



Chromatin and 3C approaches

Marc A. Marti-Renom

CNAG-CRG · ICREA

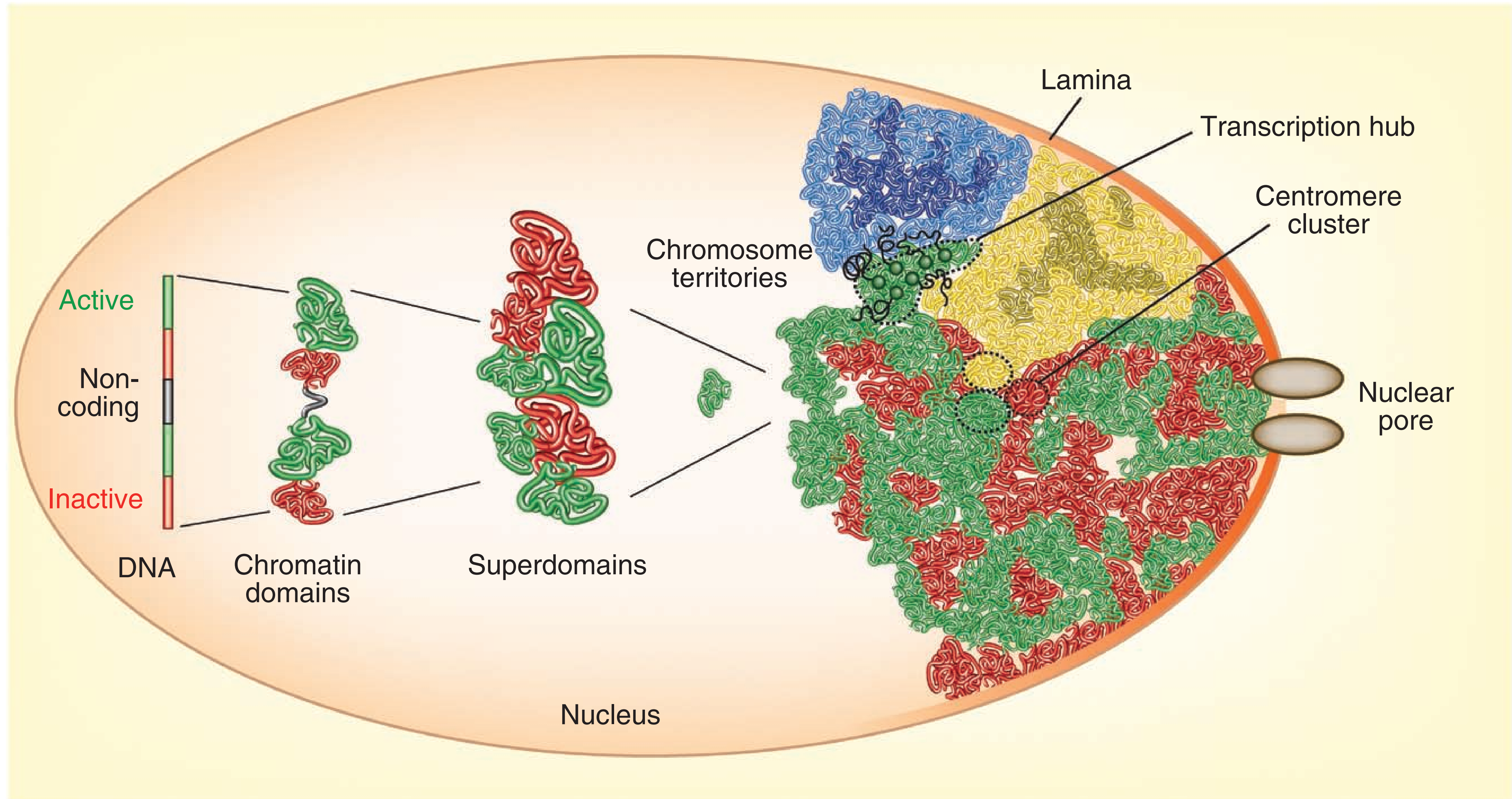
<http://marciuslab.org>
<http://3DGenomes.org>
<http://cnag.crg.eu>

cnag CRG[®] ICREA

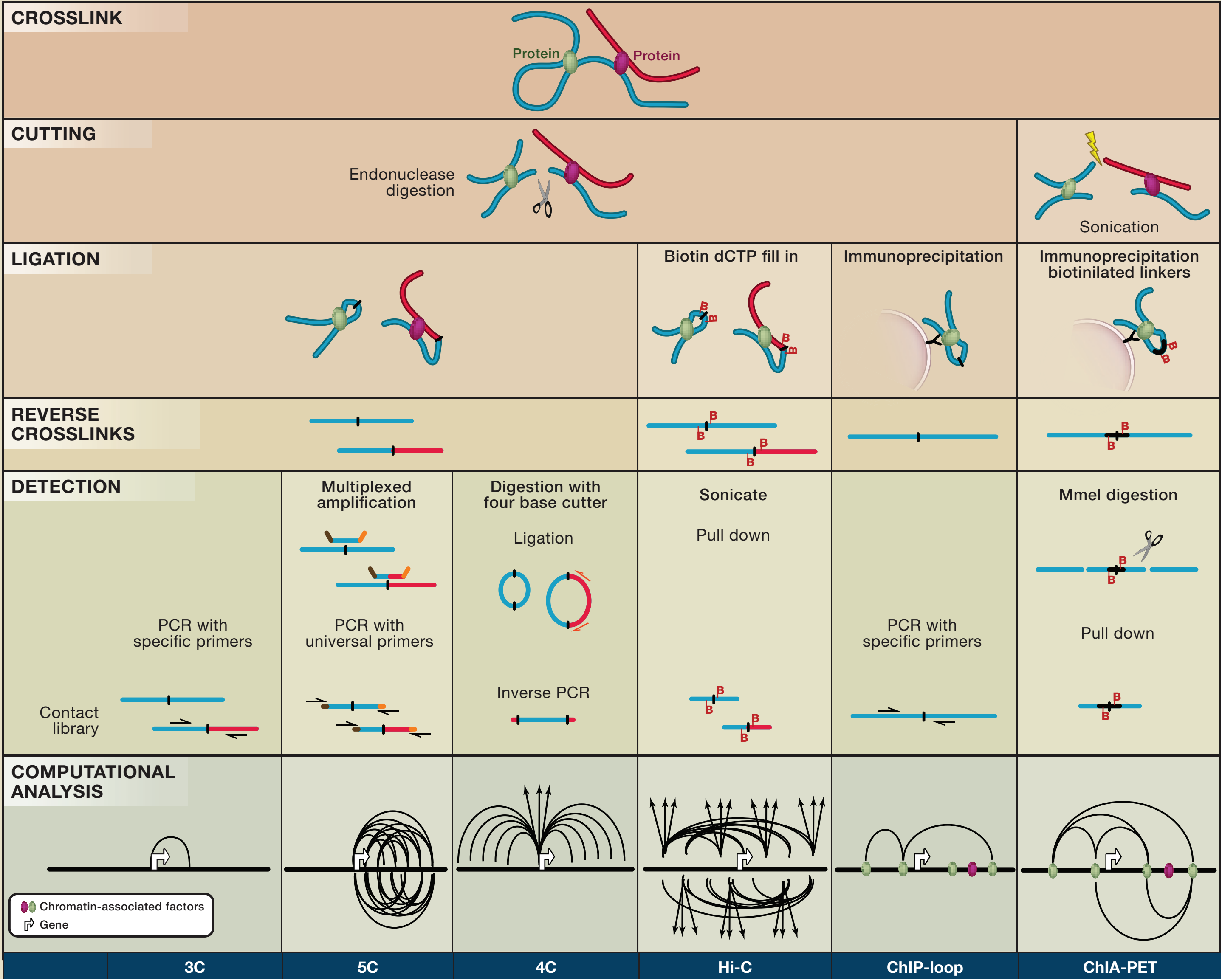
Photo by David Oliete - www.davidoliete.com

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. Laue³, Amos Tanay² & Peter Fraser²

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. Sebra² & Amos Tanay¹

ARTICLES

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

Enhancer hubs and loop collisions identified from single-allele topologies

Amin Allahyar^{1,2,7}, Carlo Vermeulen^{3,7}, Britta A. M. Bouwman³, Peter H. L. Krijger³, Marjon J. A. M. Versteegen³, Geert Geeven³, Melissa van Kranenburg³, Mark Pieterse³, Roy Straver³, Judith H. I. Haarhuis⁴, Kees Jalink⁵, Hans Teunissen⁶, Ivo J. Renkens¹, Wigard P. Kloosterman¹, Benjamin D. Rowland⁴, Elzo de Wit⁴, Jeroen de Ridder^{3*} and Wouter de Laat^{3*}

Cell

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

Graphical Abstract

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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 Díaz¹, Kai Kruse¹, Tabea Erdmann², Annette M. Staiger^{3,4,5}, German Ott³, Georg Lenz² & Juan M. Vaquerizas¹

