

CIRCULATE Galaxy cohort B Ando et al 2024

[Code ▼](#)

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

```
#Demographics Table
```

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```

rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$CohortB=="TRUE",]

circ_data_subset <- circ_data %>%
  select(
    Age,
    Gender,
    ECOG,
    pT,
    pN,
    Stage,
    ACT,
    BRAF.V600E,
    RAS,
    MSI,
    RFS.Event,
    OS.Event,
    OS.months) %>%
  mutate(
    Age = as.numeric(Age),
    Gender = factor(Gender, levels = c("Male", "Female")),
    ECOG = factor(ECOG, levels = c(0, 1)),
    pT = factor(pT, levels = c("T1-T2", "T3-T4")),
    pN = factor(pN, levels = c("N0", "N1-N2")),
    Stage = factor(Stage, levels = c("II", "III")),
    ACT = factor(ACT, levels = c("TRUE", "FALSE"), labels = c("Adjuvant Chemotherapy",
"Observation")),
    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")),
    RFS.Event = factor(RFS.Event, levels = c("TRUE", "FALSE"), labels = c("Recurrence",
"No Recurrence")),
    OS.Event = factor(OS.Event, levels = c("TRUE", "FALSE"), labels = c("Deceased", "Ali
ve")),
    OS.months = as.numeric(OS.months))
table1 <- circ_data_subset %>%
  tbl_summary(
    statistic = list(
      all_continuous() ~ "{median} ({min} - {max})",
      all_categorical() ~ "{n} ({p}%)" ) %>%
    bold_labels()
  )
table1

```

Characteristic	N = 250 ¹
Age	67 (38 - 92)
¹ Median (Range); n (%)	

Characteristic	N = 250 ¹
Gender	
Male	162 (65%)
Female	88 (35%)
ECOG	
0	228 (91%)
1	22 (8.8%)
pT	
T1-T2	29 (12%)
T3-T4	221 (88%)
pN	
N0	99 (40%)
N1-N2	151 (60%)
Stage	
II	100 (40%)
III	150 (60%)
ACT	
Adjuvant Chemotherapy	123 (49%)
Observation	127 (51%)
BRAF.V600E	
BRAF wt	248 (99%)
BRAF V600E	2 (0.8%)
RAS	
RAS wt	122 (49%)
RAS mut	128 (51%)
MSI	
MSS	247 (99%)
¹ Median (Range); n (%)	

Characteristic	N = 250 ¹
MSI-High	3 (1.2%)
RFS.Event	
Recurrence	48 (19%)
No Recurrence	202 (81%)
OS.Event	
Deceased	11 (4.4%)
Alive	239 (96%)
OS.months	22.0 (1.2 - 35.9)
¹ Median (Range); n (%)	

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```
fit1 <- as_flex_table(
  table1,
  include = everything(),
  return_calls = FALSE,
  strip_md_bold = TRUE)
```

Warning: The `strip_md_bold` argument of `as_flex_table()` is deprecated as of gtsummary 1.6.0.

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fit1

Characteristic	N = 250 ¹
Age	67 (38 - 92)
Gender	
Male	162 (65%)
Female	88 (35%)
ECOG	
0	228 (91%)
1	22 (8.8%)
pT	
T1-T2	29 (12%)

¹Median (Range); n (%)

Characteristic	N = 250 ¹
T3-T4	221 (88%)
pN	
N0	99 (40%)
N1-N2	151 (60%)
Stage	
II	100 (40%)
III	150 (60%)
ACT	
Adjuvant Chemotherapy	123 (49%)
Observation	127 (51%)
BRAF.V600E	
BRAF wt	248 (99%)
BRAF V600E	2 (0.8%)
RAS	
RAS wt	122 (49%)
RAS mut	128 (51%)
MSI	
MSS	247 (99%)
MSI-High	3 (1.2%)
RFS.Event	
Recurrence	48 (19%)
No Recurrence	202 (81%)
OS.Event	
Deceased	11 (4.4%)
Alive	239 (96%)
OS.months	22.0 (1.2 - 35.9)

¹Median (Range); n (%)

Hide

```
save_as_docx(fit1, path= "~/Downloads/table1.docx")
```

#Demographics Table by MRD ctDNA Status

Hide

```

rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$CohortB=="TRUE",]
circ_data <- circ_data[circ_data$ctDNA.MRD!="",]

circ_data_subset1 <- circ_data %>%
  select(
    Age,
    Gender,
    ECOG,
    pT,
    pN,
    Stage,
    ACT,
    BRAF.V600E,
    RAS,
    MSI,
    RFS.Event,
    OS.Event,
    OS.months) %>%
  mutate(
    Age = as.numeric(Age),
    Gender = factor(Gender, levels = c("Male", "Female")),
    ECOG = factor(ECOG, levels = c(0, 1)),
    pT = factor(pT, levels = c("T1-T2", "T3-T4")),
    pN = factor(pN, levels = c("N0", "N1-N2")),
    Stage = factor(Stage, levels = c("II", "III")),
    ACT = factor(ACT, levels = c("TRUE", "FALSE"), labels = c("Adjuvant Chemotherapy",
"Observation")),
    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")),
    RFS.Event = factor(RFS.Event, levels = c("TRUE", "FALSE"), labels = c("Recurrence",
"No Recurrence")),
    OS.Event = factor(OS.Event, levels = c("TRUE", "FALSE"), labels = c("Deceased", "Ali
ve")),
    OS.months = as.numeric(OS.months))

circ_data1 <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$CohortB=="TRUE",]
circ_data <- circ_data[circ_data$ctDNA.MRD!="",]

circ_data_subset2 <- circ_data %>%
  select(
    Age,
    Gender,
    ECOG,
    pT,
    pN,
    Stage,

```

```
ACT,
BRAf.V600E,
RAS,
MSI,
RFS.Event,
OS.Event,
OS.months,
ctDNA.MRD) %>%
mutate(
  Age = as.numeric(Age),
  Gender = factor(Gender, levels = c("Male", "Female")),
  ECOG = factor(ECOG, levels = c(0, 1)),
  pT = factor(pT, levels = c("T1-T2", "T3-T4")),
  pN = factor(pN, levels = c("N0", "N1-N2")),
  Stage = factor(Stage, levels = c("II", "III")),
  ACT = factor(ACT, levels = c("TRUE", "FALSE"), labels = c("Adjuvant Chemotherapy",
"Observation")),
  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")),
  RFS.Event = factor(RFS.Event, levels = c("TRUE", "FALSE"), labels = c("Recurrence",
"No Recurrence")),
  OS.Event = factor(OS.Event, levels = c("TRUE", "FALSE"), labels = c("Deceased", "Ali
ve")),
  OS.months = as.numeric(OS.months),
  ctDNA.MRD = factor(ctDNA.MRD, levels = c("NEGATIVE", "POSITIVE")))
Overall <- circ_data_subset1 %>%
tbl_summary(
  statistic = list(
    all_continuous() ~ "{median} ({min} - {max})",
    all_categorical() ~ "{n} ({p}%)" ) %>%
  bold_labels()
Overall
```

Characteristic	N = 247 ¹
Age	67 (38 - 92)
Gender	
Male	162 (66%)
Female	85 (34%)
ECOG	
0	225 (91%)
1	22 (8.9%)
¹ Median (Range); n (%)	

Characteristic	N = 247 ¹
pT	
T1-T2	29 (12%)
T3-T4	218 (88%)
pN	
N0	98 (40%)
N1-N2	149 (60%)
Stage	
II	99 (40%)
III	148 (60%)
ACT	
Adjuvant Chemotherapy	121 (49%)
Observation	126 (51%)
BRAF.V600E	
BRAF wt	245 (99%)
BRAF V600E	2 (0.8%)
RAS	
RAS wt	121 (49%)
RAS mut	126 (51%)
MSI	
MSS	244 (99%)
MSI-High	3 (1.2%)
RFS.Event	
Recurrence	48 (19%)
No Recurrence	199 (81%)
OS.Event	
Deceased	11 (4.5%)
¹ Median (Range); n (%)	

Characteristic	N = 247 ¹
Alive	236 (96%)
OS.months	22.0 (1.2 - 35.9)
¹ Median (Range); n (%)	

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

Characteristic	NEGATIVE, N = 212 ¹	POSITIVE, N = 35 ¹	p-value ²
Age	67 (38 - 92)	67 (43 - 82)	0.6
Gender			0.5
Male	141 (67%)	21 (60%)	
Female	71 (33%)	14 (40%)	
ECOG			0.3
0	191 (90%)	34 (97%)	
1	21 (9.9%)	1 (2.9%)	
pT			0.8
T1-T2	26 (12%)	3 (8.6%)	
T3-T4	186 (88%)	32 (91%)	
pN			<0.001
N0	95 (45%)	3 (8.6%)	
N1-N2	117 (55%)	32 (91%)	
Stage			<0.001

¹ Median (Range); n (%)

² Wilcoxon rank sum test; Pearson's Chi-squared test; Fisher's exact test

Characteristic	NEGATIVE, N = 212 ¹	POSITIVE, N = 35 ¹	p-value ²
II	96 (45%)	3 (8.6%)	
III	116 (55%)	32 (91%)	
ACT			0.004
Adjuvant Chemotherapy	96 (45%)	25 (71%)	
Observation	116 (55%)	10 (29%)	
BRAF.V600E			>0.9
BRAF wt	210 (99%)	35 (100%)	
BRAF V600E	2 (0.9%)	0 (0%)	
RAS			0.060
RAS wt	109 (51%)	12 (34%)	
RAS mut	103 (49%)	23 (66%)	
MSI			>0.9
MSS	209 (99%)	35 (100%)	
MSI-High	3 (1.4%)	0 (0%)	
RFS.Event			<0.001
Recurrence	23 (11%)	25 (71%)	
No Recurrence	189 (89%)	10 (29%)	
OS.Event			0.2
Deceased	8 (3.8%)	3 (8.6%)	
Alive	204 (96%)	32 (91%)	
OS.months	22.0 (7.5 - 35.9)	16.4 (1.2 - 34.9)	0.082

¹ Median (Range); n (%)

² Wilcoxon rank sum test; Pearson's Chi-squared test; Fisher's exact test

Hide

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

Characteristic	Table 1	Table 2		p-value ²
	N = 247 ¹	NEGATIVE, N = 212 ¹	POSITIVE, N = 35 ¹	
Age	67 (38 - 92)	67 (38 - 92)	67 (43 - 82)	0.6
Gender				0.5
Male	162 (66%)	141 (67%)	21 (60%)	
Female	85 (34%)	71 (33%)	14 (40%)	
ECOG				0.3
0	225 (91%)	191 (90%)	34 (97%)	
1	22 (8.9%)	21 (9.9%)	1 (2.9%)	
pT				0.8
T1-T2	29 (12%)	26 (12%)	3 (8.6%)	
T3-T4	218 (88%)	186 (88%)	32 (91%)	
pN				<0.001
N0	98 (40%)	95 (45%)	3 (8.6%)	
N1-N2	149 (60%)	117 (55%)	32 (91%)	
Stage				<0.001
II	99 (40%)	96 (45%)	3 (8.6%)	
III	148 (60%)	116 (55%)	32 (91%)	
ACT				0.004
Adjuvant Chemotherapy	121 (49%)	96 (45%)	25 (71%)	
Observation	126 (51%)	116 (55%)	10 (29%)	
BRAF.V600E				>0.9
BRAF wt	245 (99%)	210 (99%)	35 (100%)	
BRAF V600E	2 (0.8%)	2 (0.9%)	0 (0%)	
RAS				0.060
RAS wt	121 (49%)	109 (51%)	12 (34%)	

¹ Median (Range); n (%)² Wilcoxon rank sum test; Pearson's Chi-squared test; Fisher's exact test

	Table 1	Table 2		
Characteristic	N = 247 ¹	NEGATIVE, N = 212 ¹	POSITIVE, N = 35 ¹	p-value ²
RAS mut	126 (51%)	103 (49%)	23 (66%)	
MSI				>0.9
MSS	244 (99%)	209 (99%)	35 (100%)	
MSI-High	3 (1.2%)	3 (1.4%)	0 (0%)	
RFS.Event				<0.001
Recurrence	48 (19%)	23 (11%)	25 (71%)	
No Recurrence	199 (81%)	189 (89%)	10 (29%)	
OS.Event				0.2
Deceased	11 (4.5%)	8 (3.8%)	3 (8.6%)	
Alive	236 (96%)	204 (96%)	32 (91%)	
OS.months	22.0 (1.2 - 35.9)	22.0 (7.5 - 35.9)	16.4 (1.2 - 34.9)	0.082

¹ Median (Range); n (%)

² Wilcoxon rank sum test; Pearson’s Chi-squared test; Fisher’s exact test

Hide

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

	Table 1	Table 2		
Characteristic	N = 247 ¹	NEGATIVE, N = 212 ¹	POSITIVE, N = 35 ¹	p-value ²
Age	67 (38 - 92)	67 (38 - 92)	67 (43 - 82)	0.6
Gender				0.5
Male	162 (66%)	141 (67%)	21 (60%)	
Female	85 (34%)	71 (33%)	14 (40%)	
ECOG				0.3

¹Median (Range); n (%)

²Wilcoxon rank sum test; Pearson's Chi-squared test; Fisher's exact test

	Table 1		Table 2	
Characteristic	N = 247 ¹	NEGATIVE, N = 212 ¹	POSITIVE, N = 35 ¹	p-value ²
0	225 (91%)	191 (90%)	34 (97%)	
1	22 (8.9%)	21 (9.9%)	1 (2.9%)	
pT				0.8
T1-T2	29 (12%)	26 (12%)	3 (8.6%)	
T3-T4	218 (88%)	186 (88%)	32 (91%)	
pN				<0.001
N0	98 (40%)	95 (45%)	3 (8.6%)	
N1-N2	149 (60%)	117 (55%)	32 (91%)	
Stage				<0.001
II	99 (40%)	96 (45%)	3 (8.6%)	
III	148 (60%)	116 (55%)	32 (91%)	
ACT				0.004
Adjuvant Chemotherapy	121 (49%)	96 (45%)	25 (71%)	
Observation	126 (51%)	116 (55%)	10 (29%)	
BRAF.V600E				>0.9
BRAF wt	245 (99%)	210 (99%)	35 (100%)	
BRAF V600E	2 (0.8%)	2 (0.9%)	0 (0%)	
RAS				0.060
RAS wt	121 (49%)	109 (51%)	12 (34%)	
RAS mut	126 (51%)	103 (49%)	23 (66%)	
MSI				>0.9
MSS	244 (99%)	209 (99%)	35 (100%)	
MSI-High	3 (1.2%)	3 (1.4%)	0 (0%)	
RFS.Event				<0.001
Recurrence	48 (19%)	23 (11%)	25 (71%)	
No Recurrence	199 (81%)	189 (89%)	10 (29%)	
OS.Event				0.2
Deceased	11 (4.5%)	8 (3.8%)	3 (8.6%)	
Alive	236 (96%)	204 (96%)	32 (91%)	

¹Median (Range); n (%)²Wilcoxon rank sum test; Pearson's Chi-squared test; Fisher's exact test

	Table 1		Table 2	
Characteristic	N = 247 ¹	NEGATIVE, N = 212 ¹	POSITIVE, N = 35 ¹	p-value ²
OS.months	22.0 (1.2 - 35.9)	22.0 (7.5 - 35.9)	16.4 (1.2 - 34.9)	0.082

¹Median (Range); n (%)

²Wilcoxon rank sum test; Pearson's Chi-squared test; Fisher's exact test

[Hide](#)

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

#ctDNA Detection Rates by Window and Stages

[Hide](#)

```
#ctDNA at Baseline
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$CohortB=="TRUE",]
circ_data$ctDNA.Baseline <- factor(circ_data$ctDNA.Baseline, levels=c("NEGATIVE","POSITIVE"))
circ_data <- subset(circ_data, ctDNA.Baseline %in% c("NEGATIVE", "POSITIVE"))
circ_data$Stage <- factor(circ_data$Stage, levels=c("II", "III"))
positive_counts_by_stage <- aggregate(circ_data$ctDNA.Baseline == "POSITIVE", by=list(circ_data$Stage), FUN=sum)
total_counts_by_stage <- aggregate(circ_data$ctDNA.Baseline, by=list(circ_data$Stage), FUN=length)
combined_data <- data.frame(
  Stage = total_counts_by_stage$Group.1,
  Total_Count = total_counts_by_stage$x,
  Positive_Count = positive_counts_by_stage$x,
  Rate = (positive_counts_by_stage$x / total_counts_by_stage$x) * 100 # Convert to percentage
)
combined_data$Rate <- sprintf("%.2f%%", combined_data$Rate)
overall_total_count <- nrow(circ_data)
overall_positive_count <- nrow(circ_data[circ_data$ctDNA.Baseline == "POSITIVE",])
overall_positivity_rate <- (overall_positive_count / overall_total_count) * 100 # Convert to percentage
overall_row <- data.frame(
  Stage = "Overall",
  Total_Count = overall_total_count,
  Positive_Count = overall_positive_count,
  Rate = sprintf("%.2f%%", overall_positivity_rate)
)
combined_data <- rbind(combined_data, overall_row)
print(combined_data)
```

Stage <fctr>	Total_Count <int>	Positive_Count <int>	Rate <chr>
II	97	94	96.91%
III	148	144	97.30%
Overall	245	238	97.14%

3 rows

[Hide](#)

```
#ctDNA at MRD Window
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$CohortB=="TRUE",]
circ_data <- circ_data[circ_data$ctDNA.MRD!="",]
circ_data$ctDNA.MRD <- factor(circ_data$ctDNA.MRD, levels=c("NEGATIVE","POSITIVE"))
circ_data$Stage <- factor(circ_data$Stage, levels=c("II", "III"))
positive_counts_by_stage <- aggregate(circ_data$ctDNA.MRD == "POSITIVE", by=list(circ_data$Stage), FUN=sum)
total_counts_by_stage <- aggregate(circ_data$ctDNA.MRD, by=list(circ_data$Stage), FUN=length)
combined_data <- data.frame(
  Stage = total_counts_by_stage$Group.1,
  Total_Count = total_counts_by_stage$x,
  Positive_Count = positive_counts_by_stage$x,
  Rate = (positive_counts_by_stage$x / total_counts_by_stage$x) * 100 # Convert to percentage
)
combined_data$Rate <- sprintf("%.2f%%", combined_data$Rate)
overall_total_count <- nrow(circ_data)
overall_positive_count <- nrow(circ_data[circ_data$ctDNA.MRD == "POSITIVE",])
overall_positivity_rate <- (overall_positive_count / overall_total_count) * 100 # Convert to percentage
overall_row <- data.frame(
  Stage = "Overall",
  Total_Count = overall_total_count,
  Positive_Count = overall_positive_count,
  Rate = sprintf("%.2f%%", overall_positivity_rate)
)
combined_data <- rbind(combined_data, overall_row)
print(combined_data)
```

Stage <fctr>	Total_Count <int>	Positive_Count <int>	Rate <chr>
II	99	3	3.03%
III	148	32	21.62%

Stage <fctr>	Total_Count <int>	Positive_Count <int>	Rate <chr>
Overall	247	35	14.17%

3 rows

Hide

```
#ctDNA at Surveillance Window
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$CohortB=="TRUE",]
circ_data$ctDNA.Surveillance <- factor(circ_data$ctDNA.Surveillance, levels=c("NEGATIVE", "POSITIVE"))
circ_data <- subset(circ_data, ctDNA.Surveillance %in% c("NEGATIVE", "POSITIVE"))
circ_data$Stage <- factor(circ_data$Stage, levels=c("II", "III"))
positive_counts_by_stage <- aggregate(circ_data$ctDNA.Surveillance == "POSITIVE", by=list(circ_data$Stage), FUN=sum)
total_counts_by_stage <- aggregate(circ_data$ctDNA.Surveillance, by=list(circ_data$Stage), FUN=length)
combined_data <- data.frame(
  Stage = total_counts_by_stage$Group.1,
  Total_Count = total_counts_by_stage$x,
  Positive_Count = positive_counts_by_stage$x,
  Rate = (positive_counts_by_stage$x / total_counts_by_stage$x) * 100 # Convert to percentage
)
combined_data$Rate <- sprintf("%.2f%%", combined_data$Rate)
overall_total_count <- nrow(circ_data)
overall_positive_count <- nrow(circ_data[circ_data$ctDNA.Surveillance == "POSITIVE",])
overall_positivity_rate <- (overall_positive_count / overall_total_count) * 100 # Convert to percentage
overall_row <- data.frame(
  Stage = "Overall",
  Total_Count = overall_total_count,
  Positive_Count = overall_positive_count,
  Rate = sprintf("%.2f%%", overall_positivity_rate)
)
combined_data <- rbind(combined_data, overall_row)
print(combined_data)
```

Stage <fctr>	Total_Count <int>	Positive_Count <int>	Rate <chr>
II	94	8	8.51%
III	139	32	23.02%
Overall	233	40	17.17%

3 rows

#ctDNA MRD Detection rate Stage II vs III

Hide

```
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$CohortB=="TRUE",]
circ_data$ctDNA.MRD <- factor(circ_data$ctDNA.MRD, levels = c("NEGATIVE", "POSITIVE"))
circ_data$Stage_Grouped <- factor(ifelse(circ_data$Stage %in% c("II", "II"), "II", "II
I"))
contingency_table <- table(circ_data$Stage_Grouped, circ_data$ctDNA.MRD)
chi_square_test <- chisq.test(contingency_table)
print(contingency_table)
```

	NEGATIVE	POSITIVE
II	96	3
III	116	32

Hide

```
print(chi_square_test)
```

Pearson's Chi-squared test with Yates' continuity correction

```
data: contingency_table
X-squared = 15.364, df = 1, p-value = 8.865e-05
```

#ctDNA Surveillance Detection rate Stage II vs III

Hide

```
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$CohortB=="TRUE",]
circ_data$ctDNA.Surveillance <- factor(circ_data$ctDNA.Surveillance, levels = c("NEGATIV
E", "POSITIVE"))
circ_data$Stage_Grouped <- factor(ifelse(circ_data$Stage %in% c("II", "II"), "II", "II
I"))
contingency_table <- table(circ_data$Stage_Grouped, circ_data$ctDNA.Surveillance)
chi_square_test <- chisq.test(contingency_table)
print(contingency_table)
```

	NEGATIVE	POSITIVE
II	86	8
III	107	32

Hide

```
print(chi_square_test)
```

Pearson's Chi-squared test with Yates' continuity correction

```
data: contingency_table
X-squared = 7.3146, df = 1, p-value = 0.00684
```

#DFS by ctDNA at the MRD Window - All stages Landmark MRD timepoint

Hide

```
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$CohortB=="TRUE",]
circ_data <- circ_data[circ_data$ctDNA.MRD!="",]
circ_data <- circ_data[circ_data$DFS.MRD.months>=0,]
circ_datadf <- as.data.frame(circ_data)

survfit(Surv(time = circ_data$DFS.MRD.months, event = circ_data$DFS.Event)~ctDNA.MRD, data = circ_data)
```

```
Call: survfit(formula = Surv(time = circ_data$DFS.MRD.months, event = circ_data$DFS.Event) ~
ctDNA.MRD, data = circ_data)
```

	n	events	median	0.95LCL	0.95UCL
ctDNA.MRD=NEGATIVE	211	28	NA	NA	NA
ctDNA.MRD=POSITIVE	35	25	9.27	7.62	14.1

Hide

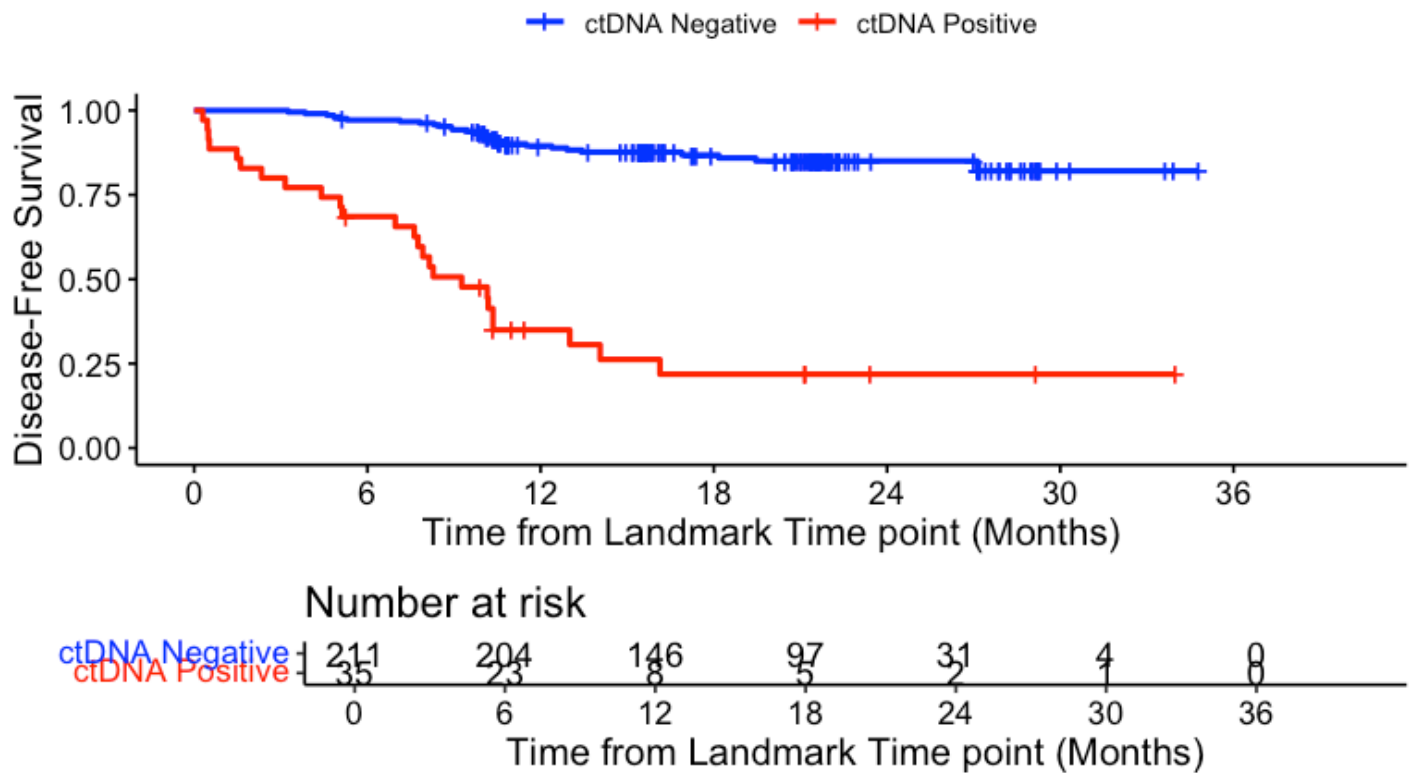
```
event_summary <- circ_data %>%
  group_by(ctDNA.MRD) %>%
  summarise(
    Total = n(),
    Events = sum(DFS.Event),
    Fraction = Events / n(),
    Percentage = (Events / n()) * 100
  )
print(event_summary)
```

ctDNA.MRD <chr>	Total <int>	Events <int>	Fraction <dbl>	Percentage <dbl>
NEGATIVE	211	28	0.1327014	13.27014
POSITIVE	35	25	0.7142857	71.42857
2 rows				

Hide

```
surv_object <-Surv(time = circ_data$DFS.MRD.months, event = circ_data$DFS.Event)
KM_curve <- survfit(surv_object ~ ctDNA.MRD, 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("blue","red"), title="DFS - ctDNA MRD window | All stages", ylab= "Disease-Free Survival", xlab="Time from Landmark Time point (Months)", legend.labs=c("ctDNA Negative", "ctDNA Positive"), legend.title="")
```

DFS - ctDNA MRD window | All stages



Hide

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

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

ctDNA.MRD=NEGATIVE

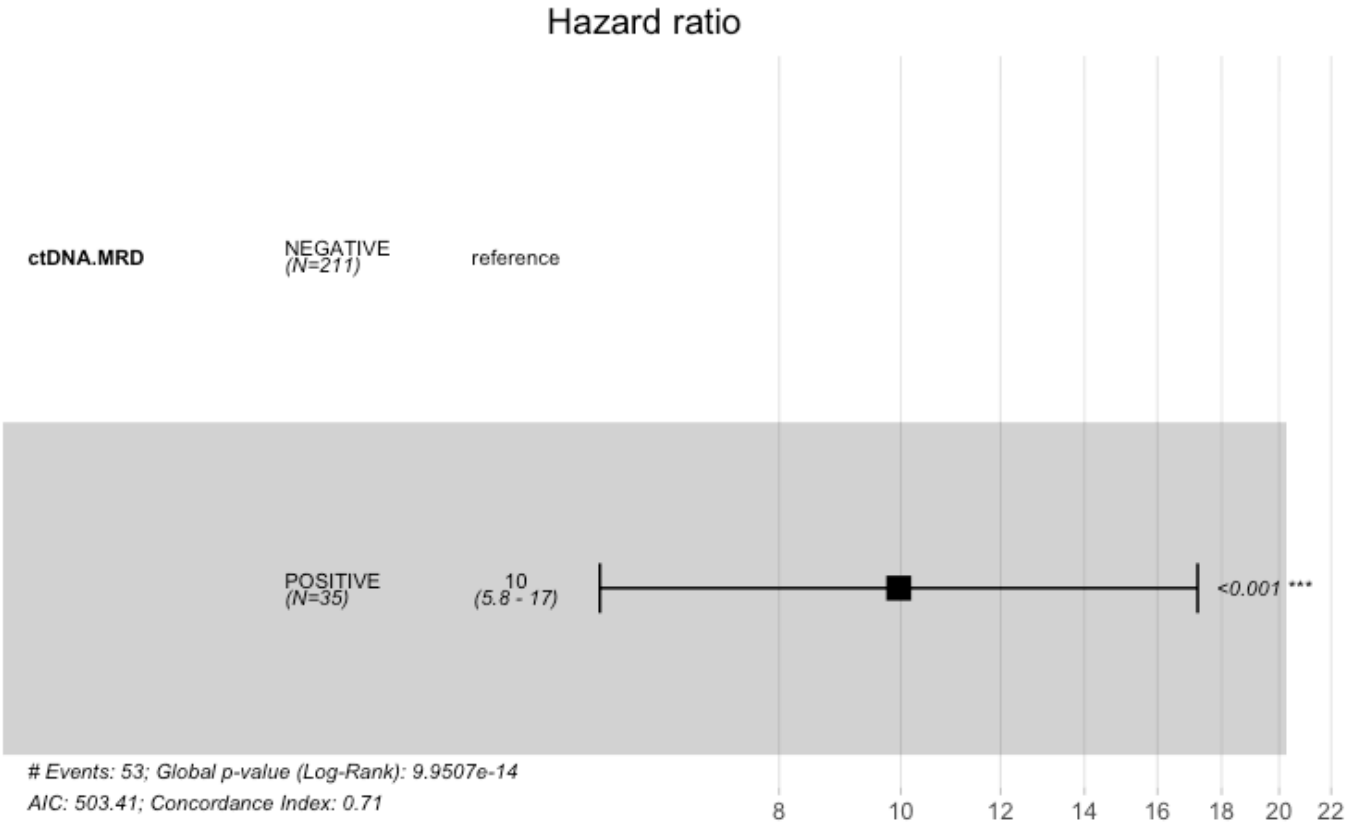
time	n.risk	n.event	survival	std.err	lower 95% CI	upper 95% CI
12	146	21	0.895	0.0218	0.843	0.930
18	97	4	0.868	0.0250	0.810	0.910
24	31	2	0.850	0.0275	0.787	0.896

ctDNA.MRD=POSITIVE

time	n.risk	n.event	survival	std.err	lower 95% CI	upper 95% CI
12	8	22	0.350	0.0830	0.1948	0.509
18	5	3	0.219	0.0792	0.0884	0.386
24	2	0	0.219	0.0792	0.0884	0.386

