



PacBio long read sequencing [↗](#)

PLOS Genetics

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EXTERNAL LINK

<https://doi.org/10.1371/journal.pgen.1007735>

THIS PROTOCOL ACCOMPANIES THE FOLLOWING PUBLICATION

Aw WC, Towarnicki SG, Melvin RG, Youngson NA, Garvin MR, Hu Y, Nielsen S, Thomas T, Pickford R, Bustamante S, Vila-Sanjurjo A, Smyth GK, Ballard JWO (2018) Genotype to phenotype: Diet-by-mitochondrial DNA haplotype interactions drive metabolic flexibility and organismal fitness. PLoS Genet 14(11): e1007735. doi: [10.1371/journal.pgen.1007735](https://doi.org/10.1371/journal.pgen.1007735)

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.).

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