
HUMAN “The Movie” by Yann Arthus-Bertrand

Structure determination of genomes and genomic domains by satisfaction of spatial restraints

Marc A. Marti-Renom
CNAG-CRG · ICREA

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

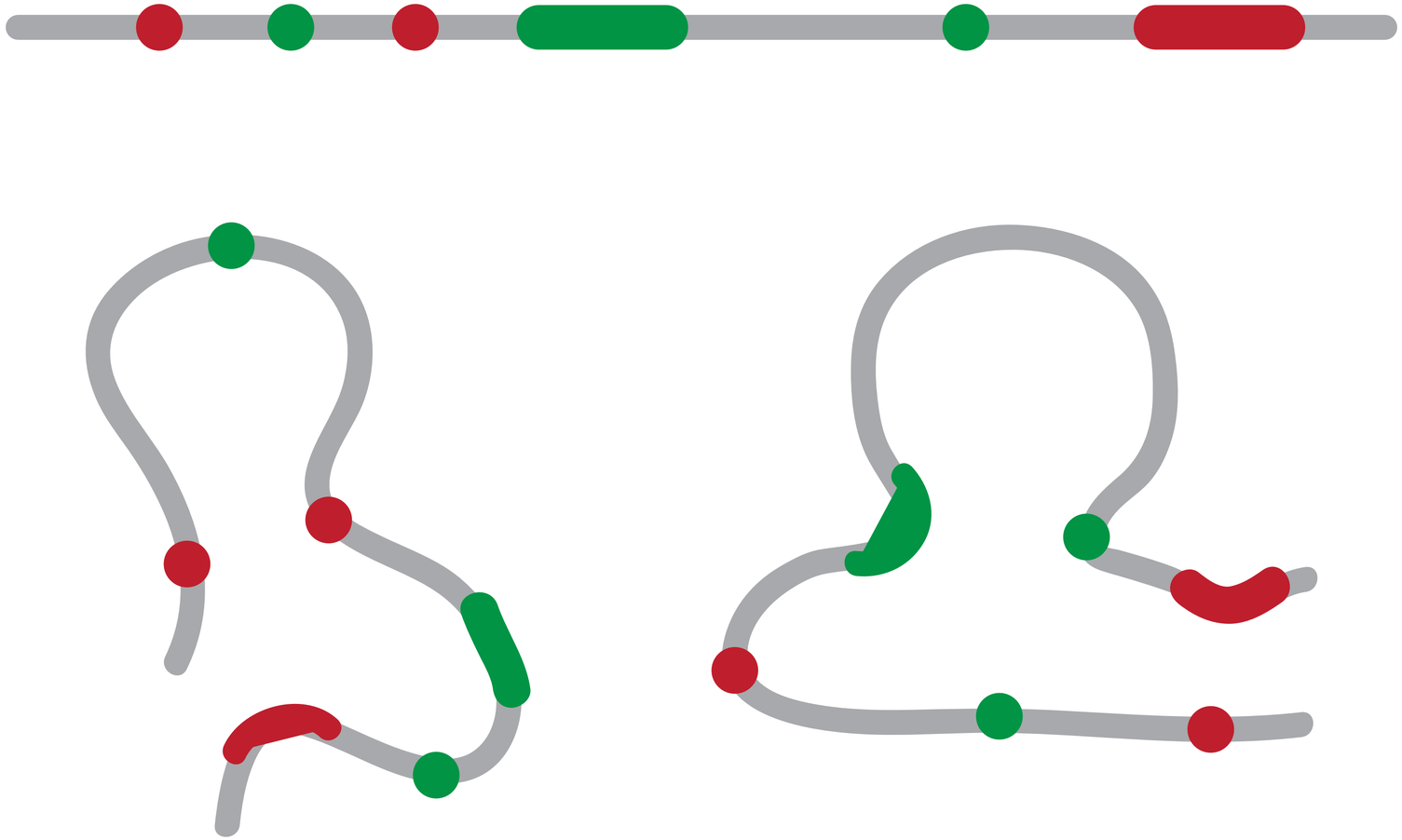
cnag CRG ICREA

All you will see in the screen will be stored here:

http://marciuslab.org/www/presentations/

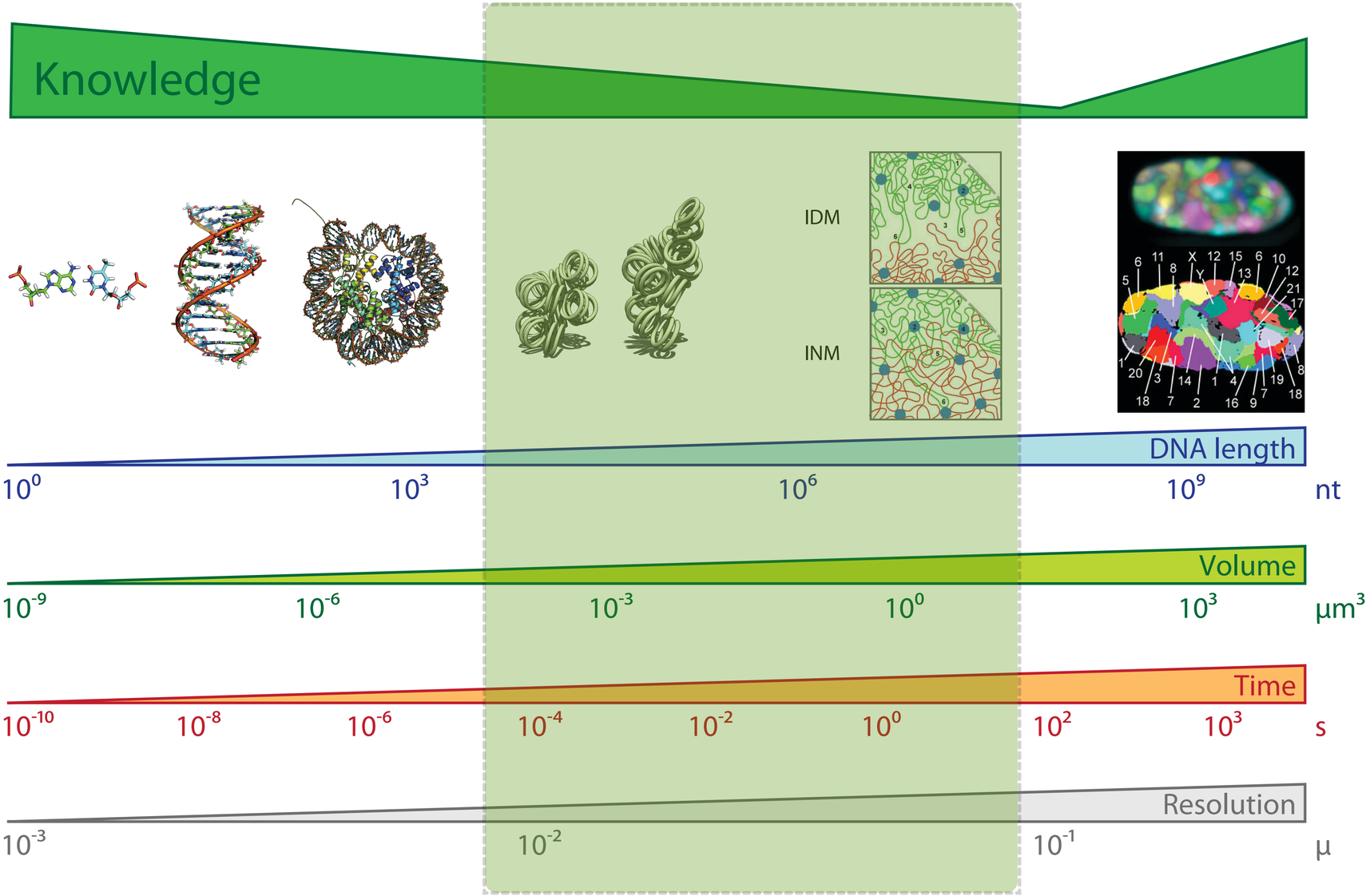
I encourage you to:

You can ask for question by using the chat or by raising your hand



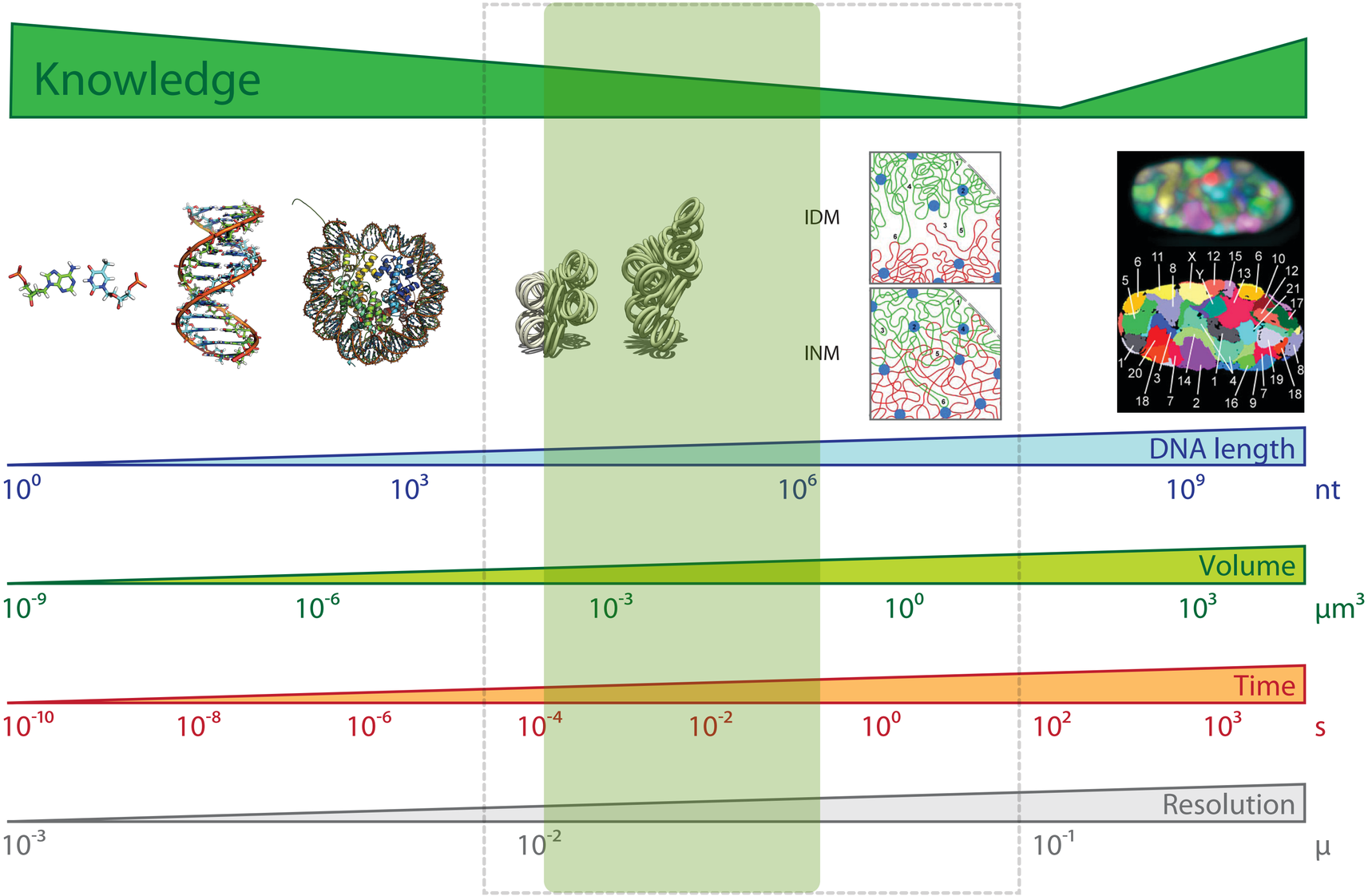
Resolution Gap

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



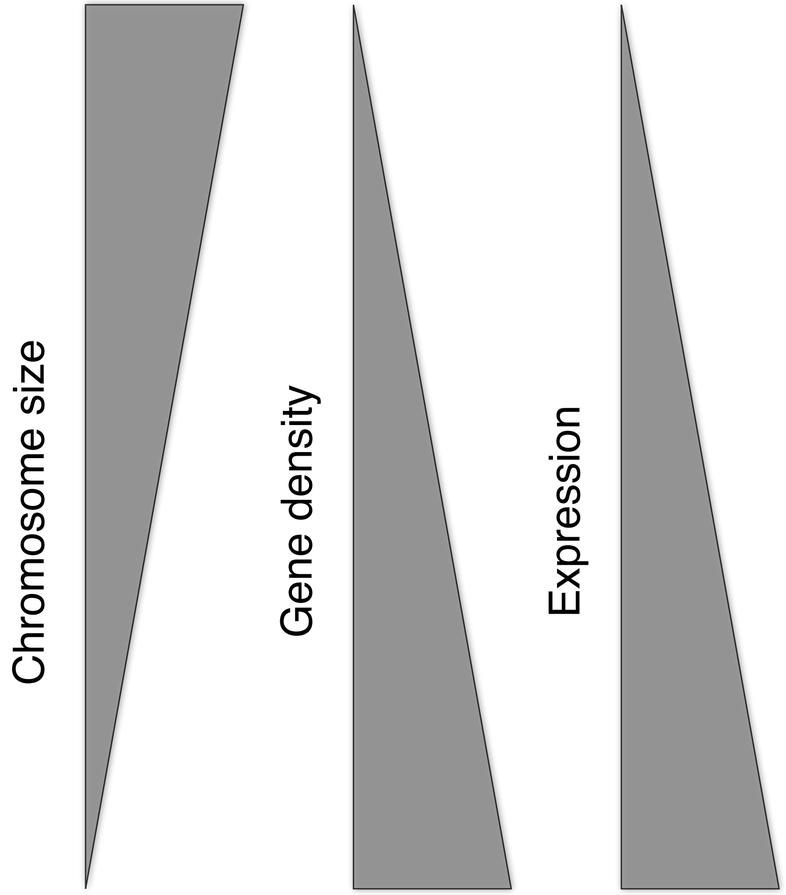
Resolution Gap

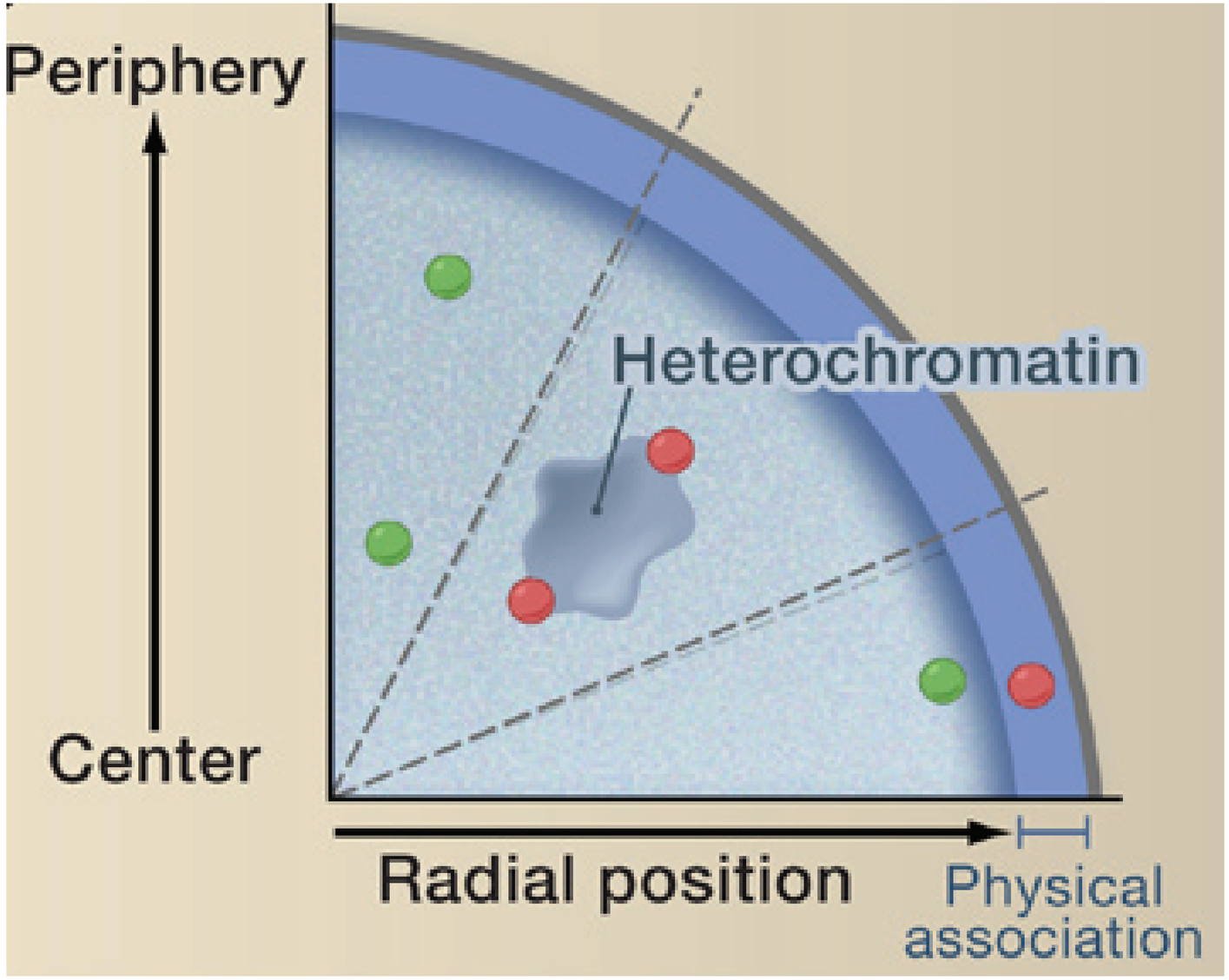
Marti-Renom, M. A. & Mirny, L. A. PLoS Comput Biol *7*, e1002125 (2011)



Level I: Radial genome organization

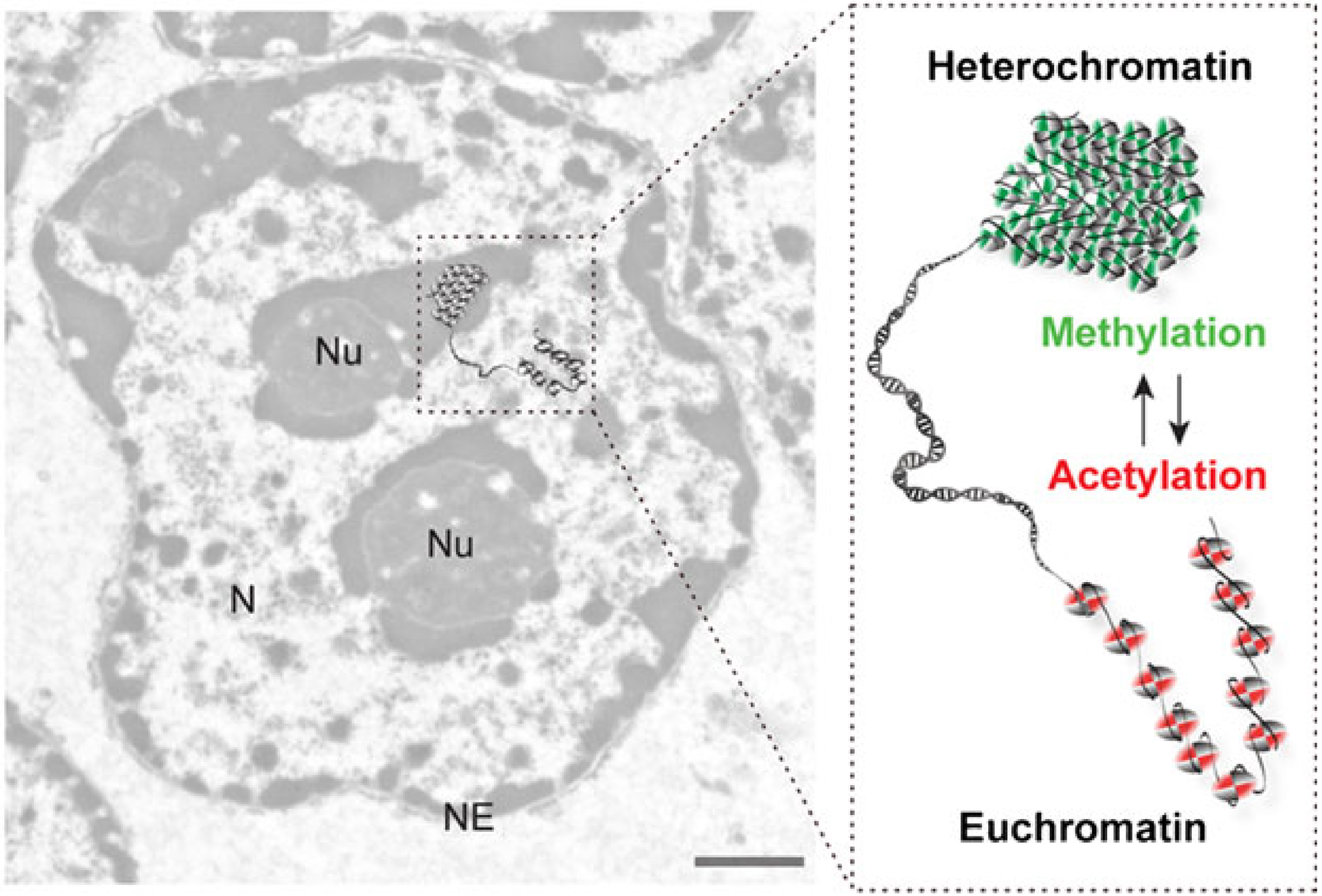
Takizawa, T., Meaburn, K. J. & Misteli, T. The meaning of gene positioning. Cell 135, 9–13 (2008).