Hide

```
circ_data$ctDNA.MRD <- factor(circ_data$ctDNA.MRD, levels=c("NEGATIVE","POSITIVE"))
cox_fit <- coxph(surv_object ~ ctDNA.MRD, data=circ_data)
ggforest(cox_fit,data = circ_data)
```



Hide

```
summary(cox_fit)
```

Call:
coxph(formula = surv_object ~ ctDNA.MRD, data = circ_data)

n= 246, number of events= 53

	coef	exp(coef)	se(coef)	z	Pr(> z)
ctDNA.MRDPOSITIVE	2.2985	9.9592	0.2795	8.222	<2e-16 ***

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

	exp(coef)	exp(-coef)	lower .95	upper .95
ctDNA.MRDPOSITIVE	9.959	0.1004	5.758	17.23

Concordance= 0.709 (se = 0.032)
Likelihood ratio test= 55.38 on 1 df, p=1e-13
Wald test = 67.61 on 1 df, p=<2e-16
Score (logrank) test = 101.2 on 1 df, p=<2e-16

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 = 9.96 (5.76-17.23); p = 0"
```

[Hide](#)

```
#Fisher test for DFS percentages at 12, 18, and 24 months
dfs_times <- c(12, 18, 24)
p_values <- sapply(dfs_times, function(time) {
  neg_count <- sum(circ_data$ctDNA.MRD == "NEGATIVE" & circ_data$DFS.MRD.months >= time & circ_data$DFS.Event == 0)
  pos_count <- sum(circ_data$ctDNA.MRD == "POSITIVE" & circ_data$DFS.MRD.months >= time & circ_data$DFS.Event == 0)
  neg_total <- sum(circ_data$ctDNA.MRD == "NEGATIVE")
  pos_total <- sum(circ_data$ctDNA.MRD == "POSITIVE")

  neg_surv <- neg_total - sum(circ_data$ctDNA.MRD == "NEGATIVE" & circ_data$DFS.Event == 1 & circ_data$DFS.MRD.months < time)
  pos_surv <- pos_total - sum(circ_data$ctDNA.MRD == "POSITIVE" & circ_data$DFS.Event == 1 & circ_data$DFS.MRD.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 12 months p-value at 18 months p-value at 24 months
3.289740e-11          6.618049e-13          2.261958e-12
```

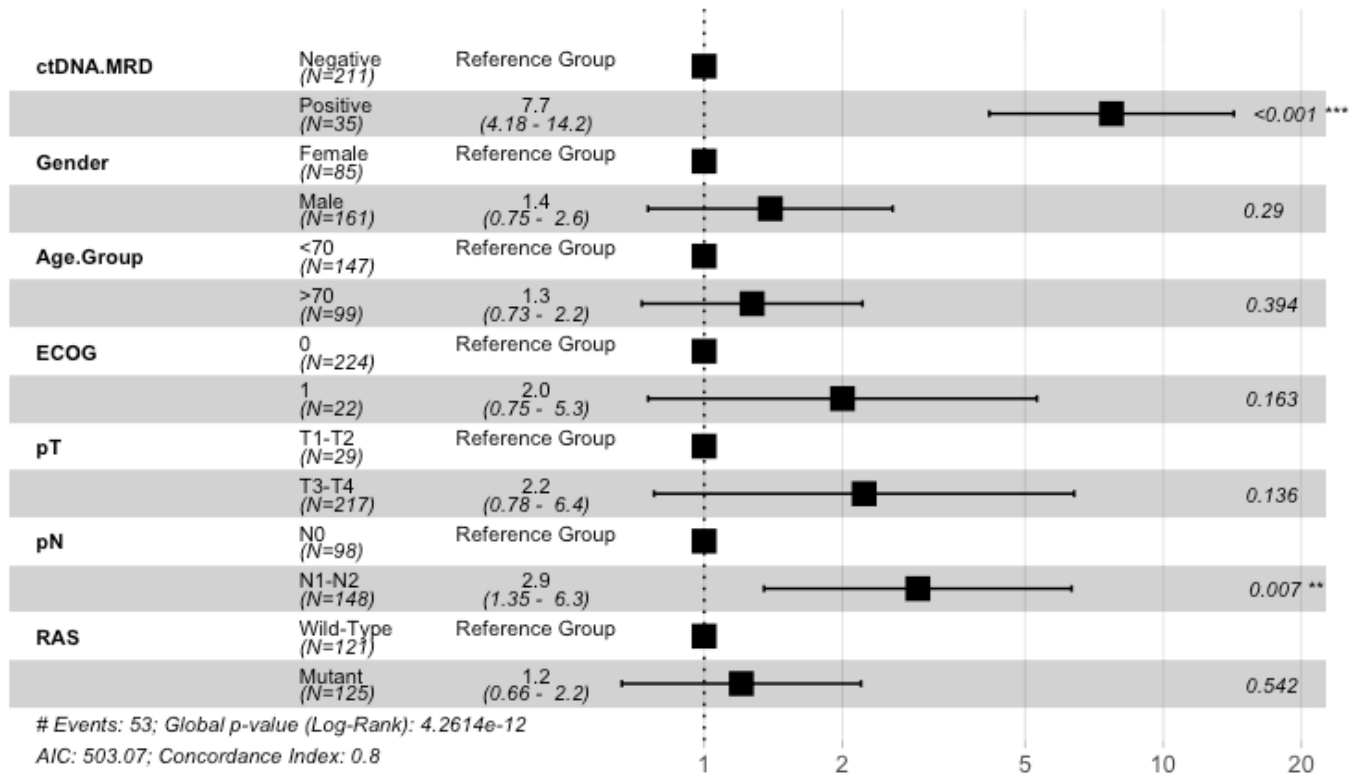
#Multivariate cox regression at MRD Window for DFS - All stages Landmark MRD timepoint

[Hide](#)

```
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$CohortB=="TRUE",]
circ_data <- circ_data[circ_data$ctDNA.MRD!="",]
circ_data <- circ_data[circ_data$DFS.MRD.months>=0,]
circ_datadf <- as.data.frame(circ_data)

circ_data$ctDNA.MRD <- factor(circ_data$ctDNA.MRD, levels=c("NEGATIVE","POSITIVE"), labels = c("Negative", "Positive"))
circ_data$Gender <- factor(circ_data$Gender, levels = c("Female", "Male"))
circ_data$Age.Group <- factor(circ_data$Age.Group, levels = c("1", "2"), labels = c("<70", ">70"))
circ_data$ECOG <- factor(circ_data$ECOG, levels = c("0", "1"))
circ_data$pT <- factor(circ_data$pT, levels = c("T1-T2", "T3-T4"))
circ_data$pN <- factor(circ_data$pN, levels = c("N0", "N1-N2"))
circ_data$RAS <- factor(circ_data$RAS, levels = c("WT", "MUT"), labels = c("Wild-Type", "Mutant"))
surv_object <- Surv(time = circ_data$DFS.MRD.months, event = circ_data$DFS.Event)
cox_fit <- coxph(surv_object ~ ctDNA.MRD + Gender + Age.Group + ECOG + pT + pN + RAS, data=circ_data)
ggforest(cox_fit, data = circ_data, main = "Multivariate Regression Model for DFS - All Stages", refLabel = "Reference Group")
```

Multivariate Regression Model for DFS - All Stages



Hide

```
test.ph <- cox.zph(cox_fit)
```

#DFS by ctDNA at the MRD Window - Stage II Landmark MRD timepoint

Hide

```
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$CohortB=="TRUE",]
circ_data <- circ_data[circ_data$ctDNA.MRD!="",]
circ_data <- circ_data[!(circ_data$Stage %in% c("III")),]
circ_data <- circ_data[circ_data$DFS.MRD.months>=0,]
circ_datadf <- as.data.frame(circ_data)

survfit(Surv(time = circ_data$DFS.MRD.months, event = circ_data$DFS.Event)~ctDNA.MRD, data = circ_data)
```

```
Call: survfit(formula = Surv(time = circ_data$DFS.MRD.months, event = circ_data$DFS.Event) ~
ctDNA.MRD, data = circ_data)
```

	n	events	median	0.95LCL	0.95UCL
ctDNA.MRD=NEGATIVE	96	6	NA	NA	NA
ctDNA.MRD=POSITIVE	3	3	13	0.493	NA

Hide

```
event_summary <- circ_data %>%
  group_by(ctDNA.MRD) %>%
  summarise(
    Total = n(),
    Events = sum(DFS.Event),
    Fraction = Events / n(),
    Percentage = (Events / n()) * 100
  )
print(event_summary)
```

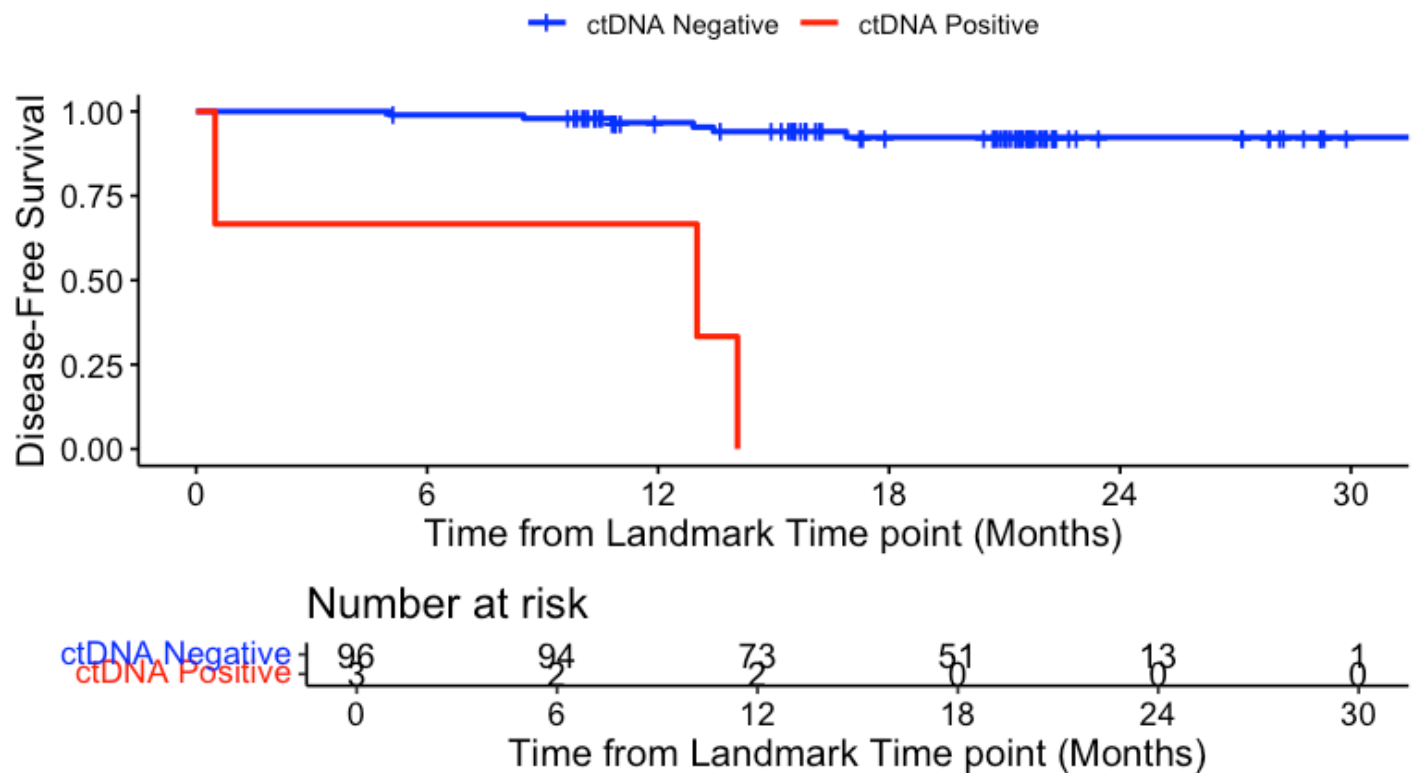
ctDNA.MRD <chr>	Total <int>	Events <int>	Fraction <dbl>	Percentage <dbl>
NEGATIVE	96	6	0.0625	6.25
POSITIVE	3	3	1.0000	100.00

2 rows

Hide

```
surv_object <- Surv(time = circ_data$DFS.MRD.months, event = circ_data$DFS.Event)
KM_curve <- survfit(surv_object ~ ctDNA.MRD, 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("blue","red"), title="DFS - ctDNA MRD window | Stage II",
  ylab= "Disease-Free Survival", xlab="Time from Landmark Time point (Months)", legend.labels=c("ctDNA Negative", "ctDNA Positive"), legend.title="")
```

DFS - ctDNA MRD window | Stage II



Hide

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

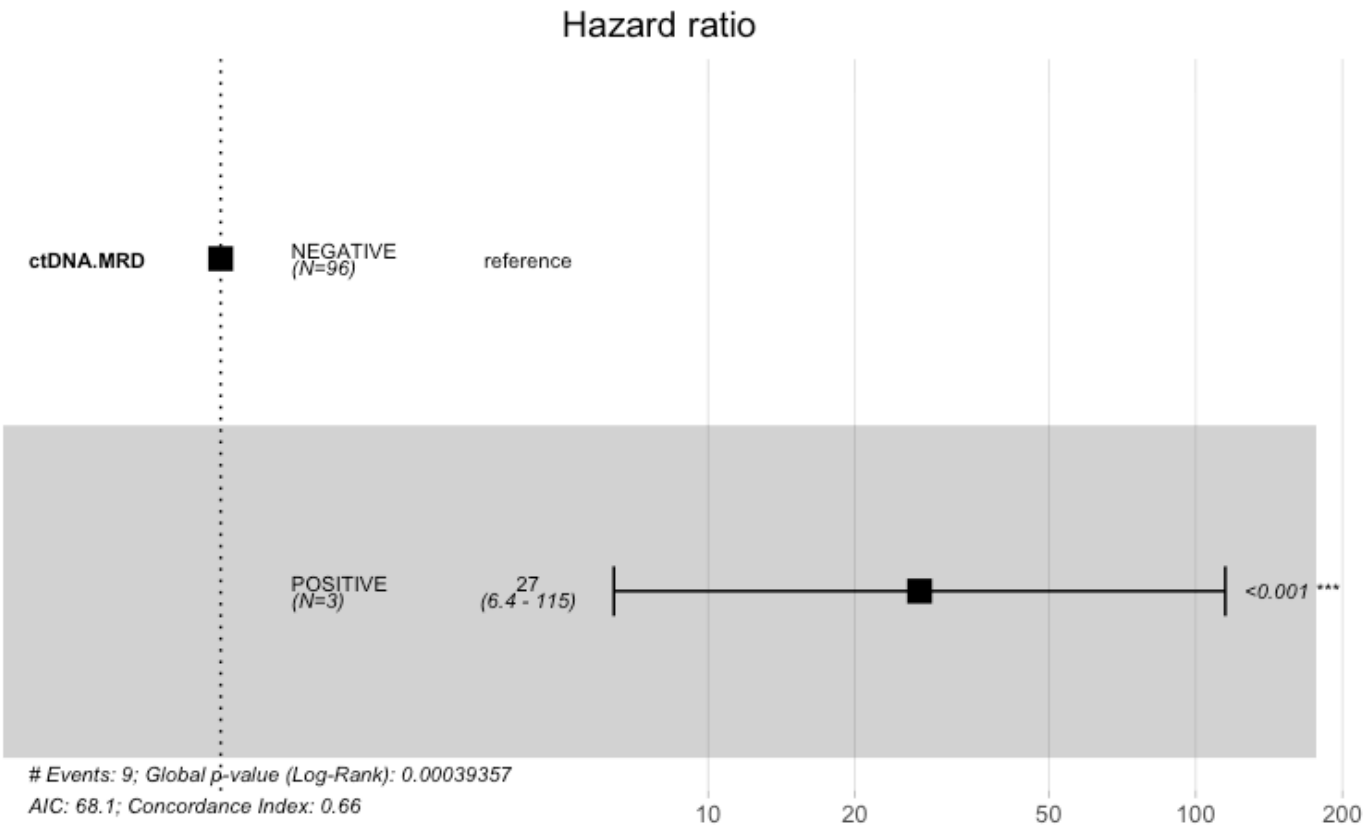
```
Call: survfit(formula = surv_object ~ ctDNA.MRD, data = circ_data,
  conf.int = 0.95, conf.type = "log-log")
```

ctDNA.MRD=NEGATIVE							
time	n.risk	n.event	survival	std.err	lower 95% CI	upper 95% CI	
12	73	3	0.967	0.0189	0.900	0.989	
24	13	3	0.923	0.0307	0.835	0.965	

ctDNA.MRD=POSITIVE							
CI	time	n.risk	n.event	survival	std.err	lower 95% CI	upper 95% CI
52	12.0000	2.0000	1.0000	0.6667	0.2722	0.0541	0.94

Hide

```
circ_data$ctDNA.MRD <- factor(circ_data$ctDNA.MRD, levels=c("NEGATIVE","POSITIVE"))
cox_fit <- coxph(surv_object ~ ctDNA.MRD, data=circ_data)
ggforest(cox_fit,data = circ_data)
```



Hide

```
summary(cox_fit)
```

Call:

```
coxph(formula = surv_object ~ ctDNA.MRD, data = circ_data)
```

```
n= 99, number of events= 9
```

	coef	exp(coef)	se(coef)	z	Pr(> z)
ctDNA.MRDPOSITIVE	3.3011	27.1423	0.7369	4.48	7.46e-06 ***

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

	exp(coef)	exp(-coef)	lower .95	upper .95
ctDNA.MRDPOSITIVE	27.14	0.03684	6.404	115

Concordance= 0.66 (se = 0.077)

Likelihood ratio test= 12.56 on 1 df, p=4e-04

Wald test = 20.07 on 1 df, p=7e-06

Score (logrank) test = 45.99 on 1 df, p=1e-11

[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 = 27.14 (6.4-115.04); p = 0"
```

[Hide](#)

```
#Fisher test for DFS percentages at 12 and 24 months
dfs_times <- c(12, 24)
p_values <- sapply(dfs_times, function(time) {
  neg_count <- sum(circ_data$ctDNA.MRD == "NEGATIVE" & circ_data$DFS.MRD.months >= time
& circ_data$DFS.Event == 0)
  pos_count <- sum(circ_data$ctDNA.MRD == "POSITIVE" & circ_data$DFS.MRD.months >= time
& circ_data$DFS.Event == 0)
  neg_total <- sum(circ_data$ctDNA.MRD == "NEGATIVE")
  pos_total <- sum(circ_data$ctDNA.MRD == "POSITIVE")

  neg_surv <- neg_total - sum(circ_data$ctDNA.MRD == "NEGATIVE" & circ_data$DFS.Event ==
1 & circ_data$DFS.MRD.months < time)
  pos_surv <- pos_total - sum(circ_data$ctDNA.MRD == "POSITIVE" & circ_data$DFS.Event ==
1 & circ_data$DFS.MRD.months < time)

  surv_matrix <- matrix(c(neg_surv, pos_surv, neg_total - neg_surv, pos_total - pos_sur
v), 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 12 months p-value at 24 months
0.1175270483          0.0005355469
```

#DFS by ctDNA at the MRD Window - Stage III Landmark MRD timepoint

Hide

```
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$Eligible=="TRUE",]
circ_data <- circ_data[circ_data$ctDNA.MRD!="",]
circ_data <- circ_data[!(circ_data$Stage %in% c("II")),]
circ_data <- circ_data[circ_data$DFS.MRD.months>=0,]
circ_datadf <- as.data.frame(circ_data)

survfit(Surv(time = circ_data$DFS.MRD.months, event = circ_data$DFS.Event)~ctDNA.MRD, da
ta = circ_data)
```

```
Call: survfit(formula = Surv(time = circ_data$DFS.MRD.months, event = circ_data$DFS.Even
t) ~
  ctDNA.MRD, data = circ_data)
```

1 observation deleted due to missingness

	n	events	median	0.95LCL	0.95UCL
ctDNA.MRD=NEGATIVE	1189	203	NA	NA	NA
ctDNA.MRD=POSITIVE	291	233	5.06	4.6	6.51

Hide

```
event_summary <- circ_data %>%
  group_by(ctDNA.MRD) %>%
  summarise(
    Total = n(),
    Events = sum(DFS.Event),
    Fraction = Events / n(),
    Percentage = (Events / n()) * 100
  )
print(event_summary)
```

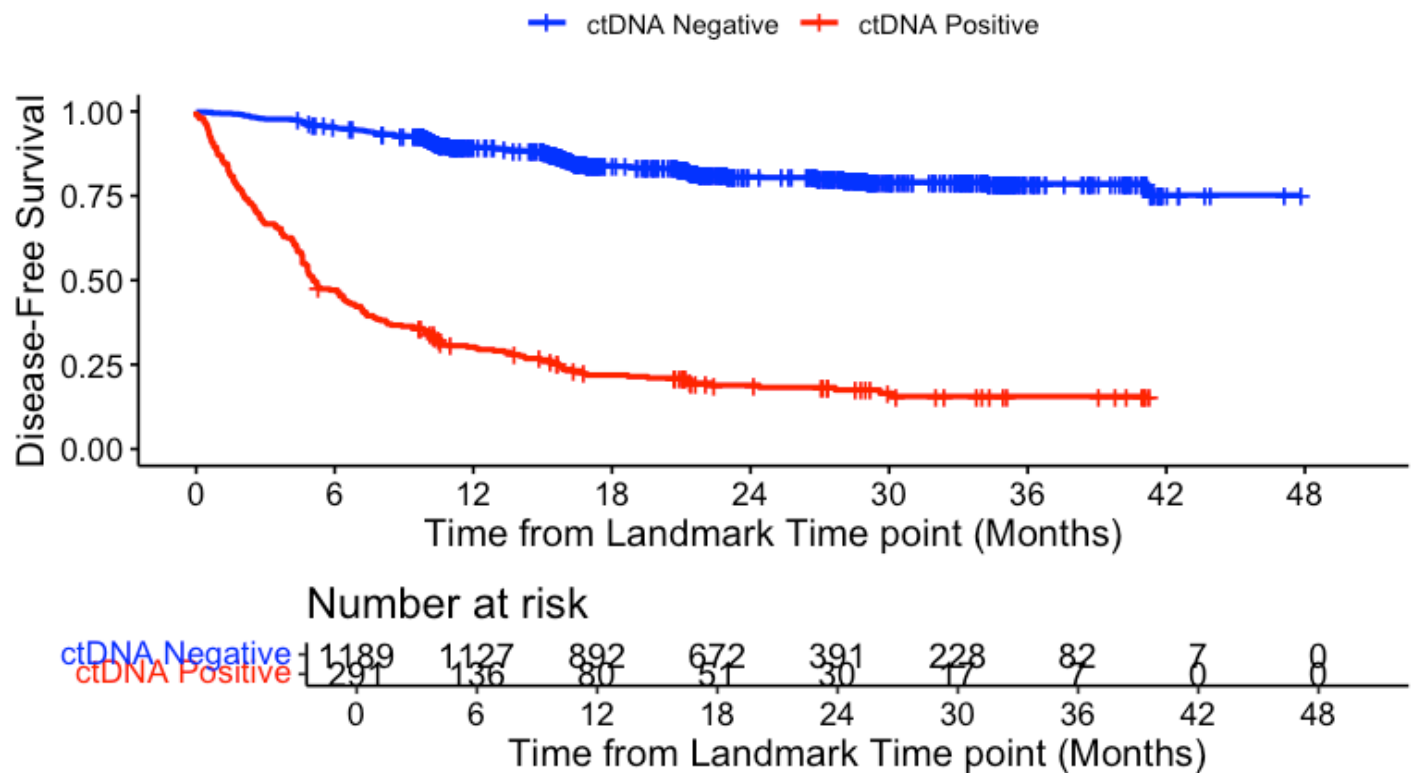
ctDNA.MRD	Total	Events	Fraction	Percentage
<chr>	<int>	<int>	<dbl>	<dbl>
NEGATIVE	1189	203	0.1707317	17.07317
POSITIVE	291	233	0.8006873	80.06873
NA	1	NA	NA	NA

3 rows

Hide

```
surv_object <-Surv(time = circ_data$DFS.MRD.months, event = circ_data$DFS.Event)
KM_curve <- survfit(surv_object ~ ctDNA.MRD, data = circ_data,conf.int=0.95,conf.type="l
og-log")
ggsurvplot(KM_curve, data = circ_data, pval = FALSE, conf.int = FALSE, risk.table = TRU
E, break.time.by=6, palette=c("blue","red"), title="DFS - ctDNA MRD window | Stage III",
ylab= "Disease-Free Survival", xlab="Time from Landmark Time point (Months)", legend.lab
s=c("ctDNA Negative", "ctDNA Positive"), legend.title="")
```

DFS - ctDNA MRD window | Stage III

[Hide](#)

```
summary(KM_curve, times= c(24, 30))
```

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

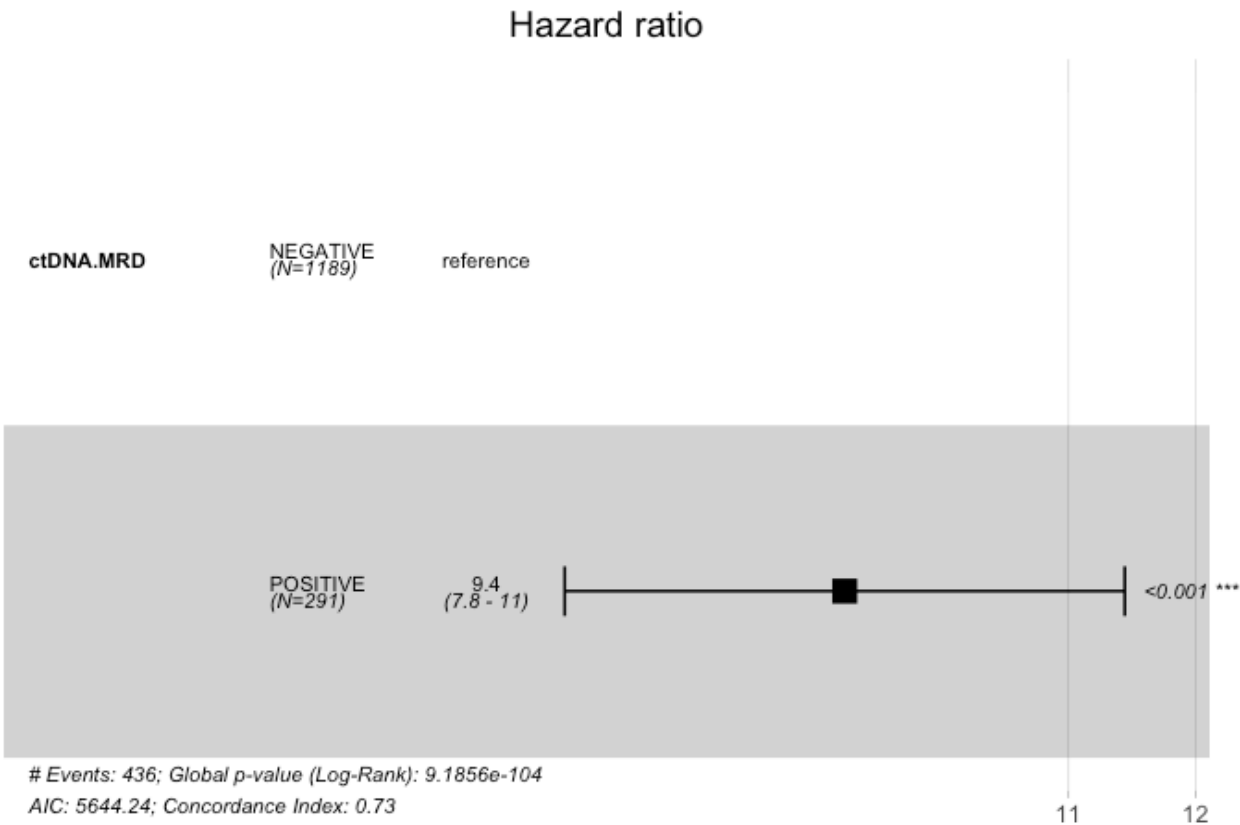
1 observation deleted due to missingness

ctDNA.MRD=NEGATIVE							
time	n.risk	n.event	survival	std.err	lower 95% CI	upper 95% CI	
24	391	195	0.806	0.0130	0.779	0.830	
30	228	6	0.791	0.0141	0.762	0.817	

ctDNA.MRD=POSITIVE							
time	n.risk	n.event	survival	std.err	lower 95% CI	upper 95% CI	
24	30	229	0.189	0.0245	0.144	0.239	
30	17	3	0.166	0.0250	0.120	0.218	

Hide

```
circ_data$ctDNA.MRD <- factor(circ_data$ctDNA.MRD, levels=c("NEGATIVE","POSITIVE"))
cox_fit <- coxph(surv_object ~ ctDNA.MRD, data=circ_data)
ggforest(cox_fit,data = circ_data)
```



Hide

```
summary(cox_fit)
```


Call:

```
coxph(formula = surv_object ~ ctDNA.MRD, data = circ_data)
```

n= 1480, number of events= 436

(1 observation deleted due to missingness)

	coef	exp(coef)	se(coef)	z	Pr(> z)
ctDNA.MRDPOSITIVE	2.24488	9.43924	0.09775	22.97	<2e-16 ***

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

	exp(coef)	exp(-coef)	lower .95	upper .95
ctDNA.MRDPOSITIVE	9.439	0.1059	7.794	11.43

Concordance= 0.729 (se = 0.011)

Likelihood ratio test= 467.9 on 1 df, p=<2e-16

Wald test = 527.5 on 1 df, p=<2e-16

Score (logrank) test = 768.2 on 1 df, p=<2e-16

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 = 9.44 (7.79-11.43); p = 0"
```

Hide

```
#Fisher test for DFS percentages at 24 and 30 months
dfs_times <- c(24, 30)
circ_data <- na.omit(circ_data[, c("ctDNA.MRD", "DFS.MRD.months", "DFS.Event")])
p_values <- sapply(dfs_times, function(time) {
  neg_count <- sum(circ_data$ctDNA.MRD == "NEGATIVE" & circ_data$DFS.MRD.months >= time
& circ_data$DFS.Event == 0)
  pos_count <- sum(circ_data$ctDNA.MRD == "POSITIVE" & circ_data$DFS.MRD.months >= time
& circ_data$DFS.Event == 0)
  neg_total <- sum(circ_data$ctDNA.MRD == "NEGATIVE")
  pos_total <- sum(circ_data$ctDNA.MRD == "POSITIVE")

  neg_surv <- neg_total - sum(circ_data$ctDNA.MRD == "NEGATIVE" & circ_data$DFS.Event ==
1 & circ_data$DFS.MRD.months < time)
  pos_surv <- pos_total - sum(circ_data$ctDNA.MRD == "POSITIVE" & circ_data$DFS.Event ==
1 & circ_data$DFS.MRD.months < time)

  surv_matrix <- matrix(c(neg_surv, pos_surv, neg_total - neg_surv, pos_total - pos_sur
v), 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 24 months p-value at 30 months
        6.506858e-91          5.794183e-92
```

#DFS by ACT treatment in MRD negative - Stage II/III

Hide

