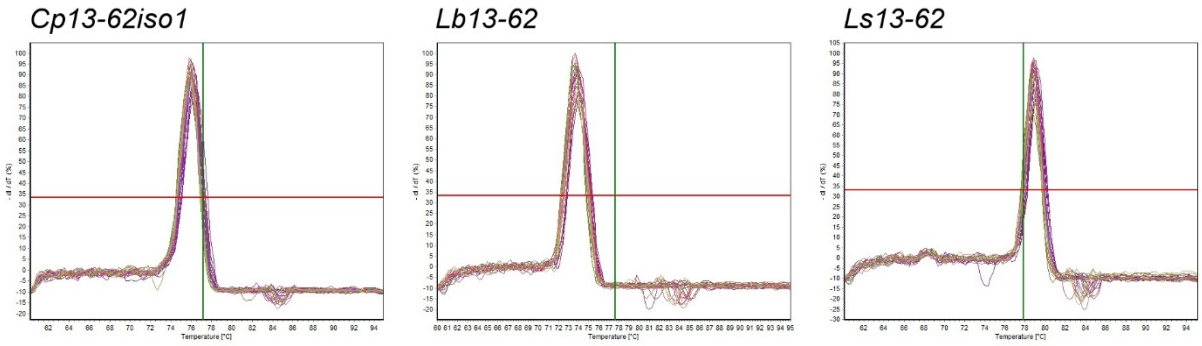
Supplementary Table S1 List of primers used in this study.

	Primer	Sequence (5´-3´)
Genome walking	Cp13-62GW_iso1_R1	GAAGAACTCGGCTTCAAGCAACTC
	Cp13-62GW_iso1_R2	GTTCAAAGGGAACTCTAAGAGACTAA
	Cp13-62GW_iso2_R1	GGGTTGGAATCTTGGCATAGCTC
	Cp13-62GW_iso2_R2	GCCAATATGGAAGTGCTGCAAAG
	Ls13-62GW_R1	TTATTATTAATGCGGCGGCGAAGGT
	Ls13-62GW_R2	TCGTTTTCTTTCTTTGCTGGGTCGT
Gene cloning	Cp13-62g_iso1_F	CAAACGGAGGGCTAGATTCAT
	Cp13-62g_iso2_F	CCTTCTTCGAAGCTTCATCAC
	Cp13-62g_iso1+2_rev	CTAAAACACACAGCCATGTACGA
	Lb13-62g_F	ACTCCACCGGTCCACTTCTTC
	Lb13-62g_R	TTCGGTAAATCGTGGGAGAAAAGAGAG
	Lb13-62g2_F	GTGAAGATCATCTAGATCAACGTACGAG
	Ls13-62g_F	CAACCCCTCGAGAAACCTAA
	Ls13-62g_R	CATGCATGCAAGACGATTATT
GUS analysis	Cp13-62p_F	CACT**TCTAGA**TCTCCCACTTCTTCTT
	Cp13-62p_iso1+2_frag_F	ACCC**TCTAGA**GCTATTACTCGTCTG
	Cp13-62p_R	TGTG**CCATGG**TTTGCTGCTGTG
	Lb13-62p_F	GTGT**GTCGAC**CATCTAGATCAACGTACG
	Lb13-62p_frag_F	GAAA**TCTAGA**TTACTCGTCAGCCATCCA
	Lb13-62p_R	TGTG**CCATGG**TTGATGCTGCGGCTTGA
	Ls13-62p_F	CACT**TCTAGA**TCTCCCACTTCTTTGCT
	Ls13-62p_R	TGTG**CCATGG**TGCGCGGCGCGT
Mutagenesis	Cp13-62p_iso1_c845t_F	GGTTCTACACCTGTCAGGCTTTCGACGGAGG
	Cp13-62p_iso1_c845t_R	CCTCCGTCGAAAGCCTGACAGGTGTAGAACC
	Cp13-62p_iso2_c904t_F	CTCCGGCCAAAGCCTGACAGCTGTAGAAC
	Cp13-62p_iso2_c904t_R	GTTCTACAGCTGTCAGGCTTTGGCCGGAG
	Lb13-62_c662t_R	AGTTTTTACACGTGTCAGGCTGTGGCGGAAGG
	Lb13-62_c662t_F	CCTTCCGCCACAGCCTGACACGTGTAAAAACT
	Ls13-62_c623t_F	TCGACACCTGTCGGGCTGCCGCCG
	Ls13-62_c623t_R	CGGCGGCAGCCCGACAGGTGTCGA
RT-qPCR	Cp13-62iso1_qPCR_F	GCAAATCGCCAAGTCTCATT
	Cp13-62iso1_qPCR_R	CATCATCGTCGTCACTGCTT
	Lb13-62_qPCR_F	CATCTCCATGGTCCTTTAAGC
	Lb13-62_qPCR_R	TCCTAAACACACTCAGCCACA
	Ls13-62_qPCR_F	GTACTCGCCGGAGATGAAAA
	Ls13-62_qPCR_R	TCGTTCCCACTCCCATAGAC
RT-PCR	Cp13-62iso1_RT-PCR_F	CCTGGCATCATGAGAAGGAT
	Cp13-62iso1_RT-PCR_R	GAACTCTGAATCGCCCTGAC
	Lb13-62_RT-PCR_F	AACCTCAGGCAACATACTCG
	Lb13-62_RT-PCR_R	CCTAAACACACTCAGCCACA
	Ls13-62_RT-PCR_F	TGAGAAACAAGCTGGGGAAC
	Ls13-62_RT-PCR_R	AGGTGAGATCTGGCGATTTG
	CpEF1α_RT-PCR_F	AGTCAAGTCCGTCGAAATGC

