

Identifying targetable alterations predictive of distant progression in glioblastoma patients undergoing standard therapy

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Background
Migratory growth is a hallmark of glioblastoma (GBM) and is a major factor in therapeutic failure.
Hypothesis: Genetic variants that predict distant progression (migratory growth) represent key treatment targets.

AIM
Identify targetable genetic variants associated with distant progression

Methods
Patients
All consecutive GBM *IDH wildtype* (wt) patients treated with standard therapy at Rigshospitalet (year 2016-21) were included.
Genomic cohort
Genomic tumor profiling (WES or WGS) was conducted in consenting patients.
Definition of distant progression
A new tumor lesion located more than 2 cm from the primary tumor.
Candidate biomarkers
Pathogenic or likely-pathogenic variants were grouped in i) gene alterations present in >5% of samples, and ii) the presence of alterations in four commonly altered signaling pathways.
Statistics
Cox regression analysis was used to model the association with time to distant progression.

Results

Table 1. Patient characteristics

	Total, n = 353	Genomic, n = 204
Median age, years (range)	59 (17 – 77)	58 (18-77)
Female, n (%)	134 (38)	70 (34)
ECOG PS, n (%)		
0-1	332 (95)	193 (96)
2	17 (5)	8 (4)
Subependymal involvement	153 (43)	85 (42)
Multicentric Disease, n (%)	45 (13)	17 (8)
Corticosteroid use, n (%)	161 (46)	82 (40)
Surgical resection, n (%)	286 (81)	180 (89)
Methylated MGMT, n (%)	148 (42)	91 (45)
Positive p53 expression, n (%)	215 (68)	129 (69)
Median PFS (95% CI), months	7.5 (6.8 – 8.2)	7.5 (7.0 – 8.0)
Resection at recurrence, n (%)	115 (35)	88 (46)
Second line treatment, n (%)	240 (74)	158 (84)
Median OS (95% CI), months	17.2 (15.8 - 18.7)	19.7 (17.0 - 22.5)

