Spatial Biology Platforms Compared: Xenium vs CosMx vs Visium HD

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Executive Summary

This comparison examines five commercial platforms: **Xenium** and **Visium HD** from **10x Genomics**; **CosMx SMI** and **GeoMx DSP**, now sold by **Bruker Spatial Biology** following Bruker's 2024 acquisition of NanoString's instrument business; and **MERSCOPE** from privately held **Vizgen**. Each platform answers a different version of the same question: where, in a tissue section, is a given gene or protein being expressed, and at what resolution. Xenium is an imaging-based in situ hybridization platform using a padlock-probe rolling-circle-amplification chemistry that 10x Genomics describes as unique among commercial in situ platforms (Source: www.10xgenomics.com), reaching transcript localization precision under 30 nanometers laterally (Source: www.10xgenomics.com). CosMx SMI, Bruker's competing single-cell imager, processes up to 3 million cells per slide and up to 26 slides per week (Source: dlmp.uw.edu) with panels scaling to 6,000-plex (Source: dlmp.uw.edu). MERSCOPE, built on Nobel-adjacent MERFISH (multiplexed error-robust fluorescence in situ hybridization) chemistry from Xiaowei Zhuang's Harvard laboratory, first shipped commercially on August 30, 2021 (Source: vizgen.com) and now offers panels up to 1,000 genes on its Ultra configuration (Source: vizgen.com). Visium HD, launched commercially on March 26, 2024 (Source: www.prnewswire.com), takes the opposite technical route: it is sequencing-based rather than imaging-based, using a continuous lawn of 2 by 2 micrometer barcoded squares to approximate single-cell resolution while capturing the whole transcriptome (Source: cdn.10xgenomics.com). GeoMx DSP takes a third route entirely, sacrificing single-cell resolution for operator-selected regions of interest at roughly 10-micron granularity and throughput of up to 40 slides per week (Source: brukerspatialbiology.com).

Peer-reviewed benchmarking provides useful evidence alongside vendor documentation, but individual studies should be interpreted in light of their disclosed funding, panels, tissues, and methods. A Nature Methods analysis of 25 Xenium datasets covering 6 million cells found Xenium the most sensitive in situ sequencing based technique, with sensitivity comparable to MERSCOPE (Source: www.nature.com). A separate Nature Communications tumor-tissue benchmark found Xenium's false discovery rate under 0.09 percent, markedly lower than CosMx or MERFISH, while CosMx detected higher raw transcript and gene counts per cell (Source: www.nature.com) (Source: www.nature.com). A January 2026 Genome Biology study from the Josep Carreras Leukaemia Research Institute and the Barcelona Supercomputing Center benchmarked five platforms head to head, Visium v1, Visium v2/CytAssist, Visium HD, Xenium, and CosMx, across six cancer types, and reported that Xenium showed consistently lower background noise and stronger spatial signal than CosMx (Source: link.springer.com).

Commercially, the market remains concentrated around two vendors following consolidation. Bruker closed its approximately $392.6 million cash acquisition of NanoString's instrument business, including GeoMx and CosMx, on May 6, 2024 (Source: www.nasdaq.com), following NanoString's Chapter 11 restructuring, and formally created a Bruker Spatial Biology division in October 2024 (Source: www.bruker.com). 10x Genomics reported full-year 2025 revenue of $642.8 million, up 5 percent from $610.8 million in 2024 (Source: www.prnewswire.com), with its spatial product line contributing roughly $178.1 million of that total across instruments and consumables (Source: www.prnewswire.com). Grand View Research pegs the global spatial transcriptomics market at $385.7 million in 2024, projected to reach $1.31 billion by 2033 at a 14.69 percent compound annual growth rate (Source: www.grandviewresearch.com). No platform wins on every axis: Xenium and CosMx compete on subcellular imaging fidelity and panel breadth, MERSCOPE competes on MERFISH's academic pedigree and flexible panel tiers, Visium HD offers a choice between broadly compatible probe-based protein-coding coverage and fresh-frozen 3′ expanded discovery, and GeoMx is principally an ROI platform optimized for region-level throughput and combined RNA-protein readouts. Its conventional quantitative RNA workflows generally require multi-cell ROIs, while its UV-cleaving area can resolve a single cell and its Discovery Proteome Atlas supports single-cell protein analysis with sensitivity constraints. Pharmaceutical and biotech organizations selecting among them in 2026 face a decision that is as much about downstream data infrastructure, panel design services, and informatics integration as it is about raw instrument specifications.

Introduction and Background

Spatial biology, the practice of measuring gene or protein expression while preserving each measurement's physical location within a tissue section, has moved from a handful of academic core facilities to a commercial instrument category with billions of dollars in projected market value. The field addresses a limitation that conventional single-cell RNA sequencing cannot: dissociating a tissue into single cells for sequencing destroys the spatial context of the tumor microenvironment, the neural circuit, or the immune infiltrate that a researcher is often trying to characterize in the first place. Spatial platforms solve this by reading out molecular signals directly on an intact tissue section, either through iterative imaging of fluorescent probes or through spatially barcoded sequencing.

This report compares five commercial platforms: 10x Genomics' **Xenium** and **Visium HD**; Bruker Spatial Biology's **CosMx SMI** and **GeoMx DSP**; and privately held Vizgen's **MERSCOPE**. Bruker acquired the CosMx and GeoMx instrument businesses from NanoString in 2024 for approximately $392.6 million in cash, assuming certain liabilities (Source: www.nasdaq.com). These platforms split into two technical families. Imaging-based platforms, Xenium, CosMx, and MERSCOPE, use rounds of fluorescent probe hybridization and optical decoding to localize individual transcripts at or near single-molecule resolution. Sequencing-based platforms, Visium HD and, to a lesser extent, GeoMx's oligo readout, spatially barcode a tissue region and then rely on a conventional next-generation sequencer to identify what was captured where.

This report compares all five platforms directly on capabilities, adoption, and peer-reviewed performance evidence, without treating any of them as a foregone winner. It draws on official vendor documentation and technical notes, financial filings and investor disclosures from 10x Genomics (NASDAQ: TXG) and Bruker (NASDAQ: BRKR), and peer-reviewed benchmarking studies published in Nature Methods, Nature Communications, and Genome Biology through early 2026. Because pharmaceutical and biotech organizations increasingly need spatial biology data to flow into broader translational medicine, regulatory, and commercial data infrastructure rather than sit in a single core facility's file server, this report also considers the organizational side of platform selection. Firms such as **IntuitionLabs**, a life-sciences and AI consultancy, note that they specialize exclusively in the pharmaceutical and life sciences industries, including biotech, medical devices, diagnostics, and CROs (contract research organizations) (Source: intuitionlabs.ai), underscoring that instrument selection is only the first step; integrating high-dimensional spatial output into existing enterprise systems is a separate and often underestimated project.

