



OPEN ACCESS

EDITED AND REVIEWED BY
Ling-Ling Chen,
Guangxi University, China

*CORRESPONDENCE
France Denoeud
✉ fdenoeud@genoscope.cns.fr

RECEIVED 30 April 2024
ACCEPTED 27 May 2024
PUBLISHED 05 June 2024

CITATION
Guenzi-Tiberi P, Istace B, Alsos IG,
The PhyloNorway Consortium, Coissac E,
Lavergne S, The PhyloAlps Consortium,
Aury J-M and Denoeud F (2024)
Corrigendum: LocoGSE, a sequence-based
genome size estimator for plants.
Front. Plant Sci. 15:1426035.
doi: 10.3389/fpls.2024.1426035

COPYRIGHT
© 2024 Guenzi-Tiberi, Istace, Alsos, The
PhyloNorway Consortium, Coissac, Lavergne,
The PhyloAlps Consortium, Aury and Denoeud.
This is an open-access article distributed under
the terms of the [Creative Commons Attribution
License \(CC BY\)](#). The use, distribution or
reproduction in other forums is permitted,
provided the original author(s) and the
copyright owner(s) are credited and that the
original publication in this journal is cited, in
accordance with accepted academic
practice. No use, distribution or reproduction
is permitted which does not comply with
these terms.

Corrigendum: LocoGSE, a sequence-based genome size estimator for plants

Pierre Guenzi-Tiberi¹, Benjamin Istace¹, Inger Greve Alsos²,
The PhyloNorway Consortium, Eric Coissac³,
Sébastien Lavergne³, The PhyloAlps Consortium,
Jean-Marc Aury¹ and France Denoeud^{1*}

¹Génomique Métabolique, Genoscope, Institut François Jacob, CEA, CNRS, Univ Evry, Université Paris-Saclay, Evry, France, ²The Arctic University Museum of Norway, UiT The Arctic University of Norway, Tromsø, Norway, ³Univ. Grenoble Alpes, Univ. Savoie Mont Blanc, CNRS, LECA (Laboratoire d'Ecologie Alpine), Grenoble, France

KEYWORDS

genome size estimation, genome size, ploidy, genome-skimming, environmental DNA, plant genomics, 1C, 1Cx

A corrigendum on

LocoGSE, a sequence-based genome size estimator for plants

by Guenzi-Tiberi P, Istace B, Alsos IG, The PhyloNorway Consortium, Coissac E, Lavergne S, The PhyloAlps Consortium, Aury J-M and Denoeud F (2024). *Front. Plant Sci.* 15:1328966. doi: 10.3389/fpls.2024.1328966

In the published article, there was an error in [Figure 2](#) as published. The same formula “ $y=1.59x R2 = 0.99$ ” was displayed on all panels, whereas it was supposed to vary across lineages. The corrected [Figure 2](#) and its caption appear below.

The authors apologize for this error and state that this does not change the scientific conclusions of the article in any way. The original article has been updated.

Publisher's note

All claims expressed in this article are solely those of the authors and do not necessarily represent those of their affiliated organizations, or those of the publisher, the editors and the reviewers. Any product that may be evaluated in this article, or claim that may be made by its manufacturer, is not guaranteed or endorsed by the publisher.

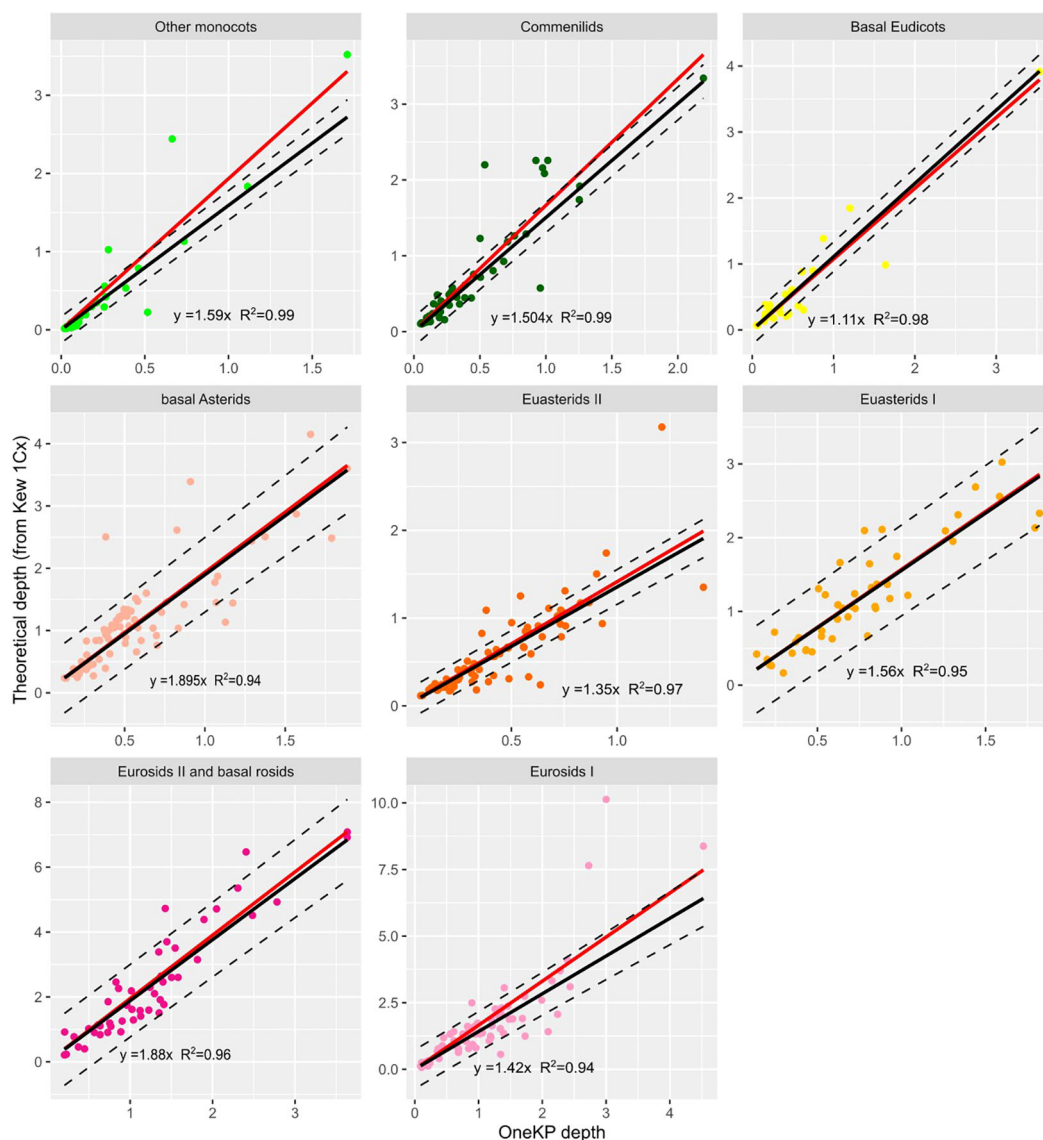


FIGURE 2 Relationship between depth on OneKP single copy genes and theoretical depth (calculated from Kew 1Cx) in the training set, for 8 plant lineages. Black line is the regression line obtained after robust regression, red line is the regression line obtained with standard regression. Regression line equations and R coefficients are displayed for each lineage.