

help("forestplotMV")

change ctdna group: Decrease from baseline: (Reference)

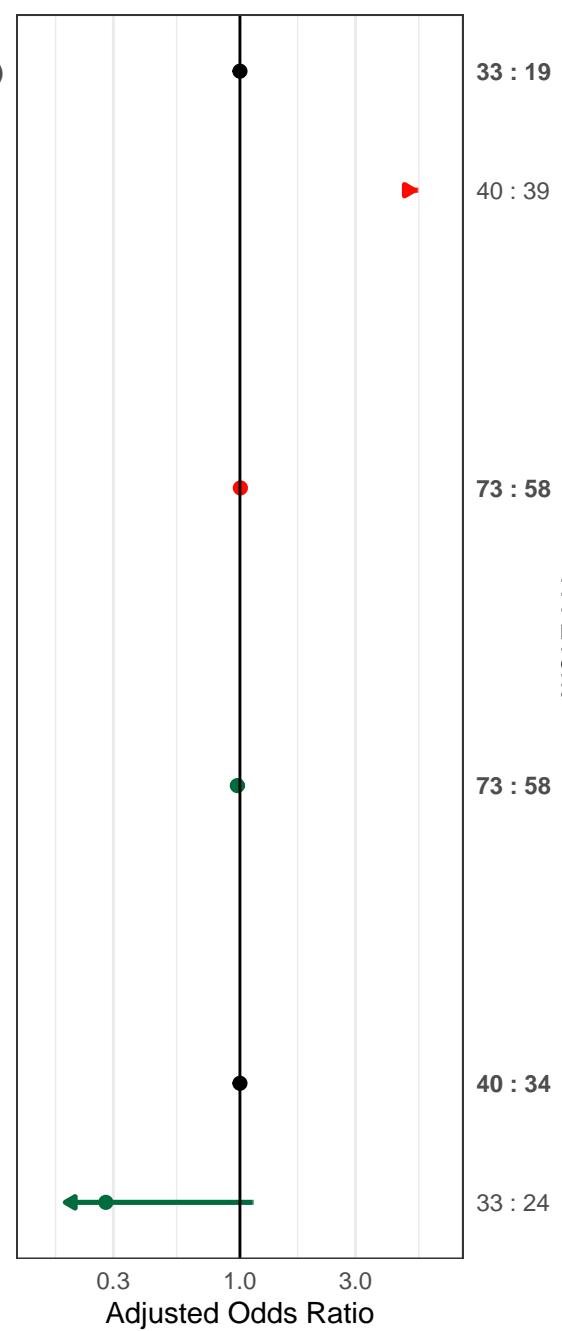
Increase from baseline: 32.56 (5.40, 639.81)

I size: 1.00 (0.99, 1.02)

age: 0.98 (0.91, 1.04)

sex: Female: (Reference)

Male: 0.28 (0.06, 1.13)



help("forestplotMV")

change ctdna group: Decrease from baseline: (Reference)

Increase from baseline: 32.56 (5.40, 639.81)

(Unadjusted): 28.74 (5.20, 540.18)

I size: 1.00 (0.99, 1.02)

(Unadjusted): 1.01 (1.00, 1.02)

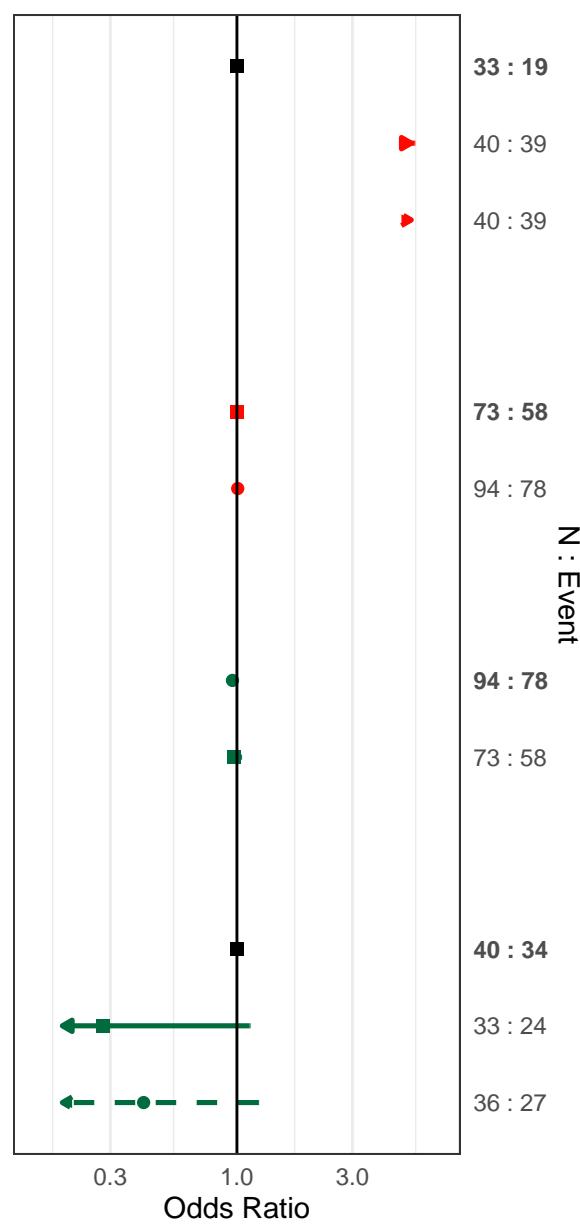
age: 0.96 (0.91, 1.00)

NA: 0.98 (0.91, 1.04)

sex: Female: (Reference)

Male: 0.28 (0.06, 1.13)

(Unadjusted): 0.41 (0.13, 1.22)



■ Adjusted ● Unadjusted

help("forestplotUV")

change ctdna group: Decrease from baseline: (Reference)

