

**MutS HOMOLOG1 silencing mediates *ORF220* substoichiometric shifting and causes male sterility in *Brassica juncea***

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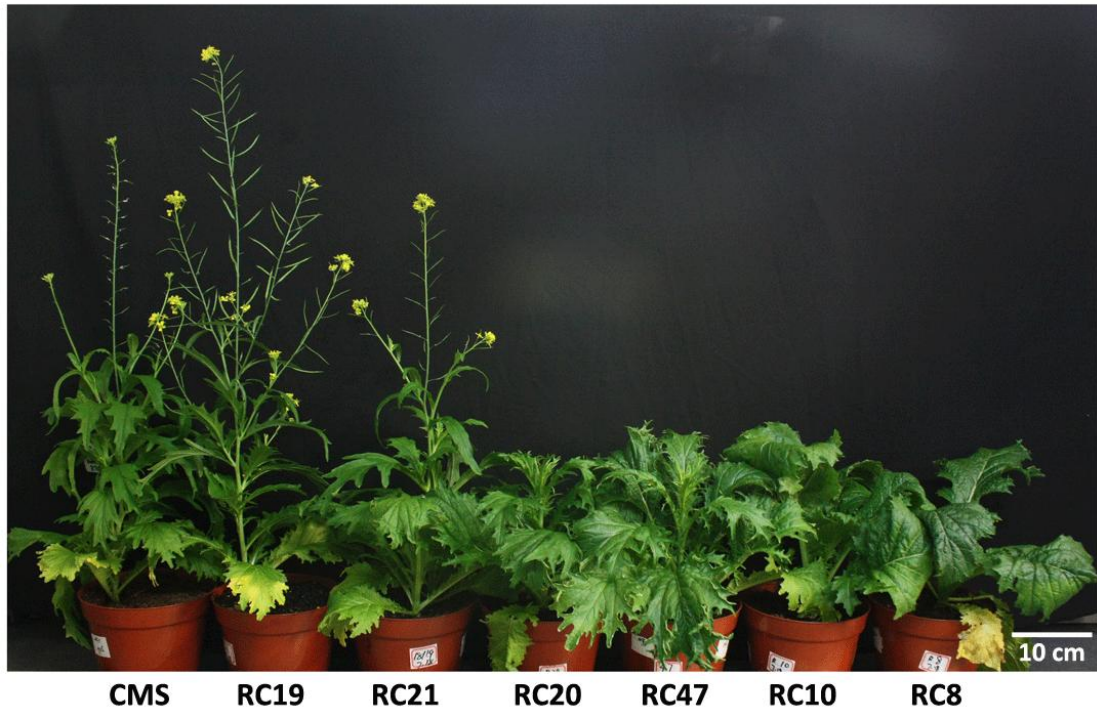


Figure S1 Candidate revertant lines of *B. juncea*.

