SUPPLEMENTARY MATERIALS

Epigenomics in 3D: importance of long-range spreading and specific interactions in epigenomic maintenance

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Supplementary Figures

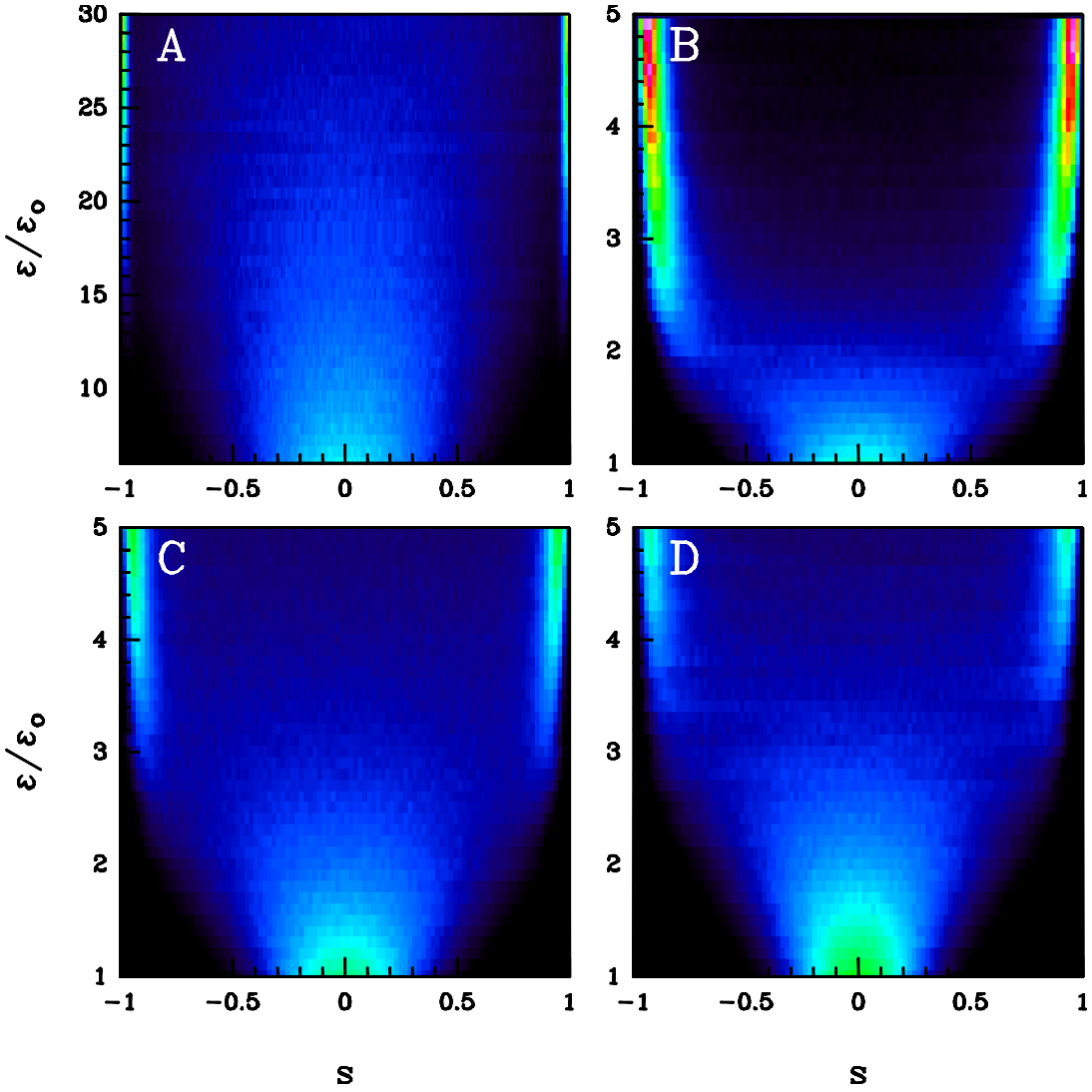

FIG. S1: **Probability density functions of the mean epigenomic state**. (A-D) Heatmaps of the Pdfs $\rho(s)$ as a function of recruitment strength ϵ/ϵ_o for the cis model ($\epsilon_t = 0$, $\epsilon = \epsilon_c$, $k_r = \epsilon_0 + \epsilon n_c$) with $\epsilon_o = 0.001$ (A), for the cis & trans models without self-attraction ($k_b = 0$, $\epsilon_c = \epsilon_t = \epsilon$, $k_r = \epsilon_0 + \epsilon(n_c + n_t)$) with $\epsilon_o = 0.001$ (B), $\epsilon_o = 0.01$ (C), $\epsilon_o = 0.001$ and $k_{int} = 1$ (D).

