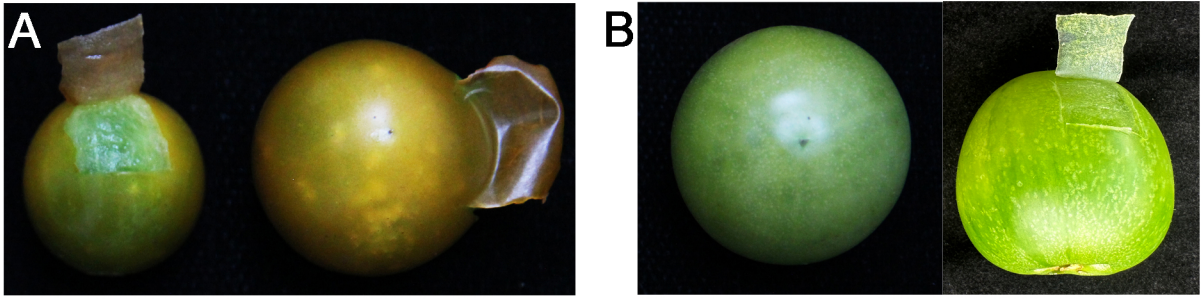
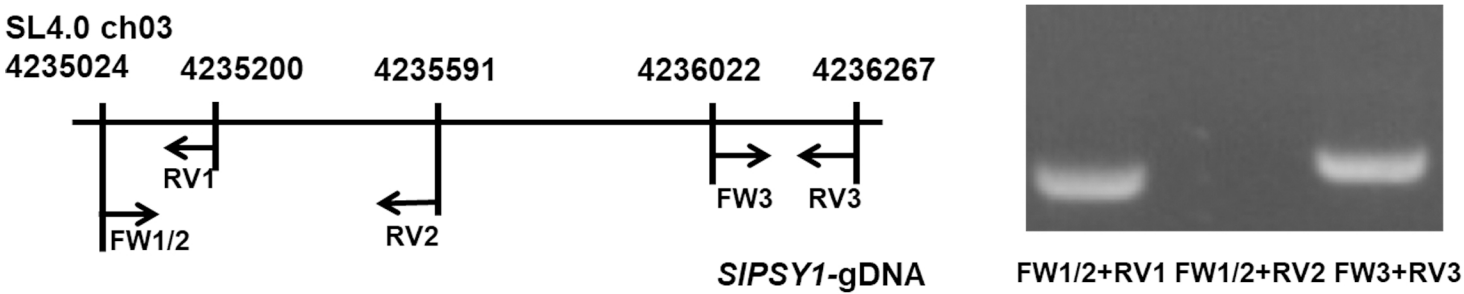
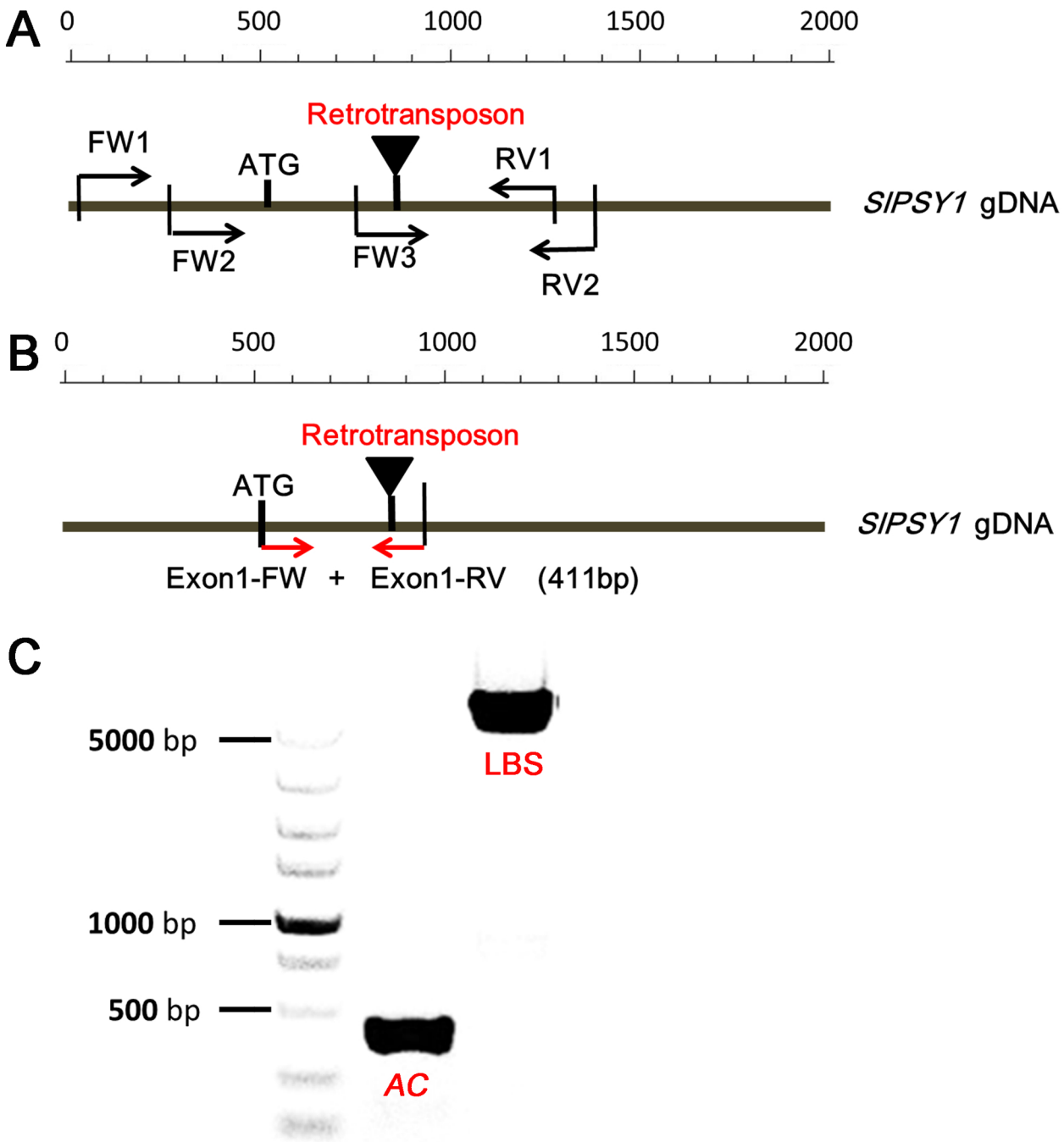


