

Powerful, real-time, long-read
sequencing in the palm
of your hand



“ Nanopore sequencing technology is advancing at an unprecedented pace, promising a future where portable sequencing will be routine in surveillance and many other fields. ”

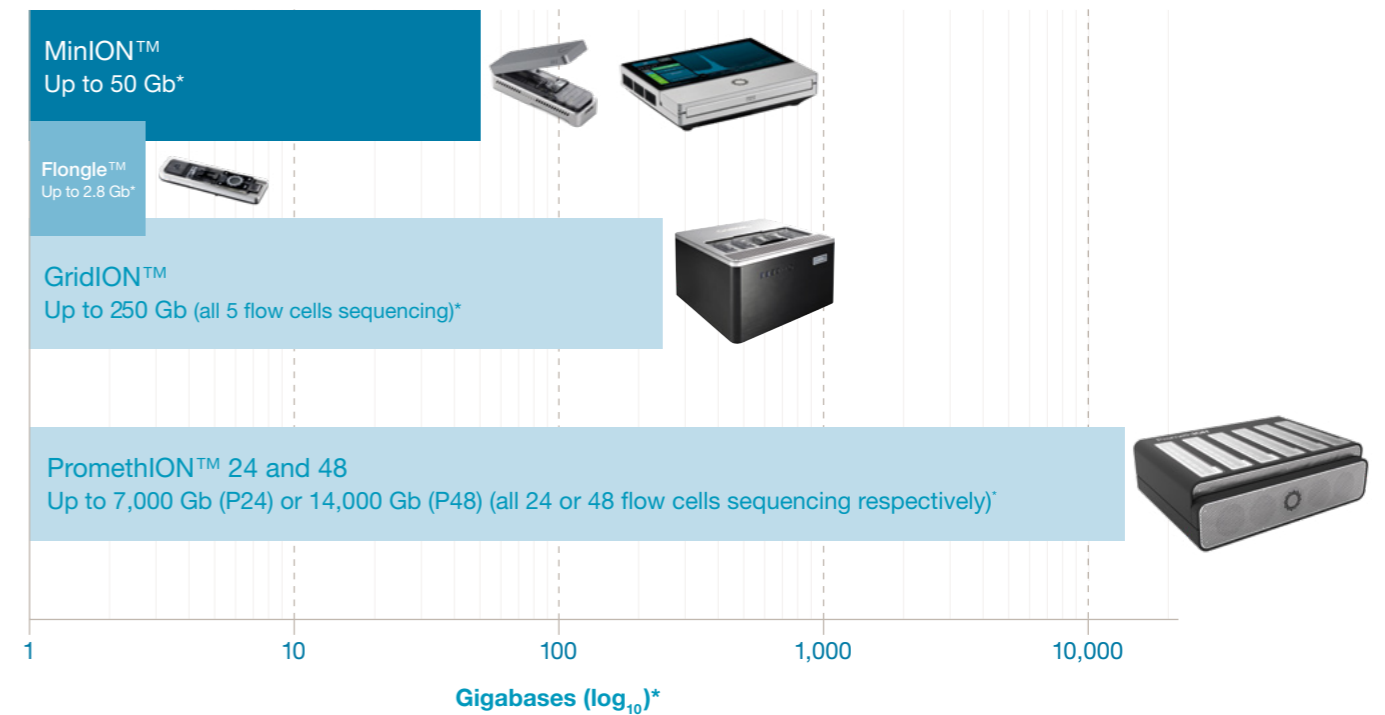
Jana Batovska, La Trobe University

“ MinION ~5 kb amplicon run basecalling all done at 34.28 Gb, I'll take that :) ”

Dr. John Tyson, University of British Columbia

Combining powerful real-time sequencing with complete portability, MinION devices deliver immediate access to gigabases of long-read data

MinION and MinION Mk1C allow you to sequence anything, anywhere — from the bench to the field — with real-time analysis providing immediate access to actionable results. The same DNA and RNA sequencing workflows are available across our products, offering unrestricted read length, from short to ultra-long, and complete scalability to suit your needs.



* Theoretical max output when system is run for 72 hours (or 16 hours for Flongle) at 420 bases / second. Outputs may vary according to library type, run conditions, etc.


