



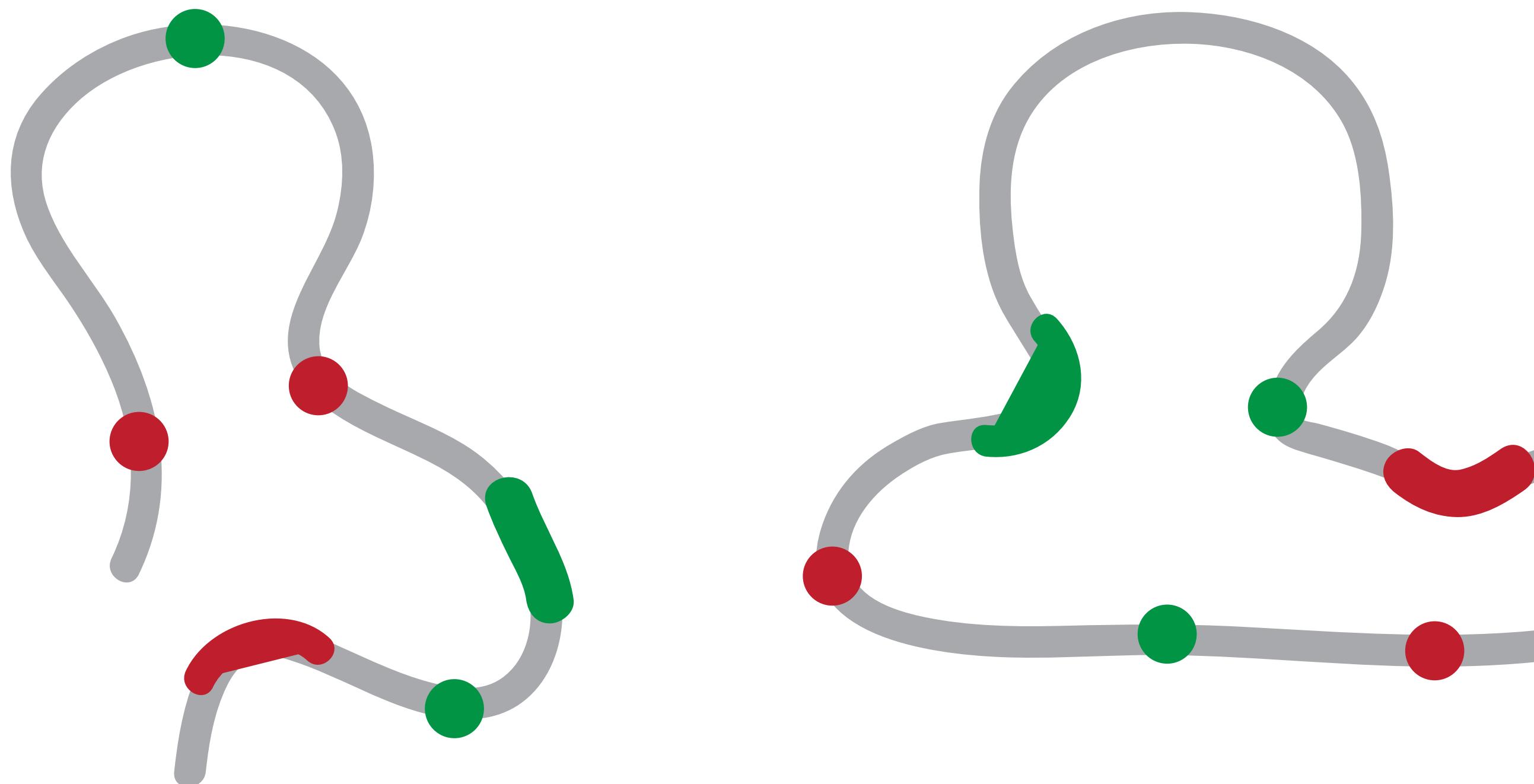
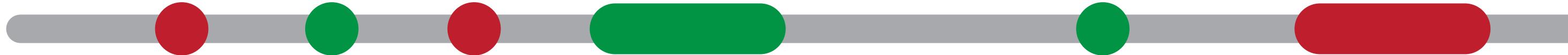
Photo by David Oliete - www.davidoliete.com

3D Genomics

Marc A. Martí-Renom
CNAG-CRG · ICREA

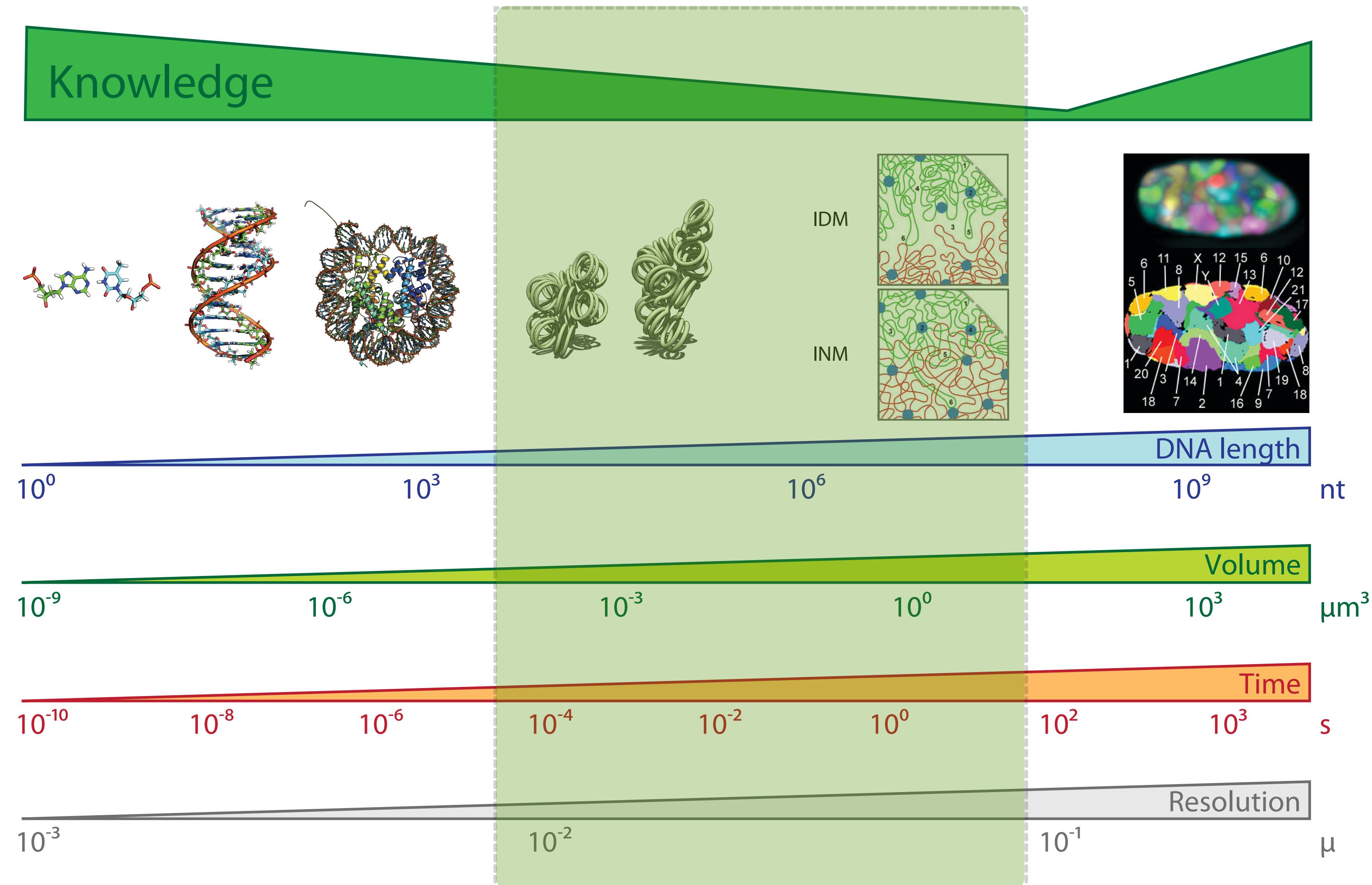
<http://marciuslab.org>
<http://3DGenomes.org>
<http://cnag.crg.eu>

