

Table S1. The primers information for the qRT-PCR

Gene id		Sequence (5'-3')	Primer length (bp)	Tm(°C)	GC%	Starting base position	Product length
Lba01g01874	F	AGGTGCTTGTTGTGAACCCA	20	60.03	50.00%	716	214
	R	CGTGCTTTAAACAGTGCCCC	20	60.04	55.00%	929	
Lba01g02344	F	GACGTGTGCTGTCAGGAGAA	20	60	55.0%	1004	150
	R	TCTTCACCGCTTTGCCAGAT	20	60	50.0%	1153	
Lba02g00136	F	TTGGACCTTTAGCGGCTCAG	20	60.04	55.00%	362	211
	R	GCACGACGATGAAGAGGAGT	20	59.83	55.00%	572	
Lba02g00994	F	AGCCACGCATCTGGAAATT	20	60.3	50.0%	468	300
	R	GGAGTCAAATGCTTCGCTGC	20	60.2	55.0%	767	
Lba03g00118	F	ATGTCACCGAGCGTGTTCTT	20	60	50.0%	368	273
	R	ATGGCTTCTTGGTCTGGAGC	20	60	55.0%	640	
Lba03g01605	F	TGCTGCTGGTATGAGTGGTG	20	60.04	55.00%	4692	162
	R	CTGTTTGTGTGACGCTGGTG	20	59.97	55.00%	4853	
Lba04g01211	F	TCCAAGTCTGTTCGAGCCAC	20	60	55.0%	937	172
	R	GCATTTTCCCTTGATGGCCC	20	59.8	55.0%	1108	
Lba05g01557	F	GCTGTTGGAAAAGTGCTCCC	20	59.7	55.0%	460	149
	R	TCCTCCTTGATTGCAGCCTT	20	59.3	50.0%	608	
Lba05g02210	F	AAGCAACTACAGCCACACGA	20	59.9	50.0%	1030	225
	R	CGCGCCATAAACAATTCGGT	20	59.9	50.0%	1254	
Lba06g01747	F	AACCTCGCTGCTGATATGGG	20	59.9	55.0%	289	158
	R	TCGGGGTAAATGCAAGCACT	20	60	50.0%	446	
Lba06g02033	F	GGGAGTTGGCAGTGAAGGAA	20	59.9	55.0%	893	181
	R	TCGGCTTCTTCCCTCAGGTC	20	59.4	55.0%	1073	

Lba07g00206	F	GAATGGACGTGGGGGAAGAG	20	60.1	60.0%	153	109
	R	TAGCTCATGCCCTGGTTTGG	20	60	55.0%	261	
Lba07g00818	F	GTGGTGAGACGAGCTGAACA	20	60	55.0%	154	254
	R	CCCCATGTTGGCTGTGGTAT	20	60	55.0%	407	
Lba07g02052	F	ACCAAGTCTCCGATGCAGTG	20	60	55.00%	62	163
	R	TCCCTGCAAGTGTCACGTAC	20	60	55.00%	224	
Lba07g02085	F	TCAGTCGCTCGAAAATGCCT	20	60	50.0%	1556	121
	R	CCCATCTCCTTTGCCTTGGT	20	60	55.0%	1676	
Lba08g02201	F	TTCAAGGATCTGACCACCGC	20	60	55.0%	1214	258
	R	GCTCTCCGTGAACCAAGACA	20	60	55.0%	1471	
Lba11g01391	F	GCCTCCTCAATCCCAACGAA	20	60	55.0%	141	149
	R	TTCCCAACACCATGTCCTCG	20	60	50.0%	289	
Lba11g01902	F	TCCTCCCAATGTTGCTGCTT	20	59.9	50.0%	444	155
	R	CAAATGCACCCGTCCCAATC	20	59.8	55.0%	598	
LbaCML38	F	CGGTGGTTCTTCTGGTTCATCAA	23	57.37	47	/	/
	R	TCTTCTGTGCCTCCTCATTAATC	25	57.24	43	/	
GAPDH	F	TGGTGCTGACTTCGTCGTTGA	21	58.12	52	/	/
	R	TTGCTAGGAGCGGAGATCACAA	22	57.52	50	/	