

# A complete genomic resource for captive marmosets

Insights into recent population  
history and biology

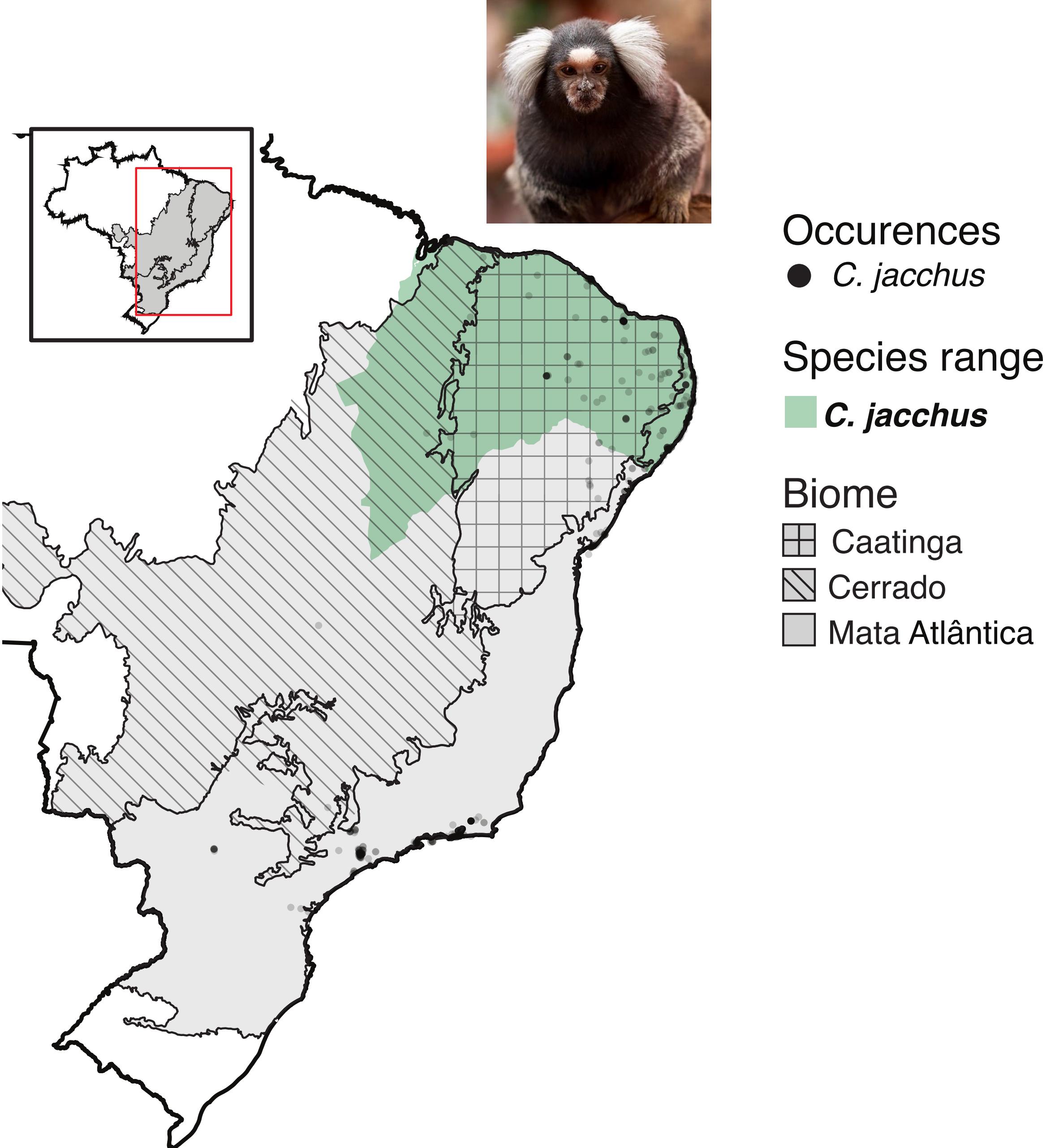
Murillo F. Rodrigues  
Marmoset Coordinating Center  
Oregon National Primate Center

September 18, 2025



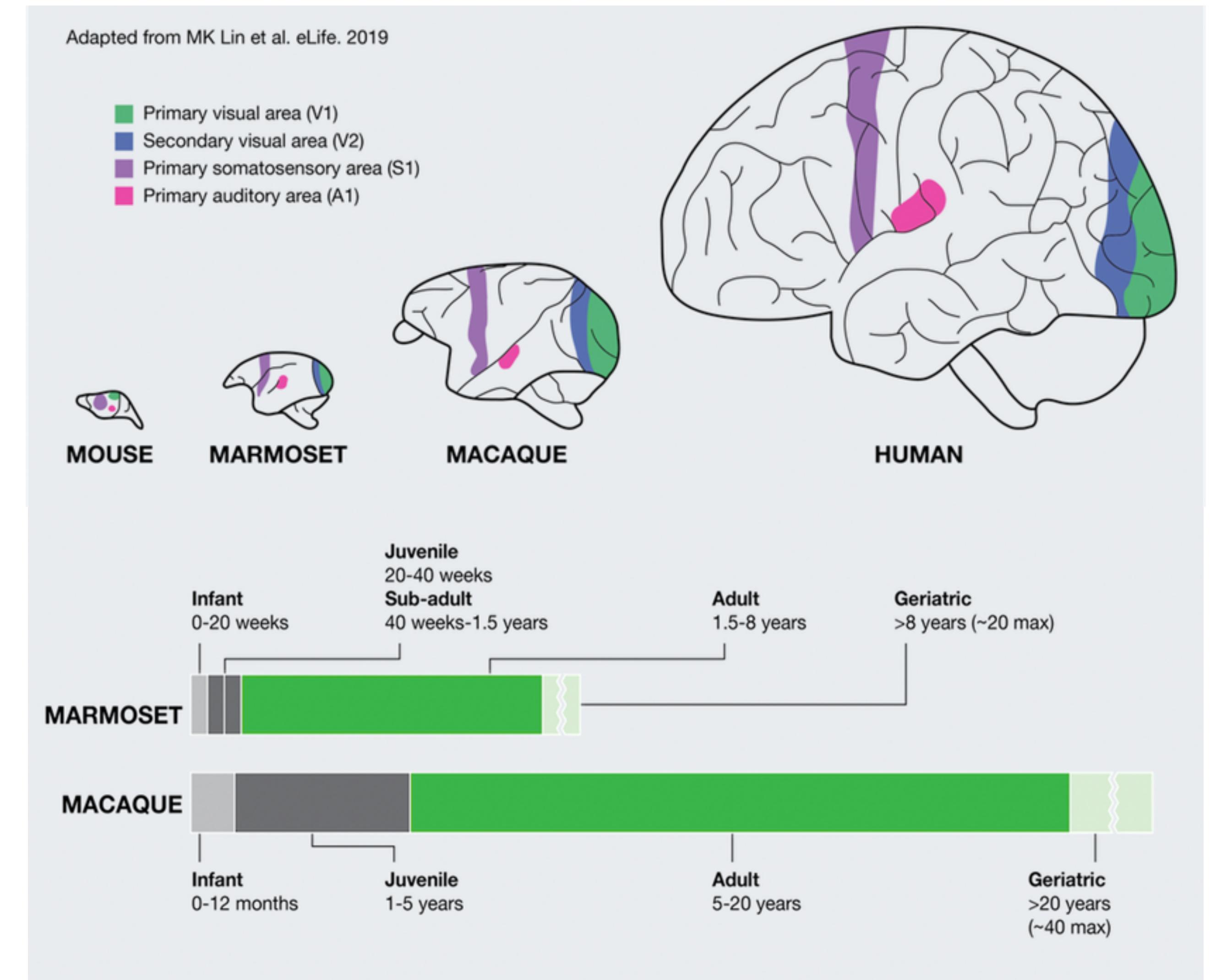
# The common marmoset

- *Callithrix* is a genus of small (<500g) New World monkeys
- Migrated from the Amazon Forest to the Atlantic Forest around 4 M.a.
- Recently, the common marmoset (*C. jacchus*) invaded the Southeast of Brazil

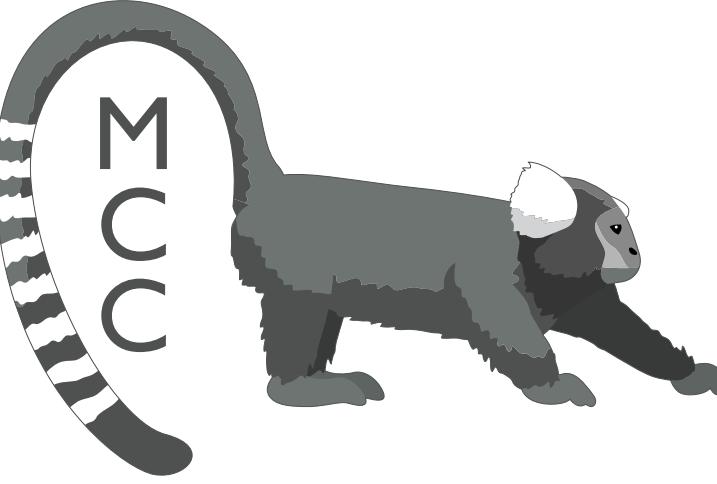


# The common marmoset: an emerging model

- Model for biomedical research
- Similar brain organization to humans
- Easier to rear and faster development



