



Distinct structural transitions of chromatin topological domains correlate with coordinated hormone-induced gene regulation

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CNAG-CRG · ICREA

<http://marciuslab.org>  
<http://3DGenomes.org>  
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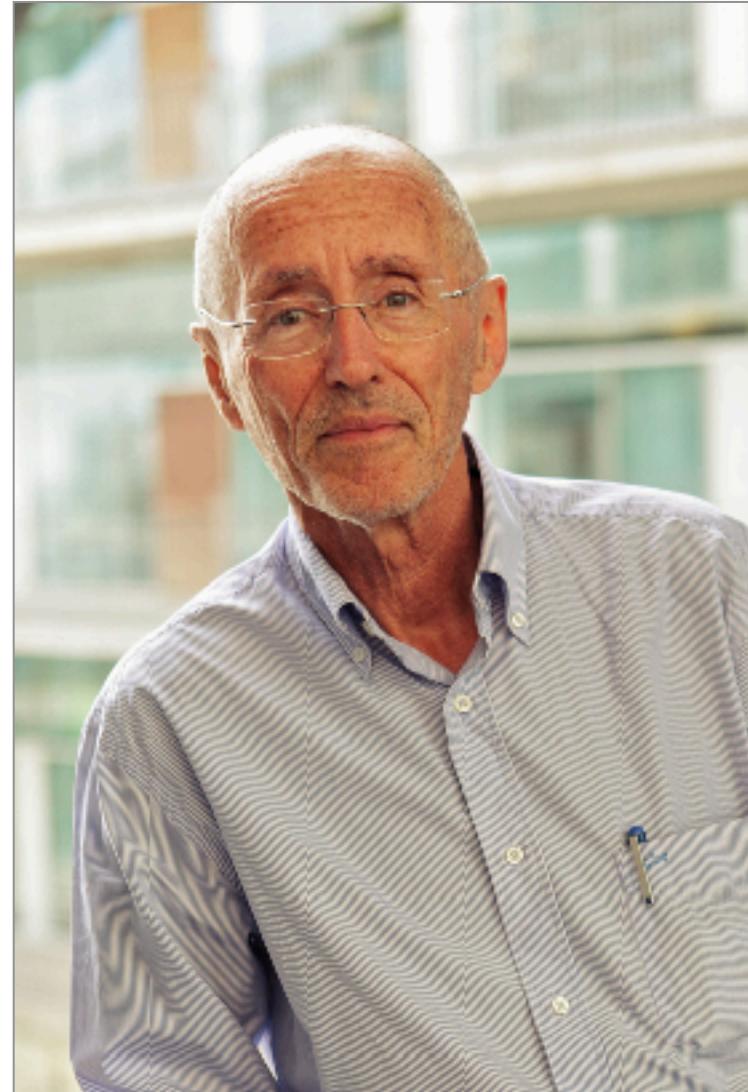
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**François Serra**  
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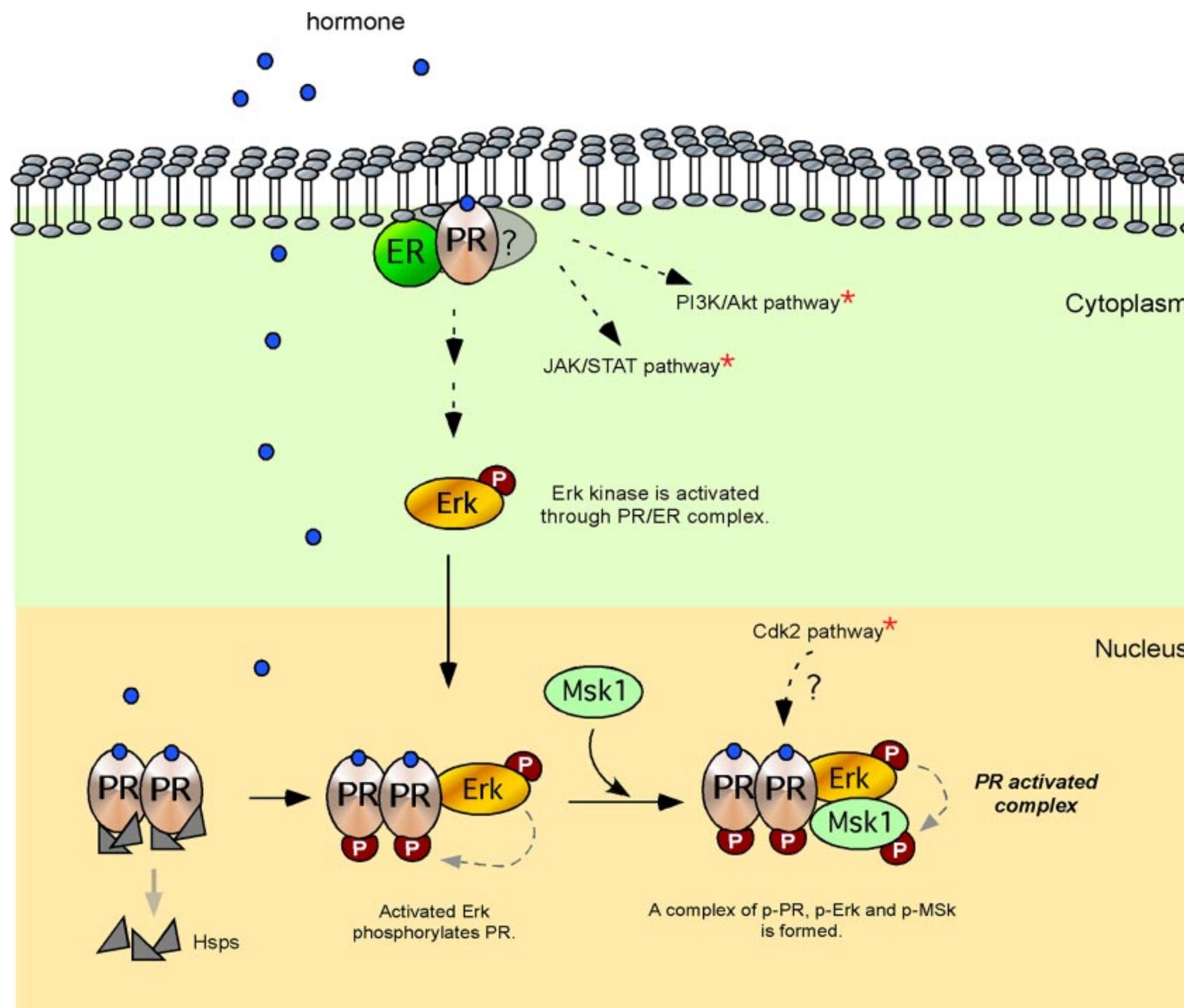


**François le Dily**  
CRG



**Miguel Beato**  
CRG

# Progesterone-regulated transcription in breast cancer



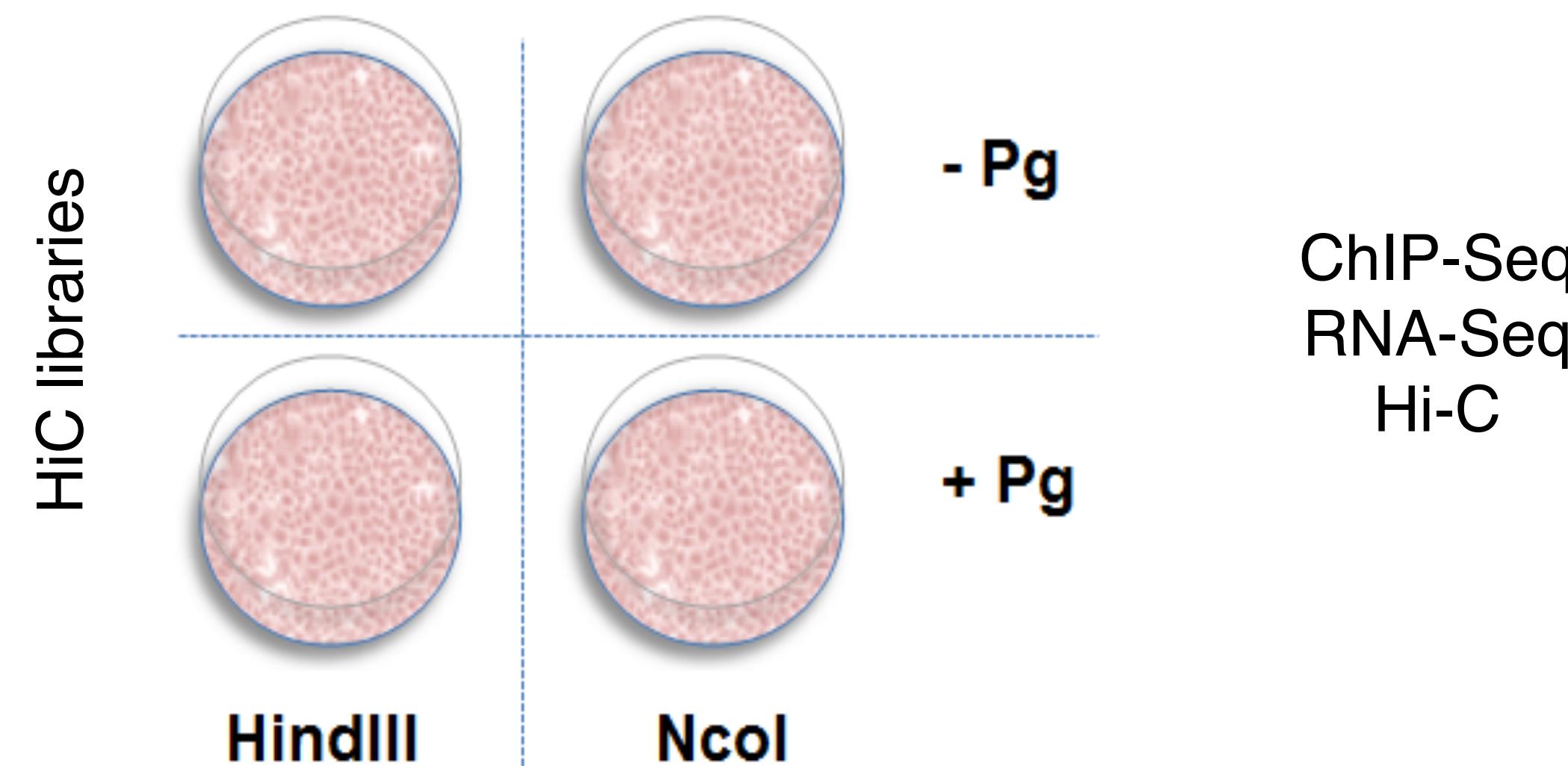
> 2,000 genes Up-regulated  
> 2,000 genes Down-regulated

