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Regularities in simple sequence repeat variations induced by a cross of resynthesized *Brassica napus* and natural *Brassica napus*

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Supplementary Table 1. Statistics data on the number of SSRs and band types amplified by 47 different primer pairs in an introgressed population and parental species.

Primer pairs	Total number of bands	Total number of polymorphic makers	Number of parental bands	Number of parental bands sequenced	Number of abnormal bands	Number of eliminated bands	Number of novel bands	P-SSR[a)]	E-SSR[b)]	N-SSR[c)]	Total number of SSR
A125	21	17	8	4	13	4	9	5	6	8	19
A17	4	4	0	0	4	4	0	0	5	0	5
A224	11	8	6	3	5	1	4	3	1	4	8
A241	2	2	0	0	2	2	0	0	2	0	2
A290	6	6	0	0	6	6	0	0	8	0	8
A291	6	6	0	0	6	6	0	0	6	0	6
A293	3	3	0	0	3	3	0	0	6	0	6
A321	9	3	6	0	3	3	0	0	3	0	3
A322	3	3	0	0	3	3	0	0	3	0	3
A34	1	1	0	0	1	1	0	0	0	0	0

A76	9	4	5	0	4	4	0	0	4	0	4
A80	11	8	6	3	5	3	2	0	0	2	2
A89	5	2	3	0	2	2	0	0	4	0	4
A9	9	3	6	0	3	3	0	0	3	0	3
cen10	6	3	3	0	3	3	0	0	0	0	0
cen29	18	10	12	4	6	5	1	0	0	0	0
cen39	20	13	14	7	6	5	1	0	4	0	4
cen48	9	5	4	0	5	5	0	0	3	0	3
cen56	8	5	3	0	5	5	0	0	1	0	1
cen65	6	5	1	0	5	5	0	0	1	0	1
cen68	7	2	5	0	2	2	0	0	2	0	2
cen71	11	2	9	0	2	2	0	0	2	0	2
H47	7	3	4	0	3	3	0	0	4	0	4
H5	10	9	1	0	9	9	0	0	5	0	5
H53	5	3	2	0	3	3	0	0	3	0	3
H6	9	5	4	0	5	5	0	0	4	0	4
Y104	11	4	7	0	4	4	0	0	0	0	0
Y12	12	2	10	0	2	2	0	0	3	0	3
Y24	6	2	4	0	2	2	0	0	2	0	2
Y28	9	1	8	0	1	1	0	0	1	0	1
Y3	12	8	4	0	8	8	0	0	2	0	2
Y30	4	2	2	0	2	2	0	0	2	0	2
Y34	18	14	4	0	14	14	0	0	0	0	0
Y36	7	4	3	0	4	4	0	0	2	0	2
Y49	11	10	7	6	4	0	4	0	6	4	10
Y5	3	1	2	0	1	1	0	0	1	0	1

Y51	3	2	1	0	2	2	0	0	1	0	1
Y6	10	3	7	0	3	3	0	0	3	0	3
Y61	8	6	4	2	4	4	0	1	3	0	4
Y66	13	12	2	1	11	4	7	0	0	0	0
Y73	4	4	0	0	4	4	0	0	2	0	2
Y77	19	19	12	12	7	3	4	9	1	2	12
Y8	15	1	14	0	1	1	0	0	0	0	0
Y80	7	7	0	0	7	7	0	0	6	0	6
Y86	15	14	6	5	9	6	3	0	1	0	1
Y88	14	5	9	0	5	5	0	0	0	0	0
Y96	13	8	5	0	8	8	0	0	1	0	1
TOTAL	430	264	211	47	219	184	35	18	117	20	155
Percentage (%)		-		10.9%	50.9%	42.8%	8.1%	11.6	75.5	12.9	-

a) SSRs detected in parental bands.
b) SSRs detected in eliminated bands.
c) SSRs detected in newborn bands.

