



Linking genomes, traits and environment across time and space: a vision for Digitization 2.0

Scott V. Edwards

Department of Organismic and Evolutionary Biology

Museum of Comparative Zoology

Harvard University

Cambridge, MA USA

<http://www.oeb.harvard.edu/faculty/edwards>



Overview –

Genomes, Environment and Digitization

- **We know genomes change over time and space...**
 - Temporal comparisons
 - Geographic comparisons
- **...but thus far we've focused on just one dimension of the genome – its sequence**
 - Genome expression and changing environments
 - Epigenetics and changing environments
- **How do we capture these data and what kinds of research will it enable?**
 - Need for renewed collection of diverse resources for genomics
 - Capturing these data and linking it to environmental change



**Museum collections in 21st century
evolutionary biology**

Gothenburg, Sweden



Museum of Southwestern Biology, U. New Mexico

Museum of Natural History, Stockholm

Gothenburg Herbarium

Gothenburg Natural History Museum

Museum für Naturkund, Berlin

Lund Museum of Zoology

Museum of Comparative Zoology, Harvard

Essig Museum of Entomology, Berkeley

Natural History and Science Museum, University of Porto

Universeum, Gothenburg

GÖTEBORGS naturhistoriska museum



Paradoxmasken
Xenoturbella bocki
En enkelt byggd djur som bara påträffats vid svenska kustlinjen.
Musichaf August Malm samlade in de allra första kända exemplaren.





Lund University Museum of Zoology





NSF PRFB SYMPOSIUM

NSF Symposium for Postdoctoral Research Fellowships in Biology
Research Using Biological Collections, Nov. 7-9, 2017

Postdoctoral fellowships in Biology - 2015

Sophie George

bio_dbi_prfb@nsf.gov, (703) 292-8470

Carter Kimsey

bio-dbi-prfb@nsf.gov, (703) 292-8470

Diane Jofuku Okamuro

dbipgr@nsf.gov, (703) 292-4400

DUE DATES

Full Proposal Deadline Date: January 8, 2015

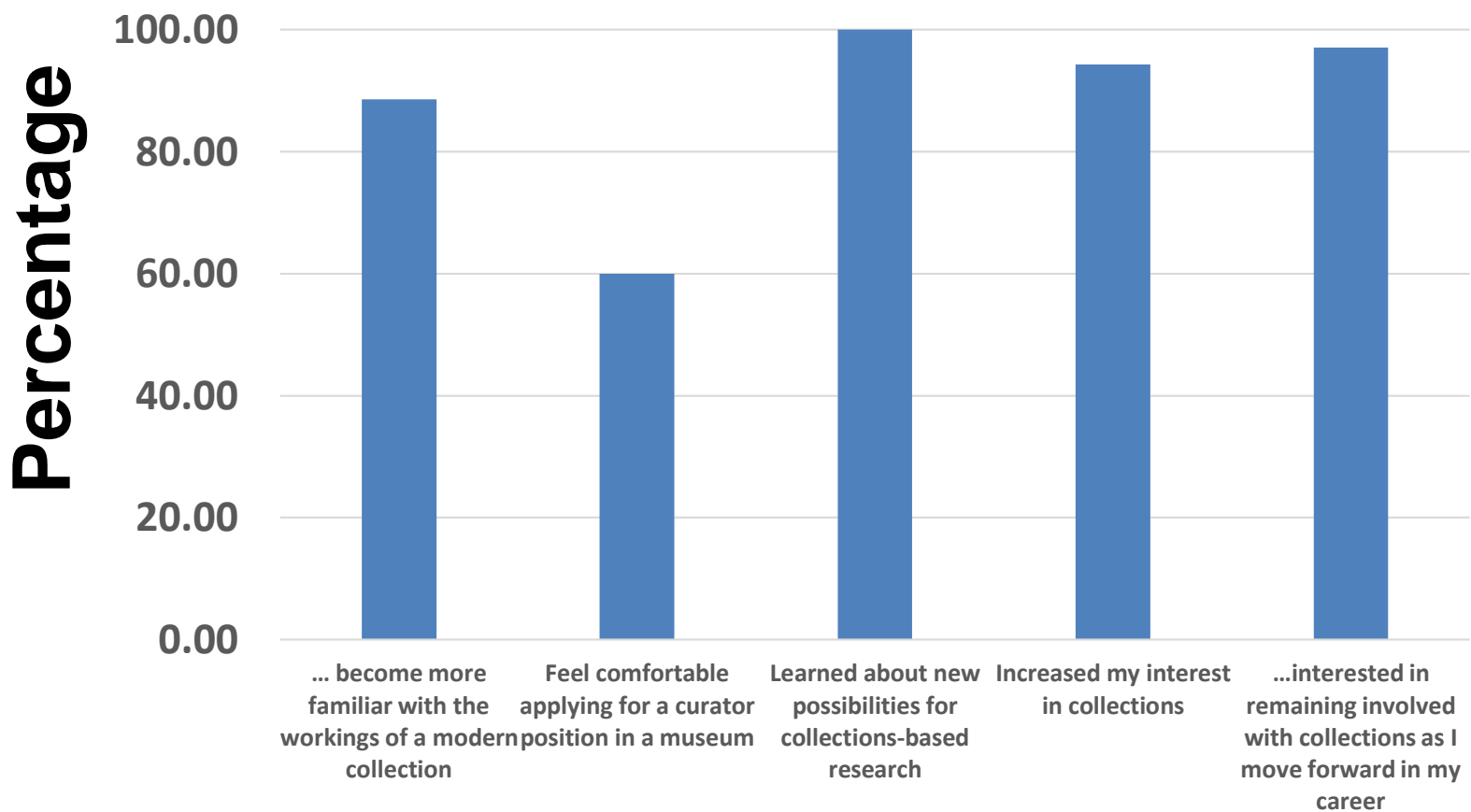
SYNOPSIS

The Directorate for Biological Sciences (BIO) awards Postdoctoral Research Fellowships in Biology to recent recipients of the doctoral degree for research and training in *selected* areas supported by BIO and with special goals for human resource development in biology. The fellowships encourage independence at an early stage of the research career to permit Fellows to pursue their research and training goals in the most appropriate research locations regardless of the availability of funding for the Fellows at that site. For FY 2015 and beyond, these BIO programs are **(1) Broadening Participation of Groups Under-represented in Biology, (2) Research Using Biological Collections, and (3) National Plant Genome Initiative (NPGI) Postdoctoral Research Fellowships**. These areas change periodically as new scientific and infrastructure opportunities present themselves. For this reason, this solicitation will be changed as necessary to reflect the areas being funded.

The fellowships are also designed to provide active mentoring of the Fellows by the sponsoring scientists who will benefit from having these talented young scientists in their research groups. The research and training plan of each fellowship must address important scientific questions within the scope of the BIO Directorate and the specific guidelines in this fellowship program solicitation. Because the fellowships are offered to postdoctoral scientists only early in their careers, NSF encourages doctoral advisors to discuss the availability of these postdoctoral fellowships in biology with their graduate students early in their doctoral programs to ensure potential applicants may take advantage of this funding opportunity. Fellowships are awards to individuals, not institutions, and are administered by the Fellows.

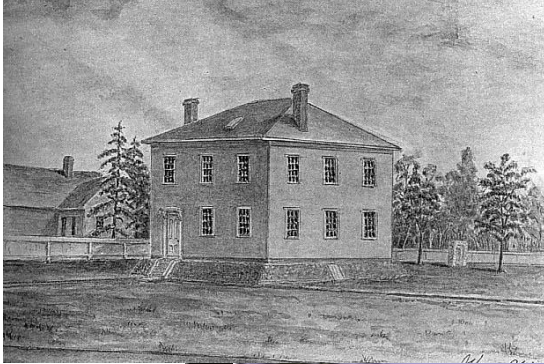
The NSF collections postdoctoral program broadens the collections community*

As a result of your postdoc, have you, do you or are you



*Based on a post-conference survey of 35 participants

Museum of Comparative Zoology: a research and teaching museum



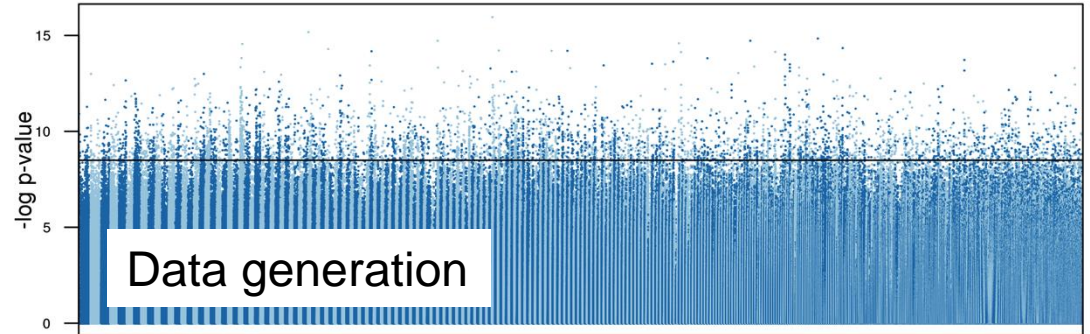
Schmitt, C. J., Cook, J., Zamudio, K., Edwards, S. V. 2018.

