

Table S1. Primers used to amplify the full-length of *NtPT2* and relative genes for Real-Time PCR.

Gene	No. ID	Primer sequences F (5' to 3')	Primer sequences R (5' to 3')
<i>NtPT2-Oe</i>	AB042951	CGAGCTCATGTCTGCAGATAA CAATC	GCTCTAGATCATTCTTCAGT TATAG
<i>NtPT2</i>	AB042951	GGCGCCTTCATTGCTGCTGTCT	CGCGAACCTTCCAACGATAT C
<i>NtPIN1a</i>	KC347302.1	GGAGCTGCAGCACAACAAAGT	ACCTTTCTTGTTATTAGTGC
<i>NtPIN1c</i>	XM_01665857 6	CTGCTGTTGTGCCACTTTATG	GAAAGAGAGAAGTGGAACT GCG
<i>NtPIN4</i>	KC433529.1	GCAGTCCCTTTACTTTCC	CCATTCTAGGCTACCATTT
<i>NtYUCC</i> 6	XM_01937386 8	GGTCCAGTAATTGTAGGAGC	TTGAGTTGCCATAAAGAAG C
<i>NtYUCC</i> 8	XM_01659238 8	ATGTGTATGGGTAAATGGTCC	CAGATTTTTCCAAGATTACA C
<i>NtYUCC</i> 9	XM_01663515 9	GCGAAGATGTGTTTGGGTAA	GCCATAAAGATGCAATACA ATC
<i>NtL25</i>	L18908	CCGTCCAAAAAATCTGACCC	TCTTCAAAGTCTTAGGTCGG

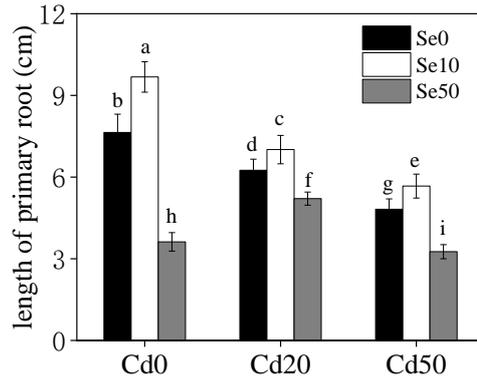


Figure S1. The length of primary root of tobacco under different Se and Cd concentration supply conditions. 14-days-old seedlings were grown in pot with sand under different Se and Cd treatments for 21 days. **Se0**: no Se; **Se10**: Se, 10 μ M; **Se50**: Se, 50 μ M; **Cd0**: no Cd; **Cd20**: Cd, 20 μ M; **Cd50**: Cd, 50 μ M. Values are presented as the means \pm SD of five biological repeats. Different letters indicate significant differences ($p < 0.05$).

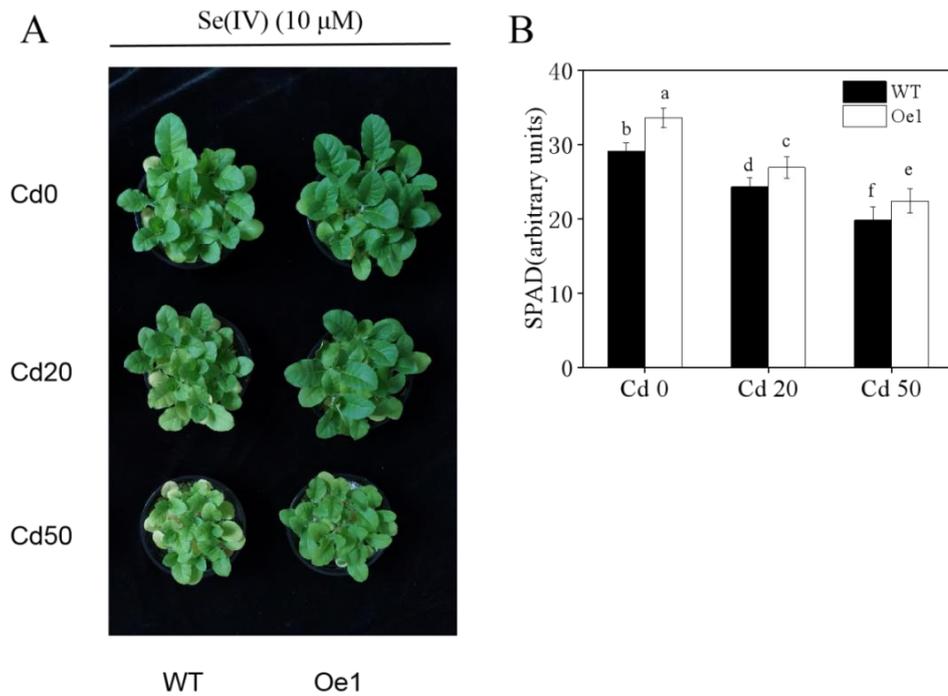


Figure S2. The phenotype and SPAD of tobacco seedlings in Se (10 μ M) and different Cd (0, 20, 50 μ M) concentrations supply conditions. WT: wild-type tobacco; Oe1: *NtPT2-Oe* transgenic tobacco. 14-days-old seedlings were grown in pot with sand under different Se and Cd treatments for 21 days. **Se0:** no Se; **Se10:** Se, 10 μ M; **Se50:** Se, 50 μ M; **Cd0:** no Cd; **Cd20:** Cd, 20 μ M; **Cd50:** Cd, 50 μ M. Values are presented as the means \pm SD of five biological repeats. Different letters indicate significant differences ($p < 0.05$). Values are presented as the means \pm SD of five biological repeats. Different letters indicate significant differences ($p < 0.05$).

