

# Bando et al 2025\_Altair Final Clinical Analysis

Code ▾

```
library(swimplot) library(coxphf) library(grid) library(gtable) library(readr) library(mosaic) library(dplyr) library(survival)
library(survminer) library(gridtext) library(ggplot2) library(scales) library(officer) library(ggthemes) library(tidyverse)
library(gtsummary) library(flextable) library(parameters) library(car) library(grid) library(ComplexHeatmap)
library(readxl) library(janitor) library(rms) library(pROC) library(DT)
```

#Demographics Table by Altair Arm

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```

rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Altair 20240729 Dataset.csv")

circ_data_subset1 <- circ_data %>%
  select(
    Age.Group,
    Sex,
    PrimSitev2,
    StageA.alt,
    p_hadNeo,
    p_TxAdjAltair,
    ctDNA1mo,
    p_AltBaselineWin,
    BRAF.V600E,
    RAS,
    MSI) %>%
  mutate(
    Age.Group = factor(Age.Group, levels = c("1", "2"), labels = c("<70", ">70")),
    Sex = factor(Sex, levels = c("Male", "Female")),
    PrimSitev2 = factor(PrimSitev2, levels = c("Right-sided colon", "Left-sided colon",
"Rectum")),
    StageA.alt = factor(StageA.alt, levels = c("I", "II", "III", "IV")),
    p_hadNeo = factor(p_hadNeo, levels=c("FALSE","TRUE"), labels = c("No", "Yes")),
    p_TxAdjAltair = factor(p_TxAdjAltair, levels=c("FALSE","TRUE"), labels = c("No", "Yes")),
    ctDNA1mo = factor(ctDNA1mo, levels = c("NEGATIVE", "POSITIVE"), labels = c("Negative", "Positive")),
    p_AltBaselineWin = factor(p_AltBaselineWin, levels = c("MRD", "OnTreatment", "Surveillance")),
    BRAF.V600E = factor(BRAF.V600E, levels = c("WT", "MUT"), labels = c("BRAF wt", "BRAF V600E")),
    RAS = factor(RAS, levels = c("WT", "MUT"), labels = c("RAS wt", "RAS mut")),
    MSI = factor(MSI, levels = c("MSS", "MSI-High")))

circ_data1 <- read.csv("Altair 20240729 Dataset.csv")

circ_data_subset2 <- circ_data1 %>%
  select(
    Age.Group,
    Sex,
    PrimSitev2,
    StageA.alt,
    p_hadNeo,
    p_TxAdjAltair,
    ctDNA1mo,
    p_AltBaselineWin,
    BRAF.V600E,
    RAS,
    MSI,
    altair.Arm) %>%
  mutate(

```

```
Age.Group = factor(Age.Group, levels = c("1", "2"), labels = c("<70", ">70")),
Sex = factor(Sex, levels = c("Male", "Female")),
PrimSitev2 = factor(PrimSitev2, levels = c("Right-sided colon", "Left-sided colon",
"Rectum")),
StageA.alt = factor(StageA.alt, levels = c("I", "II", "III", "IV")),
p_hadNeo = factor(p_hadNeo, levels=c("FALSE","TRUE"), labels = c("No", "Yes")),
p_TxAdjAltair = factor(p_TxAdjAltair, levels=c("FALSE","TRUE"), labels = c("No", "Yes")),
ctDNA1mo = factor(ctDNA1mo, levels = c("NEGATIVE", "POSITIVE"), labels = c("Negative", "Positive")),
p_AltBaselineWin = factor(p_AltBaselineWin, levels = c("MRD", "OnTreatment", "Surveillance")),
BRAF.V600E = factor(BRAF.V600E, levels = c("WT", "MUT"), labels = c("BRAF wt", "BRAF V600E")),
RAS = factor(RAS, levels = c("WT", "MUT"), labels = c("RAS wt", "RAS mut")),
MSI = factor(MSI, levels = c("MSS", "MSI-High")),
altair.Arm = factor(altair.Arm, levels=c("Control","Experimental"), labels = c("Placebo", "FTD/TPI"))
Overall <- circ_data_subset1 %>%
tbl_summary(
  statistic = list(
    all_continuous() ~ "{median} ({min} - {max})",
    all_categorical() ~ "{n} ({p}%)" ) %>%
bold_labels()
Overall
```

| Characteristic     | N = 243 <sup>1</sup> |
|--------------------|----------------------|
| Age.Group          |                      |
| <70                | 155 (64%)            |
| >70                | 88 (36%)             |
| Sex                |                      |
| Male               | 142 (58%)            |
| Female             | 101 (42%)            |
| PrimSitev2         |                      |
| Right-sided colon  | 60 (26%)             |
| Left-sided colon   | 127 (55%)            |
| Rectum             | 46 (20%)             |
| Unknown            | 10                   |
| StageA.alt         |                      |
| <sup>1</sup> n (%) |                      |

| Characteristic     | N = 243 <sup>1</sup> |
|--------------------|----------------------|
| I                  | 10 (4.1%)            |
| II                 | 58 (24%)             |
| III                | 109 (45%)            |
| IV                 | 66 (27%)             |
| p_hadNeo           | 87 (36%)             |
| p_TxAdjAltair      | 112 (46%)            |
| ctDNA1mo           |                      |
| Negative           | 113 (47%)            |
| Positive           | 130 (53%)            |
| p_AltBaselineWin   |                      |
| MRD                | 58 (24%)             |
| OnTreatment        | 33 (14%)             |
| Surveillance       | 152 (63%)            |
| BRAF.V600E         |                      |
| BRAF wt            | 234 (96%)            |
| BRAF V600E         | 9 (3.7%)             |
| RAS                |                      |
| RAS wt             | 148 (61%)            |
| RAS mut            | 95 (39%)             |
| MSI                |                      |
| MSS                | 238 (98%)            |
| MSI-High           | 5 (2.1%)             |
| <sup>1</sup> n (%) |                      |

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```
ByctDNA_MRD <- circ_data_subset2 %>%
tbl_summary(
  by = altair.Arm, # add this line to subgroup by altair.Arm
  statistic = list(
    all_continuous() ~ "{median} ({min} - {max})",
    all_categorical() ~ "{n} ({p}%)" ) %>%
add_p() %>%
bold_labels()
ByctDNA_MRD
```

| Characteristic    | Placebo<br>N = 121 <sup>1</sup> | FTD/TPI<br>N = 122 <sup>1</sup> | p-value <sup>2</sup> |
|-------------------|---------------------------------|---------------------------------|----------------------|
| Age.Group         |                                 |                                 | 0.8                  |
| <70               | 78 (64%)                        | 77 (63%)                        |                      |
| >70               | 43 (36%)                        | 45 (37%)                        |                      |
| Sex               |                                 |                                 | >0.9                 |
| Male              | 71 (59%)                        | 71 (58%)                        |                      |
| Female            | 50 (41%)                        | 51 (42%)                        |                      |
| PrimSitev2        |                                 |                                 | >0.9                 |
| Right-sided colon | 29 (25%)                        | 31 (26%)                        |                      |
| Left-sided colon  | 64 (56%)                        | 63 (53%)                        |                      |
| Rectum            | 22 (19%)                        | 24 (20%)                        |                      |
| Unknown           | 6                               | 4                               |                      |
| StageA.alt        |                                 |                                 | 0.6                  |
| I                 | 3 (2.5%)                        | 7 (5.7%)                        |                      |
| II                | 30 (25%)                        | 28 (23%)                        |                      |
| III               | 56 (46%)                        | 53 (43%)                        |                      |
| IV                | 32 (26%)                        | 34 (28%)                        |                      |
| p_hadNeo          | 41 (34%)                        | 46 (38%)                        | 0.5                  |
| p_TxAdjAltair     | 56 (46%)                        | 56 (46%)                        | >0.9                 |

<sup>1</sup> n (%)  
<sup>2</sup> Pearson's Chi-squared test; Fisher's exact test

| Characteristic   | Placebo<br>N = 121 <sup>1</sup> | FTD/TPI<br>N = 122 <sup>1</sup> | p-value <sup>2</sup> |
|--|---------------------------------|---------------------------------|----------------------|
| ctDNA1mo   |                                 |                                 | >0.9                 |
| Negative   | 56 (46%)                        | 57 (47%)                        |                      |
| Positive   | 65 (54%)                        | 65 (53%)                        |                      |
| p_AltBaselineWin   |                                 |                                 | 0.5                  |
| MRD  | 30 (25%)                        | 28 (23%)                        |                      |
| OnTreatment  | 19 (16%)                        | 14 (11%)                        |                      |
| Surveillance   | 72 (60%)                        | 80 (66%)                        |                      |
| BRAF.V600E   |                                 |                                 | 0.5                  |
| BRAF wt  | 118 (98%)                       | 116 (95%)                       |                      |
| BRAF V600E   | 3 (2.5%)                        | 6 (4.9%)                        |                      |
| RAS  |                                 |                                 | 0.2                  |
| RAS wt   | 79 (65%)                        | 69 (57%)                        |                      |
| RAS mut  | 42 (35%)                        | 53 (43%)                        |                      |
| MSI  |                                 |                                 | 0.7                  |
| MSS  | 118 (98%)                       | 120 (98%)                       |                      |
| MSI-High   | 3 (2.5%)                        | 2 (1.6%)                        |                      |
| <sup>1</sup> n (%)   |                                 |                                 |                      |
| <sup>2</sup> Pearson's Chi-squared test; Fisher's exact test |                                 |                                 |                      |

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```
merged_table <- tbl_merge(tbls=list(Overall, ByctDNA_MRD))
merged_table
```

|  | Table 1              | Table 2                         |  |
|--|----------------------|---------------------------------|--|
| Characteristic   | N = 243 <sup>1</sup> | Placebo<br>N = 121 <sup>1</sup> | FTD/TPI<br>N = 122 <sup>1</sup> p-value <sup>2</sup> |
| Age.Group  |                      |                                 | 0.8  |
| <sup>1</sup> n (%)   |                      |                                 |  |
| <sup>2</sup> Pearson's Chi-squared test; Fisher's exact test |                      |                                 |  |

| Characteristic   | Table 1              | Table 2                         |                                 | p-value <sup>2</sup> |
|--|----------------------|---------------------------------|---------------------------------|----------------------|
|  | N = 243 <sup>1</sup> | Placebo<br>N = 121 <sup>1</sup> | FTD/TPI<br>N = 122 <sup>1</sup> |                      |
| <70  | 155 (64%)            | 78 (64%)                        | 77 (63%)                        |                      |
| >70  | 88 (36%)             | 43 (36%)                        | 45 (37%)                        |                      |
| <b>Sex</b>   |                      |                                 |                                 | >0.9                 |
| Male   | 142 (58%)            | 71 (59%)                        | 71 (58%)                        |                      |
| Female   | 101 (42%)            | 50 (41%)                        | 51 (42%)                        |                      |
| <b>PrimSitev2</b>  |                      |                                 |                                 | >0.9                 |
| Right-sided colon  | 60 (26%)             | 29 (25%)                        | 31 (26%)                        |                      |
| Left-sided colon   | 127 (55%)            | 64 (56%)                        | 63 (53%)                        |                      |
| Rectum   | 46 (20%)             | 22 (19%)                        | 24 (20%)                        |                      |
| Unknown  | 10                   | 6                               | 4                               |                      |
| <b>StageA.alt</b>  |                      |                                 |                                 | 0.6                  |
| I  | 10 (4.1%)            | 3 (2.5%)                        | 7 (5.7%)                        |                      |
| II   | 58 (24%)             | 30 (25%)                        | 28 (23%)                        |                      |
| III  | 109 (45%)            | 56 (46%)                        | 53 (43%)                        |                      |
| IV   | 66 (27%)             | 32 (26%)                        | 34 (28%)                        |                      |
| <b>p_hadNeo</b>  | 87 (36%)             | 41 (34%)                        | 46 (38%)                        | 0.5                  |
| <b>p_TxAdjAltair</b>   | 112 (46%)            | 56 (46%)                        | 56 (46%)                        | >0.9                 |
| <b>ctDNA1mo</b>  |                      |                                 |                                 | >0.9                 |
| Negative   | 113 (47%)            | 56 (46%)                        | 57 (47%)                        |                      |
| Positive   | 130 (53%)            | 65 (54%)                        | 65 (53%)                        |                      |
| <b>p_AltBaselineWin</b>                                      |                      |                                 |                                 | 0.5                  |
| MRD  | 58 (24%)             | 30 (25%)                        | 28 (23%)                        |                      |
| OnTreatment  | 33 (14%)             | 19 (16%)                        | 14 (11%)                        |                      |
| Surveillance   | 152 (63%)            | 72 (60%)                        | 80 (66%)                        |                      |
| <sup>1</sup> n (%)   |                      |                                 |                                 |                      |
| <sup>2</sup> Pearson's Chi-squared test; Fisher's exact test |                      |                                 |                                 |                      |

|  | Table 1              | Table 2                         |                                 |                      |
|--|----------------------|---------------------------------|---------------------------------|----------------------|
| Characteristic   | N = 243 <sup>1</sup> | Placebo<br>N = 121 <sup>1</sup> | FTD/TPI<br>N = 122 <sup>1</sup> | p-value <sup>2</sup> |
| BRAF.V600E   |                      |                                 |                                 | 0.5                  |
| BRAF wt  | 234 (96%)            | 118 (98%)                       | 116 (95%)                       |                      |
| BRAF V600E   | 9 (3.7%)             | 3 (2.5%)                        | 6 (4.9%)                        |                      |
| RAS  |                      |                                 |                                 | 0.2                  |
| RAS wt   | 148 (61%)            | 79 (65%)                        | 69 (57%)                        |                      |
| RAS mut  | 95 (39%)             | 42 (35%)                        | 53 (43%)                        |                      |
| MSI  |                      |                                 |                                 | 0.7                  |
| MSS  | 238 (98%)            | 118 (98%)                       | 120 (98%)                       |                      |
| MSI-High   | 5 (2.1%)             | 3 (2.5%)                        | 2 (1.6%)                        |                      |
| <sup>1</sup> n (%)   |                      |                                 |                                 |                      |
| <sup>2</sup> Pearson's Chi-squared test; Fisher's exact test |                      |                                 |                                 |                      |

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```
fit1 <- as_flex_table(  
  merged_table,  
  include = everything(),  
  return_calls = FALSE  
)  
fit1
```

|                | Table 1              | Table 2                         |                                 |                      |
|----------------|----------------------|---------------------------------|---------------------------------|----------------------|
| Characteristic | N = 243 <sup>1</sup> | Placebo<br>N = 121 <sup>1</sup> | FTD/TPI<br>N = 122 <sup>1</sup> | p-value <sup>2</sup> |
| Age.Group      |                      |                                 |                                 | 0.8                  |
| <70            | 155 (64%)            | 78 (64%)                        | 77 (63%)                        |                      |
| >70            | 88 (36%)             | 43 (36%)                        | 45 (37%)                        |                      |
| Sex            |                      |                                 |                                 | >0.9                 |
| Male           | 142 (58%)            | 71 (59%)                        | 71 (58%)                        |                      |
| Female         | 101 (42%)            | 50 (41%)                        | 51 (42%)                        |                      |
| PrimSitev2     |                      |                                 |                                 | >0.9                 |

<sup>1</sup>n (%)

<sup>2</sup>Pearson's Chi-squared test; Fisher's exact test



|                         | Table 1              |                                 | Table 2                         |                      |
|-------------------------|----------------------|---------------------------------|---------------------------------|----------------------|
| Characteristic          | N = 243 <sup>1</sup> | Placebo<br>N = 121 <sup>1</sup> | FTD/TPI<br>N = 122 <sup>1</sup> | p-value <sup>2</sup> |
| Right-sided colon       | 60 (26%)             | 29 (25%)                        | 31 (26%)                        |                      |
| Left-sided colon        | 127 (55%)            | 64 (56%)                        | 63 (53%)                        |                      |
| Rectum                  | 46 (20%)             | 22 (19%)                        | 24 (20%)                        |                      |
| Unknown                 | 10                   | 6                               | 4                               |                      |
| <b>StageA.alt</b>       |                      |                                 |                                 | 0.6                  |
| I                       | 10 (4.1%)            | 3 (2.5%)                        | 7 (5.7%)                        |                      |
| II                      | 58 (24%)             | 30 (25%)                        | 28 (23%)                        |                      |
| III                     | 109 (45%)            | 56 (46%)                        | 53 (43%)                        |                      |
| IV                      | 66 (27%)             | 32 (26%)                        | 34 (28%)                        |                      |
| <b>p_hadNeo</b>         | 87 (36%)             | 41 (34%)                        | 46 (38%)                        | 0.5                  |
| <b>p_TxAdjAltair</b>    | 112 (46%)            | 56 (46%)                        | 56 (46%)                        | >0.9                 |
| <b>ctDNA1mo</b>         |                      |                                 |                                 | >0.9                 |
| Negative                | 113 (47%)            | 56 (46%)                        | 57 (47%)                        |                      |
| Positive                | 130 (53%)            | 65 (54%)                        | 65 (53%)                        |                      |
| <b>p_AltBaselineWin</b> |                      |                                 |                                 | 0.5                  |
| MRD                     | 58 (24%)             | 30 (25%)                        | 28 (23%)                        |                      |
| OnTreatment             | 33 (14%)             | 19 (16%)                        | 14 (11%)                        |                      |
| Surveillance            | 152 (63%)            | 72 (60%)                        | 80 (66%)                        |                      |
| <b>BRAF.V600E</b>       |                      |                                 |                                 | 0.5                  |
| BRAF wt                 | 234 (96%)            | 118 (98%)                       | 116 (95%)                       |                      |
| BRAF V600E              | 9 (3.7%)             | 3 (2.5%)                        | 6 (4.9%)                        |                      |
| <b>RAS</b>              |                      |                                 |                                 | 0.2                  |
| RAS wt                  | 148 (61%)            | 79 (65%)                        | 69 (57%)                        |                      |
| RAS mut                 | 95 (39%)             | 42 (35%)                        | 53 (43%)                        |                      |
| <b>MSI</b>              |                      |                                 |                                 | 0.7                  |
| MSS                     | 238 (98%)            | 118 (98%)                       | 120 (98%)                       |                      |
| MSI-High                | 5 (2.1%)             | 3 (2.5%)                        | 2 (1.6%)                        |                      |

<sup>1</sup>n (%)<sup>2</sup>Pearson's Chi-squared test; Fisher's exact test

Hide

```
save_as_docx(fit1, path = "~/Downloads/merged_table.docx")
```

#Median enrollment MTM/mL in the complete cohort

[Hide](#)

```
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Altair 20240729 Dataset.csv")
circ_datadf <- as.data.frame(circ_data)

median_val <- median(circ_data$p_AltBaselineMTM, na.rm = TRUE)
q1_val <- quantile(circ_data$p_AltBaselineMTM, 0.25, na.rm = TRUE)
q3_val <- quantile(circ_data$p_AltBaselineMTM, 0.75, na.rm = TRUE)
range_val <- range(circ_data$p_AltBaselineMTM, na.rm = TRUE)
cat("Median:", format(median_val, digits = 4), "\n")
```

Median: 0.4

[Hide](#)

```
cat("Q1 (25th percentile):", q1_val, "\n")
```

Q1 (25th percentile): 0.1096503

[Hide](#)

```
cat("Q3 (75th percentile):", q3_val, "\n")
```

Q3 (75th percentile): 1.767375

[Hide](#)

```
cat("Range:", range_val, "\n")
```

Range: 0.02627334 250.47

#Median enrollment MTM/mL by Stage

[Hide](#)

```
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Altair 20240729 Dataset.csv")
circ_datadf <- as.data.frame(circ_data)
circ_data$StageA.alt <- factor(circ_data$StageA.alt, levels = c("I", "II", "III", "IV"))

stage_summary <- circ_data %>%
  group_by(StageA.alt) %>%
  summarise(
    Median = median(p_AltBaselineMTM, na.rm = TRUE),
    Q1 = quantile(p_AltBaselineMTM, 0.25, na.rm = TRUE),
    Q3 = quantile(p_AltBaselineMTM, 0.75, na.rm = TRUE),
    Min = min(p_AltBaselineMTM, na.rm = TRUE),
    Max = max(p_AltBaselineMTM, na.rm = TRUE)
  ) %>%
  ungroup()
print(stage_summary)
```

| StageA.alt<br><fctr> | Median<br><dbl> | Q1<br><dbl> | Q3<br><dbl> | Min<br><dbl> | Max<br><dbl> |
|----------------------|-----------------|-------------|-------------|--------------|--------------|
| I                    | 0.1897622       | 0.05556848  | 1.2886383   | 0.03024498   | 121.26864    |
| II                   | 0.2941548       | 0.08791899  | 0.9805206   | 0.02627334   | 166.33426    |
| III                  | 0.3793725       | 0.11772783  | 1.4162926   | 0.02899812   | 250.47000    |
| IV                   | 0.6802357       | 0.18488692  | 2.5976302   | 0.03444433   | 40.42593     |
| 4 rows               |                 |             |             |              |              |

#Median enrollment MTM/mL by enrollment window

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```
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Altair 20240729 Dataset.csv")
circ_datadf <- as.data.frame(circ_data)
circ_data$p_AltBaselineWin <- factor(circ_data$p_AltBaselineWin, levels = c("MRD", "OnTreatment", "Surveillance"))

stage_summary <- circ_data %>%
  group_by(p_AltBaselineWin) %>%
  summarise(
    Median = median(p_AltBaselineMTM, na.rm = TRUE),
    Q1 = quantile(p_AltBaselineMTM, 0.25, na.rm = TRUE),
    Q3 = quantile(p_AltBaselineMTM, 0.75, na.rm = TRUE),
    Min = min(p_AltBaselineMTM, na.rm = TRUE),
    Max = max(p_AltBaselineMTM, na.rm = TRUE)
  ) %>%
  ungroup()
print(stage_summary)
```

| p_AltBaselineWin<br><fctr> | Median<br><dbl> | Q1<br><dbl> | Q3<br><dbl> | Min<br><dbl> | Max<br><dbl> |
|----------------------------|-----------------|-------------|-------------|--------------|--------------|
| MRD                        | 0.9724113       | 0.20765821  | 4.2230867   | 0.02650878   | 121.2686     |
| OnTreatment                | 0.8224263       | 0.23246840  | 2.1174125   | 0.06015442   | 166.3343     |
| Surveillance               | 0.2395414       | 0.08798068  | 0.9850139   | 0.02627334   | 250.4700     |
| 3 rows                     |                 |             |             |              |              |

#Median enrollment MTM/mL by enrollment window in each treatment arm

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```
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Altair 20240729 Dataset.csv")
circ_datadf <- as.data.frame(circ_data)
circ_data$p_AltBaselineWin <- factor(circ_data$p_AltBaselineWin, levels = c("MRD", "OnTreatment", "Surveillance"))
circ_data$altair.Arm <- factor(circ_data$altair.Arm, levels = c("Control", "Experimental"), labels = c("Placebo", "FTD/TPI"))

# 1. Summary statistics by p_AltBaselineWin
stage_summary <- circ_data %>%
  group_by(p_AltBaselineWin) %>%
  summarise(
    Median = median(p_AltBaselineMTM, na.rm = TRUE),
    Q1 = quantile(p_AltBaselineMTM, 0.25, na.rm = TRUE),
    Q3 = quantile(p_AltBaselineMTM, 0.75, na.rm = TRUE),
    Min = min(p_AltBaselineMTM, na.rm = TRUE),
    Max = max(p_AltBaselineMTM, na.rm = TRUE)
  ) %>%
  ungroup()
print("Summary by p_AltBaselineWin:")
```

[1] "Summary by p\_AltBaselineWin:"

Hide

```
print(stage_summary)
```

| p_AltBaselineWin<br><fctr> | Median<br><dbl> | Q1<br><dbl> | Q3<br><dbl> | Min<br><dbl> | Max<br><dbl> |
|----------------------------|-----------------|-------------|-------------|--------------|--------------|
| MRD                        | 0.9724113       | 0.20765821  | 4.2230867   | 0.02650878   | 121.2686     |
| OnTreatment                | 0.8224263       | 0.23246840  | 2.1174125   | 0.06015442   | 166.3343     |
| Surveillance               | 0.2395414       | 0.08798068  | 0.9850139   | 0.02627334   | 250.4700     |
| 3 rows                     |                 |             |             |              |              |

```
# 2. Median by p_AltBaselineWin and altair.Arm
arm_stage_summary <- circ_data %>%
  group_by(p_AltBaselineWin, altair.Arm) %>%
  summarise(
    Median = median(p_AltBaselineMTM, na.rm = TRUE),
    n = n()
  ) %>%
  ungroup()
```

`summarise()` has grouped output by 'p\_AltBaselineWin'. You can override using the `.groups` argument.

```
print("Median p_AltBaselineMTM by p_AltBaselineWin and altair.Arm:")
```

```
[1] "Median p_AltBaselineMTM by p_AltBaselineWin and altair.Arm:"
```

```
print(arm_stage_summary)
```

| p_AltBaselineWin<br><fctr> | altair.Arm<br><fctr> | Median<br><dbl> | n<br><int> |
|----------------------------|----------------------|-----------------|------------|
| MRD                        | Placebo              | 0.9724113       | 30         |
| MRD                        | FTD/TPI              | 0.8748196       | 28         |
| OnTreatment                | Placebo              | 0.9076431       | 19         |
| OnTreatment                | FTD/TPI              | 0.7410978       | 14         |
| Surveillance               | Placebo              | 0.1690072       | 72         |
| Surveillance               | FTD/TPI              | 0.2931127       | 80         |

6 rows

```
# 3. Wilcoxon test p-values for Control vs Experimental within each p_AltBaselineWin
p_values <- circ_data %>%
  filter(!is.na(p_AltBaselineMTM), !is.na(altair.Arm), !is.na(p_AltBaselineWin)) %>%
  group_by(p_AltBaselineWin) %>%
  summarise(
    p_value = tryCatch(
      wilcox.test(p_AltBaselineMTM ~ altair.Arm)$p.value,
      error = function(e) NA
    )
  )
print("Wilcoxon test p-values by p_AltBaselineWin:")
```

```
[1] "Wilcoxon test p-values by p_AltBaselineWin:"
```

[Hide](#)

```
print(p_values)
```

| <b>p_AltBaselineWin</b><br><fctr> | <b>p_value</b><br><dbl> |
|-----------------------------------|-------------------------|
| MRD                               | 0.6156082               |
| OnTreatment                       | 0.5289893               |
| Surveillance                      | 0.2198430               |
| 3 rows                            |                         |

#Median enrollment MTM/mL in Stage IV vs Non-Stage IV

[Hide](#)

```
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Altair 20240729 Dataset.csv")
circ_data <- circ_data[!(circ_data$StageA.alt %in% c("I", "II", "III")),]
circ_datadf <- as.data.frame(circ_data)

median_val <- median(circ_data$p_AltBaselineMTM, na.rm = TRUE)
q1_val <- quantile(circ_data$p_AltBaselineMTM, 0.25, na.rm = TRUE)
q3_val <- quantile(circ_data$p_AltBaselineMTM, 0.75, na.rm = TRUE)
range_val <- range(circ_data$p_AltBaselineMTM, na.rm = TRUE)
cat("Median:", format(median_val, digits = 4), "\n")
```

```
Median: 0.6802
```

[Hide](#)

```
cat("Q1 (25th percentile):", q1_val, "\n")
```

Q1 (25th percentile): 0.1848869

Hide

cat("Q3 (75th percentile):", q3\_val, "\n")

Q3 (75th percentile): 2.59763

Hide

cat("Range:", range\_val, "\n")

Range: 0.03444433 40.42593

Hide

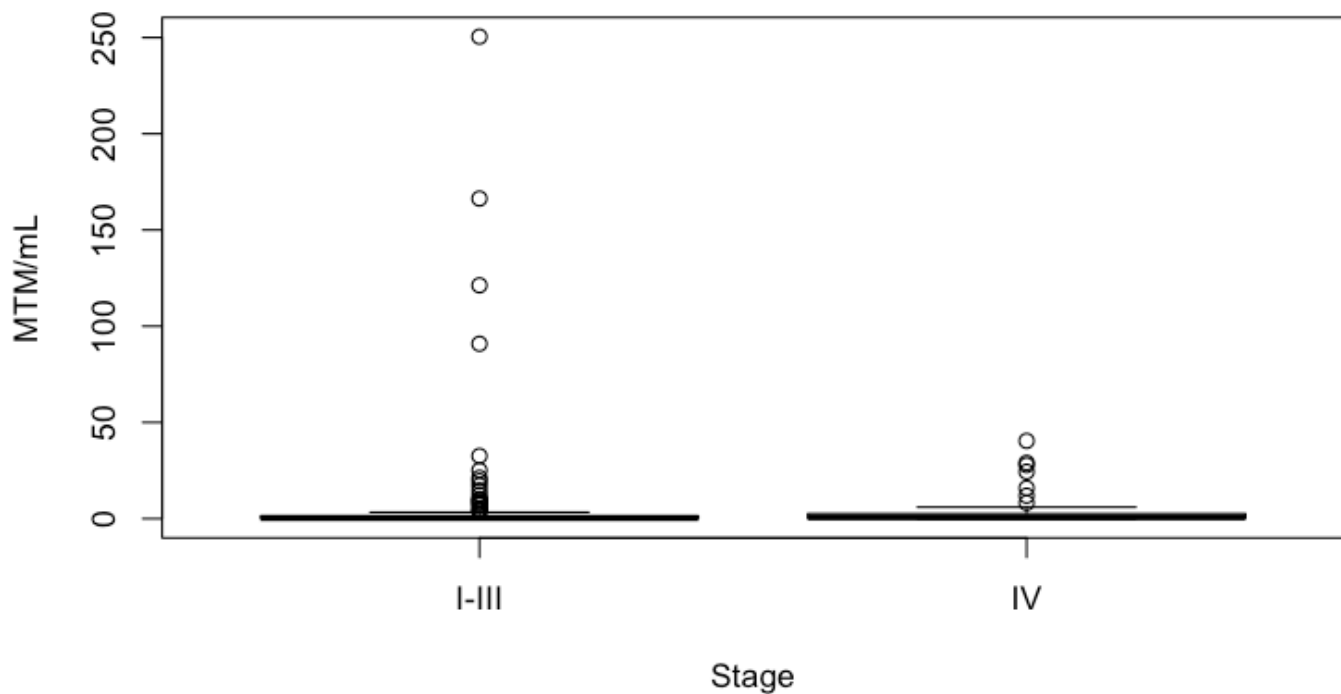
```
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Altair 20240729 Dataset.csv")
circ_datadf <- as.data.frame(circ_data)
circ_data$Stage.Final <- factor(circ_data$Stage.Final, levels = c("I-III", "IV"))
median_MTM <- aggregate(p_AltBaselineMTM ~ Stage.Final, data = circ_data, FUN = median)
print(median_MTM)
```

| Stage.Final | p_AltBaselineMTM |
|-------------|------------------|
| <fctr>      | <dbl>            |
| I-III       | 0.3199376        |
| IV          | 0.6802357        |
| 2 rows      |                  |

Hide

```
circ_data$Stage.Final <- factor(circ_data$Stage.Final, levels = c("I-III", "IV"))
boxplot(p_AltBaselineMTM~Stage.Final, data=circ_data, main="MTM/mL at enrollment", xlab
="Stage", ylab="MTM/mL", col="white",border="black")
```

## MTM/mL at enrollment


[Hide](#)

```
m1<-wilcox.test(p_AltBaselineMTM ~ Stage.Final, data=circ_data, na.rm=TRUE, exact=FALSE,
conf.int=TRUE)
print(m1)
```

Wilcoxon rank sum test with continuity correction

```
data: p_AltBaselineMTM by Stage.Final
W = 4740, p-value = 0.02394
alternative hypothesis: true location shift is not equal to 0
95 percent confidence interval:
 -0.41562942 -0.01469699
sample estimates:
difference in location
 -0.1351274
```

#Number of patients with enrolment MTM/mL > various thresholds

[Hide](#)



```
rm(list = ls())
setwd("~/Downloads")
circ_data <- read.csv("Altair 20240729 Dataset.csv")
circ_data$p_AltBaselineMTM <- as.numeric(circ_data$p_AltBaselineMTM)

# Define your cutoffs
cutoffs <- c(0.01, 0.047, 0.1, 0.179, 0.2, 0.3, 0.5, 1, 5, 8.172, 10)
total_pts <- nrow(circ_data)
for (co in cutoffs) {
  pts_above <- sum(circ_data$p_AltBaselineMTM >= co, na.rm = TRUE)
  perc <- (pts_above / total_pts) * 100
  cat("Cutoff:", co,
      "- Patients ≥ cutoff:", pts_above,
      "- Percentage:", round(perc, 2), "%\n")
}
```

```
Cutoff: 0.01 - Patients ≥ cutoff: 243 - Percentage: 100 %
Cutoff: 0.047 - Patients ≥ cutoff: 229 - Percentage: 94.24 %
Cutoff: 0.1 - Patients ≥ cutoff: 189 - Percentage: 77.78 %
Cutoff: 0.179 - Patients ≥ cutoff: 158 - Percentage: 65.02 %
Cutoff: 0.2 - Patients ≥ cutoff: 150 - Percentage: 61.73 %
Cutoff: 0.3 - Patients ≥ cutoff: 135 - Percentage: 55.56 %
Cutoff: 0.5 - Patients ≥ cutoff: 111 - Percentage: 45.68 %
Cutoff: 1 - Patients ≥ cutoff: 78 - Percentage: 32.1 %
Cutoff: 5 - Patients ≥ cutoff: 29 - Percentage: 11.93 %
Cutoff: 8.172 - Patients ≥ cutoff: 23 - Percentage: 9.47 %
Cutoff: 10 - Patients ≥ cutoff: 18 - Percentage: 7.41 %
```

#DFS1 by TAS vs Placebo - All stages & stratified for Stage & ctDNA 1mo post-surgery

[Hide](#)

```
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Altair 20240729 Dataset.csv")
circ_datadf <- as.data.frame(circ_data)

survfit(Surv(time = circ_data$DFS.months, event = circ_data$p_evtDFS1b)~altair.Arm, data
= circ_data)
```

```
Call: survfit(formula = Surv(time = circ_data$DFS.months, event = circ_data$p_evtDFS1b)
~
      altair.Arm, data = circ_data)
```

|                         | n   | events | median | 0.95LCL | 0.95UCL |
|-------------------------|-----|--------|--------|---------|---------|
| altair.Arm=Control      | 121 | 99     | 5.55   | 4.17    | 7.33    |
| altair.Arm=Experimental | 122 | 99     | 9.30   | 7.92    | 10.84   |

[Hide](#)

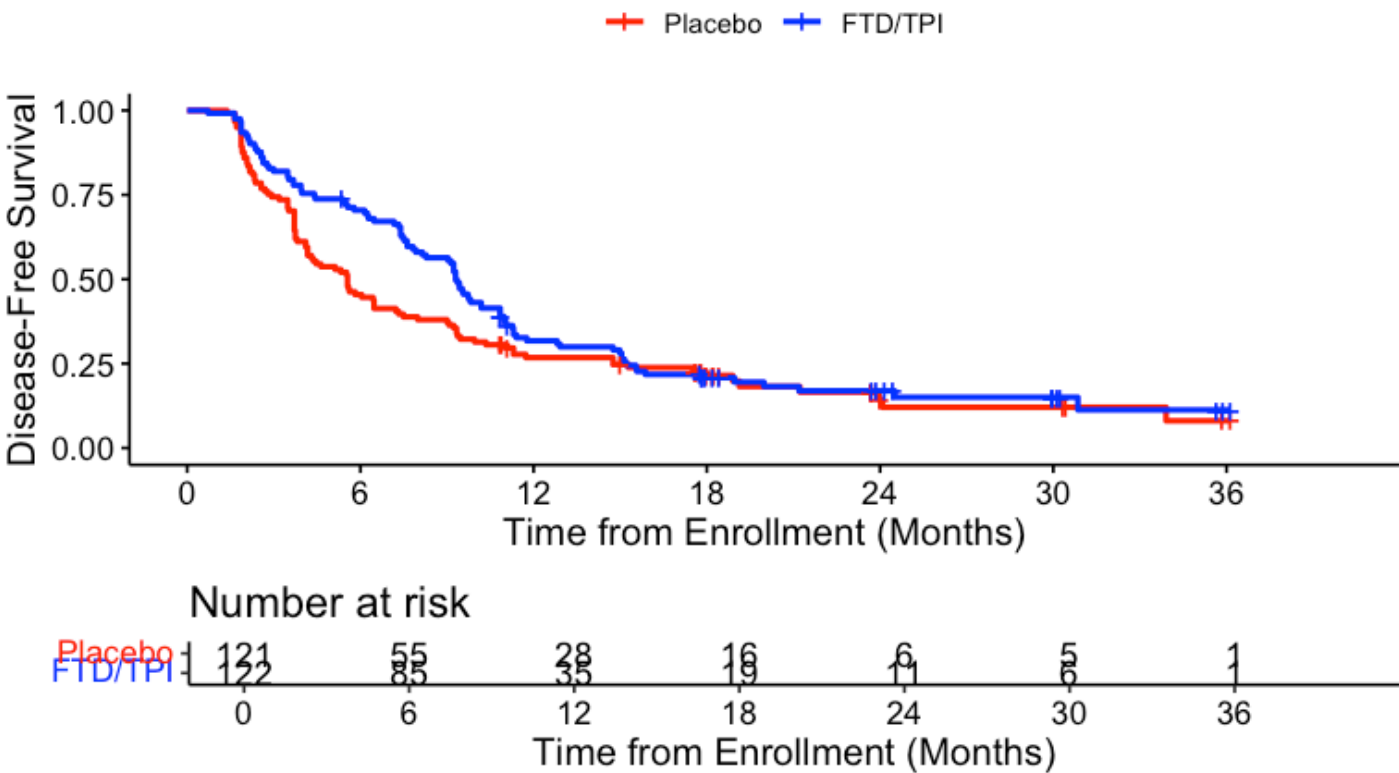
```
event_summary <- circ_data %>%
  group_by(altair.Arm) %>%
  summarise(
    Total = n(),
    Events = sum(p_evtDFS1b),
    Fraction = Events / n(),
    Percentage = (Events / n()) * 100
  )
print(event_summary)
```

| altair.Arm   | Total | Events | Fraction  | Percentage |
|--------------|-------|--------|-----------|------------|
| <chr>        | <int> | <int>  | <dbl>     | <dbl>      |
| Control      | 121   | 99     | 0.8181818 | 81.81818   |
| Experimental | 122   | 99     | 0.8114754 | 81.14754   |
| 2 rows       |       |        |           |            |

Hide

```
surv_object <-Surv(time = circ_data$DFS.months, event = circ_data$p_evtDFS1b)
KM_curve <- survfit(surv_object ~ altair.Arm, data = circ_data,conf.int=0.95,conf.type
="log-log")
ggsurvplot(KM_curve, data = circ_data, pval = FALSE, conf.int = FALSE, risk.table = TRU
E, break.time.by=6, palette=c("red","blue"), title="DFS1 by Arm - All Patients", ylab=
"Disease-Free Survival", xlab="Time from Enrollment (Months)", legend.labs=c("Placebo",
"FTD/TPI"), legend.title="")
```