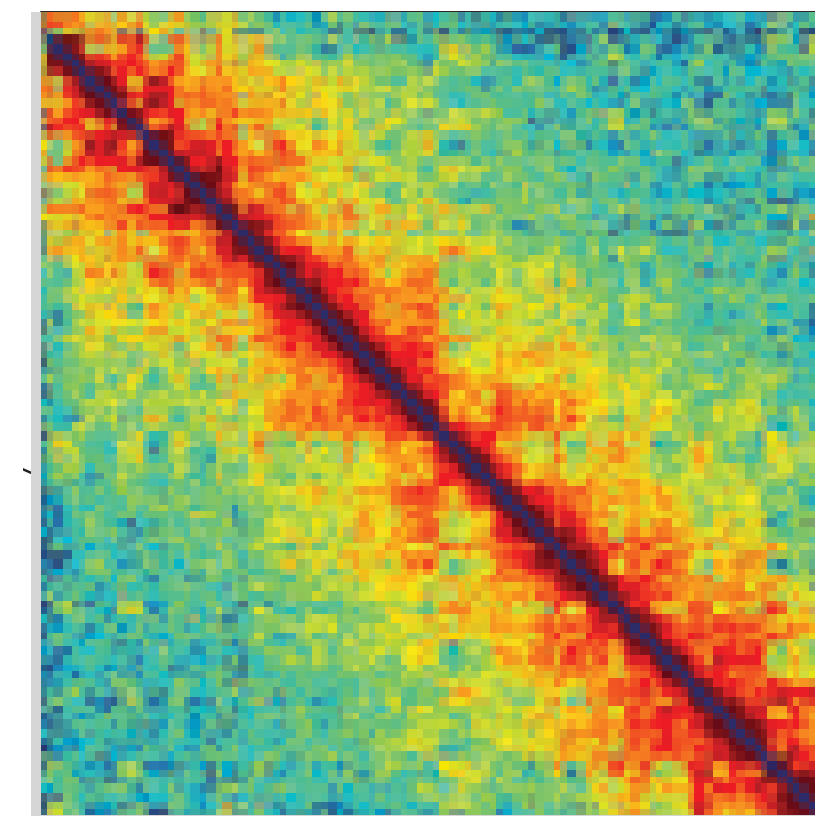
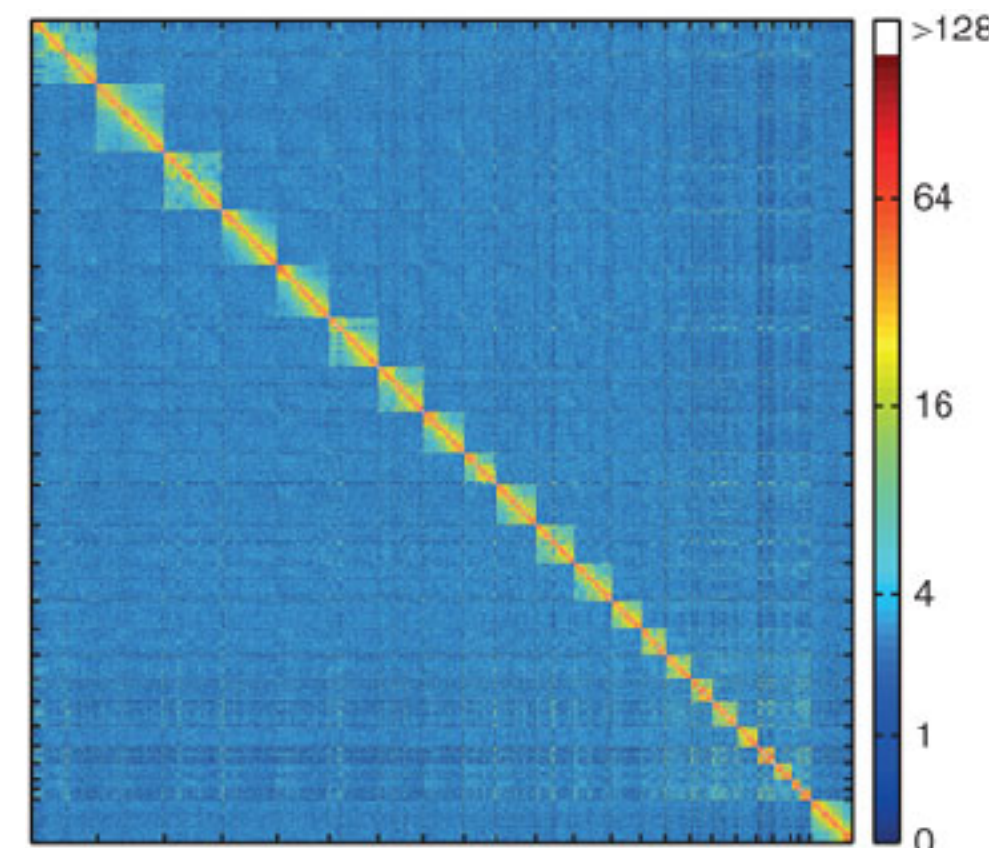
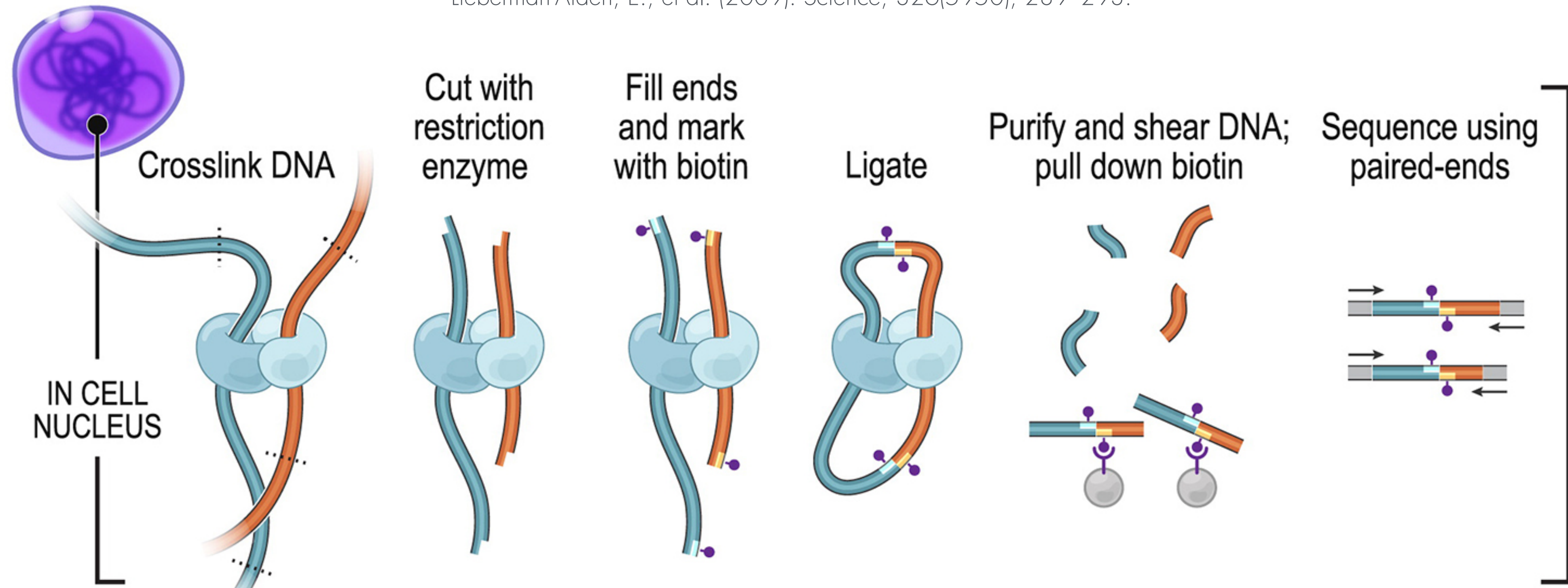
Compartment-dependent chromatin interaction dynamics revealed by liquid chromatin Hi-C

Houda Belaghzal^{1*}, Tyler Borrmann^{2*}, Andrew D. Stephens³, Denis L. Lafontaine¹, Sergey V. Venev¹, Zhiping Weng², 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.

