Outline

• Overview of Xenium Workflow
  • Supported Tissues, Block Generation, & Sectioning
  • Probe Hybridization Preparation
  • Instrument Operation Interactive Demo

• Pre-Designed Panels

• Overview of Xenium Custom Panel Design
  • Required Information & Files to Design a Custom Panel
  • Understanding the *In Situ* Optical Detection Budget
  • Understanding Probe Sets in Xenium Panel Design

• Xenium Analysis Overview

• Understanding Xenium Algorithms
  • Decoding
  • Cell Segmentation

• Understanding Xenium Outputs

• Reanalysis with Xenium Ranger

• Continuing Analysis with Community Software
Overview of Xenium Workflow

- Block Generation & Sectioning
- Probe Hybridization Preparation
- Instrument Operation Interactive Demo
A Simple Workflow: 3-6 Hours of Hands-On Time

From tissue to instrument start in 2-3 days, from instrument start to data in ~2 days

Sample Preparation | Probe hybridization, ligation, & amplification

FF or FFPE tissue sections on Xenium slides

Fixation & permeabilization (FF) or Deparaffinization & decrosslinking (FFPE)

Probe hybridization

Rolling circle amplification product

Ligation & primer hybridization for amplification

Simple ~4-6 hours hands on time workflow

Fluorescent probe hybridization, imaging & decoding | Data visualization

Xenium Analyzer

1. Fluorescent probe
2. Probe hybridization
3. Automated slide imaging
4. Probe removal
5. Cycle

Fully automated decoding and analysis
Supported Tissues, Block Generation, & Sectioning
Xenium is Compatible with a Large Variety of Tissues

Formal-fixed paraffin-embedded (FFPE)

Tissue array with 7 different human FFPE tissues run on a single Xenium slide
Xenium is Compatible with a Large Variety of FF and FFPE Tissues

Fresh Frozen (FF)
Generating FFPE Blocks for Xenium
Formal-fixed paraffin-embedded (FFPE)

FFPE Tissue Blocks

Human or Mouse FFPE Blocks

Fixation solution:
- 10% neutral buffered formalin (NBF) or 4% paraformaldehyde (PFA)

Carefully optimize fixation tissue size & time
- Over fixation → decreased RNA accessibility
- Under Fixation → RNA degradation
Sectioning FFPE Blocks for Xenium

Formal-fixed paraffin-embedded (FFPE)

Practice tissue placement on blank slide before using Xenium Slides
Xenium Sample Preparation for FFPE slides

- Deparaffinization to remove the wax
- Decrosslinking makes analytes (RNA and/or protein) accessible
  - Has a big impact on tissue adhesion and autofluorescence generation

Proceed immediately to Xenium In Situ Gene Expression - Probe Hybridization, Ligation & Amplification User Guide (CG000582)
Generating Fresh Frozen (FF) Blocks for Xenium

Fresh Frozen (FF)

**FF Tissue Embedded With OCT**

Image is representative; follow guidance in CG000579

**Human or Mouse FF Tissue**

- Tissue fresh freezing and OCT embedding
  - Fixed-frozen tissue is not supported at this time
- QC (H&E) tissue prior to placing on Xenium slide
- Section on to Xenium slide
  - 10 µm thickness
Sectioning FF Blocks for Xenium

Practice tissue placement on blank slide before using Xenium Slides
Xenium Sample Preparation
Fresh frozen sample/slides

- Fresh frozen tissue must be fixed to retain RNA
  - 4% PFA or 3.7% Formaldehyde

- Permeabilization allows RNA to be accessible and probes to enter cells

Proceed immediately to Xenium In Situ Gene Expression - Probe Hybridization, Ligation & Amplification User Guide (CG000582)
Xenium Cassette Assembly

Inspect cassette and gasket when removing from packing

1. Place dry slide in cassette
2. Press down on slide
3. Secure clips
4. Press down on all sides

After assembly, inspect all sides of cassette and gasket for tight seal
Probe Hybridization Preparation
Xenium Assay Workflow: Probe Hybridization Prep Overview

**Assay Workflow**

- Transforms RNA into detectable signatures through rolling circle amplification (RCA)
- Two slides processed in parallel
Hybridized probe

Probe Hybridization

- Probes target RNA
- Two regions independently hybridize to target RNA
  - Increases specificity
- Gene specific barcode and primer binding site
Xenium Assay Workflow - Ligation

