

Local adaptation in blue tit populations: insights from population genomics

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Merci à

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Enrique Ortega

Marie-Pierre Dubois

Blue tit long term project

Great tit in the city project

CEFE

MGX

ERC-2013-StG-337365-SHE

OSU-OREME

Outline

Concepts (10min)

The blue tits context (5min)

Genomics results (20-25min)



Concepts

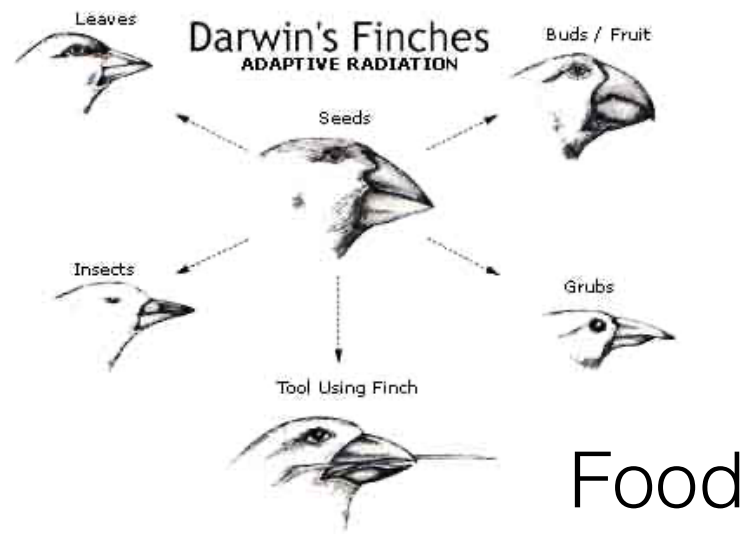
At an intra-specific scale

Fascinating traits variations & local adaptation



Sexual selection

Predation



Concepts

At an intra-specific scale

Fascinating traits variations & local adaptation

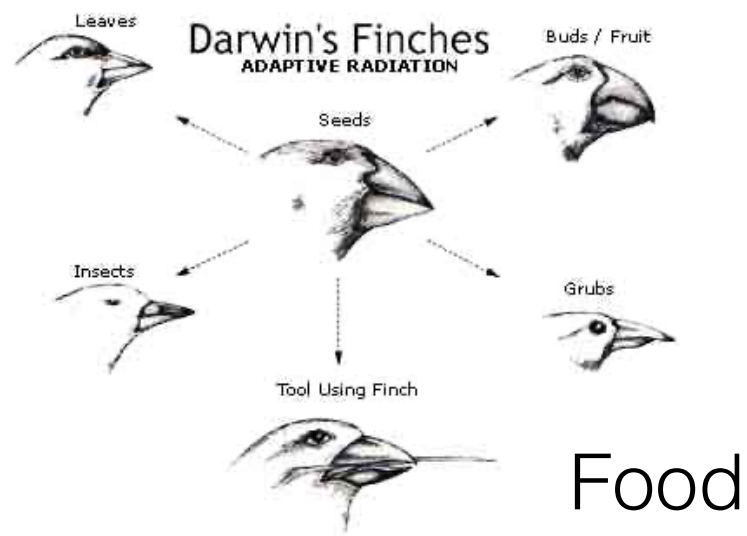


Sexual selection

Predation



Climate



Food



Pollutants

Concepts

At an intra-specific scale

Fascinating traits variations & local adaptation

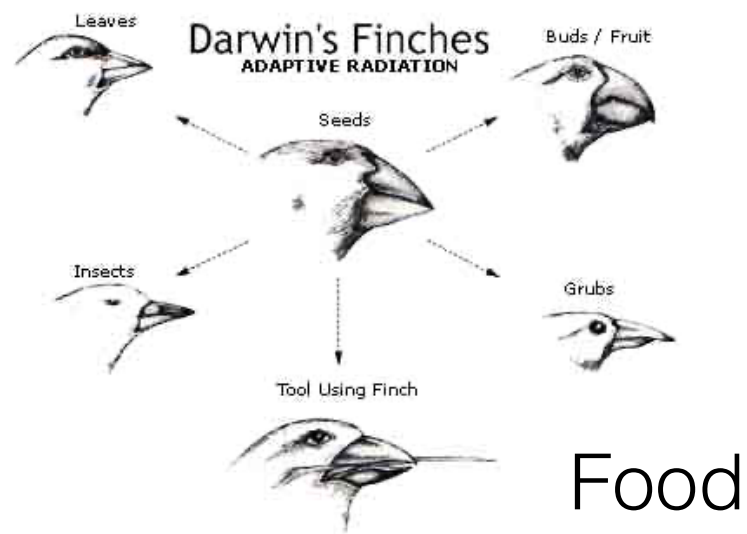


Sexual selection

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Climate



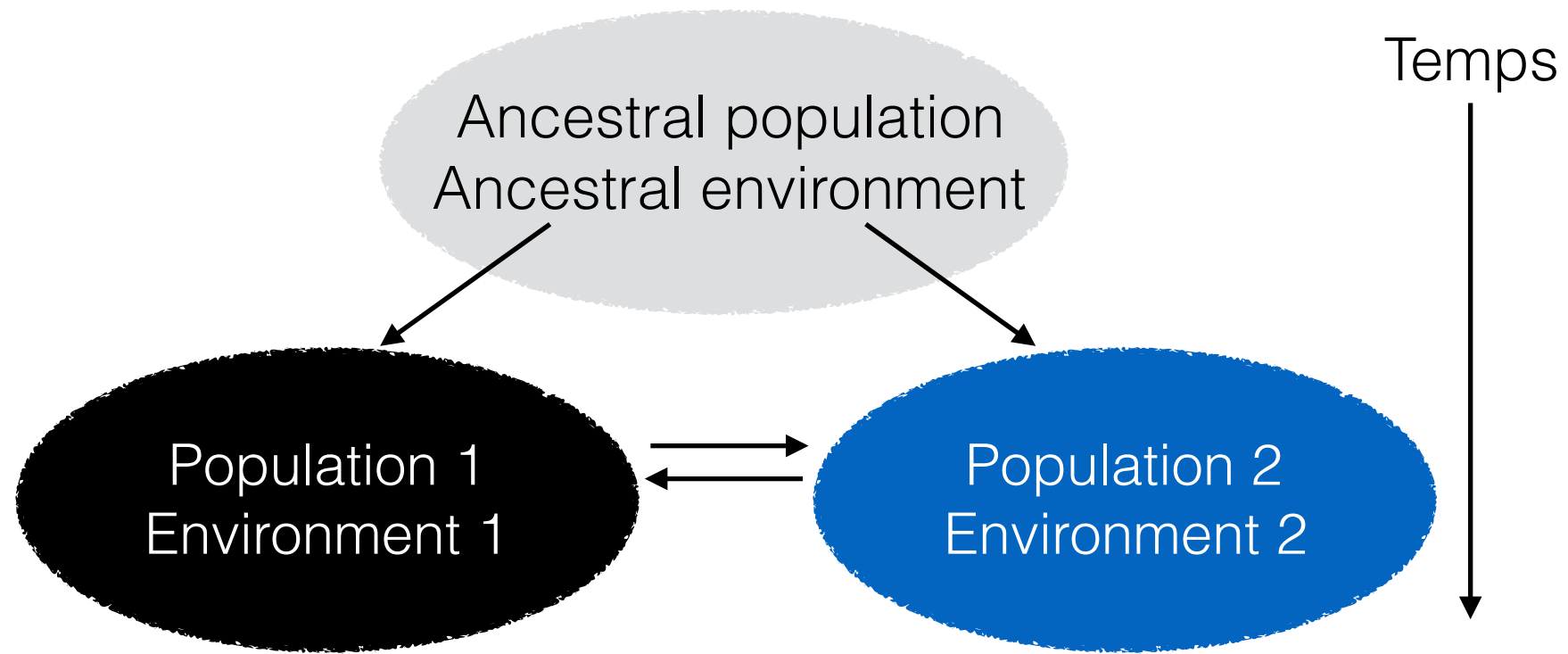
Food



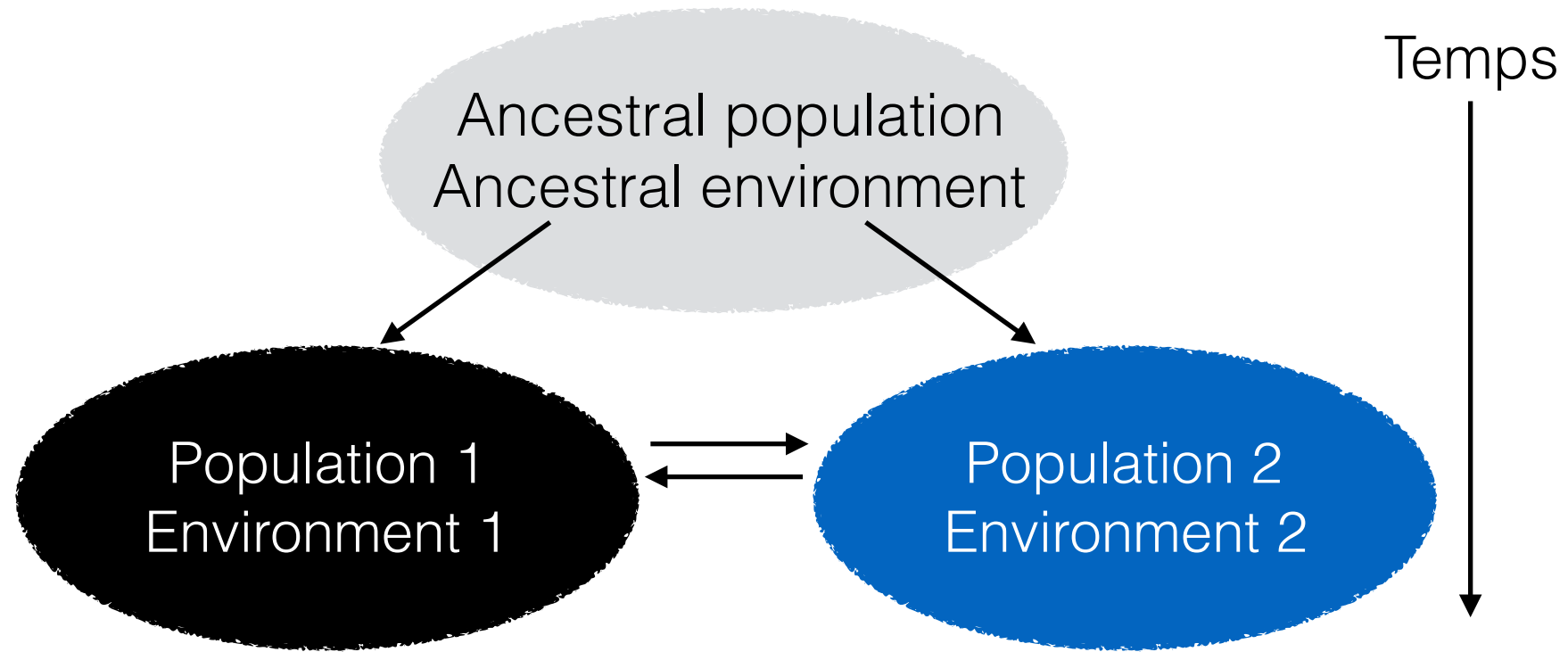
Pollutants

Understanding evolutionary mechanisms implicated in such variations and adaptations is relevant for both fundamental science and the society

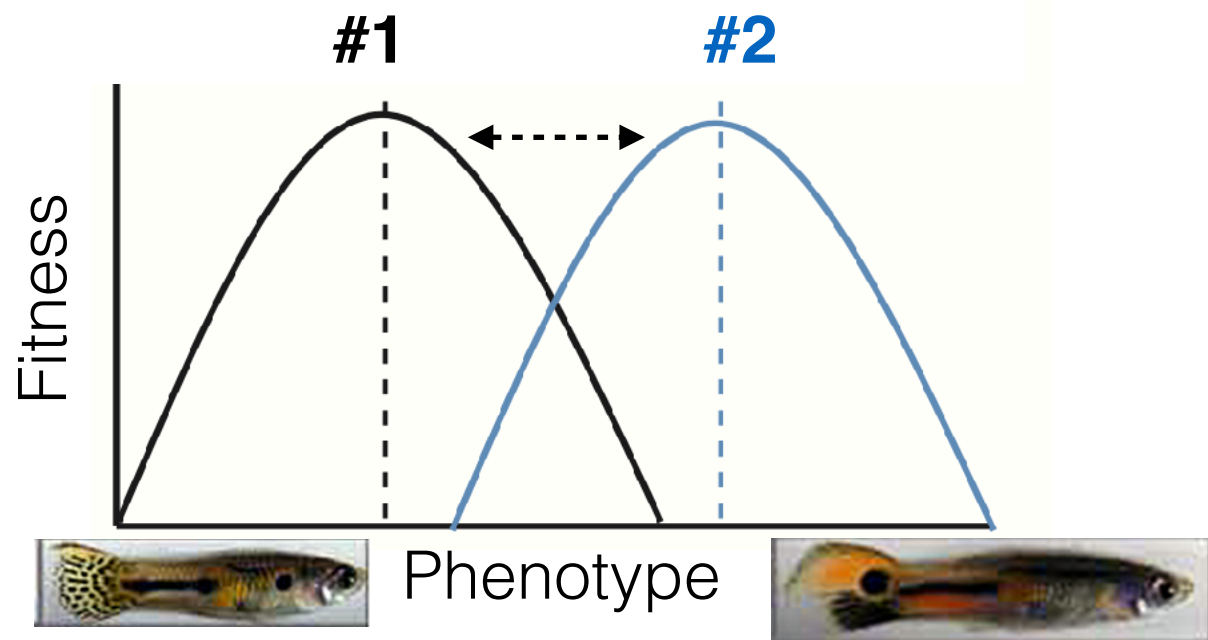
Concepts



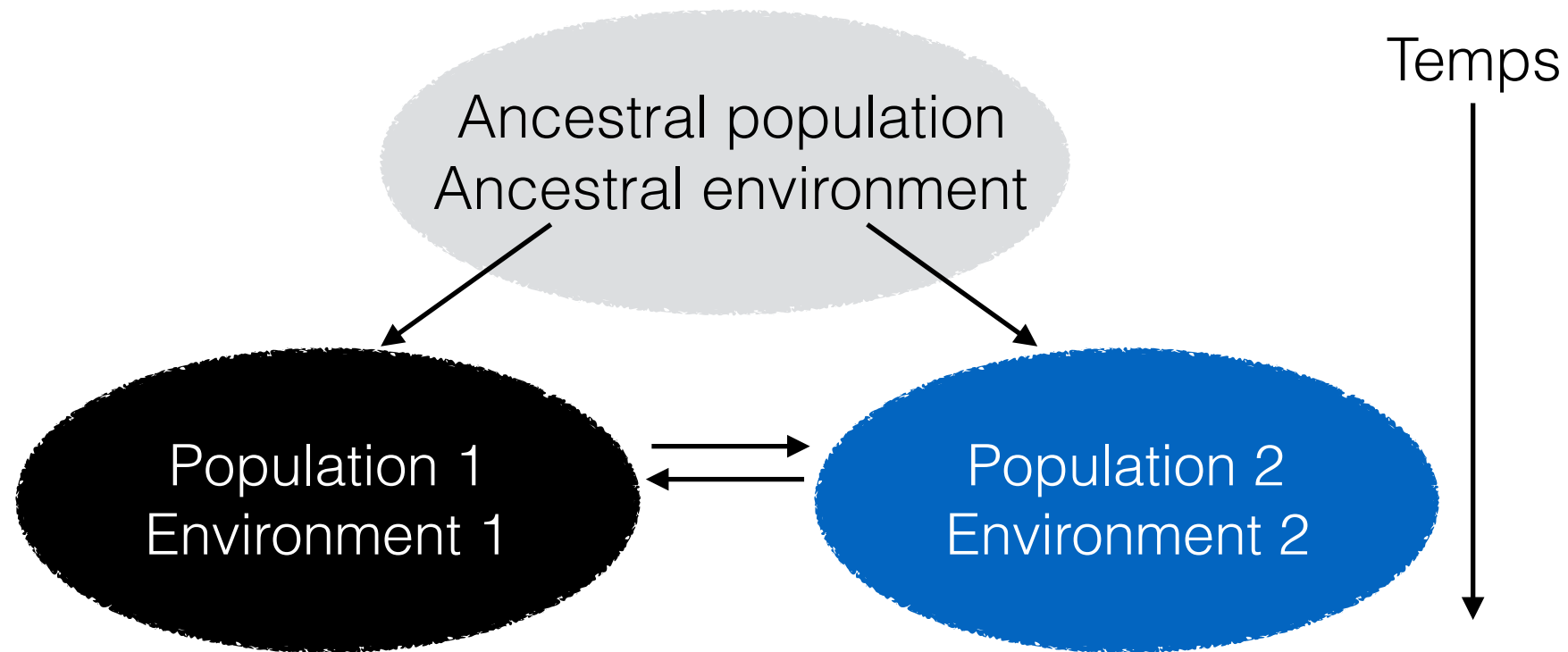
Concepts



Divergent phenotypic optimum
between environments

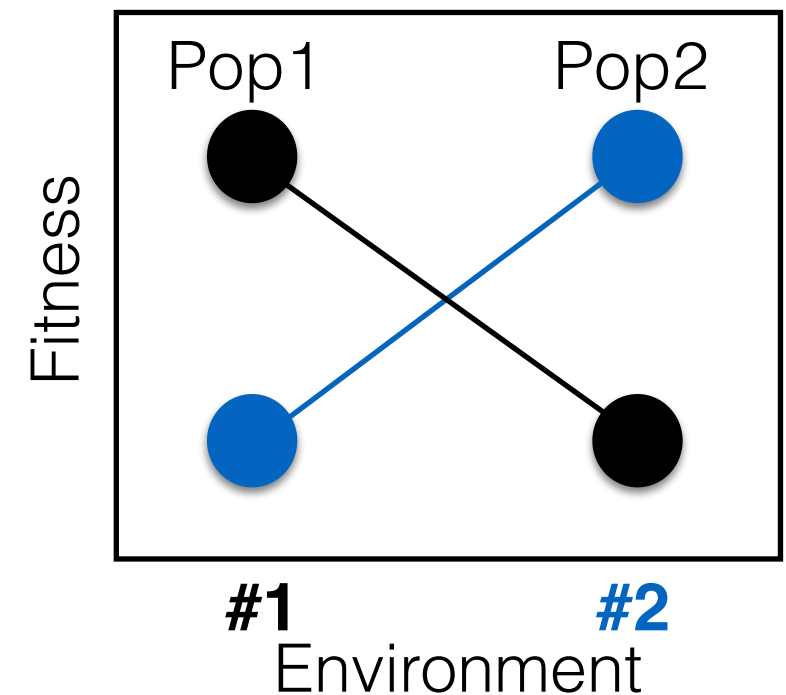
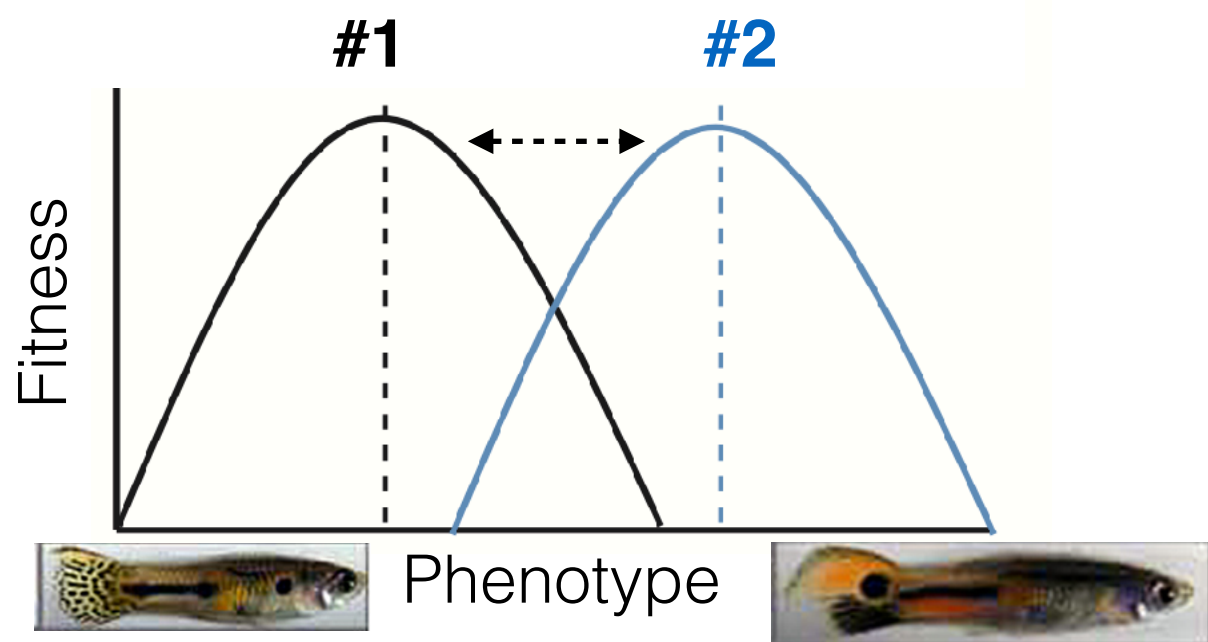


Concepts

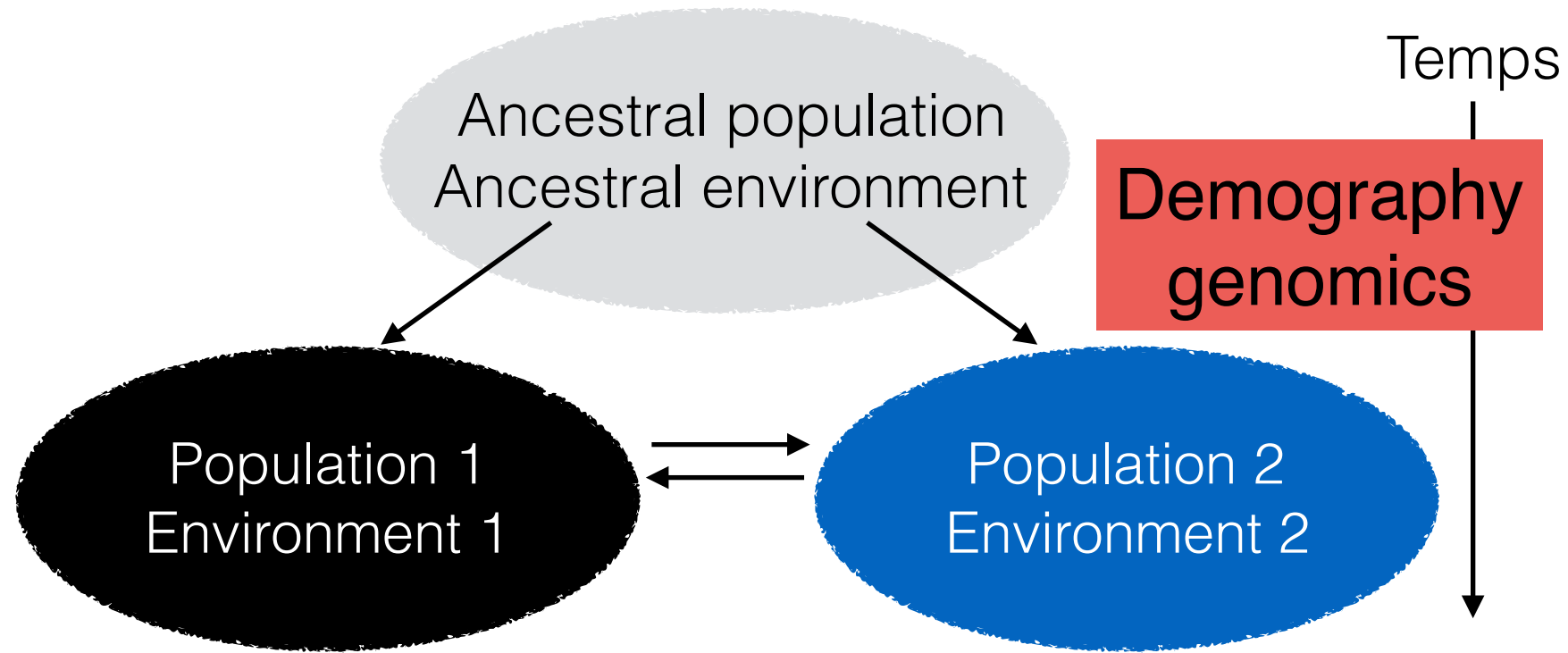


Divergent selection
Local adaptation

Divergent phenotypic optimum
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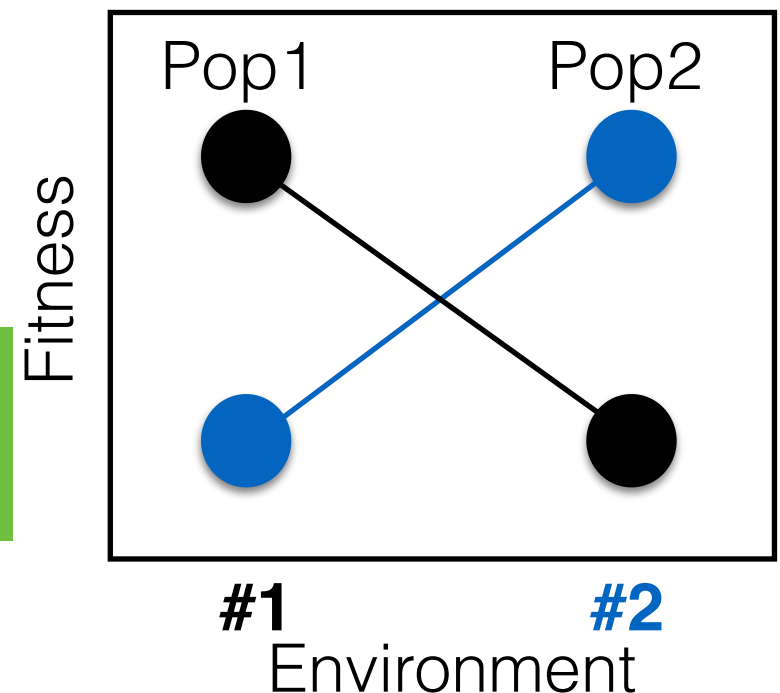
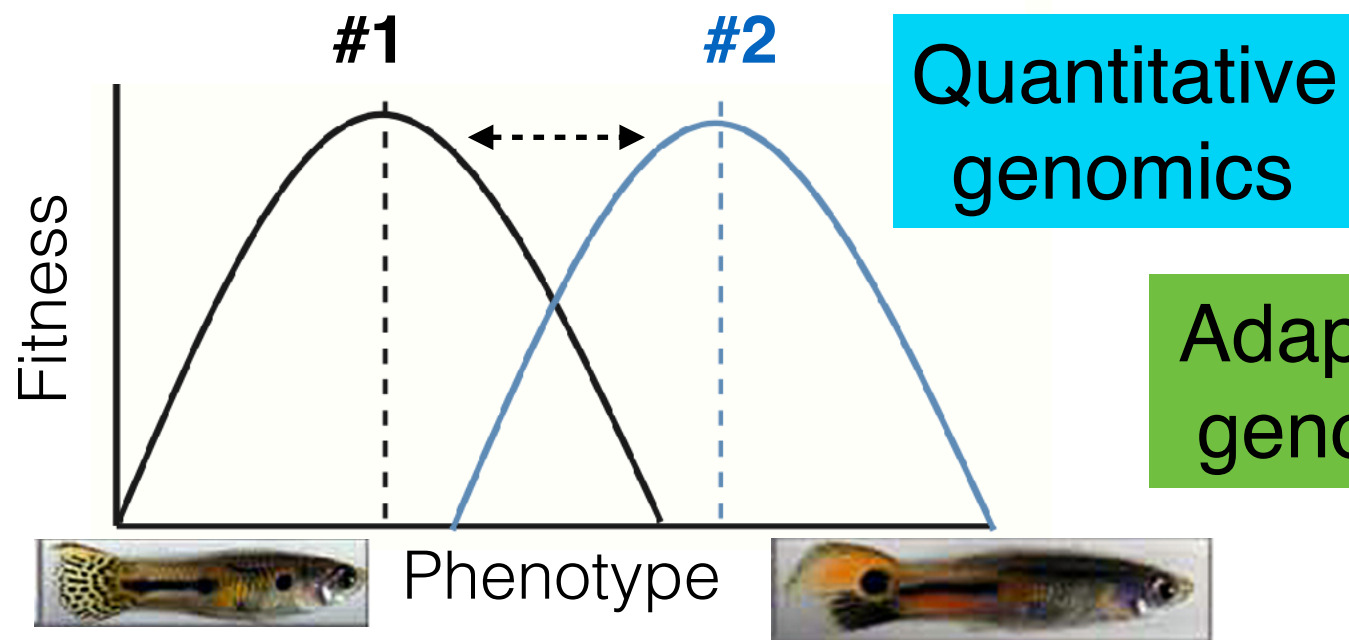


Concepts



Divergent selection
Local adaptation

Divergent phenotypic optimum
between environments



Concepts: Demography

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Adaptation is conditioned by gene flow and population size