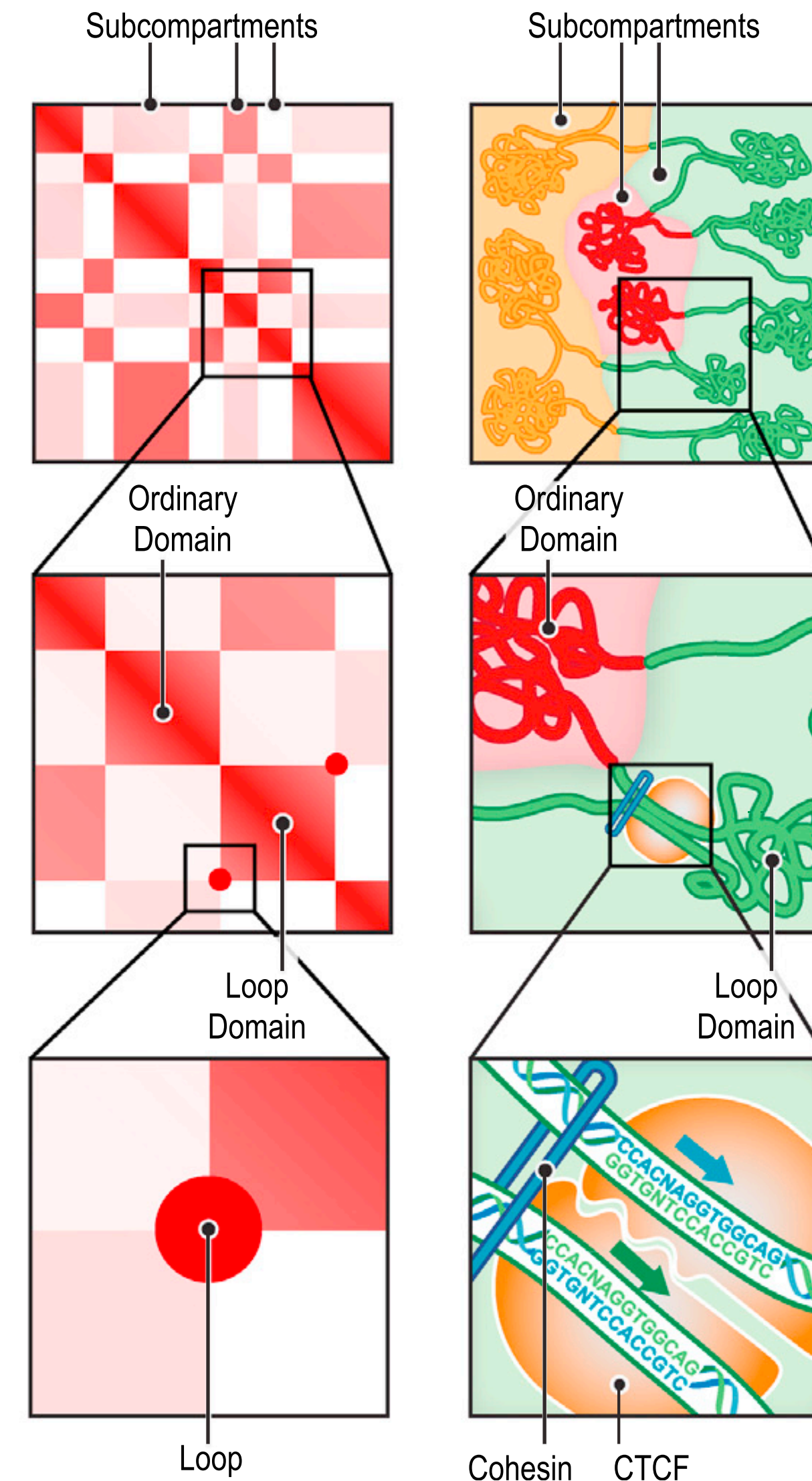
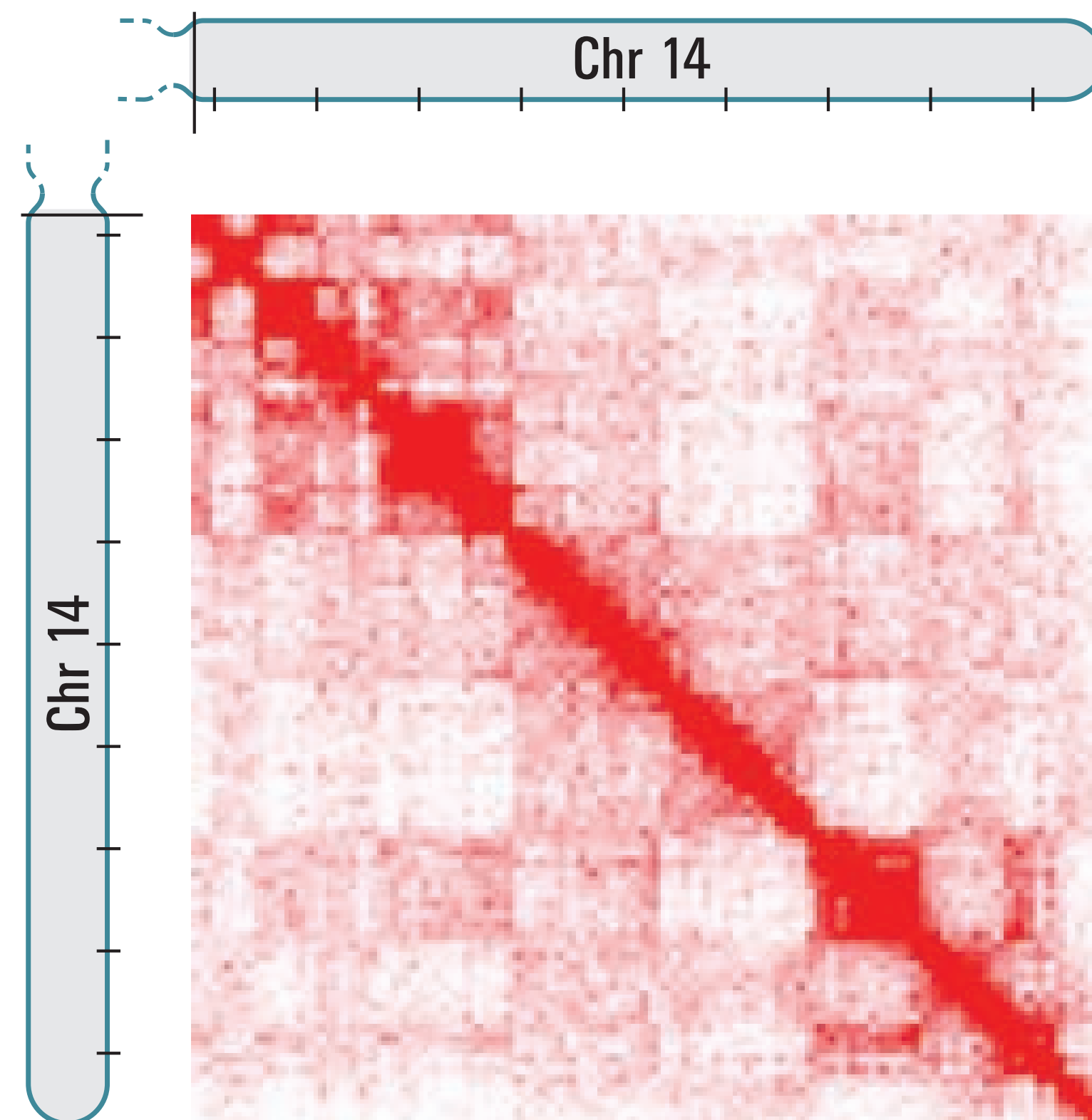
Lieberman-Aiden, E., et al. (2009). *Science*, 326(5950), 289–293.



Hierarchical genome organisation

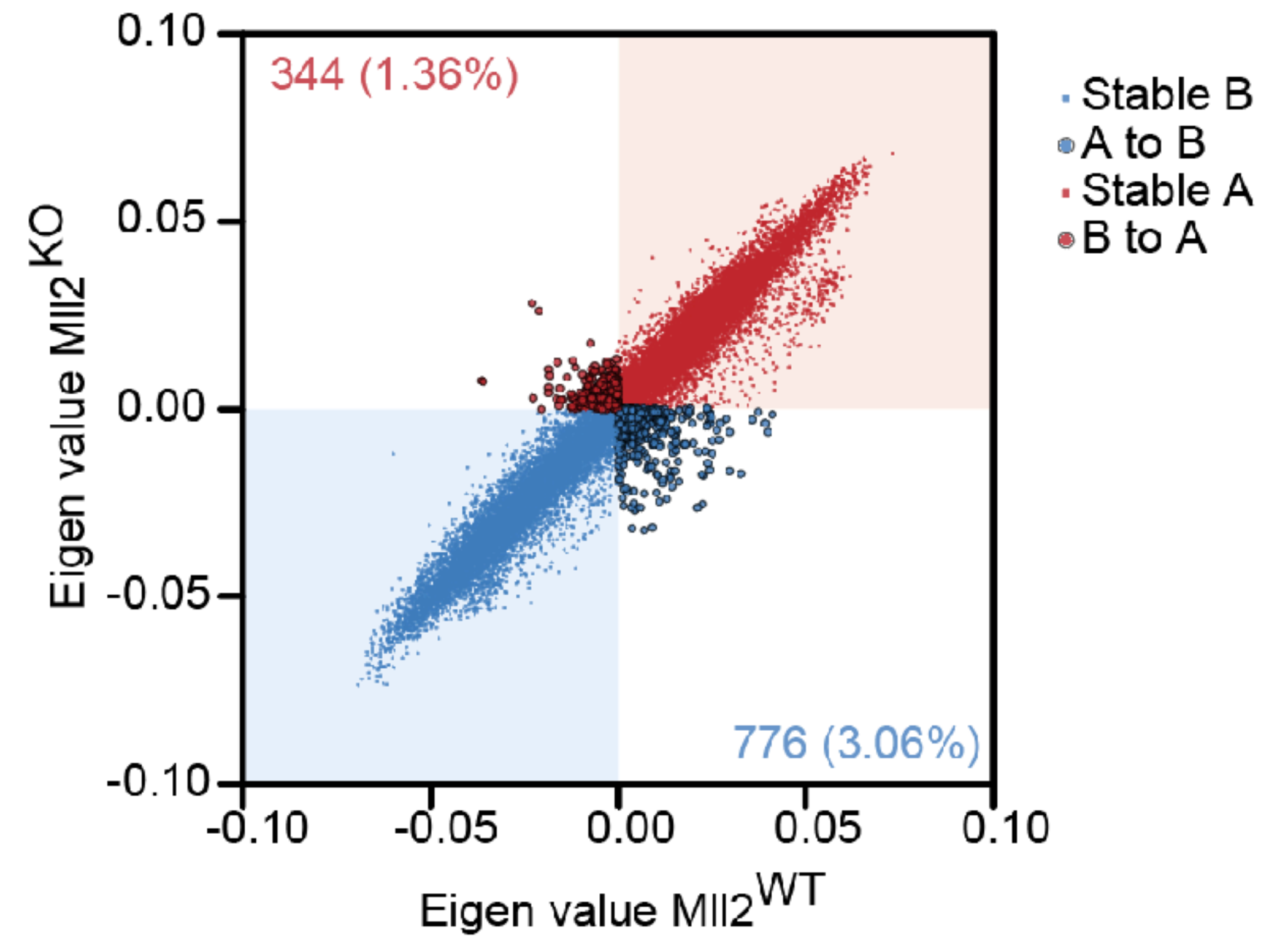
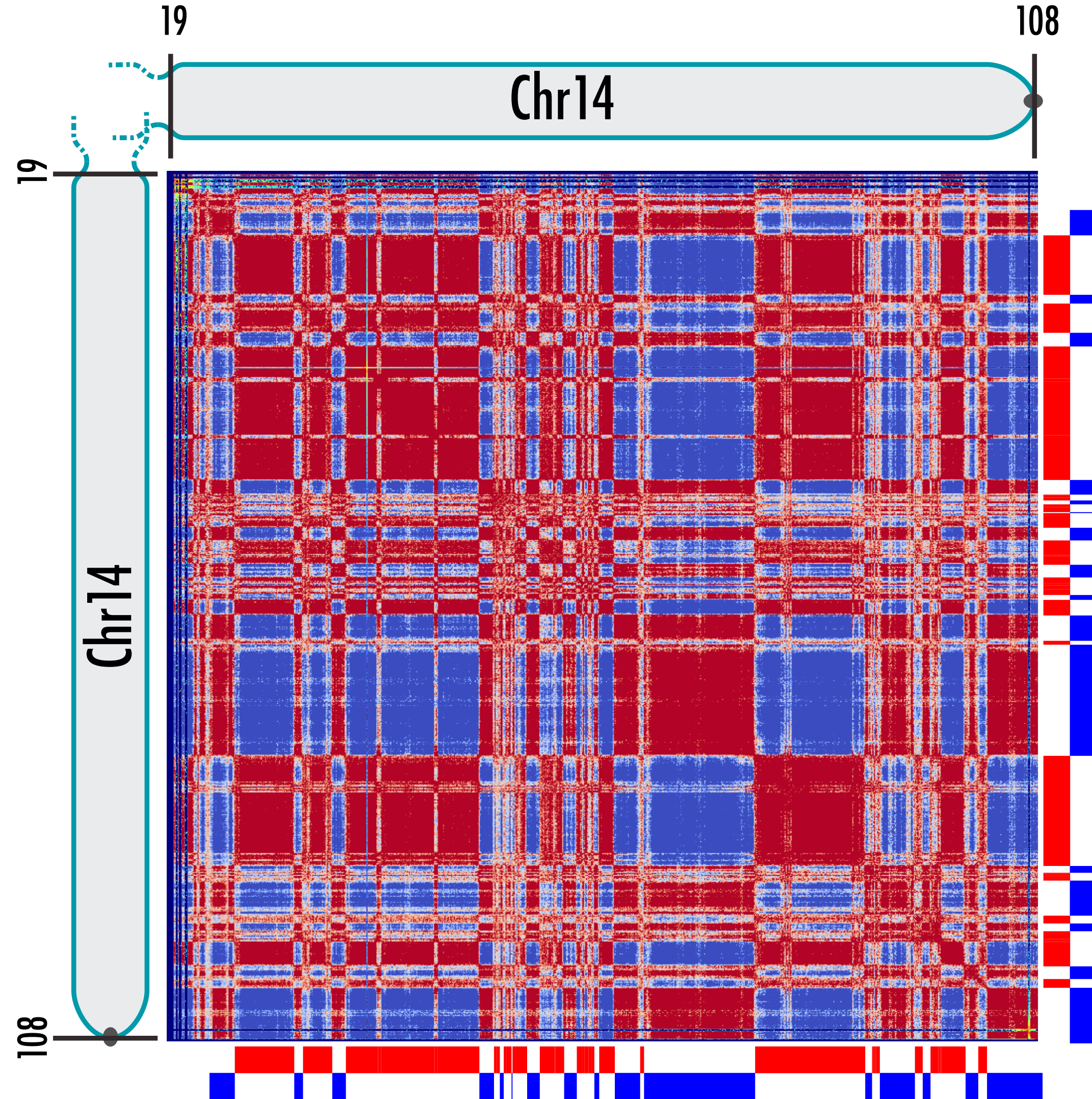
Lieberman-Aiden, E., et al. (2009). *Science*, 326(5950), 289–293.