Probe Ligation

Ligation

- Ligation seals junction between probe arms
- Generates circular DNA probe
Xenium Assay Workflow - Amplification

RNA Target Site

Amplification

- Ligation products enzymatically replicated
- Rolling Circle Amplification (RCA)
- 100s of copies of probes generated
Xenium Assay Workflow - Quenching and Staining

Xenium Assay Workflow - Autofluorescence Quenching and Nuclei Staining

**Autofluorescence Quenching**
- Proprietary autofluorescence mix
- Improves signal-to-noise ratio
- No tissue optimization required for FFPE and fresh frozen tissue

**Nuclei Staining**
- Assists in nuclei identification in overview scan
Xenium Assay Workflow - Validated Thermal Cyclers

Two slides on thermocycler adaptor

Which Thermal Cyclers Are Compatible with Xenium?

Best practices

- 10x recommends using adjustable lid models
  - Close lid and tighten until click is heard
  - Do not turn past the click
- Pre-equilibrate thermocycler adaptor
- Always run two slides at a time

E.g., Analytik Jena Biometra TAdvanced 96 SG (846-5-070-241)
Instrument Operation
Xenium On-Instrument Workflow
Xenium On-Instrument Workflow

Slide ID

Panel Information

Custom Panel
Xenium On-Instrument Workflow

Overview scan
Slide 1

Region selection:
- 12 total FoVs
- Contiguous rectangle
  - (3x4, 4x3, 2x6, 6x2)
- Avoid obvious defect - debris, low cell density, bubble, etc.

Initialize ~10-20 min
Load ~5 min
Sample Scan 1 h
Region Sel. ~10 min
Run ~24 hrs
Cleanup ~5 min
Unload ~10 min

Slide 1
Slide 2
Overview scan Slide 1
Overview scan with FoVs
Xenium On-Instrument Workflow

Xenium Analyzer Run

- During Xenium Analyzer run, instrument goes through a series of cycles
  1) First, rolling circle products are labeled with fluorescent signals
  2) Then, the signals are imaged at each cycle
  3) After imaging is complete, probes are removed to leave Rolling Circle Products available for subsequent cycles of RNA labeling
Pre-Designed Panels
Pre-Designed Panels: Design Philosophy
Expertly Curated, Experimentally Validated, Readily Available 10x In Situ Gene Panels

Data-driven approach to gene curation
• Publicly available scRNA-seq or other large datasets
  • Human Protein Atlas, Tabula Sapiens, Tabula Muris, etc
• Literature curation, especially for disease states

Eight pre-designed panels for cell typing using combinations of gene expression that uniquely label cell types

- Human & mouse
  ~ 250 to 380 genes/panel
- Six tissue specific panels
- Two multi-tissue panels
- Add up to 100 custom genes of interest
Panel and Custom Menu Offers Maximum Flexibility

Customize any panel or build your own standalone panel

Pre-designed & validated panels

- **Human Breast**
  - 280 genes

- **Human Lung**
  - 289 genes

- **Human Brain**
  - 266 genes

- **Human Multi-Tissue & Cancer**
  - 377 genes

- **Human Colon**
  - 322 genes

- **Mouse Brain**
  - 248 genes

- **Human Skin**
  - 260 genes

- **Mouse Multi-Tissue**
  - 379 genes

Add up to 100 custom targets

Coming Soon in 2024

5000 & 2000 gene panels
Overview of Xenium Custom Panel Design

- Required Information & Files to Design a Custom Panel
- Understanding the *In Situ* Optical Detection Budget
- Understanding Probe Sets in Xenium Panel Design
Build your Custom Panel Online with Xenium Panel Designer

Panel design algorithms specifically developed for 10x assays enable breadth of applications

- Design standard human and mouse gene expression **custom panels for up to 480 plex** independently

- Upgrade to advanced **custom panels** to access wide range of applications and species with 10x support

[Image: www.10xgenomics.com/products/xenium-panels]
Panel and Custom Menu Offers Maximum Flexibility

Customize any panel or build your own standalone panel

**Standalone custom**

- 480 custom genes
- 300 custom genes
- 100 custom genes
- 50 custom genes

Panels designed or under design:
- Rat
- Dog
- Zea mays
- Zebrafish
- Pig
- Mosquito
- And more…
Exclusive to Xenium: Isoform Detection
Xenium mBrain panel + custom probes for Isoforms -> Differential cell-type expression of isoforms

