Oviedo, February 09th, 2024

Dear Editor,

We thank the opportunity to submit the revised version of the manuscript “**PlantFUNCO: integrative functional genomics database reveals clues into duplicates divergence evolution (MS ID#: MBE-23-0764.R1)”.**

In this revised version, we have addressed all the minor points raised during the review process. According to the referees’ feedback, the manuscript underwent erratum correction, figure modification and minor text review. Detailed responses to the reviewers are provided below in a point-by-point manner.

We believe that our manuscript is now well suited for publication in “Molecular Biology and Evolution”, and we hope that both the reviewers and the editorial committee share our opinion.

Sincerely yours,



**Dr. Mónica Meijón**

Associate Professor

Plant Physiology

Department of Organisms and Systems Biology

University of Oviedo

Spain

Telf.: +34 985 104 796

E-mail: [meijonmonica@uniovi.es](about:blank)

**MS ID#: MBE-23-0764.R1**

**MS TITLE: PlantFUNCO: integrative functional genomics database reveals clues into duplicates divergence evolution**

***Editors’ Comments to the Author:***

Please make the minor tweaks:

1. Abstract (line 28): "... plants epigenomics and functional genomics have evolved". Epigenomics/functional genomics are the tools researchers use to study genome biology and evolution. All instances referencing epigenomics/functional genomics as an intrinsic biological process should be revised (something to the effect of "plant epigenomes" or "functional non-coding genome", which are the phenotypes in question). Another example of this error is Line 352. It's rather unfortunate that this was missed by the proof-reading service. 2. Text size in Figures 3, 6, and 7 are still too small. I would encourage the authors to identity the most pertinent information in each figure and reduce the overall complexity such that the text size can be uniformly presented. 3. Line 475: Do the authors mean "--shift -75"? If not, then the ATAC/DNase-seq peak coordinates are incorrectly placed by ~150 bp and the entire workflow needs to be rerun to correctly annotate chromatin states.

# We wish to thank the Board of Editors and the Associate Editor to give us the chance to address these minor points, and we extend our gratitude to the anonymous reviewers for their valuable and prompt feedback. Detailed responses to the minor tweaks suggested by the Editor are provided below in the answer to Reviewer 1.

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***Reviewers' comments:***

***Reviewer: 1***

*Comments to the Author:*

The authors have done an outstanding job of addressing my concerns and clarifying points of confusion. I have just a few additional minor comments that require attention prior to publication. Line numbers referenced below are from the document titled Manuscript\_Draft\_marked.docx.

# We appreciate the reviewer’s time spent on the second review round of our manuscript. We truly value the attention given to the minor points highlighted.

1. Abstract (line 28): "... plants epigenomics and functional genomics have evolved". Epigenomics/functional genomics are the tools researchers use to study genome biology and evolution. All instances referencing epigenomics/functional genomics as an intrinsic biological process should be revised (something to the effect of "plant epigenomes" or "functional non-coding genome", which are the phenotypes in question). Another example of this error is Line 352. It's rather unfortunate that this was missed by the proof-reading service.

# The reviewer is absolutely right. We have replaced “epigenomics/functional genomics” by “plants epigenome and functional non-coding genome” as suggested. This modification applies to the following lines:

**[ Abstract, Page 1, Lines 29-30]**

**[ Discussion, Page 11, Lines 353]**

**[ Discussion, Page 13, Lines 448-449]**

2. Text size in Figures 3, 6, and 7 are still too small. I would encourage the authors to identity the most pertinent information in each figure and reduce the overall complexity such that the text size can be uniformly presented.

# We agree with the reviewer’s observation. We have removed protein-coding/ortholog numbers for Figure 3, as this information is available in supplementary Table S1. Additionally, we have unified the legends, increased the text size, and adjusted the overall figure size. Furthermore, we resized Figure 6A, increased the text size for all relevant plot titles and labels, and aligned the overall figure size accordingly. Lastly, we increased the text size for all relevant titles, significance values and made adjustments to the overall figure size for Figure 7.

3. Line 475: Do the authors mean "--shift -75"? If not, then the ATAC/DNase-seq peak coordinates are incorrectly placed by ~150 bp and the entire workflow needs to be rerun to correctly annotate chromatin states.

# The reviewer is correct, and we apologise for any confusion. As stated by the reviewer, the “—shift” argument was originally set to “-75”. This erratum has been corrected.

**[ Methods, Page 14, Lines 476]**

***Reviewer: 2***

*Comments to the Author:*

The authors have addressed all of my concerns