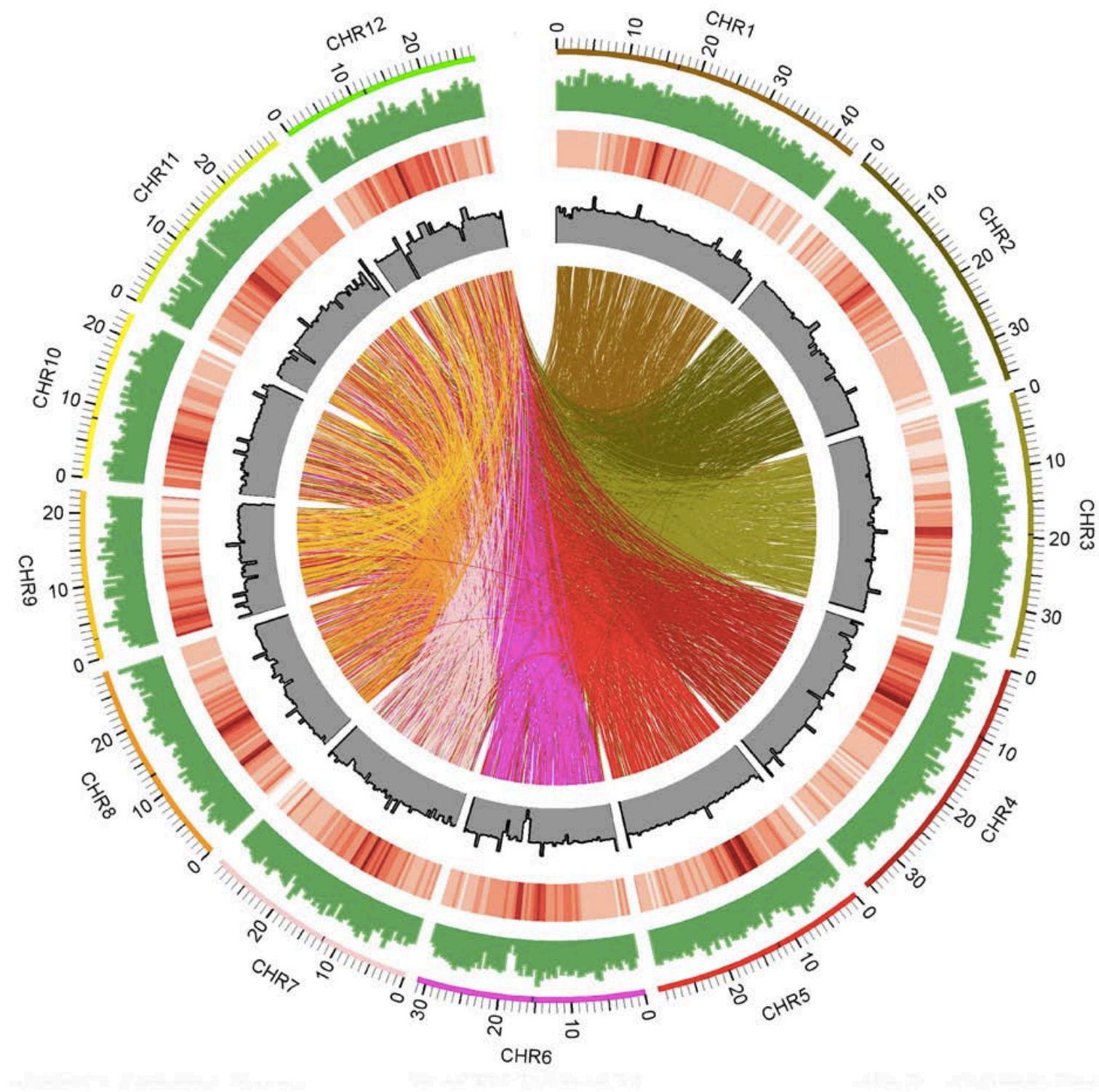




Can we use genomics to help conserve biodiversity?

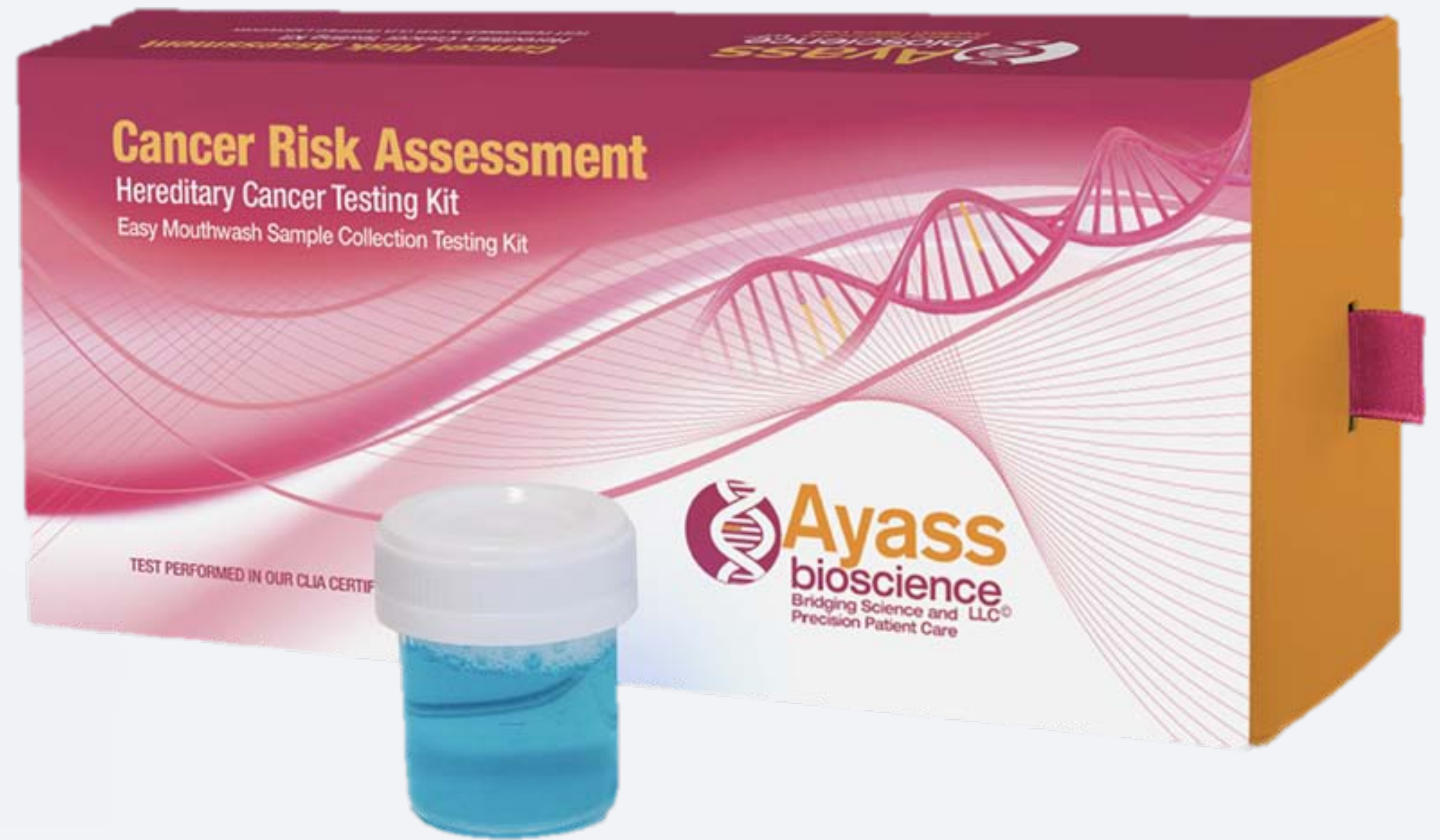


Aaron Shafer
aaronshafer@trentu.ca

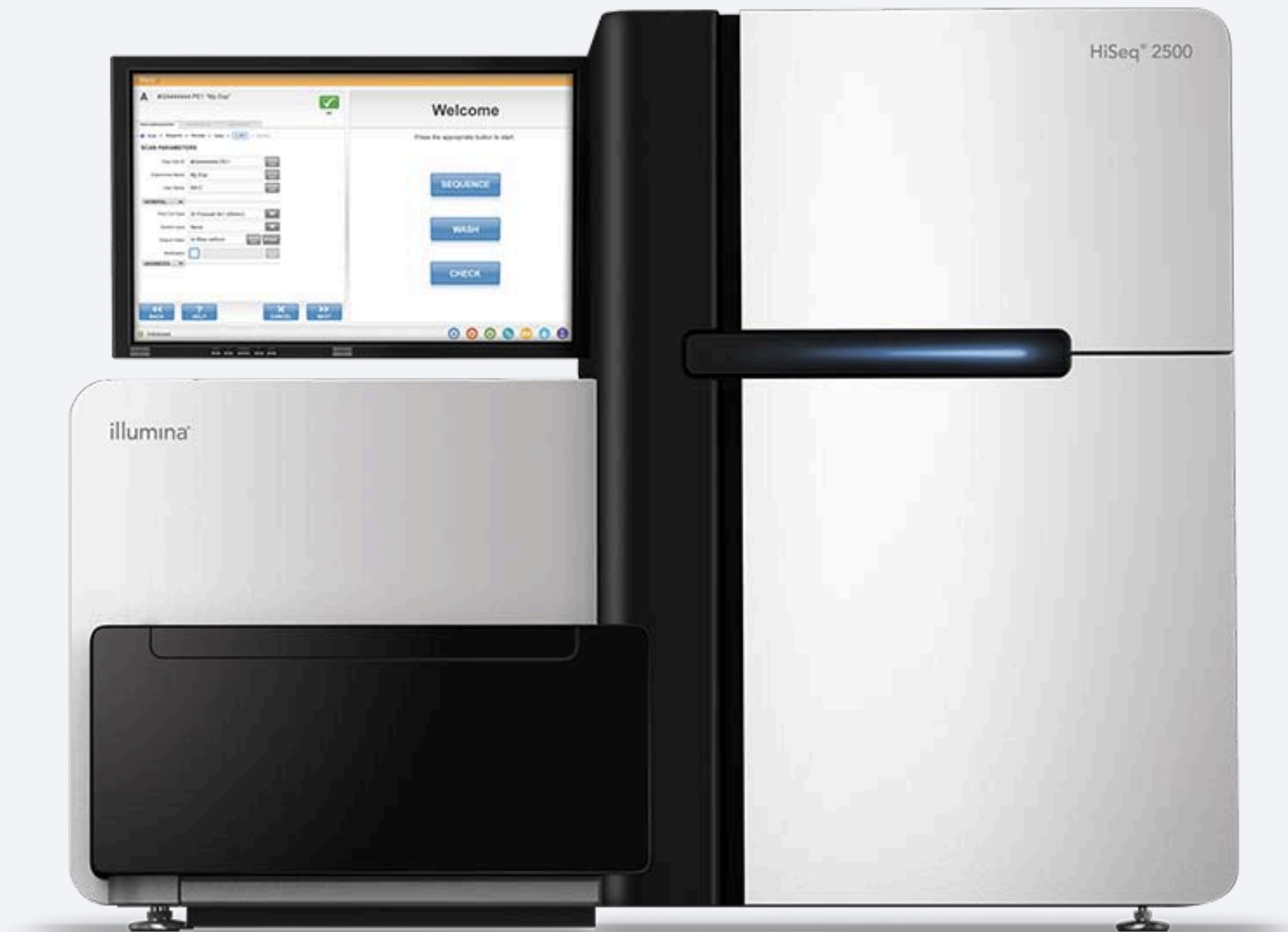


June 2024 - Biología de la conservación Cérvidos Neotropicales

▶ **Genetic information will be used to prolong your lifespan.
Can we do the same for biodiversity?**



▶ It's also a story about technology and conservation



Into the wild ca. 2010

Conservation Biology

Essay

Achieving Conservation Science that Bridges the Knowledge–Action Boundary

CARLY N. COOK,^{*†} MICHAEL B. MASCIA,[‡] MARK W. SCHWARTZ,[§] HUGH P. POSSINGHAM,^{*} AND RICHARD A. FULLER^{*}

^{*}School of Biological Sciences, University of Queensland, Brisbane, Queensland 4072, Australia
[†]School of Botany, University of Melbourne, Parkville, VIC 3010, Australia
[‡]World Wildlife Fund, 1250 24th Street NW, Washington, DC 20037, U.S.A.
[§]Department of Environmental Science & Policy, 1 Shields Avenue, University of California, Davis, CA 95616, U.S.A.

BIOTROPICA 41(5): 549–554 2009 10.1111/j.1744-7429.2009.00557.x

Bridging the Gap: How Can Information Access and Exchange Between Conservation Biologists and Field Practitioners be Improved for Better Conservation Outcomes?

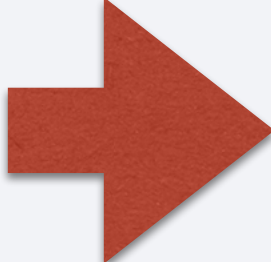
Terry Sunderland¹, Jacqueline Sunderland-Groves, Patricia Shanley, and Bruce Campbell
Centre for International Forestry Research, PO Box 0113, BOCBD, Bogor 16000, Indonesia

▶ What is in a genome?



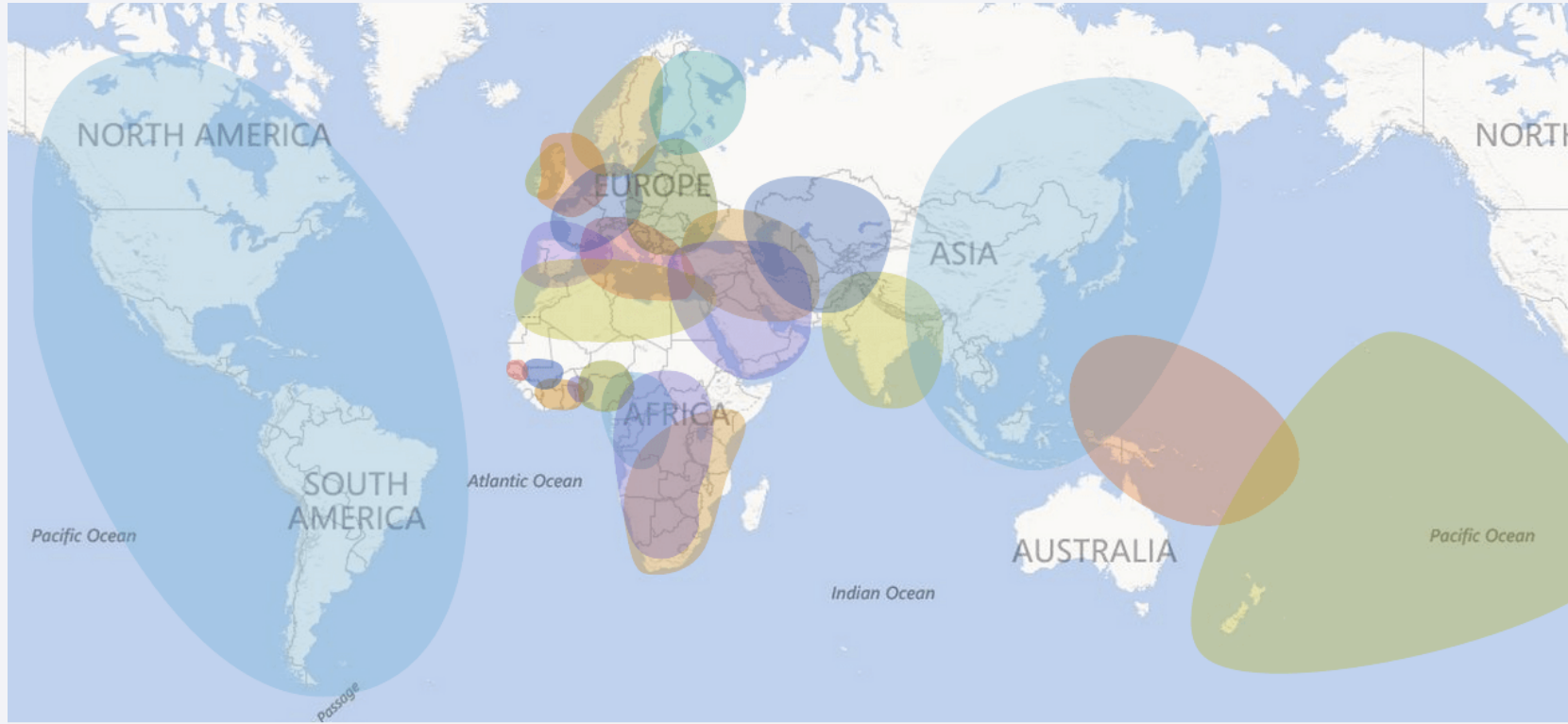
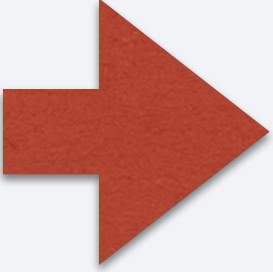
My genome

Your genome



A
T/A
T
A
C
T
A

A
T
T
A
C
G
A



▶ Genome in context: conservation **genetics** has a *rich* history

Bonnell & Selander 1976 (Science)

Elephant Seals: Genetic Variation and Near Extinction

Abstract. Blood samples from northern elephant seals (*Mirounga angustirostris*), representing five breeding colonies in California and Mexico, were surveyed electrophoretically for protein variation reflecting underlying genetic differences. No polymorphisms were found among 21 proteins encoded by 24 loci. This uniform homozygosity may be a consequence of fixation of alleles brought about by the decimation of this species by sealers in the last century.

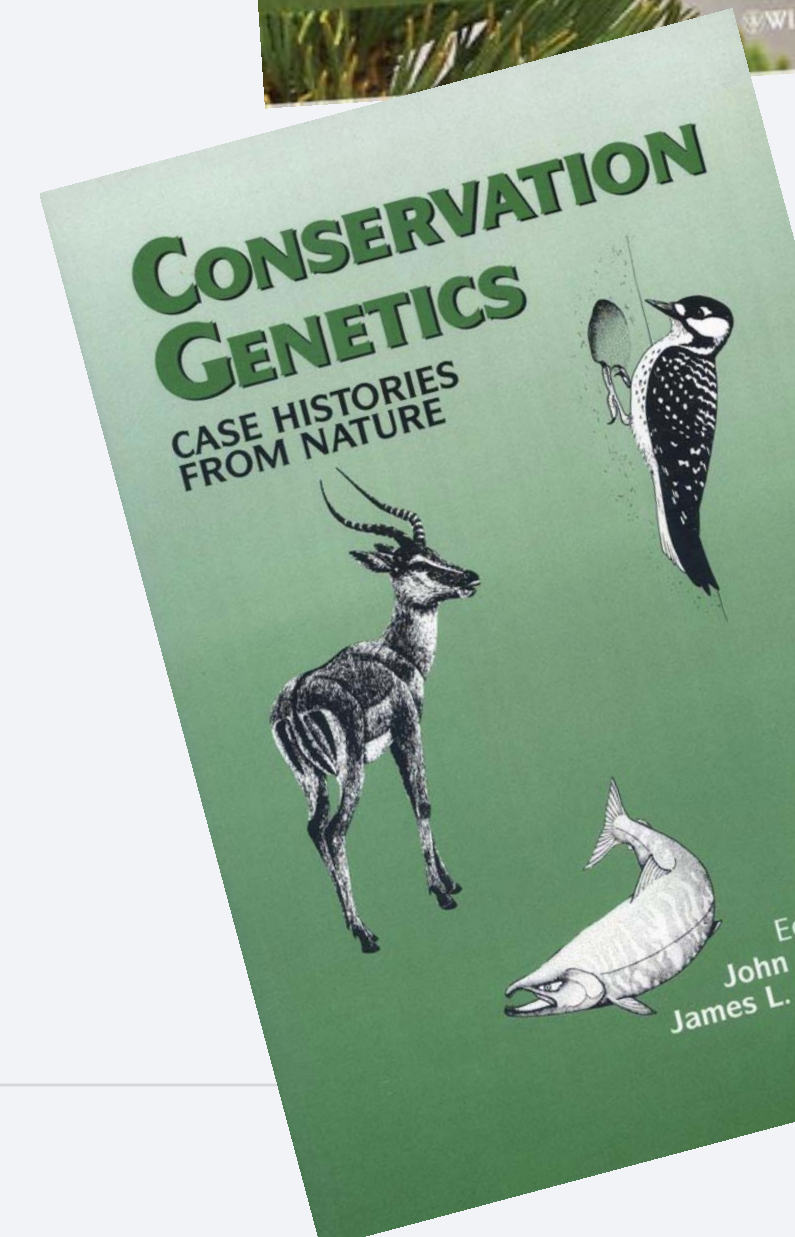
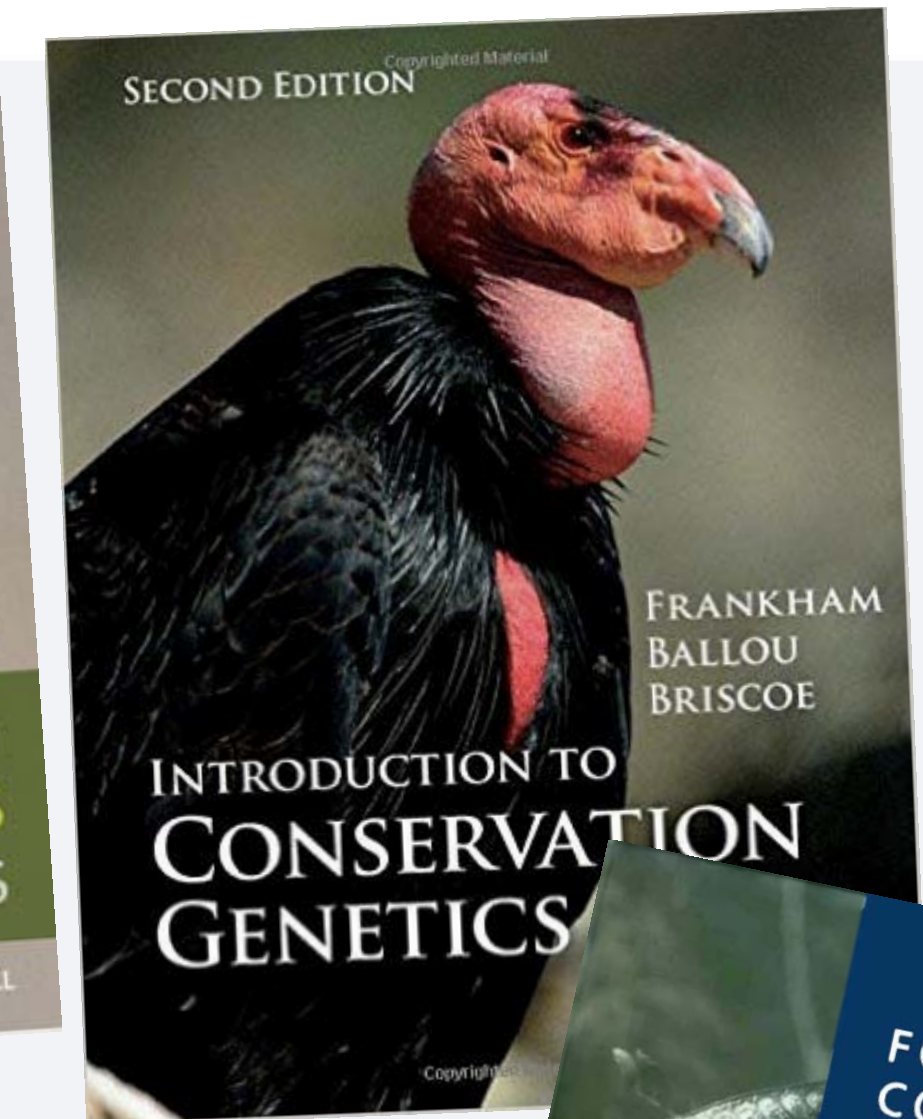
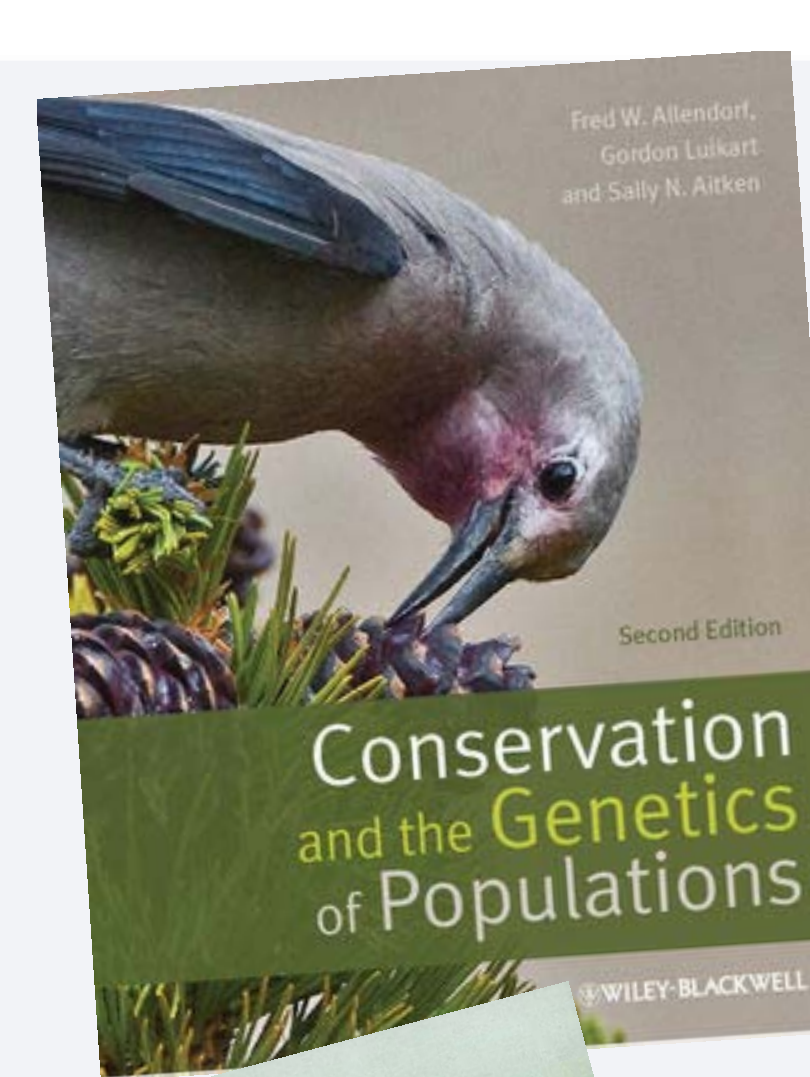
animal species. Our results also suggest that the northern elephant seal, now lacking a pool of variability with which to adapt to changing conditions, is especially vulnerable to environmental modification.

