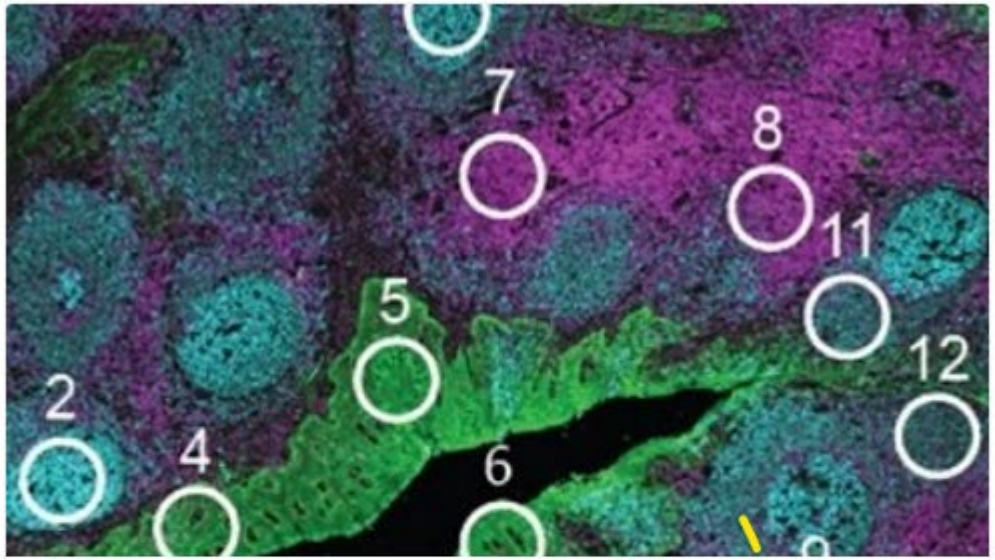
KIGene core facility



Spatial Biology

We offer full service assignments of high-plex spatial profiling of tissue sections via the nanoString/Bruker GeoMx and CosMx platforms. Our cryostat and light microscope are offered on a "hands-on" basis.

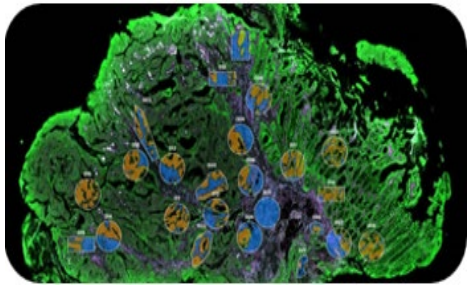


Genetic Analysis

KIGene is a well-established node at Karolinska Institutet with more than thirty years experiences of running a core facility. We offer genetic analyses, covering DNA sequencing, gene expression, genotyping, miRNA profiling and copy number variation, as well as epigenetic analysis.

Spatial Biology

platforms and applications

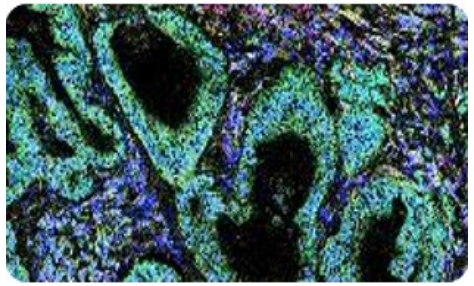


GeoMx Digital Spatial Profiler

Non-destructive profiling of expression from tissue compartments and cell populations

Whole transcriptome and 1200+ proteins (human and mouse)

FFPE and FF tissue sample



CosMx Spatial Molecular Imager

Non-biased imaging at single-cell and subcellular resolution

Whole transcriptome and 64+ proteins (human and mouse)

FFPE and FF tissue sample



Cryostar NX70 cryostat

Båda teknikerna använder hybridiseringsbaserad detektion utan amplifiering, vilket gör dem väl lämpade för potentiellt nedbrutna vävnadsprover.

https://ki.se/en/research/kigene
kigene-spatialbiology@mmk.ki.se

Research specialist: Lars Selander
Research specialist: Malin Alvehus
Senior research specialist: Ida Nilsson
Scientific director: Martin Schalling
Group leader: Catharina Lavebratt