“Museum specimens of terrestrial vertebrates are sensitive indicators of environmental change in the Anthropocene.” *Phil. Trans. R. Soc. Lond. B.*, in review.



From field to digital genome

Whole genomes and variation linked to vouchered specimens



Model organism or animal sample Digitization

Identifiers BioSample: SAMN06628349; sample name: Emu 1B-2889

Organism [Dromaius novaehollandiae \(emu\)](#)

cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Sauropsida; Sauria; Archelosauria; Archosauria; Dinosauria; Theropoda; Coelurosauria; Aves; Palaeognathae; Casuariiformes; Dromaiidae; Dromaius

Package [Model organism or animal; version 1.0](#)

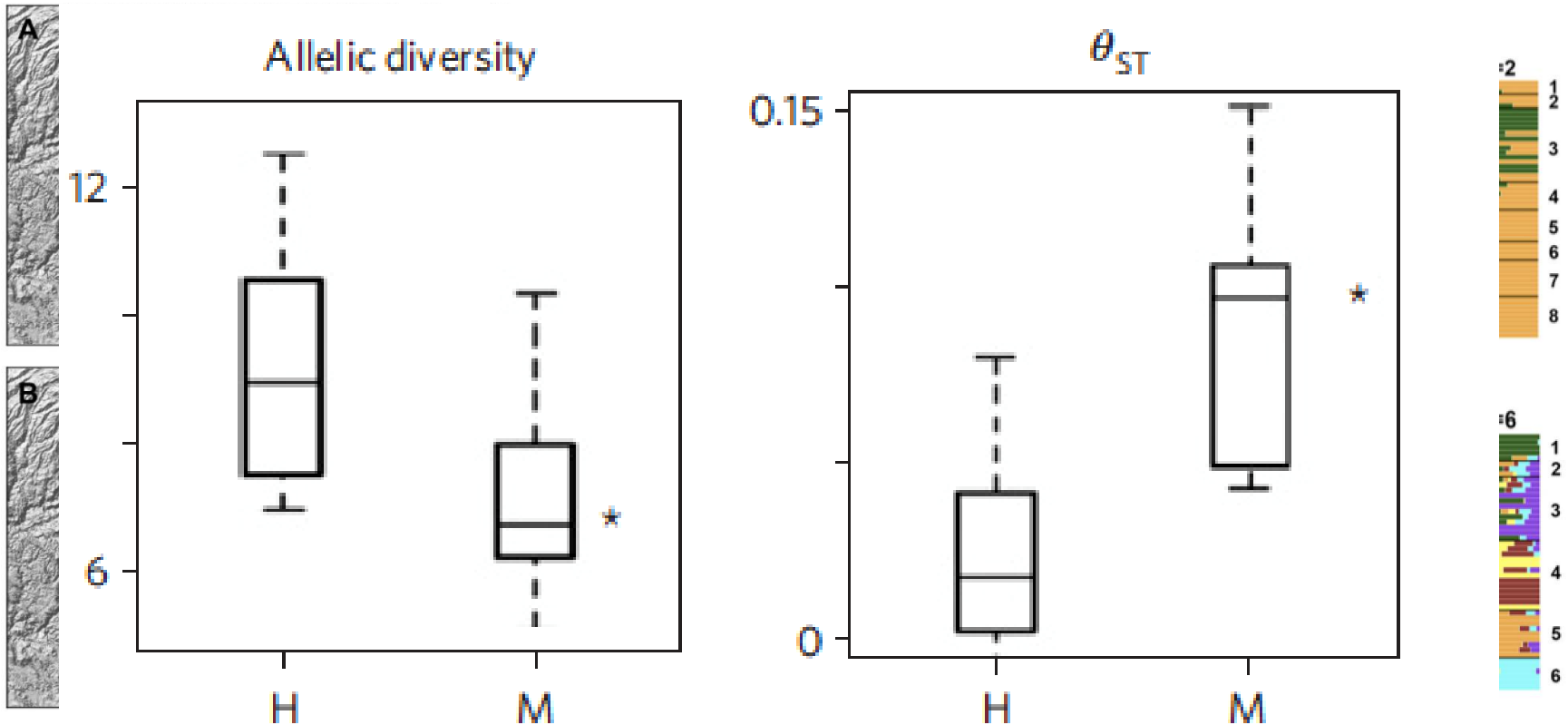
Attributes

age	missing
sex	male
tissue	liver
isolate	ROM 1B-2889
collection date	1998
environment biome	Deciduous forest
isolation source	blood preserved in ethanol
environment feature	Emu farm
environment material	tissue
geographic location	Canada: vicinity of Toronto
isolation and growth condition	http://www.informdurham.com/record/OSH0181
latitude and longitude	43.65 N 79.38 W
sample material processing	DNA isolation
sample size	1

Submission [Harvard University](#), Scott Edwards; 2017-03-22

Grinnell Resurvey Project

Population genomics over 100 years for chipmunks impacted by climate change

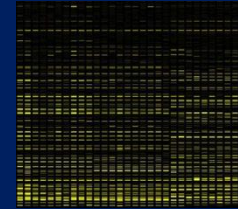


Microsatellites/exon capture from tissues & skins for ~10K exons;
Rubidge et al. 2012 *Nature Climate Change*; Good et al. in review.

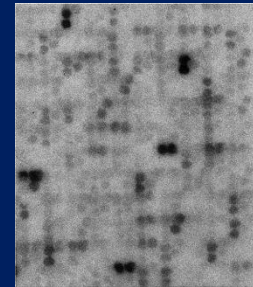
Tracking the effects of a *Mycoplasma* epizootic through time in House Finches



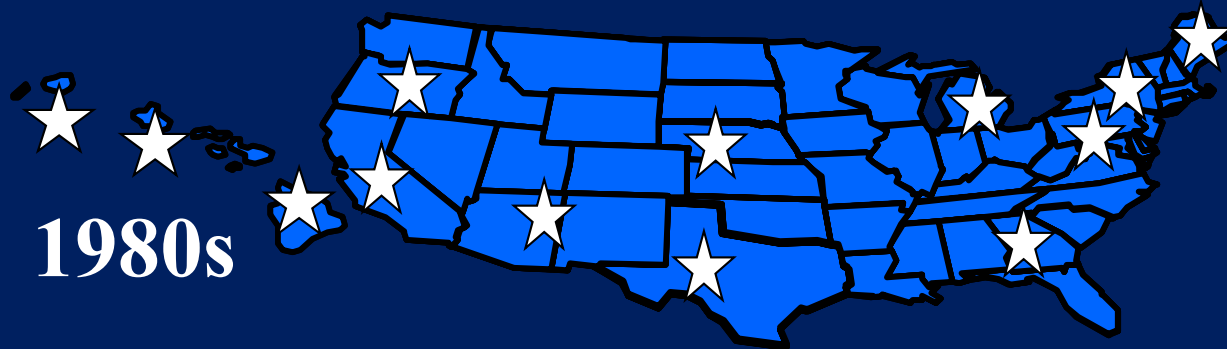
Pre-epizootic tissue collection: priceless!



