

Figure S1. Prediction of transmembrane structure of the SINRAMP protein family.

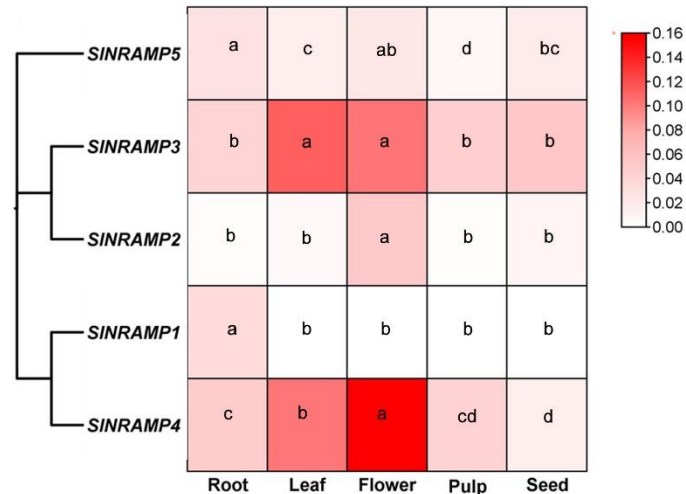


Figure S2. Tissue-specific expression profiles of the SINRAMP genes was performed in various tomato tissues.

The 14-day-old seedlings were transplanted and grown in greenhouse for four months, then SINRMAP gene family expression levels were determined in different tissues. leaves, roots, flowers, pulps and seeds were separately harvested for qRT-PCR analysis. Fold-changes of genes expression were normalized against the reference gene *SlActin* using $2^{-(\Delta\Delta Ct)}$ values. Data (means \pm SE, n = 4) sharing the same letter(s) above the error bars are not significantly different at the 0.05 level based on the Duncan's test.

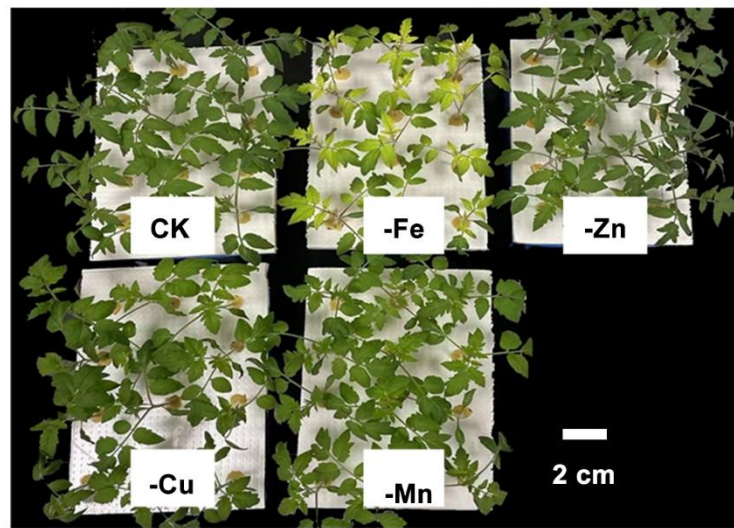


Figure S3. Photograph of the treatments

The 14-day-old seedlings were subjected to four nutrient deficiencies (-Fe, -Cu, -Zn, -Mn) for 7 days, and then the shoots and roots elements concentration, as well as SINRMAP gene family expression levels were determined.

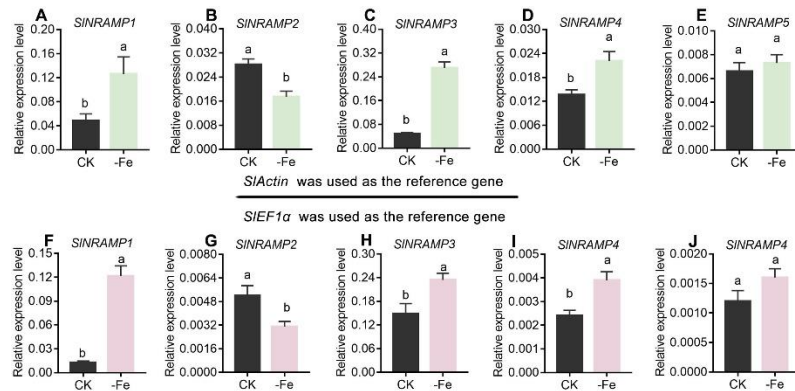


Figure S4 Expression levels of the *SINRAMP1* gene under Fe deficiency using two reference genes

