

Table S1. Primer sequences used in this study

Name	Forward (5'-3')	Reverse (5'-3')	Applications
<i>PcNRAMP1</i>	TGAAAATCCGCAAATCGC	TCCACAAAGATGTTGGTCAT	
<i>PcNRAMP2</i>	AGGATTATTCCGATGAAGTAGC	GTTGCCACAGTAAGAGCC	
<i>PcNRAMP3.1</i>	CTCCTGGTGCTGTCAATCTAA	GGCACGCCTGGAAAGAT	
<i>PcNRAMP3.2</i>	AGCTTTCAAACAAACGGGAG	TCTGATGTCATCGCTTAGCAA	
<i>PcNRAMP4</i>	TGGGAATTATTGGCATCAACA	TCTGAACACCCTCTATTATGGC	
<i>PcNRAMP5</i>	GCCCACTTGTCGCTTACT	GTGGATTGACAACCCGAAG	RT-qPCR
<i>PcNRAMP6.1</i>	ATGGCAATCTATATCCTAGCAG	CAAGTCCGTTTCCATGTTA	
<i>PcNRAMP6.2</i>	CACCACTATCAAATCGAGGTT	TTTCAAGGCAATAGCAAT	
<i>PcActin2/7</i>	CCCATTGAGCACGGTATTGT	TACGACCACTGGCATAACAGG	
<i>PcEF1α</i>	TCCCTTGTCCCAATCTCTG	ACATCCTGAAGTGGGAGACG	
<i>PcNRAMP1</i>	ATGGCGGGTTCGTCTTCTGT	CAAATCATTGCAATTACTCCTC	Clone
<i>GW-PcNRAMP1</i>	GGGGACAAGTTGTACAAAAAGCAGGCTTAATGGC GGGGACCACTTGACAAGAAAGCTGGTCTTACAA GGGTTCGTCTTCTGT	ATCATTGCAATTACTC	Gateway

Table S1. Continued

Name	Forward (5'- 3')	Reverse (5'- 3')	Applications
<i>35S-PcNRAMP1</i>	TCCATTGCCAGCTATCTGTCAC	ACTCATACTTGTATTGCGCTCCT	
<i>PcNRAMP1-RT</i>	GCACCATTGATTGAGAATTCAA	TCATACTTGTATTGCGCTCCT	The selection of transgenic lines
<i>PcActin</i>	TCATCGGAATGGAAGCTGCTGGTA	TCATCGGAATGGAAGCTGCTGGTA	
<i>PcNRAMP1^{D61A}</i>	TTGTTCAATTGCATACATTGCCCTGG	GCAATGTATGCAATTGAAACAAGGAACCCGGGA	
<i>PcNRAMP1^{G63A}</i>	GCATACATTGACCTGCAAATTTGAAACTGACCT GC	GCAGGGTCAATGTATGCAATTGAAACAAGGA	Site-directed mutations
<i>PcNRAMP1^{M236A}</i>	CACTTCTCGGTGCCATGGTTGCGCCGACAATCTC CATTC	GAATGGAGATTGTGCGCGCAACCATGGCACCGAGA AGTG	
<i>PcNRAMP1^{P405A}</i>	CGATGATTCTATCTTGAGCTCGTTGCTCTCG	CGAGCTAAAAGATAGAACATCGATGCAATAATG	

Table S2. Accession numbers of *NRAMP* genes presented in Figure. 1.