Supplementary Table 2. SSR motifs and band types amplified from 47 different primer pairs in an introgressed population and parental species

Name of primer pairs	Bands type	SSR 1	SSR 2
A125	parental	(TA)12	-
A125	parental	(T)10	(TA)12
A125	eliminated	(T)10	(TA)10
A125	eliminated	(T)10	(TA)12
A125	parental	(TA)8	-
A125	parental	(TA)7	-
A125	eliminated	(TA)8	-
A125	eliminated	(TA)8	-
A125	new	(T)10	(TA)8
A125	new	(T)10	(TA)11
A125	new	(T)10	-
A125	new	(T)10	-
A125	new	(T)10	-
A125	new	(T)10	-
A125	new	-	-
A125	new	-	-
A125	new	-	-
A17	eliminated	(TGA)6	-
A17	eliminated	(GGA)4	(TGA)4
A17	eliminated	(TGA)6	-
A17	eliminated	(TGA)6	-
A224	eliminated	(AAAT)4-(AAGA)3	-
A224	parental	(AAAT)6-(AAGA)3	-
A224	parental	(AAAT)5-(AAGA)3	-
A224	parental	(AAAT)5-(AAGA)3	-
A224	new	(AAAT)4-(AAGA)3	-
A224	new	(AAAT)4-(AAGA)3	-
A224	new	(AAAT)4-(AAGA)3	-
A224	new	(AAAT)4-(AAGA)3	-
A241	eliminated	(AT)9	-
A241	eliminated	(AT)7	-
A290	eliminated	(A)17	(TA)7-(TA)22
A290	eliminated	(A)19	(TA)8-(TA)15
A290	eliminated	(A)19	(AT)10-(TA)17
A290	eliminated	(A)19	(AT)8-(TA)18
A290	eliminated	-	-
A290	eliminated	-	-
A291	eliminated	(TAT)10	-
A291	eliminated	(TAT)11	-

A291	eliminated	(TAT)12	-
A291	eliminated	(TAT)15	-
A291	eliminated	(TAT)15	-
A291	eliminated	(TTA)5	-
A293	eliminated	(TG)7	(GTG)4
A293	eliminated	(TG)7	(GTG)4
A293	eliminated	(TG)7	(GTG)4
A321	eliminated	(ATG)4	-
A321	eliminated	(TGA)6	-
A321	eliminated	(TGA)4	-
A322	eliminated	(TAA)9	-
A322	eliminated	(TAA)11	-
A322	eliminated	(TAA)11	-
A34	eliminated	-	-
A76	eliminated	(GAT)5-(TGA)4-(TGA)6	-
A76	eliminated	(ATG)4	-
A76	eliminated	(GAT)5-(TGA)4-(TGA)6	
A76	eliminated	(ATG)4	-
A80	eliminated	-	-
A80	eliminated	-	-
A80	eliminated	-	-
A80	parental	-	-
A80	parental	-	-
A80	parental	-	-
A80	new	(AT)5	-
A80	new	(AT)5	-
A89	eliminated	(CT)9	(CAT)5-(CAT)4
A89	eliminated	(CT)9	(CAT)5-(CAT)4
A9	eliminated	(CTC)6	-
A9	eliminated	(CTC)6	-
A9	eliminated	(CTC)6	-
cen10	eliminated	-	-
cen10	eliminated	-	-
cen10	eliminated	-	-
cen29	parental	-	-
cen29	eliminated	-	-
cen29	eliminated	-	-
cen29	eliminated	-	-
cen29	eliminated	-	-
cen29	eliminated	-	-
cen29	parental	-	-
cen29	parental	-	-
cen29	parental	-	-
cen29	new	-	-

Cen39	eliminated	(TA)5	-
Cen39	eliminated	(AT)10	-
Cen39	eliminated	(AT)13	-
Cen39	eliminated	(AT)10	-
Cen39	parental	-	-
Cen39	parental	-	-
Cen39	parental	-	-
Cen39	eliminated	-	-
Cen39	parental	-	-
Cen39	parental	-	-
Cen39	parental	-	-
Cen39	parental	-	-
Cen39	new	-	-
Cen48	eliminated	(GA)33	-
Cen48	eliminated	(GA)35	-
Cen48	eliminated	(GA)34	-
Cen48	eliminated	-	-
Cen48	eliminated	-	-
Cen56	eliminated	(TC)11	-
Cen56	eliminated	-	-
Cen56	eliminated	-	-
Cen56	eliminated	-	-
Cen56	eliminated	-	-
Cen65	eliminated	(TA)8	-
Cen65	eliminated	-	-
Cen65	eliminated	-	-
Cen65	eliminated	-	-
Cen65	eliminated	-	-
Cen68	eliminated	(T)12-(GA)8	-
Cen68	eliminated	(T)10-(GA)10	-
Cen71	eliminated	(AG)5	-
Cen71	eliminated	(AG)5	-
H47	eliminated	(AG)7	-
H47	eliminated	(AG)5	(ACA)4-(TCCCT)3
H47	eliminated	(CT)10	-
H53	eliminated	(AT)8	-
H53	eliminated	(AT)5	-
H53	eliminated	(AT)17	-
H5	eliminated	(AG)12	-
H5	eliminated	(AG)12	-
H5	eliminated	(GA)10	-
H5	eliminated	(AG)11	-
H5	eliminated	(AG)12	-
H5	eliminated	-	-