High migration rate / selection

Absence of gene flow & small N_e

-> low probability of local adaptation

Concepts: Demography

Adaptation is conditioned by gene flow and population size

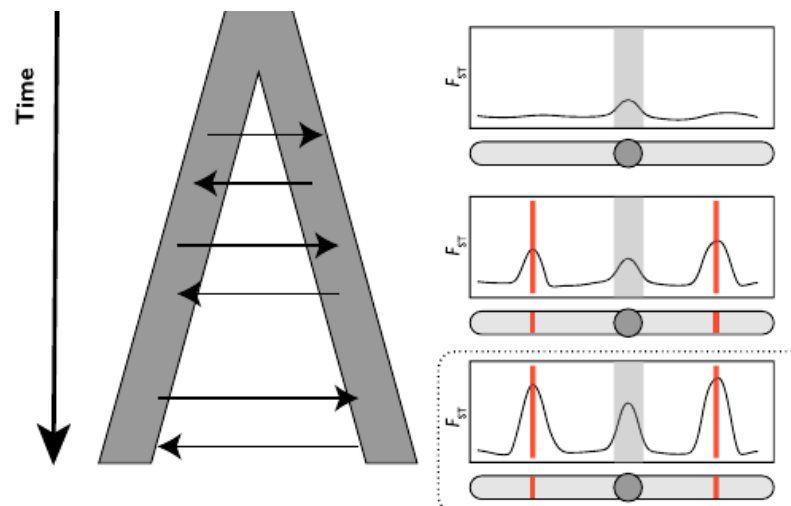
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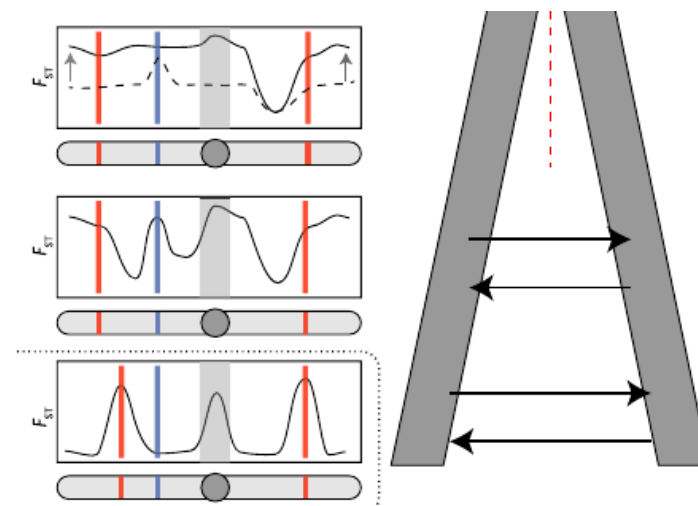
Historical demography and interpretations of genome scans

Isolation with
constant gene flow



Locus
implicated in
adaptation

Strict isolation and
secondary contact



Locus implicated
in adaptation /
incompatibilities

Concepts: Quantitative genetics

Concepts: Quantitative genetics

Origin of phenotypic variation

Génétique

Environnementale

Interaction

Concepts: Quantitative genetics

Origin of phenotypic variation

Génétique

Environnementale

Interaction

Héritabilité ($H^2 = V_G / V_P$)

$R = h^2 \times S$

Concepts: Quantitative genetics

Origin of phenotypic variation

Génétique

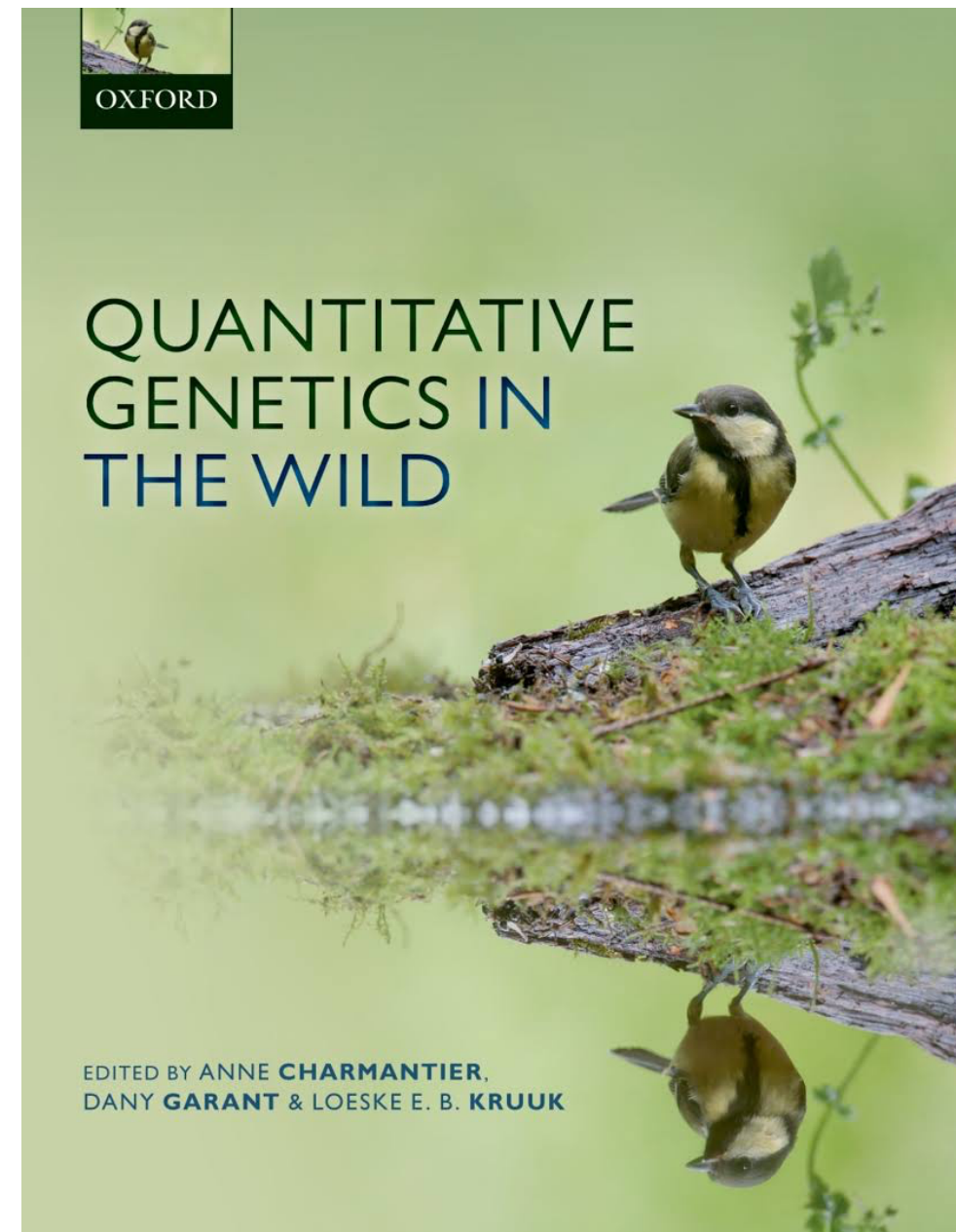
Environnementale

Interaction

Héritabilité ($H^2 = V_G / V_P$)

$R = h^2 \times S$

- > experimentations
- > quantitative genetics in the wild



Concepts: Quantitative **genomics**

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Power of genomics

SNP heritability (pedigree free; precise)

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Power of genomics

SNP heritability (pedigree free; precise)

Phenotype-Genotype associations to identify causative variants

Simple: a few large effect genes

Complex: many small effects genes

Concepts: Quantitative genomics

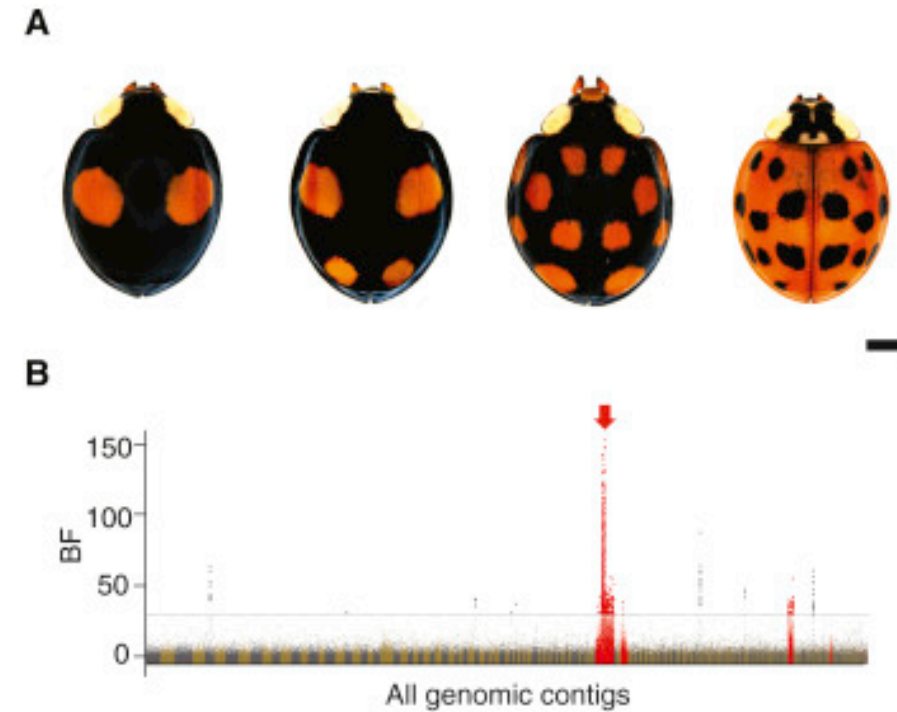
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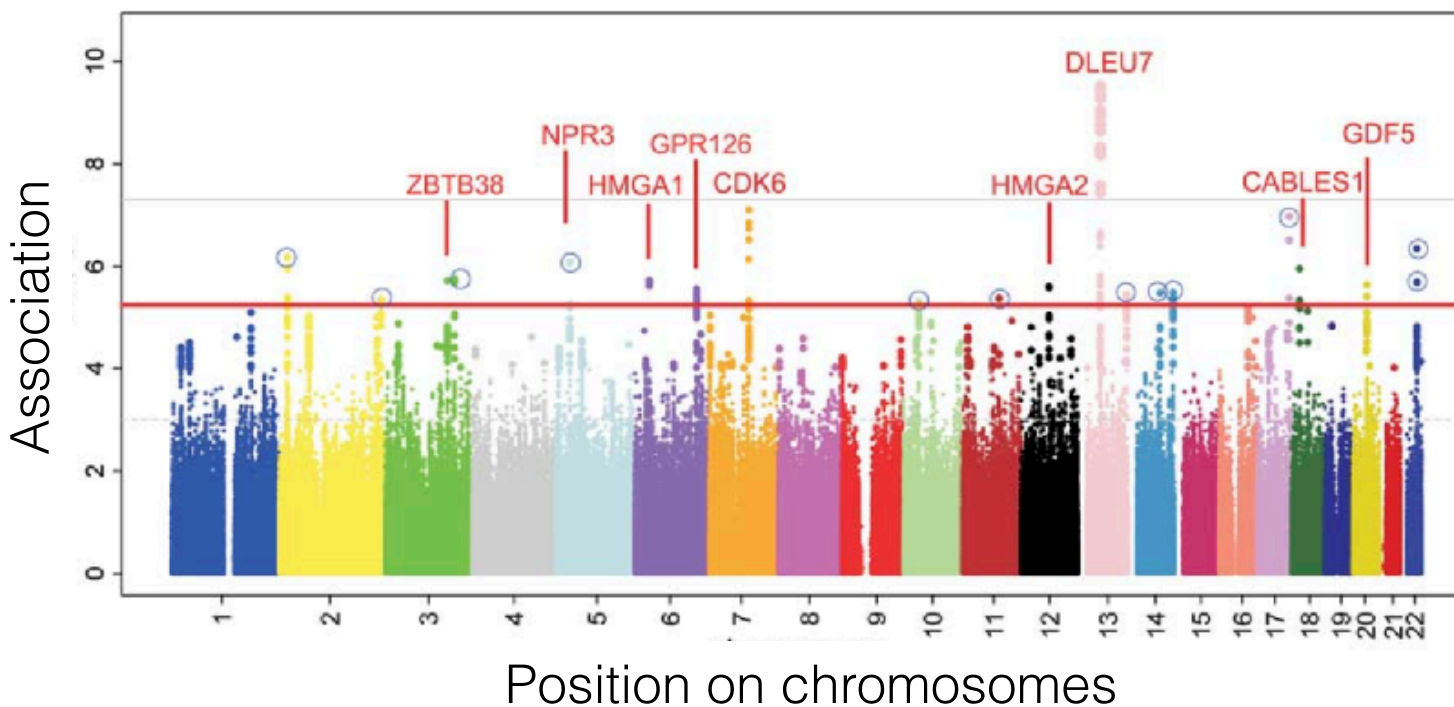
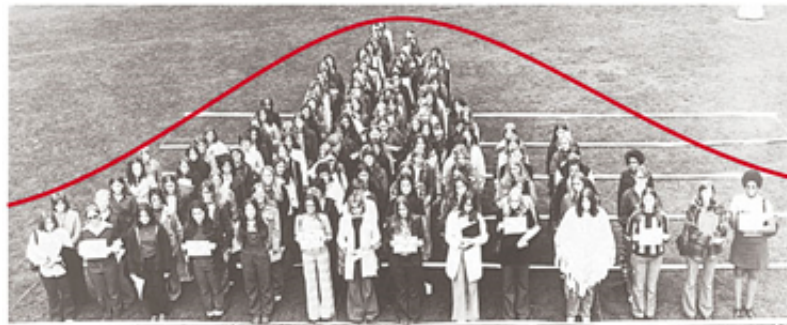
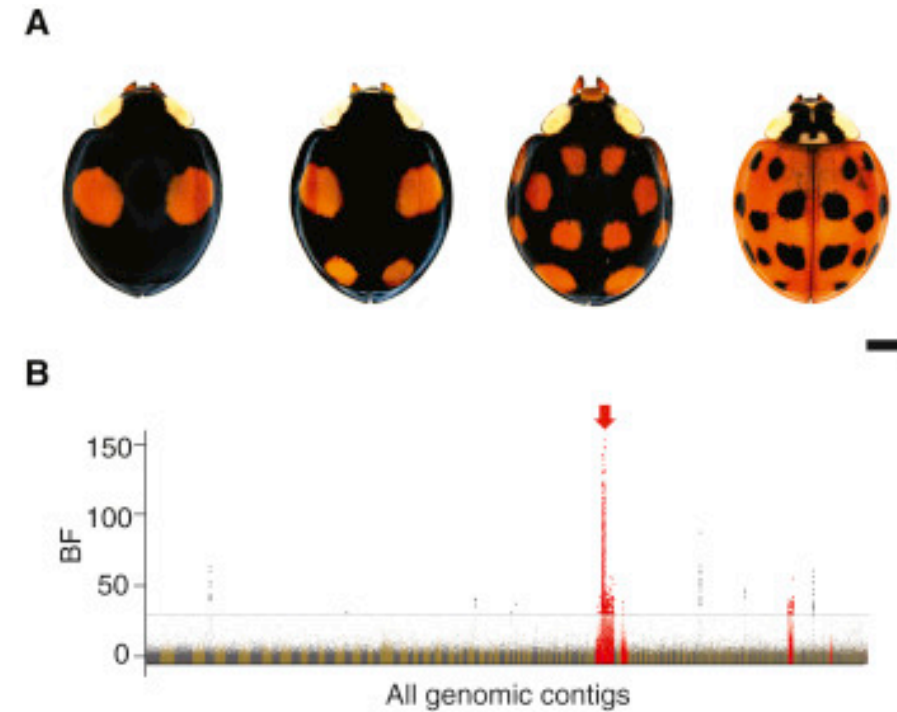
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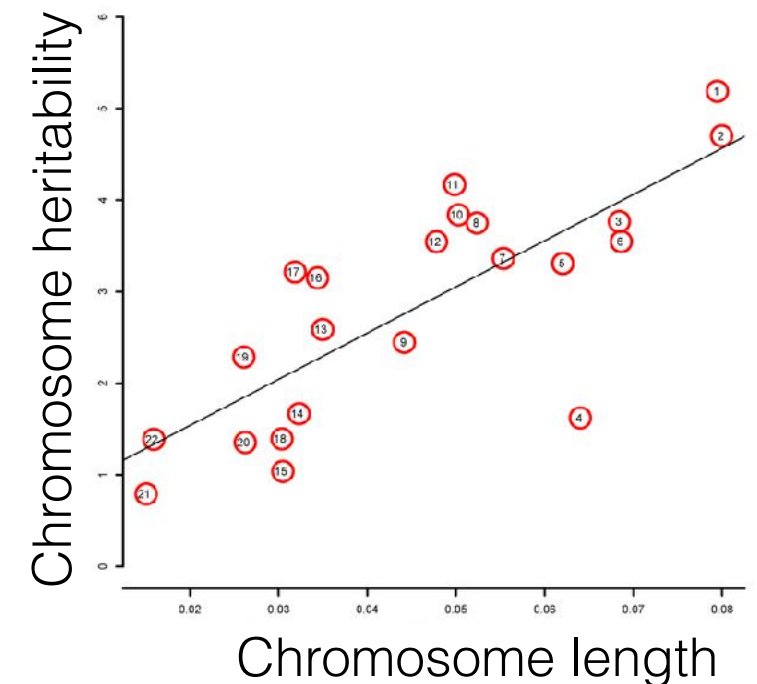
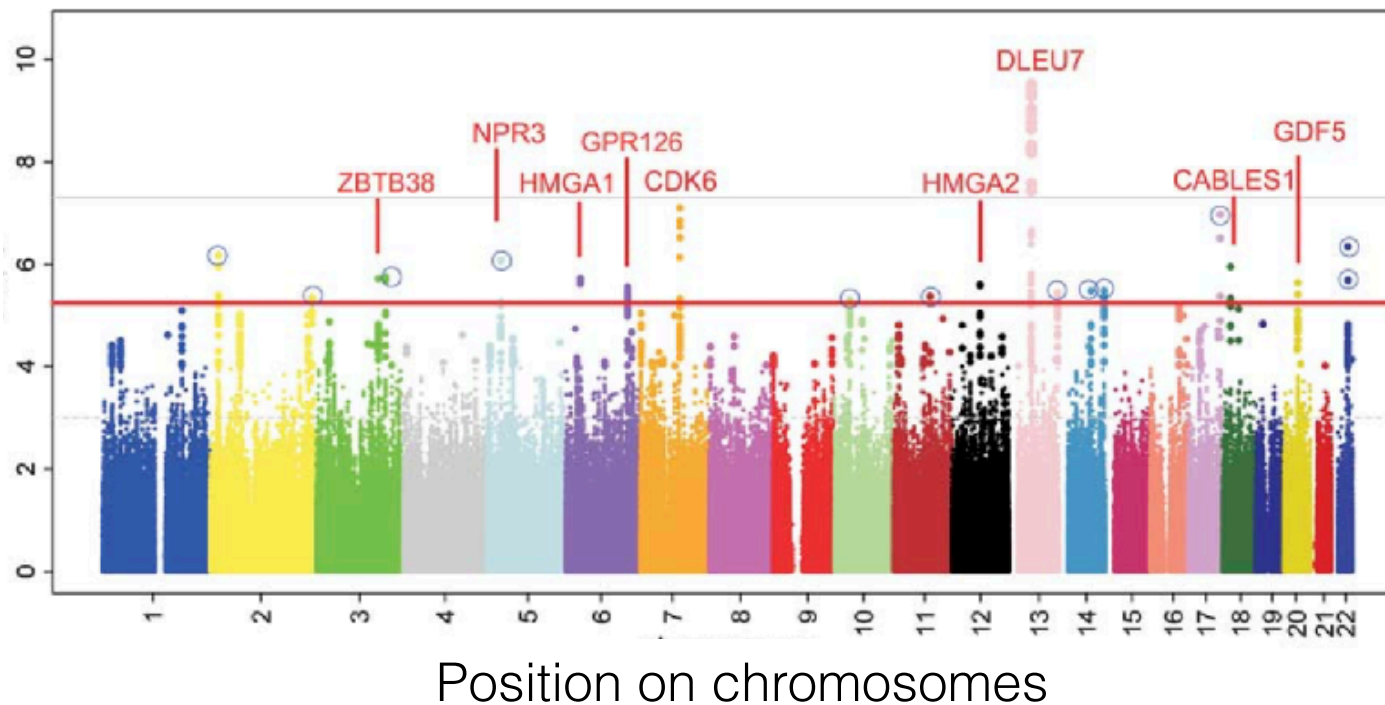
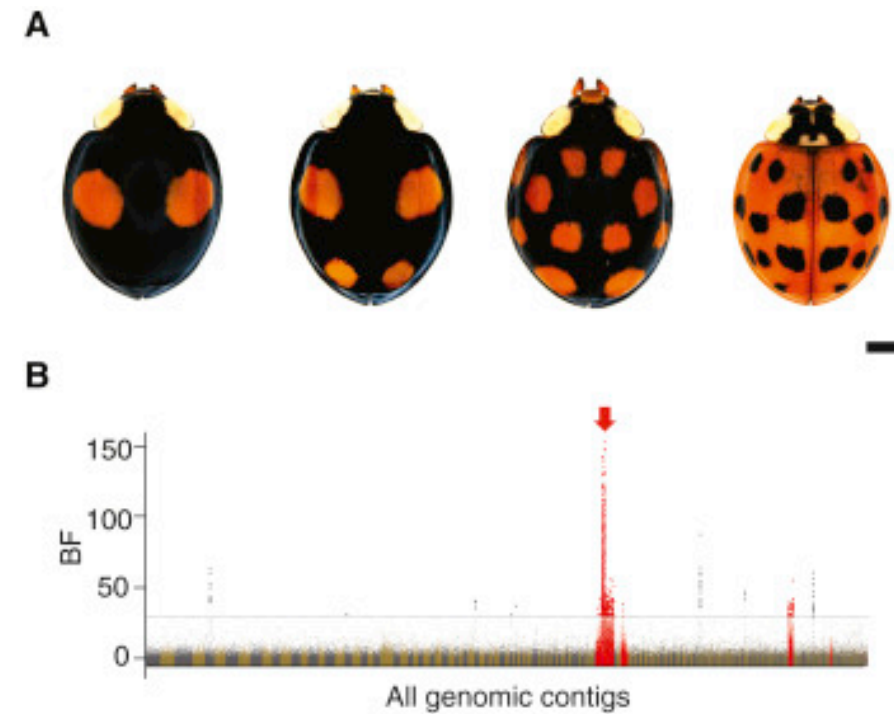
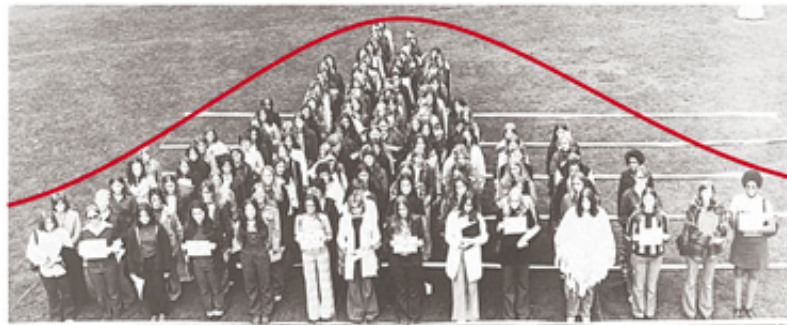
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Concepts: Adaptation genomics

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Power of genomics

Genome scans looking for footprints of divergent selection between populations



Allele frequency differences?

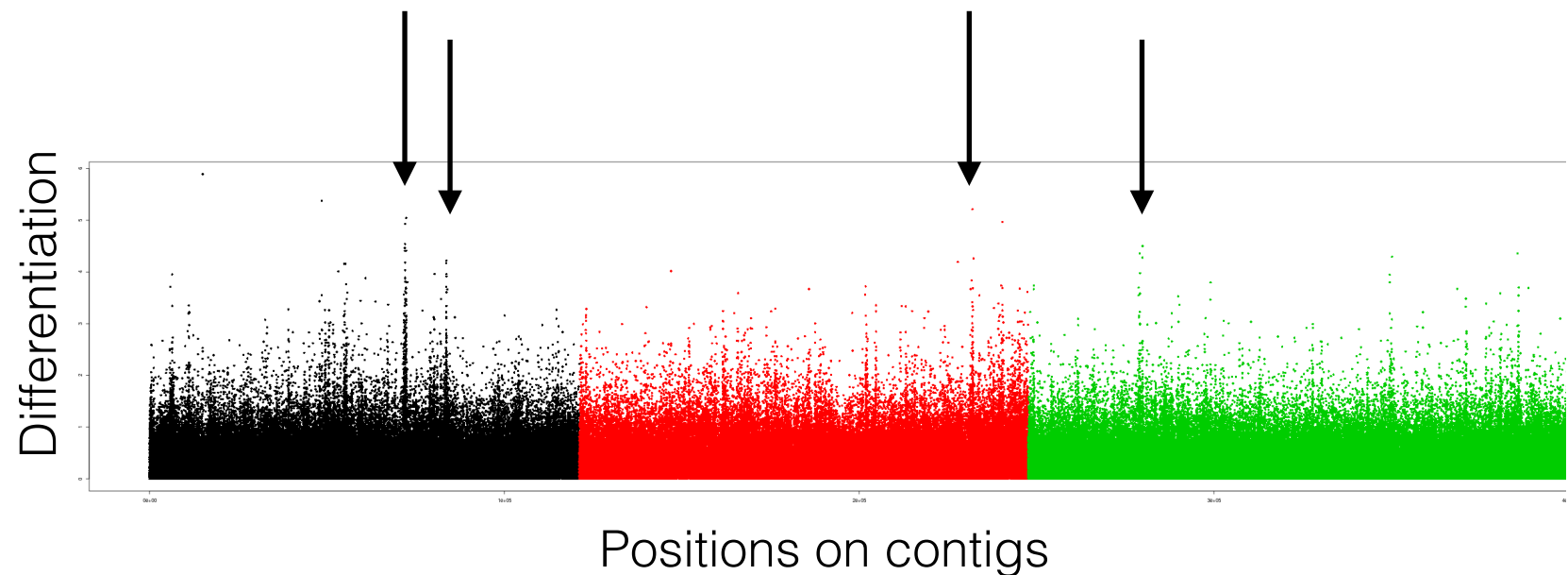
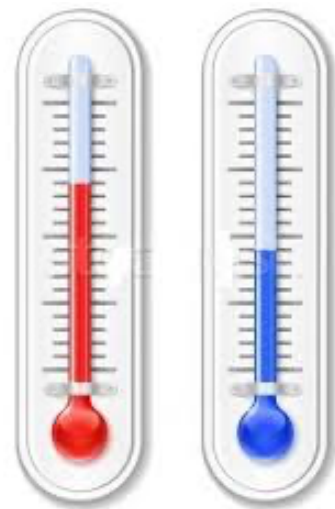
Concepts: Adaptation genomics

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Allele frequency differences?



Concepts: common goals of quantitative and adaptation genomics

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Variants' identity and characteristics?

Name

Function, regulation

Location in the genome

Type of mutation, its age, its origin...

Concepts: common goals of quantitative and adaptation genomics

Variants' identity and characteristics?

