

## Supplementary Figure S5

### Content:

- A. Primers used for cloning of *NtMTP2* promoter
- B. *In situ* analysis of the promoter sequences including 5'UTR of *NtMTP2*

### A. Primers used for cloning of *NtMTP2* promoter

NtMTP2-prom-for	CAC CTG TTA GTG TTT AGG ATA GAG TAG
NtMTP2-prom-rev	GTT TAG AAG TTC TAT GAA ATT TGG GAG A

CACC – sequence added to clone the insert into the pENTR plasmid in proper orientation.

**Cloned promoter sequence of *NtMTP2* + 5'UTR + START codon** (contig AWOK01S500825.1 position 3015 ...4286 – without ATG),

**In red** - START codon.

Underlined - sequence of the forward primer and the sequence complementary to the reverse primer.

TGTTAGTGTGTTTAGGATAGAGTAGGATATTTTTCAAGAGGGGATTGCAACGTGAGATGGTTGTAAACCTGTAATGTCAGCAT  
GTTACATCACTTTATTCTGTTTTCCCAATCGATACCTTTAGATTACATGTCAACAGCAAAAAGAAGAAAAAAAAATGAAATTT  
AGCTCACTTGCAGTCATCCTAGTACTTTTTGGTAGAAGTGAAGATTATTTGCTAATTGAGTGTTTTTTTTTCGTGCAAAGGAT  
ATTGTGGAATCGGTCGATAATAAGTGACTTTTTGATCTCTTTATTTTGGTCCAAAATAATTGTCCTTTTATATAATCAAGA  
AAAAATTAATTTTTTTTTTTAAAATTCGTCCTTATTTATATATTTCAATTGTGTCAAGTTAATAATATGTAGATTTTAATTA  
AGGGTAATTTTTCAAATATTTTTTTCTATAAGAGTATTTTTTTAAGGGTGTGCCAAATACAAAATATTATTTATTAT  
GAATGGGAGGGAGTATAAATTAGTCCTGGTCAGGGGTTAACTATGCCTTGATTGAGTGGACTACTTTTGATCGCTTGT  
GTACAAAACCTTCTATCTTTTGGACCAGCGGTTAGAAAAGATAGTAATTGTTTTACATCAAATGCTATATATCGGACTATA  
TGAAATTCAAAATAATTATTTTCAACCGTTTCAATTTATGTGACGTGTTAAAAAGAATGATCATTTTTTATAATTTTTATGT  
AATGATTTATAATCACACAAAATATATATGTCTTATTTTACCTCACAAAGTTAAAAGAATTTTTTTTTAAAATTTTGTGT  
CCAGTCAAATATATTCGACTGAAATGAAATGGAGGGCAGTAGTTATTATACTACTATTAGTACGTAGTTGTCATTGGCAA  
AGAAAACGAAGCAATATTTGTGCTTCATGATCGGGGTTAGACTTAATAGCTTGGAAAATTTAGGACAATTTAAGTTACACT  
TATTTAAAATTTAGCTGCAGCTTCGTGATTTTTCTTTTACATTACAAAACATGTAATTTTACATACAACTACAAAACAAG  
AAAATCAAAAAGATTGGTGATTATACAACCTTGACGGGTACTACGCGAAGTATCTGATTCTTTCTTGCACATCCAAACGAT  
TAATTTTTAATGGCGGAAAACGGTAATTAACCTATTACAACCTCCATGGATAATCACTTAATCAGTTGCTTTCTTTAATCACT  
CTTCATCGGCGTCTCAAATCCGAGCAATCTCCCAAATTCATAGAACTTCTAAACATG

## B. *In situ* analysis of the promoter sequence including 5'UTR of *NtMTP2*

The program PlantCARE: <http://bioinformatics.psb.ugent.be/webtools/plantcare/html/>, was used to identify *cis*-acting elements within the promoter region. For analysis the 1271 bp fragment of the promoter region (counting from the START codon upstream) was used.

