

Appendix A. The primer sequences used for expression analysis.

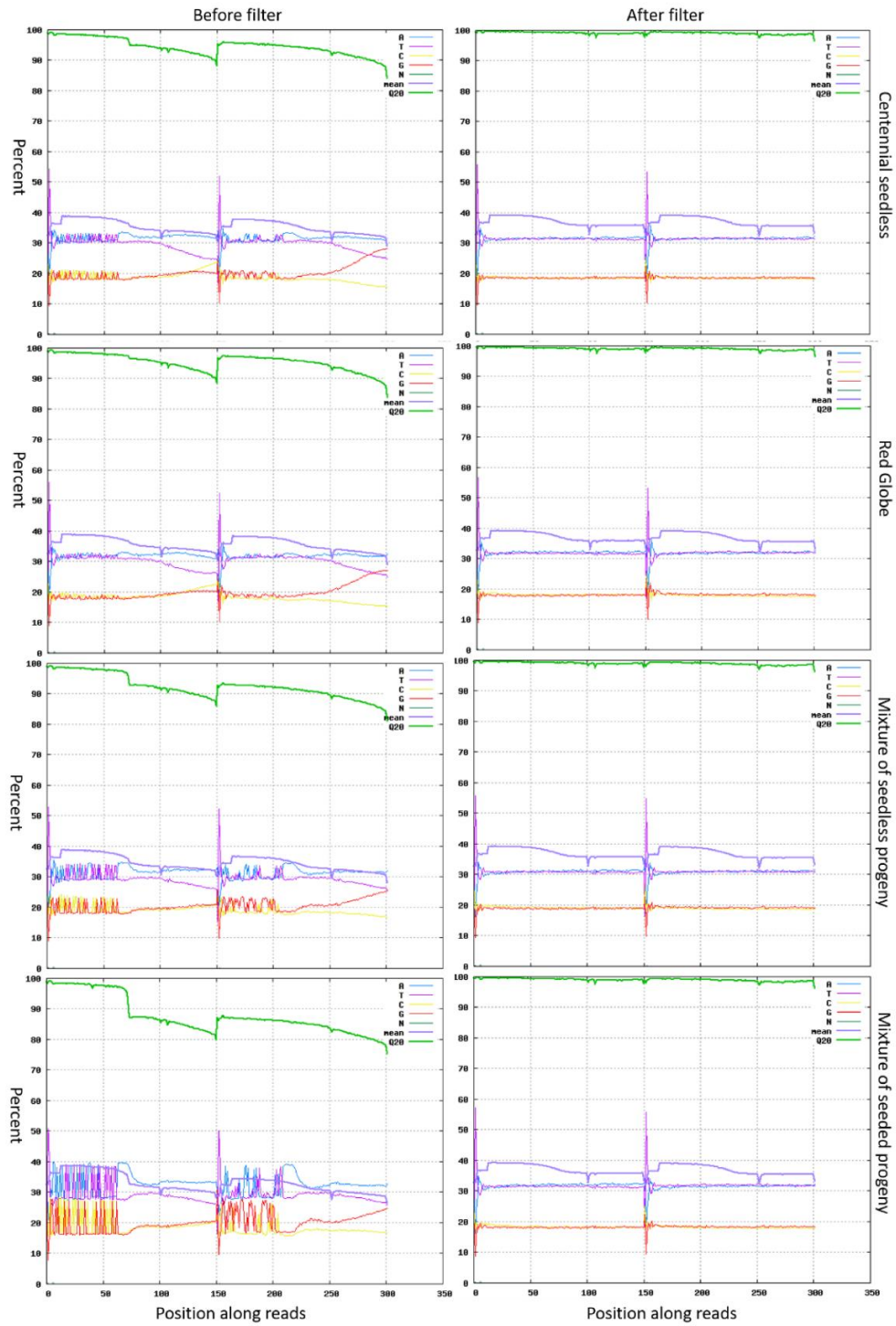
Gene name	Forward primer (5'->3')	Reverse primer (5'->3')
<i>G1</i>	TGGCTACTGCGATAAGAAAGG	AGGCACCCCAAATAATGAAAC
<i>G2</i>	CCCTATTGTGGAGCCTGTGAT	GGAACTGGCAACTTGTGGTG
<i>G3</i>	CGTCATCGCCCAATAAGC	CGTCAAGTCAGAGGAAACCC
<i>G4</i>	AGTCCGGTGAGATTCAGGTTT	GCTTTCCAGTTGTTAGGAGGC
<i>G5</i>	AGTAGAGGCGTCAACCGAGAT	TCAACAGTAACAACAGCAACCAT
<i>G6</i>	GATGGAGTAGCCCAAGTGAT	TGCGAAAAGACCAAAGAAGAGT
<i>G7</i>	TCCTGGCAATGTTGAAAAGC	TGACGAAACCTGAAACGACC
<i>G8</i>	TCTCACAAGTTGGTTGCTGG	GCCGAAATGTTTTGCTATCC
<i>G9</i>	GGGAGAATAATGCTGGTAGGG	TCCATCATAGGTAAGTGTCTTTTCG
<i>Actin 1</i>	GATTCTGGTGATGGTGTGAGT	GACAATTTCCCGTTCAGCAGT
<i>EF1-α</i>	AGGAGGCAGCCAACCTTACC	CAAACCCTGCATCACCATTC

