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# THE EVOLUTIONARY HISTORY OF DENISOVAN AND NEANDERTHAL Y CHROMOSOMES

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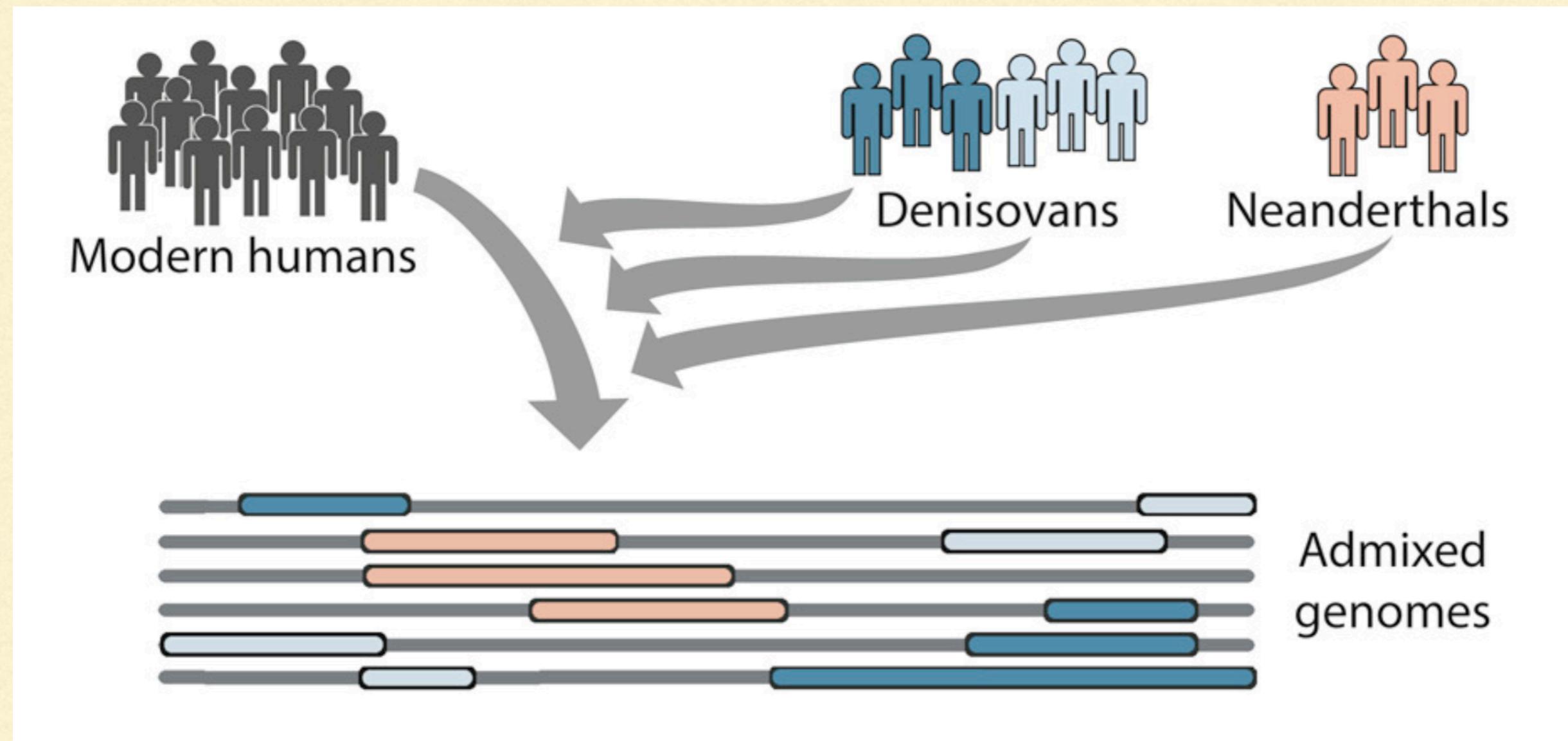
MAX-PLANCK-GESELLSCHAFT

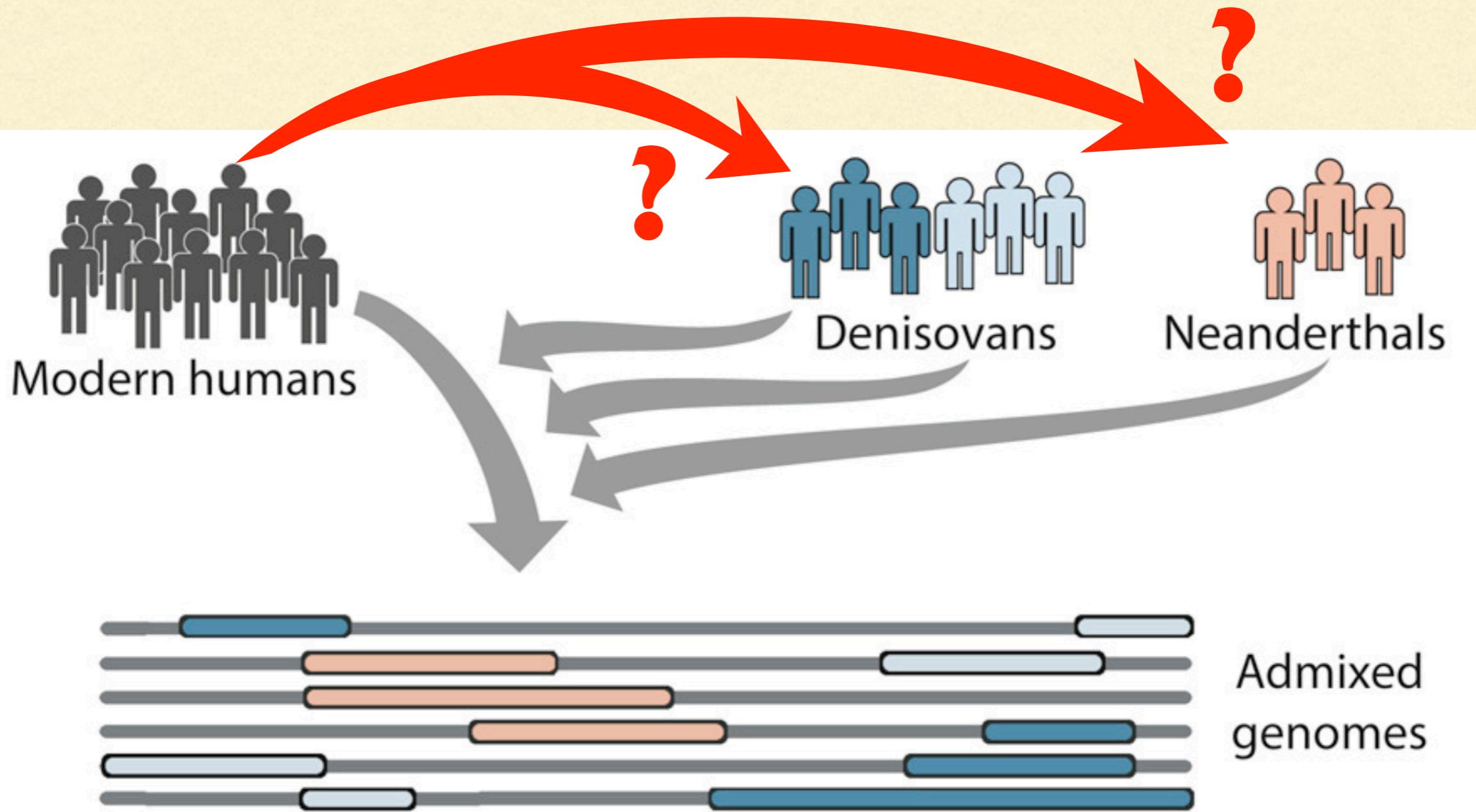
**Martin Petr**

***Max Planck Institute for  
Evolutionary Anthropology***

*Leipzig, Germany*

# ADMIXTURE FROM ARCHAIC HUMANS INTO MODERN HUMANS

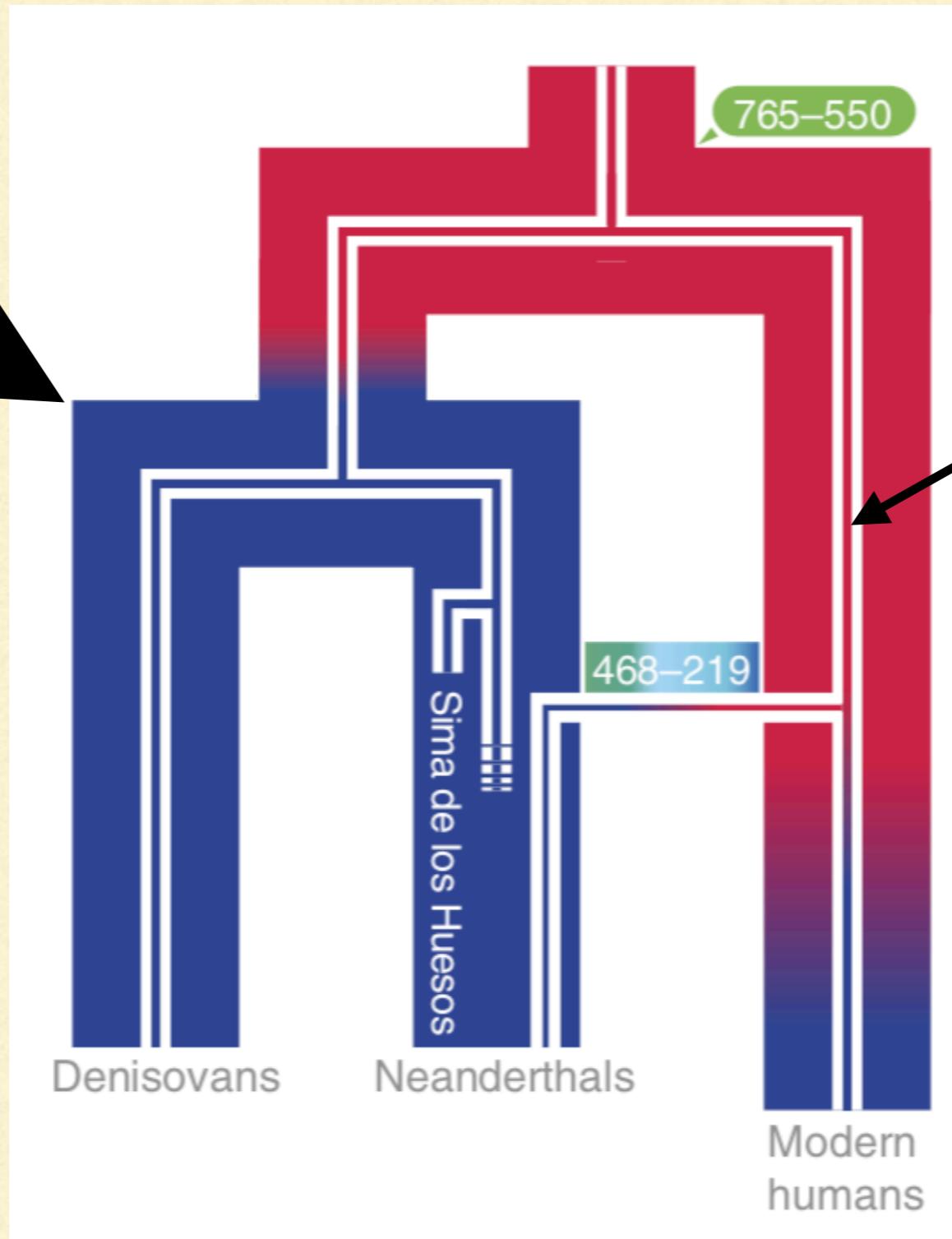
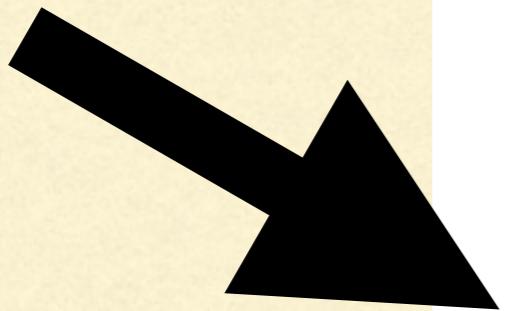




