

Supporting Materials:

**Zinc Enhances Cadmium Accumulation in Shoots
of Hyperaccumulator *Solanum nigrum* by
Improving ATP-dependent Transport and
Alleviating Toxicity**

Table S1. Transcriptome sequencing data of *S. nigrum* leaves under Zn and Cd treatment.

Samples	Read number	Base number	GC Content	%≥Q30
CK-1	32001719	9600515700	42.23	95.11
CK-2	29860166	8958049800	42.34	92.70
CK-3	26150731	7845219300	42.30	92.93
Zn-1	20303904	6091171200	42.40	95.34
Zn-2	22102926	6630877800	44.09	95.43
Zn-3	21541203	6462360900	42.50	95.08
Cd-1	26268369	7880510700	42.52	95.46
Cd-2	20641928	6192578400	42.86	95.22
Cd-3	23629249	7088774700	42.43	95.13
ZnCd-1	28995486	8698645800	42.55	91.71
ZnCd-2	22990500	6897150000	42.73	92.44
ZnCd-3	23204534	6961360200	42.63	91.49

Table S2. Primers of some genes in *S. nigrum* for qRT-PCR.

gene names	Forward (from 5' to 3')	Reverse (from 5' to 3')
<i>MT2a</i>	GGACATTGAGAAGTCCACTACC	CACCTGCTGCTTTCTCATCTA
<i>MT2b</i>	GTCTTGCTGTGGAGGAAACT	TCAGTGATTGTGCTGCTCTC
<i>MT2bX1</i>	TCCACTACCCTCACCATCAT	CCCTCCTTCTGTTGCTTTCT
<i>MT2c</i>	TCCACTACCCTCACCATCAT	CTTGCATCCATTCCCTCCTT
<i>ZIP2</i>	AAGTCGAAGTGGATGAAGAAGG	GAGTGGAACACAATGCAAGAA
<i>ZIP10</i>	GTTCTATCCCGGCCCTAAAC	TCCGGTAACACGTGCATAAA
<i>COP5.1</i>	AACTCGGCGATTGGGTATTT	CGCCGATCCTGAAGAACAA
<i>COP6.3</i>	GTCACCACCATCACCACAAA	TGGCCAGCCTGAGAATAGA
<i>YSL2</i>	CGGTGTTGTAGCAGGACTTAT	GGTCAGATAGCTCGTCTTGAAA
<i>Sultr1</i>	AAGGTCCCTGGCATACTTATTG	GTCTTCGTCAGTTAGCCATCTT
<i>OPT3.1</i>	CTTCTTCTCGTGGGTCTGTTG	CCAGCCCAATCAAGGGTAAA
<i>PTR1</i>	GTTTGTGTGCTGCCCTATCT	CCCATTCCCTCGTGCTAATATCC
<i>NRT2.5</i>	CCGCCTCTTCTCCCAATTATC	TCACAAGCTGTTCCCATAGC
<i>NRT2.7</i>	GTGTTGTTGGGCTTGCTAATG	CCACGAAATGAACGAAGGAATG
<i>ABCC15</i>	GTACAATACAGCCCTGATCTCC	GACTTCCCACTACCTGTTCTTC
<i>EF1α</i>	CAAGATCCCATTTCGTCCCAT	GGTCAAGAGCCTCAAGGAGAGTT