H5	eliminated	-	-
H5	eliminated	-	-
H5	eliminated	-	-
H6	eliminated	(AT)9	-
H6	eliminated	(AT)8	-
H6	eliminated	(AT)5	-
H6	eliminated	(AT)5	-
H6	eliminated	-	-
Y104	eliminated	-	-
Y104	eliminated	-	-
Y104	eliminated	-	-
Y104	eliminated	-	-
Y12	eliminated	(ATAA)4-(AT)9	-
Y12	eliminated	(AT)9	(ATAA)4-(AT)8
Y24	eliminated	(CT)9	-
Y24	eliminated	(CT)8	-
Y28	eliminated	(AG)10	-
Y3	eliminated	(GAA)4	-
Y3	eliminated	(GAA)4	-
Y3	eliminated	-	-
Y3	eliminated	-	-
Y3	eliminated	-	-
Y3	eliminated	-	-
Y3	eliminated	-	-
Y3	eliminated	-	-
Y30	eliminated	(AT)12	-
Y30	eliminated	(AT)14	-
Y34	eliminated	-	-
Y34	eliminated	-	-
Y34	eliminated	-	-
Y34	eliminated	-	-
Y34	eliminated	-	-
Y34	eliminated	-	-
Y34	eliminated	-	-
Y34	eliminated	-	-
Y34	eliminated	-	-
Y34	eliminated	-	-
Y34	eliminated	-	-
Y34	eliminated	-	-
Y34	eliminated	-	-
Y34	eliminated	-	-
Y34	eliminated	-	-
Y34	eliminated	-	-
Y36	eliminated	(GA)6-(GTCTG)4	-

Y36	eliminated	(AG)12-(TGGTC)3	-
Y36	eliminated	-	-
Y36	eliminated	-	-
Y49	parental	(TGAT)3-(GAT)17	-
Y49	parental	(TGAT)3-(GAT)17	-
Y49	parental	(TGAT)3-(GAT)17	-
Y49	parental	(TGAT)3-(GAT)15	-
Y49	parental	(TGAT)3-(GAT)17	-
Y49	parental	(TGAT)3-(GAT)17	-
Y49	new	(TGAT)3-(GAT)14	-
Y49	new	(TGAT)3-(GAT)14	-
Y49	new	(TGAT)3-(GAT)14	-
Y49	new	(TGAT)3-(GAT)14	-
Y5	eliminated	(CT)8	-
Y51	eliminated	(GAA)5-(AGA)5	-
Y51	eliminated	-	-
Y6	eliminated	(TGGTT)3	-
Y6	eliminated	(TGGTT)4	-
Y6	eliminated	(TGGTT)3	-
Y61	eliminated	(AGA)4	-
Y61	eliminated	(AGA)4	-
Y61	parental	(AGA)4	-
Y61	eliminated	(AGA)4	-
Y61	eliminated	-	-
Y61	parental	-	-
Y66	eliminated	-	-
Y66	eliminated	-	-
Y66	eliminated	-	-
Y66	parental	-	-
Y66	eliminated	-	-
Y66	new	-	-
Y66	new	-	-
Y66	new	-	-
Y66	new	-	-
Y66	new	-	-
Y66	new	-	-
Y66	new	-	-
Y73	eliminated	(TC)12	-
Y73	eliminated	(TC)12	-
Y73	eliminated		-
Y73	eliminated		-
Y77	parental	(GA)10	-
Y77	parental	(AG)12	-
Y77	parental	(AG)14	-

