survival.Ss.data)
summary(fit6Ss)

## Call: survfit(formula = surv_object_SS ~ Genotype, data = Survival.Ss.data,
## conf.type = "log-log")
##
##               Genotype=Ss_22
##      time      n.risk    n.event  survival   std.err
##    63.0000    24.0000     1.0000    0.9583    0.0408
## lower 95% CI upper 95% CI
##    0.7392     0.9940
##
##               Genotype=Ss_23
##      time n.risk n.event survival std.err lower 95% CI upper 95% CI
##
##               Genotype=Ss_27
##      time n.risk n.event survival std.err lower 95% CI upper 95% CI
##
```

```
##           Genotype=Ss_28
##      time n.risk n.event survival std.err lower 95% CI upper 95% CI
##
##           Genotype=Ss_24
##      time n.risk n.event survival std.err lower 95% CI upper 95% CI
##
##           Genotype=Ss_30
##      time n.risk n.event survival std.err lower 95% CI upper 95% CI
##
##           Genotype=Ss_20
##      time n.risk n.event survival std.err lower 95% CI upper 95% CI
```

```
# Plot the survival model
```

```
Genotype_only_SS<-ggsurvplot(fit6Ss, data = Survival.Ss.data, pval = TRUE,
                             risk.table=T, tables.height=0.4, conf.int = T, n.risk = TRUE )
Genotype_only_SS
```



```
# Treatment and genotype model 1
```

```
# Kaplan-Meier estimator. The "log-log" confidence interval is preferred.
```

```
fit7Ss <- survfit(surv_object_SS ~ Genotype + Treatment, data = Survival.Ss.data)
summary(fit7Ss)
```

```
## Call: survfit(formula = surv_object_SS ~ Genotype + Treatment, data = Survival.Ss.data)
##
## 1 observation deleted due to missingness
##           Genotype=Ss_22, Treatment=Control
##      time      n.risk      n.event      survival      std.err
##      63.000        8.000         1.000         0.875         0.117
## lower 95% CI upper 95% CI
```

```

##      0.673      1.000
##
##      Genotype=Ss_22, Treatment=N
## time n.risk n.event survival std.err lower 95% CI upper 95% CI
##
##      Genotype=Ss_22, Treatment=NP
## time n.risk n.event survival std.err lower 95% CI upper 95% CI
##
##      Genotype=Ss_23, Treatment=Control
## time n.risk n.event survival std.err lower 95% CI upper 95% CI
##
##      Genotype=Ss_23, Treatment=N
## time n.risk n.event survival std.err lower 95% CI upper 95% CI
##
##      Genotype=Ss_23, Treatment=NP
## time n.risk n.event survival std.err lower 95% CI upper 95% CI
##
##      Genotype=Ss_27, Treatment=Control
## time n.risk n.event survival std.err lower 95% CI upper 95% CI
##
##      Genotype=Ss_27, Treatment=N
## time n.risk n.event survival std.err lower 95% CI upper 95% CI
##
##      Genotype=Ss_27, Treatment=NP
## time n.risk n.event survival std.err lower 95% CI upper 95% CI
##
##      Genotype=Ss_28, Treatment=Control
## time n.risk n.event survival std.err lower 95% CI upper 95% CI
##
##      Genotype=Ss_28, Treatment=N
## time n.risk n.event survival std.err lower 95% CI upper 95% CI
##
##      Genotype=Ss_28, Treatment=NP
## time n.risk n.event survival std.err lower 95% CI upper 95% CI
##
##      Genotype=Ss_24, Treatment=Control
## time n.risk n.event survival std.err lower 95% CI upper 95% CI
##
##      Genotype=Ss_24, Treatment=N
## time n.risk n.event survival std.err lower 95% CI upper 95% CI
##
##      Genotype=Ss_24, Treatment=NP
## time n.risk n.event survival std.err lower 95% CI upper 95% CI
##
##      Genotype=Ss_30, Treatment=Control
## time n.risk n.event survival std.err lower 95% CI upper 95% CI
##
##      Genotype=Ss_30, Treatment=N
## time n.risk n.event survival std.err lower 95% CI upper 95% CI
##
##      Genotype=Ss_30, Treatment=NP
## time n.risk n.event survival std.err lower 95% CI upper 95% CI
##
##      Genotype=Ss_20, Treatment=Control

```

