



# Comparative study of the 3D genome in primates

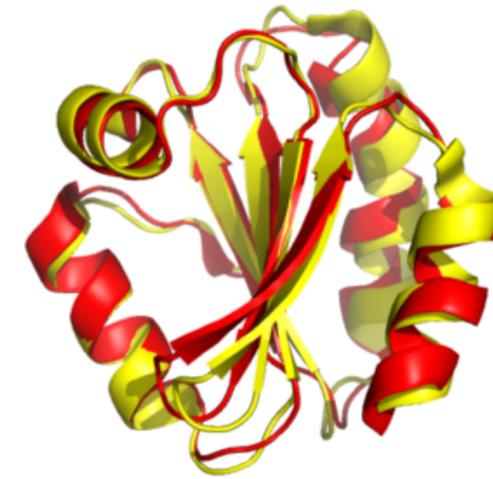
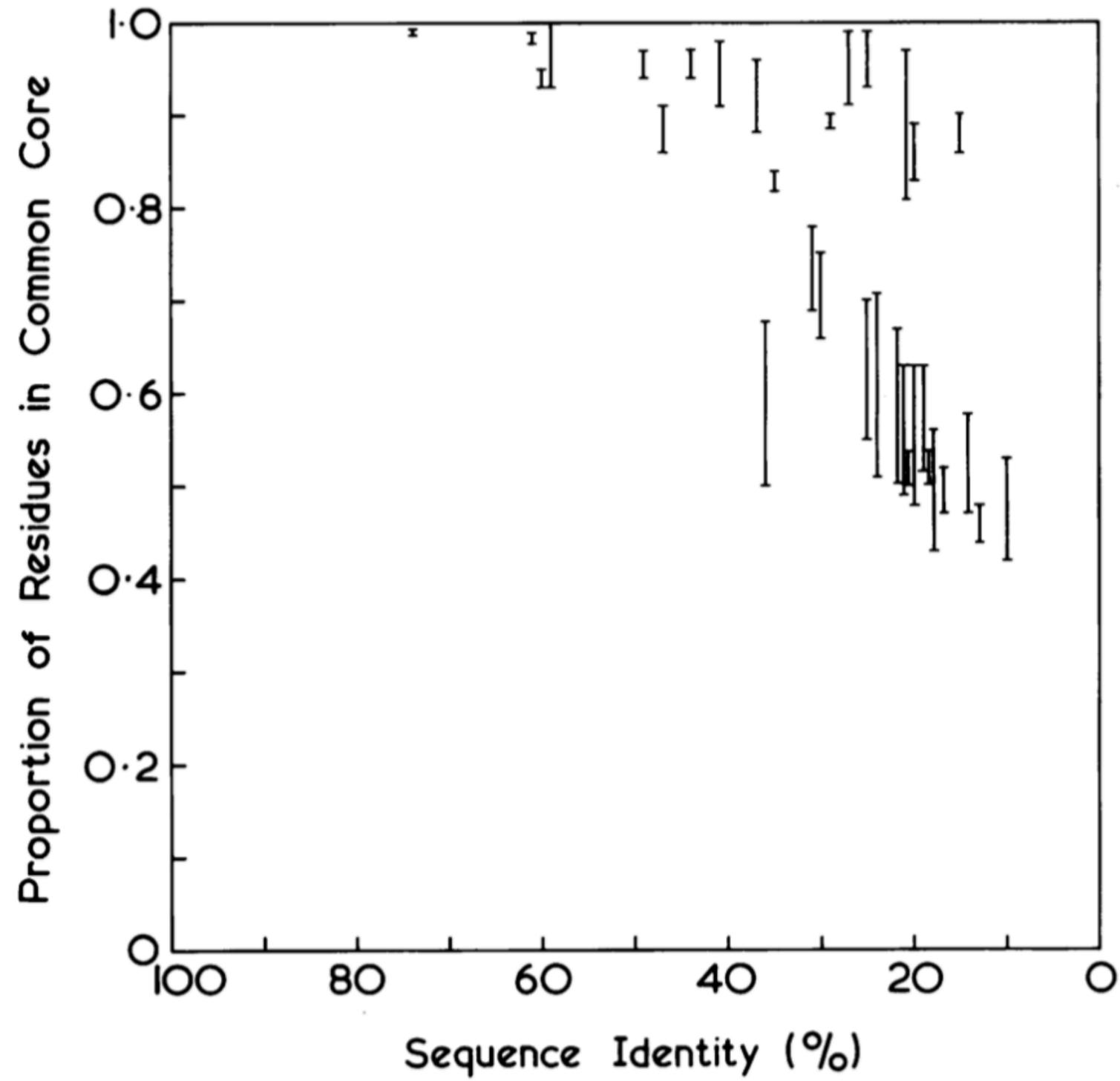
**Marc A. Marti-Renom**

CNAG-CRG · ICREA

Unpublished

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**Yasmina Cuartero**  
CNAG-CRG

In collaboration with:

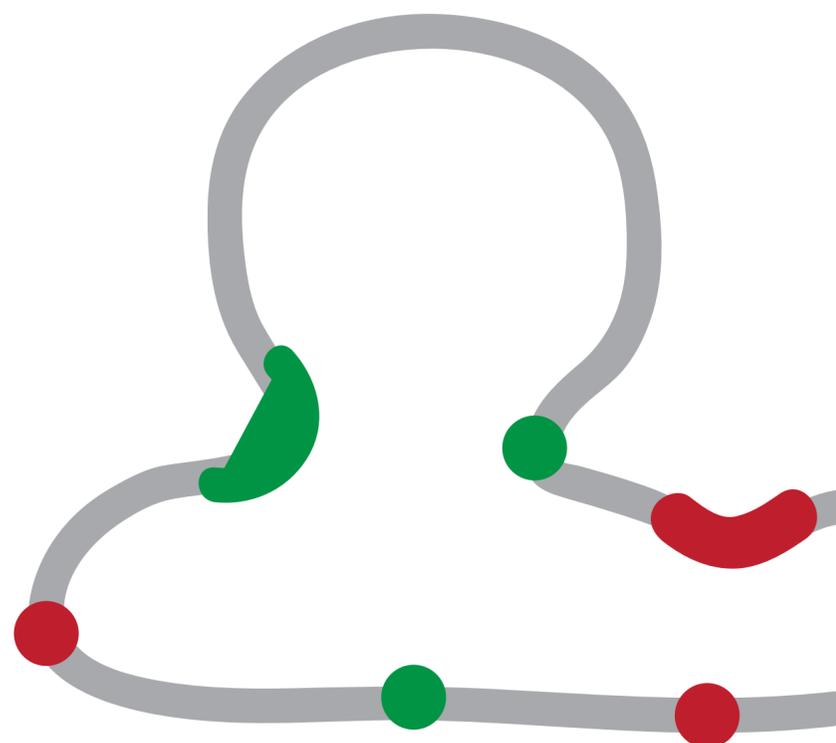
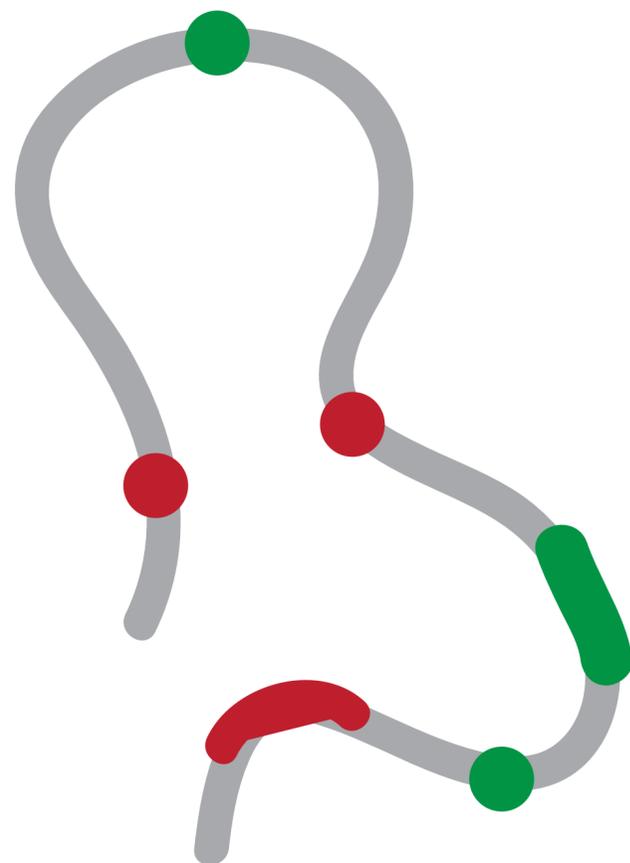
The 4DGenome Unit (CRG)

The Marquès Lab (IBE-UPF)

The Ruiz-Herrera Lab (UAB)

The Navarro Lab (EGA-UPF)

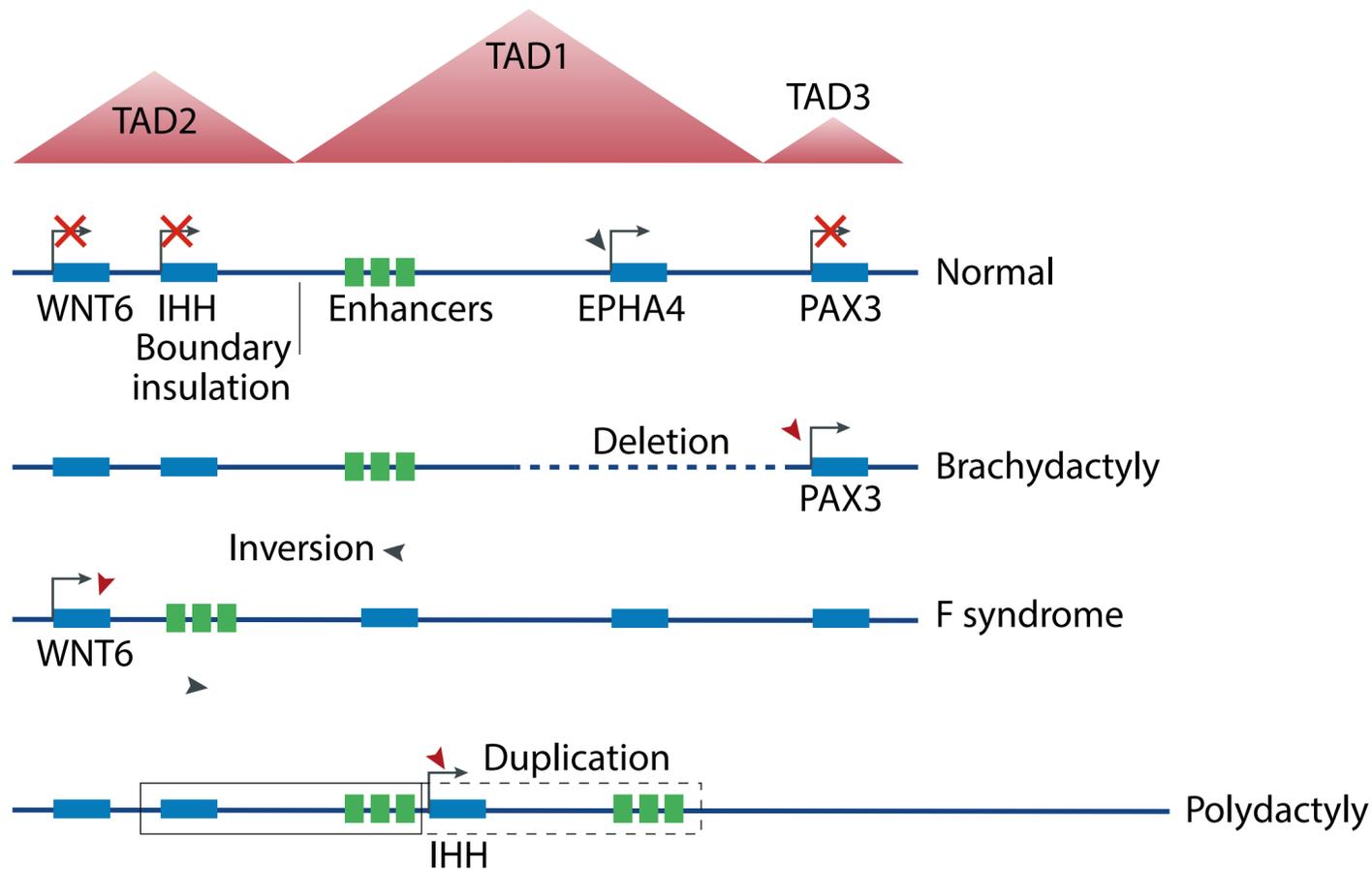
The Caceres Lab (UAB)



