experimental approach

hypothesis testing

specific gene targets

imaging-based technologies

hypothesis generation

unbiased & transcriptome wide

sequencing-based technologies

⭐ preprocess data

⭐⭐ remove low-quality spots

differing gene variance

different counts/spot

feature selection

plot mean-variance

normalize data

deconvolve cell types

compare cell type proportions across samples, conditions

spatially plot cell type proportions

highly variable or biologically relevant genes

reduce dimensionality

cluster across spots in a sample

identify differentially expressed genes across samples/ conditions based on annotations

Color key

Label A
Label B
Label C
Label D
Label E
Label F

⭐ 1. Plot spot annotation (tissue vs. background)
2. Plot genes & UMI (tissue vs. background)
3. Remove background spots
4. View distribution of genes & UMI in each tissue spot
5. Remove low-expressed genes

⭐⭐ 1. with high mitochondrial gene expression or
2. high UMI counts or gene numbers