```
##      time n.risk n.event survival std.err lower 95% CI upper 95% CI
##
##      Genotype=Ss_20, Treatment=N
##      time n.risk n.event survival std.err lower 95% CI upper 95% CI
##
##      Genotype=Ss_20, Treatment=NP
##      time n.risk n.event survival std.err lower 95% CI upper 95% CI

# Plot the survival model
Ssid_Plot<-ggsurvplot_facet(fit7Ss, data = Survival.Ss.data,
  facet.by="Treatment",
  # risk.table=T, tables.height=0.5,
  nrow = 3, alpha=0.5, conf.int = T,
  linetype=1) +theme(legend.position = "left")

Ssid_Plot
```

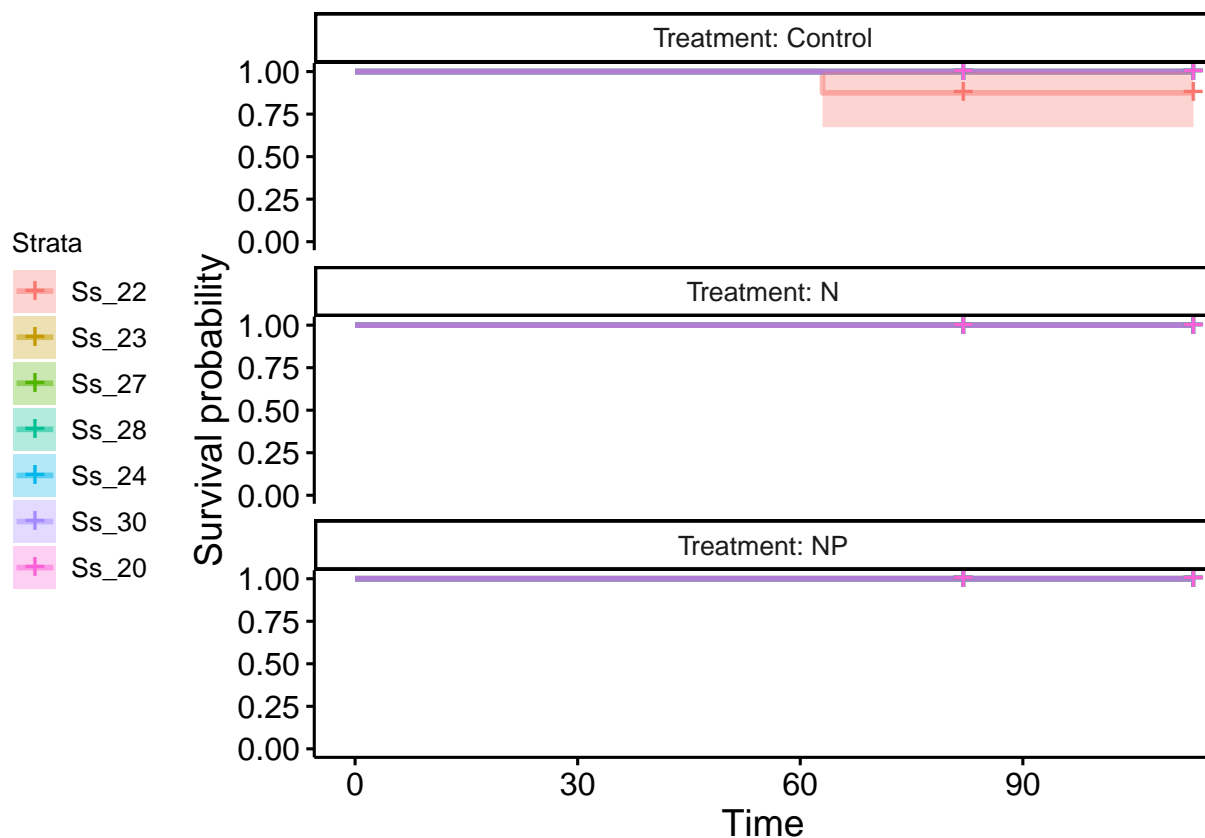
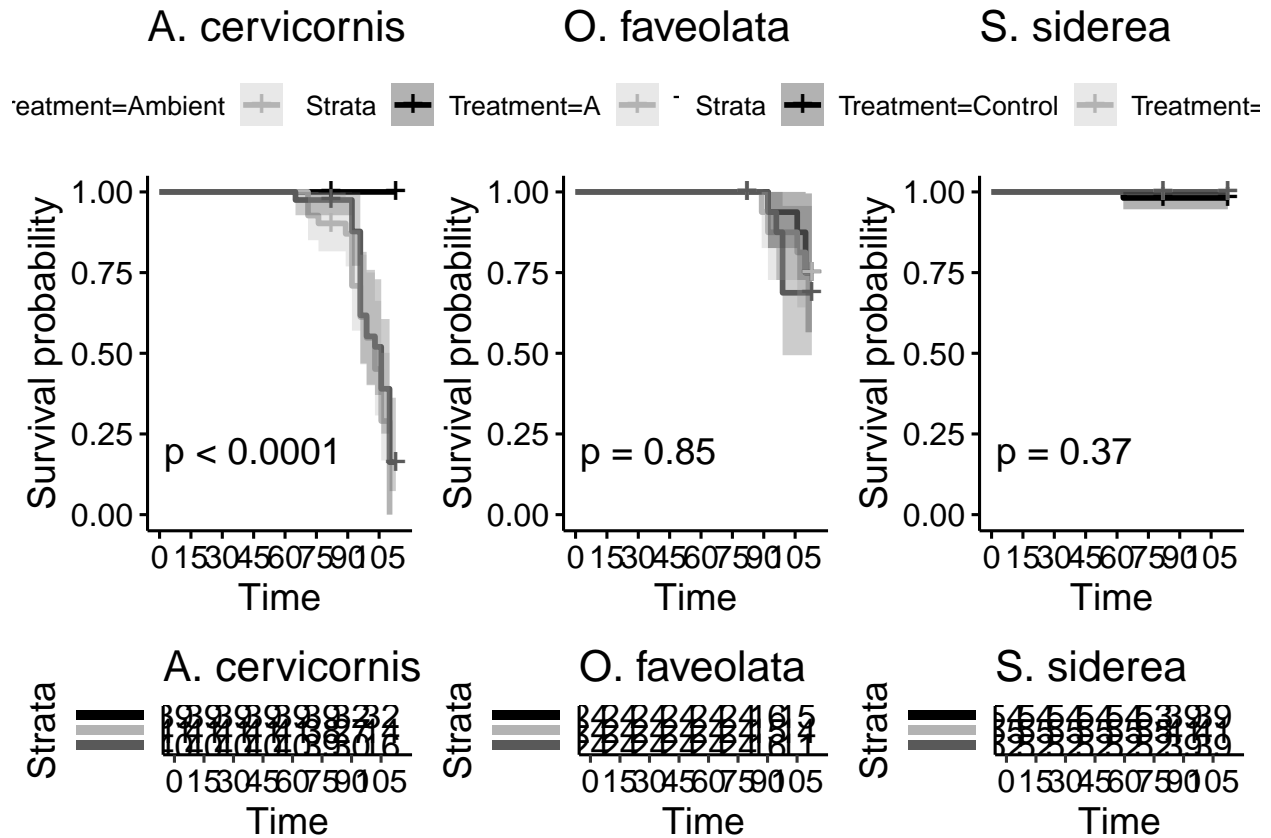


Figure 2: All Spp treatment plot

```
Survival.Trat.plot<-ggarrange(Ac_Treatment_Only$plot,
  Of_Treatment_Only$plot,
  Ss_Treatment_Only$plot,
  Ac_Treatment_Only$table,
  Of_Treatment_Only$table,
  Ss_Treatment_Only$table,
  heights = c(2, 0.7),
```