The secondary questions this report answers include how Xenium, CosMx, and MERSCOPE compare on single-cell resolution; how Visium HD stacks up against Xenium on throughput and pricing; how CosMx and GeoMx, now sibling products under one vendor, are positioned relative to each other; and which platform is best suited to a pharmaceutical sponsor's translational or biomarker discovery program as opposed to an academic core facility's broad-service model.

Xenium (10x Genomics): In Situ Hybridization at Subcellular Resolution

Capabilities

Xenium is 10x Genomics' imaging-based in situ platform, delivering what the company describes as high-plex in situ analysis at subcellular resolution with nanometer precision (Source: www.10xgenomics.com). Its chemistry relies on padlock probes and rolling circle amplification (RCA), a combination 10x states is unique among commercial in situ platforms (Source: www.10xgenomics.com). The Xenium Analyzer instrument achieves transcript localization precision under 30 nanometers in the lateral (X and Y) plane and under 150 nanometers axially (Z) (Source: www.10xgenomics.com). A single run processes two slides and up to roughly 472 square millimeters of tissue, completing a 480-gene panel in under three days or a 5,000-gene panel in under six days (Source: www.10xgenomics.com), with sample preparation requiring two to three days and four to six hours of hands-on time before the automated run begins (Source: www.10xgenomics.com).

The panel menu spans sub-500-gene targeted panels up to the 5,000-gene Xenium Prime 5K panel, customizable with up to 100 additional genes (Source: www.10xgenomics.com), and 10x Genomics states it delivered over 10,500 custom genes to Xenium customers between January 2023 and January 2025 (Source: www.10xgenomics.com). Xenium supports both fresh-frozen and formalin-fixed paraffin-embedded (FFPE) tissue in a single universal workflow (Source: www.10xgenomics.com), and the company has extended the platform with a same-cell multiomics add-on, Xenium Protein, combining RNA and protein detection on a single section (Source: www.10xgenomics.com). 10x also claims Xenium analyzes more tissue per run, 427 to 472 square millimeters, than competing imaging platforms, which it says top out around 300 square millimeters (Source: www.10xgenomics.com), a vendor claim that should be read alongside the independent benchmarks discussed later in this report. On pricing, 10x Genomics does not publish list prices; one U.S. government-facing distributor lists the Xenium Analyzer instrument under a GSA (General Services Administration) contract at approximately $394,669 per unit (Source: www.govsci.com), though this figure reflects one reseller's contract price rather than an official list price and should be treated as indicative only.

Adoption

10x Genomics commercially launched Xenium on December 8, 2022, announcing the first global shipments of the Xenium Analyzer (Source: www.prnewswire.com). By August 29, 2023, eight months after launch, the company had shipped more than 100 Xenium Analyzer instruments (Source: www.prnewswire.com). By the end of 2023, cumulative Xenium installations reached 255 units, out of 5,966 total instruments 10x Genomics had sold across its Chromium, Visium, and Xenium lines combined (Source: www.stocktitan.net). By the end of 2024, that figure had grown to more than 400 Xenium instruments installed, alongside more than 800 Visium units and more than 5,800 Chromium units (Source: www.genengnews.com). 10x Genomics reported 2024 total revenue of $610.8 million and full-year 2025 revenue of $642.8 million ($598.7 million excluding one-time patent litigation settlement revenue) (Source: www.prnewswire.com). May 29, 2024 saw the launch of the Xenium Prime 5K Pan-Tissue and Pathways panel, expanding the targeted panel ceiling to 5,000 genes (Source: www.prnewswire.com).

Strengths and Limitations

Independent, non-vendor-authored studies give the clearest read on Xenium's real-world performance relative to peers. A Nature Methods benchmarking analysis of 25 Xenium datasets spanning 6 million cells and 1.2 billion reads found Xenium to be the most sensitive in situ sequencing based technique among those it examined, with sensitivity comparable to MERSCOPE and another ISH-based method, Molecular Cartography (Source: www.nature.com); the same study noted the panels analyzed in that dataset spanned only 210 to 392 genes, narrower than some competing panels (Source: www.nature.com). A separate Nature Communications benchmark on FFPE tumor tissue found Xenium's false discovery rate under 0.09 percent, substantially lower than CosMx or MERFISH in the same comparison (Source: www.nature.com), though the same study found that CosMx, running a higher-plex panel, detected more total transcripts and unique genes per cell (Source: www.nature.com), a real tradeoff between panel breadth and per-target specificity rather than a simple win for either platform. Xenium's principal limitation relative to Visium HD and GeoMx WTA (whole transcriptome atlas) panels is that it remains a targeted, panel-based method even at its 5,000-gene ceiling, rather than an unbiased whole-transcriptome readout.

CosMx SMI (Bruker Spatial Biology): High-Plex Single-Cell Imaging

Capabilities

CosMx SMI (Spatial Molecular Imager) is Bruker's single-cell and subcellular imaging platform, acquired along with the rest of NanoString's instrument business in 2024. Grant documentation for the platform specifies system throughput of up to 3 million cells per slide, up to 4 slides per run, and up to 26 slides per week (Source: dlmp.uw.edu), with subcellular resolution of 120 nanometers and transcript localization precision under 50 nanometers (Source: dlmp.uw.edu). Multiplexing capacity scales to 6,000-plex RNA panels and up to 76-plex protein panels, with a flexible scan area up to 300 square millimeters per slide, compatible with FFPE, fresh-frozen tissue, organoids, and cultured cells (Source: dlmp.uw.edu). The optical system uses custom water-immersion optics with 1.1 numerical aperture (NA) and 22.78X magnification, imaging five fluorophores per cycle across a 0.51 by 0.51 millimeter field of view (Source: dlmp.uw.edu). A demonstration dataset using the 960-plex panel classified more than 800,000 cells across 8 slides from 5 non-small-cell lung cancer (NSCLC) FFPE tumors (Source: dlmp.uw.edu).

