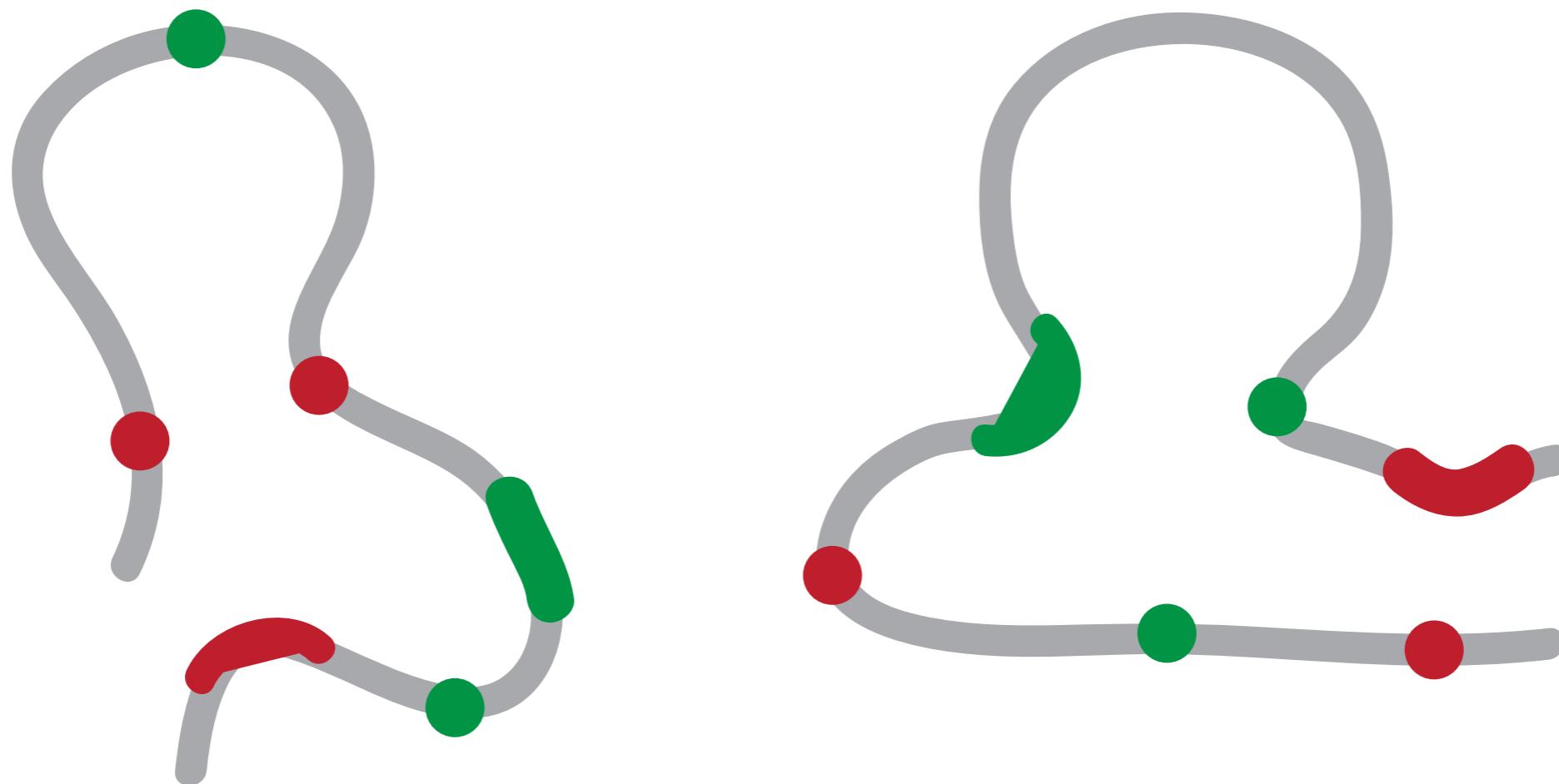


Chromatin structure and Hi-C data

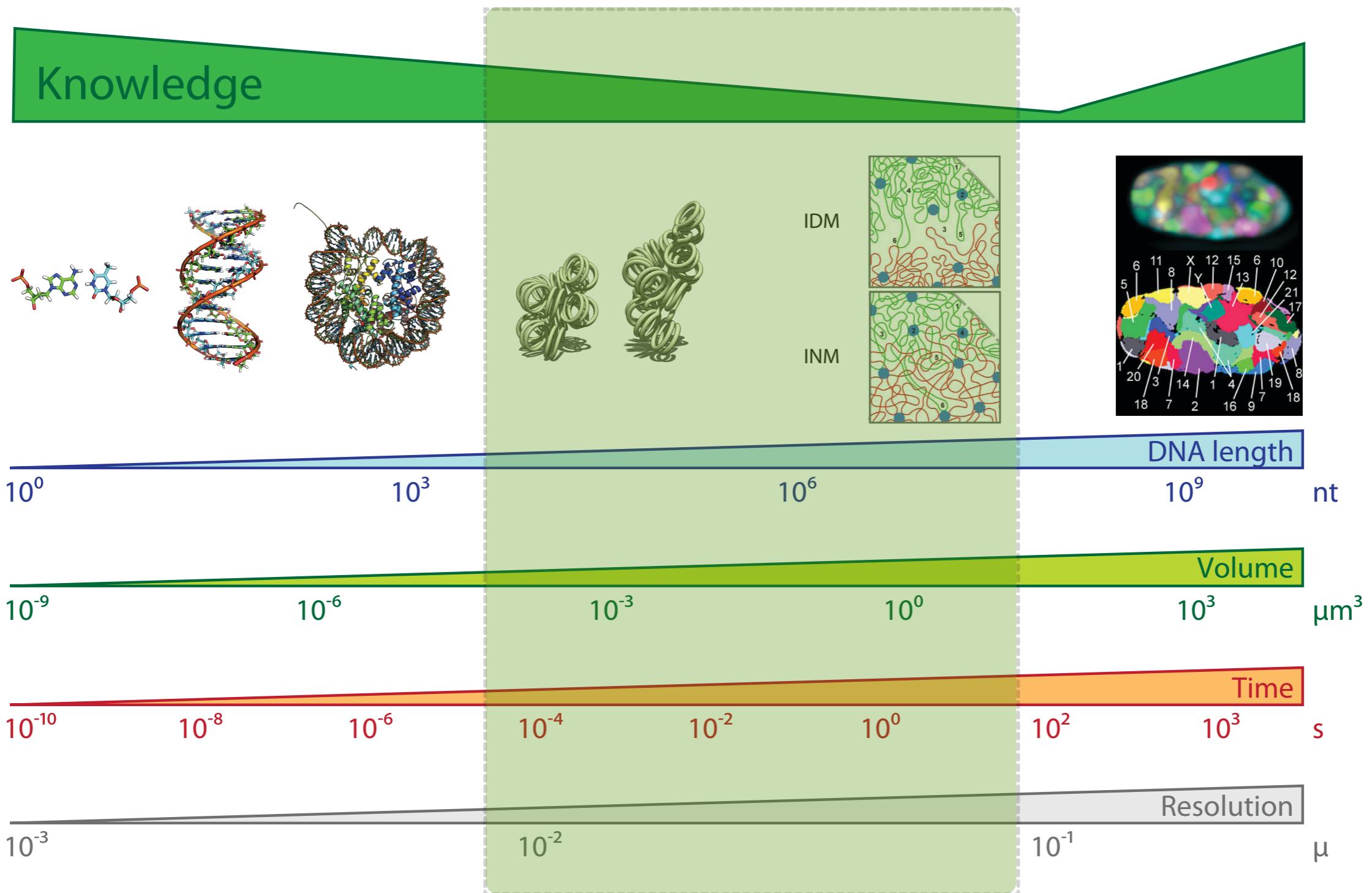
François Serra, Marco Di Stefano & Marc A. Martí-Renom
Structural Genomics Group (CNAG-CRG)