**Regulation in 3D?**

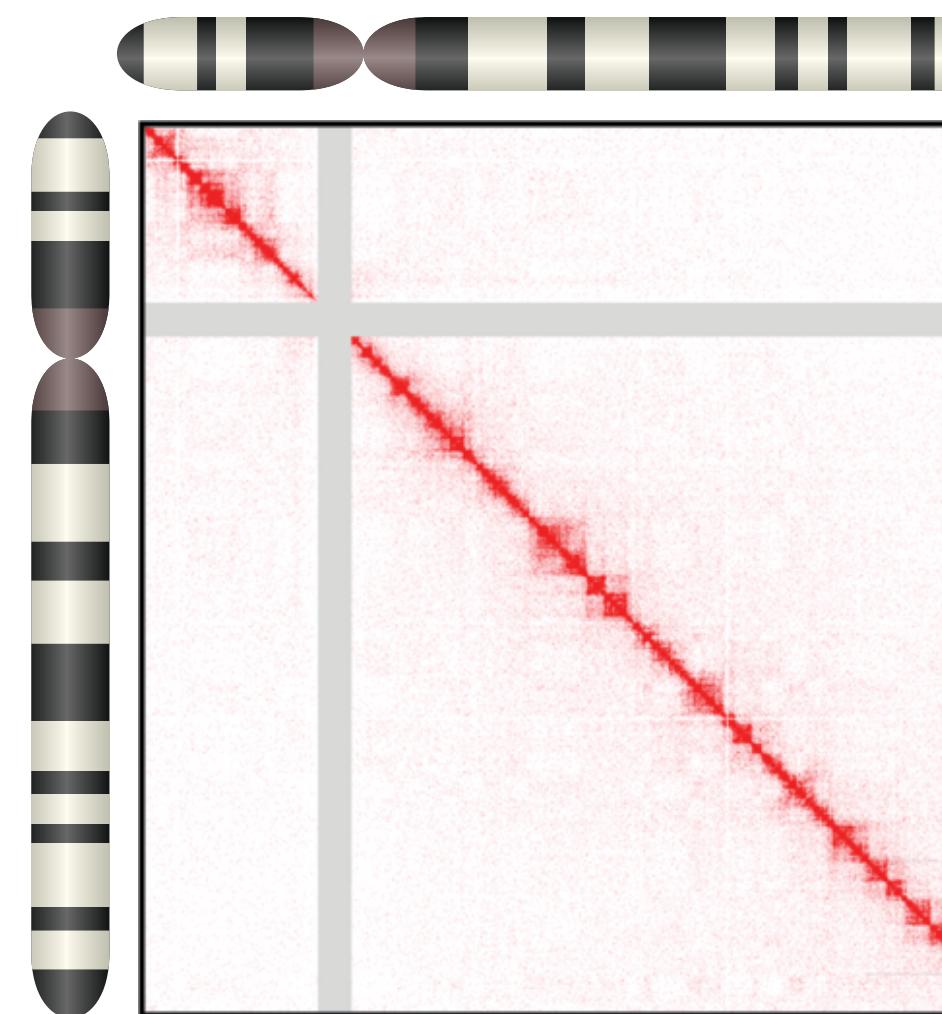
Vicent *et al* 2011, Wright *et al* 2012, Ballare *et al* 2012

Le Dily, F. et al. Genes & Dev (2014)

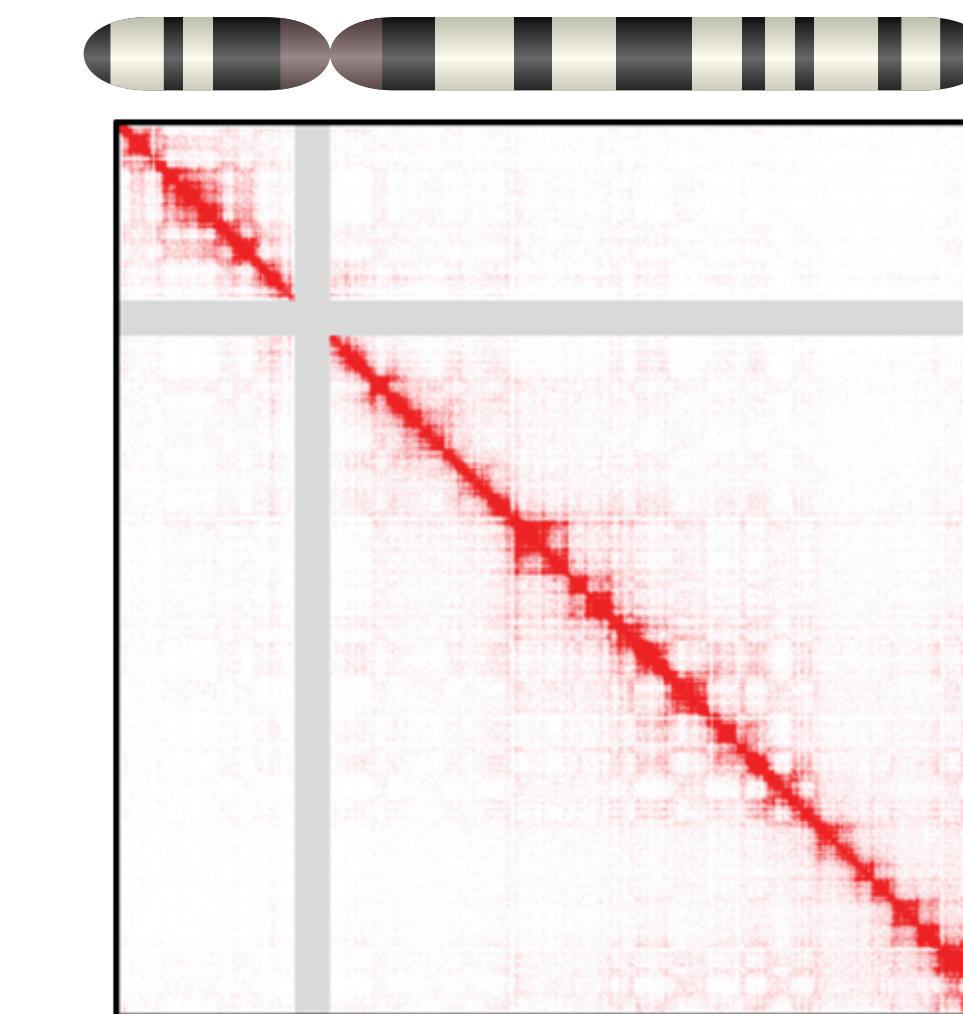
# Experimental design



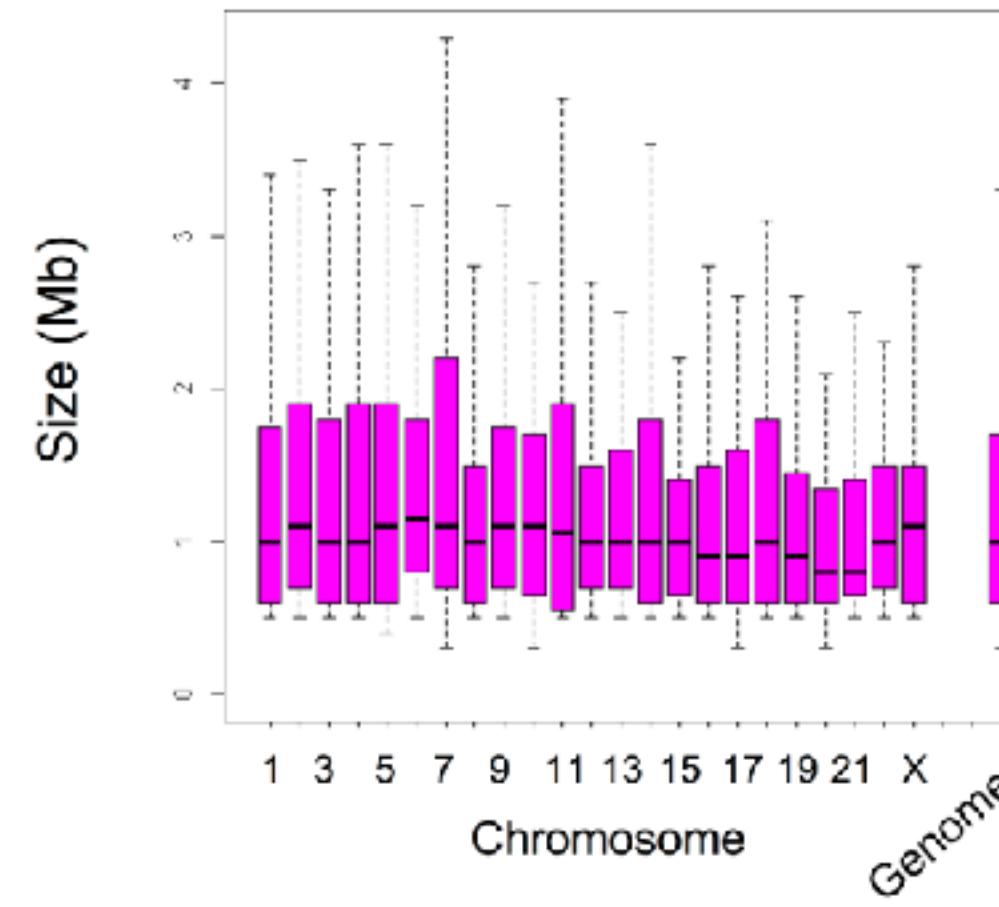
Chr.18 (Hind III)



