BMC Bioinformatics

Publisher Correction to: TrancriptomeReconstructoR: data-driven annotation of complex transcriptomes

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The original article can be found online at https://doi.org/10.1186/s12859-021-04208-2.

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Following the publication of the original article [1], the authors identified missing additional files and references. The Additional files 1 and 2 including the references have been added to the original article.

The original article [1] has been corrected.

The publisher apologizes to the authors and readers for the inconvenience.

Supplementary Information

The online version contains supplementary material available at https://doi.org/10.1186/s12859-021-04259-5.

Additional file 1. Vignette to TranscriptomeReconstructoR. The file describes an example pipeline for *de novo* calling of gene and transcript models by TranscriptomeReconstructoR, as well as detailed description of the algorithm.

Additional file 2. Supplementary Figures S1–S4. **Fig. S1**. Comparison of gene borders between TAIR10 and Araport11. **Fig. S2**. Metagene plot of PAS signal around TSS of sppRNA-containing genes. **Fig. S3**. Example of a novel gene encoding transient RNA. **Fig. S4**. Example of a gene misannotated in TAIR10 and Araport11.

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