Supplementary Figure 6. Condensin association along fission yeast chromosome 2.

Cells of strain Y252 (h-leu-32 nda3-KM311 cnd2-Pk9) were grown in rich YE4S medium at 32°C, and arrested in metaphase by shift to the restrictive temperature of the nda3-KM311 cold sensitive allele of 20°C for 6 hours. Cells were processed for chromatin immunoprecipitation against the Pk epitope-tagged Cnd2 subunit of the fission yeast condensin complex (ortholog of the budding yeast Brn1 subunit). The binding profile of Cnd2-Pk9 along fission yeast chromosome 2, relative to a whole genome DNA sample, is shown. Every bar represents the average of 11 oligonucleotide probes within 250 bp windows. Peaks in dark blue have been identified according to the following criteria: Signal intensities were smoothed using a sliding 2.25 kb window. Local maxima were identified, and those with a smoothed signal intensity above 0.55 were considered a peak. Peaks extend from their maximum to both sides for as long as the raw signal intensity remains above 0.1. The peak position was defined as the maximum point within the peak.

103 peaks were identified with these criteria along chromosome 2. This may be an underestimate of the actual number of association sites, some of which may not have been recognised by our peak picking parameters.

The location of these condensin binding sites with respect to the nearest tRNA and ribosomal protein gene is given below. (A) 21 of the 103 peaks lie within 5 kb of a tRNA gene. (B) Of the remaining 82 peaks, 20 lie within 5 kb of a gene encoding a ribosomal protein component. This suggests that, like in budding yeast, condensin binding sites are enriched at tRNA genes and ribosomal protein genes along fission yeast chromosome 2.

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![Graph showing condensin association along fission yeast chromosome 2. Peaks in dark blue represent signal intensities smoothed using a sliding 2.25 kb window. Peaks extend from their maximum to both sides for as long as the raw signal intensity remains above 0.1. The peak position is defined as the maximum point within the peak. The number of condensin peaks is shown on the y-axis, and the distance from the nearest tRNA gene in kb is shown on the x-axis.](image-url)