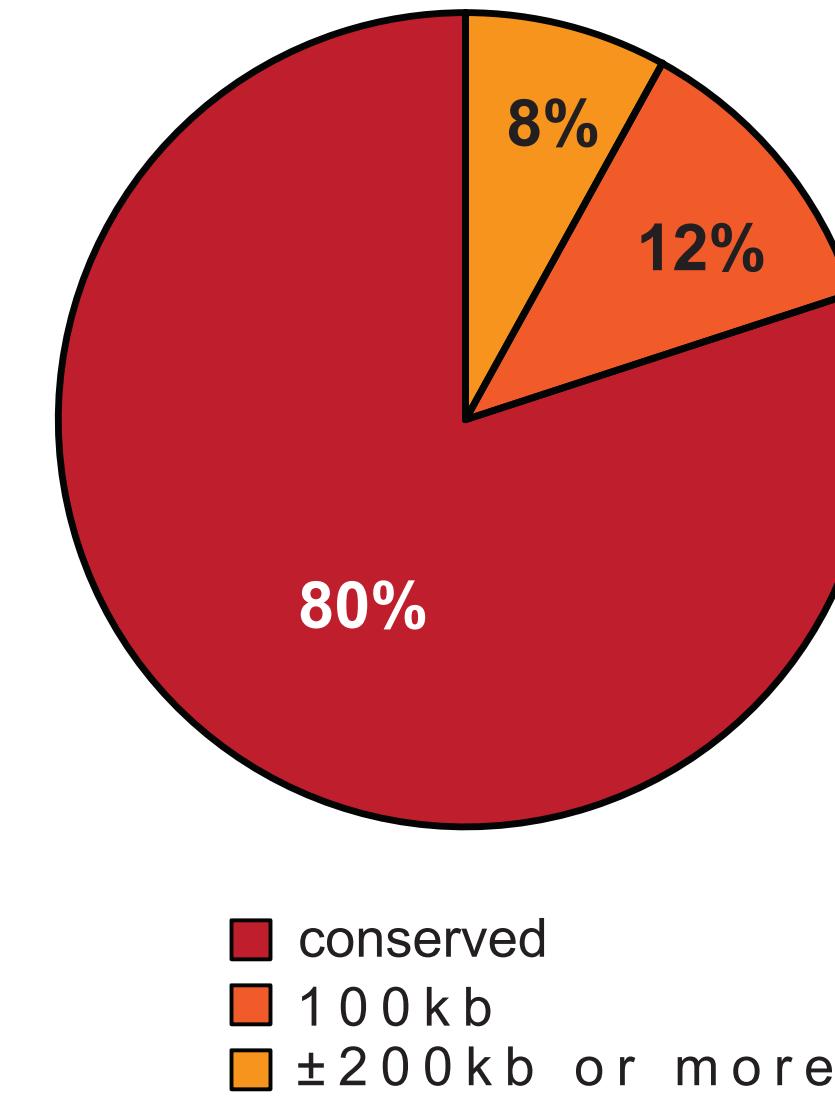
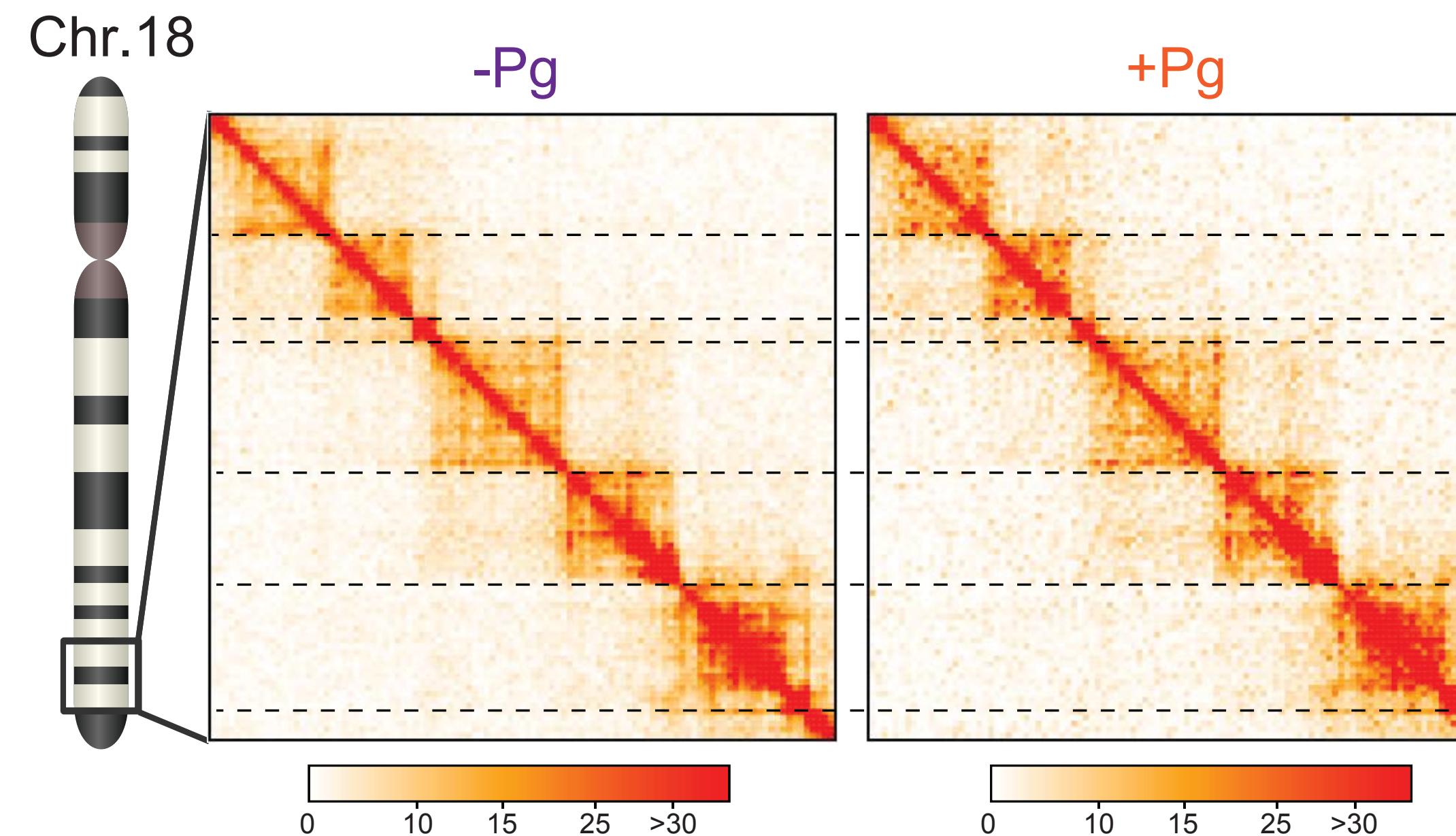
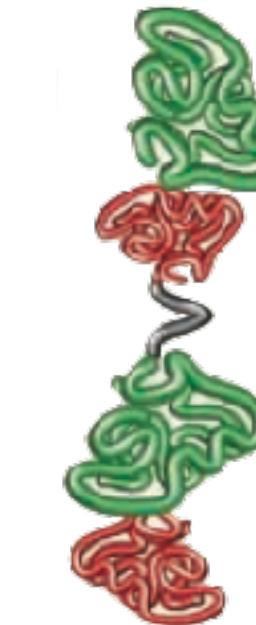
Chr.18 (Ncol)



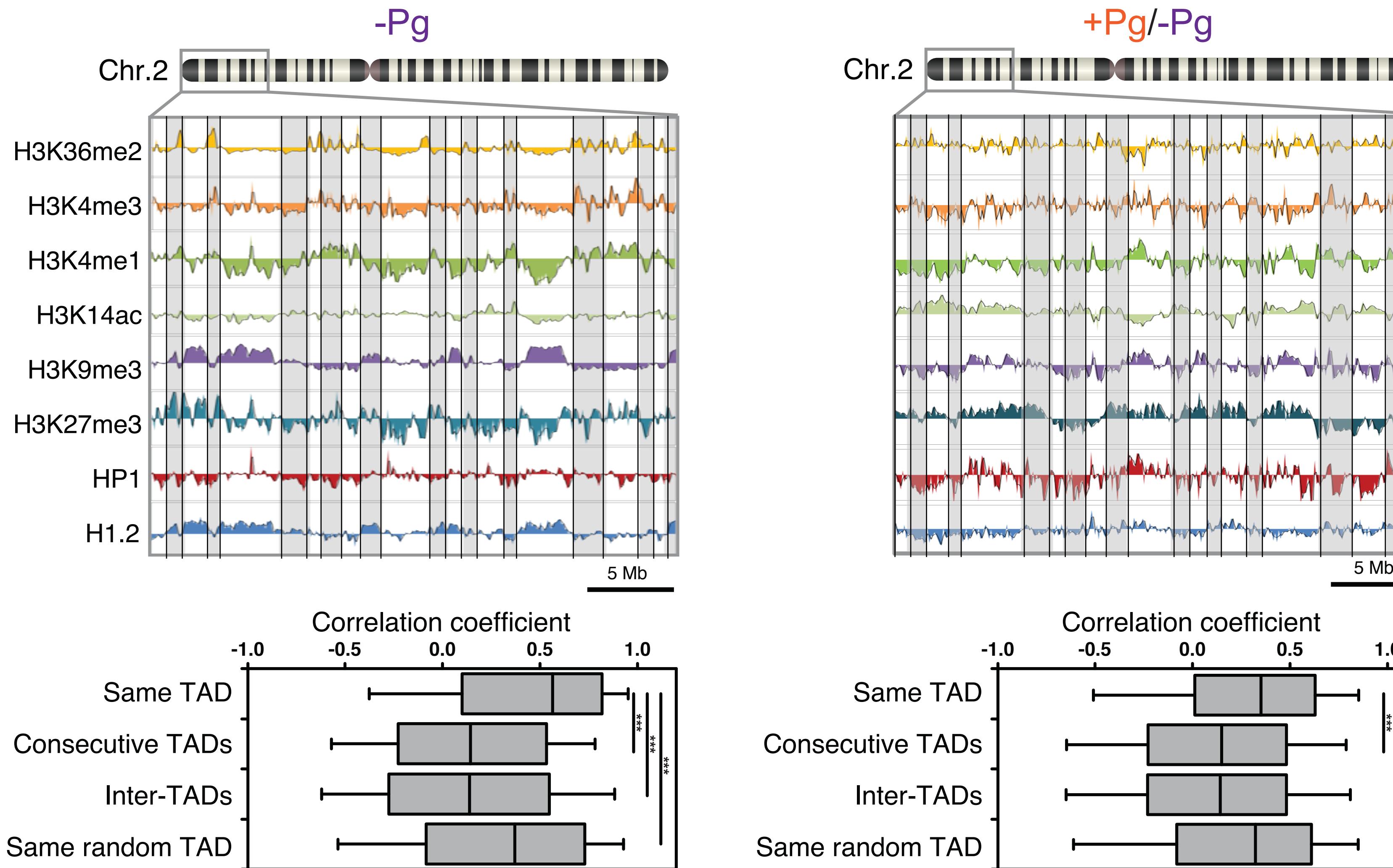
# Are there TADs? how robust?



