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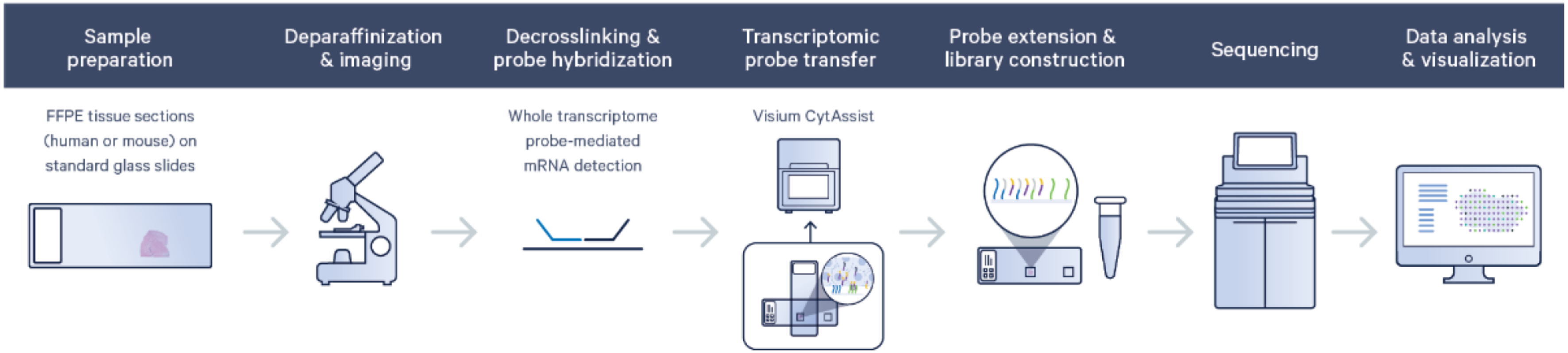
Spatial Gene Expression – 10x Genomics Visium CytAssist

Initial QC: RNA quality is important for high-quality data. Therefore, DV200-values of FFPE sections are assessed first. Samples must have a DV200-value > 30%.



Sample preparation → Deparaffinization & imaging → Decrosslinking & probe hybridization → Transcriptomic probe transfer → Probe extension & library construction → Sequencing → Data analysis & visualization

FFPE tissue sections (human or mouse) on standard glass slides

Whole transcriptome probe-mediated mRNA detection

Visium CytAssist

Figure 1: Workflow using Visium CytAssist. **Sample Prep:** FFPE sections are placed positively charged slides. **Imaging:** Sections can be H&E or IF stained and imaged. **Probe hybridization:** Sections are decrosslinked and probes hybridize to transcripts (transcripts targeted: ~18.000 for human sections or ~20.000 for mouse sections). **Transcriptomic probe transfer:** Probes get transferred to the Visium slide in the CytAssist instrument. **Probe extension and library construction**: Probes captured on the Visium slide get extended and thereby receive the spatial barcode. Released probes are build into libraries for **sequencing**. **Data analysis and Visualization** is performed using SpaceRanger.

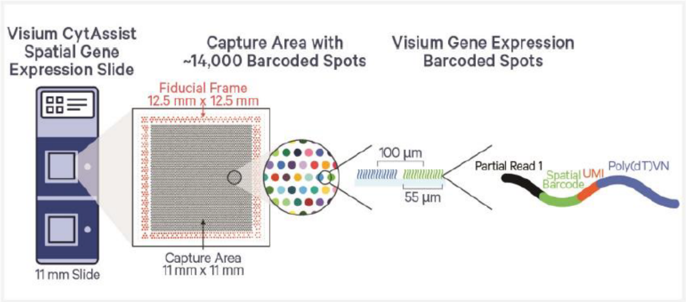


Figure 2: Closer view of Visium slide. Each capture spot has a unique spatial barcode.
11 mm slides have ~14.000 barcoded spots.
6.5 mm slides have ~5.000 barcoded spots.

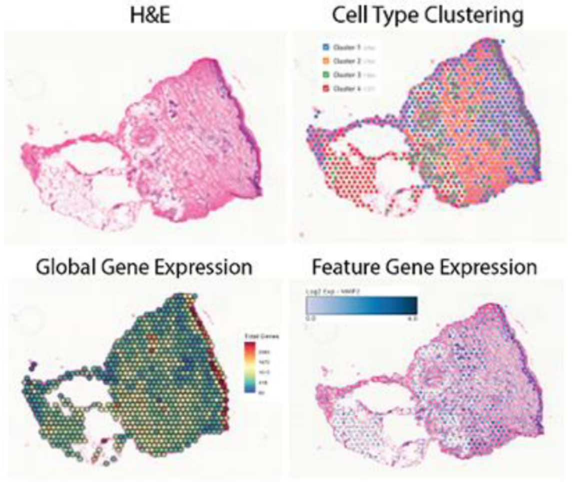


Figure 3: Data from transcriptome-wide gene expression allows to assess individual gene expression, cell type annotation, and global gene expression. Transcriptomic data can be visualized and shown in an overlay with the microscopic image. Visium thereby connects histology and genomics.