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



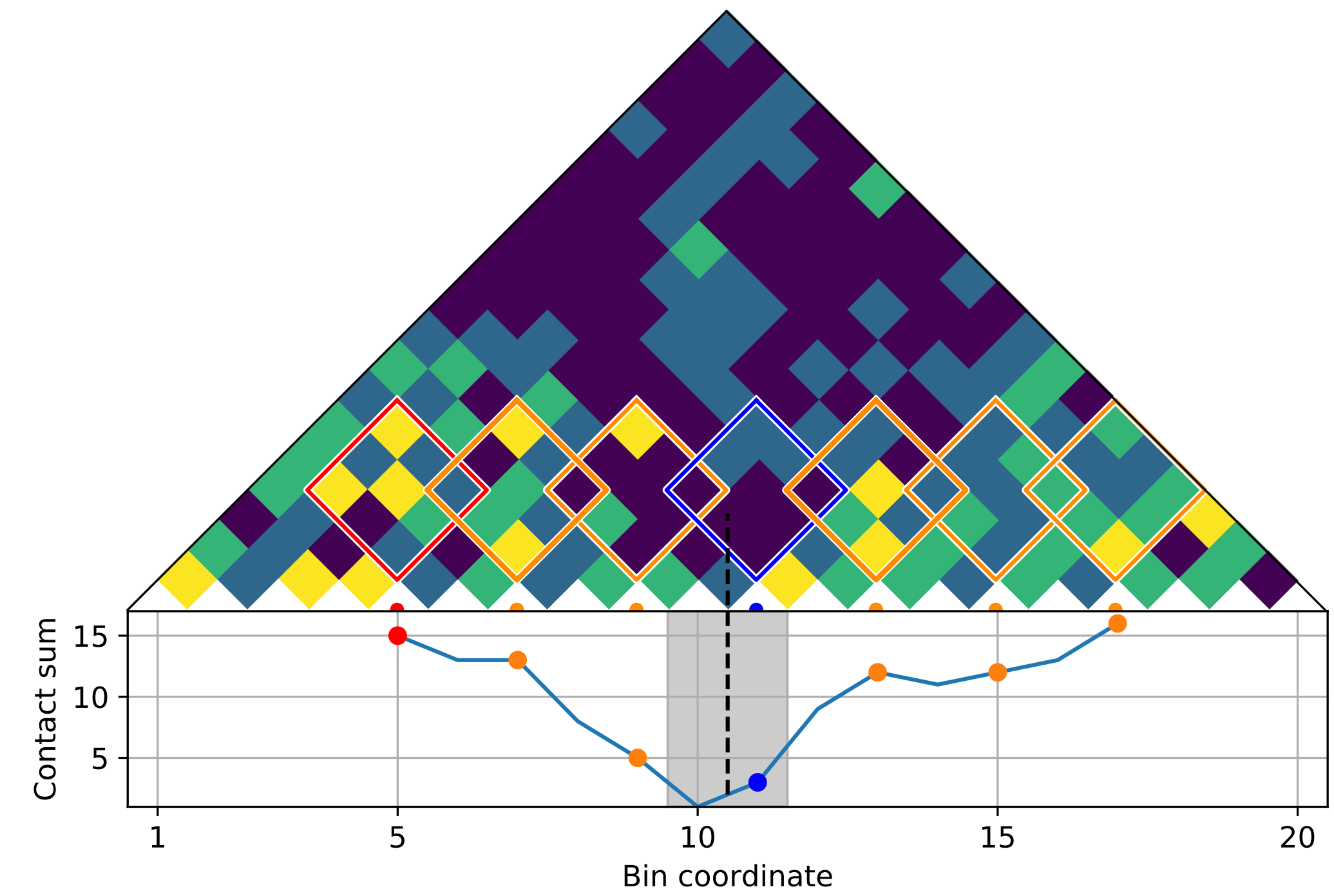
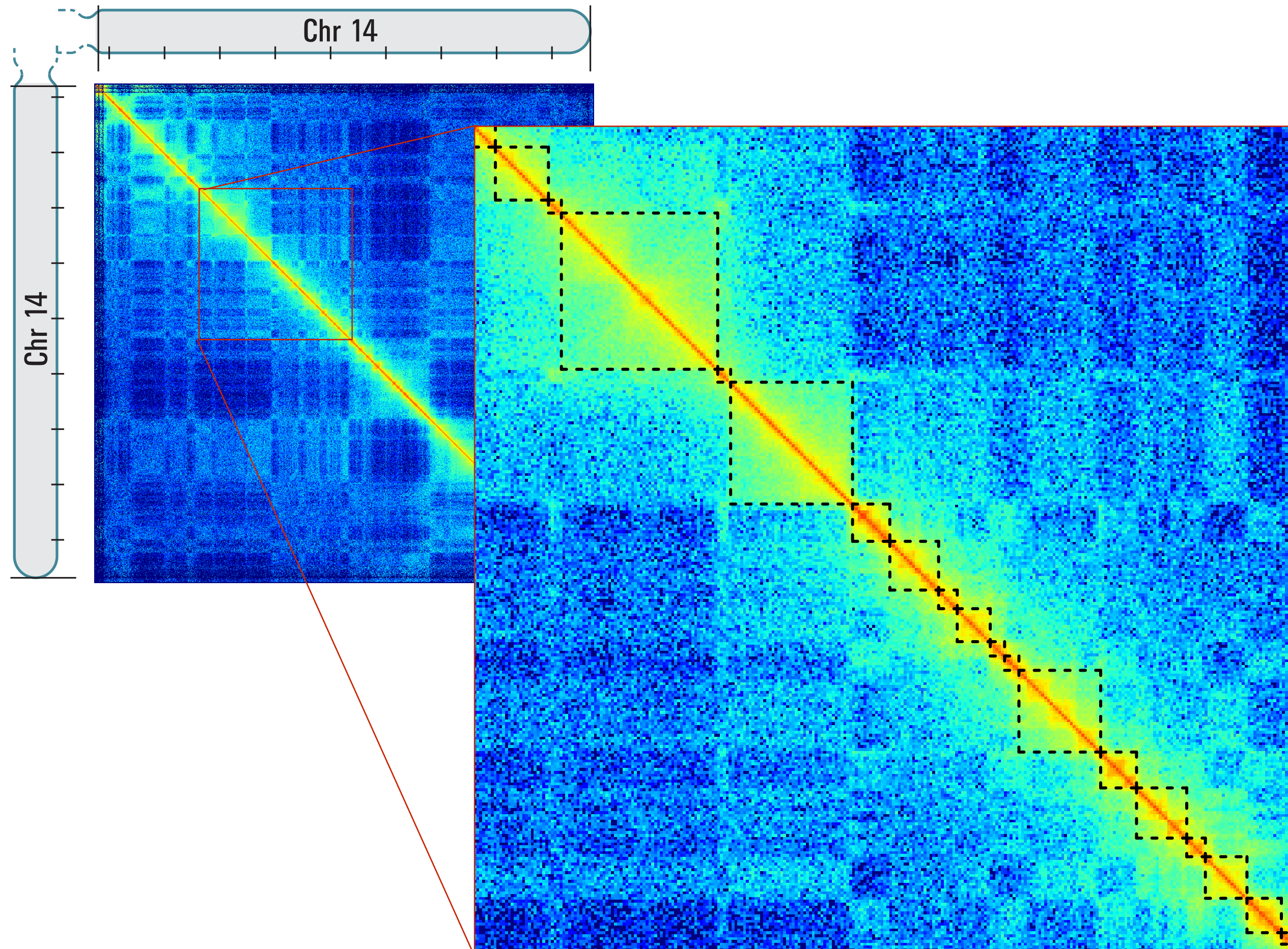
A/B Compartment

