



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>

HUMAN “The Movie” by Yann Arthus-Bertrand

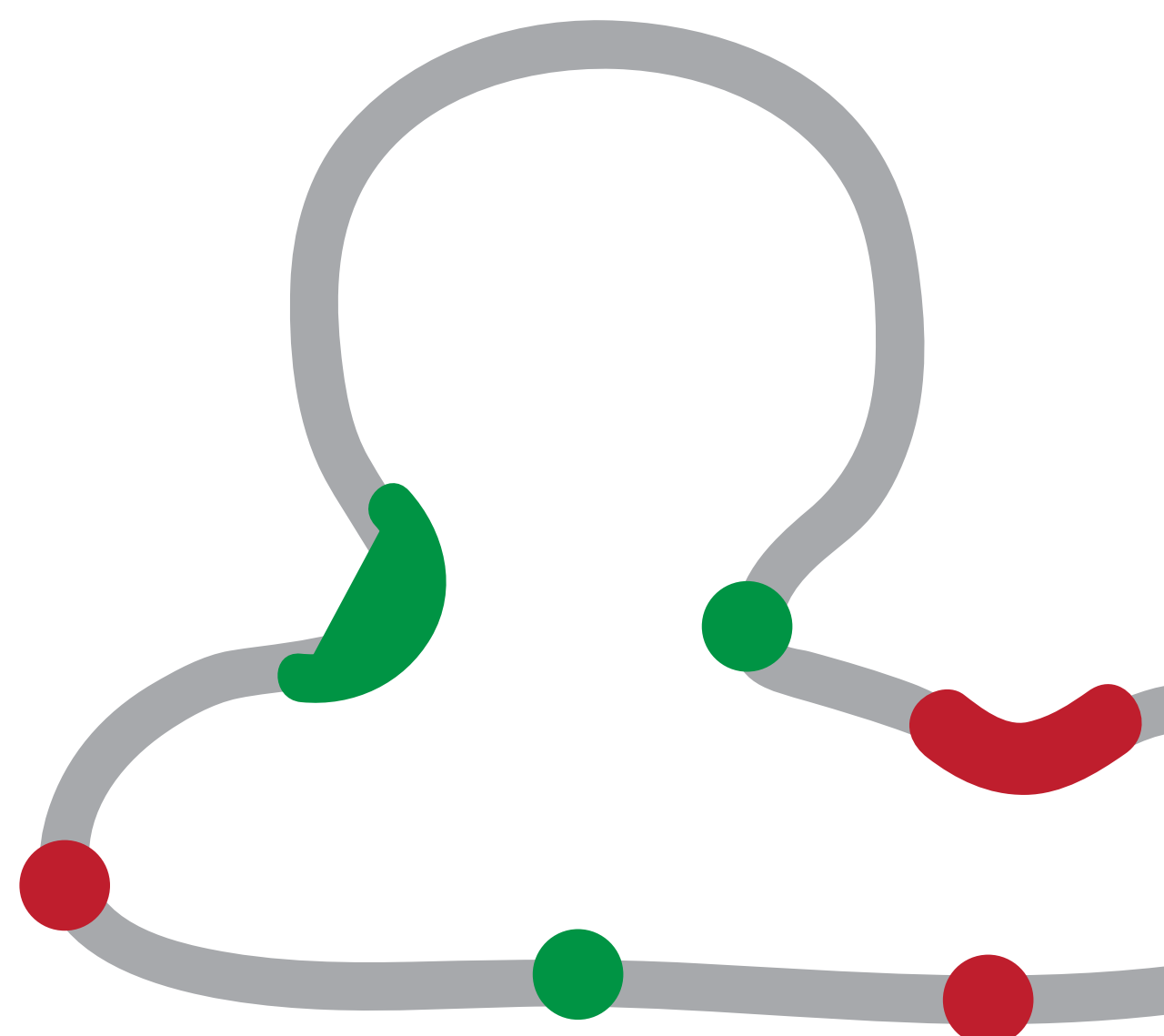
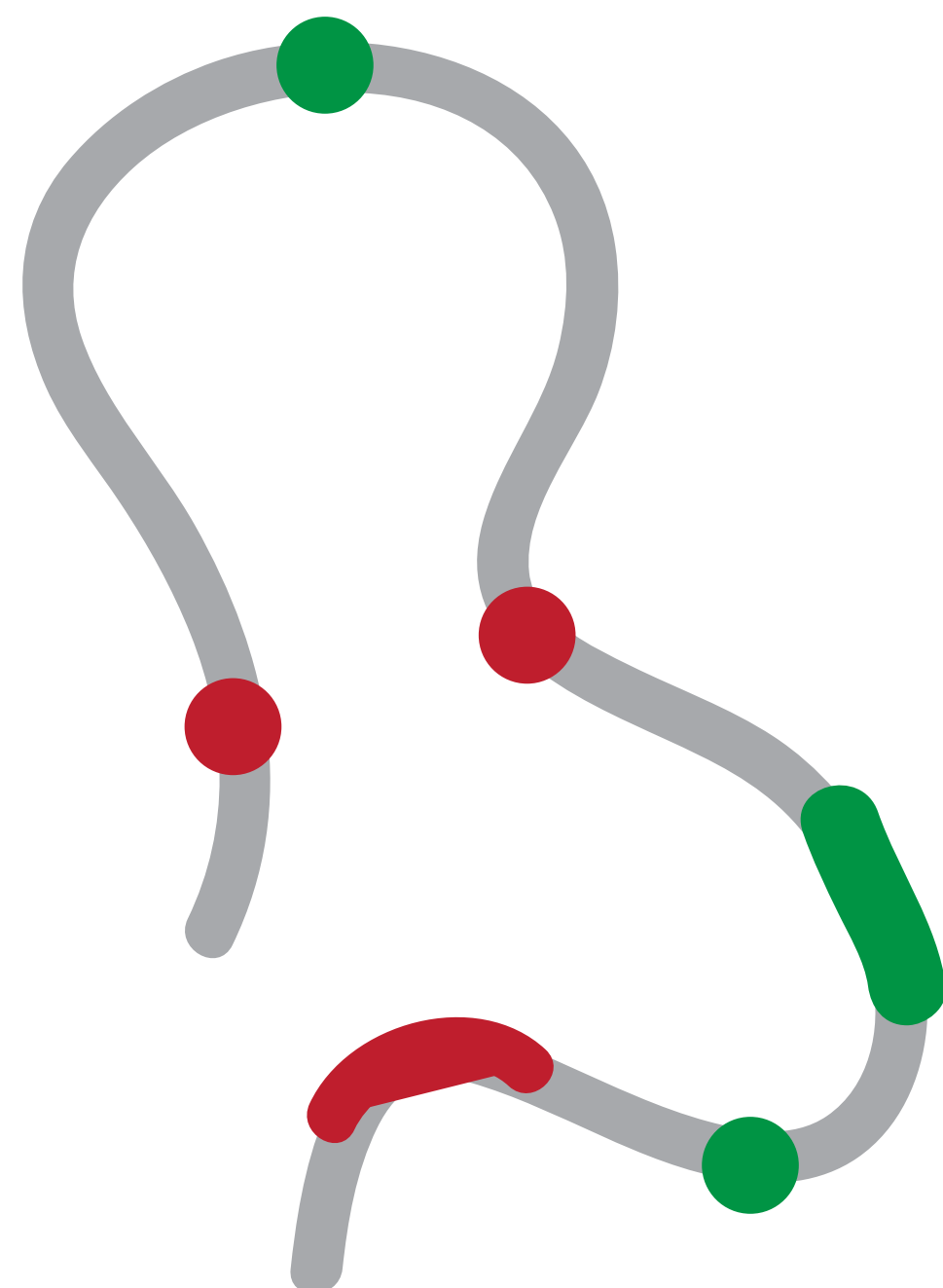
cnag CRG[®] ICREA

All you will see in the screen is here:

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

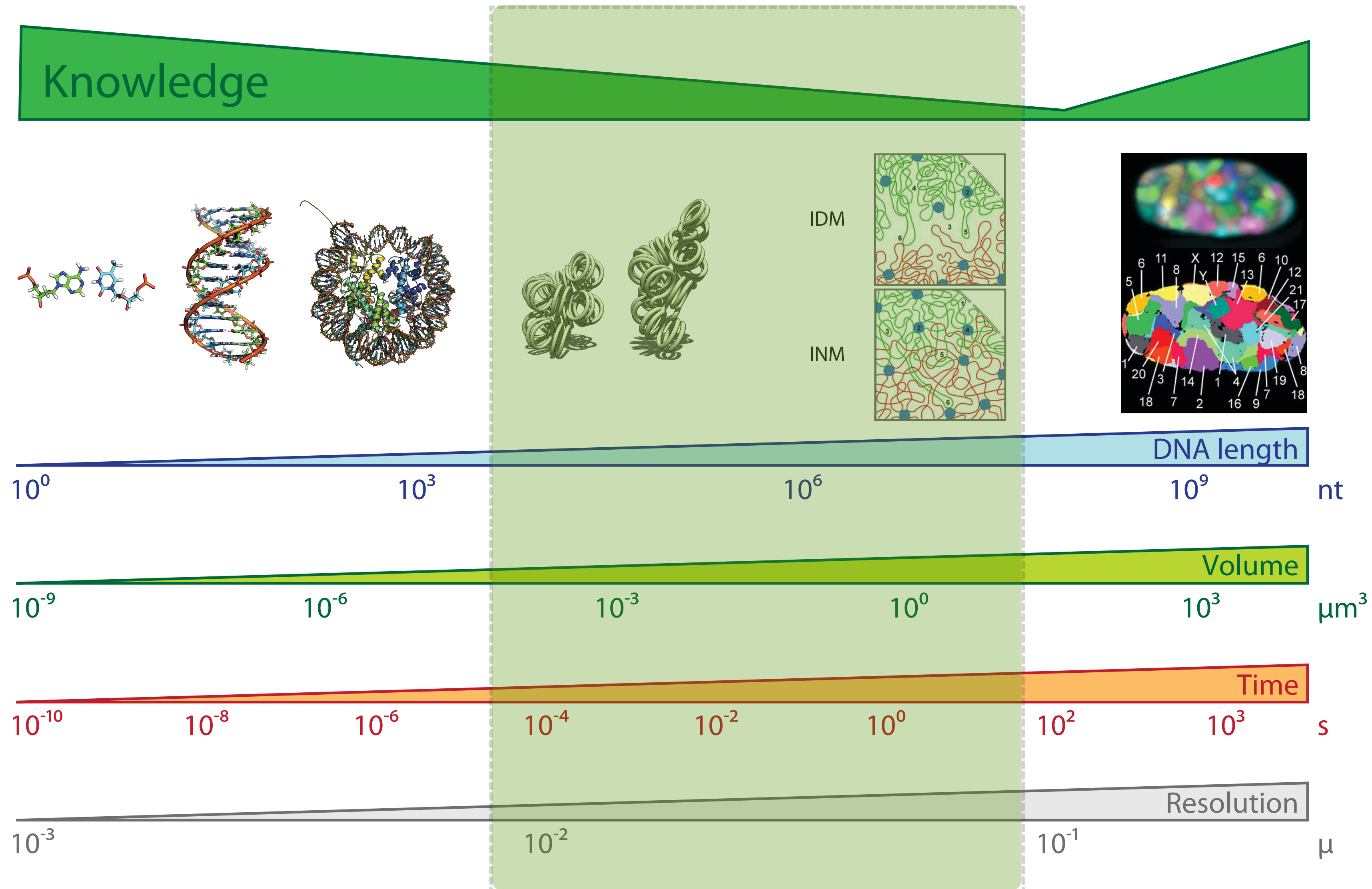
I encourage you to:

