



Upgrade your DNA extraction with Fire Monkey

January 2026

The Fire Monkey chemistry can be utilized in a magnetic beads format that has been automated on several robotic instruments for high quality and multiplexed High Molecular Weight-DNA (HMW-DNA) extractions; extracts do not require overnight resting and are immediately ready to use.



From multiple samples sample to DNA in **2h**



Magnetic beads
Automatable format



➤ **100kb**
Average extract size



FIRE MONKEY
HMW-DNA
Automation

Hybrid

Single extract for short and long reads



No O/N resting

Immediately ready to use



Multiplexing potential **96x**



Multiplexed extractions

Up to 96x HMW-DNA extracts per run, fully automated

Faster processing

Immediately ready to use in 2 hours, no overnight resting

Extensive validation

Superior performance on several robotic instruments

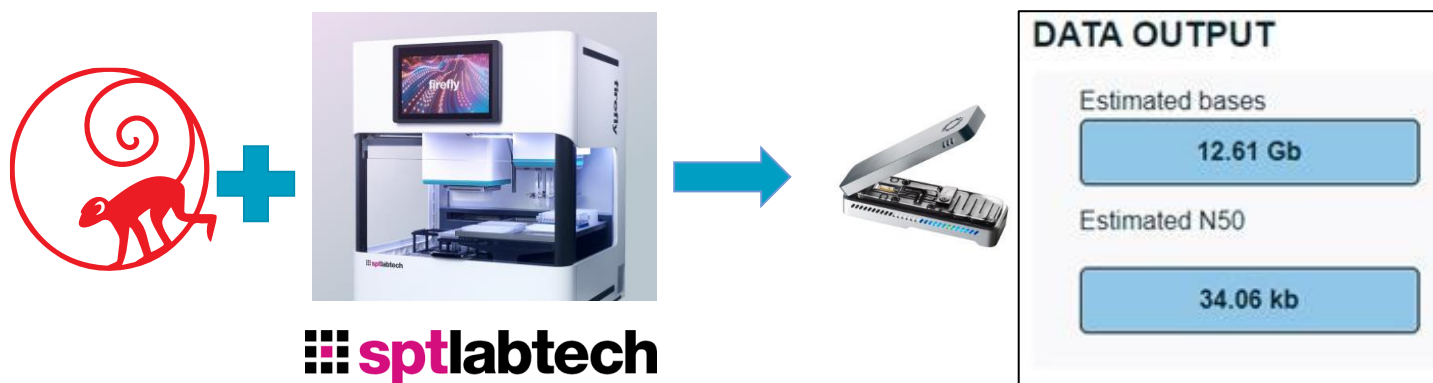
Hybrid assemblies

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

Proof of concept

Automated Fire Monkey HMW-DNA extractions from mammalian and bacterial cells have been successfully performed on several instruments such as Firefly (SPT Labtech), oKtopure (LGC Biosearch) and Kingfisher (ThermoFisher Scientific). Depending on robot specifications extractions were either fully or part-automated and in all cases generated high quality Oxford Nanopore Technologies (ONT) long read sequencing data.

Fire Monkey / Firefly SPT Labtech – Fully automated & miniaturised HMW-DNA extractions



- A miniaturized volume version of the Fire Monkey magnetic beads protocol was transferred to the Firefly machine
- *E coli* samples HMW-DNA extractions were fully automated from bacterial cell pellet to DNA extract
- An extract was ran on the ONT LSK114/R10/MinION platform without post-extraction size-depletion
- At 46 hrs of sequencing the N50 value was 34kb
- Flow cell was washed and re-loaded half-way generating more than 12Gb of data
- Fully automated miniaturized HMW-DNA extractions will reduce overall material cost and tackle one of the major challenges for the adaptation of routine long-read sequencing according to the NHS National Genomics Education Programme (GeNotes 10/02/2025):

“Input DNA should ideally be in long fragments (high molecular weight DNA), which can be a challenge for standard automated laboratory DNA isolation methods.”

