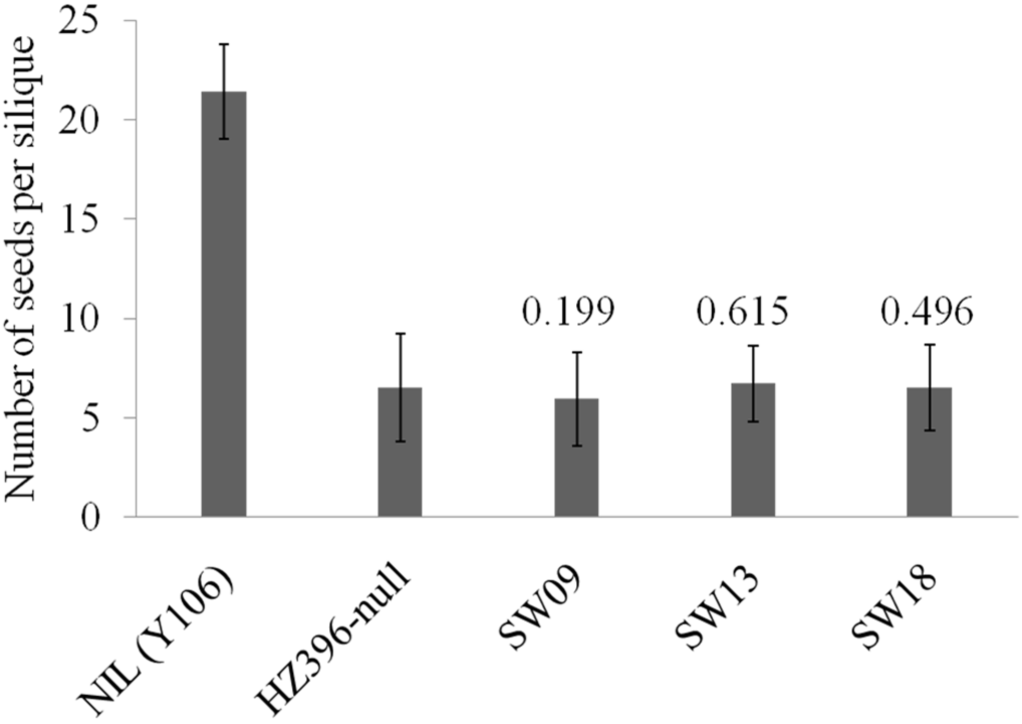
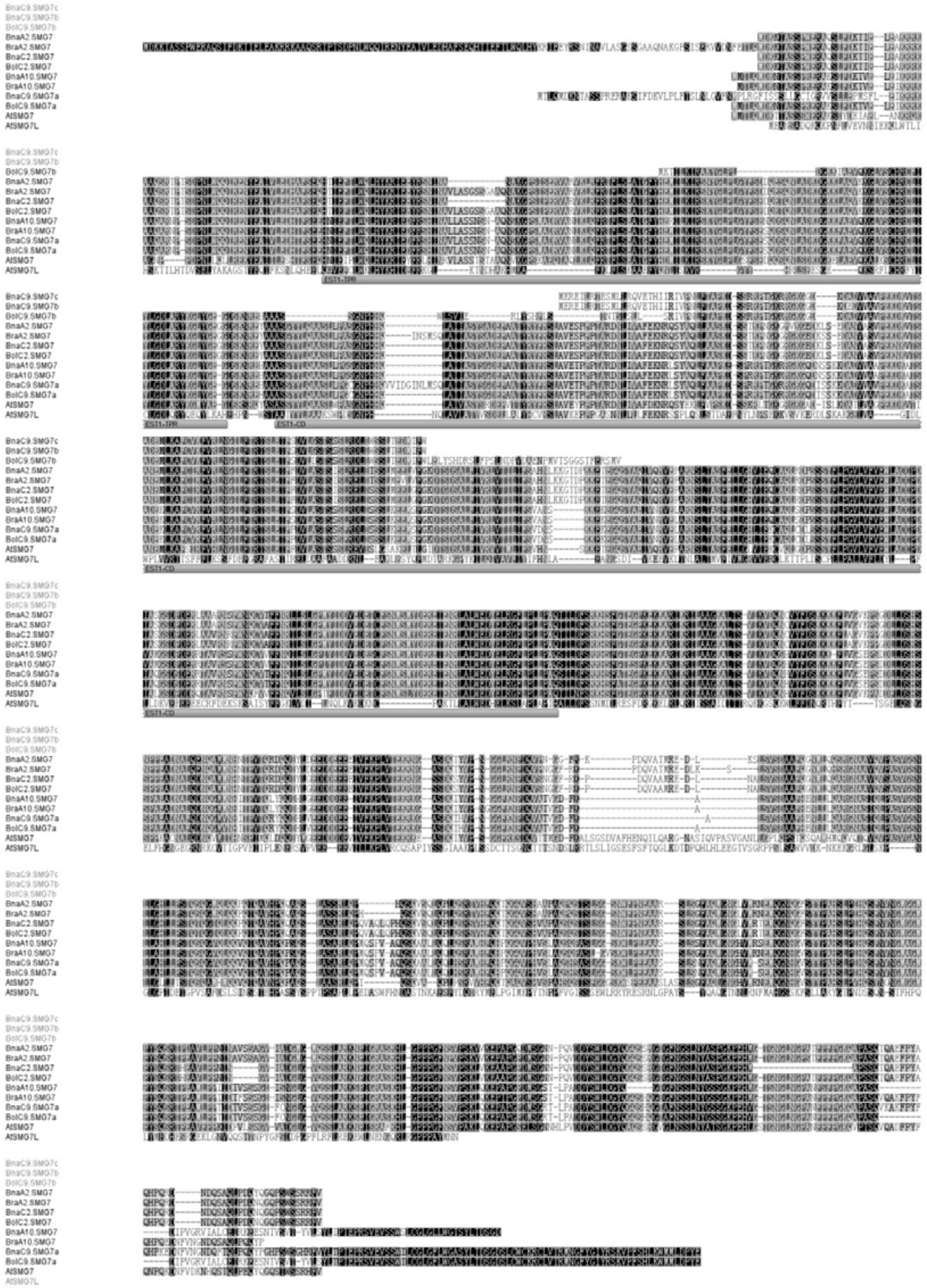
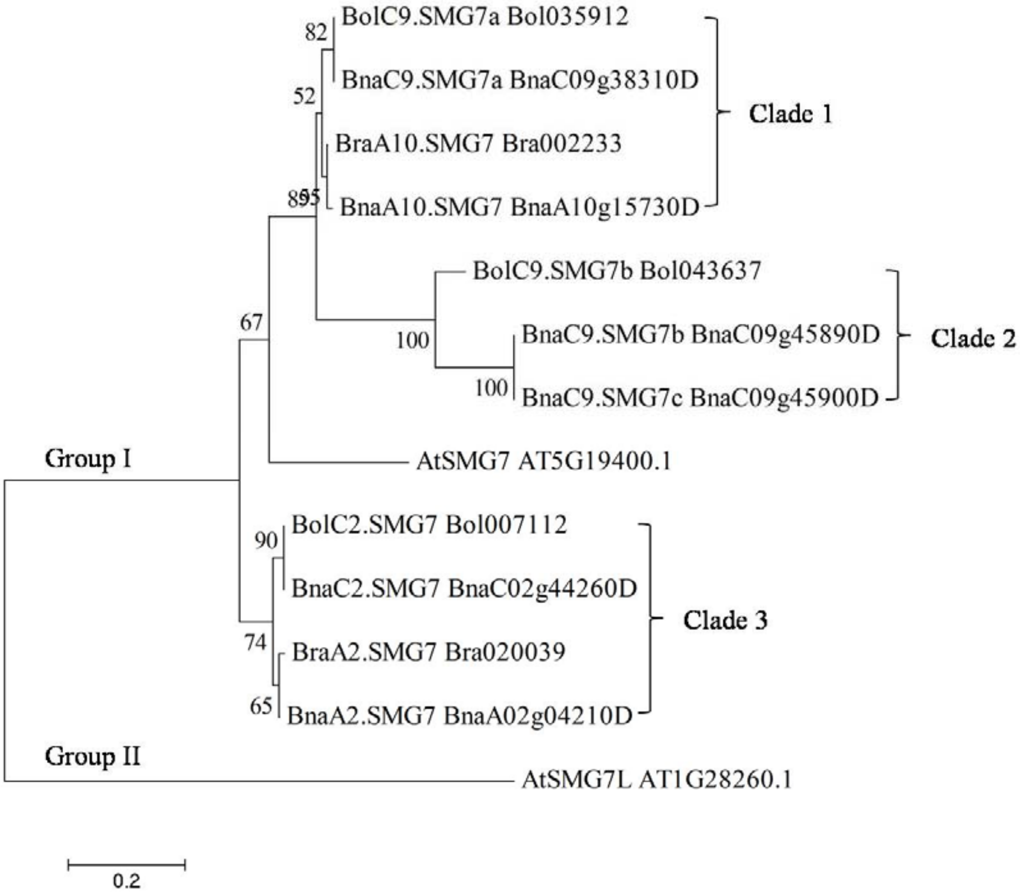
Supplemental Material



