**READ FULL-LENGTH TRANSCRIPTS**
**NO ASSEMBLY REQUIRED**

**The Iso-Seq™ method** provides full-length cDNA sequences from the 5’ end of transcripts to their poly-A tails - eliminating the need for transcript reconstruction and inference - giving **complete, unambiguous information about alternatively spliced exons, transcriptional start sites**, and poly-adenylation sites. Confidently characterize the full complement of isoforms within targeted genes, or across an entire transcriptome.

- Accurately characterize full-length mRNA and IncRNA transcripts
- Discover novel genes, isoforms, and fusions
- Generate evidence-based gene annotations
- Improve quantitative accuracy of RNA-seq data with sample-specific gene models
- Detect allele-specific isoform expression
- Sequence intact, polycistronic operons from the mRNA of bacterial and metagenomic samples

**COMPLEX ISOFORMS OF THE NEUREXIN 1α GENE DETECTED USING THE ISO-SEQ METHOD**

Transcript map of 247 unique alternatively spliced isoforms (~1.5 kb each) of the Neurexin 1α gene generated with a targeted Iso-Seq method.

Number and differential isoform usage of the neurexin 1α gene across three brain regions

[www.pacb.com/isoseq](http://www.pacb.com/isoseq)
FROM RNA TO A COMPLETE REPERTOIRE OF FULL-LENGTH TRANSCRIPT ISOFORMS

Iso-Seq Sample Preparation
- Prepare full-length cDNA transcripts from as low as 1 ng of polyA+ RNA or 2 ng of total RNA
- Select for transcripts > 3 kb with size-selection protocol options
- Use with standard target enrichment methods
- Multiplex transcripts or full transcriptomes with sample barcoding

SMRT® Sequencing with PacBio® Systems
- Take advantage of the Sequel™ System for high-throughput projects to reduce costs and generate 7X more reads compared with the PacBio RS II
- Directly sequence full-length transcripts with read lengths averaging ~10 kb
- Scale throughput based on project needs
  - Profile multiplexed targeted samples in a single SMRT Cell
  - Survey whole transcriptomes in 1-2 SMRT Cells on the Sequel System
  - Increase sequencing depth for more comprehensive transcriptome characterization

Data analysis with SMRT Analysis or PacBio DevNet
- Iso-Seq analysis: Output high-quality, full-length transcript sequences with no assembly required
- No reference genome required

KEY REFERENCES

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