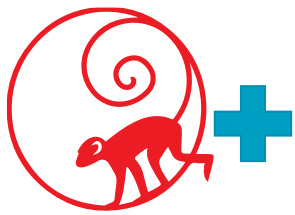
<https://www.genomicseducation.hee.nhs.uk/genotes/knowledge-hub/long-read-sequencing/>

- Find our Fire Monkey SPT Labtech Application note here:

<https://www.sptlabtech.com/news/spt-labtech-and-revolugen-demonstrate-fully-automated-bead-based-high-molecular-weight-dna-extraction>

Proof of concept

Fire Monkey / oKtopure LGC Biosearch– Semi automated HMW-DNA extractions



DATA OUTPUT

Estimated bases

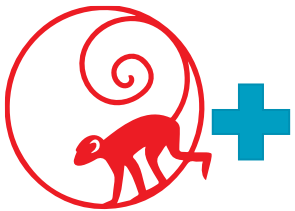
21.03 Gb

Estimated N50

44.89 kb

- White blood cells from 1ml of horse blood were lysed off deck and the plate was transferred to the oKtopure machine
- An extract was ran on the ONT LSK114/R10/MinION platform without post-extraction size-depletion
- At 72 hrs of sequencing the N50 value was 45kb
- Flow cell was washed and re-loaded after 24 and 48 hrs of sequencing way generating 21Gb of data
- This amount of data could be extrapolated 5x onto a PromethION flow cell that could allow the coverage of a mammalian genome 30x with long reads

Fire Monkey / Kingfisher ThermoFisher Scientific– Semi automated HMW-DNA extractions



DATA OUTPUT

Estimated bases

13.92 Gb

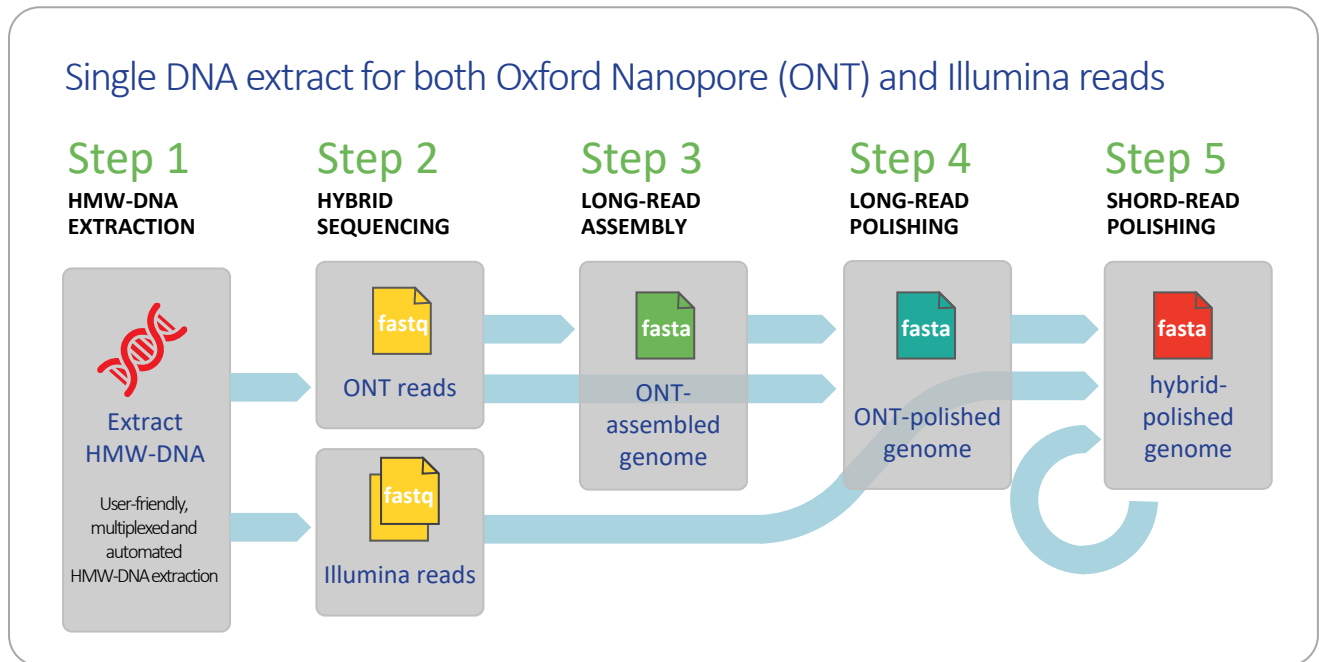
Estimated N50

26.56 kb

- *E coli* pellets were treated with 100µl of DNA/RNA Shield (Zymo Research) for 10mins at RT
- Samples were mixed with solutions and beads and added to plate/instrument
- Proteinase K lysis, washes, and elution performed on deck with no manual intervention
- Pooled replicates were prepped was ran on the ONT LSK114/R10/MinION platform without post-extraction size-depletion
- Single run produced 14Gb with a read N50 of 27kb

Hybrid assemblies

Because the Fire Monkey magnetic beads version has been automated on several robotic instruments 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.



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>