DFS1 by Arm - All Patients



Hide

```
summary(KM_curve, times= c(6, 12, 18, 24))
```

```
Call: survfit(formula = surv_object ~ altair.Arm, data = circ_data,
  conf.int = 0.95, conf.type = "log-log")
```

| altair.Arm=Control |        |         |          |         |        |        |       |        |
|--------------------|--------|---------|----------|---------|--------|--------|-------|--------|
| time               | n.risk | n.event | survival | std.err | lower  | 95% CI | upper | 95% CI |
| 6                  | 55     | 66      | 0.455    | 0.0453  | 0.3642 |        | 0.540 |        |
| 12                 | 28     | 22      | 0.268    | 0.0408  | 0.1916 |        | 0.350 |        |
| 18                 | 16     | 5       | 0.215    | 0.0391  | 0.1443 |        | 0.296 |        |
| 24                 | 6      | 4       | 0.145    | 0.0394  | 0.0785 |        | 0.231 |        |

| altair.Arm=Experimental |        |         |          |         |       |        |       |        |
|-------------------------|--------|---------|----------|---------|-------|--------|-------|--------|
| time                    | n.risk | n.event | survival | std.err | lower | 95% CI | upper | 95% CI |
| 6                       | 85     | 36      | 0.705    | 0.0413  | 0.615 |        | 0.777 |        |
| 12                      | 35     | 46      | 0.318    | 0.0428  | 0.236 |        | 0.402 |        |
| 18                      | 19     | 12      | 0.208    | 0.0380  | 0.139 |        | 0.287 |        |
| 24                      | 11     | 3       | 0.169    | 0.0370  | 0.104 |        | 0.248 |        |

Hide

```

circ_data$altair.Arm <- factor(circ_data$altair.Arm, levels=c("Control","Experimental"),
labels = c("Placebo", "FTD/TPI"))
circ_data$Disease.Stage <- factor(circ_data$Disease.Stage, levels=c("Stage II or lower", "StageIII", "M1"))
circ_data$ctDNA1mo <- factor(circ_data$ctDNA1mo, levels=c("NEGATIVE","POSITIVE"), labels = c("Negative", "Positive"))
cox_fit_stratified <- coxph(surv_object ~ altair.Arm + strata(Disease.Stage) + strata(ctDNA1mo), data = circ_data)
summary(cox_fit_stratified)

```

Call:

```
coxph(formula = surv_object ~ altair.Arm + strata(Disease.Stage) +
      strata(ctDNA1mo), data = circ_data)
```

n= 243, number of events= 198

|                   | coef    | exp(coef) | se(coef) | z      | Pr(> z ) |
|-------------------|---------|-----------|----------|--------|----------|
| altair.ArmFTD/TPI | -0.2337 | 0.7916    | 0.1448   | -1.614 | 0.107    |

|                   | exp(coef) | exp(-coef) | lower .95 | upper .95 |
|-------------------|-----------|------------|-----------|-----------|
| altair.ArmFTD/TPI | 0.7916    | 1.263      | 0.596     | 1.051     |

Concordance= 0.555 (se = 0.021 )

Likelihood ratio test= 2.6 on 1 df, p=0.1

Wald test = 2.6 on 1 df, p=0.1

Score (logrank) test = 2.61 on 1 df, p=0.1

[Hide](#)

```

# Extract values for HR, 95% CI, and p-value
cox_fit_summary_stratified <- summary(cox_fit_stratified)
HR_stratified <- cox_fit_summary_stratified$coefficients[2]
lower_CI_stratified <- cox_fit_summary_stratified$conf.int[3]
upper_CI_stratified <- cox_fit_summary_stratified$conf.int[4]
p_value_stratified <- cox_fit_summary_stratified$coefficients[5]
label_text_stratified <- paste0("HR = ", round(HR_stratified, 2),
                                " (", round(lower_CI_stratified, 2), "-",
                                round(upper_CI_stratified, 2), "); p = ",
                                round(p_value_stratified, 3))
print(label_text_stratified)

```

```
[1] "HR = 0.79 (0.6-1.05); p = 0.107"
```

#DFS1 by TAS vs Placebo - Excluding QC patients

[Hide](#)

```
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Altair 20240729 Dataset.csv")
circ_data <- circ_data[circ_data$QC.Exclude=="FALSE",]
circ_datadf <- as.data.frame(circ_data)

survfit(Surv(time = circ_data$DFS.months, event = circ_data$p_evtDFS1b)~altair.Arm, data
= circ_data)
```

Call: survfit(formula = Surv(time = circ\_data\$DFS.months, event = circ\_data\$p\_evtDFS1b) ~ altair.Arm, data = circ\_data)

|                         | n   | events | median | 0.95LCL | 0.95UCL |
|-------------------------|-----|--------|--------|---------|---------|
| altair.Arm=Control      | 117 | 99     | 5.52   | 4.11    | 6.47    |
| altair.Arm=Experimental | 118 | 99     | 9.30   | 7.82    | 10.18   |

Hide

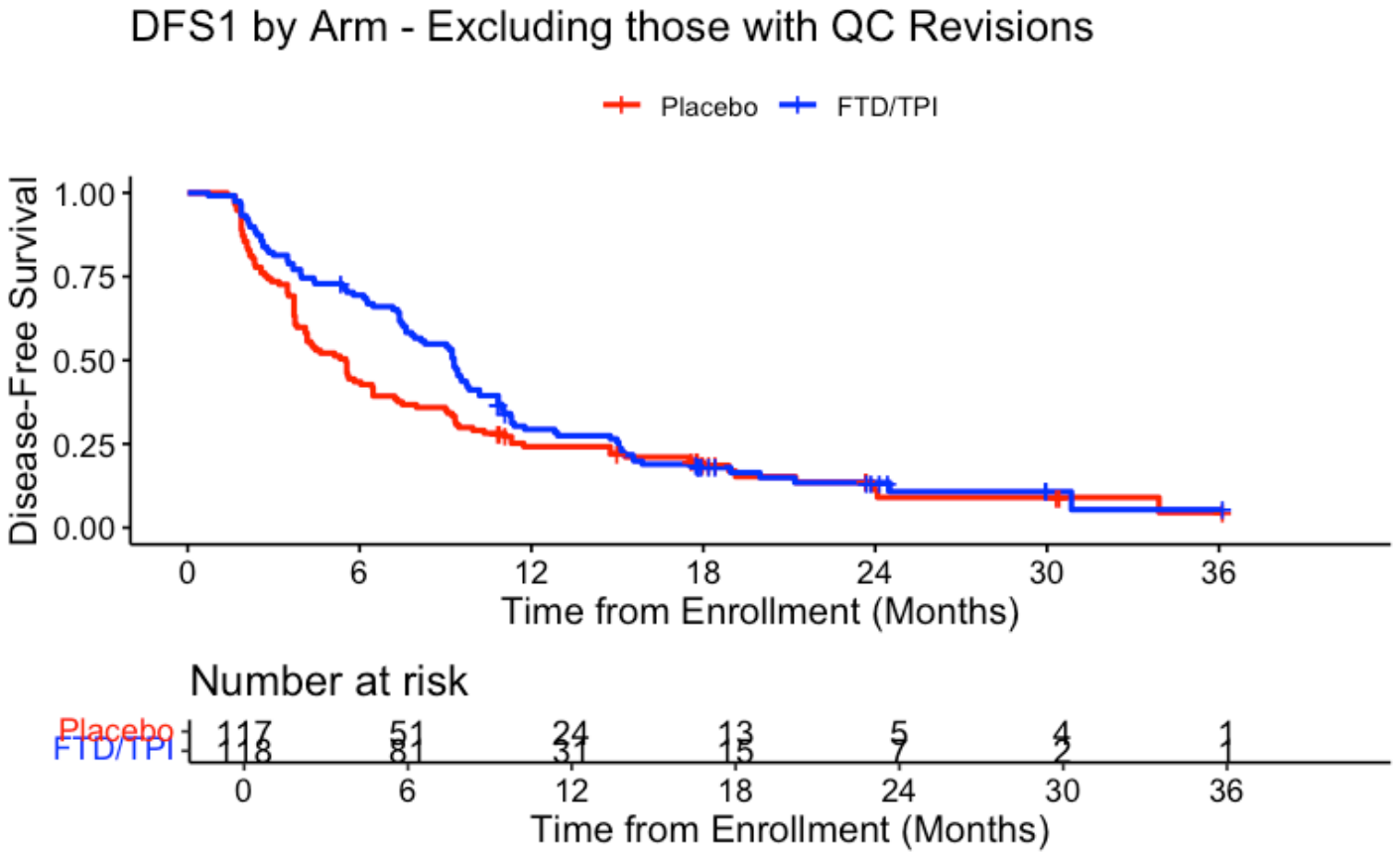
```
event_summary <- circ_data %>%
  group_by(altair.Arm) %>%
  summarise(
    Total = n(),
    Events = sum(p_evtDFS1b),
    Fraction = Events / n(),
    Percentage = (Events / n()) * 100
  )
print(event_summary)
```

| altair.Arm   | Total | Events | Fraction  | Percentage |
|--------------|-------|--------|-----------|------------|
| <chr>        | <int> | <int>  | <dbl>     | <dbl>      |
| Control      | 117   | 99     | 0.8461538 | 84.61538   |
| Experimental | 118   | 99     | 0.8389831 | 83.89831   |

2 rows

Hide

```
surv_object <-Surv(time = circ_data$DFS.months, event = circ_data$p_evtDFS1b)
KM_curve <- survfit(surv_object ~ altair.Arm, data = circ_data,conf.int=0.95,conf.type
=="log-log")
ggsurvplot(KM_curve, data = circ_data, pval = FALSE, conf.int = FALSE, risk.table = TRU
E, break.time.by=6, palette=c("red","blue"), title="DFS1 by Arm - Excluding those with Q
C Revisions", ylab= "Disease-Free Survival", xlab="Time from Enrollment (Months)", legen
d.labs=c("Placebo", "FTD/TPI"), legend.title="")
```



Hide

```
summary(KM_curve, times= c(6, 12, 18, 24))
```

```
Call: survfit(formula = surv_object ~ altair.Arm, data = circ_data,
  conf.int = 0.95, conf.type = "log-log")
```

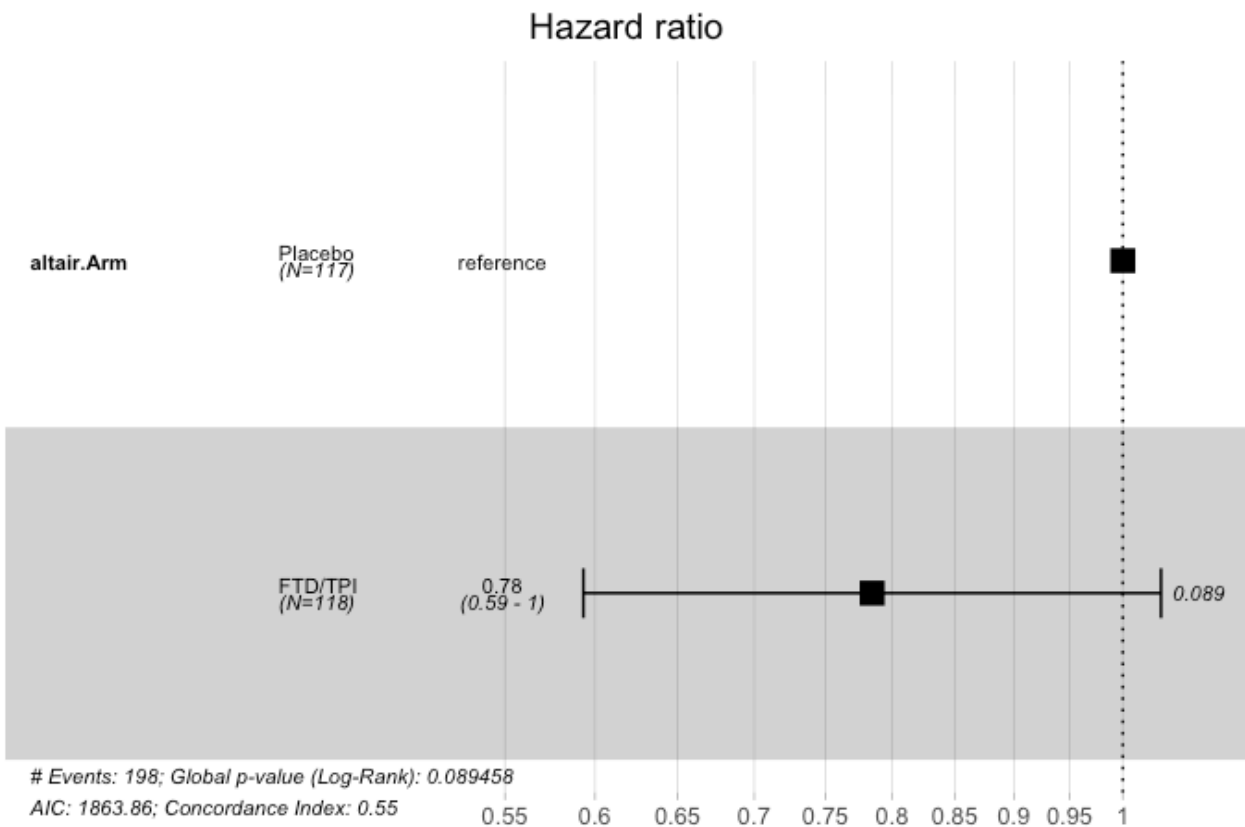
| altair.Arm=Control |        |         |          |         |              |              |  |
|--------------------|--------|---------|----------|---------|--------------|--------------|--|
| time               | n.risk | n.event | survival | std.err | lower 95% CI | upper 95% CI |  |
| 6                  | 51     | 66      | 0.436    | 0.0458  | 0.3450       | 0.523        |  |
| 12                 | 24     | 22      | 0.242    | 0.0402  | 0.1679       | 0.324        |  |
| 18                 | 13     | 5       | 0.186    | 0.0381  | 0.1186       | 0.266        |  |
| 24                 | 5      | 4       | 0.113    | 0.0373  | 0.0532       | 0.198        |  |

| altair.Arm=Experimental |        |         |          |         |              |              |  |
|-------------------------|--------|---------|----------|---------|--------------|--------------|--|
| time                    | n.risk | n.event | survival | std.err | lower 95% CI | upper 95% CI |  |
| 6                       | 81     | 36      | 0.695    | 0.0424  | 0.6027       | 0.769        |  |
| 12                      | 31     | 46      | 0.294    | 0.0427  | 0.2131       | 0.379        |  |
| 18                      | 15     | 12      | 0.179    | 0.0367  | 0.1143       | 0.257        |  |
| 24                      | 7      | 3       | 0.135    | 0.0355  | 0.0746       | 0.212        |  |

Hide

```
circ_data$altair.Arm <- factor(circ_data$altair.Arm, levels=c("Control","Experimental"),
labels = c("Placebo", "FTD/TPI"))
cox_fit <- coxph(surv_object ~ altair.Arm, data=circ_data)
ggforest(cox_fit,data = circ_data)
```



Hide

```
summary(cox_fit)
```

```
Call:
coxph(formula = surv_object ~ altair.Arm, data = circ_data)

n= 235, number of events= 198

              coef exp(coef) se(coef)      z Pr(>|z|)
altair.ArmFTD/TPI -0.2425    0.7847  0.1426 -1.7  0.0891 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

              exp(coef) exp(-coef) lower .95 upper .95
altair.ArmFTD/TPI    0.7847      1.274    0.5933    1.038

Concordance= 0.554 (se = 0.02 )
Likelihood ratio test= 2.88 on 1 df,  p=0.09
Wald test               = 2.89 on 1 df,  p=0.09
Score (logrank) test = 2.9 on 1 df,  p=0.09
```

Hide

```
cox_fit_summary <- summary(cox_fit)

# Extract values for HR, 95% CI, and p-value
HR <- cox_fit_summary$coefficients[2]
lower_CI <- cox_fit_summary$conf.int[3]
upper_CI <- cox_fit_summary$conf.int[4]
p_value <- cox_fit_summary$coefficients[5]
label_text <- paste0("HR = ", round(HR, 2), " (", round(lower_CI, 2), "-", round(upper_C
I, 2), "); p = ", round(p_value, 3))
print(label_text)
```

```
[1] "HR = 0.78 (0.59-1.04); p = 0.089"
```

#DFS1 by TAS vs Placebo - Excluding Mets patients

Hide

```
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Altair 20240729 Dataset.csv")
circ_data <- circ_data[circ_data$Mets.Exclude=="FALSE",]
circ_datadf <- as.data.frame(circ_data)

survfit(Surv(time = circ_data$DFS.months, event = circ_data$p_evtDFS1b)~altair.Arm, data
= circ_data)
```



```
Call: survfit(formula = Surv(time = circ_data$DFS.months, event = circ_data$p_evtDFS1b)
~
      altair.Arm, data = circ_data)

      n events median 0.95LCL 0.95UCL
altair.Arm=Control    119     97   5.55    4.17    7.49
altair.Arm=Experimental 112     90   9.43    9.04   10.84
```

Hide

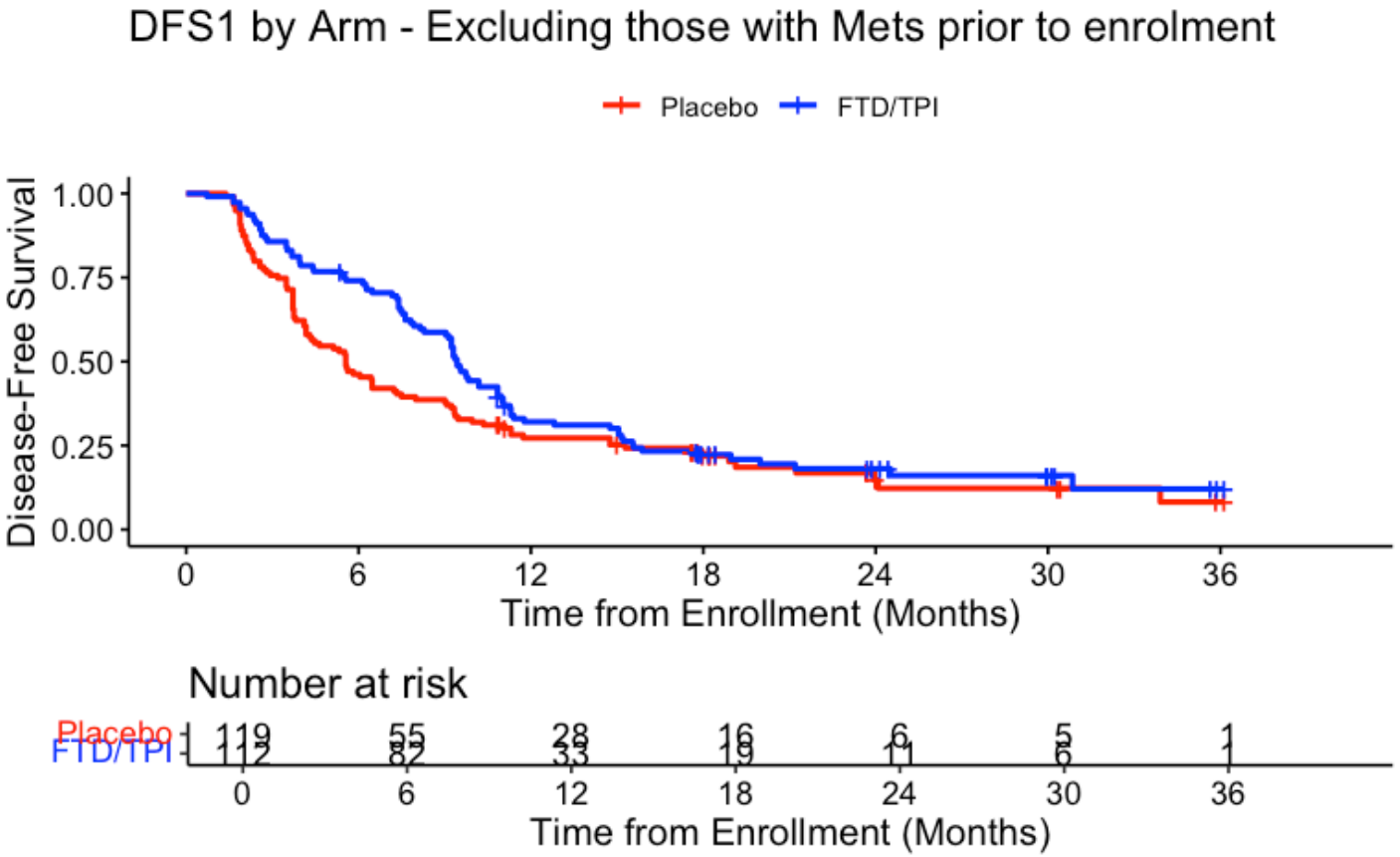
```
event_summary <- circ_data %>%
  group_by(altair.Arm) %>%
  summarise(
    Total = n(),
    Events = sum(p_evtDFS1b),
    Fraction = Events / n(),
    Percentage = (Events / n()) * 100
  )
print(event_summary)
```

| altair.Arm   | Total | Events | Fraction  | Percentage |
|--------------|-------|--------|-----------|------------|
| <chr>        | <int> | <int>  | <dbl>     | <dbl>      |
| Control      | 119   | 97     | 0.8151261 | 81.51261   |
| Experimental | 112   | 90     | 0.8035714 | 80.35714   |

2 rows

Hide

```
surv_object <-Surv(time = circ_data$DFS.months, event = circ_data$p_evtDFS1b)
KM_curve <- survfit(surv_object ~ altair.Arm, data = circ_data,conf.int=0.95,conf.type
="log-log")
ggsurvplot(KM_curve, data = circ_data, pval = FALSE, conf.int = FALSE, risk.table = TRU
E, break.time.by=6, palette=c("red","blue"), title="DFS1 by Arm - Excluding those with M
ets prior to enrolment", ylab= "Disease-Free Survival", xlab="Time from Enrollment (Mont
hs)", legend.labs=c("Placebo", "FTD/TPI"), legend.title="")
```



Hide

```
summary(KM_curve, times= c(6, 12, 18, 24))
```

```
Call: survfit(formula = surv_object ~ altair.Arm, data = circ_data,
  conf.int = 0.95, conf.type = "log-log")
```

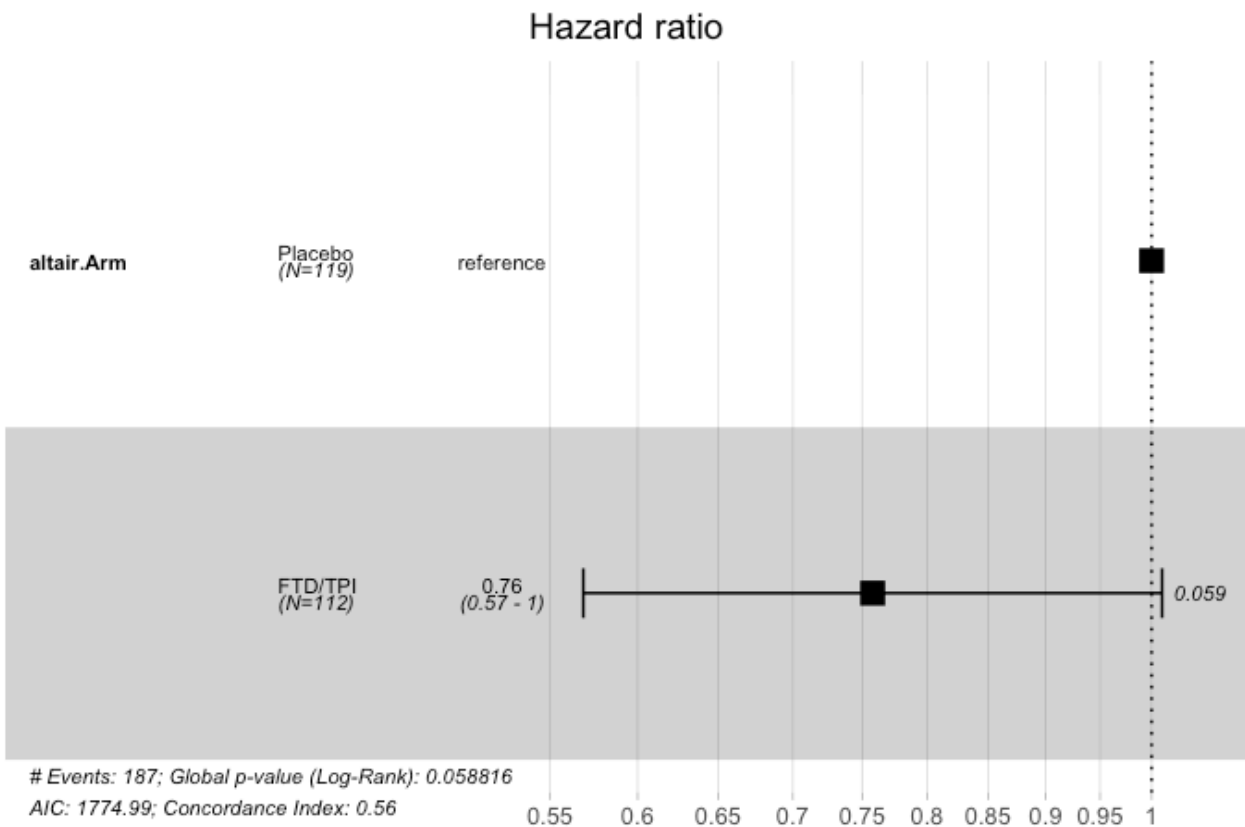
| altair.Arm=Control |        |         |          |         |              |              |  |
|--------------------|--------|---------|----------|---------|--------------|--------------|--|
| time               | n.risk | n.event | survival | std.err | lower 95% CI | upper 95% CI |  |
| 6                  | 55     | 64      | 0.462    | 0.0457  | 0.3708       | 0.549        |  |
| 12                 | 28     | 22      | 0.272    | 0.0413  | 0.1950       | 0.355        |  |
| 18                 | 16     | 5       | 0.219    | 0.0397  | 0.1467       | 0.300        |  |
| 24                 | 6      | 4       | 0.147    | 0.0400  | 0.0798       | 0.235        |  |

| altair.Arm=Experimental |        |         |          |         |              |              |  |
|-------------------------|--------|---------|----------|---------|--------------|--------------|--|
| time                    | n.risk | n.event | survival | std.err | lower 95% CI | upper 95% CI |  |
| 6                       | 82     | 29      | 0.741    | 0.0414  | 0.649        | 0.812        |  |
| 12                      | 33     | 46      | 0.321    | 0.0447  | 0.235        | 0.409        |  |
| 18                      | 19     | 10      | 0.223    | 0.0404  | 0.149        | 0.306        |  |
| 24                      | 11     | 3       | 0.181    | 0.0394  | 0.112        | 0.264        |  |

Hide

```
circ_data$altair.Arm <- factor(circ_data$altair.Arm, levels=c("Control","Experimental"),
labels = c("Placebo", "FTD/TPI"))
cox_fit <- coxph(surv_object ~ altair.Arm, data=circ_data)
ggforest(cox_fit,data = circ_data)
```



Hide

```
summary(cox_fit)
```

Call:

```
coxph(formula = surv_object ~ altair.Arm, data = circ_data)
```

n= 231, number of events= 187

|                   | coef    | exp(coef) | se(coef) | z      | Pr(> z ) |
|-------------------|---------|-----------|----------|--------|----------|
| altair.ArmFTD/TPI | -0.2773 | 0.7579    | 0.1468   | -1.889 | 0.0589   |

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

|                   | exp(coef) | exp(-coef) | lower .95 | upper .95 |
|-------------------|-----------|------------|-----------|-----------|
| altair.ArmFTD/TPI | 0.7579    | 1.32       | 0.5684    | 1.01      |

Concordance= 0.559 (se = 0.02 )

Likelihood ratio test= 3.57 on 1 df, p=0.06

Wald test = 3.57 on 1 df, p=0.06

Score (logrank) test = 3.59 on 1 df, p=0.06

[Hide](#)

```
cox_fit_summary <- summary(cox_fit)
```

```
# Extract values for HR, 95% CI, and p-value
```

```
HR <- cox_fit_summary$coefficients[2]
```

```
lower_CI <- cox_fit_summary$conf.int[3]
```

```
upper_CI <- cox_fit_summary$conf.int[4]
```

```
p_value <- cox_fit_summary$coefficients[5]
```

```
label_text <- paste0("HR = ", round(HR, 2), " (", round(lower_CI, 2), "-", round(upper_CI, 2), "); p = ", round(p_value, 3))
```

```
print(label_text)
```

```
[1] "HR = 0.76 (0.57-1.01); p = 0.059"
```

#DFS1 by TAS vs Placebo - Stage I-III

[Hide](#)

```
rm(list=ls())
```

```
setwd("~/Downloads")
```

```
circ_data <- read.csv("Altair 20240729 Dataset.csv")
```

```
circ_data <- circ_data[!(circ_data$StageA.alt %in% c("IV")),]
```

```
circ_datadf <- as.data.frame(circ_data)
```

```
survfit(Surv(time = circ_data$DFS.months, event = circ_data$p_evtDFS1b)~altair.Arm, data = circ_data)
```

```
Call: survfit(formula = Surv(time = circ_data$DFS.months, event = circ_data$p_evtDFS1b)
~
      altair.Arm, data = circ_data)

              n events median 0.95LCL 0.95UCL
altair.Arm=Control      89      67   6.05    4.63    9.23
altair.Arm=Experimental 88      68   9.27    7.62   10.97
```

Hide

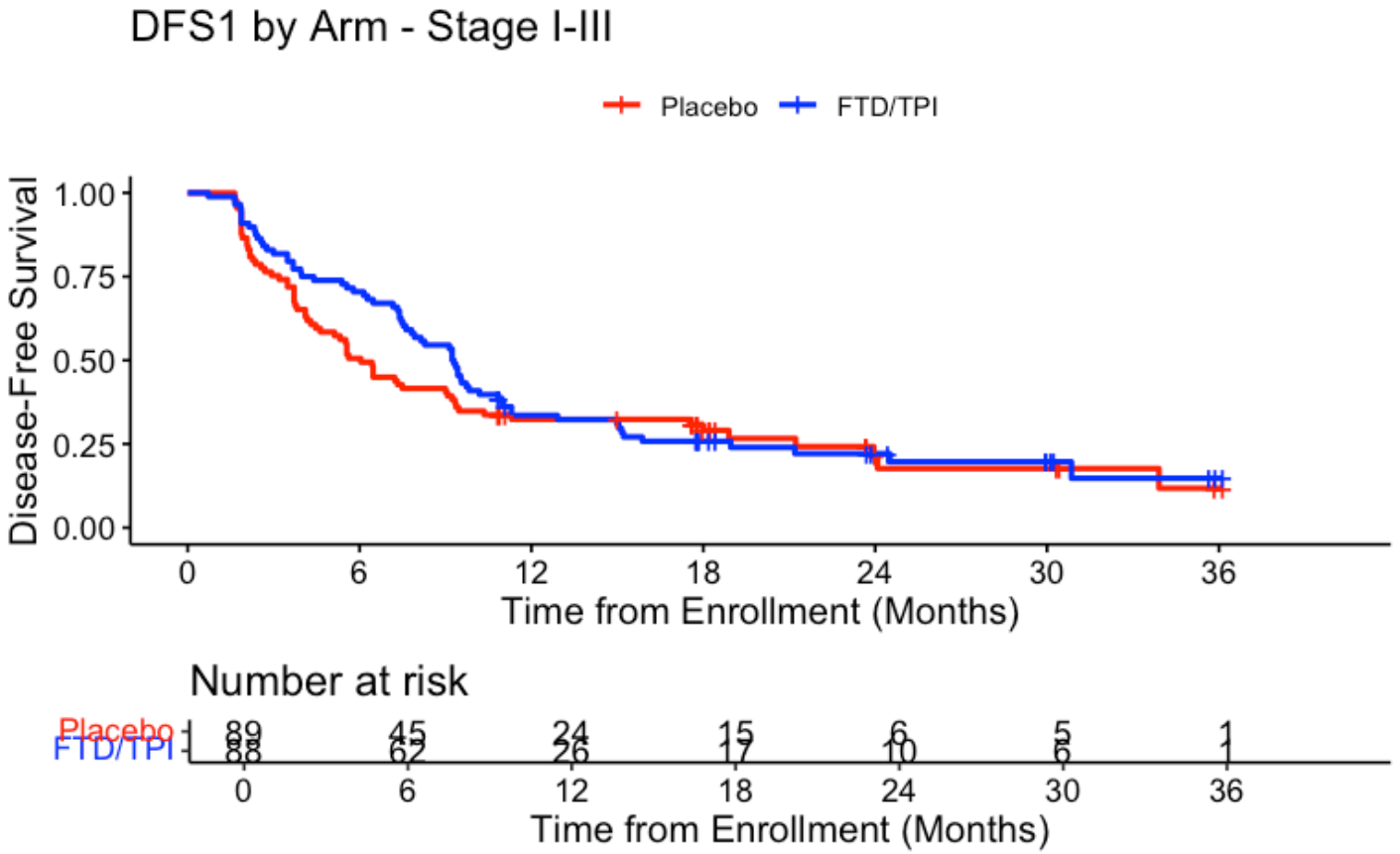
```
event_summary <- circ_data %>%
  group_by(altair.Arm) %>%
  summarise(
    Total = n(),
    Events = sum(p_evtDFS1b),
    Fraction = Events / n(),
    Percentage = (Events / n()) * 100
  )
print(event_summary)
```

| altair.Arm   | Total | Events | Fraction  | Percentage |
|--------------|-------|--------|-----------|------------|
| <chr>        | <int> | <int>  | <dbl>     | <dbl>      |
| Control      | 89    | 67     | 0.7528090 | 75.28090   |
| Experimental | 88    | 68     | 0.7727273 | 77.27273   |

2 rows

Hide

```
surv_object <-Surv(time = circ_data$DFS.months, event = circ_data$p_evtDFS1b)
KM_curve <- survfit(surv_object ~ altair.Arm, data = circ_data,conf.int=0.95,conf.type
="log-log")
ggsurvplot(KM_curve, data = circ_data, pval = FALSE, conf.int = FALSE, risk.table = TRU
E, break.time.by=6, palette=c("red","blue"), title="DFS1 by Arm - Stage I-III", ylab= "D
isease-Free Survival", xlab="Time from Enrollment (Months)", legend.labs=c("Placebo", "F
TD/TPI"), legend.title="")
```



Hide

```
summary(KM_curve, times= c(6, 12, 18, 24))
```

```
Call: survfit(formula = surv_object ~ altair.Arm, data = circ_data,
  conf.int = 0.95, conf.type = "log-log")
```

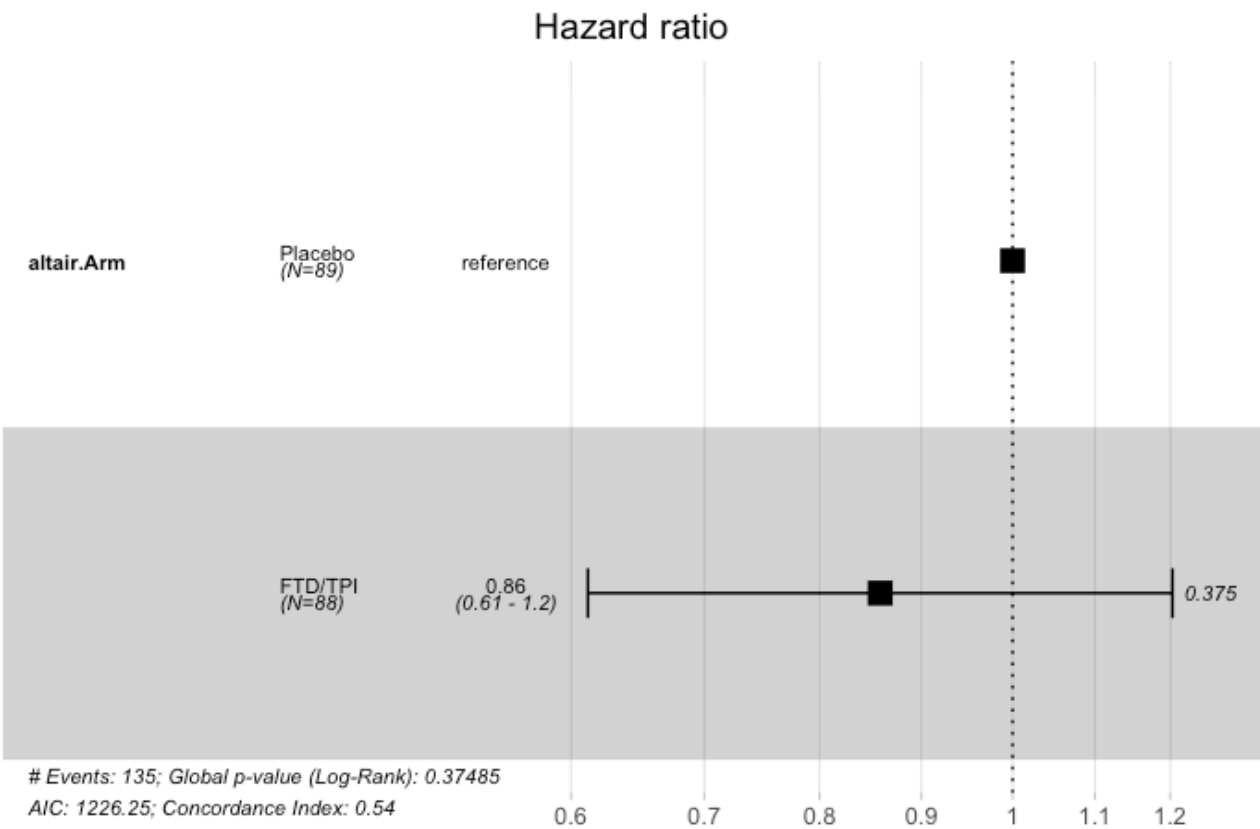
| altair.Arm=Control |        |         |          |         |              |              |  |
|--------------------|--------|---------|----------|---------|--------------|--------------|--|
| time               | n.risk | n.event | survival | std.err | lower 95% CI | upper 95% CI |  |
| 6                  | 45     | 44      | 0.506    | 0.0530  | 0.398        | 0.604        |  |
| 12                 | 24     | 16      | 0.324    | 0.0499  | 0.229        | 0.422        |  |
| 18                 | 15     | 2       | 0.291    | 0.0500  | 0.197        | 0.391        |  |
| 24                 | 6      | 3       | 0.212    | 0.0537  | 0.118        | 0.324        |  |

| altair.Arm=Experimental |        |         |          |         |              |              |  |
|-------------------------|--------|---------|----------|---------|--------------|--------------|--|
| time                    | n.risk | n.event | survival | std.err | lower 95% CI | upper 95% CI |  |
| 6                       | 62     | 26      | 0.705    | 0.0486  | 0.597        | 0.788        |  |
| 12                      | 26     | 32      | 0.336    | 0.0509  | 0.238        | 0.435        |  |
| 18                      | 17     | 6       | 0.258    | 0.0480  | 0.170        | 0.355        |  |
| 24                      | 10     | 2       | 0.221    | 0.0477  | 0.136        | 0.320        |  |