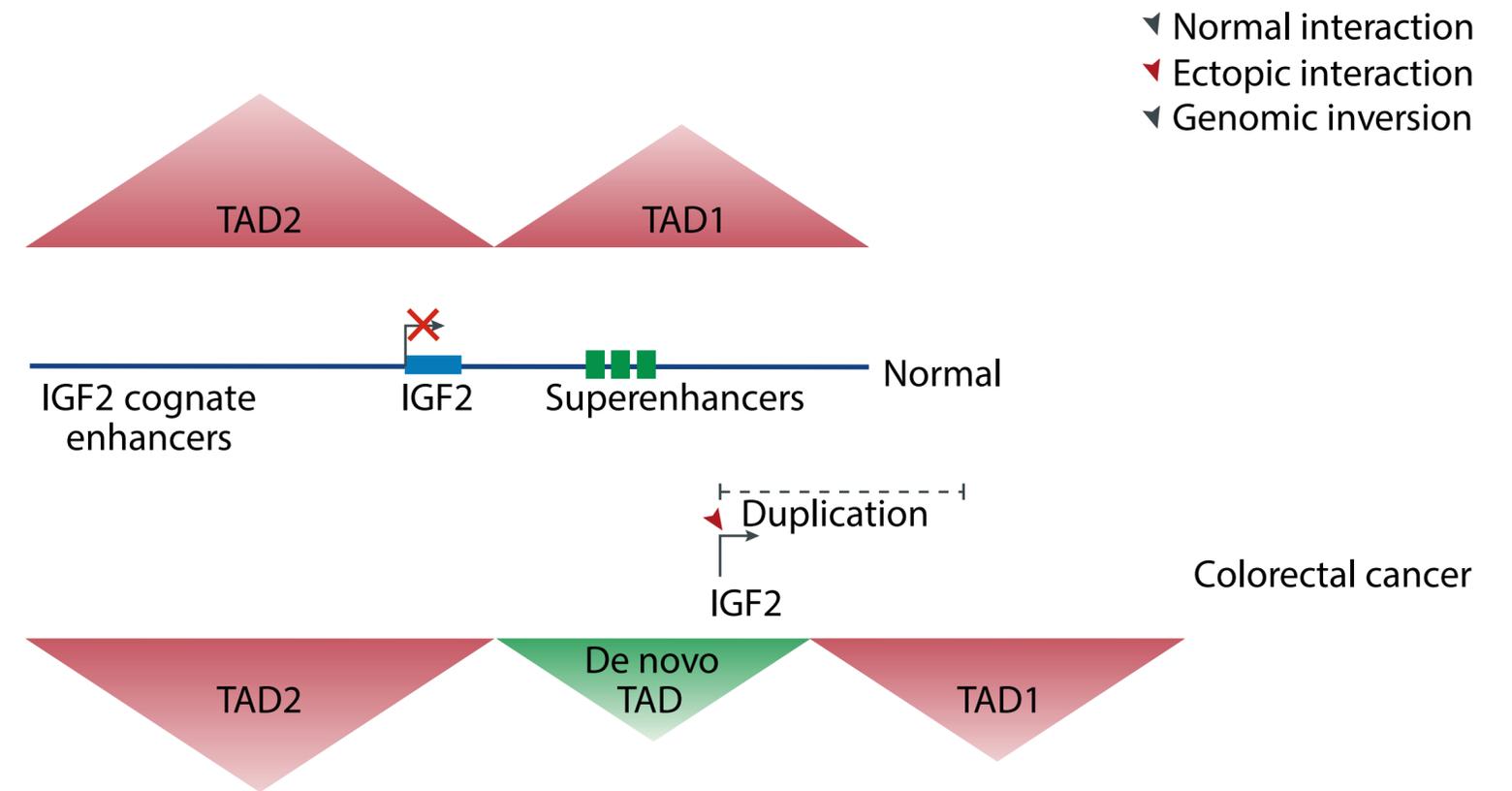


# Is 3D at all relevant?

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



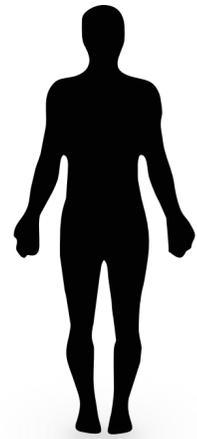
Lupianez, D. G. et al. Cell 161, 1012–1025 (2015)



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

- ▼ Normal interaction
- ▼ Ectopic interaction
- ▼ Genomic inversion

# Hi-C matrices from lymphoblasts in seven primates



Human



Chimpanzee



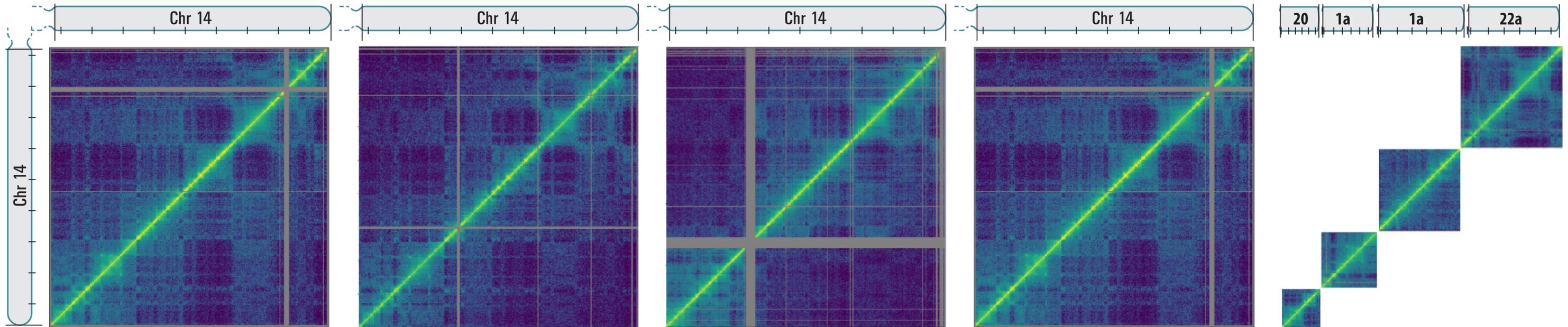
Gorilla



Orangutan



Gibbon



Macaque

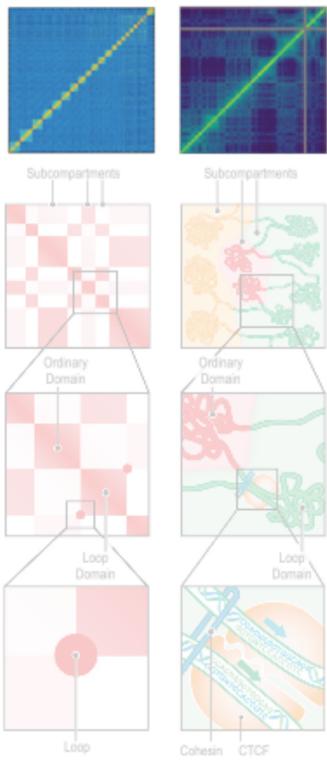


Marmoset



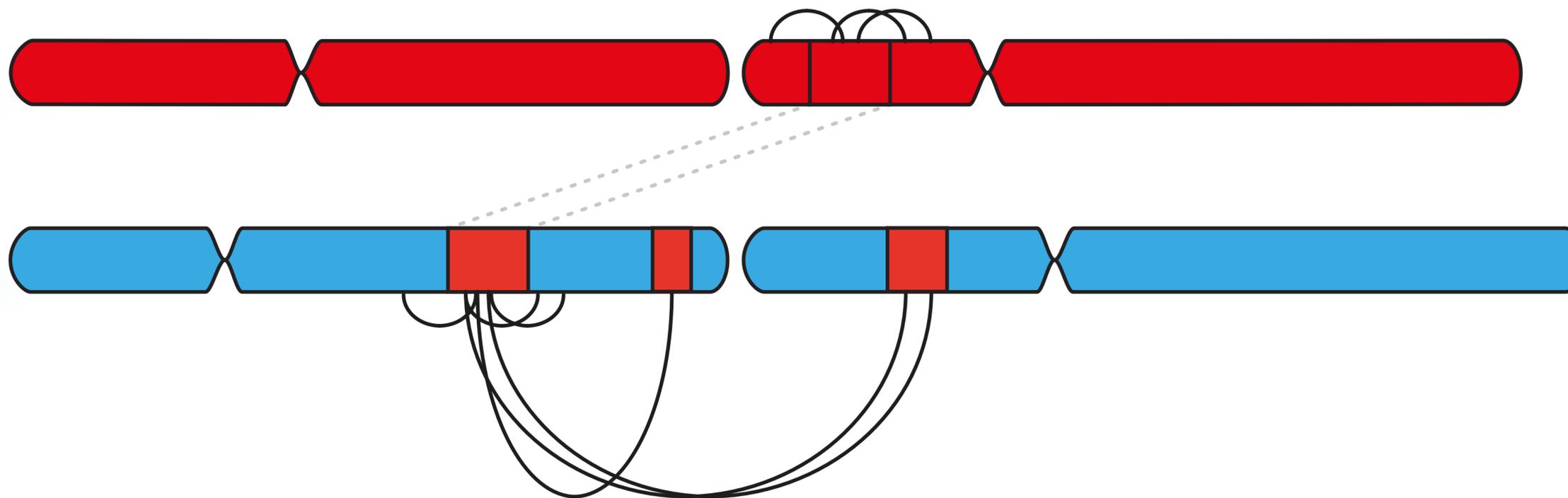
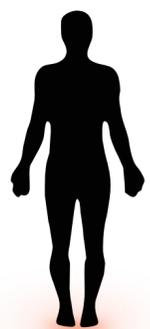
Mouse

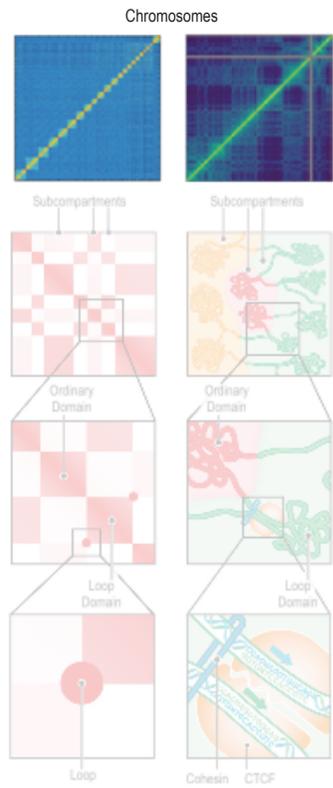
Chromosomes



# Synteny breakpoints in 3D

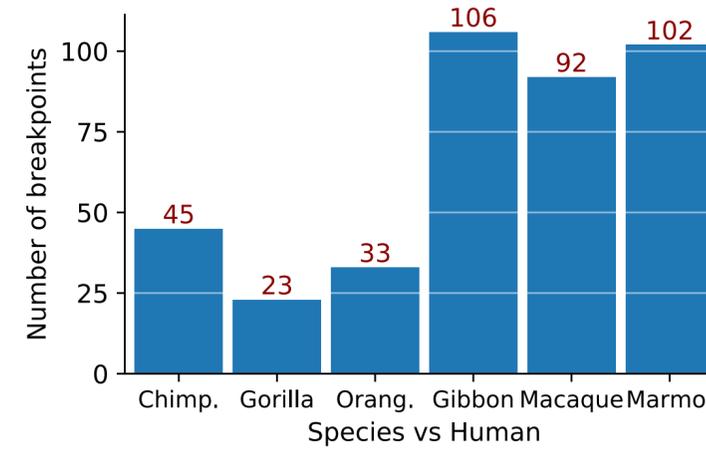
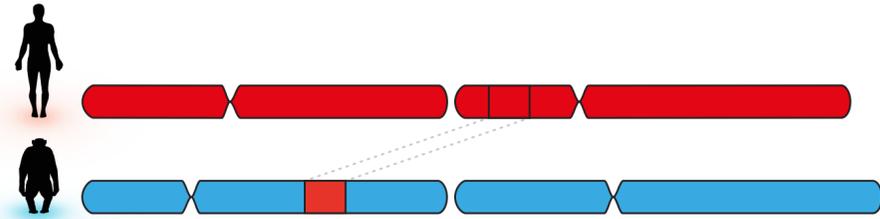
Two regions of at least 100 kb separated by more than 750 kb (including trans chromosomal)  
Common detections from Ruiz-Herrera's Lab (@300Kb res) and our lab (ENSEMBLE @1Kb res)