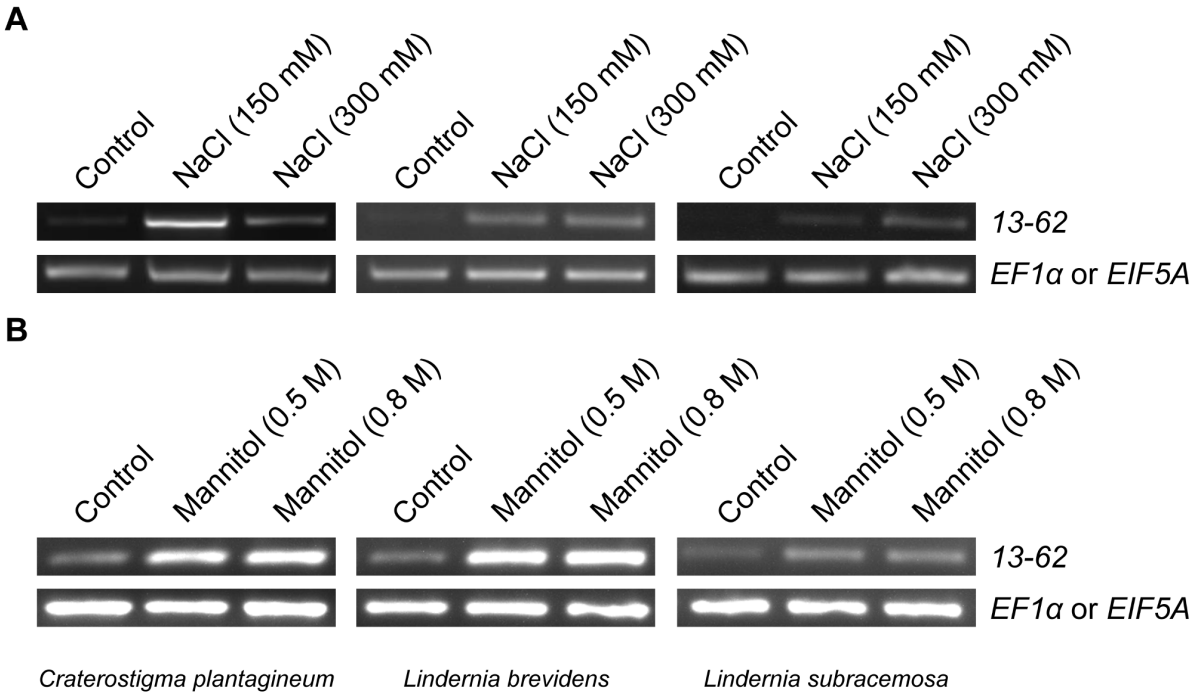
RT-PCR	CpEF1α_RT-PCR_R	CACTTGGCACCCTTCTTAGC
	LbEIF5A_RT-PCR_F	GGGAAAGGACCTTGTTGTGA
	LbEIF5A_RT-PCR_R	TGGGCTCATTACTCCACTGA
	LsEIF5A_RT-PCR_F	TGGGTGGTTTTTATCAATGTCC
	LsEIF5A_RT-PCR_R	GGTTGAGTGATAACACAGTAGCAAA
	Ot13-62_RT-PCR_F	ACACCGCAGGCCAAGAAG
	Ot13-62_RT-PCR_R	TAGATGAAGCTCCTGGCGATG
	OtALAD_RT-PCR_F	GATGAGGCAGAAGGAGCAGAT
	OtALAD_RT-PCR_R	GGCGAAGTAGGACAGGATGAT

