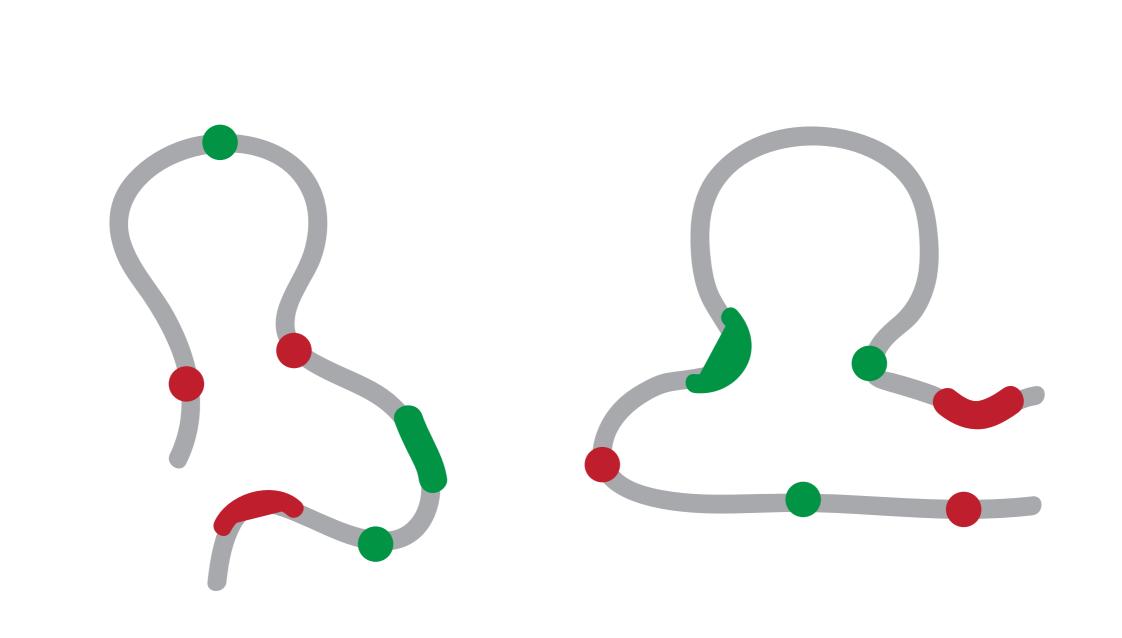
Exploring the time dependent structural rearrangements of SOX2 locus in mouse using the TADdyn tool

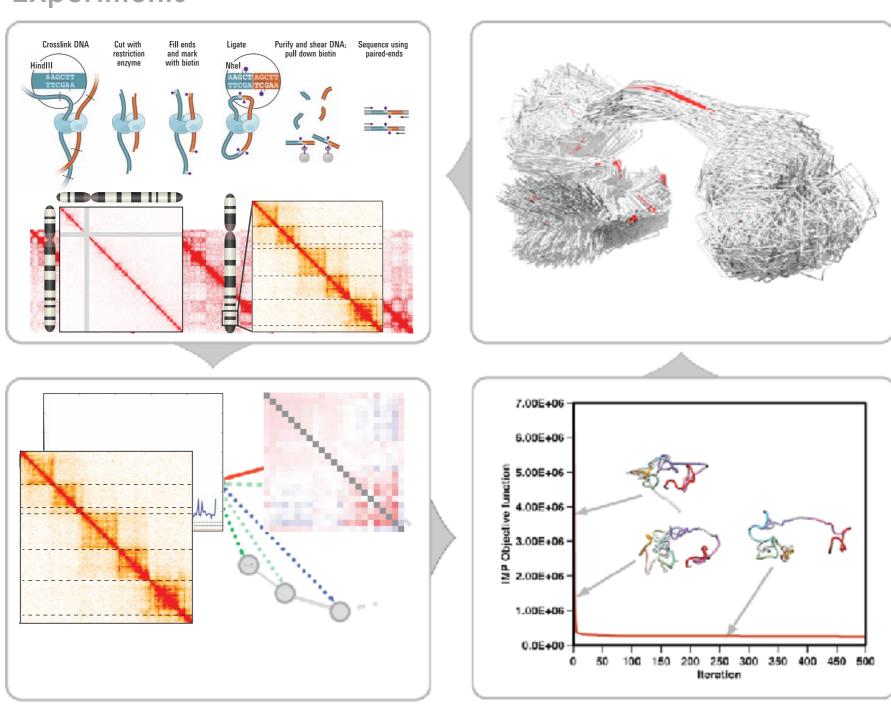
Marc A. Marti-Renom
Structural Genomics Group (ICREA, CNAG-CRG)





Hybrid Method Baù, D. & Marti-Renom, M. A. Methods 58, 300–306 (2012).

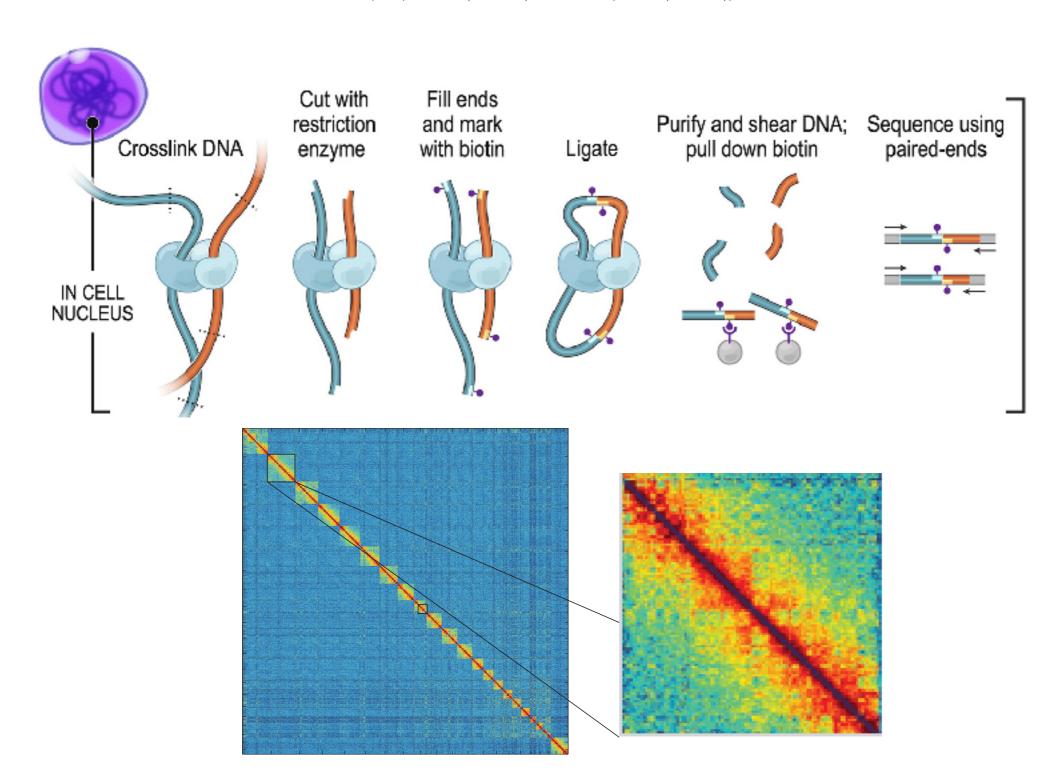
Experiments



Computation

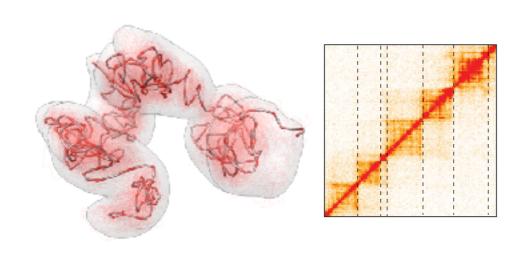
Chromosome Conformation Capture

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.

