# Supplementary Data

## A novel strategy of transcription regulation by intra-genic nucleosome ordering

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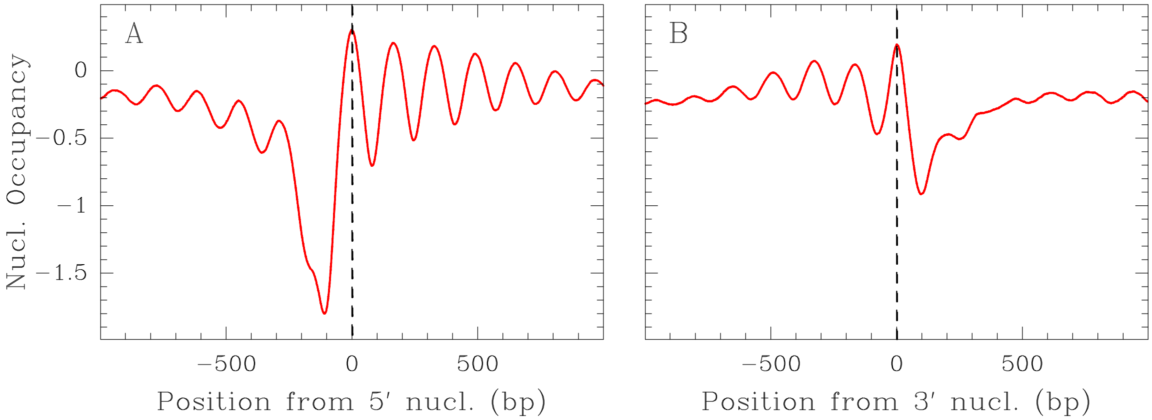

Figure S1: Average (4554 yeast genes) *in vivo* nucleosome occupancy profile around (A) the first flanking nucleosome downstream the TSS (5′ nucleosome) and (B) the first flanking nucleosome upstream the TTS (3′ nucleosome). Data retrieved from (Lee et al., 2007).

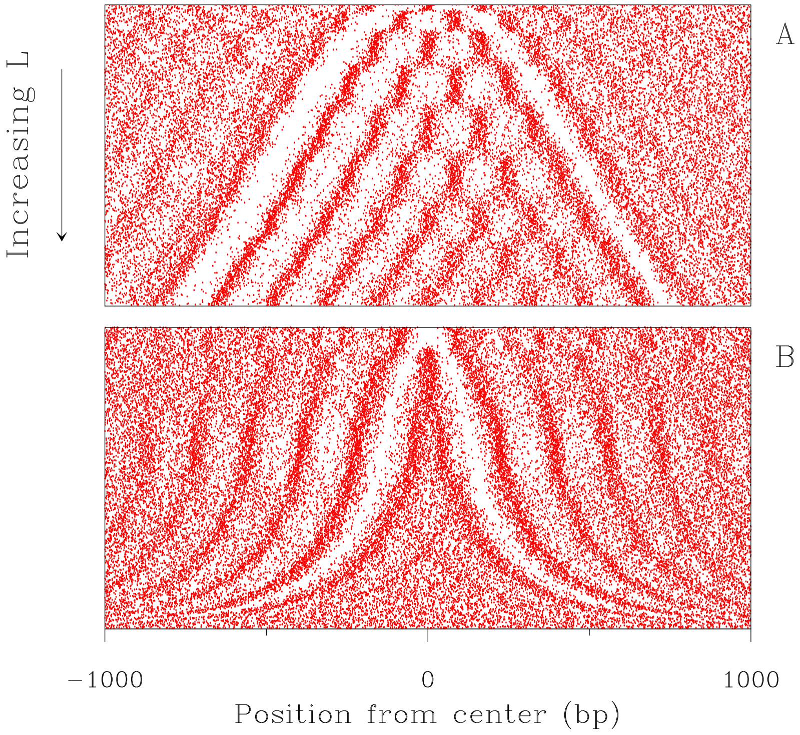

Figure S2: 2D map of local minima (red points) of the experimental nucleosome occupancy profiles of yeast genes (A) and intergenic regions (B); nucleosomes occupy the white zones. The first 2500 genes and the total 3300 intergenic regions were centered at the middle of $L$ and ordered from the top to bottom according to the distance $L$ between the left $5'$ and right $3'$ most nucleosomes. Data retrieved from (Lee et al., 2007).