Gene Name	Locus names or Accession nos. or AGI codes	Species
<i>AtNRAMP1</i>	AT1G80830	<i>Arabidopsis thaliana</i>
<i>AtNRAMP2</i>	AT1G47240	<i>A. thaliana</i>
<i>AtNRAMP3</i>	AT2G23150	<i>A. thaliana</i>
<i>AtNRAMP4</i>	AT5G67330	<i>A. thaliana</i>
<i>AtNRAMP5</i>	AT4G18790	<i>A. thaliana</i>
<i>AtNRAMP6</i>	AT1G15960	<i>A. thaliana</i>
<i>OsNRAMP1</i>	Os07g0258400	<i>Oryza sativa</i>
<i>OsNRAMP2</i>	Os03g0208500	<i>O. sativa</i>
<i>OsNRAMP3</i>	Os06g0676000	<i>O. sativa</i>
<i>OsNRAT1</i>	Os02g0131800	<i>O. sativa</i>
<i>OsNRAMP5</i>	Os07g0257200	<i>O. sativa</i>
<i>OsNRAMP6</i>	Os01g0503400	<i>O. sativa</i>
<i>OsNRAMP7</i>	Os12g0581600	<i>O. sativa</i>
<i>PcNRAMP1</i>	Spta717-Potri.001G044900	<i>Populus × canescens</i>
<i>PcNRAMP2</i>	Spta717-Potri.002G121000	<i>P. × canescens</i>
<i>PcNRAMP3.1</i>	Spta717-Potri.007G050600	<i>P. × canescens</i>
<i>PcNRAMP3.2</i>	Spta717-Potri.007G050700	<i>P. × canescens</i>
<i>PcNRAMP4</i>	Spta717-Potri.002G080400	<i>P. × canescens</i>
<i>PcNRAMP5</i>	Spta717-Potri.002G080500	<i>P. × canescens</i>
<i>PcNRAMP6.1</i>	Spta717-Potri.005G181000	<i>P. × canescens</i>
<i>PcNRAMP6.2</i>	Spta717-Potri.005G181100	<i>P. × canescens</i>
<i>PtNRAMP1</i>	Potri.001G044900	<i>Populus trichocarpa</i>
<i>PtNRAMP2</i>	Potri.002G121000	<i>P. trichocarpa</i>
<i>PtNRAMP3.1</i>	Potri.007G050600	<i>P. trichocarpa</i>
<i>PtNRAMP3.2</i>	Potri.007G050700	<i>P. trichocarpa</i>

Table S2. Continued

Gene Name	Locus names or Accession nos. or AGI codes	Species
<i>PtNRAMP4</i>	Potri.002G080400	<i>P. trichocarpa</i>
<i>PtNRAMP5</i>	Potri.002G080500	<i>P. trichocarpa</i>
<i>PtNRAMP6.1</i>	Potri.005G181000	<i>P. trichocarpa</i>
<i>PtNRAMP6.2</i>	Potri.005G181100	<i>P. trichocarpa</i>

Table S3. Characteristics of the sequences of *PcNRAMP* genes and their proteins

Gene name	Accession number	Chromosomal	Length of CDS	Number of amino	Molecular	Theoretical pI	Grand average of	Transmembrane
		location	(bp)	acids (aa)	weight (kDa)		hydropathicity	helices
<i>PcNRAMP1</i>	Potri.001G044900	1	1626	541	58.65	8.6	0.571	12
<i>PcNRAMP2</i>	Potri.002G121000	2	1611	536	58.61	5.19	0.496	11
<i>PcNRAMP3.1</i>	Potri.007G050600	7	1518	505	55.51	5.01	0.65	11
<i>PcNRAMP3.2</i>	Potri.007G050700	7	1503	500	54.64	4.93	0.667	11
<i>PcNRAMP4</i>	Potri.002G080400	2	1659	552	60.1	8.23	0.442	12
<i>PcNRAMP5</i>	Potri.002G080500	2	1641	546	58.96	7.06	0.548	12
<i>PcNRAMP6.1</i>	Potri.005G181000	5	1746	581	63.4	7.56	0.512	12
<i>PcNRAMP6.2</i>	Potri.005G181100	5	1758	585	63.95	8.42	0.463	10

Table S4. Biomass of WT and transgenic lines (*PcNRAMP1*-OE5, *PcNRAMP1*-OE8, *PcNRAMP1*-OE9) of *P. × canescens* treated with either 0 (−Cd) or 100 (+Cd) µM CdCl₂ for 2 weeks. Data indicate means ± SE (n = 4). Different letters after the values indicate significant differences between the treatments. P-values of the two-way ANOVAs of genotype (G), Cd and their interactions (G × Cd) are also indicated. *: P<0.05; **: P<0.01; ***: P<0.001; ****: P<0.0001; ns: not significant.

