

Supplemental information

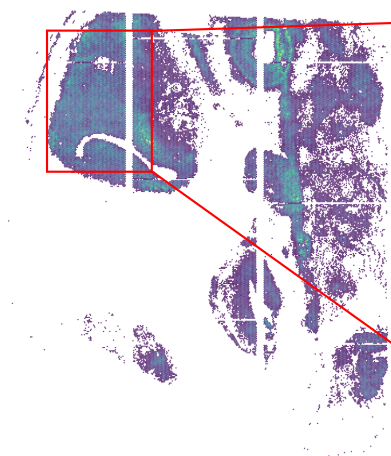
Open-ST: High-resolution spatial transcriptomics

in 3D

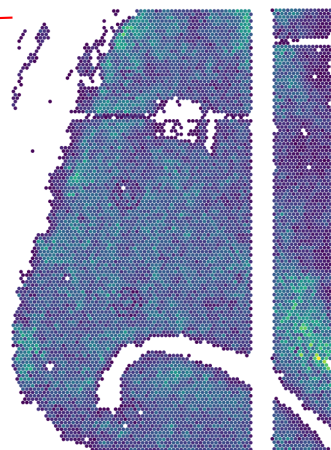
Marie Schott, Daniel León-Periñán, Elena Splendiani, Leon Strenger, Jan Robin Licha, Tancredi Massimo Pentimalli, Simon Schallenberg, Jonathan Alles, Sarah Samut Tagliaferro, Anastasiya Boltengagen, Sebastian Ehrig, Stefano Abbiati, Steffen Dommerich, Massimiliano Pagani, Elisabetta Ferretti, Giuseppe Macino, Nikos Karaiskos, and Nikolaus Rajewsky

Methods S1: selection of regions of interest for the different spatial technologies in the benchmarking analysis, related to STAR Methods “Benchmarking analysis”.

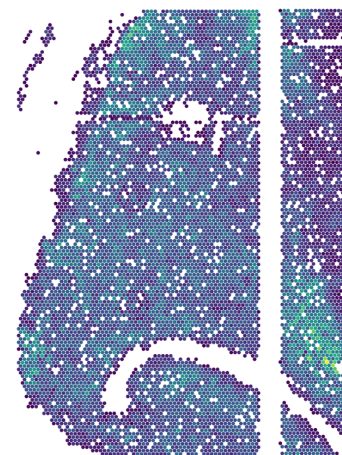
Open-ST
e13 mouse brain rep1
full sample



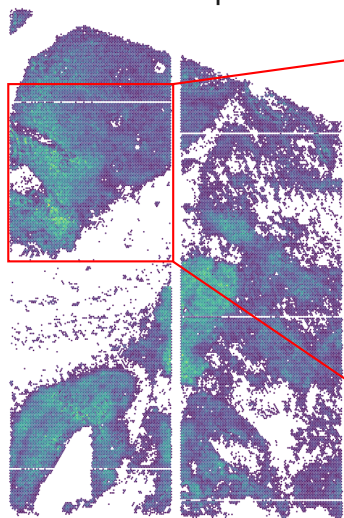
selected region of interest
8592 pseudo cells



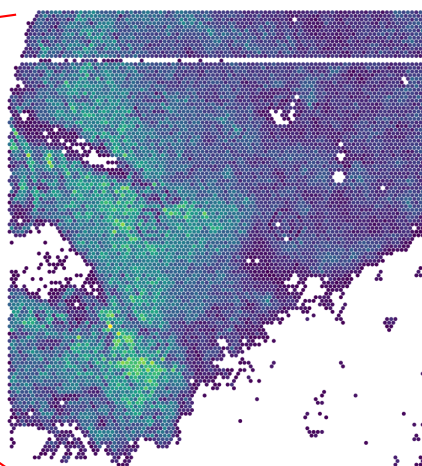
randomly sampled
7855 pseudo cell
(1mm² total area)



