

**Title: The Mutation of Glu at Amino Acid 3838 of AtMDN1 Provokes Pleiotropic Development Phenotypes in Arabidopsis**

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**Supplementary information**

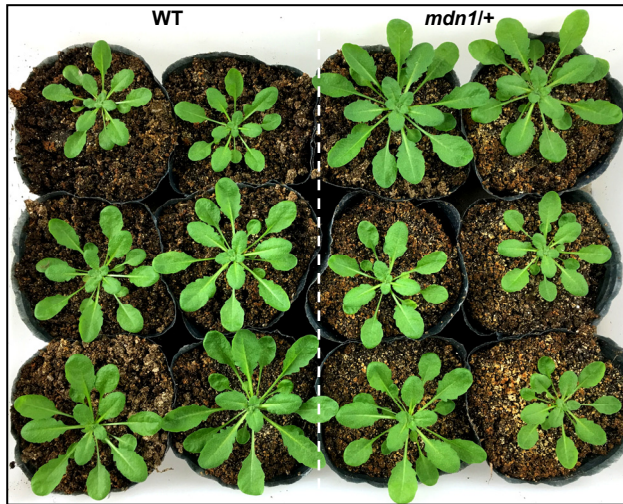
Supplementary Figure 1. Phenotype of *mdn1* heterozygote.

Supplementary Figure 2. Conservation analysis of MDN1 proteins.

Supplementary Figure 3. Expression pattern analysis of *AtMDN1* using public database.

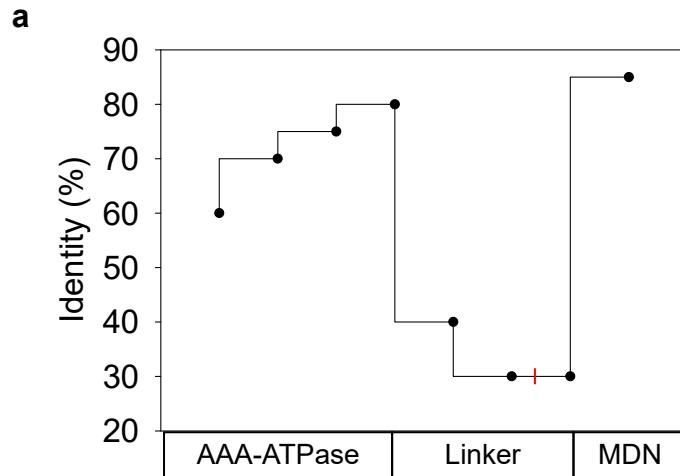
Supplementary Figure 4. Pearson correlation analysis of different samples. rep, repeats.

Supplementary Table 1. Key primers used in this study.



**Supplementary Figure 1. Phenotype of *mdn1* heterozygote.**

Wild type and heterozygote of *mdn1* are grown for 4 weeks under normal conditions.