```
ncol = 3, nrow = 2)
Survival.Trat.plot
```

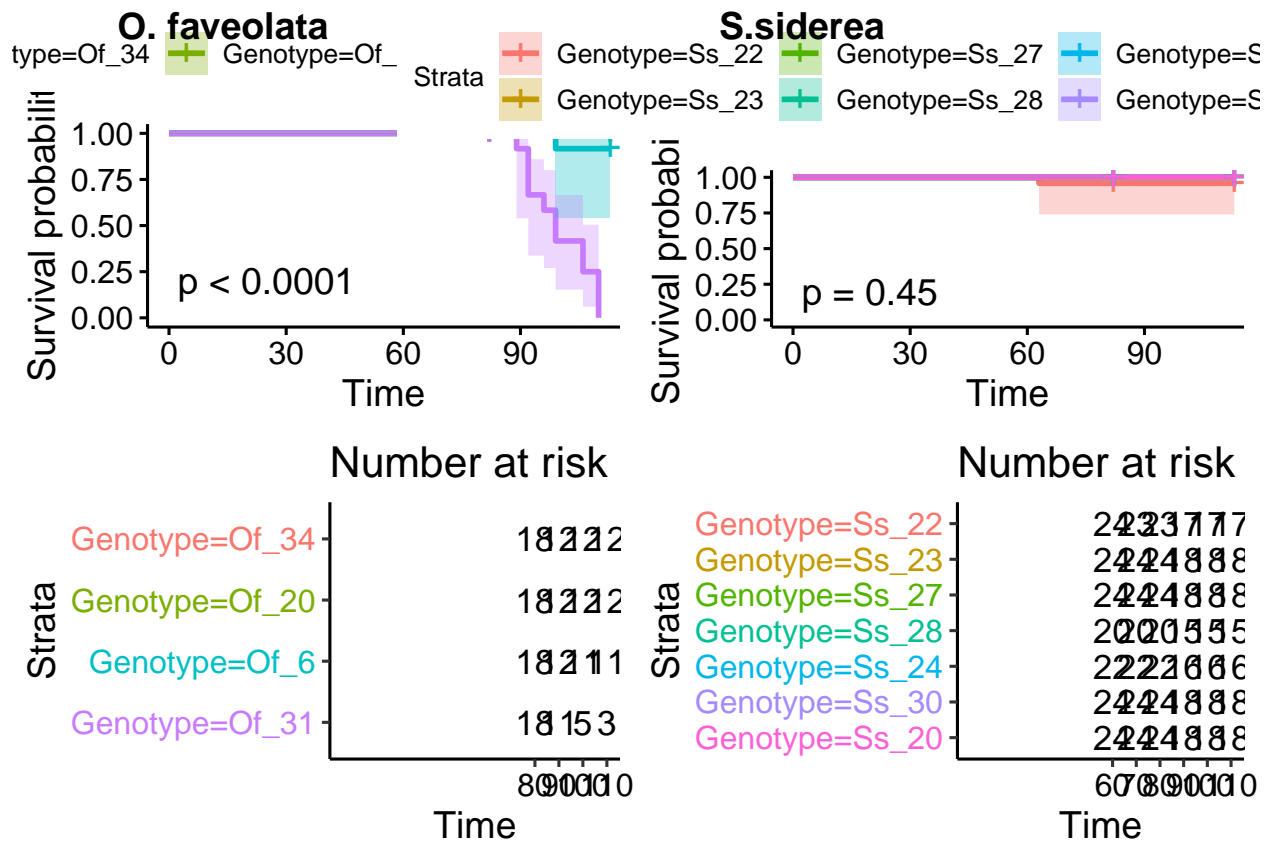


