

Supplementary Table 1 The CIS regulatory elements between *TpNRAMP3* and *OsNRAMP3*.

Gene	Cis-acting element	Function
<i>TpNRAMP3</i>	3-AF1 binding site	Light responsive element
	5' UTR Py-rich stretch	Element conferring high transcription levels
	A-box	Cis-acting regulatory element
	ABRE	Cis-acting element involved in the abscisic acid responsiveness
	AE-box	Part of a module for light response
	CAAT-box	Common cis-acting element in promoter and enhancer regions
	CAT-box	Cis-acting regulatory element related to meristem expression
	CCGTCC-box	Cis-acting regulatory element related to meristem specific activation
	CGTCA-motif	Cis-acting regulatory element involved in the MeJA- responsiveness
	G-box	Cis-acting regulatory element involved in light responsiveness
	GAG-motif	Part of a light responsive element
	GARE-motif	Gibberellin-responsive element
	GCN4_motif	Cs-regulatory element involved in endosperm expression
	GT1-motif	Light responsive element
	I-box	Part of a light responsive element
	L-box	Part of a light responsive element
	Skn-1_motif	Cis-acting regulatory element required for endosperm expression
	Sp1	Light responsive element
	TATA-box	Core promoter element around -30 of transcription start

	TATC-box	Cis-acting element involved in gibberellin-responsiveness
	TC-rich repeats	Cis-acting element involved in defense and stress responsiveness
	TCA-element	Cis-acting element involved in salicylic acid responsiveness
	TCT-motif	Part of a light responsive element
	TGACG-motif	Cis-acting regulatory element involved in the MeJA-responsiveness
<i>OsNRAMP3</i>	ABRE	Cis-acting element involved in the abscisic acid responsiveness
	ACE	Cis-acting element involved in light responsiveness
	ATCT-motif	Part of a conserved DNA module involved in light responsiveness
	CAAT-box	Common cis-acting element in promoter and enhancer regions
	CAT-box	Cis-acting regulatory element related to meristem expression
	CGTCA-motif	Cis-acting regulatory element involved in the MeJA- responsiveness
	G-box	Cis-acting regulatory element involved in light responsiveness
	GAG-motif	Part of a light responsive element
	GARE-motif	Gibberellin-responsive element
	GCN4_motif	Cis-regulatory element involved in endosperm expression
	I-box	Part of a light responsive element
	MBS	MYB binding site involved in drought-inducibility
	Skn-1_motif	Cis-acting regulatory element required for endosperm expression
	Sp1	Light responsive element
	TATA-box	Core promoter element around -30 of transcription start
	TCT-motif	Part of a light responsive element
	TGACG-motif	Cis-acting regulatory element involved in the MeJA-responsiveness

Circadian	Cis-acting regulatory element involved in circadian control
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rbcS-CMA7a	Part of a light responsive element
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Note: yellow marked the *TpNRAMP3*-specific CIS regulatory elements; green marked the *OsNRAMP3*-specific CIS regulatory elements.

