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In vivo chromatin signatures at nucleosome inhibitory energy barriers (NIEBs) predicted by physical model

In eukaryotes, DNA is wrapped around histones to form nucleosomes, the building blocks of chromatin. The condensation of the genome is not the only function of this organization and chromatin acts as a substrate of many processes: replication, transcription, DNA reparation. Even if most of the genome is thought to be covered by nucleosomes, physical modeling predicts some nucleosome inhibitory energy barriers (NIEBs) based on the DNA sequence. It has recently been shown that the predicted NIEBs is ubiquitous from yeast to mammals and correlate with in vivo data. Physical modeling, confirmed by in vivo results, highlights the statistical positioning of nucleosomes at the borders of those barriers. Based on MNase-sequencing and MNase-ChIP-sequencing data, we characterized the chromatin signature at NIEBs borders. We show that the model outperform initial expectation, predicting correctly nucleosomes over kilobases at the border of NIEBs. The model predicts a first nucleosome perfectly positioned follows by arrays of nucleosomes of different repeat lengths. We then highlight a very dynamic structure at NIEBs border suggesting that the energetic profile encoded in DNA sequence, and resulting from evolution, could be the base for chromatin organization and plasticity.

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