



Photo by David Oliete - [www.davidoliête.com](http://www.davidoliете.com)

Chromatin and 3C approaches

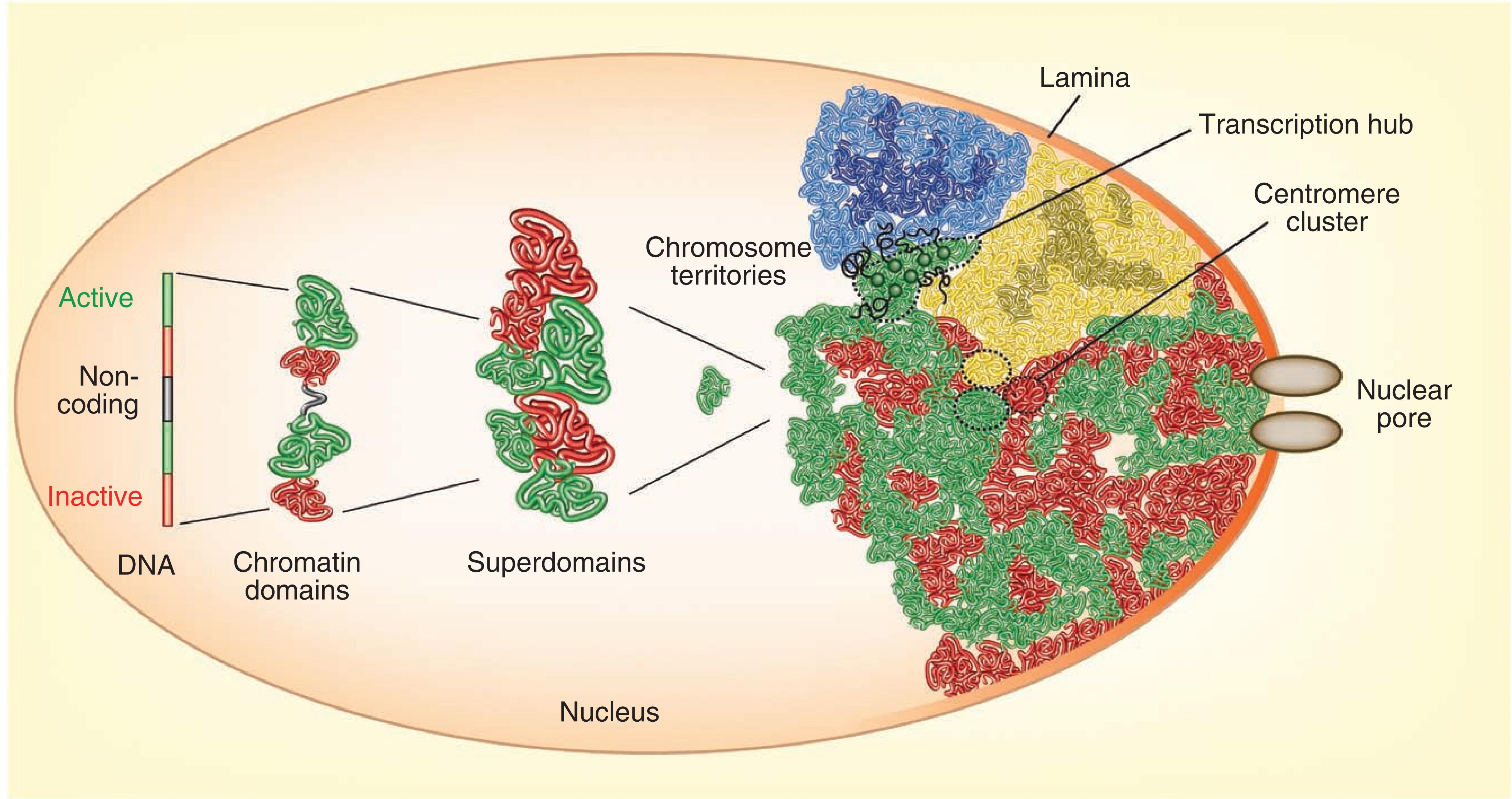
Marc A. Martí-Renom
CNAG-CRG · ICREA

<http://marciuslab.org>
<http://3DGenomes.org>
<http://cnag.crg.eu>

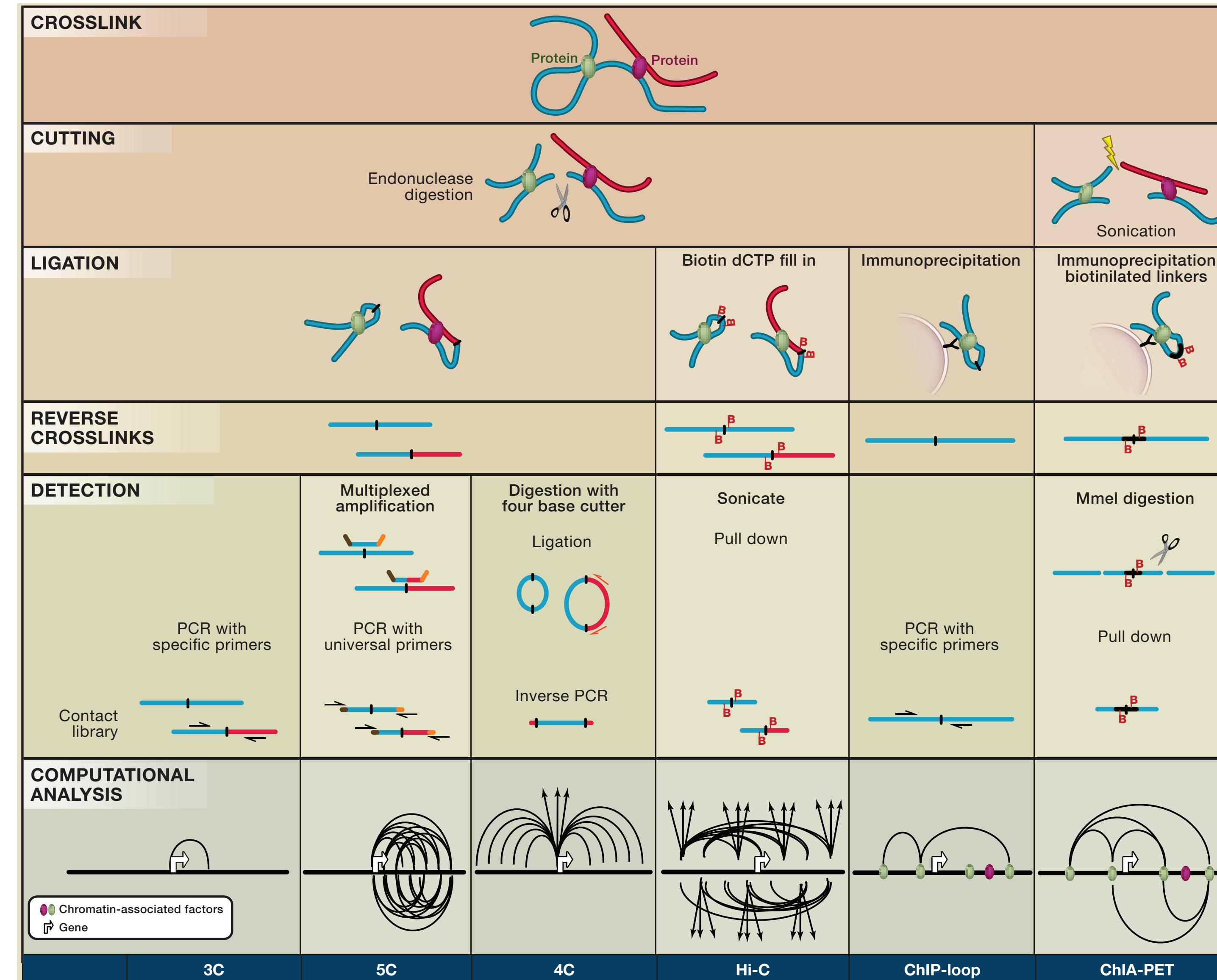
cnag CRG · ICREA

Complex genome organization

Cavalli, G. & Misteli, T. Functional implications of genome topology. *Nat Struct Mol Biol* 20, 290–299 (2013).



