

CORRECTION

Open Access



Author Correction: Hidden genomic features of an invasive malaria vector, *Anopheles stephensi*, revealed by a chromosome-level genome assembly

Mahul Chakraborty^{1†}, Arunachalam Ramaiah^{1,2,3†}, Adriana Adolfi⁴, Paige Halas⁴, Bhagyashree Kaduskar^{2,3}, Luna Thanh Ngo¹, Suvratha Jayaprasad⁵, Kiran Paul⁵, Saurabh Whadgar⁵, Subhashini Srinivasan^{3,5}, Suresh Subramani^{3,6,7}, Ethan Bier^{2,7}, Anthony A. James^{4,7,8} and J. J. Emerson^{1,9*}

Correction to: *BMC Biol* 19, 1-16 (2021)
<https://doi.org/10.1186/s12915-021-00963-z>

The original article [1] contained an error in Fig. 3 and omitted a Funding source which the authors would like to correct.

Due to a labeling error in one of our Iso-Seq samples, the RNA sample that was collected 24h after blood feeding was labeled as 324 by the sequencing center because they unknowingly removed a separator between the replicate number and the sample name. The error resulted in a different ordering of categories than we would have chosen, though this doesn't actually affect the interpretations we made in the manuscript. The corrected Fig. 3 can be viewed ahead in this correction article.

Although the error does not affect any conclusion, it remains technically inaccurate and merits correction.

We also did not acknowledge funding from the United States National Science Foundation (NSF) to J.J.E. for

development of the sex chromosome inference approach. This is an important oversight, as NSF requires acknowledgment. The grant number is: NSF grant IOS-1656260.

Author details

¹Department of Ecology and Evolutionary Biology, University of California, Irvine, CA 92697, USA. ²Section of Cell and Developmental Biology, University of California, La Jolla, San Diego, CA 92093-0335, USA. ³Tata Institute for Genetics and Society, Center at inStem, Bangalore, Karnataka 560065, India. ⁴Department of Microbiology & Molecular Genetics, University of California, Irvine, CA 92697, USA. ⁵Institute of Bioinformatics and Applied Biotechnology, Bangalore, KA 560100, India. ⁶Section of Molecular Biology, University of California, La Jolla, San Diego, CA 92093-0322, USA. ⁷Tata Institute for Genetics and Society, University of California, La Jolla, San Diego, CA 92093-0335, USA. ⁸Department of Molecular Biology & Biochemistry, University of California, Irvine, CA 92697, USA. ⁹Center for Complex Biological Systems, University of California, Irvine, CA 92697, USA.

Published online: 02 May 2022

Reference

1. Chakraborty M, et al. Hidden genomic features of an invasive malaria vector, *Anopheles stephensi*, revealed by a chromosome-level genome assembly. *BMC Biol.* 2021;19:1–16. <https://doi.org/10.1186/s12915-021-00963-z>.

The original article can be found online at <https://doi.org/10.1186/s12915-021-00963-z>.

*Correspondence: jje@uci.edu

[†]Mahul Chakraborty and Arunachalam Ramaiah contributed equally to this work.

⁹Center for Complex Biological Systems, University of California, Irvine, CA 92697, USA

Full list of author information is available at the end of the article



© The Author(s) 2022. **Open Access** This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if changes were made. The images or other third party material in this article are included in the article's Creative Commons licence, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons licence and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this licence, visit <http://creativecommons.org/licenses/by/4.0/>. The Creative Commons Public Domain Dedication waiver (<http://creativecommons.org/publicdomain/zero/1.0/>) applies to the data made available in this article, unless otherwise stated in a credit line to the data.