# MODERN → ARCHAIC HUMAN GENE FLOW

## — AUTOSOMAL DNA VS MITOCHONDRIAL DNA

autosomal DNA



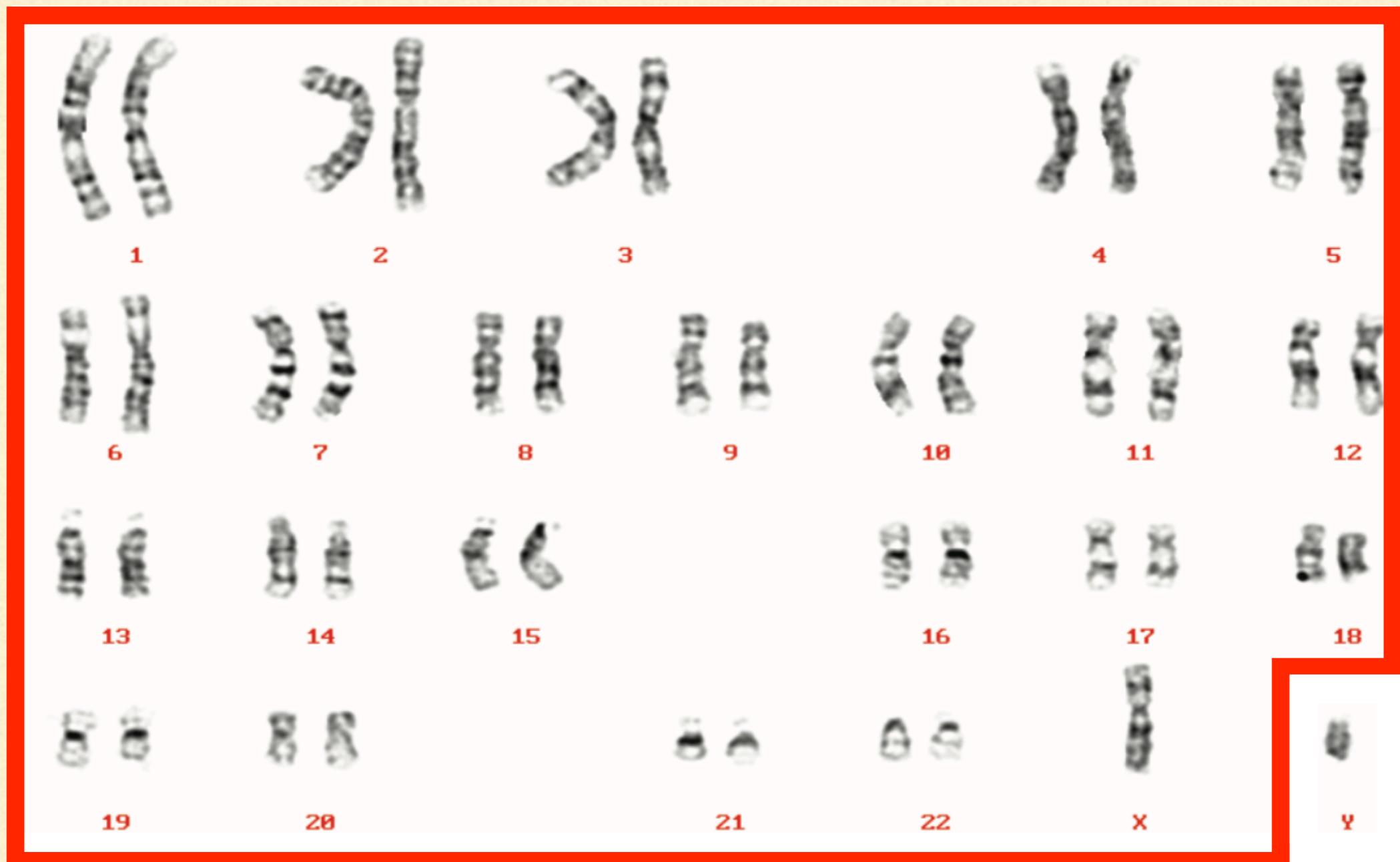
mtDNA

Meyer et al. *Nature* 2014.  
Posth et al. *Nat Comm.* 2017

# SO FAR, HIGH QUALITY ARCHAICS WERE FEMALE

—Y CHROMOSOMES LARGELY A MYSTERY

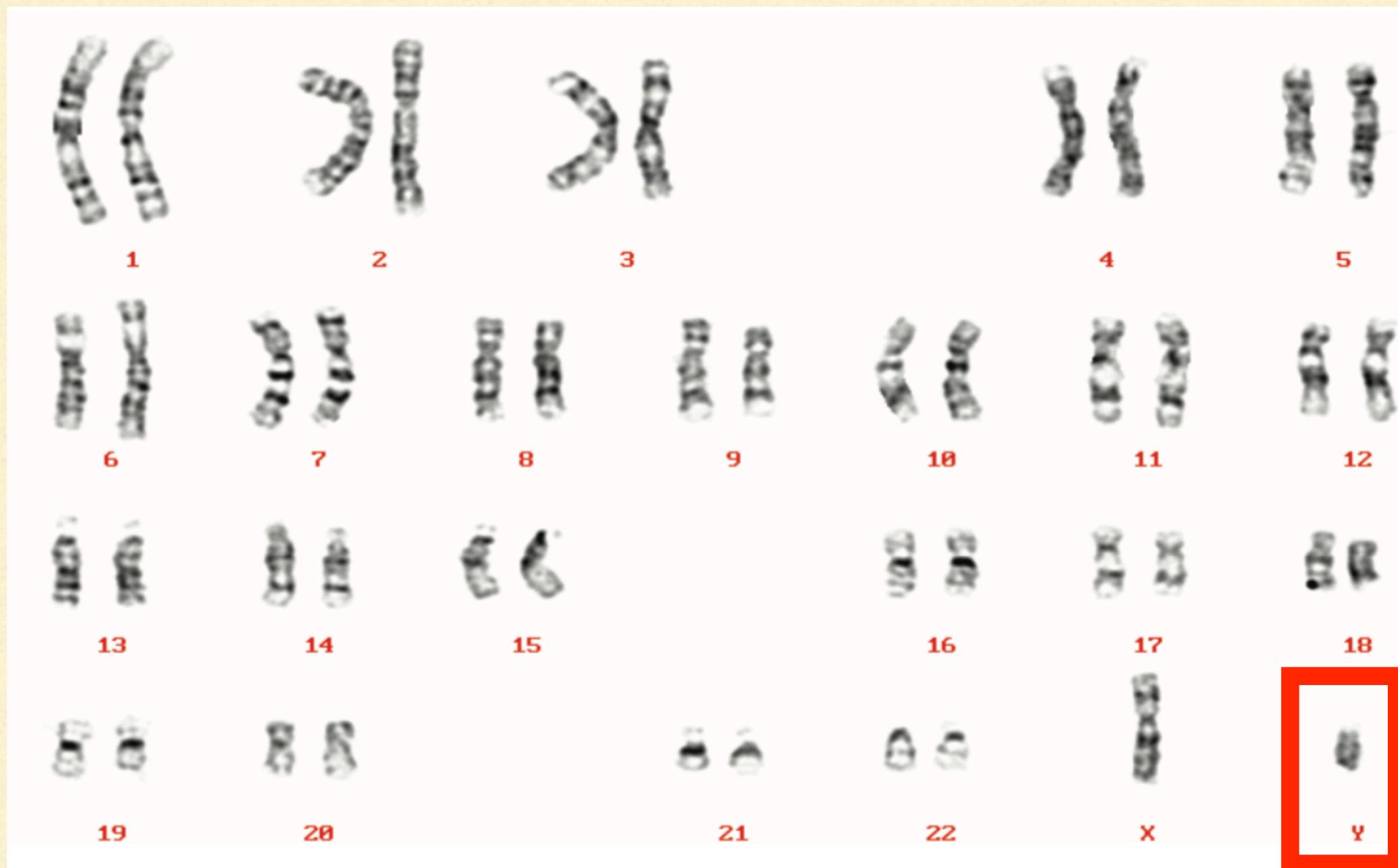
human chromosomes:



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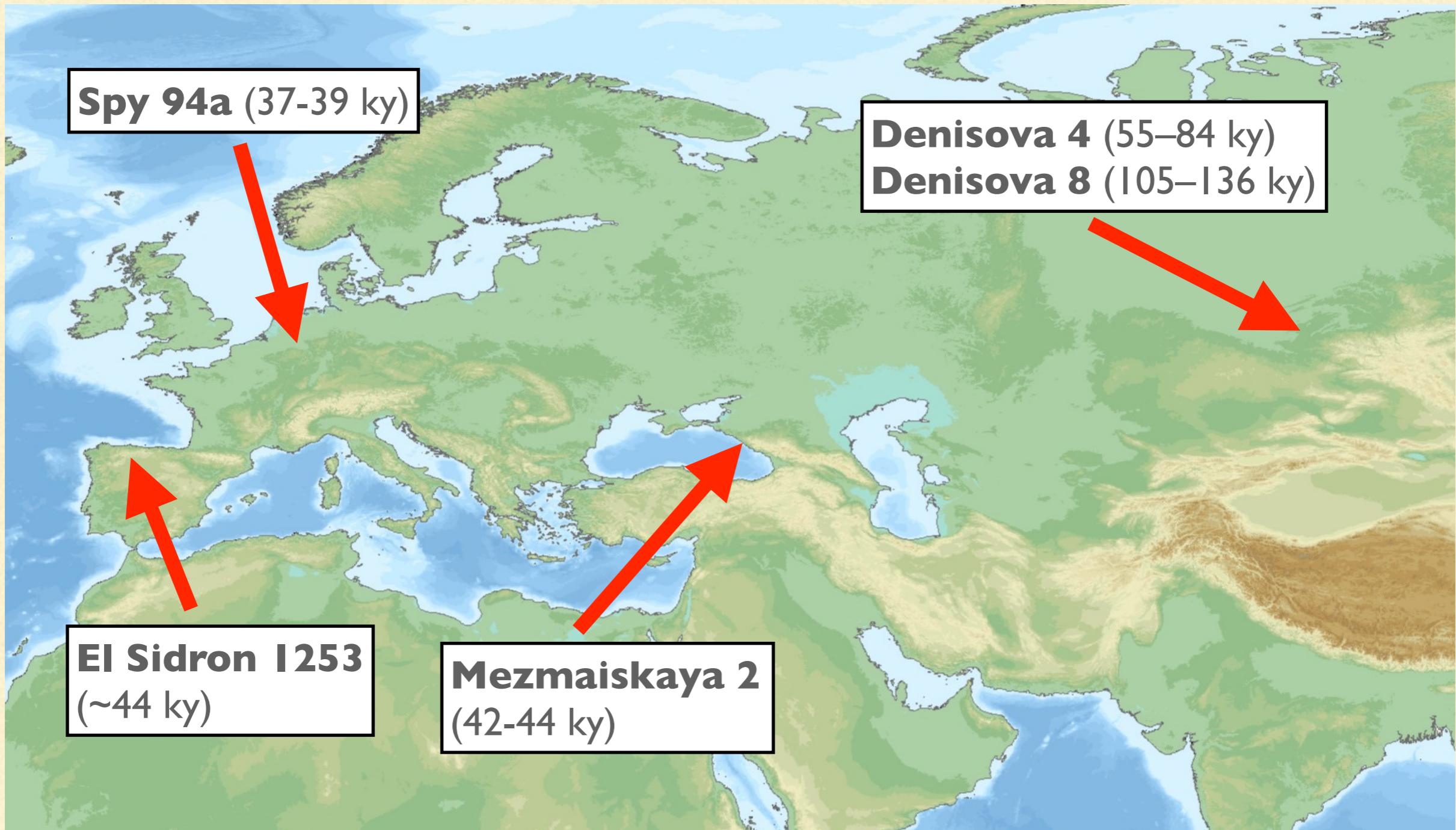
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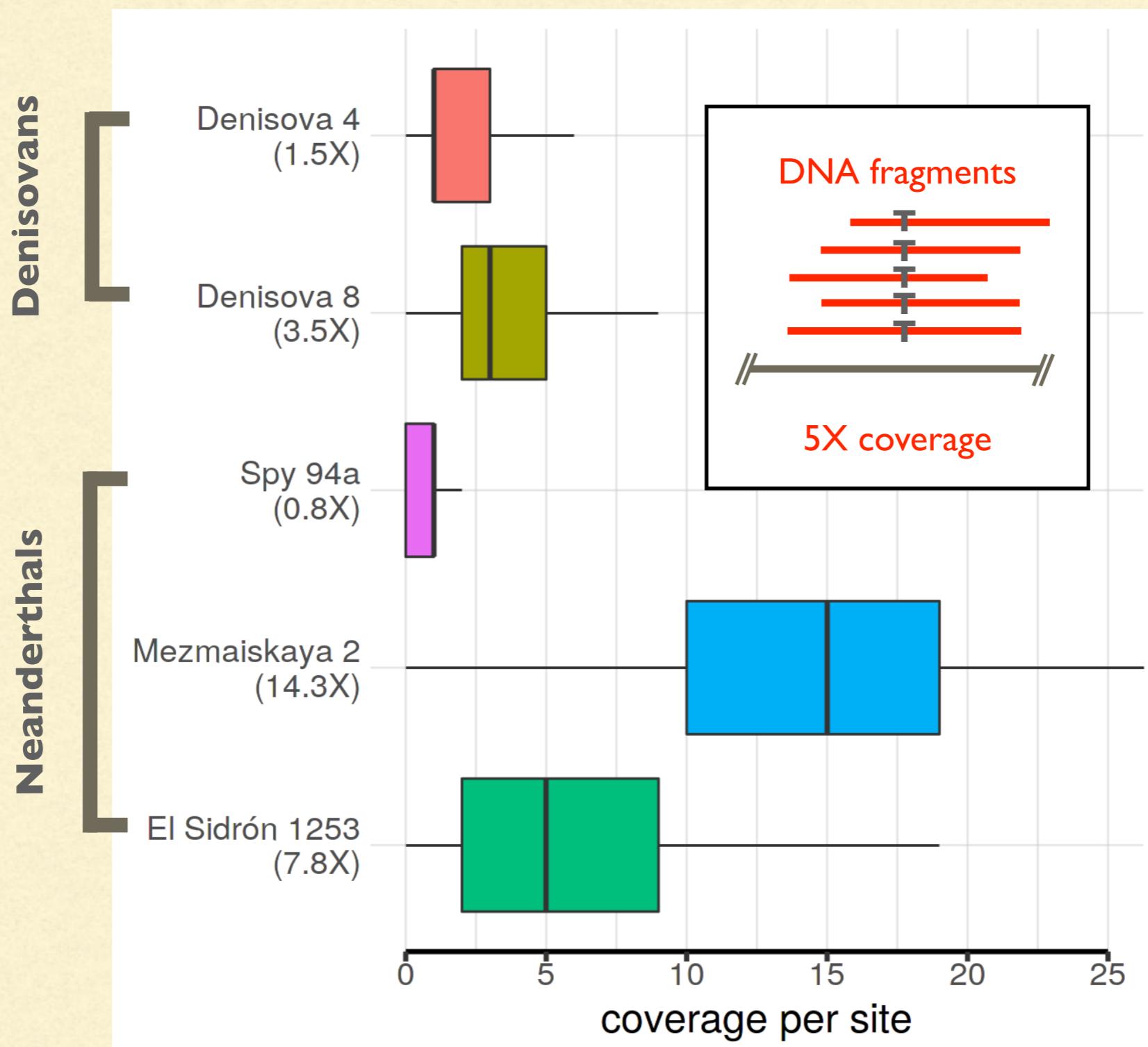
# FOCUSING ON Y CHROMOSOMES

—ARCHAIC HUMAN MALES



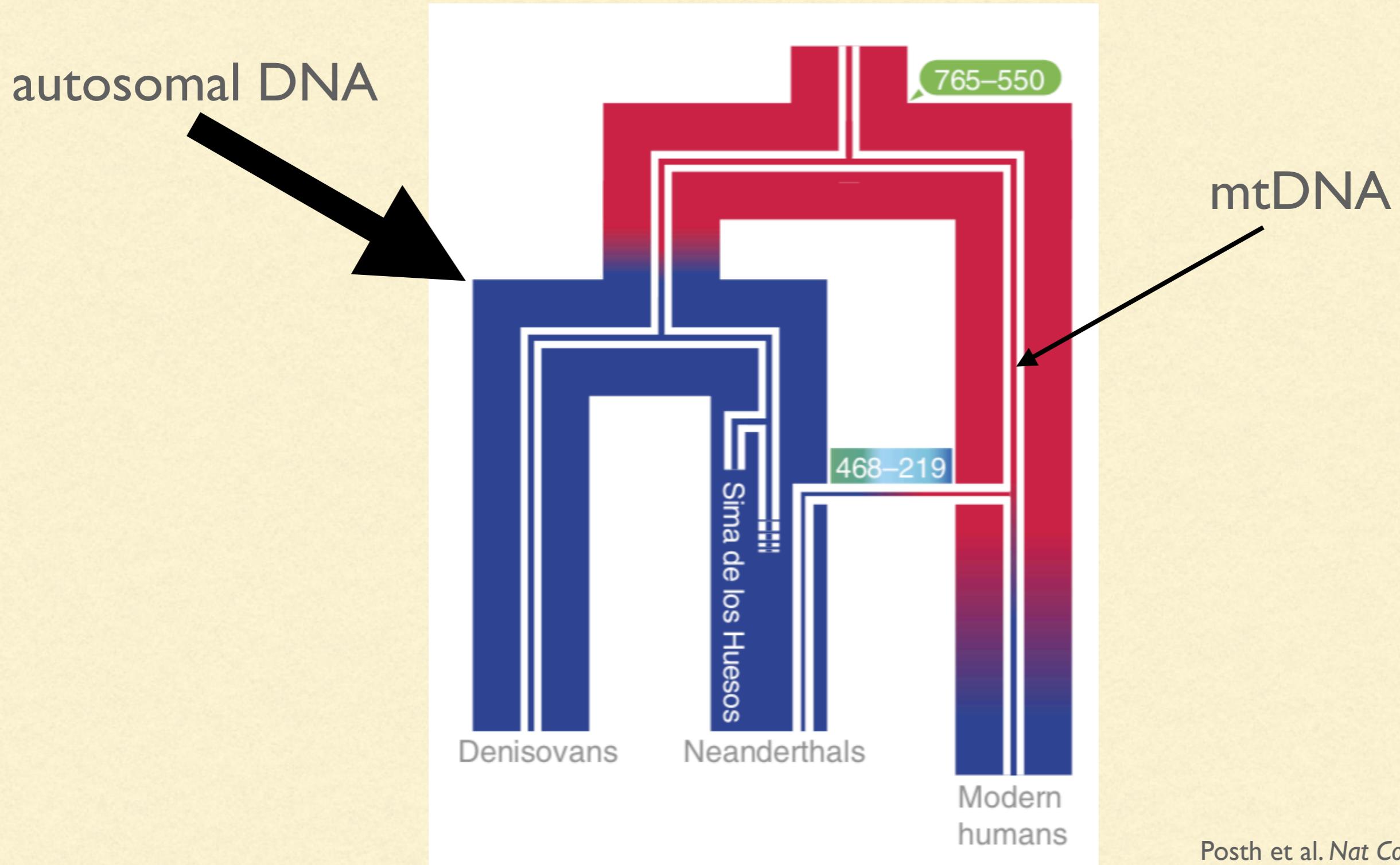
# COVERAGE OF Y CHROMOSOMES

(USING “WHOLE CHROMOSOME CAPTURE” METHOD)

