



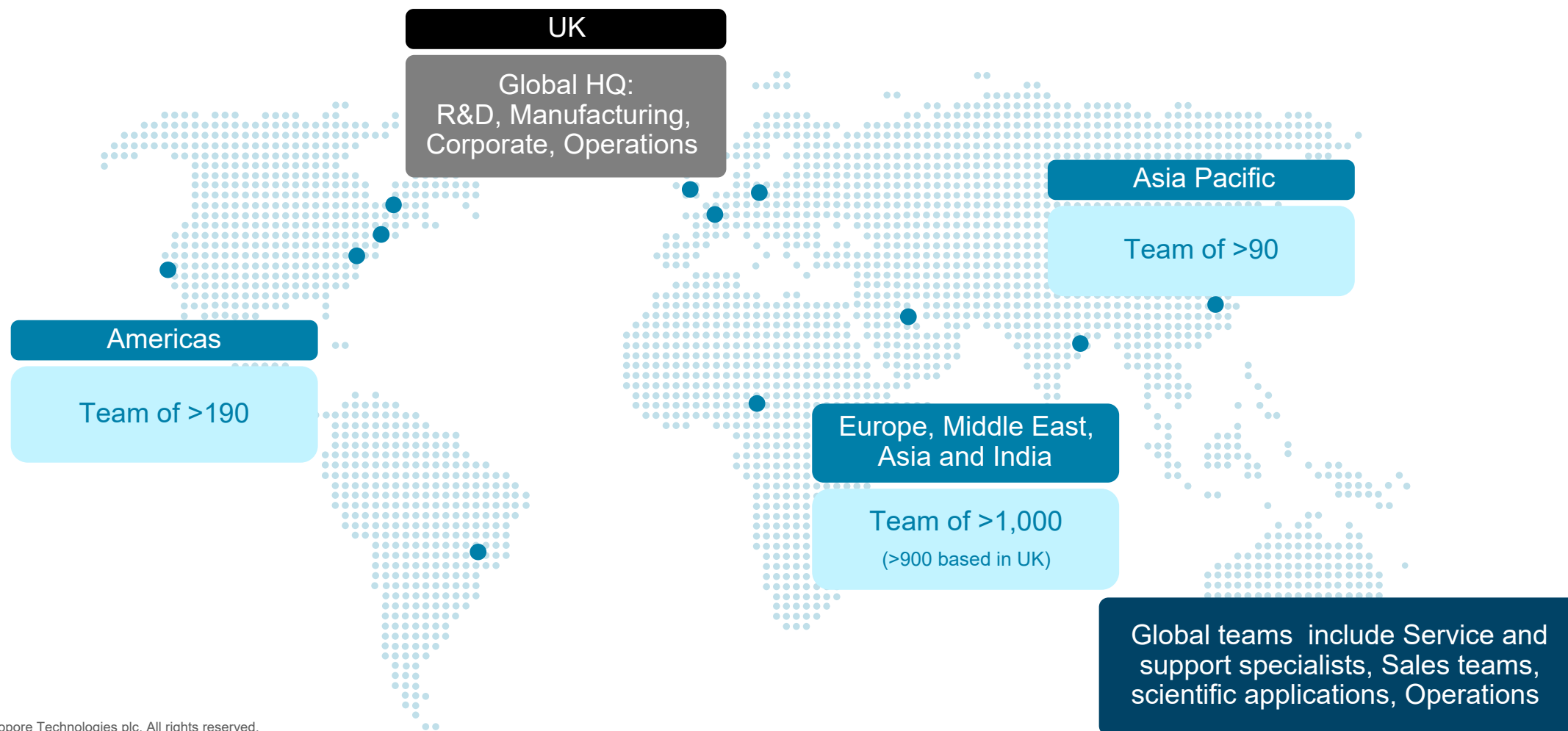
# GENERATE **ULTRA-RICH** **DATA** FOR ANSWERS WITH IMPACT

Jonghwa Ahn, Ph.D  
Senior Field Applications Scientist  
Oxford Nanopore Technologies





# A UK-headquartered company with an international footprint





# Nanopore sequencing: An end-to-end platform

Comprehensive solutions for library preparation, sequencing and data analysis

Platform technology: Flexibility and control at every stage



## Prepare

- ✓ Output optimised
- ✓ Speed optimised
- ✓ Manual & Automated

## Sequence

- ✓ Field devices
- ✓ Lab devices
- ✓ Low & high output platforms  
(low \$ / test & low \$ / Gb)

