

Genomic region	Nucles.	<i>t::HHF2</i>						<i>scc1-73</i>					
		<i>Fuzziness</i> (%)	<i>p-val.</i>	<i>Occupancy</i> <i>decrease</i> (%)	<i>p-val.</i>	<i>Occupancy</i> <i>increase</i> (%)	<i>p-val.</i>	<i>Fuzziness</i> (%)	<i>p-val.</i>	<i>Occupancy</i> <i>decrease</i> (%)	<i>p-val.</i>	<i>Occupancy</i> <i>increase</i> (%)	<i>p-val.</i>
genome	66279	1516 (2.3)		2685 (4.05)		1304 (2)		77 (0.12)		375 (0.6)		328 (0.5)	
IGR	19557	374 (1.9)	3e-6	826 (4.2)	6e-3	530 (2.7)	3e-18	28 (0.14)	0.04	154 (0.8)	1e-11	134 (0.7)	1.5e-3
ORF	52047	1331 (2.6)	2e-21	2164 (4.2)	5e-4	762 (1.5)	2e-61	60 (0.12)	0.11	214 (0.4)	1e-8	183 (0.35)	5e-37
Pericentromere	1726	43 (2.5)	0.05	71 (4.1)	0.05	37 (2.1)	0.06	2 (0.12)	0.27	8 (0.46)	0.14	5 (0.29)	0.04
rDNA*	106	0 (<1)	n.a.	8 (7.5)	0.04	0 (<0.9)	n.a.	0 (<1)	n.a.	0 (<0.9)	n.a.	1 (0.94)	0.33
tDNA	285	2 (0.7)	0.03	3 (1.1)	2e-3	7 (2.5)	0.13	0 (<0.4)	n.a.	0 (<0.4)	n.a.	8 (2.8)	2e-4
Telomeres	784	15 (1.9)	0.08	26 (3.3)	0.04	51 (6.5)	1e-13	2 (0.26)	0.17	2 (0.25)	0.15	18 (2.3)	6e-7
<i>X-element</i>	134	15 (11)	4e-7	0 (<0.8)	n.a.	24 (17.9)	2e-16	0 (<0.74)	n.a.	0 (<0.8)	n.a.	13 (9.7)	1e-12
<i>Y-element</i>	671	0 (<0.15)	n.a.	26 (3.9)	0.08	35 (5.2)	2e-7	2 (0.3)	0.14	2 (0.3)	0.2	11 (1.6)	1e-3
<i>Telom. repeat</i>	28	0 (<3.6)	n.a.	0 (<3.6)	n.a.	14 (50%)	4e-17	0 (<3.6)	n.a.	0 (<3.6)	n.a.	1 (3.6)	0.14

Table S2. 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 of obtaining 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, analyzed as a single copy.