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CORRECTION
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Corrigendum: Transcriptomics Identifies Modules of Differentially Expressed Genes and Novel Cyclotides in *Viola pubescens*

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A Corrigendum on

Transcriptomics Identifies Modules of Differentially Expressed Genes and Novel Cyclotides in *Viola pubescens*
by Sternberger, A. L., Bowman, M. J., Kruse, C. P. S., Childs, K. L., Ballard, H. E., and Wyatt, S. E. (2019). Front. Plant Sci. 10:156. doi: 10.3389/fpls.2019.00156

In our original article, there was a mistake in the legend for **Figure 1** as published. The descriptions of the figure labels (A) and (B) were switched. The correct legend appears below.

"*Viola pubescens* var. scabriuscula bearing **(A)** cleistogamous and **(B)** chasmogamous flowers. Photographs were taken over native populations located in Sells Park, Athens County, Ohio, 45701 (39°20′40.6″N 82°04′31.9″W)."

Additionally, there was a mistake in **Table 1** as published. In the first column, "# of scaffolds > 10 kbp" should be "# of scaffolds > 1 K nt." The corrected **Table 1** appears below.

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

TABLE 1 | Summary statistics of the *V. pubescens* genome assembly via ABySS and CEGMA and BUSCO assessments of genome completeness.

# of scaffolds	157,722
Total size of scaffolds (bp)	318,370,682
Longest scaffold (bp)	86,685
# of scaffolds > 1 K nt	80,885
N50 length (bp)	3,500
Average length of break (>25 N's) between contigs in scaffold	45
Scaffold %N	0.06
Percent in scaffolded contigs	3.2
Percent in unscaffolded contigs	96.8
CEGMA Partial (%)	94, $n = 248$
CEGMA Complete (%)	76, $n = 248$
BUSCO	C: 79.7% [D:13.5%], F: 8.9%, M: 11.4%, $n = 2121$

C, complete; D, duplicated; F, fragmented; M, missing; n, gene number.