Genotype	Cd (µM)	Root	Wood	Bark	Leaf	Whole plant
WT	0	0.64 ± 0.08 b	1.83 ± 0.48 c	1.38 ± 0.10 a	7.50 ± 0.29 a	11.34 ± 0.73 a
	100	0.31 ± 0.01 a	1.00 ± 0.13 ab	0.72 ± 0.01 b	5.62 ± 0.27 b	7.69 ± 0.34 b
	0	0.58 ± 0.17 ab	1.97 ± 0.48 c	1.34 ± 0.12 a	7.58 ± 1.2 a	11.47 ± 1.74 a
<i>PcNRAMP1</i> -OE5	100	0.37 ± 0.02 ab	0.84 ± 0.04 a	0.73 ± 0.07 b	5.42 ± 0.16 b	7.34 ± 0.06 b
	0	0.53 ± 0.03 ab	1.71 ± 0.06 bc	1.50 ± 0.20 a	7.31 ± 0.62 a	11.05 ± 0.51 a
<i>PcNRAMP1</i> -OE8	100	0.33 ± 0.03 a	0.95 ± 0.05 ab	0.61 ± 0.04 b	5.26 ± 0.26 b	7.15 ± 0.21 b
	0	0.60 ± 0.14 b	2.26 ± 0.22 c	1.40 ± 0.48 a	7.42 ± 0.23 a	11.80 ± 0.66 a
<i>PcNRAMP1</i> -OE9	100	0.33 ± 0.02 a	0.77 ± 0.08 a	0.66 ± 0.06 b	5.33 ± 0.28 b	7.08 ± 0.40 b
	G	ns	ns	ns	ns	ns
<i>P</i> -values	Cd	**	****	****	****	****
	G x Cd	ns	ns	ns	ns	ns

Table S5. Concentrations of Mn, Fe, Zn, Ca and Mg in different tissues of WT and transgenic lines (*PcNRAMP1*-OE5, *PcNRAMP1*-OE8, *PcNRAMP1*-OE9) of *P. × canescens* treated with either 0 (−Cd) or 100 (+Cd) µM CdCl₂ for 2 weeks. Data indicate means ± SE (n = 4). Different letters after the values indicate significant differences between the treatments. P-values of the two-way ANOVAs of genotype (G), Cd and their interactions (G × Cd) are also indicated. *: P<0.05; **: P<0.01; ***: P<0.001; ****: P<0.0001; ns: not significant.

Genotype	Cd (µM)	Root						Wood			
		Mn	Fe	Zn	Ca	Mg	Mn	Fe	Zn	Ca	Mg
		(µg g ⁻¹ DW)	(µg g ⁻¹ DW)	(µg g ⁻¹ DW)	(mg g ⁻¹ DW)	(mg g ⁻¹ DW)	(µg g ⁻¹ DW)	(µg g ⁻¹ DW)	(µg g ⁻¹ DW)	(mg g ⁻¹ DW)	(mg g ⁻¹ DW)
WT	0	14.11 ± 1.94 a	275.80 ± 48.88 a	30.87 ± 4.03 ab	1.75 ± 0.53 a	6.50 ± 0.28 c	2.18 ± 0.22 a	152.73 ± 17.52 a	12.60 ± 0.94 a	0.75 ± 0.01 ab	0.46 ± 0.06 a
	100	11.28 ± 4.09 a	570.98 ± 31.70 b	48.05 ± 5.02 cd	4.20 ± 0.14 c	1.03 ± 0.08 ab	0.46 ± 0.07 a	136.65 ± 3.52 a	13.69 ± 3.08 ab	0.65 ± 0.01 a	0.36 ± 0.06 a
<i>PcNRAMP1</i> -OE5	0	156.19 ± 9.49 b	691.88 ± 117.55 b	40.63 ± 3.29 bc	1.62 ± 0.11 a	0.70 ± 0.05 a	47.62 ± 12.58 b	338.37 ± 18.50 b	18.42 ± 1.36 cd	0.97 ± 0.03 c	0.33 ± 0.03 a
	100	9.62 ± 0.89 ab	1041.06 ± 61.22 c	27.00 ± 2.98 a	3.09 ± 0.16 b	0.71 ± 0.01 a	1.92 ± 0.2 a	126.93 ± 9.01 a	14.36 ± 0.94 ab	0.87 ± 0.04 bc	0.42 ± 0.08 a
<i>PcNRAMP1</i> -OE8	0	183.90 ± 8.66 bc	708.94 ± 33.50 b	48.62 ± 0.7 cd	1.62 ± 0.05 a	0.94 ± 0.03 ab	46.24 ± 0.99 b	298.96 ± 19.18 b	21.75 ± 0.50 de	1.16 ± 0.05 d	0.34 ± 0.03 a
	100	4.24 ± 1.19 a	927.35 ± 18.83 c	37.5 ± 0.47 ab	3.23 ± 0.16 b	0.73 ± 0.02 a	0.8 ± 0.14 a	124.11 ± 0.23 a	18.24 ± 0.78 bc	0.91 ± 0.01 c	0.44 ± 0.05 a
<i>PcNRAMP1</i> -OE9	0	171.68 ± 7.65 c	713.26 ± 61.33 b	56.61 ± 2.18 d	1.62 ± 0.18 a	1.17 ± 0.01 b	58.01 ± 2.62 b	303.47 ± 8.10 b	24.95 ± 1.35 e	1.36 ± 0.12 e	0.35 ± 0.04 a
	100	9.80 ± 0.98 ab	1106.96 ± 71.60 c	47.99 ± 3.63 cd	3.37 ± 0.18 b	0.74 ± 0.04 a	1.16 ± 0.4 a	124.89 ± 1.97 a	19.88 ± 0.61 d	0.96 ± 0.03 c	0.47 ± 0.02 a
<i>P</i> -values	G	****	****	**	*	**	****	****	****	****	ns
	Cd	****	****	ns	****	***	****	****	*	****	ns
	G × Cd	****	ns	**	ns	**	****	****	ns	*	ns