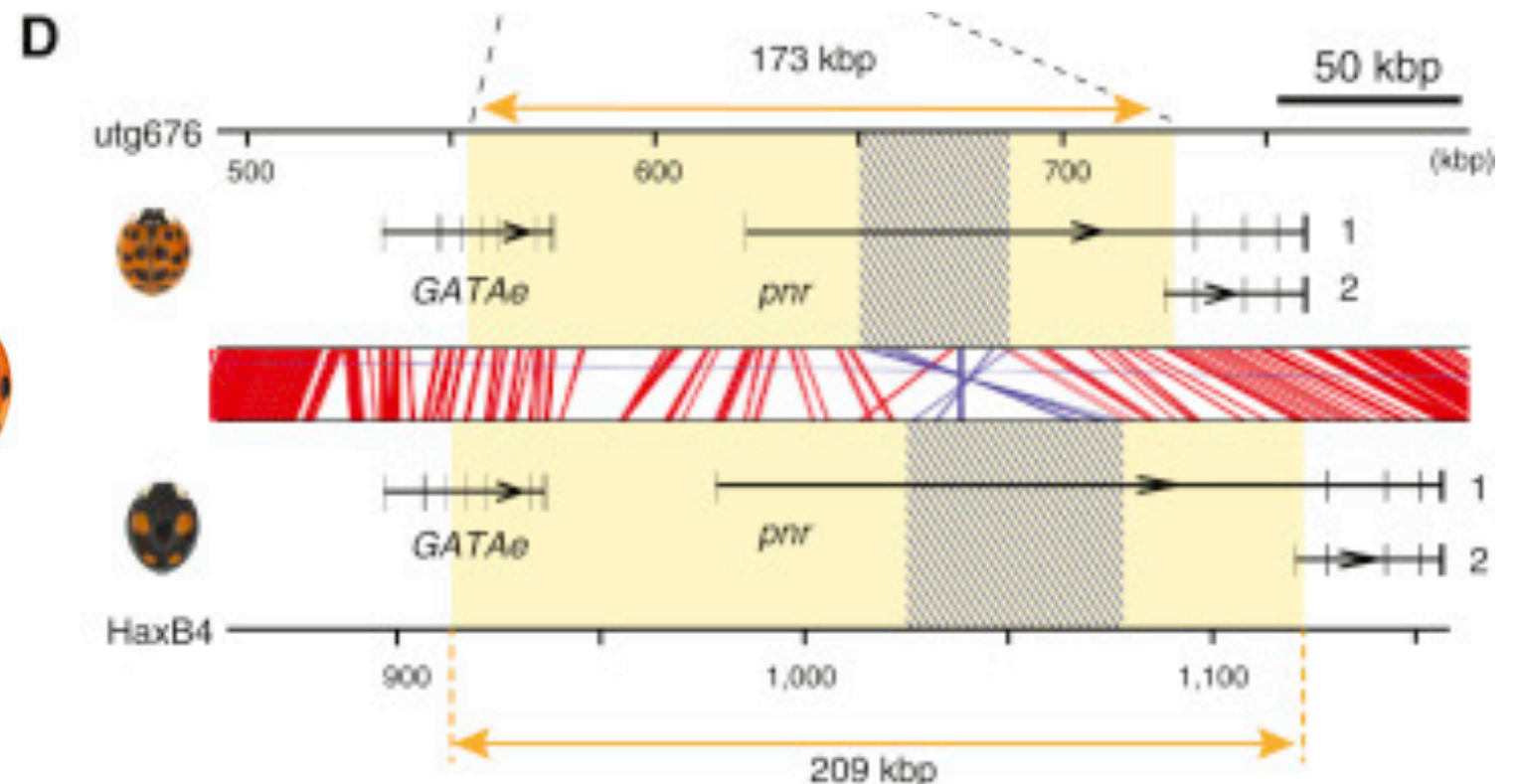
Name

Function, regulation

Location in the genome

Type of mutation, its age, its origin...

highly divergent sequence of ~170 kb
in the *cis*-regulatory regions of *pannier*,
with a 50 kb **inversion** between color forms



The blue tit context

Cyanistes caeruleus



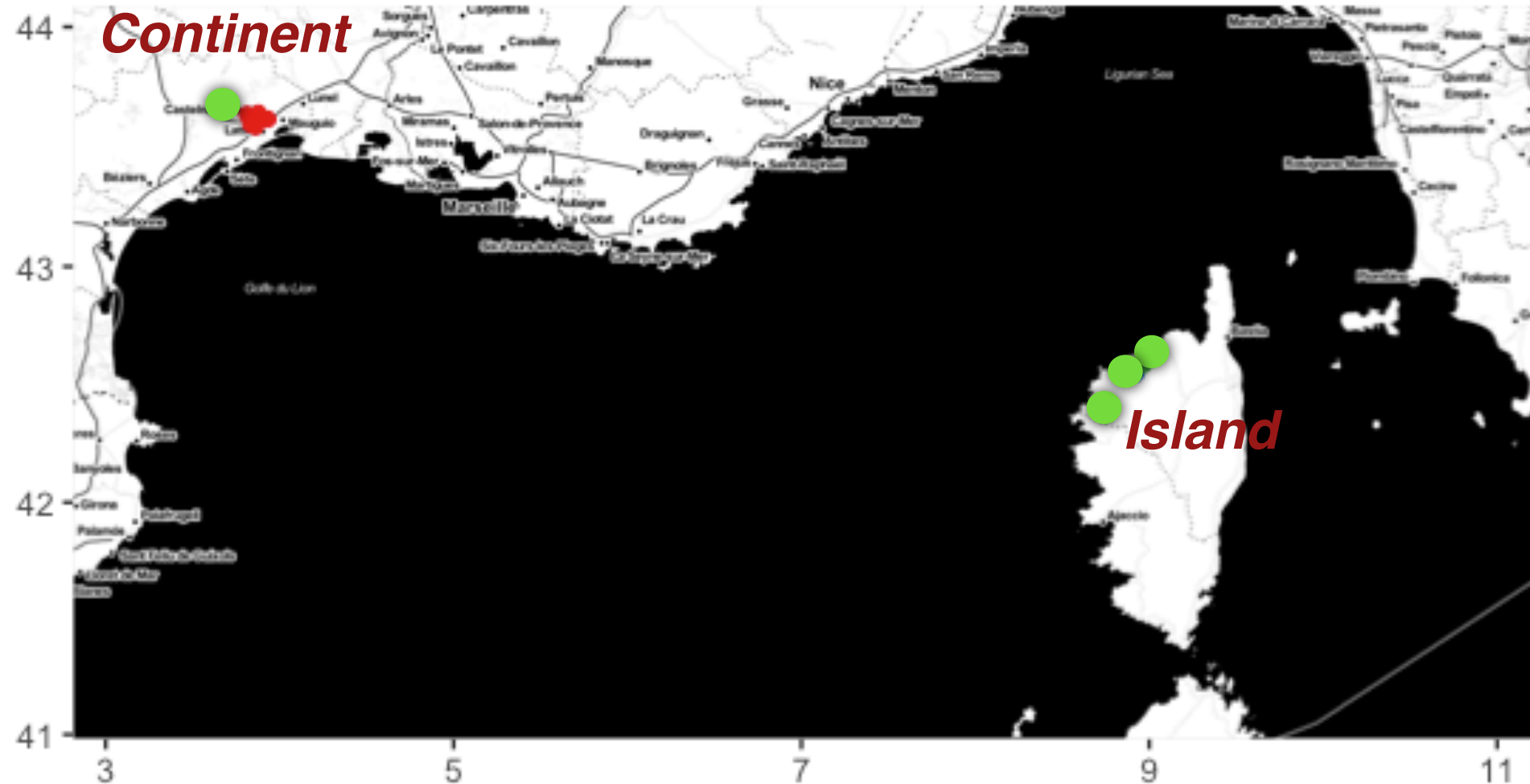
The blue tit context

Divergence at two spatial scales

Deciduous



Evergreen



The blue tit context

Divergence at two spatial scales

Deciduous



Evergreen



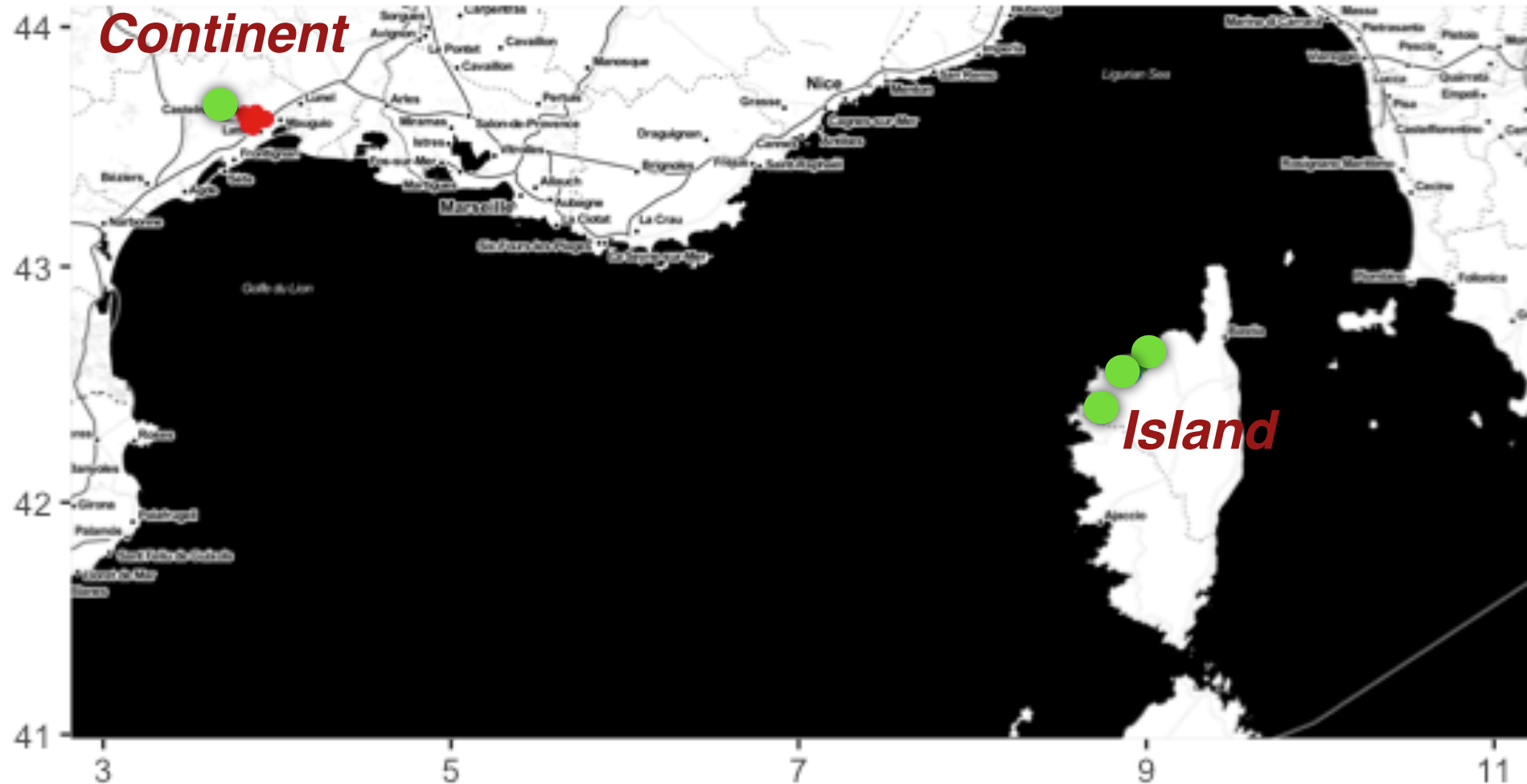
REVIEW AND SYNTHESSES

Mediterranean blue tits as a case study of local adaptation

Anne Charmantier,¹ Claire Doutrelant,¹ Gabrielle Dubuc-Messier,^{1,2} Amélie Fargevieille¹ and Marta Szulkin¹

¹ Centre d'Ecologie Fonctionnelle et Evolutive, Campus CNRS, Montpellier, France

² Département des sciences biologiques, Université du Québec à Montréal, Succursale centre-ville, QC, Canada



The blue tit context

Phenotypic divergence

Phenology

Morphology

+ Comportement, couleur ...

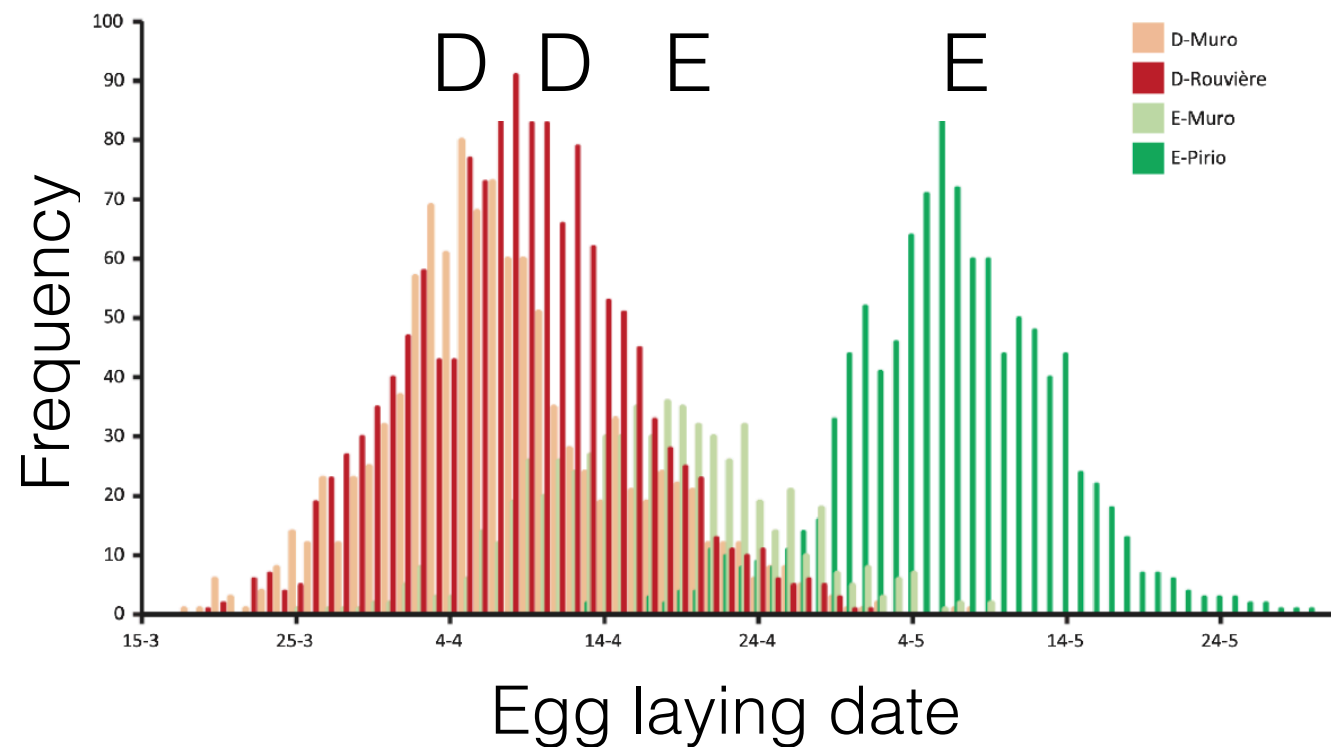
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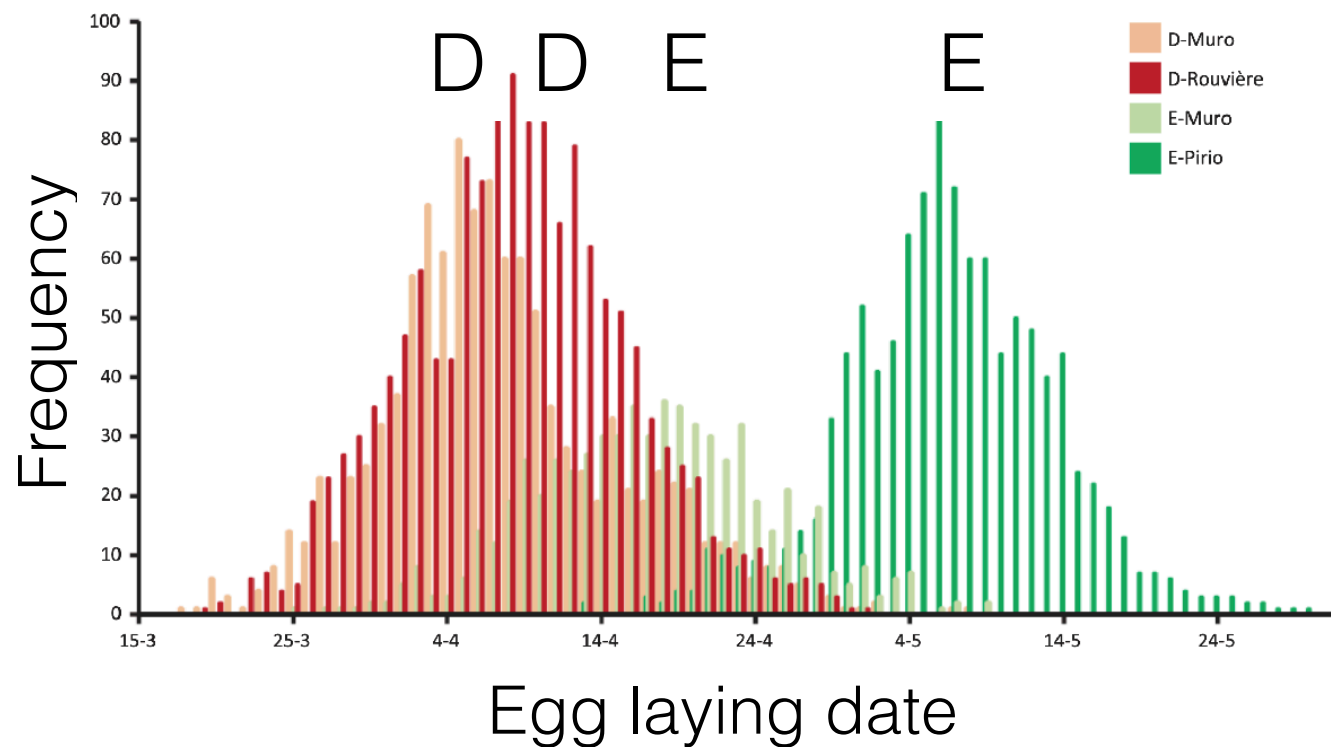


Phenological differences in blue tits coincide with phenological differences in caterpillar and oaks

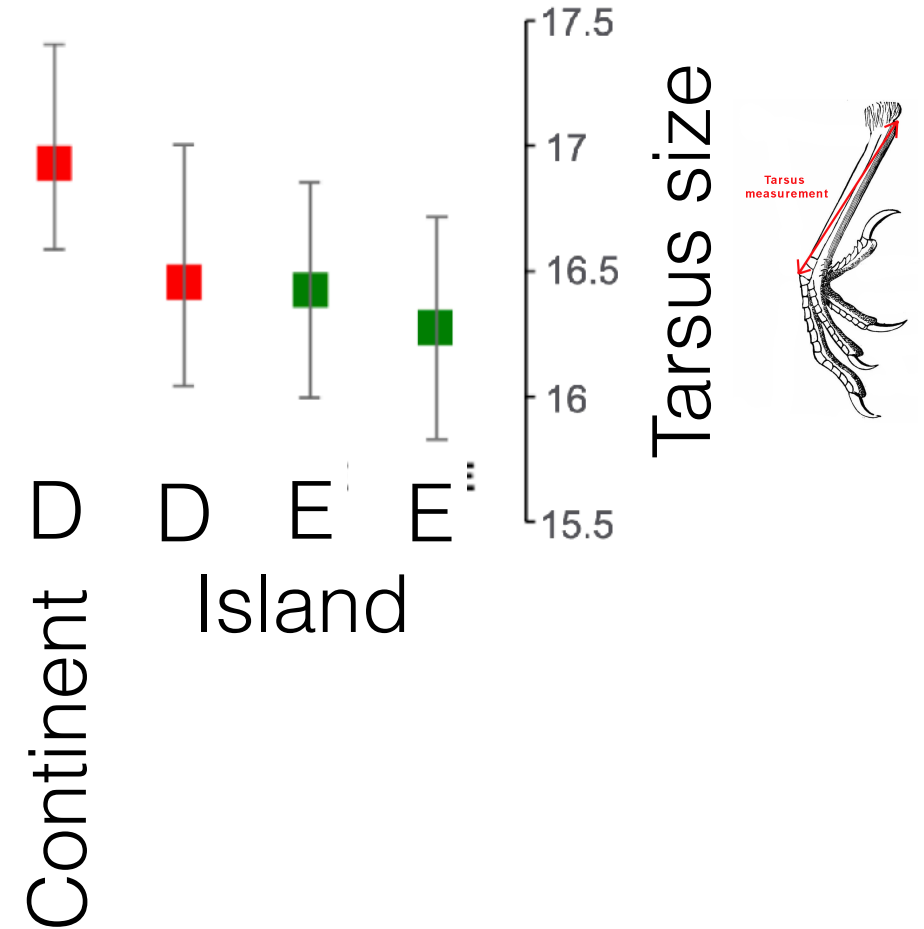
The blue tit context

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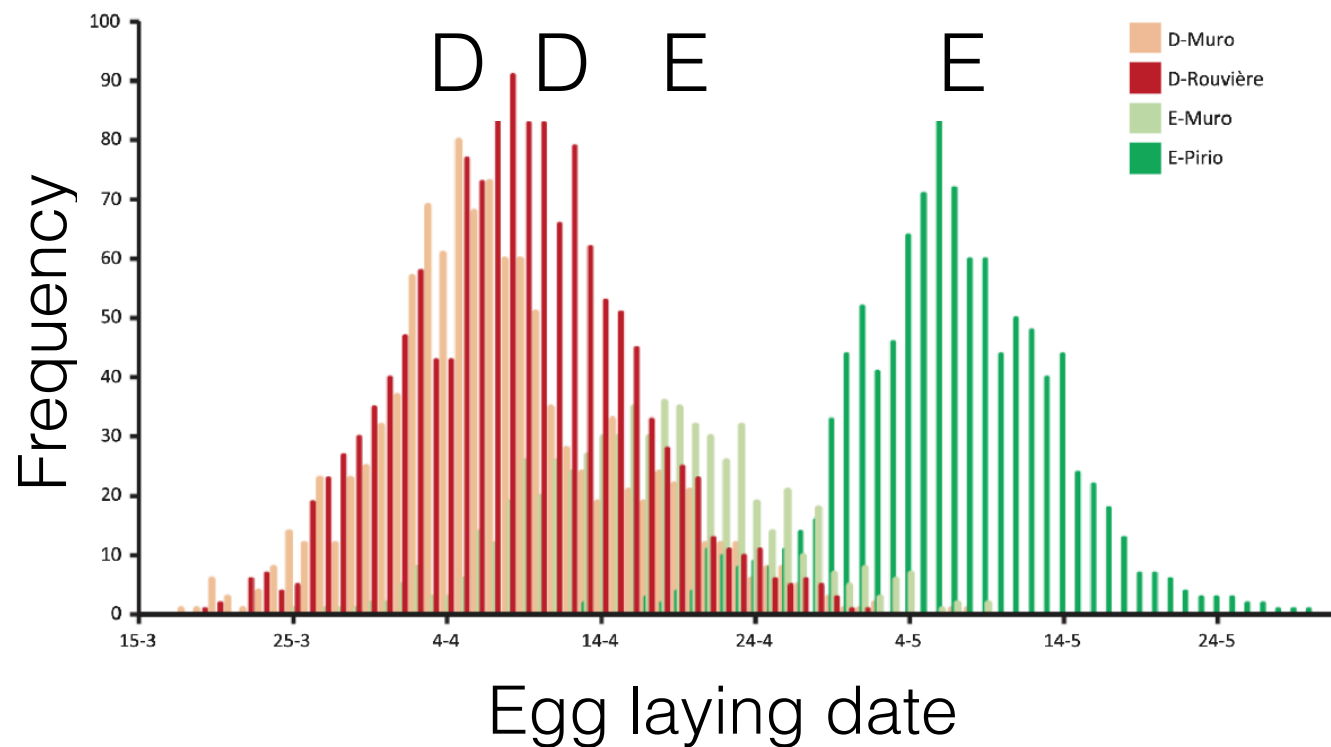
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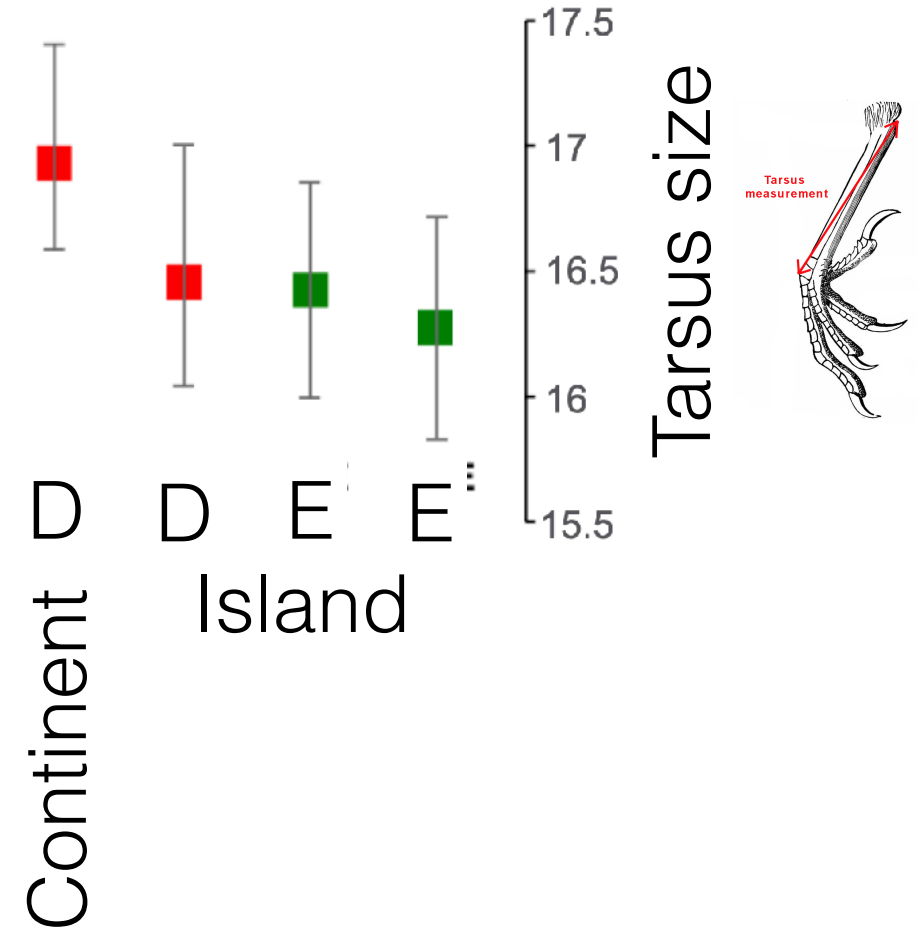
The blue tit context

Phenotypic divergence

Phenology
Morphology
+ Comportement, couleur ...



Phenological differences in blue tits coincide with phenological differences in caterpillar and oaks



Traits' heritability

tarsus length: 0.42–0.60
body mass: 0.27–0.64
wing length: 0.22–0.32
laying date: 0.20–0.43

The blue tit context

What are the genomic bases and the evolutionary mechanisms responsible of the these heritable and potentially adaptative phenotypic differences?

The blue tit context

What are the genomic bases and the evolutionary mechanisms responsible of these heritable and potentially adaptive phenotypic differences?

Demographic scenario & parameters

Scenario of divergence between populations?
Historical & contemporary N_e , m ?

Quantitative genomics

Traits' heritability?
Genomic architecture of traits variations?

Population genomics

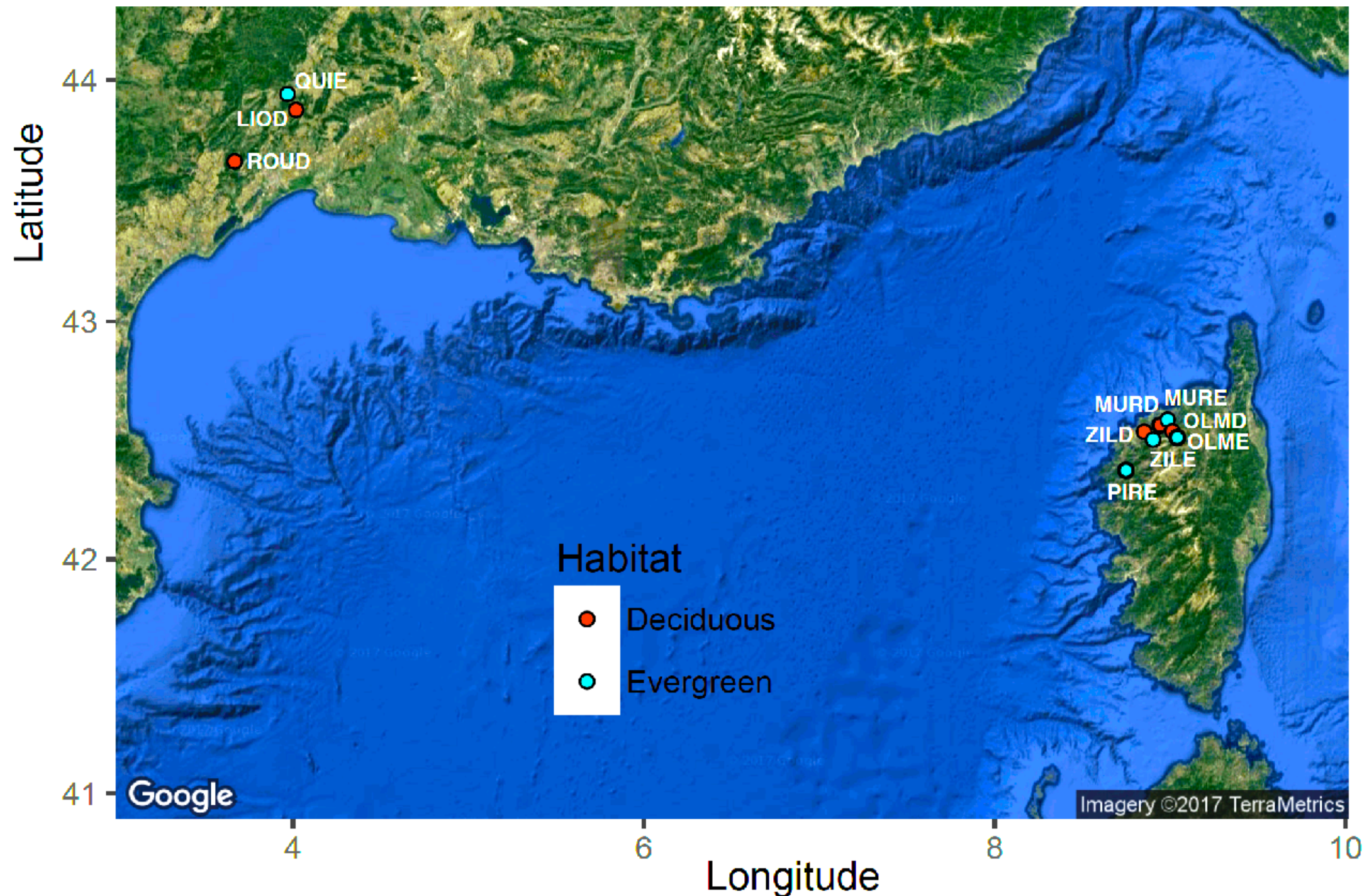
Genomic footprints of divergent selection?
Relatively to local recombination rate and inversions?

