



Supplementary Fig. S1 Phenotype of peels in green ripe fruits. Green ripe fruits phenotype of yellow colour peel **(A)** and colourless peel **(B)** in the F2 generation of *M82* × LBS.

SL4.0 ch03

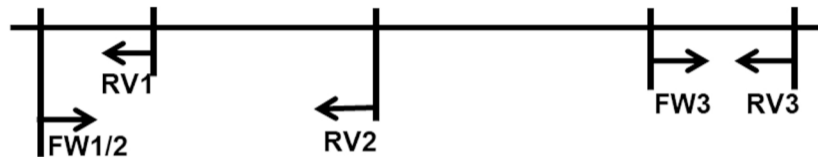
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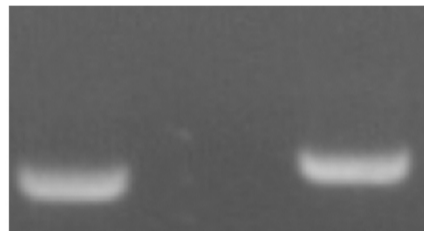
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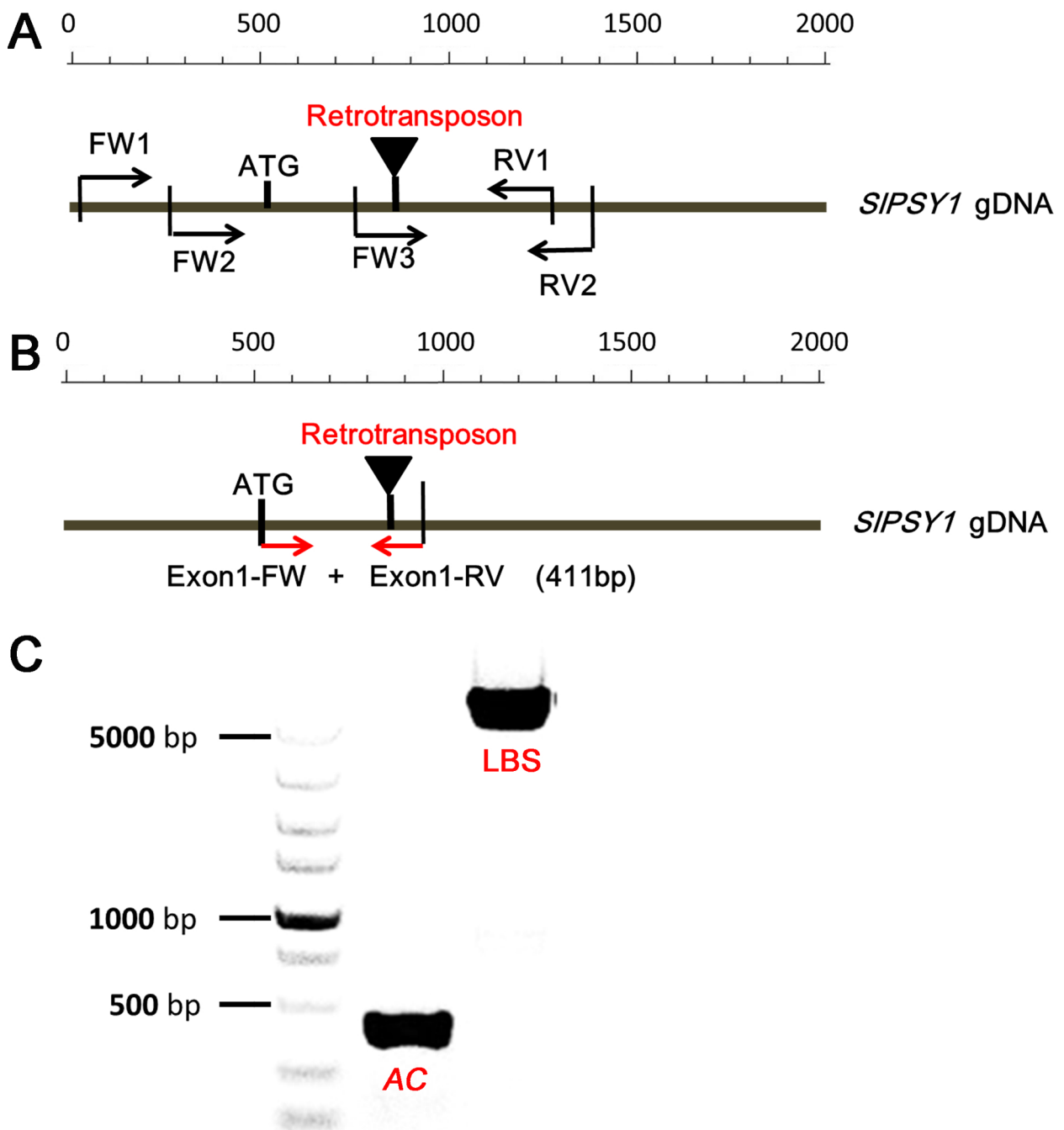