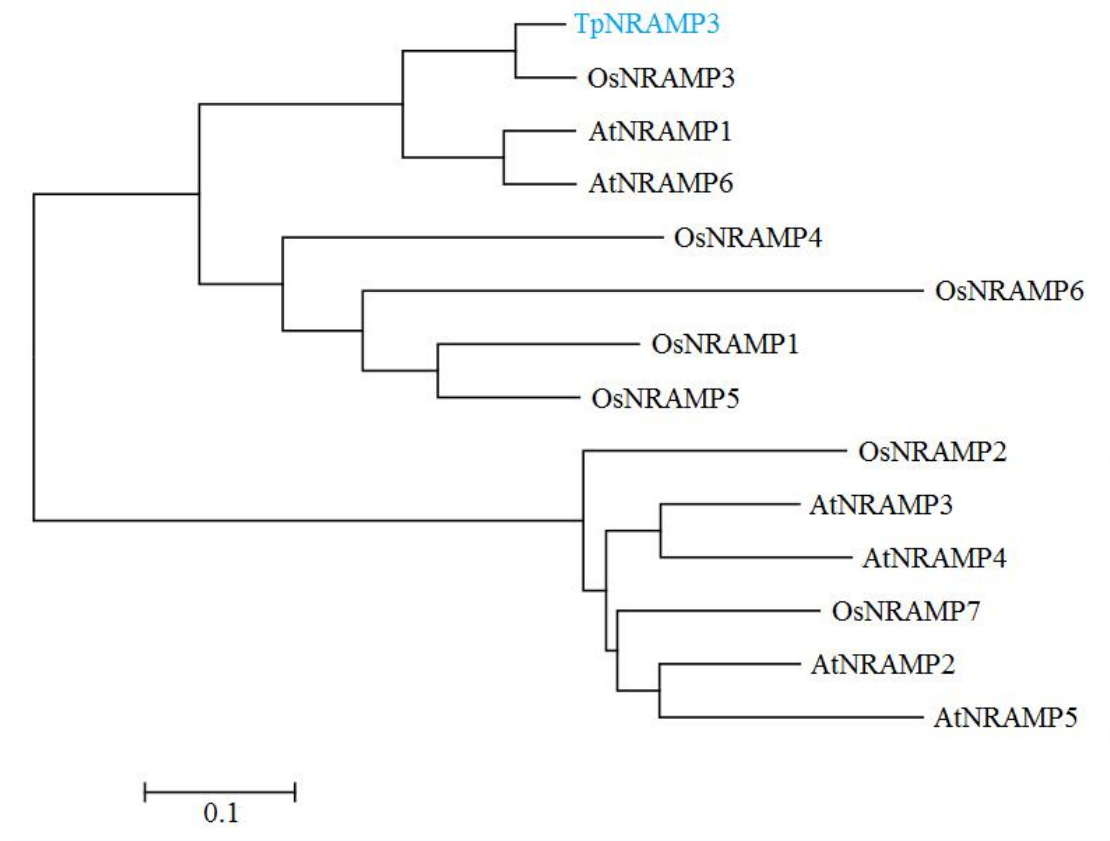


Fig S1. TpNRAMP3 is closely grouped with OsNRAMP3.

TpNRAMP3 (KX165384), 7 OsNRAMP proteins and 6 AtNRAMP proteins, including OsNRAMP1 (AK121534), OsNRAMP2 (L81152), OsNRAMP3 (AK070574), OsNRAMP4 (LOC_Os02g03900), OsNRAMP5 (AK070788), OsNRAMP6 (XM_015762723), OsNRAMP7 (LOC_Os12G39180), AtNRAMP1 (AF165125), AtNRAMP2 (AF141204), AtNRAMP3 (AF202539), AtNRAMP4 (AF202540), AtNRAMP5 (NM_117995.2), AtNRAMP6 (NM_101464.4), were aligned using Vector NTI 11.5.1; the phylogenetic tree of the NRAMP proteins was constructed using MEGA5.