```
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$CohortB=="TRUE",]
circ_data <- circ_data[circ_data$ctDNA.MRD!="",]
circ_data <- circ_data[circ_data$ctDNA.MRD=="NEGATIVE",]
circ_data$DFS.months=circ_data$DFS.months-2
circ_data <- circ_data[circ_data$DFS.months>=0,]
circ_datadf <- as.data.frame(circ_data)

survfit(Surv(time = circ_data$DFS.months, event = circ_data$DFS.Event)~ACT, data = circ_
data)
```

Call: survfit(formula = Surv(time = circ_data\$DFS.months, event = circ_data\$DFS.Event) ~
ACT, data = circ_data)

	n	events	median	0.95LCL	0.95UCL
ACT=FALSE	115	16	NA	NA	NA
ACT=TRUE	96	12	NA	NA	NA

Hide

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

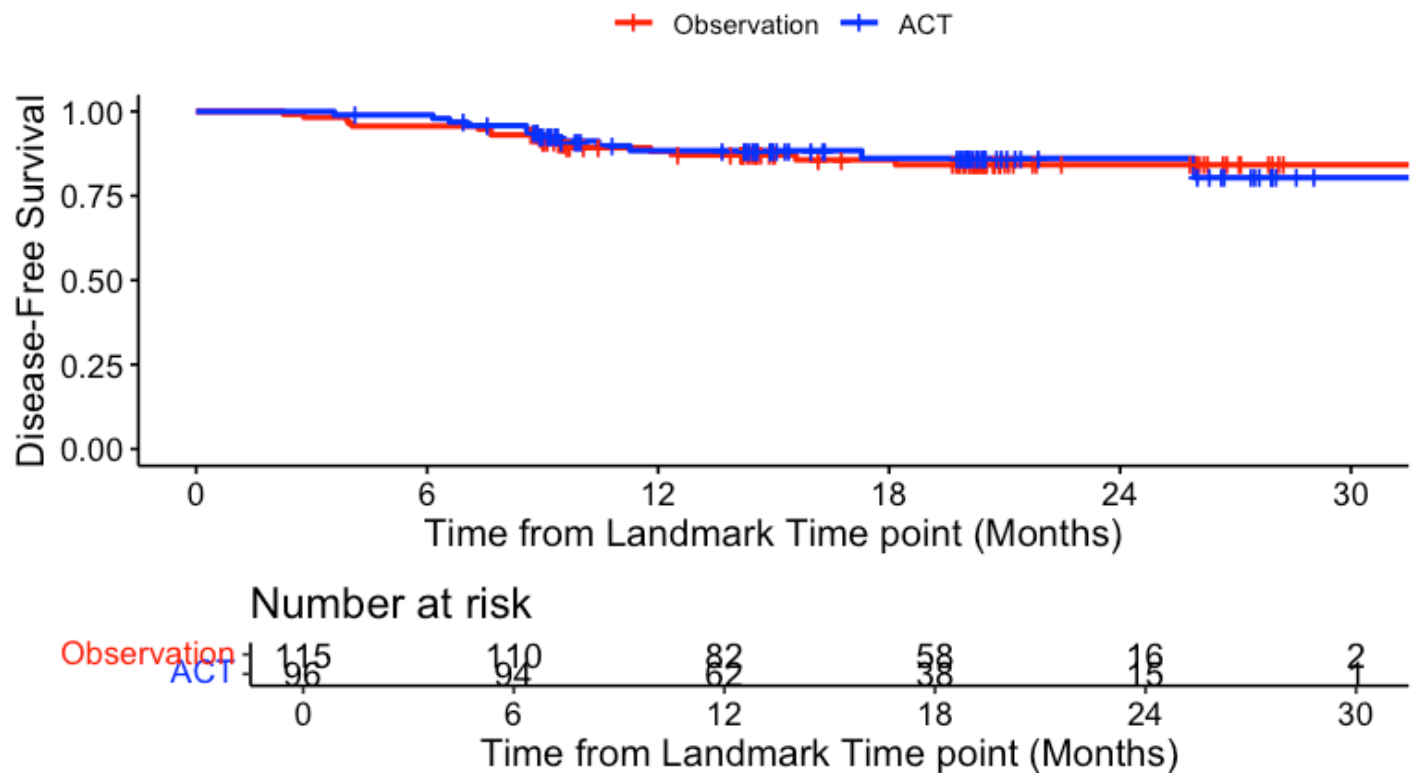
ACT <lgl>	Total <int>	Events <int>	Fraction <dbl>	Percentage <dbl>
FALSE	115	16	0.1391304	13.91304
TRUE	96	12	0.1250000	12.50000

2 rows

Hide

```
surv_object <- Surv(time = circ_data$DFS.months, event = circ_data$DFS.Event)
KM_curve <- survfit(surv_object ~ ACT, 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="DFS - ctDNA MRD Negative ACT vs Observation | Stage II/III",
  ylab= "Disease-Free Survival", xlab="Time from Landmark Time point (Months)", legend.labs=c("Observation", "ACT"), legend.title="")
```

DFS - ctDNA MRD Negative ACT vs Observation | Stage II/III



Hide

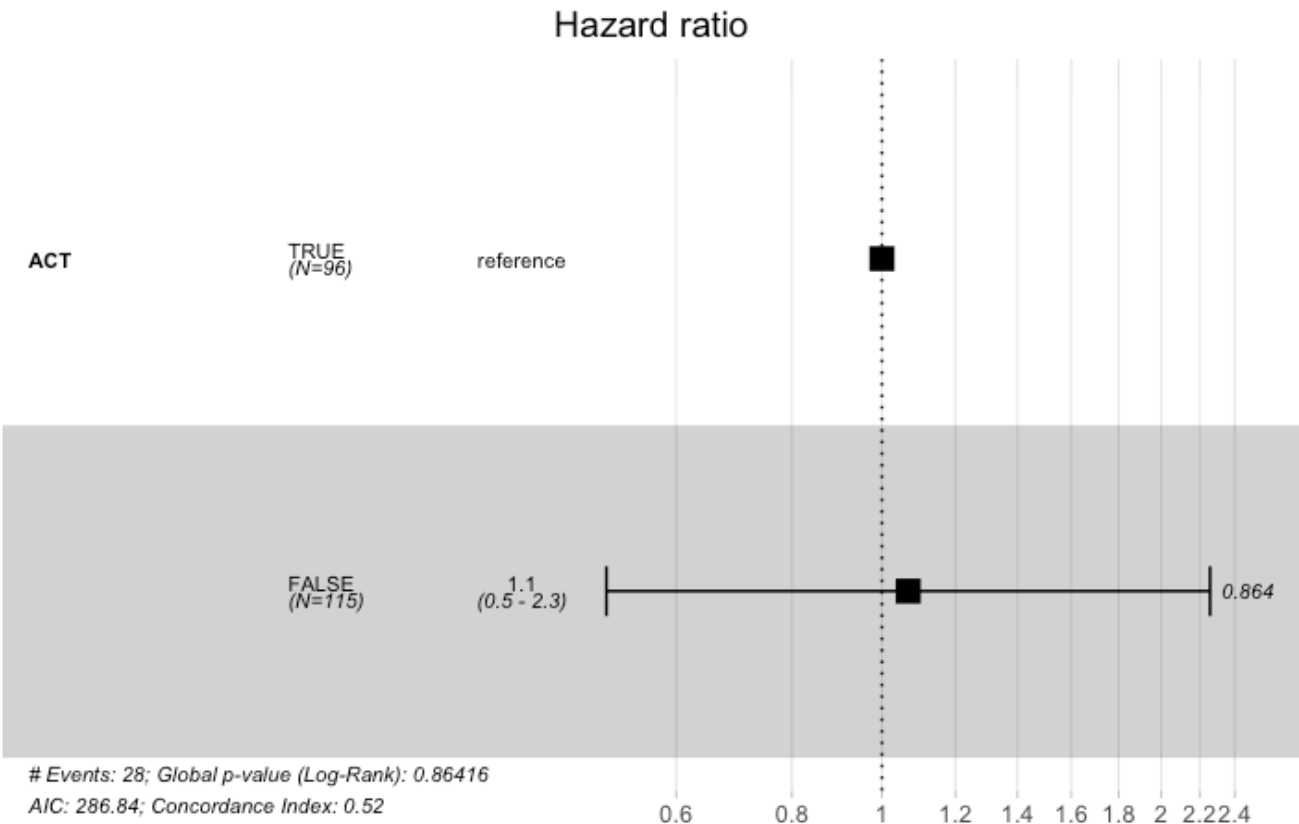
```
summary(KM_curve, times= c(24))
```

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

		ACT=FALSE					
	time	n.risk	n.event	survival	std.err	lower 95% CI	upper 95%
CI	24.0000	16.0000	16.0000	0.8419	0.0373	0.7521	0.90
13							
		ACT=TRUE					
	time	n.risk	n.event	survival	std.err	lower 95% CI	upper 95%
CI	24.0000	15.0000	11.0000	0.8612	0.0407	0.7574	0.92
28							

Hide

```
circ_data$ACT <- factor(circ_data$ACT, levels=c("TRUE","FALSE"))
cox_fit <- coxph(surv_object ~ ACT, data=circ_data)
ggforest(cox_fit,data = circ_data)
```



Hide

```
summary(cox_fit)
```

Call:

```
coxph(formula = surv_object ~ ACT, data = circ_data)
```

n= 211, number of events= 28

	coef	exp(coef)	se(coef)	z	Pr(> z)
ACTFALSE	0.06529	1.06747	0.38220	0.171	0.864

	exp(coef)	exp(-coef)	lower .95	upper .95
ACTFALSE	1.067	0.9368	0.5047	2.258

Concordance= 0.517 (se = 0.048)

Likelihood ratio test= 0.03 on 1 df, p=0.9

Wald test = 0.03 on 1 df, p=0.9

Score (logrank) test = 0.03 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 = 1.07 (0.5-2.26); p = 0.864"
```

[Hide](#)

```
#Fisher test for DFS percentages at 24
dfs_times <- c(24)
p_values <- sapply(dfs_times, function(time) {
  neg_count <- sum(circ_data$ACT == "TRUE" & circ_data$DFS.months >= time & circ_data$DFS.Event == 0)
  pos_count <- sum(circ_data$ACT == "FALSE" & circ_data$DFS.months >= time & circ_data$DFS.Event == 0)
  neg_total <- sum(circ_data$ACT == "TRUE")
  pos_total <- sum(circ_data$ACT == "FALSE")

  neg_surv <- neg_total - sum(circ_data$ACT == "TRUE" & circ_data$DFS.Event == 1 & circ_data$DFS.months < time)
  pos_surv <- pos_total - sum(circ_data$ACT == "FALSE" & circ_data$DFS.Event == 1 & circ_data$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 24 months
0.6811626
```

[Hide](#)

```
#Adjusted HR "ACT vs no ACT" - Non ACT as reference
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$CohortB=="TRUE",]
circ_data <- circ_data[circ_data$ctDNA.MRD!="",]
circ_data <- circ_data[circ_data$ctDNA.MRD=="NEGATIVE",]
circ_data$DFS.months=circ_data$DFS.months-2
circ_data <- circ_data[circ_data$DFS.months>=0,]
circ_datadf <- as.data.frame(circ_data)

circ_data$ACT <- factor(circ_data$ACT, levels=c("FALSE","TRUE"))
circ_data$Age.Group <- factor(circ_data$Age.Group, levels = c("1", "2"), labels = c("<70", "≥70"))
circ_data$Gender <- factor(circ_data$Gender, levels = c("Female", "Male"))
circ_data$Stage <- factor(circ_data$Stage, levels = c("II", "III"))
circ_data$ECOG <- factor(circ_data$ECOG, levels=c("0","1"))
surv_object <- Surv(time = circ_data$DFS.months, event = circ_data$DFS.Event)
cox_fit <- coxph(surv_object ~ ACT + Gender + Age.Group + Stage + ECOG, data=circ_data)
summary(cox_fit)
```

Call:

```
coxph(formula = surv_object ~ ACT + Gender + Age.Group + Stage +
      ECOG, data = circ_data)
```

n= 211, number of events= 28

	coef	exp(coef)	se(coef)	z	Pr(> z)
ACTTRUE	-0.5269	0.5904	0.4211	-1.251	0.21080
GenderMale	0.1145	1.1213	0.4081	0.280	0.77910
Age.Group≥70	0.3280	1.3883	0.4022	0.816	0.41472
StageIII	1.5211	4.5774	0.4886	3.113	0.00185 **
ECOG1	0.5215	1.6846	0.5509	0.947	0.34383

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

	exp(coef)	exp(-coef)	lower .95	upper .95
ACTTRUE	0.5904	1.6937	0.2587	1.348
GenderMale	1.1213	0.8918	0.5039	2.495
Age.Group≥70	1.3883	0.7203	0.6311	3.054
StageIII	4.5774	0.2185	1.7569	11.926
ECOG1	1.6846	0.5936	0.5722	4.960

Concordance= 0.71 (se = 0.043)

Likelihood ratio test= 12.82 on 5 df, p=0.03

Wald test = 11.73 on 5 df, p=0.04

Score (logrank) test = 12.73 on 5 df, p=0.03

#DFS by ACT treatment in MRD positive - Stage II/III

Hide

```
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$CohortB=="TRUE",]
circ_data <- circ_data[circ_data$ctDNA.MRD!="",]
circ_data <- circ_data[circ_data$ctDNA.MRD=="POSITIVE",]
circ_data$DFS.months=circ_data$DFS.months-2
circ_data <- circ_data[circ_data$DFS.months>=0,]
circ_datadf <- as.data.frame(circ_data)
```

```
survfit(Surv(time = circ_data$DFS.months, event = circ_data$DFS.Event)~ACT, data = circ_data)
```

Call: survfit(formula = Surv(time = circ_data\$DFS.months, event = circ_data\$DFS.Event) ~ ACT, data = circ_data)

	n	events	median	0.95LCL	0.95UCL
ACT=FALSE	6	5	5.62	1.22	NA
ACT=TRUE	25	16	9.33	6.97	NA

Hide

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

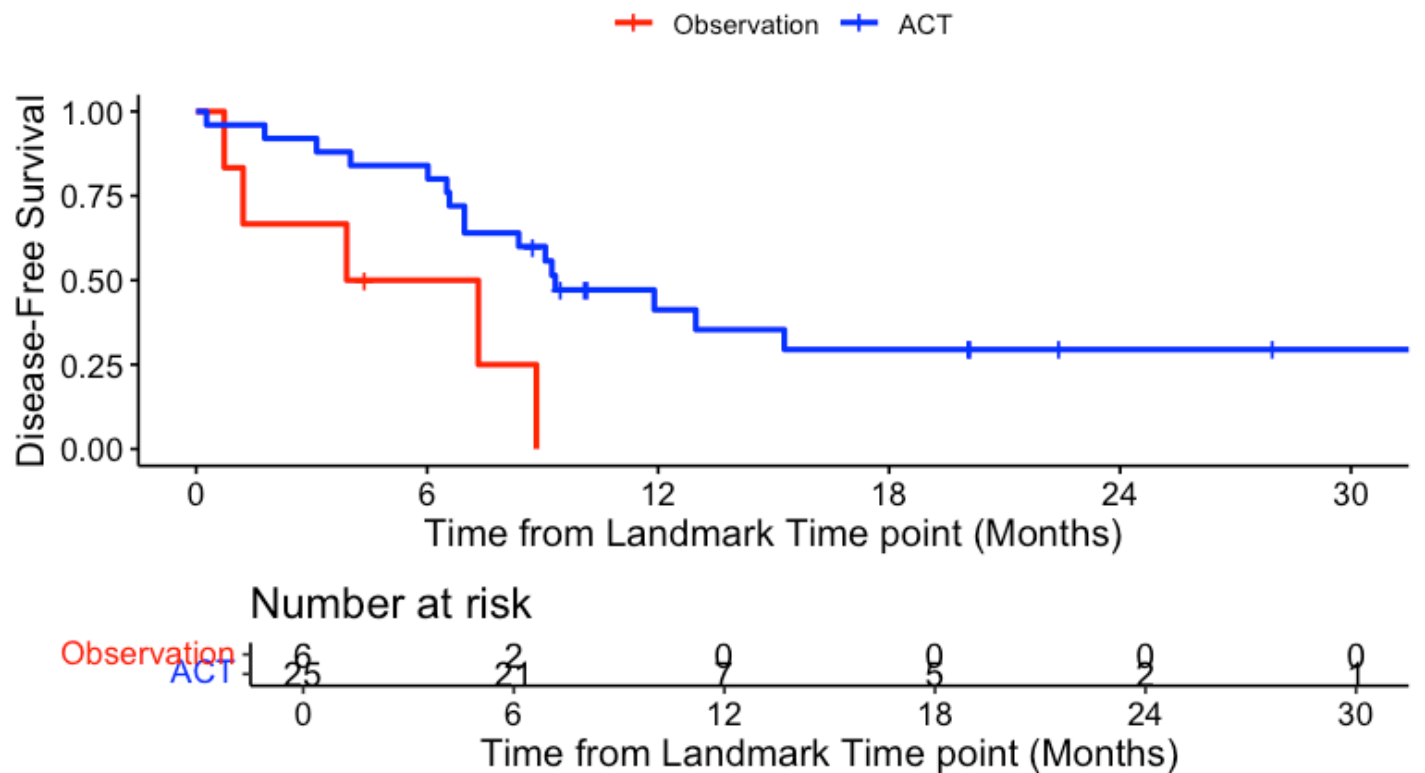
ACT <lgl>	Total <int>	Events <int>	Fraction <dbl>	Percentage <dbl>
FALSE	6	5	0.8333333	83.33333
TRUE	25	16	0.6400000	64.00000

2 rows

Hide

```
surv_object <- Surv(time = circ_data$DFS.months, event = circ_data$DFS.Event)
KM_curve <- survfit(surv_object ~ ACT, 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="DFS - ctDNA MRD Positive ACT vs Observation | Stage II/III",
  ylab= "Disease-Free Survival", xlab="Time from Landmark Time point (Months)", legend.labs=c("Observation", "ACT"), legend.title="")
```

DFS - ctDNA MRD Positive ACT vs Observation | Stage II/III

[Hide](#)

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

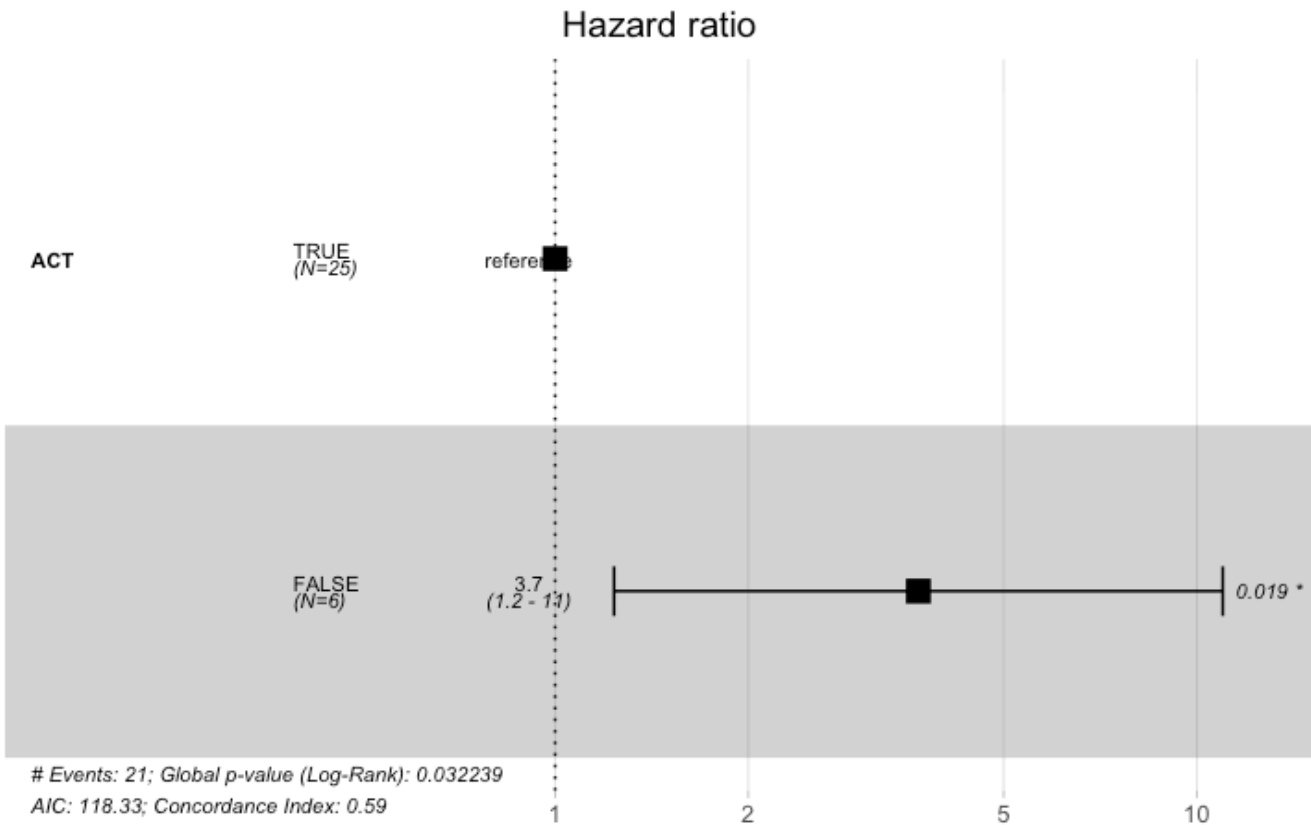
```
Call: survfit(formula = surv_object ~ ACT, data = circ_data, conf.int = 0.95,
  conf.type = "log-log")
```

ACT=FALSE							
CI	time	n.risk	n.event	survival	std.err	lower 95% CI	upper 95%
04	6.000	2.000	3.000	0.500	0.204	0.111	0.8

ACT=TRUE							
time	n.risk	n.event	survival	std.err	lower 95% CI	upper 95% CI	
6	21	4	0.840	0.0733	0.628	0.937	
24	2	12	0.295	0.1026	0.118	0.497	

Hide

```
circ_data$ACT <- factor(circ_data$ACT, levels=c("TRUE","FALSE"))
cox_fit <- coxph(surv_object ~ ACT, data=circ_data)
ggforest(cox_fit,data = circ_data)
```



Hide

```
summary(cox_fit)
```

Call:

```
coxph(formula = surv_object ~ ACT, data = circ_data)
```

```
n= 31, number of events= 21
```

	coef	exp(coef)	se(coef)	z	Pr(> z)
ACTFALSE	1.3036	3.6825	0.5572	2.339	0.0193 *

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

	exp(coef)	exp(-coef)	lower .95	upper .95
ACTFALSE	3.682	0.2716	1.235	10.98

Concordance= 0.593 (se = 0.045)

Likelihood ratio test= 4.59 on 1 df, p=0.03

Wald test = 5.47 on 1 df, p=0.02

Score (logrank) test = 6.25 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_CI, 2), "); p = ", round(p_value, 3))
```

```
print(label_text)
```

```
[1] "HR = 3.68 (1.24-10.98); p = 0.019"
```

[Hide](#)

```
#Adjusted HR "ACT vs no ACT" – Non ACT as reference
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$CohortB=="TRUE",]
circ_data <- circ_data[circ_data$ctDNA.MRD!="",]
circ_data <- circ_data[circ_data$ctDNA.MRD=="POSITIVE",]
circ_data$DFS.months=circ_data$DFS.months-2
circ_data <- circ_data[circ_data$DFS.months>=0,]
circ_datadf <- as.data.frame(circ_data)

circ_data$ACT <- factor(circ_data$ACT, levels=c("FALSE","TRUE"))
circ_data$Age.Group <- factor(circ_data$Age.Group, levels = c("1", "2"), labels = c("<70", "≥70"))
circ_data$Gender <- factor(circ_data$Gender, levels = c("Female", "Male"))
circ_data$Stage <- factor(circ_data$Stage, levels = c("II", "III"))
circ_data$ECOG <- factor(circ_data$ECOG, levels=c("0","1"))
surv_object <- Surv(time = circ_data$DFS.months, event = circ_data$DFS.Event)
cox_fit <- coxph(surv_object ~ ACT + Gender + Age.Group + Stage + ECOG, data=circ_data)
summary(cox_fit)
```

Call:

```
coxph(formula = surv_object ~ ACT + Gender + Age.Group + Stage +
      ECOG, data = circ_data)
```

n= 31, number of events= 21

	coef	exp(coef)	se(coef)	z	Pr(> z)
ACTTRUE	-1.27835	0.27850	0.59142	-2.162	0.0307 *
GenderMale	0.35495	1.42611	0.51244	0.693	0.4885
Age.Group≥70	0.12911	1.13782	0.45951	0.281	0.7787
StageIII	0.08804	1.09203	0.81274	0.108	0.9137
ECOG1	1.40597	4.07950	1.13540	1.238	0.2156

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

	exp(coef)	exp(-coef)	lower .95	upper .95
ACTTRUE	0.2785	3.5907	0.08738	0.8876
GenderMale	1.4261	0.7012	0.52236	3.8935
Age.Group≥70	1.1378	0.8789	0.46231	2.8003
StageIII	1.0920	0.9157	0.22204	5.3708
ECOG1	4.0795	0.2451	0.44071	37.7622

Concordance= 0.632 (se = 0.066)

Likelihood ratio test= 6.01 on 5 df, p=0.3

Wald test = 6.81 on 5 df, p=0.2

Score (logrank) test = 7.76 on 5 df, p=0.2

#DFS by ctDNA at 3 months - All stages Landmark 3 months timepoint

Hide

```
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$CohortB=="TRUE",]
circ_data <- circ_data[circ_data$ctDNA.3months!="",]
circ_data <- circ_data[circ_data$DFS.3mo.months>=0,]
circ_datadf <- as.data.frame(circ_data)

survfit(Surv(time = circ_data$DFS.3mo.months, event = circ_data$DFS.Event)~ctDNA.3months, data = circ_data)
```

Call: survfit(formula = Surv(time = circ_data\$DFS.3mo.months, event = circ_data\$DFS.Event) ~ ctDNA.3months, data = circ_data)

	n	events	median	0.95LCL	0.95UCL
ctDNA.3months=NEGATIVE	204	31	NA	NA	NA
ctDNA.3months=POSITIVE	19	14	8.28	5.59	NA

Hide

```
event_summary <- circ_data %>%
  group_by(ctDNA.3months) %>%
  summarise(
    Total = n(),
    Events = sum(DFS.Event),
    Fraction = Events / n(),
    Percentage = (Events / n()) * 100
  )
print(event_summary)
```

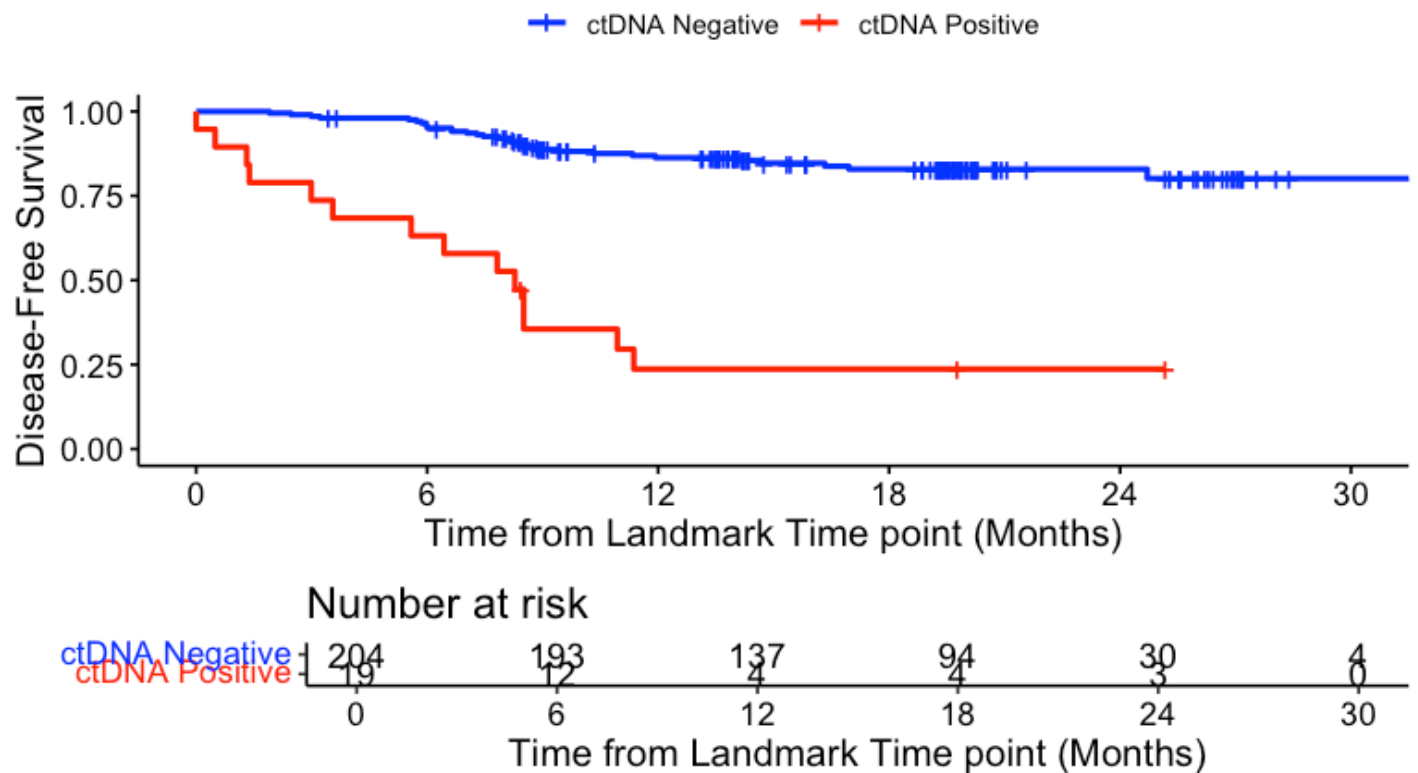
ctDNA.3months <chr>	Total <int>	Events <int>	Fraction <dbl>	Percentage <dbl>
NEGATIVE	204	31	0.1519608	15.19608
POSITIVE	19	14	0.7368421	73.68421

2 rows

Hide

```
surv_object <-Surv(time = circ_data$DFS.3mo.months, event = circ_data$DFS.Event)
KM_curve <- survfit(surv_object ~ ctDNA.3months, 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("blue","red"), title="DFS - ctDNA 3 months | All stages", ylab= "Disease-Free Survival", xlab="Time from Landmark Time point (Months)", legend.labs=c("ctDNA Negative", "ctDNA Positive"), legend.title="")
```

DFS - ctDNA 3 months | All stages



Hide

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