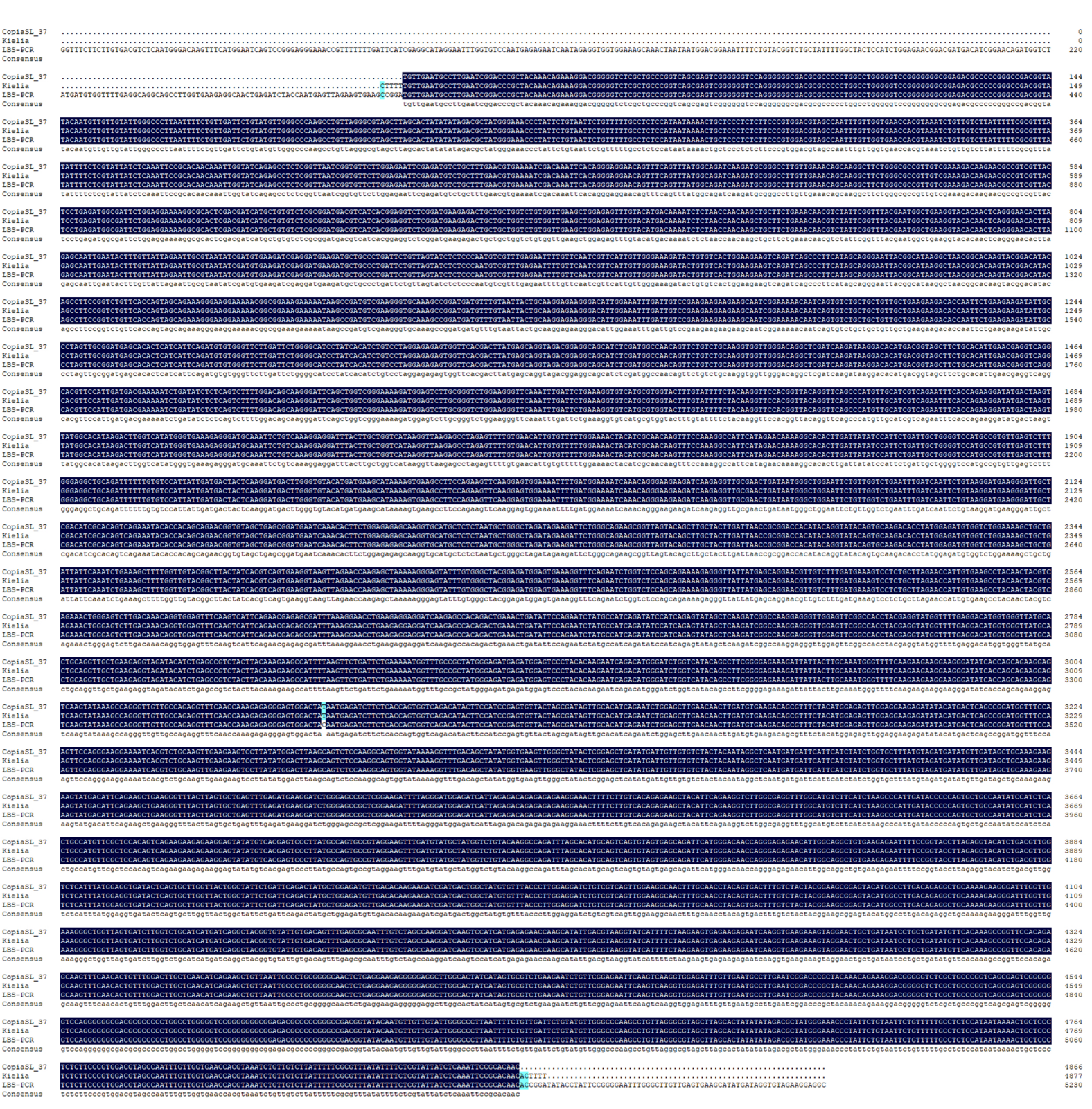
Supplementary Fig. S1 Phenotype of peels in green ripe fruits. Green ripe fruits phenotype of yellow colour peel **(A)** and colourless peel **(B)** in the F2 generation of *M82* × LBS.