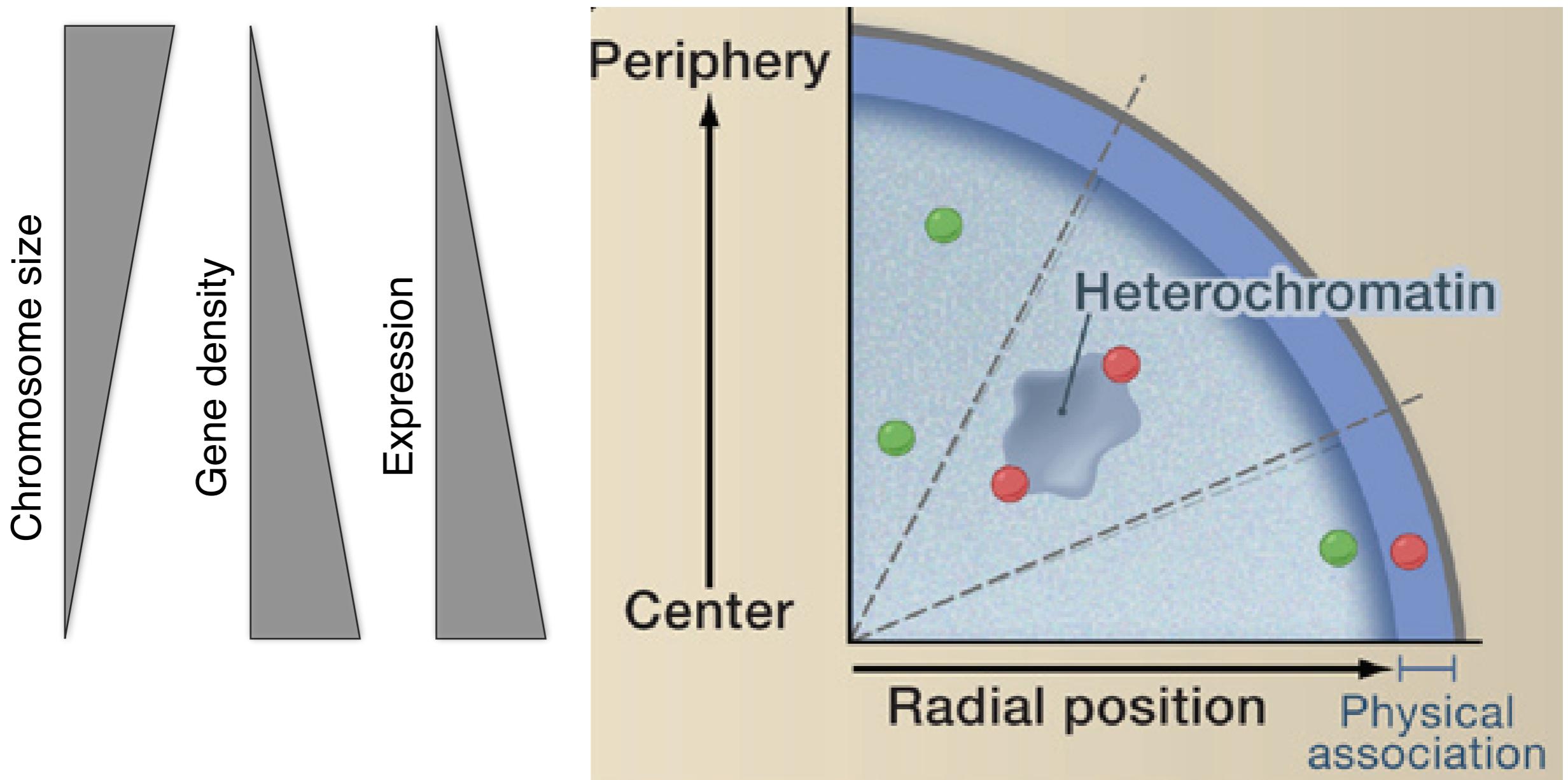
Resolution Gap

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

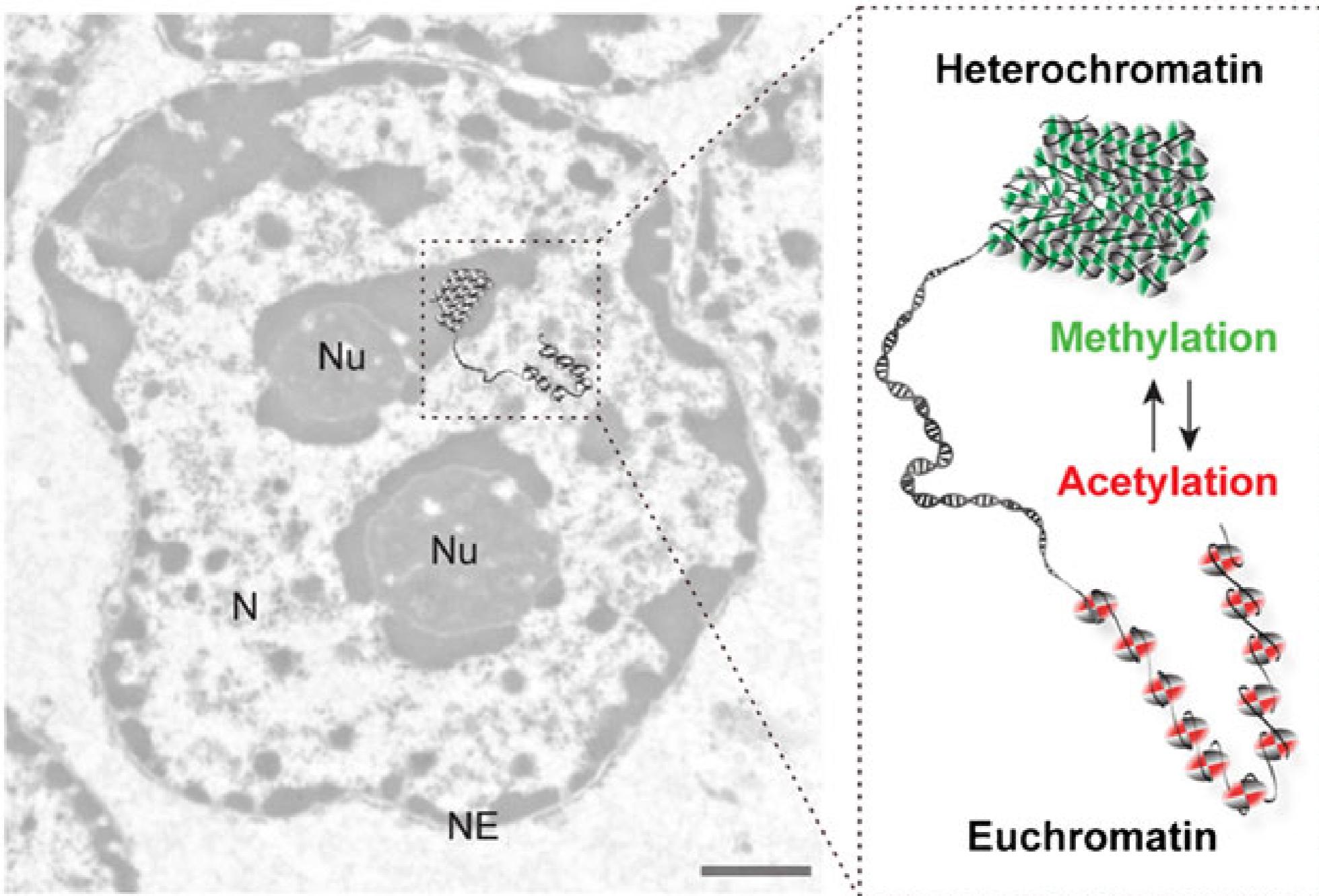


Level I: Radial genome organization

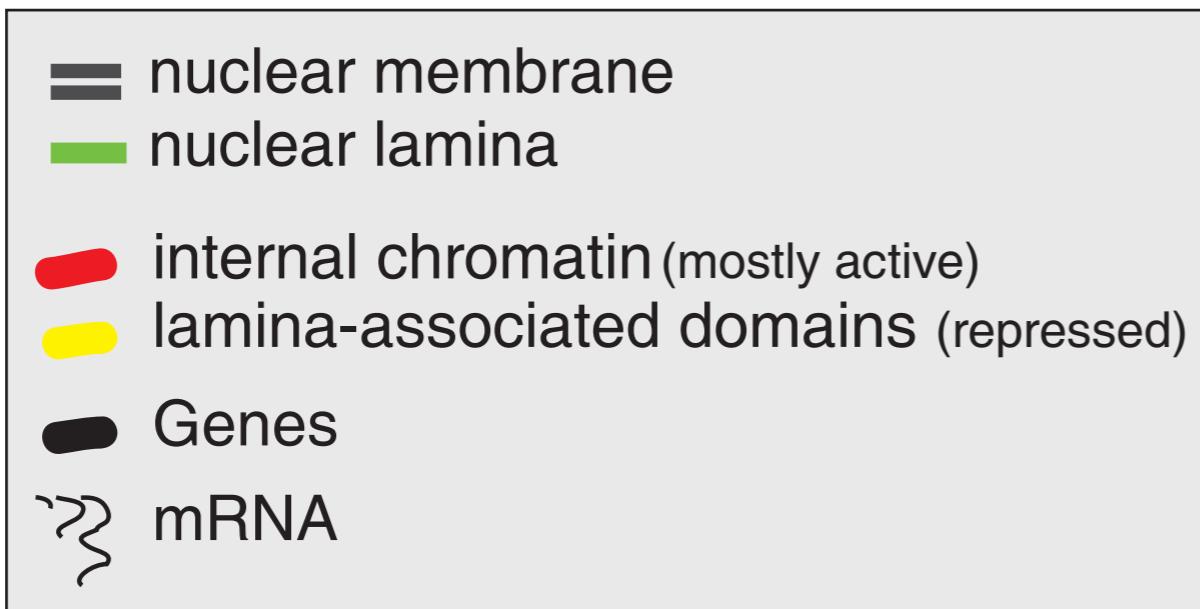
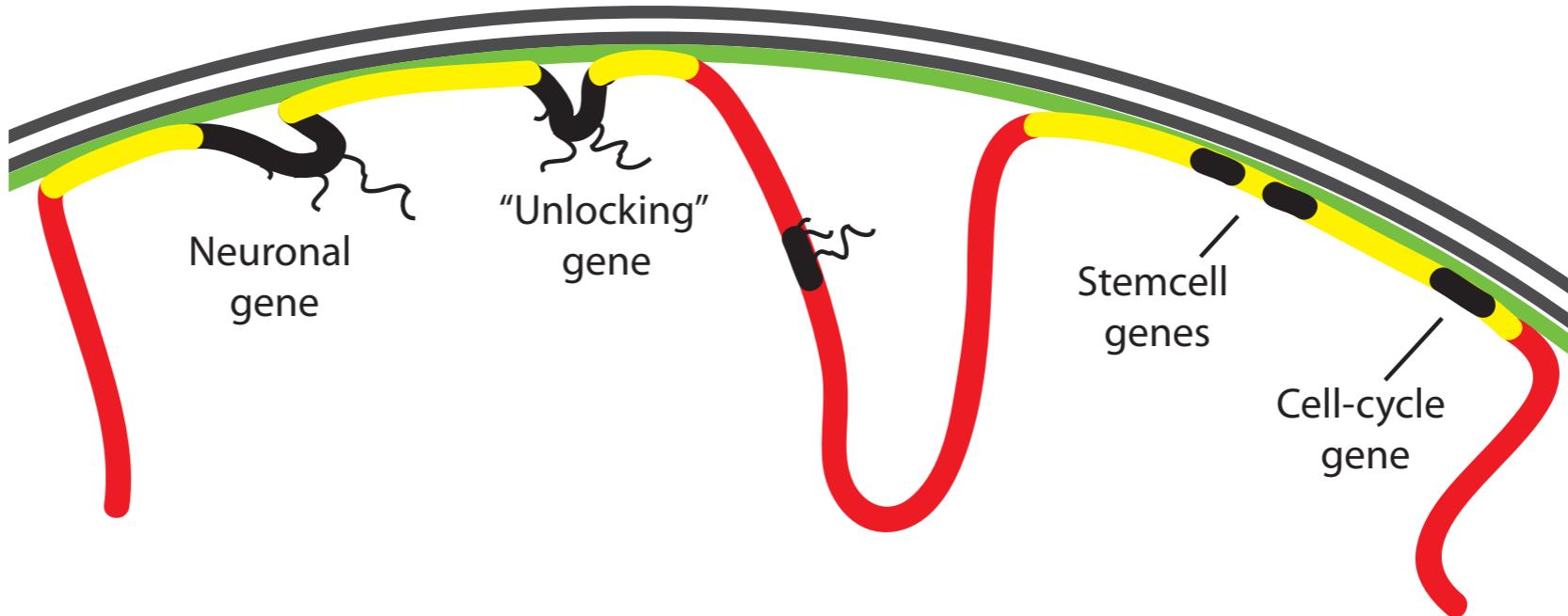
Takizawa, T., Meaburn, K. J. & Misteli, T. The meaning of gene positioning. Cell 135, 9–13 (2008).



