

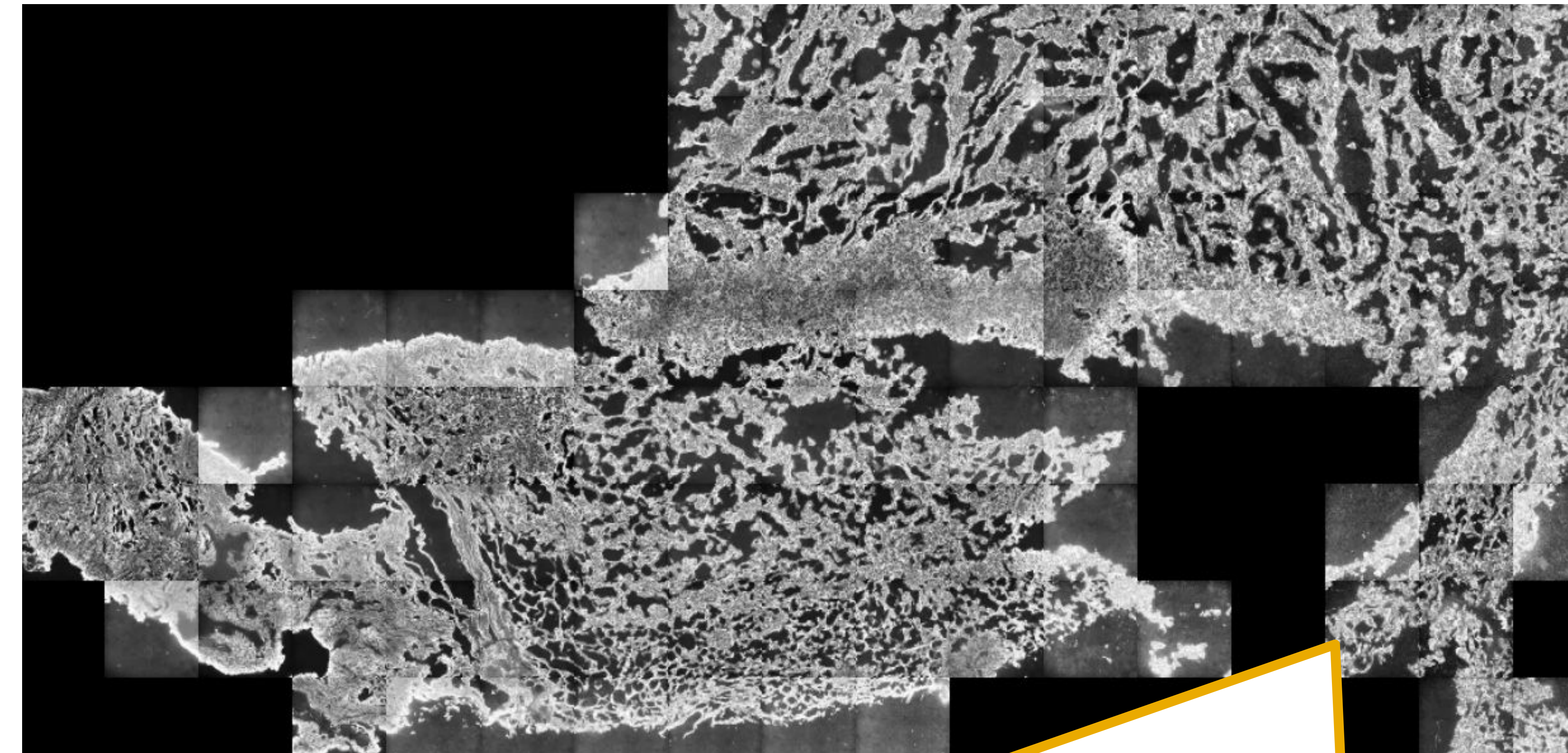
webFISH: Cloud-Based Spatial Genomics Visualization

Facilitating new biological insights with a **robust and responsive** interface that enables seamless exploration of high-dimensional spatial genomic data.