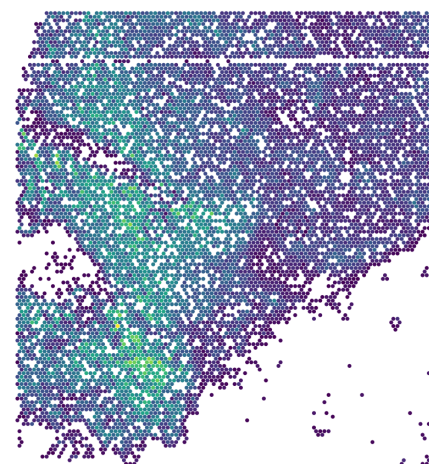
Open-ST
e13 mouse brain rep2
full sample



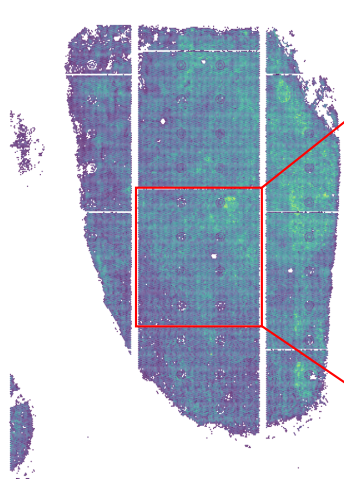
selected region of interest
9358 pseudo cells



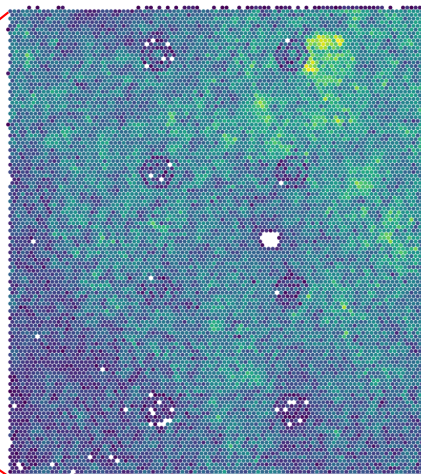
randomly sampled
7855 pseudo cell
(1mm² total area)



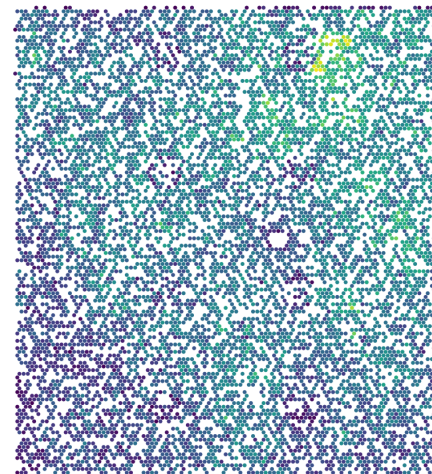
Open-ST
healthy lymph node
full sample



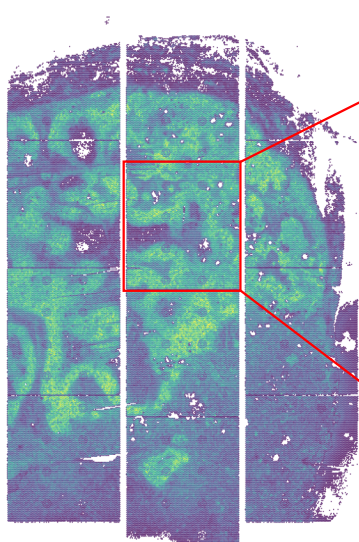
selected region of interest
12715 pseudo cells



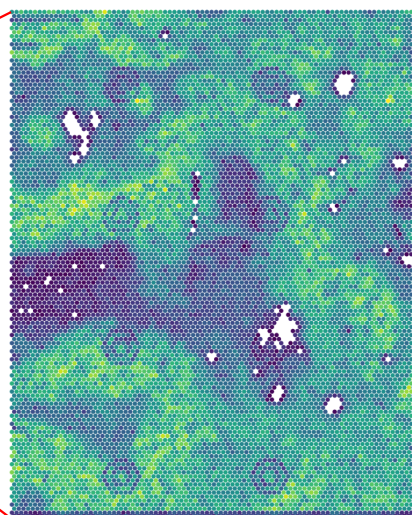
randomly sampled
7855 pseudo cell
(1mm² total area)



