



Figure 1. Spatial organization of the epigenome. (A) Chromatin interaction map for an ~ 1 Mb region of the genome in *Drosophila* embryos (data from the laboratories of Giacomo Cavalli and Amos Tanay). The interaction strength between two specific genomic regions is given by the heat map corresponding to their coordinates on the x - and y -axes. The presence of distinct topological domains is indicated by the patterns of squares on the heat map diagonal, with steep decreases in interaction strength when passing beyond the domain. The topological domain borders are denoted by gray lines. The linear profiles for binding of the insulator protein, CP190, and the histone modifications, H3K4me3 and H3K27me3, are shown above the map, along with a color-coding for the epigenetic “state” of each topological domain (“null” domains, devoid of known epigenetic marks are indicated in black; “active” domains, marked by H3K4me3, are indicated in green; domains repressed by the mark H3K27me3 are indicated in red). Key functional organization principles of the genome are shown in the insets. (B) A subset of the interaction map, rotated by 45° , is shown to highlight the topological domain organization of the genome. This inset shows a large null domain, physically segregated from a small active domain, with the border between them containing a binding site for the insulator protein CP190 (shown schematically below). (C) A specific interdomain interaction between two small active domains, kept separate from the surrounding repressive chromatin, is highlighted in a subset of the interaction map and schematically shown below the map.