

Table S1: Chromosomal distribution of CNV events in eight *B. napus* lines.

Lines	Ascona		English Giant		Hansen × Gaspard		Milena		Pacific		Pirola		Tina		Wilhelmsburger		Sum Del	Sum Dup	Total
Chromosomes	Del	Dup	Del	Dup	Del	Dup	Del	Dup	Del	Dup	Del	Dup	Del	Dup	Del	Dup			
A01	0	0	3	2	2	3	2	5	2	2	1	1	5	3	6	7	21	23	44
A02	3	4	3	1	2	0	9	0	3	2	4	3	10	8	12	0	46	18	64
A03	0	1	6	0	2	4	1	3	2	3	2	12	2	5	4	12	19	40	59
A04	1	1	2	1	1	1	1	1	1	3	1	1	4	2	2	0	13	10	23
A05	0	1	3	1	1	1	1	0	0	0	2	0	9	0	5	1	21	4	25
A06	3	4	9	25	1	2	6	3	2	3	7	1	3	5	3	4	34	47	81
A07	4	1	8	1	1	0	3	1	3	1	2	0	7	1	5	0	33	5	38
A08	4	3	5	1	2	3	8	3	9	3	7	2	8	2	7	2	50	19	69
A09	3	0	8	17	10	1	6	1	5	16	7	2	15	24	19	21	73	82	155
A10	2	0	0	0	0	0	1	0	1	1	1	0	0	1	2	1	7	3	10
Total	20	15	47	49	22	15	38	17	28	34	34	22	63	51	65	48	317	251	568
C01	7	2	5	0	1	0	4	0	0	3	2	0	7	0	10	0	36	5	41
C02	2	1	11	5	0	1	6	2	5	3	4	2	18	7	7	11	53	32	85
C03	4	7	6	0	6	3	3	2	2	5	17	6	8	7	20	3	66	33	99
C04	1	2	1	1	0	2	2	4	2	3	2	1	1	4	9	2	18	19	37
C05	0	3	1	5	1	1	0	3	0	3	2	2	5	2	2	6	11	25	36
C06	11	1	0	0	2	1	1	2	11	2	11	3	11	1	18	0	65	10	75
C07	2	1	3	0	0	0	2	2	0	2	1	1	3	2	2	2	13	10	23
C08	0	4	0	1	0	2	4	3	6	0	2	1	30	1	16	0	58	12	70
C09	1	1	13	8	1	5	7	3	4	3	2	3	17	1	22	12	67	36	103
Total	28	22	40	20	11	15	29	21	30	24	43	19	100	25	106	36	387	182	569
Grand total	48	37	87	69	33	30	67	38	58	58	77	41	163	76	171	84	704	433	1137

Table S2: Characteristics of CNVs including CNV number, deletion to duplication ratio, average CNV size and percentage of CNVs larger or smaller than average in eight *B. napus* lines.

	Ascona		English Giant		HANSEN x GASPARD		Milena	
	Del	Dup	Del	Dup	Del	Dup	Del	Dup
CNV number	48	37	87	69	33	30	67	38
Deletion to duplication ratio	1.29	-	1.26	-	1.1	-	1.76	-
Average CNV size (kb)	3.06	1.91	3.54	3.37	2.35	3.15	4.90	1.93
Median CNV size (kb)	2.10	1.75	2.30	2.92	1.62	2.82	2.81	1.94
Larger than average (%)	37.5	43.24	24.14	28.99	39.39	36.67	23.88	50
Smaller than average (%)	62.5	56.76	75.86	71.01	60.61	63.33	76.12	50
	Pacific		Pirola		Tina		Wilhelsburger	
	Del	Dup	Del	Dup	Del	Dup	Del	Dup
CVN number	58	58	77	41	163	76	171	84
Deletion to duplication ratio	1	-	1.87	-	2.14	-	2.03	-
Average CNV size (kb)	2.73	2.69	3.44	2.72	3.73	2.62	4.03	2.56
Median CNV size (kb)	1.99	2.19	1.92	2.19	2.32	2.59	2.41	2.52
Larger than average (%)	37.93	39.66	28.57	39.02	25.15	50	22.81	50
Smaller than average (%)	62.07	60.34	71.43	60.98	74.85	50	77.19	50

Table S3: The number of RGAs affected by CNV events in eight *B. napus* lines.

