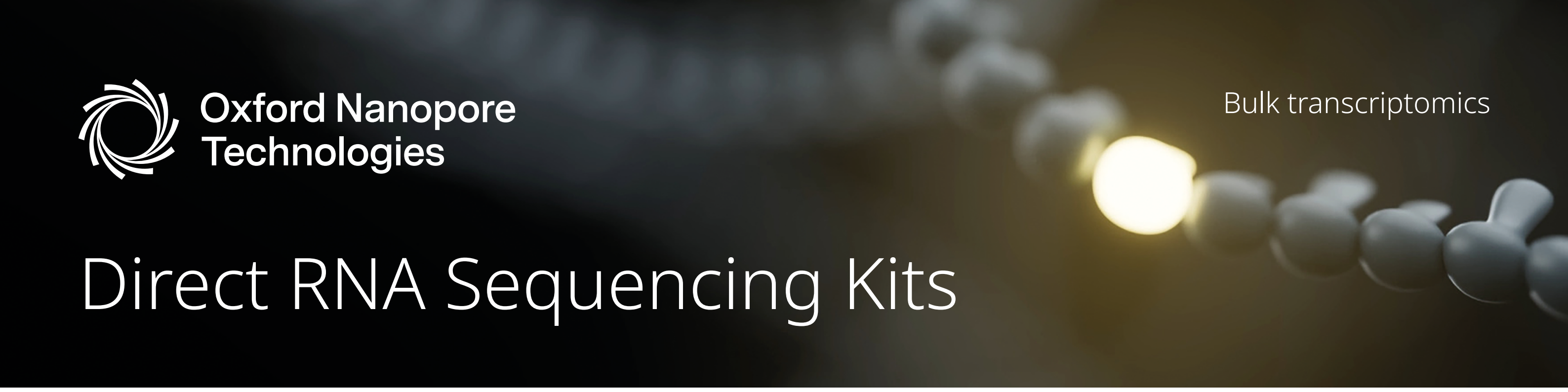


Oxford Nanopore Technologies

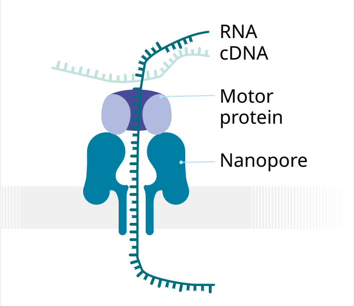
Bulk transcriptomics

Direct RNA Sequencing Kits

See RNA as it truly exists — full length, with modifications intact

RNA modifications shape transcript structure and function, playing essential roles in cellular processes. For example, m^6A has been shown to affect protein expression by regulating mRNA splicing, stability, and translation. But their true impact can only be understood when measured in the context of full-length RNA molecules.

Direct RNA sequencing reads native, full-length RNA molecules, preserving sequence and modification information along entire transcripts without amplification. In a single assay, you can simultaneously detect up to eight RNA modifications at base resolution, identify transcript isoforms, and quantify gene and transcript expression levels.



Oxford Nanopore sequencing is the only available technology that directly reads native, full-length RNA molecules.

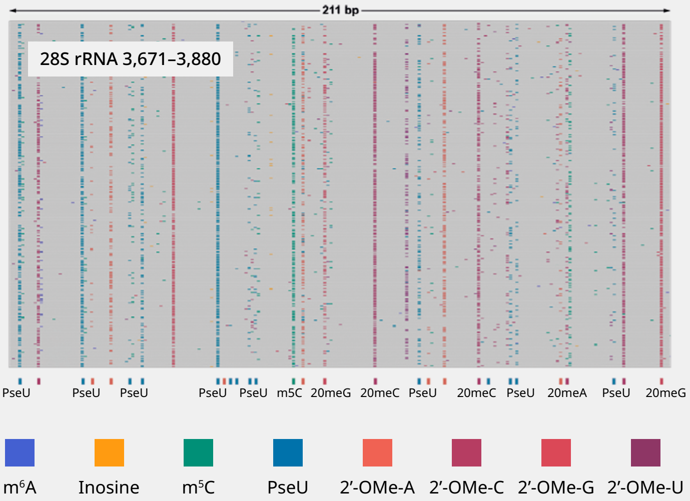
Capture transcriptomic and epitranscriptomic variation, in one go

Full-length reads span entire transcripts, including splice junctions and poly(A) tails, so you can see the full diversity of isoforms in your samples. You can link RNA modifications to specific transcripts and track co-modification patterns along the same molecule. This is unlike short-read RNA-seq, which fragments RNA and erases RNA modifications during cDNA preparation, breaking these connections and obscuring isoform diversity.

