SUPPLEMENTAL FIGURES - Polymer coil-globule phase transition is a universal folding principle of Drosophila epigenetic domains - Lesage et al.

**Figure 1** Radii of gyration $R_g$ calculated from the dataset of Boettiger et al. [? ] for the three sets of domains: active (red), inactive (black) and repressed (blue). (a) Data are represented as boxplots, showing the interquartile range (IQR: 25 to 75 percentile), with whiskers adding and subtracting additional 1.5 IQR. Points indicate the mean, errorbars are the standard error of the mean (i.e. the sample standard deviation over the square root of the sample size). Solid lines are power laws ($A L^\nu$) fitted to the series of mean values, weighted by standard errors of the mean. Corresponding Flory exponents $\nu$ are 0.34 (active), 0.30 (inactive), 0.19 (repressed). (b) Medians from the same datasets are indicated by the horizontal segments. Notches display the confidence interval around the median based on the median $\pm 1.57$ IQR over the square root of the sample size. Solid lines are power laws ($A L^\nu$) fitted to the series of median values. Corresponding Flory exponents $\nu$ are 0.36 (active), 0.31 (inactive), 0.22 (repressed). (a, b) Dashed lines, shown for reference, represent the typical scaling laws for random walk polymers ($\nu = 0.5$, green), self-avoiding walk polymers ($\nu = 3/5$, orange) and globule polymers ($\nu = 1/3$, blue).
Figure 2 Selected histograms from the on-lattice simulations for different polymer lengths $N$ from 10 to 2649, obtained with interaction energies $\varepsilon = 0.20$ (orange), $\varepsilon = 0.31$ (purple) and $\varepsilon = 0.44$ (green). Dashed lines correspond to the theoretical model of the free energy $\mathcal{F}_N(t;\varepsilon) = a_1(\varepsilon)Nt + a_2(\varepsilon)Nt^2 + a_3(\varepsilon)(Nt)^{-2/3} + a_4(\varepsilon)(Nt^2)^{2/3} + 1.13 \ln Nt$. 

SUPPLEMENTAL FIGURES - Polymer coil-globule phase transition is a universal folding principle of Drosophila epigenetic domains - Lesage et al.
Figure 3 Parameter distribution inferred from data by Bayesian analysis for active (red) domain measurements. On the diagonal: parameter distributions, marginalized on all other parameters. Off diagonal: distributions marginalized on each parameter couple (see legends). In all graphs, blue lines indicate the position of the mean value of the corresponding parameters.
Figure 4. Parameter distribution inferred from data by Bayesian analysis for inactive (black) domain measurements. On the diagonal: parameter distributions, marginalized on all other parameters. Off diagonal: distributions marginalized on each parameter couple (see legends). In all graphs, blue lines indicate the position of the mean value of the corresponding parameters. The active and repressed cases are presented in SI Fig.s
Figure 5  Parameter distribution inferred from data by Bayesian analysis for repressed (blue) domain measurements. On the diagonal: parameter distributions, marginalized on all other parameters. Off diagonal: distributions marginalized on each parameter couple (see legends). In all graphs, light blue lines indicate the position of the mean value of the corresponding parameters, used as best parameter estimates in table in Table 1.
Figure 6. The ensemble of data histograms with the corresponding theoretical distribution obtained using the parameters obtained from the fit for active domains. Outliers that have been filtered out by the procedure described in Materials and Methods.
Figure 7 The ensemble of data histograms with the corresponding theoretical distribution obtained using the parameters obtained from the fit for inactive domains. Outliers that have been filtered out by the procedure described in Materials and Methods.
Figure 8: The ensemble of data histograms with the corresponding theoretical distribution obtained using the parameters obtained from the fit for repressed domains. Outliers that have been filtered out by the procedure described in Materials and Methods.
Figure 9 Medians of $R_g$ as a function of the domain length $L$ calculated from the analytical model with the parameter sets of Table 1: active (red line), inactive (black line), repressed (blue line). Boxplots (same colors respectively) correspond to the experimental data from Ref. [?], as in Fig. 1. Medians are indicated by the horizontal segment. Dashed lines are obtained from previous fitting curves by deconvolution, hence correspond to the behavior expected in a typical haploid system. The orange dotted line represents the $\nu = 3/5$ typical scaling law. Complementary information with respect to Fig. 4.