Genetic Analysis

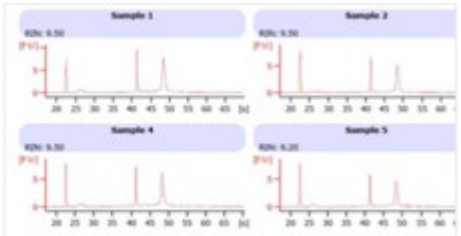
platforms and applications



ABI 3730 PRISM DNA Analyzers

Sanger DNA sequencing analysis

Fragment length analysis



Agilent 2100 BioAnalyzer, Nanodrop 1000, Qubit 2.0

Quantity and quality control of RNA, DNA and protein



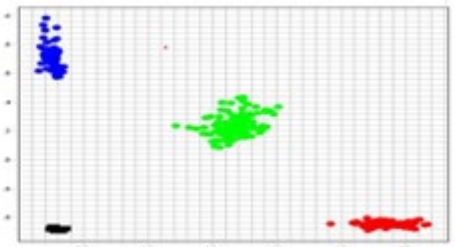
nanoString/Bruker nCounter analysis system

Gene expression (800 targets)

miRNA profiling

Protein expression analysis

Copy number variation



QuantStudio 6 and 7 FLEX instrument

Real-time gene expression analysis

SNP analysis (real-time or end-point analysis)



Oxford Nanopore Promethion 2 integrated

Real-time long-read sequencing

Direct calling of DNA and RNA modifications

“Hands-on” service

Användaren bokar och använder plattformen på egen hand efter genomgången introduktionskurs.

“Hands-off” service

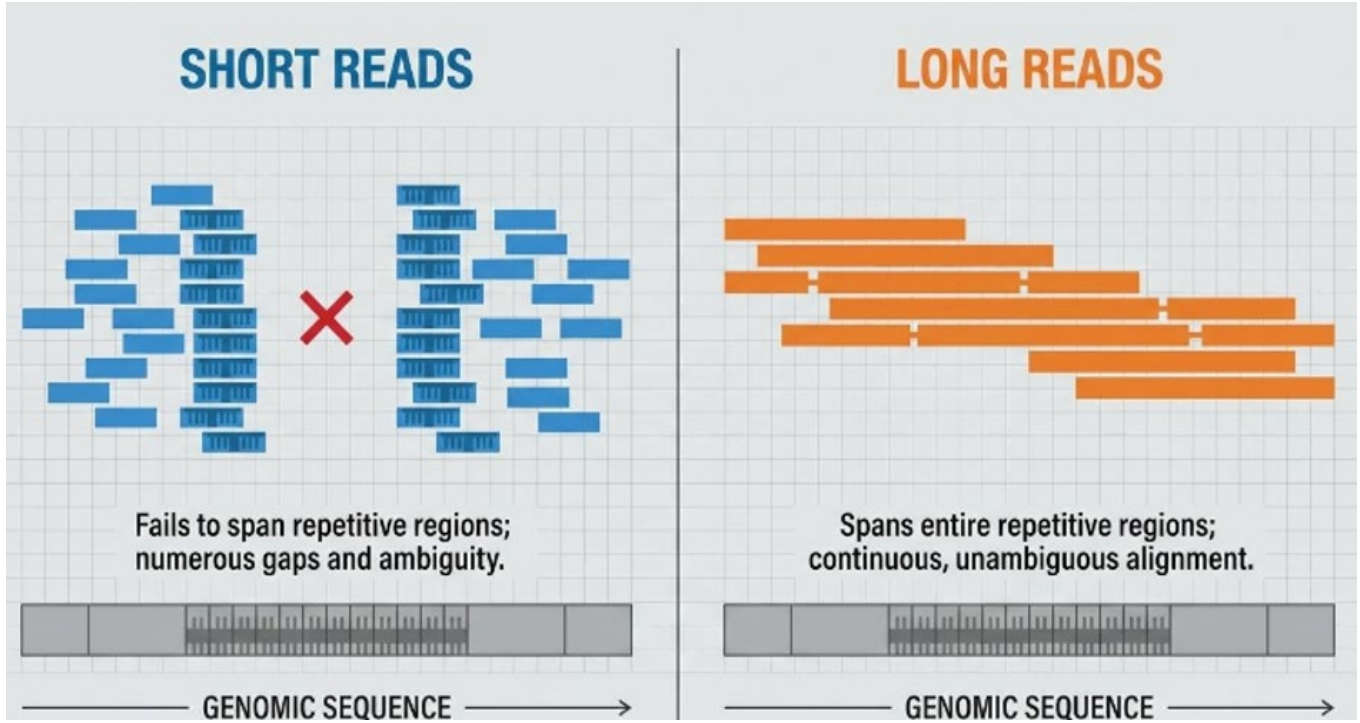
Vi utför analyserna.

