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**