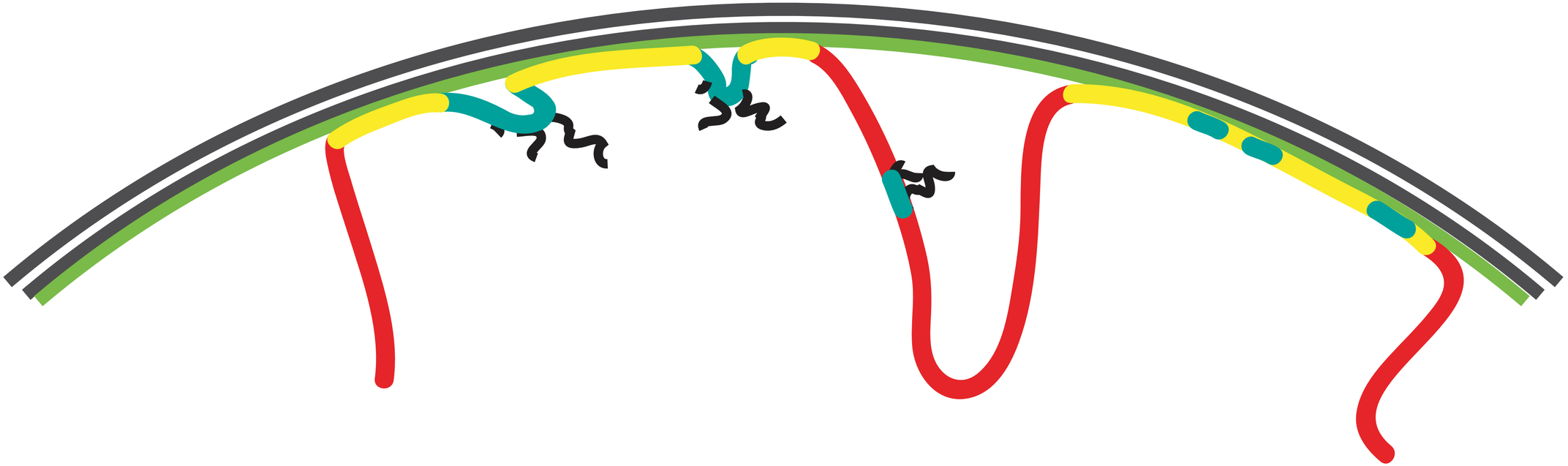


Level II: Euchromatin vs heterochromatin

Electron microscopy



Level III: Lamina-genome interactions



nuclear membrane
nuclear lamina

internal chromatin (mostly active)
lamina-associated domains (repressed)

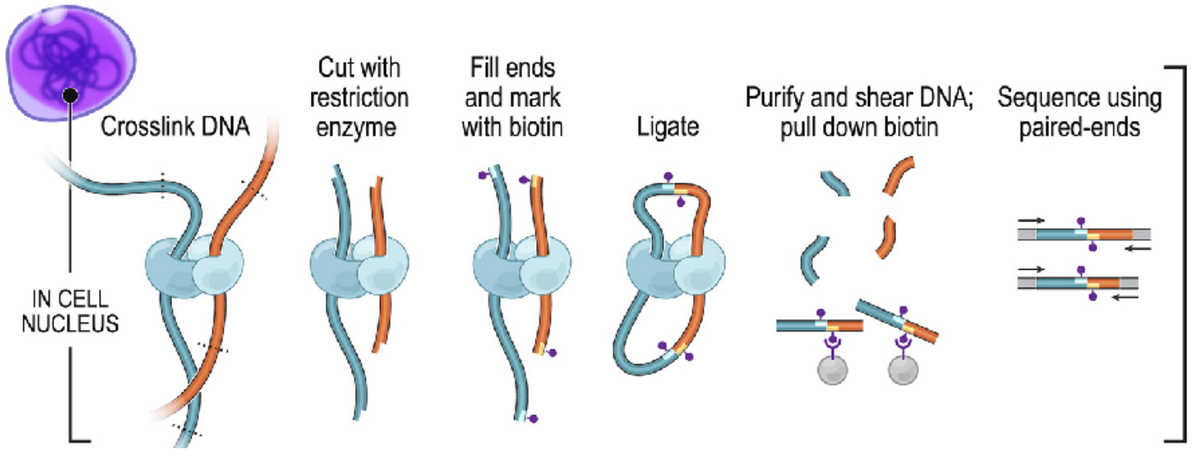
Genes

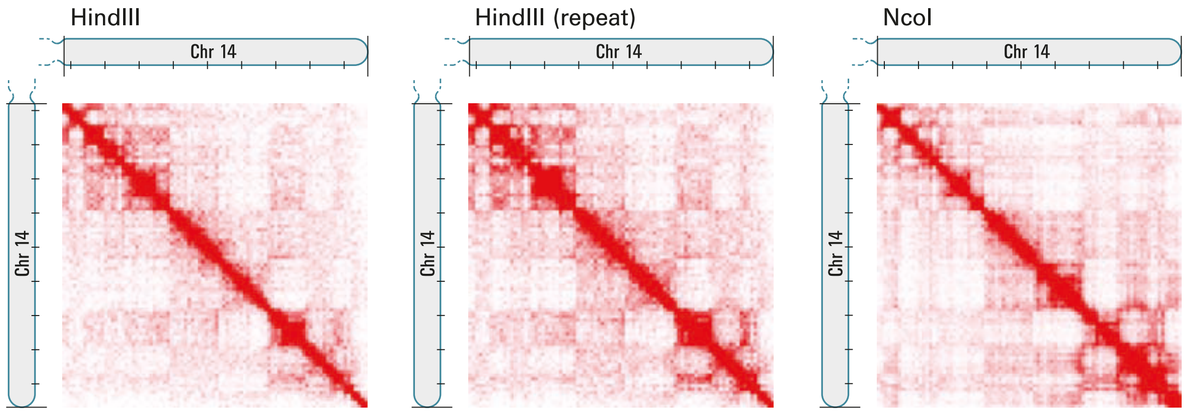
mRNA

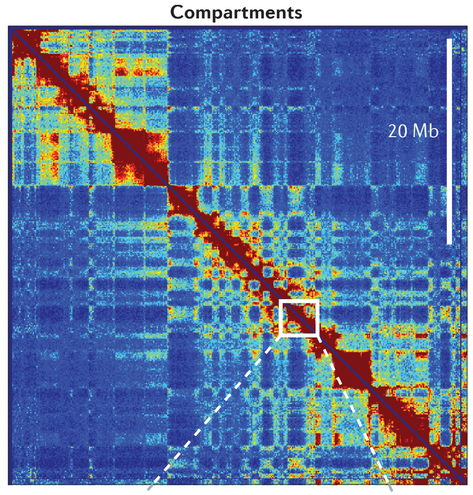
Adapted from Molecular Cell 38, 603-613, 2010

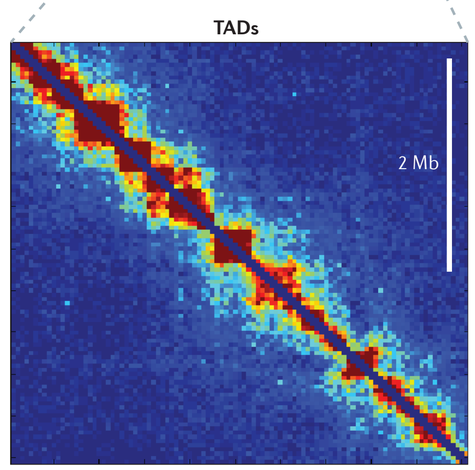
Level IV: Higher-order organization

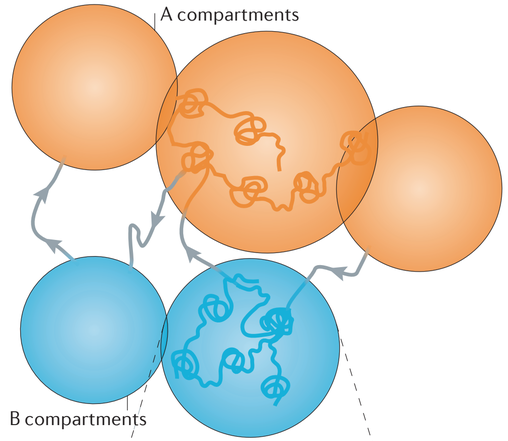
Dekker, J., Marti-Renom, M. A. & Mirny, L. A. Nat Rev Genet 14, 390–403 (2013).

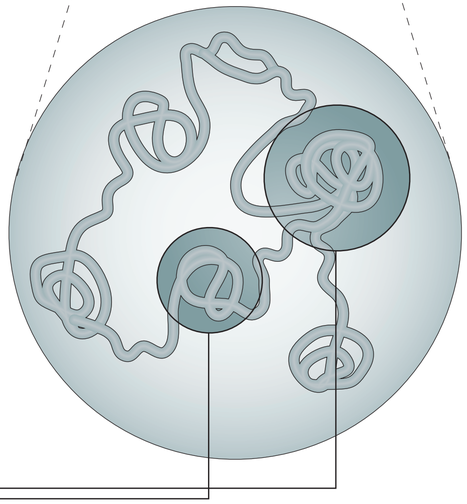




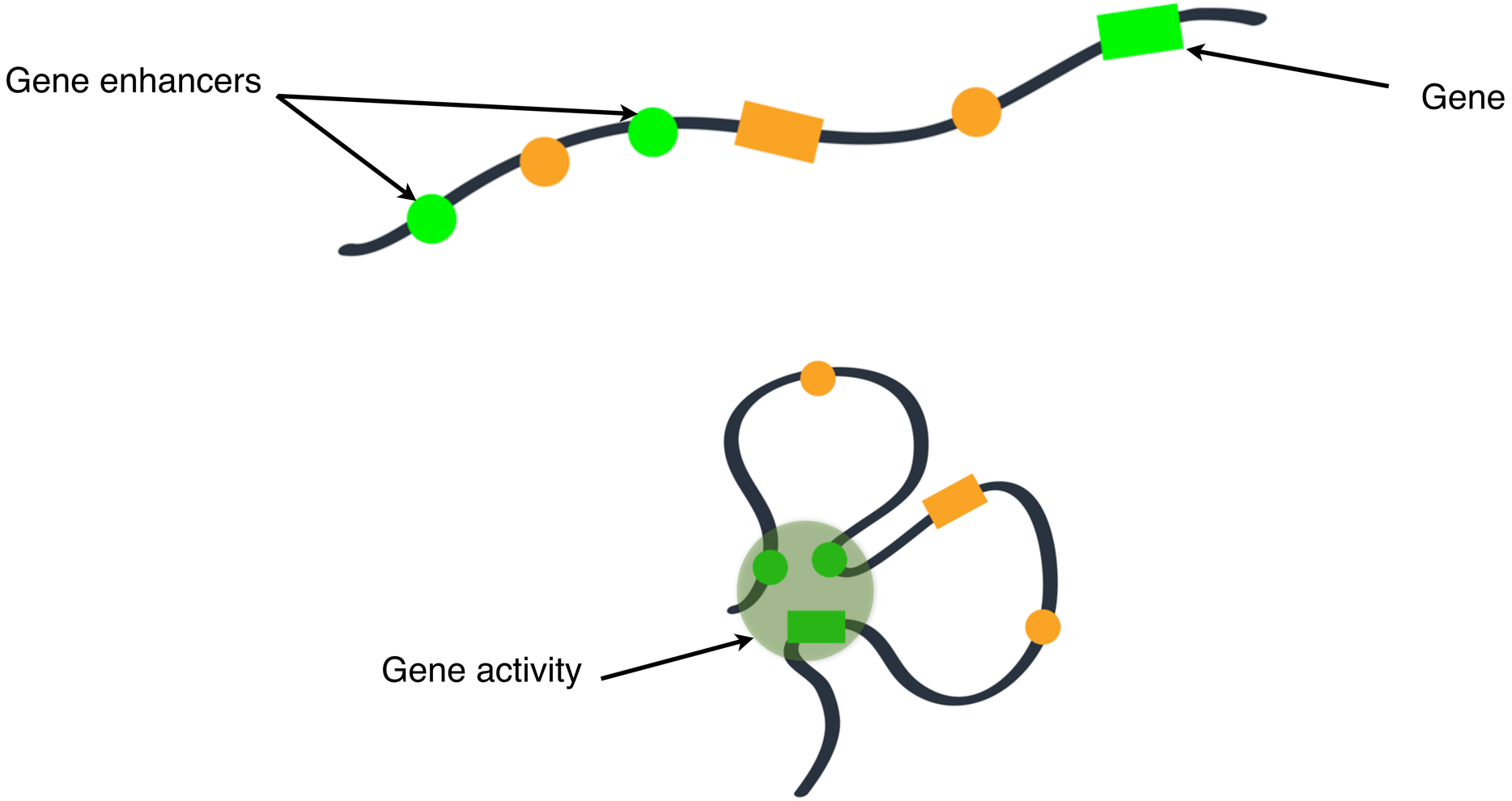






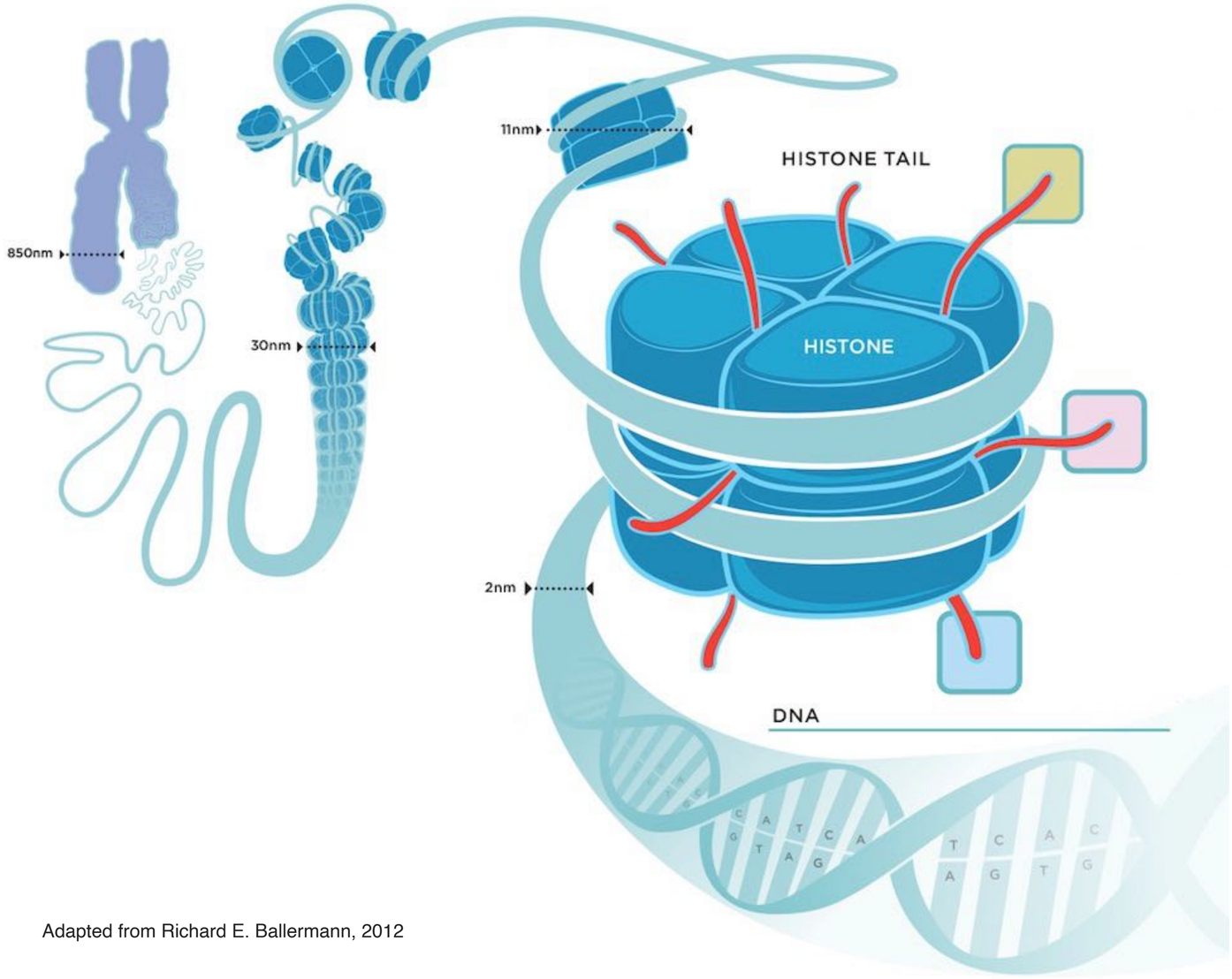


Level V: Chromatin loops



Level VI: Nucleosome

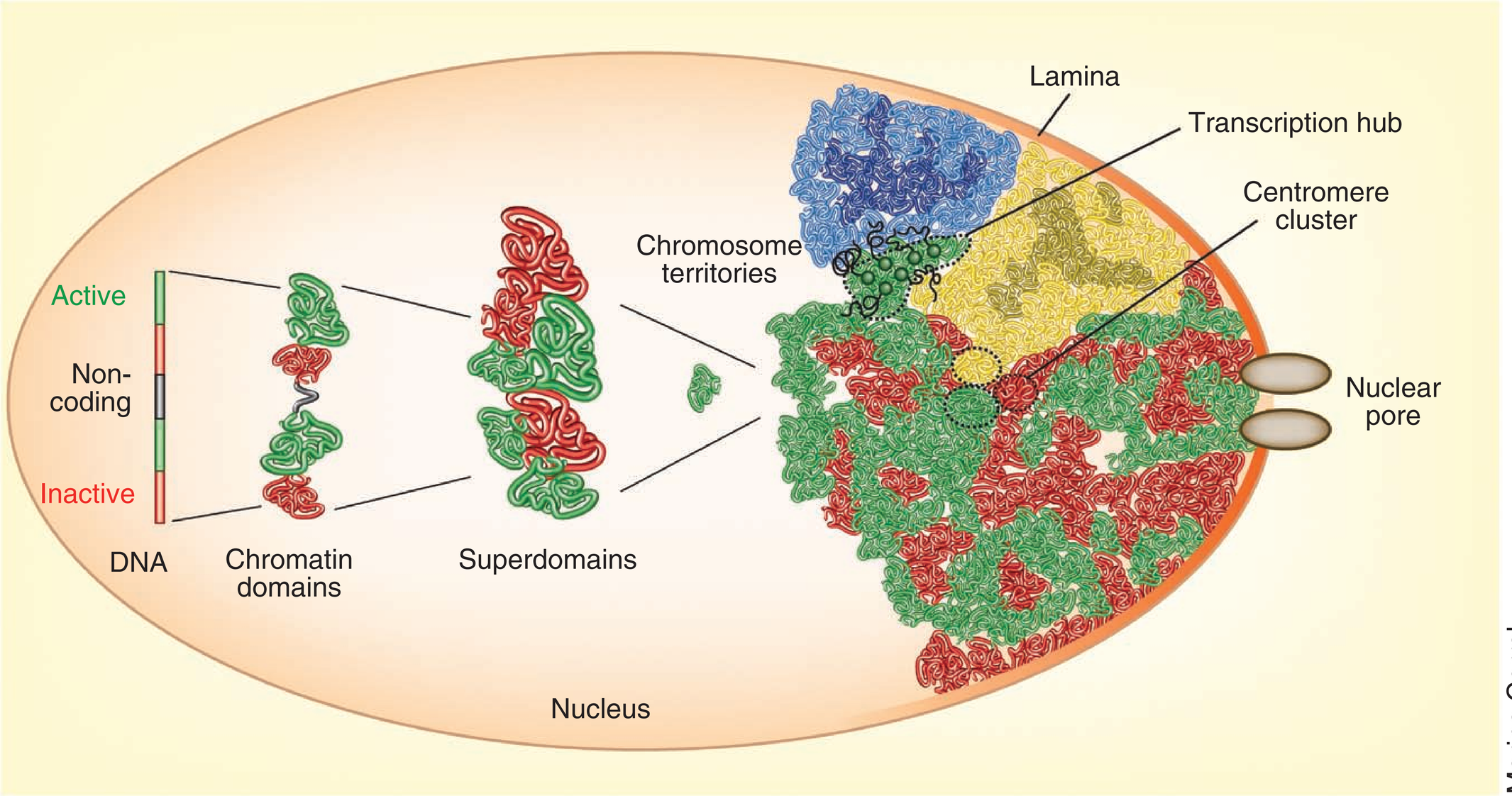
Chromosome **Chromatin fibre** **Nucleosome**



Adapted from Richard E. Ballermann, 2012

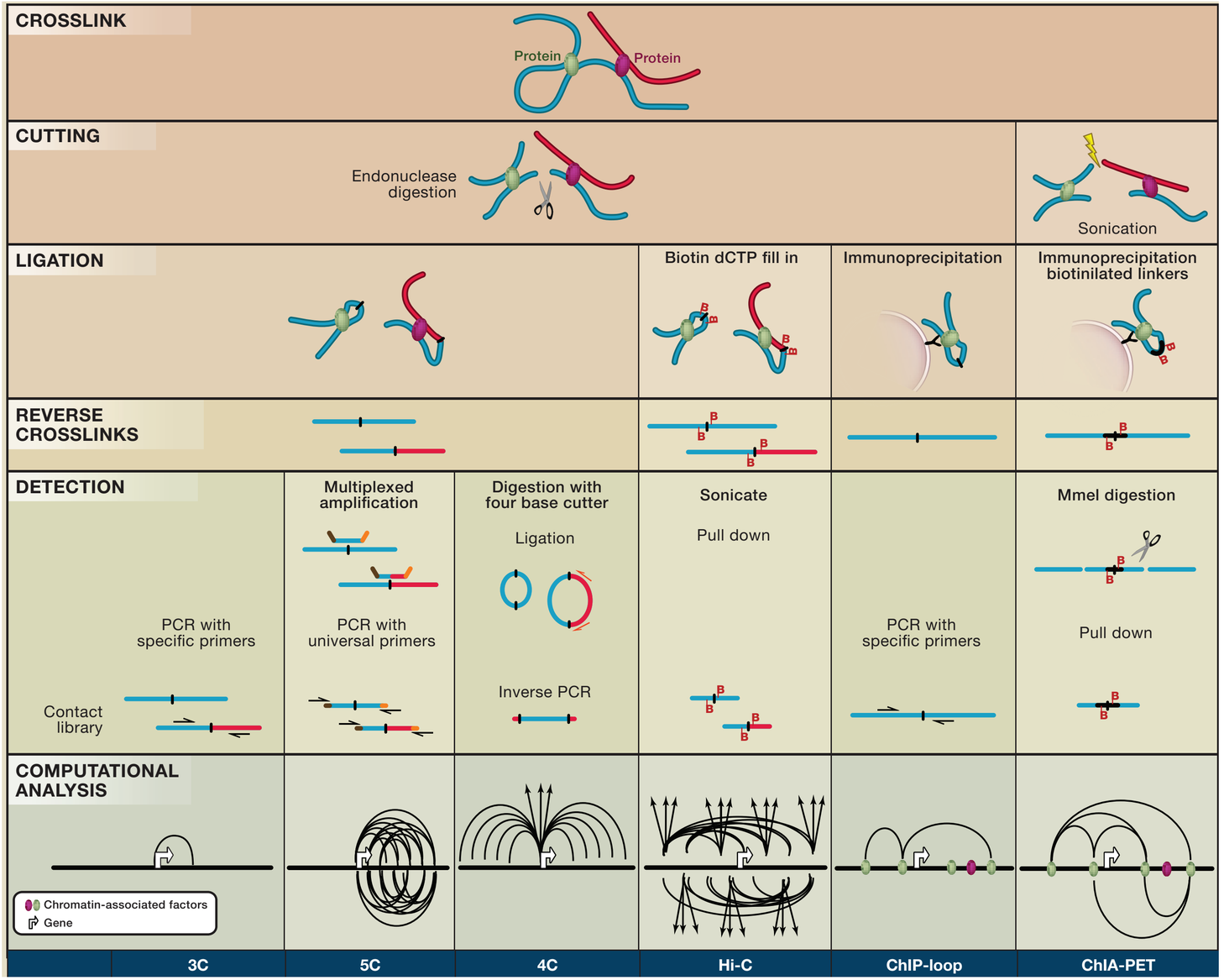
Complex genome organization

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



Marina Corral

Chromosome Conformation Capture



Hakim, O., & Misteli, T. (2012). SnapShot: Chromosome Confirmation Capture. Cell, 148(5), 1068–1068.e2.