As of February 2026, Bruker markets CosMx as capable of multiomic imaging, the whole transcriptome plus 64 or more proteins, from a single FFPE or fresh-frozen tissue section (Source: brukerspatialbiology.com), and is developing a CosMx Mouse Whole Transcriptome assay with early access planned for spring 2026 (Source: brukerspatialbiology.com). The CosMx Human Whole Transcriptome panel covers approximately 19,000 RNA targets across essentially all protein-coding genes (Source: brukerspatialbiology.com), while the CosMx Human 6K Discovery Panel profiles 6,000 RNA targets plus more than 400 ligand-receptor pairs and can be customized with up to 200 additional targets (Source: brukerspatialbiology.com). In a self-reported comparison table, Bruker states CosMx's whole-transcriptome mode captures all cells on a section with zero cell loss, versus roughly 35 percent cell loss typically associated with dissociation-based single-cell RNA sequencing (Source: brukerspatialbiology.com), a vendor claim rather than an independently replicated measurement.

Adoption

Bruker closed its acquisition of NanoString's instrument business, encompassing nCounter, GeoMx, CosMx, and AtoMx, for approximately $392.6 million in cash on May 6, 2024 (Source: www.nasdaq.com), the year after NanoString had generated approximately $168 million in revenue in 2023 (Source: www.nasdaq.com). At the time of the acquisition, NanoString's underlying technologies had enabled more than 7,000 peer-reviewed publications (Source: www.nasdaq.com), a figure Bruker's current spatial biology homepage still cites as "7,000 Publications and counting" (Source: brukerspatialbiology.com). Bruker projected the acquired business would be dilutive to non-GAAP earnings per share by $0.15 to $0.20 for the remainder

of 2024, targeting near-break-even performance by 2026 (Source: www.nasdaq.com). In October 2024, Bruker formally created a dedicated Bruker Spatial Biology division combining GeoMx, CosMx, and AtoMx with Canopy Biosciences and Bruker Spatial Genomics (Source: www.bruker.com). A University of Glasgow researcher quoted on Bruker's site describes CosMx's large capture area as enabling characterization of "100s of samples weekly" using tissue microarrays drawn from clinical trial cohorts (Source: brukerspatialbiology.com).

Strengths and Limitations

CosMx's principal strength is raw multiplexing and per-cell detection depth: the independent Nature Communications benchmark referenced above found CosMx detected the highest transcript and unique gene counts per cell among the platforms it tested (Source: www.nature.com). Its principal weakness in the same body of independent literature is signal specificity: the same benchmark found CosMx's false discovery rate the highest among the platforms compared, and a separate PMC (PubMed Central)-indexed study similarly reported Xenium consistently showed higher expression counts on matched genes than CosMx in tumor tissue microarrays, with Xenium showing the lowest false discovery rate of the platforms tested while CosMx showed the highest (Source: pmc.ncbi.nlm.nih.gov). The same study found CosMx recovered fewer distinct cell types in breast tissue than Xenium, identifying only six cell subtypes where Xenium resolved more (Source: pmc.ncbi.nlm.nih.gov). Instrument list pricing is not publicly disclosed by Bruker; prospective buyers are directed to a quote-request process rather than a published price sheet.

MERSCOPE (Vizgen): MERFISH-Based Spatial Genomics

Capabilities

MERSCOPE runs Vizgen's MERFISH chemistry, which the company describes as combinatorial labeling, sequential imaging, and error-robust barcoding (Source: vizgen.com), technology originally developed in Xiaowei Zhuang's Harvard laboratory and marketed by Vizgen as the first commercially available high-plex single-cell spatial genomics platform (Source: vizgen.com). Current gene panel imaging kits come in three multiplexing tiers: 18-bit encoding for up to 140 genes, 21-bit for up to 300 genes, and 27-bit for up to 1,000 genes (Source: vizgen.com), and custom panels built on the newer MERFISH 2.0 chemistry can target up to 960 genes (Source: vizgen.com). The base MERSCOPE instrument supports up to 1 square centimeter of imageable tissue per flow chamber, with throughput up to 3.0 square centimeters of tissue per week; the higher-end MERSCOPE Ultra configuration raises that ceiling to 9.0 square centimeters per week (Source: info.vizgen.com), using FCX-S (1.25 square centimeter) and FCX-L (3.0 square centimeter) flow chambers, multiplex capacity up to 1,000 genes, and transcript localization precision of 20 nanometers or better in the X and Y planes (Source: info.vizgen.com). MERSCOPE Ultra pairs a back-thinned cooled sCMOS (scientific complementary metal-oxide-semiconductor) camera with 58 terabytes of on-instrument storage (Source: info.vizgen.com). Both configurations run validated workflows for fresh-frozen and FFPE tissue while preserving morphology and spatial context (Source: vizgen.com).

Adoption

Vizgen began shipping the first commercial MERSCOPE instruments on August 30, 2021, to the Salk Institute, UC Irvine, and Beth Israel Deaconess Medical Center (Source: vizgen.com), following an earlier $14 million seed round from ARCH Venture Partners and Northpond Ventures in early 2020 (Source: endpoints.news). MERSCOPE's full U.S. commercial launch followed on January 18, 2022 (Source: vizgen.com). In January 2026, Vizgen closed a $48 million financing round led by ARCH Venture Partners and co-led by M Ventures and Northpond Ventures (Source: vizgen.com), which Vizgen's chief executive, Rob Carson, described as putting the company "on a march to profitability" following resolution of prior litigation (Source: vizgen.com). Vizgen was co-founded by Xiaowei Zhuang, David Walt, and Jeffrey Moffitt, and is headquartered in Waltham, Massachusetts with research and development based in Cambridge, Massachusetts (Source: vizgen.com). Since late 2024, the company states its customers have published more than 100 new high-impact peer-reviewed articles using the platform, alongside the rollout of MERFISH 2.0 chemistry (Source: vizgen.com).

Strengths and Limitations

MERSCOPE's clearest strength is flexibility across panel sizes and its academic pedigree, tracing directly to the laboratory that invented MERFISH; a large-scale application of that pedigree is discussed in the Case Studies section below. Independent benchmarking, however, complicates the sensitivity picture. A June 2025 Genome Biology comparison of imaging-based spatial platforms on tumor cryosections found MERSCOPE's false discovery rate at 5.23 percent, over ten times higher than Xenium's in the same comparison (Source: pmc.ncbi.nlm.nih.gov), even as the same study found Xenium the highest-correlating platform against an RNAscope reference standard at r equals 0.82 (Source: pmc.ncbi.nlm.nih.gov). As with CosMx, no public MERSCOPE or MERSCOPE Ultra instrument list price is available; Vizgen operates a quote-request sales model rather than a published price list.

