Table S5. Cohesin distribution in wild-type and histone-depleted cells at the indicated genomic regions. A peak of Scc1 is defined as a DNA fragment with continuous Scc1 signals that are both positive (relative to the untagged strain) and with a $p < 0.05$. A peak signal was calculated as the sum of these positive signals. Genomic regions with Scc1 and peaks of Scc1 at a particular genomic region are defined by at least 1 bp overlapping.