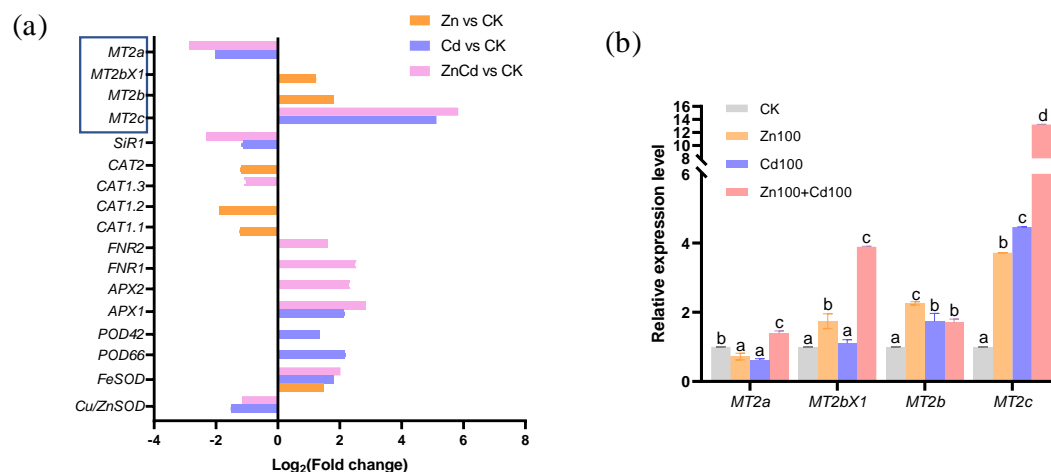


Figure S1. Expression levels of DEGs involved in antioxidant protection in leaves of *S. nigrum* by transcriptome (a) and qRT-PCR (b). Plant was exposed to a complete Hoagland solution (CK) or with 100 $\mu\text{mol}\cdot\text{L}^{-1}$ Zn (Zn100), 100 $\mu\text{mol}\cdot\text{L}^{-1}$ Cd (Cd100) and 100 $\mu\text{mol}\cdot\text{L}^{-1}$ Zn +100 $\mu\text{mol}\cdot\text{L}^{-1}$ Cd (Zn100+Cd100) for 10 days. Expression level of genes by transcriptome was showed use Log₂(Fold change) between sample sets (Zn vs CK, Cd vs CK and ZnCd vs CK). Relative expression level of MT genes by qRT-PCR denoted by different letters refer to the significant differences ($p < 0.05$, Duncan's test). *MT2a*, *MT2b*, *MT2bX1*, *MT2c*: metallothionein family members; *SiR*: sulfite reductase; *CAT*: catalase; *FNR*: ferredoxin-NADP reductase; *APX*: L-ascorbate peroxidase; *POD*: peroxidase; *FeSOD*: iron superoxidase dismutase; *Cu/ZnSOD*: copper, zinc superoxidase dismutase.

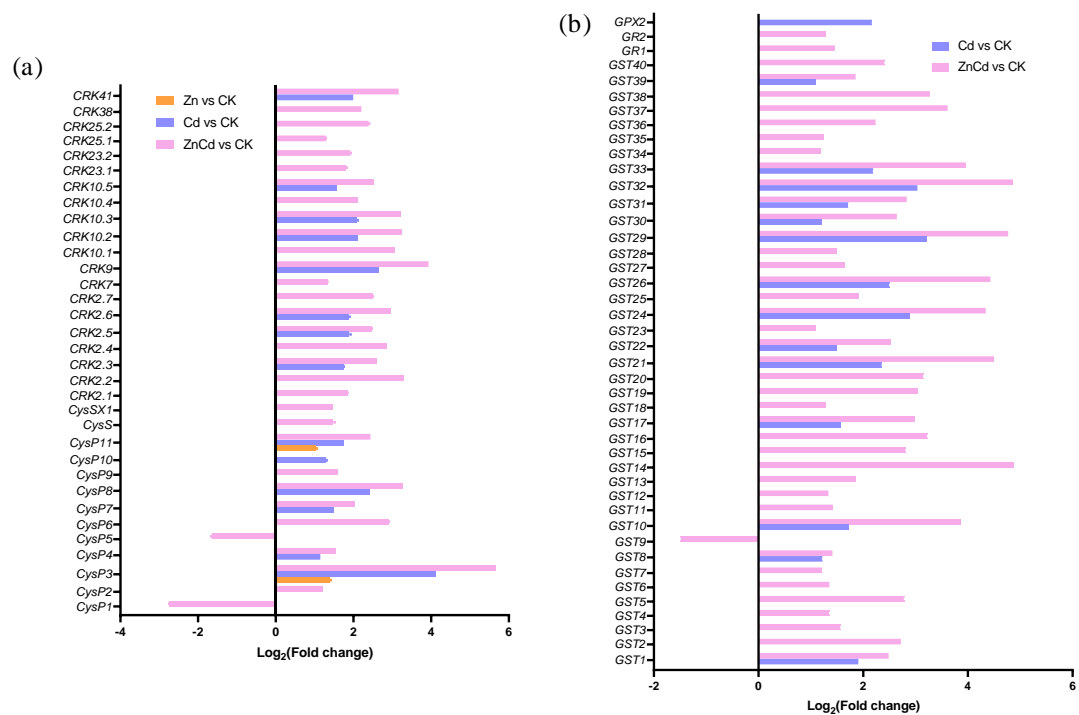


Figure S2. Expression levels of genes involved in cysteine (a) and glutathione (b) metabolism in leaves of *S. nigrum* by transcriptome. Plant was exposed to a complete Hoagland solution (CK) or with 100 $\mu\text{mol}\cdot\text{L}^{-1}$ Zn (Zn100), 100 $\mu\text{mol}\cdot\text{L}^{-1}$ Cd (Cd100) and 100 $\mu\text{mol}\cdot\text{L}^{-1}$ Zn+100 $\mu\text{mol}\cdot\text{L}^{-1}$ Cd (Zn100+Cd100) for 10 days. Expression level of gene was showed use Log₂(Fold change) between sample sets (Zn vs CK, Cd vs CK and ZnCd vs CK). GRK: cysteine-rich receptor-like protein kinase; CysS: cysteine synthase; CysP: cysteine proteinase precursor; GPX: glutathione peroxidase; GR: glutathione reductase; GST: glutathione S-transferase.