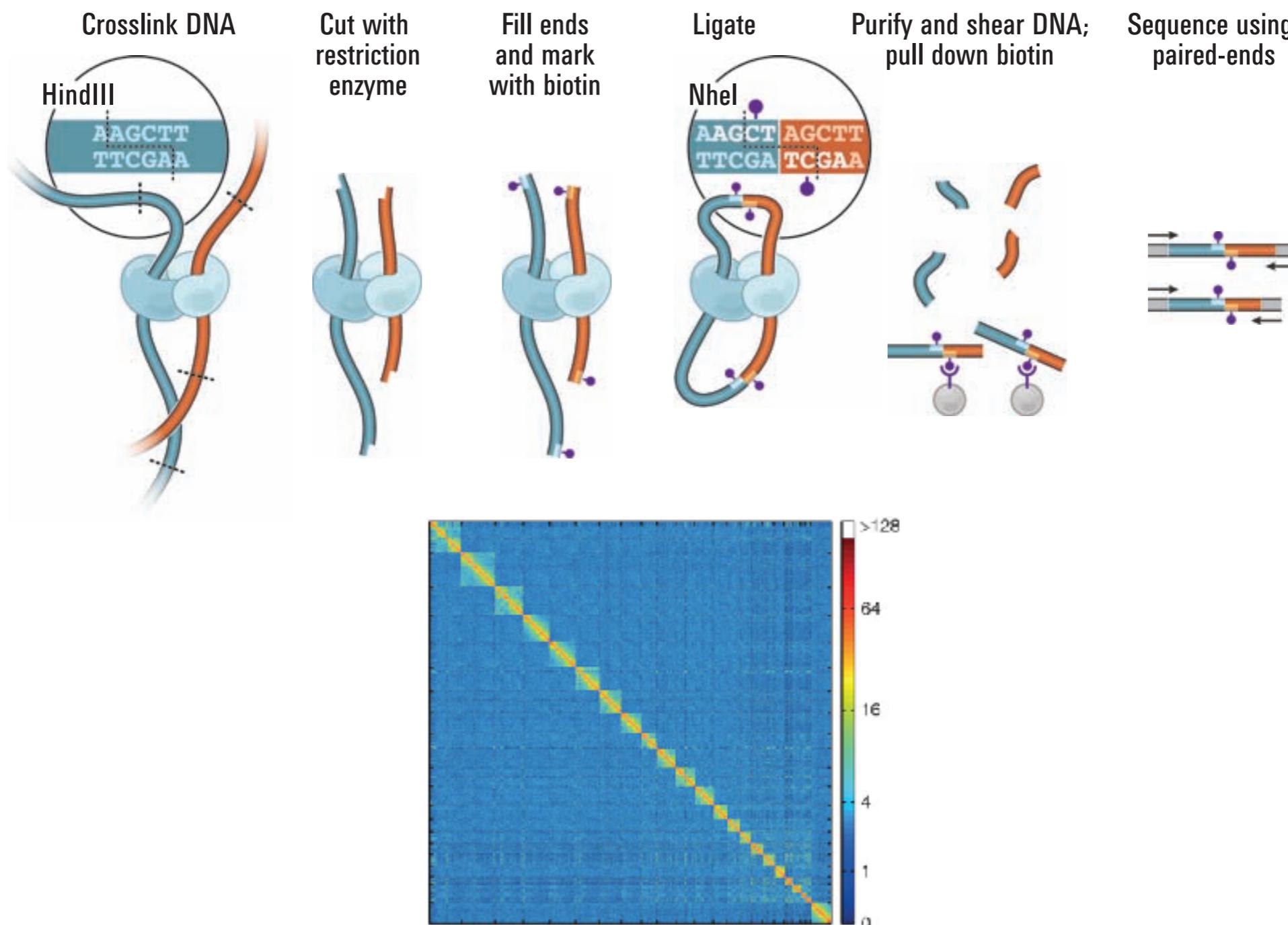
Level II: Euchromatin vs heterochromatin



Level III: Lamina-genome interactions



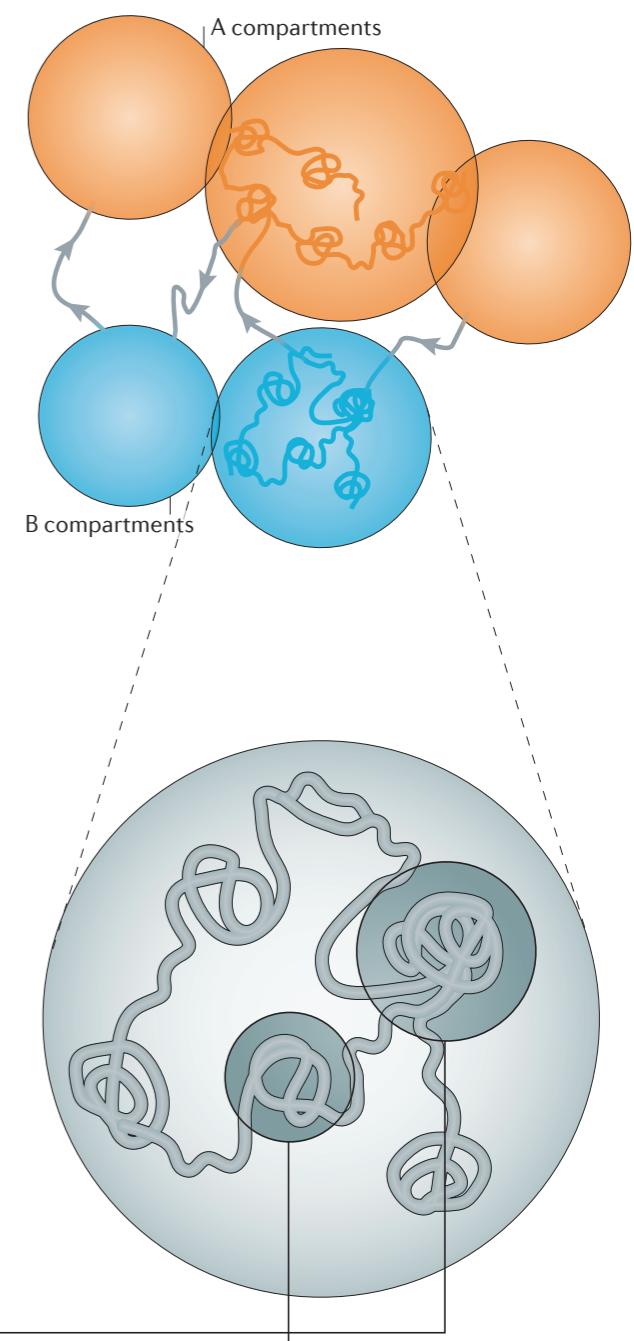
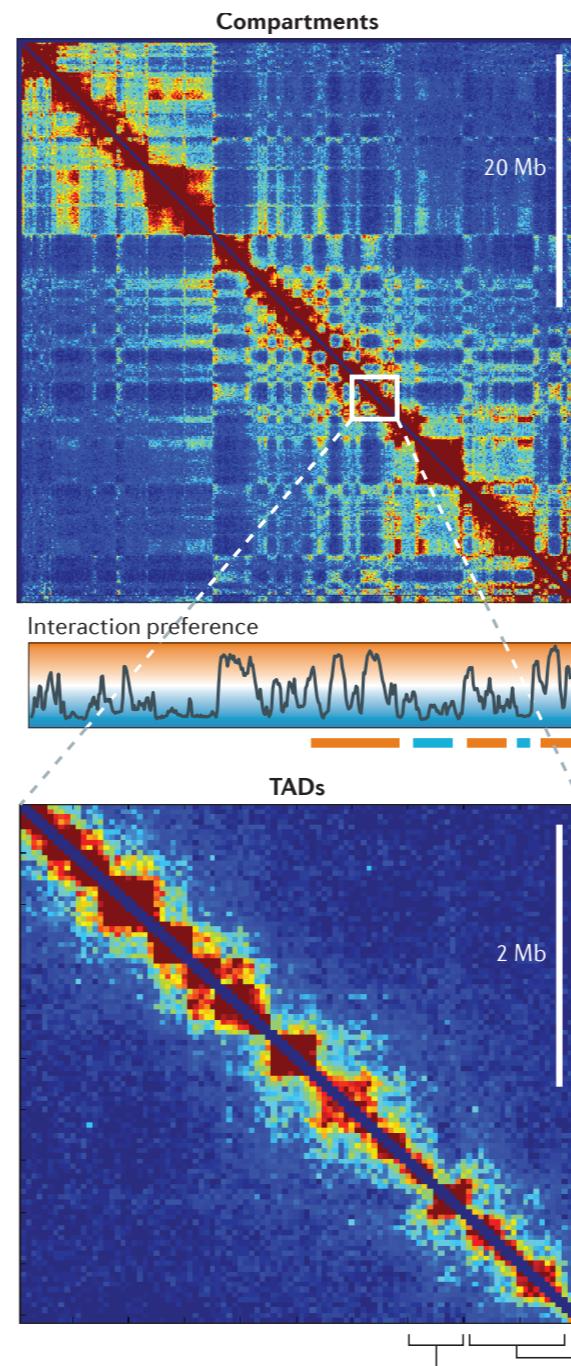
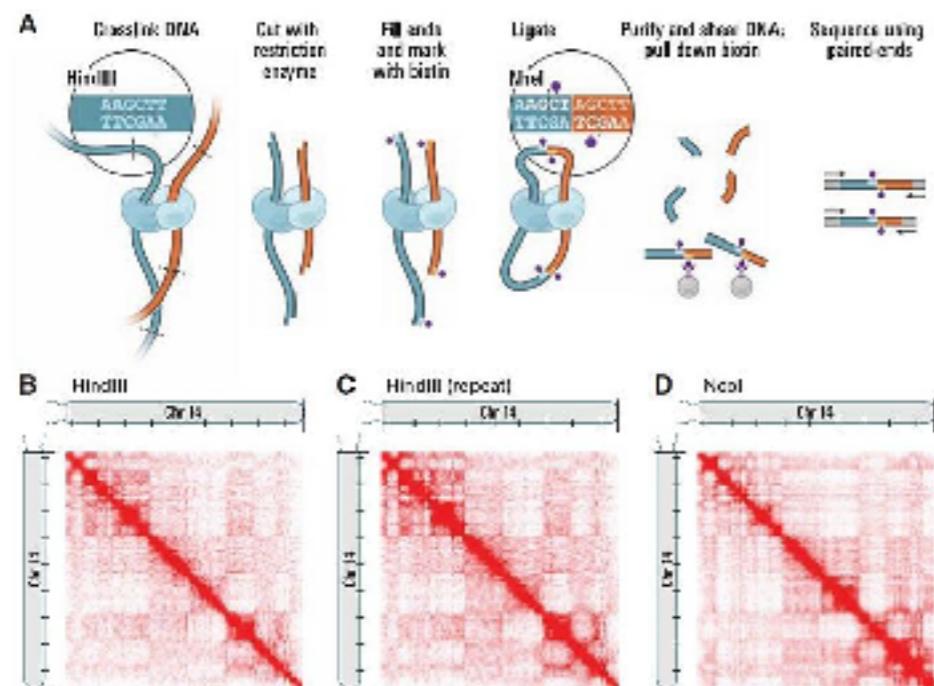
Level IV: Higher-order organization



