

Proteomics of Homeobox7 Enhanced Salt Tolerance in *Mesembryanthemum crystallinum*

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Supplementary data

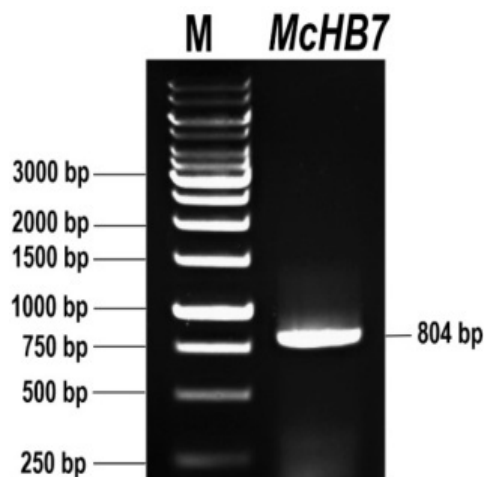


Figure S1 Cloning *McHB7* from ice plant leaves

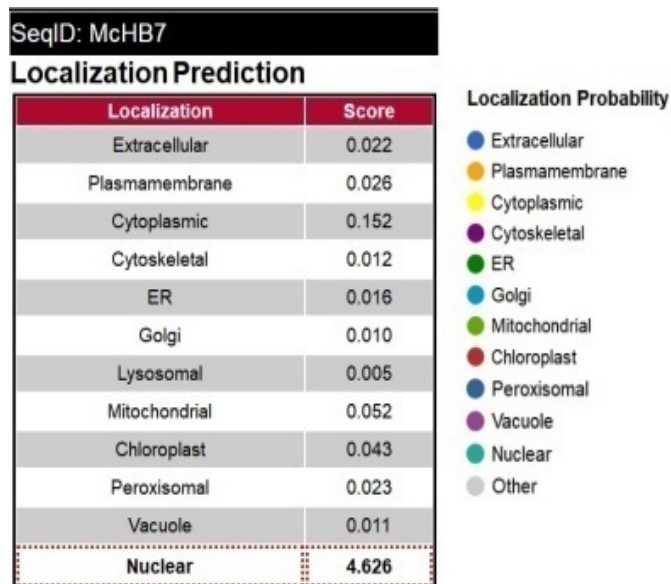


Figure S2 Subcellular localization prediction with CELLO2GO

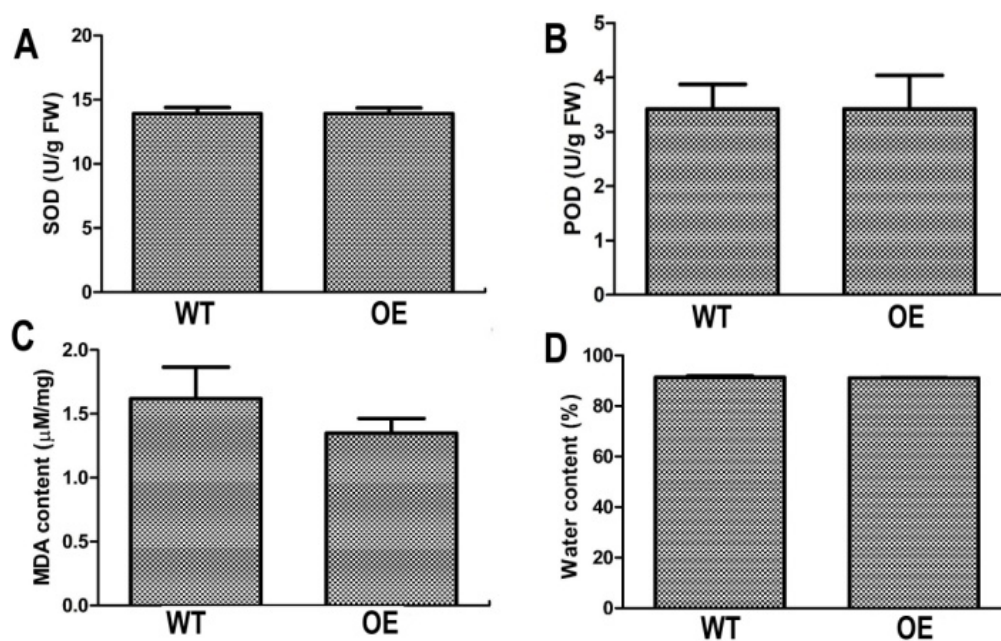
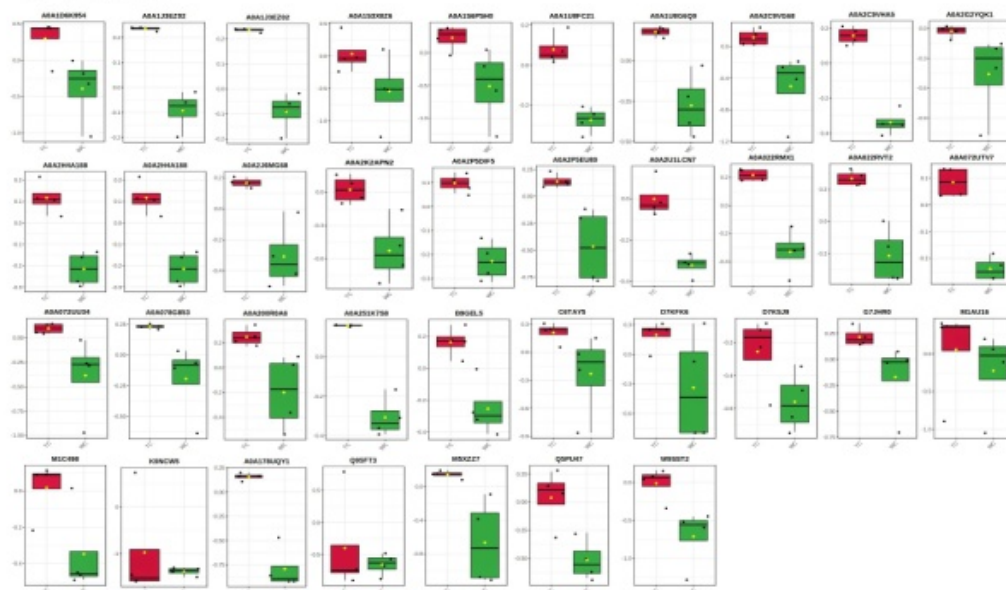