**b**

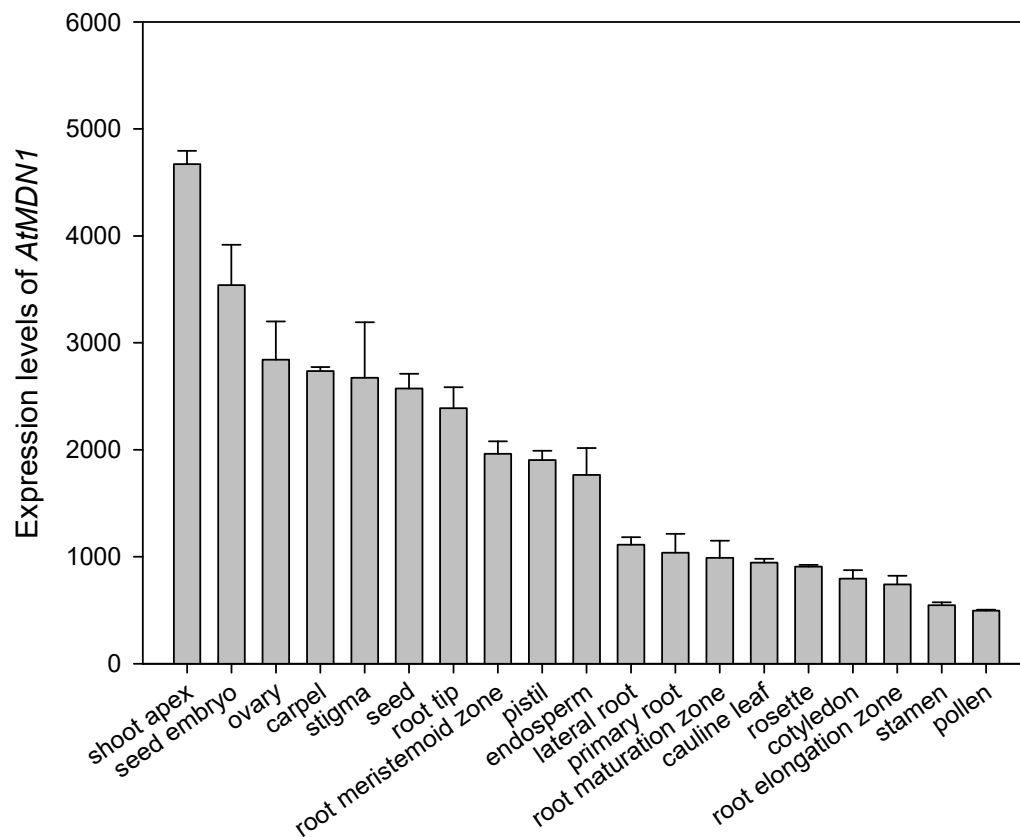
<i>A. thaliana</i>	ISQSLVEFIETSNVGEFRRRLQLLFCFLLQL
<i>D. rerio</i>	VSSSLQAFIEGSTLGEFVSRLSMLLGFHCHI
<i>S. cerevisiae</i>	LVSSLNLFFSKSTLGEFNARLDLVKAFYKHI
<i>M. musculus</i>	LVSTLQAFIEGSSLGEFHVRLQMLLVFHCHV
<i>H. sapiens</i>	LVSTLQAFIEGSSLGEFHVRLQMLLVFHCHV

GEF

**Supplementary Figure 2. Conservation analysis of MDN1 proteins.**

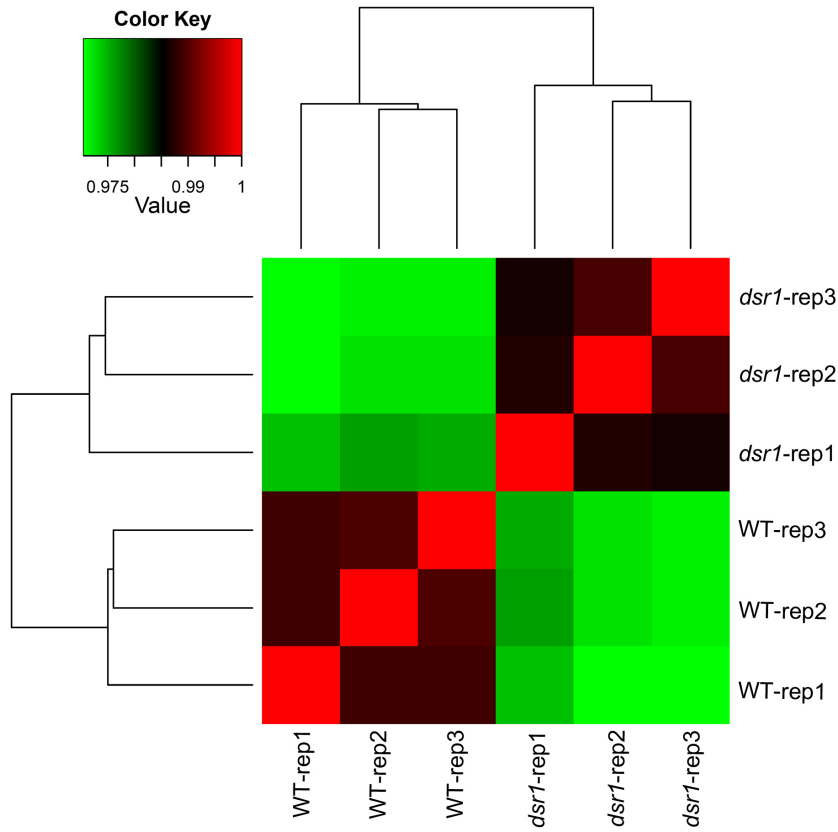
(a) Conservation analysis of the AAA, the linker, and the MIDAS (MDN) domains in MDN1 homologues of organisms showed in **b** and Fig. 3a. The red bar indicates the mutation site of *dsr1*.

