The Iso-Seq™ application generates full-length cDNA sequences, from the poly-A tail to the 5’ end of transcripts - eliminating the need for transcript reconstruction and inference - giving complete, unambiguous information about alternatively spliced exons, transcriptional start sites, and poly-adenylation sites. Be confident in the characterization of the full complement of isoforms within targeted genes, or across an entire transcriptome.

- Directly detect full-length mRNA and lncRNA transcripts
- Discover novel genes, gene isoforms, and gene fusion events
- Evidence-based gene annotation
- Improve quantitation accuracy of RNA-seq data with sample-specific gene models
- Detect allele-specific transcript isoform expressions

Complex Isoforms of Neurexin 1α Gene Detected Using Isoform Sequencing with PacBio

A. Transcript map of 247 unique alternatively spliced isoforms of the Neurexin 1α gene (~4-5 kb) generated with a targeted Iso-Seq method.¹
B. Neurexin 1α isoform variants distribution detected across three cell types.²

www.pacb.com/isoseq
From RNA to Evidence-based Gene Models

**Iso-Seq Sample Preparation**
- Prepare full-length transcripts with from total RNA (~50 ng) or mRNA
- Optional size-selection protocol for transcripts > 3 kb
- Support for targeted genes and multiplexing

**SMRT® Sequencing on the PacBio® RS II**
- Sequence full-length transcripts up to 10 kb
- Scalable throughput:
  - Profile multiplexed targeted transcripts in a single SMRT Cell
  - Increase sequencing depth for more comprehensive transcriptome characterization

**Iso-Seq Analysis in SMRT Analysis**
- No assembly required; no inference of isoforms
- Output high-quality, full-length transcript sequences
- Fully de novo, no genome reference required
- Open-source computational pipeline

**References**