Supplementary Table 2

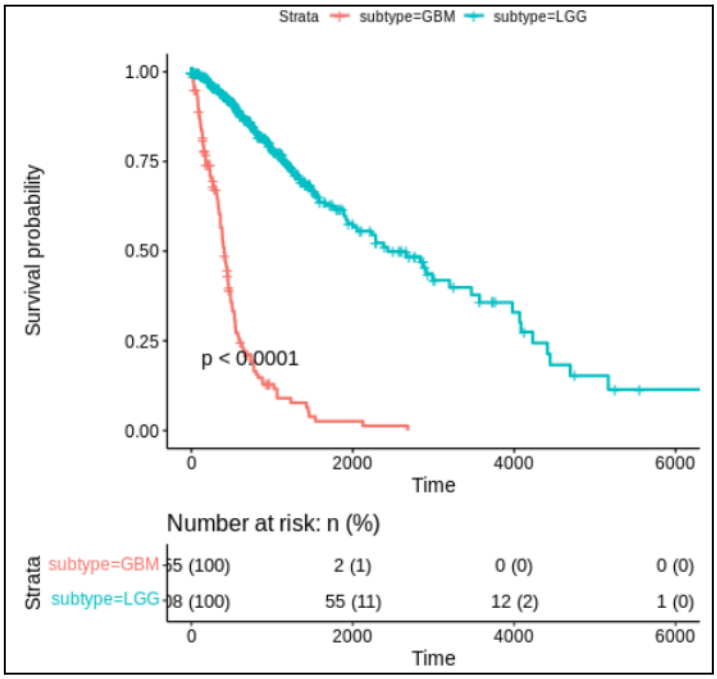
Comprehensive survival analysis results of each glioma subtype and key mutation

We conducted a survival analysis for each subtype, and each identified mutation from the first step was leveraged only from clinical data. This ensured that specific subtypes or the selected mutations had a significant impact, whether advantageous or detrimental to a patient's survival. The Kaplan-Meier method was applied to estimate the survival probability at different time intervals. We considered the length of time from the date of metastatic lung cancer diagnosis to the date of death or last follow-up as the overall survival time. Patients still alive at the time of analysis were censored at the most recent assessment date.

Diffuse Glioma

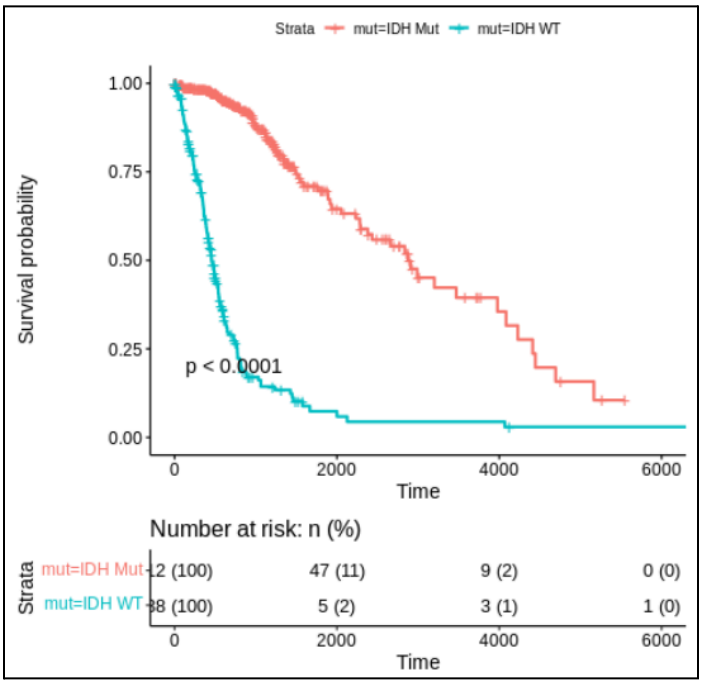
Subtype - GBM vs LGG

Kaplan-Meier analysis demonstrates significantly improved overall survival in LGG compared to GBM patients ($p<0.0001$), reflecting fundamental biological differences between these subtypes.



