Genome of Drosophila melanogaster

Academic Press - The three



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Notes: Rev. ed. of: The genetic variations of Drosophila melanogaster

/ D.L. Lindsley and E.H. Grell. 1968.

This edition was published in 1992



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Due to their low occurrence, these interactions are also less reproducible than intra-arm interactions, especially at low sequencing depth. For comparison, we also generated a population of structures using only Hi-C data, referred to hereafter as a control model.

Drosophila melanogaster

Each probe on the array is represented by a vertical line, the color of which indicates the relative binding of the protein ranging from white equals background level to black equals strongest binding. Right panel: The position of FISH probes used for this study, relative to the pericentromeric regions of each chromosome chrX, chr2, chr4.

Drosophila melanogaster Genome Project

This gene cluster is brought together by nearby active domains, which form frequent interactions. C DamID profile of GAL4-DBD and ChIP profile of Gaf visualized in the same SOM matrix as in A and B. Topological associated domains TADs are defined by observing an increased probability of interaction between chromatin regions in a domain relative to interactions between domains.

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The genome encodes approximately 13,600 genes, somewhat fewer than the smaller Caenorhabditis elegans genome, but with comparable functional diversity. These genes were transcriptionally silenced and late-replicating. Therefore, both A and E are interpreted as ensemble averages.

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