CASE STUDY

Company: A precision medicine startup leveraging spatial metabolomics for oncology and metabolic disease research, focused on identifying spatially-resolved biomarkers for drug discovery.

Pain Point: Traditional metabolomics methods either lose spatial resolution (bulk) or tissue structure (single-cell). Existing tools lack support for multi-isotope labeling, outlier QC, and scalable automation, slowing translational research and delaying therapeutic development.

Approach: Elucidata deployed its integrated platform Polly for data orchestration, visualization, and LC-MS analysis to process and harmonize 100+ spatial metabolomics samples. The pipeline enabled isotopic labeling support (13C, 15N), natural abundance correction, and built-in QC, accelerating insight generation for metabolic flux analysis.

What the Customer Says

"Our workflows couldn't handle the complexity of labeled spatial metabolomics at scale. Elucidata's platform gave us high-quality data outputs within hours, not weeks while preserving critical spatial and isotopic context."

– Senior Scientist, Spatial Biology

Key Challenges

Loss of spatial resolution with conventional bulk or single-cell metabolomics

Manual, time-consuming LC-MS analysis for multi-isotope labeled samples

No built-in NA correction or outlier detection in existing tools

Fragmented workflows, requiring multiple platforms for a single study

How We Helped

1. Processed **100+ spatial samples** using our Integrated LC-MS Data solution
2. Orchestrated **spatial segmentation, automated QC, and visualizations**
3. Performed **NA correction** and delivered **fractional enrichment outputs**
4. Enabled **automated peak picking** with manual override flexibility
5. Provided **cohort-based comparative visualizations** in real time

Impact

<5 mins/sample from raw data to actionable outputs	**>90% reduction in QC-related reruns**
100+ samples processed at scale with multi-isotope compatibility	**6X faster** spatial metabolomics workflow with Polly