listen AND speak
not necessarily in this order... 😊



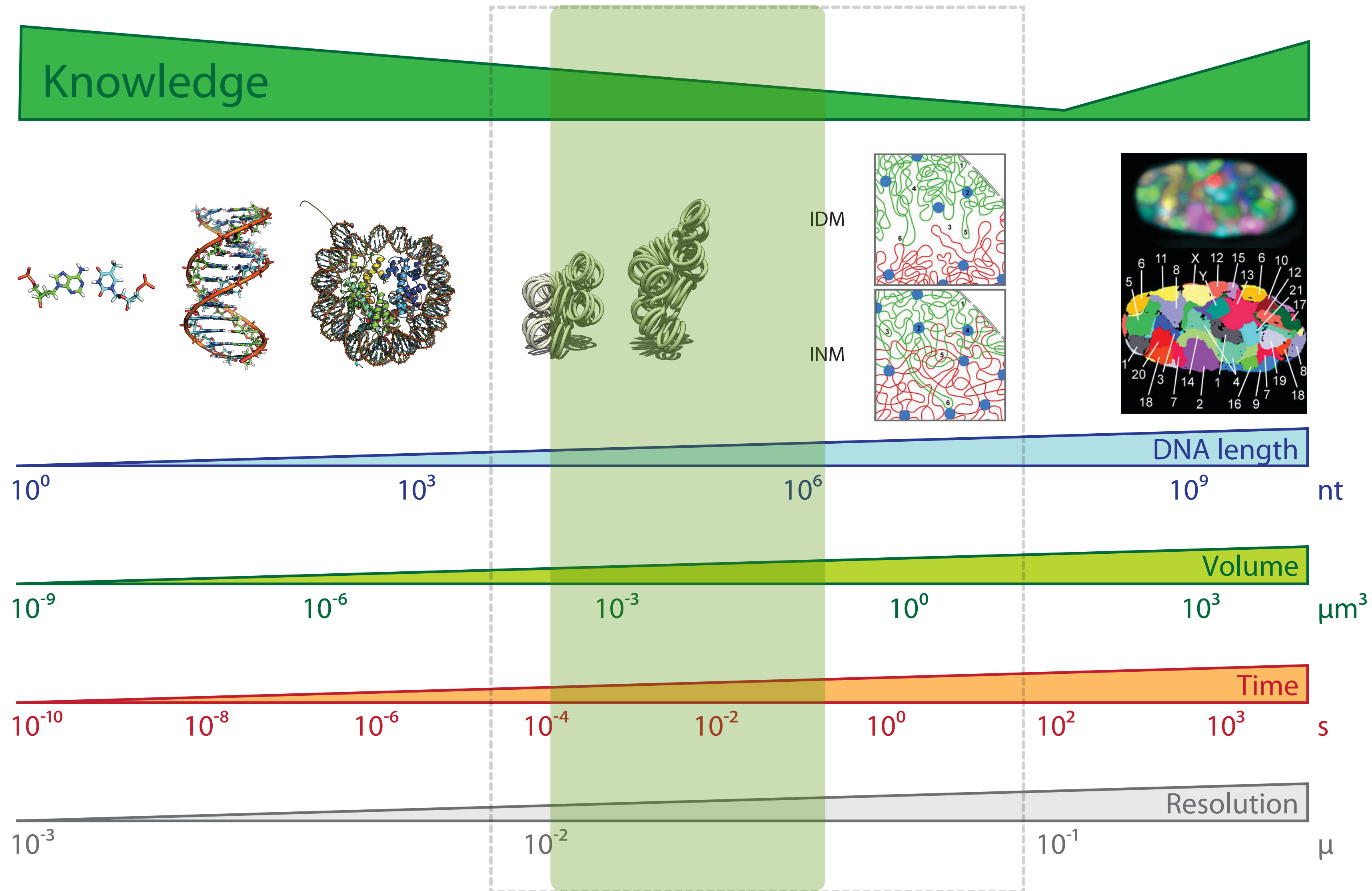
Resolution Gap

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



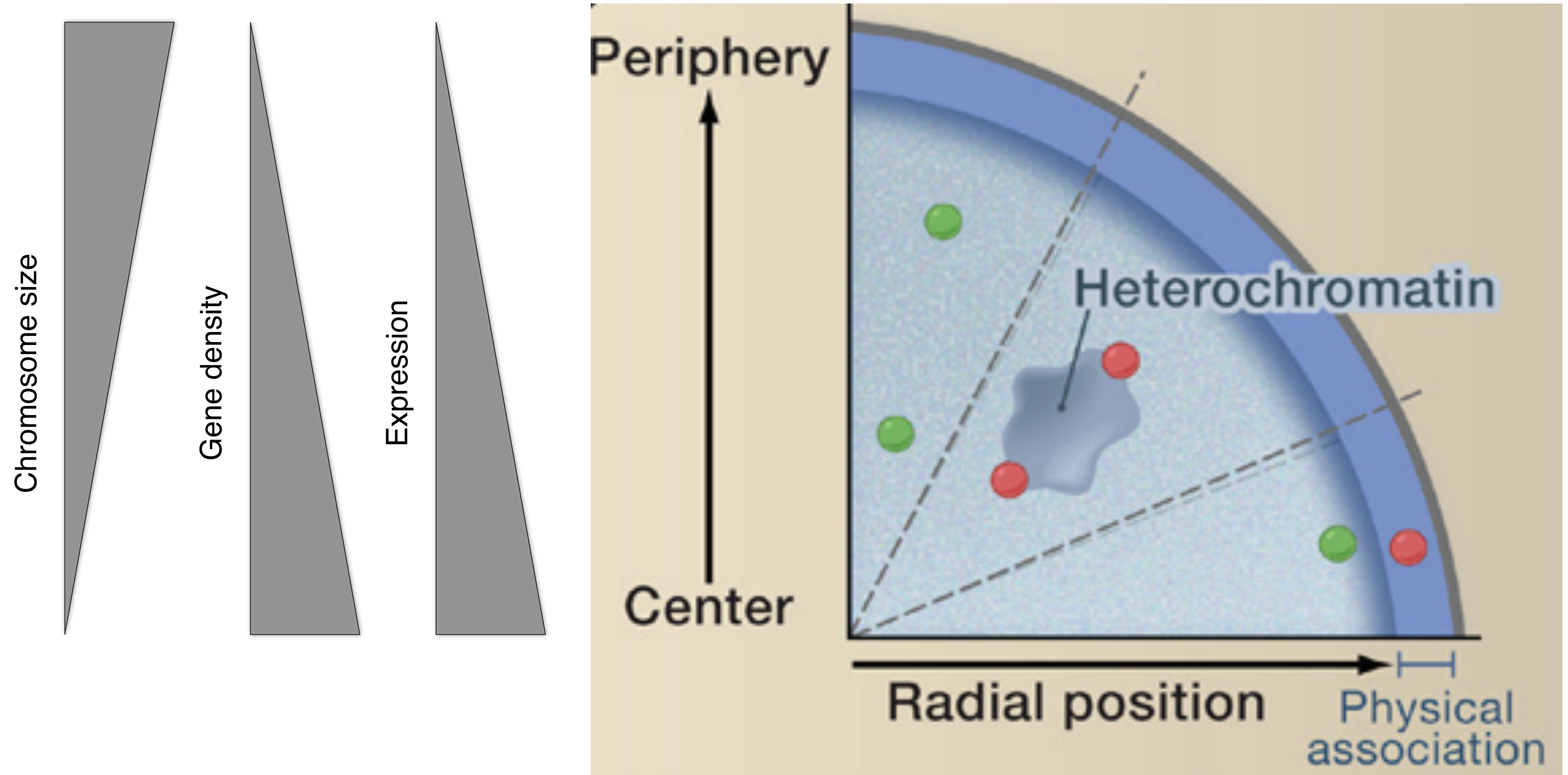
Resolution Gap

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



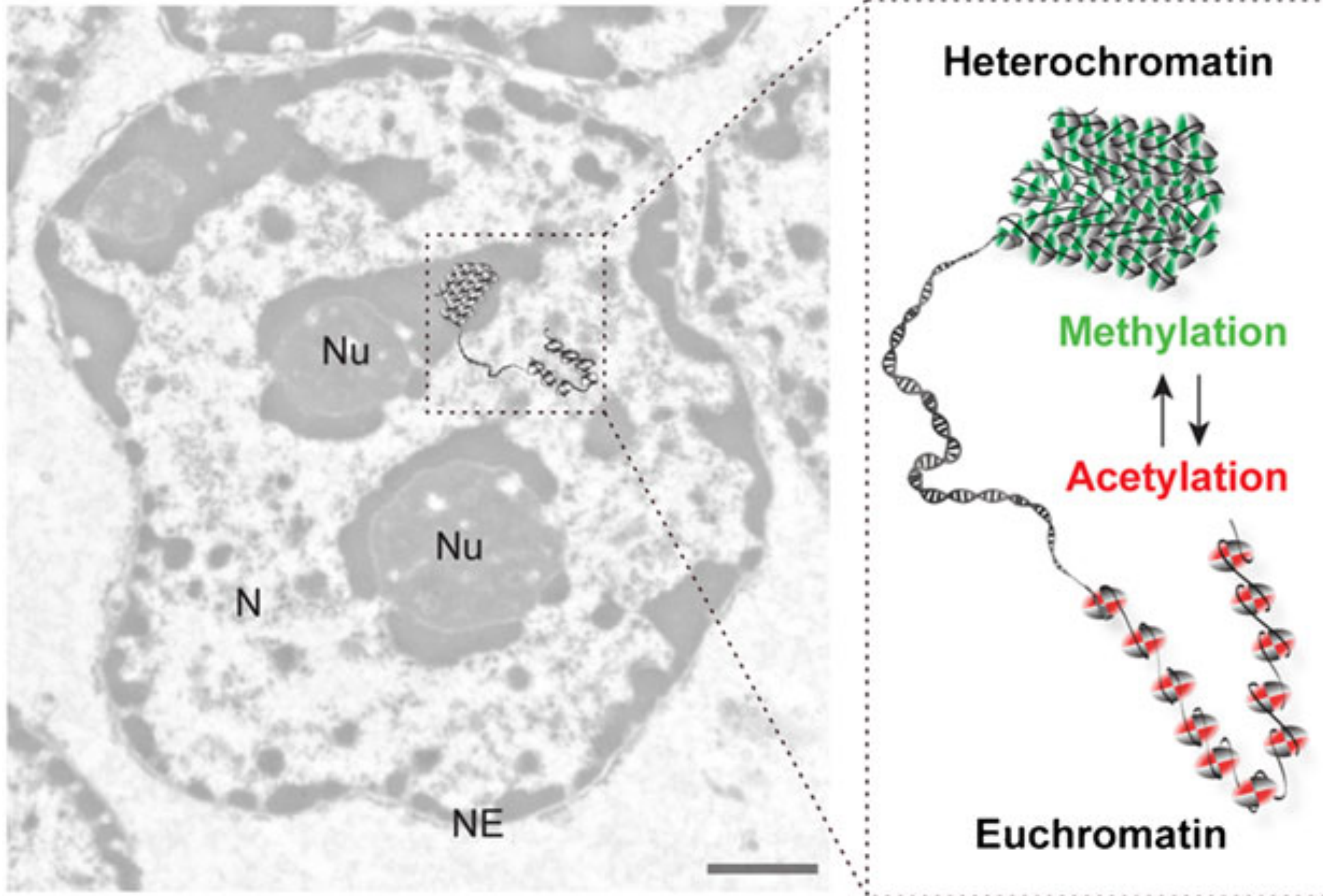
Level I: Radial genome organization

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

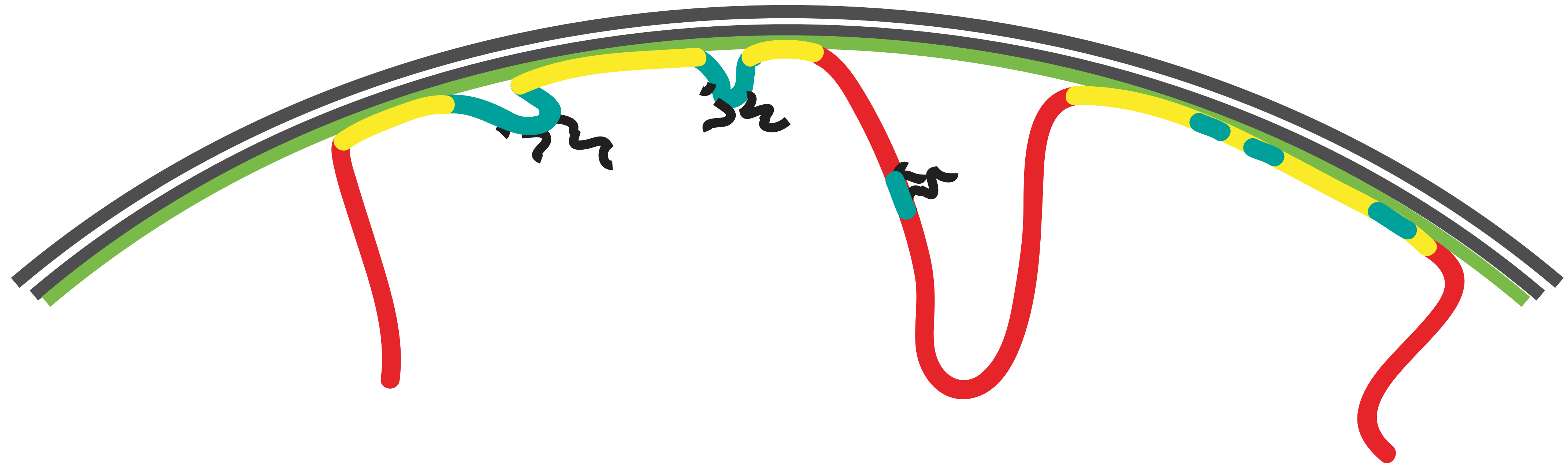


Level II: Euchromatin vs heterochromatin

Electron microscopy



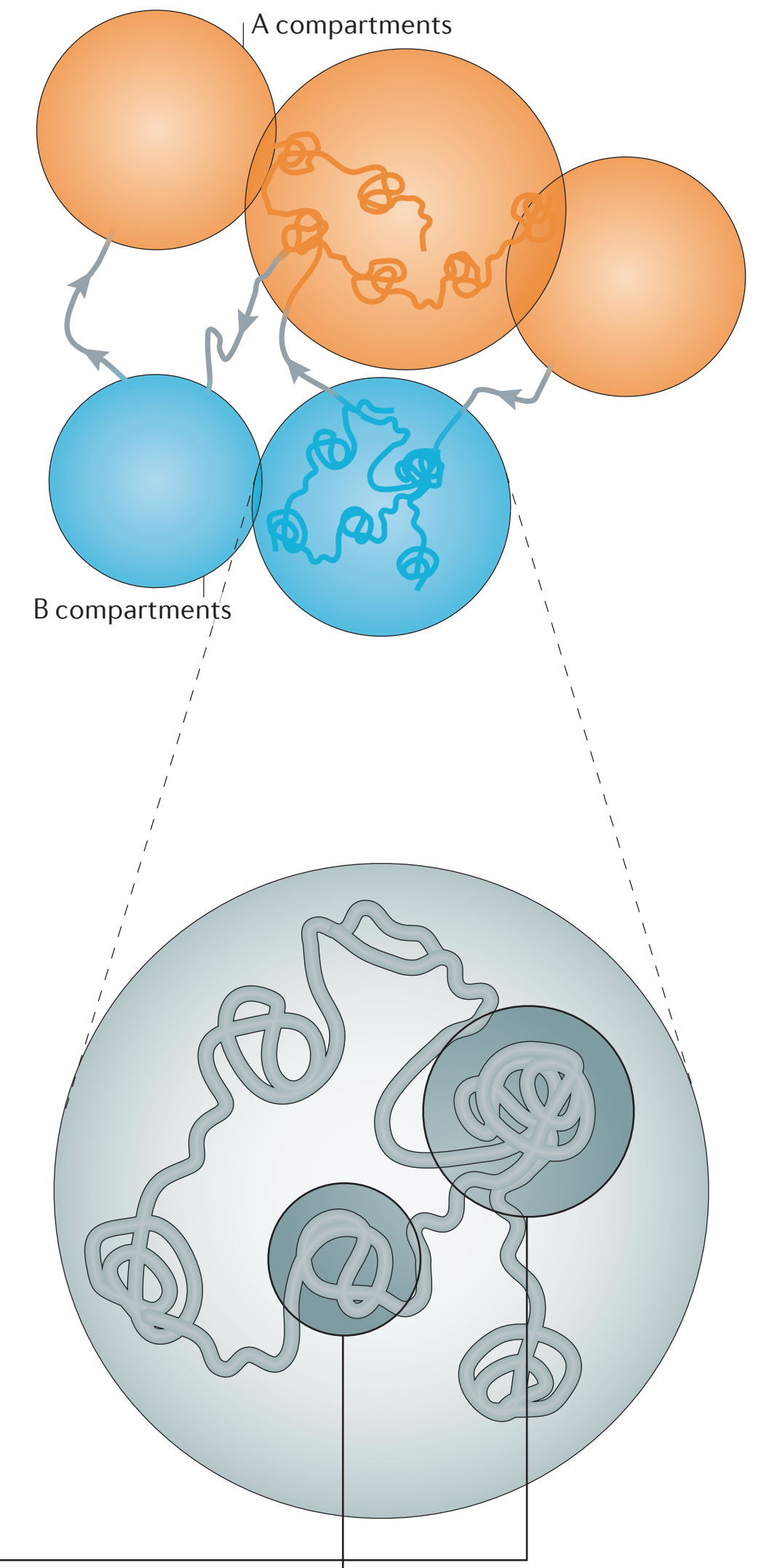
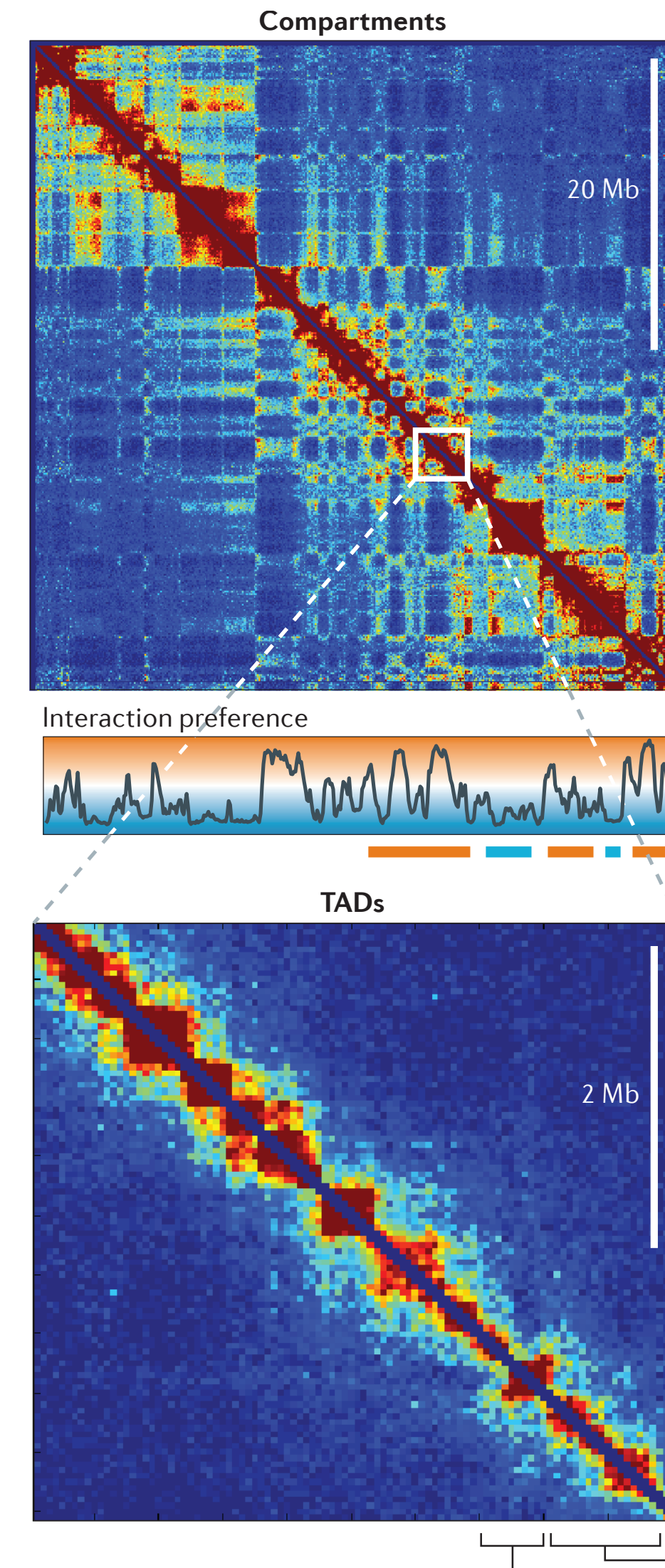
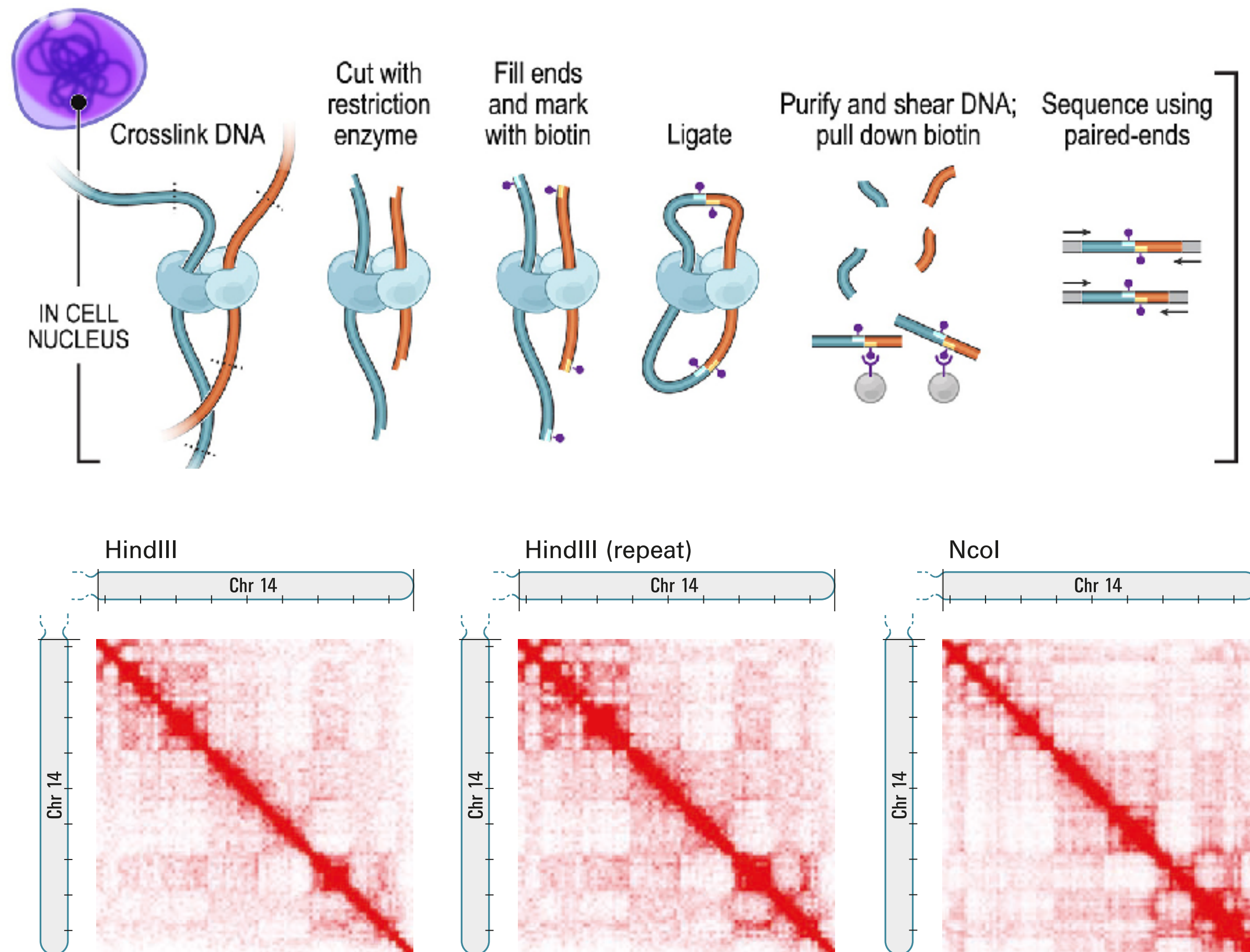
Level III: Lamina-genome interactions



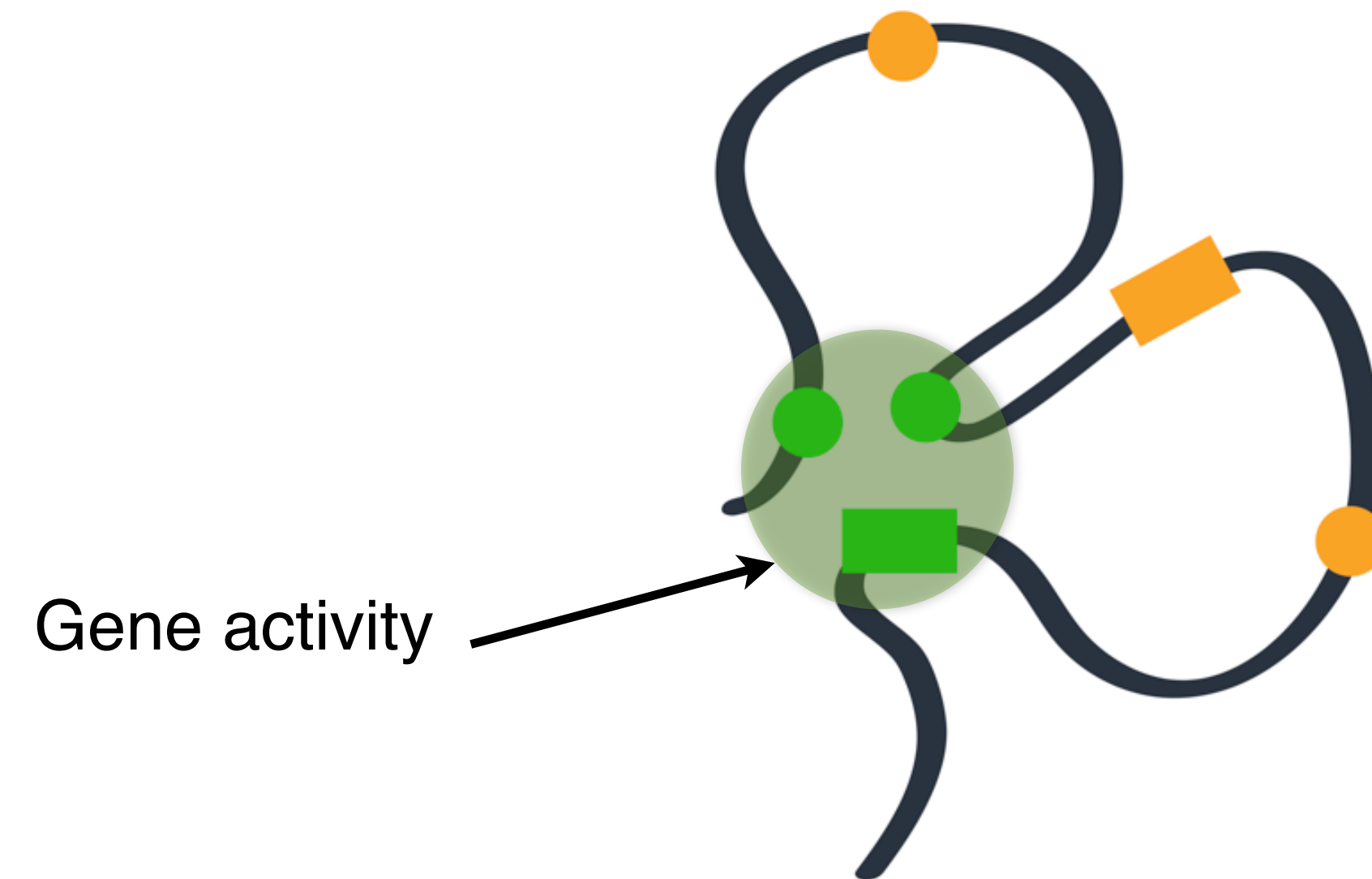
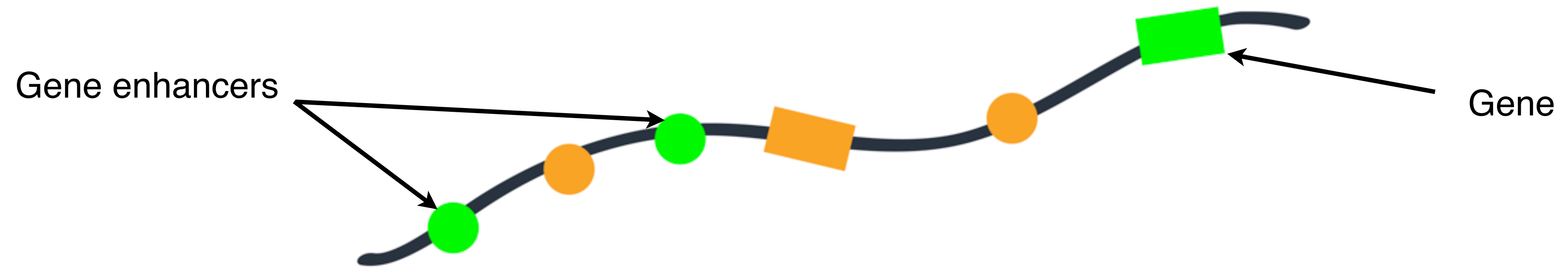
- nuclear membrane
- nuclear lamina
- internal chromatin (mostly active)
- lamina-associated domains (repressed)
- Genes
- mRNA

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

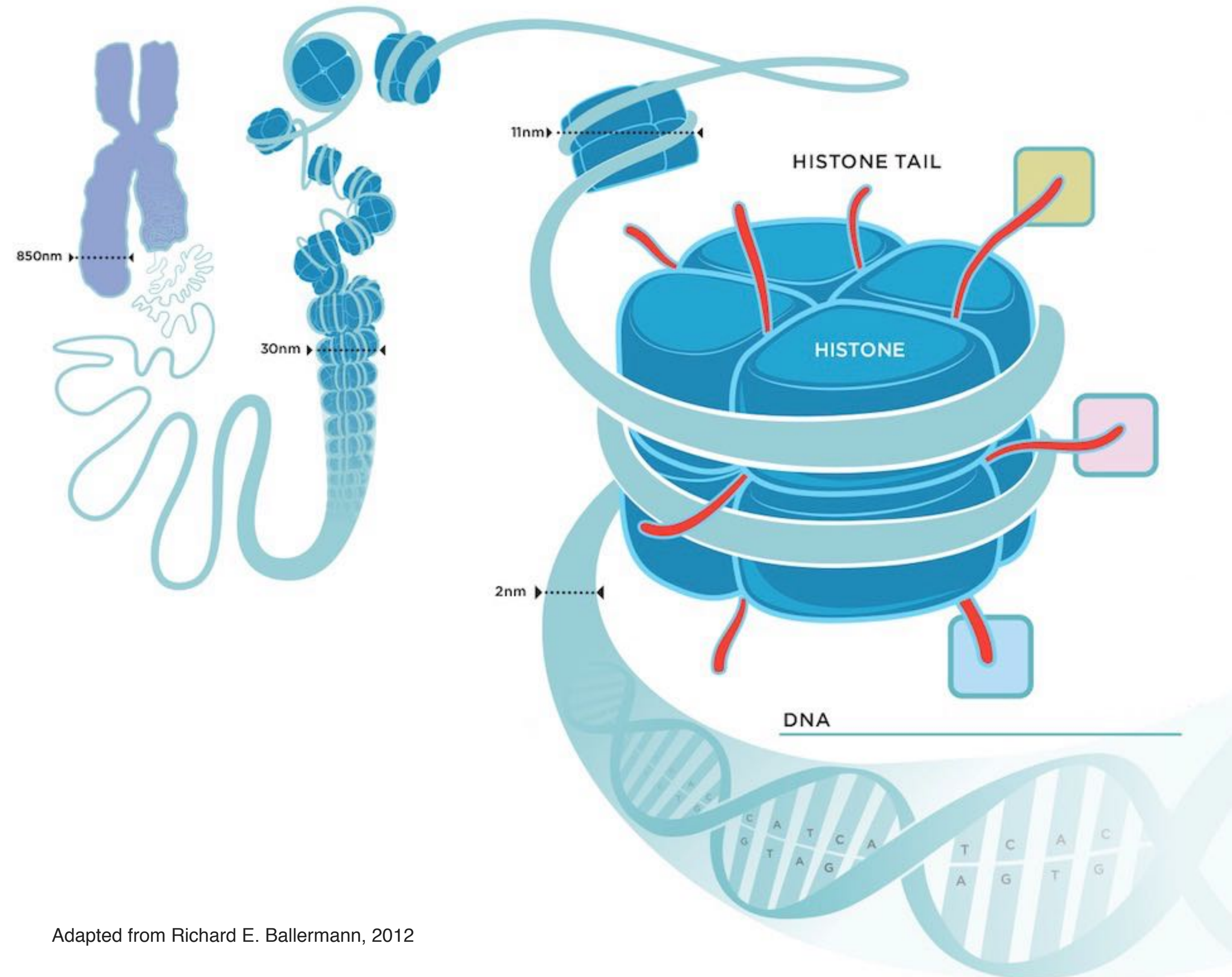


Level VI: Nucleosome

Chromosome

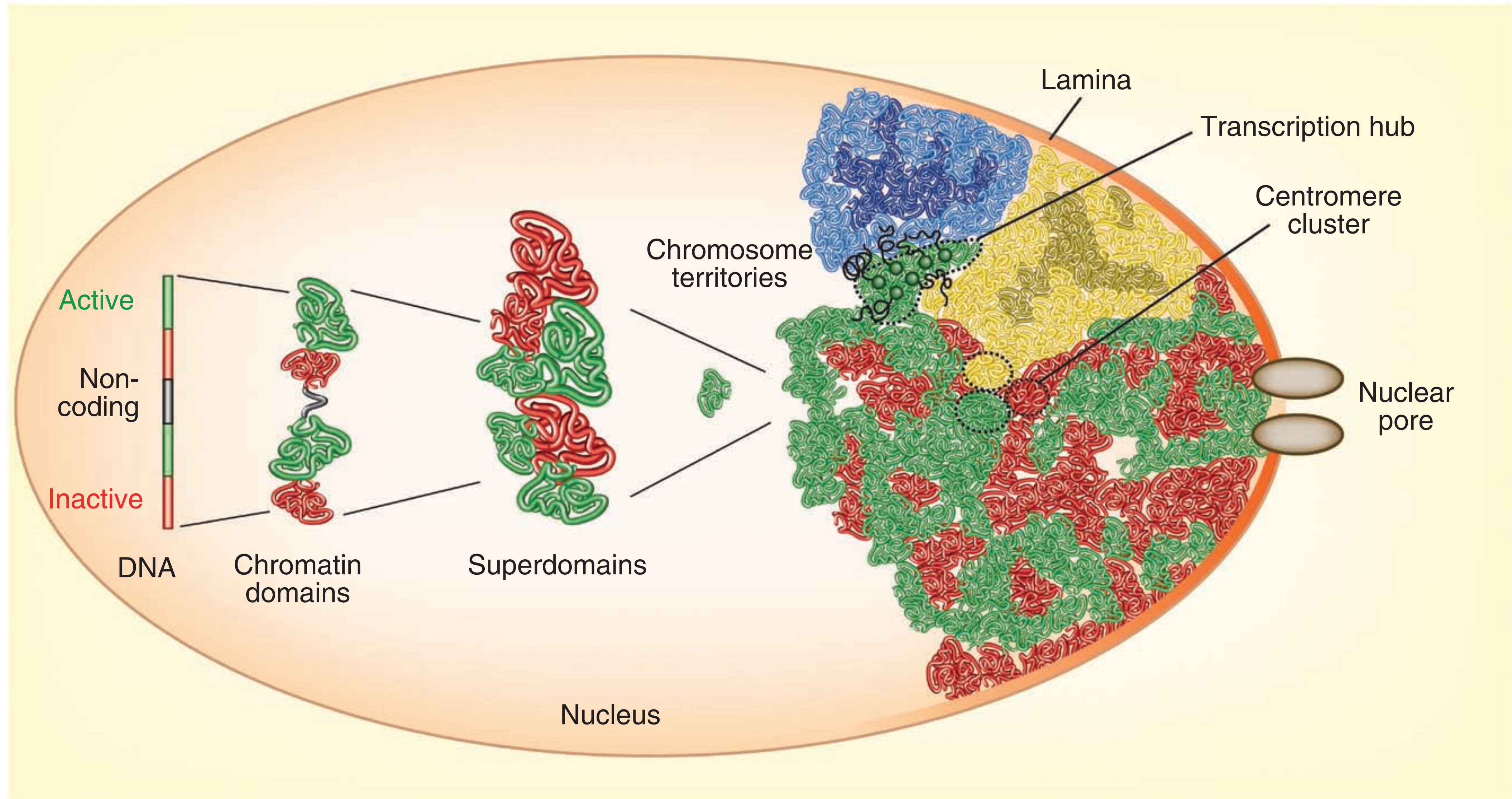
Chromatin fibre

Nucleosome



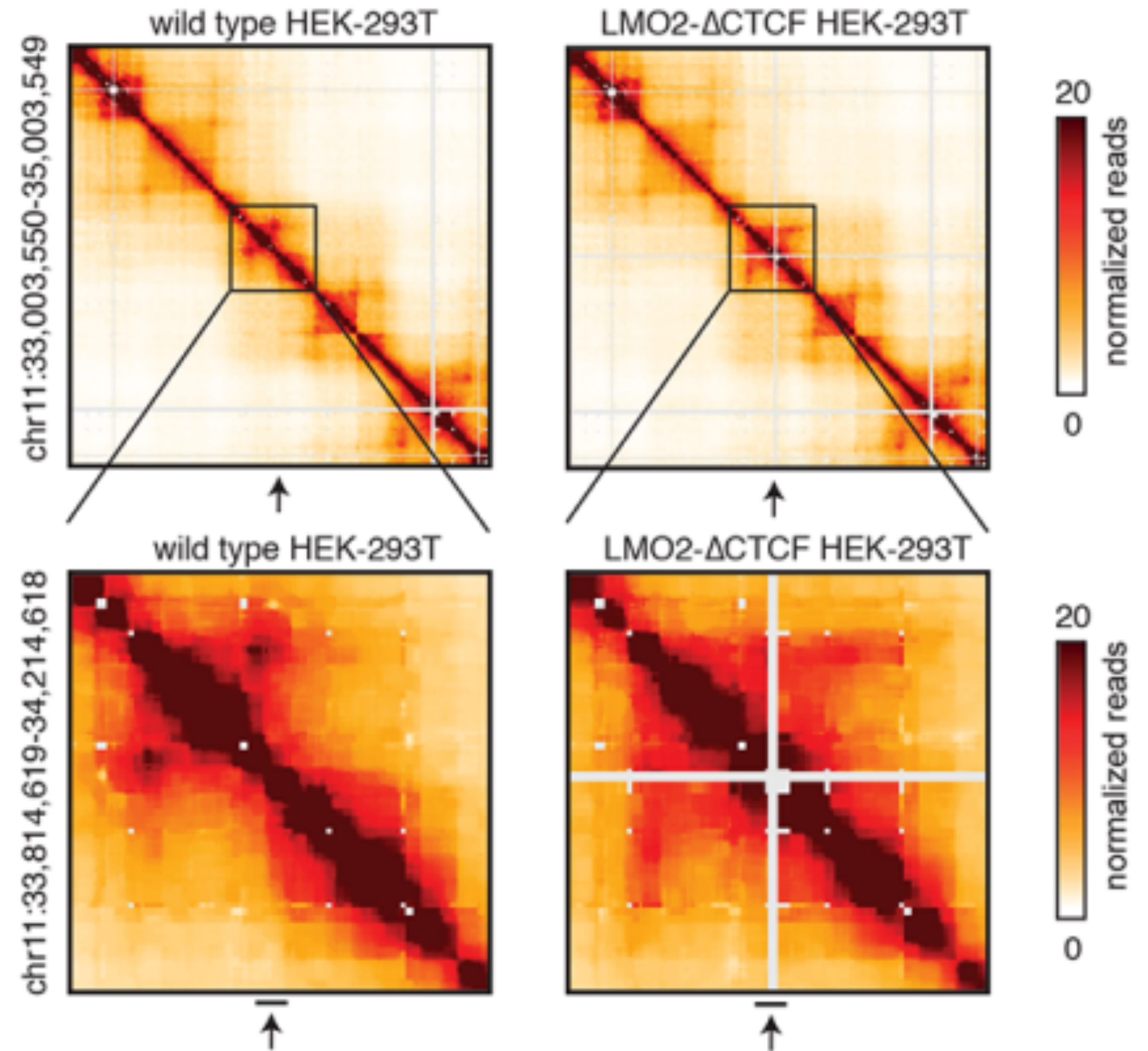
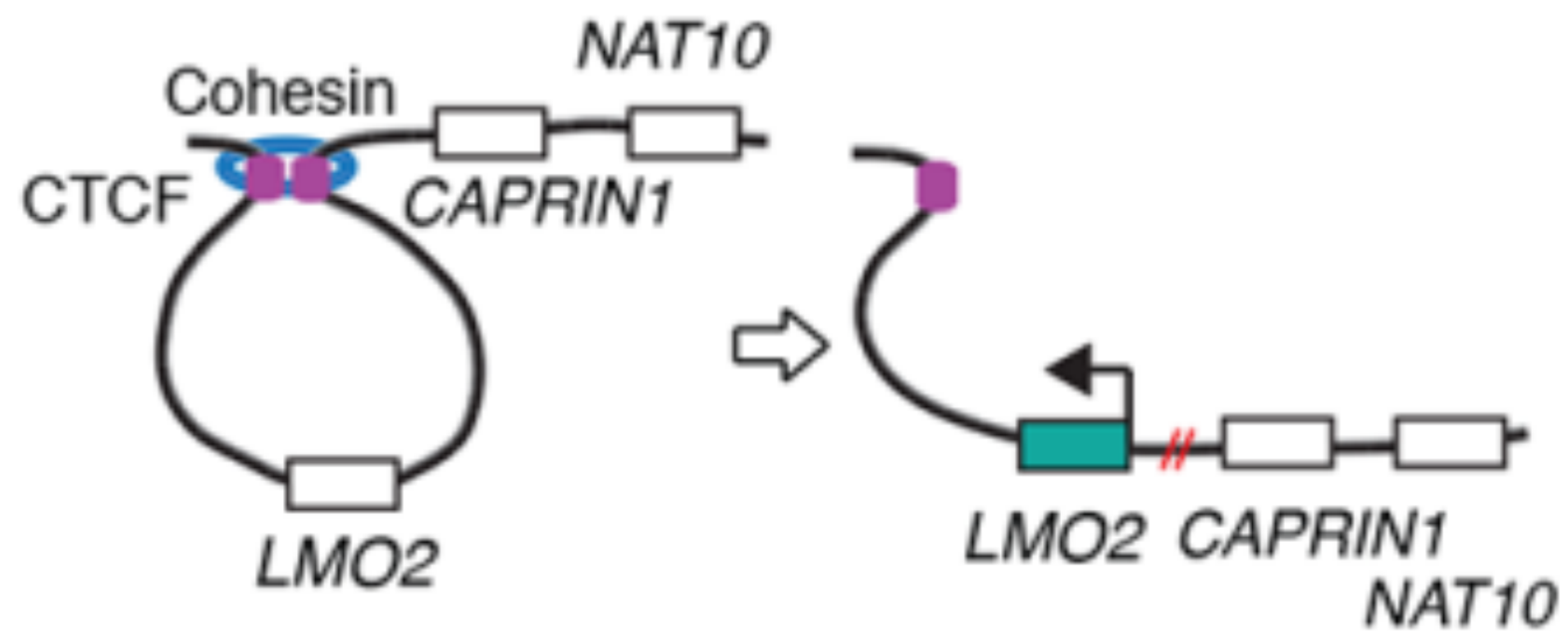
Complex genome organization