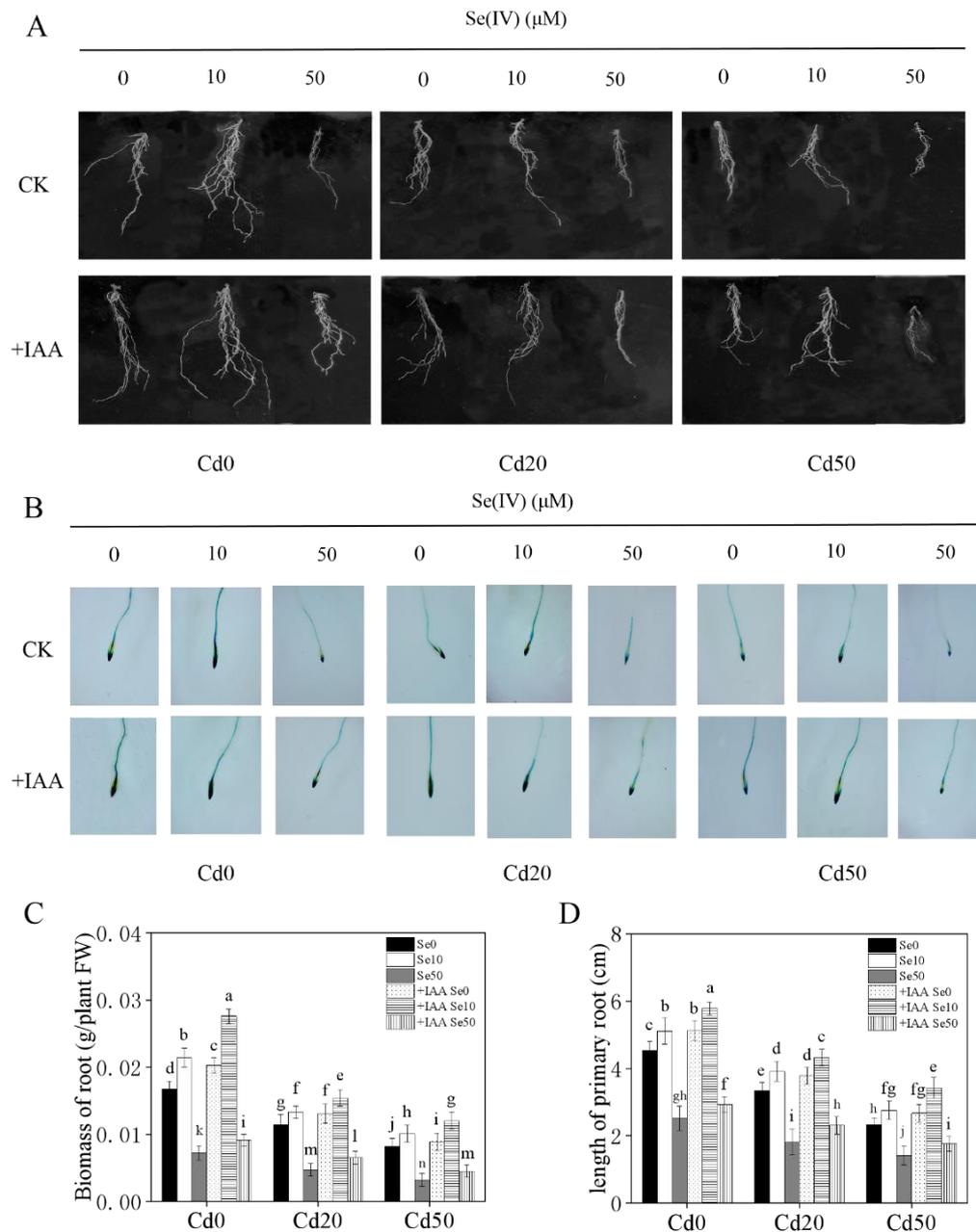


Figure S3. Characterization of root and histochemical localization of *DR5::GUS* transgenic tobacco under Se and Cd supply conditions with adding IAA (100 nM). A, The phenotype of root under different Se and Cd concentration supply conditions with adding IAA (100 nM); B, Histochemical localization of *DR5::GUS* transgenic tobacco under different Se and Cd concentration supply conditions with adding IAA; C, Biomass of root in tobacco under different Se and Cd concentration supply conditions with adding IAA (100 nM), D, Length of primary root of tobacco under different Se and Cd concentration supply conditions with adding IAA (100 nM). 14-days-old seedlings were grown in pot with sand under different Se (0, 10, 50 μM) and Cd (0, 20, 50 μM) concentrations with adding IAA (100 nM) for 7 days. **Se0**: no Se; **Se10**: Se, 10 μM ; **Se50**: Se, 50 μM ; **Cd0**: no Cd; **Cd20**: Cd, 20 μM ; **Cd50**: Cd, 50 μM . **CK**: control, no IAA. Values are presented as the means \pm SD of five biological repeats. Different letters indicate significant differences ($p < 0.05$).

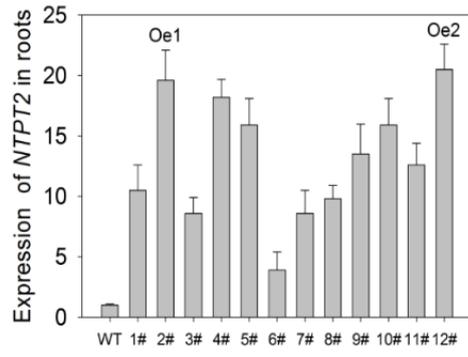


Figure S4. Expression of *NtPT2* in roots of twelve transgenic lines. Values are presented as the means \pm SD of five biological repeats. Different letters indicate significant differences ($p < 0.05$).