Demographic history and recombination shape the genomic landscape of a broadly distributed Pacific salmon

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GenomeCanada

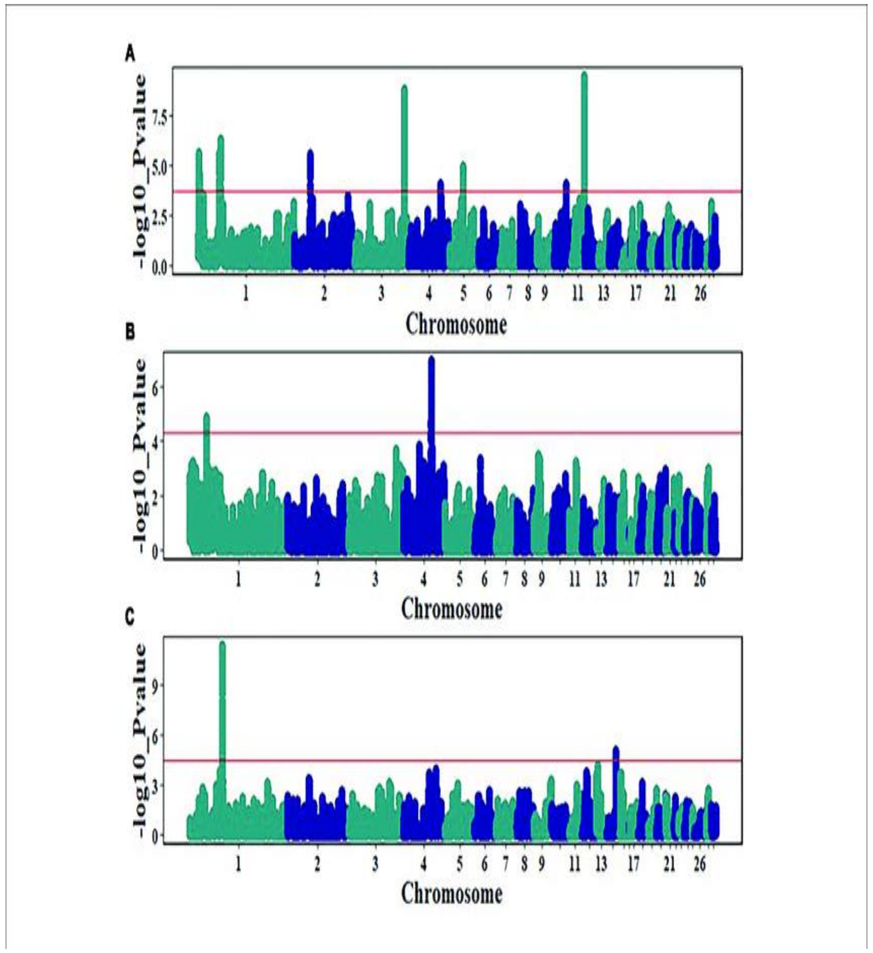
EPIC4

UMR 5175 CENTRE D'ECOLOGIE FONCTIONNELLE & EVOLUTIVE

cnrs

Local adaptation and beyond

- Genome scans for evidence of natural selection are now routine



Walugembe et al. 2019 *Front. Genetics*

Local adaptation and beyond

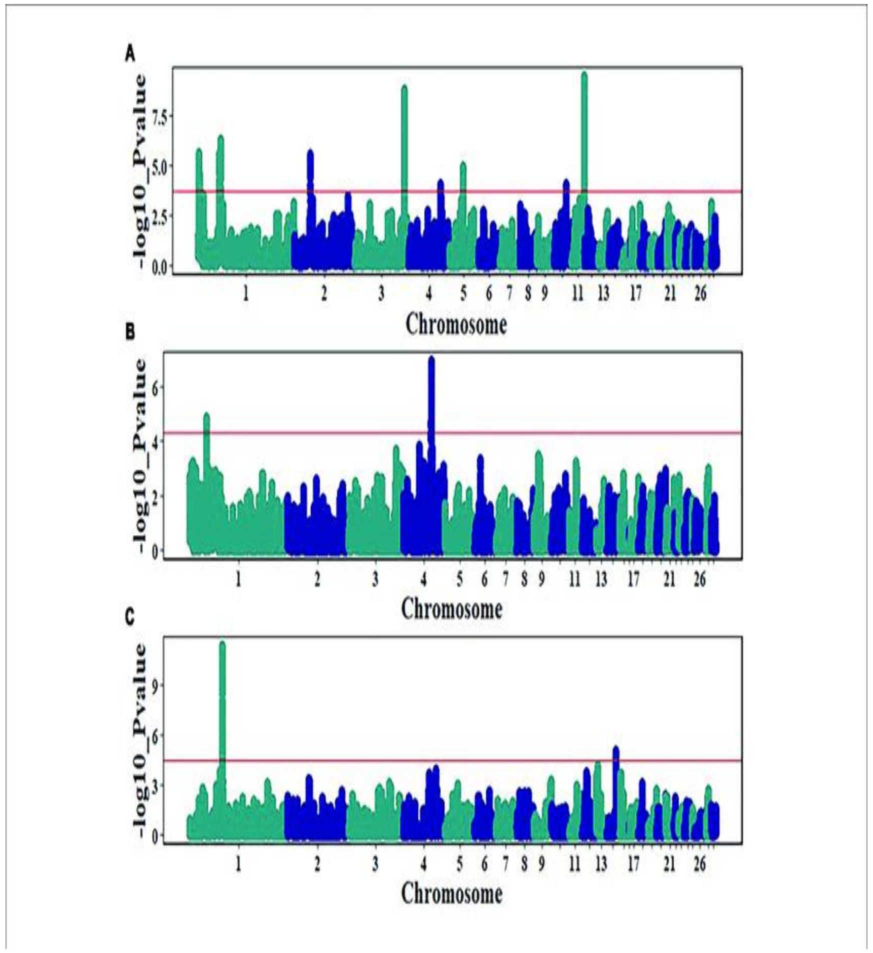
- Genome scans for evidence of natural selection are now routine
- Increasingly used in conservation genomics