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



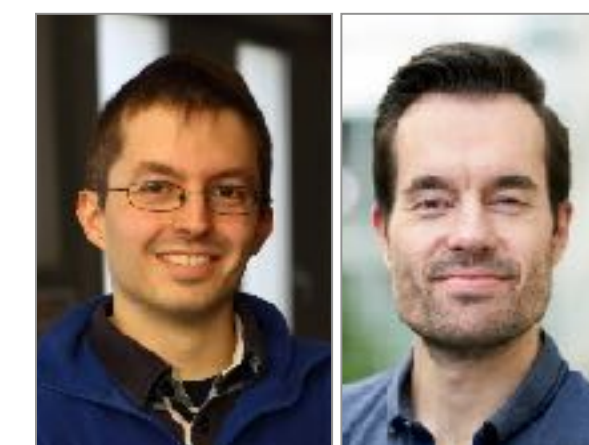
TADs are functional units

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





Dynamics of gene activation

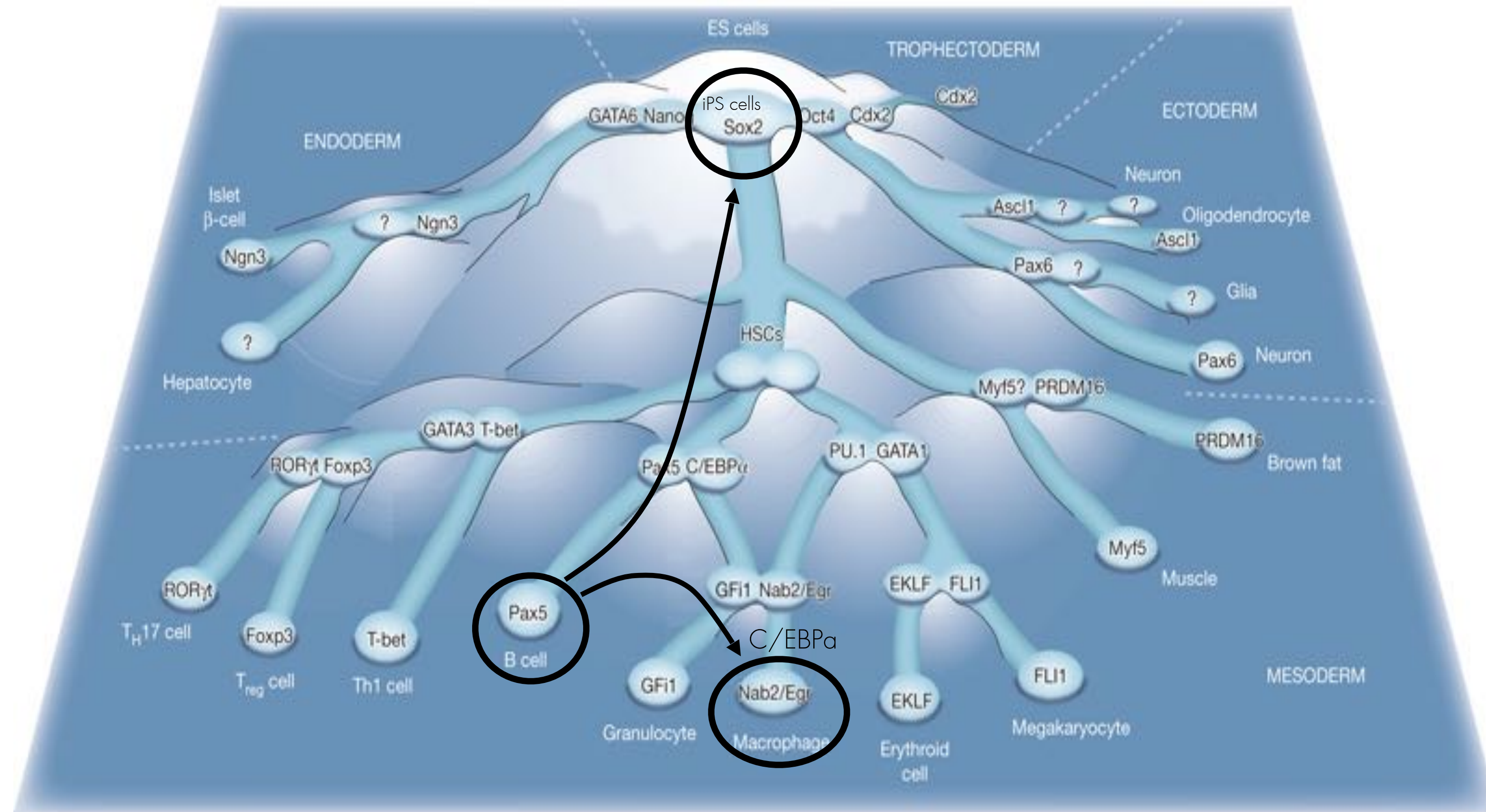


Marco di Stefano
Ralph Stadhouders
with Graf Lab (CRG, Barcelona)

Nature Genetics (2018) 50 238–249 & BioRxived

Transcription factors dictate cell fate

Graf & Enver (2009) Nature



Transcription factors (TFs) determine cell identity through gene regulation

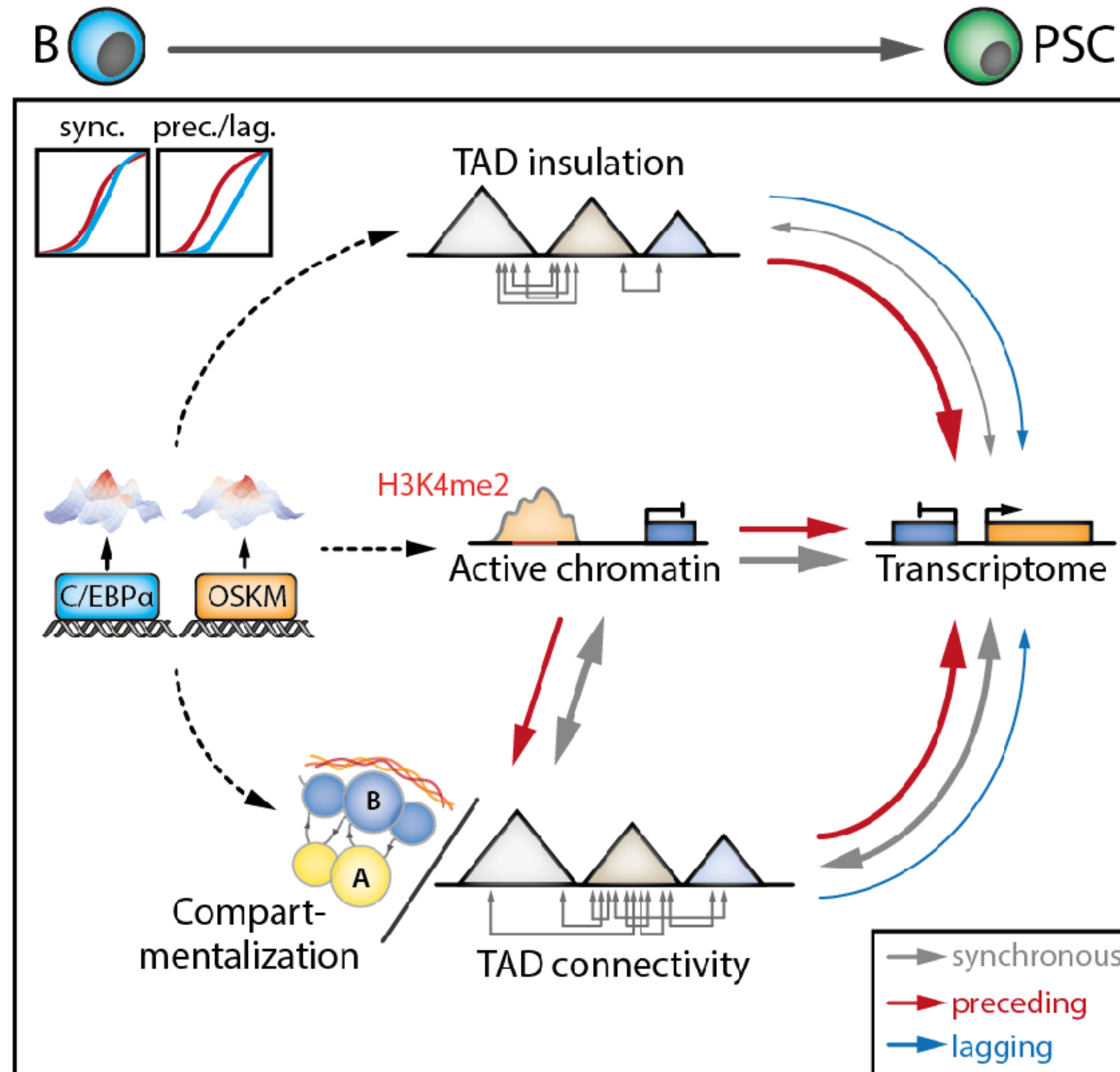
Normal 'forward' differentiation

Cell fates can be converted by enforced TF expression

Transdifferentiation or reprogramming

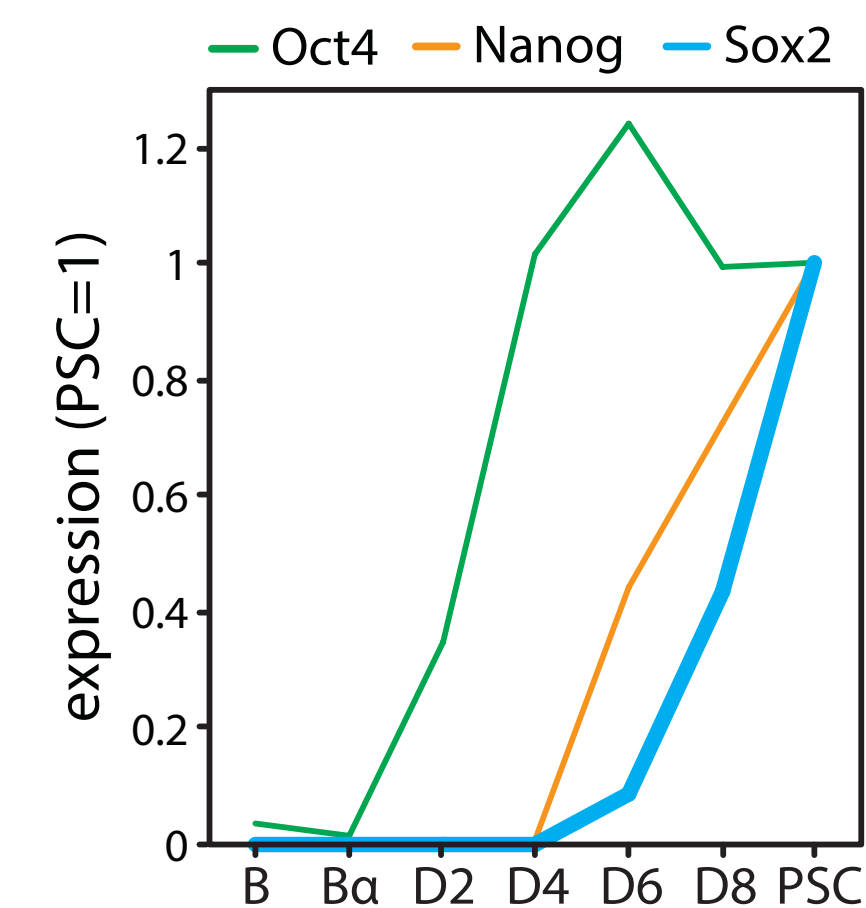
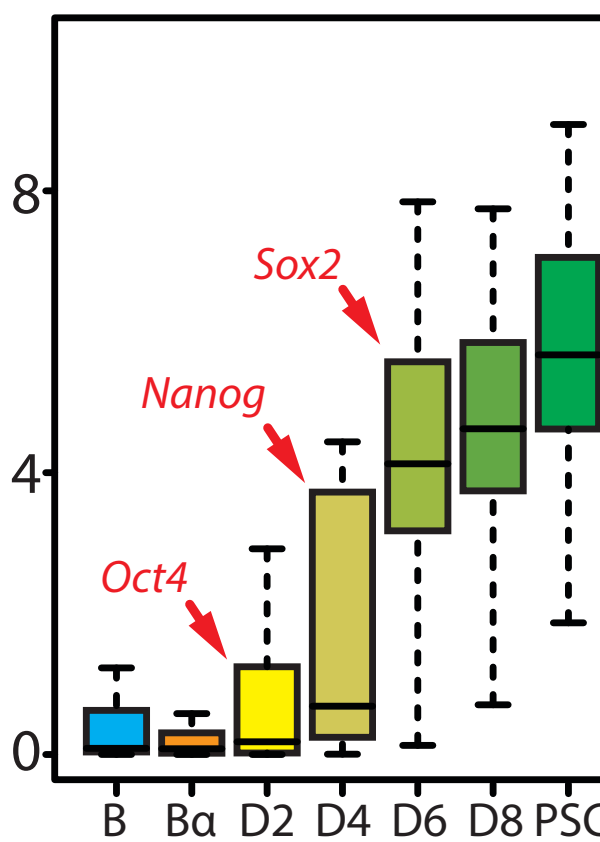
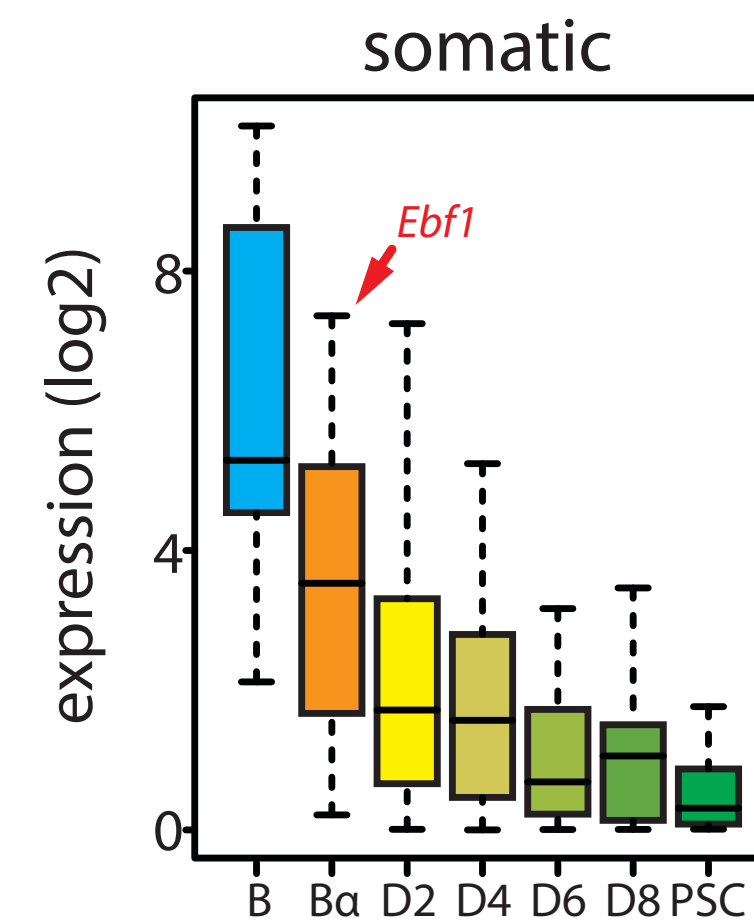
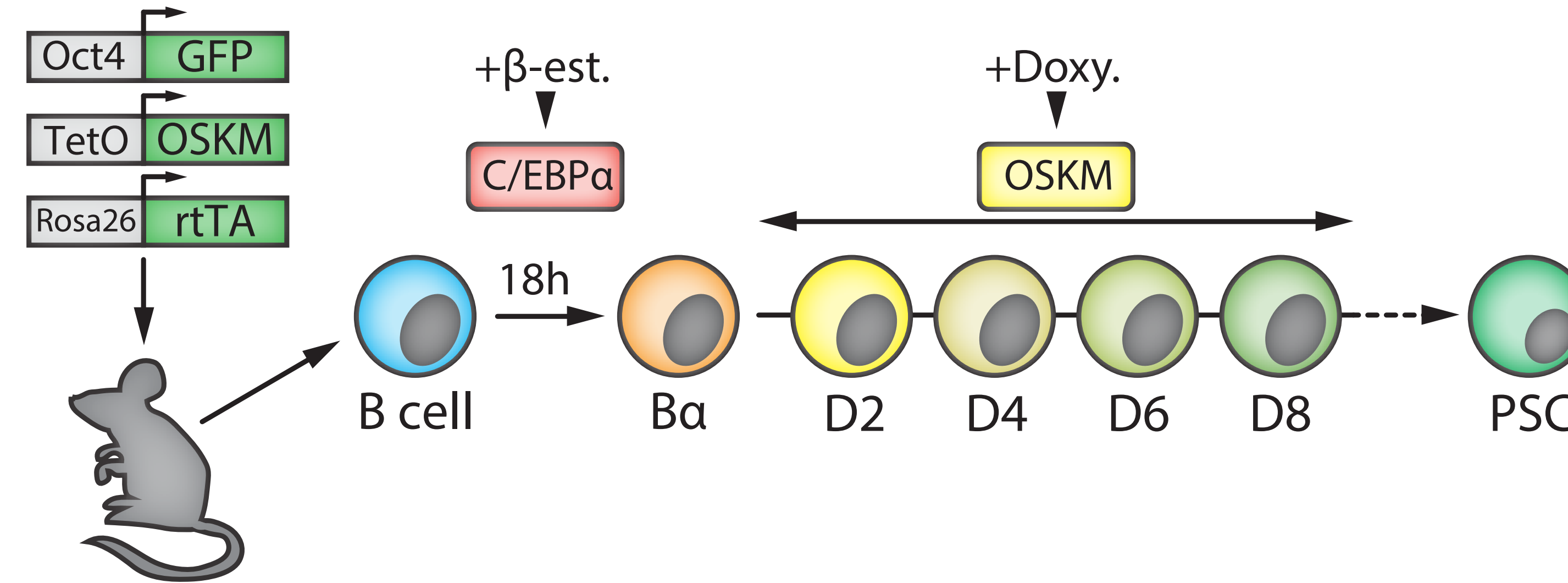
Interplay: topology, gene expression & chromatin

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



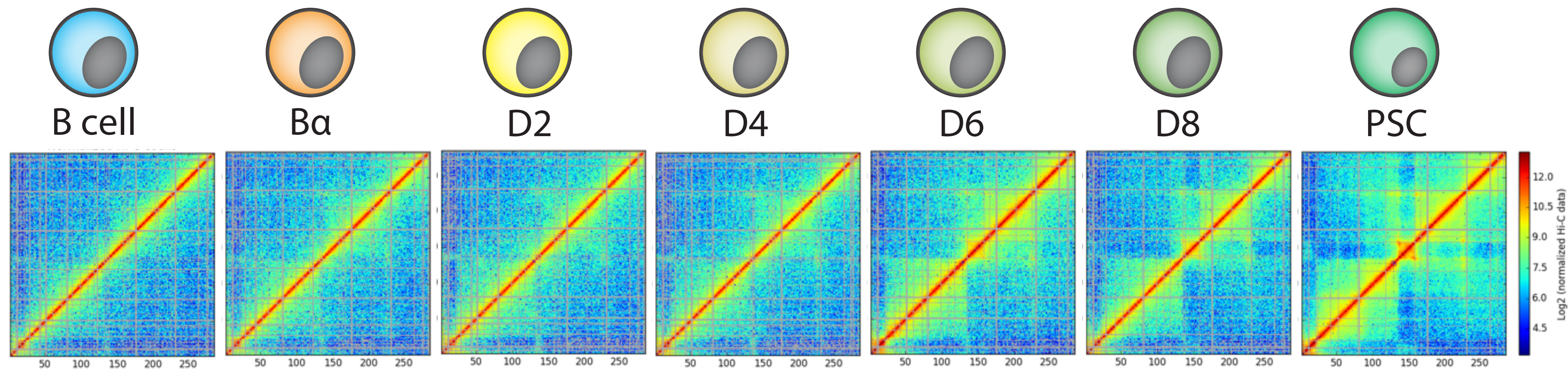
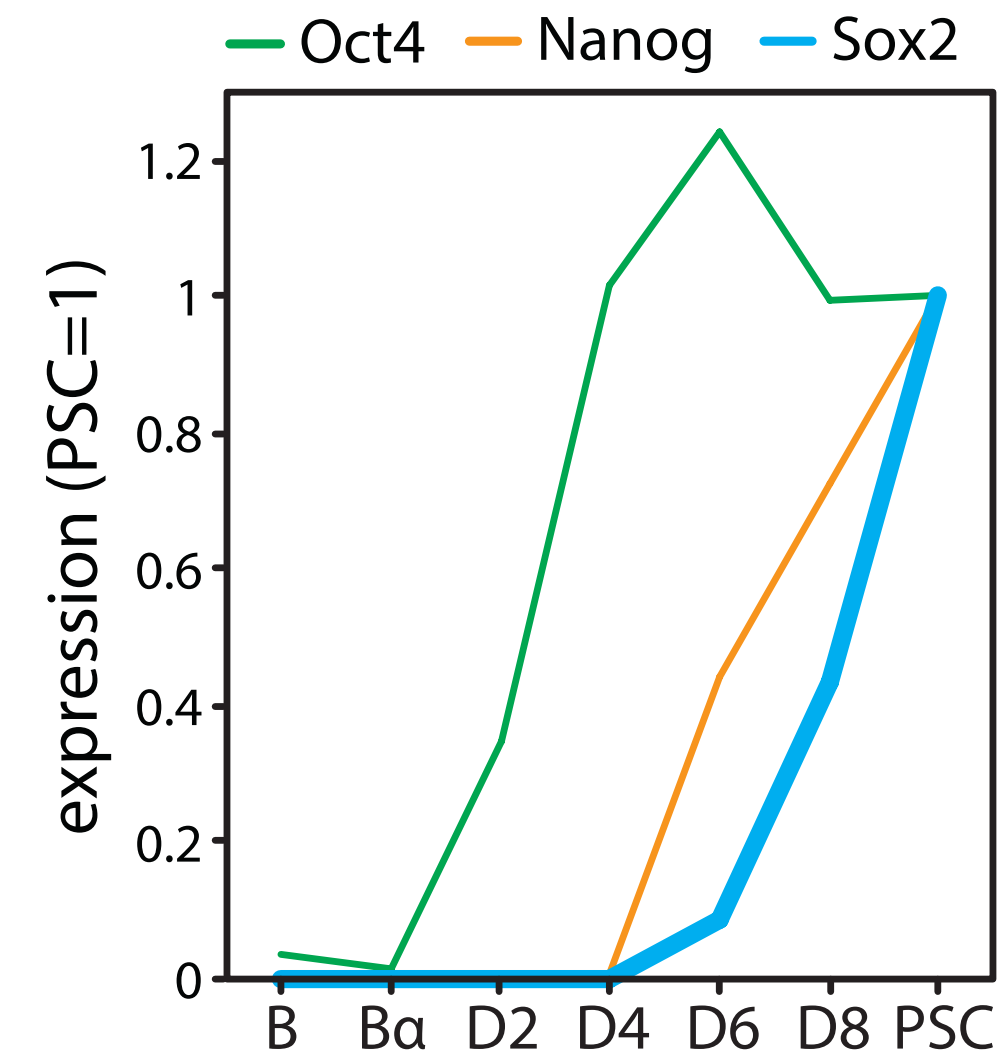
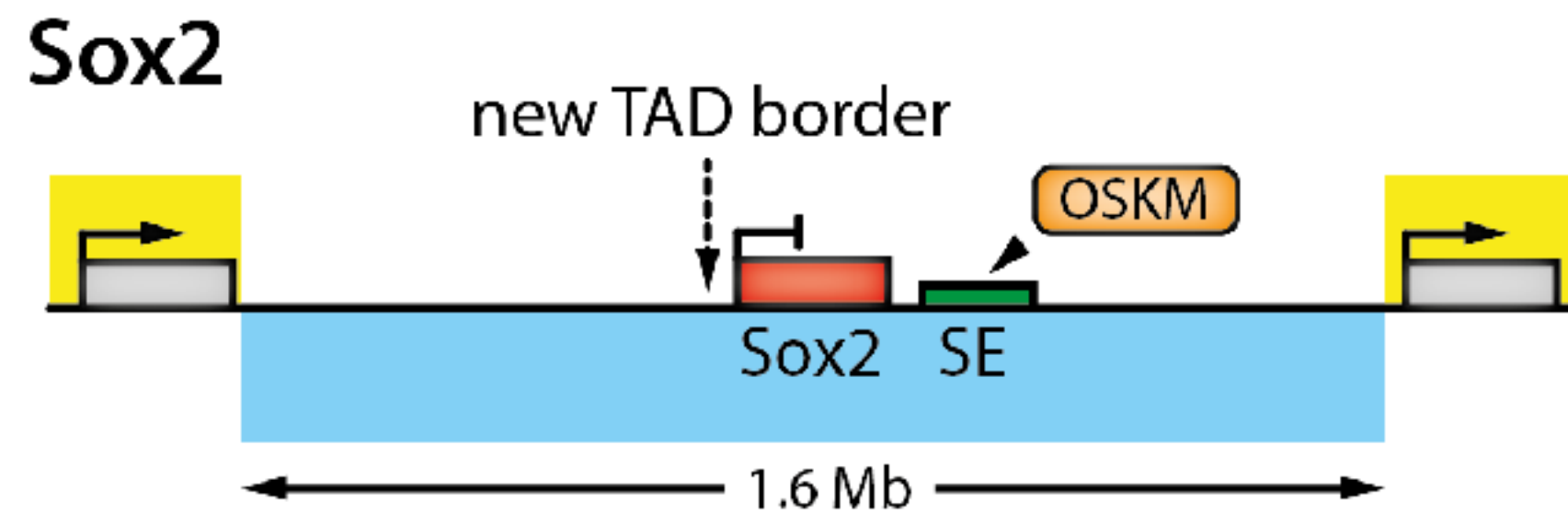
Reprogramming from B to PSC