Table S5. Continued

Genotype	Cd (μM)	Bark						Leaf			
		Mn	Fe	Zn	Ca	Mg	Mn	Fe	Zn	Ca	Mg
		(μg g ⁻¹ DW)	(μg g ⁻¹ DW)	(μg g ⁻¹ DW)	(mg g ⁻¹ DW)	(mg g ⁻¹ DW)	(μg g ⁻¹ DW)	(μg g ⁻¹ DW)	(μg g ⁻¹ DW)	(mg g ⁻¹ DW)	(mg g ⁻¹ DW)
WT	0	13.8 ± 1.56 a	140.21 ± 9.05 a	136.48 ± 16.39 a	12.85 ± 1.57 b	2.73 ± 0.55 b	28.21 ± 1.77 b	240.54 ± 3.77 bc	53.24 ± 1.20 ab	7.04 ± 0.96 d	3.48 ± 0.43 d
	100	3.75 ± 0.15 a	108.72 ± 7.92 a	114.49 ± 11.36 a	6.82 ± 0.169 a	2.37 ± 0.52 ab	7.97 ± 0.91 a	228.60 ± 9.76 b	37.49 ± 2.58 a	2.60 ± 0.04 a	1.42 ± 0.26 ab
<i>PcNRAMP1-OE5</i>	0	332.66 ± 36.57 b	775.91 ± 31.92 b	155.03 ± 11.01 ab	11.84 ± 0.92 b	1.78 ± 0.03 ab	51.91 ± 12.71 c	283.50 ± 24.19 cd	71.94 ± 9.51 cd	7.91 ± 0.74 d	2.25 ± 0.35 c
	100	16.58 ± 1.71 a	155.24 ± 0.09 a	121.34 ± 16.22 a	7.75 ± 0.34 a	1.51 ± 0.16 a	21.15 ± 1.57 ab	171.94 ± 20.98 a	40.74 ± 4.42 a	3.56 ± 0.07 ab	1.26 ± 0.01 a
<i>PcNRAMP1-OE8</i>	0	337.68 ± 6.96 b	778.16 ± 43.45 b	193.79 ± 7.05 bc	11.87 ± 0.48 b	1.75 ± 0.04 ab	54.03 ± 7.15 c	298.65 ± 4.06 d	82.7 ± 4.02 de	7.38 ± 0.65 d	2.13 ± 0.24 bc
	100	7.94 ± 1.94 a	145.22 ± 5.73 a	120.39 ± 10.85 a	7.93 ± 0.06 a	1.46 ± 0.13 a	12.35 ± 1.27 a	171.62 ± 13.36 a	66.7 ± 2.23 bc	4.22 ± 0.19 ab	1.27 ± 0.02 a
<i>PcNRAMP1-OE9</i>	0	359.33 ± 20.97 b	715.89 ± 19.65 b	226.96 ± 11.50 c	11.90 ± 0.15 b	1.72 ± 0.05 ab	51.38 ± 5.22 c	308.29 ± 18.45 d	93.45 ± 6.70 e	6.86 ± 1.32 cd	2.01 ± 0.20 b
	100	9.35 ± 0.45 a	150.20 ± 9.51 a	119.45 ± 6.72 a	8.45 ± 0.30 a	1.41 ± 0.15 a	14.31 ± 0.57 ab	180.62 ± 21.12 a	85.69 ± 8.68 de	4.88 ± 0.40 bc	1.28 ± 0.06 a
G		****	****	**	ns	*	*	ns	****	ns	*
<i>P-values</i>		Cd	****	****	****	ns	****	****	***	****	****
G × Cd		****	****	**	ns	ns	ns	**	ns	ns	ns