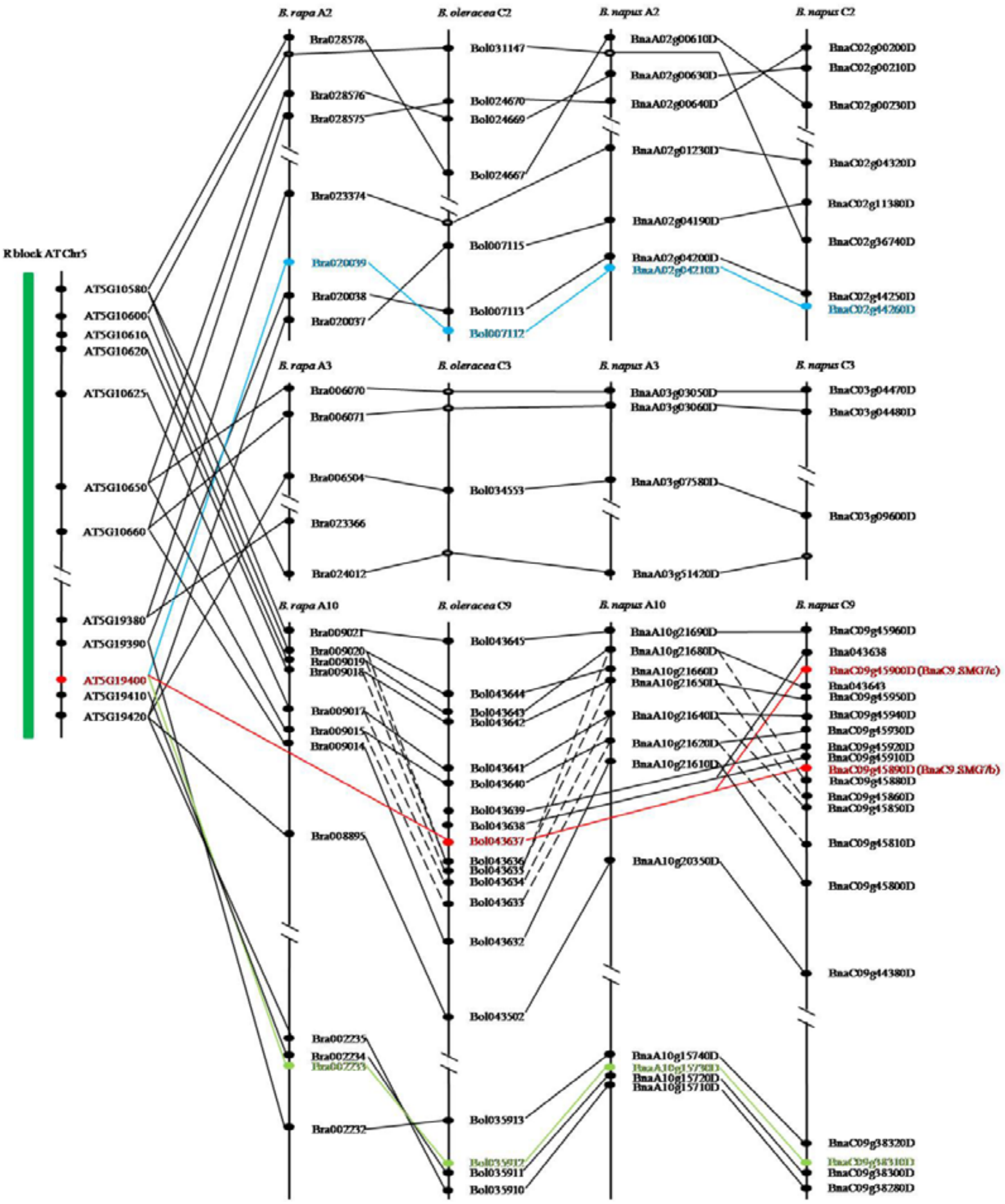
Supplementary Figure S1. Number of seeds per silique in NIL(Y106), HZ396-null and *BnaC9.RING*-transgenic T_0 lines. A two-tailed Student's t test between HZ396-null and *BnaC9.RING*-transgenic plants was used to generate the *P* value. Error bars represent the standard deviations.



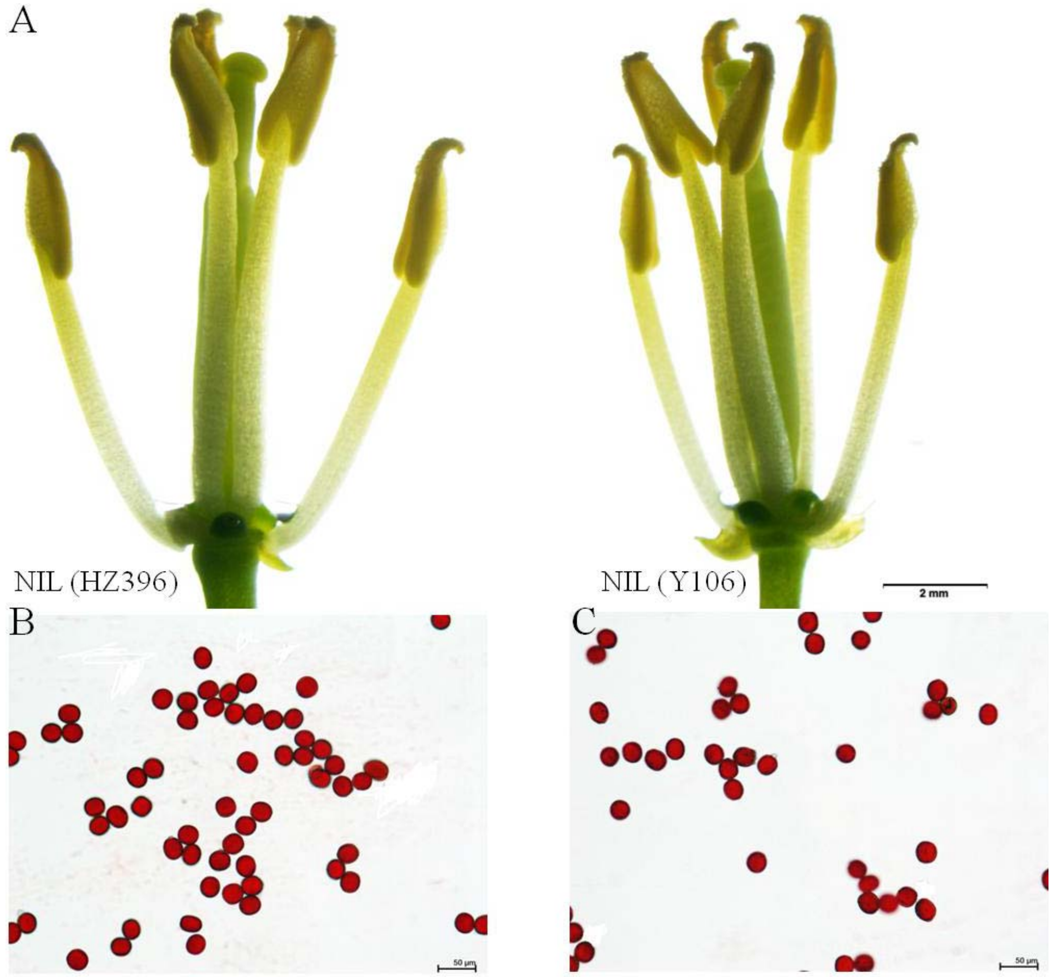
Supplementary Figure S2. Comparison of the amino acid sequences of *Brassicaceae* SMG7. The following protein sequences were used for the alignment: *Brassica rapa* BraA2.SMG7 (Bra020039), *Brassica rapa* BraA10.SMG7 (Bra002233), *Brassica oleracea* BolC2.SMG7 (Bol007112), *Brassica oleracea* BolC9.SMG7a (Bol035912), *Brassica oleracea* BolC9.SMG7b (Bol043637), *Brassica napus* BnaA2.SMG7 (BnaA02g04210D), *Brassica napus* BnaA10.SMG7 (BnaA10g15730D), *Brassica napus* BnaC2.SMG7 (BnaC02g44260D), *Brassica napus* BnaC9.SMG7a (BnaC09g38310D), *Brassica napus* BnaC9.SMG7b (BnaC09g45890D) and *Brassica napus* BnaC9.SMG7c (BnaC09g45900D). The alignment of SMG7 amino acid sequences was performed with Geneious 4.8.3. Gray bars represent the conserved EST-TPR or EST-CD domain.