Chromosome Conformation Capture



ARTICLE

doi:10.1038/nature12593

Single-cell Hi-C reveals cell-to-cell variability in chromosome structure

Takashi Nagano^{1*}, Yaniv Lubling^{2*}, Tim J. Stevens^{3*}, Stefan Schoenfelder¹, Eitan Yaffe², Wendy Dean⁴, Ernest D. Lue³, Amos Tanay² & Peter Fraser¹

LETTER

doi:10.1038/nature20158

Capturing pairwise and multi-way chromosomal conformations using chromosomal walks

Pedro Olivares-Chauvet¹, Zohar Mukamel¹, Aviezer Lifshitz¹, Omer Schwartzman¹, Noa Oded Elkayam¹, Yaniv Lubling¹, Gintaras Deikus², Robert P. Sebra³ & Amos Tanay¹

nature
genetics

ARTICLES

<https://doi.org/10.1038/s41588-018-0161-5>

Enhancer hubs and loop collisions identified from single-allele topologies

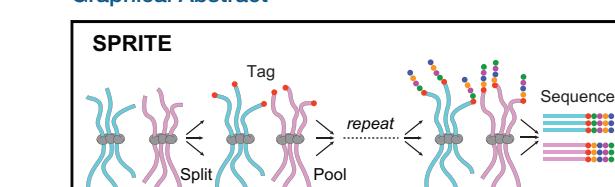
Amin Allahyar^{1,2}, Carlo Vermeulen^{3,7}, Britta A. M. Bouwman³, Peter H. L. Krijger³, Marjon J. A. M. Versteegen³, Geert Geenen³, Melissa van Kranenburg³, Mark Pieterse³, Roy Straver^{3,1}, Judith H. I. Haarhuis⁴, Kees Jalink⁵, Hans Teunissen⁶, Ivo J. Renkens¹, Wigard P. Kloosterman¹, Benjamin D. Rowland¹, Elzo de Wit⁶, Jeroen de Ridder^{3,*} and Wouter de Laat^{3*}

Resource

Cell

Higher-Order Inter-chromosomal Hubs Shape 3D Genome Organization in the Nucleus

Graphical Abstract



Authors
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ARTICLE

DOI: 10.1038/s41467-018-06961-0 OPEN

Chromatin conformation analysis of primary patient tissue using a low input Hi-C method

Noelia Diaz¹, Kai Kruse¹, Tabea Erdmann², Annette M. Staiger^{3,4,5}, German Ott³, Georg Lenz² & Juan M. Vaquerizas¹

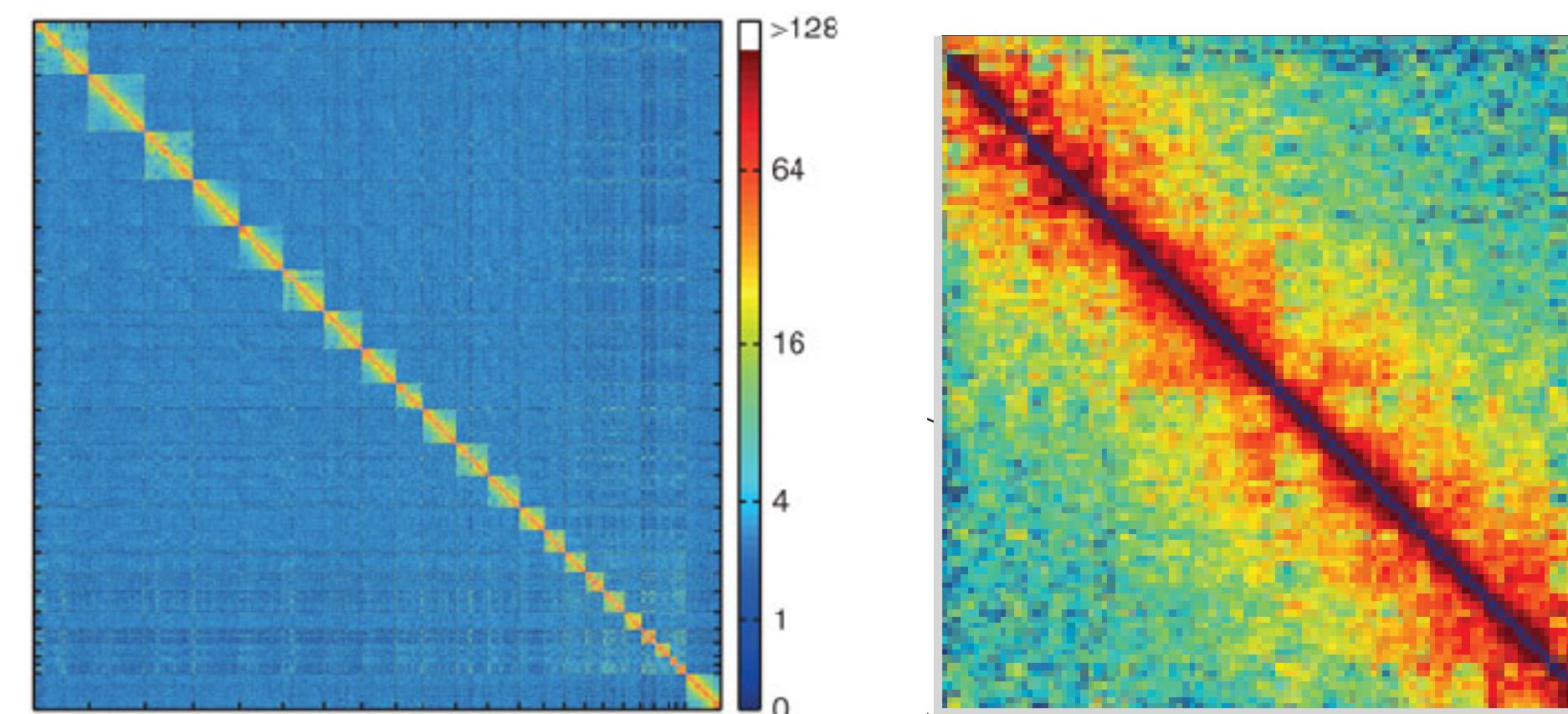
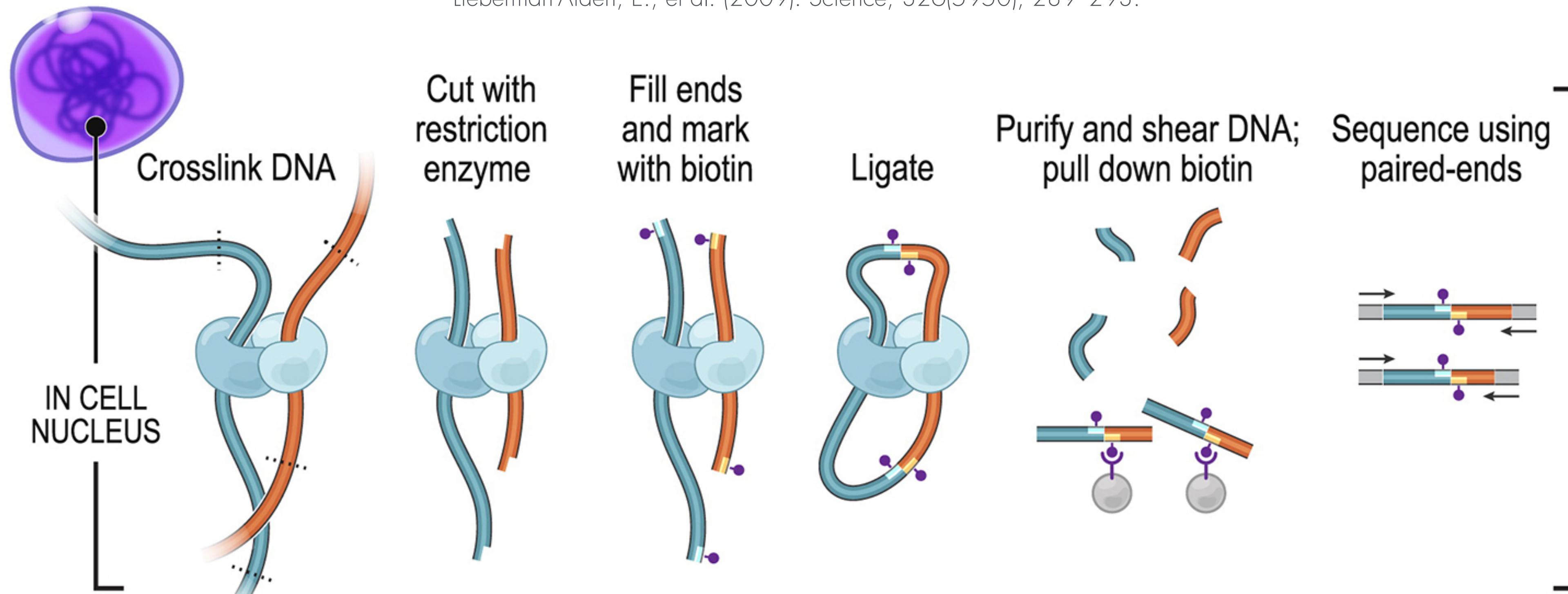
Compartment-dependent chromatin interaction dynamics revealed by liquid chromatin Hi-C

Houda Belaghzal¹, Tyler Borrman², Andrew D. Stephens³, Denis L. Lafontaine¹, Sergey V. Veney¹, Zhiping Weng³, John F. Marko^{3,4}, Job Dekker^{1,5,6#}

Chromosome Conformation Capture

Dekker, J., Rippe, K., Dekker, M., & Kleckner, N. (2002). Science, 295(5558), 1306–1311.