Visium HD (10x Genomics): Sequencing-Based Whole Transcriptome Spatial Mapping

Capabilities

Visium HD is architecturally distinct from Xenium, CosMx, and MERSCOPE: rather than imaging fluorescent probes cycle by cycle, it spatially barcodes a tissue region and reads the result out on a standard next-generation sequencer. 10x Genomics commercially launched Visium HD Spatial Gene Expression on March 26, 2024, describing it as enabling whole-transcriptome spatial discovery at single-cell-scale resolution from FFPE tissue (Source: www.prnewswire.com), with 10x's chief technology officer Michael Schnall-Levin calling it "the most requested product in our history" (Source: www.prnewswire.com). The underlying slide architecture replaces the 55-micrometer hexagonal spots of standard Visium with a continuous lawn of contiguous 2 by 2 micrometer barcoded squares and no gaps between capture areas (Source: www.prnewswire.com), confirmed in 10x's own technical documentation describing the slides as a continuous lawn of oligos rather than discrete spots (Source: cdn.10xgenomics.com). Visium HD offers two capture area sizes, 6.5 by 6.5 millimeters and 11 by 11 millimeters, with two capture areas per slide, and is compatible with human, mouse, and rat tissue plus a species-agnostic 3 prime assay (Source: www.10xgenomics.com). The Visium HD whole-transcriptome (WT) panel assay is probe-based and compatible with fresh frozen, fixed frozen, and FFPE tissue, while the Visium HD 3 prime assay is poly(A) capture based and restricted to fresh-frozen tissue (Source: cdn.10xgenomics.com).

Crucially, Visium HD runs exclusively on the Visium CytAssist instrument, not a dedicated imager: probes are hybridized to tissue and precisely transferred onto the barcoded slide via the CytAssist (Source: www.10xgenomics.com), and the resulting spatially barcoded libraries are sequenced on standard Illumina instruments including the NovaSeq 6000, NextSeq 2000, or NovaSeq X series (Source: www.10xgenomics.com). This means Visium HD's capital cost profile differs fundamentally from Xenium, CosMx, or MERSCOPE: a laboratory with an existing Illumina sequencer and CytAssist instrument does not need to buy a new dedicated imaging platform to run Visium HD, though sequencing depth and reagent costs scale with the number of samples processed rather than being fixed per instrument-run the way imaging platform costs are.

Adoption

10x Genomics explicitly positions Visium HD and Xenium as complementary rather than competing products within its own portfolio: whole-transcriptome, sequencing-based Visium HD for unbiased discovery, versus targeted, imaging-based Xenium Prime 5K for up to 5,000 genes at subcellular resolution (Source: www.10xgenomics.com). Xenium's readout, by contrast, relies on multiple rounds of fluorescent probe hybridization and imaging on the Xenium Analyzer, a fundamentally different mechanism from Visium HD's sequencing-based approach (Source: www.10xgenomics.com). A bioRxiv preprint from December 2024, cited by 10x as supporting evidence, reported Visium HD showed superior spatial fidelity compared with other commercially available sequencing-based spatial transcriptomics platforms (Source: www.10xgenomics.com). A June 2025 Nature Genetics paper used Visium HD to map immune cell interactions in the colorectal cancer tumor microenvironment (Source: www.10xgenomics.com), and a March 2025 Frontiers in Oncology paper authored by Bristol Myers Squibb scientists used the related Visium for FFPE assay to identify cholesterol metabolism as a factor in colorectal cancer immunotherapy resistance (Source: www.frontiersin.org) (Source: www.frontiersin.org), illustrating pharmaceutical-sector adoption of 10x's sequencing-based spatial line specifically.

Strengths and Limitations

Visium HD's strengths depend on the assay selected. The HD WT Panel is a sequencing-efficient, probe-based option for protein-coding gene coverage across FFPE, fresh-frozen, and fixed-frozen tissue; HD 3′ uses poly(A) capture for expanded whole-transcriptome discovery from fresh-frozen tissue (10x Genomics. For both assays, the 2 by 2 micrometer bins provide single-cell-scale profiling through spatial barcodes and computational analysis rather than direct visualization of individual transcripts within cells; turnaround also depends on sequencer queue and depth rather than a fixed imaging-run duration. Neither 10x Genomics nor its resellers publish a public list price for Visium HD reagent kits or the CytAssist instrument; academic core facilities typically publish their own per-sample pass-through pricing, which was outside the scope of vendor-sourced figures verifiable for this report.

GeoMx DSP (Bruker Spatial Biology): Region of Interest Digital Spatial Profiling

Capabilities

GeoMx DSP (Digital Spatial Profiler) is principally a region-of-interest (ROI), biology-driven profiling platform: rather than imaging every cell, researchers select tissue compartments to profile (Source: brukerspatialbiology.com). Its UV-cleaving area can resolve a single cell, but Bruker recommends at least 20 cells per ROI for protein analysis and 100 for RNA analysis in conventional quantitative workflows because smaller ROIs can yield insufficient signal. GeoMx selects those regions of interest down to roughly 10-micron resolution using a digital micromirror array that exposes only the masked tissue area to ultraviolet light, releasing photocleavable oligonucleotide barcodes from that region alone, and supports throughput of up to 40 slides per week with unattended overnight runs (Source: brukerspatialbiology.com). The GeoMx Human Whole Transcriptome Atlas panel provides an unbiased view of more than 18,000 protein-coding genes and is validated for both FFPE and fresh-frozen tissue, read out via next-generation sequencing rather than imaging (Source: brukerspatialbiology.com). On the protein side, GeoMx assays enable quantitative spatial analysis of up to 1,200 proteins from a single FFPE or fresh-frozen section using photocleavable oligonucleotide-barcoded antibodies (Source: brukerspatialbiology.com), and as of February 2026 Bruker's Discovery Proteome Atlas extends this further, profiling more than 1,200 protein targets in a single assay alongside whole-transcriptome RNA data (Source: brukerspatialbiology.com).