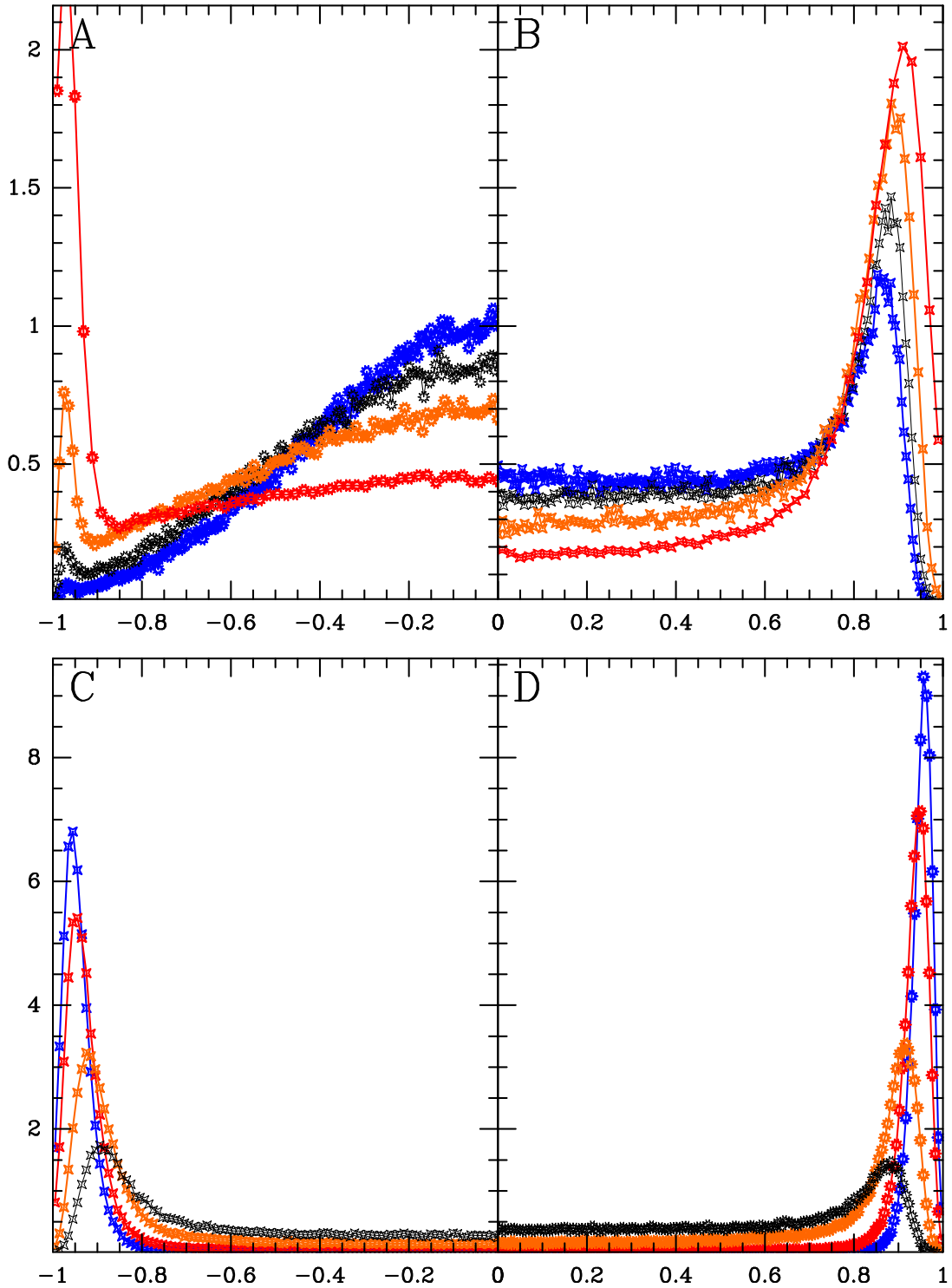

FIG. S2: **Finite size effect**. (A) Pdf $\rho(s)$ (the half-part, $s < 0$) for $\epsilon/\epsilon_o = 18.6$ for the cis model ($\epsilon_t = 0$, $\epsilon = \epsilon_c$, $k_r = \epsilon_0 + \epsilon n_c$) with $\epsilon_o = 0.001$ and (B) (the half-part, $s > 0$) for the cis & trans models for $\epsilon/\epsilon_o = 18.6$ without self-attraction ($k_b = 0$, $\epsilon_c = \epsilon_t = \epsilon$, $k_r = \epsilon_0 + \epsilon(n_c + n_t)$) with $\epsilon_o = 0.001$, for a chain with $N = 50$ monomers (red), 100 (orange), 150 (black) and 200 (blue). (C,D) for the cis & trans models (see B) for $N = 100$ (C) and $N = 150$ (D) with $k_b/k_u = 0$ (black), 0.1 (orange), 0.1625 (red) and 0.1875 (blue) (B).