MICHAEL L. BONNELL

Thimann Laboratories, University
of California, Santa Cruz 95060

ROBERT K. SELANDER

Department of Zoology,
University of Texas, Austin 78712





Genome in context: Convention on Biological Diversity & various legislative acts



Target 4 (and 20):*maintain and restore the genetic diversity within and between populations of native, **wild** and domesticated species to maintain their **adaptive** potential*

ENDANGERED SPECIES ACT OF 1973

As Amended through the
108th Congress

Department of the Interior
U.S. Fish and Wildlife Service
Washington, D.C. 20240

Distinct Population Segment: *quantitative genetic separation.... differ in genetic characteristics...*

▶ Genome in context: A conservation **genetics** gap emerges

Evolutionary Applications Open Access
Evolutionary Applications ISSN 1752-4571

PERSPECTIVE

The conservation genetics juggling act: integrating genetics and ecology, science and policy

Susan M. Haig,¹ Mark. P. Miller,¹ Renee Bellinger,² Hope M. Draheim,³ Dacey M. Mercer⁴ and Thomas D. Mullins¹

¹ U.S. Geological Survey, Forest and Rangeland Ecosystem Science Center, Corvallis, OR, USA
² Department of Biology, Tropical Conservation Biology and Environmental Science, University of Hawaii, Hilo, HI, USA
³ Pacific States Marine Fisheries Commission, Eagle Fish Genetics Laboratory, Eagle, ID, USA
⁴ Hatfield Marine Science Center, Oregon State University, Newport, OR, USA

life cycle. As a federal laboratory, we are often addressing the needs of the U.S. Fish and Wildlife Service in their efforts to list, de-list, or recover species. **Nevertheless, there remains an overall communication gap between research geneticists and biologists who are charged with implementing their results.** Therefore, we outline the need for a National Center for Small Population Biology to ameliorate this problem and provide organizations charged with making status decisions firmer ground from which to make their critical decisions.

Contents lists available at ScienceDirect

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ELSEVIER journal homepage: www.elsevier.de/jnc

Short communication

Conservation Genetic Resources for Effective Species Survival (ConGRESS): Bridging the divide between conservation research and practice



REVIEWS REVIEWS REVIEWS
... Antonio^a, Giorgio Bertorelle^a, Josef Bryja^c, Margarida Fernandes^d, ... Ceder^b, Heidi C. Hauffeⁱ,

Counting the books while the library burns: why conservation monitoring programs need a plan for action

David B Lindenmayer^{1*}, Maxine D. ...

Diversity

Where's the Conservation in Conservation Genetics?

CRISTIANO VERNESI,^{*} MICHAEL W. BRUFORD,[†] GIORGIO BERTORELLE,[‡] ELENA PECCHIOLI,^{*} ANNAPAOLA RIZZOLI,^{*} AND HEIDI C. HAUFFE^{*§}

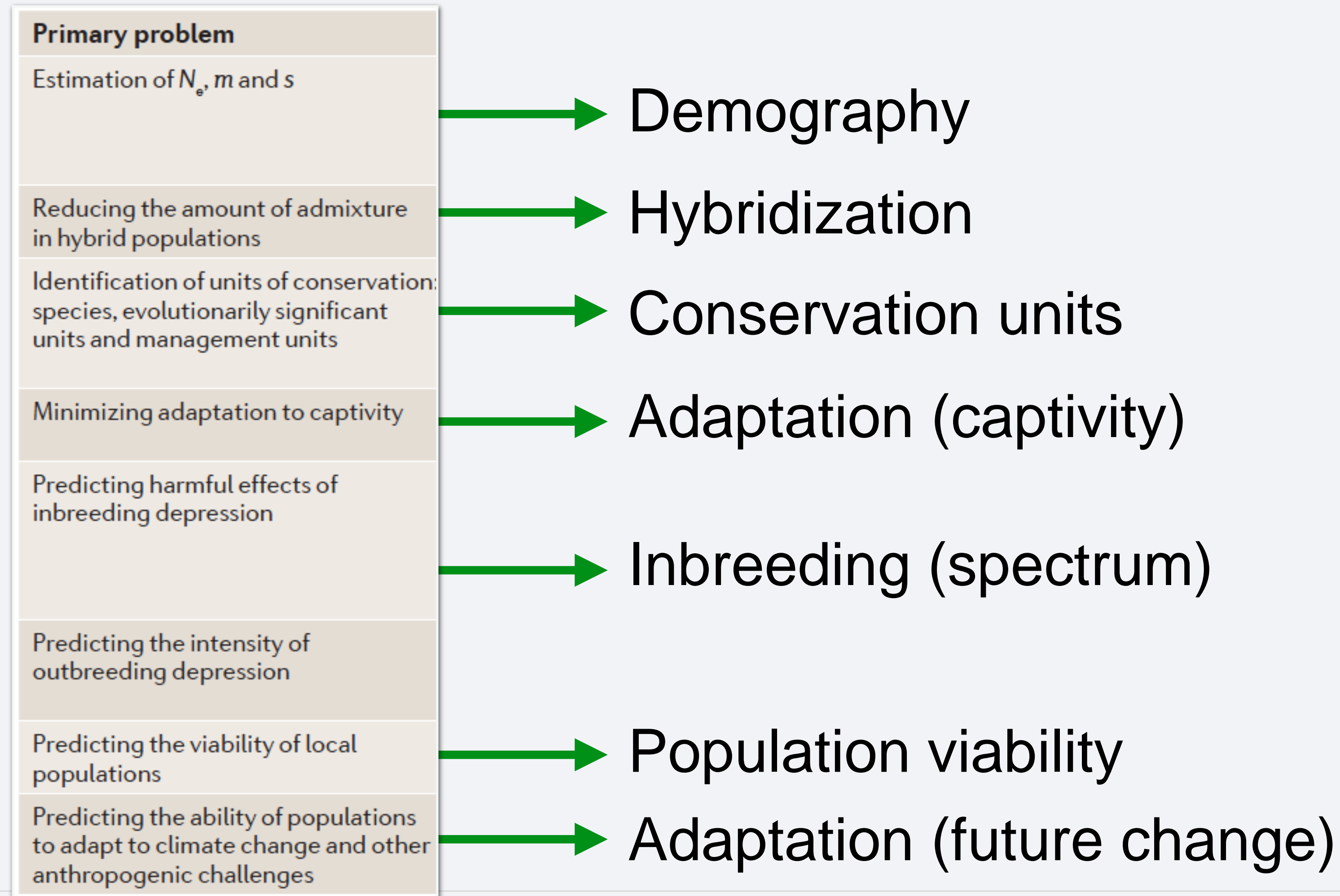
^{*}Centro di Ecologia Alpina, Fondazione Edmund Mach, 38040 Viote del Monte Bondone, Trento, Italy
[†]Cardiff School of Biosciences, University of Cardiff, Cardiff CF10 3US, United Kingdom
[‡]Department of Biology and Evolution, University of Ferrara, Via L. Borsari, 46, 44100 Ferrara, Italy

▶ Genomics enters the conservation discussion

All selected articles predate 2010



▶ Conservation genetics problems have genomic solutions!



▶ Conservation genetics problems have genomic solutions!

More markers and adaptive loci is the answer

Primary problem	Possible genomic solution
Estimation of N_e , m and s	Increasing the number of markers , reconstructing pedigrees and using haplotype information will provide greater power to estimate and monitor N_e and m , as well as to identify migrants, estimate the direction of migration and estimate s for individual loci within a population
Reducing the amount of admixture in hybrid populations	Genome scanning of many markers will help to identify individuals with greater amounts of admixture so that they can be removed from the breeding pool
Identification of units of conservation: species, evolutionarily significant units and management units	The incorporation of adaptive genes and gene expression will augment our understanding of conservation units based on neutral genes. The use of individual-based landscape genetics will help to identify boundaries between conservation units more precisely
Minimizing adaptation to captivity	Numerous markers throughout the genome could be monitored to detect whether populations are becoming adapted to captivity
Predicting harmful effects of inbreeding depression	Understanding the genetic basis of inbreeding depression will facilitate the prediction of the effectiveness of purging. Genotyping of individuals at loci associated with inbreeding depression will allow the selection of individuals as founders or mates in captive populations. Pedigree reconstruction will allow more powerful tests of inbreeding depression
Predicting the intensity of outbreeding depression	Understanding the divergence of populations at adaptive genes will help to predict effects on fitness when these genes are combined. Detecting chromosomal rearrangements will help to predict outbreeding depression
Predicting the viability of local populations	Incorporating genotypes that affect vital rates and the genetic architecture of inbreeding depression will improve population viability models
Predicting the ability of populations to adapt to climate change and other anthropogenic challenges	Understanding adaptive genetic variation will help to predict the response to a rapidly changing environment or to harvesting by humans and allow the selection of individuals for assisted migration

▶ Conservation genetics problems have genomic solutions!

More markers and adaptive loci is the answer

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Increased resolution
 "Adaptive loci"

▣ Conservation genet(om)ic climate in two parts

Part I. Questioning the solutions

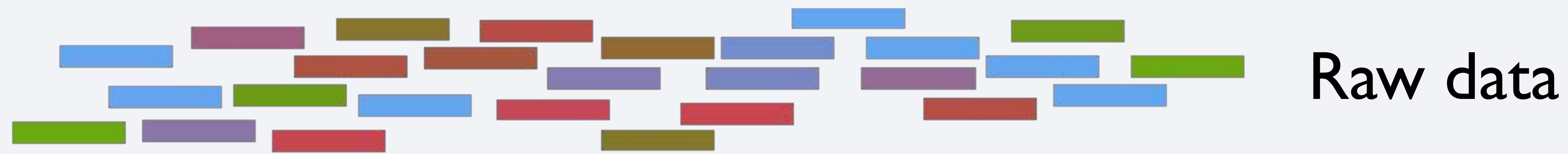
Part II. Empirical examples and a way forward

- Its okay to do basic and fundamental research!
- Basic and fundamental research will have applications (to conservation)

▣ Questioning the solutions

- We are in the midst of a Biodiversity crisis
- Very good intentions coupled with a demand to publish
- Various levels of experience handling and analyzing genomic data
- **Human genomics is not wildlife genomics**
 - e.g. 23andMe has SNP data on 1,000,000s people

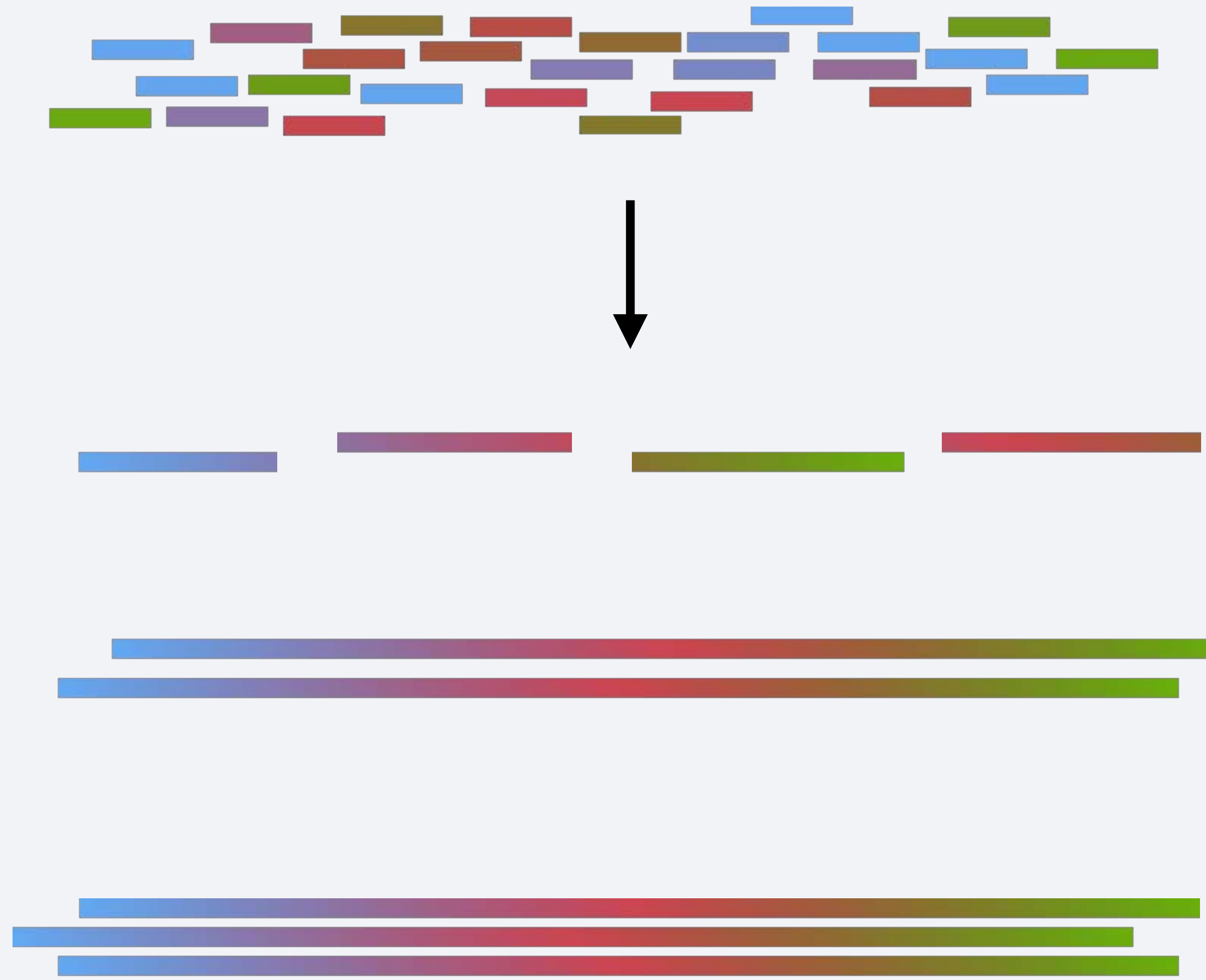
▶ No standard way to generate genomic (SNP) data



- Many ways to go from raw sequencing data to SNPs (pipelines)
- No standardized way to filter your data (leave as is; remove *wonky* SNPs)
- Lots of missing data (more SNPs) → less missing data (fewer SNPs)

▶ 312 permutations (all more-or-less used)

