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 HSE

 E-BOX

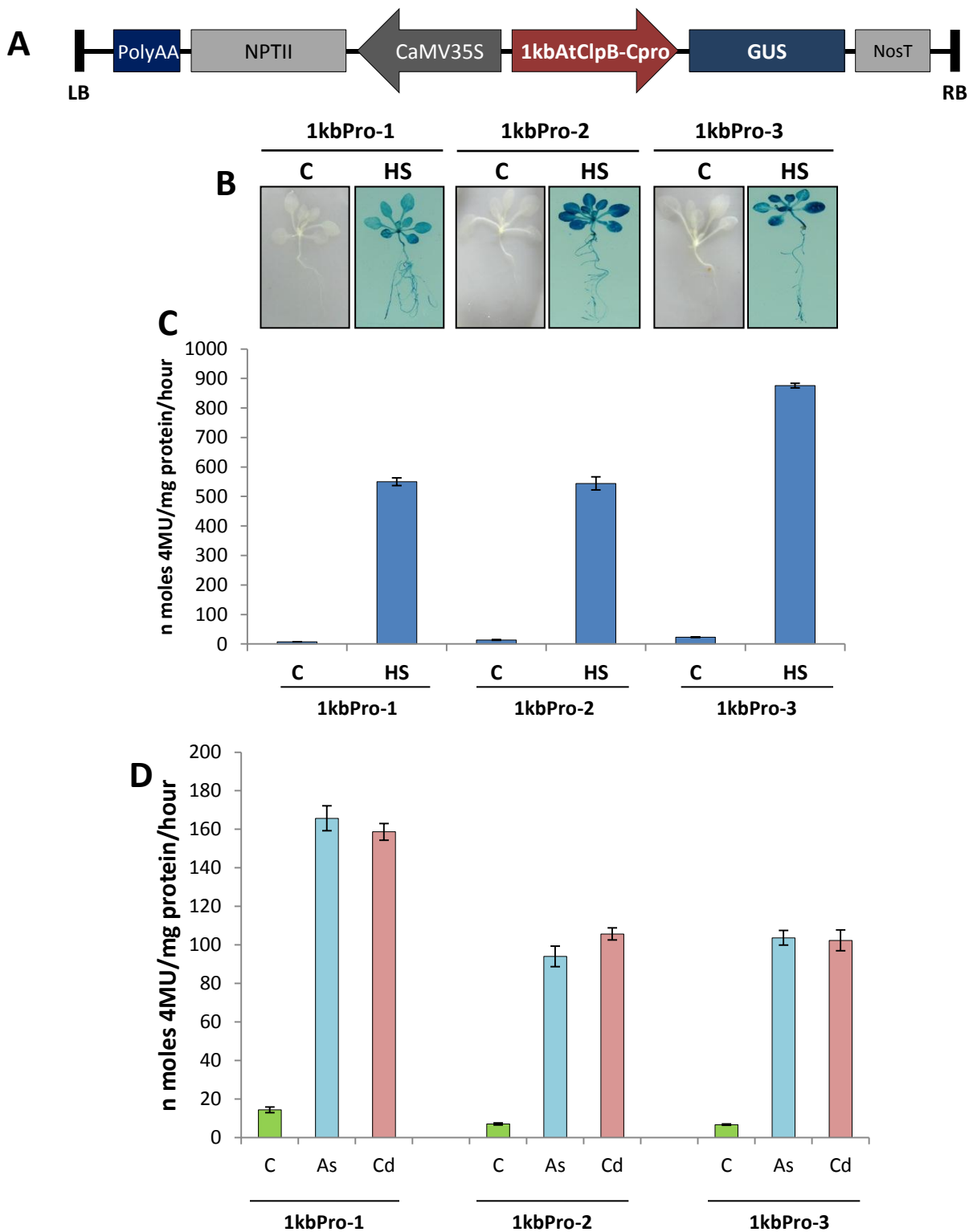
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