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*      20      *      40      *      60      *      80      *      100     *      120     *      140     *      160     *
R19 : AATGAGTCCGCTTCAATATTCACAAACCGCTACTAGATAGATATCAGATATTATGGATACGATTCATTCAGAGGTCCTTGGGGTAAAGGTATAGACACGGAGAGTCAAAATCTGTGCTAAAAGCGTGGAGGTCGAGCTCTTCAAGGCAATATAGAA : 170
MF : AATGAGTCCGCTTCAATATTCACAAACCGCTACTAGATAGATATCAGATATTATGGATACGATTCATTCAGAGGTCCTTGGGGTAAAGGTATAGACACGGAGAGTCAAAATCTGTGCTAAAAGCGTGGAGGTCGAGCTCTTCAAGGCAATATAGAA : 170
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*      180      *      200     *      220     *      240     *      260     *      280     *      300     *      320     *      340
R19 : ATGGATAAGTTCGGCAGCGGATCGGGAATCTGGGATCTTCTTATCTAATGAATGGGGGAGGAGTCCGCTTGAATATCGCCCGTCCGCCCCCGAGTATATGATTCAACAGGAATCAACAGAGGTAAGTATGATCAATCAACCTCGTAAATGCCCC : 340
MF : ATGGATAAGTTCGGCAGCGGATCGGGAATCTGGGATCTTCTTATCTAATGAATGGGGGAGGAGTCCGCTTGAATATCGCCCGTCCGCCCCCGAGTATATGATTCAACAGGAATCAACAGAGGTAAGTATGATCAATCAACCTCGTAAATGCCCC : 340
ATGGATAAGTTCGGCAGCGGATCGGGAATCTGGGATCTTCTTATCTAATGAATGGGGGAGGAGTCCGCTTGAATATCGCCCGTCCGCCCCCGAGTATATGATTCAACAGGAATCAACAGAGGTAAGTATGATCAATCAACCTCGTAAATGCCCC
*      360      *      380     *      400     *      420     *      440     *      460     *      480     *      500
R19 : GGTAAACCAGCAGTAAGTAAGTACTTTAGGGATGGTCATACCATTGATGACACTTGGACAGGATGGAGTTACCAAAATGGGACTATCGGGTGGGTAATGAAATAGACGCGTGGGGATTCGAGGCTCTCTTCTTGGACCTTAA : 510
MF : GGTAAACCAGCAGTAAGTAAGTACTTTAGGGATGGTCATACCATTGATGACACTTGGACAGGATGGAGTTACCAAAATGGGACTATCGGGTGGGTAATGAAATAGACGCGTGGGGATTCGAGGCTCTCTTCTTGGACCTTAA : 510
GTTAAACCAGCAGTAAGTAAGTACTTTAGGGATGGTCATACCATTGATGACACTTGGACAGGATGGAGTTACCAAAATGGGACTATCGGGTGGGTAATGAAATAGACGCGTGGGGATTCGAGGCTCTCTTCTTGGACCTTAA
*      520      *      540     *      560     *      580     *      600     *      620     *      640     *      660     *      680
R19 : TAAAGAGAAACCGAGTCTCTTGGTCGTAATCTGAATAGGGGGAACCTCCGCTGATCTTACTTCGGAACAAACATTTAGATTAGGCTGGTCACACTGGAATGTGATTAATCCATAGGGGATCTTCCAAATAGAGAACTCTAGGAGCAAGCAAGAA : 680
MF : TAAAGAGAAACCGAGTCTCTTGGTCGTAATCTGAATAGGGGGAACCTCCGCTGATCTTACTTCGGAACAAACATTTAGATTAGGCTGGTCACACTGGAATGTGATTAATCCATAGGGGATCTTCCAAATAGAGAACTCTAGGAGCAAGCAAGAA : 680
TAAAGAGAAACCGAGTCTCTTGGTCGTAATCTGAATAGGGGGAACCTCCGCTGATCTTACTTCGGAACAAACATTTAGATTAGGCTGGTCACACTGGAATGTGATTAATCCATAGGGGATCTTCCAAATAGAGAACTCTAGGAGCAAGCAAGAA
*      700      *      720     *      740     *      760     *      780     *      800     *      820     *      840
R19 : GAAGGCTCTAATCTTTTATGATTCAGGTTAGCTTATTGGAACAGATAGCAACAACATTTACCCGATGGTATTTTTGATTTTCCAAATGGATTCACCTCAATTAATGGAAATTTTTTGAATACGAAATATACCTTCGTTGGTCTCCGATCAAA : 850
MF : GAAGGCTCTAATCTTTTATGATTCAGGTTAGCTTATTGGAACAGATAGCAACAACATTTACCCGATGGTATTTTTGATTTTCCAAATGGATTCACCTCAATTAATGGAAATTTTTTGAATACGAAATATACCTTCGTTGGTCTCCGATCAAA : 850
GAAGGCTCTAATCTTTTATGATTCAGGTTAGCTTATTGGAACAGATAGCAACAACATTTACCCGATGGTATTTTTGATTTTCCAAATGGATTCACCTCAATTAATGGAAATTTTTTGAATACGAAATATACCTTCGTTGGTCTCCGATCAAA
*      860      *      880     *      900     *      920     *      940     *      960     *      980     *      1000    *      1020
R19 : GAATCTCTGTTAGGCACTTCGTAACCATCATACATAGCTGTTGATCAGATTTCAATCTTCTGTTTCGCTAGGCAATATGTCCATGGA : 1020
MF : GAATCTCTGTTAGGCACTTCGTAACCATCATACATAGCTGTTGATCAGATTTCAATCTTCTGTTTCGCTAGGCAATATGTCCATGGA : 1019
GATTTCTGTTAGGCACTTCGTAACCATCATACATAGCTGTTGATCAGATTTCAATCTTCTGTTTCGCTAGGCAATATGTCCATGGA
*      1040     *      1060    *      1080    *      1100    *      1120    *      1140    *      1160    *      1180
R19 : ATGGACAGATCTTCGCGCTAAGTAAATGGGAACCTTCTCCGTTACATTACATGAATCTTATTTCATTCAACCGGAAAAGGCAATTTTTTCAACAT : 1190
MF : ATGGACAGATCTTCGCGCTAAGTAAATGGGAACCTTCTCCGTTACATTACATGAATCTTATTTCATTTCAGGAAAGGCAATTTTTTCAACAT : 1189
ATGGACAGATCTTCGCGCTAAGTAAATGGGAACCTTCTCCGTTACATTACATGAATCTTATTTCATTTCAGGAAAGGCAATTTTTTCAACAT
*      1200     *      1220    *      1240    *      1260    *      1280    *      1300    *      1320    *      1340    *      1360
R19 : TCTCGGATAGGATATAGACGGAAAATCCATTAGAAATGAACATATTGGTCTTAGGCCATCTCTGGCCTGAAACCAATTCAGAGTGGTTCTTCCGTAATCTTGATAAACAGCGTTATATATAGATATAGGAGGATCTGTTGGGAAATAGAACCCCTTT : 1360
MF : TCTCGGATAGGATATAGACGGAAAATCCATTAGAAATGAACATATTGGTCTTAGGCCATCTCTGGCCTGAAACCAATTCAGAGTGGTTCTTCCGTAATCTTGATAAACAGCGTTATATATAGATATAGGAGGATCTGTTGGGAAATAGAACCCCTTT : 1359
TCTCGGATAGGATATAGACGGAAAATCCATTAGAAATGAACATATTGGTCTTAGGCCATCTCTGGCCTGAAACCAATTCAGAGTGGTTCTTCCGTAATCTTGATAAACAGCGTTATATATAGATATAGGAGGATCTGTTGGGAAATAGAACCCCTTT
*      1380     *      1400    *      1420    *      1440    *      1460    *      1480    *      1500    *      1520
R19 : GACATCTCTCATCTGAAAGATCTTCGATGTGAAAACACAGGAAAGGGCTGATCTTGAATAGAAAGAGTGGATCTCGGGGTCACAAA : 1530
MF : GACATCTCTCATCTGAAAGATCTTCGATGTGAAAACACAGGAAAGGGCTGATCTTGAATAGAAAGAGTGGATCTCGGGGTCACAAA : 1529
GACATCTCTCATCTGAAAGATCTTCGATGTGAAAACACAGGAAAGGGCTGATCTTGAATAGAAAGAGTGGATCTCGGGGTCACAAA
*      1540     *      1560    *      1580    *      1600    *      1620    *      1640    *      1660    *      1680
R19 : CTGGAGAACTCCGAAATATCTGCTGAACCTCATTTTTCATCAATATCTCCGCTCGCCGAAATCGGCGGGAATGGCAATCCCAATTCAGCTTTCGATGAAATCAATAGAAAACGCGCGGGCCGATATCTAGGACGCCAACTATCTGAA : 1700
MF : CTGGAGAACTCCGAAATATCTGCTGAACCTCATTTTTCATCAATATCTCCGCTCGCCGAAATCGGCGGGAATGGCAATCCCAATTCAGCTTTCGATGAAATCAATAGAAAACGCGCGGGCCGATATCTAGGACGCCAACTATCTGAA : 1699
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CTCCGAGAACCTCCGAAATATCTGCTGAACCTCATTTTTCATCAATATCTCCGCTCGCCGAAATCGGCGGGAATGGCAATCCCAATTCAGCTTTCGATGAAATCAATAGAAAACGCGCGGGCCGATATCTAGGACGCCAACTATCTGAA
*      1720     *      1740    *      1760    *      1780    *      1800    *      1820    *      1840    *      1860
R19 : TGAATAAATCTCCCTCTATCTGTTCGCGGTCGAGGACGCTCTCTCCTCCCTTCTCAAACTCCGATTGTAATTTTCTAGAGAAATCTCGATCAAGATAGAAACAGATCCATCTGCAATATATAAGGGATCCCTTGGTCGGCAAGAAAAGCAATGTCAAT : 1870
MF : TGAATAAATCTCCCTCTATCTGTTCGCGGTCGAGGACGCTCTCTCCTCCCTTCTCAAACTCCGATTGTAATTTTCTAGAGAAATCTCGATCAAGATAGAAACAGATCCATCTGCAATATATAAGGGATCCCTTGGTCGGCAAGAAAAGCAATGTCAAT : 1869
TGAATAAATCTCCCTCTATCTGTTCGCGGTCGAGGACGCTCTCTCCTCCCTTCTCAAACTCCGATTGTAATTTTCTAGAGAAATCTCGATCAAGATAGAAACAGATCCATCTGCAATATATAAGGGATCCCTTGGTCGGCAAGAAAAGCAATGTCAAT
*      1880
R19 : GATCATTAACAACCTGCAAT : 1895
MF : GATCATTAACAACCTGCAAT : 1894
GATCATTAACAACCTGCAAT

