Table S3 The lengths of the chromosomes after individual and consensus analysis allowing to detect the chromosomes with high cost of consensus ordering: data on six BC maize sets

Chr#	Phase	set1	set2	set3	set4	set5	set6
1	before	243.6	212.0	226.8	184.9	202.5	234.2
	after	245.7	212.1	226.8	184.9	203.6	234.2
2	before	146.5	144.8	121.2	60.5	170.3	95.5
	after	146.5	167.6	123.4	61.5	170.4	95.5
	after-crt	146.5	144.8	123.4	61.5	170.3	95.5
3	before	154.1	167.8	147.9	172.8	140.3	117.0
	after	154.1	167.8	147.9	172.8	144.6	117.0
4	before	100.6	158.9	142.0	144.4	123.9	105.
	after	100.6	158.7	142.0	144.4	123.9	105.2
5	before	143.5	157.5	158.3	162.3	136.2	151.2
	before-crt	143.5	157.5	135.2	162.3	136.2	151.
	after	143.5	157.5	166.4	163.5	136.2	151.
	after-crt	143.5	157.5	137.8	163.5	136.2	151.
	before	104.5	139.6	53.6	120.9	125.6	83.4
6	after	104.5	139.8	53.6	211.8	128.9	83.4
	after-crt	104.5	139.7	53.6	120.7	125.7	83.4
	before	111.9	139.8	191.7	111.8	124.3	92.0
7	before-crt	111.9	139.8	162.8	111.8	124.3	92.0
	after	111.9	139.8	200.6	111.8	124.3	92.0
	after-crt	111.9	139.8	167.2	111.8	124.3	92.0
8	before	133.4	141.8	114.5	104.6	145.7	86.7
	after	133.4	141.8	121.0	104.6	145.7	86.7
9	before	132.3	119.1	136.3	139.8	97.8	46.2
	after	132.3	119.1	136.3	139.8	97.8	46.2
10	before	97.2	114.1	112.1	75.9	109.3	58.9
	after	97.2	114.2	115.3	75.9	111.5	58.9

Notes: *before* – the lengths (in cM) of the map variants after individual analysis of separate sets but before the consensus analysis; *before-crt* – the same as *before* but after removing some markers of chromosomes 5 and 7 in set #3; *after* - the legths of the map variants after the consensus analysis; *after-crt* – the same as *after* but after removing some markers of set2-Chr2, set3-Chr5, set4-Chr6, and set3-Chr7

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