https://ki.se/en/research/kigene

kigene@mmk.ki.se

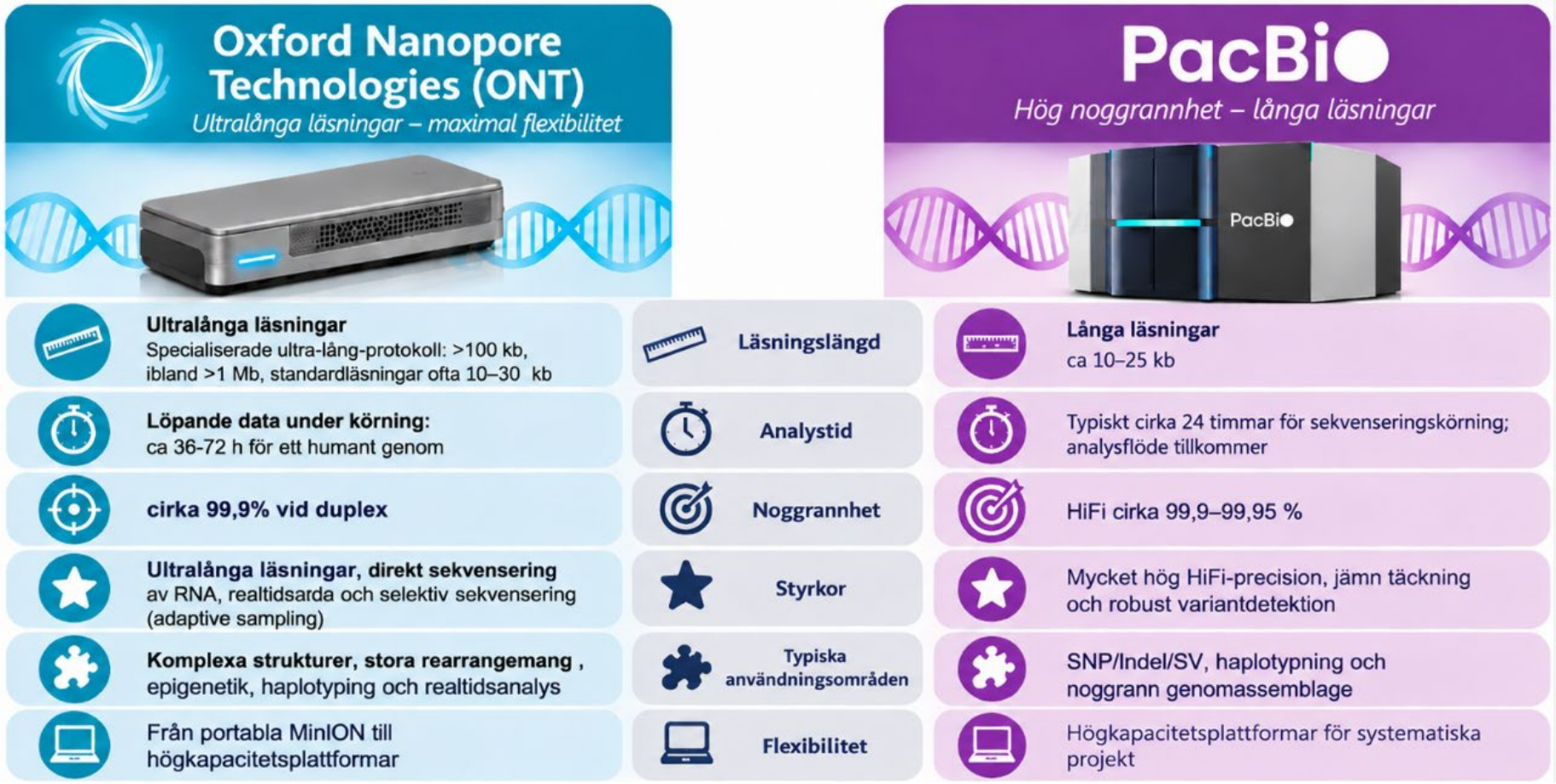
Research specialist: Annika Eriksson
Research engineer: Katarina Gell
Research specialist : Malin Alvehus
Scientific director: Martin Schalling
Group leader: Catharina Lavebratt

