Table S1. Accumulation of Cd in *A. thaliana.* Plants were grown hydroponically for two weeks before transferring to a fresh medium containing the indicated concentrations of $CdCl_2$ for the indicated time. Plants were harvested at the bolting stage. Roots and shoots were collected and Cd content was analysed by ICP-MS. Shown are arithmetic means ± S.D (*n* = 2-4)

	Cadmium Accumulation (µg g^{-1} dry biomass)	
Growth conditions	**Root**	**Shoot**
25 µM $CdCl_2$; 3 days	2212.1 ± 174.3	1565.6 ± 145.1
1 µM $CdCl_2$;10 days	789.9 ±59.4	291.7 ±14.0
2.5 µM $CdCl_2$; 10 days	1259.8 ± 62.7	715.9 ± 1.1

Table S2. Cloning primers used in this study

Name	**5´ → 3´**
COPT2-F	GCCGCCTCGAGCATTAGTATCATGGATCATGATCAC
COPT2-R	GCGGCGAATTCACAAACGCAGCCTGAAGAC
att*B-COPT2*-F	TCGTCGGGGACAACTTTGTACAAAAAAGTTGGATTAGTATCATGGATCATGATCAC ATG
att*B-COPT2*-R	GGCGGCCGCACAACTTTGTACAAGAAAGTTGGGTTGTTCAACAAACGCAGCCT
COPT2-M111A-F	GGTGATGCTCGCTGTTGCTTCCTTTAACGCAGGTGT
COPT2-M111A-R	ACACCTGCGTTAAAGGAAGCAACAGCGAGCATCACC
COPT2-1-LP	CTGTGTCGTGAGGTTTTGAGG
COPT2-1-RP	TCTTGAGTGTGTACACAGCGG
COPT2-2-LP	GAGACAGAGAGCGTACATGCC
COPT2-2-RP	TTTATGGGGAATTCCCAAAAG
COPT1-LP	TCCTCCTCCTCACATTCACAC
COPT1-RP	CCTACATTACCCGATTTGCTG
LBb1.3	ATTTTGCCGATTTCGGAAC

Table S3. qPCR primers used in this study

Gene	**5′ → 3′**
Actin 2-F	GACCTTTAACTCTCCCGCTA
Actin 2-R	GGAAGAGAGAAACCCTCGTA
COPT1-F	CATGTCGTTTAACGCCGGTGTGTT
COPT1-R	CCGGAAAGTTTGGCTTCCGAACAA
COPT2-F	TGGTGATGCTCGCTGTTATGTCCT
COPT2-R	TCTGGTCATCGGAGGGTTTCTTGA
COPT3-F	AATGTATTGGGTCTGTCTCGCCGT
COPT3-R	GCCACGAAGACTCCTCCATTGAA
COPT4-F	AGACCGTCACTGTTACACCCAACA
COPT4-R	AGTGCATACATCCCACGGTCAGAA
COPT5-F	ATCAATACCTCGAGAATCGCCGCA
COPT5-R	AGCTGCAAGCATCAGCAAGTAACC
COPT6-F	ACACTCAAGACAGGCCTT
COPT6-R	CGAAGAGCATGAAACCCAC
SPL7-F	GAGCTGGAGGGCTATATCCG
SPL7-R	GGAAGAGGCTCGATGACTGT
miR398b/c-F	GGATCTCGACAGGGTTGATATG
miR398b/c-F	AAGAGCTCAGCAGGGGTGACCTG
FSD1-F	ACTTACAGCTTCCCAAGACAC
FSD1-R	TGCTGTGAATCCCCTTGTG
CSD1-F	TTCTGGCCTTAAGCCTGGTC
CSD1-R	CGACATGCTGGTGATCTAGG
CSD2-F	CATGACACACGGAGCTCCAG
CSD2-R	GAGCTGGAGGGCTATATCCG
F-box-F	TTTCGGCTGAGAGGTTCGAGT
F-box-R	GATTCCAAGACGTAAAGCAGATCAA