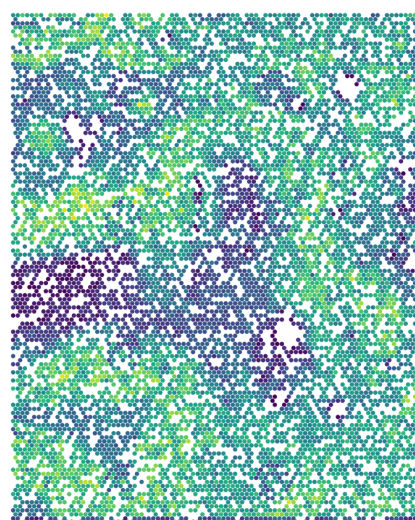
Open-ST
metastatic lymph node
full sample



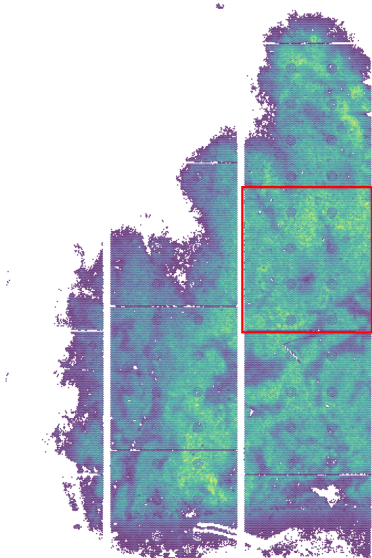
selected region of interest
12825 pseudo cells



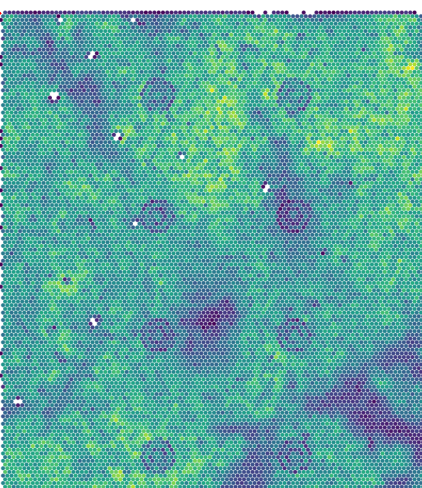
randomly sampled
7855 pseudo cell
(1mm² total area)



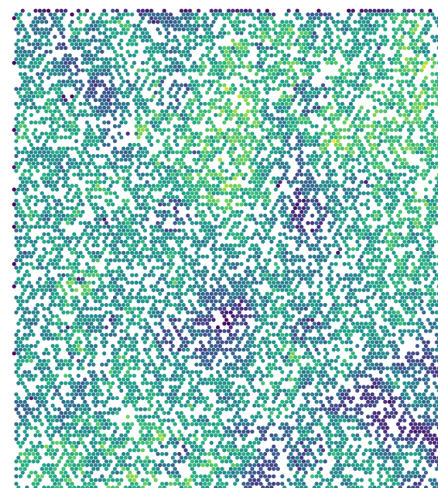
Open-ST
primary tumor (HNSCC)
full sample



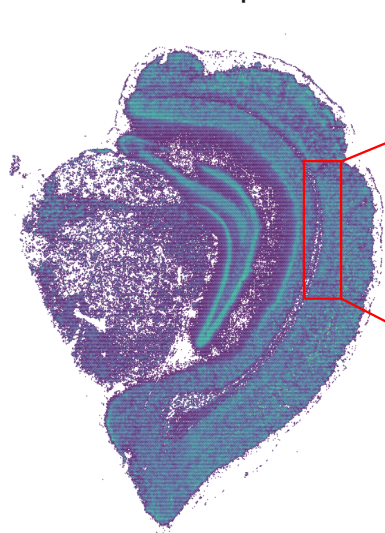
selected region of interest
12921 pseudo cells