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 Schoenfelder[1], Eitan Yaffe[2], Wendy Dean[4], Ernest D. Laue[3], Amos Tanay[2] & Peter Fraser[1]

LETTER

doi:10.1038/nature20158

Capturing pairwise and multi-way chromosomal conformations using chromosomal walks

Pedro Olivares-Chauvet[1], Zohar Mukamel[1], Aviezer Lifshitz[1], Omer Schwartzman[1], Noa Oded Elkayam[1], Yaniv Lubling[1], Gintaras Deikus[2], Robert P. Sebra[2] & Amos Tanay[1]

nature genetics ARTICLES

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

Enhancer hubs and loop collisions identified from single-allele topologies

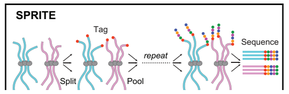
Amin Allahyar[1,2,7], Carlo Vermeulen[3,7], Britta A. M. Bouwman[3], Peter H. L. Krijger[3], Marjon J. A. M. Verstegen[3], Geert Geeven[3], Melissa van Kranenburg[3], Mark Pieterse[3], Roy Straver[1], Judith H. I. Haarhuis[4], Kees Jalink[5], Hans Teunissen[6], Ivo J. Renkens[1], Wigard P. Kloosterman[1], Benjamin D. Rowland[4], Elzo de Wit[4], Jeroen de Ridder[1]* and Wouter de Laat[3]*

Resource

Cell

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

Graphical Abstract



Authors

Sofia A. Quinodoz, Noah Ollikainen, Barbara Tabak, ..., Patrick McDonel, Manuel Garber, Mitchell Guttman

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mguttman@caltech.edu

nature COMMUNICATIONS

ARTICLE

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

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

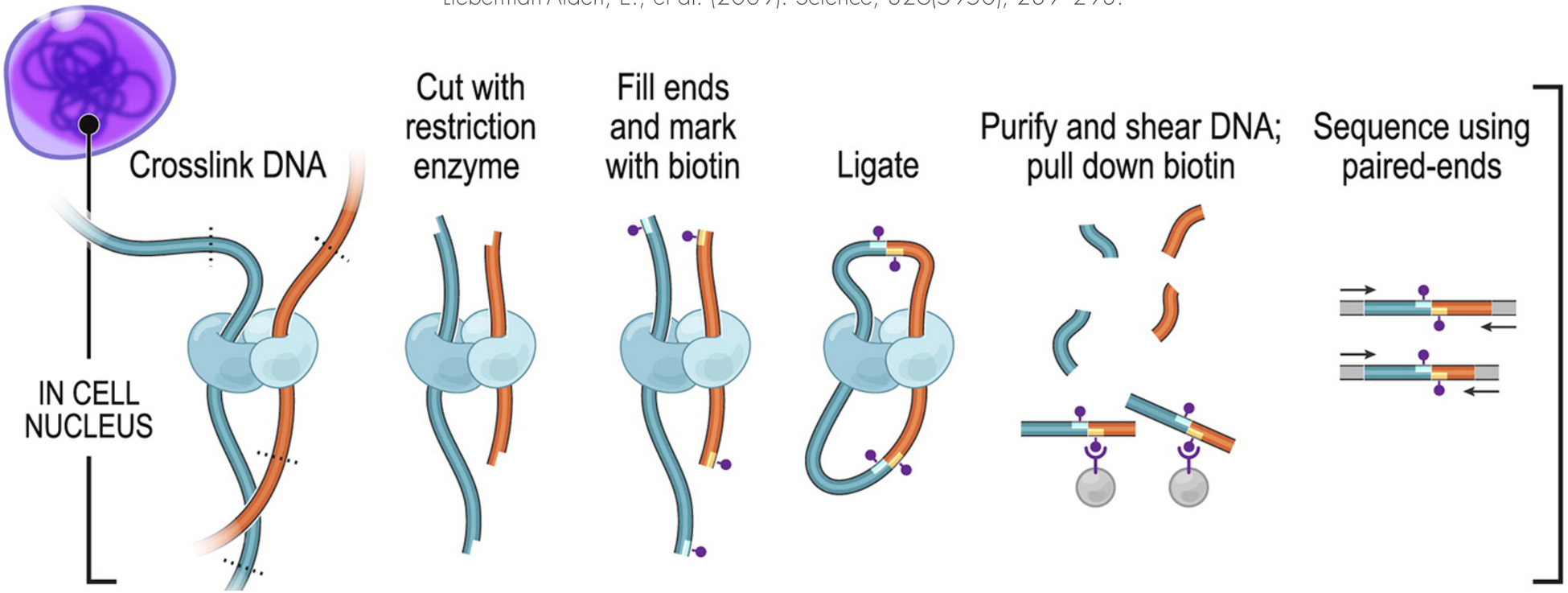
Noelia Díaz[1], Kai Kruse[1], Tabea Erdmann[2], Annette M. Staiger[3,4,5], German Ott[3], Georg Lenz[2] & Juan M. Vaquerizas[1]

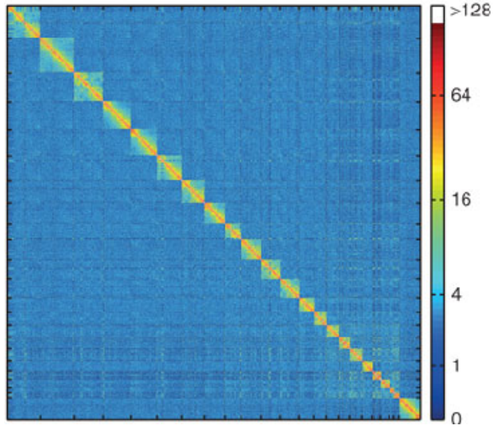
Compartment-dependent chromatin interaction dynamics revealed by liquid chromatin Hi-C

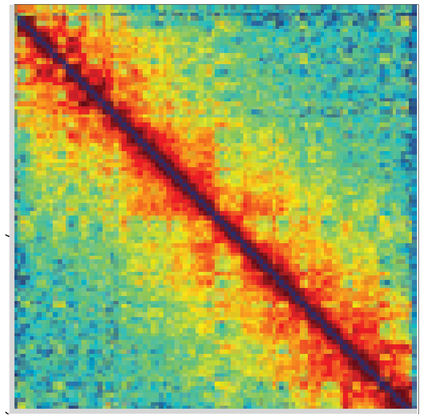
Houda Belaghzal[1*], Tyler Borrman[2*], Andrew D. Stephens[3], Denis L. Lafontaine[1], Sergey V. Venev[1], Zhiping Weng[2], John F. Marko[3,4], Job Dekker[1, 5, 6 #]

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.

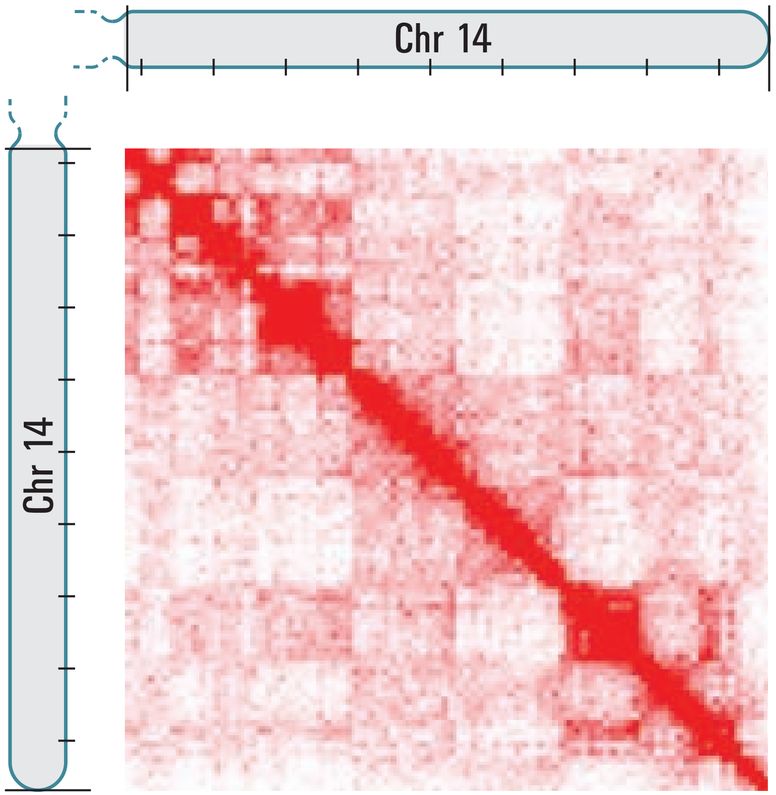


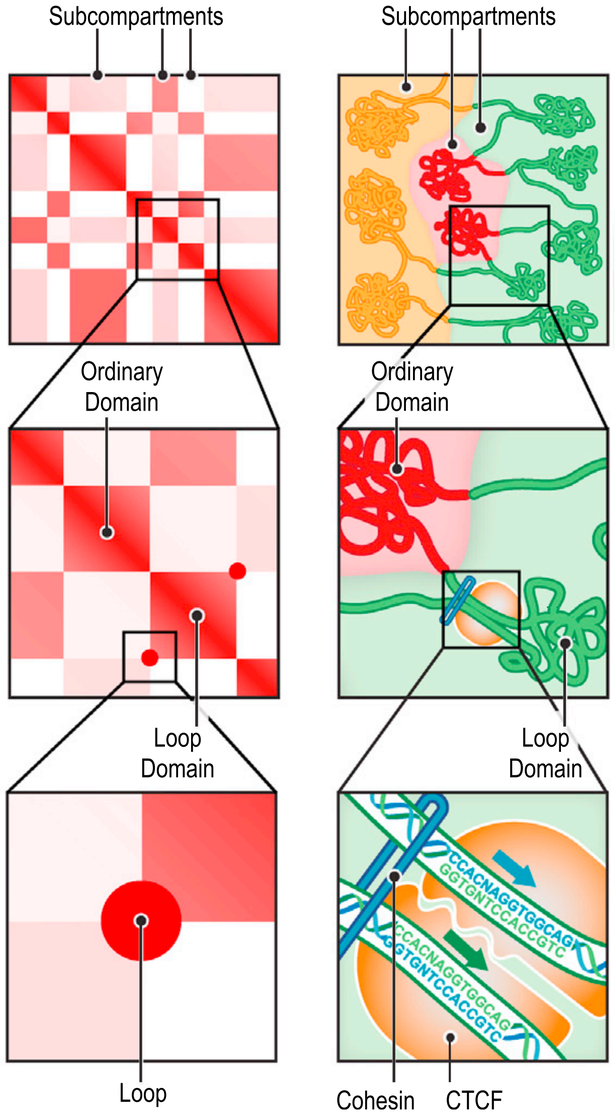




Hierarchical genome organisation

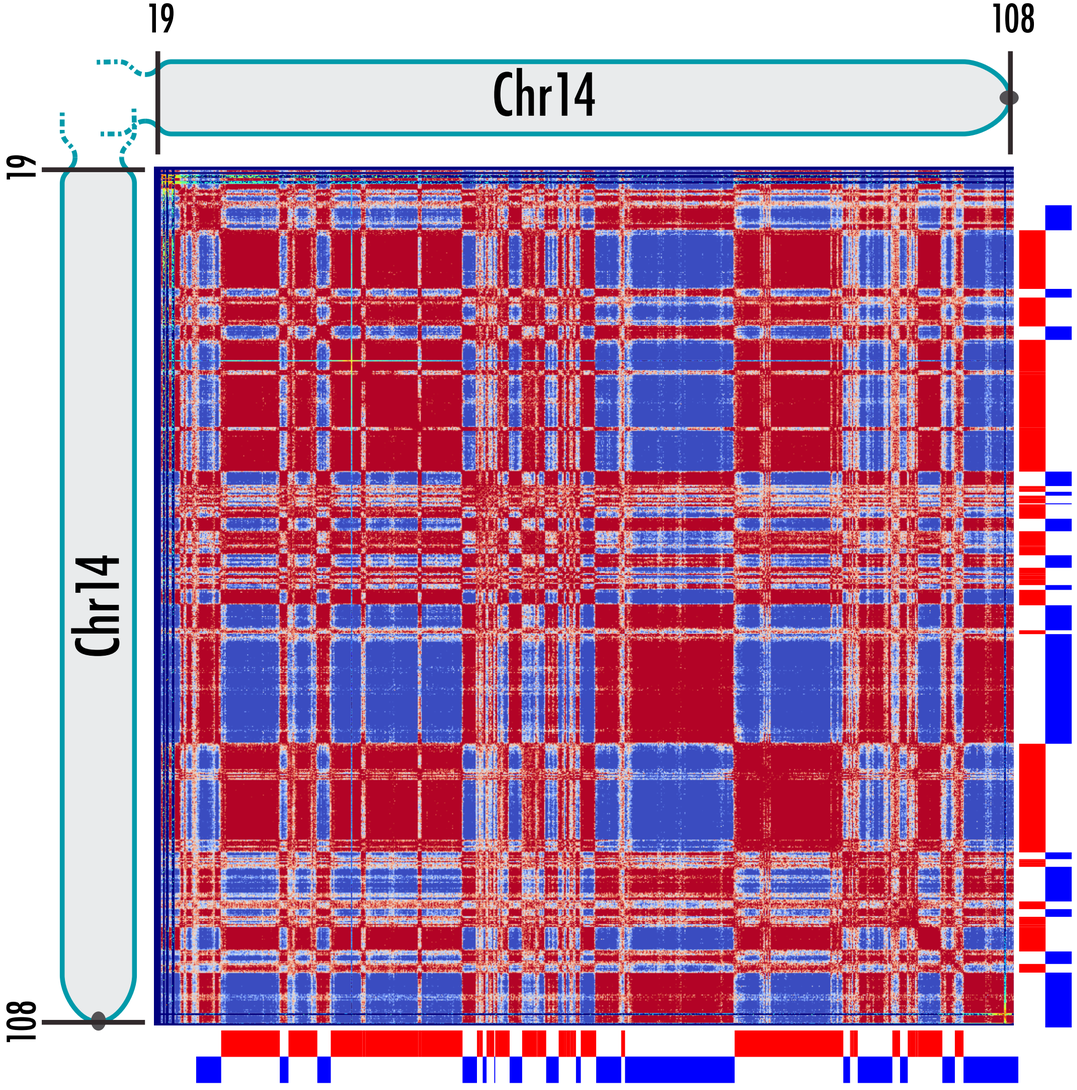
Lieberman-Aiden, E., et al. (2009). Science, 326(5950), 289–293.
Rao, S. S. P., et al. (2014). Cell, 1–29.

