

## Upgrade your DNA extraction with Fire Monkey

June 2026



Fire Monkey is a spin-column based Nucleic Acid Isolation and Purification (NAIP) kit that performs High Molecular Weight-DNA (HMW-DNA) extraction; extracts do not require overnight resting and are immediately ready to use.

|                                                    |                                                                                                     |
|----------------------------------------------------|-----------------------------------------------------------------------------------------------------|
| <p>From sample to DNA in <b>1h</b></p>             | <p><b>Hybrid</b><br/>Single extract for short and long reads</p>                                    |
| <p><b>Spin column</b><br/>User-friendly format</p> | <p><b>No O/N resting</b><br/>Immediately ready to use</p>                                           |
| <p><b>&gt; 100kb</b><br/>Average extract size</p>  | <p><b>FIRE MONKEY HMW-DNA Extraction kit</b><br/>Mammalian cells throughput up to <b>160 Gb</b></p> |

### Simpler operation

HMW-DNA from an easy, familiar spin column format

### Faster processing

Immediately ready to use in one hour, no overnight resting

### Extensive validation

Superior performance independently verified

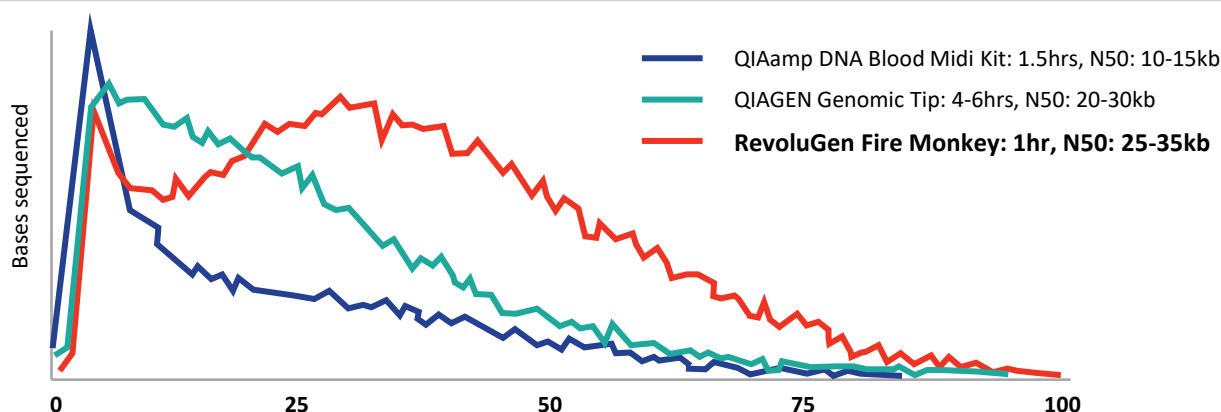
### Hybrid assemblies

A single extract can be used for both short and long read sequencing

# External validation

Both mammalian and bacterial protocols have been validated on ONT, Illumina and 10x Genomics workflows and results have been published in peer-reviewed journals. Validation of the kit was performed by ONT in 2018 and is continuously being carried out by several KOLs including UKHSA and Quadram Institute labs etc.

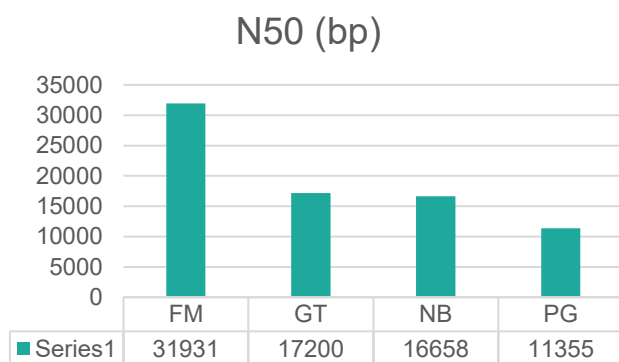
## Fire Monkey – Oxford Nanopore validation in 2018



- Oxford Nanopore Technologies (ONT) validated the FM kit on white blood cells against two Qiagen products
- Fire Monkey produced the highest N50 values in a fraction of extraction time compared to Qiagen's industry standard product
- Data available on ONT website: search 'RevoluGen' and select posts older than 2 years

## Fire Monkey – Interlaboratory evaluation in July 2025

Inter-laboratory evaluation of HMW-DNA extraction kits on ONT sequencing performance taken place at 4 labs in the UK, France, Spain and Germany (Qiagen labs) comparing Fire Monkey (FM), Genomic Tip (GT, Qiagen), Gentra Puregene (PG, Qiagen) and Nanobind (NB, PacBio). FM extracts produced the highest N50 values and were the only ones out of the 4 kits that did not require overnight incubation (Devonshire et al 2025, <https://pmc.ncbi.nlm.nih.gov/articles/PMC12305982/>).