Hide

```
circ_data$altair.Arm <- factor(circ_data$altair.Arm, levels=c("Control","Experimental"),
labels = c("Placebo", "FTD/TPI"))
cox_fit <- coxph(surv_object ~ altair.Arm, data=circ_data)
ggforest(cox_fit,data = circ_data)
```



Hide

```
summary(cox_fit)
```

Call:

```
coxph(formula = surv_object ~ altair.Arm, data = circ_data)
```

n= 177, number of events= 135

|                   | coef    | exp(coef) | se(coef) | z      | Pr(> z ) |
|-------------------|---------|-----------|----------|--------|----------|
| altair.ArmFTD/TPI | -0.1532 | 0.8580    | 0.1725   | -0.888 | 0.375    |

|                   | exp(coef) | exp(-coef) | lower .95 | upper .95 |
|-------------------|-----------|------------|-----------|-----------|
| altair.ArmFTD/TPI | 0.858     | 1.166      | 0.6118    | 1.203     |

Concordance= 0.537 (se = 0.023 )

Likelihood ratio test= 0.79 on 1 df, p=0.4

Wald test = 0.79 on 1 df, p=0.4

Score (logrank) test = 0.79 on 1 df, p=0.4

[Hide](#)

```
cox_fit_summary <- summary(cox_fit)
```

```
# Extract values for HR, 95% CI, and p-value
```

```
HR <- cox_fit_summary$coefficients[2]
```

```
lower_CI <- cox_fit_summary$conf.int[3]
```

```
upper_CI <- cox_fit_summary$conf.int[4]
```

```
p_value <- cox_fit_summary$coefficients[5]
```

```
label_text <- paste0("HR = ", round(HR, 2), " (", round(lower_CI, 2), "-", round(upper_CI, 2), "); p = ", round(p_value, 3))
```

```
print(label_text)
```

```
[1] "HR = 0.86 (0.61-1.2); p = 0.375"
```

#DFS1 by TAS vs Placebo - Stage I-II

[Hide](#)

```
rm(list=ls())
```

```
setwd("~/Downloads")
```

```
circ_data <- read.csv("Altair 20240729 Dataset.csv")
```

```
circ_data <- circ_data[!(circ_data$StageA.alt %in% c("III","IV")),]
```

```
circ_datadf <- as.data.frame(circ_data)
```

```
survfit(Surv(time = circ_data$DFS.months, event = circ_data$p_evtDFS1b)~altair.Arm, data = circ_data)
```



```
Call: survfit(formula = Surv(time = circ_data$DFS.months, event = circ_data$p_evtDFS1b)
~
      altair.Arm, data = circ_data)
```

|                         | n  | events | median | 0.95LCL | 0.95UCL |
|-------------------------|----|--------|--------|---------|---------|
| altair.Arm=Control      | 33 | 20     | 18.0   | 5.52    | NA      |
| altair.Arm=Experimental | 35 | 23     | 10.8   | 9.23    | NA      |

Hide

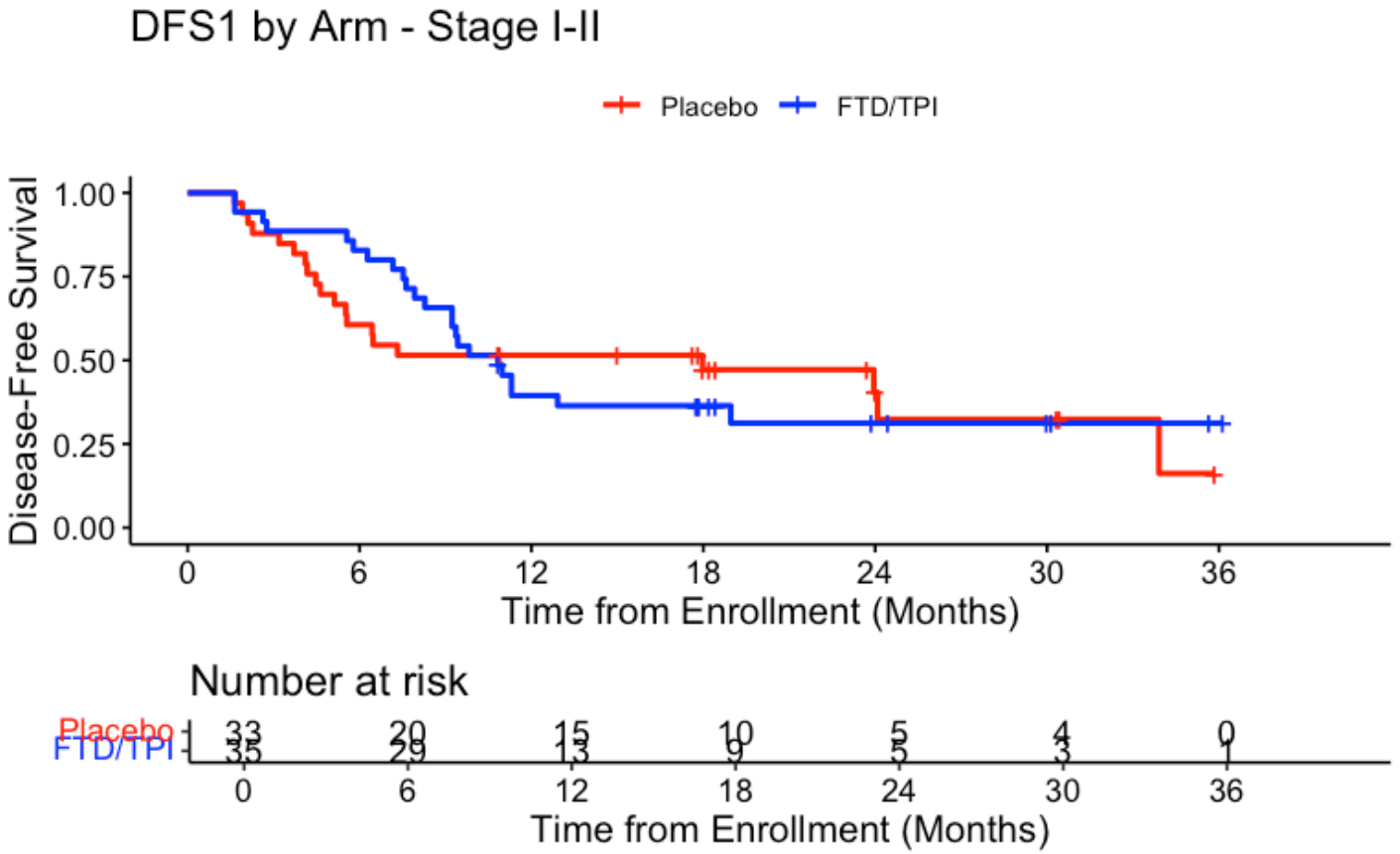
```
event_summary <- circ_data %>%
  group_by(altair.Arm) %>%
  summarise(
    Total = n(),
    Events = sum(p_evtDFS1b),
    Fraction = Events / n(),
    Percentage = (Events / n()) * 100
  )
print(event_summary)
```

| altair.Arm   | Total | Events | Fraction  | Percentage |
|--------------|-------|--------|-----------|------------|
| <chr>        | <int> | <int>  | <dbl>     | <dbl>      |
| Control      | 33    | 20     | 0.6060606 | 60.60606   |
| Experimental | 35    | 23     | 0.6571429 | 65.71429   |

2 rows

Hide

```
surv_object <-Surv(time = circ_data$DFS.months, event = circ_data$p_evtDFS1b)
KM_curve <- survfit(surv_object ~ altair.Arm, data = circ_data,conf.int=0.95,conf.type
="log-log")
ggsurvplot(KM_curve, data = circ_data, pval = FALSE, conf.int = FALSE, risk.table = TRU
E, break.time.by=6, palette=c("red","blue"), title="DFS1 by Arm - Stage I-II", ylab= "Di
sease-Free Survival", xlab="Time from Enrollment (Months)", legend.labs=c("Placebo", "FT
D/TPI"), legend.title="")
```



Hide

```
summary(KM_curve, times= c(6, 12, 18, 24))
```

```
Call: survfit(formula = surv_object ~ altair.Arm, data = circ_data,
  conf.int = 0.95, conf.type = "log-log")
```

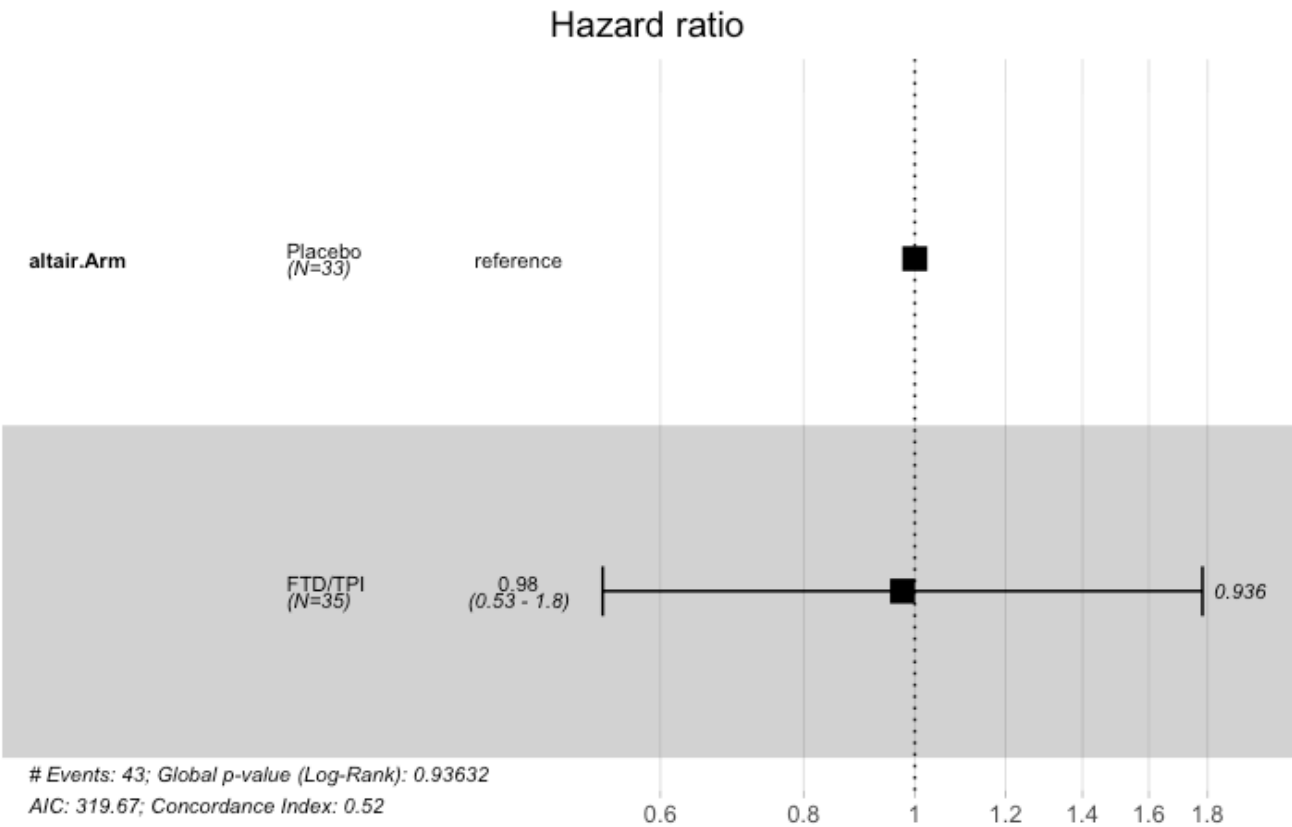
| altair.Arm=Control |        |         |          |         |              |              |  |
|--------------------|--------|---------|----------|---------|--------------|--------------|--|
| time               | n.risk | n.event | survival | std.err | lower 95% CI | upper 95% CI |  |
| 6                  | 20     | 13      | 0.606    | 0.0851  | 0.420        | 0.749        |  |
| 12                 | 15     | 3       | 0.515    | 0.0870  | 0.335        | 0.669        |  |
| 18                 | 10     | 1       | 0.472    | 0.0897  | 0.292        | 0.633        |  |
| 24                 | 5      | 1       | 0.405    | 0.0991  | 0.215        | 0.587        |  |

| altair.Arm=Experimental |        |         |          |         |              |              |  |
|-------------------------|--------|---------|----------|---------|--------------|--------------|--|
| time                    | n.risk | n.event | survival | std.err | lower 95% CI | upper 95% CI |  |
| 6                       | 29     | 6       | 0.829    | 0.0637  | 0.658        | 0.919        |  |
| 12                      | 13     | 15      | 0.395    | 0.0834  | 0.234        | 0.551        |  |
| 18                      | 9      | 1       | 0.364    | 0.0823  | 0.209        | 0.521        |  |
| 24                      | 5      | 1       | 0.312    | 0.0855  | 0.158        | 0.480        |  |

Hide

```
circ_data$altair.Arm <- factor(circ_data$altair.Arm, levels=c("Control","Experimental"),
labels = c("Placebo", "FTD/TPI"))
cox_fit <- coxph(surv_object ~ altair.Arm, data=circ_data)
ggforest(cox_fit,data = circ_data)
```



Hide

```
summary(cox_fit)
```

Call:

```
coxph(formula = surv_object ~ altair.Arm, data = circ_data)
```

n= 68, number of events= 43

|                   | coef     | exp(coef) | se(coef) | z     | Pr(> z ) |
|-------------------|----------|-----------|----------|-------|----------|
| altair.ArmFTD/TPI | -0.02455 | 0.97575   | 0.30719  | -0.08 | 0.936    |

|                   | exp(coef) | exp(-coef) | lower .95 | upper .95 |
|-------------------|-----------|------------|-----------|-----------|
| altair.ArmFTD/TPI | 0.9757    | 1.025      | 0.5344    | 1.782     |

Concordance= 0.52 (se = 0.043 )

Likelihood ratio test= 0.01 on 1 df, p=0.9

Wald test = 0.01 on 1 df, p=0.9

Score (logrank) test = 0.01 on 1 df, p=0.9

[Hide](#)

```
cox_fit_summary <- summary(cox_fit)
```

```
# Extract values for HR, 95% CI, and p-value
```

```
HR <- cox_fit_summary$coefficients[2]
```

```
lower_CI <- cox_fit_summary$conf.int[3]
```

```
upper_CI <- cox_fit_summary$conf.int[4]
```

```
p_value <- cox_fit_summary$coefficients[5]
```

```
label_text <- paste0("HR = ", round(HR, 2), " (", round(lower_CI, 2), "-", round(upper_CI, 2), "); p = ", round(p_value, 3))
```

```
print(label_text)
```

```
[1] "HR = 0.98 (0.53-1.78); p = 0.936"
```

#DFS1 by TAS vs Placebo - Stage III

[Hide](#)

```
rm(list=ls())
```

```
setwd("~/Downloads")
```

```
circ_data <- read.csv("Altair 20240729 Dataset.csv")
```

```
circ_data <- circ_data[!(circ_data$StageA.alt %in% c("I", "II", "IV")),]
```

```
circ_datadf <- as.data.frame(circ_data)
```

```
survfit(Surv(time = circ_data$DFS.months, event = circ_data$p_evtDFS1b)~altair.Arm, data = circ_data)
```

```
Call: survfit(formula = Surv(time = circ_data$DFS.months, event = circ_data$p_evtDFS1b)
~
      altair.Arm, data = circ_data)
```

|                         | n  | events | median | 0.95LCL | 0.95UCL |
|-------------------------|----|--------|--------|---------|---------|
| altair.Arm=Control      | 56 | 47     | 5.44   | 3.71    | 9.00    |
| altair.Arm=Experimental | 53 | 45     | 7.82   | 6.14    | 9.73    |

Hide

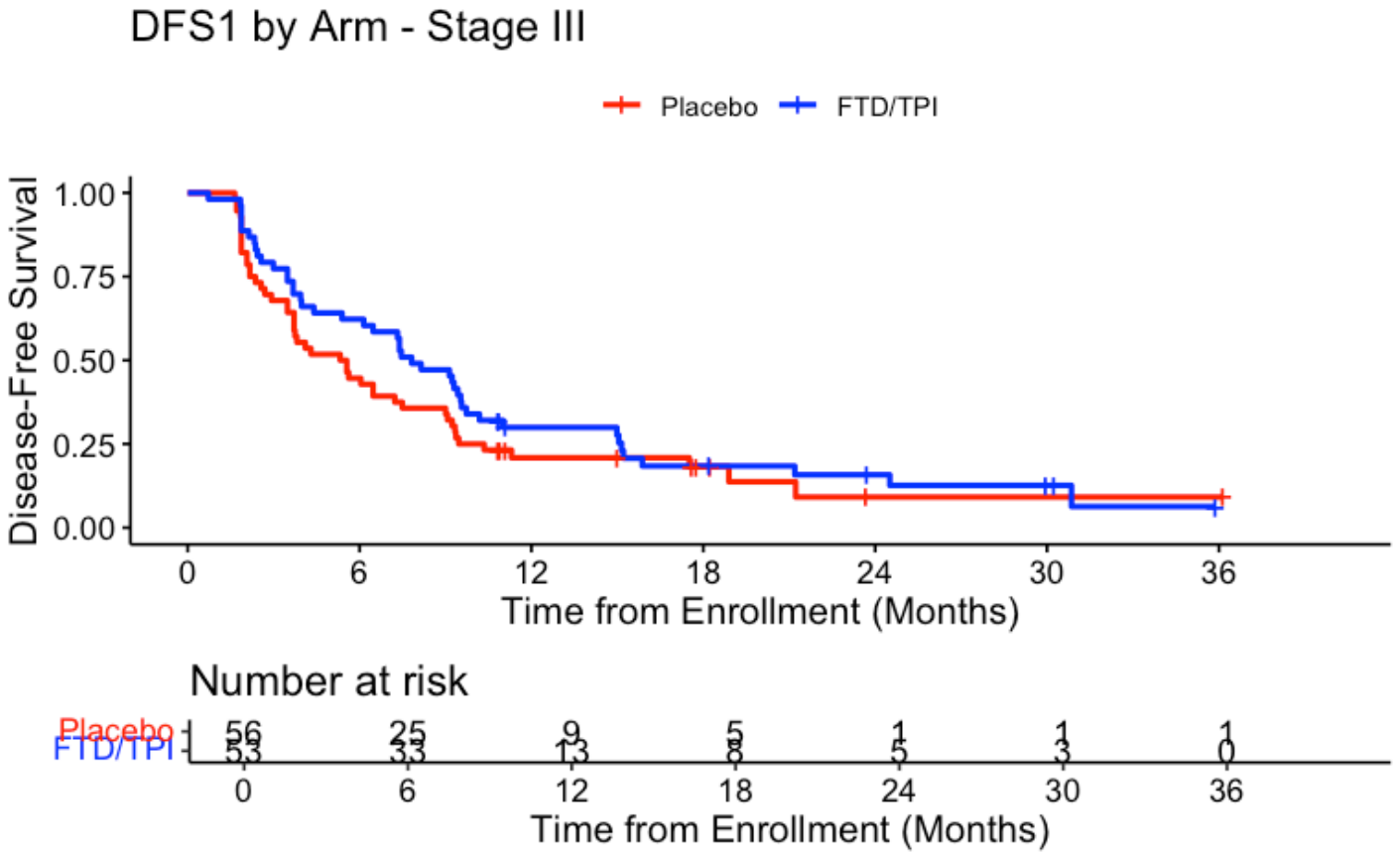
```
event_summary <- circ_data %>%
  group_by(altair.Arm) %>%
  summarise(
    Total = n(),
    Events = sum(p_evtDFS1b),
    Fraction = Events / n(),
    Percentage = (Events / n()) * 100
  )
print(event_summary)
```

| altair.Arm   | Total | Events | Fraction  | Percentage |
|--------------|-------|--------|-----------|------------|
| <chr>        | <int> | <int>  | <dbl>     | <dbl>      |
| Control      | 56    | 47     | 0.8392857 | 83.92857   |
| Experimental | 53    | 45     | 0.8490566 | 84.90566   |

2 rows

Hide

```
surv_object <-Surv(time = circ_data$DFS.months, event = circ_data$p_evtDFS1b)
KM_curve <- survfit(surv_object ~ altair.Arm, data = circ_data,conf.int=0.95,conf.type
="log-log")
ggsurvplot(KM_curve, data = circ_data, pval = FALSE, conf.int = FALSE, risk.table = TRU
E, break.time.by=6, palette=c("red","blue"), title="DFS1 by Arm - Stage III", ylab= "Dis
ease-Free Survival", xlab="Time from Enrollment (Months)", legend.labs=c("Placebo", "FT
D/TPI"), legend.title="")
```



Hide

```
summary(KM_curve, times= c(6, 12, 18, 24))
```

```
Call: survfit(formula = surv_object ~ altair.Arm, data = circ_data,
  conf.int = 0.95, conf.type = "log-log")
```

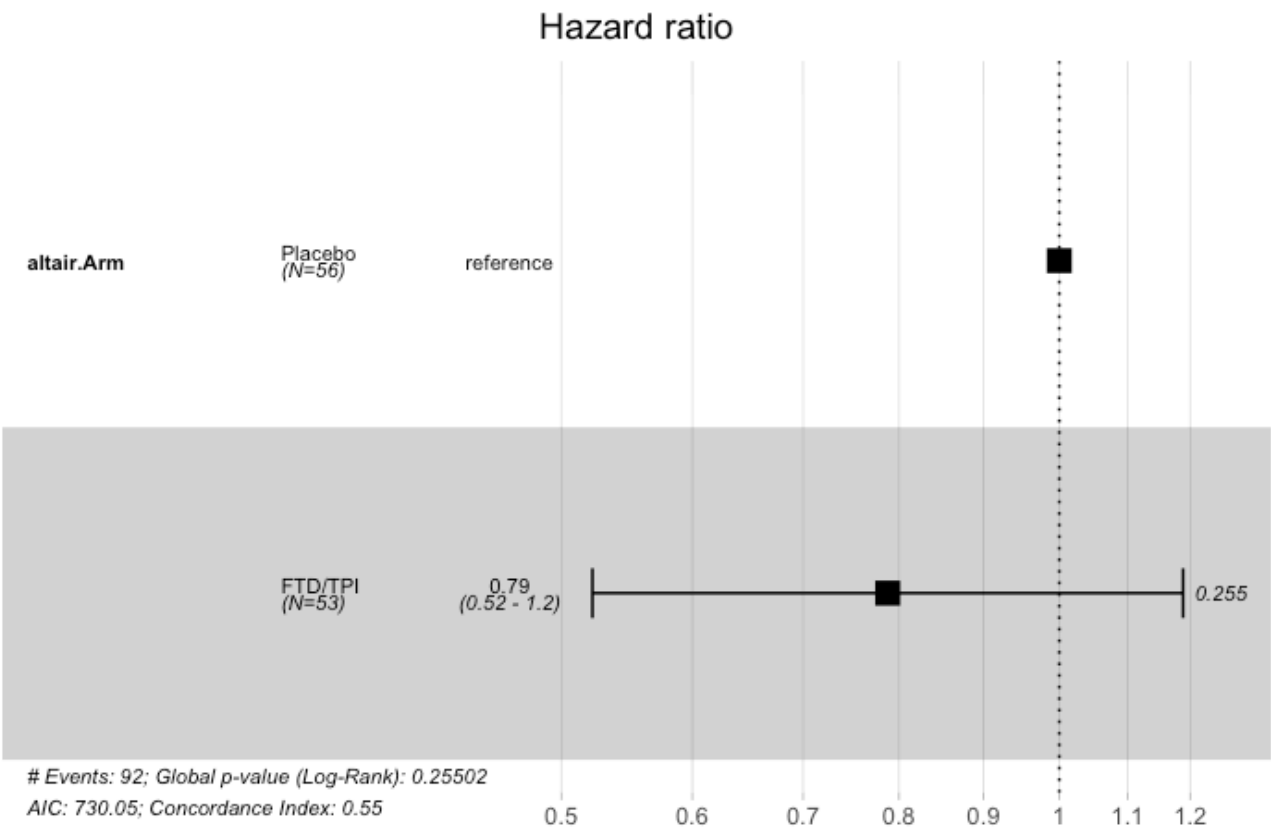
| altair.Arm=Control |        |         |          |         |              |              |  |
|--------------------|--------|---------|----------|---------|--------------|--------------|--|
| time               | n.risk | n.event | survival | std.err | lower 95% CI | upper 95% CI |  |
| 6                  | 25     | 31      | 0.4464   | 0.0664  | 0.3142       | 0.570        |  |
| 12                 | 9      | 13      | 0.2089   | 0.0553  | 0.1129       | 0.325        |  |
| 18                 | 5      | 1       | 0.1828   | 0.0542  | 0.0914       | 0.299        |  |
| 24                 | 1      | 2       | 0.0914   | 0.0531  | 0.0212       | 0.226        |  |

| altair.Arm=Experimental |        |         |          |         |              |              |  |
|-------------------------|--------|---------|----------|---------|--------------|--------------|--|
| time                    | n.risk | n.event | survival | std.err | lower 95% CI | upper 95% CI |  |
| 6                       | 33     | 20      | 0.623    | 0.0666  | 0.4784       | 0.738        |  |
| 12                      | 13     | 17      | 0.299    | 0.0633  | 0.1826       | 0.425        |  |
| 18                      | 8      | 5       | 0.184    | 0.0561  | 0.0900       | 0.305        |  |
| 24                      | 5      | 1       | 0.158    | 0.0539  | 0.0705       | 0.277        |  |

Hide

```
circ_data$altair.Arm <- factor(circ_data$altair.Arm, levels=c("Control","Experimental"),
labels = c("Placebo", "FTD/TPI"))
cox_fit <- coxph(surv_object ~ altair.Arm, data=circ_data)
ggforest(cox_fit,data = circ_data)
```



Hide

```
summary(cox_fit)
```

Call:

```
coxph(formula = surv_object ~ altair.Arm, data = circ_data)
```

n= 109, number of events= 92

|                   | coef    | exp(coef) | se(coef) | z      | Pr(> z ) |
|-------------------|---------|-----------|----------|--------|----------|
| altair.ArmFTD/TPI | -0.2388 | 0.7876    | 0.2098   | -1.138 | 0.255    |

|                   | exp(coef) | exp(-coef) | lower .95 | upper .95 |
|-------------------|-----------|------------|-----------|-----------|
| altair.ArmFTD/TPI | 0.7876    | 1.27       | 0.5221    | 1.188     |

Concordance= 0.545 (se = 0.029 )

Likelihood ratio test= 1.3 on 1 df, p=0.3

Wald test = 1.3 on 1 df, p=0.3

Score (logrank) test = 1.3 on 1 df, p=0.3

[Hide](#)

```
cox_fit_summary <- summary(cox_fit)
```

```
# Extract values for HR, 95% CI, and p-value
```

```
HR <- cox_fit_summary$coefficients[2]
```

```
lower_CI <- cox_fit_summary$conf.int[3]
```

```
upper_CI <- cox_fit_summary$conf.int[4]
```

```
p_value <- cox_fit_summary$coefficients[5]
```

```
label_text <- paste0("HR = ", round(HR, 2), " (", round(lower_CI, 2), "-", round(upper_CI, 2), "); p = ", round(p_value, 3))
```

```
print(label_text)
```

```
[1] "HR = 0.79 (0.52-1.19); p = 0.255"
```

#DFS1 by TAS vs Placebo - Stage IV

[Hide](#)

```
rm(list=ls())
```

```
setwd("~/Downloads")
```

```
circ_data <- read.csv("Altair 20240729 Dataset.csv")
```

```
circ_data <- circ_data[!(circ_data$StageA.alt %in% c("I", "II", "III")),]
```

```
circ_datadf <- as.data.frame(circ_data)
```

```
survfit(Surv(time = circ_data$DFS.months, event = circ_data$p_evtDFS1b)~altair.Arm, data = circ_data)
```



```
Call: survfit(formula = Surv(time = circ_data$DFS.months, event = circ_data$p_evtDFS1b)
~
      altair.Arm, data = circ_data)
```

|                         | n  | events | median | 0.95LCL | 0.95UCL |
|-------------------------|----|--------|--------|---------|---------|
| altair.Arm=Control      | 32 | 32     | 3.96   | 3.71    | 7.98    |
| altair.Arm=Experimental | 34 | 31     | 9.76   | 7.62    | 11.76   |

Hide

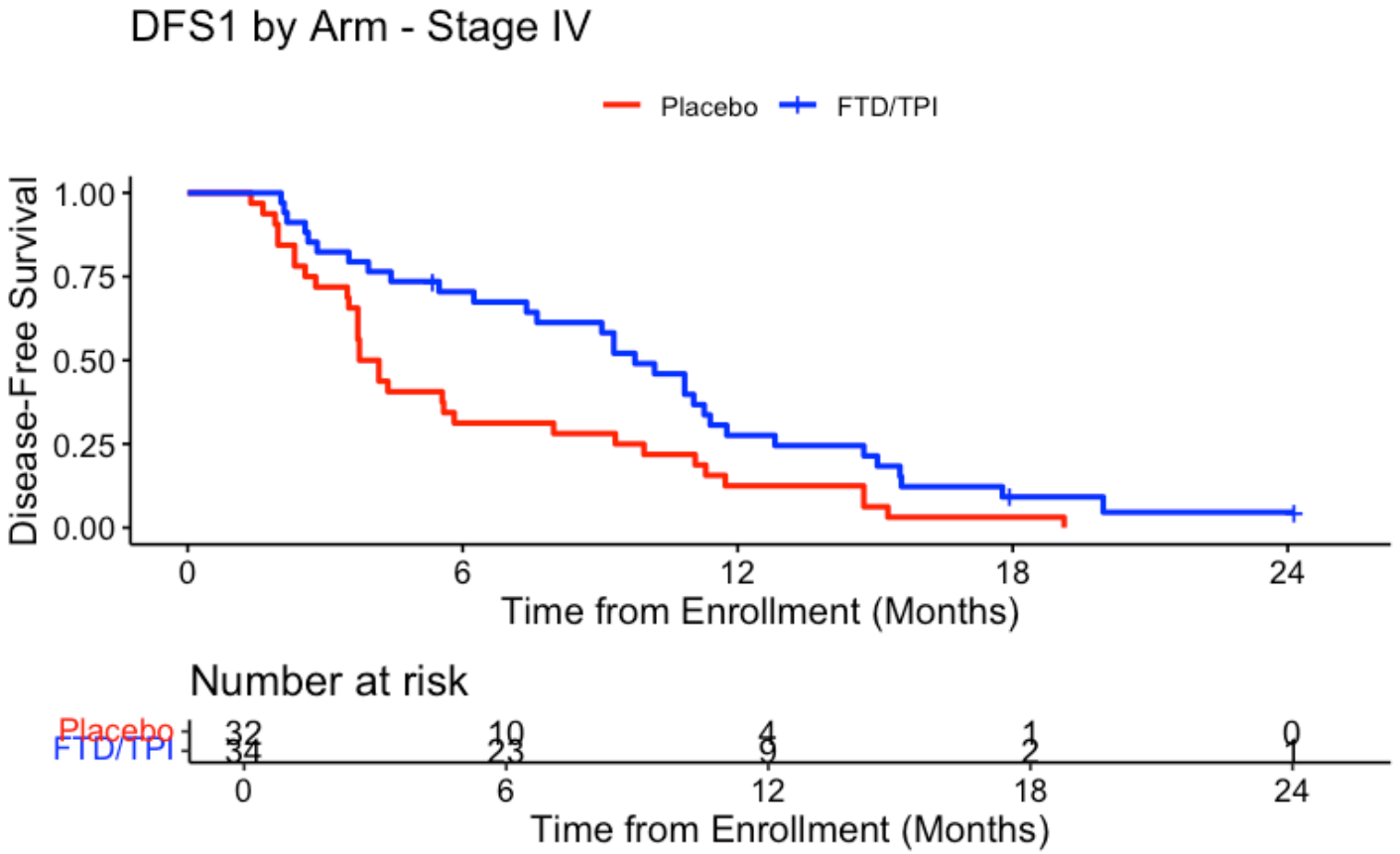
```
event_summary <- circ_data %>%
  group_by(altair.Arm) %>%
  summarise(
    Total = n(),
    Events = sum(p_evtDFS1b),
    Fraction = Events / n(),
    Percentage = (Events / n()) * 100
  )
print(event_summary)
```

| altair.Arm   | Total | Events | Fraction  | Percentage |
|--------------|-------|--------|-----------|------------|
| <chr>        | <int> | <int>  | <dbl>     | <dbl>      |
| Control      | 32    | 32     | 1.0000000 | 100.00000  |
| Experimental | 34    | 31     | 0.9117647 | 91.17647   |

2 rows

Hide

```
surv_object <-Surv(time = circ_data$DFS.months, event = circ_data$p_evtDFS1b)
KM_curve <- survfit(surv_object ~ altair.Arm, data = circ_data,conf.int=0.95,conf.type
="log-log")
ggsurvplot(KM_curve, data = circ_data, pval = FALSE, conf.int = FALSE, risk.table = TRU
E, break.time.by=6, palette=c("red","blue"), title="DFS1 by Arm - Stage IV", ylab= "Dise
ase-Free Survival", xlab="Time from Enrollment (Months)", legend.labs=c("Placebo", "FTD/
TPI"), legend.title="")
```



Hide

```
summary(KM_curve, times= c(6, 12, 18, 24))
```

```
Call: survfit(formula = surv_object ~ altair.Arm, data = circ_data,
  conf.int = 0.95, conf.type = "log-log")
```

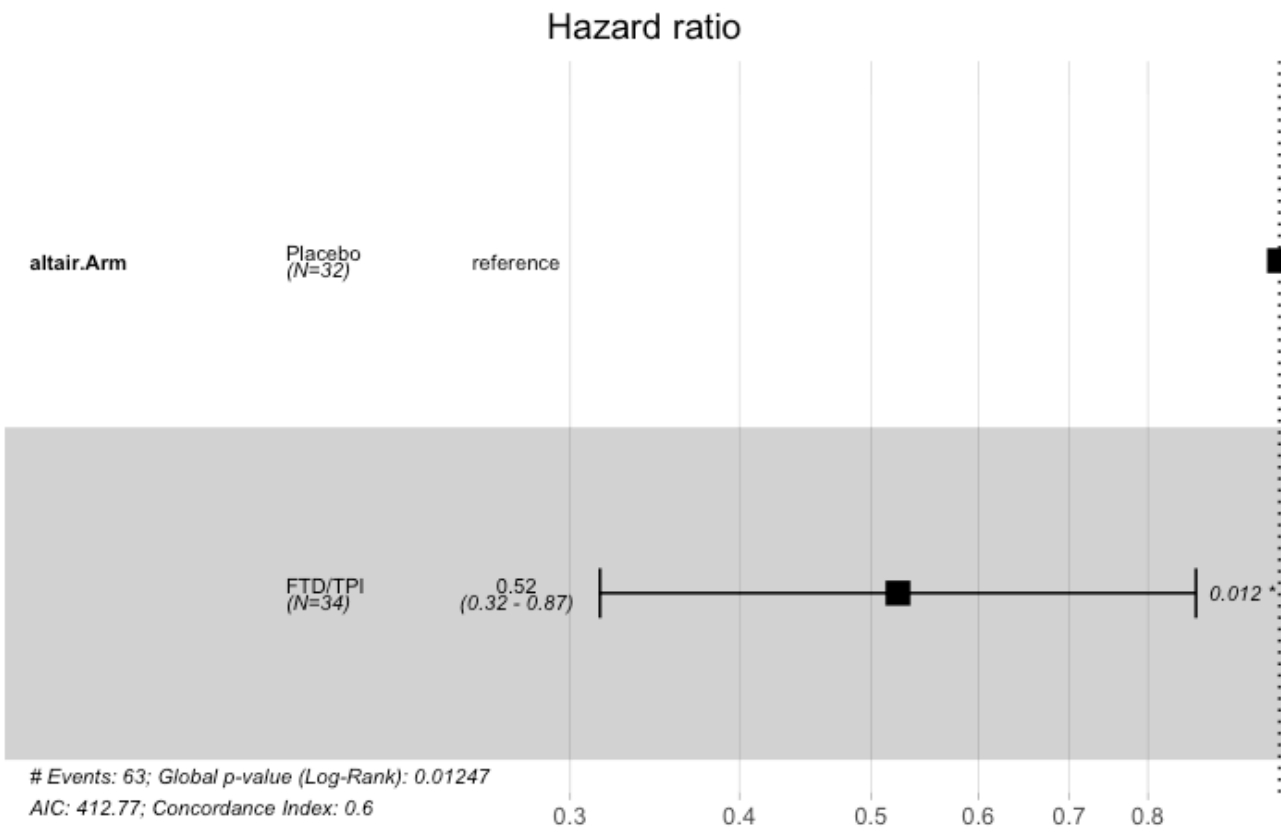
| altair.Arm=Control |        |         |          |         |              |              |  |
|--------------------|--------|---------|----------|---------|--------------|--------------|--|
| time               | n.risk | n.event | survival | std.err | lower 95% CI | upper 95% CI |  |
| 6                  | 10     | 22      | 0.3125   | 0.0819  | 0.16376      | 0.473        |  |
| 12                 | 4      | 6       | 0.1250   | 0.0585  | 0.03950      | 0.262        |  |
| 18                 | 1      | 3       | 0.0312   | 0.0308  | 0.00237      | 0.137        |  |

| altair.Arm=Experimental |        |         |          |         |              |              |  |
|-------------------------|--------|---------|----------|---------|--------------|--------------|--|
| time                    | n.risk | n.event | survival | std.err | lower 95% CI | upper 95% CI |  |
| 6                       | 23     | 10      | 0.7047   | 0.0785  | 0.52049      | 0.829        |  |
| 12                      | 9      | 14      | 0.2757   | 0.0780  | 0.13790      | 0.433        |  |
| 18                      | 2      | 6       | 0.0919   | 0.0505  | 0.02355      | 0.219        |  |
| 24                      | 1      | 1       | 0.0460   | 0.0412  | 0.00431      | 0.175        |  |

Hide

```
circ_data$altair.Arm <- factor(circ_data$altair.Arm, levels=c("Control","Experimental"),
labels = c("Placebo", "FTD/TPI"))
cox_fit <- coxph(surv_object ~ altair.Arm, data=circ_data)
ggforest(cox_fit,data = circ_data)
```



Hide

```
summary(cox_fit)
```

```
Call:
coxph(formula = surv_object ~ altair.Arm, data = circ_data)

n= 66, number of events= 63

              coef exp(coef) se(coef)      z Pr(>|z|)
altair.ArmFTD/TPI -0.6474    0.5234  0.2580 -2.509  0.0121 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

              exp(coef) exp(-coef) lower .95 upper .95
altair.ArmFTD/TPI    0.5234      1.911    0.3157    0.8679

Concordance= 0.596 (se = 0.034 )
Likelihood ratio test= 6.24 on 1 df,  p=0.01
Wald test               = 6.3 on 1 df,  p=0.01
Score (logrank) test = 6.5 on 1 df,  p=0.01
```