Trends in Ecology & Evolution
Volume 27, Issue 9, September 2012, Pages 489-496

Opinion

Harnessing genomics for delineating conservation units

W. Chris Funk [1], John K. McKay [2], Paul A. Hohenlohe [3], Fred W. Allendorf [4]



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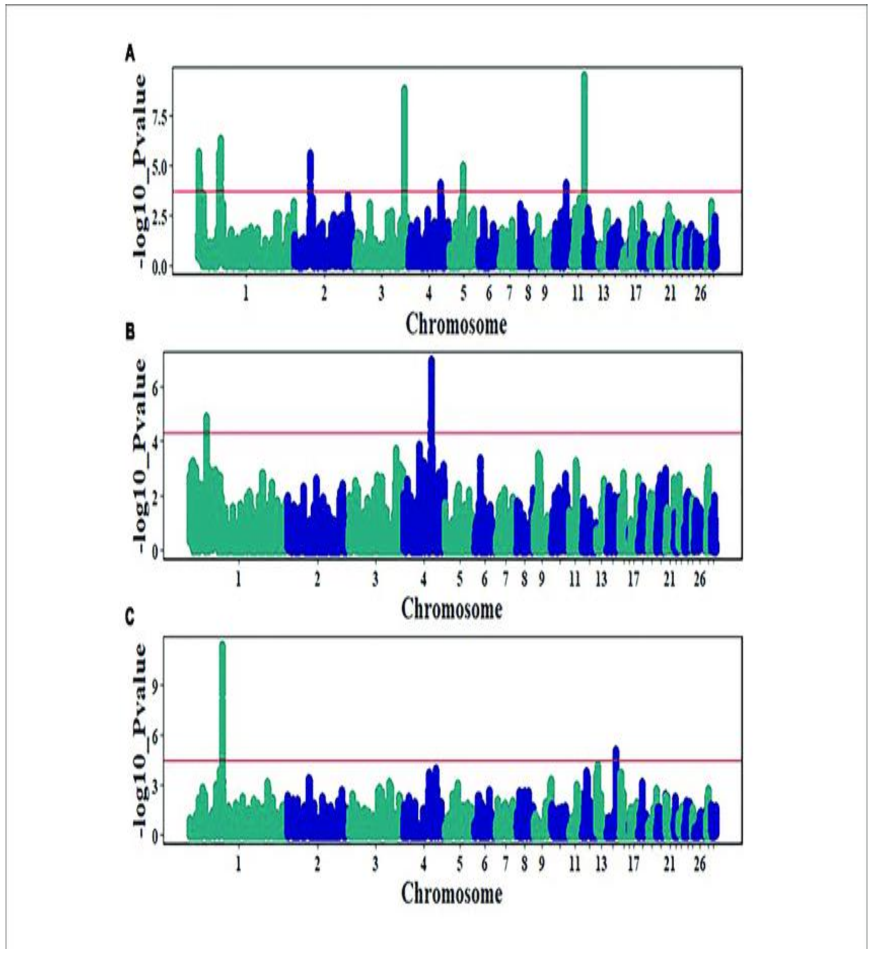
Local adaptation and beyond

- Genome scans for evidence of natural selection are now routine
- Increasingly used in conservation genomics
- The speed and efficacy of natural selection, however, is greatly influenced by a population' demographic history



Walugembe et al. 2019 *Front. Genetics*

Evolutionary Applications
Open Access
Evolutionary approaches to environmental, biomedical and socio-economic issues

PERSPECTIVE | Open Access

Genomics and conservation units: The genetic basis of adult migration timing in Pacific salmonids

Robin S. Waples, Steven T. Lindley

First published: 01 August 2018 | https://doi.org/10.1111/eva.12687 | Citations: 23

Trends in Ecology & Evolution
Volume 33, Issue 11, November 2018, Pages 827-839
CellPress