The 14-day-old seedlings were subjected to four nutrient deficiencies (-Fe, -Cu, -Zn, -Mn) for 7 days, and then *SINRMAP1* expression levels in roots was determined. The gene expression level was normalized against the reference gene *SlActin* (A-E) and *SlEF1α*(F-J) using $2^{(-\Delta Ct)}$ values. Data (means \pm SE, n = 5), different letters indicate significant differences (p < 0.05, Duncan's test)

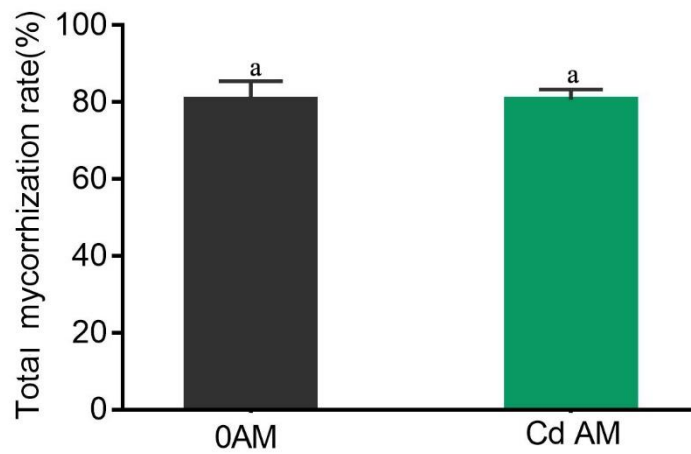







Figure S5 Total mycorrhization of mycorrhizal tomato plants grown in Cd free (0AM) and 100 μ M Cd (CdAM) for 35 days.

The 14-day-old seedlings were inoculated with or without AMF under Cd stress for 35 days, and then total mycorrhization of mycorrhizal tomato plants was determined. Data (means \pm SE, n = 3), Different letters indicate significant differences ($p < 0.05$, Duncan's test)

Table S1 The list of SINRAMP family gene in different plants

plant species	Gene name	Geng ID	plant species	Gene name	Geng ID
<i>Arabidopsis thaliana</i>	<i>AtNRAMP1</i>	AT1G80830.1	<i>Glycine Max</i>	<i>GmNRAMP1a</i>	Glyma.01G190700.1
	<i>AtNRAMP2</i>	AT1G47240.1		<i>GmNRAMP1b</i>	Glyma.11G051500.1
	<i>AtNRAMP3</i>	AT2G23150.1		<i>GmNRAMP2a</i>	Glyma.05G101700.1
	<i>AtNRAMP4</i>	AT5G67330.1		<i>GmNRAMP2b</i>	Glyma.17G165200.1
	<i>AtNRAMP5</i>	AT4G18790.1		<i>GmNRAMP3a</i>	Glyma.04G044000.1
	<i>AtNRAMP6</i>	AT1G15960.1		<i>GmNRAMP3b</i>	Glyma.06G044200.1
	<i>StNRAMP1</i>	PGSC0003DMG400023310		<i>GmNRAMP4b</i>	Glyma.16G027800.1
	<i>StNRAMP2</i>	PGSC0003DMT400064287		<i>GmNRAMP5a</i>	Glyma.07G023600.2
	<i>StNRAMP3</i>	PGSC0003DMT400055473		<i>GmNRAMP5b</i>	Glyma.08G218200.1
	<i>StNRAMP4</i>	PGSC0003DMT400055484		<i>GmNRAMP6a</i>	Glyma.13G369900.1
<i>Solanum tuberosum</i>	<i>StNRAMP5</i>	PGSC0003DMT400023921		<i>GmNRAMP6b</i>	Glyma.15G003500.1
	<i>OsNRAMP1</i>	Os07t0258400-03	<i>Solanum Lycopersicum</i>	<i>GmNRAMP7</i>	Glyma.06G115800.2
	<i>OsNRAMP2</i>	Os03t0208500-01		<i>SINRMAP1</i>	Solyc11g018530.2.1
	<i>OsNRAMP3</i>	Os06t0676000-01		<i>SINRMAP2</i>	Solyc04g078250.3.1
	<i>OsNRAMP4</i>	Os02t0131800-01		<i>SINRMAP3</i>	Solyc02g092800.3.1
	<i>OsNRAMP5</i>	Os07t0257200-01		<i>SINRMAP4</i>	Solyc03g116900.3.1
	<i>OsNRAMP6</i>	Os01t0503400-03		<i>SINRMAP5</i>	Solyc09g007870.3.1
<i>Oryza sativa</i>	<i>OsNRAMP7</i>	Os12t0581600-01			

Table S2 Analysis of the ten conserved motifs of SINRAMP family proteins in tomato

