

cDNA-PCR Sequencing Kits

Annotate the transcriptome with confidence

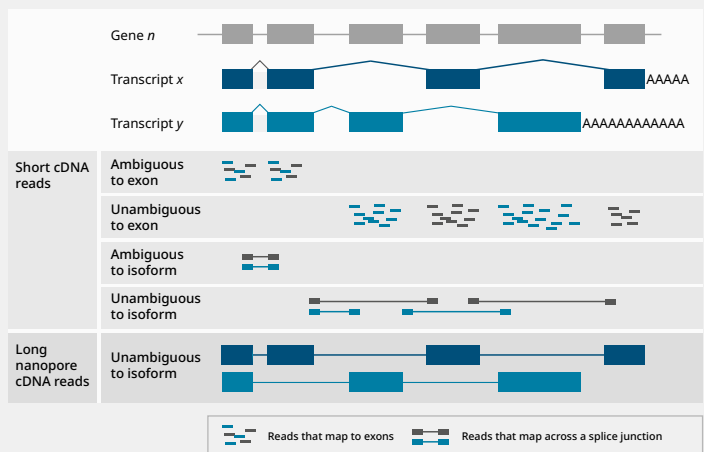
Understanding the transcriptome is essential for studying gene regulation in health and disease. Through alternative splicing, a single gene can generate multiple transcript isoforms, increasing protein diversity to support normal cell function. When this process is disrupted, abnormal splice variants can arise, some of which have been linked to rare diseases and cancer¹.

Investigating alternative splicing is challenging because transcripts from a single gene can share many exons, making them difficult to distinguish². Short-read sequencing captures only small fragments of transcripts, typically covering only a single splice junction, limiting isoform identification and quantification.

Oxford Nanopore cDNA-PCR Sequencing Kits overcome these limitations by capturing full-length transcripts. By spanning all splice junctions in a single read, confidently identify, reconstruct, and quantify all transcripts for alternative splicing research, genome annotation, and differential transcript analysis.

Resolve complete transcripts with long nanopore reads.

Transcript isoforms are difficult to distinguish due to their similarities. Short-read sequencing generates fragmented reads that may only map to individual exons or splice junctions, resulting in ambiguous results. Nanopore reads of unrestricted length span entire transcripts, capturing all splice junctions within single reads for unambiguous transcript identification.



See the whole picture with full-length transcripts

Oxford Nanopore cDNA sequencing is designed to capture transcripts in full. Flexible input requirements support low amounts of poly(A)⁺ or total RNA while still delivering high read outputs.

Highly selective amplification adapters target the 3' ends of the poly(A) tail, reducing internal priming, a known limitation of other long-read cDNA technologies, and enabling estimation of poly(A) tail length. By avoiding stringent size selection, transcripts of all lengths are captured, revealing a representative view of the transcriptome and deeper insights into transcript diversity than ever before.



Unrestricted read lengths

Sequence any length of transcript with minimal internal priming



Low input requirements

Start with as little as 10 ng poly(A)⁺ RNA or 500 ng total RNA



High read output

Generate 60–80M reads per PromethION™ Flow Cell across 1–24 barcodes



Simple workflow

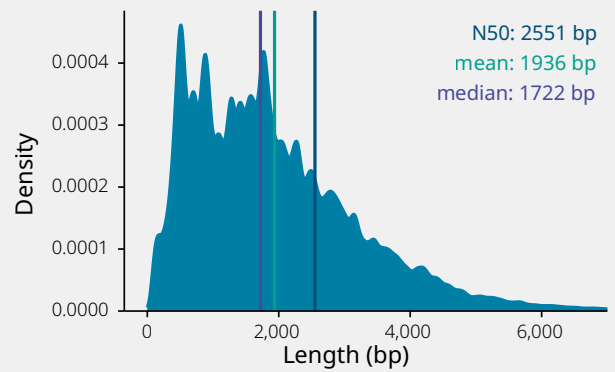
Complete cDNA-PCR Sequencing Kit library preparation in one day, with two hours of hands-on time

Generate even longer cDNA reads

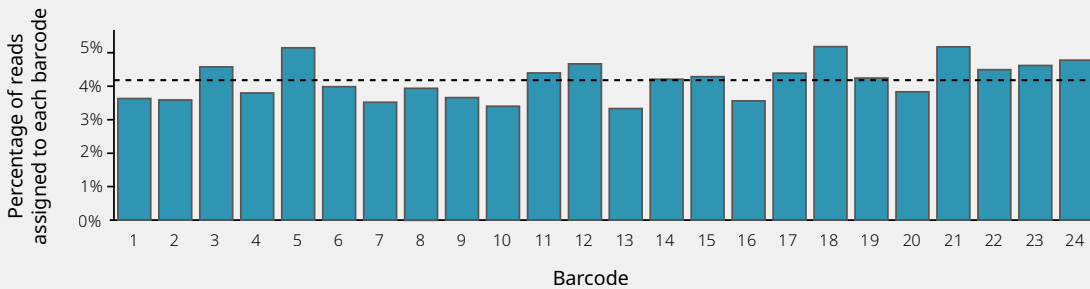
With the latest protocol updates to the **cDNA-PCR Sequencing Kits**, generate longer cDNA reads with a median length of ~1.8 kb*, whilst retaining balanced barcodes. Discover novel isoforms, annotate genomes, and quantify transcripts with confidence.

Universal Human Reference RNA was prepared using the cDNA-PCR Barcoding Kit for a 24-plex sequencing run, resulting in a median read length of 1722 bp (right), with reads uniformly represented across all barcodes in replicates of three (below).

Unlock full-length transcripts with long reads.



Sequence up to 24 samples in a single run with reads balanced across all barcodes.



	cDNA-PCR Sequencing Kit	cDNA-PCR Barcoding Kit
Product codes	SQK-PCS114 (6 reactions)	SQK-PCB114.24 (6 reactions)
Compatible flow cells	PromethION Flow Cell (DNA) MinION™ Flow Cell (DNA)	
Multiplex options	1	1–24
Input sample types	Total RNA and poly(A)+ RNA	
Recommended input	500 ng total RNA or 10 ng poly(A)+ RNA per sample	
Typical output	PromethION: 60–80M reads MinION: 10–15M reads	
Typical read length (median)*	~1.8 kb	
Library preparation time	<8 hours	

*For Universal Human Reference RNA; typical read length is dependent on sample type.



Find out more: nanopore.com/rna-and-cdna-sequencing



References:

1. Tao, Y. and Zhang, Q. et al. *Signal Transduct. Target. Ther.* 9(1):26 (2024). DOI: <https://doi.org/10.1038/s41392-024-01734-2>
2. Heberle, B.A. and Brandon, J.A. et al. *Nat. Biotechnol.* 43(4):635–646 (2025). DOI: <https://doi.org/10.1038/s41587-024-02245-9>

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phone +44 (0)845 034 7900

email support@nanoporetech.com

[oxford-nanopore-technologies](https://www.linkedin.com/company/oxford-nanopore-technologies)

@nanopore

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