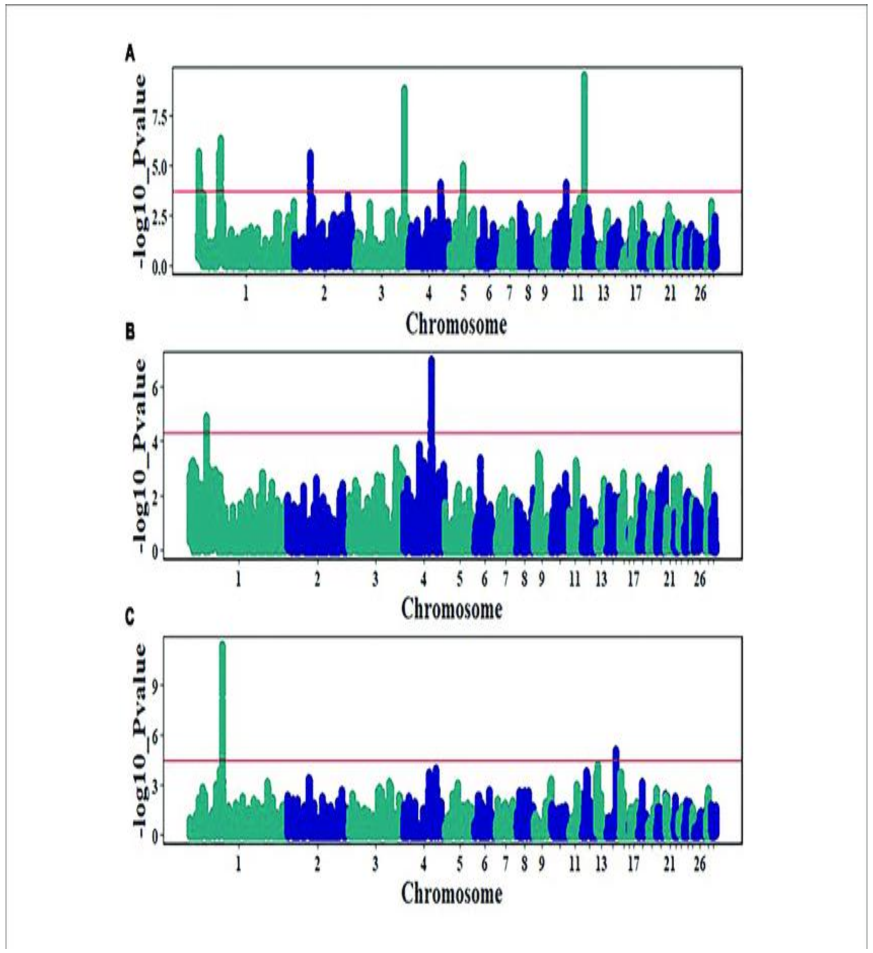
Opinion

The Peril of Gene-Targeted Conservation

Marty Kardos [1], Aaron B.A. Shafer [2]

Local adaptation and beyond

- Genome scans for evidence of natural selection are now routine
- Increasingly used in conservation genomics
- The speed and efficacy of natural selection, however, is greatly influenced by a population' demographic history
- Deleterious variants have received far less attention



Walugembe et al. 2019 *Front. Genetics*

On the importance of demography

- For North American biota, the importance of glaciations has been well-documented

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Secondary Contact scenario

On the importance of demography

- For North American biota, the importance of glaciations has been well-documented

Expansion scenario

On the importance of demography

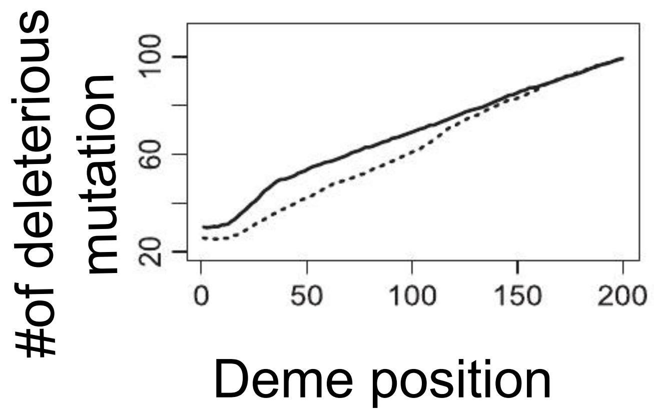
- For North American biota, the importance of glaciations has been well-documented
- New genomic data can help elucidate complex demographic histories

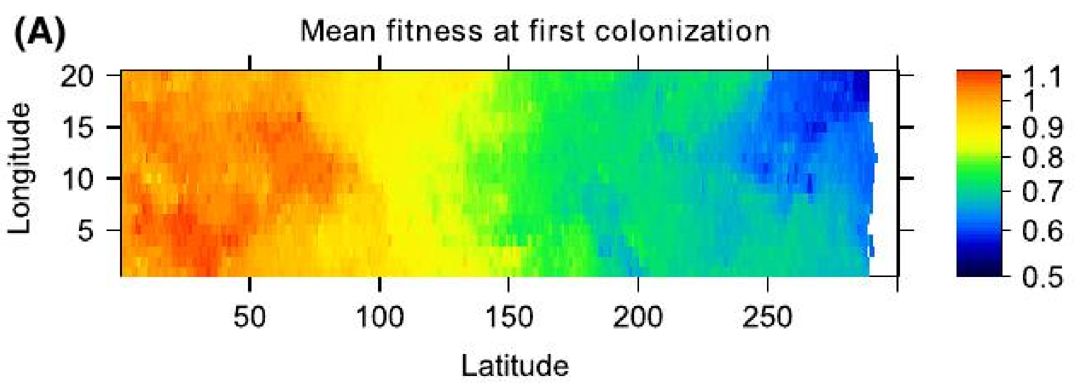
Expansion scenario

On the importance of demography

- For North American biota, the importance of glaciations has been well-documented
- New genomic data can help elucidate complex demographic histories
- How did recolonization shape the genomic landscape of variants, especially deleterious ones

Expansion load:

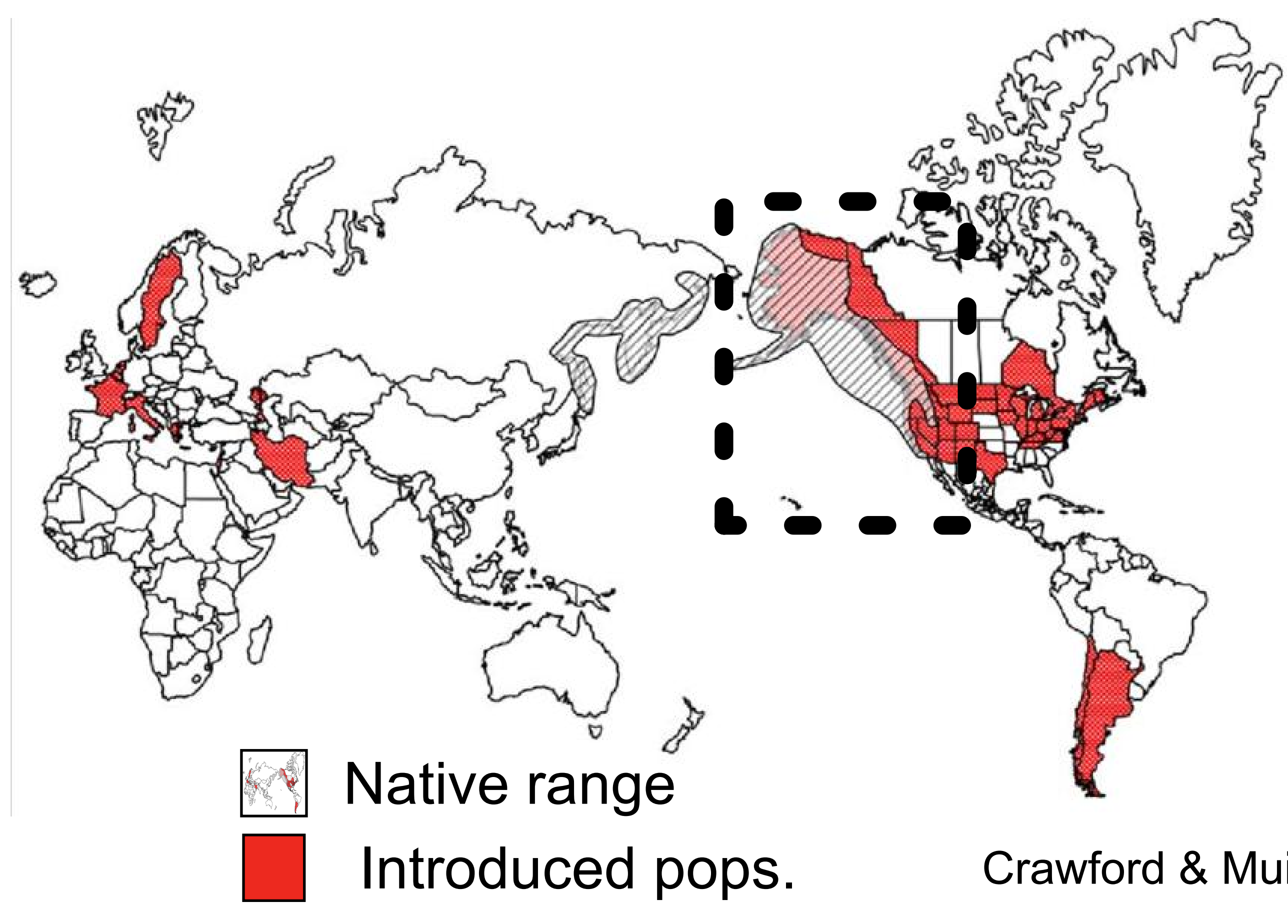




Peischl et al. 2013 *Mol Ecol*

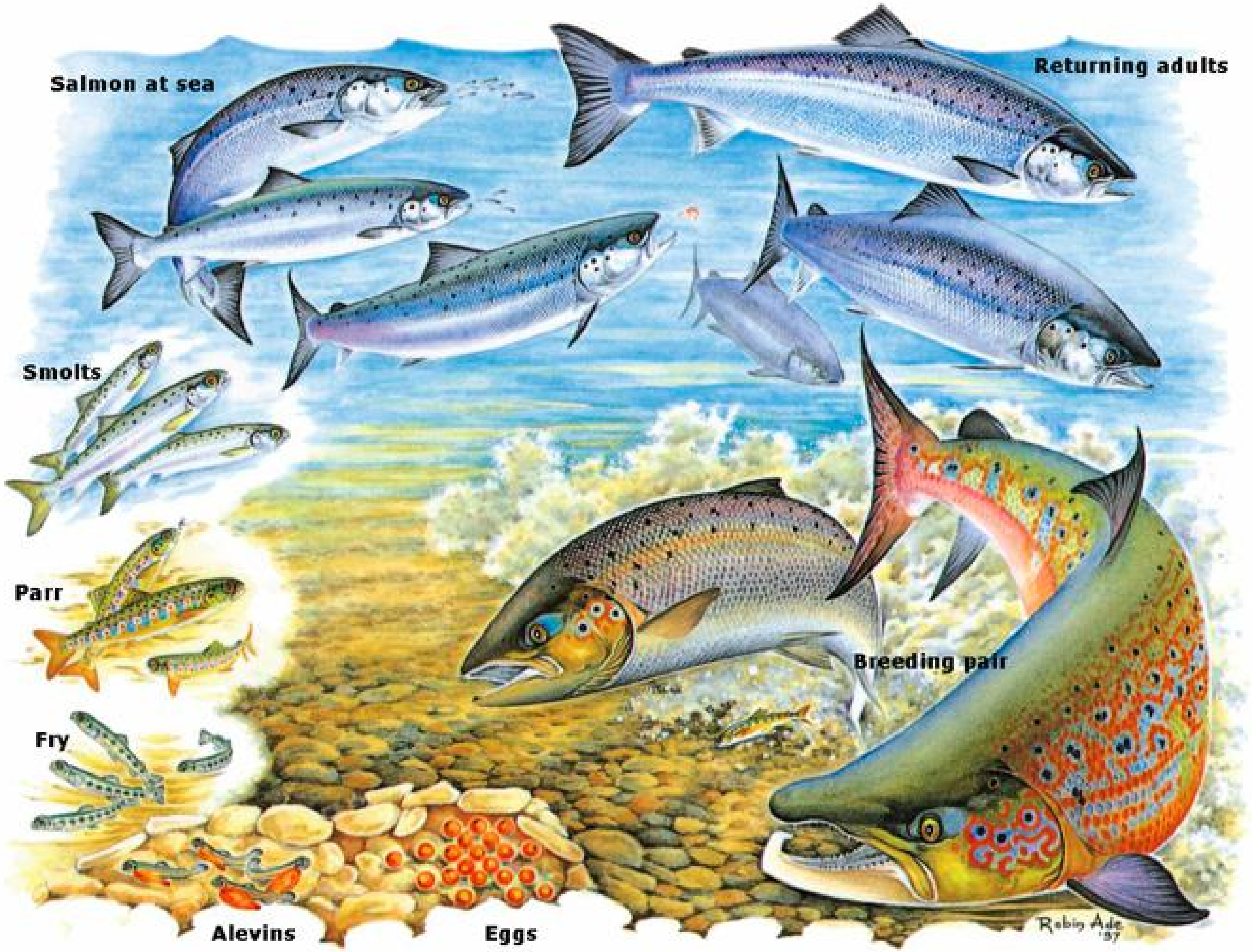
Coho salmon *Oncorhynchus kisutch*

(c) Joseph Tomelleri



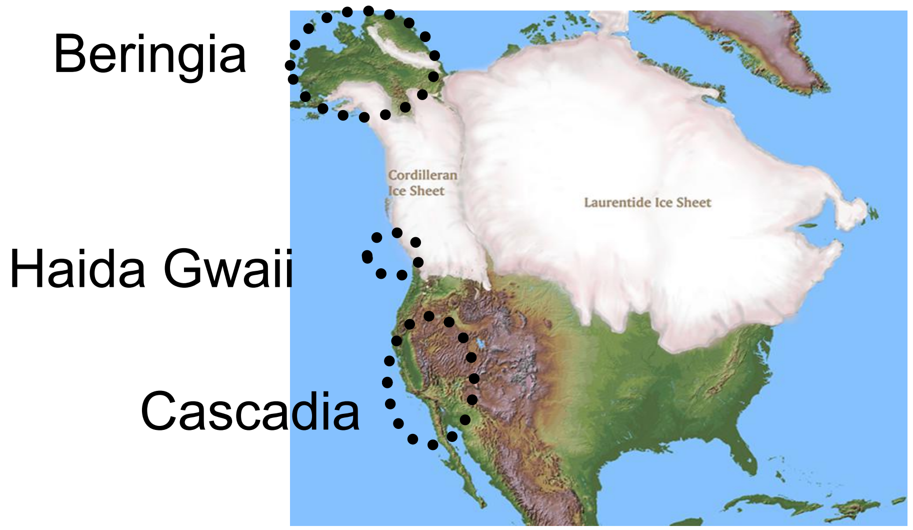
Crawford & Muir 2008

Coho salmon *Oncorhynchus kisutch*



Objectives:

1. Test alternative hypotheses of **number** and **location** of glacial refugia



2. Describe the impacts of **post-glacial recolonization** on the accumulation of **deleterious variants**

3. Test the **effect of recombination** on the efficacy of selection

Sampling

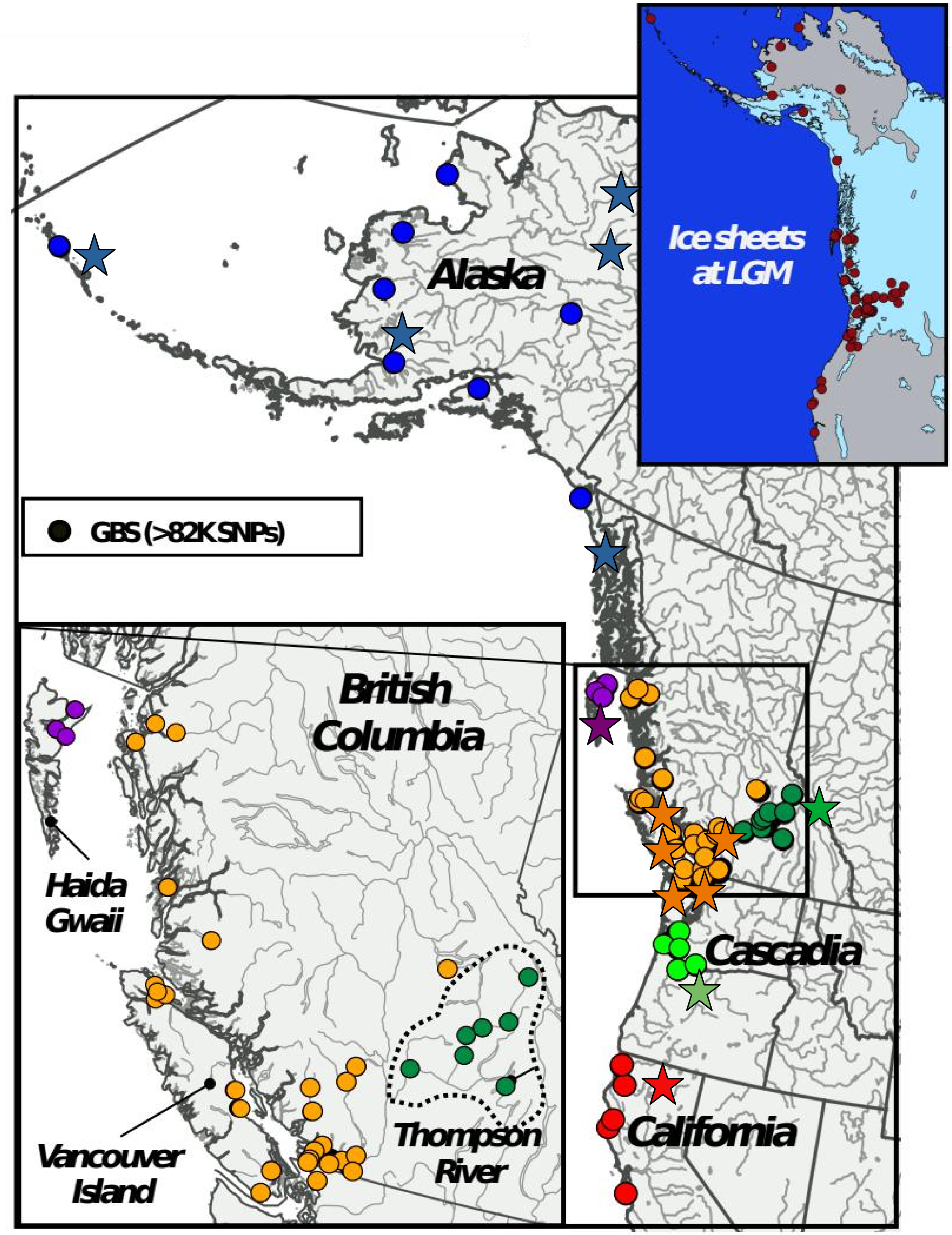
Genotyping-by-sequencing (GBS)