Motif	Logo	Sequence	Width	Annotation
1		YIWAIGLLAAGQSSTITGTYAG QFIMGGFLDLRLKKWLRALIT RSCAIVP	50	NRAMP
2		IQLLAARJGVATGRHLAELCR EEYPKW	27	NRAMP
3		GAVIMPHNLFHLSALVQSRKI P	22	NRAMP
4		VSIAYLDPGNLEGD LQAGAIA GYSLLW	27	NRAMP
5		WAGVLITGLDCFLFLLZNYG VRKLEALFAVLIAMAVSF	41	NRAMP

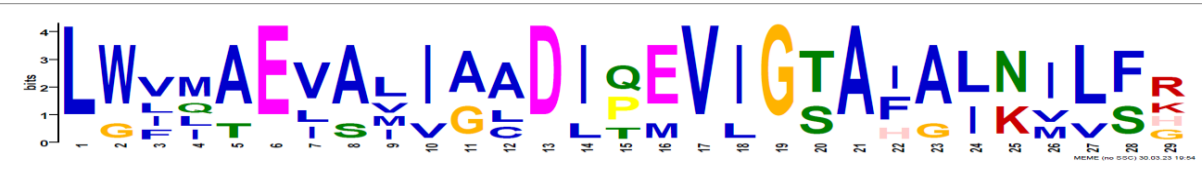



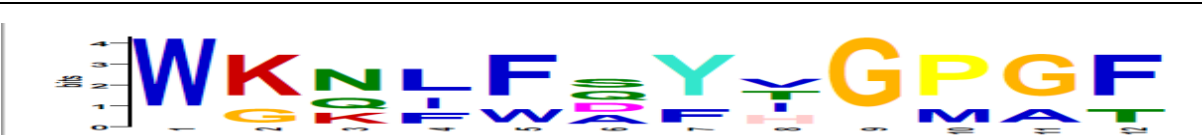
6	 <p>LWVMAEVAIAADIQEVIGTAFALNLF</p>	LWVMAEVAIAADIQEVIGTAF AJNILFR	29	NRAMP
7	 <p>VILSFZJPFALIPLLKLVSSETIMGVHKISVSMKVJSW</p>	VILSFZJPFALIPLLKLVSSETIM GVHKISVSMKVJSW	38	NRAMP
8	 <p>RKGVGKEALNYYLIESGFALLISFLINLFVTSVFGKVFY</p>	RKGVGKEALNYYLIESGFALL ISFLINLFVTSVFGKVFY	40	NRAMP
9	 <p>WFGYAKPNGNELLAGLFIPKLSGKGATQ</p>	WFGYAKPNGNELLAGLFIPK LSGKGATQ	29	NRAMP
10	 <p>WKNLFAYVGPFGF</p>	WKNLFAYVGPFGF	12	NRAMP

Table S3 The genomic location of SINRAMP family genes

Gene name	Gene ID	Genomic Location
<i>SINRAMP1</i>	Solyc11g018530.2.1	Chr11:8645242-8648856
<i>SINRAMP2</i>	Solyc04g078250.3.1	Chr4:63109871-63113592
<i>SINRAMP3</i>	Solyc02g092800.3.1	Chr2:54402272-54405963
<i>SINRAMP4</i>	Solyc03g116900.3.1	Chr3:67650010-67659122
<i>SINRAMP5</i>	Solyc09g007870.3.1	Chr9:1399607-1407814