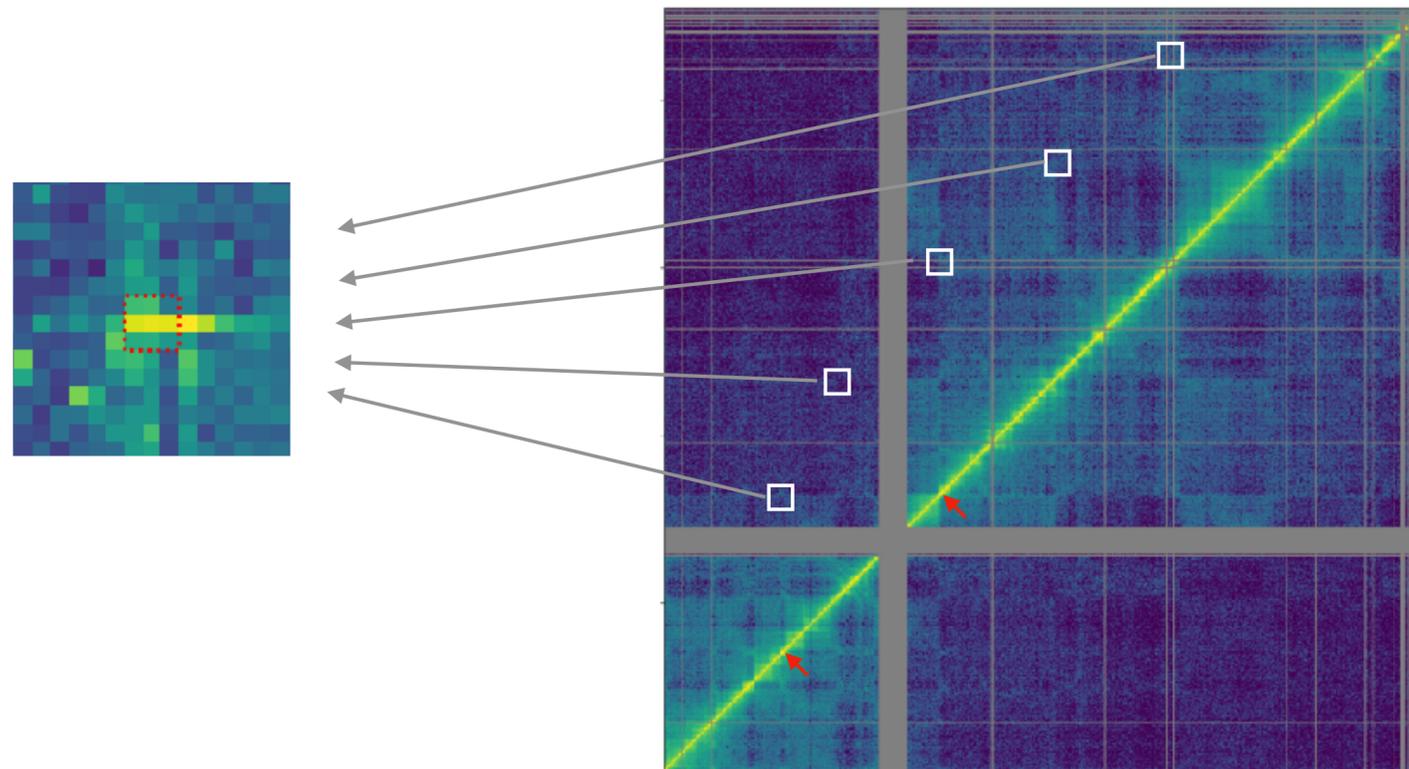


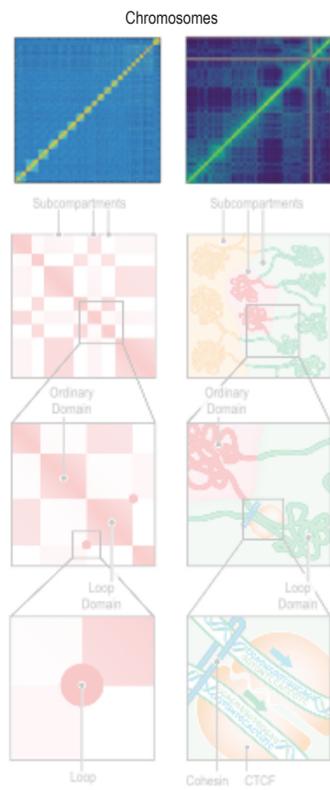
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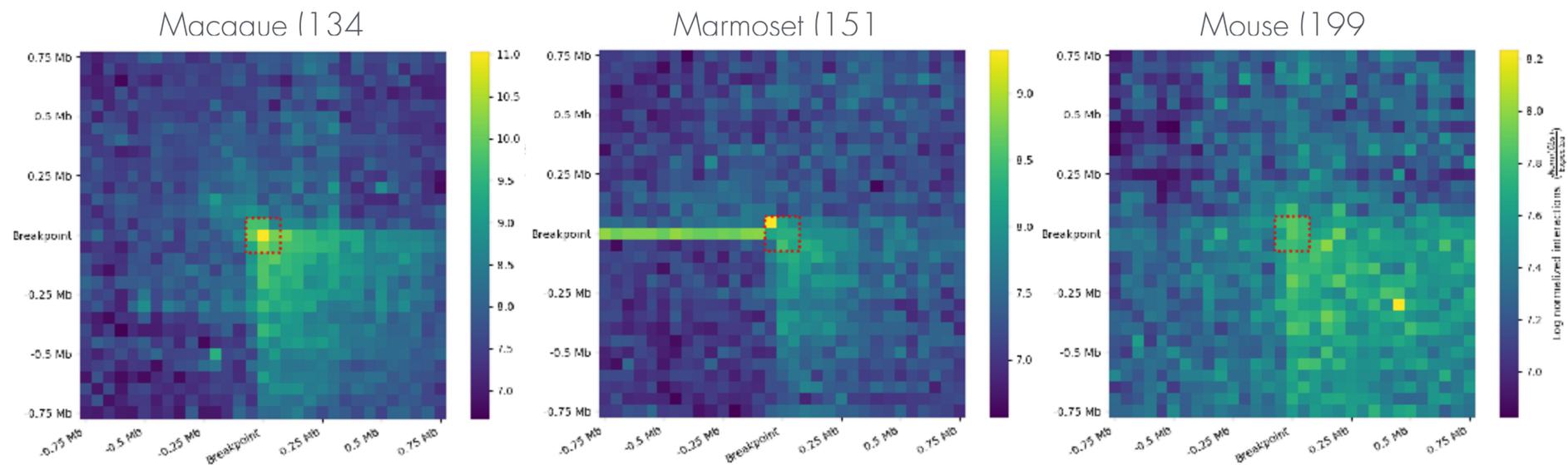
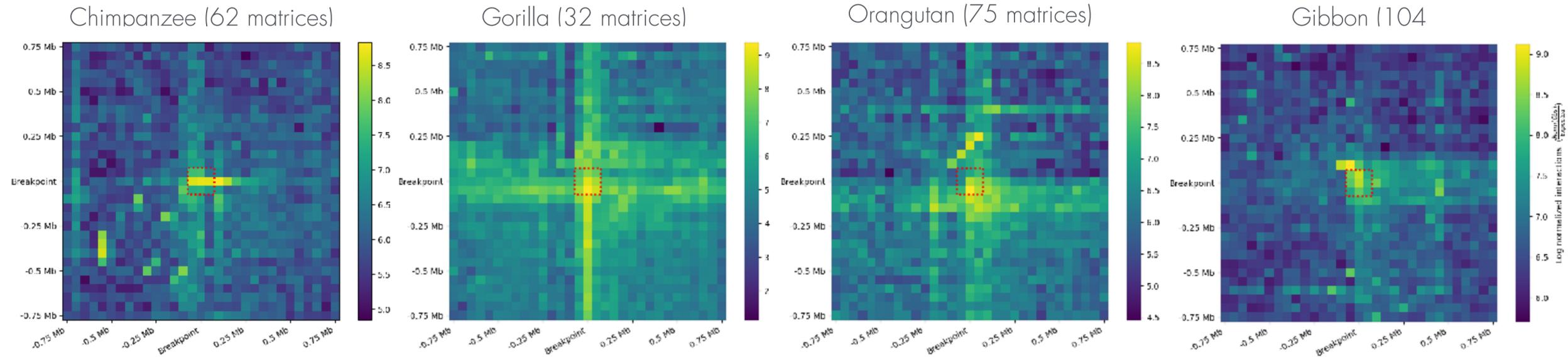
Chimp chr14

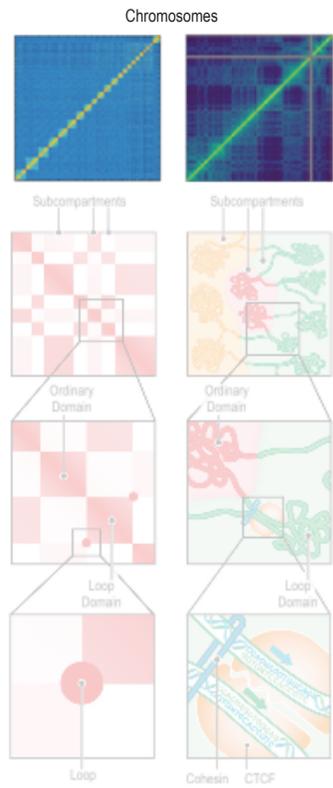




# Synteny breakpoints in 3D

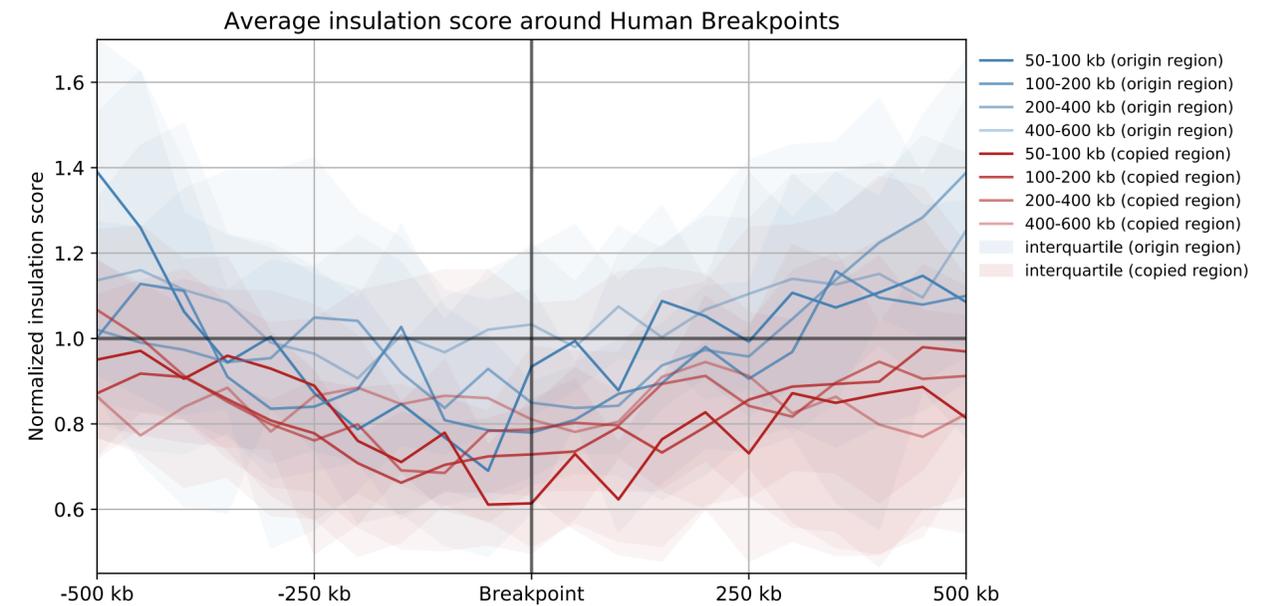
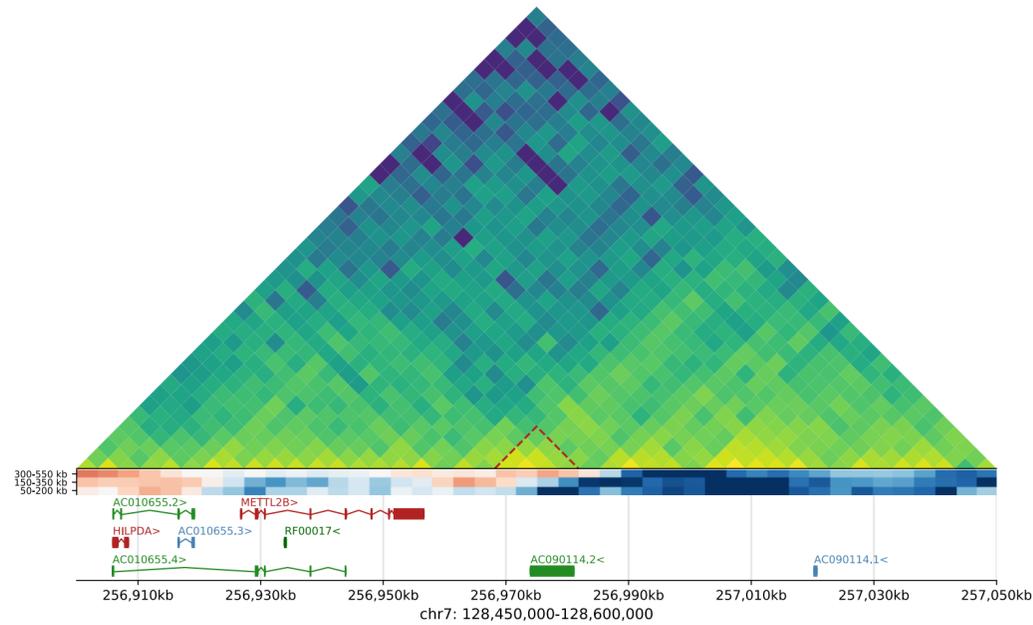
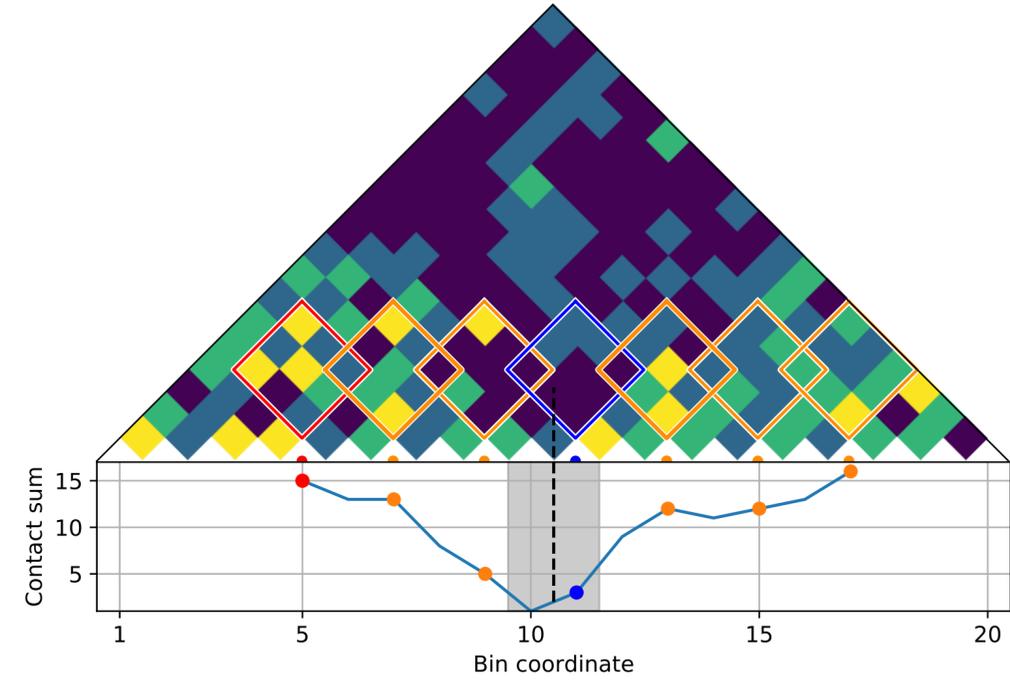
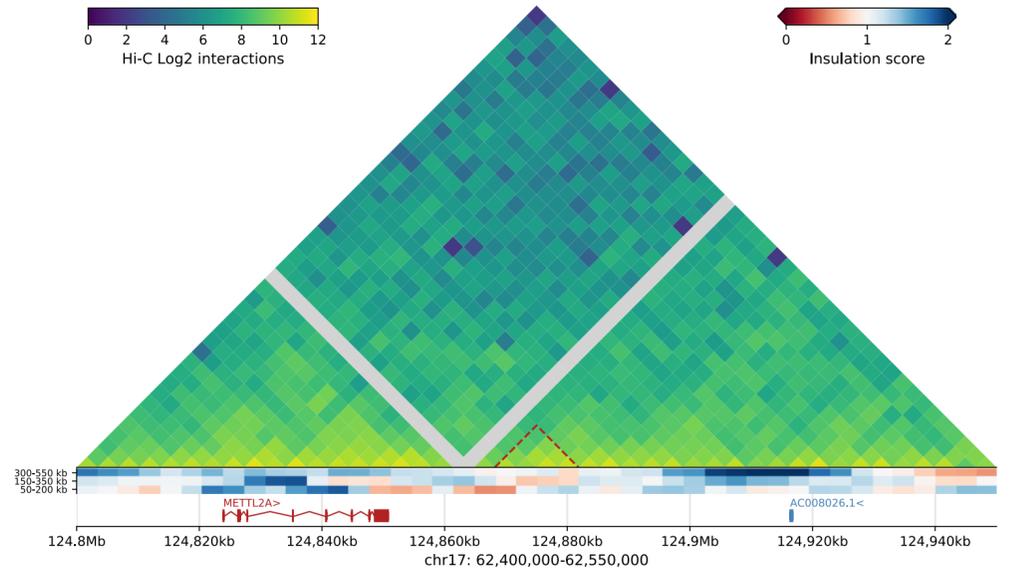
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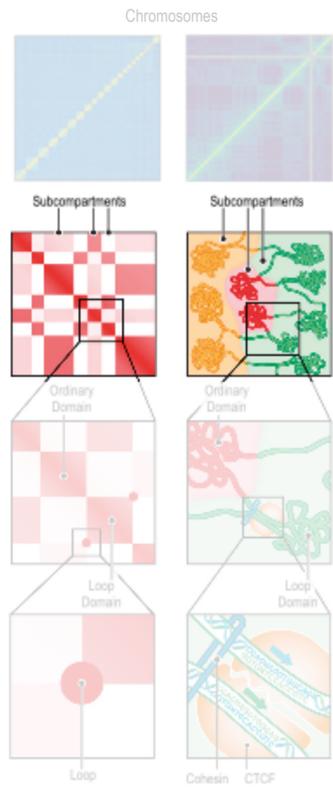