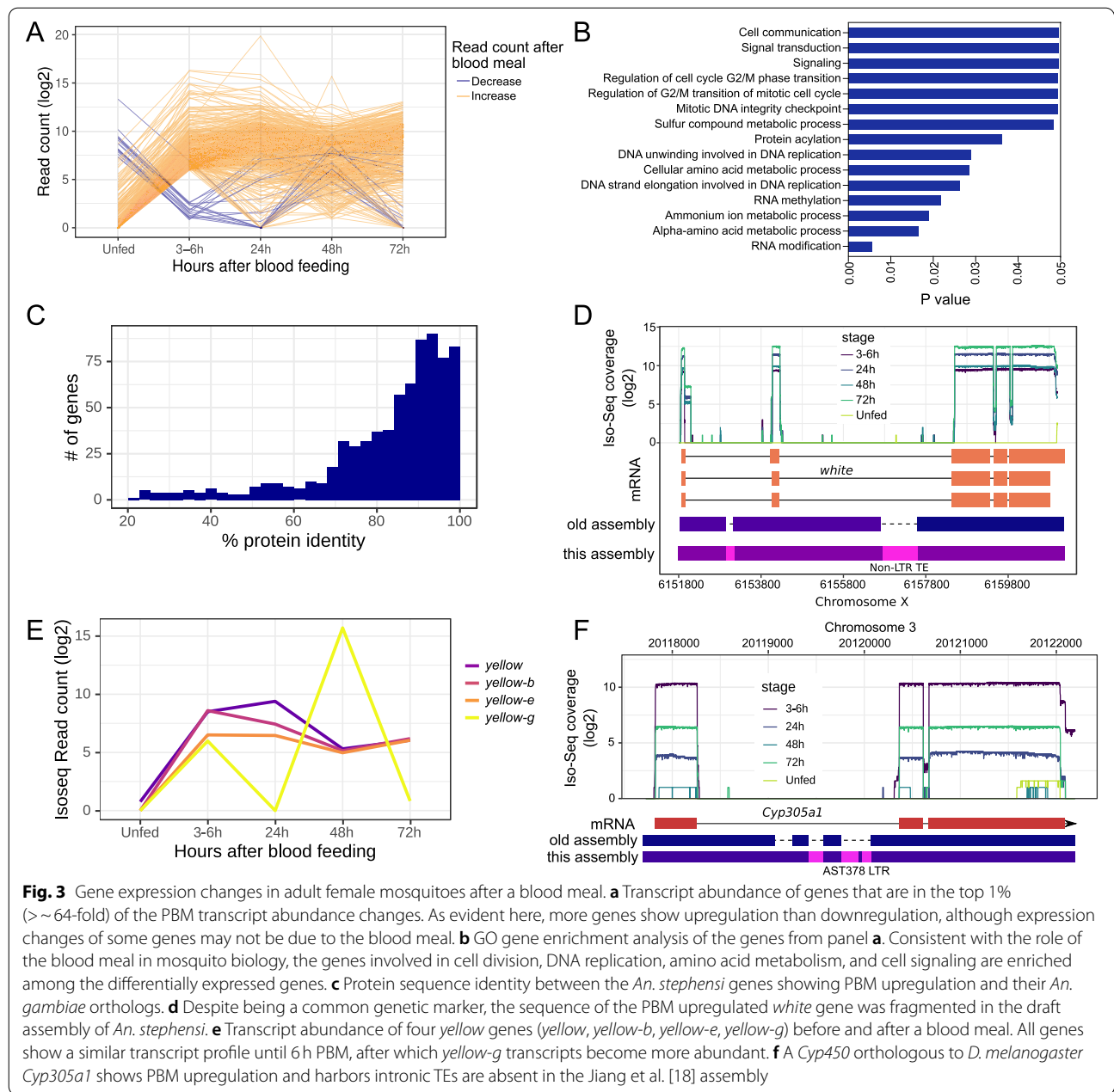


Fig. 3 Gene expression changes in adult female mosquitoes after a blood meal. **a** Transcript abundance of genes that are in the top 1% (> ~ 64-fold) of the PBM transcript abundance changes. As evident here, more genes show upregulation than downregulation, although expression changes of some genes may not be due to the blood meal. **b** GO gene enrichment analysis of the genes from panel **a**. Consistent with the role of the blood meal in mosquito biology, the genes involved in cell division, DNA replication, amino acid metabolism, and cell signaling are enriched among the differentially expressed genes. **c** Protein sequence identity between the *An. stephensi* genes showing PBM upregulation and their *An. gambiae* orthologs. **d** Despite being a common genetic marker, the sequence of the PBM upregulated *white* gene was fragmented in the draft assembly of *An. stephensi*. **e** Transcript abundance of four *yellow* genes (*yellow*, *yellow-b*, *yellow-e*, *yellow-g*) before and after a blood meal. All genes show a similar transcript profile until 6 h PBM, after which *yellow-g* transcripts become more abundant. **f** A *Cyp450* orthologous to *D. melanogaster Cyp305a1* shows PBM upregulation and harbors intronic TEs are absent in the Jiang et al. [18] assembly