Supplementary Figure S1



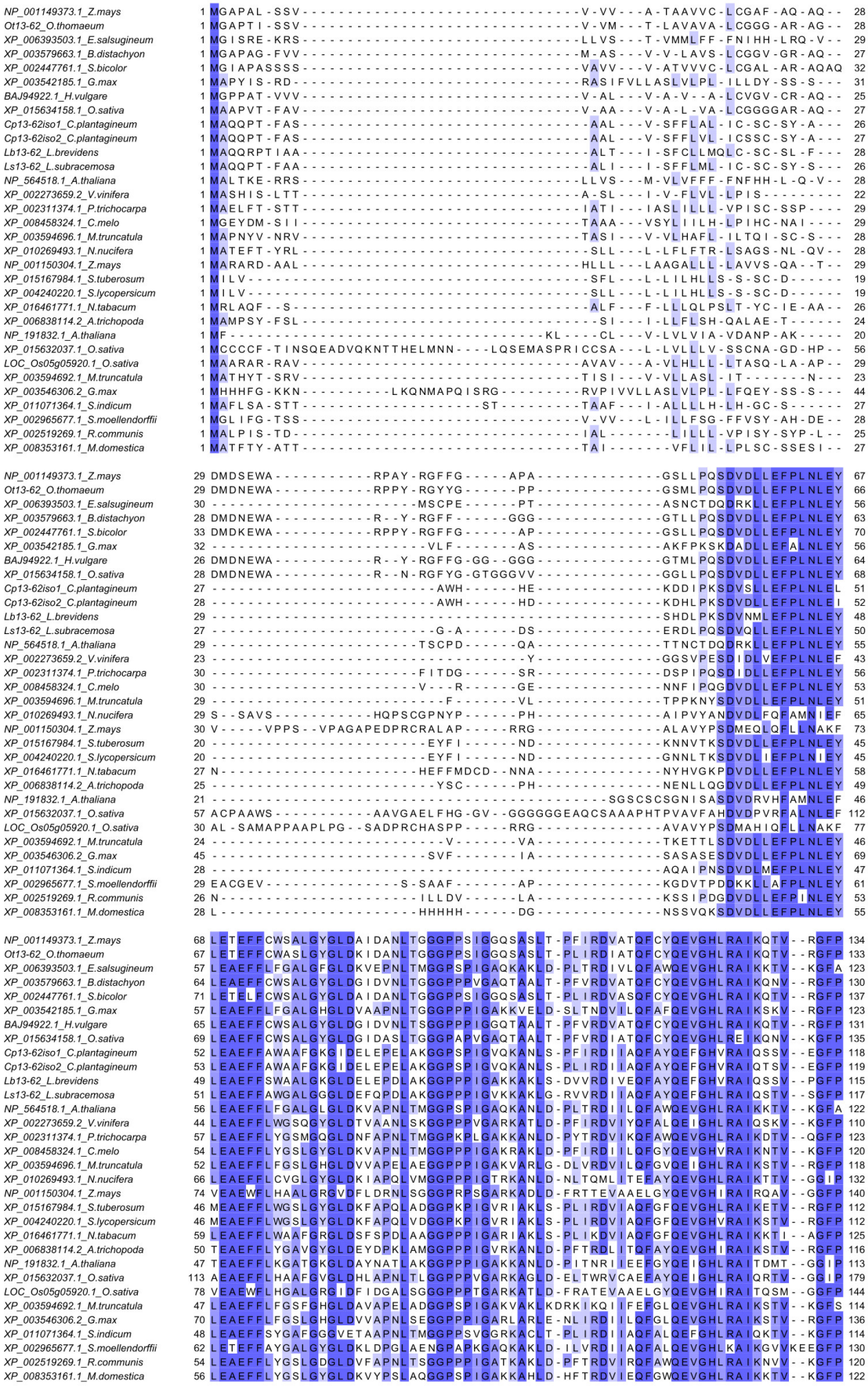
Supplementary Figure S1 Specificity of the primer pairs used to amplify *13-62* in RT-qPCR amplifications. Dissociation curves were obtained from three biological repeats with three technical repeats each.