Cell typing with base panel

Snap-25 isoforms are differentially localized

Snap25 isoforms have regional localization (especially during development) involved with plasticity of neurons
Advanced Customization Enables Broader Applications
Unique padlock chemistry affords key applications with additional ones in development

Available Now
- Isoform/Translocations
- Diverse Species
- Xenografts
- Exogenous Sequences

Coming Soon
- Expressed SNVs
- TCR/BCR Profiling*

*Determine the V and J gene of the heavy and light chains paired for each T/B cell.
Required Information & Files to Design a Custom Panel
What Do You Need To Get Started With Panel Design?

- **A gene list**
  Selection of genes for elucidating biology of interest
  - Panel design app will recommend genes to remove, but will not recommend genes to include

- **A single cell reference**
  The panel design app has a selection of curated references from CELLxGENE that can be used if they work with the experimental model (mouse & human)
  - Can be either Chromium (fresh or Flex) or Visium (with reference-free deconvolution)
  - Matched reference is recommended, but is not required
  - Reference **must** be in 10x MEX or h5 format

- **Additionally for Advanced custom only (custom targets)**
  The sequence of the target transcript
The Importance of Single Cell Reference Data

Having closely matched scRNA-seq data is desirable

1. Determines how much optical budget the panel is using
2. Place highly expressed genes in the same cell type on optically distant barcodes
3. Provides a basis for choosing probeset coverage reduction

If you don’t have scRNA-seq data, you can use publicly available data from sources such as CELLxGENE

1. It is particularly important to find the best scRNA-seq dataset you can when you are working in diseased tissue
What is the In-situ Optical Detection Budget?

Careful panel design for optimal spot detection & high accuracy gene identification

Optical detection budget
Upper limit of spots that can be resolved in a single image

- Detection of genes is carefully divided in different cycles to avoid optical detection limit
- Gene expression per cell from scRNA-seq is used as a reference to select genes that maximize spot detection efficiency

Like **all** imaging based technologies, only a finite number of fluorescent signals can be distinguished within a given area or volume

<table>
<thead>
<tr>
<th>Detection Cycle/Channel</th>
<th>Distance of Events</th>
<th>Events (Detected/Present)</th>
<th>Optical Crowding</th>
</tr>
</thead>
<tbody>
<tr>
<td>A Different</td>
<td>Close</td>
<td>2/2</td>
<td>No</td>
</tr>
<tr>
<td>B Same</td>
<td>Far</td>
<td>2/2</td>
<td>No</td>
</tr>
<tr>
<td>C Same</td>
<td>Close</td>
<td>1/2</td>
<td>Yes</td>
</tr>
</tbody>
</table>
Optical Budget Considerations For Panel Design

Optical budget is reserved for add-on genes in 10x pre-designed panels

- Single Cell Gene Expression data is used to quantify the expression of a gene in the relevant cell type
- Ideally, select genes with a mean expression of at least 4/2 transcripts per cell
Highly expressed genes in an imaging based in situ panel need to be carefully evaluated.

Extremely highly expressed genes (EHEGs) can utilize all or most of the allocated optical detection budget for a particular cell, limiting detection of other genes within the cell.

- However, EHEGs can be included in the assay based on the biology of interest.
- Consider what cell types they are expressed in, and what information you are hoping to obtain from that cell type.

**EXAMPLE: Insulin**

- Highly expressed only in pancreatic beta cells.
- Including INS on your panel will effectively label beta cells.
- The remaining expression profile of the beta cells will be hard to determine.
- The other cell types in your experiment will be unaffected by the high expression of INS in beta cells.
Understanding Probesets in Xenium Panel Design

General info

By default, every gene on a panel has 8 probesets

- A probeset is one or more probes that cover every isoform of a given gene
- Some genes cannot have 8 probesets due to a variety of factors:
  - Gene length
  - Repeat content / GC content
  - Sites of known variation
- Some genes have zero probesets due to the above factors; if this is true for a gene you want on your panel, please contact 10x support
Understanding Probesets in Xenium Panel Design

