Library
Indian Institute of Science Education and Research
Mohali

DSpace@IISERMohali (/jspui/)
/ Publications of IISER Mohali (/jspui/handle/123456789/4)
/ Research Articles (/jspui/handle/123456789/9)

Please use this identifier to cite or link to this item: http://hdl.handle.net/123456789/253

Title:	Large-Scale Functional Organization of Long-Range Chromatin Interaction Networks
Authors:	Sandhu, K.S. (/jspui/browse?type=author&value=Sandhu%2C+K.S.)
Keywords:	RNA polymerase II Chromatin assembly and disassembly
Issue Date:	2012
Publisher:	Elsevier B.V.
Citation:	Cell Reports, 2 (5), pp. 1207-1219.
Abstract:	Chromatin interactions play important roles in transcription regulation. To better understand the underlying evolutionary and functional constraints of these interactions, we implemented a systems approach to examine RNA polymerase-II-associated chromatin interactions in human cells. We found that 40% of the total genomic elements involved in chromatin interactions converged to a giant, scale-free-like, hierarchical network organized into chromatin communities. The communities were enriched in specific functions and were syntenic through evolution. Disease-associated SNPs from genome-wide association studies were enriched among the nodes with fewer interactions, implying their selection against deleterious interactions by limiting the total number of interactions, a model that we further reconciled using somatic and germline cancer mutation data. The hubs lacked disease-associated SNPs, constituted a nonrandomly interconnected core of key cellular functions, and exhibited lethality in mouse mutants, supporting an evolutionary selection that favored the nonrandom spatial clustering of the least-evolving key genomic domains against random genetic or transcriptional errors in the genome. Altogether, our analyses reveal a systems-level evolutionary framework that shapes functionally compartmentalized and error-tolerant transcriptional regulation of human genome in three dimensions. It is becoming increasingly clear that genes are not autonomous transcriptional units; instead, they physically interact with one another to coordinate transcriptional regulation. Using a network approach, Ruan and colleagues unravel an evolutionarily constrained systems organization of transcription-associated chromatin in the human genome. Their observations provide a possible chromatin-level explanation for how disease-associated mutations evolve and how key cellular genes escape genetic and transcriptional errors.
Description:	Only IISERM authors are available in the record.
URI:	http://www.sciencedirect.com/science/article/pii/S2211124712003269 (http://www.sciencedirect.com/science/article/pii/S2211124712003269) http://dx.doi.org/10.1016/j.celrep.2012.09.022 (http://dx.doi.org/10.1016/j.celrep.2012.09.022)
Appears in Collections:	Research Articles (/jspui/handle/123456789/9)

Files in This Item:

File	Description	Size	Format	
Need to add pdf.odt (/jspui/bitstream/123456789/253/3/Need%20to%20add%20pdf.odt)		8.63 kB	OpenDocument Text	View/Open (/jspui/bitstream/123456

Show full item record (/jspui/handle/123456789/253?mode=full) (/jspui/handle/123456789/253/statistics)

Items in DSpace are protected by copyright, with all rights reserved, unless otherwise indicated.