

Table S1. Identification of SUSs in *I. batatas*, *I. trifida*, and *I. triloba*.

	Gene Name	Gene ID	Chr.	Gene Position
<i>I. batatas</i>	<i>IbSUS1</i>	<i>g505.t1</i>	LG1	2793890-2798579
	<i>IbSUS2</i>	<i>g5497.t1</i>	LG2	8562714-8568830
	<i>IbSUS3</i>	<i>g29617.t1</i>	LG7	31576704-31580891
	<i>IbSUS4</i>	<i>g30039.t1</i>	LG7	34437879-34441970
	<i>IbSUS5</i>	<i>g31210.t1</i>	LG8	5471709-5476663
	<i>IbSUS6</i>	<i>g55056.t1</i>	LG13	27660772-27665566
	<i>IbSUS7</i>	<i>g55074.t1</i>	LG13	27792067-27797658
	<i>IbSUS8</i>	<i>g55342.t1</i>	LG13	29268770-29272895
	<i>IbSUS9</i>	<i>g60893.t1</i>	LG15	6468996-6473927
<i>I. trifida</i>	<i>ItfSUS1</i>	<i>Itf05g23040.t1</i>	Chr05	23388562-23393210
	<i>ItfSUS2</i>	<i>Itf04g24160.t1</i>	Chr04	25686043-25692389
	<i>ItfSUS3</i>	<i>Itf03g05100.t1</i>	Chr03	3101581-3105775
	<i>ItfSUS4</i>	<i>Itf11g07860.t1</i>	Chr11	4351197-4356462
	<i>ItfSUS5</i>	<i>Itf02g04900.t1</i>	Chr02	6055942-6060284
	<i>ItfSUS6</i>	<i>Itf02g07130.t1</i>	Chr02	7203732-7209455
	<i>ItfSUS7</i>	<i>Itf06g18950.t1</i>	Chr06	21194480-21199532
<i>I. triloba</i>	<i>ItbSUS1</i>	<i>Itb05g23720.t1</i>	Chr05	28786401-28791478
	<i>ItbSUS2</i>	<i>Itb04g23580.t1</i>	Chr04	28590171-28596707
	<i>ItbSUS3</i>	<i>Itb03g05100.t1</i>	Chr03	3419915-3424462
	<i>ItbSUS4</i>	<i>Itb11g08290.t1</i>	Chr11	5423033-5428557
	<i>ItbSUS5</i>	<i>Itb02g00230.t1</i>	Chr02	198892-202920
	<i>ItbSUS6</i>	<i>Itb02g02420.t1</i>	Chr02	1386690-1392450
	<i>ItbSUS7</i>	<i>Itb06g17400.t1</i>	Chr06	21252081-21257133

Table S2. Primers used in this study.

Gene	Forward Primer	Reverse Primer
<i>actin</i>	AGCAGCATGAAGATTAAGGTTGT AGCAC	TGGAAAATTAGAAGCACTTCCTGT GAAC
<i>IbSUS1</i>	AACAAAATGCGACCAGGAAC	ACCAAATTCCTCATCGGTGTA
<i>IbSUS2</i>	AGGTGTTTGGGAGTTTGTGC	ACCCCATTTCCAATTGATGA
<i>IbSUS3</i>	TCAATCTGGTTGTGGTTGGA	GCGGTAGAGTTCGCTGTTTC
<i>IbSUS4</i>	GTGGTTGGAGGTTCTTTGA	GCGGTAGAGTTCGCTGTTTC
<i>IbSUS5</i>	GAACAGGCTGCTGAGCTCTT	CGCCATAACTTGCGGTATTT
<i>IbSUS6</i>	AACTAGGTTGTTGCCGGATG	GCAACATCCTCGGTGAAAGT
<i>IbSUS7</i>	CCTGCCAATGGTAACTTCGT	CGTCTTGCCCTTGTTATTGGT
<i>IbSUS8</i>	TTCTTGCCAATTCACAGCAG	TGCCTGAAACAACCTCTGCAC
<i>IbSUS9</i>	GCCAACCCTTACCAAGTCAA	GGACGTTTTGGAGTGTCGTT