# Duplications

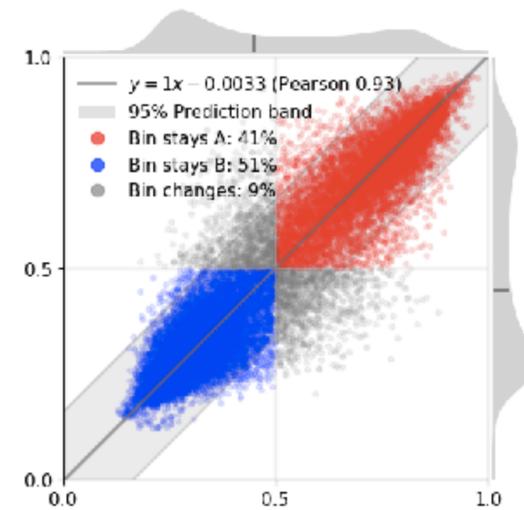
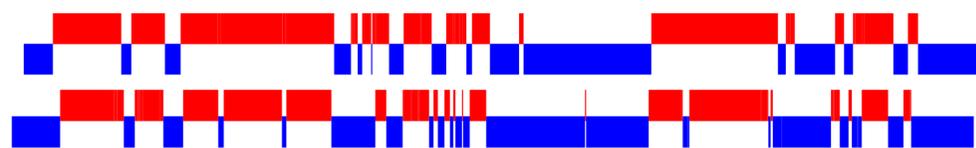
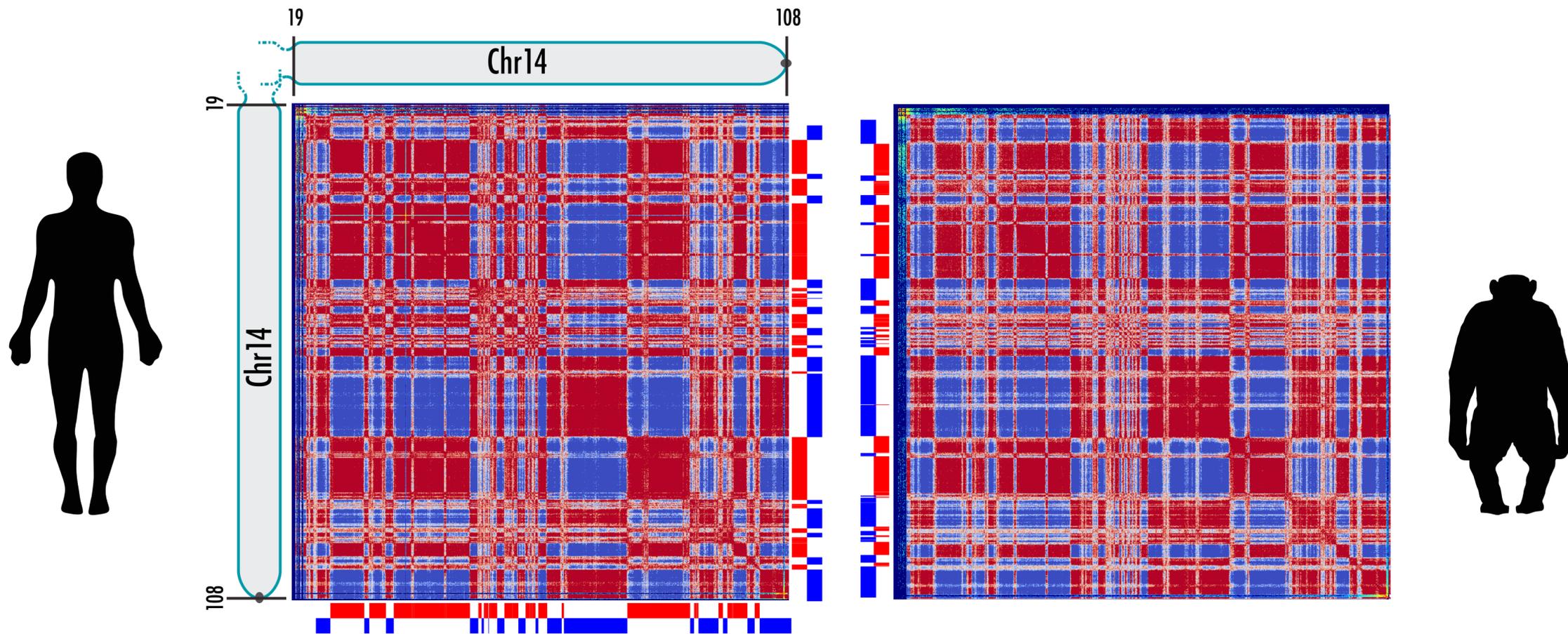
Duplicated METTL2 locus in human with respect to primates





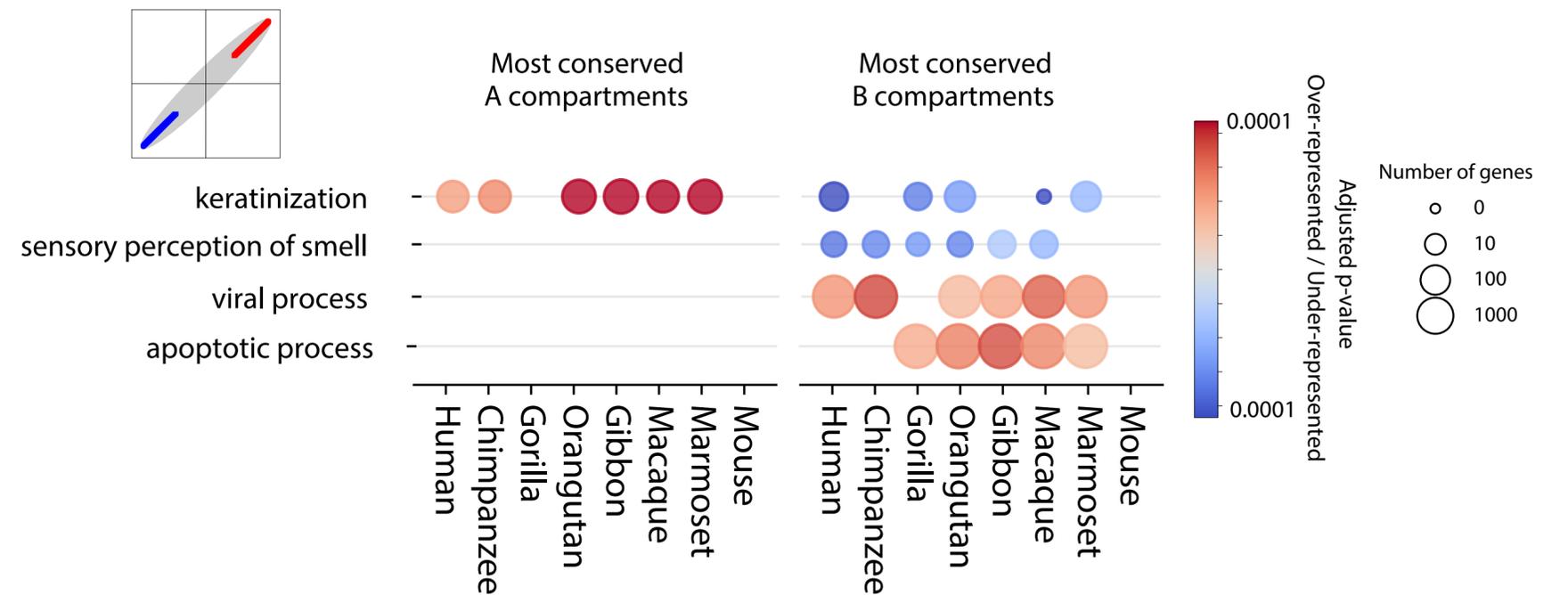
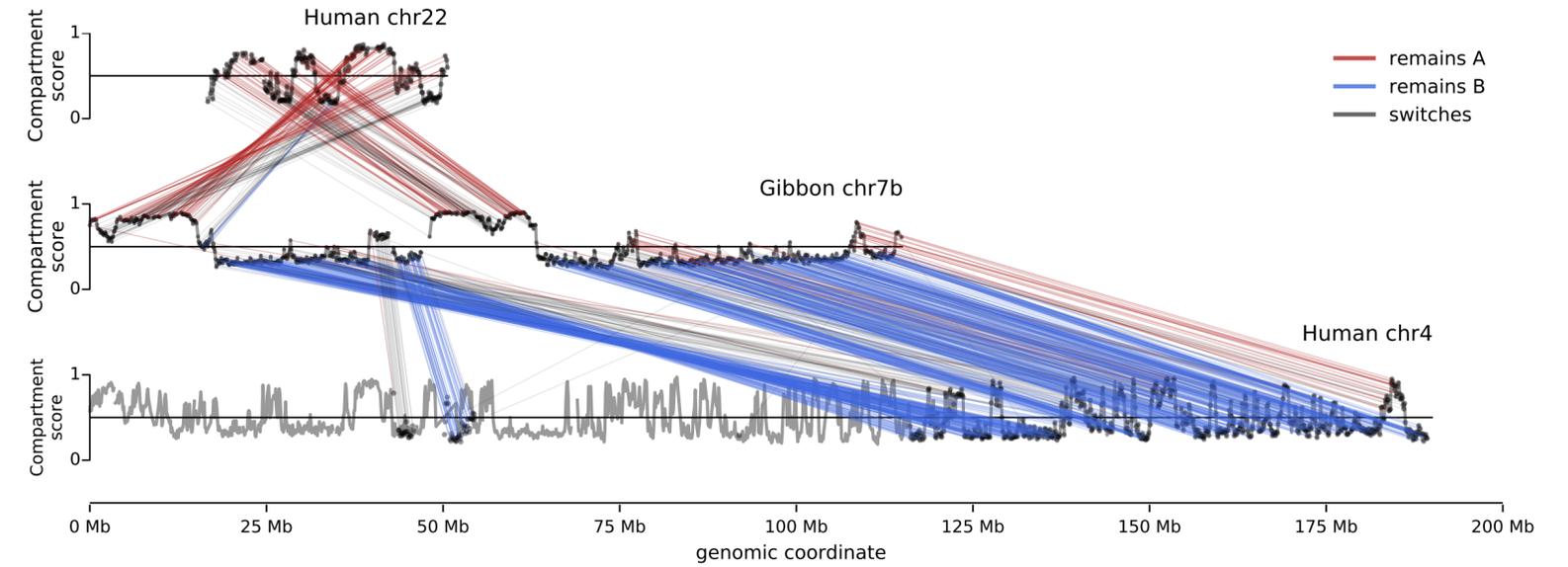
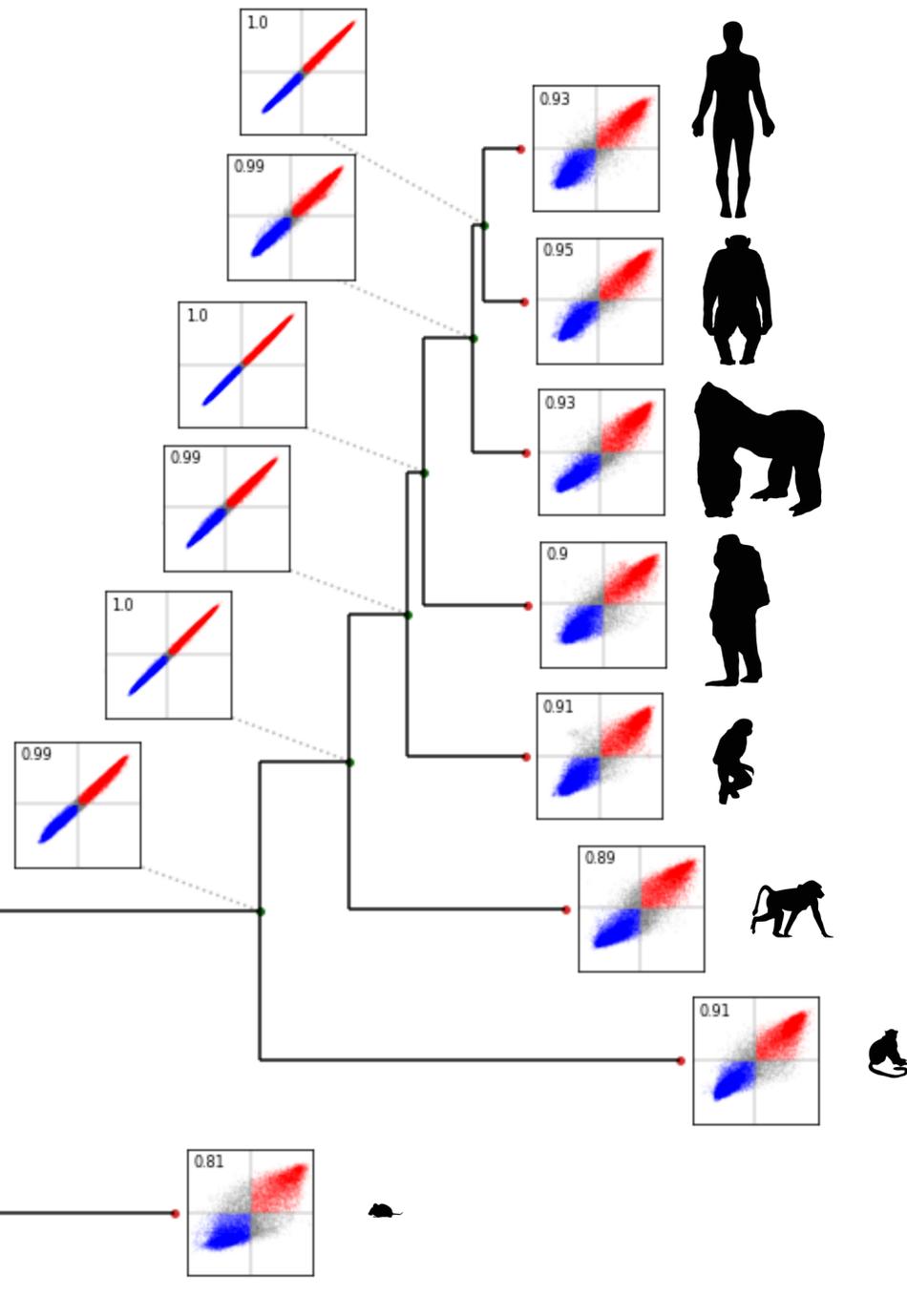
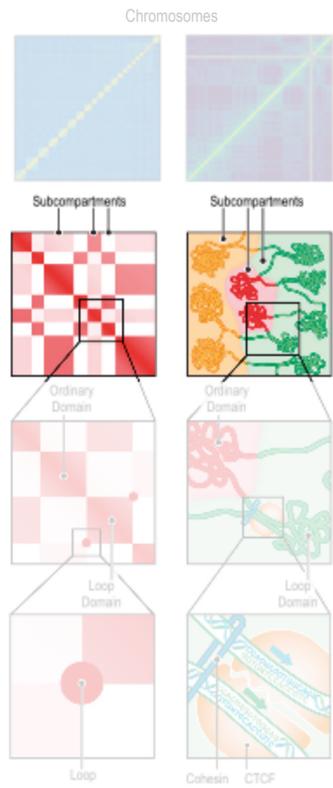
# Genome compartments