Figure S3 Physiological parameters in OE ice plant. (A) SOD activity of OE and WT ice plants. (B) POD activity. (C) MDA content. (D) Water content.

A OEC/WTC



B OES/WTs



Figure S4 Significantly increased proteins in transgenic ice plant leaves under control and salt stress treatment. **(A)** Increased proteins under control conditions. **(B)** Increased proteins under salt stress conditions

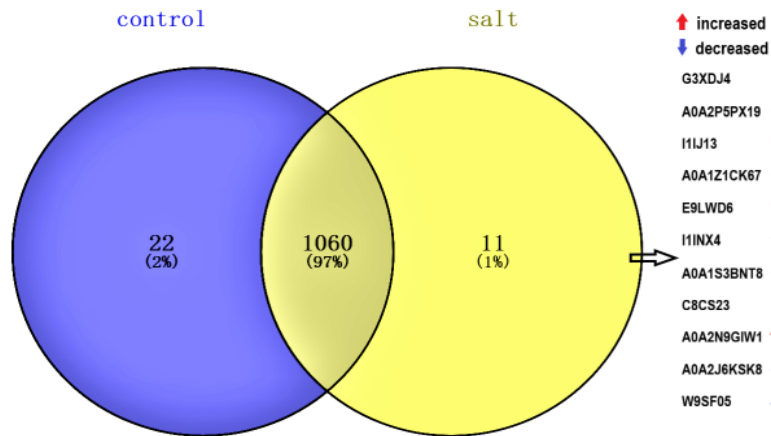


Figure S5 Identified proteins under control and salt stress conditions.

