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

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🌐 Long-read sequencing and data processing

🔗 In 1 collection

Peter Kilfeather[1]

[1]University of Oxford

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Peter Kilfeather

ABSTRACT

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

Protocol

1 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)[57]. Transcript level quantification was then performed using Salmon (v1.4.0, RRID:SCR_017036)[58].