

Our goal: to enable the analysis of anything, by anyone, anywhere



THE MINION MK1C: PORTABLE,
CONNECTED SEQUENCING + ANALYSIS + SCREEN

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AGENDA

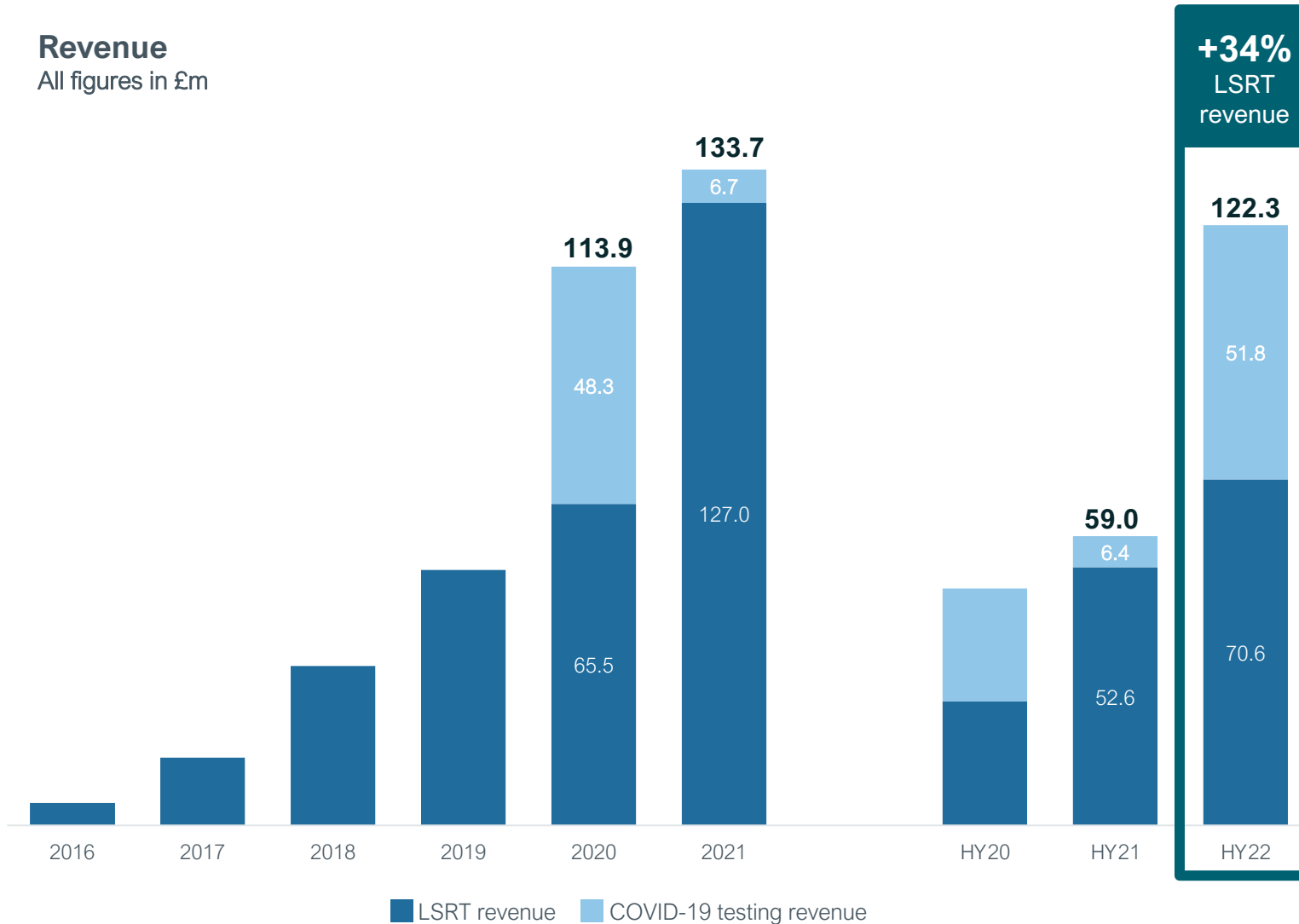
Introduction – Gordon Sanghera, CEO

HY22 Financial review – Tim Cowper, CFO

HY22 Business review – Gordon Sanghera, CEO

Continued robust underlying growth in core LSRT business

Revenue
All figures in £m



Core LSRT business

LSRT revenue
£70.6m
(HY21: £52.6m)

COVID-19 sequencing revenue
~£15-18m
(HY21: ~£6-8m)

Revenue from the EGP¹
£5.8m
(HY21: £9.8m)

¹The Emirati Genome Program
HY22 COVID-19 testing revenue of £51.8m reflects the settlement of the contract with the DHSC

HY 2022 highlights



GROWING, DIVERSE USER COMMUNITY

>7,300 active customer accounts¹

Rapid increase in publications

>3,500 publications to date²
(31 Dec: 2,466)



OPERATIONAL GROWTH

Strong financial position
£602.6m³ cash

Continued scale-up of manufacturing operations

Global headcount >900
(31 Dec: 803)



AGILE INNOVATION

First early access P2 solo shipments

Further chemistry and kit upgrades

Release of Remora

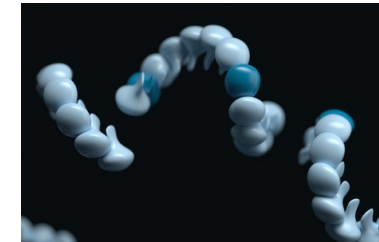
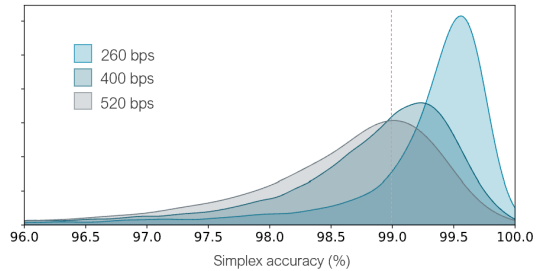
Release of Short Fragment Mode

¹ Customers active in the last 12 months

² The number of scientific publications that include nanopore sequencing, as publicly available in online resources as at 6 September 2022.

³ Cash, cash equivalents and treasury deposits

Innovation drivers of growth



PLATFORM UPGRADE: Q20+

R10.4.1 pore and Kit 14:

Nanopore high outputs with raw read accuracy over 99%

High consensus accuracy, variant calling performance & market leading methylation

Duplex enabled for Q30 read accuracy

PROMETHION UPGRADES

Hardware and compute:

P24 & P48 device upgrades for Q20+ chemistry

Included in device warranty

PromethION A100 compute now shipping
2 – 4x increase in compute capacity for integrated analysis

P2 LAUNCH

Broadening PromethION base:

P2 from only \$10,455: accessible to many labs

Enables human WGS for under \$1,000

Highly suited for other large genomes, single cell & transcriptomic applications

SHORT FRAGMENT MODE

ANY read length:

Generate over 100 million reads / PromethION flow cell

Analyse methylation patterns in cell free DNA

Comfortably run panels whilst also sequencing ultra-long samples on the same device

one platform – any experiment

HY22 Financial Review

Tim Cowper, CFO

HY22 Financial highlights¹

▶ **Core LSRT revenue up 34% to £70.6m**

Total revenue £122.3m including DHSC settlement. Core revenue inline with expectations; FY22 guidance unchanged

▶ **LSRT gross margin up 3.7pts to 54.8%**

In line with expectations driven by recycling of electrical components, improvements in manufacturing techniques and automation

▶ **Adjusted EBITDA² £(34.6)m (HY21: £(19.2)m)**

Higher gross profit offset by increased operating expenses, in particular headcount, to support long term sustainable growth