All the benefits of long-read, real-time nanopore sequencing in a portable, low-cost device



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How will you use your MinION?

From the bench to the field, MinION devices are being utilised throughout the world to deliver new insights and actionable, real-time results for a range of applications.

 Whole genome sequencing

 Targeted sequencing

 RNA sequencing

 Metagenomics

 Epigenetics



 Clinical research

 Cancer research

 Transcriptome analysis

 Human genomics

 Basic genome research



Image courtesy of Dr. Sarah Stewart Johnson, Georgetown University.

 Environmental research

 Animal research

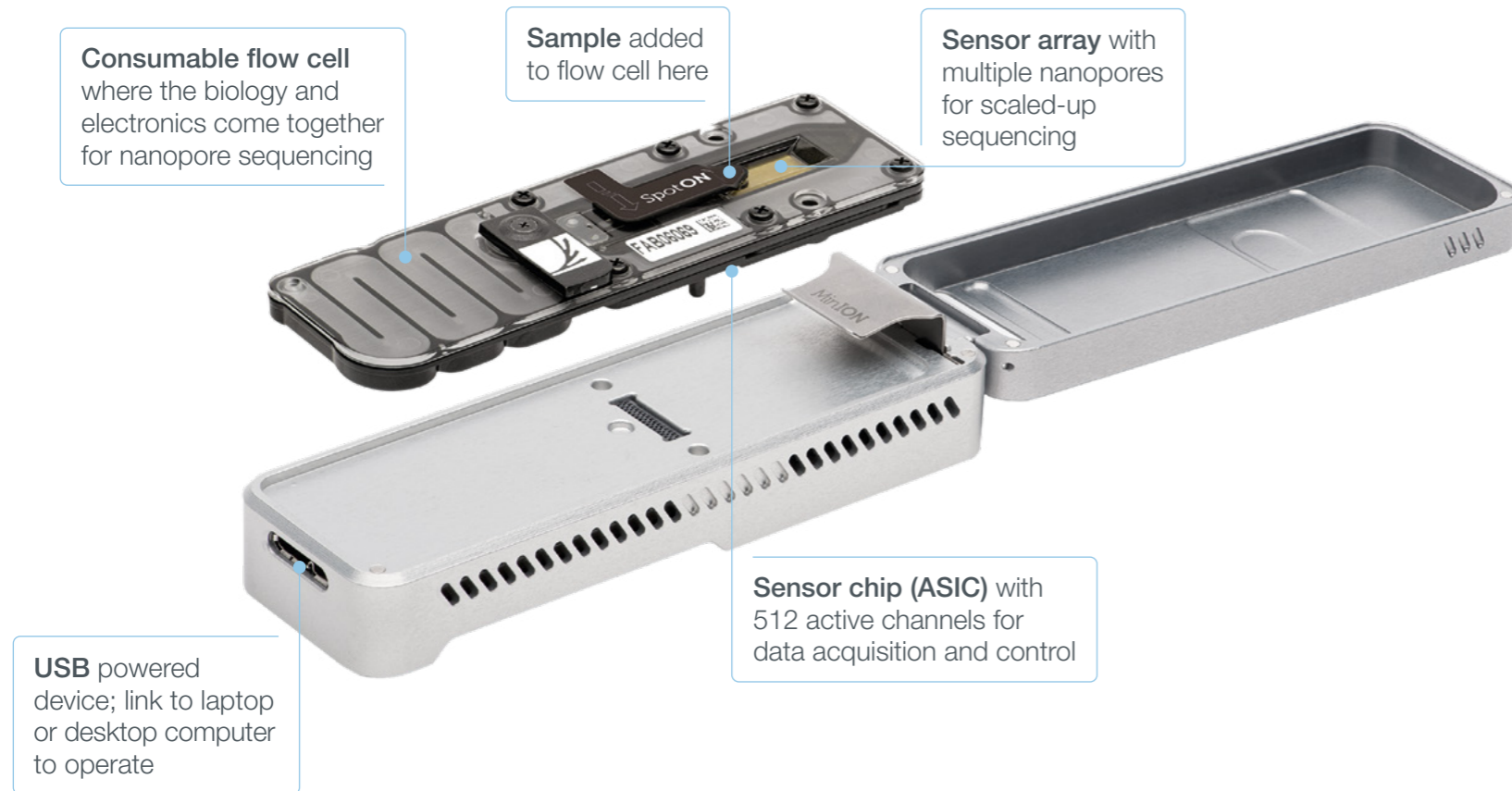