cnag CRG^R ICREA



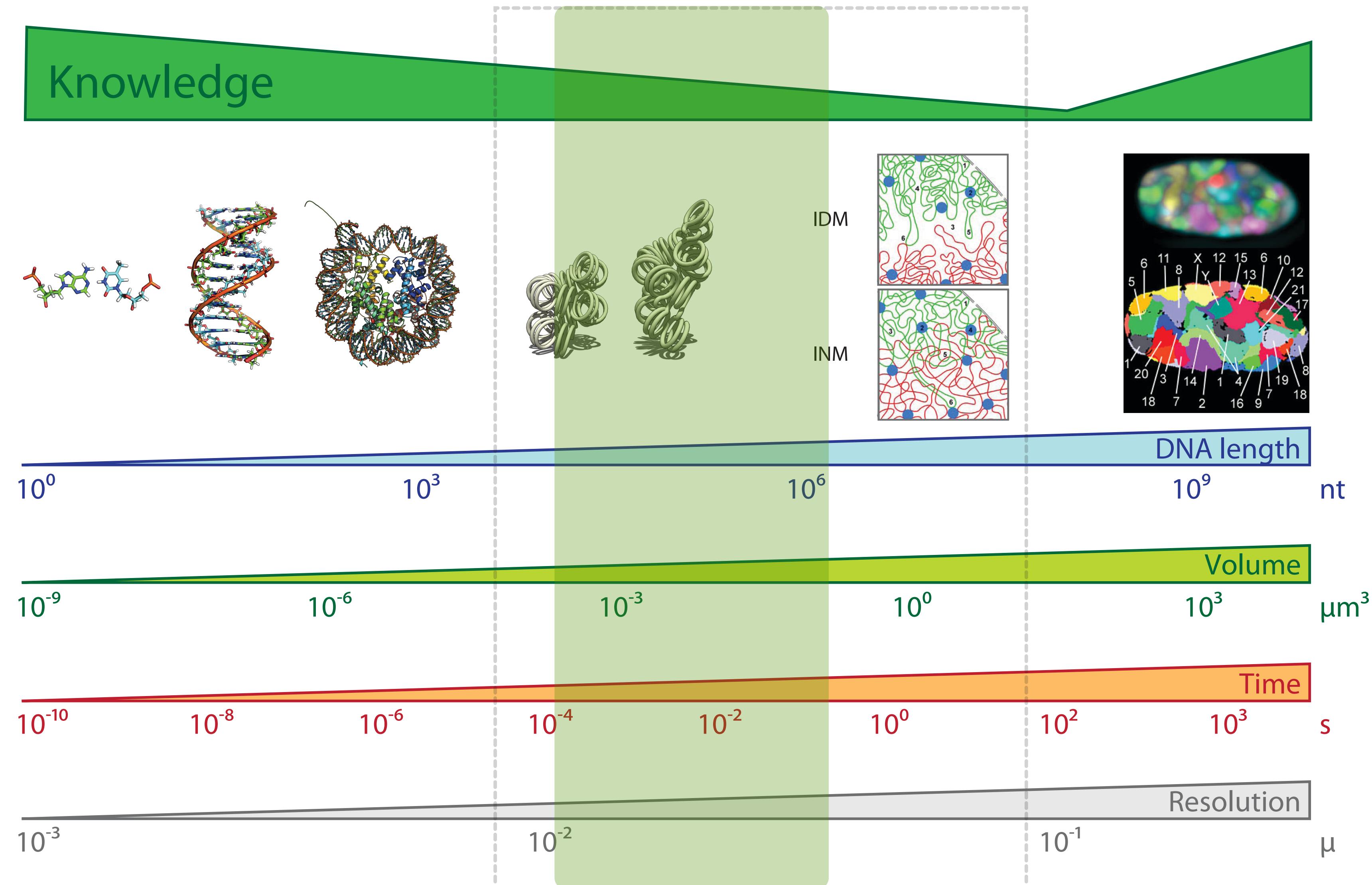
Resolution Gap

Marti-Renom, M. A. & Mirny, L. A. PLoS Comput Biol 7, e1002125 (2011)