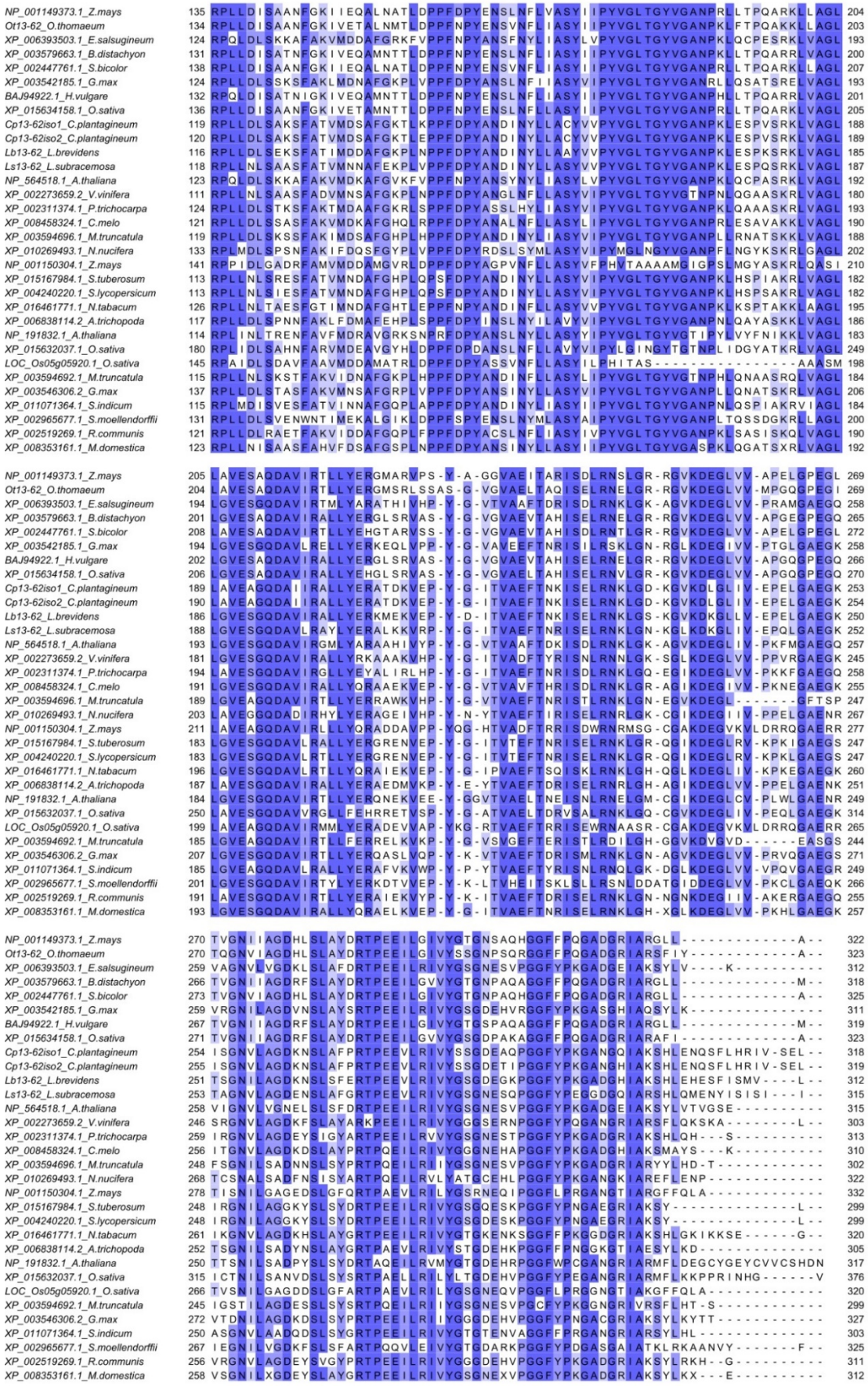
Supplementary Figure S2



Supplementary Figure S2 RT-PCR analysis of *Craterostigma plantagineum*, *Lindernia brevidens*, and *Lindernia subracemosa 13-62* expression in response to salt and osmotic stress. (A) 13-62 expression in response to salt treatments. cDNA was prepared from detached leaves incubated for 24 h in water (control), or in either 150 mM or 300 mM NaCl solutions (B) 13-62 expression in response to mannitol treatments. cDNA was prepared from detached leaves incubated for 48h in water (control), or in 0.5 M or 0.8 M mannitol solutions. cDNA samples in (A) and (B) were amplified with primers specific for the Cp13-62 (Cp13-62_RT-PCR_F and Cp13-62_RT-PCR_R), Lb13-62 (Lb13-62_RT-PCR_F and Lb13-62_RT-PCR_R), or Ls13-62 (Ls13-62_RT-PCR_F and Ls13-62_RT-PCR_R) transcripts. Expression of the elongation factor 1α (*EF1α*) gene or of the eukaryotic translation initiation factor 5A (*EIF5A*) gene was analysed as a control for cDNA preparations of *C. plantagineum* or *L. brevidens* and *L. subracemosa*, respectively. All primer sequences are listed in Supp. Table 1.

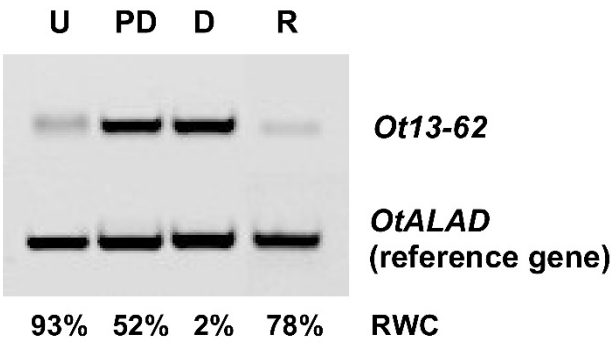
Supplementary Figure S3





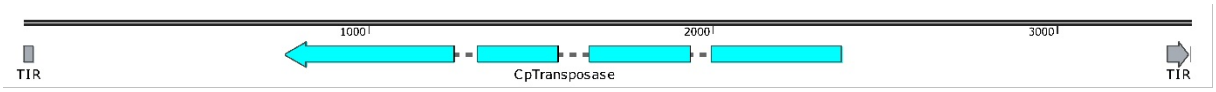
Supplementary Figure S3 Alignment of amino acid sequences of *13-62* protein homologs in selected Embryophyta.

Supplementary Figure S4



Supplementary Figure S4 RT-PCR analysis of *Oropetium thomaeum 13-62* (*Ot13-62*) expression during dehydration and rehydration. cDNA was prepared from untreated (U), partially dehydrated (PD), desiccated (D), and 24 h rehydrated (R) leaves and amplified with primers specific for the *Ot13-62* transcript (Ot13-62_RT-PCR_F and Ot13-62_RT-PCR_R, Supp. Table 1). Transcript expression of the aminolevulinic acid dehydratase (ALAD) was analysed as a control for cDNA preparations. Relative water content (RWC) of leaves used for cDNA preparations is indicated.