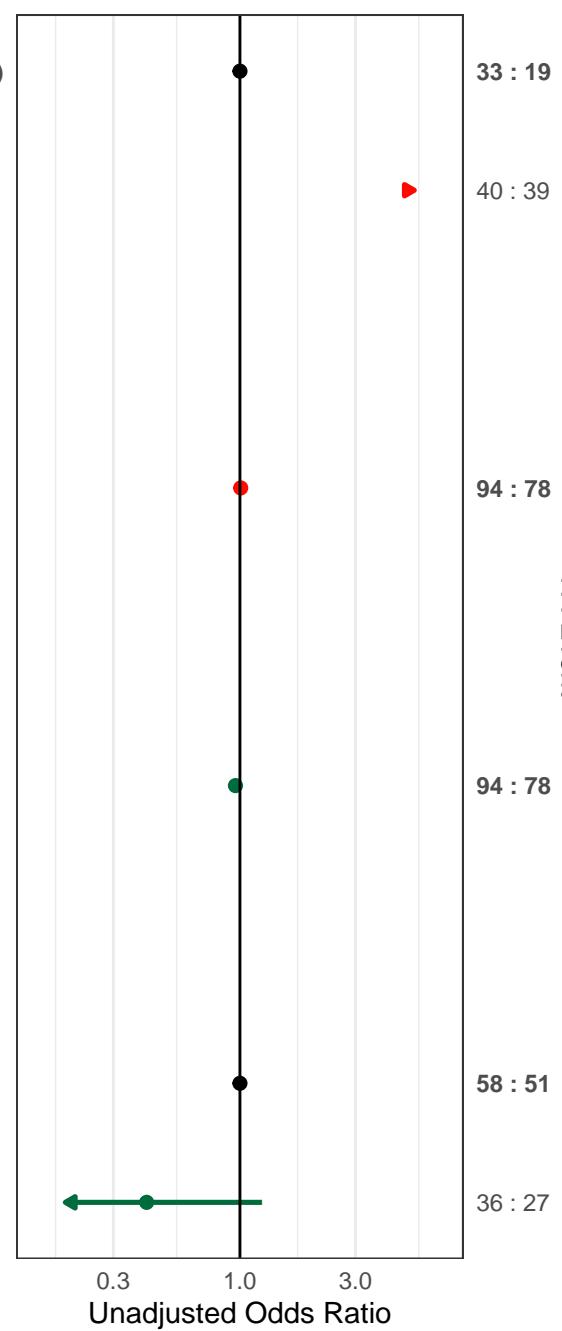
Increase from baseline: 28.74 (5.20, 540.18)

I size: 1.01 (1.00, 1.02)

age: 0.96 (0.91, 1.00)

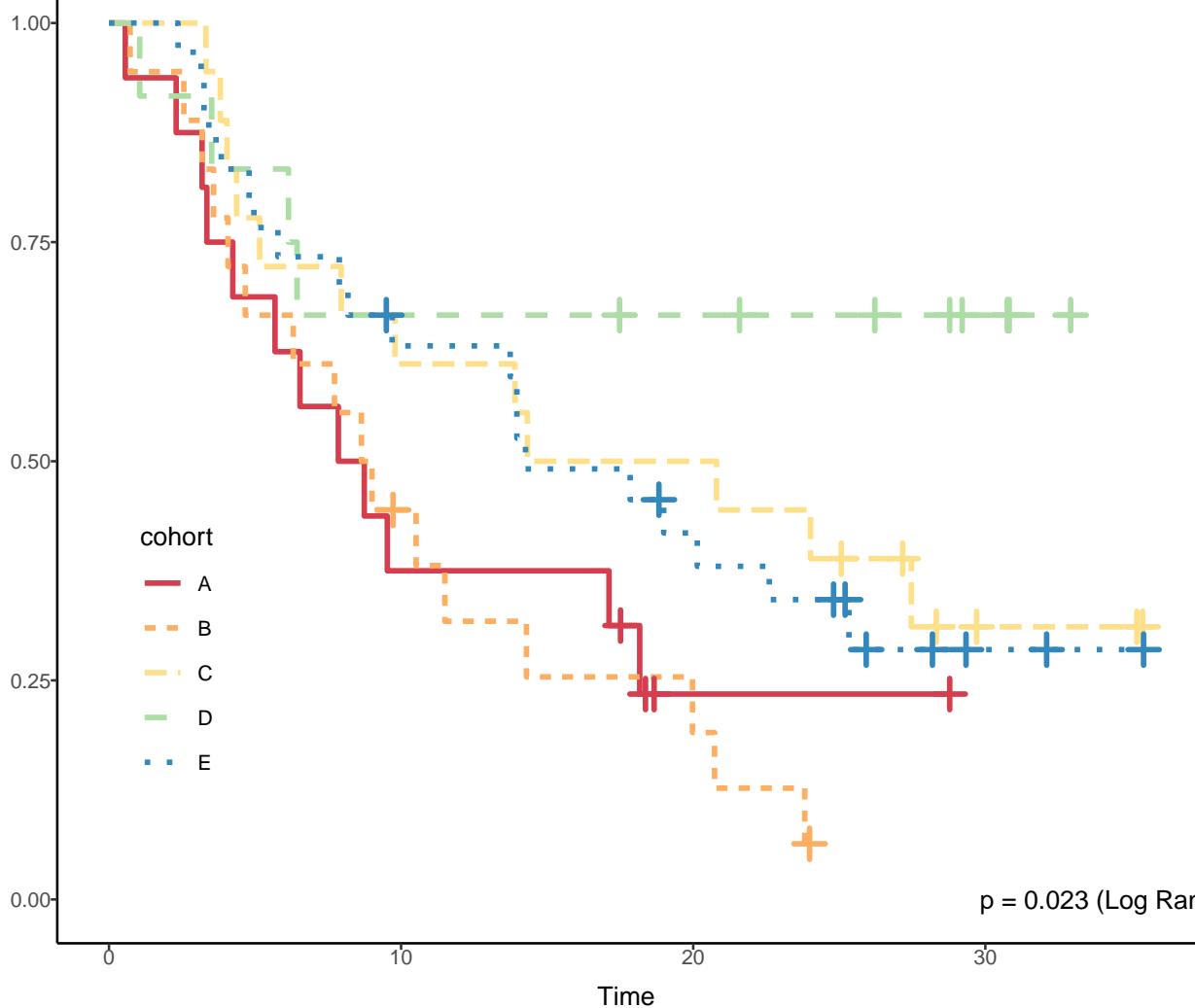
sex: Female: (Reference)