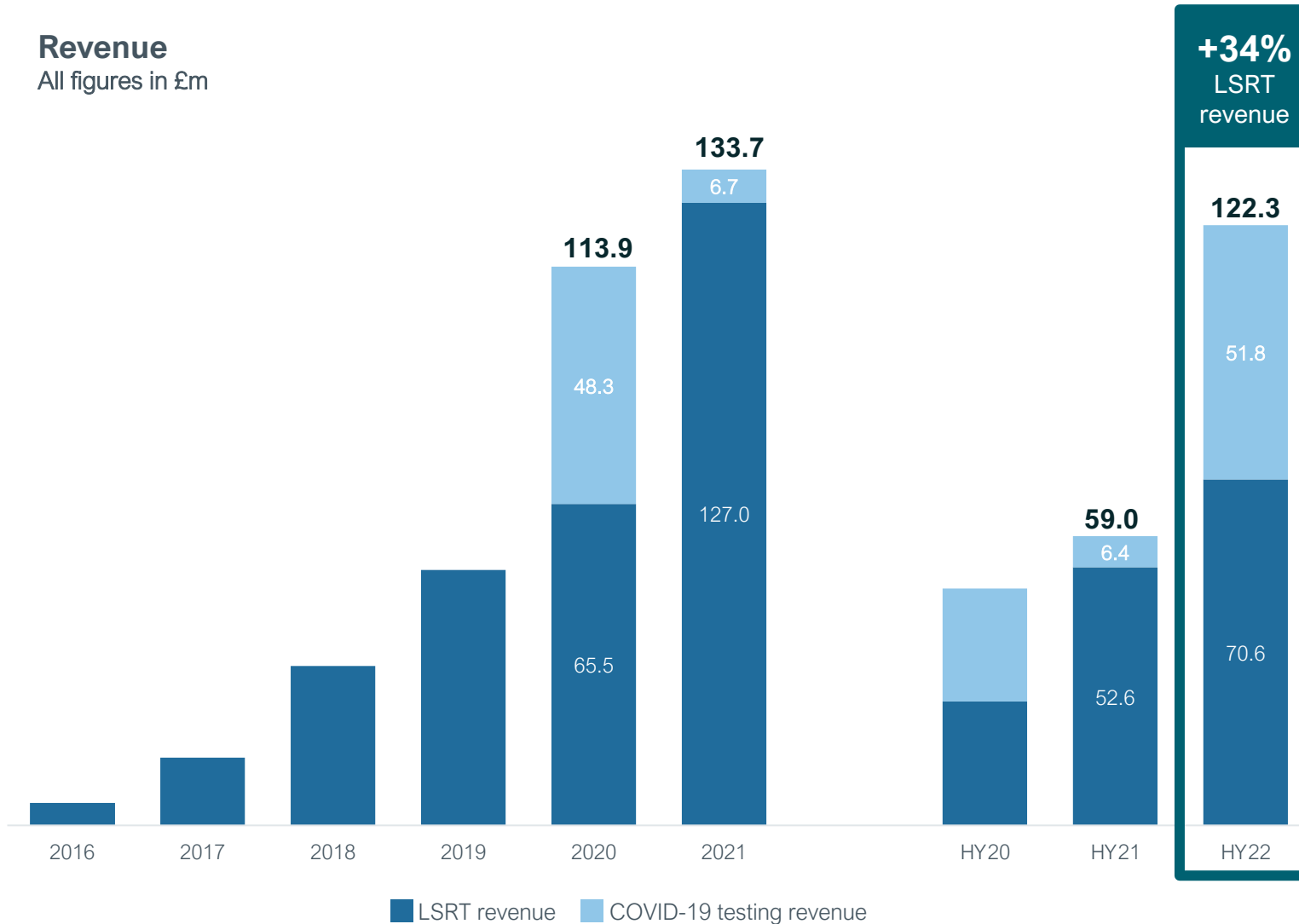
▶ **Cash, cash equivalents and treasury deposits £602.6m (FY21: £618.2m)**

¹ All growth rates are year-on-year unless stated otherwise

² Adjusted EBITDA, being EBITDA, adjusted for Share-based payments (Founder LTIP), Employer's social security charge on pre-IPO share-based payments and impairments and revenue and expenses associated with the settlement of the COVID-19 testing contract with the DHSC