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



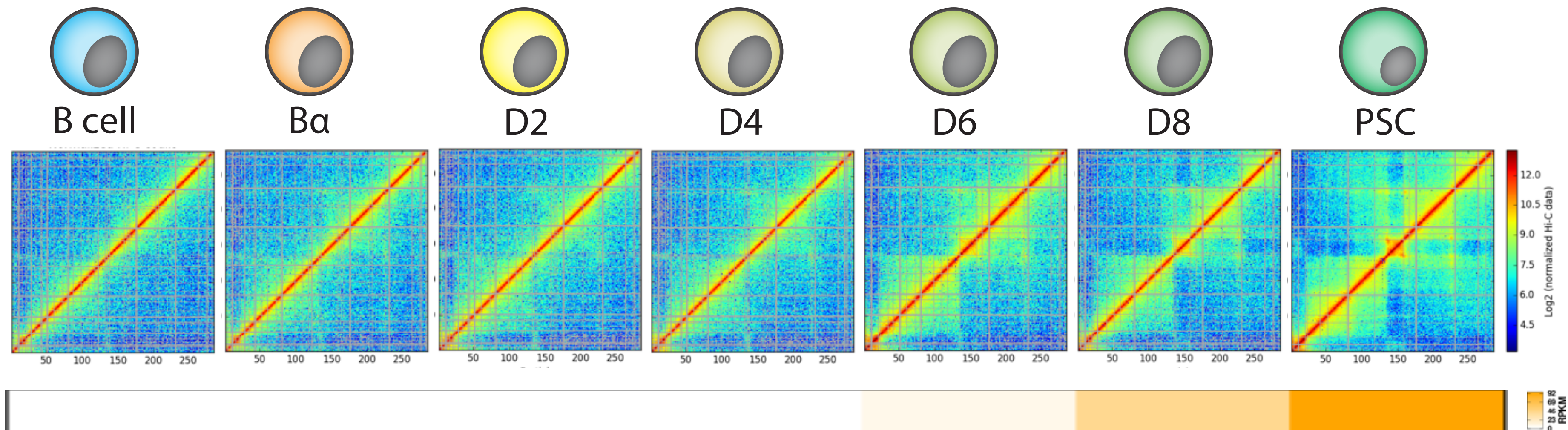
Hi-C maps of reprogramming from B to PSC

The SOX2 locus



Hi-C maps of reprogramming from B to PSC

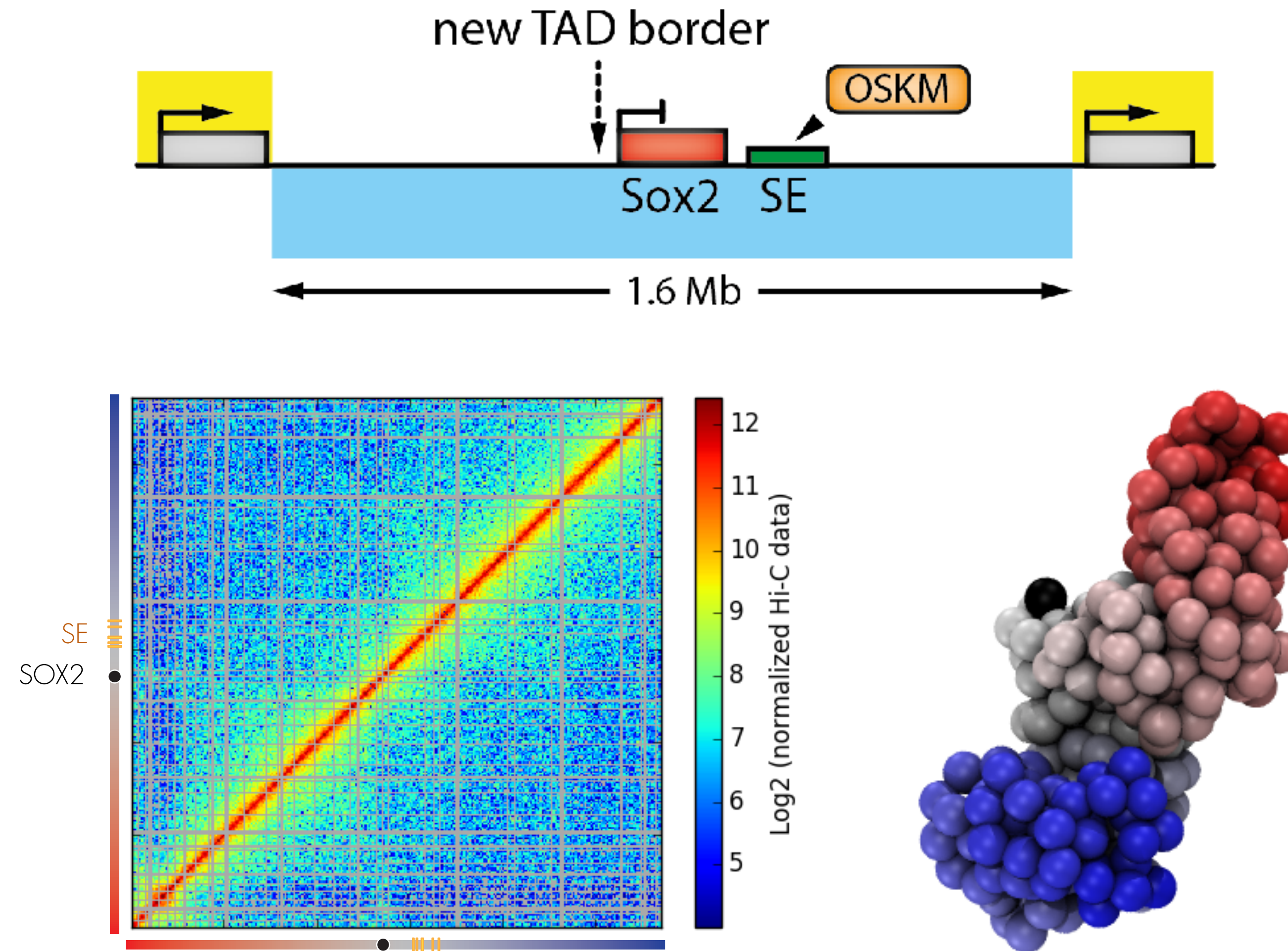
The SOX2 locus



How do these structural rearrangements interplay with the transcription activity?

What are the main drivers of structural transitions?

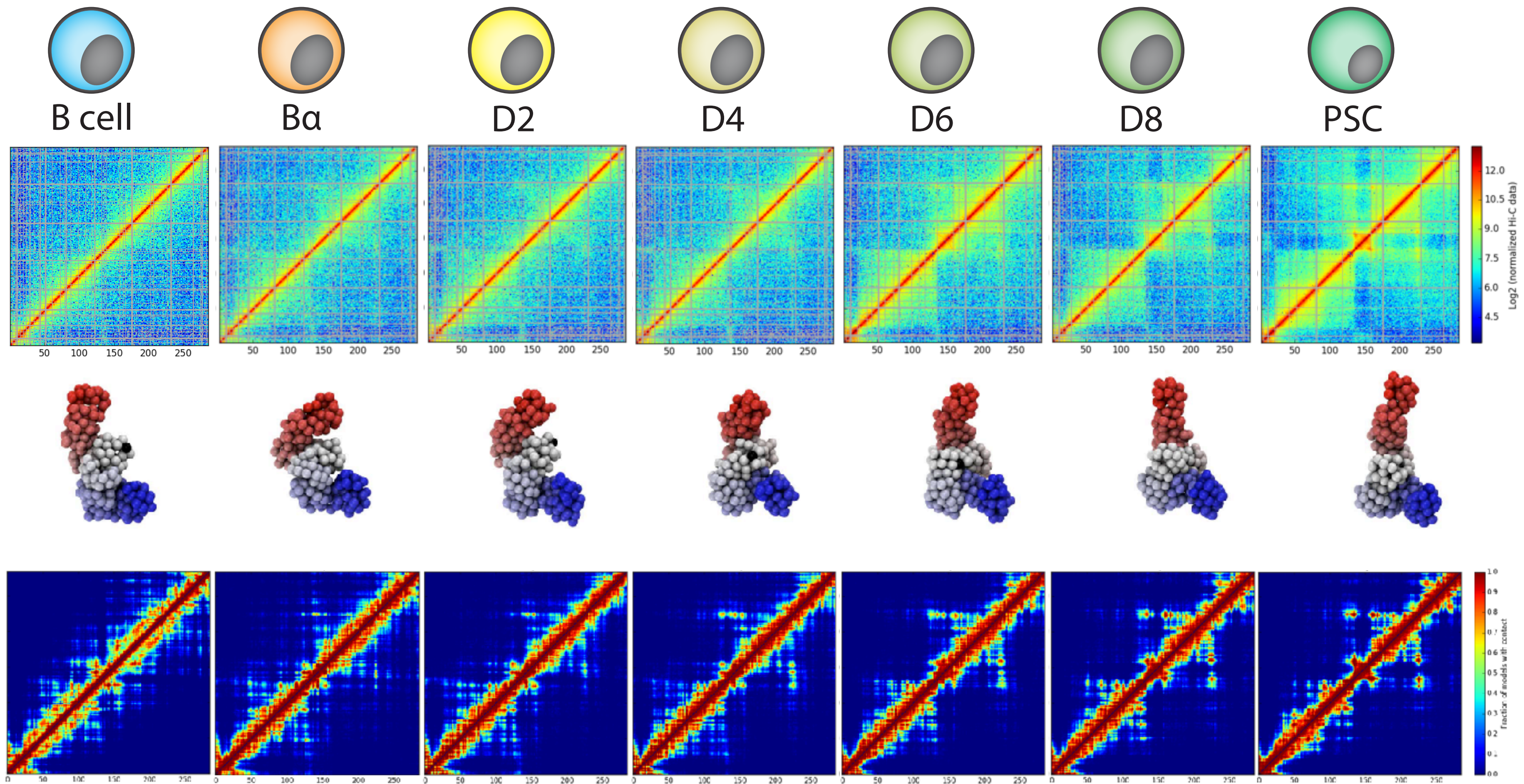
TADbit modeling of SOX2 from B cells Hi-C



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

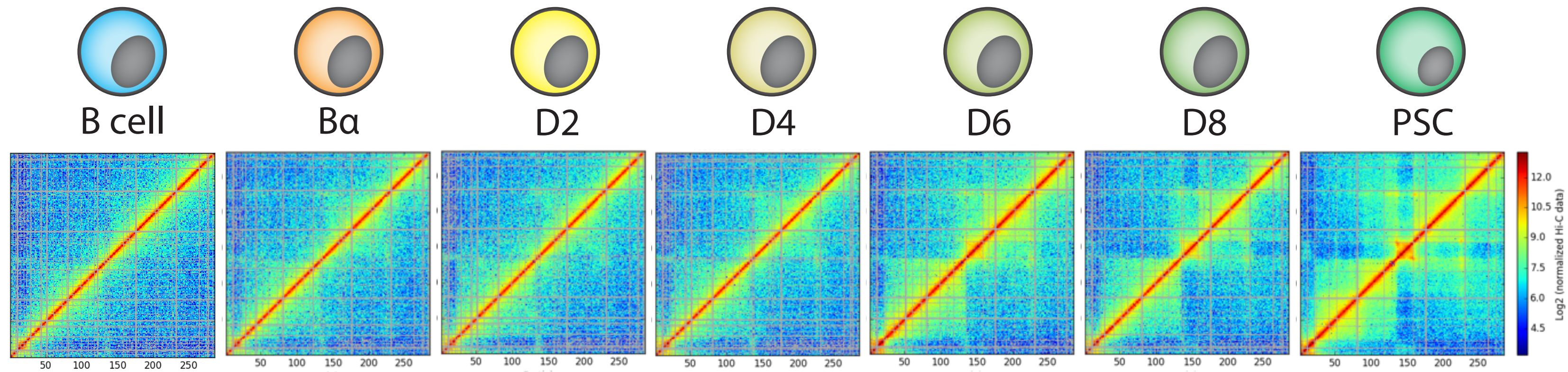
Models of reprogramming from B to PSC

The SOX2 locus



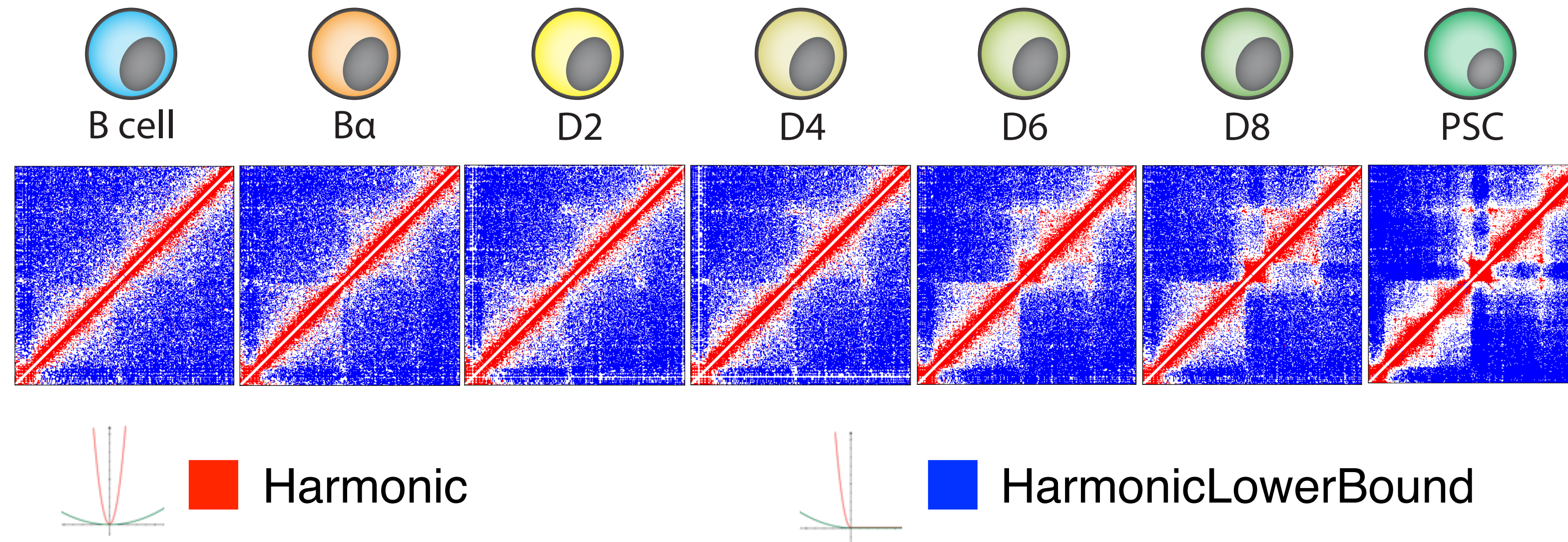
TADdyn: from time-series Hi-C maps to dynamic restraints

The SOX2 locus



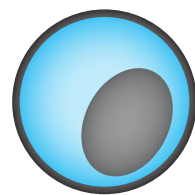
TADdyn: from time-series Hi-C maps to dynamic restraints

The SOX2 locus

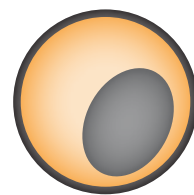


TADdyn: from time-series Hi-C maps to dynamic restraints

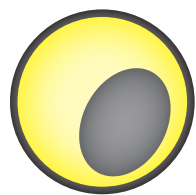
The SOX2 locus



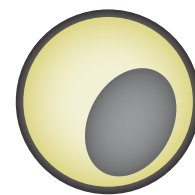
B cell



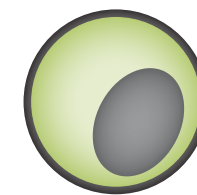
B α



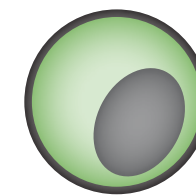
D2



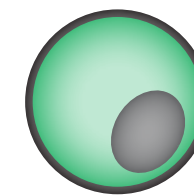
D4



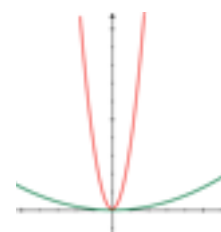
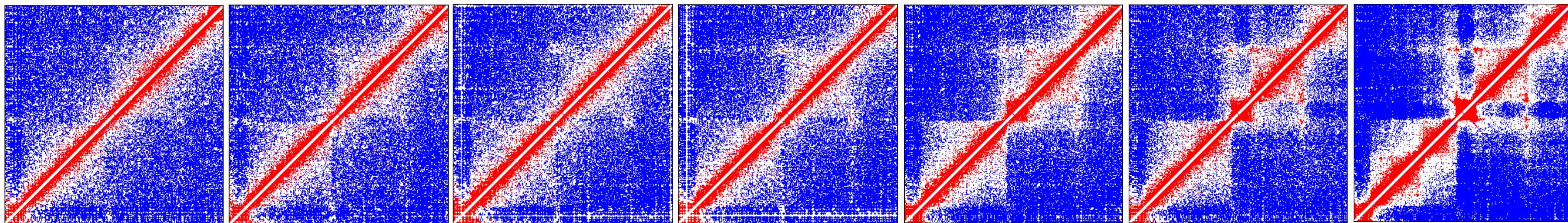
D6