SIPSY1-gDNA



FW1/2+RV1 FW1/2+RV2 FW3+RV3

Supplementary Fig. S2 PCR analysis of the *PSY1* gene. Three fragments were designed for PCR-based analysis of *PSY1* gene presence or not. The genomic positions of these fragments were showed in the left. And the amplification of these fragments was showed in the right.

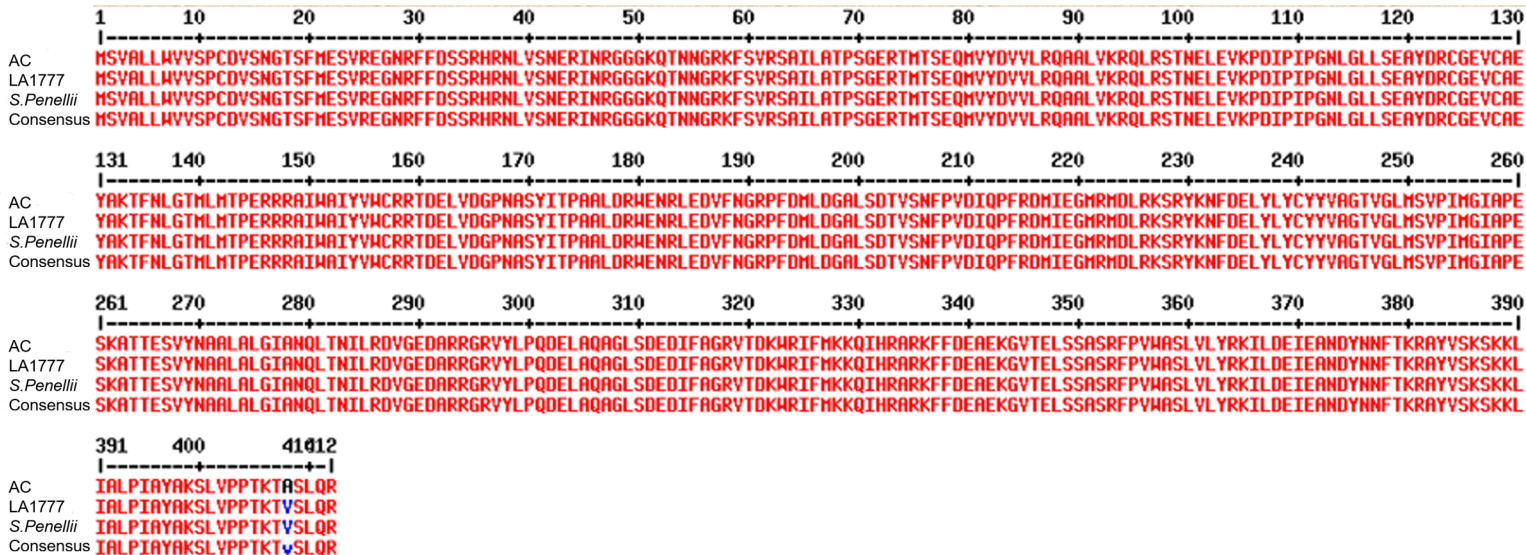


Supplementary Fig. S3 Identification of a transposon in the first exon of the *PSY1* gene in LBS. **(A)** Tail PCR-based analysis of the *PSY1* gene in LBS. The *PSY1*-specific primers (FW1/FW2/FW3 and RV1/RV2) and four short arbitrary degenerate primers were used to amplify the fragment using genomic DNA from LBS. **(B)** A pair of *PSY1*-specific primers (Exon1-FW and Exon1-RV) were used for amplification of the fragment of the *PSY1* gene in LBS. **(C)** Amplification products of genomic DNA fragment using the *PSY1*-specific primers Exon1-FW and Exon1-RV in AC and LBS. A fragment of expected size of 411 bp was amplified in the tomato control AC genome, whereas a much larger DNA product of about 5 kb was generated using LBS genomic DNA. The expected size of the PCR product would be about 5.2 kb comprising a retrotransposon of 4866 bp and the flanking sequence (411 bp) of exon 1 of the *PSY1* gene in LBS.

CopiaSL_37	0
Kielia	0
LBS-FCR	GGTTTCTTCTGTAGGCTCAATGGGACAGTTTTCAGGATCAGTCGGGAGGAAACCGTTTTTTTGTTCATCGAGGACATAGAAATTTGGTCTCAATGAGAAATCAATAGAGTGGTGGAAAGCAACTAATAAGGACGGAATTTTCTGACGGCTGCTATTTTGGCTACTCCATCTGGAGACGAGCATGACATCGGACAGATGGTCT	220