The blue tit context

Sampling

4 + 6 populations

In order to increase the coverage of the environmental mosaic



The blue tit context

Sampling

At the nest or using nets

Blood sample

1250 individuals sequenced



Sequencing

RAD-Sequencing



Sbfl enzyme



MGX Montpellier



Stacks

Read mapping on
great tit genome

93% reads mapped

50k to 145k filtered

454 to 947 individuals filtered

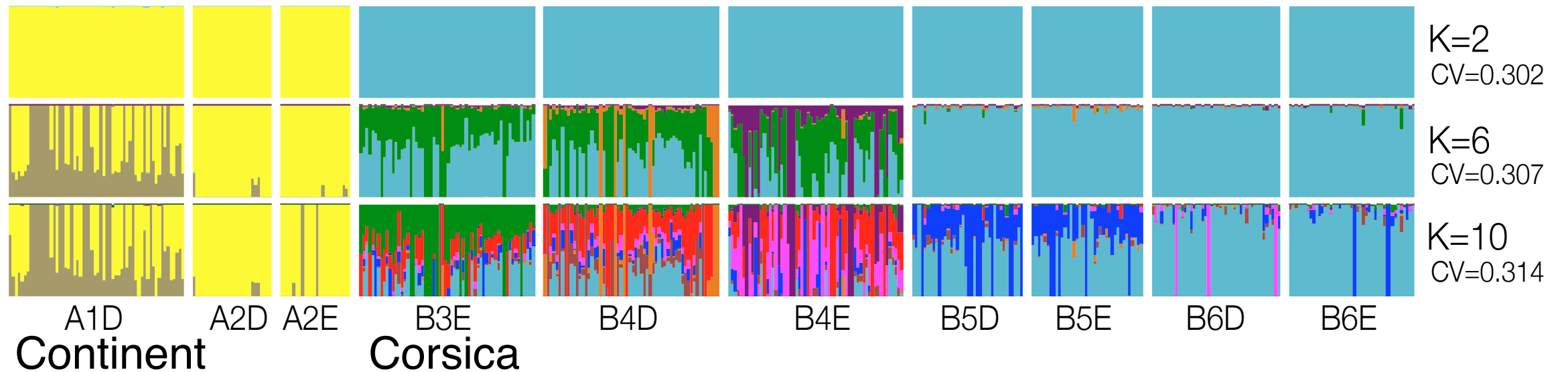
49.2x as median read depth

0.98 as median genotyping rate

Population structure

Population structure

Admixture



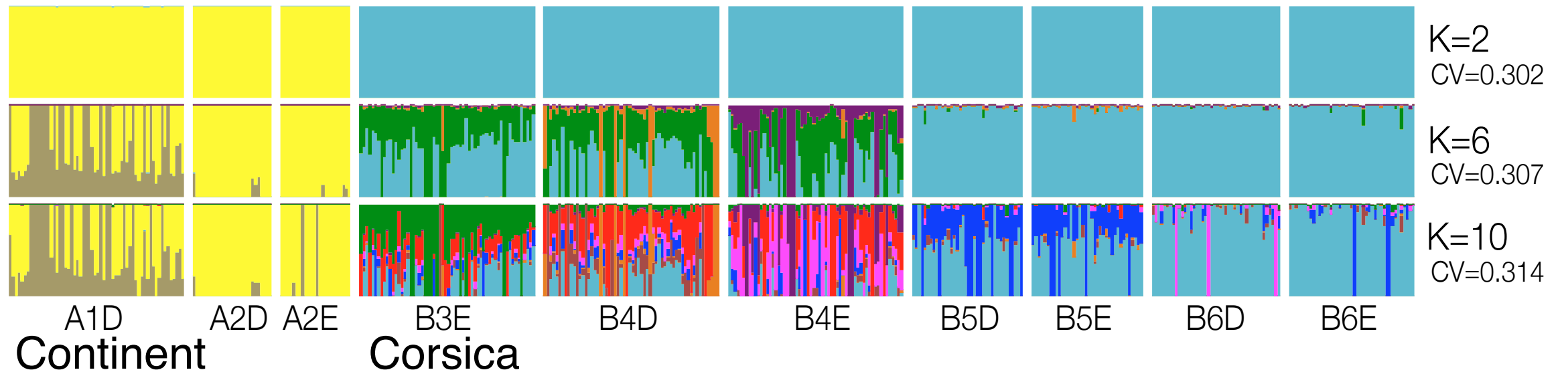
Large structure
between Corsica
and the continent,

Very little structure
between adjacent
populations

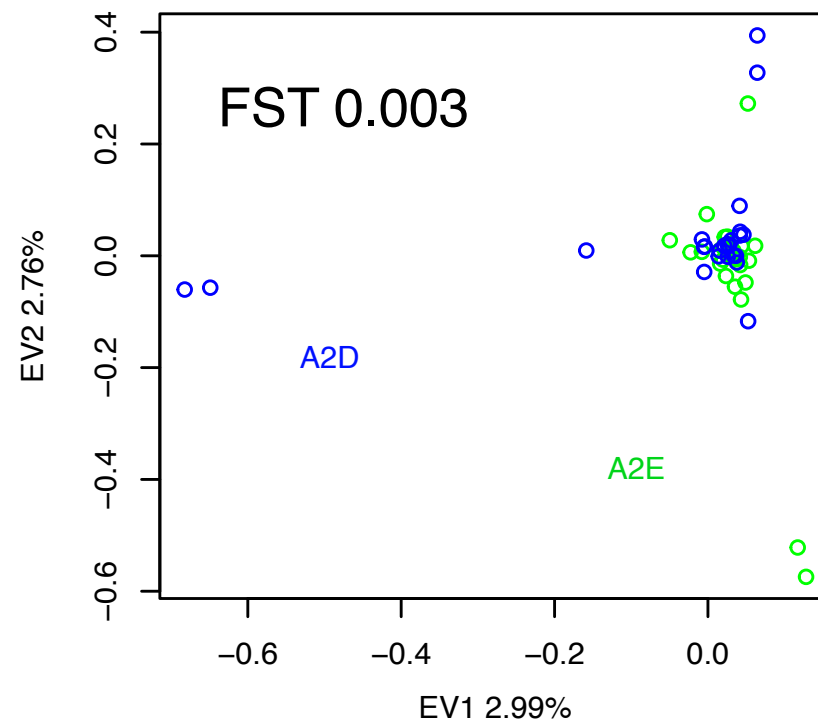
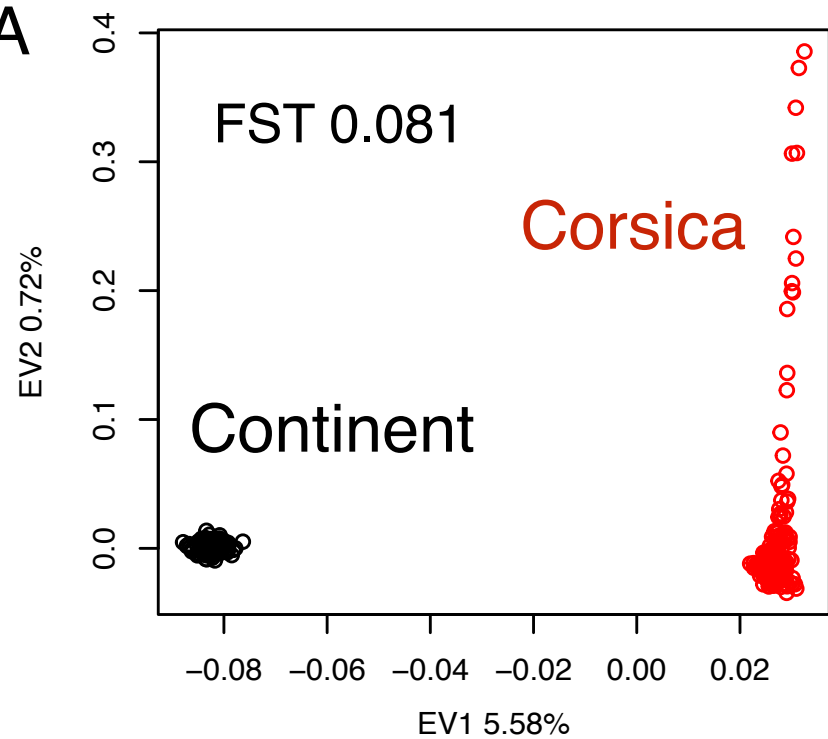
Population structure

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Admixture



PCA



Large structure between Corsica and the continent,
Very little structure between adjacent populations

Demographic analyses

Demographic history and parameters at the two spatial scales:

- i) Between each neighboring population pairs
- ii) Between Corsica Island and Continent

Demographic analyses

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ABC framework

Model choice

equilibrium

secondary contact

divergence with ancestral migration

panmixia

isolation with migration

strict isolation

& parameters estimations
for the best models



Quentin Rougemont

Demographic analyses

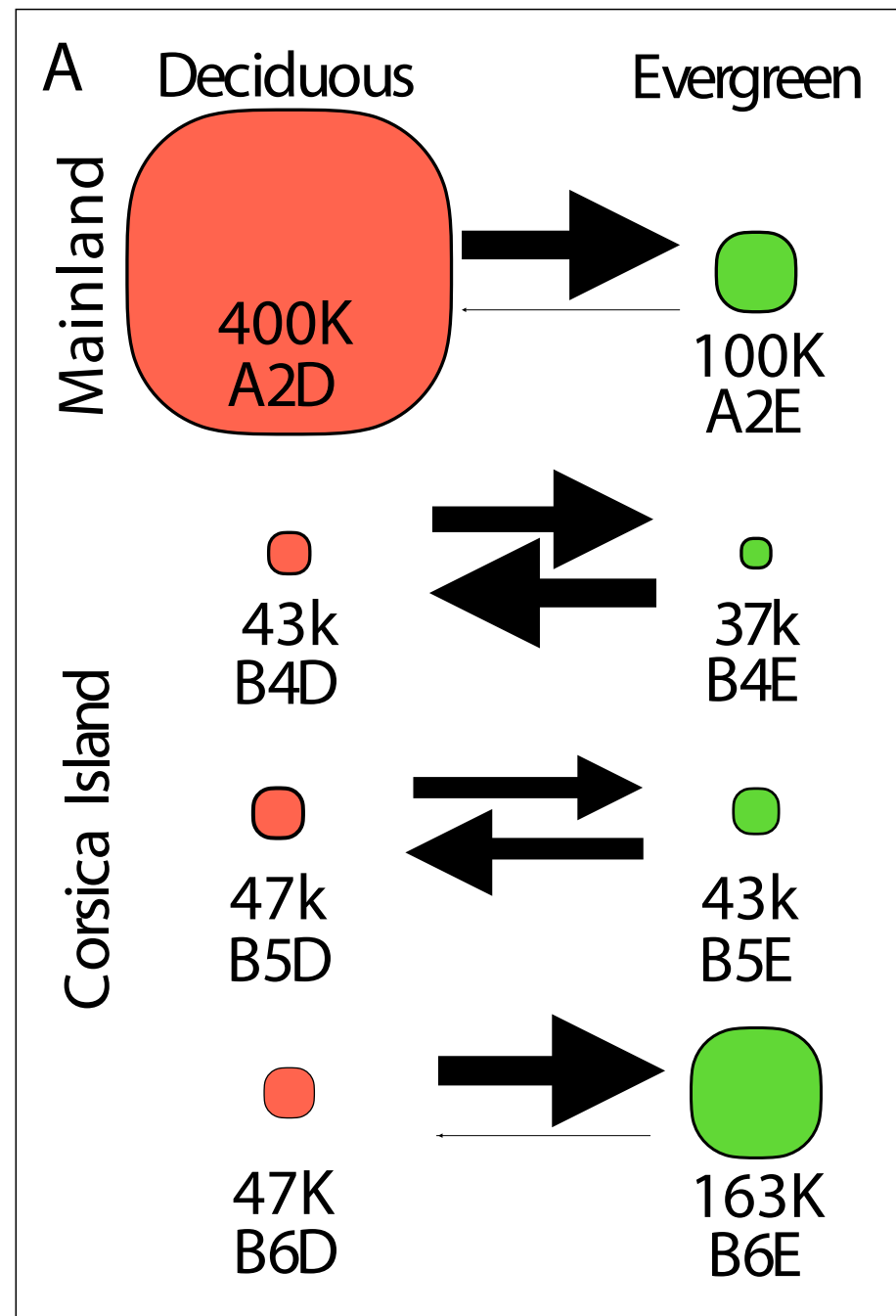
i) Between each neighboring population pairs

$P(\text{isolation with migration}) = 0,74$

$P(\text{equilibrium}) = 0.94$

$P(\text{equilibrium}) = 0.95$

$P(\text{equilibrium}) = 0.99$



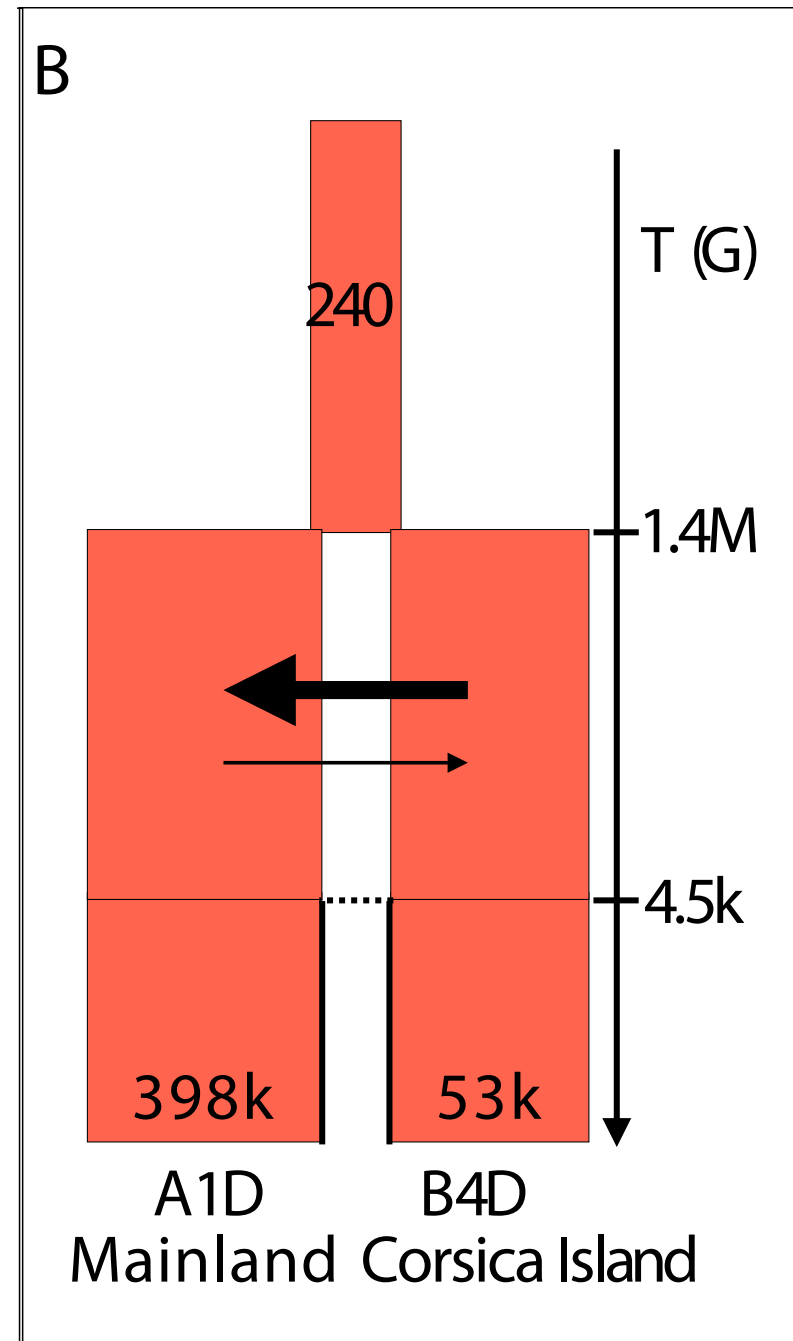
-> Constant gene flow between 'populations'

-> Will likely limit adaptation and large effect genes

Demographic analyses

ii) Between Corsica Island and Continent

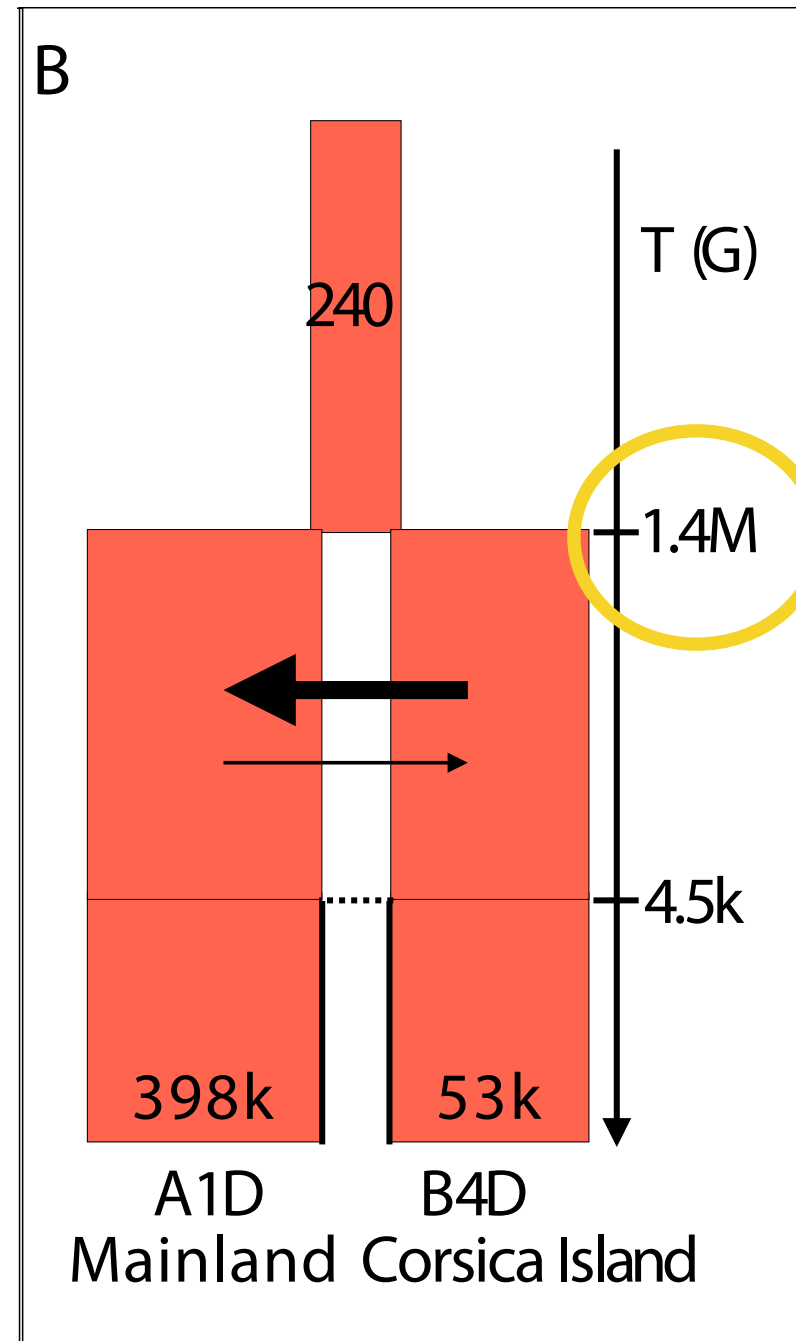
$P(\text{ancient migration}) = 0,99$



Demographic analyses

ii) Between Corsica Island and Continent

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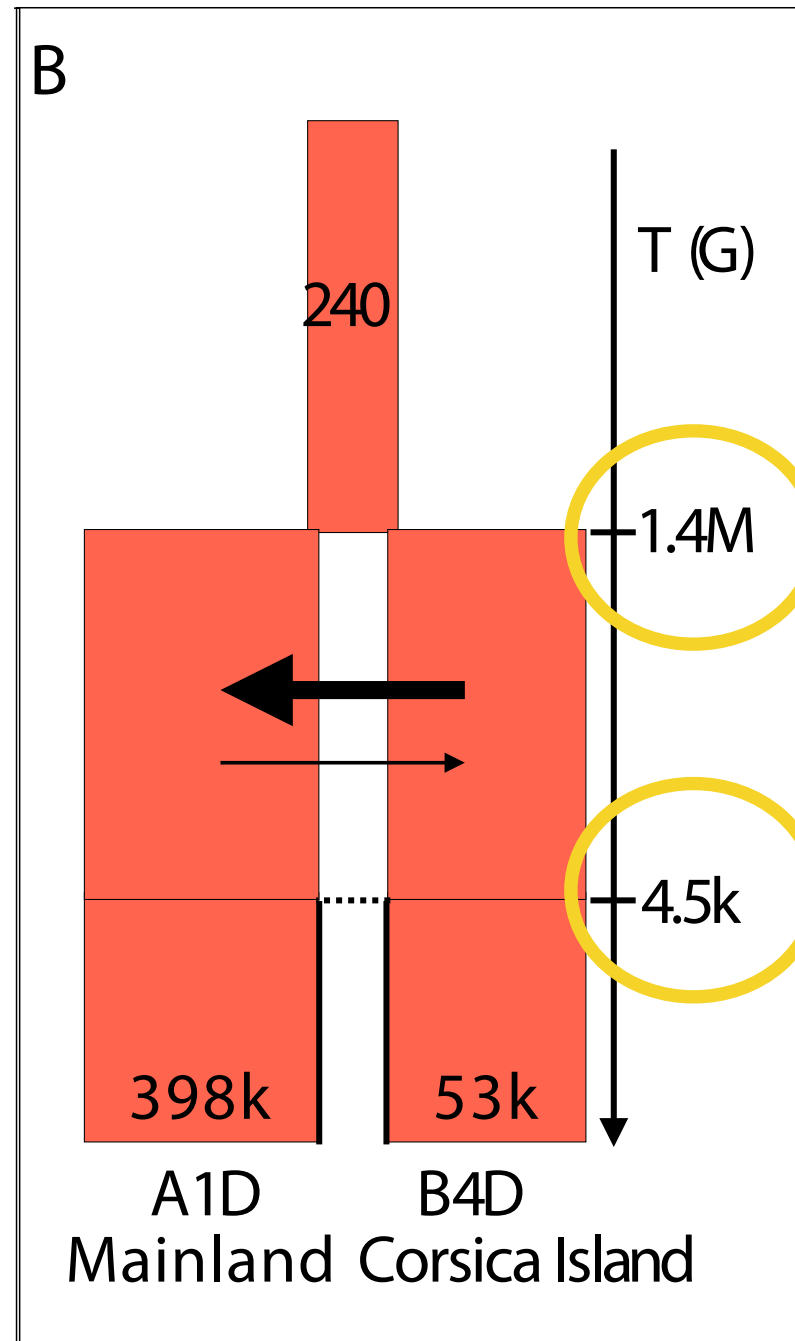


-> Coherent with the history of diversification of the blue tits complex

Demographic analyses

ii) Between Corsica Island and Continent

$P(\text{ancient migration}) = 0,99$



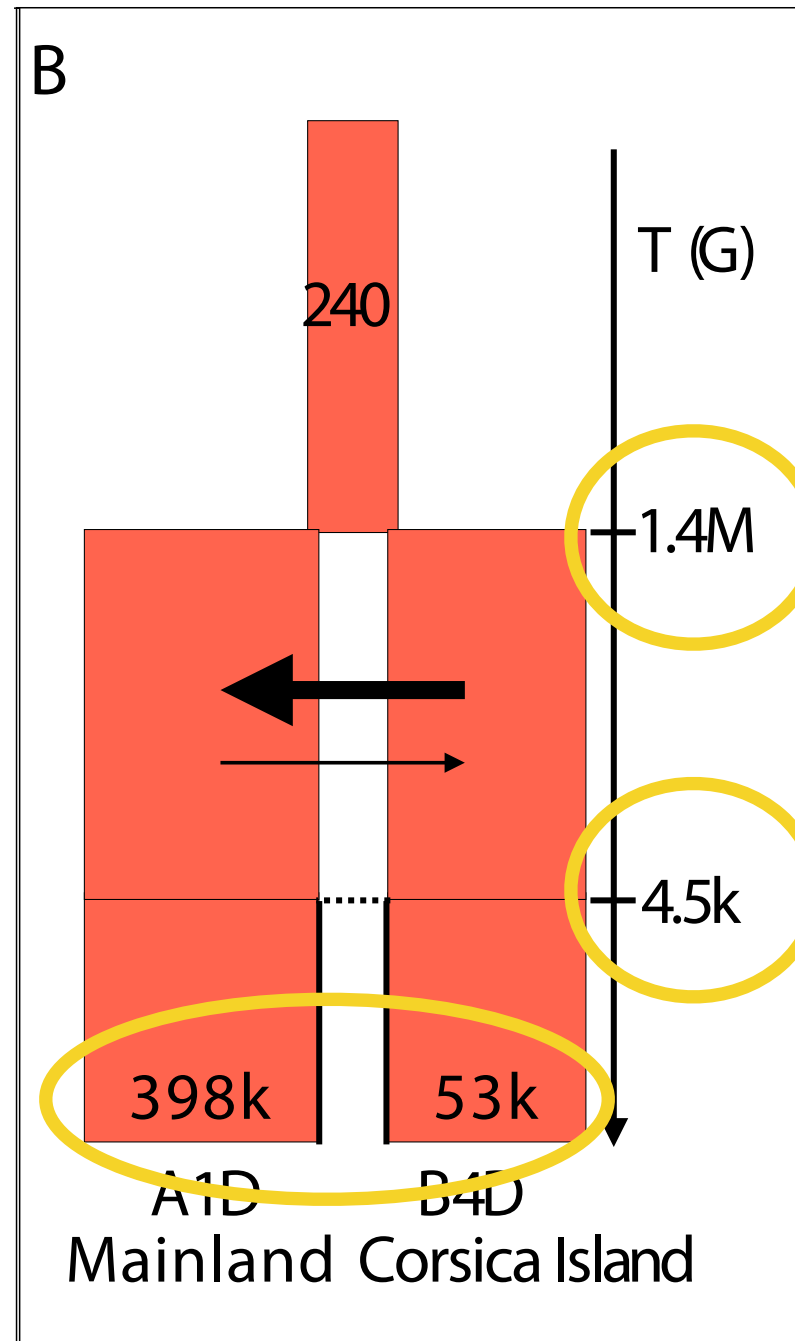
-> Coherent with the history of diversification of the blue tits complex

-> Coherent with the end of last glaciation and rise of sea level between continent and Corsica, precluding gene flow

Demographic analyses

ii) Between Corsica Island and Continent

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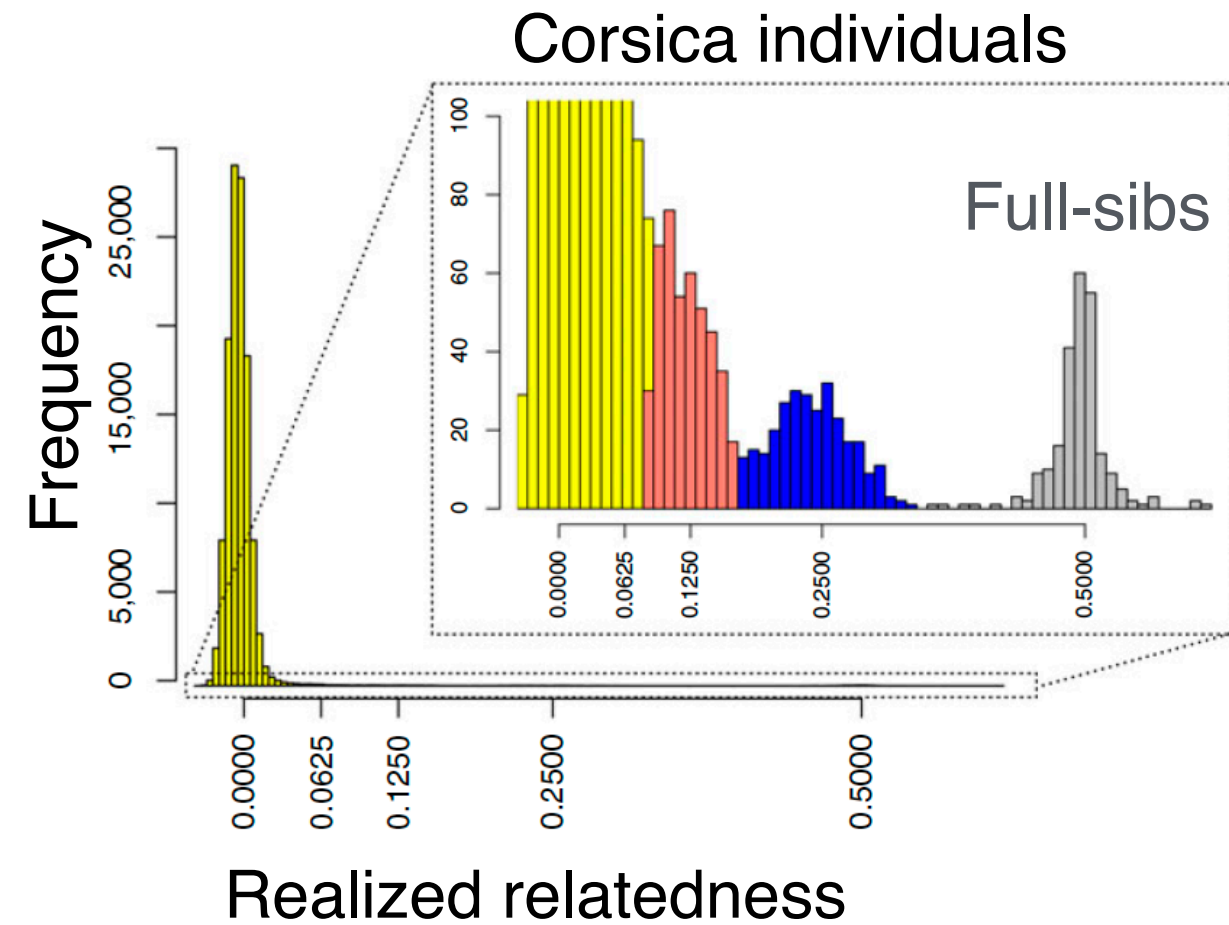
-> Large N_e , coherent with low differentiation (0.08) between both groups

