

Spatial designed for unimaginable scale



Atera

Atera provides unmatched spatial throughput and performance, allowing you to scale single cell spatial imaging studies beyond all previous limitations. With flexible run configurations and a > 500 mm² imageable area

per slide, Atera maximizes tissue throughput while offering the flexibility to tailor your experimental design to your needs. Capture your biology in exquisite detail with sensitivity equivalent to single cell assays. Our whole transcriptome assay enables unprecedented spatial biology experiments, including the ability to profile up to 800 whole transcriptome samples of 1 cm² each per year on one instrument. Never choose between spatial resolution and panel plex again.

Highlights

- Up to 800 1 cm² whole transcriptome samples per year
- > 500 mm² imageable area per slide for > 2,000 mm² total tissue per run when using all 4 slides
- Standard, off-the-shelf slide compatibility, with flexible run configurations
- Run 18,000-gene Atera WTA (whole transcriptome) and 1,000-gene Atera Select panels, with optional stacking of up to two 1,000-gene panels (stacking of up to three 1,000-gene panels coming soon)

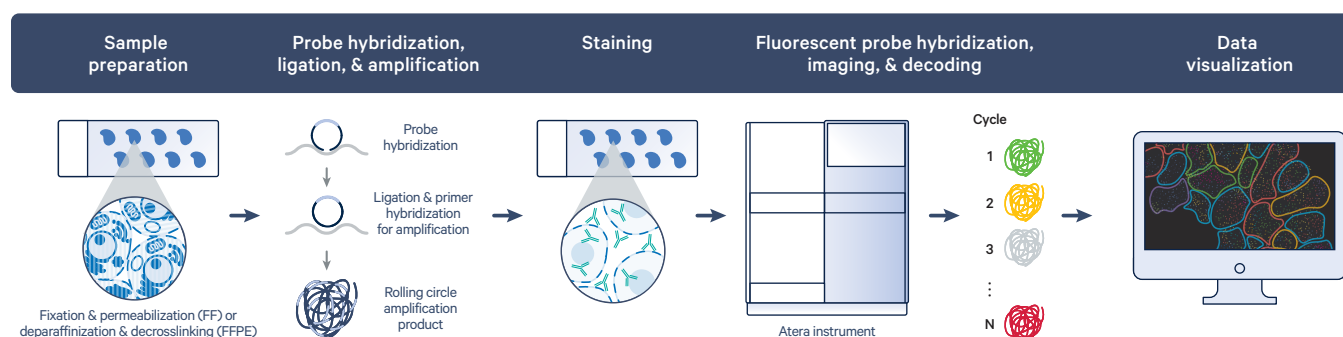


Figure 1. One universal workflow for unmatched, whole transcriptome spatial insights from your fresh frozen and FFPE tissue. After sectioning tissue onto a standard glass slide, probes from your chosen panel are bound, ligated, and amplified on-slide using a universal workflow. Following multimodal tissue staining, slides are then loaded onto the Atera instrument where fluorescence imaging, decoding, and analysis is performed automatically on-instrument.

