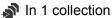


FEB 07, 2024

## Cong-read sequencing and data processing



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DOI:

dx.doi.org/10.17504/protocols.io. bp2l6x5pklqe/v1

**Protocol Citation:** Peter Kilfeather 2024. Long-read sequencing and data processing. **protocols.io** https://dx.doi.org/10.17504/protoc ols.io.bp2l6x5pklqe/v1

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**Protocol status:** Working We use this protocol and it's working

Created: Feb 07, 2024

## **ABSTRACT**

Long-read sequencing and data processing methods from Kilfeather, Khoo et al., 2024

Oct 7 2024



Last Modified: Feb 07, 2024

PROTOCOL integer ID: 94800

## **Funders Acknowledgement:**

Aligning Science Across Parkinson's Grant ID: ASAP-020370 Monument Trust Discovery Award from Parkinson's UK Grant ID: J-1403

## **Protocol**

Twelve TRAP samples and three TOTAL samples were sequenced using the Oxford Nanopore Technologies MinION platform. TRAP samples were equally divided by age and genotype (N = 3 per age:genotype). Library preparation was performed using the cDNA-PCR kit (SQK-PCS109). Raw fast5 data was basecalled and demultiplexed using Guppy (v4.5.2). Read data from FASTQ files were aligned to the mm10 genome (Gencode M25 GRCm38.p6) using minimap2 (v2.18, RRID:SCR\_018550)<sup>57</sup>. Transcript level quantification was then performed using Salmon (v1.4.0, RRID:SCR\_017036)<sup>58</sup>.