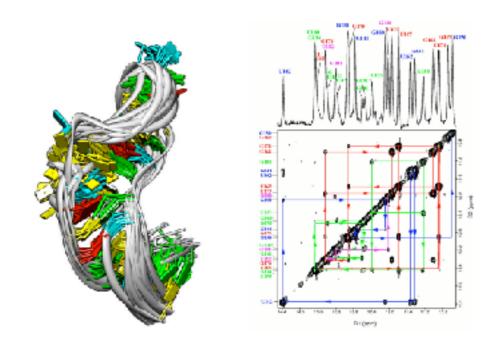


Restraint-based Modeling

Baù, D. & Marti-Renom, M. A. Methods 58, 300–306 (2012).



Chromosome structure determination 3C-based data

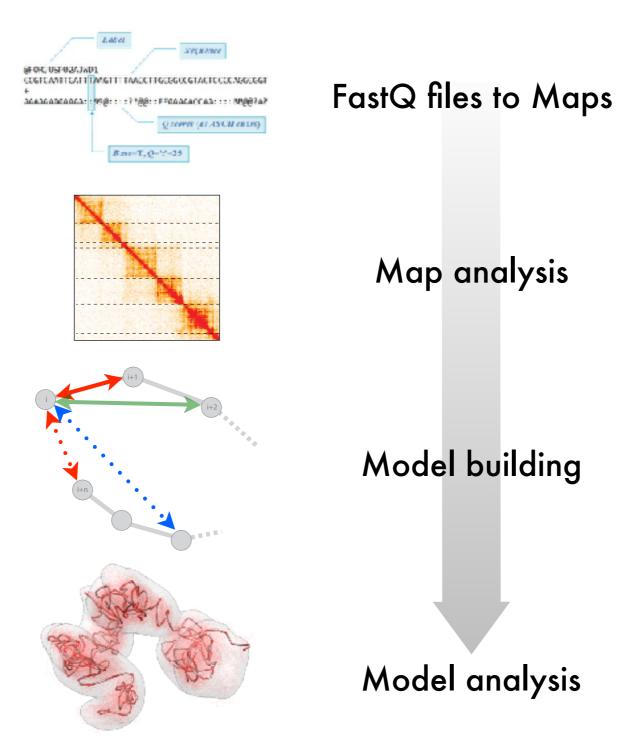


Biomolecular structure determination 2D-NOESY data

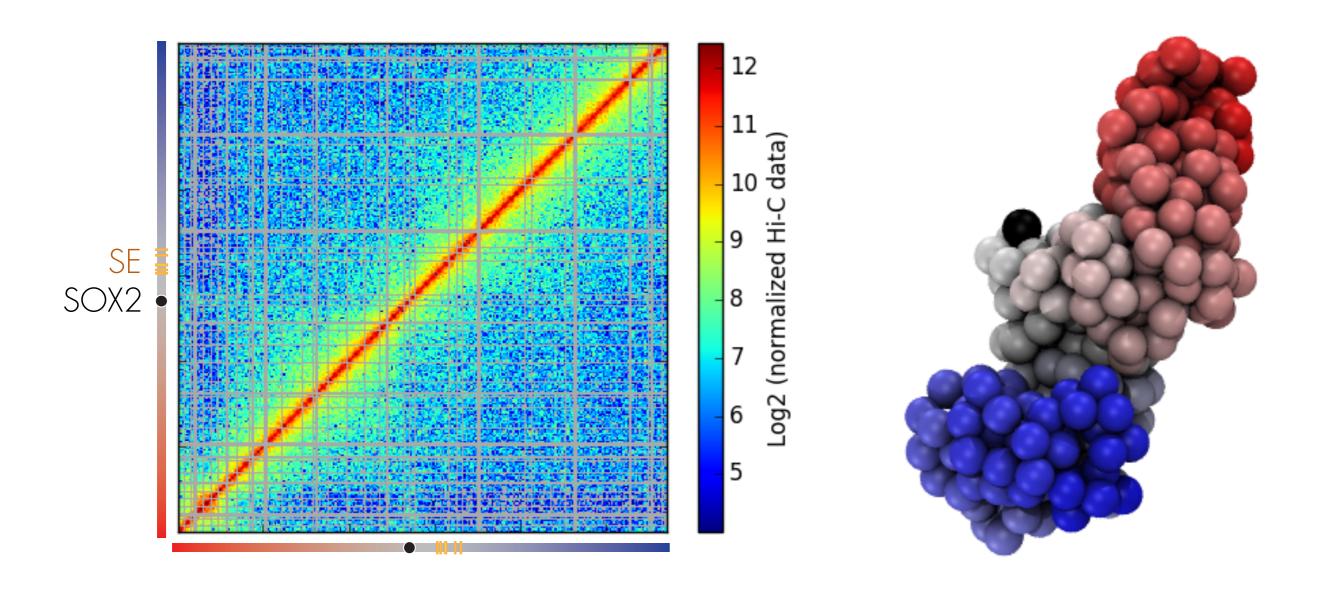


http://3DGenomes.org

Serra, F., Baù, D. et al. PLOS CB (2017)