Chromosome 14



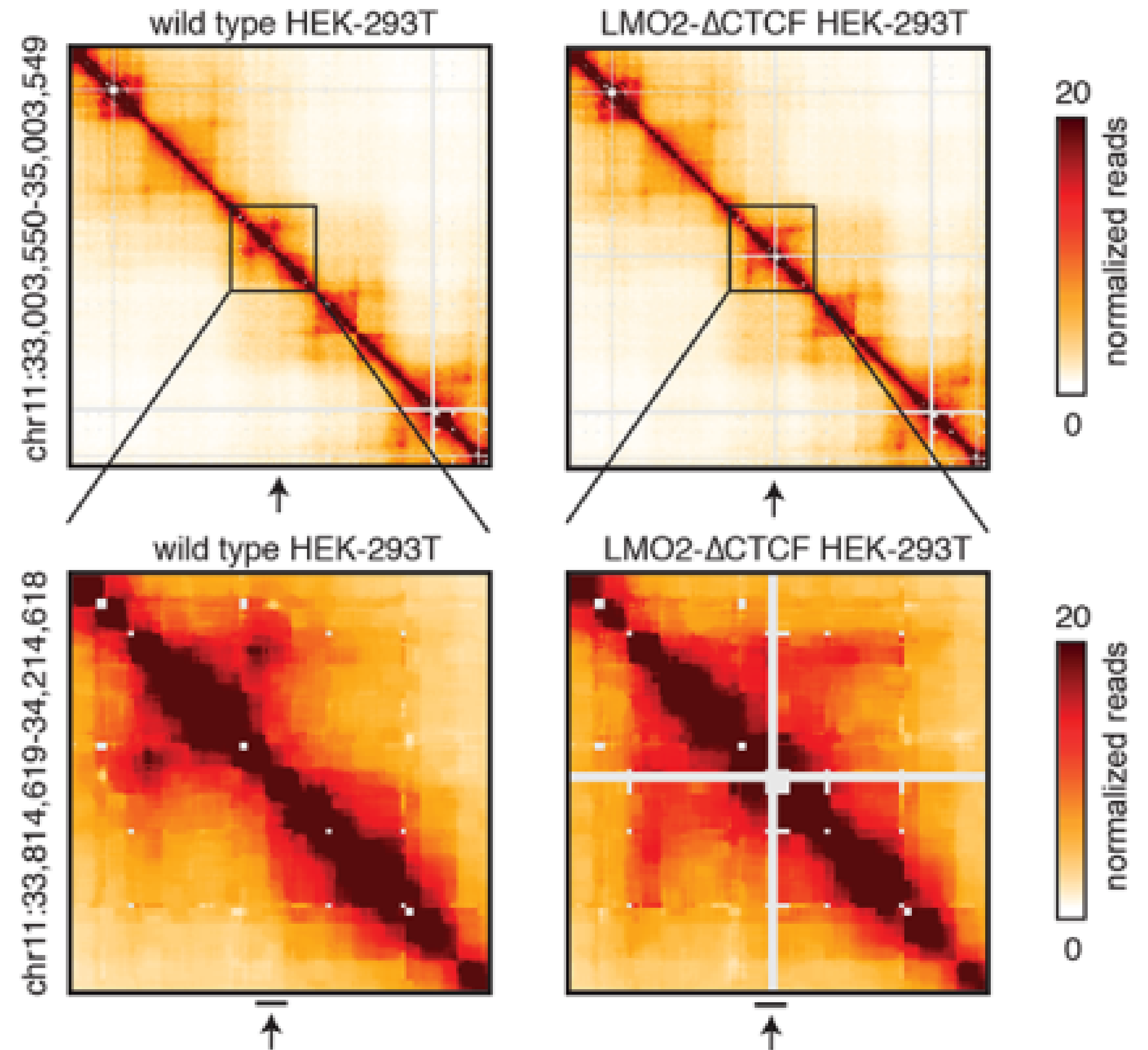
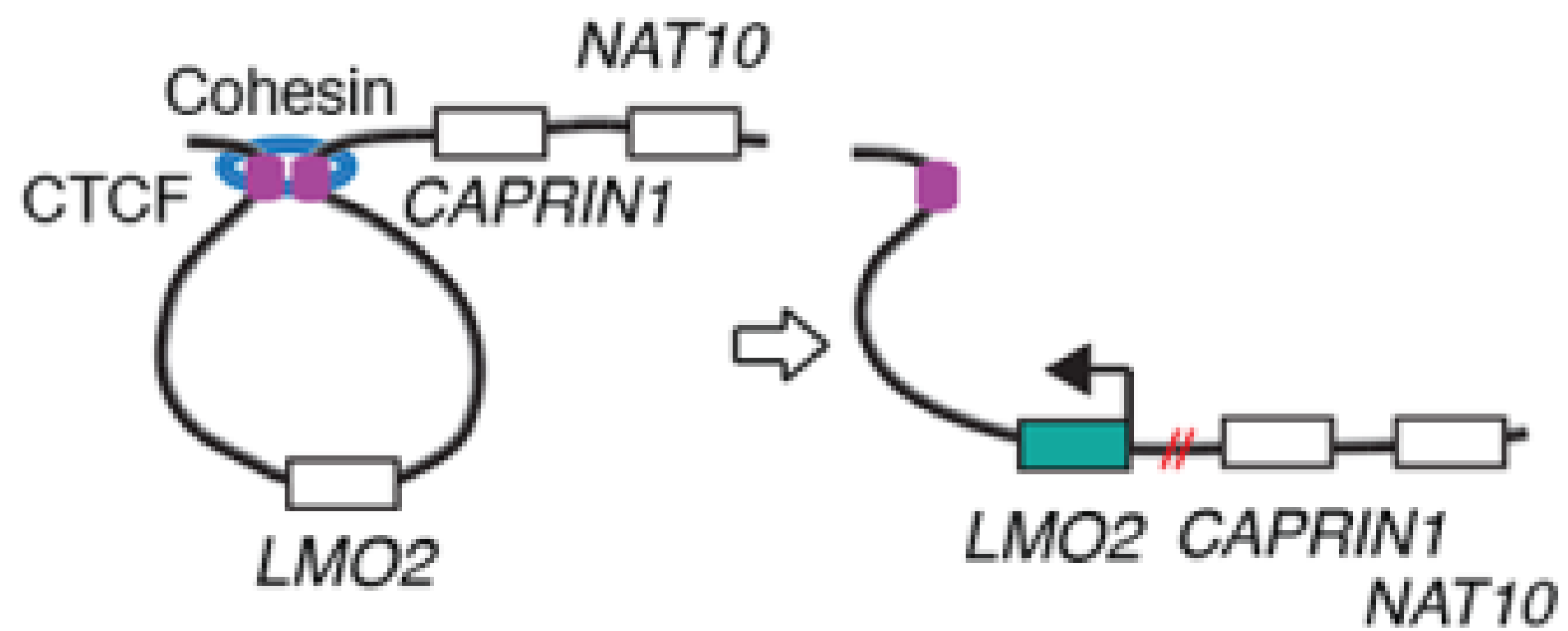
TADs

