Glioblastoma

Ivy Glioblastoma Atlas project

This is the online help for the Ivy Glioblastoma Atlas Project web application.

The Ivy Glioblastoma Atlas Project is a foundational resource for exploring the anatomic and genetic basis of glioblastoma at the cellular and molecular levels. The project is organized into six studies that were designed to identify genes enriched in glioblastoma. Three of those studies were based on anatomic structures or features of glioblastoma and three were focused on putative cancer stem cells.

Ivy Glioblastoma Studies

Color Key	Study	Description
	Anatomic Structures ISH Survey	Primary screen of 8 tumors with probes for 343 genes enriched in glioblastoma.
	Anatomic Structures RNA-Seq	Screen of 5 structures (Leading Edge, Infiltrating Tumor, Cellular Tumor, Microvascular Proliferation, and Pseudopalisading Cells Around Necrosis) identified by H&E staining. A total of 122 RNA samples were generated from 10 tumors.
	Anatomic Structures ISH for Enriched Genes	Subsequent screen of 29 tumors with probes for 37 genes enriched in glioblastoma structures identified in Anatomic Structures RNA-Seq Study.
	Cancer Stem Cells ISH Survey	Primary screen of 16 tumors with probes for 55 genes enriched in putative cancer stem cells, resulting in a 20 probe reference set, which was then used in an extensive screen of 42 tumors.
	Cancer Stem Cells RNA-Seq	Screen of 35 clusters of putative cancer stem cells identified by ISH with a 17 reference probe subset (validated in the Cancer Stem Cells ISH Survey). A total of 148 RNA samples were generated from 34 tumors.
	Cancer Stem Cells ISH for Enriched Genes	Subsequent screen of 37 tumors with probes for 76 genes enriched in clusters of putative cancer stem cells identified in the Cancer Stem Cells RNA-Seq Study.

DATA SETS:

The Ivy Glioblastoma Atlas Project web application includes data sets generated with multiple data modalities:

In Situ Hybridization (ISH) Image Data:

- ISH images (22,000) acquired with 20x objective for 0.50m/pixel resolution of 15K x 18K pixel images
- H&E images (12,000) acquired with 20x objective for 0.50m/pixel resolution of 15K x 18K pixel images
- Annotated anatomic structures in all H&E images
- Counts of cell nuclei for anatomic structures in all H&E images

RNA-Sequencing Data: from anatomic structures and putative cancer stem cell clusters

- RNA-Seq profiles for 270 laser-microdissected samples. The profiles have 15 million mapped reads and the samples include tissue from anatomic structures or putative cancer stem cell clusters.

Clinical and Other Data

- De-identified clinical data for 41 patients including age, gender, initial KPS, neurosurgery (resection number), hemisphere, chemotherapy, radiation therapy, recurrence by 6 months, and multifocality
- MRI anonymized scans (42)
- Resected tumor images (42) with tissue block subdivisions and orientation of tumor in brain
- Mutations: Epidermal growth factor receptor (EGFR) amplification, PTEN gene deletion
- MGMT gene methylation status

Related Resources

Ivy GAP Clinical and Genomic Database: Partner database with additional clinical, genomic, and transcriptome data for Ivy GAP.
The Cancer Genome Atlas (TCGA): NIH-funded initiative for genomic mapping of cancers, including glioblastoma.