**N50 values in number of base pairs (bp) adapted from Supplementary Table 3 of study**

Pooled cell line extracts from the 4 kits were sequenced on the PromethION in parallel. The FM extracts generated the highest N50 value.

| HMW-DNA extraction kit            | Extraction time | Overnight treatment |
|-----------------------------------|-----------------|---------------------|
| <b>Fire Monkey (FM) RevoluGen</b> | <b>1hr</b>      | <b>NO</b>           |
| Genomic Tip (GT) Qiagen           | 4-6hrs          | YES                 |
| Nanobind (NB) PacBio              | 1hr             | YES                 |
| Gentra Puregene (PG) Qiagen       | 1-2hrs          | YES                 |

**Extraction workflow comparison adapted from the Materials and Methods of the study and kits Instructions For Use.**

The Fire Monkey kit is the only kit that combines short extraction time with no need for overnight incubation.

# External validation

| Institute / Organization                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | Sequencing Platform                                                                                                                                                                            | Publication                                                                                                                                                                                                                                       |
|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|  Quadram Institute<br>Science • Health • Food • Innovation                                                                                                                                                                                                                                                                                                                                                                                                                                                        |  illumina®                                                                                                    | Emergence of Resistance to Fluoroquinolones and Third-Generation Cephalosporins in <i>Salmonella Typhi</i> in Lahore, Pakistan<br>Rasheed F et al, (2020) Microorganisms 8 (9) 1336                                                               |
|  UEA<br>University of East Angles<br> Quadram Institute<br>Science • Health • Food • Innovation                                                                                                                                                                                                                                                                                                                                  |  Oxford NANOPORE technologies                                                                                 | Emergence of ciprofloxacin heteroresistance in foodborne <i>Salmonella enterica</i> serovar Agona<br>Zhang CZ et al, (2020) Journal of Antimicrobial Chemotherapy 75(10) 2773                                                                     |
|  Canadian Food Inspection Agency<br> UK Health Security Agency                                                                                                                                                                                                                                                                                                                                                                   |  Oxford NANOPORE technologies                                                                                 | Complete Genome Assemblies of the Rare <i>Salmonella enterica</i> Serovar Adjame Using Nanopore and Illumina Sequence Reads<br>Gao R et al, (2020) Microbiol Resour Announc 9(35): e00280-20                                                      |
|  SpeedX                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | <b>PCR</b>                                                                                                                                                                                     | Nucleic Acid Ratio Determination (Patent Application)<br>Todd AV & Lima NE (2020) Pub. No.: US 2020/0199651                                                                                                                                       |
|  Dana-Farber Cancer Institute<br> HARVARD UNIVERSITY                                                                                                                                                                                                                                                                                                                                                                            |  10X GENOMICS<br> illumina® | Determination of complete chromosomal haplotypes by bulk DNA sequencing<br>Tourdot RW et al, (2021) Genome Biology. Volume 22, Article 139                                                                                                        |
|  UNIVERSITY OF BATH<br> FROSLN<br> THE UNIVERSITY OF EDINBURGH<br> UK Health Security Agency                                                                                                                                                           |  Oxford NANOPORE technologies                                                                               | Acquisition and loss of CTX-M plasmids in <i>Shigella</i> species associated with MSM transmission in the UK<br>Locke R et al, (2021) Microbial Genomics. Volume 7, Issue 8                                                                       |
|  UK Health Security Agency                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |  Oxford NANOPORE technologies                                                                               | Analysis of a small outbreak of Shiga toxin-producing <i>Escherichia coli</i> O157:H7 using long-read sequencing<br>Greig DR et al, (2021) Microbial Genomics. Volume 7, Issue 3                                                                  |
|  UEA<br>University of East Angles<br> NORWICH MEDICAL SCHOOL<br> Quadram Institute<br>Science • Health • Food • Innovation<br> UK Health Security Agency<br> FROSLN |  Oxford NANOPORE technologies                                                                               | Characterization of a pESI-like plasmid and analysis of multidrug-resistant <i>Salmonella enterica</i> Infantis isolates in England and Wales<br>Lee WWY et al, (2021) Microbial Genomics. Volume 7, Issue 10                                     |
|  LIVERPOOL SCHOOL OF TROPICAL MEDICINE<br>Since 1898                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  Oxford NANOPORE technologies                                                                               | First identification of bla NDM-5 producing <i>Escherichia coli</i> from neonates and a HIV infected adult in Tanzania<br>Manyahi J et al, (2022) Journal of Medical Microbiology. Volume 71, Issue 2                                             |
|  UK Health Security Agency                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |  Oxford NANOPORE technologies                                                                               | Use of Nanopore Sequencing to Characterise the Genomic Architecture of Mobile Genetic Elements Encoding blaCTX-M-15 in <i>Escherichia coli</i> Causing Travellers' Diarrhoea<br>Bird MT et al, (2022) Front. Microbiol. Volume 13, Article 862234 |
|  Quadram Institute<br>Science • Health • Food • Innovation                                                                                                                                                                                                                                                                                                                                                                                                                                                      |  Oxford NANOPORE technologies                                                                               | Impact of <i>Salmonella</i> genome rearrangement on gene expression<br>Waters EV et al, (2022) Evolution Letters Volume 6, Issue 6, pages: 426-437                                                                                                |
|  UK Health Security Agency<br> Quadram Institute<br>Science • Health • Food • Innovation                                                                                                                                                                                                                                                                                                                                     |  Oxford NANOPORE technologies                                                                               | Dynamics of <i>Salmonella enterica</i> and antimicrobial resistance in the Brazilian poultry industry and global impacts on public health<br>Alikhan NF et al, (2022) PLOS Genetics 18(6): e1010174                                               |