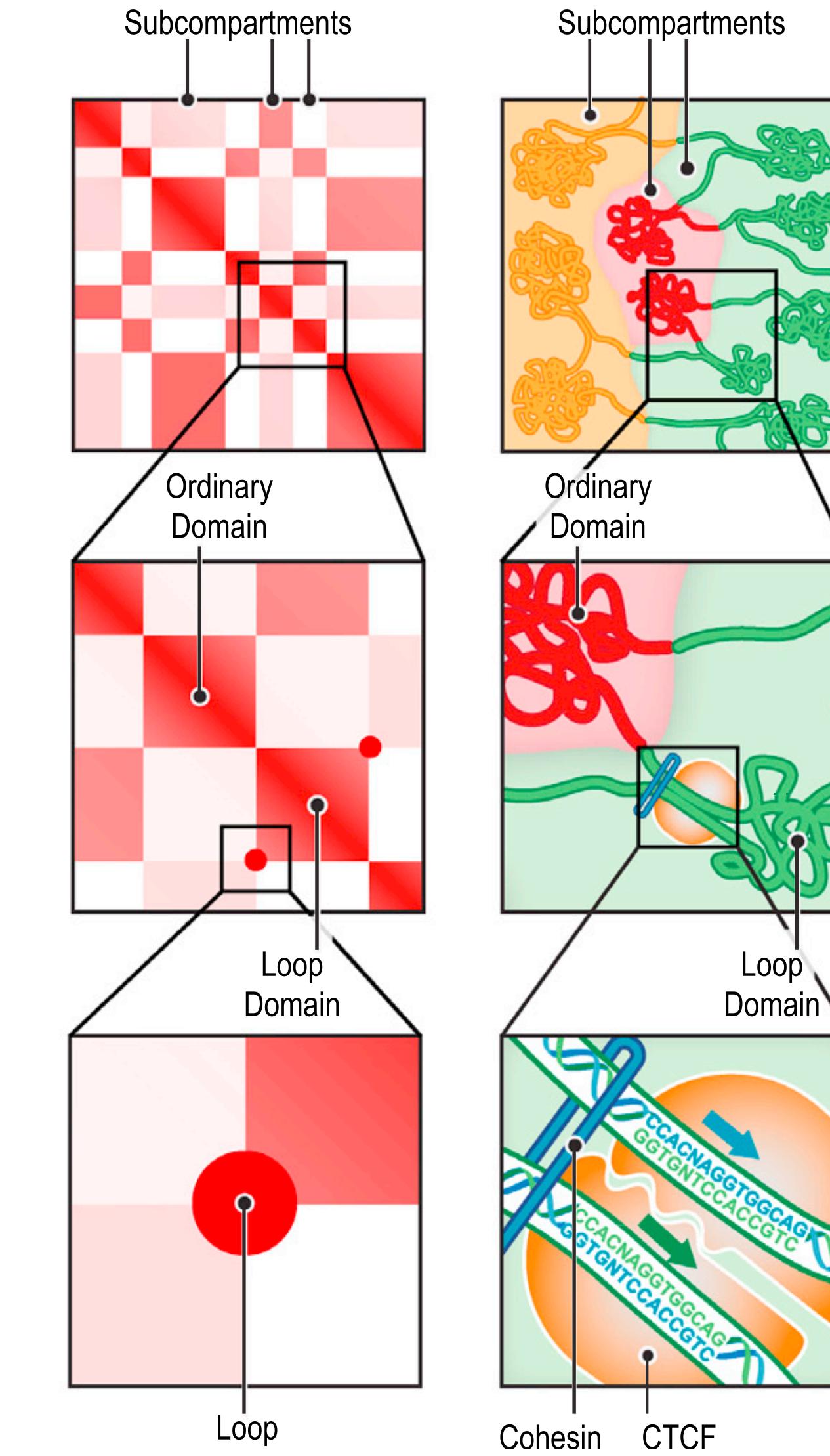
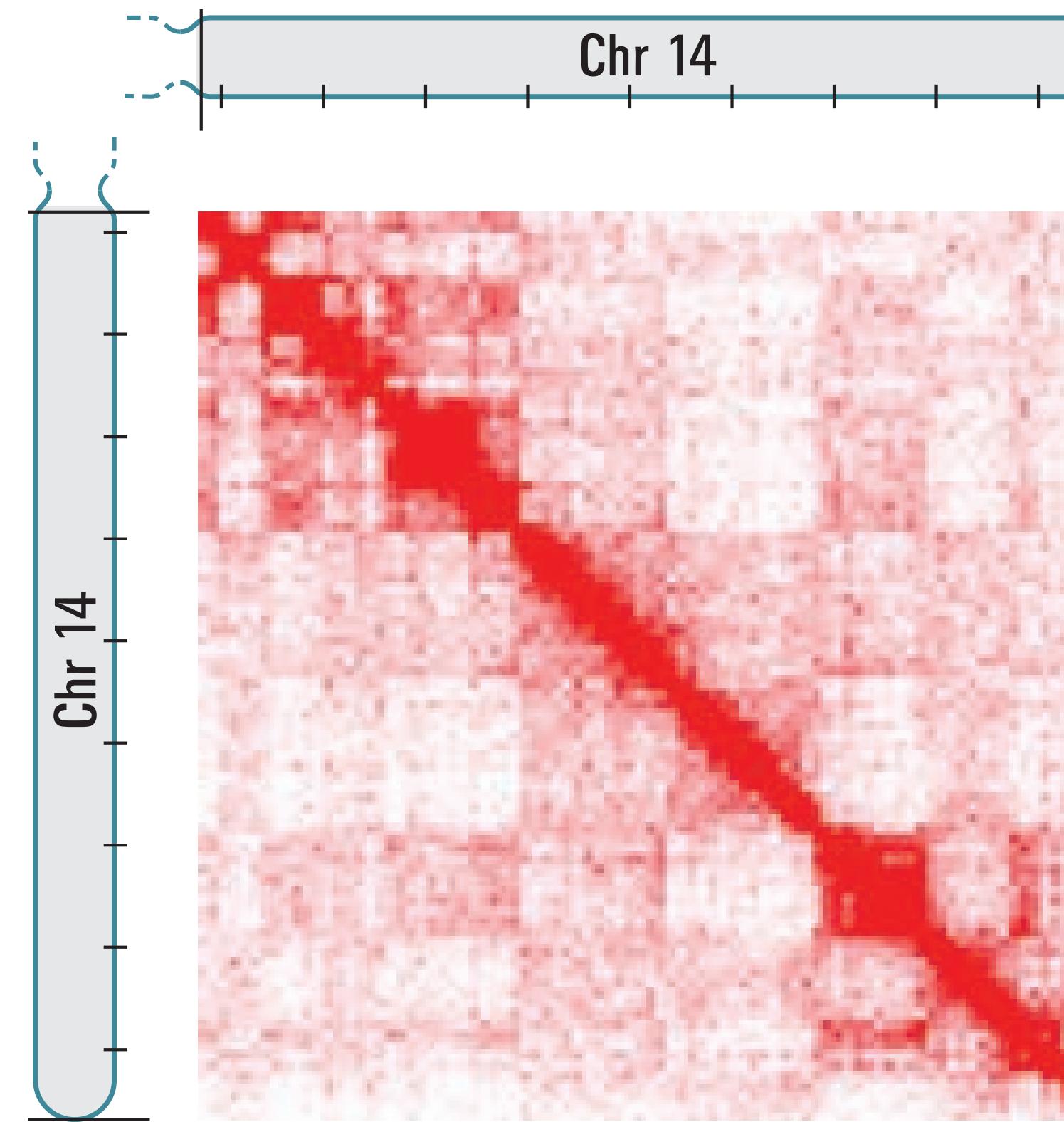
Lieberman-Aiden, E., et al. (2009). Science, 326(5950), 289–293.