Långa vs korta läsningar



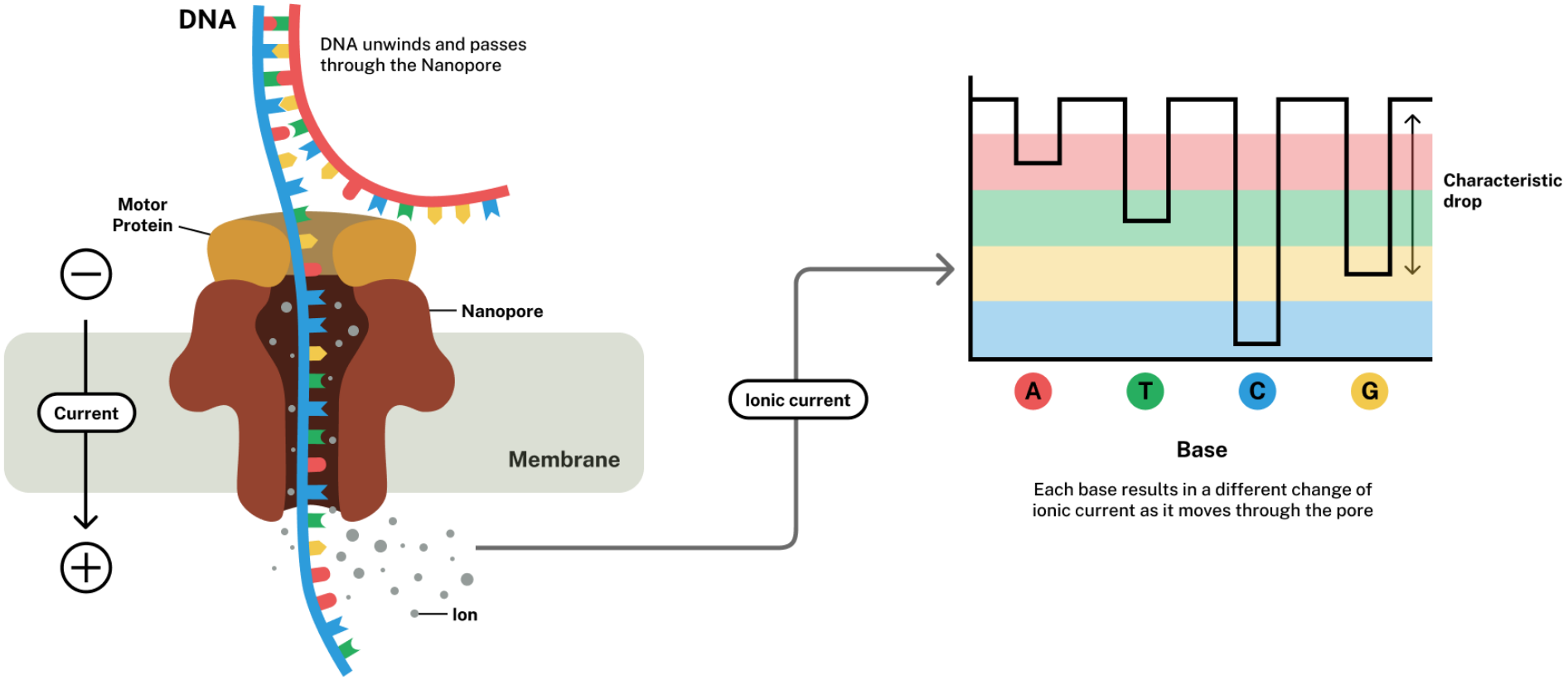
- Möjliggör analys av komplexa regioner
- Bättre de novo assembly
- Bättre detektion av strukturella genetiska variationer
- Direkt analys av DNA-metylering och RNA-modifieringar
- Realtidssekvensering
- Analys av nativt DNA och RNA- ingen PCR bias
- Bättre haplotyping/ genomisk fasning