Assay sensitivity

**Assay Sensitivity:** Number of transcripts detected per gene

The number of probesets for a gene have a roughly linear relationship with the sensitivity of the gene on the panel

- For highly expressed genes, reducing the probeset count will reduce the sensitivity i.e., fewer transcripts detected
- Recommendation: At least 3 probesets per gene
  - For some applications, single probeset per target can be used

**Note:**

- Reducing probeset count enables analysis of highly expressed genes
- Increasing probeset count enables analysis of lowly expressed genes
What to Think About When You Are Picking Your Gene List

1. What is the goal of my panel?
   1. Cell typing or something more?

2. How much am I willing to accept potential optical crowding?
   1. Lower sensitivity isn’t necessarily bad, depending on what you said to #1

3. Can I pick genes for my panel that give me the goals I want in #1 without picking highly expressed genes?

4. Can I pick non-redundant genes that represent my biology of interest?
   1. Only a single HLA class I gene
   2. Avoid multiple mitochondrial genes
   3. Representative gene from my pathway of interest

5. Are the genes I am interested in ubiquitously and/or highly expressed (collagen, immunoglobulins)

6. Are the genes I am interested in very lowly expressed?

7. Can I use co-expressed genes to infer my biological question without using a highly expressed gene?
Overview of the Xenium Panel Design Workflow

1. You will be asked to select one or more curated single cell references and/or upload your own single cell reference(s)

2. You will provide a gene list which is validated against the 10x Genomics 2020-A reference

3. The application will run the panel design algorithm
   1. Detects genes that are highly expressed and recommends either removing the gene or reducing the number of probesets for that gene
   2. If more genes are provided than the panel specification, recommends genes to drop based on the cell-typing efficiency of the panel
   3. Assigns genes to barcodes based on the expression profile to make the most of the optical budget

4. The application generates a summary report that shows you the recommended panel adjustments and how much of the optical budget is being used

5. Allows you to iterate on the panel by adjusting the gene list, manually change probeset counts, or use different single cell references
Xenium Analysis Overview
Common File Formats for Ease of Use

10x has extensive experience optimizing single cell and spatial data formats

Single-cell tools (filtering, clustering, trajectory analysis) continue to work with Xenium data

Usable data immediately after run ends

Seamless integration with Seurat, Squidpy, stLearn, Giotto, and Voyager
Usable Data Immediately After Your Run Ends

No additional steps of analysis time required to analyze and visualize your data

**ONBOARD ANALYSIS**

- Imaging
- Decoding
- Segmentation
- Cell assignment
- Clustering

**Morphology images**

**Localized Transcripts**

**Cell Segmentation**

**Unsupervised Clustering**
Xenium Explorer – Powerful interactive native visualization

Visualization is no longer just static plots
Understanding Xenium Algorithms

- Decoding
- Cell Segmentation
Decoding
A codebook is simply a collection of codewords assigned to genes.

Codewords determine when fluorescent signals (puncta) are expected across cycles and channels.

Each Xenium panel uses a codebook that contains 40 negative control codewords; each panel also includes 20 negative control probe sets (except the Xenium Mouse Brain Gene Expression Panel, which has 27).
Xenium Decoding

Decoding example of a single transcript across cycles and channels

- Example codeword: AEAEEDECEEEBEEE
- Using a probabilistic model that takes signal intensities, similarity to known codewords, and other attributes into account, Xenium can decode the example codeword to sub-pixel accuracy

See more at our [Overview of Xenium Algorithms](#) support page
Xenium decoding outputs include calibrated quality scores

- A Phred-scale calibrated quality score (Q-score) is assigned to each decoded transcript to signify the confidence in the decoded transcript identity

- This is just a re-scaling of the probability of error that a reported gene decoding is incorrect
  - Q-score = $-10 \times \log_{10}(P_{err})$

<table>
<thead>
<tr>
<th>Q-score</th>
<th>Error probability ($P_{err}$)</th>
</tr>
</thead>
<tbody>
<tr>
<td>10</td>
<td>10%</td>
</tr>
<tr>
<td>20*</td>
<td>1%</td>
</tr>
<tr>
<td>30</td>
<td>0.1%</td>
</tr>
</tbody>
</table>

*Xenium Q-score threshold >20 << 1% of reported transcripts are incorrectly decoded*
Xenium Measures $P_{err}$ Via Negative Control Codewords

- By definition, a call made to negative control codeword is an error.
- A call to a gene codeword might be correct or might be an error.
- We observe:
  - $D_g$ - number of puncta that decode to genes
  - $D_c$ - number of puncta that decode to controls
- Some errors are not observed because the error goes to another gene codeword - Correcting for that gives us:
  - $P_{err} = D_c / D_g \times N_g / N_c$
- So, we have an *in situ* measure of $P_{err}$, based on negative control codewords counts.