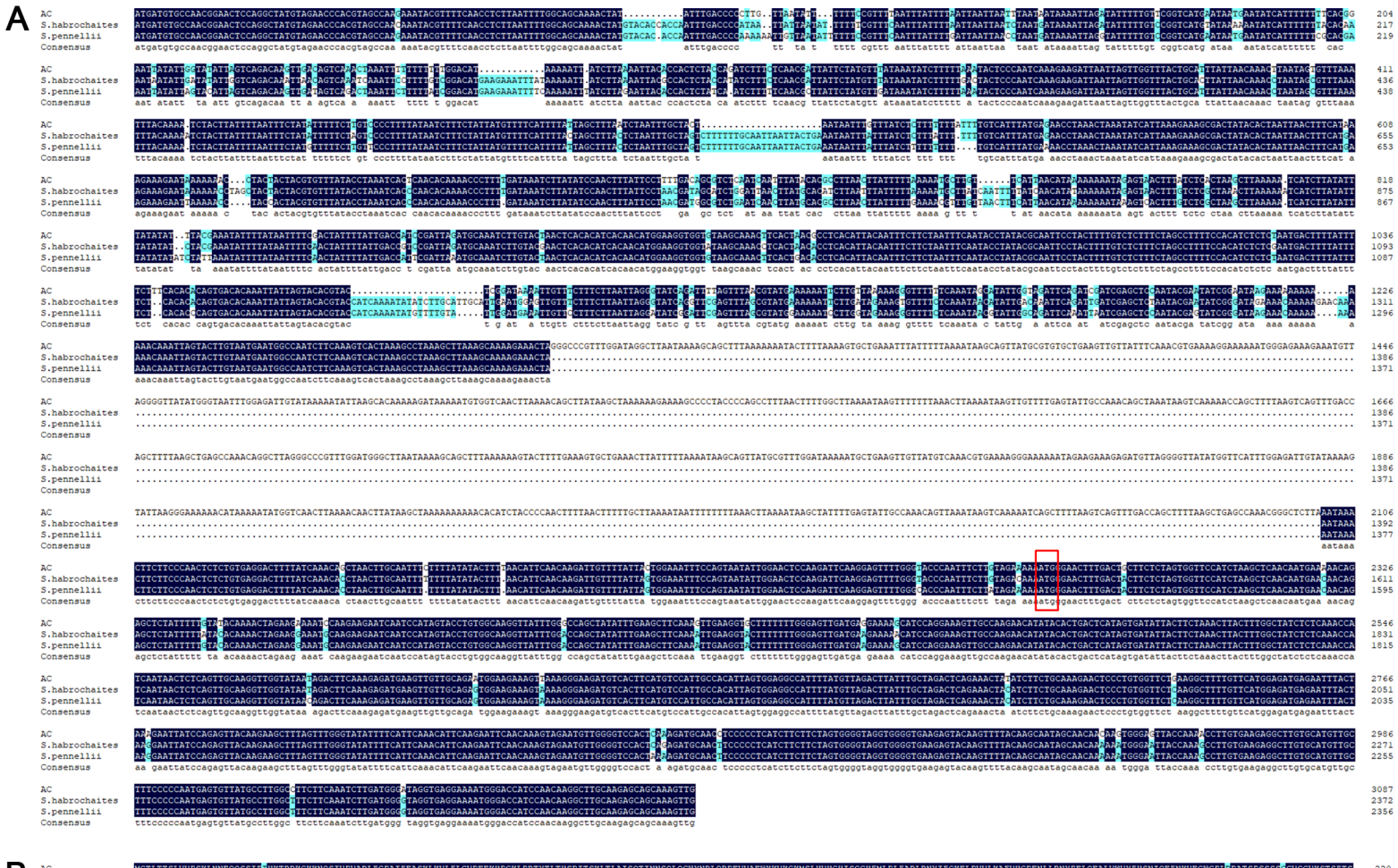
Supplementary Fig. S2 PCR analysis of the *PSY1* gene. Three fragments were designed for PCR-based analysis of *PSY1* gene presence or not. The genomic positions of these fragments were showed in the left. And the amplification of these fragments was showed in the right.