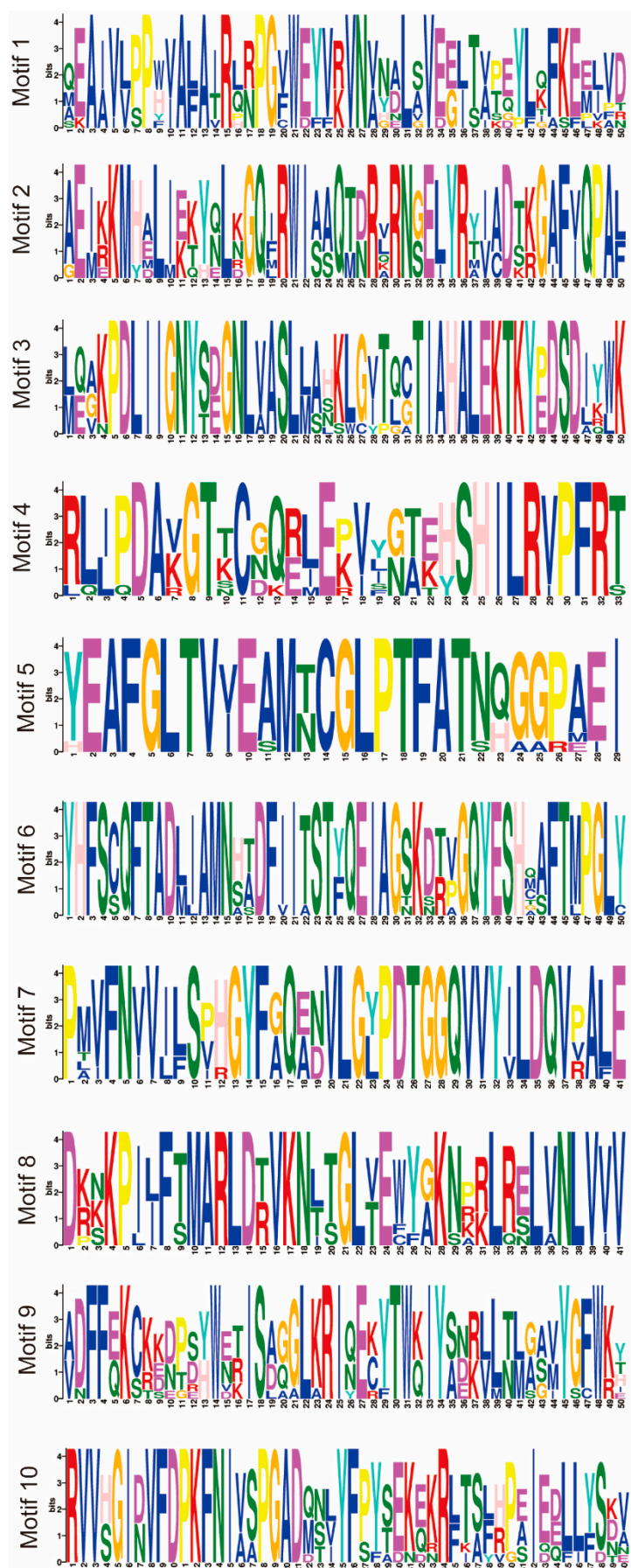


Figure S1. Sequence logos of the 10 conserved motifs.