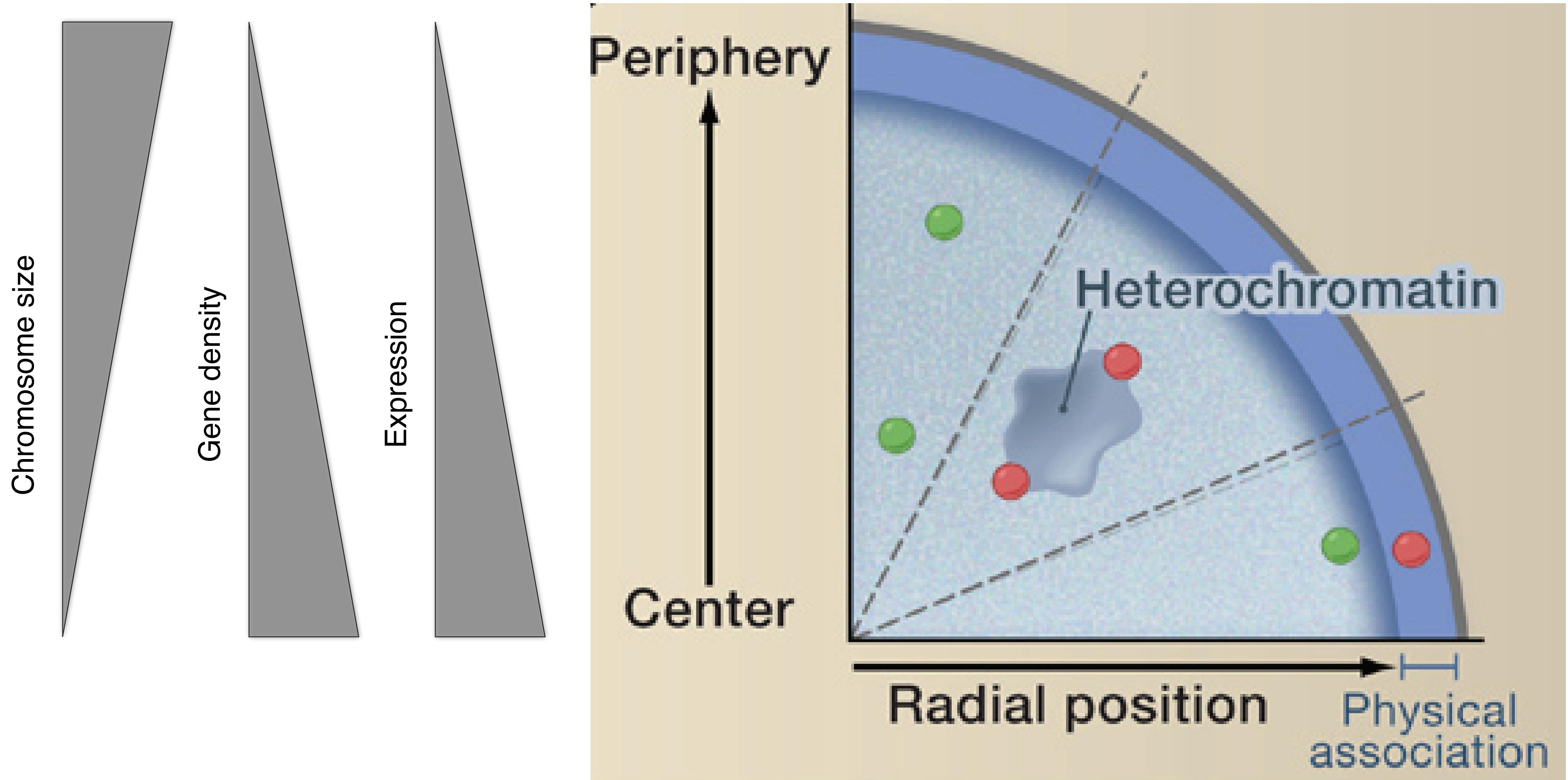
Resolution Gap

Marti-Renom, M. A. & Mirny, L. A. PLoS Comput Biol 7, e1002125 (2011)



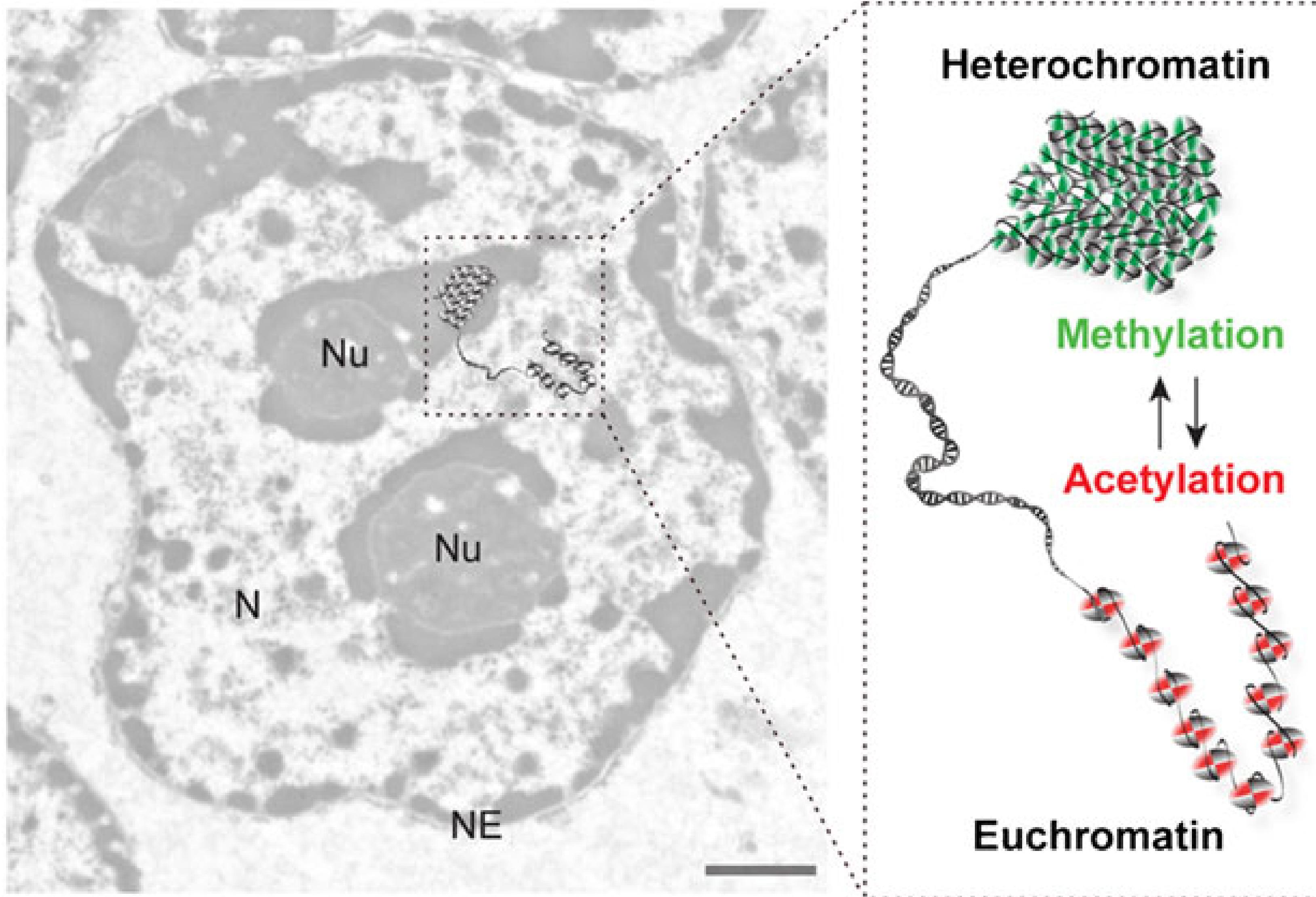
Level I: Radial genome organization

Takizawa, T., Meaburn, K. J. & Misteli, T. The meaning of gene positioning. Cell 135, 9–13 (2008).

