

Table S2 Parameters of two genetic maps constructed by the bi-filtering method (Map B) and the conventional method (Map C) in the HJ-DH population of *B. napus*

LG	Map B					Map C ^a					
	Total marker	SSR marker	SNP marker	Length (cM)	Average distance (cM/marker)	Total marker	SSR marker	SNP marker	mHemi-SNP and Pseudo-simple SNP	Length (cM)	Average distance (cM/marker)
A1	128	19	109	128.8	1.01	129	19	110	6	105.1	0.81
A2	177	15	162	99.2	0.56	190	15	175	13	144.8	0.76
A3	185	47	138	199.6	1.08	196	47	149	12	233.2	1.19
A4	47	10	37	58.3	1.24	51	11	40	3	69.5	1.36
A5	73	16	57	63.2	0.87	74	16	58	1	83.5	1.13
A6	74	16	58	66.4	0.90	78	16	62	4	87.4	1.12
A7	171	33	138	128.1	0.75	187	33	154	16	155.9	0.83
A8	77	17	60	68.9	0.89	81	17	64	4	79.9	0.99
A9	94	34	60	112.7	1.20	97	36	61	1	143.9	1.48
A10	88	18	70	64.9	0.74	93	20	73	4	90.3	0.97
Subtotal	1114	225	889	990.1	0.89	1176	230	946	64	1193.5	1.07
C1	94	18	76	74.8	0.80	117	18	99	18	190.1	1.62
C2	96	21	75	100.1	1.04	102	21	81	7	127.1	1.25
C3	55	22	33	103.5	1.88	59	22	37	4	110.4	1.87
C4	132	40	92	153.6	1.16	142	40	102	10	200.2	1.41
C5	136	27	109	145.2	1.07	140	27	113	4	186.9	1.34
C6	91	26	65	64.1	0.70	99	27	72	7	100.7	1.02
C7	108	15	93	77	0.71	112	15	97	4	93.7	0.84
C8	121	32	89	144.6	1.20	131	32	99	11	172.3	1.32
C9	67	15	52	167.3	2.50	37	16	21	3	102.5	2.77
Subtotal	900	216	684	1030.2	1.14	939	218	721	65	1283.9	1.49
Total	2014	441	1573	2020.3	1.00	2115	448	1667	132	2477.4	1.27

^aThe data of Map C is come from Cai *et al.* [30].