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.

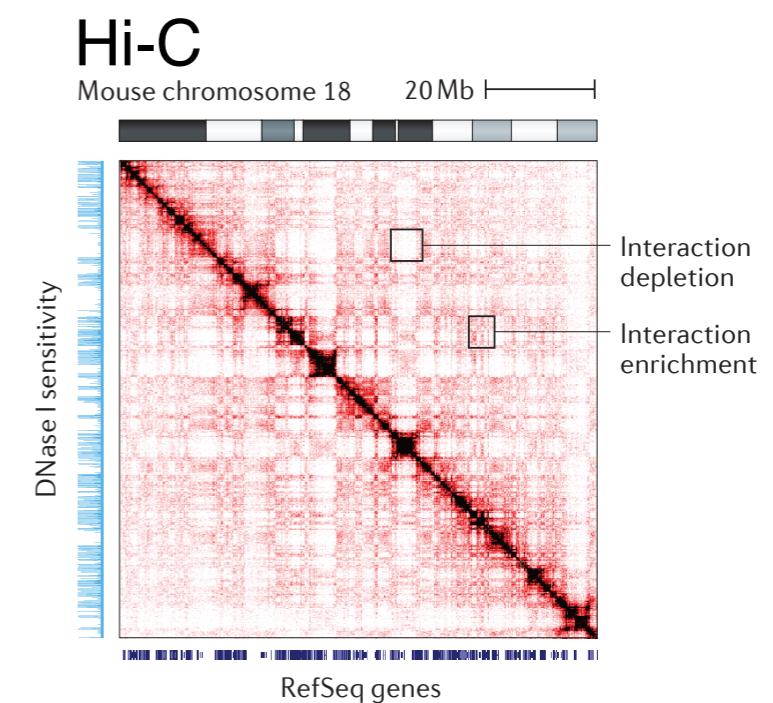
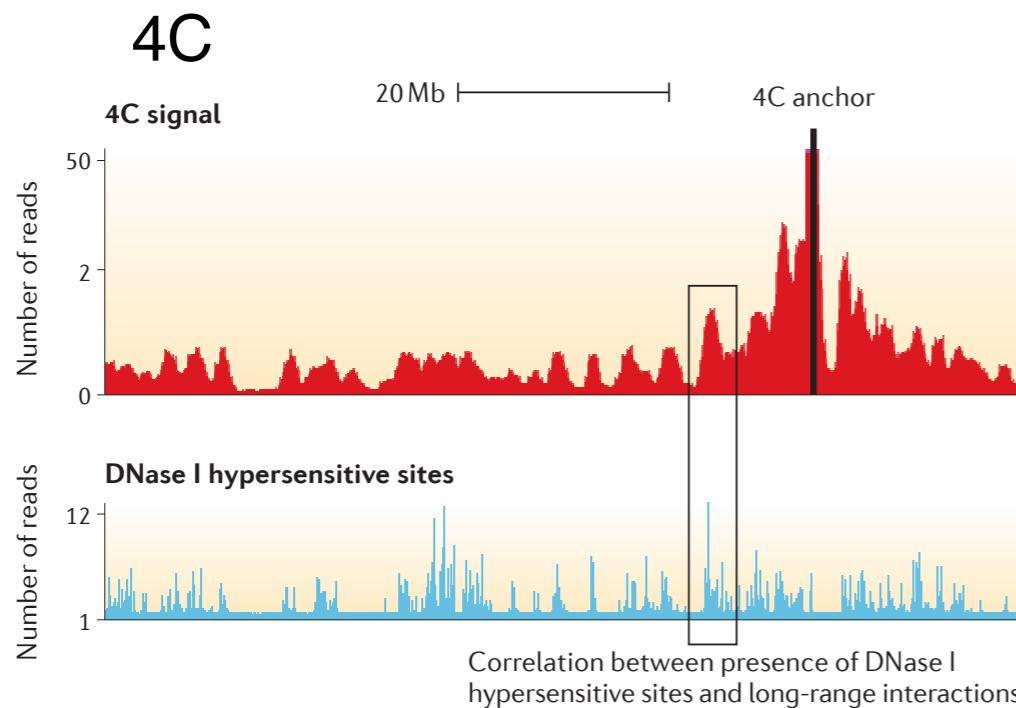
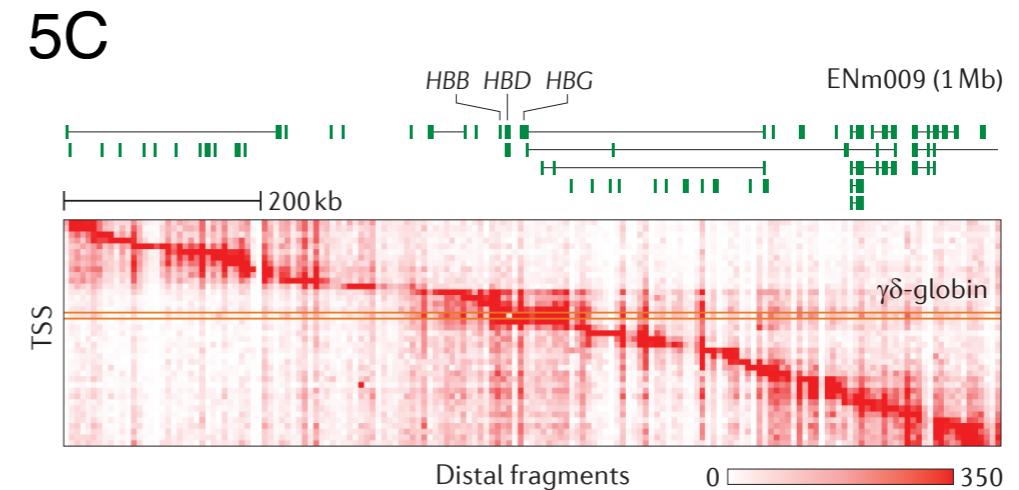
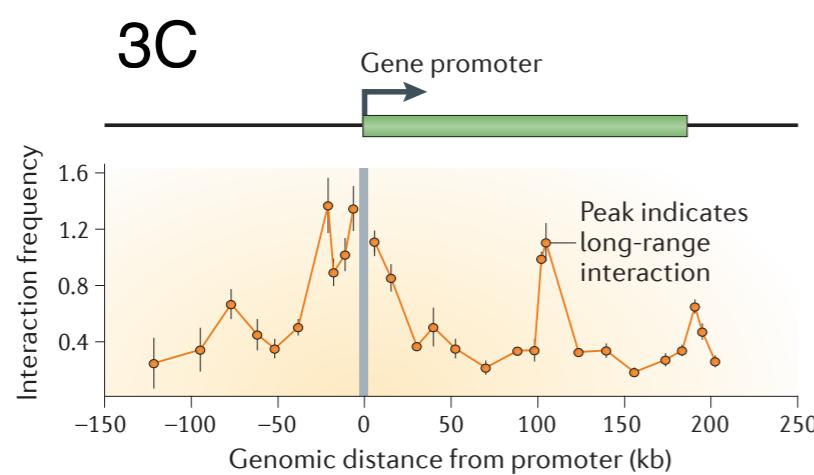
Level IV: Higher-order organization