# External validation

| Institute / Organization                                                                                                                           | Sequencing Platform                                                                                                                                                                                 | Publication                                                                                                                                                                                                                                                                       |
|----------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <br>UK Health Security Agency                                     | <br>NANOPORE technologies                                                                                          | Outbreak of sexually transmitted, extensively drug-resistant <i>Shigella sonnei</i> in the UK, 2021-22: a descriptive epidemiological study<br>Charles H et al, (2022) The Lancet Infectious Diseases 22: 1503-1510                                                               |
| <br>UK Health Security Agency                                     | <br>NANOPORE technologies                                                                                          | Characterization of a P1-bacteriophage-like plasmid (phage-plasmid) harbouring bla CTX-M-15 in <i>Salmonella enterica</i> serovar Typhi<br>Greig DR et al, (2022) Microbial Genomics Volume 8, Issue 12                                                                           |
| <br>LIVERPOOL SCHOOL OF TROPICAL MEDICINE<br>Since 1898           | <br>NANOPORE technologies<br>     | Intracellular Transposition of Mobile Genetic Elements Associated with the Colistin Resistance Gene mcr-1<br>Goodman RN et al, (2022) Microbiology Spectrum e03278-22                                                                                                             |
| <br>USGS<br>science for a changing world                          | <br>10x GENOMICS<br>              | Multi-omics responses in tree swallow ( <i>Tachycineta bicolor</i> ) nestlings from the Maumee Area of Concern, Maumee River, Ohio<br>Tseng CY et al, (2023) Science of The Total Environment Volume 856, Part 2, 159130                                                          |
| <br>Quadram Institute<br>Science • Health • Food • Innovation    | <br>NANOPORE technologies                                                                                         | Uropathogenic <i>Escherichia coli</i> population structure and antimicrobial susceptibility in Norfolk, UK<br>Carter C et al, (2023) Journal of Antimicrobial Chemotherapy Volume 78, Pages 2028-2036                                                                             |
| <br>CNRGH<br>CENTRE NATIONAL DE RECHERCHES EN GÉNOMIQUE HUMAINE | <br>NANOPORE technologies                                                                                        | High diagnostic potential of short and long genome sequencing with transcriptome analysis in exome-negative development disorders<br>Lecoquierre F et al, (2023) Human Genetics Volume 142, Pages 773-783                                                                         |
| <br>UK Health Security Agency                                   | <br>NANOPORE technologies                                                                                        | Surveillance of antimicrobial resistant Shiga toxin-producing <i>E. coli</i> O157:H7 in England, 2016–2020<br>Greig DR et al, (2023) Journal of Antimicrobial Chemotherapy Volume 78, Issue 9, Pages 2263-2273                                                                    |
| <br>LIVERPOOL SCHOOL OF TROPICAL MEDICINE<br>Since 1898         | <br>NANOPORE technologies                                                                                        | Development of pBACpAK entrapment vector derivatives to detect intracellular transfer of mobile genetic elements within chloramphenicol resistant bacterial isolates<br>Goodman RN et al, (2023) Journal of Microbiological Methods Volume 213, Issue 9, 106813                   |
| <br>Quadram Institute<br>Science • Health • Food • Innovation   | <br>NANOPORE technologies<br> | FakA impacts antiseptic susceptibility in <i>Staphylococcus aureus</i> and <i>Enterococcus faecalis</i><br>Gaya MS et al, (2024) bioRxiv<br><a href="https://www.biorxiv.org/content/10.1101/2024.02.13.580087v1">https://www.biorxiv.org/content/10.1101/2024.02.13.580087v1</a> |
| <br>UK Health Security Agency                                   | <br>NANOPORE technologies                                                                                        | Re-analysis of an outbreak of Shiga toxin-producing <i>Escherichia coli</i> O157:H7 associated with raw drinking milk using Nanopore sequencing<br>Greig DR et al, (2024) Nature Scientific Reports Volume 14, Article number 5821                                                |
| <br>Quadram Institute<br>Science • Health • Food • Innovation   | <br>NANOPORE technologies                                                                                        | From acute to persistent infection: revealing phylogenomic variations in <i>Salmonella</i> Agona<br>Waters EV et al, (2024) PLOS Pathogens 20(10): e1012679                                                                                                                       |