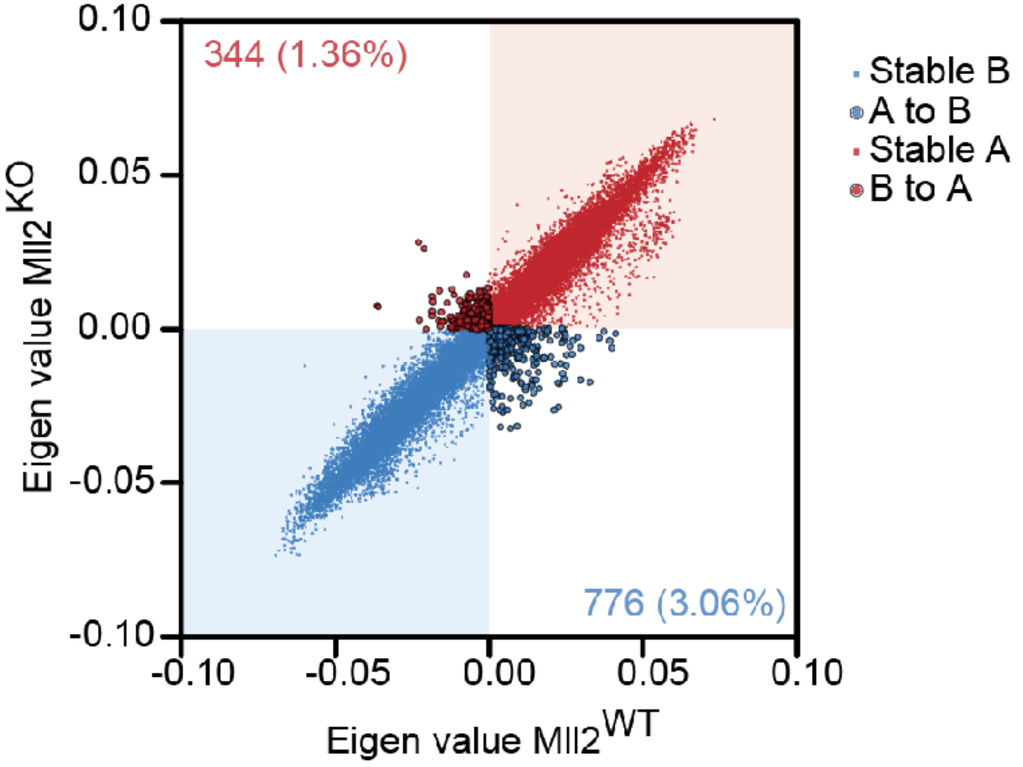




A/B Compartment

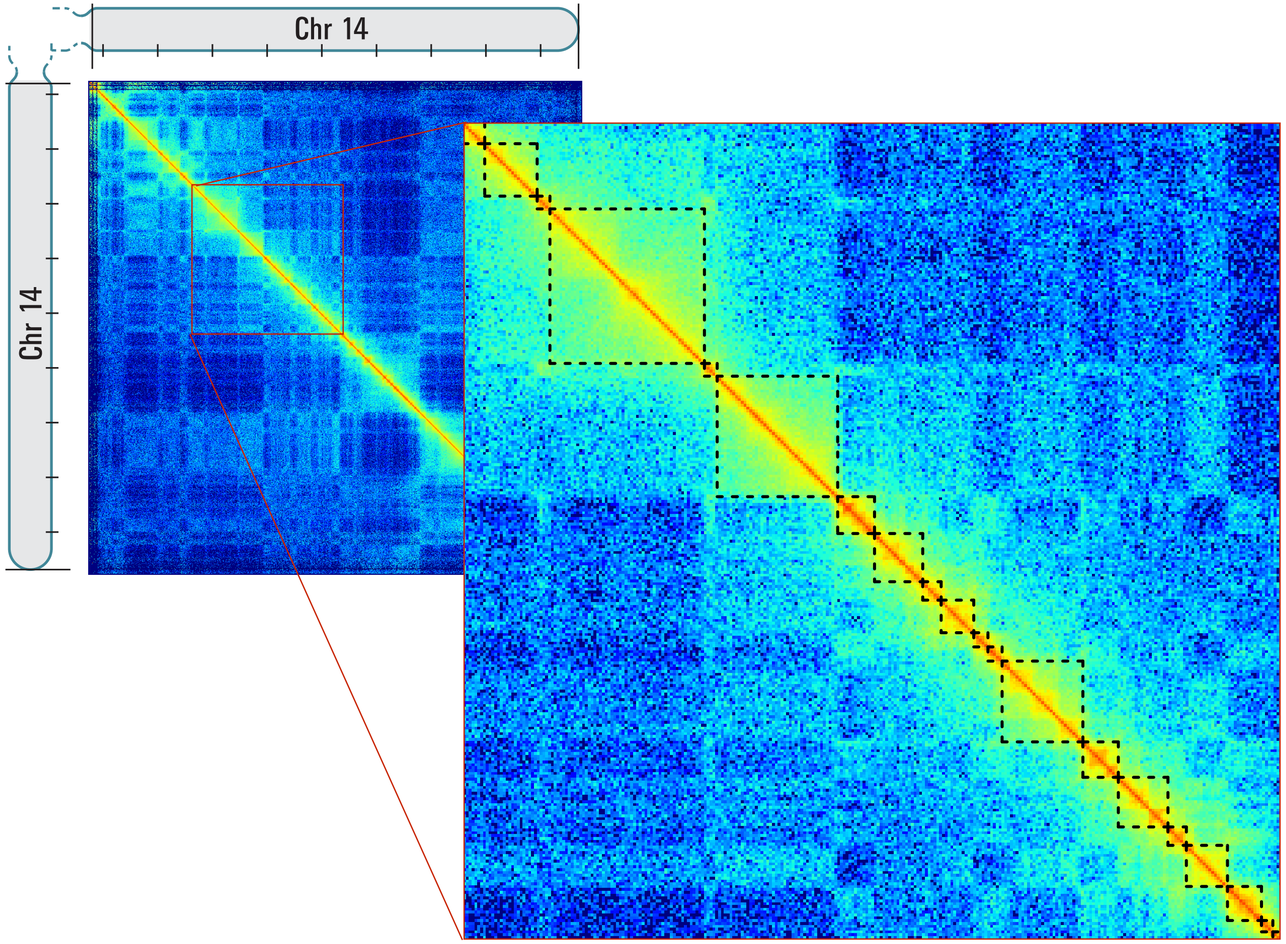
Chromosome 14

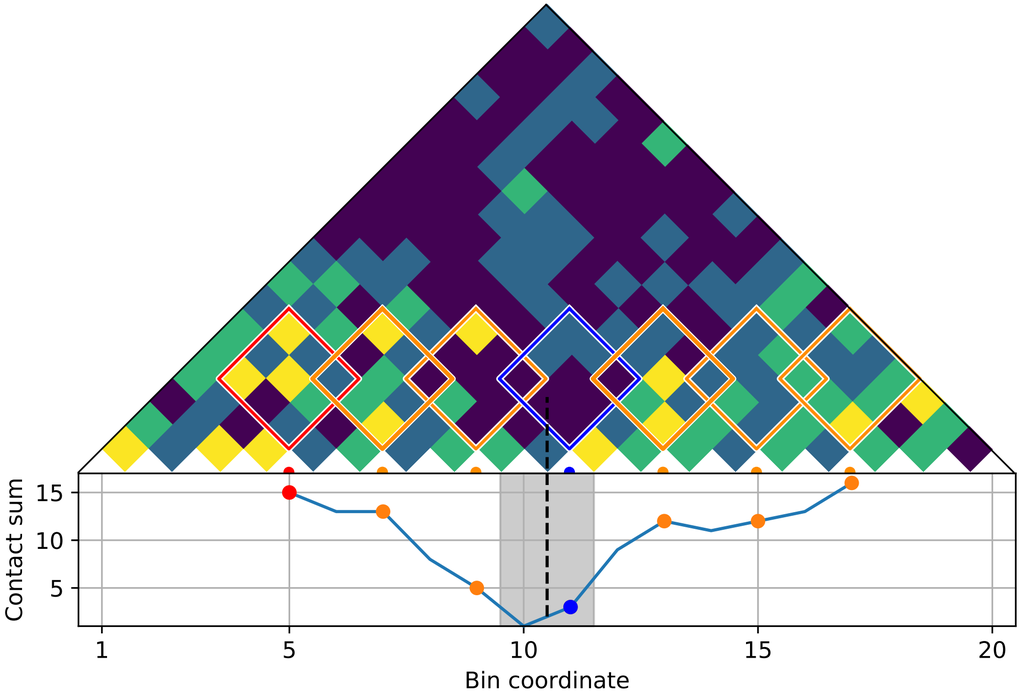




TADs

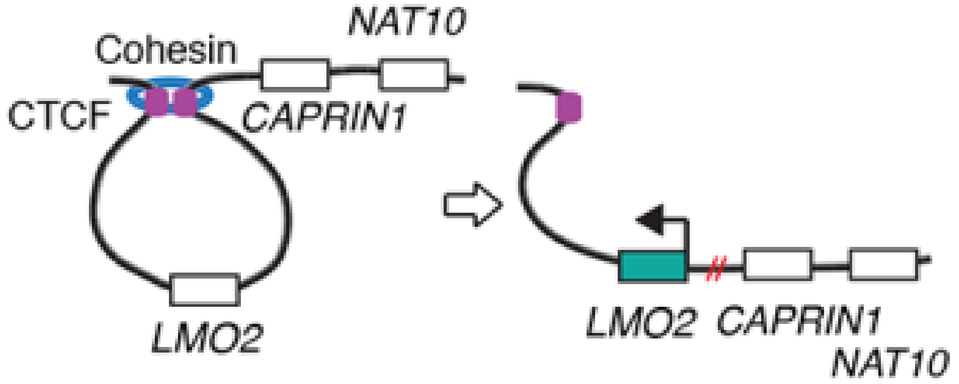
Chromosome 14

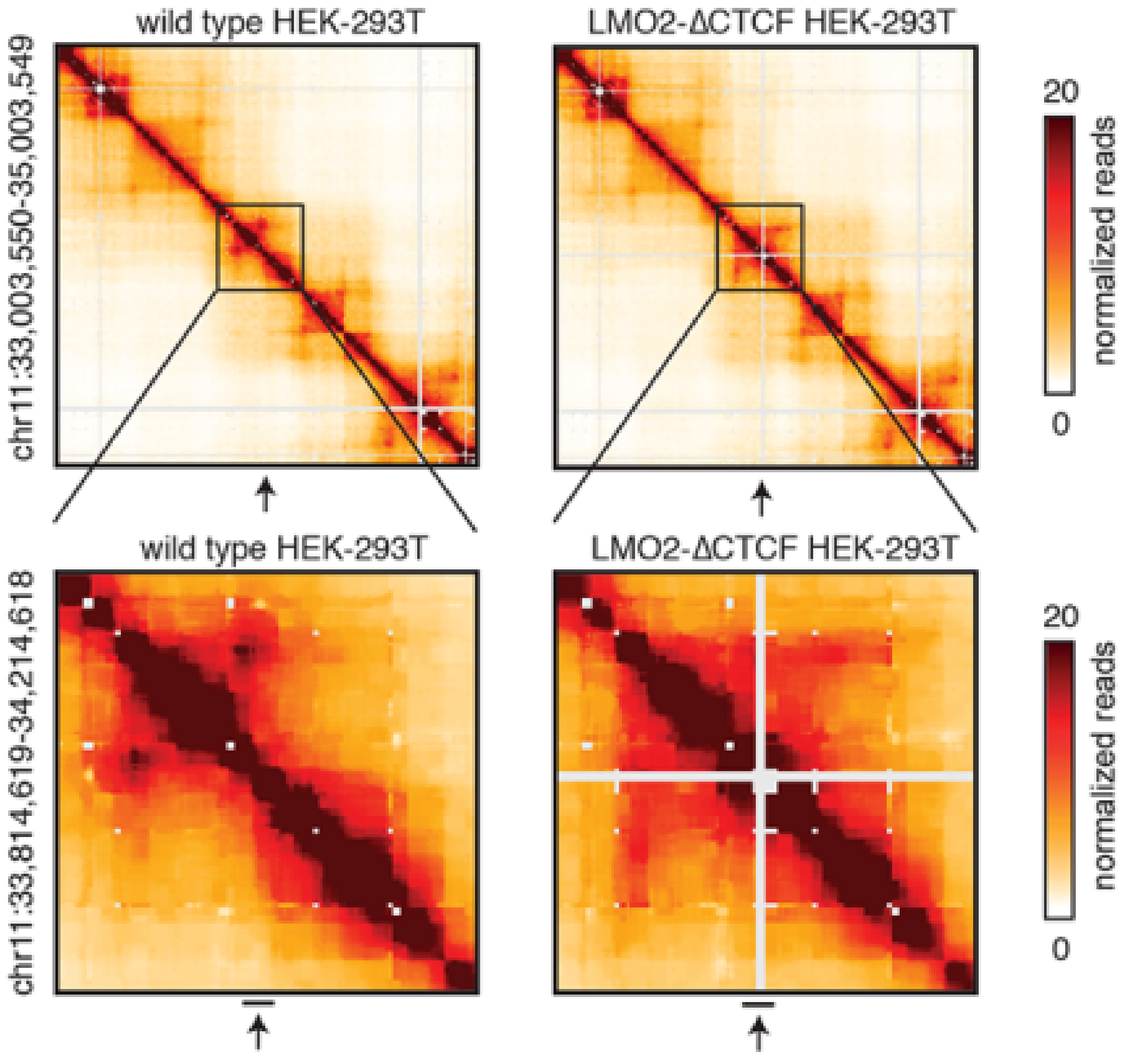




TADs are functional units

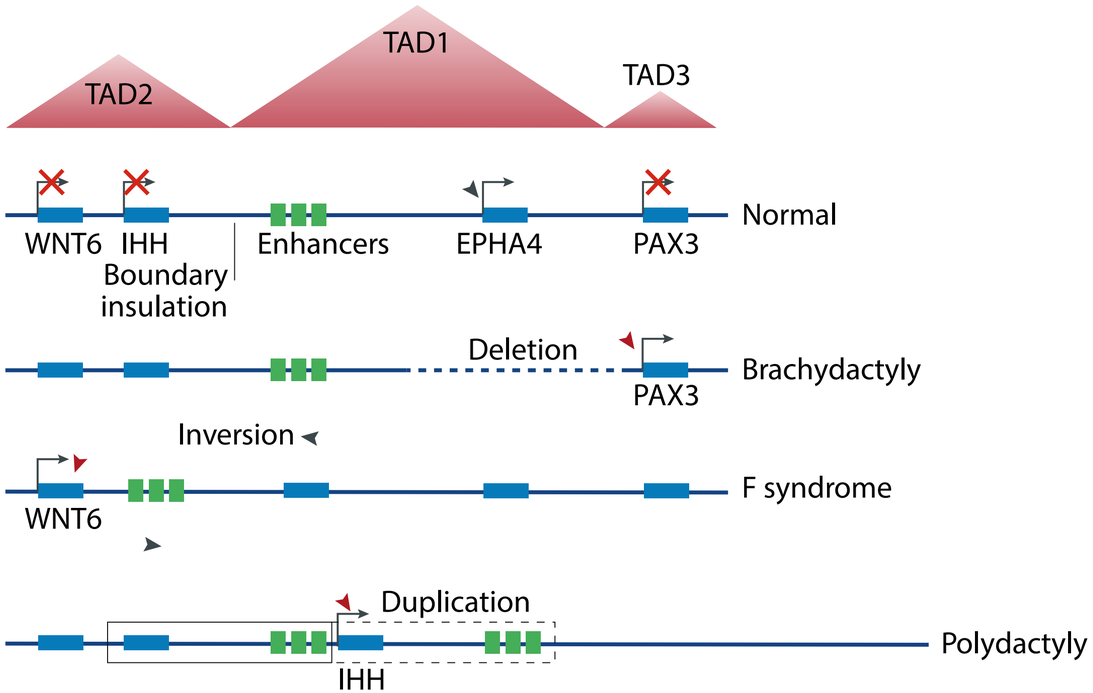
Hnisz, D., et al. (2016). Science



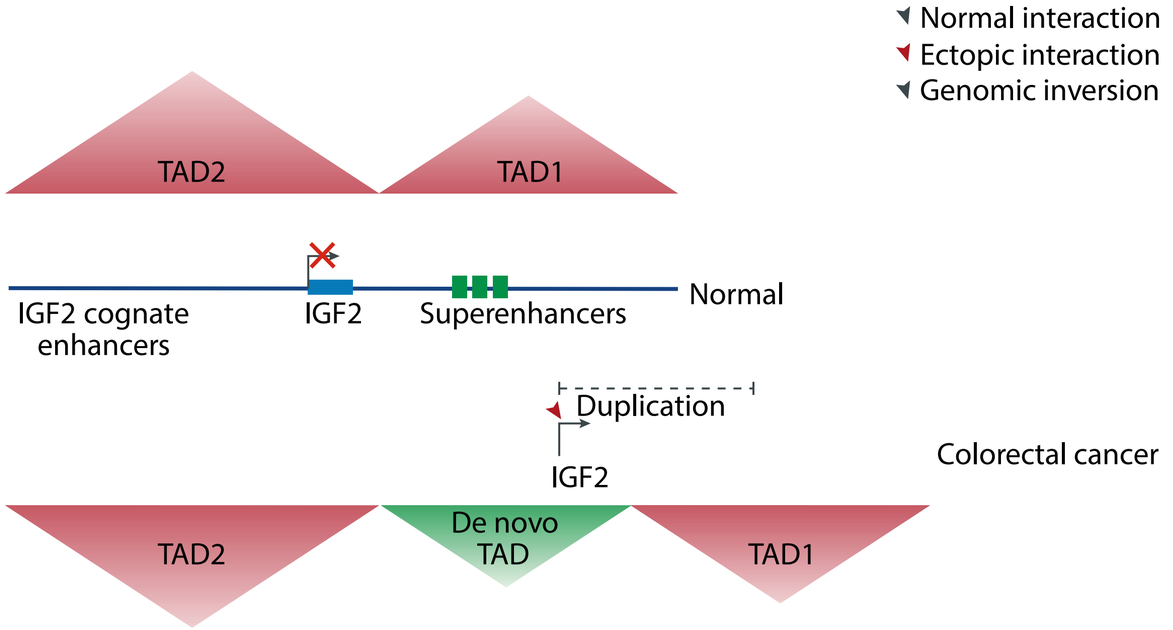


TADs are functional units

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



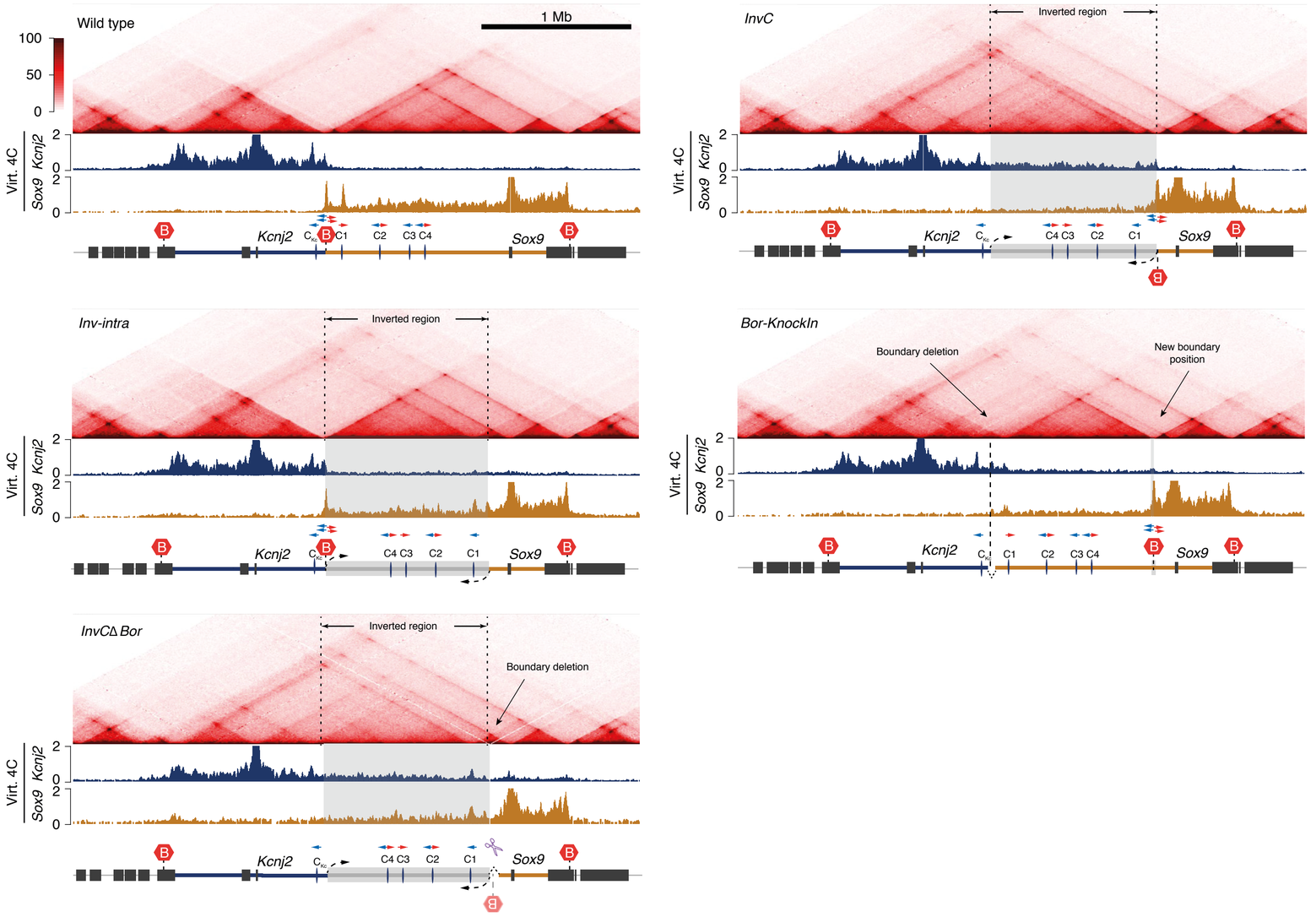
Lupianez, D. G. et al. Cell 161, 1012–1025 (2015)



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

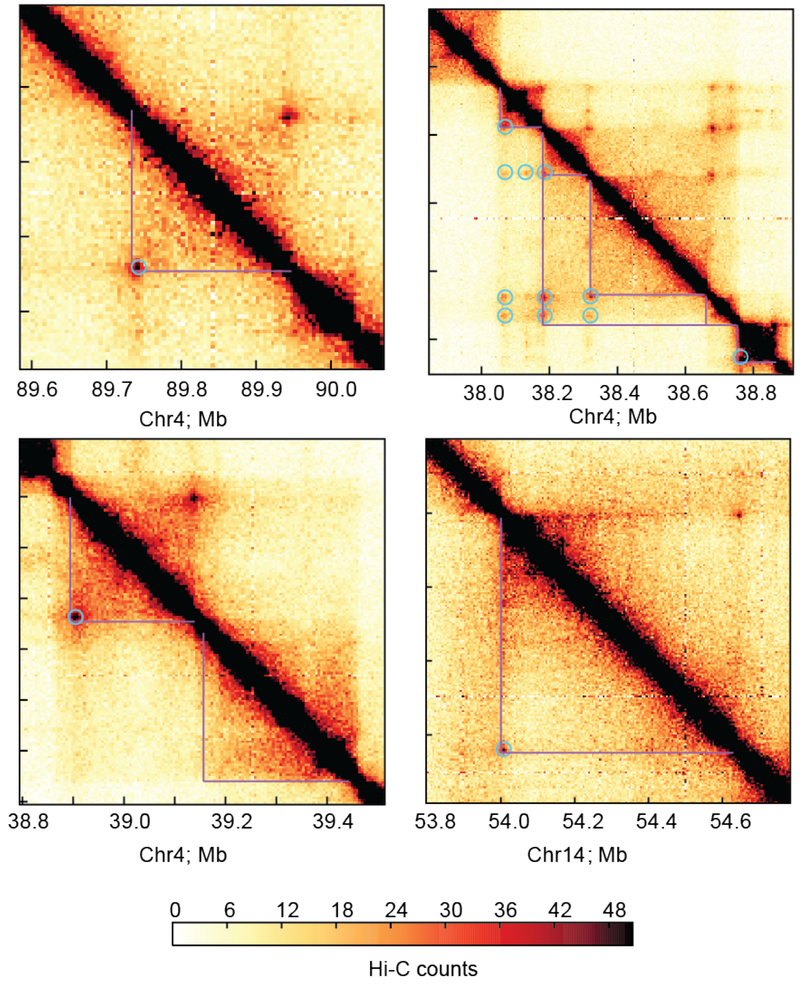
TADs are functional units

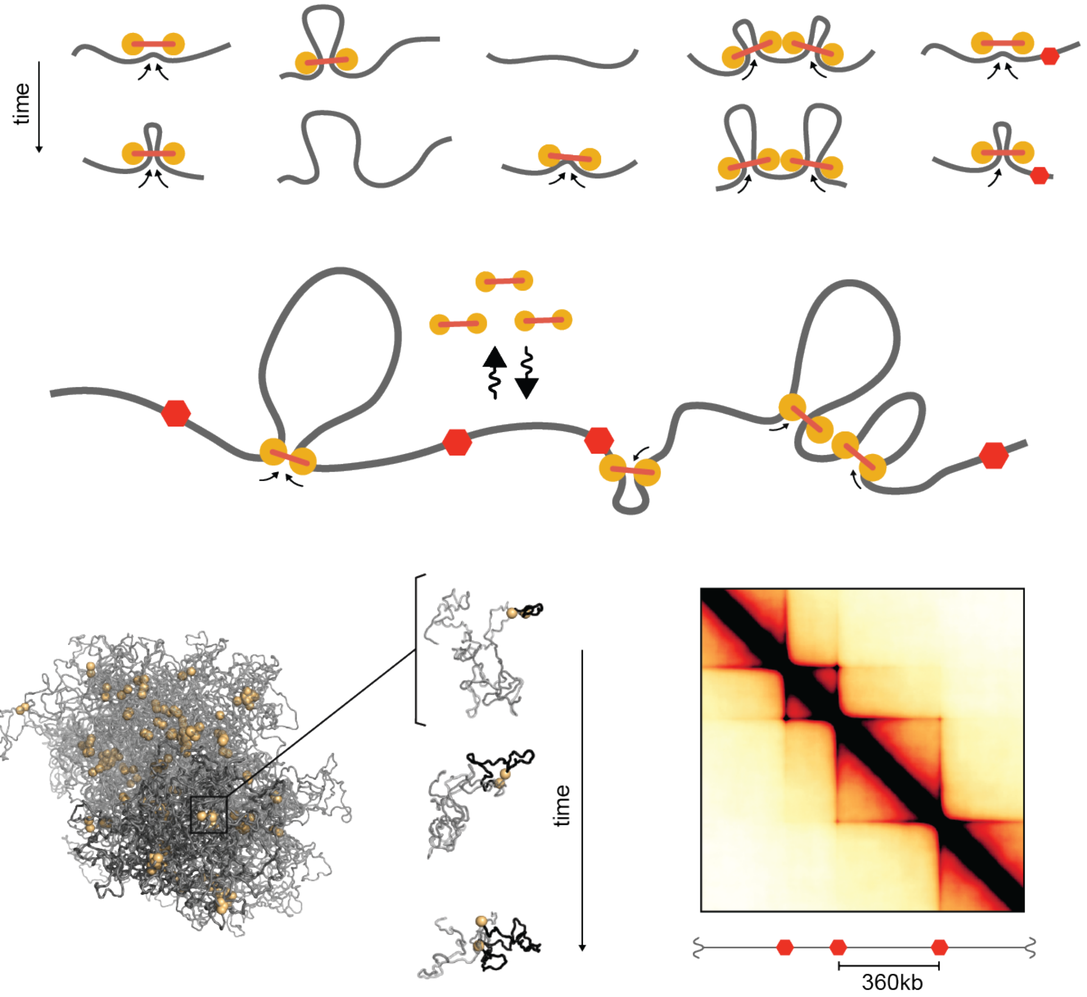
Despang, et al. (2019). Nature Genetics 51,1263–1271 (2019)