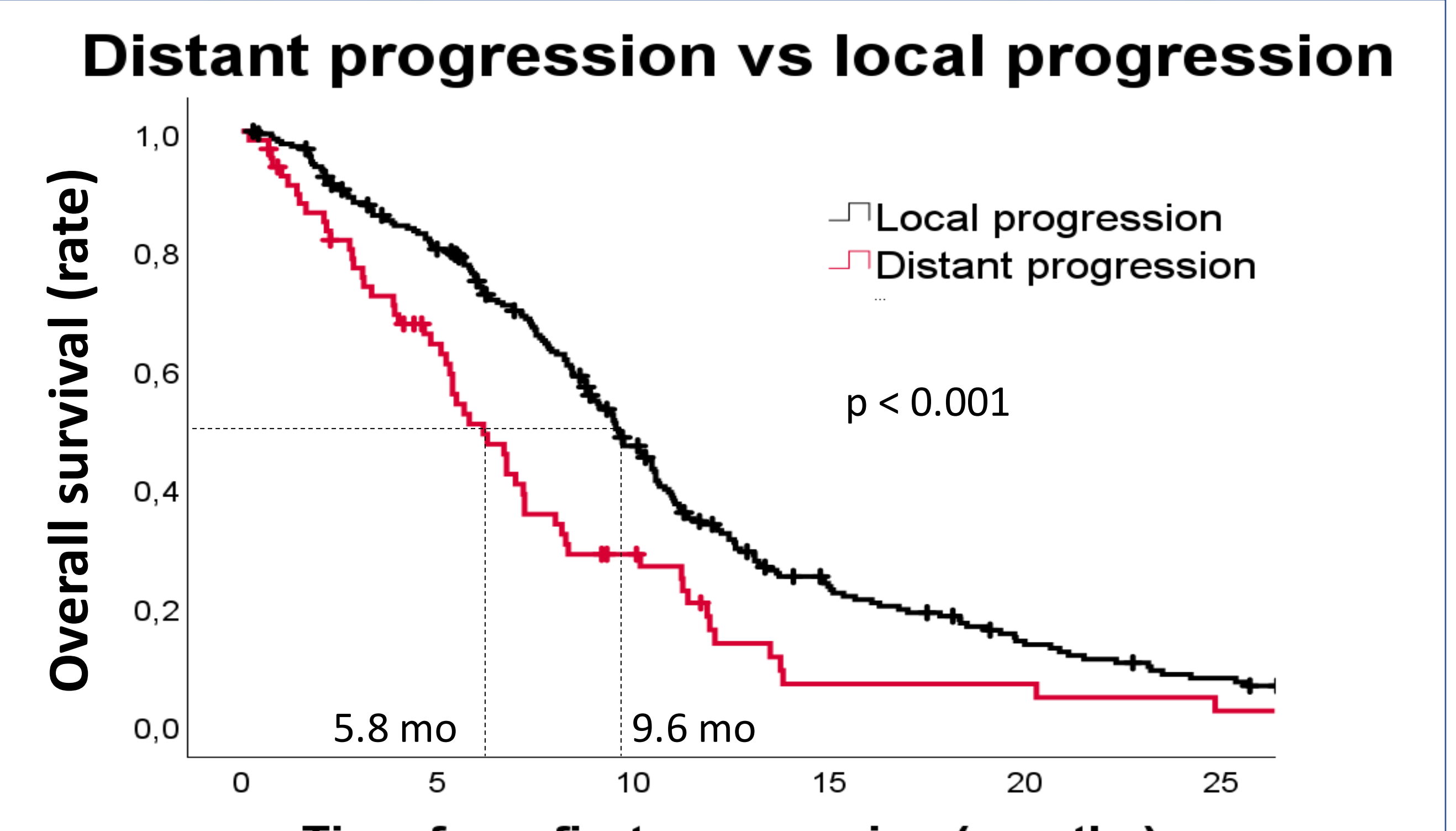