Hierarchical genome organisation

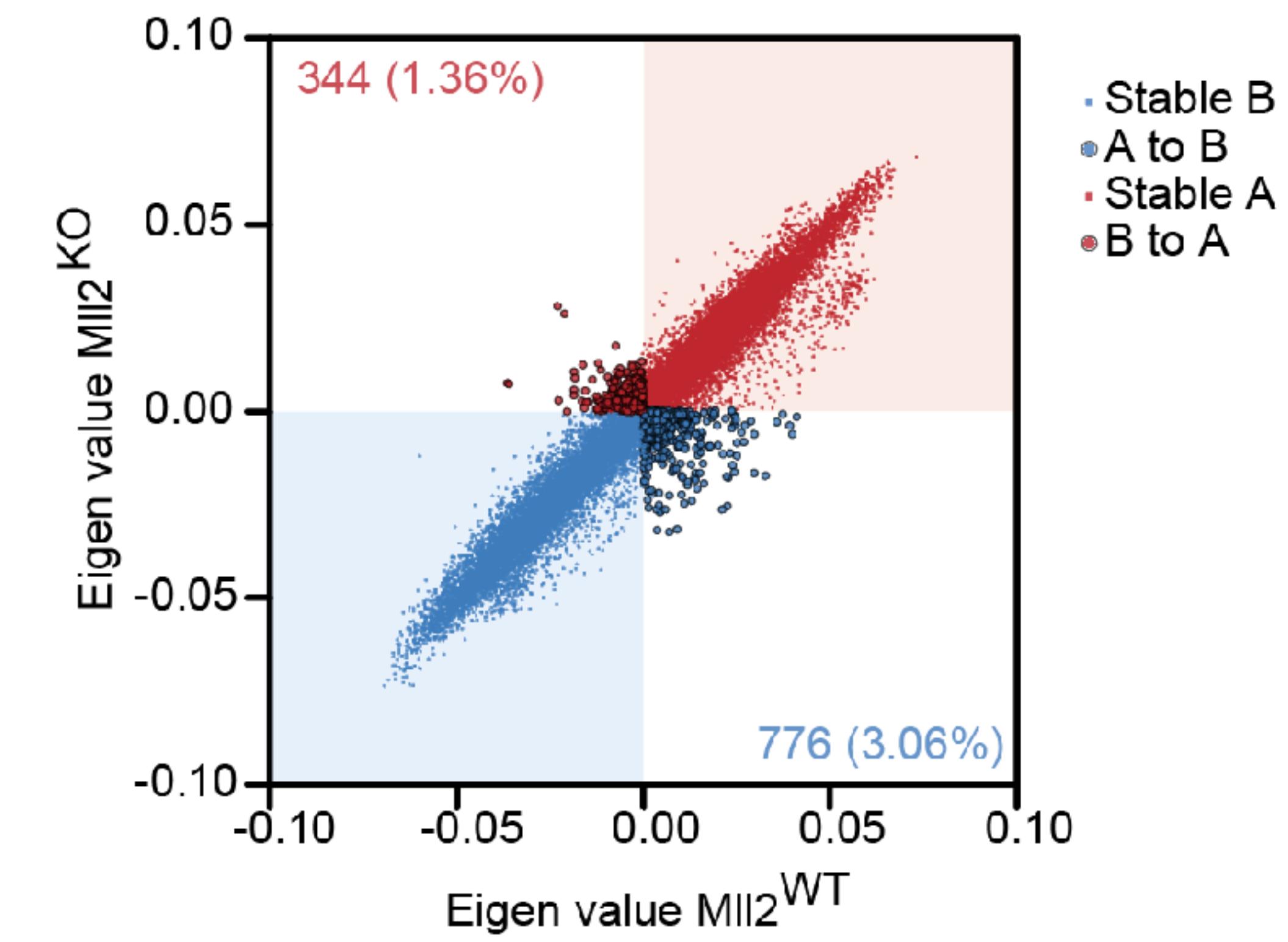
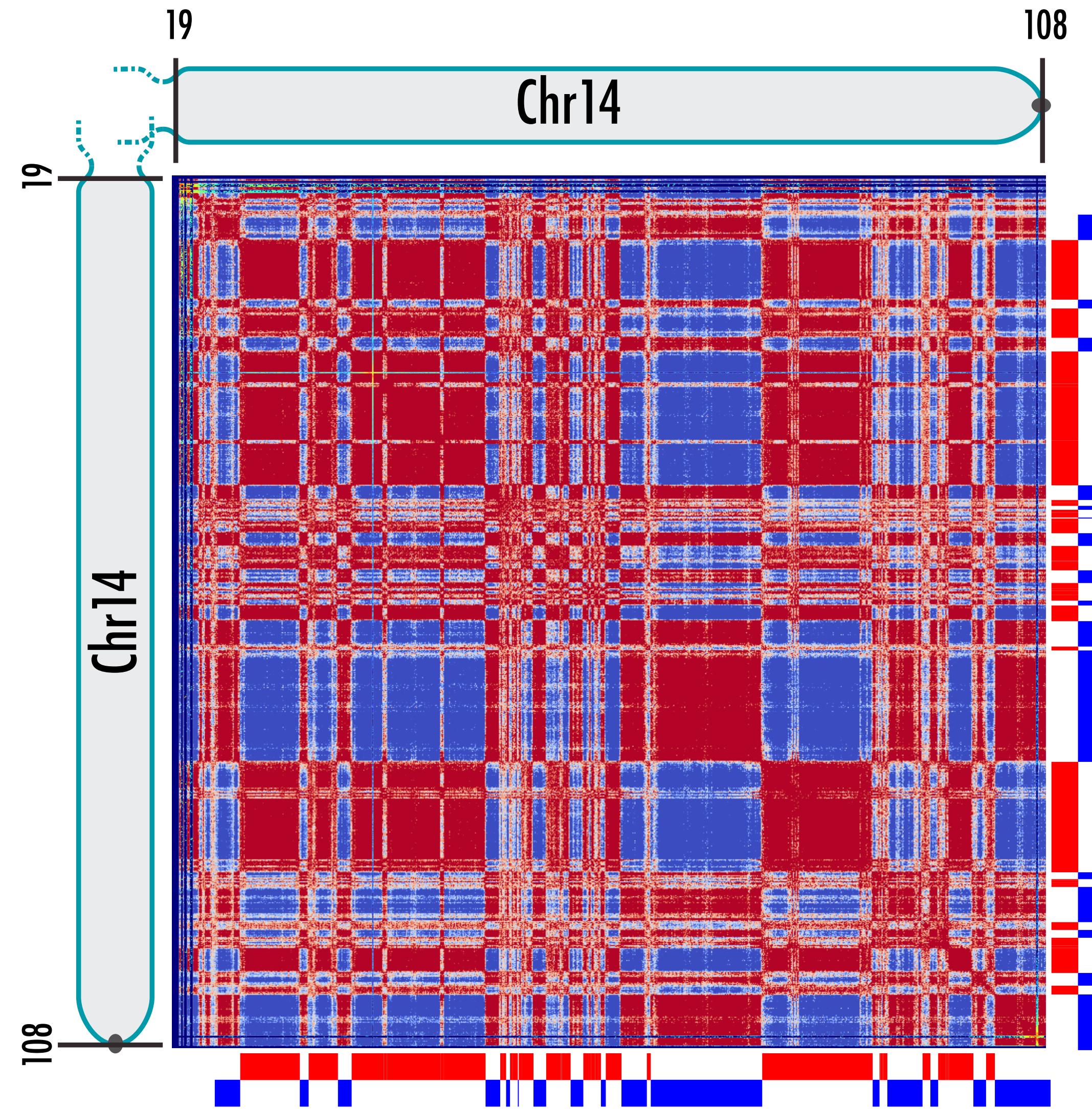
Lieberman-Aiden, E., et al. (2009). Science, 326(5950), 289–293.

Rao, S. S. P., et al. (2014). Cell, 1–29.



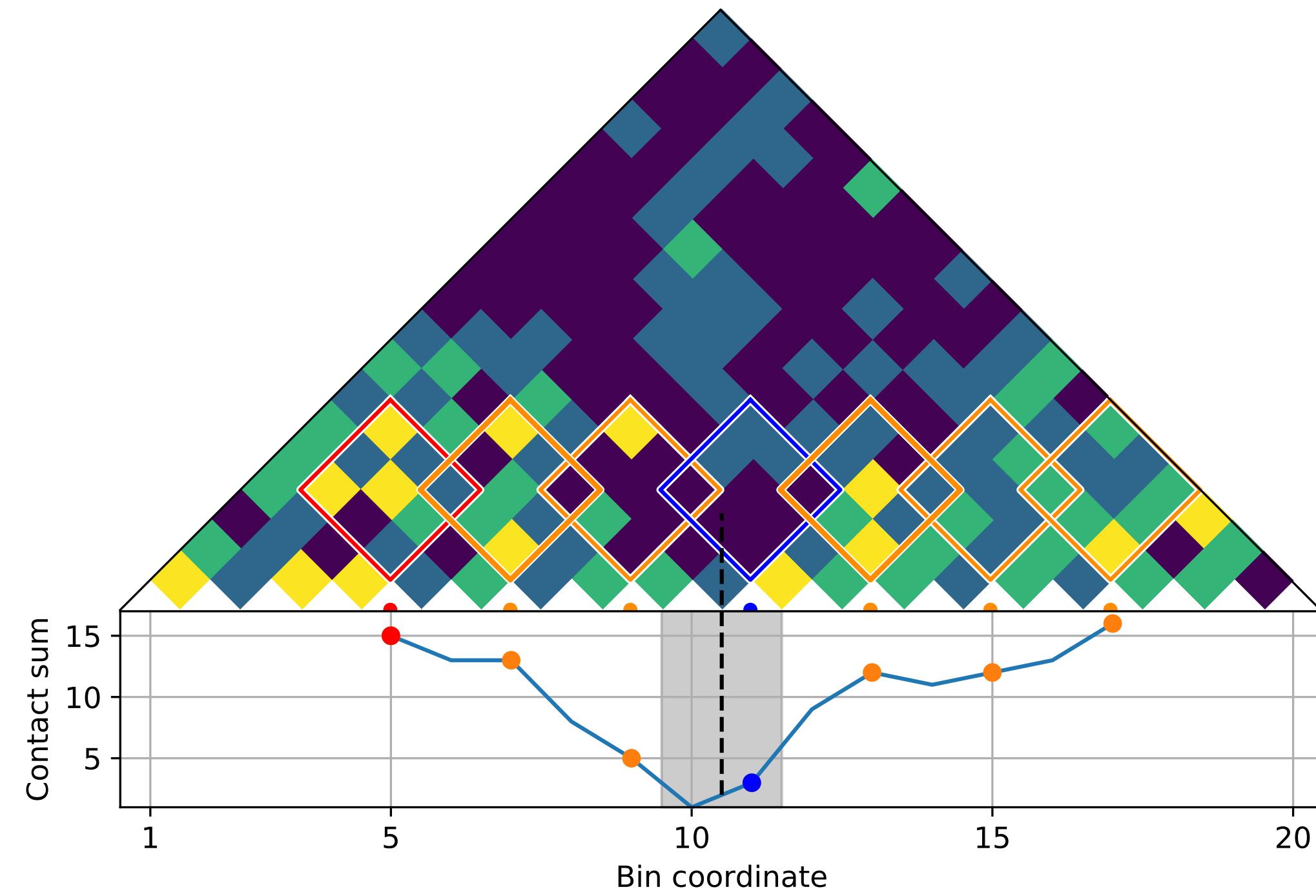
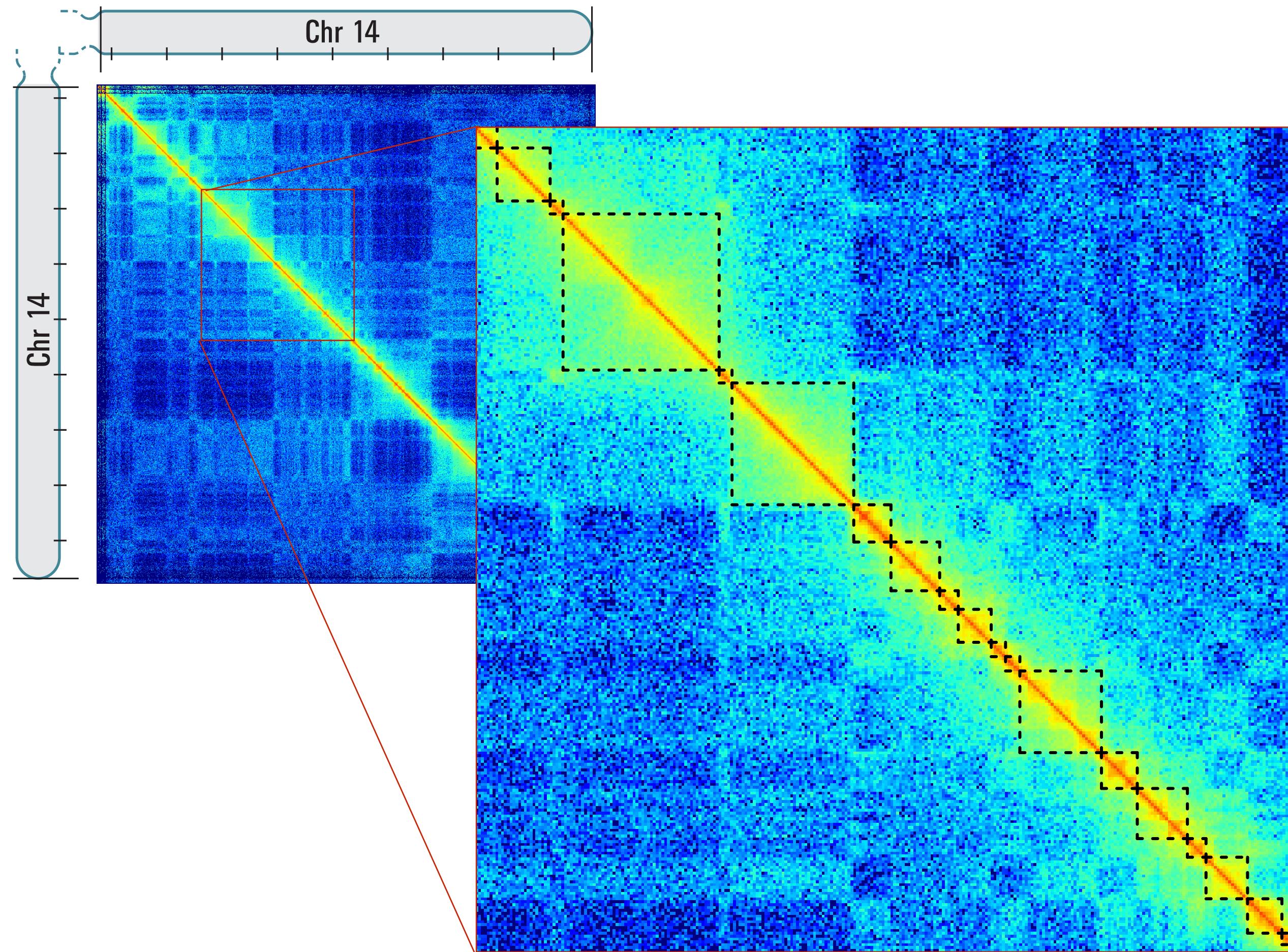
A/B Compartiment