TADbit modeling of SOX2 from B cells Hi-C

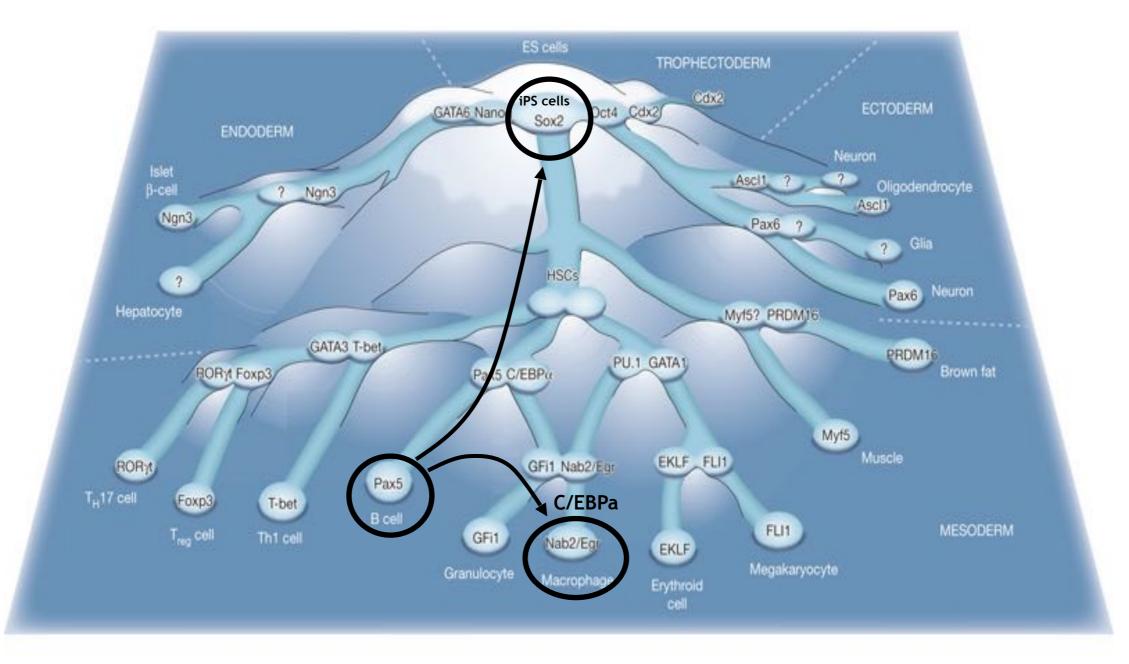


Optimal IMP parameters

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

Transcription factors dictate cell fate

Graf & Enver (2009) Nature



Transcription factors (TFs) determine cell identity through gene regulation

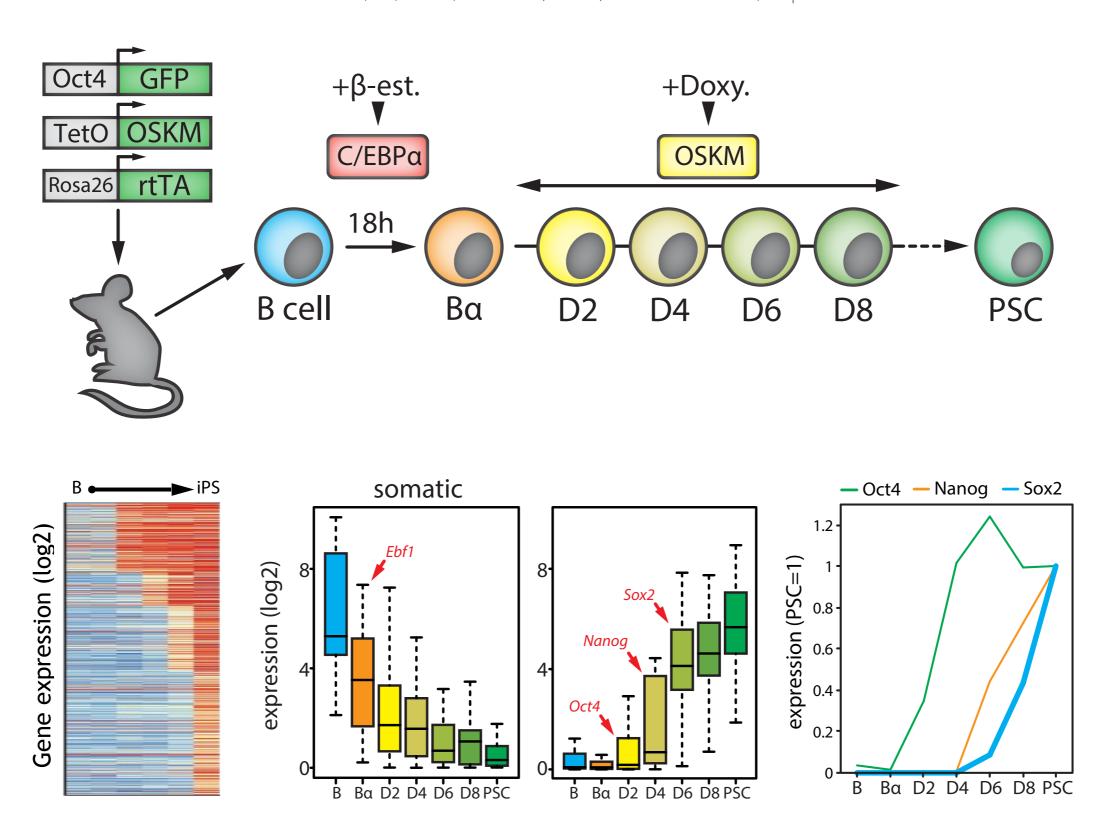
Normal 'forward' differentiation

Cell fates can be converted by enforced TF expression

Transdifferentiation or reprogramming

Reprogramming from B to PSC

Stadhouders, R., Vidal, E. et al. (2017) Nature Genetics, in press.