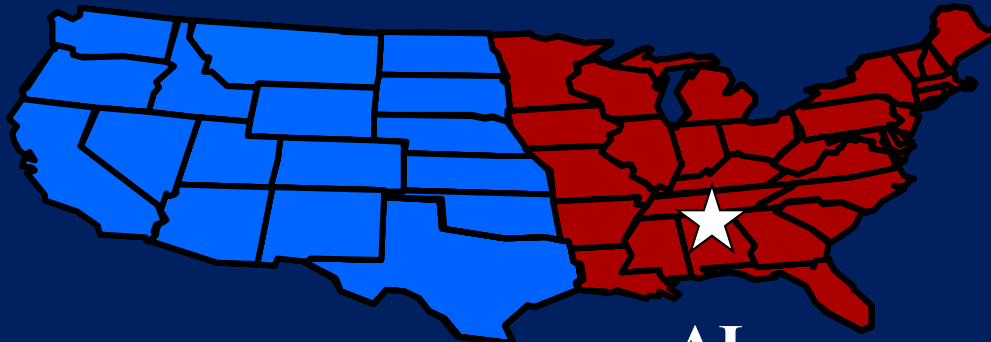
Ongoing collections During the epizootic



Diverse data types emerging from single study system

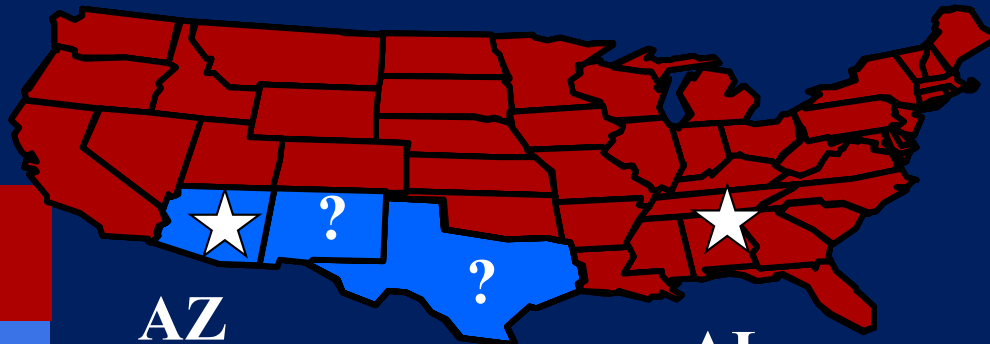


1980s



2001

AL



2007

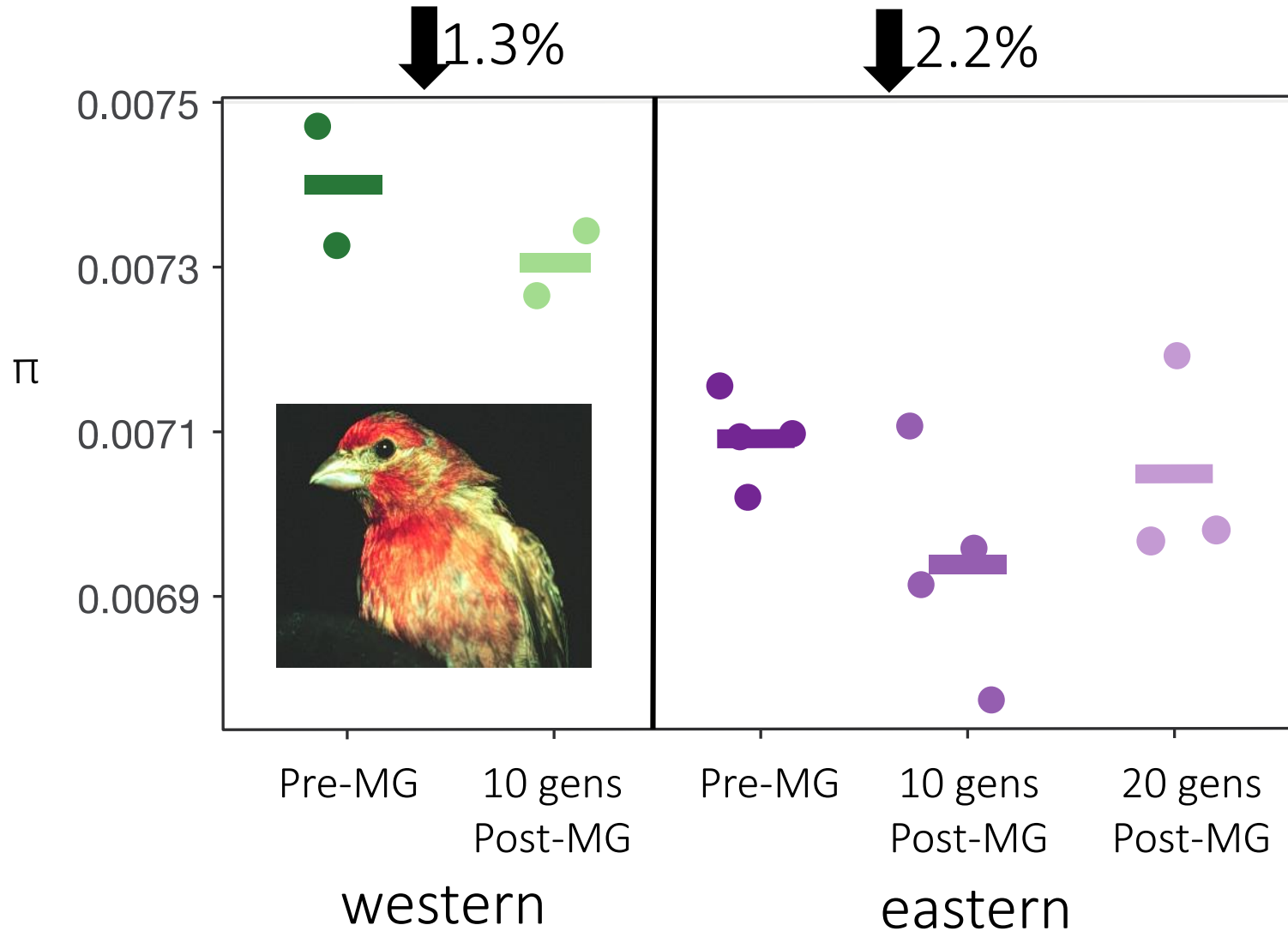
AZ

AL

Mycoplasma exposed areas

Mycoplasma unexposed areas

Whole-genome sequencing reveals serial bottlenecks due to introductions and disease