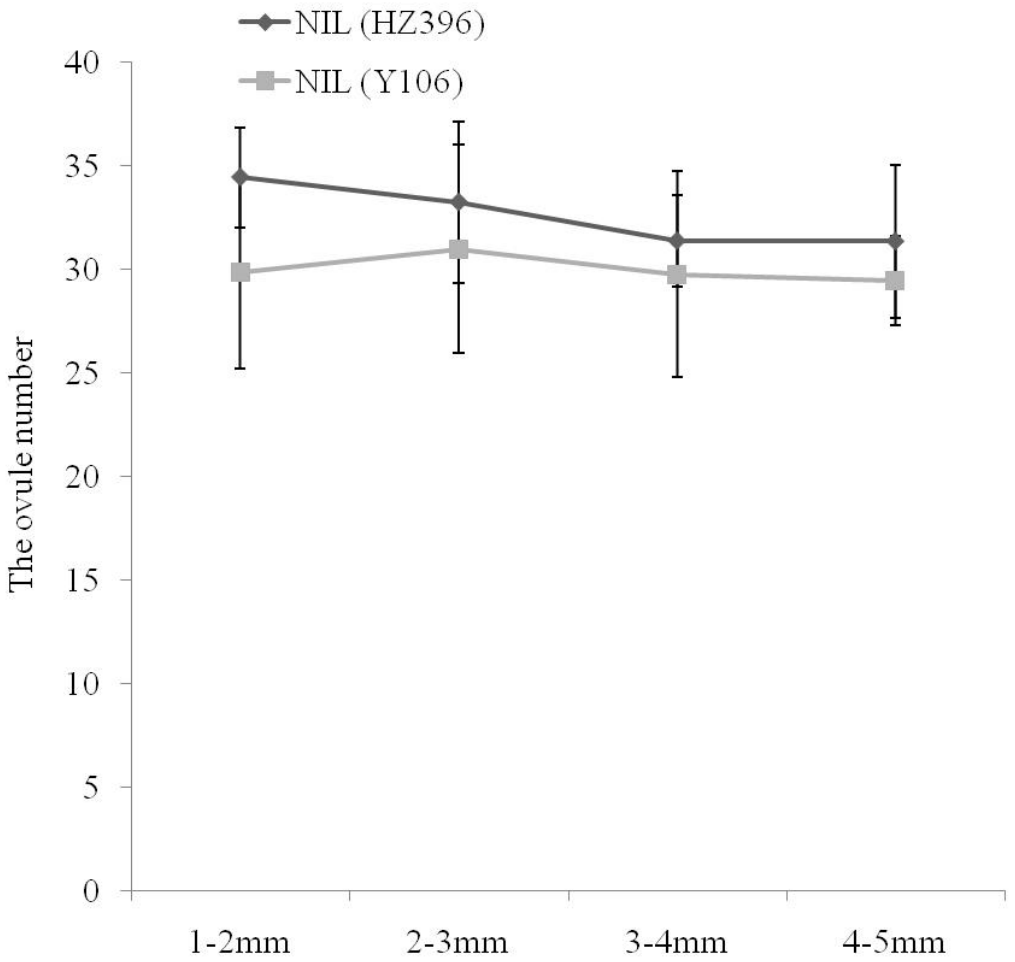
Supplementary Figure S3. Phylogenetic tree of the *Brassicaceae* SMG7 proteins. The bootstrap neighbor-joining phylogenetic tree was constructed using MEGA 4.0. The lengths of the branches refer to the amino acid variation rates.



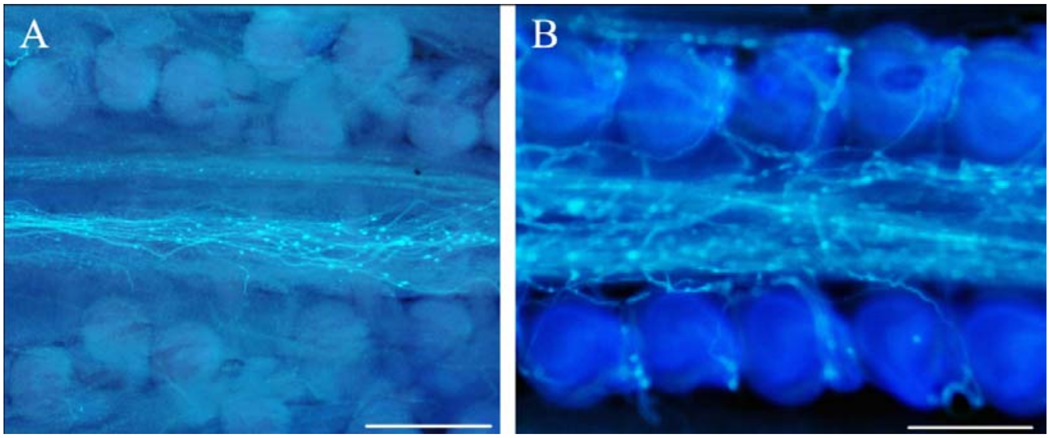
Supplementary Figure S4. Origin and evolution analysis of the *SMG7* homologs. Syntenic analysis of the genomic regions spanning *SMG7* and its homologs from the Arabidopsis, *B. rapa*, *B. oleracea* and *B. napus* genomes. The region including *BnaC9.SMG7b* and *BnaC9.SMG7c* and their flanking genes on the C9 chromosome of the *B. napus* genome was corrected based on the partial sequences of BAC clone HBnB016G24. The green bar represents the ancestral karyotype R block (Schranz et al., 2006). The loci individually depicted by blue, red and green ellipses represent the *SMG7* homologs in the A or C genomes, which are connected by blue, red and green solid lines, respectively. The black filled ellipses represent homologs, which are connected by solid or dotted lines, whereas the hollow white ellipses represent the absence of a homologous gene in the expected positions.



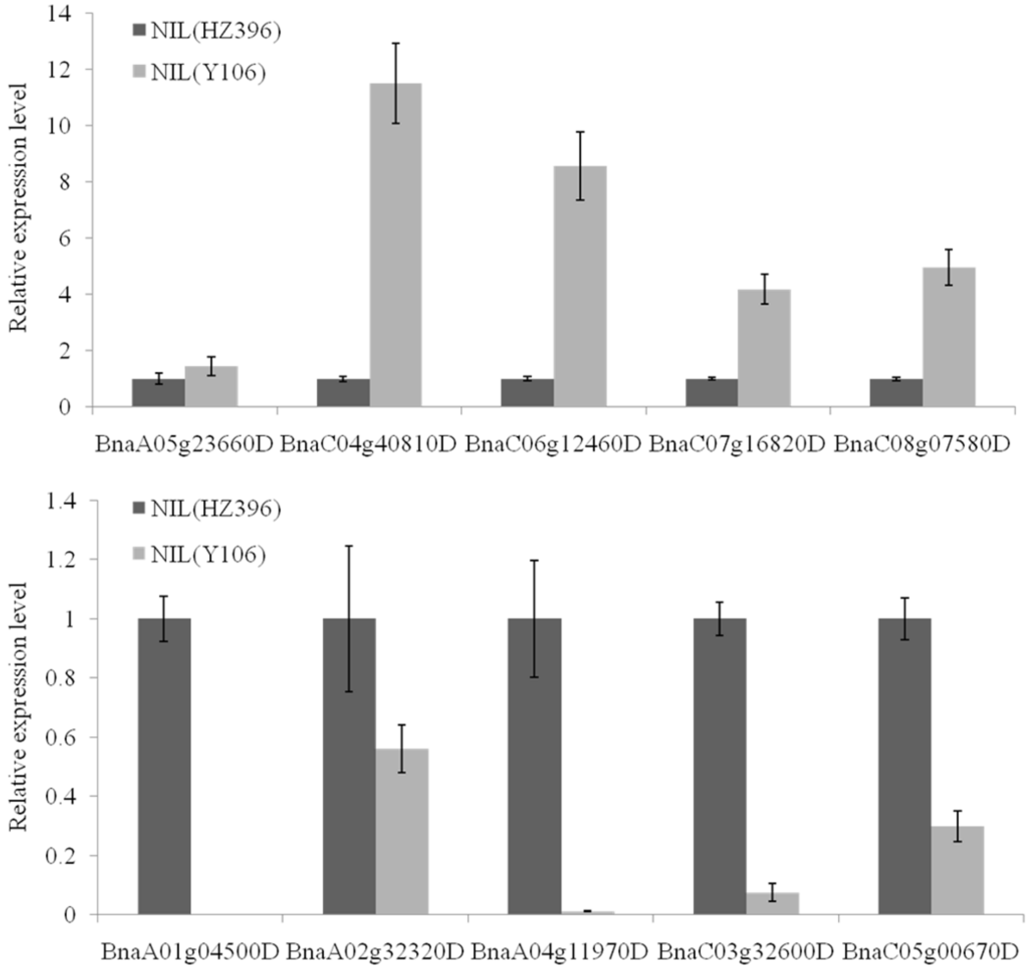
Supplementary Figure S5. Flower phenotype and pollen fertility of NIL(HZ396) and NIL(Y106). A, Flower morphology of NIL(HZ396) and NIL(Y106) after the removal of petals. Bar=2 mm. B and C, Carmine acetate staining of NIL(HZ396) and NIL(Y106) pollen. Bars=50 µm.



Supplementary Figure S6. Quantitative analysis of ovule number in NIL(HZ396) and NIL(Y106). Ovaries from NIL(HZ396) and NIL(Y106) with sizes of 1-2, 2-3, 3-4 and 4-5 mm before pollination. Error bars represent the standard deviations.

