

Supplementary file S1

Table S1. Summary of studies on abiotic stress-related genes which contribute to enhancing abiotic stress tolerance in *Betula platyphylla*.

Gene name	Gene type	OE/RE	Family	Abiotic stress type	Dose/degree	Type of transformation	RNA extraction	Reverse transcription	High expression	Location	References
<i>BplMYB46</i>	TF	OE	R2R3-MYB	salt osmotic stress	200 mM NaCl for salt stress 200 mM mannitol for osmotic stress	Agrobacterium-mediated transformation	N.A.	N.A.	N.A.	nucleus	(Guo et al. 2018)
<i>BpHOX2</i>	TF	OE	HD-Zip 1	osmotic stress	9% (w/v) PEG6000	Agrobacterium-mediated transformation	N.A.	N.A.	mature stems and leaves	nucleus	(Tan et al. 2020)
<i>BplMYB46</i>	TF	OE	R2R3-MYB	salt stress osmotic stress	200 mM NaCl for 24 h 300 mM mannitol for 24 h	Particle bombardment	N.A.	N.A.	mature tissue of stems	nucleus	(Guo et al. 2017b)
<i>BpHMG6</i>		OE	High mobility group	salt stress	200 mM NaCl	N.A.	CTAB	PrimeScript™ RT reagent Kit (TaKaRa)	N.A.	nucleus	(Lei et al. 2021)

<i>BpHSP9</i>		OE	heat shock proteins	heat stress	37°C for 1.5, 3, 6, 12, 24, 48 or 72 h	Agrobacterium-mediated transformation	Plant RNeasy Extraction Kit (BioTeKe)	PrimeScript™ RT Reagent Kit (TaKaRa)	stem and leaves	chloroplast, nucleus, extracellular and mitochondria	(Liu et al. 2018)
<i>BpUVR8</i>		OE	UVR	UV-B radiation	1.5 μmol m ⁻² s ⁻¹	Agrobacterium-mediated transformation	CTAB	PrimeScript first-strand cDNA synthesis kit (Takara)	leaves	nucleus	(Li et al. 2018)
<i>BpBZR1</i>	TF	OE	BZR	salt stress	0.4 M NaCl for 6, 12, 24, 48, and 72 h	Agrobacterium-mediated transformation	RNeasy Extraction Kit (BioTeKe)	TranScript® One-Step gDNA Removal and cDNA Synthesis SuperMix (TransGen)	leaves	nucleus	(Lv et al. 2020a)
<i>BpERF13</i>	TF	OE	AP2/ERF	cold stress	4 °C	Agrobacterium-mediated transformation	CTAB	Prime-Script™ RT reagent kit with gDNA Eraser (Takara)	roots	nucleus	(Lv et al. 2019)
<i>BpIERD15</i>		OE	ERD	Drought stress	20% (w/v) PEG6000	Agrobacterium-mediated transformation	CTAB	Toyo Spinning Kit (TOYOBO SYBR qPCR Mix, QPS-201)	mature leaves	N.A.	(Lv et al. 2020b)

<i>BpMYB46</i>	TF	OE	MYB	salt stress osmotic stress	200 mM NaCl for 6, 12, 24, and 48 h 200 mM Mannitol for 6, 12, 24, and 48 h	Agrobacterium-mediated transformation	CTAB	PrimeScript™ RT reagent Kit (Takara Bio)	N.A.	nucleus	(Wang et al. 2019b)
LncRNA280 68.1 and LncRNA305 05.2	lncRNAs	OE		cadmium stress	600 μM CdCl ₂ for 24 h	Agrobacterium-mediated transformation	CTAB	TransScript One-Step gDNA Removal and cDNA Synthesis SuperMix (Transgen)	N.A.	N.A.	(Wen et al. 2020)
<i>BpERF2</i> and <i>BpMYB102</i>	TF	OE	AP2/ERF and MYB	drought stress	20% (w/v) PEG6000 for 48 h	Agrobacterium-mediated transformation	CTAB	Primescript™ RT reagent kit (Takara)	N.A.	N.A.	(Wen et al. 2019)
<i>BpERF11</i>	TF	RE	AP2/ERF	salt stress osmotic stress	50 mM NaCl for 2 h 100 mM mannitol for 2 h	Agrobacterium-mediated transformation	CTAB	PrimeScript™ RT Reagent Kit (Takara)	N.A.	nucleus	(Zhang et al. 2016)
<i>BpARF1</i>	TF	RE	ARF	drought stress	300 mM mannitol	N.A.	N.A.	N.A.	young leaves	nucleus or mitochondrial	(Li et al. 2020a)

<i>BpNAC012</i>	TF	OE	NAC	salt and osmotic stress	200 mM NaCl or 300 mM mannitol solution	Agrobacterium-mediated transformation	N.A.	PrimeScript™ RT Reagent Kit (Takara)	leaves	N.A.	(Hu et al. 2019)
<i>BpNAC002</i> , <i>BpNAC003</i> , <i>BpNAC004</i> , <i>BpNAC019</i> , <i>BpNAC025</i> , <i>BpNAC026</i> , <i>BpNAC032</i> , <i>BpNAC052</i> , <i>BpNAC054</i> , <i>BpNAC063</i> , <i>BpNAC092</i> , and <i>BpNAC108</i>	TF	OE	NAC	cold stress	4 °C for 0.5, 1, 2, 2.5, and 3 h	N.A.	CTAB	N.A.	roots and sylem	N.A.	(Chen et al. 2019)

BpIMYB46: *Betula platyphylla* myeloblastosis 46 gene; *BpHOX2*: *B. platyphylla* homeobox-leucine zipper 2 gene ; *BpHMG6*: *B. platyphylla* high-mobility group 6 gene; *BpHSP9*: *B. platyphylla* heat shock protein 9 gene; *BpUVR8*: *B. platyphylla* UV resistance locus 8 gene; *BpBZRI*: *B. platyphylla* brassinazole-resistant 1 gene; *BpERF13*: *B. platyphylla* ethylene response factor 13 gene; *BpLERD15*: *B. platyphylla* early response to dehydration 15 gene; *BpERF2*: *B. platyphylla* ethylene response factor 2 gene; *BpMYB102*: *B. platyphylla* myeloblastosis 102 gene; *BpERF11*: *B. platyphylla* ethylene responsive factor 11 gene; *BpARF1*: *B. platyphylla* auxin response factor 1 gene; *BpNACs*: *B. platyphylla* No apical meristem (NAM), Arabidopsis transcription activation factor (ATAF1/2), Cup-shaped cotyledon (CUC2) genes; LncRNA28068.1: Long non-coding RNAs 28068.1; LncRNA30505.2: Long non-coding RNAs 30505.2; OE:Over-expressing; RE: repressed-expressing;; PEG: Polyethylene glycol; NaCl: Sodium chloride; CTAB: Cetyltrimethylammonium Bromide; N.A.:no detailed comments