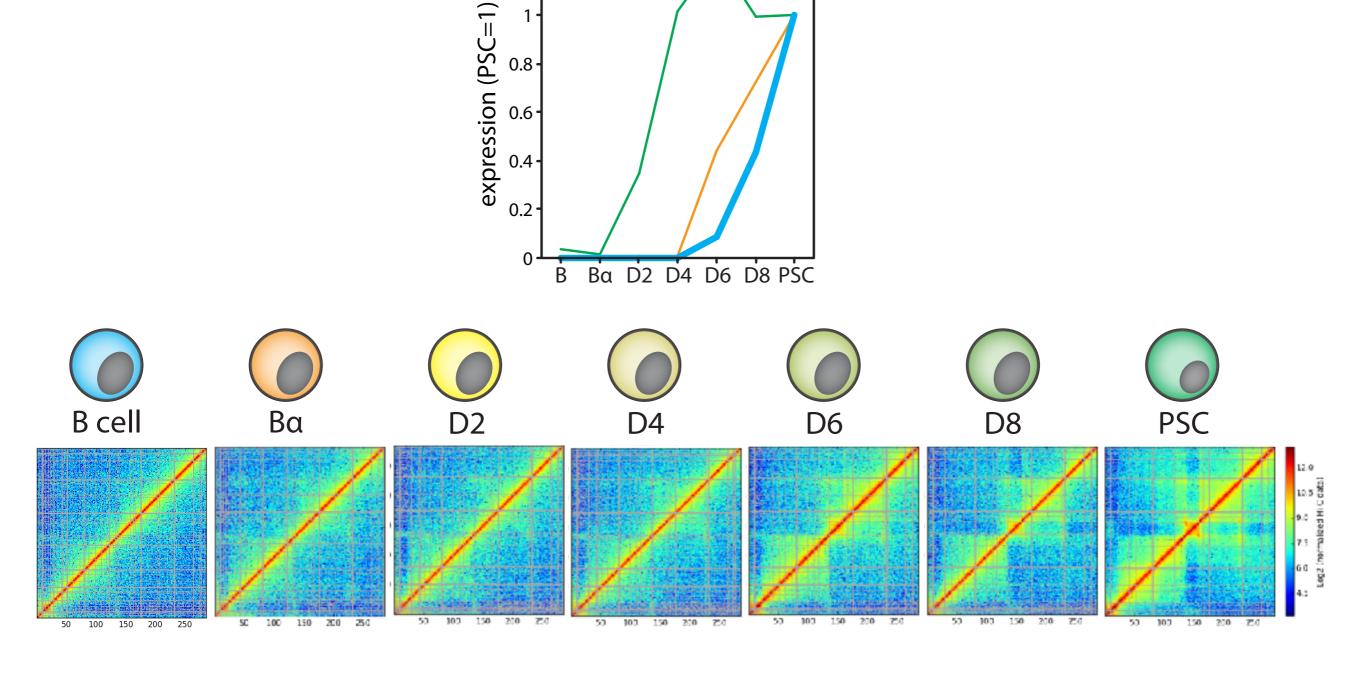


Hi-C maps of reprogramming from B to PSC

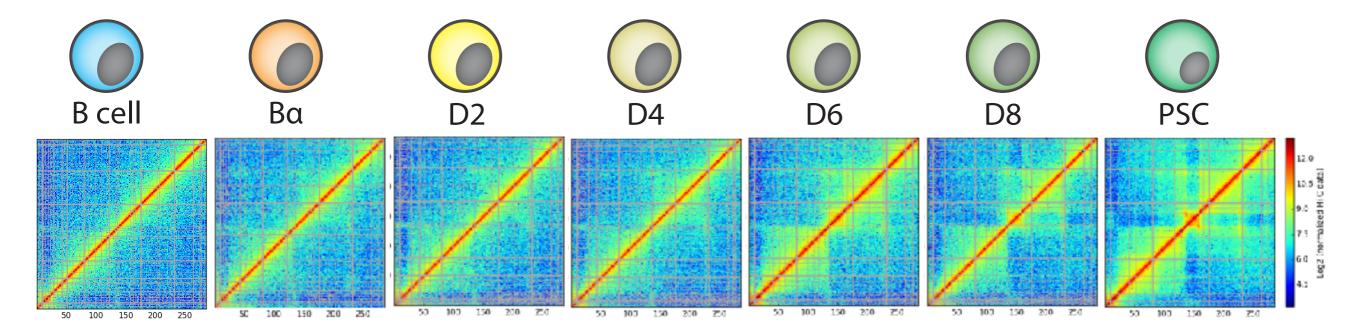
The SOX2 locus

— Oct4 — Nanog — Sox2

1.2



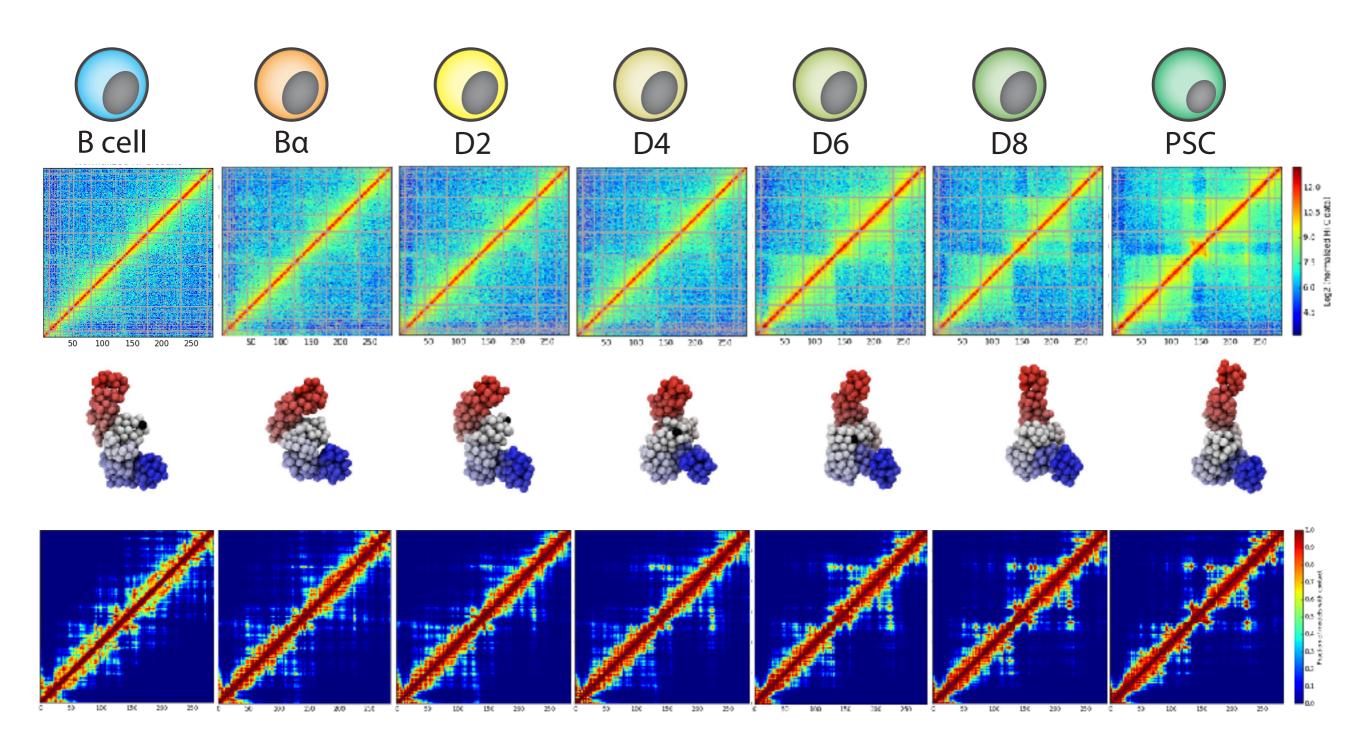
Hi-C maps of reprogramming from B to PSC The SOX2 locus



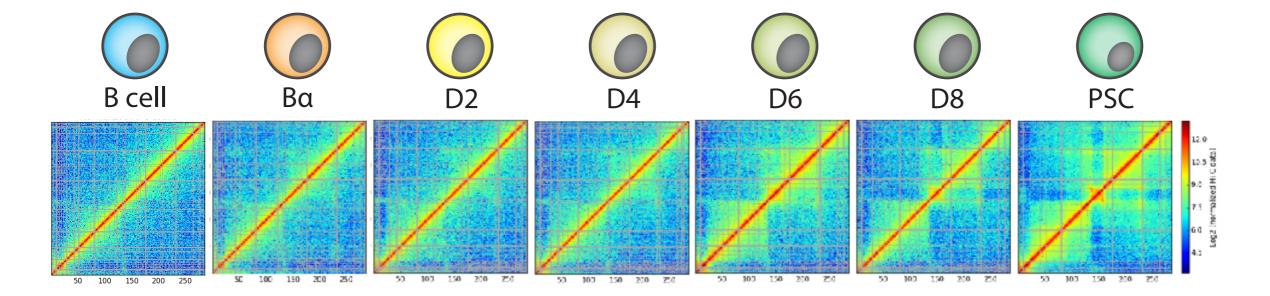
How does these structural rearrangements interplay with the transcription activity?

What are the main drivers of structural transitions?

