CORRECTION

Correction to: High-throughput miRNA deep sequencing in response to drought stress in sugarcane

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Correction to: 3 Biotech (2021) 11:312
https://doi.org/10.1007/s13205-021-02857-x

The authors have inadvertently duplicated Fig. 8 as Fig. 9. Correction to Fig. 9 is given below. The authors regret any inconvenience caused as a result of this error.

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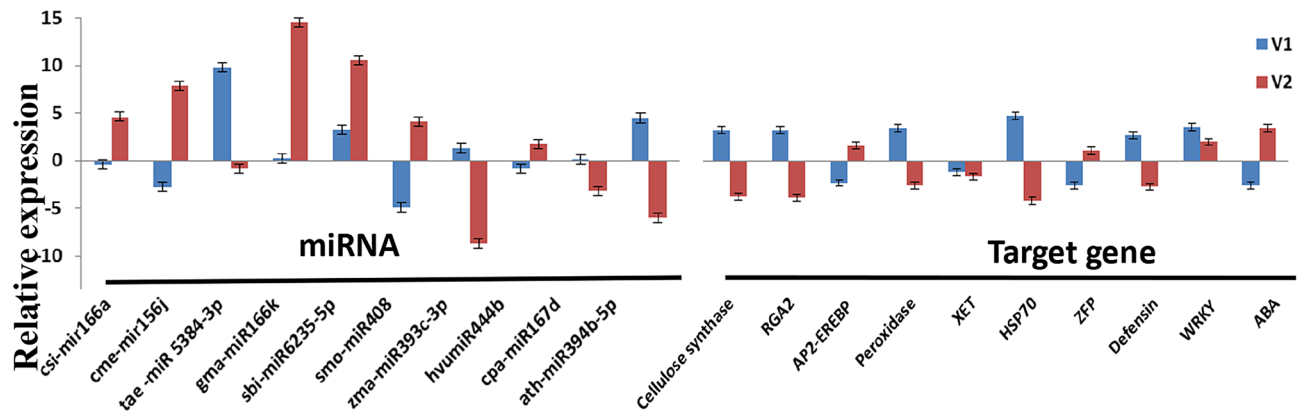
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Fig. 9 Expression profiling of miRNAs and predicted target genes of drought susceptible Co 8021 (V1) and drought tolerant Co 06022 (V2) sugarcane cultivars subjected to 10 days drought stress. The target genes are cellulose synthase, *RGA2*-Disease resistance protein RGA2, *AP2-EREBP*-AP2-EREBP transcription factor, peroxidase, *XET*-Xyloglucan endotransglucosylase hydrolase, *HSP 70*-heat shock protein 70-kDa, *ZFP*-zinc finger domain superfamily protein, defensin, *WRKY*-WRKY transcription factor and *ABA*-abscisic acid. In qRT-PCR each bar represents the average of three replicates and error bars indicate SE