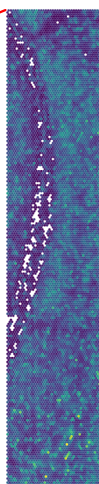
randomly sampled
7855 pseudo cell
(1mm² total area)



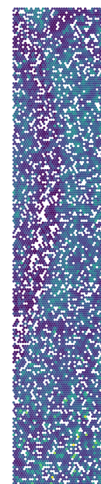
Stereo-seq
adult mouse brain
full sample



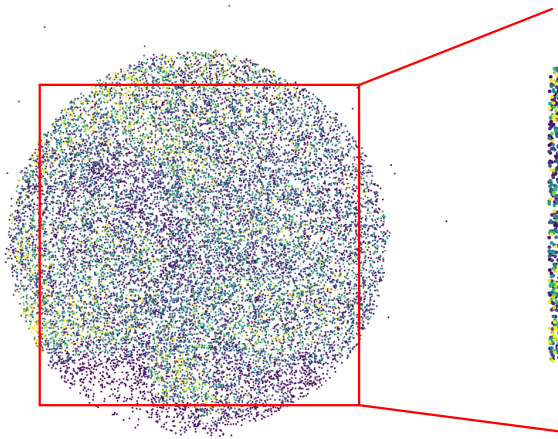
selected region of interest
9566 pseudo-cells



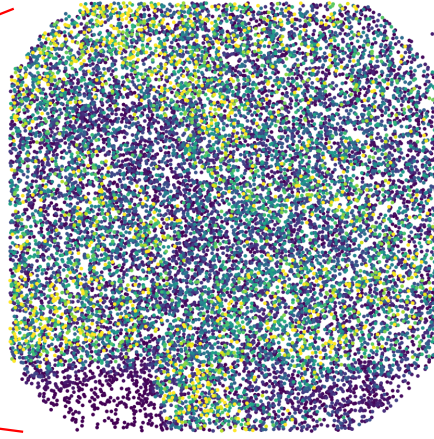
randomly sampled
7855 pseudo cell
(1mm² total area)



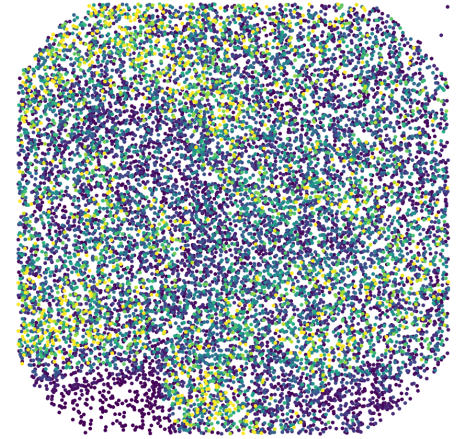
Slide-seq
e9.5 mouse brain
full sample



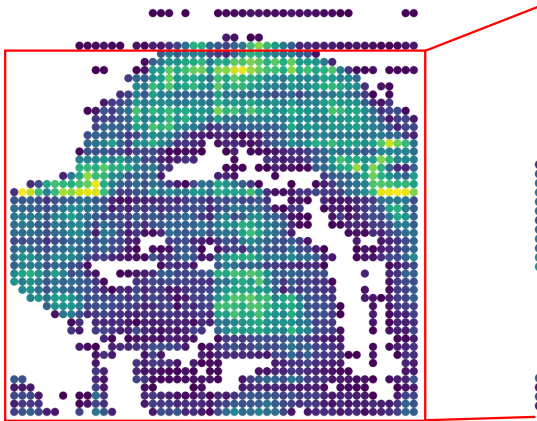
selected region of interest
14430 beads



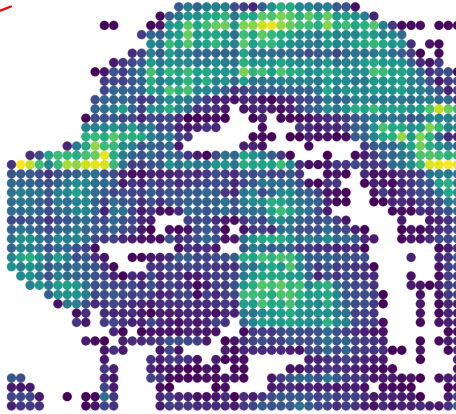
randomly sampled
12738 beads
(1mm² total area)



