# Abstract 111: Association of MGMT status with survival in low and high-grade IDH-mutant astrocytomas

**WashU** Medicine

Katherine Schwetye<sup>1</sup>, Omar Butt<sup>1</sup>, Manmeet Ahluwalia<sup>2</sup>, Sonikpreet Aulakh<sup>3</sup>, Gilbert Youssef <sup>4</sup>, Joanne Xiu<sup>5</sup>, Theodore Nicolaides<sup>5</sup>, Negar Sadeghipour<sup>5</sup>, Patricia Pittman<sup>5</sup>, Christian Davidson<sup>5</sup> <sup>1</sup>Washington University, <sup>2</sup>Miami Cancer Institute, <sup>3</sup>West Virginia University, <sup>4</sup>Dana Farber Cancer Center, <sup>5</sup>Caris Life Sciences

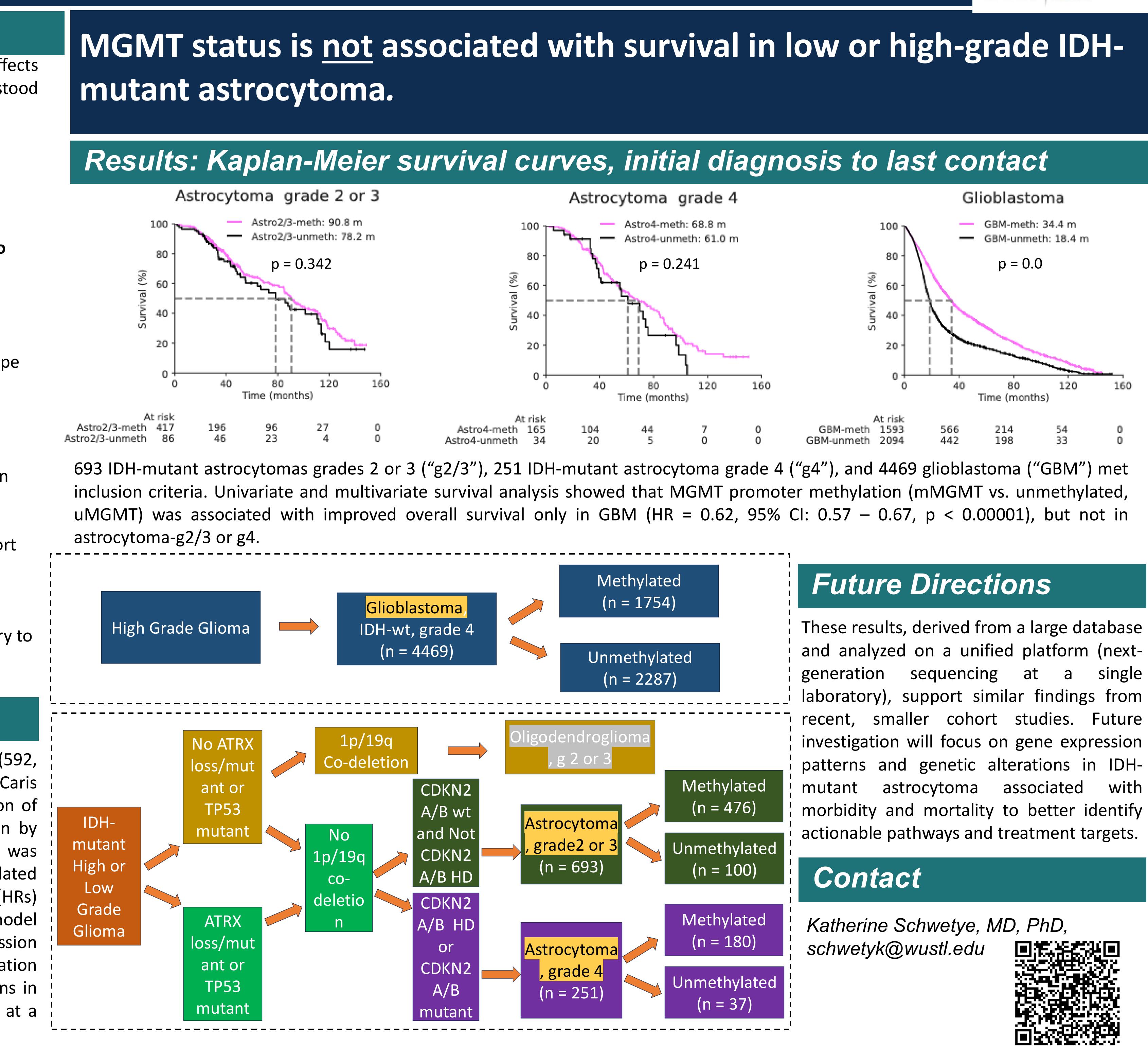
## Background

methylation status affects MGMT promoter How survival in IDH-mutant astrocytomas is less understood than in IDH-wildtype GBM.

- MGMT is a DNA repair enzyme Alleviates temozolomide damaged lesions
- High MGMT expression leads to resistance to temozolomide
- Hypermethylation of MGMT promoter leads to silencing of transcription, increasing sensitivity to temozolomide
- IDH mutants **lose** native enzymatic activity
- Acquires novel activity to promote epigenetic changes
- Leads to <u>Glioma</u> <u>CpG</u> <u>Island</u> <u>Methylation</u> <u>Phenotype</u> (G-CIMP)
- Multiple techniques measure MGMT promoter methylation:
  - Pyrosequencing
  - Methylation-specific polymerase chain reaction (PCR)
  - Direct Sanger sequencing
- Limitations include low quantitative accuracy, short read length, and low sample throughput
- We used a large database of next-generation sequencing (NGS) and whole-transcriptome sequencing (WTS) performed in a single laboratory to determine the role of MGMT status on survival in IDH-mutant astrocytomas and in GBM.

### Methods

10,181 glioma samples were analyzed by NGS (592, NextSeq, or WES, NovaSeq) and WTS (NovaSeq) at Caris Life Sciences (Phoenix, AZ), including determination of methylation status of the MGMT promoter region by pyrosequencing. Real-world overall survival was obtained from insurance claims data and calculated from initial diagnosis to last contact. Hazard ratios (HRs) were analyzed using Cox proportional hazards model and p values (log-rank test). Multivariate regression analysis was performed on age, gender, radiation treatment, temozolomide treatment, and mutations in different biomarkers. Fisher's exact test was used at a significance level of 0.05.





CARIS<sup>®</sup> PRECISION ONCOLOGY

single associated with