Nanopore vs PacBio

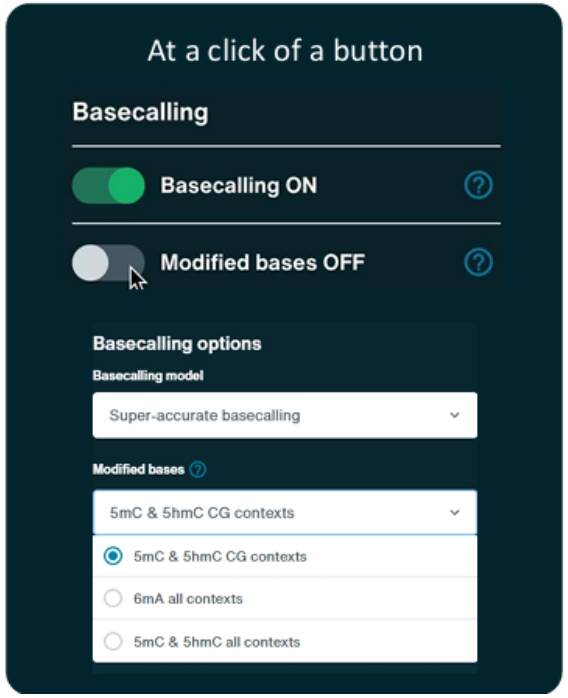


- Ultralång sekvensering
  - > 100 kb (4 Mb är rapporterat)
- Direkt RNA-sekvensering
  - Möjliggör analys av RNA-modifieringar
- Adaptiv Sampling
  - Riktad sekvensering utan laborativ anrikning

Nanopore-sekvensering



Epigenetik



Oxford Nanopore Technologies

Modified Base Models

Dorado – basecalling software integrated in MinKNOW

	Model	Context	Raw Read Accuracy	MinKNOW	Dorado
DNA	5mC/5hmC (mammal/plant)	CpG	99.2%	✓	✓
		All	98.7%	✓	✓
	4mC/5mC (bacterial)	All	97.6%	✓	✓
	6mA	All	99.7%	✓	✓
RNA	m6A	DRACH	99.7%	✓	✓
		All	98.7%	✓	✓
	PseU	All	97.6%	✓	✓
	m5C	All	97.9%	✓	✓
	Inosine	All	98.8%	✓	✓
	2'Ome-A/C/U/G	All	>96.7%*	coming soon	✓

*Different values for A, C, U and G.
See https://nanoporetech.com/platform/accuracy

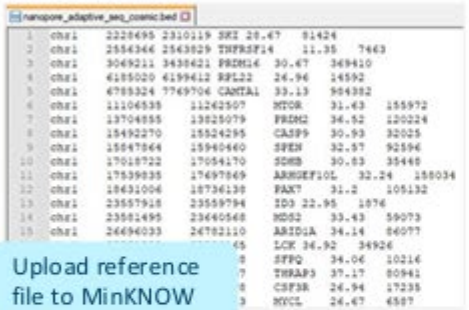
© 2026 Oxford Nanopore Technologies plc. All rights reserved.
Oxford Nanopore Technologies products are RUO. Products labelled/branded as Oxford Nanopore Diagnostics may be RUO or may be regulated as in-vitro diagnostic devices in some jurisdictions.