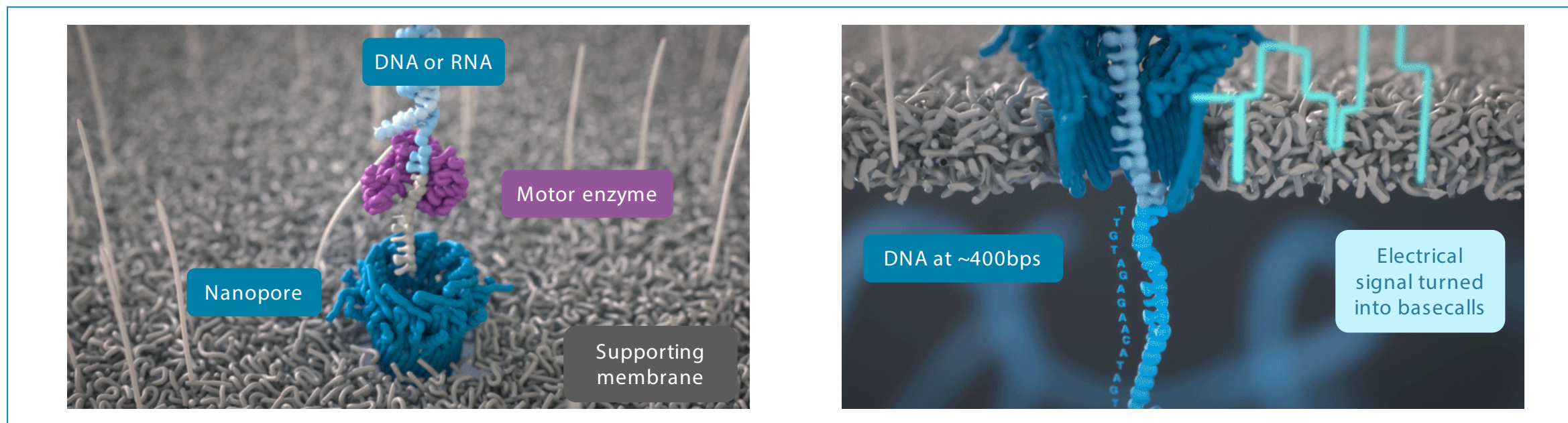
## Analyse

- ✓ Accessible
- ✓ Scalable
- ✓ Versatile



# Nanopore sequencing: how it works

An adapted DNA/RNA strand is passed through a nanopore, an electrical signal is interpreted into sequence data