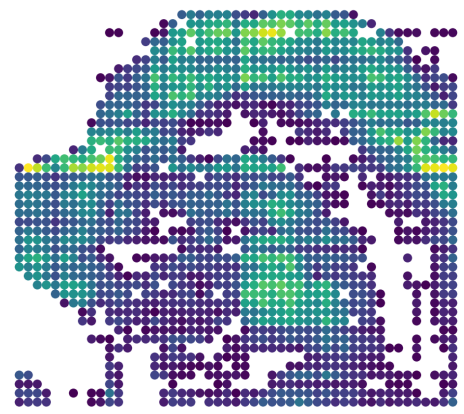
DBiT-seq
e11 mouse tail
full sample



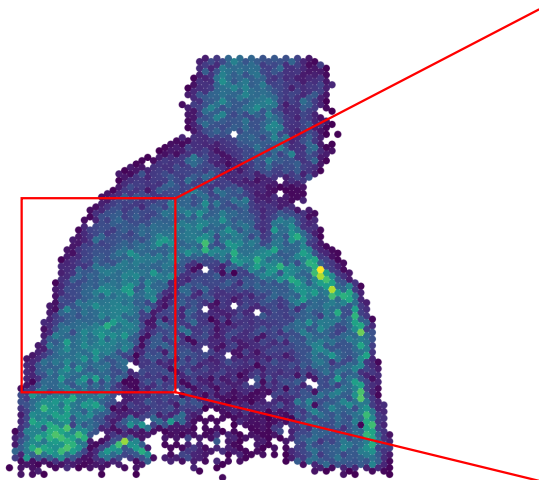
selected region of interest
1625 pixels



randomly sampled
1600 pixels
(1mm² total area)



Visium
adult mouse brain
full sample



selected region of interest
600 spots



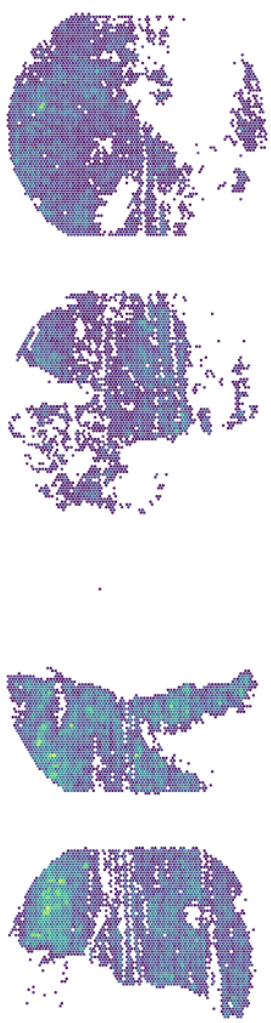
randomly sampled
420 spots
(1mm² total area)



Seq-scope
adult mouse liver
full sample



selected region of interest
10740 pseudo cells



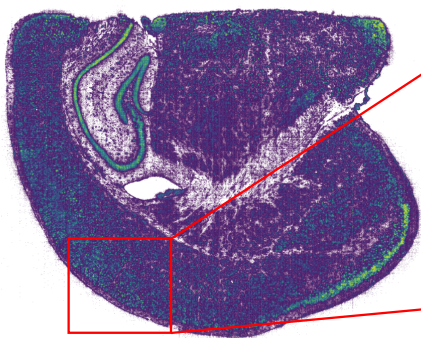
randomly sampled
7855 pseudo cell
(1mm² total area)



Visium HD
adult mouse brain
full sample



selected region of interest
334765 bins (2um)



randomly sampled
250000 pseudo cell
(1mm² total area)