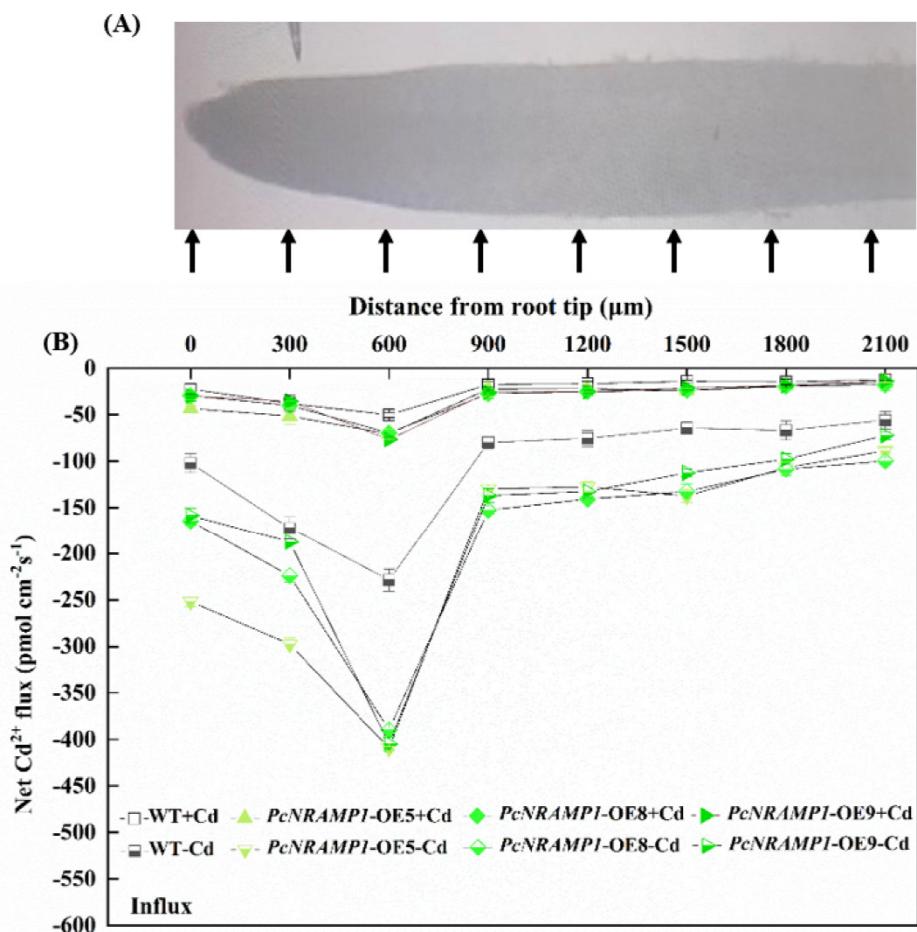


Figure S1. Root tip and net Cd²⁺ fluxes along root apexes. (A-B) Root tip and net Cd²⁺ fluxes along root apexes of WT and transgenic lines (*PcNRAMP1-OE5*, *PcNRAMP1-OE8*, *PcNRAMP1-OE9*) of *P. × canescens* exposed to either 0 (−Cd) or 100 (+Cd) μM CdCl₂ for 2 weeks. Data indicate means ± SE (n = 4).