## Features

Direct sequencing of  
DNA and RNA

PCR free,  
no amplification bias

Read  
length-agnostic

Real-time  
analysis

Chemistry on bespoke  
electronics

## Benefits

Richer information  
including epigenetics

Simpler workflows, Richer  
information including  
epigenetics

One platform for any  
sample; see the true scope  
in your biology

Rapid results  
Intelligent analyses  
e.g. adaptive sampling

Scalable, from small to large  
formats Low-cost



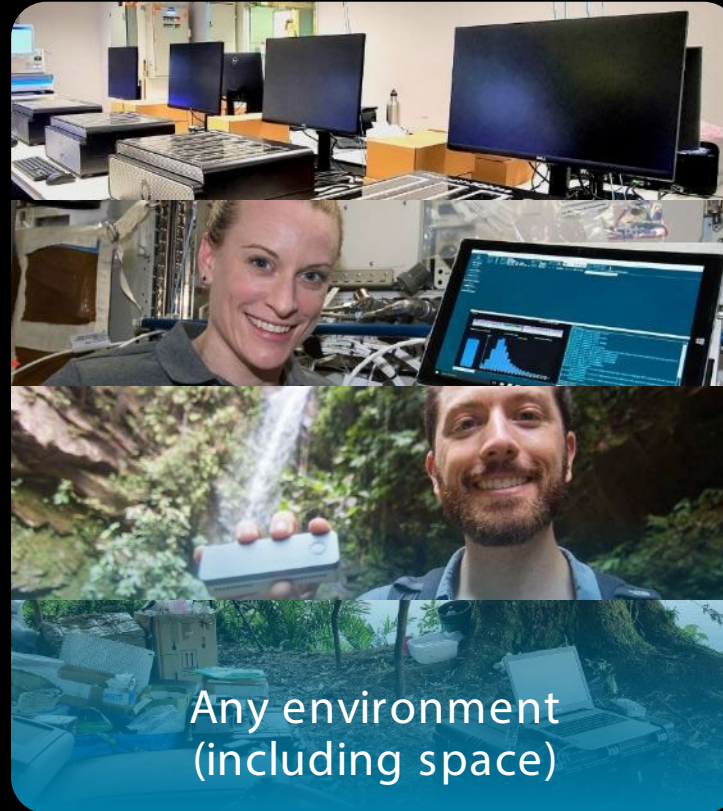


# Our vision is to enable the analysis of anything, by anyone, anywhere

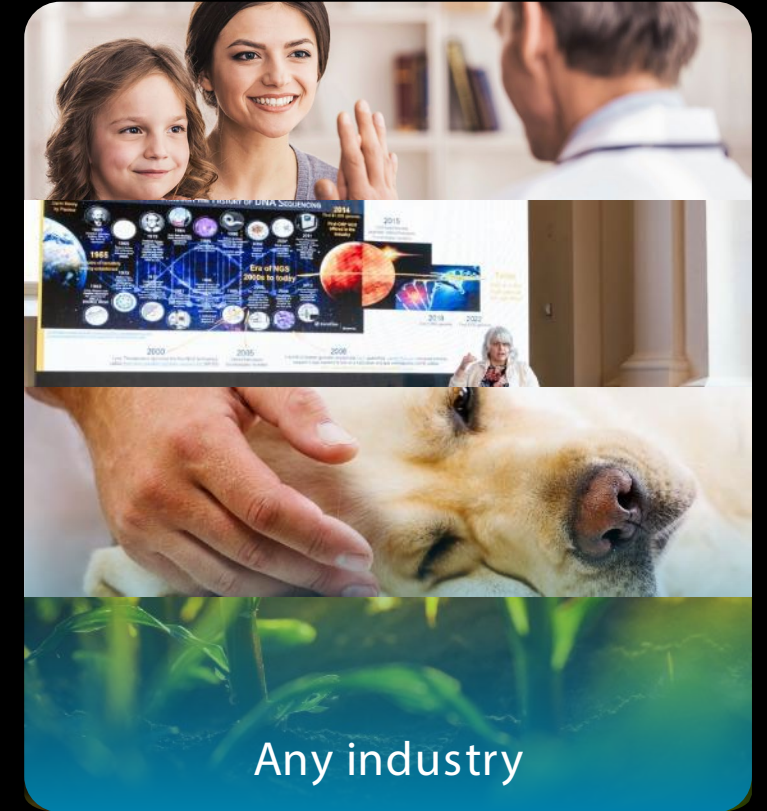
Our mission: We empower people to explore and answer biological questions with our transformative technology platform



Any community



Any environment  
(including space)



Any industry



We continue to innovate for research – and lock down for applied/clinical uses

01.

02.

03.

04.



Beta

Registration based  
Early Access

Open Early  
Access

Released



Q-Line

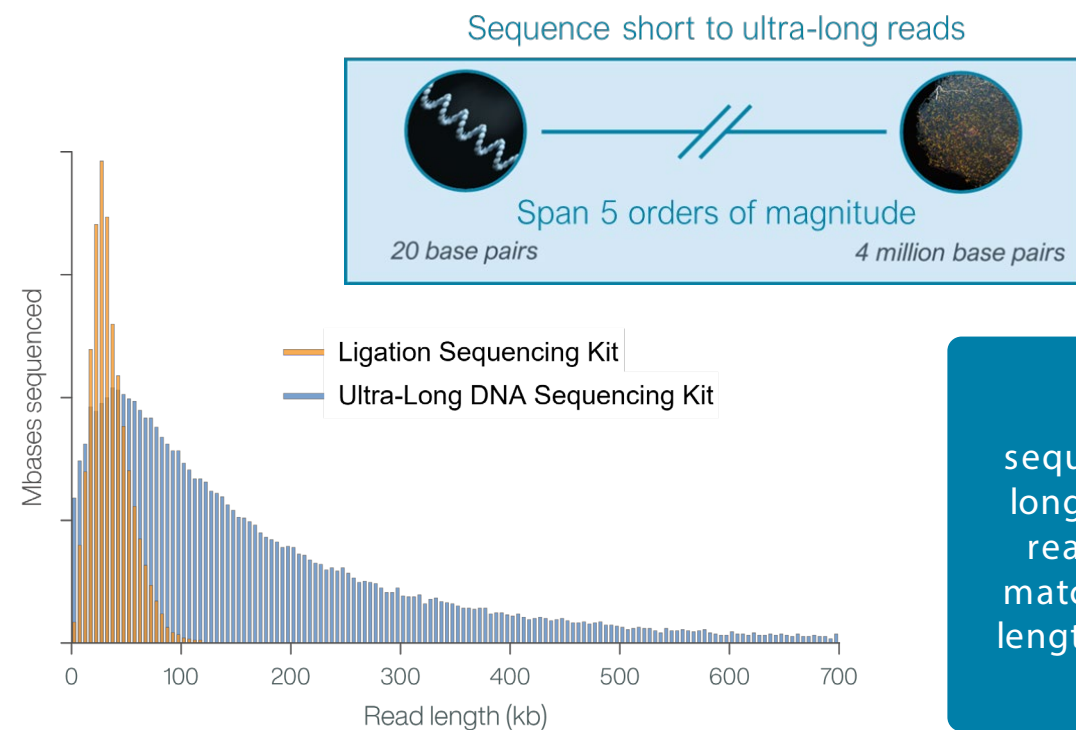
Locked down software & chemistry  
Robust platforms



