Table 1. Primer sequences used for qRT-PCR.

Gene ID	Forward Primer Sequence (5′-3′)	Reverse Primer Sequence (5′-3′)
GAPDH	GTACGACAACGAATGGGGTTA	TCATATCAGCAGCACCAGCA
Sme2.5_01907.1_g00015.1	AACCAGACAGCAAGAATCA	CAACCAACATCACCATTAGG
Sme2.5_00108.1_g00003.1	TCACTACTAATCCTCAACTCC	AATTCCTACCACTCAATGCT
Sme2.5_04516.1_g00001.1	GGATTCGGAGAGCATACG	GGTGAGGTGATACTGGAAC
Sme2.5_00538.1_g00012.1	TTCACTGCCAATCAATCCA	TTCCAACCAACTTCCTGTAA

Table 2. Pearson correlation coefficient analysis of WT and *dwf* RNA-seq samples.

	dwf-1	*dwf*-2	*dwf*-3	WT-1	WT-2	WT-3
dwf-1	1	0.979	0.988	0.907	0.941	0.93
dwf-2	0.979	1	0.986	0.921	0.955	0.943
dwf-3	0.988	0.986	1	0.915	0.949	0.938
WT-1	0.907	0.921	0.915	1	0.961	0.984
WT-2	0.941	0.955	0.949	0.961	1	0.981
WT-3	0.93	0.943	0.938	0.984	0.981	1