Table S1. *IbBAGs* homologous genes in Tanzania genome.

Gene	Tanzania Hap-A	Tanzania Hap-B	Tanzania Hap-C	Tanzania Hap-D	Tanzania Hap-E	Tanzania Hap-F
IbBAG1	*Ibat.Tzn_v2.05AG015480.1*	*Ibat.Tzn_v2.05CG015580.1*	*Ibat.Tzn_v2.05DG015700.1*		*Ibat.Tzn_v2.05FG014950.1*	*Ibat.Tzn_v2.05AG015480.1*
IbBAG2	*Ibat.Tzn_v2.05AG029870.1*	*Ibat.Tzn_v2.05BG000990.1*	*Ibat.Tzn_v2.05CG000740.1*	*Ibat.Tzn_v2.05DG001450.1*		*Ibat.Tzn_v2.05EG000670.1*
IbBAG3	*Ibat.Tzn_v2.13AG004740.1*	*Ibat.Tzn_v2.13CG004830.1*	*Ibat.Tzn_v2.13DG004570.1*	*Ibat.Tzn_v2.13EG005310.1*	*Ibat.Tzn_v2.13FG004680.1*	*Ibat.Tzn_v2.13AG004740.1*
IbBAG4	*Ibat.Tzn_v2.12AG022340.1*	*Ibat.Tzn_v2.12CG026600.1*	*Ibat.Tzn_v2.12DG024550.1*	*Ibat.Tzn_v2.12EG028340.1*	*Ibat.Tzn_v2.12FG024760.1*	*Ibat.Tzn_v2.12AG022340.1*
IbBAG5	*Ibat.Tzn_v2.12AG023470.1*	*Ibat.Tzn_v2.12BG025080.1*	*Ibat.Tzn_v2.12CG027020.1*		*Ibat.Tzn_v2.12EG028760.1*	*Ibat.Tzn_v2.12FG025260.1*
IbBAG6	*Ibat.Tzn_v2.01AG006180.1*	*Ibat.Tzn_v2.10BG006020.1*	*Ibat.Tzn_v2.06CG021770.1*	*Ibat.Tzn_v2.15DG014340.1*		*Ibat.Tzn_v2.15FG015460.1*
IbBAG7		*Ibat.Tzn_v2.03BG027040.1*		*Ibat.Tzn_v2.03EG030000.1*	*Ibat.Tzn_v2.03FG035200.1*	
IbBAG8	*Ibat.Tzn_v2.03AG030970.1*	*Ibat.Tzn_v2.03BG026520.1*	*Ibat.Tzn_v2.03DG028400.1*	*Ibat.Tzn_v2.03EG029610.1*	*Ibat.Tzn_v2.03FG034260.1*	*Ibat.Tzn_v2.03AG030970.1*
IbBAG9	*Ibat.Tzn_v2.11AG000870.1*	*Ibat.Tzn_v2.11BG000280.1*	*Ibat.Tzn_v2.11CG000720.1*		*Ibat.Tzn_v2.11EG000360.1*	
IbBAG10	*Ibat.Tzn_v2.10AG019300.1*	*Ibat.Tzn_v2.10CG017990.1*	*Ibat.Tzn_v2.10DG024450.1*	*Ibat.Tzn_v2.10EG019630.1*	*Ibat.Tzn_v2.10FG020210.1*	*Ibat.Tzn_v2.10AG019300.1*
IbBAG11		*Ibat.Tzn_v2.08BG008200.1*	*Ibat.Tzn_v2.08CG010360.1*	*Ibat.Tzn_v2.08DG010550.1*	*Ibat.Tzn_v2.08EG010380.1*	*Ibat.Tzn_v2.08FG011200.1*
IbBAG12	*Ibat.Tzn_v2.01AG004900.1*	*Ibat.Tzn_v2.01BG006030.1*		*Ibat.Tzn_v2.01EG002170.1*	*Ibat.Tzn_v2.01FG006150.1*	*Ibat.Tzn_v2.01AG004900.1*
IbBAG13	*Ibat.Tzn_v2.07AG015660.2*	*Ibat.Tzn_v2.07BG012420.1*	*Ibat.Tzn_v2.07CG013870.1*	*Ibat.Tzn_v2.07DG013280.1*	*Ibat.Tzn_v2.07EG013900.2*	
IbBAG14	*Ibat.Tzn_v2.07AG015660.2*	*Ibat.Tzn_v2.07BG012420.1*	*Ibat.Tzn_v2.07CG013870.1*	*Ibat.Tzn_v2.07DG013280.1*	*Ibat.Tzn_v2.07EG013900.2*	
IbBAG15	*Ibat.Tzn_v2.09AG011320.1*	*Ibat.Tzn_v2.09BG008260.1*	*Ibat.Tzn_v2.09CG006910.2*	*Ibat.Tzn_v2.09DG009730.1*	*Ibat.Tzn_v2.09EG011030.3*	*Ibat.Tzn_v2.09FG009600.3*

Table S2. Identification of *BAG* family genes in *I. batatas*, *I. trifida*, and *I. triloba*.