Chromosome 14



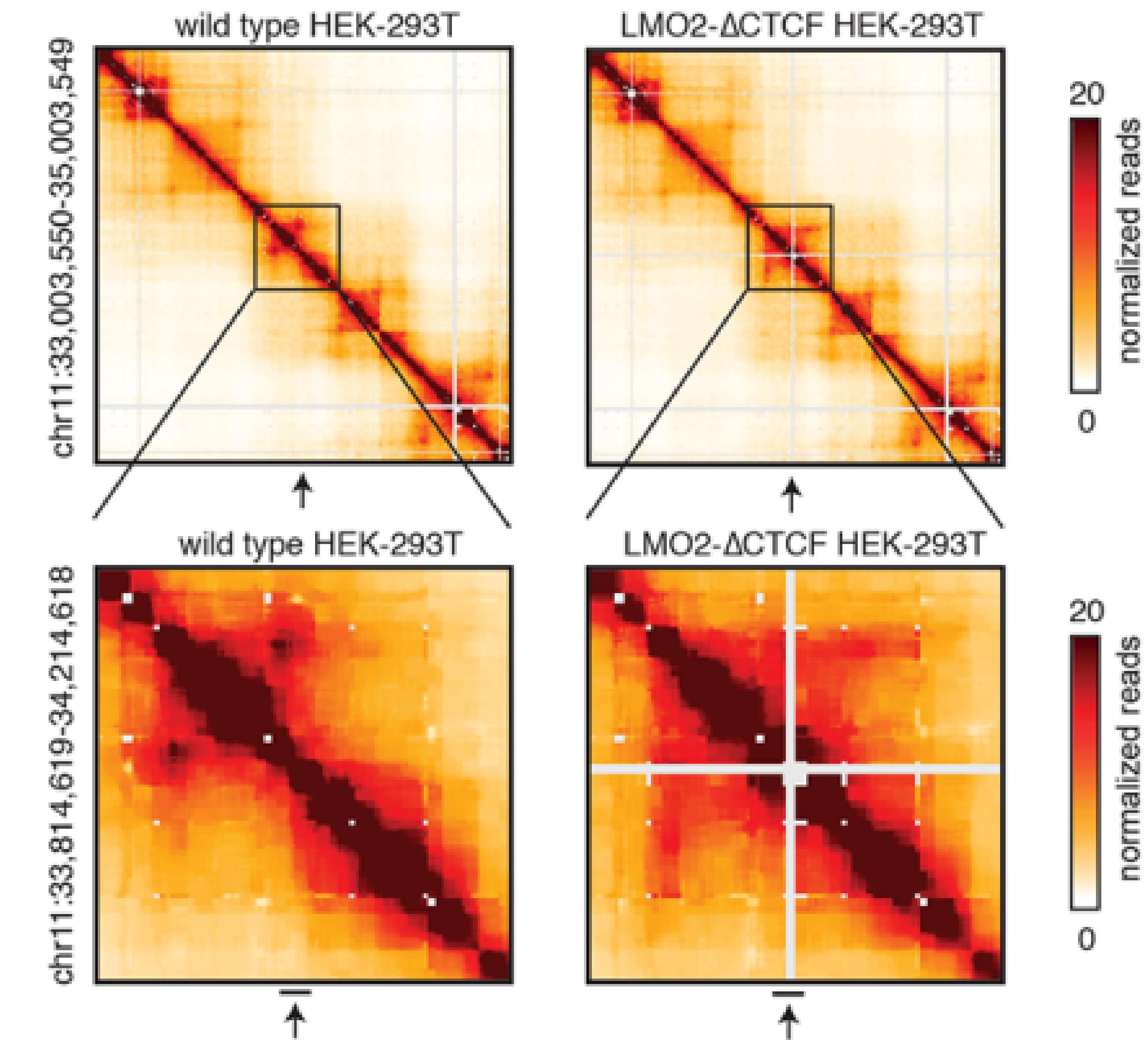
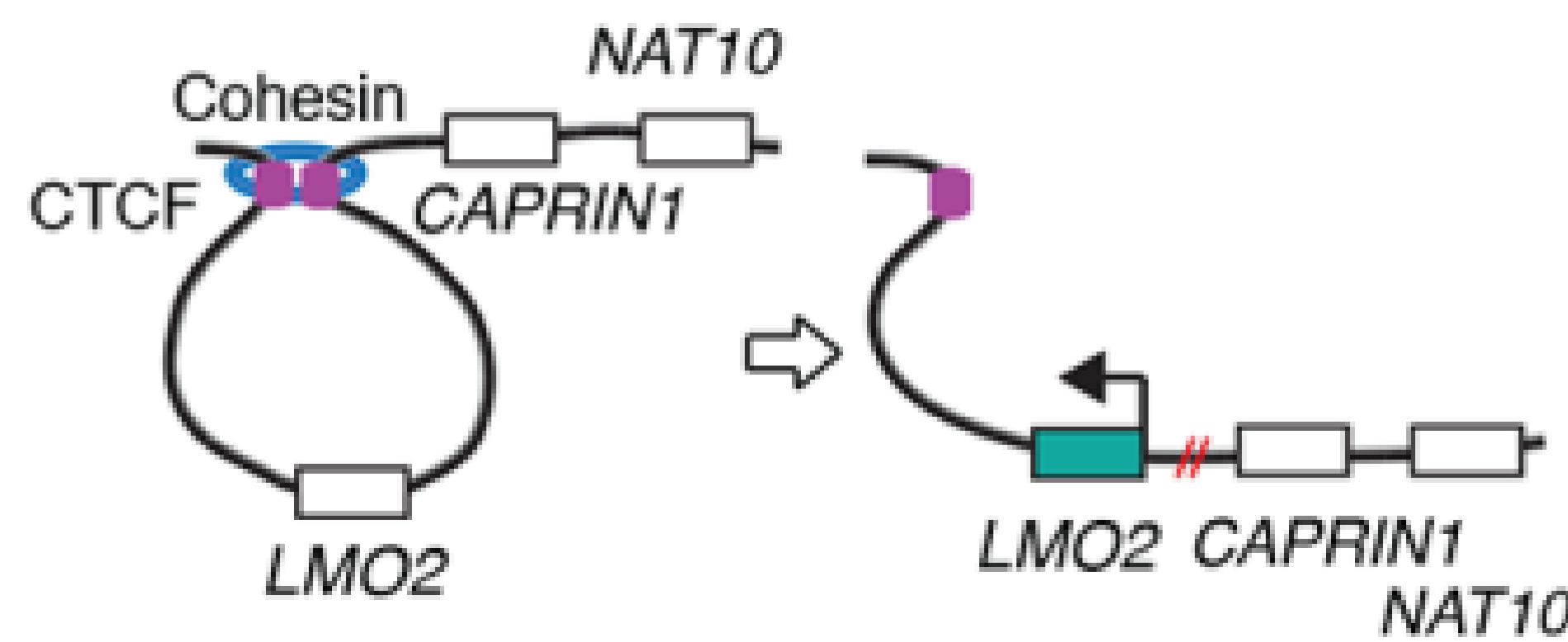
TADs

