

# Library Preparation Methods

## PolyA Selection

Enriches mRNA by capturing poly-adenylated transcripts

## Ribosomal Depletion

Removes rRNA to capture all RNA types including non-coding

## Strand Specificity

Preserves information about which DNA strand was transcribed

## UMI Incorporation

Unique Molecular Identifiers enable accurate quantification

## 3' Tag-seq

Sequences only 3' ends - cost effective for counting

## Full-length Coverage

Complete transcript coverage for isoform analysis

Trade-off: **Cost vs. Information Content**