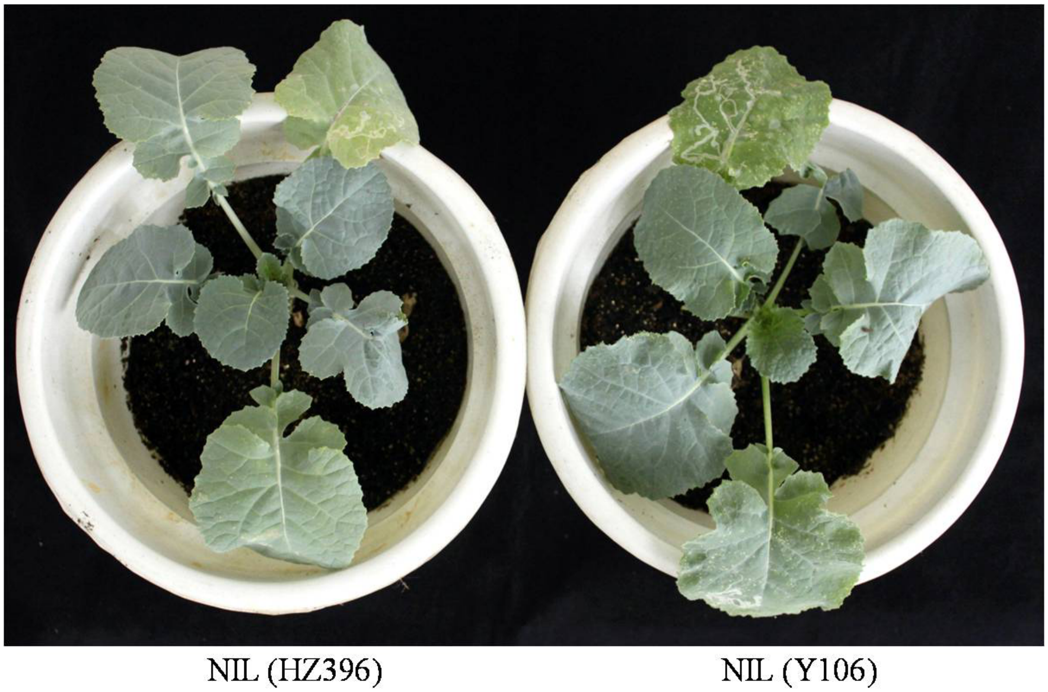


Supplementary Figure S7. Fluorescence micrographs of pollen tube germination and growth in NIL(HZ396) and NIL(Y106). A, Pollen grain germination 72 h after artificial pollination on NIL(HZ396). B, Pollen grain germination 72 h after artificial pollination on NIL(Y106). Bars=500 μm.

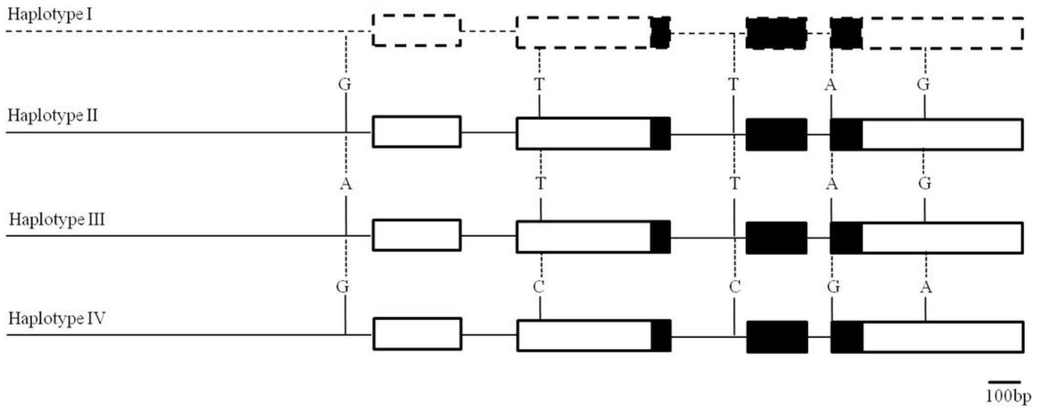


Supplementary Figure S8. qPCR confirmation of the differentially expressed genes (DEGs) between NIL(HZ396) and NIL(Y106). Total RNA was extracted from ovaries during meiotic stages with length <1 mm before pollination. Error bars represent standard errors from three independent RNA samples.

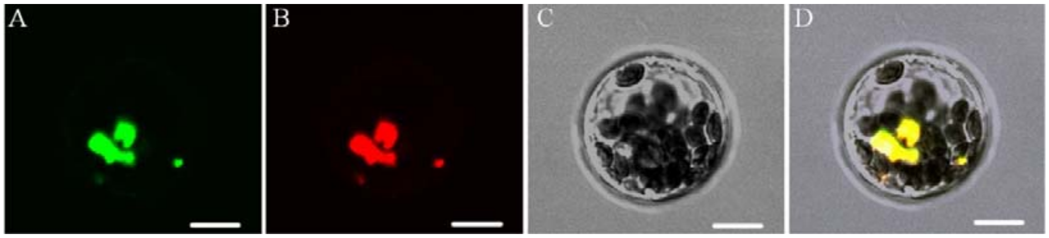
Supplementary Figure S9. Statistics of alternative splicing (AS) events in NIL(HZ396) and NIL(Y106). TSS: Alternative 5' first exon (transcription start site); TTS: Alternative 3' last exon (transcription terminal site); SKIP: Skipped exon (SKIP_ON, SKIP_OFF pair); XSKIP: Approximate SKIP (XSKIP_ON, XSKIP_OFF pair); MSKIP: Multi-exon SKIP(MSKIP_ON, MSKIP_OFF pair); XMSKIP: Approximate MSKIP (XMSKIP_ON, XMSKIP_OFF pair); IR: Intron retention (IR_ON, IR_OFF pair); XIR: Approximate IR (XIR_ON, XIR_OFF pair); MIR: Multi-IR (MIR_ON, MIR_OFF pair); XMIR: Approximate MIR (XMIR_ON, XMIR_OFF pair); AE: Alternative exon ends (5', 3', or both); XAE: Approximate AE.



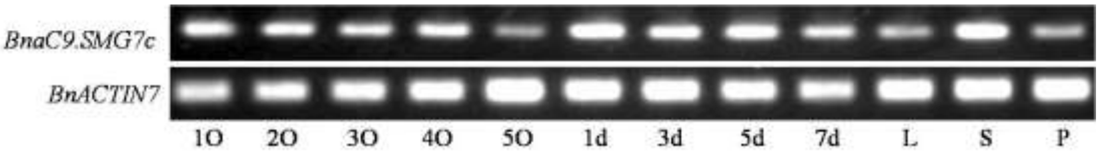
Supplementary Figure S10. Ten-week-old NIL(HZ396) and NIL(Y106) plants.



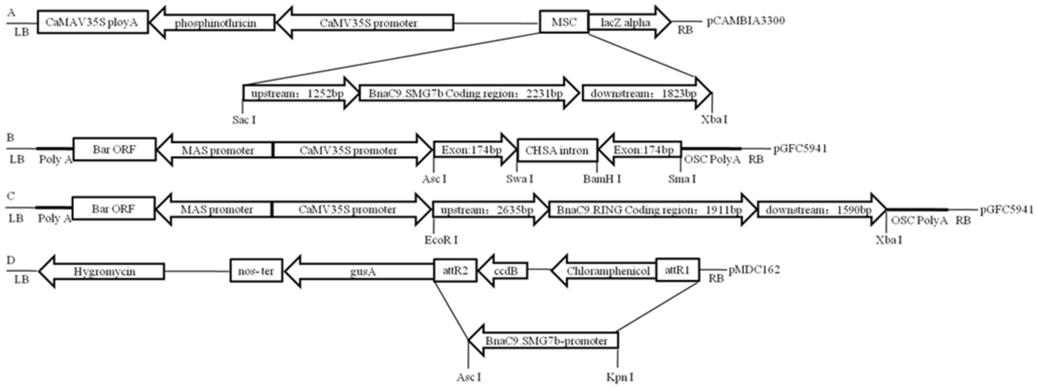
Supplementary Figure S11. Gene structure and natural variations of *BnaC9.SMG7b*. Black lines represent 5’ upstream regions and introns. Black bars represent exons and white bars represent 5’ and 3’ untranslated regions. Bar=100 bp.



Supplementary Figure S12. BnaC9.SMG7c subcellular localization. Co-localization of BnaC9.SMG7c-GFP (A) and AtDCP1-RFP (B) in the P-bodies. The bright-field image (C) and merged images (D) are also shown. Bars=10 μm.



Supplementary Figure S13. Expression patterns of *BnaC9.SMG7c* by RT-PCR. 1O-5O, ovary from NIL(Y106) with <1, 1-2, 2-3, 3-4 and 4-5 mm before pollination; 1d-7d, ovary from NIL(Y106) grown for 1, 3, 5 and 7 days after pollination; L, leaves; S, stamens; P, pedicels. *BnACTIN7* expression was used as a control.



Supplementary Figure S14. Schematic presentation of transgenic constructs. A, The genetic complementation construct of *BnaC9.SMG7b*. B, The RNAi construct of *BnaC9.SMG7b*. C, The genetic complementation construct of *BnaC9.RING*. D, The promoter analysis construct of *BnaC9.SMG7b*.

Supplementary Table S1. Progeny testing of the seven recombinants occurring in the interval between SRC9-298 and SRC9-397 in the autumn of 2012 in Wuhan.

	Number of seeds per silique of BC_4F_2 progenies of the recombinants (%)						
NO.	3U20	3U82	5U19	3U42	3U92	5U73	T8-15
1	28.1	27	26.6	10.8	10.6	13.2	16
2	25.8	28.2	9.8	7	12.6	12.4	9.7
3	23.4	25.7	17.9	14.5	10.7	14.9	5.7
4	30.5	16.3	23.3	12.8	12	10.4	15.4
5	27.5	18	26.4	15.7	16.1	15.1	15.3
6	27.4	27.1	26.5	16.9	8.8	18.1	16.5
7	25.1	10.9	23.9	12.6	10.2	13.7	15.7
8	9.7	8.2	8	13.3	12.2	18.3	
9	14.1	7	26.9	12.1	12.8	12.4	
10	9.7	14	18.3	13.2	12.8	12.9	
Mean ± s.e.m	22.1±2.5	18.3±2.6	20.8±2.2	12.9±0.9	11.9±0.6	14.1±0.8	13.5±1.6
Range	9.7-30.5	7-28.2	8-26.9	7-16.9	8.8-16.1	10.4-18.3	5.7-16.5
qSS.C9 genotype[a]	H	H	H	B	B	B	B

[a] *qSS.C9* genotype deduced by progeny testing. B, homozygous for HZ396 genotype; H, heterozygote.