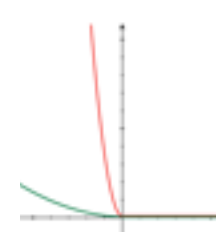
D8



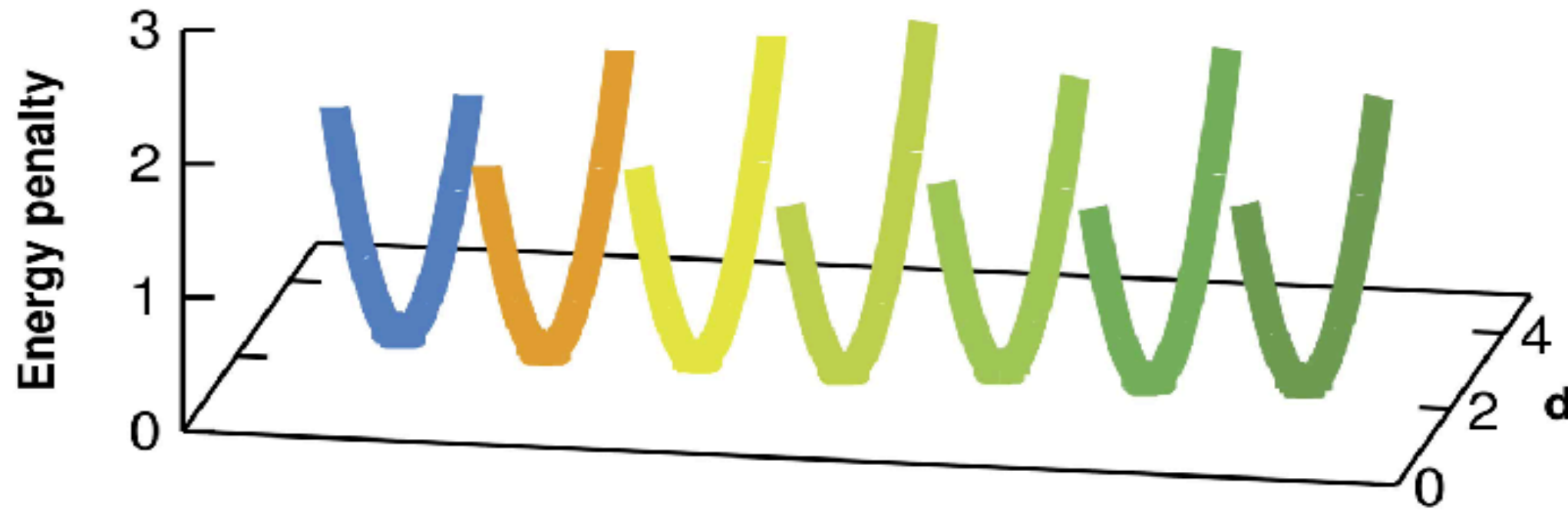
PSC



Harmonic



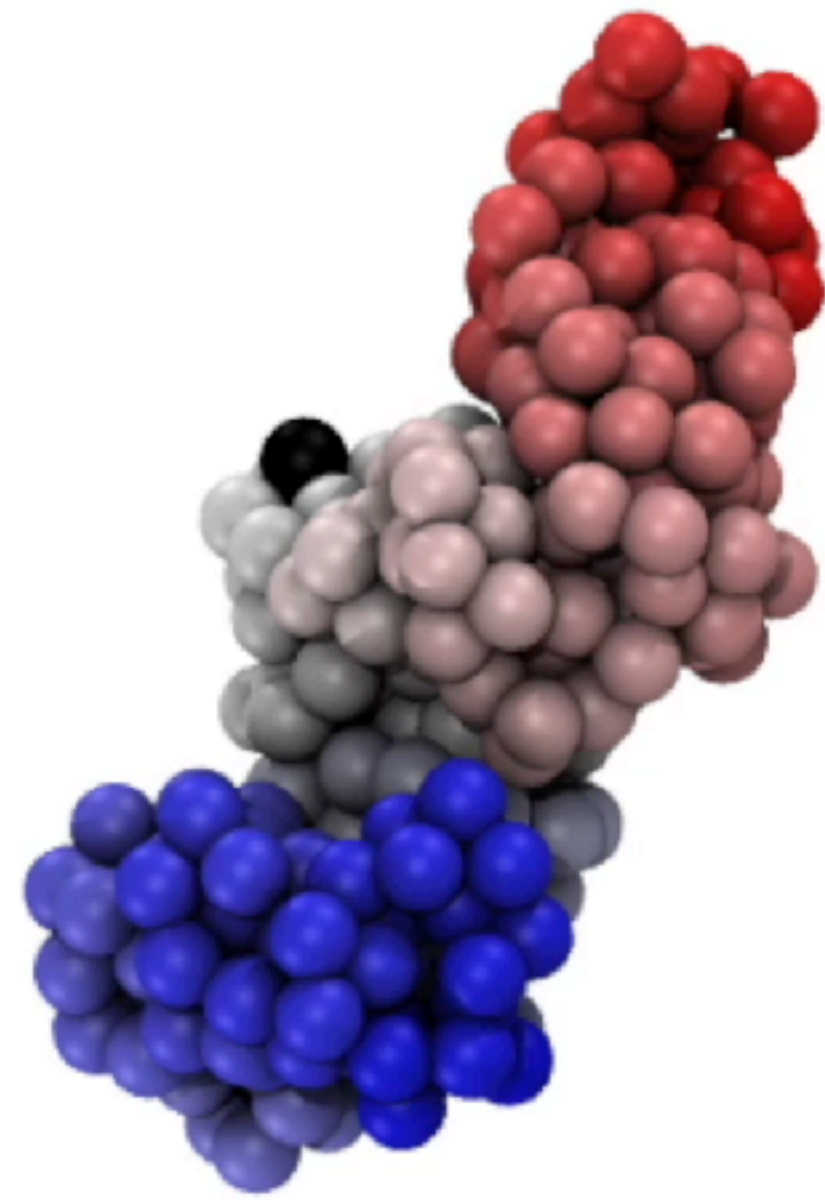
HarmonicLowerBound



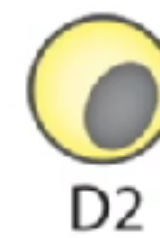
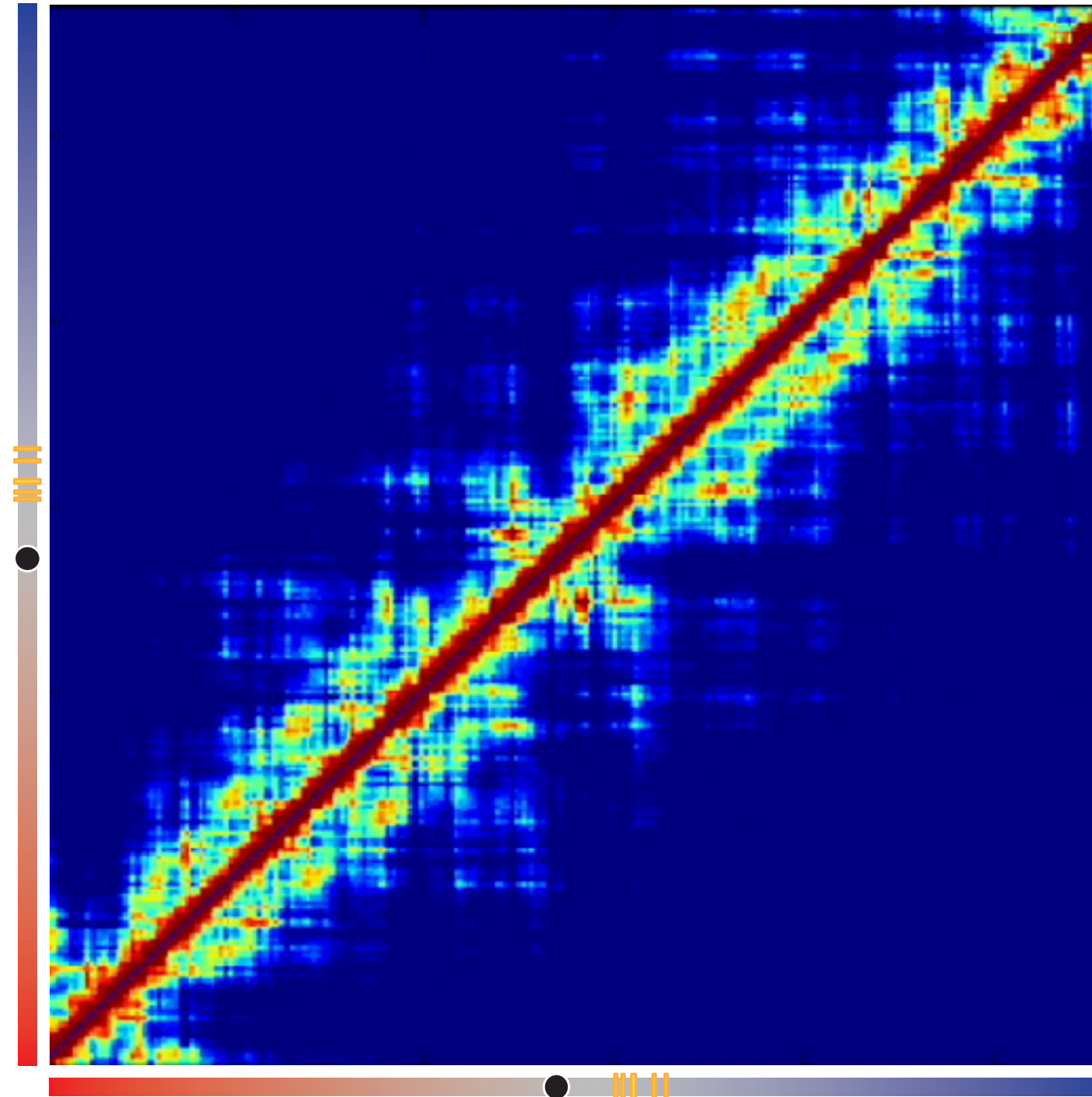
Transition	Stable	Vanishing	Raising
B -> B α	18,612	6,984	7,290
B α -> D2	18,512	7,390	6,687
D2 -> D4	18,369	6,830	6,893
D4 -> D6	18,971	6,291	7,289
D6 -> D8	20,167	6,093	6,250
D8 -> ES	20,679	5,738	6,173

SOX2 locus structural changes from B to PSC

Contacts

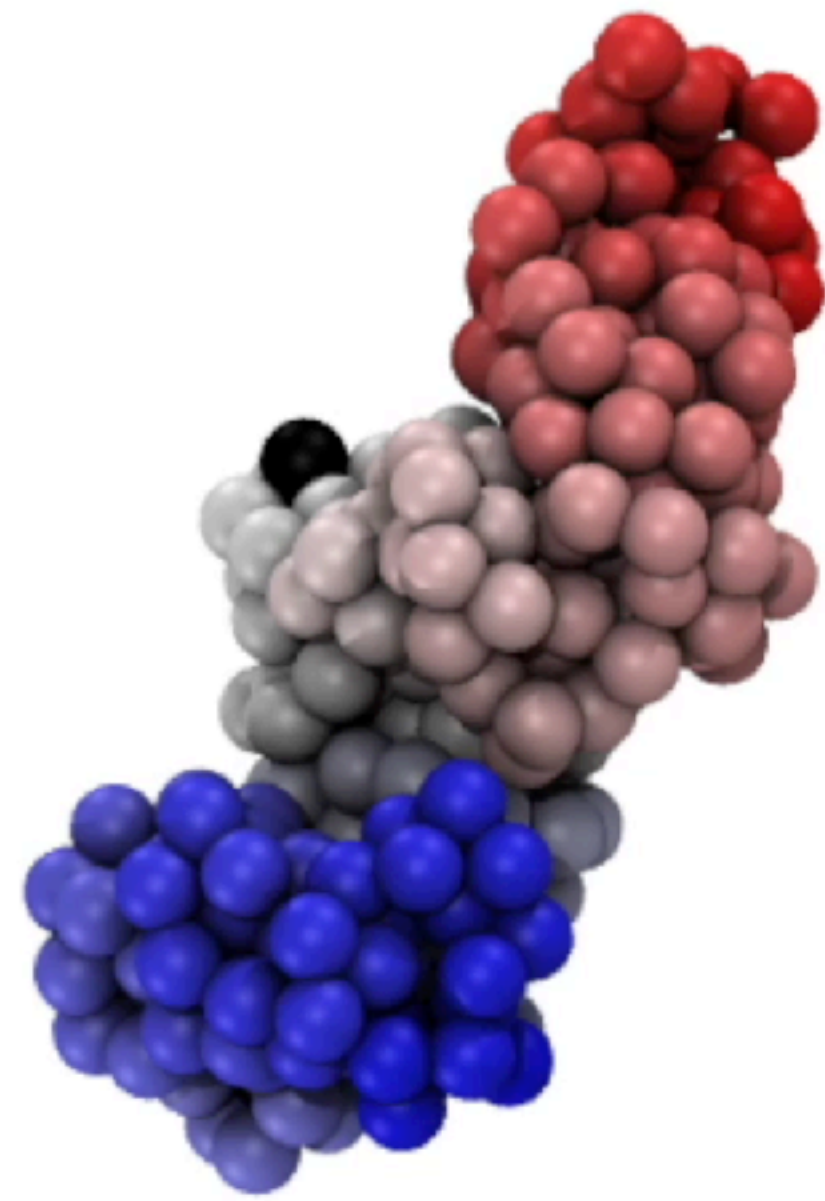


SE
SOX2

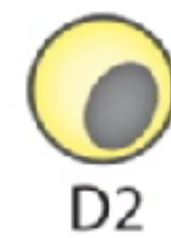
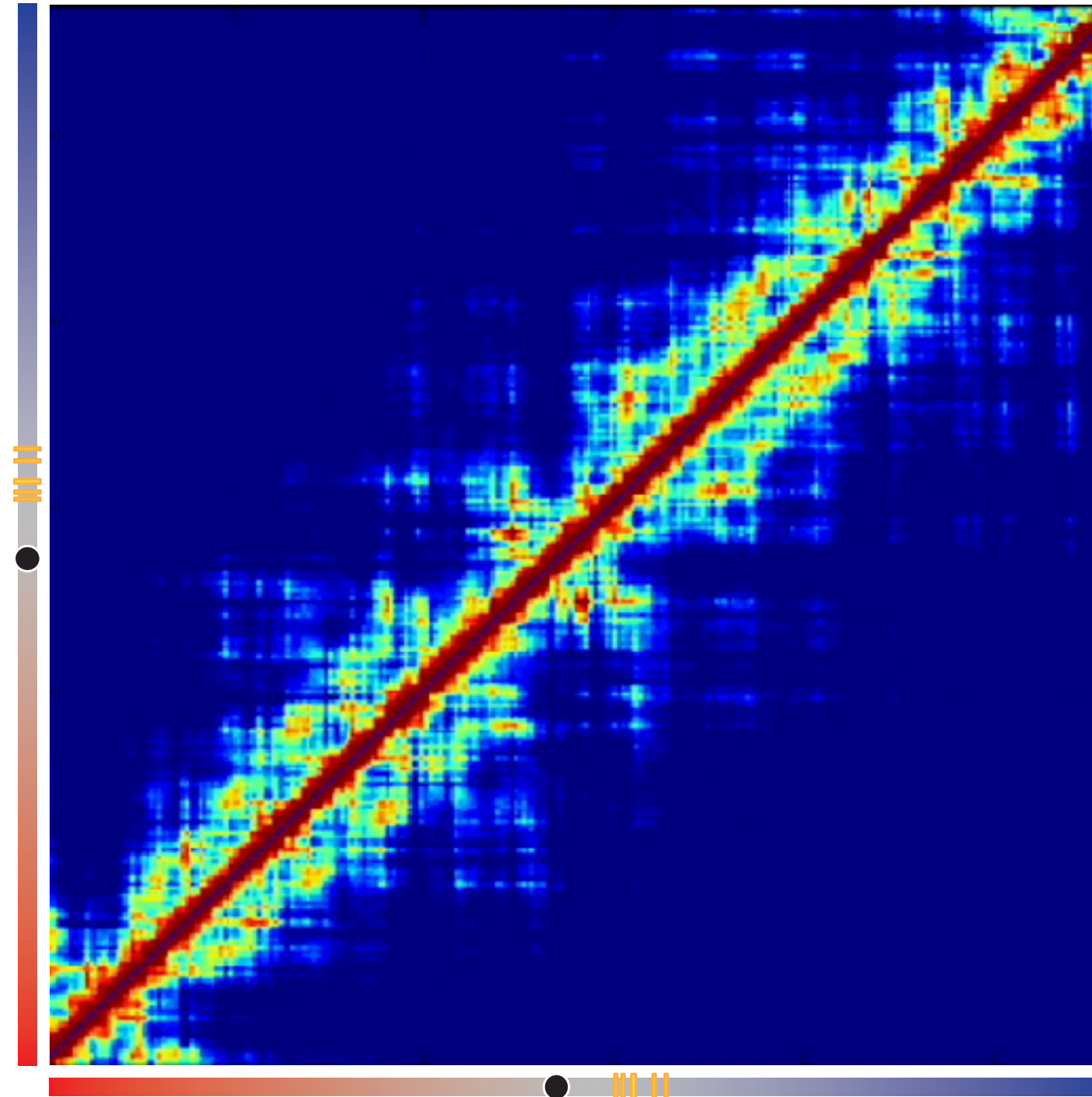


SOX2 locus structural changes from B to PSC

Contacts

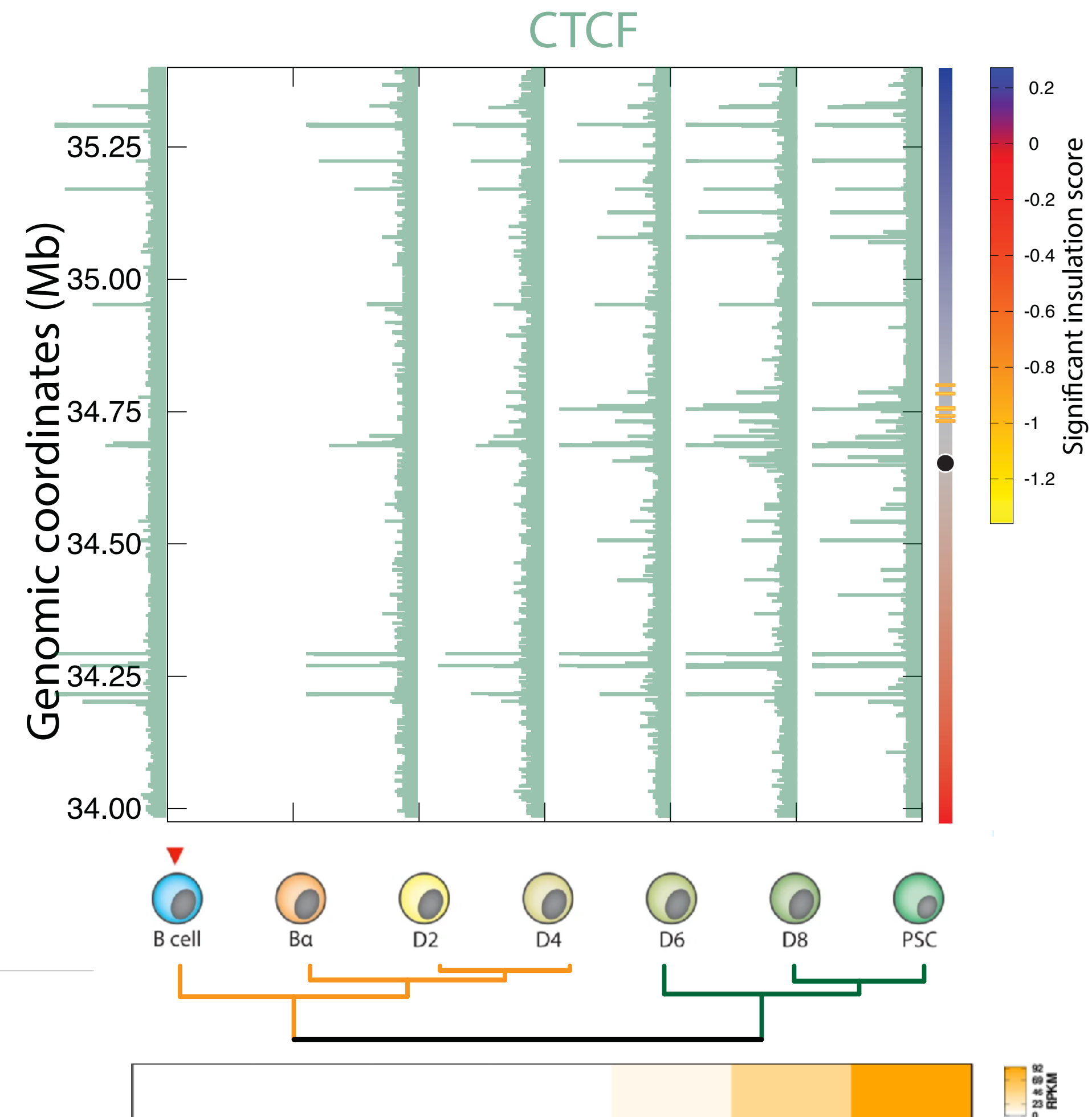
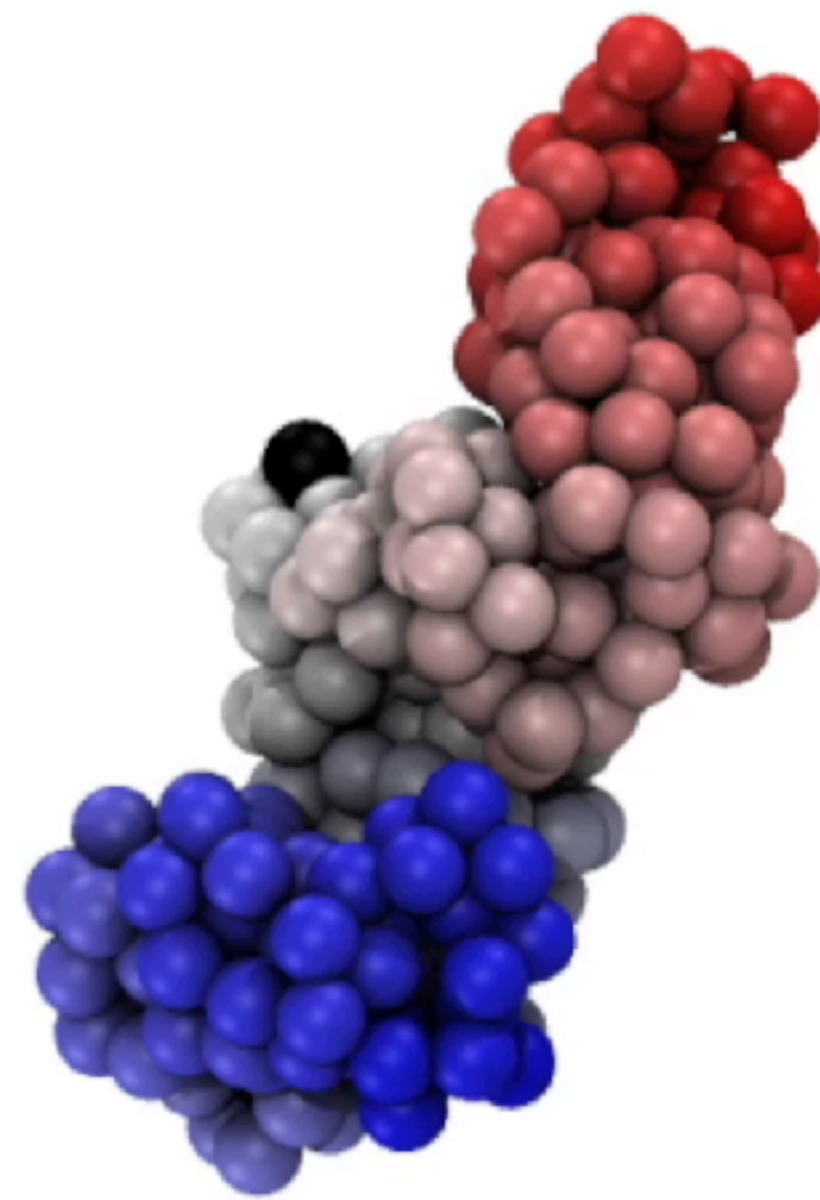


SE
SOX2



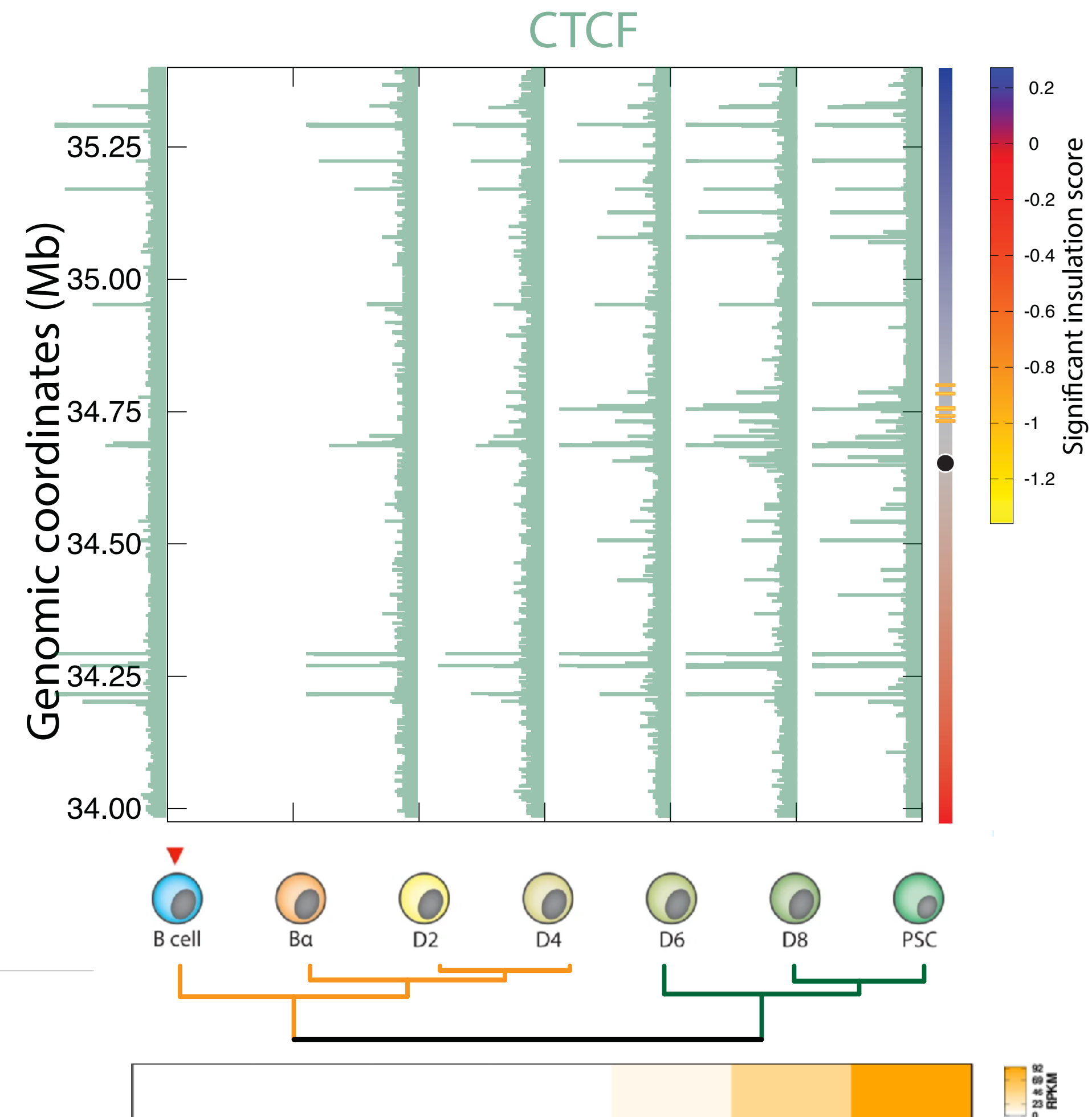
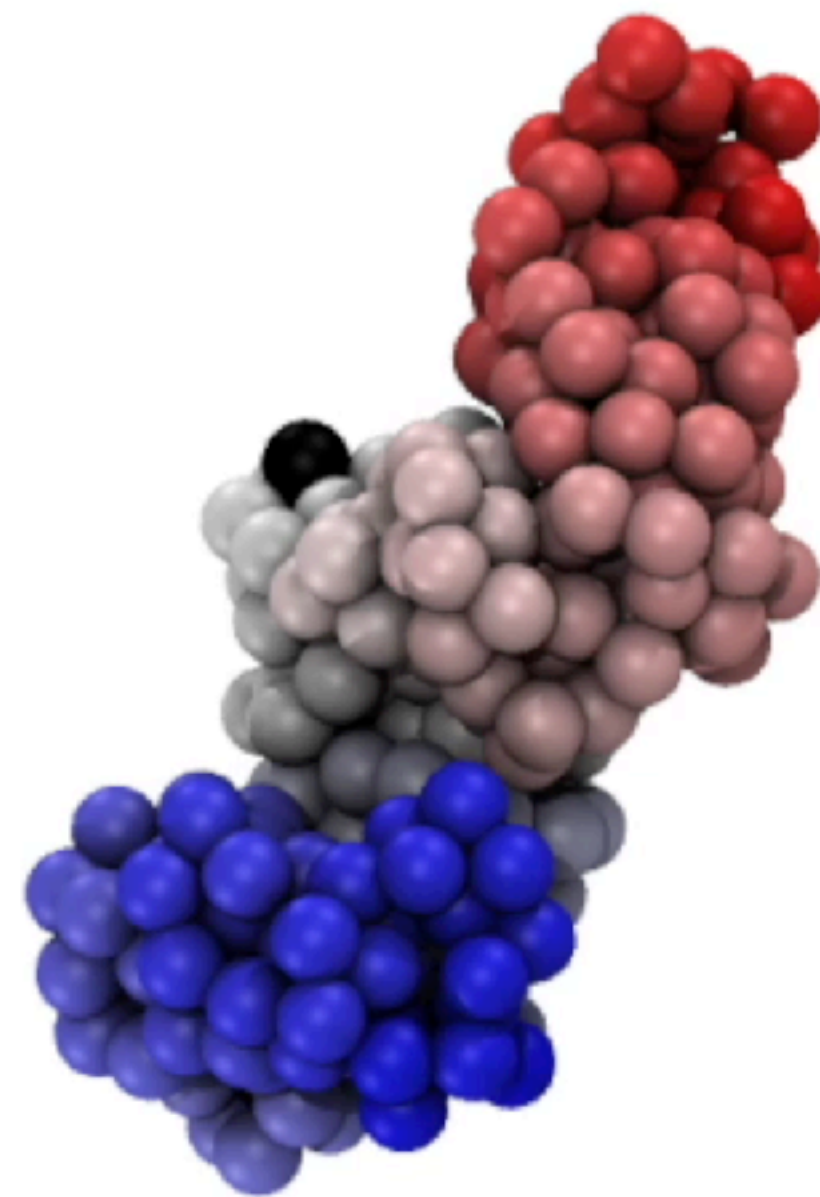
SOX2 locus structural changes from B to PSC

