

		IGR with altered nuc. in <i>scc1-73</i> (286)	IGR with up nuc. in <i>scc1-73</i> (129)	IGR with down nuc. in <i>scc1-73</i> (151)
Scc1-binding IGR (1720)	<i>overlap.</i>	84	32	50
	<i>obs/exp</i> (<i>p-val</i>)	1.12 (0.02)	0.96 (0.08)	1.27 (0.01)
		ORF with altered nuc. in <i>scc1-73</i> (358)	ORF with up nuc. in <i>scc1-73</i> (157)	ORF with down nuc. in <i>scc1-73</i> (206)
Scc1-binding ORF (2363)	<i>overlap.</i>	167	80	91
	<i>obs/exp</i> (<i>p-val</i>)	1.14 (0.03)	1.24 (0.002)	1.07 (0.03)

Table S6. The effect of cohesin inactivation on chromatin structure is more severe in cohesin-associated regions. The probability that *scc1-73* alters nucleosomes in Scc1-binding IGR or Scc1-binding ORF if the altered genomic regions in *scc1-73* cells were randomly distributed was determined by a hypergeometric test. The rate between the observed and expected frequencies of common genomic regions is also shown. The number of regions in each case is indicated in parenthesis.