

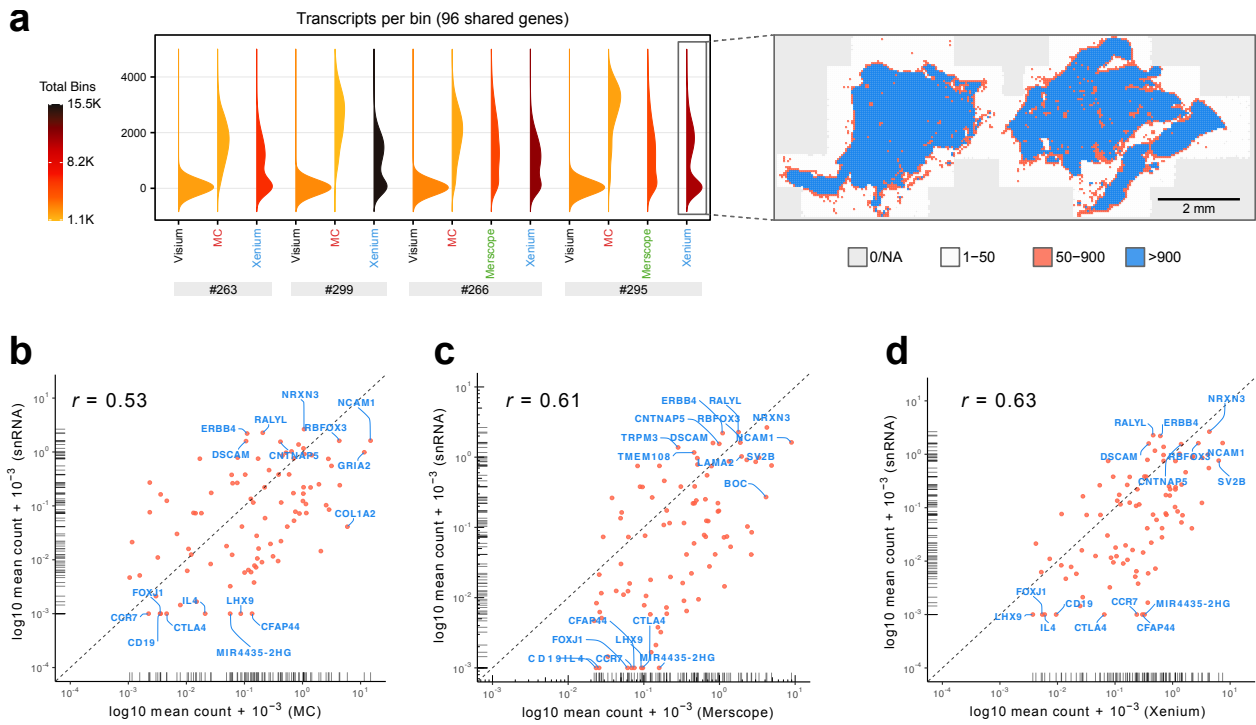


Fig. S5. Sensitivity analysis of *iST* methods

(a) Tissue location of cells with high and low transcript distribution for the spatial binning analysis shown in **Fig. 3a** for sample MB295 on Xenium. The cell population with fewer transcripts per bin is enriched in the outer regions of the tissue. (b) Correlation of snRNA-seq with MC for the shared panel of 96 genes in snRNA-seq. The dashed line indicates the equivalent number of transcripts detected by the two methods being compared. The snRNA-seq analysis was conducted using the Chromium v2 chemistry, which has a reported detection efficiency of 14-15% (v3 chemistry 30-32%) according to the manufacturer (<https://kb.10xgenomics.com/hc/en-us/articles/360001539051-What-fraction-of-mRNA-transcripts-are-captured-per-cell>). (c) Same as panel b, but for the correlation of snRNA-seq with Merscope. (d) Same as panel b, but for the correlation of snRNA-seq with Xenium.