

Fossilized chromosomes from woolly mammoth

Marc A. Marti-Renom CNAG-CRG · ICREA

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Marcela Sandoval Velasco (ex) Gilbert Lab



Olga Dudchenko Aiden Lab

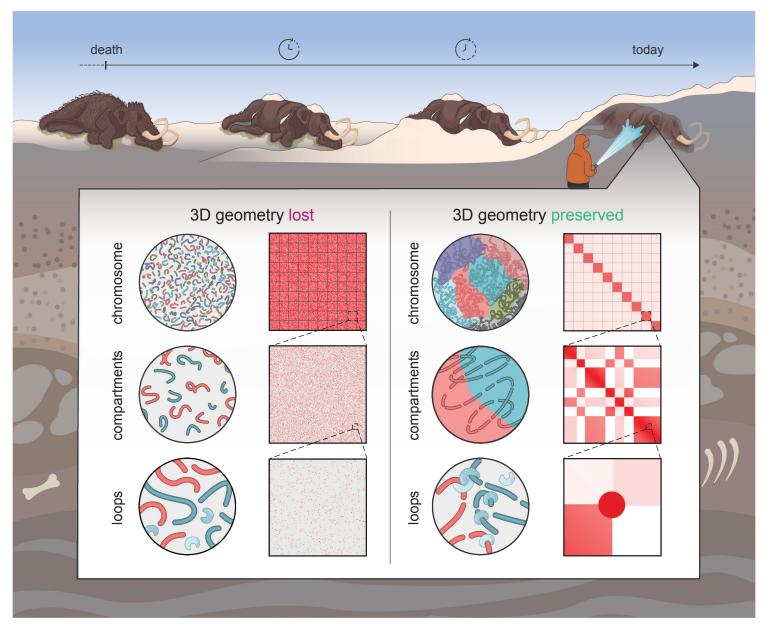


Juan Antonio Rodríguez (ex) Marti-Renom Lab



Cynthia Perez Estrada (ex) Aiden Lab

What happens to the nucleus in 10s of thousands of years?



A "whoolly" phenomenal sample



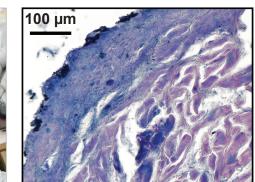
Dan Fisher UMich, Museum of Paleontology

Valeri Plotnikov Sakha Academy of Sciences

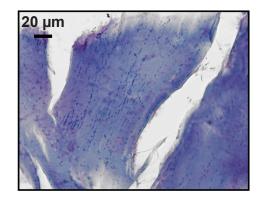
- Found in permafrost in the summer of 2018
- Belaya Gora in Yakutia, Russia
- Date >45,000 years

Photo credit: Chris Waddle









Limitations of (a)DNA-Seq

What is in the genome?

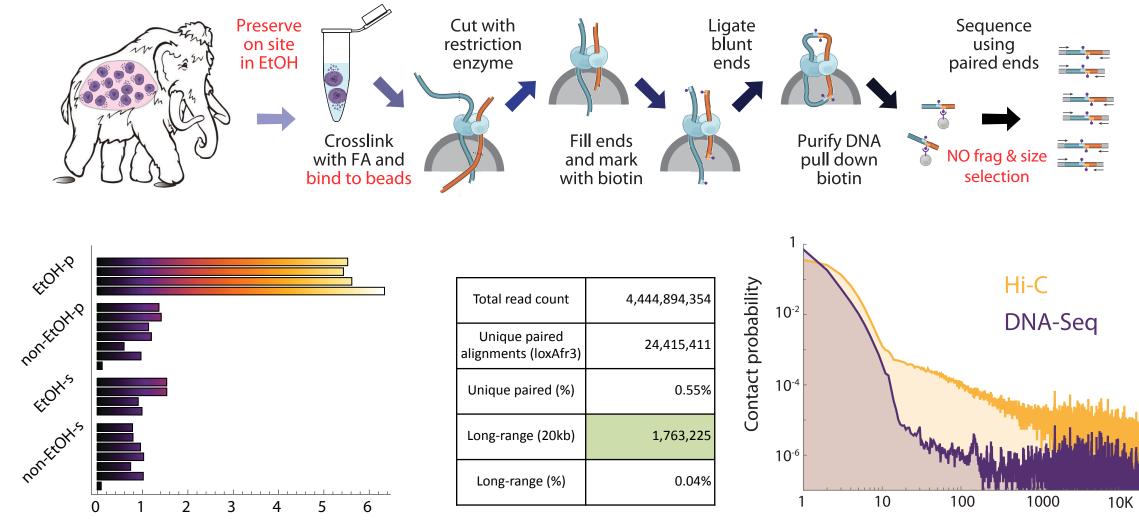
Need chrom-length de novo assemblies! aDNA-Seq relies on modern references

What is expressed in individual tissues? Need to probe transcriptional activity!