-> Coherent with the history of diversification of the blue tits complex

-> Coherent with the end of last glaciation and rise of sea level between continent and Corsica, precluding gene flow

Quantitative genomic analyses

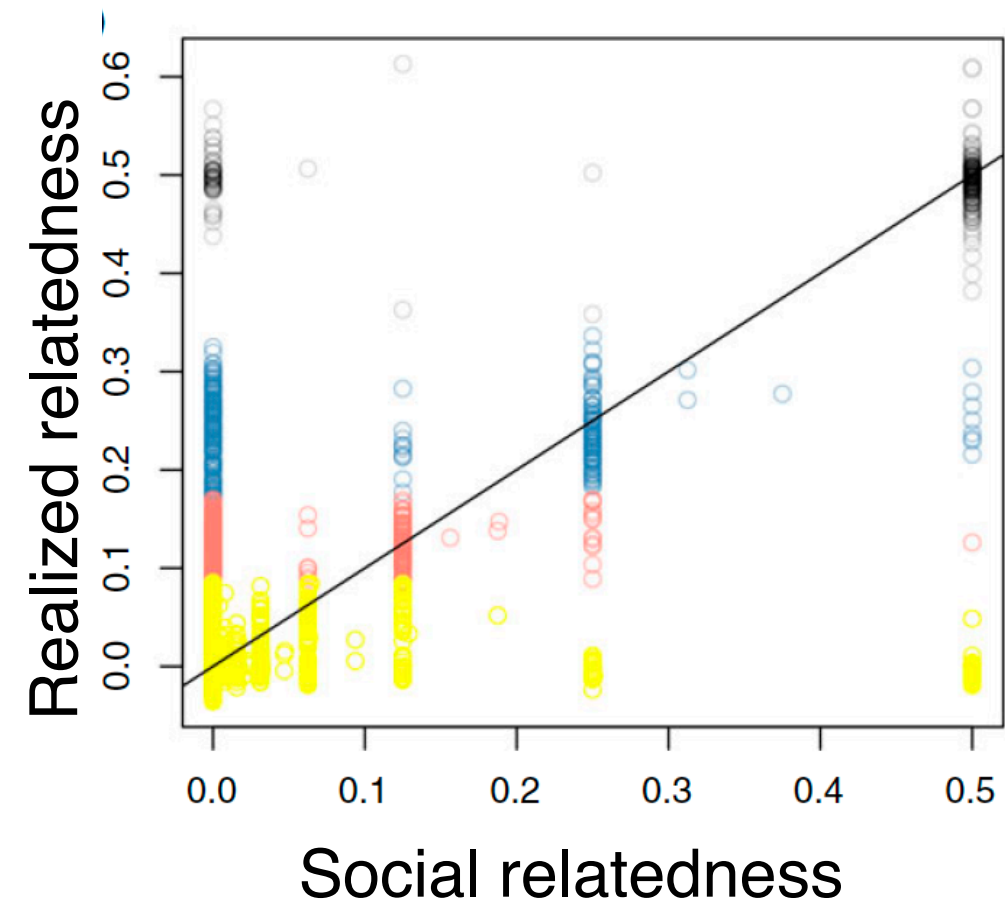
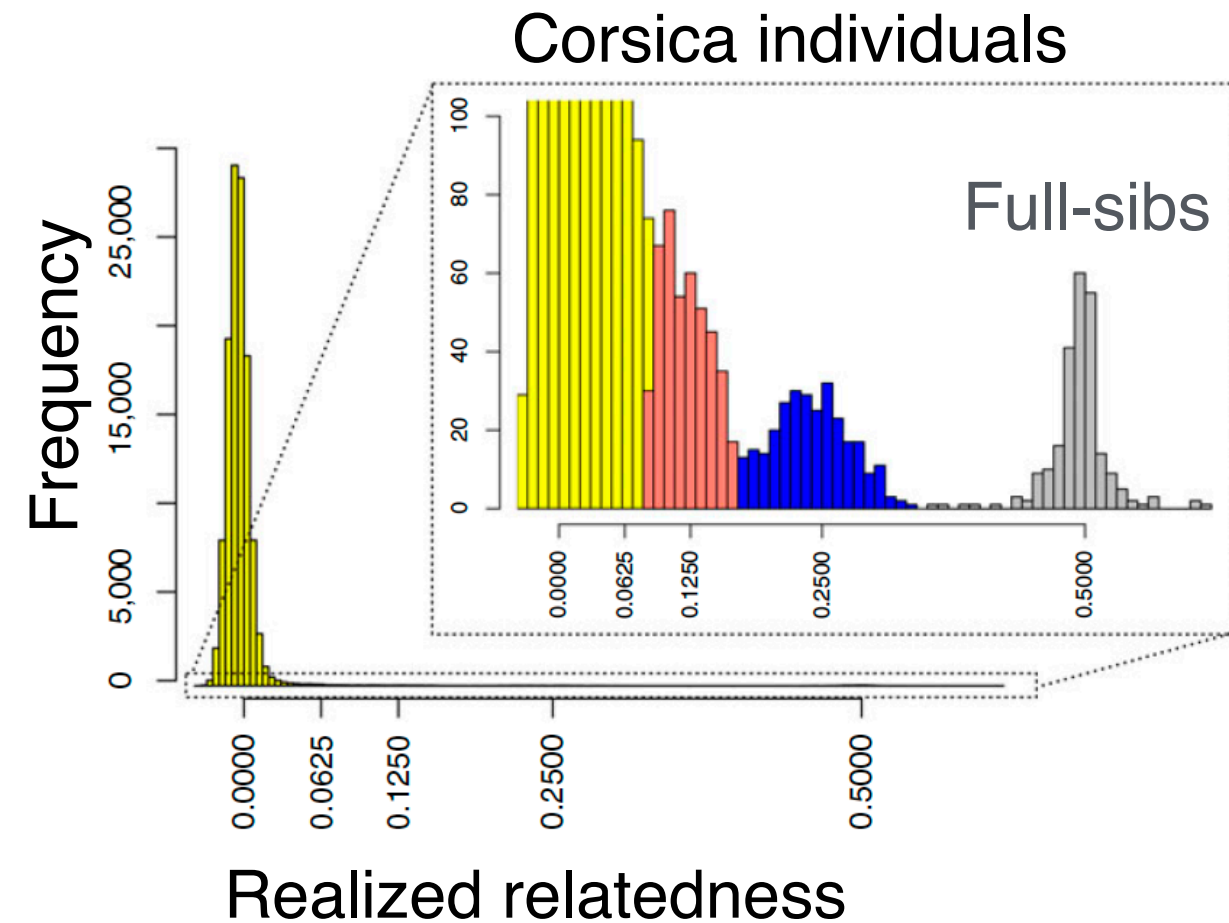
Measuring relatedness among individuals



-> Precise estimate of relatedness

Quantitative genomic analyses

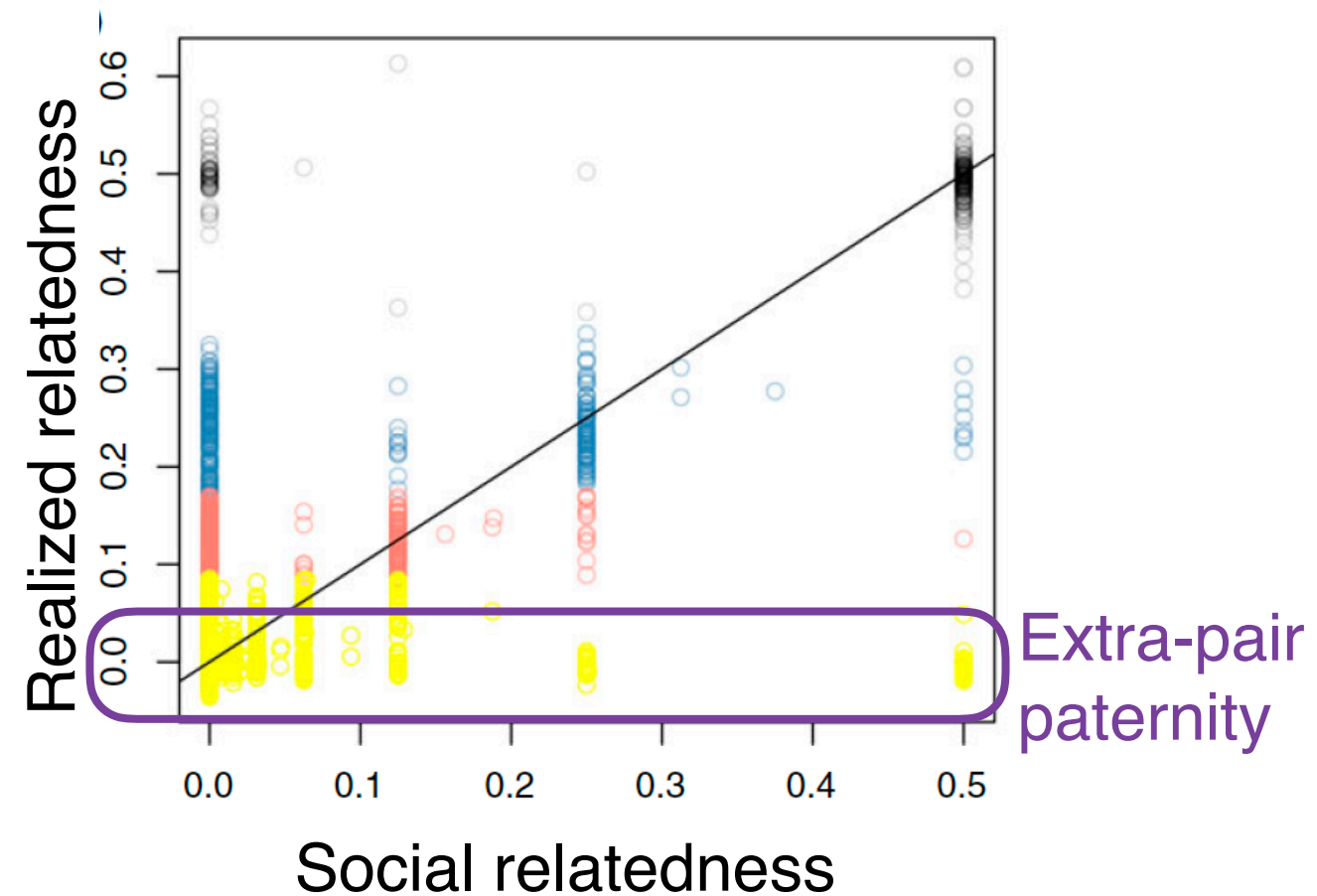
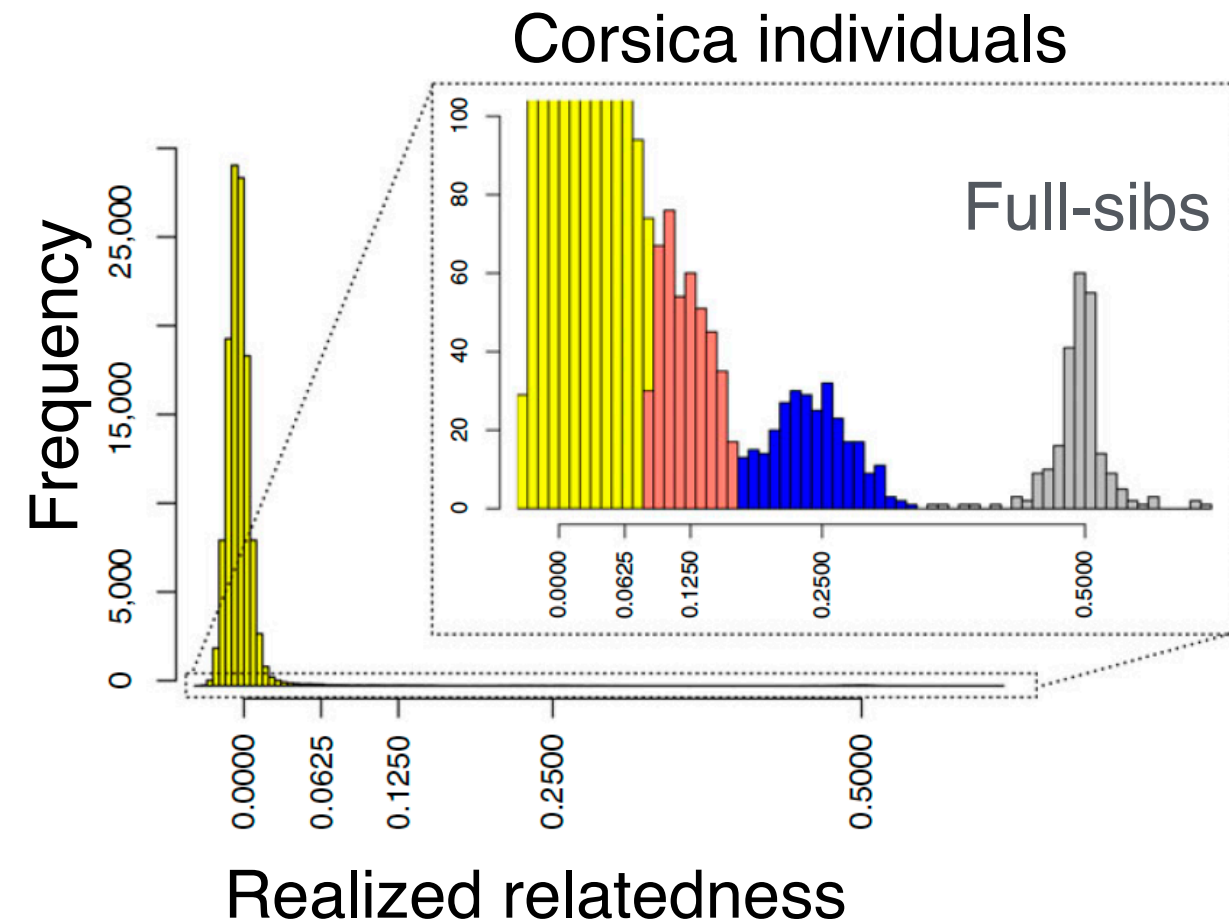
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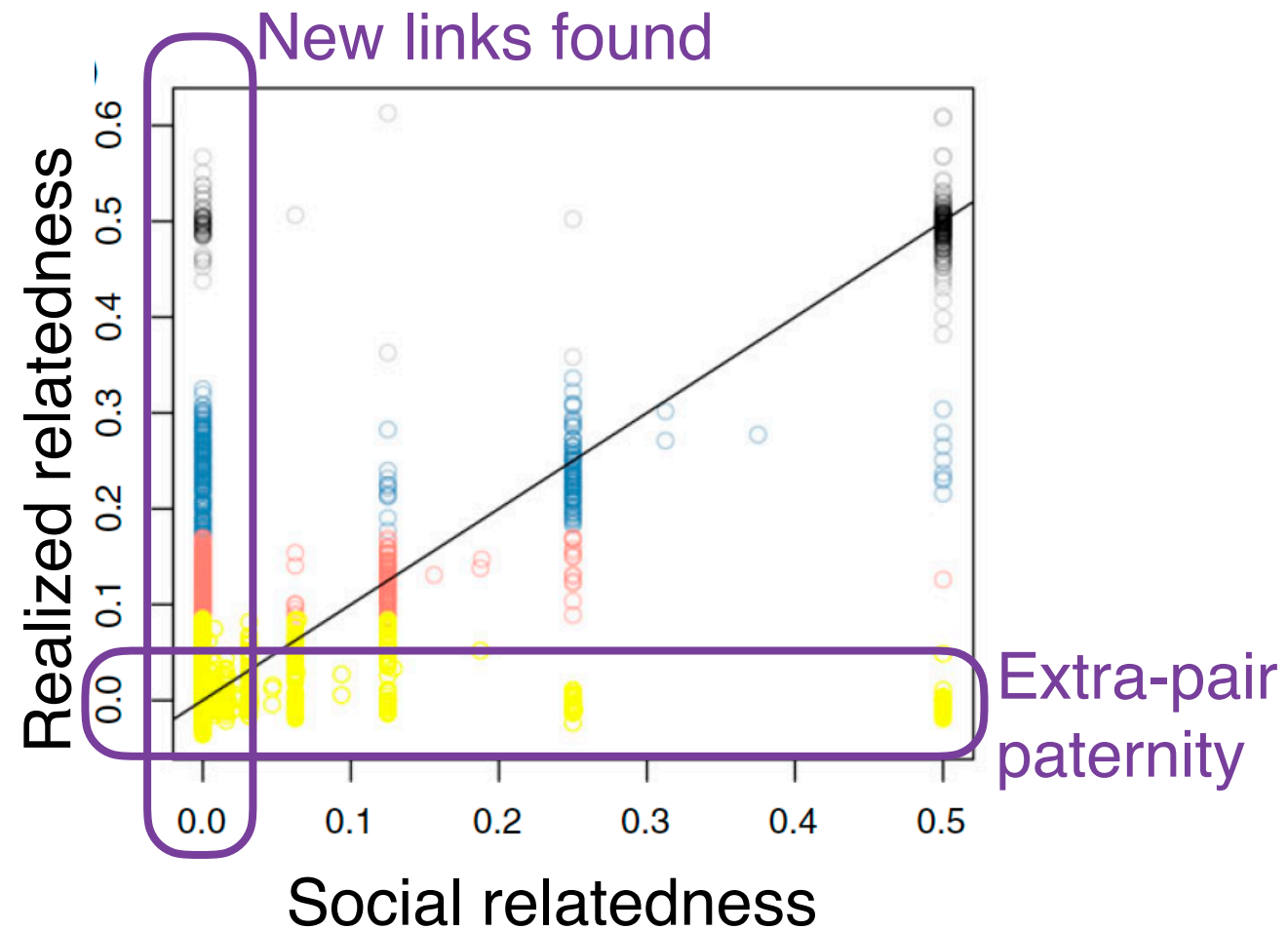
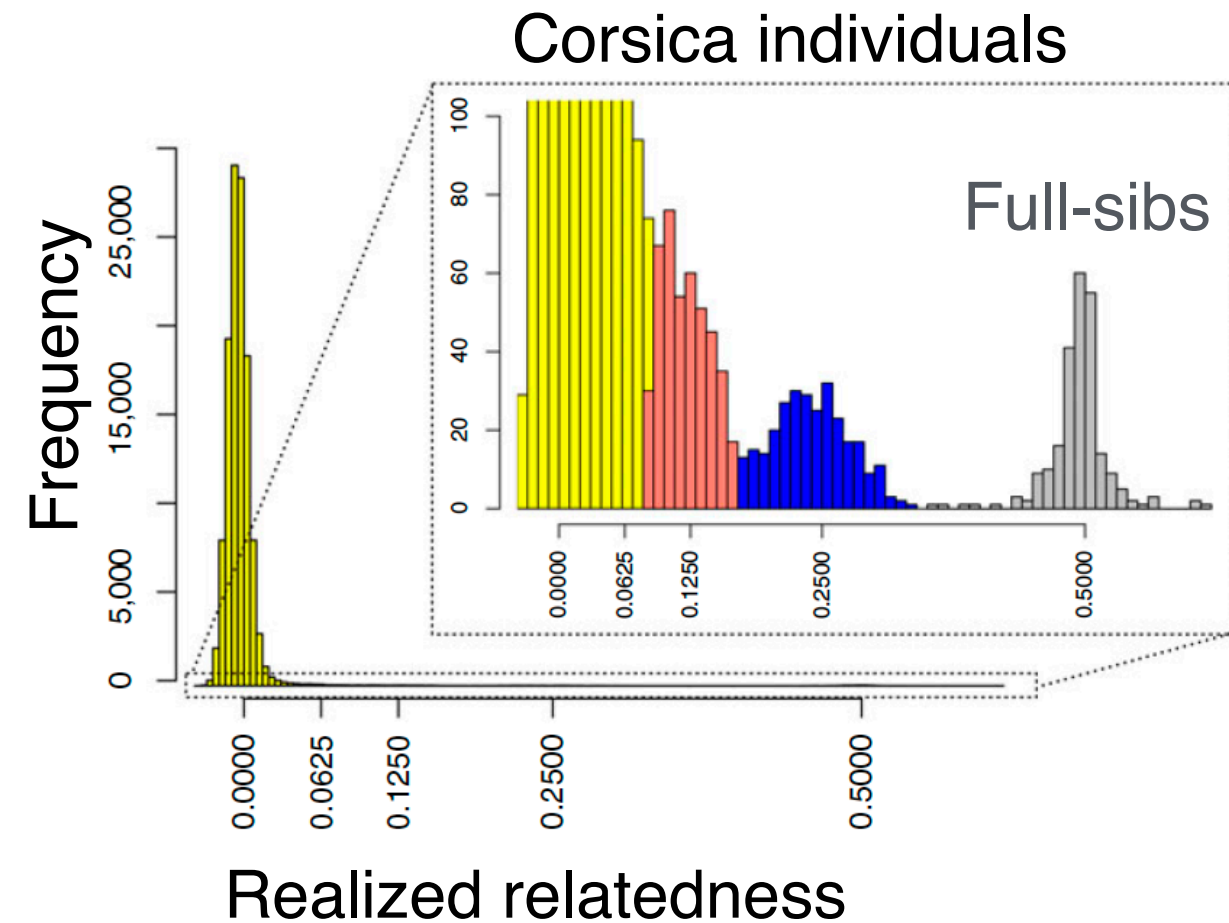


-> Precise estimate of relatedness

-> Extra-pair paternities solved
(as well as their propagation in
the pedigree)

Quantitative genomic analyses

Measuring relatedness among individuals



-> Precise estimate of relatedness

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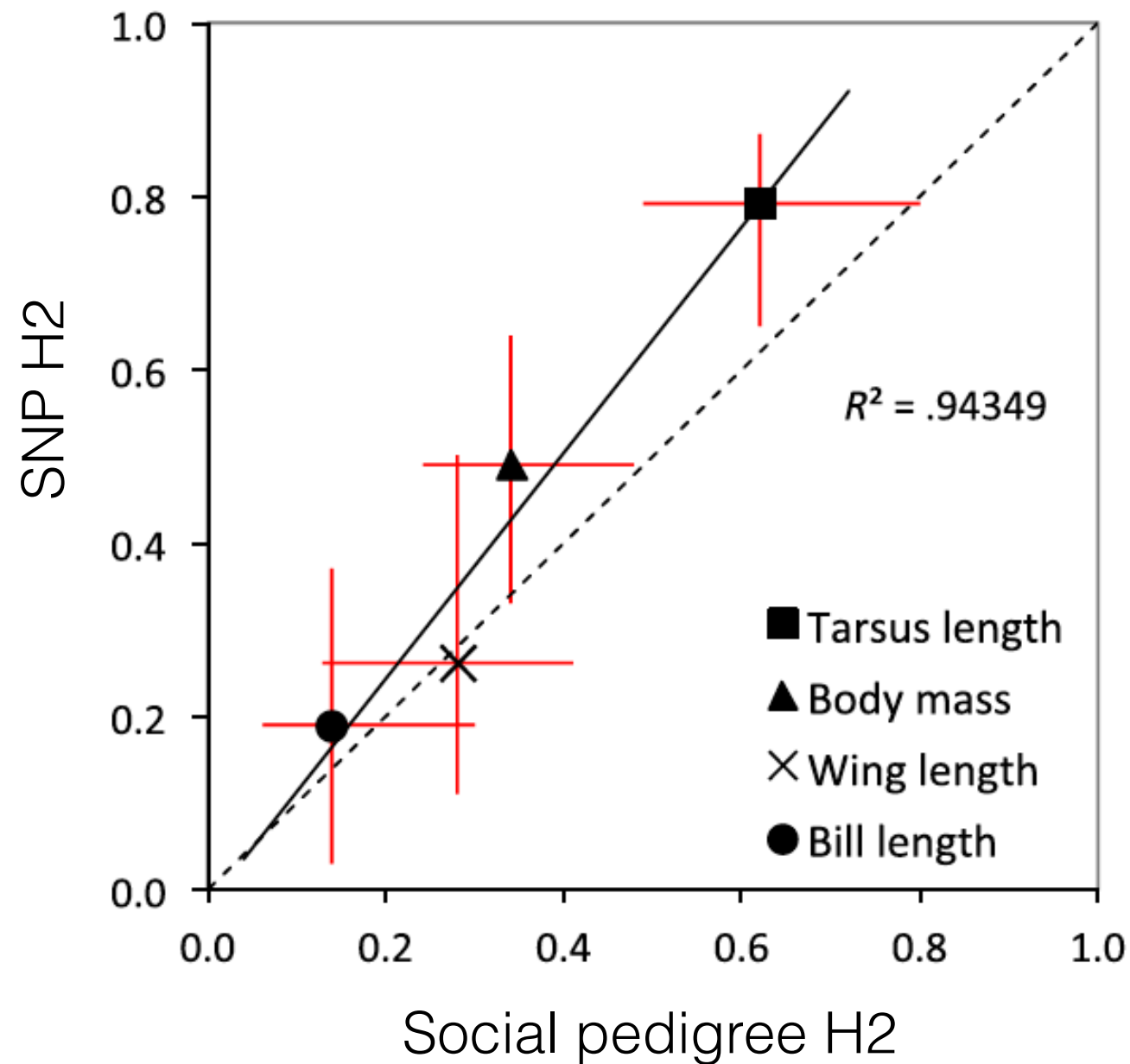
More links per individual

Quantitative genomic analyses

Heritability of phenotypic traits: SNP vs social

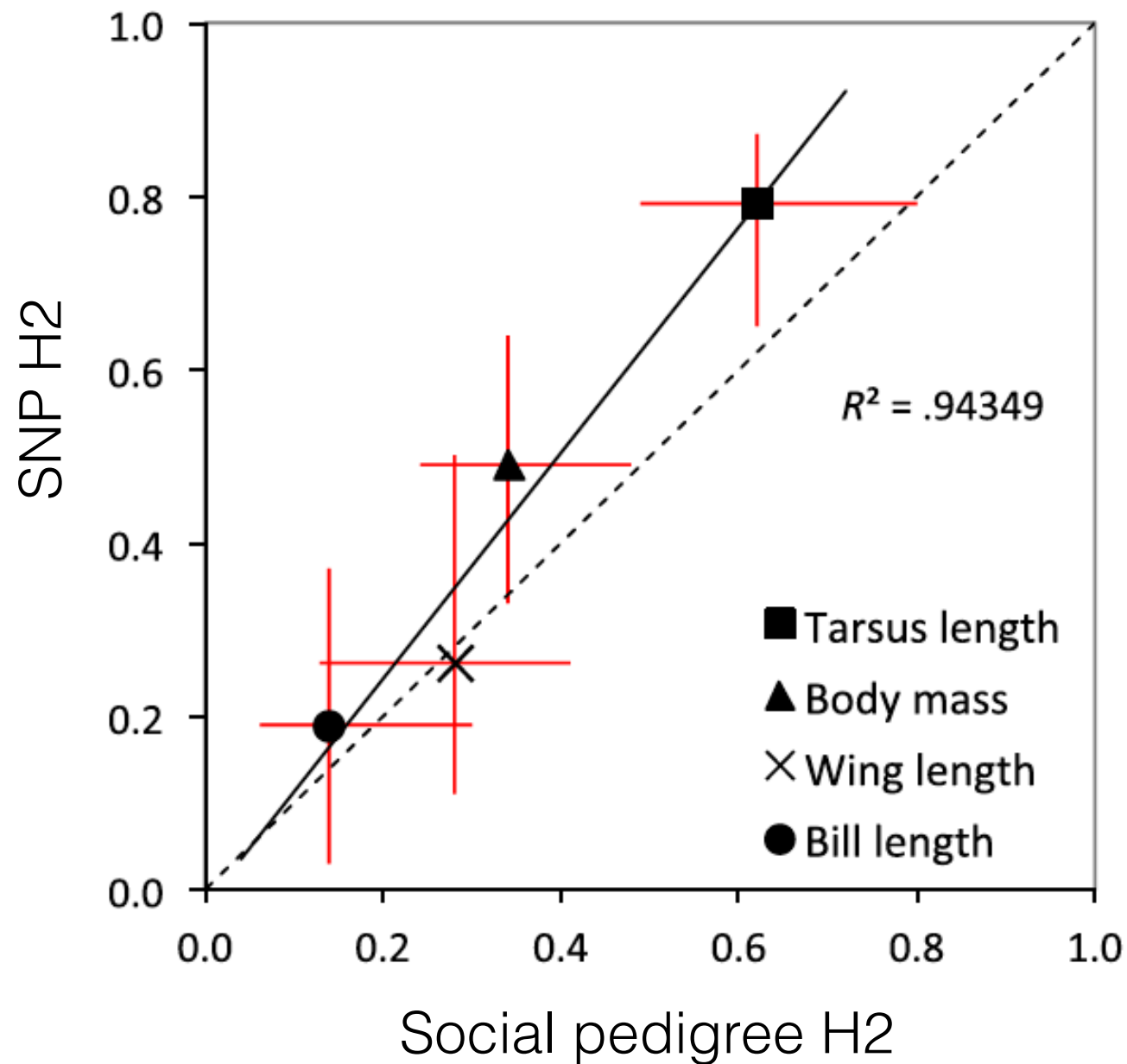
Quantitative genomic analyses

Heritability of phenotypic traits: SNP vs social



Quantitative genomic analyses

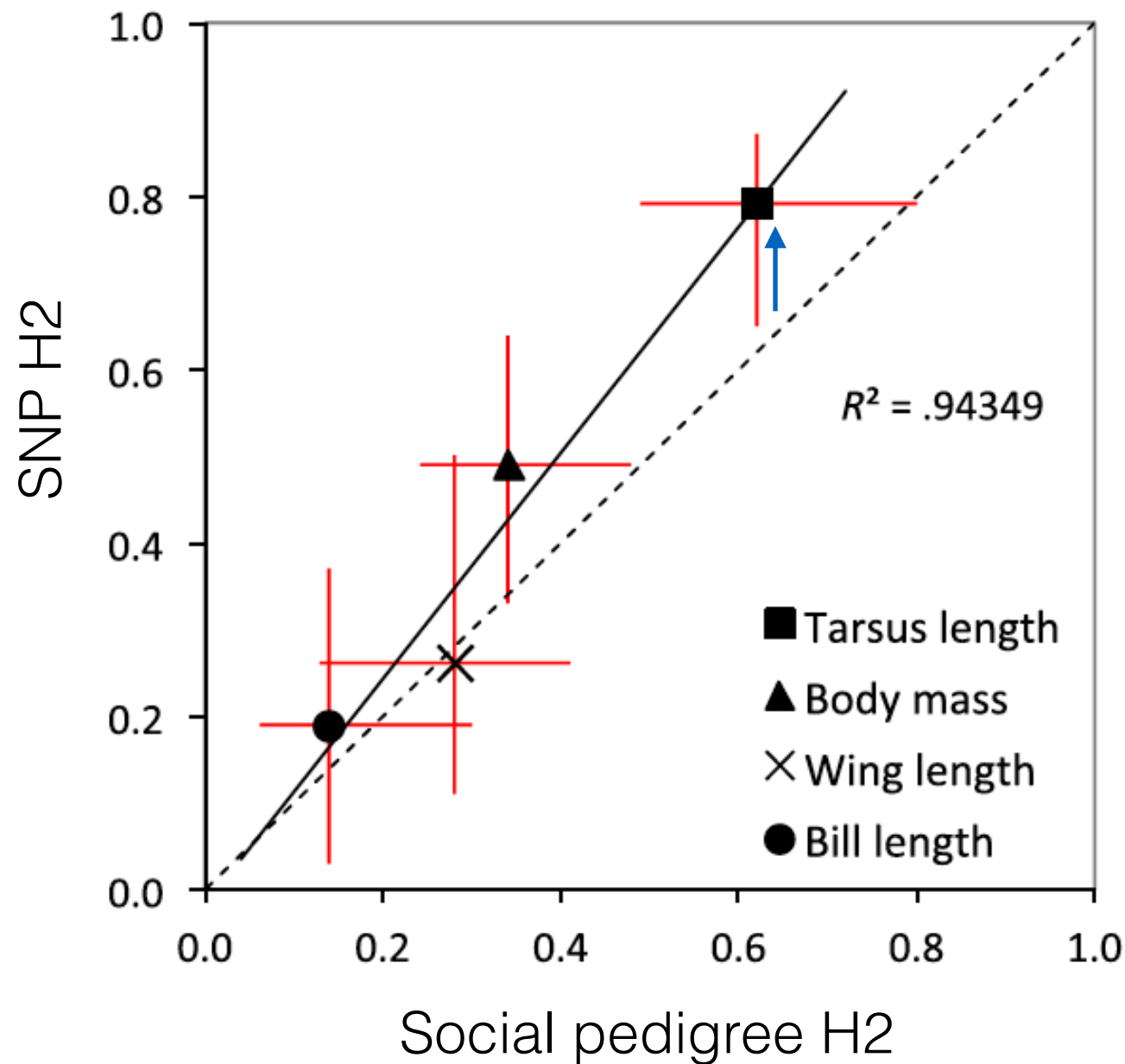
Heritability of phenotypic traits: SNP vs social