# Marmoset Coordinating Center



- There are over 2,500 captive marmosets in the US scattered over many colonies
- Coordinating breeding efforts is necessary
  - Track individuals
  - Provide breeding guidelines
  - Genomic survey of the captive marmoset population



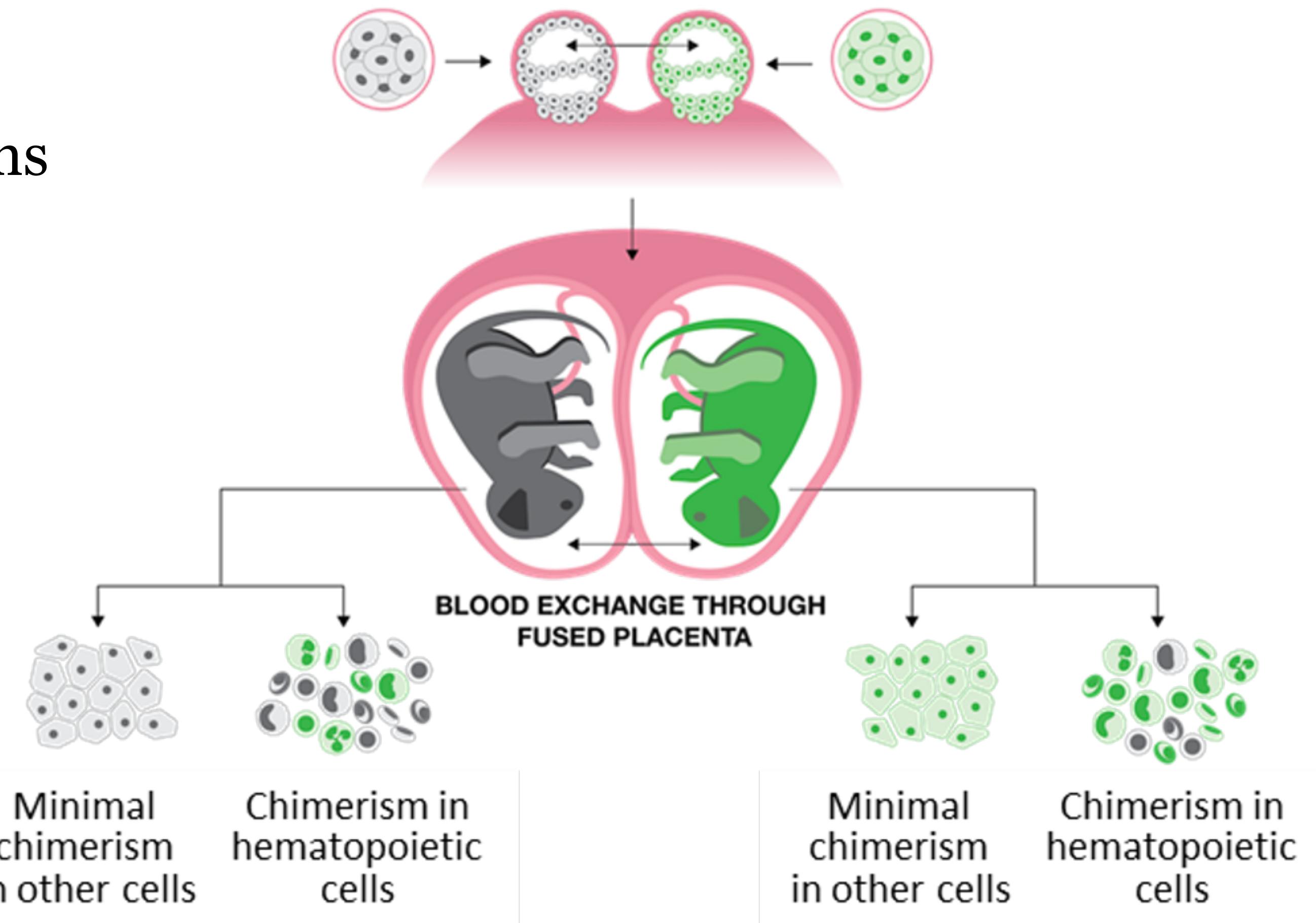
See [mcc.ohsu.edu](http://mcc.ohsu.edu) for more information!

# Genomics is complicated by chimerism

- Marmosets commonly give birth to twins

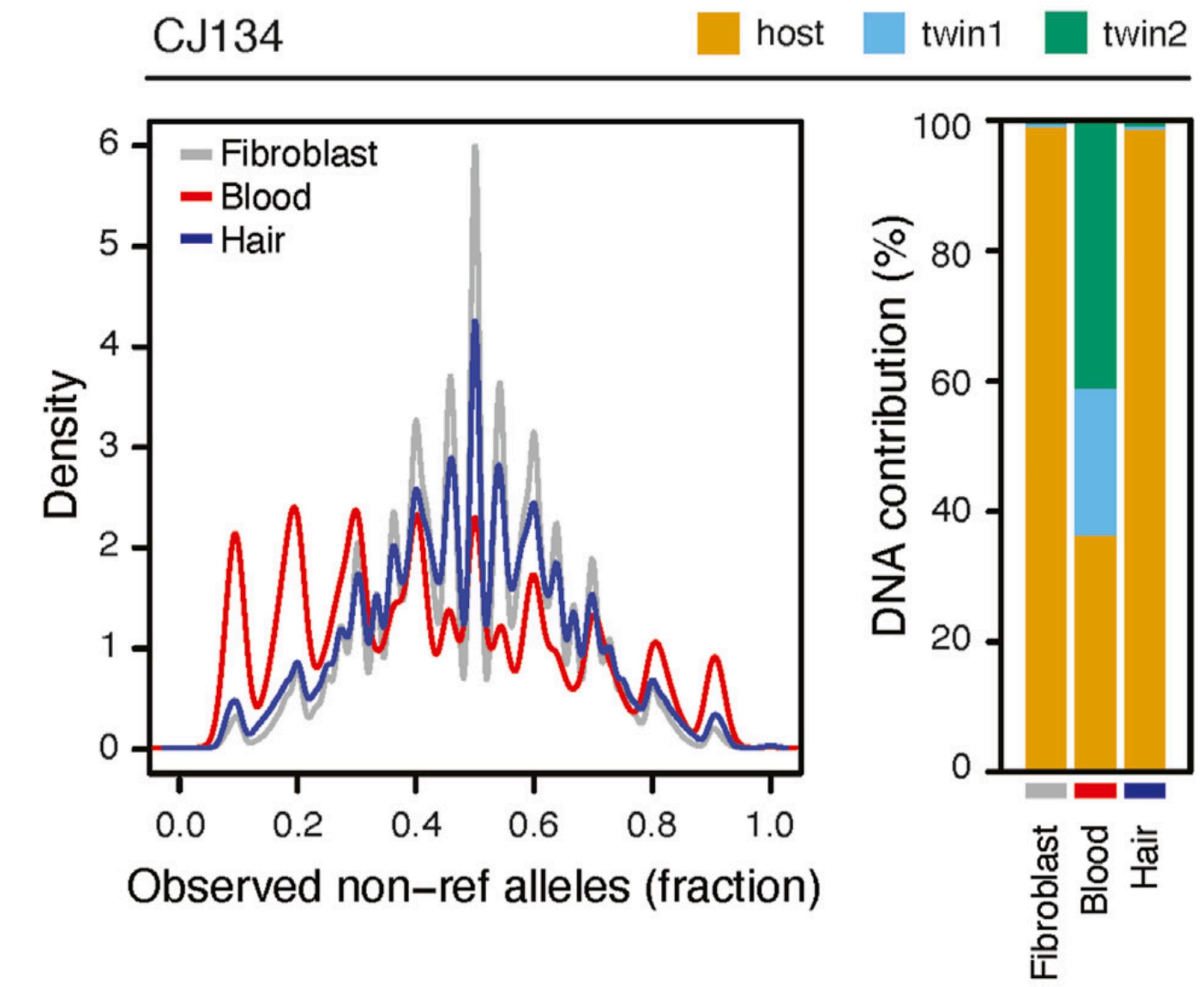
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  - Twins exchange blood through the placenta
  - Blood remains chimeric throughout their lives