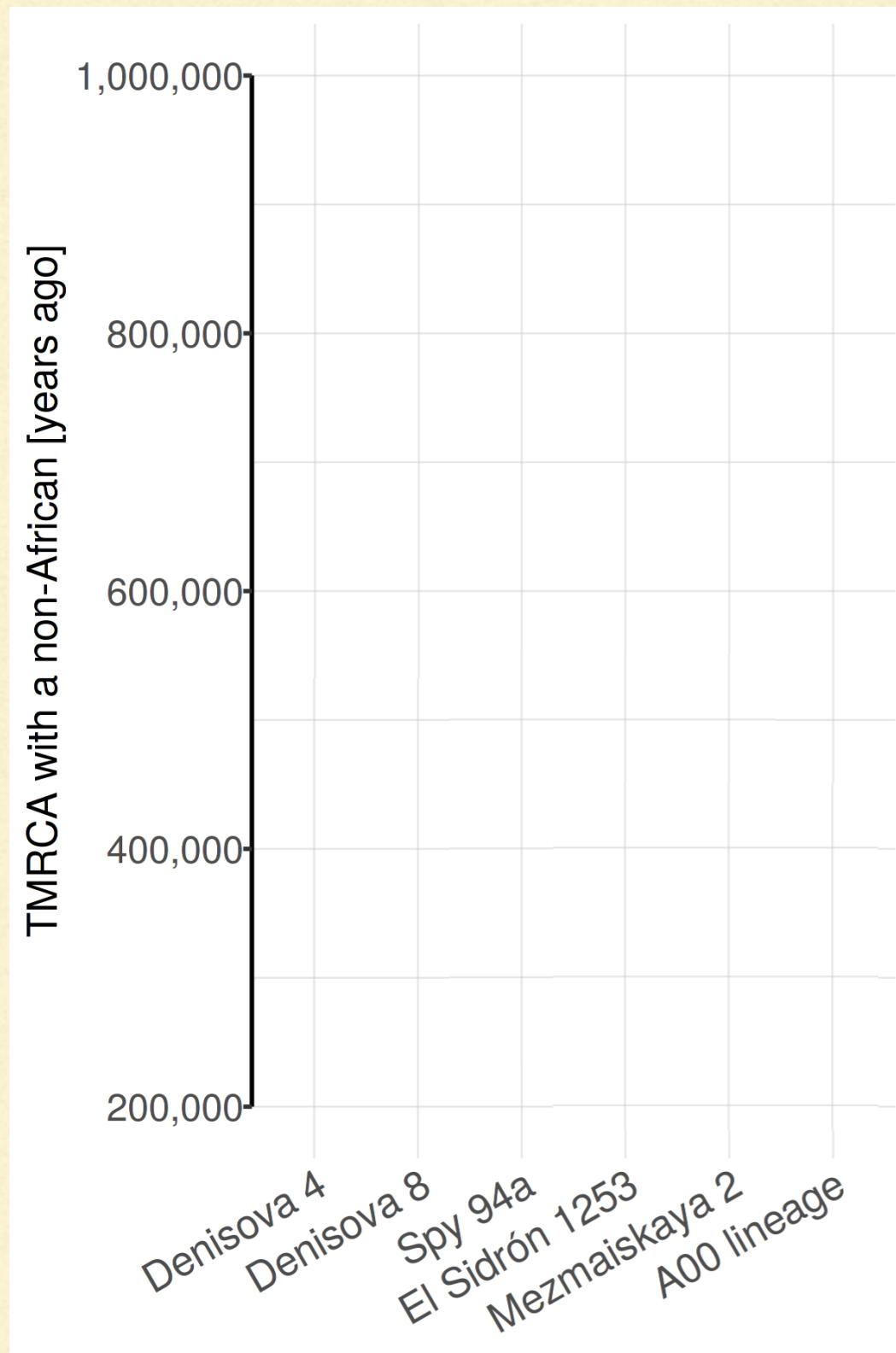


# DISCORDANT AUTOSOMAL AND MT DATA

## ... WHAT ABOUT Y CHROMOSOMES?

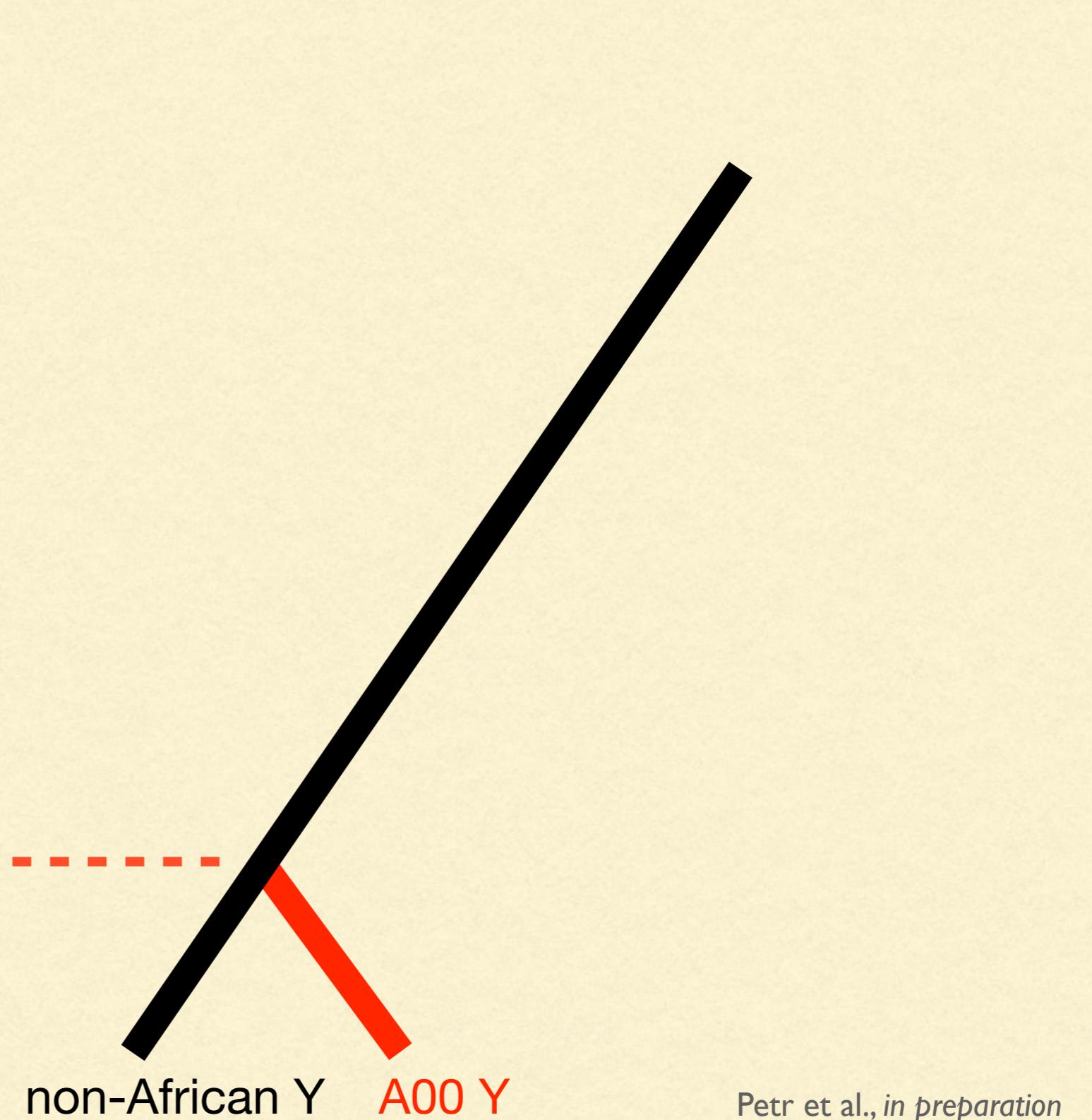
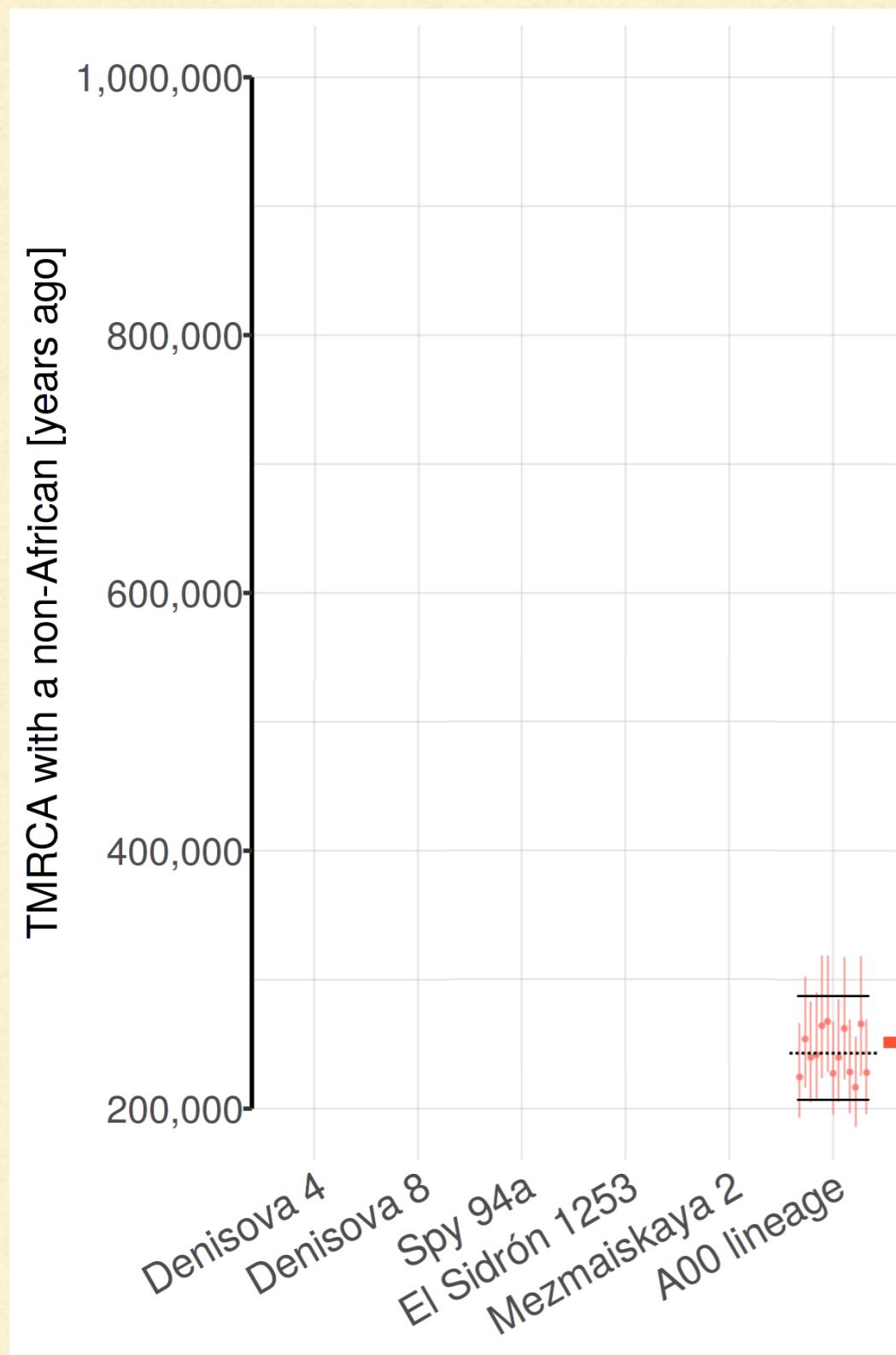


# ESTIMATES OF TMRCA WITH MODERN HUMAN Y CHROMOSOMES

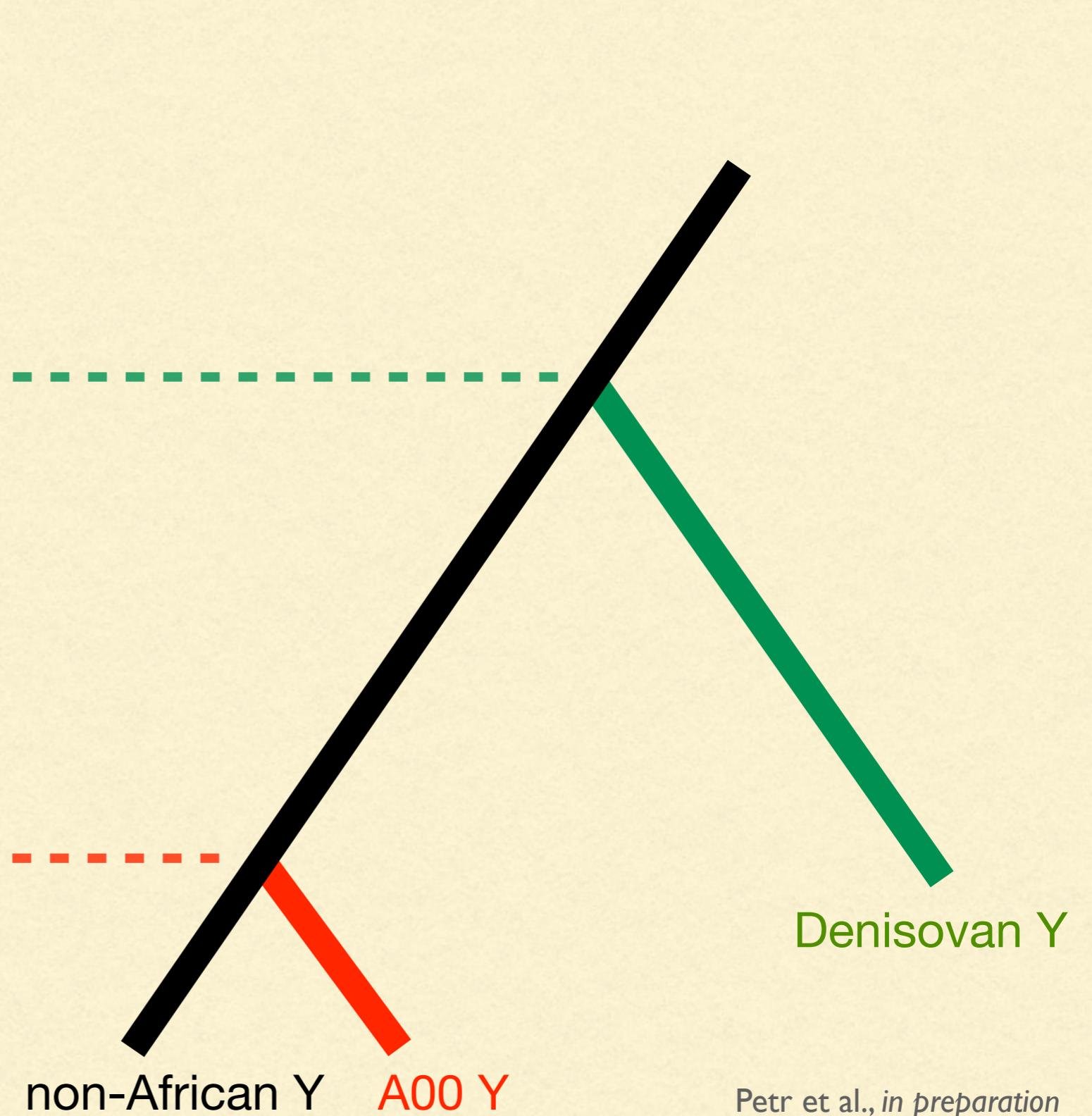
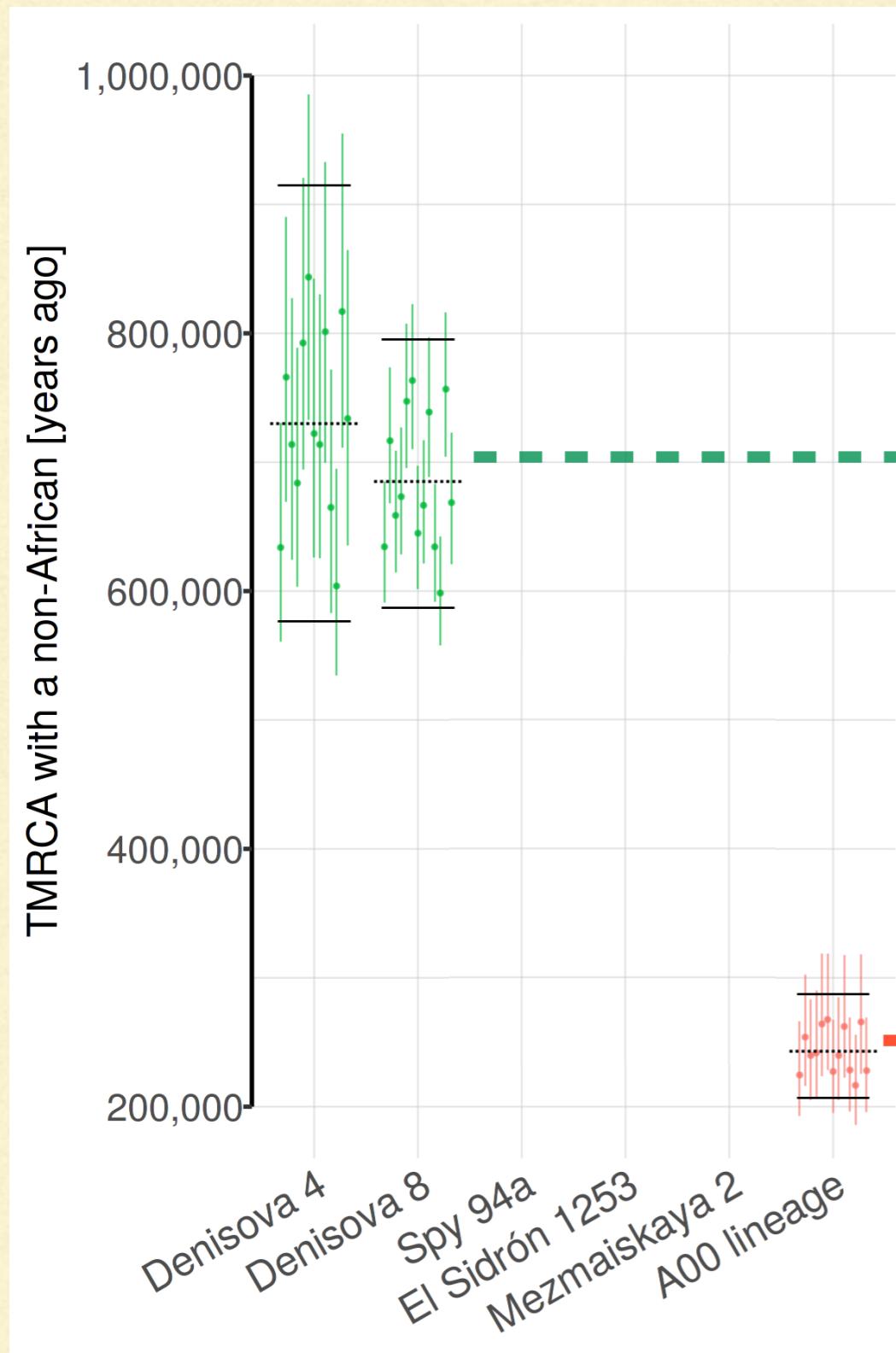