Continued robust underlying growth in core LSRT business

Revenue
All figures in £m



Core LSRT business

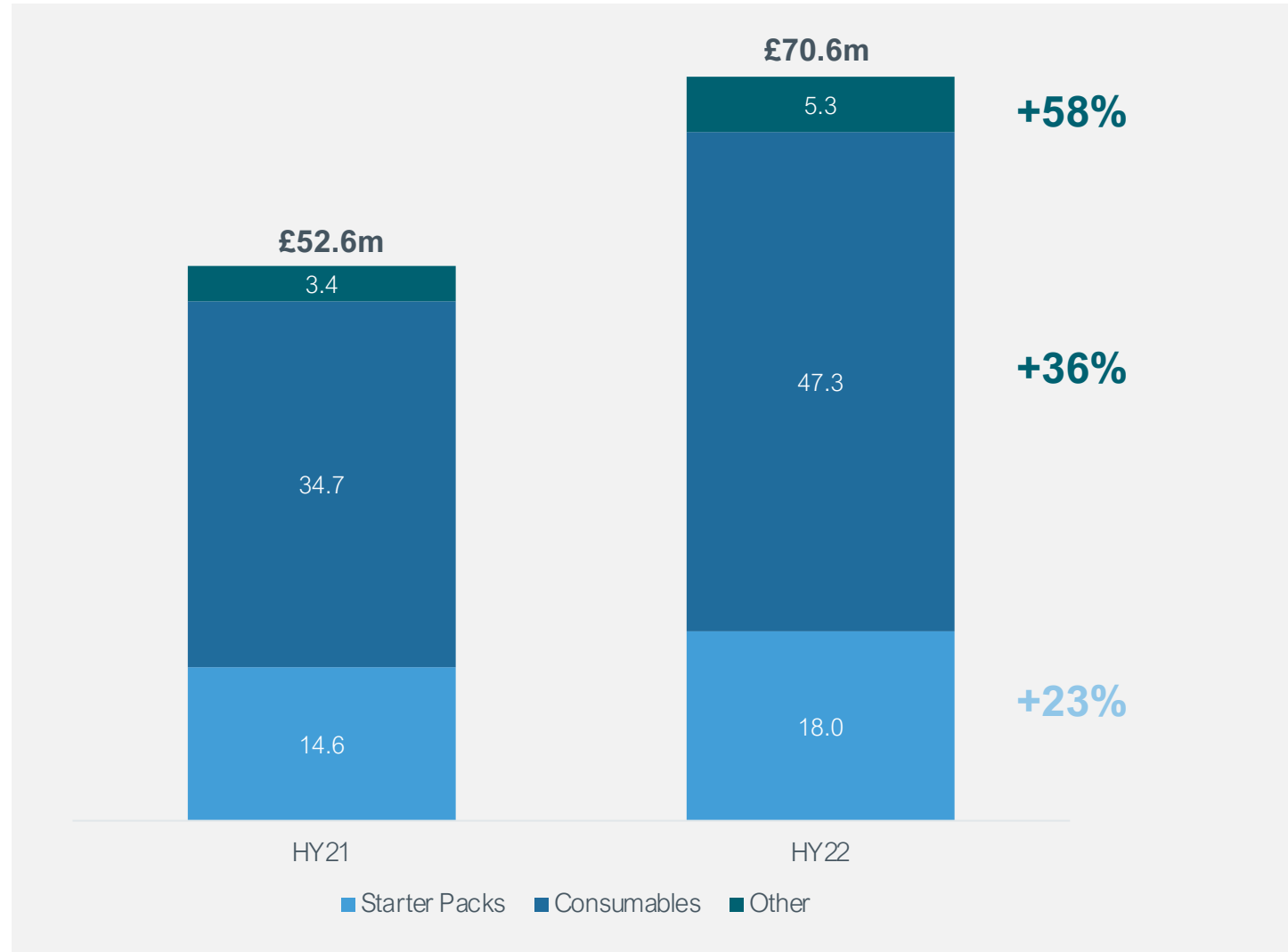
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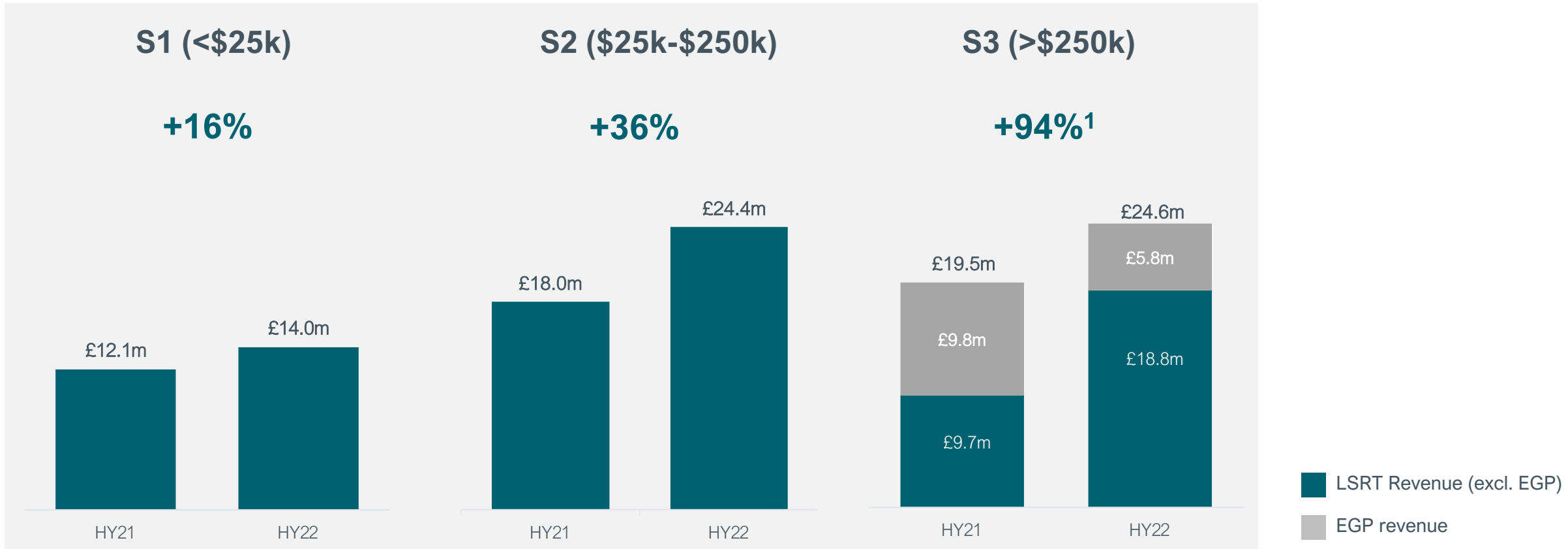
Core LSRT revenue growth in HY22 driven by increased utilisation



Increased utilisation reflected in strong consumables revenue growth

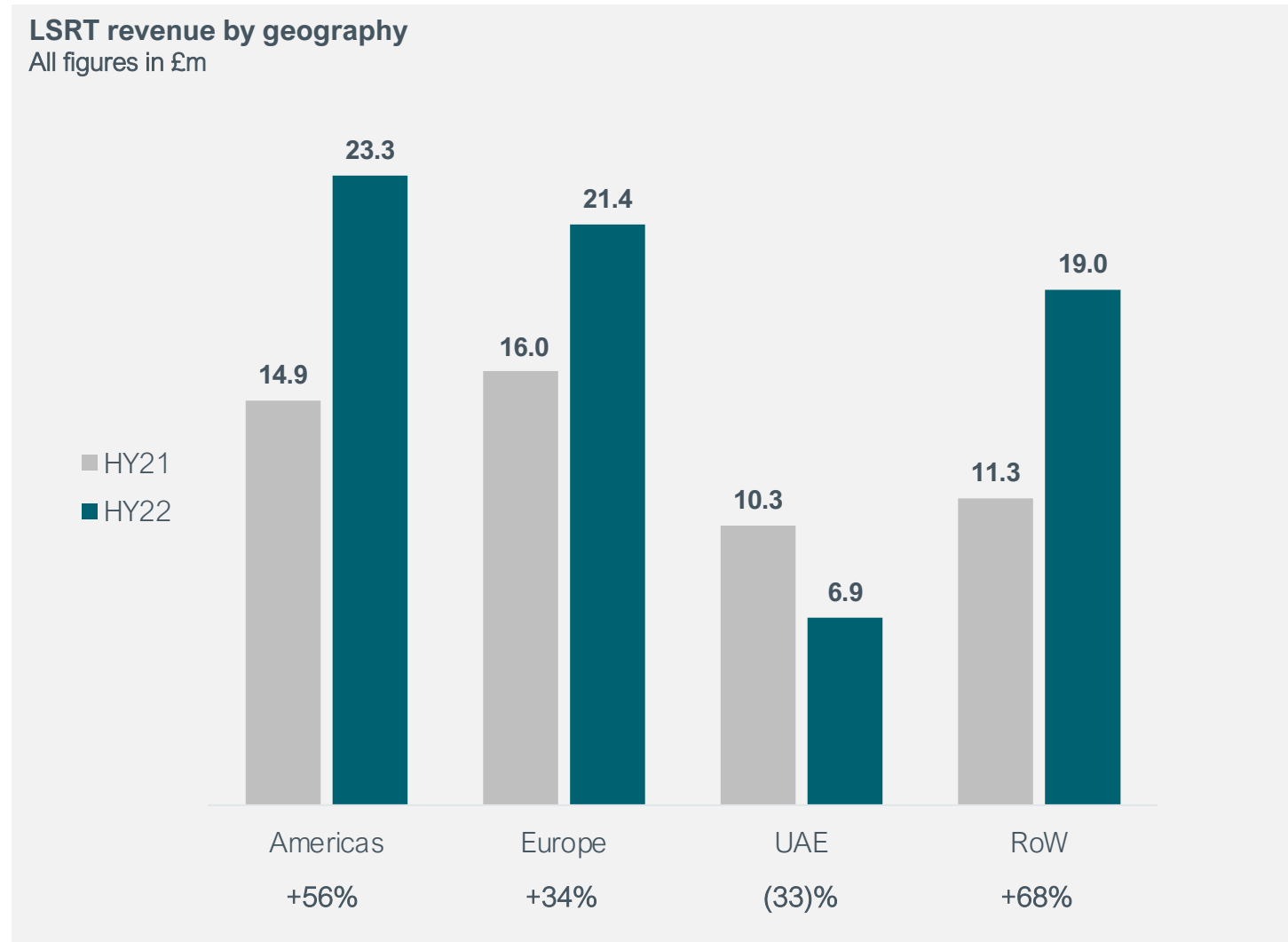
Starter pack revenue driven by both new customer acquisition and customer expansion

LSRT revenue growth underpinned by expansion and diversification of user base



Revenue from indirect customers was £7.5m (HY21: £3.0m) a 150% year-on-year increase