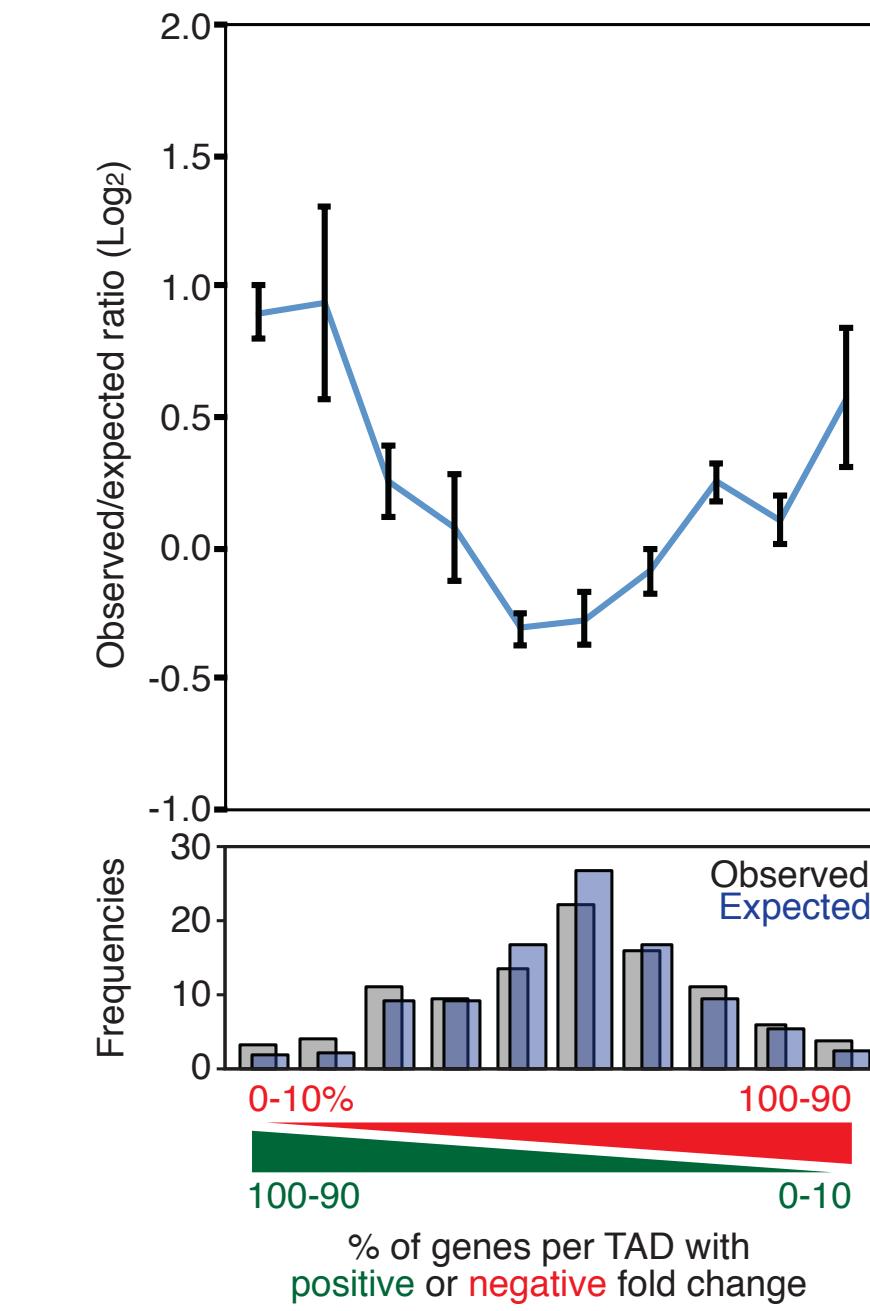
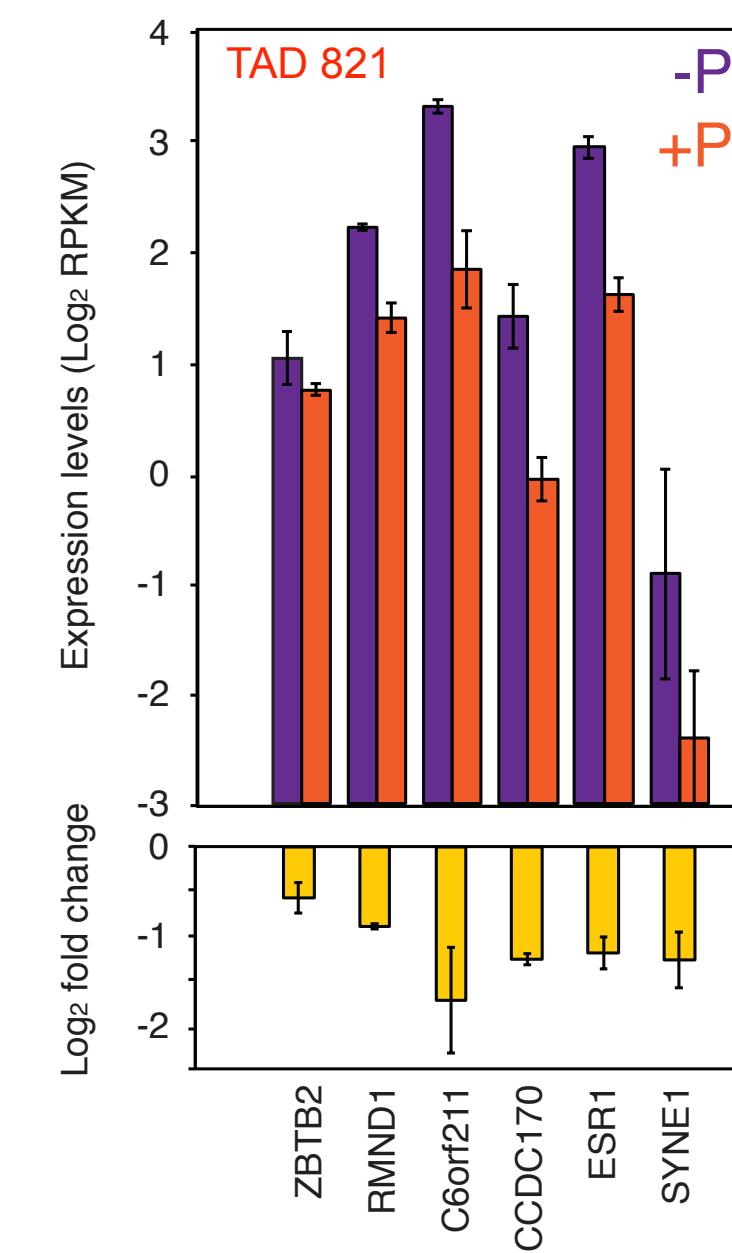
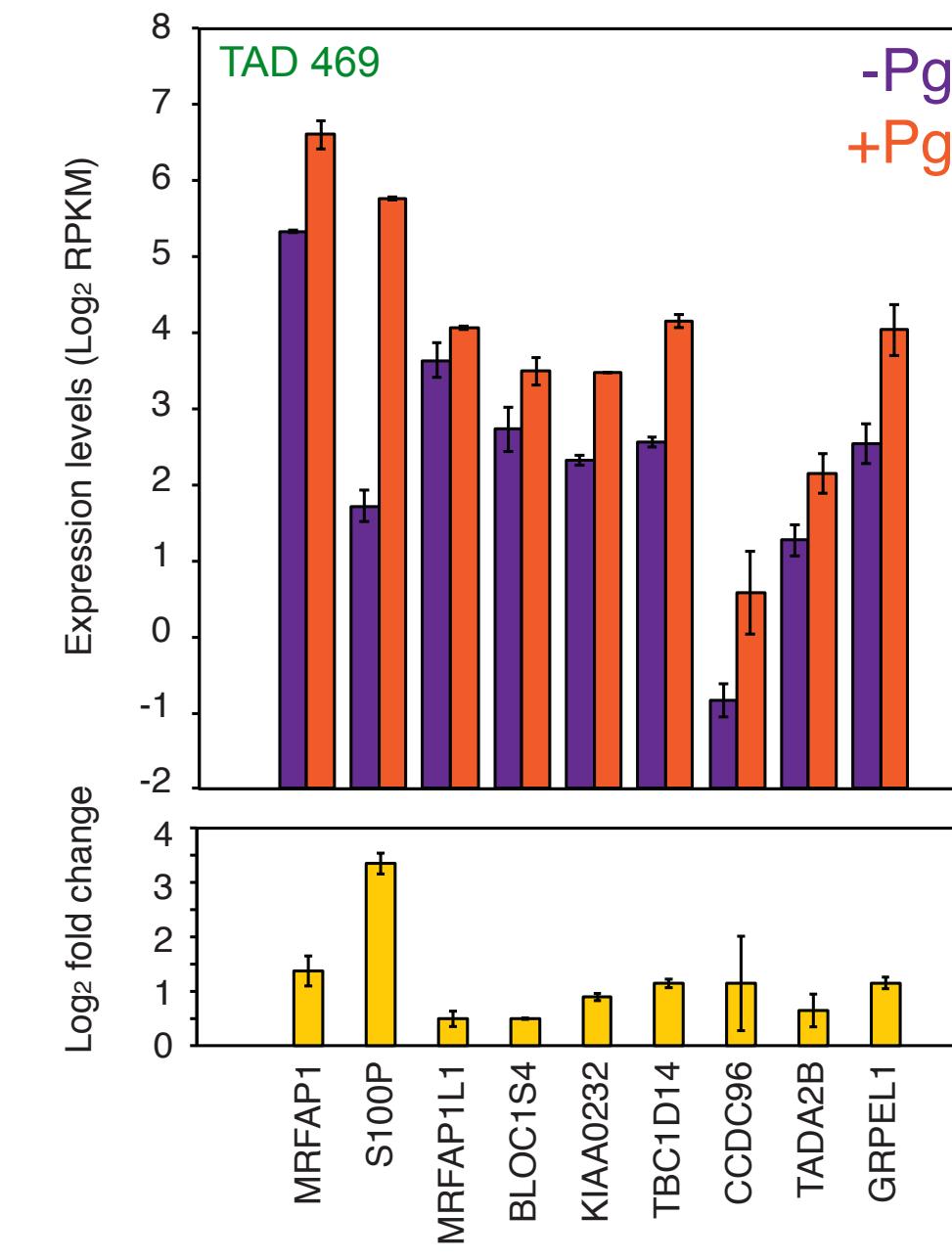
>2,000 detected TADs



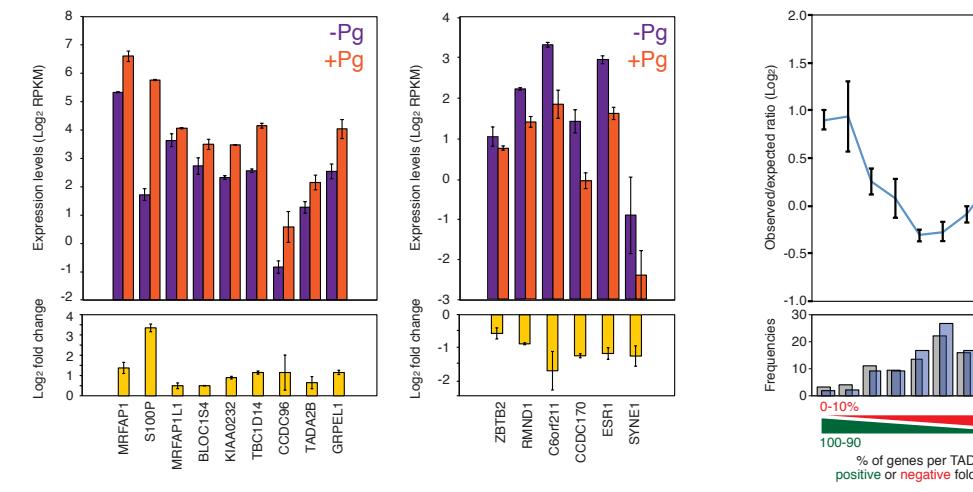
# Are TADs homogeneous?