How expression patterns arise? Need to probe genetic regulation!



Paleo-HiC improves endogenous long-range contact recovery



% of Hi-C read pairs aligning to loxAfr3

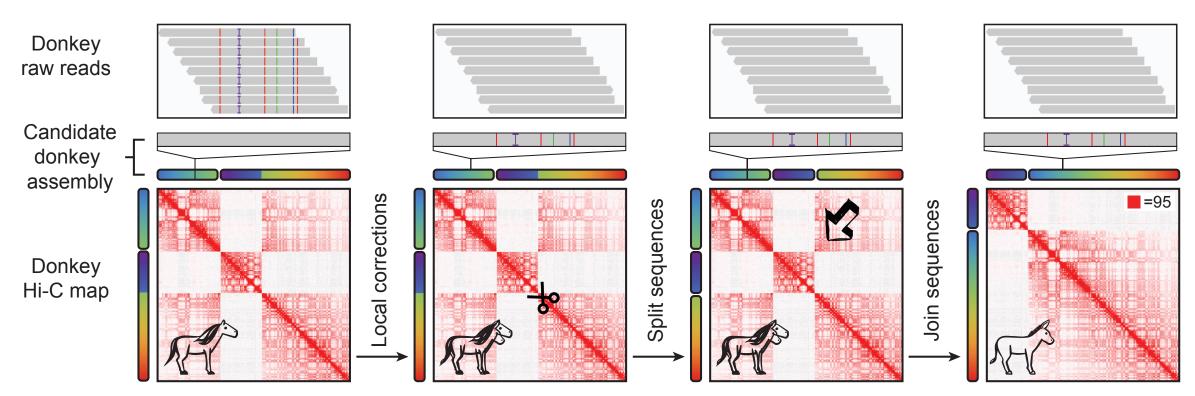
Distance (bp)