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





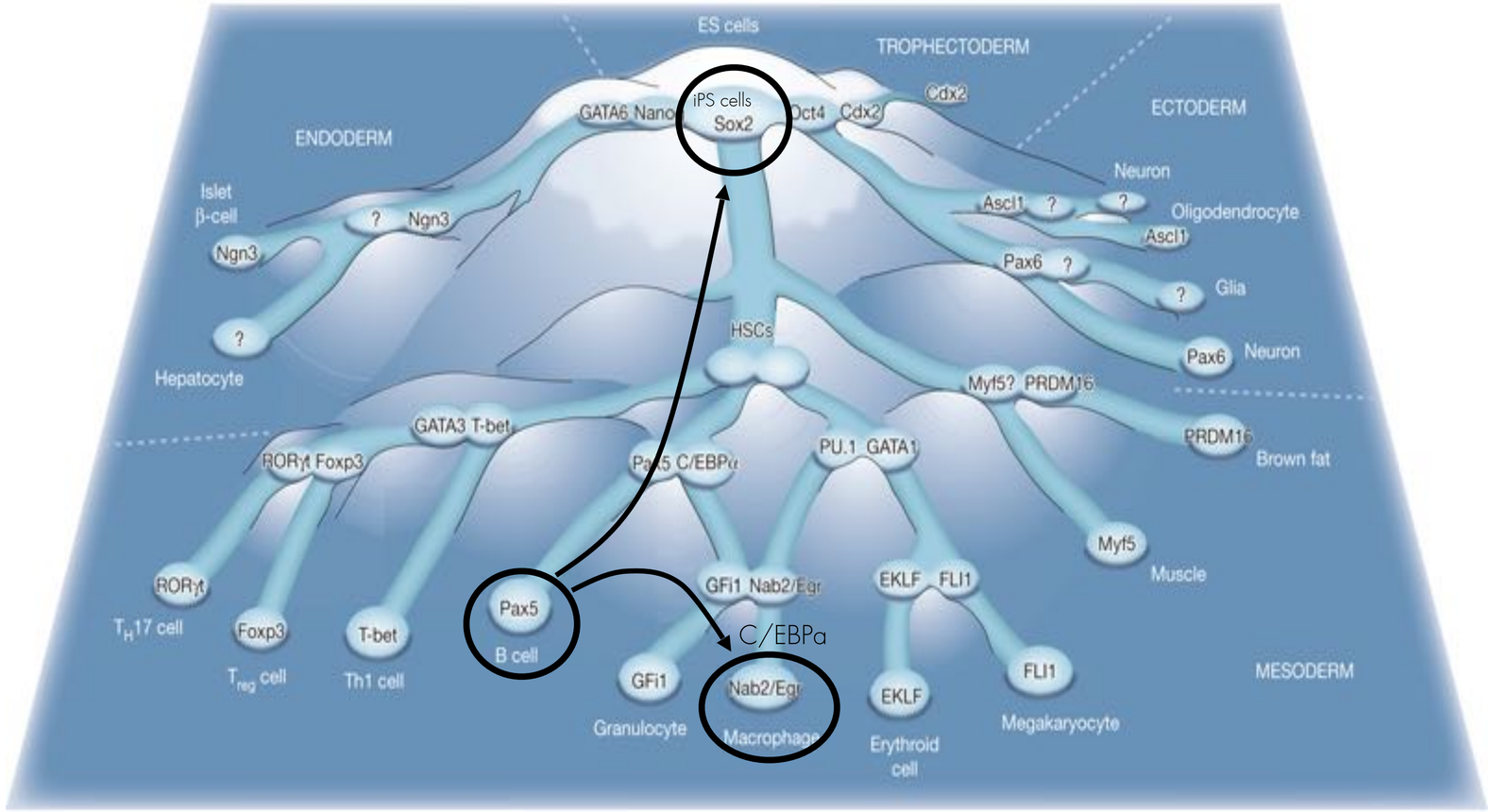
Dynamics of gene activation


Marco di Stefano
Ralph Stadhouders
with Graf Lab (CRG, Barcelona)

Nature Genetics (2018) 50 p238
Nature Communications (2020) 11 p2564

Transcription factors dictate cell fate

Graf & Enver (2009) Nature



Transcription factors (TFs) determine cell identity through gene regulation

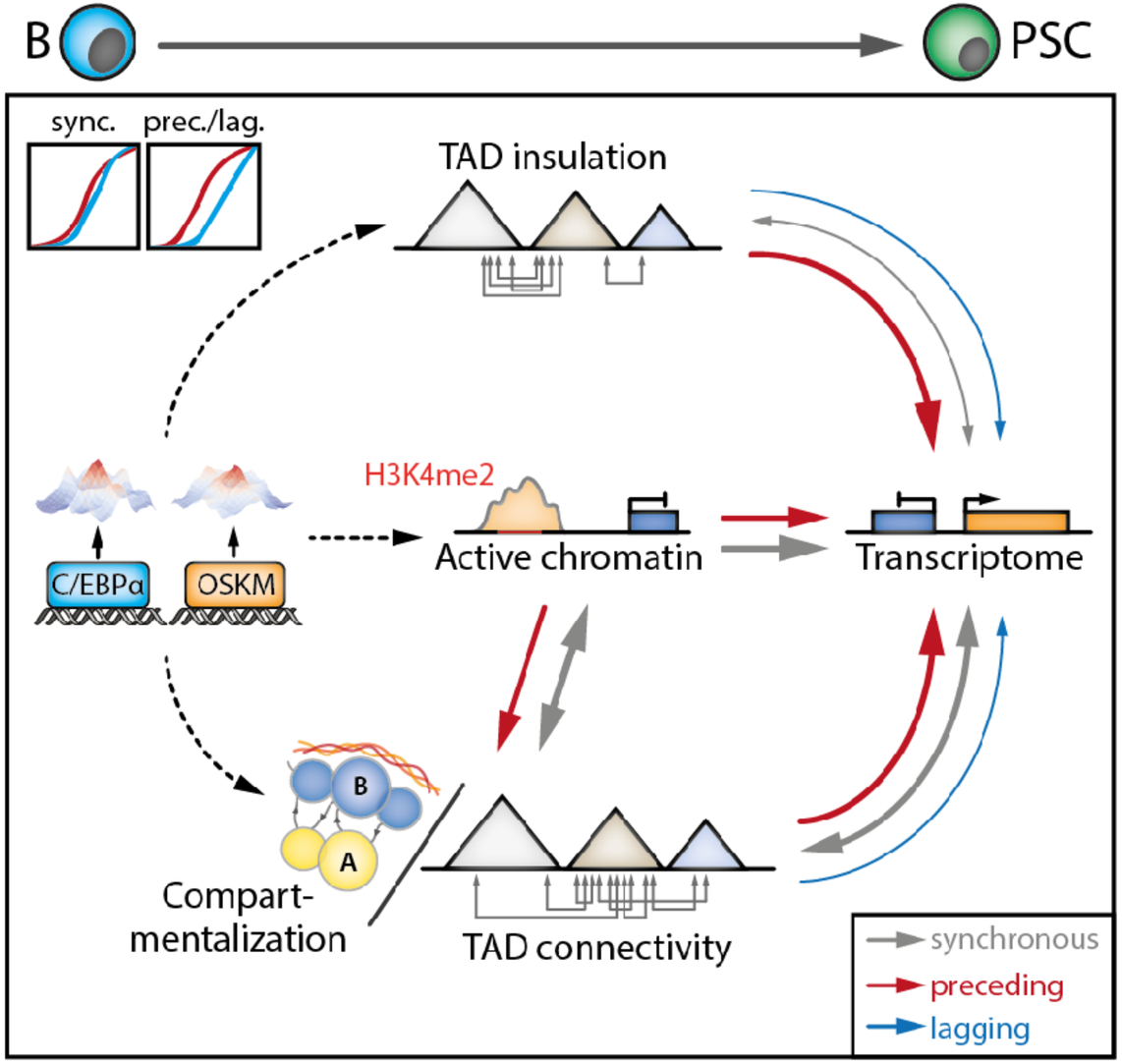
Normal 'forward' differentiation

Cell fates can be converted by enforced TF expression

Transdifferentiation or reprogramming

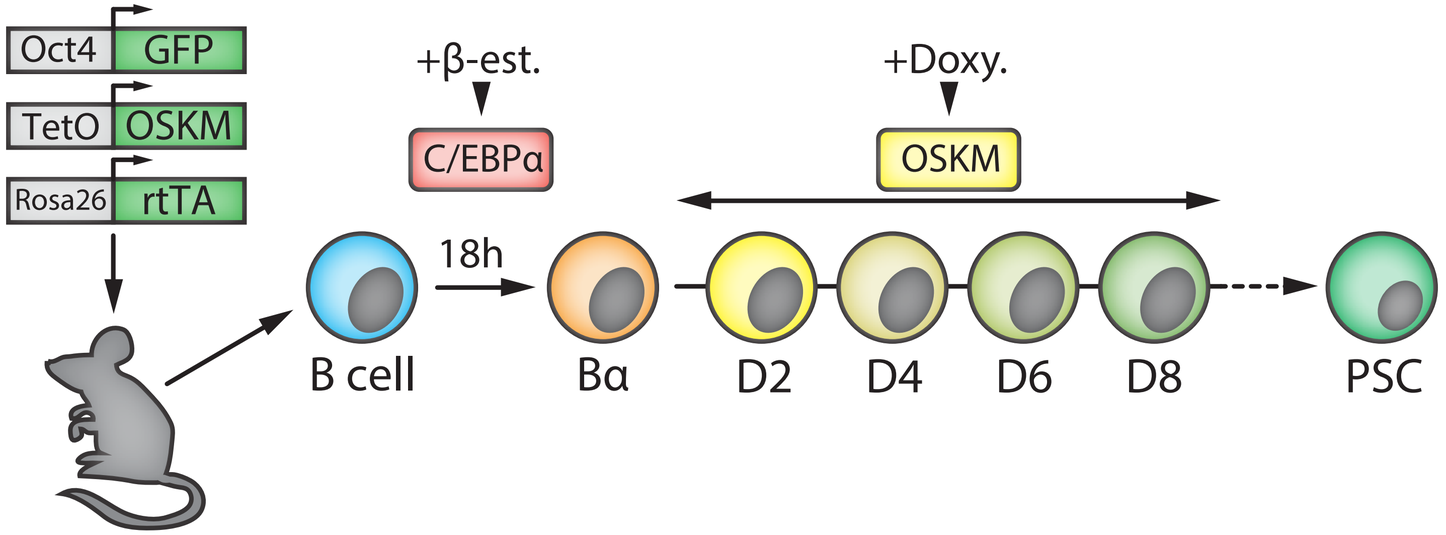
Interplay: topology, gene expression & chromatin

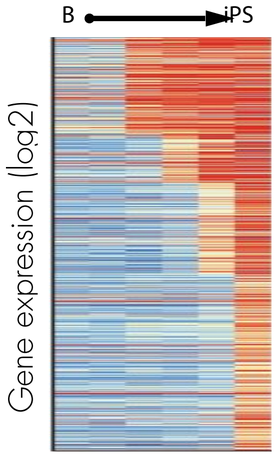
Stadhouders, R., Vidal, E. et al. (2018) Nature Genetics

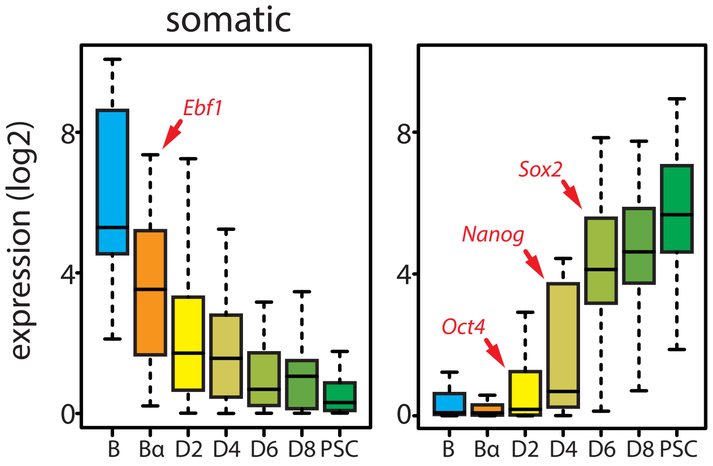


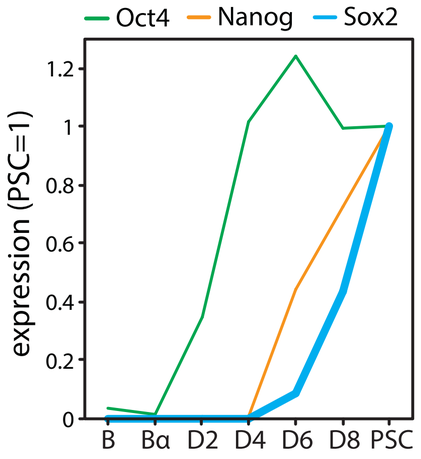
Reprogramming from B to PSC

Stadhouders, R., Vidal, E. et al. (2018) Nature Genetics



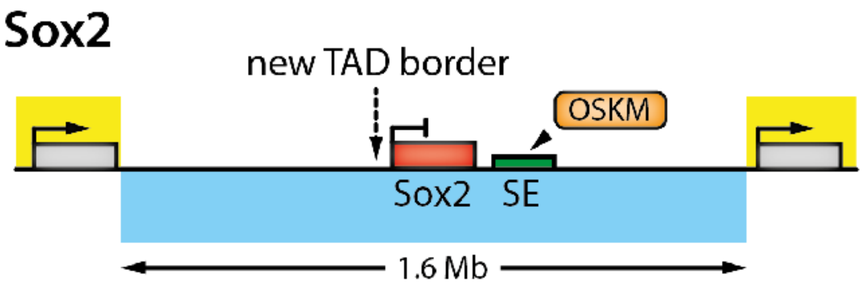


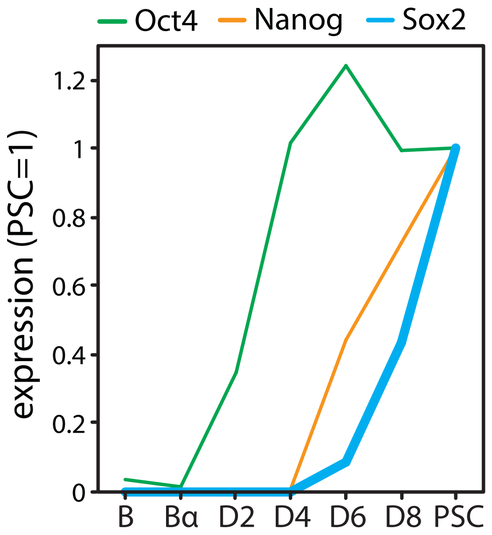


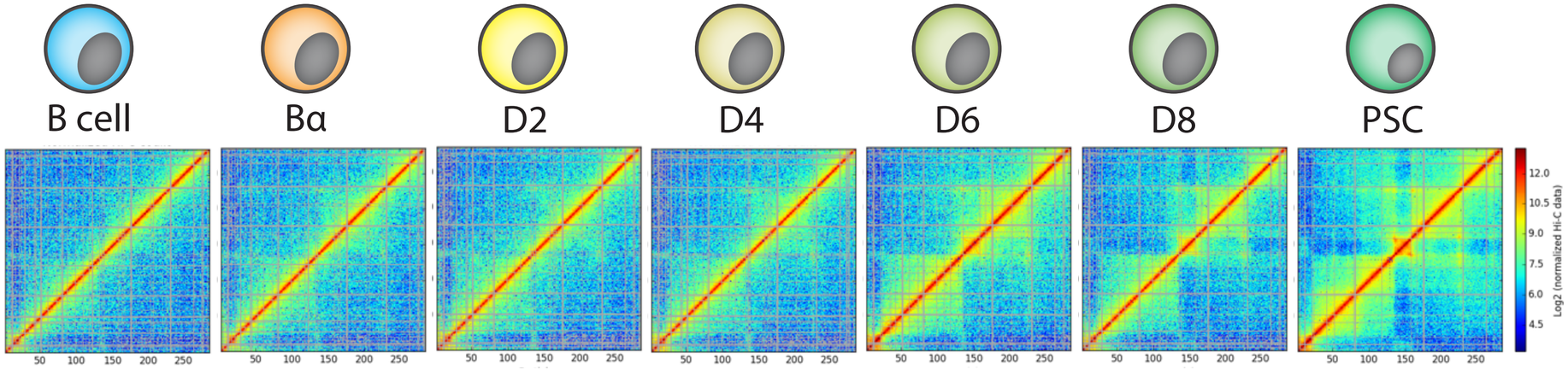


Hi-C maps of reprogramming from B to PSC

The SOX2 locus

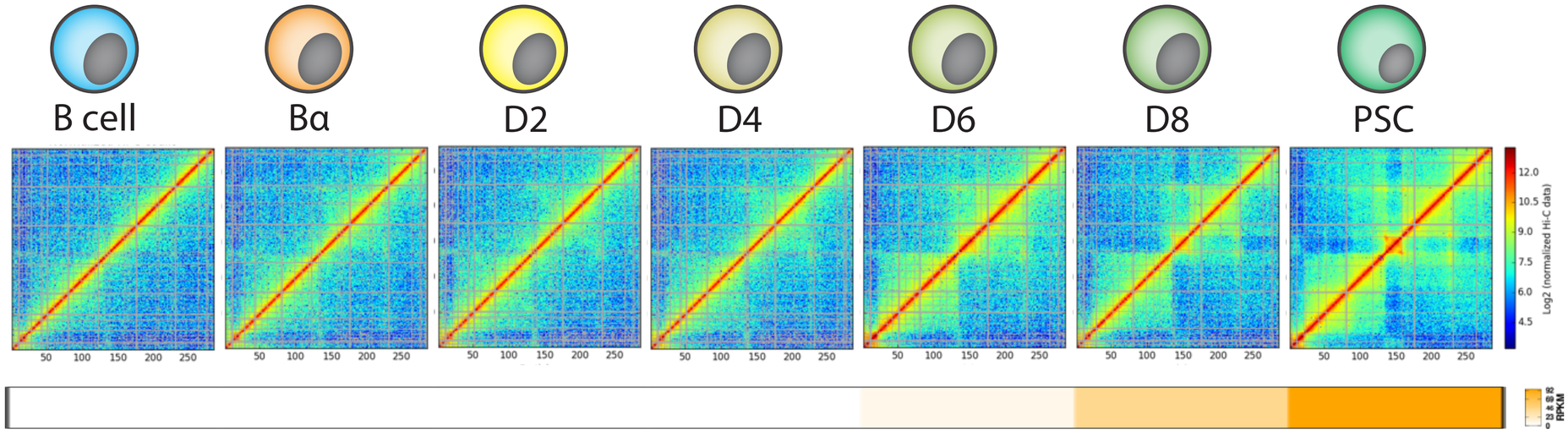






Hi-C maps of reprogramming from B to PSC

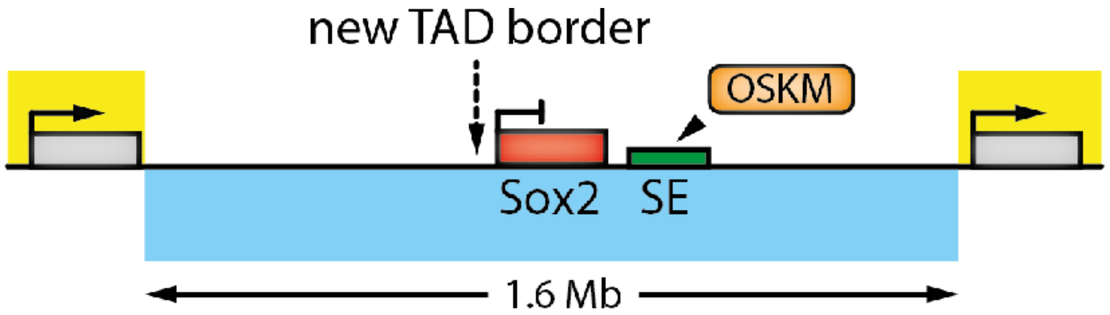
The SOX2 locus

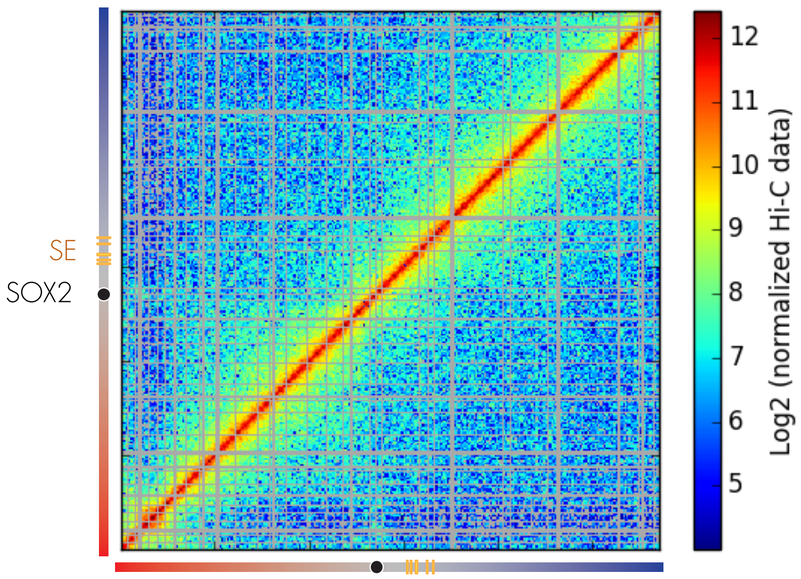


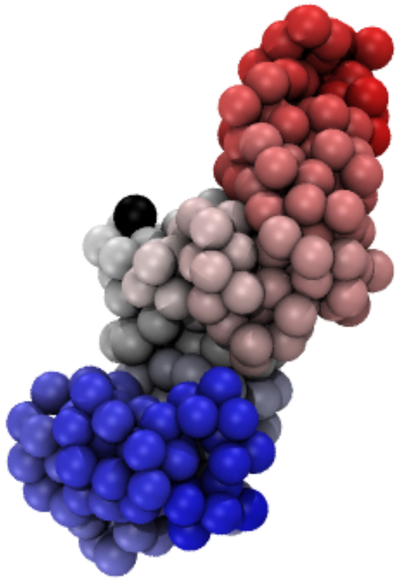
How does these structural rearrangements interplay with the transcription activity?

What are the main drivers of structural transitions?