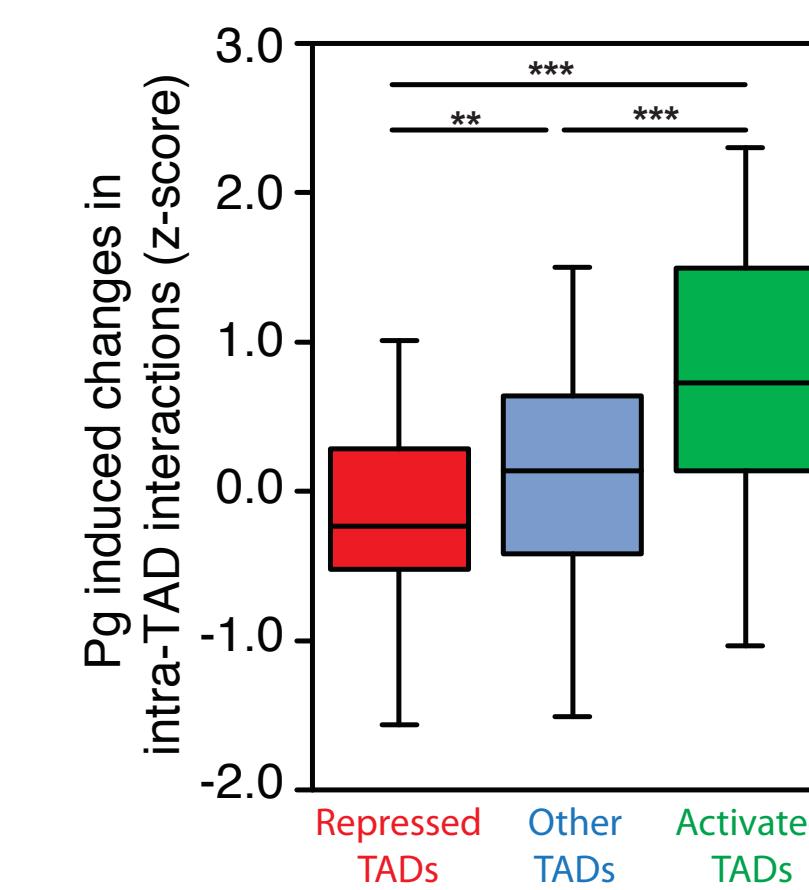
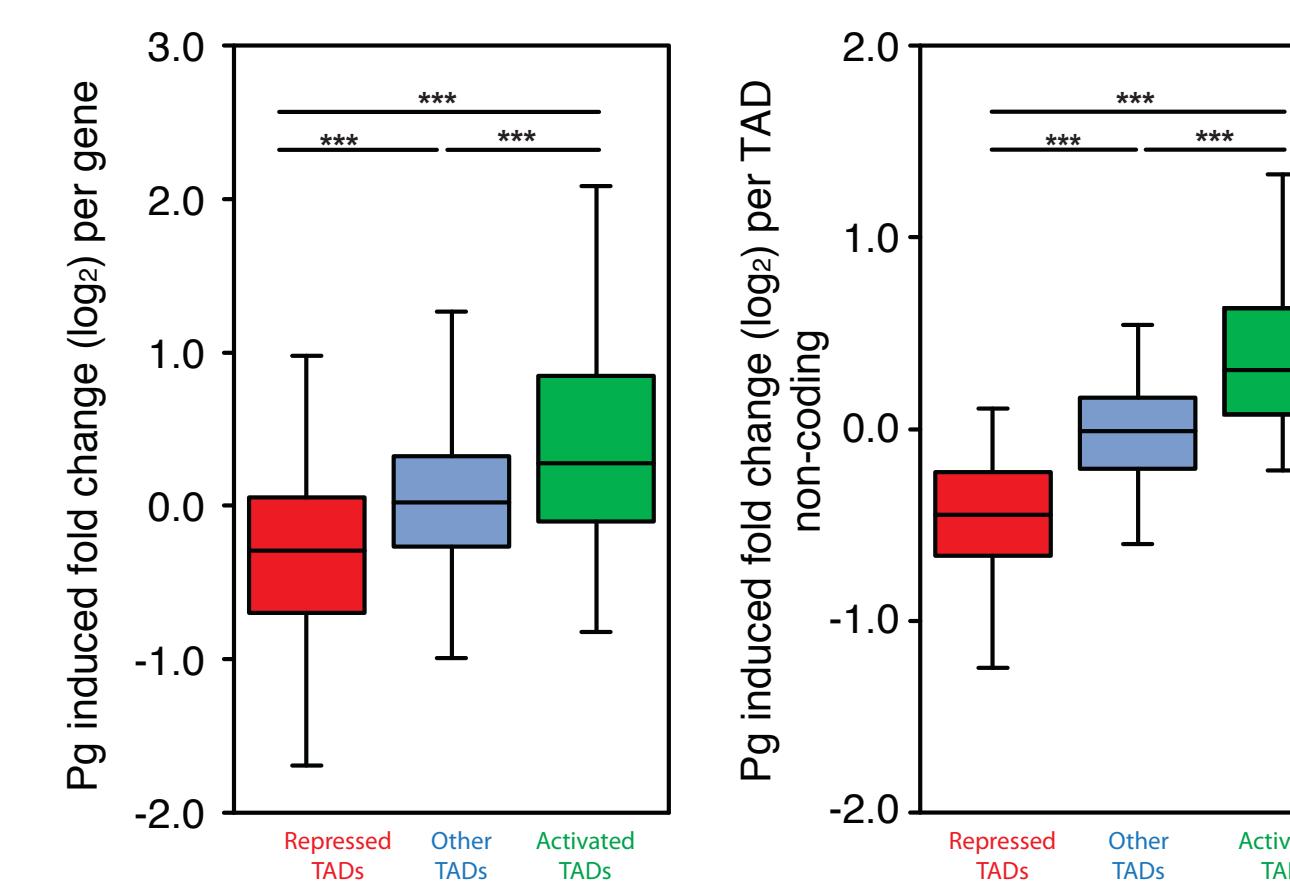
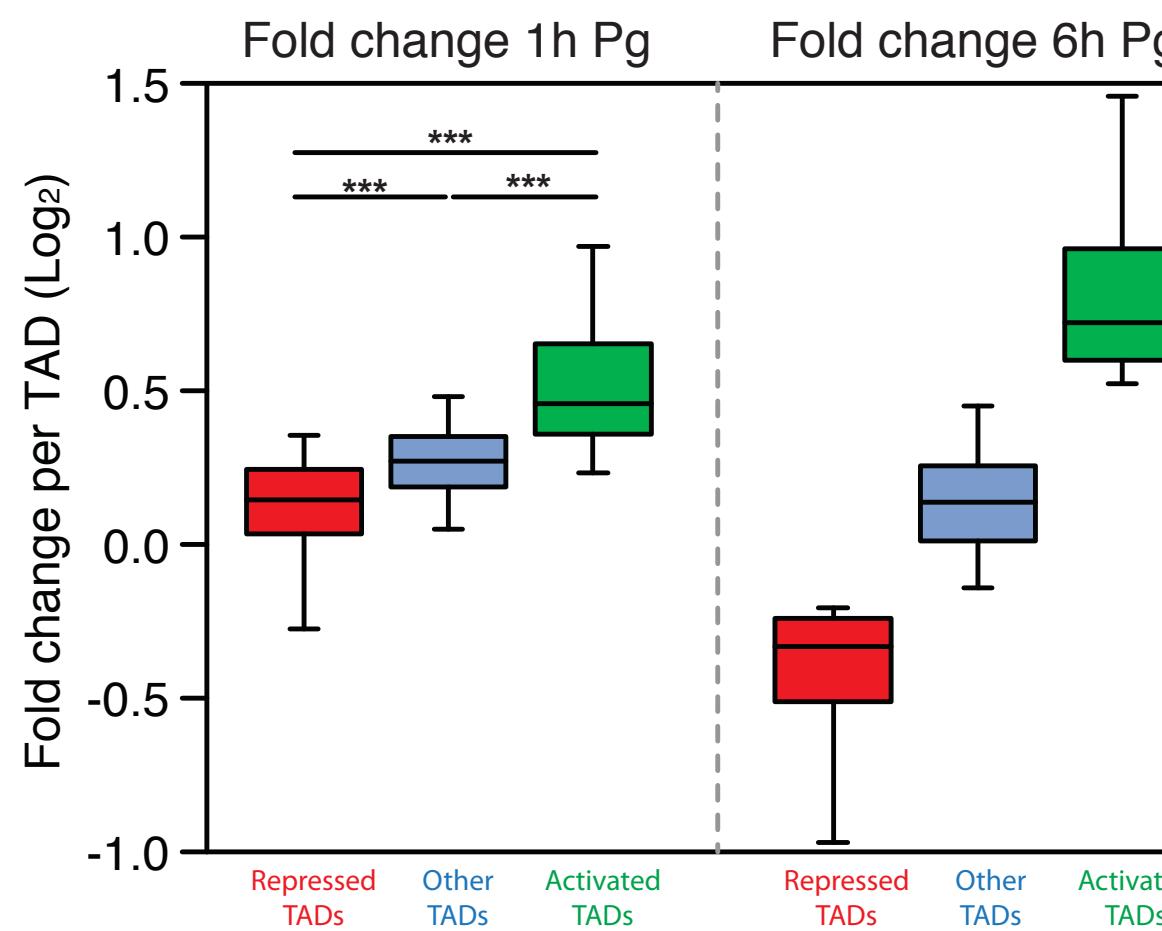
# Do TADs respond differently to Pg treatment?



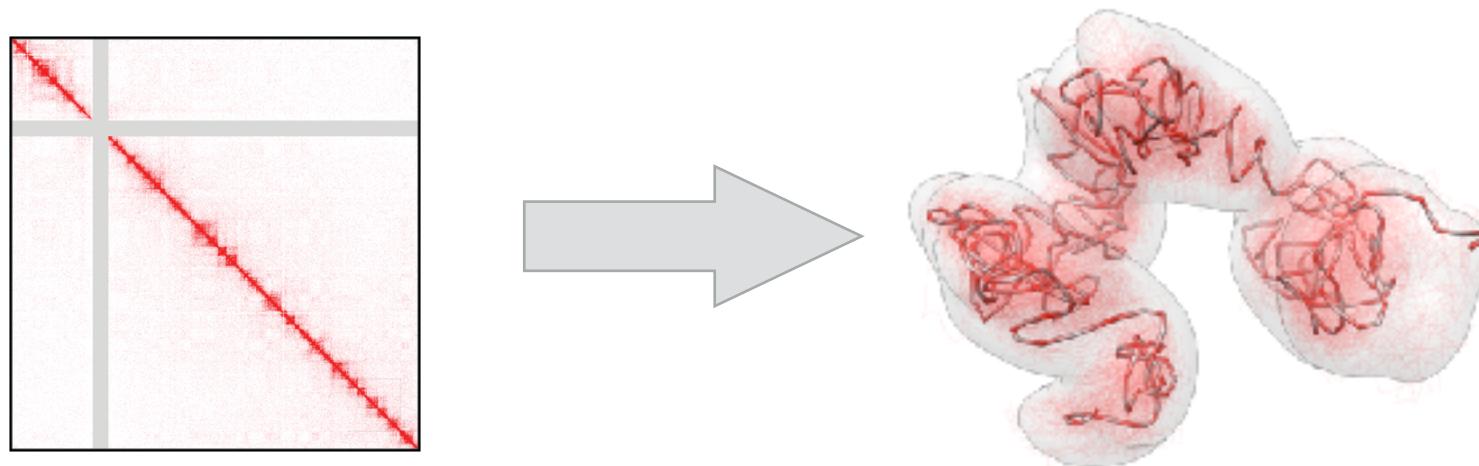
# Do TADs respond differently to Pg treatment?



