PRODUCT DATASHEET

High-Output Long-Read RNA Isoform Sequencing (Kinnex)

Product Overview

Full-length mRNA sequencing using long-read technologies can capture complete transcript isoforms, allowing researchers to perform differential isoform analysis, identify novel isoforms, and fusion transcripts. Prior to the development of MAS-seq (Multiplexed Arrays Isoform Sequencing), this capability has been constrained by throughput limitations. MAS-seq leverages programmable cDNA concatenation to generate optimal libraries for maximized throughput on the PacBio Revio platform. Broad Clinical Labs is offering the commercialized version of MAS-seq for bulk RNA isoform sequencing, **Kinnex Full Length RNA kit**, which boosts the output of RNA isoform sequencing 8-fold on the PacBio sequencers

Input Requirements

- Total RNA that meets the following criteria:
    - >45 ng/µL
    - >30 µL
    - >7.0 RQS
- Minimum sample metadata, including collaborator participant ID, collaborator sample ID, biological sex of participant.

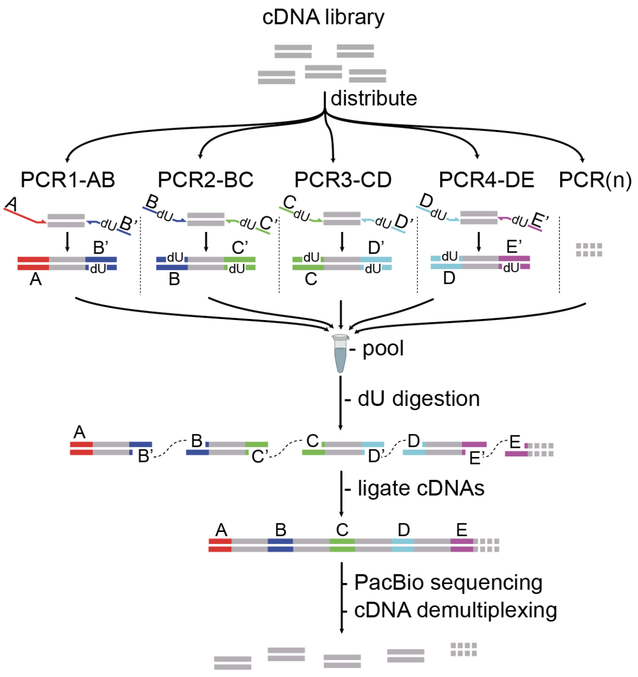
Data Deliverable

- 30-50 million de-concatenated HiFi S-reads Sequences per array
- de-concatenated, de-multiplexed, aggregated BAM file
- QC metrics

What's Included

- Sample Receipt and QC
- MAS library construction
- Sequencing on the Pacific Biosciences Revio^{TM} platform
- Sample de-concatenation and demultiplexing
- Data delivery to a customer-owned Google cloud-based platform

Figure 1. Schematic of MAS-seq workflow.



Version: 16704279