Appendix B. The primer sequences used for SNaPshot analysis.

Gene ID	Gene name	PCR primer(5'—3')	PCR product length and GC content	SNP type	Extend the primer direction	Extended product	Extension of primers
GSVIVG01011008001	<i>G2</i>	F-TTTACCTATTGTGGAGCCTGTG R-TTCTTTGAAGTTGCTGACCGT	428bp; 44.6%	[C/T]	F	CT	AGCATTCTGAATCTATCCAAG
GSVIVG01011006001	<i>G4</i>	F-GAGAAGACTGTTTTGGTTGTTGG R-GGATACTTCCATACTTGGCTTTG	369bp; 40.9%	[G/T]	F	GT	TTTTTTTTTTTTTTTTTTTTTACTT GACCAAATATGGCATAA
GSVIVG01000995001	<i>G8</i>	F-ATGGAGGATTTGGCAGGGAC R-GGTATGGTGCTCTTTGGGTTT	444bp; 41.2%	[A/G]	F	AG	TTTTTTTTTGTGATGATCTTCACAA GTTGGTT

Appendix C. Base information before and after filtering. ‘C’ represents ‘Centennial seedless’, ‘R’ ‘Red Globe’, ‘S’ ‘Seeded progeny’, and ‘SL’ ‘seedless progeny’.

Sample	Before Filter					After Filter					Depth of Sequencing Coverage (X)
	Clean Data (bp)	Q20(%)	Q30(%)	N (%)	GC (%)	HQ Clean Data(bp)	Q20 (%)	Q30 (%)	N (%)	GC (%)	
C	9142732900 (100.00%)	8633714754 (94.43%)	8358040466 (91.42%)	3475671 (0.04%)	3545317329 (38.78%)	7690945589 (84.12%)	7616403713 (99.03%)	7408891257 (96.33%)	505298 (0.01%)	2854893663 (37.12%)	16
R	10897982872 (100.00%)	10389407838 (95.33%)	10058729515 (92.30%)	4151971 (0.04%)	4143648805 (38.02%)	9139871825 (83.87%)	9052837925 (99.05%)	8810861994 (96.40%)	601635 (0.01%)	3311229182 (36.23%)	19
SL	8413745368 (100.00%)	7768132426 (92.33%)	7504719160 (89.20%)	3167524 (0.04%)	3311491966 (39.36%)	7106136706 (84.46%)	7031566603 (98.95%)	6826888959 (96.07%)	453719 (0.01%)	2711817819 (38.16%)	15
S	10005311944 (100.00%)	8781970198 (87.77%)	8480365921 (84.76%)	3822020 (0.04%)	3841287060 (38.39%)	7928006616 (79.24%)	7844872273 (98.95%)	7620510603 (96.12%)	494672 (0.01%)	2900864989 (36.59%)	17



