Table 10. Primary constriction gaps after siRNA-mediated down-regulation

			Primary constriction cohesion		
Treatment	**Chromosome**	**n***	**Normal**[†]	**PCG**[†]	**FI_{Total}**[‡]
Untransfected	2	263	97.34	2.66	1.0
GAPD	2	329	96.01	3.99	1.5×
SMC1L1	2	238	89.92	10.08	3.79×
CSPG6	2	313	87.11	12.89	4.85×
STAG2	2	260	94.62	5.38	2.02×
MRE11A	2	294	87.76	12.24	4.60×
Untransfected	4	263	95.44	4.56	1.0
GAPD	4	329	96.35	3.65	0.80×
SMC1L1	4	238	84.45	15.55	3.41×
CSPG6	4	313	84.59	15.41	3.38×
STAG2	4	260	91.54	8.46	1.86×
MRE11A	4	294	90.82	9.18	2.01×
Untransfected	7	263	100.00	0.00	NA[§]
GAPD	7	329	99.69	0.31	1.0[§]
SMC1L1	7	238	90.34	9.66	31.16×[§]
CSPG6	7	313	86.48	13.50	43.55×[§]
STAG2	7	260	96.15	3.85	12.42×[§]
MRE11A	7	294	95.58	4.42	14.26×[§]
Untransfected	13	263	99.24	0.76	1.0
GAPD	13	329	98.77	1.23	1.62×
SMC1L1	13	238	88.66	11.34	14.92×
CSPG6	13	313	86.16	13.84	18.21×
STAG2	13	260	98.46	1.54	2.02×
MRE11A	13	294	95.58	4.42	5.82×

*Number of mitotic spreads included in the analyses.

[†] Values represent percentages.

[‡] FI_{Total} represents the relative fold increase of the PCG for the indicated condition over that of the untransfected control population.

[§] Because no aberrant primary constriction cohesion defects were observed in the untransfected population, the GAPD control value was substituted in the calculation of FI_{Total}. NA, Not applicable.