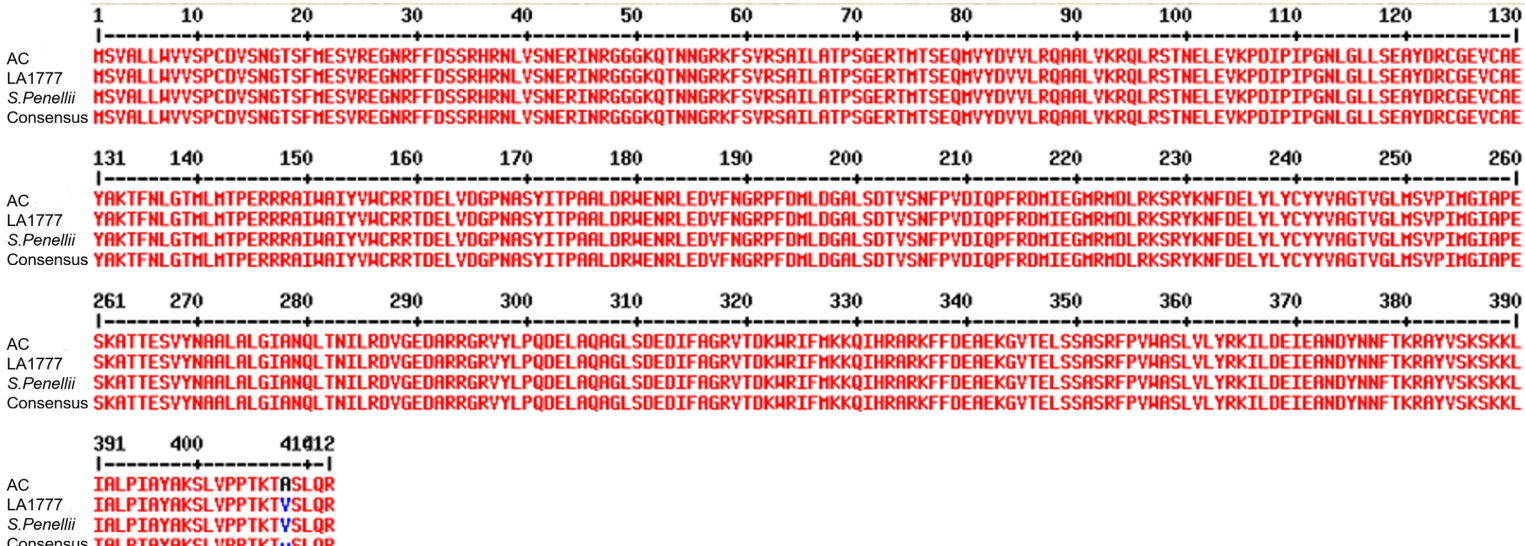
Supplementary Fig. S3 Identification of a transposon in the first exon of the *PSY1* gene in LBS. **(A)** Tail PCR-based analysis of the *PSY1* gene in LBS. The *PSY1*-specific primers (FW1/FW2/FW3 and RV1/RV2) and four short arbitrary degenerate primers were used to amplify the fragment using genomic 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.



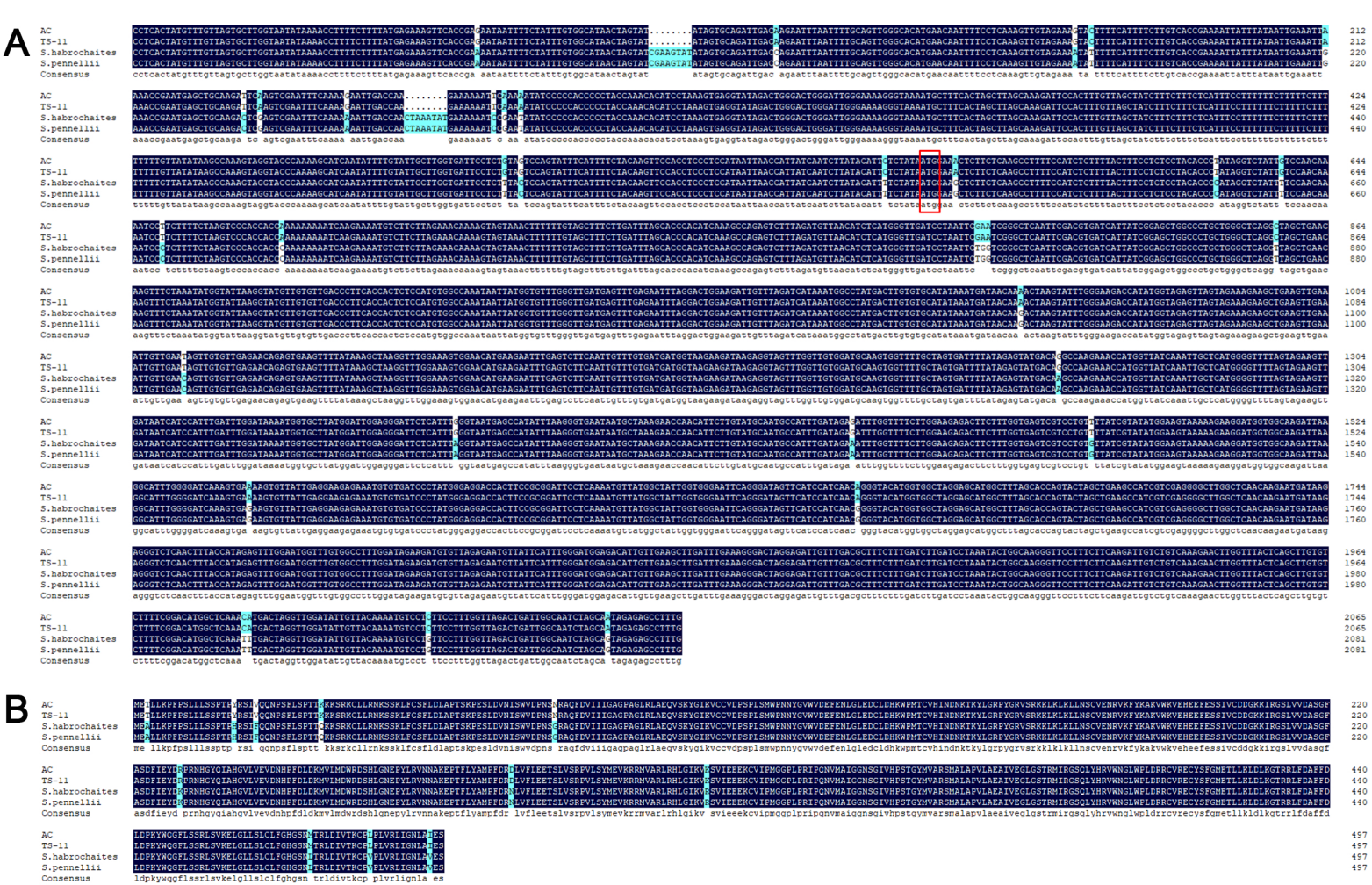
Supplementary Fig. S4 Identification of the nature of the retrotransposon in LBS. DNA sequences of two highly homologous retrotransposons were aligned with the genomic DNA sequence flanking the transposon insert. The two transposons are identical in their core sequences and differ only in the sequence extensions at the beginning and in the end of the transposons. *Solanum lycopersicum* retrotransposon 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.