With direct RNA sequencing, you can simultaneously detect and quantify RNA modifications along native molecules.

Detect multiple RNA modifications in the same read at single-base resolution. Go beyond enrichment-based methods, such as MeRIP-seq that identifies broad regions, and measure the stoichiometry of modifications at each position — delivering a comprehensive view of transcriptomic and epitranscriptomic diversity.

Sequencing reads from a 211 bp region of human 28S ribosomal RNA (rRNA), generated using the Direct RNA Sequencing Kit, with detected modifications mapped (right).



Eight RNA modifications

Detect eight different RNA modifications simultaneously: m^6A, inosine, m^5C, PseU, 2′-OMe-A, 2′-OMe-C, 2′-OMe-G, 2′-OMe-U

Full-length transcripts

Preserve co-modification patterns along the same molecule and unambiguously map modifications to isoforms with full-length reads

Fast and simple workflow

Go from purified RNA to loading the sequencer in under 3 hours, with only 1.5 hours of hands-on time

Highly accurate gene counting

Generate accurate, quantitative measurements without PCR bias, as each RNA strand is read once

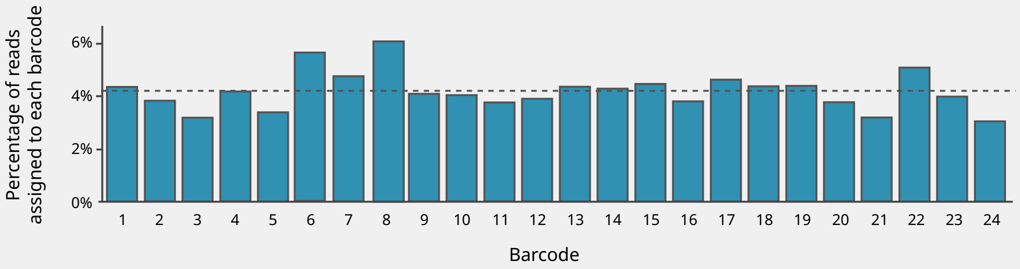
Do more with every sequencing run

Unlock multiplexed direct RNA sequencing with our new **Direct RNA Barcoding Kit**. Sequence up to 24 samples in a single run and gain greater control over the number of reads you generate for each sample, with the opportunity to reduce per-sample costs.

Optimised barcoding to boost output while preserving accuracy.

Both the barcodes and protocol for the Direct RNA Barcoding Kit have been optimised to deliver balanced barcode performance, while maintaining the read length, read output, and modification accuracy of the singleplex Direct RNA Sequencing Kit.

Reads assigned to each barcode in a 24-plex sequencing run of RNA Control Sample (EXP-RCS001) prepared with the Direct RNA Barcoding Kit (below).



	Direct RNA Sequencing Kit	Direct RNA Barcoding Kit
Product codes	SQK-RNA004 (6 reactions) SQK-RNA004-XL (48 reactions)	SQK-DRB004.24 (6 reactions)
Compatible flow cells	PromethION™ Flow Cell (RNA) MinION™ Flow Cell (RNA)	
Multiplex options	1	4–24
Input sample types	Total RNA and polyA(+) RNA	PolyA(+) RNA
Recommended input	1 µg total RNA or 300 ng poly(A)+ RNA	450 fmol poly(A)+ RNA per barcode
Typical output[*]	PromethION: 10–25M reads MinION: 3–6M reads	
Typical read length (median)[†]	~900 bp	
Modifications	m^6A, inosine, m^5C, PseU, 2′-OMe-A, 2′-OMe-C, 2′-OMe-G, 2′-OMe-U	
Library preparation time	~160 minutes	~370 minutes

[*] Typical output is lower for total RNA samples compared with poly(A)+ RNA samples.

[†] For Universal Human Reference RNA; typical read length is dependent on sample type.

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

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FL_1338(EN)_V1_08May2026