TAD borders



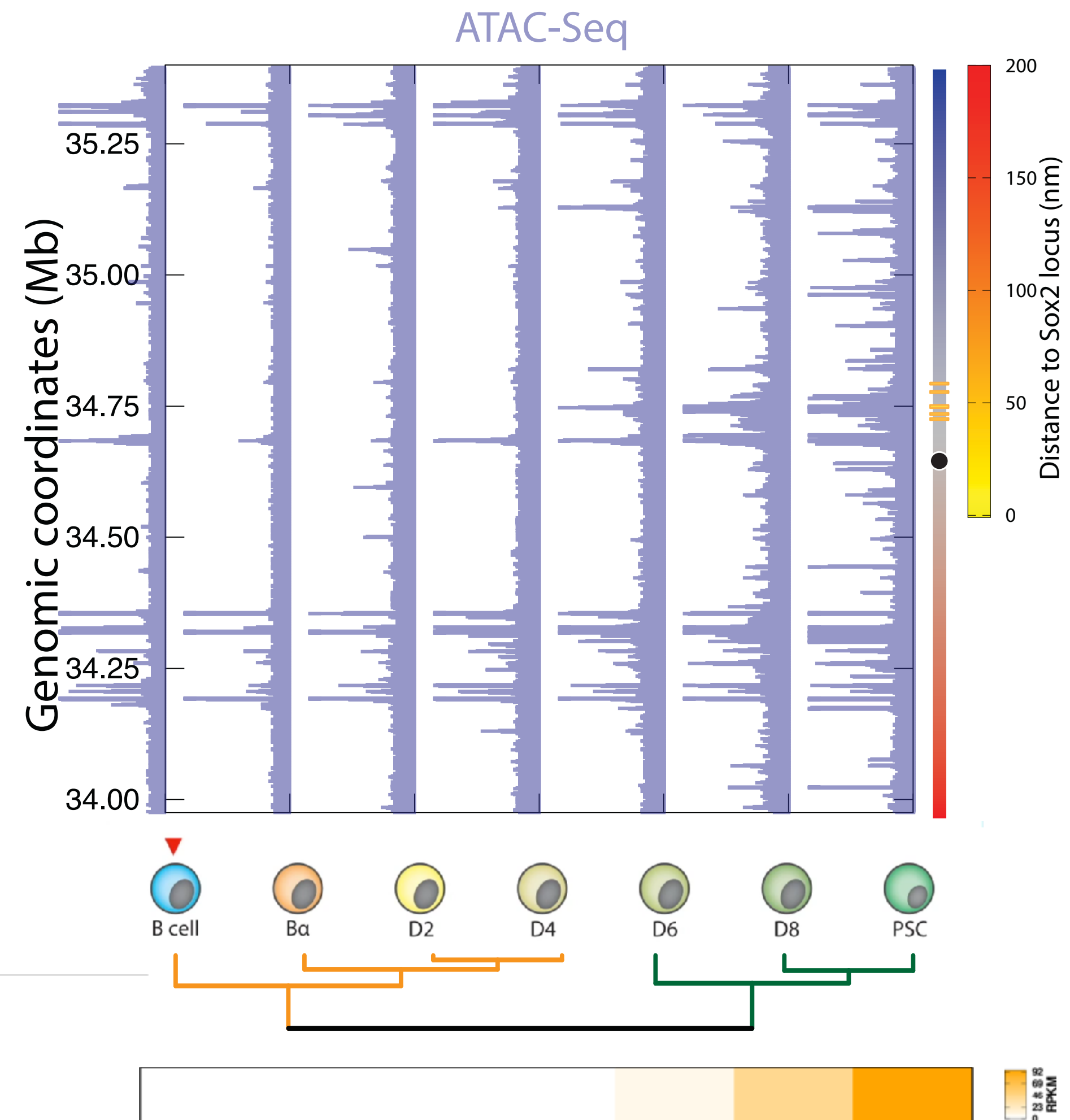
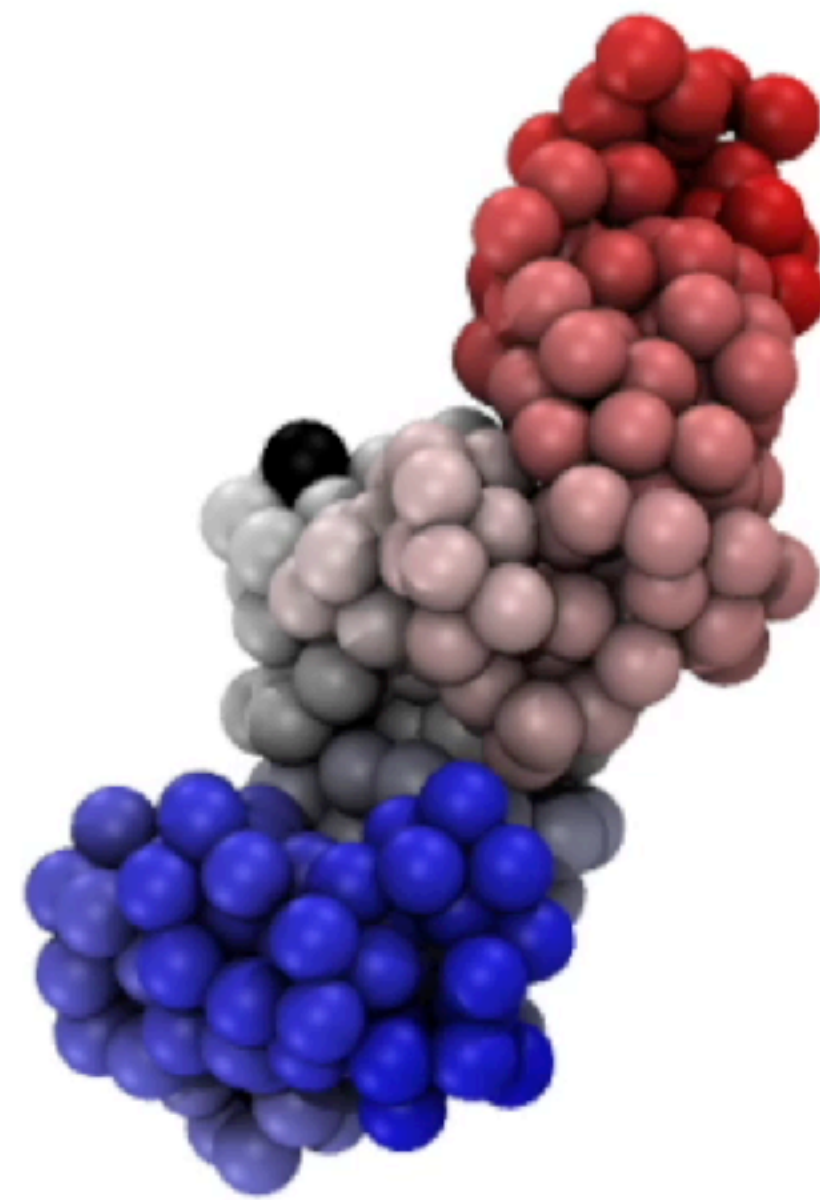
SOX2 locus structural changes from B to PSC

TAD borders



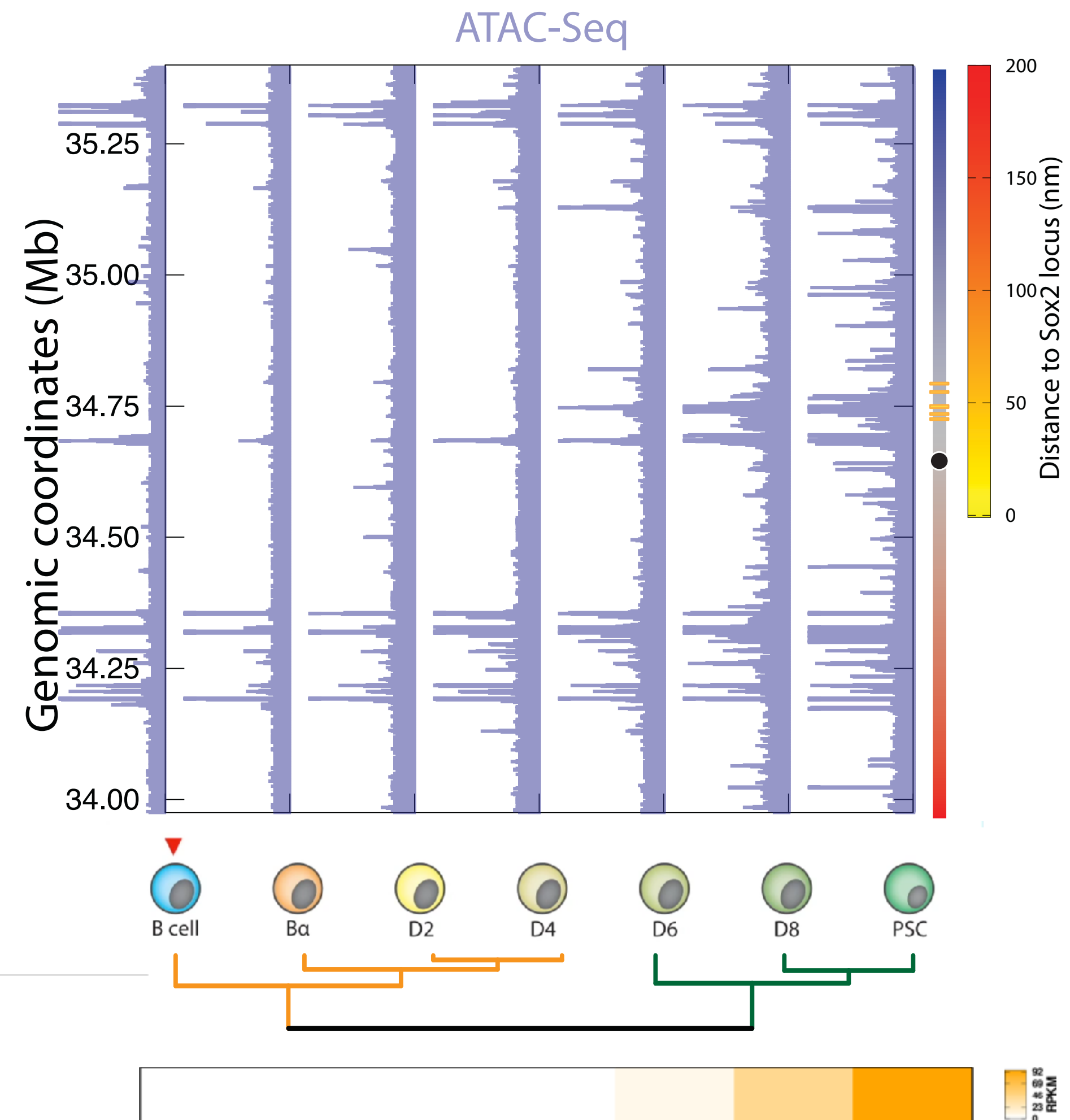
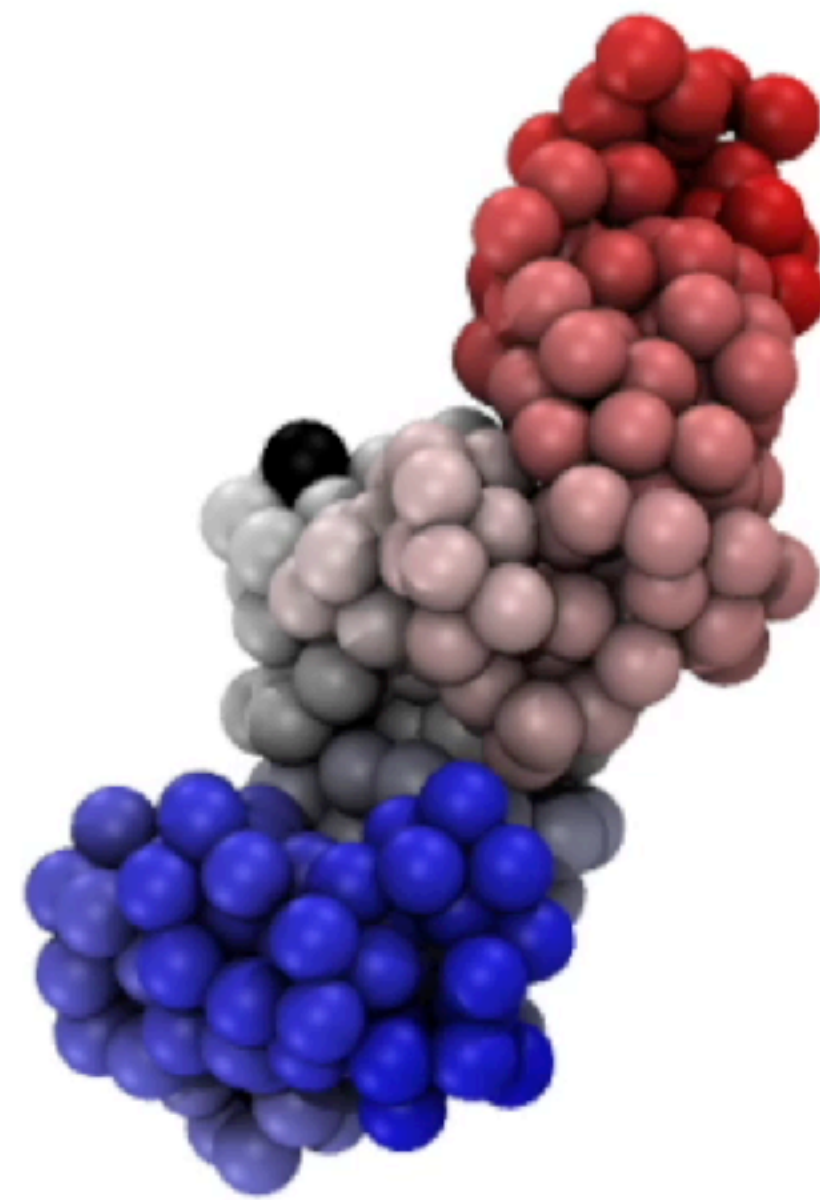
SOX2 locus structural changes from B to PSC

Distance to regulatory elements



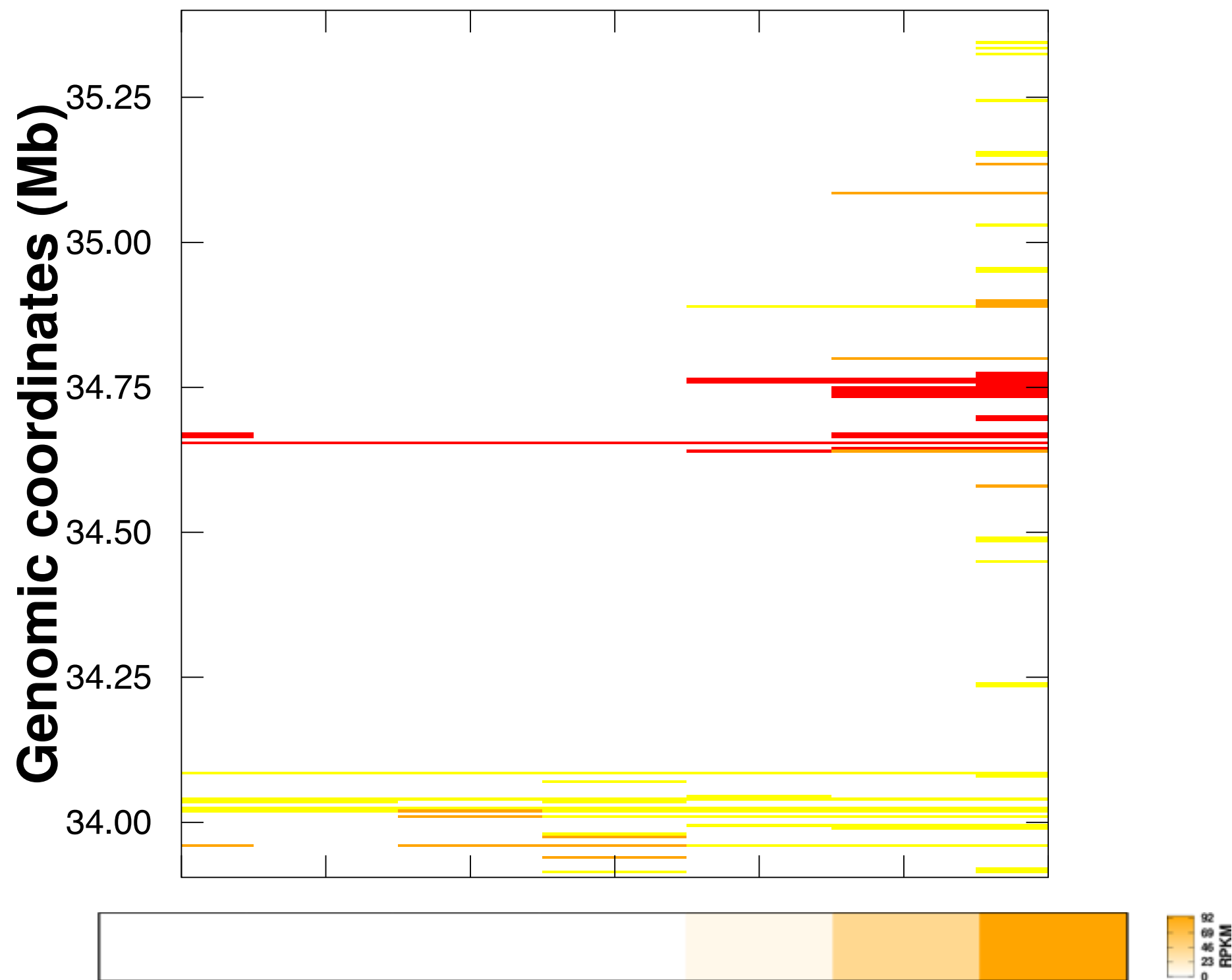
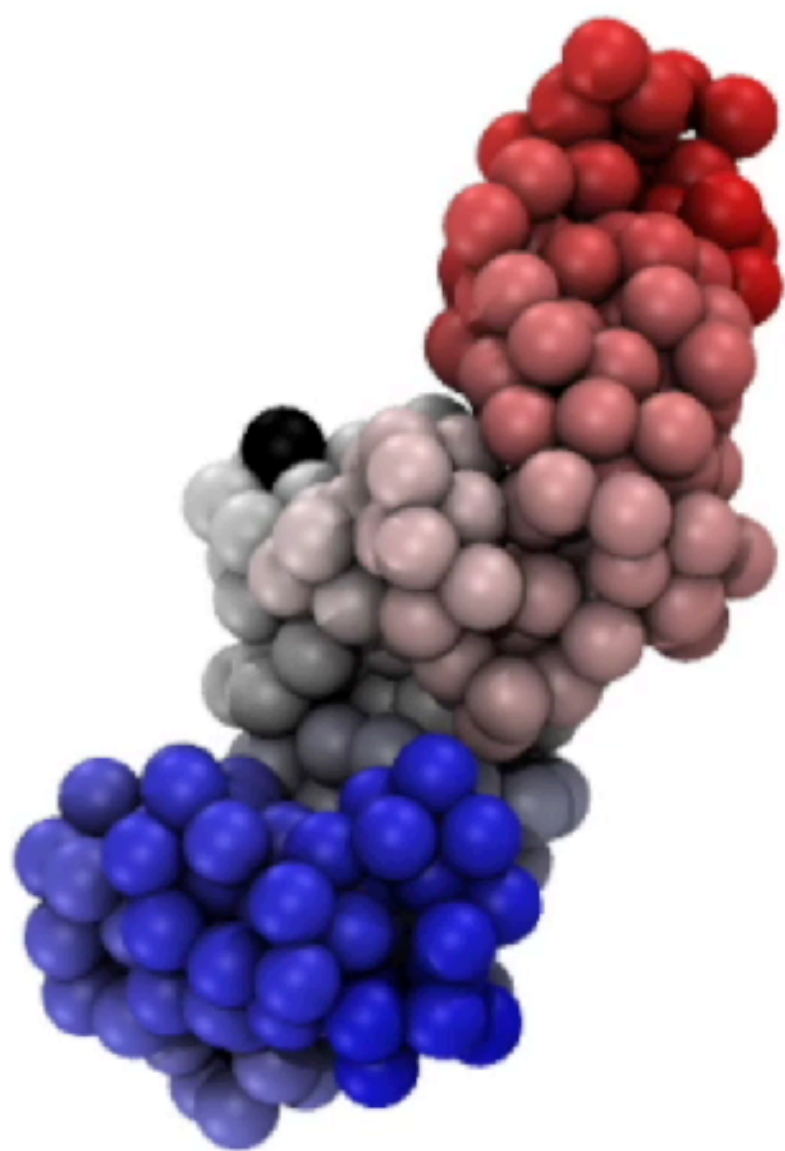
SOX2 locus structural changes from B to PSC

Distance to regulatory elements



SOX2 locus structural changes from B to PSC

Chromatin Activity

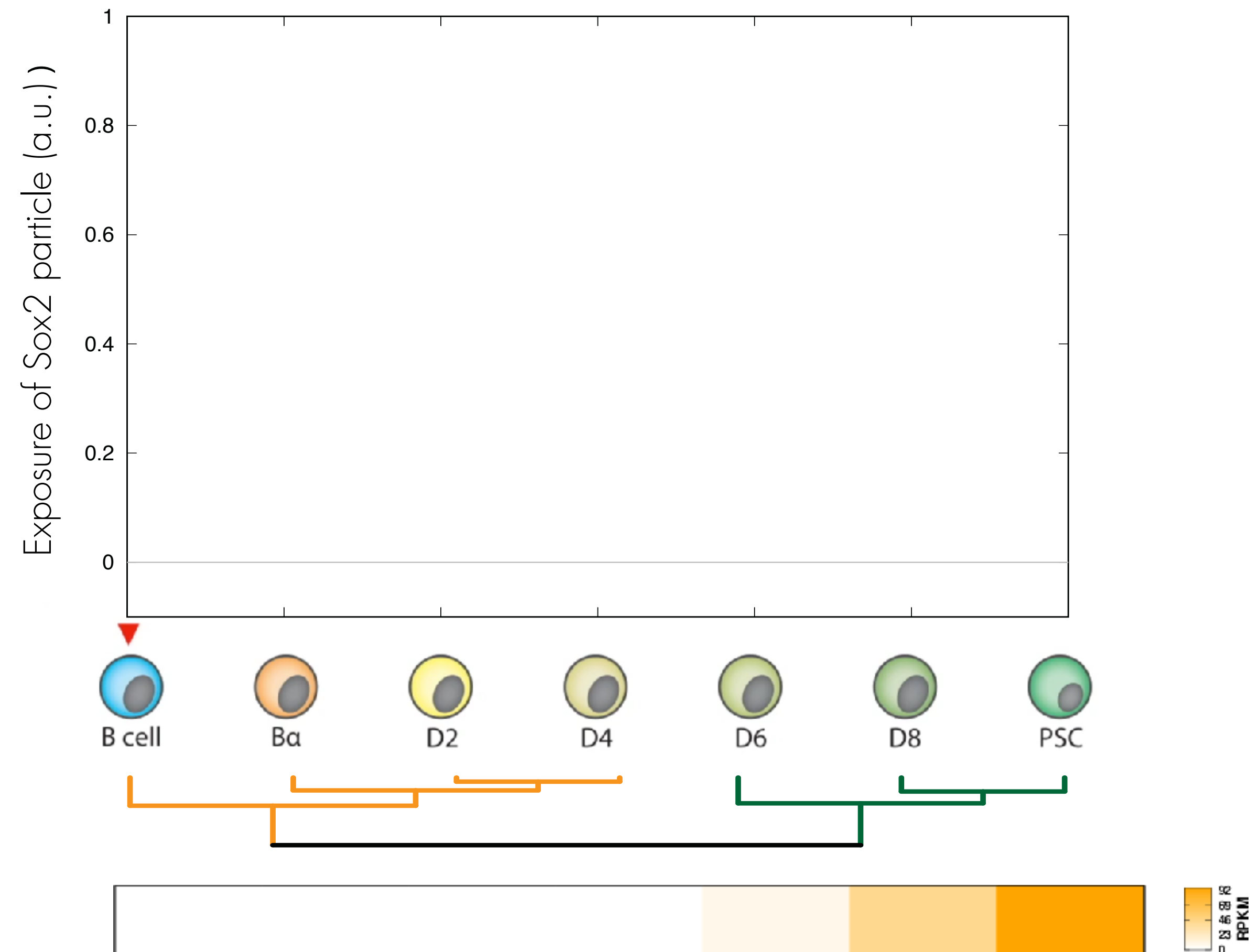


	B	Ba	D2	D4	D6	D8	PSC
A	9	6	7	13	13	22	48
AP	4	1	4	4	4	13	23
APD	3	1	1	1	4	10	15



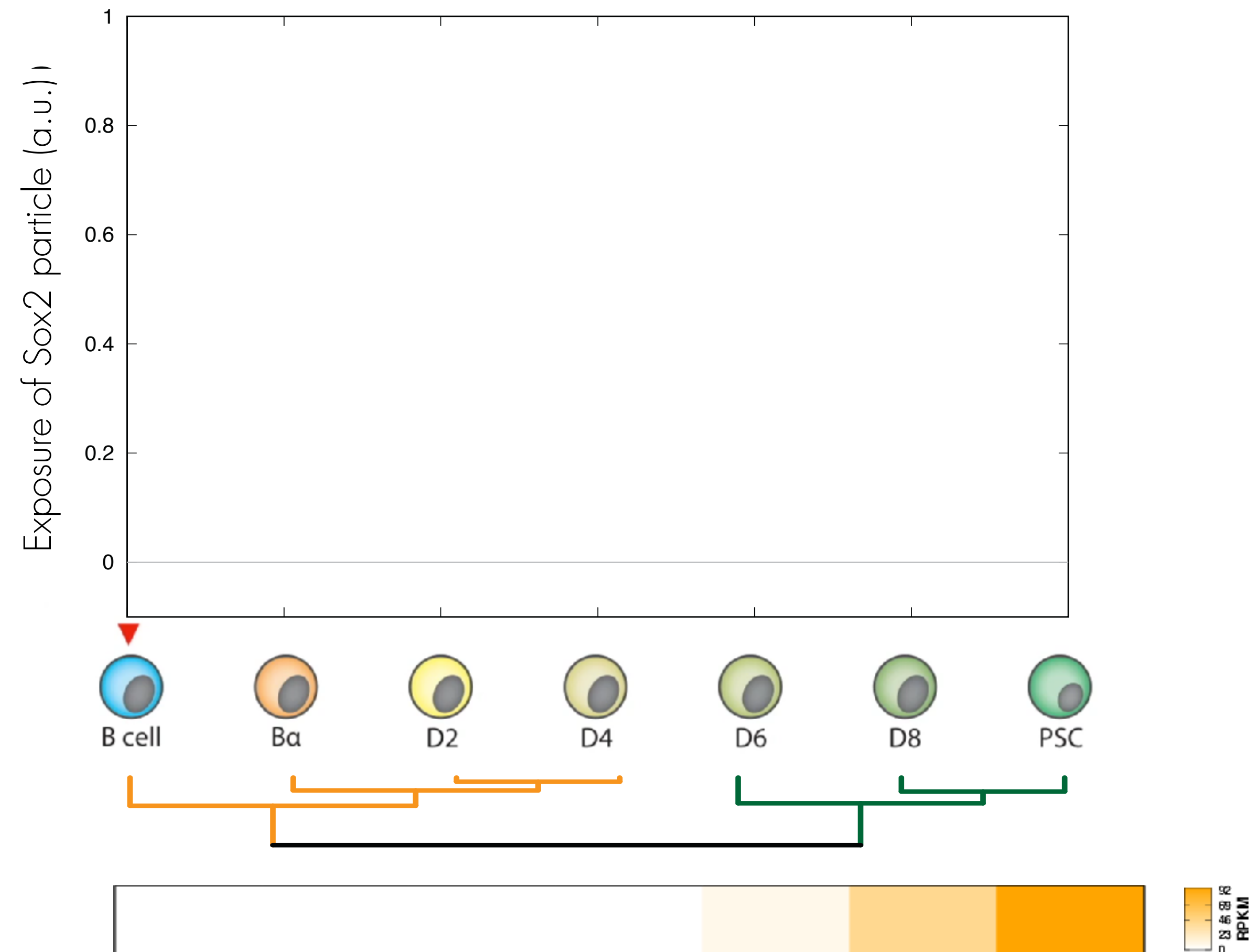
SOX2 locus structural changes from B to PSC