Arabidopsis	**Homologous gene in *I. batatas*/ *I. trifida*/ *I. triloba***	**Gene ID**	**Gene name**
Group Ⅰ： *AT5G52060/AtBAG1* *AT5G62100/AtBAG2* *AT5G07220/AtBAG3*	*I. batatas*	*g1642.t1*	*IbBAG1*
		g20550.t1	*IbBAG5*
		g23383.t1	*IbBAG6*
		g25310.t1	*IbBAG7*
	I. trifida	*itf03g12810.t1*	*ItfBAG3*
		itf05g14330.t1	*ItfBAG6*
		itf12g25060.t1	*ItfBAG13*
	I. triloba	*itb03g13440.t1*	*ItbBAG3*
		itb05g14970.t1	*ItbBAG6*
		itb12g25410.t1	*ItbBAG13*
Group Ⅱ： *AT3G51780/AtBAG4* *AT1G12060/AtBAG5*	*I. batatas*	*g4176.t1*	*IbBAG2*
		g15882.t1	*IbBAG3*
		g34788.t1	*IbBAG10*
		g39432.t1	*IbBAG11*
		g46511.t1	*IbBAG12*
		g49380.t1	*IbBAG13*
		g49384.t1	*IbBAG14*
		g58853.t1	*IbBAG15*
	I. trifida	*itf01g03220.t1*	*ItfBAG1*
		itf03g01800.t1	*ItfBAG2*
		itf05g00940.t1	*ItfBAG5*
		itf07g14940.t1	*ItfBAG7*
		itf08g09020.t1	*ItfBAG8*
		itf09g09430.t1	*ItfBAG9*
		itf10g17930.t1	*ItfBAG10*
		itf13g03550.t1	*ItfBAG14*
	I. triloba	*itb01g03520.t1*	*ItbBAG1*
		itb03g01750.t1	*ItbBAG2*
		itb05g00360.t1	*ItbBAG5*
		itb07g16910.t1	*ItbBAG7*
		itb08g09640.t1	*ItbBAG8*
		itb09g10270.t1	*ItbBAG9*
		itb10g18190.t1	*ItbBAG10*
		itb13g05240.t1	*ItbBAG14*
Group Ⅲ： *AT2G46240/AtBAG6* *AT5G62390/AtBAG7*	*I. batatas*	*g20498.t1*	*IbBAG4*
		g25374.t1	*IbBAG8*
		g30328.t1	*IbBAG9*
	I. trifida	*itf03g13330.t1*	*ItfBAG4*
		itf11g00190.t1	*ItfBAG11*
		itf12g24570.t1	*ItfBAG12*

		itb03g13970.t1	*ItbBAG4*
	I. triloba	*itb11g00170.t1*	*ItbBAG11*
		itb12g24940.t1	*ItbBAG12*

Table S3. Primers used in this study.

Gene	Forward Primer	Reverse Primer
IbBAG1	GTGCAGAAACGGGGTCCA	CCCAGTTGGCCCTGTCAG
IbBAG4	AAGACGAGCTCGATGCCG	CGGTCACGGCATCCAAGT
IbBAG5	ACTCCACAGCAGCAGCAG	GTGGGCGTCGGAAAGTGA
IbBAG7	AACAACAGCCGGGGATGG	CTGCCCCGAGAGCTGAAG
IbBAG8	GGGTCTTGGCCCTGGAAC	CGCCGTCCACGTGTACTT
IbBAG9	CAAGGTCTGAAGGCGCCA	GGGGTTTTCTCCGCCGAA
IbBAG11	GAGGTTGTTTTCATGGCGGC	AGTGCTACCAACAATGGCAGA
IbBAG15	GGCGGTGAGGAAATCGCT	GGTAACAGTGGCGGCAGT