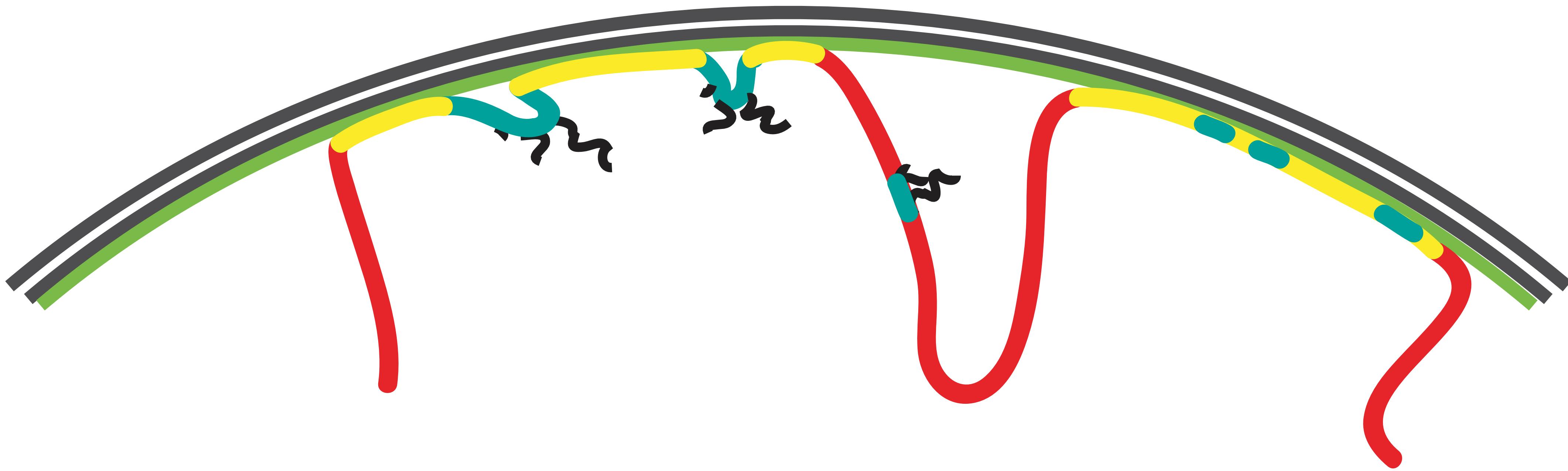


Level II: Euchromatin vs heterochromatin

Electron microscopy



Level III: Lamina-genome interactions