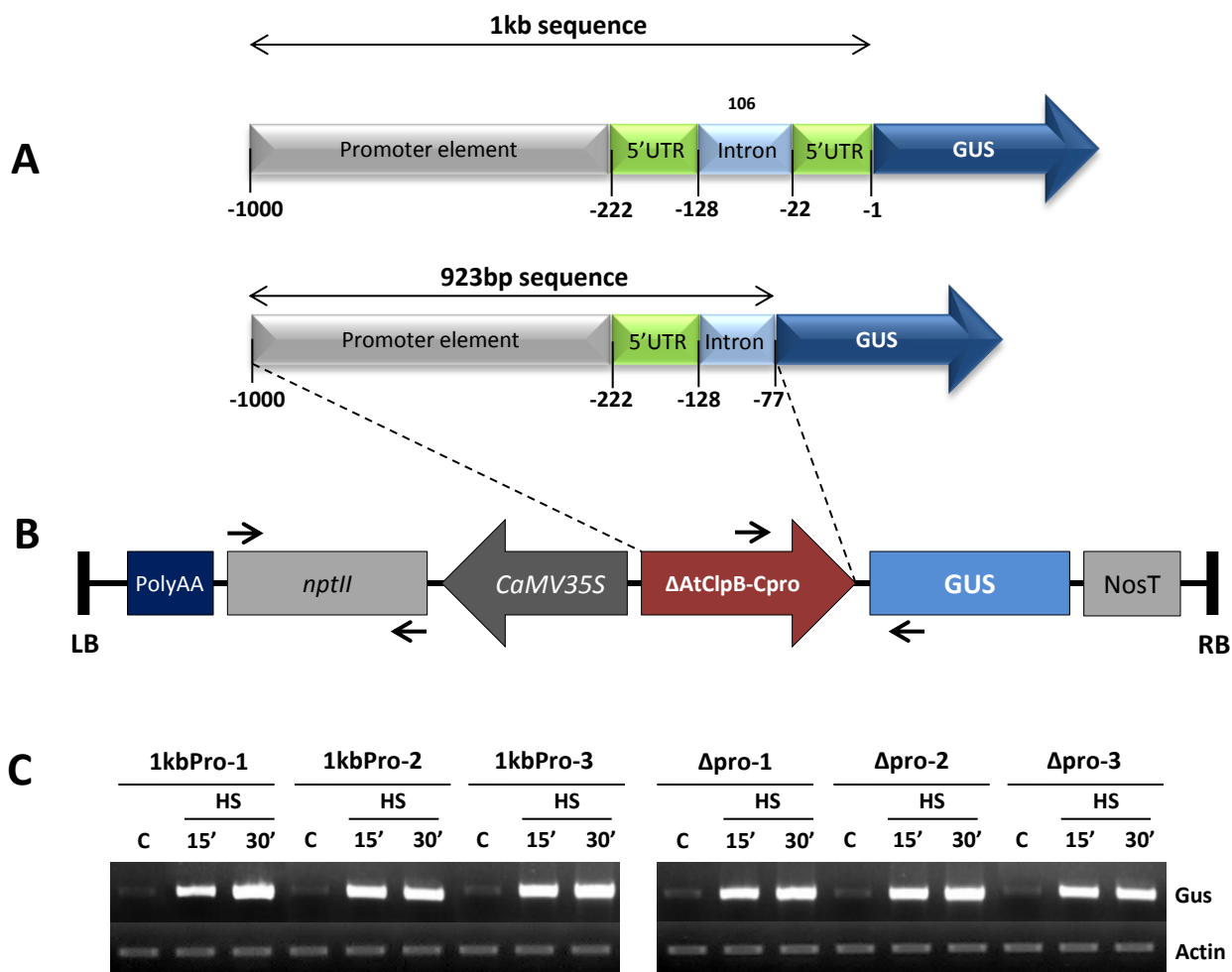
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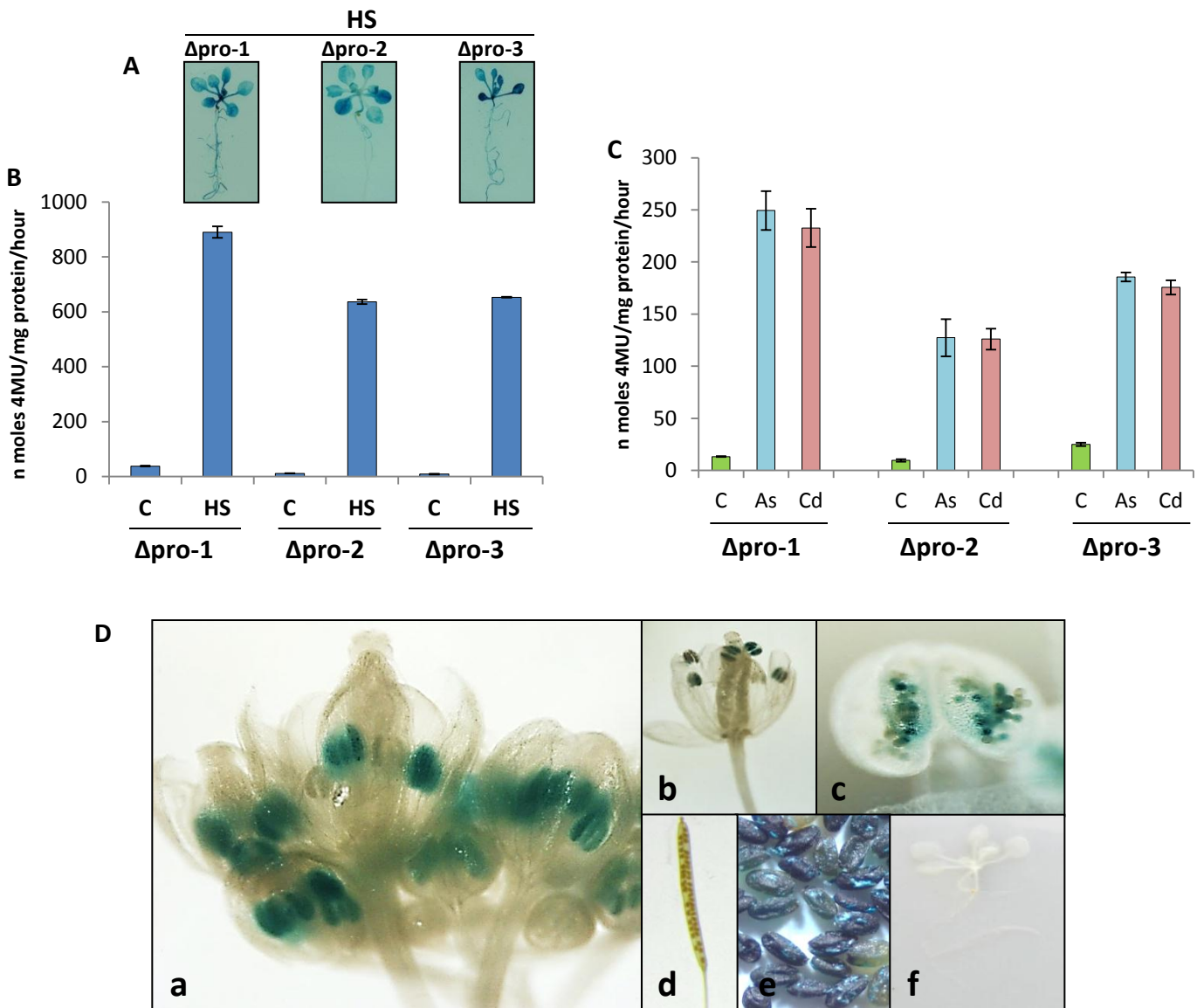
**Fig. S1.** Nucleotide sequence of 1kb upstream (from ATG) promoter region of *AtClpB-C* gene. Both positive and negative strands are shown. Positions of various regulatory cis-elements noted in this sequence are marked.