Y77	parental	(AT)7-(AG)8	-
Y77	parental	(AG)15	-
Y77	eliminated	(AG)13	-
Y77	parental	(AG)14	-
Y77	parental	(AG)13	-
Y77	parental	(AT)5-(AG)13	-
Y77	parental	(AG)13	-
Y77	new	(AG)14	-
Y77	new	(AG)14	-
Y77	parental	-	-
Y77	eliminated	-	-
Y77	eliminated	-	-
Y77	parental	-	-
Y77	new	-	-
Y77	new	-	-
Y8	eliminated	-	-
Y80	eliminated	(TGA)4	-
Y80	eliminated	(TC)5-(CT)6	-
Y80	eliminated	(TC)11-(TTGAT)5	-
Y80	eliminated	(TGA)5	-
Y80	eliminated	(TGA)5	-
Y80	eliminated	(TGA)4	-
Y80	eliminated	-	-
Y86	eliminated	(CAAAT)3-(GA)6	-
Y86	eliminated	-	-
Y86	eliminated	-	-
Y86	eliminated	-	-
Y86	eliminated	-	-
Y86	parental	-	-
Y86	parental	-	-
Y86	parental	-	-
Y86	parental	-	-
Y86	parental	-	-
Y86	new	-	-
Y86	new	-	-
Y86	new	-	-
Y88	eliminated	-	-
Y88	eliminated	-	-
Y88	eliminated	-	-
Y88	eliminated	-	-
Y88	eliminated	-	-
Y96	eliminated	(AC)5	-
Y96	eliminated	-	-
Y96	eliminated	-	-

Y96	eliminated	-	-
Y96	eliminated	-	-
Y96	eliminated	-	-
Y96	eliminated	-	-
Y96	eliminated	-	-

Supplementary Table 3. Details of primer pairs which produce bands that are eliminated and/or new bands in an introgressed population.

Name	Forward sequence 5'-3'	F-TM[a)]	Reverse sequence	R-TM[b)]	Product size
A125	AAACCAAGACCAGCCCATTT	60.7	GGTATGTCAGCAGTCACGTCC	60.6	235
A17	CAAGGCGAAACAGAGAGGAG	60.1	ACATAGACGGGAACAGACGC	60.1	218
A224	GACCAGCATCGCTTACGAAC	60.8	ACCCATTGGTCAAACGTGAG	60.8	279
A241	TCCAGGGAAGAAGACCCTTT	60.0	CCGGCTGCAAAGAGTAGAAC	60.0	144
A290	CAGAATCTTGTGCTTACCGTTGT	60.6	GTGGCAACTTATGGTGGCTT	60.0	250
A291	ACATGTCAGCGACAAGTCTTAATAAC	60.0	CAGCAGTCAAGGAAGAAAGCA	60.7	160
A293	ATGTGTGTGTGTGTGGGTCC	60.2	AGCCACATCAGAGCTCGAAA	61.1	232
A321	TTGCTTCGGTATCCCATCTC	60.0	AATTTCAAATCCCCAGAAACG	60.2	203
A322	TGCAGATAAAAGCTCTTAAGGACAA	60.7	ACACAAGAACTTGCCCCAAC	60.0	264
A34	CAAACACACAAACAACCCACA	60.3	AATGCAGGTGTTGGGAGAAG	60.1	271
A76	CGCTCGTTTCTTCGAATTGT	60.4	CCTCAACCCCACCACTATCA	60.8	241
A80	GCATCCGTGCGAGTTAGAAT	60.2	GGTCCTCACGCAAAGATTGT	60.1	267
A89	GTTGCCTCGGTCACATCTTT	60.1	TCGCCGTTGAGATAGGTTTC	60.2	277
A9	CAACACCTCAGAGCCTTCGT	60.4	CTGTCGCCGTTCTCTTTCTC	60.1	198
Cen10	GGCCTAAAAGAGGAGTTGGG	60.1	TGTGTGACCCCTCAAACTGA	60.1	316
Cen29	GCTTCTTCTGCACCACCTTC	60.0	GATGATGGCAAATGGGAAAC	60.1	438
Cen39	GACAGCGACACTTGCGTAAA	60.1	CTTTTCTTCTCGACGTTGCC	60.0	438
Cen48	GGTGCCTTGTCCCTACAAAA	60.0	AAATATCTTCCCAGGCCCAC	60.2	436
Cen56	GGAACGACTTCCTCCCGTAT	60.3	TGTTTAGAGAATGGGGACCG	59.9	426
Cen65	AATTTTTAAGCCCGCATCG	60.0	TTATCCGCATGGTTTGAGAA	59.1	191
Cen68	TTCGAATTTCATCACCACGA	60.0	CAACGGTCCGTAACTGGTCT	60.0	328