Structural exposure



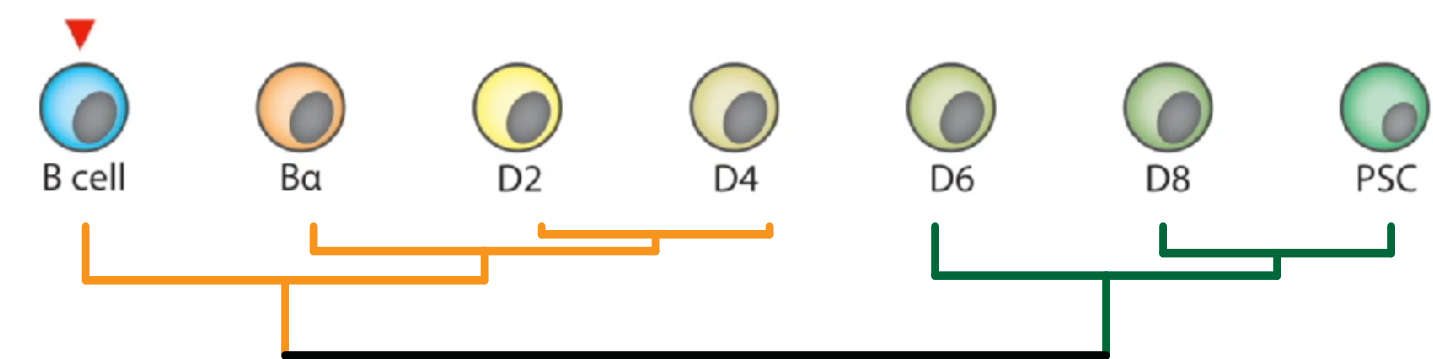
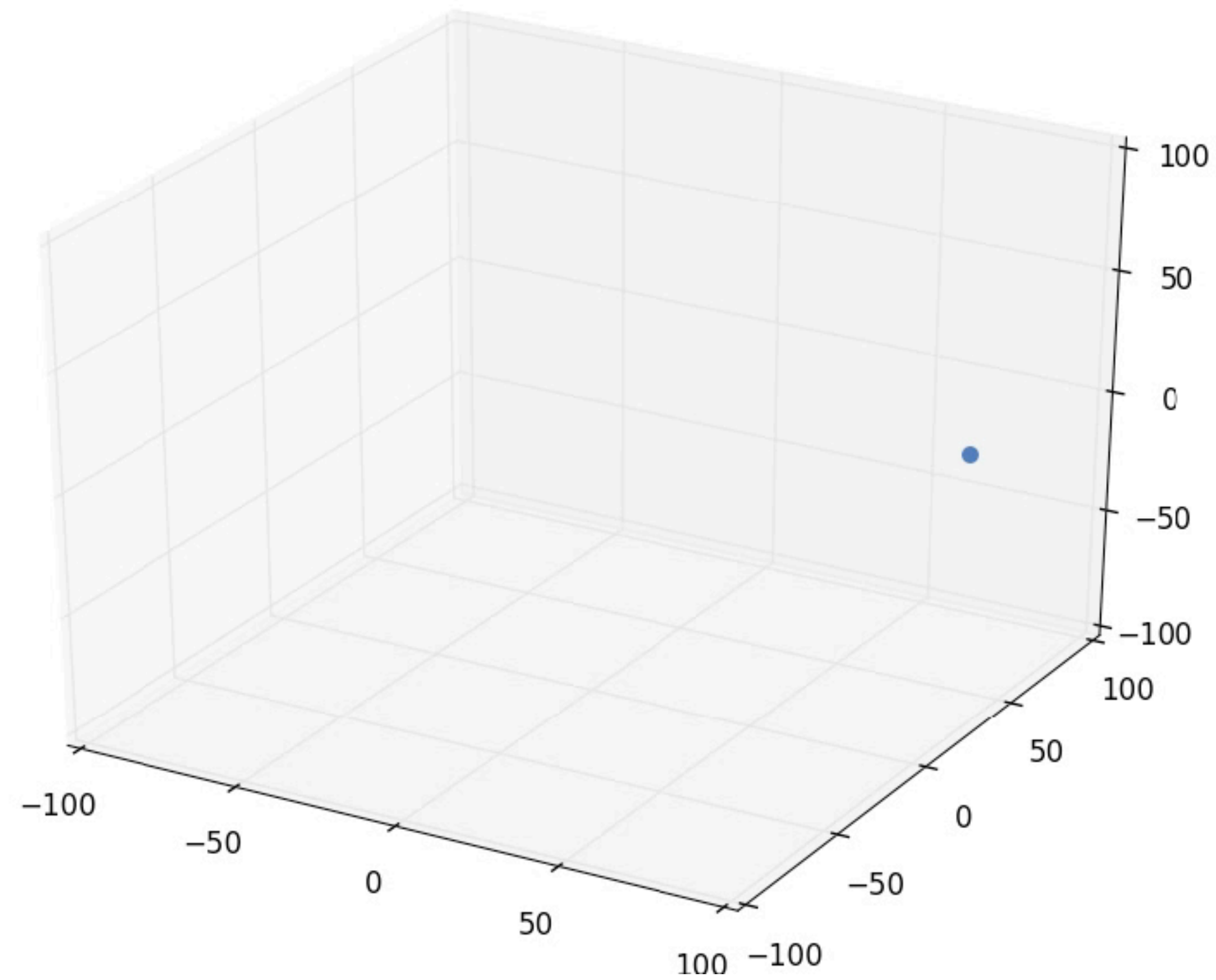
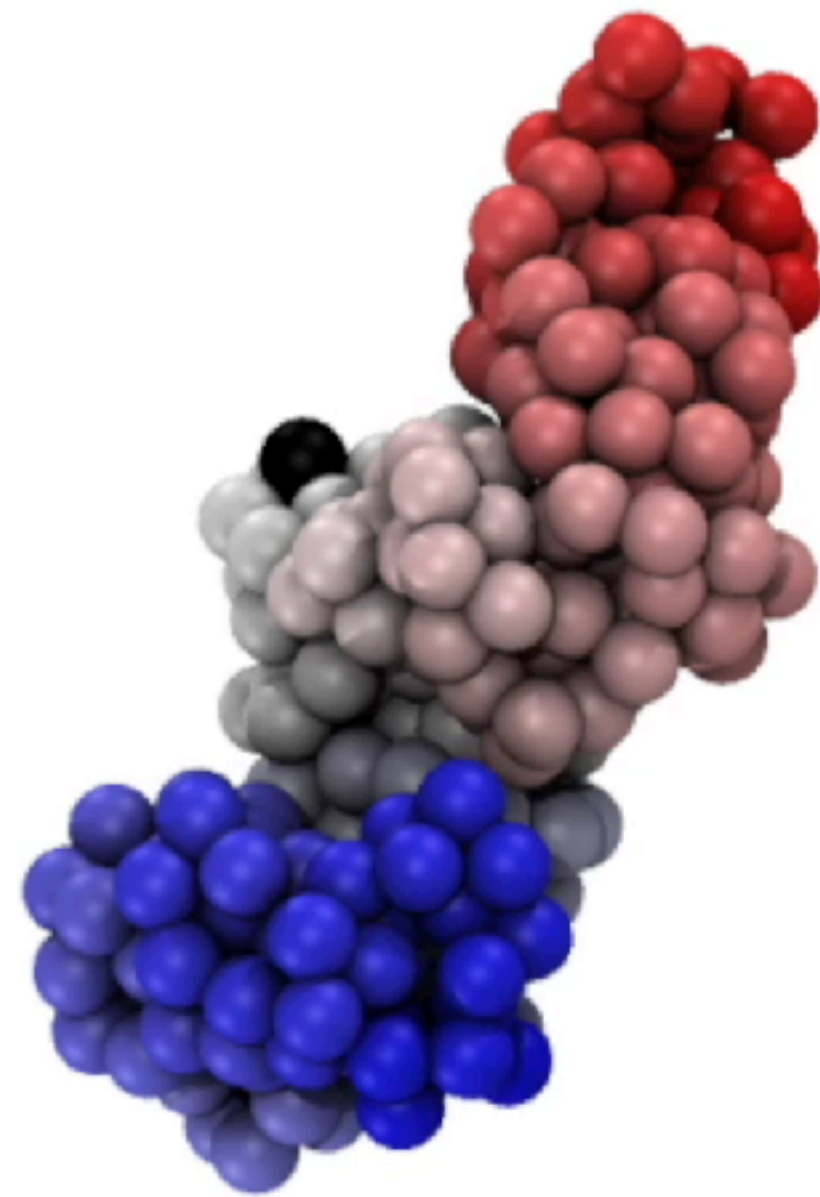
SOX2 locus structural changes from B to PSC

Structural exposure



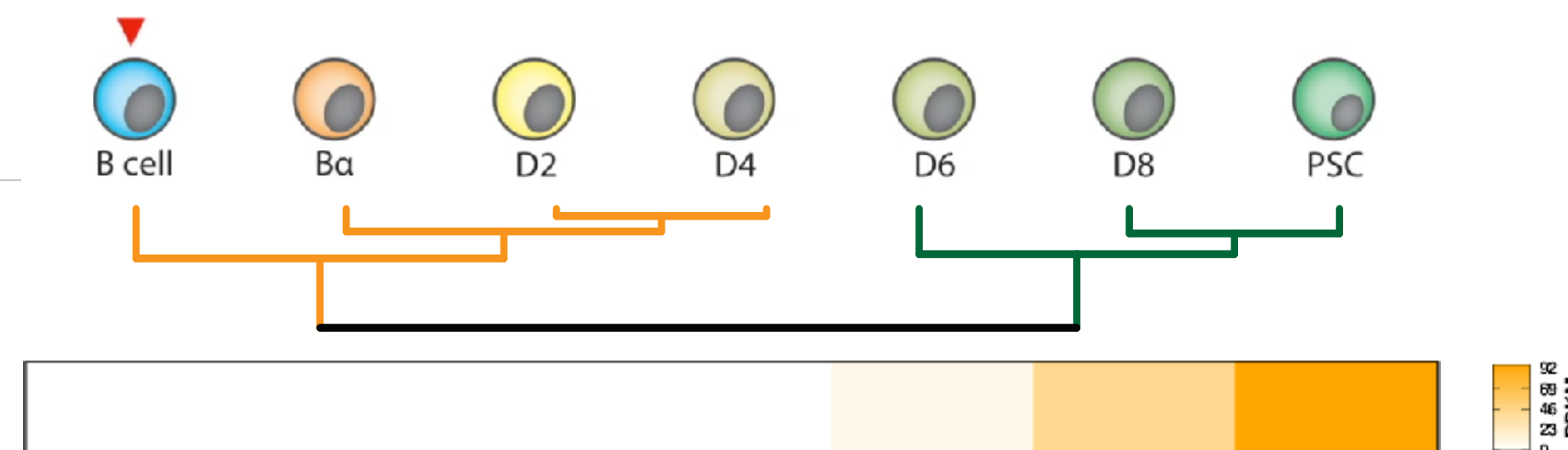
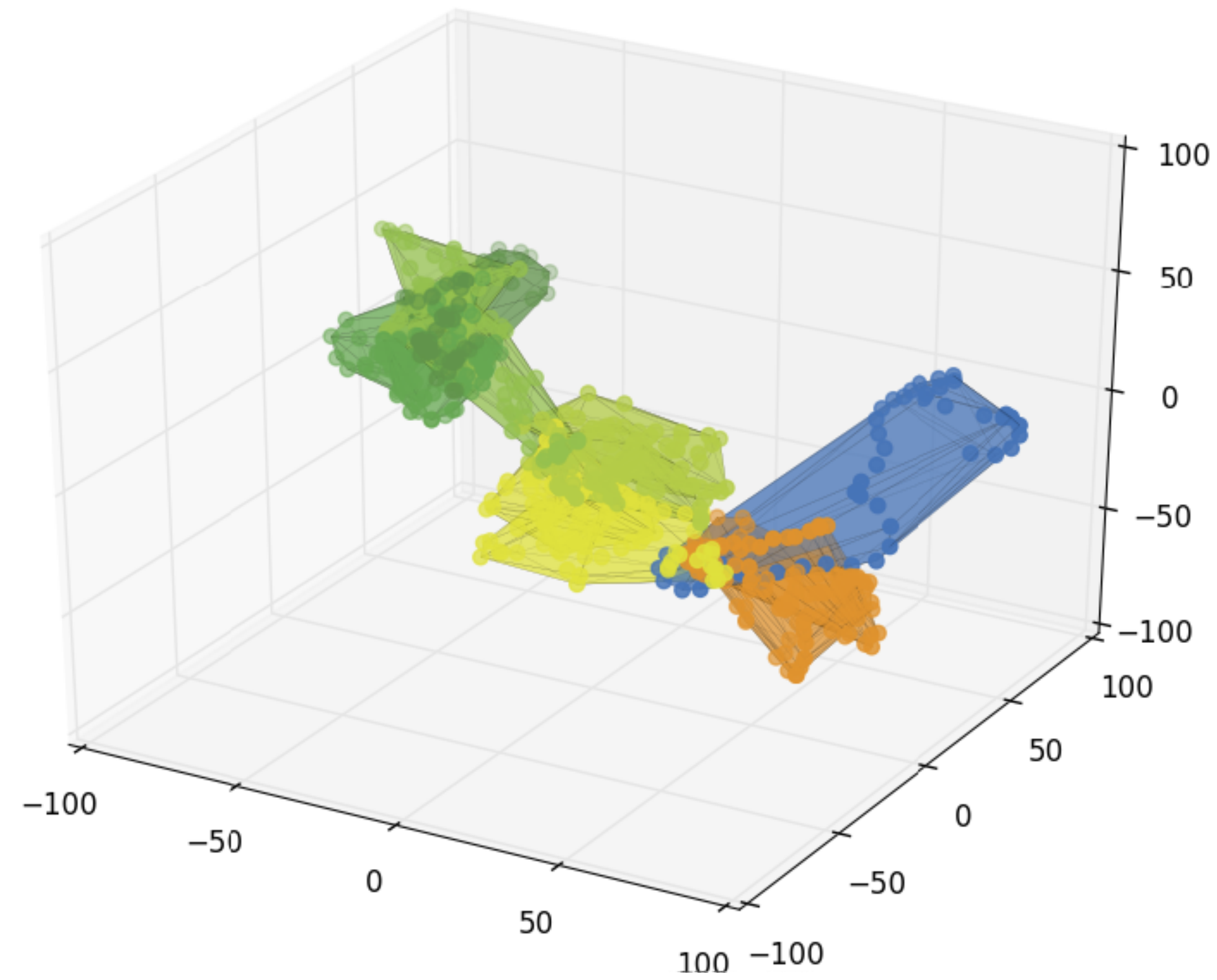
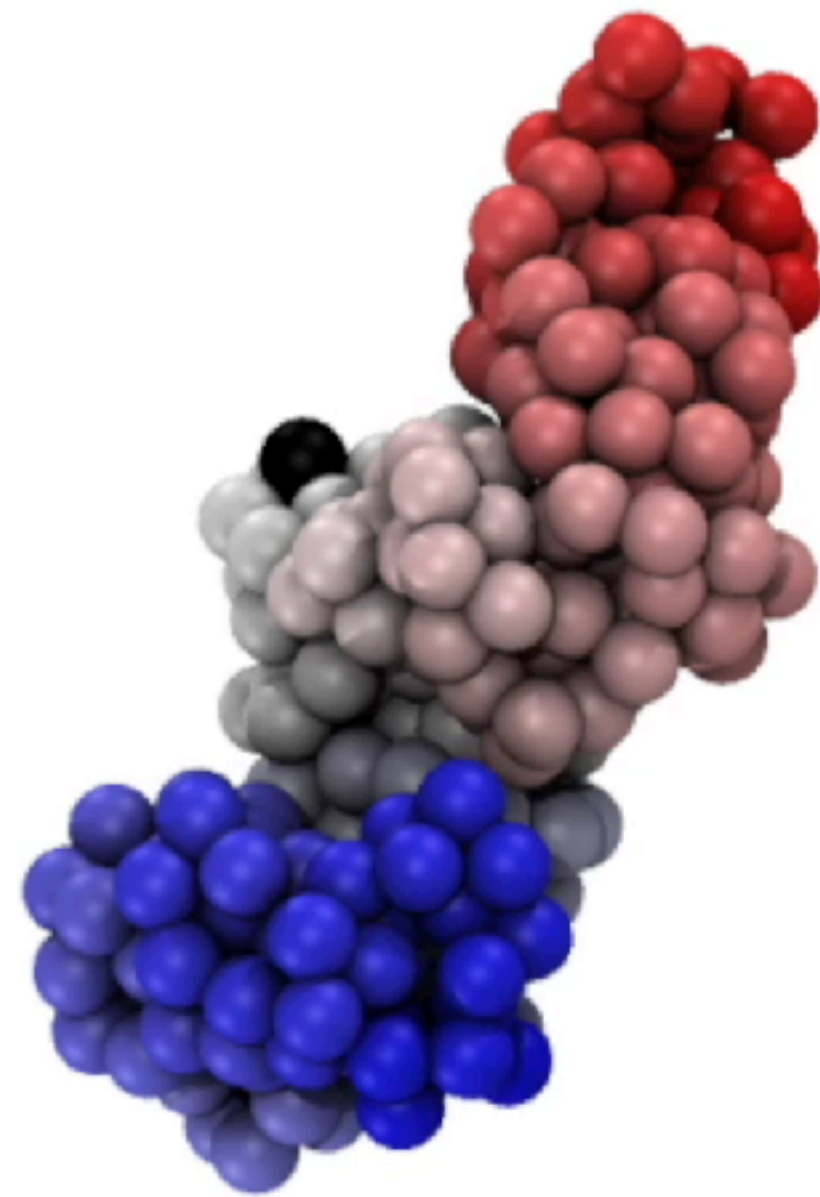
SOX2 locus dynamics changes from B to PSC

SOX2 displacement



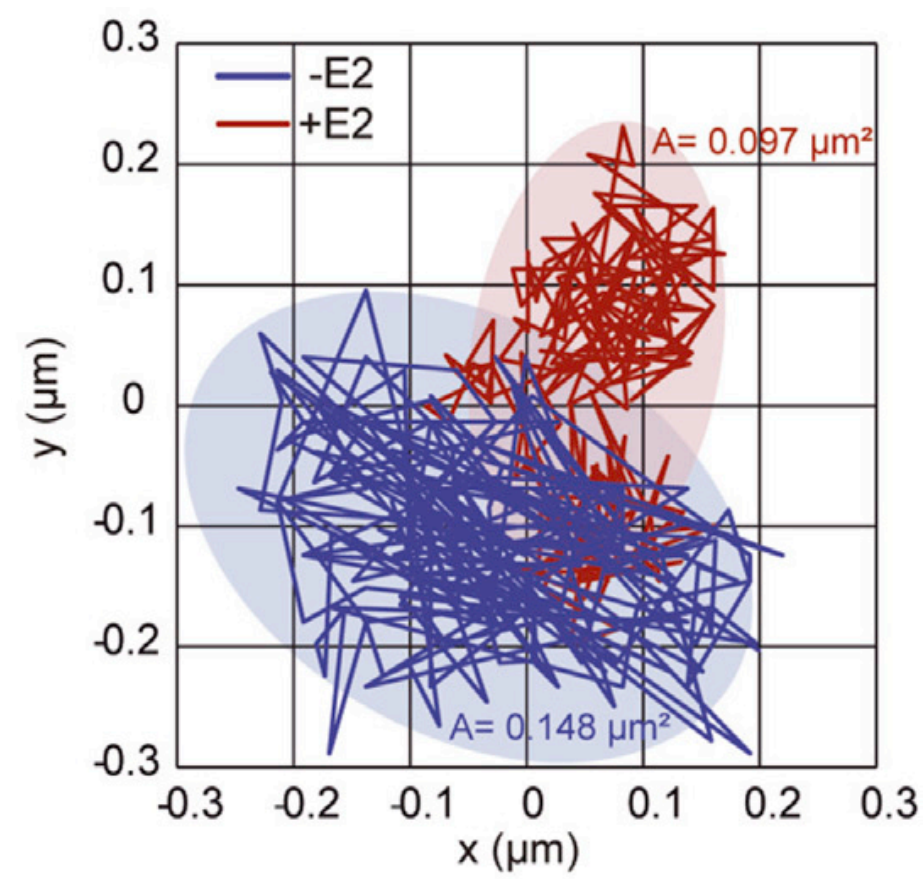
SOX2 locus dynamics changes from B to PSC

SOX2 displacement



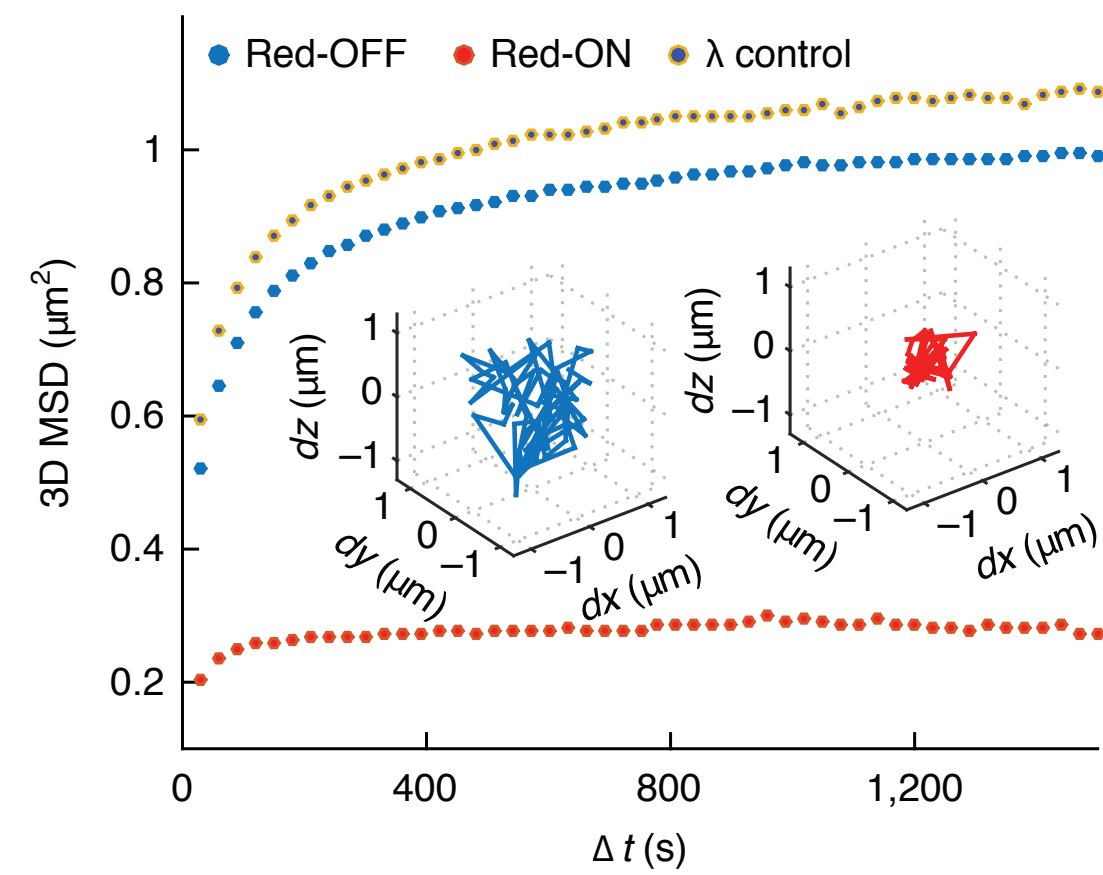
SOX2 locus dynamics changes from B to PSC

