



OPEN ACCESS

EDITED AND REVIEWED BY

Zulfiqar Ali,
University of Agriculture, Faisalabad,
Pakistan

*CORRESPONDENCE

Wei Yan
yanwei@jaas.ac.cn

RECEIVED 28 October 2023
ACCEPTED 17 November 2023
PUBLISHED 29 November 2023

CITATION

Xu T, Meng S, Zhu X, Di J, Zhu Y, Yang X and Yan W (2023) Corrigendum: Integrated GWAS and transcriptomic analysis reveal the candidate salt-responsive genes regulating Na^+/K^+ balance in barley (*Hordeum vulgare* L.). *Front. Plant Sci.* 14:1329188.
doi: 10.3389/fpls.2023.1329188

COPYRIGHT

© 2023 Xu, Meng, Zhu, Di, Zhu, Yang and Yan. 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: Integrated GWAS and transcriptomic analysis reveal the candidate salt-responsive genes regulating Na^+/K^+ balance in barley (*Hordeum vulgare* L.)

Tingting Xu, Shan Meng, Xiaopin Zhu, Jiachun Di, Yin Zhu, Xin Yang and Wei Yan*

Institute of Germplasm Resources and Biotechnology, Jiangsu Key Laboratory for Agrobiolog, Jiangsu Provincial Platform for Conservation and Utilization of Agricultural Germplasm, Jiangsu Academy of Agricultural Sciences, Nanjing, China

KEYWORDS

barley, GWAS, RNA-Seq, salt tolerance, Na^+/K^+ balance, candidate genes

A Corrigendum on

Integrated GWAS and transcriptomic analysis reveal the candidate salt-responsive genes regulating Na^+/K^+ balance in barley (*Hordeum vulgare* L.)

by Xu T, Meng S, Zhu X, Di J, Zhu Y, Yang X and Yan W (2023) *Front. Plant Sci.* 13:1004477.
doi: 10.3389/fpls.2022.1004477

In the published article, there was an error in Figure 4. The image in Figure 6 was used as the image in Figure 4. The corrected Figure 4 appears 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.

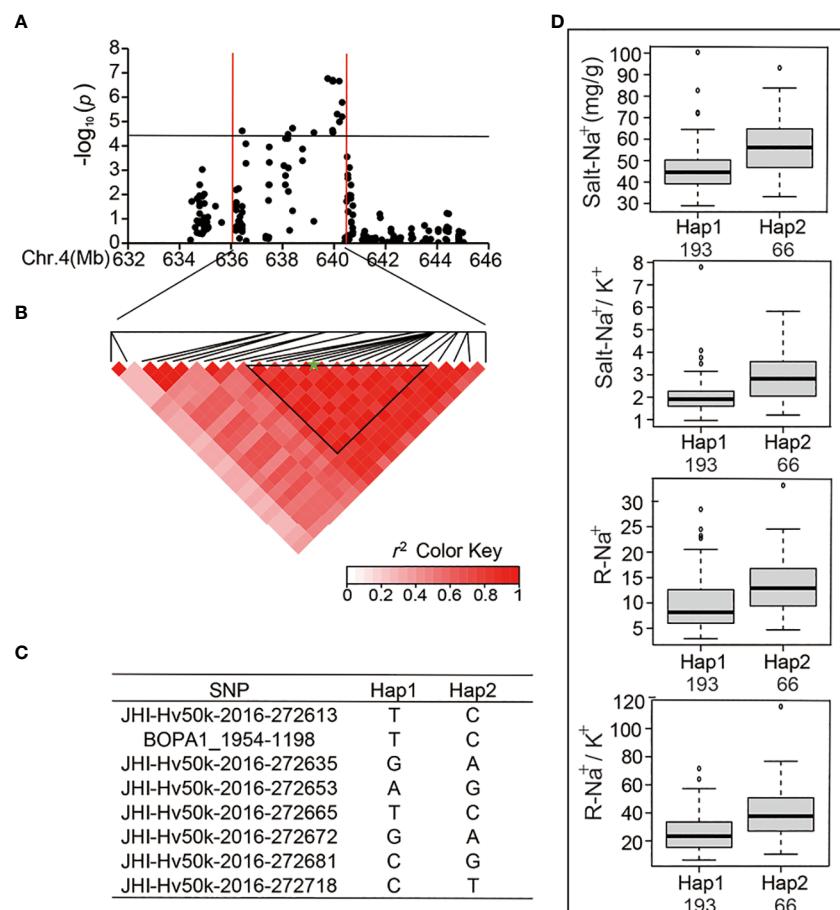


FIGURE 4

Analysis of the SNP peak and the candidate genes on chromosome 4. **(A)** Manhattan plots for Chr 4. The black line represents the significance threshold ($P < 10^{-4.40}$) and a red line indicates the position of the strong SNP peak. **(B)** LD based on pairwise r^2 values between the SNPs estimated on Chr 4. The black inverted triangles indicate 8 significantly associated SNPs that were repeatedly detected. The green five-pointed star indicates the strongest SNP with the highest threshold. **(C)** Haplotypes were found among the barley accessions using the 8 SNPs. **(D)** Phenotypic differences of Salt- Na^+ , Salt- Na^+/K^+ , R- Na^+ , and R- Na^+/K^+ between the two haplotypes.