Riktad sekvensering av utvalda regioner

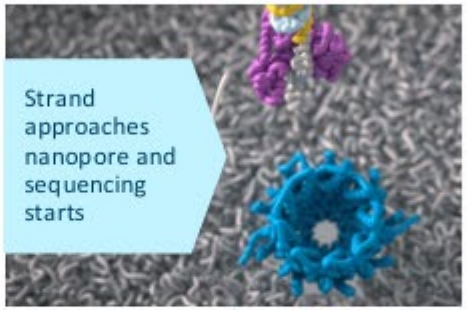
Adaptive sampling

Targeted sequencing

How does adaptive sampling work?



Upload reference file to MinKNOW

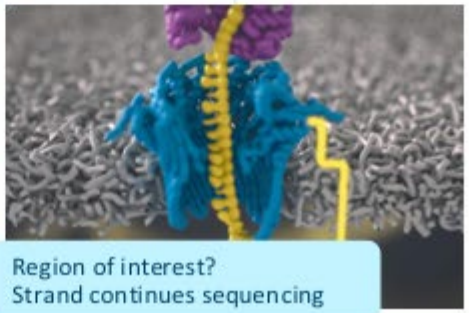


Strand approaches nanopore and sequencing starts

Real-time basecalling and alignment

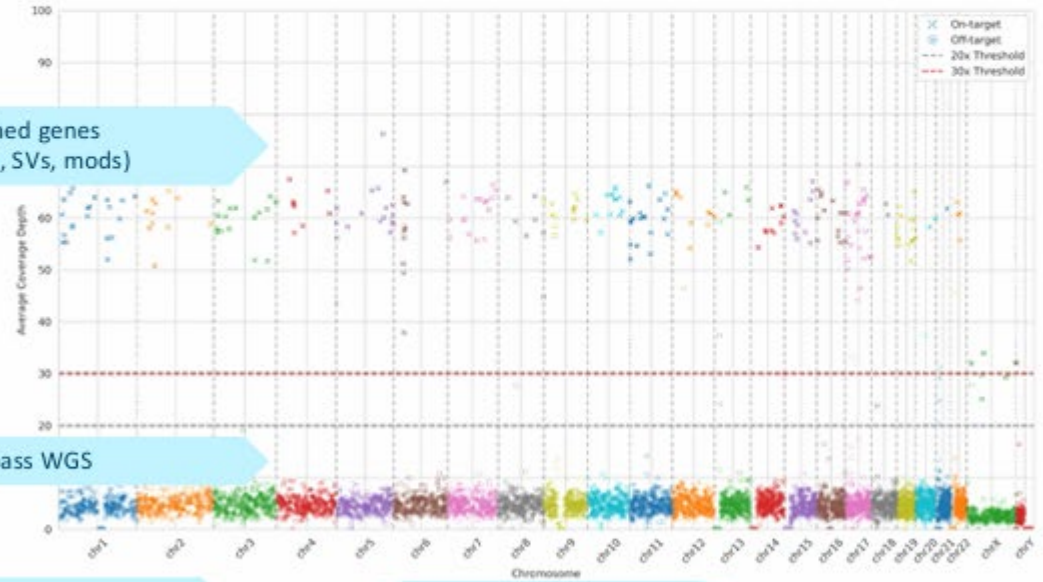


Not region of interest? Strand rejected



Region of interest? Strand continues sequencing

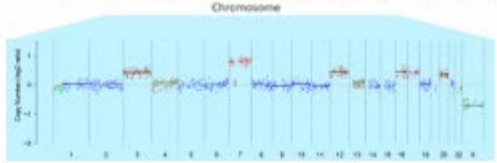
What do you get?



Enriched genes (SNVs, SVs, mods)

Low pass WGS

Detect large chromosomal gains / losses and PRS from low pass WGS



Sequencing coverage across the genome, depicting low-pass whole-genome coverage and >30x enrichment for target loci.

