BMC Genomics

CORRECTION

Correction to: Predicting and clustering plant *CLE* genes with a new method developed specifically for short amino acid sequences

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　　Following the publication of the original article [1], it was reported that there was an error in Fig. 7 whereby the yellow triangles showing the cleavage sites were not present. The corrected Fig. 7 is included in this Correction article, and the original article has been corrected.

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Reference
1.　Zhang Z, Liu L, Kucukoglu M, et al. Predicting and clustering plant *CLE* genes with a new method developed specifically for short amino acid sequences. BMC Genomics. 2020;21:709. https://doi.org/10.1186/s12864-020-07114-8.

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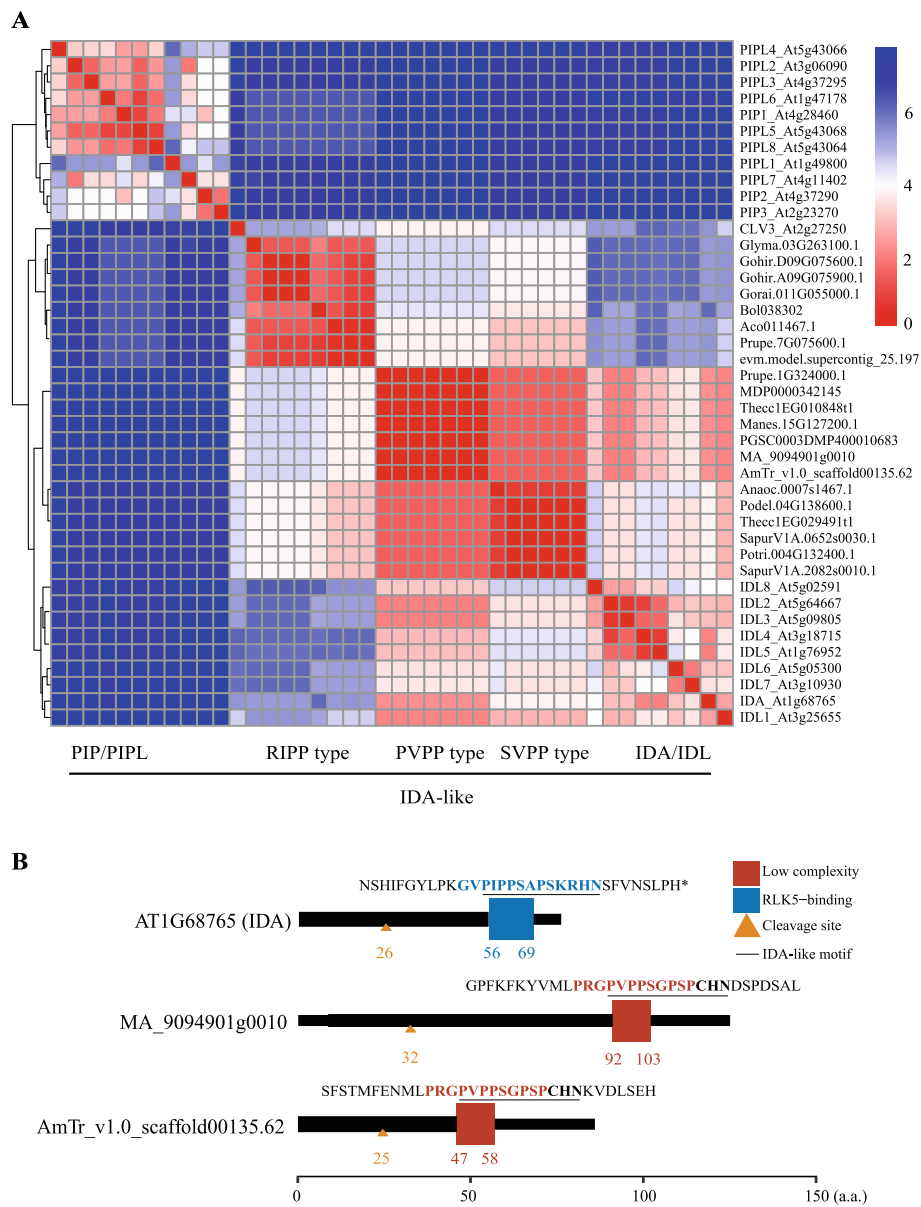Full list of author information is available at the end of the article

Fig. 7 Clustering analysis of IDA-like CLE motifs and Arabidopsis IDA/IDL motifs. **a** Clustering of IDA-like CLE motifs and Arabidopsis IDA/IDL, PIP/PIPL and CLV3 motifs. The heat map indicates the Euclidean distance of each pair of motifs. Red represents short distances. Blue represents long distances. A shorter Euclidean distance implies a higher similarity. **b** Protein domain schematic diagram of *Arabidopsis* IDA and two "PVPP-type" IDA-like CLE candidates. Protein domains were predicted using SMART. Blue box: RLK5-binding domain; red-brown box: low complexity domain; pale-brown triangle: location of the cleavage site of the signal peptide for the secretory pathway; black underline: IDA or IDA-like motif