Male: 0.41 (0.13, 1.22)



Kaplan–Meier Plot

Survival Probability



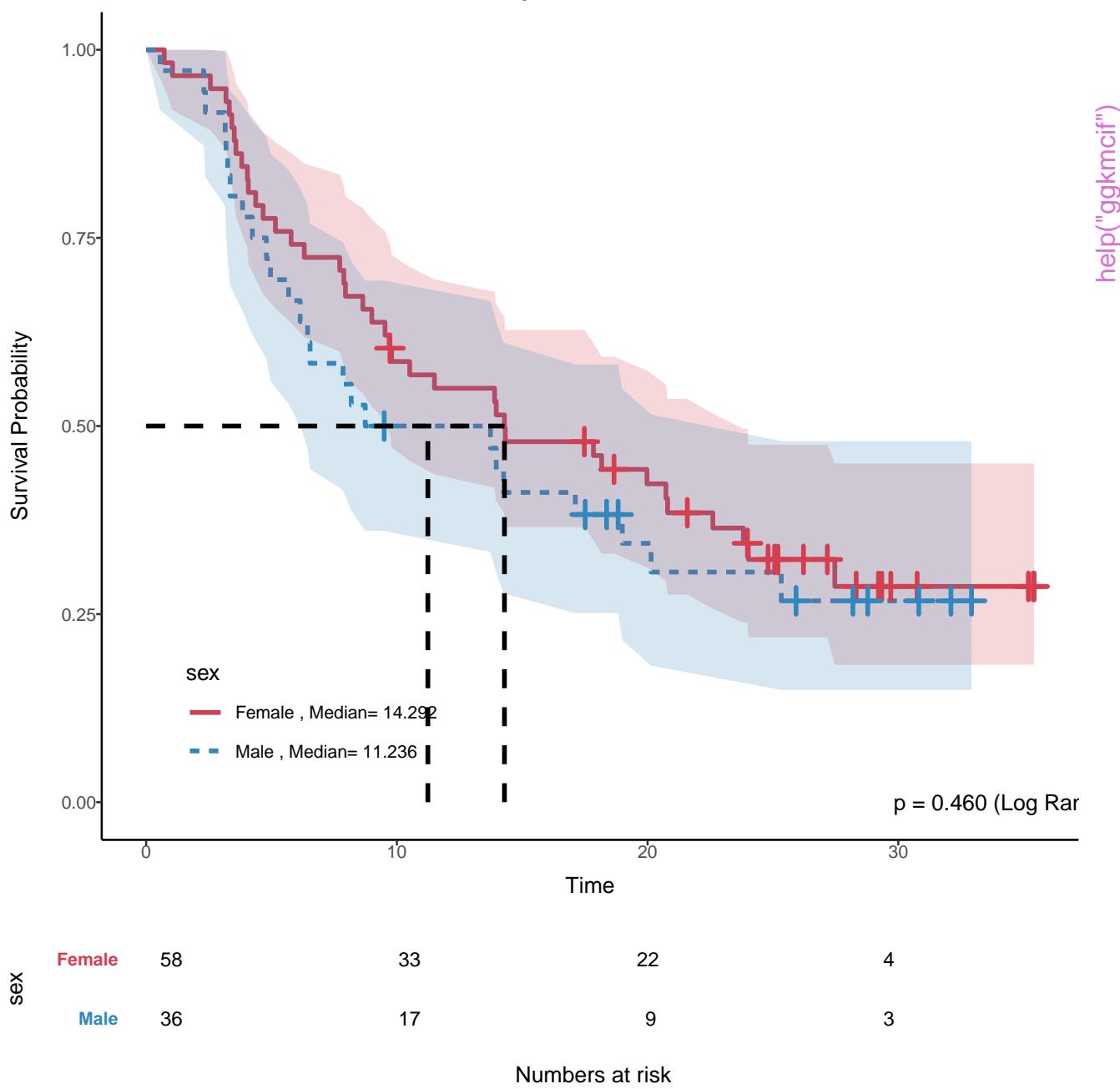
cohort

A	16	6	1	0
B	18	7	3	0
C	18	11	9	2
D	12	8	7	3
E	30	18	11	2

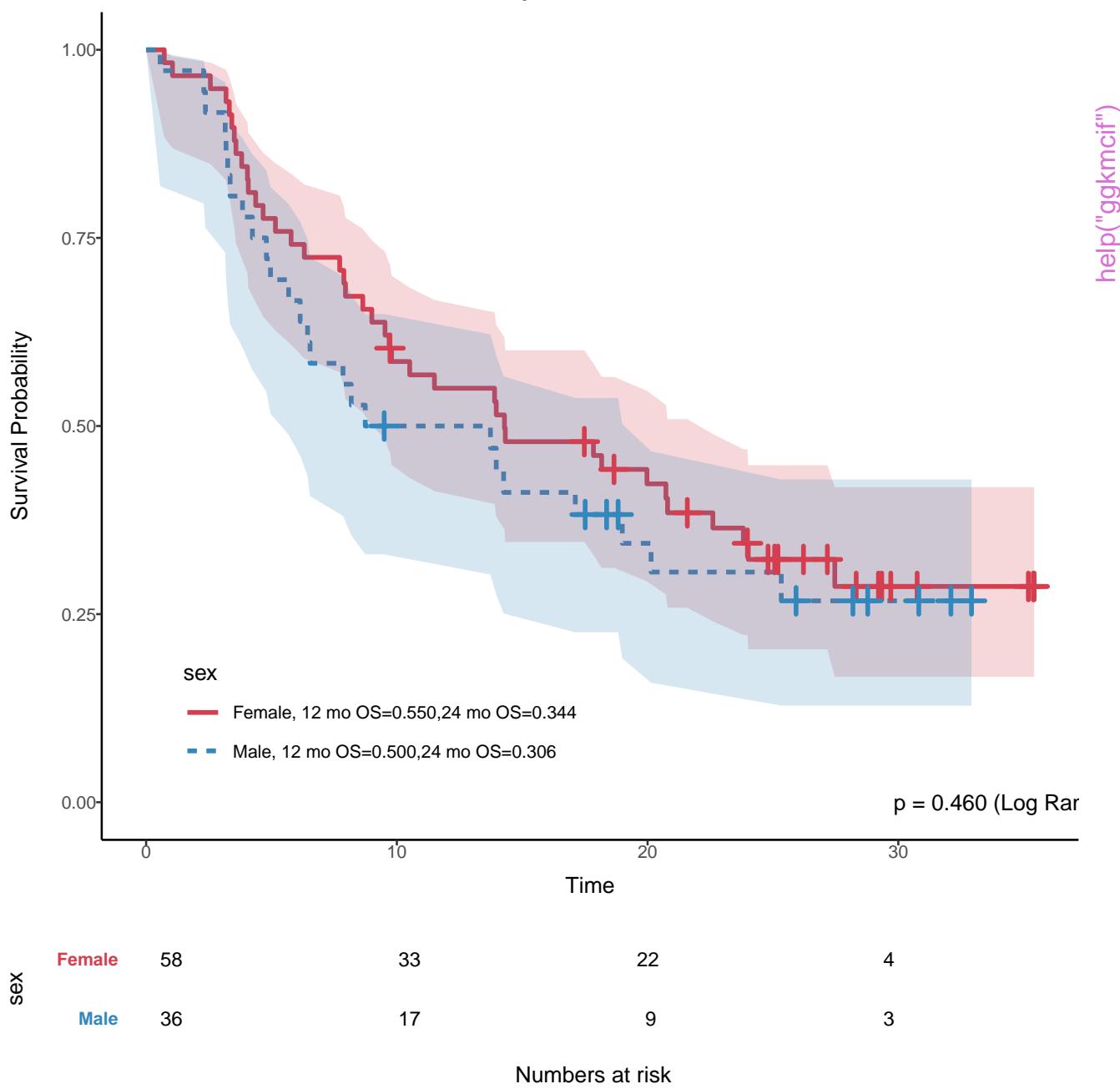
Numbers at risk

help("ggkmcf")