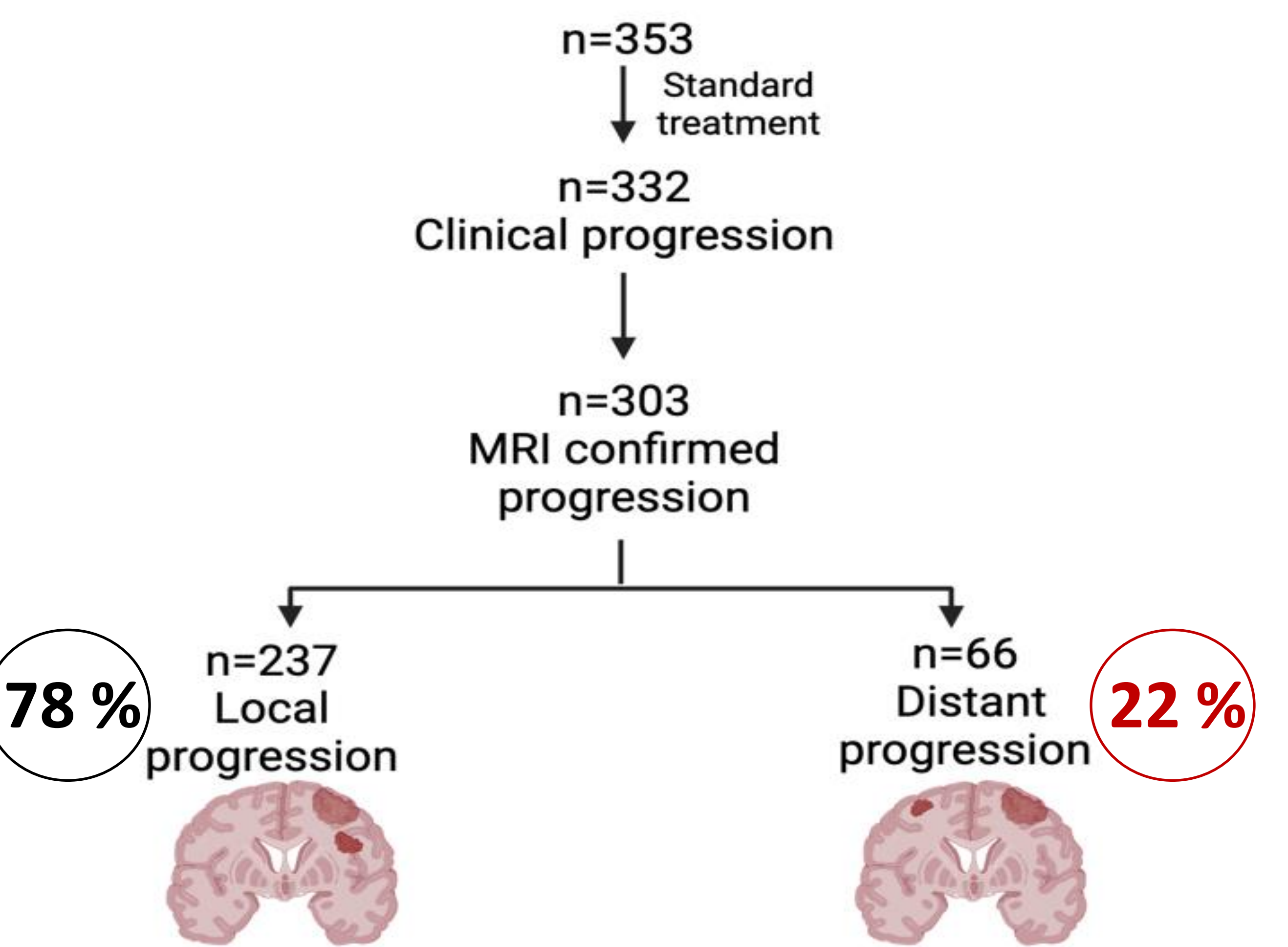