```
Call: survfit(formula = surv_object ~ ctDNA.3months, data = circ_data,
  conf.int = 0.95, conf.type = "log-log")
```

ctDNA.3months=NEGATIVE

time	n.risk	n.event	survival	std.err	lower 95% CI	upper 95% CI
12	137	26	0.863	0.0252	0.805	0.905
24	30	4	0.829	0.0293	0.762	0.879

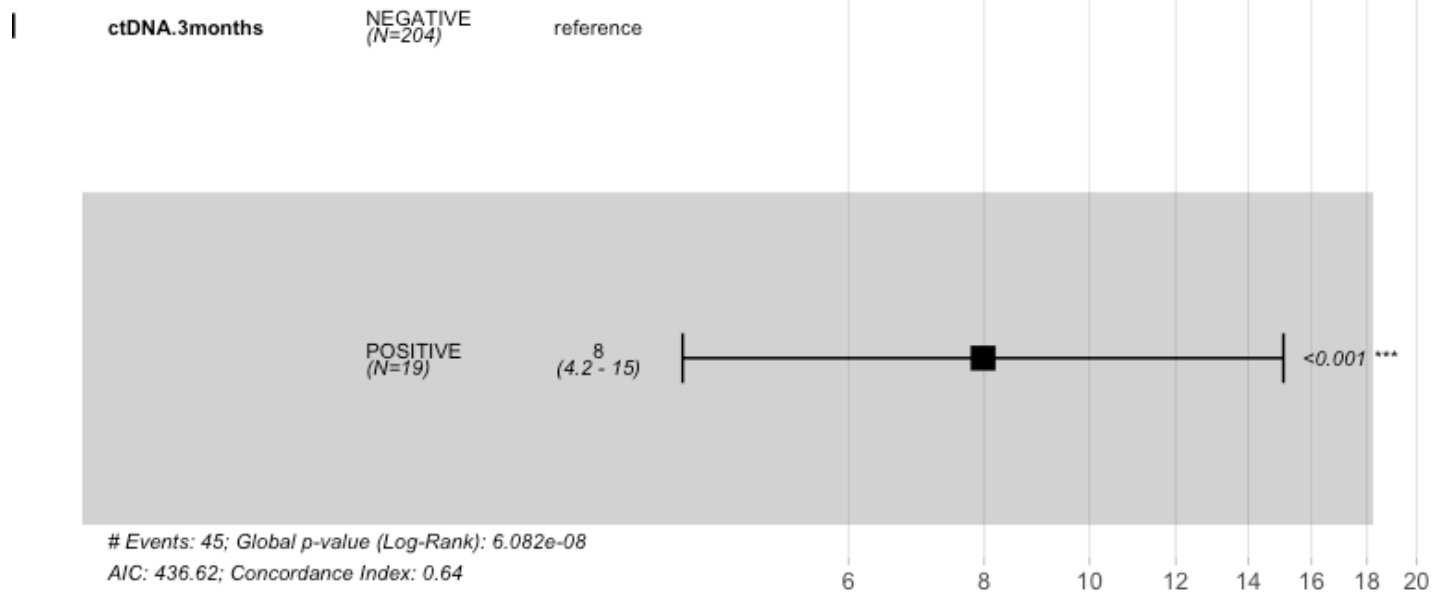
ctDNA.3months=POSITIVE

time	n.risk	n.event	survival	std.err	lower 95% CI	upper 95% CI
12	4	14	0.237	0.101	0.0758	0.447
24	3	0	0.237	0.101	0.0758	0.447

[Hide](#)

```
circ_data$ctDNA.3months <- factor(circ_data$ctDNA.3months, levels=c("NEGATIVE","POSITIVE"))
cox_fit <- coxph(surv_object ~ ctDNA.3months, data=circ_data)
ggforest(cox_fit,data = circ_data)
```

Hazard ratio


[Hide](#)

```
summary(cox_fit)
```


Call:

```
coxph(formula = surv_object ~ ctDNA.3months, data = circ_data)
```

n= 223, number of events= 45

	coef	exp(coef)	se(coef)	z	Pr(> z)
ctDNA.3monthsPOSITIVE	2.0768	7.9792	0.3247	6.397	1.58e-10 ***

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

	exp(coef)	exp(-coef)	lower .95	upper .95
ctDNA.3monthsPOSITIVE	7.979	0.1253	4.223	15.08

Concordance= 0.641 (se = 0.034)

Likelihood ratio test= 29.34 on 1 df, p=6e-08

Wald test = 40.92 on 1 df, p=2e-10

Score (logrank) test = 57.62 on 1 df, p=3e-14

[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 = 7.98 (4.22-15.08); p = 0"
```

[Hide](#)

```
#Fisher test for DFS percentages at 12 and 24 months
dfs_times <- c(12, 24)
p_values <- sapply(dfs_times, function(time) {
  neg_count <- sum(circ_data$ctDNA.3months == "NEGATIVE" & circ_data$DFS.3mo.months >= time & circ_data$DFS.Event == 0)
  pos_count <- sum(circ_data$ctDNA.3months == "POSITIVE" & circ_data$DFS.3mo.months >= time & circ_data$DFS.Event == 0)
  neg_total <- sum(circ_data$ctDNA.3months == "NEGATIVE")
  pos_total <- sum(circ_data$ctDNA.3months == "POSITIVE")

  neg_surv <- neg_total - sum(circ_data$ctDNA.3months == "NEGATIVE" & circ_data$DFS.Event == 1 & circ_data$DFS.3mo.months < time)
  pos_surv <- pos_total - sum(circ_data$ctDNA.3months == "POSITIVE" & circ_data$DFS.Event == 1 & circ_data$DFS.3mo.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 12 months p-value at 24 months
2.546518e-08        1.138180e-07
```

#DFS by ctDNA at 6 months - All stages Landmark 6 months timepoint

[Hide](#)

```
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$CohortB=="TRUE",]
circ_data <- circ_data[circ_data$ctDNA.6months!="",]
circ_data <- circ_data[circ_data$DFS.6mo.months>=0,]
circ_datadf <- as.data.frame(circ_data)

survfit(Surv(time = circ_data$DFS.6mo.months, event = circ_data$DFS.Event)~ctDNA.6months, data = circ_data)
```

```
Call: survfit(formula = Surv(time = circ_data$DFS.6mo.months, event = circ_data$DFS.Event) ~
ctDNA.6months, data = circ_data)
```

	n	events	median	0.95LCL	0.95UCL
ctDNA.6months=NEGATIVE	173	21	NA	NA	NA
ctDNA.6months=POSITIVE	9	7	3.68	2.6	NA

[Hide](#)

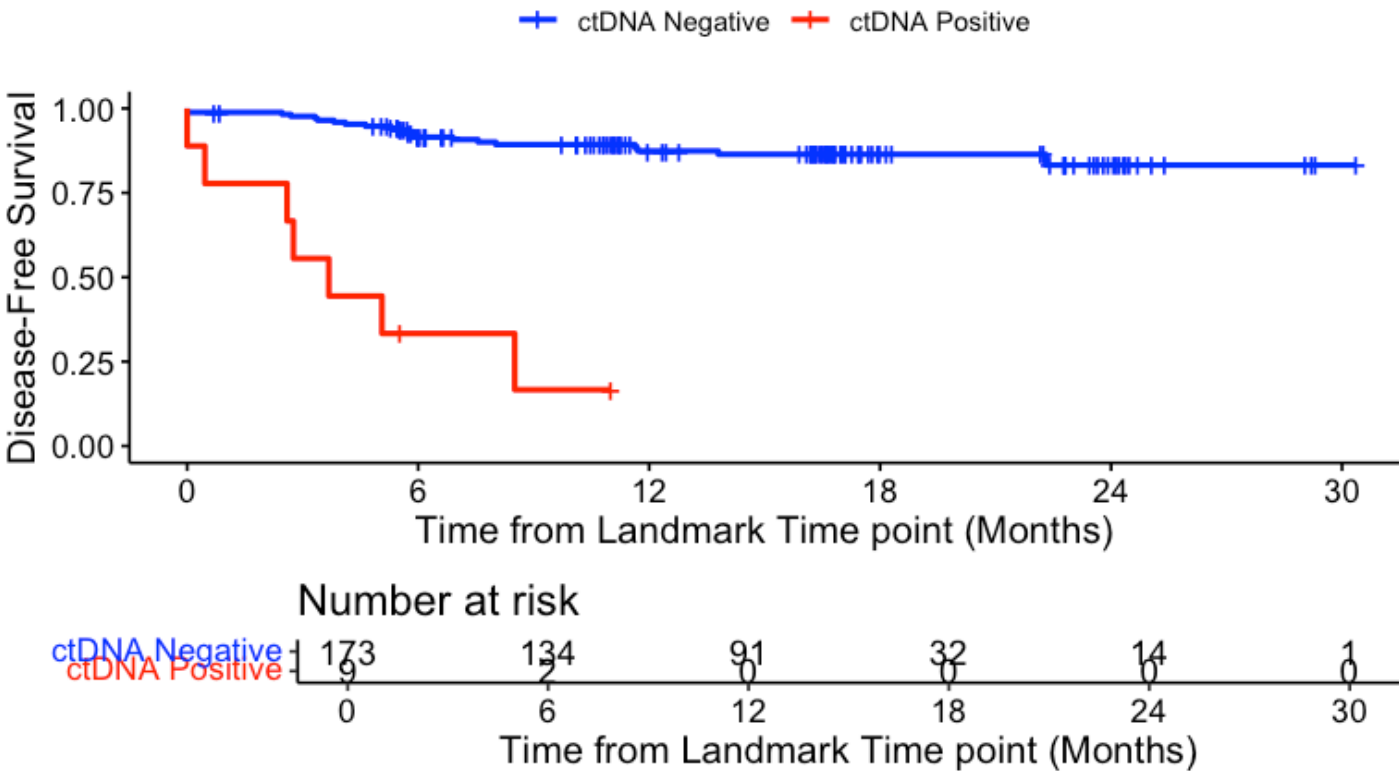
```
event_summary <- circ_data %>%
  group_by(ctDNA.6months) %>%
  summarise(
    Total = n(),
    Events = sum(DFS.Event),
    Fraction = Events / n(),
    Percentage = (Events / n()) * 100
  )
print(event_summary)
```

ctDNA.6months <chr>	Total <int>	Events <int>	Fraction <dbl>	Percentage <dbl>
NEGATIVE	173	21	0.1213873	12.13873
POSITIVE	9	7	0.7777778	77.77778
2 rows				

[Hide](#)

```
surv_object <- Surv(time = circ_data$DFS.6mo.months, event = circ_data$DFS.Event)
KM_curve <- survfit(surv_object ~ ctDNA.6months, 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("blue","red"), title="DFS - ctDNA 6 months | All stages", ylab= "Disease-Free Survival", xlab="Time from Landmark Time point (Months)", legend.labels=c("ctDNA Negative", "ctDNA Positive"), legend.title="")
```

DFS - ctDNA 6 months | All stages



Hide

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

```
Call: survfit(formula = surv_object ~ ctDNA.6months, data = circ_data,
  conf.int = 0.95, conf.type = "log-log")
```

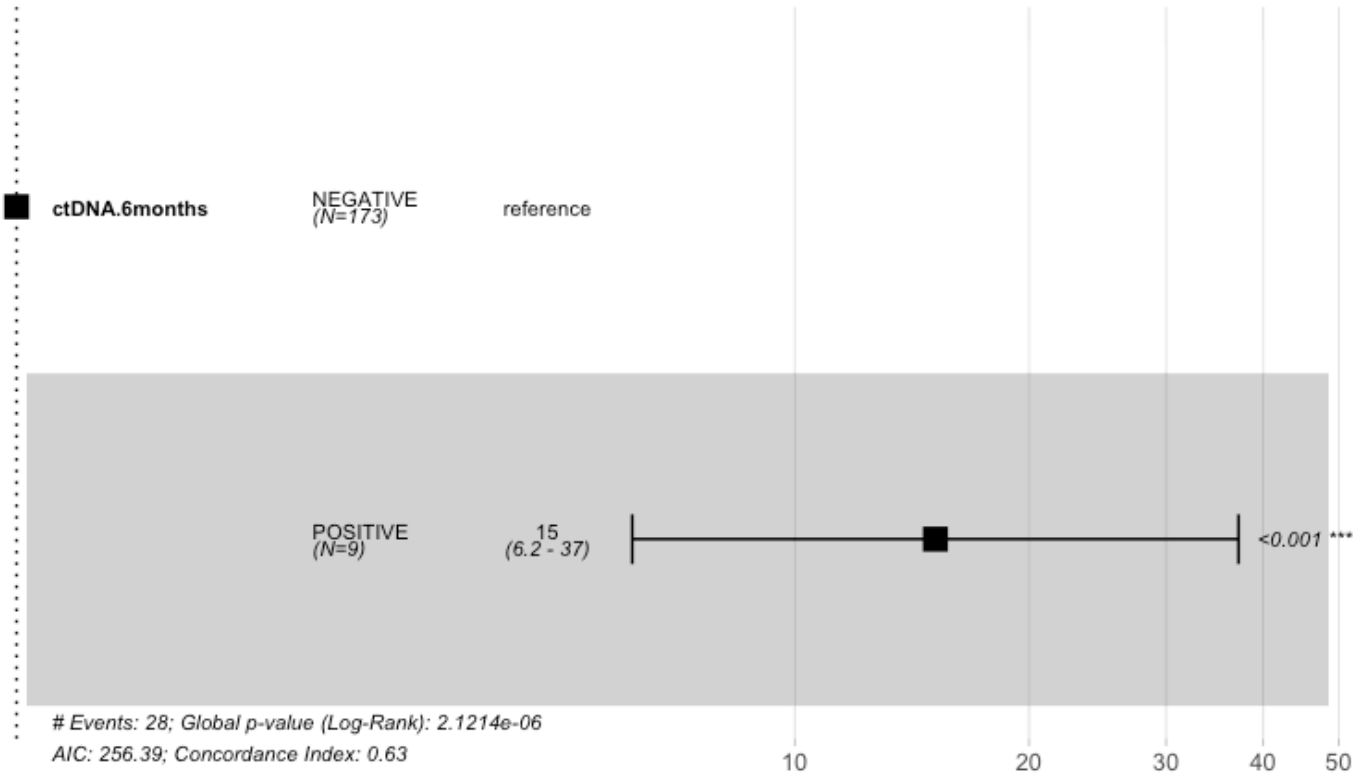
ctDNA.6months=NEGATIVE							
time	n.risk	n.event	survival	std.err	lower 95% CI	upper 95% CI	
6	134	14	0.915	0.0217	0.861	0.949	
24	14	7	0.832	0.0420	0.730	0.898	

ctDNA.6months=POSITIVE							
CI	time	n.risk	n.event	survival	std.err	lower 95% CI	upper 95% CI
26	6.0000	2.0000	6.0000	0.3333	0.1571	0.0783	0.62

Hide

```
circ_data$ctDNA.6months <- factor(circ_data$ctDNA.6months, levels=c("NEGATIVE", "POSITIV
E"))
cox_fit <- coxph(surv_object ~ ctDNA.6months, data=circ_data)
ggforest(cox_fit, data = circ_data)
```

Hazard ratio



Hide

```
summary(cox_fit)
```

Call:
coxph(formula = surv_object ~ ctDNA.6months, data = circ_data)

n= 182, number of events= 28

	coef	exp(coef)	se(coef)	z	Pr(> z)
ctDNA.6monthsPOSITIVE	2.7187	15.1598	0.4577	5.94	2.85e-09 ***

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

	exp(coef)	exp(-coef)	lower .95	upper .95
ctDNA.6monthsPOSITIVE	15.16	0.06596	6.182	37.18

Concordance= 0.628 (se = 0.042)
Likelihood ratio test= 22.48 on 1 df, p=2e-06
Wald test = 35.29 on 1 df, p=3e-09
Score (logrank) test = 62.3 on 1 df, p=3e-15

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 = 15.16 (6.18-37.18); p = 0"
```

[Hide](#)

```
#Fisher test for DFS percentages at 6 and 24 months
dfs_times <- c(6, 24)
p_values <- sapply(dfs_times, function(time) {
  neg_count <- sum(circ_data$ctDNA.6months == "NEGATIVE" & circ_data$DFS.6mo.months >= time & circ_data$DFS.Event == 0)
  pos_count <- sum(circ_data$ctDNA.6months == "POSITIVE" & circ_data$DFS.6mo.months >= time & circ_data$DFS.Event == 0)
  neg_total <- sum(circ_data$ctDNA.6months == "NEGATIVE")
  pos_total <- sum(circ_data$ctDNA.6months == "POSITIVE")

  neg_surv <- neg_total - sum(circ_data$ctDNA.6months == "NEGATIVE" & circ_data$DFS.Event == 1 & circ_data$DFS.6mo.months < time)
  pos_surv <- pos_total - sum(circ_data$ctDNA.6months == "POSITIVE" & circ_data$DFS.Event == 1 & circ_data$DFS.6mo.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 24 months
5.667547e-05        2.922826e-05
```

#DFS by ctDNA Clearance ACT-treated at 3 months - all stages

[Hide](#)

```
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$CohortB=="TRUE",]
circ_data <- circ_data[circ_data$ctDNA.MRD!="",]
circ_data <- circ_data[circ_data$ACT==TRUE,]
circ_datadf <- as.data.frame(circ_data)

circ_data$ctDNA.Dynamics <- NA #first we create the variable for the ctDNA & NAC combina
tion, and we assign values
circ_data <- circ_data %>%
  mutate(ctDNA.Dynamics = case_when(
    ctDNA.MRD == "POSITIVE" & ctDNA.3months == "NEGATIVE" ~ 1,
    ctDNA.MRD == "POSITIVE" & ctDNA.3months == "POSITIVE" ~ 2
  ))

circ_data <- circ_data[circ_data$DFS.3mo.months>=0,]
survfit(Surv(time = circ_data$DFS.3mo.months, event = circ_data$DFS.Event)~ctDNA.Dynamic
s, data = circ_data)
```

Call: survfit(formula = Surv(time = circ_data\$DFS.3mo.months, event = circ_data\$DFS.Event) ~
ctDNA.Dynamics, data = circ_data)

97 observations deleted due to missingness

	n	events	median	0.95LCL	0.95UCL
ctDNA.Dynamics=1	16	8	14.16	6.01	NA
ctDNA.Dynamics=2	8	7	8.05	5.59	NA

[Hide](#)

```
event_summary <- circ_data %>%
  group_by(ctDNA.Dynamics) %>%
  summarise(
    Total = n(),
    Events = sum(DFS.Event),
    Fraction = Events / n(),
    Percentage = (Events / n()) * 100
  )
print(event_summary)
```

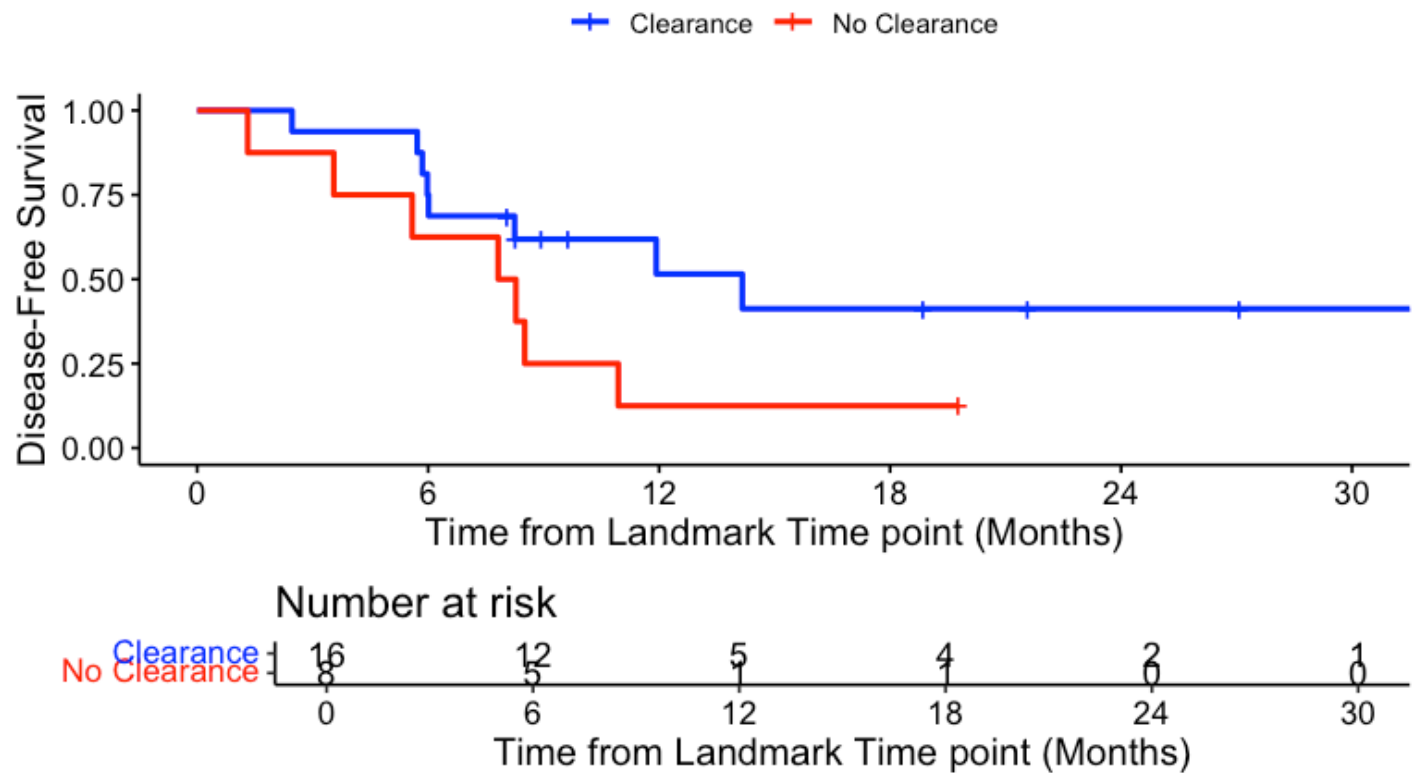
ctDNA.Dynamics <dbl>	Total <int>	Events <int>	Fraction <dbl>	Percentage <dbl>
1	16	8	0.500	50.0
2	8	7	0.875	87.5
NA	97	NA	NA	NA

3 rows

Hide

```
surv_object <- Surv(time = circ_data$DFS.3mo.months, event = circ_data$DFS.Event)
KM_curve <- survfit(surv_object ~ ctDNA.Dynamics, 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("blue","red"), title="DFS - ctDNA Clearance from MRD to 3 months ACT-treated | All Stages", ylab= "Disease-Free Survival", xlab="Time from Landmark Time point (Months)", legend.labs=c("Clearance", "No Clearance"), legend.title="")
```


DFS - ctDNA Clearance from MRD to 3 months ACT-treated | All St



Hide

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

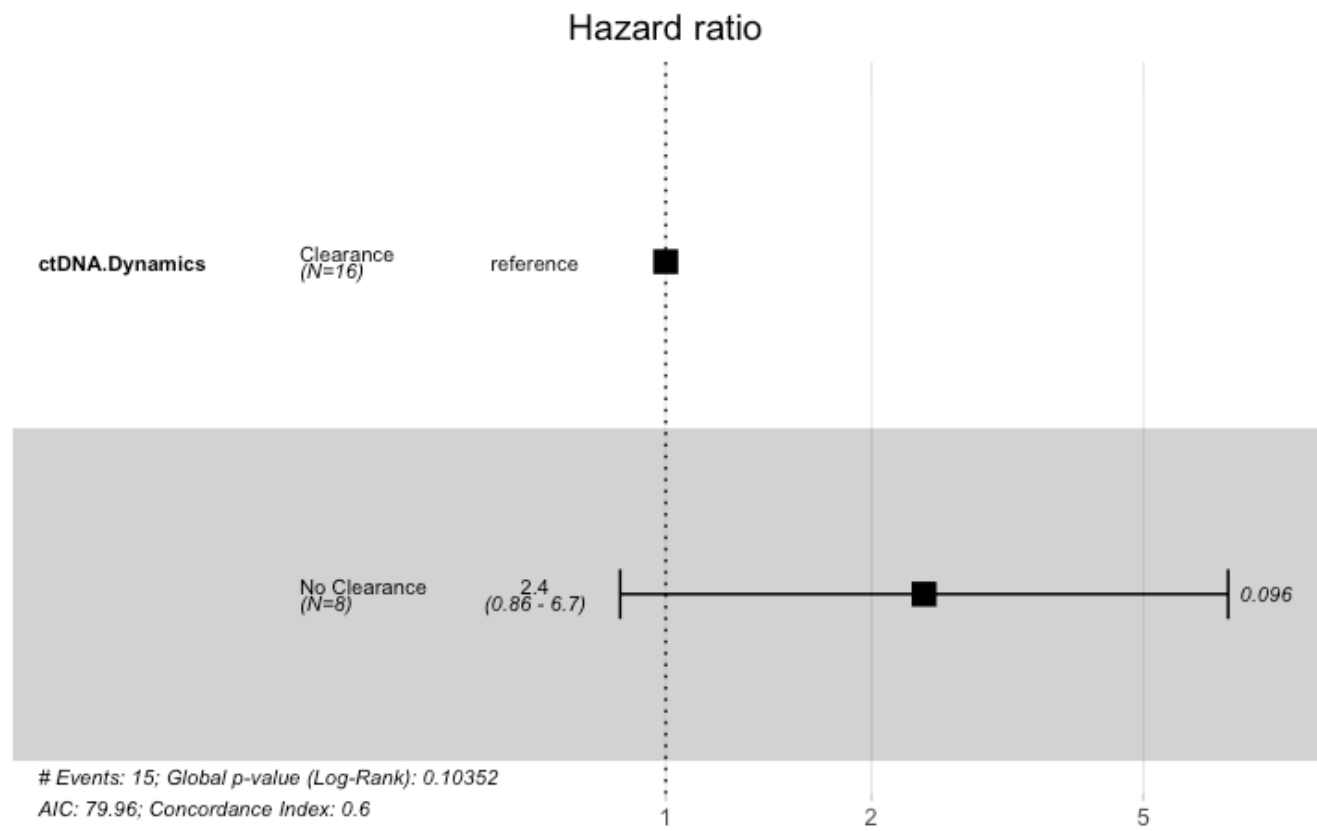
```
Call: survfit(formula = surv_object ~ ctDNA.Dynamics, data = circ_data,
  conf.int = 0.95, conf.type = "log-log")

97 observations deleted due to missingness
      ctDNA.Dynamics=1
time n.risk n.event survival std.err lower 95% CI upper 95% CI
  12      5      7    0.516  0.139    0.229    0.742
  24      2      1    0.413  0.145    0.146    0.665

      ctDNA.Dynamics=2
time n.risk n.event survival std.err lower 95% CI upper 95%
CI
12.00000  1.00000  7.00000  0.12500  0.11693  0.00659  0.422
71
```

Hide

```
circ_data$ctDNA.Dynamics <- factor(circ_data$ctDNA.Dynamics, levels=c("1","2"), labels =
c("Clearance", "No Clearance"))
cox_fit <- coxph(surv_object ~ ctDNA.Dynamics, data=circ_data)
ggforest(cox_fit,data = circ_data)
```



Hide

```
summary(cox_fit)
```

Call:
coxph(formula = surv_object ~ ctDNA.Dynamics, data = circ_data)

n= 24, number of events= 15
(97 observations deleted due to missingness)

	coef	exp(coef)	se(coef)	z	Pr(> z)
ctDNA.DynamicsNo Clearance	0.8707	2.3885	0.5227	1.666	0.0958

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

	exp(coef)	exp(-coef)	lower .95	upper .95
ctDNA.DynamicsNo Clearance	2.389	0.4187	0.8574	6.654

Concordance= 0.605 (se = 0.066)
Likelihood ratio test= 2.65 on 1 df, p=0.1
Wald test = 2.77 on 1 df, p=0.1
Score (logrank) test = 2.95 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_CI, 2), "); p = ", round(p_value, 3))
print(label_text)
```

```
[1] "HR = 2.39 (0.86-6.65); p = 0.096"
```

Hide

```
#Fisher test for DFS percentages at 12 and 24 months
dfs_times <- c(12)
circ_data <- na.omit(circ_data[, c("ctDNA.Dynamics", "DFS.3mo.months", "DFS.Event")])
p_values <- sapply(dfs_times, function(time) {
  neg_count <- sum(circ_data$ctDNA.Dynamics == "Clearance" & circ_data$DFS.3mo.months >=
time & circ_data$DFS.Event == FALSE)
  pos_count <- sum(circ_data$ctDNA.Dynamics == "No Clearance" & circ_data$DFS.3mo.months
>= time & circ_data$DFS.Event == FALSE)
  neg_total <- sum(circ_data$ctDNA.Dynamics == "Clearance")
  pos_total <- sum(circ_data$ctDNA.Dynamics == "No Clearance")

  neg_surv <- neg_total - sum(circ_data$ctDNA.Dynamics == "Clearance" & circ_data$DFS.Event == TRUE & circ_data$DFS.3mo.months < time)
  pos_surv <- pos_total - sum(circ_data$ctDNA.Dynamics == "No Clearance" & circ_data$DFS.Event == TRUE & circ_data$DFS.3mo.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 12 months
0.07907586
```

```
#DFS by ctDNA Clearance ACT-treated at 6 months - all stages
```

Hide

```
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$CohortB=="TRUE",]
circ_data <- circ_data[circ_data$ctDNA.MRD!="",]
circ_data <- circ_data[circ_data$ACT==TRUE,]
circ_datadf <- as.data.frame(circ_data)

circ_data$ctDNA.Dynamics <- NA #first we create the variable for the ctDNA & NAC combina
tion, and we assign values
circ_data <- circ_data %>%
  mutate(ctDNA.Dynamics = case_when(
    ctDNA.MRD == "POSITIVE" & ctDNA.6months == "NEGATIVE" ~ 1,
    ctDNA.MRD == "POSITIVE" & ctDNA.6months == "POSITIVE" ~ 2
  ))

circ_data <- circ_data[circ_data$DFS.6mo.months>=0,]
survfit(Surv(time = circ_data$DFS.6mo.months, event = circ_data$DFS.Event)~ctDNA.Dynamic
s, data = circ_data)
```

Call: survfit(formula = Surv(time = circ_data\$DFS.6mo.months, event = circ_data\$DFS.Event) ~
ctDNA.Dynamics, data = circ_data)

106 observations deleted due to missingness

	n	events	median	0.95LCL	0.95UCL
ctDNA.Dynamics=1	13	5	NA	5.52	NA
ctDNA.Dynamics=2	2	2	2.68	2.60	NA

[Hide](#)

```
event_summary <- circ_data %>%
  group_by(ctDNA.Dynamics) %>%
  summarise(
    Total = n(),
    Events = sum(DFS.Event),
    Fraction = Events / n(),
    Percentage = (Events / n()) * 100
  )
print(event_summary)
```