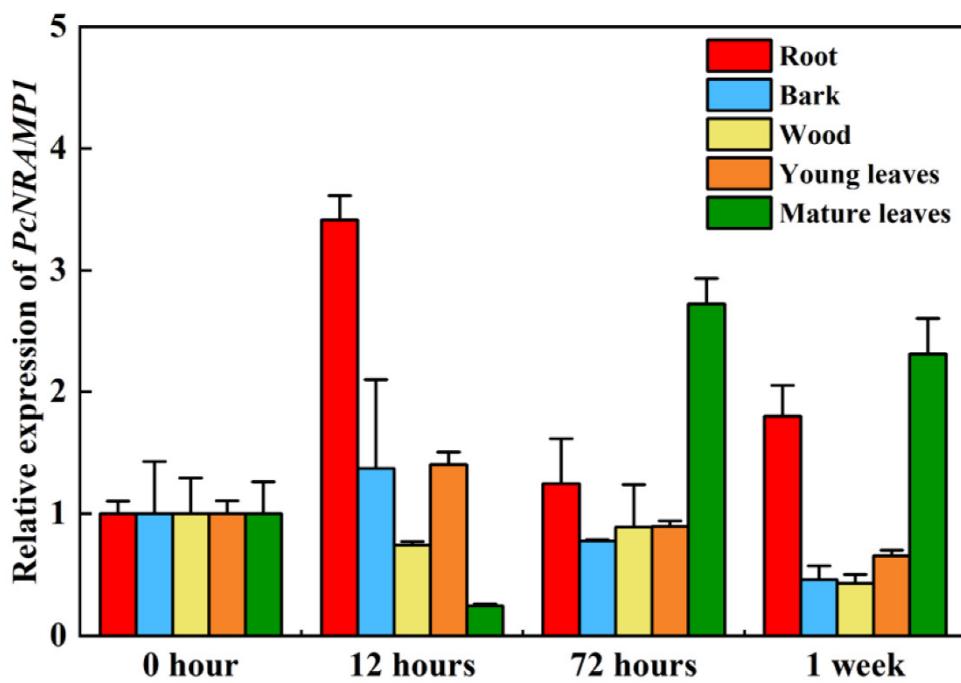


Figure S2. The expression levels of *PcNRAMP1* in different tissues of *P. × canescens* exposed to Cd for different times. Bars indicate means \pm SE ($n = 4$). The expression level of *PcNRAMP1* was set to 1 in different tissues at the beginning of the treatment (0 hour), and the corresponding fold changes were calculated at the other time points.

