23.09.2020

Science news

By G.Timokhin

1. A new 3D-genomics method has been introduced





- Single Cell
- Multiple Scales
- High genomic throughput

- 1. High-resolution conformation tracing of whole chromosomes by sequential hybridization
- 2. A multiplexed errorrobust fluorescence *in situ* hybridization (MERFISH)-based method for genome-scale chromatin tracing
- 3. Helps to characterize chromatin domains, compartments, and *trans*chromosomal interactions and their relationship to transcription in single cells



2. Large-Scale Topological Changes Restrain Malignant Progression in Colorectal Cancer

Cell		Log in	Register	Subscribe	Claim	Q :	
	ARTICLE I VOLUME 182, ISSUE 6, P1474-1489.E23, SEPTEMBER 17, 2020 Large-Scale Topological Changes Restrain Malignant	Purchase	E Subscribe	Save Share	Reprints	C Request	
<	Progression in Colorectal Cancer Sarah E. Johnstone ¹⁰ • Alejandro Reyes ¹⁰ • Yifeng Qi • Bin Zhang • Martin J. Aryee ? • Bradley E. Bernstein ? ¹¹ • Show all authors • Show footnotes		Res	Cancer	Genome	Торог	>
	Published: August 24, 2020 • DOI: https://doi.org/10.1016/j.cell.2020.07.030 • (R) Check for updates	Hum	Ran color	Normal Normal Normal	∵ ⊁ Plu	mX Metric	y xs



- The third compartment appears
- A and B compartments are mixed
- Epigenetic modifications restrain malignization

- 1. A and B compartments are "mixed" in the nuclei of tumour cells
- 2. The third "I" compartment appears: characterised by hypomethylation and polycomb H3K27me3 modification — this hypomethylation restrains oncogenes
- 3. Similar shifts were evident in non-malignant cells that have accumulated excess divisions



3. For more 3D-genomics insights I recommend The 3D genome Nature collection

nature research

nature > collection

COLLECTION | 02 SEPTEMBER 2019

The 3D genome

The three-dimensional configuration of the genome is complex, dynamic and crucial for gene regulation. In the past few years, technological advances in chromosome conformation capture methods and in microscopy techniques revealed how the organization of the genome is interconnected with nuclear architecture and can vary between cell types and during cell differentiation and development. This collection includes recent articles from across the Nature group of journals and showcases both the latest advances in the methodologies used to study genome organization, and our recent understanding of how genome organization and nuclear architecture regulate gene expression, cell fate and cell function in physiology and disease. The content of this collection has been chosen by the editors of *Nature Reviews Molecular Cell Biology*. show less





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Reviews

REVIEW ARTICLE 17 DEC 2019 Nature Reviews Genetics	Methods for mapping 3D chromosome architecture How chromosomes are positioned and folded within the nucleus has implications for gene regulation. In this Review, Kempfer and Pombo describe and evaluate methods for studying chromosome architecture and outline the insights they are providing about nuclear organization. Rieke Kempfer & Ana Pombo	
REVIEW ARTICLE 2 SEP 2019 Nature Reviews Molecular Cell Biology	Control of DNA replication timing in the 3D genome Different genomic regions are replicated at different times during the S phase of the cell cycle, forming early- and late-replicating domains that occupy different locations in the nucleus. The recent identification of specific DNA sequences and long non-coding RNAs show more Claire Marchal, Jiao Sima & David M. Gilbert	
REVIEW ARTICLE 13 JUN 2019 Nature Reviews Molecular Cell Biology	The role of 3D genome organization in development and cell differentiation The 3D organization of the genome is crucial for gametogenesis, embryogenesis and cell differentiation through its modulation of transcription, DNA replication and cell division. Recent studies have highlighted the roles of 3D chromatin dynamics, such as the show more Hui Zheng & Wei Xie	Nederative Decremente Retrieve Decremente De
REVIEW ARTICLE 13 MAY 2019 Nature Reviews Genetics	Long-range enhancer–promoter contacts in gene expression control For appropriate control of gene expression, enhancers must communicate with the right target genes at the right time, typically over large genomic distances. In this Review, Schoenfelder and Fraser discuss our latest understanding of long-range enhancer–promoter show more	

Stefan Schoenfelder & Peter Fraser