**Fig. S2.** Analysis of Gus expression in 1kbAtClpB-Cpro:Gus plants under stress conditions. (A) Schematic representation of the 1kbAtClpB-Cpro:Gus construct. (B) Qualitative analysis of Gus in the 1kbPro-1, 1kbPro-2 and 1kbPro-3 seedlings. Histochemical Gus staining of the control [C] and heat stressed [HS; 38°C/2h] seedlings is shown. (C) Quantitative estimation of Gus activity by MUG assay. (D) Gus expression analysis in 1kbPro-1, 1kbPro-2 and 1kbPro-3 lines under heavy metal (arsenic and cadmium) stress. Graphs represent the quantitative estimation of Gus activity by MUG assays.

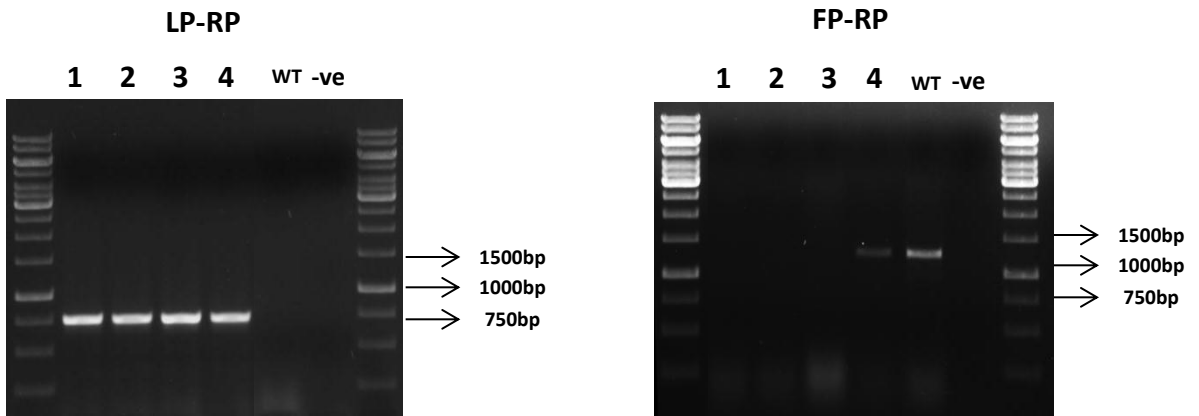
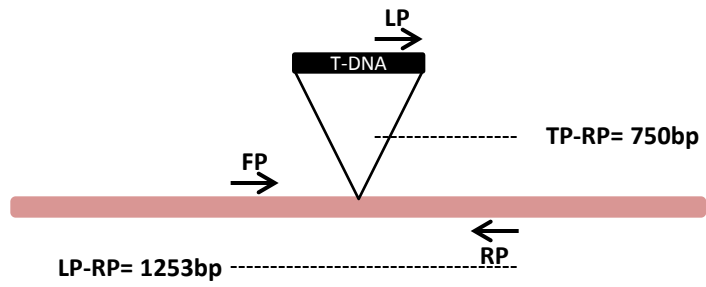


**Fig. S3.** (A) Schematic representation of 1kbAtClpB-Cpro and  $\Delta$ AtClpB-Cpro fragments. Nucleotide region deleted from the 1kb promoter is shown. (B) Diagrammatic representation of  $\Delta$ AtClpB-Cpro:Gus construct. (C) sqRT-PCR showing the comparison between transcript expression levels in 1kbPro and  $\Delta$ pro seedlings under C and HS (38°C/15' and 30') conditions.