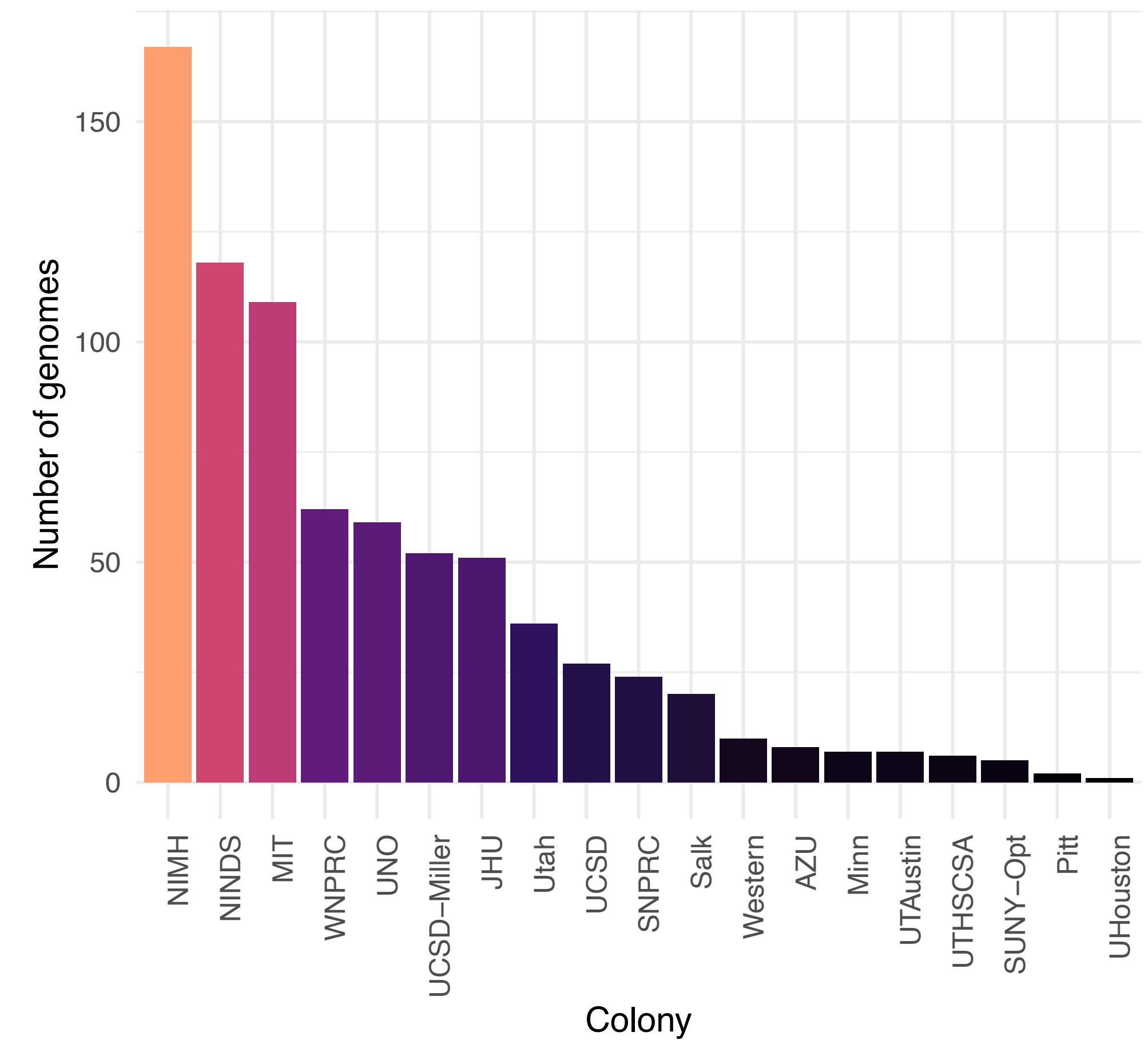
# Genomics is complicated by chimerism

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  - Blood remains chimeric throughout their lives
- Hair follicles are not chimeric and much easier to obtain



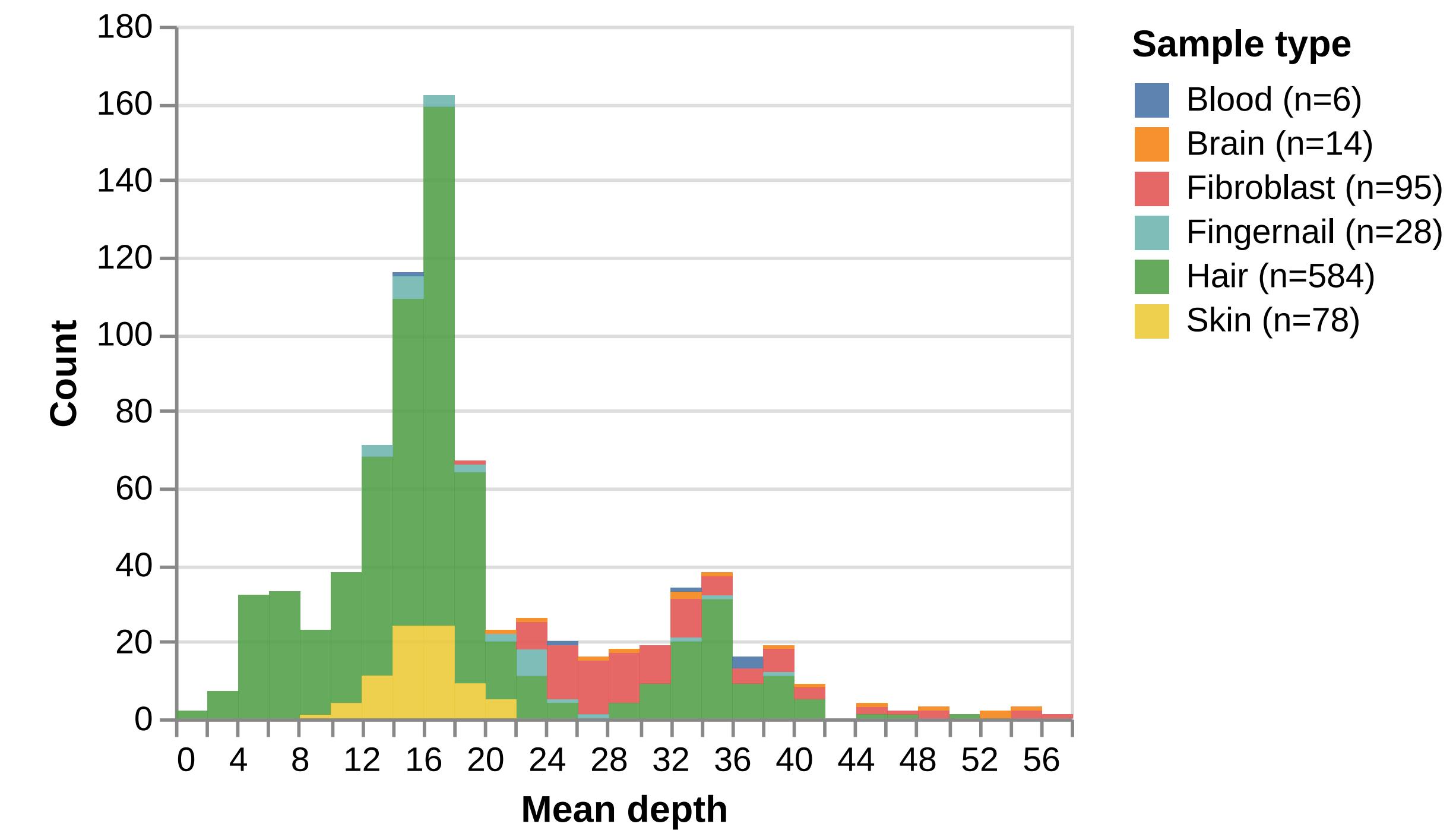
# Data

- Whole-genome sequences for 805 captive marmoset genomes
  - 578 genomes generated by MCC
  - 193 genomes generated by collaborators (e.g., MIT)
  - 34 genomes obtained from SRA for two asian centers