Consensus	
CopiaSL_37	144
Kielia	144
LBS-FCR	144
Consensus	144
CopiaSL_37	364
Kielia	364
LBS-FCR	364
Consensus	364
CopiaSL_37	584
Kielia	584
LBS-FCR	584
Consensus	584
CopiaSL_37	804
Kielia	804
LBS-FCR	804
Consensus	804
CopiaSL_37	1024
Kielia	1024
LBS-FCR	1024
Consensus	1024
CopiaSL_37	1244
Kielia	1244
LBS-FCR	1244
Consensus	1244
CopiaSL_37	1464
Kielia	1464
LBS-FCR	1464
Consensus	1464
CopiaSL_37	1684
Kielia	1684
LBS-FCR	1684
Consensus	1684
CopiaSL_37	1904
Kielia	1904
LBS-FCR	1904
Consensus	1904
CopiaSL_37	2124
Kielia	2124
LBS-FCR	2124
Consensus	2124
CopiaSL_37	2344
Kielia	2344
LBS-FCR	2344
Consensus	2344
CopiaSL_37	2564
Kielia	2564
LBS-FCR	2564
Consensus	2564
CopiaSL_37	2784
Kielia	2784
LBS-FCR	2784
Consensus	2784
CopiaSL_37	3004
Kielia	3004
LBS-FCR	3004
Consensus	3004
CopiaSL_37	3224
Kielia	3224
LBS-FCR	3224
Consensus	3224
CopiaSL_37	3444
Kielia	3444
LBS-FCR	3444
Consensus	3444
CopiaSL_37	3664
Kielia	3664
LBS-FCR	3664
Consensus	3664
CopiaSL_37	3884
Kielia	3884
LBS-FCR	3884
Consensus	3884
CopiaSL_37	4104
Kielia	4104
LBS-FCR	4104
Consensus	4104
CopiaSL_37	4324
Kielia	4324
LBS-FCR	4324
Consensus	4324
CopiaSL_37	4544
Kielia	4544
LBS-FCR	4544
Consensus	4544
CopiaSL_37	4764
Kielia	4764
LBS-FCR	4764
Consensus	4764
CopiaSL_37	4984
Kielia	4984
LBS-FCR	4984
Consensus	4984
CopiaSL_37	5204
Kielia	5204
LBS-FCR	5204
Consensus	5204