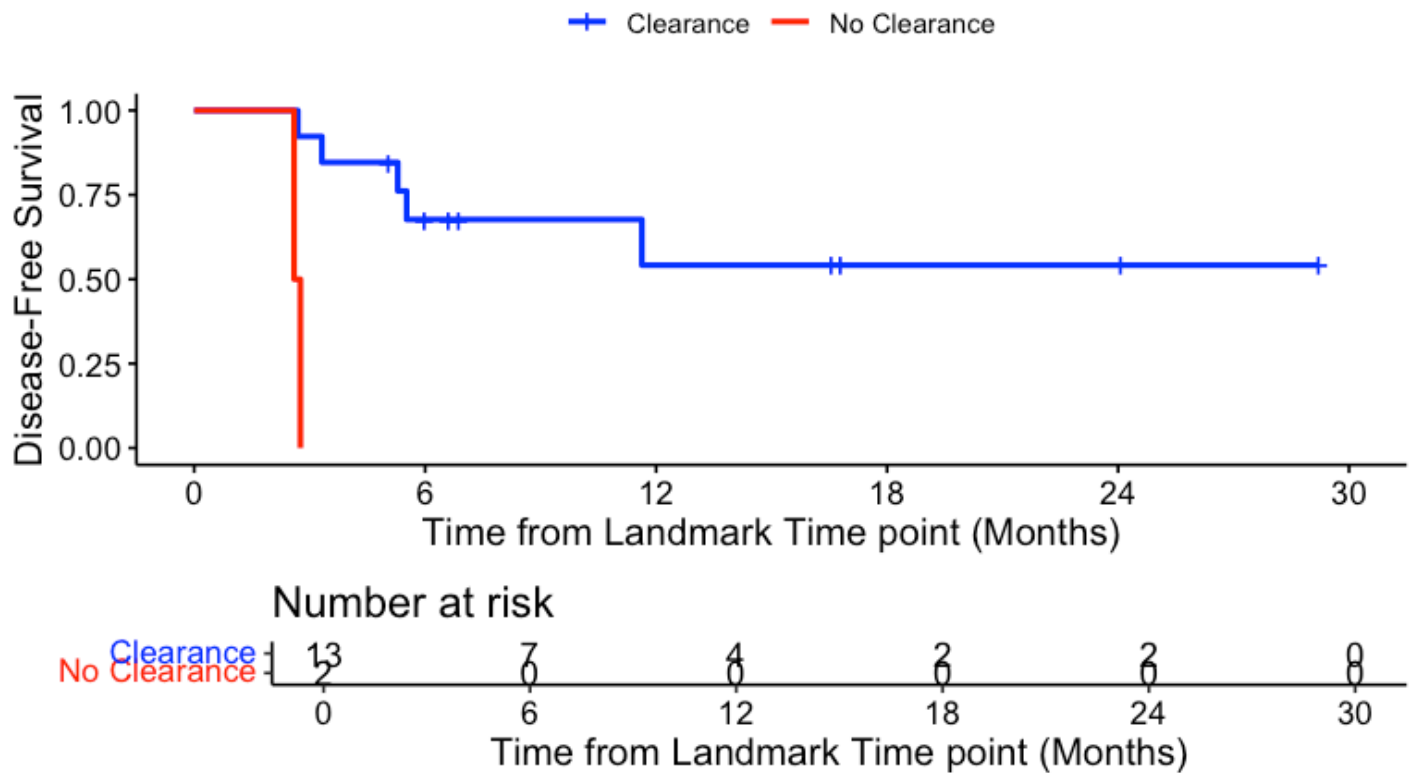
ctDNA.Dynamics <dbl>	Total <int>	Events <int>	Fraction <dbl>	Percentage <dbl>
1	13	5	0.3846154	38.46154
2	2	2	1.0000000	100.00000
NA	106	NA	NA	NA

3 rows

Hide

```
surv_object <-Surv(time = circ_data$DFS.6mo.months, event = circ_data$DFS.Event)
KM_curve <- survfit(surv_object ~ ctDNA.Dynamics, 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("blue","red"), title="DFS - ctDNA Clearance from MRD to 6 months ACT-treated | All Stages", ylab= "Disease-Free Survival", xlab="Time from Landmark Time point (Months)", legend.labs=c("Clearance", "No Clearance"), legend.title="")
```

DFS - ctDNA Clearance from MRD to 6 months ACT-treated | All S



Hide

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

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

106 observations deleted due to missingness

ctDNA.Dynamics=1

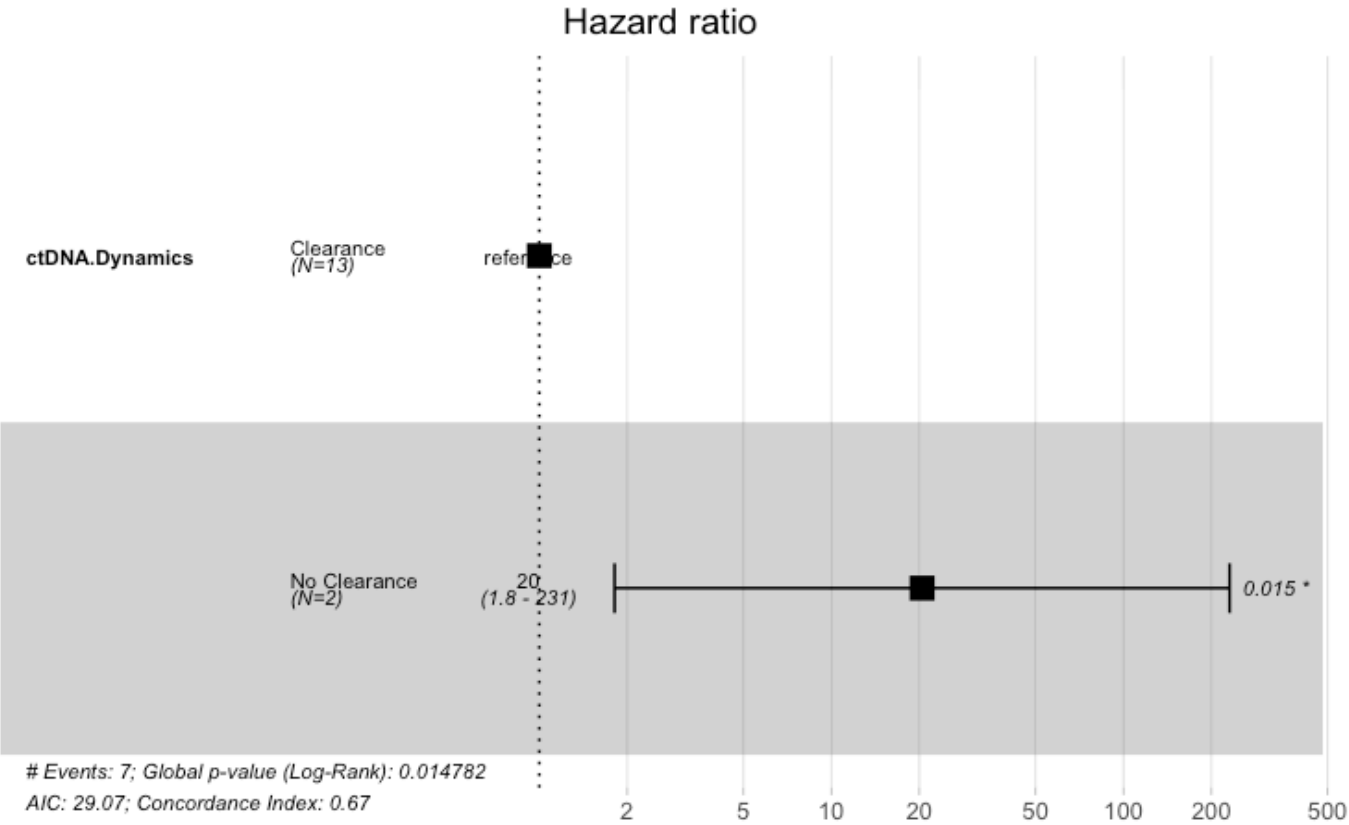
time	n.risk	n.event	survival	std.err	lower 95% CI	upper 95% CI
12	4	5	0.542	0.162	0.204	0.789
24	2	0	0.542	0.162	0.204	0.789

ctDNA.Dynamics=2

time	n.risk	n.event	survival	std.err	lower 95% CI	upper 95% CI
12	4	5	0.542	0.162	0.204	0.789
24	2	0	0.542	0.162	0.204	0.789

Hide

```
circ_data$ctDNA.Dynamics <- factor(circ_data$ctDNA.Dynamics, levels=c("1","2"), labels =
c("Clearance", "No Clearance"))
cox_fit <- coxph(surv_object ~ ctDNA.Dynamics, data=circ_data)
ggforest(cox_fit,data = circ_data)
```



Hide

```
summary(cox_fit)
```

Call:
coxph(formula = surv_object ~ ctDNA.Dynamics, data = circ_data)

n= 15, number of events= 7
(106 observations deleted due to missingness)

	coef	exp(coef)	se(coef)	z	Pr(> z)
ctDNA.DynamicsNo Clearance	3.017	20.438	1.237	2.44	0.0147 *

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

	exp(coef)	exp(-coef)	lower .95	upper .95
ctDNA.DynamicsNo Clearance	20.44	0.04893	1.81	230.8

Concordance= 0.669 (se = 0.087)
Likelihood ratio test= 5.94 on 1 df, p=0.01
Wald test = 5.95 on 1 df, p=0.01
Score (logrank) test = 11.68 on 1 df, p=6e-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 = 20.44 (1.81-230.77); p = 0.015"
```

#Percentages of MRD negative with molecular recurrence (returned positive) post-MRD

[Hide](#)

```
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$CohortB=="TRUE",]
circ_data <- circ_data[circ_data$ctDNA.MRD != "" & circ_data$Lead.Time >= 0, ]
circ_data <- circ_data[circ_data$ctDNA.MRD=="NEGATIVE",]
circ_data <- circ_data[circ_data$PostMRDPos.Event=="TRUE",]
circ_datadf <- as.data.frame(circ_data)

# Convert days to months
circ_data$PostMRDPos.months <- circ_data$PostMRDPos/30.437

# Define the intervals: 0-6, 6-9, 9-12, 12-15, 15-18, 18-21, 21-24, >24 months
breaks <- c(0, 6, 9, 12, 15, 18, 21, 24, 48)
labels <- c("0-6m", "6-9m", "9-12m", "12-15m", "15-18m", "18-21m", "21-24m", ">24m")

# Categorize p_drelReturned_months into intervals
circ_data$p_drelReturned_intervals <- cut(circ_data$PostMRDPos.months, breaks = breaks,
labels = labels, right = FALSE)

# Examine the distribution of the intervals
table(circ_data$p_drelReturned_intervals)
```

0-6m	6-9m	9-12m	12-15m	15-18m	18-21m	21-24m	>24m
9	5	7	1	4	0	0	0

[Hide](#)


```
# Get the counts for each interval
interval_counts <- table(circ_data$p_drelReturned_intervals)

# Calculate the percentages
interval_percentages <- 100 * interval_counts / sum(interval_counts)

# Combine the counts and percentages for a clearer overview
interval_summary <- data.frame(Counts = interval_counts, Percentages = interval_percentages)

# Calculate the total number of observations
total_observations <- sum(interval_counts)

# Add the total number of observations to the summary
interval_summary$TotalObservations <- c(rep(NA, length(interval_counts)-1), total_observations)

# Print the summary with total observations
print(interval_summary)
```

Counts.Var1 <fctr>	Counts.Freq <int>	Percentages.Var1 <fctr>	Percentages.Freq <dbl>	TotalObservations <int>
0-6m	9	0-6m	34.615385	NA
6-9m	5	6-9m	19.230769	NA
9-12m	7	9-12m	26.923077	NA
12-15m	1	12-15m	3.846154	NA
15-18m	4	15-18m	15.384615	NA
18-21m	0	18-21m	0.000000	NA
21-24m	0	21-24m	0.000000	NA
>24m	0	>24m	0.000000	26
8 rows				

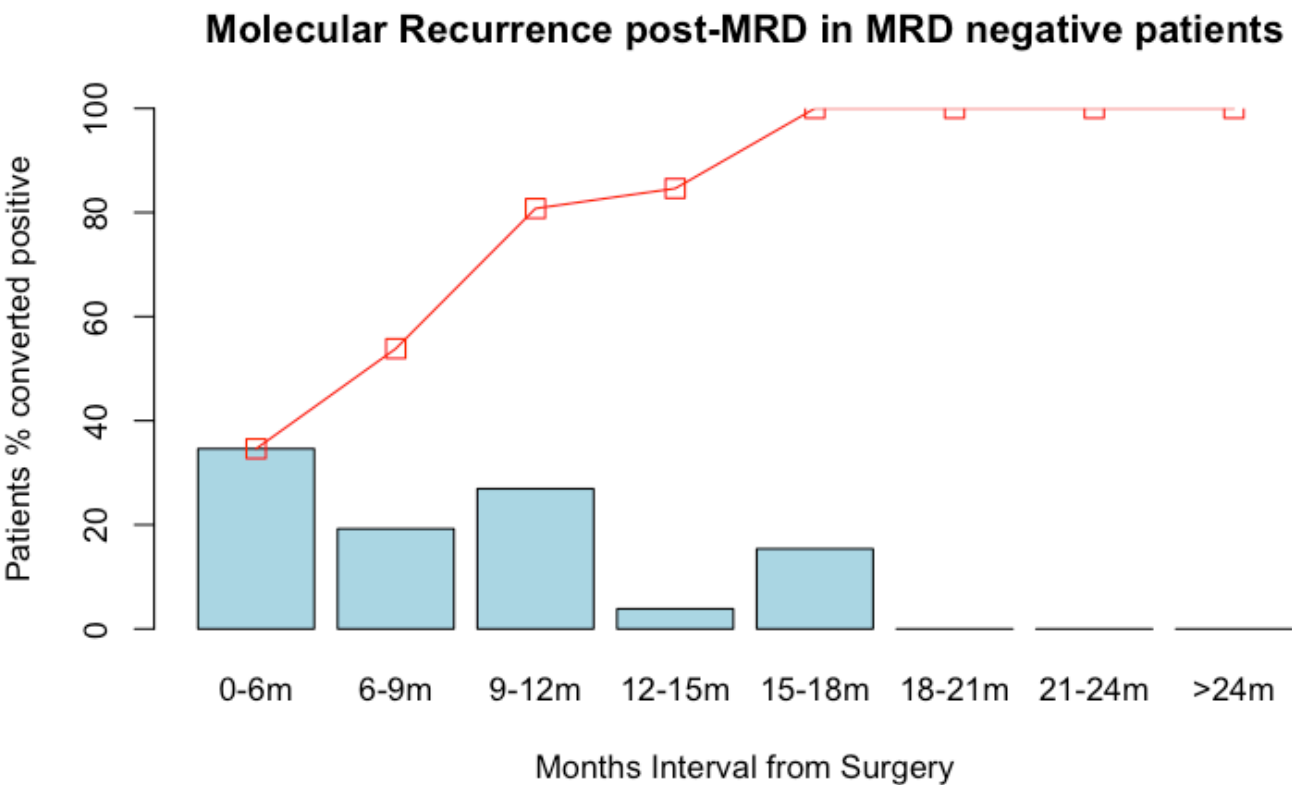
[Hide](#)

```
# Calculate cumulative percentages
cumulative_percentages <- cumsum(interval_percentages)

# Combine the counts, percentages, and cumulative percentages for a clearer overview
interval_summary <- data.frame(Counts = interval_counts, Percentages = interval_percentages, CumulativePercentages = cumulative_percentages, TotalObservations = c(rep(NA, length(interval_counts)-1), total_observations))

bp <- barplot(interval_percentages,
               main="Molecular Recurrence post-MRD in MRD negative patients",
               xlab="Months Interval from Surgery",
               ylab="Patients % converted positive",
               col="lightblue",
               ylim=c(0, 100))

# Add the cumulative percentages to the plot
points(bp, cumulative_percentages, type="o", pch=22, col="red", cex=1.5)
```



Hide

```
print(interval_summary)
```

	Counts.Var1 <fctr>	Counts.Freq <int>	Percentages.Var1 <fctr>	Percentages.Freq <dbl>	CumulativePercentages <dbl>
	0-6m	0-6m	9	0-6m	34.615385

	Counts.Var1 <fctr>	Counts.Freq <int>	Percentages.Var1 <fctr>	Percentages.Freq <dbl>	CumulativePercentag <dbl>
6-9m	6-9m	5	6-9m	19.230769	53.846154
9-12m	9-12m	7	9-12m	26.923077	80.769231
12-15m	12-15m	1	12-15m	3.846154	84.615385
15-18m	15-18m	4	15-18m	15.384615	100.000000
18-21m	18-21m	0	18-21m	0.000000	100.000000
21-24m	21-24m	0	21-24m	0.000000	100.000000
>24m	>24m	0	>24m	0.000000	100.000000

8 rows | 1-6 of 6 columns

#DFS by ctDNA MRD positive vs ctDNA negative with molecular recurrence at Surveillance - 3 groups

Hide

```
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$CohortB=="TRUE",]
circ_data <- circ_data[circ_data$ctDNA.MRD!="",]
circ_datadf <- as.data.frame(circ_data)

circ_data$ctDNA.Dynamics <- NA #first we create the variable for the ctDNA & NAC combination, and we assign values
circ_data <- circ_data %>%
  mutate(ctDNA.Dynamics = case_when(
    ctDNA.MRD == "NEGATIVE" & ctDNA.Surveillance=="NEGATIVE" ~ 1,
    ctDNA.MRD == "NEGATIVE" & ctDNA.Surveillance=="POSITIVE" ~ 2,
    ctDNA.MRD == "POSITIVE" ~ 3
  ))

circ_data <- circ_data[circ_data$DFS.MRD.months>=0,]
survfit(Surv(time = circ_data$DFS.MRD.months, event = circ_data$DFS.Event)~ctDNA.Dynamics, data = circ_data)
```

```
Call: survfit(formula = Surv(time = circ_data$DFS.MRD.months, event = circ_data$DFS.Event) ~
```

```
ctDNA.Dynamics, data = circ_data)
```

7 observations deleted due to missingness

```

              n events median 0.95LCL 0.95UCL
ctDNA.Dynamics=1 180      10      NA      NA      NA
ctDNA.Dynamics=2  24      14    13.44    10.55      NA
ctDNA.Dynamics=3  35      25     9.27     7.62    14.1

```

[Hide](#)

```

event_summary <- circ_data %>%
  group_by(ctDNA.Dynamics) %>%
  summarise(
    Total = n(),
    Events = sum(DFS.Event),
    Fraction = Events / n(),
    Percentage = (Events / n()) * 100
  )
print(event_summary)

```

ctDNA.Dynamics <dbl>	Total <int>	Events <int>	Fraction <dbl>	Percentage <dbl>
1	180	10	0.05555556	5.555556
2	24	14	0.58333333	58.333333
3	35	25	0.71428571	71.428571
NA	7	4	0.57142857	57.142857

4 rows

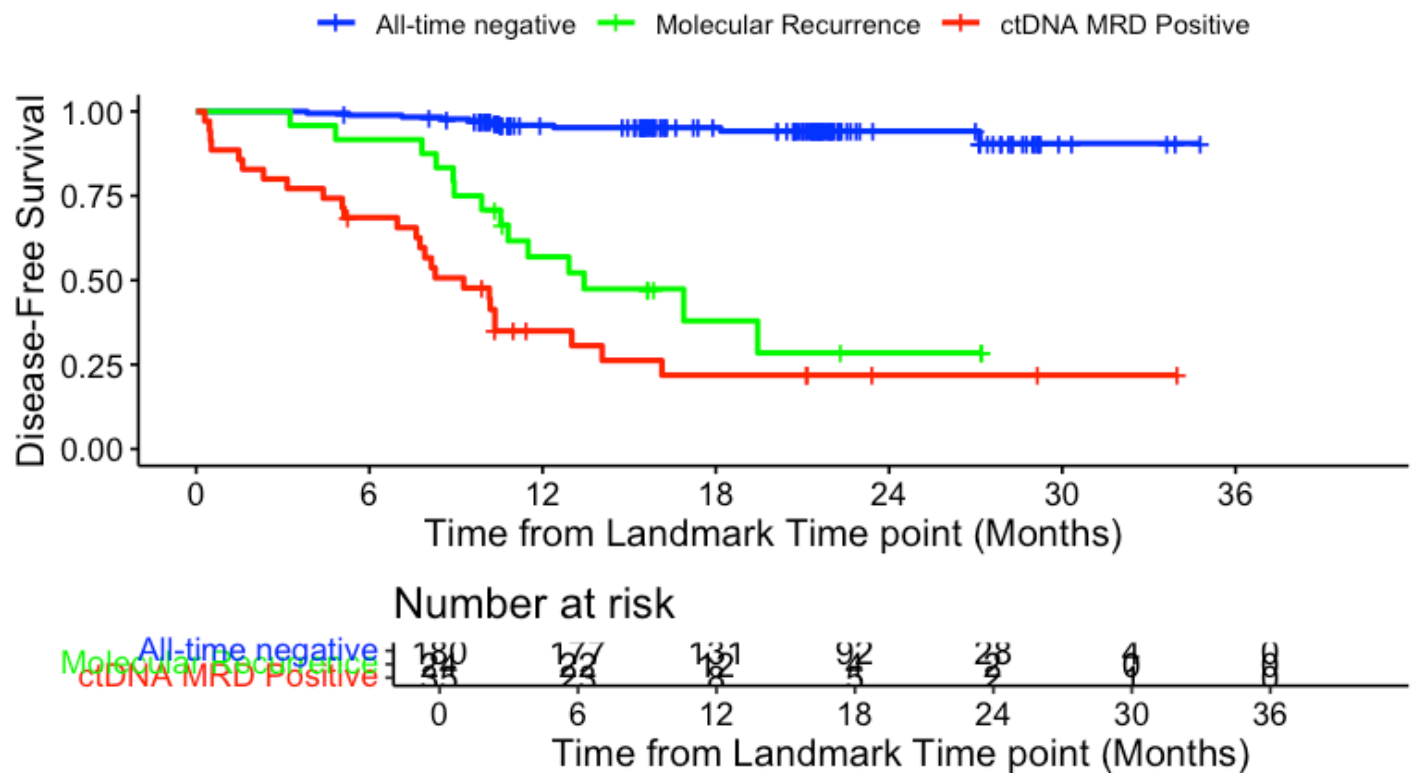
[Hide](#)

```

surv_object <- Surv(time = circ_data$DFS.MRD.months, event = circ_data$DFS.Event)
KM_curve <- survfit(surv_object ~ ctDNA.Dynamics, 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("blue","green","red"), title="DFS - ctDNA MRD Pos vs Neg with Molecular Recurrence at Surveillance Window", ylab= "Disease-Free Survival", xlab="Time from Landmark Time point (Months)", legend.labs=c("All-time negative", "Molecular Recurrence", "ctDNA MRD Positive"), legend.title="")

```

DFS - ctDNA MRD Pos vs Neg with Molecular Recurrence at Surve



Hide

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

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

7 observations deleted due to missingness

ctDNA.Dynamics=1

time	n.risk	n.event	survival	std.err	lower 95% CI	upper 95% CI
12	131	7	0.959	0.0151	0.916	0.98
24	28	2	0.942	0.0194	0.889	0.97

ctDNA.Dynamics=2

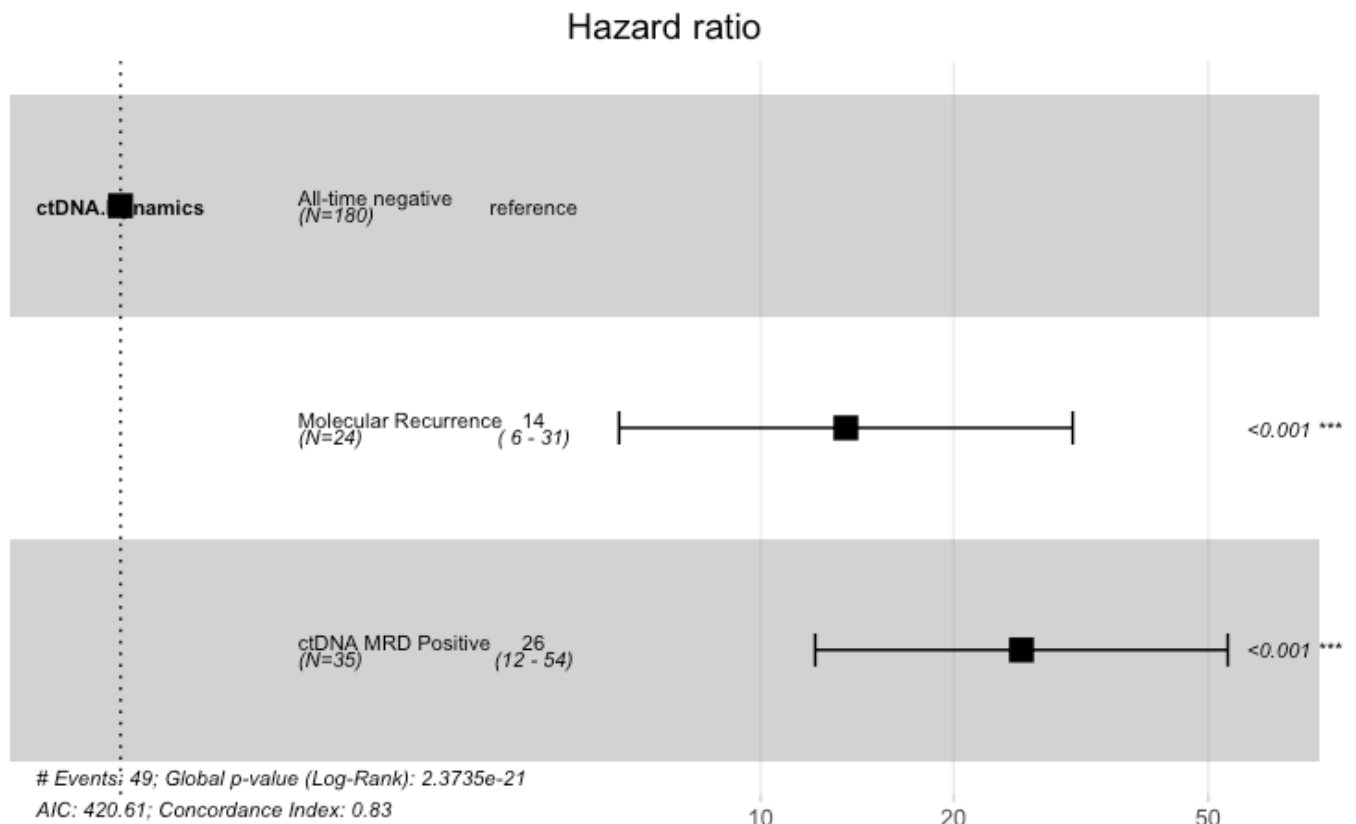
time	n.risk	n.event	survival	std.err	lower 95% CI	upper 95% CI
12	12	10	0.569	0.104	0.3457	0.742
24	2	4	0.285	0.122	0.0863	0.525

ctDNA.Dynamics=3

time	n.risk	n.event	survival	std.err	lower 95% CI	upper 95% CI
12	8	22	0.350	0.0830	0.1948	0.509
24	2	3	0.219	0.0792	0.0884	0.386

[Hide](#)

```
circ_data$ctDNA.Dynamics <- factor(circ_data$ctDNA.Dynamics, levels=c("1","2","3"), label
ls = c("All-time negative", "Molecular Recurrence", "ctDNA MRD Positive"))
cox_fit <- coxph(surv_object ~ ctDNA.Dynamics, data=circ_data)
ggforest(cox_fit, data = circ_data)
```


[Hide](#)

```
summary(cox_fit)
```

Call:

```
coxph(formula = surv_object ~ ctDNA.Dynamics, data = circ_data)
```

n= 239, number of events= 49

(7 observations deleted due to missingness)

	coef	exp(coef)	se(coef)	z	Pr(> z)
ctDNA.DynamicsMolecular Recurrence	2.6086	13.5800	0.4162	6.267	3.68e-10 ***
ctDNA.DynamicsctDNA MRD Positive	3.2402	25.5396	0.3786	8.559	< 2e-16 ***

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

	exp(coef)	exp(-coef)	lower .95	upper .95
ctDNA.DynamicsMolecular Recurrence	13.58	0.07364	6.006	30.70
ctDNA.DynamicsctDNA MRD Positive	25.54	0.03915	12.162	53.63

Concordance= 0.834 (se = 0.029)

Likelihood ratio test= 94.98 on 2 df, p=<2e-16

Wald test = 74.17 on 2 df, p=<2e-16

Score (logrank) test = 146.1 on 2 df, p=<2e-16

[Hide](#)

```
#Fisher test for DFS percentages at 12 and 24 months – All time negative vs Molecular Re
currence
```

```
dfs_times <- c(12, 24)
```

```
circ_data <- na.omit(circ_data[, c("ctDNA.Dynamics", "DFS.MRD.months", "DFS.Event")])
```

```
p_values <- sapply(dfs_times, function(time) {
```

```
  neg_count <- sum(circ_data$ctDNA.Dynamics == "All-time negative" & circ_data$DFS.MRD.m
onths >= time & circ_data$DFS.Event == 0)
```

```
  pos_count <- sum(circ_data$ctDNA.Dynamics == "Molecular Recurrence" & circ_data$DFS.MR
D.months >= time & circ_data$DFS.Event == 0)
```

```
  neg_total <- sum(circ_data$ctDNA.Dynamics == "All-time negative")
```

```
  pos_total <- sum(circ_data$ctDNA.Dynamics == "Molecular Recurrence")
```

```
  neg_surv <- neg_total - sum(circ_data$ctDNA.Dynamics == "All-time negative" & circ_dat
a$DFS.Event == 1 & circ_data$DFS.MRD.months < time)
```

```
  pos_surv <- pos_total - sum(circ_data$ctDNA.Dynamics == "Molecular Recurrence" & circ_
data$DFS.Event == 1 & circ_data$DFS.MRD.months < time)
```

```
  surv_matrix <- matrix(c(neg_surv, pos_surv, neg_total - neg_surv, pos_total - pos_sur
v), 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 12 months p-value at 24 months
8.575063e-07 6.424306e-10

Hide

```
#Repeat analysis to run Fisher test for All time negative vs ctDNA Positive
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$CohortB=="TRUE",]
circ_data <- circ_data[circ_data$ctDNA.MRD!="",]

circ_data$ctDNA.Dynamics <- NA #first we create the variable for the ctDNA & NAC combina
tion, and we assign values
circ_data <- circ_data %>%
  mutate(ctDNA.Dynamics = case_when(
    ctDNA.MRD == "NEGATIVE" & ctDNA.Surveillance=="NEGATIVE" ~ 1,
    ctDNA.MRD == "NEGATIVE" & ctDNA.Surveillance=="POSITIVE" ~ 2,
    ctDNA.MRD == "POSITIVE" ~ 3
  ))

circ_data <- circ_data[circ_data$DFS.MRD.months>=0,]

surv_object <- Surv(time = circ_data$DFS.MRD.months, event = circ_data$DFS.Event)
KM_curve <- survfit(surv_object ~ ctDNA.Dynamics, data = circ_data, conf.int=0.95, conf.ty
pe="log-log")
summary(KM_curve, times= c(12, 24))
```

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

7 observations deleted due to missingness

ctDNA.Dynamics=1

time	n.risk	n.event	survival	std.err	lower 95% CI	upper 95% CI
12	131	7	0.959	0.0151	0.916	0.98
24	28	2	0.942	0.0194	0.889	0.97

ctDNA.Dynamics=2

time	n.risk	n.event	survival	std.err	lower 95% CI	upper 95% CI
12	12	10	0.569	0.104	0.3457	0.742
24	2	4	0.285	0.122	0.0863	0.525

ctDNA.Dynamics=3

time	n.risk	n.event	survival	std.err	lower 95% CI	upper 95% CI
12	8	22	0.350	0.0830	0.1948	0.509
24	2	3	0.219	0.0792	0.0884	0.386

Hide


```

circ_data$ctDNA.Dynamics <- factor(circ_data$ctDNA.Dynamics, levels=c("1","2","3"), labels = c("All-time negative","Molecular Recurrence", "ctDNA MRD Positive"))

#Fisher test for DFS percentages at 12 and 24 months – All time negative vs ctDNA Positive
dfs_times <- c(12, 24)
circ_data <- na.omit(circ_data[, c("ctDNA.Dynamics", "DFS.MRD.months", "DFS.Event")])
p_values <- sapply(dfs_times, function(time) {
  neg_count <- sum(circ_data$ctDNA.Dynamics == "All-time negative" & circ_data$DFS.MRD.months >= time & circ_data$DFS.Event == 0)
  pos_count <- sum(circ_data$ctDNA.Dynamics == "ctDNA MRD Positive" & circ_data$DFS.MRD.months >= time & circ_data$DFS.Event == 0)
  neg_total <- sum(circ_data$ctDNA.Dynamics == "All-time negative")
  pos_total <- sum(circ_data$ctDNA.Dynamics == "ctDNA MRD Positive")

  neg_surv <- neg_total - sum(circ_data$ctDNA.Dynamics == "All-time negative" & circ_data$DFS.Event == 1 & circ_data$DFS.MRD.months < time)
  pos_surv <- pos_total - sum(circ_data$ctDNA.Dynamics == "ctDNA MRD Positive" & circ_data$DFS.Event == 1 & circ_data$DFS.MRD.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 12 months	p-value at 24 months
2.382798e-15	1.933852e-17

[Hide](#)