SOX2 displacement



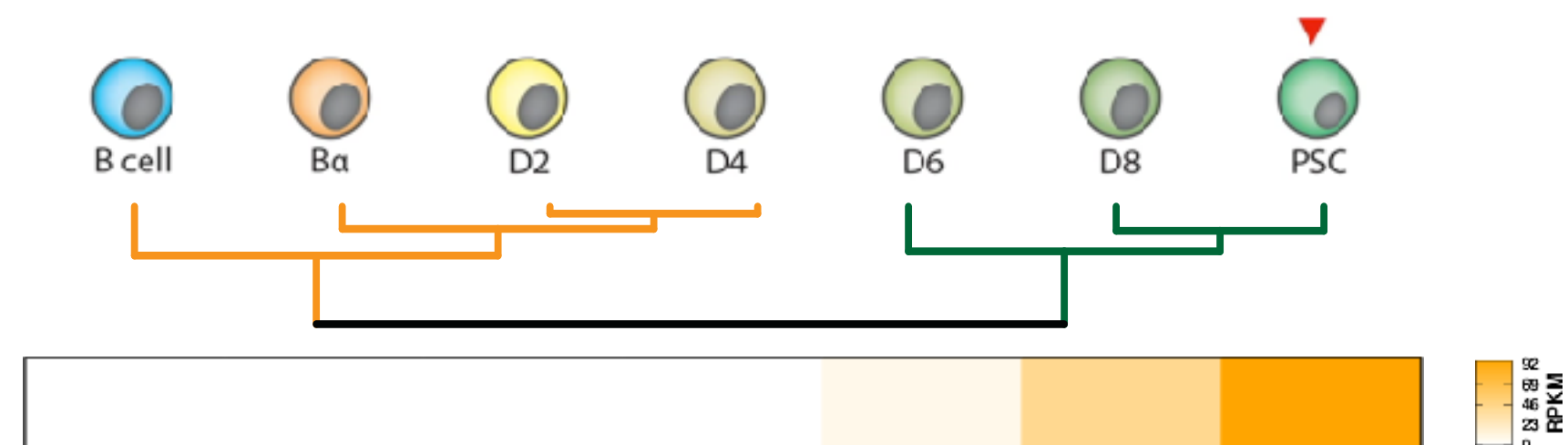
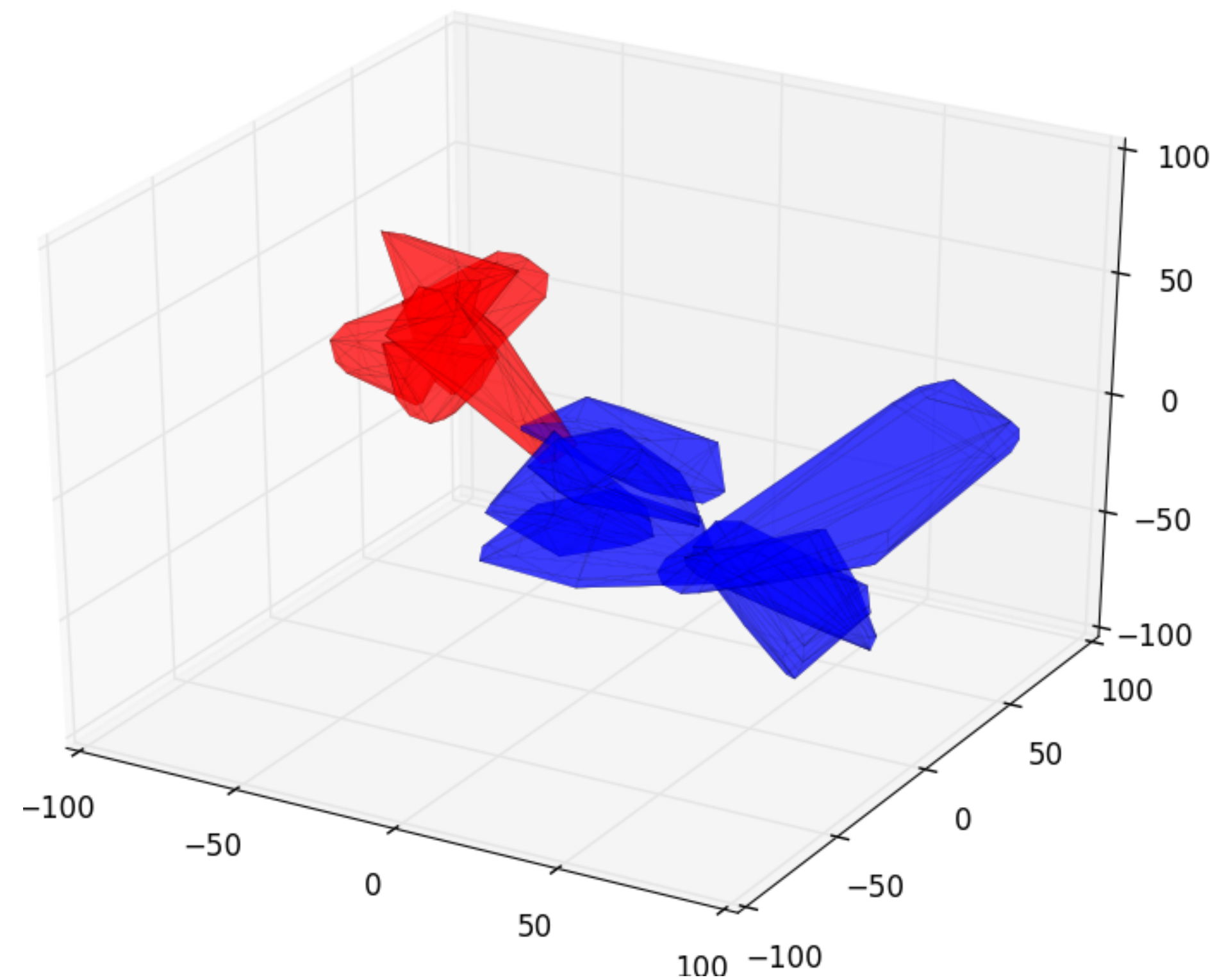
Two dimensional trajectories and area explored over 50s of the CCND1 locus recored before -E2 and after +E2 activation.

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



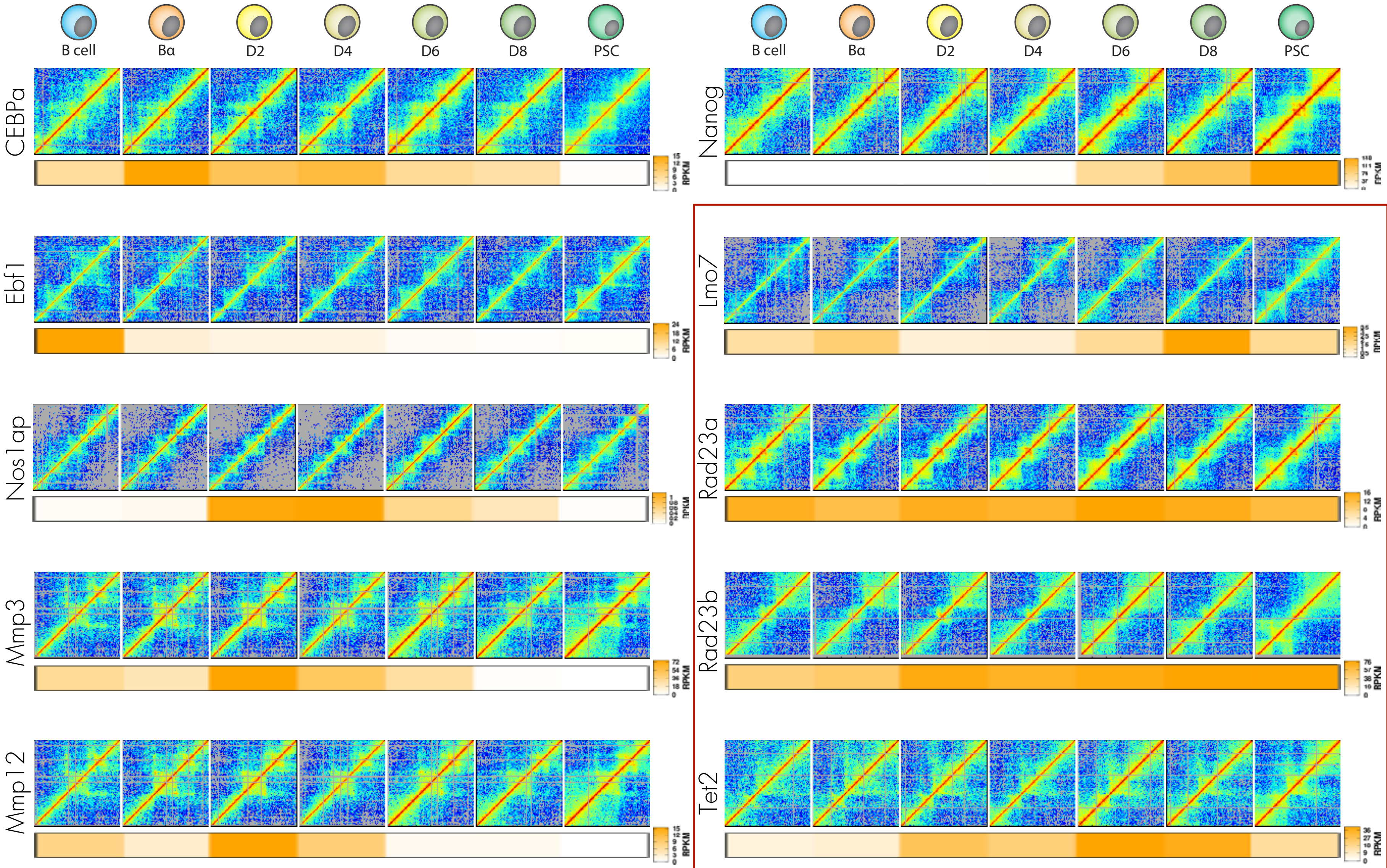
Transcription affects the 3D topology of the enhancer-promoted enhancing its temporal stability and is associated with further spatial compaction.

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

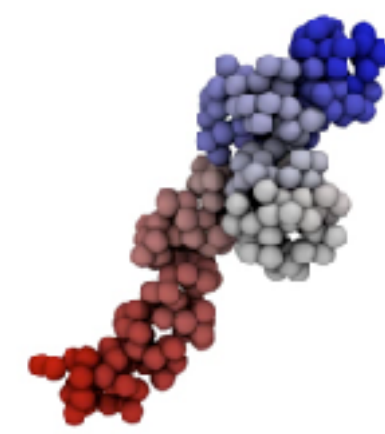


Structural changes from B to PSC

Other 10 loci

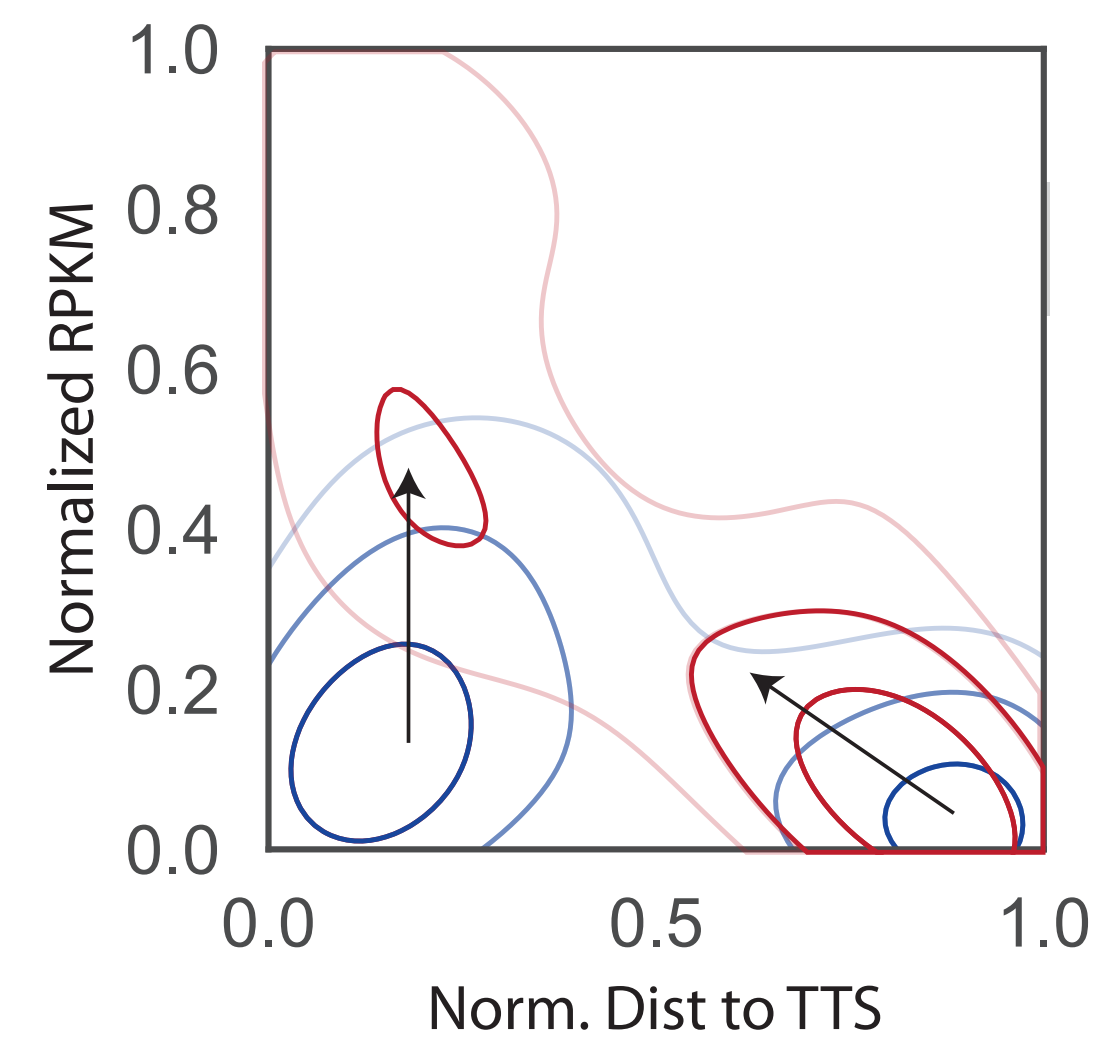
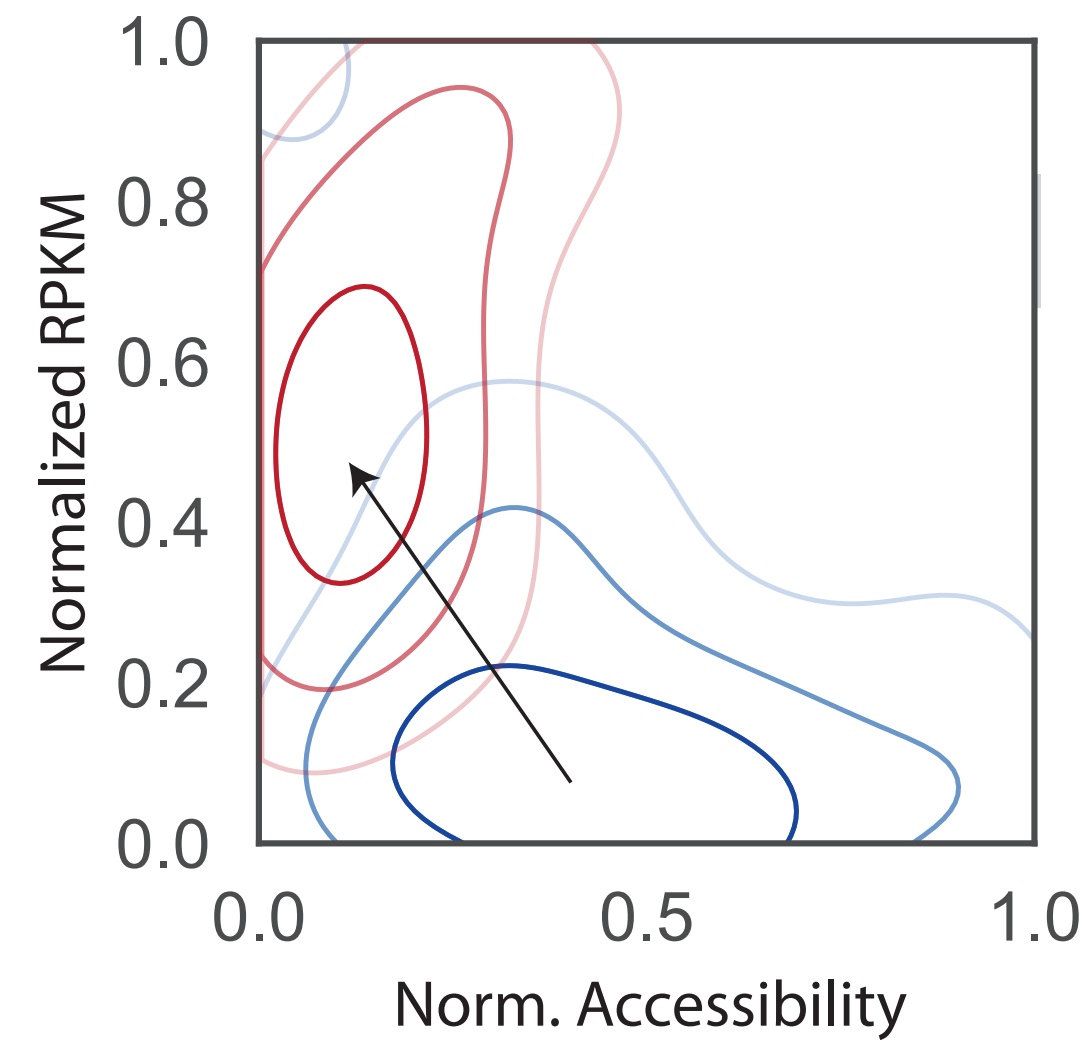


Always active

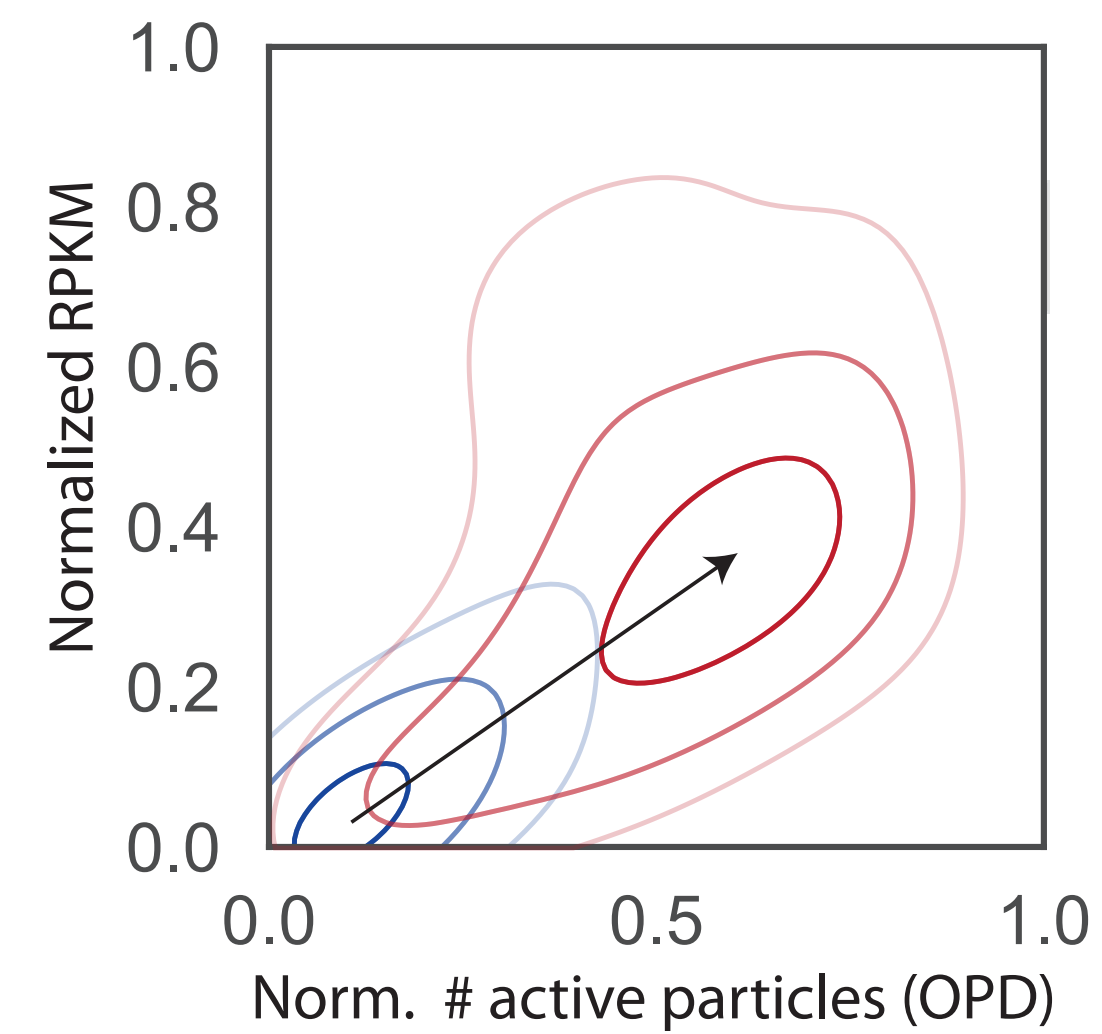
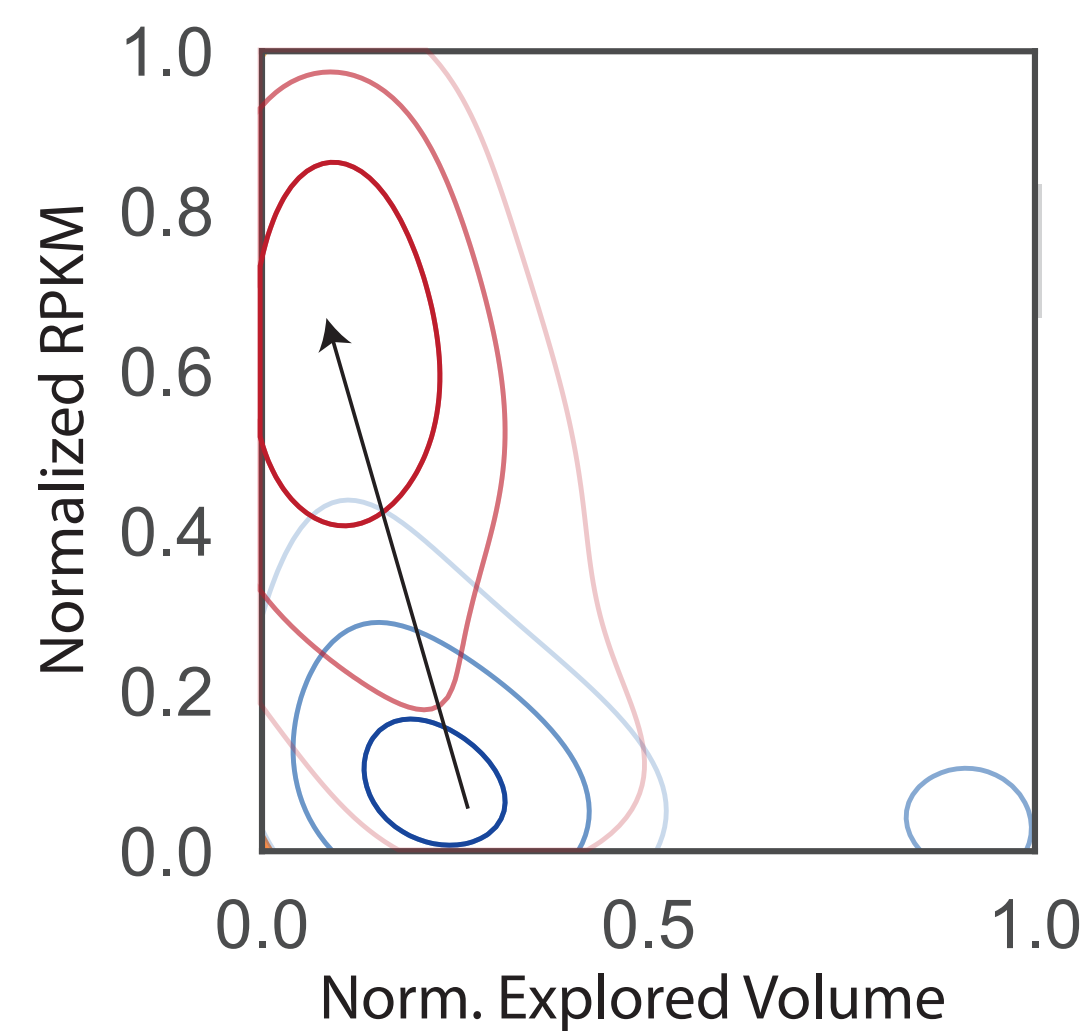


Dynamics of gene activation

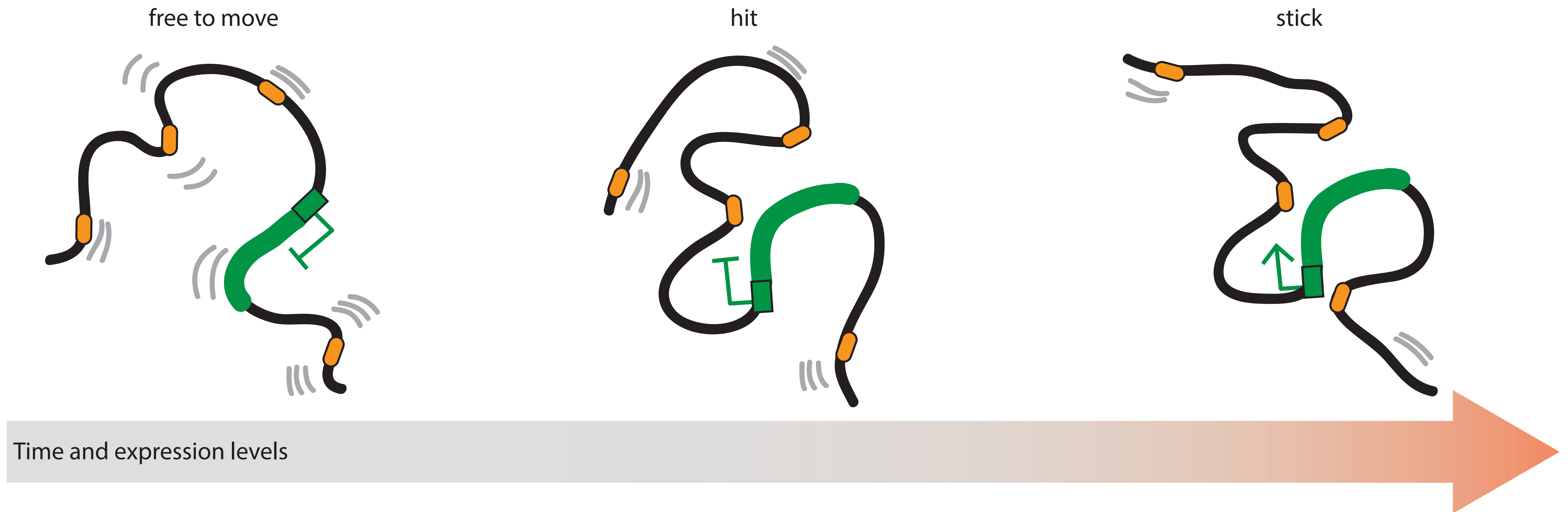
Trends in all 11 loci



Active loci
Switching loci



A “hit-and-stick” model for gene activation



<http://marciuslab.org>
<http://3DGenomes.org>

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