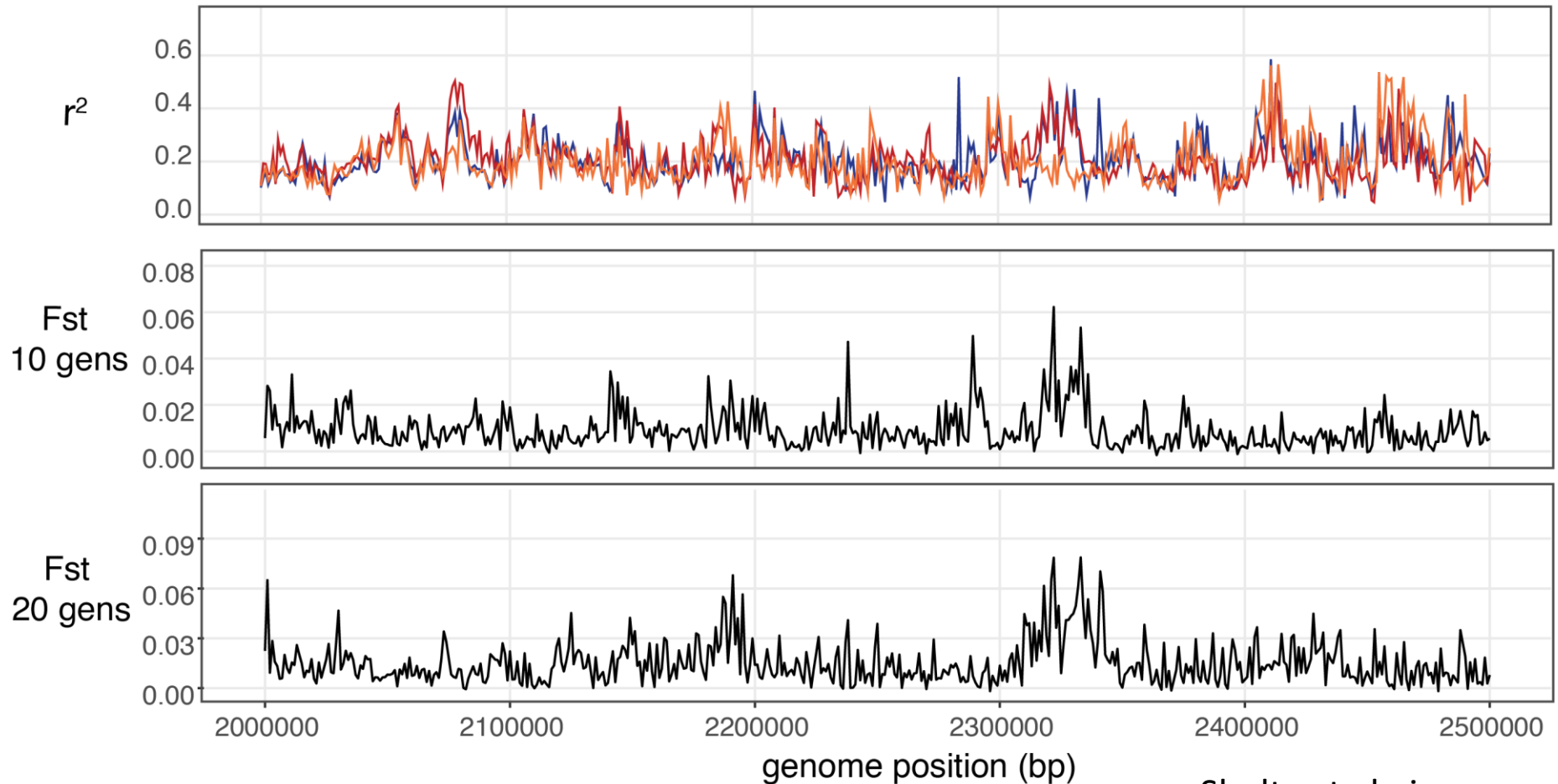


Whole-genome sequencing reveals subtle signatures of disease-induced natural selection

1990

2001

2014

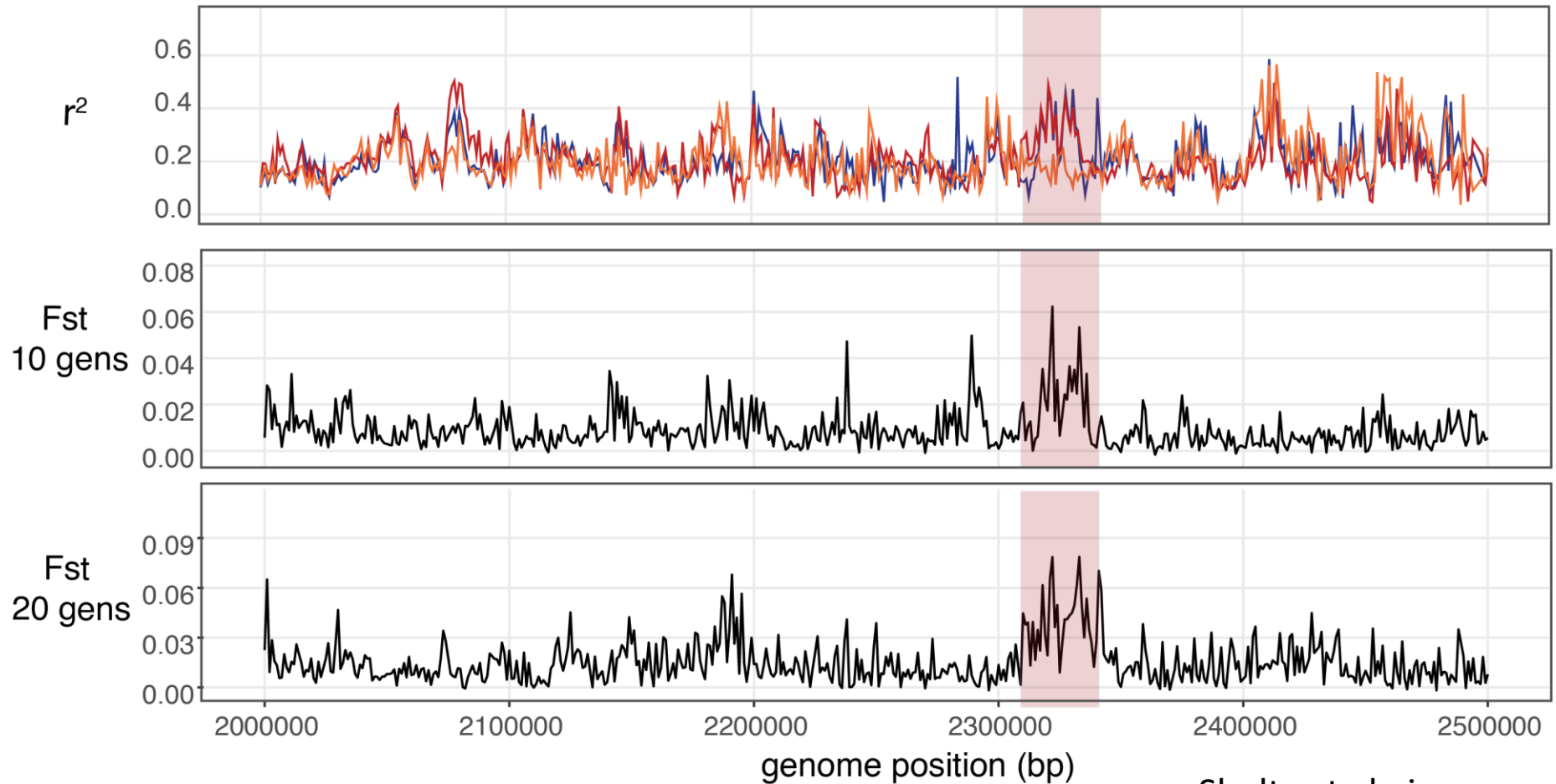


Whole-genome sequencing reveals subtle signatures of disease-induced natural selection