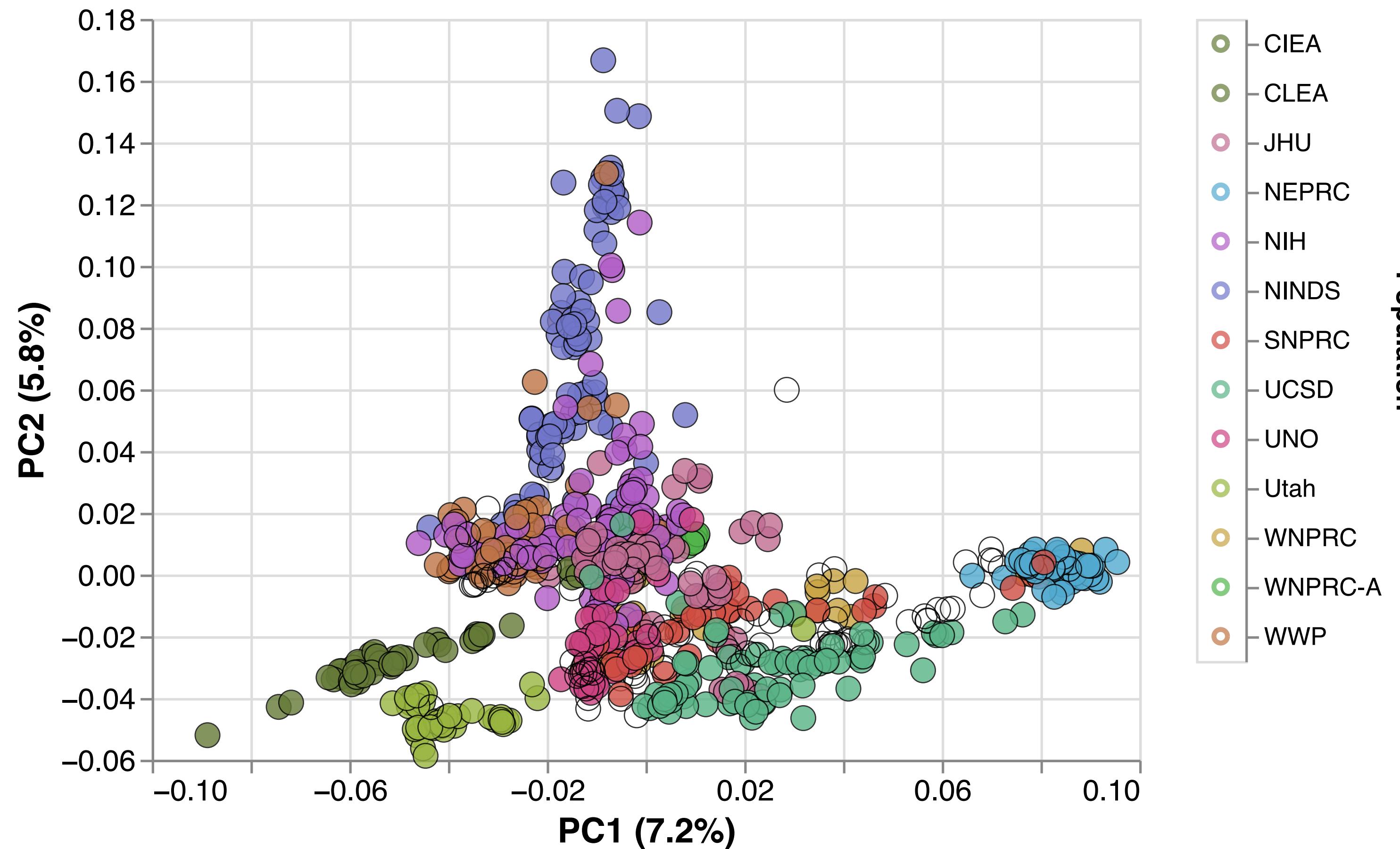
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  - 34 genomes obtained from SRA for two asian centers
- Sample types: hair follicles (majority), fibroblast, fingernail, skin punches, and blood



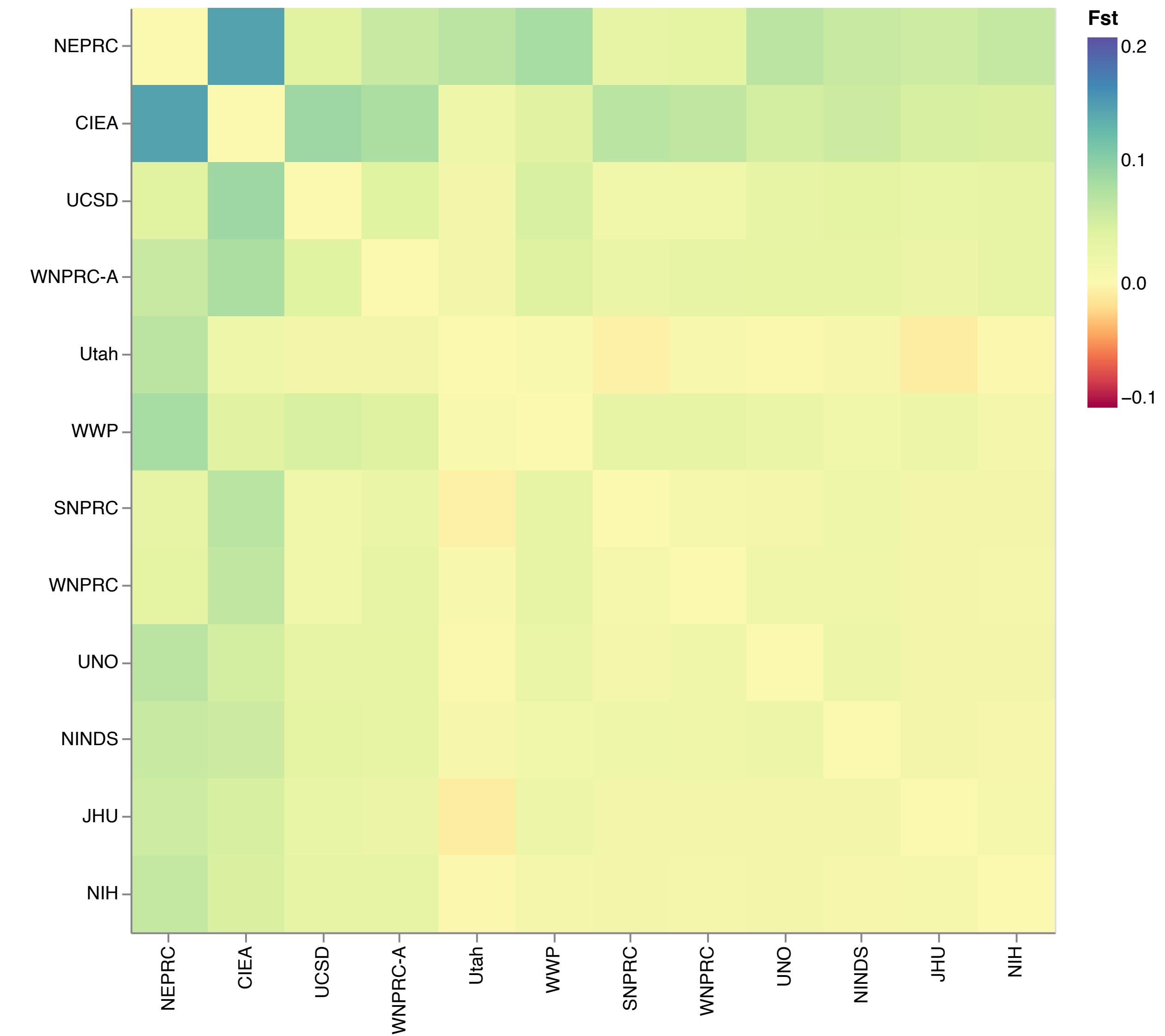
# Genetic structure across colonies

- Homogeneous clusters:  
**CIEA**, **Utah** and **NEPRC**
- Main axis of variation: **CIEA** - **NEPRC**
- Apparent mixing or shared origin between **NINDS**, **NIH**, **JHU**, **UNO**, **SNPRC**, **UCSD**



