Identifying genomic markers of response to immune checkpoint blockade (for example, PD-1 blockade) may benefit cancer patients by providing predictive biomarkers for patient stratification and identifying resistance mechanisms for therapeutic targeting. Gliomas typically have a low tumor mutational burden (TMB) and a highly immunosuppressive microenvironment—two features associated with immunotherapy resistance. Nevertheless, recent work has suggested that a subset of patients with high-TMB (hypermutated) gliomas might benefit from PD-1 blockade [1)]

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