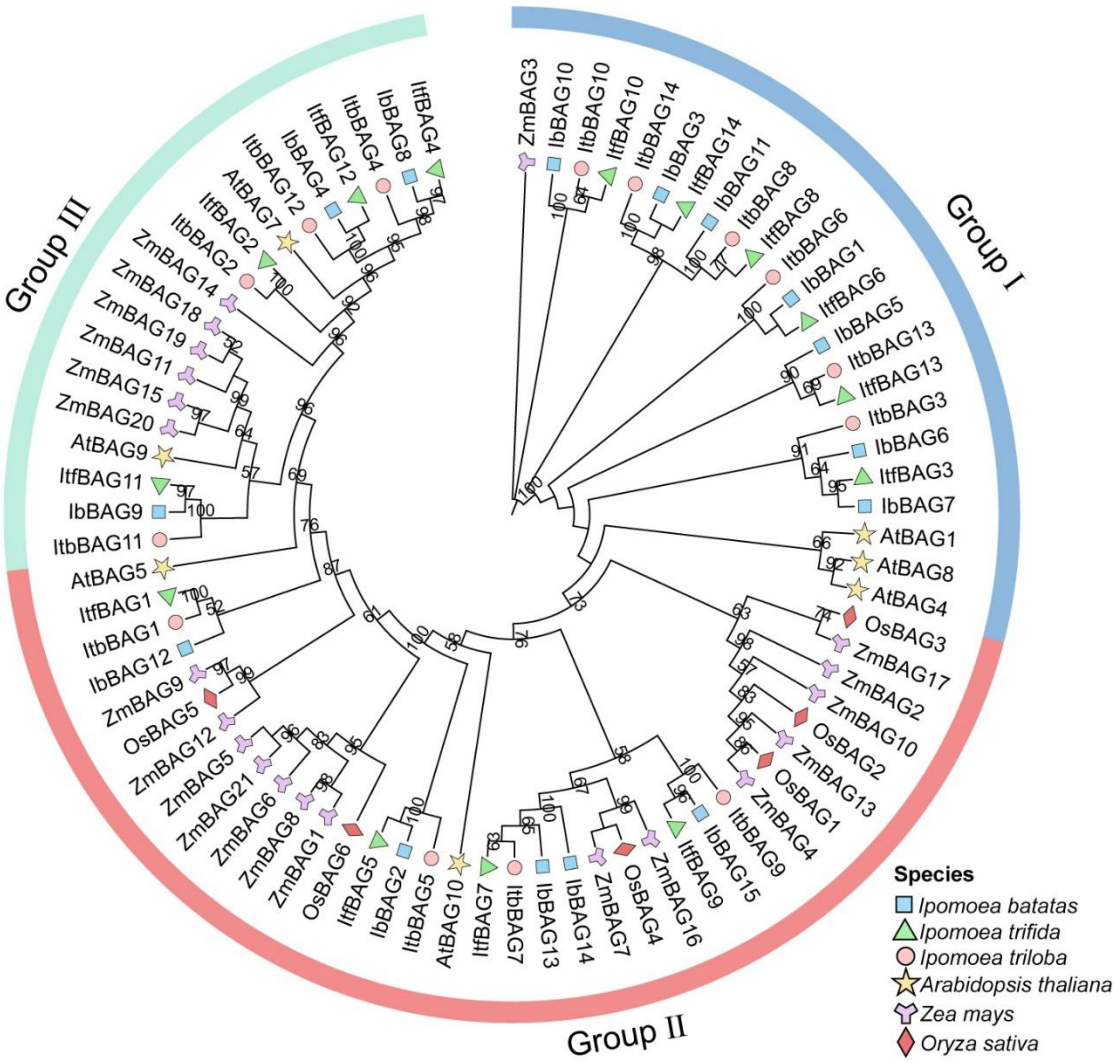

Figure S1. Phylogenetic analysis of the BAG proteins from seven plant species (i.e., *I. batatas*, *I. trifida*, *I. triloba, Arabidopsis thaliana, Oryza sativa* L., and *Zea mays*). A total of 77 BAGs were divided into three subgroups (Group Ⅰ to Group Ⅲ) according to the evolutionary distance. The pink circles, blue squares, green triangles, yellow stars, purple wyes and red diamonds respectively represent the 15 IbBAGs in *I. batatas*, 14 ItfBAGs in *I. trifida*, 14 ItbBAGs in I. *triloba*, 7 AtBAGs in *Arabidopsis thaliana*, 6 OsBAGs in *Oryza sativa* L., and 21 ZmBAGs in *Zea mays*.

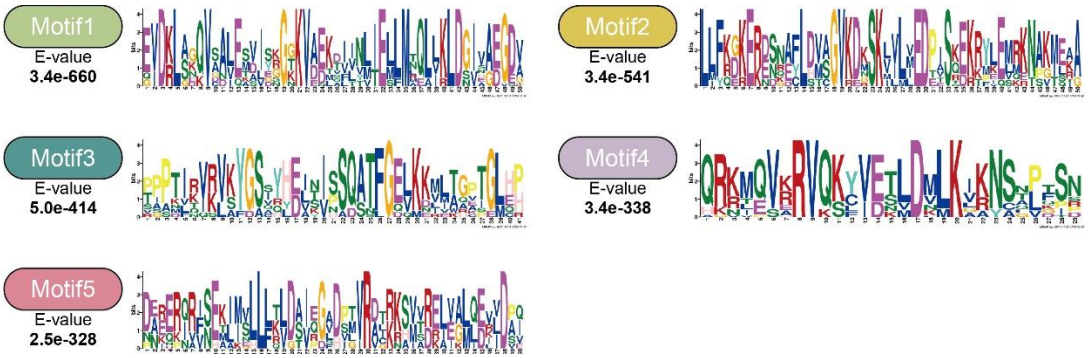

Figure S2. Conserved motifs analysis of IbBAGs in *I. batatas*.