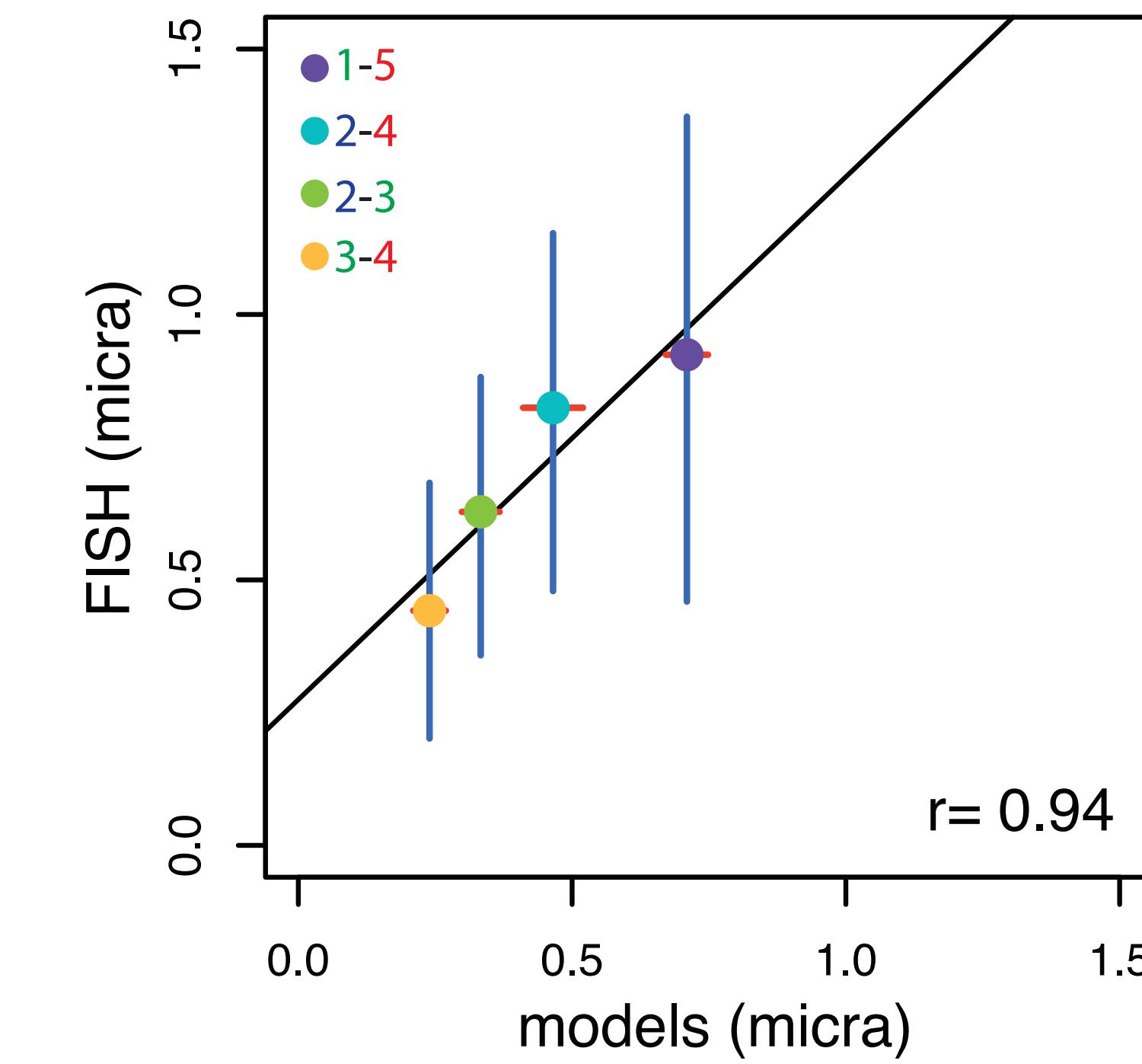
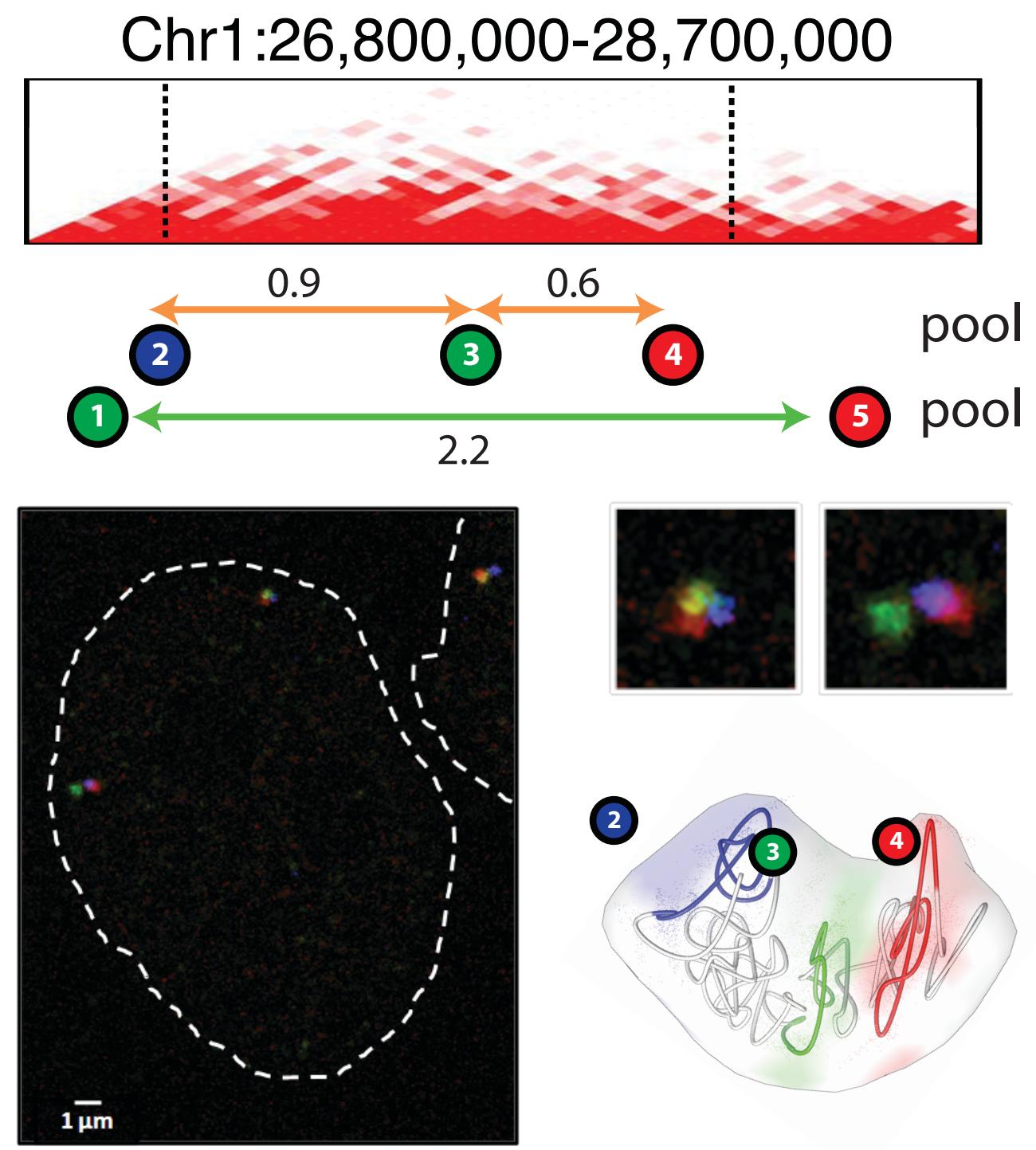
Pg induced fold change per TAD (6h)



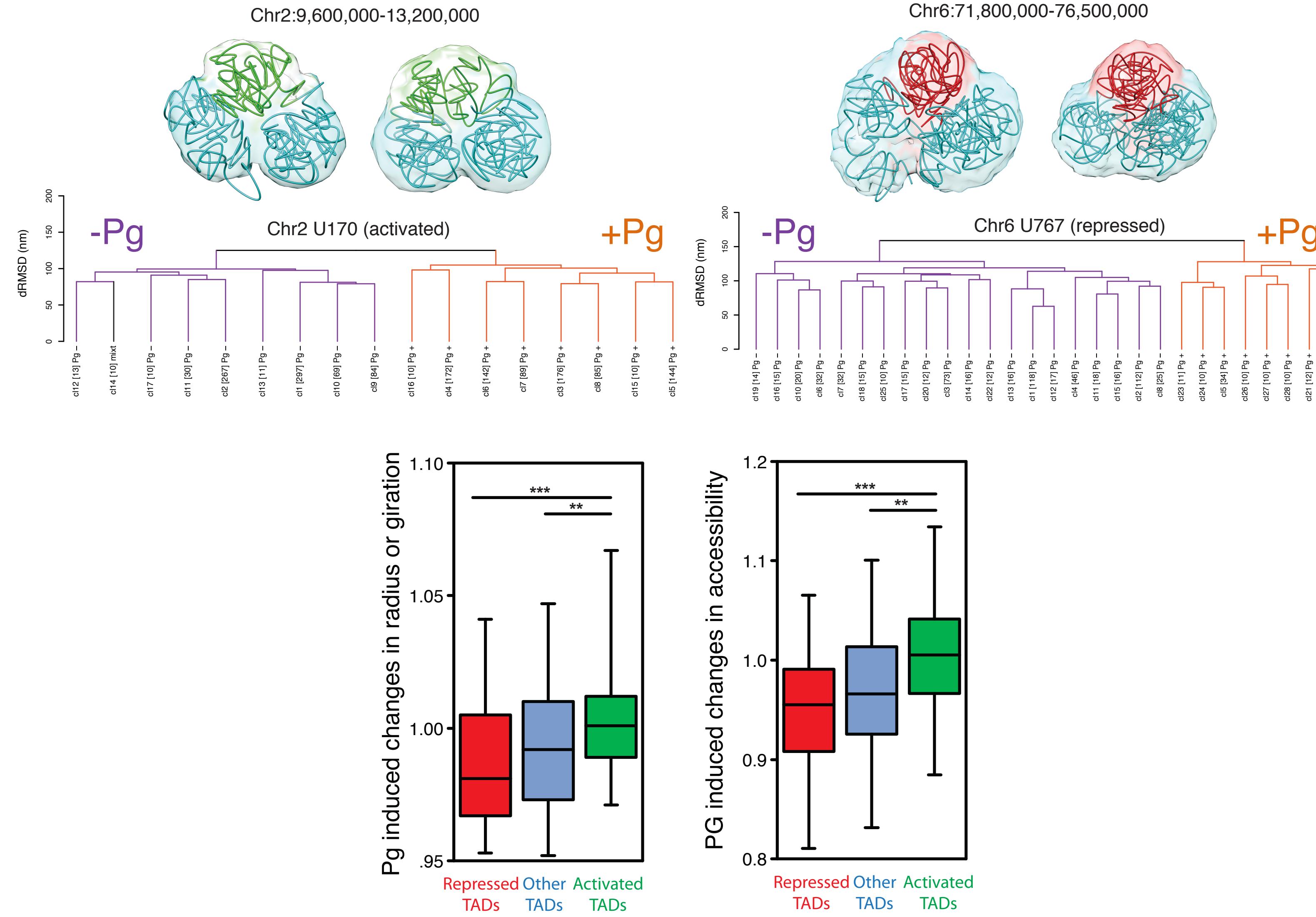
# Modeling 3D TADs



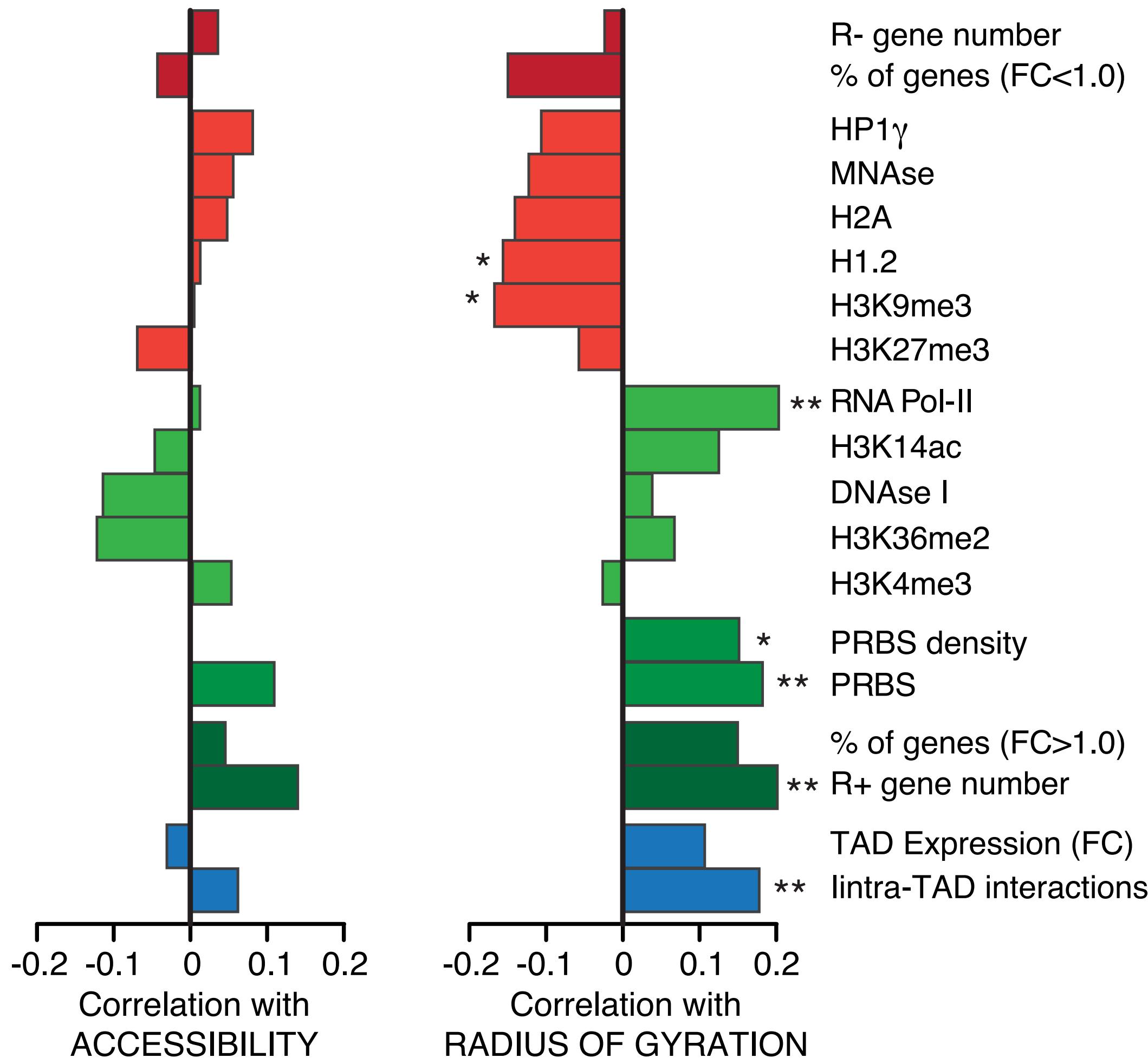
61 genomic regions containing 209 TADs covering 267Mb