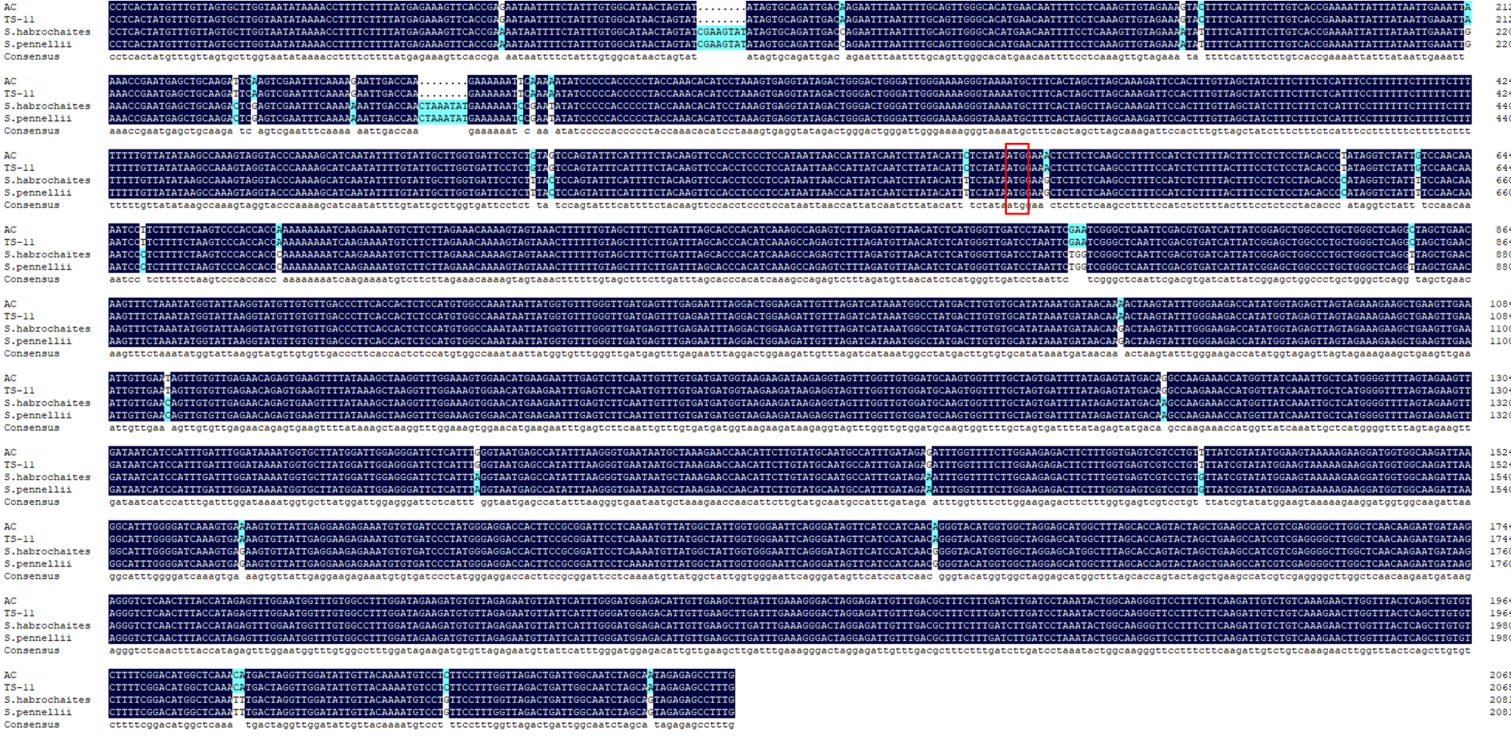
Supplementary Fig. S4 Identification of the nature of the retrotransposon in LBS. DNA sequences flanking the retrotransposon insert. The two transposons are identical in their core sequences and differ only in the sequence extensions at the beginning and in the end of the transposons.

Solanum lycopersicum Kielia (GenBank: EU195798.2) has a short extension of 5 bases at the beginning of its core sequence and an extension of 6 bases in the end of its core sequence, as compared with *Solanum lycopersicum* LTR retrotransposon:CopiaSL_37 (GenBank: LC012665.1). Analysis of the DNA sequences flanking the retrotransposon in LBS reveals that the transposon in LBS is CopiaSL_37.