SUPPLEMENTAL FIGURE LEGENDS

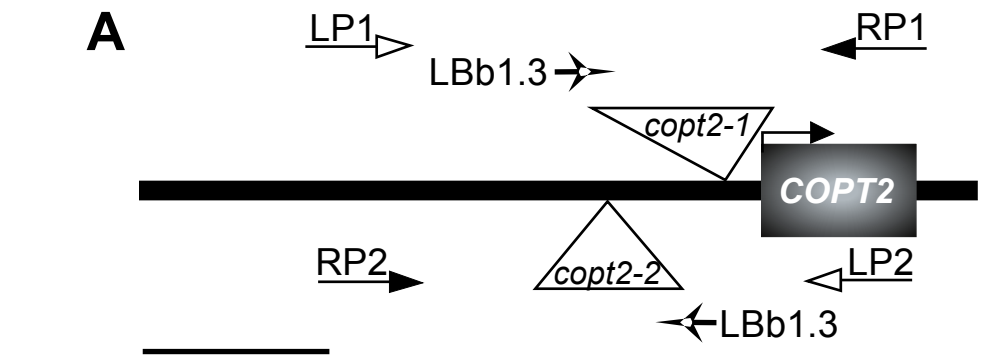
Figure S1. Basic characterization of *copt2-1* and *copt2-2* alleles. **A.** Genomic structure of *COPT2* (start codon indicated by horizontal black arrow on the black box labeled *COPT2*). Note that *COPT2* does not contain introns. Triangles indicate T-DNA insertions located 89 and 455 bp in the genomic region upstream of *COPT2* ORF in the *copt2-1 (copt2-1)* and *copt2-2 (copt2-2)* alleles, respectively. Positions of primers used for genotyping the *copt2-1* allele are indicated as arrows above and for the *copt2-2* allele below the schematic representation of the genomic structure of *COPT2*. Note that the T-DNA insertion for *copt2-1* is oriented towards the *COPT2* coding region, while the T-DNA insertion within the *copt2-2* allele is oriented in the opposite direction. Scale bar = 500 bp. **B**. Comparison of PCR products using both LBb1.3 + RP1/2 and LP1/2 + RP1/2 primer combinations and genomic DNA (gDNA) isolated from *copt2-1 (copt2-1)* and *copt2-2 (copt2-2)* mutant plants, respectively, shows that both mutants bear homozygous T-DNA insertions, in contrast to wild-type plants (Wt). LBb1.3 + RP1/2 primers used to detect T-DNA insertions produce a ~0.6 kb product for *copt2-1* and *copt2-2*, suggesting a presence of T-DNA inserts. Primer pairs LP1/RP1 and LP2/RP2 detect genomic fragments lacking the T-DNA insert and thus, PCR products of the indicated size are present in the gDNA from the wild-type but not from homozygous *copt2-1* or *copt2-2* alleles. **C**. RT-PCR detection of full-length *COPT2* transcripts (482 bp, 27 cycles) using COPT2-F and COPT2-R (Table S2) in roots of 14-day old Wt, *copt2-1* and *copt2-2* seedlings show the lack of the detectable *COPT2* transcript, in contrast to wild-type plants. *Actin2* was used as a loading control and detected using qPCR primers (141 bp Table S3). Note: 30 cycles show a faint band in *copt2-1* seedlings (not shown).

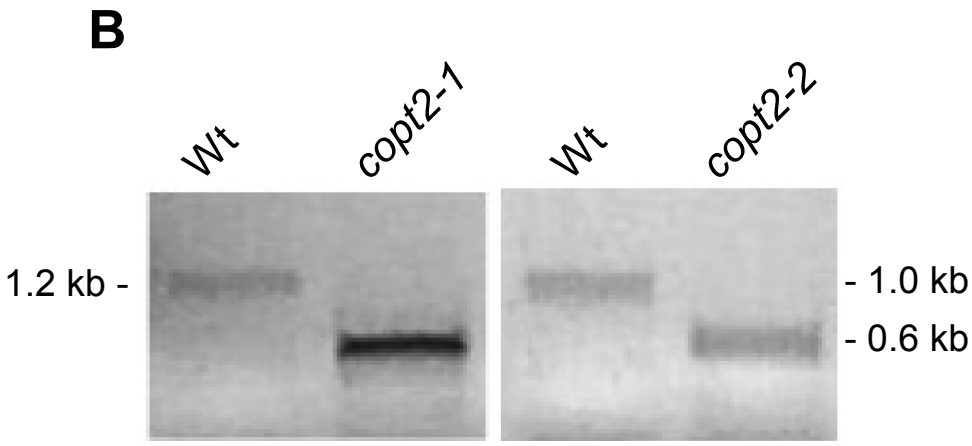
Figure S2. A. Genomic structure of *COPT1* (start codon indicated by horizontal black arrow). Note that *COPT1* does not contain introns. Gray arrowheads indicate a T-DNA insertion with a predicted location 93 bp in the promoter region of *COPT1* in the *copt1-1 (**copt1-1**)* mutant, according to the flanking sequence associated with the SALK_067183 allele. Arrowheads seen above the genomic structure indicate LP (**LP**), RP (**RP**), LBb1.3 (**LBb1.3**) primer positions. Scale bar = 500 bp. **B**. Comparison of PCR products using both LBb1.3 + RP and LP + RP primer combinations in gDNA isolated from *copt1-1 (**copt1-1**)* mutant plants indicate that the *copt1-1* allele contains homozygous T-DNA insertions, in contrast to wild-type plants (**Wt**).

LBb1.3 + RP primers used to detect T-DNA produce a ~0.8 kb product while LP + RP primers used to detect non-T-DNA bearing plants result in a 1.2 kb product.

