

Supplementary materials

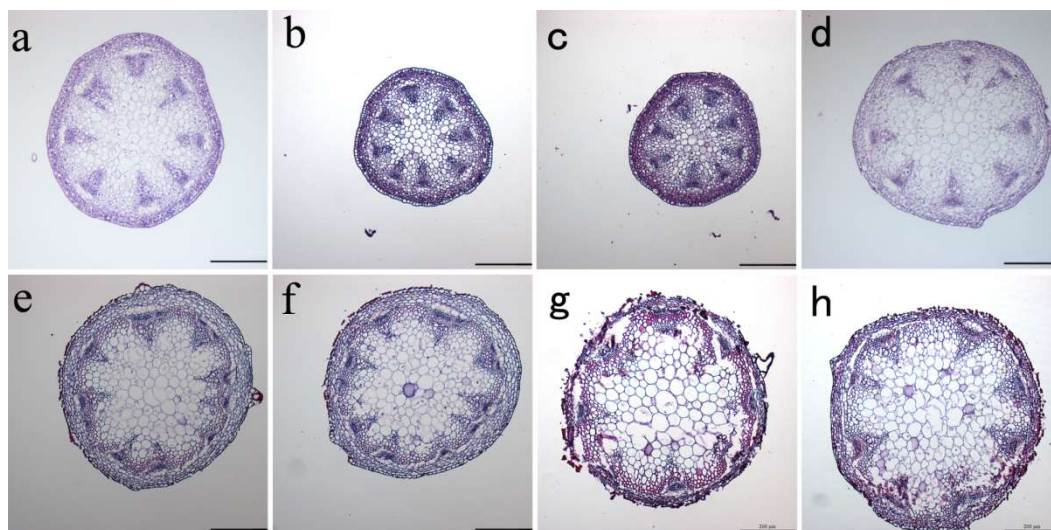


Figure S1. (a–d) Plants growth status at T1 stage. (a) is wild-type (WT), (b) is GABI_355H03 (*hdt1-1*), (c) is GABI_768H10 (*hdt1-2*) and (d) is CT. (e–h) Plants growth status at T2 stage. (e) is wild-type (WT), (f) is GABI_355H03 (*hdt1-1*), (g) is GABI_768H10 (*hdt1-2*) and (h) is CT. Scale bars = 200 μm (a–h)

Table S1. Area analysis of stem in WT and *hdt1*

Area	WT	<i>hdt1</i>	Difference (<i>hdt1</i> vs. WT)	<i>p</i> -Value
Pith (mm^2)	0.3194 ± 0.0197	0.1923 ± 0.0115	–39.82%	$p < 0.01$
Xylem (mm^2)	0.1222 ± 0.0118	0.0899 ± 0.0031	–26.43%	$0.01 < p < 0.01$
Phloem (mm^2)	0.0432 ± 0.0028	0.0394 ± 0.0023	–9.05%	$0.01 < p < 0.05$

The analyses were performed based on WT and *hdt1* stems at T3 stage. Data shown are average $\pm$ SD. *p*-values were determined by Student's *t* test ($n \geq 10$).

Table S2. Primer information used for reverse transcription-polymerase chain reaction (RT-PCR)

Primer Name	Sequence(5'-3')
AtActin2F	5' CATCCTCCGTCTTGACCTTGC 3'
AtActin2R	5' CAAACGAGGGCTGGAACAAG 3'
AT5G13330-F	5' TAAATCGGATCAACATCAACCAG 3'
AT5G13330-R	5' CGAAAGTCCCGAGCCAGA 3'
AT3G22640-F	5' GGTAGGGTTTGGTATTTATGCG 3'
AT3G22640-R	5' TTTGGCTCGTGAACAGTTTCT 3'
AT5G28640-F	5' TTCAACGCAACCTAATGTACCTAG 3'
AT5G28640-R	5' AATCATCCCACCACCAGCA 3'
AT2G42840-F	5' TTCTGTTGCTTCCGTAAGGTTT 3'
AT2G42840-R	5' GGAGTTGAAGGAGAAGGGTCGT 3'
AT5G17420-F	5' TTCCAGCCATCTGTCTCCT 3'
AT5G17420-R	5' CTAAGTCCGCTCCATCTCAA 3'
AT5G44030-F	5' GCCGTTTGTCTTCTCACCG 3'
AT5G44030-R	5' TGATGCTTACACCACTCCACC 3'
AT5G01040-F	5' CCAGGCGGATGGGTTGT 3'
AT5G01040-R	5' CGGAGTTGGCCCGTTTT 3'
AT5G60020-F	5' CGATTCCTTGCAGATAACCCAG 3'
AT5G60020-R	5' CCAAGCCATCCTCAGACCC 3'
AT3G23030-F	5' GAAGAATCTACACCTCCTACCAA 3'
AT3G23030-R	5' CTCCGTCCATACTCACTTTCA 3'
AT3G15540-F	5' ATGATGATCTAGCCTTTGCTCTTG 3'
AT3G15540-R	5' TTCGCAGTTGTCACCATCTTTC 3'
AT5G07310-F	5' AATCAACAAGATCCTAACCCACC 3'
AT5G07310-R	5' GCTGCCCCACTTTCCCCAT 3'
AT2G47520-F	5' AAGAAGCGTAAACCCGTCTCA 3'
AT2G47520-R	5' TGGCCTCTGCCTTATCCCT 3'

Table S3. qRT-PCR corroboration of differentially expressed genes.

Gene ID		Change Fold	
		Transcriptomic Data	qRT-PCR
AT5G13330	<i>ERF113</i>	-1.9415	-1.3577
AT3G22640	<i>PAP85</i>	-10.417	-2.3427
AT5G28640	<i>GIF1</i>	-4.6295	-1.8356
AT2G42840	<i>PDF1</i>	-5.894	-2.6308
AT5G44030	<i>CESA4</i>	2.0603	1.9431
AT5G17420	<i>CESA7</i>	1.7013	1.1501
AT5G01040	<i>LAC8</i>	7.5751	2.7969
AT5G60020	<i>LAC17</i>	2.4538	1.9139
AT3G15540	<i>IAA19</i>	1.7525	1.2624
AT3G23030	<i>IAA2</i>	1.6792	1.4578
AT5G07310	<i>ERF115</i>	3.0198	2.1857
AT2G47520	<i>ERF071</i>	8.1782	2.1967
Pearson correlation coefficient		0.921433	

Fold-change: Log₂ (*hdt1*/wild type).