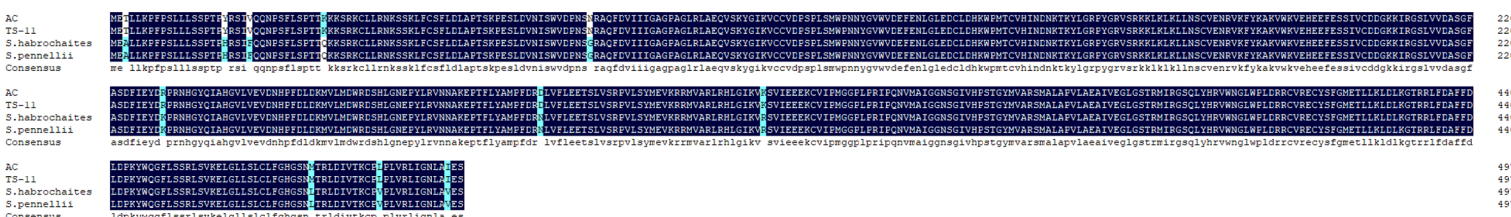


Supplementary Fig. S6 Amino acid sequence alignment of the deduced PSY1 proteins in AC, *S. habrochaites* and *S. pennellii*.

A



B

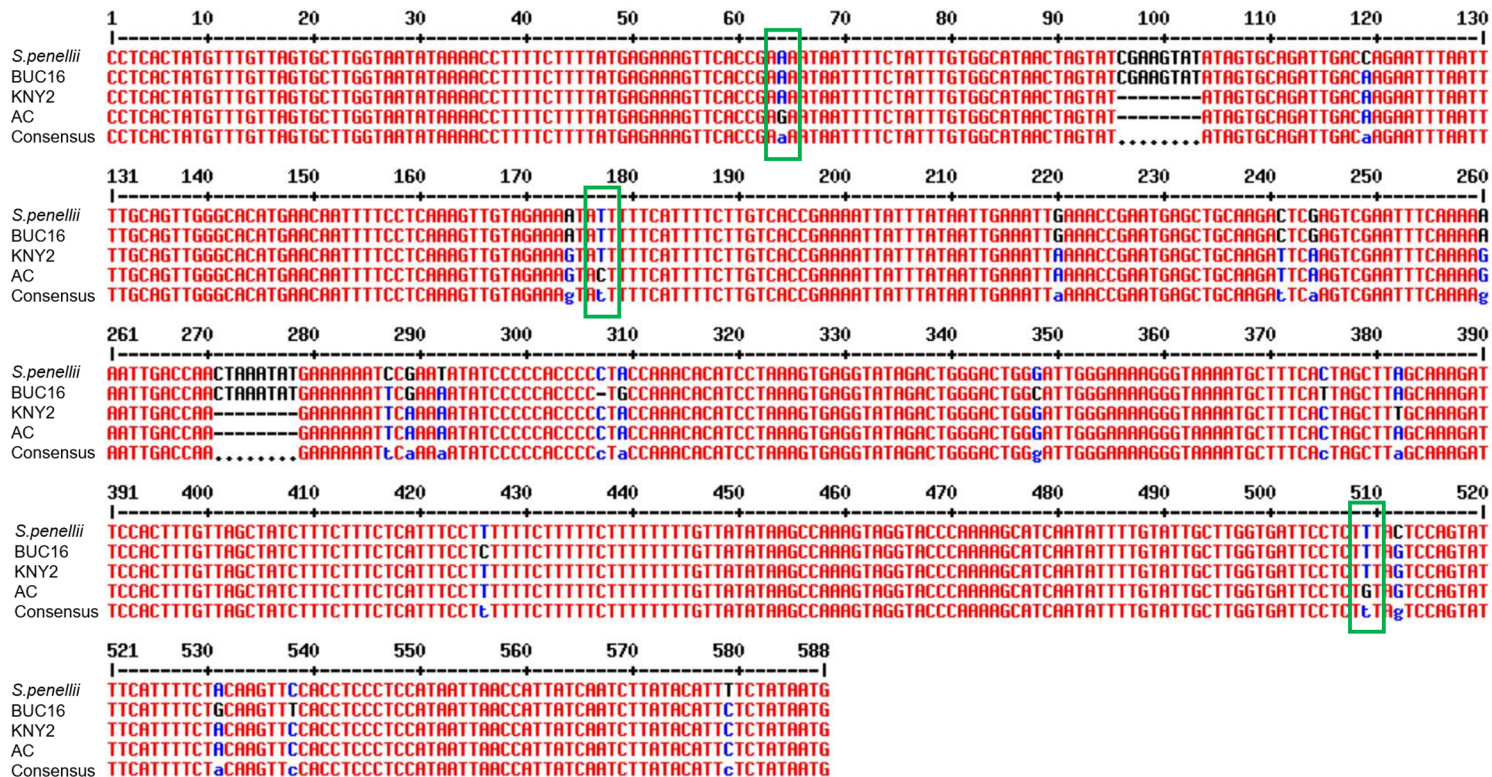


Supplementary Fig. S7 Sequence analysis of the *CYC-B* gene in AC, TS-11, *S. habrochaites* and *S. pennellii*. (A)

Alignment of the promoter and CDS sequences of the *CYC-B* gene in AC, TS-11, *S. habrochaites* and *S. pennellii*.

The translation initiation site (ATG) is marked by a red box. Nucleotide differences are highlighted in blue.

(B) Amino acid sequence alignment of the deduced *CYC-B* proteins in AC, TS-11, *S. habrochaites* and *S. pennellii*.



Supplementary Fig. S8 Alignment of the promoter sequences of the *CYC-B* gene in *S. pennellii*, BUC16, KNY2 and AC. The reported SNP positions are marked by green boxes. The tomato inbred lines BUC16 and KNY2 have been reported in Hwang et al., 2016.

1 **Supplementary Table S1** Segregation of fruit colours in *M82* × *LBS* segregating
2 populations.

Generation	Total plants	No. of plants with fruit color in				Expected ratio	χ^2 value
		Red/Pink	Yellow	Purple	Green		
F1	25	25(Red)	0	0	0		
F2	943	550	169	154	70	9:3:3:1	6.636

3

Supplementary Table S2 Sequences of primers used in this study.

Primer name	Sequence (5'-3')
SGR1-RNAi-FW1	AAAAAGCAGGCTACTTCCCCCTCATCTTCTTCTG
SGR1-RNAi-RV1	CCATAACAAGGCAACAGACATTCCCAAATAAATAATGCTGCTTCCA
PSY1-RNAi-FW2	TGGAAGCAGCATTATTTATTTGGGAATGTCTGTTGCCTTGTTATGG
