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Corrigendum: Integrated analysis of small RNAs, transcriptome and degradome sequencing reveal the drought stress network in *Agropyron mongolicum* Keng

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Agropyron mongolicum Keng, drought resistance, microRNAs, transcriptome, degradome, integration analysis, co-expression network

A Corrigendum on:

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By Fan B, Sun F, Yu Z, Zhang X, Yu X, Wu J, Yan X, Zhao Y, Nie L, Fang Y and Ma Y (2022) *Front. Plant Sci.* 13:976684. doi: 10.3389/fpls.2022.976684

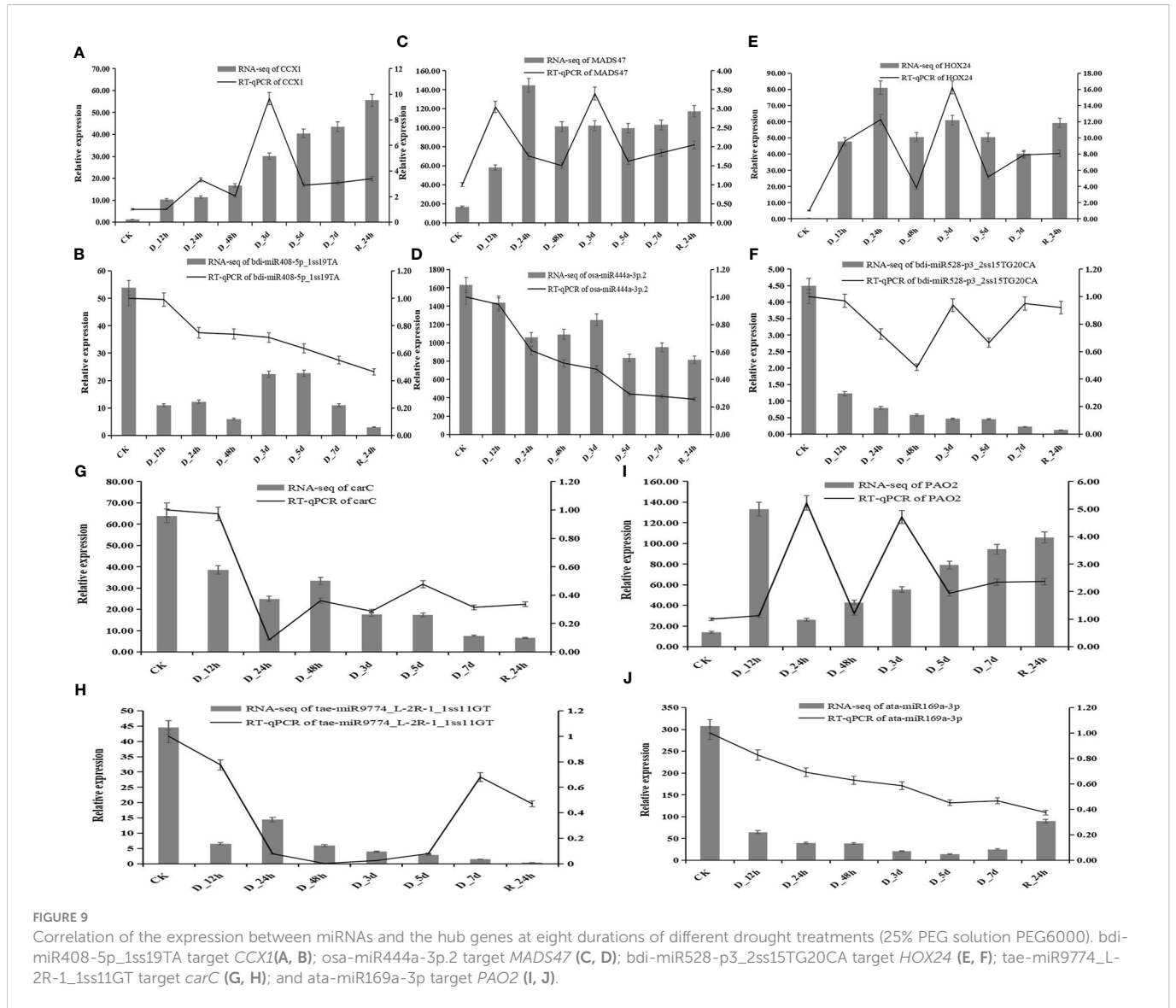
In the published article, there was an error in [Figure 9](#). [Figure 9](#) should have been a bar graph of RT-qPCR, but since the relative expression trends of RT-qPCR are the same to that of RNA-seq, we unintentionally put the bar graph of gene expression from RNA-seq in [Figure 9](#). We have corrected [Figure 9](#) to a combined graph from the gene expression of RT-qPCR and RNA-seq.

In the last sentence of “Correlation analysis of miRNAs and their candidate hub genes for drought resistance”, “The relative expression of tae-miR9774_L-2R-1_1ss11GT increased overall, but the relative expression of its target genes decreased”, the first “increased” should be “decreased”, and “but the relative expression of its target genes decreased” should be removed.

The corrected sentence appears below:

“The relative expression of tae-miR9774_L-2R-1_1ss11GT and target gene *carC* decreased overall”.

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



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