TADbit modeling of SOX2 from B cells Hi-C





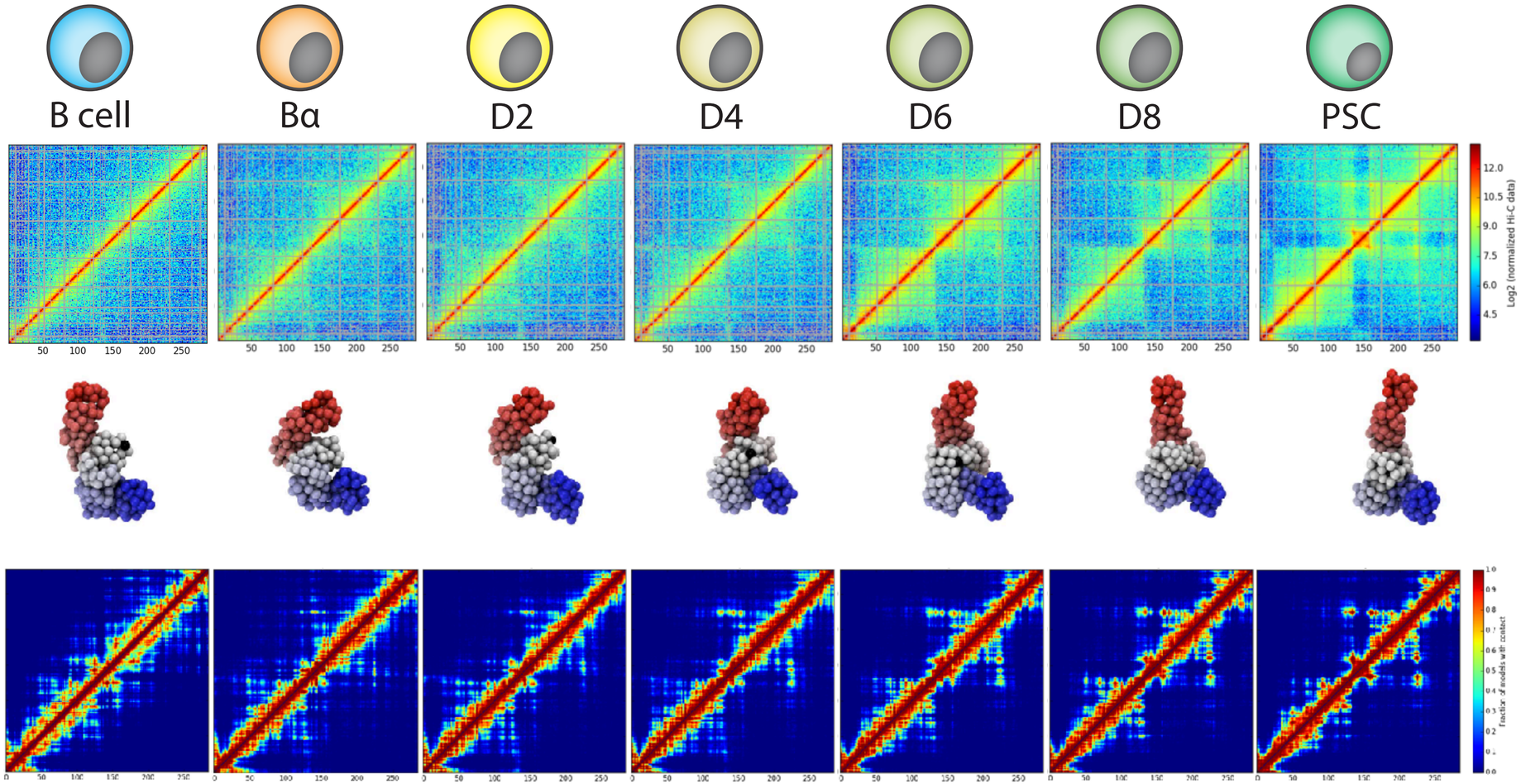


Optimal IMP parameters

lowfreq=0 , upfreq=1 , maxdist=200nm, dcutoff=125nm, particle size=50nm (5kb)

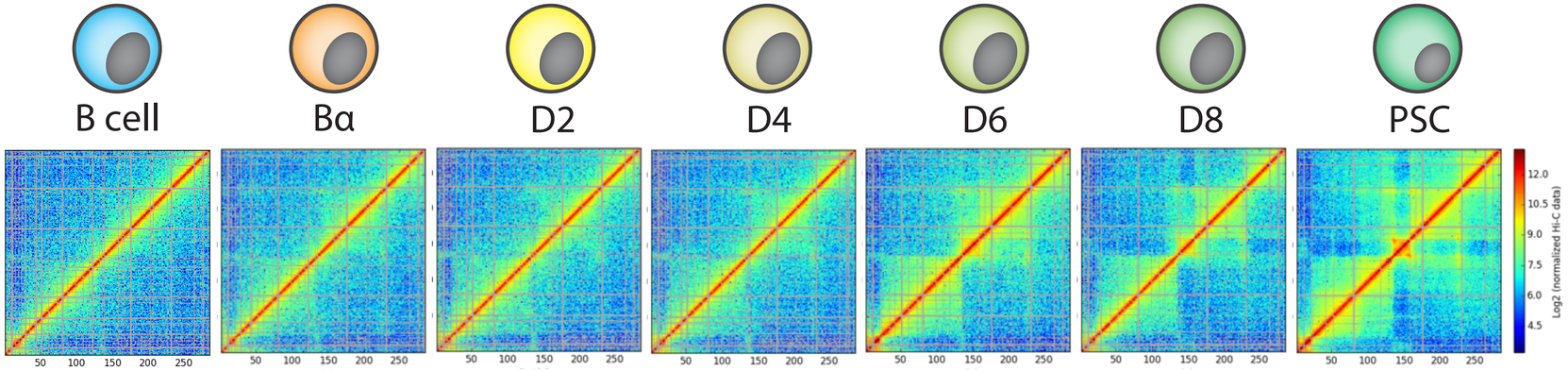
Models of reprogramming from B to PSC

The SOX2 locus



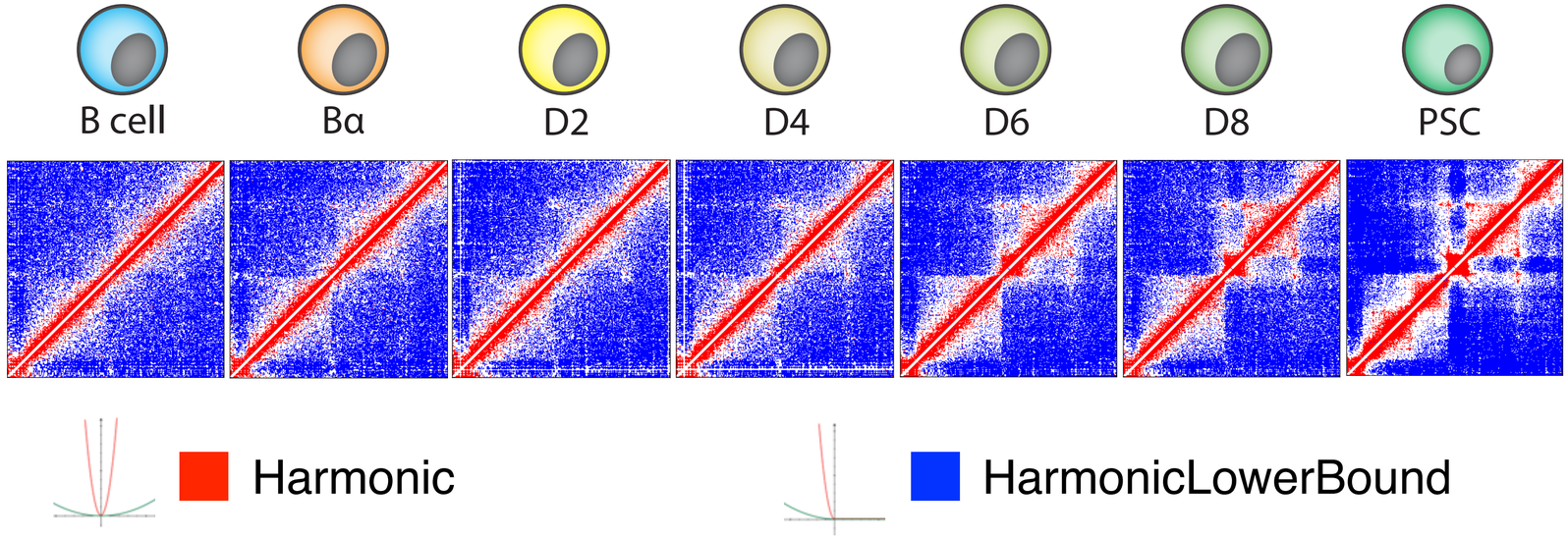
TADdyn: from time-series Hi-C maps to dynamic restraints

The SOX2 locus



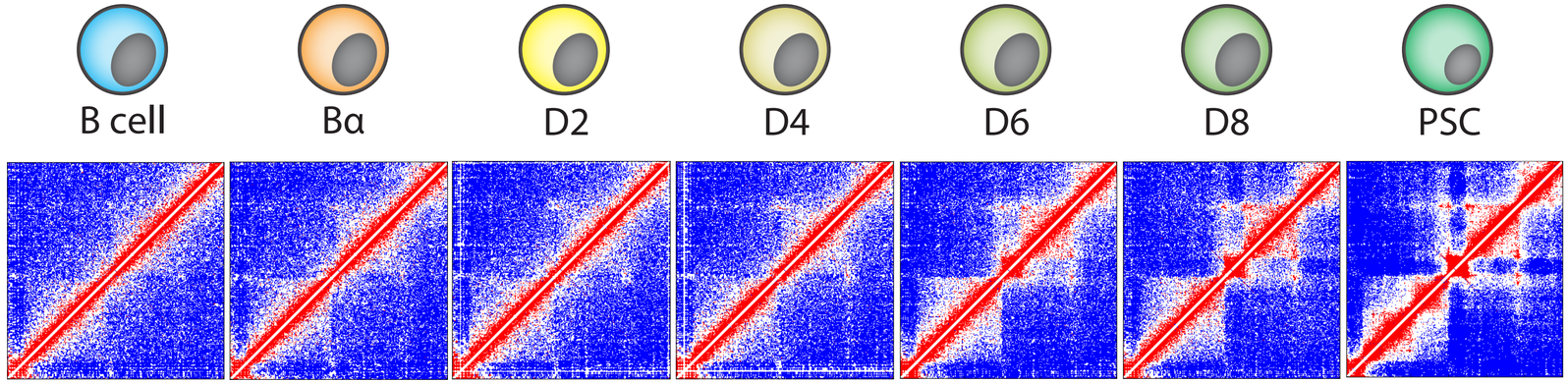
TADdyn: from time-series Hi-C maps to dynamic restraints

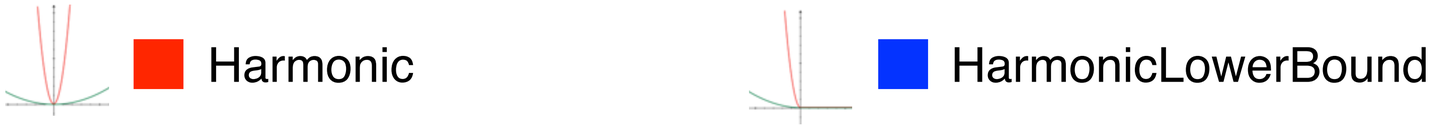
The SOX2 locus

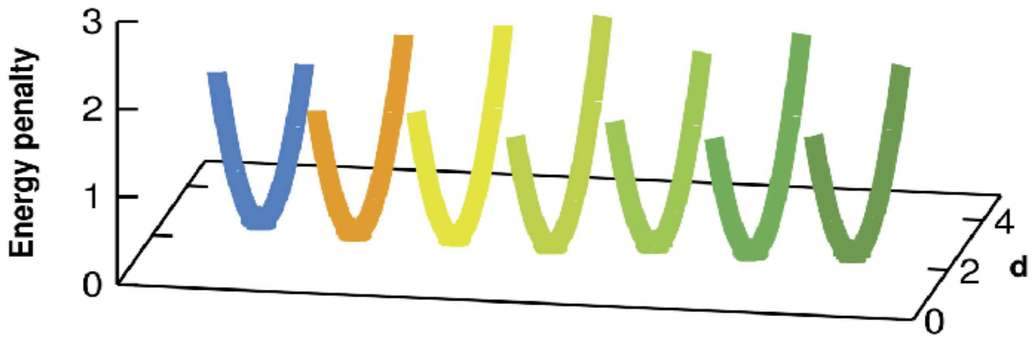


TADdyn: from time-series Hi-C maps to dynamic restraints

The SOX2 locus



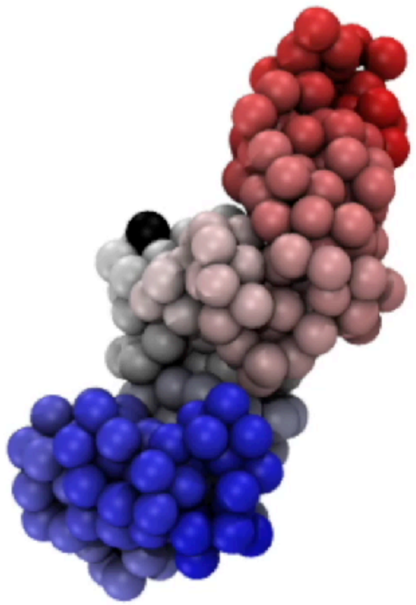


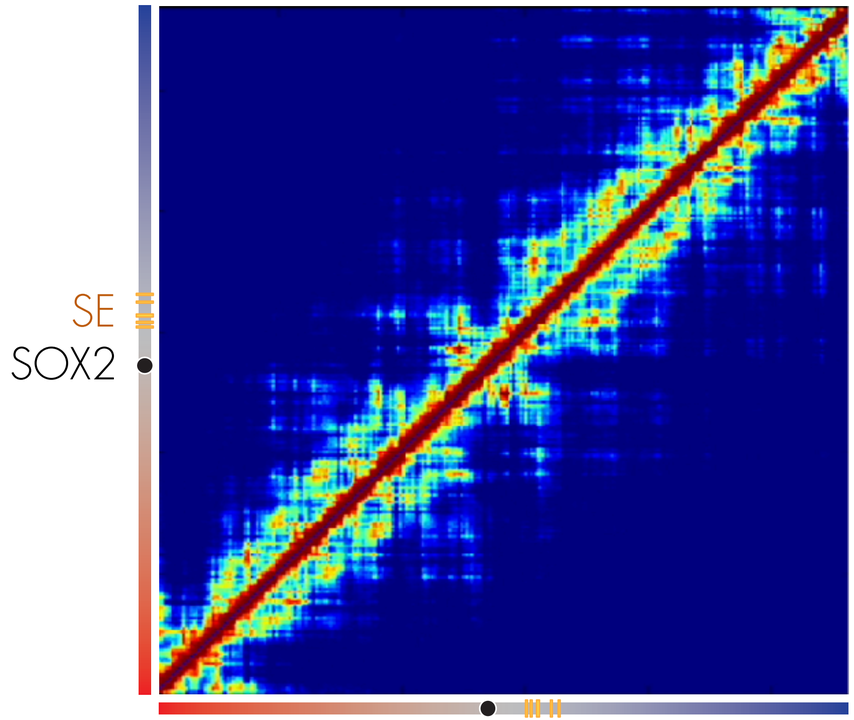


Transition	Stable	Vanishing	Raising
B -> Bα	18,612	6,984	7,290
Bα -> D2	18,512	7,390	6,687
D2 -> D4	18,369	6,830	6,893
D4 -> D6	18,971	6,291	7,289
D6 -> D8	20,167	6,093	6,250
D8 -> ES	20,679	5,738	6,173