non-African Y

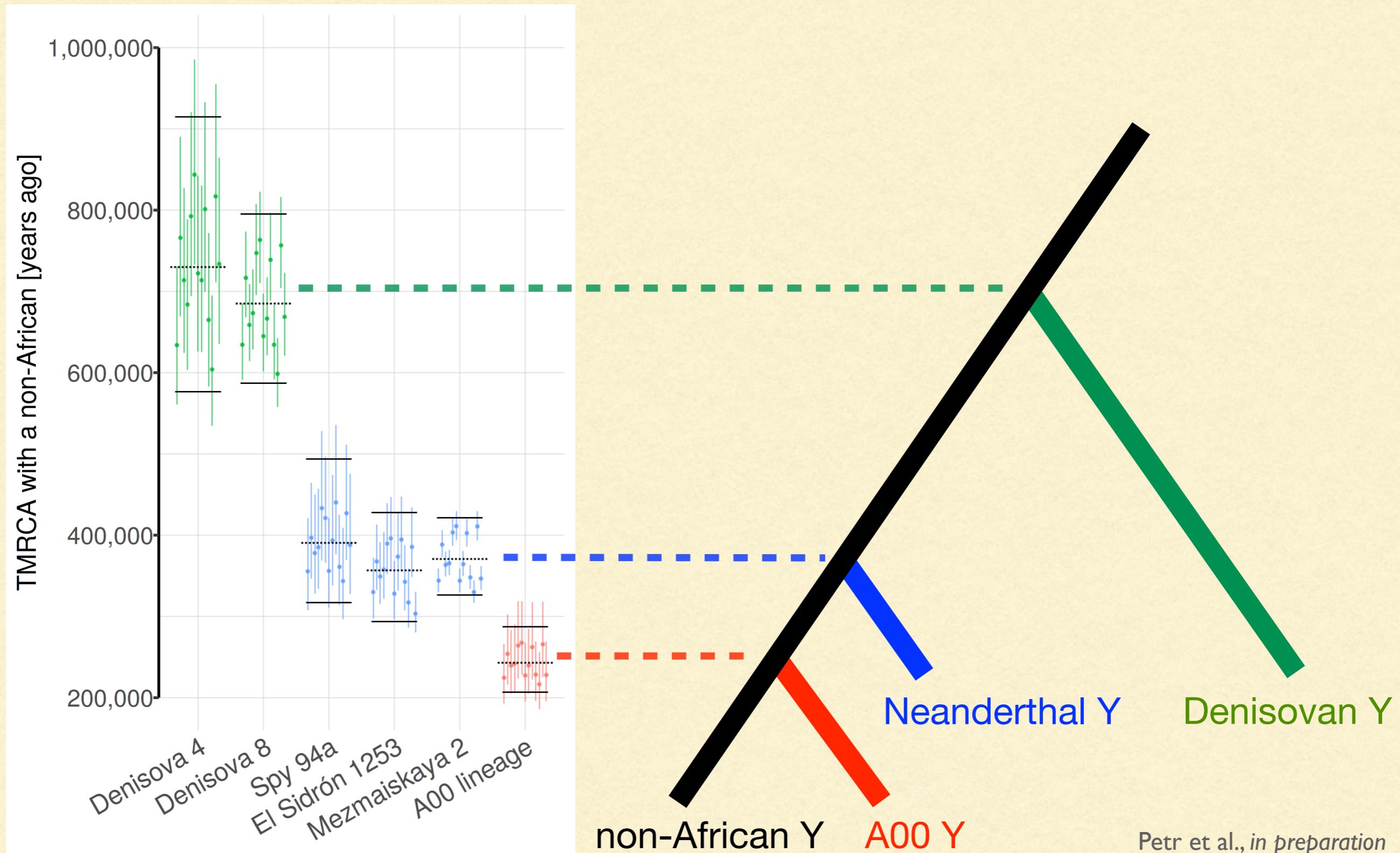
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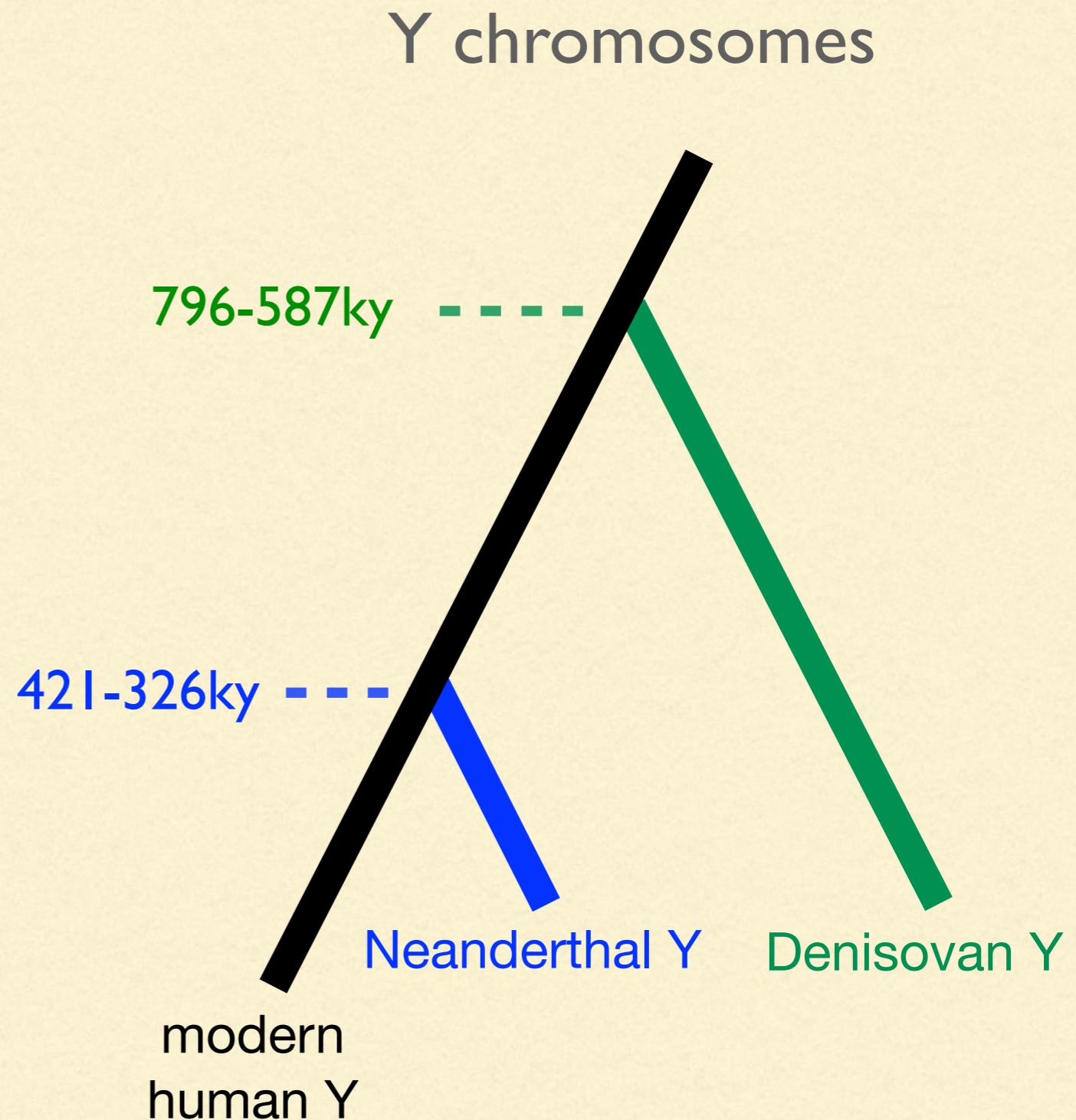
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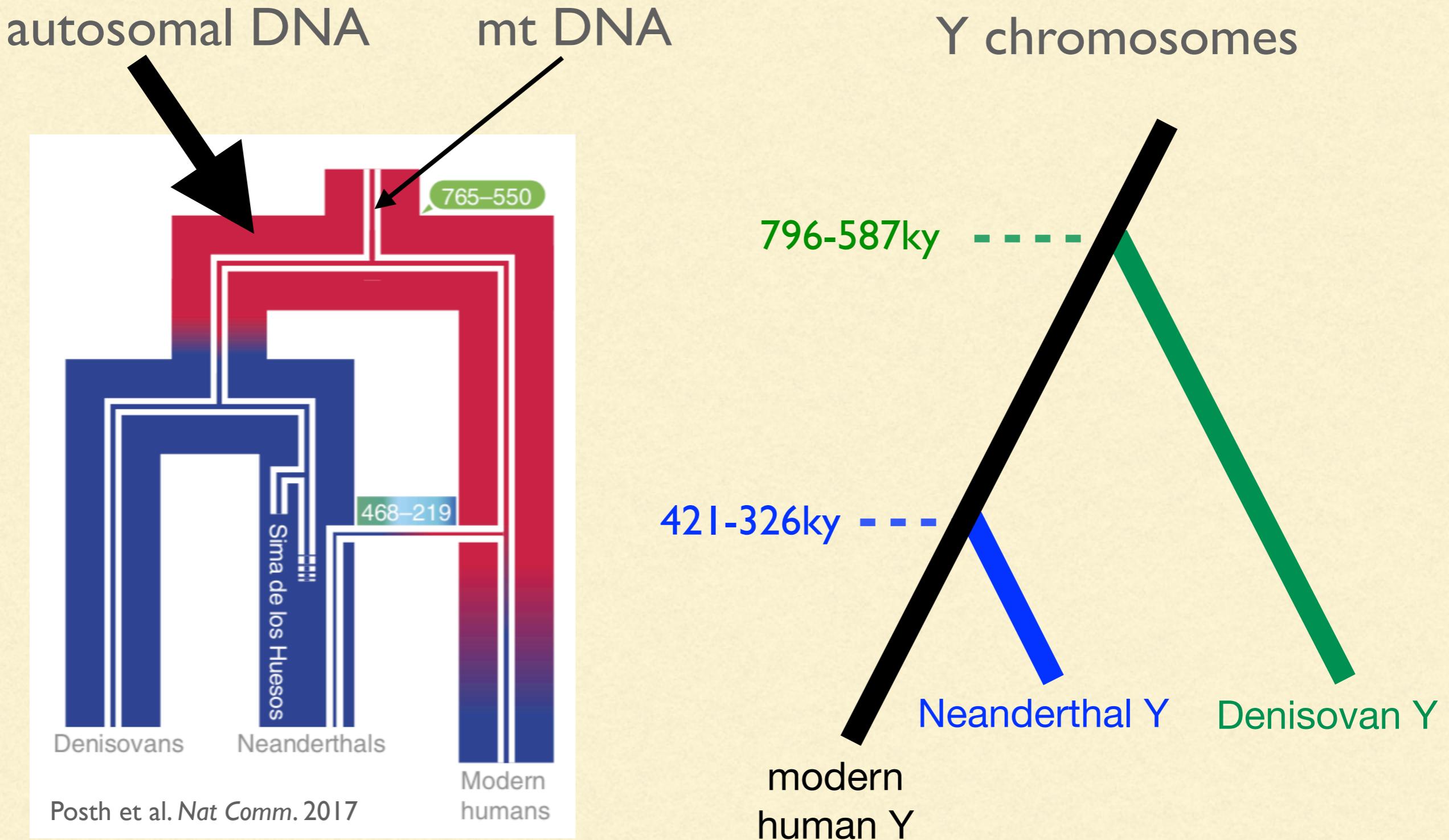
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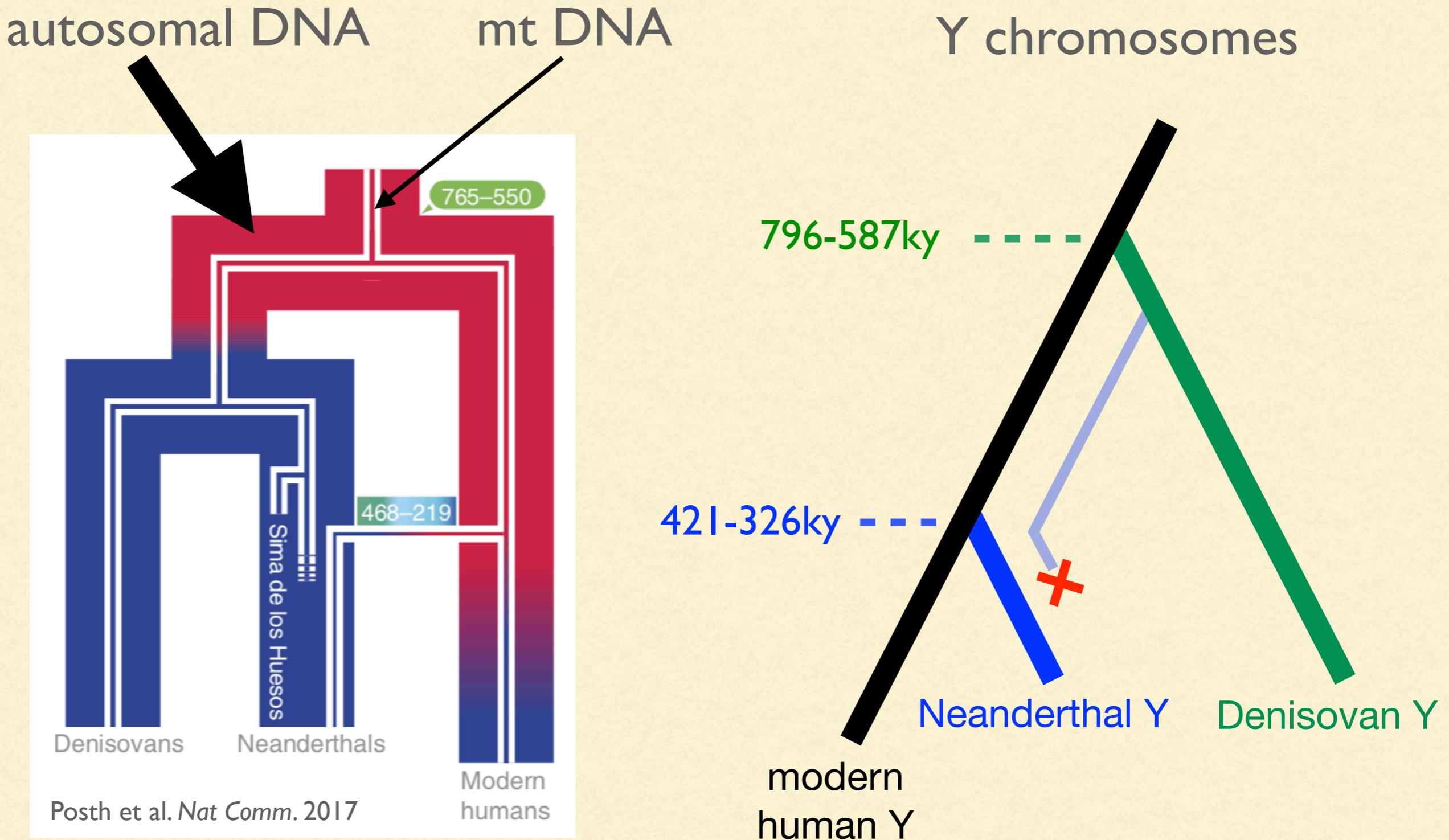
# REPLACEMENT OF NEANDERTHAL Y CHROMOSOMES?