Cen71	GACTGTTGGAGCATGGGTTT	60.0	CTCACGCCTCAGCTCTCTCT	60.0	485
Y104	AAAGCGAAGAACACGGAAAC	59.4	CTTGTCCGGTCAGATTTGGT	60.0	361
Y12	CATAACTCGGGGTCCAAAAA	59.8	CTTTCTCGATCCTCCCCTTC	60.1	372
Y24	GGTCTTGCTTGGAGTTCGAG	60.0	GAAACATTTCGTCAGCAGCA	60.0	202
Y28	TATGCAAAACCCACAGGTCA	60.0	AATGTCGAAAAGGTCGCATC	60.1	134
Y3	AGAAGAAAATGGGCATCGTG	60.1	GAGTAGGCTCAGTGCGTTCC	60.0	152
Y30	GGTTGTCCAGAGGACCAGAA	60.1	TGTCATGTCGGTTCGTGACT	60.2	354
Y34	GATTTGGGATGGGGAAAGTT	60.0	TTACCCTACCGAAAACGACG	60.0	302
Y36	TGATTGCTCGTTGACCAGAG	60.0	GCGTGCGAGAGAATCTTACC	60.0	348
Y49	TCGGTTTCCTGAGCTGAAGT	60.0	TCGTGGCGACTCTTCTTTTT	60.0	339
Y5	TTACCCACCTTGGCTTCATC	59.9	GCGTTTCGTCCTCTTCTCAC	60.0	154
Y51	CTTCCAAGCTCATACCCGAA	60.2	CACACGACGTCTCTTTGCAC	60.5	109
Y6	CTGCAACAATGCAAACAACC	60.2	TTGCGAAACGAGAGACAATG	60.0	277
Y61	GAACAGTCTACAGCCGGAGC	60.0	ACCGACCTACAAATACCCCC	59.9	242
Y66	TCATTTCTCCCGACCATAGC	60.0	ACTATGCATGTTTGCCCCTC	60.0	362
Y73	CTTCGTCTCTCTGTCCCCTG	60.0	GAACCGTGATCCGTCGTACT	60.0	379
Y77	TGCTCTCGTTGCATACCTTG	60.0	TATGATTTGCTTTGCTTGCG	60.0	264
Y8	ACCTTTGAACGGTTGGTCAG	60.0	CGCGGGTGTTTATTTTCAGT	60.0	311
Y80	ATTGAACCCGATTGGACTTG	59.8	TGCTAACTGCATGCAACCTC	60.0	239
Y86	CAACGAAAACAGATCGAGCA	60.0	GTCGGAGAGATGGATGGAGA	60.2	359
Y88	TTCTCTCCATGTTGTGCGTC	59.8	ACAAGACGGCAAAGATTGCT	59.9	380
Y96	TGCTCTGGCTCTTTCGGTAT	60.0	TTTAGCGTGTGAGCATCTCC	59.0	315
H47	GGAAGCCTCTGTGCGAAAAA	52.0	TGCCGACGATTTGATAGAGGA	52.0	175
H5	GGAATCCTACGGAAGAGCAA	52.0	AAGGTAACGGTGGCAGTGAG	54.0	150
H53	CCCAAATACGAAAACAAAGTTTGAC	53.0	AGGATCTCATCCGCTTTCCA	52.0	137
H6	CGAGTTTTTGTGTGTACGTATAGTAAT	54.0	CCAAAGTGCGTAAAGGAAGG	52.0	305

a) Melting temperature of forward sequences

b) Melting temperature of reverse sequences