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



Level IV: Higher-order organization

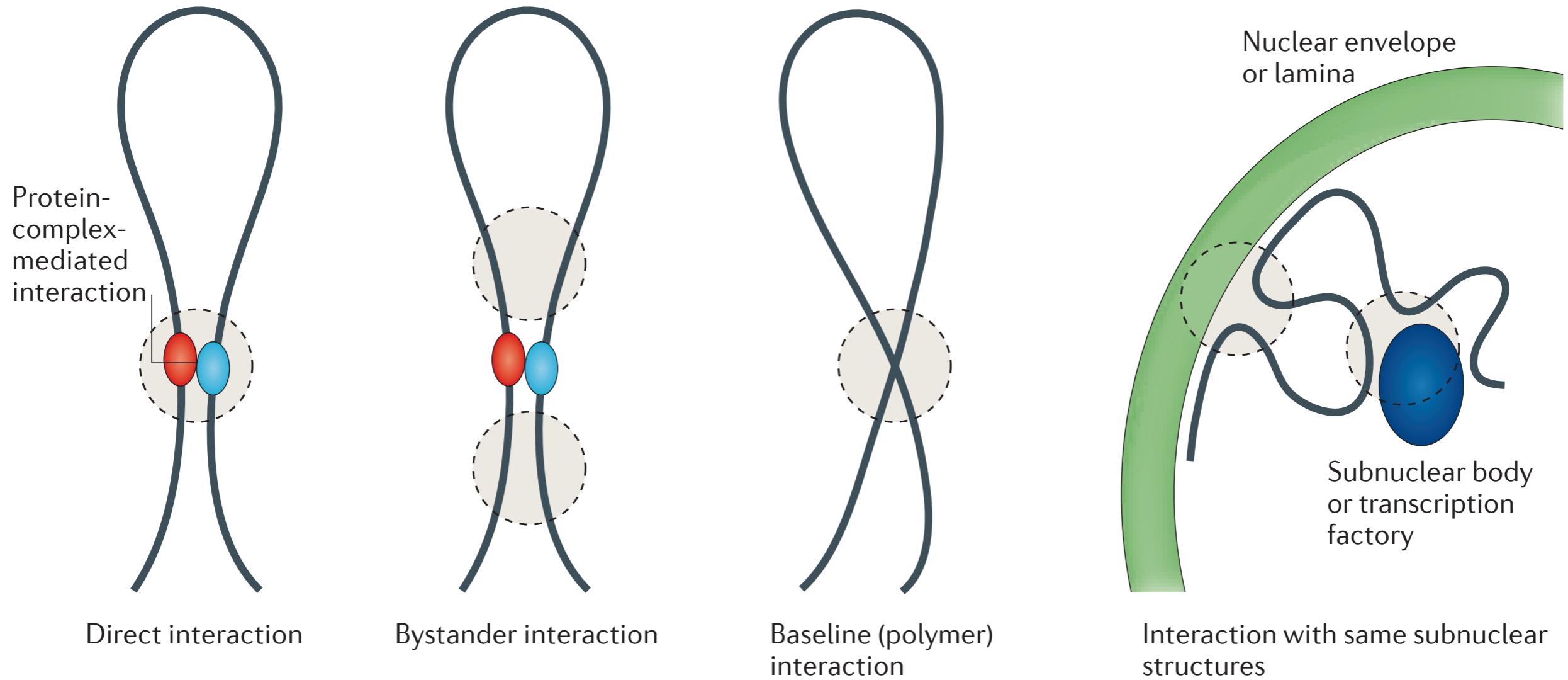
Insights from 3C-based technologies



Adapted from Dekker et al., (2013) Nat Rev Genetics

Level IV: Higher-order organization

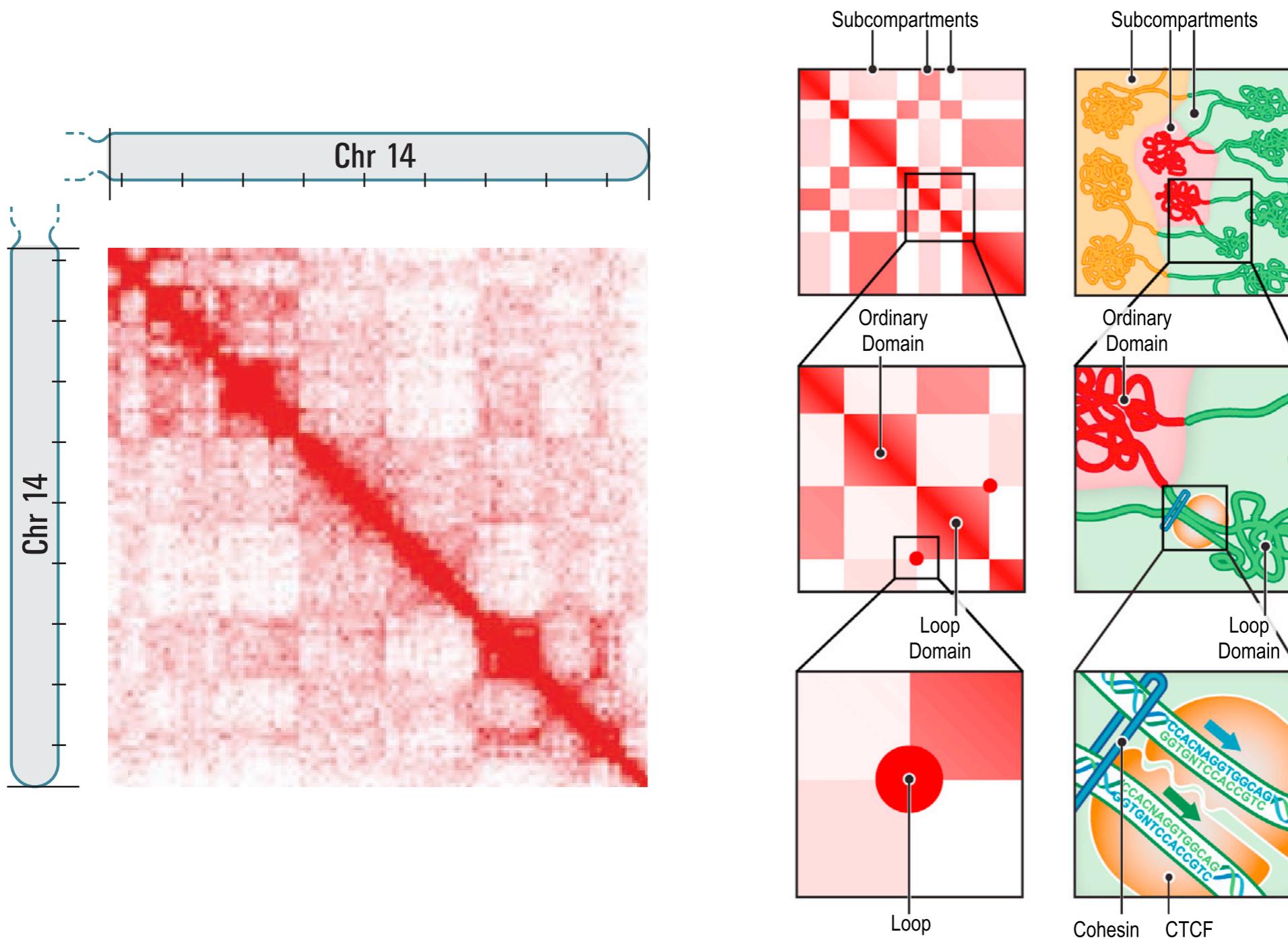
Interpreting chromatin interaction data



Adapted from Dekker et al., (2013) Nat Rev Genetics

Level IV: Higher-order organization

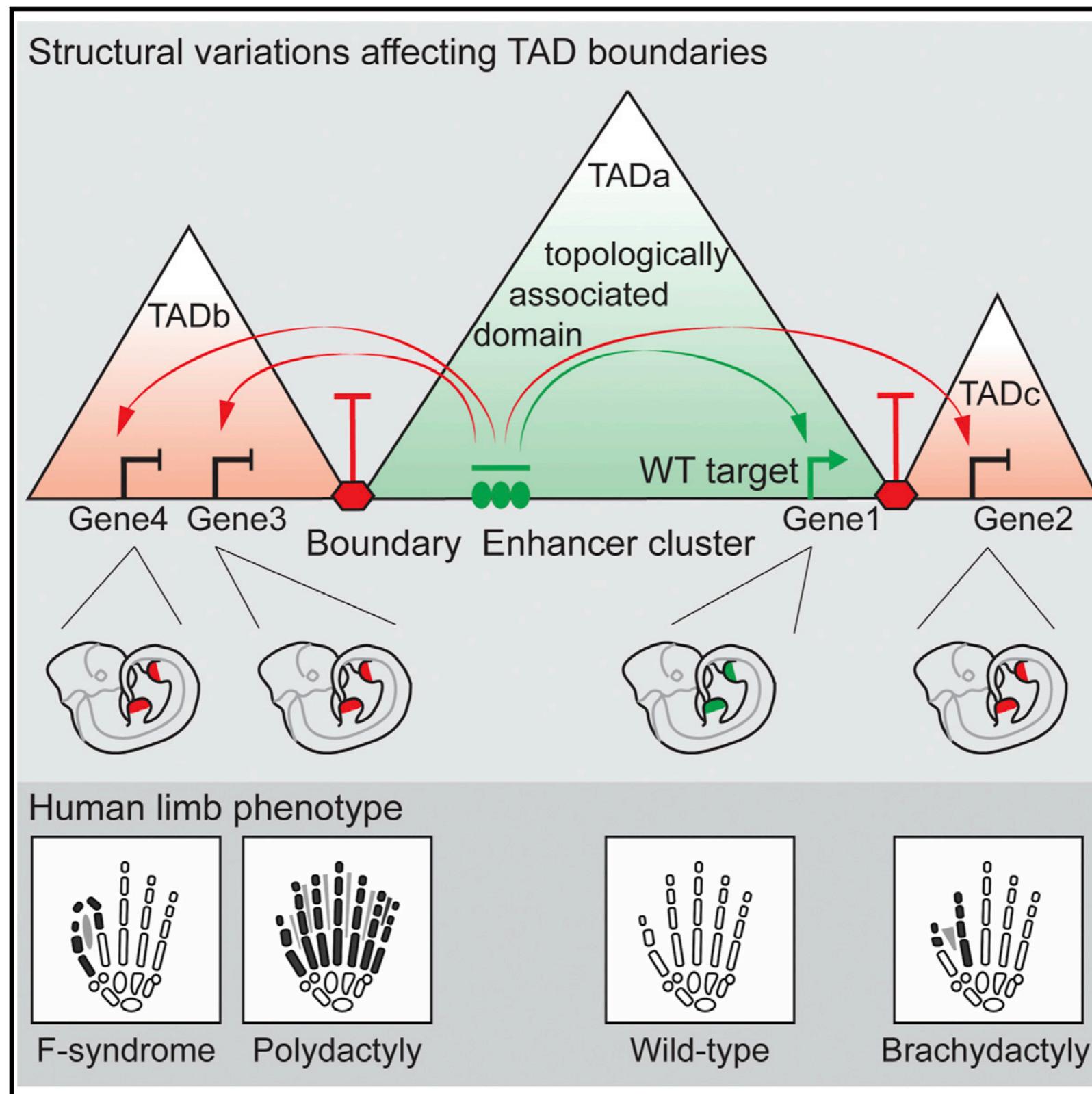
Hierarchical genome organisation



Lieberman-Aiden, E., et al. (2009). Science, 326(5950), 289–293.
Rao, S. S. P., et al. (2014). Cell, 1–29.