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PROBLEM:

**MT AND Y REPLACEMENT UNLIKELY**

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**population genetics theory:**

introgression at X% → probability of replacement = X%

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**population genetics theory:**

introgression at X% → probability of replacement = X%

**basic probability theory:**

P[mtDNA replacement] = 3%

P[Y chromosome replacement] = 3%

P[**both** mtDNA **and** Y replaced] = 3% × 3% → **0.09%**

POSSIBLE SOLUTION:

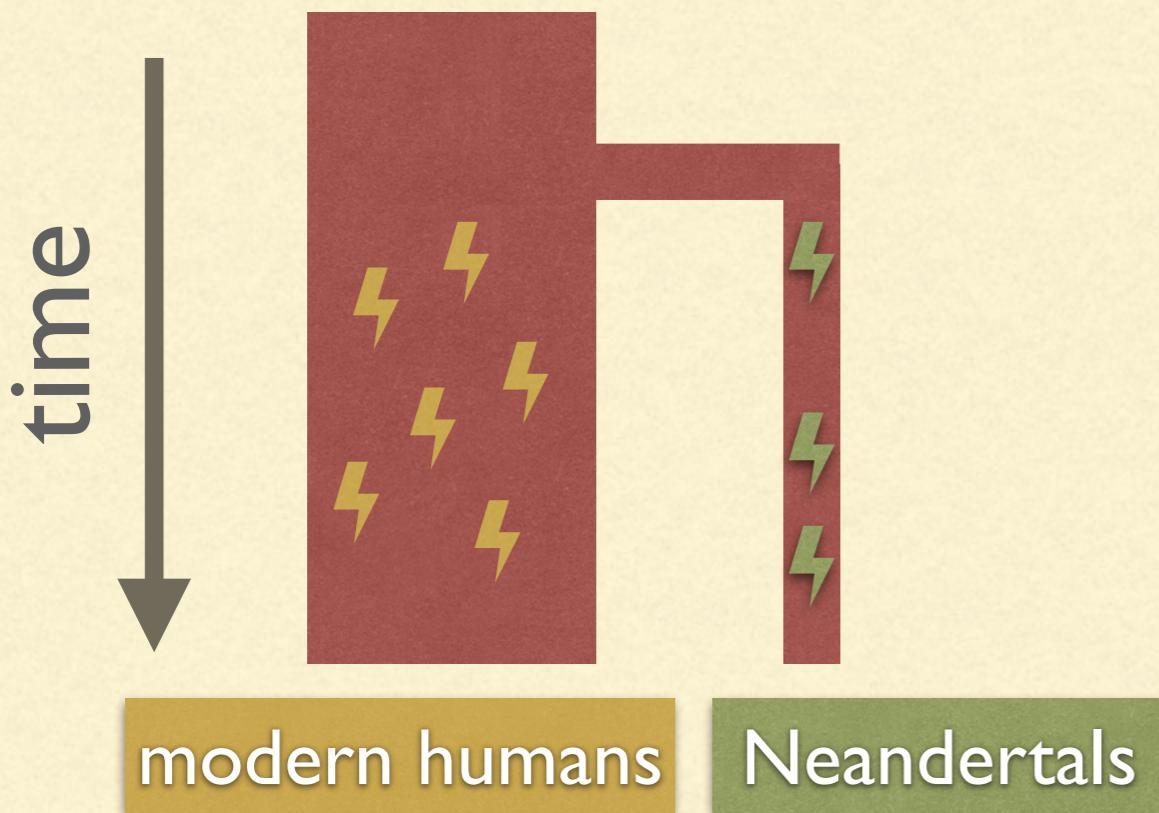
# **INTROGRESSION NOT NEUTRAL**

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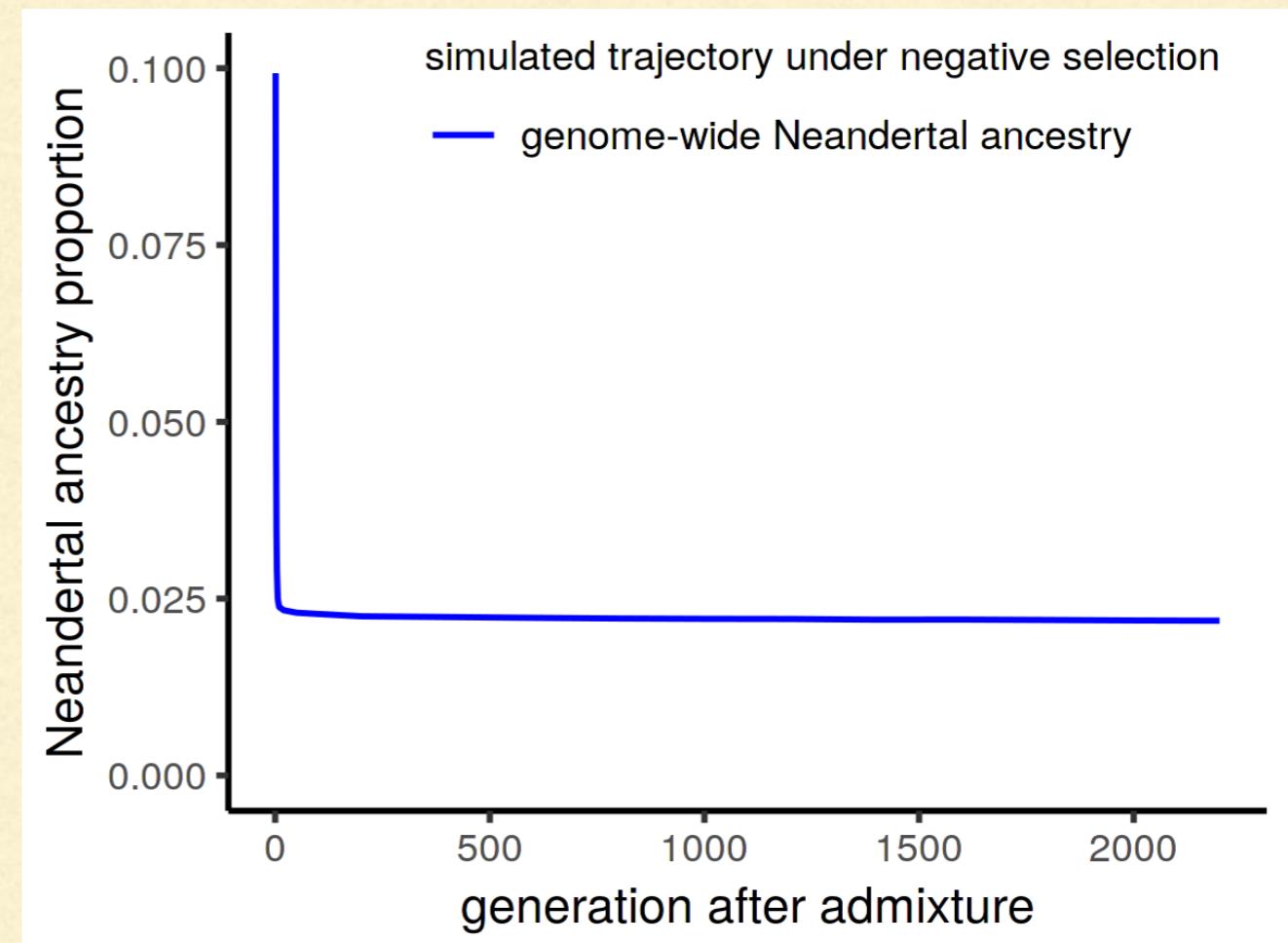
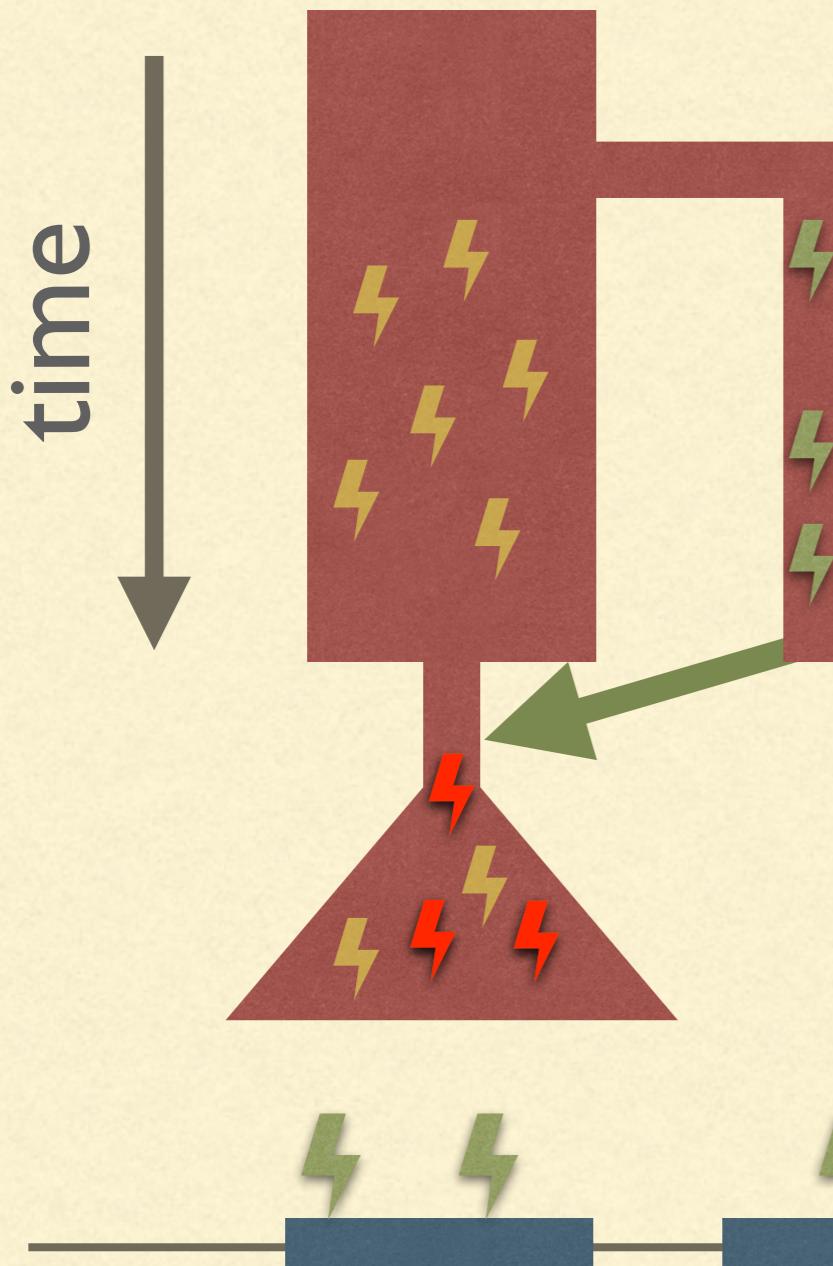
⚡ ⚡ - deleterious mutations



POSSIBLE SOLUTION:

# INTROGRESSION NOT NEUTRAL

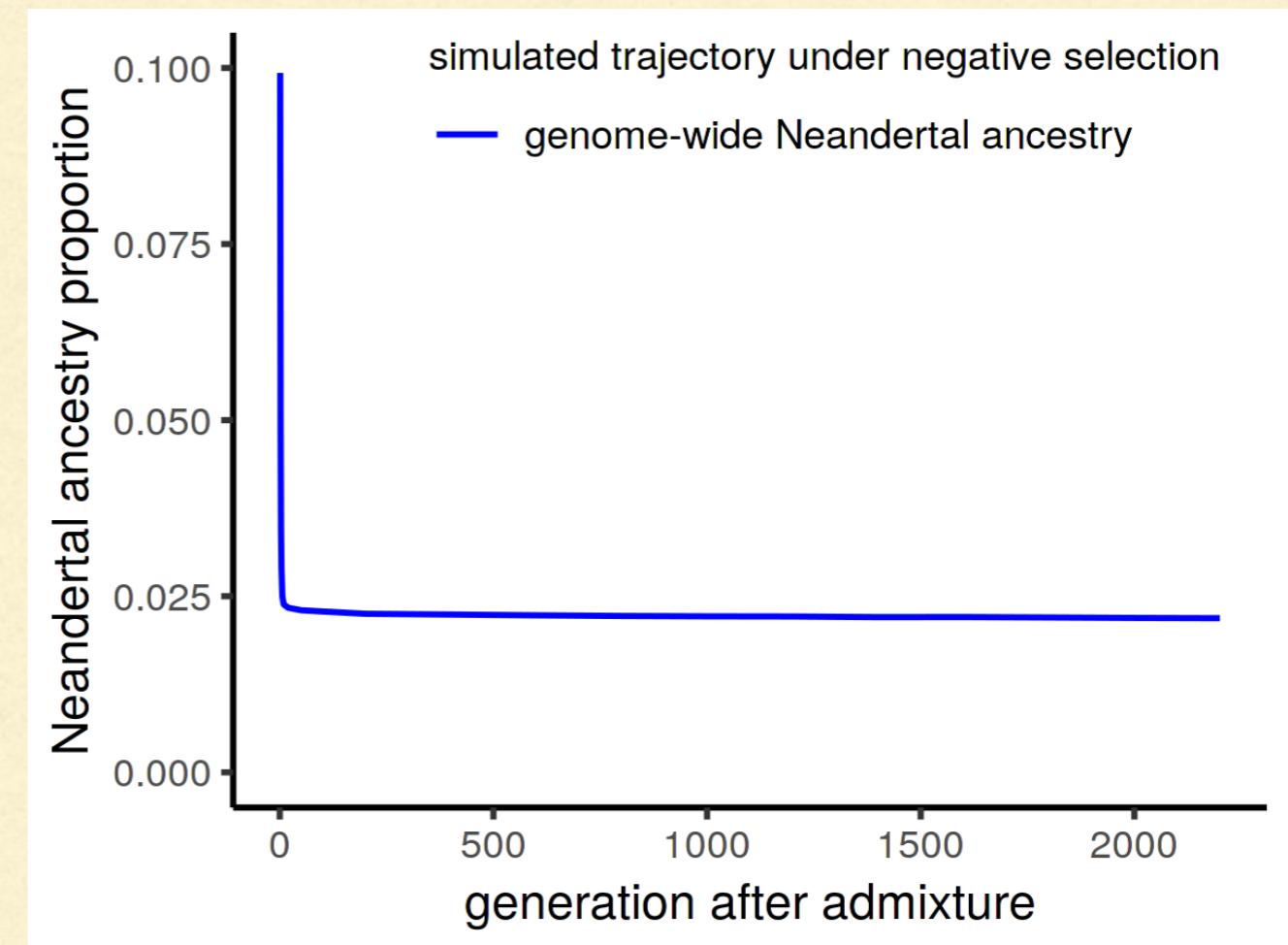
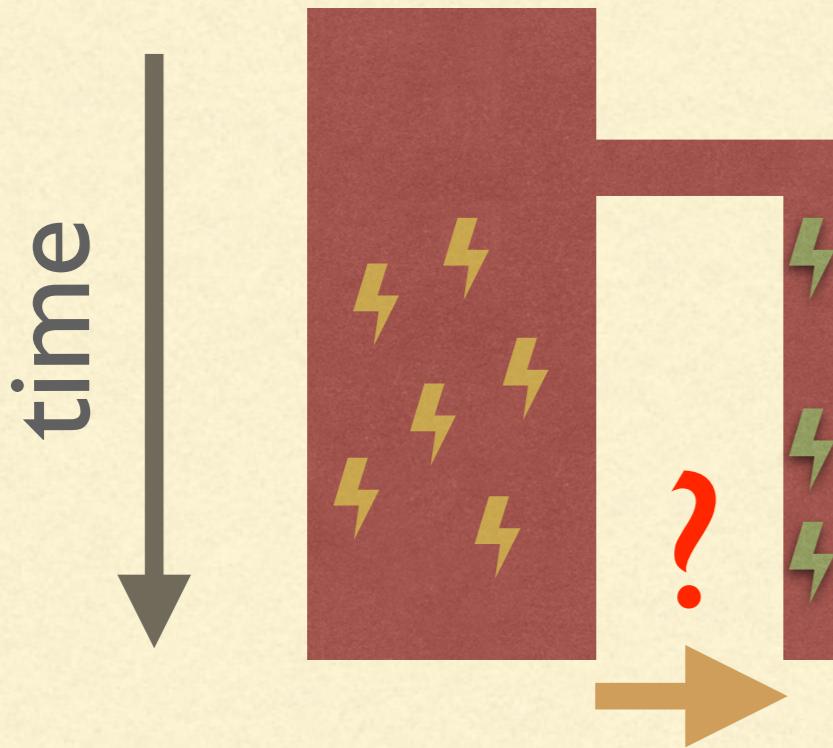
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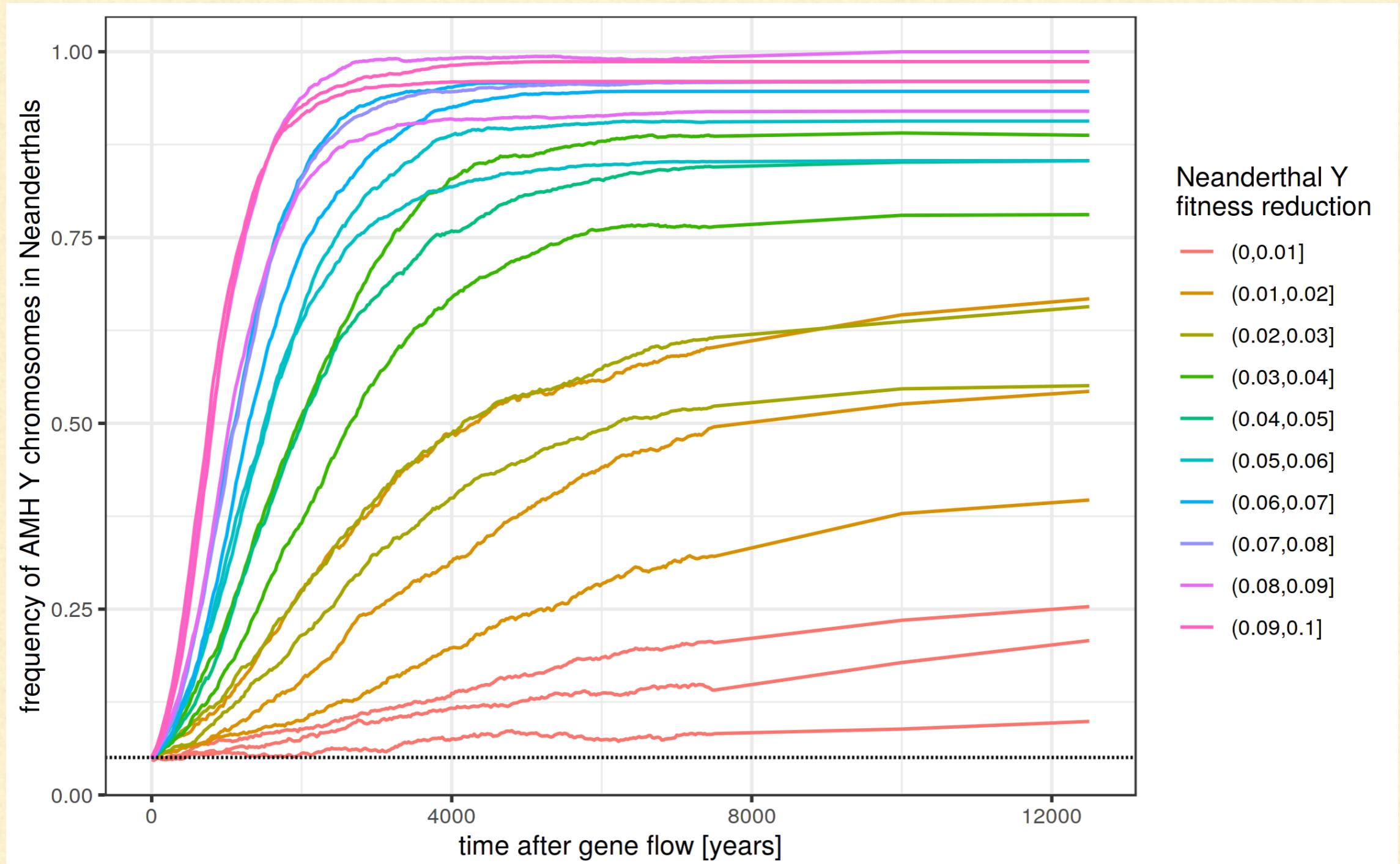
POSSIBLE SOLUTION:

# INTROGRESSION NOT NEUTRAL

⚡ ⚡ - deleterious mutations



# LOWER FITNESS OF NEANDERTHAL Y STRONGLY FAVOURS MODERN HUMAN Y!



# CONCLUSIONS

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- Study of full archaic Y chromosomes finally possible!

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  - AMH-Denisovan TMRCA ~700 kya
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- Y of Sima de los Huesos should be “Denisovan-like”.

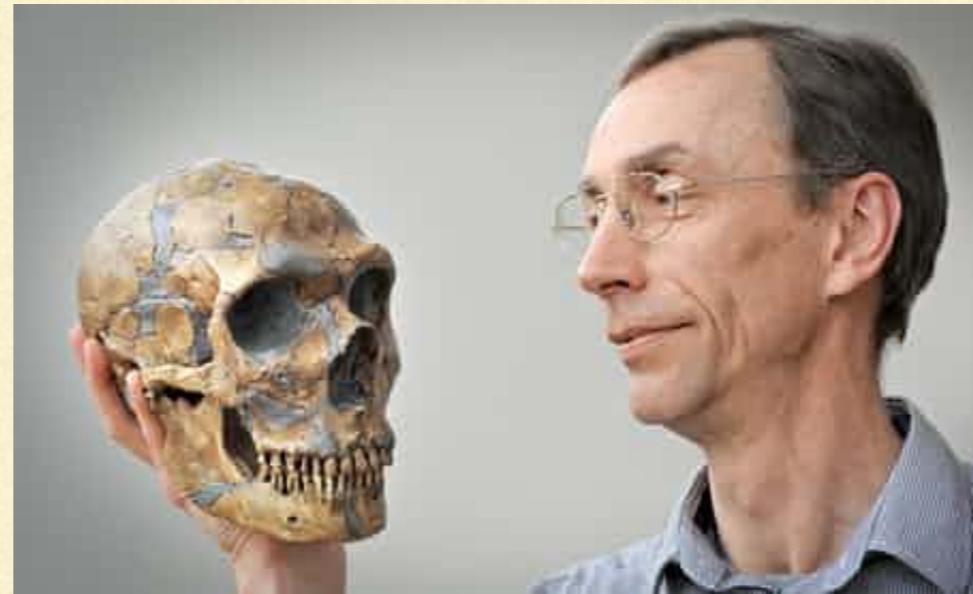
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  - Neanderthal Y replaced via AMH gene flow?
- Y of Sima de los Huesos should be “Denisovan-like”.
- Functional implications for future archaic Y studies.



**Mateja Hajdinjak**

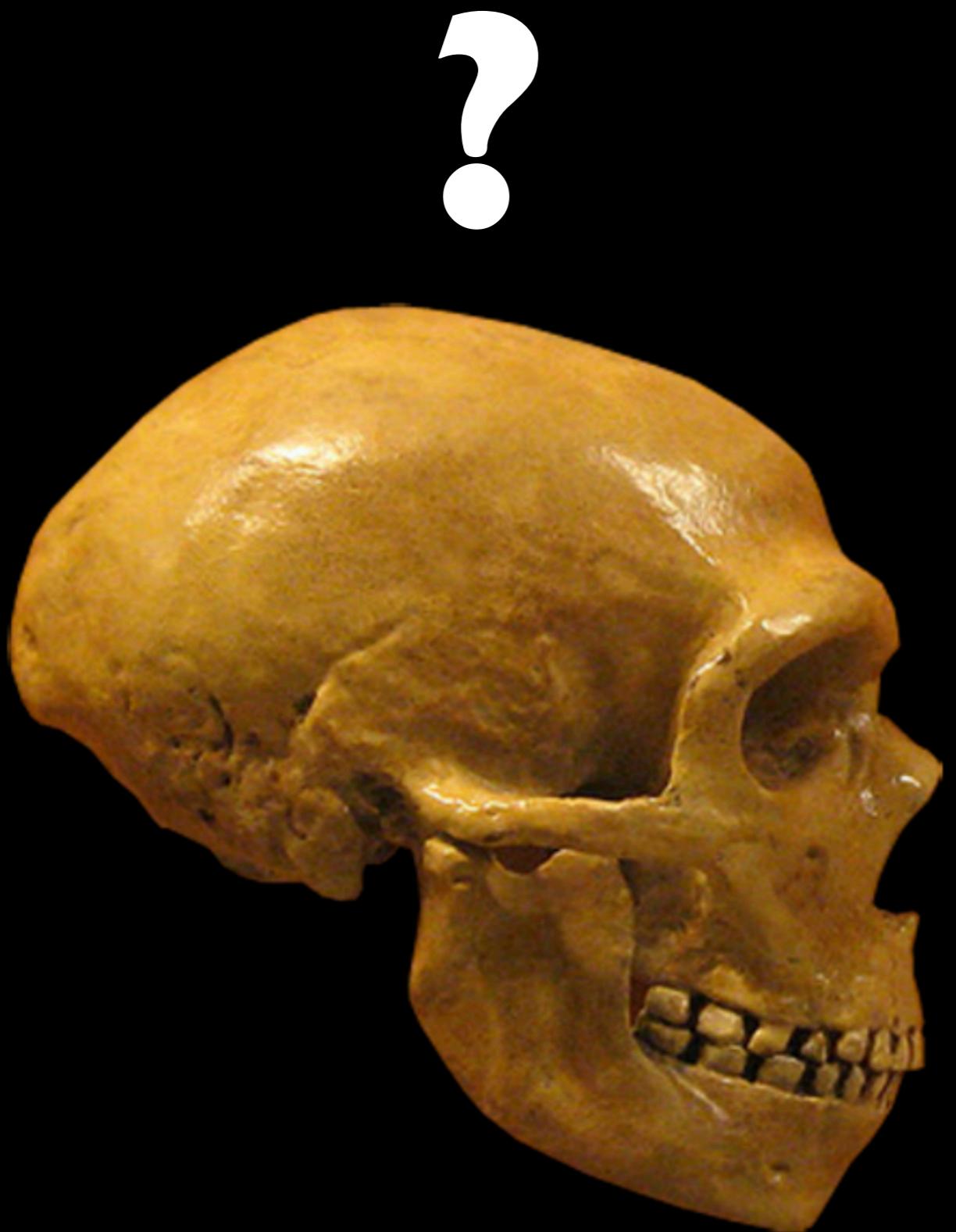


**Svante Pääbo**



**Janet Kelso**

**Qiaomei Fu, Elena Essel, Hélène Rougier, Isabelle Crevecoeur, Patrick Semal, Liubov V. Golovanova, Vladimir B. Doronichev, Carles Lalueza-Fox, Marco de la Rasilla, Antonio Rosas, Michael V. Shunkov, Maxim B. Kozlikin, Anatoli P. Derevianko, Matthias Meyer, Benjamin Vernot**



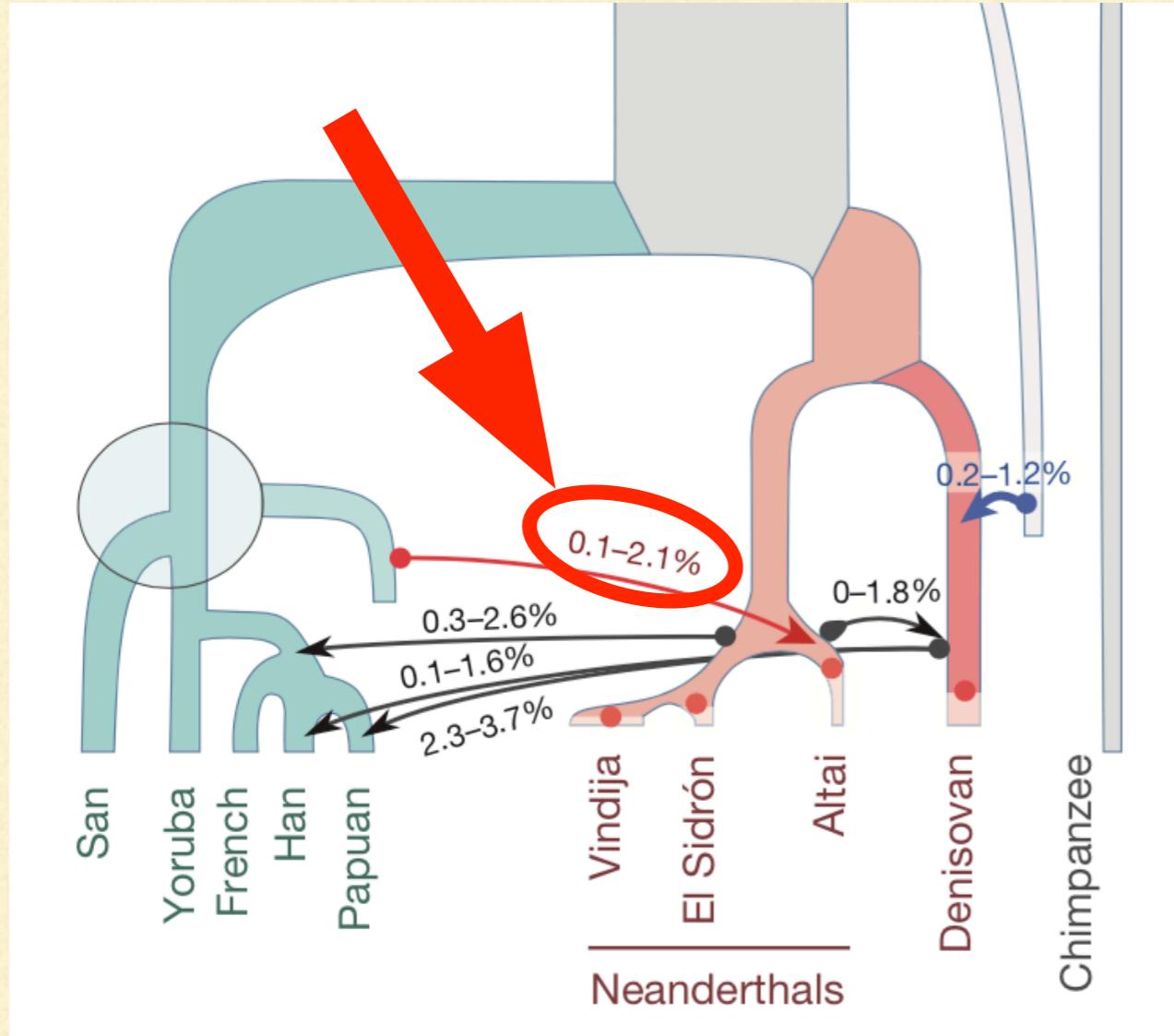
?



?



