

Genomic region	Nucles.	<i>t::HHF2</i>		<i>scc1-73</i>	
		<i>Altered nucleosomes (%)</i>	<i>p-value</i>	<i>Altered nucleosomes (%)</i>	<i>p-value</i>
genome	66279	4431 (6.69)		768 (1.16)	
IGR	19557	1478 (7.56)	8.6e-10	317 (1.62)	8.1e-13
ORF	52047	3298 (6.34)	1.9e-12	437 (0.84)	8.1e-42
Pericentric chromatin	1726	125 (7.24)	0.024	15 (0.87)	0.051
rDNA*	106	8 (7.55)	0.14	1 (0.94)	0.36
tDNA	285	11 (3.86)	0.014	8 (2.8)	0.012
Telomeres	784	83 (10.59)	1.1e-5	20 (2.55)	6.0e-4

Table S1. Comparison of the number and percentage of nucleosomes altered after histone depletion (in *t::HHF2* cells) or cohesin inactivation (in *scc1-73* cells) in the indicated genomic regions relative to the whole genome. A hypergeometric test was used to determine the probability to obtain the indicated percentages of altered nucleosomes at the indicated genomic regions if their distribution along the genome were random. Significantly higher (green) and lower (red) percentages are highlighted. *rDNA is analyzed as a single copy.