Conservation of the A/B compartments



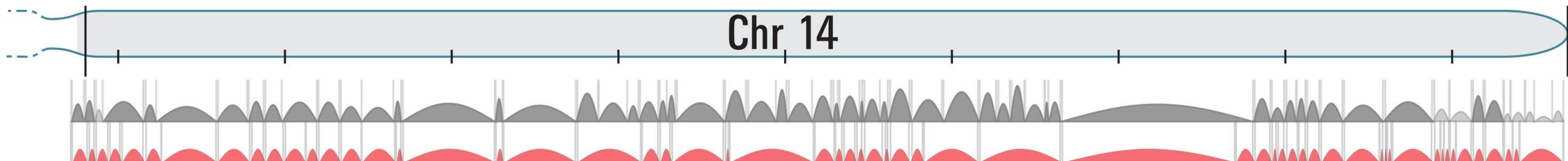
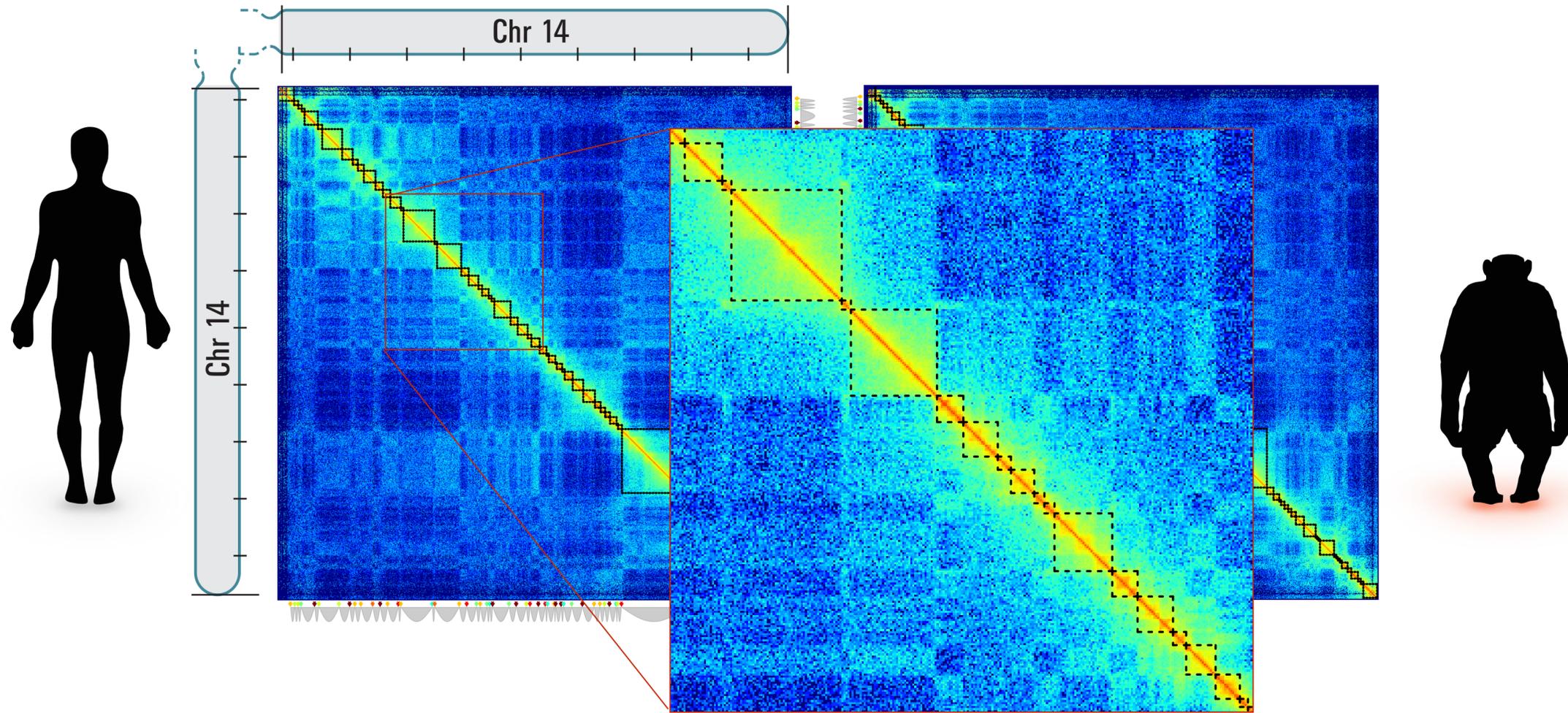
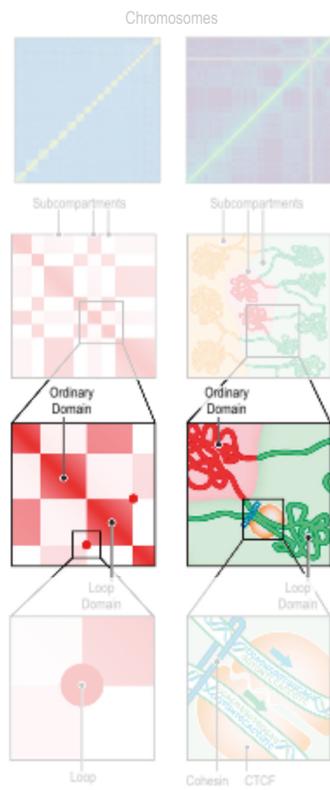
# Genome compartments

Conservation of the A/B compartments



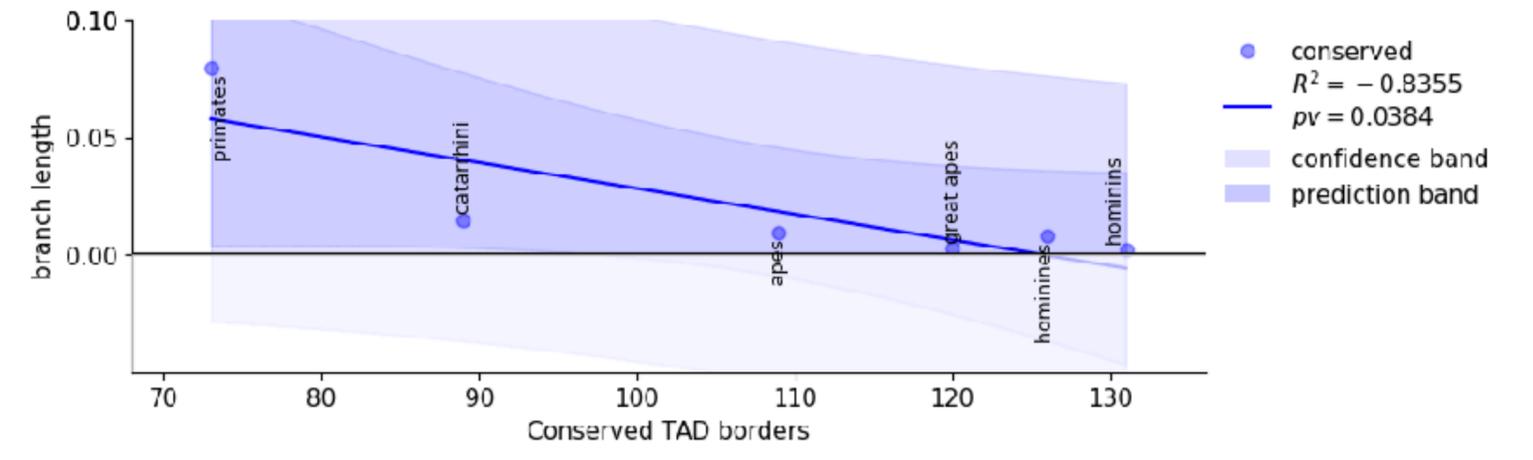
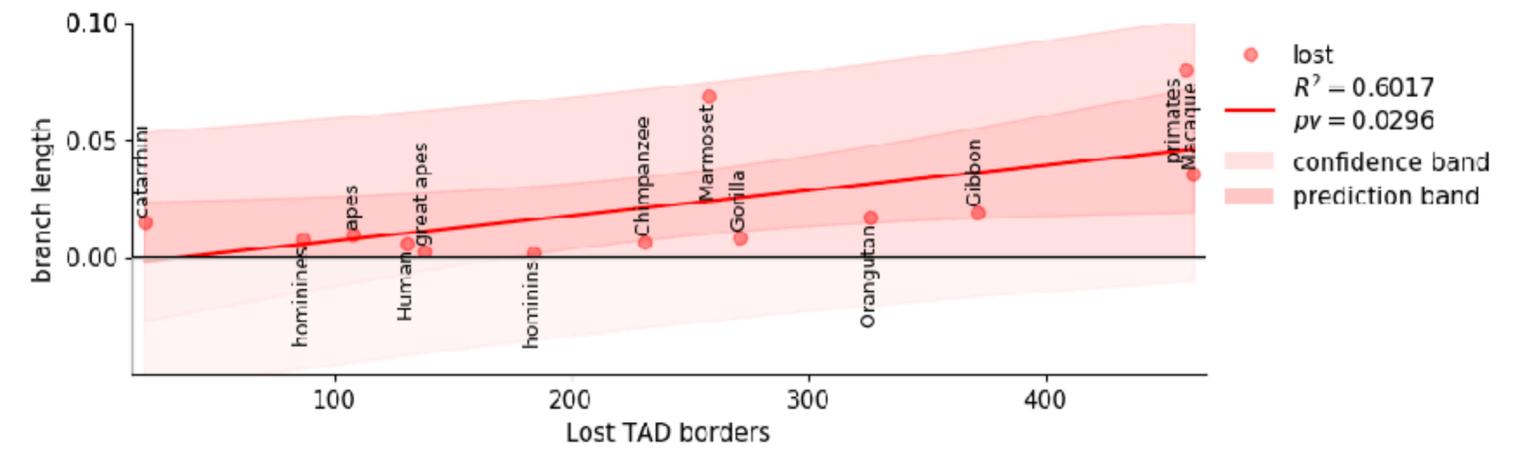
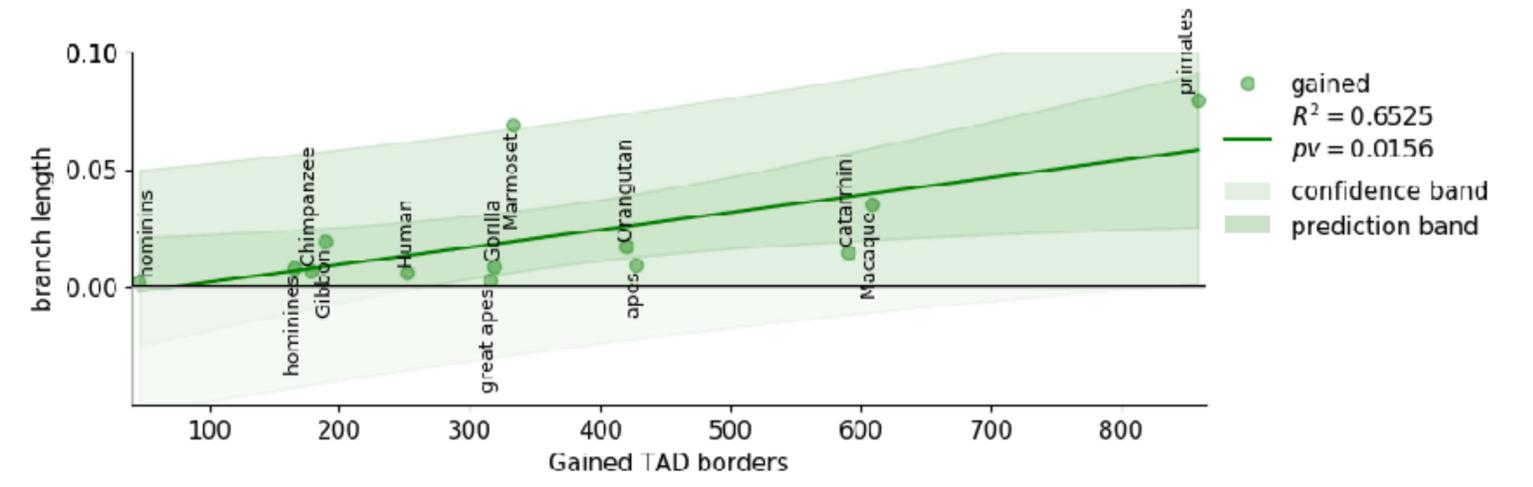
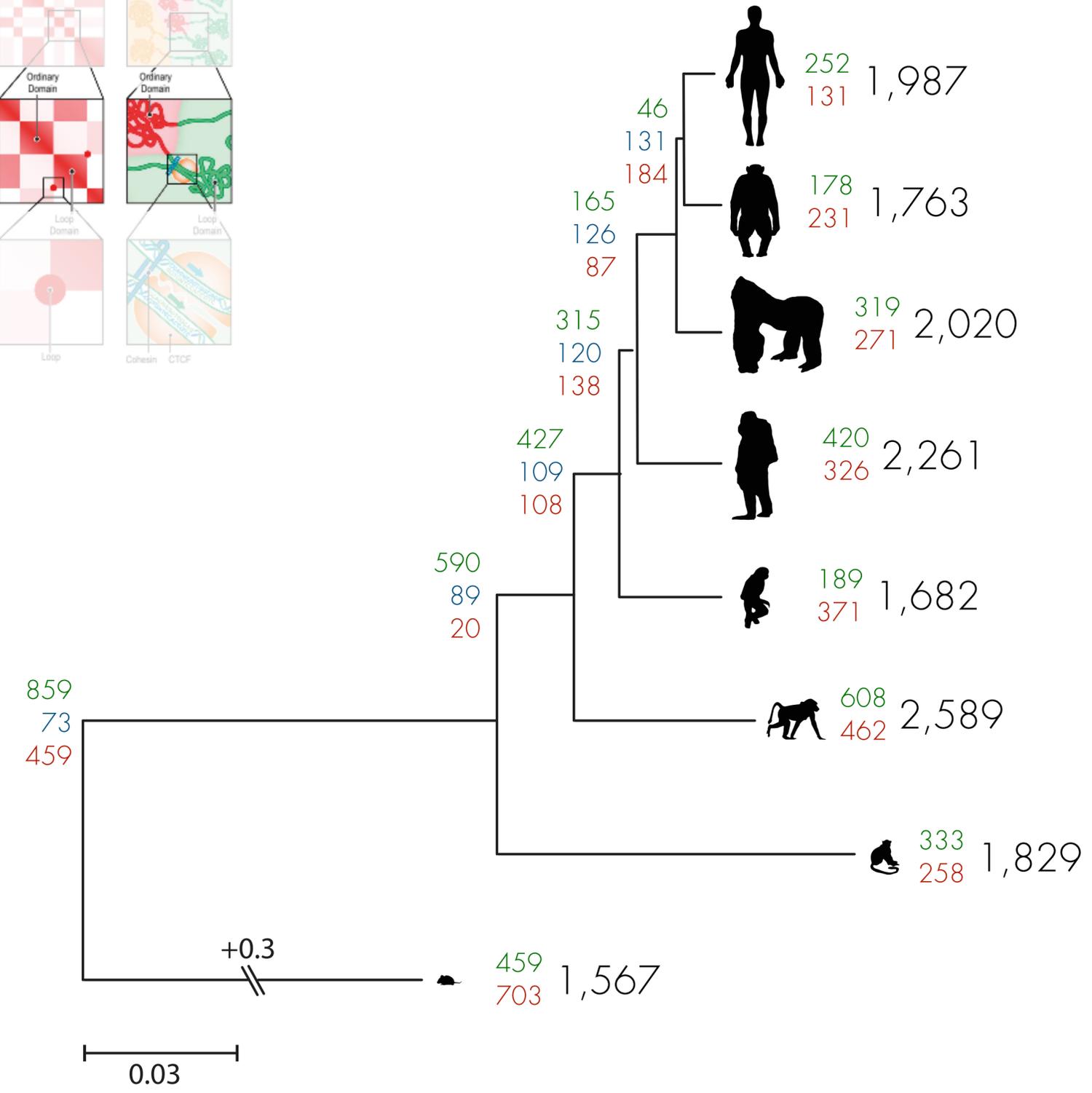
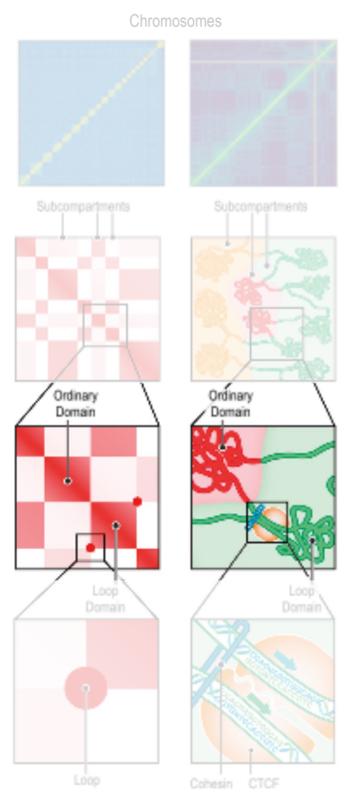
# Genome Topologically Associating Domains

