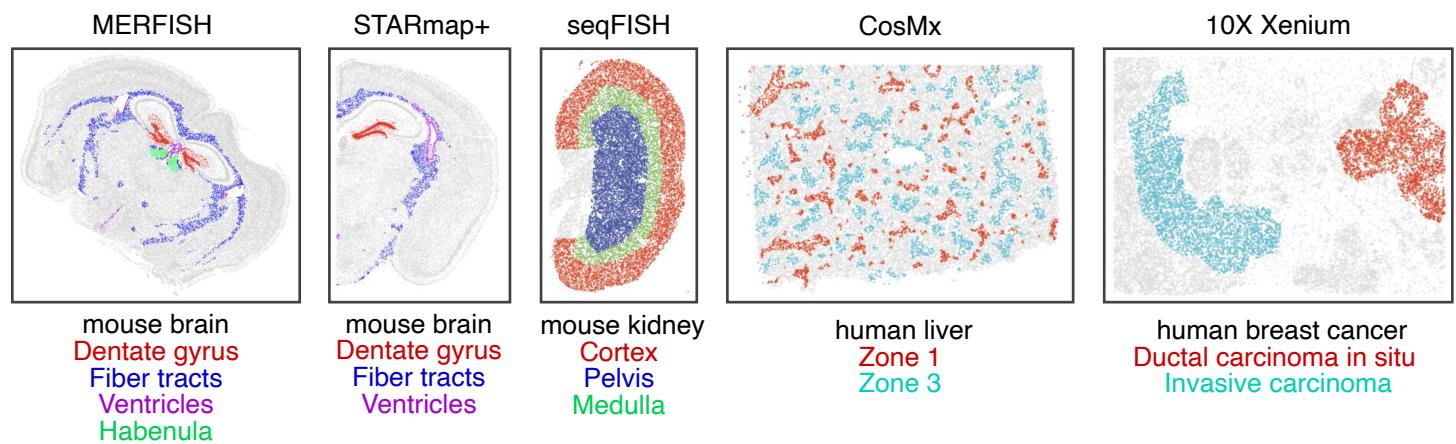
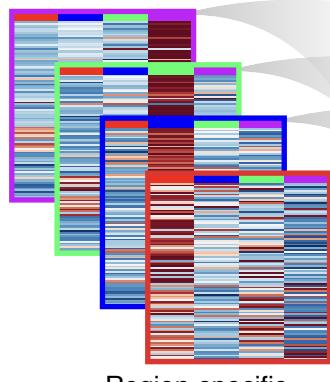


1. Imaging-based spatially resolved transcriptomics data with tissue region annotations

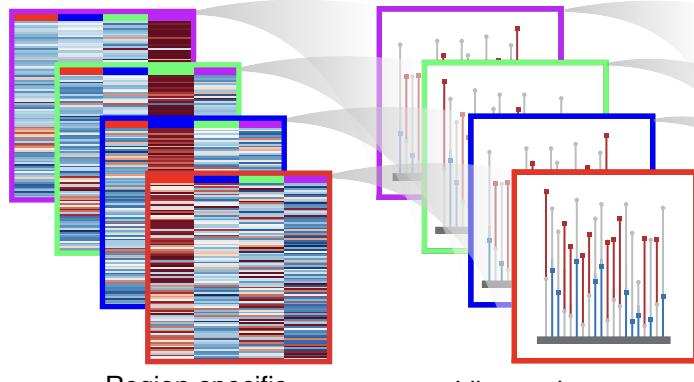


2. Targeted gene panels

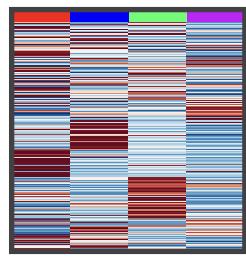


Region-specific skewed gene panels

3. Expression normalization

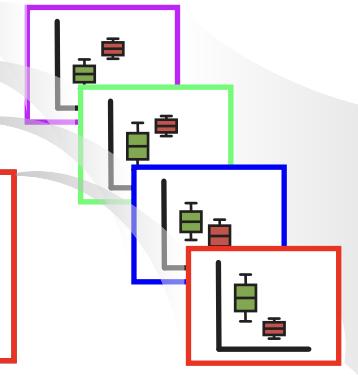


Library size
scTransform
DESeq2
TMM
Cell volume/area



Original gene panel

4. Downstream analysis



Differential gene expression
Gene expression fold change
Spatially variable genes

5. Compare results between gene panels