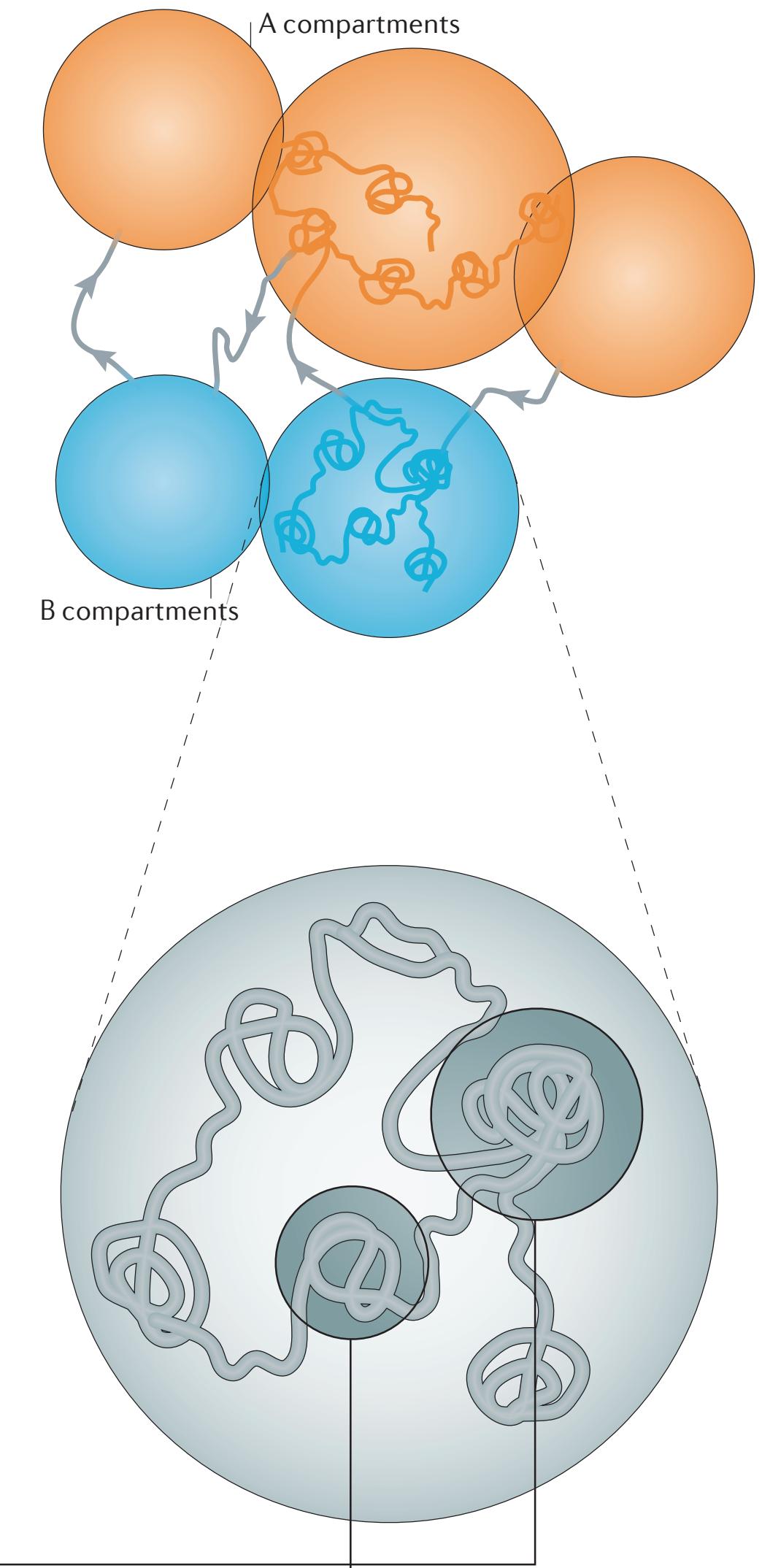
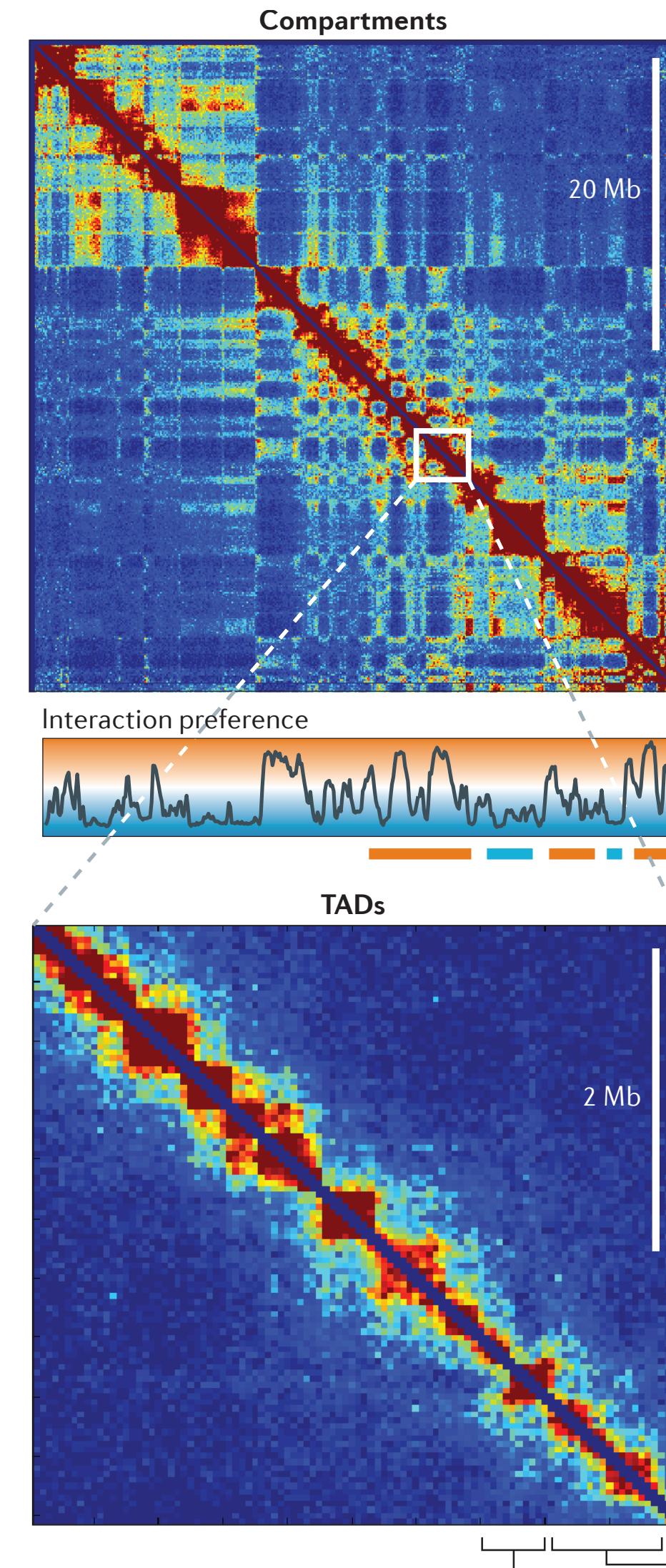
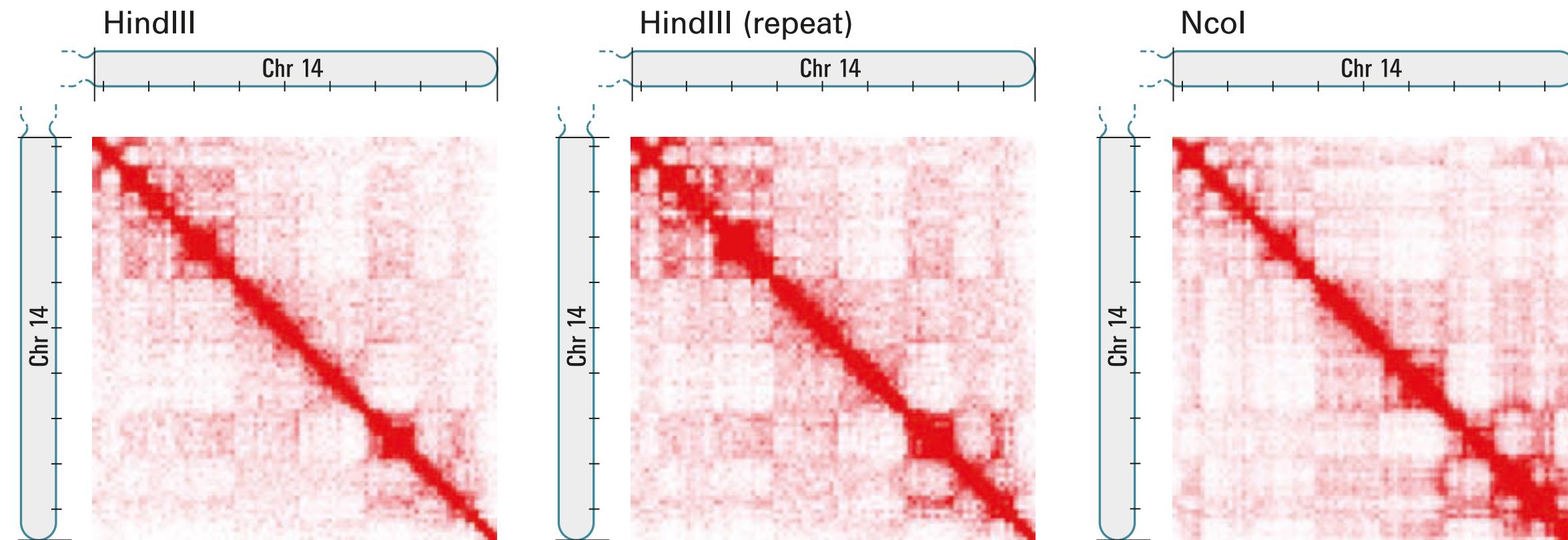
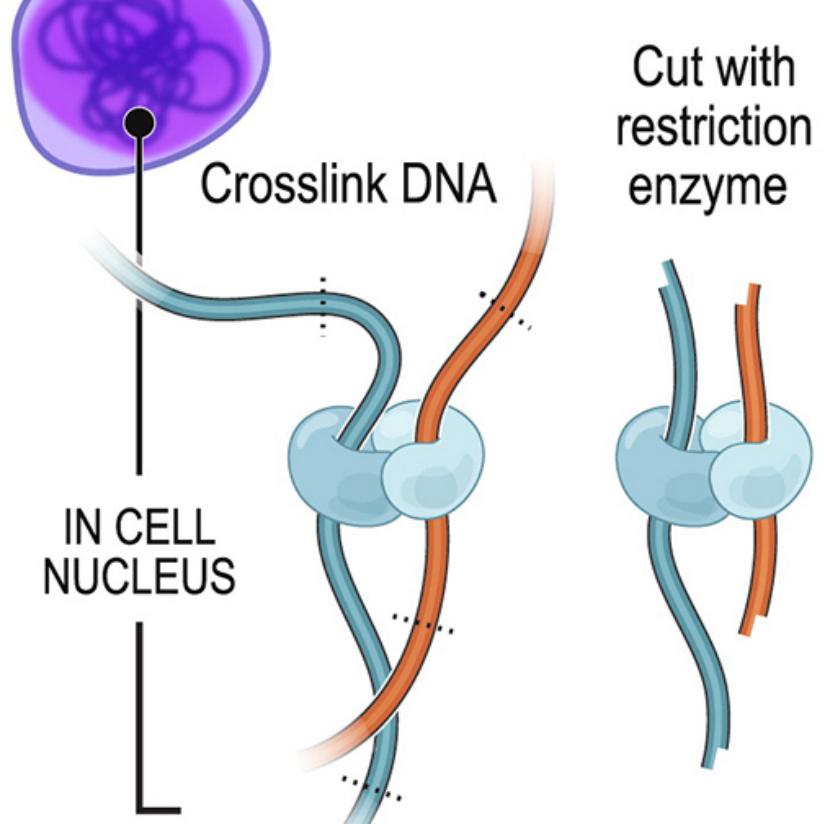