- 1,957 individuals from 58 sampling locations
- 82K SNPs after QC filters

Whole genome re-seq ★

- 71 ind/14 sampling locations
- SNPs called with GATK (30X)
- Outgroups (3 species)

- **GBS dataset 2: (GEA)**
  - 7,945 individuals 211 locations
  - 45 K SNP after QC filters



GitHub

GBS SNP calling: github.com/QuentinRougemont/stacks_workflow
Full genomes: github.com/QuentinRougemont/gatk_haplotype

GBS based results:

PLOS GENETICS

RESEARCH ARTICLE

Demographic history shaped geographical patterns of deleterious mutation load in a broadly distributed Pacific Salmon

Quentin Rougemont[1]*, Jean-Sébastien Moore[1], Thibault Leroy[2,3], Eric Normandeau[1], Eric B. Rondeau[4,5], Ruth E. Withler[6], Donald M. Van Doornik[7], Penelope A. Crane[8], Kerry A. Naish[9], John Carlos Garza[10], Terry D. Beacham[6], Ben F. Koop[4,5], Louis Bernatchez[1]

1 Département de Biologie, Institut de Biologie Intégrative et des Systèmes (IBIS), Université Laval, Québec, Québec, Canada, **2** ISEM, Univ. Montpellier, CNRS, EPHE, IRD, Montpellier, France, **3** Department of Botany & Biodiversity Research, University of Vienna, Vienna, Austria, **4** Centre for Biomedical Research, University of Victoria, Victoria, BC, Canada, **5** Department of Biology, University of Victoria, Victoria, BC, Canada, **6** Department of Fisheries and Ocean, Pacific Biological Station, Nanaimo, British Columbia, Canada, **7** National Oceanic and Atmospheric Administration, National Marine Fisheries Service, Northwest Fisheries Science Center, Manchester Research Station, Port Orchard, Washington, United States of America, **8** Conservation Genetics Laboratory, U.S. Fish and Wildlife Service, Anchorage, Alaska, United States of America, **9** School of Aquatic and Fishery Sciences, University of Washington, Seattle, WA, United States of America, **10** Fisheries Ecology Division, Southwest Fisheries Science Center, National Marine Fisheries Service and Institute of Marine Sciences, University of California–Santa Cruz, Santa Cruz, California, United States of America