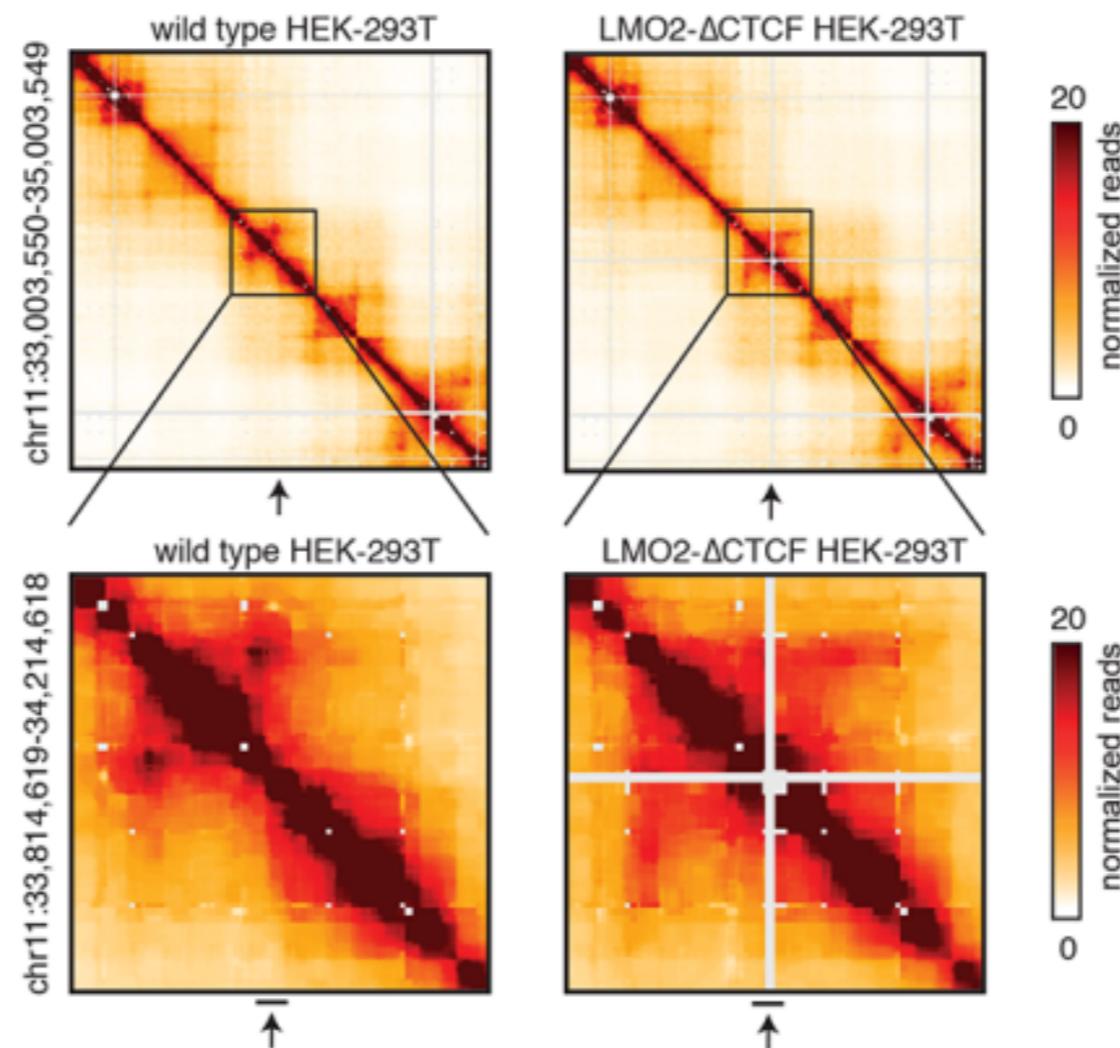
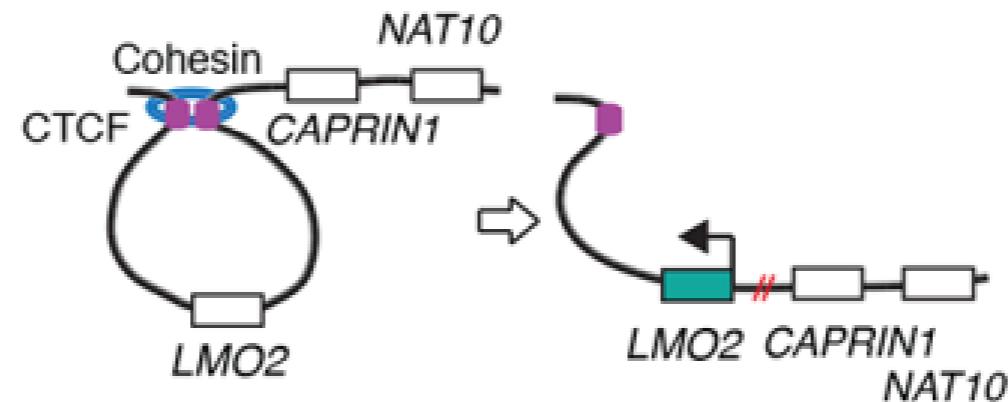
Level IV: Higher-order organization