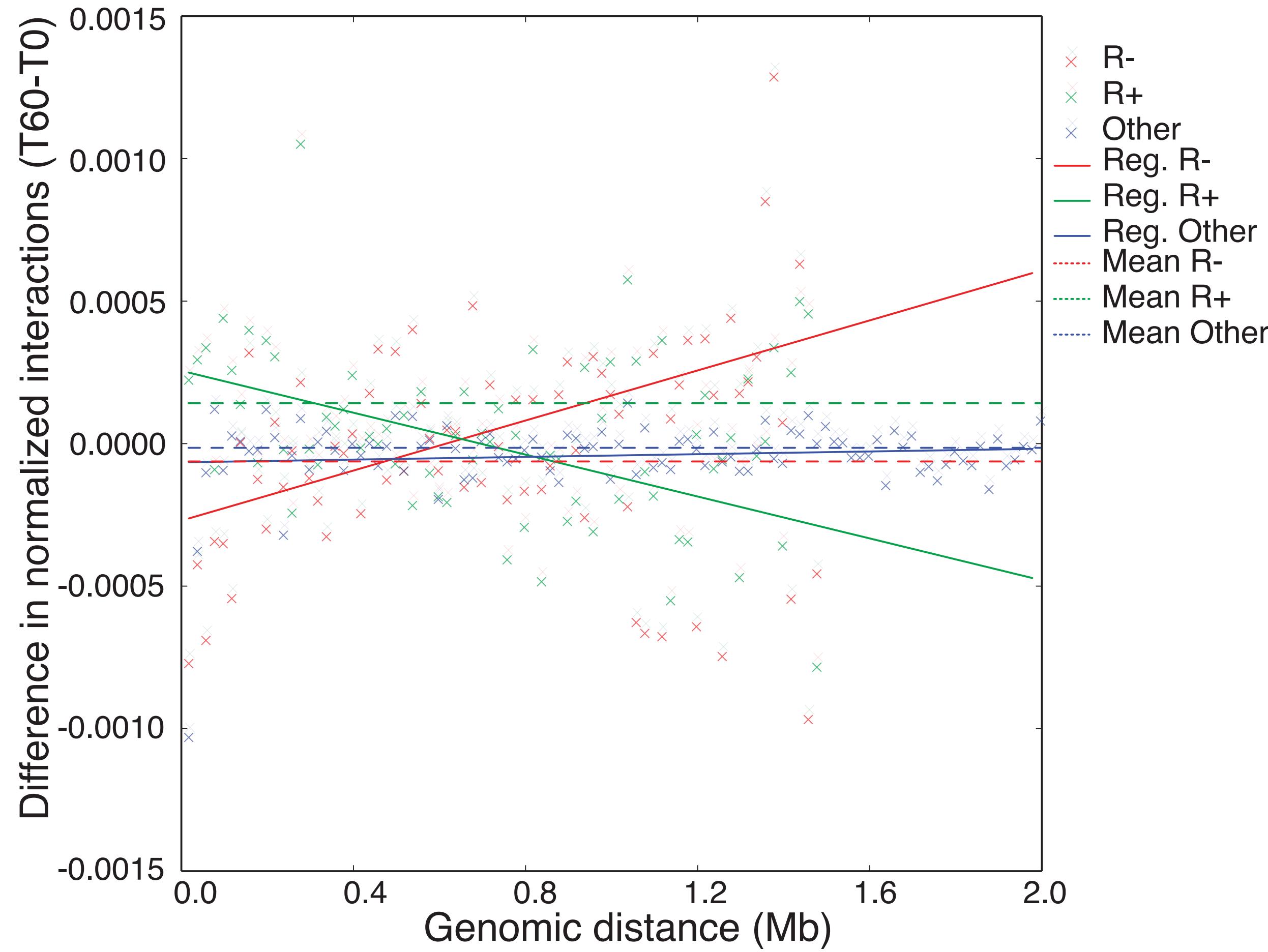
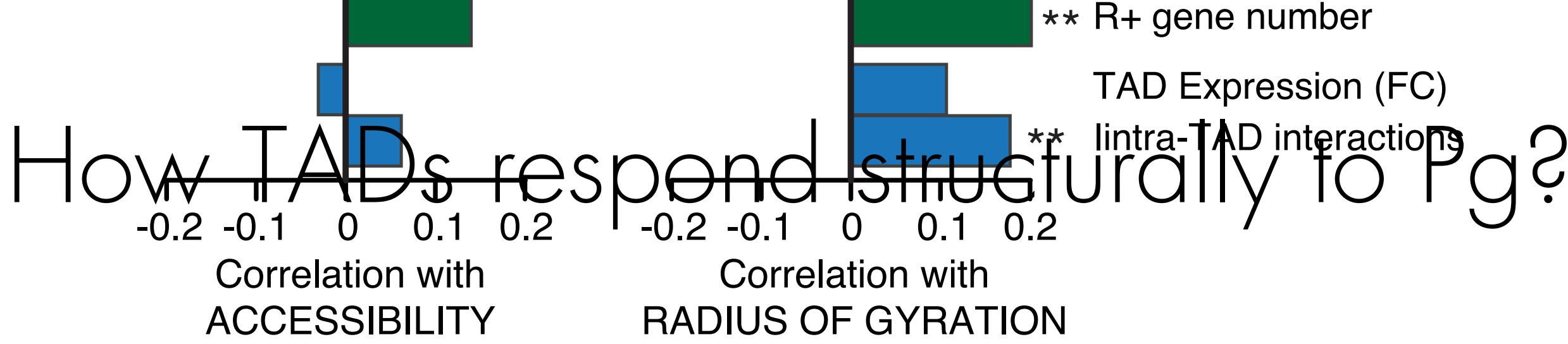


# How TADs respond structurally to Pg?



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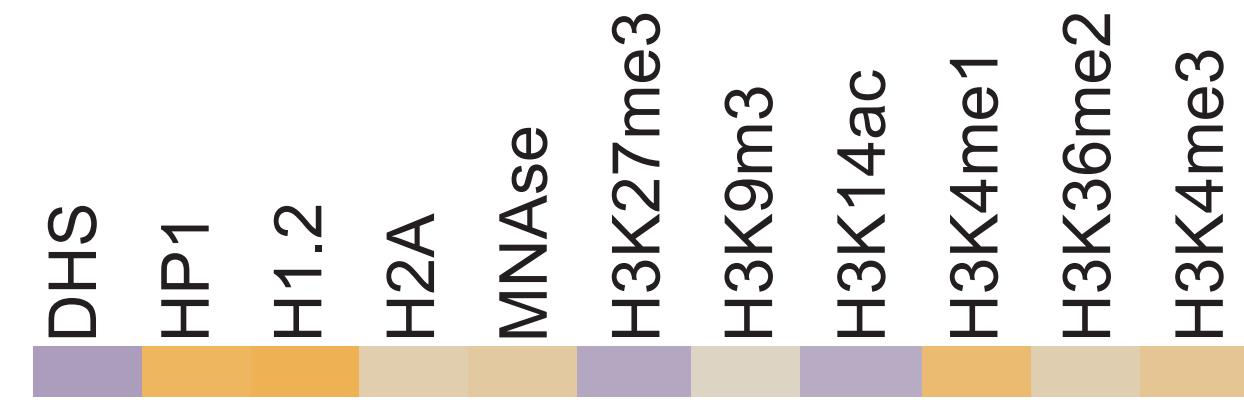
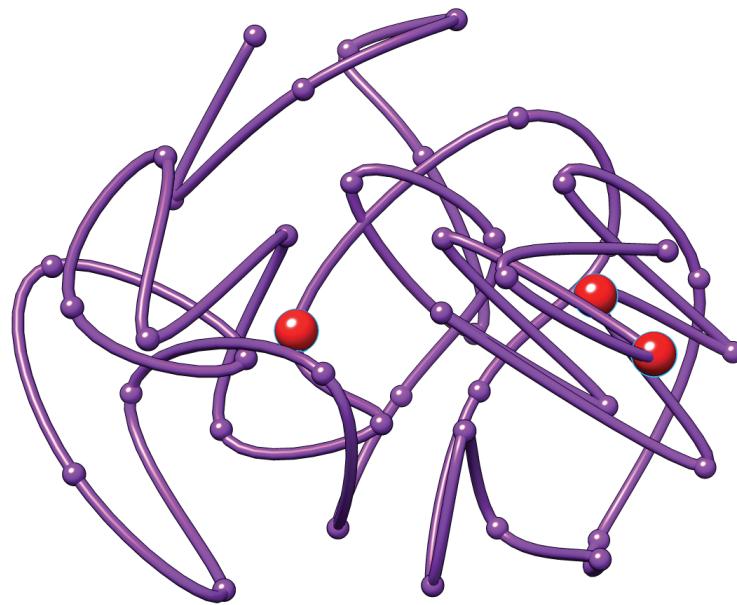