Adoption

GeoMx's combined transcriptomic and proteomic capability is frequently the deciding factor cited by adopting labs. A University of York researcher quoted on Bruker's site states the deciding factor in obtaining GeoMx DSP was its ability to look at both transcriptomic and proteomic information from the same platform (Source: brukerspatialbiology.com). A Wake Forest researcher similarly describes relying on GeoMx to complement CosMx, using GeoMx for broader hypothesis testing and CosMx SMI specifically for true subcellular spatial analysis of cell-cell interactions (Source: brukerspatialbiology.com), a direct end-user illustration of Bruker's own positioning of GeoMx and CosMx as complementary tools addressing regional versus single-cell resolution respectively (Source: www.bruker.com). GeoMx's oncology adoption extends into pharmaceutical-relevant clinical trial cohorts: a European Urology study from researchers affiliated with UNC Lineberger Comprehensive Cancer Center used GeoMx proteomic digital spatial profiling on muscle-invasive bladder cancer samples drawn from two named neoadjuvant chemoimmunotherapy trials, LCCC1520 (pembrolizumab) and BLASST-1 (nivolumab) (Source: pubmed.ncbi.nlm.nih.gov).

Strengths and Limitations

GeoMx's principal strength is its reported throughput and multiomic breadth per slide: Bruker reports up to 40 slides per week with unattended overnight runs. This figure should not be used to rank GeoMx against platforms reported in tissue-area or other non-equivalent throughput units. That is also its principal limitation for conventional quantitative RNA workflows: these generally rely on multi-cell ROIs, so research requiring routine cell-by-cell transcript mapping is better served by Xenium, CosMx, or MERSCOPE. GeoMx's UV-cleaving area can resolve a single cell, and its Discovery Proteome Atlas describes single-cell protein analysis, although smaller ROIs may have limited sensitivity. As with the other platforms in this comparison, Bruker does not publish a public list price for the GeoMx DSP instrument.

Feature Comparison

Table 1 below summarizes the core technical specifications of all five platforms side by side, drawing on vendor documentation and technical notes verified for this report.

PLATFORM	VENDOR	TECHNOLOGY TYPE	RESOLUTION	MAXIMUM MULTIPLEXING	SAMPLE TYPES	THROUGHPUT
Xenium	10x Genomics	Imaging (padlock probe RCA) (Source: www.10xgenomics.com)	Subcellular, XY < 30 nm, Z < 150 nm (Source: www.10xgenomics.com)	Up to 5,000 genes (Xenium Prime 5K), plus Xenium Protein add-on (Source: www.10xgenomics.com)	FFPE and fresh frozen, single universal workflow (Source: www.10xgenomics.com)	2 slides/run, ~472 mm² tissue, 480-gene panel in < 3 days, 5,000-gene panel in < 6 days (Source: www.10xgenomics.com)
CosMx SMI	Bruker Spatial Biology	Imaging (cyclic hybridization/imaging/cleavage) (Source: dlmp.uw.edu)	Subcellular, 120 nm, precision < 50 nm (Source: dlmp.uw.edu)	Human 6K Discovery: 6,000 RNA targets; Human WTX: ~19,000 RNA targets (CosMx Human Whole Transcriptome Assay product bulletin	FFPE, fresh frozen, organoids, cultured cells (Source: dlmp.uw.edu)	Up to 3 million cells/slide, 4 slides/run, 26 slides/week (Source: dlmp.uw.edu)
MERSCOPE	Vizgen	Imaging (MERFISH combinatorial barcoding) (Source: vizgen.com)	Subcellular, XY precision ≤ 20 nm (Ultra) (Source: info.vizgen.com)	Up to 1,000 genes (27-bit panels) (Source: vizgen.com)	FFPE and fresh frozen, validated workflows (Source: vizgen.com)	Up to 3.0 cm²/week (base), up to 9.0 cm²/week (Ultra) (Source: info.vizgen.com)
Visium HD	10x Genomics	Sequencing (spatially barcoded NGS via CytAssist) (Source: www.10xgenomics.com)	2 x 2 µm contiguous bins, near single cell scale (Source: cdn.10xgenomics.com)	Whole transcriptome, unbiased, no fixed gene ceiling (Source: www.prnewswire.com)	WT panel: FFPE, fixed frozen, fresh frozen; 3' assay: fresh frozen only (Source: cdn.10xgenomics.com)	2 capture areas/slide, 6.5x6.5 mm or 11x11 mm; throughput bound by sequencer, not imager (Source: www.10xgenomics.com)
GeoMx DSP	Bruker Spatial Biology	Region of interest profiling, DMD-based UV release + NGS/nCounter readout (Source: brukerspatialbiology.com)	Region-level; ROIs can physically be as small as 10 µm, but Bruker recommends at least 20 cells for protein and 100 cells for RNA quantification, not single-cell profiling (Bruker GeoMx DSP knowledge base	18,000+ genes (WTA) or up to 1,200 proteins (Source: brukerspatialbiology.com)	FFPE and fresh frozen (Source: brukerspatialbiology.com)	Up to 40 slides/week, unattended overnight (Source: brukerspatialbiology.com)

The table makes clear that no single specification column has one winner. Based on vendor-reported specifications—not an independently normalized performance ranking—Xenium and MERSCOPE report the smallest transcript-localization precision values; CosMx reports the highest cells-per-slide capacity and offers both a 6,000-target discovery panel and a human whole-transcriptome assay covering approximately 19,000 RNA targets; Visium HD's HD WT Panel offers probe-based protein-coding coverage across the broadest sample types, while its fresh-frozen HD 3′ assay supports expanded discovery; and GeoMx reports the highest slides-per-week throughput because it forgoes single-cell profiling. Buyers should read vendor-published throughput and precision numbers, particularly Bruker's and 10x Genomics' own comparison claims, as upper-bound figures achieved under optimized conditions rather than guaranteed performance on any given tissue type, a caveat that motivates the peer-reviewed benchmarking data presented next.

Performance and Benchmarks

Vendor specification sheets describe what a platform is capable of under ideal conditions; peer-reviewed benchmarking studies assess particular tissues, panels, segmentation methods, and metrics. The studies summarized here identify trade-offs—for example, lower background or stronger spatial coherence for Xenium in some comparisons and broader panel coverage or higher raw per-cell counts for CosMx—but do not establish a universal platform ranking.

Table 2 summarizes five peer-reviewed benchmarking studies published between 2025 and 2026 that directly compared two or more of the five platforms covered in this report.