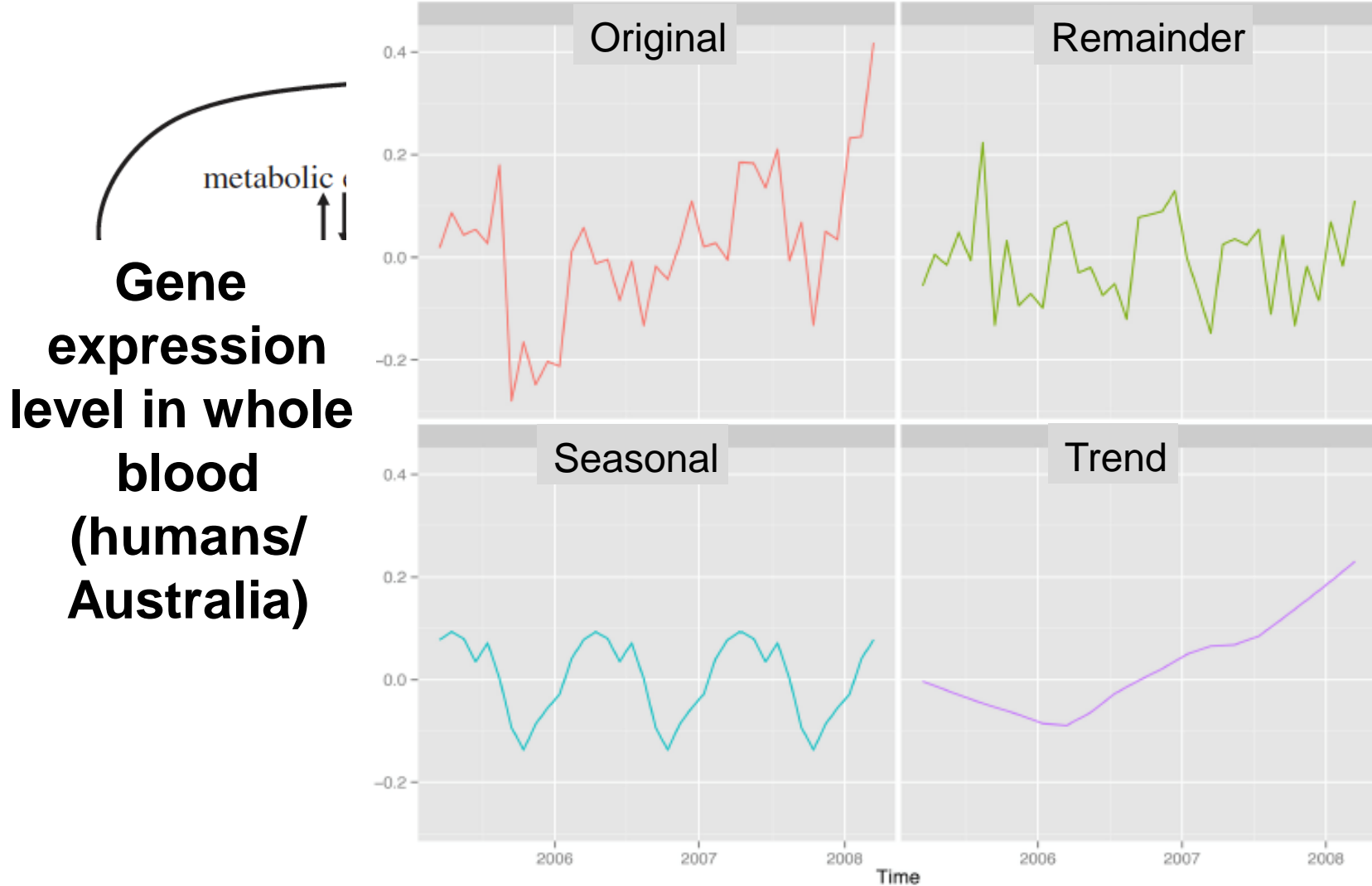
1990

2001

2014

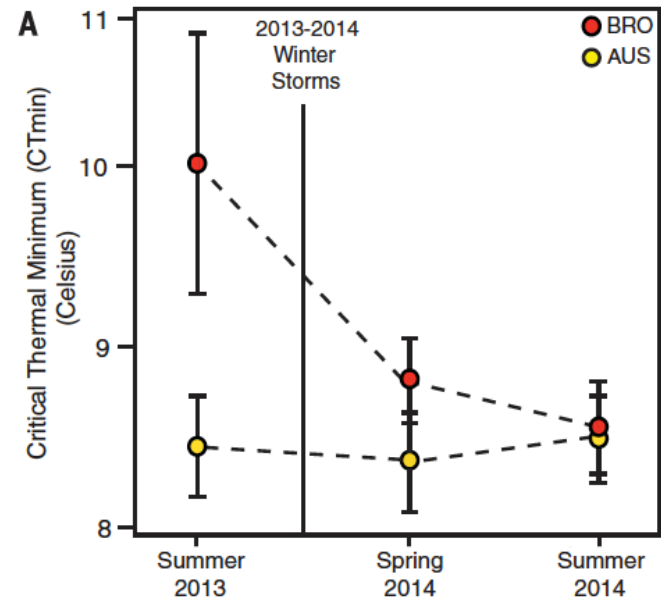
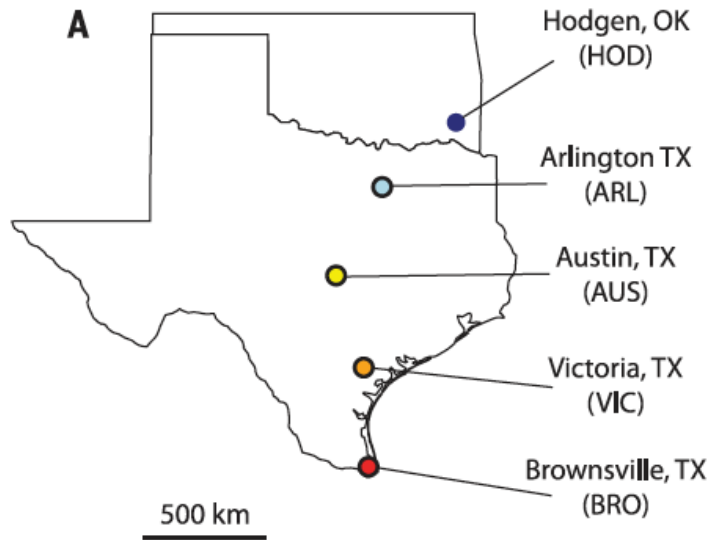
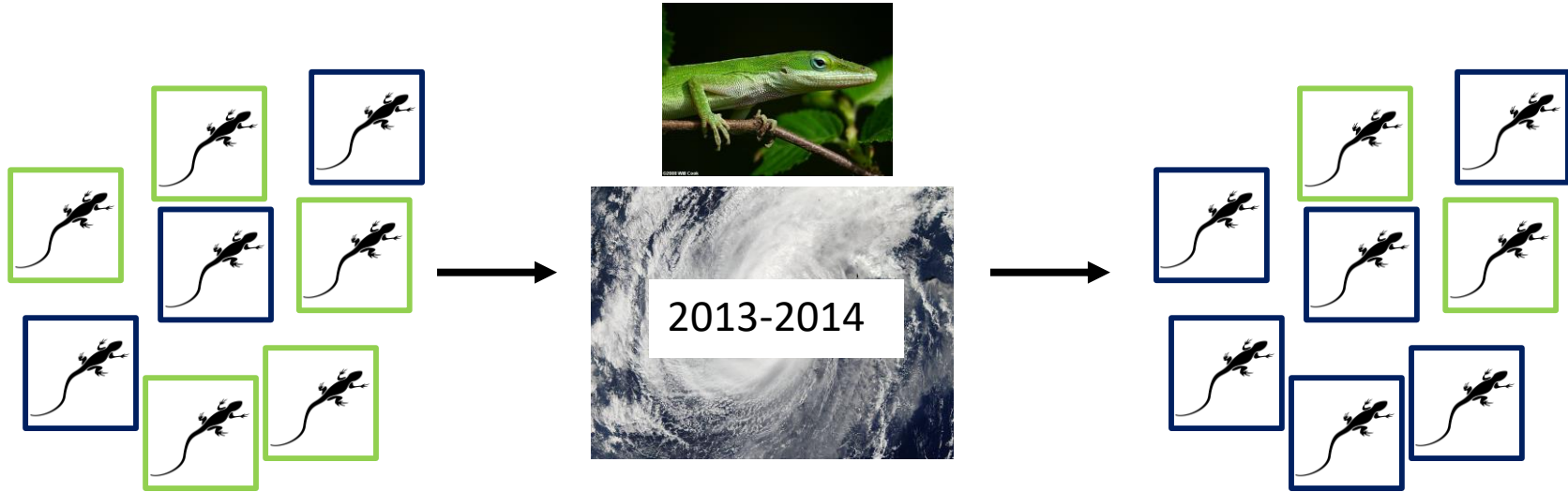


The genome is dynamically expressed and modified in space and time...

