

Table S2. Statistics for centromere coupling experiments

genotype	number of spreads scored	average number of Mtw1 foci	standard deviation	P value vs <i>ZIP1</i>	P value vs <i>zip1Δ</i>
<i>ZIP1</i>	207	16.45	3.16		****
<i>zip1-N1</i>	165	15.90	2.51	ns	****
<i>zip1-NM1</i>	100	18.69	3.74	****	ns
<i>zip1-NM2</i>	200	18.76	3.98	****	ns
<i>zip1-M1</i>	153	17.18	3.60	ns	****
<i>zip1-N2</i>	152	17.56	3.49	*	**
<i>zip1-MC1</i>	155	16.97	3.65	ns	****
<i>zip1-MC2</i>	104	16.09	3.12	ns	****
<i>zip1-C1</i>	303	19.41	3.69	****	ns
<i>zip1-C2</i>	254	16.53	3.37	ns	****
<i>zip1Δ</i>	257	19.19	3.77	****	

Significance was evaluated with the Kruskal-Wallis test with Dunn's correction for multiple comparisons, performed using Prism 6.0.

ns, $P > 0.05$, * $P \leq 0.05$, ** $P \leq 0.01$, *** $P \leq 0.001$, **** $P \leq 0.0001$