	Ascona		English Giant		Hansen × Gaspard		Milena		Pacific		Pirola		Tina		Wilhelsburger		Sum of Del	Sum of Dup	Total
RGAs	Del	Dup	Del	Dup	Del	Dup	Del	Dup	Del	Dup	Del	Dup	Del	Dup	Del	Dup			
CN	1	2	5	2	0	0	2	1	1	1	3	0	2	3	7	2	21	11	32
CNL	5	2	2	3	0	2	5	4	2	3	7	1	10	7	10	6	41	28	69
NBS	1	0	5	0	1	1	5	1	2	2	3	1	7	1	6	5	30	11	41
NL	6	1	8	2	3	0	8	3	7	7	11	1	12	4	11	5	66	23	89
OTHER	0	0	1	1	1	0	1	0	1	0	2	0	1	1	4	0	11	2	13
TN	4	0	2	0	2	0	0	0	2	0	3	0	5	1	5	0	23	1	24
TNL	1	3	0	1	0	5	7	3	6	4	4	6	16	4	12	0	46	26	72
TX	2	0	1	1	2	0	3	0	2	0	2	1	9	1	9	2	30	5	35
Sum	20	8	24	10	9	8	31	12	23	17	35	10	62	22	64	20	268	107	375
RLK	20	23	48	50	16	18	24	17	27	31	32	23	73	41	79	51	319	254	573
RLP	8	6	15	9	8	4	12	9	8	10	10	8	28	13	28	13	117	72	189
Sum	28	29	63	59	24	22	36	26	35	41	42	31	101	54	107	64	436	326	762
Total	48	37	87	69	33	30	67	38	58	58	77	41	163	76	171	84	704	433	1137

Table S4: The number of singletons and clustered RGAs affected by CNV across 563 *R* genes.

RGAs	In cluster				Singleton				Sum of Del	Sum of Dup	Sum of Both	Total
	Del	Dup	Both	Sum	Del	Dup	Both	Sum				
CN	5	2	2	9	2	0	0	2	7	2	2	11
CNL	12	7	3	22	7	3	0	10	19	10	3	32
NBS	12	3	2	17	2	2	0	4	14	5	2	21
NL	11	4	2	17	8	4	4	16	19	8	6	33
OTHER	2	1	0	3	2	1	0	3	4	2	0	6
TN	9	1	0	10	1	0	0	1	10	1	0	11
TNL	18	8	3	29	2	0	1	3	20	8	4	32
TX	10	4	0	14	3	1	0	4	13	5	0	18
Sum of NBS-LRR and TX	79	30	12	121	27	11	5	43	106	41	17	164
RLK	71	31	8	110	89	101	19	209	160	132	27	319
RLP	30	14	9	53	14	9	4	27	44	23	13	80
Sum of TM-LRR	101	45	17	163	103	110	23	236	204	155	40	399
Total	180	75	29	284	130	121	28	279	310	196	57	563

Table S5: Distribution and number of the singletons and clustered *R* genes affected by CNV across the chromosomes.

Chromosome	<i>R</i> genes number	Clustered <i>R</i> genes number	Clusters number	Singleton <i>R</i> genes number	Clustered <i>R</i> genes affected by CNV	Singletons <i>R</i> genes affected by CNV
A01	66	24	11	42	6	16
A02	75	40	12	35	22	13
A03	87	28	14	59	12	22
A04	60	31	13	29	8	5
A05	52	22	9	30	8	8
A06	104	50	20	54	21	24
A07	90	41	17	49	12	8
A08	85	40	16	45	16	12
A09	140	63	25	77	35	39
A10	41	15	6	26	1	4
C01	107	55	23	52	10	14
C02	115	58	19	57	26	15
C03	149	49	19	100	21	27
C04	83	33	16	50	5	13
C05	91	34	13	57	5	10
C06	118	75	24	43	29	7
C07	75	31	9	44	2	4
C08	95	53	19	42	28	5
C09	135	51	21	84	17	33
Sum	1,768	793	306	975	284	279

