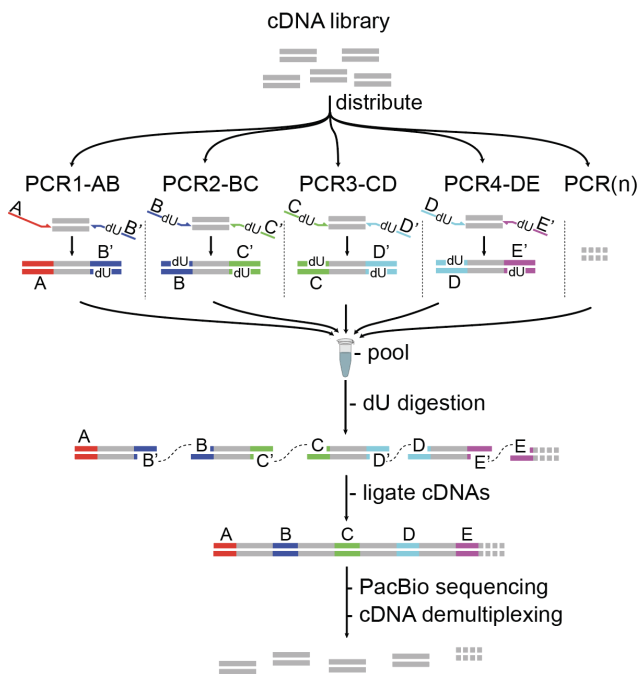


# High-Output Long-Read RNA Isoform Sequencing (MAS-seq)

## Product Overview

Multiplexed Arrays Isoform Sequencing (MAS-seq) is a novel library preparation approach that enables high-throughput long-read sequencing of full-length cDNA libraries<sup>1</sup>. Our MAS-seq service is compatible with multiple full-length cDNA library types, including bulk cDNA, 10x 5' Single Cell Gene Expression cDNA, 10x 3' Single Cell Gene Expression cDNA, and 10x Visium cDNA libraries. The combined accuracy and throughput enabled by MAS-seq greatly enhances quantification of RNA isoforms, particularly from read-intensive approaches such as single-cell and spatial RNA sequencing.

Alternative splicing is a core biological process that enables profound and essential diversification of gene function. Short-read RNA sequencing approaches fail to accurately resolve RNA isoforms and therefore primarily enable gene expression measurements - an isoform unaware representation of the transcriptome. Conversely, full-length RNA sequencing using long-read technologies are able to capture complete transcript isoforms, but their utility has been constrained by throughput limitations. MAS-seq, a technique for programmably concatenating cDNAs into single molecules optimal for long-read sequencing, addresses these challenges.



**Figure 1.** Schematic of MAS-seq workflow.

## What's Included

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

## Input Requirements

- 100µL full-length (pre-sheared) cDNA ≥6ng/µL from any of the following: Bulk cDNA libraries; 10x 5' Single Cell Gene Expression cDNA libraries, 10x 3' Single Cell Gene Expression cDNA libraries, or 10x Visium cDNA libraries.
- Minimum sample metadata, including collaborator participant ID, collaborator sample ID, biological sex of participant.

## Data Deliverable

- 50-80 million de-concatenated HiFi DNA sequences

<sup>1</sup> Al'Khafaji, A.M., Smith, J.T., Garimella, K.V. et al. High-throughput RNA isoform sequencing using programmed cDNA concatenation. *Nat Biotechnol* (2023). <https://doi.org/10.1038/s41587-023-01815-7>