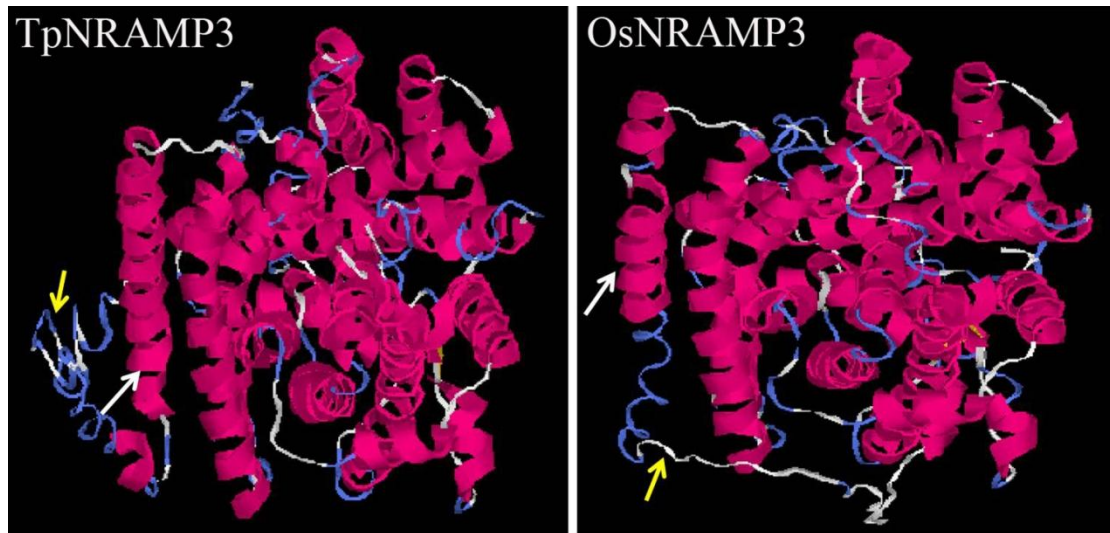


Fig S2. Protein structures of TpNRAMP3 and OsNRAMP3.

The protein structures of TpNRAMP3 and OsNRAMP3 were predicted using the software of I-TASSER. The white arrows represented the α -helix; the yellow arrows represented the random coil.

OsNRAMP3	(1)	MSGPMQRSSQPQFIS ¹⁰⁰ SVERNN-QSNGPGTPLIDSIDVDQIVIPEKNSWKN
TpNRAMP3	(1)	MSGPRQGSSQPQFMT ¹⁰⁰ SVGQNNLSNGPGTPLIDSIDVDQIVIPEKNSWKN
OsNRAMP3	(50)	LFSYIGPGFLVSIAYIDPGNFETDLQAGAQYKYELLWIIILIASCAALIIQ
TpNRAMP3	(51)	<u>LFSYIGPGFLVSIAYIDPGNFETDLQAGAQYKYELLWIIILIASCAALVIQ</u>
		TM1 TM2
OsNRAMP3	(100)	SLAARLGVVVTGKHLAEHCRAEYPKATNFILWILAE LAVVACDIPEVIGTA
TpNRAMP3	(101)	<u>SLAASLGVVVTGKHLAEHCRAEYPKVTNFILWILAE LAVVACDIPEVIGTA</u>
		TM3
OsNRAMP3	(150)	FALNMLFKIPVWCGVLITGLSTLM ¹⁰⁰ LLLQOYGVRKLEFLIAILVSLIATC
TpNRAMP3	(151)	<u>FALNMLFKIPITWCGVLITGLSTLM¹⁰⁰LLFLQOYGVRKLEFLIAFLVFLIATC</u>
		TM4 TM5
OsNRAMP3	(200)	FLVELGYSKPNSSEVV ¹⁰⁰ RGLFVPEIKGNGATGLAISLLGAMVMPHNFLHLS
TpNRAMP3	(201)	<u>FLVELGYSKPNSSEVV¹⁰⁰RGLFVPEIKGDGATGLAISLLGAMVMPHNFLHLS</u>
OsNRAMP3	(250)	ALVLSRKVPRSVHGIKEACRFYMIESAFALTIAFLINISIIISVSGAVCGS
TpNRAMP3	(251)	ALVLSRKVPRSVHGIKEACRFYMIESAFALTVAFLINISIIISVSGAVCSA
		TM6
OsNRAMP3	(300)	DNLSPEDQMNCSDLDLNKASFL ¹⁰⁰ LKNV LGNWSSKLFVAVALLASGQSSTITG
TpNRAMP3	(301)	DNLNPEDRMNCNDLDLNKASFL ¹⁰⁰ LKNV LGNWSSKVF ¹⁰⁰ SIALLASGQSSTITG
		TM7
OsNRAMP3	(350)	TYAGQYVMQGF ¹⁰⁰ DLRMTPIRNLLTRSLAILPSLIVSIIGGSSAAGQLII
TpNRAMP3	(351)	<u>TYAGQYVMQGF¹⁰⁰DLRMTPIRNLLTRSLAIVPSLIVSLIGGSSAAGKLII</u>
		TM8
OsNRAMP3	(400)	IASMILSFELPFALVPLLKFTSS ¹⁰⁰ RTKMGQHTNSKAISVITWIGIGSFIVVI
TpNRAMP3	(401)	<u>IASMILSFELPFALVPLLKFTSS¹⁰⁰RTKMGPHNTNSRFISVLTWAIIGSFIMVI</u>
		TM9 TM10
OsNRAMP3	(450)	NTYFLITSFV ¹⁰⁰ KLLLHNGLSTVSQVFSGIFGFLGMLIYMAAILYL ¹⁰⁰ VFRKNR
TpNRAMP3	(451)	<u>NIYFLITSFVR¹⁰⁰LLLHSGLSTVSQVFSGIFGFLGMLIYIAAILYL¹⁰⁰VFRKNR</u>
		TM11
OsNRAMP3	(500)	KATLPLLEGDS ¹⁰⁰ TVRIVGRDTATEGEGSLGHL ¹⁰⁰ PREDISSMQLPQORTASDL
TpNRAMP3	(501)	KCTLPLLECD ¹⁰⁰ AKLGDAG---HTEGEGSLGHL ¹⁰⁰ PREDISSMQLPHQRPASDL
OsNRAMP3	(550)	D
TpNRAMP3	(548)	D