# The benefits of PCR-free sequencing

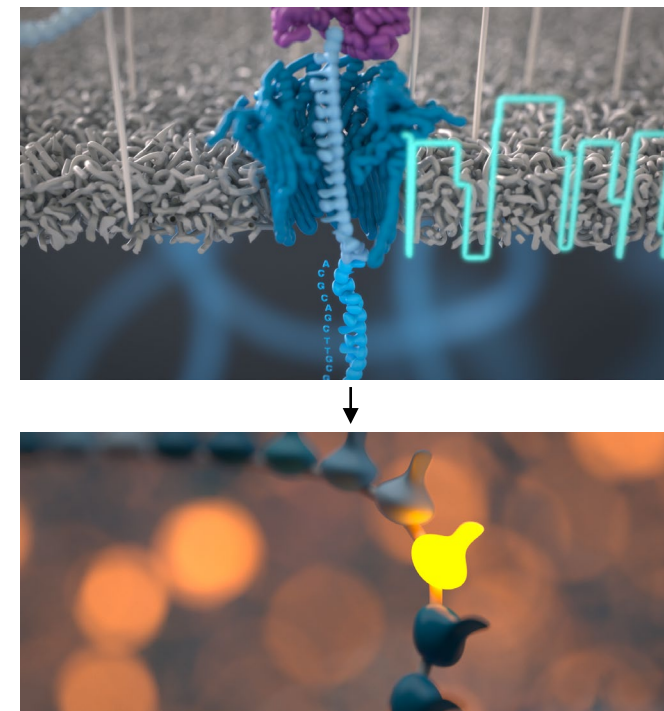
Avoid the limitations of short read technologies

## Unrestricted read lengths



Nanopore sequencing delivers long and ultra-long read lengths that match the fragment length in your library