Table 1. List of *cis*-acting elements found in promoter MTP2; all elements were marked by colours on the promoter sequence below

Cis-acting regulatory elements	Sequence	Position in <i>NtMTP2</i> promoter sequence (bp upstream ATG)	Function	References
<b>Metals responsive sequences</b>				
<b>MRE1</b>	TGCACAT	1118	heavy metal-responsive elements	Zhang and Liu, 2017
<b>MRE2</b>	ATTTAGC TGC	979		
<b>IDE2</b>	CAAGTTT/ A	377, 774	sequence the iron deficiency-responsive element	Ogo et al. 2008
<b>Light responsive sequences</b>				
<b>BOX4</b>	ATTAAT	328	part of a conserved DNA module involved in light responsiveness from <i>Petroselinum crispum</i>	Weisshaar et al. 1991; Hiratsuka K et al. 1997.
<b>GT1-motif</b>	GGTTAA	520	light responsive element from <i>Arabidopsis thaliana</i>	Hagen et al. 1992
<b>Phytohormone responsive sequences</b>				
<b>ABRE</b>	ACGTG	47, 689	<i>cis</i> -acting element involved in the abscisic acid responsiveness from <i>Arabidopsis thaliana</i> ,	Shen and Ho, 1995
<b>TGACG-element</b>	AACGAC	687, 1084	<i>cis</i> -acting regulatory element involved in the MeJA-responsiveness from <i>Hordeum vulgare</i>	Rouster et al. 1997
<b>Regulation of plant development</b>				
<b>MYB-binding sites</b>	CAACAG	130	MYB binding sites correlated with trichome-specific expression	Fasani et al. 2017
<b>General regulatory elements</b>				
<b>TATA-box</b>	ATATAA	multi-position	core promoter element around -30 of transcription start site	Basehoar et al. 2004
<b>CAAT-box</b>	CAAAT	multi-position	common <i>cis</i> -acting element in promoter and enhancer regions from <i>Pisum sativum</i>	Frangeul et al. 2004