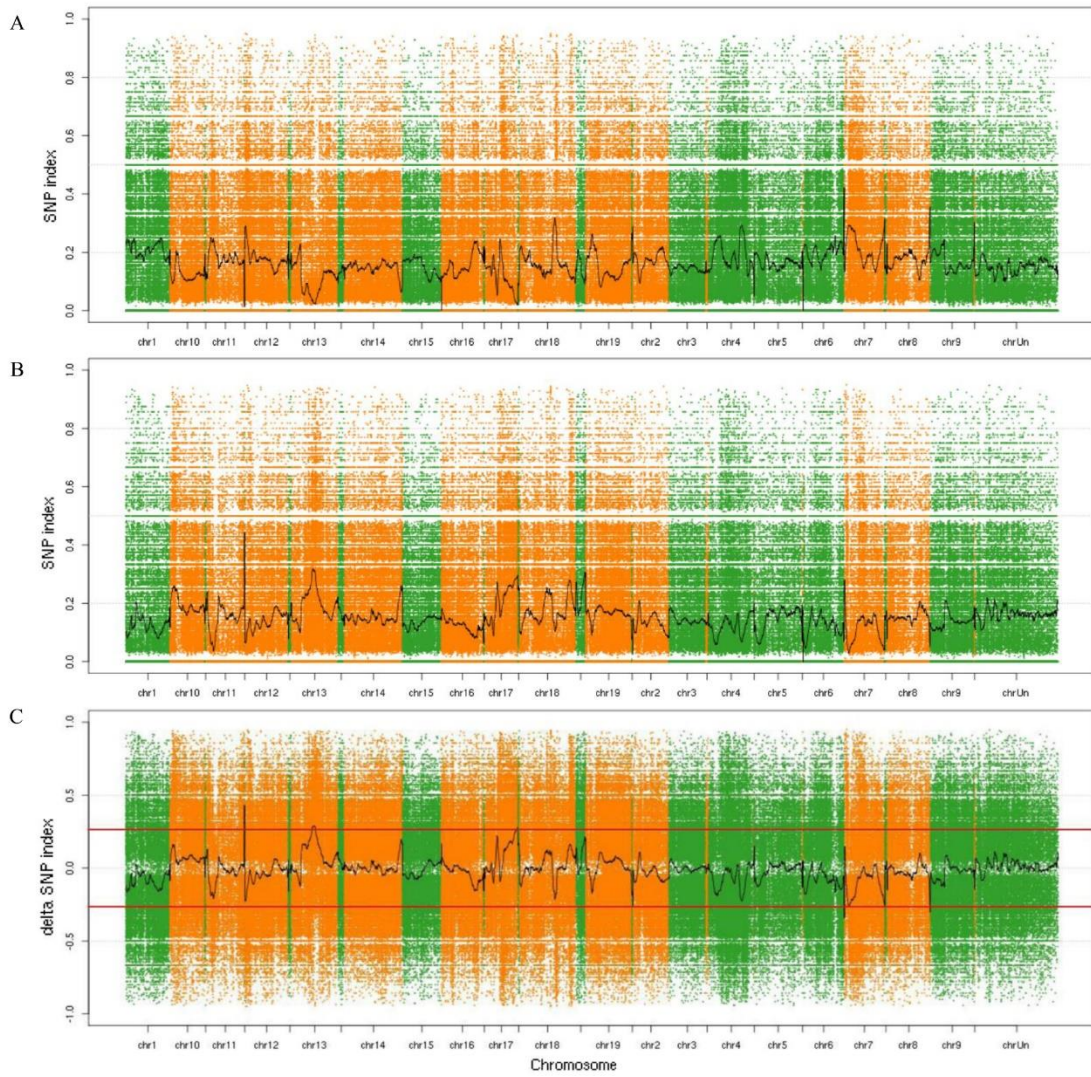
Appendix D. Base composition and quality value distribution after data filtering. Lines A, T, C and G indicate the percentages of the corresponding bases at each position. Mean refers to the average quality of all bases at each position, while Q20 and Q30 indicate the percentages of bases with quality values not less than 20 and 30, respectively.

Appendix E. Reads information before and after filtering. ‘C’ represents ‘Centennial seedless’, ‘R’ ‘Red Globe’, ‘S’ ‘Seeded progeny’, and ‘SL’ ‘seedless progeny’.

Sample	Clean Reads Num	HQ Clean Reads Num (%)	Read Length	Adapter (%)	Low Quality (%)	Poly A(%)	N(%)
C	60547900	57160754 (94.41%)	151/151	31027138 (102.48%)	875868 (2.89%)	0 (0%)	14923 (0.05%)
R	72172072	68761692 (95.27%)	151/151	37849198 (104.88%)	560746 (1.55%)	0 (0%)	17630 (0.05%)
SL	55720168	50978504 (91.49%)	151/151	18803012 (67.5%)	1480010 (5.31%)	0 (0%)	13622 (0.05%)
S	66260344	56263426 (84.91%)	151/151	18806616 (56.76%)	3615472 (10.91%)	0 (0%)	16674 (0.05%)

Appendix F. Number of DEGs containing functional variants.