Table S4 The analysis of collinear gene pairs between different plants

Collinear plant 1	Collinear plant 2	collinear gene pairs
<i>Arabidopsis thaliana</i>	<i>Glycine Max</i>	<p><i>AtNRAMP2</i> : <i>GmNRAMP3a/GmNRAMP3b</i>; <i>AtNRAMP6</i> : <i>GmNRAMP5a/GmNRAMP5b/GmNRAMP6a/GmNRAMP6b</i>; <i>AtNRAMP3</i> : <i>GmNRAMP1a/GmNRAMP2a/GmNRAMP3b/ GmNRAMP1b/GmNRAMP2b</i>; <i>AtNRAMP4</i>: <i>GmNRAMP1a/ GmNRAMP3a/GmNRAMP2a/GmNRAMP3b/GmNRAMP1b/ GmNRAMP2b</i></p>
<i>Glycine Max</i>	<i>Solanum Lycopersicon</i>	<p><i>SINRAMP5</i>: Glyma.03G181400.3/Glyma.10G058300.4/Glyma.13G145100.4/Glyma.19G182151.1; Solyc04g078220.3.1: <i>GmNRAMP1a/GmNRAMP3a/GmNRAMP2a/GmNRAMP3b/GmNRAMP1b/GmNRAMP2b</i>; <i>SINRAMP4</i> : <i>GmNRAMP5a/ GmNRAMP5b/GmNRAMP6a/GmNRAMP6b</i>; <i>SINRAMP3</i>: <i>GmNRAMP1a/GmNRAMP3a/GmNRAMP2a/GmNRAMP3b/GmNRAMP1b/GmNRAMP2b</i></p>
<i>Solanum lycopersicum</i>	<i>Solanum tuberosum</i>	<p><i>SINRAMP5</i>:<i>StNRAMP4</i> <i>SINRAMP3</i>:<i>StNRAMP2/StNRAMP3</i> <i>SINRAMP1</i>: <i>StNRAMP5</i></p>
<i>Solanum tuberosum</i>	<i>Medicago sativa</i>	<p><i>MtNRAMP5</i>: <i>StNRAMP2/StNRAMP3</i> <i>MtNRAMP1</i>: <i>StNRAMP5</i> <i>MtNRAMP4</i>: <i>StNRAMP2/StNRAMP3</i> <i>MtNRAMP7</i>: <i>StNRAMP2/StNRAMP3</i></p>
<i>Medicago sativa</i>	<i>Oryza sativa</i>	<p><i>OsNRAMP2</i>: <i>MtNRAMP4</i> <i>OsNRAMP2</i>: <i>MtNRAMP7</i> <i>OsNRAMP2</i>: <i>MtNRAMP5</i></p>

Table S5 The best templates of SINRAMP family proteins selected from the SwissModel template library for building 3D structure models

Gene name	Template	Sequence identity (%)	Range	Coverage	GMQE	QMEANDisCo global score	Description
<i>SINRAMP1</i>	5m8k.1.A	33.04	29 - 492	0.86	0.59	0.64 ± 0.05	Divalent metal cation transporter MntH
<i>SINRAMP2</i>	5m8k.1.A	31.3	72 - 487	0.79	0.53	0.63 ± 0.05	Divalent metal cation transporter MntH
<i>SINRAMP3</i>	5m8k.1.A	31.7	1 - 433	0.96	0.66	0.64 ± 0.05	Divalent metal cation transporter MntH
<i>SINRAMP4</i>	5m8k.1.A	34.37	37 - 496	0.85	0.58	0.65 ± 0.05	Divalent metal cation transporter MntH
<i>SINRAMP5</i>	5m8k.1.A	24.56	11 - 465	0.34	0.20	0.59 ± 0.05	Divalent metal cation transporter MntH

Table S6 The cis-acting elements in the promoter regions of SINRAMP family genes

Classification	Motif name	Function	Number of motif of <i>SINRMAP</i> family genes				
			<i>SINRAM</i> <i>P1</i>	<i>SINRAM</i> <i>P2</i>	<i>SINRAM</i> <i>P3</i>	<i>SINRAM</i> <i>P4</i>	<i>SINRAM</i> <i>P5</i>
Gene transcription	CAAT-box	common cis-acting element in promoter and enhancer regions	16	12	15	16	17
	TATA-box	core promoter element around -30 of transcription start	110	38	50	91	61
	chs-CMA1a	part of a light responsive element			1		
	LAMP-element	part of a light responsive element	1	1			
	TCT-motif	part of a light responsive element	3		1		
	GATA-motif	part of a light responsive element	1			1	
	AE-box	part of a module for light response	3	2			
Plant growth and development	I-box	part of a light responsive element	1				1
	AT1-motif	part of a light responsive module		1			
	Gap-box	part of a light responsive element					1
	TCCC-motif	part of a light responsive element		1			
	ATCT-motif	part of a conserved DNA module involved in light responsiveness			2	3	
	Box 4	part of a conserved DNA module involved in light responsiveness	2	1	4	2	
	ACE	cis-acting element involved in light responsiveness		1			
	G-Box	cis-acting regulatory element involved in light responsiveness		3	3	1	1
	3-AF1 binding site	light responsive element					1

Abiotic and biotic stresses	GT1-motif	light responsive element	1	1	1		
	CAT-box	cis-acting regulatory element related to meristem expression				2	
	O2-site	cis-acting regulatory element involved in zein metabolism regulation	2	1			1
	circadian	cis-acting regulatory element involved in circadian control					2
	ARE	cis-acting regulatory element essential for the anaerobic induction					3
	TC-rich repeats	cis-acting element involved in defense and stress responsiveness	1			1	2
	W box	wound responsive		3		1	
	STRE	heat shock protein-related element	1	2	1	1	3
	WUN-motif	Wound-responsive element	1	2			
	MBS	MYB binding site involved in drought-inducibility	2	1		3	1
	CCAAT-box	MYBHv1 binding site				1	
	MYB	MYB binding site	4	4	3	9	10
	MYB recognition site	MYB recognition site				1	
	Myb	MYb binding site		1	1	4	1
	MYB-like sequence	MYB-like sequence	1		1		2
<u>Phytohormone reponsive</u>	MYC	MYC binding site	2	1	3	4	4
	MRE	MYB binding site involved in light responsiveness	1		3		
	ABRE3a	cis-acting element involved in the abscisic acid responsiveness		1		1	

