Electronic Supplementary Material (ESI) for Molecular BioSystems
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Nucleosome Positioning and Nucleosome Stacking: Two Faces of The Same Coin.

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SUPPLEMENTARY MATERIAL

Table 1A: Comparison of the Kurtosis and Skewness obtained using the Statistical positonning model to the experimental data

Kurtosis is a measure of the distribution "peakedness"(= $\frac{\mu_4}{\sigma^4}$, where μ_n is the nth moment, and σ the standard deviation), whereas skewness is a measure of the curve assymetry (= $\frac{\mu_3}{\sigma^3}$).

Nucleosome	Experimental kurtosis	Experimental skewness	Model kurtosis	Model skewness
+2	2.793	0.167	2.355	0.651
+3	2.383	0.068	2.034	0.389
+4	2.081	-0.0914	1.863	0.089
+5	2.090	0.0180	1.879	-0.136
+6	1.940	0.107	1.847	-0.183
+7	1.854	0.0682	1.986	0.858
+8	1.809	0.0544	1.863	-0.775
+9	1.803	0,00230	2.767	-1.073
+10	1.791	-0.0268	5.866	-1.519
+11	1.804	-0.0308	1.782	-0.011
+12	1.809	-0.0197	6.068	1.491

Table 1B: Comparison of the Kurtosis and Skewness obtained using the Gaussian mixture model to the experimental data

Kurtosis is a measure of the distribution "peakedness"(= $\frac{\mu_4}{\sigma^4}$, where μ_n is the nth moment, and σ the standard deviation), whereas skewness is a measure of the curve assymetry (= $\frac{\mu_3}{\sigma^3}$).

Nucleosome	Experimental kurtosis	Experimental skewness	Model kurtosis	Model skewness
+2	2.793	0.167	2.860	0.239
+3	2.383	0.068	2.312	0.125
+4	2.081	-0.0914	2.012	-0.0274
+5	2.090	0.0180	2.080	0.0088
+6	1.940	0.107	1.964	0.0763
+7	1.854	0.0682	1.899	0.0603
+8	1.809	0.0544	1.872	0.0855
+9	1.803	0,00230	1.854	-0.0168
+10	1.791	-0.0268	1.820	-0.0392
+11	1.804	-0.0308	1.799	0,00821
+12	1.809	-0.0197	1.792	-0.00755

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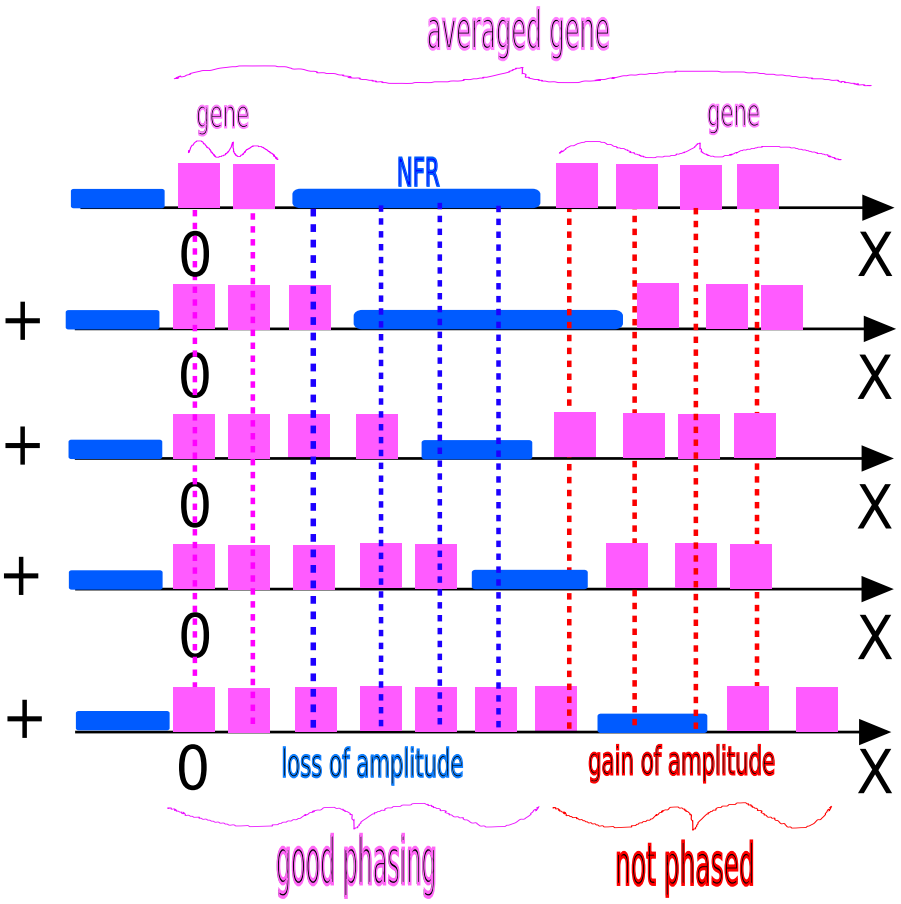

Figure S 1: The loss of amplitude A_i is due to the presence of NFRs at the end of genes. The variances $\{\sigma_i^2\}$ increase after the $+\mathbf{6}$, because the nucleosome phasing decreases while i increases, as shown.

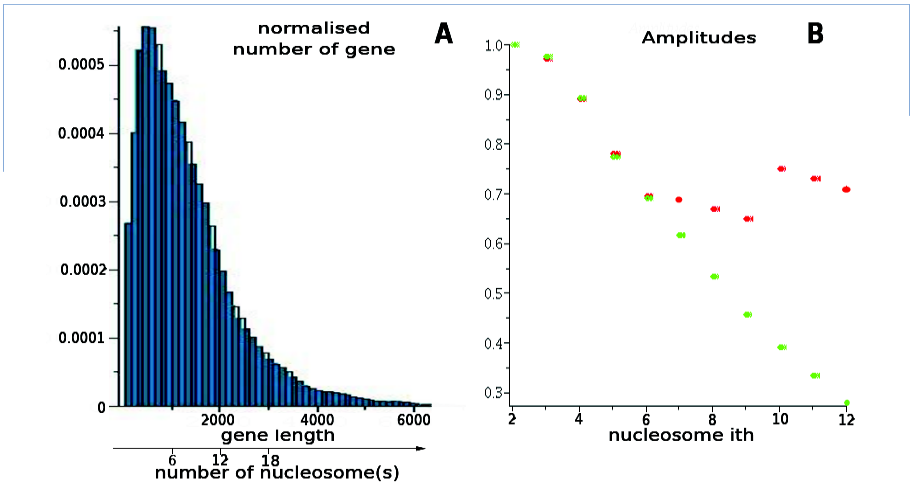

Figure S 2: The loss of amplitude A_i can be quantitatively explained be the gene length distribution found in *Saccharomyces Cerevisæ*. A: Gene length distribution (in bp and in nucleosomes). B: In green, relative amount of genes having a length of at least i nucleosomes. In red: Amplitudes of the nucleosomal density peaks as found in our gaussian mixture model.

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Figure S 3: The two plausible strcutures for the 167 bp NRl chromatin fiber. Two nucleosomes are represented.