- nuclear membrane
- nuclear lamina
- internal chromatin (mostly active)
- lamina-associated domains (repressed)
- Genes
- mRNA

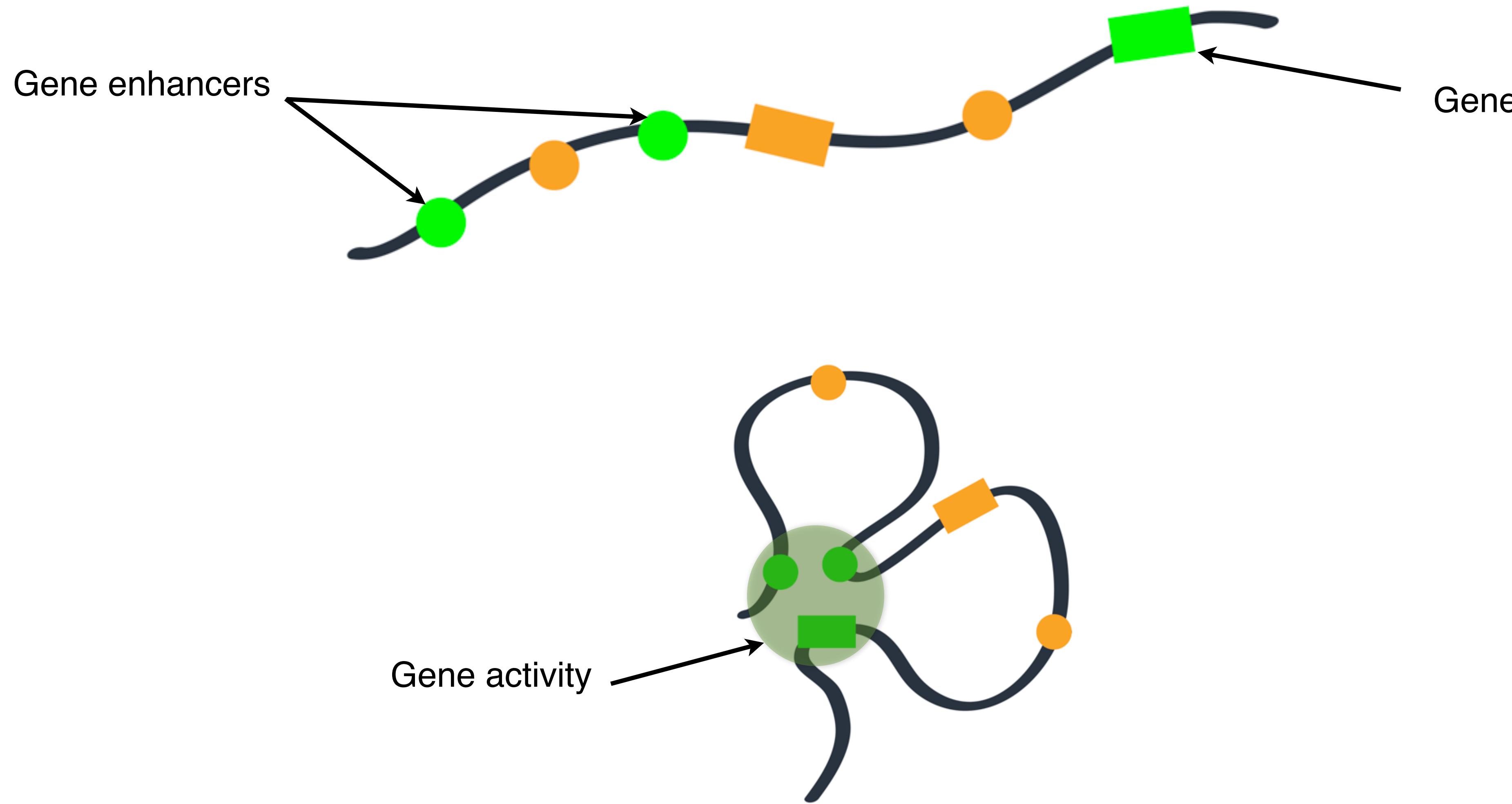
Adapted from Molecular Cell 38, 603-613, 2010

Level IV: Higher-order organization

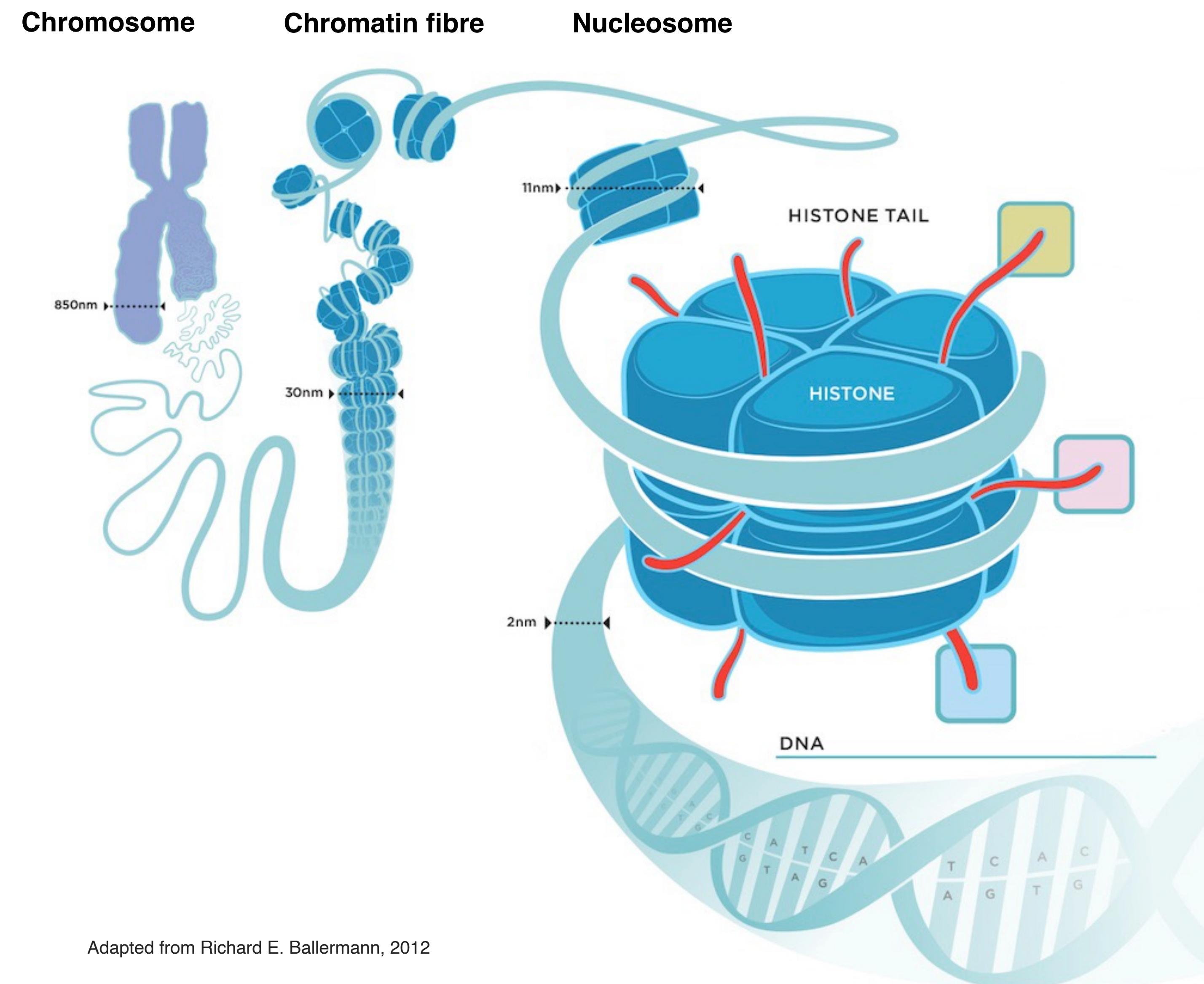
Dekker, J., Marti-Renom, M. A. & Mirny, L. A. Nat Rev Genet 14, 390–403 (2013).