(b) Conservation analysis of the GEF motif in MDN1 homologues of *Danio rerio* (XP\_003200751.2), *Saccharomyces cerevisiae* (NP\_013207.1), *Mus musculus* (XP\_006537539.1) and *Homo sapiens* (NP\_055426.1).



**Supplementary Figure 3. Expression pattern analysis of *AtMDN1* using public database.**

Tissue-specific expression pattern of *AtMDN1*. The data are collected from Genevestigator.



**Supplementary Figure 4.** Pearson correlation analysis of different samples. rep, repeats.

## Supplementary Table 1. Key primers used in this study.

Purpose	Primer name	Sequence (5'-3')
<i>AtMDN1 promoter</i>	forward (P1)	ATCCAAAATGGTCAGCTG
	reverse (P2)	TGAAACCTGTTGACAAAC
qRT- PCR	<i>MDN1</i> -forward	GTCACATGATCGGTCTAG
	<i>MDN1</i> -reverse	CCCTGTTTCTCCTACTAAG
	<i>PCAP2</i> -forward	ACCGGAGGAAATAATTGC
	<i>PCAP2</i> -reverse	CTGGCTTCTTCTCTTCCA
	<i>GOX3</i> -forward	GATGGAATATGAGAAGATCG
	<i>GOX3</i> -reverse	GGCATAGAAATATTAACCCTA
	<i>FER2</i> - forward	CTACCCCTTTTGTTCCTC
	<i>FER2</i> - reverse	CTGTCAAAGTAGGCATAC
	<i>PER1</i> - forward	GGTCCTGACAGTAAGATAA
	<i>PER1</i> - reverse	GTGGCGATCTTGTTATTG
	<i>RAD50</i> - forward	GACACTGAATCGAGAAAG
	<i>RAD50</i> - reverse	CCTGTTCCGTCTTCTTTA
	<i>EM6</i> -forward	GAAGGATATCAGCAGATG
	<i>EM6</i> -reverse	GGTCCTGAATTGGATTG
	<i>CRC</i> -forward	TGGTGAAGTACTATAAGA
	<i>CRC</i> -reverse	TCTGCTTCTTCTCAGGAG
	<i>SMC3</i> -forward	CTCGTGCTAATCCTTACTA
	<i>SMC3</i> -reverse	TCCGTTTATTTCTGTTTC
	<i>TOP2</i> -forward	GACCTTACTTCTCATTGC
	<i>TOP2</i> -reverse	GCACAACATCAATTCAA
	<i>GRF5</i> -forward	CTCTCATTACCAACAAC
	<i>GRF5</i> -reverse	AGCAGAATAAGTAGTAGAAGA
	<i>ELIP2</i> -forward	CAAGCCTAAGGTGAGTAC
	<i>ELIP2</i> -reverse	TCCCTTTGATAACTCCATG
	<i>PAP85</i> -forward	TCTCCTTATCTCCATAGC
	<i>PAP85</i> -reverse	GGAACCAATCACTGAAAC
<i>Actin2</i> -forward	CTTCGTCTTCCACTTCAG	
<i>Actin2</i> -reverse	ATCATACCAGTCTCAACAC	