Revenue growth diversified by geography

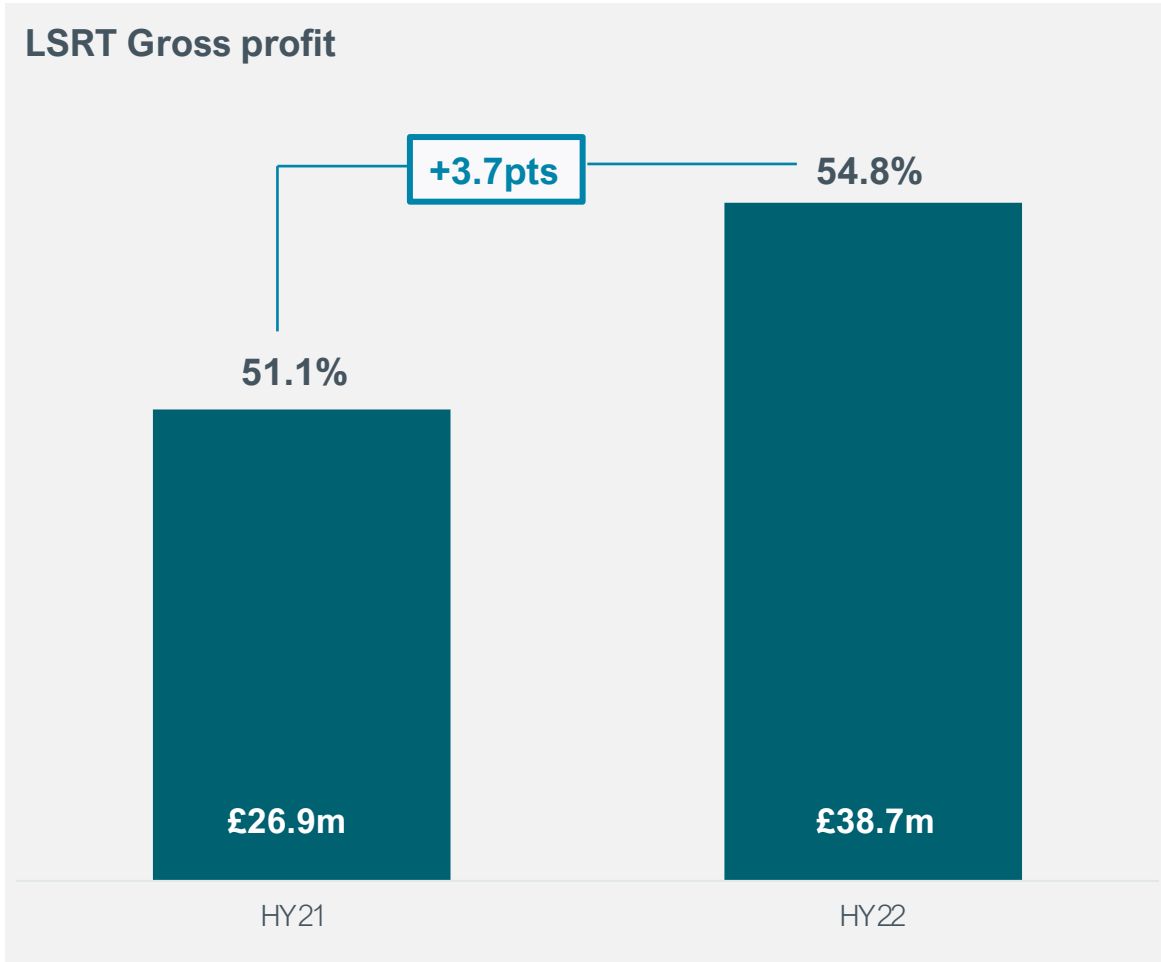


Strong growth in Americas and Europe reflects increase in commercial resources

RoW revenue reflects strong COVID-19 sequencing business in China

UAE impacted by £4m year-on-year decrease in EGP revenue

Improving margins in core LSRT business



Total Gross profit (including DHSC) increased from £30.2m to £78.0m

Total Gross margin (including DHSC) increased from 51.2% to 63.7%

Continued investment in innovation and commercial infrastructure

	HY22 £m	HY21 £m
Adjusted Research and development expenses	34.6	24.2
Capitalised development expenses	9.0	4.3
Total R&D and capitalised development expenses	43.6	28.5
Employers' social security taxes on pre-IPO share awards	(9.4)	6.4
Less: Capitalised development expenses	(9.0)	(4.3)
Research and Development expenses as reported	25.2	30.6
Adjusted S,G & A expenses	49.9	37.9
Share-based payment expenses on Founder LTIP	35.4	0.9
Employers' social security taxes on pre-IPO share awards	(11.0)	4.0
Expenses associated with settlement of DHSC COVID-19 testing contract	1.4	-
S,G & A expenses as reported	75.7	42.8

Adjusted EBITDA

	HY22 £m	HY21 £m
Loss before tax	(27.6)	(44.4)
Depreciation & Amortisation	16.1	12.0
Other	(0.2)	0.4
EBITDA	(11.7)	(32.0)
Founder LTIP	35.4	0.9
Employers Social Security on pre-IPO Share Awards	(20.4)	11.3
Settlement of DHSC COVID-19 testing contract	(37.9)	0.0
Other	0.0	0.5
Adjusted EBITDA	(34.6)	(19.2)

Strong balance sheet

	HY22 £m	FY21 £m
Non-current assets	89.0	91.3
Current assets		
Inventory	73.1	63.1
Trade and other receivables	54.9	54.8
R&D tax credit recoverable	5.6	14.3
Assets held for sale	15.6	0.0
Cash and cash equivalents	471.6	487.8
Other financial assets	132.4	130.6
Total assets	842.3	841.9
Non-current liabilities	(27.7)	(32.8)
Current liabilities	(88.5)	(105.0)
Net assets	726.1	704.0
Total Equity	726.1	704.0

Increase in inventory reflects higher stock levels of core components to manage global supply chain risk

£602.6m

cash, cash equivalents and short-term treasury deposits

Financial guidance; reaffirming FY22 and FY23 targets

FY 2022 Guidance	<p>LSRT revenue: £145m to £160m <i>No change</i></p>
FY 2023 Guidance	<p>LSRT revenue: £190m to £220m <i>No change</i></p> <p>Gross margin: >60% <i>No change</i></p>
Medium Term (3-5 years) Guidance	<p>Compound annual revenue growth: >30% <i>No change</i></p> <p>Gross margin: >65% <i>No change</i></p> <p>Adjusted EBITDA: Breakeven by 2026 <i>No change</i></p>

FY22 revenue guidance accounts for an expected decline in COVID-19 sequencing revenue in HY22 and £15-20m of revenue from the EGP, the Group's largest customer

HY22 Business Review

Gordon Sanghera, CEO

Highly differentiated products driving increased adoption

Electronic sensing platform enabling:

Accessibility:

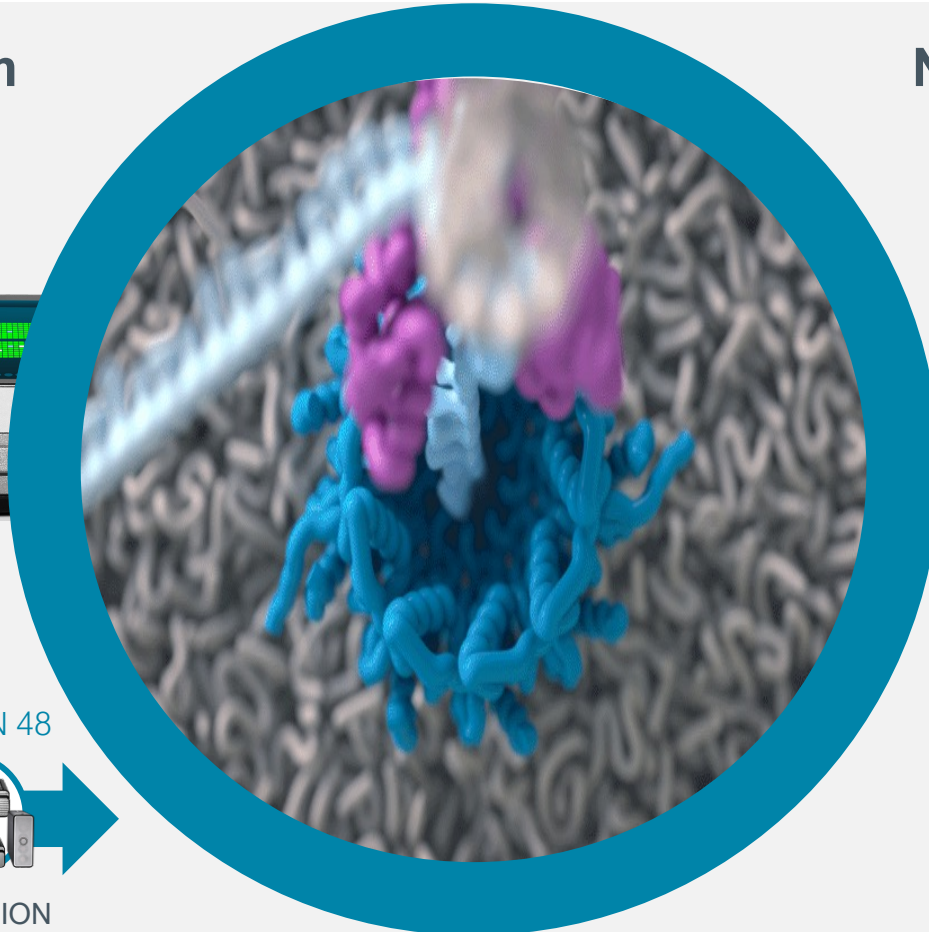
MinION from \$1,000
Price per Gb from \$2-3

Real-Time:

Rapid sample prep
Data streams in real-time

Scalability:

One platform scaled from Flongle to PromethION 48

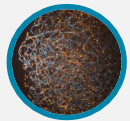


Native DNA/RNA delivering information rich data:

Of any read length:

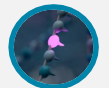


From 20 bases
to 4 mega bases



with strong performance across:

SNP Detection



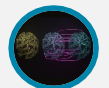
SV Detection



Assembly

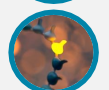


Phasing



Full Methylation

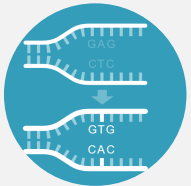
5mC, 5hmC, 6mA, all context



Richness of content delivering complete genomes

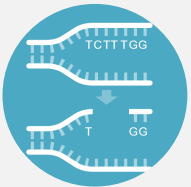
Today, traditional SBS enables:

Single Nucleotide Variants



- e.g. Sickle cell disease

Insertion / deletions



- e.g. Cystic Fibrosis

“We identified 2,855 dark CDS regions across 748 protein-coding genes that were dark

There are 76 dark genes with known mutations associated with 326 human diseases

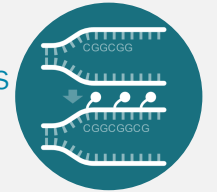
Systematic analysis of dark and camouflaged genes reveals disease-relevant genes hiding in plain sight”

Mark Ebbert et al. (2019)
Genome Biology 20:97

Nanopore *additionally* enables:

Methylation

- e.g. fragile x syndrome
- DNA methylation patterns are globally disrupted in cancer



Structural Variations

- e.g. cancer, Alzheimer's, Parkinson's, Prader-Willi syndrome



Copy Number Variation

- e.g. cancer, autism, schizophrenia, ADHD

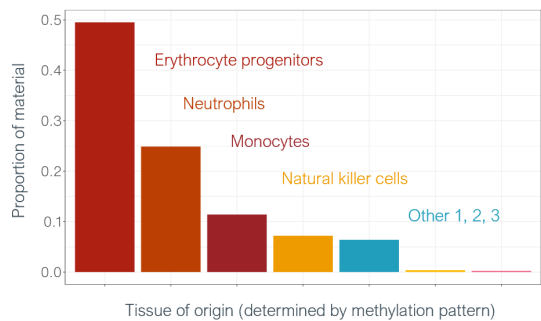
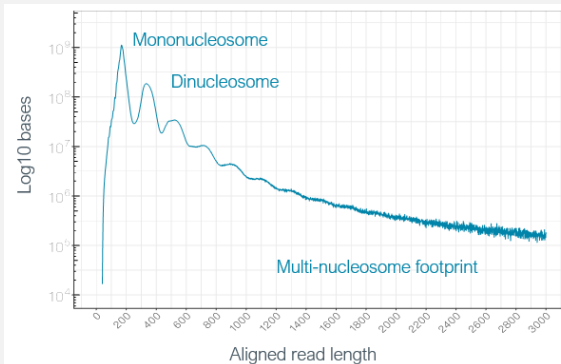


Methylation detection in cell free DNA

A new paradigm with Remora and Short Fragment Mode

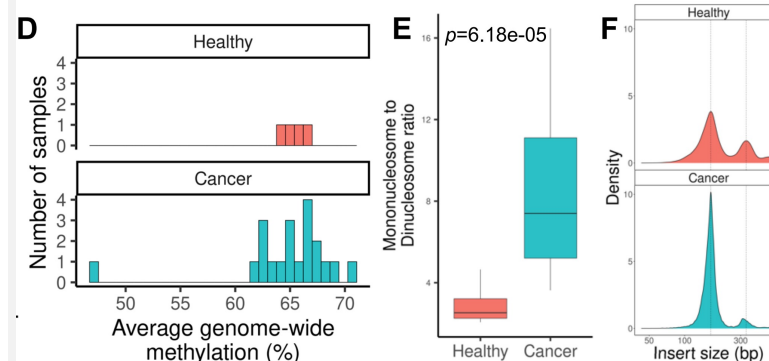
INITIAL CLIVEOME DATA UNCOVERS NUCLEOSOME FOOTPRINT

'Whilst SFM is designed to sequence small fragments, nanopore's ability to sequence any length reveals a samples full cfDNA footprint'



'Additionally, methylation patterns can be used for tissue of origin detection'

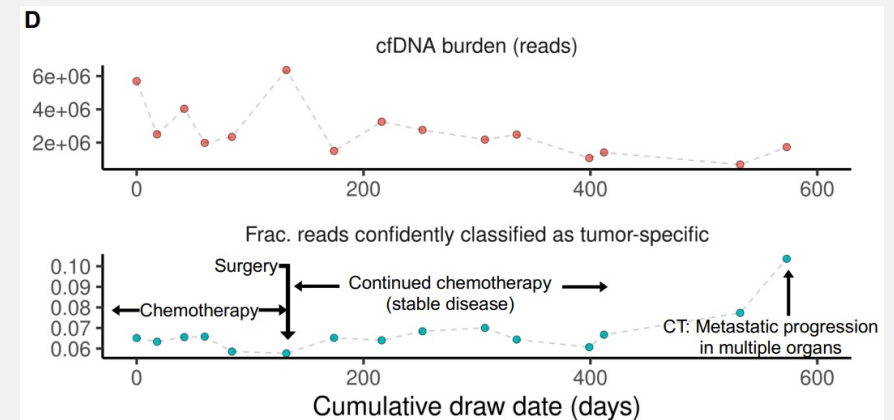
STANFORD: SHOW SIGNIFICANT VARIANCE IN cfDNA METHYLATION PATTERNS BETWEEN CANCER SAMPLES AND HEALTHY CONTROLS¹