Hide

```
cox_fit_summary <- summary(cox_fit)

# Extract values for HR, 95% CI, and p-value
HR <- cox_fit_summary$coefficients[2]
lower_CI <- cox_fit_summary$conf.int[3]
upper_CI <- cox_fit_summary$conf.int[4]
p_value <- cox_fit_summary$coefficients[5]
label_text <- paste0("HR = ", round(HR, 2), " (", round(lower_CI, 2), "-", round(upper_C
I, 2), "); p = ", round(p_value, 3))
print(label_text)
```

```
[1] "HR = 0.52 (0.32-0.87); p = 0.012"
```

#DFS1 by TAS vs Placebo - ctDNA positive post-surgery

Hide

```
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Altair 20240729 Dataset.csv")
circ_data <- circ_data[circ_data$ctDNA1mo == "POSITIVE",]
circ_data <- subset(circ_data, !is.na(p_MRD))
circ_datadf <- as.data.frame(circ_data)

survfit(Surv(time = circ_data$DFS.months, event = circ_data$p_evtDFS1b)~altair.Arm, data
= circ_data)
```

```
Call: survfit(formula = Surv(time = circ_data$DFS.months, event = circ_data$p_evtDFS1b)
~
      altair.Arm, data = circ_data)

              n events median 0.95LCL 0.95UCL
altair.Arm=Control      65     58   4.17    3.71    6.47
altair.Arm=Experimental 65     55   7.92    7.16   10.84
```

Hide

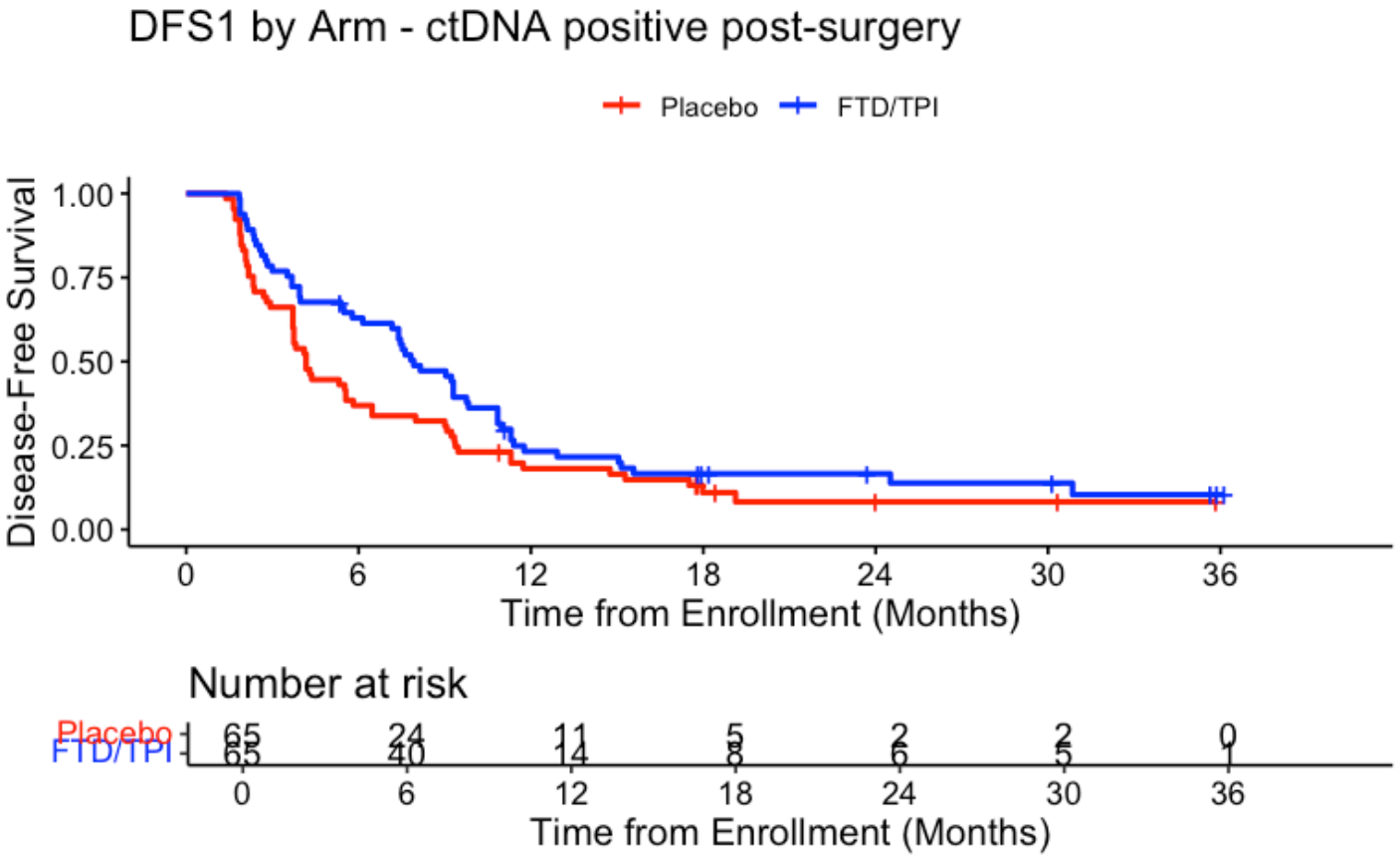
```
event_summary <- circ_data %>%
  group_by(altair.Arm) %>%
  summarise(
    Total = n(),
    Events = sum(p_evtDFS1b),
    Fraction = Events / n(),
    Percentage = (Events / n()) * 100
  )
print(event_summary)
```

| altair.Arm   | Total | Events | Fraction  | Percentage |
|--------------|-------|--------|-----------|------------|
| <chr>        | <int> | <int>  | <dbl>     | <dbl>      |
| Control      | 65    | 58     | 0.8923077 | 89.23077   |
| Experimental | 65    | 55     | 0.8461538 | 84.61538   |

2 rows

Hide

```
surv_object <-Surv(time = circ_data$DFS.months, event = circ_data$p_evtDFS1b)
KM_curve <- survfit(surv_object ~ altair.Arm, data = circ_data,conf.int=0.95,conf.type
="log-log")
ggsurvplot(KM_curve, data = circ_data, pval = FALSE, conf.int = FALSE, risk.table = TRU
E, break.time.by=6, palette=c("red","blue"), title="DFS1 by Arm - ctDNA positive post-su
rgery", ylab= "Disease-Free Survival", xlab="Time from Enrollment (Months)", legend.labs
=c("Placebo", "FTD/TPI"), legend.title="")
```



Hide

```
summary(KM_curve, times= c(6, 12, 18, 24))
```

```
Call: survfit(formula = surv_object ~ altair.Arm, data = circ_data,
  conf.int = 0.95, conf.type = "log-log")
```

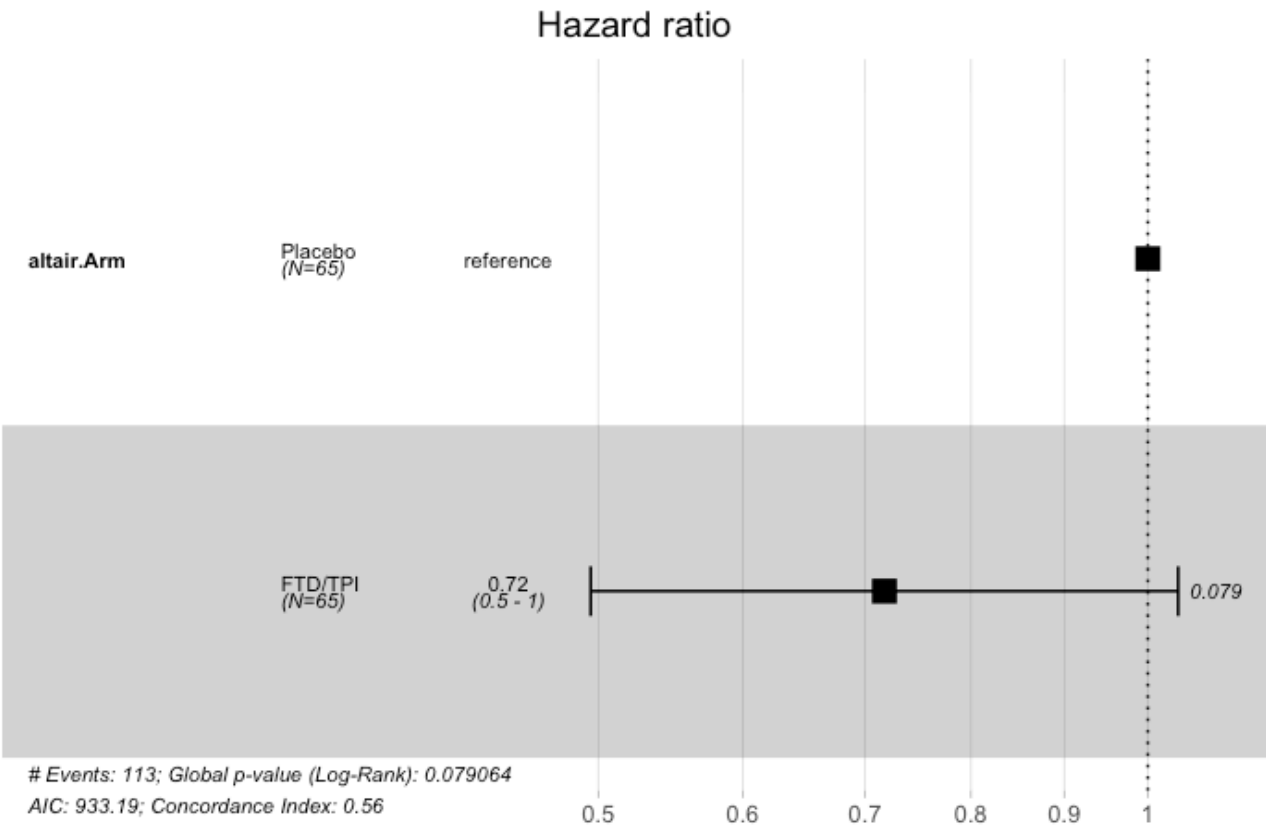
| altair.Arm=Control |        |         |          |         |              |              |  |
|--------------------|--------|---------|----------|---------|--------------|--------------|--|
| time               | n.risk | n.event | survival | std.err | lower 95% CI | upper 95% CI |  |
| 6                  | 24     | 41      | 0.3692   | 0.0599  | 0.2540       | 0.485        |  |
| 12                 | 11     | 12      | 0.1813   | 0.0482  | 0.0985       | 0.284        |  |
| 18                 | 5      | 4       | 0.1099   | 0.0408  | 0.0464       | 0.204        |  |
| 24                 | 2      | 1       | 0.0824   | 0.0388  | 0.0270       | 0.178        |  |

| altair.Arm=Experimental |        |         |          |         |              |              |  |
|-------------------------|--------|---------|----------|---------|--------------|--------------|--|
| time                    | n.risk | n.event | survival | std.err | lower 95% CI | upper 95% CI |  |
| 6                       | 40     | 24      | 0.630    | 0.0600  | 0.5002       | 0.734        |  |
| 12                      | 14     | 25      | 0.233    | 0.0534  | 0.1374       | 0.343        |  |
| 18                      | 8      | 4       | 0.166    | 0.0473  | 0.0863       | 0.269        |  |
| 24                      | 6      | 0       | 0.166    | 0.0473  | 0.0863       | 0.269        |  |

Hide

```
circ_data$altair.Arm <- factor(circ_data$altair.Arm, levels=c("Control","Experimental"),
labels = c("Placebo", "FTD/TPI"))
cox_fit <- coxph(surv_object ~ altair.Arm, data=circ_data)
ggforest(cox_fit,data = circ_data)
```



Hide

```
summary(cox_fit)
```

Call:

```
coxph(formula = surv_object ~ altair.Arm, data = circ_data)
```

n= 130, number of events= 113

|                   | coef    | exp(coef) | se(coef) | z      | Pr(> z ) |
|-------------------|---------|-----------|----------|--------|----------|
| altair.ArmFTD/TPI | -0.3323 | 0.7173    | 0.1891   | -1.757 | 0.0789   |

----

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

|                   | exp(coef) | exp(-coef) | lower .95 | upper .95 |
|-------------------|-----------|------------|-----------|-----------|
| altair.ArmFTD/TPI | 0.7173    | 1.394      | 0.4952    | 1.039     |

Concordance= 0.56 (se = 0.026 )

Likelihood ratio test= 3.08 on 1 df, p=0.08

Wald test = 3.09 on 1 df, p=0.08

Score (logrank) test = 3.12 on 1 df, p=0.08

Hide

```
cox_fit_summary <- summary(cox_fit)
```

```
# Extract values for HR, 95% CI, and p-value
```

```
HR <- cox_fit_summary$coefficients[2]
```

```
lower_CI <- cox_fit_summary$conf.int[3]
```

```
upper_CI <- cox_fit_summary$conf.int[4]
```

```
p_value <- cox_fit_summary$coefficients[5]
```

```
label_text <- paste0("HR = ", round(HR, 2), " (", round(lower_CI, 2), "-", round(upper_CI, 2), "); p = ", round(p_value, 3))
```

```
print(label_text)
```

```
[1] "HR = 0.72 (0.5-1.04); p = 0.079"
```

Hide



```
#Fisher test for DFS percentages at 6, 12, 18 and 24 months
dfs_times <- c(6, 12, 18, 24)
p_values <- sapply(dfs_times, function(time) {
  neg_count <- sum(circ_data$altair.Arm == "FTD/TPI" & circ_data$DFS.months >= time & circ_data$p_evtDFS1b == 0)
  pos_count <- sum(circ_data$altair.Arm == "Placebo" & circ_data$DFS.months >= time & circ_data$p_evtDFS1b == 0)
  neg_total <- sum(circ_data$altair.Arm == "FTD/TPI")
  pos_total <- sum(circ_data$altair.Arm == "Placebo")

  neg_surv <- neg_total - sum(circ_data$altair.Arm == "FTD/TPI" & circ_data$p_evtDFS1b == 1 & circ_data$DFS.months < time)
  pos_surv <- pos_total - sum(circ_data$altair.Arm == "Placebo" & circ_data$p_evtDFS1b == 1 & circ_data$DFS.months < time)

  surv_matrix <- matrix(c(neg_surv, pos_surv, neg_total - neg_surv, pos_total - pos_surv), nrow = 2)
  test_result <- fisher.test(surv_matrix)
  return(test_result$p.value)
})
names(p_values) <- paste0("p-value at ", dfs_times, " months")
print(p_values)
```

| p-value at 6 months | p-value at 12 months | p-value at 18 months | p-value at 24 months |
|---------------------|----------------------|----------------------|----------------------|
| 0.004815238         | 0.522656471          | 0.466593017          | 0.320823902          |

#DFS1 by TAS vs Placebo - ctDNA negative post-surgery

[Hide](#)

```
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Altair 20240729 Dataset.csv")
circ_data <- circ_data[circ_data$ctDNA1mo == "NEGATIVE",]
circ_data <- subset(circ_data, !is.na(ctDNA1mo))
circ_datadf <- as.data.frame(circ_data)

survfit(Surv(time = circ_data$DFS.months, event = circ_data$p_evtDFS1b)~altair.Arm, data = circ_data)
```

```
Call: survfit(formula = Surv(time = circ_data$DFS.months, event = circ_data$p_evtDFS1b) ~
  altair.Arm, data = circ_data)
```

|                         | n  | events | median | 0.95LCL | 0.95UCL |
|-------------------------|----|--------|--------|---------|---------|
| altair.Arm=Control      | 56 | 41     | 6.85   | 5.55    | 18.9    |
| altair.Arm=Experimental | 57 | 44     | 10.18  | 9.23    | 15.0    |

[Hide](#)

```
event_summary <- circ_data %>%
  group_by(altair.Arm) %>%
  summarise(
    Total = n(),
    Events = sum(p_evtDFS1b),
    Fraction = Events / n(),
    Percentage = (Events / n()) * 100
  )
print(event_summary)
```

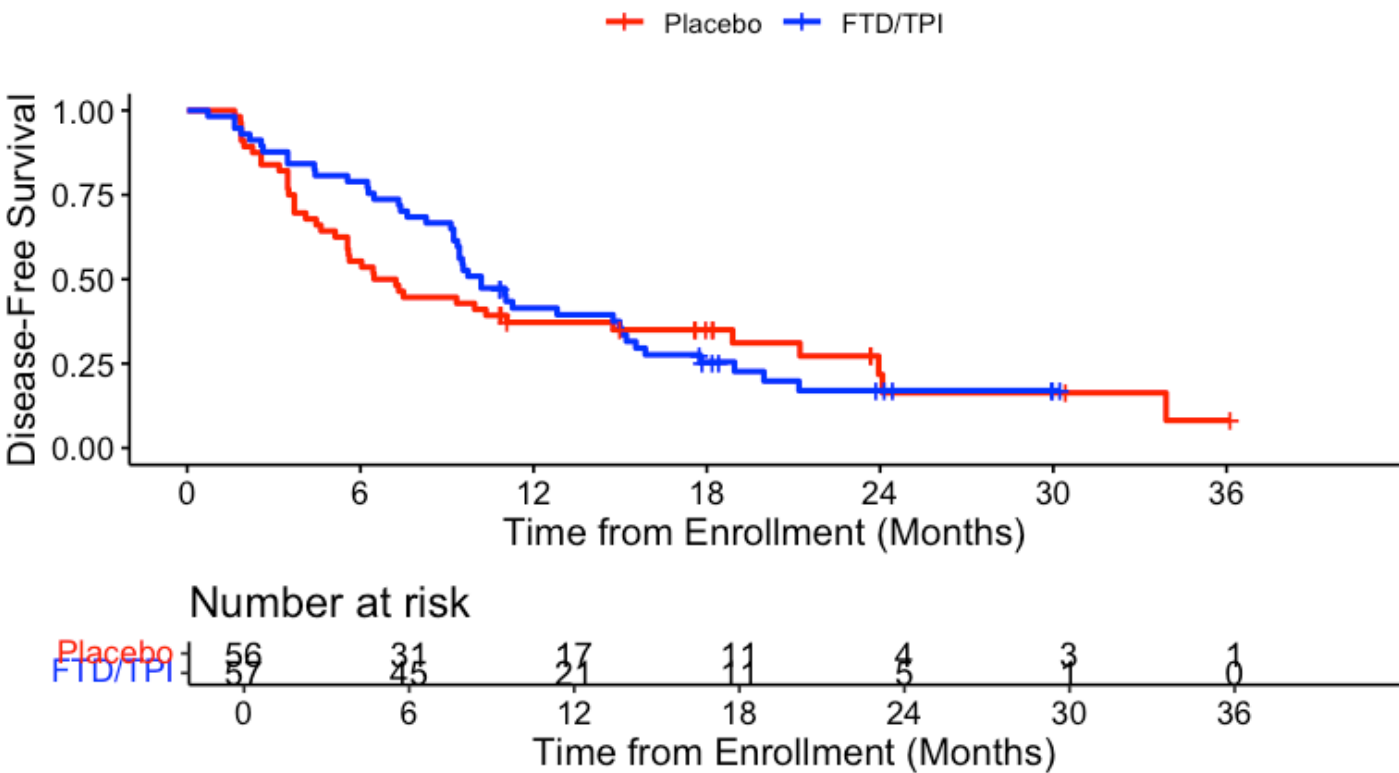
| altair.Arm   | Total | Events | Fraction  | Percentage |
|--------------|-------|--------|-----------|------------|
| <chr>        | <int> | <int>  | <dbl>     | <dbl>      |
| Control      | 56    | 41     | 0.7321429 | 73.21429   |
| Experimental | 57    | 44     | 0.7719298 | 77.19298   |

2 rows

Hide

```
surv_object <-Surv(time = circ_data$DFS.months, event = circ_data$p_evtDFS1b)
KM_curve <- survfit(surv_object ~ altair.Arm, data = circ_data,conf.int=0.95,conf.type
="log-log")
ggsurvplot(KM_curve, data = circ_data, pval = FALSE, conf.int = FALSE, risk.table = TRU
E, break.time.by=6, palette=c("red","blue"), title="DFS1 by Arm - ctDNA negative post-su
rgery", ylab= "Disease-Free Survival", xlab="Time from Enrollment (Months)", legend.labs
=c("Placebo", "FTD/TPI"), legend.title="")
```

DFS1 by Arm - ctDNA negative post-surgery



Hide

```
summary(KM_curve, times= c(6, 12, 18, 24))
```

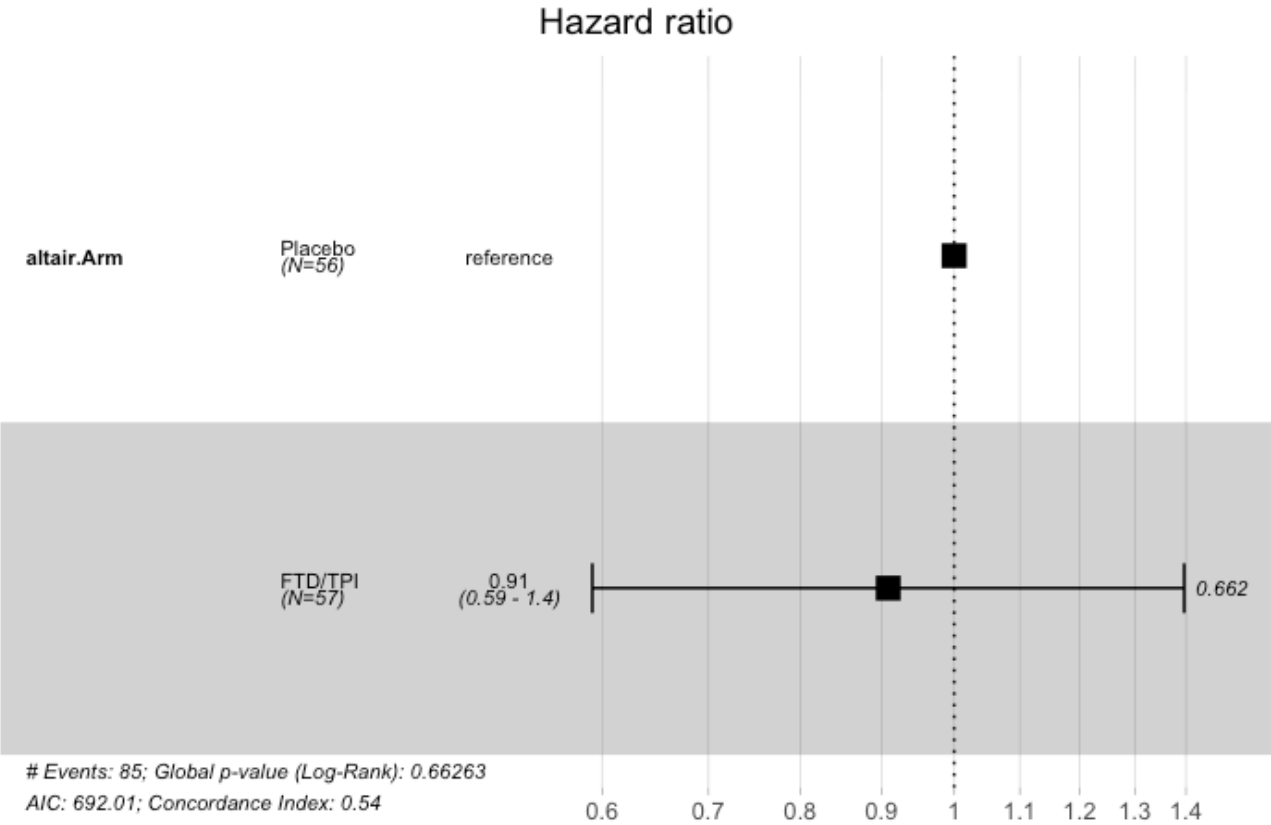
```
Call: survfit(formula = surv_object ~ altair.Arm, data = circ_data,
  conf.int = 0.95, conf.type = "log-log")
```

```
altair.Arm=Control
time n.risk n.event survival std.err lower 95% CI upper 95% CI
  6      31      25   0.554  0.0664   0.4147   0.672
 12      17      10   0.372  0.0650   0.2472   0.497
 18       11       1   0.350  0.0648   0.2272   0.476
 24        4       3   0.218  0.0742   0.0943   0.374
```

```
altair.Arm=Experimental
time n.risk n.event survival std.err lower 95% CI upper 95% CI
  6      45      12   0.789  0.0540   0.6592   0.875
 12      21      21   0.414  0.0661   0.2848   0.539
 18      11       8   0.255  0.0602   0.1471   0.378
 24       5       3   0.170  0.0567   0.0771   0.294
```

Hide

```
circ_data$altair.Arm <- factor(circ_data$altair.Arm, levels=c("Control","Experimental"),
  labels = c("Placebo", "FTD/TPI"))
cox_fit <- coxph(surv_object ~ altair.Arm, data=circ_data)
ggforest(cox_fit,data = circ_data)
```



Hide

```
summary(cox_fit)
```

Call:  
coxph(formula = surv\_object ~ altair.Arm, data = circ\_data)

n= 113, number of events= 85

|                   | coef     | exp(coef) | se(coef) | z      | Pr(> z ) |
|-------------------|----------|-----------|----------|--------|----------|
| altair.ArmFTD/TPI | -0.09568 | 0.90875   | 0.21911  | -0.437 | 0.662    |

|                   | exp(coef) | exp(-coef) | lower .95 | upper .95 |
|-------------------|-----------|------------|-----------|-----------|
| altair.ArmFTD/TPI | 0.9088    | 1.1        | 0.5915    | 1.396     |

Concordance= 0.538 (se = 0.03 )  
Likelihood ratio test= 0.19 on 1 df, p=0.7  
Wald test = 0.19 on 1 df, p=0.7  
Score (logrank) test = 0.19 on 1 df, p=0.7

Hide

```
cox_fit_summary <- summary(cox_fit)

# Extract values for HR, 95% CI, and p-value
HR <- cox_fit_summary$coefficients[2]
lower_CI <- cox_fit_summary$conf.int[3]
upper_CI <- cox_fit_summary$conf.int[4]
p_value <- cox_fit_summary$coefficients[5]
label_text <- paste0("HR = ", round(HR, 2), " (", round(lower_CI, 2), "-", round(upper_CI, 2), "); p = ", round(p_value, 3))
print(label_text)
```

[1] "HR = 0.91 (0.59–1.4); p = 0.662"

#DFS2 by TAS vs Placebo - All stages

Hide

```
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Altair 20240729 Dataset.csv")
circ_datadf <- as.data.frame(circ_data)

survfit(Surv(time = circ_data$DFS2.months, event = circ_data$p_evtDFS2)~altair.Arm, data = circ_data)
```

Call: survfit(formula = Surv(time = circ\_data\$DFS2.months, event = circ\_data\$p\_evtDFS2) ~ altair.Arm, data = circ\_data)

|                         | n   | events | median | 0.95LCL | 0.95UCL |
|-------------------------|-----|--------|--------|---------|---------|
| altair.Arm=Control      | 121 | 100    | 5.55   | 4.17    | 7.33    |
| altair.Arm=Experimental | 122 | 99     | 9.30   | 7.92    | 10.84   |

Hide

```
event_summary <- circ_data %>%
  group_by(altair.Arm) %>%
  summarise(
    Total = n(),
    Events = sum(p_evtDFS2),
    Fraction = Events / n(),
    Percentage = (Events / n()) * 100
  )
print(event_summary)
```

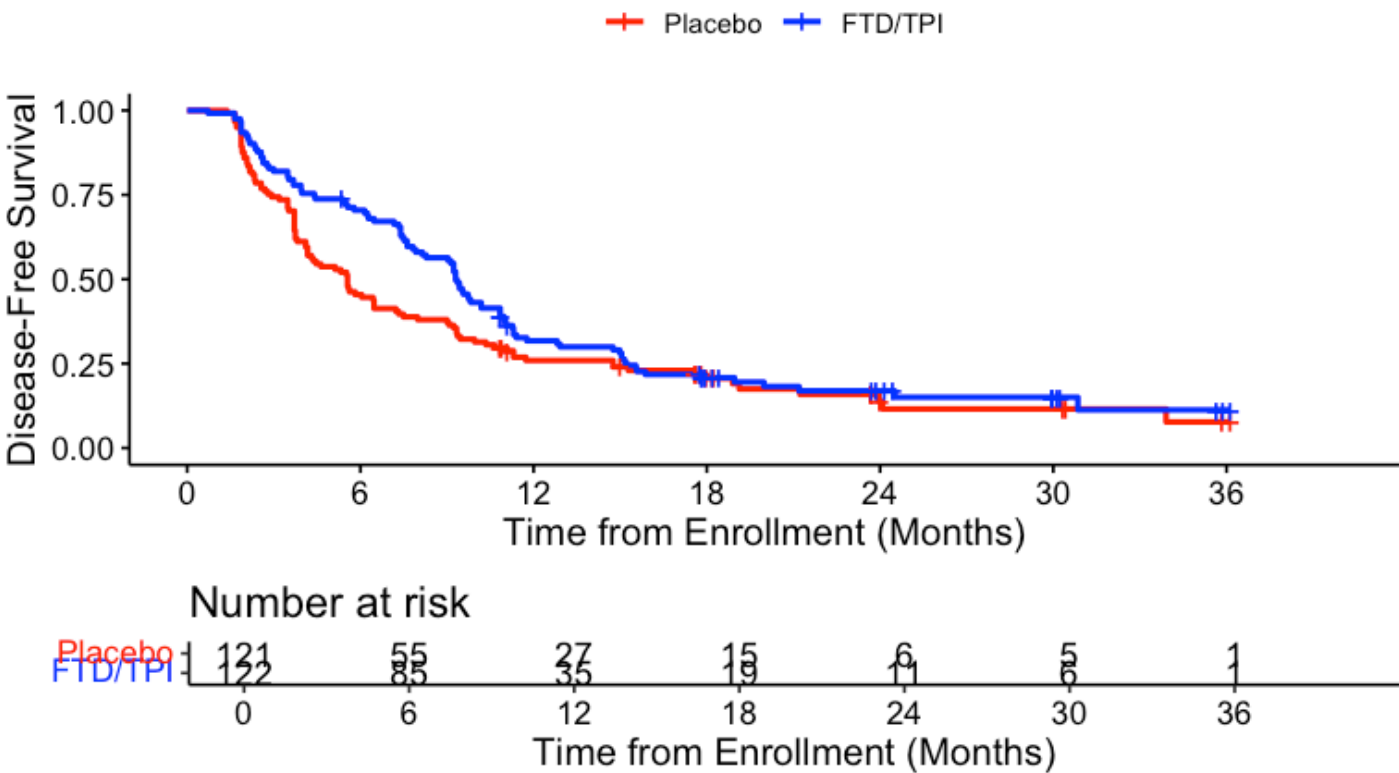
| altair.Arm<br><chr> | Total<br><int> | Events<br><int> | Fraction<br><dbl> | Percentage<br><dbl> |
|---------------------|----------------|-----------------|-------------------|---------------------|
| Control             | 121            | 100             | 0.8264463         | 82.64463            |

| altair.Arm<br><chr> | Total<br><int> | Events<br><int> | Fraction<br><dbl> | Percentage<br><dbl> |
|---------------------|----------------|-----------------|-------------------|---------------------|
| Experimental        | 122            | 99              | 0.8114754         | 81.14754            |
| 2 rows              |                |                 |                   |                     |

Hide

```
surv_object <-Surv(time = circ_data$DFS2.months, event = circ_data$p_evtDFS2)
KM_curve <- survfit(surv_object ~ altair.Arm, data = circ_data,conf.int=0.95,conf.type
="log-log")
ggsurvplot(KM_curve, data = circ_data, pval = FALSE, conf.int = FALSE, risk.table = TRU
E, break.time.by=6, palette=c("red","blue"), title="DFS2 by Arm", ylab= "Disease-Free Su
rvival", xlab="Time from Enrollment (Months)", legend.labs=c("Placebo", "FTD/TPI"), lege
nd.title="")
```

DFS2 by Arm



Hide

```
summary(KM_curve, times= c(6, 12, 18, 24))
```

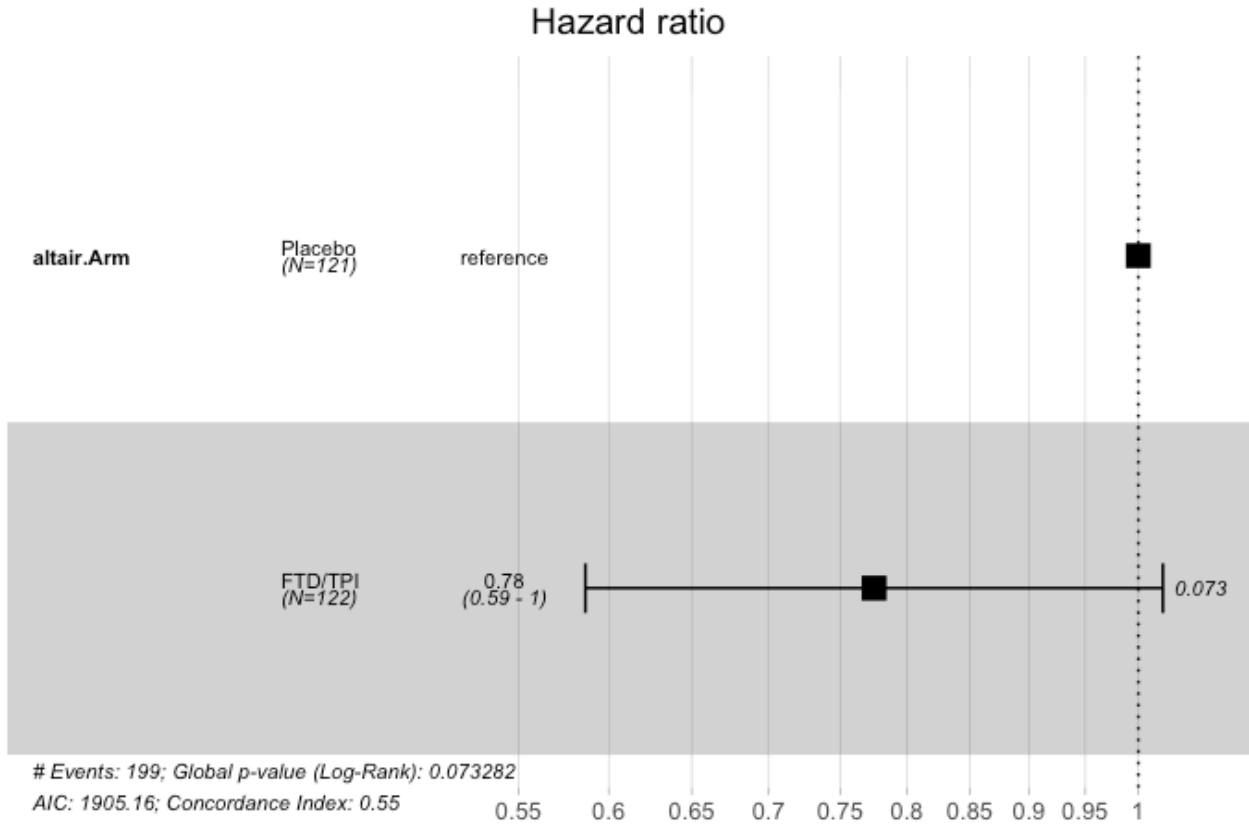
```
Call: survfit(formula = surv_object ~ altair.Arm, data = circ_data,
  conf.int = 0.95, conf.type = "log-log")
```

```
altair.Arm=Control
time n.risk n.event survival std.err lower 95% CI upper 95% CI
  6      55      66   0.455  0.0453   0.3642   0.540
 12      27      23   0.259  0.0404   0.1842   0.341
 18      15       5   0.206  0.0386   0.1366   0.286
 24       6       4   0.139  0.0383   0.0746   0.223
```

```
altair.Arm=Experimental
time n.risk n.event survival std.err lower 95% CI upper 95% CI
  6      85      36   0.705  0.0413   0.615   0.777
 12      35      46   0.318  0.0428   0.236   0.402
 18      19      12   0.208  0.0380   0.139   0.287
 24      11       3   0.169  0.0370   0.104   0.248
```

Hide

```
circ_data$altair.Arm <- factor(circ_data$altair.Arm, levels=c("Control","Experimental"),
labels = c("Placebo", "FTD/TPI"))
cox_fit <- coxph(surv_object ~ altair.Arm, data=circ_data)
ggforest(cox_fit,data = circ_data)
```



Hide

```
summary(cox_fit)
```

Call:  
coxph(formula = surv\_object ~ altair.Arm, data = circ\_data)

n= 243, number of events= 199

|                   | coef    | exp(coef) | se(coef) | z      | Pr(> z ) |
|-------------------|---------|-----------|----------|--------|----------|
| altair.ArmFTD/TPI | -0.2549 | 0.7750    | 0.1421   | -1.793 | 0.073 .  |

---  
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

|                   | exp(coef) | exp(-coef) | lower .95 | upper .95 |
|-------------------|-----------|------------|-----------|-----------|
| altair.ArmFTD/TPI | 0.775     | 1.29       | 0.5866    | 1.024     |

Concordance= 0.552 (se = 0.019 )  
Likelihood ratio test= 3.21 on 1 df, p=0.07  
Wald test = 3.22 on 1 df, p=0.07  
Score (logrank) test = 3.23 on 1 df, p=0.07

Hide



```
cox_fit_summary <- summary(cox_fit)

# Extract values for HR, 95% CI, and p-value
HR <- cox_fit_summary$coefficients[2]
lower_CI <- cox_fit_summary$conf.int[3]
upper_CI <- cox_fit_summary$conf.int[4]
p_value <- cox_fit_summary$coefficients[5]
label_text <- paste0("HR = ", round(HR, 2), " (", round(lower_CI, 2), "-", round(upper_CI, 2), "); p = ", round(p_value, 3))
print(label_text)
```

[1] "HR = 0.78 (0.59–1.02); p = 0.073"

#OS by TAS vs Placebo - All stages

Hide

```
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Altair 20240729 Dataset.csv")
circ_datadf <- as.data.frame(circ_data)

survfit(Surv(time = circ_data$OS.months, event = circ_data$p_evt0S)~altair.Arm, data = circ_data)
```

Call: survfit(formula = Surv(time = circ\_data\$OS.months, event = circ\_data\$p\_evt0S) ~ altair.Arm, data = circ\_data)

|                         | n   | events | median | 0.95LCL | 0.95UCL |
|-------------------------|-----|--------|--------|---------|---------|
| altair.Arm=Control      | 121 | 10     | NA     | NA      | NA      |
| altair.Arm=Experimental | 122 | 14     | NA     | NA      | NA      |

Hide

```
event_summary <- circ_data %>%
  group_by(altair.Arm) %>%
  summarise(
    Total = n(),
    Events = sum(p_evt0S),
    Fraction = Events / n(),
    Percentage = (Events / n()) * 100
  )
print(event_summary)
```