 Plant research

 Microbiology

 Microbiome

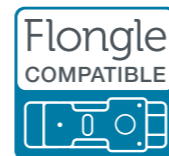
Portable DNA/RNA sequencing for anyone

Small enough to fit in a pocket and powerful enough to deliver gigabases of data, the USB-powered MinION allows researchers to rapidly generate actionable biological insights across a wide range of application areas.



MinION

Specification	
Weight 87 g (103 g with flow cell)	Size W 105 mm H 23 mm D 33 mm



Choose your MinION Starter Pack

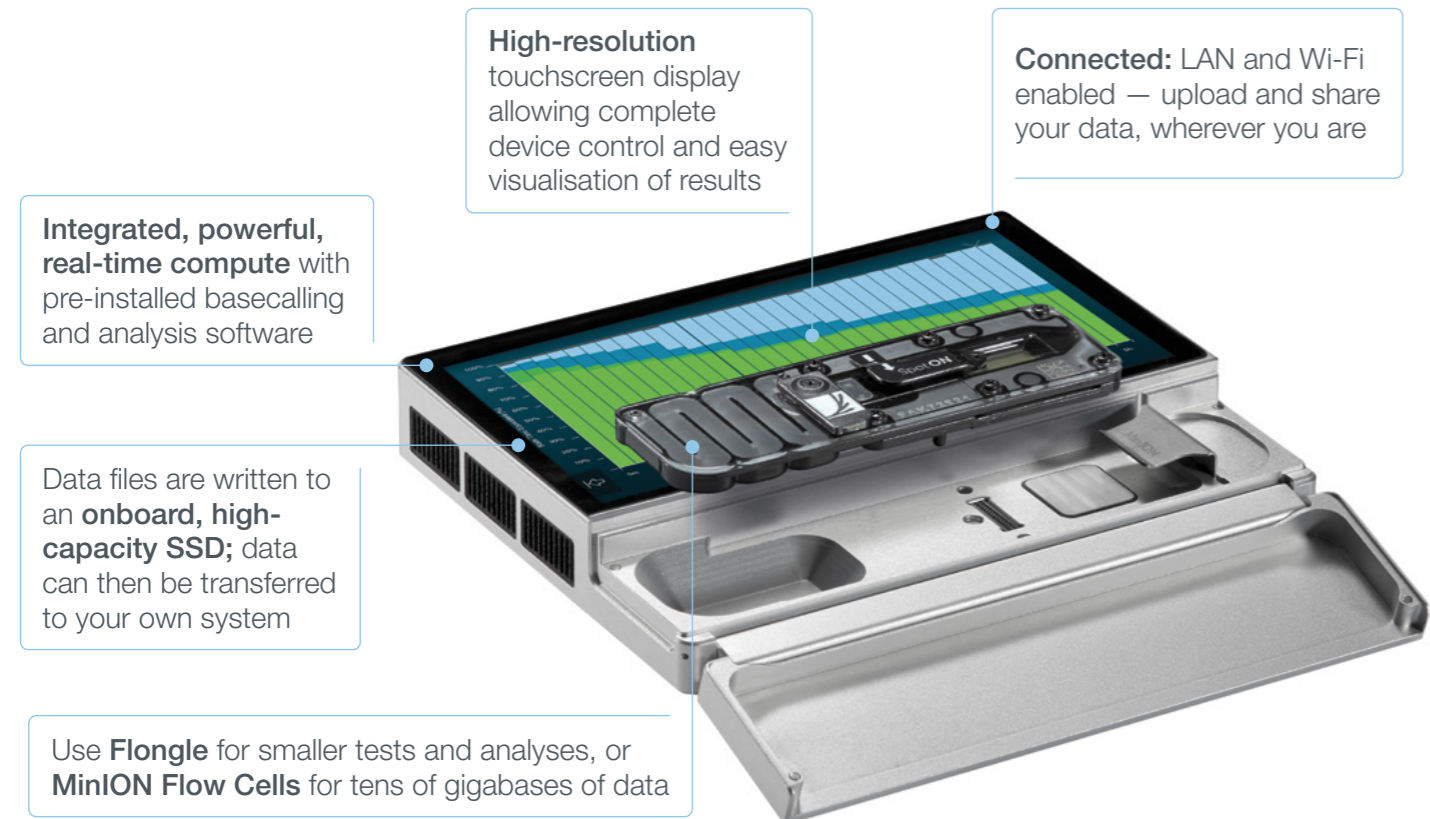
	Recommended	
	Basic	Enhanced
MinION device	1	1
Flow cells	1*	4
Sequencing kits	1	1
Wash kits	1	1
Community Support	Included	Included
Training included†	-	1-day workshop
	\$1,000	\$3,300