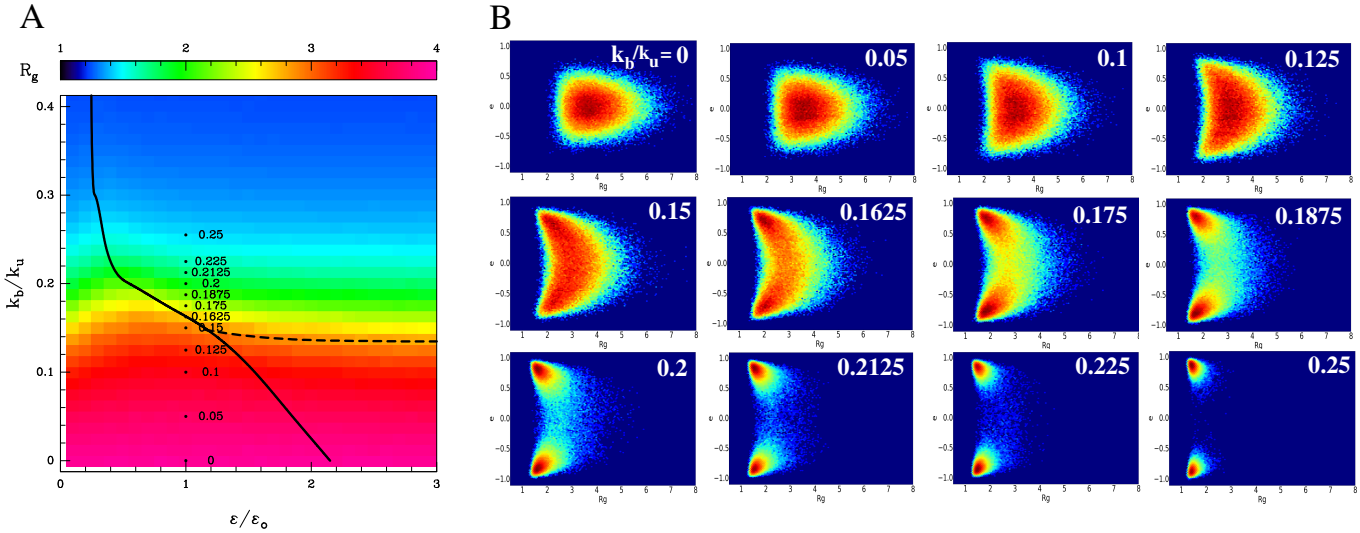

FIG. S3: **Large-scale coupling between 1D and 3D** (A) Heatmap of the radius of gyration R_g (see Mat. & Meth.) as a function of the attraction k_b/k_u and recruitment strength ϵ/ϵ_o for the cis & trans model with $k_u = 0.001$, $\epsilon_o = 0.001$, $\epsilon_c = \epsilon_t$. As in Fig. 4 A, the monostable and multimodal/bistable regions are demarcated by the transition black curve and the limit between multimodality and bistability is represented by the black dashed line. (B) Heatmaps of the 2D Pdf $\rho(R_g, s)$ for the same model as in (A) with $\epsilon/\epsilon_0 = 1$ and increasing values of self-attraction, from $k_b/k_u = 0$ to $k_b/k_u = 0.25$ (see (A)).

