



FIGURE S1 Identification of target plants in progeny populations of MAALs. (A–B) FISH using a B genome–specific probe demonstrates the target plant with the chromosome complement of 18C+1B. Blue indicates the DAPI counterstaining of chromosomes, and the red signal indicates the probe specifically for the B genome chromosome (B–cent, the PBNBH35 sub–sequence) (Bar, 5  $\mu$ m). (C) SSR marker detection of plants with *B. nigra* chromosome. M, marker; CC, *B. oleracea*; BB, *B. nigra*; B1–B8, the plants with corresponding *B. nigra* chromosome respectively.

**Table S1 Summary of MAALs, non-MAALs, CC and BB sequencing data aligned to the reference genome**

Samples	Reads Number	Data			Alignment Rate	Reference genome
		Size	Q20	Q30		
CCB1-1	38.82M	5.81Gb	0.987	0.954	92.84%	CC+B01
CCB1-2	40.52M	6.06Gb	0.9867	0.9529	92.29%	CC+B01
CCB1-3	40.31M	6.30Gb	0.9873	0.9543	92.40%	CC+B01
CCn1-1	44.35M	6.64Gb	0.9895	0.9613	93.41%	CC+B01
CCn1-2	39.91M	5.97Gb	0.9873	0.9549	93.08%	CC+B01
CCn1-3	39.63M	5.93Gb	0.987	0.9539	92.87%	CC+B01
CCB4-1	46.92M	7.02Gb	0.9882	0.9575	93.25%	CC+B04
CCB4-2	40.61M	6.08Gb	0.9882	0.955	93.51%	CC+B04
CCB4-3	40.94M	6.13Gb	0.9877	0.9556	93.46%	CC+B04
CCn4-1	37.33M	5.59Gb	0.9883	0.9567	93.29%	CC+B04
CCn4-2	43.17M	6.46Gb	0.988	0.9567	93.26%	CC+B04
CCn4-3	39.77M	5.95Gb	0.9882	0.9567	93.25%	CC+B04
CCB5-1	40.31M	6.03Gb	0.9868	0.9532	92.53%	CC+B05
CCB5-2	40.82M	6.11Gb	0.9873	0.9548	92.81%	CC+B05
CCB5-3	40.75M	6.10Gb	0.9878	0.9561	92.91%	CC+B05
CCn5-1	40.19M	6.01Gb	0.9864	0.9517	93.03%	CC+B05
CCn5-2	42.01M	6.29Gb	0.9875	0.9551	93.52%	CC+B05
CCn5-3	41.04M	6.14Gb	0.9874	0.9548	93.01%	CC+B05
CCB6-1	44.09M	6.60Gb	0.9873	0.9544	92.60%	CC+B06
CCB6-2	39.99M	5.98Gb	0.9875	0.955	92.56%	CC+B06
CCB6-3	40.20M	6.01Gb	0.9873	0.9546	92.69%	CC+B06
CCn6-1	39.59M	5.92Gb	0.9856	0.9491	93.12%	CC+B06
CCn6-2	44.97M	6.73Gb	0.9883	0.9579	93.30%	CC+B06
CCn6-3	44.03M	6.59Gb	0.9897	0.9623	92.96%	CC+B06
CCB8-1	37.83M	5.66Gb	0.9874	0.9525	88.66%	CC+B08
CCB8-2	42.64M	6.38Gb	0.9873	0.9524	88.99%	CC+B08
CCB8-3	43.78M	6.55Gb	0.9871	0.9516	89.31%	CC+B08
CCn8-1	42.46M	6.36Gb	0.9879	0.9548	92.84%	CC+B08
CCn8-2	37.81M	5.66Gb	0.9881	0.9549	91.53%	CC+B08
CCn8-3	41.29M	6.18Gb	0.9876	0.9532	89.94%	CC+B08
CC-1	43.13M	6.46Gb	0.9882	0.957	93.39%	CC
CC-2	40.34M	6.04Gb	0.9881	0.9569	93.61%	CC
CC-3	42.46M	6.35Gb	0.9878	0.9561	93.61%	CC
BB-1	40.65M	6.08Gb	0.9882	0.9568	82.01%	BB
BB-2	41.14M	6.16Gb	0.9879	0.9565	86.15%	BB
BB-3	42.75M	6.40Gb	0.9887	0.9588	87.52%	BB