# Long-term isolation between colonies

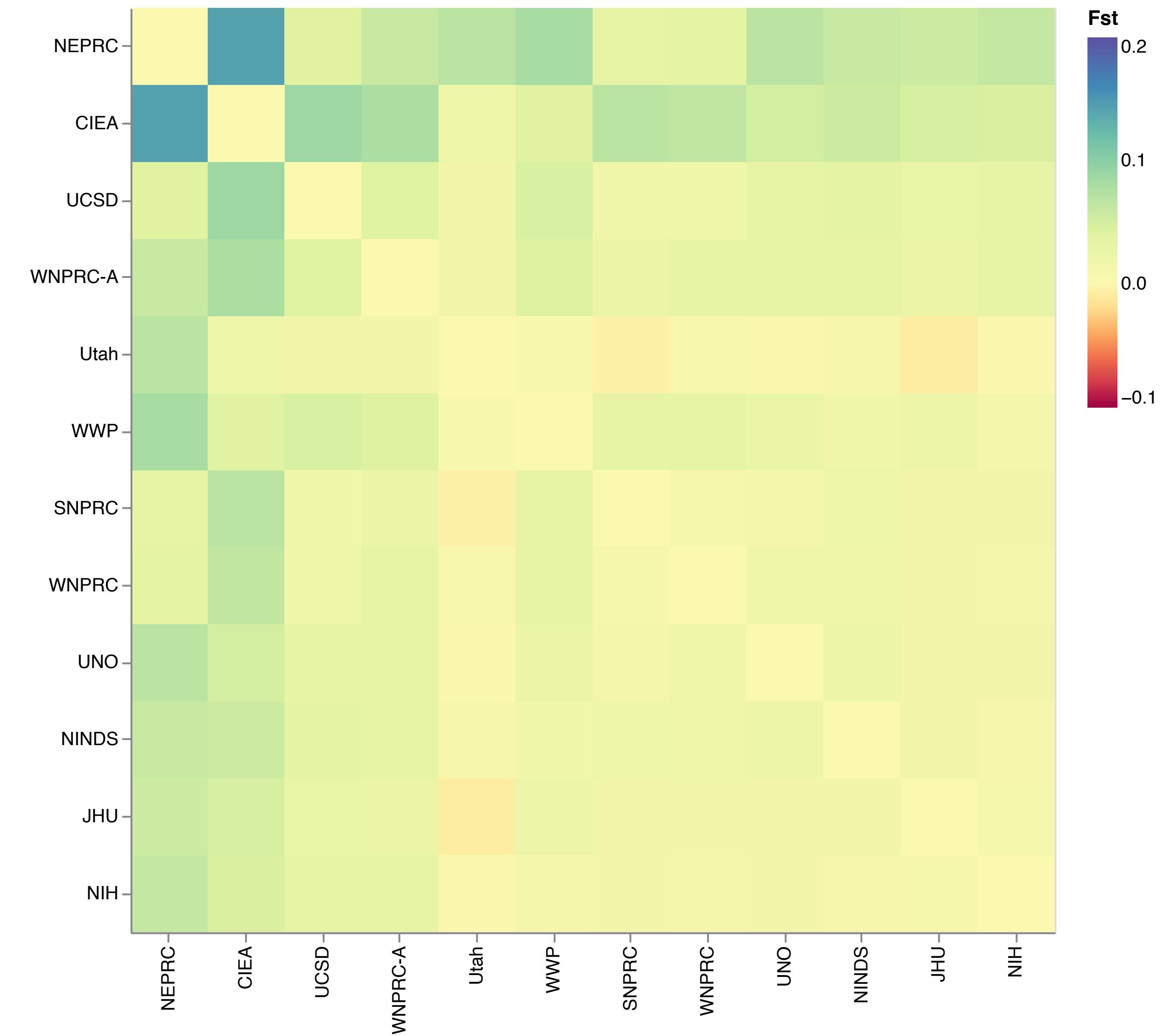
- Most colonies are not well differentiated, with FST ranging from 0 to 0.05



Results

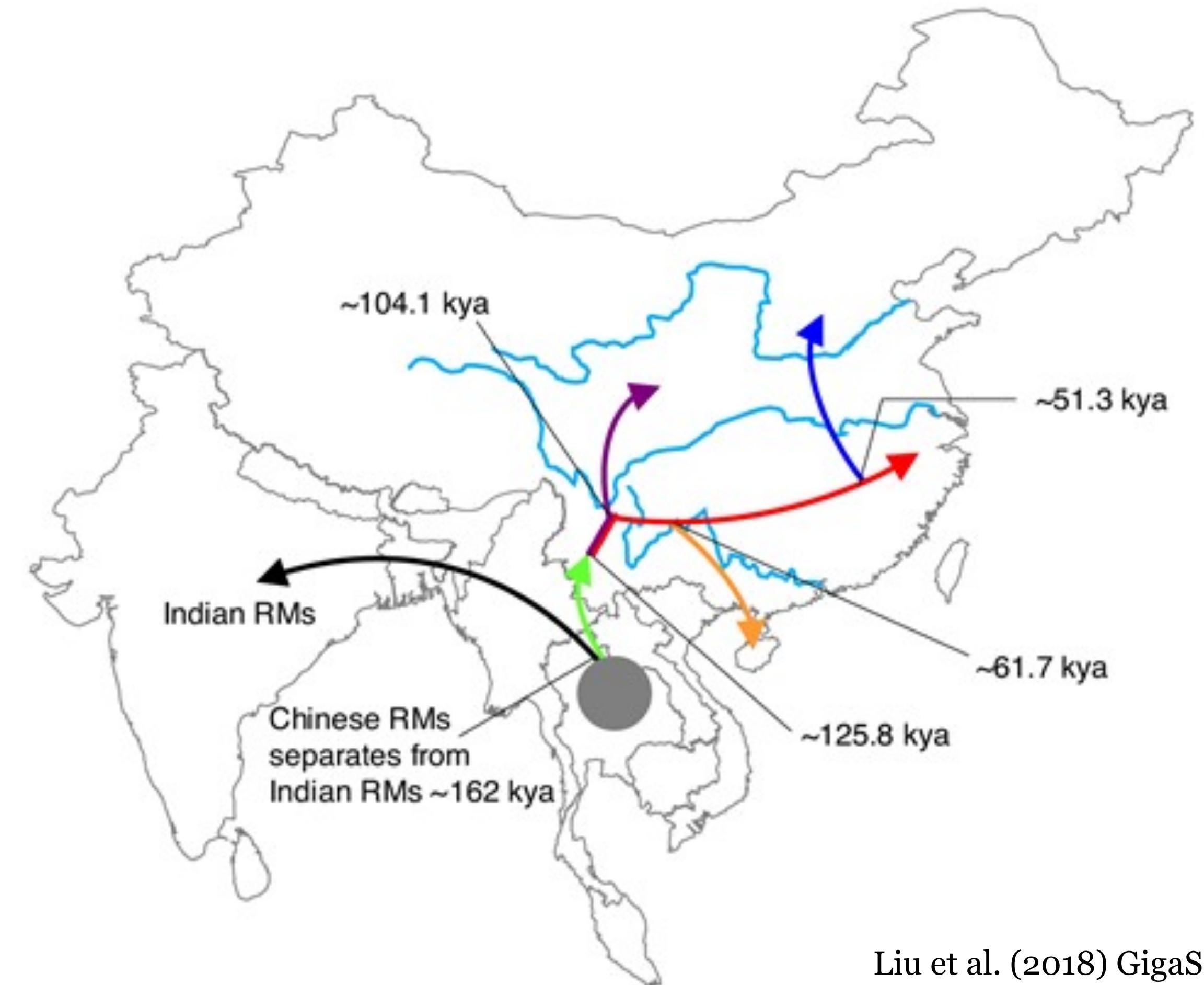
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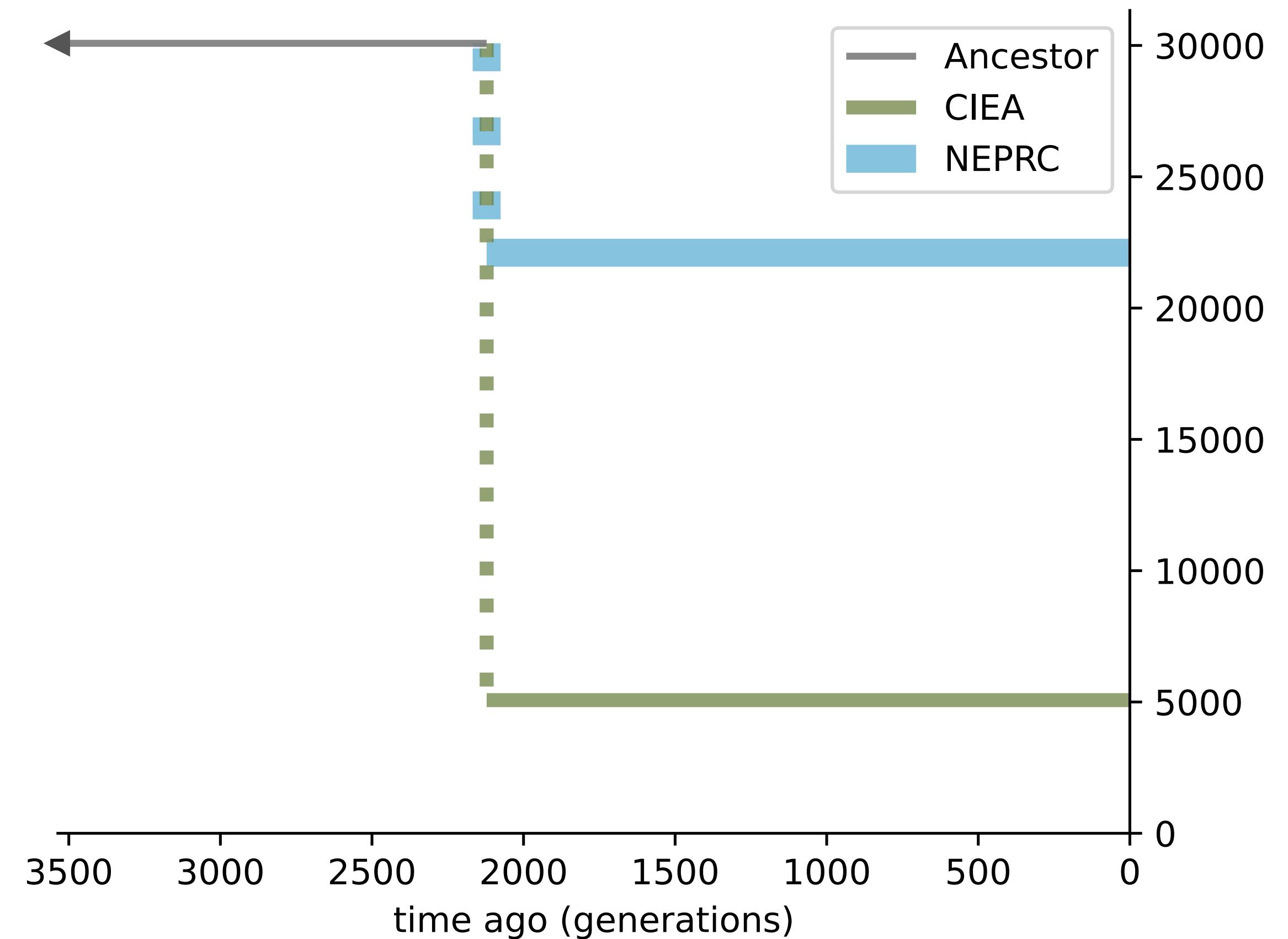
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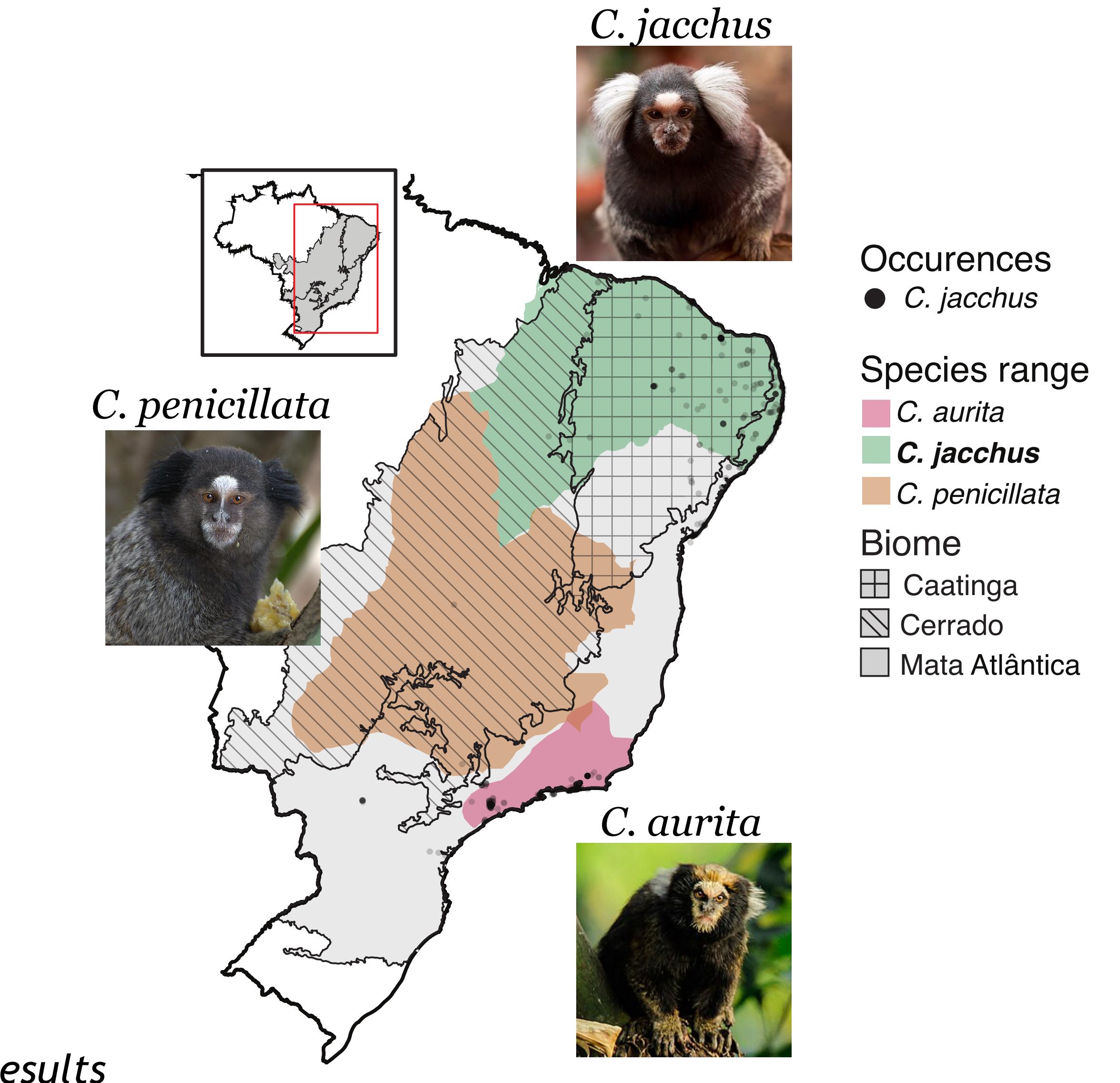
Liu et al. (2018) GigaScience