```
#Repeat analysis to run Fisher test for Molecular Recurrence vs ctDNA Positive
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$CohortB=="TRUE",]
circ_data <- circ_data[circ_data$ctDNA.MRD!="",]

circ_data$ctDNA.Dynamics <- NA #first we create the variable for the ctDNA & NAC combina
tion, and we assign values
circ_data <- circ_data %>%
  mutate(ctDNA.Dynamics = case_when(
    ctDNA.MRD == "NEGATIVE" & ctDNA.Surveillance=="NEGATIVE" ~ 1,
    ctDNA.MRD == "NEGATIVE" & ctDNA.Surveillance=="POSITIVE" ~ 2,
    ctDNA.MRD == "POSITIVE" ~ 3
  ))

circ_data <- circ_data[circ_data$DFS.MRD.months>=0,]

surv_object <- Surv(time = circ_data$DFS.MRD.months, event = circ_data$DFS.Event)
KM_curve <- survfit(surv_object ~ ctDNA.Dynamics, data = circ_data, conf.int=0.95, conf.ty
pe="log-log")
summary(KM_curve, times= c(12, 24))
```

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

7 observations deleted due to missingness

ctDNA.Dynamics=1

time	n.risk	n.event	survival	std.err	lower 95% CI	upper 95% CI
12	131	7	0.959	0.0151	0.916	0.98
24	28	2	0.942	0.0194	0.889	0.97

ctDNA.Dynamics=2

time	n.risk	n.event	survival	std.err	lower 95% CI	upper 95% CI
12	12	10	0.569	0.104	0.3457	0.742
24	2	4	0.285	0.122	0.0863	0.525

ctDNA.Dynamics=3

time	n.risk	n.event	survival	std.err	lower 95% CI	upper 95% CI
12	8	22	0.350	0.0830	0.1948	0.509
24	2	3	0.219	0.0792	0.0884	0.386

Hide

```

circ_data$ctDNA.Dynamics <- factor(circ_data$ctDNA.Dynamics, levels=c("1","2","3"), labels = c("All-time negative","Molecular Recurrence", "ctDNA MRD Positive"))

#Fisher test for DFS percentages at 12 and 24 months – Molecular Recurrence vs ctDNA Positive
dfs_times <- c(12, 24)
circ_data <- na.omit(circ_data[, c("ctDNA.Dynamics", "DFS.MRD.months", "DFS.Event")])
p_values <- sapply(dfs_times, function(time) {
  neg_count <- sum(circ_data$ctDNA.Dynamics == "Molecular Recurrence" & circ_data$DFS.MRD.months >= time & circ_data$DFS.Event == 0)
  pos_count <- sum(circ_data$ctDNA.Dynamics == "ctDNA MRD Positive" & circ_data$DFS.MRD.months >= time & circ_data$DFS.Event == 0)
  neg_total <- sum(circ_data$ctDNA.Dynamics == "Molecular Recurrence")
  pos_total <- sum(circ_data$ctDNA.Dynamics == "ctDNA MRD Positive")

  neg_surv <- neg_total - sum(circ_data$ctDNA.Dynamics == "Molecular Recurrence" & circ_data$DFS.Event == 1 & circ_data$DFS.MRD.months < time)
  pos_surv <- pos_total - sum(circ_data$ctDNA.Dynamics == "ctDNA MRD Positive" & circ_data$DFS.Event == 1 & circ_data$DFS.MRD.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)

```

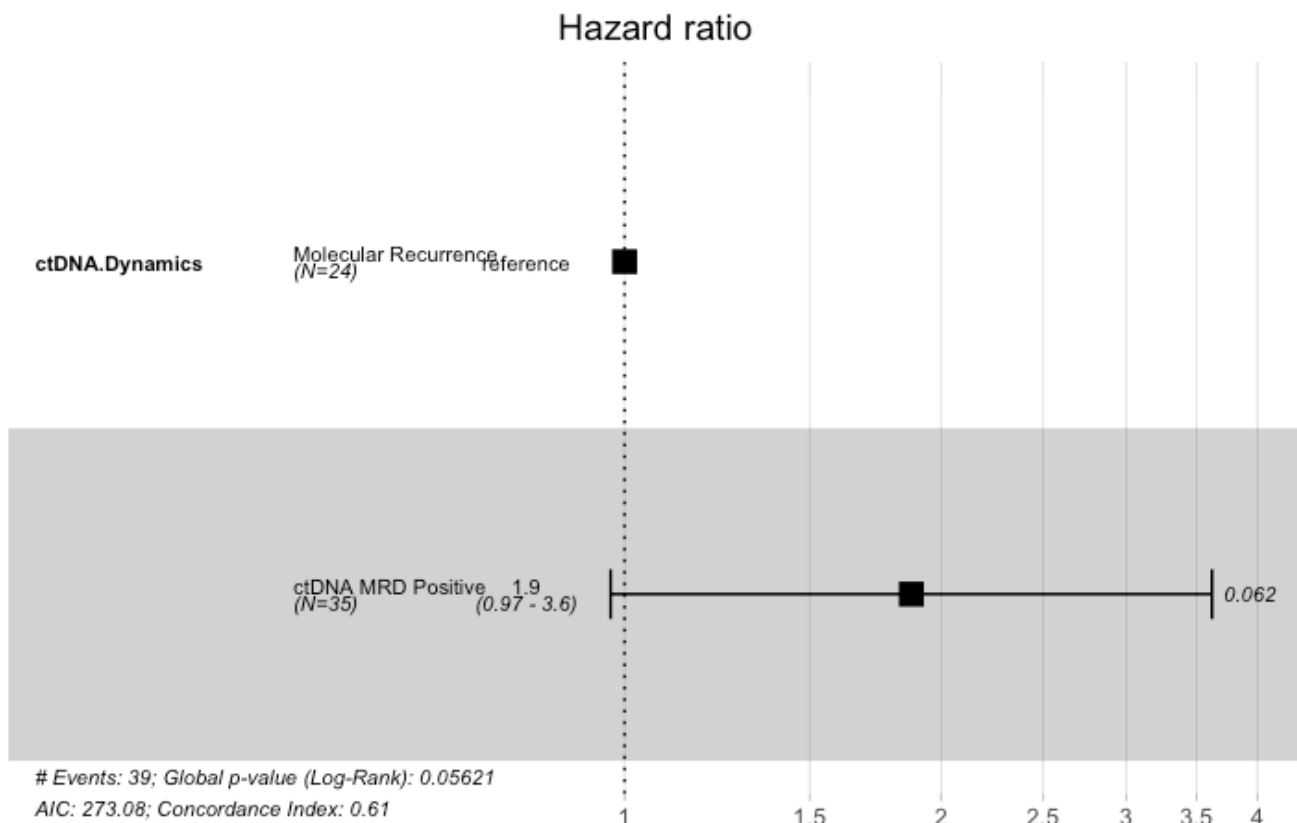
p-value at 12 months	p-value at 24 months
0.1214065	0.4023373

[Hide](#)

```
#Repeat to compare HRS for Molecular Recurrence vs ctDNA MRD positive
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$CohortB=="TRUE",]
circ_data <- circ_data[circ_data$ctDNA.MRD!="",]
circ_datadf <- as.data.frame(circ_data)

circ_data$ctDNA.Dynamics <- NA #first we create the variable for the ctDNA & NAC combina
tion, and we assign values
circ_data <- circ_data %>%
  mutate(ctDNA.Dynamics = case_when(
    ctDNA.MRD == "NEGATIVE" & ctDNA.Surveillance=="NEGATIVE" ~ 1,
    ctDNA.MRD == "NEGATIVE" & ctDNA.Surveillance=="POSITIVE" ~ 2,
    ctDNA.MRD == "POSITIVE" ~ 3
  ))

circ_data <- circ_data[circ_data$DFS.MRD.months>=0,]
surv_object <- Surv(time = circ_data$DFS.MRD.months, event = circ_data$DFS.Event)
circ_data$ctDNA.Dynamics <- factor(circ_data$ctDNA.Dynamics, levels=c("2","3"), labels =
c("Molecular Recurrence", "ctDNA MRD Positive"))
cox_fit <- coxph(surv_object ~ ctDNA.Dynamics, data=circ_data)
ggforest(cox_fit,data = circ_data)
```


[Hide](#)

```
summary(cox_fit)
```

Call:

```
coxph(formula = surv_object ~ ctDNA.Dynamics, data = circ_data)
```

```
n= 59, number of events= 39
```

```
(187 observations deleted due to missingness)
```

	coef	exp(coef)	se(coef)	z	Pr(> z)
ctDNA.DynamicsctDNA MRD Positive	0.6281	1.8741	0.3361	1.869	0.0616

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

	exp(coef)	exp(-coef)	lower .95	upper .95
ctDNA.DynamicsctDNA MRD Positive	1.874	0.5336	0.9699	3.621

```
Concordance= 0.608 (se = 0.037 )
```

```
Likelihood ratio test= 3.65 on 1 df, p=0.06
```

```
Wald test = 3.49 on 1 df, p=0.06
```

```
Score (logrank) test = 3.6 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 = 1.87 (0.97-3.62); p = 0.062"
```

#DFS by ctDNA at the Surveillance Window - All stages Landmark 10 weeks

[Hide](#)

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

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

```
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
```

```
circ_data <- circ_data[circ_data$CohortB=="TRUE",]
```

```
circ_data <- circ_data[circ_data$ctDNA.Surveillance!="",]
```

```
circ_data$DFS.months=circ_data$DFS.months-2.5
```

```
circ_data <- circ_data[circ_data$DFS.months>=0,]
```

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

```
survfit(Surv(time = circ_data$DFS.months, event = circ_data$DFS.Event)~ctDNA.Surveillance, data = circ_data)
```

```
Call: survfit(formula = Surv(time = circ_data$DFS.months, event = circ_data$DFS.Event) ~
      ctDNA.Surveillance, data = circ_data)
```

	n	events	median	0.95LCL	0.95UCL
ctDNA.Surveillance=NEGATIVE	193	10	NA	NA	NA
ctDNA.Surveillance=POSITIVE	40	30	8.79	7.16	12

Hide

```
event_summary <- circ_data %>%
  group_by(ctDNA.Surveillance) %>%
  summarise(
    Total = n(),
    Events = sum(DFS.Event),
    Fraction = Events / n(),
    Percentage = (Events / n()) * 100
  )
print(event_summary)
```

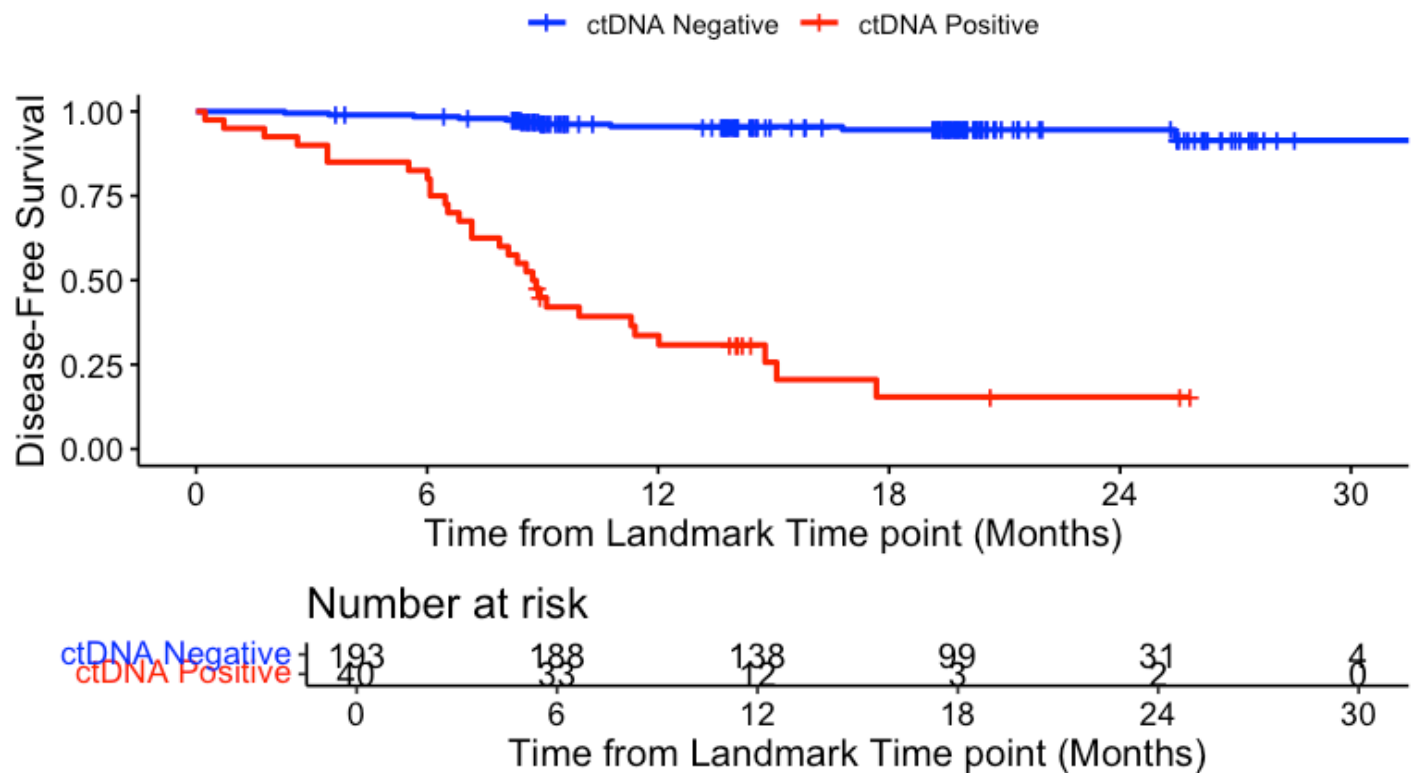
ctDNA.Surveillance	Total	Events	Fraction	Percentage
<chr>	<int>	<int>	<dbl>	<dbl>
NEGATIVE	193	10	0.05181347	5.181347
POSITIVE	40	30	0.75000000	75.000000

2 rows

Hide

```
surv_object <-Surv(time = circ_data$DFS.months, event = circ_data$DFS.Event)
KM_curve <- survfit(surv_object ~ ctDNA.Surveillance, 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("blue","red"), title="DFS - ctDNA Surveillance window | All stages", ylab= "Disease-Free Survival", xlab="Time from Landmark Time point (Months)", legend.labs=c("ctDNA Negative", "ctDNA Positive"), legend.title="")
```

DFS - ctDNA Surveillance window | All stages



Hide

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

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

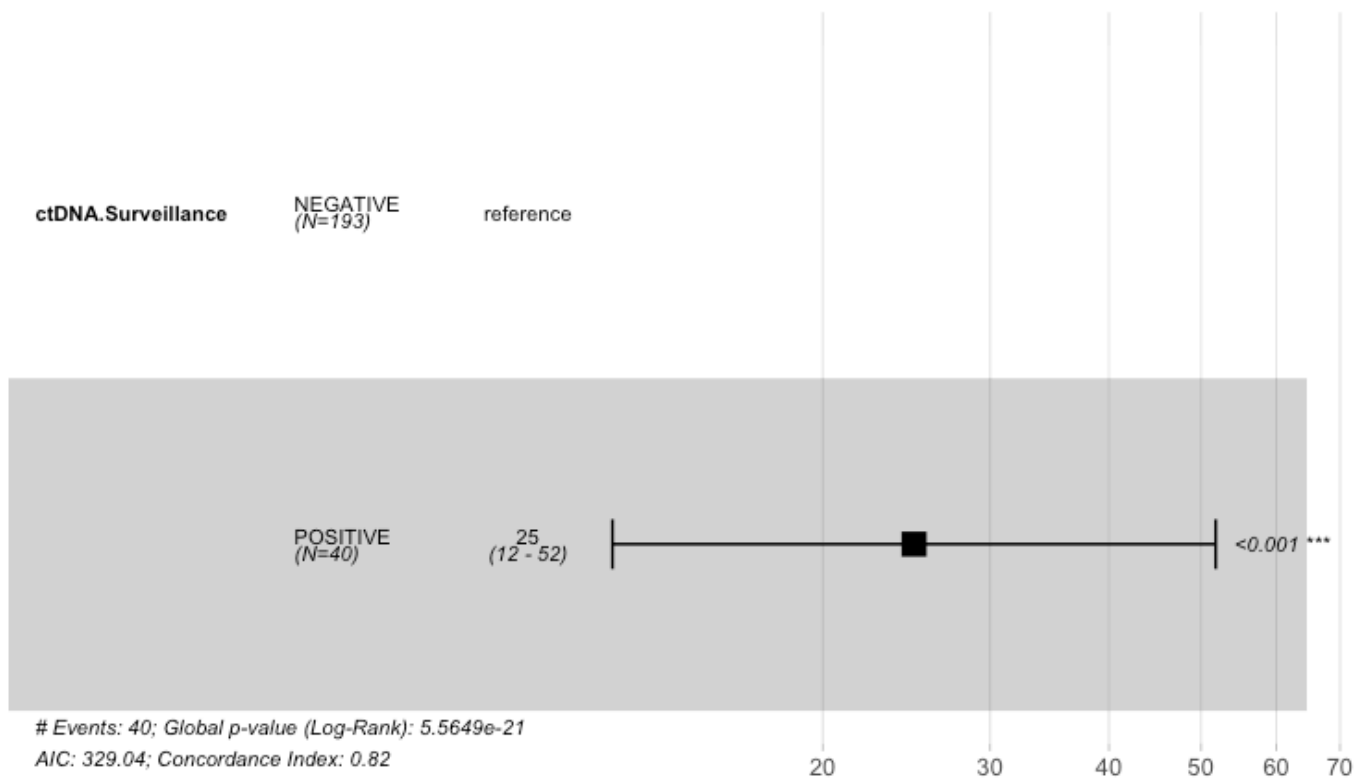
```
ctDNA.Surveillance=NEGATIVE
time n.risk n.event survival std.err lower 95% CI upper 95% CI
 12   138     8    0.955  0.0156    0.912    0.977
 24    31     1    0.946  0.0181    0.896    0.972
```

```
ctDNA.Surveillance=POSITIVE
time n.risk n.event survival std.err lower 95% CI upper 95% CI
 12    12    26    0.336  0.0765    0.1940    0.485
 24     2     4    0.154  0.0733    0.0461    0.321
```

[Hide](#)

```
circ_data$ctDNA.Surveillance <- factor(circ_data$ctDNA.Surveillance, levels=c("NEGATIVE", "POSITIVE"))
cox_fit <- coxph(surv_object ~ ctDNA.Surveillance, data=circ_data)
ggforest(cox_fit, data = circ_data)
```

Hazard ratio


[Hide](#)

```
summary(cox_fit)
```


Call:

```
coxph(formula = surv_object ~ ctDNA.Surveillance, data = circ_data)
```

n= 233, number of events= 40

	coef	exp(coef)	se(coef)	z	Pr(> z)
ctDNA.SurveillancePOSITIVE	3.2170	24.9530	0.3726	8.633	<2e-16 ***

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

	exp(coef)	exp(-coef)	lower .95	upper .95
ctDNA.SurveillancePOSITIVE	24.95	0.04008	12.02	51.8

Concordance= 0.822 (se = 0.033)

Likelihood ratio test= 88.32 on 1 df, p=<2e-16

Wald test = 74.53 on 1 df, p=<2e-16

Score (logrank) test = 156.3 on 1 df, p=<2e-16

[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 = 24.95 (12.02-51.8); p = 0"
```

[Hide](#)

```
#Fisher test for DFS percentages at 12 and 24 months
dfs_times <- c(12, 24)
circ_data <- na.omit(circ_data[, c("ctDNA.Surveillance", "DFS.months", "DFS.Event")])
p_values <- sapply(dfs_times, function(time) {
  neg_count <- sum(circ_data$ctDNA.Surveillance == "NEGATIVE" & circ_data$DFS.months >=
time & circ_data$DFS.Event == 0)
  pos_count <- sum(circ_data$ctDNA.Surveillance == "POSITIVE" & circ_data$DFS.months >=
time & circ_data$DFS.Event == 0)
  neg_total <- sum(circ_data$ctDNA.Surveillance == "NEGATIVE")
  pos_total <- sum(circ_data$ctDNA.Surveillance == "POSITIVE")

  neg_surv <- neg_total - sum(circ_data$ctDNA.Surveillance == "NEGATIVE" & circ_data$DFS.Event == 1 & circ_data$DFS.months < time)
  pos_surv <- pos_total - sum(circ_data$ctDNA.Surveillance == "POSITIVE" & circ_data$DFS.Event == 1 & circ_data$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 12 months	p-value at 24 months
1.175567e-17	2.041854e-21

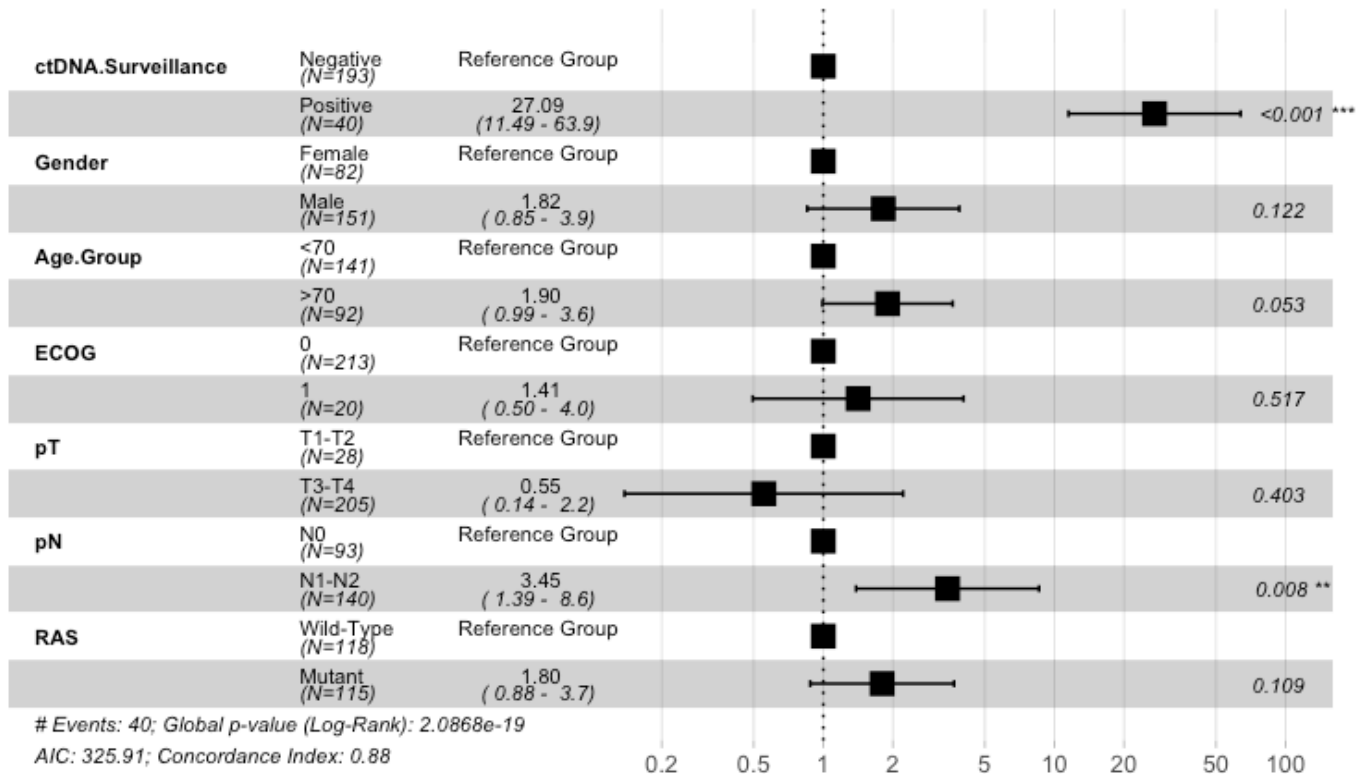
#Multivariate cox regression at Surveillance Window for DFS - All stages Landmark 10 weeks

Hide

```
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$CohortB=="TRUE",]
circ_data <- circ_data[circ_data$ctDNA.Surveillance!="",]
circ_data$DFS.months=circ_data$DFS.months-2.5
circ_data <- circ_data[circ_data$DFS.months>=0,]
circ_datadf <- as.data.frame(circ_data)

circ_data$ctDNA.Surveillance <- factor(circ_data$ctDNA.Surveillance, levels=c("NEGATIVE", "POSITIVE"), labels = c("Negative", "Positive"))
circ_data$Gender <- factor(circ_data$Gender, levels = c("Female", "Male"))
circ_data$Age.Group <- factor(circ_data$Age.Group, levels = c("1", "2"), labels = c("<70", ">70"))
circ_data$PrimSite <- factor(circ_data$PrimSite, levels = c("Left-sided colon", "Right-sided colon"))
circ_data$ECOG <- factor(circ_data$ECOG, levels = c("0", "1"))
circ_data$pT <- factor(circ_data$pT, levels = c("T1-T2", "T3-T4"))
circ_data$pN <- factor(circ_data$pN, levels = c("N0", "N1-N2"))
circ_data$RAS <- factor(circ_data$RAS, levels = c("WT", "MUT"), labels = c("Wild-Type", "Mutant"))
surv_object <- Surv(time = circ_data$DFS.months, event = circ_data$DFS.Event)
cox_fit <- coxph(surv_object ~ ctDNA.Surveillance + Gender + Age.Group + ECOG + pT + pN + RAS, data=circ_data)
ggforest(cox_fit, data = circ_data, main = "Multivariate Regression Model for DFS - All Stages", refLabel = "Reference Group")
```

Multivariate Regression Model for DFS - All Stages



Hide

```
test.ph <- cox.zph(cox_fit)
```

#DFS by ctDNA Dynamics from MRD to 6 months - all stages

Hide

```
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$CohortB=="TRUE",]
circ_data <- circ_data[circ_data$ctDNA.MRD!="",]
circ_data <- circ_data[circ_data$DFS.6mo.months>=0,]
circ_datadf <- as.data.frame(circ_data)

circ_data$ctDNA.Dynamics <- NA #first we create the variable for the ctDNA & NAC combina
tion, and we assign values
circ_data <- circ_data %>%
  mutate(ctDNA.Dynamics = case_when(
    ctDNA.MRD == "NEGATIVE" & ctDNA.6months == "NEGATIVE" ~ 1,
    ctDNA.MRD == "POSITIVE" & ctDNA.6months == "NEGATIVE" ~ 2,
    ctDNA.MRD == "NEGATIVE" & ctDNA.6months == "POSITIVE" ~ 3,
    ctDNA.MRD == "POSITIVE" & ctDNA.6months == "POSITIVE" ~ 4
  ))

survfit(Surv(time = circ_data$DFS.6mo.months, event = circ_data$DFS.Event)~ctDNA.Dynamic
s, data = circ_data)
```

```
Call: survfit(formula = Surv(time = circ_data$DFS.6mo.months, event = circ_data$DFS.Event) ~
```

```
ctDNA.Dynamics, data = circ_data)
```

66 observations deleted due to missingness

```
      n events median 0.95LCL 0.95UCL
ctDNA.Dynamics=1 157      16      NA      NA      NA
ctDNA.Dynamics=2  14       5      NA    5.52      NA
ctDNA.Dynamics=3   4       2    8.51    0.00      NA
ctDNA.Dynamics=4   5       5    2.76    2.60      NA
```

[Hide](#)

```
event_summary <- circ_data %>%
  group_by(ctDNA.Dynamics) %>%
  summarise(
    Total = n(),
    Events = sum(DFS.Event),
    Fraction = Events / n(),
    Percentage = (Events / n()) * 100
  )
print(event_summary)
```

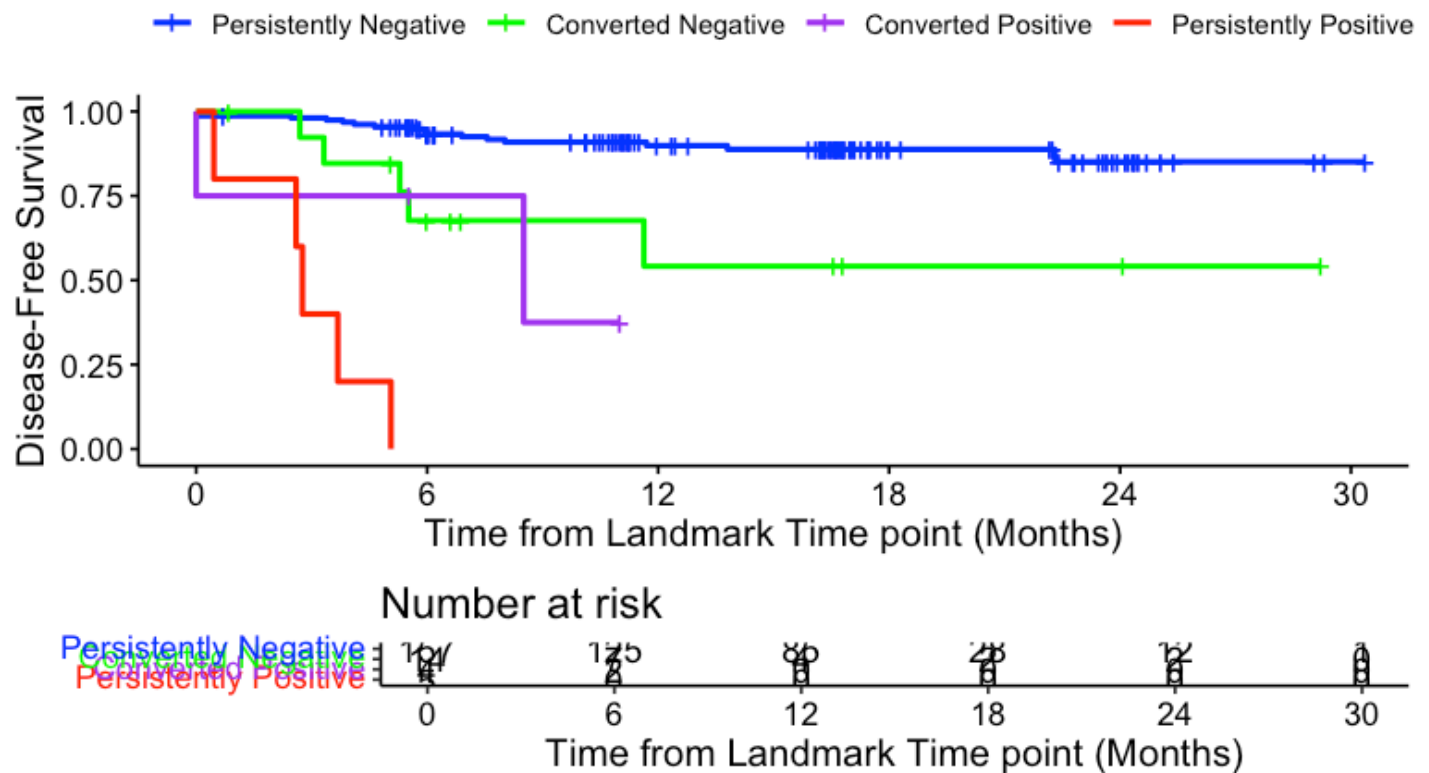
ctDNA.Dynamics <dbl>	Total <int>	Events <int>	Fraction <dbl>	Percentage <dbl>
1	157	16	0.1019108	10.19108
2	14	5	0.3571429	35.71429
3	4	2	0.5000000	50.00000
4	5	5	1.0000000	100.00000
NA	66	NA	NA	NA

5 rows

[Hide](#)