**Table S2 Uneven distributions of DEGs of *trans*-effects across all chromosomes in each of comparisons between MAAL and CC per chromosome**

Chr	Total genes	CCB1 VS CC		CCB4 VS CC		CCB5 VS CC		CCB6 VS CC		CCB8 VS CC	
		DEGs	Ratio (%)	DEGs	Ratio (%)						
C1	5960	200	3.36 <sup>a</sup>	104	1.74 <sup>a</sup>	79	1.33 <sup>abc</sup>	262	4.40 <sup>ab</sup>	1080	18.12 <sup>ab</sup>
C2	6603	167	2.53 <sup>bcd</sup>	82	1.24 <sup>bc</sup>	50	0.76 <sup>c</sup>	204	3.09 <sup>c</sup>	1031	15.61 <sup>c</sup>
C3	9084	271	2.98 <sup>ad</sup>	150	1.65 <sup>a</sup>	146	1.61 <sup>b</sup>	376	4.14 <sup>ab</sup>	1679	18.48 <sup>ab</sup>
C4	7140	181	2.54 <sup>bcd</sup>	98	1.37 <sup>abc</sup>	60	0.84 <sup>ac</sup>	336	4.71 <sup>b</sup>	1205	16.88 <sup>bc</sup>
C5	6371	107	1.68 <sup>e</sup>	50	0.78 <sup>d</sup>	61	0.96 <sup>ac</sup>	220	3.45 <sup>acd</sup>	1124	17.64 <sup>abc</sup>
C6	5289	115	2.17 <sup>ce</sup>	76	1.44 <sup>abc</sup>	49	0.93 <sup>ac</sup>	190	6.59 <sup>abcd</sup>	924	17.47 <sup>abc</sup>
C7	6353	148	2.33 <sup>bc</sup>	85	1.34 <sup>abc</sup>	61	0.96 <sup>ac</sup>	199	3.13 <sup>cd</sup>	1120	17.63 <sup>abc</sup>
C8	6134	173	2.82 <sup>abd</sup>	96	1.57 <sup>ac</sup>	87	1.42 <sup>ab</sup>	256	4.17 <sup>abd</sup>	1173	19.12 <sup>a</sup>
C9	7276	172	2.36 <sup>bc</sup>	81	1.11 <sup>b</sup>	75	1.03 <sup>abc</sup>	220	3.02 <sup>c</sup>	1263	17.36 <sup>abc</sup>

<sup>a,b,c,d,e</sup> Different groups were calculated by chi-square ( $p < 0.05$ )

**Table S3 Primer sequences for the DEGs used in qRT-PCR assays and relative changes in expression.**

Gene ID	Forward Sequence	Reverse Sequence
BolC1t05740H	CCGTTGGATGGTTCGGTGA	TGGAGCATTTCGGCTAAGAT
BniB01g000740.2N.1	TCTTGGCGATTCAGAGAGCG	CCGTTATCTCCGGTGGACTC
BniB04g026360.2N.1	GATCCATGGAAAGGAGAAGAATGG	CCTTAGGCCAAGGCTTCCT
BniB05g014860.2N.1	GAGGAGTTTAAGATTGAGCACAGC	GTTTCACCGGAGGGATCAGA
BniB06g045130.2N.1	CGGATGGCGAAATGGTGGATG	CCGTCTCTGTCTTCGTTGAGC
BniB08g013480.2N.1	TCCTCTTGGGTGAAGCATTTCG	GCTTGAAAGTGTAAGGCTGAGG
Actin	AGGTCTTGTTCCAGCCATCG	TGGTGCAAGTGCTGTGATCT