

PacBio Iso-seq

Full-length RNA-seq



The Role of Long-Reads in Transcript Isoform Discovery and RNA Analysis

PacBio High Fidelity (HiFi) Sequencing utilizes Single Molecule, Real-Time (SMRT) technology to deliver long reads (10-25kb) with unparalleled accuracy $\geq 99.9\%$, or Q30). HiFi sequencing provides the most complete and accurate view of the genome, transcriptome, and epigenome, taking research to the next level.

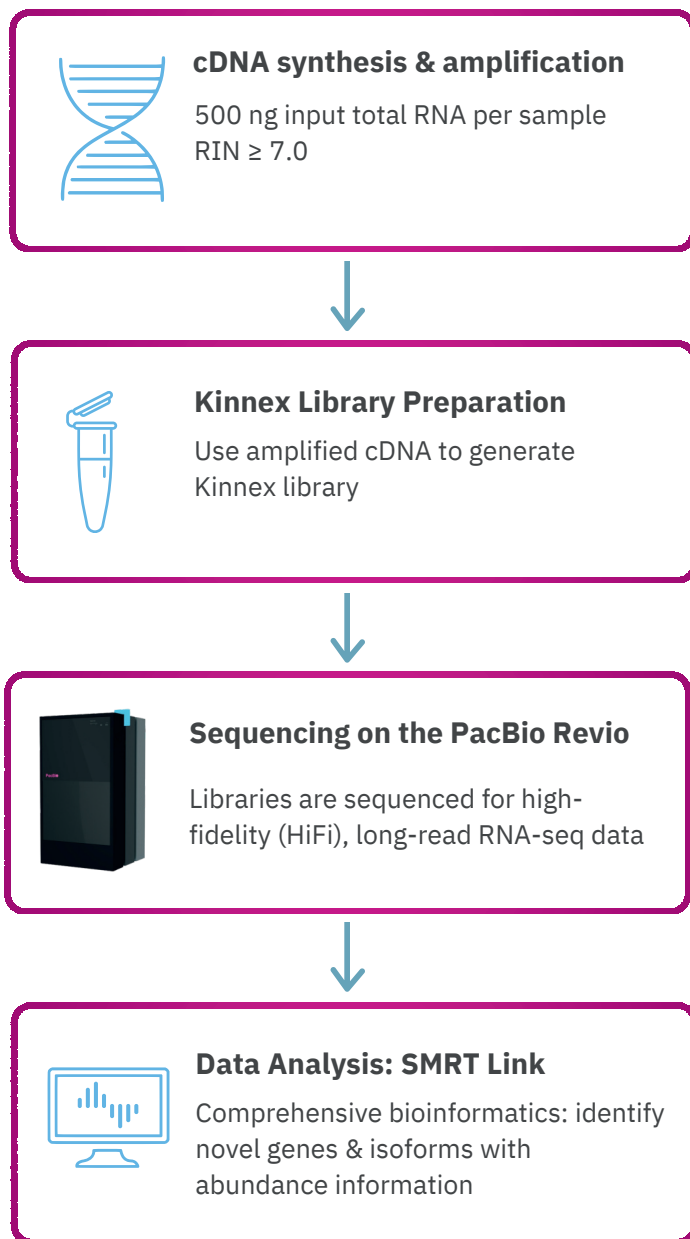
Accurately characterizing transcript isoforms is essential for understanding gene regulation, cellular diversity, and disease mechanisms. However, short-read platforms typically generate reads of 100–200 base pairs, which must be aligned and stitched together to approximate full transcripts.

PacBio HiFi and the Iso-seq Advantage: A Full-Length Solution

Key Advantage	Applications
Accurate delineation of exon-intron boundaries	Alternative Splicing Characterization
Direct observation of full-length splice variants	Novel isoform discovery and transcriptome annotation
Reliable detection of 5' and 3' UTR diversity	Fusion transcript detection in oncology
Unambiguous identification of fusion transcripts	Allele-specific and phased transcript

PACBIO LONG-READ RNA-SEQ (ISO-SEQ)

Workflow



Service Benefits

Fast, Flexible Turnaround

- Standard 4-6 weeks
- 3 week expedited upon request

1:1, PhD-Level Support

- 1:1 support from our PhD-level scientists, customized workflows available

Trusted, High-Quality Service

- CLIA/CAP compliant processes ensure reproducibility and reliable results

Advanced Bioinformatic Support

- Expert analysis pipelines for isoform discovery & custom pipelines for tailored solutions



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