

Figure S1: Amino acid alignments of AtHMA2 and AtHMA3 according to ClustalW multiple alignment.

The transmembrane segments (TMD), Metal Binding Domain (MBD), HMA, and P-ATPase signatures are indicated. The arrow indicates the position of the base pair deletion in the gene encoding *AtHMA3*, which was observed in the Col-0 ecotype genome. This deletion induces a premature stop codon immediately downstream.

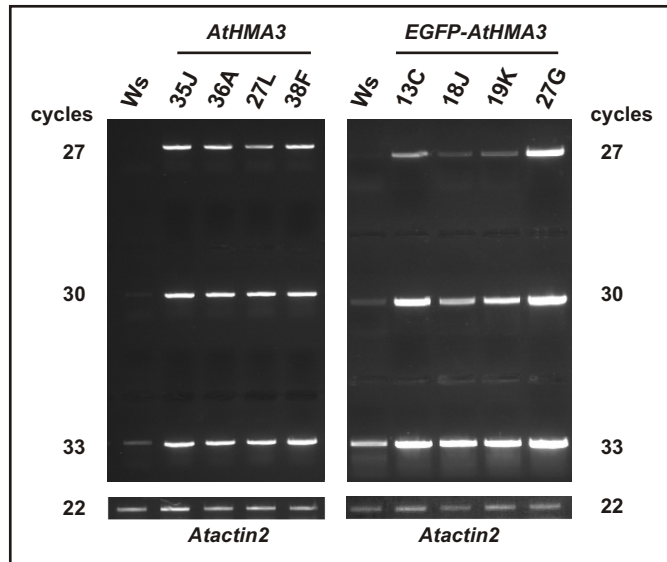


Figure S2: AtHMA3 transcripts are enhanced in 35S::AtHMA3 and 35S::EGFP::AtHMA3 overexpressing plants.

A 630 bp fragment of the AtHMA3 cDNA was amplified by RT-PCR, using total extracted RNAs from leaves of the various lines (wild-type Ws and overexpressing lines 35J, 36A, 27L, 38F, 13C, 18J, 19K and 27G). Atactin 2 cDNA was used as control.

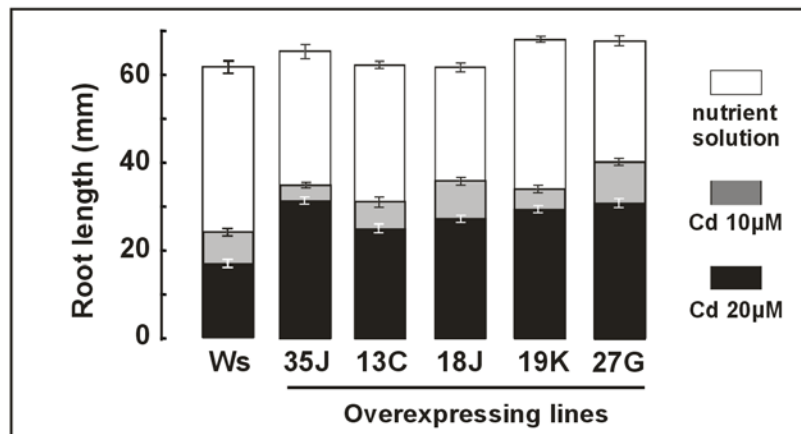


Figure S3: Root lengths of wild-type and various *35S::AtHMA3* and *35S::EGFP::AtHMA3* overexpressing lines under metal stress.

Experiments were performed as described in the legend of figure 3.