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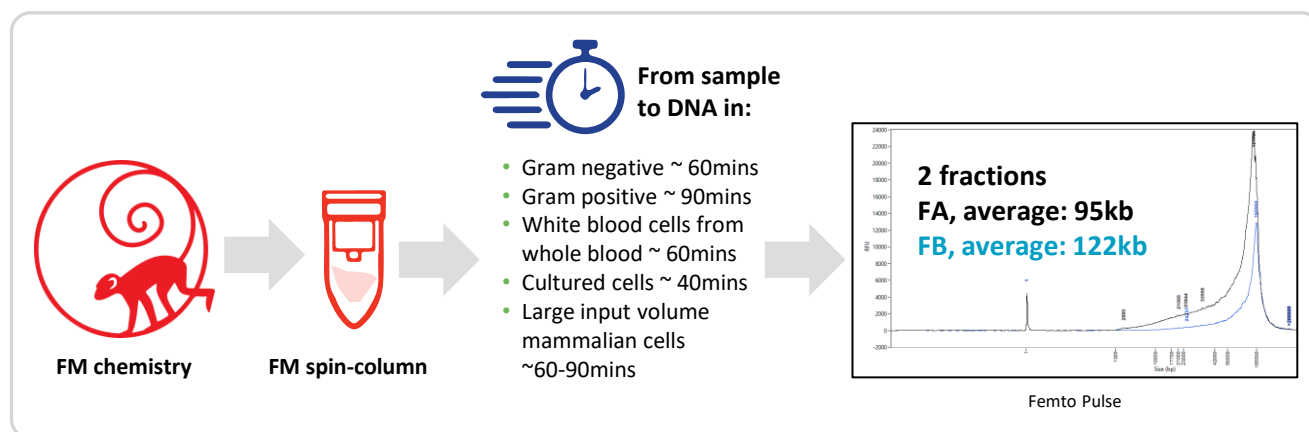
| Institute / Organization                                                                                                                         | Sequencing Platform                                                                              | Publication                                                                                                                                                                                                                                                   |
|--------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <br>LIVERPOOL SCHOOL OF TROPICAL MEDICINE<br>Since 1898         |                 | Molecular mechanisms of re-emerging chloramphenicol susceptibility in extended-spectrum beta-lactamase-producing <i>Enterobacteriales</i><br>Graf FE et al, (2024) Nature Communications Volume 15, Article number 9019                                       |
| <br>S-L o L<br>Siraj - Long-read Lab                            |                 | Comparative evaluation of commercial DNA isolation approaches for nanopore-only bacterial genome assembly and plasmid recovery<br>Kruasuwan W et al, (2024) Nature Scientific Reports Volume 14, Article number 27672                                         |
| <br>Quadram Institute<br>Science • Health • Food • Innovation   |                 | Phage-plasmid borne methionine tRNA ligase mediates epidemiologically relevant antimicrobial survival<br>Tam YL et al, (2025) medRxiv <a href="https://doi.org/10.1101/2024.10.27.24316207">https://doi.org/10.1101/2024.10.27.24316207</a>                   |
| <br>CNRGH<br>CENTRE NATIONAL DE RECHERCHE EN GÉNÉTIQUE HUMAINE  |                 | Parental germline mosaicism in genome-wide phased <i>de novo</i> variants: Recurrence risk assessment and implications for precision genetic counselling<br>Lecoquierre F et al, (2025) PLOS Genetics 21(3): e1011651                                         |
| <br>UK Health Security Agency                                  |                | Hybrid strains of enterotoxigenic/Shiga toxin-producing <i>Escherichia coli</i> , United Kingdom, 2014–2023<br>Rodwell EV et al, (2025) Journal of Medical Microbiology 74:001946                                                                             |
| <br>Quadram Institute<br>Science • Health • Food • Innovation | <br>illumina® | Genomic diversity of non-typhoidal <i>Salmonella</i> found in patients suffering from gastroenteritis in Norfolk, UK<br>Rudder SJ et al, (2025) Microbial Genomics 11:001468                                                                                  |
| <br>LIVERPOOL SCHOOL OF TROPICAL MEDICINE<br>Since 1898       |               | Comparative genomics of blood and faecal <i>E. coli</i> and <i>K. pneumoniae</i> isolates from neonates with bloodstream infections in Tanzania<br>Goodman RN et al, (2025) Nature Communications Biology Volume 8, Article number 1603                       |
| <br>Quadram Institute<br>Science • Health • Food • Innovation |               | Population structure and gene flux of <i>Listeria monocytogenes</i> ST121 reveal prophages as a candidate driver of adaptation and persistence in food production environments<br>Gutierrez AV et al, (2025) Microbial Genomics Volume 11, Issue 4, 11:001397 |
| <br>Quadram Institute<br>Science • Health • Food • Innovation |               | Characterization of a <i>Listeria monocytogenes</i> plasmid with antibiotic and stress resistance genes<br>Barker CR et al, (2025) Microbial Genomics Volume 11, Issue 7, 11:001445                                                                           |
| <br>UK Health Security Agency                                 |               | Large-scale genomic characterization of phage-plasmids in clinical <i>Enterobacteriaceae</i> isolates<br>Nair S et al, (2025) bioRxiv <a href="https://doi.org/10.1101/2025.09.12.675607">https://doi.org/10.1101/2025.09.12.675607</a>                       |
| <br>& others<br>QIAGEN                                        |               | Interlaboratory evaluation of high molecular weight DNA extraction methods for long-read sequencing and structural variant analysis<br>Devonshire AS et al, (2025) BMC Genomics 26:698                                                                        |
| <br>Chula<br>Chulalongkorn University                         |               | Biocontrol mechanisms and antimicrobial gene expression of <i>Bacillus</i> 63-10 and impact on microbial ecosystems of fruit; quality and shelf life<br>Manowan P et al, (2025) Food Control Volume 172, 111160                                               |

