

CORRECTION

Open Access



Correction: Exploring crop genomes: assembly features, gene prediction accuracy, and implications for proteomics studies

Qussai Abbas¹, Mathias Wilhelm^{2,3}, Bernhard Kuster^{3,4}, Brigitte Poppenberger⁵ and Dmitrij Frishman^{1*}

Correction: *BMC Genomics* 25, 619 (2024)

<https://doi.org/10.1186/s12864-024-10521-w>

Following publication of the original article, it was noticed that the sensitivity and specificity values of GALBA were reported incorrectly, leading to an error

in Fig. 4, and 4b. The incorrect and correct versions of Fig. 4a and b. are given in this correction article.

The online version of the original article can be found at <https://doi.org/10.1186/s12864-024-10521-w>.

*Correspondence:

Dmitrij Frishman
dimitri.frischmann@tum.de

¹Chair of Bioinformatics, TUM School of Life Sciences, Technical University of Munich, Freising, Germany

²Computational Mass Spectrometry, TUM School of Life Sciences, Technical University of Munich, Freising, Germany

³Munich Data Science Institute, Technical University of Munich, Garching, Germany

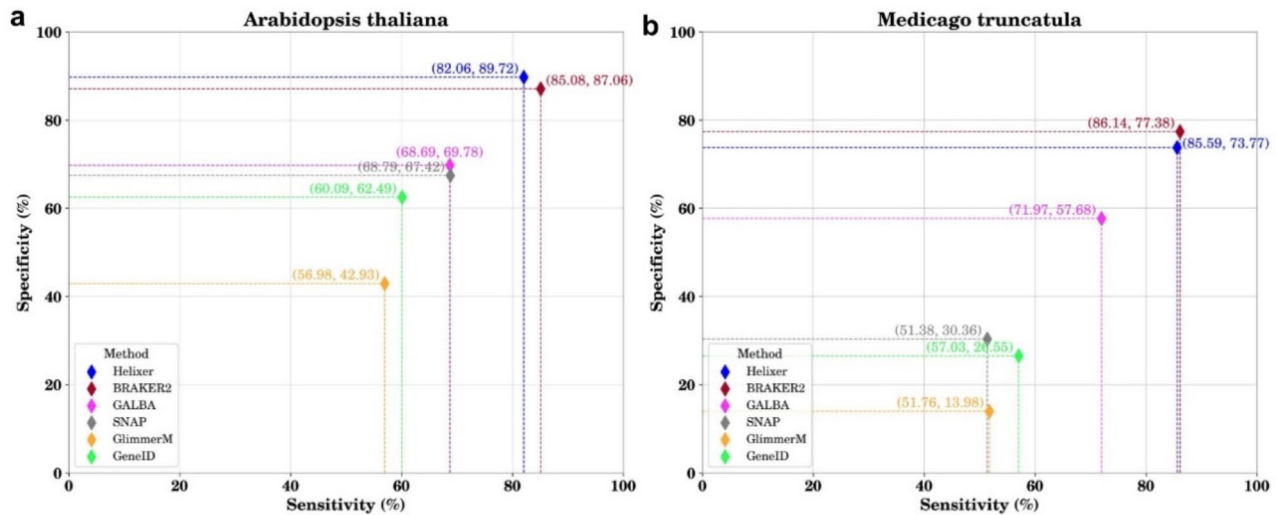
⁴Chair of Proteomics and Bioanalytics, TUM School of Life Sciences, Technical University of Munich, Freising, Germany

⁵Biotechnology of Horticultural Crops, TUM School of Life Sciences, Technical University of Munich, Freising, Germany

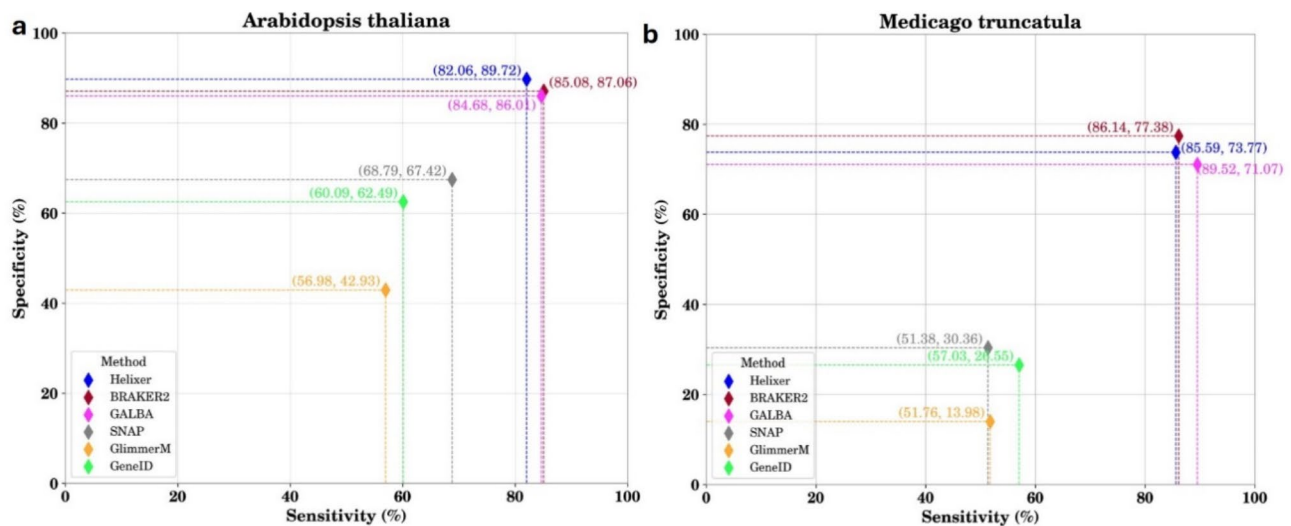


© The Author(s) 2024. **Open Access** This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, 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.

Incorrect figure panels:



Correct Fig. 4a and b:



The following text in the ‘Benchmarking gene prediction tools’ relating to Fig. 4 has been corrected as a result of this correction.

Original text:

The benchmarking of the selected gene prediction tools was conducted against the well-curated reference annotations of the *Arabidopsis thaliana* and *Medicago truncatula* model plant genomes. These tools do not rely on species-specific transcriptomics or proteomics data. Comparative analysis revealed that BRAKER2, GALBA and Helixer exhibited superior performance in terms of

sensitivity and specificity compared to the other tools assessed (Fig. 4a and b).

Corrected text:

The benchmarking of the selected gene prediction tools was conducted against the well-curated reference annotations of the *Arabidopsis thaliana* and *Medicago truncatula* model plant genomes. These tools do not rely on species-specific transcriptomics or proteomics data. Comparative analysis revealed that BRAKER2, GALBA and Helixer exhibited superior performance in terms of sensitivity and specificity compared to the other

tools assessed (Fig. 4a and b). While GALBA was specifically designed to work well with genomes that present challenges for BRAKER2—such as large genomes with abundant repeats and high GC content—it will not be included in this study and will be evaluated in future research.

The original article has been updated.

Published online: 19 September 2024

Publisher's note

Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.