* Includes voucher for second free flow cell.
 † A wide range of training and support services are available, for more information visit store.nanoporetech.com/services.

Buy now store.nanoporetech.com

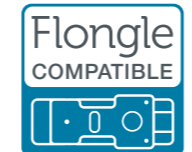
Fully integrated, portable sequencing and analysis

MinION Mk1C combines the real-time, rapid, portable sequencing of MinION and Flongle with powerful integrated computing and a high-resolution touchscreen — offering a complete, go-anywhere solution for DNA and RNA sequencing and analysis.



MinIONMk1C

Specification	
Weight 420 g	Size W 140 mm H 30 mm D 114 mm



Choose your MinION Mk1C plan

	Basic	Enhanced	CapEx*
MinION Mk1C device	1	1	1
Flow cells	6	12	-
Sequencing kits	1	2	-
Wash kits	1	1	-
Software licence and device warranty†	12 months	12 months	12 months
Community Support	Included	Included	Included
Training included‡	-	1-day workshop	-
	\$4,900	\$9,900	\$9,300

* Device purchase.
 † Extended warranties available.
 ‡ A wide range of training and support services are available, visit store.nanoporetech.com/services for more information.

Buy now store.nanoporetech.com

A complete and streamlined workflow for rapid access to actionable results



Prepare

- Streamlined library preps — in as little as 10 minutes, with multiplexing options
- Scale according to your needs — same chemistry and kits used for Flongle, MinION, GridION Mk1, and PromethION
- Automate library preparation using the portable, USB-powered VoITRAX

Sequence

- Sequence what you need, when and where you need it
- Read lengths determined by your sample and experimental needs
- MinION devices sequence DNA and RNA directly — meaning no amplification bias and retained modification information
- Run smaller sequencing tests and experiments or cost-effectively check your sample quality using Flongle on MinION

Analyse

- Real-time results for time-critical applications such as pathogen identification
- User controlled run time — stop sequencing when sufficient data generated, wash and reuse flow cell
- Portable data analysis using MinION Mk1C or combine MinION with a laptop
- Output raw signal or basecalled .fastq files for use in custom analysis pipelines

Applications include:

- Rapid metagenomic species identification and antibiotic resistance profiling
- Accurate high-coverage microbial genome assemblies (DNA and RNA)
- Enhanced large genome analysis (e.g. cancer samples) through accurate mapping of structural variation, repetitive regions, and phasing
- Quantify and characterise RNA splice variants, isoforms and fusion transcripts

Enhance your MinION sequencing workflow...

Prepare

Automated library preparation for nanopore sequencing.

- Small, USB-powered device
- Minimal hands-on time
- Reproducible results

nanopore.com/products

VolTRAX



Sequence

Adapting MinION devices for smaller, rapid tests and analyses. Delivering as much as 2.8 Gb* data, Flongle is suitable for:

- Smaller samples (e.g. targeted regions and smaller genomes)
- Rapid sample ID or quality checking
- Low-cost regular testing

nanopore.com/products

Flongle



Analyse

Providing straightforward, best-practice data analysis workflows and interactive tutorials — from basic quality control to genome assembly.