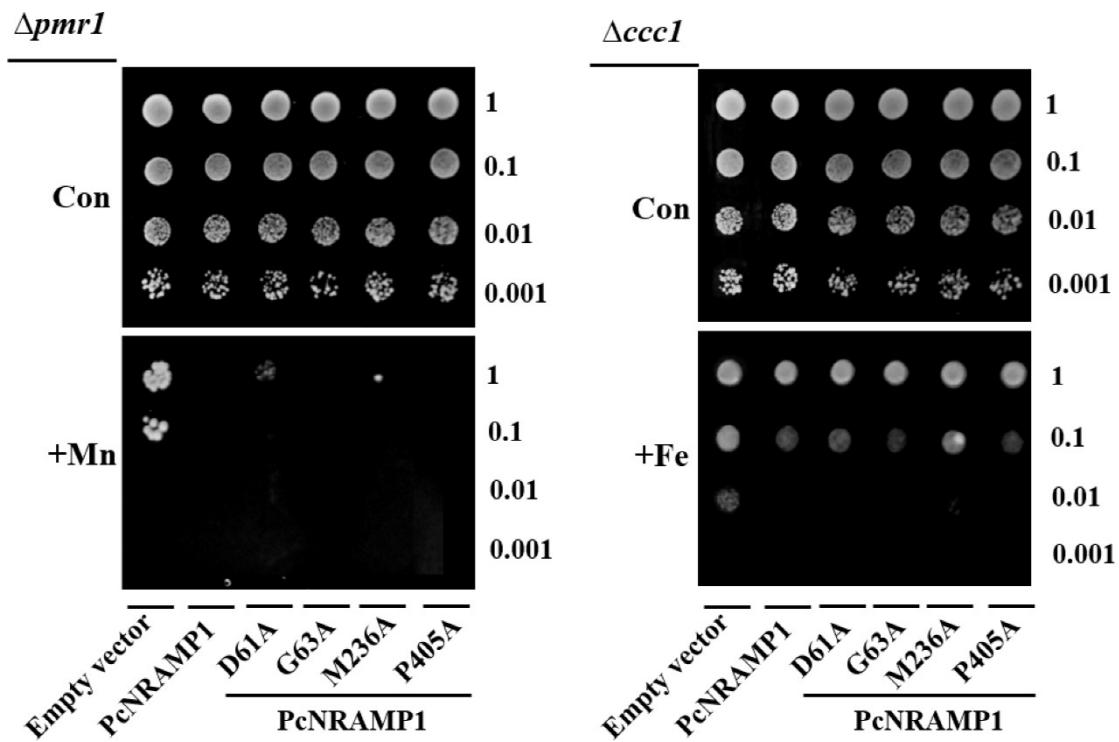


Figure S3. The growth status of yeast mutant strains $\Delta pmr1$ and $\Delta ccc1$ cells transformed with empty vector (pYES2), $PcNRAMP1$, or the mutated $PcNRAMP1$. The growth status of yeast mutant strains $\Delta pmr1$ and $\Delta ccc1$ hypersensitive to excess Mn and Fe, respectively, cells in which empty vector (pYES2), $PcNRAMP1$, or the mutated $PcNRAMP1$ ($PcNRAMP1^{D61A}$, $PcNRAMP1^{G63A}$, $PcNRAMP1^{M236A}$ and $PcNRAMP1^{P405A}$) was transformed. The yeast cells diluted with OD600 nm of 1-0.001 were cultured in the plate with galactose under either control (Con) or other bivalent metals including 1 (+Mn) mM $MnSO_4$ and 8 (+Fe) mM $FeSO_4$ for 4 days.

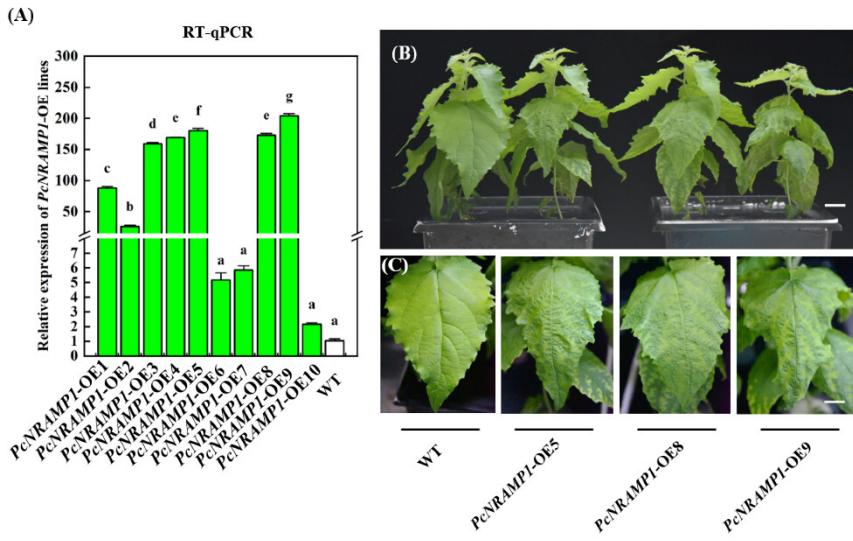


Figure S4. The selection of transgenic lines and the phenotypes of WT and poplars overexpressing *PcNRAMP1*. (A) The selection of transgenic lines. (B-C) The phenotypes of the aboveground plant and mature leaves (LPI=8) of WT and *PcNRAMP1*-overexpressed *P. × canescens* supplied with one-fourth Hoagland solution for 1 month. Scale bars in panels B and C indicate 5 and 2 cm, respectively.