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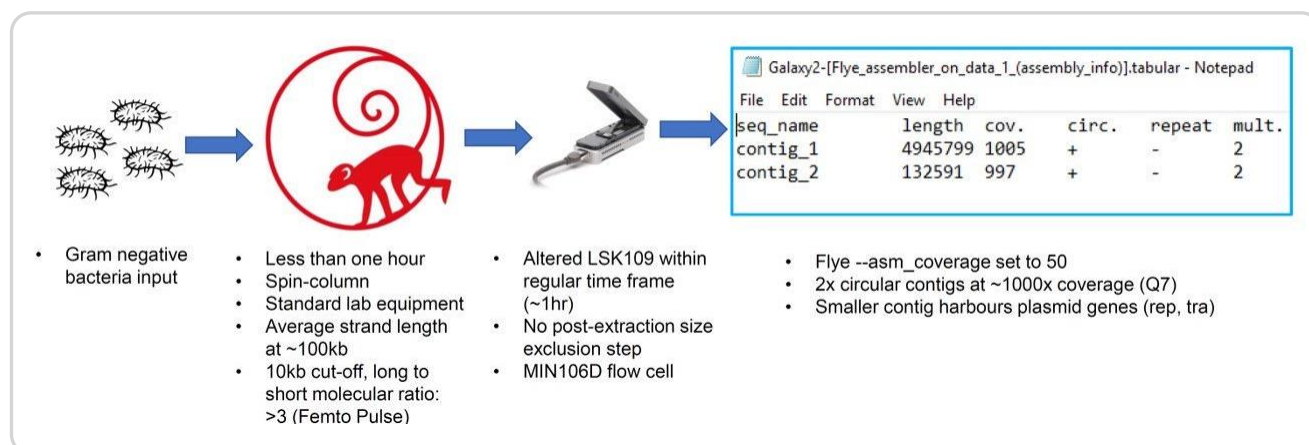
| Institute / Organization                                                                                                                       | Sequencing Platform                                                                                                  | Publication                                                                                                                                                                                                                                                                                                     |
|------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <br>Quadram Institute<br>Science • Health • Food • Innovation | <br>Oxford NANOPORE<br>technologies | <p>Rapid Preparation of Electrocompetent <i>Listeria monocytogenes</i> and enhancement of transformation efficiency with cAMP supplementation</p> <p>Gutierrez AV et al, (2026) Journal of Food Protection 100753</p>                                                                                           |
| <br>Quadram Institute<br>Science • Health • Food • Innovation | <br>illumina®                       | <p>Salmonella Genomic Markers for Risk to Food Safety</p> <p>Waters EV et al, (2026) bioRxiv <a href="https://doi.org/10.64898/2026.03.27.714810">https://doi.org/10.64898/2026.03.27.714810</a></p>                                                                                                            |
| <br>LIVERPOOL SCHOOL<br>OF TROPICAL MEDICINE<br>Since 1898    | <br>Oxford NANOPORE<br>technologies | <p>Antimicrobial activity of polymyxin A, and characterisation of the cognate biosynthetic gene cluster within the genome of the producing <i>Paenibacillus polymyxa</i></p> <p>McLeman A et al, (2026) bioRxiv <a href="https://doi.org/10.64898/2026.05.29.728749">doi.org/10.64898/2026.05.29.728749</a></p> |