```
ggsave(file="Outputs/Survival.Treat.plot.svg", plot=Survival.Trat.plot, width=7.5, height=6)
```

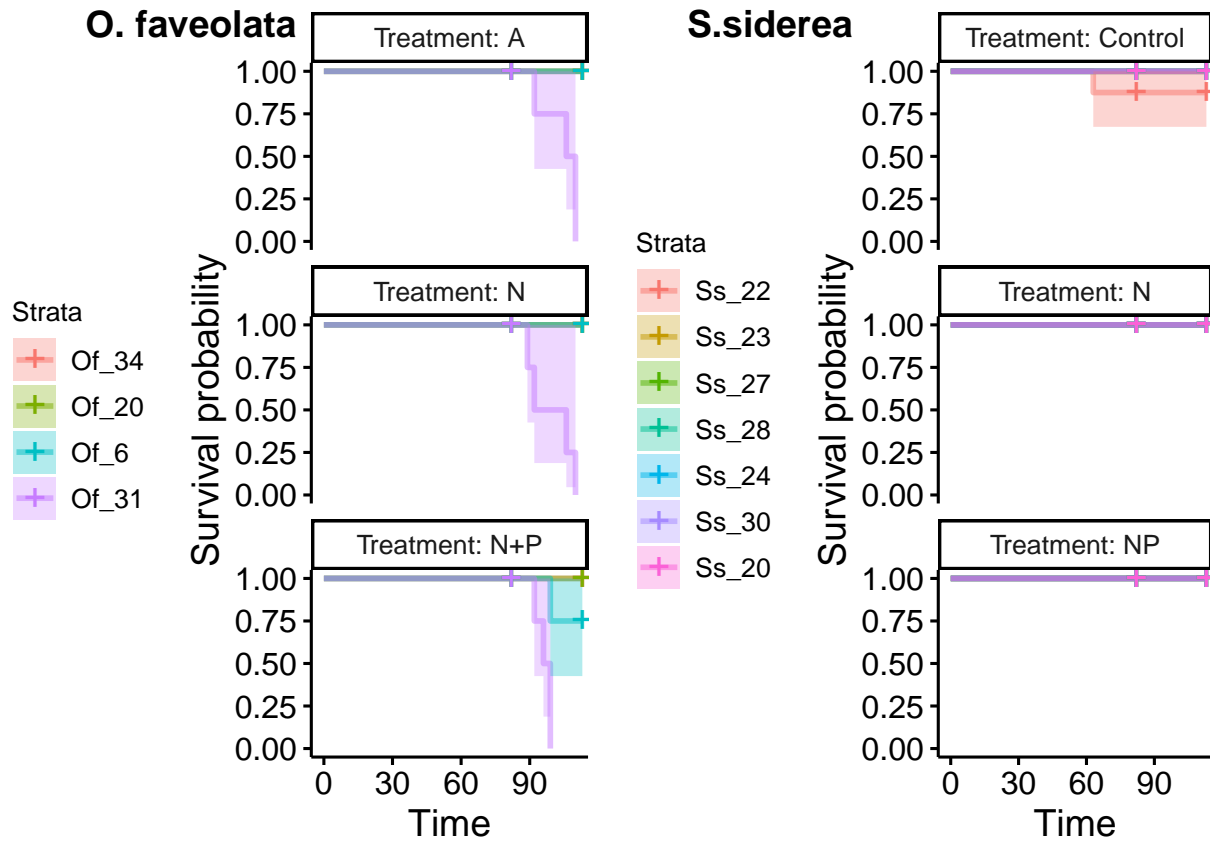
Supplementary plots by colonies (Symbiont communities)

```
SupplementarySurvivalA<-ggarrange(Genotype_only_OF$plot,Genotype_only_SS$plot,
  Genotype_only_OF$table ,Genotype_only_SS$table,
  labels = c("O. faveolata", "S.siderea"),
  ncol = 2, nrow = 2)
```

```
SupplementarySurvivalA
```



```
SupplementarySurvivalB<-ggarrange(Ofav_Plot, Ssid_Plot, labels = c("O. faveolata", "S. siderea"),
  ncol = 2, nrow = 1)
SupplementarySurvivalB
```

Packages used

```
# Creates bibliography
#knitr::write_bib(c(.packages()), "packages.bib")
```

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- Wickham, Hadley, Romain François, Lionel Henry, and Kirill Müller. 2019. *Dplyr: A Grammar of Data Manipulation*. <https://CRAN.R-project.org/package=dplyr>.
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