# Ivy Glioblastoma Studies

<table>
<thead>
<tr>
<th>Color Key</th>
<th>Study</th>
<th>Description</th>
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<tbody>
<tr>
<td></td>
<td><strong>Anatomic Structures ISH Survey</strong></td>
<td>Primary screen of 8 tumors with probes for 343 genes enriched in glioblastoma.</td>
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<td><strong>Anatomic Structures RNA-Seq</strong></td>
<td>Screen of 5 structures (Leading Edge, Infiltrating Tumor, Cellular Tumor, Microvascular Proliferation, and Pseudopalisading Cells Around Necrosis) identified by H&amp;E staining. A total of 122 RNA samples were generated from 10 tumors.</td>
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<td><strong>Anatomic Structures ISH for Enriched Genes</strong></td>
<td>Subsequent screen of 29 tumors with probes for 37 genes enriched in glioblastoma structures identified in Anatomic Structures RNA-Seq Study.</td>
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<td><strong>Cancer Stem Cells ISH Survey</strong></td>
<td>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.</td>
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<td><strong>Cancer Stem Cells RNA-Seq</strong></td>
<td>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.</td>
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<td><strong>Cancer Stem Cells ISH for Enriched Genes</strong></td>
<td>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.</td>
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**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-Seq 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.