-> high correlation
between SNP and
social h2

Quantitative genomic analyses

Heritability of phenotypic traits: SNP vs social

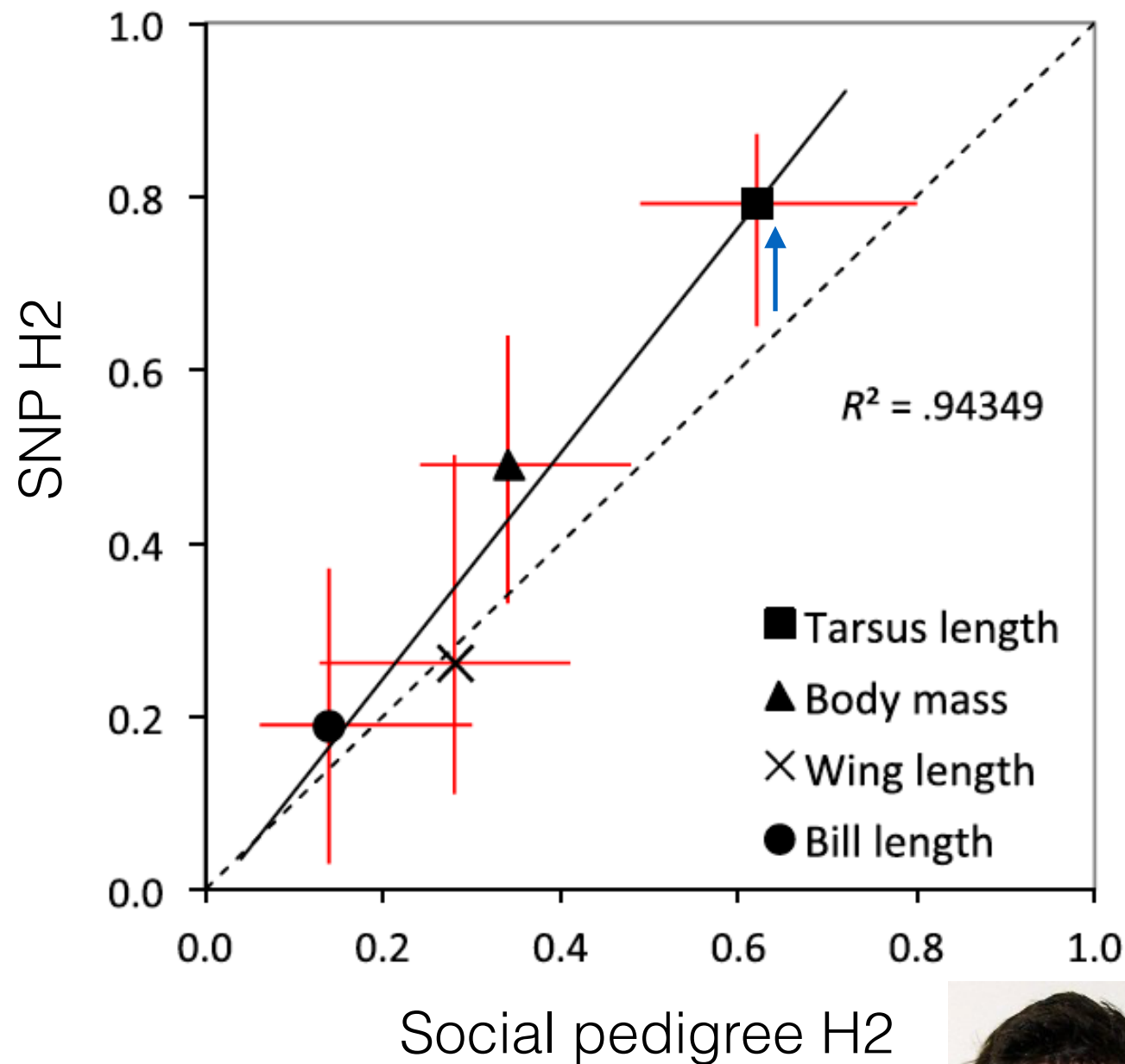


-> high correlation between SNP and social h2

-> higher h2 with the SNP than with the social pedigree
-corrected extra-pair
-no missing links

Quantitative genomic analyses

Heritability of phenotypic traits: SNP vs social



-> high correlation between SNP and social h2

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Boris Delahaie

Quantitative genomic analyses

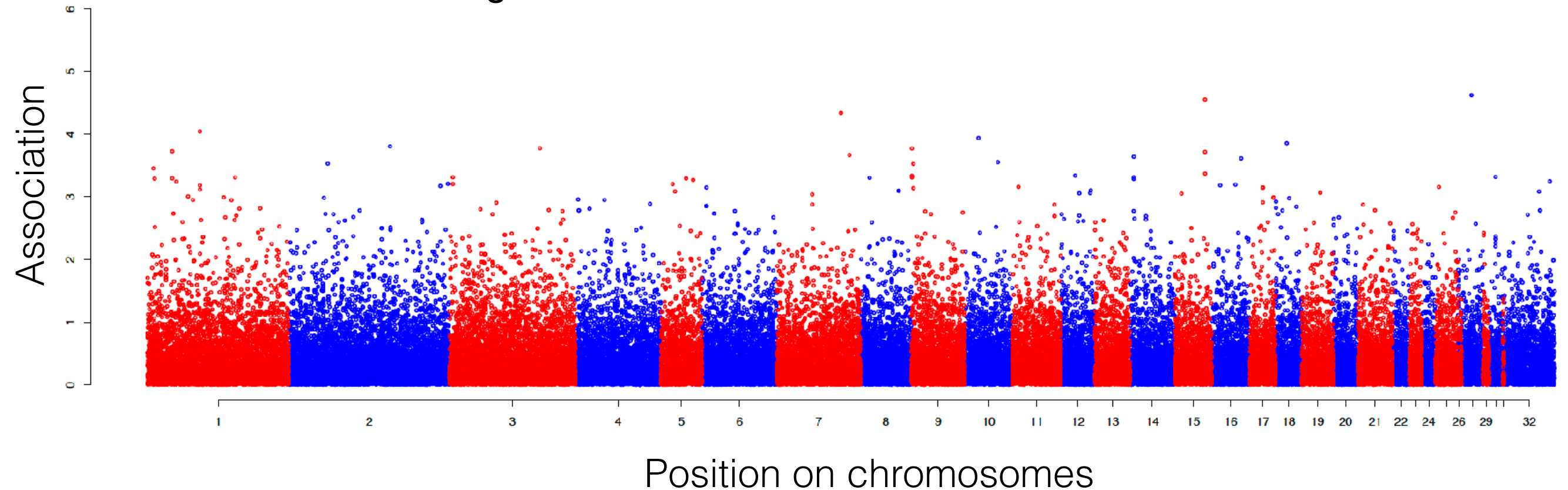
Large effect genes?

GWAS for tarsus length in Corsican birds

Quantitative genomic analyses

Large effect genes?

GWAS for tarsus length in Corsican birds



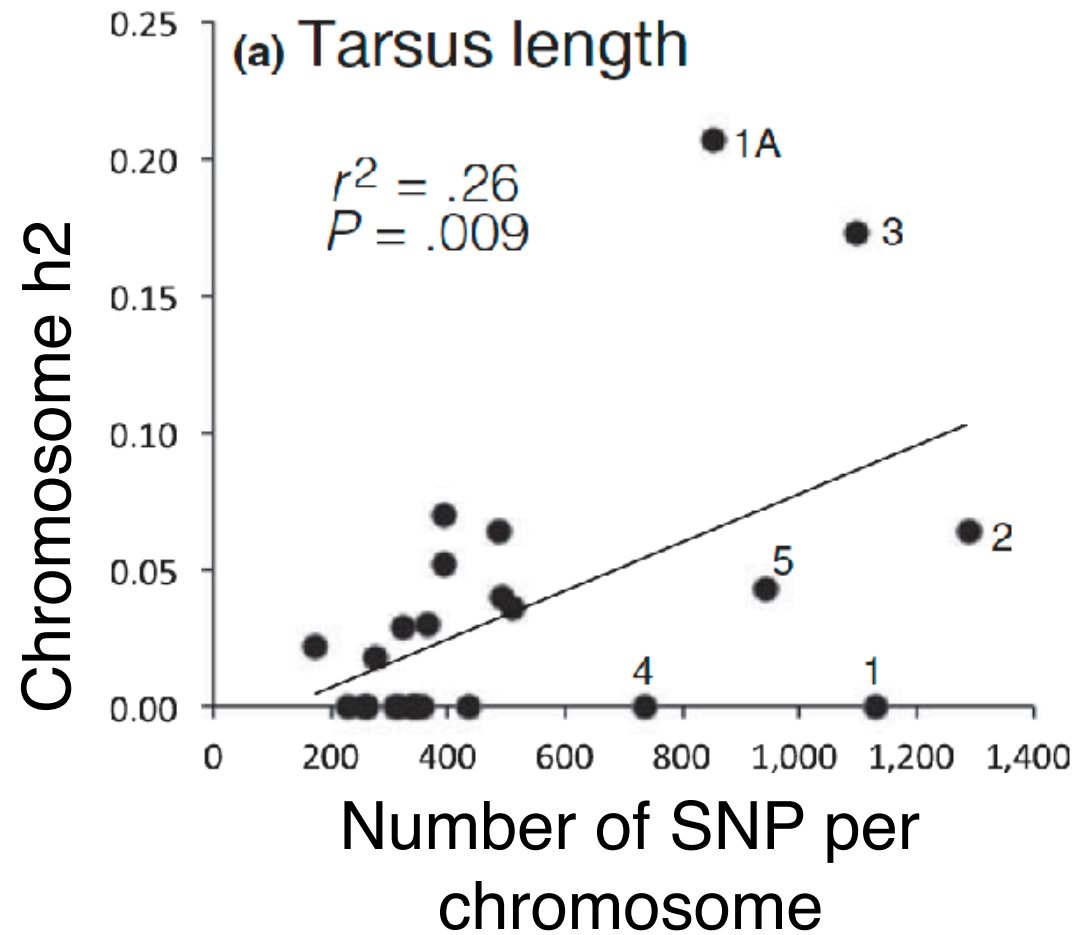
-> No large effects genes
Compatible with an infinitesimal model

Quantitative genomic analyses

Infinitesimal model?

Quantitative genomic analyses

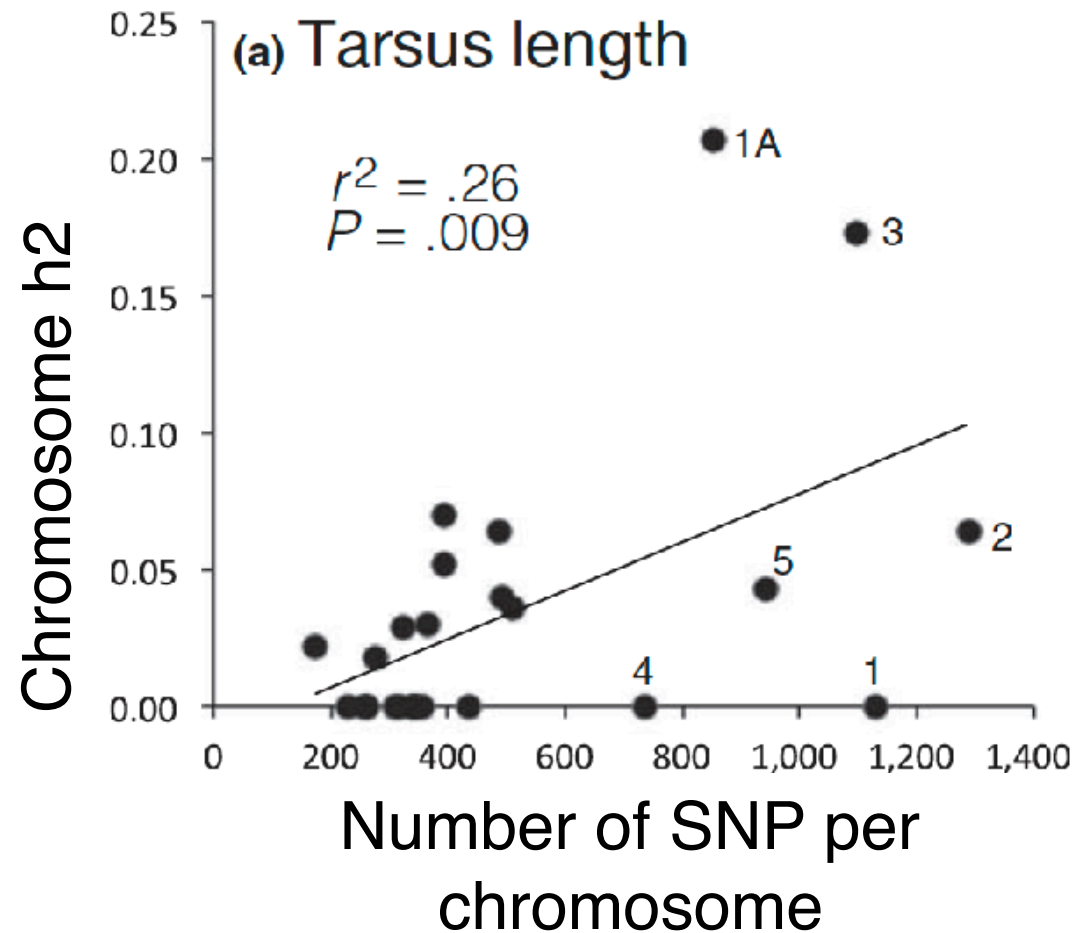
Infinitesimal model?



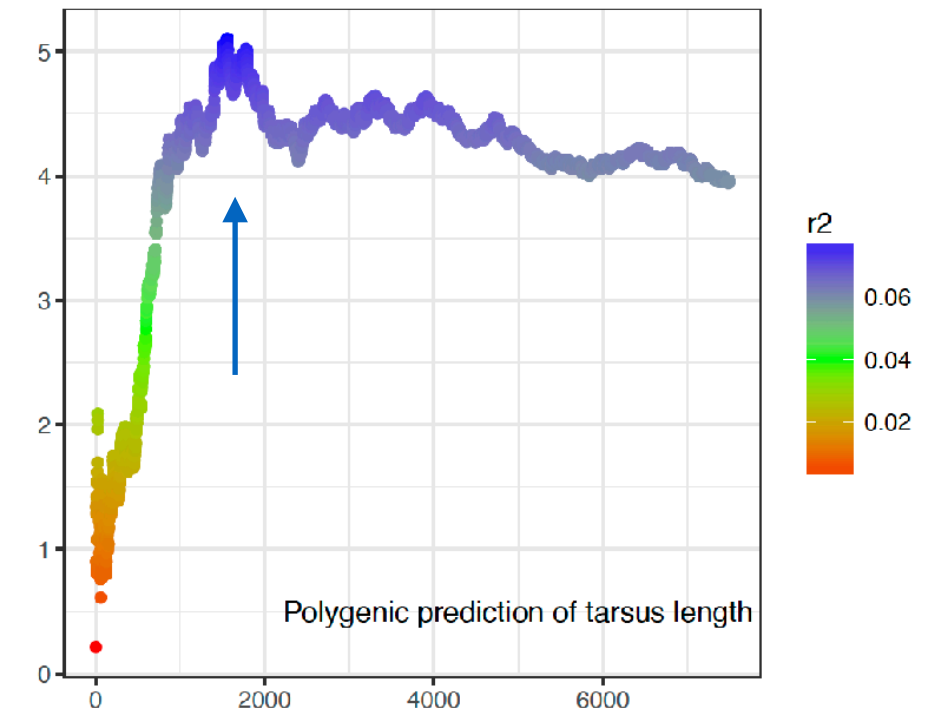
-> Compatible with an infinitesimal model

Quantitative genomic analyses

Infinitesimal model?



$-\log_{10}(P)$
Polygenic
prediction of
tarsus length



Number of SNP from the
GWAS, by increasing Pvalue

-> Compatible with an infinitesimal model

Adaptation genomics

Genome scans: looking for outlier SNPs between populations

Adaptation genomics

Genome scans: looking for outlier SNPs between populations

Bayescan

Using the demographic
parameters estimated

RDA loadings

Adaptation genomics

Genome scans: looking for outlier SNPs between populations

Bayescan

Using the demographic
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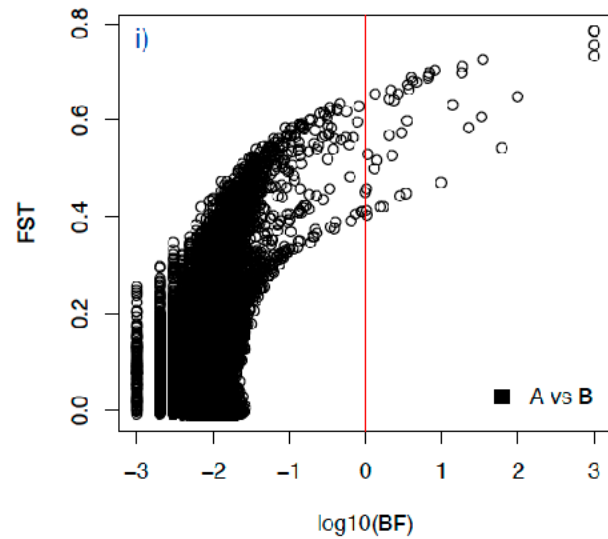
Corsica vs
continent

Deciduous vs
evergreen

Adaptation genomics

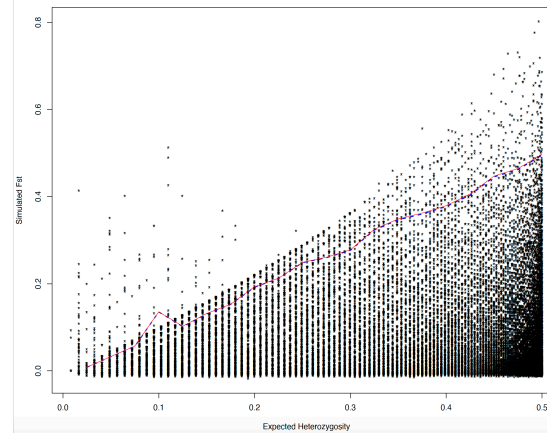
Genome scans: looking for outlier SNPs between populations

Bayescan

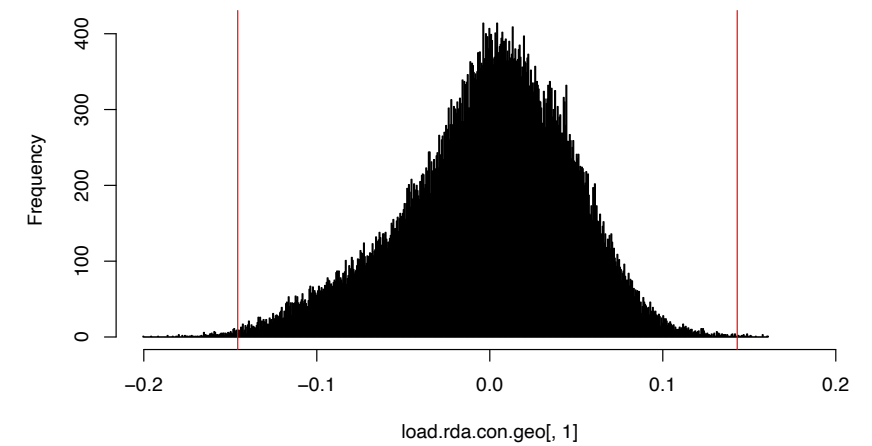


Corsica vs
continent

Using the demographic
parameters estimated



RDA loadings



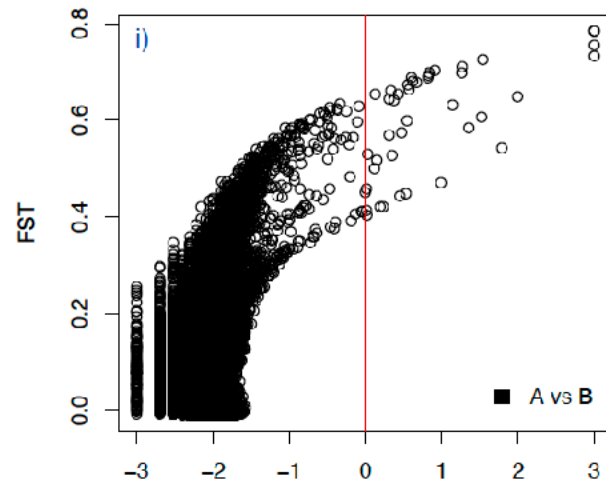
Deciduous vs
evergreen

Some outliers between Corsican and continental pop.

Adaptation genomics

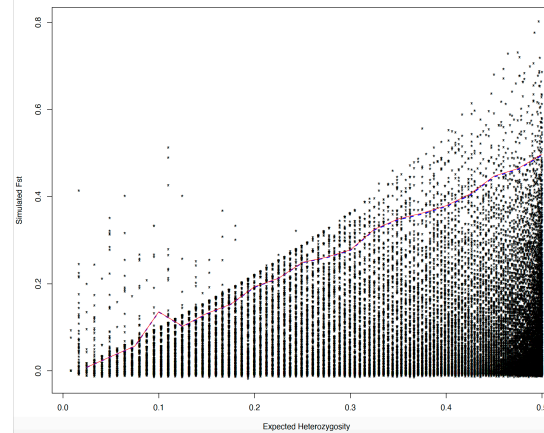
Genome scans: looking for outlier SNPs between populations

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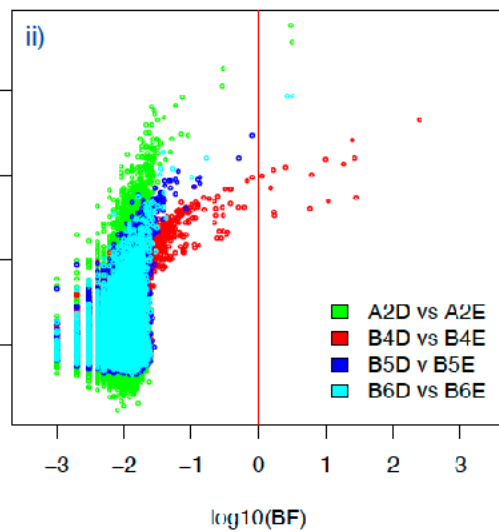
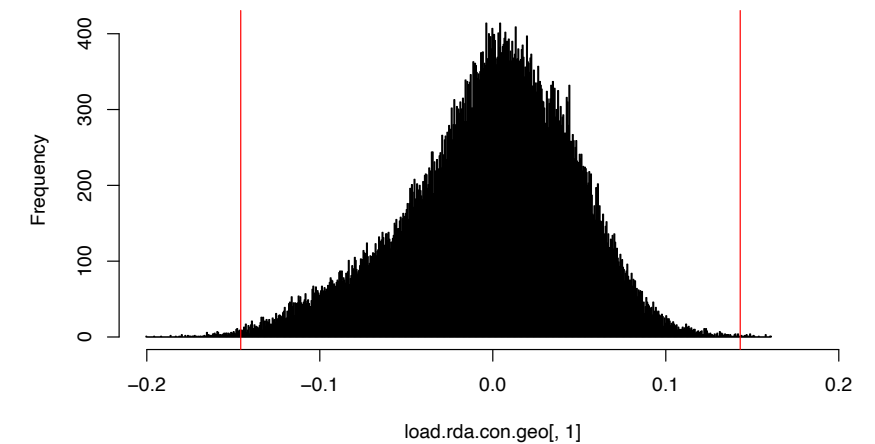


Corsica vs
continent

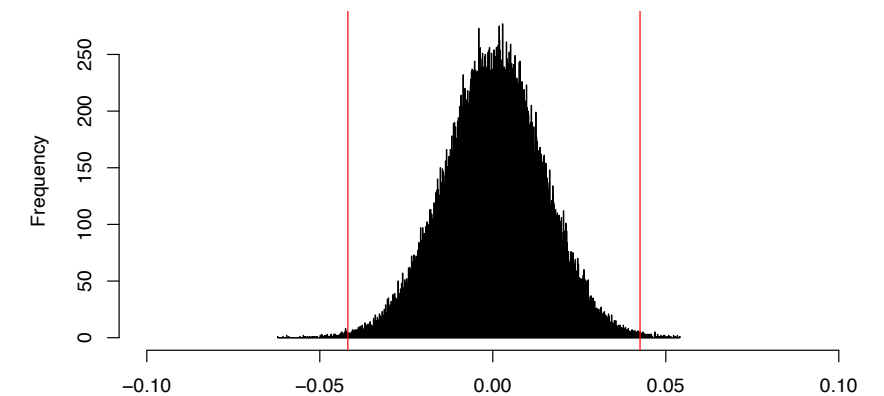
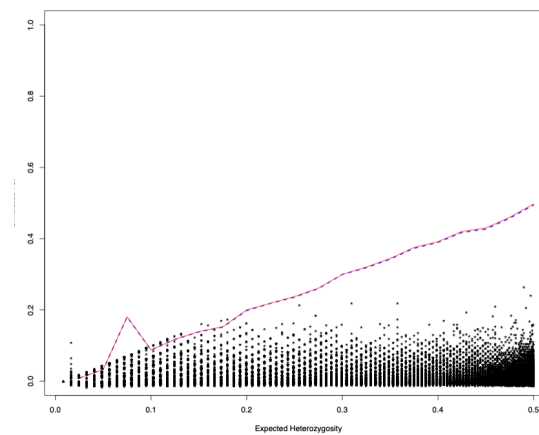
Using the demographic
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RDA loadings