Supplementary Table S2. Number of seeds per silique in five T_1 *BnaC9.SMG7b*-transgenic rapeseed lines.

NO.	SS05	SS06	SS13	SS40	SS47
1	20.2	19.5	21.5	21.2	22.6
2	20.1	22.9	20.3	19.4	21.5
3	21.9	18.7	19.2	18.3	22.7
4	17.0	24.4	21.7	18.2	17.0
5	22.9	25.3	22.1	21.2	22.3
6	19.4	19.7	21.8	18.3	18.7
7	19.3	21.1	20.6	20.1	21.3
8	19.6	21.8	18.4	17.0	19.7
9	20.7	23.7	19.6	24.0	22.7
10	19.3	21.9	19.3	20.0	20.8
Mean ± s.e.m	20.0±0.5	21.9±0.7	20.5±0.4	19.8±0.6	20.9±0.6
Range	17.0-22.9	18.7-25.3	18.4-22.1	17.0-24.0	17.0-22.7

Supplementary Table S3. Number of seeds per silique and *BnaC9.SMG7b* expression level in Ri2-8 and Ri2-14 T_1 families of 7-5 RNAi-transformed plants.

Plant	Number of seeds per silique	Relative expression level	Correlation coefficient
Ri2-8 T_1 family			0.714[a]
Ri2-8-1	5.6±0.8	0.64±0.03	
Ri2-8-2	4.2±1.0	0.73±0.03	
Ri2-8-3	9.7±0.9	0.68±0.06	
Ri2-8-4	7.6±1.6	0.82±0.07	
Ri2-8-5	22.8±1.0	1.03±0.02	
Ri2-8-6	21.3±1.1	0.70±0.02	
Ri2-8-7	13.1±1.5	0.81±0.08	
Ri2-8-9	28.3±1.0	1.20±0.09	
Ri2-8-10	8.1±1.1	0.94±0.10	
Ri2-8-11	9.7±0.9	0.87±0.03	
Ri2-8-12	11.4±1.1	0.86±0.09	
Ri2-8-13	20.0±1.4	1.21±0.13	
Ri2-8-14	32.8±1.7	1.61±0.11	
Ri2-8-15	31.1±0.9	0.91±0.02	
Ri2-14 T_1 family			0.761[b]
Ri2-14-1	10.7±1.1	1.01±0.08	
Ri2-14-2	25.5±1.5	1.17±0.07	
Ri2-14-3	25.7±1.4	1.14±0.09	
Ri2-14-4	7.5±0.6	0.86±0.04	
Ri2-14-5	27.6±1.6	1.53±0.05	
Ri2-14-6	20.5±0.7	1.29±0.03	
Ri2-14-7	11.1±0.8	1.15±0.007	

Number of seeds per silique and expression are given as mean ± s.e.m. Relative expression level of the *BnaC9.SMG7b* gene in each progeny was determined by qPCR with the RNA isolated from flower buds. [a] indicates $P<0.01$ for the correlation coefficient of the Ri2-8 T_1 family, and [b] indicates $P<0.05$ for the correlation coefficient of the Ri2-14 T_1 family.

Supplementary Table S4. Confocal laser scanning microscopy observations of NIL(Y106) and NIL(HZ396) ovules.

Ovule genotype	Normal FG[a] (%)	Abnormal FG[b] (%)
NIL(Y106)	55 (96.5%)	2 (3.5%)
NIL(HZ396)	44 (34.4%)	84 (65.6%)

[a] normal female gametophyte at stage FG5. [b] ovule with no female gametophyte.

Supplementary Table S5. Quantitative analysis of initial ovule number and number of seeds per silique in NIL(Y106) and NIL(HZ396).

Ovule genotype	NO of ovule initiation	Number of seeds per silique	Proportion of abortion ovule numbers (%)
NIL(Y106)	34.3±0.3	27.6±0.7	19.5%
NIL(HZ396)	34.4±0.3	10.4±0.5	69.8%

Data are given as mean ± s.e.m.

Supplementary Table S6. Meiosis during megasporogenesis in NIL(Y106) and NIL(HZ396).

	Dyad (%)	Triad (%)	Tetrad1 (%)	Total
NIL(Y106)	41 (9.45%)	157 (36.17%)	236 (54.38%)	434
NIL(HZ396)	45 (11.28%)	140 (35.09%)	214 (53.63%)	399

Supplementary Table S7. Part of DEGs expression quantification in NIL(HZ396) and NIL(Y106) by RNA-seq.

Gene ID	NIL(HZ396)	NIL(Y106)
BnaA05g23660D	45.2679449	92.3895353
BnaC04g40810D	12.3068881	55.0821331
BnaC06g12460D	10.7016418	45.5111242
BnaC07g16820D	24.1322023	77.0075567
BnaC08g07580D	19.7445292	70.3664484
BnaA01g04500D	129.222325	0
BnaA02g32320D	61.7484733	17.7258992
BnaA04g11970D	358.612017	4.59017776
BnaC03g32600D	125.958324	59.5746475
BnaC05g00670D	670.778909	265.302508

Supplementary Table S8. Meiotic genes expression quantification in NIL(HZ396) and NIL(Y106) by RNA-seq.

Gene family	Gene ID	NIL(HZ396)	NIL(Y106)
Entry into meiosis			
BnAGO9	BnaA02g05290D	49.3659622	82.33667686
	BnaA10g14440D	1.107458467	0.851700717
	BnaC09g36780D	1.975006991	3.13598695
	BnaC09g36860D	0	0.018798532
BnCDC45	BnaA03g37670D	3.091703106	3.52102192
	BnaA07g05080D	1.682906433	3.194329164
	BnaC03g74180D	3.627816788	5.234455858
BnMEI1[a]	BnaA07g33480D	4.0961519	7.17287678
	BnaC06g38030D	3.52774858	7.36563184
BnSW11	BnaA02g11280D	3.079670849	2.509166783
	BnaA10g08080D	0.75887258	0.651617693
	BnaC02g15840D	0.861586509	1.798917603
	BnaC09g27720D	7.237326679	11.9246432
BnXRI1	BnaA06g30010D	5.505114064	7.782530417
	BnaA09g03120D	5.636378723	7.72051318
	BnaC07g26700D	9.471440535	12.6285537
	BnaC09g02540D	5.363663216	8.908185457
Recombination: DSB formation			
BnDFO	BnaA10g04520D	1.036968744	2.821191476
	BnaC05g04880D	6.463771835	6.014167875
BnH2AX	BnaA06g05170D	86.3502485	95.88013536
	BnaA08g26730D	31.31113827	34.24290548
	BnaA09g48670D	0	0.116077646
	BnaC05g06450D	108.6105109	109.4612199
BnPHS1	BnaA03g14800D	5.546848144	7.302996885
	BnaC03g17840D	6.979530211	8.168643913
BnPRD1	BnaA03g24590D	0.72057029	1.703428582
	BnaC03g29300D	1.269872751	2.074887917
BnPRD2	BnaA02g08030D	0.24091193	0.274365344
	BnaA10g11740D	2.044874847	2.105856393
	BnaC02g11140D	0.803604066	0.717799063
	BnaC09g33470D	2.267960796	2.663152843
BnPRD3[a]	BnaA06g35310D	3.70060041	8.53985049
	BnaA10g00300D	5.58474404	8.01194344
	BnaC05g00390D	3.06078607	3.90078928
	BnaC07g20440D	4.69827208	10.5664721
BnSPO11-1	BnaA01g29970D	3.131855094	5.761672232
	BnaC01g37870D	1.011830107	2.149195198
BnSPO11-2	BnaA09g11340D	0.688590793	0.697075206

	BnaC09g11780D	0.413154476	0.653508005
Recombination: early DSB repair			
BnATM	BnaA06g20800D	2.137878903	2.502912598
	BnaC03g53260D	6.100832774	6.88895593
BnATR	BnaA04g12720D	23.89073168	18.7755024
	BnaC04g33820D	1.238362521	1.977738616
BnBRCA2(IV), BnBRCA2(V)	BnaA03g00230D	0.150777639	0.243262721
	BnaA05g13130D	2.007571487	2.88680058
	BnaC03g00130D	2.131026921	3.0561526
	BnaC06g42060D	2.32872433	3.448350079
BnCOM1[a]	BnaA04g05720D	1.83289904	3.59696378
	BnaC04g28430D	2.87435946	6.66537638
BnMCM8[a]	BnaA05g28830D	1.46115188	2.77341627
	BnaC05g43310D	0.78509653	1.65577091
BnMRE11	BnaA10g07340D	2.770725725	4.190862724
	BnaC09g30690D	14.03283981	14.95849429
BnNBS1	BnaA05g33420D	7.290310223	7.911722151
BnRAD50	BnaA03g14800D	5.546848144	7.302996885
	BnaC03g17840D	6.979530211	8.168643913
BnRAD51	BnaA03g08120D	3.013697058	6.946086319
	BnaA10g14690D	5.575003207	6.950874522
	BnaC03g10300D	18.2919285	21.54479516
	BnaC09g37020D	4.864463583	8.24767947
BnRAD51B	BnaA04g17220D	0.044846682	0.085123607
	BnaC04g39830D	4.068374037	4.943645994
BnRAD51C	BnaA05g04710D	4.016269558	6.270772372
	BnaC04g04170D	1.055443474	1.335560039
BnRAD51D	BnaA08g29130D	0.699608246	1.021483282
BnRPA1A	BnaA07g04290D	3.757769408	3.540093129
	BnaC07g47810D	5.375174817	5.735677427
BnRPA1C	BnaA02g23910D	58.5871356	64.66933901
	BnaA09g17670D	2.281331236	3.748184624
	BnaC02g31570D	56.91812798	49.2756239
	BnaC09g18720D	2.69640678	3.412037908
BnXRCC3	BnaA03g10270D	0.455770844	0.432549924
	BnaC03g12950D	0.075715178	0.646718312
Recombination: IH bias			
BnAHP2	BnaC05g08840D	0.213816701	0.243507628
BnMND1	BnaA03g49390D	2.506929547	3.541142045
BnXRCC2	BnaA09g06860D	4.704967734	6.358136073
	BnaC09g06360D	3.788679668	4.432994956
Recombination: CO and NCO outcome			
BnARP6	BnaA08g00100D	18.5526953	21.91236772
	BnaC03g71020D	17.73679515	17.76923147