Conservation of TADs



# Genome Topologically Associating Domains

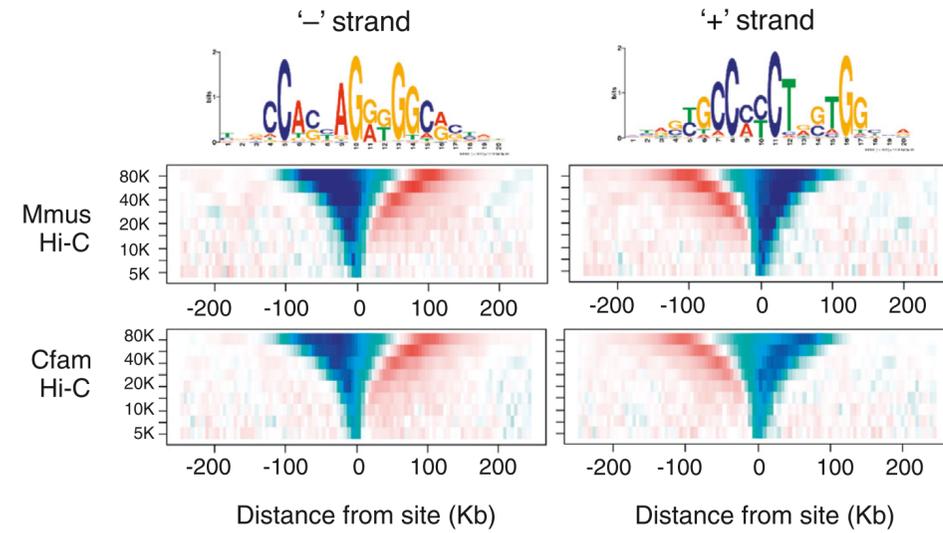
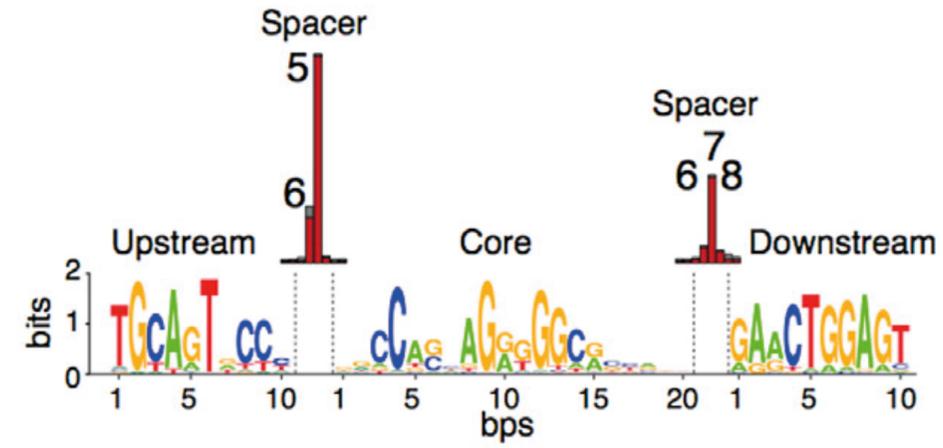
Conservation of TADs



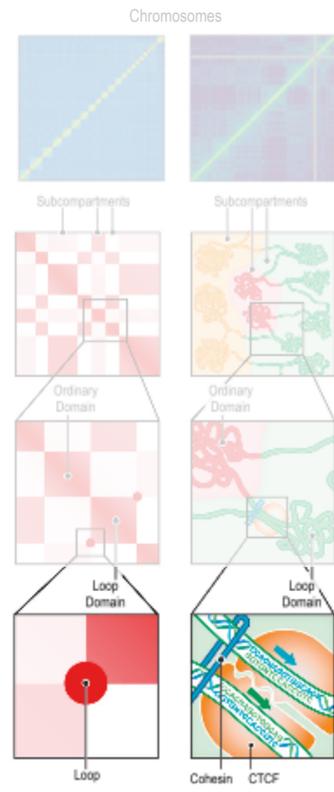


# Loops

Conservation of CTCF sites

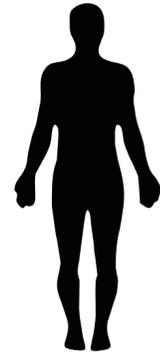


Vietri Rudan, et al. Cell Rep. 2015 Mar 03; 10(8) 1297-1309  
 Nakahashi et al. Cell Rep. 2013 May 30; 3(5) 1678-1689



# Loops

Conservation of CTCF sites



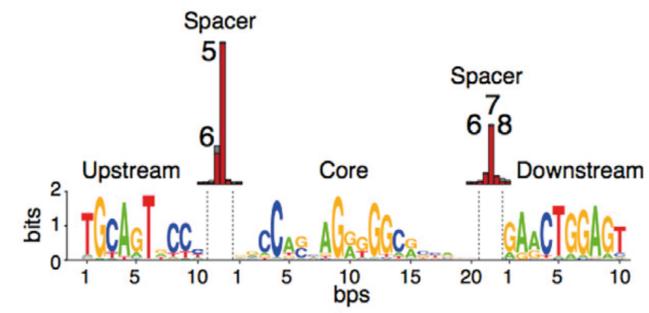
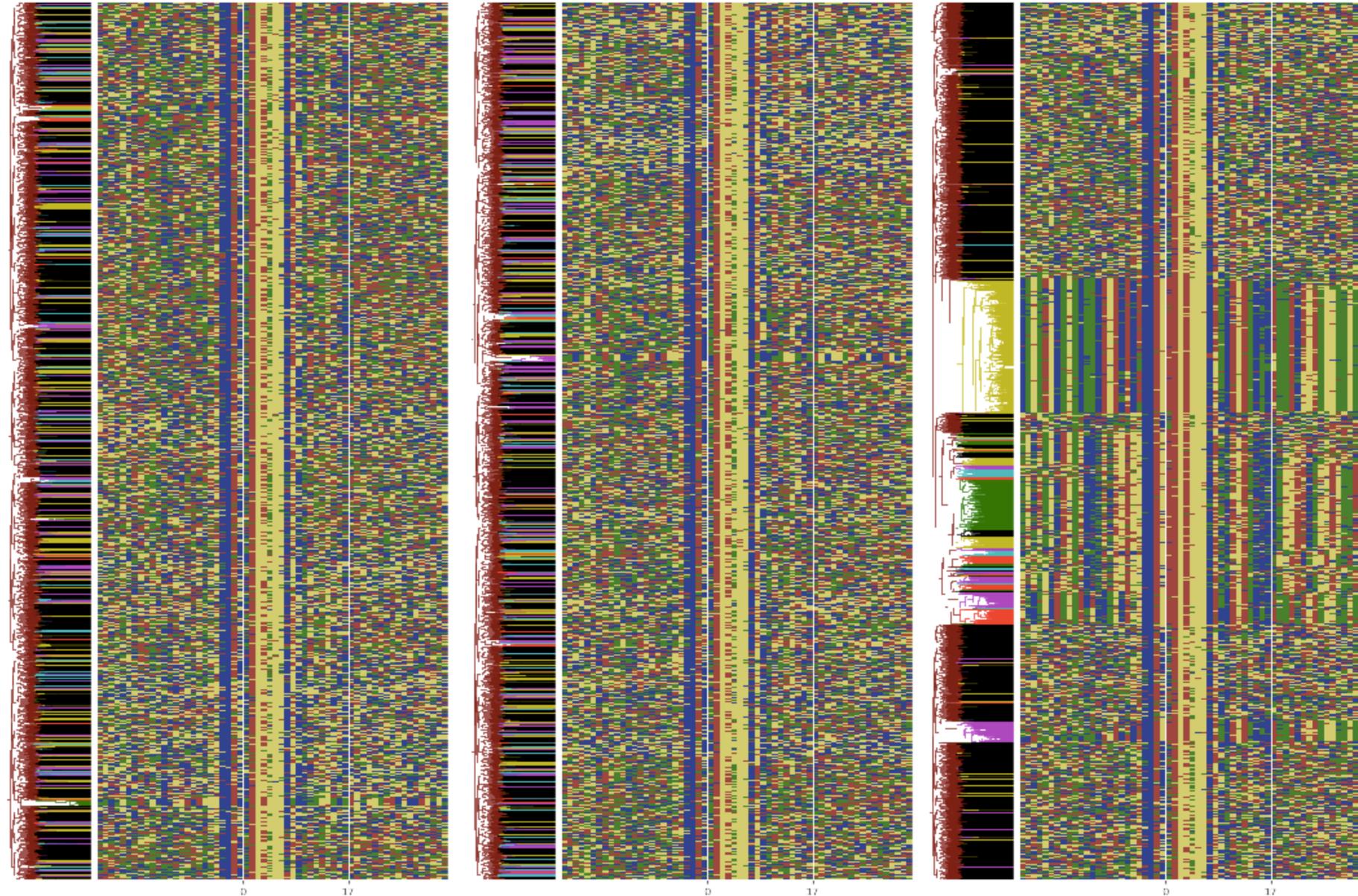
Human