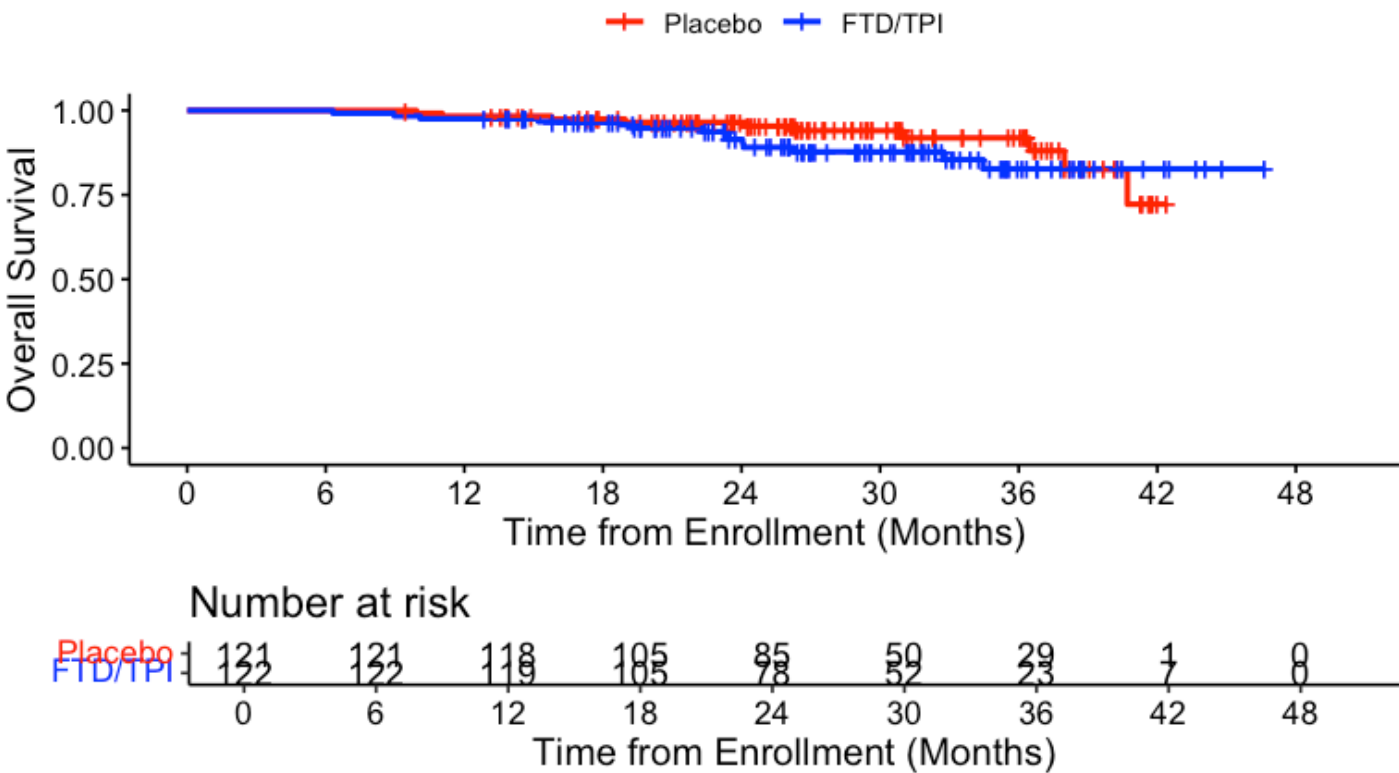
| altair.Arm<br><chr> | Total<br><int> | Events<br><int> | Fraction<br><dbl> | Percentage<br><dbl> |
|---------------------|----------------|-----------------|-------------------|---------------------|
| Control             | 121            | 10              | 0.08264463        | 8.264463            |
| Experimental        | 122            | 14              | 0.11475410        | 11.475410           |

2 rows

Hide

```
surv_object <-Surv(time = circ_data$OS.months, event = circ_data$p_evtOS)
KM_curve <- survfit(surv_object ~ altair.Arm, data = circ_data, conf.int=0.95, conf.type
="log-log")
ggsurvplot(KM_curve, data = circ_data, pval = FALSE, conf.int = FALSE, risk.table = TRUE, break.time.by=6, palette=c("red","blue"), title="OS by Arm - All Patients", ylab= "Overall Survival", xlab="Time from Enrollment (Months)", legend.labs=c("Placebo", "FTD/TP I"), legend.title="")
```

OS by Arm - All Patients



Hide

```
summary(KM_curve, times= c(6, 12, 18, 24))
```

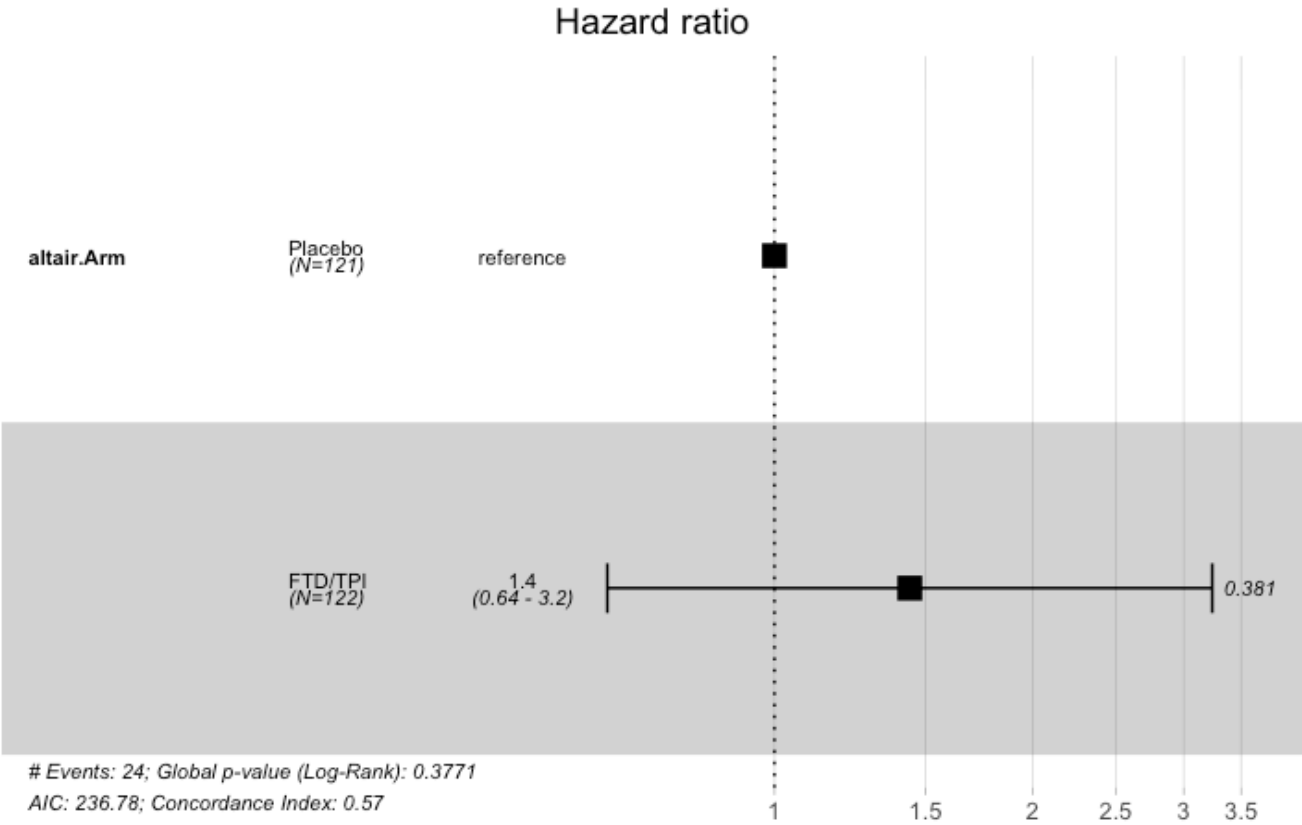
```
Call: survfit(formula = surv_object ~ altair.Arm, data = circ_data,
  conf.int = 0.95, conf.type = "log-log")
```

|                    |        |         |          |         |              |              |  |  |
|--------------------|--------|---------|----------|---------|--------------|--------------|--|--|
| altair.Arm=Control |        |         |          |         |              |              |  |  |
| time               | n.risk | n.event | survival | std.err | lower 95% CI | upper 95% CI |  |  |
| 6                  | 121    | 0       | 1.000    | 0.0000  | 1.000        | 1.000        |  |  |
| 12                 | 118    | 2       | 0.983    | 0.0117  | 0.935        | 0.996        |  |  |
| 18                 | 105    | 1       | 0.974    | 0.0146  | 0.923        | 0.992        |  |  |
| 24                 | 85     | 1       | 0.965    | 0.0172  | 0.909        | 0.987        |  |  |

|                         |        |         |          |         |              |              |  |  |
|-------------------------|--------|---------|----------|---------|--------------|--------------|--|--|
| altair.Arm=Experimental |        |         |          |         |              |              |  |  |
| time                    | n.risk | n.event | survival | std.err | lower 95% CI | upper 95% CI |  |  |
| 6                       | 122    | 0       | 1.000    | 0.0000  | 1.000        | 1.000        |  |  |
| 12                      | 119    | 3       | 0.975    | 0.0140  | 0.926        | 0.992        |  |  |
| 18                      | 105    | 1       | 0.967    | 0.0163  | 0.914        | 0.987        |  |  |
| 24                      | 78     | 5       | 0.914    | 0.0277  | 0.840        | 0.955        |  |  |

Hide

```
circ_data$altair.Arm <- factor(circ_data$altair.Arm, levels=c("Control","Experimental"),
labels = c("Placebo", "FTD/TPI"))
cox_fit <- coxph(surv_object ~ altair.Arm, data=circ_data)
ggforest(cox_fit,data = circ_data)
```



Hide

```
summary(cox_fit)
```

Call:  
coxph(formula = surv\_object ~ altair.Arm, data = circ\_data)

n= 243, number of events= 24

|                   | coef   | exp(coef) | se(coef) | z     | Pr(> z ) |
|-------------------|--------|-----------|----------|-------|----------|
| altair.ArmFTD/TPI | 0.3631 | 1.4378    | 0.4142   | 0.877 | 0.381    |

|                   | exp(coef) | exp(-coef) | lower .95 | upper .95 |
|-------------------|-----------|------------|-----------|-----------|
| altair.ArmFTD/TPI | 1.438     | 0.6955     | 0.6385    | 3.238     |

Concordance= 0.574 (se = 0.054 )  
Likelihood ratio test= 0.78 on 1 df, p=0.4  
Wald test = 0.77 on 1 df, p=0.4  
Score (logrank) test = 0.78 on 1 df, p=0.4

Hide

```
cox_fit_summary <- summary(cox_fit)

# Extract values for HR, 95% CI, and p-value
HR <- cox_fit_summary$coefficients[2]
lower_CI <- cox_fit_summary$conf.int[3]
upper_CI <- cox_fit_summary$conf.int[4]
p_value <- cox_fit_summary$coefficients[5]
label_text <- paste0("HR = ", round(HR, 2), " (", round(lower_CI, 2), "-", round(upper_CI, 2), "); p = ", round(p_value, 3))
print(label_text)
```

[1] "HR = 1.44 (0.64–3.24); p = 0.381"

#DFS1 by ctDNA MRD enrollment timepoint TAS vs Placebo

Hide

```
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Altair 20240729 Dataset.csv")
circ_data <- circ_data[circ_data$p_AltBaselineWin=="MRD",]
circ_datadf <- as.data.frame(circ_data)

survfit(Surv(time = circ_data$DFS.months, event = circ_data$p_evtDFS1b)~altair.Arm, data = circ_data)
```

Call: survfit(formula = Surv(time = circ\_data\$DFS.months, event = circ\_data\$p\_evtDFS1b) ~ altair.Arm, data = circ\_data)

|                         | n  | events | median | 0.95LCL | 0.95UCL |
|-------------------------|----|--------|--------|---------|---------|
| altair.Arm=Control      | 30 | 26     | 4.17   | 3.71    | 7.98    |
| altair.Arm=Experimental | 28 | 22     | 7.77   | 5.39    | 11.30   |

Hide

```
event_summary <- circ_data %>%
  group_by(altair.Arm) %>%
  summarise(
    Total = n(),
    Events = sum(p_evtDFS1b),
    Fraction = Events / n(),
    Percentage = (Events / n()) * 100
  )
print(event_summary)
```

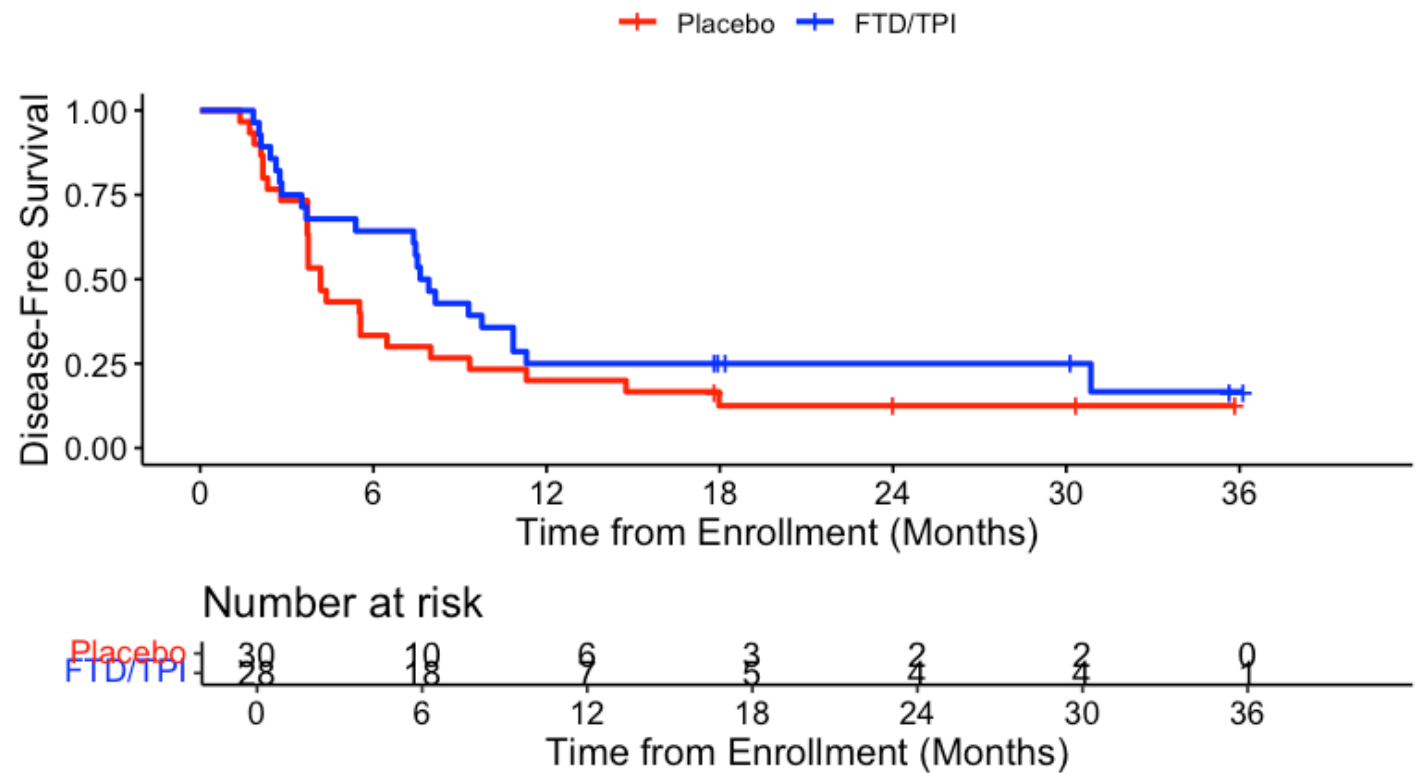
| altair.Arm<br><chr> | Total<br><int> | Events<br><int> | Fraction<br><dbl> | Percentage<br><dbl> |
|---------------------|----------------|-----------------|-------------------|---------------------|
| Control             | 30             | 26              | 0.8666667         | 86.66667            |

| altair.Arm<br><chr> | Total<br><int> | Events<br><int> | Fraction<br><dbl> | Percentage<br><dbl> |
|---------------------|----------------|-----------------|-------------------|---------------------|
| Experimental        | 28             | 22              | 0.7857143         | 78.57143            |
| 2 rows              |                |                 |                   |                     |

Hide

```
surv_object <-Surv(time = circ_data$DFS.months, event = circ_data$p_evtDFS1b)
KM_curve <- survfit(surv_object ~ altair.Arm, data = circ_data,conf.int=0.95,conf.type
="log-log")
ggsurvplot(KM_curve, data = circ_data, pval = FALSE, conf.int = FALSE, risk.table = TRU
E, break.time.by=6, palette=c("red","blue"), title="DFS1 by Arm - ctDNA MRD Enrollment",
ylab= "Disease-Free Survival", xlab="Time from Enrollment (Months)", legend.labs=c("Plac
ebo", "FTD/TPI"), legend.title="")
```

DFS1 by Arm - ctDNA MRD Enrollment



Hide

```
summary(KM_curve, times= c(6, 12, 18, 24))
```

Call: `survfit(formula = surv_object ~ altair.Arm, data = circ_data, conf.int = 0.95, conf.type = "log-log")`

altair.Arm=Control

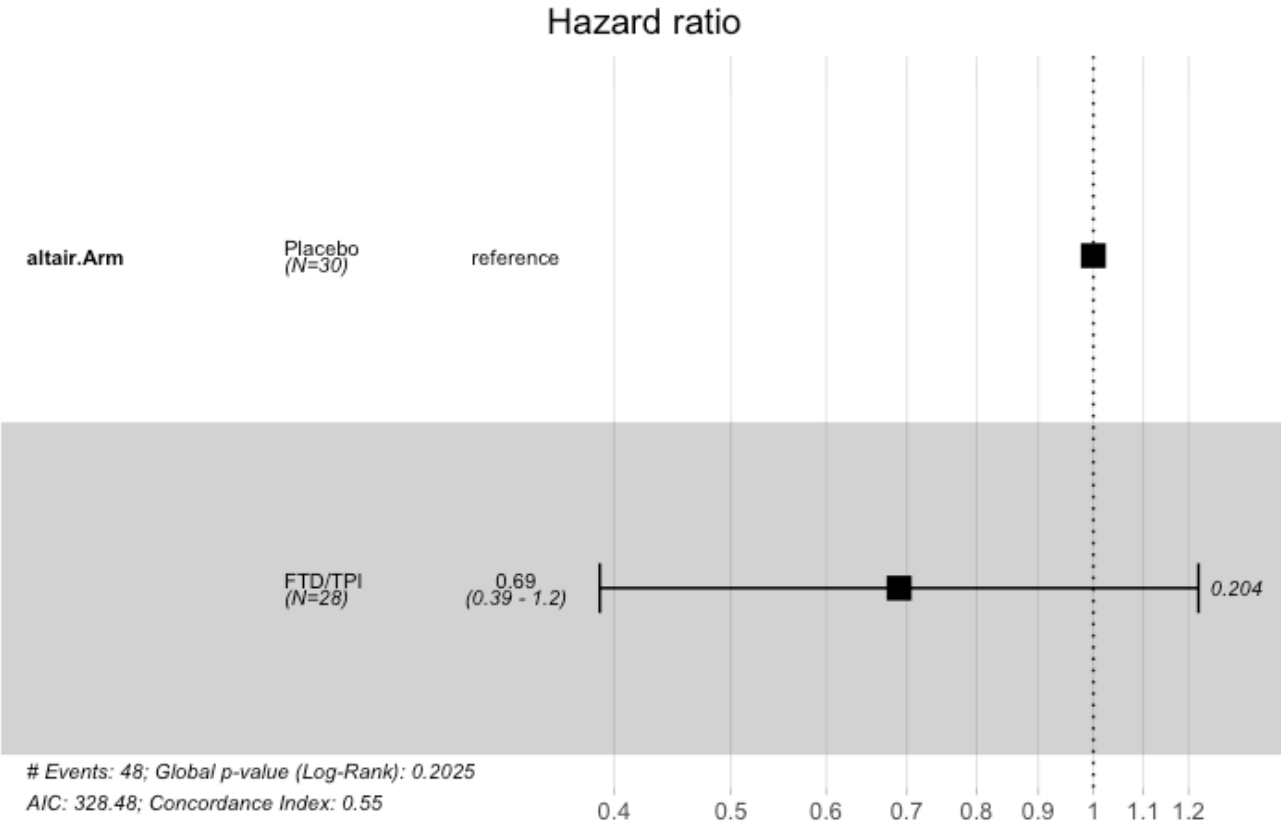
| time | n.risk | n.event | survival | std.err | lower 95% CI | upper 95% CI |
|------|--------|---------|----------|---------|--------------|--------------|
| 6    | 10     | 20      | 0.333    | 0.0861  | 0.1753       | 0.500        |
| 12   | 6      | 4       | 0.200    | 0.0730  | 0.0812       | 0.356        |
| 18   | 3      | 2       | 0.125    | 0.0625  | 0.0357       | 0.273        |
| 24   | 2      | 0       | 0.125    | 0.0625  | 0.0357       | 0.273        |

altair.Arm=Experimental

| time | n.risk | n.event | survival | std.err | lower 95% CI | upper 95% CI |
|------|--------|---------|----------|---------|--------------|--------------|
| 6    | 18     | 10      | 0.643    | 0.0906  | 0.438        | 0.789        |
| 12   | 7      | 11      | 0.250    | 0.0818  | 0.111        | 0.418        |
| 18   | 5      | 0       | 0.250    | 0.0818  | 0.111        | 0.418        |
| 24   | 4      | 0       | 0.250    | 0.0818  | 0.111        | 0.418        |

Hide

```
circ_data$altair.Arm <- factor(circ_data$altair.Arm, levels=c("Control","Experimental"),
labels = c("Placebo", "FTD/TPI"))
cox_fit <- coxph(surv_object ~ altair.Arm, data=circ_data)
ggforest(cox_fit,data = circ_data)
```



Hide

```
summary(cox_fit)
```

Call:  
coxph(formula = surv\_object ~ altair.Arm, data = circ\_data)

n= 58, number of events= 48

|                   | coef    | exp(coef) | se(coef) | z      | Pr(> z ) |
|-------------------|---------|-----------|----------|--------|----------|
| altair.ArmFTD/TPI | -0.3714 | 0.6897    | 0.2921   | -1.271 | 0.204    |

|                   | exp(coef) | exp(-coef) | lower .95 | upper .95 |
|-------------------|-----------|------------|-----------|-----------|
| altair.ArmFTD/TPI | 0.6897    | 1.45       | 0.3891    | 1.223     |

Concordance= 0.555 (se = 0.04 )  
Likelihood ratio test= 1.62 on 1 df, p=0.2  
Wald test = 1.62 on 1 df, p=0.2  
Score (logrank) test = 1.63 on 1 df, p=0.2

Hide



```
cox_fit_summary <- summary(cox_fit)

# Extract values for HR, 95% CI, and p-value
HR <- cox_fit_summary$coefficients[2]
lower_CI <- cox_fit_summary$conf.int[3]
upper_CI <- cox_fit_summary$conf.int[4]
p_value <- cox_fit_summary$coefficients[5]
label_text <- paste0("HR = ", round(HR, 2), " (", round(lower_CI, 2), "-", round(upper_CI, 2), "); p = ", round(p_value, 3))
print(label_text)
```

```
[1] "HR = 0.69 (0.39-1.22); p = 0.204"
```

[Hide](#)

```
#Fisher test for DFS percentages at 6, 12, 18 and 24 months
dfs_times <- c(6, 12, 18, 24)
p_values <- sapply(dfs_times, function(time) {
  neg_count <- sum(circ_data$altair.Arm == "FTD/TPI" & circ_data$DFS.months >= time & circ_data$p_evtDFS1b == 0)
  pos_count <- sum(circ_data$altair.Arm == "Placebo" & circ_data$DFS.months >= time & circ_data$p_evtDFS1b == 0)
  neg_total <- sum(circ_data$altair.Arm == "FTD/TPI")
  pos_total <- sum(circ_data$altair.Arm == "Placebo")

  neg_surv <- neg_total - sum(circ_data$altair.Arm == "FTD/TPI" & circ_data$p_evtDFS1b == 1 & circ_data$DFS.months < time)
  pos_surv <- pos_total - sum(circ_data$altair.Arm == "Placebo" & circ_data$p_evtDFS1b == 1 & circ_data$DFS.months < time)

  surv_matrix <- matrix(c(neg_surv, pos_surv, neg_total - neg_surv, pos_total - pos_surv), nrow = 2)
  test_result <- fisher.test(surv_matrix)
  return(test_result$p.value)
})
names(p_values) <- paste0("p-value at ", dfs_times, " months")
print(p_values)
```

| p-value at 6 months | p-value at 12 months | p-value at 18 months | p-value at 24 months |
|---------------------|----------------------|----------------------|----------------------|
| 0.03454285          | 0.75694899           | 0.32484791           | 0.32484791           |

#DFS1 by ctDNA On-treatment timepoint TAS vs Placebo

[Hide](#)

```
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Altair 20240729 Dataset.csv")
circ_data <- circ_data[circ_data$p_AltBaselineWin=="OnTreatment",]
circ_datadf <- as.data.frame(circ_data)

survfit(Surv(time = circ_data$DFS.months, event = circ_data$p_evtDFS1b)~altair.Arm, data
= circ_data)
```

```
Call: survfit(formula = Surv(time = circ_data$DFS.months, event = circ_data$p_evtDFS1b)
~
      altair.Arm, data = circ_data)
```

|                         | n  | events | median | 0.95LCL | 0.95UCL |
|-------------------------|----|--------|--------|---------|---------|
| altair.Arm=Control      | 19 | 16     | 9.07   | 4.30    | 17.5    |
| altair.Arm=Experimental | 14 | 13     | 6.64   | 2.99    | NA      |

Hide

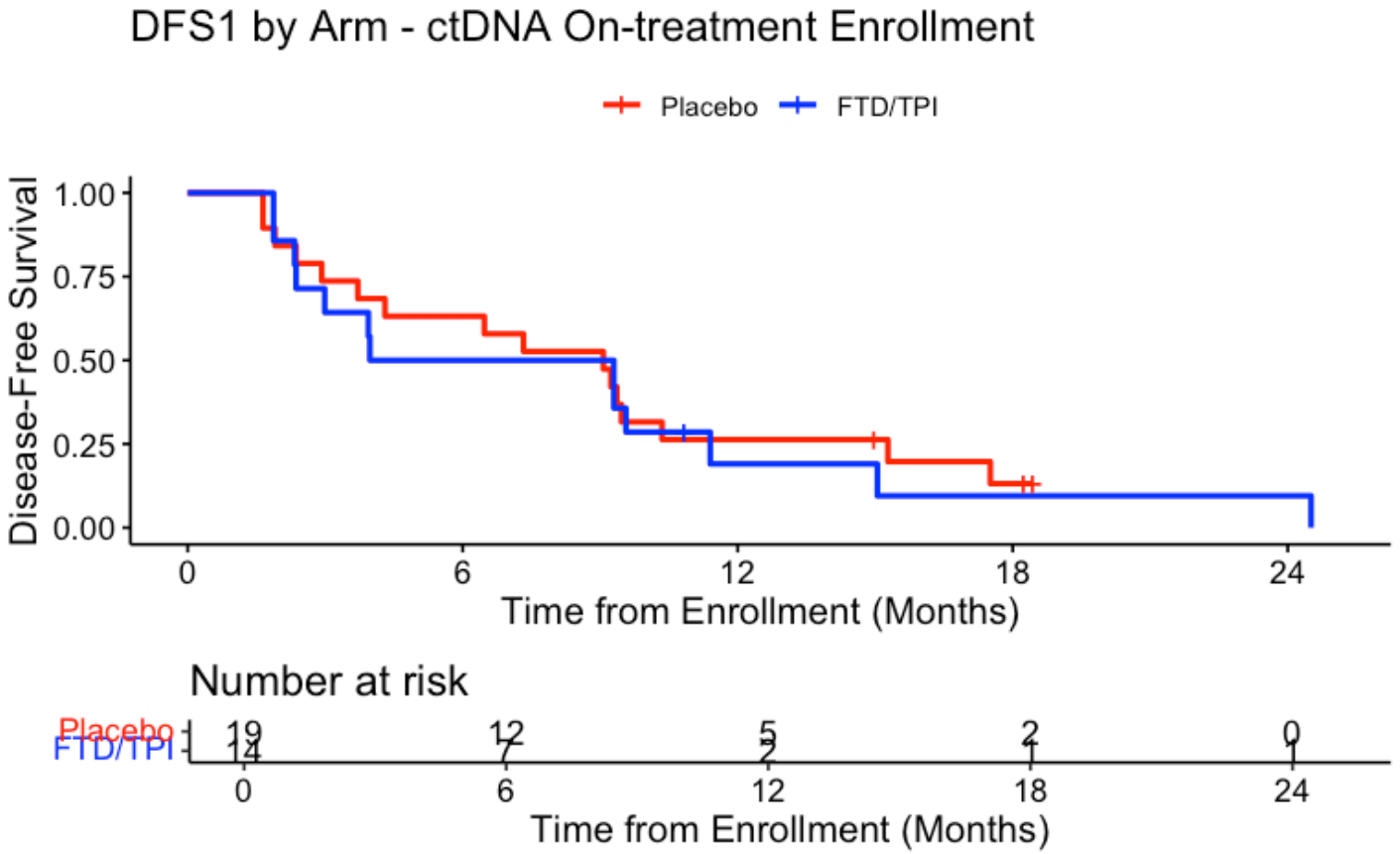
```
event_summary <- circ_data %>%
  group_by(altair.Arm) %>%
  summarise(
    Total = n(),
    Events = sum(p_evtDFS1b),
    Fraction = Events / n(),
    Percentage = (Events / n()) * 100
  )
print(event_summary)
```

| altair.Arm   | Total | Events | Fraction  | Percentage |
|--------------|-------|--------|-----------|------------|
| <chr>        | <int> | <int>  | <dbl>     | <dbl>      |
| Control      | 19    | 16     | 0.8421053 | 84.21053   |
| Experimental | 14    | 13     | 0.9285714 | 92.85714   |

2 rows

Hide

```
surv_object <-Surv(time = circ_data$DFS.months, event = circ_data$p_evtDFS1b)
KM_curve <- survfit(surv_object ~ altair.Arm, data = circ_data,conf.int=0.95,conf.type
=="log-log")
ggsurvplot(KM_curve, data = circ_data, pval = FALSE, conf.int = FALSE, risk.table = TRU
E, break.time.by=6, palette=c("red","blue"), title="DFS1 by Arm - ctDNA On-treatment Enr
ollment", ylab= "Disease-Free Survival", xlab="Time from Enrollment (Months)", legend.la
bs=c("Placebo", "FTD/TPI"), legend.title="")
```



Hide

```
summary(KM_curve, times= c(6, 12, 18, 24))
```

```
Call: survfit(formula = surv_object ~ altair.Arm, data = circ_data,
  conf.int = 0.95, conf.type = "log-log")
```

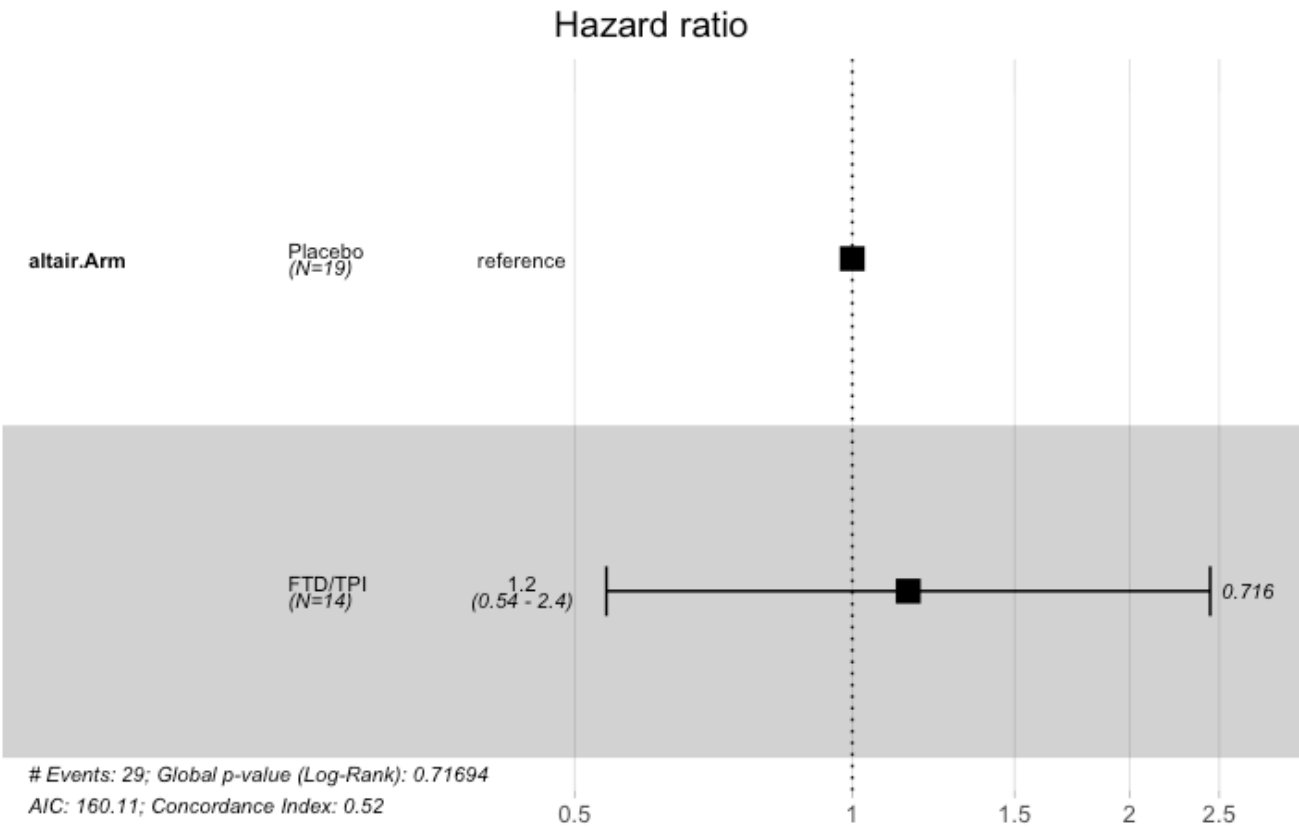
| altair.Arm=Control |        |         |          |         |              |              |  |
|--------------------|--------|---------|----------|---------|--------------|--------------|--|
| time               | n.risk | n.event | survival | std.err | lower 95% CI | upper 95% CI |  |
| 6                  | 12     | 7       | 0.632    | 0.1107  | 0.3790       | 0.804        |  |
| 12                 | 5      | 7       | 0.263    | 0.1010  | 0.0958       | 0.468        |  |
| 18                 | 2      | 2       | 0.132    | 0.0829  | 0.0240       | 0.332        |  |

| altair.Arm=Experimental |        |         |          |         |              |              |  |
|-------------------------|--------|---------|----------|---------|--------------|--------------|--|
| time                    | n.risk | n.event | survival | std.err | lower 95% CI | upper 95% CI |  |
| 6                       | 7      | 7       | 0.5000   | 0.1336  | 0.22859      | 0.722        |  |
| 12                      | 2      | 4       | 0.1905   | 0.1119  | 0.03612      | 0.437        |  |
| 18                      | 1      | 1       | 0.0952   | 0.0876  | 0.00635      | 0.335        |  |
| 24                      | 1      | 0       | 0.0952   | 0.0876  | 0.00635      | 0.335        |  |

Hide

```
circ_data$altair.Arm <- factor(circ_data$altair.Arm, levels=c("Control","Experimental"),
labels = c("Placebo", "FTD/TPI"))
cox_fit <- coxph(surv_object ~ altair.Arm, data=circ_data)
ggforest(cox_fit,data = circ_data)
```



Hide

```
summary(cox_fit)
```

Call:

```
coxph(formula = surv_object ~ altair.Arm, data = circ_data)
```

n= 33, number of events= 29

|                   | coef   | exp(coef) | se(coef) | z     | Pr(> z ) |
|-------------------|--------|-----------|----------|-------|----------|
| altair.ArmFTD/TPI | 0.1399 | 1.1502    | 0.3846   | 0.364 | 0.716    |

|                   | exp(coef) | exp(-coef) | lower .95 | upper .95 |
|-------------------|-----------|------------|-----------|-----------|
| altair.ArmFTD/TPI | 1.15      | 0.8694     | 0.5413    | 2.444     |

Concordance= 0.516 (se = 0.053 )

Likelihood ratio test= 0.13 on 1 df, p=0.7

Wald test = 0.13 on 1 df, p=0.7

Score (logrank) test = 0.13 on 1 df, p=0.7

[Hide](#)

```
cox_fit_summary <- summary(cox_fit)
```

```
# Extract values for HR, 95% CI, and p-value
```

```
HR <- cox_fit_summary$coefficients[2]
```

```
lower_CI <- cox_fit_summary$conf.int[3]
```

```
upper_CI <- cox_fit_summary$conf.int[4]
```

```
p_value <- cox_fit_summary$coefficients[5]
```

```
label_text <- paste0("HR = ", round(HR, 2), " (", round(lower_CI, 2), "-", round(upper_C  
I, 2), "); p = ", round(p_value, 3))
```

```
print(label_text)
```

```
[1] "HR = 1.15 (0.54-2.44); p = 0.716"
```

[Hide](#)

```
#Fisher test for DFS percentages at 6, 12, 18 and 24 months
dfs_times <- c(6, 12, 18, 24)
p_values <- sapply(dfs_times, function(time) {
  neg_count <- sum(circ_data$altair.Arm == "FTD/TPI" & circ_data$DFS.months >= time & circ_data$p_evtDFS1b == 0)
  pos_count <- sum(circ_data$altair.Arm == "Placebo" & circ_data$DFS.months >= time & circ_data$p_evtDFS1b == 0)
  neg_total <- sum(circ_data$altair.Arm == "FTD/TPI")
  pos_total <- sum(circ_data$altair.Arm == "Placebo")

  neg_surv <- neg_total - sum(circ_data$altair.Arm == "FTD/TPI" & circ_data$p_evtDFS1b == 1 & circ_data$DFS.months < time)
  pos_surv <- pos_total - sum(circ_data$altair.Arm == "Placebo" & circ_data$p_evtDFS1b == 1 & circ_data$DFS.months < time)

  surv_matrix <- matrix(c(neg_surv, pos_surv, neg_total - neg_surv, pos_total - pos_surv), nrow = 2)
  test_result <- fisher.test(surv_matrix)
  return(test_result$p.value)
})
names(p_values) <- paste0("p-value at ", dfs_times, " months")
print(p_values)
```

| p-value at 6 months | p-value at 12 months | p-value at 18 months | p-value at 24 months |
|---------------------|----------------------|----------------------|----------------------|
| 0.4969359           | 1.0000000            | 1.0000000            | 1.0000000            |