STUDY (JOURNAL, DATE)	PLATFORMS COMPARED	KEY FINDING
Nature Methods, March 2025 (Source: www.nature.com)	Xenium, MERSCOPE, Molecular Cartography (25 Xenium datasets, 6 million cells)	Xenium the most sensitive in situ sequencing based technique, comparable to MERSCOPE
PMC (PubMed Central)-indexed FFPE benchmark (Source: pmc.ncbi.nlm.nih.gov)	Xenium, CosMx, MERFISH	Xenium showed 14.6-fold more counts than CosMx on matched genes in a breast tumor TMA (tissue microarray); Xenium retained 95 to 97 percent of cells post-filtering (Source: pmc.ncbi.nlm.nih.gov)
Nature Communications, September 2025 (Source: www.nature.com)	Xenium, CosMx, MERFISH	Xenium's FDR (false discovery rate) under 0.09 percent; CosMx detected higher total transcript and unique gene counts per cell
Genome Biology, June 2025 (Source: pmc.ncbi.nlm.nih.gov)	Xenium, MERSCOPE, RNAscope HiPlex, Molecular Cartography, Visium	Xenium highest correlation with RNAscope reference (r equals 0.82); MERSCOPE FDR of 5.23 percent, over ten times Xenium's
Genome Biology, January 2026 (Source: link.springer.com)	Visium v1, Visium v2/CytAssist, Visium HD, Xenium, CosMx (six cancer types)	Xenium showed consistently lower background noise and stronger spatial signal than CosMx despite comparable cell-type calls

The January 2026 Genome Biology study, conducted jointly by the Josep Carreras Leukaemia Research Institute and the Barcelona Supercomputing Center, is a comprehensive investigator-led, peer-reviewed comparison that systematically benchmarked five commercial spatial transcriptomics platforms—Visium v1, Visium v2/CytAssist, Visium HD, Xenium, and CosMx—on matched FFPE tumor sections across six cancer types. Its acknowledgements state that NanoString and Longwood Laboratories funded the CosMx experiments, while 10x Genomics and Bonsai Labs funded the Xenium experiments (Source: link.springer.com). Its finding of broadly comparable cell-type patterns alongside different raw-data characteristics should not be read as functional interchangeability: the study also reported gene-specific differences, including examples in which CosMx localization was more biologically faithful and signals that a Xenium panel did not contain. Earlier work, including the Genome Biology tumor-cryosection study from June 2025, additionally found that imaging-based platforms as a class detected 2.3 to 2.5-fold higher transcript counts per cell than single-nucleus RNA sequencing on matched genes (Source: pmc.ncbi.nlm.nih.gov), reinforcing the broader case for spatial platforms over dissociation-based sequencing regardless of which specific spatial vendor is chosen. Notably, none of these peer-reviewed studies benchmark GeoMx DSP against the single-cell imaging platforms on identical metrics. GeoMx is principally an ROI platform, and its conventional quantitative RNA workflows generally require multi-cell ROIs; its UV-cleaving area can nevertheless resolve a single cell, and current DPA materials describe single-cell protein analysis with sensitivity limitations. Comparisons involving GeoMx in the literature instead commonly focus on concordance with bulk RNA sequencing or other region-based protein assays rather than per-cell sensitivity or false discovery rate.

Data Analysis and Evidence

The spatial biology instrument market sits within a broader spatial transcriptomics market that Grand View Research estimated at $385.7 million globally in 2024, projecting growth to $1.31 billion by 2033 at a 14.69 percent compound annual growth rate (CAGR) from 2025 to 2033 (Source: www.grandviewresearch.com) (Source: www.grandviewresearch.com). That growth rate implies the category will more than triple in size over the coming decade, driven in large part by pharmaceutical and biotech adoption for translational biomarker work rather than academic research alone.

At the corporate level, 10x Genomics reported full-year 2025 revenue of $642.8 million, a 5 percent increase from $610.8 million in 2024 (Source: www.prnewswire.com), with the spatial product line contributing $34.1 million in instrument revenue and $144.0 million in consumables revenue, roughly $178.1 million combined (Source: www.prnewswire.com). Full-year 2025 gross margin across the company was 69 percent, up from 68 percent in 2024 (Source: www.prnewswire.com). On the Bruker side, full-year 2025 total company revenue reached $3.44 billion, up 2.1 percent from $3.37 billion in 2024 (Source: ir.bruker.com), and Q1 2026 revenue reached $823.4 million, up 2.7 percent year over year (Source: ir.bruker.com); neither release isolates spatial-biology-segment revenue from Bruker's broader life-science and diagnostics reporting, a data gap worth flagging for anyone trying to size Bruker's spatial business specifically against 10x Genomics' more granular disclosure.

Installed-base figures show the relative maturity of each vendor's spatial franchise. 10x Genomics had shipped 255 Xenium instruments by the end of 2023, alongside 531 Visium and 5,180 Chromium units, for 5,966 instruments total (Source: www.stocktitan.net), and grew to more than 400 Xenium units, more than 800 Visium units, and more than 5,800 Chromium units by the end of 2024 (Source: www.genengnews.com). NanoString's pre-acquisition 2023 revenue was approximately $168 million (Source: www.nasdaq.com), against which Bruker's approximately $392.6 million acquisition price (Source: www.nasdaq.com) implies a purchase multiple of roughly 2.3 times trailing annual revenue, consistent with an asset acquisition out of Chapter 11 bankruptcy proceedings rather than a strategic premium acquisition of a healthy standalone company. Competitive tension between the two dominant vendors surfaced directly in patent litigation: in late December 2024, a U.S. District Court upheld a roughly $31.6 million patent-infringement award against NanoString (by then Bruker) tied to its GeoMx product, a win for 10x Genomics (Source: www.genengnews.com), a reminder that the intellectual property underlying these chemistries remains actively contested even as the two companies market their platforms as addressing different market segments.

Case Studies and Real-World Examples

MD Anderson Cancer Center: Xenium in a Dedicated Institutional Core

The University of Texas MD Anderson Cancer Center operates a CPRIT (Cancer Prevention and Research Institute of Texas) Advanced Spatial Genomics core facility directed by Dr. Nicholas Navin (Source: www.mdanderson.org), whose instrumentation list confirms an installed 10x Genomics Xenium Analyzer that the core describes as a state-of-the-art single-cell spatial imaging platform (Source: www.mdanderson.org). The same list also includes a Visium CytAssist, so this is an example of a major cancer center operating Xenium for imaging-based single-cell spatial work, not evidence that it has standardized exclusively on Xenium.