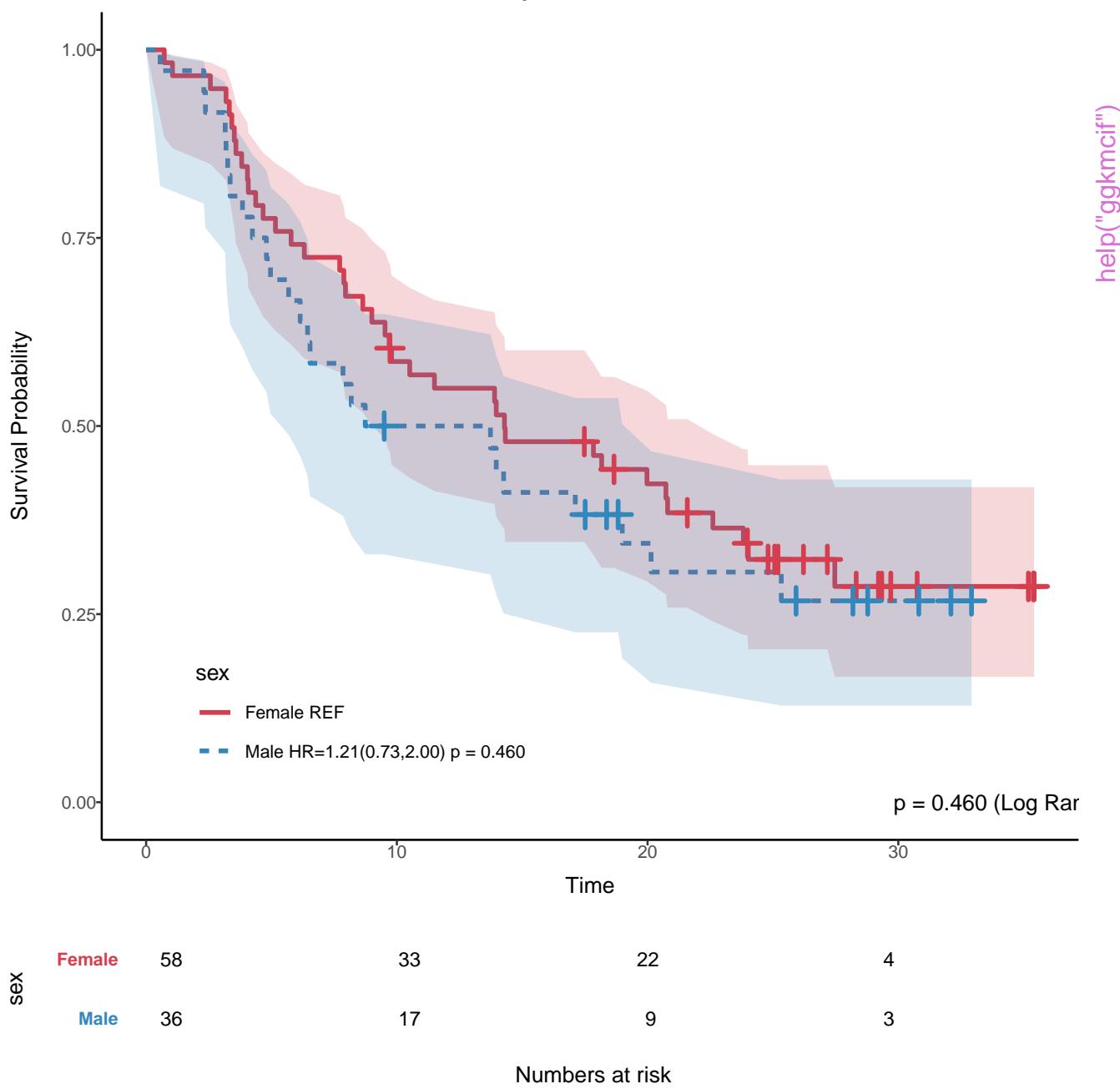
Kaplan–Meier Plot



Kaplan–Meier Plot



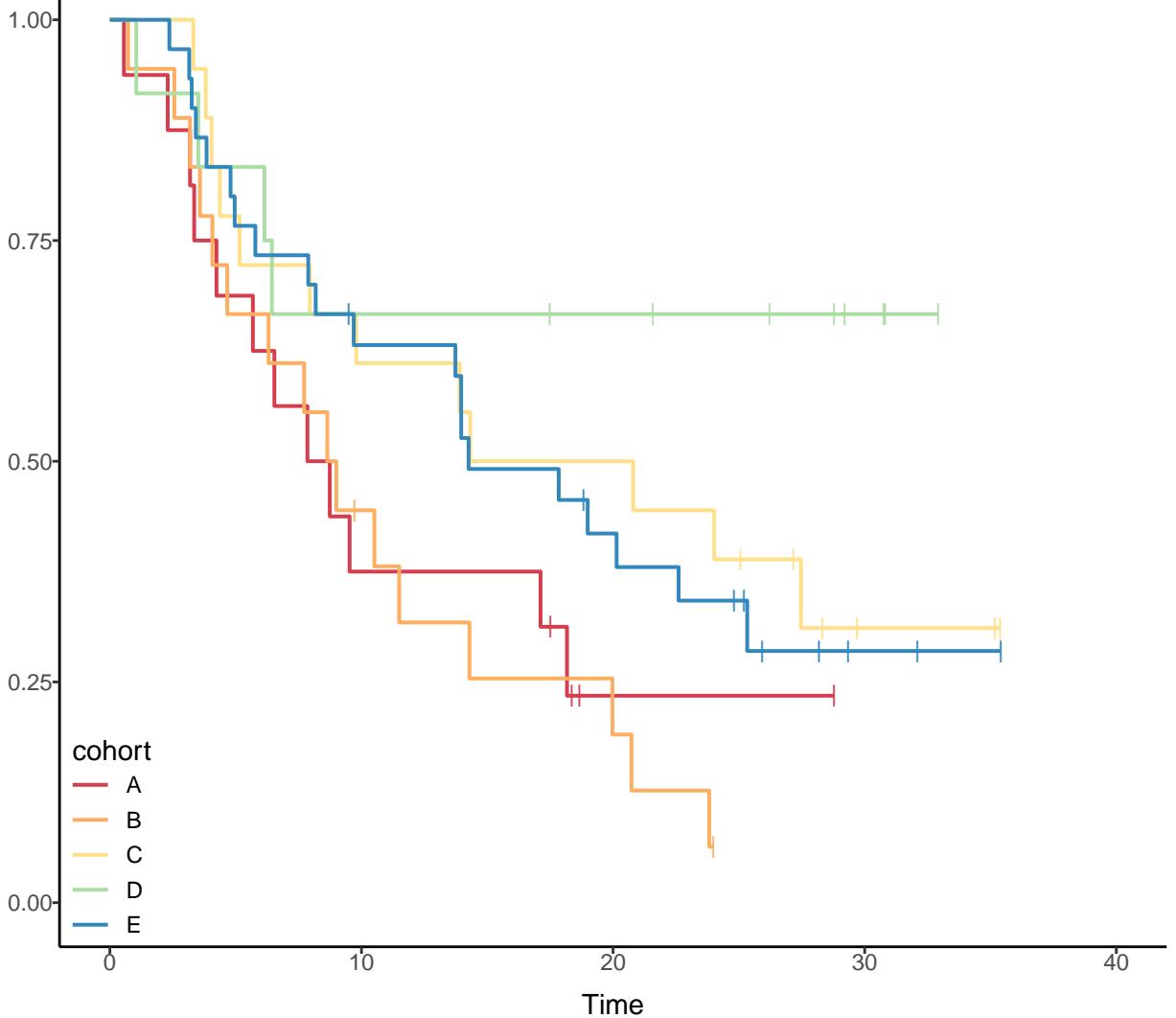
Kaplan–Meier Plot



help("ggkmcif")

$p = 0.023$ (Log Rank)

