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## Glioblastoma heterogeneity at single cell resolution

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## Abstract

Glioblastoma (GBM) is one of the deadliest types of cancer and highly refractory to chemoradiation and immunotherapy. One of the main reasons for this resistance to therapy lies within the heterogeneity of the tumor and its associated microenvironment. The vast diversity of cell states, composition of cells, and phenotypical characteristics makes it difficult to accurately classify GBM into distinct subtypes and find effective therapies. The advancement of sequencing technologies in recent years has further corroborated the heterogeneity of GBM at the single cell level. Recent studies have only begun to elucidate the different cell states present in GBM and how they correlate with sensitivity to therapy. Furthermore, it has become clear that GBM heterogeneity not only depends on intrinsic factors but also strongly differs between new and recurrent GBM, and treatment naïve and experienced patients. Understanding and connecting the complex cellular network that underlies GBM heterogeneity will be indispensable in finding new ways to tackle this deadly disease. Here, we present an overview of the multiple layers of GBM heterogeneity and discuss novel findings in the age of single cell technologies.

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