Deciduous vs
evergreen



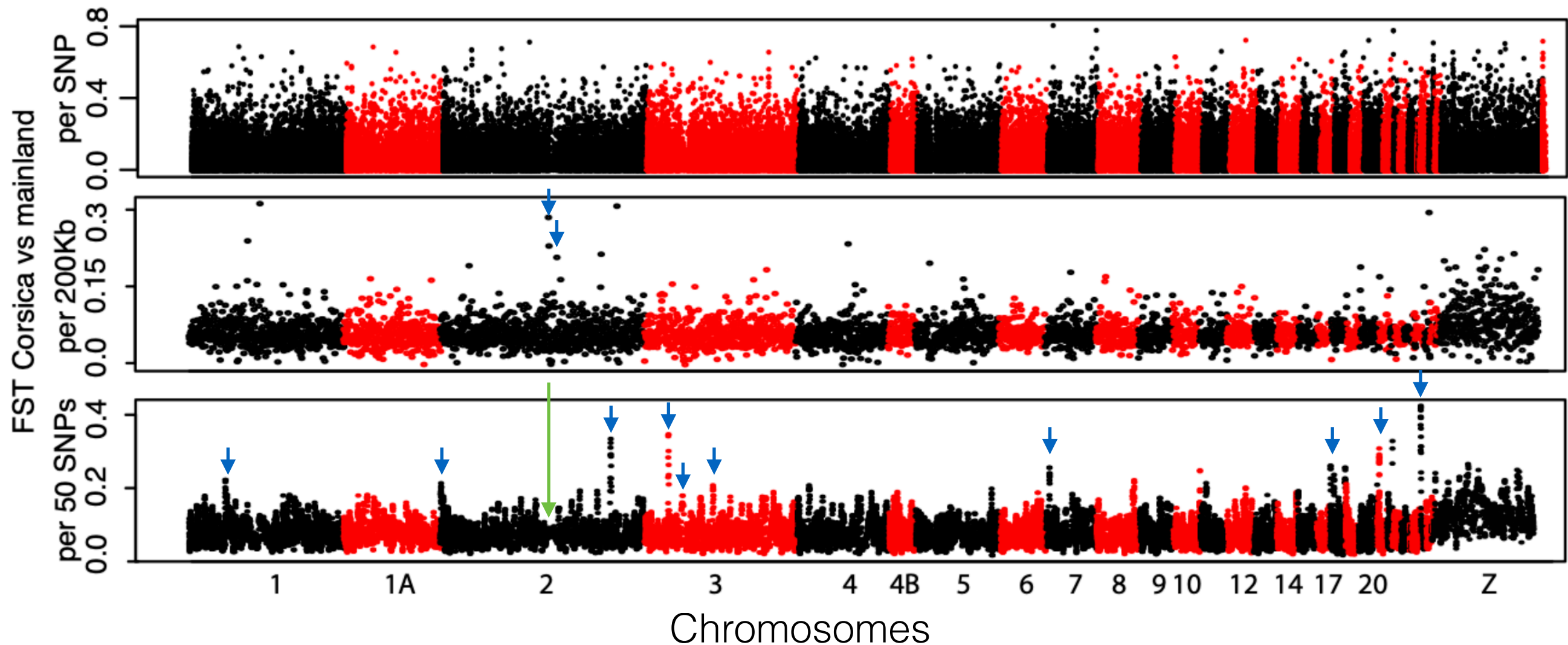
Some outliers between Corsican and continental pop.
Few to no outliers between heterogeneous habitats
-> Coherent with the demography of the populations

Adaptation genomics

Genome scans: looking for outlier WINDOWS

Adaptation genomics

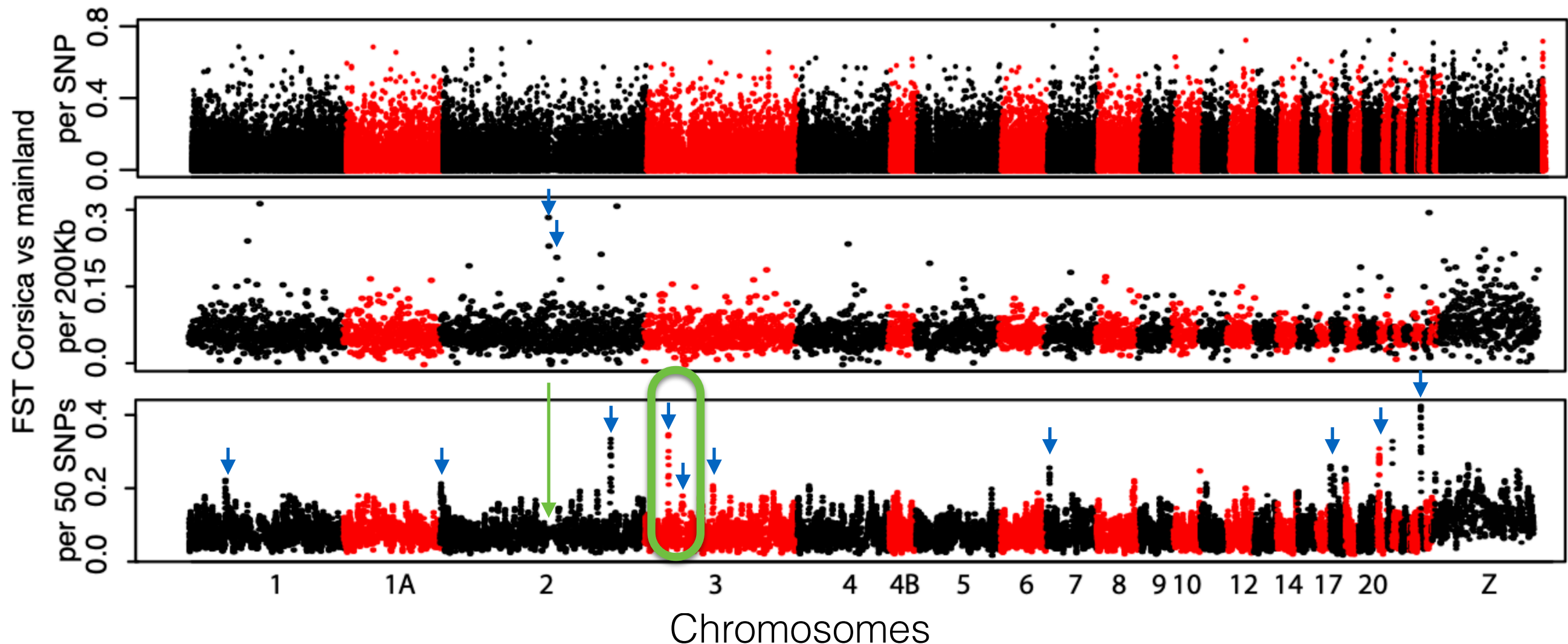
Genome scans: looking for outlier WINDOWS



- > No large and distinct F_{ST} peak,
 - > Windows more efficient when scaled to recombination rate (here via scaling windows by n SNPs)
- ...no particularly relevant gene ontologies yet...

Adaptation genomics

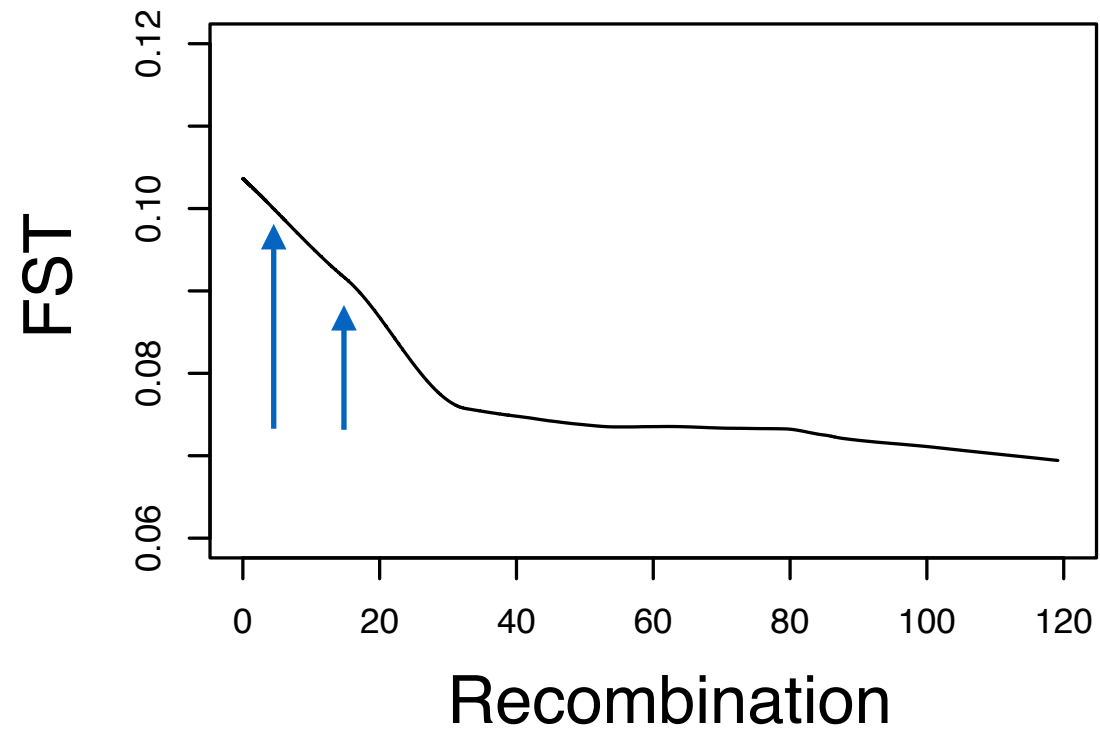
Genome scans: looking for outlier WINDOWS



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Adaptation genomics

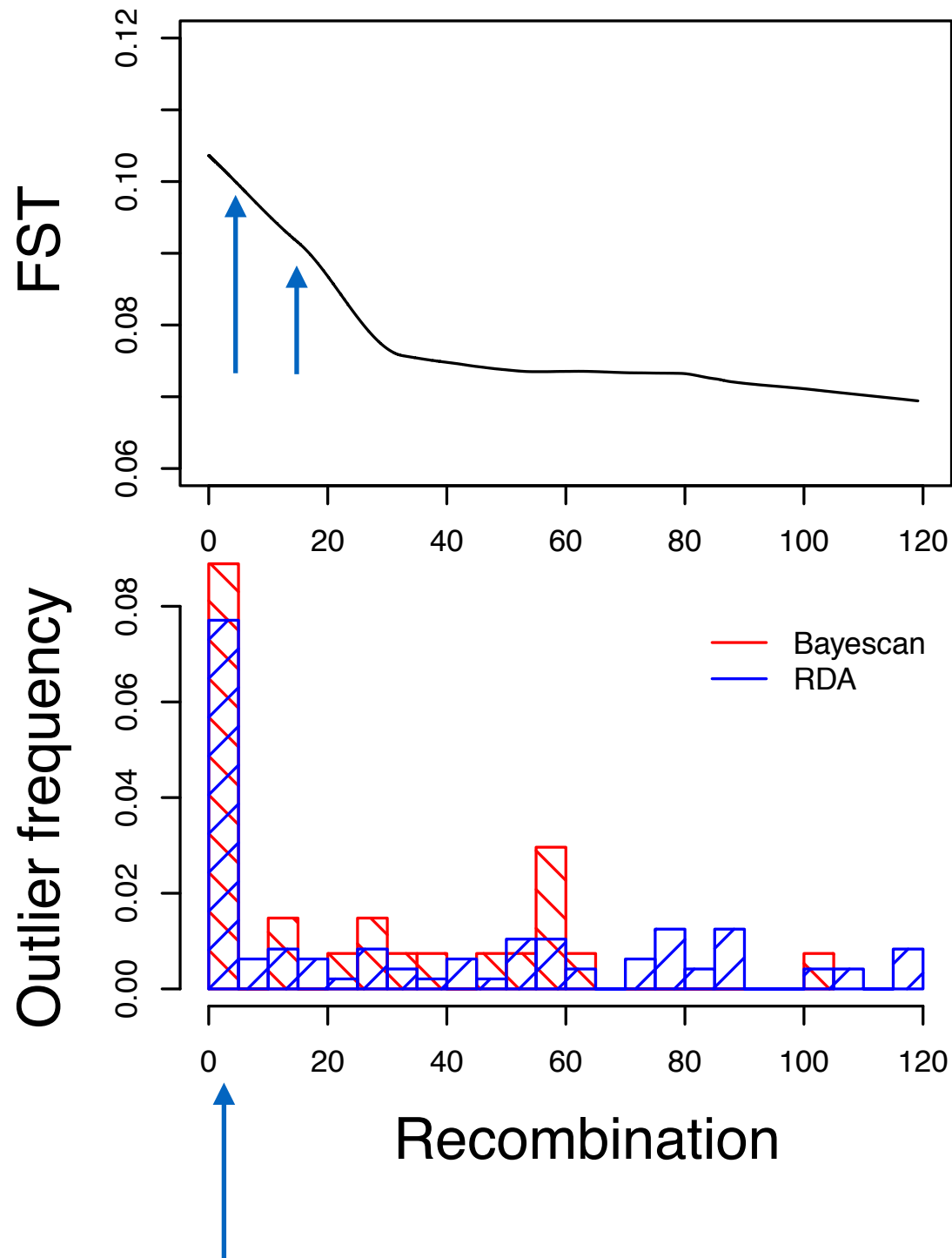
Genome scans outliers & recombination rate



-> Larger differentiation in regions with reduced recombination

Adaptation genomics

Genome scans outliers & recombination rate



-> Larger differentiation in regions with reduced recombination

-> Large proportion FST outliers Corsica vs continent in recombination cold spots

Neutral envelope should integrate local recombination value?