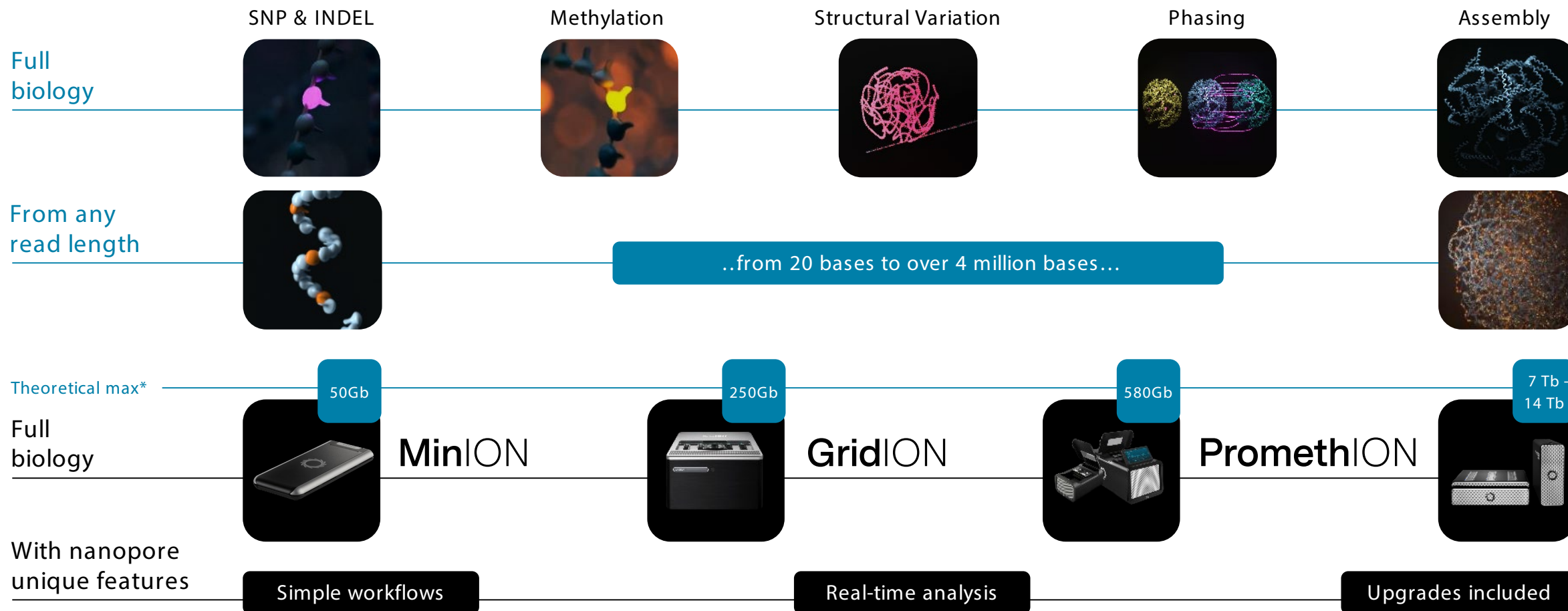
## Methylation included







# ONE sequencing platform

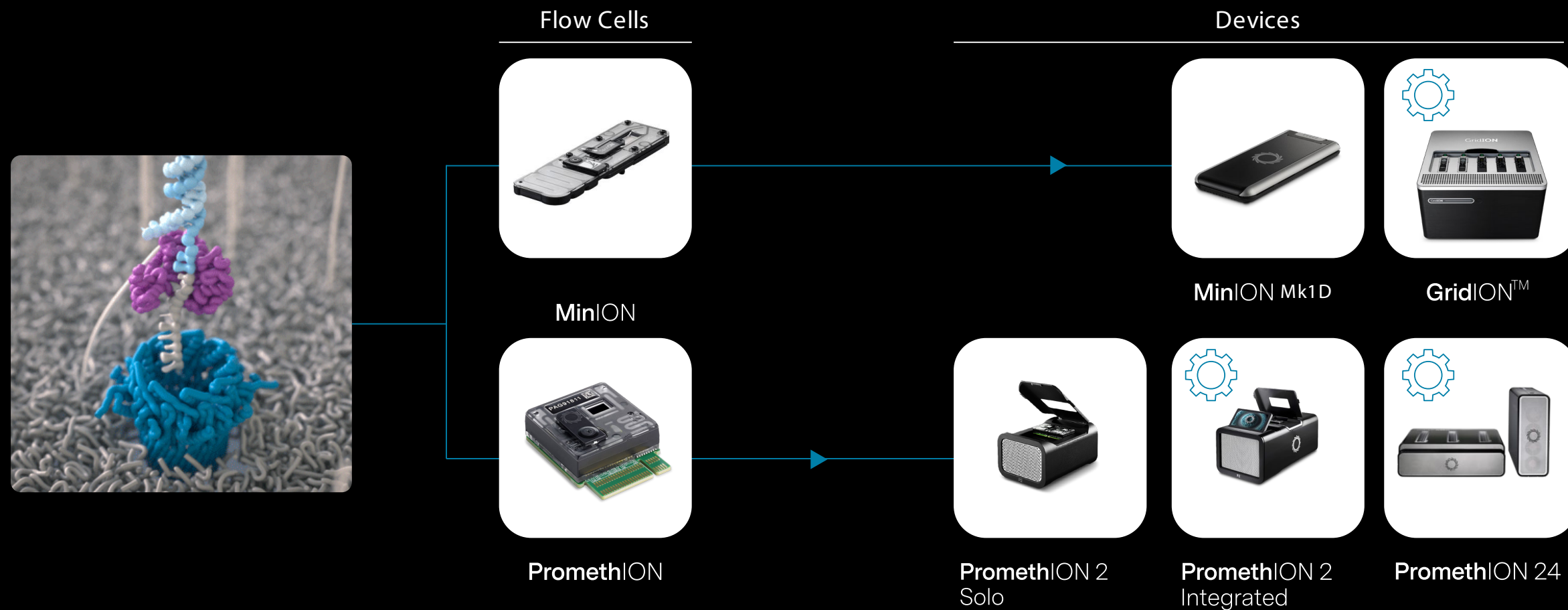


\*Theoretical max output when system is run for 72 hours at 400 bases / second. Outputs may vary according to library type, run conditions, etc.





