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Title: Insulated domain organization and regulation of metazoan genomes

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Abstract:

CCCTC-binding factor (CTCF) compartmentalizes the metazoan genomes into epigenetically insulated chromatin domains, several aspects of which remain poorly understood. In this thesis, we attempted to address the following key questions: 1) Do insulated chromatin domains regulate the genome in an allele-specific manner? 2) How are the transcriptional states of chromatin domains concurrently regulated during development? The first part of the thesis highlights that the CTCF mediated looping guides the majority of the mono-allelic expression of the genome and alludes the widespread allele-specificity of CTCF mediated genome architecture. The second part suggests that the biased visibility in the high throughput chromatin conformation (Hi-C) datasets can be reliably repurposed to quantitate the chromatin compaction across genome. We identified novel condensed domains that are dynamically associated with the developmental regulation of concurrent transcriptional states of genes. Altogether, the thesis presents non-trivial insights to allele-specific and domain-wide

transcriptional regulation guided through CTCF-mediated genome architecture.

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