Study shows higher variance in genome-wide methylation in cancer samples

Mononucleosome to dinucleosome ratio is different between cancer samples and controls

Longitudinal research study (in days) tracks methylation patterns in patients as they undergo treatment and detect changes in sample health

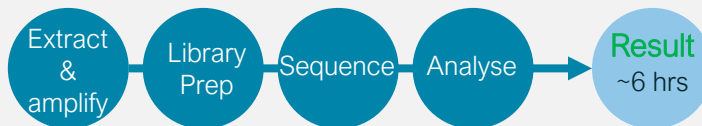


Rapid, distributed pathogen sequencing for public health decision making

...and beyond public health into potential management of infectious disease

RAPID PNEUMONIA METAGENOMICS¹

Pneumonia affects 10-30% of ventilated patients, drives 50% of antimicrobial prescriptions and has 10-15% attributable mortality



Work by GSTT

- 250 samples tested (150 same day)
- 45% of results informed antimicrobial prescribing changes
- 15% contained hard to identify infections

Approach has potential to replace culture in clinical workflows

AMR TUBERCULOSIS

Drug resistant TB accounts for 1 in 3 deaths from antimicrobial resistance



Collaboration with WHO, FIND, UNITAD

- Targeted sequencing assay detecting drug resistance from sputum
- Evaluation of 392 controls complete (specificity, sensitivity >98%, LOD 100 TB cells / ml)
- 3 site evaluation of over 700 samples underway

Working closely with several countries for which TB control is vital to their health systems

OUTBREAK SURVEILLANCE

Monkeypox – from one case in May to over 16,000 in July²

First draft genome sequence of Monkeypox virus associated with the suspected multi-country outbreak, May 2022 (confirmed case in Portugal)

Monkeypox | Genome Reports

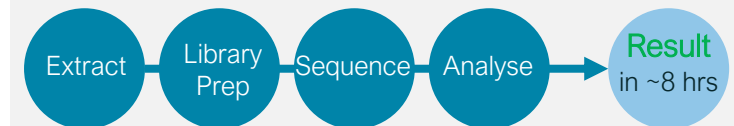
vborges

3 May 20

Joana Isidro¹, Vítor Borges¹, Miguel Pinto¹, Rita Ferreira¹, Daniel Sobral¹, Alexandra Nunes¹, João Dourado Santos¹, Maria José Borrego³, Sofia Núnzio², Ana Pelerito², Rita Cordeiro², João Paulo Gomes^{1*}.

¹ Bioinformatics Unit, Department of Infectious Diseases, National Institute of Health Doutor Ricardo Jorge (INSA), Lisbon, Portugal

SARS-CoV2 surveillance continues as we track new variants



From as little as \$9.55 per sample



Oxford
NANOPORE
Technologies

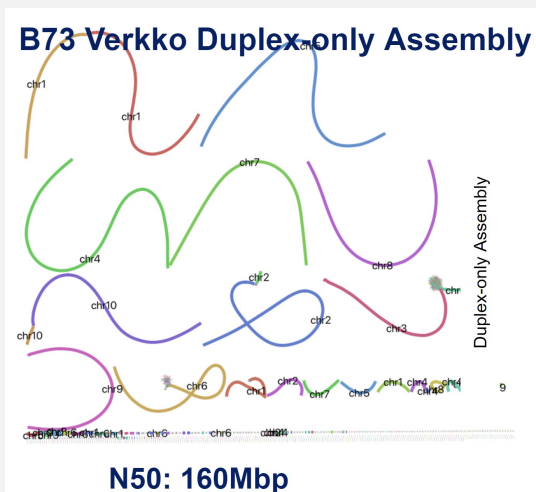
¹ Source: Guys and St Thomas NHS Trust

² <https://www.who.int/director-general/speeches/detail/who-director-general-s-statement-on-the-press-conference-following-IHR-emergency-committee-regarding-the-multi-country-outbreak-of-monkeypox--23-july-2022>

Continuing to break boundaries

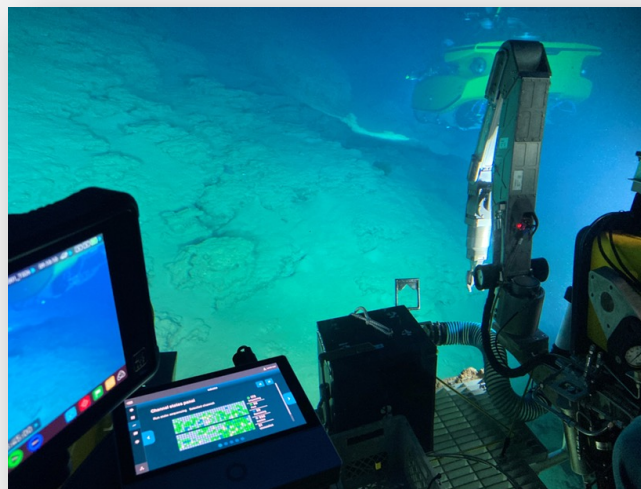
And taking sequencing to the heart of the sample

TELOMERE-TELOMERE PLANTS



- Highly contiguous assembly of maize in collaboration between keygen and JHU to deliver perfectly assembled chromosomes

OCEAN X



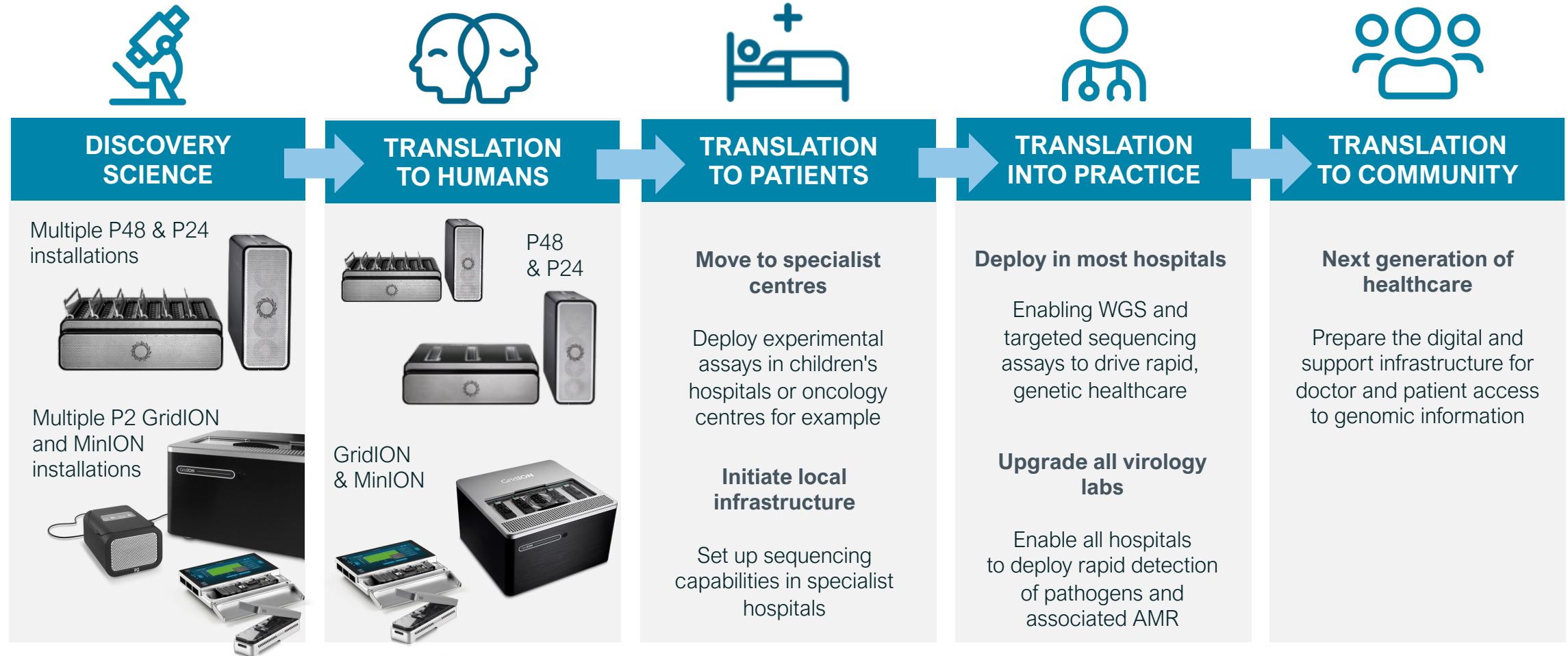
- Sequencing at depth takes on new meaning with sequencing at 272m underwater proving the technology can be utilised in deep sea exploration