IDH: Mut vs WT

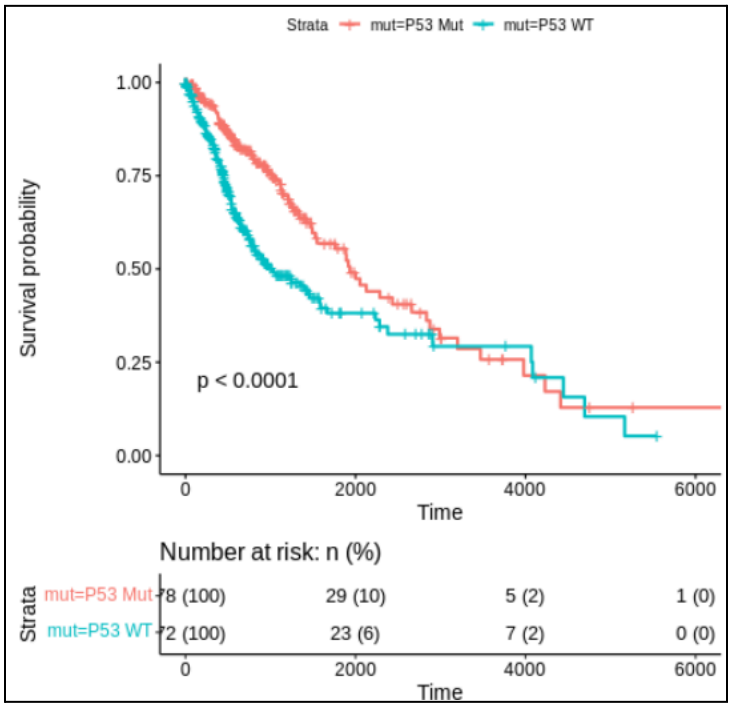
IDH-mutant gliomas show markedly better survival outcomes compared to IDH-wildtype (p<0.0001), confirming IDH status as a crucial prognostic marker.



TP53: Mut vs WT

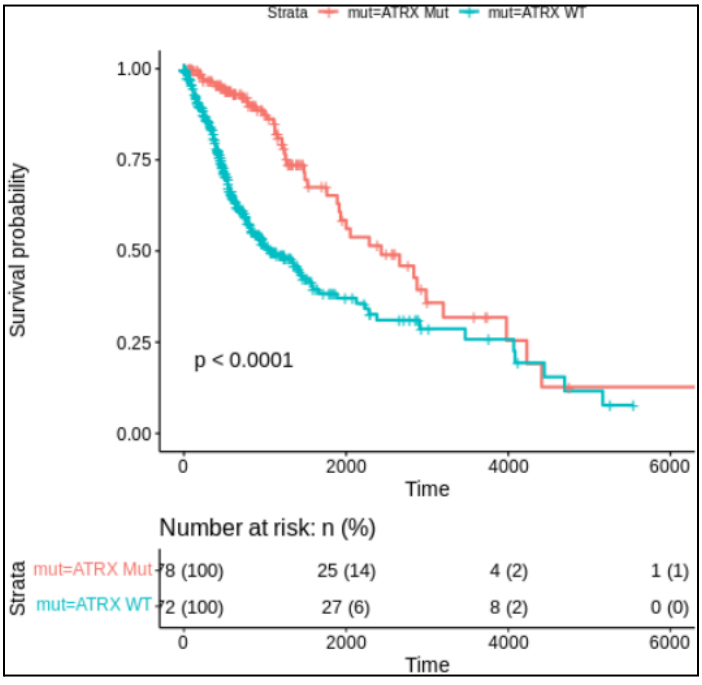
TP53 mutation status exhibits differential survival impact (p<0.0001), suggesting

its role as a prognostic indicator in glioma progression.