```
surv_object <- Surv(time = circ_data$DFS.6mo.months, event = circ_data$DFS.Event)
KM_curve <- survfit(surv_object ~ ctDNA.Dynamics, 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("blue","green","purple", "red"), title="DFS - ctDNA Dynamics from MRD to 6 months | All Stages", ylab= "Disease-Free Survival", xlab="Time from Landmark Time point (Months)", legend.labs=c("Persistently Negative", "Converted Negative", "Converted Positive", "Persistently Positive"), legend.title="")
```

DFS - ctDNA Dynamics from MRD to 6 months | All Stages



Hide

```
summary(KM_curve, times= c(24))
```

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

66 observations deleted due to missingness

	time	ctDNA.Dynamics=1 n.risk	n.event	survival	std.err	lower 95% CI	upper 95% CI
CI	24.000	12.000	16.000	0.851	0.045	0.736	0.9
19							

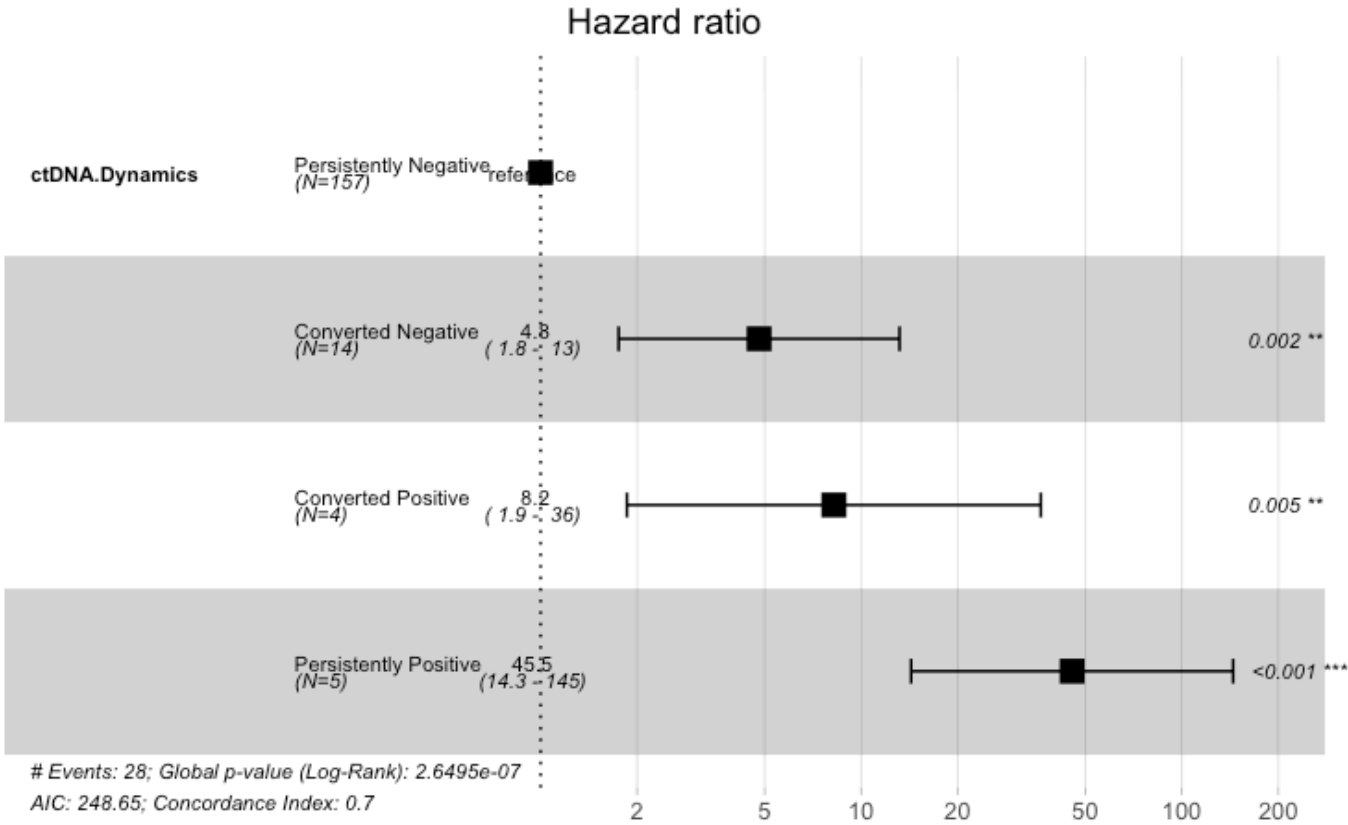
	time	ctDNA.Dynamics=2 n.risk	n.event	survival	std.err	lower 95% CI	upper 95% CI
CI	24.000	2.000	5.000	0.542	0.162	0.204	0.7
89							

```
ctDNA.Dynamics=3
time n.risk n.event survival std.err lower 95% CI upper 95% CI
```

```
ctDNA.Dynamics=4
time n.risk n.event survival std.err lower 95% CI upper 95% CI
```

[Hide](#)

```
circ_data$ctDNA.Dynamics <- factor(circ_data$ctDNA.Dynamics, levels=c("1","2","3", "4"),
labels = c("Persistently Negative", "Converted Negative","Converted Positive", "Persistently Positive"))
cox_fit <- coxph(surv_object ~ ctDNA.Dynamics, data=circ_data)
ggforest(cox_fit,data = circ_data)
```



Hide

```
summary(cox_fit)
```

```
Call:
coxph(formula = surv_object ~ ctDNA.Dynamics, data = circ_data)

n= 180, number of events= 28
(66 observations deleted due to missingness)
```

	coef	exp(coef)	se(coef)	z	Pr(> z)
ctDNA.DynamicsConverted Negative	1.5689	4.8013	0.5147	3.048	0.00230 **
ctDNA.DynamicsConverted Positive	2.1062	8.2170	0.7582	2.778	0.00547 **
ctDNA.DynamicsPersistently Positive	3.8173	45.4828	0.5900	6.470	9.8e-11 ***

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

	exp(coef)	exp(-coef)	lower .95	upper .95
ctDNA.DynamicsConverted Negative	4.801	0.20828	1.751	13.17
ctDNA.DynamicsConverted Positive	8.217	0.12170	1.859	36.32
ctDNA.DynamicsPersistently Positive	45.483	0.02199	14.310	144.57

Concordance= 0.697 (se = 0.048)
Likelihood ratio test= 33.4 on 3 df, p=3e-07
Wald test = 46.4 on 3 df, p=5e-10
Score (logrank) test = 106.2 on 3 df, p=<2e-16

#Table with recurrence sites by ctDNA at the MRD Window

Hide

```
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$CohortB=="TRUE",]
circ_data <- circ_data[circ_data$RFS.Event=="TRUE",]

circ_data_subset1 <- circ_data %>%
  select(
    Rel.Site) %>%
  mutate(
    Rel.Site = factor(Rel.Site, levels = c("Local", "Lymph Node", "Liver", "Lung", "Peri
toneum", "Brain"))))

circ_data_subset2 <- circ_data %>%
  select(
    Rel.Site,
    ctDNA.MRD) %>%
  mutate(
    Rel.Site = factor(Rel.Site, levels = c("Local", "Lymph Node", "Liver", "Lung", "Peri
toneum", "Brain")),
    ctDNA.MRD = factor(ctDNA.MRD, levels = c("NEGATIVE", "POSITIVE")))
Overall <- circ_data_subset1 %>%
  tbl_summary(
    statistic = list(
      all_continuous() ~ "{median} ({min} - {max})",
      all_categorical() ~ "{n} ({p}%))" %>%
    bold_labels()
  Overall
```

Characteristic	N = 48 ¹
Rel.Site	
Local	4 (8.3%)
Lymph Node	5 (10%)
Liver	17 (35%)
Lung	18 (38%)
Peritoneum	3 (6.3%)
Brain	1 (2.1%)
¹ n (%)	

Hide

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

Characteristic	NEGATIVE, N = 23 ¹	POSITIVE, N = 25 ¹	p-value ²
Rel.Site	<0.001		
Local	2 (8.7%)	2 (8.0%)	
Lymph Node	1 (4.3%)	4 (16%)	
Liver	2 (8.7%)	15 (60%)	
Lung	15 (65%)	3 (12%)	
Peritoneum	2 (8.7%)	1 (4.0%)	
Brain	1 (4.3%)	0 (0%)	
¹ n (%)			
² Fisher's exact test			

Hide

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

	Table 1	Table 2		
Characteristic	N = 48 ¹	NEGATIVE, N = 23 ¹	POSITIVE, N = 25 ¹	p-value ²
Rel.Site				<0.001
Local	4 (8.3%)	2 (8.7%)	2 (8.0%)	
Lymph Node	5 (10%)	1 (4.3%)	4 (16%)	
Liver	17 (35%)	2 (8.7%)	15 (60%)	
¹ n (%)				
² Fisher's exact test				

	Table 1	Table 2		
Characteristic	N = 48 ¹	NEGATIVE, N = 23 ¹	POSITIVE, N = 25 ¹	p-value ²
Lung	18 (38%)	15 (65%)	3 (12%)	
Peritoneum	3 (6.3%)	2 (8.7%)	1 (4.0%)	
Brain	1 (2.1%)	1 (4.3%)	0 (0%)	

¹ n (%)
² Fisher's exact test

Hide

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

	Table 1	Table 2		
Characteristic	N = 48 ¹	NEGATIVE, N = 23 ¹	POSITIVE, N = 25 ¹	p-value ²
Rel.Site				<0.001
Local	4 (8.3%)	2 (8.7%)	2 (8.0%)	
Lymph Node	5 (10%)	1 (4.3%)	4 (16%)	
Liver	17 (35%)	2 (8.7%)	15 (60%)	
Lung	18 (38%)	15 (65%)	3 (12%)	
Peritoneum	3 (6.3%)	2 (8.7%)	1 (4.0%)	
Brain	1 (2.1%)	1 (4.3%)	0 (0%)	

¹n (%)
²Fisher's exact test

Hide

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

#MTM/mL levels at the MRD Window by Radiological Recurrence

Hide

```
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$CohortB=="TRUE",]
circ_data <- circ_data[circ_data$ctDNA.MRD!="",]
circ_data <- circ_data[circ_data$DFS.MRD.months>=0,]
circ_data <- as.data.frame(circ_data)

# Transform p_MRD_MTM with log10
circ_data$p_MRD_MTM <- as.numeric(as.character(circ_data$p_MRD_MTM))
circ_data$RFS.Event <- factor(circ_data$RFS.Event, levels = c("FALSE", "TRUE"), labels =
c("No Recurrence", "Recurrence"))
summary_stats <- circ_data %>%
  group_by(RFS.Event) %>%
  summarise(
    median_p_MRD_MTM = median(p_MRD_MTM, na.rm = TRUE),
    range_p_MRD_MTM = paste0(min(p_MRD_MTM, na.rm = TRUE), " - ", max(p_MRD_MTM, na.rm =
TRUE))
  )
print(summary_stats)
```

RFS.Event <fctr>	median_p_MRD_MTM <dbl>	range_p_MRD_MTM <chr>
No Recurrence	0.00000000	0 - 9.694491335
Recurrence	0.06305439	0 - 645.7568074

2 rows

Hide

```
m3_1v2 <- wilcox.test(p_MRD_MTM ~ RFS.Event,
                      data = circ_data[circ_data$RFS.Event %in% c("No Recurrence", "Recu
rrence"), ],
                      na.rm = TRUE)
print(m3_1v2)
```

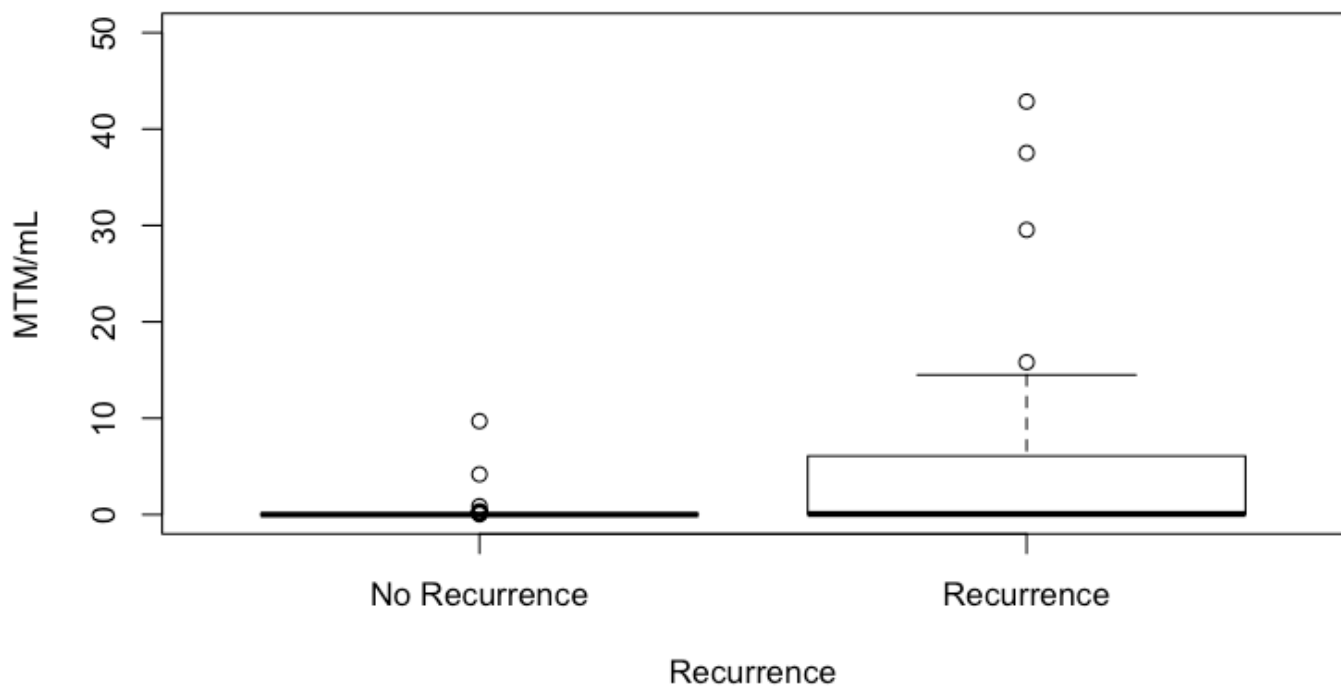
Wilcoxon rank sum test with continuity correction

data: p_MRD_MTM by RFS.Event
W = 2458, p-value < 2.2e-16
alternative hypothesis: true location shift is not equal to 0

Hide

```
boxplot(p_MRD_MTM~RFS.Event, data=circ_data, main="ctDNA MRD Window MTM - Recurrence", x
lab="Recurrence", ylab="MTM/mL", col="white",border="black", ylim = c(0, 50))
```

ctDNA MRD Window MTM - Recurrence



#MTM/mL levels at the MRD Window by Radiological Recurrence Sites

Hide

```
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$CohortB=="TRUE",]
circ_data <- circ_data[circ_data$RFS.Event=="TRUE",]
circ_data <- circ_data[circ_data$ctDNA.MRD!="",]
circ_data <- circ_data[circ_data$DFS.MRD.months>=0,]
circ_data <- as.data.frame(circ_data)

# Transform p_MRD_MTM with log10
circ_data$p_MRD_MTM <- as.numeric(as.character(circ_data$p_MRD_MTM))
circ_data$Rel.Site <- factor(circ_data$Rel.Site, levels = c("Liver", "Lymph Node", "Local", "Peritoneum", "Lung", "Brain"))
summary_stats <- circ_data %>%
  group_by(Rel.Site) %>%
  summarise(
    median_p_MRD_MTM = median(p_MRD_MTM, na.rm = TRUE),
    range_p_MRD_MTM = paste0(min(p_MRD_MTM, na.rm = TRUE), " - ", max(p_MRD_MTM, na.rm = TRUE))
  )
print(summary_stats)
```

Rel.Site	median_p_MRD_MTM	range_p_MRD_MTM
<fctr>	<dbl>	<chr>
Liver	1.66880485	0 - 645.7568074
Lymph Node	4.10239125	0 - 42.85542855
Local	0.07993897	0 - 0.2238338905
Peritoneum	0.00000000	0 - 15.80708422
Lung	0.00000000	0 - 11.24115557
Brain	0.00000000	0 - 0
6 rows		

Hide

```
kruskal_test <- kruskal.test(p_MRD_MTM ~ Rel.Site, data = circ_data)
print(kruskal_test)
```

Kruskal-Wallis rank sum test

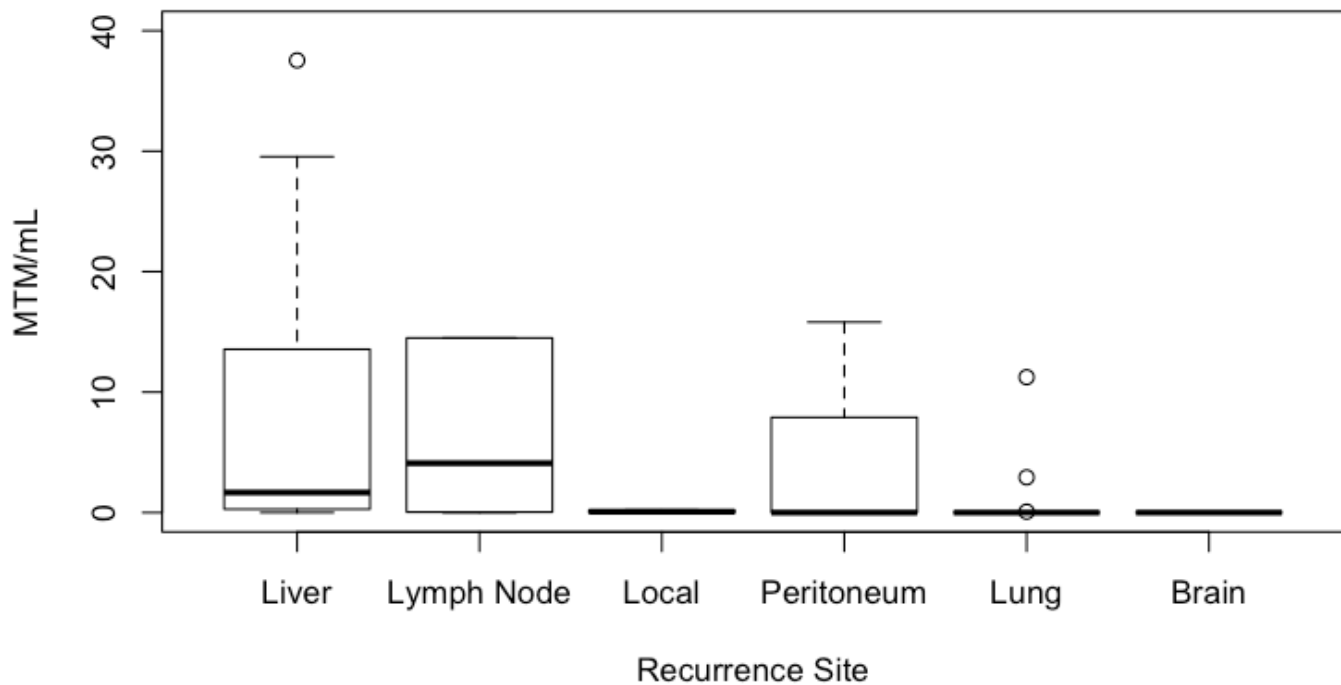
data: p_MRD_MTM by Rel.Site

Kruskal-Wallis chi-squared = 20.366, df = 5, p-value = 0.001067

Hide

```
boxplot(p_MRD_MTM~Rel.Site, data=circ_data, main="ctDNA MRD Window MTM - Recurrence Site", xlab="Recurrence Site", ylab="MTM/mL", col="white",border="black", ylim = c(0, 40))
```

ctDNA MRD Window MTM - Recurrence Site



#Barplot with Recurrence Sites (Liver vs Others) by ctDNA at the MRD Window

Hide

```
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$CohortB=="TRUE",]
circ_data <- circ_data[circ_data$RFS.Event=="TRUE",]

circ_data$ctDNA.MRD <- factor(circ_data$ctDNA.MRD, levels = c("NEGATIVE", "POSITIVE"), l
abels = c("Negative", "Positive"))
circ_data$Rel.Site <- factor(circ_data$Rel.Site, levels = c("Liver", "Lymph Node", "Loca
l", "Peritoneum", "Lung", "Brain"))
contingency_table <- table(circ_data$Rel.Site, circ_data$ctDNA.MRD)
chi_square_test <- chisq.test(contingency_table)
```

Warning: Chi-squared approximation may be incorrect

Hide

```
print(chi_square_test)
```

Pearson's Chi-squared test

```
data: contingency_table  
X-squared = 21.028, df = 5, p-value = 0.0008004
```

[Hide](#)

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

Fisher's Exact Test for Count Data

```
data: contingency_table  
p-value = 5.02e-05  
alternative hypothesis: two.sided
```

[Hide](#)

```
print(contingency_table)
```

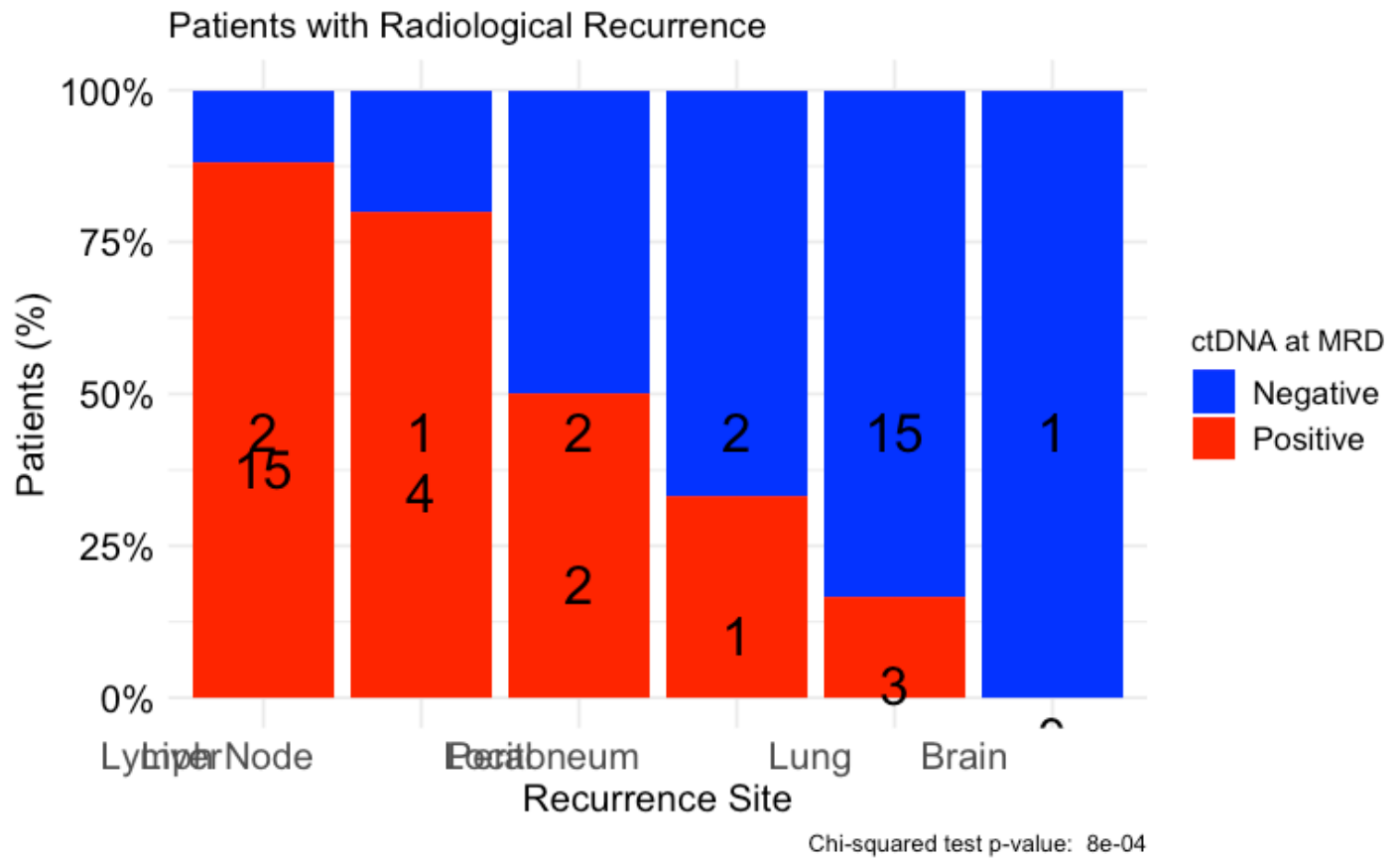
	Negative	Positive
Liver	2	15
Lymph Node	1	4
Local	2	2
Peritoneum	2	1
Lung	15	3
Brain	1	0

[Hide](#)


```

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 = "Patients with Radiological Recurrence",
        x = "Recurrence Site",
        y = "Patients (%)",
        fill = "ctDNA at MRD",
        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("Negative" = "blue", "Positive" = "red")) + # 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

```



#Detection ctDNA rates based on sites of relapse

Hide

```

# Remove existing objects and set the working directory
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$CohortB=="TRUE",]
circ_data <- circ_data[circ_data$RFS.Event=="TRUE",]

# Create a table of counts for the "Rel.Site" variable
relsite_counts <- table(circ_data$Rel.Site)
relsite_df <- as.data.frame(relsite_counts)
names(relsite_df) <- c("Rel.Site", "Count")
circ_data_pos_mrd <- circ_data[circ_data$ctDNA.MRD=="POSITIVE",]
circ_data_pos_anytime <- circ_data[circ_data$ctDNA.anytime=="POSITIVE",]
pos_counts_mrd <- table(circ_data_pos_mrd$Rel.Site)
pos_counts_anytime <- table(circ_data_pos_anytime$Rel.Site)
relsite_df$MRDPos_Count <- ifelse(is.na(match(relsite_df$Rel.Site, names(pos_counts_mrd))), 0, pos_counts_mrd[match(relsite_df$Rel.Site, names(pos_counts_mrd))])
relsite_df$MRDPos_Count[is.na(relsite_df$MRDPos_Count)] <- 0
relsite_df$AnytimePos_Count <- ifelse(is.na(match(relsite_df$Rel.Site, names(pos_counts_anytime))), 0, pos_counts_anytime[match(relsite_df$Rel.Site, names(pos_counts_anytime))])
relsite_df$AnytimePos_Count[is.na(relsite_df$AnytimePos_Count)] <- 0
relsite_df$Percent <- (relsite_df$Count / sum(relsite_df$Count)) * 100
relsite_df$MRDPos_Percent <- (relsite_df$MRDPos_Count / relsite_df$Count) * 100
relsite_df$AnytimePos_Percent <- (relsite_df$AnytimePos_Count / relsite_df$Count) * 100
total_observations <- sum(relsite_df$Count)
total_pos_mrd <- sum(relsite_df$MRDPos_Count)
total_pos_anytime <- sum(relsite_df$AnytimePos_Count)
total_row <- data.frame(Rel.Site = "Total", Count = total_observations, MRDPos_Count = total_pos_mrd, AnytimePos_Count = total_pos_anytime, Percent = 100, MRDPos_Percent = (total_pos_mrd / total_observations) * 100, AnytimePos_Percent = (total_pos_anytime / total_observations) * 100)
relsite_df <- rbind(relsite_df, total_row)
print(relsite_df)

```

Rel.Site <fctr>	Co... <int>	MRDPos_C... <dbl>	AnytimePos_Count <dbl>	Percent <dbl>	MRDPos_Perc... <dbl>	AnytimePos
Brain	1	0	0	2.083333	0.00000	
Liver	17	15	17	35.416667	88.23529	1
Local	4	2	4	8.333333	50.00000	1
Lung	18	3	10	37.500000	16.66667	
Lymph Node	5	4	5	10.416667	80.00000	1
Peritoneum	3	1	3	6.250000	33.33333	1
Total	48	25	39	100.000000	52.08333	

7 rows

Hide

```
ft <- flextable(relsite_df)
doc <- read_docx() %>%
  body_add_flextable(value = ft)
print(doc, target = "relsite_df.docx")
```

#MRD Window - Sensitivity and Specificity calculations - All Cohorts

Hide

```
#All Patients
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$CohortB=="TRUE",]
circ_data$ctDNA.MRD <- factor(circ_data$ctDNA.MRD, levels=c("NEGATIVE","POSITIVE"))
circ_data$RFS.Event <- factor(circ_data$RFS.Event, levels=c("FALSE","TRUE"))
circ_data$RFS.Event <- factor(ifelse(circ_data$RFS.Event == "FALSE", "NEGATIVE", "POSITIVE"))
conf_matrix <- table(circ_data$ctDNA.MRD, circ_data$RFS.Event)

# Calculate sensitivity and specificity manually
true_positives <- conf_matrix["POSITIVE", "POSITIVE"]
false_negatives <- conf_matrix["NEGATIVE", "POSITIVE"]
true_negatives <- conf_matrix["NEGATIVE", "NEGATIVE"]
false_positives <- conf_matrix["POSITIVE", "NEGATIVE"]
sensitivity <- true_positives / (true_positives + false_negatives)
specificity <- true_negatives / (true_negatives + false_positives)
ppv <- true_positives / (true_positives + false_positives)
npv <- true_negatives / (true_negatives + false_negatives)
print(paste("Sensitivity - All pts: ", sensitivity*100))
```

```
[1] "Sensitivity - All pts: 52.0833333333333"
```

Hide

```
print(paste("Specificity - All pts: ", specificity*100))
```

```
[1] "Specificity - All pts: 94.9748743718593"
```

Hide

```
print(paste("Positive Predictive Value (PPV) - All pts: ", ppv * 100))
```

```
[1] "Positive Predictive Value (PPV) - All pts: 71.4285714285714"
```

Hide

```
print(paste("Negative Predictive Value (NPV) – All pts: ", npv * 100))
```

```
[1] "Negative Predictive Value (NPV) – All pts: 89.1509433962264"
```

Hide

```
#Stage II Patients
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$CohortB=="TRUE",]
circ_data <- circ_data[circ_data$Stage=="II",]
circ_data$ctDNA.MRD <- factor(circ_data$ctDNA.MRD, levels=c("NEGATIVE","POSITIVE"))
circ_data$RFS.Event <- factor(circ_data$RFS.Event, levels=c("FALSE","TRUE"))
circ_data$RFS.Event <- factor(ifelse(circ_data$RFS.Event == "FALSE", "NEGATIVE", "POSITIVE"))
conf_matrix <- table(circ_data$ctDNA.MRD, circ_data$RFS.Event)

# Calculate sensitivity and specificity manually
true_positives <- conf_matrix["POSITIVE", "POSITIVE"]
false_negatives <- conf_matrix["NEGATIVE", "POSITIVE"]
true_negatives <- conf_matrix["NEGATIVE", "NEGATIVE"]
false_positives <- conf_matrix["POSITIVE", "NEGATIVE"]
sensitivity <- true_positives / (true_positives + false_negatives)
specificity <- true_negatives / (true_negatives + false_positives)
ppv <- true_positives / (true_positives + false_positives)
npv <- true_negatives / (true_negatives + false_negatives)
print(paste("Sensitivity – Stage II: ", sensitivity*100))
```