Hi-C assisted assembly

Dubchenko et al. Science. 2017 Apr 7;356(6333):92-95

Initialize with horse assembly

Final donkey assembly

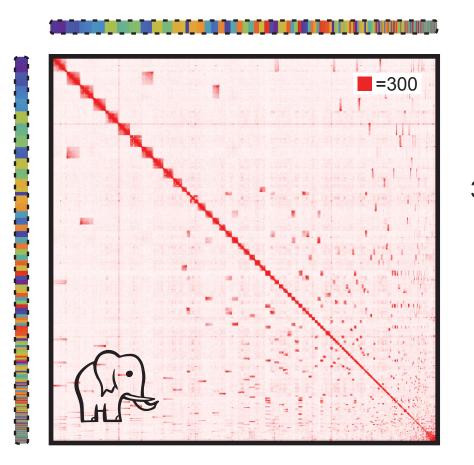


correct · split · orient · order

This is a Hi-C from mammoth

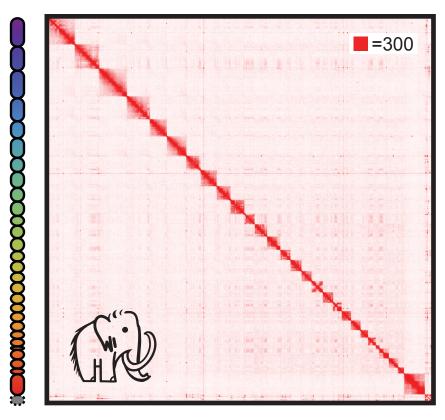
based on Loxafr3.0

PaleoHi-C vs Loxafr3.0, fragmentary African elephant assembly



3D assisted assembly

PaleoHi-C vs MamPri_Loxafr3.0_assisted_HiC, chromosome-length mammoth assembly



Limitations of (a)DNA-Seq

Hallmarks of a successful Hi-C experiment

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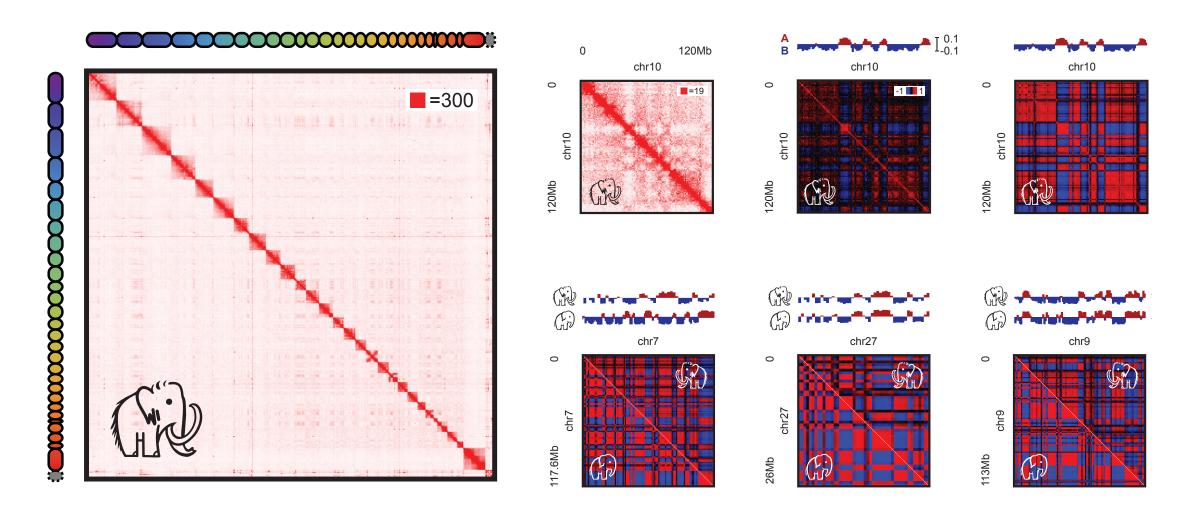
How expression patterns arise? Need to probe genetic regulation!



- Chromosome territories

Facilitates de novo assembly of whole chromosomes

Compartments preserved in a 52K years old sample



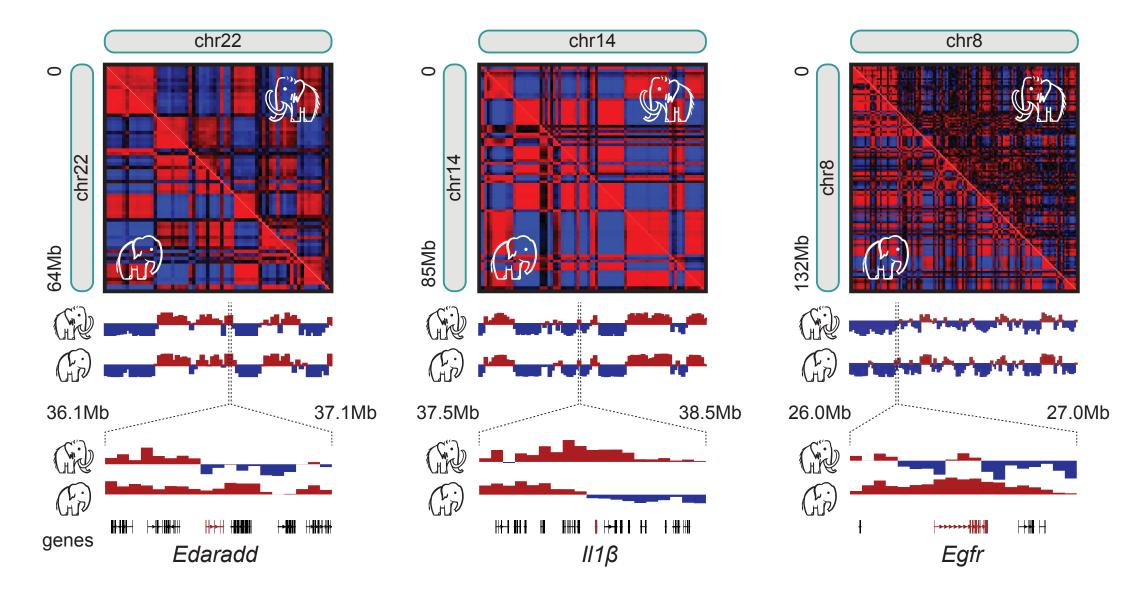
Tissue specific compartmentalization chr18

chr18 chr18 chr18 chr18 chr18 chr18 chr18

0

84Mb

Mammoth Altered Regulation Sequences (MARS)



Limitations of (a)DNA-Seq

Hallmarks of a successful Hi-C experiment

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How expression patterns arise?