Figure 1. Kaplan-Meier plot of post-progression survival for patients with distant vs. local progression.

Table 2. Multivariate analysis of the clinical cohort modelling time to distant progression

Covariate	HR (95%CI) p-value
MGMT, un-methylated vs. methylated	2.69 (1.70-4.25) <0.001
Corticosteroid use, yes vs. no	0.93 (0.60 – 1.45) 0.75
Age, per 10-year increase	1.02 (0.85 – 1.22) 0.81
Multicentric vs. single lesion	2.54 (1.42 – 4.54) 0.002
ECOG PS, 1-2 vs 0	0.90 (0.57 – 1.43) 0.67
Biopsy vs. resection	1.48 (0.80 – 2.76) 0.21

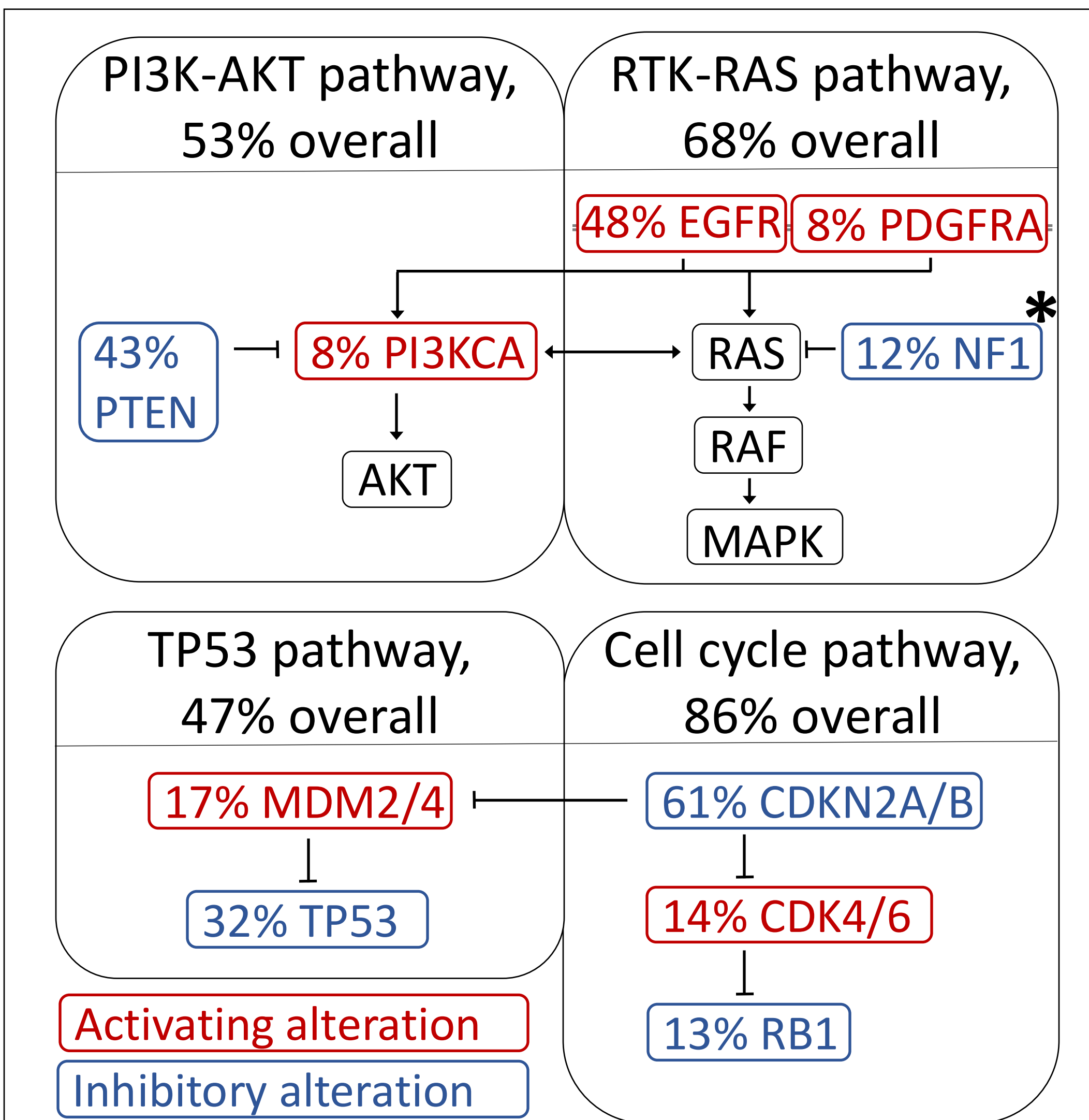


Figure 2. Candidate genetic alterations incl. frequency (%) analyzed by univariate analysis.
* *NF1* alteration showed association with distant progression (HR=3.46, 95%CI: 1.51-7.94, p=0.003).

Table 3. Multivariate analysis of the genomic cohort modelling time to distant progression

Covariate	HR (95%CI) p-value
NF1 alteration vs. NF1 wildtype	3.22 (1.37-7.61) 0.008
MGMT, un-methylated vs. methylated	2.82 (1.28-6.21) 0.01
Multicentric vs. single lesion	1.95 (0.58 – 6.61) 0.28