Data Upload

- ❖ Allows scientists to add new experimental data to the website, such as gene information, cell boundaries, images of different stains, etc.
- ❖ **Expands the lab's current analysis pipeline**

Why this is useful: Scientists are able to quickly input new data to visualize it, making our website **easy to integrate with their research.**



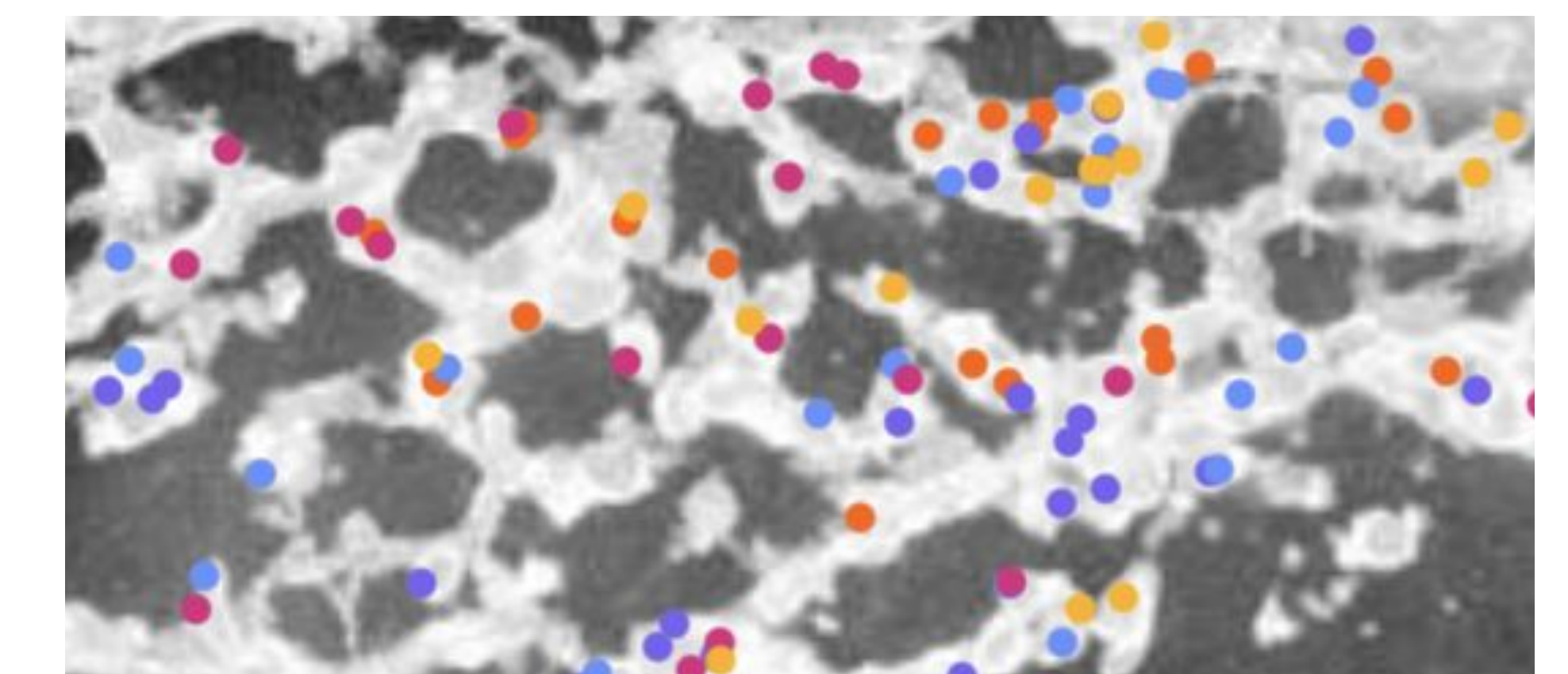
Stain Layer

- ❖ One or more microscope images (e.g., tissue biopsies, embryos, cell cultures)
- ❖ Images are **stitched together** and **tiled** for efficient rendering

Why this is useful: Easily navigable tiled imagery provides a comprehensive **overview of entire experiment.** Automatic tiling eliminates the need for experimenters to examine each microscope image individually.