Kontakta oss

kigene@mmk.ki.se

CMM L8:00

Oxford Nanopore Technologies

Flexibility for your library preparation

Kits to match specific experimental needs

	DNA					RNA	
	Output optimised	Speed optimised	Ultra-long reads optimised	Low input optimised	Targeted sequencing	Direct RNA	cDNA
	Ligation Sequencing Kit	**Rapid Sequencing Kit**	**Ultra-Long DNA Sequencing Kit**	**Rapid PCR Barcoding Kit**	**16S Barcoding Kit**	**Direct RNA Sequencing Kit**	**cDNA-PCR Sequencing Kit**
Preparation time	60 mins	10 mins	200* mins +1xO/N incubation	15 mins + PCR	45 mins + PCR	135 mins	~225 mins + PCR
Input recommendation	400-1000 ng gDNA 100-200 fmol amplicons	50 - 200 ng	6M Cells	1 - 5 ng	10 ng	300 ng poly(A)+ RNA or 1 µg total RNA	10ng poly(A)+ RNA or 500 ng total RNA
Fragmentation	Optional	Transposase-based	Transposase-based	Transposase-based	-	Optional	Yes
Amplification	No	No	No	Yes	Yes	No	Yes
Barcode options	Native Barcoding Kits 24 & 96 plex	Rapid Barcoding Kits 24 & 96 plex	-	24 plex	24 plex	*Direct RNA 24plex*	cDNA-PCR Barcoding Kit 24 plex
Typical output	●●●	●●○	●●○	●●○	●●○	20M	>100M
Adaptive sampling	✓	✓	✓	✓		*In development*	*In development*
Methylation included	✓	✓	✓			✓	
Highlights	• Base modifications preserved and included • Automatable workflows on various liquid handlers, and XL kits enable production-scale sequencing			Ideal for low input	Adaptive sampling - software-controlled enrichment	Base modifications preserved and included with the Direct RNA Sequencing Kit	

* Includes DNA extraction

© 2026 Oxford Nanopore Technologies plc. All rights reserved.
Oxford Nanopore Technologies products are RUO. Products labelled/branded as Oxford Nanopore Diagnostics may be RUO or may be regulated as in-vitro diagnostic devices in some jurisdictions.

