

**Table S1.** Oligonucleotide primers used in this work.

Primer	Sequence (5'-3')	Use
abi1-2-LP	AGGAAACCCCTTATTGAAATTC	Identification of <i>abi1-2</i> allele (use with LBa1)
abi1-2-RP	CTCTGTTCTGCTGATCATCT	
hab1-1-LP	ACAATGGCTTGTAGGTTGCTG	Identification of <i>hab1-1</i> allele (use with LBa1)
hab1-1-RP	GCTTCAGGTTCTGGTCTTGAAC	
LBa1	TGGTTCACGTAGTGGGCCATCG	Identification of <i>abi1-2</i> and <i>hab1-1</i>
abi3-F	GCGATGAAGCAGCTTTTAAAGCGAATT	Identification of <i>abi3-8</i> by dCAPS marker. The <i>EcoRI</i> digestion products are either 180 bp + 20 bp ( <i>abi3-8</i> ) or 200 bp (wild type allele)
abi3-R	GGTGGAGGAACCCATGTTGAAG	
abi4-F	GTCACGTGCTCAGCTCAACTT	Identification of <i>abi4-1</i> by dCAPS marker. The <i>NlaIV</i> digestion products are either 191 bp ( <i>abi4-1</i> ) or 161 bp + 30 bp (wild type allele)
abi4-R	TTAAAAGGGATACCGTACGGAC	
abi5-F	GAGTCGTCCATGGCGCAAG	Identification of <i>abi5-7</i> by dCAPS marker. The <i>BamHI</i> digestion products are either 207 bp ( <i>abi5-7</i> ) or 187 bp + 20 bp (wild type allele)
abi5-R	GATTGTTATTATCTCCTCTGGGAT	
pHRS1-F	AATGAGCTCAGCTAGTTTTTCGAGTTCAAGCTAG	Amplifying the 5' flanking sequence of <i>HRS1</i> (1617 bp) for preparing complementation and <i>pHRS1::HRS1-GFP</i> lines
pHRS1-R	ATTAAGCTTGATGATACTTTAGGGACTTAATTT	
HRS1-F1	TTAAAGCTTATGATTAATAAAGTTCAGC	Amplifying the genomic sequence of <i>HRS1</i> (1615 bp) for preparing complementation lines
HRS1-R1	TTAGGATCCTTAATTATCTTGACGTA	
HRS1-F2	TTAAAGCTTATGATTAATAAAGTTCAGC	Amplifying the cDNA sequence of <i>HRS1</i> (1032 bp) for constructing <i>pHRS1::HRS1-GFP</i> transgenic lines
HRS1-R2	TAAGTCGACCATTATCTTGACGTAATG	
HRS1-F3	AACATTTTCGTAGTCGTCGGTG	Specific for <i>HRS1</i> transcripts, used in quantitative PCR assay
HRS1-R3	ACGGGTAGAAGAAGACATCGC	
ABI3-F	ACAGGGATGGAAACCAGAAAA	Specific for <i>ABI3</i> transcripts, used in quantitative PCR assay
ABI3-R	TTCCAAACACGAGAGGTTCC	
ABI4-F	AGGGACAATTCCAACACCAAC	Specific for <i>ABI4</i> transcripts, used in quantitative PCR assay
ABI4-R	CCACTTCCTCCTTGTTCCCTG	
ABI5-F	AACCTAATCCAAACCCGAACC	Specific for <i>ABI5</i> transcripts, used in quantitative PCR assay
ABI5-R	TACCCTCCTCCTGTCTCT	
ACT8-F	ATATGCCTATCTACGAGGGTTTC	Specific for <i>ACT8</i> transcripts, used in quantitative PCR assay as internal standard
ACT8-R	ATACAATTTCCCGTTCTGTGT	

The underlined nucleotides form *SacI* (GAGCTC), *HindIII* (AAGCTT), *BamHI* (GGATCC) or *SalI* (GTCGAC) restriction digestion sites.