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PacBio long read sequencing 🔗

📖 **PLOS Genetics**

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EXTERNAL LINK

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THIS PROTOCOL ACCOMPANIES THE FOLLOWING PUBLICATION

☐ EN-DNeasy-Blood--Tissue-Handbook.pdf

PROTOCOL STATUS

Working

1   The mtDNA was extracted using a DNeasy kit (Qiagen).

2   Sequencing was performed using PacBio RSII Chemistry P6-C4, 10kb template preparation and sequencing with 3.24 ug input DNA at the Ramaciotti Center at University of New South Wales (UNSW).

3   PacBio long-read sequencing of the Alstonville and Japan mtDNA produced 882.56 Mb of raw data.

4   Read lengths averaged 5,573 bases with longest read length of 24,822 bases and mean coverage of 40X for each mtDNA.

5   Sequences were assembled using FALCON 1.8.2 (Pacific Biosciences of California, Inc.) and aligned and annotated to the *D. melanogaster* A + T rich region using Geneious 9.1.8 (Biomatters Ltd.).