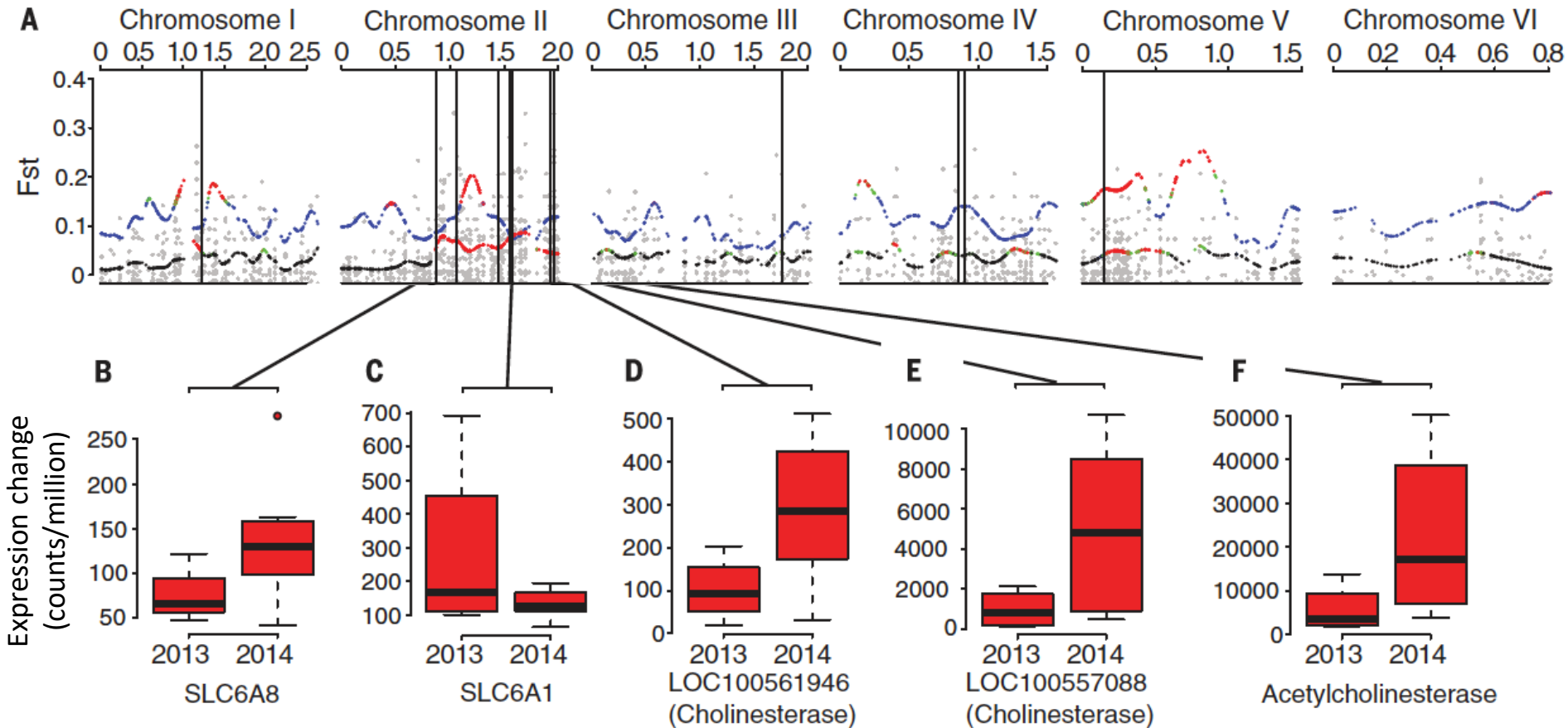


...but museums are unprepared for capturing this dynamism

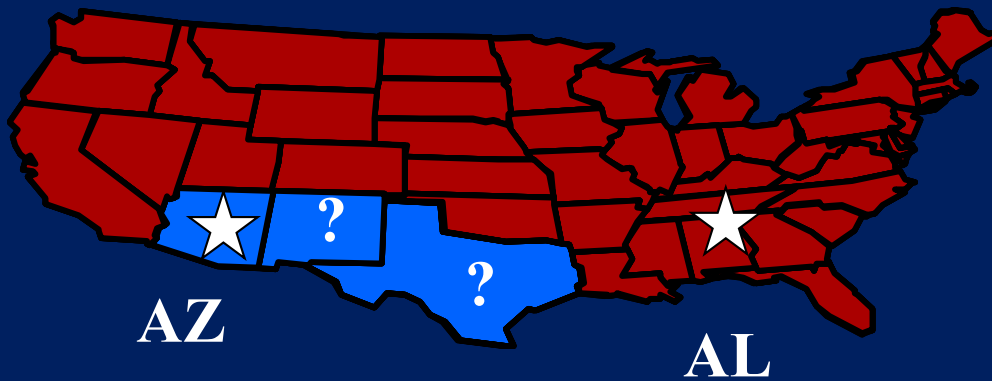
Rapid phenotypic evolution triggered by the 2013-2014 polar vortex



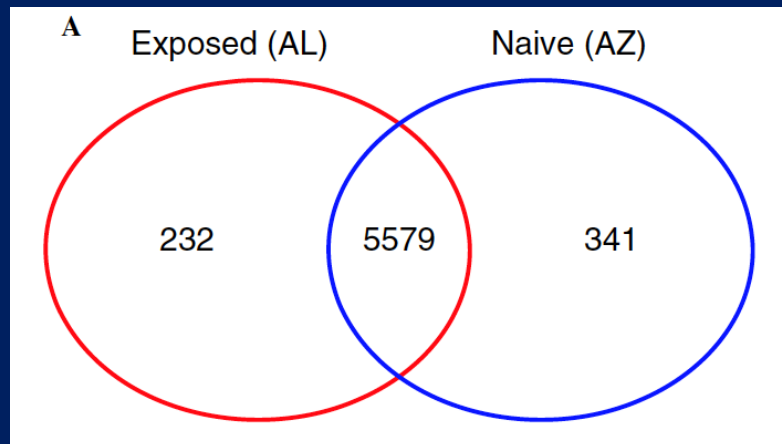
Rapid sequence and expression evolution triggered by the 2013-2014 polar vortex



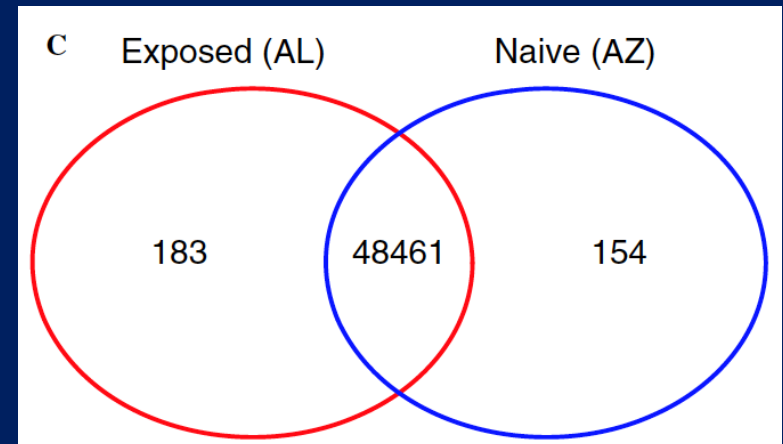
Expression comparisons in House Finches are limited to geography, not time

