

Description of Additional Supplementary Files

Supplementary Data 1: Normalized NanoString counts matrix for full SickKids patient cohort

Supplementary Data 2: Immunohistochemistry quantification for comparison with NanoString gene counts

Supplementary Data 3: Sample type and subtype for overall SickKids patient cohort

Supplementary Data 4: Genes on custom NanoString immuno-oncology panel

Supplementary Data 5: Tumor inflammation signature scores for PBTA patient cohort

Supplementary Data 6: Immune signature GSVA scores, using gene sets from Bagaev et al, Cancer Cell 2021

Supplementary Data 7: PROGENy pathway activation scores for PBTA samples

Supplementary Data 8: Pearson correlation values for TIS with COSMIC SBS signatures

Supplementary Data 9: Clinical, pathologic, and molecular annotation for SickKids low-grade glioma cohort

Supplementary Data 10: Differential expression testing for BRAF mutant vs. BRAF fused LGG

Supplementary Data 11: Consensus clusters for BRAF mutant low-grade gliomas

Supplementary Data 12: Estimated tumor content for BRAF mutant low-grade gliomas

Supplementary Data 13: Clinical and molecular annotations for SickKids high-grade glioma cohort

Supplementary Data 14: TIS scores for primary vs progression/recurrent diffuse midline gliomas

Supplementary Data 15: SNV effect breakdown for PBTA high-grade gliomas

Supplementary Data 16: CNV breakdown for PBTA high-grade gliomas

Supplementary Data 17: Clinical data for MMRD HGG patient cohort

Supplementary Data 18: Outcome data and tumor mutation burden for immune checkpoint inhibitor treated MMRD HGGs

Supplementary Data 19: Breakdown of variants types from WES data for MMRD HGGs

Supplementary Data 20: TP53 variant types for MMRD HGGs

Supplementary Data 21: Sample QC metrics and pass/fail status compared to sample age

Supplementary Data 22: NanoString vs RNAseq TIS scores for validation samples