Shafer et al. (2017) *Methods in Ecology & Evolution*



RAD data

denovo assembly of RAD loci



“Cheap” reference

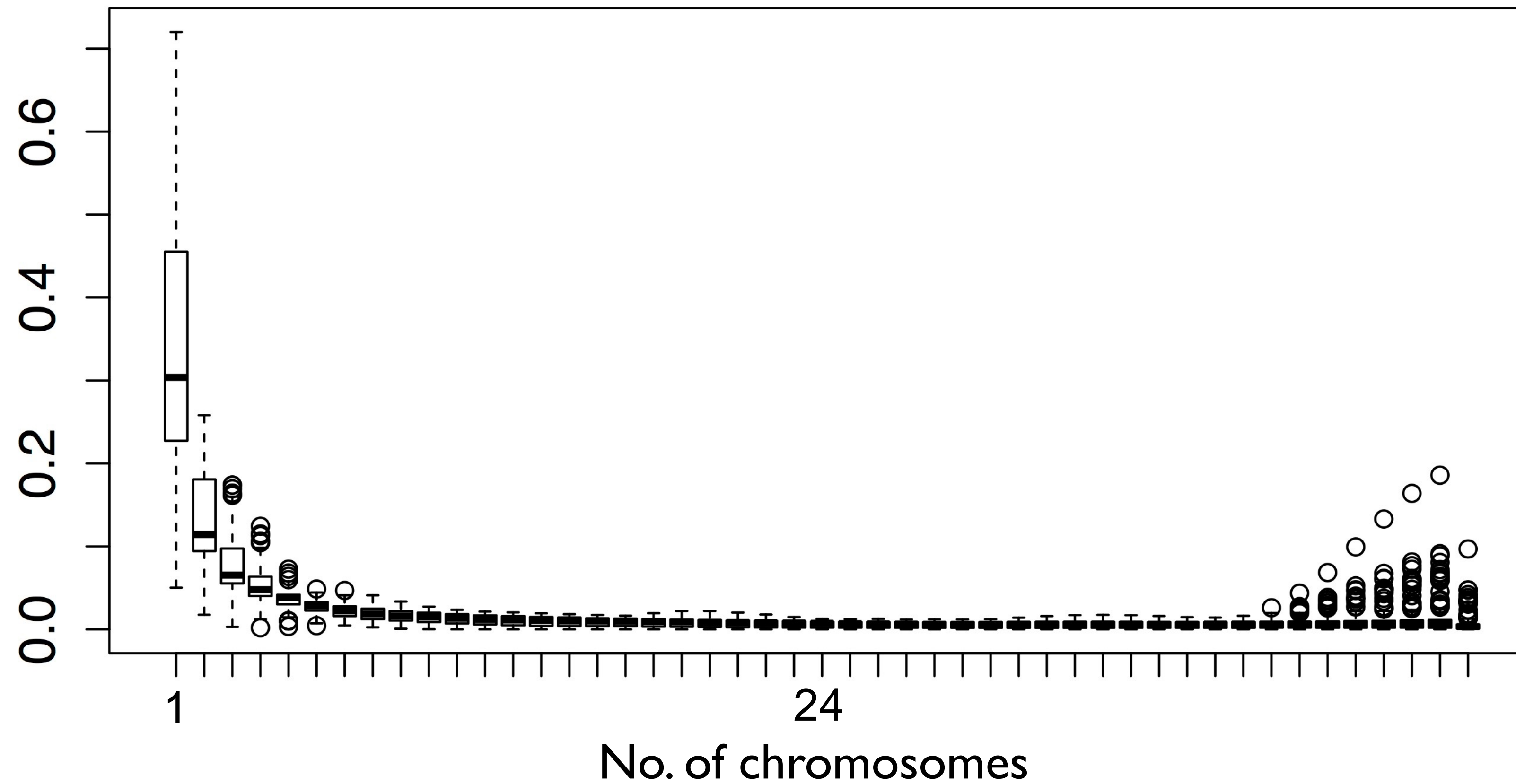


High quality related reference



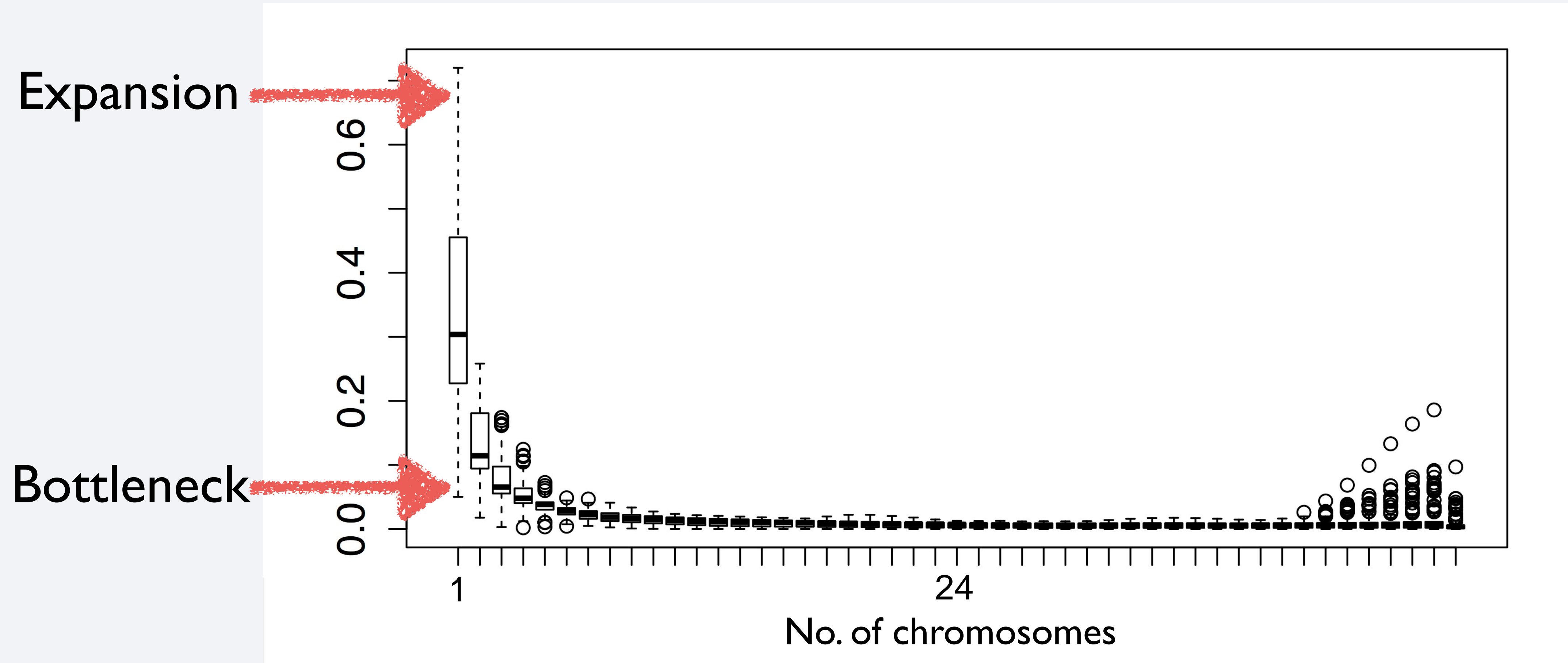
▶ Site-frequency spectra from sea lion data

Shafer et al. (2017) *Methods in Ecology & Evolution*



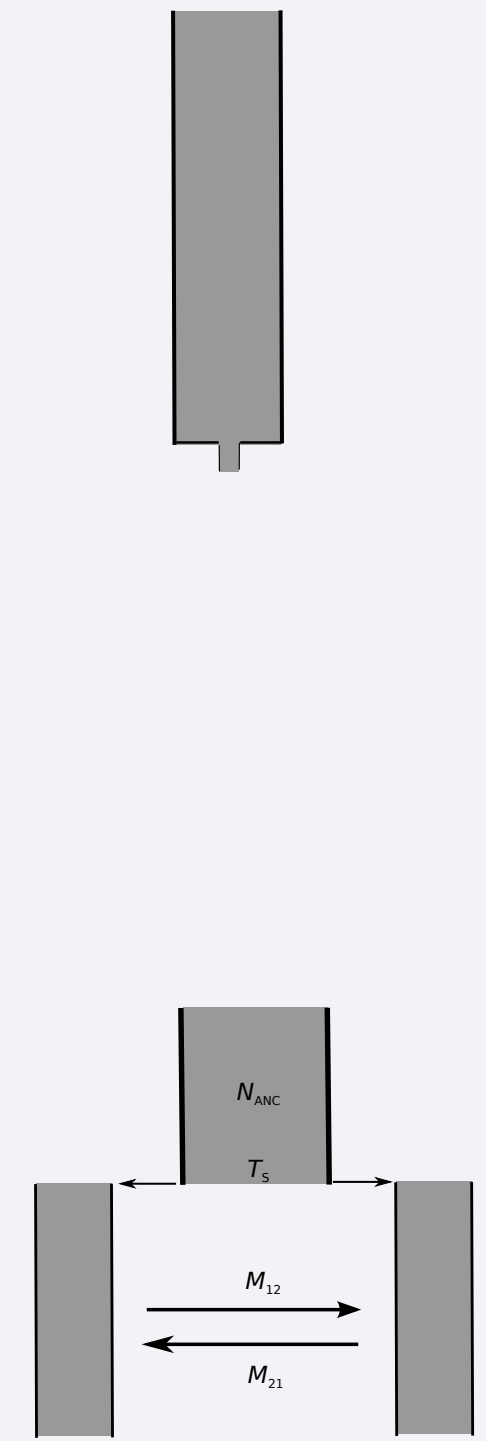
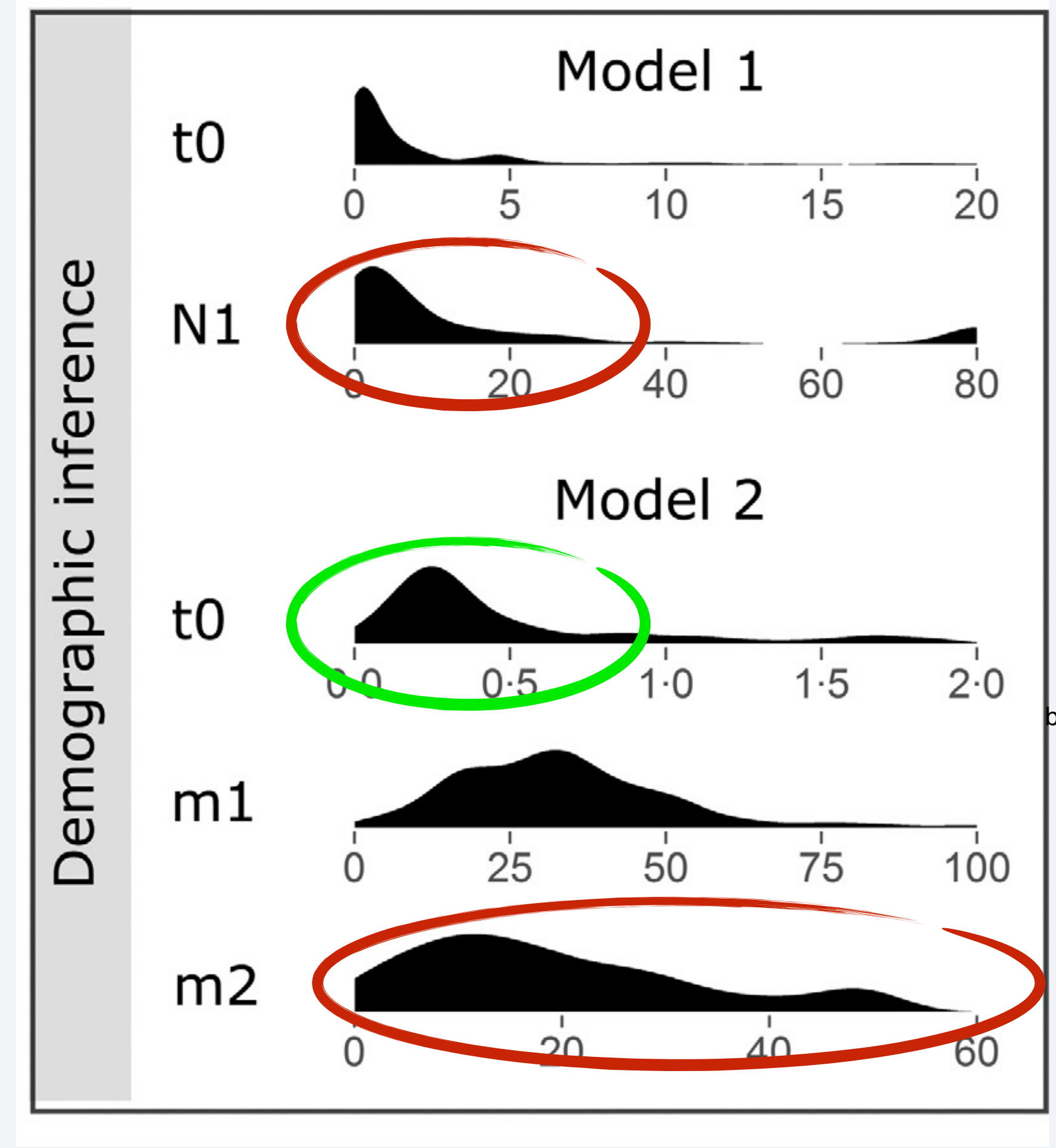
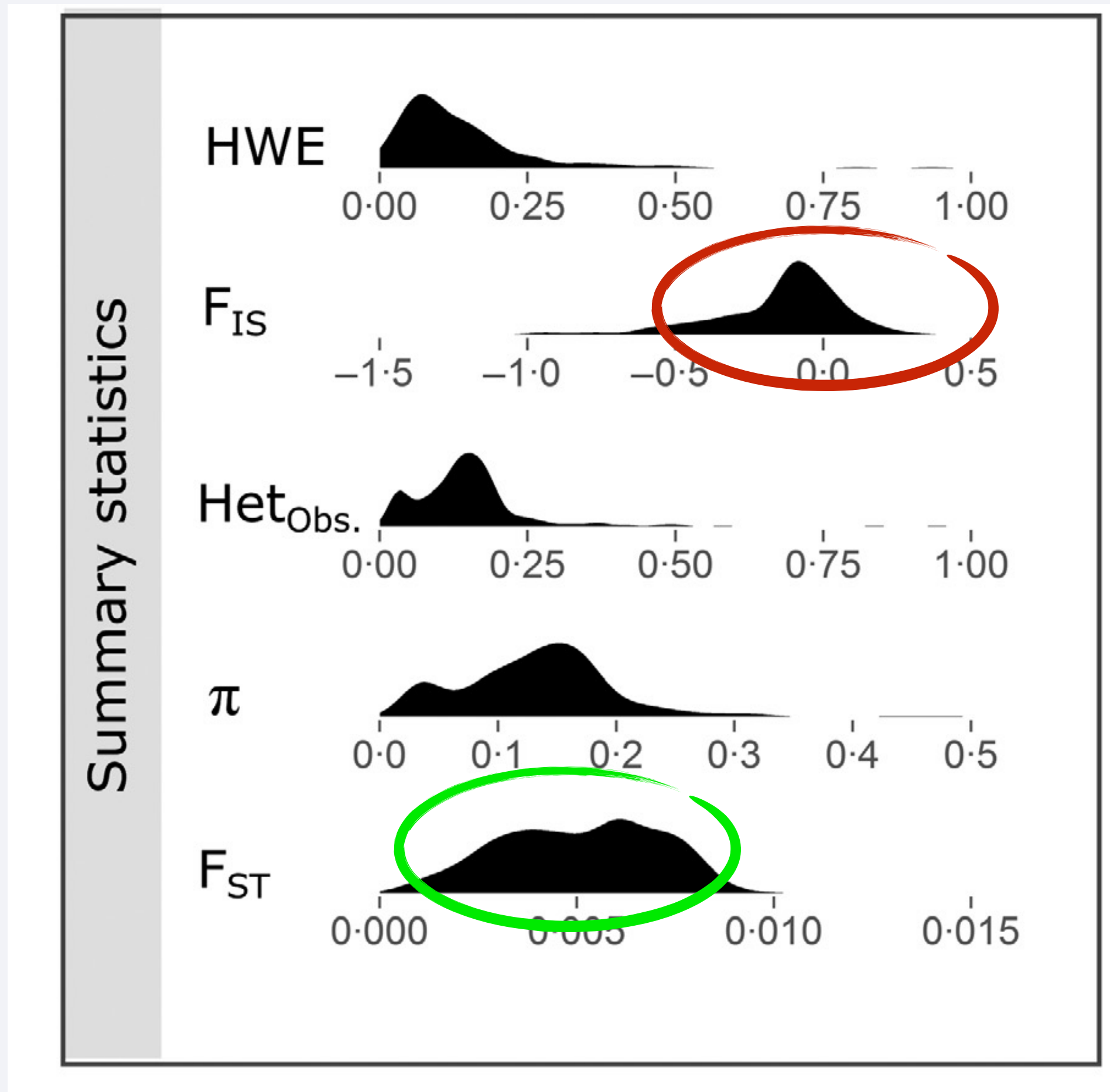
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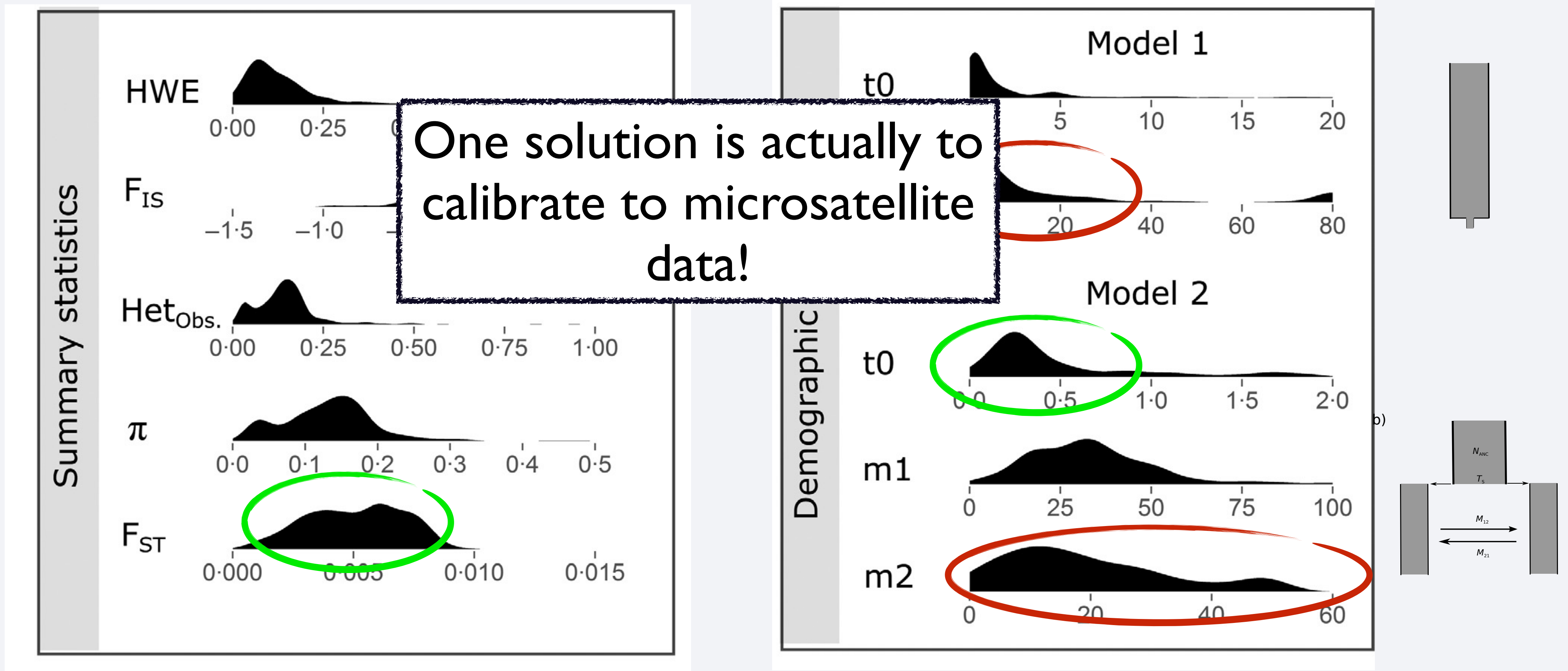
▶ Site-frequency spectra from sea lion data

Shafer et al. (2017) *Methods in Ecology & Evolution*



▶ Site-frequency spectra from sea lion data

Shafer et al. (2017) *Methods in Ecology & Evolution*



▶ Thinking a bit about local adaptation

McMahon et al. (2014) Evolutionary Applications

As argued above, we think that 'local adaptation' is the most important issue where genomics can contribute to conservation science. We want to stress that we do not see 'local adaptation' as different from the issue of 'preserving genetic variation' or 'identifying ecotypes'. These aspects are instead tightly linked. Without genetic variation, there can be no local adaptation, and without local adaptation, no ecotypes. Further, simply because local adaptation is the most important aspect, this does not exclude, for example 'estimation of demographic parameters'. Our argument is simply that the first is more important, not that the second is unimportant.

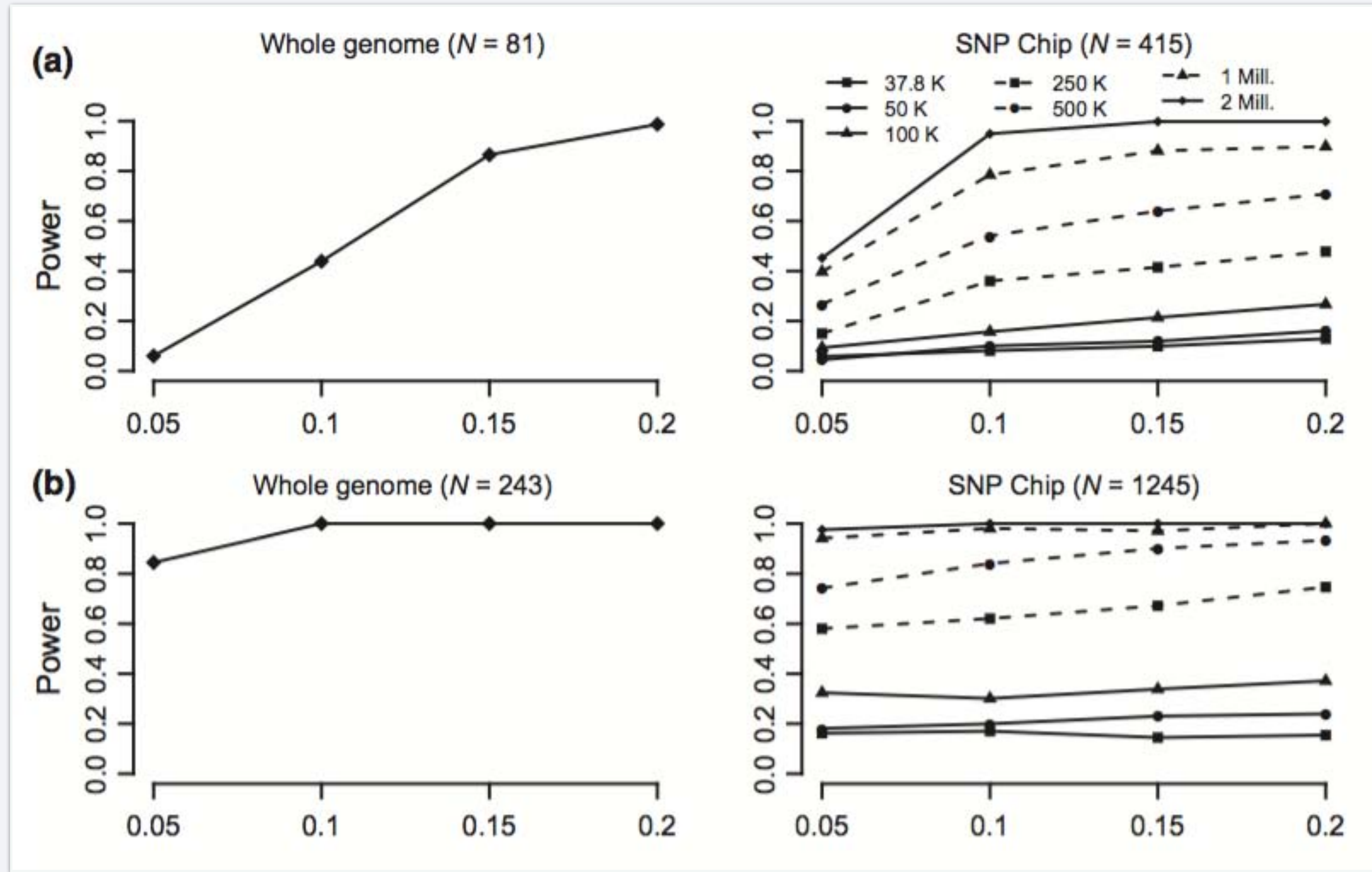
Conclusions and perspectives

We predict that genomics will make a difference primarily in determining which parts of the genomes are responsible for local adaptation and therefore important to preserve.