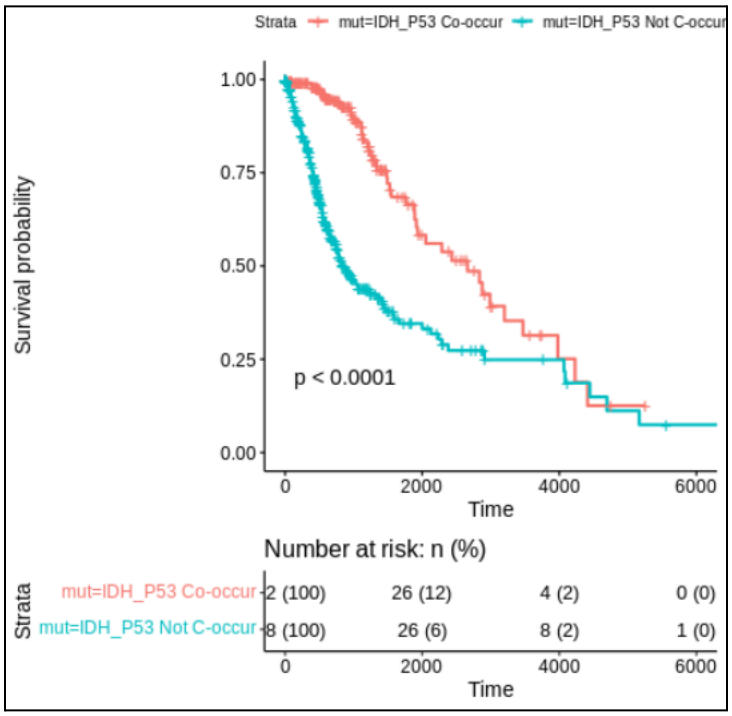
ATRX: Mut vs WT

ATRX-mutant patients demonstrate distinct survival patterns compared to wildtype (p<0.0001), particularly in association with IDH mutation.



IDH+TP53: Mut vs WT

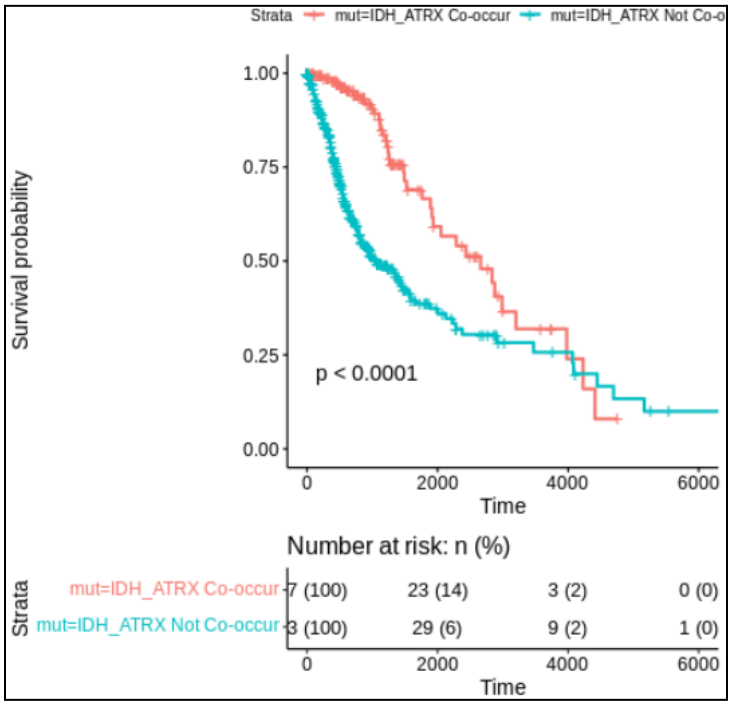
Co-occurrence of IDH and TP53 mutations shows a significant survival advantage compared to wild-type cases (p<0.0001), indicating synergistic prognostic value.