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Figure S2 Comparison of mitochondrial DNA from CMS and revertant lines of *B. juncea*.

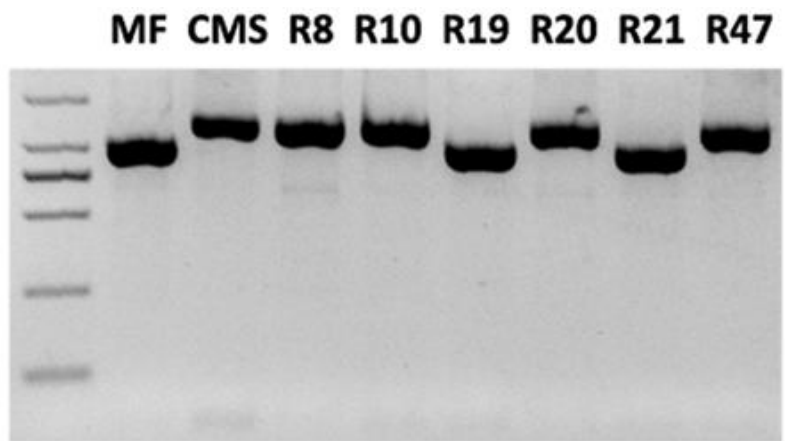


Figure S3 Mitochondrial genome rearrangement of the *atpA* gene.

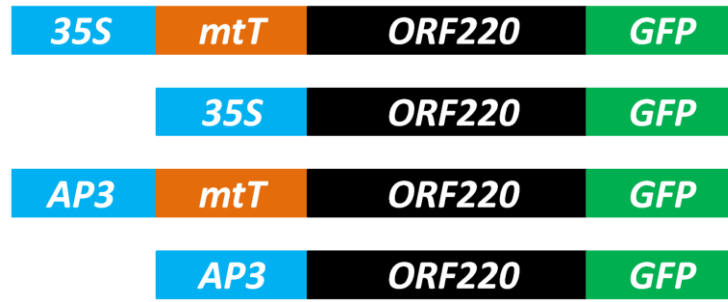


Figure S4 Schematic diagram of ORF220 gene construction.