Stage	Up-regulated DEGs	Down-regulated DEGs	Total DEGs
Stage 1	1862	563	2425
Stage 2	2146	842	2988
Stage 3	1877	451	2328



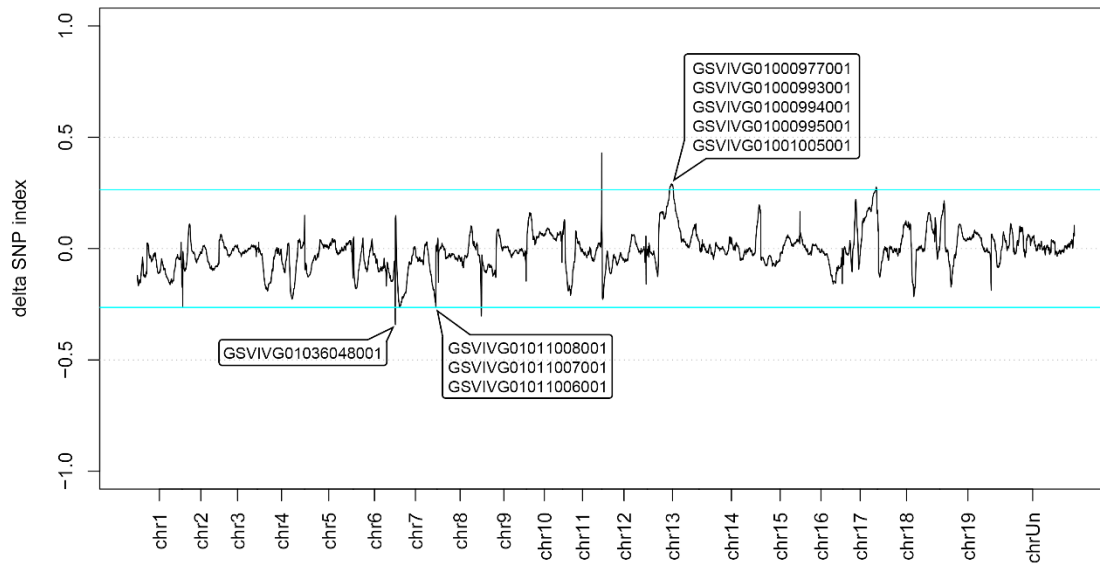
Appendix G. Distribution of the SNP-index. The x-axis indicates the chromosomal position and each spot represents a SNP. Average values of SNP-index or delta SNP are indicated by the black lines. A, SNP-index plot of ‘Seeded’ bulk pool; B, SNP-index plot of ‘Seedless’ bulk pool; C, Plot of delta SNP-index. The red line indicates the threshold line.

Appendix H. Functional variants in the valley.

Chr	Start	End	Ref	Mut	Structure_gene	Function_type
chr6	21418457	21418457	C	G	GSVIVG01036048001	nonsynonymous
chr7	2257286	2257286	G	A	GSVIVG01011008001	nonsynonymous
chr7	2266373	2266373	C	T	GSVIVG01011007001	nonsynonymous
chr7	2266664	2266664	C	T	GSVIVG01011007001	nonsynonymous
chr7	2278664	2278664	A	C	GSVIVG01011006001	nonsynonymous
chr7	2285223	2285223	A	C	GSVIVG01011005001	nonsynonymous
chr7	2285268	2285268	C	A	GSVIVG01011005001	nonsynonymous
chr8	22124410	22124410	T	A	GSVIVG01033258001	nonsynonymous
chr8	22124434	22124434	G	A	GSVIVG01033258001	nonsynonymous
chr8	22231576	22231576	G	C	GSVIVG01033245001	nonsynonymous
chr8	22233901	22233901	C	T	GSVIVG01033244001	nonsynonymous
chr8	22233903	22233903	C	G	GSVIVG01033244001	nonsynonymous
chr8	22265929	22265929	A	G	GSVIVG01033240001	nonsynonymous

Appendix I. Functional variants in the peak.