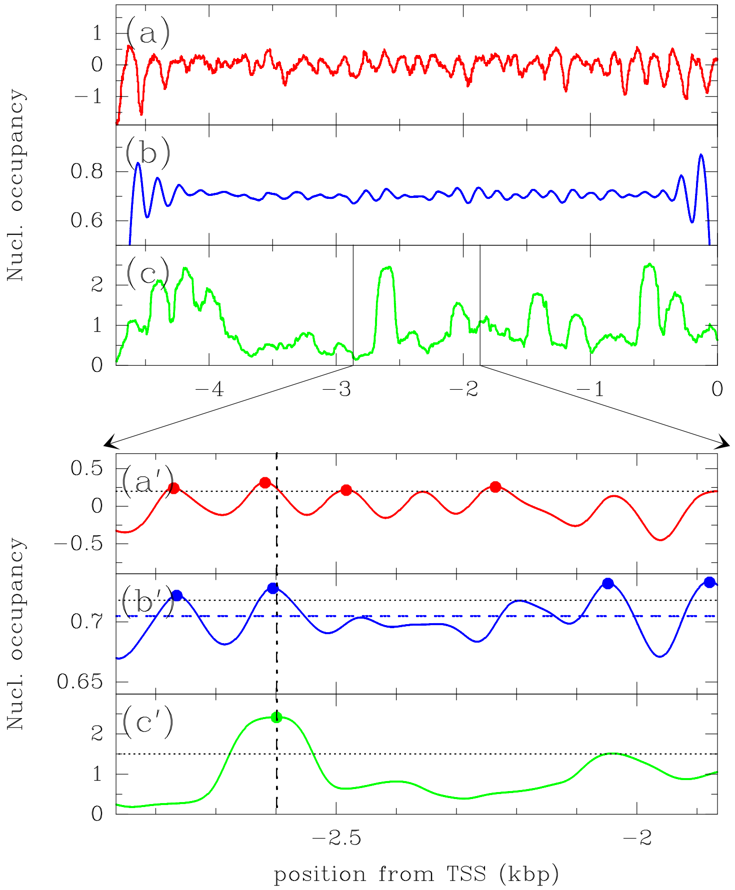

Figure S3: Example of nucleosome occupancy profile along a large gene. Profile of the KOG1 gene ($TSS$ = 480731, $TTS$ = 475999) on yeast chromosome VIII: (a) *in vivo* data from (Lee et al., 2007); (b) theoretical model when introducing between the bordering energy barriers the sequence dependent energy profile predicted by the model II (Vaillant et al., 2007); (c) *in vitro* data from (Kaplan et al., 2009). (a'-c') represent a zoom on the 1 *kbp* central region of the KOG1 gene; the horizontal black dotted lines correspond to the thresholds (see Materials and Methods) used to detect the well positioned nucleosomes (dots); the vertical line marks the location of a nucleosome detected *in vitro* as well as *in vivo* and also predicted by our theoretical modeling. In (b'), the blue dashed-line corresponds to the prediction of out toy model with energy barriers bordering a flat energy potential.

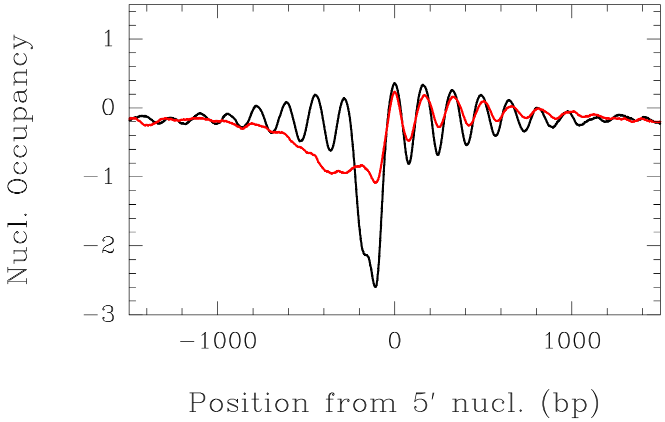

Figure S4: Mean experimental nucleosome occupancy profiles (data retrieved from Lee et al. (2007)) for the two classes OPN (red) and DPN (black) yeast genes defined by Tirosh and Barkai (2008), when aligned on the 5′ nucleosome.

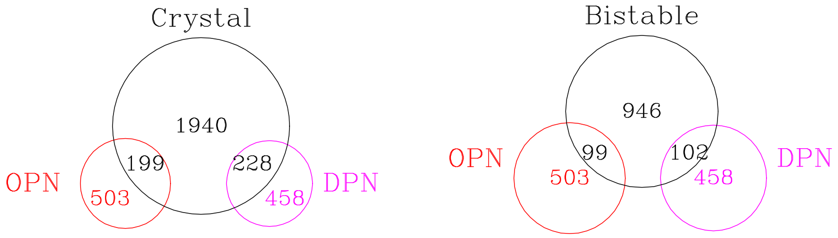

Figure S5: Venn diagrams showing the repartition of DPN and OPN yeast genes (Tirosh and Barkai, 2008) among crystal and bistable genes.

| **GO-term** | **Bistable** | **Crystal-like** |
|---|---|---|
| cytoskeleton organization and biogenesis | 18 | 14 |
| translation | 46 | 127 |
| cytokinesis | 18 | 16 |
| response to stress | 23 | 66 |
| pseudohyphal growth | 14 | 14 |
| amino acid and derivative metabolic process | 33 | 43 |
| protein modification | 55 | 82 |
| signal transduction | 14 | 16 |
| vitamin metabolic process | 3 | 13 |
| conjugation | 9 | 9 |
| DNA metabolic process | 74 | 117 |
| transport | 84 | 135 |
| cell budding | 10 | 11 |
| transcription | 33 | 76 |
| cell homeostasis | 11 | 13 |
| biological process unknown | 262 | 516 |
| lipid metabolic process | 18 | 44 |
| electron transport | 2 | 8 |
| meiosis | 13 | 18 |
| vesicle mediated transport | 27 | 59 |
| carbohydrate metabolic process | 16 | 36 |
| ribosome biogenesis and assembly | 51 | 104 |
| cellular respiration | 9 | 21 |
| organelle organization and biogenesis | 37 | 75 |
| sporulation | 6 | 8 |
| protein catabolic process | 14 | 29 |
| generation of precursor metabolites and energy | 8 | 13 |
| cell cycle | 27 | 52 |
| RNA metabolic process | 49 | 90 |
| anatomical structure morphogenesis | 5 | 8 |
| cell wall organization and biogenesis | 25 | 46 |
| membrane organization and biogenesis | 11 | 21 |
| nuclear organization and biogenesis | 5 | 10 |

Table S1: Numbers of *S. cerevisiae* genes displaying a given Gene Ontology (GO) that are classified as bi-stable or crystal-like.

# References

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Lee, W., Tillo, D., Bray, N., Morse, R. H., Davis, R. W., Hughes, T. R., and Nislow, C. (2007). A high-resolution atlas of nucleosome occupancy in yeast. *Nat. Genet.* **39**:1235–1244.

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