TADs are functional units



Level IV: Higher-order organization

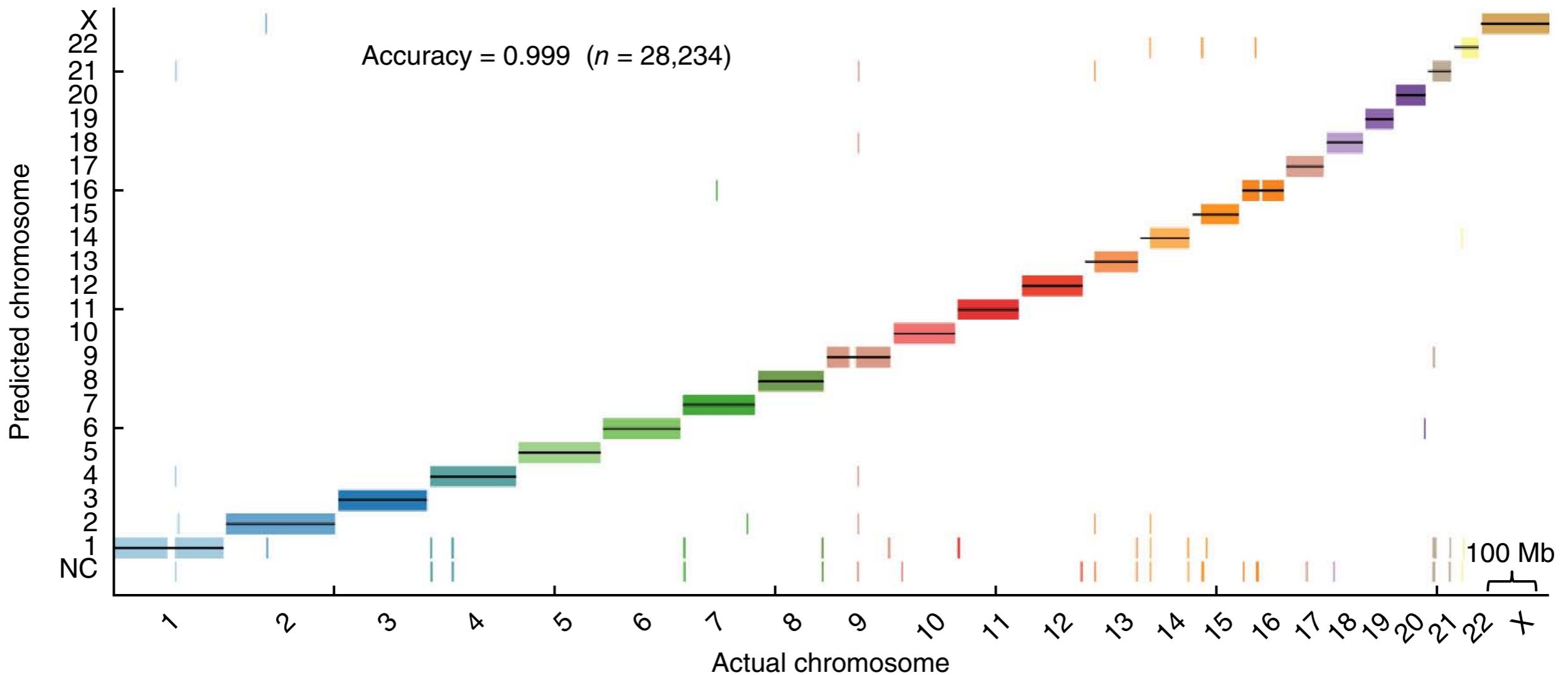
TADs are functional units



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

3C Detour...
desirable side effects

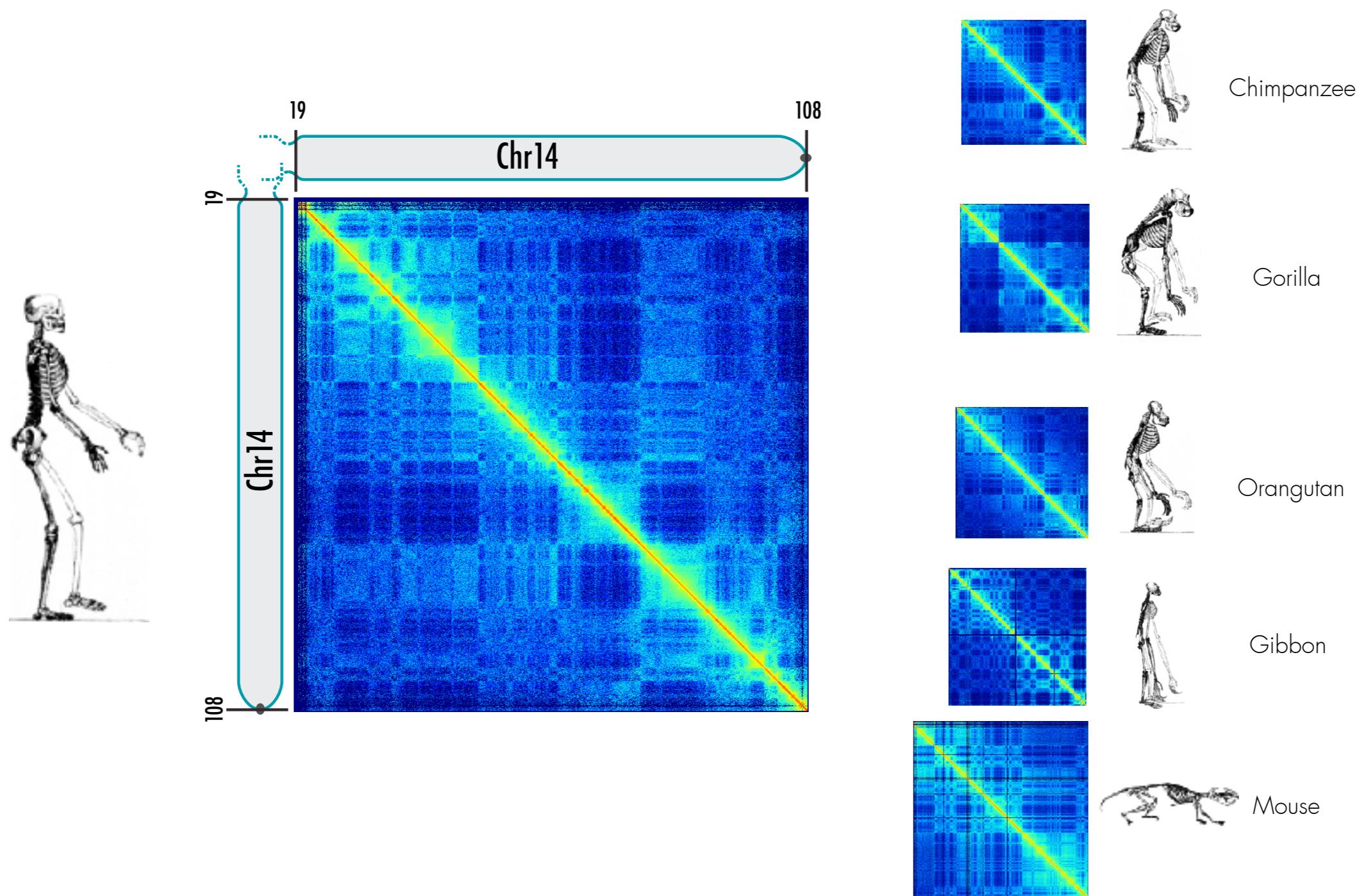
Chromosome Conformation Capture for de-novo assembly



Kaplan, N., & Dekker, J. (2013). High-throughput genome scaffolding from *in vivo* DNA interaction frequency. *Nature Biotechnology*, 31(12), 1143–1147.