## Kuhlwilm et al. *Nature*. 2016



## Hubisz et al. *bioRxiv*. 2019

- at least 3% gene flow
- **200-300 kya**

# **“WHOLE CHROMOSOME CAPTURE”**

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**goal: capture and sequence ~6.9 Mb of the entire Y**

human Y  
reference  
sequence

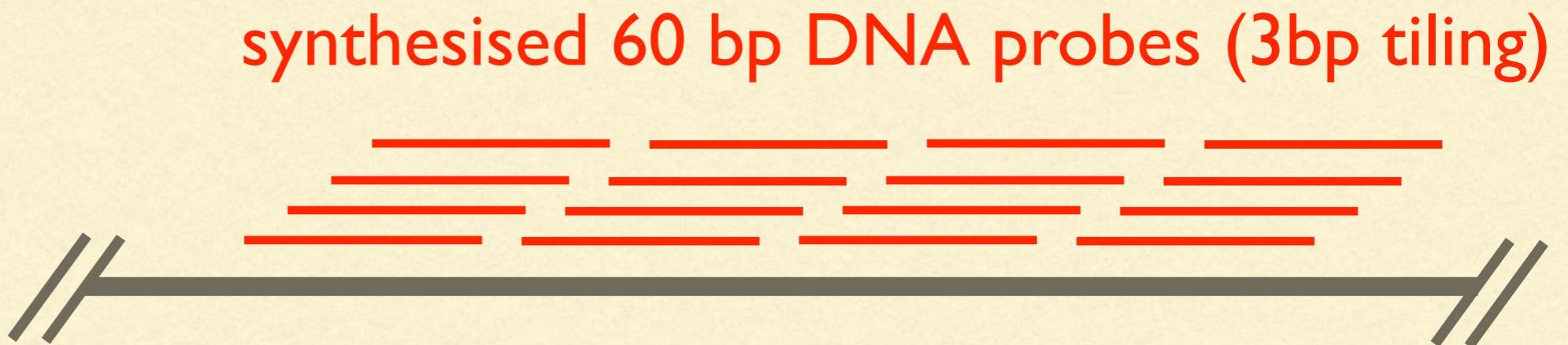


# “WHOLE CHROMOSOME CAPTURE”

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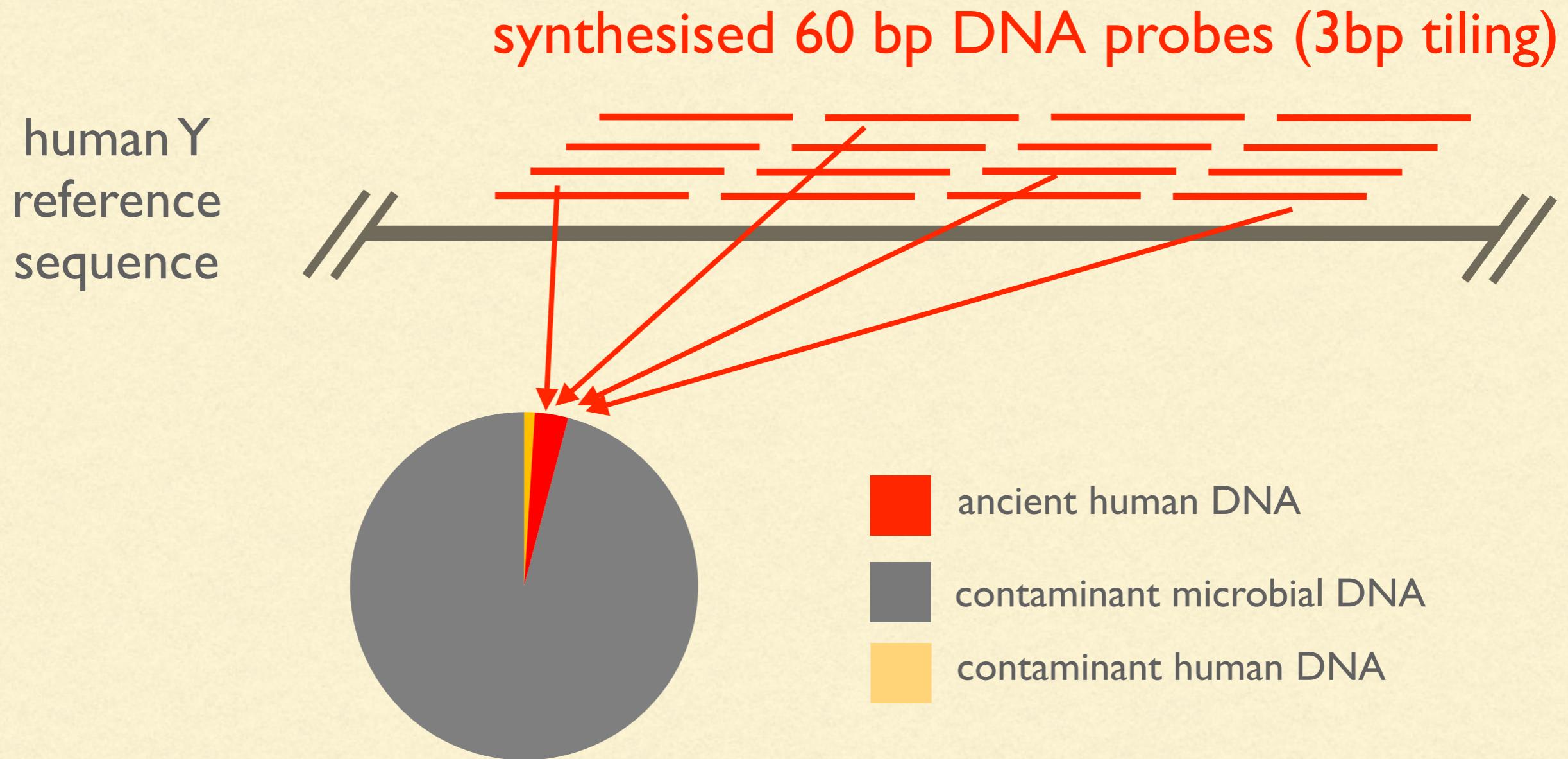
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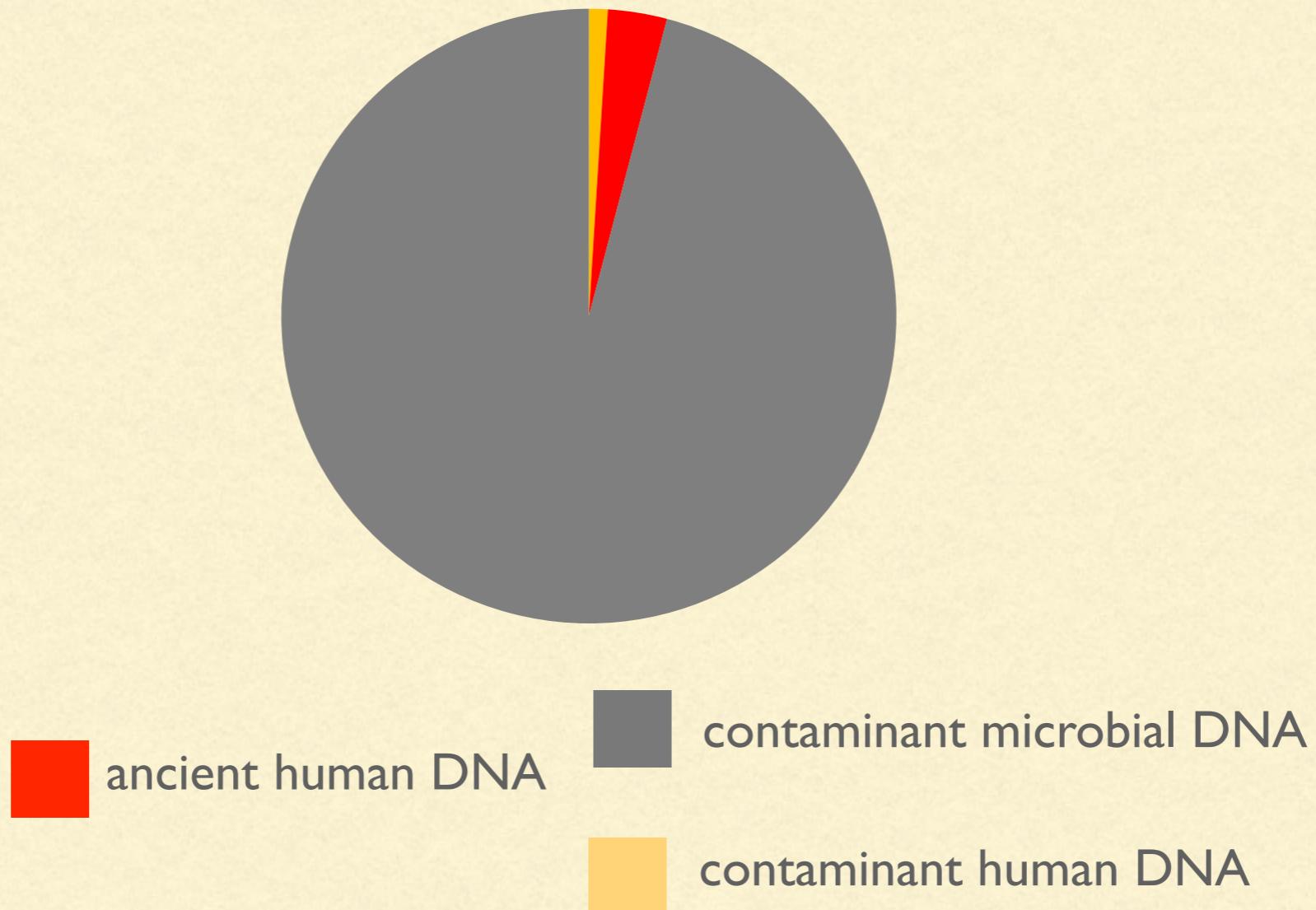
**goal: capture and sequence ~6.9 Mb of the entire Y**



# ANCIENT DNA CHALLENGES...

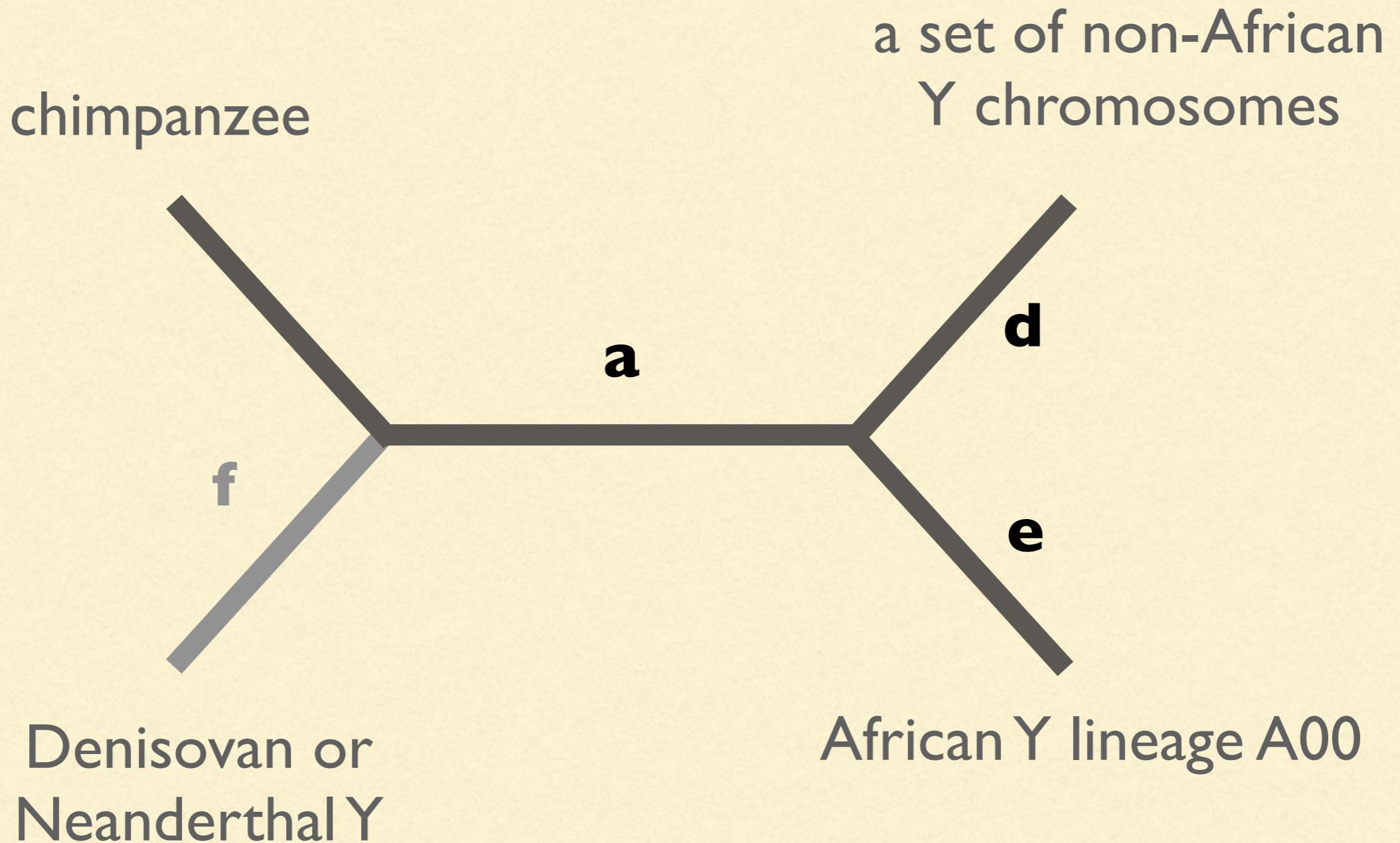
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Total DNA extracted from a tooth/bone:



# ESTIMATING TMRCA

WITH MODERN HUMAN Y CHROMOSOMES



# COVERAGE OF CAPTURED Y CHROMOSOMES

Denisovans

Denisova 4 20X  
10X  
2X

Denisova 8 20X  
10X  
2X

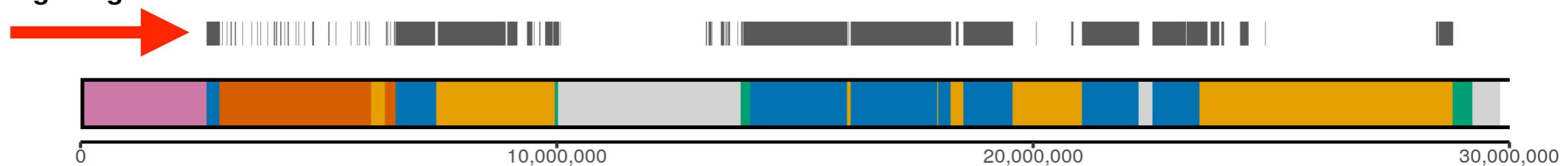
Neanderthals

Spy 94a 20X  
10X  
2X

Mezmaiskaya 2 20X  
10X  
2X

El Sidrón 1253 20X  
10X  
2X

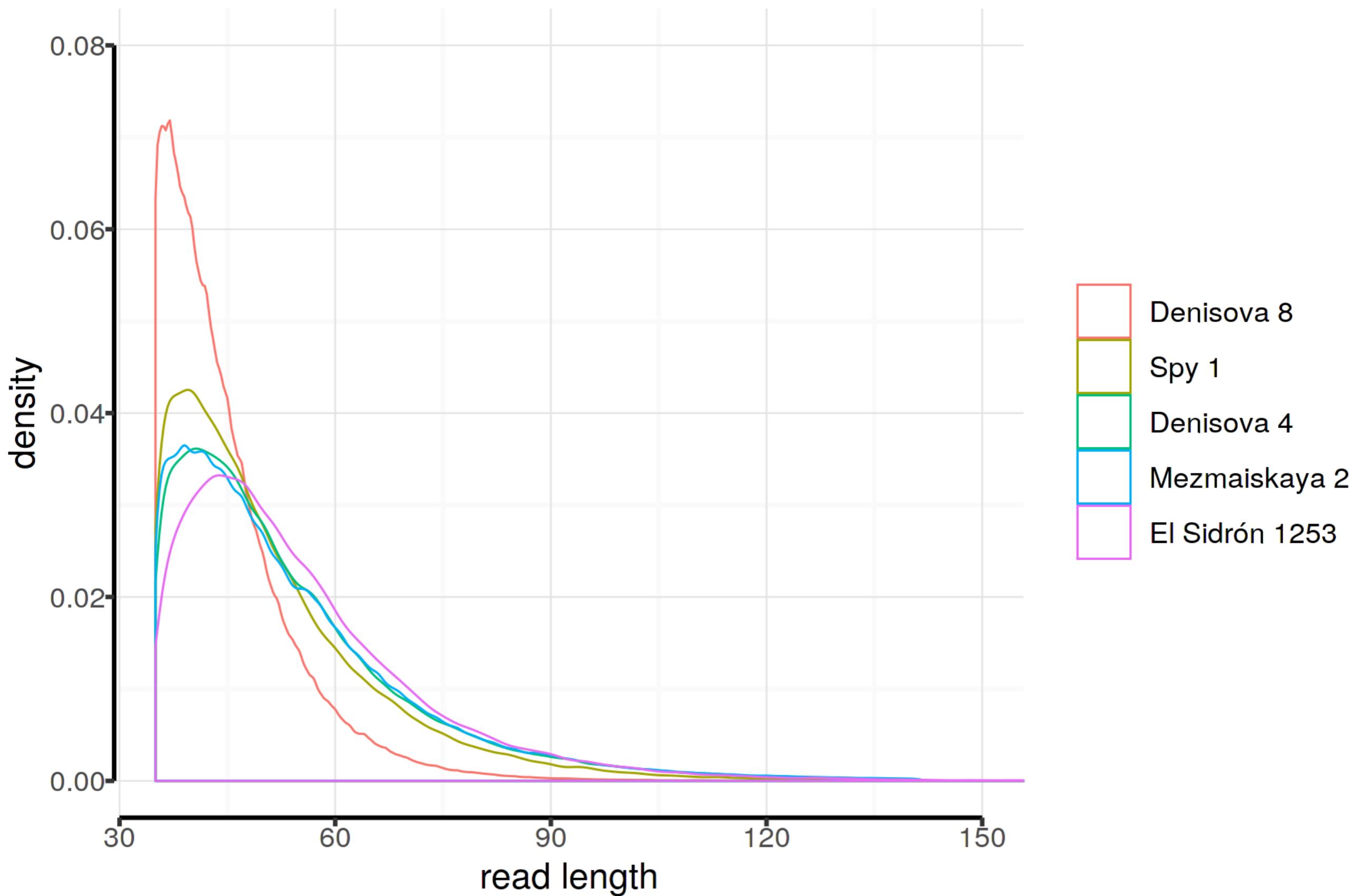
target regions



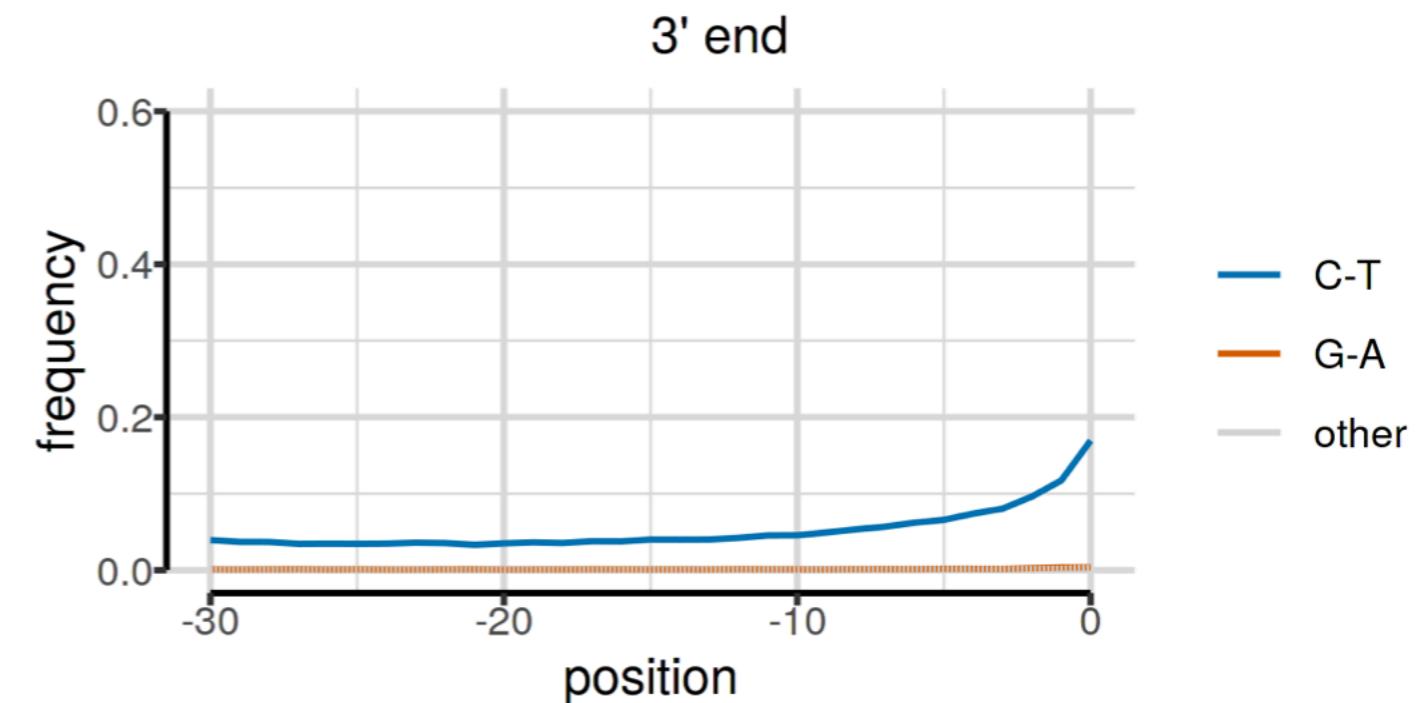
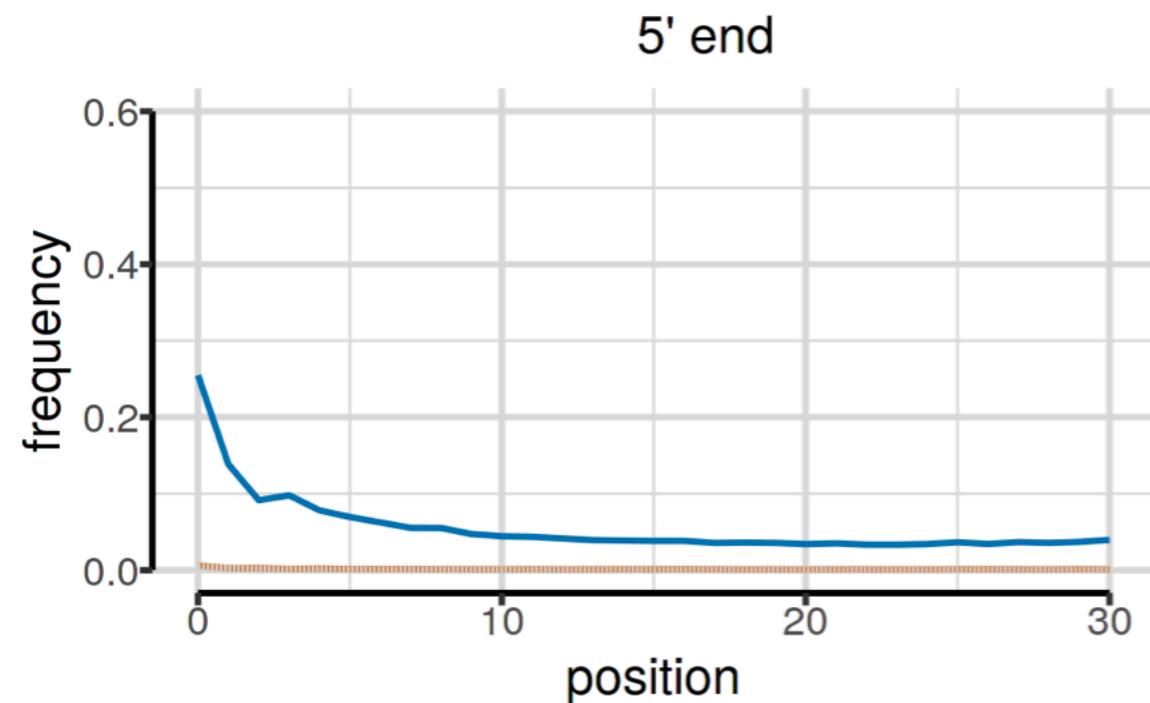
ampliconic  
heterochromatic  
pseudo-autosomal  
X-degenerate  
X-transposed  
others

# COVERAGE OF CAPTURED **Y CHROMOSOMES**

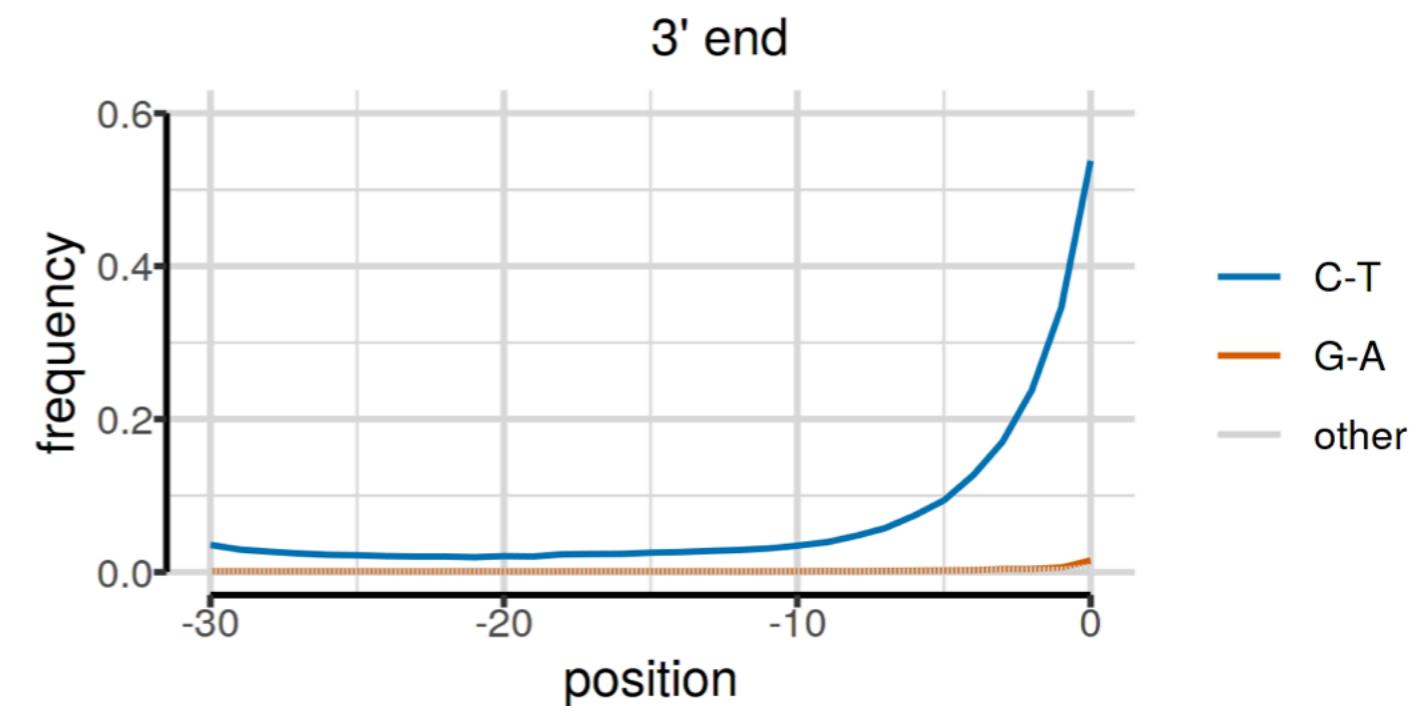
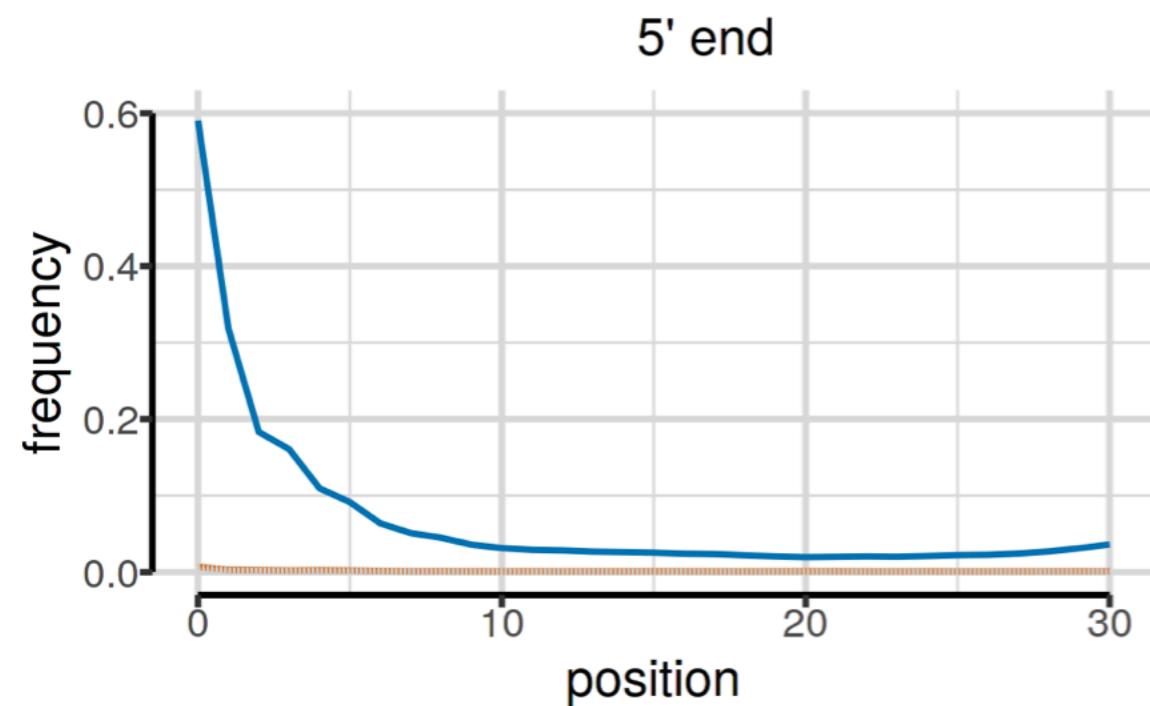
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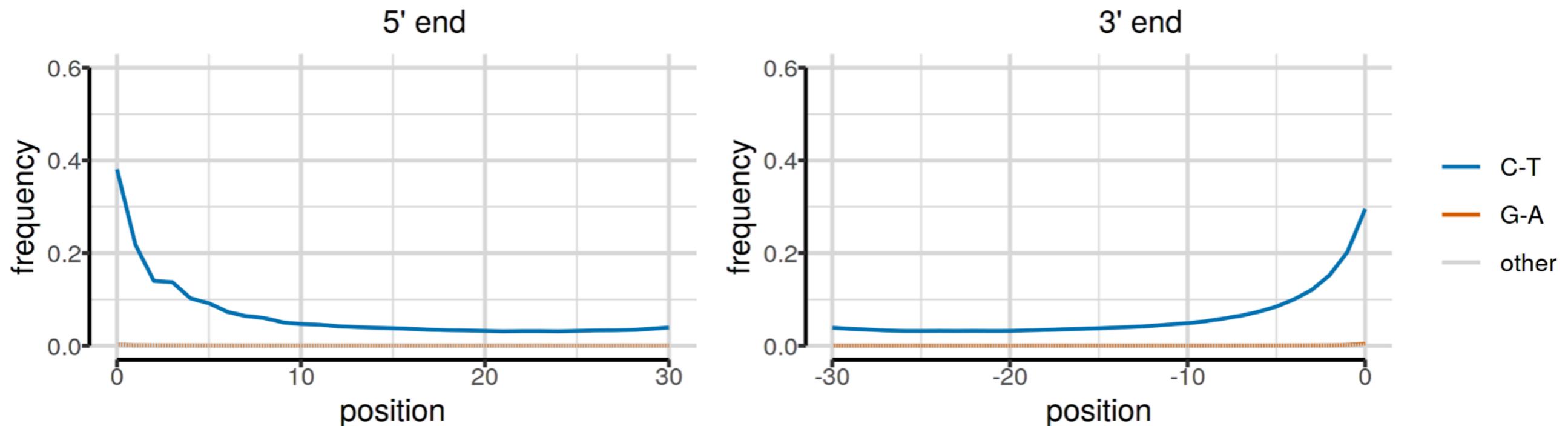
## Denisova 4



## Denisova 8



## Mezmaiskaya 2



## Spy 94a

