Supplementary Methods: Nucleosee retrieval power

We have tested Nucleosee retrieval power against two different nucleosome position datasets on *S. pombe*. The first dataset includes 74,288 nucleosomes retrieved by the DANPOS tool [Chen et al 2013] from the nucleosome occupancy map of [Gonzalez et al. 2016] generated by microccocal nuclease digestion (DANPOS parameter *height* was set to 1). The second dataset includes 73,945 nucleosome unique positions reported by [Moyle-Heyrman et al, 2013] on their nucleosome map generated by a chemical method without MNase digestion. Both maps were generated in two biological replicates.

In both cases, we used Nucleosee to pre-process the average coverage from the two replicates with 3 discretization levels (*d*=3) and windows of 30 bps (*w*=30). Then we used Nucleosee to search for *abcba*, individual nucleosome patterns, with up to *v*=2 variations. We obtained 85,547 matches for González et al. maps and 76,518 matches for Moyle-Heyrman et al. maps. We calculated nucleosome positions as the middle point of the Nucleosee matches, which are given as patterns of coordinates intervals. In the case of single nucleosome patterns, such point will approximately map to the dyad center. This approximation has a margin error of 30 bps, which is the discretization window size.

For each dataset, we considered the reported nucleosome positions as positives. In order to compute specificity and sensitivity, we defined negatives as the center positions of 150 bps regions which are located at least 75 bps away from reported nucleosomes on both directions.

Finally, we identified true positives and negatives by identifying which positions reported by our method are closer than a given distance to DANPOS or Moyle-Heyrman et al. positives or negatives. We defined a range of distances from 0 bps to 250 bps to generate ROC curves for DANPOS (Sup. Fig. 1) and Moyle-Heyrman et al. (Sup. Fig 2) comparisons. Given the discretization resolution, we consider correct distances below 40 bps (red dot in Sup. Figs. 1 and 2). In the case of the DANPOS comparison such distance reports a Nucleosee sensitivity of 87.9% and a specificity of 68.5%. In the case of Moyle-Heyrman et al. comparison the sensitivity is 73.8% and the specificity 83.6%.

Sensitivity decays quickly for error distances below 30 bps, although this is mainly due to the discretization resolution used to pre-process data with Nucleosee. Sensitivity does not significantly increase with larger error distances, while specificity steeply decreases, suggesting that the Nucleosee retrieval power can be correctly characterized with a 30-40 bps margin error.