BnBLAP75	BnaA09g06650D	1.056810039	2.031008112
	BnaC09g05950D	2.381419898	3.490583001
BnCDKG1	BnaC02g42490D	24.00616529	36.77840543
BnFANCM	BnaA05g18180D	2.793890072	4.354569966
	BnaC05g27760D	3.098265088	4.810352395
BnHEI10[a]	BnaA05g14420D	2.93421221	4.53199203
	BnaA06g00910D	1.76557286	4.55558987
	BnaC03g69660D	3.1539716	6.20425502
	BnaC06g06360D	3.23699338	6.63964133
BnMER3[a]	BnaA02g29040D	2.05494471	4.94160585
	BnaC02g37070D	1.32408251	3.55068848
BnMHF1	BnaA03g13400D	8.870033114	9.722331954
	BnaC03g16220D	7.549729269	12.65830902
BnMHF2	BnaA07g34380D	3.831188012	3.952167461
	BnaC03g70530D	1.525308675	1.061570562
	BnaC06g39210D	10.32755029	12.01458908
BnMHL1	BnaA03g23940D	2.509805365	3.479856865
	BnaC03g28480D	4.343362273	5.518259988
BnMHL3	BnaA03g53380D	2.114033612	4.142558833
	BnaC07g45660D	4.49209934	7.343762371
BnMSH2	BnaA03g34810D	2.591832253	4.15862397
BnMSH4[a]	BnaA08g08260D	1.49979069	3.55844586
BnMSH5[a]	BnaA05g20450D	2.34023885	6.4681952
BnMUS81	BnaA09g20790D	9.021846838	10.76840565
BnPTD	BnaA06g38110D	3.693151097	5.885737836
	BnaC05g49280D	11.66013743	11.01182346
BnRFC1	BnaA02g05420D	29.60298865	37.80334093
	BnaC08g49560D	0.094849274	0.108020195
BnRBR	BnaA01g30730D	5.061142328	6.633106254
	BnaA03g32200D	6.774862458	5.133912396
	BnaA05g26760D	13.19074544	16.37060044
	BnaC03g37490D	2.019907424	2.362808801
	BnaC05g40780D	12.02666434	13.68040049
BnSHOC1[a]	BnaA03g12670D	0.45169902	1.47547585
	BnaC03g15550D	0.60418818	1.4829455
BnZIP4	BnaA06g30240D	12.95961057	15.86580961
	BnaC07g26460D	17.11186423	19.13308265
Recombination: control of CO distribution			
BnAXR1	BnaA08g28200D	4.45631689	4.261072504
	BnaA09g50410D	6.495395704	8.476137874
	BnaA10g03210D	5.140251423	6.145469556
	BnaC05g03220D	13.55157193	14.63508729
	BnaC08g44060D	1.818108746	2.622727346
	BnaC08g46380D	6.366166986	7.091187824

BnPSS1	BnaA06g38300D	2.703404228	2.52679559
	BnaC05g11410D	3.031089589	3.420892491
	BnaC08g39040D	0.560031231	1.022112274
Axis-SC			
BnASY1[a]	BnaA07g26350D	8.08536014	25.4448534
	BnaC06g26770D	0.89366017	1.84771041
	BnaC06g28450D	2.78705724	8.77188388
BnASY3	BnaC04g00500D	12.27461768	17.13249355
BnZYP1[a]	BnaA07g20670D	1.49916053	5.10741641
	BnaA07g34050D	2.06771417	17.5352784
	BnaC06g20530D	4.79538075	10.8205759
	BnaC06g38690D	6.30460919	13.5752357
Sister chromatid cohesion			
BnCTF7	BnaA03g51450D	8.095466842	10.67085214
	BnaA08g12500D	0.402073704	1.001670029
	BnaC03g67630D	1.943356238	4.06840768
	BnaC07g50930D	4.710829161	8.228208817
BnSCC2	BnaA02g02660D	6.783273864	10.19749368
	BnaA10g18670D	4.858390595	7.729974593
	BnaC02g06100D	0.880665496	1.1323698
BnSCC3	BnaA05g00110D	44.54816308	61.42347134
	BnaC04g51720D	0.174031902	0.247747811
BnSMC2	BnaA06g17360D	2.528346126	4.742600953
	BnaA06g21840D	5.696215095	7.7490712
	BnaC03g74950D	10.84214309	12.47755727
BnSMC3	BnaA03g22510D	0.256162498	0
	BnaC03g72770D	0.560031231	0.027256327
	BnaC04g38670D	21.4314635	26.31630096
BnSGO1, BnSGO2	BnaA07g09410D	2.745099618	2.158627788
	BnaC07g12350D	9.176475867	10.7187035
BnSYN1[a]	BnaA10g24970D	2.44111773	5.57546569
	BnaC09g49900D	1.49873232	2.84474779
BnSYN3	BnaA09g37900D	2.333775632	2.115328011
	BnaC04g23000D	2.125246723	0.844946147
	BnaC08g29760D	3.972623041	7.363321754
BnPANS1	BnaA03g01210D	2.735093964	2.868980824
	BnaA10g25920D	5.714884985	8.249098467
BnTTN8	BnaA03g37440D	0.376133465	0.164755368
	BnaA09g34490D	23.6982843	31.97017658
	BnaC03g43960D	1.807321301	1.480086714
	BnaC08g25430D	23.94544432	29.04498132
Cell cycle control: spindle–cytokinesis			
BnATK1	BnaA09g19860D	21.56025411	28.91793474
	BnaC09g21860D	21.0367089	27.61639233

BnCDKA;1	BnaA01g20470D	13.41102068	15.22026408
	BnaC01g25750D	18.7945605	24.13903502
	BnaC03g52880D	6.02603741	7.671854483
	BnaC08g20460D	0.120622111	0
BnCYCB3;1[a]	BnaA06g10930D	4.50157765	7.12945094
	BnaA08g23620D	2.30134291	3.16051039
	BnaC05g12450D	8.81984754	13.506279
	BnaC08g16920D	4.93245143	7.16089366
BnJASON[a]	BnaA08g28700D	9.99975383	19.4426328
	BnaC08g01870D	7.09961856	11.47549
BnMMD1[a]	BnaA02g12370D	15.4538664	32.1657266
BnMPK4	BnaA03g26950D	16.64843151	19.52835687
	BnaC03g31910D	48.58910209	49.39786635
BnNACK2	BnaA06g19570D	5.906780144	8.681767863
BnOSD1[a]	BnaA09g37090D	9.72455461	18.5245993
	BnaC08g28850D	13.5334054	21.7693159
BnPS1[a]	BnaA07g05890D	16.1150548	23.2469015
	BnaA08g06420D	1.43926562	1.81135117
	BnaA10g09600D	6.18313873	12.791739
	BnaC07g48210D	5.22695816	9.34892027
	BnaC08g06940D	1.36828143	1.43971815
	BnaC09g31940D	4.93826406	8.22242932
BnSDS[a]	BnaA06g09550D	0.46551879	2.33523507
	BnaA08g31410D	0.7519154	2.66826708
	BnaA09g45480D	1.36423608	4.4817579
	BnaC05g10920D	0.39681096	2.20162627
	BnaC08g16420D	0.45940504	3.14542108
	BnaC08g39330D	0.3840165	2.55115959
BnSKP1[a]	BnaA02g17620D	181.85469	191.766039
	BnaA07g21520D	188.134783	231.623014
	BnaA07g32230D	104.293451	117.013432
	BnaC02g23320D	52.9051577	56.0864113
	BnaC05g15660D	66.3980048	0
	BnaC06g22030D	366.258725	402.528256
	BnaC06g36600D	115.197839	131.153409
BnSMG7	BnaA02g04210D	13.55235271	14.5444385
	BnaA10g15730D	14.29953816	15.52103359
	BnaC02g44260D	0.77926661	0.805303033
	BnaC09g38310D	15.78776183	15.92843249
	BnaC09g45890D	0	0.613145116
	BnaC09g45900D	0.522654983	0.595111436
BnTAM[a]	BnaA02g03470D	12.4044015	12.0471034
	BnaA07g33530D	2.98282585	3.34555571
	BnaC02g07160D	0.52877367	1.04226928

BnTDM1[a]	BnaC06g38120D	7.48268662	18.1239553
	BnaA03g44650D	3.02250106	5.96649797
	BnaC07g36490D	4.59420161	7.34338212

[a] indicates that these gene families are anaylzed by qPCR.

Supplementary Table S9. *qSS.C9* genotypes, haplotypes and number of seeds per silique in 84 accessions.