# Sample types

Sample types covered are Gram negative and Gram positive cells, white blood cells from whole blood, and cultured mammalian cells (Figure 1). Fire Monkey HMW-DNA is library ready and can enable a complete assembly with ~1000x coverage of the chromosome and recovery of a ~130kb plasmid one 1 MinION flow cell (Bacteria, Figure 2), as well as generate 160Gb of total data with 40x coverage at an N50 of 51kb on a PromethION flow cell (Mammalian, Figure 3).



**Figure 1.** Sample types covered by the Fire Monkey HMW-DNA spin-column protocols. Fire Monkey extracts HMW-DNA with average strand lengths of appx. 100kb and above for Fraction A (FA) and Fraction B (FB) from bacterial and mammalian cell samples. The extract does not require size selection prior to ONT library preps.



**Figure 2.** An *E. coli* Fire Monkey extract (Fraction B) run on LSK109/MinION enabled a complete assembly with ~1000x coverage of the chromosome (Flye, Q7) and recovery of a ~130kb plasmid. No size selection was performed post-extraction.

## Run statistics

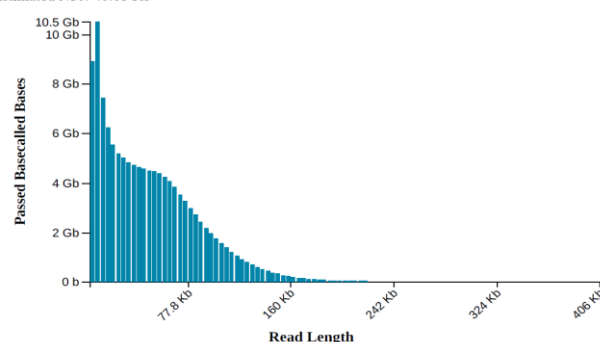
| 96hrs run               | Throughput (Gb) | Reads #          | Read N50 (kb) |
|-------------------------|-----------------|------------------|---------------|
| All data                | 160.3           | 12,952,997       | 38,6          |
| Pass data Q>7           | 136.5           | 10,262,206       | 40,3          |
| 100kb+ data Q>7         | 13.3            | 108,878          | 118,8         |
| <b>Top 40x coverage</b> | <b>109.42</b>   | <b>2,907,649</b> | <b>51,5</b>   |

