

## CORRECTION

# Correction: Transcriptomic analysis reveals the roles of gibberellin-regulated genes and transcription factors in regulating bolting in lettuce (*Lactuca sativa* L.)

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The gene LsWRKY (Lsat\_1\_v5\_gn\_6\_12161) incorrectly did not appear in [Fig 4](#). Please see the corrected [Fig 4](#) here.

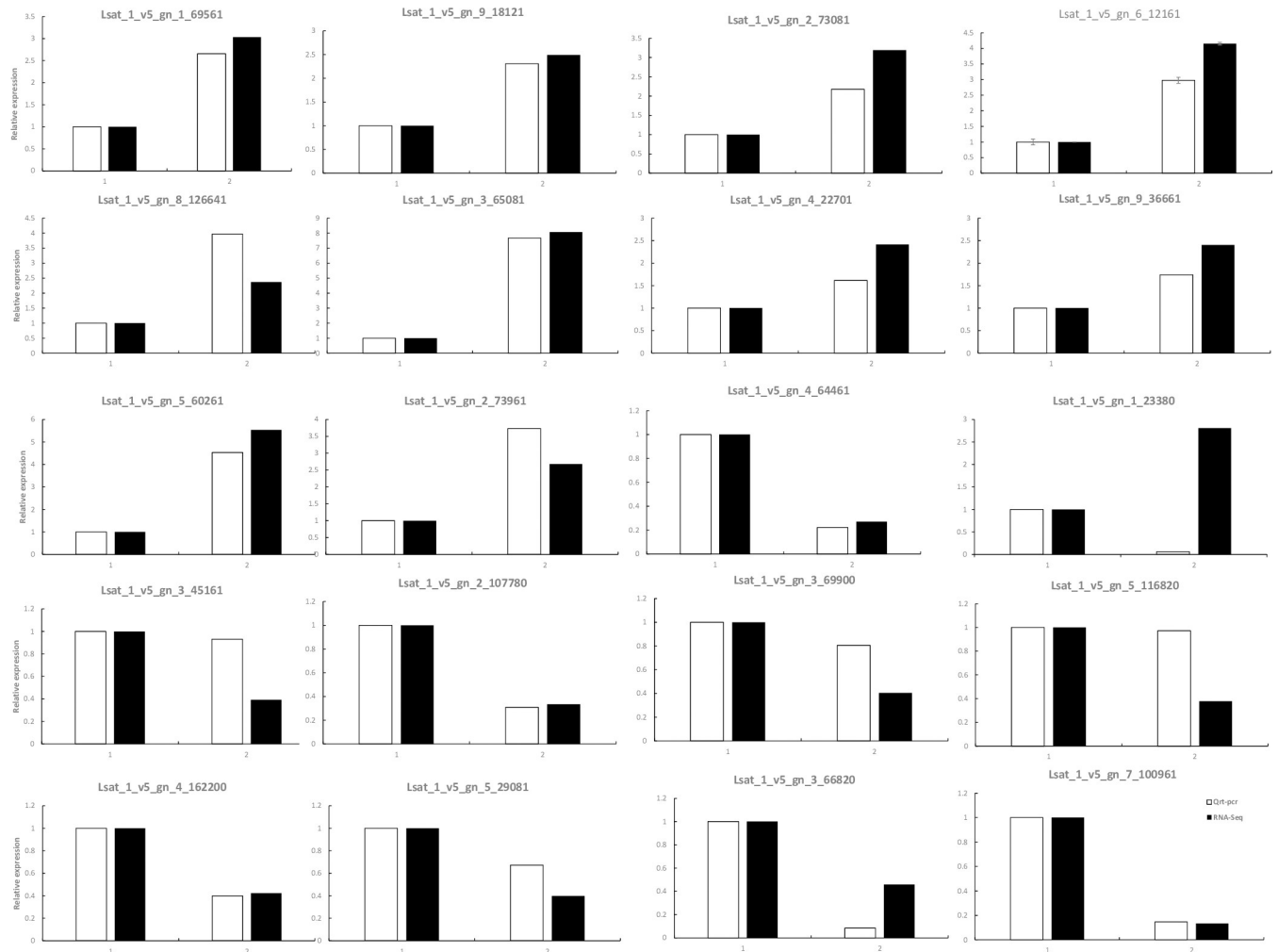


## OPEN ACCESS

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**Fig 4. Verification of differentially expressed genes by RT-qPCR.** Twenty genes were chosen for RT-qPCR validation. The white and black bars represent the relative expression levels of each gene in the control and high-temperature groups, as detected by RT-qPCR and RNA-Seq, respectively. To plot the RNA-Seq data, gene expression in the control group was set to be the same as that observed by RT-qPCR, and relative expression in the high-temperature group was calculated using the fold-change detected by RNA-Seq. The bars represent the standard deviation (n = 3); 1 represents the control temperature, and 2 represents the high temperature. Asterisks indicate that the gene transcriptions are significantly different between control and treatment group (unpaired t test,  $P < 0.05$ ).

<https://doi.org/10.1371/journal.pone.0221609.g001>

## Reference

1. Liu X, Lv S, Liu R, Fan S, Liu C, Liu R, et al. (2018) Transcriptomic analysis reveals the roles of gibberellin-regulated genes and transcription factors in regulating bolting in lettuce (*Lactuca sativa* L.). PLoS ONE 13(2): e0191518. <https://doi.org/10.1371/journal.pone.0191518> PMID: 29415067