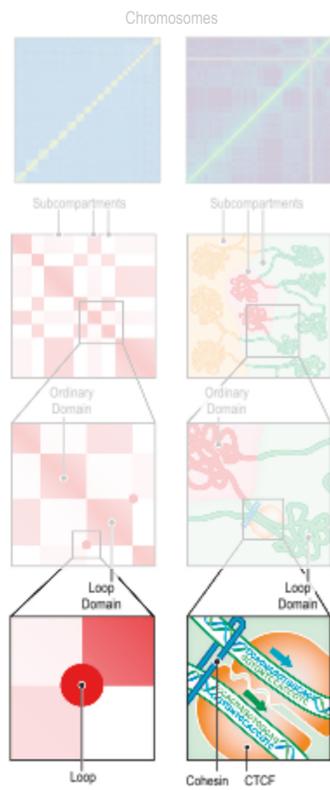
Gibbon



Mouse

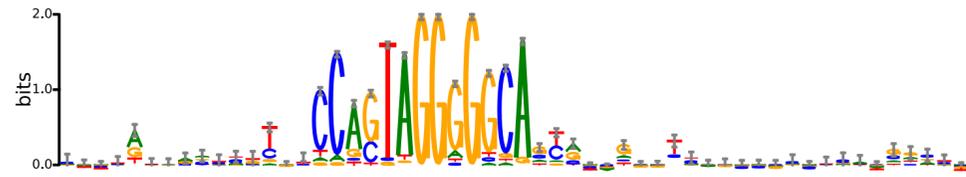




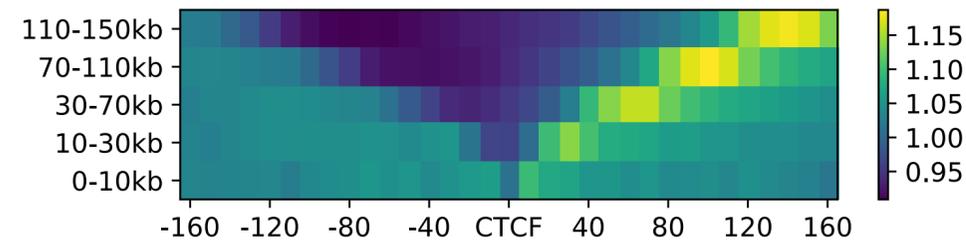


# Loops

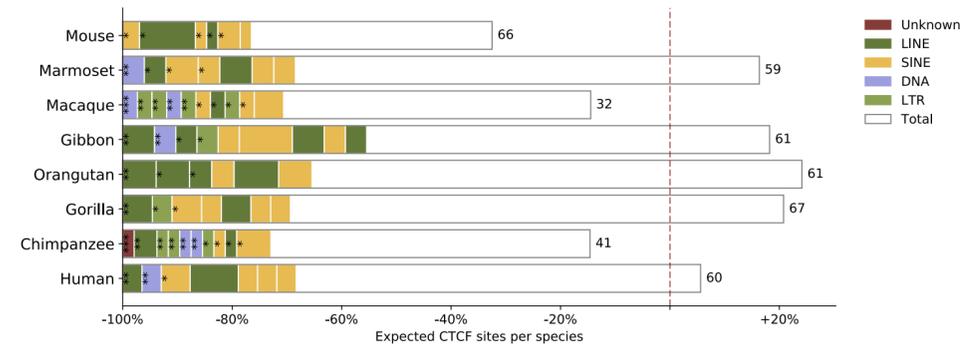
Conservation of CTCF sites



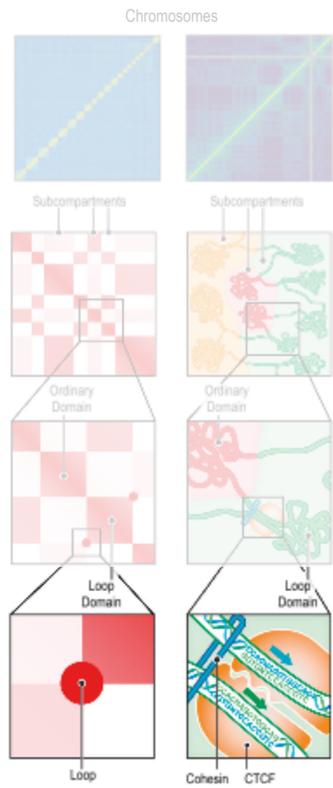
- Motif (nucleotide content)



- Insulation/looping (interaction directionality)



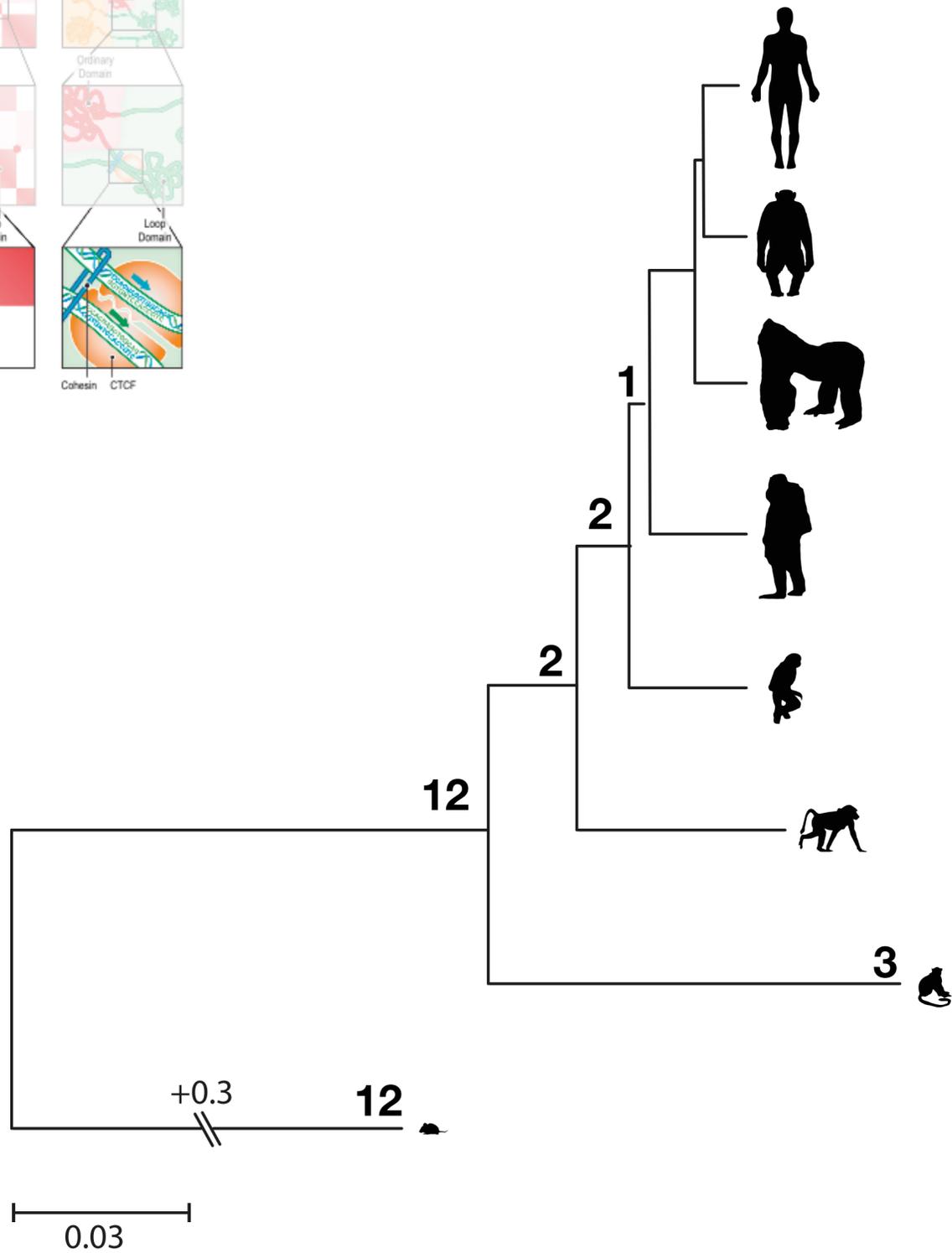
- Enrichment in repetitive elements

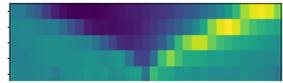
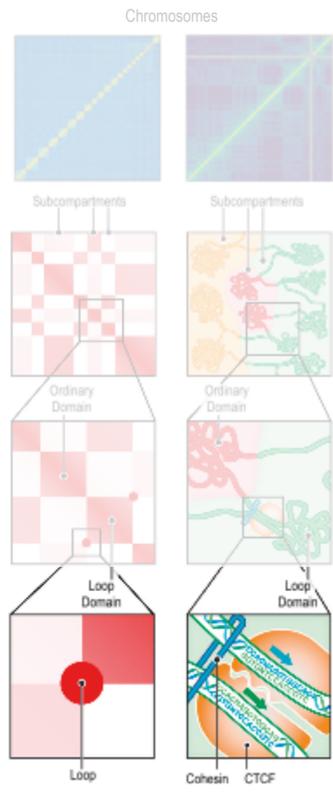


# Loops

Conservation of CTCF sites

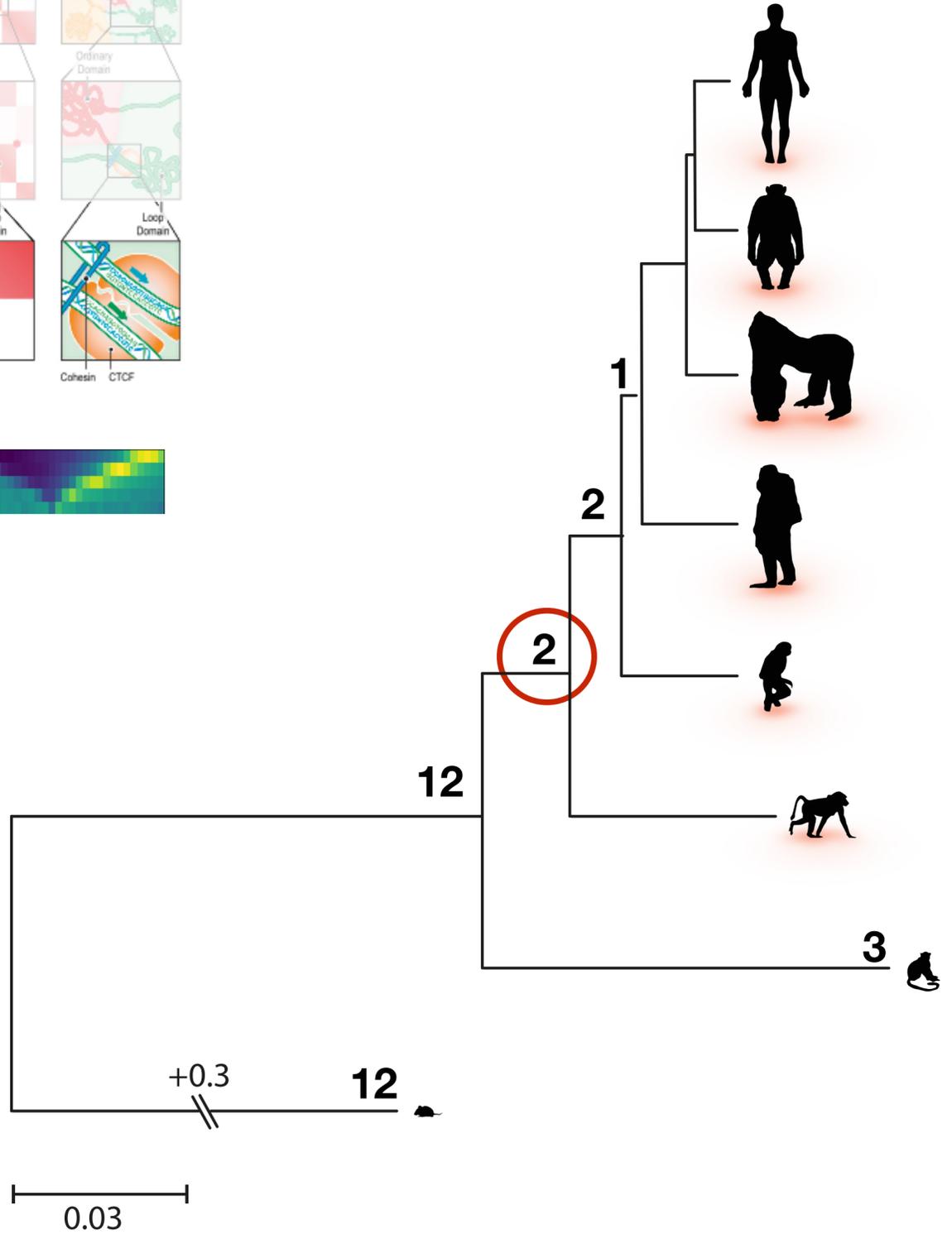
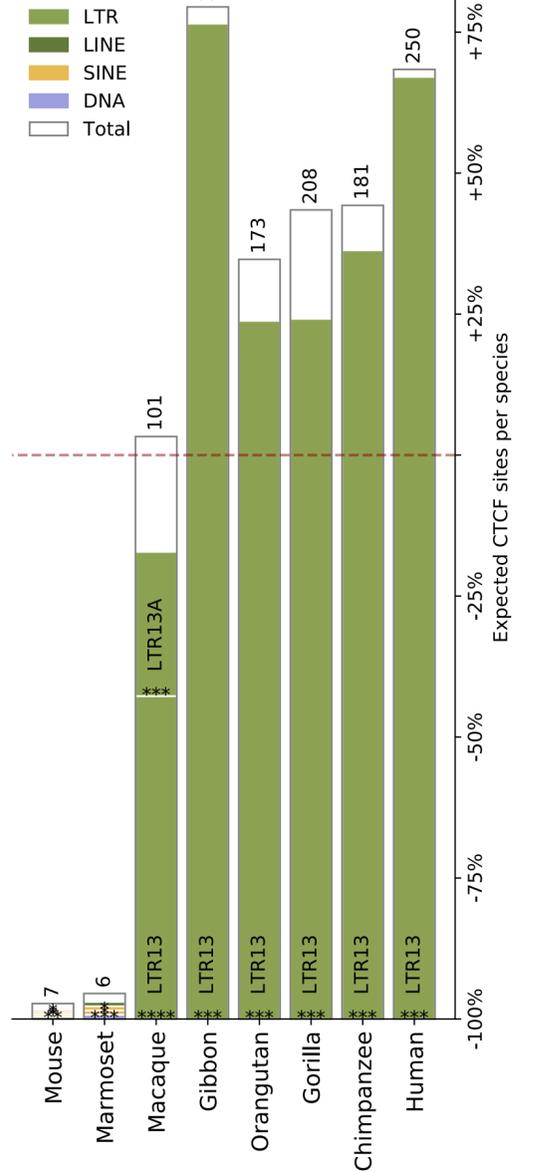
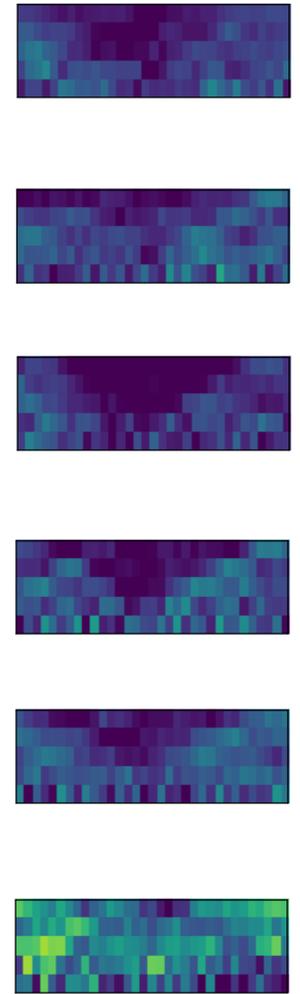
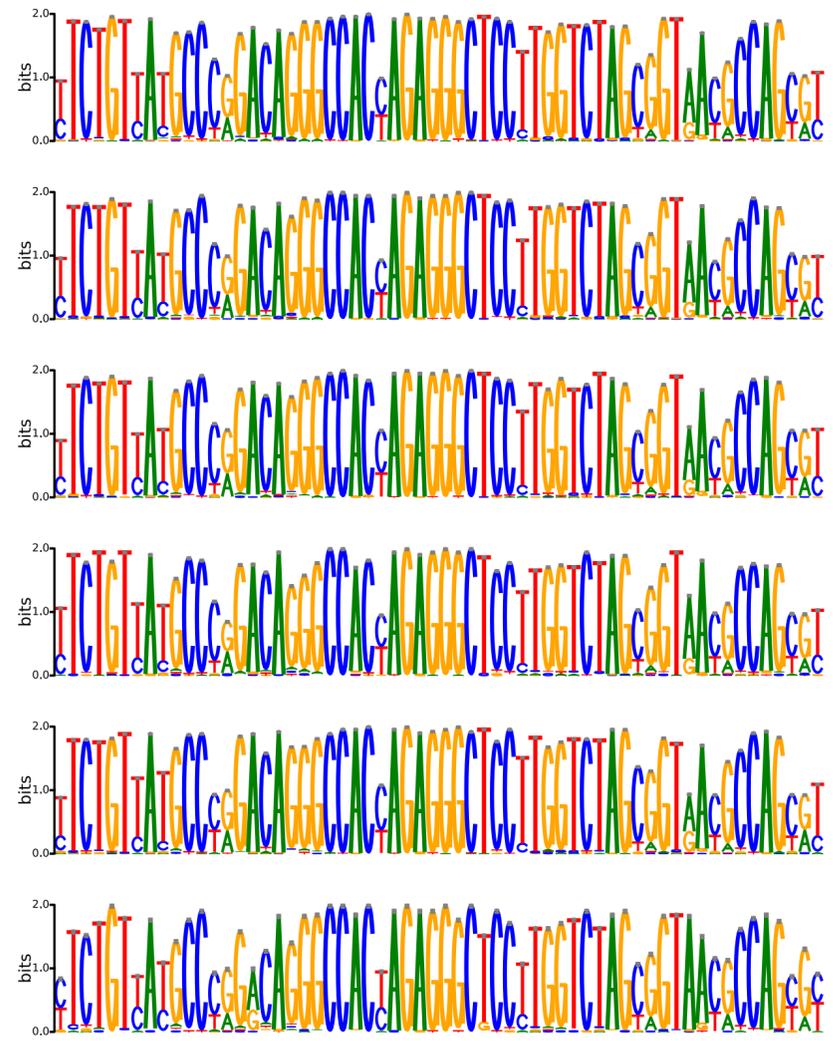
Few events of genome expansion through transposons involving CTCF sites