RNA IN SPACE



- The ISS continues to track its surfaces as we look to broadening boundaries of space exploration
- Teams have gone from sample to sequence with no culture step

We are at the beginning of our transformational journey



2022 outlook



Commercial



Expand teams Geographically



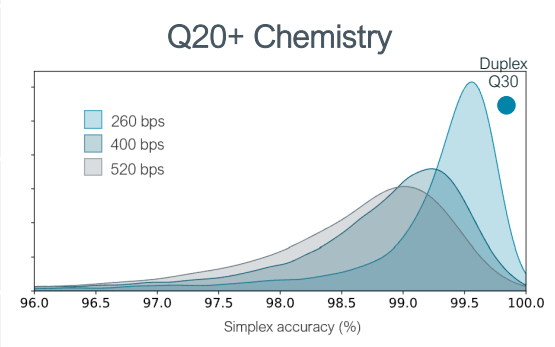
Deepen customer facing teams (sales, TS, CS)



Continue to develop leading digital interface



Innovation



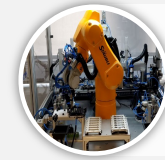
Our Q20+ chemistry enables high accuracy nanopore sequencing



Operations



Increasing logistics footprint



Focus on production automation



Continue to develop our talent

Appendix

Strong growth in active customer accounts

	30 Jun 2022	31 Dec 2021	Change
S1 (<\$25k)			
Number of active customer accounts	6,350	5,501	+15%
Avg. Revenue per customer account (\$000s)	5.5	5.8	(5)%
S2 (\$25k-\$250k)			
Number of customer accounts	912	782	+17%
Avg. Revenue per customer account (\$000s)	66.5	67.7	(2)%
S3 (>\$250k)			
Number of active customer accounts	69	56	+23%
Avg. Revenue per customer account (\$000s) ¹	649.7	629.9	+3%
Indirect			
Number of active customer accounts	7	6	+17%
Avg. Revenue per customer account (\$000s)	2,737.0	2,238.0	+22%

>7,300
active customers²

>990
active customers added³

Summary income statement

	HY22	HY21
	£m	£m
Revenue	122.3	59.0
Cost of Sales	(44.4)	(28.7)
Gross profit	78.0	30.2
<i>Gross margin %</i>	63.7%	51.2%
Operating expenses		
Research and development expenses	(25.2)	(30.6)
Selling, general & administrative expenses	(75.7)	(42.8)
Loss from operations	(23.0)	(43.2)
Other	(4.6)	(1.2)
Loss before tax	(27.6)	(44.4)

Introduction to Oxford Nanopore Technologies

1

Single molecule sensing platform

Building on DNA/RNA to enable the multi-omics world of tomorrow

2

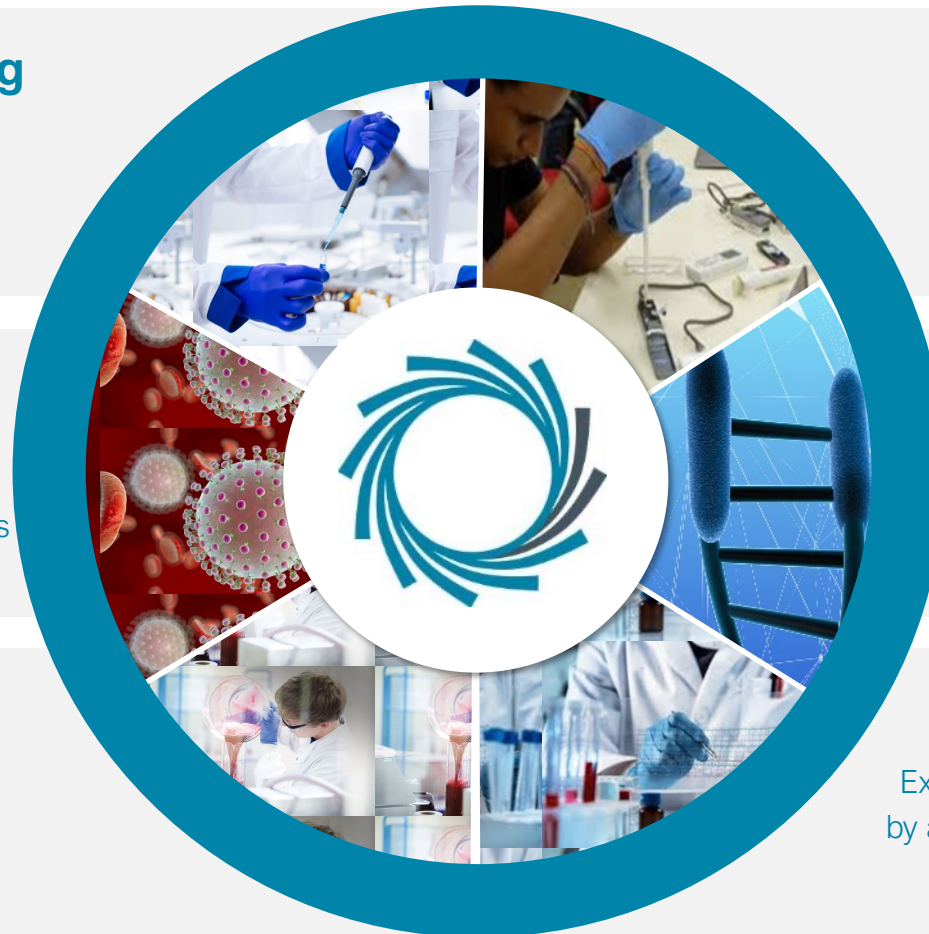
DNA/RNA Sequencing market

\$5.8* billion opportunity for sequencing in 2021 with potential \$10s of billions in future applied markets