Survival Probability



At risk

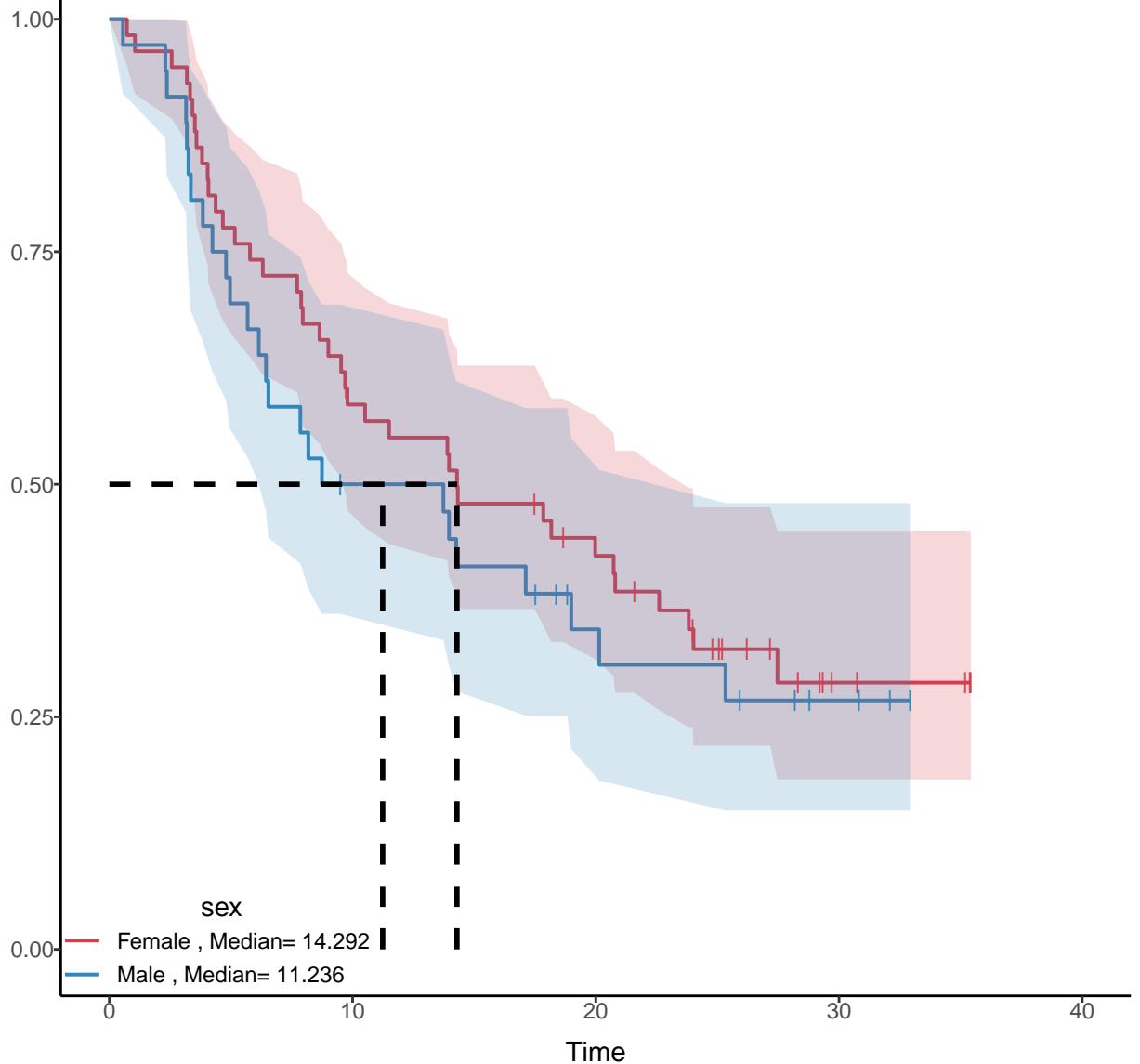
A	16	6	1	0	0
B	18	7	3	0	0
C	18	11	9	2	0
D	12	8	7	3	0
E	30	18	11	2	0

help("ggkmcif2_2025")

$p = 0.460$ (Log Rank)

help("ggkmcif2_2025")

