

Locus dependent role of CTCF sites in enhancer-promoter transcriptional regulation

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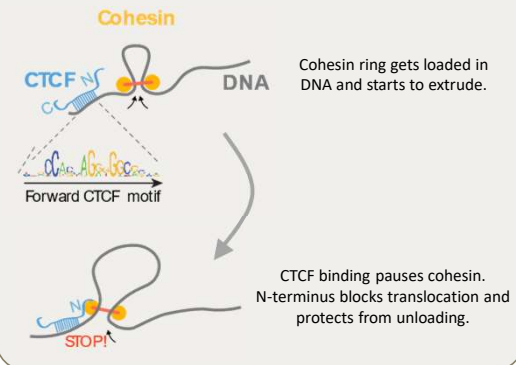
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INTRODUCTION

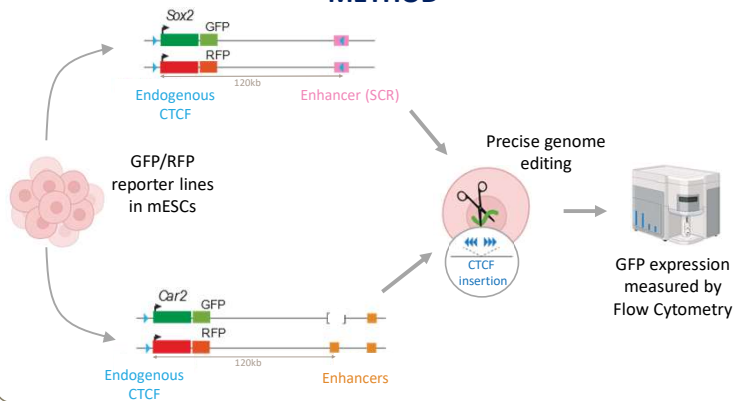
The regulation of communication between enhancers and promoters plays a key role in transcriptional patterning during cell differentiation. When separated by a long distance, the relative 3D positioning of the Cis-Regulatory Elements (CRE) to the promoter relies on the 3D folding of the DNA [1], enabled by the cohesin complex and its cofactors and delimited by CCTC-binding factors (CTCFs) [2]. The role of CTCF sites in gene regulation has only been studied in a handful of loci and its role as an enhancer blocker was recently challenged by a study working on the effect of the CTCF boundary in the *Sox2* locus. Authors reported that the *Sox2* enhancer can bypass artificial insertion of CTCF sites, to regulate the *Sox2* gene [3]. Furthermore, depleting CTCF and the subunits of the cohesin complex (RAD21, WAPL [4]; NIPBL, PDS5 Nora Lab, unpublished) only has a mild effect on *Sox2* expression, indicating loop extrusion is largely dispensable for *Sox2* regulation. In order to identify which genes actually rely on loop extrusion, the Nora lab performed RNA-seq in mouse ES Cells (mESCs) after acute degradation of NIPBL, a protein necessary for the loop extrusion activity but dispensable for the mitotic functions of cohesin (unpublished), and CTCF [5]. Among the down-regulated genes upon depletion, *Car2* has been identified as a CTCF-Cohesin sensitive gene while *Sox2* was only mildly affected (Nora Lab, unpublished).

Following those observations, one of the goals in the Nora Lab is to identify the differences in loop-extrusion sensitiveness between *Car2* and *Sox2* and more generally, to understand how the genomic context may render a given gene sensitive or not to the loop extrusion pathway. During my internship in the Nora Lab, I specifically investigated the role of CTCF sites in the regulation of both *Car2* and *Sox2*.

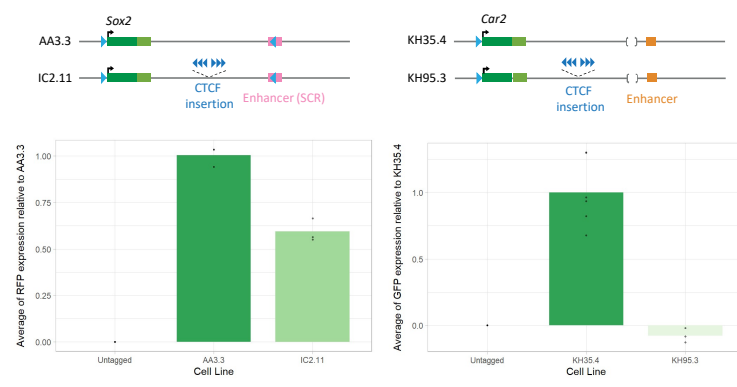
MODEL OF COHESIN-CTCF MEDIATED DNA LOOP EXTRUSION