Detecting genetic basis to phenotypes is [very] difficult in wild populations

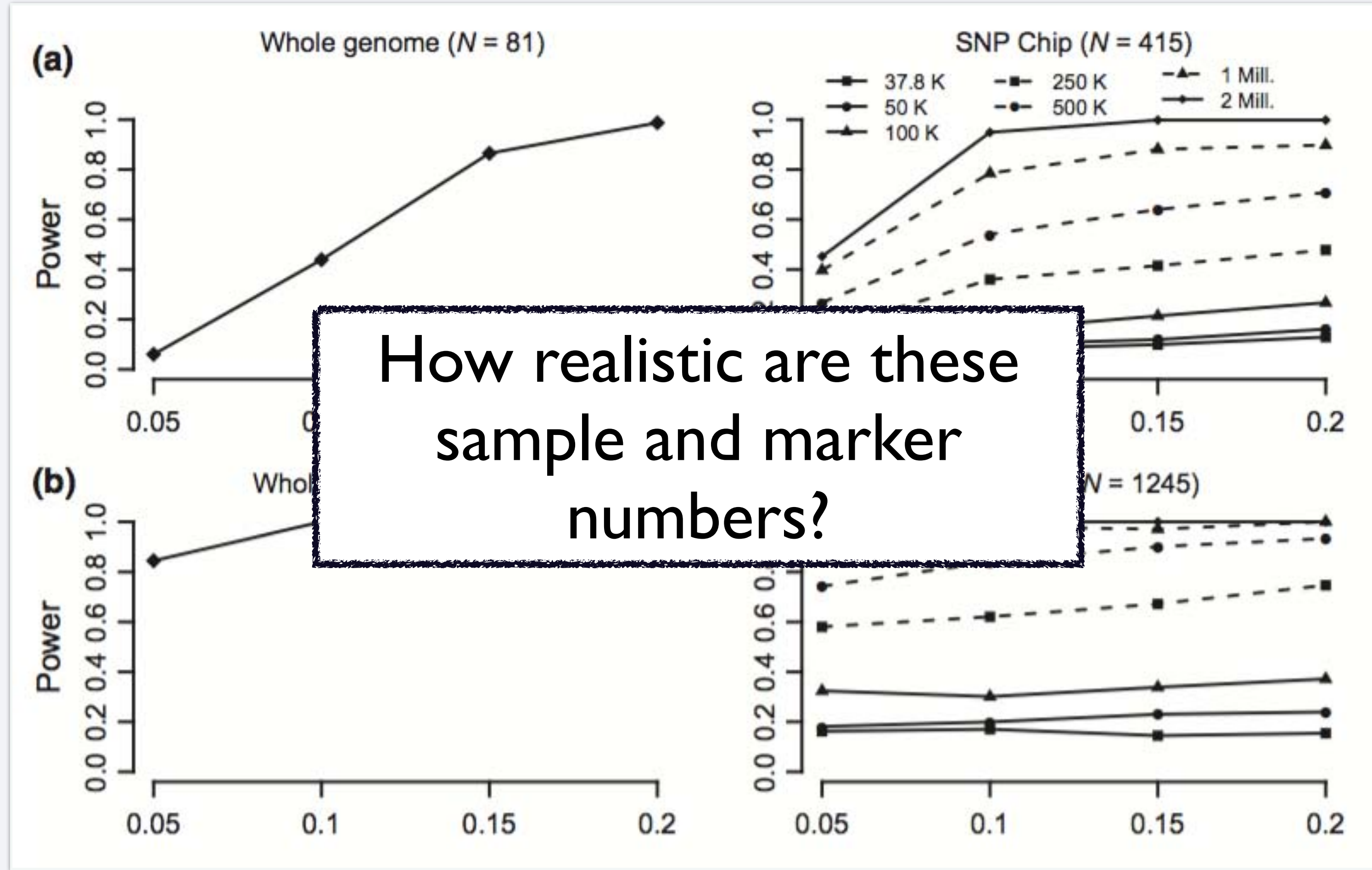
Kardos et al. (2016) Molecular Ecology





Detecting genetic basis to phenotypes is [very] difficult in wild populations

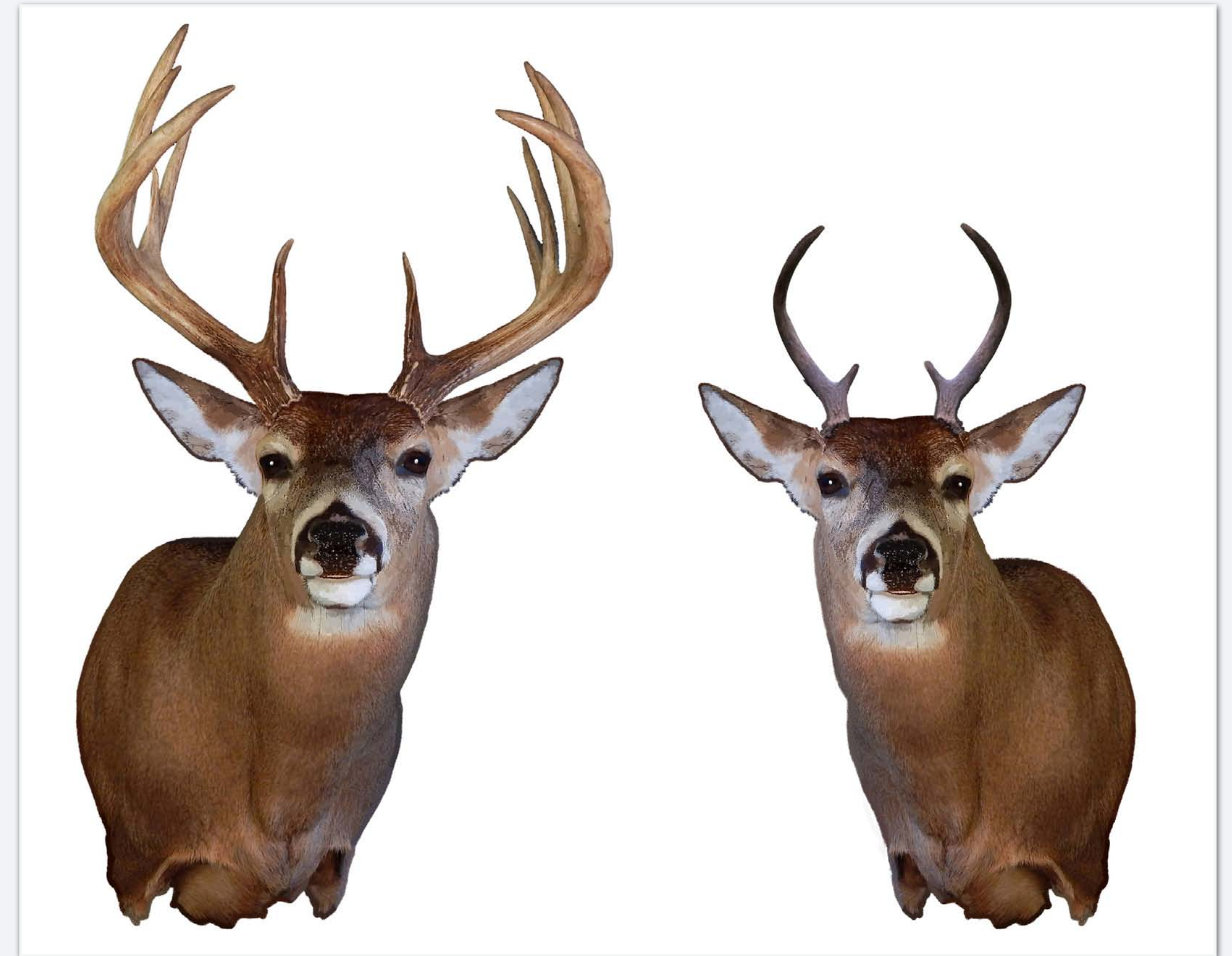
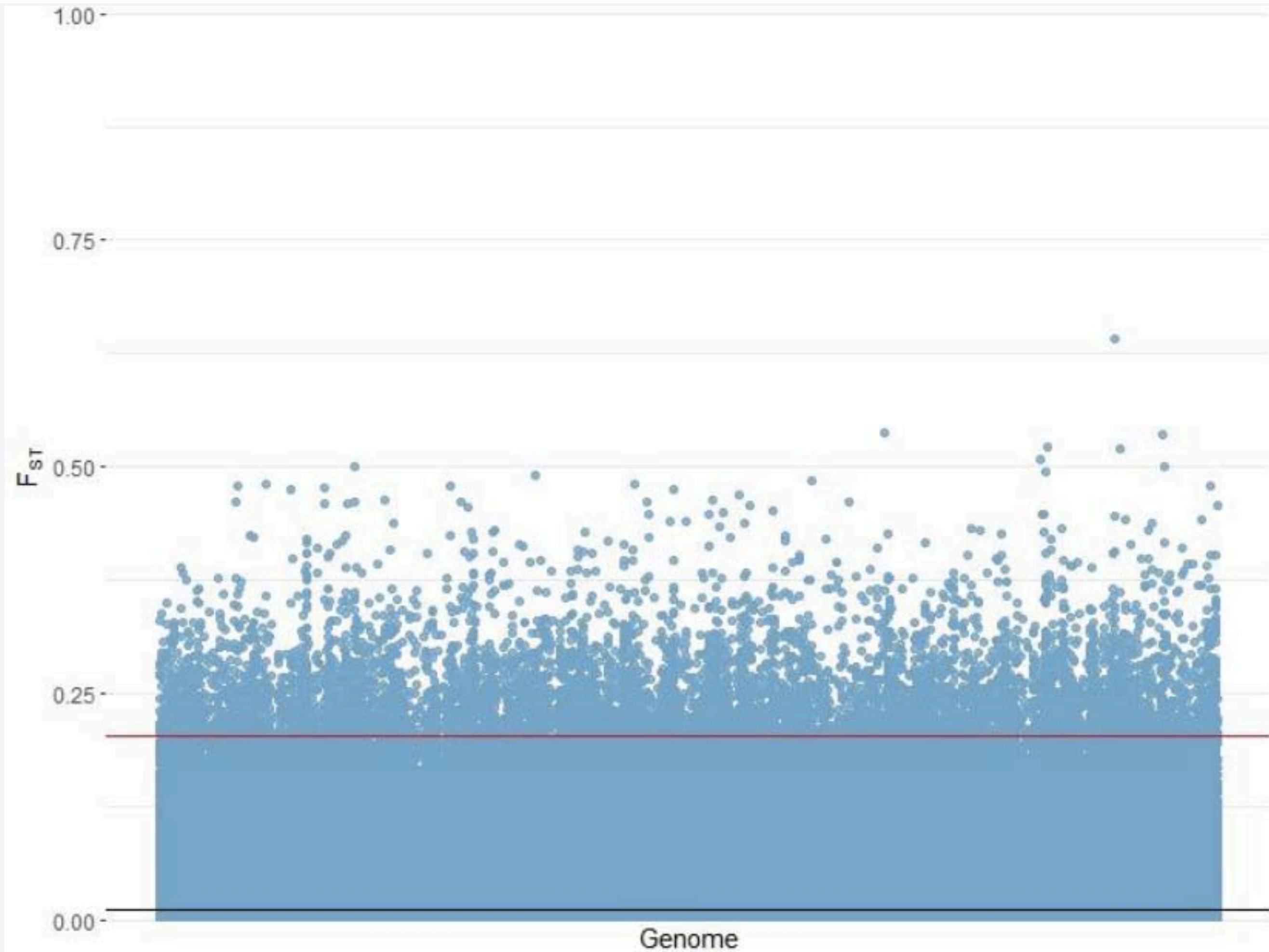
Kardos et al. (2016) Molecular Ecology





Detecting genetic basis to phenotypes is [very] difficult in wild populations

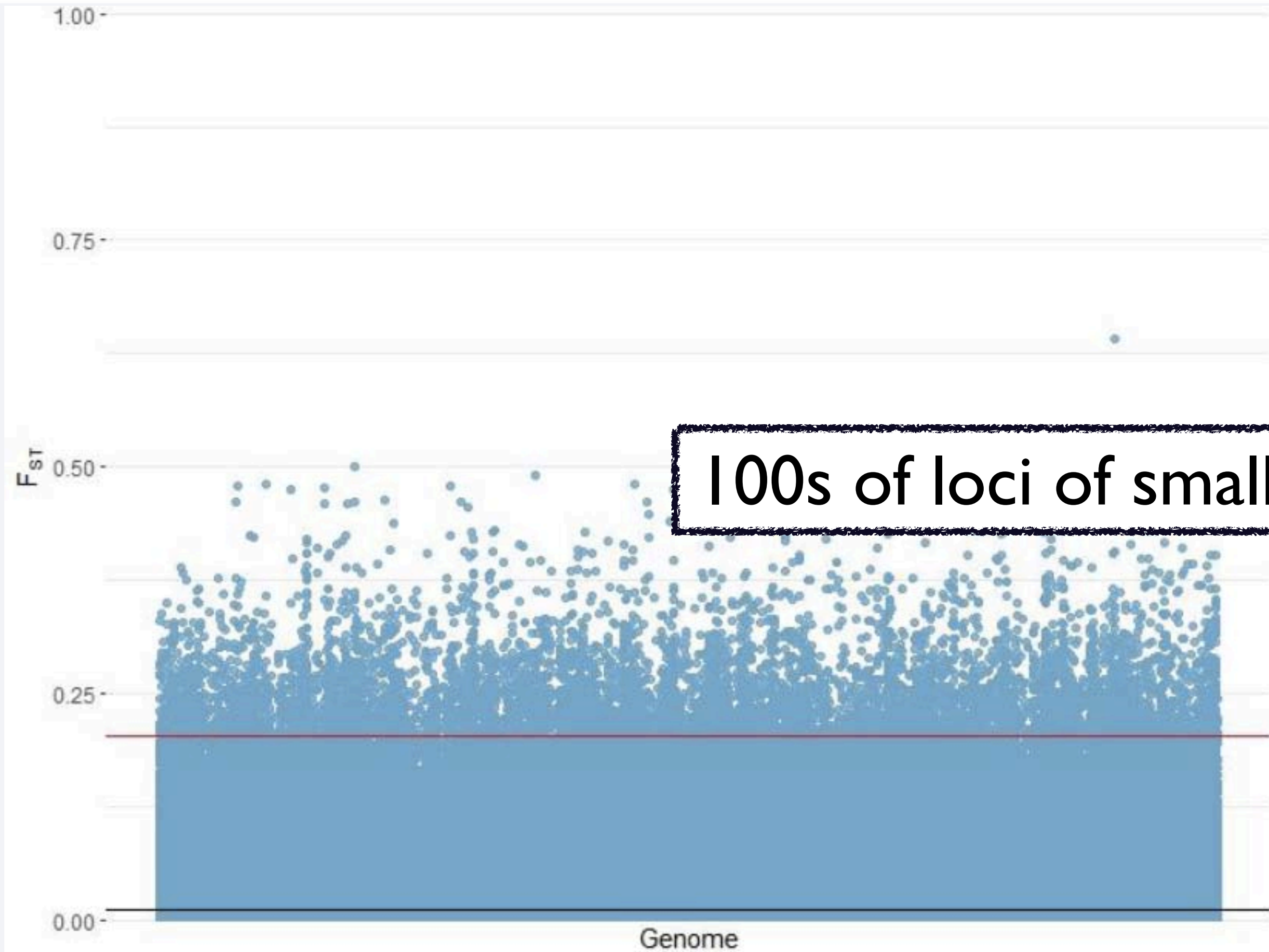
Anderson et al. 2022 BMC Genomics



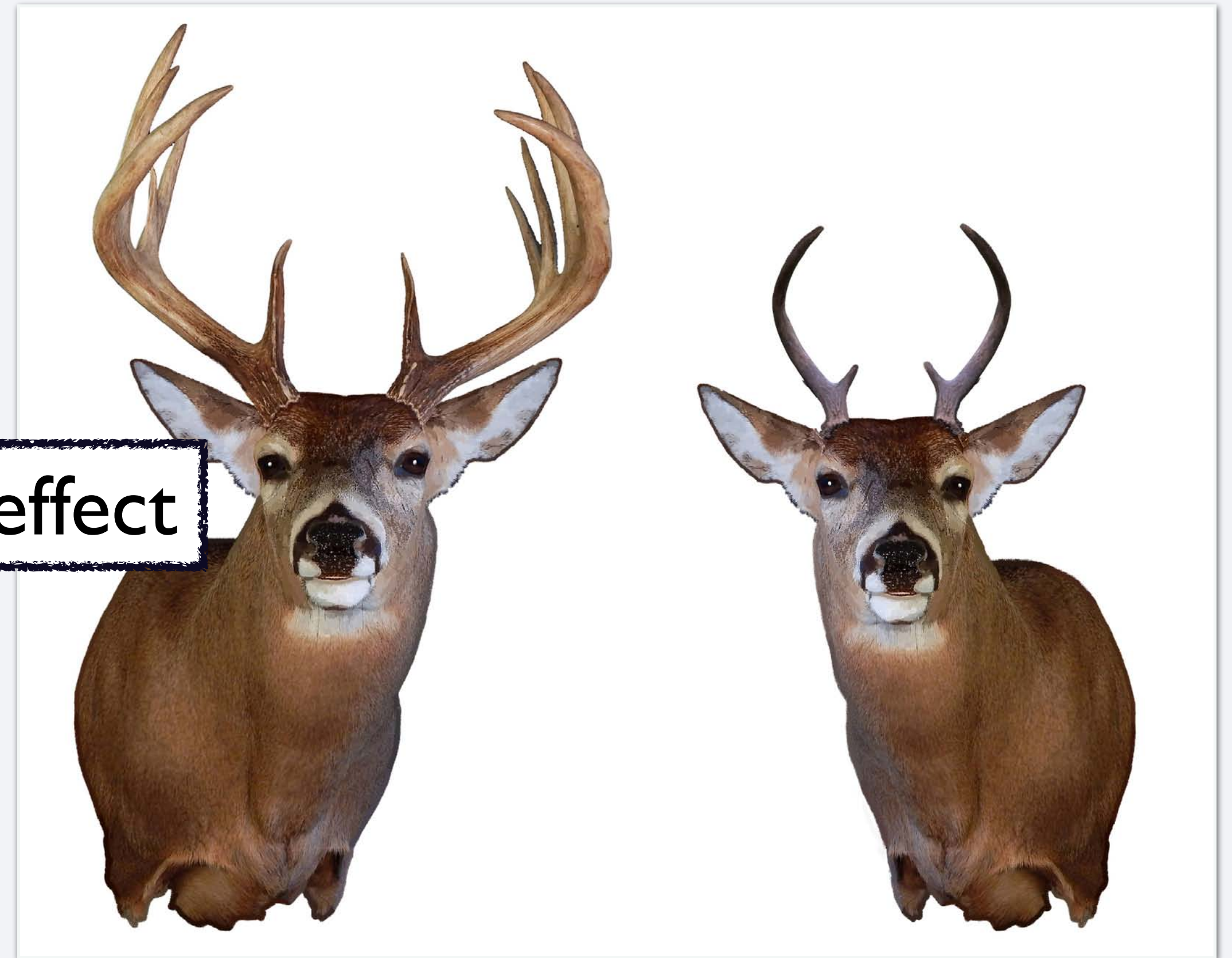


Detecting genetic basis to phenotypes is [very] difficult in wild populations

Anderson et al. (2022) BMC Genomics



100s of loci of small effect



▣ Questioning the genomics solution

- No standardized way to call SNPs
- Bioinformatics pipeline influences demographic inference
- GWAS / local adaptation very difficult
- Epigenetic influences (i.e. not inherited SNPs)
- **Long recognized in the human world**

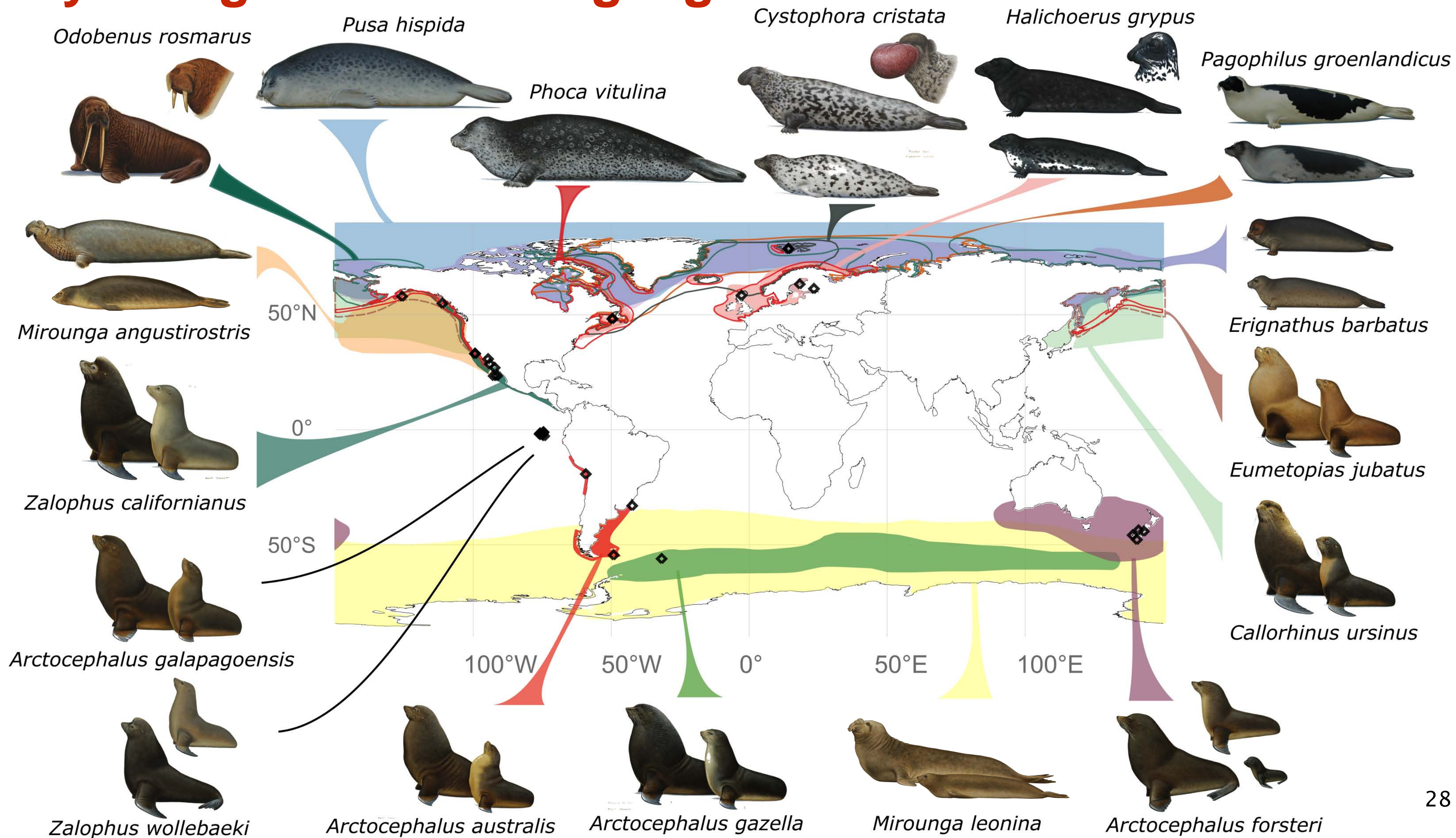
▣ Conservation genet(om)ic climate in two parts

Part I. Questioning the solutions

Part II. Empirical examples and a way forward

- Its okay to do basic and fundamental research!
- **Basic and fundamental research** will have applications (to conservation)

Story 1: A genetic warning signal



- ▶ The most important metric of all:

Effective population size (N_e) is a population genetics convention describing the number of breeding individuals in an ideal population that would lose genetic variation at the same rate as the observed population.