Figure S3. RT-PCR comparison of the transcript abundance of *COPT1, COPT2* and *COPT6* in the wild-type (***Wt***) and a triple *copt1-1copt2-1copt6-1* mutant (***copt1copt2copt6***) of *A. thaliana.* Plants were grown on solid ½ MS medium for 10 days prior RNA extraction and cDNA synthesis. *COPT1 (**COPT1**), COPT2 (**COPT2**)* and *COPT6 (**COPT6**)* transcripts were detected using qPCR primer pairs (Table S3) and *Actin2* (***ACTIN2***) as a loading control. Reactions were run for 27 cycles before detection.

Figure S1





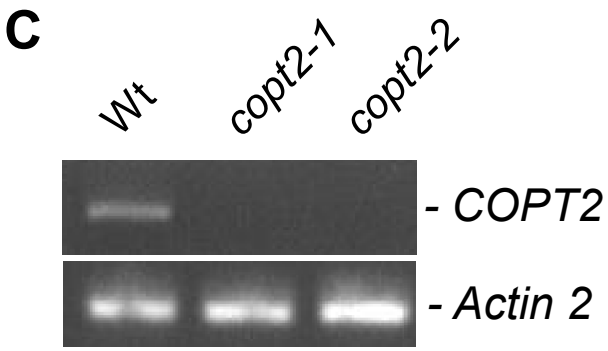


Figure S2

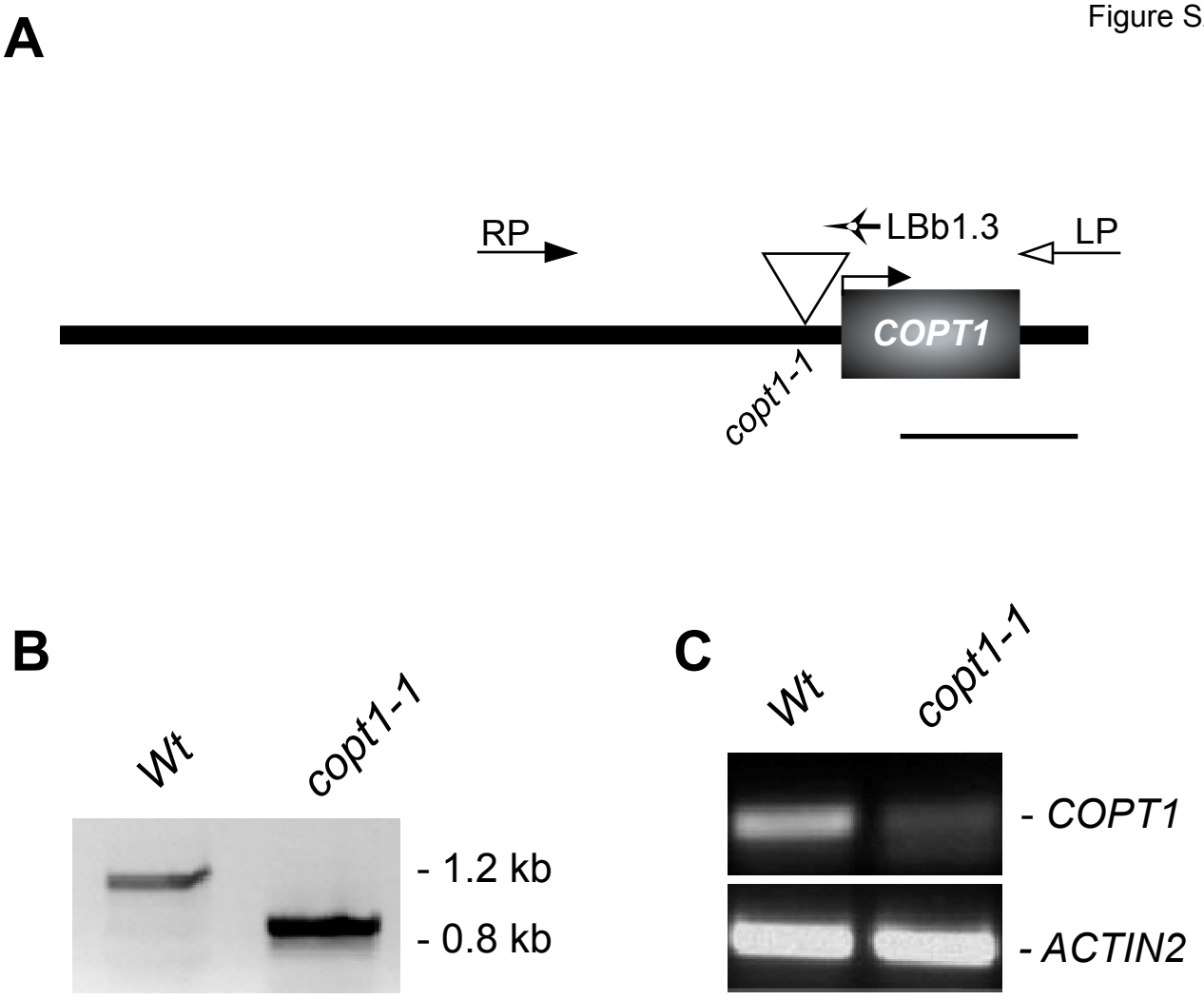


Figure S3