- Minimal installation requirements
- Interactive tutorials for your data
- Fully customisable

nanopore.com/analyse

EPI2ME Labs



...with data analysis in real time

EPI2ME

Real time data analysis workflows accessed through the cloud or locally using MinION Mk1C†.

Example workflows:

What's In My Pot (WIMP)

Species-level identification and quantification of microbes from metagenomic samples

ARMA Builds on WIMP with full antibiotic resistance profiling

16S Genus-level identification of bacteria and archaea in metagenomic samples

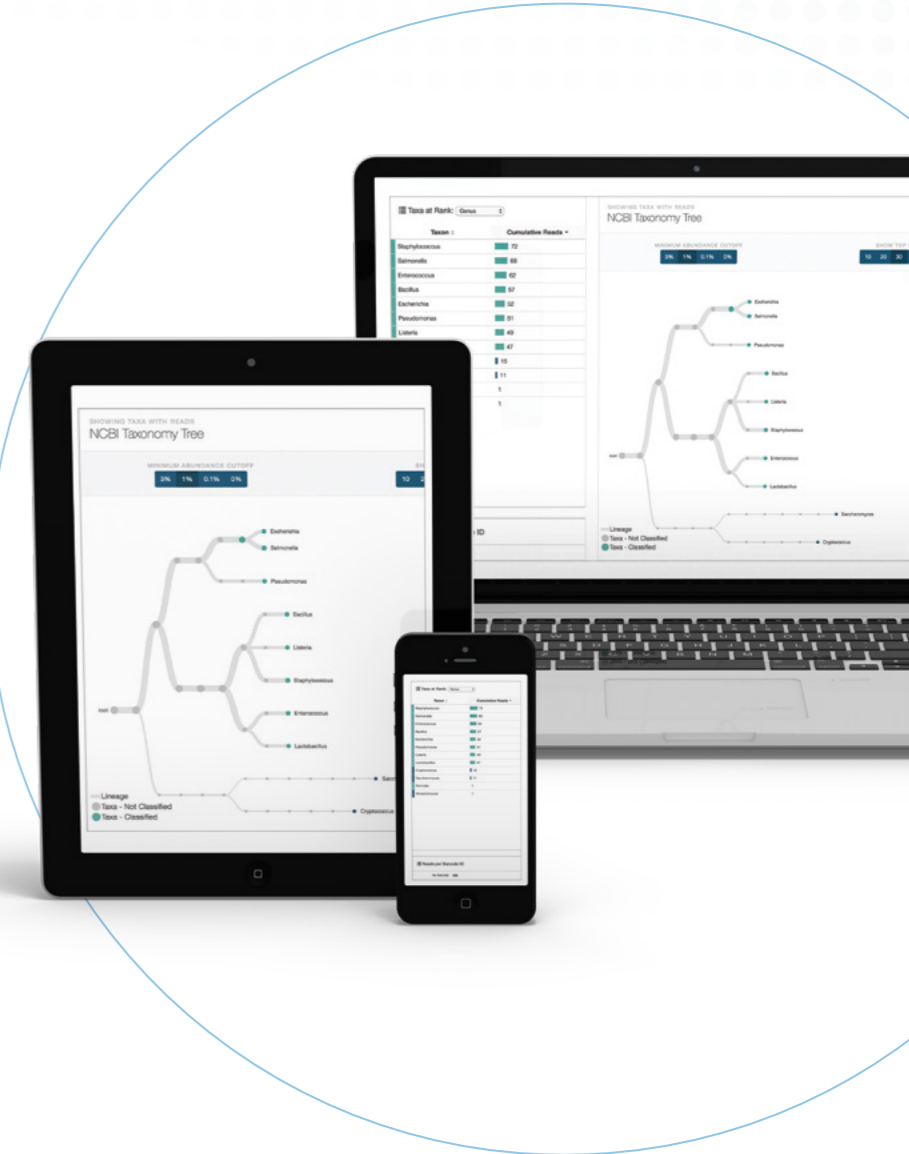
Custom Reference Alignment

Align genomes to any reference sequence

Human SV

Map and identify structural variation across the whole human genome

nanopore.com/analyse



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† Coming soon.



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BR_1002(EN)_V5_16May2021