Supplementary Figure S5



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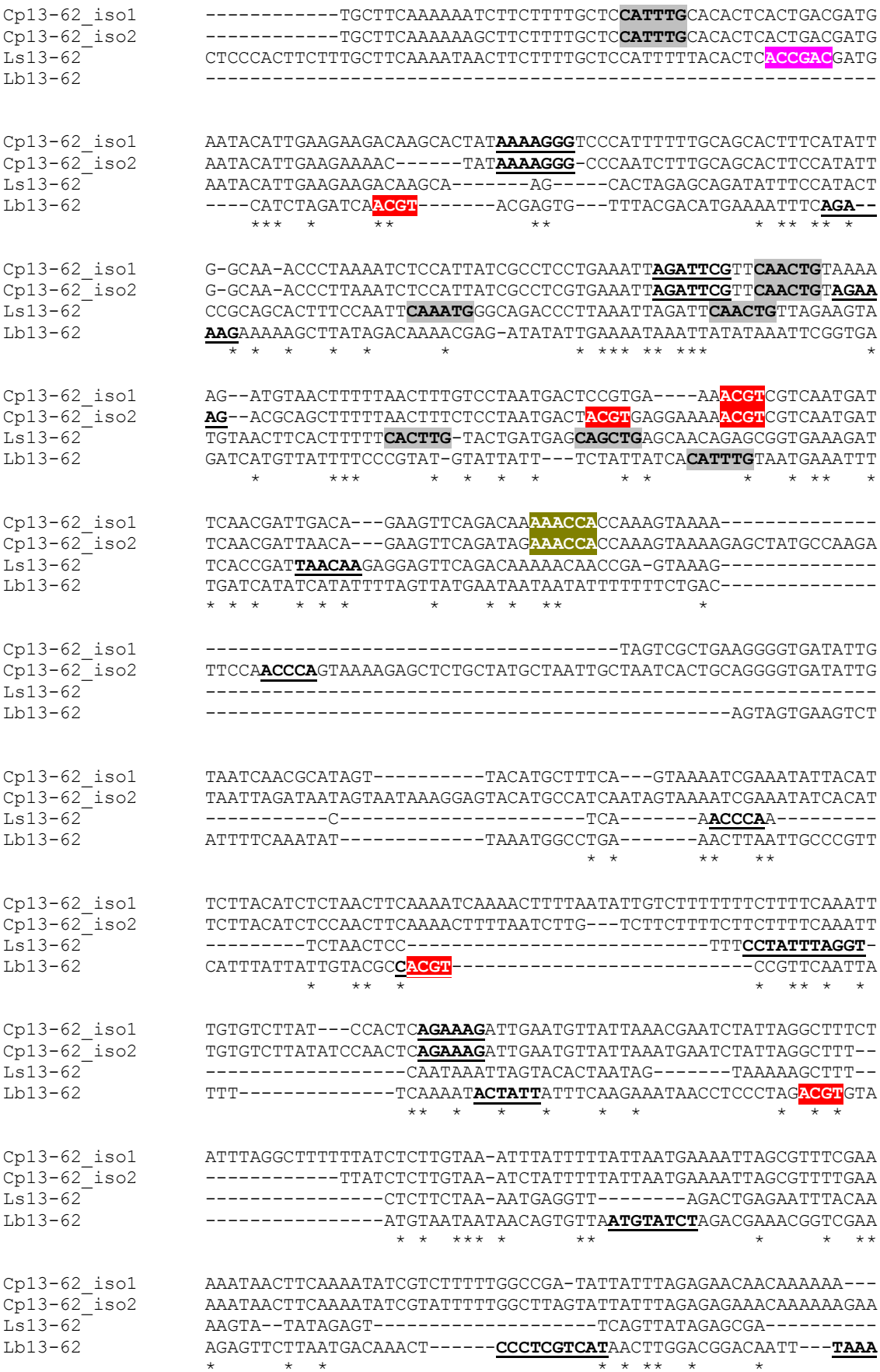
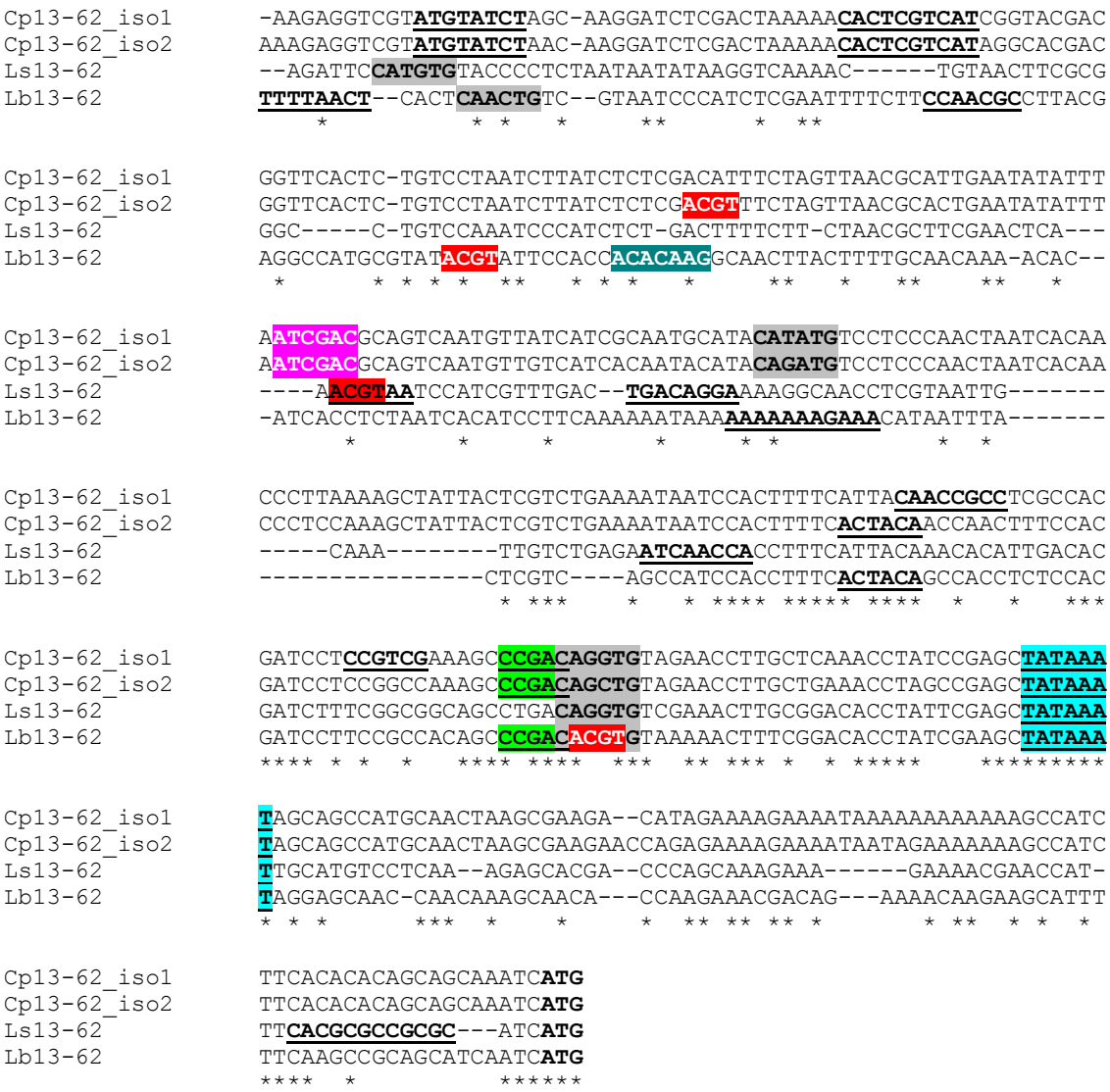
Supplementary Figure S5 Sequence of the transposable element identified in the *Lb13-62* genomic locus. Putative terminal inverted repeat (TIR) sequences and transposase coding sequence are indicated in grey and light blue, respectively.