IDH+ATRX: Mut vs WT

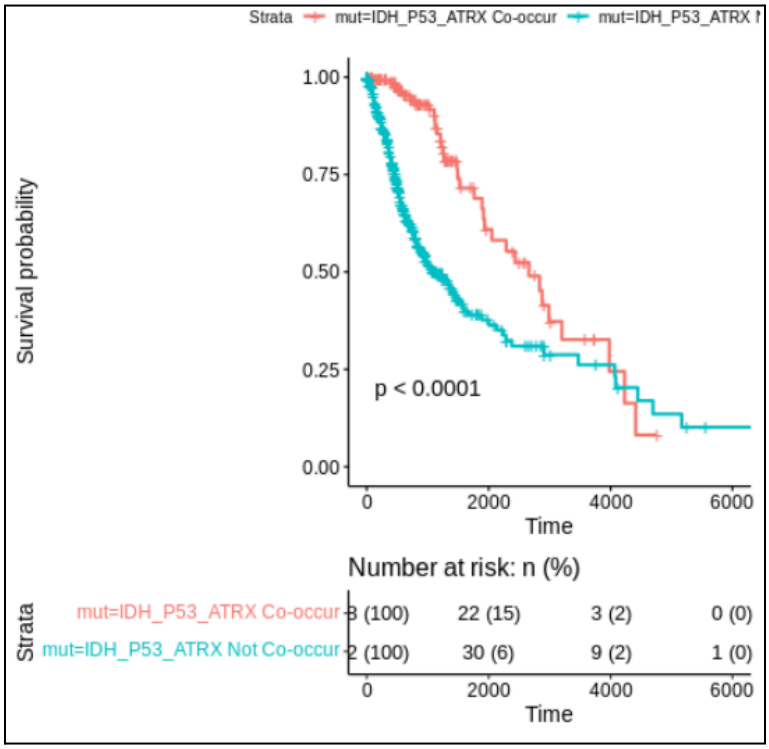
Combined IDH and ATRX mutations are associated with improved survival

outcomes (p<0.0001), characteristic of astrocytic lineage tumours.



IDH+P53+ATRX: Mut vs WT

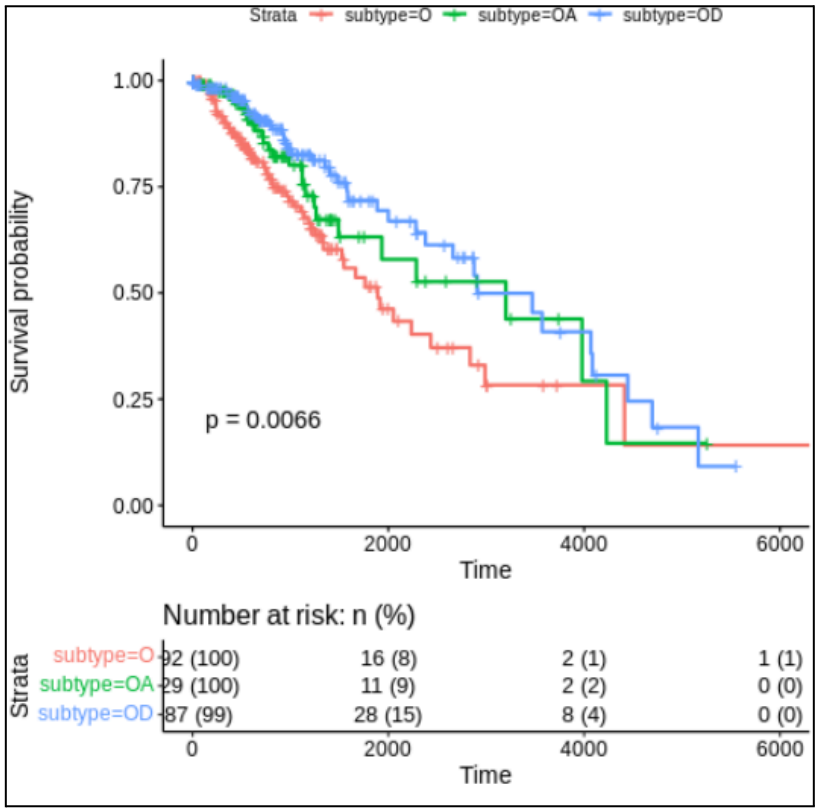
Triple-positive mutations (IDH/TP53/ATRX) define a distinct prognostic subgroup with significantly altered survival patterns (p<0.0001).