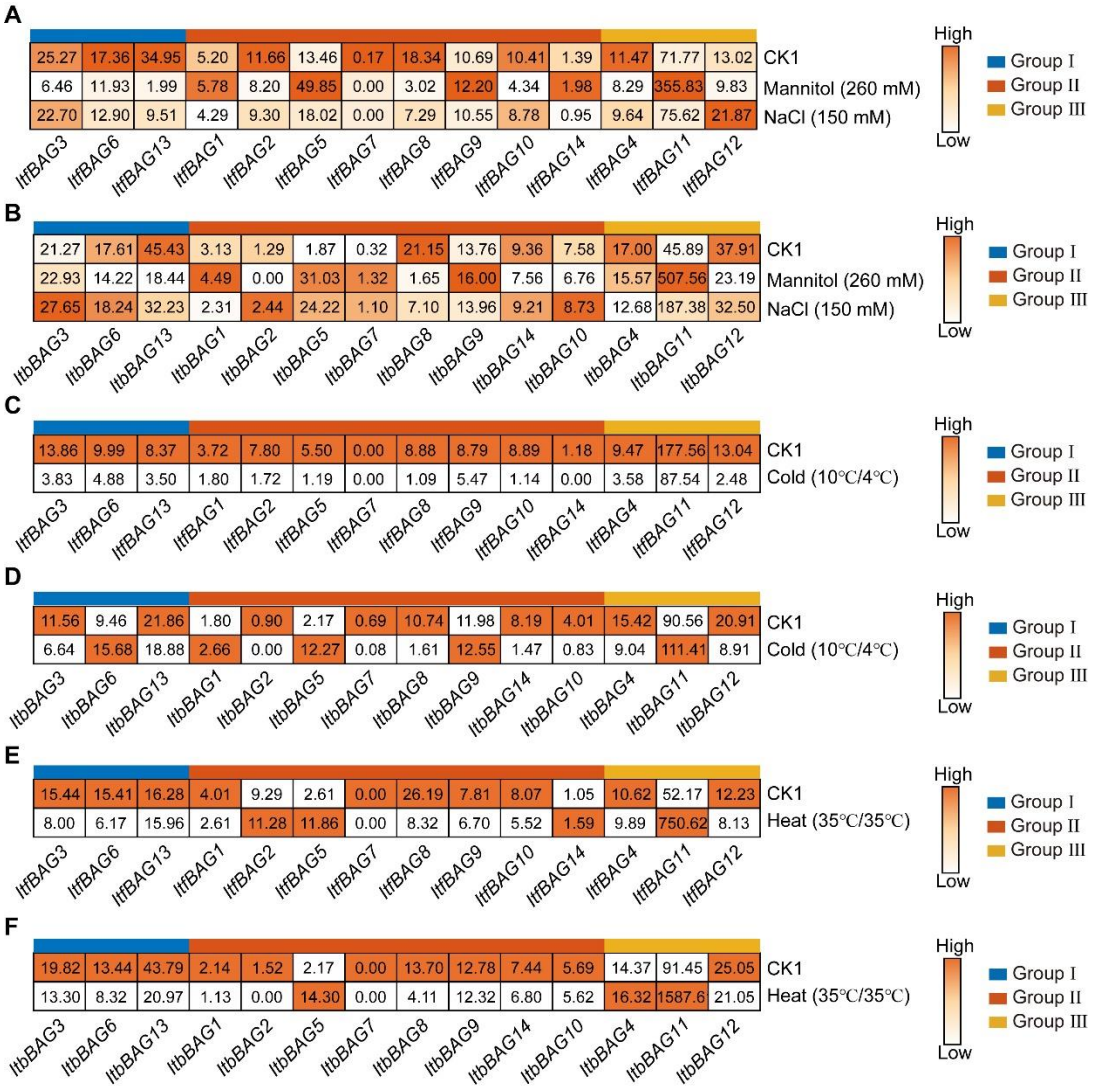

Figure S3. Gene expression patterns of *BAGs* in response to different abiotic stress (Mannitol, NaCl, cold and heat) in *I. trifida* and *I. triloba* as determined by RNA-seq. FPKM was shown in the boxes.