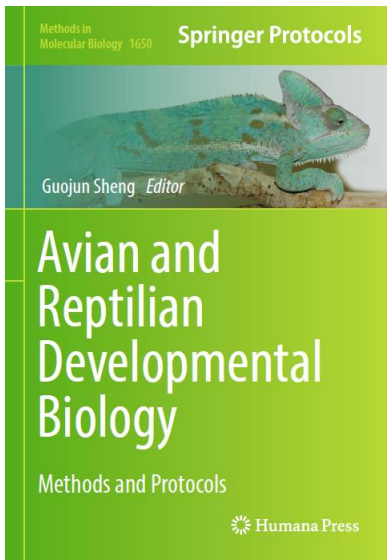


Expression differences



Splice variant differences

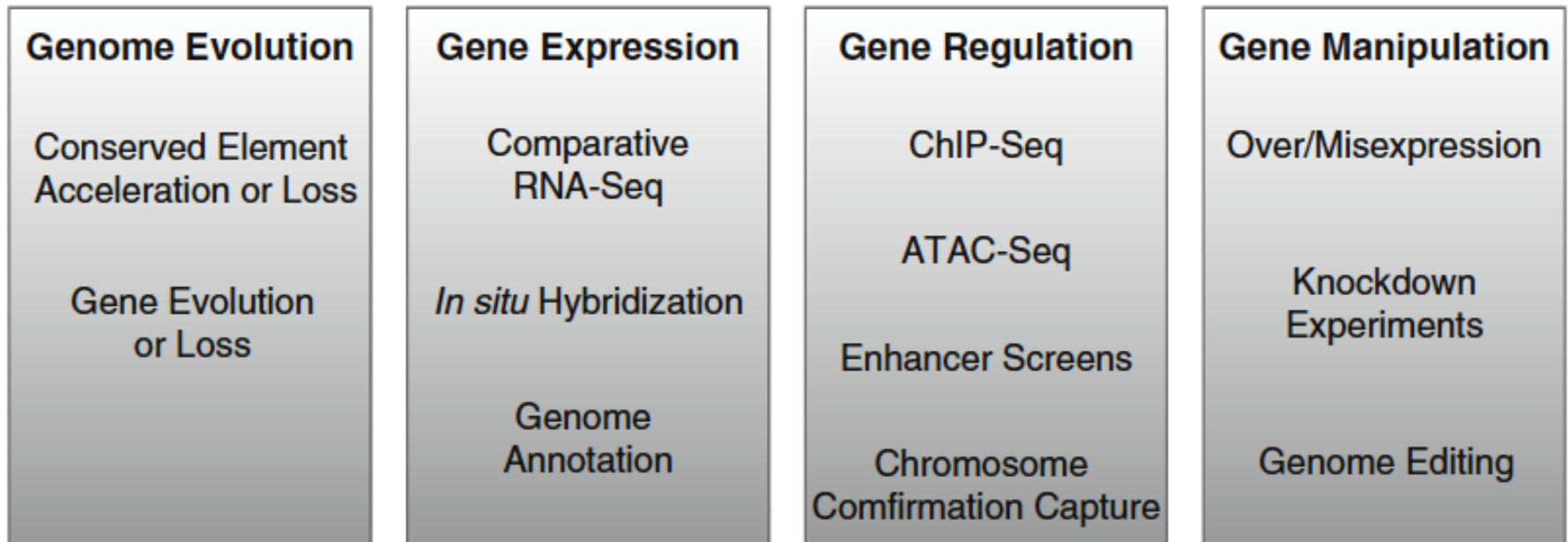




Comparative Genomics as a Foundation for **Eco-evolutionary** Studies in Birds

Phil Grayson, Simon Y.W. Sin, Timothy B. Sackton, and Scott V. Edwards

Draft Genome

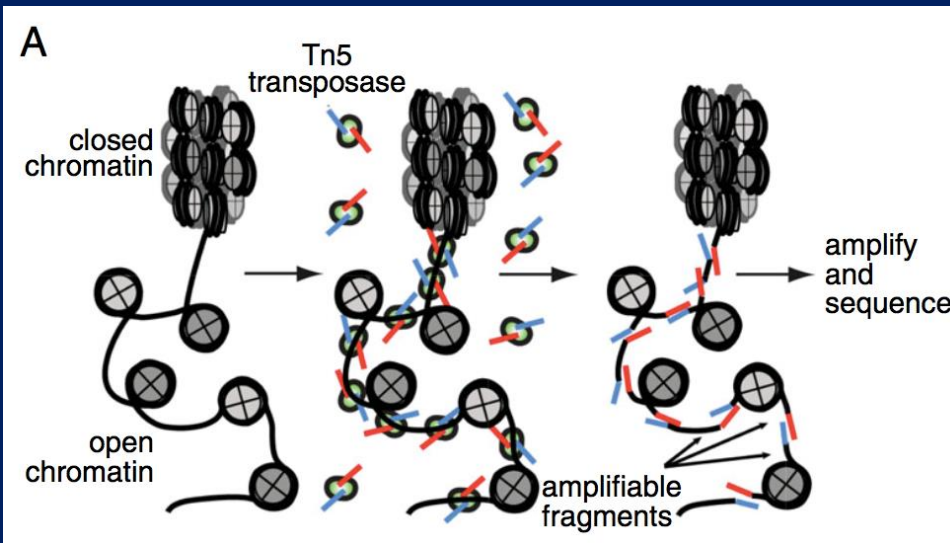


Assay for Transposase-Accessible Chromatin

ATAC-Seq identifies DNA with open chromatin, accessible to transcription factors



Stage HH24-25 chickens and rheas

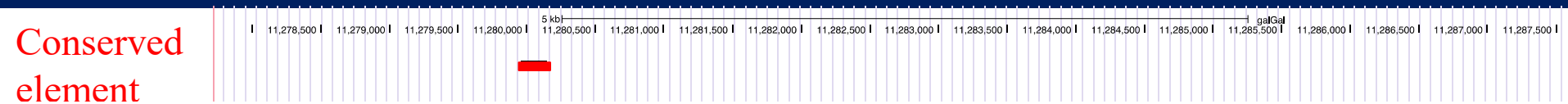


Buenrostro et al. 2015. *Curr Protoc. Biol.* 2015; 109: 21.29.1–21.29.9.



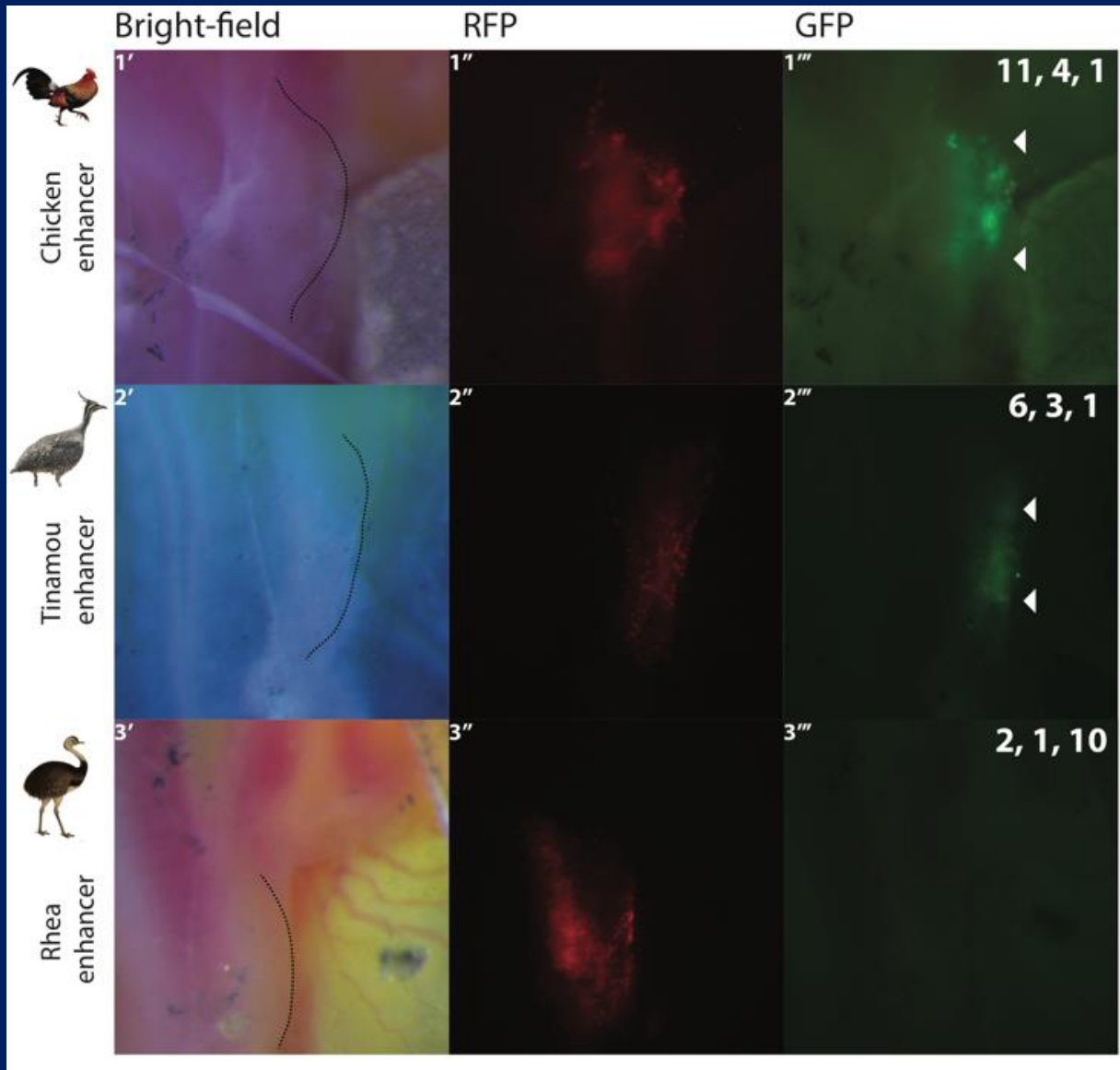
Chromatin state varies by species, development time...and probably environment

Ratite noncoding element 1317692 is contained under chicken ATAC peaks ...