## Filtered Canu assembly

| Horse genome length (Gb) | Number of contigs | Contig N50 (kb) | Longest contig (kb) |
|--------------------------|-------------------|-----------------|---------------------|
| 2.562                    | 759               | 25,481          | 86,755              |

## Read Length Histogram Estimated Bases - Outliers Discarded

Estimated N50: 40.65 Kb



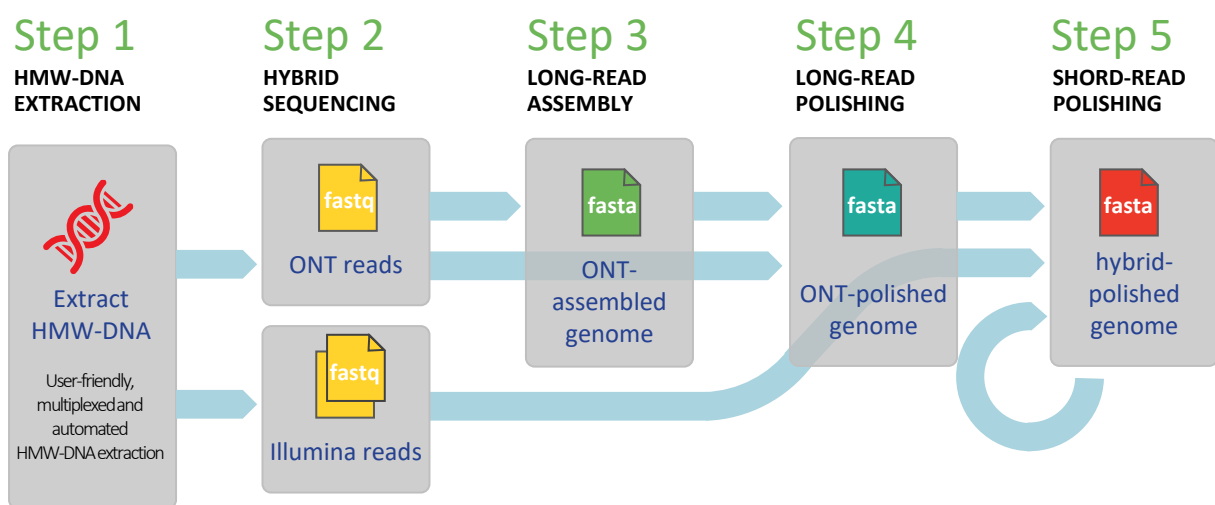
**Figure 3.** A white blood cell Fire Monkey extract ran on LSK110/PromethION enabled 40x coverage at N50: 51kb. No size selection was performed post-extraction.

- Sample type : horse white blood cells from 1ml blood
- 1 hour spin column Fire Monkey
- No size selection post extraction (pooled Fractions + B)
- LSK110 / Single PromethION flow cell
- 96hrs run, 3 flushes
- 160.3Gb of total data, 15Gb within last 24hrs
- 13.3Gb 100kb+ Q>7
- Top 40x coverage with read N50: 51.5kb
- Horse genome is ~2.5 billion bases long
- Genome assembled in 759 contigs with a contig N50 of ~25.5 million bases long (longest contig ~86.8 millions bases)

# Hybrid assemblies

Because Fire Monkey is as user-friendly as any spin column kit it gives Illumina sequencing laboratories the option, at little extra cost, to keep the same sample extract for both their initial short read sequencing and for any subsequent long read sequencing they may decide to perform at some point in the future. It also provides a minimally disruptive entry point into long read sequencing as it uses a spin column protocol that everyone is already familiar with. If Fire Monkey is adopted as the standard extraction protocol for their short read sequencing needs, any long read sequencing can therefore be performed on exactly the same original sample that the Fire Monkey kit extracted without any further cost, reprocessing problems or potential handling errors.

## Single DNA extract for both Oxford Nanopore (ONT) and Illumina reads



### Adapted from:

Wick *et al* (2022) Assembling the perfect bacterial genome using Oxford Nanopore and Illumina sequencing.  
<https://preprints.scielo.org/index.php/scielo/preprint/view/5053/9840>

## HOW TO ORDER



## Fire Monkey 10 Column Kit

To place an order and for more  
information please [Click here](#)