Survival Probability



At risk	
Female	58
Male	36

33
17

22
9

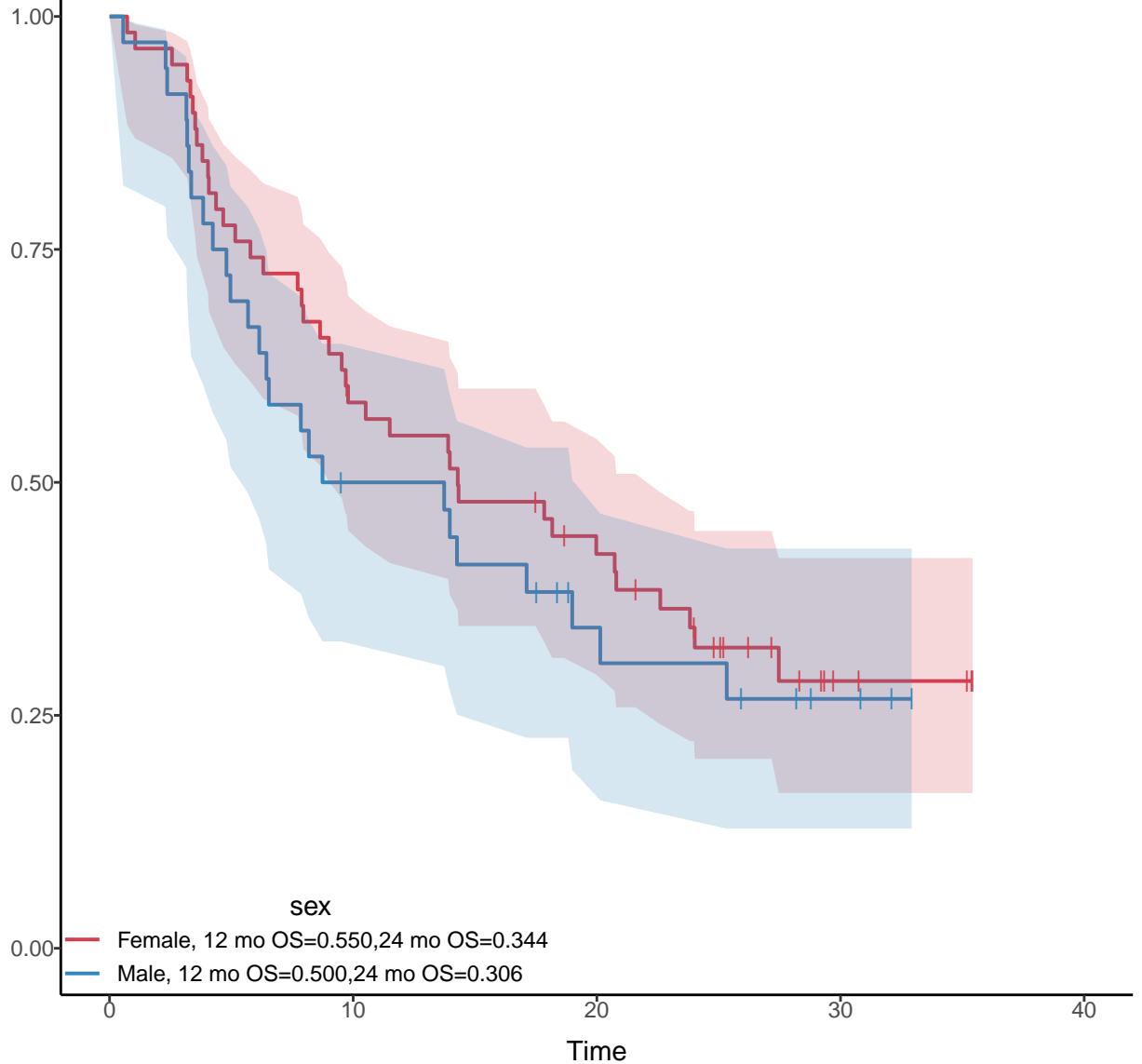
4
3

0
0

$p = 0.460$ (Log Rank)

help("ggkmcif2_2025")