**A**

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At3G24230 : MHWIATRNAVVSIPKWR--FFFRSSYRYYSLLKSSILLNRRYSEGISCTDGGKSLRRTTAS--KKVKT--SSDVLTDKDLSHLWVWKERLQT : 89
BjuA074077 : MHWIATRNAVVSIPRWRSEAFIFRSPFRTHSSLLKSSILLNRRYSEDRYCLDGGKSVRGITTSKKVKTKSSDVLTDKDLSHLWVWKERLQT : 94
BjuB062106 : MHWIATRNAVVSIPRWRSEAFIFRSPFRTHSSLLKSSILLNRRYSEDRYCLDGGKSVRGITTSKKVKTKSSDVLTDKDLSHLWVWKERLQT : 93
MHWIATRNAVVSIP4WRsfaFIFRSP5RThSSLLKpSp 6LLN RYSer yCLgDgKS6RgITTaSSKKVTKs DVLTDKDLSHL6WVWKERLQT

At3G24230 : CKKPSTLQIERIMYTNLLGLDPSLRNGSLKDGNLNWEMLQFKSRFPREVLLCFVGGFYEAIGIDACIIVEYAGLNPFPGGLRSDSPKAGCP66 : 183
BjuA074077 : CKKPSTLQIERIMYTNLLGLDPSLRNGSLKDGNLNWEMLQFKSRFPREVLLCFVGGFYEAIGIDACIIVEYAGLNPFPGGLRSDSPKAGCFV : 188
BjuB062106 : CKKPSTLQIERIMYTNLLGLDPSLRNGSLKDGNLNWEMLQFKSRFPREVLLCFVGGFYEAIGIDACIIVEYAGLNPFPGGLRSDSPKAGCFV : 187
CKKPSTLQIERIMYTNLLGLDPSLRNGSLKDGNLNWEMLQFKSRFPREVLLCFVGGFYEAIGIDACIIVEYAGLNPFPGGLRSDS PKAGCP66

At3G24230 : NLRQTDLDDLRNGYSVCIVVEEQGPTPARSRKGRFISGHAHPGSPYVYGI VGVHDHDLDFPEMEVVGISRSARGYCMISIFETMKAYSLDDGLT : 277
BjuA074077 : NLRQTDLDDLRNGYSVCIVVEEQGPTPARSRKGRFISGHAHPGSPYVYGI VGVHDHDLDFPEMEVVGISRSARGYCMISIFETMKAYSLDDGLT : 282
BjuB062106 : NLRQTDLDDLRNGYSVCIVVEEQGPTPARSRKGRFISGHAHPGSPYVYGI VGVHDHDLDFPEMEVVGISRSARGYCMISIFETMKAYSLDDGLT : 281
NLRQTDLDDLRNGYSVCIVVEEQGPTPARSRKGRFISGHAHPGSPYVYGI VGVHDHDLDFPEMEVVGISRSARGYCMISIFETMKAYSLDDGLT

At3G24230 : EEALVTKLRRCHHLEFLHASLRNASGTCRWGFGEGGLWGCESGRNFEWFEFGDTLSELLSKVKVIVYGLDDEVSRFNVNVPENRPRLHLG : 371
BjuA074077 : EEALVTKLRRCHHLEFLHASLRNASGTCRWGFGEGGLWGCESGRNFEWFEFGDTLSELLSKVKVIVYGLDDEVSRFNVNVPENRPRLHLG : 376
BjuB062106 : EEALVTKLRRCHHLEFLHASLRNASGTCRWGFGEGGLWGCESGRNFEWFEFGDTLSELLSKVKVIVYGLDDEVSRFNVNVPENRPRLHLG : 375
EEALVTKLRRCHHLEFLHASLRNASGTCRWGFGEGGLWGCESGRNFEWFEFGDTLSELL34V4IVYGLDDEVSRFNVNVPENRPRLHLG

At3G24230 : TATQIGALPTEGIPCLLKVLLPSTCSGLPSLYVRDLLNPPAYDIALKIQTCKLMSTVTCSEPEFTCVSSAKIVKLEQREANYIEFCRKNV : 465
BjuA074077 : TATQIGALPTEGIPCLLKVLLPSTCSGLPSLYVRDLLNPPAYDIALKIQTCKLMSTVTCSEPEFTCVSSAKIVKLEQREANYIEFCRKNV : 470
BjuB062106 : TATQIGALPTEGIPCLLKVLLPSTCSGLPSLYVRDLLNPPAYDIALKIQTCKLMSTVTCSEPEFTCVSSAKIVKLEQREANYIEFCRKNV : 469
TATQIGALPTEGIPCLLKVLLPSTCSGLPSLY6RDLNPPAYDIALKIQTCKLMST6TCS6PEFTCVSSAKIVKLEQREANYIEFCRKNV

At3G24230 : LDFVLMHMRHPEIVEILKLLMPTWVATGLKIDFETVNECHWASD3IGEMISLDD1ESHQNVSKa6N6NEFFYDMESSWRGFKVGIHIEET : 559
BjuA074077 : LDFVLMHMRHPEIVEILKLLMPTWVATGLKIDFETVNECHWASD3IGEMISLDD1ESHQNVSKa6N6NEFFYDMESSWRGFKVGIHIEET : 564
BjuB062106 : LDFVLMHMRHPEIVEILKLLMPTWVATGLKIDFETVNECHWASD3IGEMISLDD1ESHQNVSKa6N6NEFFYDMESSWRGFKVGIHIEET : 563
LDFVLMHMRHPEIVEILKLLMPTWVATGLKIDFETVNECHWASD3IGEMISLDD1ESHQNVSKa6N6NEFFYDMESSWRGFKVGIHIEET