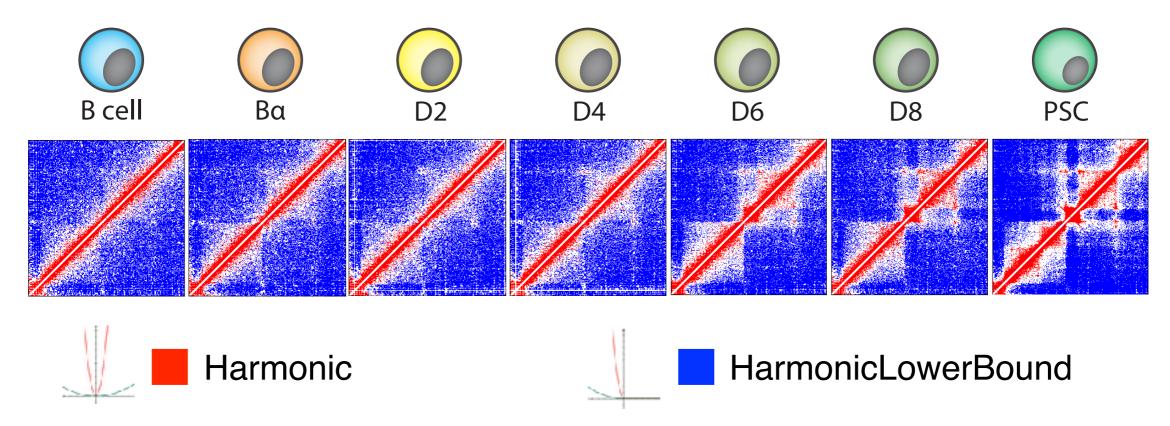
Models of reprogramming from B to PSC



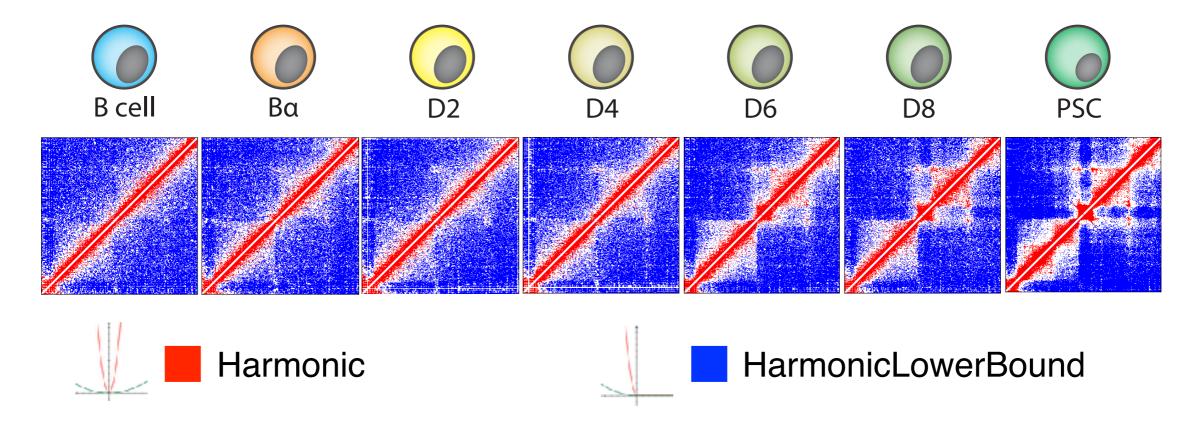
TADdyn: from time-series Hi-C maps to dynamic restraints

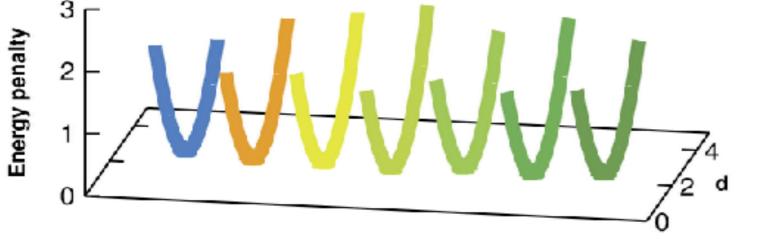


TADdyn: from time-series Hi-C maps to dynamic restraints



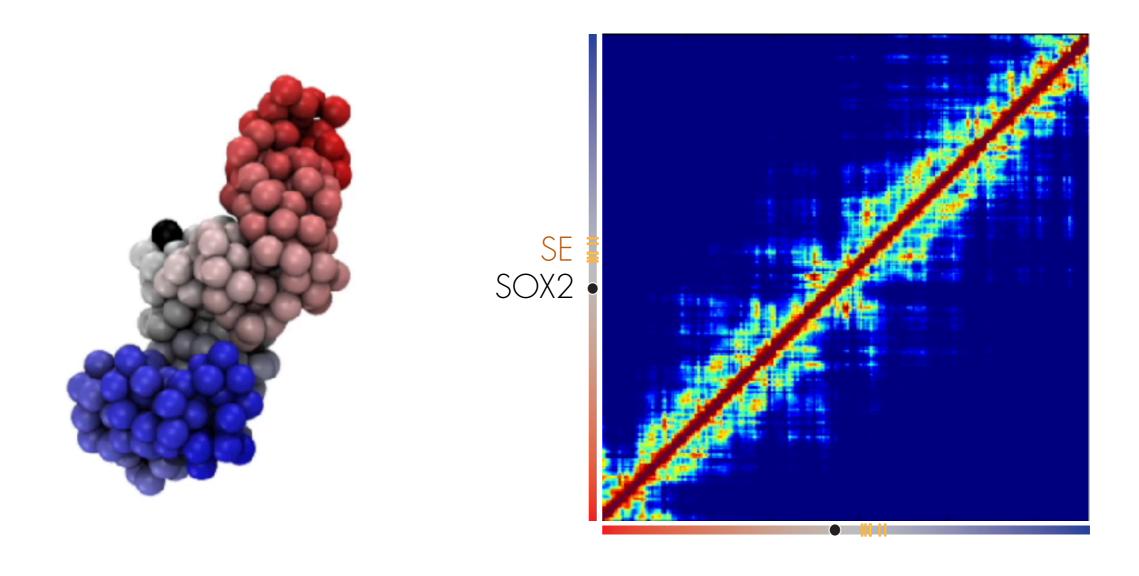
TADdyn: from time-series Hi-C maps to dynamic restraints





Transition	Stable	Vanishing	Raising
B -> B α	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