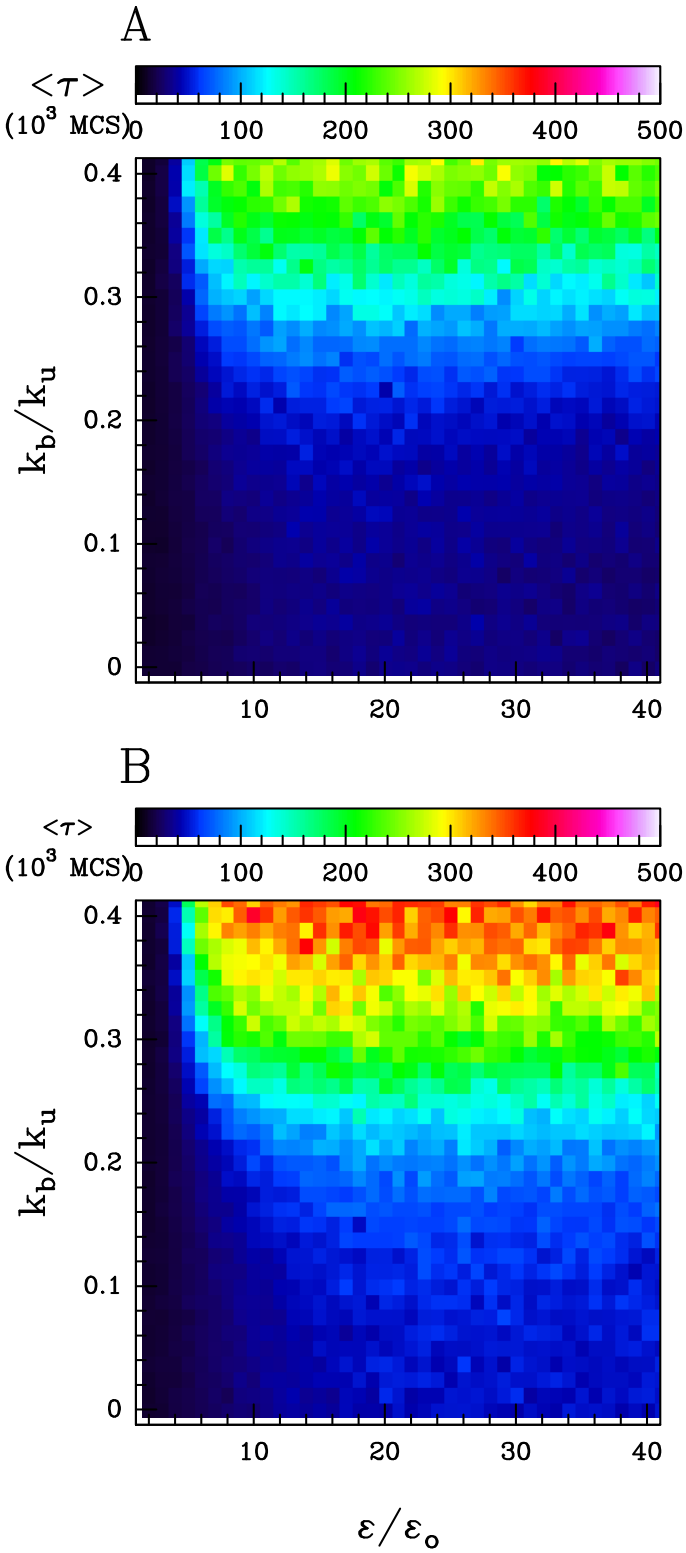

FIG. S4: **Maintenance of two neighbouring epigenomic domains**. Same as in Fig. 6 A,B, but (A) (no boundary) and (B) (boundary) now correspond to the heatmaps of (absolute) stability time (see Mat. & Meth.) $\langle\tau\rangle$.