At3G24230 : TCVKSAEALSLAVEDFHPHISRIKAmASLGGsKGEIYA4EHESVWFKGRFPTS6WgTAGEeQIKQLKPAIDSKGKVGVEEFTTqKVE : 653
BjuA074077 : TCVKSAEALSLAVEDFHPHISRIKAmASLGGsKGEIYA4EHESVWFKGRFPTS6WgTAGEeQIKQLKPAIDSKGKVGVEEFTTqKVE : 658
BjuB062106 : TCVKSAEALSLAVEDFHPHISRIKAmASLGGsKGEIYA4EHESVWFKGRFPTS6WgTAGEeQIKQLKPAIDSKGKVGVEEFTTqKVE : 657
TCVKSAAEALSLAV EDFHPHISRIKAmASLGGsKGEI YA4EHESVWFKGRFPTS6WgTAGEeQIKQLKPAIDSKGKVGVEEFTTqKVE

At3G24230 : AIVRYHEASENANARVLELLELRLSARQTKINIVFASMLIVIAKALFESHACGRRRKKWFPTLVGFSDEANPLDGGATRMKILGLSPYWF : 746
BjuA074077 : AIVRYHEASENANARVLELLELRLSARQTKINIVFASMLIVIAKALFESHACGRRRKKWFPTLVGFSDEANPLDGGATRMKILGLSPYWF : 752
BjuB062106 : AIVRYHEASENANARVLELLELRLSARQTKINIVFASMLIVIAKALFESHACGRRRKKWFPTLVGFSDEANPLDGGATRMKILGLSPYWF : 751
AIVRYHEASENANARVLELLELRLSARQTKINIVFASMLIVIAKALFESHACGRRRKKWFPTLVGFSDEANPLDGGATRMKILGLSPYWF

At3G24230 : DVASGTAVHNTVDMQSLFLLTGFGNGGKSSLLRSCAAALLGIGEMVFAESAYIPHFDSIMLHMKSYSFVQDGKSSFCVEMSEIRSVSQATS : 840
BjuA074077 : DVASGTAVHNTVDMQSLFLLTGFGNGGKSSLLRSCAAALLGIGEMVFAESAYIPHFDSIMLHMKSYSFVQDGKSSFCVEMSEIRSVSQATS : 846
BjuB062106 : DVASGTAVHNTVDMQSLFLLTGFGNGGKSSLLRSCAAALLGIGEMVFAESAYIPHFDSIMLHMKSYSFVQDGKSSFCVEMSEIRSVSQATS : 845
DVASGTAVHNTVDMQSLFLLTGFGNGGKSSLLRSCAAALLGIGEMVFAESAYIPHFDSIMLHMKSYSFVQDGKSSFCVEMSEIRSVSQATS

At3G24230 : RSVLIDEICRGTEATAGTCIAGSV6ESLdASGCLGIVSTHLHGIFDLPLTARN6TYKAMGAENVEGQTKPTWKLTDGVCRESLAFETAKREGV : 934
BjuA074077 : RSVLIDEICRGTEATAGTCIAGSV6ESLdASGCLGIVSTHLHGIFDLPLTARN6TYKAMGAENVEGQTKPTWKLTDGVCRESLAFETAKREGV : 940
BjuB062106 : RSVLIDEICRGTEATAGTCIAGSV6ESLdASGCLGIVSTHLHGIFDLPLTARN6TYKAMGAENVEGQTKPTWKLTDGVCRESLAFETAKREGV : 939
4SVLIDEICRGTEATAGTCIAGSV6ESLdASGCLGIVSTHLHGIFDLPLTARN6TYKAMGAENVEGQTKPTWKLTDGVCRESLAFETAKREGV

At3G24230 : PESVIQRAEALYLSVYAKDaSgVV4P kt tSS1N 2IsKFVsERSLEKDLAKAI6KICGKRM Epgv6ECLSIGARELPPPSTVGSSCVY : 1028
BjuA074077 : PESVIQRAEALYLSVYAKDaSgVV4P kt tSS1N 2IsKFVsERSLEKDLAKAI6KICGKRM Epgv6ECLSIGARELPPPSTVGSSCVY : 1032
BjuB062106 : PESVIQRAEALYLSVYAKDaSgVV4P kt tSS1N 2IsKFVsERSLEKDLAKAI6KICGKRM Epgv6ECLSIGARELPPPSTVGSSCVY : 1033
PE 6IQRAEALYLSVYAKDaS gVV4P kt tSS1N 2IsKFVsERSLEKDLAKAI6KICGKRM Epgv6ECLSIGARELPPPSTVGSSCVY