ABRE4	cis-acting element involved in the abscisic acid responsiveness		1		1	
as-1	SA and oxidative responsiveness	1	1		3	1
TCA	cis-acting element involved in salicylic acid responsiveness		1	2		
ERE	ethylene response element	1	3	6	4	
TCA-element	cis-acting element involved in salicylic acid responsiveness				2	2
ABRE	cis-acting element involved in the abscisic acid responsiveness		2	3	1	
TGA-element	auxin-responsive element		1	1		
AuxRR-core	cis-acting regulatory element involved in auxin responsiveness				1	
GARE-motif	gibberellin-responsive element		1		1	1
TGACG-motif	cis-acting regulatory element involved in the MeJA-responsiveness	1	1		3	1
CGTCA-motif	cis-acting regulatory element involved in the MeJA-responsiveness	1	1		3	1

Table S7 Expression levels of SINRAMP family genes in tomato were subjected to Fe, Cu, Mn, Zn deficiency.

Treatments		<i>SINRAMP1</i>	<i>SINRAMP2</i>	<i>SINRAMP3</i>	<i>SINRAMP4</i>	<i>SINRAMP5</i>
Roots	CK	0.048±0.012b	0.028±0.002b	0.049±0.003b	0.014±0.001c	0.007±0.001a
	-Fe	0.126±0.028a	0.017±0.002c	0.270±0.020a	0.022±0.002b	0.006±0.000a
	-Zn	0.037±0.005b	0.028±0.003b	0.054±0.002b	0.015±0.001c	0.006±0.000a
	-Cu	0.013±0.001b	0.039±0.004a	0.035±0.001b	0.029±0.002a	0.005±0.000a
	-Mn	0.069±0.028ab	0.029±0.006b	0.046±0.003b	0.026±0.002ab	0.007±0.000a
Leaves	CK	0.0001±0.00005b	0.017±0.002a	0.074±0.004b	0.036±0.005b	0.019±0.003b
	-Fe	0.0004±0.00012a	0.006±0.001b	0.365±0.021a	0.103±0.022a	0.027±0.002a
	-Zn	0.0002±0.0005ab	0.017±0.001a	0.055±0.004b	0.031±0.002b	0.025±0.002a
	-Cu	0.0001±0.004b	0.018±0.002a	0.081±0.003b	0.036±0.006b	0.016±0.001b
	-Mn	0.0002±0.0006ab	0.014±0.001a	0.057±0.005b	0.026±0.003b	0.024±0.001a

The 14-day-old seedlings were subjected to four nutrient deficiencies (-Fe, -Cu, -Zn, -Mn) for 7 days, and then SINRMAP gene family expression levels in roots and leaves was determined. The gene expression level was normalized against the reference gene *SlActin* using $2^{(-\Delta Ct)}$ values. Data (means ±SE, n = 5), Different letters indicate significant differences (p <0.05, Duncan's test)

Table S8 Primers of SINRAMP family genes selected for qRT-PCR analysis

Gene	NCBI Acc. Num.	Forward (5' to 3')	Reverse (5' to 3')
<i>SlActin</i>	112697914	TTCCGTTGCCCAGAGGTCCT	TCGCCCTTTGAAATCCACATC
<i>SINRMAP1</i>	112706038	AGTTGGGACCACACAAGAAC	TGTTGCTTATCAGCCAACC
<i>SINRMAP2</i>	112717764	ACTATGCTGGTCAATGAGACA	AACGCTGGCAGTTTCTCAA
<i>SINRMAP3</i>	112766867	TGGTTAACTGGATTGTTGGCTGCTGGAC	ATGAATTCAAAGAAGGGGGATCAGGGCA
<i>SINRMAP4</i>	112706457	ACGTATGCAGTTGCCTCAG	GACGATACGAGTTCTAACTG
<i>SINRMAP5</i>	112764447	CAGAGTGTAATCAACTTGGTGC	GGGTTACCAAGGATTTTCCAC
<i>SIEF1α</i>	X14449	GGAACCTGAGAAGGAGCCTAAG	CAACACCAACAGCAACAGTCT