Gene Layer

- ❖ Techniques developed by the Cai Lab allow scientists to measure gene expression **within** tissue samples (colored dots below; colors correspond to specific genes)



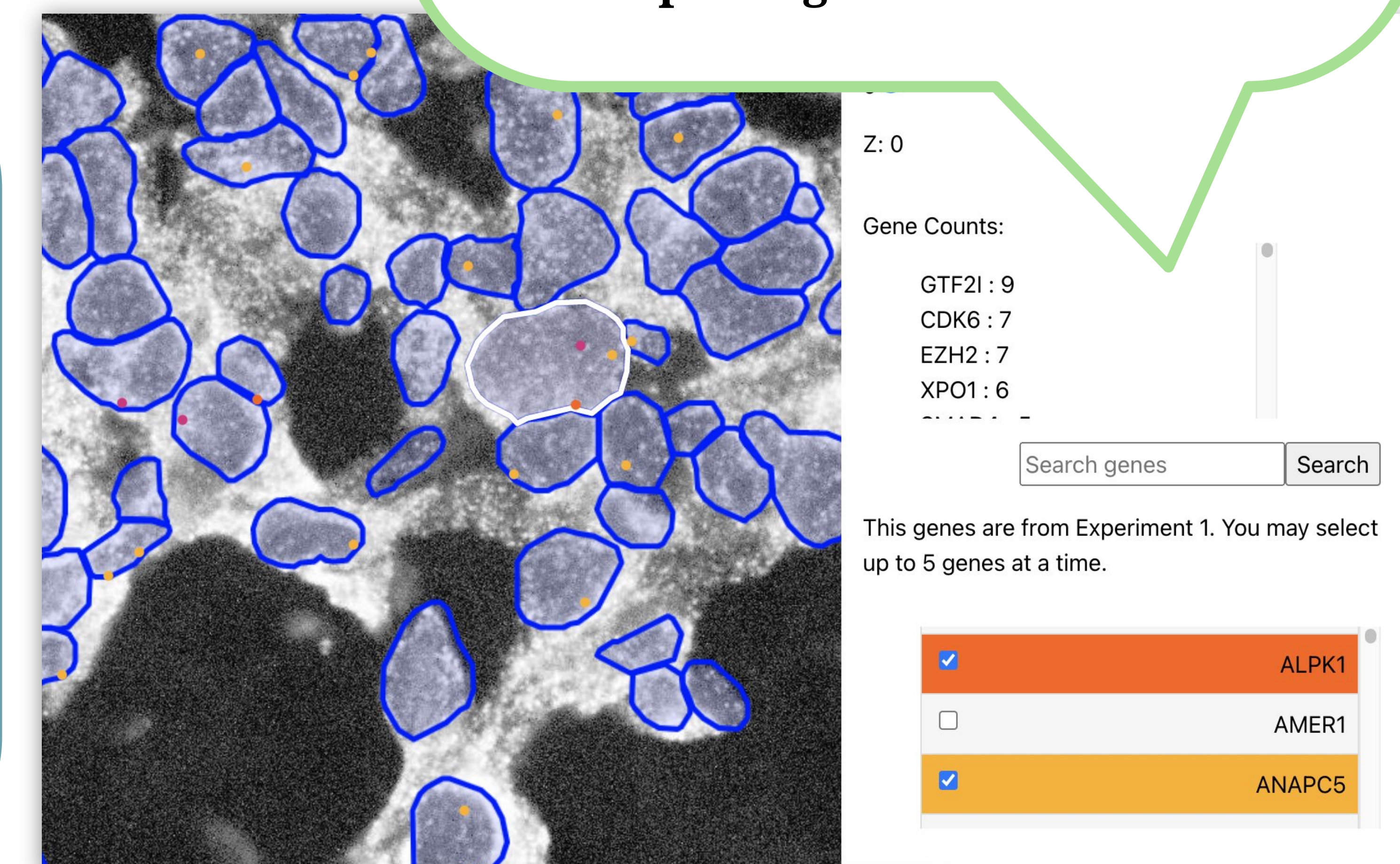
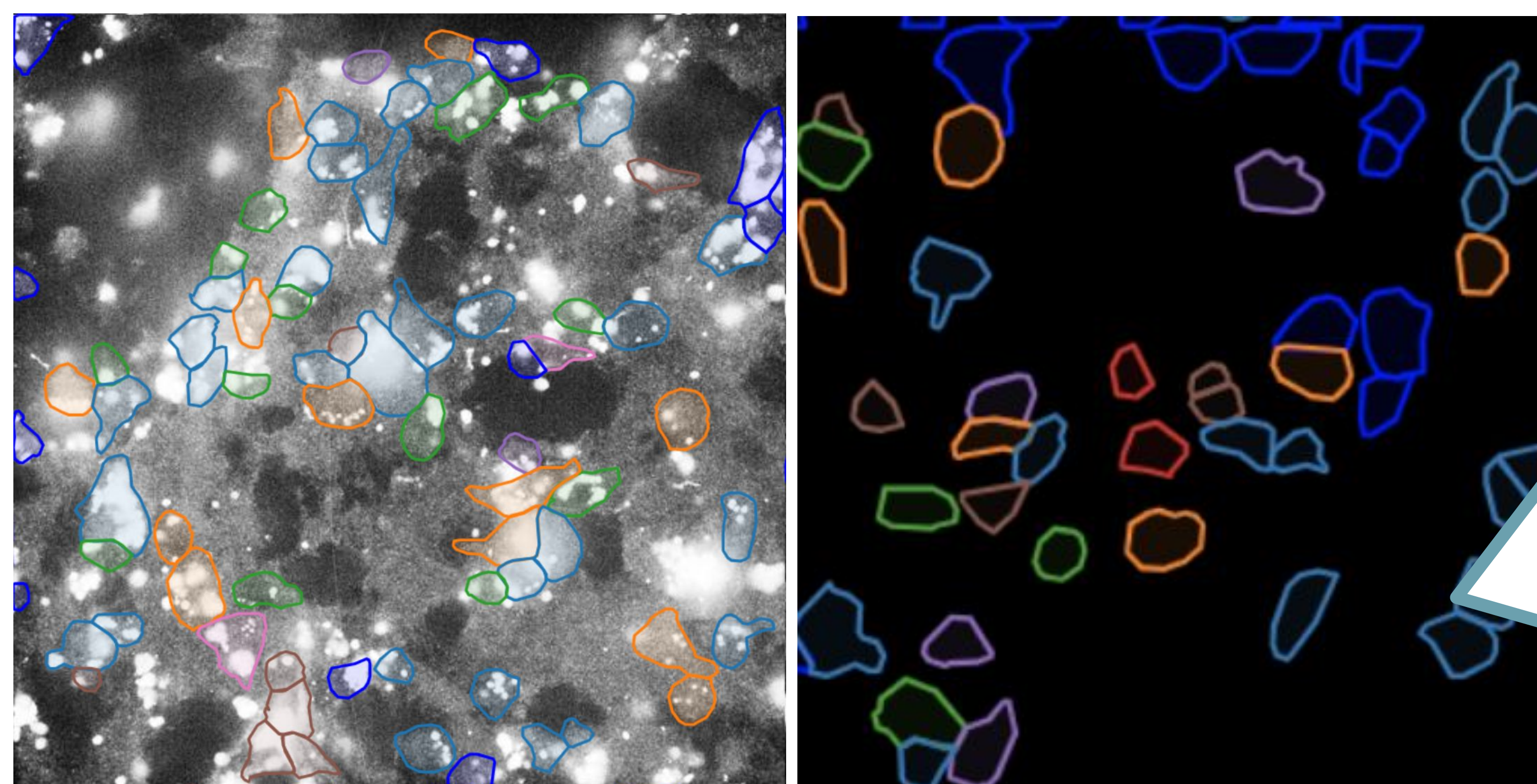
- ❖ In our interface, the user can select up to 5 genes to display at once
- ❖ Selecting a cell (below, white outline) displays the **number of times each gene is expressed** within that cell

Why this is useful: Analyzing gene expression in their native environment leads to **new biological insights.** It is the basis of **spatial genomics.**

Cell Layer

- ❖ Cells are displayed through their **boundaries** (computed offline), which are **outlined & clickable**
- ❖ Boundary colors can be used to indicate **cell type**
- ❖ Boundaries are stored as **polygon vectors**, which allows for efficient rendering

Why this is useful: Scientists often want to **compare gene expression across cells.** Outlining cell boundaries provides scientists with a **visual summary** of gene expression within cells.



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