# Model for TAD regulation

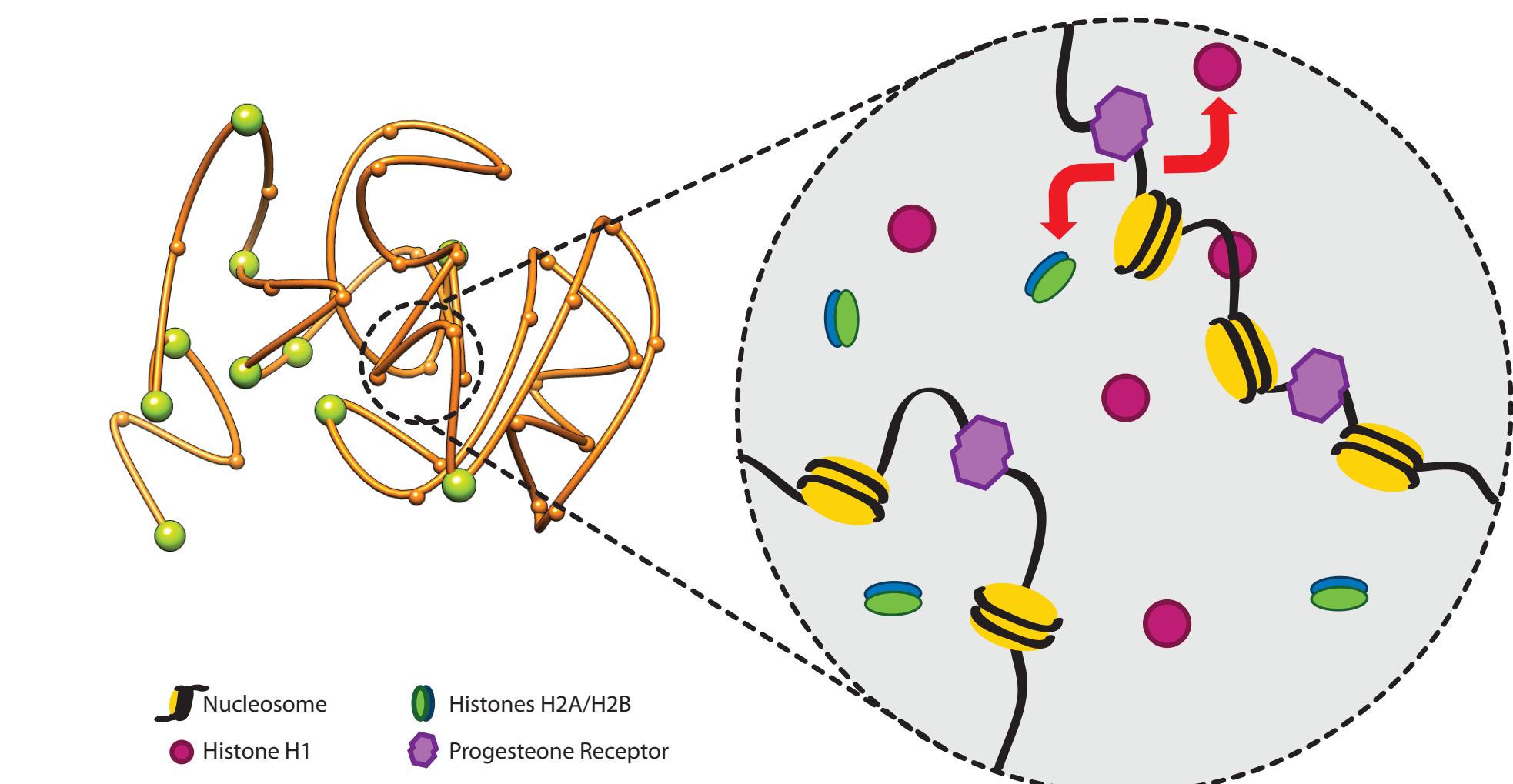
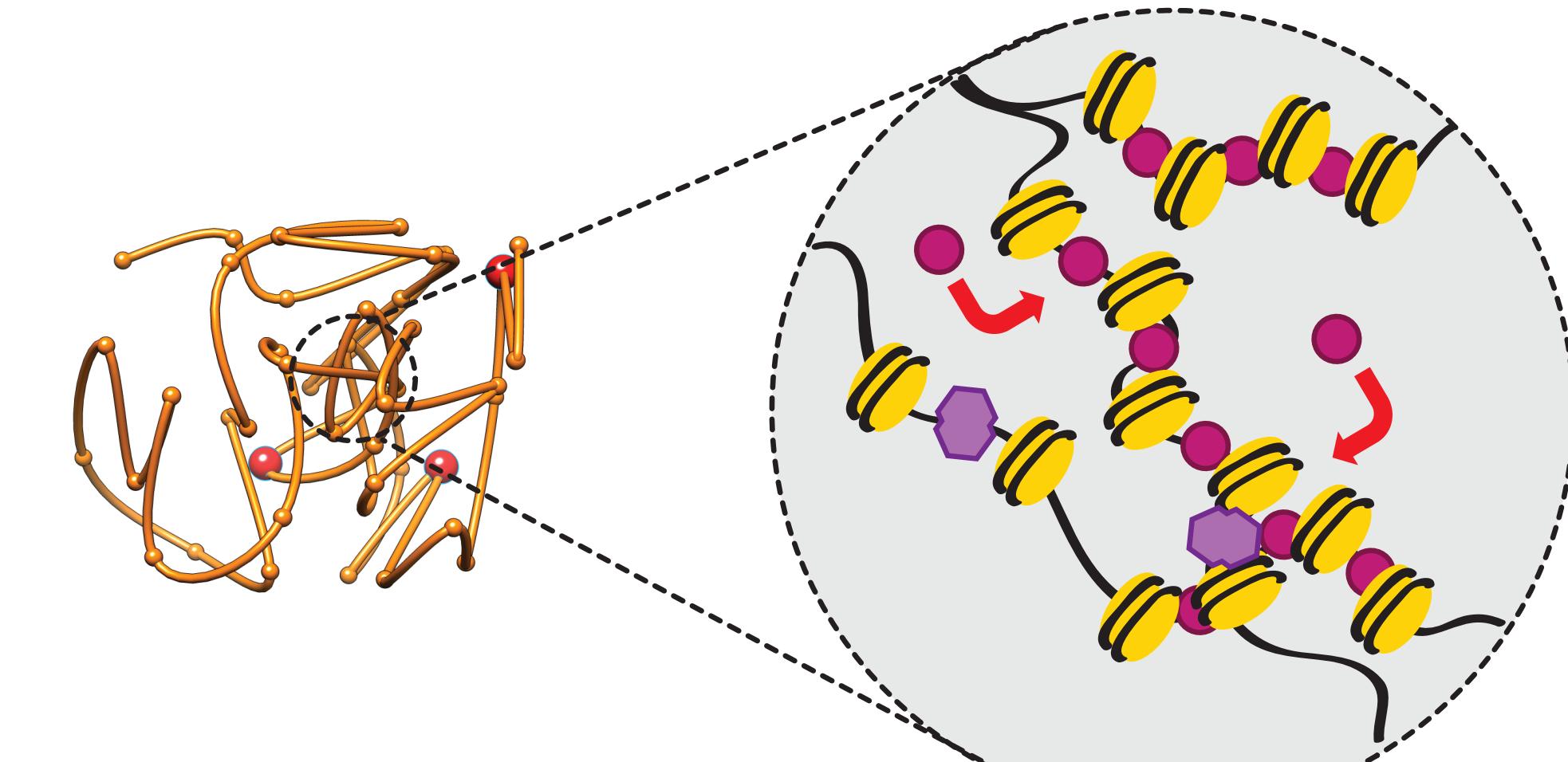
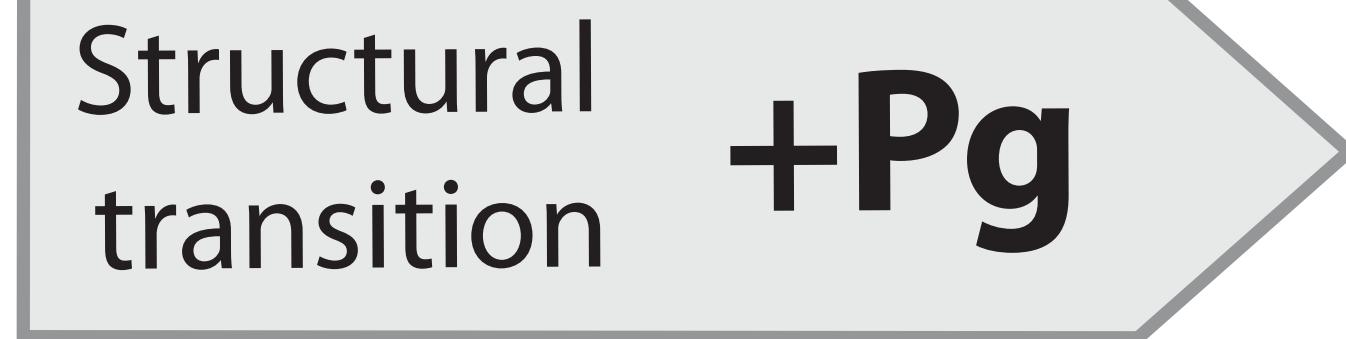
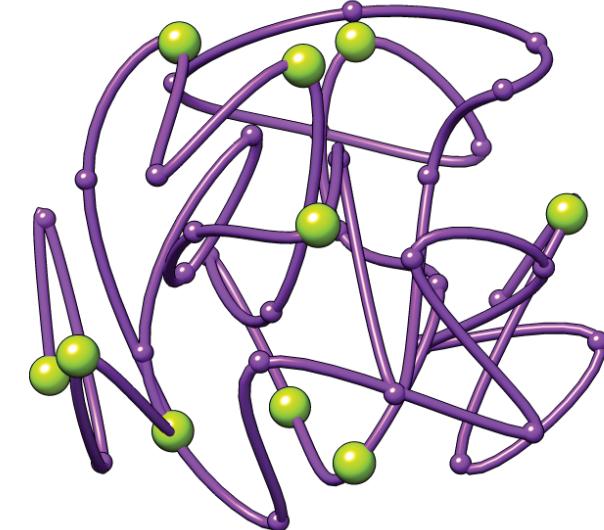
## Repressed TAD

chr1 U41



## Activated TAD

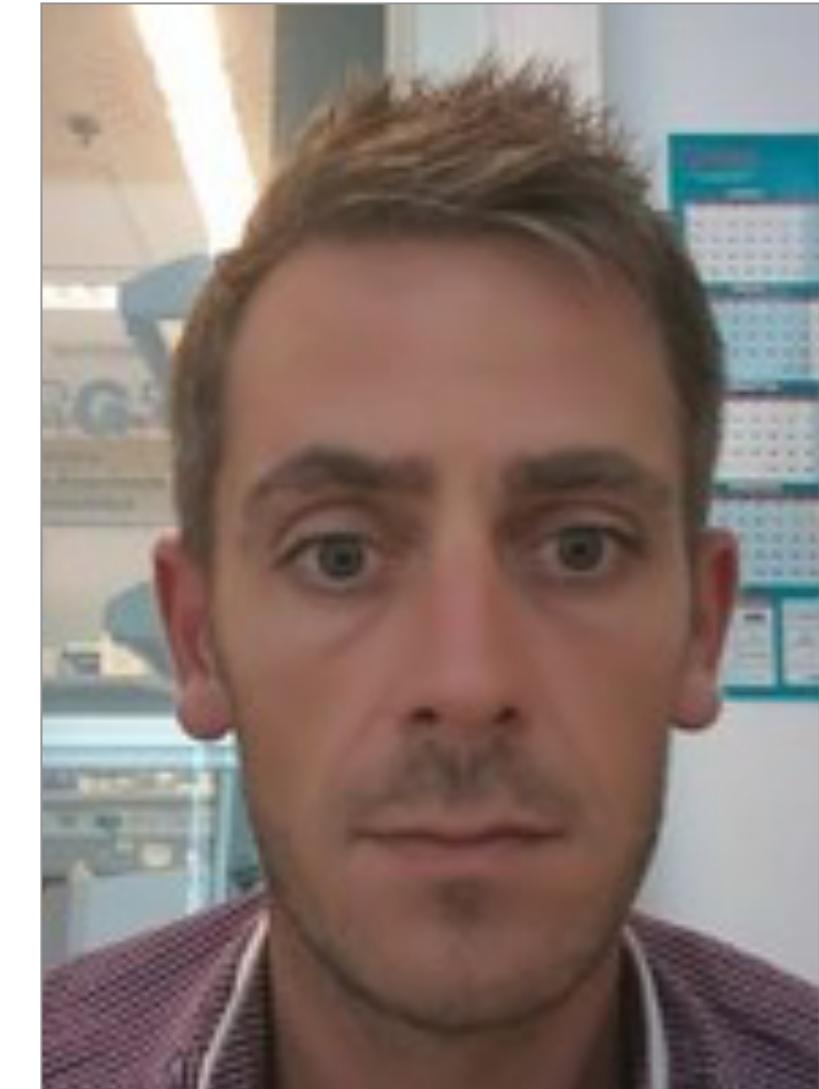
chr2 U207





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## CRG



# Miguel Beato

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