Contacts









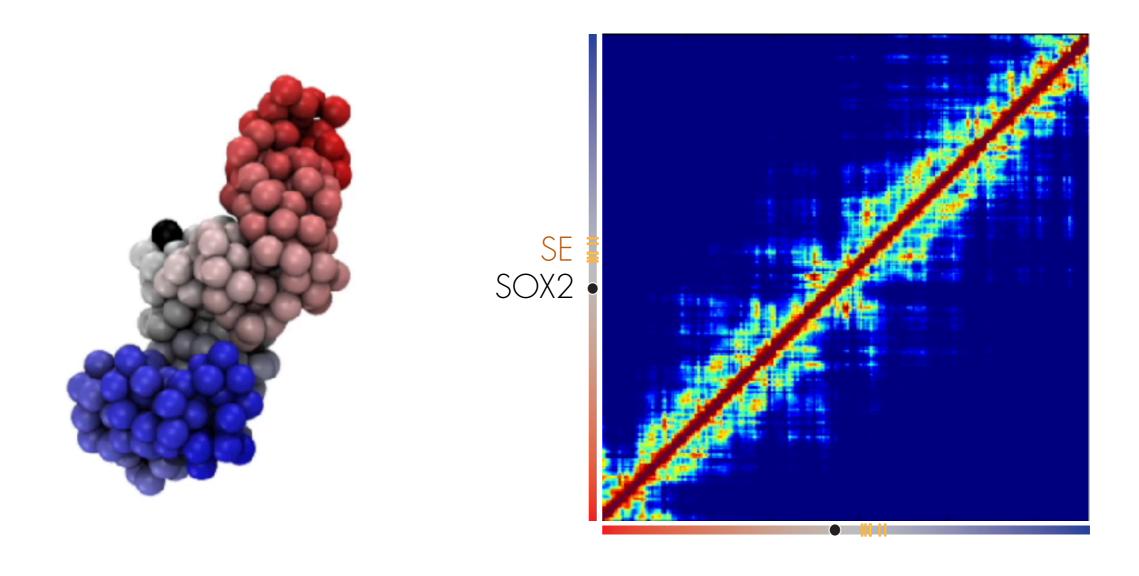








Contacts









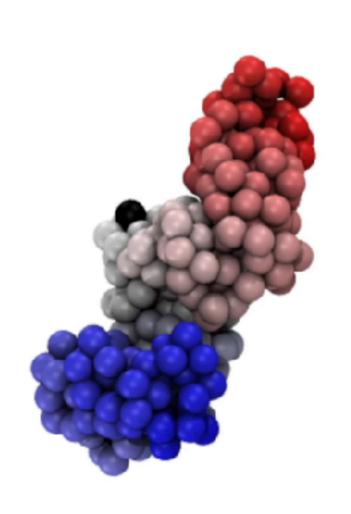


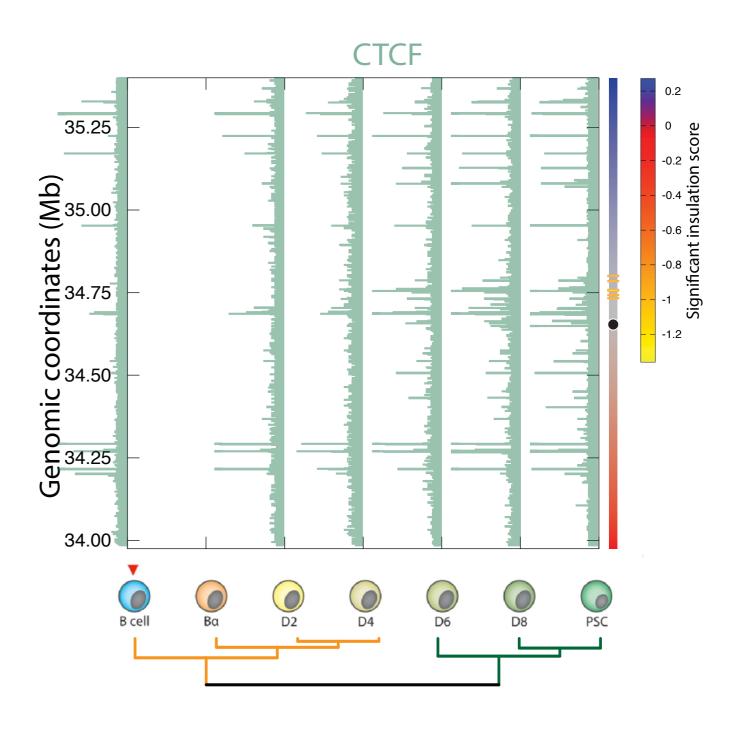




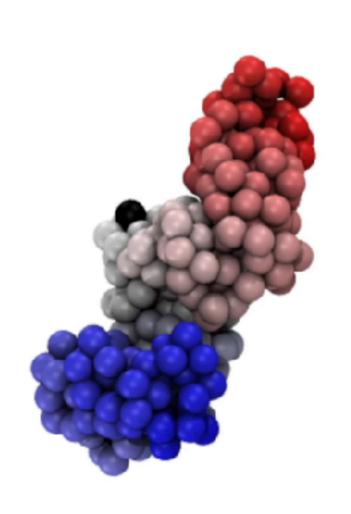


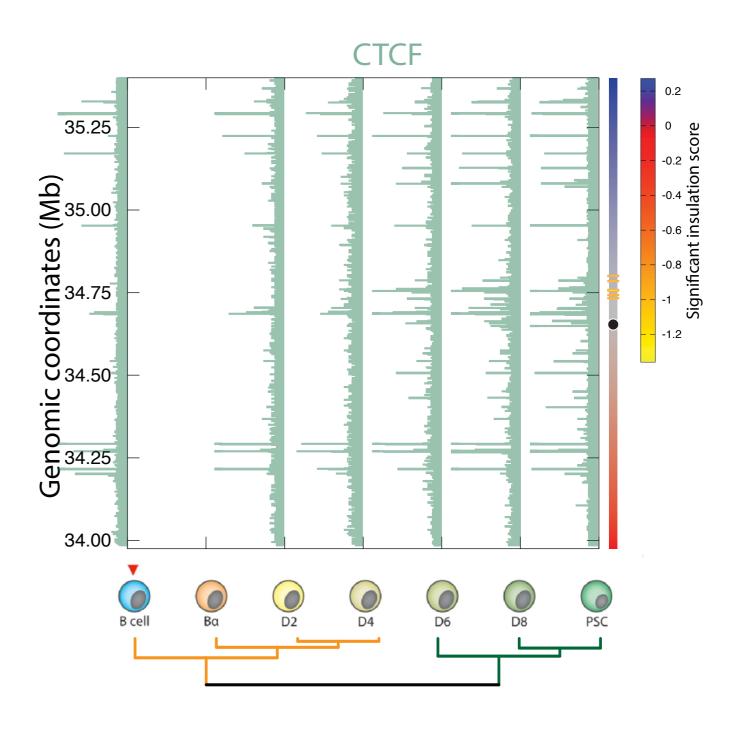
TAD borders



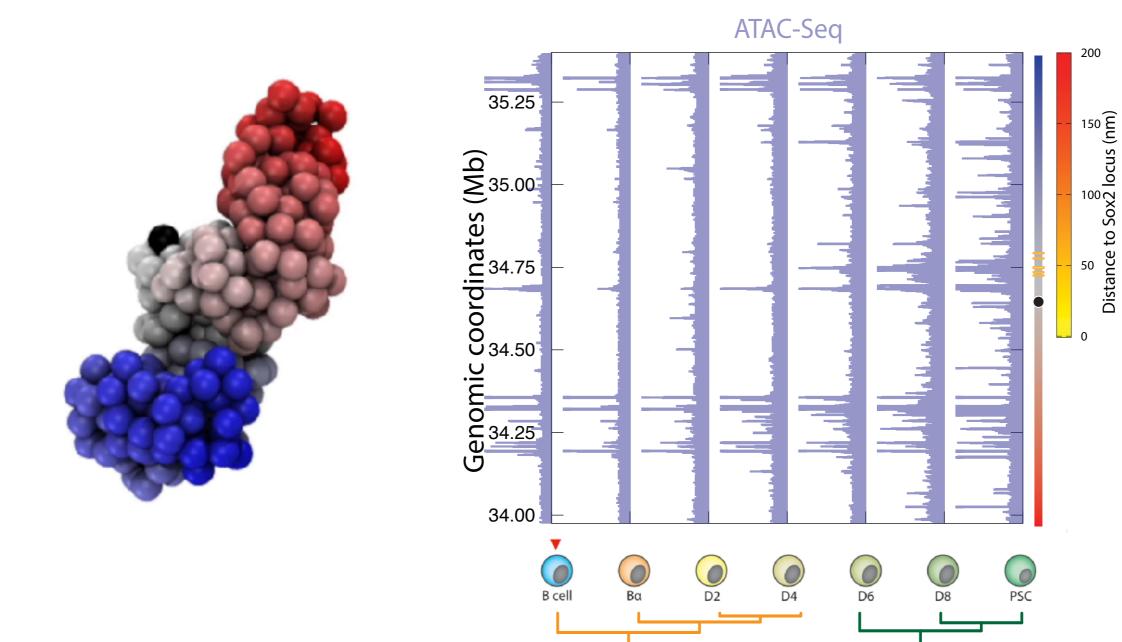


TAD borders

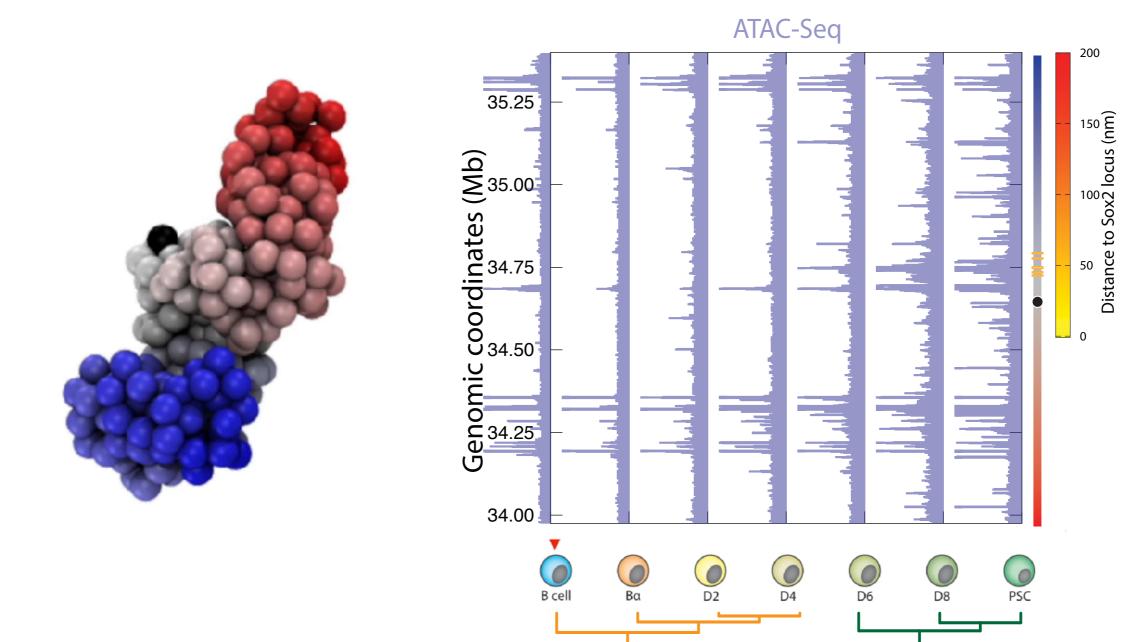




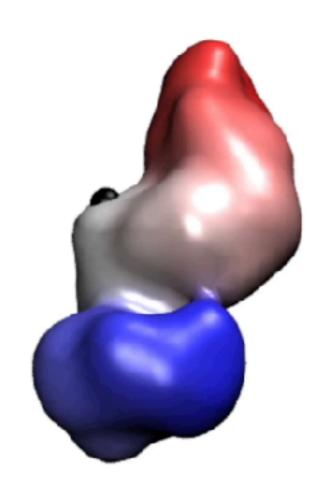
Distance to regulatory elements

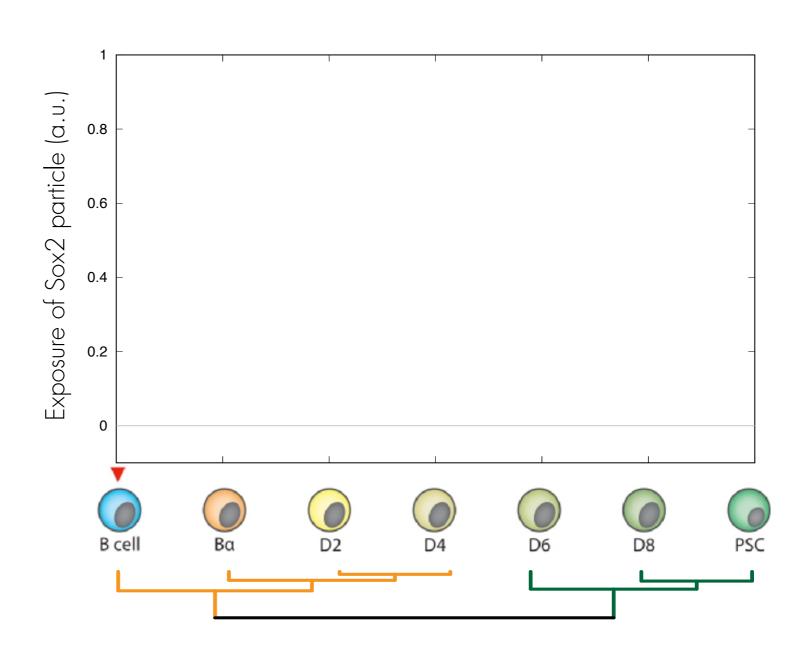


Distance to regulatory elements