#DFS1 by ctDNA Surveillance timepoint TAS vs Placebo

[Hide](#)

```
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Altair 20240729 Dataset.csv")
circ_data <- circ_data[circ_data$p_AltBaselineWin=="Surveillance",]
circ_datadf <- as.data.frame(circ_data)

survfit(Surv(time = circ_data$DFS.months, event = circ_data$p_evtDFS1b)~altair.Arm, data = circ_data)
```

```
Call: survfit(formula = Surv(time = circ_data$DFS.months, event = circ_data$p_evtDFS1b) ~
  altair.Arm, data = circ_data)
```

|                         | n  | events | median | 0.95LCL | 0.95UCL |
|-------------------------|----|--------|--------|---------|---------|
| altair.Arm=Control      | 72 | 57     | 5.57   | 4.11    | 9.33    |
| altair.Arm=Experimental | 80 | 64     | 9.73   | 9.13    | 11.76   |

[Hide](#)

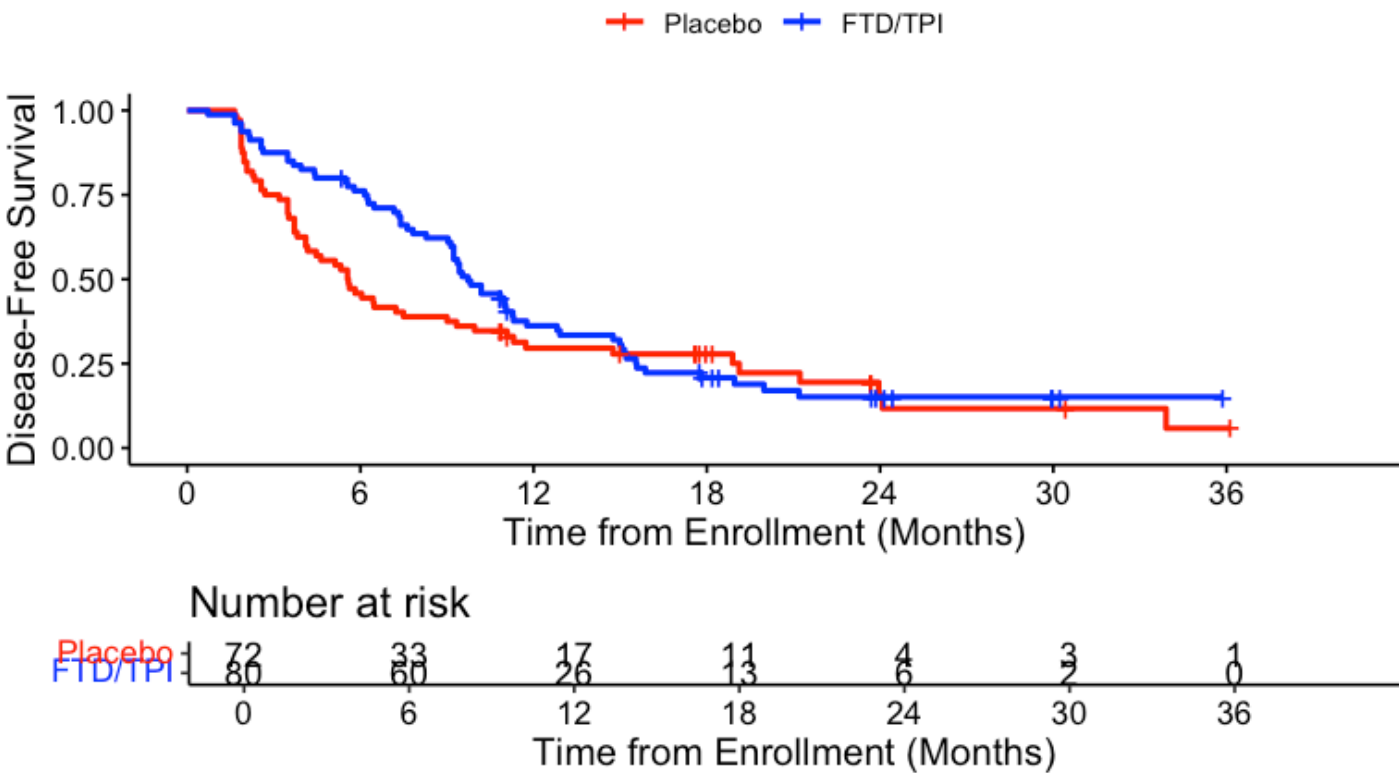
```
event_summary <- circ_data %>%
  group_by(altair.Arm) %>%
  summarise(
    Total = n(),
    Events = sum(p_evtDFS1b),
    Fraction = Events / n(),
    Percentage = (Events / n()) * 100
  )
print(event_summary)
```

| altair.Arm<br><chr> | Total<br><int> | Events<br><int> | Fraction<br><dbl> | Percentage<br><dbl> |
|---------------------|----------------|-----------------|-------------------|---------------------|
| Control             | 72             | 57              | 0.7916667         | 79.16667            |
| Experimental        | 80             | 64              | 0.8000000         | 80.00000            |
| 2 rows              |                |                 |                   |                     |

Hide

```
surv_object <-Surv(time = circ_data$DFS.months, event = circ_data$p_evtDFS1b)
KM_curve <- survfit(surv_object ~ altair.Arm, data = circ_data,conf.int=0.95,conf.type
="log-log")
ggsurvplot(KM_curve, data = circ_data, pval = FALSE, conf.int = FALSE, risk.table = TRU
E, break.time.by=6, palette=c("red","blue"), title="DFS1 by Arm - ctDNA Surveillance Enr
ollment", ylab= "Disease-Free Survival", xlab="Time from Enrollment (Months)", legend.la
bs=c("Placebo", "FTD/TPI"), legend.title="")
```

DFS1 by Arm - ctDNA Surveillance Enrollment



Hide

```
summary(KM_curve, times= c(6, 12, 18, 24))
```

Call: `survfit(formula = surv_object ~ altair.Arm, data = circ_data, conf.int = 0.95, conf.type = "log-log")`

| altair.Arm=Control |        |         |          |         |        |        |       |        |
|--------------------|--------|---------|----------|---------|--------|--------|-------|--------|
| time               | n.risk | n.event | survival | std.err | lower  | 95% CI | upper | 95% CI |
| 6                  | 33     | 39      | 0.458    | 0.0587  | 0.3408 |        | 0.568 |        |
| 12                 | 17     | 11      | 0.296    | 0.0551  | 0.1933 |        | 0.406 |        |
| 18                 | 11     | 1       | 0.278    | 0.0545  | 0.1780 |        | 0.388 |        |
| 24                 | 4      | 4       | 0.156    | 0.0565  | 0.0657 |        | 0.281 |        |

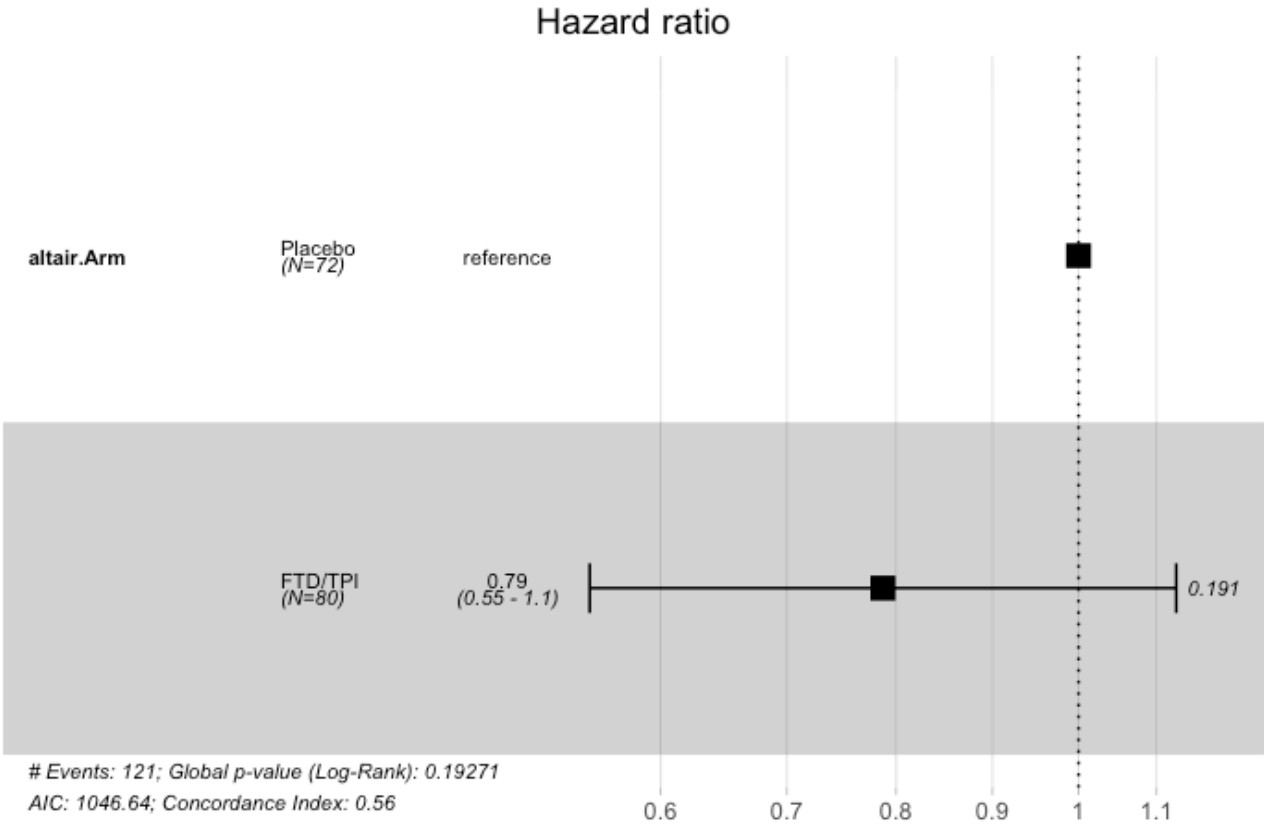
  

| altair.Arm=Experimental |        |         |          |         |        |        |       |        |
|-------------------------|--------|---------|----------|---------|--------|--------|-------|--------|
| time                    | n.risk | n.event | survival | std.err | lower  | 95% CI | upper | 95% CI |
| 6                       | 60     | 19      | 0.762    | 0.0477  | 0.6525 |        | 0.841 |        |
| 12                      | 26     | 31      | 0.362    | 0.0547  | 0.2568 |        | 0.468 |        |
| 18                      | 13     | 11      | 0.208    | 0.0473  | 0.1243 |        | 0.307 |        |
| 24                      | 6      | 3       | 0.151    | 0.0443  | 0.0774 |        | 0.248 |        |

Hide

```
circ_data$altair.Arm <- factor(circ_data$altair.Arm, levels=c("Control","Experimental"),
labels = c("Placebo", "FTD/TPI"))
cox_fit <- coxph(surv_object ~ altair.Arm, data=circ_data)
ggforest(cox_fit,data = circ_data)
```





Hide

```
summary(cox_fit)
```

Call:  
coxph(formula = surv\_object ~ altair.Arm, data = circ\_data)

n= 152, number of events= 121

|                   | coef    | exp(coef) | se(coef) | z      | Pr(> z ) |
|-------------------|---------|-----------|----------|--------|----------|
| altair.ArmFTD/TPI | -0.2391 | 0.7873    | 0.1829   | -1.307 | 0.191    |

|                   | exp(coef) | exp(-coef) | lower .95 | upper .95 |
|-------------------|-----------|------------|-----------|-----------|
| altair.ArmFTD/TPI | 0.7873    | 1.27       | 0.5501    | 1.127     |

Concordance= 0.559 (se = 0.025 )  
Likelihood ratio test= 1.7 on 1 df, p=0.2  
Wald test = 1.71 on 1 df, p=0.2  
Score (logrank) test = 1.72 on 1 df, p=0.2

Hide

```
cox_fit_summary <- summary(cox_fit)

# Extract values for HR, 95% CI, and p-value
HR <- cox_fit_summary$coefficients[2]
lower_CI <- cox_fit_summary$conf.int[3]
upper_CI <- cox_fit_summary$conf.int[4]
p_value <- cox_fit_summary$coefficients[5]
label_text <- paste0("HR = ", round(HR, 2), " (", round(lower_CI, 2), "-", round(upper_CI, 2), "); p = ", round(p_value, 3))
print(label_text)
```

```
[1] "HR = 0.79 (0.55-1.13); p = 0.191"
```

[Hide](#)

```
#Fisher test for DFS percentages at 6, 12, 18 and 24 months
dfs_times <- c(6, 12, 18, 24)
p_values <- sapply(dfs_times, function(time) {
  neg_count <- sum(circ_data$altair.Arm == "FTD/TPI" & circ_data$DFS.months >= time & circ_data$p_evtDFS1b == 0)
  pos_count <- sum(circ_data$altair.Arm == "Placebo" & circ_data$DFS.months >= time & circ_data$p_evtDFS1b == 0)
  neg_total <- sum(circ_data$altair.Arm == "FTD/TPI")
  pos_total <- sum(circ_data$altair.Arm == "Placebo")

  neg_surv <- neg_total - sum(circ_data$altair.Arm == "FTD/TPI" & circ_data$p_evtDFS1b == 1 & circ_data$DFS.months < time)
  pos_surv <- pos_total - sum(circ_data$altair.Arm == "Placebo" & circ_data$p_evtDFS1b == 1 & circ_data$DFS.months < time)

  surv_matrix <- matrix(c(neg_surv, pos_surv, neg_total - neg_surv, pos_total - pos_surv), nrow = 2)
  test_result <- fisher.test(surv_matrix)
  return(test_result$p.value)
})
names(p_values) <- paste0("p-value at ", dfs_times, " months")
print(p_values)
```

| p-value at 6 months | p-value at 12 months | p-value at 18 months | p-value at 24 months |
|---------------------|----------------------|----------------------|----------------------|
| 0.0001278464        | 0.3959706440         | 0.4666619773         | 0.6942842858         |

#Barplot with enrollment timepoint at any time by Arm

[Hide](#)

```
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Altair 20240729 Dataset.csv")

circ_data$altair.Arm <- factor(circ_data$altair.Arm, levels=c("Control","Experimental"),
labels = c("Placebo", "FTD/TPI"))
circ_data$p_AltBaselineWin <- factor(circ_data$p_AltBaselineWin, levels = c("MRD", "OnTreatment", "Surveillance"), labels = c("MRD", "On Treatment", "Surveillance"))
contingency_table <- table(circ_data$altair.Arm, circ_data$p_AltBaselineWin)
chi_square_test <- chisq.test(contingency_table)
print(chi square test)
```

Pearson's Chi-squared test

```
data: contingency_table
X-squared = 1.2435, df = 2, p-value = 0.537
```

Hide

```
fisher_exact_test <- fisher.test(contingency_table)
print(fisher exact test)
```

## Fisher's Exact Test for Count Data

```
data: contingency_table
p-value = 0.5471
alternative hypothesis: two.sided
```

Hide

```
print(contingency table)
```

|         | MRD On Treatment Surveillance |    |    |
|---------|-------------------------------|----|----|
| Placebo | 30                            | 19 | 72 |
| FTD/TPI | 28                            | 14 | 80 |

Hide

```
p_values <- c(chi_square_test$p.value, fisher_exact_test$p.value)
p_adjusted <- p.adjust(p_values, method = "bonferroni")
names(p_adjusted) <- c("Chi-Square Test", "Fisher's Exact Test")
print(p_adjusted)
```

## Chi-Square Test Fisher's Exact Test

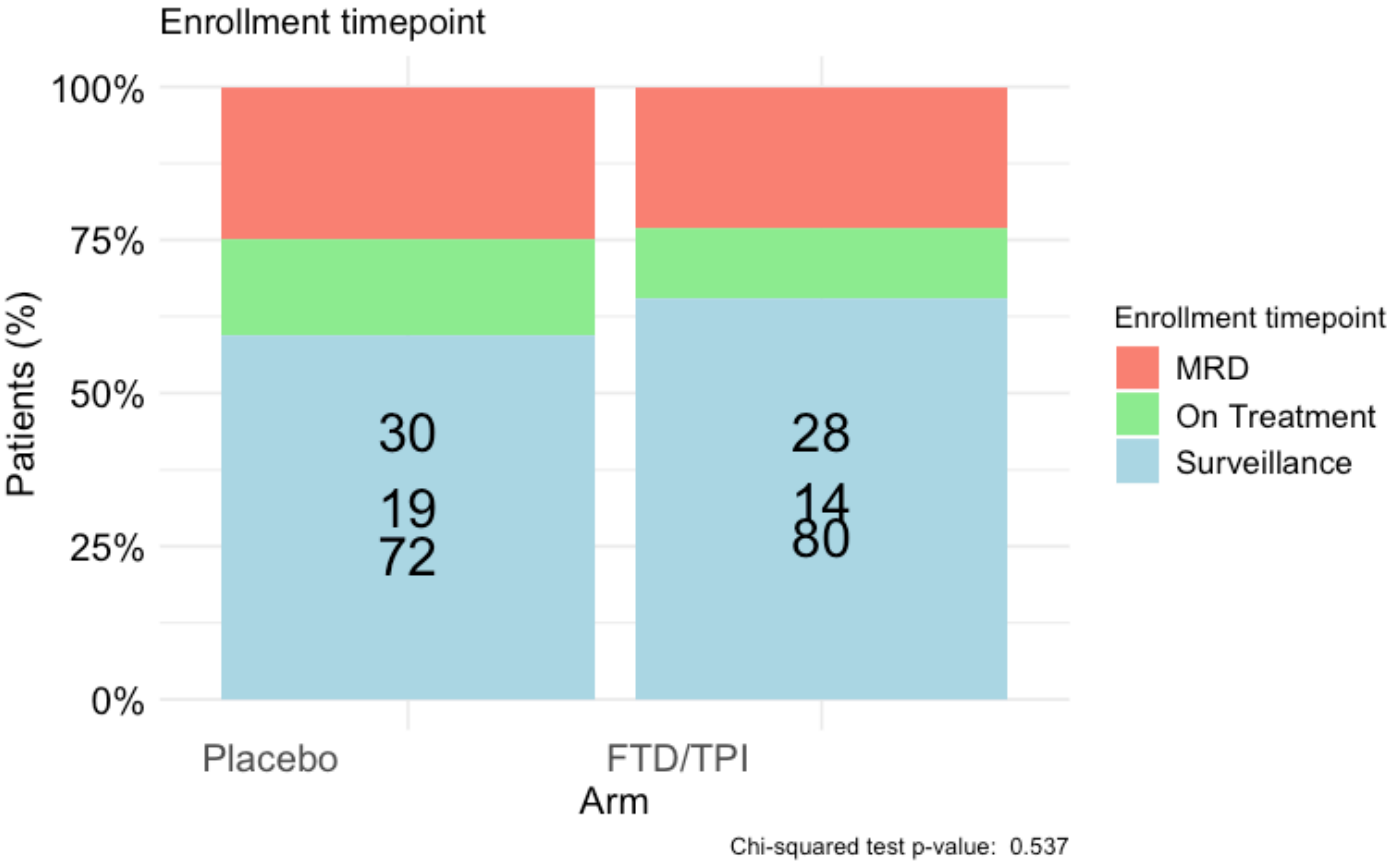
1

1

```

table_df <- as.data.frame(contingency_table)
table_df$Total <- ave(table_df$Freq, table_df$Var1, FUN = sum)
table_df$Percentage <- table_df$Freq / table_df$Total
table_df$MiddlePercentage <- table_df$Percentage / 2
ggplot(table_df, aes(x = Var1, y = Percentage, fill = Var2)) +
  geom_bar(stat = "identity") +
  geom_text(aes(y = MiddlePercentage, label = Freq), position = "stack", color = "black",
    vjust = 1.5, size = 7) +
  theme_minimal() +
  labs(title = "Enrollment timepoint",
    x = "Arm",
    y = "Patients (%)",
    fill = "Enrollment timepoint",
    caption = paste("Chi-squared test p-value: ", format.pval(chi_square_test$p.value))) +
  scale_y_continuous(labels = scales::percent_format()) +
  scale_fill_manual(values = c("Surveillance" = "lightblue", "On Treatment" = "lightgreen", "MRD" = "salmon")) + # define custom colors
  theme(axis.text.x = element_text(angle = 0, hjust = 1.5, size = 14), # increase x-axis text size
    axis.text.y = element_text(size = 14, color = "black"), # increase y-axis text size
    axis.title.x = element_text(size = 14, color = "black"), # increase x-axis label size
    axis.title.y = element_text(size = 14, color = "black"), # increase y-axis label size
    legend.text = element_text(size = 12, color = "black")) # increase Recurrence label size

```



Hide

```
#Calculate median MTM/mL for enrollment timepoint
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Altair 20240729 Dataset.csv")
result <- circ_data %>%
  group_by(p_AltBaselineWin) %>%
  summarise(
    Median = median(p_AltBaselineMTM, na.rm = TRUE),
    Range = paste(min(p_AltBaselineMTM, na.rm = TRUE), max(p_AltBaselineMTM, na.rm = TRUE), sep = " - ")
  )
print(result)
```

| p_AltBaselineWin | Median    | Range                       |
|------------------|-----------|-----------------------------|
| <chr>            | <dbl>     | <chr>                       |
| MRD              | 0.9724113 | 0.026508782 - 121.2686353   |
| OnTreatment      | 0.8224263 | 0.06015441805 - 166.3342558 |
| Surveillance     | 0.2395414 | 0.02627334075 - 250.47      |

3 rows

#DFS1 by TAS vs Placebo - All stages MTM/mL based on the lowest MTM/mL upon which the trial is positive

Hide

```
#Pts with MTM/mL≥0.047
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Altair 20240729 Dataset.csv")

total_pts <- nrow(circ_data)
pts_MTM <- nrow(circ_data[circ_data$p_AltBaselineMTM >= 0.047,])
percentage_pts_MTM <- (pts_MTM / total_pts) * 100
print(paste0("Percentage of patients with MTM ≥ 0.047: ", round(percentage_pts_MTM, 2),
"%"))
```

[1] "Percentage of patients with MTM ≥ 0.047: 94.24%"

Hide

```
circ_data <- circ_data[circ_data$p_AltBaselineMTM>=0.047,]
circ_datadf <- as.data.frame(circ_data)

survfit(Surv(time = circ_data$DFS.months, event = circ_data$p_evtDFS1b)~altair.Arm, data
= circ_data)
```

Call: survfit(formula = Surv(time = circ\_data\$DFS.months, event = circ\_data\$p\_evtDFS1b) ~ altair.Arm, data = circ\_data)

|                         | n   | events | median | 0.95LCL | 0.95UCL |
|-------------------------|-----|--------|--------|---------|---------|
| altair.Arm=Control      | 112 | 96     | 5.42   | 4.11    | 6.47    |
| altair.Arm=Experimental | 117 | 98     | 9.30   | 7.82    | 10.18   |

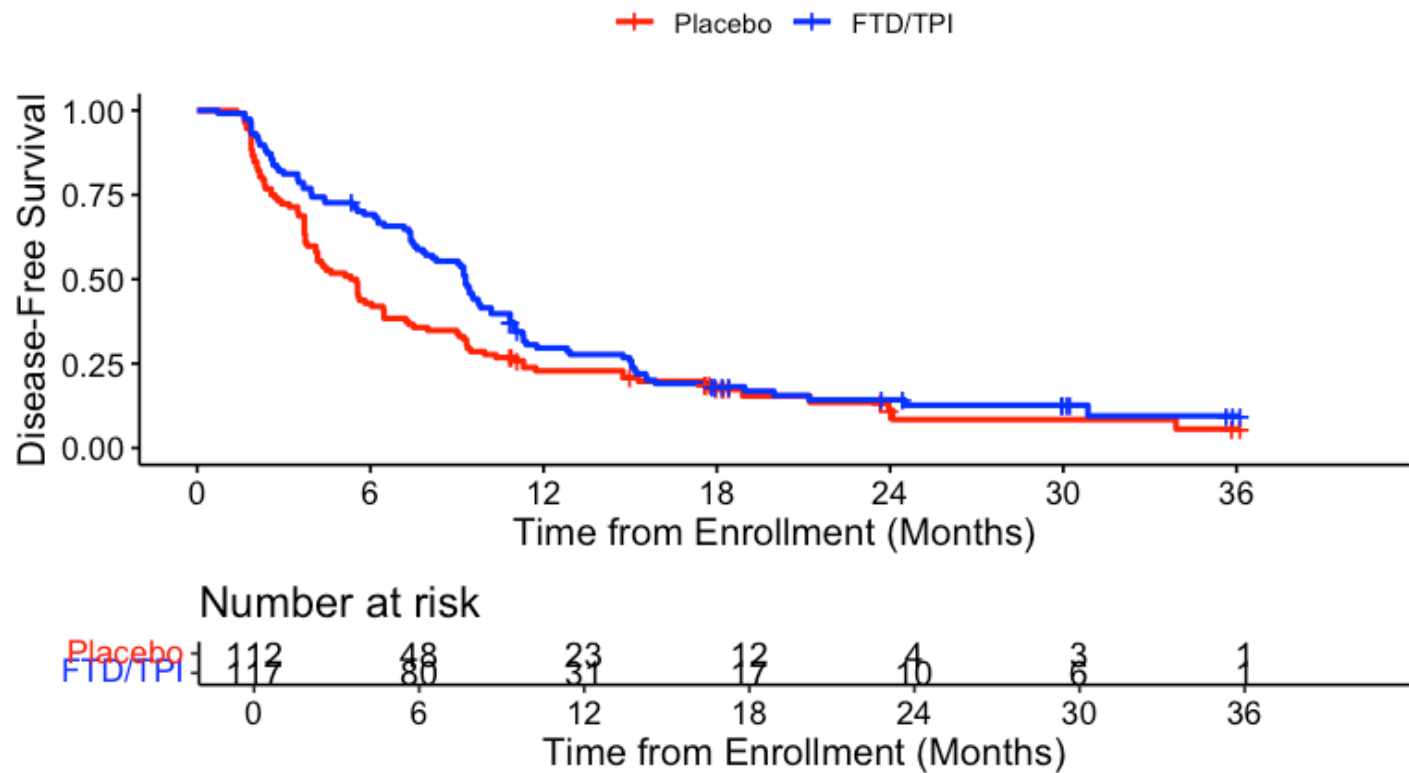
Hide

```
event_summary <- circ_data %>%
  group_by(altair.Arm) %>%
  summarise(
    Total = n(),
    Events = sum(p_evtDFS1b),
    Fraction = Events / n(),
    Percentage = (Events / n()) * 100
  )
print(event_summary)
```

| altair.Arm<br><chr> | Total<br><int> | Events<br><int> | Fraction<br><dbl> | Percentage<br><dbl> |
|---------------------|----------------|-----------------|-------------------|---------------------|
| Control             | 112            | 96              | 0.8571429         | 85.71429            |
| Experimental        | 117            | 98              | 0.8376068         | 83.76068            |
| 2 rows              |                |                 |                   |                     |

```
surv_object <- Surv(time = circ_data$DFS.months, event = circ_data$p_evtDFS1b)
KM_curve <- survfit(surv_object ~ altair.Arm, data = circ_data, conf.int=0.95, conf.type
="log-log")
ggsurvplot(KM_curve, data = circ_data, pval = FALSE, conf.int = FALSE, risk.table = TRUE,
break.time.by=6, palette=c("red","blue"), title="DFS1 by Arm - MTM/mL  $\geq 0.047$ ", ylab=
"Disease-Free Survival", xlab="Time from Enrollment (Months)", legend.labs=c("Placebo",
"FTD/TPI"), legend.title="")
```

DFS1 by Arm - MTM/mL  $\geq 0.047$



Hide

```
summary(KM_curve, times= c(6, 12, 18, 24))
```

```
Call: survfit(formula = surv_object ~ altair.Arm, data = circ_data,
  conf.int = 0.95, conf.type = "log-log")
```

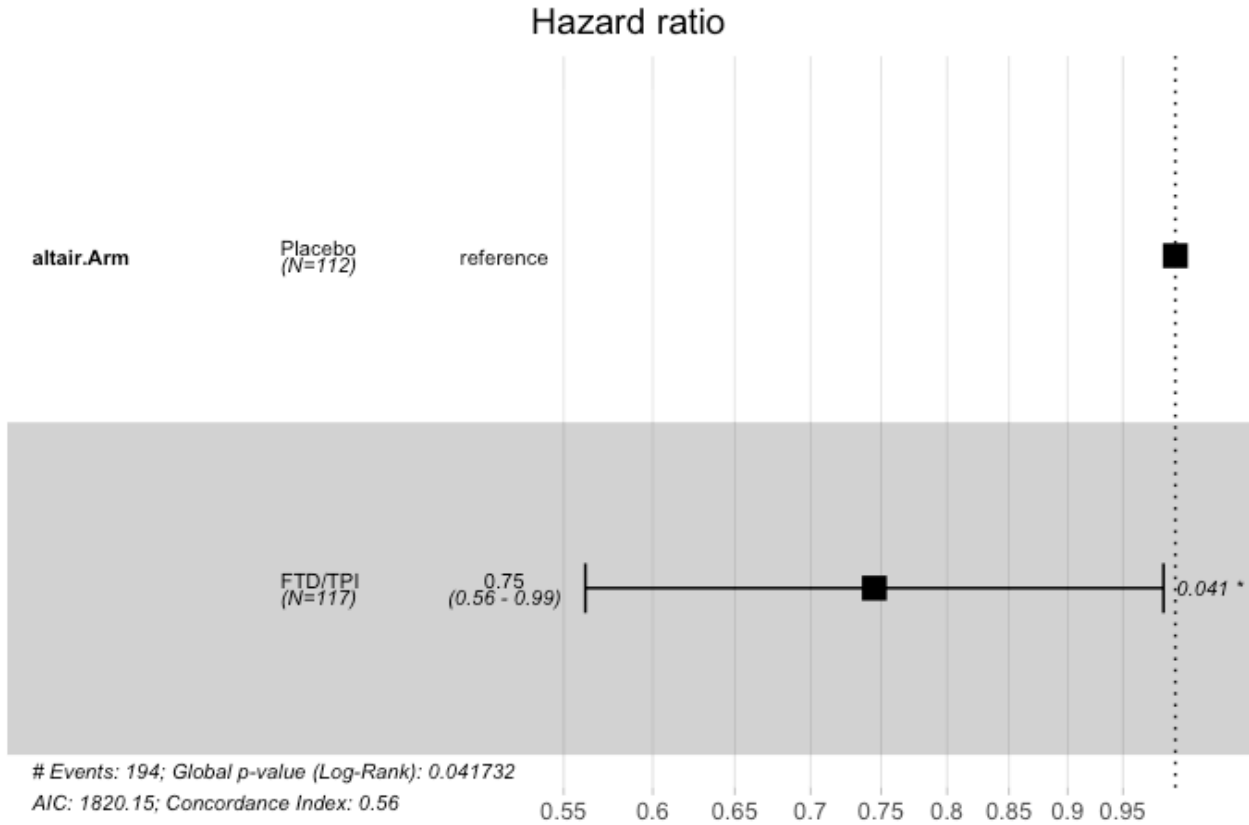
| altair.Arm=Control |        |         |          |         |        |        |       |        |
|--------------------|--------|---------|----------|---------|--------|--------|-------|--------|
| time               | n.risk | n.event | survival | std.err | lower  | 95% CI | upper | 95% CI |
| 6                  | 48     | 64      | 0.429    | 0.0468  | 0.3360 |        | 0.518 |        |
| 12                 | 23     | 22      | 0.228    | 0.0401  | 0.1552 |        | 0.310 |        |
| 18                 | 12     | 5       | 0.173    | 0.0374  | 0.1074 |        | 0.252 |        |
| 24                 | 4      | 3       | 0.112    | 0.0375  | 0.0524 |        | 0.198 |        |

| altair.Arm=Experimental |        |         |          |         |        |        |       |        |
|-------------------------|--------|---------|----------|---------|--------|--------|-------|--------|
| time                    | n.risk | n.event | survival | std.err | lower  | 95% CI | upper | 95% CI |
| 6                       | 80     | 36      | 0.692    | 0.0427  | 0.5995 |        | 0.767 |        |
| 12                      | 31     | 45      | 0.296    | 0.0430  | 0.2150 |        | 0.382 |        |
| 18                      | 17     | 12      | 0.182    | 0.0370  | 0.1158 |        | 0.259 |        |
| 24                      | 10     | 3       | 0.143    | 0.0352  | 0.0824 |        | 0.219 |        |

Hide

```
circ_data$altair.Arm <- factor(circ_data$altair.Arm, levels=c("Control","Experimental"),
  labels = c("Placebo", "FTD/TPI"))
cox_fit <- coxph(surv_object ~ altair.Arm, data=circ_data)
ggforest(cox_fit,data = circ_data)
```





Hide

```
summary(cox_fit)
```

Call:  
coxph(formula = surv\_object ~ altair.Arm, data = circ\_data)

n= 229, number of events= 194

|                   | coef    | exp(coef) | se(coef) | z      | Pr(> z ) |
|-------------------|---------|-----------|----------|--------|----------|
| altair.ArmFTD/TPI | -0.2942 | 0.7451    | 0.1442   | -2.041 | 0.0413 * |

---  
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

|                   | exp(coef) | exp(-coef) | lower .95 | upper .95 |
|-------------------|-----------|------------|-----------|-----------|
| altair.ArmFTD/TPI | 0.7451    | 1.342      | 0.5617    | 0.9884    |

Concordance= 0.558 (se = 0.02 )  
Likelihood ratio test= 4.15 on 1 df, p=0.04  
Wald test = 4.16 on 1 df, p=0.04  
Score (logrank) test = 4.19 on 1 df, p=0.04

Hide

```
cox_fit_summary <- summary(cox_fit)

# Extract values for HR, 95% CI, and p-value
HR <- cox_fit_summary$coefficients[2]
lower_CI <- cox_fit_summary$conf.int[3]
upper_CI <- cox_fit_summary$conf.int[4]
p_value <- cox_fit_summary$coefficients[5]
label_text <- paste0("HR = ", round(HR, 2), " (", round(lower_CI, 2), "-", round(upper_CI, 2), "); p = ", round(p_value, 3))
print(label_text)
```

```
[1] "HR = 0.75 (0.56-0.99); p = 0.041"
```

Hide

```
#Pts with MTM/mL<0.047
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Altair 20240729 Dataset.csv")

total_pts <- nrow(circ_data)
pts_MTM <- nrow(circ_data[circ_data$p_AltBaselineMTM < 0.047,])
percentage_pts_MTM <- (pts_MTM / total_pts) * 100
print(paste0("Percentage of patients with MTM < 0.047: ", round(percentage_pts_MTM, 2), "%"))
```

```
[1] "Percentage of patients with MTM < 0.047: 5.76%"
```

Hide

```
circ_data <- circ_data[circ_data$p_AltBaselineMTM<0.047,]
circ_datadf <- as.data.frame(circ_data)

survfit(Surv(time = circ_data$DFS.months, event = circ_data$p_evtDFS1b)~altair.Arm, data = circ_data)
```

```
Call: survfit(formula = Surv(time = circ_data$DFS.months, event = circ_data$p_evtDFS1b) ~
      altair.Arm, data = circ_data)
```

|                         | n | events | median | 0.95LCL | 0.95UCL |
|-------------------------|---|--------|--------|---------|---------|
| altair.Arm=Control      | 9 | 3      | NA     | 19.1    | NA      |
| altair.Arm=Experimental | 5 | 1      | NA     | NA      | NA      |

Hide

```
event_summary <- circ_data %>%
  group_by(altair.Arm) %>%
  summarise(
    Total = n(),
    Events = sum(p_evtDFS1b),
    Fraction = Events / n(),
    Percentage = (Events / n()) * 100
  )
print(event_summary)
```

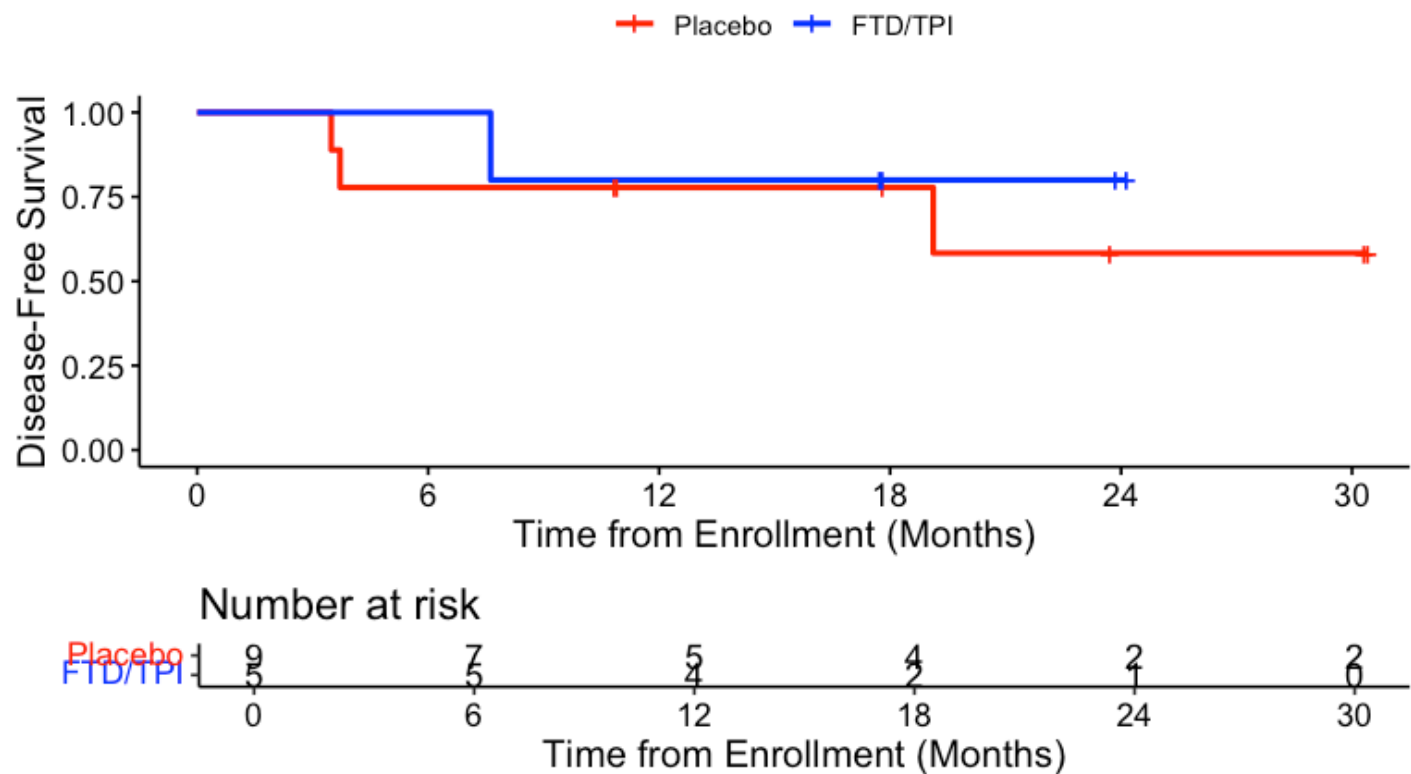
| altair.Arm<br><chr> | Total<br><int> | Events<br><int> | Fraction<br><dbl> | Percentage<br><dbl> |
|---------------------|----------------|-----------------|-------------------|---------------------|
| Control             | 9              | 3               | 0.3333333         | 33.33333            |
| Experimental        | 5              | 1               | 0.2000000         | 20.00000            |