▣ What is measured?

Census population size (N_c)

Effective population size (N_e)

▣ What is measured?

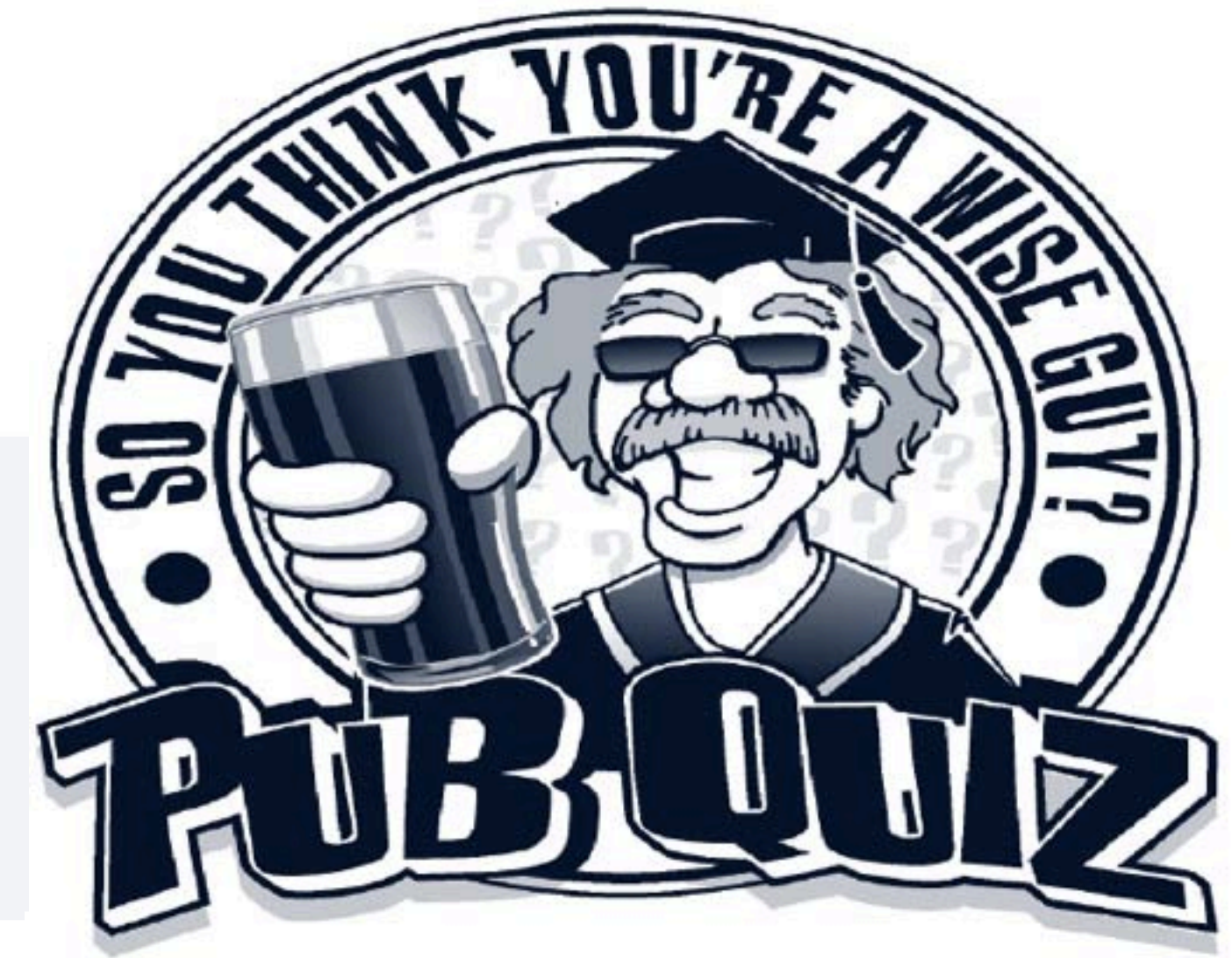
$$\theta_W = \theta_\pi = 4N_e\mu$$

▶ What is measured?

```
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```

$$= 4N_e$$
A silhouette diagram illustrating the evolution of man from an ape-like ancestor. It shows five stages of a creature, starting from a crouching ape on the left and progressing through intermediate forms to a fully upright, walking human on the right.

▶ What is measured?



$$0.00074 = 4N_e \quad 1.8E-08$$

▣ What is measured?

Human N_c

7,346,235,000

Human N_e

~10,472 *****This is the value nature operates with!**

▣ And by the way:

Target 4

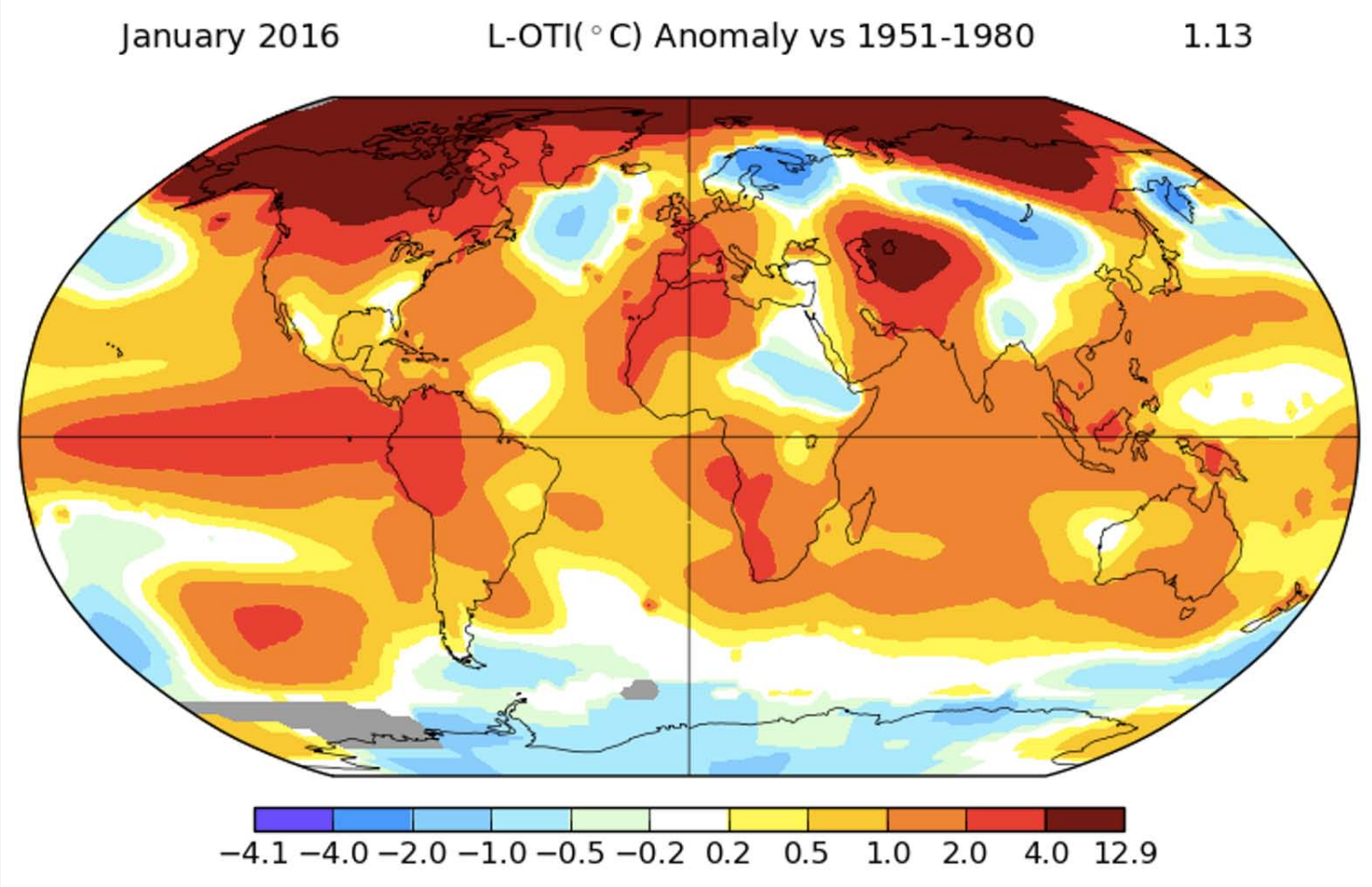
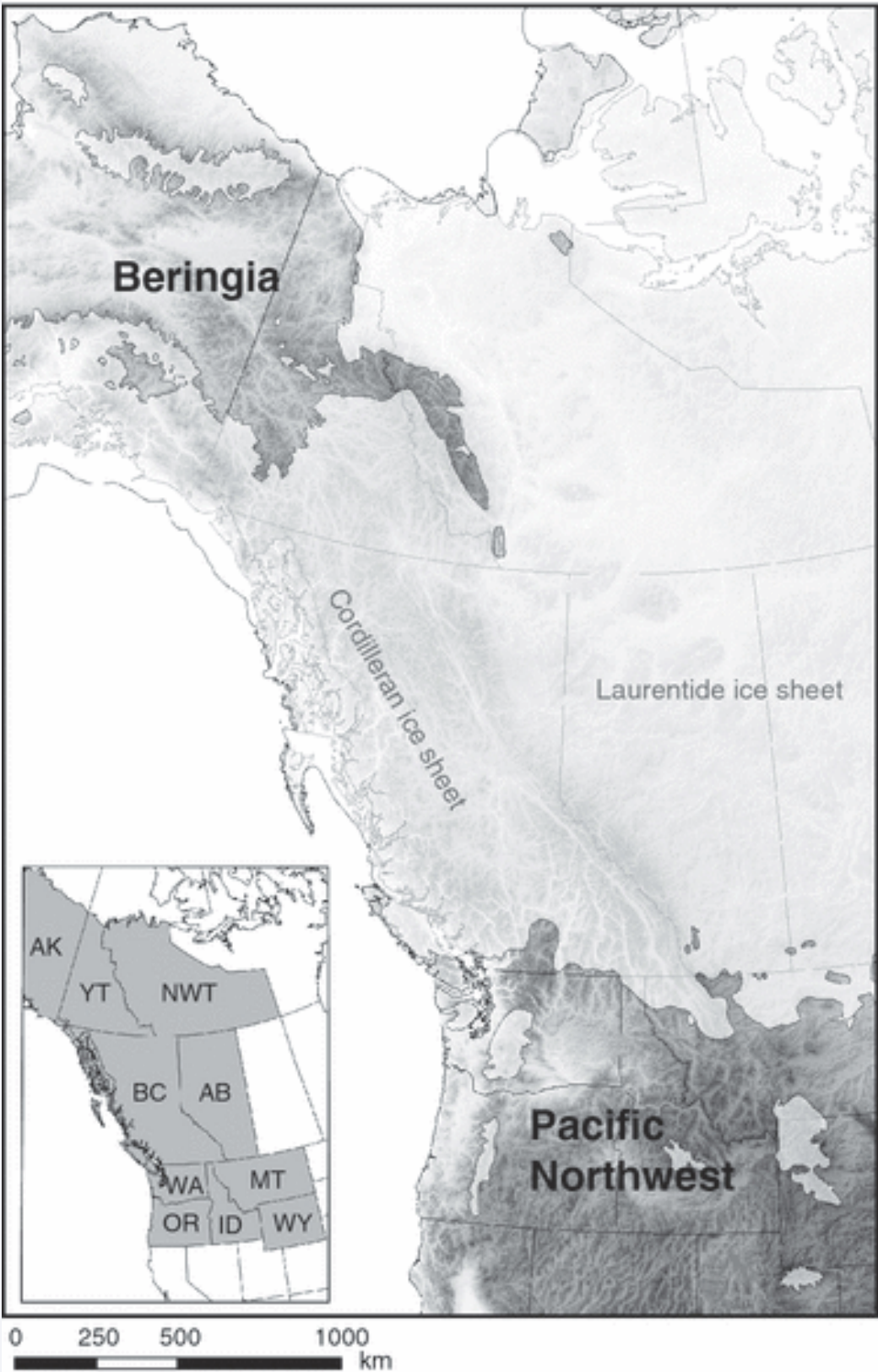
Halt Species Extinction, Protect Genetic Diversity, and Manage Human-Wildlife Conflicts

Ensure urgent management actions to halt human induced extinction of known threatened species and for the recovery and conservation of species, in particular threatened species, to significantly reduce extinction risk, as well as to maintain and restore the genetic diversity within and between populations of native, wild and domesticated species to maintain their adaptive potential, including through in situ and ex situ conservation and sustainable management practices, and effectively manage human-wildlife interactions to minimize human-wildlife conflict for coexistence.



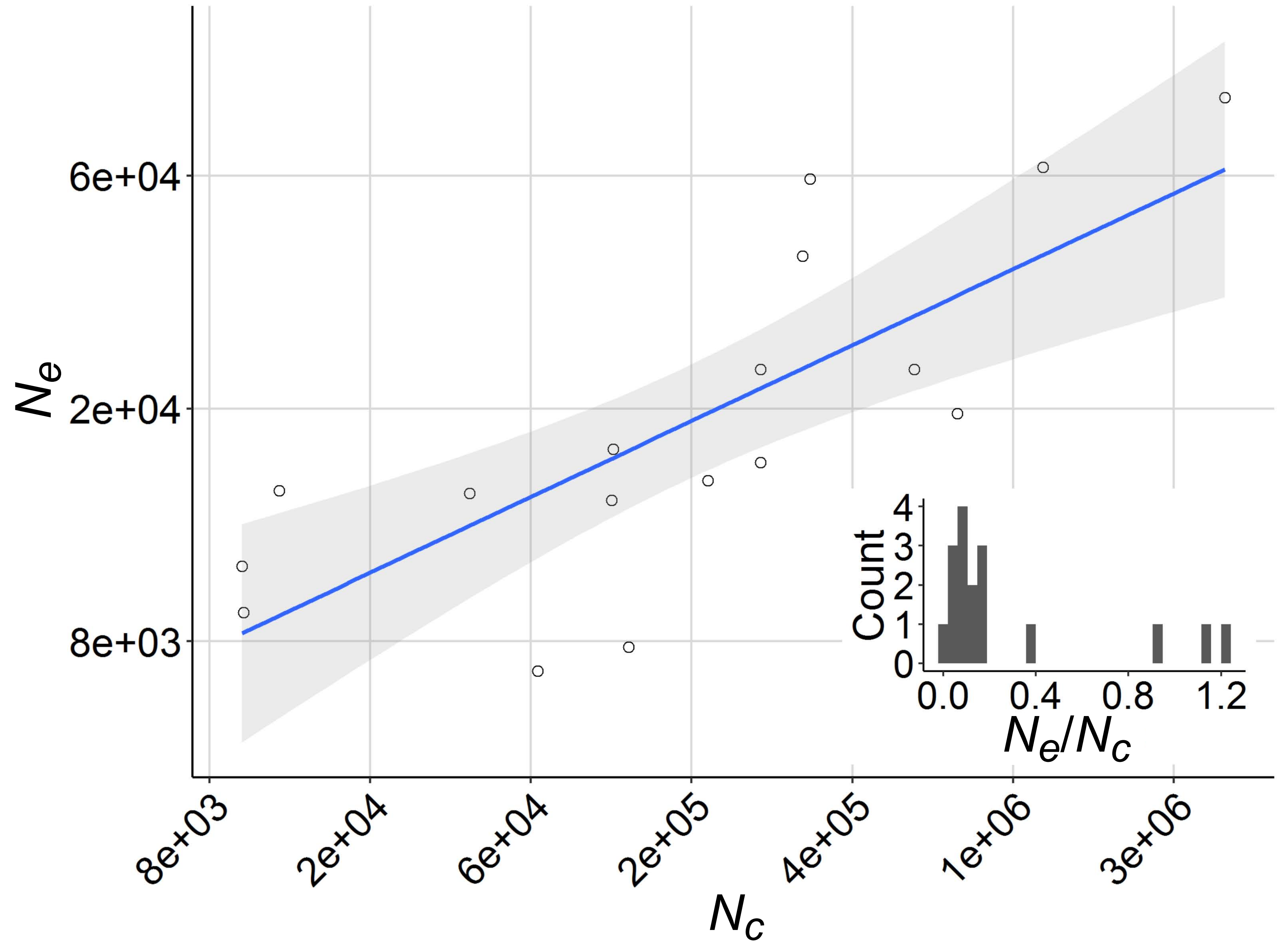
▶ Back to seals: what has influenced N_e (i.e. genetic diversity)?

Past \longrightarrow Present



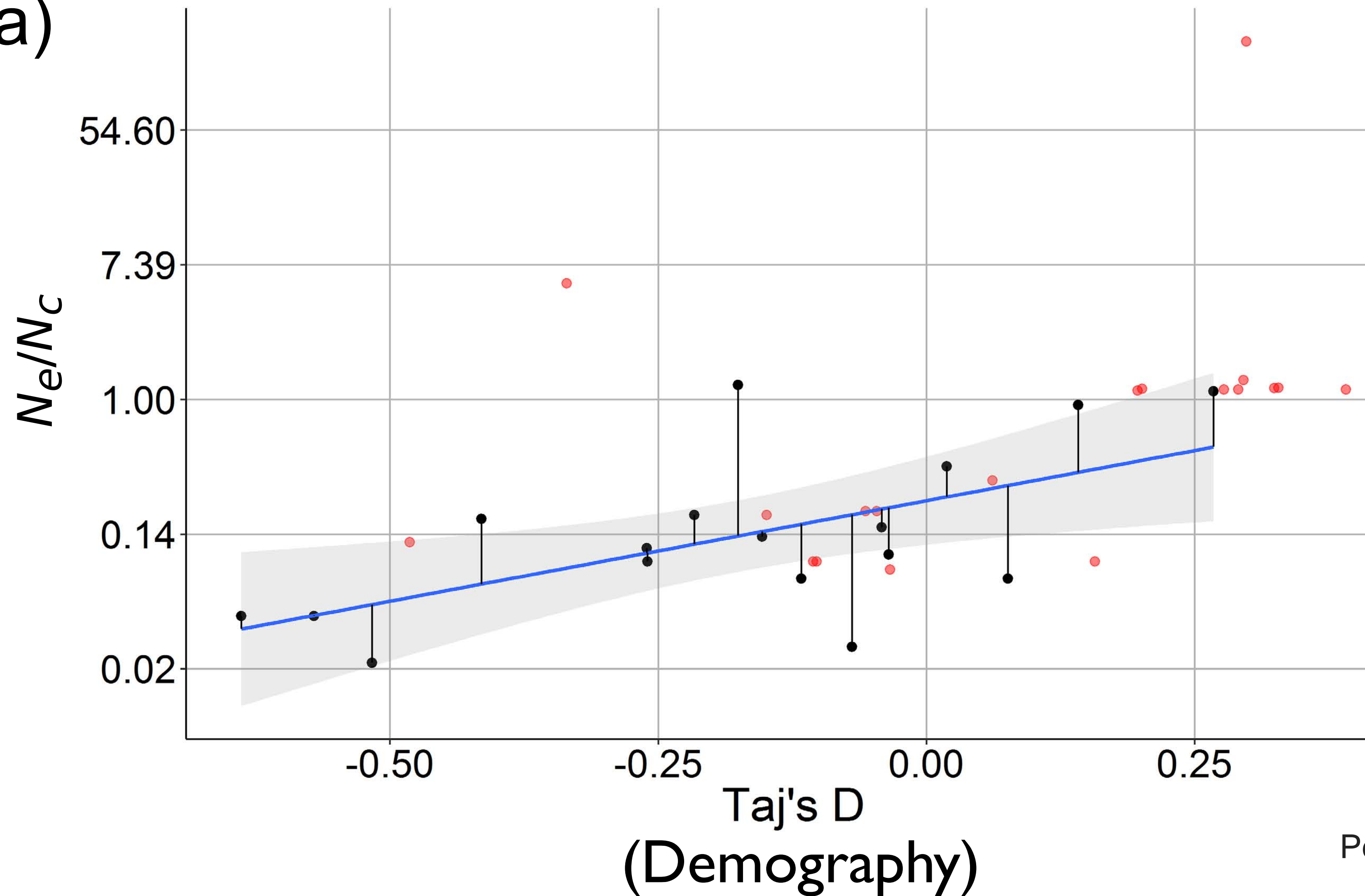
N_e is correlated to N_c

$$\theta_{\pi} = 4N_e\mu$$



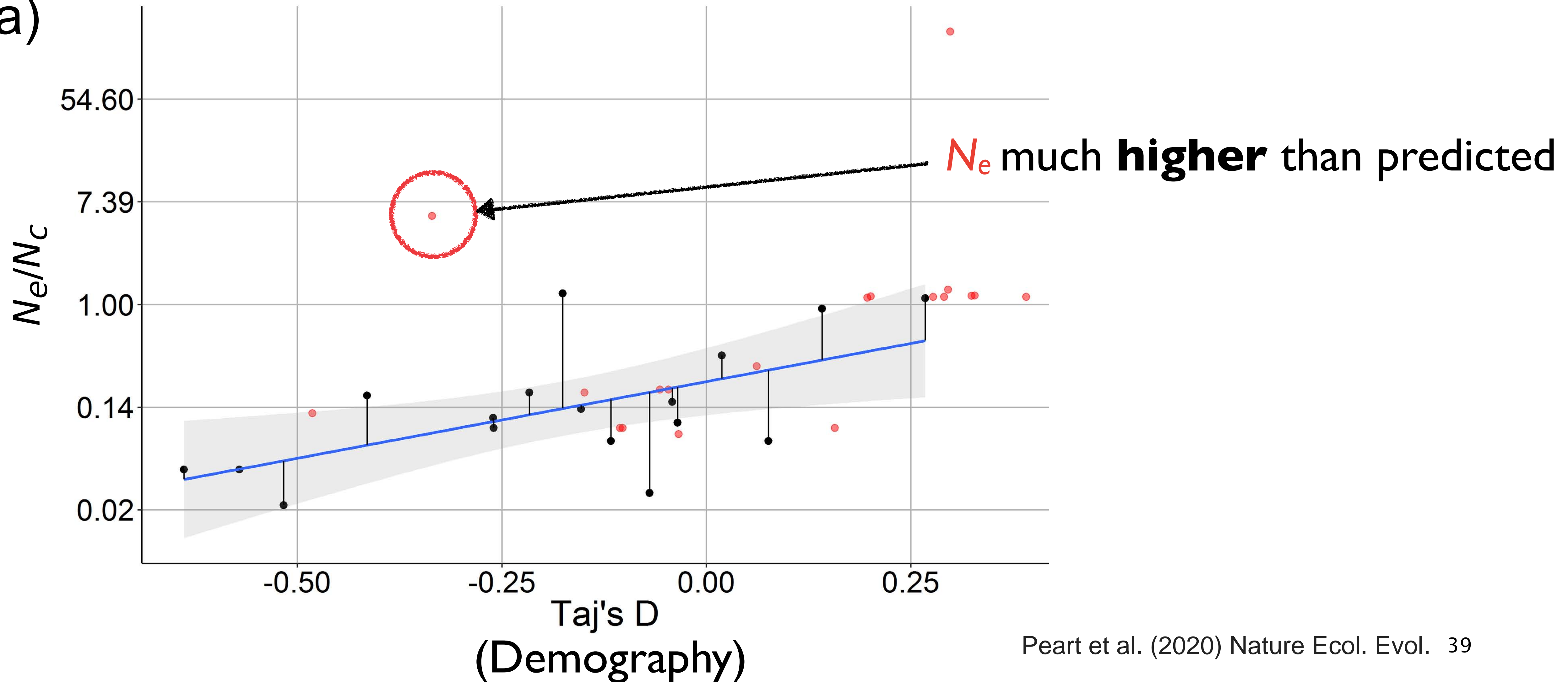
We then built a model trying to understand $N_e:N_c$

(a)



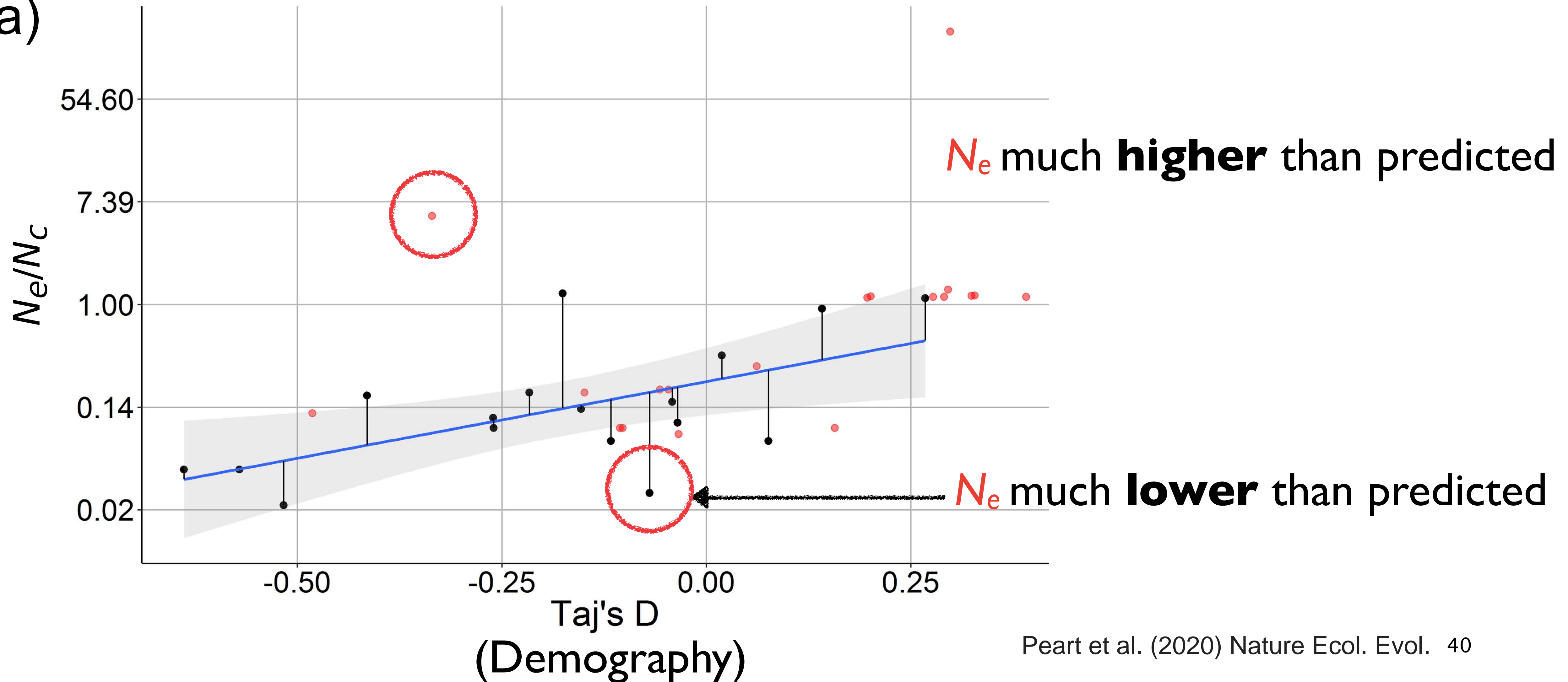
We then built a model trying to understand $N_e:N_c$

(a)



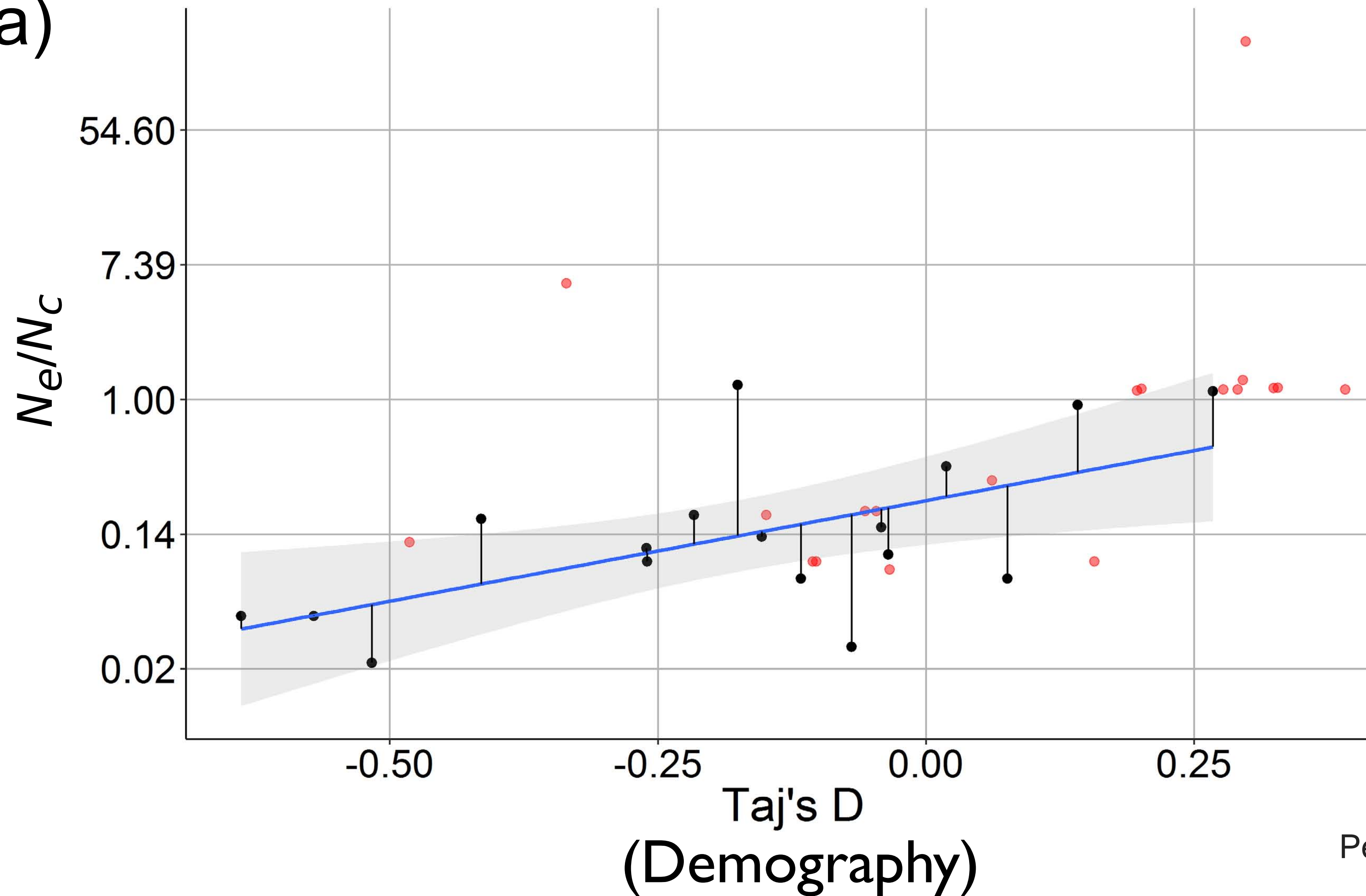
We then built a model trying to understand $N_e:N_c$

(a)

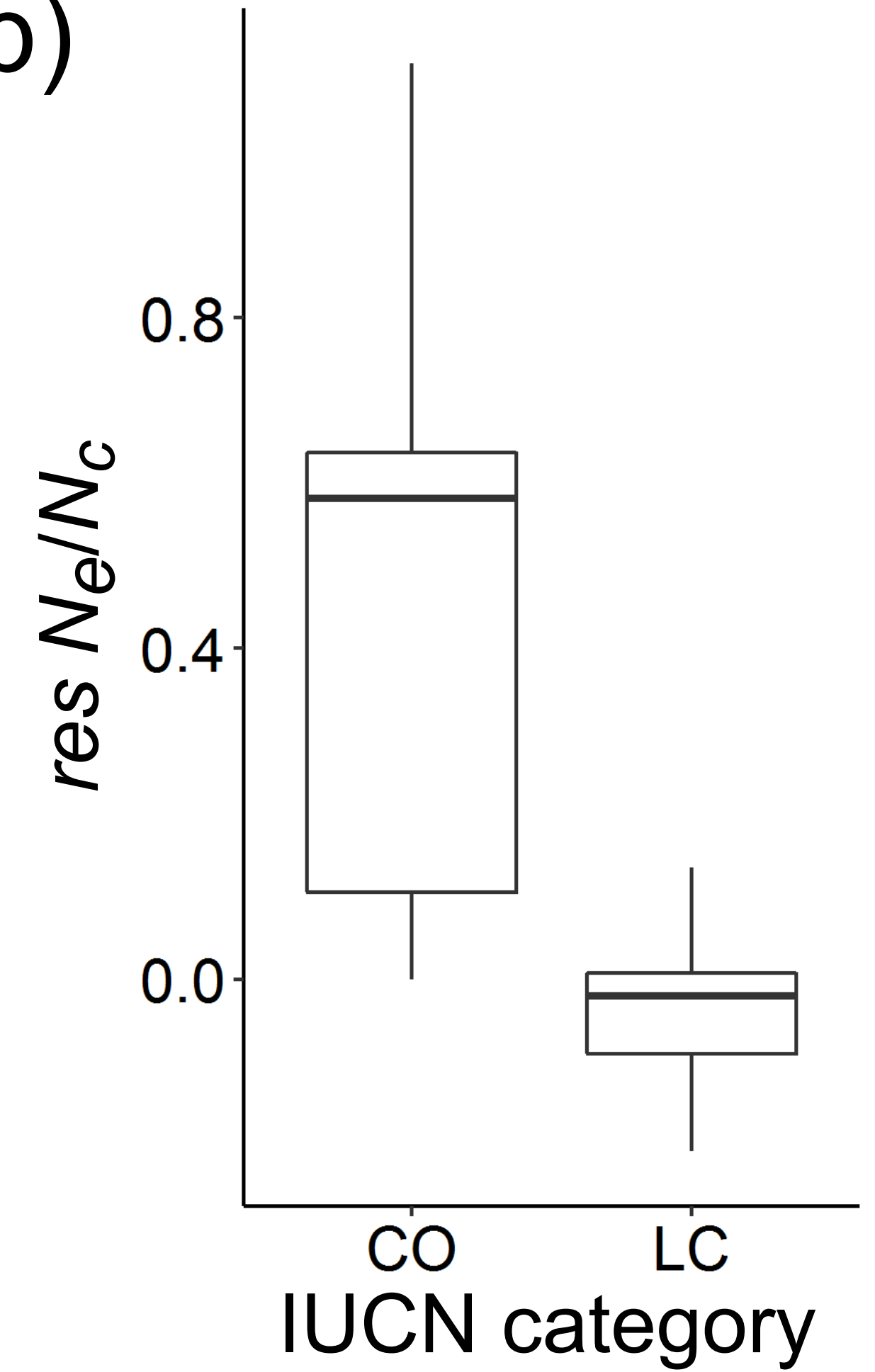


We then built a model trying to understand $N_e:N_c$

(a)



(b)



▣ Story 1: A genetic warning signal - explained

Effective population size (N_e) *is slow to respond to change*

Census population size (N_c) *responds immediately to change*

Can use this model to identify at risk species

If species allowed to recover (N_c), loss of genetic diversity (N_e) will be minimized

▶ Story 1: A genetic warning signal - expanded

SPECIAL SECTION

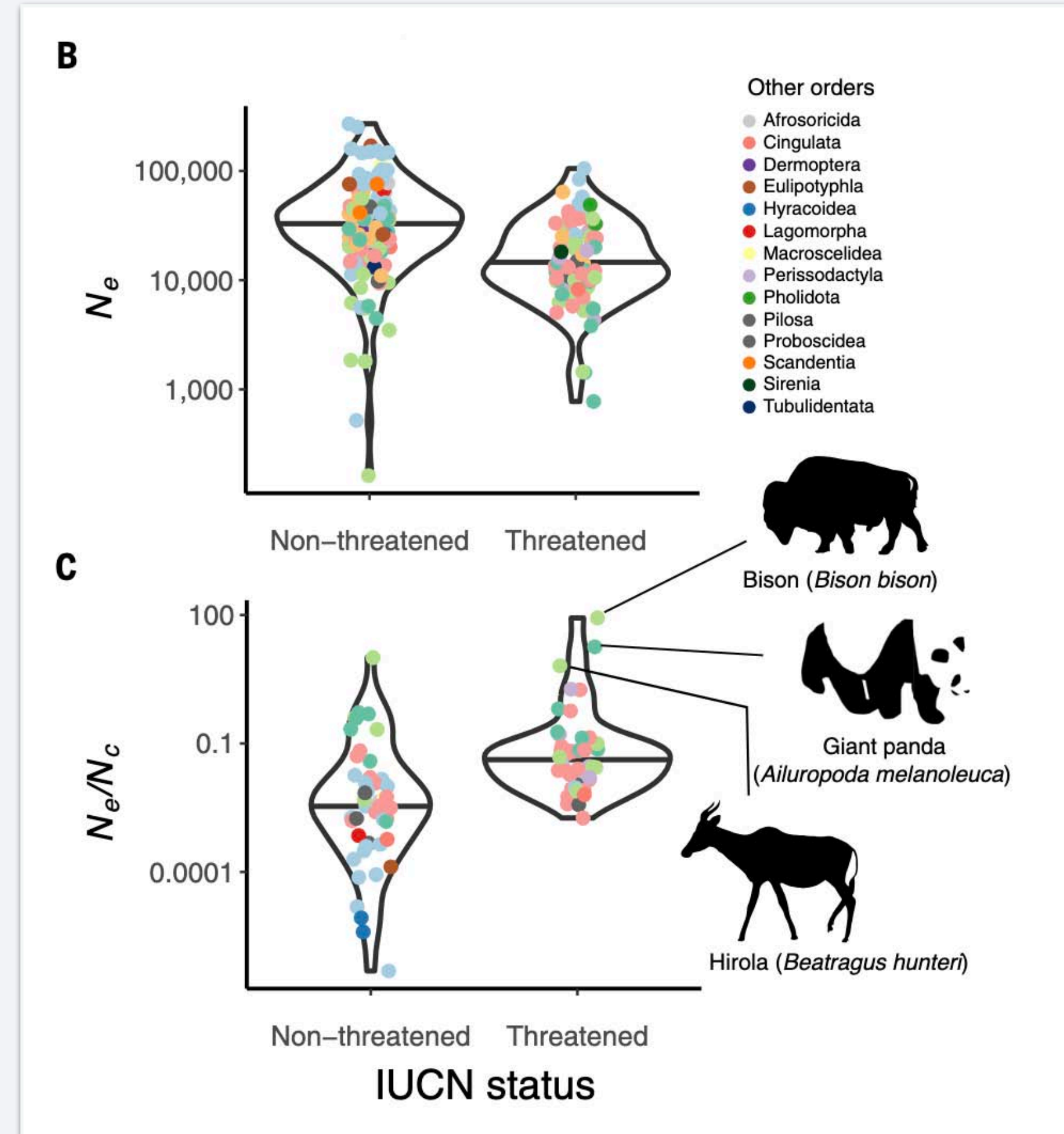
ZOONOMIA

RESEARCH ARTICLE SUMMARY