Survival Probability



sex

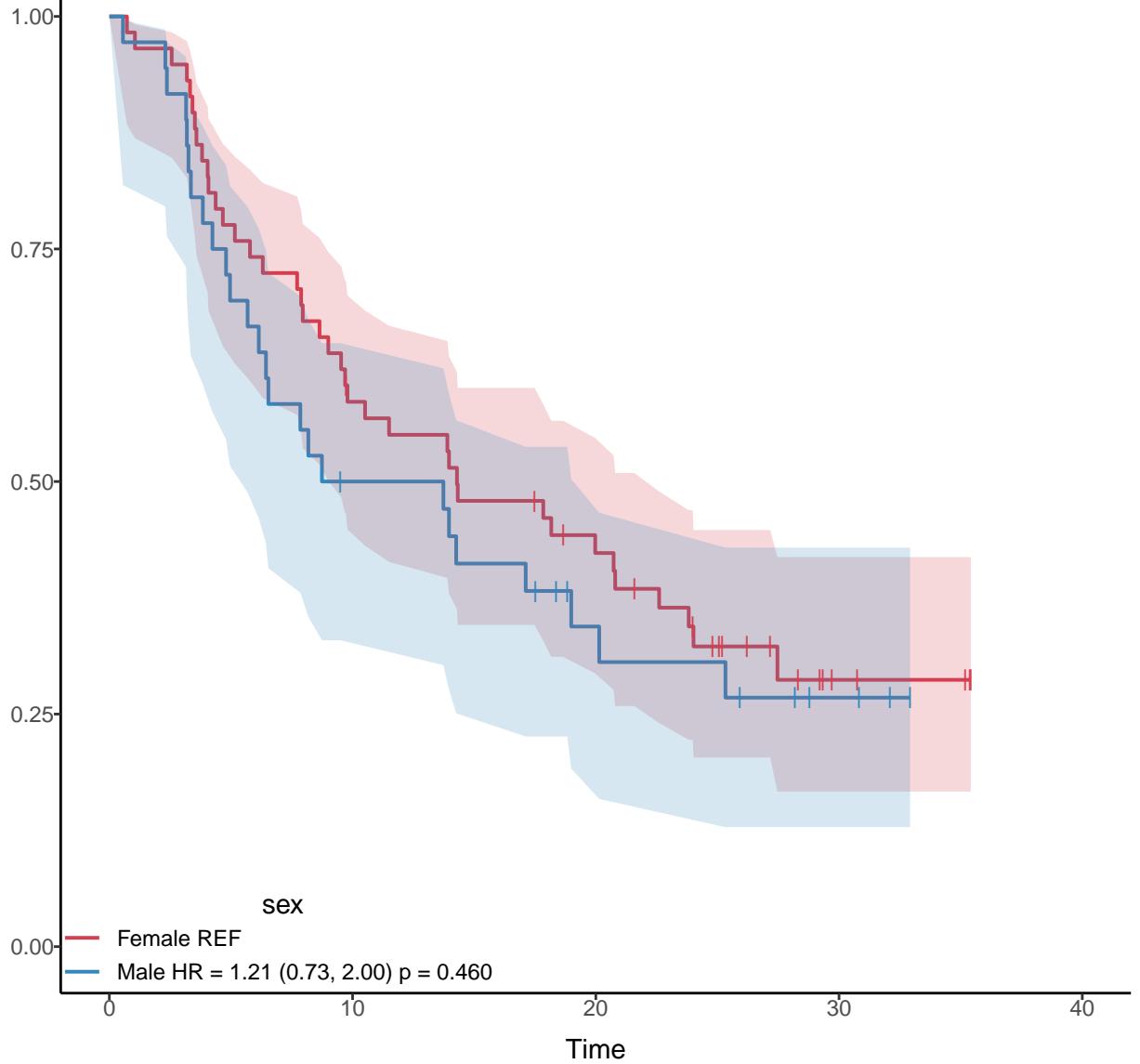
At risk

Female	58	33	22	4	0
Male	36	17	9	3	0

$p = 0.460$ (Log Rank)

help("ggkmcif2_2025")