At3G24230 : VMRRPDKRLYIGQTDDELEGRIRAHRAKEGLQSSFLYLVQCGKSMACQLETLLINQLHEQCYSLANLADGKHRNFQTSSTSS6 ASDVVSIS : 1118
BjuA074077 : VMRRPDKRLYIGQTDDELEGRIRAHRAKEGLQSSFLYLVQCGKSMACQLETLLINQLHEQCYSLANLADGKHRNFQTSSTSS6 ASDVVSIS : 1122
BjuB062106 : VMRRPDKRLYIGQTDDELEGRIRAHRAKEGLQSSFLYLVQCGKSMACQLETLLINQLHEQCYSLANLADGKHRNFQTSSTSS6 ASDVVSIS : 1123
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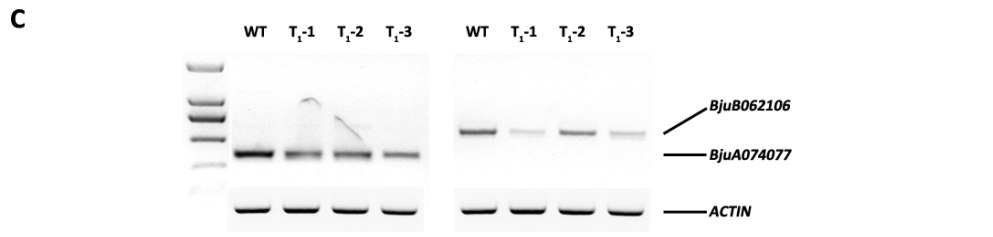
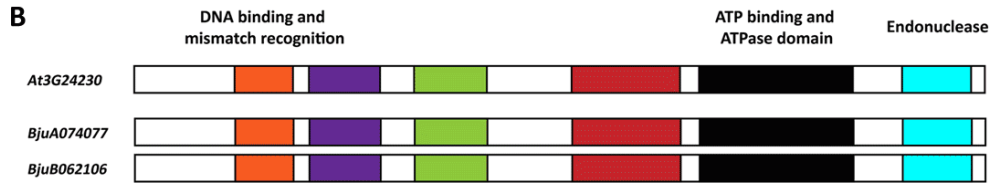


Figure S5 *MSH1* from *B. juncea* and comparison with its ortholog in *A. thaliana*.

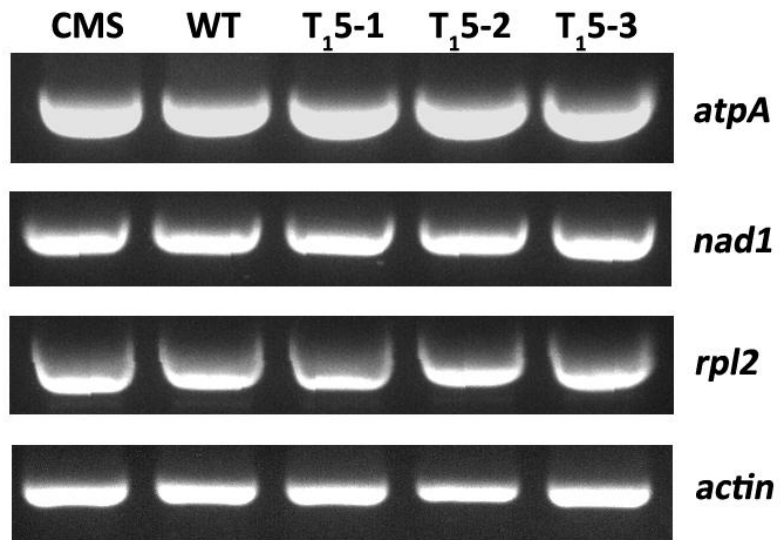


Figure S6 Substoichiometric shifting of mitochondrial genes in MSH1-RNAi lines relative to wild type.

