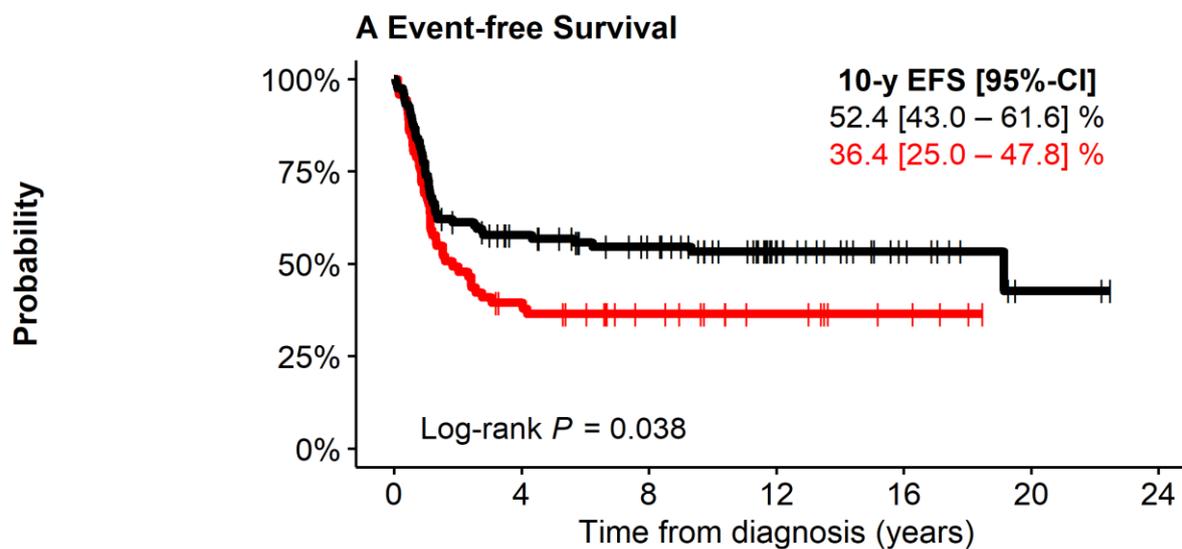


## Supplementary Material

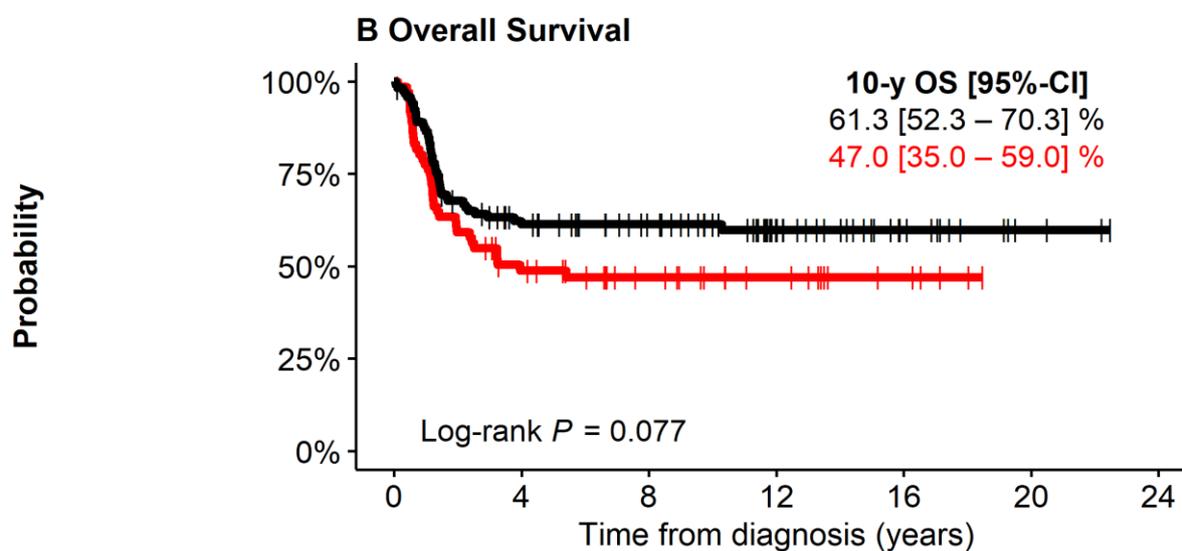
### Supplementary Figure S1

EFS and OS of 190 study group patients with *MYCN* amplification by stage (1, 2, 3, 4S vs. stage 4 aged <18 months)