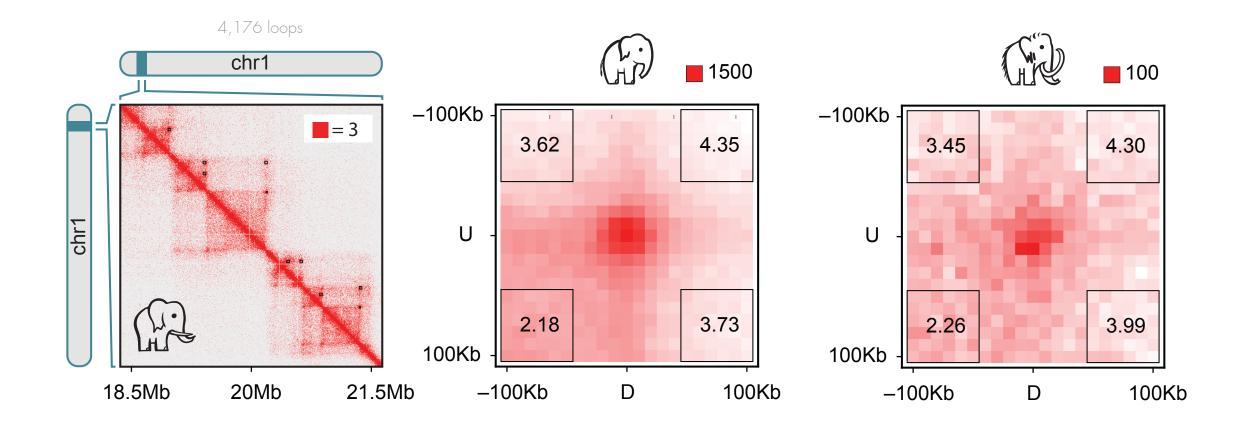
Need to probe genetic regulation!



- Facilitates de novo assembly of whole chromosomes
- Active and inactive chromatin compartments Probes **Transcriptional activity**

Paleo-hic recovers loop signatures!

Rao, Huntley et al., Cell 2014



Limitations of (a)DNA-Seq

Hallmarks of a successful Hi-C experiment

- Chromosome territories

What is in the genome?

Need chrom-length de novo assemblies! aDNA-Seq relies on modern references



What is expressed in individual tissues? Need to probe transcriptional activity!

How expression patterns arise?

Need to probe genetic regulation!