Chromosome 14



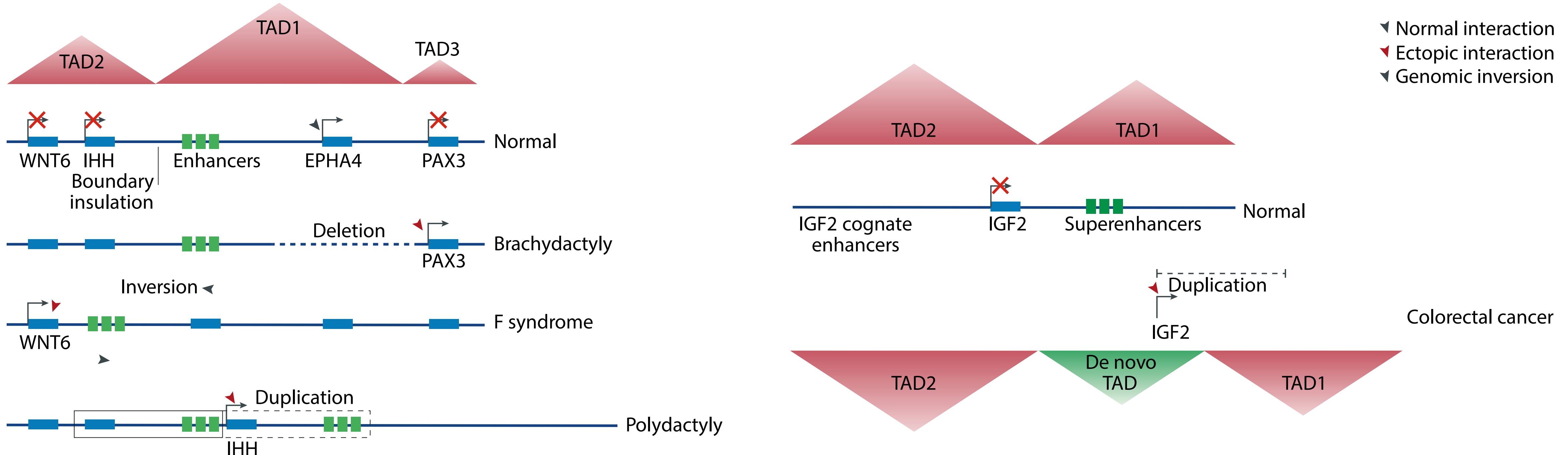
TADs are functional units

Hnisz, D., et al. (2016). Science



TADs are functional units

Figure adapted from Hui Zheng and Wei Xie. *Nature Reviews Molecular Cell Biology* (2019)

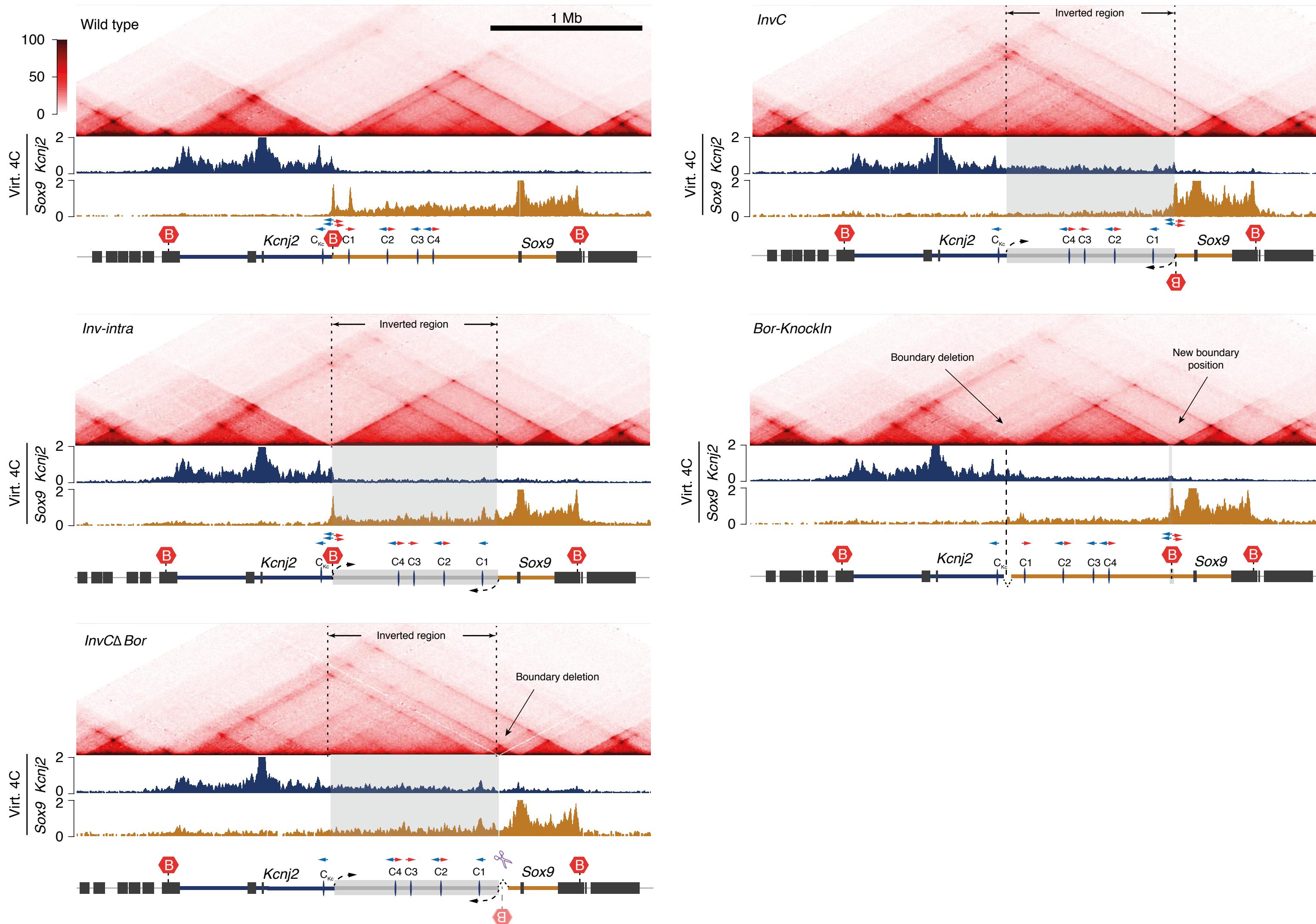


Lupianez, D. G. et al. *Cell* 161, 1012–1025 (2015)

Flavahan, W. A. et al. *Nature* 529, 110–114 (2016).