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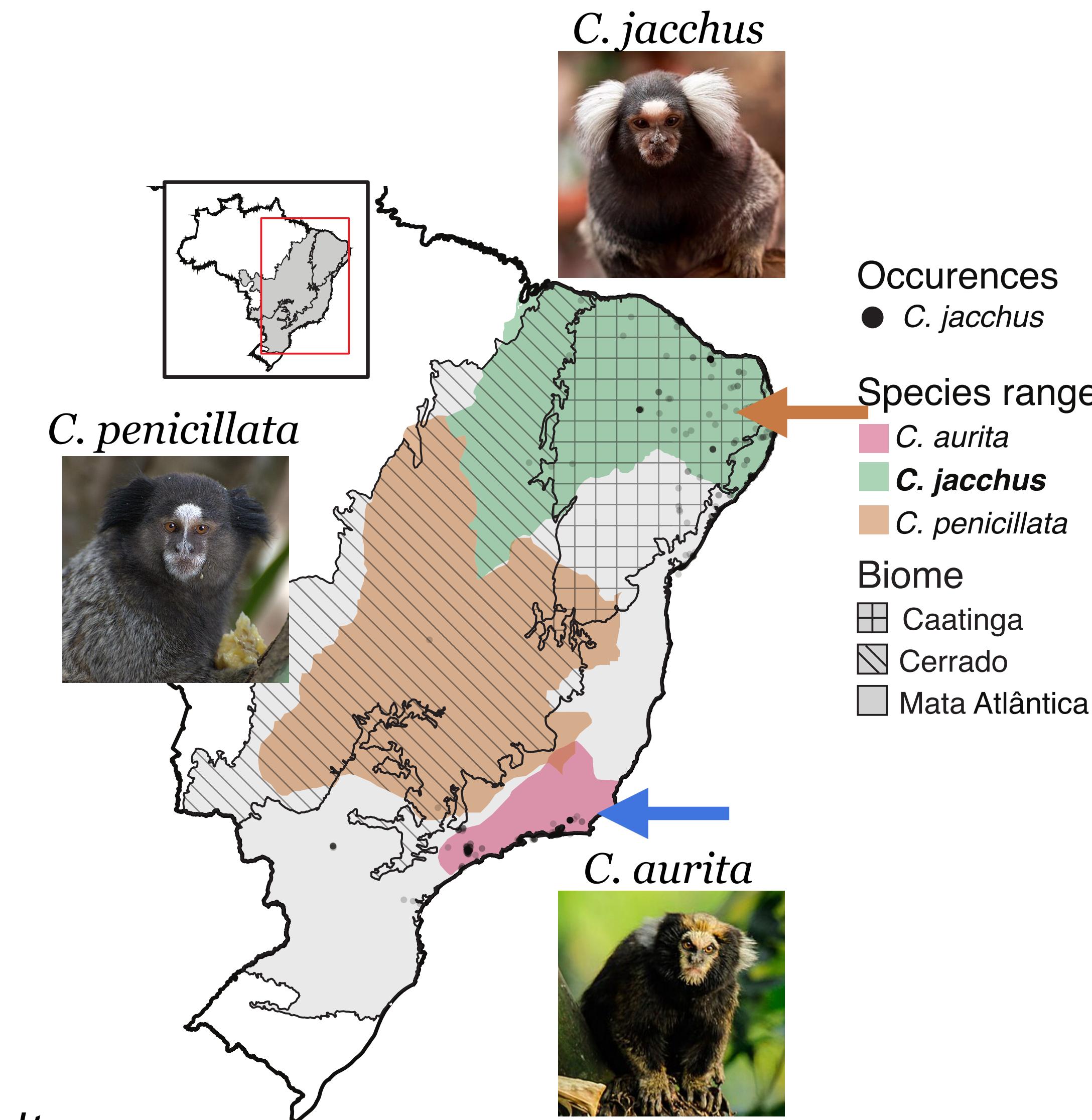
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- Estimated split between **CIEA - NEPRC** around 2200 generations ago