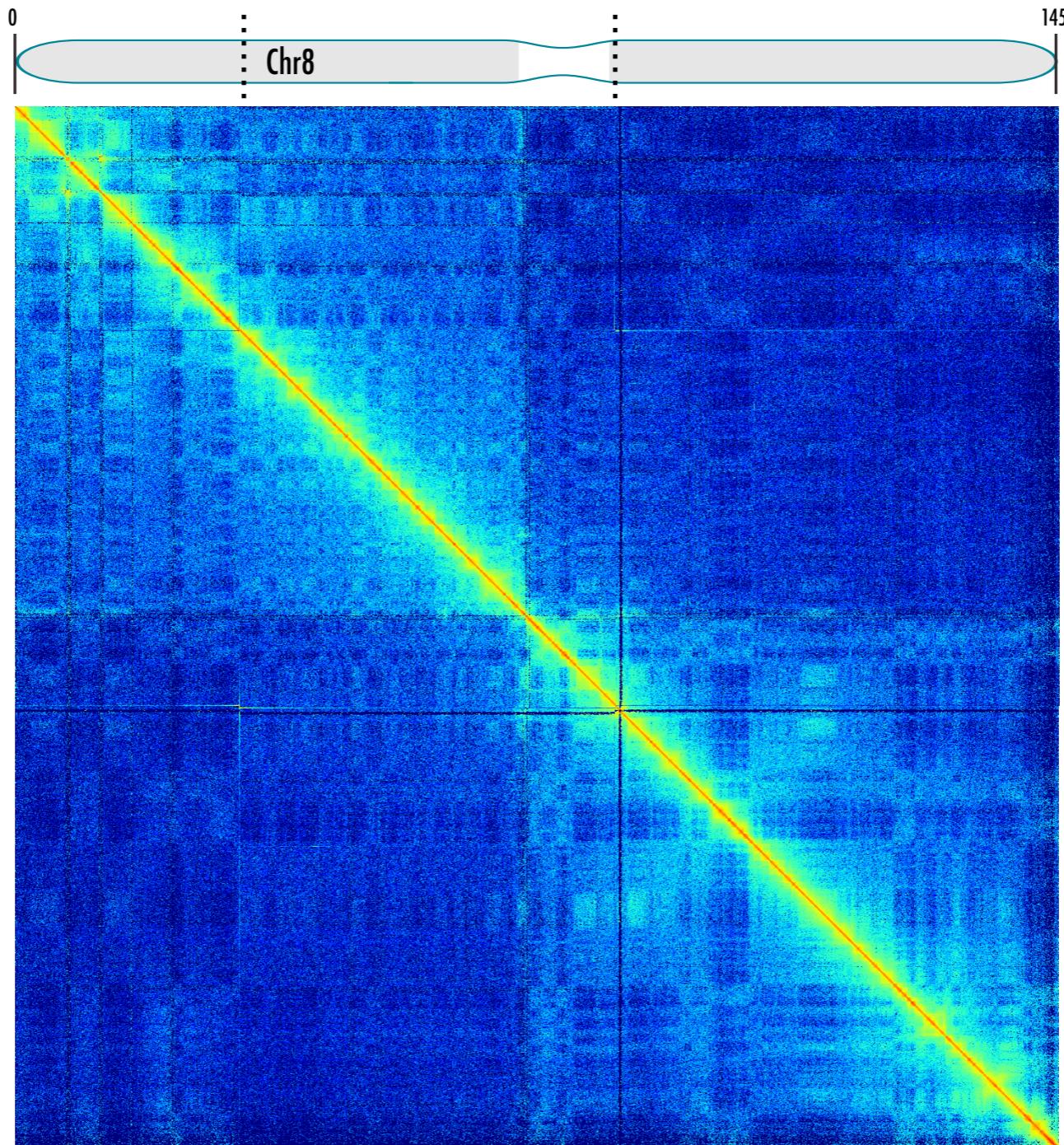
Great apes lymphoblast maps

Chromosome 14

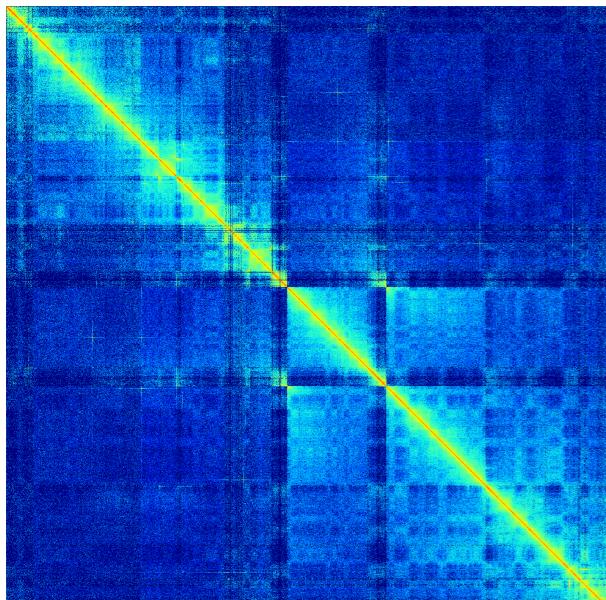


Assembly error detection

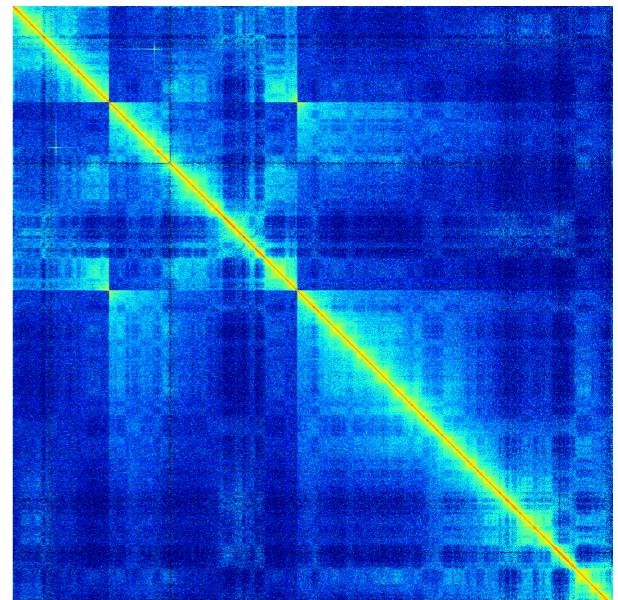
Chromosome 8 Gorilla



Chr 7

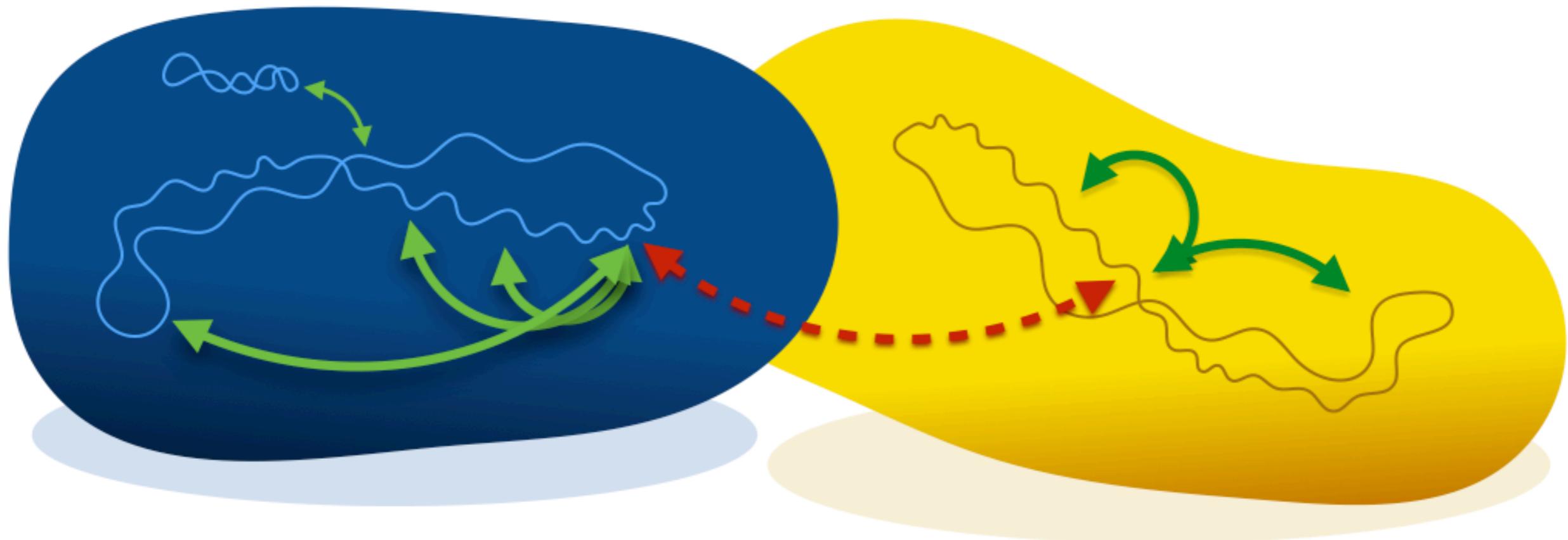


Chr 12



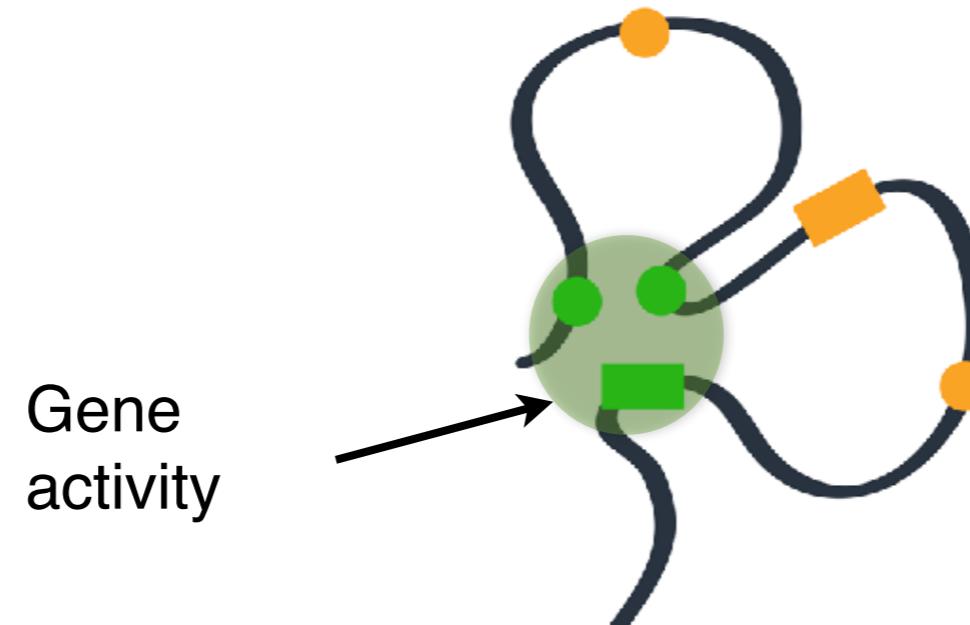
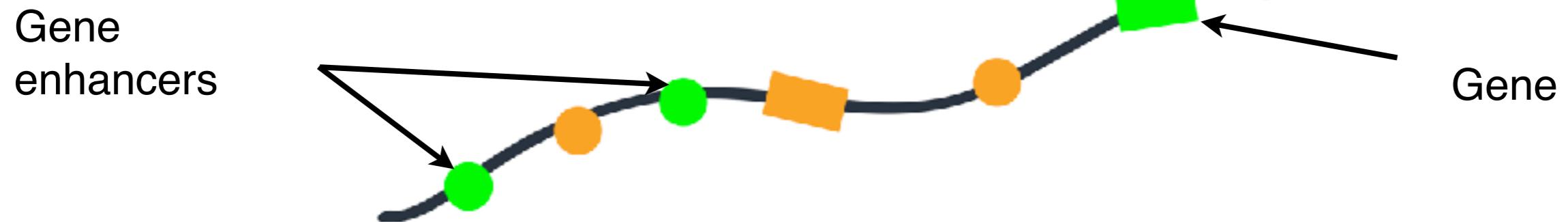
GGO8 has an inversion of the region corresponding to HSA8:30.0-86.9Mb
Aylwyn Scally (Department of Genetics, University of Cambridge)

Chromosome Conformation Capture for meta genomics

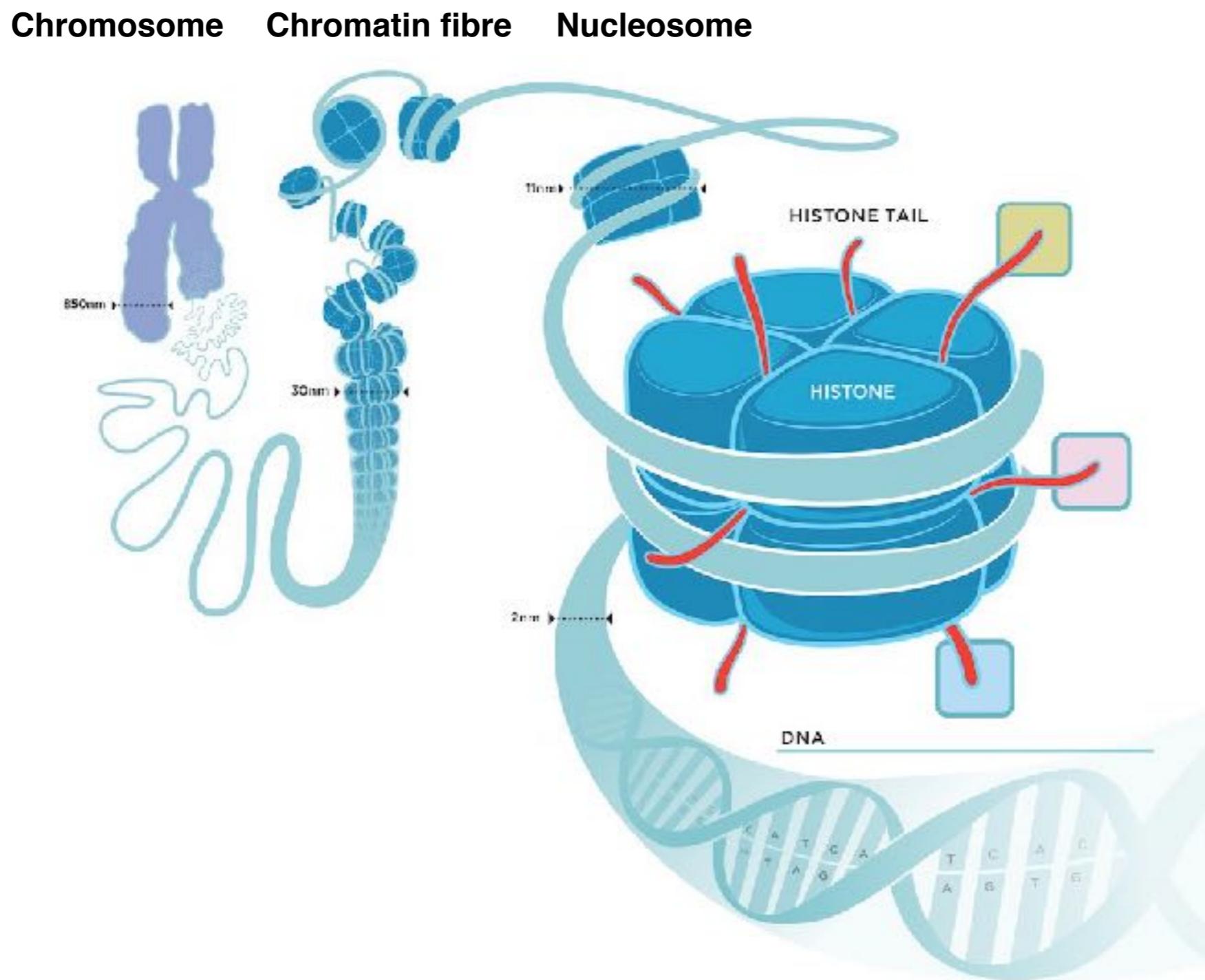


Beitel, C. W., Froenicke, L., Lang, J. M., Korf, I. F., Michelmore, R. W., Eisen, J. A., & Darling, A. E. (2014). Strain- and plasmid-level deconvolution of a synthetic metagenome by sequencing proximity ligation products. doi:10.7287/peerj.preprints.260v1

Level V: Chromatin loops



Level VI: Nucleosome



Adapted from Richard E. Ballermann, 2012

Complex genome organization

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