>MTP2prom

+ GTTAGTGTTT AGGATAGAGT AGGATATTTT CAAGAGGGGA TTGCAACGT GAGATGGTTG TAAACCTGTA

+ AGAGCAT GTTACATCAC TTTATTCTGT TTCCCAATCG ATACCTTTAG ATTACATGT AACAGCAAAA

+ AGAAGAAAAA AAATGAAATT TAGCTCACTT GCAGTCATCC TAGTACTTTT GGTAGAAGTG AAGATTATTT

+ GCTAATTGAG TGTTTTTTTT CGTGCAAAGG ATATTGTGGA ATCGGTCGAT AATAAGTGAC TTTTGTATCT

+ CTTTATTTTG GTCCAAAATA ATTGTCCTTT TATATAATCA AGAAAAAATT AATTTTTTTT TTTAAAATTC

IDE2

+ GTCCTTATT ATATATTCAA TTGTGCAAG TTAATAATAT GTAGATTTTA ATTAAGGGTA ATTTTCAAAA

+ TATTTTTTTT CTATAAGAGT AATTTTTTTT AAGGGTGTGC CAAATACAAA ATATTATTT ATTATGAATG

+ GGAGGGAGTA TAAATTAGTC CTGGTCAGGG GTTAACTACTA TGCCTTGATT GAGTGGACTA CTTTTGATCG

+ CTTGTTGTAC AAAACCTTTCT ATCTTTTGGA CCAGCGGTTA GAAAAGATAG TAATTGTTTT ACATCAAATG

+ CTATATATCG GACTATATGA AATTCAAAAAT AATTATTTCA CCCGTTTCAATTTATGTGAC GTTTAAAAA

+ GAATGATCAT TTTTATAAT TTTTATGTAA TGATTTATAA TCACACAAAA TATATATGTC TTATTTTACC

IDE2

+ TCACAAGTTT AAAAGAATTT TTTTTTAAA ATTTTGTGTC CAGTCAAATA TATTCGACTG AAATGAAATG

+ GAGGGCAGTA GTTATTATAC TACTATTAGT ACGTAGTTGT CATTGGCAAA AGAAAACGAA GCAATATTG

+ TCGTTCATGA TCGGGGTTAG ACTTAATAGC TTGAAATTT TAGGACAATT TAA GTTACAC TTATTAAAAT

MRE2

+ TTAGCTGCAG CTTCGTGATT TTTCTTTTAC ATTACAAAAAC ATGTAATTTT ACATACAAAC TACAAAAACA

+ AGAAAATCAA AAAAGATTGG TGATTATACA ACTTGACGGG TACTACGCGA AGTATCTGAT TCTTTCTGTC

MRE1

+ ACATCCAAAC GATTAATTTT TAATGGCGGA AAACGGTAAT TAACTATTAC AACTCCATGG ATAATCACTT

+ AATCAGTTGC TTTCTTTAAT CACTCTTCAT CGGCGTCTCA AATCCGAGCA ATCTCTCCAA ATTTTCATAGA

+ ACTTCTAAA

## References:

1. Basehoar, A.D., Zanton, S., Pugh, B. 2004. Identification and Distinct Regulation of Yeast TATA Box-Containing Genes. *Cell*, 116(5):699-709.
2. Fasani<sup>1</sup>, E., DalCorso<sup>1</sup>, G., Varotto, C., Li, M., Visioli, G., Mattarozzi, M., Furini, A. 2017. The MTP1 promoters from *Arabidopsis halleri* reveal cis-regulating elements for the evolution of metal tolerance. *New Phytol.* 214, 1614–1630.
3. Frangeul, L., Glaser, P., Rusniok, C., Buchrieser, C., Duchaud, E., Dehoux, P., Kunst, F. 2004. CAAT-Box, contigs-Assembly and Annotation Tool-Box for genome sequencing projects. *Bioinformatics*, 20(5):790–797.
4. Hagen, G., Muller, S., Beato, M., Suske, G. 1992. Cloning by recognition site screening of two novel GT box binding proteins: a family of Sp1 related genes. *Nucl. Acids Res.* 20(21), 5519–5525.
5. Hiratsuka, K., Chua, N.H. 1997. Light regulated transcription in higher plants. *J. Plant. Res.* 110(1), 131–139.
6. Ogo, Y., Kobavashi, T., Itai, R.N., Nakanishi, H., Kakei, Y., Takahashi, M., Toki, S., Mori, S., Nishizawa, N.K. 2008. A Novel NAC Transcription Factor, IDEF2, That Recognizes the Iron Deficiency-responsive Element 2 Regulates the Genes Involved in Iron Homeostasis in Plants. *J. Biol. Chem.* 283, 13407-13417.
7. Shen, Q., Ho, T.H. 1995. Functional dissection of an abscisic acid (ABA)-inducible gene reveals two independent ABA-responsive complexes each containing a G-box and a novel cis-acting element.. *The Plant Cell.* 7, 295-307.
8. Weisshaar, B., Block, A., Armstrong, G.A., Herrmann, A., Schulze-Lefert, P., Hahlbrock, K. 1991. Regulatory elements required for light-mediated expression of the *Petroselinum crispum* chalcone synthase gene. *Symp. Soc. Exp. Biol.* 45,191-210.
9. Rouster, J., Leah, R., Mundy, J., Cameron-Mills, V. 1997. Identification of a methyl jasmonate-responsive region in the promoter of a lipoxygenase 1 gene expressed in barley grain. *The Plan J.* 11(3), 513-523.
10. Zhang, M., Liu, B. 2017. Identification of a rice metal tolerance protein OsMTP11 as a manganese transporter. *PLoS ONE* 12(4), 1-23.