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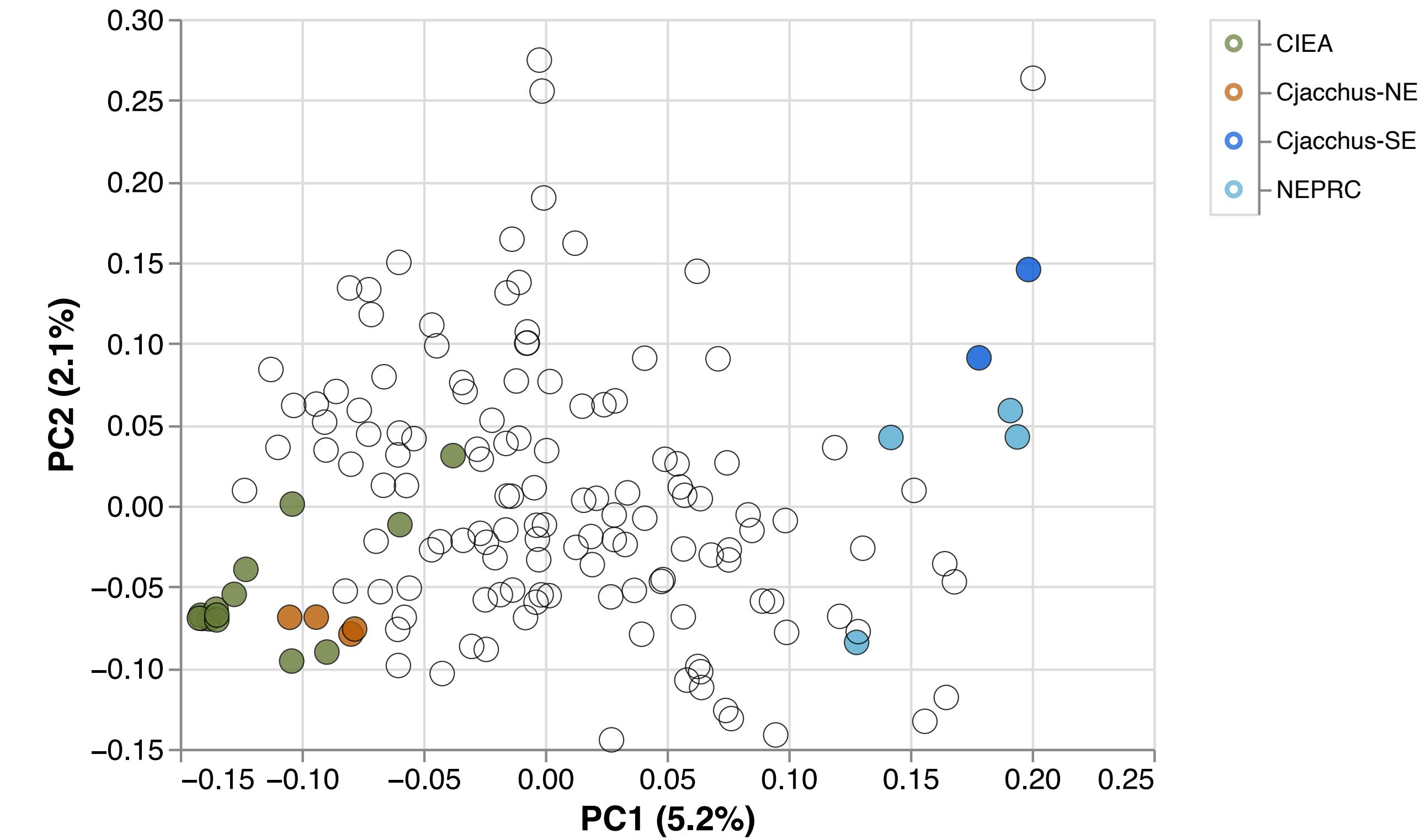