Negative Control Codewords are a random subset of codewords, with identical properties to gene codewords.
Xenium Q-Scores are Based on Empirical Calibration

Q-score calibration procedure:
1. Divide “raw” calls into bins according to confidence score
2. Within each bin, compute empirical $P_{err}$, based on formula
3. Convert $P_{err}$ to Q-score and assign to all calls in the bin

This guarantees that Xenium Q-scores are always well calibrated
• All counts regardless of Q-score are included in Xenium outputs

• The threshold for inclusion in secondary analysis is Q20

• This threshold is applied per-transcript

• Overall $P_{err}$ of calls > Q20: 0.05%
  - Only a small fraction of calls are at Q20
  - Most calls are > Q20
  - Therefore, the average decoding error rate is < 1%

Q-score distribution (Mouse Pup FFPE dataset)
Cell Segmentation
A Comprehensive Approach to Cell Segmentation

- Pathology
- Cell Morphology
- Stain Development
- Training and Benchmark Data
- Computational Methods
- Quantitative Performance Metrics

- Epithelial tissue
- Nervous tissue
- Connective tissue
- Muscle tissue
- Immune cells
- Adipocytes
- Fibroblasts

- Endothelial
- Glial
- Lining
- Neurons
- Microglia
- Astrocytes
- Oligodendrocytes
- Neurons

- Bone
- Blood
- Cartilage
- Stroma

- Smooth
- Cardiac
- Skeletal

- Pathology
- Cell Morphology
- Stain Development
- Training and Benchmark Data
- Computational Methods
- Quantitative Performance Metrics
Setting the Foundation with Xenium Nucleus Segmentation

State-of-the-art nucleus segmentation

A critical foundation for membrane, cytoplasm, and transcript-based methods

Human Cerebellum  Human Tonsil  Human Lung  Mouse Brain

See more in the segmentation section of our Overview of Xenium Algorithms support page
Shipping Q1 2024: Xenium Multi-Modal Segmentation

Xenium Multi-tissue Stain Mix

Membrane Antibody Cocktail

Interior Antibody Cocktail

Cytoplasmic RNA Stain

DAPI Nuclear Stain

Cell boundary & interior stain

Membrane segmentation

Interior stain with nuclear expansion

Nuclear expansion
Distinct Advantages of 4 Channel Cell Morphology Images

FFPE human colon

Nuclei

Interior antibody stain

Cytoplasmic RNA stain

Membrane antibody stain

Merge
Multi-Modal Segmentation - Built for Broad Tissue Coverage

FFPE human colon with cells colored based on clustering from Human Multi-Tissue panel
Understanding Xenium Outputs
Region Selection Occurs After an Overview Scan

See more in our Xenium Analyzer User Guide

Overview Scan
Layout and features seen following completion

Region Selection Guidance
Instructions to properly select regions

Options Panel
Toggle views on/off and adjust channels

Sample Area
Shows image of scanned sample

Region Information
View, add, edit or delete regions
Each Selected Region Produces a Separate Output Directory

- Each Xenium run can analyze two slides; each slide has an area of 12 x 24 mm divided into approximately 19 x 33 FOV (Fields of View)
- Slides can have multiple regions, which produce separate output bundles
- Output size is a function of tissue area and sample-specific factors like tissue shape, number of cells, number of decoded transcripts, and percent of high-quality transcripts

<table>
<thead>
<tr>
<th>Tissue</th>
<th>Tissue area (cm²)</th>
<th>Estimated output directory size (GB)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Core needle biopsy</td>
<td>0.01</td>
<td>0.2</td>
</tr>
<tr>
<td>Hemisphere of coronal mouse brain</td>
<td>0.5</td>
<td>10</td>
</tr>
<tr>
<td>Full coronal mouse brain</td>
<td>1</td>
<td>20</td>
</tr>
<tr>
<td>Tissue section covering entire sample area</td>
<td>2.35</td>
<td>60</td>
</tr>
</tbody>
</table>