Chr	Start	End	Ref	Mut	Structure_gene	Function_type
chr13	10640109	10640109	G	A	GSVIVG01011286001	nonsynonymous
chr13	10642235	10642235	C	G	GSVIVG01011286001	nonsynonymous
chr13	10644278	10644278	C	T	GSVIVG01011287001	nonsynonymous
chr13	10645827	10645827	C	T	GSVIVG01011287001	nonsynonymous
chr13	10652197	10652197	G	C	GSVIVG01011287001	nonsynonymous
chr13	10990570	10990570	G	A	GSVIVG01000974001	nonsynonymous
chr13	11040377	11040377	A	T	GSVIVG01000977001	nonsynonymous
chr13	11046108	11046108	C	T	GSVIVG01000978001	nonsynonymous
chr13	11046126	11046126	T	C	GSVIVG01000978001	nonsynonymous
chr13	11080403	11080403	G	T	GSVIVG01000979001	nonsynonymous
chr13	11080408	11080408	A	G	GSVIVG01000979001	nonsynonymous
chr13	11081171	11081171	T	C	GSVIVG01000979001	nonsynonymous
chr13	11081188	11081188	A	G	GSVIVG01000979001	nonsynonymous
chr13	11117569	11117569	T	A	GSVIVG01000981001	nonsynonymous
chr13	11117570	11117570	T	A	GSVIVG01000981001	nonsynonymous
chr13	11117575	11117575	G	A	GSVIVG01000981001	nonsynonymous
chr13	11123918	11123918	G	C	GSVIVG01000982001	nonsynonymous
chr13	11124014	11124014	A	G	GSVIVG01000982001	nonsynonymous
chr13	11222492	11222492	G	A	GSVIVG01000993001	nonsynonymous
chr13	11223120	11223120	T	C	GSVIVG01000993001	nonsynonymous
chr13	11223228	11223228	C	A	GSVIVG01000993001	nonsynonymous
chr13	11223476	11223476	C	T	GSVIVG01000993001	stopgain
chr13	11229443	11229443	G	A	GSVIVG01000994001	nonsynonymous
chr13	11240814	11240814	G	A	GSVIVG01000995001	nonsynonymous
chr13	11330135	11330135	T	C	GSVIVG01001004001	nonsynonymous
chr13	11336347	11336347	T	C	GSVIVG01001005001	nonsynonymous
chr13	11337398	11337398	G	C	GSVIVG01001005001	nonsynonymous
chr13	11800114	11800114	G	A	GSVIVG01010687001	nonsynonymous
chr13	11804731	11804731	G	A	GSVIVG01010688001	nonsynonymous
chr13	11976345	11976345	A	G	GSVIVG01010700001	nonsynonymous
chr13	11978511	11978511	G	A	GSVIVG01010700001	nonsynonymous
chr13	11979844	11979844	C	T	GSVIVG01010700001	nonsynonymous
chr13	12223560	12223560	C	T	GSVIVG01010709001	nonsynonymous
chr13	12223660	12223660	G	A	GSVIVG01010709001	nonsynonymous
chr13	12225287	12225287	G	C	GSVIVG01010710001	nonsynonymous
chr17	16705573	16705573	A	G	GSVIVG01029408001	nonsynonymous
chr17	16799260	16799260	C	T	GSVIVG01029412001	nonsynonymous
chr17	16799569	16799569	G	A	GSVIVG01029412001	nonsynonymous



Appendix J. Distribution of candidate genes based on expression analysis from transcriptome data.

Appendix K. Motif analysis of mutant sequences.

Gene Name	Ref	Mutant	Amino Acid Change	MOTIF
<i>G1</i>	C	G	G-A	ML domain
<i>G2</i>	G	A	A-V	Low complexity region
<i>G3</i>	C	T	S-F	Low complexity region
	C	T	S-F	none
<i>G4</i>	T	G	I-S	none
<i>G5</i>	T	A	H-Q	none
	G	A	G-S	none
<i>G6</i>	T	C	M-T	none
	C	A	S-Y	none
	C	T	Q-stopgain	none
<i>G7</i>	G	A	E-K	none
<i>G8</i>	G	A	A-T	none
<i>G9</i>	T	C	N-D	none
	G	C	P-A	none