Chromosome 14



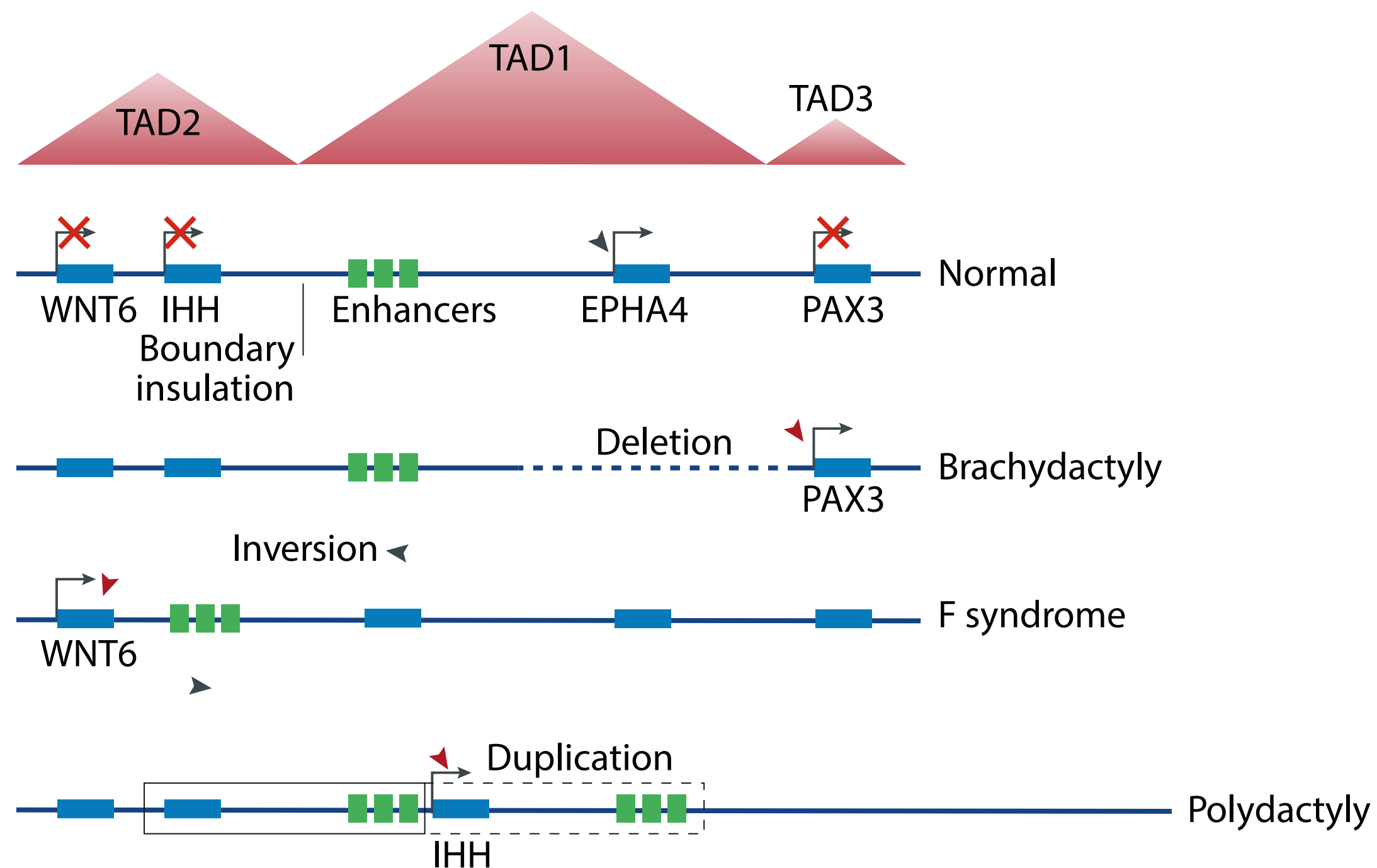
TADs are functional units

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

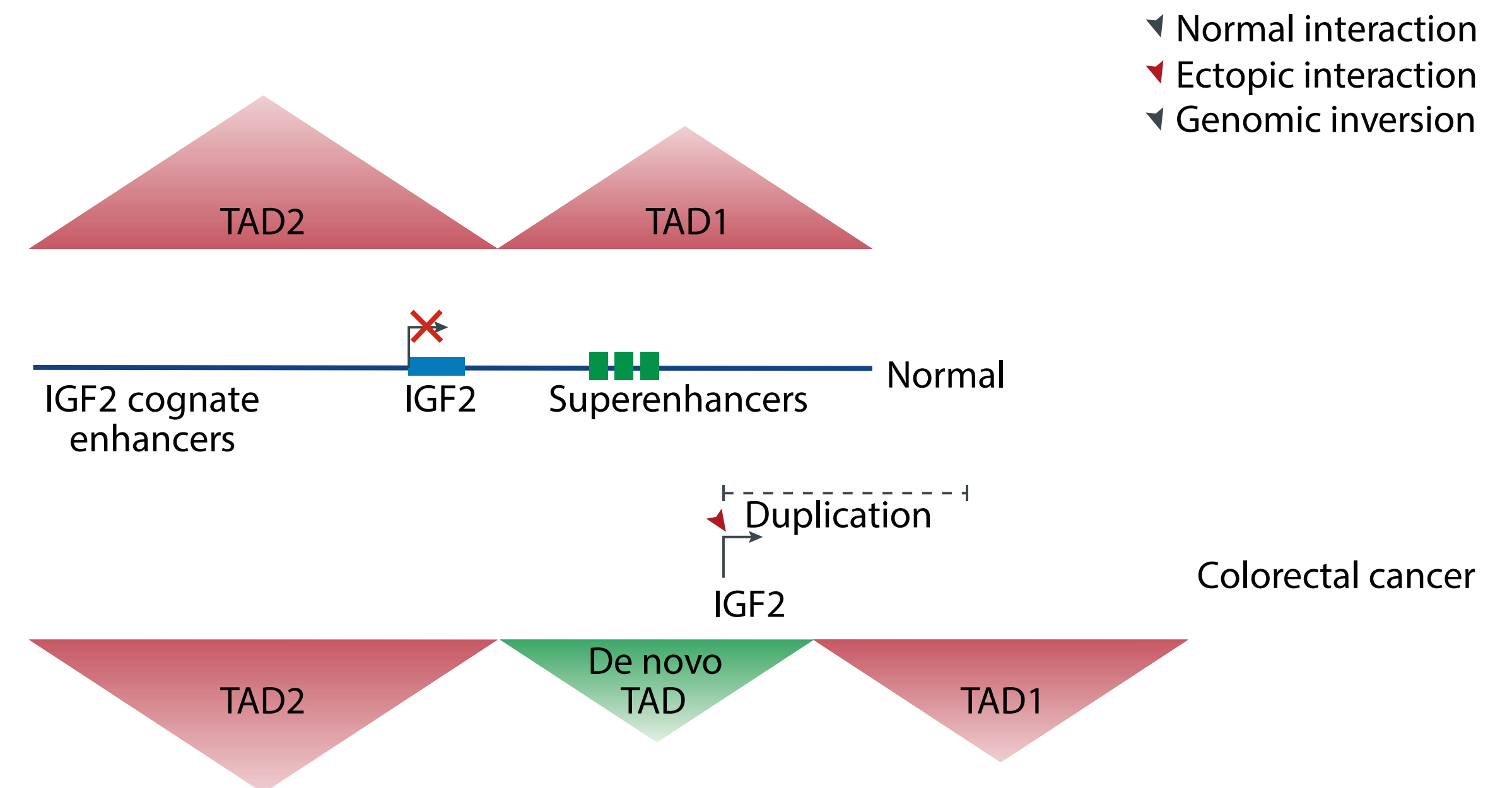


TADs are functional units

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



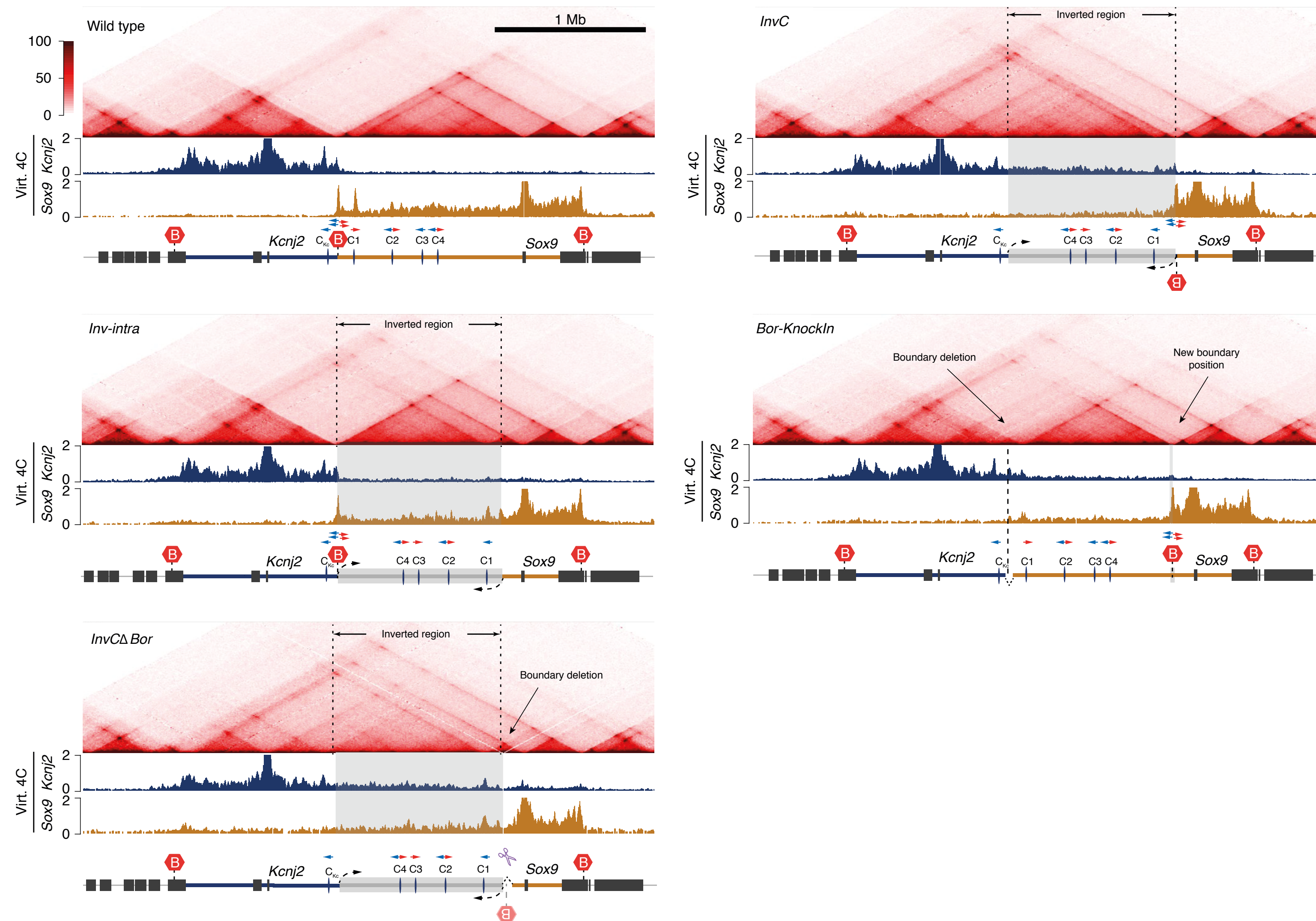
Lupianez, D. G. et al. Cell 161, 1012–1025 (2015)