The table shows estimated output directory sizes as a function of tissue area, assuming the sample has similar properties to a model mouse brain coronal section.
Gain immediate confidence in your data with key metrics and plots

Sample Region Summary
- Region name: whole_body
- Slide ID: 00009507
- Cassette name: mousepup_base_419
- Preparation method: ffpe

Analysis Summary Is Available On-Instrument

Key Metrics
- Median transcripts per cell: 113
- Number of cells detected: 1,355,849
- Decoded transcripts per 100 µm²: 130.6
- Total high quality decoded transcripts: 191,407,876

See more at our Overview of the Xenium Analysis Summary support page
Analysis Summary Is Available On-Instrument

Gain immediate confidence in your data with key metrics and plots

See more at our [Overview of the Xenium Analysis Summary](#) support page
Xenium Onboard Analysis Output Formats

**Morphology images**

**Transcripts w/ calibrated Q-scores**

**Cell segmentation**

**Cell-feature matrix & clustering**

See more at our [Understanding Xenium Outputs](#) support page
Reanalysis with Xenium Ranger
Xenium Ranger Enables Reanalysis & Custom Segmentation

Three pipelines with more in development

**Xenium Ranger** is run on a range of Linux distributions to reanalyze Xenium data and produce an output bundle that can be viewed in Xenium Explorer

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**Resegment**

Resegment Xenium data by adjusting cell expansion distance or nucleus intensity filter or by using our latest nucleus segmentation model.

---

**Import Segmentation**

Reassign transcripts in Xenium Ranger using segmentation results produced by 3rd party tools (Cellpose, Baysor, etc.) and visualize in Xenium Explorer.

---

**Relabel**

Correct the gene panel applied to decoded transcripts so a run doesn’t have to be restarted or aborted due to user error.
Cell boundaries on an H&E image of epithelial cells in human colon tissue show that reducing expansion distance to 5µm leads to more accurate cell boundaries for this sample.
Import-Segmentation: Leverage Alternative Methods

Image and transcript-based segmentation and QC in Xenium Explorer

Use the segmentation method which is best suited to your samples and experimental question and import results in Xenium Ranger

Supported segmentation formats:

- **Cellpose**: labeled mask in TIFF or NumPy NPY format
- **QuPath**: polygons in GeoJSON format
- **Baysor**: transcript-based segmentation outputs

Segmentation on post-Xenium IF images is possible by providing a transformation matrix which can be generated in Xenium Explorer
Continuing Analysis with Community Developed Tools & Software
Community Developed Tools Enable Path to Conclusions

An example

Cell Segmentation Refinement
- Refining cell segmentation based on transcriptional composition with Baysor
- Augmenting segmentation with post-Xenium IF imaging

Single Cell Style Analysis & Data Integration
- Clustering, cell typing, and differential expression
- QC, normalization
- Sample de-array, aggregation, batch correction

Spatial Context Analysis
- Layering histopathology annotations
- Spatial trajectory analysis
- Neighborhood enrichment analysis

Xenium Explorer Visualization & Validation
10x Provides Analysis Guides
Facilitate your continued journey with Xenium Analysis

- **Continuing Your Journey after Xenium Analyzer**: overview of community-developed tools

- **Using Baysor to Perform Xenium Cell Segmentation**

- **H&E to Xenium DAPI Image Registration with Fiji** (alternative to Xenium Explorer alignment)

*Note: Installing and running Baysor requires computational skill and compute infrastructure. The Baysor Analysis Guide was written using a previous version of Baysor - we recommend following Baysor instructions for installation.*
Conclusion
"The Xenium platform is providing us with unprecedented insight into the molecular pathology of disease at an incredible resolution."

Dr. Simon Gregory
Duke University

"It works like a charm, does the job as per specs and beyond. As I said it before, it's a cut above the rest."

Luciano Martelotto, PhD
University of Adelaide
Exceptional Launch Year
Early customer success, from install to insight
Biology’s Most Comprehensive Toolkit

Support a large diversity of samples

Provide robust pipelines and understandable data formats

Sample prep

Data analysis
Thank you!

Please attend our CytAssist GEX Workshop
Sprague Hall 105 - Jan 24th - 1:30 – 3 PM

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