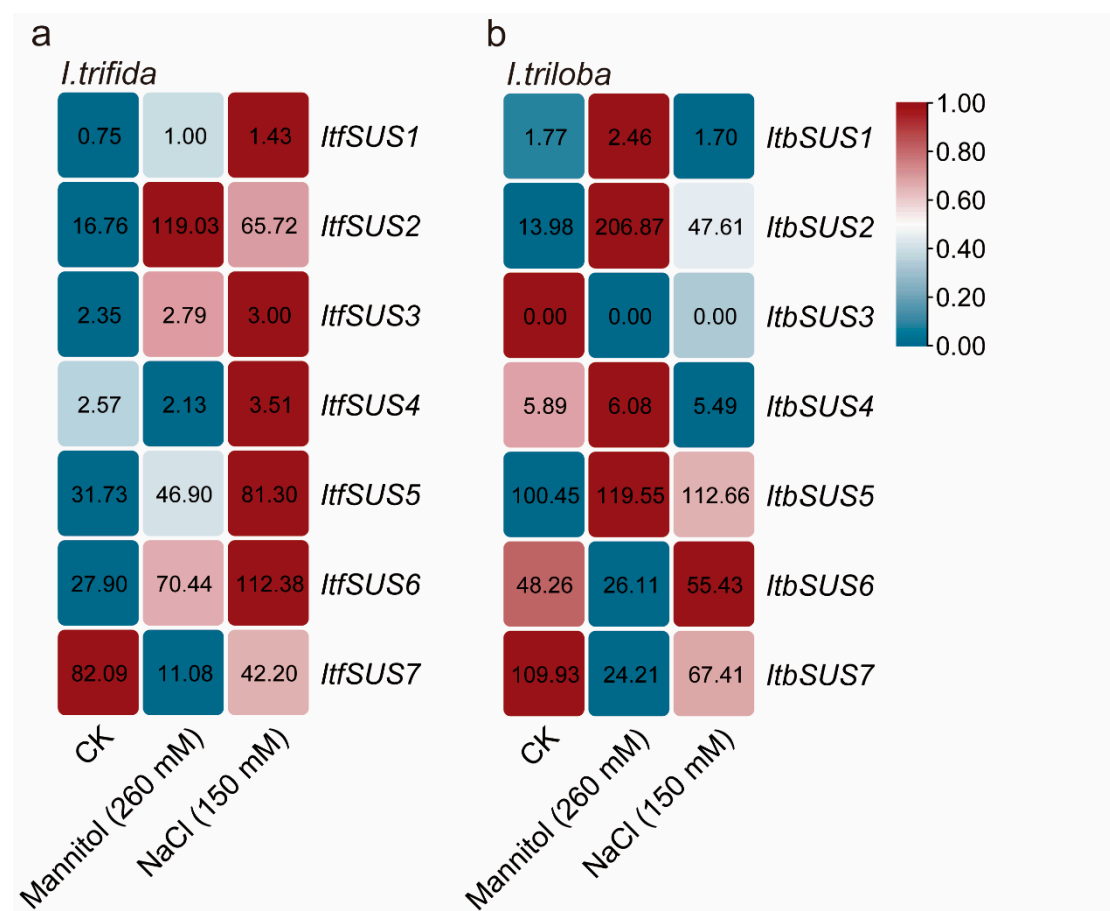


Figure S2. Expression analysis of *ItfSUS*s (a) and *ItbSUS*s (b) in response to drought and salt stresses as determined by RNA-seq. FPKM values are shown in the boxes.

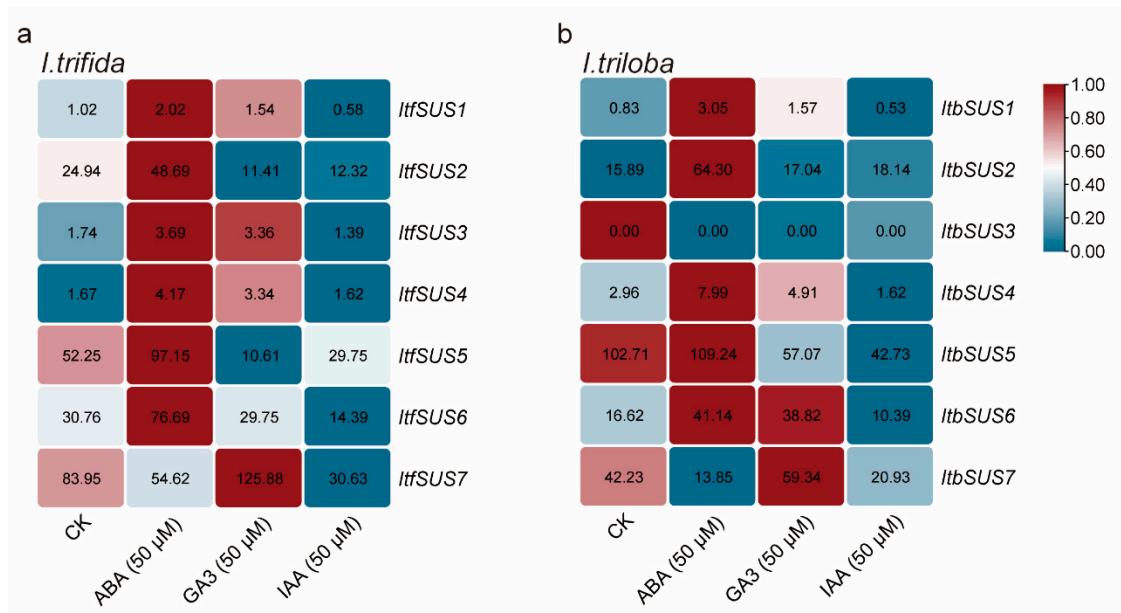


Figure S3. Expression analysis of *ItfSUSs* (**a**) and *ItbSUSs* (**b**) in response to different hormones (ABA, GA3, and IAA) as determined by RNA-seq. FPKM values are shown in the boxes.