For more about library prep kits visit
nanoporetech.com/prepare

PCR-fri biblioteksprepparation

Converting sample into a format compatible with nanopore sequencing

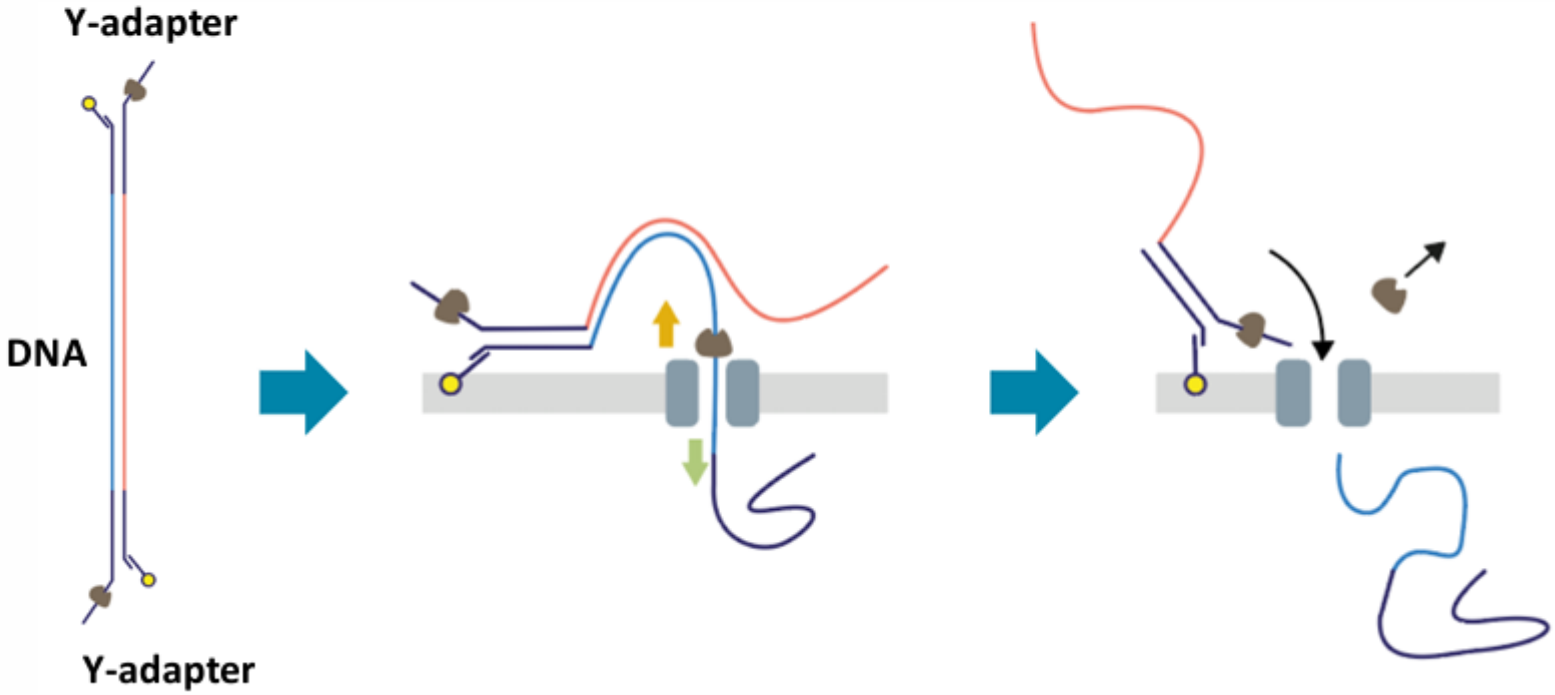
Library prep for nanopore sequencing

Attachment of “sequencing Y-adapter”

Motor protein pre-bound to the adapter

Adapter facilitates tethering

Both strands can be sequenced



PCR-fri biblioteksprepparation

Ligation-based kits: optimised for output and accuracy

Simple, straightforward prep

- ~60 min library prep

Highly versatile

- Range of input samples: gDNA, cDNA, amplicons
- Base modifications preserved
- Control of fragment length: optional fragmentation and/or size selection

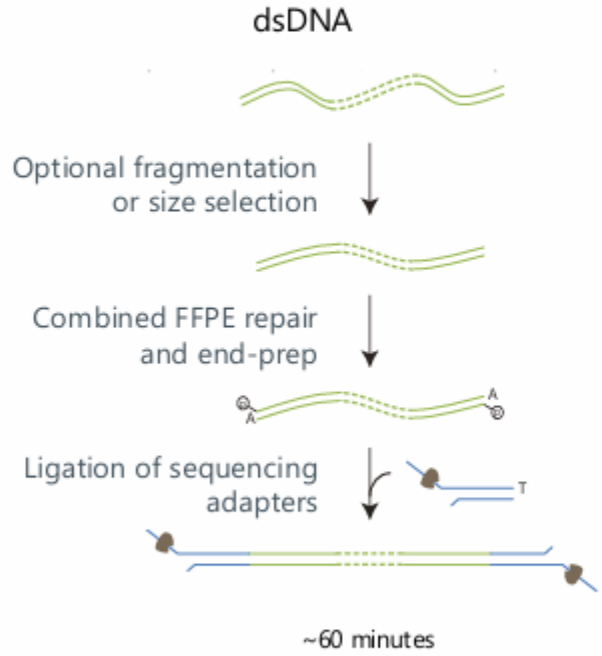
Multiplexing options

- Multiplex up to 96 samples

Find out more about DNA library prep kits:
nanoporetech.com/prepare

© 2026 Oxford Nanopore Technologies plc. All rights reserved.
Oxford Nanopore Technologies products are RUO. Products labelled/branded as Oxford Nanopore Diagnostics may be RUO or may be regulated as in-vitro diagnostic devices in some jurisdictions.

Ligation Sequencing Kit



Native Barcoding Kit