PSY1-RNAi-RV2	AGAAAGCTGGGTTCGGCTTCACTTCTAACTCATTGG
attB1	GGGACAAGTTTGTACAAAAAAGCAGGCT
attB2	GGGACCACTTTGTACAAGAAAGCTGGGT
SGR1-qPCR-FW	GTAGGTGGGGTGAAGAGTACAAGTT
SGR1-qPCR-RV	CACCATCCTAAACTTGATGTTCTTG
PSY1-qPCR-FW	TGGAAGGTGACAAAAAGAAAGACA
PSY1-qPCR-RV	CCATTATTAGTTTGCTTTCCACCAC
PSY1-DET-FW	GAATGTCTGTTGCCTTGTTATGG
PSY1-DET-RV	GCTTTATCTTTGAAGAGAGGCAGTT
LD-1	ACGATGGACTCCAGAGCGGCCGC(G/C/A)N(G/C/A)NNNGGAA
LD-2	ACGATGGACTCCAGAGCGGCCGC(G/C/T)N(G/C/T)NNNGGTT
LD-3	ACGATGGACTCCAGAGCGGCCGC(G/C/A)(G/C/A)N(G/C/A)NNNCCAA
LD-4	ACGATGGACTCCAGAGCGGCCGC(G/C/T)(G/A/T)N(G/C/T)NNNCGGT
PSY1-TAIL-RV1	TCAAGCTAGTCAAGCTCGGATT
PSY1-TAIL-RV2	GAACAGCAACGCAAATGAAAAT
PSY1-TAIL-FW1	GATATGTTGTACTCGAACGAGGGTC
PSY1-TAIL-FW2	CTGTTTGAGTGAGGAAAAGTTGGTT
PSY1-TAIL-FW3	GATGGTCTATGATGTGGTTTTGAGG
PSY1-LBS-gDNA-FW1/2	GAATGTCTGTTGCCTTGTTATGG
PSY1-LBS-gDNA-RV1	TTTCCGTCCATTATTAGTTTGCTT
PSY1-LBS-gDNA-RV2	CCCTTCTTCTCTCGGGAGTCAT
PSY1-LBS-gDNA-FW3	GTATGGTGCAGAAGAACAGATGAA
PSY1-LBS-gDNA-RV3	CAGCAAAAGTGACATCAAACGC
SGR1-cDNA-DET-FW	ATGGGAACTTTGACTACTTCTCTAGTG
SGR1-cDNA-DET-RV	TCAACTTTGCTGCTCTTGCAA
ProSGR1-PNL-OE-FW	TGCATCCAACGCGTTGGGAGCTCATGACTCCGCCATACTTACCAA
ProSGR1-PNL-OE-RV	TCTCATTAAAGCAGGACTCTAGA TGCTGCTTCCACAAACCCTA
ProSGR1-AC-OE-FW	TGCATCCAACGCGTTGGGAGCTCGCTGAATGATGTGCCAACGG
ProSGR1-AC-OE-RV	TCTCATTAAAGCAGGACTCTAGATGCTGCTTCCACAAACCCTA
35S-CYCB-OE-FW	CATTTGGAGAGGACACGCTCGAGTGTATTGCTTGGTGATTCCTCTG
35S-CYCB-OE-RV	TCTCATTAAAGCAGGACTCTAGAGGCTTTAAGAGGAACAGAGTGG
CYCB-CR-DT1-FW	GAATCTAACAGTGTAGTTTGTGTTGGACAATAGACCTATGTTTTAGAGCTAGAAATAG