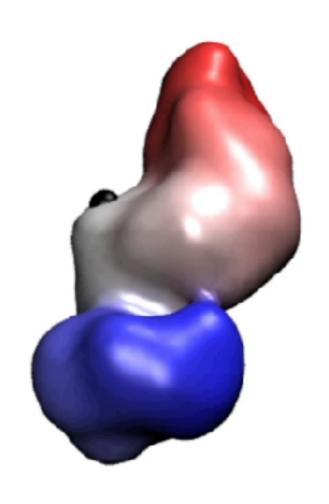


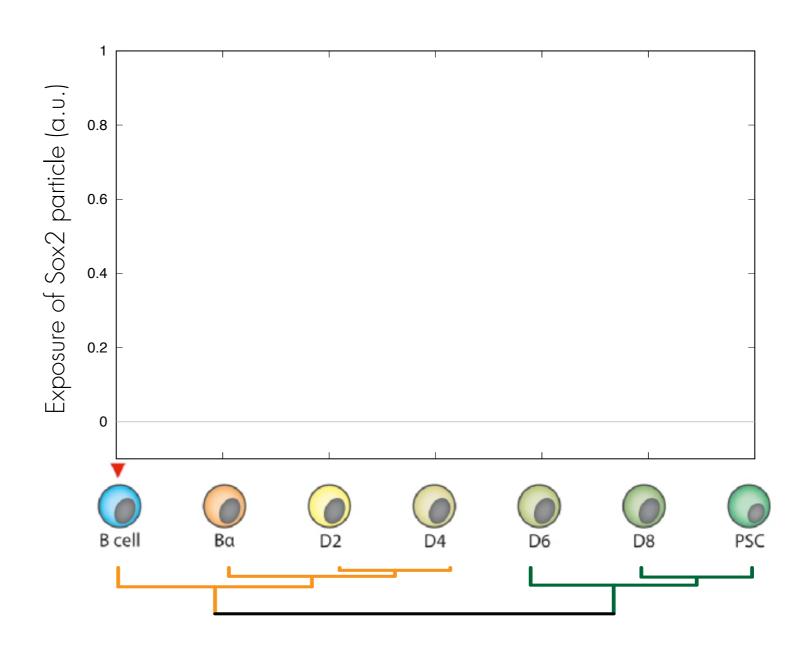
Structural exposure





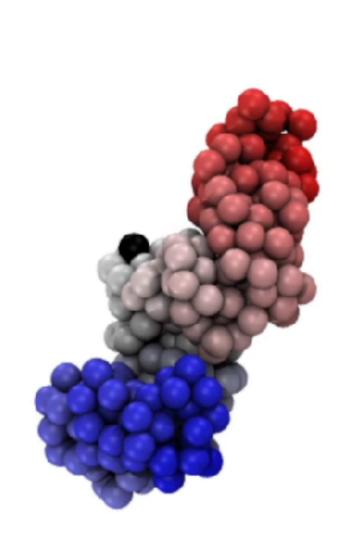
Structural exposure

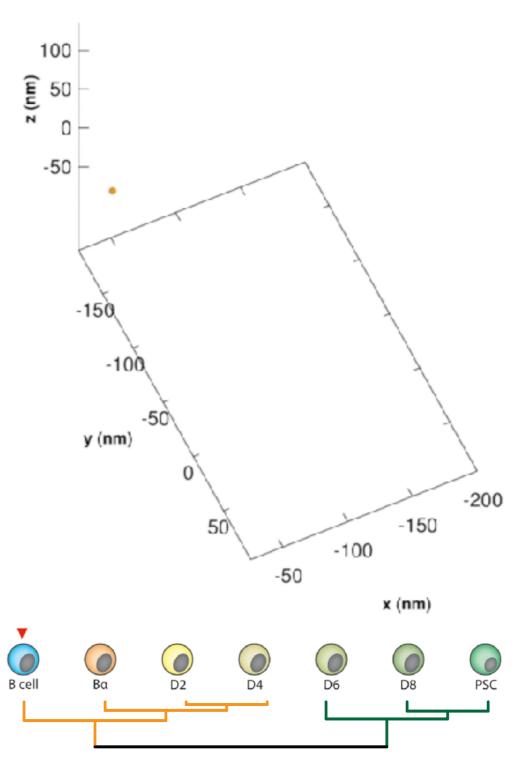




SOX2 locus dynamics changes from B to PSC

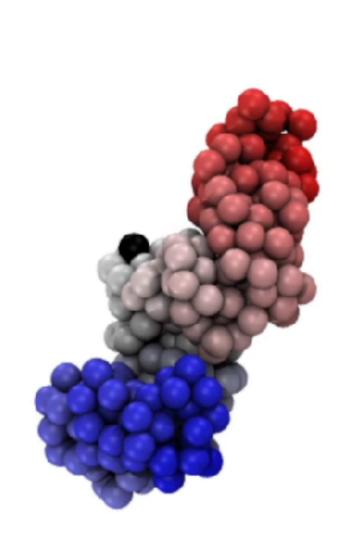
SOX2 displacement

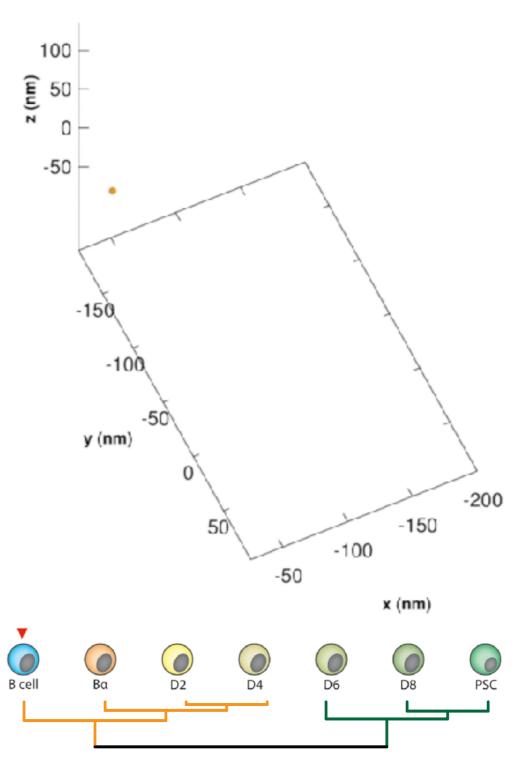




SOX2 locus dynamics changes from B to PSC

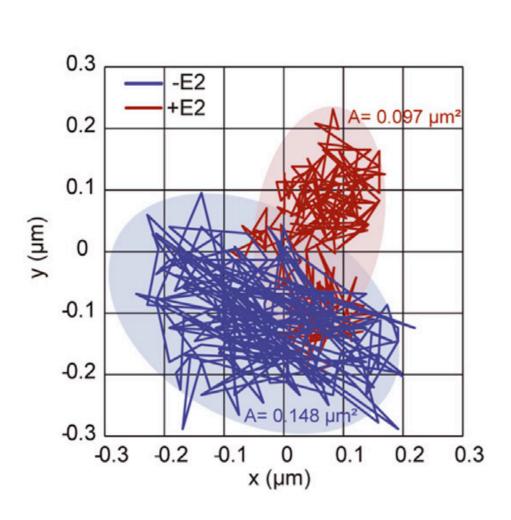
SOX2 displacement





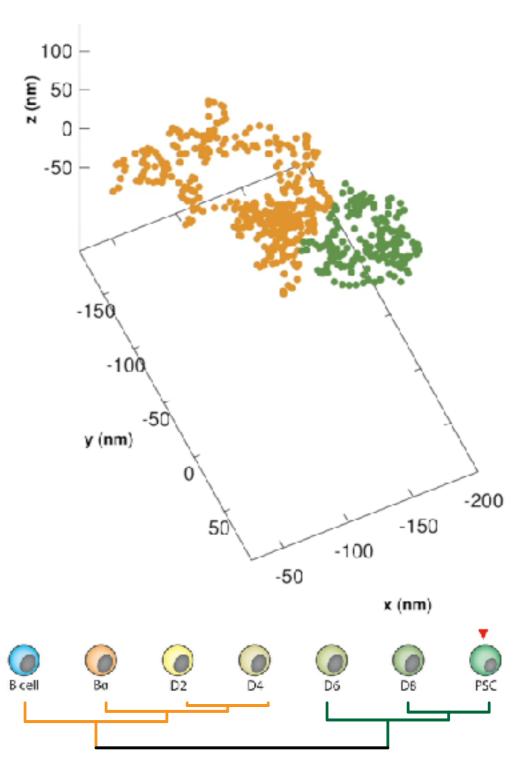
SOX2 locus dynamics changes from B to PSC

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, Blophys J. 113, 1383-1394 (2017).



A "cage" model for transcriptional activation

The Sox2 transcriptional activation is preceded by major structural rearrangements involving the formation of a small "cage" domain.











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Julen Mendieta
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In collaboration with Ralph Stadhouders (Erasmus MC) and Thomas Graf (CRG)

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