# One core technology at any scale

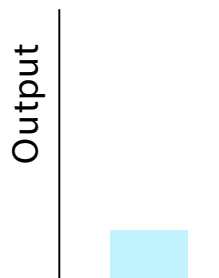




# It starts with a flow cell

A single chemistry delivered across increasing number of nanopores

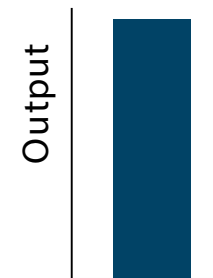
## MinION



### Choose MinION™

- ✓ 10-20 Gb of Ultra-long reads
- ✓ Multiplex small genomes
- ✓ Low-pass sequencing of larger genomes
- ✓ From \$600

## PromethION



### Choose PromethION™

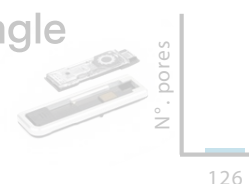
- ✓ Generate hundreds of Gigabases of data
- ✓ Sequence large genomes to high coverage
- ✓ From \$900



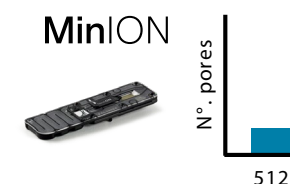
# MinION™ Flow Cells

Flexible and versatile for multiple applications

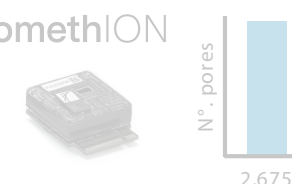
Flongle



MinION



PromethION



15-35 Gb native gDNA reads  
(read N50 ~25 kb)

Multiplexed sequencing of  
up to 96 samples with PCR  
or PCR-free barcoding

Highly accurate full-  
length plasmid  
sequencing



Wash and re-use for  
multiple successive libraries  
with Flow Cell Wash Kit

10-20 Gb ultra-long  
native DNA reads  
(>50 kb read N50)

Plus: direct methylation detection, direct  
RNA sequencing, read lengths from short  
(20 bases) to ultra-long (>4 million bases), ...



# The MinION™ Mk1D devices

Sequencing of anything,  
anywhere by anyone in  
real-time



Simple installation and operation  
with reproducible results

Improved thermal regulation enables  
reproducible results in ambient  
temperature 10-35°C

For small genomes, metagenomics,  
targeted sequencing, and more





# Mk1D IT specification

**Important** - Only USB-C ports are supported to connect your MinION Mk1D to your computer. Ensure the computer you purchase has a USB-C port available. USB-A to USB-C adapters or USB-A to USB-C cables are not supported. USB-A ports typically cannot deliver enough power for the MinION Mk1D and may compromise sequencing performance.

Component	Windows, Linux	macOS
Operating system	Windows 10/11, Ubuntu 20.04/22.04 LTS	macOS
Peripheral	USB Type-C (USB 2.0 speeds or greater)	USB Type-C (USB 2.0 speeds or greater)
Memory	16 GB or higher	16 GB or higher
GPU	NVIDIA RTX 4070 or higher	Apple M3 Max
CPU	Intel or AMD Processor with at least 4 cores/8 threads	Apple M3 Max
Storage	1 TB SSD or greater	1 TB SSD or greater

**We recommend internal solid-state storage for MinKNOW installation as well as data output/acquisition. Solid-state drives are much faster than traditional hard drives and are able to keep up with the flow of data generated during a sequencing run.**

## Example laptops meeting spec (non exhaustive list)



Razer blade 18 (RTX 4070 or greater)



Apple MacBook Pro 14" M3 Max

Benchmarked to run all different basecalling models of over a 72 hour run

# Thank you

---

Oxford Nanopore Technologies, the Wheel icon, AmPORE-TB, ElysION, EPI2ME, Flongle, GridION, MinION, MinKNOW, PromethION, and TraxION are registered trademarks or the subject of trademark applications of Oxford Nanopore Technologies plc in various countries. Information contained herein may be protected by patents or patents pending of Oxford Nanopore Technologies plc. All other brands and names contained are the property of their respective owners.

© 2025 Oxford Nanopore Technologies plc. All rights reserved.

Oxford Nanopore Technologies products are not intended for use for health assessment or to diagnose, treat, mitigate, cure, or prevent any disease or condition.