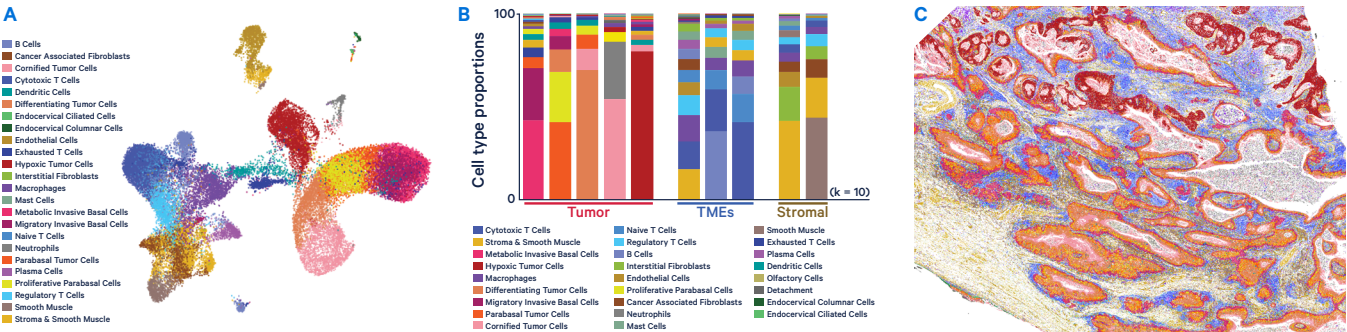


Figure 2. Spatial localization of major cell types in a clinical cervical cancer sample. **A.** UMAP (717,576 cells detected and 1.04B transcripts over ≥ 20) from FFPE stage III-B invasive squamous cell carcinoma of the human cervix using Atera WTA. **B.** Niche analysis for cell types detected in the cervical tumor microenvironment with Atera WTA. **C.** Representative spatial distribution of cells from cervical tissue.

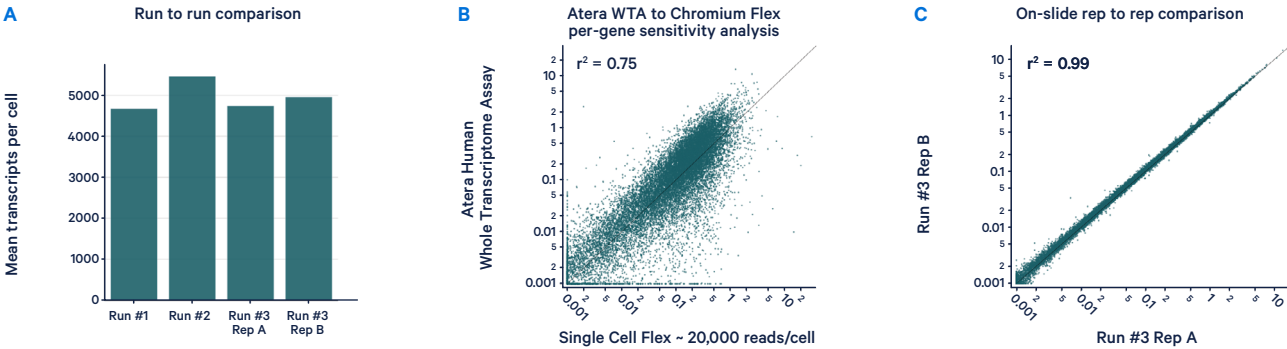


Figure 3. Sensitivity, specificity, and robustness of Atera. **A.** Sensitivity (transcript count per cell) of multiple replicates of FFPE human testis across several runs. **B.** Per-gene pseudobulk correlation analysis in human FFPE testis comparing Atera WTA to Chromium Single Cell Flex Apex. **C.** Representative plot of a correlation of transcript counts between two technical replicates in human testis using Atera WTA on the same slide.

Product specifications

Atera instrument specifications		Atera output and throughput	
Product numbers	1001128 (Atera instrument)	Resolution	Transcript XY-localization precision of < 30-nm and Z-localization precision of < 150-nm Pixel size: ~0.2 $\mu\text{m}/\text{pixel}$
Dimensions (W x D x H)	52.9" x 35.9" x 63.6" 134.5 cm x 91.3 cm x 161.5 cm	Sample preparation	2-3 days sample prep with 3-4 hours of hands-on time
Weight	1,350 lb 614 kg	Data output file formats	Cell-feature matrices: AnnData Transcripts and segmentation boundaries: Zarr Tissue images: OME-TIFF
Electrical requirements	100-240 VAC, 50-60 Hz, 1,600 W	Total tissue area analyzable per run	> 1,000 mm^2 for 2 slides > 2,000 mm^2 for 4 slides
Operating temperatures / Humidity	19-25°C (66-77°F), 30-80% relative humidity	Throughput	Atera Whole Transcriptome Assay • 7 days per run, 800 WTA samples of 1 cm^2 / year Atera Select Assays • up to 1,000 genes: 29 hours per run • up to 2,000 genes: 52 hours per run • up to 3,000 genes: 75 hours per run Note: Throughput estimates are for completion of data acquisition of a four-slide run with 4 cm^2 sample area per slide and 10 μm tissue thickness. Data acquisition and analysis are parallelized for up to two runs.
Cloud connectivity	Native compatibility with 10x Genomics Cloud instrument management for run monitoring and data egress to connected directories		
Ethernet link speed	Up to 10 Gbps		

Contact us
[10xgenomics.com](https://www.10xgenomics.com) | info@10xgenomics.com