Allen Institute for Brain Science: MERSCOPE at Whole-Organ Scale

The Allen Institute for Brain Science generated the spatial layer of its widely cited 2023 whole-mouse-brain cell-type atlas using Vizgen's MERSCOPE platform (Source: www.nature.com), published in Nature on December 13, 2023. The dataset comprised approximately 4.3 million MERFISH-profiled cells across 59 coronal brain sections (Source: www.nature.com), making it among the largest published single-platform spatial datasets from any of the five platforms compared in this report and a direct demonstration of MERSCOPE's suitability for whole-organ-scale atlasing projects rather than single-tumor-section studies.

UNC Lineberger Comprehensive Cancer Center: GeoMx in Named Immunotherapy Trials

Researchers affiliated with UNC Lineberger Comprehensive Cancer Center used the GeoMx platform to perform proteomic digital spatial profiling of muscle-invasive bladder cancer (MIBC) samples drawn from two named neoadjuvant chemoimmunotherapy trials, LCCC1520 (pembrolizumab) and BLASST-1 (nivolumab), publishing the results in European Urology in December 2023 (Source: pubmed.ncbi.nlm.nih.gov). This case demonstrates GeoMx's specific role in clinical trial biomarker analysis, where region-level proteomic profiling of pre- and post-treatment biopsies, rather than single-cell imaging, was the appropriate technical fit for correlating spatial protein expression with checkpoint-inhibitor response.

Washington University School of Medicine: CosMx Within the HuBMAP Consortium

Washington University School of Medicine's Jain Lab published an open laboratory protocol for CosMx spatial transcriptomics under funding from the NIH (National Institutes of Health) Human BioMolecular Atlas Program (HuBMAP) consortium, crediting NIDDK (National Institute of Diabetes and Digestive and Kidney Diseases) grant U54DK134301 (Source: www.protocols.io), and the protocol explicitly names the commercial platform used as Bruker NanoString's CosMx technology (Source: www.protocols.io). This case shows CosMx's adoption within a federally funded, multi-institutional tissue-atlas consortium alongside the single-institution and single-vendor examples above, indicating the platform's role in large collaborative mapping efforts as well as individual cancer center cores.

Josep Carreras Leukaemia Research Institute and Barcelona Supercomputing Center: A Five-Platform Head-to-Head

The Josep Carreras Leukaemia Research Institute (Badalona, Spain) and the Barcelona Supercomputing Center jointly ran a comprehensive investigator-led, peer-reviewed technical benchmark comparing five commercial spatial transcriptomics platforms—Visium v1, Visium v2/CytAssist, Visium HD, Xenium, and CosMx—on matched FFPE tumor sections spanning six cancer types, published in Genome Biology in January 2026. The paper discloses that NanoString and Longwood Laboratories funded the CosMx experiments and that 10x Genomics and Bonsai Labs funded the Xenium experiments (Source: link.springer.com). Unlike the single-platform institutional cores above, this case is itself a direct answer to the question this report was written to address: which platform performs best under identical experimental conditions, and its finding that Xenium showed consistently lower background noise and stronger spatial signal than CosMx despite comparable cell-type calls (Source: link.springer.com) is among the most direct, recent, and methodologically rigorous pieces of evidence available on relative platform performance as of 2026.

Implications and Future Directions

Bruker's February 2026 AGBT (Advances in Genome Biology and Technology) conference announcements point toward platform convergence rather than continued specialization. The company's spatial biology portfolio now explicitly groups GeoMx DSP and CosMx SMI, alongside CellScape and PaintScape instruments, as a cohesive multiomic ecosystem spanning DNA, RNA, and protein measurement (Source: brukerspatialbiology.com), and the same announcement introduced expanded CosMx capabilities for spatial microRNA (miRNA) and T-cell receptor (TCR) assays at subcellular resolution (Source: brukerspatialbiology.com). Notably, Bruker's own materials describe a new spatial discovery mode in its AtoMx Spatial Informatics Platform that prepares data exports specifically for conversational large language models (Source: brukerspatialbiology.com), a signal that vendors themselves now anticipate downstream AI-assisted analysis as a standard part of the spatial biology workflow rather than an afterthought.

That anticipated AI layer sits on top of a more basic and frequently underestimated challenge: getting large spatial datasets—including multi-gigapixel imaging data from Xenium, CosMx, and MERSCOPE, and sequencing libraries or count matrices from GeoMx and Visium HD—into a pharmaceutical sponsor's existing translational medicine, regulatory, and commercial data infrastructure in a form that cross-functional teams beyond the generating laboratory can actually use. This is squarely the kind of problem that life-sciences-focused data engineering and AI consultancies are built to address rather than something a spatial biology vendor's own software typically solves end to end. IntuitionLabs, for instance, describes its data engineering practice as providing robust data pipelines, integration, warehousing, and business intelligence for actionable insights (Source: intuitionlabs.ai), the kind of capability a pharmaceutical organization needs once its translational biology group has already chosen a spatial platform and generated the first several terabytes of imaging or count-matrix data. Given that Grand View Research projects the broader spatial transcriptomics market to grow at a 14.69 percent CAGR through 2033 (Source: www.grandviewresearch.com), the volume of this integration problem across the pharmaceutical industry is likely to grow roughly in step with instrument adoption, independent of which specific vendor or vendors a given organization standardizes on.

Looking forward, the clearest structural trend is that the choice is increasingly not "Xenium or CosMx or MERSCOPE" in isolation, but which combination of a single-cell imaging platform, a whole-transcriptome sequencing-based platform, and, where proteomic and region-level throughput matters, a GeoMx-style ROI platform, best serves a given research and clinical development portfolio. Continued patent litigation between 10x Genomics and Bruker over core chemistries (Source: www.genengnews.com) suggests further legal disputes remain plausible even as the companies pursue complementary rather than head-to-head product positioning within their own portfolios.

Frequently Asked Questions (FAQs)

How do Xenium, CosMx, and MERSCOPE compare on single-cell resolution? All three are imaging-based platforms capable of subcellular resolution. Xenium achieves transcript localization precision under 30 nanometers laterally (Source: www.10xgenomics.com), CosMx achieves 120-nanometer subcellular resolution with sub-50-nanometer transcript localization precision (Source: dlmp.uw.edu), and MERSCOPE Ultra reports transcript localization precision of 20 nanometers or better (Source: info.vizgen.com). Independent benchmarking, rather than these vendor specification sheets, is the more reliable guide to real-world performance: Xenium has repeatedly scored best on false discovery rate and correlation with reference methods across multiple 2025 and 2026 peer-reviewed studies (Source: www.nature.com) (Source: pmc.ncbi.nlm.nih.gov).