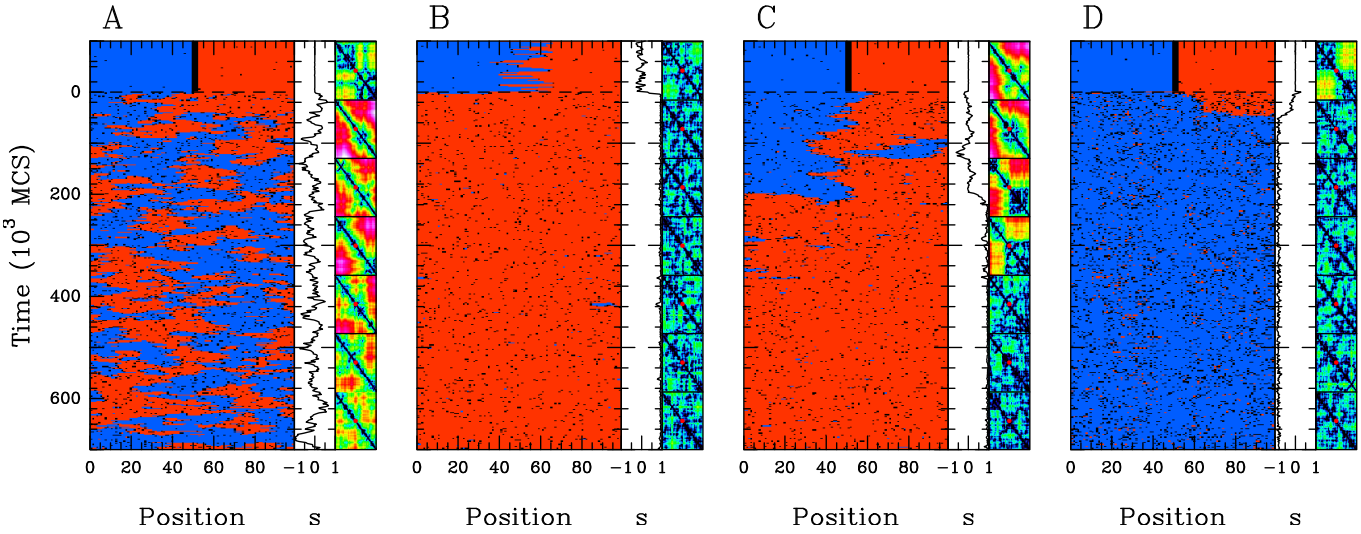

FIG. S5: **Maintenance of two neighbouring epigenomic domains** Relaxation dynamics of the A-I compartmentalization (same as in Fig. 6 $(\mathrm{A,B})_{1,2}$) with $\epsilon_o = 0.001$, $k_{int} = 1$ when considering only cis-spreading in the relaxation phase ($\epsilon_t = 0$, $k_b/k_u = 0.28$ $(t > 0)$) (A), an initial compartmentalization $(t < 0)$ with a fuzzy 1D boundary (see Mat. and Meth.) and $k_b/k_u = 0.28$ in the relaxation phase (B), an initial compartmentalization with the A and I compartments in the coil state (ie $k_b/k_u = 0$ for $t < 0$) and $k_b/k_u = 0.28$ $(t > 0)$ (C), a symetrical recruitment ($\epsilon_c = \epsilon_t$, $\epsilon_o = 0.001$) and a flexible chain ($k_{int} = 0$) in the relaxation phase (D).

Supplementary movie

Movie S1: Folding and epigenome dynamics of a 100 monomer isolated chain for: $\epsilon_c = \epsilon_t = \epsilon_o = 0.001$, $k_b/k_u = 0.1750$, $k_{int} = 0$ (see the corresponding 2D Pdf $\rho(Rg, s)$ in Fig. S1 B). Total duration: 2000 frames, a frame every 2000 MCS.