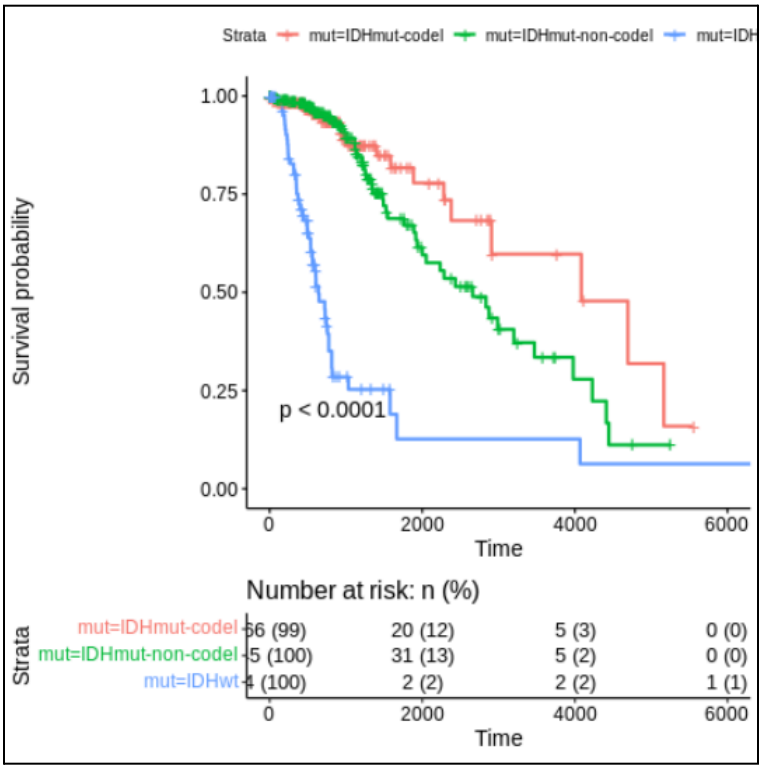
Low-Grade Glioma

Stratification by IDH and 1p/19q status reveals three distinct prognostic groups: IDH-mutant/1p19q-codeletion oligodendrogliomas showing the best prognosis, followed by IDH-mutant non-codeleted astrocytomas, and IDH-wildtype tumours with poorest outcomes ($p<0.0001$).