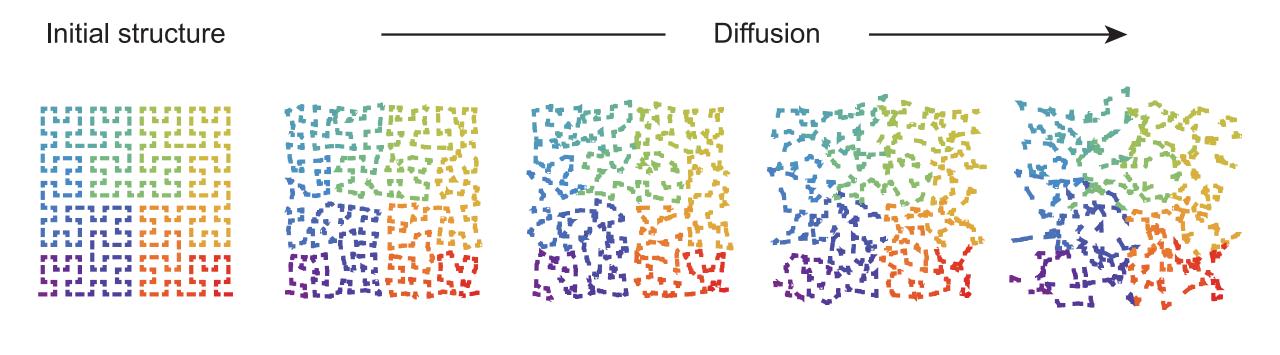


Probes Transcriptional activity

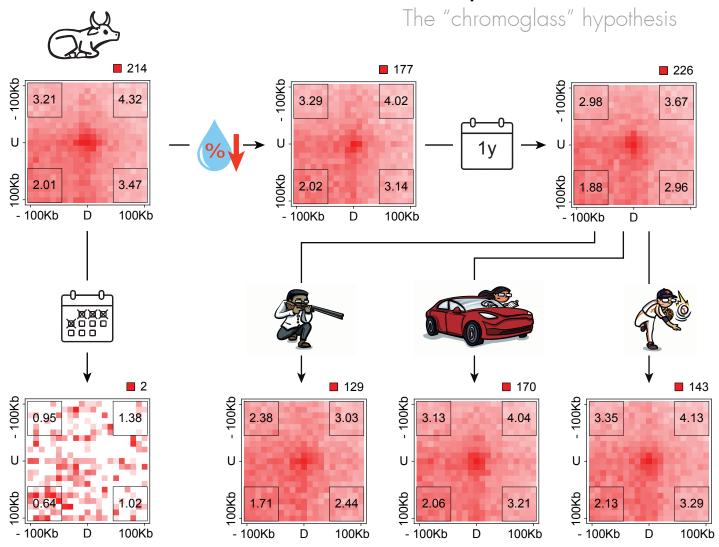
- Chromatin Loops Reveals **regulation of individual genes**

How is this possible? (q.k.a. reviewer #3)

The "chromoglass" hypothesis



How is this possible? (q.k.a. reviewer #3)



THREE-DIMENSIONAL GENOME ARCHITECTURE PERSISTS IN A 52,000-YEAR-OLD WOOLLY MAMMOTH SKIN SAMPLE

Marcela Sandoval-Velasco[#], Olga Dudchenko^{#,†}, Juan Antonio Rodríguez#, Cynthia Pérez Estrada#, Marianne Dehasque, Claudia Fontsere, Sarah S.T. Mak, Rugayya Khan, Vinícius G. Contessoto, Antonio B. Oliveira Junior, Achyuth Kalluchi, Bernardo J. Zubillaga Herrera, Jiyun Jeong, Renata P. Roy, Ishawnia Christopher, David Weisz, Arina D. Omer, Sanjit S. Batra, Muhammad S. Shamim, Neva C. Durand, Brendan O'Connell, Alfred L. Roca, Maksim V. Plikus, Mariya A. Kusliy, Svetlana A. Romanenko, Natalya A. Lemskaya, Natalya A. Serdyukova, Svetlana A. Modina, Polina L. Perelman, Elena A. Kizilova, Sergei I. Baiborodin, Nikolai B. Rubtsov, Gur Machol, Krisha Rath, Ragini Mahajan, Parwinder Kaur, Andreas Gnirke, Isabel Garcia-Treviño, Rob Coke, Joseph P. Flanagan, Kelcie Pletch, Aurora Ruiz-Herrera, Valerii Plotnikov, Innokentiy S. Pavlov, Naryya I. Pavlova, Albert V. Protopopov, Michele Di Pierro, Alexander S. Graphodatsky, Eric S. Lander, M. Jordan Rowley, Peter G. Wolynes, José N. Onuchic, Love Dalén, Marc A. Marti-Renom[†], M. Thomas P. Gilbert[†],

> Erez Lieberman Aiden† Cell 2024



Take home messages:



- Chromosome fossils also enable to assemble the entire genome of extinct species.
- Chromosome fossils help to interpret how the genomes of those species were organized in space as well as its functional activity.
- Key mammoth genes associated with hair follicle development were active in mammoth compared to modern elephants.
- Specific loop interactions in the genome regulating gene expression were also visible and conserved in the mammoth sample.
- Chromoglass (a glass-like-state of the chromosomes) allowed the genome structure to be physically conserved over such long period of time.

https://tinyurl.com/MammothPaper

Mammoth foot Photo credit: Love Dalén



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











Generalitat de Catalunya



National Human Genome Research Institute