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Check for updates

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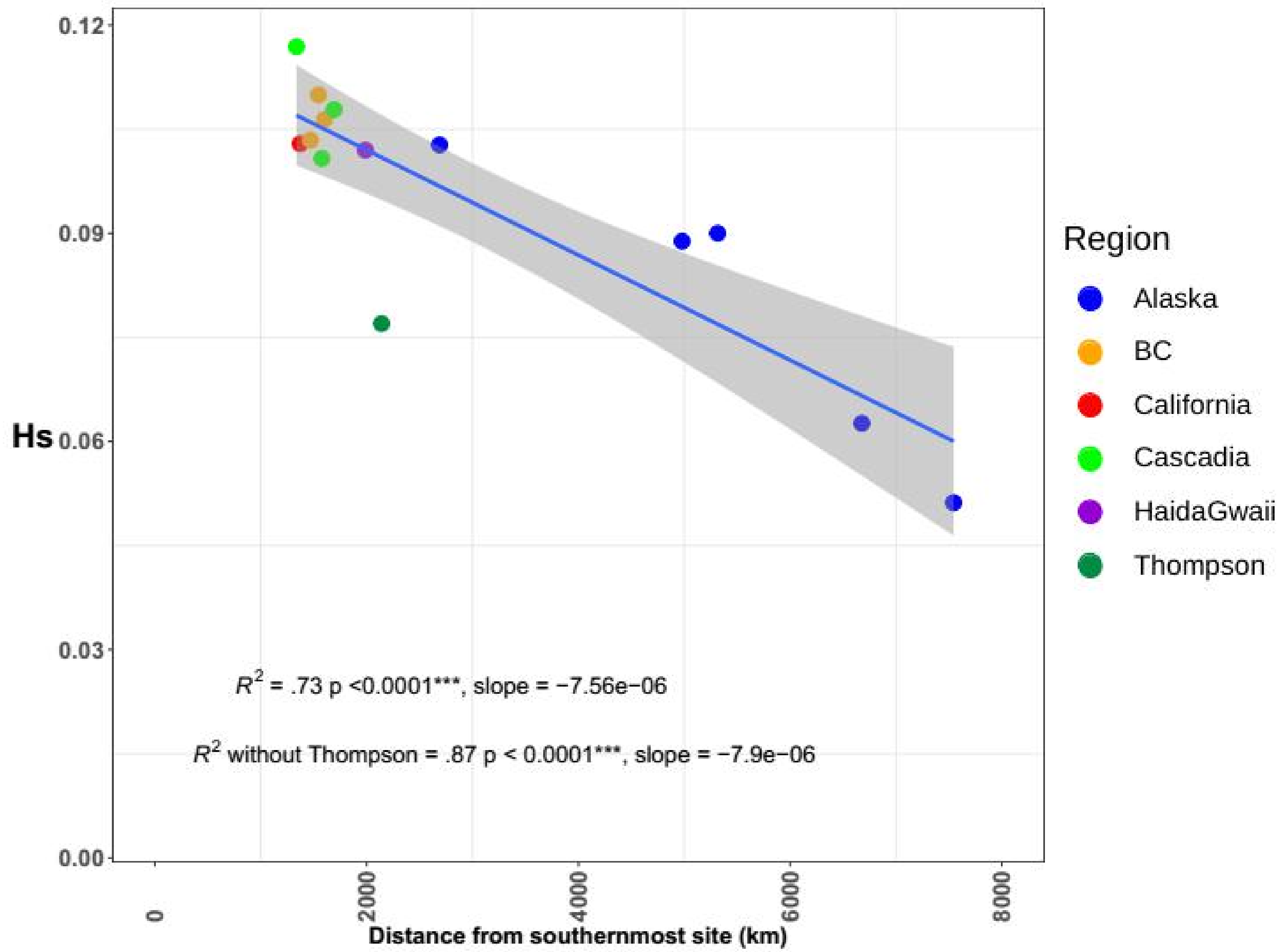
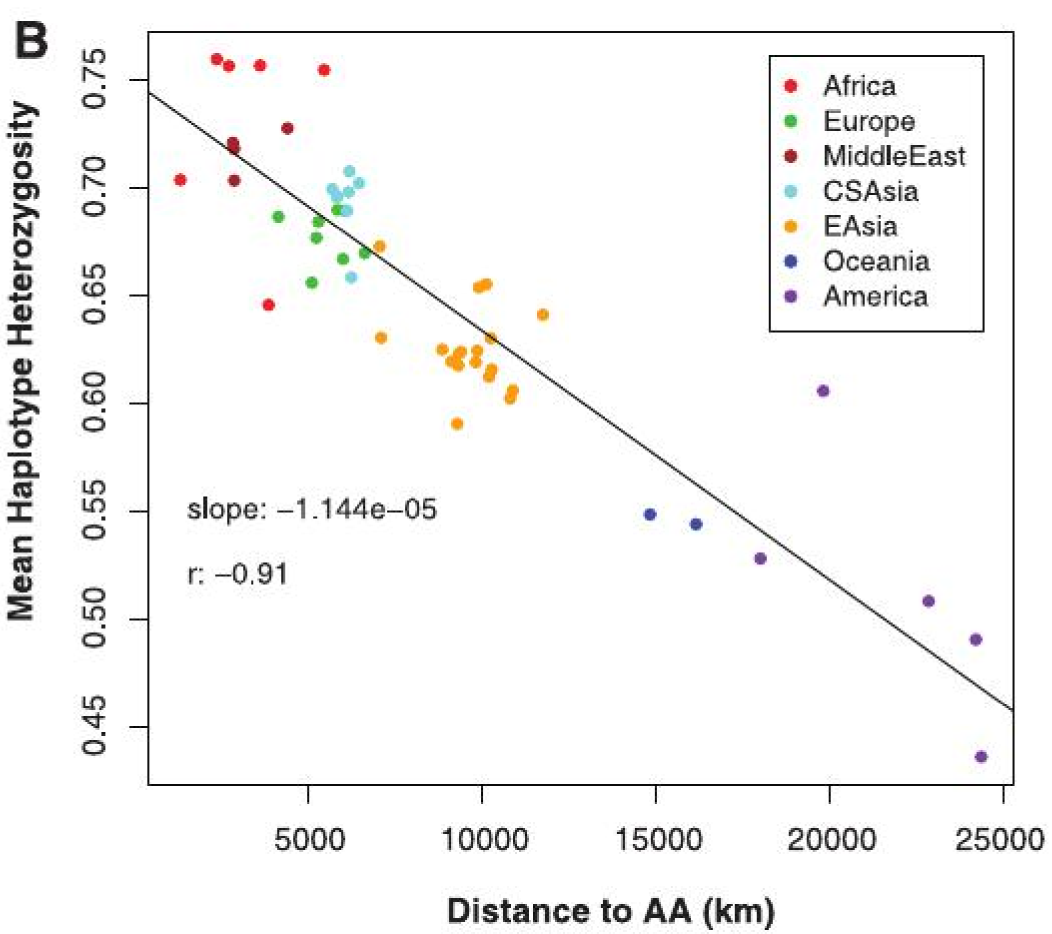
Abstract

Evidence for a single refugium south of ice sheets:
WGS data :