Accessions	SNP1	SNP2	SNP3	SNP4	SNP5	Number of seeds per silique	*qSS.C9* haplotype[a]	Geographical/Collection region
	promoter region	coding region						
g187	—	—	—	—	—	12.3±1.3	Type I	China
HZ396	—	—	—	—	—	9.6±1.7	Type I	Hubei, China
g035	—	—	—	—	—	13.5±0.4	Type I	Hubei, China
g080	—	—	—	—	—	18.2±0.7	Type I	Hubei, China
g048	—	—	—	—	—	14.4±0.6	Type I	Sichuan, China
g099	—	—	—	—	—	16.3±1.2	Type I	Europe
g163	—	—	—	—	—	11.6±1.6	Type I	Europe
g169	—	—	—	—	—	14.7±0.2	Type I	Europe
g028	G	T	T	A	G	18.1±1.9	Type II	Australia
g037	G	T	T	A	G	19.5±1.0	Type II	Australia
g039	G	T	T	A	G	23.1±1.0	Type II	Australia
g133	G	T	T	A	G	15.2±0.1	Type II	Canada
g027	G	T	T	A	G	20.8±3.4	Type II	Canada
g183	G	T	T	A	G	15.0±1.9	Type II	China
g184	G	T	T	A	G	17.6±3.0	Type II	China
g109	G	T	T	A	G	23.8±1.2	Type II	China
g086	G	T	T	A	G	10.6±1.0	Type II	Hubei, China
g076	G	T	T	A	G	14.5±1.2	Type II	Hubei, China
g003	G	T	T	A	G	14.6±0.9	Type II	Hubei, China
g085	G	T	T	A	G	14.7±4.4	Type II	Hubei, China
g171	G	T	T	A	G	16.1±0.9	Type II	Hubei, China
925A	G	T	T	A	G	16.1±1.2	Type II	Hubei, China
g087	G	T	T	A	G	16.4±1.8	Type II	Hubei, China
g013	G	T	T	A	G	17.5±2.0	Type II	Hubei, China

g157	G	T	T	A	G	17.7±1.3	Type II	Hubei, China
HZ165	G	T	T	A	G	18.0±0.8	Type II	Hubei, China
g002	G	T	T	A	G	18.5±1.5	Type II	Hubei, China
H29A	G	T	T	A	G	18.8±0.9	Type II	Hubei, China
WHR	G	T	T	A	G	18.9±0.5	Type II	Hubei, China
g051	G	T	T	A	G	19.0±1.4	Type II	Hubei, China
g146	G	T	T	A	G	19.1±1.0	Type II	Hubei, China
616A	G	T	T	A	G	19.1±0.8	Type II	Hubei, China
春 R2	G	T	T	A	G	19.1±1.3	Type II	Hubei, China
g061	G	T	T	A	G	19.4±1.8	Type II	Hubei, China
R11	G	T	T	A	G	19.9±0.7	Type II	Hubei, China
g172	G	T	T	A	G	20.1±2.7	Type II	Hubei, China
5148DH	G	T	T	A	G	20.3±1.0	Type II	Hubei, China
HS5X	G	T	T	A	G	20.6±0.6	Type II	Hubei, China
g075	G	T	T	A	G	20.6±1.3	Type II	Hubei, China
245A	G	T	T	A	G	20.9±0.3	Type II	Hubei, China
987A	G	T	T	A	G	20.9±1.1	Type II	Hubei, China
g001	G	T	T	A	G	21.1±0.6	Type II	Hubei, China
g064	G	T	T	A	G	21.2±1.2	Type II	Hubei, China
g016	G	T	T	A	G	21.4±1.5	Type II	Hubei, China
g004	G	T	T	A	G	21.7±1.1	Type II	Hubei, China
g015	G	T	T	A	G	21.8±1.4	Type II	Hunan, China
HZ168	G	T	T	A	G	22.2±1.1	Type II	Hubei, China
ZS11X	G	T	T	A	G	23.0±0.5	Type II	Hubei, China
g074	G	T	T	A	G	23.1±3.1	Type II	Hubei, China
195-14A	G	T	T	A	G	23.2±0.7	Type II	Hubei, China
g158	G	T	T	A	G	23.5±2.4	Type II	Hubei, China
8307R	G	T	T	A	G	23.6±0.3	Type II	Hubei, China
g063	G	T	T	A	G	24.0±0.1	Type II	Hubei, China

L135R	G	T	T	A	G	24.6±0.3	Type II	Hubei, China
7-6R	G	T	T	A	G	25.4±0.4	Type II	Hubei, China
Y106	G	T	T	A	G	26.0±0.7	Type II	Hubei, China
g049	G	T	T	A	G	26.4±2.3	Type II	Hubei, China
g062	G	T	T	A	G	26.5±2.2	Type II	Hubei, China
Y147	G	T	T	A	G	27.5±0.9	Type II	Hubei, China
7-5DH	G	T	T	A	G	28.1±0.3	Type II	Hubei, China
YY9X	G	T	T	A	G	14.0±1.1	Type II	Guizhou, China
HY16X	G	T	T	A	G	19.7±0.5	Type II	Shanghai, China
g052	G	T	T	A	G	24.2±2.1	Type II	Shanghai, China
g147	G	T	T	A	G	18.0±0.1	Type II	Sichuan, China
g050	G	T	T	A	G	23.3±3.4	Type II	Sichuan, China
g088	G	T	T	A	G	23.7±1.7	Type II	Sichuan, China
g014	G	T	T	A	G	23.4±1.6	Type II	Yunnan, China
g110	G	T	T	A	G	24.3±2.7	Type II	Yunnan, China
ZY50X	G	T	T	A	G	17.4±0.3	Type II	Zhejiang, China
2013ZL6	G	T	T	A	G	21.0±0.6	Type II	Zhejiang, China
ZS72X	G	T	T	A	G	21.8±0.8	Type II	Zhejiang, China
g121	G	T	T	A	G	14.9±0.7	Type II	Europe
g026	G	T	T	A	G	15.8±0.5	Type II	Europe
g025	G	T	T	A	G	20.1±1.4	Type II	Europe
g181	G	T	T	A	G	20.4±1.0	Type II	Europe
g148	G	T	T	A	G	21.4±1.7	Type II	Europe
g122	G	T	T	A	G	25.8±0.5	Type II	Europe
wester	A	T	T	A	G	16.7±1.1	Type III	Australia
g040	A	T	T	A	G	20.2±1.9	Type III	Australia
g038	A	T	T	A	G	23.0±0.9	Type III	Canada
g073	A	T	T	A	G	23.8±2.0	Type III	Hubei, China
MY12X	A	T	T	A	G	23.1±0.4	Type III	Sichuan, China

g145	A	T	T	A	G	24.9±0.8	Type III	Europe
HZX	G	C	C	G	A	25.5±1.4	Type IV	Hubei, China

[a] *qSS.C9* haplotype is determined and grouped by sequencing the promoter region and gene region of *qSS.C9* in the accessions. Data are given as mean ± s.e.m.

Supplementary Table S10. Number of seeds per silique in three haplotypes.

qSS.C9 haplotype	Range	Mean ± s.e.m	*P* values	
Haplotype I (n=8)	9.6-18.2	13.8±1.0		
Haplotype II (n=69)	10.6-28.1	20.4±0.4	9.72E-05[a]	
Haplotype III (n=6)	16.7-24.9	22.0±1.2	0.000384[b]	0.277[c]

P values were generated by a two-tailed Student's t test. [a], [b] and [c] indicate the *P* value calculated, respectively, between Haplotype I and Haplotype II, Haplotype I and Haplotype III, and Haplotype II and Haplotype III. Data are given as mean ± s.e.m.

Supplementary Table S11. Quantitative analysis of initial ovule number and number of seeds per silique in 15 *B. napus* germplasms.

Accessions	NO of ovule initiation	Number of seeds per silique	Proportion of abortion ovule numbers (%)	*P* values
Westar	23.6±0.6[a]	16.7±0.9	29.2%	8E-06
ZS4R	23.8±0.2[a]	21.4±0.8	10.1%	6E-04
ZY50X	26.0±0.4[b]	18.7±0.7	28.1%	2E-09
HY15X	26.3±0.2[bc]	22.5±0.3	14.5%	6E-09
HZ165	27.4±0.4[bcd]	18.4±0.5	32.8%	2E-12
195A-14	27.6±0.4[cd]	24.9±0.5	9.8%	1E-04
ZS11X	28.1±0.6[d]	27.7±0.6	3.9%	0.728
HZ168	28.3±0.4[d]	21.7±0.9	23.3%	3E-09
7-6	28.5±0.4[d]	26.6±0.3	6.7%	5E-04
R5200	28.6±0.3[d]	26.0±0.4	9.1%	3E-04
Y106	30.2±0.5[e]	26.0±0.4	13.9%	1E-06
80-5213	30.6±0.4[e]	23.0±0.9	24.8%	1E-05
80-5215	30.7±0.4[e]	29.2±0.7	4.9%	0.239
80-5214	31.1±0.4[e]	22.1±0.8	28.9%	2E-07
7-5DH	32.4±0.6[f]	26.2±1.0	19.1%	5E-06

[a] Different alphabetical letters following means indicate significant differences (*P*=0.01). Data are given as mean ± s.e.m. *P* values were generated by a two-tailed Student's t test.

Supplementary Table S12. Summary of primers used in this study.