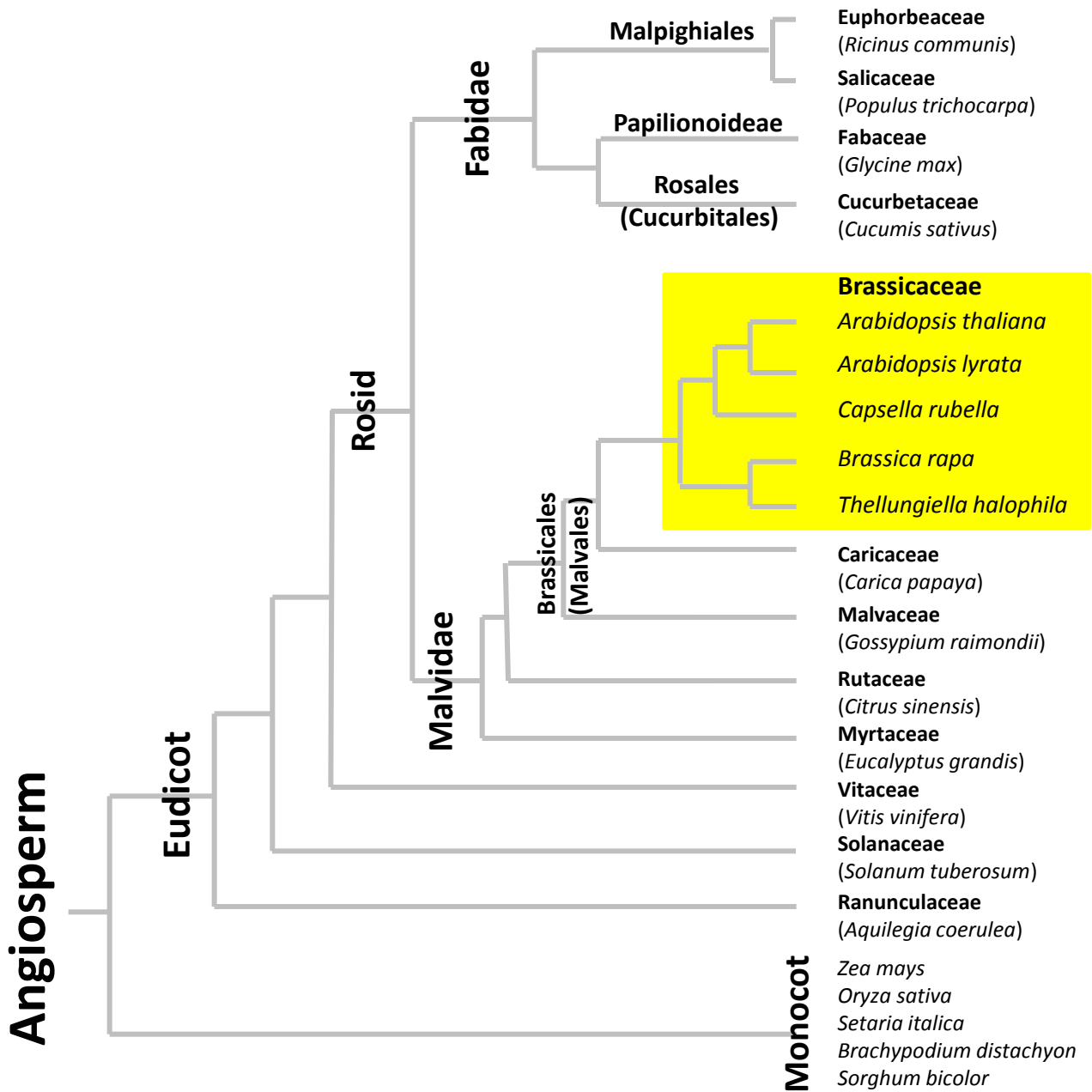


**Fig. S4.** Analysis of Gus expression in  $\Delta AtClpB-Cpro:Gus$  plants. (A) Qualitative (histochemical staining) and (B) quantitative estimation (MUG assay) of Gus expression in the  $\Delta pro-1$ ,  $\Delta pro-2$  and  $\Delta pro-3$  lines under C and HS (38°C/2h) conditions. (C) Quantitative estimation of Gus in the  $\Delta pro-1$ ,  $\Delta pro-2$  and  $\Delta pro-3$  lines under heavy metal (arsenic and cadmium) stress. (D) Histochemical staining for Gus expression in  $\Delta AtClpB-Cpro:Gus$  plants under unstressed (control) conditions at different developmental stages. (a) inflorescence, (b) single flower, (c) anther showing microspores, (d) young silique, (e) mature imbibed seeds and (f) 10-d-old seedlings are shown.