2 rows

Hide

```
surv_object <- Surv(time = circ_data$DFS.months, event = circ_data$p_evtDFS1b)
KM_curve <- survfit(surv_object ~ altair.Arm, data = circ_data, conf.int=0.95, conf.type
="log-log")
ggsurvplot(KM_curve, data = circ_data, pval = FALSE, conf.int = FALSE, risk.table = TRU
E, break.time.by=6, palette=c("red","blue"), title="DFS1 by Arm - MTM/mL <0.047", ylab=
"Disease-Free Survival", xlab="Time from Enrollment (Months)", legend.labs=c("Placebo",
"FTD/TPI"), legend.title="")
```

DFS1 by Arm - MTM/mL <0.047



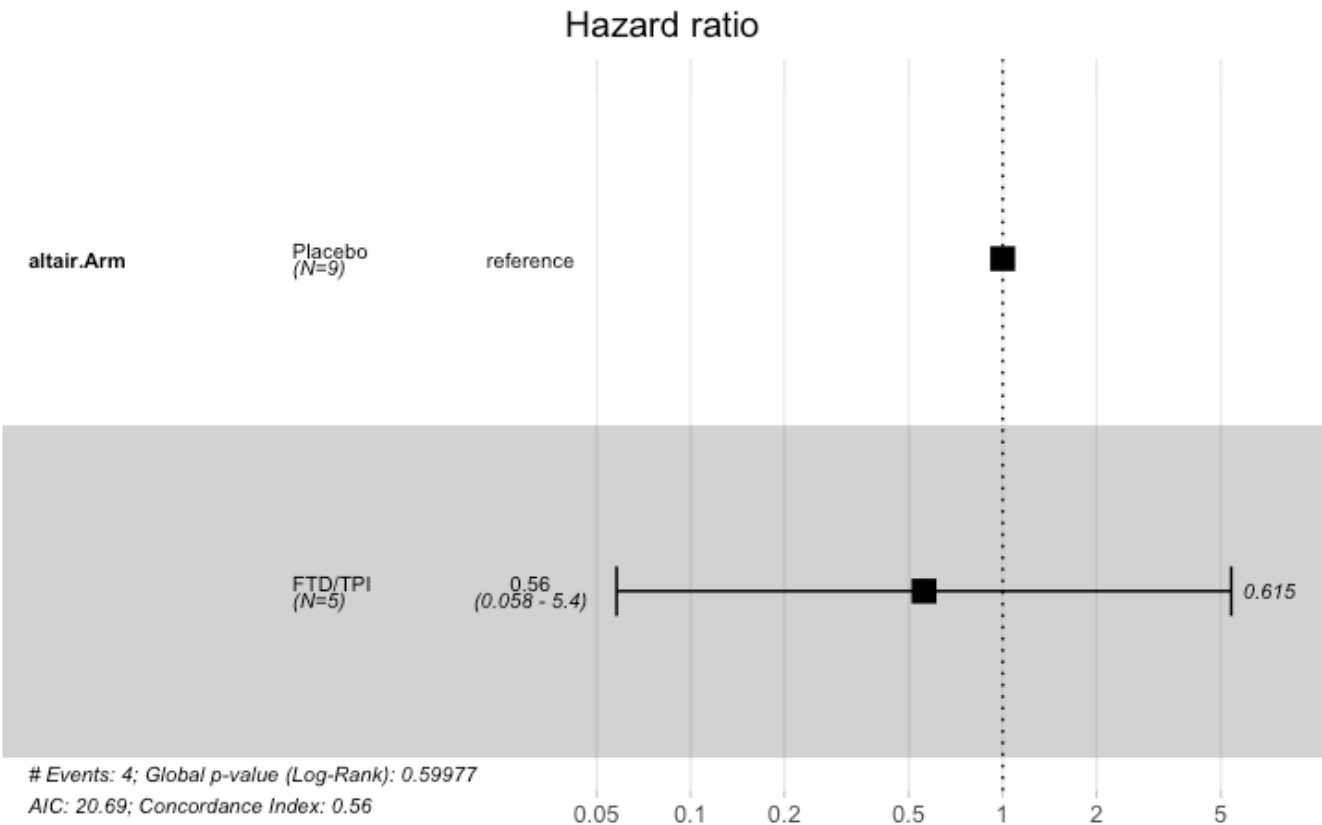
```
summary(KM_curve, times= c(6, 12, 18, 24))
```

```
Call: survfit(formula = surv_object ~ altair.Arm, data = circ_data,
  conf.int = 0.95, conf.type = "log-log")
```

| altair.Arm=Control |        |         |          |         |              |              |  |
|--------------------|--------|---------|----------|---------|--------------|--------------|--|
| time               | n.risk | n.event | survival | std.err | lower 95% CI | upper 95% CI |  |
| 6                  | 7      | 2       | 0.778    | 0.139   | 0.365        | 0.939        |  |
| 12                 | 5      | 0       | 0.778    | 0.139   | 0.365        | 0.939        |  |
| 18                 | 4      | 0       | 0.778    | 0.139   | 0.365        | 0.939        |  |
| 24                 | 2      | 1       | 0.583    | 0.198   | 0.157        | 0.855        |  |

| altair.Arm=Experimental |        |         |          |         |              |              |  |
|-------------------------|--------|---------|----------|---------|--------------|--------------|--|
| time                    | n.risk | n.event | survival | std.err | lower 95% CI | upper 95% CI |  |
| 6                       | 5      | 0       | 1.0      | 0.000   | 1.000        | 1.000        |  |
| 12                      | 4      | 1       | 0.8      | 0.179   | 0.204        | 0.969        |  |
| 18                      | 2      | 0       | 0.8      | 0.179   | 0.204        | 0.969        |  |
| 24                      | 1      | 0       | 0.8      | 0.179   | 0.204        | 0.969        |  |

```
circ_data$altair.Arm <- factor(circ_data$altair.Arm, levels=c("Control","Experimental"),
labels = c("Placebo", "FTD/TPI"))
cox_fit <- coxph(surv_object ~ altair.Arm, data=circ_data)
ggforest(cox_fit,data = circ_data)
```



Hide

```
summary(cox_fit)
```

Call:

```
coxph(formula = surv_object ~ altair.Arm, data = circ_data)
```

n= 14, number of events= 4

|                   | coef    | exp(coef) | se(coef) | z      | Pr(> z ) |
|-------------------|---------|-----------|----------|--------|----------|
| altair.ArmFTD/TPI | -0.5812 | 0.5592    | 1.1566   | -0.502 | 0.615    |

|                   | exp(coef) | exp(-coef) | lower .95 | upper .95 |
|-------------------|-----------|------------|-----------|-----------|
| altair.ArmFTD/TPI | 0.5592    | 1.788      | 0.05795   | 5.397     |

Concordance= 0.561 (se = 0.12 )

Likelihood ratio test= 0.28 on 1 df, p=0.6

Wald test = 0.25 on 1 df, p=0.6

Score (logrank) test = 0.26 on 1 df, p=0.6

Hide

```
cox_fit_summary <- summary(cox_fit)
```

```
# Extract values for HR, 95% CI, and p-value
```

```
HR <- cox_fit_summary$coefficients[2]
```

```
lower_CI <- cox_fit_summary$conf.int[3]
```

```
upper_CI <- cox_fit_summary$conf.int[4]
```

```
p_value <- cox_fit_summary$coefficients[5]
```

```
label_text <- paste0("HR = ", round(HR, 2), " (", round(lower_CI, 2), "-", round(upper_CI, 2), "); p = ", round(p_value, 3))
```

```
print(label_text)
```

```
[1] "HR = 0.56 (0.06-5.4); p = 0.615"
```

Hide

```
#Analysis for Likelihood-Ratio Interaction P value
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Altair 20240729 Dataset.csv")
circ_data$p_evtDFS1b <- as.logical(circ_data$p_evtDFS1b)
circ_data$DFS.months <- as.numeric(circ_data$DFS.months)

circ_data$altair.Arm <- factor(circ_data$altair.Arm, levels=c("Control","Experimental"),
labels = c("Placebo", "FTD/TPI"))
circ_data$ctDNA.MTM <- NA
circ_data <- circ_data %>%
  mutate(ctDNA.MTM = case_when(
    p_AltBaselineMTM<0.047 ~ 1,
    p_AltBaselineMTM>=0.047 ~ 2
  ))
circ_data$ctDNA.MTM <- factor(circ_data$ctDNA.MTM, levels=c("1","2"), labels = c("<0.047", "≥0.047"))
surv_object <- Surv(time = circ_data$DFS.months, event = circ_data$p_evtDFS1b)
cox_model_main <- coxph(surv_object ~ ctDNA.MTM + altair.Arm, data = circ_data)
cox_model_interaction <- coxph(surv_object ~ ctDNA.MTM * altair.Arm, data = circ_data)
lrt_result <- anova(cox_model_main, cox_model_interaction, test = "LRT")
print(lrt_result)
```

#### Analysis of Deviance Table

```
Cox model: response is surv_object
Model 1: ~ ctDNA.MTM + altair.Arm
Model 2: ~ ctDNA.MTM * altair.Arm
loglik Chisq Df Pr(>|Chi|)
1 -937.59
2 -937.54 0.0991 1 0.753
```

#DFS1 by TAS vs Placebo - MTM/mL as continuous variable

Hide

```

rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Altair 20240729 Dataset.csv")
circ_data$p_evtDFS1b <- as.logical(circ_data$p_evtDFS1b)
circ_data$DFS.months <- as.numeric(circ_data$DFS.months)
circ_data$p_AltBaselineMTM <- as.numeric(circ_data$p_AltBaselineMTM)
circ_data$altair.Arm <- factor(circ_data$altair.Arm, levels=c("Control","Experimental"),
labels = c("Placebo", "FTD/TPI"))

#####
# 3. Define cutoffs (0.01 to 100 on a normal numeric scale)
#####
cutoffs <- seq(0.01, 100, length.out = 50)

# Prepare a data frame to store results
results_df <- data.frame(
  cutoff = cutoffs,
  HR      = NA_real_,
  HR_low  = NA_real_,
  HR_hi   = NA_real_,
  pval    = NA_real_,
  n_included = NA_integer_
)

#####
# 4. Loop over each cutoff: subselect data and fit Cox model (Placebo vs. TAS-102)
#####
for (i in seq_along(cutoffs)) {

  current_cutoff <- cutoffs[i]

  # Subset: patients with p_AltBaselineMTM >= current_cutoff
  sub_data <- circ_data %>%
    filter(p_AltBaselineMTM >= current_cutoff)

  # Re-factor in case any level is dropped
  sub_data$altair.Arm <- factor(sub_data$altair.Arm, levels = c("Placebo", "FTD/TPI"))

  # Only run the Cox model if both arms have at least some minimal data
  arm_counts <- table(sub_data$altair.Arm)
  if (length(arm_counts) == 2 && all(arm_counts >= 2)) {

    fit <- coxph(Surv(DFS.months, p_evtDFS1b) ~ altair.Arm, data = sub_data)
    fit_sum <- summary(fit)

    # Extract HR, 95% CI, and p-value
    hr      <- fit_sum$conf.int[,"exp(coef)"][1]
    hr_conf_low <- fit_sum$conf.int[,"lower .95"][1]
    hr_conf_hi  <- fit_sum$conf.int[,"upper .95"][1]
    pval      <- fit_sum$coefficients[,"Pr(>|z|)"][1]

    # Store in results_df

```

```
results_df$HR[i]      <- hr
results_df$HR_low[i]  <- hr_conf_low
results_df$HR_hi[i]   <- hr_conf_hi
results_df$pval[i]    <- pval
results_df$n_included[i] <- nrow(sub_data)

} else {
  results_df$n_included[i] <- nrow(sub_data)
}
}
```



[illegible]

```
G2; H2; Warning h in coxph.fit(X, Y, istrat, offset, init, control, weights = weights, :
Ran out of iterations and did not converge g
G2; H2; Warning h in coxph.fit(X, Y, istrat, offset, init, control, weights = weights, :
Ran out of iterations and did not converge g
G2; H2; Warning h in coxph.fit(X, Y, istrat, offset, init, control, weights = weights, :
Ran out of iterations and did not converge g
```

Hide

```
#####
# 5. Plot: x-axis on log scale, y-axis with breaks at 0.05, 0.1, 0.25, 0.5, 1, 2
#####
plot_df <- results_df %>%
  filter(!is.na(HR))

# Plot
p <- ggplot(plot_df, aes(x = cutoff, y = HR)) +
  # Ribbon for confidence intervals
  geom_ribbon(aes(ymin = HR_low, ymax = HR_hi), alpha = 0.2) +
  # Line for the HR
  geom_line(size = 1) +
  # Reference line at HR=1
  geom_hline(yintercept = 1, linetype = "dashed", color = "red") +

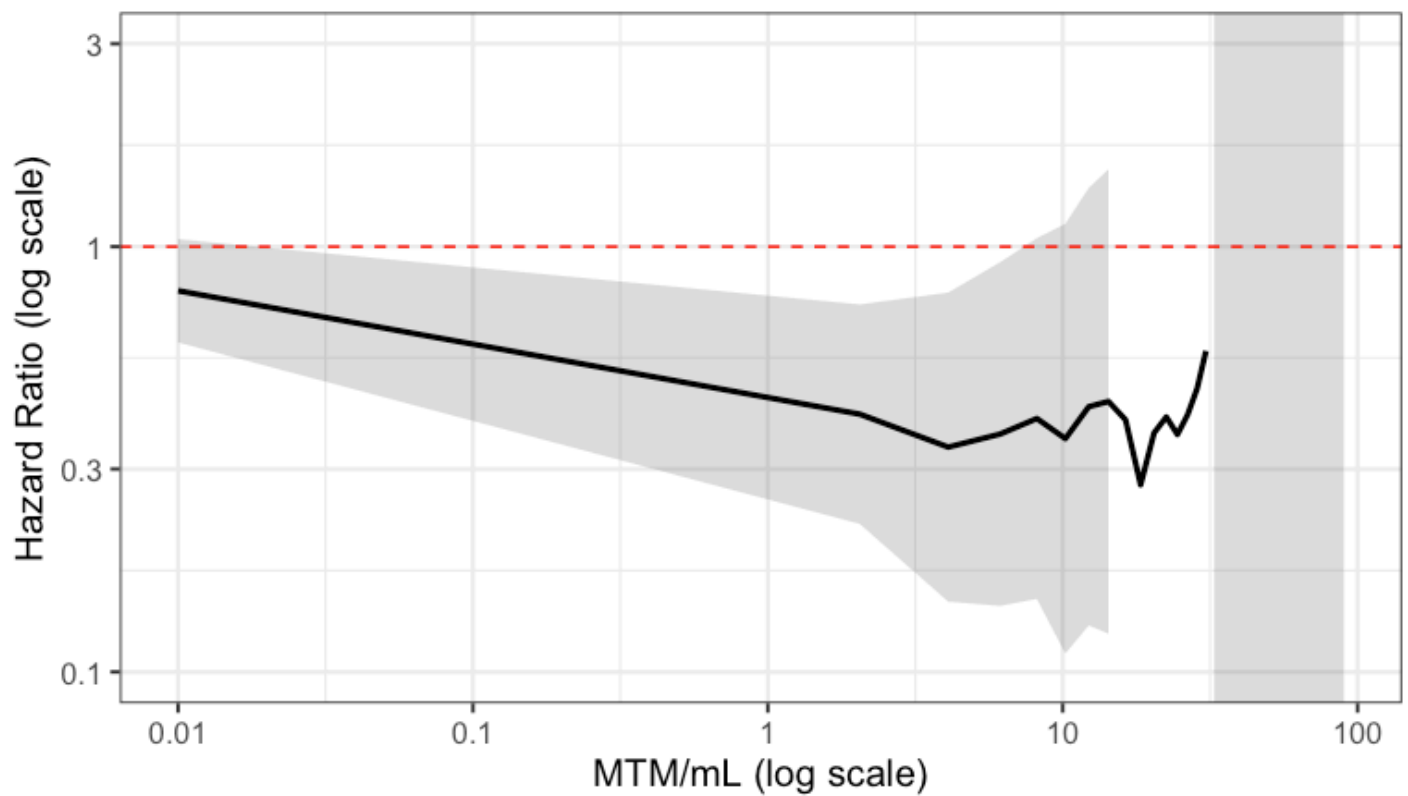
  # X-axis on log scale
  scale_x_log10(
    breaks = c(0.01, 0.1, 1, 10, 100),
    labels = c("0.01", "0.1", "1", "10", "100")
  ) +

  # Y-axis on normal (linear) scale with specific breaks
  scale_y_log10(
    breaks = c(0.1, 0.3, 1, 3),
    labels = c("0.1", "0.3", "1", "3"),
    limits = c(0.1, 3) # Adjust or remove if needed
  ) +

  theme_bw(base_size = 14) +
  labs(
    title = "Hazard Ratio (Placebo vs. TAS-102) by MTM/mL",
    x = "MTM/mL (log scale)",
    y = "Hazard Ratio (log scale)"
  )

print(p)
```

## Hazard Ratio (Placebo vs. TAS-102) by MTM/mL


[Hide](#)

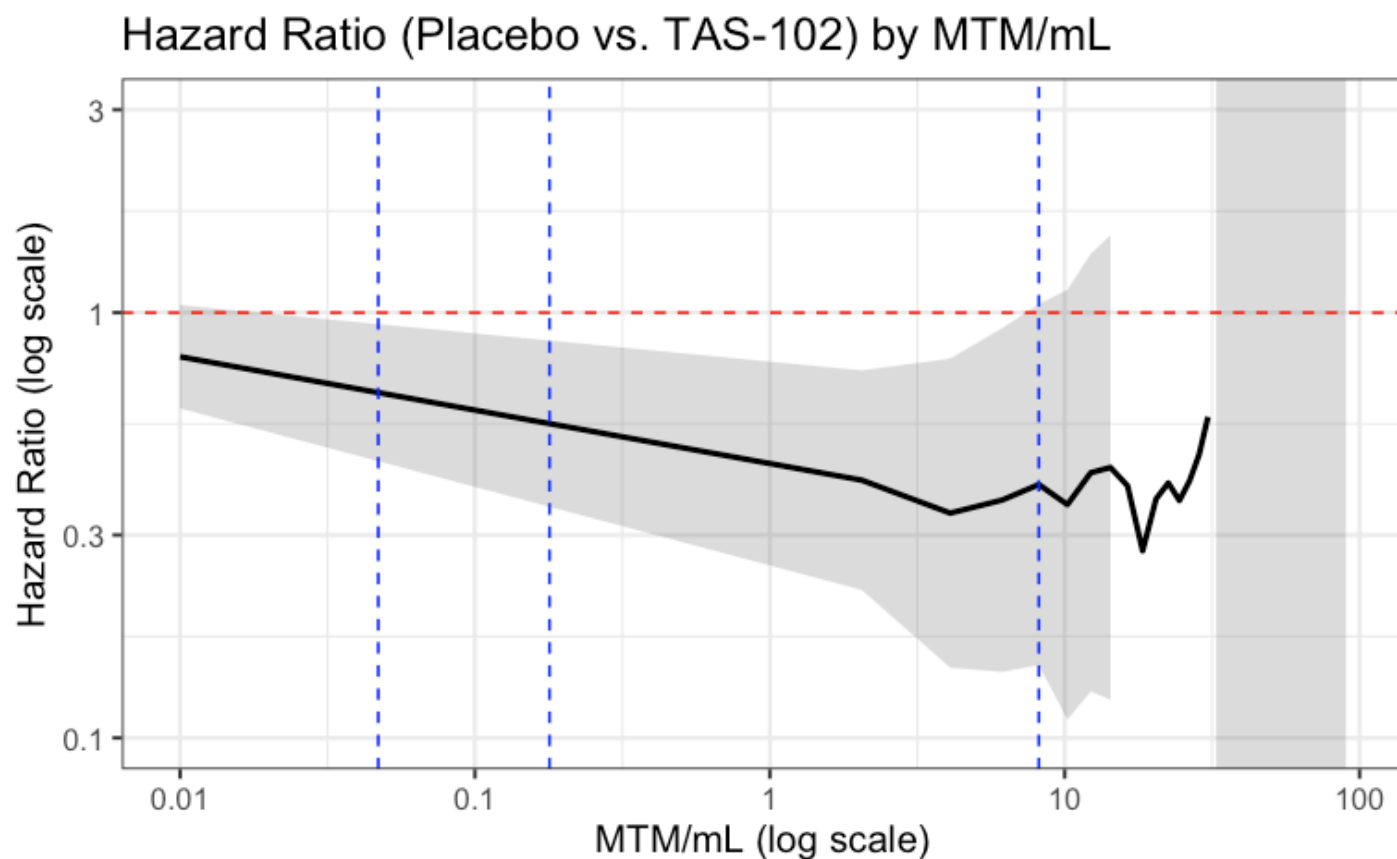
```
# Find the 2nd MTM cutoff where the upper bound of the confidence interval (HR_hi) crosses HR = 1
crossing_point <- results_df %>%
  filter(HR_hi >= 1) %>%
  slice(2) # Select the 2nd occurrence

# Print the cutoff value where HR_hi crosses 1
print(crossing_point$cutoff)
```

```
[1] 8.172449
```

[Hide](#)

```
#####
# 6. (Optional) Add vertical lines for specific cutoffs
#####
p +
  geom_vline(
    xintercept = c(0.047, 0.179, 8.172),
    linetype    = "dashed",
    color       = "blue"
  ) +
  annotate(
    "text",
    x      = c(0.179, 8.172),
    y      = max(plot_df$HR_hi, na.rm = TRUE),
    label  = c("0.179", "8.172"),
    vjust  = -0.5,
    color  = "blue"
  )
)
```



#Histogram for number of patients per enrolment MTM/mL

Hide

```
rm(list = ls())
setwd("~/Downloads")

df <- read.csv("Altair 20240729 Dataset.csv")
df$p_evtDFS1b <- as.logical(df$p_evtDFS1b)
df$DFS.months <- as.numeric(df$DFS.months)
df$p_AltBaselineMTM <- as.numeric(df$p_AltBaselineMTM)

# Clean the data
df <- df %>% filter(!is.na(p_AltBaselineMTM), p_AltBaselineMTM > 0)

# Descriptive stats (note: use the correct column name)
ppm_range <- range(df$p_AltBaselineMTM)
lowest_ppm <- ppm_range[1]
highest_ppm <- ppm_range[2]
median_ppm <- median(df$p_AltBaselineMTM)

cat("Lowest PPM value :", lowest_ppm, "\n")
```

Lowest PPM value : 0.02627334

[Hide](#)

```
cat("Highest PPM value:", highest_ppm, "\n")
```

Highest PPM value: 250.47

[Hide](#)

```
cat("Median PPM value :", median_ppm, "\n")
```

Median PPM value : 0.4

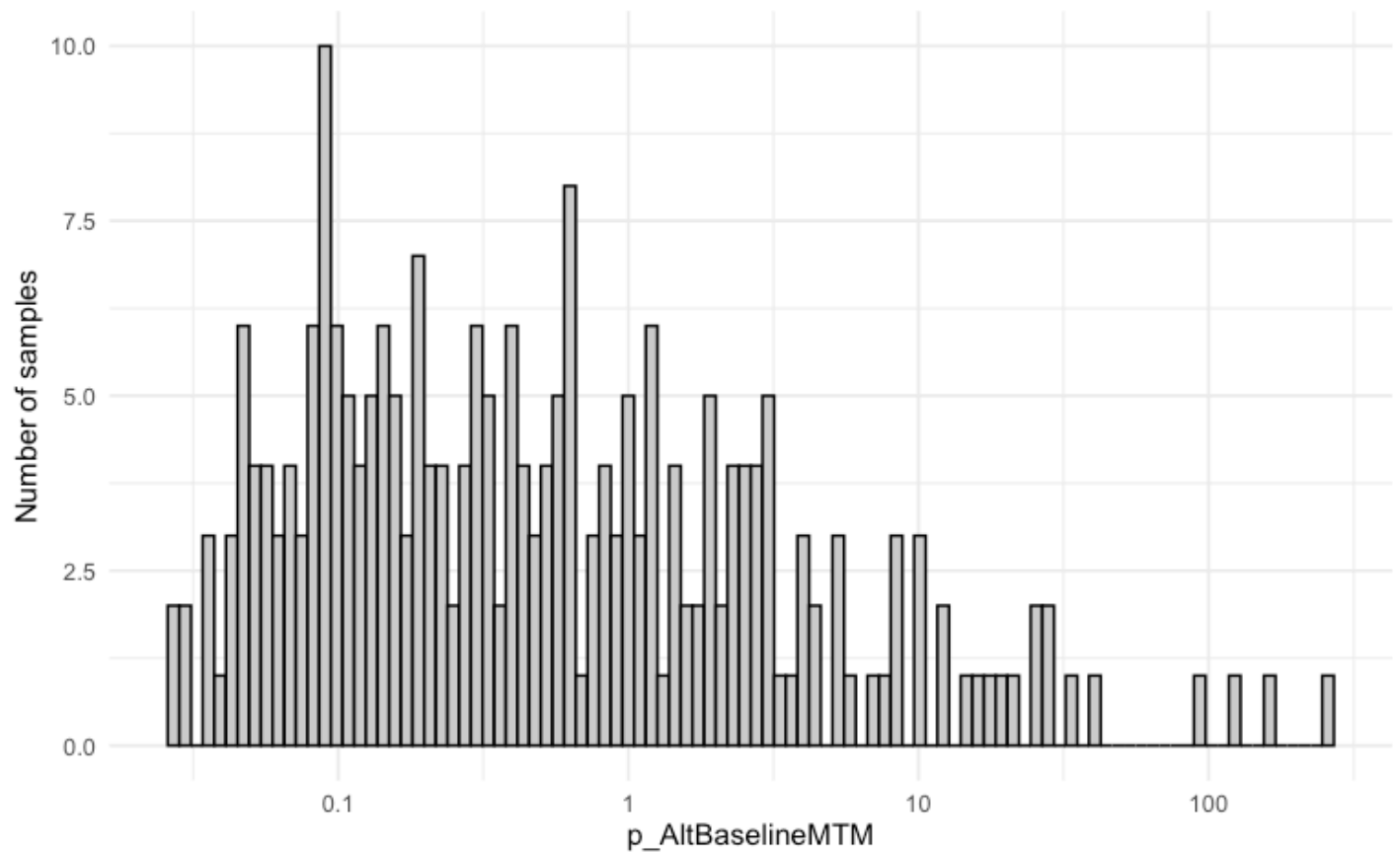
[Hide](#)

```
cat("Full range      :", lowest_ppm, "to", highest_ppm, "\n\n")
```

Full range : 0.02627334 to 250.47

[Hide](#)

```
# Histogram with custom log-scale breaks
ggplot(df, aes(x = p_AltBaselineMTM)) +
  geom_histogram(bins = 100, fill = "gray80", color = "black") +
  scale_x_log10(
    breaks = c(0.01, 0.1, 1, 10, 100),
    labels = c("0.01", "0.1", "1", "10", "100")
  ) +
  labs(x = "p_AltBaselineMTM", y = "Number of samples") +
  ylim(0, 10) +
  theme_minimal()
```



#Enrollment MTM/mL by ctDNA clearance in TAS-102 vs Placebo Arms

Hide

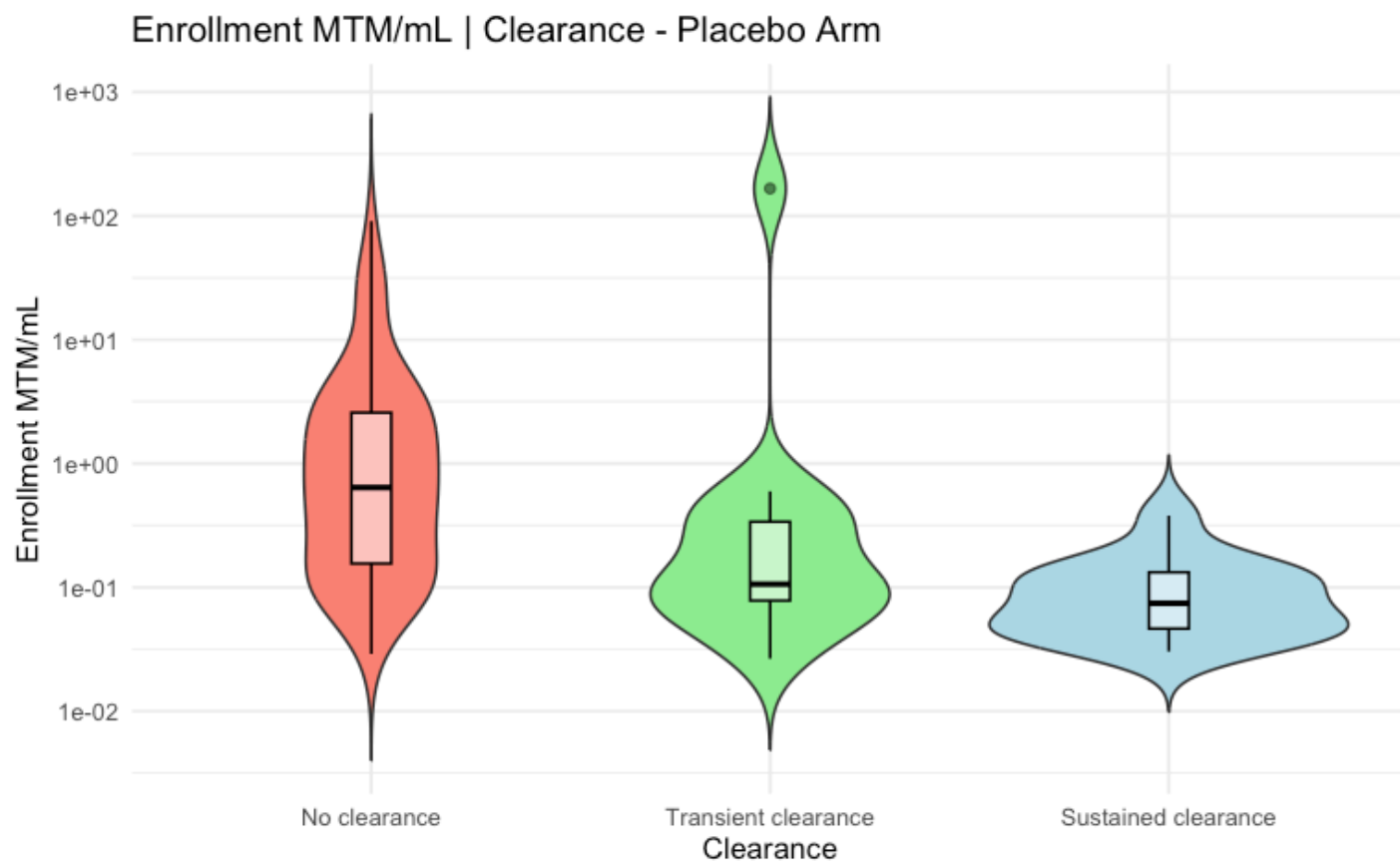
```
#Placebo
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Altair 20240729 Dataset.csv")
circ_data <- circ_data[circ_data$altair.group.SAP_MSv2!="1b = Exclude: No on-Tx TPs",]
circ_data <- circ_data[circ_data$altair.Arm=="Control",]

# Transform p_MRD_MTM with log10
circ_data$p_AltBaselineMTM <- as.numeric(as.character(circ_data$p_AltBaselineMTM))
circ_data$p_evtDFS1b <- factor(circ_data$p_evtDFS1b, levels=c("TRUE","FALSE"), labels =
c("Recurrence", "No Recurrence"))
circ_data$altair.resultPatW <- factor(circ_data$altair.resultPatW, levels=c("No clearanc
e", "Transient clearance", "Sustained clearance"))
median_p_MRD_MTM <- aggregate(p_AltBaselineMTM ~ altair.resultPatW, data = circ_data, FU
N = median)
print(median_p_MRD_MTM)
```

| altair.resultPatW<br><fctr> | p_AltBaselineMTM<br><dbl> |
|-----------------------------|---------------------------|
| No clearance                | 0.63992898                |
| Transient clearance         | 0.10612747                |
| Sustained clearance         | 0.07446615                |
| 3 rows                      |                           |

Hide

```
# Create violin plot with log10 scale on y-axis
ggplot(circ_data, aes(x=altair.resultPatW, y=p_AltBaselineMTM, fill=altair.resultPatW))
+
  geom_violin(trim=FALSE) +
  scale_fill_manual(values=c("Sustained clearance"="lightblue", "Transient clearance"="l
ightgreen", "No clearance"="salmon")) +
  geom_boxplot(width=0.1, fill="white", colour="black", alpha=0.5) +
  scale_y_log10(breaks=c(0.001, 0.01, 0.1, 1, 10, 100, 1000, 10000)) +
  labs(title="Enrollment MTM/mL | Clearance - Placebo Arm", x="Clearance", y="Enrollment
MTM/mL") +
  theme_minimal() +
  theme(legend.position="none")
```


[Hide](#)

```
m3_1v2 <- wilcox.test(p_AltBaselineMTM ~ altair.resultPatW,
  data = circ_data[circ_data$altair.resultPatW %in% c("Sustained clearance", "Transient clearance"), ],
  na.rm = TRUE)
print(m3_1v2)
```

Wilcoxon rank sum exact test

data: p\_AltBaselineMTM by altair.resultPatW  
 W = 153, p-value = 0.09254  
 alternative hypothesis: true location shift is not equal to 0

[Hide](#)

```
m3_1v3 <- wilcox.test(p_AltBaselineMTM ~ altair.resultPatW,
  data = circ_data[circ_data$altair.resultPatW %in% c("Sustained clearance", "No clearance"), ],
  na.rm = TRUE)
print(m3_1v3)
```



Wilcoxon rank sum test with continuity correction

data: p\_AltBaselineMTM by altair.resultPatW  
W = 1053, p-value = 4.344e-06  
alternative hypothesis: true location shift is not equal to 0

Hide

```
m3_2v3 <- wilcox.test(p_AltBaselineMTM ~ altair.resultPatW,
                      data = circ_data[circ_data$altair.resultPatW %in% c("Transient cle
arance", "No clearance"), ],
                      na.rm = TRUE)
print(m3_2v3)
```

Wilcoxon rank sum test with continuity correction

data: p\_AltBaselineMTM by altair.resultPatW  
W = 1010, p-value = 0.002179  
alternative hypothesis: true location shift is not equal to 0

Hide

```
# Create a table with p-values
p_value_table <- data.frame(
  Comparison = c("Sustained vs Transient", "Sustained vs No Clearance", "Transient vs No
Clearance"),
  P_Value = c(m3_1v2$p.value, m3_1v3$p.value, m3_2v3$p.value)
)
print(p_value_table)
```

| Comparison                | P_Value      |
|---------------------------|--------------|
| <chr>                     | <dbl>        |
| Sustained vs Transient    | 9.253992e-02 |
| Sustained vs No Clearance | 4.344491e-06 |
| Transient vs No Clearance | 2.179474e-03 |
| 3 rows                    |              |

Hide

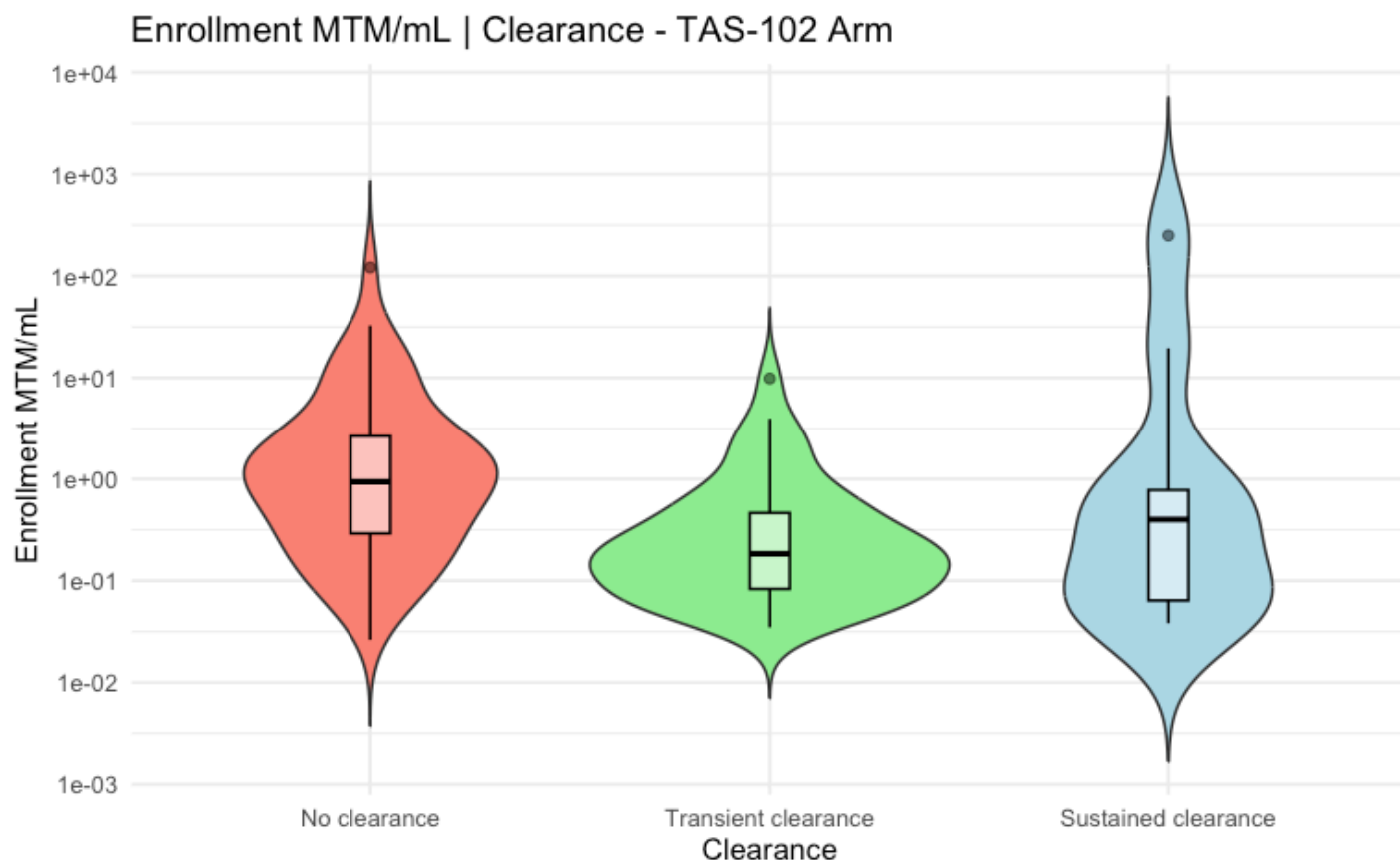
```
#TAS-102
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Altair 20240729 Dataset.csv")
circ_data <- circ_data[circ_data$altair.group.SAP_MSv2!="1b = Exclude: No on-Tx TPs",]
circ_data <- circ_data[circ_data$altair.Arm=="Experimental",]

# Transform p_MRD_MTM with log10
circ_data$p_AltBaselineMTM <- as.numeric(as.character(circ_data$p_AltBaselineMTM))
circ_data$p_evtDFS1b <- factor(circ_data$p_evtDFS1b, levels=c("TRUE","FALSE"), labels =
c("Recurrence", "No Recurrence"))
circ_data$altair.resultPatW <- factor(circ_data$altair.resultPatW, levels=c("No clearance", "Transient clearance", "Sustained clearance"))
median_p_MRD_MTM <- aggregate(p_AltBaselineMTM ~ altair.resultPatW, data = circ_data, FUN = median)
print(median_p_MRD_MTM)
```

| altair.resultPatW   | p_AltBaselineMTM |
|---------------------|------------------|
| <fctr>              | <dbl>            |
| No clearance        | 0.9419575        |
| Transient clearance | 0.1840031        |
| Sustained clearance | 0.4000000        |
| 3 rows              |                  |