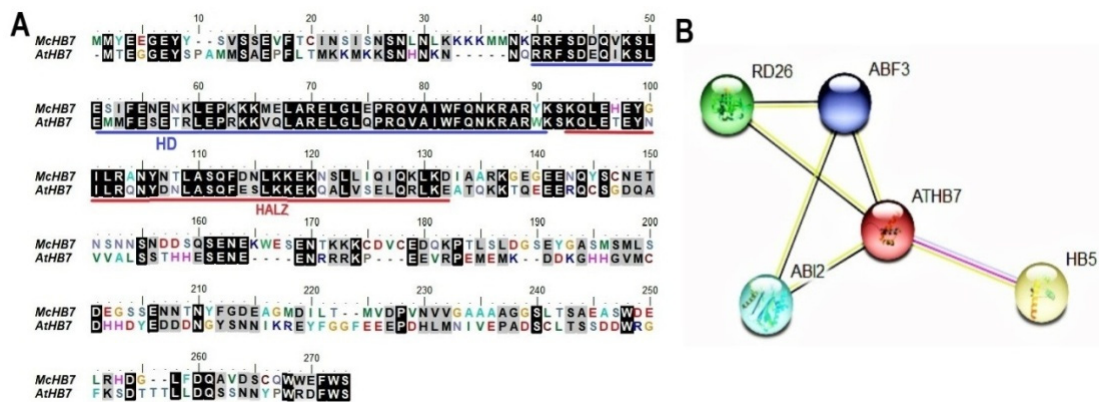


Figure S6 Alignment with *AtHB7* and *McHB7*. (A) Alignment of *AtHB7* and *McHB7*. (B) Protein-protein interaction network of *AtHB7*.

Table S1. List of primers sequences for cloning and quantitative real-time PCR

Gene name	Primer sequence(5'-3')
cMcHB7	F: ATGATGTATGAAGAAGGAGAA R: TCACGACCAAAATTTCCACCA
gMcHB7	F: CGCCCATGGATGATGTATGAAGAAGGAGAA R: CGGACTAGT CGACCAAAATTTCCACCATTG
McPIP1;2	F: GATGCCAAGAGGAGTGCTAG R: GTTCCAGTGATTGGGATGGTT
rtMcHB7	F: CGAGACGAACAGCAATAATAGT R: CTTCACACACATCGCATTCT
pMcHB7	F: CGCGGATCCATGATGTATGAAGAAGGAGAA R:CGGTCTAGATCAGGCGCCTTTGTCATCGTCATCCTTGTAGTCTCCGCC TTTATCGTCATCGTCTTTATAATCTCCGCCTTTGTCATCGTCATCCTTGTA GTCTCCGCCCGACCAAAATTTCCACCATTG

cMcHB7 was the primer for *McHB7* gene cloning; gMcHB7 was the primer for GFP ligation, the underlines were *NcoI* and *Spe I* restriction sites, respectively; McPIP1;2 was the internal primer for RT-qPCR; rtMcHB7 was the primer for *McHB7* quantification using RT-qPCR; and pMcHB7 was the primer for overexpression vector construction, the underlines were *Bam HI* and *XbaI*, respectively.