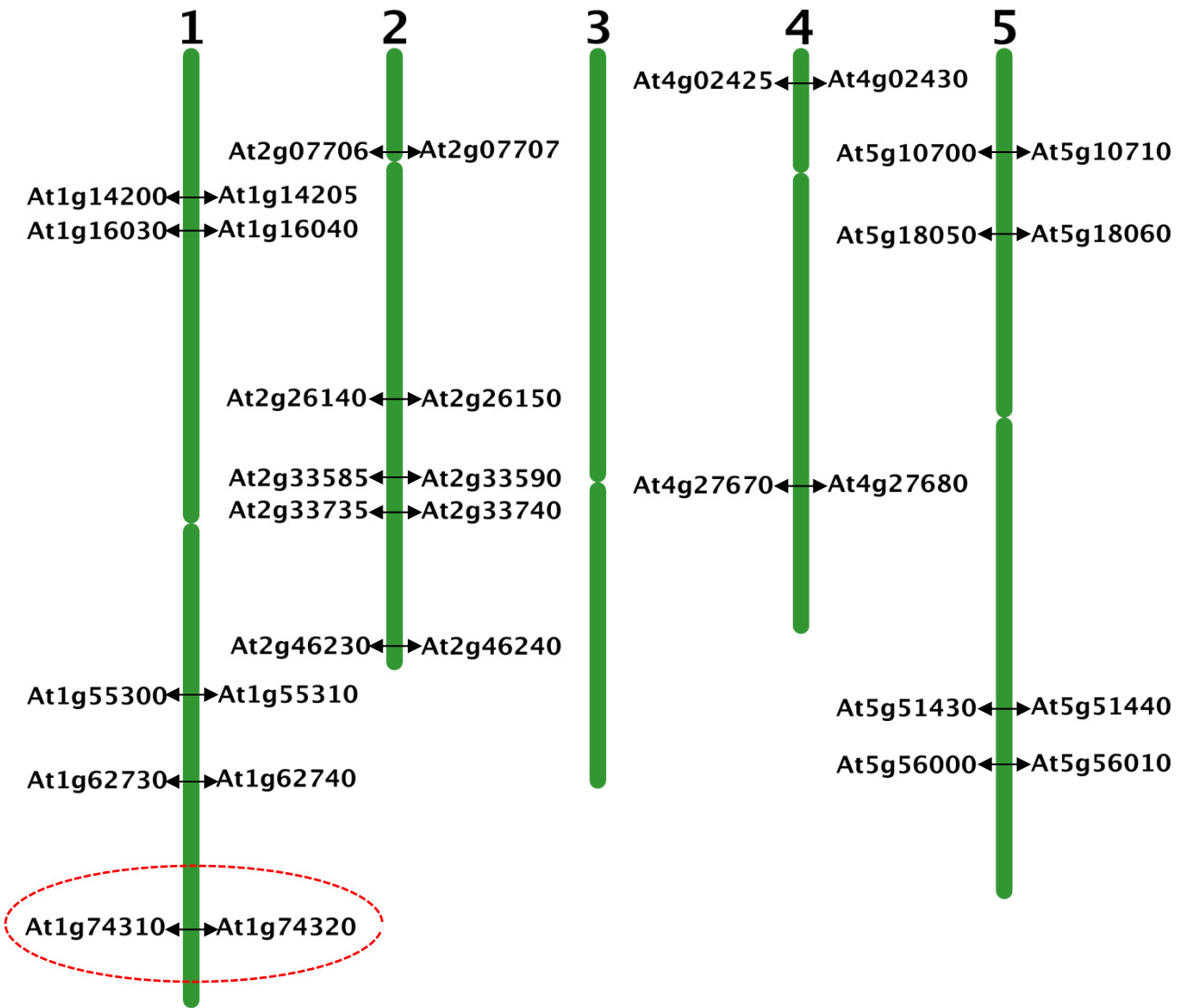




**Fig. S6.** Confirmation PCR to analyze the status of 4 individual mutant plants raised from *Salk\_014505* T<sub>3</sub> seeds. Primers used are indicated by arrows on the above diagrammatic representation. Out of the four lines, line no. 1, 2, 3 are homozygous and 4 is heterozygous.



**Fig. S7.** Genes homologous to At1g74310 (*ClpB-C*) and At1g74320 (*AtCK2*) were identified in several plant genera covering different families across the angiosperm including both dicots and monocots in plant database Phytozome (<http://www.phytozome.net>) and looked for their genomic organization. The families and genera analyzed are represented in the above diagrammatic sketch. Details of the locus id of the homologous genes is provided separately in Table S1. Genera along with the family with conservation in the divergent organization of the two genes are marked by a yellow box. Distance between the TSSs of the two genes among the highlighted genera is mentioned in the Table S1.



**Fig. S8.** Genomic organization of the 16 heat up-regulated divergent gene pairs in Arabidopsis (with intergenic region between TSSs <1.5 kb), analyzed using the “Chromosome Map Tool” (<http://www.arabidopsis.org/jsp/ChromosomeMap/tool.jsp>) of The Arabidopsis Information Resource (TAIR) and modified for better representation. Positions