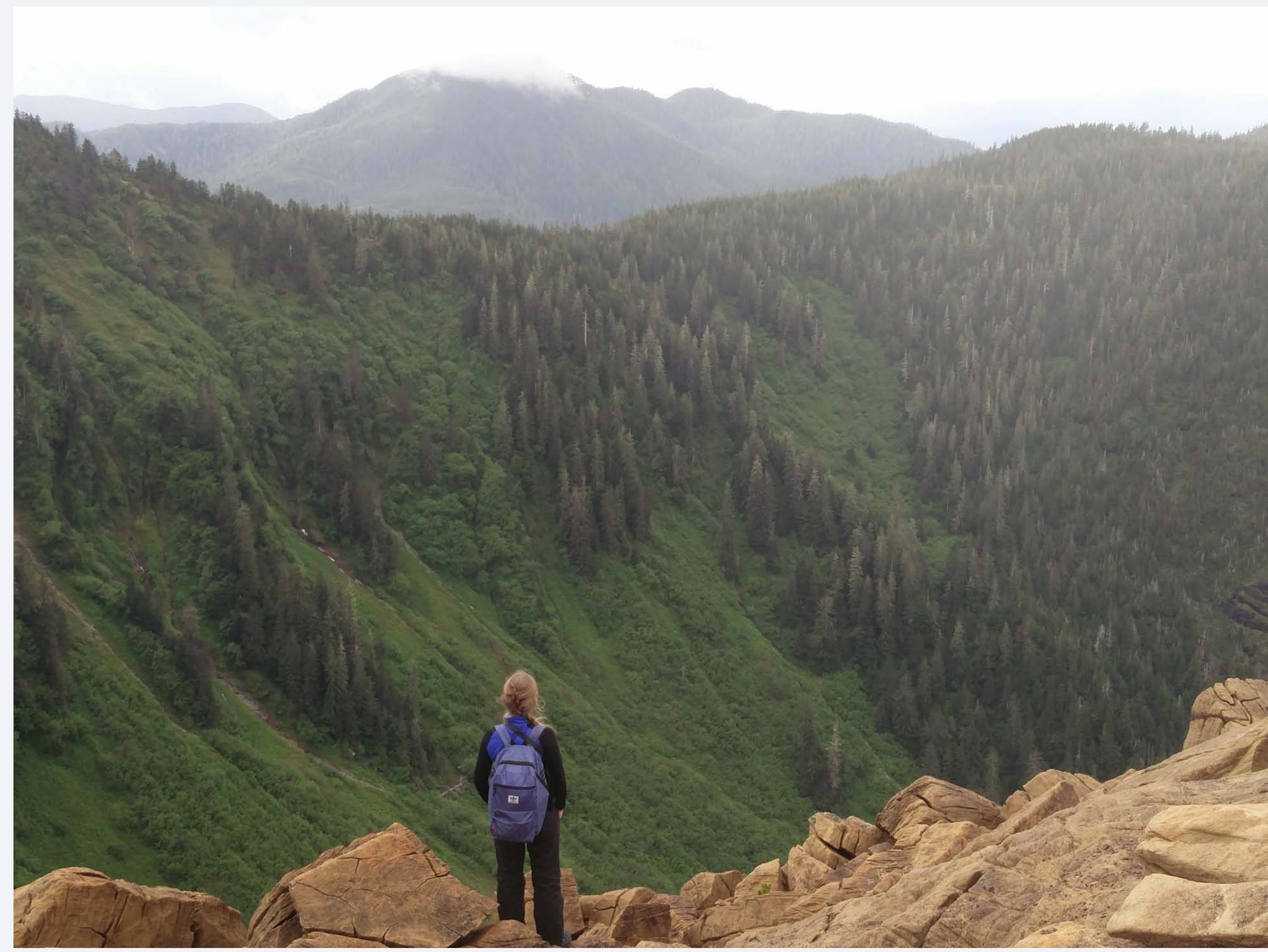
ZOONOMIA

The contribution of historical processes to contemporary extinction risk in placental mammals

Aryn P. Wilder*†, Megan A. Supple*†, Ayshwarya Subramanian, Anish Mudide, Ross Swofford, Aitor Serres-Armero, Cynthia Steiner, Klaus-Peter Koepfli, Diane P. Genereux, Elinor K. Karlsson, Kerstin Lindblad-Toh, Tomas Marques-Bonet, Violeta Munoz Fuentes, Kathleen Foley, Wynn K. Meyer, Zoonomia Consortium, Oliver A. Ryder*†, Beth Shapiro*†

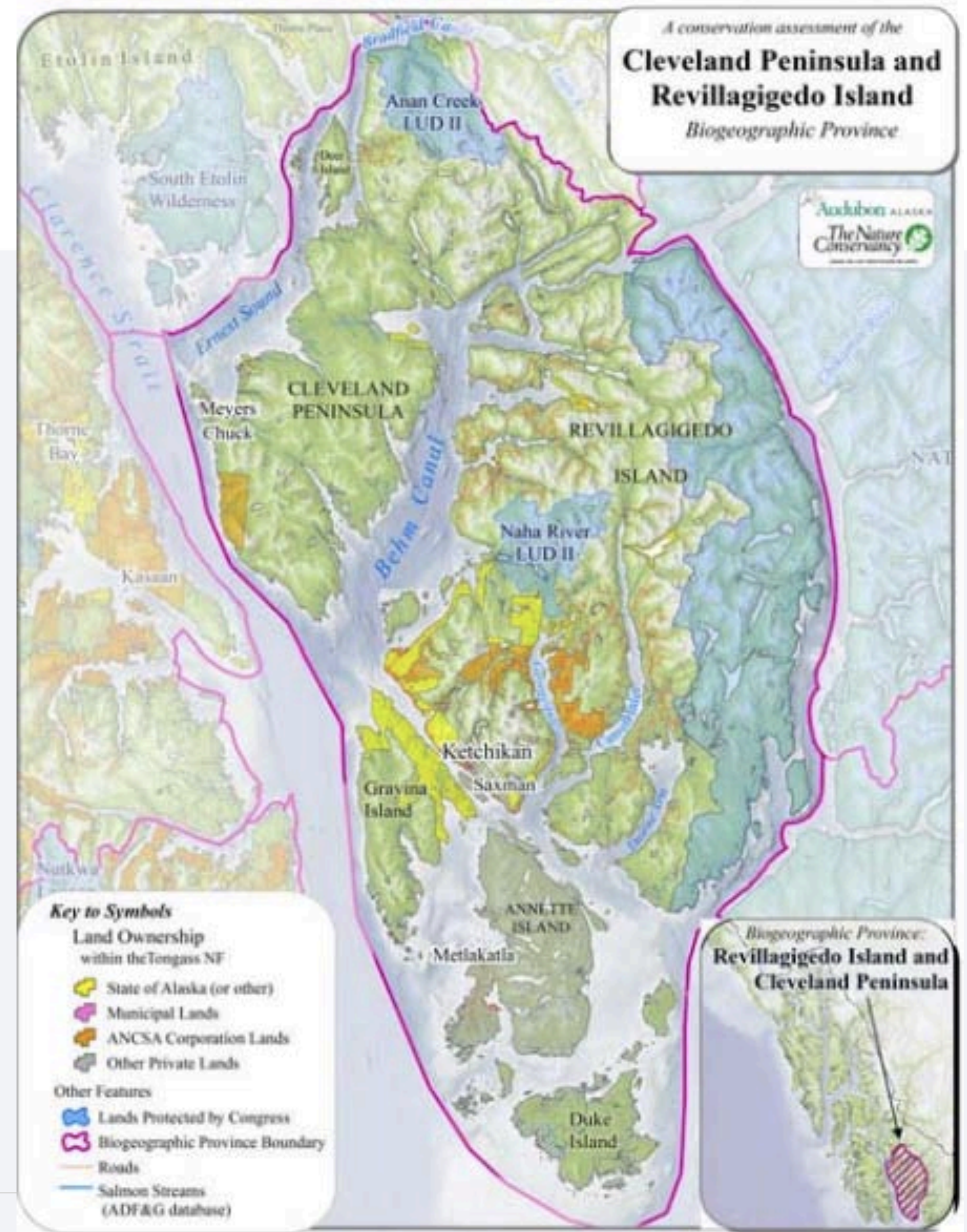


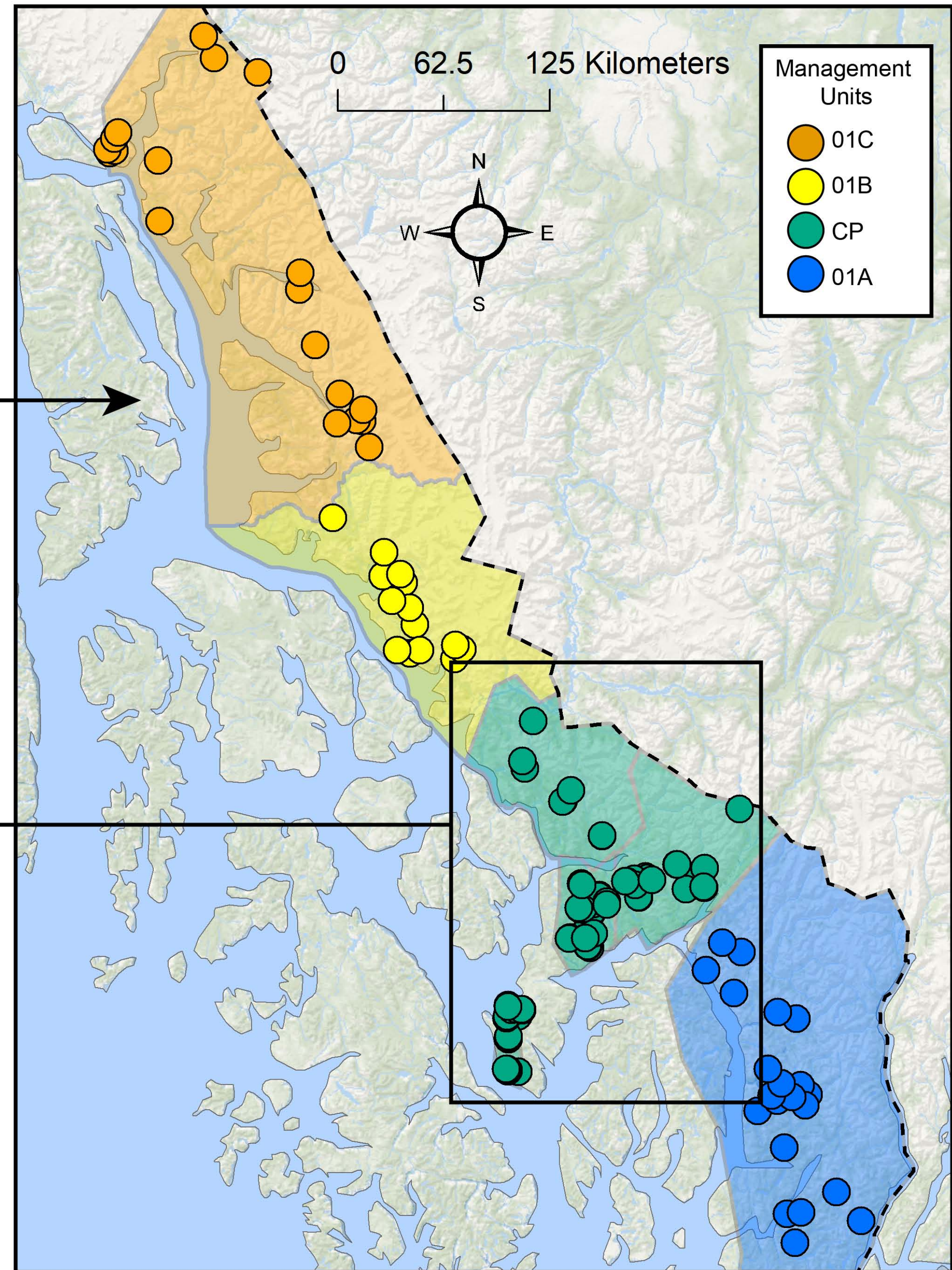
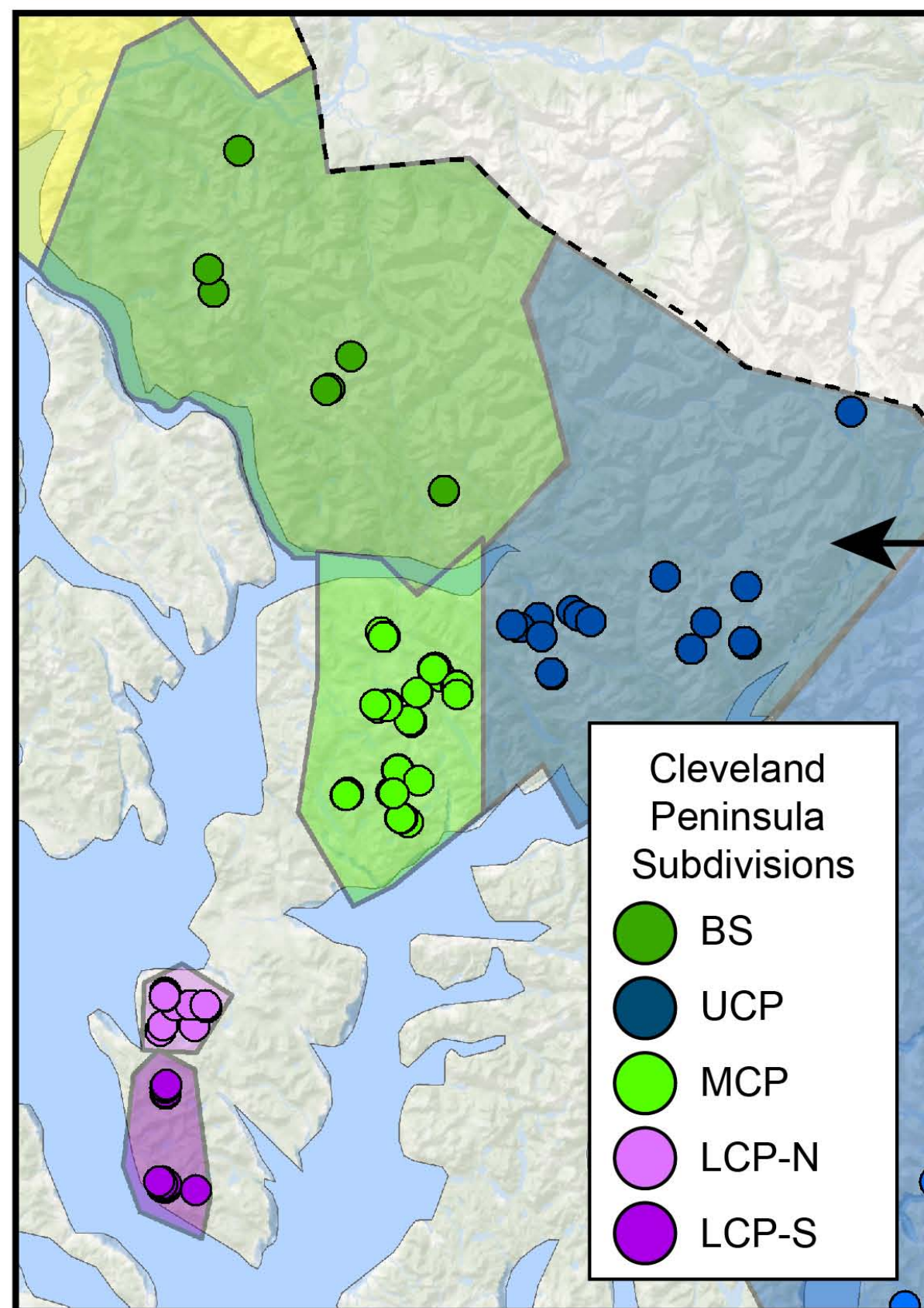
▶ Story 2: The extinction vortex



▶ Story 2: The Cleveland Peninsula

White et al. (2021) J. Wildlife Mgt.

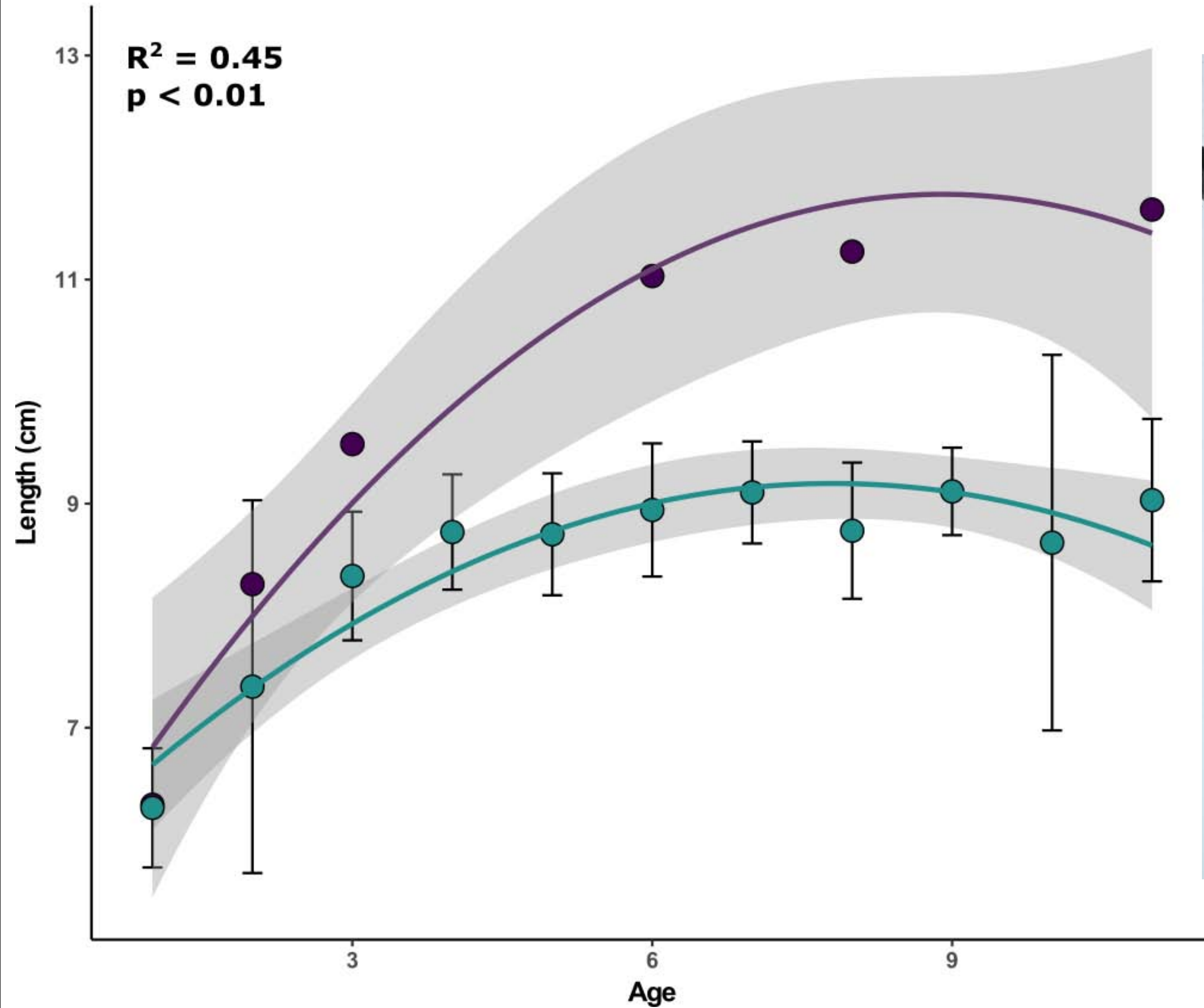




The "mountain goat" in the room

White et al. (2021) J. Wildlife Mgt.

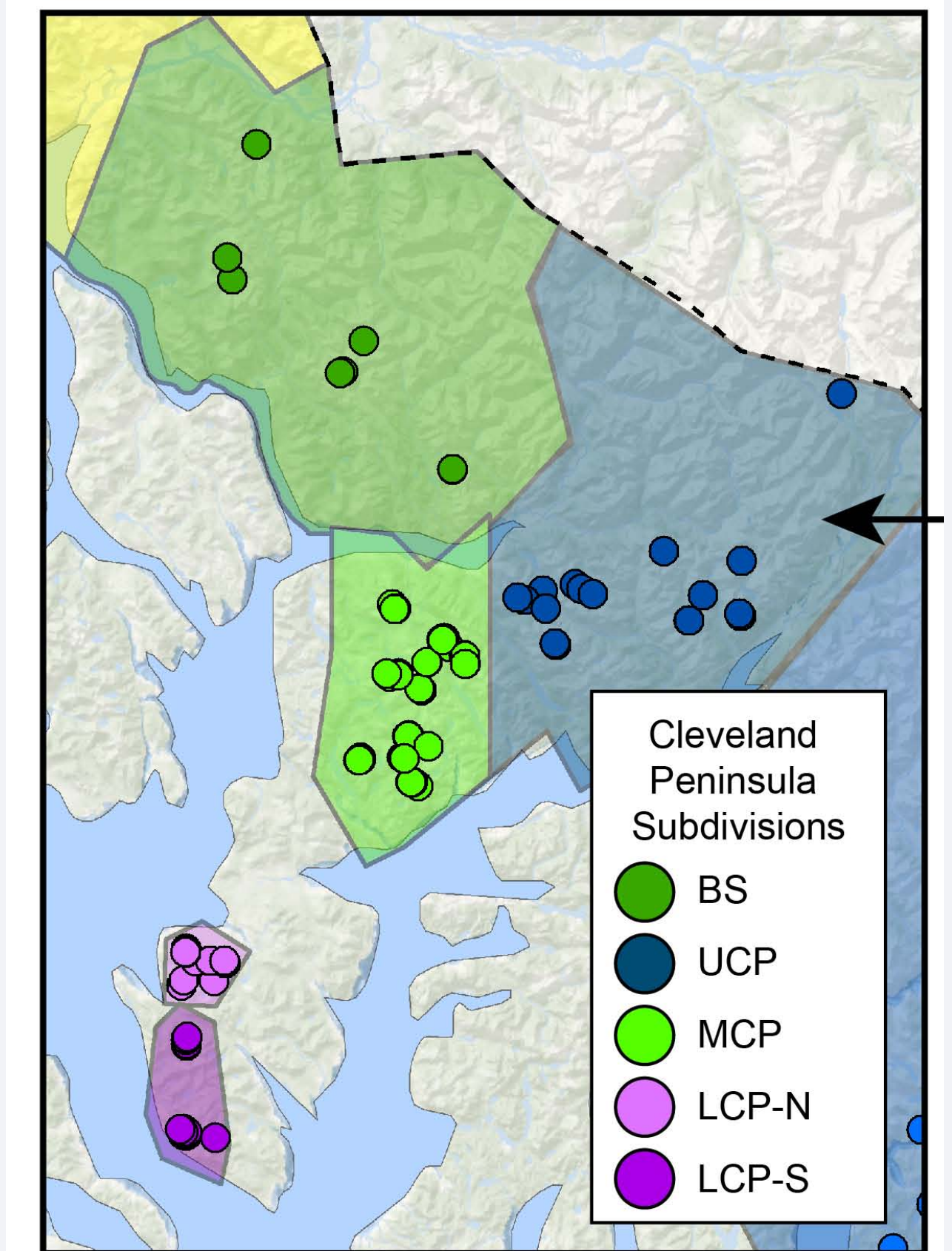
Horn Length between Cleveland and SE Alaska



Minimal diversity and signatures consistent with inbreeding

White et al. (2021) J. Wildlife Mgt.

Population	Subdivision	No. of Alleles	Observed Heterozygosity	Fixation Index	N_e estimate
Cleveland Peninsula	Upper	3.9 ± 0.56	0.34 ± 0.04	0.30 ± 0.06	14.7-17.5
	Middle	4.8 ± 0.64	0.31 ± 0.04	0.37 ± 0.05	27.3-47.7
	Lower North	4.4 ± 0.46	0.23 ± 0.04	0.50 ± 0.07	7.3-14.9
	Lower South	4.3 ± 0.44	0.28 ± 0.04	0.38 ± 0.05	4.8-7.9



▶ Story 2: The extinction vortex

White et al. (2021) J. Wildlife Mgt.

MANAGEMENT IMPLICATIONS

Given the geographic isolation, phenotypic differences, and the genetic distinctiveness reported here, this current harvest moratoria and separate hunting is warranted on the LCP (e.g. Moritz 1994, Fraser and Bernatchez 2001). These data suggest a sustainable harvest unlikely on the LCP given the genetic parameters and population numbers; if the population demographically recovers, any future harvest should be limited to adult males (Gonzalez-Voyer et al. 2003) and consideration should be given to alternating harvest years given the high extirpation risk (Hamel

▣ Conservation genet(om)ic climate in two parts

Part I. Questioning the solutions

Part II. Empirical examples and a way forward

- Its okay to do basic and fundamental research!
- **Basic and fundamental research** will have applications (to conservation)

▶ Story 1: Political hurdles remain



Quick guide to the Aichi Biodiversity Genetic diversity maint

By 2020, the genetic diversity of cultivated plants and farmed and domesticated animals and of wild relatives of cultivated plants and domesticated animals and of other socio-economically as well as culturally valuable species, is maintained and strategies need to be developed and implemented for minimizing genetic erosion and safeguarding their genetic diversity.