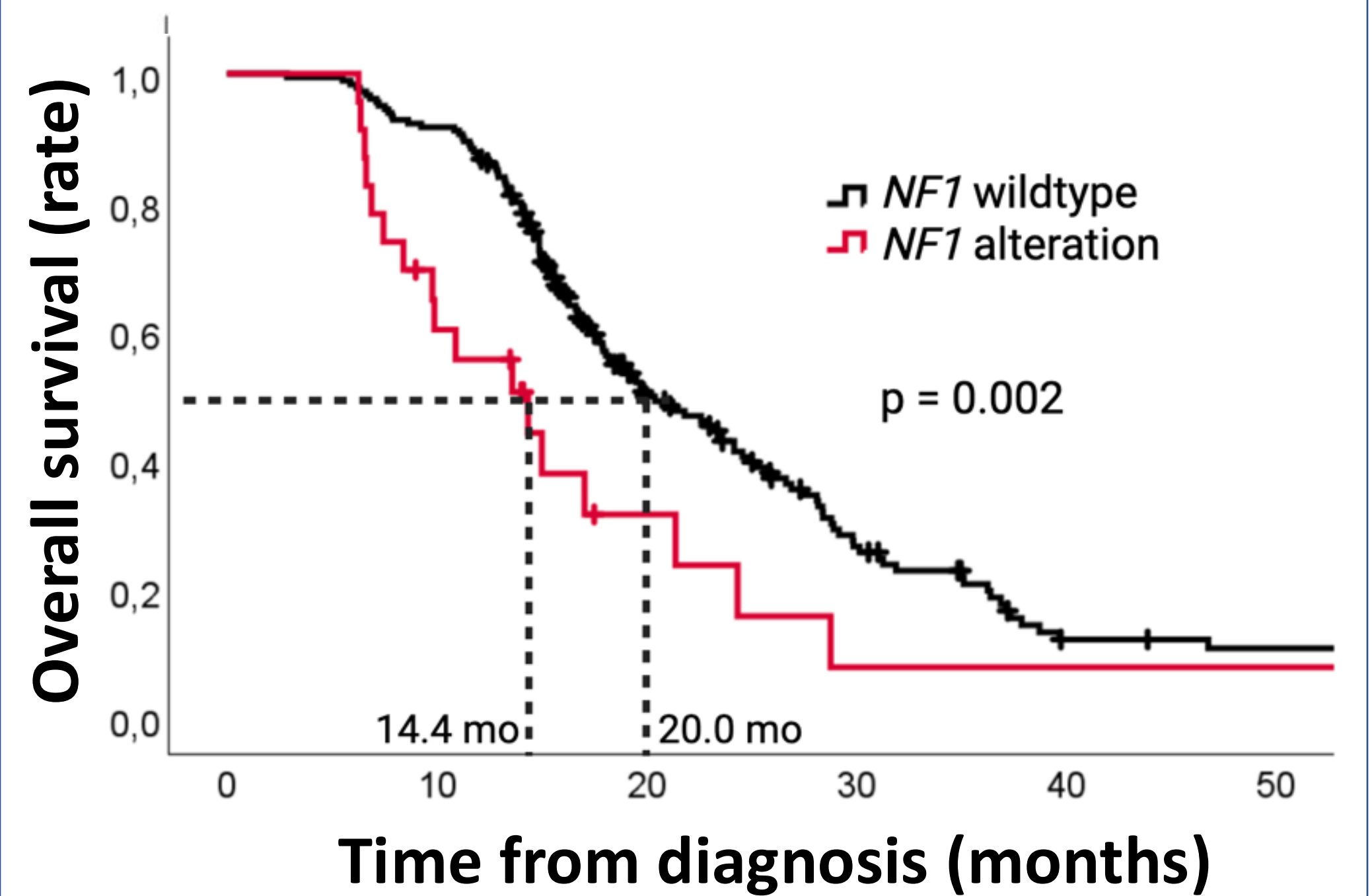
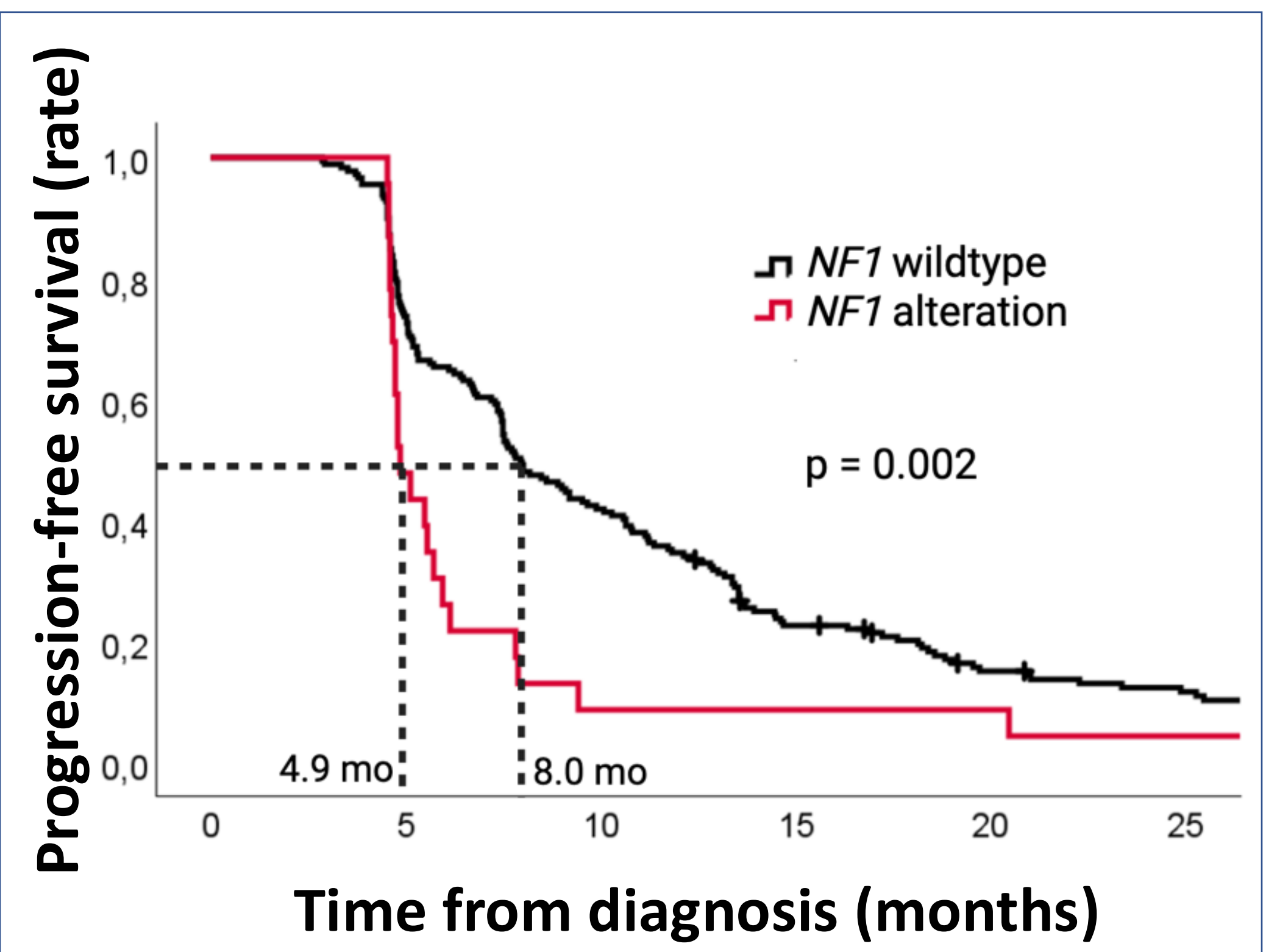


Figure 3. Kaplan-Meier plots of PFS and OS for *NF1* altered and *NF1*wt glioblastoma

Conclusion

- Distant progression is an aggressive growth pattern associated with poor survival.
- Clinical predictors of distant progression:
 - Unmethylated MGMT
 - Multicentric tumor
- NF1* alteration predicts distant progression (migratory growth).
- NF1* alteration is an independent predictor of poor progression-free survival and overall survival.
- NF1* alteration serves as a potential target for personalized therapy.

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