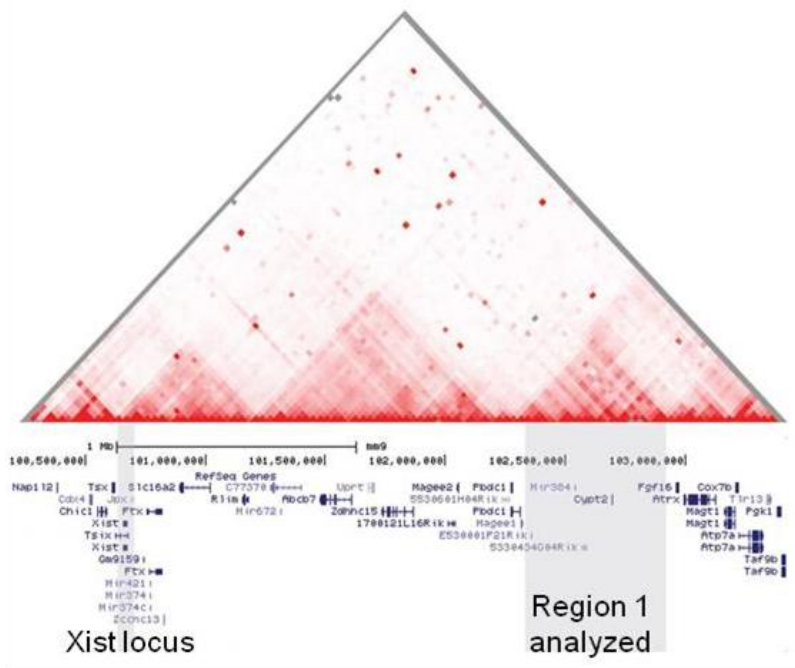
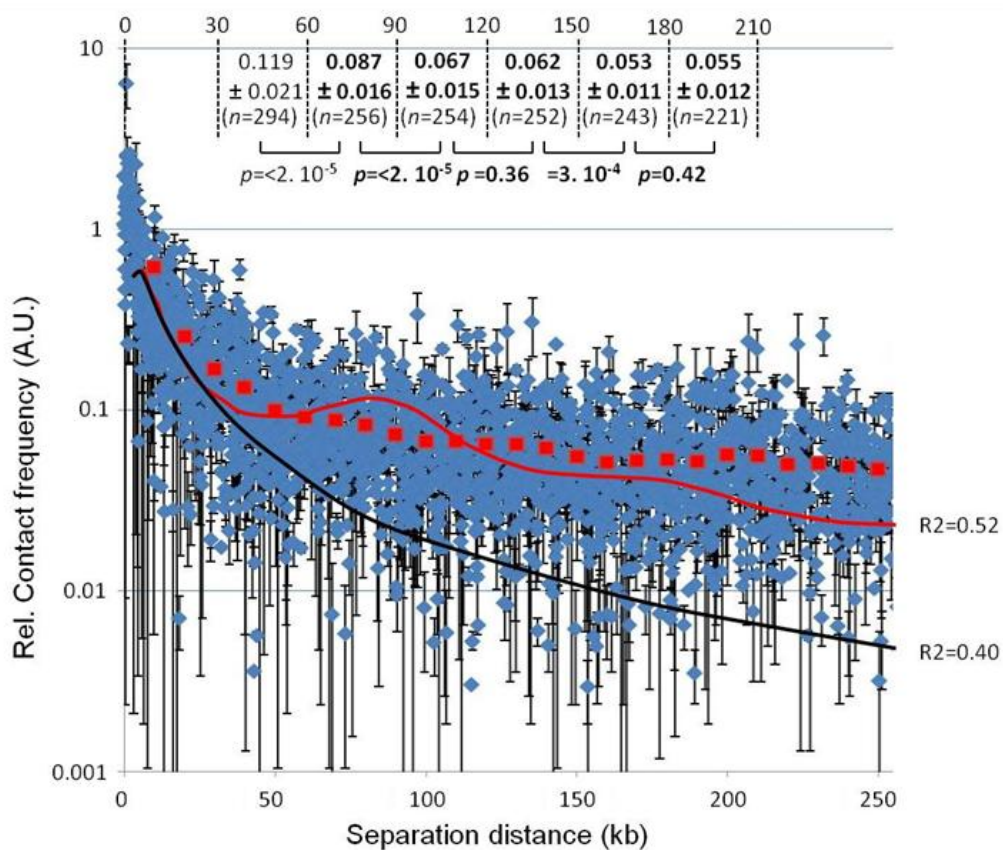


A



B



Additional file 4 : fitting the statistical helix model to contact frequencies quantified by 5C experiments in mECS: (a) 5C Matrix from data obtained in mESC [2] indicating the 572kb gene-poor region (region 1) with no apparent locus-specific interaction (chrX:102,338,477-102,910,171) that we used to fit polymer models. (b) “Virtual 3C” profiles were reconstructed from region 1 and data were compiled in a single graph. Error bars are standard error of the mean of two 5C experiments. Dashed lines delimit supranucleosomal domains that encompass separation distances where contact frequencies are alternatively lower and higher (see *Methods*). The graph shows the best fit analyses obtained with the unconstrained chromatin model [eqs. 1 and 2] (black curve) or the statistical helix model [eqs. 1 and 3] (red curve). Correlation coefficients (R^2) are indicated on the graph. For each supranucleosomal domains, the mean contact frequencies and the number (n) of experimental points are indicated on the graph. p -values (Mann-Whitney U -test) account for the significance of the differences observed between the experimental means of two adjacent domains.