SOX2 locus structural changes from B to PSC

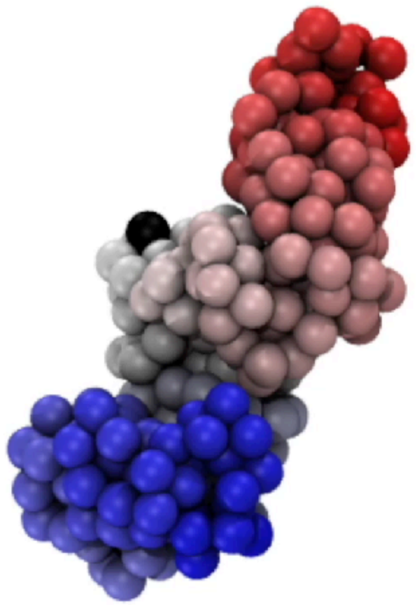
Contacts

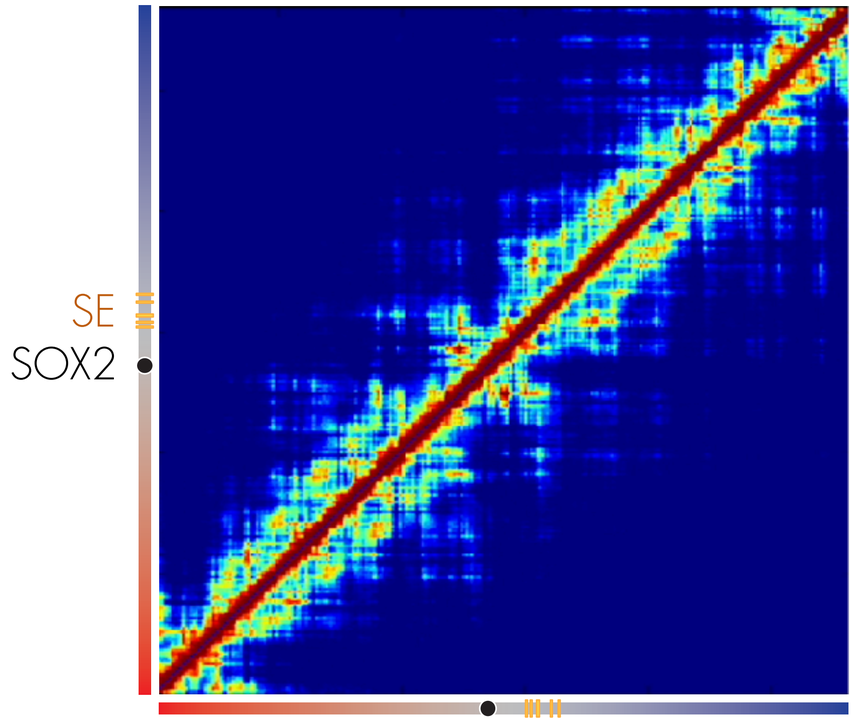




SOX2 locus structural changes from B to PSC

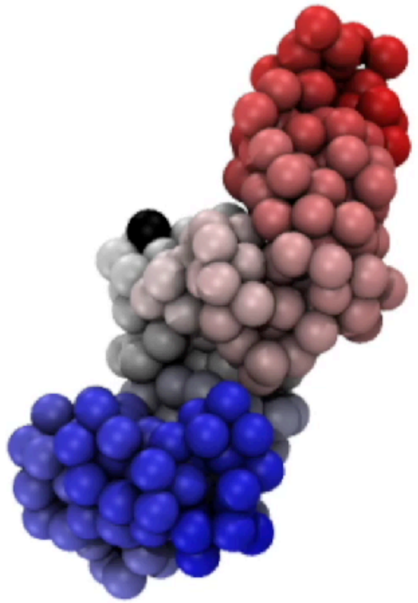
Contacts

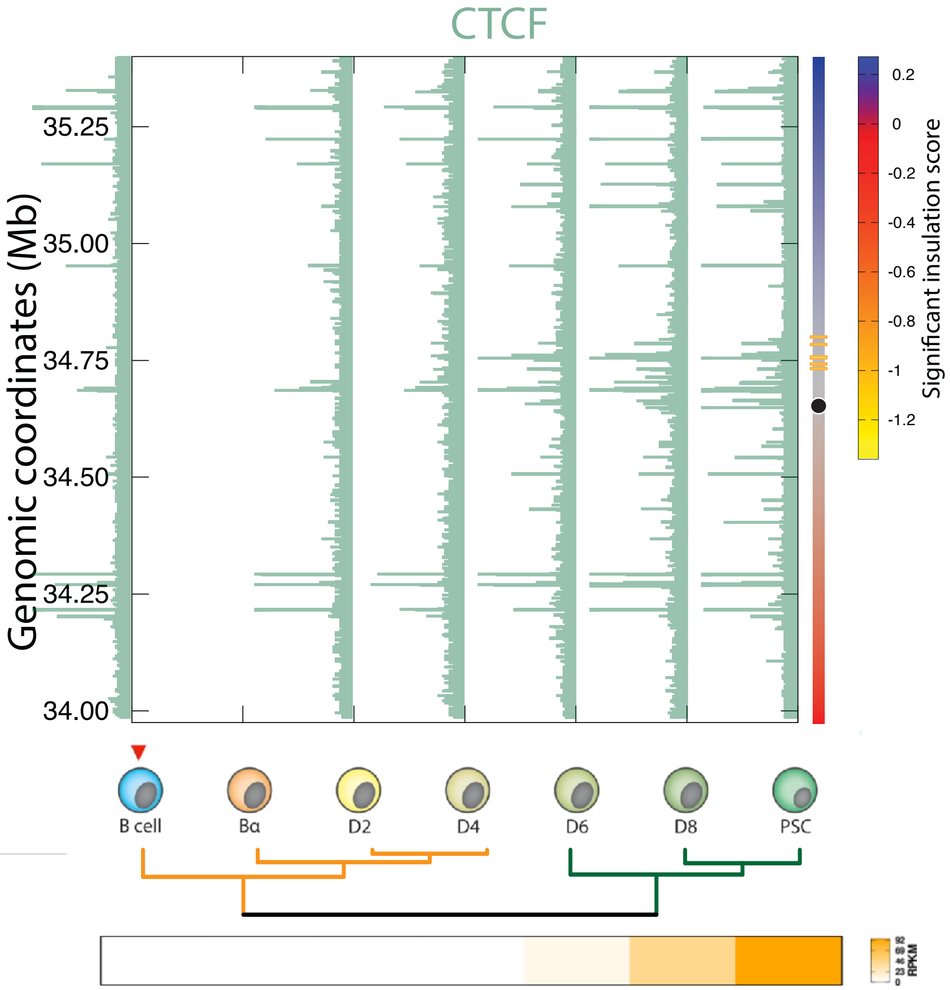




SOX2 locus structural changes from B to PSC

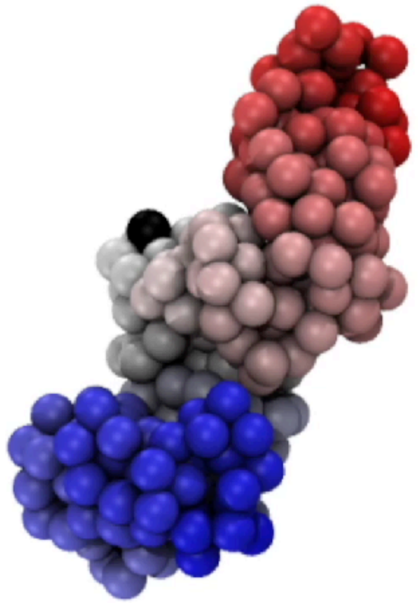
TAD borders

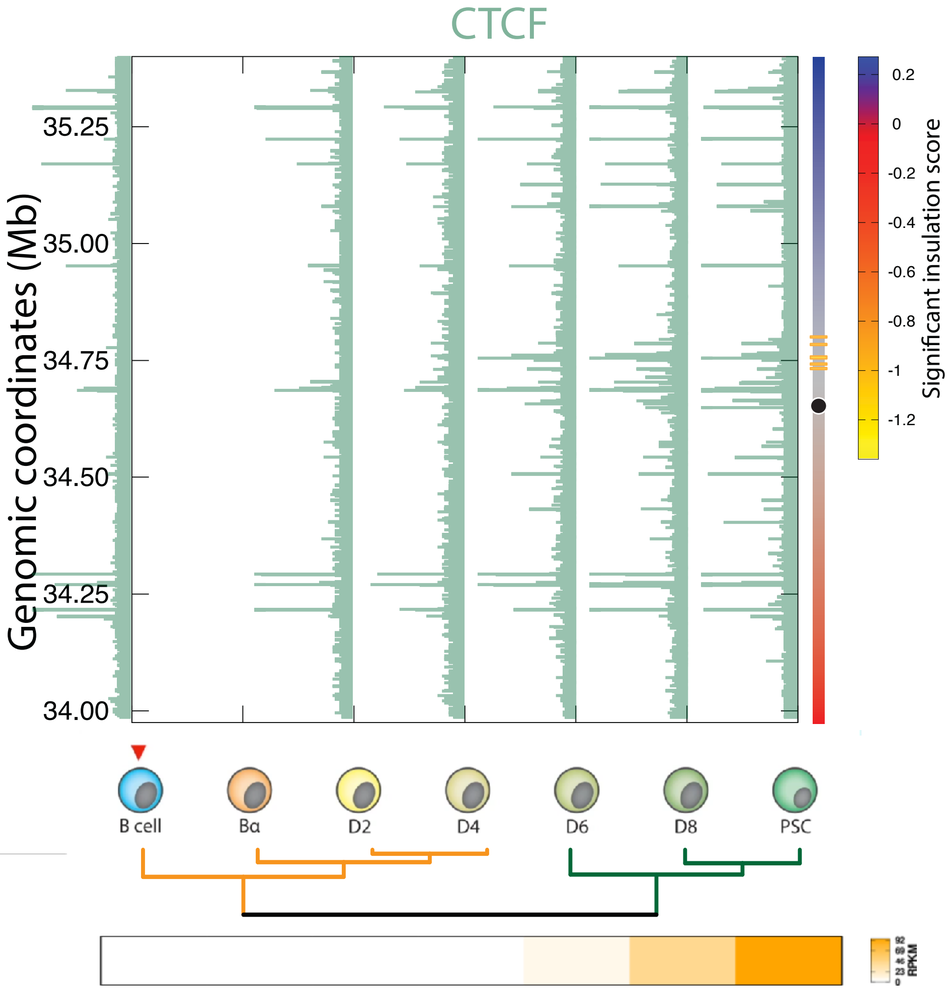




SOX2 locus structural changes from B to PSC

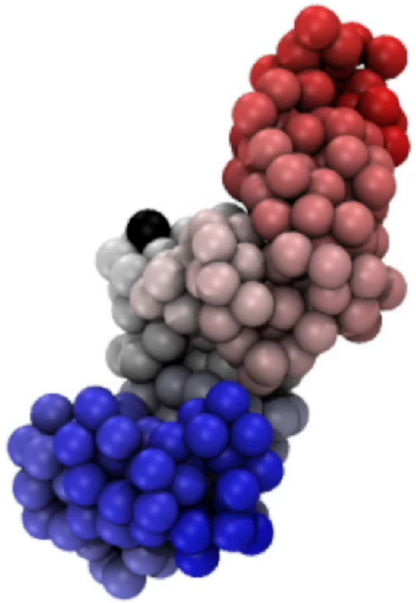
TAD borders

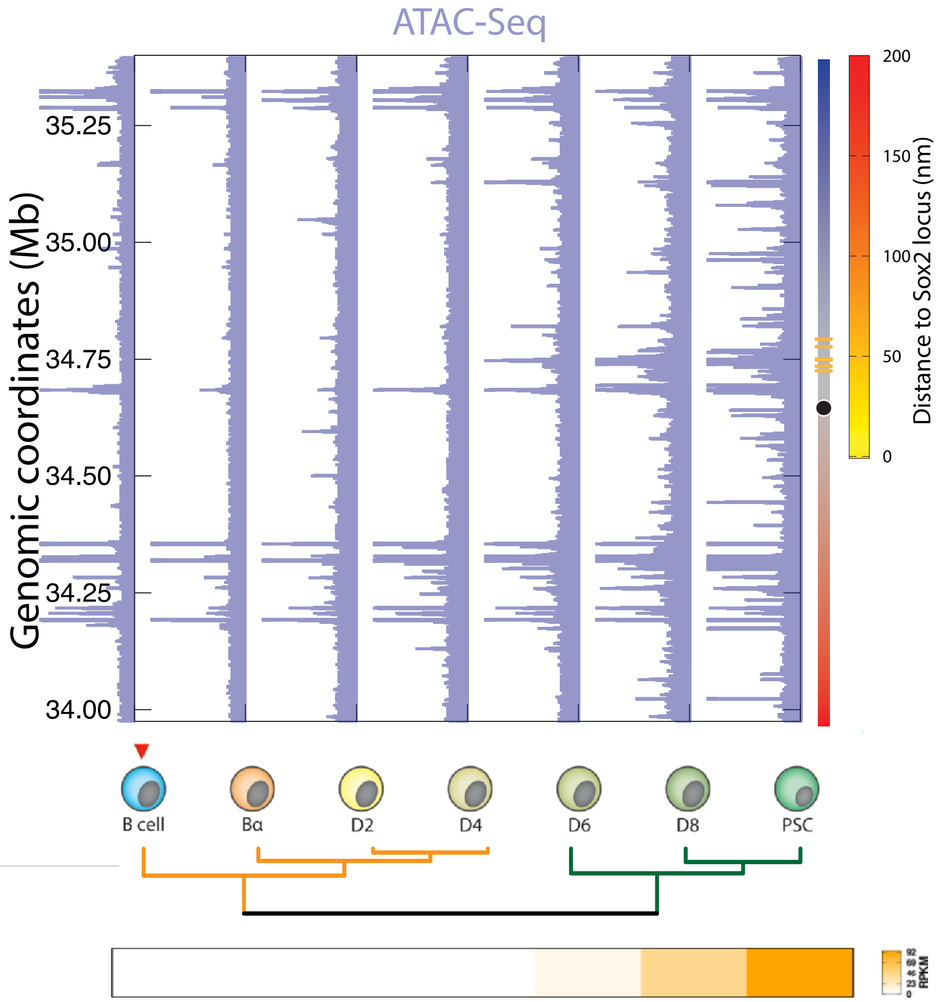




SOX2 locus structural changes from B to PSC

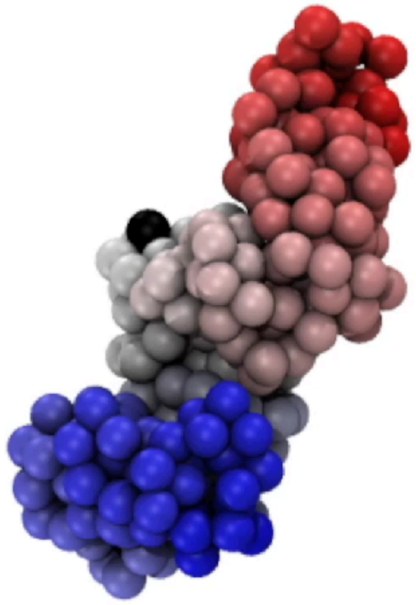
Distance to regulatory elements

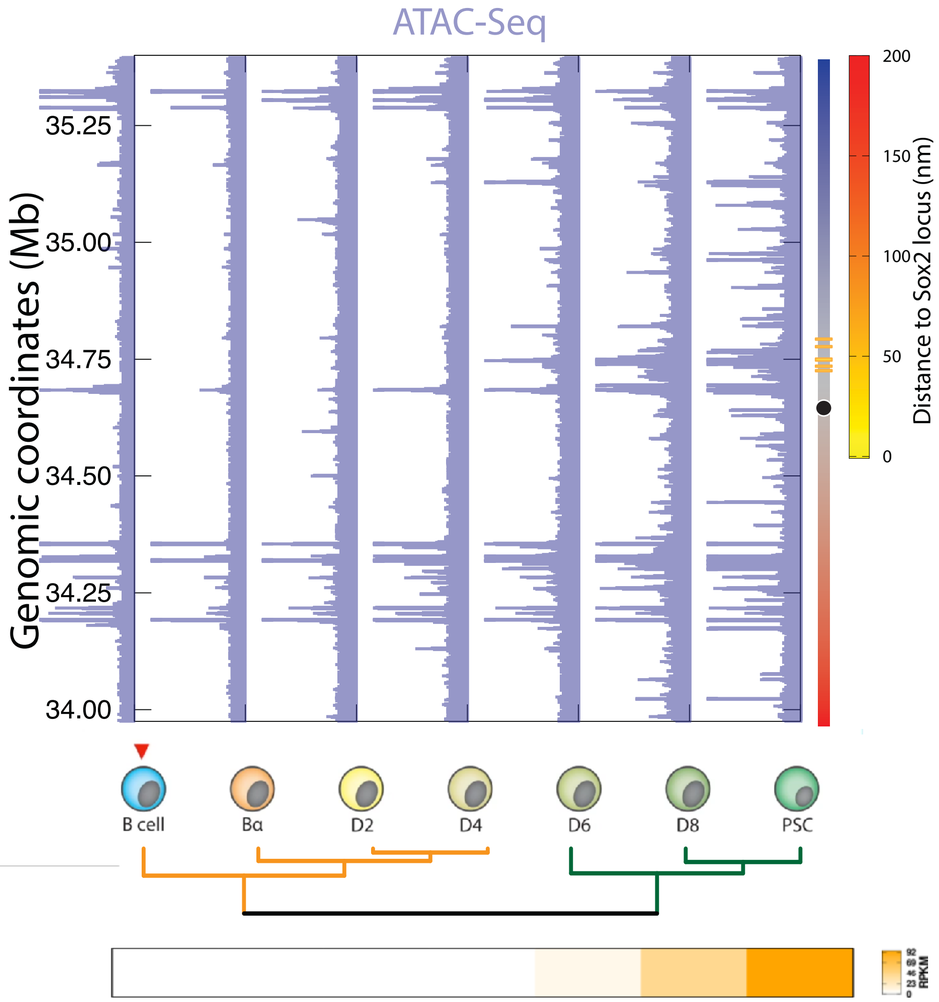




SOX2 locus structural changes from B to PSC

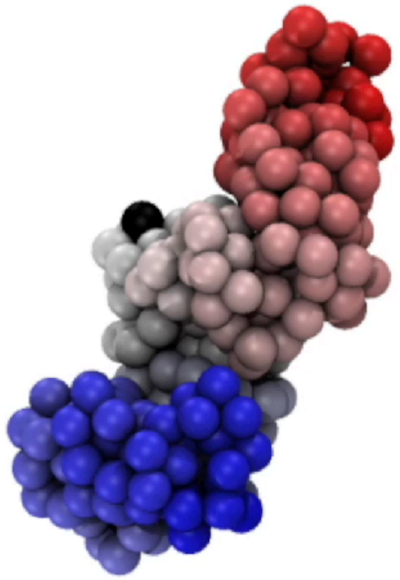
Distance to regulatory elements

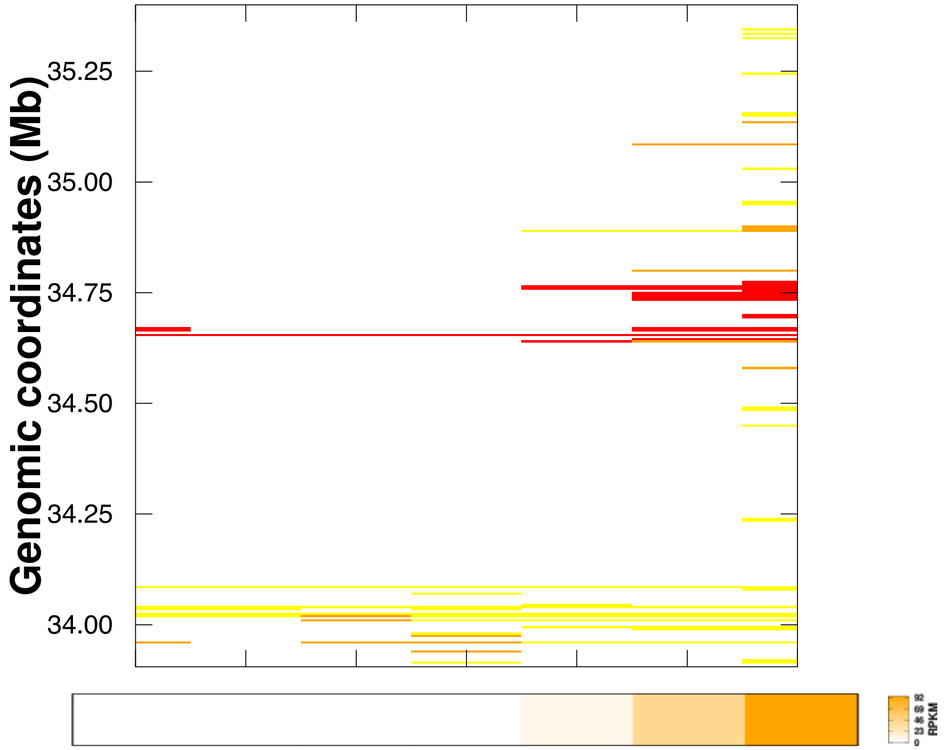




SOX2 locus structural changes from B to PSC

Chromatin Activity

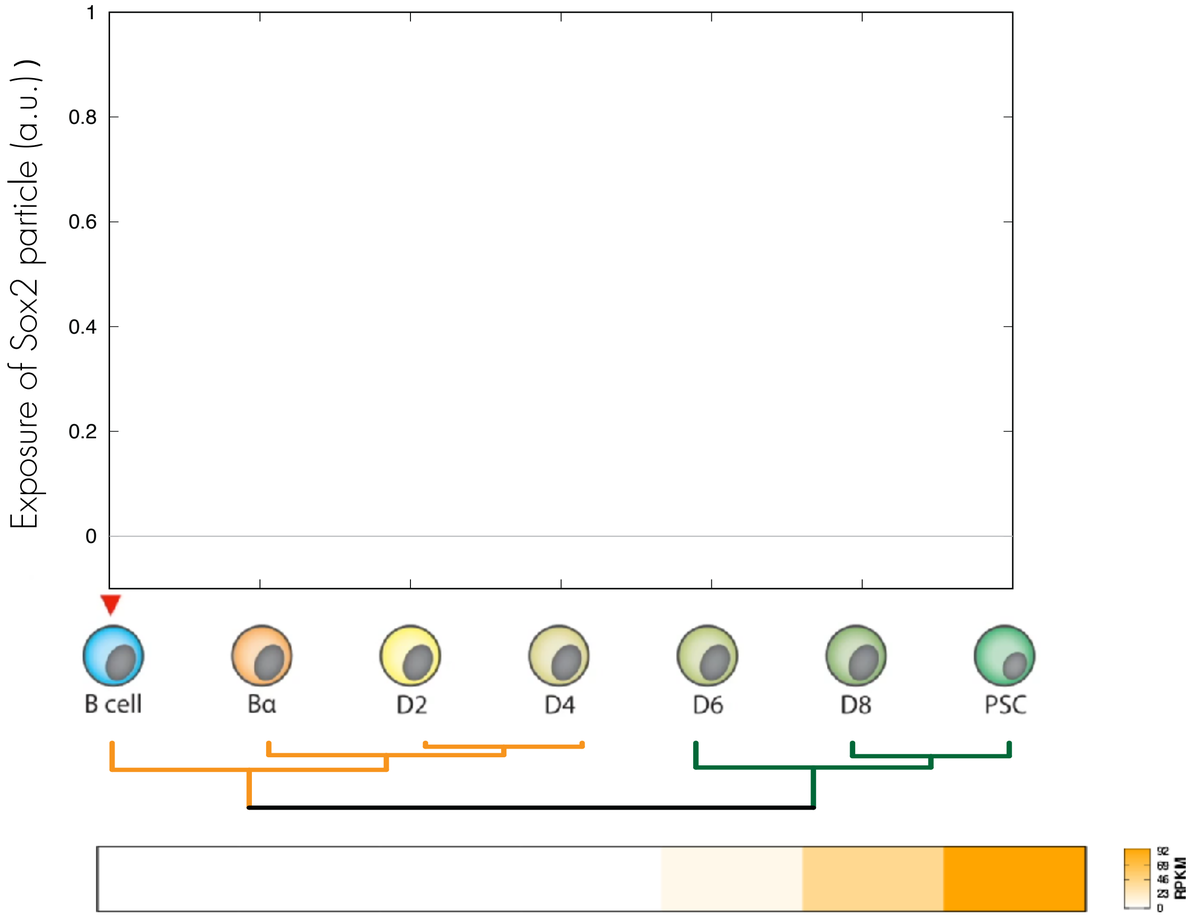




	B	Ba	D2	D4	D6	D8	PSC
A	9	6	7	13	13	22	48
AP	4	1	4	4	4	13	23
APD	3	1	1	1	4	10	15

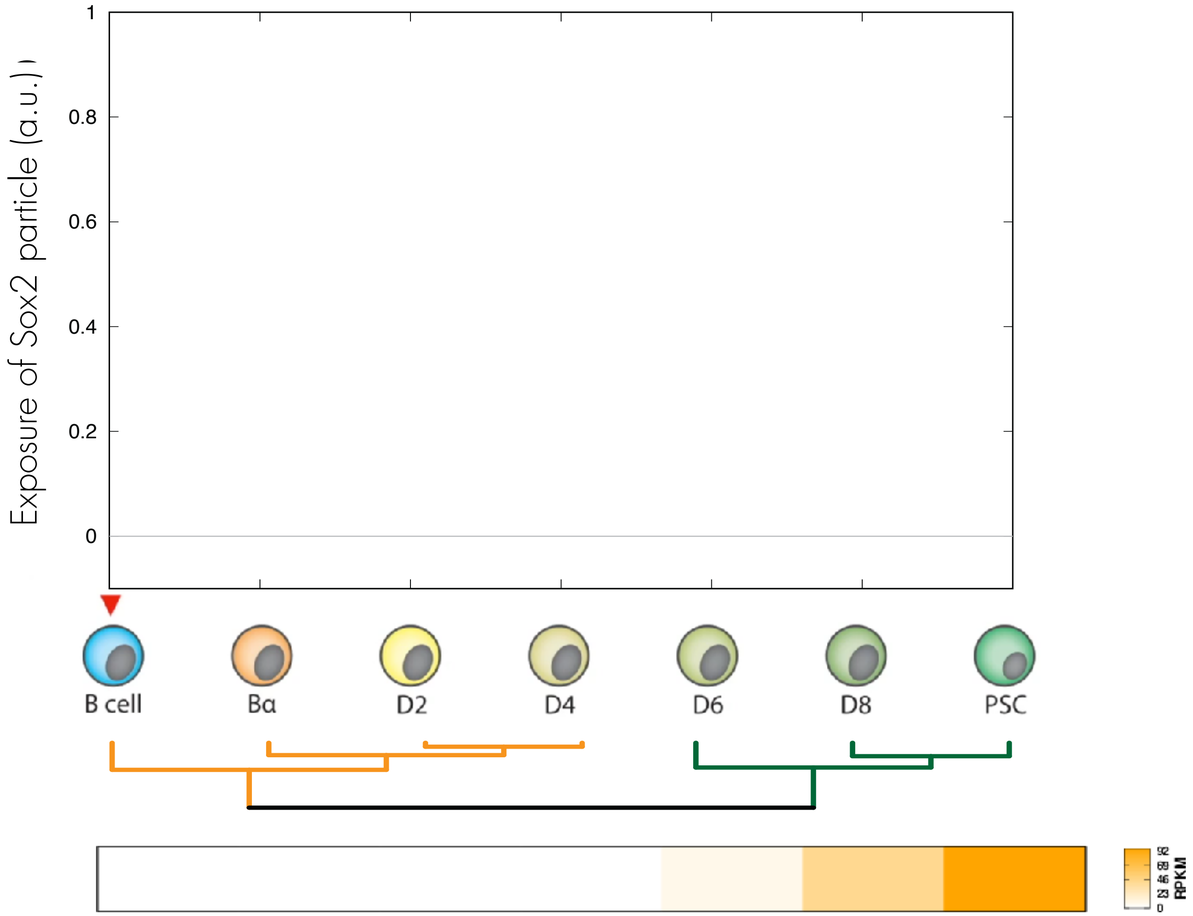
SOX2 locus structural changes from B to PSC

Structural exposure



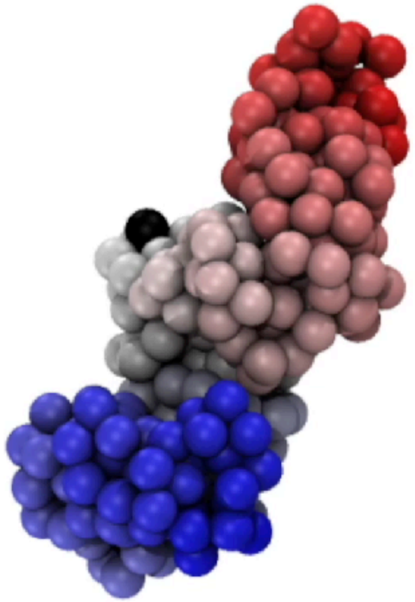
SOX2 locus structural changes from B to PSC