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

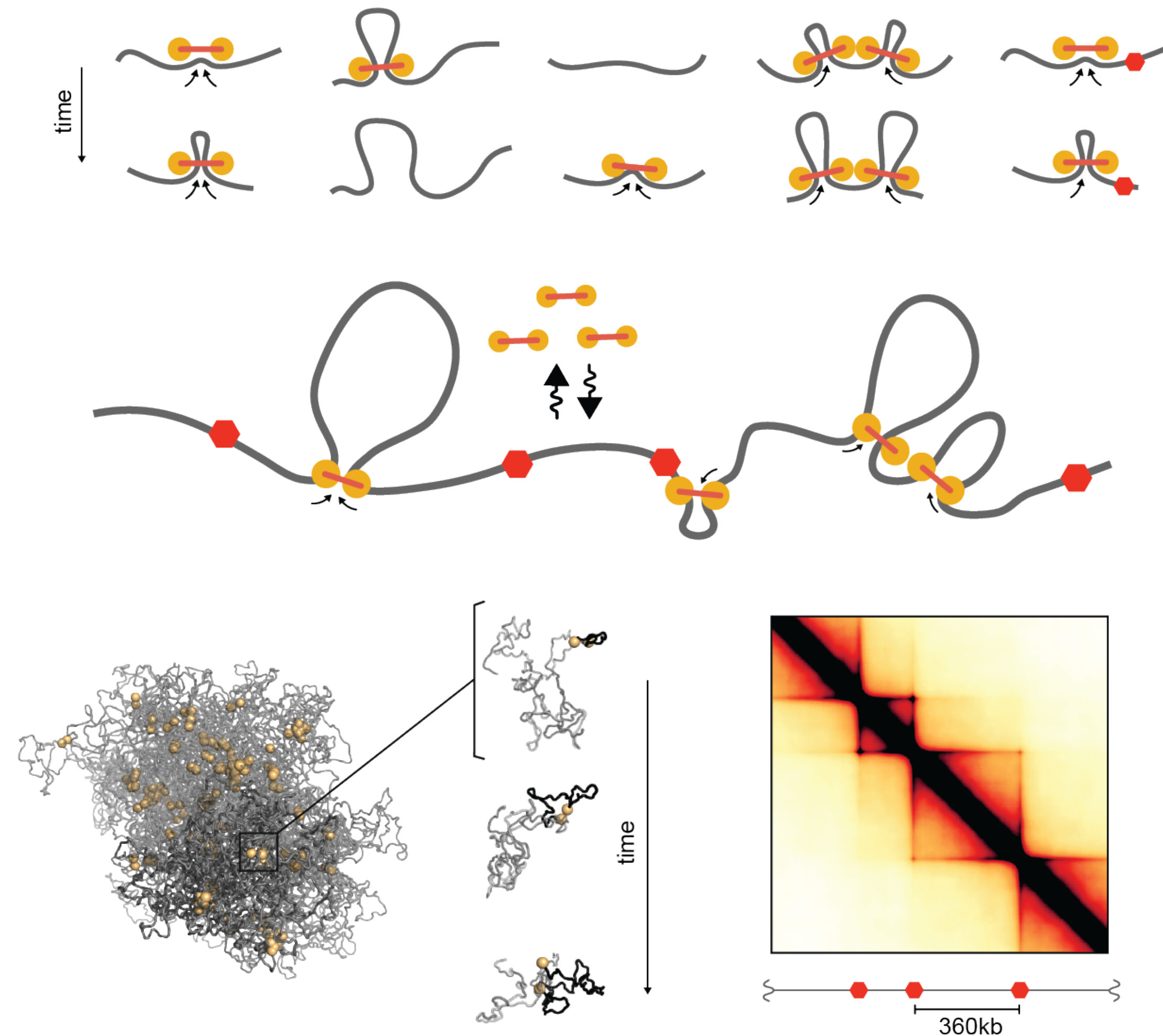
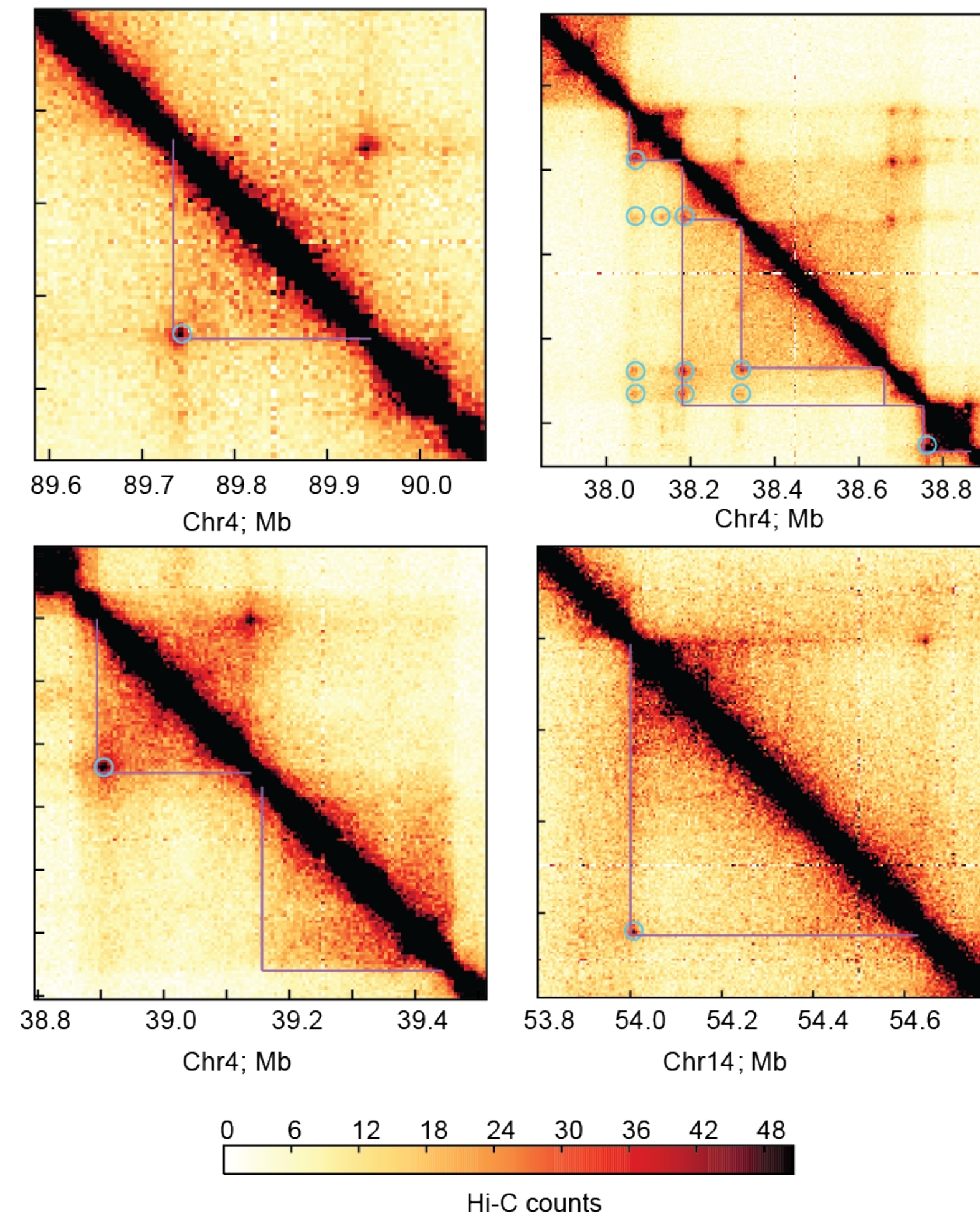
TADs are functional units

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



Loop-extrusion as a TAD forming mechanism

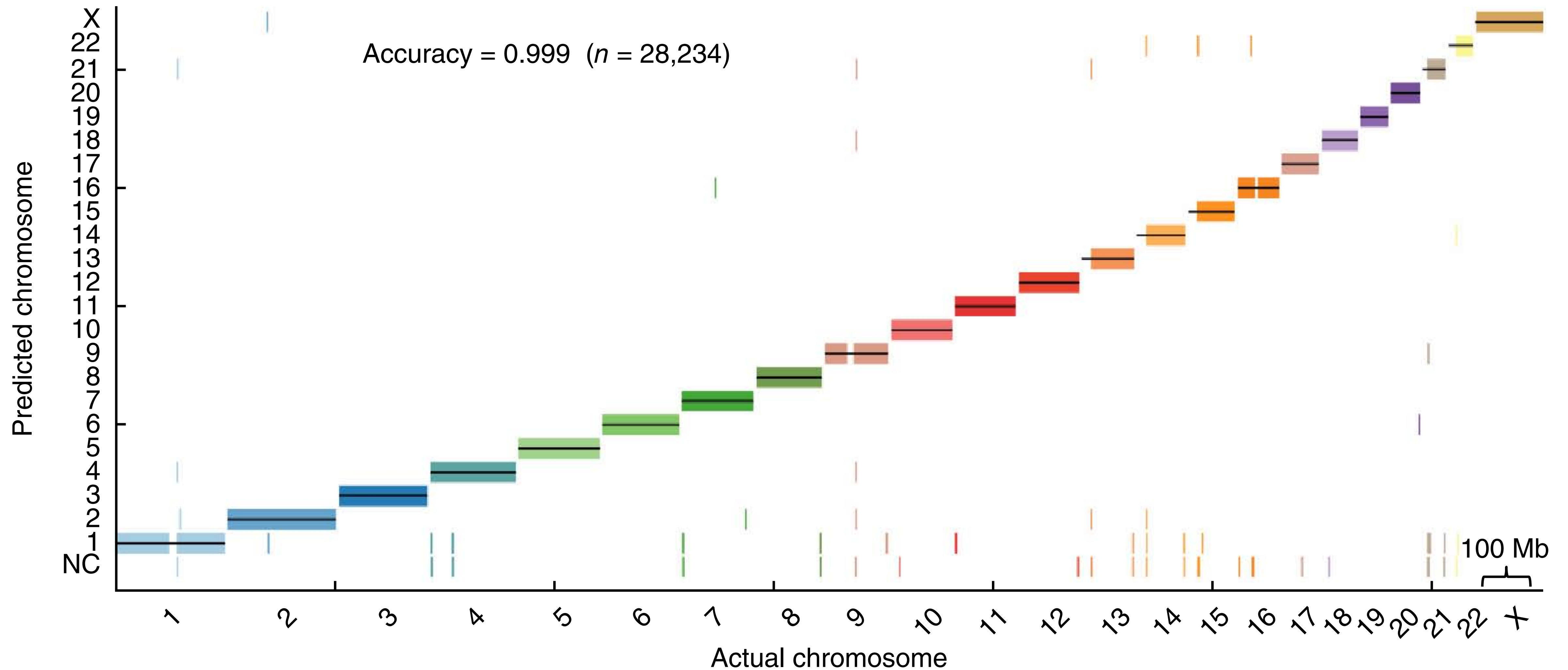
Fudenberg, G., Imakaev, M., Lu, C., Goloborodko, A., Abdennur, N., & Mirny, L. A. (2018).
Cold Spring Harb Symp Quant Biol 2017. 82: 45-55



