

Table S1. Numbers of clusters of RAD51, LigIV, γ H2AX, RNAPII, and S9.6 detected on single metaphase chromosome plates in individual plants.

* RNAPII and S9.6 clusters were counted together with γ H2AX clusters on the same cytological slide.

**NC – Non-checked.

Genotype	Plate No.	Number of clusters per single chromosome plate				
		RAD51	LigIV	γ H2AX	RNAPII *	S9.6 *
B26	1	65	37	127	NC	NC**
	2	62	43	149	NC	NC
	3	54	26	184	NC	NC
	4	60	76	185	NC	NC
	5	69	40	140	NC	NC
	6	57	44	109	NC	NC
	7	67	36	101	NC	NC
	8	58	75	124	NC	NC
	9	59	61	148	NC	NC
	10	58	35	102	NC	NC
average		60.9	47.3	136.9	NC	NC
SE		± 4.8	± 17.3	± 30.5	NC	NC
B60	1	85	99	115	NC	NC
	2	115	86	102	NC	NC
	3	99	50	103	NC	NC
	4	112	60	90	NC	NC
	5	88	69	93	NC	NC
	6	92	55	110	NC	NC
	7	114	81	124	NC	NC
	8	98	62	117	NC	NC
	9	75	82	85	NC	NC
	10	92	56	130	NC	NC
	11		94		NC	NC
average		97.0	72.2	106.9		
SE		± 13.3	± 16.9	± 14.9		
B70	1	58	51	63	5	2
	2	59	55	64	4	0
	3	36	48	68	4	0
	4	42	52	75	4	0
	5	96	66	83	5	1
	6	92	56	84	4	2
	7	37	63	85	5	0
	8	95	70	86	6	0
	9	59	75	96	4	1
	10	61	50	127	4	2
average		63.5	58.6	83.1	4.5	0.8
SE		± 23.2	± 9.3	± 18.8	± 0.7	± 0.9
B81	1	73	108	73	1	1
	2	45	109	73	2	2

	3	44	116	51	3	1
	4	69	108	48	5	4
	5	53	110	60	4	3
	6	64	128	50	7	5
	7	51	148	57	4	2
	8	61	187	71	8	8
	9	55	126	76	2	0
	10	48	134	52	1	1
average		56.3	127.4	61.1	3.7	2.7
SE		± 10.1	± 24.8	± 11.1	± 2.4	± 2.3
B91	1	78	85	72	NC	NC
	2	40	96	69	NC	NC
	3	46	82	107	NC	NC
	4	45	105	58	NC	NC
	5	74	100	82	NC	NC
	6	70	134	82	NC	NC
	7	34	159	89	NC	NC
	8	69	163	49	NC	NC
	9	53	156	54	NC	NC
	10	62	156	39	NC	NC
average		57.1	123.6	70.1		
SE		± 15.5	± 33.2	± 20.6		
TR34	1	61	69	146	6	4
	2	73	53	164	7	0
	3	68	57	97	7	0
	4	84	57	113	6	0
	5	76	63	97	0	5
	6	82	65	94	2	0
	7	75	49	123	5	2
	8	77	61	96	0	2
	9	72	47	98	6	0
	10	71	48	243	6	2
	11	63	56			
average		72.9	56.8	127.1	4.5	1.5
SE		± 7.1	± 7.2	± 47.2	± 2.8	± 1.8
TR43	1	58	89	114	NC	NC
	2	64	59	74	NC	NC
	3	62	77	69	NC	NC
	4	58	82	87	NC	NC
	5	59	64	77	NC	NC
	6	90	56	110	NC	NC
	7	87	87	131	NC	NC
	8	88	124	106	NC	NC
	9	77	141	105	NC	NC
	10	75	112	109	NC	NC
average		71.8	89.1	98.2		

SE		±13.2	±28.4	±20.3		
TR52	1	84	78	79	7	5
	2	63	36	105	7	6
	3	69	57	107	3	2
	4	69	53	108	6	1
	5	70	52	110	2	4
	6	53	53	115	7	3
	7	64	52	118	7	7
	8	55	62	129	5	0
	9	81	49	125	2	1
	10	66	53	135	8	2
	11			178	8	4
average		67.4	54.5	119.0	5.6	3.2
SE		±9.8	±10.6	±24.6	±2.3	±2.2
TR67	1	38	61	81	NC	NC
	2	56	49	60	NC	NC
	3	52	76	131	NC	NC
	4	60	67	88	NC	NC
	5	28	86	99	NC	NC
	6	46	82	109	NC	NC
	7	75	95	86	NC	NC
	8	52	116	152	NC	NC
	9	71	86	99	NC	NC
	10	66	97	113	NC	NC
average		54.4	81.5	101.8		
SE		±14.6	±19.4	±26.2		
TR82	1	84	104	90	12	6
	2	40	136	100	8	10
	3	64	99	106	6	6
	4	60	79	198	15	8
	5	60	92	143	6	5
	6	40	138	106	8	8
	7	50	127	118	6	2
	8	57	91	134	18	6
	9	57	136	114	6	9
	10	54	111	118	6	4
average		56.6	111.3	122.7	9.1	6.4
SE		±12.6	±22.9	±30.7	±4.4	±2.4

Table S2. Primer combinations for real-time quantitative PCR.

No.		Sequence	NCBI Reference Sequence
1.	Actin-F	AGATGATGCACCAAGGGCTG	XM_037590498.1
2.	Actin-R	CCCCATCCCTACCATGACAC	
3.	MRE11-F	GGACGCAGCGAACGAAGTAA	XM_037623921.1
4.	MRE11-R	TTTCCGTCCACTTTGTGGGA	
5.	KU70-F	GATTGGGCAGACCTTGCAGA	XM_037583509.1
6.	KU70-R	GCGCCGACAGGTAAGTTTTC	
7.	LigIV-F	ACAAAGATCTGGCCGACGAG	XM_037631088.1
8.	LigIV-R	CATACATGCTACCCCGAGCC	
9.	RAD51-F	CGAGCACCTCCAGGCATCT	XM_037612996.1
10.	RAD51-R	CTCCACTGTGCAAAGACCAGC	
11.	BRCA1-F	AAATGTGCTTGCTGCGGAGT	XM_037565827.1
12.	BRCA1-R	TGAAGTGGAAGCTTTTGCGAC	
13.	MSH2-F	TGCATACAGCCACTGATCTGG	XM_037548313.1
14.	MSH2-R	AACACATGTCCAAATGGGCC	
15.	MLH1-F	ACACCCCTGATATGGATCGC	XM_037603461.1
16.	MLH1-R	TCTTTCTCAACGTCCCAGGC	