Fig S3. Alignments between TpNRAMP5 and OsNRAMP5.

Black lines marked the transmembrane domains predicted by SOSUI. The shaded residues represented their consensus positions were 100%, but their identity positions were 0%.

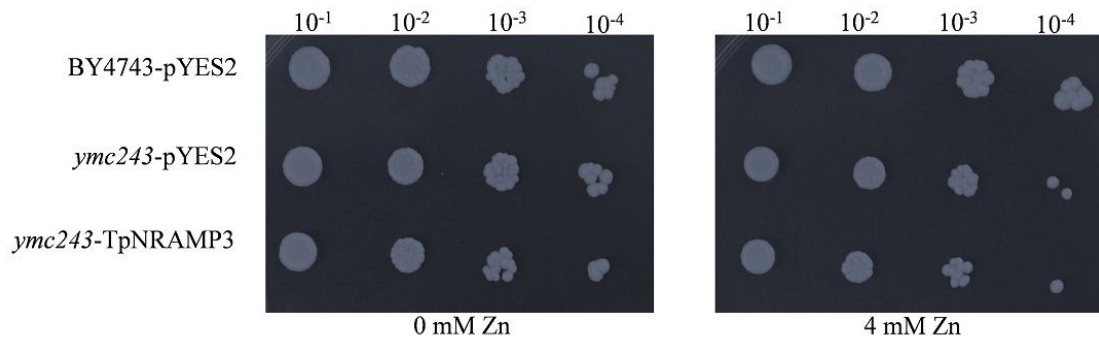


Fig S4. Zn sensitivity of TpNRAMP3 in yeast.

Expression of *TpNRAMP3* in Zn sensitive strain $\Delta zrc1$ did not affect the yeast growth when compared with expressing pYES2 in $\Delta zrc1$.

