

Description of Additional Supplementary Files

Supplementary Data 1: Differentially expressed genes in invasive vs. non-invasive PDX models. Table summarizing the results of differential expression analysis comparing invasive GBM PDX models to non-invasive models.

Supplementary Data 2: Gene signatures for DiG and LiG up/downregulated genes. Transcriptional signatures defining distal and local invasion patterns. The table lists the top 75 genes significantly upregulated or downregulated in distally invading gliomas (DiG) and locally invading gliomas (LiG).

Supplementary Data 3: Visium sample information and source. Metadata for all samples utilized in the spatial transcriptomics (10x Genomics Visium) analysis. Columns include unique sample names, corresponding model names, and the data source (indicating whether the data was generated in this study or obtained from public repositories).

Supplementary Data 4: Gene signatures for spatial transcriptomics programs. List of transcriptional signatures identified through spatial analysis. These include spatial DiG/LiG programs, spatial associated with vascular, defined by malignant cells in close spatial proximity to nonmalignant vascular cells, as well as metaprogram (MP) derived signatures: spatial DiG (MP), spatial tumor core (MP), and periphery DiG program (MP), representing malignant cells that have invaded furthest into the cortical layers.

Supplementary Data 5: CODEX panel information. Detailed specifications for the antibody panel used in CODEX imaging. The table provides information on the protein target, clone, manufacturer, catalog number, post-conjugation dilution, and the specific cell type/marker category for each antibody