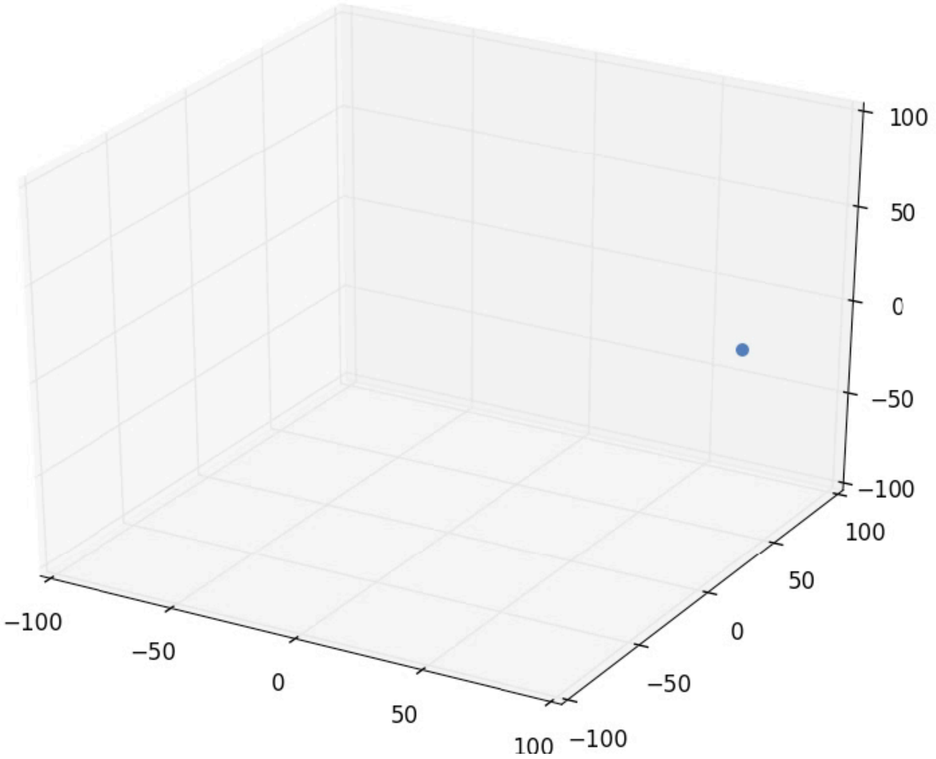
Structural exposure

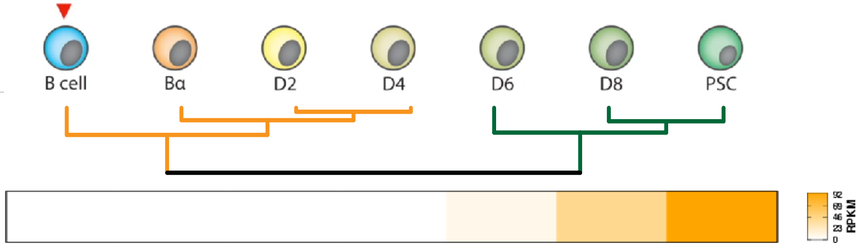


SOX2 locus dynamics changes from B to PSC

SOX2 displacement

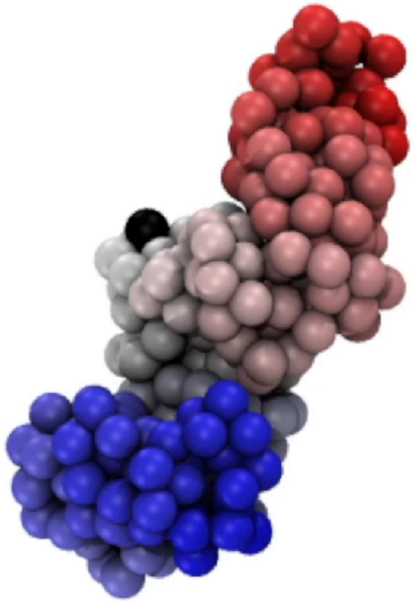


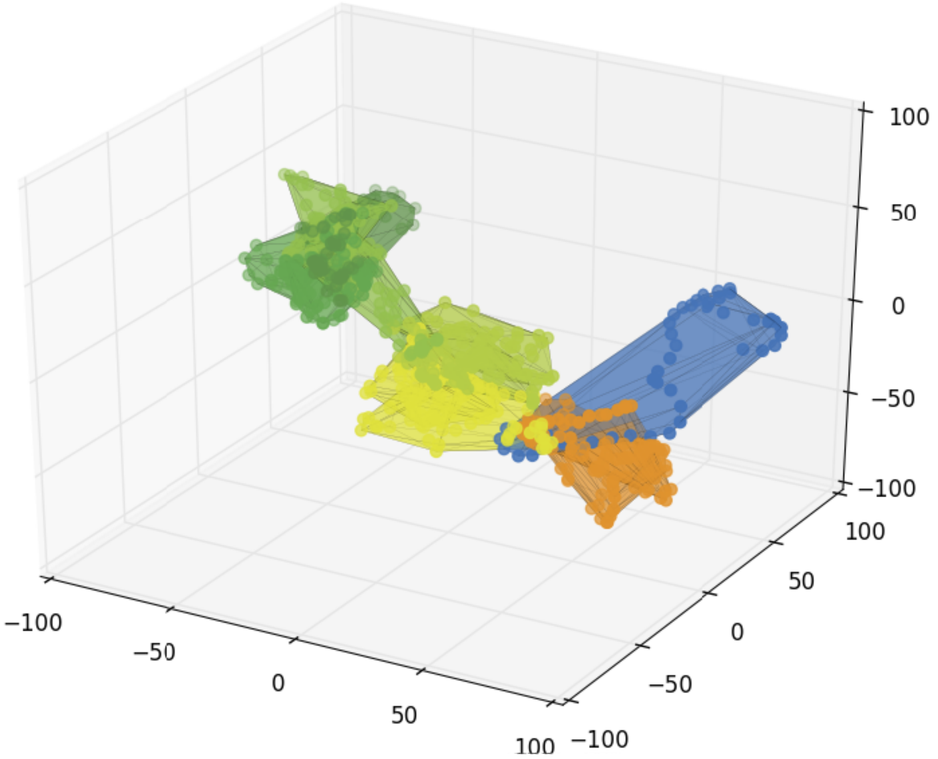


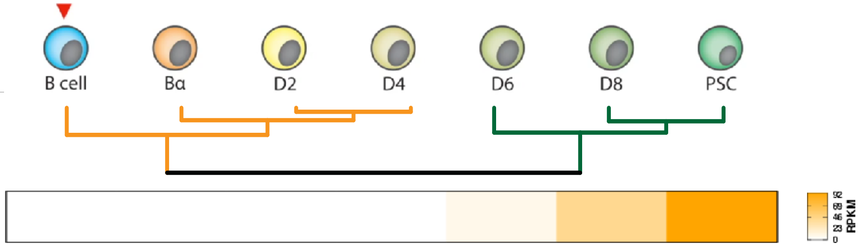


SOX2 locus dynamics changes from B to PSC

SOX2 displacement

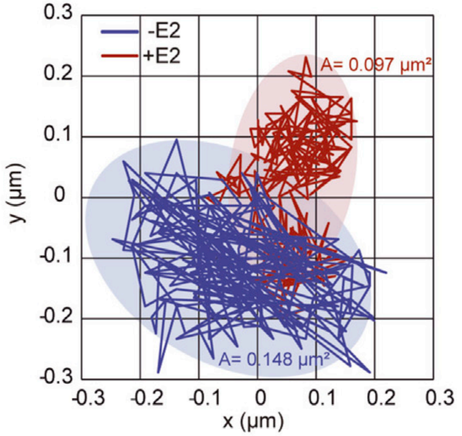






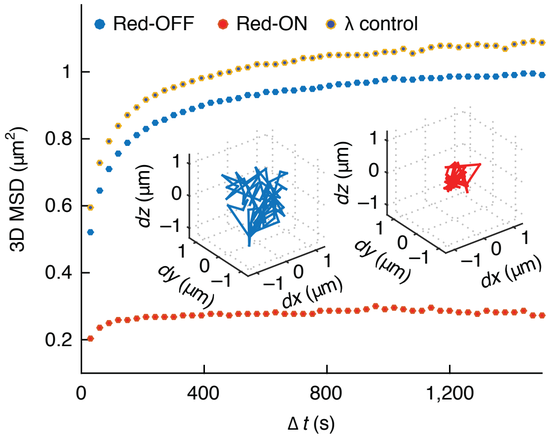
SOX2 locus dynamics changes from B to PSC

SOX2 displacement



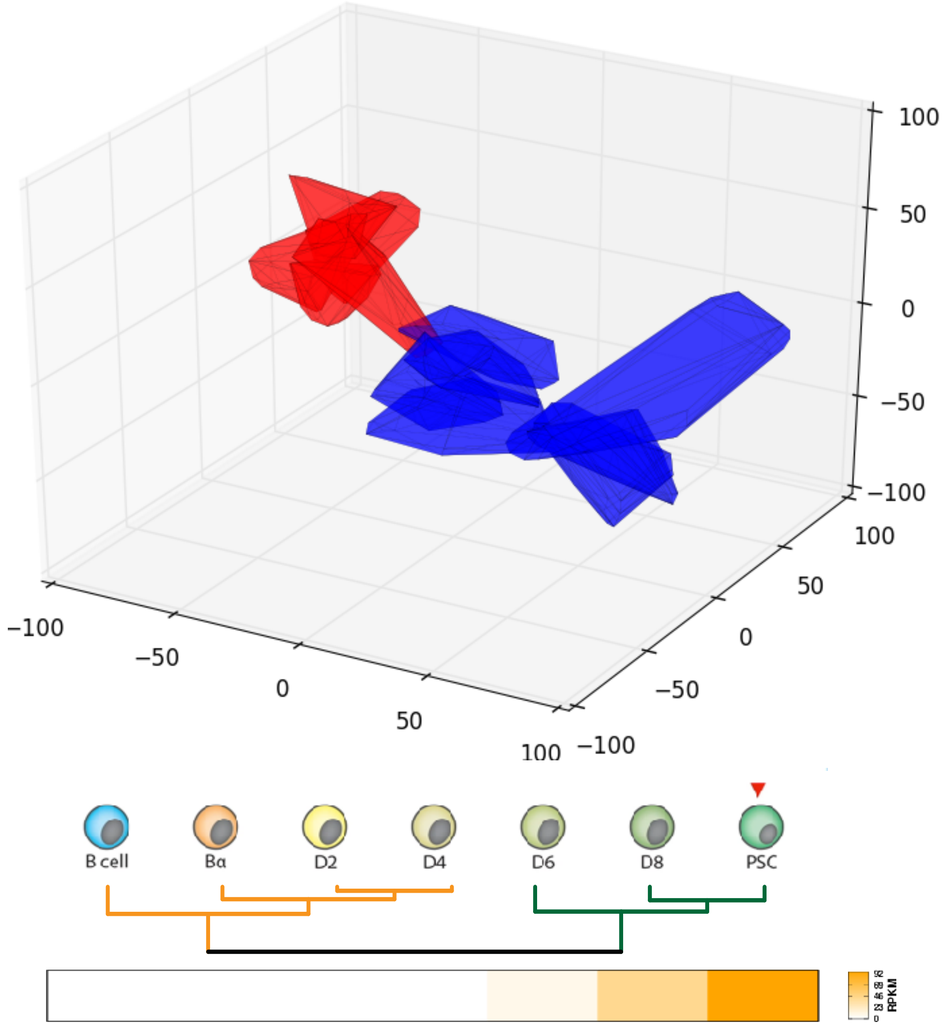
Two dimensional trajectories and area explored over 50s of the CCND1 locus recored before -E2 and after +E2 activation.

Germier ,T., et al, (2017) Biophys J.



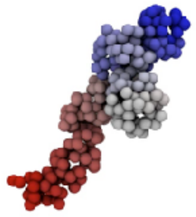
Transcription affects the 3D topology of the enhancer-promoted enhancing its temporal stability and is associated with further spatial compaction.

Chen ,T., et al, (2018) Nat. Genetics

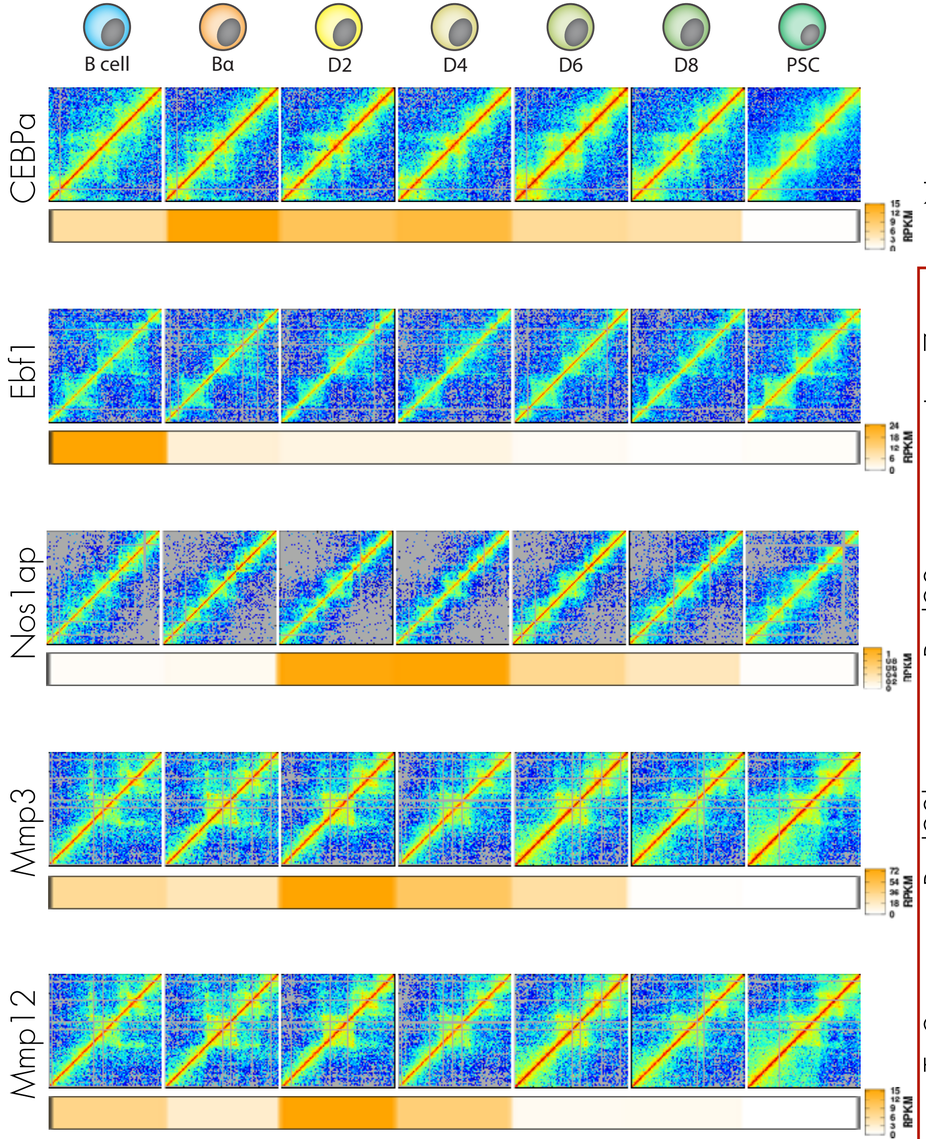


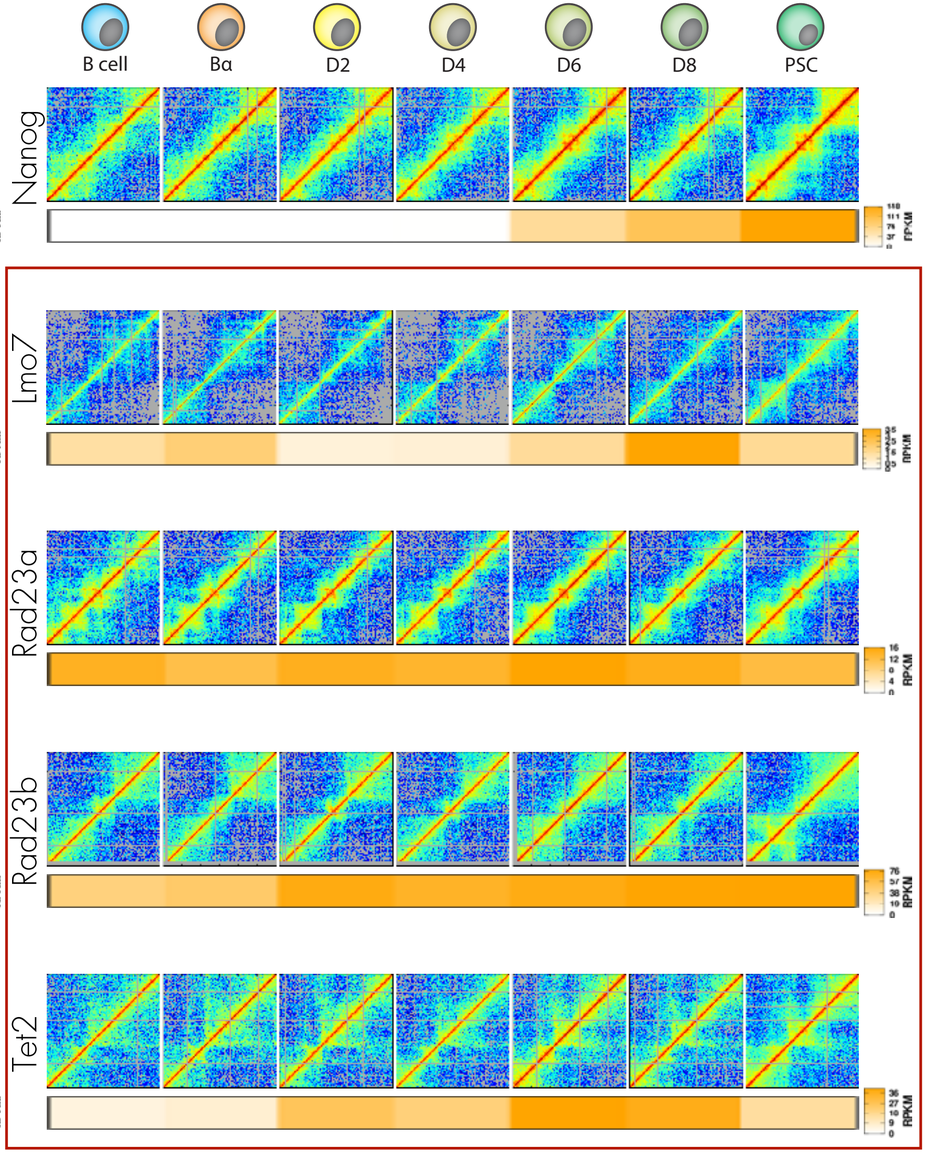
Structural changes from B to PSC

Other 10 loci



Switch

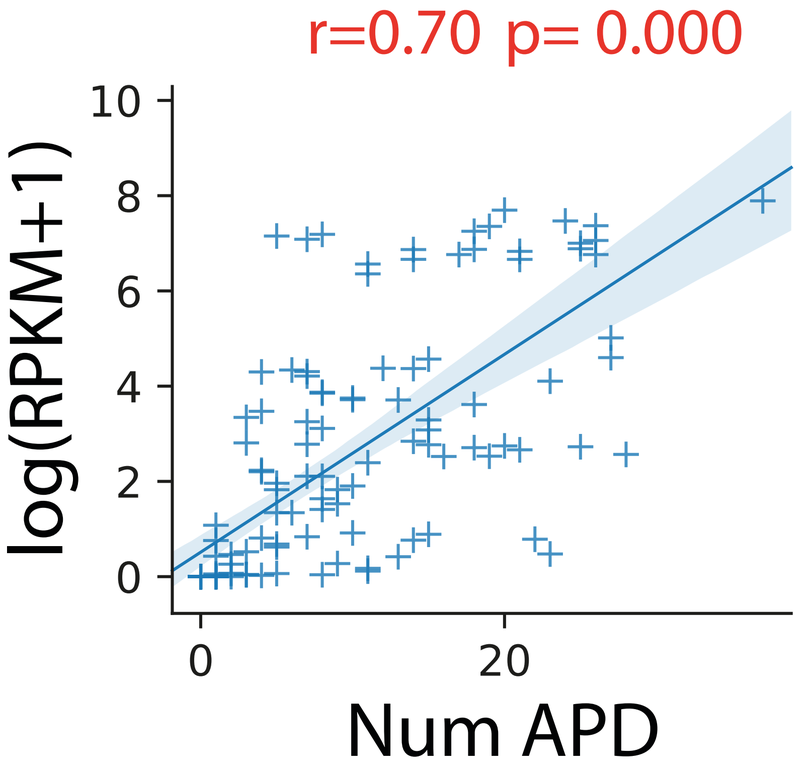


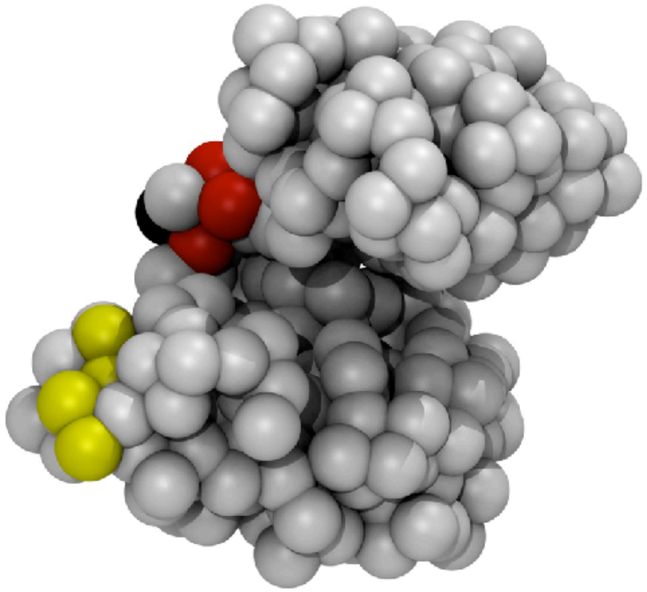


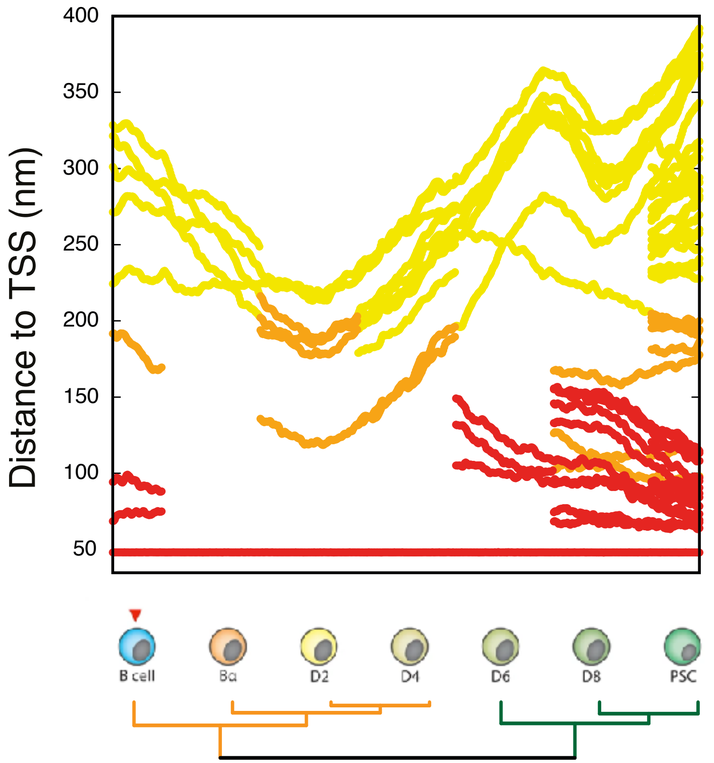
Always active

Dynamics of gene activation

3D enhancer hubs







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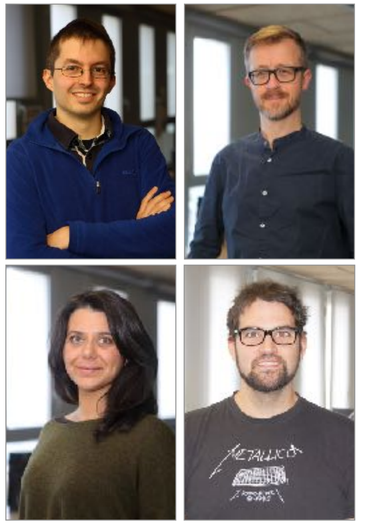

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