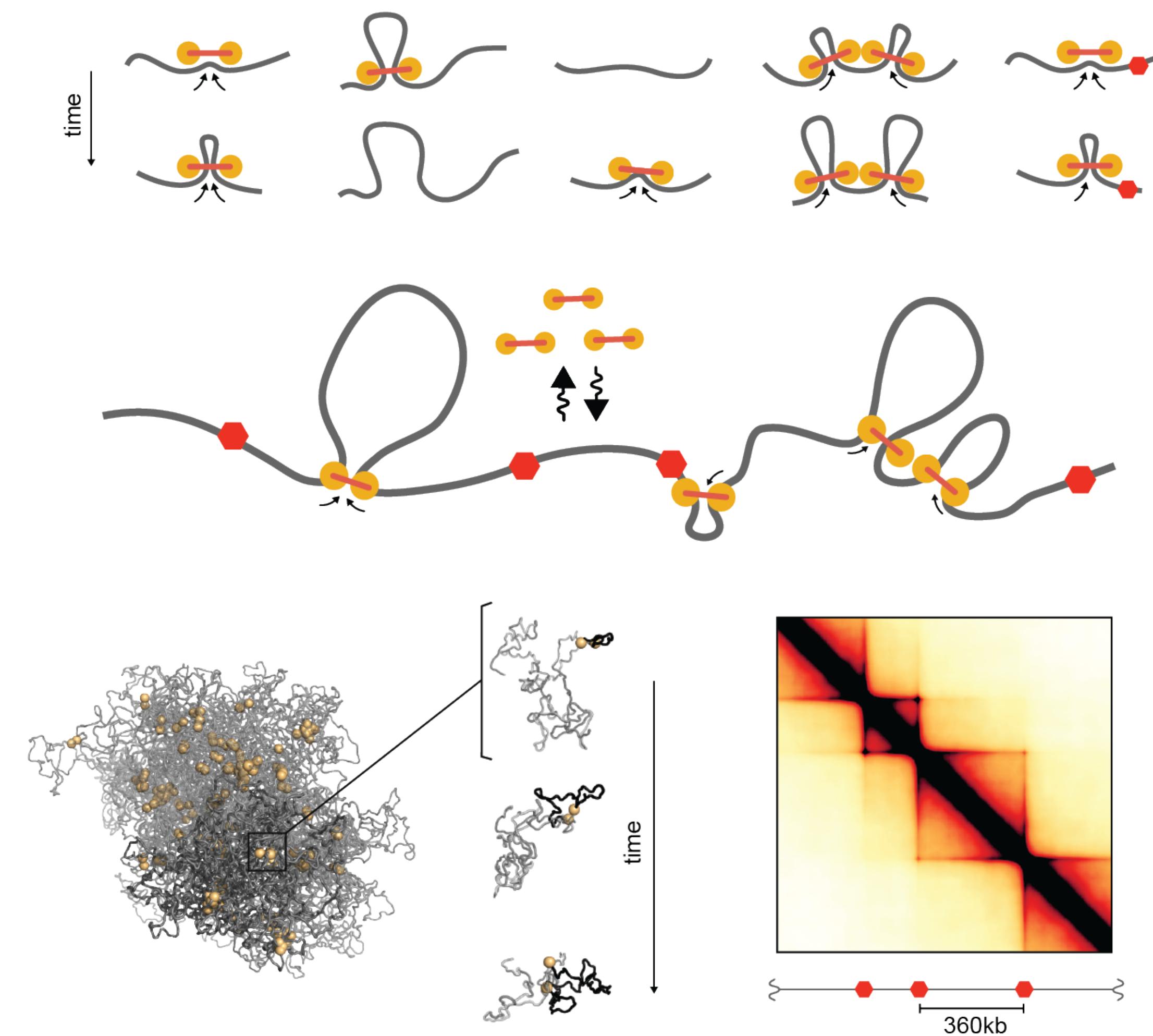
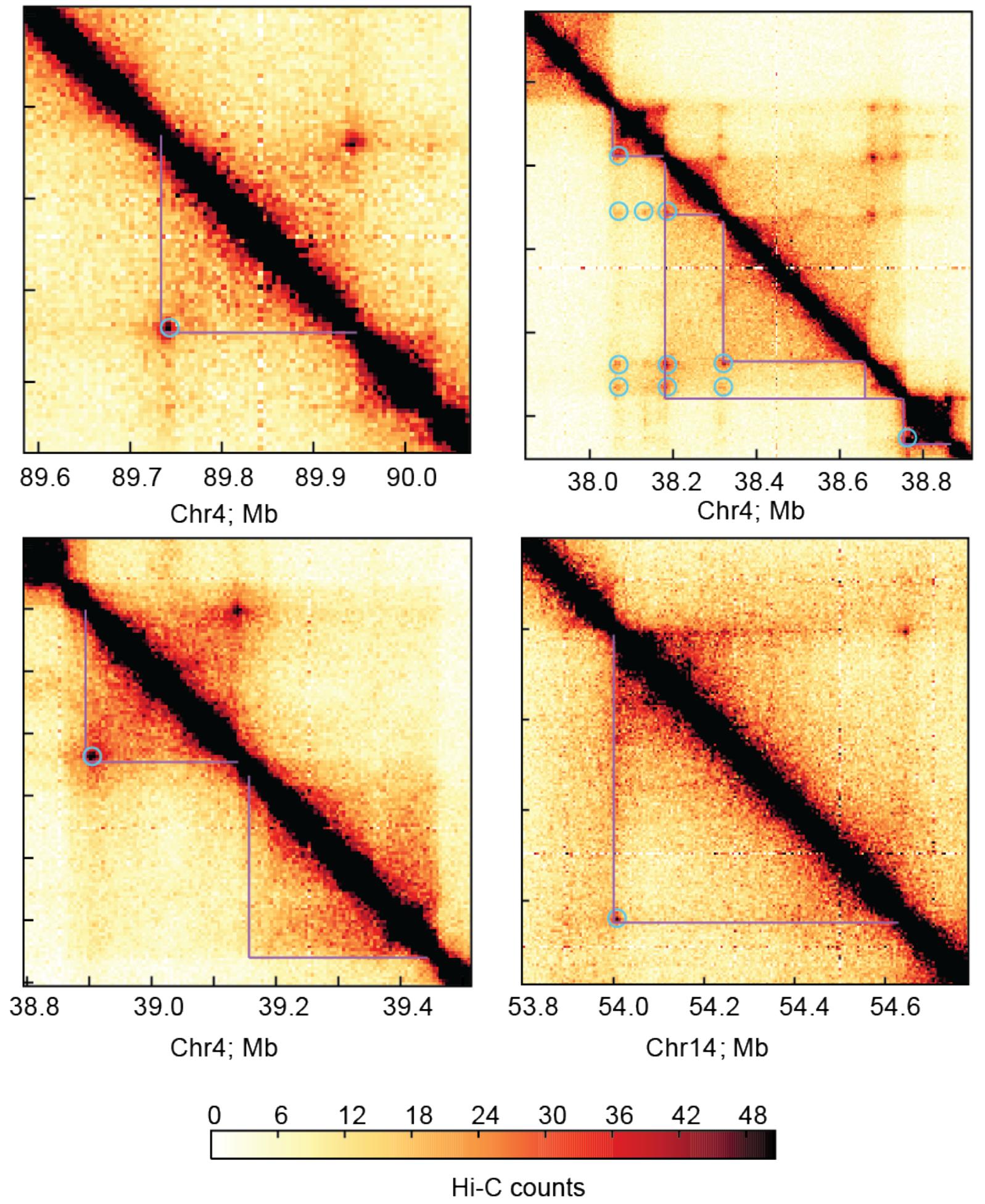
TADs are functional units

Despang, et al. (2019). Nature Genetics 51, 1263–1271 (2019)



Loop-extrusion as a TAD forming mechanism

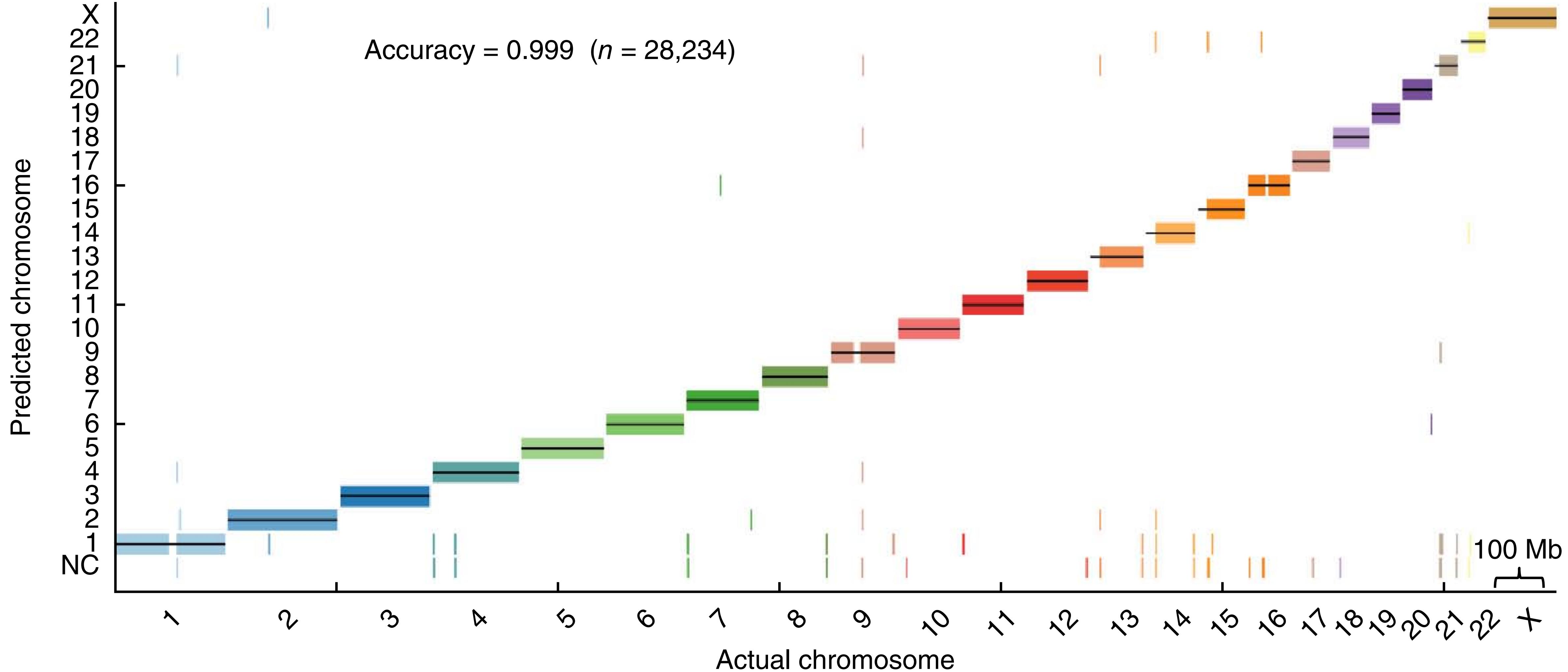
Fudenberg, G., Imakaev, M., Lu, C., Goloborodko, A., Abdennur, N., & Mirny, L. A. (2018).
Cold Spring Harb Symp Quant Biol 2017. 82: 45-55



