## Murine glioma model

Glioblastoma genetically engineered mouse models make it possible to pinpoint genetic alterations involved in tumor initiation and progression, but tumors are usually composed of cells with specific, homogeneous genetic changes, and thus cannot completely reflect the intratumoral genomic and phenotypic heterogeneity of glioblastoma

Immune profiling analyses and single cell sequencing of implanted and spontaneous tumors from Qk/trp53/Pten mice as well as from glioblastoma patients revealed intratumoral immune components that were predominantly myeloid cells (e.g. monocytes, macrophages, and microglia) with minor populations of T, B, and NK cells. When comparing spontaneous and implanted mouse samples, we found that there were more neutrophils, T, and NK cells in the implanted model. Neutrophils, T, and NK cells were increased in abundance in samples derived from human high-grade glioma (HGG) compared to those derived from low-grade glioma (LGG). Overall, our data demonstrate that our implanted and spontaneous QPP models recapitulate the immunosuppressive myeloid dominant nature of the tumor microenvironment of human gliomas. The model provides a suitable tool for investigating the complex immune compartment of gliomas and it may contribute to a better understanding of the resistance of human glioblastoma to currently available immunotherapy<sup>1)</sup>

Contemporary literature indicates that the GL261 model has been most frequently used. However, further research using SMA-560, CT-2A, GL26, and 4C8 tumors seems likely to reveal additional glioma immunotherapy applications for these models as well. Given the promise of immunotherapy as part of a multimodal treatment paradigm for Glioblastoma, such in vivo models will continue to prove invaluable in the future <sup>2)</sup>.

## 1)

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