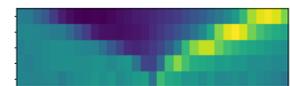
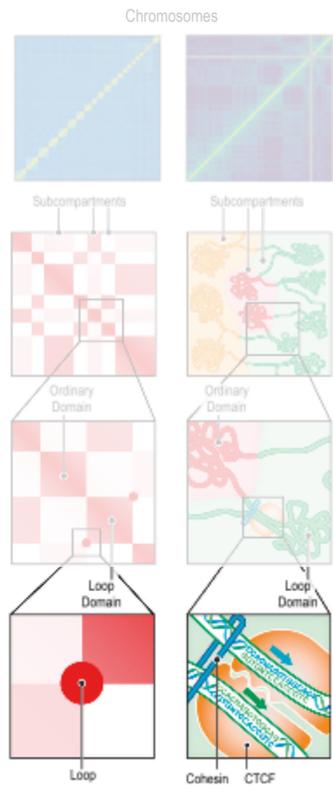


# Loops

Conservation of CTCF sites

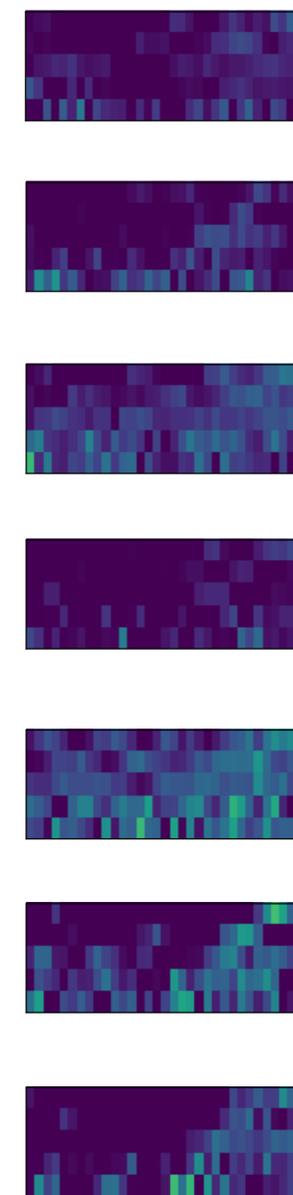
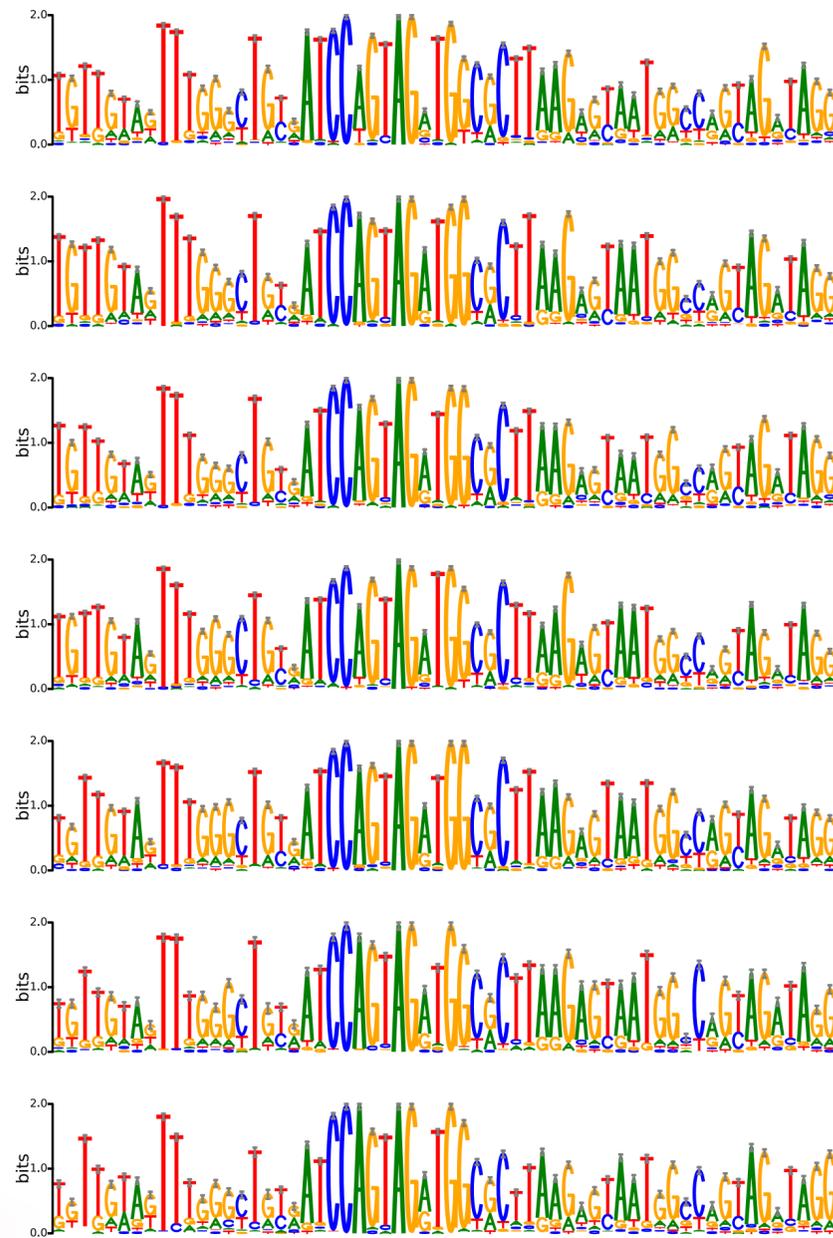
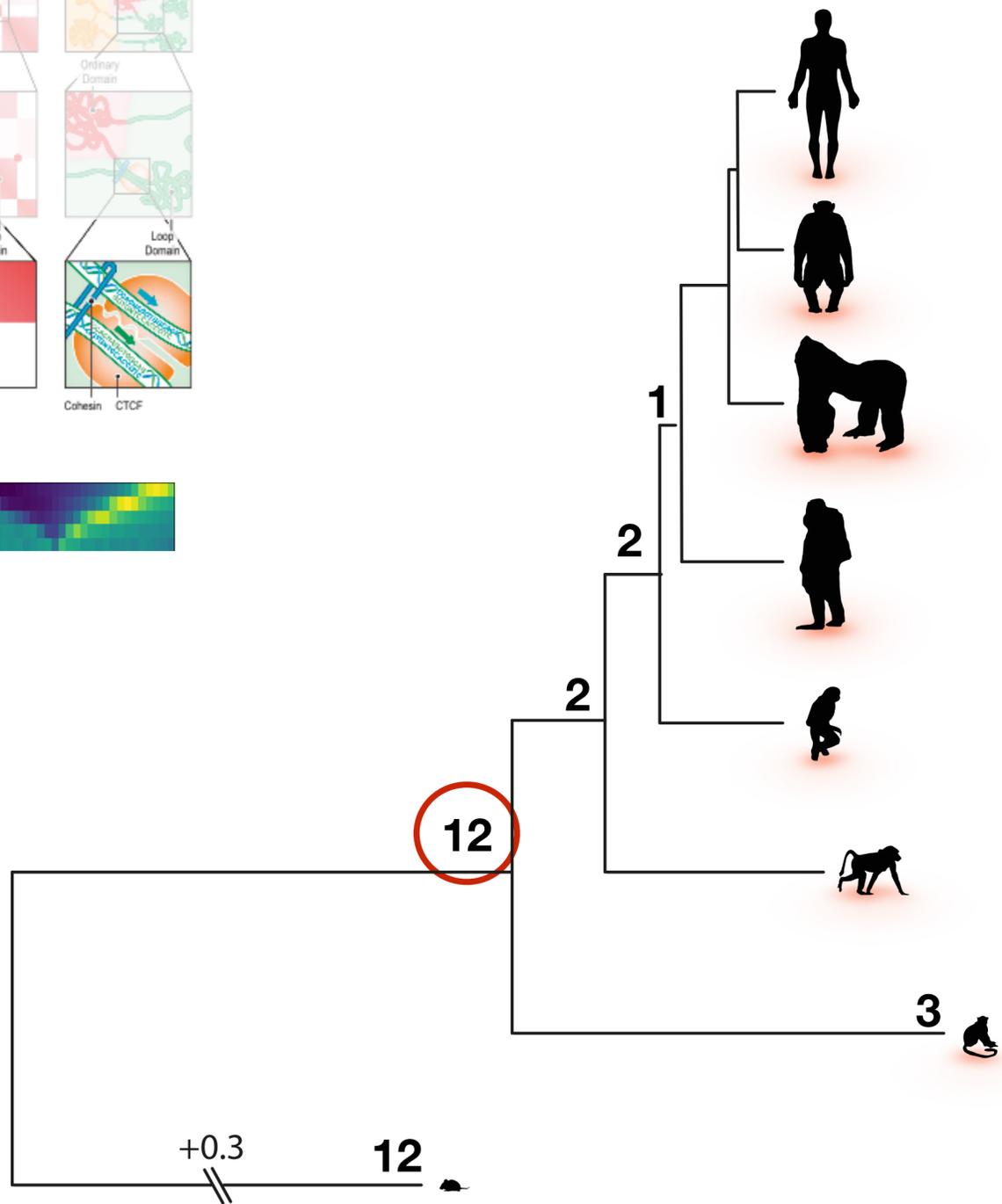


LTR 13 (Long Terminal Repeat) for HERVK13 endogenous retrovirus

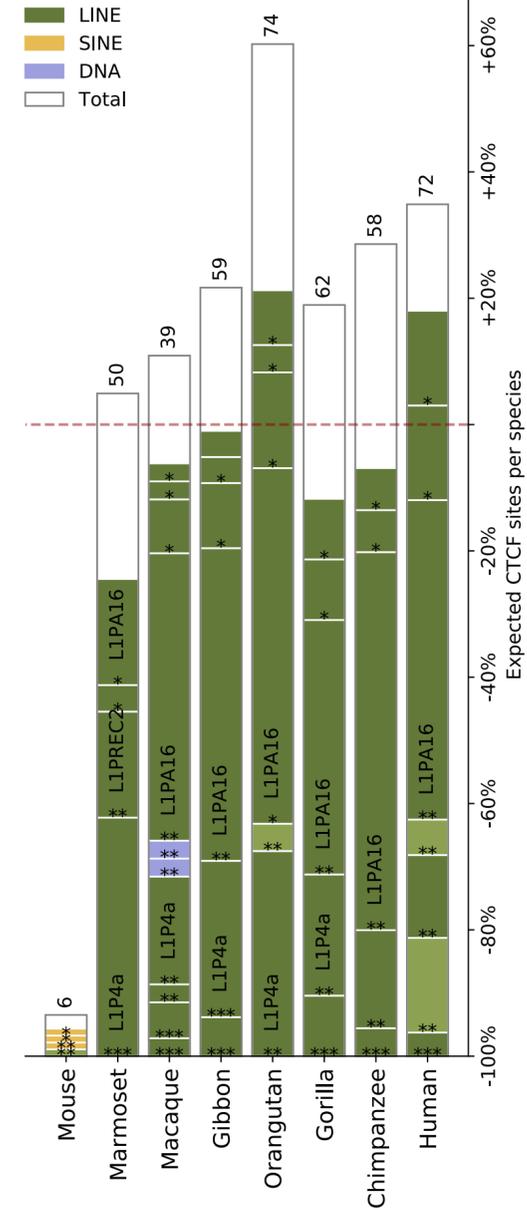


# Loops

Conservation of CTCF sites



■ LTR  
■ LINE  
■ SINE  
■ DNA  
 Total



3' end of L1 retrotransposon, L1PA16\_3end subfamily



# Summary

- Conservation of 3D structure after chromosomal rearrangements.
- Recently duplicated regions are more isolated from surrounding DNA.
- Compartments are very conserved in primates; detectable changes may not be related to cell-specific features.
- TAD borders conserved with similar selective strength against gain and loss
- New, but few primate specific expansions carrying CTCF sites
- Selection against the creation of new and strong CTCF sites

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

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**cnag**

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Centre for Genomic Regulation

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