Table S2 Posphorylated proteins

Accession	Description	Peptides	Unique Peptides
Q40185	Chlorophyll a-b binding protein	4	2
A0A022RT96	Chlorophyll a-b binding protein	6	2
A0A078II53	Glutamine synthetase	3	2
A0A1D8DAB1	Ribulose biphosphate carboxylase large chain	2	2
A0A0A0QMA2	Ribulose biphosphate carboxylase large chain	3	3
B8BPB7	Uncharacterized protein	3	2
A0A1S4CJP2	ribulose biphosphate carboxylase/oxygenase activase 1, chloroplastic isoform X1	10	2
A0A087H1T9	Glutamine synthetase	2	2
A0A2R6XLV7	Uncharacterized protein	8	2
K4AXU0	Uncharacterized protein	13	2
A0A1Y0KLB7	Ribulose biphosphate carboxylase large chain	3	2
A0A2P6U3A8	Rubisco activase	3	2
Q2HW53	Ferredoxin-dependent glutamate synthase; Glutamate synthase, large subunit region 1 and 3, putative; Glutamate synthase	14	2
I3SU63	Fructose-bisphosphate aldolase	3	2
B9HKC1	Uncharacterized protein	4	3
A0A2P5AJP3	Chlorophyll a-b binding protein	6	2
A0A1S4BC47	Chlorophyll a-b binding protein	5	3
M7YTH1	Chlorophyll a-b binding protein	8	2
Q41423	Chlorophyll a-b binding protein	5	2
A0A2P5DIF5	Chlorophyll a-b binding protein	6	4
Q9TKH0	Ribulose biphosphate carboxylase large chain	3	2
A0A0S2LMW5	ATP synthase subunit beta	2	2
W1P4U4	Chlorophyll a-b binding protein	8	2
A0A178VDH1	CSP41A OS=Arabidopsis thaliana	4	2
M5X4I0	Malate dehydrogenase	6	2
K3YTH6	Uncharacterized protein	2	2
G0WYB2	Ribulose biphosphate carboxylase large chain	2	2
A0A0B5H5B4	Ribulose biphosphate carboxylase large chain	3	2
A0A1U8G7Q4	phosphoglucomutase	9	3
C5IFT7	Chlorophyll a-b binding protein	5	3
A0A218W3S5	Uncharacterized protein	6	2
B9HRB0	Uncharacterized protein	3	2
A0A2N9J3G3	Chlorophyll a-b binding protein	5	2
M1AAF6	Uncharacterized protein	4	4

Table S3 *Cis*-acting elements in the upstream promoter of *AtHB7*

site name	sequence	function
MBS	CAACTG	MYB binding site involved in drought-inducibility
as-1	TGACG	an Oxidative Stress-Responsive Element
WUN-motif	AAATTTCCT	wound-responsive element
ABRE	ACGTG	involved in the abscisic acid responsiveness
GARE-motif	TCTGTTG	gibberellin-responsive element
LAMP-element	CTTTATCA	part of a light responsive element
MRE	AACCTAA	MYB binding site involved in light responsiveness
GCN4_motif	TGAGTCA	involved in endosperm expression
CCAAT-box	CAACGG	MYBHv1 binding site
ACE	CTAACGTATT	involved in light responsiveness
TGACG-motif	TGACG	involved in the MeJA-responsiveness
GATA-motif	AAGATAAGATT	part of a light responsive element
GT1-motif	GGTTAA	light responsive element
ARE	AAACCA	<i>cis</i> -acting regulatory element essential for the anaerobic induction
TC-rich repeats	ATTCTCTAAC	defense and stress responsiveness
P-box	CCTTTTG	gibberellin-responsive element
LTR	CCGAAA	low-temperature responsiveness
TATC-box	TATCCCA	gibberellin-responsiveness
CAT-box	GCCACT	related to meristem expression
3-AF1 binding site	TAAGAGAGGA A	light responsive element
TCT-motif	TCTTAC	part of a light responsive element
G-box	TAACACGTAG	involved in light responsiveness
TCA-element	CCATCTTTTT	involved in salicylic acid responsiveness
Box 4	ATTAAT	part of a conserved DNA module involved in light responsiveness
O2-site	GATGATGTGG	involved in zein metabolism regulation
Sp1	GGGCGG	light responsive element
GA-motif	ATAGATAA	part of a light responsive element
CGTCA-motif	CGTCA	involved in the MeJA-responsiveness
AE-box	AGAAACAA	part of a module for light response
chs-CMA1a	TTACTTAA	part of a light responsive element
Box II	ACACGTAGA	part of a light responsive element