Supplementary Figure S6





Name	Consensus sequence	Name	Consensus sequence
TATA Box	TATAAAT	BPC1	AGAAAG
ABRE	ACGT	ARR10	AGATTCG
DRE (DREB1B)	CCGAC	GAMYB	CAACCGCC
MYB1AT	WAACCA	HSFA1E	CCGTCG
DRECRTCOREAT	RCCGAC	MYB-15	TAACAA
CBFHV -CRT/DRE	ATCGAC	ASR-1	ACCCA
DPBF	ACACAAG (ACACNNG)	AGL15	TTTCCTATTTAGGT
MYCCONSENSUSAT	CANNTG	NAC6	ACGTAA
MYC (erd1)	CATGTG	ATH1	TGACAGGA
MYC (rd22)	CAGCTG	At4g36620	ATCAACCA
ATHSFA1D	ACTACA	ERF13	CACGCGCCGCGCA
DOF	AAAAAAAGAAA	OCSBF-1	CACGT
TEIL	ATGTATCT	HSFA4A	ACTATT
HBP-1a	CCCTCGTCAT/CACTCGTCAT	GT-1	TAAATTTTAACT
PBF	AAAAGGG	At5g54070	CCAACG

Supplementary Figure S6 Putative *cis*-acting elements identified in the *13-62* promoter. *13-62* promoter sequences were aligned with ClustalX software. Putative abscisic acid (ABA)- and dehydration-responsive and ABA were identified from

promoter sequences and are indicated on the sequence alignment. The translational start codon is indicated in bold.