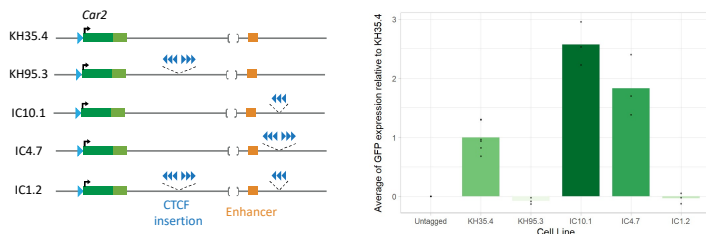
METHOD



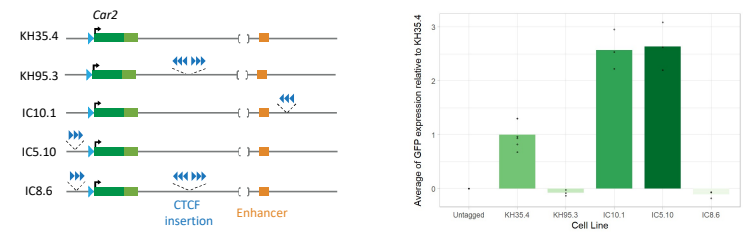
1. CTCF sites insulation strength depends on the genomic context



2. CTCF sites at the enhancer boost *Car2* expression but is not sufficient to bypass intergenic insulation



3. CTCF sites at the promoter boost *Car2* expression but is not sufficient to bypass intergenic insulation



CONCLUSION AND PERSPECTIVES

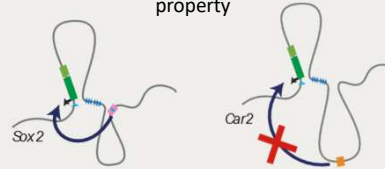
While I did not discover why *Sox2* and *Car2* have different sensitivity to CTCF/cohesin, these data show that CTCF sites can have contrasting effects depending on the nature of the gene (cohesin sensitive or non-sensitive) but also depending on its relative position to the promoter and the enhancers within a single locus. Moreover, it shows that reinforcing CTCF binding in the *Car2* promoter is sufficient to up-regulate its expression. Furthermore, CTCF insulation bypass needs more than the tethering of enhancer or promoter only. One possible explanation is that we need the combination of both a strong CTCF site at the promoter or at the enhancer in pair to enable the insulation bypass.

In future experiments, it would be interesting to test the above hypothesis by creating a triple CTCF insertion at the promoter, the enhancer and the intergenic loci. Finally to properly explore the hypothesis of loop stacking, the Nora lab will look at the 3D conformation of some of cell lines I have generated with a DNA FISH chromatin tracing approach by microscopy invented by collaborators [6].

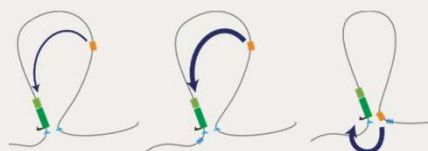
Overall, these results provide new insights into the role played by CTCF sites in enhancer-promoter communication and open new sides of transcriptional regulation to be explored.

GRAPHICAL ABSTRACT

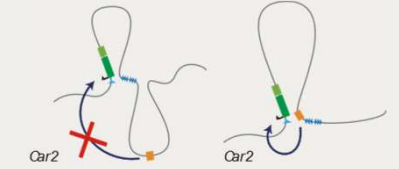
Locus-dependent CTCF insulating property



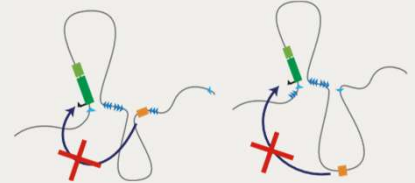
Strong CTCF sites at promoter or enhancer increase *Car2* activity



A same CTCF site, 2 contrasting roles



No insulation bypass even with strong CTCF sites at promoter or enhancer



References

- Zuin, J. et al. (2022) 'Nonlinear control of transcription through enhancer-promoter interactions', *Nature*, 604(7906), pp. 571-577. Available at: <https://doi.org/10.1038/s41586-022-04570-y>.
- Nora, E.P. et al. (2020) 'Molecular basis of CTCF binding polarity in genome folding', *Nature Communications*, 11(1), p. 5612. Available at: <https://doi.org/10.1038/s41467-020-19283-x>.
- Chakraborty, S. et al. (2023) 'Enhancer-promoter interactions can bypass CTCF-mediated boundaries and contribute to phenotypic robustness', *Nature Genetics*, 55(2), pp. 280-290. Available at: <https://doi.org/10.1038/s41588-022-01295-6>.
- Liu, N.Q. et al. (2021) 'WAPL maintains a cohesin loading cycle to preserve cell-type specific distal gene regulation', *Nature genetics*, 53(1), pp. 100-109. Available at: <https://doi.org/10.1038/s41588-020-00744-4>.
- Nora, E.P. et al. (2017) 'Targeted Degradation of CTCF Decouples Local Insulation of Chromosome Domains from Genomic Compartmentalization', *Cell*, 169(5), pp. 930-944.e22. Available at: <https://doi.org/10.1016/j.cell.2017.05.004>.
- Mateo, L.J. et al. (2019) 'Visualizing DNA folding and RNA in embryos at single-cell resolution', *Nature*, 568(7750), pp. 49-54. Available at: <https://doi.org/10.1038/s41586-019-1035-4>.