

Table S1. Comparison of DNA array-based spatial transcriptomic assays

ST method	DNA features	Barcode sequencing for each array	Feature diameter(s) (μm)	Feature center distance(s) (μm)	Percentage of array area covered by features ^a	Feature density (features per mm^2)	Array substrate ^b	Tissue used for ST assays ^c	cDNA synthesis & amplification methods ^d	Mean UMIs ^e	Data
Visium	Spotted DNAs	No	55	100	27%	~110	Glass	Mouse OB, 10- μm thickness, tissue fixation & permeabilization	TSO & PCR	15,377/55 μm	GSE153859 (10.1101/2020.08.24.252296)
DBiT-seq	Microfluidic wells	No	1) 10 2) 20 3) 50	1) 20 2) 40 3) 100	25%	1) 2500 2) 625 3) 100	Microfluidic channel-divided tissue	Mouse embryo, 7- μm thickness, tissue fixation & permeabilization	TSO & PCR	~5,000/10 μm	GSE137986 (10.1016/j.cel.2020.10.026)
Slide-seqV2	Assembled beads	Yes	10	10	78%	1×10^4	Glass	Mouse OB, 10- μm thickness, fresh frozen	RPE & PCR	494/10 μm	(10.1038/s41587-020-0739-1)
HDST	Assembled beads	Yes	2	3	34%	1.07×10^5	Silicon	Mouse OB, 10- μm thickness, tissue fixation & permeabilization	T7 aRNA	12/10 μm or 2/2 μm	GSE130682 (10.1038/s41592-019-0548-y)
Seq-Scope	Illumina DNA clusters	Yes	≥ 0.5	≤ 0.8	$\leq 70\%$	$\leq 1.5 \times 10^6$	Linear PAA coating	Mouse liver, 10- μm thickness, tissue fixation & permeabilization	RPE & PCR	$\sim 1000/10 \mu\text{m}$	GSE169706 (10.1016/j.cel.2021.05.010)
Stereo-seq	DNA nanoballs	Yes	0.22	1) 0.5 2) 0.715	1) 15% 2) 7%	1) 4×10^6 2) 1.96×10^6	Silicon	Mouse OB, 10- μm thickness, tissue fixation & permeabilization	RPE & PCR	$\sim 1450/10 \mu\text{m}$ or 59/2 μm	GSE153164 (10.1016/j.cel.2022.04.003)
Pixel-seq	Polonies	No	~1	~1	> 90%	$\leq 1 \times 10^6$	Crosslinked PAA gel	Mouse OB, 10- μm thickness, fresh frozen	TSO & PCR	977/10 μm or 47/2 μm	GSE186097

Notes:

^a: The percentages for Visium, DBiT-Seq, Slide-seqV2, HDST, and Stereo-seq were calculated based on reported feature sizes, densities, and spatial patterns.

The percentage for Seq-scope was measured by analyzing a reported cluster image of the flowcell hybridized with the highest template concentration (100 pM).

^b: PAA, polyacrylamide.

^c: Different RNA capturing conditions were used in ST methods and some captured RNAs from multiple cell layers from a whole tissue section.

^d: TSO, template-switching oligo; RPE, random priming and extension; T7 aRNA, T7 RNA polymerase-based amplification.

Different amplification methods have different yields. RPE can increase the capture efficiency.

^e: UMI counts were obtained from the original publications.

Table S2. Consumable lists for the stamping and sequencing-based polony gel fabrication

Table S3. Comparison of DNA cluster and DNA nanoball-based assays

	Seq-Scope ^a	Stereo-seq ^b	Pixel-seq ^c	
			Sequenced gel	Stamped gel
DNA array size(s) (mm ²)	30.4 (1 × 0.8) × 38 tiles	50 - 200 10 × 5, 10 × 10, or 20 × 10	147 (7 × 7) × 3	294 (7 × 7) × 6
Array fabrication cost (per mm ²)	~\$150	~\$35	~\$2.20	~\$0.06
Array fabrication time (hour)	~17	~9	~36	~7
Library preparation time (hour)	~19	~9		~6
Library sequencing platform(s)	Illumina and BGI platforms	MGI DNBSEQ-Tx		NovaSeq 6000

^a: Array cost is based on MiSeq v3 flowcells used in the original publication. Times were calculated based on the reported protocol.

^b: Arrays were subdivided from a large chip up to 13.2 × 13.2 cm². Times were calculated based on the reported protocol.

^c: Detailed cost analysis is in Table S2. Compared with Seq-Scope and Stereo-seq, the sequencing-based gel fabrication had a much lower cost partly because polony gels were fabricated on standard coverslips or glass slides instead of using commercial sequencing flowcells, and a longer time mainly due to the use of an in-house built sequencer with a much slower imaging speed than commercial sequencers.