Primer name	Sequence 5'–3'	Purpose
SCC9-136L	CGTCAAGCCAATAGCAGAATCG	fine mapping
SCC9-136R	CTTGGTGGCGTGTTTCTTGTTC	
SRC9-298L	TCCACCTTCGGATTCTCTCCCTCT	fine mapping
SRC9-298R	TGTCTTCTTCTGTTCACCGCCACT	
STC9-114L	ATGGTTCTGCCTCGAAAAGCAAC	fine mapping
STC9-114R	GAGATGAACTCCCAACAATTGCC	
SRC9-397L	GGTTTTGGCACACGGATTAAAGAAACA	fine mapping and BAC screening
SRC9-397R	CGTGCTAAGCATGGGGTAATAACACT	
STC9-108L	ATCGGTGTTTCAGTTACAGG	fine mapping and BAC screening
STC9-108R	CGAAATCCACGTAACAATTC	
STC9-164L	CAACCCTACAAAGATGAGCTAAGACG	fine mapping and the *BnaC9.SMG7b* and *BnaC9.SMG7c* homologous copies analysis
STC9-164R	TGGATGATGACTTTGCAGATGG	
STC9-271L	CATGATTACGAATTCGAGCTCGGTACCCTTACAAGTAGAGCATGGAC	*BnaC9.SMG7b* Complementation test
STC9-271R	TGCCTGCAGGTCGACTCTAGATAACTGAGGTTGAGCTGGCTCCTCG	
SWC9-012L	ATTTGAAAAATCTCAGAATTCCTTCCTCTGCGTTCCACCTCCAGAT	*BnaC9.RING* Complementation test
SWC9-012R	GGTCTTAATTAACTCTCTAGACTTGCCGACCGGTGAAGTAGTCTCT	
C9RNAi-2L	TTACCGCTCCCAAAGACTCG	*BnaC9.SMG7b* RNAi test
C9RNAi-2R	GGGTAAAAAGAATCCCGTTGAG	
STC9-175L	TTTGGCGCGCCGGTAAAACCCCATGTTGCTTC	Pro$_{BnaC9.SMG7b}$-GUS construction
STC9-175R	CGGGGTACCCTTACAAGTAGAGCATGGAC	
STC9-368L	GGAGAGGACAGGGTACCCGGGATGGAGAGGGAGATTCTAAGAACCG	BnaC9.SMG7b- GFP and BnaC9.SMG7c-GFP construction
STC9-368R	GGCAGCGGCAGCAGCCGGATCCCAAAAAATCATATCTTCCGTTAAGC	
STC9-391L	ATCAGTGATAGGGATAGATCTGGATGTCTCAAAACGGGAAGATAATC	AtDCP1-RFP construction
STC9-391R	ACCTGGTGCTCCGCCAGATCTTTGTTGAAGTGCATTTTGTAAAGTTC	
STC9-300L	AGGACACAAGCAGAGGTTTAAGC	qPCR analysis of BnaC9.SMG7b expression
STC9-300R	TTGGATCAGAAGGATTCCGAGC	
STC9-333L	CGGCTGATCGGTGGCACTGTTG	RT-PCR analysis of BnaC9.SMG7c expression
STC9-333R	AAGGATTCCGAGGGTGAGCACG	
STC9-043L	AGATGCTCAAAGCATTCTGCG	qPCR analysis of BnaC9.SMG7b expression in RNAi-transformed plants
STC9-043R	CTCGTAGACTGCTGCTAGTGGA	
STC9-452L	GGCTCAACCTTAGATTCACAGA	qPCR analysis of BnaA05g23660D expression
STC9-452R	GTATCTAACTGCTAGGATCGCG	
STC9-455L	CCCTTTGCGCCAGTTCATCTAG	qPCR analysis of BnaC04g40810D expression
STC9-455R	CATAGGCCACACTGAGCTAAGC	
STC9-457L	GTTGGGCTCAAGTTGACAGGCA	qPCR analysis of BnaC06g12460D expression
STC9-457R	GGTGTAAGCTCATTGGAAATGACC	
STC9-458L	CTAACTGCTGCTCAAGCCCTTTC	qPCR analysis of BnaC07g16820D expression
STC9-458R	TCTCTGCCTCGTCGAGTGTG	
STC9-460L	GAGCTTTGCTTCCGGTGCTGGA	qPCR analysis of BnaC08g07580D expression
STC9-460R	ACAACTCCGTTAGCCGAAGGG	
STC9-463L	GGGTTCGATGCCAATTGCCAAG	qPCR analysis of BnaA01g04500D expression
STC9-463R	GCAATAAGCCGATAACCATTGAC	

STC9-465L	GCCTGCTCATGTAGTCATATGC	qPCR analysis of BnaA02g32320D expression
STC9-465R	GCTCGAACAAGATCCTTGAGC	
STC9-467L	AGAAGCCGTGTCCGCCTAAAGC	qPCR analysis of BnaA04g11970D expression
STC9-467R	CCCAAACTTAGGGTGTGGA	
STC9-469L	TTGGCTGAGATCGGTCGTTACAC	qPCR analysis of BnaC03g32600D expression
STC9-469R	GGCAGAAGCAGCCACTTTACCG	
STC9-471L	CGATCGACGGCTATTACATTCCA	qPCR analysis of BnaC05g00670D expression
STC9-471R	TCCTTTTCCCGGCGCTAAAC	
STC9-198L	GAGGAATCTACCCAAGGAG	qPCR analysis of BnTAM expression
STC9-198R	GAGCGGAGATTCTAGATCC	
STC9-206L	GGATTCAAGAAGAAGCTGAG	qPCR analysis of BnTDM1 expression
STC9-206R	CTTTCTCTTGCTCGACAGTC	
STC9-340L	GCATGAGACTCTCTACCTCACAATG	qPCR analysis of BnCYCB3;1 expression
STC9-340R	CCTAGGATGCCAATAGTCCTCG	
STC9-342L	CAGAGGCGAGAGACCGATTG	qPCR analysis of BnOSD1 expression
STC9-342R	GCGAACTGGATGTTCGAACAC	
STC9-348L	CAATGTTCTGCAATGGAGCTTC	qPCR analysis of BnSDS expression
STC9-348R	CTTCAATTCTGGTGGCCAGAG	
STC9-414L	CTTGTGGCACTATACCTGCGACG	qPCR analysis of BnJASON expression
STC9-414R	GGCCTTCCCAACTCTTCACAAGC	
STC9-417L	CCCCAAACACTCGCTGTTAG	qPCR analysis of BnPS1 expression
STC9-417R	CACTCTTGTTGGTCCGGACCTG	
STC9-418L	ATGTACCAACCTCGGAGCAAGG	qPCR analysis of BnMMD1 expression
STC9-418R	GGGAACCGAGAAGCTCTATAGC	
STC9-420L	GAATCGTTCGAGGTCGATGAG	qPCR analysis of BnSKP1 expression
STC9-420R	GCAGTACTCGATAACCTTGGCG	
STC9-423L	TGGCTGCTAAGTACAAGTGGGC	qPCR analysis of BnMEI1 expression
STC9-423R	CATTCCCTTACGCTGGTCTG	
STC9-424L	AGGCTGGAAGACAGTGAAACCAG	qPCR analysis of BnPRD3 expression
STC9-424R	TAGCTCCTTTGGCGTCCCC	
STC9-427L	GGAGGCAAAGATCCTCATGATG	qPCR analysis of BnCOM1 expression
STC9-427R	TTCCGCCACTTGAATTCTCTGC	
STC9-428L	CTCTTCGCCGAGTGGTAGAG	qPCR analysis of BnMCM8 expression
STC9-428R	GAACTGCAGCATTCATACATGG	
STC9-432L	GACTCAGTCATGGAAGTACCATTG	qPCR analysis of BnMSH5 expression
STC9-432R	TCTACCCATTGGTGTGGCACAC	
STC9-434L	GTCTTACATTCTCCAAGGCGTTG	qPCR analysis of BnMER3 expression
STC9-434R	GACGACTGTATGTGCAGGCAG	
STC9-437L	CACCGTCAGCTGATGATAAGACC	qPCR analysis of BnSHOC1 expression
STC9-437R	CGTGTGCAATCCTAGCTTCATGG	
STC9-438L	AAGGCCGTGCCATTTCCAC	qPCR analysis of BnHEI10 expression
STC9-438R	GGAGAAATTCCAGCCATCGCC	
STC9-441L	CACTCCGATGAGCAGCAATG	qPCR analysis of BnASY1 expression
STC9-441R	CGCTTCGAGTACTGCAGGATAG	

STC9-442L	CAACGAGAATGCTAAGCTCAGG	qPCR analysis of BnZYP1 expression
STC9-442R	CAGCTTCTTGAACCTGAGAAGCC	
STC9-445L	GCCAGTGACCACTCACACAGAC	qPCR analysis of BnSYN1 expression
STC9-445R	GTAGAAGAGTTGAGCTGCAGCG	
STC9-379L	AAGAGGTGGCCTGGATGGCCG	RT-PCR/qPCR analysis of BnaA03g28670D ±PTC transcription
STC9-379R	GCATGAAATGTAAGGCACGG	
STC9-380L	AAGAGGTGGCCTGGATGGCCG	RT-PCR/qPCR analysis of BnaA03g28670D -PTC transcription
STC9-380R	GGTAGAGATGATTCGGGCTCTTC	
BnACTIN7-L	CCCTGGAATTGCTGACCGTA	RT-PCR/qPCR control for *B. napus*
BnACTIN7-R	TGGAAAGTGCTGAGGGATGC	