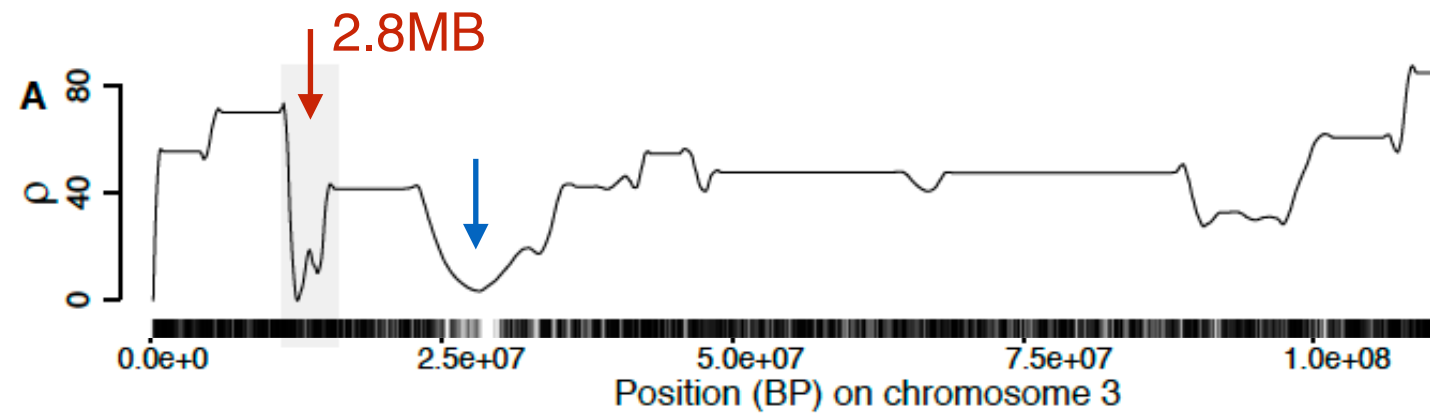
Adaptation genomics

Genome scans: Looking for inversions

Adaptation genomics

Genome scans: Looking for inversions

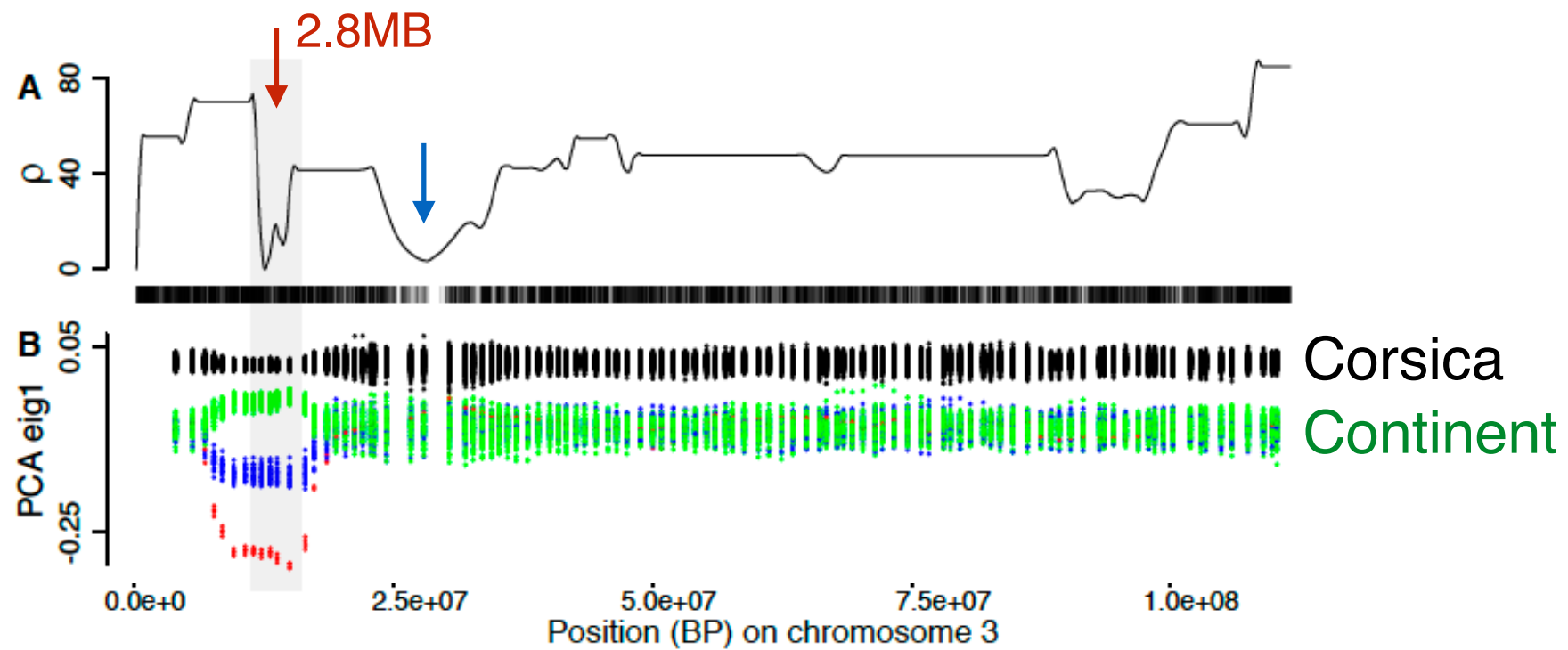
Detection



Adaptation genomics

Genome scans: Looking for inversions

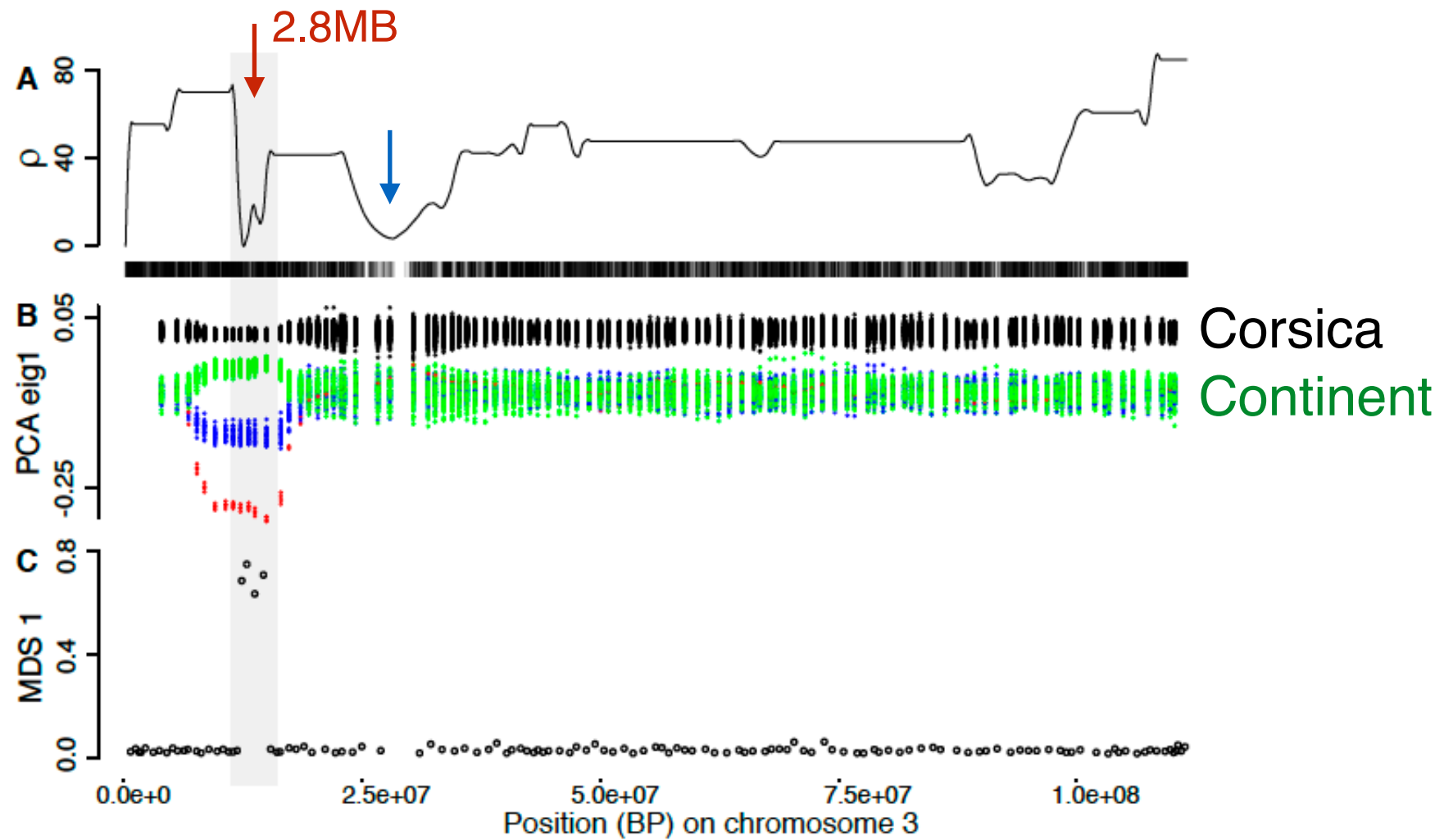
Detection



Adaptation genomics

Genome scans: Looking for inversions

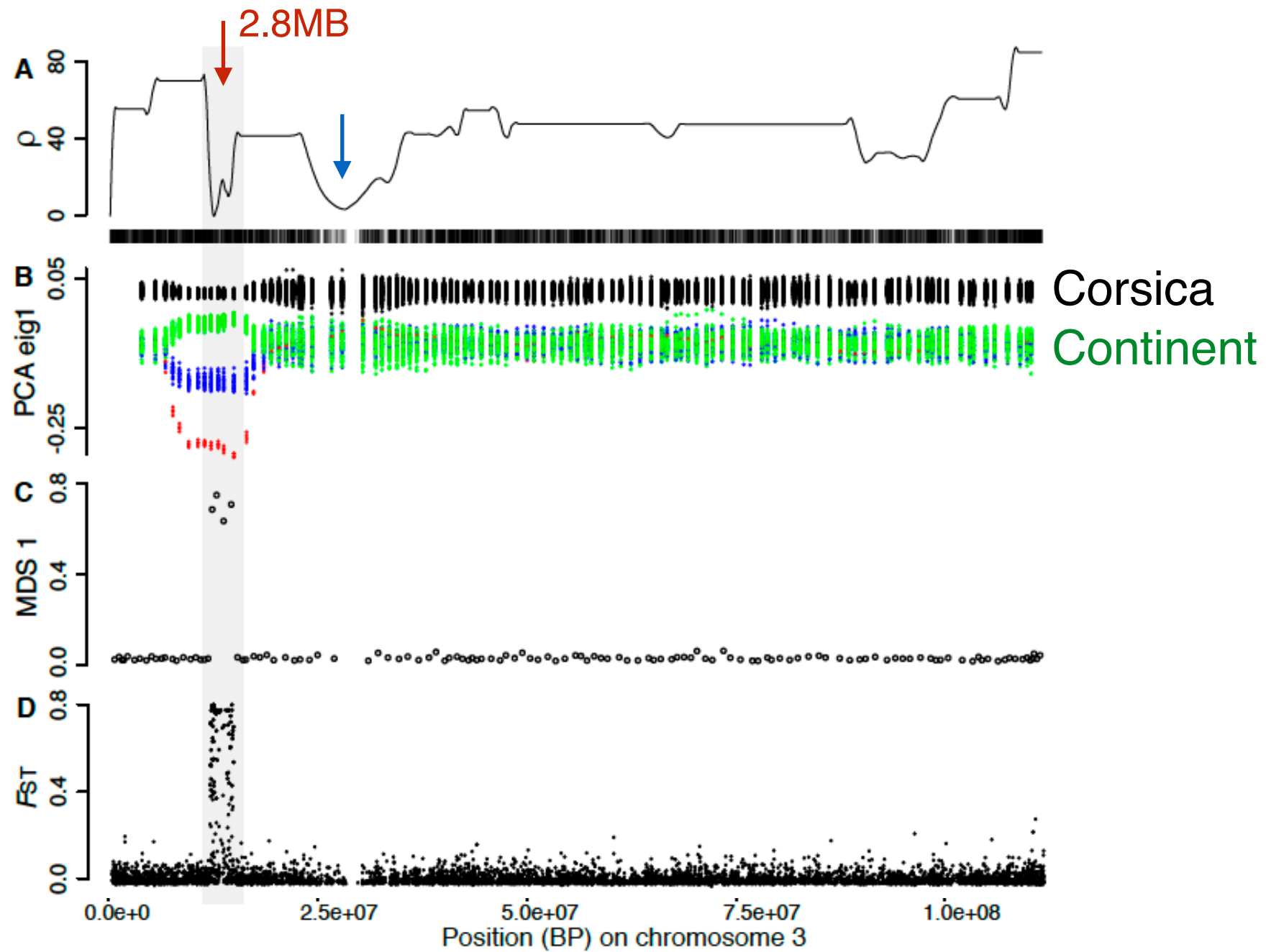
Detection



Adaptation genomics

Genome scans: Looking for inversions

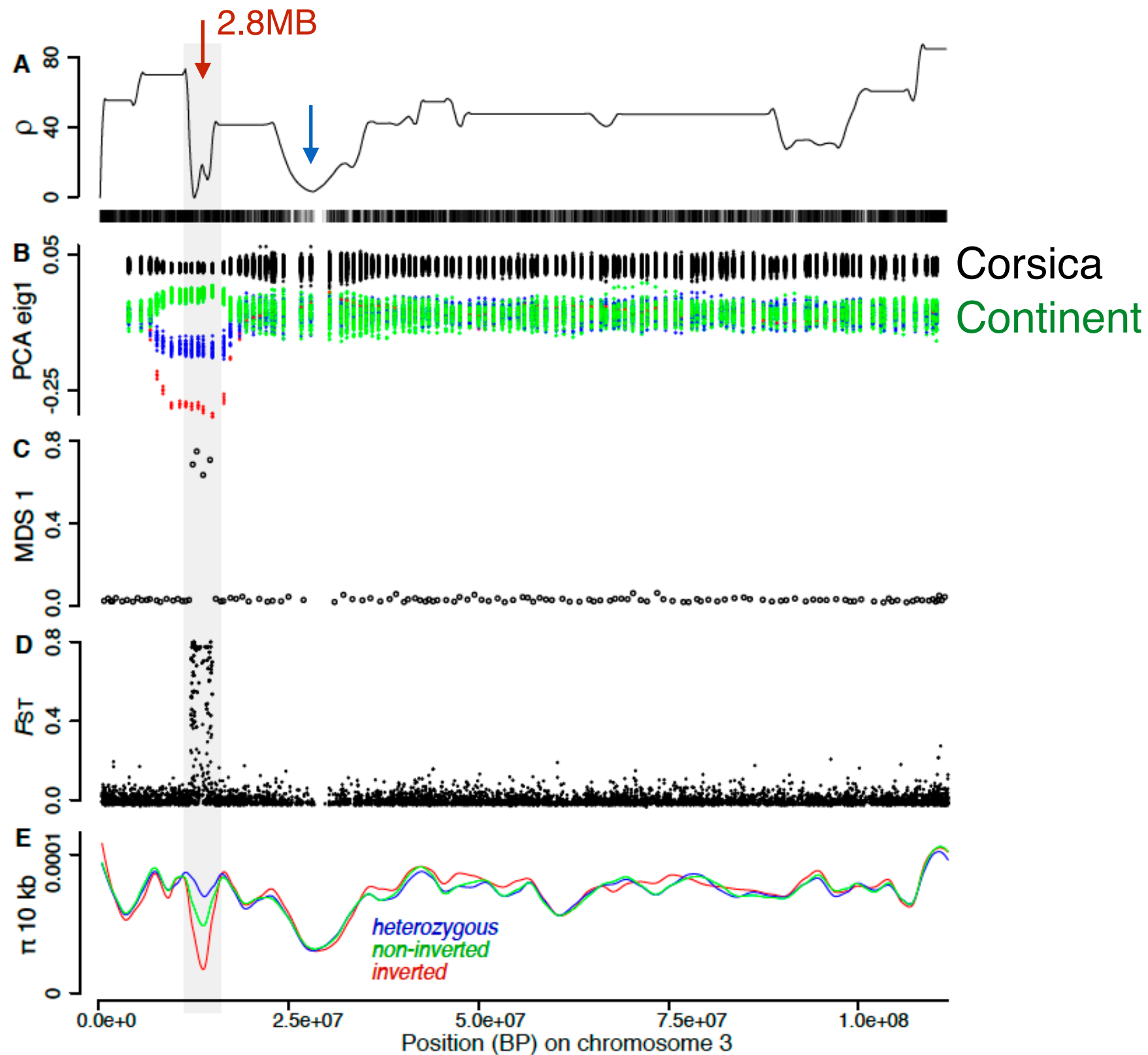
Detection



Adaptation genomics

Genome scans: Looking for inversions

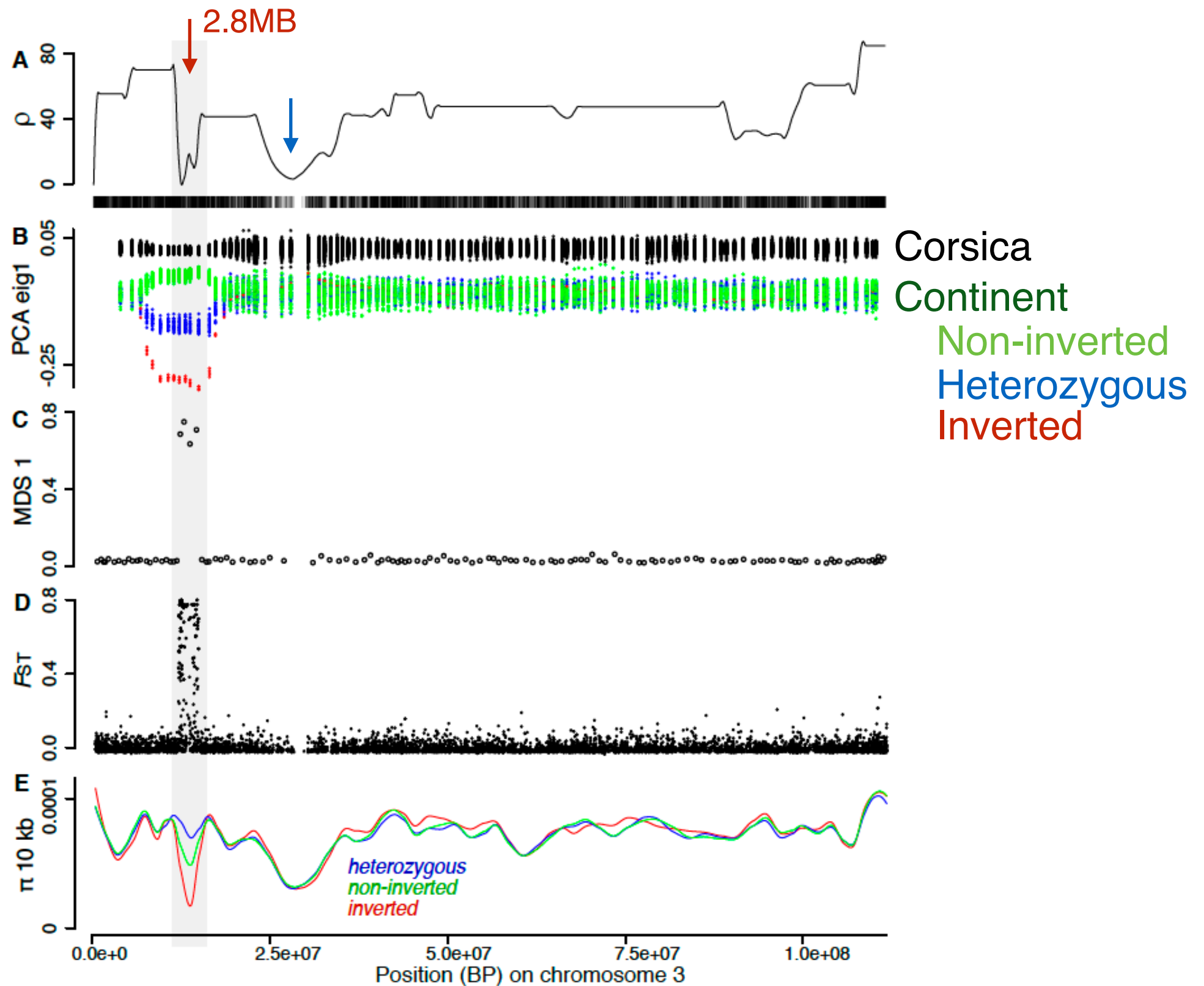
Detection



Adaptation genomics

Genome scans: Looking for inversions

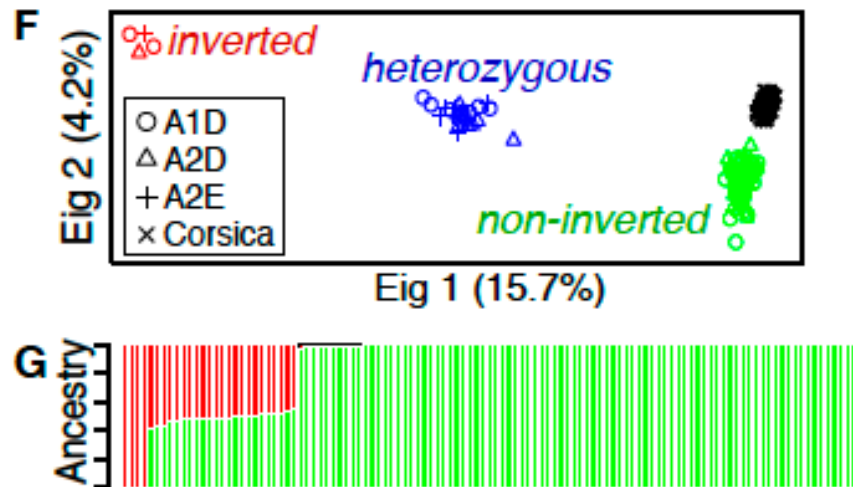
Detection



Adaptation genomics

Genome scans: Looking for inversions

Characteristics



No enrichment in an habitat

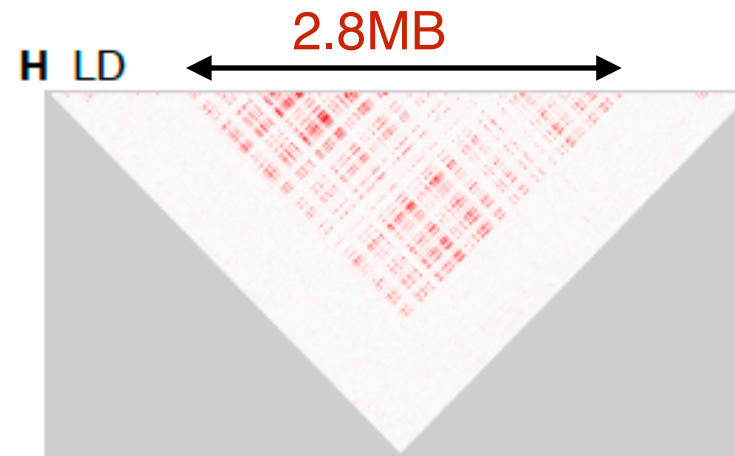
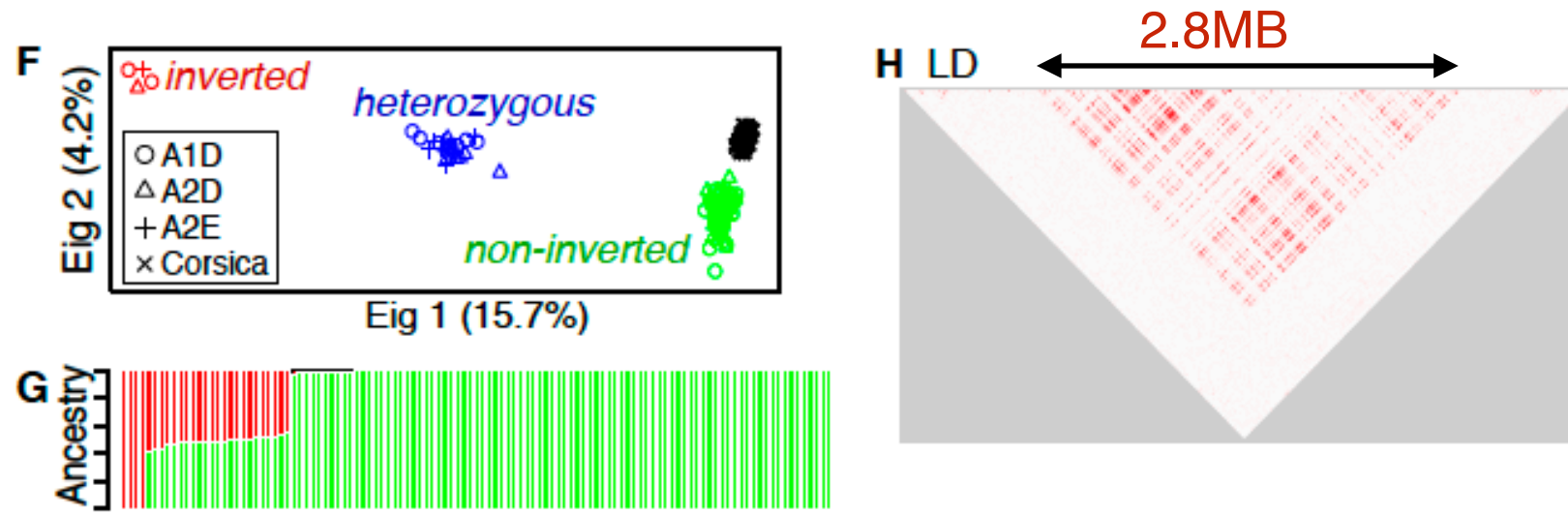
No HWE deviation (no deficit of homozygous)

No enrichment for non-synonymous nor deleterious variants (but little power)

Adaptation genomics

Genome scans: Looking for inversions

Characteristics



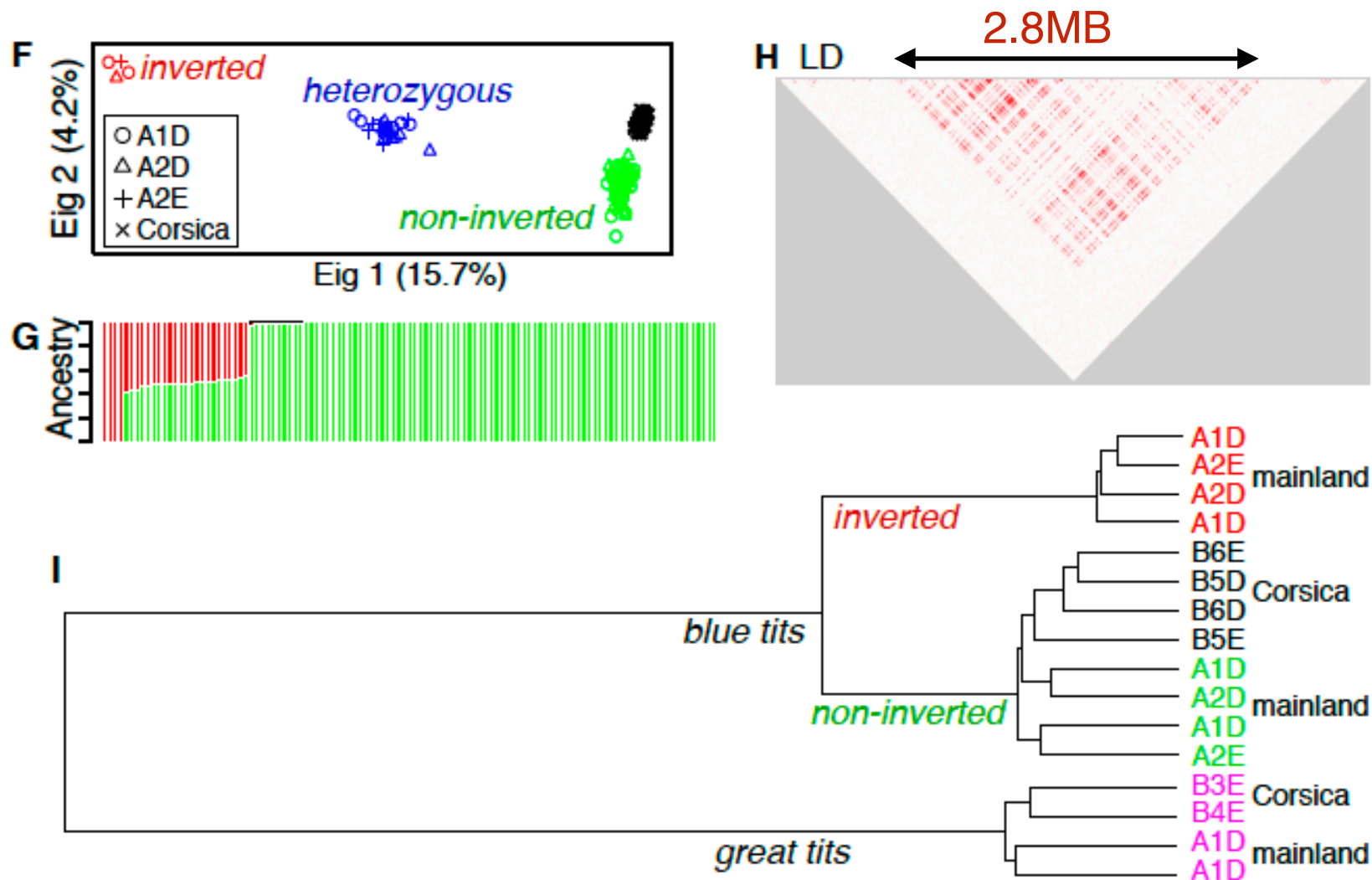
No enrichment in an habitat
No HWE deviation (no deficit of homozygous)
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Reduced recombination

Adaptation genomics

Genome scans: Looking for inversions

Characteristics



No enrichment in an habitat
No HWE deviation (no deficit of homozygous)
No enrichment for non-synonymous nor deleterious variants (but little power)

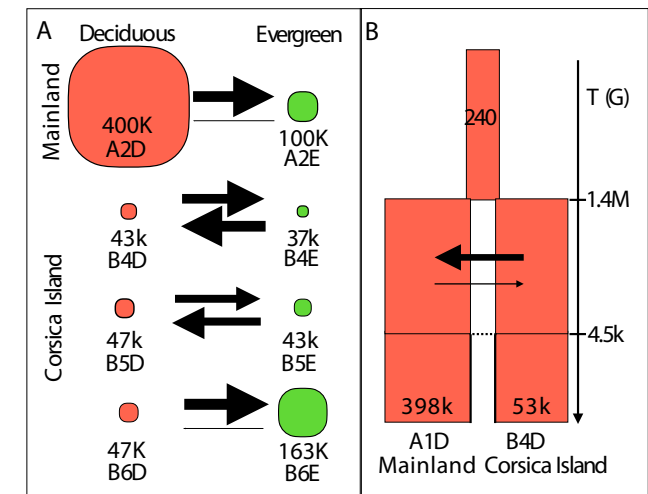
Reduced recombination

Old polymorphism (2x divergence Corsica-Continent)
Strangely absent from Corsica
Role?

Discussion / conclusion

✓ Demography of populations

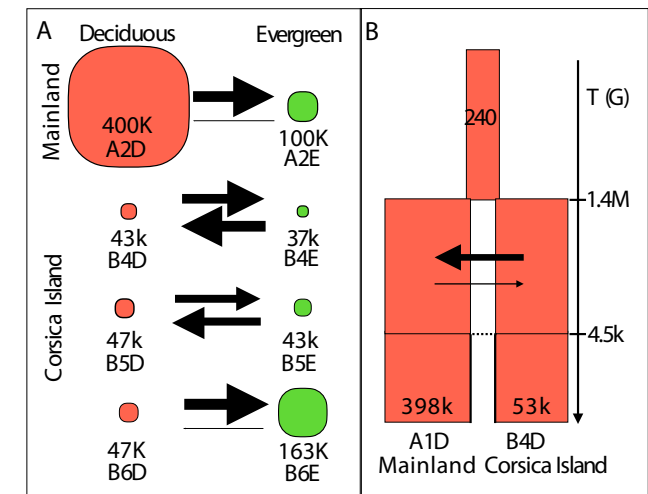
- ✓ Corsica-Continent: Divergence with ancestral migration until the end of the last glaciation; small m , large N_e
- ✓ Deciduous-Evergreen: equilibrium; large m & N_e



Discussion / conclusion

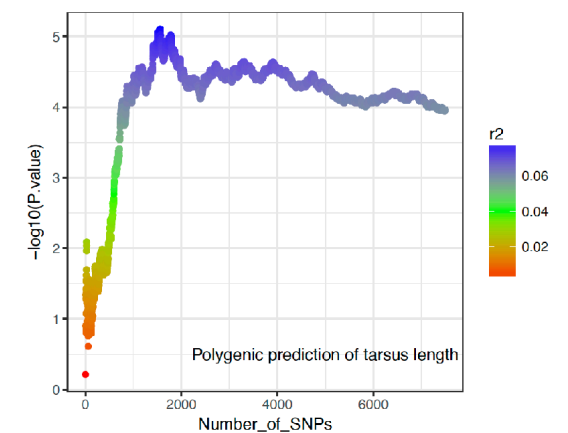
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✓ Quantitative genomics

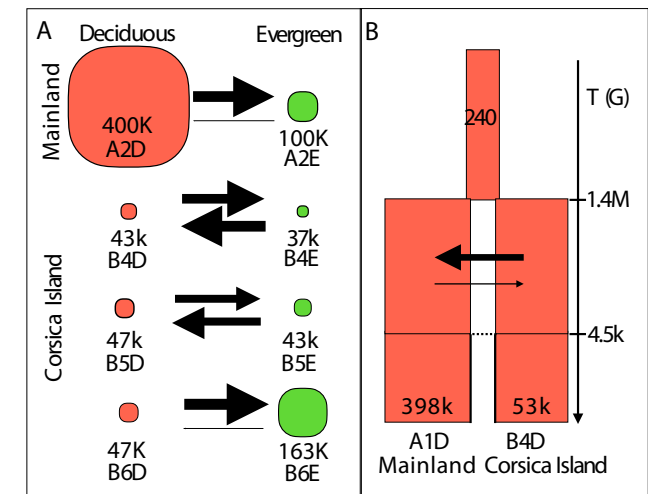
- ✓ Heritability unbiased by extra-pair paternity
- ✓ Traits variations explained by infinitesimal models



Discussion / conclusion

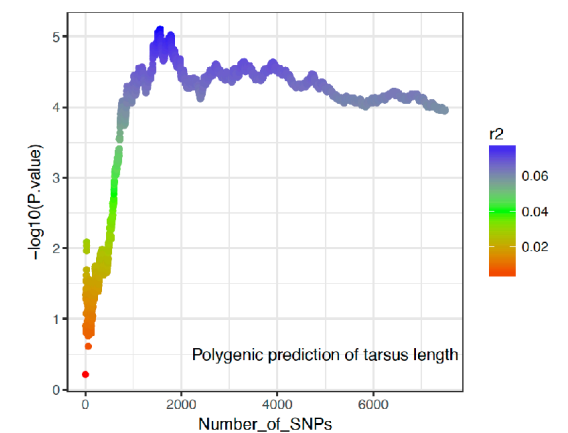
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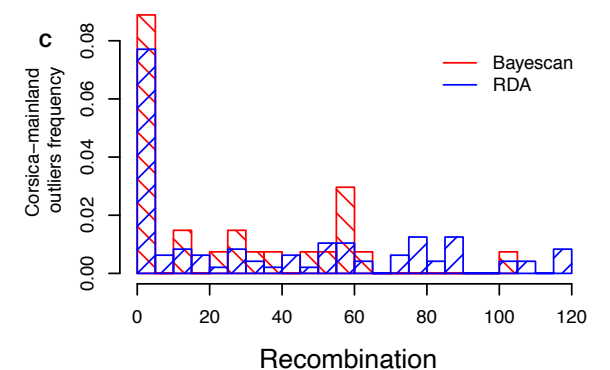
✓ Quantitative genomics

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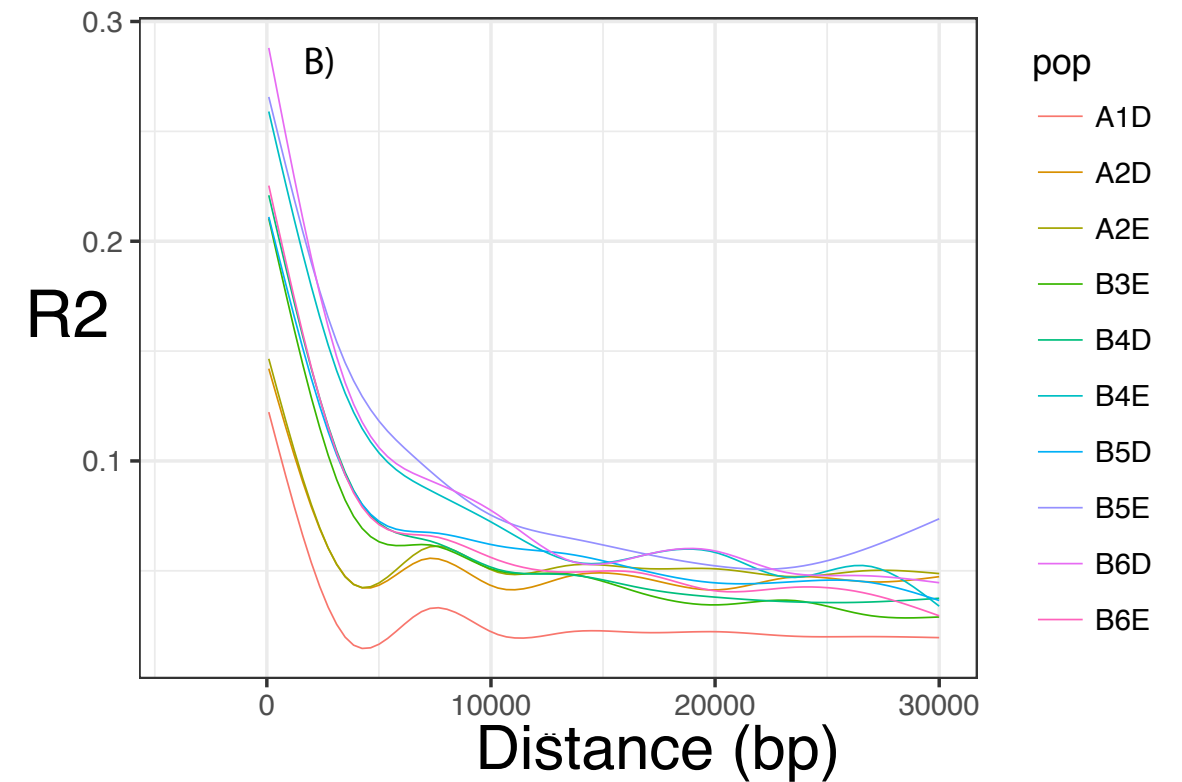
✓ Adaptation genomics

- ✓ Corsica-Continent: Significant outlier; in regions of reduced recombination; old inversion in continental birds
- ✓ Deciduous-Evergreen: Few outliers



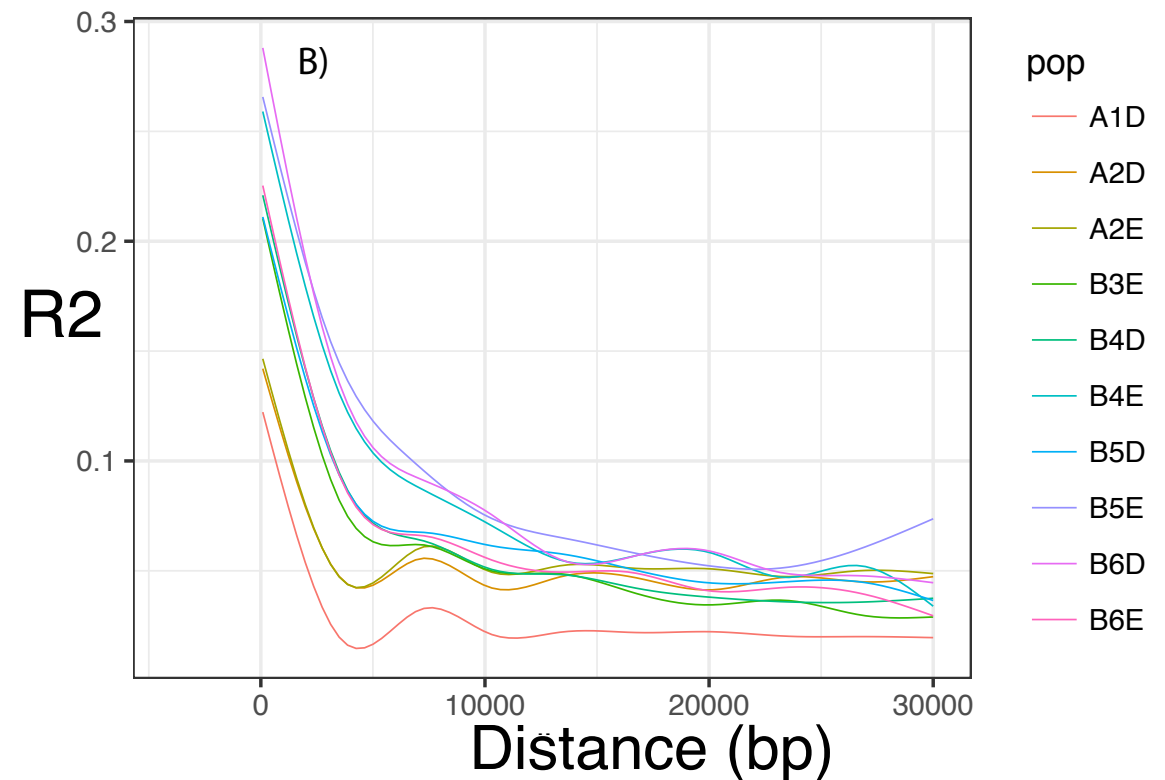
Discussion / conclusion

- ✓ Quantitative genomics
- ✓ More markers



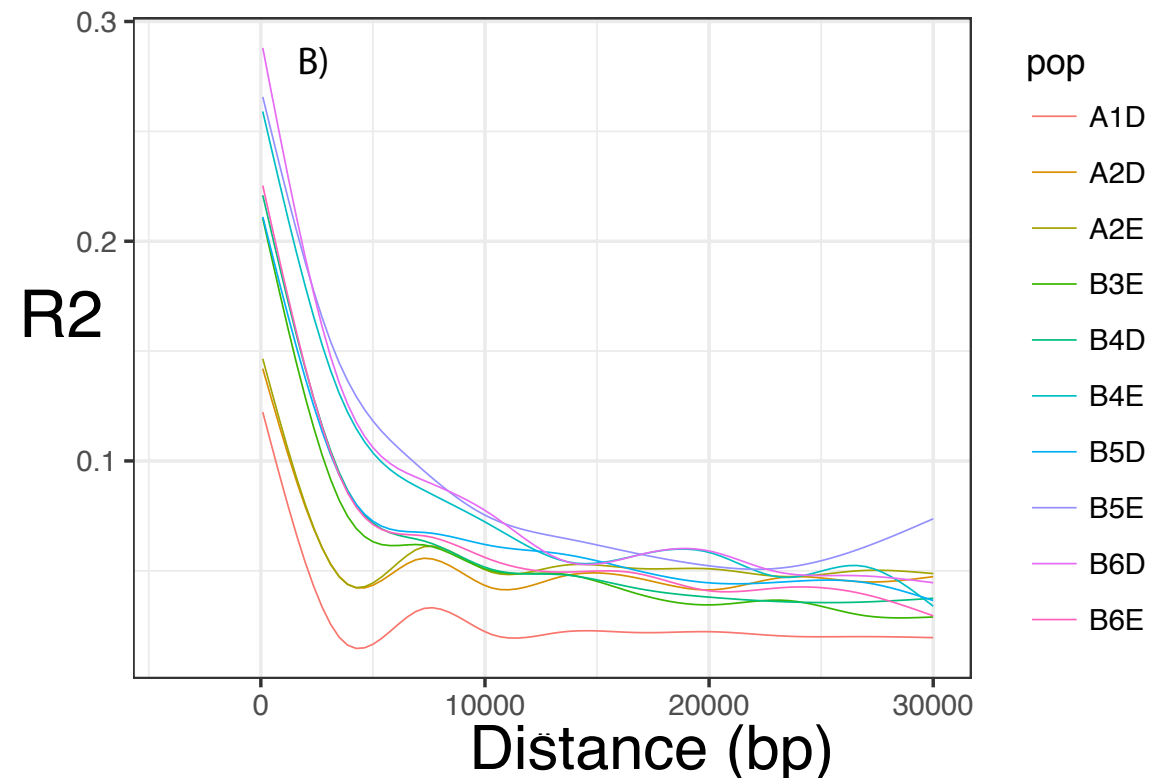
Discussion / conclusion

- ✓ Quantitative genomics
 - ✓ More markers
 - ✓ More individuals
 - ✓ Disassociate the pedigree from the environment (eg Tarsus)
 - ✓ Other traits (eg resistance to avian malaria)



Discussion / conclusion

- ✓ Quantitative genomics
 - ✓ More markers
 - ✓ More individuals
 - ✓ Disassociate the pedigree from the environment (eg Tarsus)
 - ✓ Other traits (eg resistance to avian malaria)
- ✓ Adaptation genomics
 - ✓ Full genomes
 - ✓ Role, geographic distribution, history, of the inversion? -> full sequence + genotyping more birds with a simple test



References

MOLECULAR ECOLOGY RESOURCES

SPECIAL ISSUE: ASSOCIATION MAPPING IN NATURAL POPULATIONS

Heritability estimates from genomewide relatedness matrices in wild populations: Application to a passerine, using a small sample size

C. Perrier , B. Delahaie, A. Charmantier

First published: 17 April 2018 | <https://doi.org/10.1111/1755-0998.12886>

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Charles Perrier , Quentin Rougemont, Anne Charmantier

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Charles Perrier , Anne Charmantier

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Merci !