Subtype - O/OA/OD



IDH mut + 1p19q codel/ IDH mut + non-codel/ IDH wt

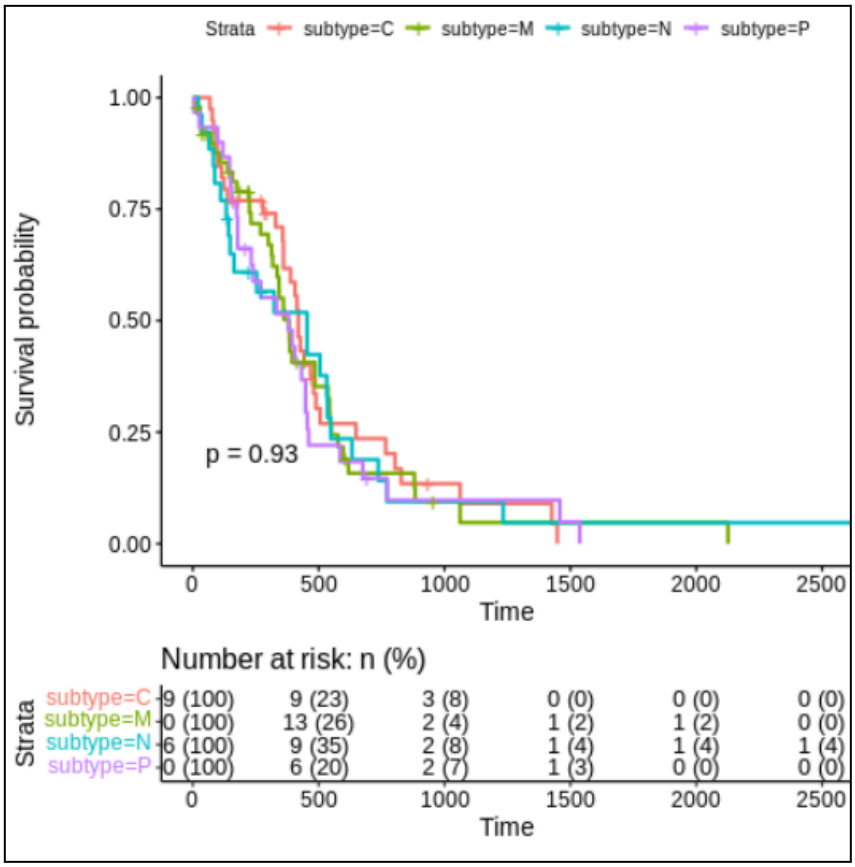


Glioblastoma Multiforme

Subtype - C/M/N/P

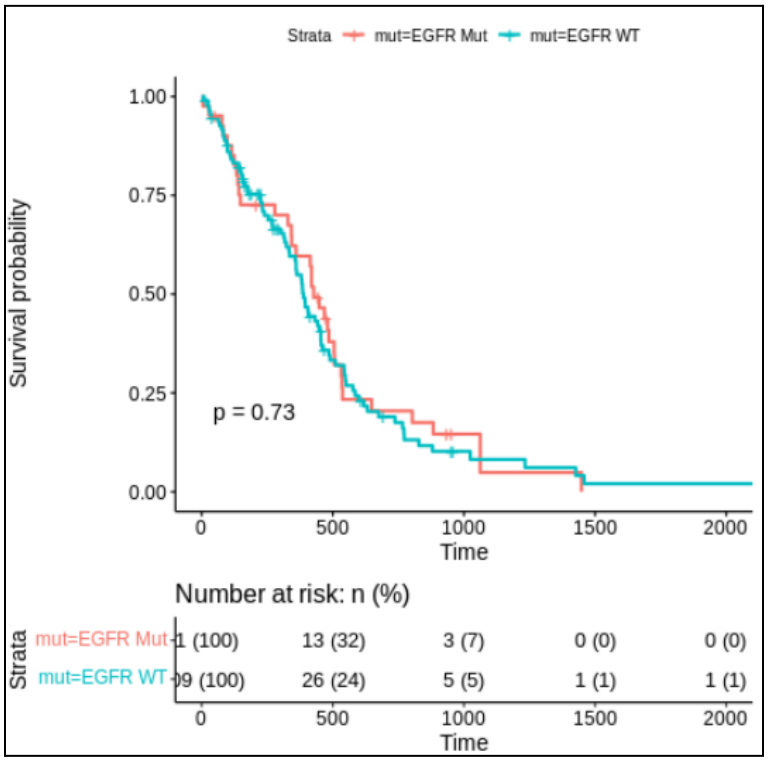
Survival analysis across Classical(C), Mesenchymal(M), Neural(N), and

Proneural(P) subtypes did not have significant prognostic differences (p=0.93).



EGFR: Mut vs WT

EGFR-mutant GBM patients did not demonstrate significantly altered survival patterns compared to wild type.



PTEN: Mut vs WT

PTEN mutation status does not significantly correlate with survival outcomes.