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# Oxford Nanopore sequencing and library construction

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In 1 collection

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Hongling Zhou

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## ABSTRACT

This is a protocol for Oxford Nanopore sequencing and library construction, which was used in the humpback puffer genome sequence.

## DOI

[dx.doi.org/10.17504/protocols.io.btignkbw](https://dx.doi.org/10.17504/protocols.io.btignkbw)

## PROTOCOL CITATION

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<https://dx.doi.org/10.17504/protocols.io.btignkbw>

## COLLECTIONS ⓘ

**Protocols for &#34;Chromosome-level genome assembly of the humpback puffer, *Tetraodon palembangensis*&#34;**

## FORK NOTE

## FORK FROM

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## CREATED

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## LAST MODIFIED

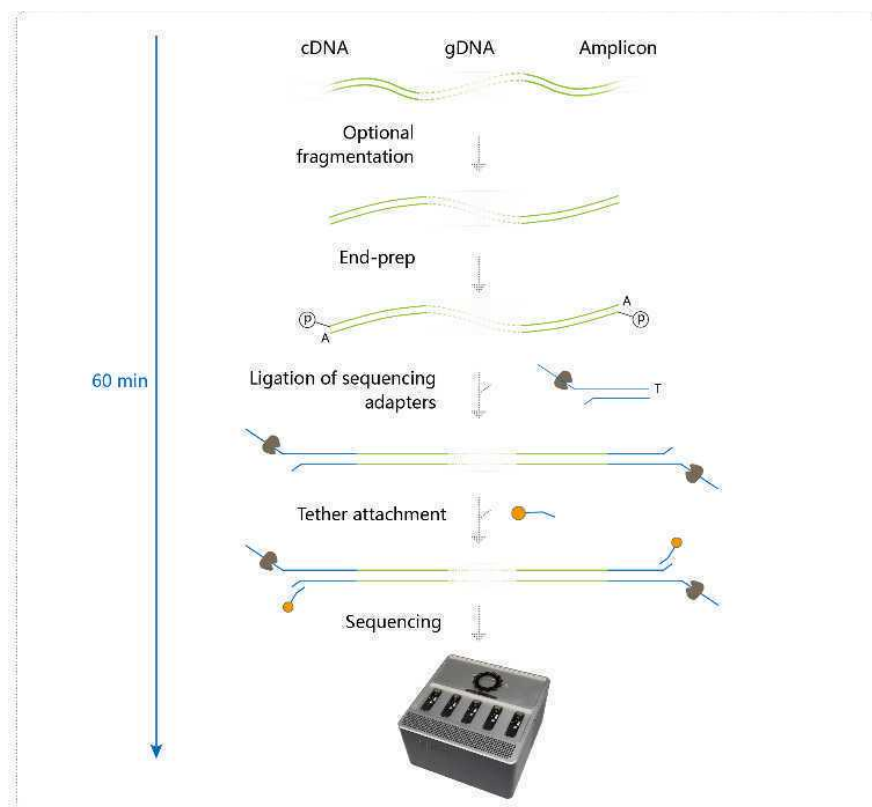
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## PROTOCOL INTEGER ID

48424

## 1 ONT Library preparation and Quality Control

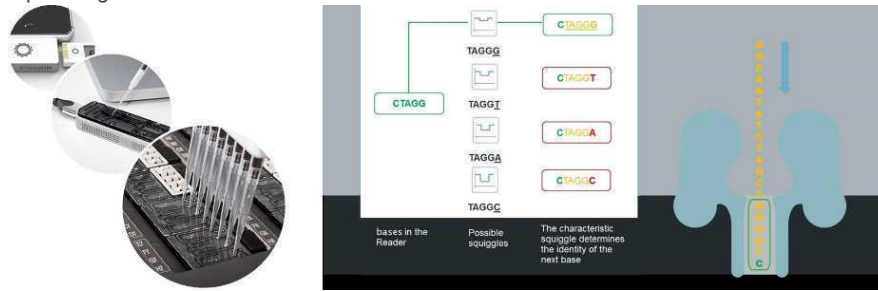
- 1.1 After obtaining the qualified DNA, the large size fraction was selected by automated gel electrophoresis (BluePippin).
- 1.2 Next, the DNA was treated with the end-repair/dA tailing module.
- 1.3 After purification, adapter ligation was performed using ligation sequencing kit (LSK109, Oxford Nanopore Technologies).
- 1.4 Finally, DNA library was quantified by Qubit.



Library construction process

## 2 DNA Sequencing

- 2.1 A certain concentration and volume of DNA library was loaded onto a flow cell- PromethION cell R9.4.1, which was then transferred to Nanopore PromethION sequencer for real-time single molecule sequencing.



Nanopore single molecule real-time sequencing