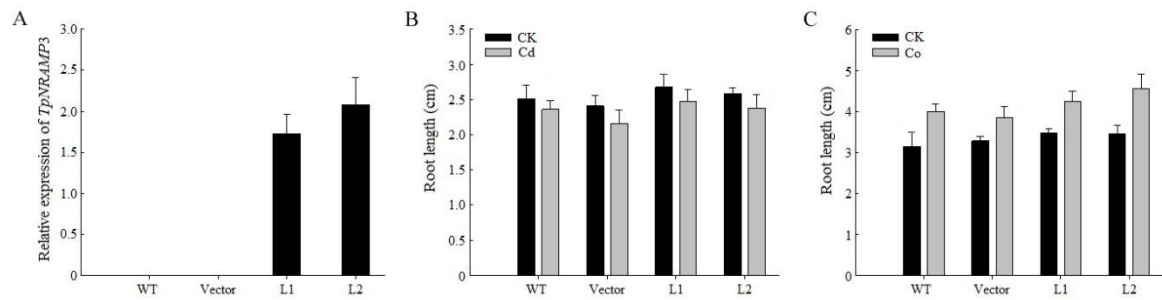


Fig S5. Expression of *TpNRAMP3* in transgenic *Arabidopsis* (A); and root length of transgenic *Arabidopsis* grown on 1/2 MS medium with 25 μ M Cd (B) and 80 μ M Co (C) stress for 10 days. Value was mean \pm standard deviation (three biological replicates).

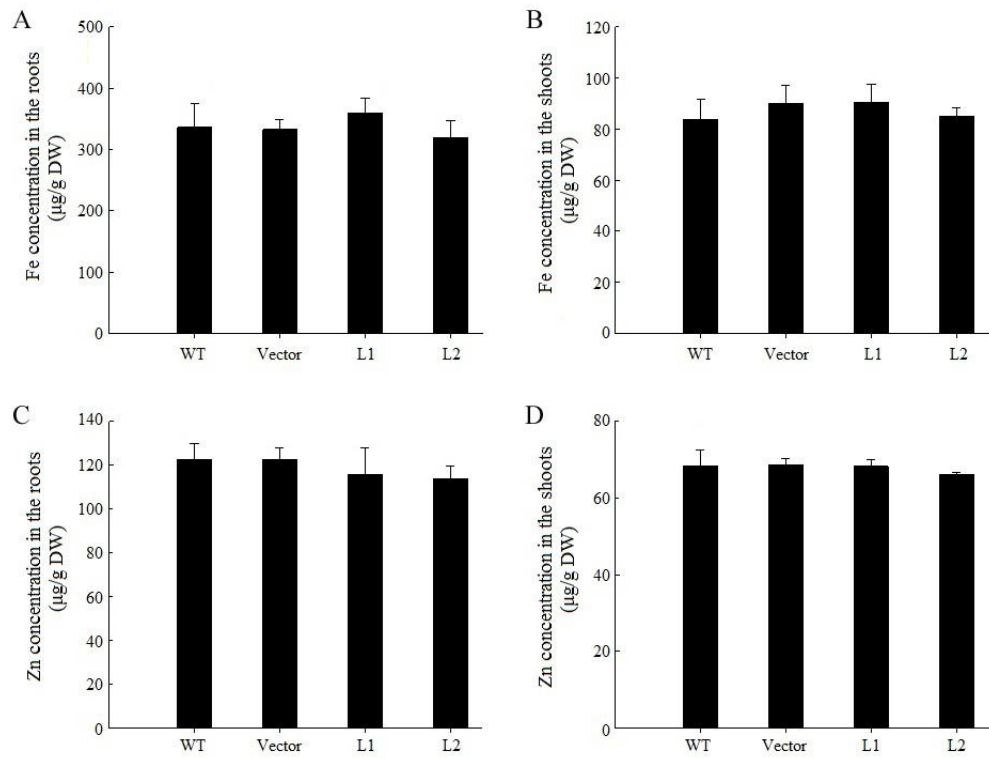


Fig S6. Fe and Zn accumulations in *TpNRAMP5* transgenic *Arabidopsis*.

A-B: Fe concentration in roots (A) and shoots (B); C-D: Zn concentration in roots (C) and shoots (D). Value was mean \pm standard deviation (three biological replicates).