#### Numbers at risk (study group)

Stage 4 <18 months	71	26	16	9	4	0	0
Stages 1,2,3 and 4S	119	60	46	24	10	2	0

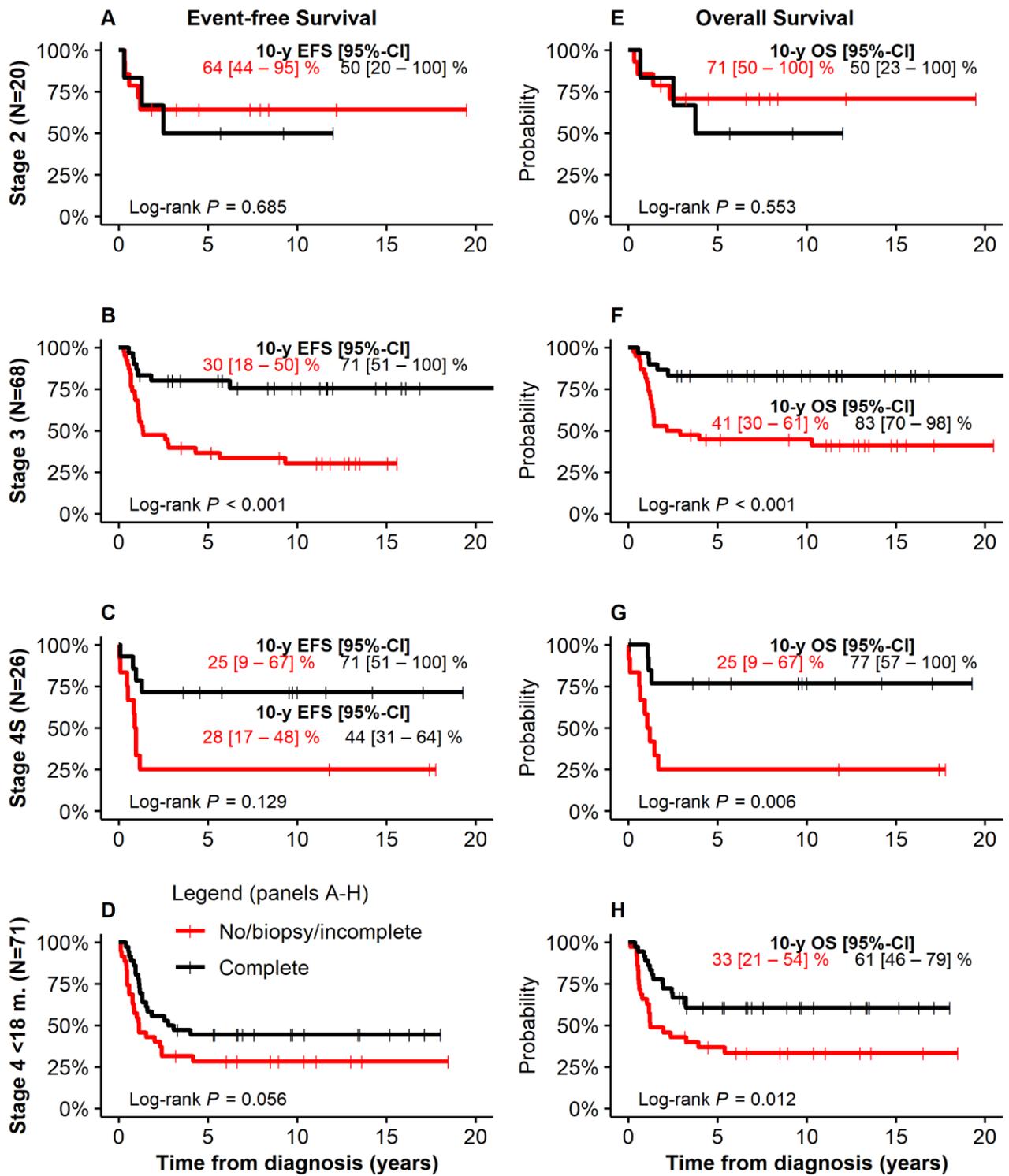


#### Numbers at risk (study group)

Stage 4 <18 months	71	31	20	12	5	0	0
Stages 1,2,3 and 4S	119	64	50	28	12	3	0

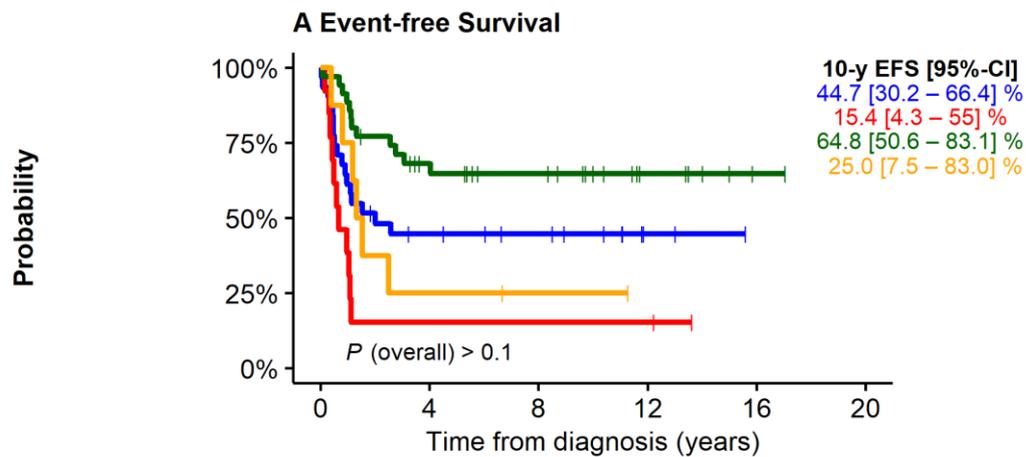
### Supplementary Figure S2

EFS and OS of 185 study group patients by stage and best result of surgical resection



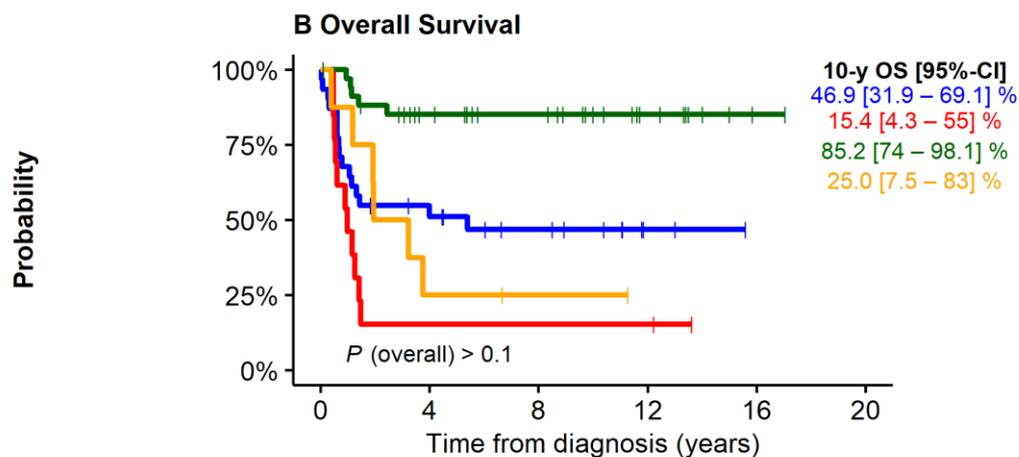
### Supplementary Figure S3

EFS and OS of 87 study group patients by independent risk factors 'presence of mutation' (mutation vs. no mutation) and 'best result of surgical resection'\* (no/incomplete/ biopsy vs. complete)



**Numbers at risk (study group)**

No/incomplete/ biopsy, no mut.	31	12	9	2	0	0
No/incomplete/ biopsy, mut.	13	2	2	2	0	0
Complete, no mut.	35	20	15	6	1	0
Complete, mutation	8	2	1	0	0	0



**Numbers at risk (study group)**

No/incomplete/ biopsy, no mut.	31	14	9	2	0	0
No/incomplete/ biopsy, mut.	13	2	2	2	0	0
Complete, no mut.	35	23	18	8	1	0
Complete, mutation	8	2	1	0	0	0

\*If more than one surgical intervention, the best result was counted.

**Pairwise comparisons (Log-rank p-values, Bonferroni-Holm adjusted)**

**EFS:**

No/incomplete/biopsy, no mutation vs. Complete, no mutation: 0.059

No/incomplete/biopsy, no mutation vs. No/incomplete/biopsy, mutation: 0.059

No/incomplete/biopsy, no mutation vs. Complete, mutation: N.A. (curves cross)  
Complete, no mutation vs. No/incomplete/biopsy, mutation: < 0.001  
Complete, no mutation vs. Complete, mutation: 0.057  
No/incomplete/biopsy, mutation vs. Complete, mutation: 0.155

**OS:**

No/incomplete/biopsy, no mutation vs. Complete, no mutation: 0.002  
No/incomplete/biopsy, no mutation vs. No/incomplete/biopsy, mutation: 0.065  
No/incomplete/biopsy, no mutation vs. Complete, mutation: N.A. (curves cross)  
Complete, no mutation vs. No/incomplete/biopsy, mutation: < 0.001  
Complete, no mutation vs. Complete, mutation: 0.001  
No/incomplete/biopsy, mutation vs. Complete, mutation: 0.164