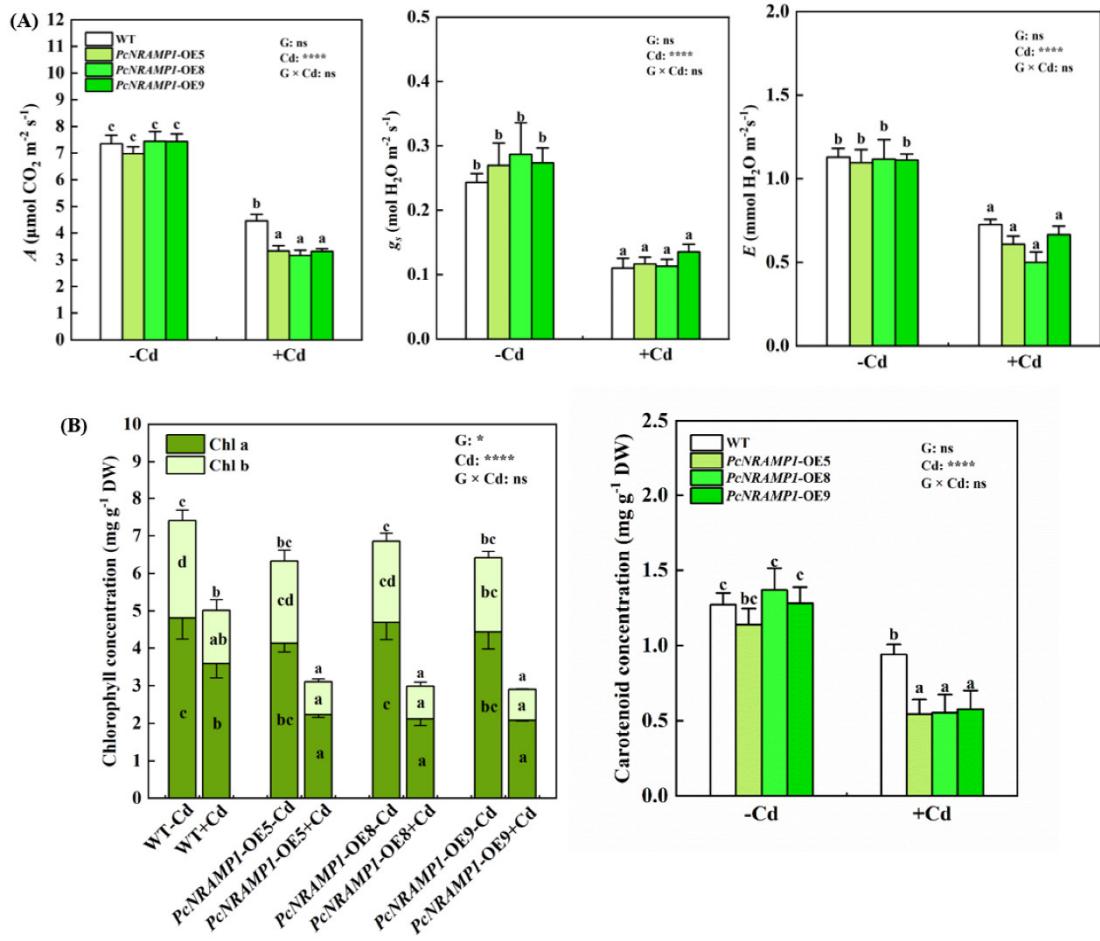


Figure S5. Photosynthesis and chlorophyll concentrations of WT and transgenic lines.

(A-B) The photosynthetic characteristics and chlorophyll concentrations of WT and *PcNRAMP1-OE5*, *PcNRAMP1-OE8*, *PcNRAMP1-OE9* of *P. × canescens* treated with either 0 (-Cd) or 100 (+Cd) $\mu\text{M CdCl}_2$ for 2 weeks. Data indicate means \pm SE (n = 4). Different letters on the bars indicate significant differences between the treatments. *P*-values of the two-way ANOVAs of genotype (G), Cd and their interactions (G \times Cd) are also indicated. *: $P < 0.05$; **: $P < 0.01$; ***: $P < 0.001$; ****: $P < 0.0001$; ns: not significant.