of the divergent gene pairs with their locus id on the 5 chromosomes (numbered 1-5) of Arabidopsis are shown. The *AtClpB-C* (*At1g74310*) : *AtCK2* (*At1g74320*) divergent gene pair is encircled. Functional annotation, fold up-regulation and distance between the gene pairs are provided in separately in Table S2.



**Table S3.** Primers used in the study.

	Primers	5' to 3' sequence
1	Primers for 1kb promoter cloning	
	1kbpro_Fwd	5' GCGAAGCTTGTTTTGAAGGAAAATCACAG 3'
	1kbpro_Rev	5' GGCCTCGAGCTTCGATTAGCTTTTGTAAATC 3'
2	Reverse primer for deletion analysis	
	$\Delta$ UTRpro_Rev	5' GGCCTCGAGTCACAAACACAAAAACACACA 3'
3	Primer for bidirectional promoter cloning	
	1329pro_Fwd	5' CGGGATCCTTGAATGCCACACACAAAG 3'
	1329pro_Rev	5' CGGGATCCCTTCGATTAGCTTTTGTAAATC 3'
4	sqRT-PCR primers for Gus	
	Gus_Fwd	5' CTACCGTACCTCGATTACCC 3'
	Gus_Rev	5' CGCTTTGGACATACCATCCG 3'
5	sqRT-PCR primers for GFP	
	GFP_Fwd	5' CGGGATCCATGGTAGATCTGACTAGTAAAG 3'
	GFP_Rev	5' GTGCCGCTTCATATGATCTGG 3'
6	Primers for mutant zygosity analysis	
	Salk_LP	5' TCTTTTCAGTACCACCCATCG 3'
	Salk_RP	5' GAGAACAAGATTGTCGCGATC 3'
	pROK2_LbP	5' GCGTGGACCGCTTGCTGCAACT 3'
7	Primers for AtClpB-C Q-PCR analysis	
	At101_F	5' TCTTGAACAGGCTTGACGAGATT 3'
	At101_R	5' GAAGCCGAGCTACTTTCCTCAAC 3'
8	Primers for AtCK Q-PCR analysis	
	AtCK_F	5' TCGAGCAGTATTGGTTAACAAAGC 3'
	AtCK_R	5' TCTTCTGGGTTGGGTCCATAG 3'