Hide

```
# Create violin plot with log10 scale on y-axis
ggplot(circ_data, aes(x=altair.resultPatW, y=p_AltBaselineMTM, fill=altair.resultPatW))
+
  geom_violin(trim=FALSE) +
  scale_fill_manual(values=c("Sustained clearance"="lightblue", "Transient clearance"="lightgreen", "No clearance"="salmon")) +
  geom_boxplot(width=0.1, fill="white", colour="black", alpha=0.5) +
  scale_y_log10(breaks=c(0.001, 0.01, 0.1, 1, 10, 100, 1000, 10000)) +
  labs(title="Enrollment MTM/mL | Clearance - TAS-102 Arm", x="Clearance", y="Enrollment MTM/mL") +
  theme_minimal() +
  theme(legend.position="none")
```


[Hide](#)

```
m3_1v2 <- wilcox.test(p_AltBaselineMTM ~ altair.resultPatW,
  data = circ_data[circ_data$altair.resultPatW %in% c("Sustained cle
arance", "Transient clearance"), ],
  na.rm = TRUE)
print(m3_1v2)
```

Wilcoxon rank sum exact test

data: p\_AltBaselineMTM by altair.resultPatW  
W = 241, p-value = 0.7395  
alternative hypothesis: true location shift is not equal to 0

[Hide](#)

```
m3_1v3 <- wilcox.test(p_AltBaselineMTM ~ altair.resultPatW,
  data = circ_data[circ_data$altair.resultPatW %in% c("Sustained cle
arance", "No clearance"), ],
  na.rm = TRUE)
print(m3_1v3)
```

Wilcoxon rank sum test with continuity correction

data: p\_AltBaselineMTM by altair.resultPatW  
W = 449, p-value = 0.09739  
alternative hypothesis: true location shift is not equal to 0

Hide

```
m3_2v3 <- wilcox.test(p_AltBaselineMTM ~ altair.resultPatW,
                      data = circ_data[circ_data$altair.resultPatW %in% c("Transient cle
arance", "No clearance"), ],
                      na.rm = TRUE)
print(m3_2v3)
```

Wilcoxon rank sum test with continuity correction

data: p\_AltBaselineMTM by altair.resultPatW  
W = 2201, p-value = 5.386e-06  
alternative hypothesis: true location shift is not equal to 0

Hide

```
# Create a table with p-values
p_value_table <- data.frame(
  Comparison = c("Sustained vs Transient", "Sustained vs No Clearance", "Transient vs No
Clearance"),
  P_Value = c(m3_1v2$p.value, m3_1v3$p.value, m3_2v3$p.value)
)
print(p_value_table)
```

| Comparison                | P_Value      |
|---------------------------|--------------|
| <chr>                     | <dbl>        |
| Sustained vs Transient    | 7.395008e-01 |
| Sustained vs No Clearance | 9.738952e-02 |
| Transient vs No Clearance | 5.386244e-06 |
| 3 rows                    |              |

#DFS1 by ctDNA Clearance with 3 groups - All stages

Hide

```
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Altair 20240729 Dataset.csv")
circ_data <- circ_data[circ_data$altair.group.SAP_MSv2!="1b = Exclude: No on-Tx TPs",]

circ_data$altair.resultPatW <- factor(circ_data$altair.resultPatW, levels=c("No clearanc
e", "Transient clearance", "Sustained clearance"))
survfit(Surv(time = circ_data$DFS.months, event = circ_data$p_evtDFS1b)~altair.resultPat
W, data = circ_data)
```

```
Call: survfit(formula = Surv(time = circ_data$DFS.months, event = circ_data$p_evtDFS1b)
~
      altair.resultPatW, data = circ_data)
```

|                                       | n   | events | median | 0.95LCL | 0.95UCL |
|---------------------------------------|-----|--------|--------|---------|---------|
| altair.resultPatW=No clearance        | 147 | 140    | 4.37   | 3.75    | 5.82    |
| altair.resultPatW=Transient clearance | 63  | 45     | 11.76  | 11.01   | 15.54   |
| altair.resultPatW=Sustained clearance | 25  | 5      | NA     | 33.91   | NA      |

Hide

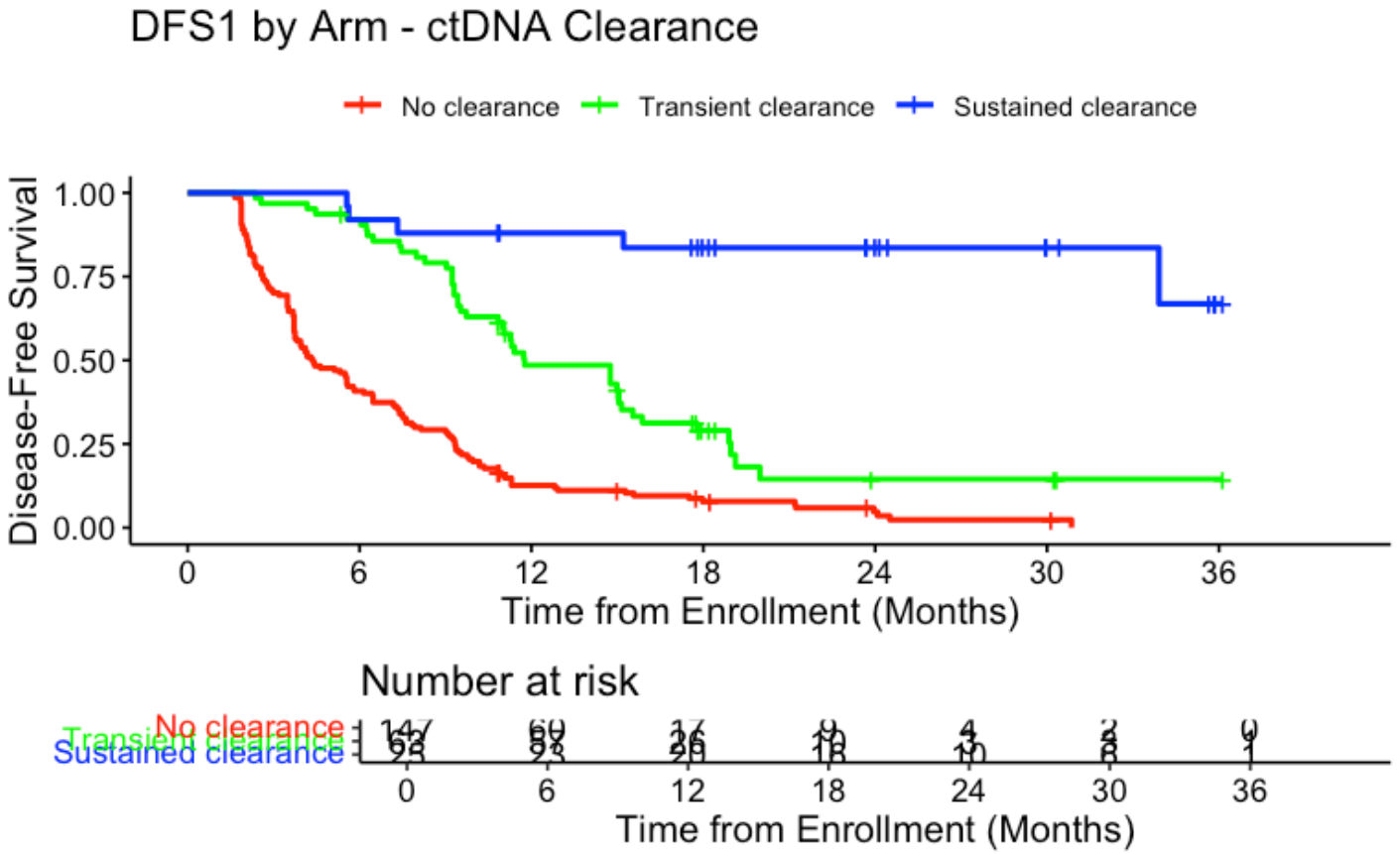
```
event_summary <- circ_data %>%
  group_by(altair.resultPatW) %>%
  summarise(
    Total = n(),
    Events = sum(p_evtDFS1b),
    Fraction = Events / n(),
    Percentage = (Events / n()) * 100
  )
print(event_summary)
```

| altair.resultPatW<br><fctr> | Total<br><int> | Events<br><int> | Fraction<br><dbl> | Percentage<br><dbl> |
|-----------------------------|----------------|-----------------|-------------------|---------------------|
| No clearance                | 147            | 140             | 0.9523810         | 95.23810            |
| Transient clearance         | 63             | 45              | 0.7142857         | 71.42857            |
| Sustained clearance         | 25             | 5               | 0.2000000         | 20.00000            |

3 rows

Hide

```
surv_object <-Surv(time = circ_data$DFS.months, event = circ_data$p_evtDFS1b)
KM_curve <- survfit(surv_object ~ altair.resultPatW, data = circ_data,conf.int=0.95,con
f.type="log-log")
ggsurvplot(KM_curve, data = circ_data, pval = FALSE, conf.int = FALSE, risk.table = TRU
E, break.time.by=6, palette=c("red","green","blue"), title="DFS1 by Arm - ctDNA Clearanc
e", ylab= "Disease-Free Survival", xlab="Time from Enrollment (Months)", legend.labs=c
("No clearance", "Transient clearance", "Sustained clearance"), legend.title="")
```



Hide

```
summary(KM_curve, times= c(6, 12, 18, 24))
```

```
Call: survfit(formula = surv_object ~ altair.resultPatW, data = circ_data,
  conf.int = 0.95, conf.type = "log-log")
```

```
altair.resultPatW=No clearance
```

| time | n.risk | n.event | survival | std.err | lower 95% CI | upper 95% CI |
|------|--------|---------|----------|---------|--------------|--------------|
| 6    | 60     | 87      | 0.4082   | 0.0405  | 0.3284       | 0.4862       |
| 12   | 17     | 41      | 0.1262   | 0.0277  | 0.0782       | 0.1861       |
| 18   | 9      | 6       | 0.0787   | 0.0232  | 0.0412       | 0.1319       |
| 24   | 4      | 3       | 0.0472   | 0.0199  | 0.0183       | 0.0975       |

```
altair.resultPatW=Transient clearance
```

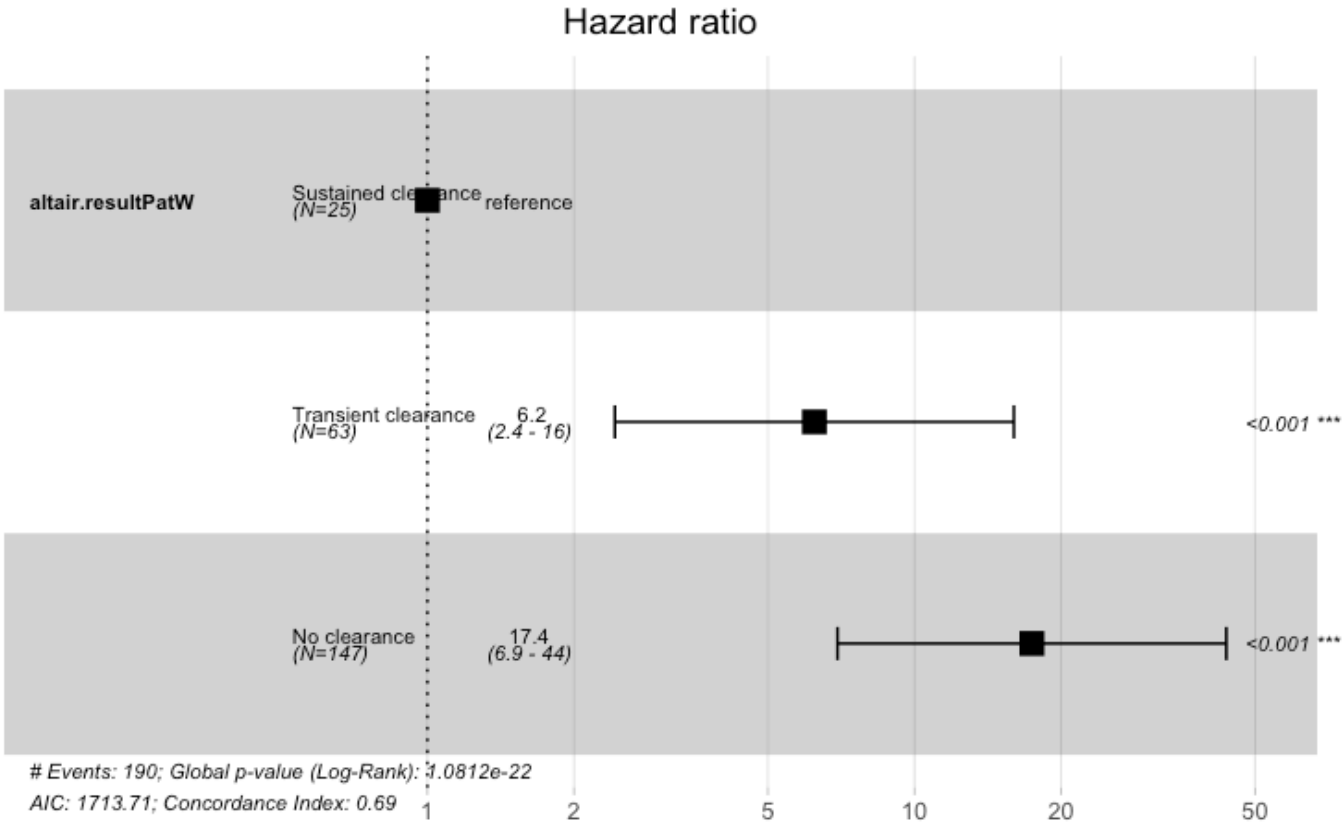
| time | n.risk | n.event | survival | std.err | lower 95% CI | upper 95% CI |
|------|--------|---------|----------|---------|--------------|--------------|
| 6    | 57     | 5       | 0.920    | 0.0342  | 0.8192       | 0.966        |
| 12   | 26     | 26      | 0.485    | 0.0653  | 0.3530       | 0.605        |
| 18   | 10     | 10      | 0.290    | 0.0619  | 0.1767       | 0.414        |
| 24   | 3      | 4       | 0.145    | 0.0600  | 0.0531       | 0.281        |

```
altair.resultPatW=Sustained clearance
```

| time | n.risk | n.event | survival | std.err | lower 95% CI | upper 95% CI |
|------|--------|---------|----------|---------|--------------|--------------|
| 6    | 23     | 2       | 0.920    | 0.0543  | 0.716        | 0.979        |
| 12   | 20     | 1       | 0.880    | 0.0650  | 0.673        | 0.960        |
| 18   | 16     | 1       | 0.836    | 0.0752  | 0.619        | 0.935        |
| 24   | 10     | 0       | 0.836    | 0.0752  | 0.619        | 0.935        |

[Hide](#)

```
circ_data$altair.resultPatW <- factor(circ_data$altair.resultPatW, levels=c("Sustained c
learance", "Transient clearance", "No clearance"))
cox_fit <- coxph(surv_object ~ altair.resultPatW, data=circ_data)
ggforest(cox_fit,data = circ_data)
```



Hide

```
summary(cox_fit)
```

Call:  
coxph(formula = surv\_object ~ altair.resultPatW, data = circ\_data)

n= 235, number of events= 190

|                                      | coef   | exp(coef) | se(coef) | z     | Pr(> z ) |     |
|--------------------------------------|--------|-----------|----------|-------|----------|-----|
| altair.resultPatWTransient clearance | 1.8292 | 6.2286    | 0.4812   | 3.801 | 0.000144 | *** |
| altair.resultPatWNo clearance        | 2.8576 | 17.4200   | 0.4690   | 6.094 | 1.1e-09  | *** |

---  
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

|                                      | exp(coef) | exp(-coef) | lower .95 | upper .95 |
|--------------------------------------|-----------|------------|-----------|-----------|
| altair.resultPatWTransient clearance | 6.229     | 0.16055    | 2.425     | 16.00     |
| altair.resultPatWNo clearance        | 17.420    | 0.05741    | 6.948     | 43.67     |

Concordance= 0.686 (se = 0.017 )  
Likelihood ratio test= 101.2 on 2 df, p=<2e-16  
Wald test = 64.59 on 2 df, p=9e-15  
Score (logrank) test = 87.72 on 2 df, p=<2e-16

Hide

```
cox_fit_summary <- summary(cox_fit)
```



#OS by ctDNA Clearance with 3 groups - All stages

Hide

```
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Altair 20240729 Dataset.csv")
circ_data <- circ_data[circ_data$altair.group.SAP_MSv2!="1b = Exclude: No on-Tx TPs",]

circ_data$altair.resultPatW <- factor(circ_data$altair.resultPatW, levels=c("No clearance", "Transient clearance", "Sustained clearance"))
survfit(Surv(time = circ_data$OS.months, event = circ_data$p_evt0S)~altair.resultPatW, data = circ_data)
```

Call: survfit(formula = Surv(time = circ\_data\$OS.months, event = circ\_data\$p\_evt0S) ~ altair.resultPatW, data = circ\_data)

|                                       | n   | events | median | 0.95LCL | 0.95UCL |
|---------------------------------------|-----|--------|--------|---------|---------|
| altair.resultPatW=No clearance        | 147 | 19     | NA     | 40.7    | NA      |
| altair.resultPatW=Transient clearance | 63  | 2      | NA     | NA      | NA      |
| altair.resultPatW=Sustained clearance | 25  | 0      | NA     | NA      | NA      |

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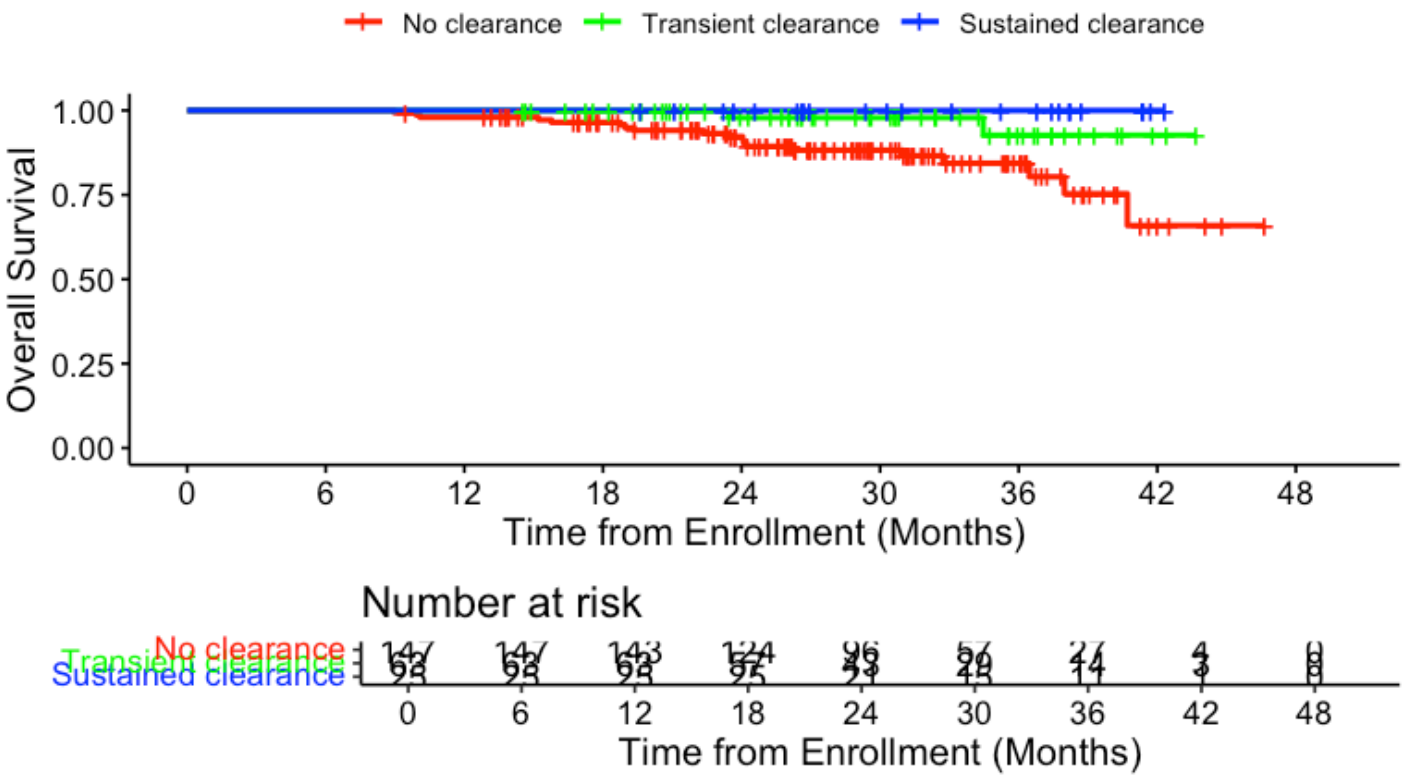
```
event_summary <- circ_data %>%
  group_by(altair.resultPatW) %>%
  summarise(
    Total = n(),
    Events = sum(p_evt0S),
    Fraction = Events / n(),
    Percentage = (Events / n()) * 100
  )
print(event_summary)
```

| altair.resultPatW<br><fctr> | Total<br><int> | Events<br><int> | Fraction<br><dbl> | Percentage<br><dbl> |
|-----------------------------|----------------|-----------------|-------------------|---------------------|
| No clearance                | 147            | 19              | 0.12925170        | 12.925170           |
| Transient clearance         | 63             | 2               | 0.03174603        | 3.174603            |
| Sustained clearance         | 25             | 0               | 0.00000000        | 0.000000            |
| 3 rows                      |                |                 |                   |                     |

Hide

```
surv_object <-Surv(time = circ_data$OS.months, event = circ_data$p_evtOS)
KM_curve <- survfit(surv_object ~ altair.resultPatW, data = circ_data, conf.int=0.95, conf.type="log-log")
ggsurvplot(KM_curve, data = circ_data, pval = FALSE, conf.int = FALSE, risk.table = TRUE, break.time.by=6, palette=c("red","green","blue"), title="OS by Arm - ctDNA Clearance", ylab= "Overall Survival", xlab="Time from Enrollment (Months)", legend.labs=c("No clearance", "Transient clearance", "Sustained clearance"), legend.title="")
```

OS by Arm - ctDNA Clearance



Hide

```
summary(KM_curve, times= c(6, 12, 18, 24))
```

Call: `survfit(formula = surv_object ~ altair.resultPatW, data = circ_data, conf.int = 0.95, conf.type = "log-log")`

| altair.resultPatW=No clearance |        |         |          |         |              |              |  |
|--------------------------------|--------|---------|----------|---------|--------------|--------------|--|
| time                           | n.risk | n.event | survival | std.err | lower 95% CI | upper 95% CI |  |
| 6                              | 147    | 0       | 1.000    | 0.0000  | 1.000        | 1.000        |  |
| 12                             | 143    | 3       | 0.979    | 0.0117  | 0.938        | 0.993        |  |
| 18                             | 124    | 2       | 0.965    | 0.0155  | 0.917        | 0.985        |  |
| 24                             | 96     | 5       | 0.923    | 0.0237  | 0.860        | 0.958        |  |

| altair.resultPatW=Transient clearance |        |         |          |         |              |              |  |
|---------------------------------------|--------|---------|----------|---------|--------------|--------------|--|
| time                                  | n.risk | n.event | survival | std.err | lower 95% CI | upper 95% CI |  |
| 6                                     | 63     | 0       | 1.000    | 0.0000  | 1.000        | 1.000        |  |
| 12                                    | 63     | 0       | 1.000    | 0.0000  | 1.000        | 1.000        |  |
| 18                                    | 57     | 0       | 1.000    | 0.0000  | NA           | NA           |  |
| 24                                    | 43     | 1       | 0.978    | 0.0215  | 0.856        | 0.997        |  |

| altair.resultPatW=Sustained clearance |        |         |          |         |              |              |  |
|---------------------------------------|--------|---------|----------|---------|--------------|--------------|--|
| time                                  | n.risk | n.event | survival | std.err | lower 95% CI | upper 95% CI |  |
| 6                                     | 25     | 0       | 1        | 0       | 1            | 1            |  |
| 12                                    | 25     | 0       | 1        | 0       | 1            | 1            |  |
| 18                                    | 25     | 0       | 1        | 0       | 1            | 1            |  |
| 24                                    | 21     | 0       | 1        | 0       | NA           | NA           |  |

Hide

```

circ_data$altair.resultPatW <- factor(circ_data$altair.resultPatW, levels=c("Sustained c
learance", "Transient clearance", "No clearance"))
cox_fit <- coxphf(surv_object ~ altair.resultPatW, data=circ_data)
summary(cox_fit)

```

```
coxphf(formula = surv_object ~ altair.resultPatW, data = circ_data)
```

Model fitted by Penalized ML

Confidence intervals and p-values by Profile Likelihood

|                                      |            | coef     | se(coef) | exp(coef) | lower 0.95 | upper 0.95 |
|--------------------------------------|------------|----------|----------|-----------|------------|------------|
| Chisq                                | p          |          |          |           |            |            |
| altair.resultPatWTransient clearance |            | 1.004483 | 1.609325 | 2.730495  | 0.221318   | 377.0473   |
| 0.5145106                            | 0.47319272 |          |          |           |            |            |
| altair.resultPatWNo clearance        |            | 2.324182 | 1.489576 | 10.218322 | 1.391342   | 1302.7825  |
| 5.8730349                            | 0.01537452 |          |          |           |            |            |

Likelihood ratio test=9.503886 on 2 df, p=0.008634899, n=235

Wald test = 5.724023 on 2 df, p = 0.05715369

Covariance-Matrix:

|                                      | altair.resultPatWTransient clearance | altair.resultP |
|--------------------------------------|--------------------------------------|----------------|
| atWNo clearance                      |                                      |                |
| altair.resultPatWTransient clearance | 2.589926                             |                |
| 2.162201                             |                                      |                |
| altair.resultPatWNo clearance        | 2.162201                             |                |
| 2.218837                             |                                      |                |

Hide

```
cox_fit_summary <- summary(cox_fit)
```

```
coxphf(formula = surv_object ~ altair.resultPatW, data = circ_data)
```

Model fitted by Penalized ML  
Confidence intervals and p-values by Profile Likelihood

|  |            | coef                                 | se(coef)       | exp(coef) | lower 0.95 | upper 0.95 |
|--|------------|--------------------------------------|----------------|-----------|------------|------------|
| Chisq  | p          |                                      |                |           |            |            |
| altair.resultPatWTransient clearance                         | 1.004483   | 1.609325                             | 2.730495       | 0.221318  | 377.0473   |            |
| 0.5145106  | 0.47319272 |                                      |                |           |            |            |
| altair.resultPatWNo clearance                                | 2.324182   | 1.489576                             | 10.218322      | 1.391342  | 1302.7825  |            |
| 5.8730349  | 0.01537452 |                                      |                |           |            |            |
| Likelihood ratio test=9.503886 on 2 df, p=0.008634899, n=235 |            |                                      |                |           |            |            |
| Wald test = 5.724023 on 2 df, p = 0.05715369                 |            |                                      |                |           |            |            |
| Covariance-Matrix:   |            |                                      |                |           |            |            |
|  |            | altair.resultPatWTransient clearance | altair.resultP |           |            |            |
| atWNo clearance  |            |                                      |                |           |            |            |
| altair.resultPatWTransient clearance                         |            |                                      | 2.589926       |           |            |            |
| 2.162201   |            |                                      |                |           |            |            |
| altair.resultPatWNo clearance                                |            |                                      | 2.162201       |           |            |            |
| 2.218837   |            |                                      |                |           |            |            |

#DFS1 by TAS vs Placebo - Central review data - All stages & stratified for Stage & ctDNA 1mo post-surgery

Hide

```
rm(list = ls())
setwd("~/Downloads")
circ_data <- read.csv("Altair 20250903 Central Imaging Dataset.csv")
circ_data <- as.data.frame(circ_data)

circ_data$altair.Arm <- factor(circ_data$altair.Arm, levels = c("Control","Experimental"), labels = c("Placebo","FTD/TPI"))
circ_data$Disease.Stage <- factor(circ_data$Disease.Stage, levels = c("Stage II or lower","StageIII","M1"))
circ_data$ctDNA1mo <- factor(circ_data$ctDNA1mo, levels = c("NEGATIVE","POSITIVE"), labels = c("Negative","Positive"))

event_summary <- circ_data %>% group_by(altair.Arm) %>% summarise(Total = n(), Events = sum(p_evtDFS1b), Fraction = Events / n(), Percentage = (Events / n()) * 100)
print(event_summary)
```

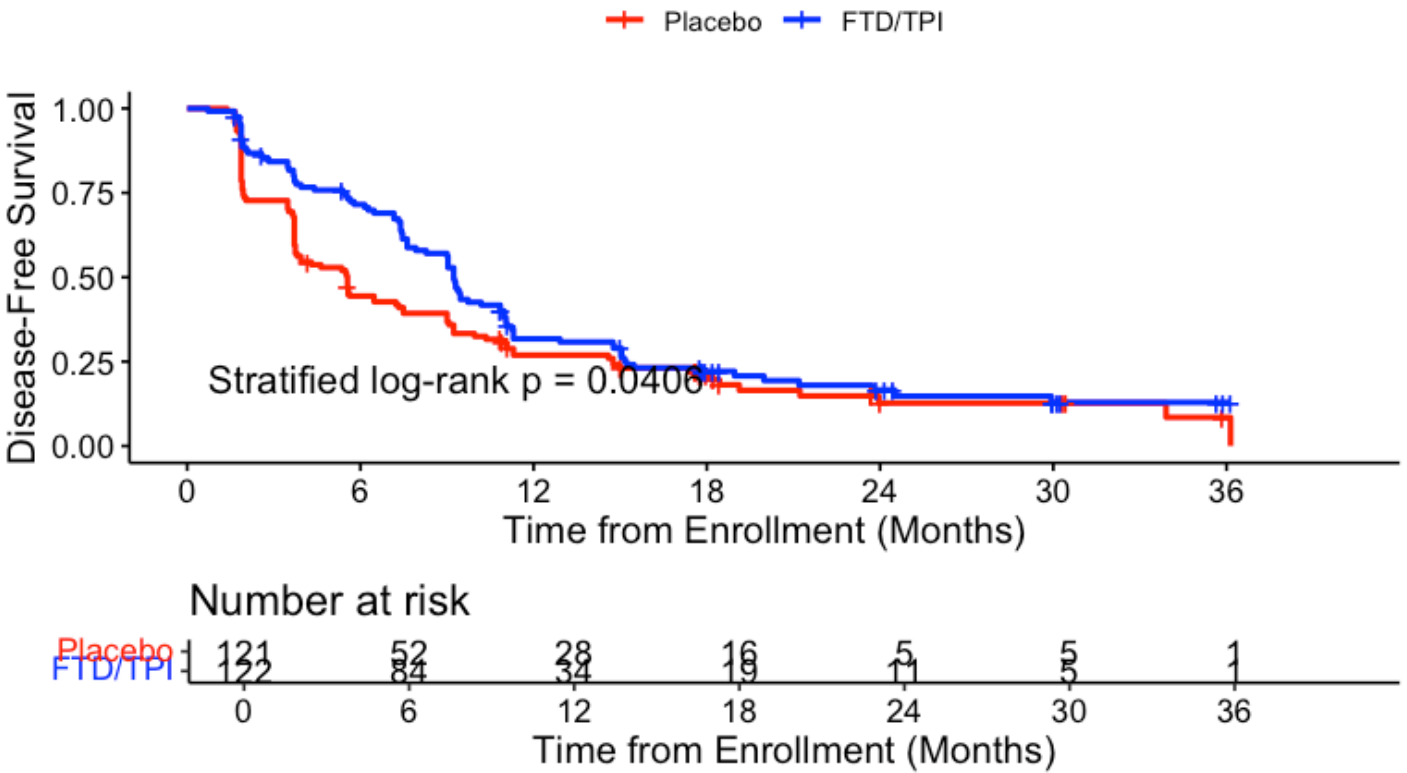
| altair.Arm<br><fctr> | Total<br><int> | Events<br><int> | Fraction<br><dbl> | Percentage<br><dbl> |
|----------------------|----------------|-----------------|-------------------|---------------------|
| Placebo              | 121            | 100             | 0.8264463         | 82.64463            |
| FTD/TPI              | 122            | 96              | 0.7868852         | 78.68852            |
| 2 rows               |                |                 |                   |                     |

```
surv_object <- Surv(time = circ_data$DFS.months, event = circ_data$p_evtDFS1b)
KM_curve <- survfit(surv_object ~ altair.Arm, data = circ_data, conf.int = 0.95, conf.type = "log-log")

# --- Stratified log-rank test (exactly as in primary analysis) ---
# Use survdiff with the same stratification factors
sd_strat <- survdiff(surv_object ~ altair.Arm + strata(Disease.Stage, ctDNA1mo), data = circ_data)
# For two groups, df = 1
p_strat_logrank <- 1 - pchisq(sd_strat$chisq, df = 1)

# KM plot with the stratified p-value displayed
ggsurvplot(KM_curve, data = circ_data, pval = sprintf("Stratified log-rank p = %.4f", p_strat_logrank), conf.int = FALSE, risk.table = TRUE, break.time.by = 6, palette = c("red", "blue"), title = "DFS1 by Arm - All Patients", ylab = "Disease-Free Survival", xlab = "Time from Enrollment (Months)", legend.labs = c("Placebo", "FTD/TPI"), legend.title = "")
```

DFS1 by Arm - All Patients



Hide

```
print(summary(KM_curve, times = c(6, 12, 18, 24)))
```

Call: `survfit(formula = surv_object ~ altair.Arm, data = circ_data, conf.int = 0.95, conf.type = "log-log")`

| altair.Arm=Placebo |        |         |          |         |              |              |  |
|--------------------|--------|---------|----------|---------|--------------|--------------|--|
| time               | n.risk | n.event | survival | std.err | lower 95% CI | upper 95% CI |  |
| 6                  | 52     | 67      | 0.444    | 0.0453  | 0.3542       | 0.530        |  |
| 12                 | 28     | 20      | 0.269    | 0.0412  | 0.1923       | 0.352        |  |
| 18                 | 16     | 6       | 0.210    | 0.0386  | 0.1397       | 0.290        |  |
| 24                 | 5      | 5       | 0.127    | 0.0379  | 0.0649       | 0.212        |  |

| altair.Arm=FTD/TPI |        |         |          |         |              |              |  |
|--------------------|--------|---------|----------|---------|--------------|--------------|--|
| time               | n.risk | n.event | survival | std.err | lower 95% CI | upper 95% CI |  |
| 6                  | 84     | 34      | 0.716    | 0.0413  | 0.6254       | 0.788        |  |
| 12                 | 34     | 46      | 0.318    | 0.0434  | 0.2347       | 0.403        |  |
| 18                 | 19     | 10      | 0.222    | 0.0395  | 0.1494       | 0.303        |  |
| 24                 | 11     | 4       | 0.166    | 0.0381  | 0.0996       | 0.247        |  |

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```
cox_fit_stratified <- coxph(surv_object ~ altair.Arm + strata(Disease.Stage) + strata(ct
DNA1mo), data = circ_data)
cox_fit_summary_stratified <- summary(cox_fit_stratified)
print(cox_fit_summary_stratified)
```

Call:

```
coxph(formula = surv_object ~ altair.Arm + strata(Disease.Stage) +
      strata(ctDNA1mo), data = circ_data)
```

n= 243, number of events= 196

|                   | coef    | exp(coef) | se(coef) | z      | Pr(> z ) |
|-------------------|---------|-----------|----------|--------|----------|
| altair.ArmFTD/TPI | -0.3048 | 0.7372    | 0.1462   | -2.085 | 0.0371 * |

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

|                   | exp(coef) | exp(-coef) | lower .95 | upper .95 |
|-------------------|-----------|------------|-----------|-----------|
| altair.ArmFTD/TPI | 0.7372    | 1.356      | 0.5536    | 0.9819    |

Concordance= 0.565 (se = 0.021 )

Likelihood ratio test= 4.34 on 1 df, p=0.04

Wald test = 4.35 on 1 df, p=0.04

Score (logrank) test = 4.38 on 1 df, p=0.04

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```
HR_stratified      <- cox_fit_summary_stratified$conf.int["altair.ArmFTD/TPI","exp(coe
f)"]
lower_CI_stratified <- cox_fit_summary_stratified$conf.int["altair.ArmFTD/TPI","lower .9
5"]
upper_CI_stratified <- cox_fit_summary_stratified$conf.int["altair.ArmFTD/TPI","upper .9
5"]

# --- Use SCORE (log-rank) p-value from the Cox fit ---
if (!is.null(cox_fit_summary_stratified$score)) {
  score_stat <- cox_fit_summary_stratified$score
} else {
  score_stat <- as.numeric(cox_fit_summary_stratified$sctest["test"])
}
p_value_score <- 1 - pchisq(score_stat, df = 1)

# (Optional) Wald p-value for reference
p_value_wald <- as.numeric(cox_fit_summary_stratified$wald["pvalue"])

# Label using SCORE p-value
label_text_stratified <- paste0(
  "HR = ", round(HR_stratified, 2),
  " (", round(lower_CI_stratified, 2), "-",
  round(upper_CI_stratified, 2), "); p (score) = ",
  format.pval(p_value_score, digits = 3)
)
print(label_text_stratified)
```

```
[1] "HR = 0.74 (0.55-0.98); p (score) = 0.036"
```

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```
#print both p-values side-by-side:  
cat(sprintf("Stratified log-rank (survdif) p = %.4f\n", p_strat_logrank))
```

```
Stratified log-rank (survdif) p = 0.0406
```

[Hide](#)

```
cat(sprintf("Cox score-test p = %.4f (Wald p = %.4f)\n", p_value_score, p_value_wald))
```

```
Cox score-test p = 0.0364 (Wald p = 0.0371)
```