S2 Table. Distribution of crossover types among all spores

Chromosome III	***S. c. ZIP1***		***K.l. ZIP1***		***S. c. ZIP1 msh4Δ***		***K.l. ZIP1 msh4Δ***	
genotype	# spores	**% total**	# spores	**% total**	# spores	**% total**	# spores	**% total**
Total number of spores	**2341**		**3249**		**3636**		**4383**	
Parental	730	**31.2**	1162	**35.8**	2051	**56.4**	1883	**43.0**
Single CO								
HIS4-CEN3	230	9.8	334	10.3	191	5.3	344	7.8
CEN3-MAT	168	7.2	389	12.0	186	5.1	492	11.2
MAT-RAD18	450	19.2	351	10.8	604	16.6	471	10.7
RAD18-HMR	225	9.6	326	10.0	384	10.6	437	10.0
total % single CO		**45.8**		**43.1**		**37.5**		**39.8**
Double CO								
HIS4-CEN3; MAT-RAD	127	5.4	95	2.9	47	1.3	118	2.7
HIS4-CEN3; RAD18-HMR	83	3.5	68	2.1	22	0.6	108	2.5
HIS4-CEN3; CEN3-MAT	55	2.3	113	3.5	28	0.8	114	2.6
CEN3-MAT; MAT-RAD18	58	2.5	115	3.5	25	0.7	105	2.4
CEN3-MAT; RAD18-HMR	51	2.2	99	3.0	26	0.7	125	2.9
MAT-RAD18; RAD18-HMR	62	2.6	79	2.4	52	1.4	77	1.8
HIS4-CEN3; MAT-RAD18	12	0.5	4	0.1	1	0.0	0	0.0
total % double CO		**19.1**		**17.6**		**5.5**		**14.8**
Triple CO								
HIS4-CEN3-MAT-RAD18	34	1.5	23	0.7	3	0.1	25	0.6
CEN3-MAT-RAD18-HMR	12	0.5	23	0.7	4	0.1	22	0.5
HIS4-CEN3-MAT; RAD18-HMR	17	0.7	24	0.7	7	0.2	28	0.6
HIS4-CEN3; MAT-RAD18-HMR	24	1.0	36	1.1	3	0.1	28	0.6
total % triple CO		**3.7**		**3.3**		**0.5**		**2.3**
Quadruple CO								
HIS4-CEN3-MAT-RAD18-HMR	3	**0.1**	8	**0.2**	2	**0.1**	**6**	**0.1**