Data Preprocessing

Cell Filtering
Remove low-quality cells and empty droplets

Gene Filtering
Exclude genes detected in too few cells

Normalization Methods
Account for sequencing depth and composition

Imputation Strategies
Handle dropout events (use with caution)

Batch Effects
Technical variation from sample processing

💡 **Quality control is critical for downstream analysis**

Raw Data	→	Cell Filtering	→	Gene Filtering	→	Normalize	→	Select HVGs	→	Ready for Analysis
20,000 cells		nGene, %mito -3,000 cells		Min cells/gene 17,000 cells		Depth + scale		~2000 genes		

QC Metrics: nGene: 200-6000   nUMI: 500-50000   %mito < 10%   %ribo: varies   Doublets: <5%