The genetic diversity of cultivated plants and farmed or domesticated animals and of wild relatives is in decline as is the genetic diversity of other socio-economically and culturally valuable species. The genetic diversity which remains needs to be maintained and strategies need to be developed and implemented to minimize the current erosion of genetic diversity, particularly as it offers options for increasing the resilience of agricultural systems and for adaptation to changing conditions (including the escalating impacts of climate change).



Mike Bruford

@MikeBruford

Following



The UK continues to interpret Target 13 (genetic diversity) in terms of domestic species and wild relatives ONLY, wilfully ignoring socio-economically and culturally valuable species! The message is clear - genetic diversity in wild animals and plants doesn't matter. Grr. 😡



Gernot Segelbacher

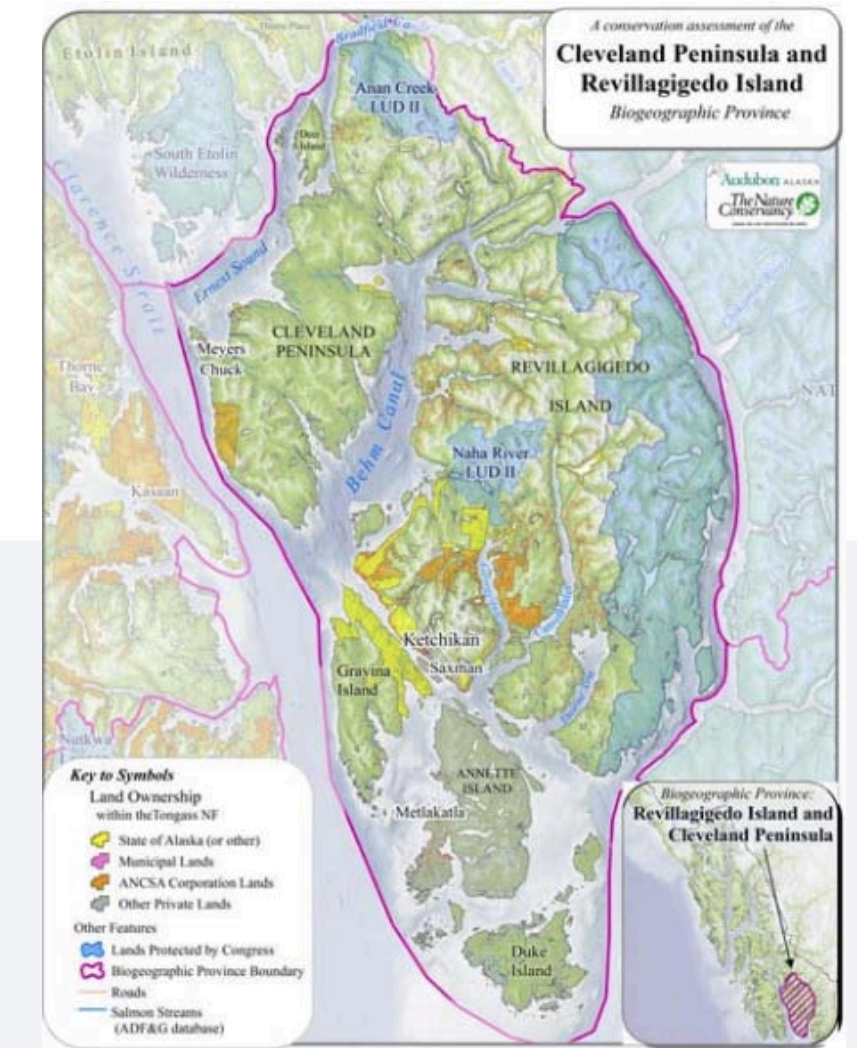
@gsegelbacher

Following



Germany the same - but just been through 5th and 6th report of Switzerland - and they are actually including a genetic monitoring of wild species

▶ **Story 2: Political hurdles remain**



Alaska Board of Game voted 4:3 to open the hunt

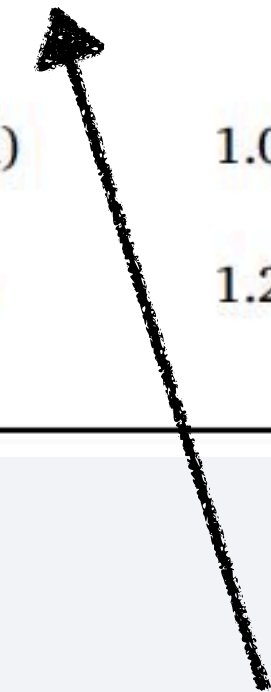
Units 1A and 1B, that portion on the Cleveland Peninsula south of the divide between Yes Bay and Santa Anna Inlet, created a resident and nonresident draw hunt with a bag limit of one male goat, and season dates of August 1-December 31. ADF&G may issue up to six permits.
Effective July 1, 2020.

▶ A way forward: recognizing and understanding the "gap"

Genomics and the challenging translation into conservation practice

Aaron B.A. Shafer¹, Jochen B.W. Wolf¹, Paulo C. Alves², Linnea Bergström¹, Michael W. Bruford³, Ioana Brännström¹, Guy Colling⁴, Love Dalén⁵, Luc De Meester⁶, Robert Ekblom¹, Katie D. Fawcett⁷, Simone Fior⁸, Mehrdad Hajibabaei⁹, Jason A. Hill¹⁰, A. Rus Hoesel¹¹, Jacob Höglund¹, Evelyn L. Jensen¹², Johannes Krause¹³, Torsten N. Kristensen¹⁴, Michael Krützen¹⁵, John K. McKay¹⁶, Anita J. Norman¹⁷, Rob Ogden¹⁸, E. Martin Österling¹⁹, N. Joop Ouborg²⁰, John Piccolo¹⁹, Danijela Popović²¹, Craig R. Primmer²², Floyd A. Reed²³, Marie Roumet⁸, Jordi Salmons²⁴, Tamara Schenekar²⁵, Michael K. Schwartz²⁶, Gernot Segelbacher²⁷, Helen Senn¹⁸, Jens Thaulow²⁸, Mia Valtonen²⁹, Andrew Veale¹², Philippine Vergeer³⁰, Nagarjun Vijay¹, Carles Vilà³¹, Matthias Weissensteiner¹, Lovisa Wennerström¹⁰, Christopher W. Wheat¹⁰, and Piotr Zieliński³²

