

Table 1 Suppl. Primers used in the study.

Primer name	Primer sequence (5'-3')
<i>SIWHY2-QRT-F</i>	CGGTTTACTGTTCTGTCAC
<i>SIWHY2-QRT-R</i>	CTCCGCCTCCATTAGTTGTG
<i>EF-1α-F</i>	GGAACCTTGAGAAGGAGCCTAAG
<i>EF-1α-R</i>	CAACACCAACAGCAACAGTCT
<i>NtUbiquitin-F</i>	TCCAGGACAAGGAGGGTAT
<i>NtUbiquitin-R</i>	CATCAACAACAGGCAACCTAG
<i>NtMnSOD-F</i>	AGCTACATGACGCCATTTCC
<i>NtMnSOD-R</i>	CCCTGTAAAGCAGCACCTTC
<i>NtAPX-F</i>	CAAATGTAAGAGGAACTCAGAGGA
<i>NtAPX-R</i>	CAGCCTTGAGCCTCATGGTACCG
<i>NtPR1a-F</i>	CCGTTGAGATGTGGGTCGAT
<i>NtPR1a-R</i>	CAACACGAACCGAGTTACGC
<i>NtPR2-F</i>	CATAACCTTCCACTCTTA
<i>NtPR2-R</i>	AAGAAAGTGGGACATCAG
<i>NtAOX1a-F</i>	GGATGACCCGAAGTGTGTTG
<i>NtAOX1a-R</i>	GCTTTCTTGTCGTGCTGCTTA
<i>NtAOX1b-F</i>	TGGCTCANCATCGTGG
<i>NtAOX1b-R</i>	CGTTCTCAATGTTGCC CTTGT
<i>NtCOX1-F</i>	ATAGAGGAGTTCCAGAAGTGT
<i>NtCOX1-R</i>	AGTTTCCTTCCTGTAAGCCT
<i>NtORF1-F</i>	AGATGTATCAGCCCAGACTT
<i>NtORF1-R</i>	ACGACTCTCTCTGGCACAAC

Table 2 Suppl. Prediction of subcellular localization of *SIWHY2* using software program *TargetP 1.1*. (<http://www.cbs.dtu.dk/services/TargetP/>). Numbers given under the cTP, mTP, SP, and others represent the localization probabilities of *SIWHY2* in different subcellular regions (length - the length of amino acid sequence; cTP - chloroplast transit peptide; mTP - mitochondrial targeting peptide; SP - secretory pathway signal peptide).

Gene	Length	cTP	mTP	SP	Others
<i>SIWHY2</i>	241	0.015	0.928	0.006	0.384