SIDE EFFECTS

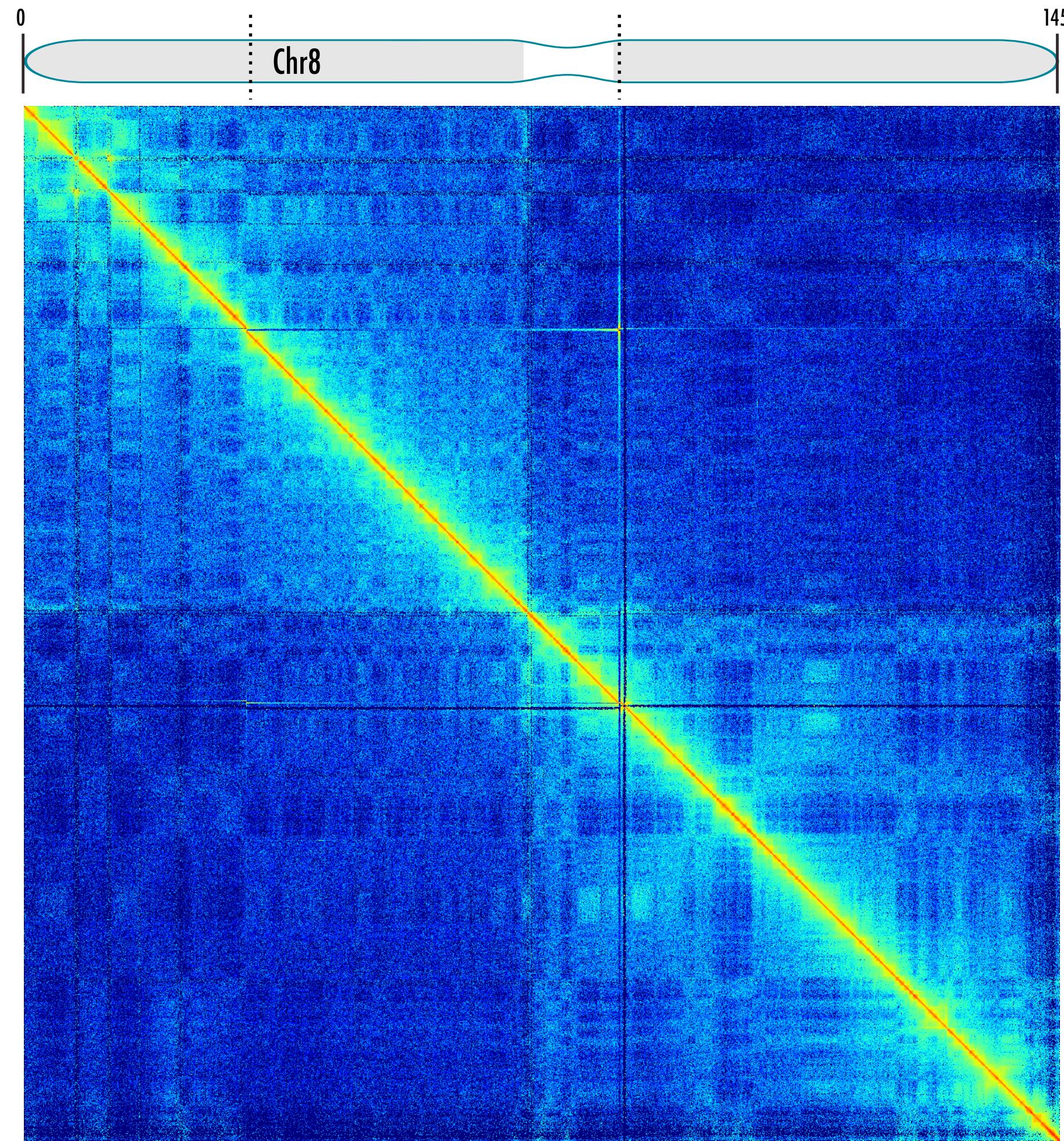
Hi-C for de-novo assembly

Kaplan, N., & Dekker, J. (2013). Nature Biotechnology, 31(12), 1143–1147.

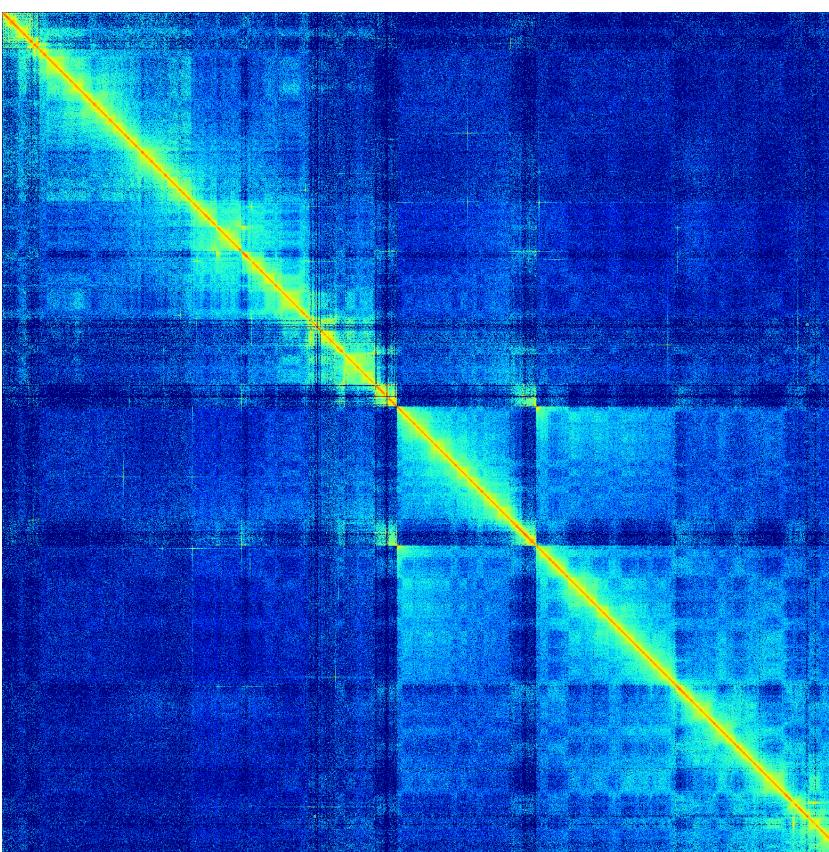


Assembly error detection

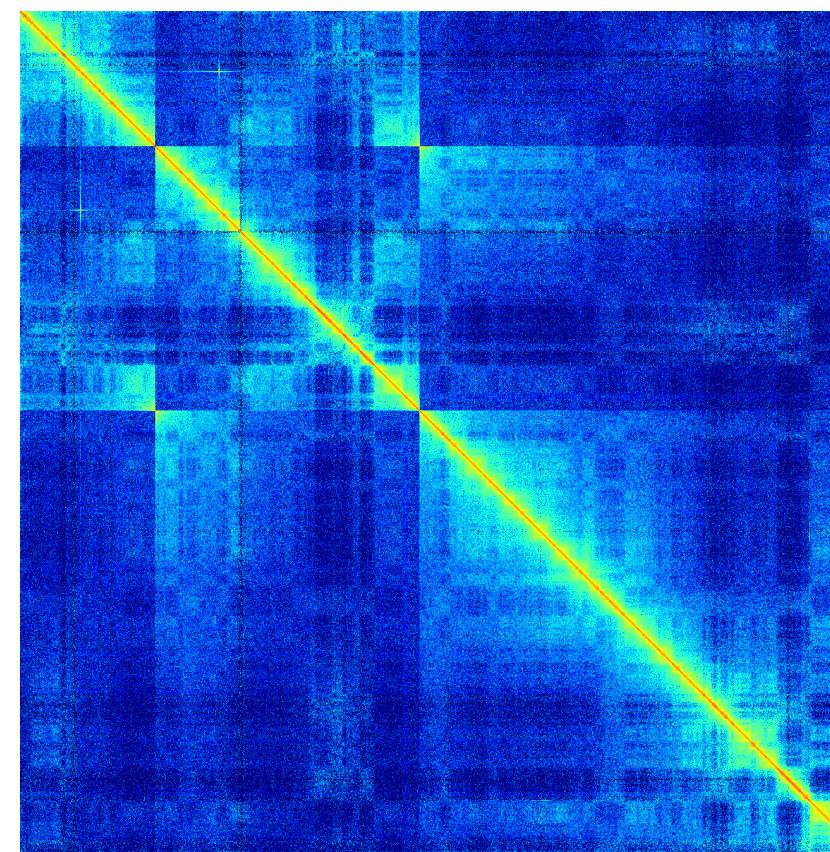
Chromosome 8 Gorilla



Chr 7



Chr 12



GGO8 has an inversion of the region corresponding to HSA8:30.0-86.9Mb
Aylwyn Scally (Department of Genetics, University of Cambridge)

Hi-C for meta genomics

Beitel, C. W., Froenicke, L., Lang, J. M., Korf, I. F., Michelmore, R. W., Eisen, J. A., & Darling, A. E. (2014). Strain- and plasmid-level deconvolution of a synthetic metagenome by sequencing proximity ligation products. doi:10.7287/peerj.preprints.260v1

Romain Koszul