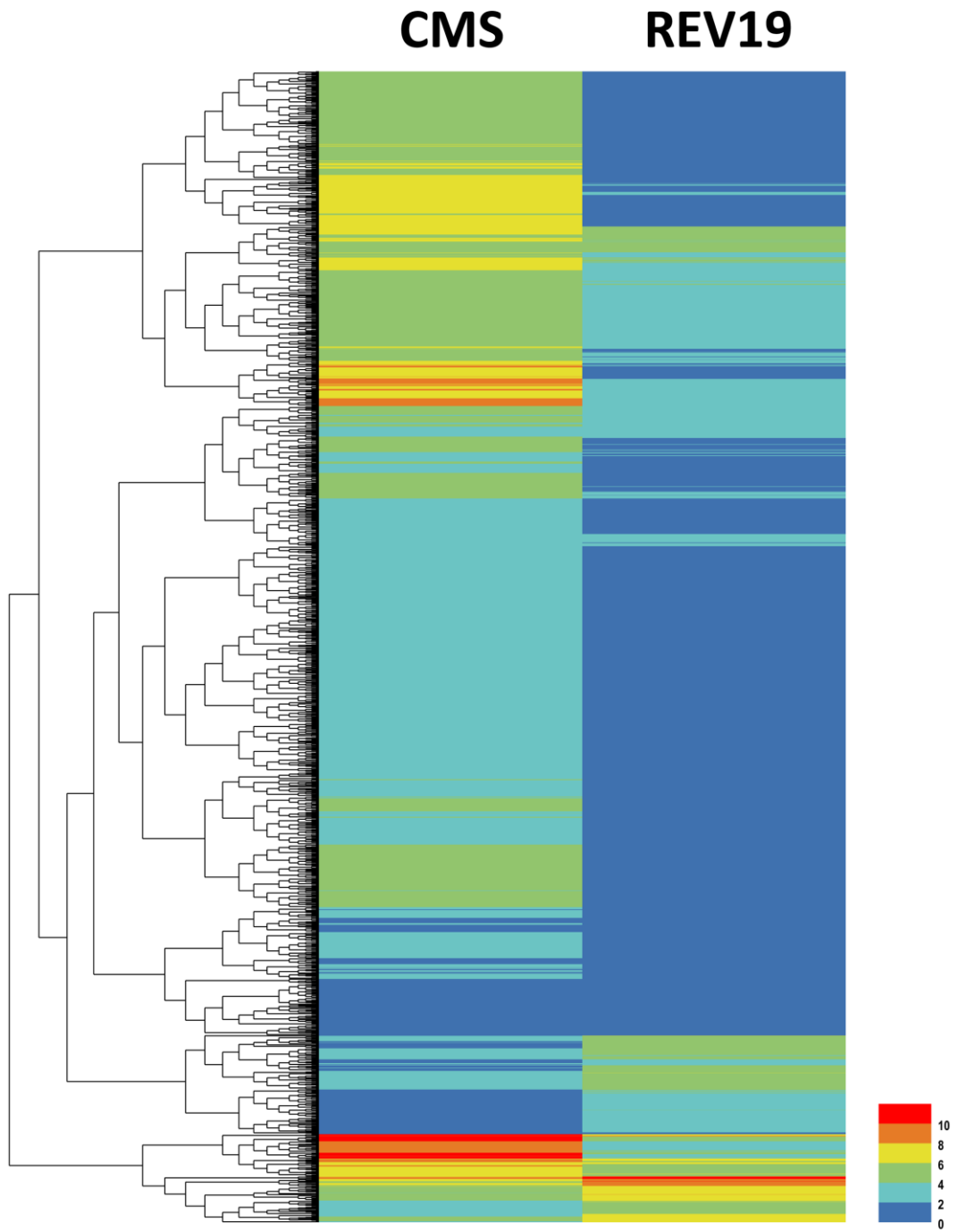


Figure S7 Genes differentially expressed between CMS and REV19 lines of *B. juncea* by RNA-seq.



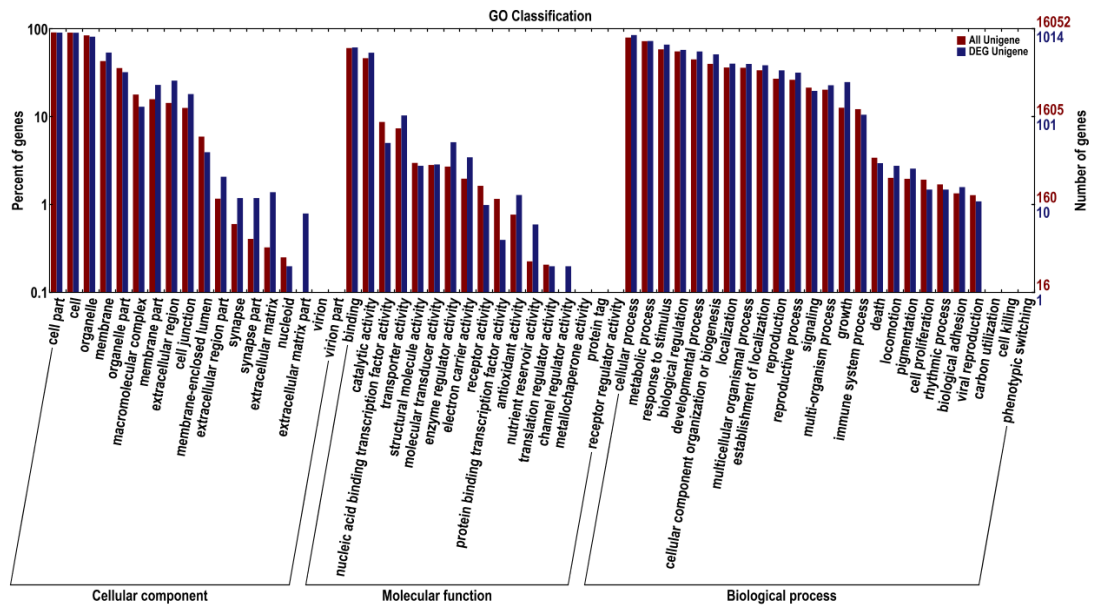


Figure S8 Gene Ontology (GO) enrichment analysis of differentially expressed genes.