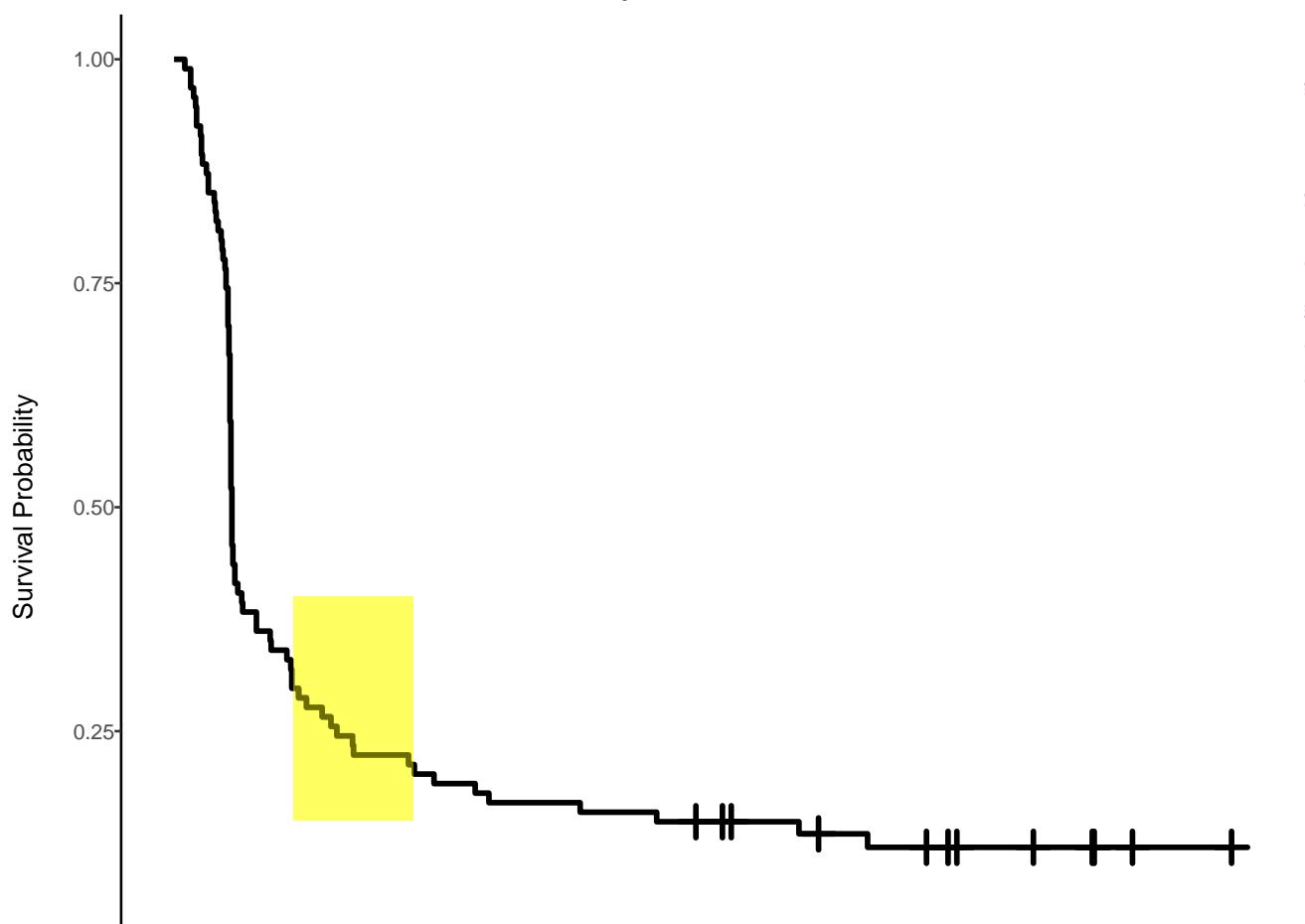
Survival Probability



At risk

Female	58	33	22	4	0
Male	36	17	9	3	0

Kaplan–Meier Plot



help("ggkmcf_paste")

Numbers at risk

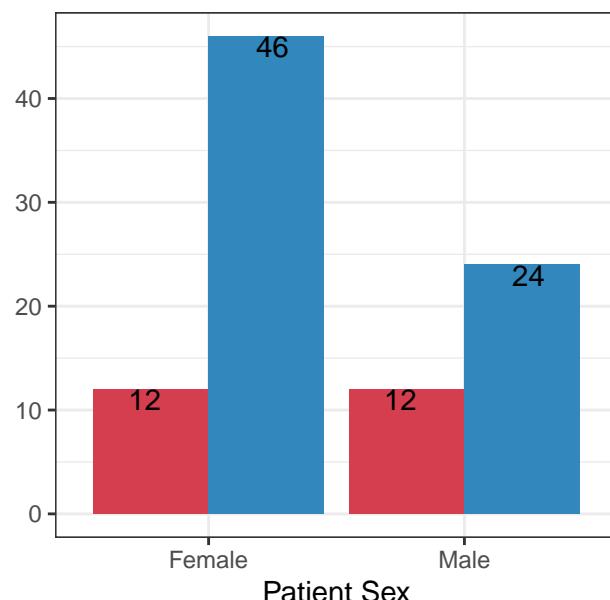
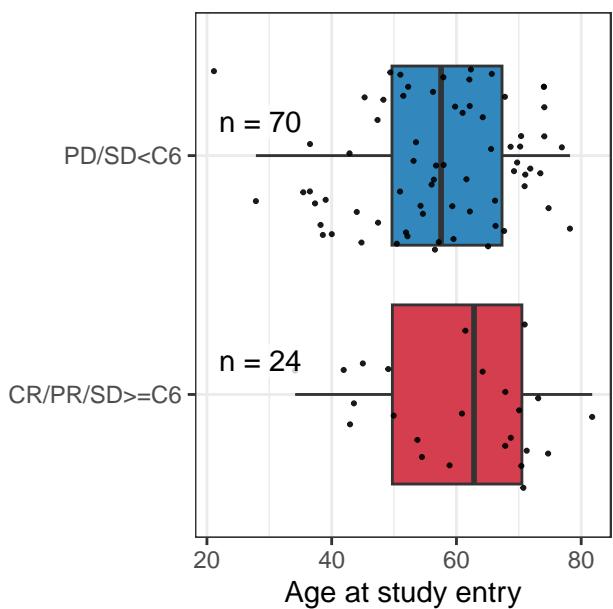
94

18

11

4

Clinical Beneficial Response



help("plotuv")