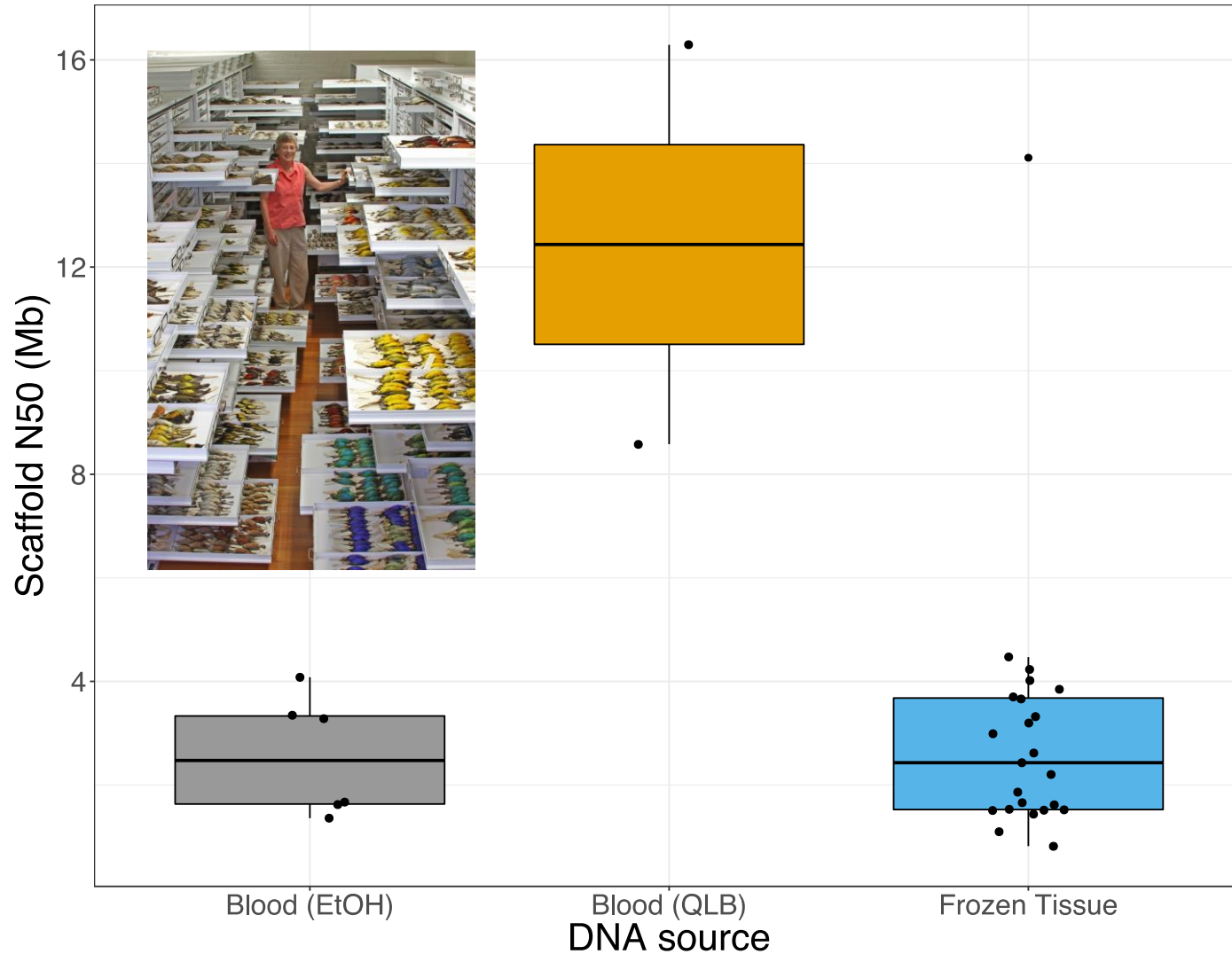
... but the rhea is missing this peak

Chromatin state predicts the ability of noncoding regions to drive gene expression



Genomically-informed cryo-collections produce high-quality genomes

Genome quality



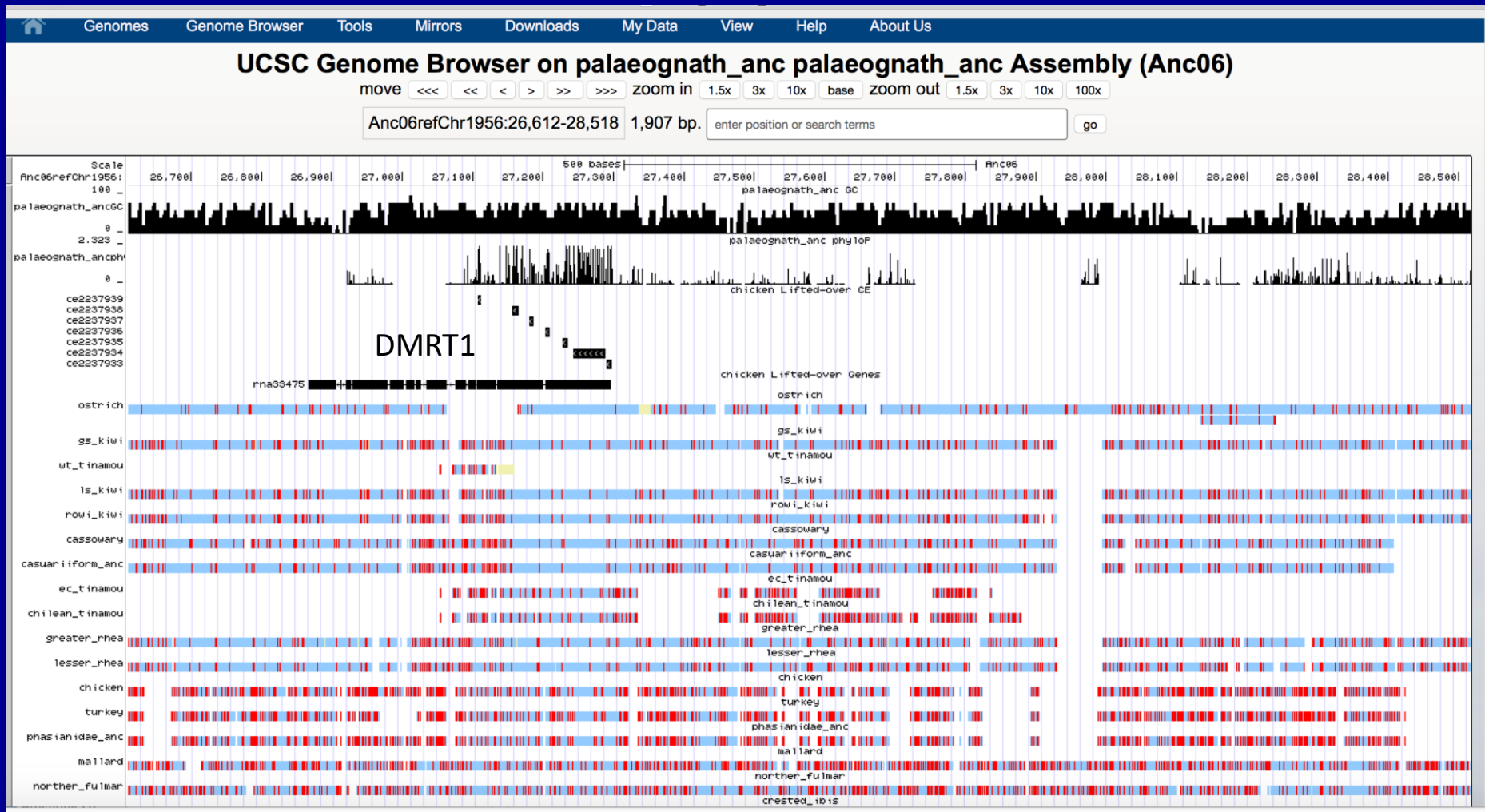
Based on 31 reference-quality genomes of birds in Edwards lab

Genomically-informed field collections facilitate a greater diversity of temporal studies



Tissue sample types

Genomic data are easy to digitize; linking them to specimens and environments is harder

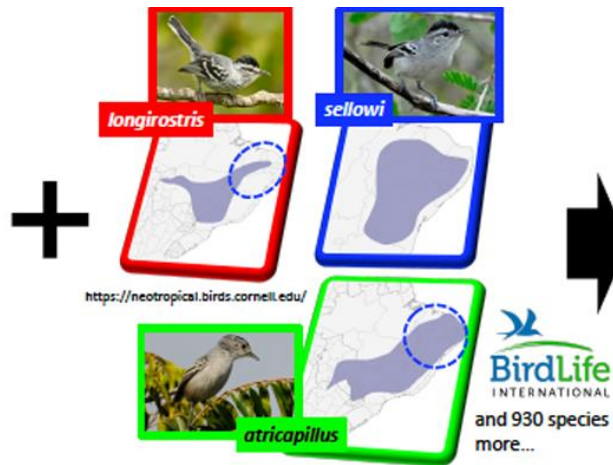


Vision: from genomes and epigenomes to global change

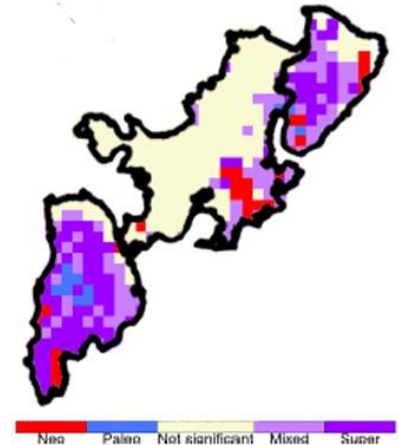
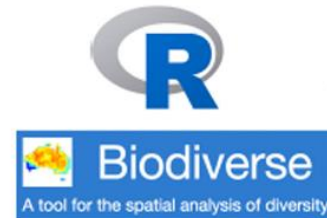
Genomes



Environments



Spatial/Temporal Change



Courtesy J. Tonini, poster

Acknowledgements:
Edwards Lab and colleagues
Thank you!