SIDE EFFECTS

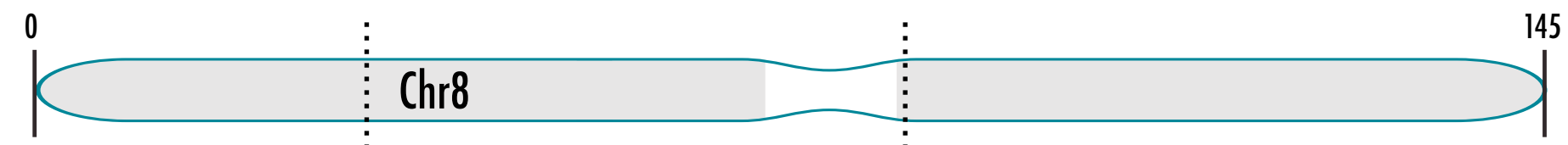
Hi-C for de-novo assembly

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

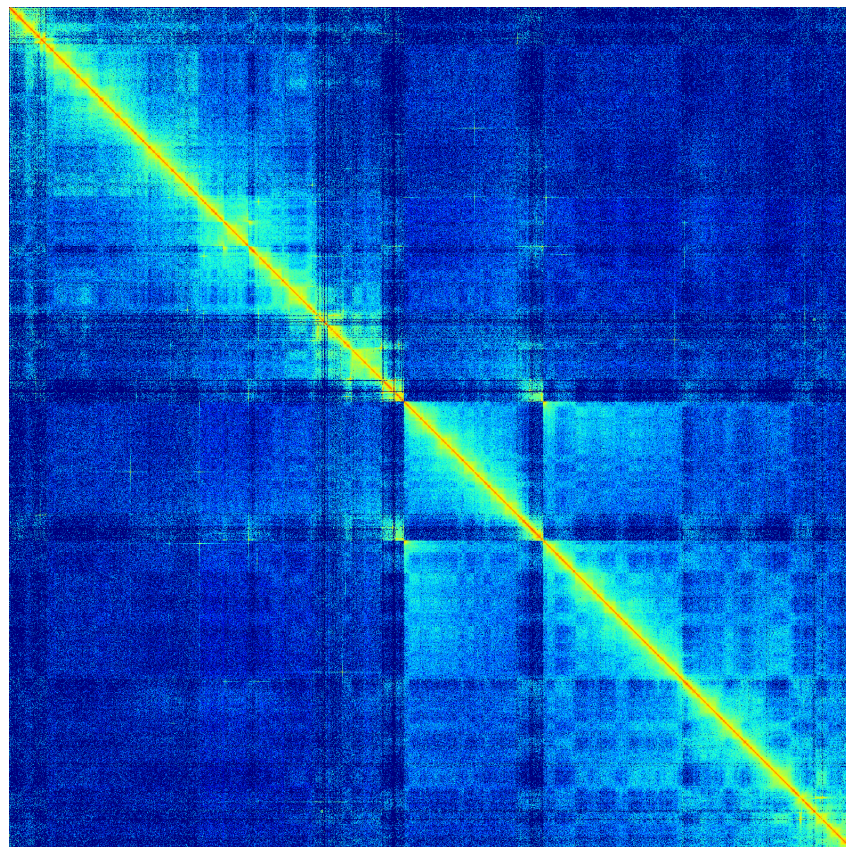


Assembly error detection

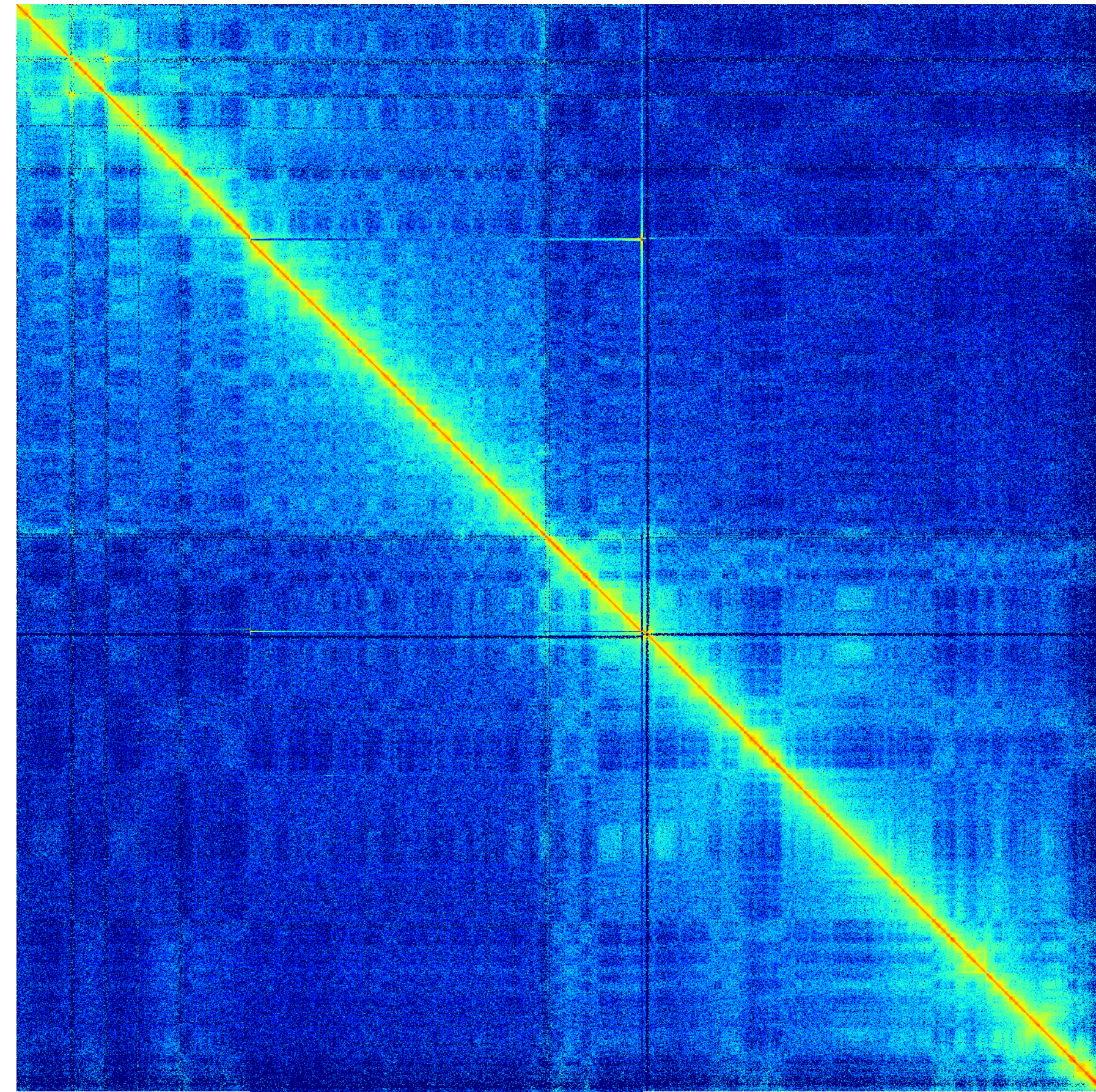
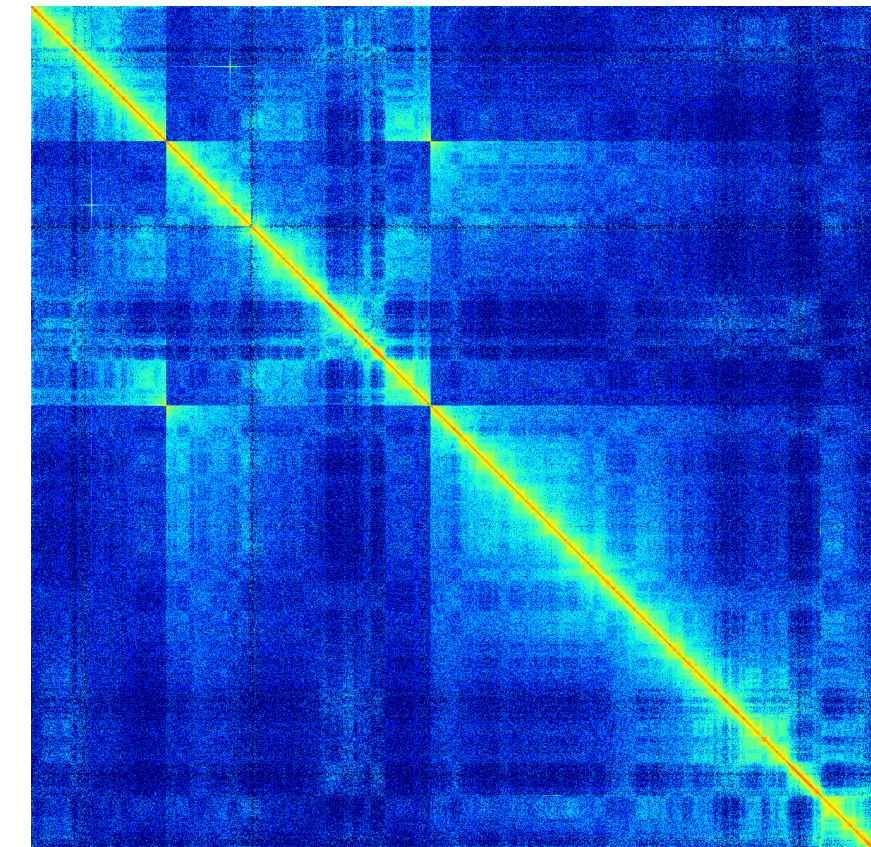
Chromosome 8 Gorilla



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., Micheltore, 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](#)