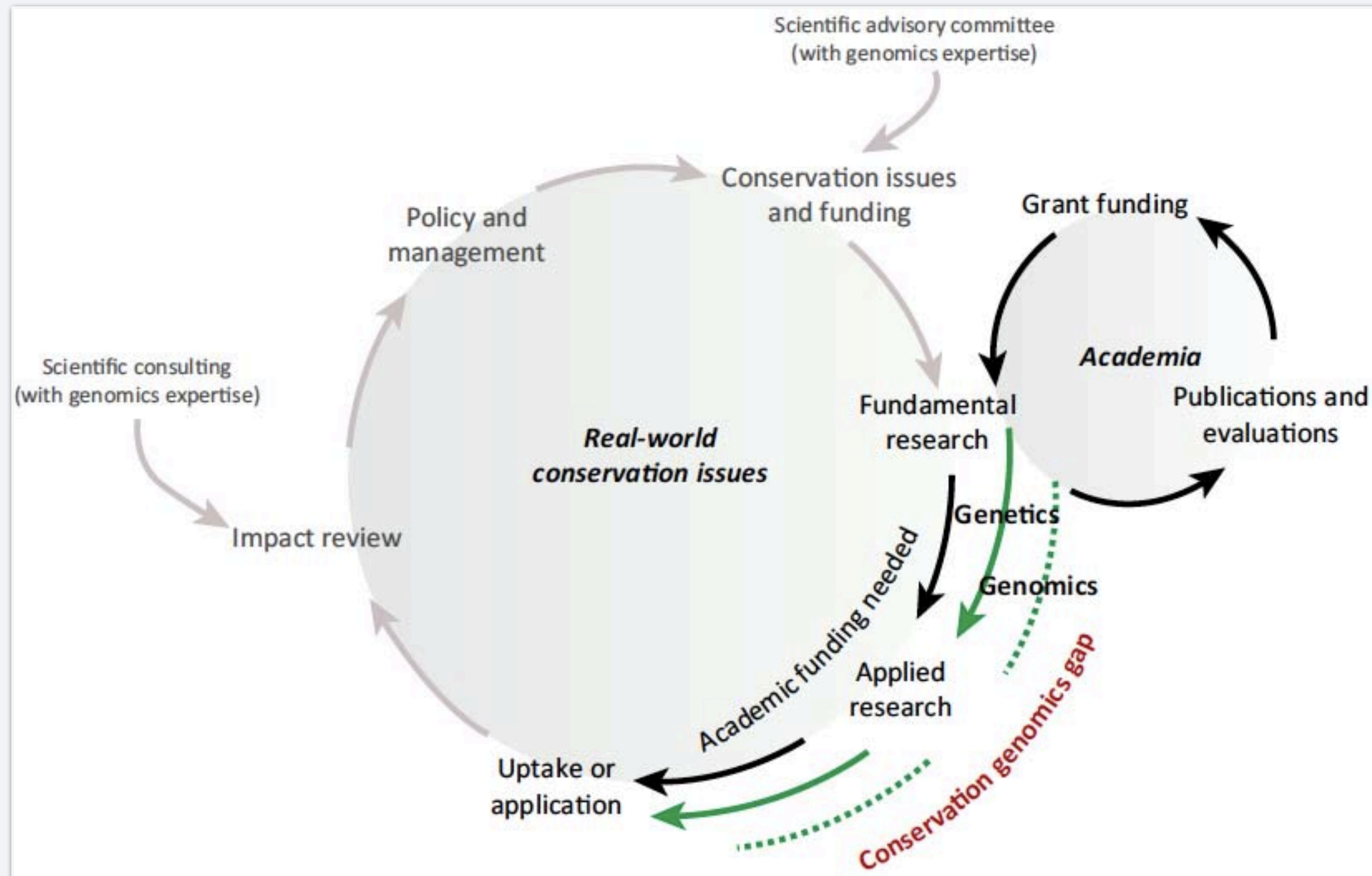
Variable	β (SE)	p-Value	Odds ratio (95% CI)
Intercept	- 1.28 (0.28)	< 0.001	
Proportion of non-academic authors	0.91 (0.47)	0.05	2.49 (1.00, 6.24)
Global conservation status			
1 (Vulnerable or threatened)	1.06 (0.35)	0.002	2.88 (1.46, 5.67)
2 (Critically endangered or possibly extinct)	1.21 (0.48)	0.012	3.35 (1.31, 8.57)



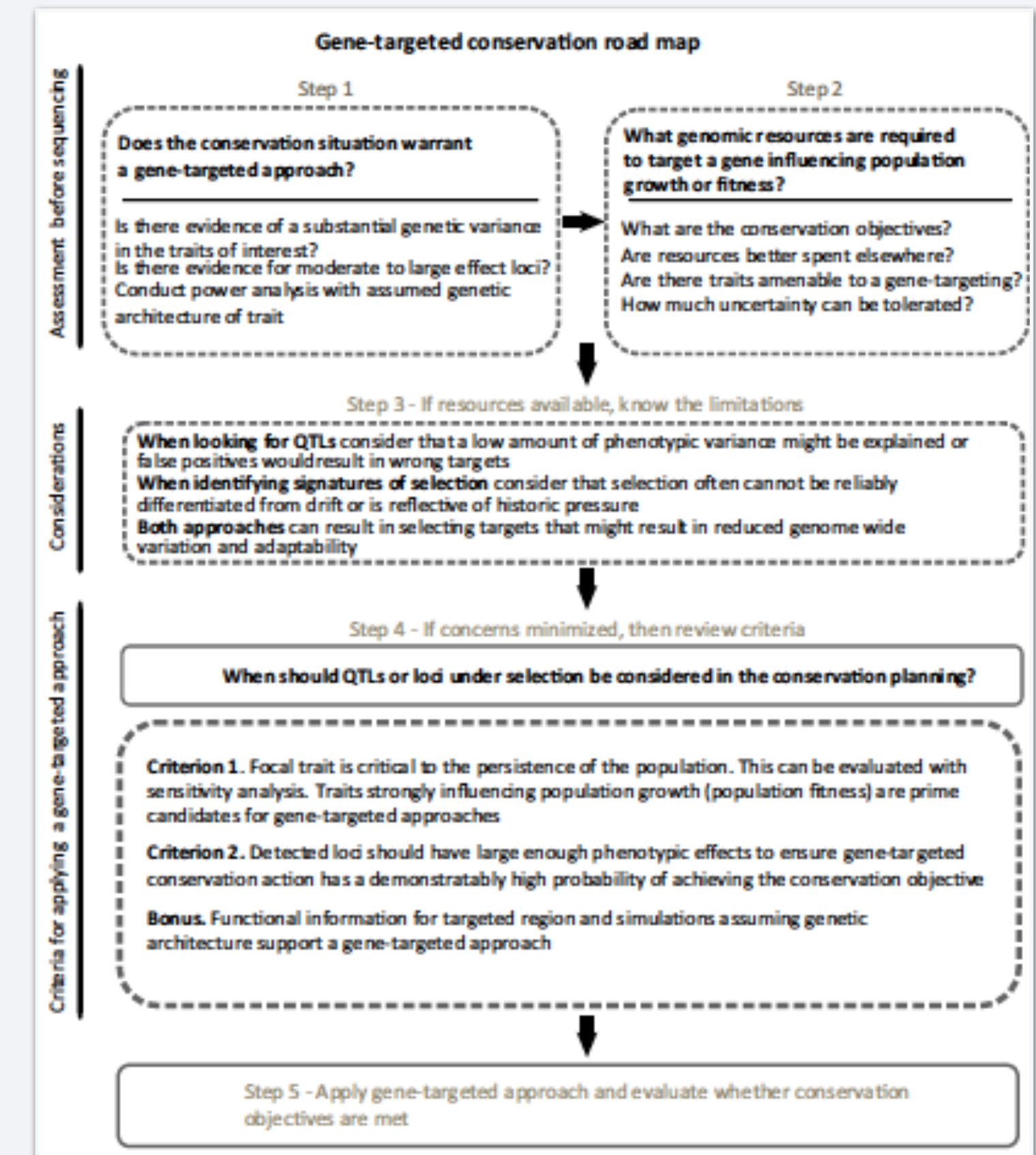
Collaborate with non-academics

▶ A way forward: bridging the "gap"

Restructure funding & evaluation




A road map forward







▣ A way forward: standard operating procedures

nature reviews genetics <https://doi.org/10.1038/s41576-024-00738-6>

Review article  Check for updates

Next-generation data filtering in the genomics era

William Hemstrom ^{1,4} , Jared A. Grummer^{2,4}, Gordon Luikart² & Mark R. Christie ^{1,3} 

▶ Writing letters can make a difference!

which was completed in 2017. A nomination was received from both LCC and Chilkat Tribal Village for ACECs. An ACEC—Research Natural Area (RNA) of 77,797 acres in the North Block of the planning area is being considered. If approved, the ACEC would preclude the issuing of special recreation permits for helicopters and UAS (Unmanned Aerial System) use within the area. An ACEC would also restrict placement or construction of structures within the designated area and include a Right-of-Way (ROW) avoidance area. Portions of the ACEC—RNA on Takshanuk Ridge would be a ROW exclusion area and no surface disturbing activities would occur on these lands. Off-Road Vehicles used in support of military fire emergency or

values including Oregon sheep, peregrine falcon, terrestrial and avian

Summary:

The Final Environmental Impact Statement (FEIS) for the Proposed Haines Amendment to the Ring of Fire Resource Management Plan (RMP) (BLM 2019a) failed to adequately analyze cumulative effects on goat populations by not adequately considering climate change and helicopter activity stressors.

Summary:

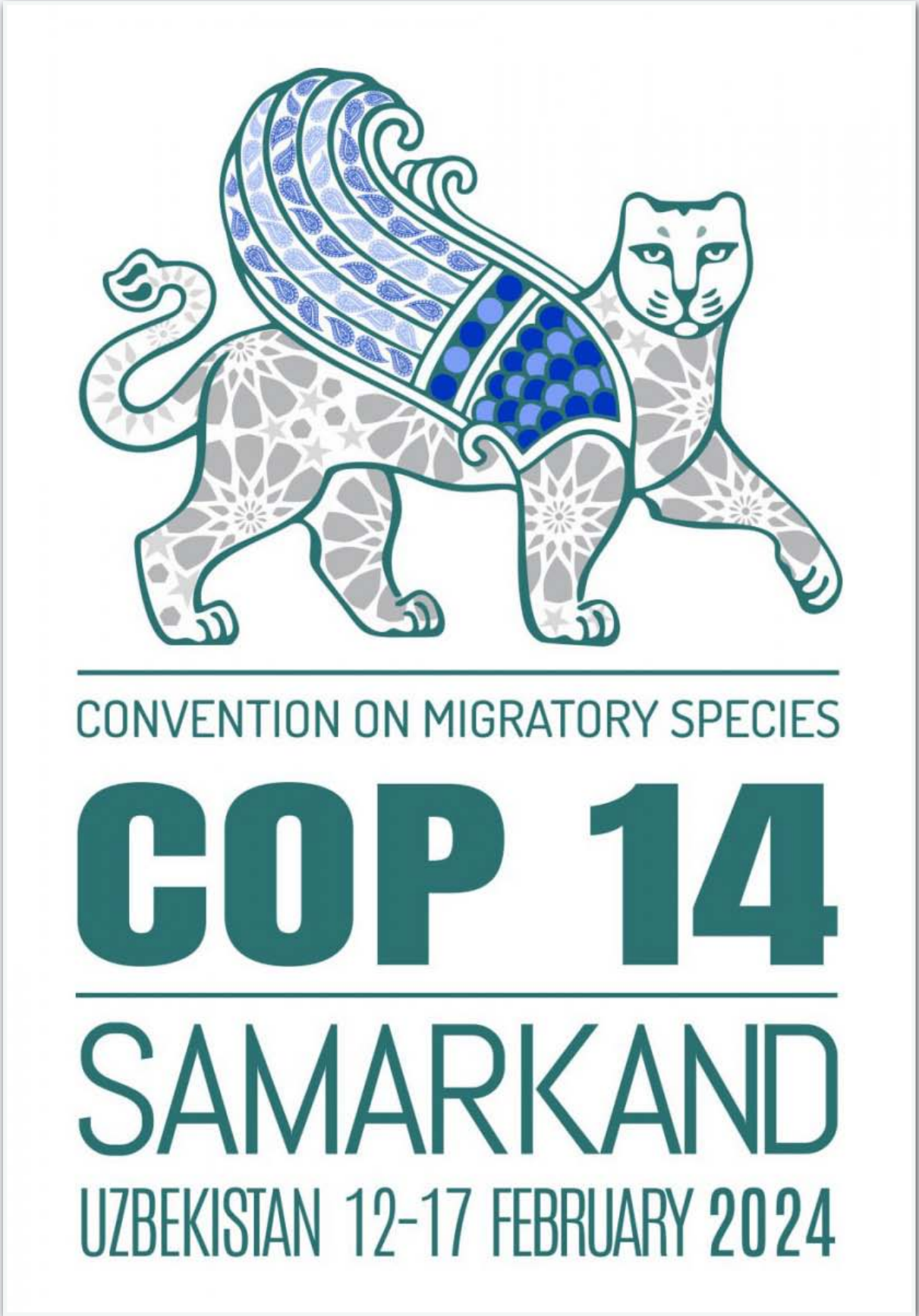
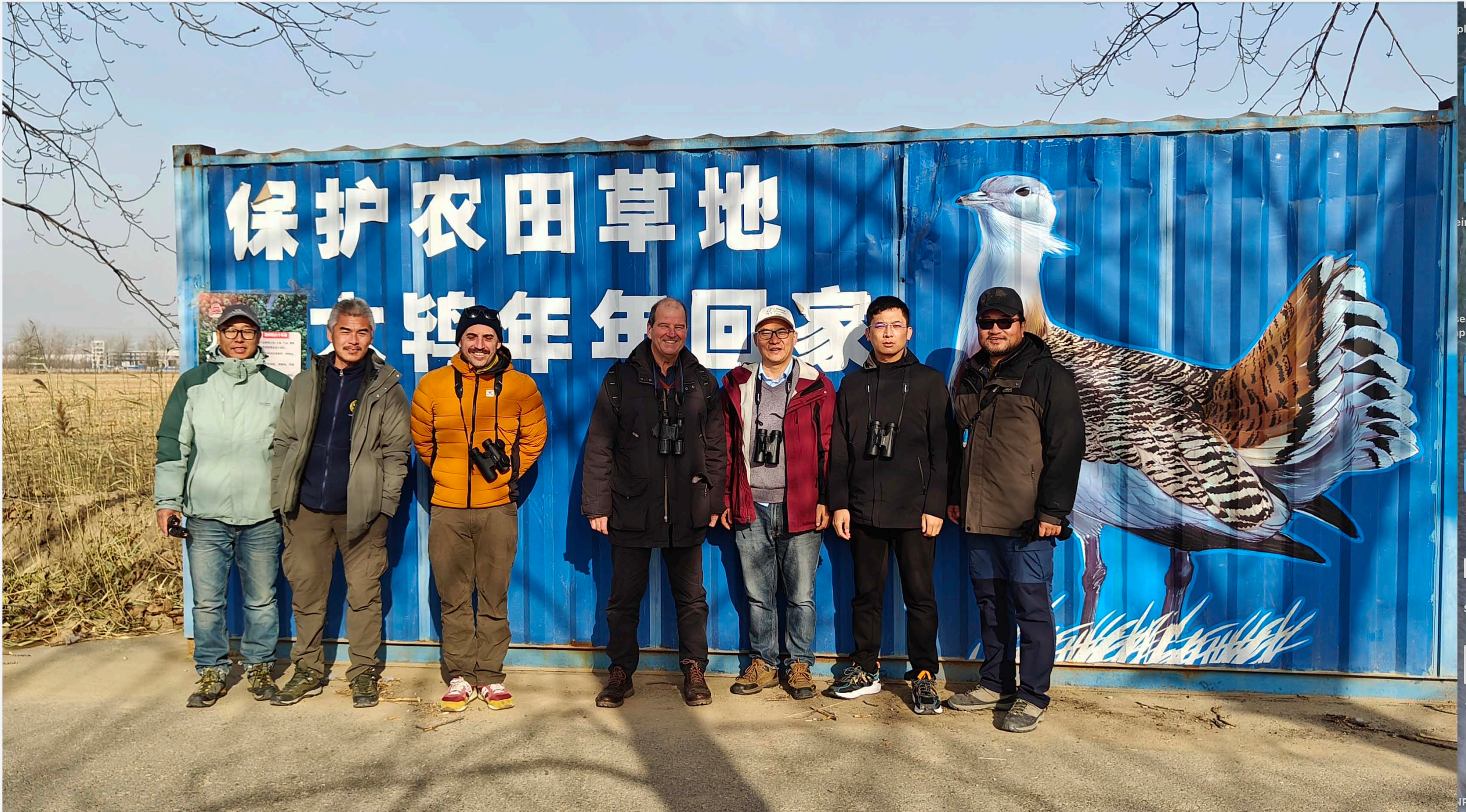
The BLM failed to conduct meaningful consultation and coordination with the Chilkat Indian Village Council as required by BLM Handbook 1780-1, the ANILCA, and under the Environmental Justice Executive Order 12898.

DEPARTMENT OF THE INTERIOR

Bureau of Land Management

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▶ **Writing letters can make a difference!**



▶ Thanks!

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