3

Growing user community

Customers in >120 countries doing ground-breaking science



Agile innovation

Delivering continuous improvement and intellectual property creation

4

Scaled operations

In-house manufacturing and global distribution

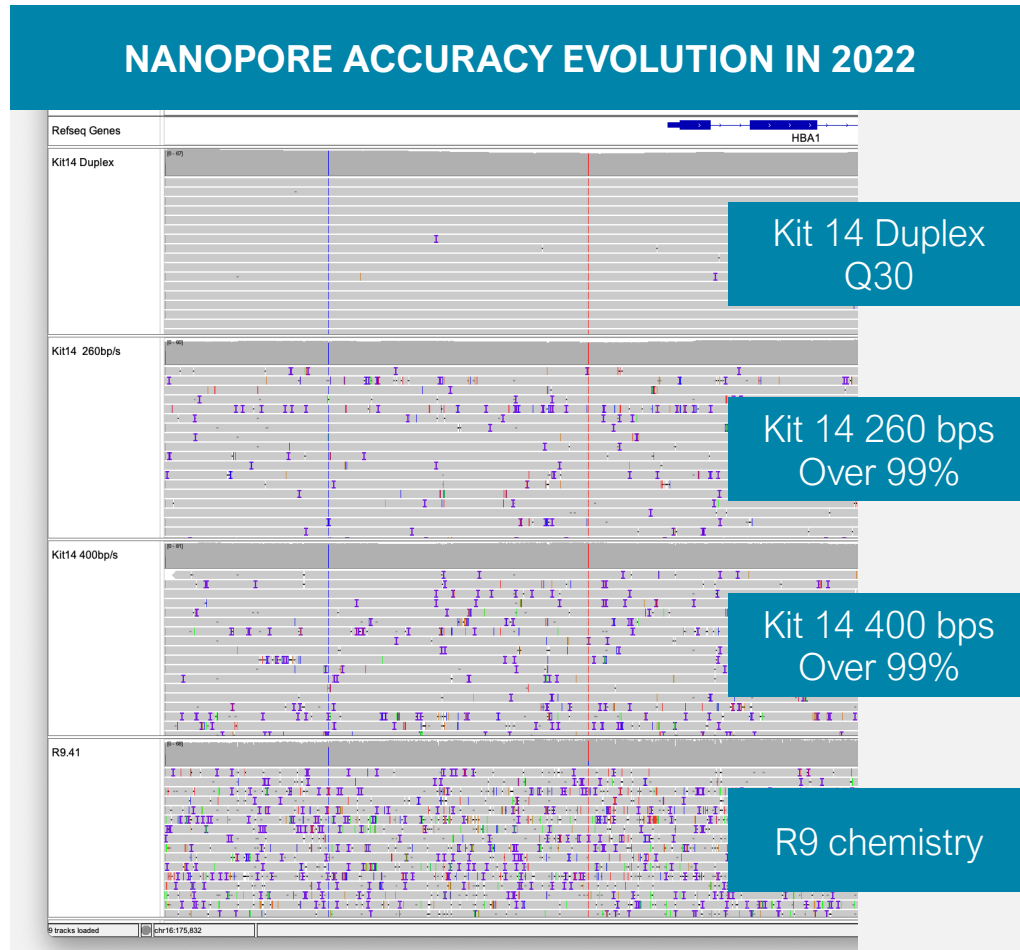
5

Our people

Experienced, driven leadership enabled by a highly ambitious and talented global team expanded to over 900¹

6

Platform upgrade to Q20+ with Kit 14 and R10.4.1 release



Duplex data shown to be extremely accurate

Accuracy improvements in crop genome assembly
Q20+ early access program

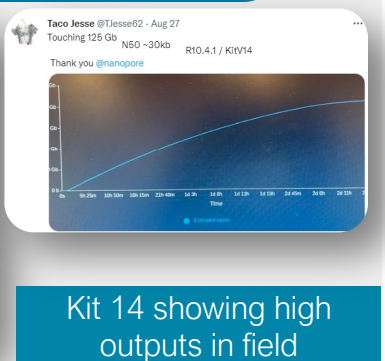
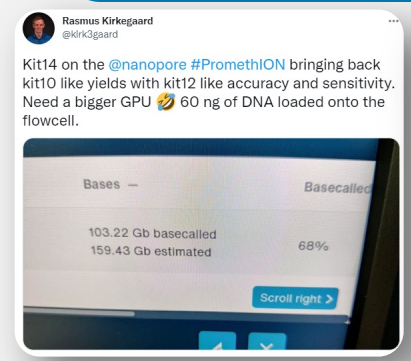
Duplex ONLY melon assembly

- Total duplex set ~17 Gb (~10% of total simplex yield)
- Subset 15.5 Gb, read N50 of 30.3 Kb (~35X coverage)

Data	R10.4 duplex	R10.4 duplex	R10.4 duplex	PacBio HiFi (35X)
Analysis tool	HiFiasm v0.16.1	Flye 2.9 HiFi	Flye 2.9 --nano-hq	HiFiasm v0.16.1
# contigs	166	221	203	348
Assembly size (Mb)	408	373	371	406
N50 contig size (Mb)	19.2	7.6	13.4	12.4
N50 index	9	14	9	9
Max contig size (Mb)	27.9	20.9	26.9	34.9
QV score	47	56	52	49

Conclusion: ONT Q20+ duplex only assembly similar in contiguity but outperforming PacBio HiFi in consensus accuracy

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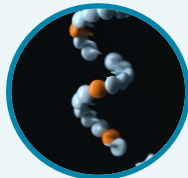
Kit 14 showing high outputs in field

Technology enablers for growth

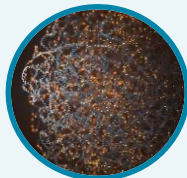
Embedding capabilities into simple user workflows

NANOPORE INFORMATION RICH DATA ...SCALABLE, ACCESSIBLE AND REAL-TIME

**ANY
Fragment
Length**



20 base pairs

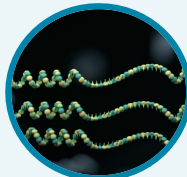


to...4 Mb + "ultra-long"

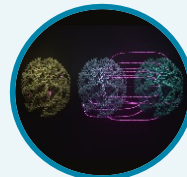
**Full Biology
from single
experiment**



SNP detection



SV detection



Phasing



Assembly

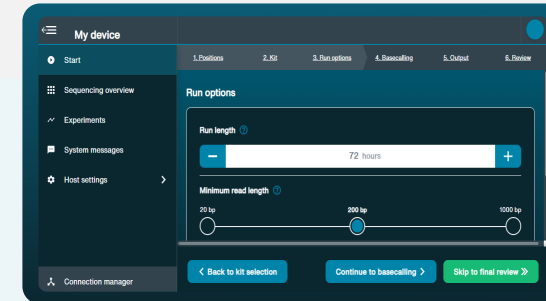
**FULL
Methylation
included**



5mC & 5hmC

*6mA and all
context models
coming soon*

**Short
Fragment
mode**



*Released in
MinKNOW
Software
March 2022*

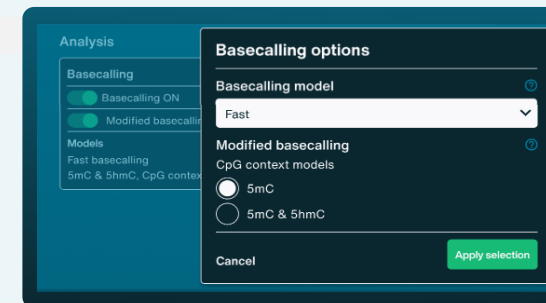
**Bioinformatics
development**



**EPI2ME
Labs**

*Available
through
EPI2ME &
EPI2ME labs*

**Remora
Integrated
Methylation**



*Released in
MinKNOW
Software
May 2022*


We are at the beginning of our transformational journey



Genomics
england


Cancer 2.0

Using nanopore to characterising SVs & methylation signatures for improved diagnosis and care in NHS



Ultra-rapid WGS

Improved critical care outcomes with rapid WGS¹ in less than 8 hours² with 12% high diagnostic yields



Liquid biopsy for MRD monitoring

Characterisation cfDNA methylomes of cancer patients for potential longitudinal monitoring



Intraoperative DNA methylation

Classification of brain tumours with methylation to improve neurosurgical strategy decisions

Next generation of healthcare

Prepare the digital and support infrastructure for doctor and patient access to genomic information

Thank you

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