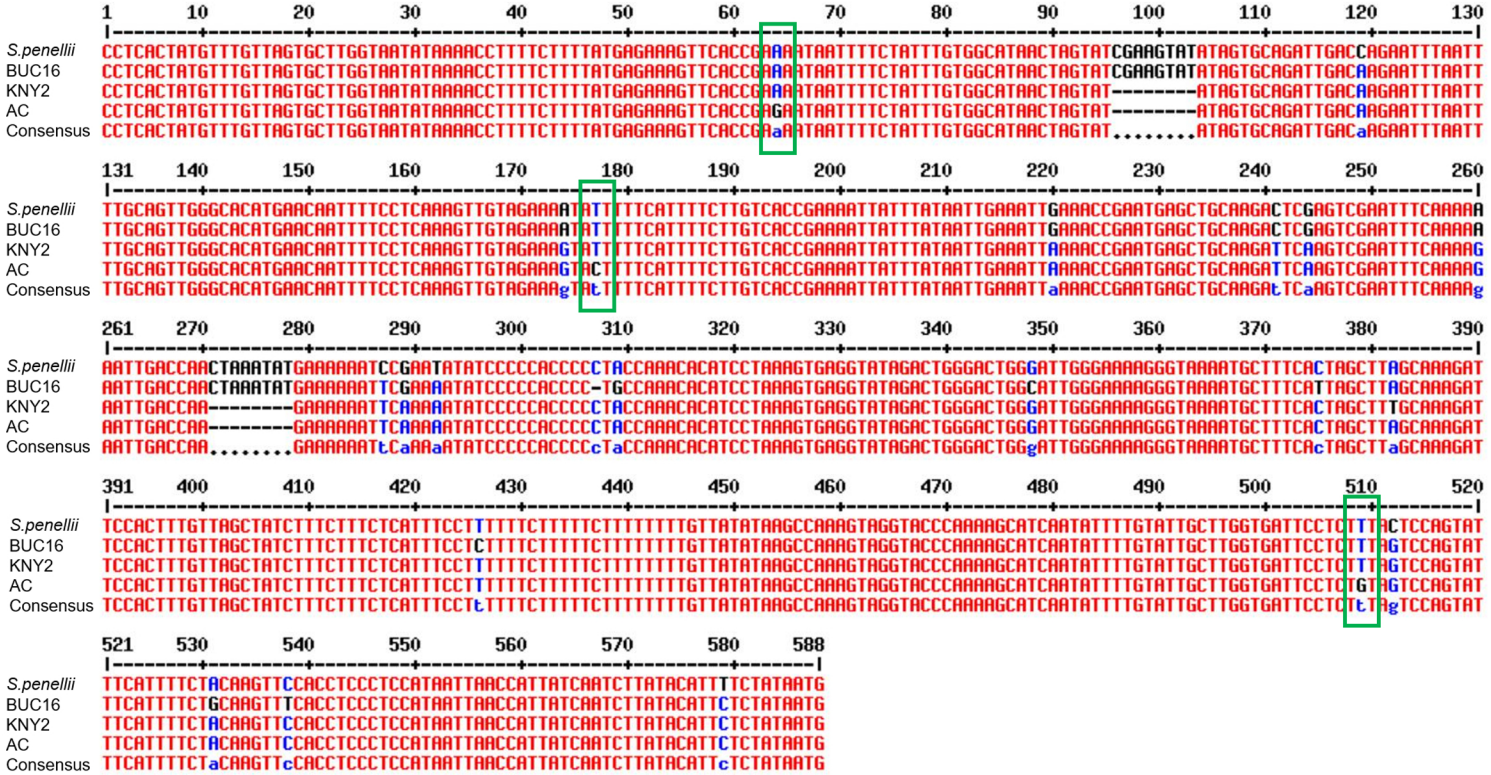
Supplementary Fig. S5 Sequence analysis of the *SGR1* gene in *AC*, *S. habrochaites* and *S. pennellii*. **(A)** Alignment of the promoter and CDS sequences of the *SGR1* gene in *AC*, *S. habrochaites* and *S. pennellii*. The translation initiation site (ATG) is marked by a red box. Nucleotide sequence differences are highlighted in blue. **(B)** Amino acid sequence alignment of the deduced SGR1 proteins in *AC*, *S. habrochaites* and *S. pennellii*.



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



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 red box. Nucleotide sequence 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.

Supplementary Table S1 Segregation of fruit colours in *M82* ×LBS segregating 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

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	AGAAAGCTGGGTCGGCTTCACTTCTAACTCATTGG
attB1	GGGGACAAGTTTGTACAAAAAAGCAGGCT
attB2	GGGGACCACTTTGTACAAGAAAGCTGGGT
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	TCTCATTAAAGCAGGACTCTAGAGGCTTTTAAGAGGAACAGAGTGG
CYCB-CR-DT1-FW	GAATCTAACAGTGTAGTTTGTTGTTGGACAATAGACCTATGTTTTAGAGCTAGAAATAG

CYCB-CR-DT2-RV	GCTATTTCTAGCTCTAAAACGATTCGAATTAGGATCAACCCAAACTACACTGTTAGATT
CYCB-CR-DET-FW	TGTATTGCTTGGTGATTCCTCTG
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	GCTATTTCTAGCTCTAAAACGTGAATCTGATGAAGTTTGGCAAACTACACTGTTAGATT
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	AGTTAAACGTCTTTGCATACTCTGC

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