Level V: Chromatin loops

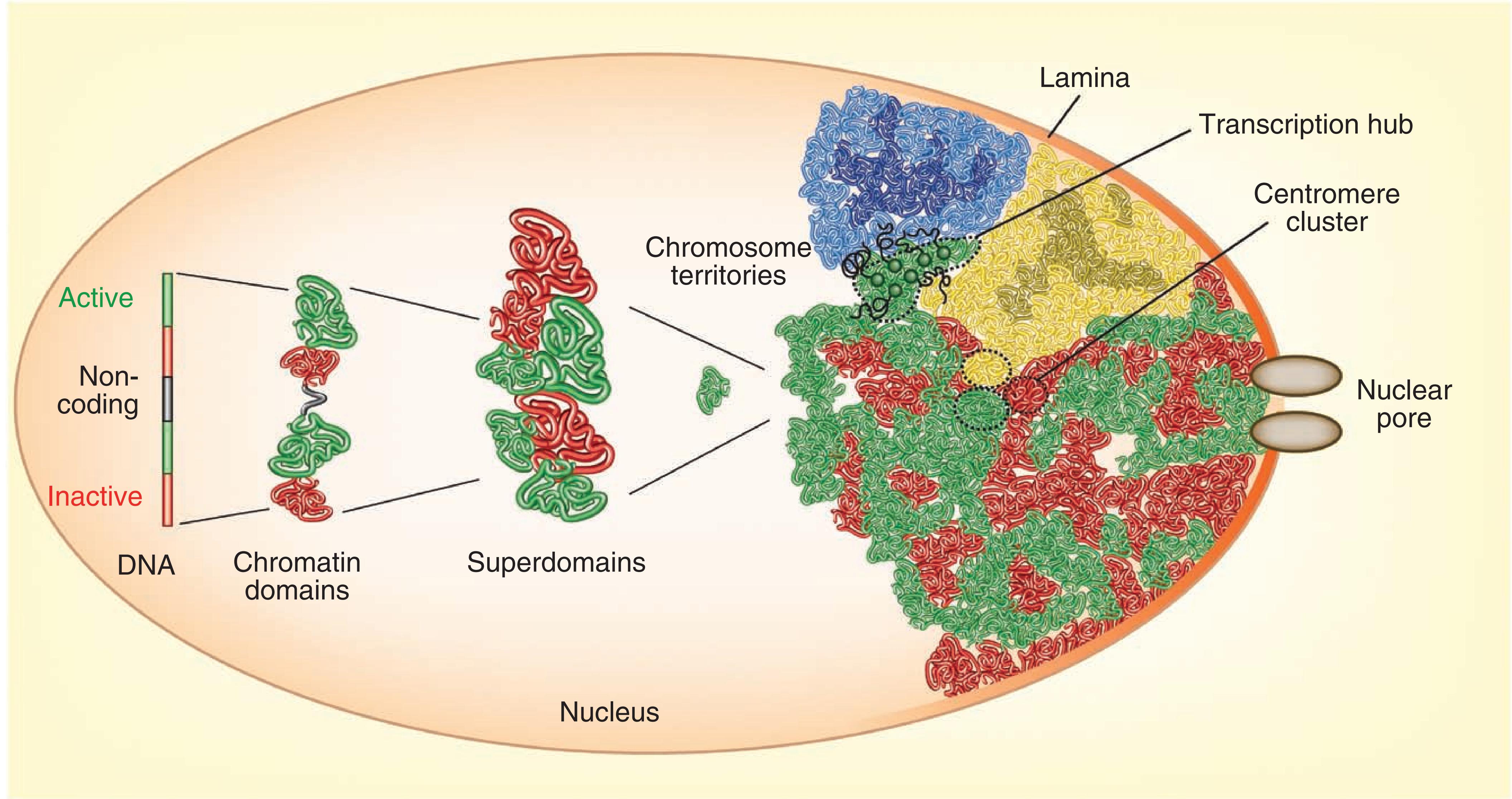


Level VI: Nucleosome



Complex genome organization

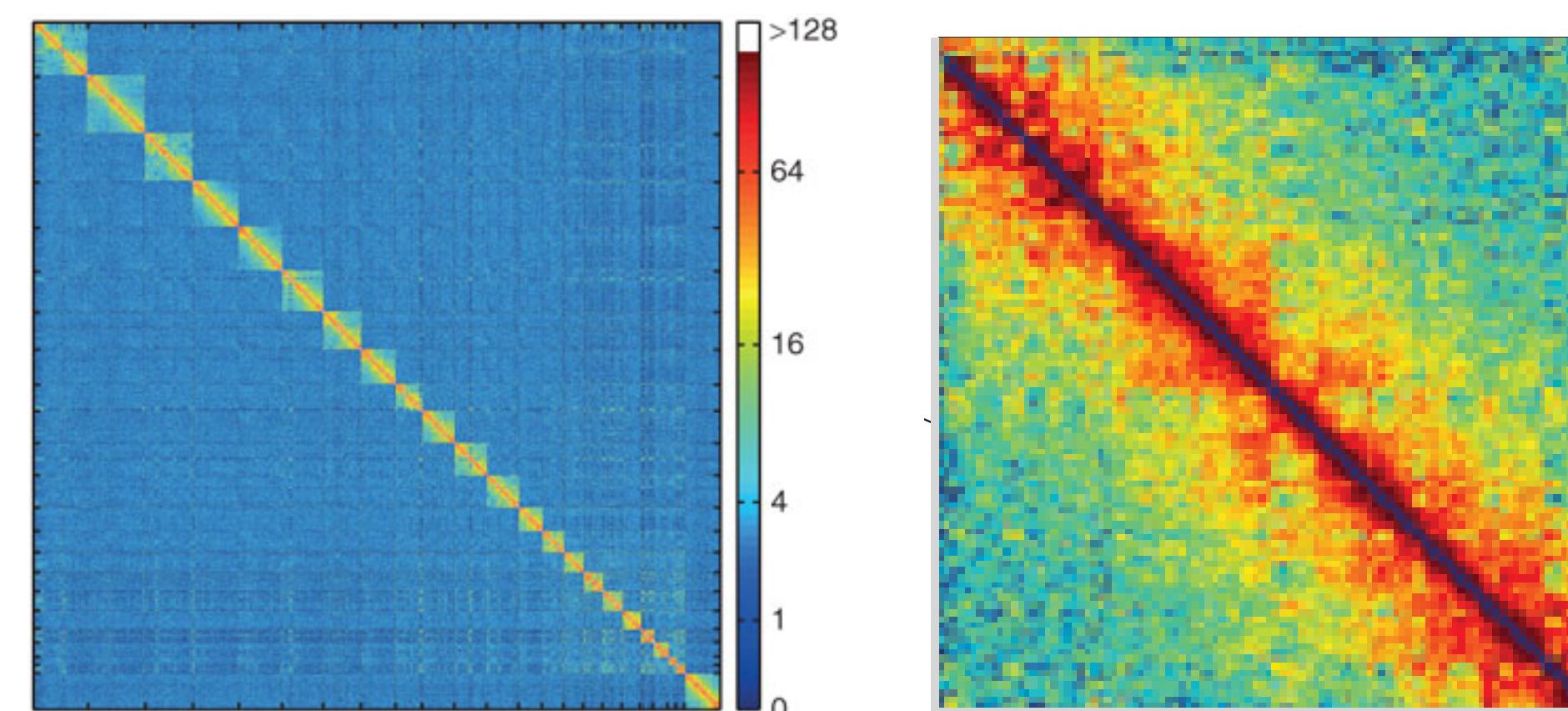
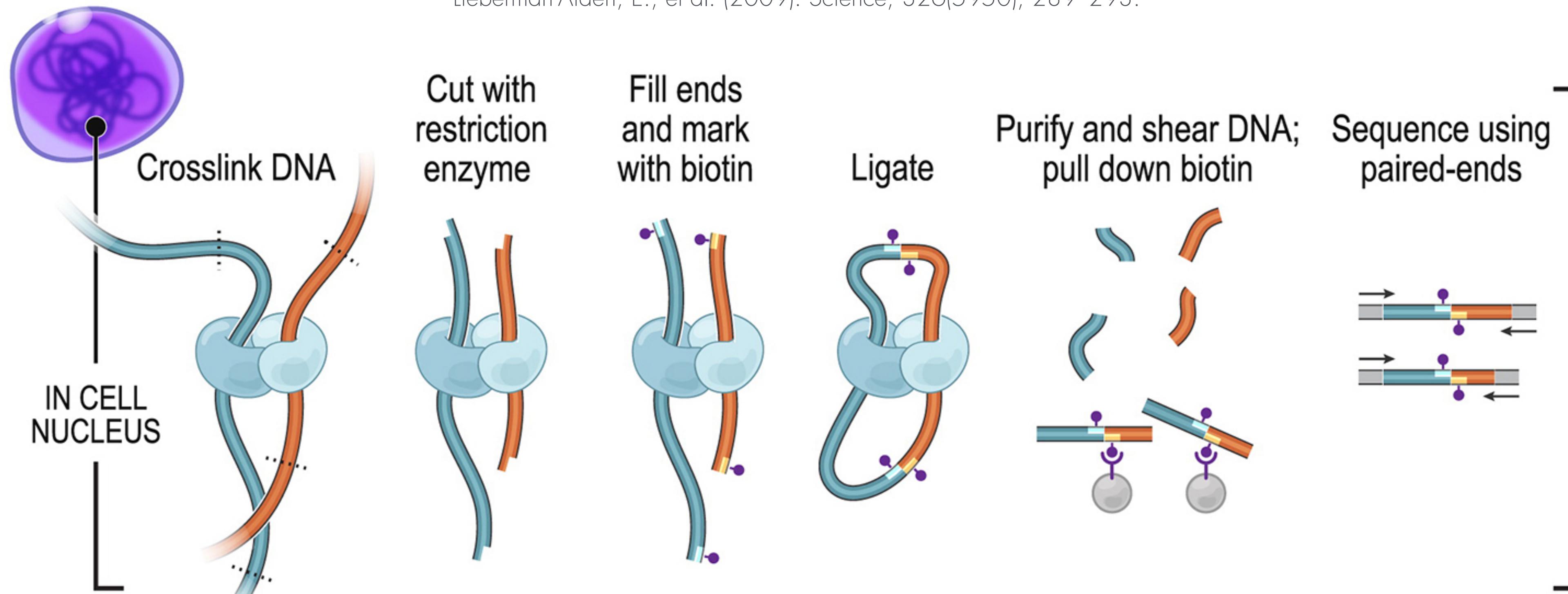
Cavalli, G. & Misteli, T. Functional implications of genome topology. *Nat Struct Mol Biol* 20, 290–299 (2013).