CYCB-CR-DT2-RV	GCTATTTCTAGCTCTAAAACGATTCTGAATTAGGATCAACCCAAACTACACTGTTAGATT
CYCB-CR-DET-FW	TGTATTGCTTGGTGATTCTCTG
CYCB-CR-DET-RV	TTCAACAATTTCAACTTCAGCTTCT
35S-PSY1-PNL-OE-FW	CATTTGGAGAGGACACGCTCGAGGAATGTCTGTTGCCTTGTTATGG
35S-PSY1-PNL-OE-RV	TCTCATTAAAGCAGGACTCTAGAGCTTTATCTTTGAAGAGAGGCAGTT
Rin-CR-DT1-FW	GAATCTAACAGTGTAGTTTGGTGGTATCTCTCCAATGTCTGTTTTAGAGCTAGAAATAG
Rin-CR-DT2-RV	GCTATTTCTAGCTCTAAAACGTGAATCTGATGAAGTTTGGCAAACACTACACTGTTAGATT
Rin-CR-DET-FW	TTTTTGTGTCACATAAGCATCAGG
Rin-CR-DET-RV	TCAATATTGAGTTGGCCTACACAC
GF-DET-FW	GGATCCGTGCCGTCTATTGT
GF-DET-RV	TGCATCTCTGAGTGGACCCC
MYB12-Pro-FW1	TTATGAAAGTGACGAACAACCGAC
MYB12-Pro-RV1	ATTTAAGTTGATCGTCACGGCC
MYB12-Pro-RV2	AGCTAAATAAGATGCAATTAAATGGC
PSY1-Exon1-FW	GAATGTCTGTTGCCTTGTTATGG
PSY1-Exon1-RV	AGTTAAACGTCTTTCATACTCTGC

Supplementary Table S3 Reaction programs of TAIL-PCR.

Reaction stage	Cycle No.	Temperature °C	Time S	Temperature °C	Time S	Temperature °C	Time S	
Primary	1	94	180					
	5	94	30	62	60	72	180	
	1	94	30	25	120	*	180	
	15	94	30	62	60	72	150	
			94	30	62	60	72	150
			94	30	45	60	72	150
	1	72	60					
	1	16	300					
Secondary	1	94	180					
	12	94	30	65	60	72	150	
			94	30	65	60	72	150
			94	30	45	60	72	150
	1	72	600					
	1	16	300					
Tertiary	1	94	180					
	25	94	30	45	60	72	150	
	1	72	600					
	1	16	300					

*, 25 °C, 150 s ramping to 72 °C at 0.2 °C/s