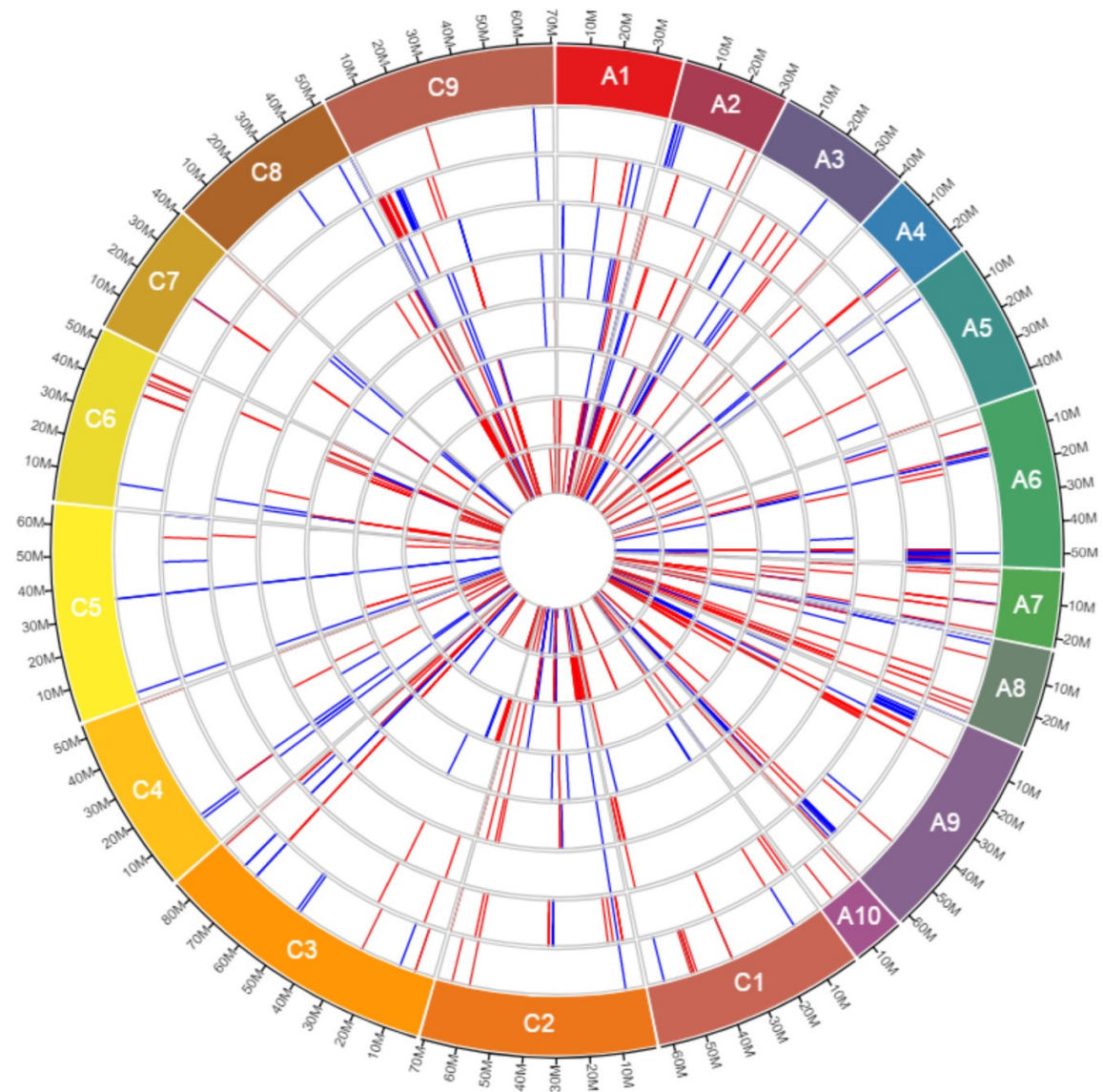


Figure S1: The position of CNV events (red and blue lines represents deletions and duplications, respectively) across the chromosomes of eight *B. napus* lines. The tracks from outer to inner show chromosomes, Ascona, English Giant, Hansen × Gaspard, Milena, Pacific, Pirola, Tina and Wilhelsburger.