How does Visium HD compare with Xenium on throughput and pricing? Visium HD is sequencing-based, running on the Visium CytAssist instrument and a standard Illumina sequencer (Source: www.10xgenomics.com), so its turnaround time depends on sequencer queue and read depth rather than a fixed imaging run. Xenium runs a fixed protocol of under three days for a 480-gene panel or under six days for a 5,000-gene panel on a dedicated Xenium Analyzer (Source: www.10xgenomics.com). Neither vendor publishes a public list price; one GSA-contract reseller listing put the Xenium Analyzer at approximately $394,669 per unit (Source: www.govsci.com), while Visium HD's cost structure is spread across CytAssist instrument, reagent kit, and sequencing costs rather than a single imager purchase.

Is CosMx or GeoMx better for a given project? They are not really substitutes for one another under Bruker's own positioning: GeoMx is a region of interest platform aimed at broader hypothesis testing and combined transcriptomic-proteomic profiling (Source: brukerspatialbiology.com), while CosMx is aimed at true subcellular, single-cell spatial analysis of cell-cell interactions (Source: brukerspatialbiology.com). A project needing single-cell mapping should default to CosMx; a project needing rapid, high-throughput regional screening across many slides, up to 40 per week (Source: brukerspatialbiology.com), should default to GeoMx.

Which platform is best for single-cell resolution overall? Among the platforms compared here, Xenium, CosMx, and MERSCOPE all offer dedicated single-cell to subcellular transcript imaging; Visium HD approximates it through computational binning of sequencing reads rather than direct single-molecule imaging. GeoMx is principally an ROI platform: conventional quantitative RNA workflows generally require multi-cell ROIs, although its UV-cleaving area can resolve a single cell and its Discovery Proteome Atlas supports single-cell protein analysis with sensitivity limitations. Peer-reviewed multi-platform benchmarks through early 2026 have reported stronger Xenium signal specificity in some comparisons (Source: link.springer.com), while CosMx has led on raw multiplex depth and total transcript counts per cell in the same body of literature (Source: www.nature.com).

Which spatial transcriptomics platform should a pharmaceutical or biotech organization buy? No single answer applies across all use cases. The choice depends on whether the project needs broad sample compatibility with probe-based protein-coding coverage (Visium HD WT Panel), fresh-frozen expanded whole-transcriptome discovery (Visium HD 3′), direct single-cell/subcellular imaging with a panel suited to the biological question (Xenium, CosMx, or MERSCOPE), or rapid region-level throughput with combined RNA and protein readout (GeoMx). Benchmarks should inform assay-specific evaluation rather than a default recommendation: their results depend on tissue, panel content, segmentation, and the metric being compared (Genome Biology. Given that instrument list prices are largely undisclosed across all five platforms, organizations evaluating a purchase should request vendor quotes directly and weigh total cost of ownership, including consumables, panel design, and data infrastructure integration, rather than instrument price alone.

How does GeoMx DSP differ fundamentally from the other platforms? GeoMx is the only platform in this comparison that is architecturally a region-of-interest profiler. Xenium, CosMx, and MERSCOPE directly image transcripts at single-cell/subcellular resolution, while Visium HD provides single-cell-scale spatial profiling through barcoded bins. GeoMx uses a digital micromirror array to selectively release oligonucleotide barcodes from operator-defined tissue regions (Source: brukerspatialbiology.com). Conventional quantitative RNA workflows are generally interpreted as aggregate signal from multi-cell ROIs, because Bruker recommends at least 100 cells per RNA ROI for sufficient signal; however, the UV-cleaving area can resolve a single cell, and the Discovery Proteome Atlas describes single-cell protein analysis with sensitivity constraints.

Conclusion

Xenium, CosMx SMI, MERSCOPE, Visium HD, and GeoMx DSP represent five genuinely distinct technical approaches to spatial biology rather than five interchangeable versions of the same instrument. Xenium and CosMx compete most directly on imaging-based single-cell resolution. Published benchmarks identify trade-offs between specificity, signal, panel content, and per-cell detection, but their results are assay- and study-specific rather than a universal ranking; the January 2026 Genome Biology comparison, for example, used mid-2025 capabilities and disclosed vendor funding of the CosMx and Xenium experiments. MERSCOPE offers a flexible, academically pedigreed alternative built on MERFISH chemistry, well suited to large-scale atlasing projects. Visium HD abandons the imaging approach entirely in favor of sequencing-based single-cell-scale profiling: its HD WT Panel is probe-based with protein-coding gene coverage and broad tissue compatibility, while its fresh-frozen HD 3′ assay supports expanded whole-transcriptome discovery, complementing rather than replacing 10x Genomics' own Xenium line (10x Genomics. GeoMx DSP occupies a different niche altogether, emphasizing higher regional throughput and combined RNA and protein readouts. Its conventional quantitative RNA workflows generally use multi-cell ROIs, while its UV-cleaving area can resolve a single cell and its Discovery Proteome Atlas supports single-cell protein analysis with sensitivity limitations—a profile that can suit clinical trial biomarker cohorts better than tumor microenvironment cell-mapping studies.

Commercially, the platforms compared here are offered by 10x Genomics, Bruker Spatial Biology—which acquired NanoString's instrument business in 2024—and independent company Vizgen. All three continue to invest heavily: Bruker's February 2026 roadmap additions, 10x Genomics' continuing Xenium and Visium HD panel expansions, and Vizgen's January 2026 financing round all point toward further capability growth rather than market stagnation. For a pharmaceutical or biotech organization, the practical decision rarely reduces to a single "best" platform. It instead depends on whether the immediate scientific question calls for unbiased discovery, maximum single-cell specificity, maximum multiplex depth, or rapid region-level throughput, paired with a realistic plan for integrating whatever terabytes of imaging or count-matrix data the chosen platform produces into the organization's broader translational and regulatory data infrastructure. Given the pace of platform updates evident through mid-2026, any organization making this decision should treat vendor specification sheets as a starting point and independent peer-reviewed benchmarking as the deciding evidence.

Tags: spatial biology, spatial transcriptomics, xenium, cosmx, merscope, visium hd, geomx dsp, 10x genomics, bruker spatial biology, spatial omics

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