```
[1] "Sensitivity – Stage II: 37.5"
```

Hide

```
print(paste("Specificity – Stage II: ", specificity*100))
```

```
[1] "Specificity – Stage II: 100"
```

Hide

```
print(paste("Positive Predictive Value (PPV) – Stage II: ", ppv * 100))
```

```
[1] "Positive Predictive Value (PPV) – Stage II: 100"
```

Hide

```
print(paste("Negative Predictive Value (NPV) – Stage II: ", npv * 100))
```

```
[1] "Negative Predictive Value (NPV) - Stage II: 94.7916666666667"
```

Hide

```
#Stage III Patients
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$CohortB=="TRUE",]
circ_data <- circ_data[circ_data$Stage=="III",]
circ_data$ctDNA.MRD <- factor(circ_data$ctDNA.MRD, levels=c("NEGATIVE","POSITIVE"))
circ_data$RFS.Event <- factor(circ_data$RFS.Event, levels=c("FALSE","TRUE"))
circ_data$RFS.Event <- factor(ifelse(circ_data$RFS.Event == "FALSE", "NEGATIVE", "POSITIVE"))
conf_matrix <- table(circ_data$ctDNA.MRD, circ_data$RFS.Event)

# Calculate sensitivity and specificity manually
true_positives <- conf_matrix["POSITIVE", "POSITIVE"]
false_negatives <- conf_matrix["NEGATIVE", "POSITIVE"]
true_negatives <- conf_matrix["NEGATIVE", "NEGATIVE"]
false_positives <- conf_matrix["POSITIVE", "NEGATIVE"]
sensitivity <- true_positives / (true_positives + false_negatives)
specificity <- true_negatives / (true_negatives + false_positives)
ppv <- true_positives / (true_positives + false_positives)
npv <- true_negatives / (true_negatives + false_negatives)
print(paste("Sensitivity - Stage III: ", sensitivity*100))
```

```
[1] "Sensitivity - Stage III: 55"
```

Hide

```
print(paste("Specificity - Stage III: ", specificity*100))
```

```
[1] "Specificity - Stage III: 90.7407407407407"
```

Hide

```
print(paste("Positive Predictive Value (PPV) - Stage III: ", ppv * 100))
```

```
[1] "Positive Predictive Value (PPV) - Stage III: 68.75"
```

Hide

```
print(paste("Negative Predictive Value (NPV) - Stage III: ", npv * 100))
```

```
[1] "Negative Predictive Value (NPV) - Stage III: 84.4827586206897"
```

#MRD Window - Sensitivity and Specificity calculations - no ACT treated

Hide

```
#All Patients
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$CohortB=="TRUE",]
circ_data <- circ_data[circ_data$ACT==FALSE,]
circ_data$ctDNA.MRD <- factor(circ_data$ctDNA.MRD, levels=c("NEGATIVE","POSITIVE"))
circ_data$RFS.Event <- factor(circ_data$RFS.Event, levels=c("FALSE","TRUE"))
circ_data$RFS.Event <- factor(ifelse(circ_data$RFS.Event == "FALSE", "NEGATIVE", "POSITIVE"))
conf_matrix <- table(circ_data$ctDNA.MRD, circ_data$RFS.Event)

# Calculate sensitivity and specificity manually
true_positives <- conf_matrix["POSITIVE", "POSITIVE"]
false_negatives <- conf_matrix["NEGATIVE", "POSITIVE"]
true_negatives <- conf_matrix["NEGATIVE", "NEGATIVE"]
false_positives <- conf_matrix["POSITIVE", "NEGATIVE"]
sensitivity <- true_positives / (true_positives + false_negatives)
specificity <- true_negatives / (true_negatives + false_positives)
ppv <- true_positives / (true_positives + false_positives)
npv <- true_negatives / (true_negatives + false_negatives)
print(paste("Sensitivity - All pts: ", sensitivity*100))
```

```
[1] "Sensitivity - All pts: 42.8571428571429"
```

Hide

```
print(paste("Specificity - All pts: ", specificity*100))
```

```
[1] "Specificity - All pts: 99.047619047619"
```

Hide

```
print(paste("Positive Predictive Value (PPV) - All pts: ", ppv * 100))
```

```
[1] "Positive Predictive Value (PPV) - All pts: 90"
```

Hide

```
print(paste("Negative Predictive Value (NPV) - All pts: ", npv * 100))
```

```
[1] "Negative Predictive Value (NPV) - All pts: 89.6551724137931"
```

Hide

```
#Stage II Patients
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$CohortB=="TRUE",]
circ_data <- circ_data[circ_data$ACT==FALSE,]
circ_data <- circ_data[circ_data$Stage=="II",]
circ_data$ctDNA.MRD <- factor(circ_data$ctDNA.MRD, levels=c("NEGATIVE","POSITIVE"))
circ_data$RFS.Event <- factor(circ_data$RFS.Event, levels=c("FALSE","TRUE"))
circ_data$RFS.Event <- factor(ifelse(circ_data$RFS.Event == "FALSE", "NEGATIVE", "POSITIVE"))
conf_matrix <- table(circ_data$ctDNA.MRD, circ_data$RFS.Event)

# Calculate sensitivity and specificity manually
true_positives <- conf_matrix["POSITIVE", "POSITIVE"]
false_negatives <- conf_matrix["NEGATIVE", "POSITIVE"]
true_negatives <- conf_matrix["NEGATIVE", "NEGATIVE"]
false_positives <- conf_matrix["POSITIVE", "NEGATIVE"]
sensitivity <- true_positives / (true_positives + false_negatives)
specificity <- true_negatives / (true_negatives + false_positives)
ppv <- true_positives / (true_positives + false_positives)
npv <- true_negatives / (true_negatives + false_negatives)
print(paste("Sensitivity - Stage II: ", sensitivity*100))
```

```
[1] "Sensitivity - Stage II: 16.6666666666667"
```

[Hide](#)

```
print(paste("Specificity - Stage II: ", specificity*100))
```

```
[1] "Specificity - Stage II: 100"
```

[Hide](#)

```
print(paste("Positive Predictive Value (PPV) - Stage II: ", ppv * 100))
```

```
[1] "Positive Predictive Value (PPV) - Stage II: 100"
```

[Hide](#)

```
print(paste("Negative Predictive Value (NPV) - Stage II: ", npv * 100))
```

```
[1] "Negative Predictive Value (NPV) - Stage II: 93.3333333333333"
```

[Hide](#)


```
#Stage III Patients
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$CohortB=="TRUE",]
circ_data <- circ_data[circ_data$ACT==FALSE,]
circ_data <- circ_data[circ_data$Stage=="III",]
circ_data$ctDNA.MRD <- factor(circ_data$ctDNA.MRD, levels=c("NEGATIVE","POSITIVE"))
circ_data$RFS.Event <- factor(circ_data$RFS.Event, levels=c("FALSE","TRUE"))
circ_data$RFS.Event <- factor(ifelse(circ_data$RFS.Event == "FALSE", "NEGATIVE", "POSITIVE"))
conf_matrix <- table(circ_data$ctDNA.MRD, circ_data$RFS.Event)

# Calculate sensitivity and specificity manually
true_positives <- conf_matrix["POSITIVE", "POSITIVE"]
false_negatives <- conf_matrix["NEGATIVE", "POSITIVE"]
true_negatives <- conf_matrix["NEGATIVE", "NEGATIVE"]
false_positives <- conf_matrix["POSITIVE", "NEGATIVE"]
sensitivity <- true_positives / (true_positives + false_negatives)
specificity <- true_negatives / (true_negatives + false_positives)
ppv <- true_positives / (true_positives + false_positives)
npv <- true_negatives / (true_negatives + false_negatives)
print(paste("Sensitivity - Stage III: ", sensitivity*100))
```

```
[1] "Sensitivity - Stage III: 53.3333333333333"
```

[Hide](#)

```
print(paste("Specificity - Stage III: ", specificity*100))
```

```
[1] "Specificity - Stage III: 97.1428571428571"
```

[Hide](#)

```
print(paste("Positive Predictive Value (PPV) - Stage III: ", ppv * 100))
```

```
[1] "Positive Predictive Value (PPV) - Stage III: 88.8888888888889"
```

[Hide](#)

```
print(paste("Negative Predictive Value (NPV) - Stage III: ", npv * 100))
```

```
[1] "Negative Predictive Value (NPV) - Stage III: 82.9268292682927"
```

```
#MRD Window - Sensitivity and Specificity calculations - ACT treated
```

[Hide](#)

```
#All Patients
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$CohortB=="TRUE",]
circ_data <- circ_data[circ_data$ACT==TRUE,]
circ_data$ctDNA.MRD <- factor(circ_data$ctDNA.MRD, levels=c("NEGATIVE","POSITIVE"))
circ_data$RFS.Event <- factor(circ_data$RFS.Event, levels=c("FALSE","TRUE"))
circ_data$RFS.Event <- factor(ifelse(circ_data$RFS.Event == "FALSE", "NEGATIVE", "POSITIVE"))
conf_matrix <- table(circ_data$ctDNA.MRD, circ_data$RFS.Event)

# Calculate sensitivity and specificity manually
true_positives <- conf_matrix["POSITIVE", "POSITIVE"]
false_negatives <- conf_matrix["NEGATIVE", "POSITIVE"]
true_negatives <- conf_matrix["NEGATIVE", "NEGATIVE"]
false_positives <- conf_matrix["POSITIVE", "NEGATIVE"]
sensitivity <- true_positives / (true_positives + false_negatives)
specificity <- true_negatives / (true_negatives + false_positives)
ppv <- true_positives / (true_positives + false_positives)
npv <- true_negatives / (true_negatives + false_negatives)
print(paste("Sensitivity - All pts: ", sensitivity*100))
```

```
[1] "Sensitivity - All pts: 59.2592592592593"
```

[Hide](#)

```
print(paste("Specificity - All pts: ", specificity*100))
```

```
[1] "Specificity - All pts: 90.4255319148936"
```

[Hide](#)

```
print(paste("Positive Predictive Value (PPV) - All pts: ", ppv * 100))
```

```
[1] "Positive Predictive Value (PPV) - All pts: 64"
```

[Hide](#)

```
print(paste("Negative Predictive Value (NPV) - All pts: ", npv * 100))
```

```
[1] "Negative Predictive Value (NPV) - All pts: 88.5416666666667"
```

[Hide](#)

```
#Stage II Patients
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$CohortB=="TRUE",]
circ_data <- circ_data[circ_data$ACT==TRUE,]
circ_data <- circ_data[circ_data$Stage=="II",]
circ_data$ctDNA.MRD <- factor(circ_data$ctDNA.MRD, levels=c("NEGATIVE","POSITIVE"))
circ_data$RFS.Event <- factor(circ_data$RFS.Event, levels=c("FALSE","TRUE"))
circ_data$RFS.Event <- factor(ifelse(circ_data$RFS.Event == "FALSE", "NEGATIVE", "POSITIVE"))
conf_matrix <- table(circ_data$ctDNA.MRD, circ_data$RFS.Event)

# Calculate sensitivity and specificity manually
true_positives <- conf_matrix["POSITIVE", "POSITIVE"]
false_negatives <- conf_matrix["NEGATIVE", "POSITIVE"]
true_negatives <- conf_matrix["NEGATIVE", "NEGATIVE"]
false_positives <- conf_matrix["POSITIVE", "NEGATIVE"]
sensitivity <- true_positives / (true_positives + false_negatives)
specificity <- true_negatives / (true_negatives + false_positives)
ppv <- true_positives / (true_positives + false_positives)
npv <- true_negatives / (true_negatives + false_negatives)
print(paste("Sensitivity - Stage II: ", sensitivity*100))
```

```
[1] "Sensitivity - Stage II: 100"
```

[Hide](#)

```
print(paste("Specificity - Stage II: ", specificity*100))
```

```
[1] "Specificity - Stage II: 100"
```

[Hide](#)

```
print(paste("Positive Predictive Value (PPV) - Stage II: ", ppv * 100))
```

```
[1] "Positive Predictive Value (PPV) - Stage II: 100"
```

[Hide](#)

```
print(paste("Negative Predictive Value (NPV) - Stage II: ", npv * 100))
```

```
[1] "Negative Predictive Value (NPV) - Stage II: 100"
```

[Hide](#)

```
#Stage III Patients
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$CohortB=="TRUE",]
circ_data <- circ_data[circ_data$ACT==TRUE,]
circ_data <- circ_data[circ_data$Stage=="III",]
circ_data$ctDNA.MRD <- factor(circ_data$ctDNA.MRD, levels=c("NEGATIVE","POSITIVE"))
circ_data$RFS.Event <- factor(circ_data$RFS.Event, levels=c("FALSE","TRUE"))
circ_data$RFS.Event <- factor(ifelse(circ_data$RFS.Event == "FALSE", "NEGATIVE", "POSITIVE"))
conf_matrix <- table(circ_data$ctDNA.MRD, circ_data$RFS.Event)

# Calculate sensitivity and specificity manually
true_positives <- conf_matrix["POSITIVE", "POSITIVE"]
false_negatives <- conf_matrix["NEGATIVE", "POSITIVE"]
true_negatives <- conf_matrix["NEGATIVE", "NEGATIVE"]
false_positives <- conf_matrix["POSITIVE", "NEGATIVE"]
sensitivity <- true_positives / (true_positives + false_negatives)
specificity <- true_negatives / (true_negatives + false_positives)
ppv <- true_positives / (true_positives + false_positives)
npv <- true_negatives / (true_negatives + false_negatives)
print(paste("Sensitivity - Stage III: ", sensitivity*100))
```

```
[1] "Sensitivity - Stage III: 56"
```

[Hide](#)

```
print(paste("Specificity - Stage III: ", specificity*100))
```

```
[1] "Specificity - Stage III: 87.6712328767123"
```

[Hide](#)

```
print(paste("Positive Predictive Value (PPV) - Stage III: ", ppv * 100))
```

```
[1] "Positive Predictive Value (PPV) - Stage III: 60.8695652173913"
```

[Hide](#)

```
print(paste("Negative Predictive Value (NPV) - Stage III: ", npv * 100))
```

```
[1] "Negative Predictive Value (NPV) - Stage III: 85.3333333333333"
```

```
#Surveillance Window - Sensitivity and Specificity calculations - All Cohorts
```

[Hide](#)

```
#All Patients
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$CohortB=="TRUE",]
circ_data$ctDNA.Surveillance <- factor(circ_data$ctDNA.Surveillance, levels=c("NEGATIVE", "POSITIVE"))
circ_data$RFS.Event <- factor(circ_data$RFS.Event, levels=c("FALSE", "TRUE"))
circ_data$RFS.Event <- factor(ifelse(circ_data$RFS.Event == "FALSE", "NEGATIVE", "POSITIVE"))
conf_matrix <- table(circ_data$ctDNA.Surveillance, circ_data$RFS.Event)

# Calculate sensitivity and specificity manually
true_positives <- conf_matrix["POSITIVE", "POSITIVE"]
false_negatives <- conf_matrix["NEGATIVE", "POSITIVE"]
true_negatives <- conf_matrix["NEGATIVE", "NEGATIVE"]
false_positives <- conf_matrix["POSITIVE", "NEGATIVE"]
sensitivity <- true_positives / (true_positives + false_negatives)
specificity <- true_negatives / (true_negatives + false_positives)
ppv <- true_positives / (true_positives + false_positives)
npv <- true_negatives / (true_negatives + false_negatives)
print(paste("Sensitivity - All pts: ", sensitivity*100))
```

```
[1] "Sensitivity - All pts: 83.3333333333333"
```

[Hide](#)

```
print(paste("Specificity - All pts: ", specificity*100))
```

```
[1] "Specificity - All pts: 94.9238578680203"
```

[Hide](#)

```
print(paste("Positive Predictive Value (PPV) - All pts: ", ppv * 100))
```

```
[1] "Positive Predictive Value (PPV) - All pts: 75"
```

[Hide](#)

```
print(paste("Negative Predictive Value (NPV) - All pts: ", npv * 100))
```

```
[1] "Negative Predictive Value (NPV) - All pts: 96.8911917098446"
```

[Hide](#)

```
#Stage II Patients
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$CohortB=="TRUE",]
circ_data <- circ_data[circ_data$Stage=="II",]
circ_data$ctDNA.Surveillance <- factor(circ_data$ctDNA.Surveillance, levels=c("NEGATIVE", "POSITIVE"))
circ_data$RFS.Event <- factor(circ_data$RFS.Event, levels=c("FALSE", "TRUE"))
circ_data$RFS.Event <- factor(ifelse(circ_data$RFS.Event == "FALSE", "NEGATIVE", "POSITIVE"))
conf_matrix <- table(circ_data$ctDNA.Surveillance, circ_data$RFS.Event)

# Calculate sensitivity and specificity manually
true_positives <- conf_matrix["POSITIVE", "POSITIVE"]
false_negatives <- conf_matrix["NEGATIVE", "POSITIVE"]
true_negatives <- conf_matrix["NEGATIVE", "NEGATIVE"]
false_positives <- conf_matrix["POSITIVE", "NEGATIVE"]
sensitivity <- true_positives / (true_positives + false_negatives)
specificity <- true_negatives / (true_negatives + false_positives)
ppv <- true_positives / (true_positives + false_positives)
npv <- true_negatives / (true_negatives + false_negatives)
print(paste("Sensitivity - Stage II: ", sensitivity*100))
```

```
[1] "Sensitivity - Stage II: 100"
```

[Hide](#)

```
print(paste("Specificity - Stage II: ", specificity*100))
```

```
[1] "Specificity - Stage II: 96.6292134831461"
```

[Hide](#)

```
print(paste("Positive Predictive Value (PPV) - Stage II: ", ppv * 100))
```

```
[1] "Positive Predictive Value (PPV) - Stage II: 62.5"
```

[Hide](#)

```
print(paste("Negative Predictive Value (NPV) - Stage II: ", npv * 100))
```

```
[1] "Negative Predictive Value (NPV) - Stage II: 100"
```

[Hide](#)

```
#Stage III Patients
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$CohortB=="TRUE",]
circ_data <- circ_data[circ_data$Stage=="III",]
circ_data$ctDNA.Surveillance <- factor(circ_data$ctDNA.Surveillance, levels=c("NEGATIVE", "POSITIVE"))
circ_data$RFS.Event <- factor(circ_data$RFS.Event, levels=c("FALSE", "TRUE"))
circ_data$RFS.Event <- factor(ifelse(circ_data$RFS.Event == "FALSE", "NEGATIVE", "POSITIVE"))
conf_matrix <- table(circ_data$ctDNA.Surveillance, circ_data$RFS.Event)

# Calculate sensitivity and specificity manually
true_positives <- conf_matrix["POSITIVE", "POSITIVE"]
false_negatives <- conf_matrix["NEGATIVE", "POSITIVE"]
true_negatives <- conf_matrix["NEGATIVE", "NEGATIVE"]
false_positives <- conf_matrix["POSITIVE", "NEGATIVE"]
sensitivity <- true_positives / (true_positives + false_negatives)
specificity <- true_negatives / (true_negatives + false_positives)
ppv <- true_positives / (true_positives + false_positives)
npv <- true_negatives / (true_negatives + false_negatives)
print(paste("Sensitivity - Stage III: ", sensitivity*100))
```

```
[1] "Sensitivity - Stage III: 80.6451612903226"
```

[Hide](#)

```
print(paste("Specificity - Stage III: ", specificity*100))
```

```
[1] "Specificity - Stage III: 93.5185185185185"
```

[Hide](#)

```
print(paste("Positive Predictive Value (PPV) - Stage III: ", ppv * 100))
```

```
[1] "Positive Predictive Value (PPV) - Stage III: 78.125"
```

[Hide](#)

```
print(paste("Negative Predictive Value (NPV) - Stage III: ", npv * 100))
```

```
[1] "Negative Predictive Value (NPV) - Stage III: 94.392523364486"
```

```
#Surveillance Window - Sensitivity and Specificity calculations - non ACT treated
```

[Hide](#)

```
#All Patients
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$CohortB=="TRUE",]
circ_data <- circ_data[circ_data$ACT==FALSE,]
circ_data$ctDNA.Surveillance <- factor(circ_data$ctDNA.Surveillance, levels=c("NEGATIVE", "POSITIVE"))
circ_data$RFS.Event <- factor(circ_data$RFS.Event, levels=c("FALSE", "TRUE"))
circ_data$RFS.Event <- factor(ifelse(circ_data$RFS.Event == "FALSE", "NEGATIVE", "POSITIVE"))
conf_matrix <- table(circ_data$ctDNA.Surveillance, circ_data$RFS.Event)

# Calculate sensitivity and specificity manually
true_positives <- conf_matrix["POSITIVE", "POSITIVE"]
false_negatives <- conf_matrix["NEGATIVE", "POSITIVE"]
true_negatives <- conf_matrix["NEGATIVE", "NEGATIVE"]
false_positives <- conf_matrix["POSITIVE", "NEGATIVE"]
sensitivity <- true_positives / (true_positives + false_negatives)
specificity <- true_negatives / (true_negatives + false_positives)
ppv <- true_positives / (true_positives + false_positives)
npv <- true_negatives / (true_negatives + false_negatives)
print(paste("Sensitivity - All pts: ", sensitivity*100))
```

```
[1] "Sensitivity - All pts: 100"
```

[Hide](#)

```
print(paste("Specificity - All pts: ", specificity*100))
```

```
[1] "Specificity - All pts: 95.0980392156863"
```

[Hide](#)

```
print(paste("Positive Predictive Value (PPV) - All pts: ", ppv * 100))
```

```
[1] "Positive Predictive Value (PPV) - All pts: 75"
```

[Hide](#)

```
print(paste("Negative Predictive Value (NPV) - All pts: ", npv * 100))
```

```
[1] "Negative Predictive Value (NPV) - All pts: 100"
```

[Hide](#)


```
#Stage II Patients
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$CohortB=="TRUE",]
circ_data <- circ_data[circ_data$ACT==FALSE,]
circ_data <- circ_data[circ_data$Stage=="II",]
circ_data$ctDNA.Surveillance <- factor(circ_data$ctDNA.Surveillance, levels=c("NEGATIVE", "POSITIVE"))
circ_data$RFS.Event <- factor(circ_data$RFS.Event, levels=c("FALSE", "TRUE"))
circ_data$RFS.Event <- factor(ifelse(circ_data$RFS.Event == "FALSE", "NEGATIVE", "POSITIVE"))
conf_matrix <- table(circ_data$ctDNA.Surveillance, circ_data$RFS.Event)

# Calculate sensitivity and specificity manually
true_positives <- conf_matrix["POSITIVE", "POSITIVE"]
false_negatives <- conf_matrix["NEGATIVE", "POSITIVE"]
true_negatives <- conf_matrix["NEGATIVE", "NEGATIVE"]
false_positives <- conf_matrix["POSITIVE", "NEGATIVE"]
sensitivity <- true_positives / (true_positives + false_negatives)
specificity <- true_negatives / (true_negatives + false_positives)
ppv <- true_positives / (true_positives + false_positives)
npv <- true_negatives / (true_negatives + false_negatives)
print(paste("Sensitivity - Stage II: ", sensitivity*100))
```

```
[1] "Sensitivity - Stage II: 100"
```

[Hide](#)

```
print(paste("Specificity - Stage II: ", specificity*100))
```

```
[1] "Specificity - Stage II: 95.5223880597015"
```

[Hide](#)

```
print(paste("Positive Predictive Value (PPV) - Stage II: ", ppv * 100))
```

```
[1] "Positive Predictive Value (PPV) - Stage II: 57.1428571428571"
```

[Hide](#)

```
print(paste("Negative Predictive Value (NPV) - Stage II: ", npv * 100))
```

```
[1] "Negative Predictive Value (NPV) - Stage II: 100"
```

[Hide](#)

```
#Stage III Patients
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$CohortB=="TRUE",]
circ_data <- circ_data[circ_data$ACT==FALSE,]
circ_data <- circ_data[circ_data$Stage=="III",]
circ_data$ctDNA.Surveillance <- factor(circ_data$ctDNA.Surveillance, levels=c("NEGATIVE", "POSITIVE"))
circ_data$RFS.Event <- factor(circ_data$RFS.Event, levels=c("FALSE", "TRUE"))
circ_data$RFS.Event <- factor(ifelse(circ_data$RFS.Event == "FALSE", "NEGATIVE", "POSITIVE"))
conf_matrix <- table(circ_data$ctDNA.Surveillance, circ_data$RFS.Event)

# Calculate sensitivity and specificity manually
true_positives <- conf_matrix["POSITIVE", "POSITIVE"]
false_negatives <- conf_matrix["NEGATIVE", "POSITIVE"]
true_negatives <- conf_matrix["NEGATIVE", "NEGATIVE"]
false_positives <- conf_matrix["POSITIVE", "NEGATIVE"]
sensitivity <- true_positives / (true_positives + false_negatives)
specificity <- true_negatives / (true_negatives + false_positives)
ppv <- true_positives / (true_positives + false_positives)
npv <- true_negatives / (true_negatives + false_negatives)
print(paste("Sensitivity - Stage III: ", sensitivity*100))
```

```
[1] "Sensitivity - Stage III: 100"
```

[Hide](#)

```
print(paste("Specificity - Stage III: ", specificity*100))
```

```
[1] "Specificity - Stage III: 94.2857142857143"
```

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```
print(paste("Positive Predictive Value (PPV) - Stage III: ", ppv * 100))
```

```
[1] "Positive Predictive Value (PPV) - Stage III: 84.6153846153846"
```

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```
print(paste("Negative Predictive Value (NPV) - Stage III: ", npv * 100))
```

```
[1] "Negative Predictive Value (NPV) - Stage III: 100"
```

```
#Surveillance Window - Sensitivity and Specificity calculations - ACT treated
```

[Hide](#)

```
#All Patients
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$CohortB=="TRUE",]
circ_data <- circ_data[circ_data$ACT==TRUE,]
circ_data$ctDNA.Surveillance <- factor(circ_data$ctDNA.Surveillance, levels=c("NEGATIVE", "POSITIVE"))
circ_data$RFS.Event <- factor(circ_data$RFS.Event, levels=c("FALSE", "TRUE"))
circ_data$RFS.Event <- factor(ifelse(circ_data$RFS.Event == "FALSE", "NEGATIVE", "POSITIVE"))
conf_matrix <- table(circ_data$ctDNA.Surveillance, circ_data$RFS.Event)

# Calculate sensitivity and specificity manually
true_positives <- conf_matrix["POSITIVE", "POSITIVE"]
false_negatives <- conf_matrix["NEGATIVE", "POSITIVE"]
true_negatives <- conf_matrix["NEGATIVE", "NEGATIVE"]
false_positives <- conf_matrix["POSITIVE", "NEGATIVE"]
sensitivity <- true_positives / (true_positives + false_negatives)
specificity <- true_negatives / (true_negatives + false_positives)
ppv <- true_positives / (true_positives + false_positives)
npv <- true_negatives / (true_negatives + false_negatives)
print(paste("Sensitivity - All pts: ", sensitivity*100))
```

```
[1] "Sensitivity - All pts: 71.4285714285714"
```

[Hide](#)

```
print(paste("Specificity - All pts: ", specificity*100))
```

```
[1] "Specificity - All pts: 94.7368421052632"
```

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```
print(paste("Positive Predictive Value (PPV) - All pts: ", ppv * 100))
```

```
[1] "Positive Predictive Value (PPV) - All pts: 75"
```

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```
print(paste("Negative Predictive Value (NPV) - All pts: ", npv * 100))
```

```
[1] "Negative Predictive Value (NPV) - All pts: 93.75"
```

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```
#Stage II Patients
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$CohortB=="TRUE",]
circ_data <- circ_data[circ_data$ACT==TRUE,]
circ_data <- circ_data[circ_data$Stage=="II",]
circ_data$ctDNA.Surveillance <- factor(circ_data$ctDNA.Surveillance, levels=c("NEGATIVE", "POSITIVE"))
circ_data$RFS.Event <- factor(circ_data$RFS.Event, levels=c("FALSE", "TRUE"))
circ_data$RFS.Event <- factor(ifelse(circ_data$RFS.Event == "FALSE", "NEGATIVE", "POSITIVE"))
conf_matrix <- table(circ_data$ctDNA.Surveillance, circ_data$RFS.Event)

# Calculate sensitivity and specificity manually
true_positives <- conf_matrix["POSITIVE", "POSITIVE"]
false_negatives <- conf_matrix["NEGATIVE", "POSITIVE"]
true_negatives <- conf_matrix["NEGATIVE", "NEGATIVE"]
false_positives <- conf_matrix["POSITIVE", "NEGATIVE"]
sensitivity <- true_positives / (true_positives + false_negatives)
specificity <- true_negatives / (true_negatives + false_positives)
ppv <- true_positives / (true_positives + false_positives)
npv <- true_negatives / (true_negatives + false_negatives)
print(paste("Sensitivity - Stage II: ", sensitivity*100))
```

```
[1] "Sensitivity - Stage II: 100"
```

[Hide](#)

```
print(paste("Specificity - Stage II: ", specificity*100))
```

```
[1] "Specificity - Stage II: 100"
```

[Hide](#)

```
print(paste("Positive Predictive Value (PPV) - Stage II: ", ppv * 100))
```

```
[1] "Positive Predictive Value (PPV) - Stage II: 100"
```

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```
print(paste("Negative Predictive Value (NPV) - Stage II: ", npv * 100))
```

```
[1] "Negative Predictive Value (NPV) - Stage II: 100"
```

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```
#Stage III Patients
rm(list=ls())
setwd("~/Downloads")
circ_data <- read.csv("Galaxy Data_20240603 Complete Dataset.csv")
circ_data <- circ_data[circ_data$CohortB=="TRUE",]
circ_data <- circ_data[circ_data$ACT==TRUE,]
circ_data <- circ_data[circ_data$Stage=="III",]
circ_data$ctDNA.Surveillance <- factor(circ_data$ctDNA.Surveillance, levels=c("NEGATIVE", "POSITIVE"))
circ_data$RFS.Event <- factor(circ_data$RFS.Event, levels=c("FALSE", "TRUE"))
circ_data$RFS.Event <- factor(ifelse(circ_data$RFS.Event == "FALSE", "NEGATIVE", "POSITIVE"))
conf_matrix <- table(circ_data$ctDNA.Surveillance, circ_data$RFS.Event)

# Calculate sensitivity and specificity manually
true_positives <- conf_matrix["POSITIVE", "POSITIVE"]
false_negatives <- conf_matrix["NEGATIVE", "POSITIVE"]
true_negatives <- conf_matrix["NEGATIVE", "NEGATIVE"]
false_positives <- conf_matrix["POSITIVE", "NEGATIVE"]
sensitivity <- true_positives / (true_positives + false_negatives)
specificity <- true_negatives / (true_negatives + false_positives)
ppv <- true_positives / (true_positives + false_positives)
npv <- true_negatives / (true_negatives + false_negatives)
print(paste("Sensitivity - Stage III: ", sensitivity*100))
```

```
[1] "Sensitivity - Stage III: 70"
```

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```
print(paste("Specificity - Stage III: ", specificity*100))
```

```
[1] "Specificity - Stage III: 93.1506849315068"
```

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```
print(paste("Positive Predictive Value (PPV) - Stage III: ", ppv * 100))
```

```
[1] "Positive Predictive Value (PPV) - Stage III: 73.6842105263158"
```

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```
print(paste("Negative Predictive Value (NPV) - Stage III: ", npv * 100))
```

```
[1] "Negative Predictive Value (NPV) - Stage III: 91.8918918918919"
```