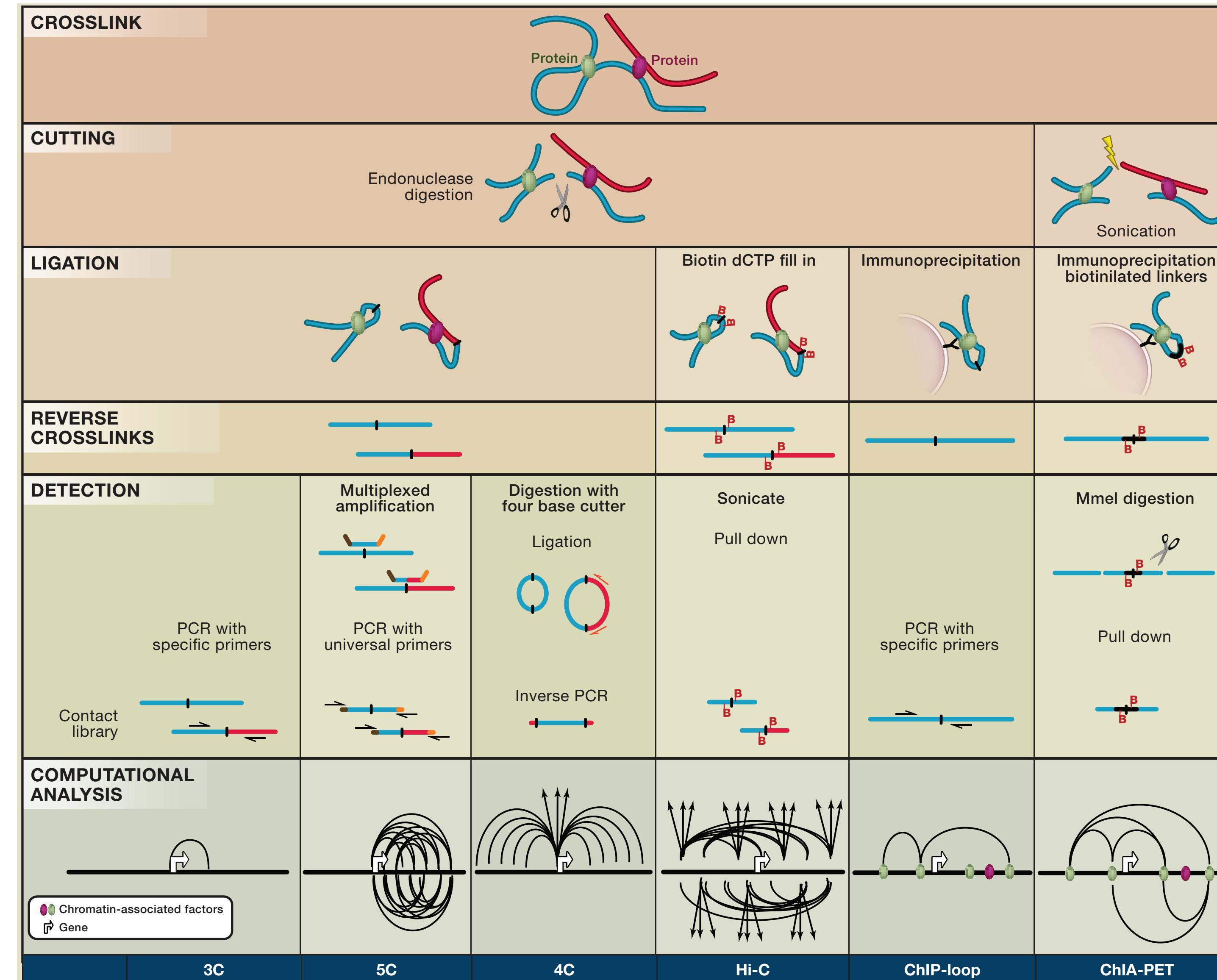
Chromosome Conformation Capture

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.



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

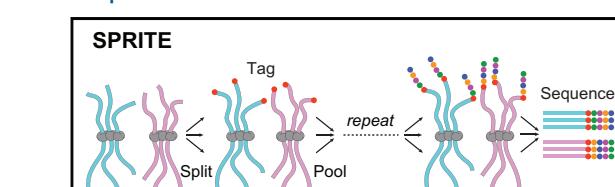
Amin Allahyar^{1,2}, Carlo Vermeulen^{3,7}, Britta A. M. Bouwman³, Peter H. L. Krijger³, Marjon J. A. M. Versteegen³, Geert Geelen³, Melissa van Kranenburg³, Mark Pieterse³, Roy Straver^{3,1}, Judith H. I. Haarhuis⁴, Kees Jalink⁵, Hans Teunissen⁶, Ivo J. Renkens¹, Wigard P. Kloosterman¹, Benjamin D. 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



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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#}