# Long-term isolation between colonies



NEPRC clusters with Southeast,

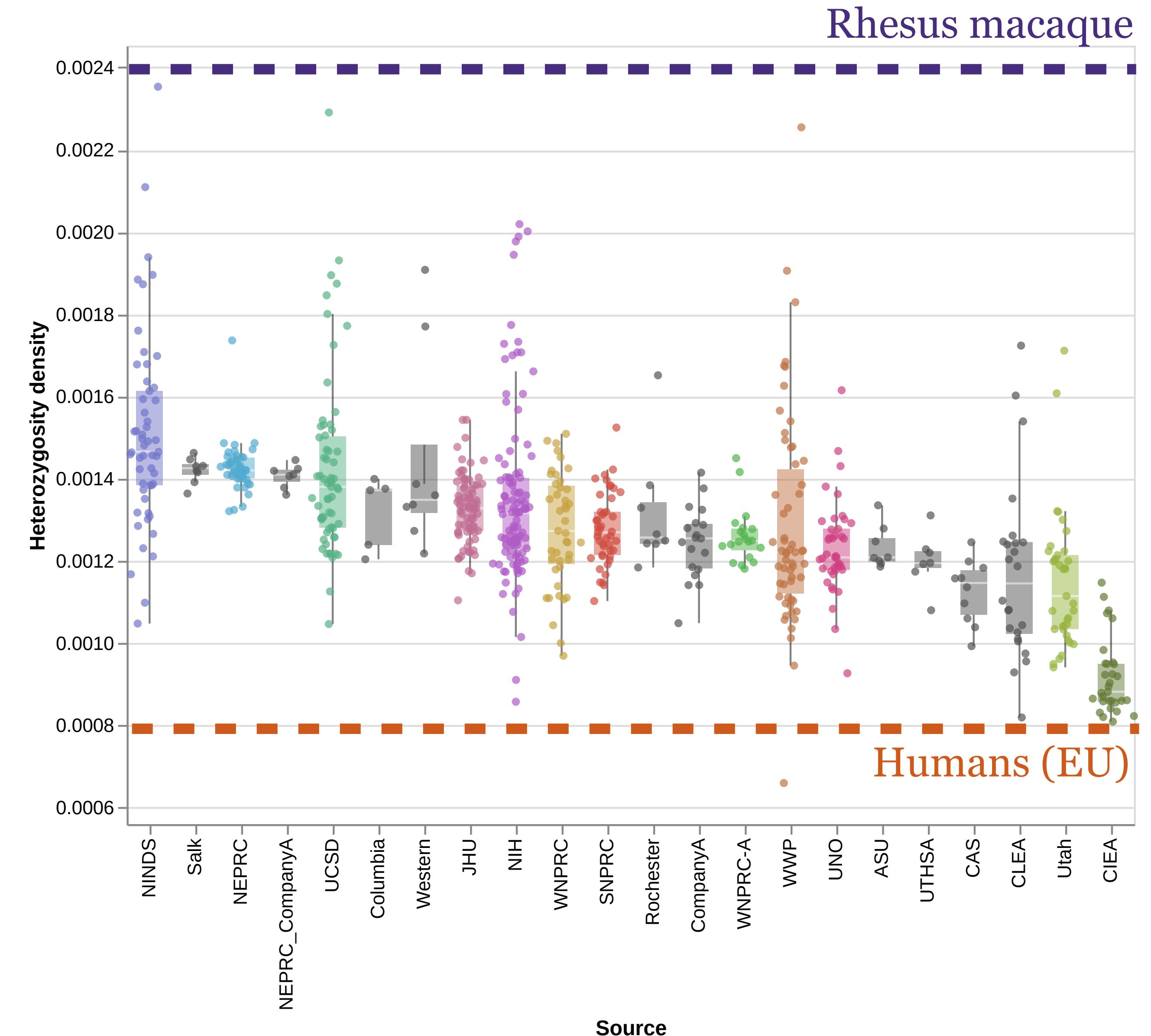
whereas CIEA clusters with Northeast



Low coverage wild-caught genomes from Malukiewicz et al. (2025) bioRxiv

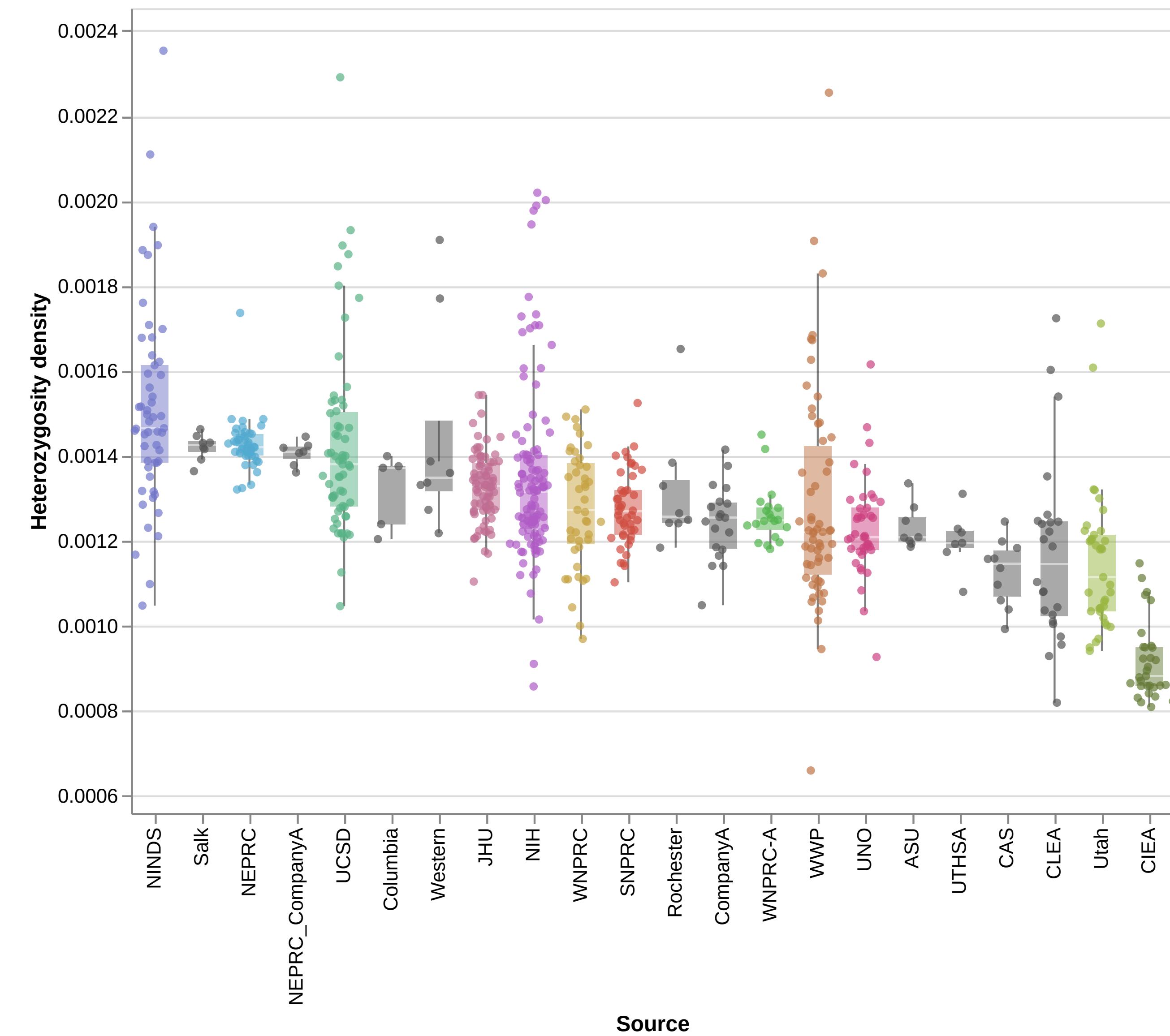
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- A lot of variation across individuals and colonies!
- **CIEA** in particular harbors the least amount of variation
- **NEPRC**, likely admixed, has high levels of diversity

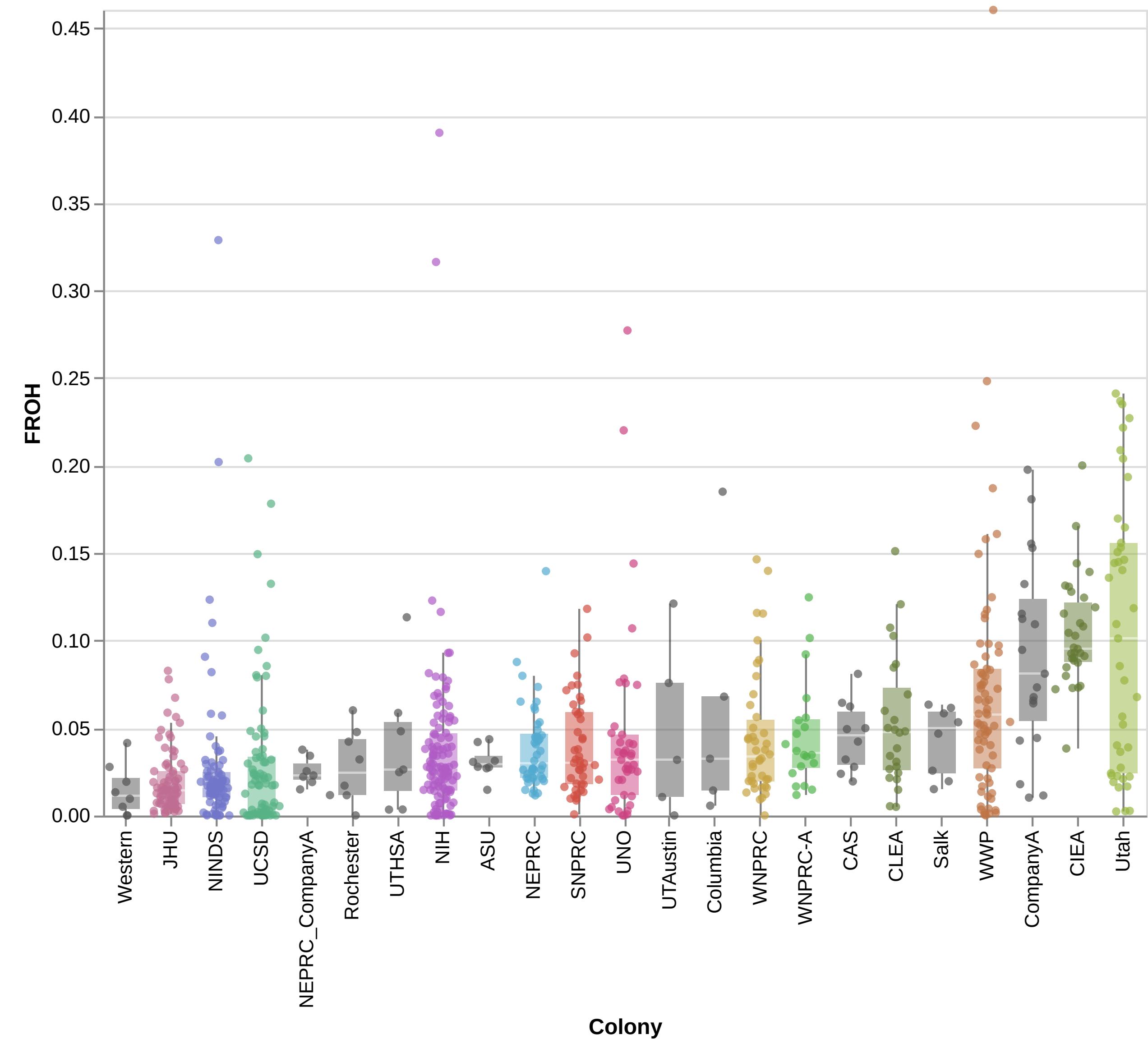


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- Recent inbreeding leads to long runs of homozygosity
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- Recent inbreeding leads to long runs of homozygosity
- In humans, FROH is no more than ~0.05 (Amish)
- More isolated centers have more inbreeding; average FROH in **CIEA** and **Utah** is ~0.1!
- Breeding strategy can reduce genomic inbreeding: NEPRC x CompanyA

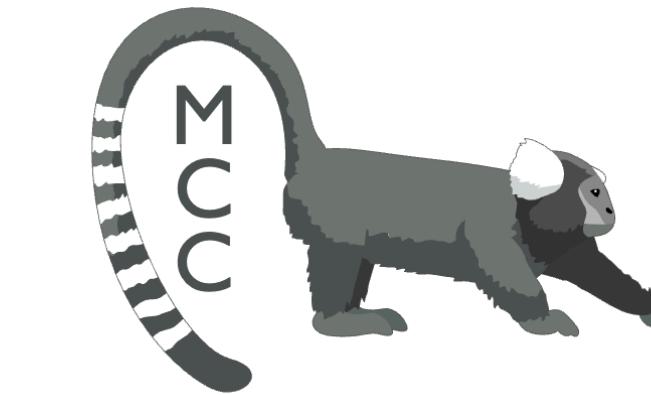


# Summary

- Moderate population structure across colonies (CIEA-NEPRC)
  - This reflects the different wild origins of captive marmosets, with NEPRC animals likely originating from an admixed population of *C. jacchus* in Southeast Brazil
  - Consequences for experiments, as genetic homogeneity is often desired
- High variation in levels of heterozygosity driven by inbreeding and population structure
- Inbreeding levels seems reasonable, but isolated colonies show early warning signs
- Breeding practices can alleviate inbreeding and increase levels of genetic diversity

**Thank you!**

# Acknowledgements



Marmoset Coordinating Center

## Coordination

Don Conrad

## Analysis

Jeff Wall

Karina Ray

Ben Bimber

Ric del Rosario

Joanna Malukiewicz

Jamie Ivy



Oregon National  
Primate Center



UC San Diego



Wisconsin National Primate Research Center

Over 60 years of life-saving research and humane animal care

## Design and support

Katinka Conrad



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