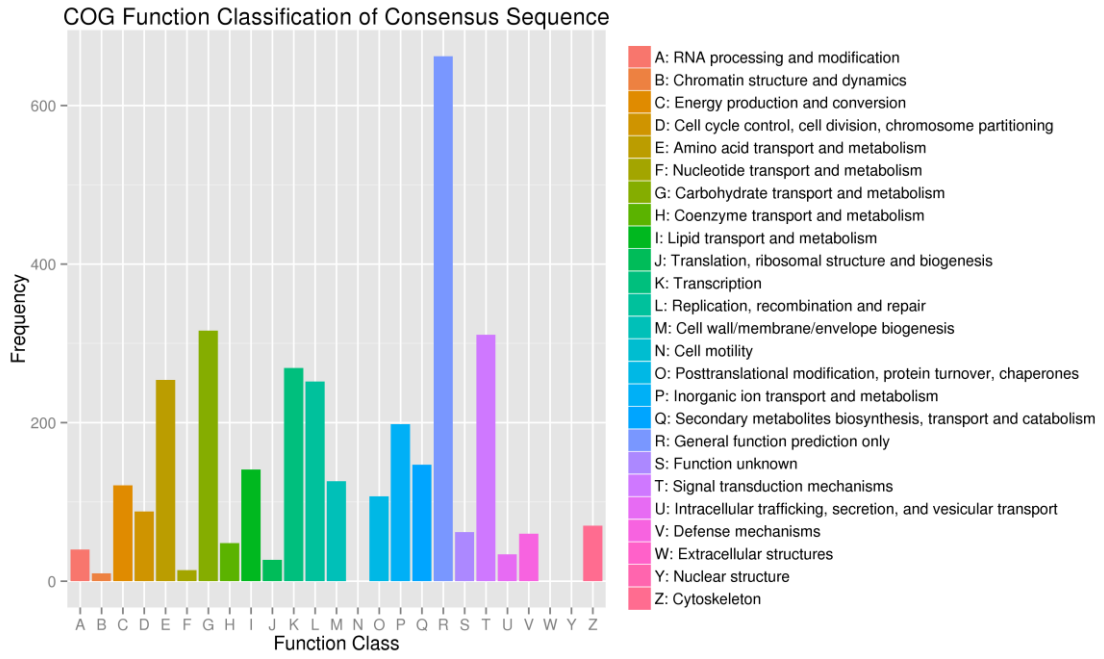


Figure S9 Clusters of Orthologous Groups (COG) analysis of differentially expressed genes.

Table S1 Primers used in this study

<b>Gene</b>	<b>Forward primer</b>	<b>Reverse primer</b>
<i>ORF220-SSS</i>	ATGCCTCAACTGGATAAATTCACTT	TCATCGATAGAGATCGAGAATTTTCG
<i>atpA</i>	GCTGCTTACAGGAGTTAGCC	GTCCAATCGCTACATAGACA
<i>ACTIN</i>	CGCCGAGCGGGAAATCGTC	GGAAAGTGCTGAGGGATGC
<i>ORF220-Construction</i>	CGAAACCAACTGCTTTCACA	TTCGTTTCATCCTGGCTCTCT
<i>AP3 promoter</i>	CAGTAACTGTGGCCAACTTAGT	ATTCTTCTCTTTTGTTTAATCTTT
<i>mt-targeted</i>	CCATGGCTTCTCGGAGGCTTCT	CGCTGCGGAGGTAGCGTACTG
<i>RT-MSH1-A</i>	AAGAATACGTGCGCATAGGG	AAGCAAAAACGGCATAACATTG
<i>RT-MSH1-B</i>	GCTTCATCGGACAATAGCCAC	CCTGCCGTTTGCAATATCTC
<i>Q-ORF220</i>	GGAGATTCGAAGCCTACAGC	ATCGAGGATCTCGTTCATCC
<i>Q-AMS</i>	TACCGGGAGGATTAGTGGAG	TCATGTTAATCGTTGCGGTT
<i>Q-AP3</i>	GGTGTGTGTGATGCTAGGG	CAACATCAGAAACCGTTTGG
<i>Q-C2H2</i>	ACAACACGATGAGGGCAATA	AAGCATTCCCTGAATTGGAC
<i>Q-DYT1</i>	CATGGGAAGTGAACCTGTGG	TTAGGTATCGGTCCAAGCC
<i>Q-GH3</i>	AAGCGCAACACATTTACTCG	ACTTTCGCGTCCTTGAGTTT
<i>Q-MYB99</i>	GAGGTTGGAICTAGAAAGGG	GCTTGCTCCACGTGTTCTTA
<i>Q-MYB103</i>	CACGGTGGAATACGTACAGC	CCACCACTTCTCCCTCAAT
<i>Q-MS1</i>	CTCATGGGAAGTTGGTCCTT	GCAACGGAGGTTAAGAGAGG
<i>Q-MS2</i>	GCGGTTAAAGAACGAGGTGT	TCTGTTTGCAACCCAATGTT
<i>Q-PI</i>	GCTGCAACAACAAGAGATGG	GGTTGAATCGGCTGAACTCT
<i>Q-SHN1</i>	CTGACATCTCAGCCTCCTCA	AGACTTGCAGCATTTCTCTCA
<i>Q-SPL</i>	GTACTIONCAACGAGGCGACAA	GATGTAGCCACTGGAAACGA
<i>Q-SPL8</i>	GCTCGATTTCACTTCCAACA	TACAGCCTGCTCACGAAATC
<i>Q-WUS</i>	CCAAGAGAGCGGTAACAACA	AGGATTCTGATCTGCTCCGT
<i>Q-4CL3</i>	CACCGTTATCACCACAGAGG	GTGCCAGAGGAGAAAGGAAG
<i>Q-25S</i>	CGGTTCTCTCGTACTAGGTTGA	CCGTCGTGAGACAGGTTAGTTTT

Table S2 Statistic of candidate revertant event from CMS *B. juncea*

CMS plant number	Seed number	Sterile	Fertile
1	5	5	0
2	5	5	0
3	4	4	0
4	4	4	0
5	3	3	0
6	3	3	0
7	3	3	0
8	2	2	0
9	2	2	0
10	2	2	0
11	2	2	0
12	2	2	0
13	1	1	0
14	1	1	0
15	1	1	0
16	1	1	0
17	1	1	0
18	1	1	0
19	7	5	2
20	1	1	0
21	1	1	0
22	1	1	0
From No. 23 - No.39	0	0	0
Total	53	51	2

Table S3 Statistic of fertility of ORF220 expression in *Arabidopsis*

	<i>ORF220</i>		<i>mt target-ORF220</i>	
	Sterile	Fertile	Sterile	Fertile
35S promoter	0	20	17	42
AP3 promoter	1	13	28	0