- Genetic diversity generally decreases from South to North



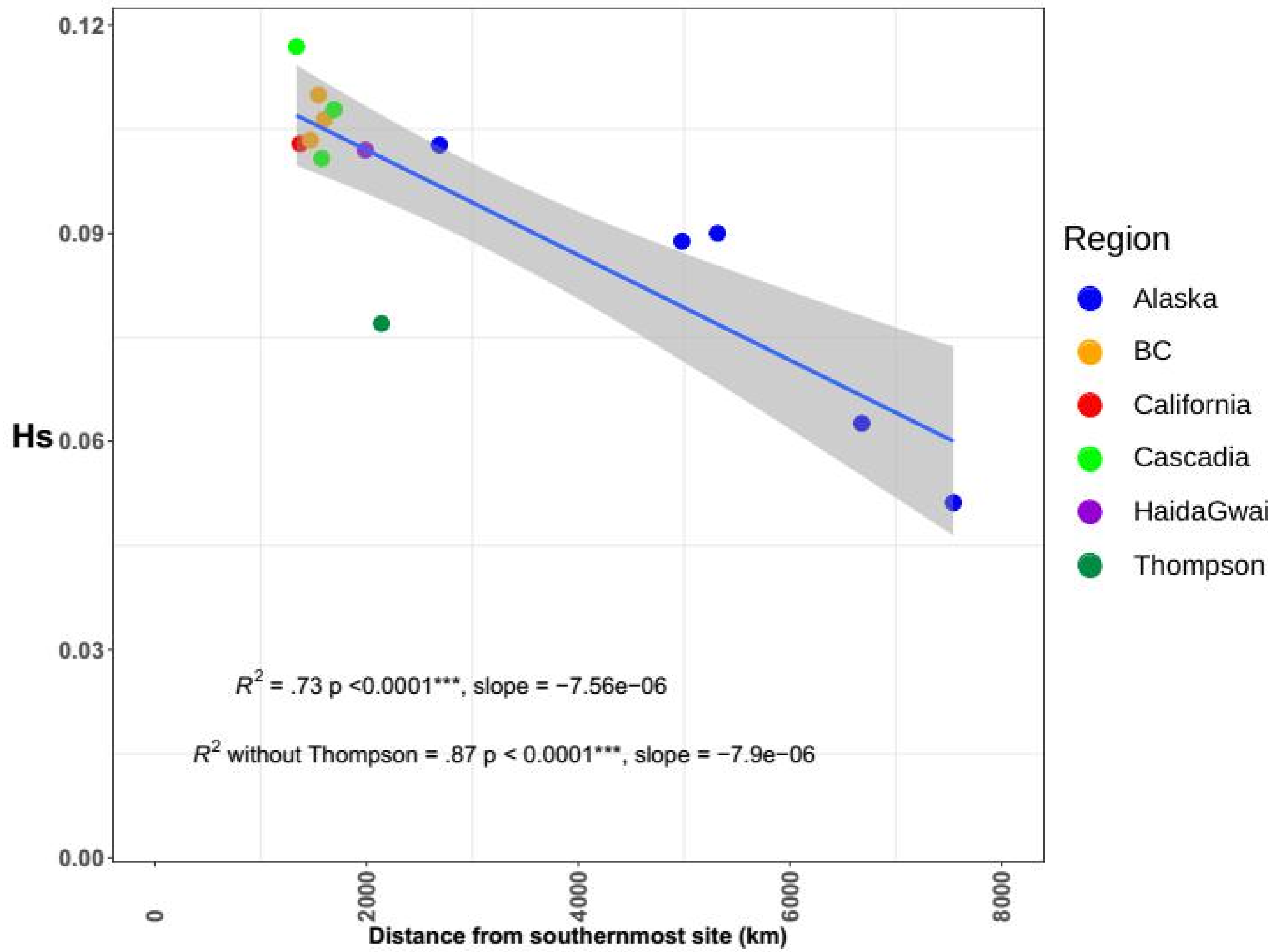


Evidence for a single refugium south of ice sheets:

WGS data :

- Genetic diversity generally decreases from South to North

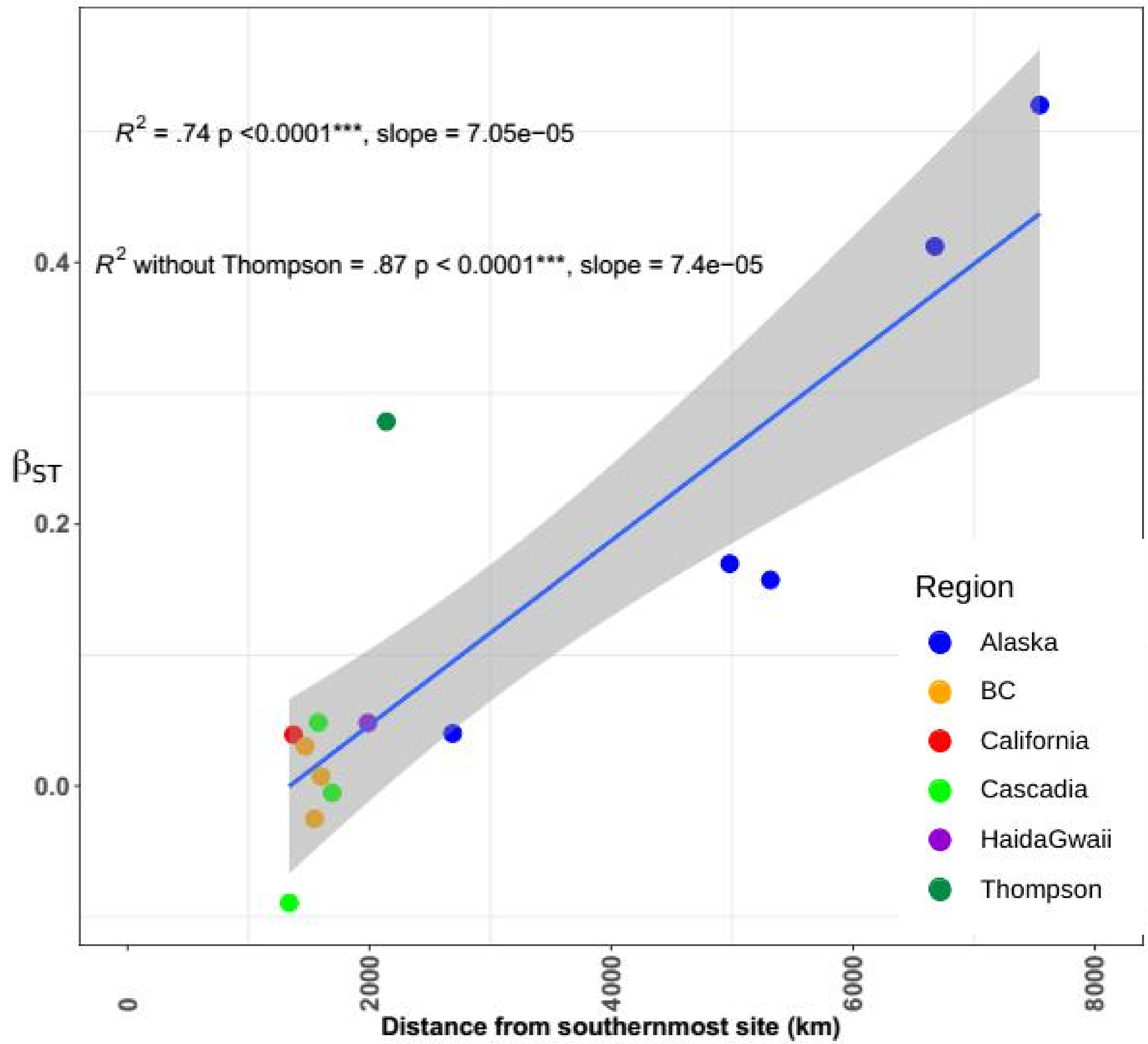
- Pronounced reduction in Het in Thompson River - *consistent with recent population declines*



Southern population are more ancestral:

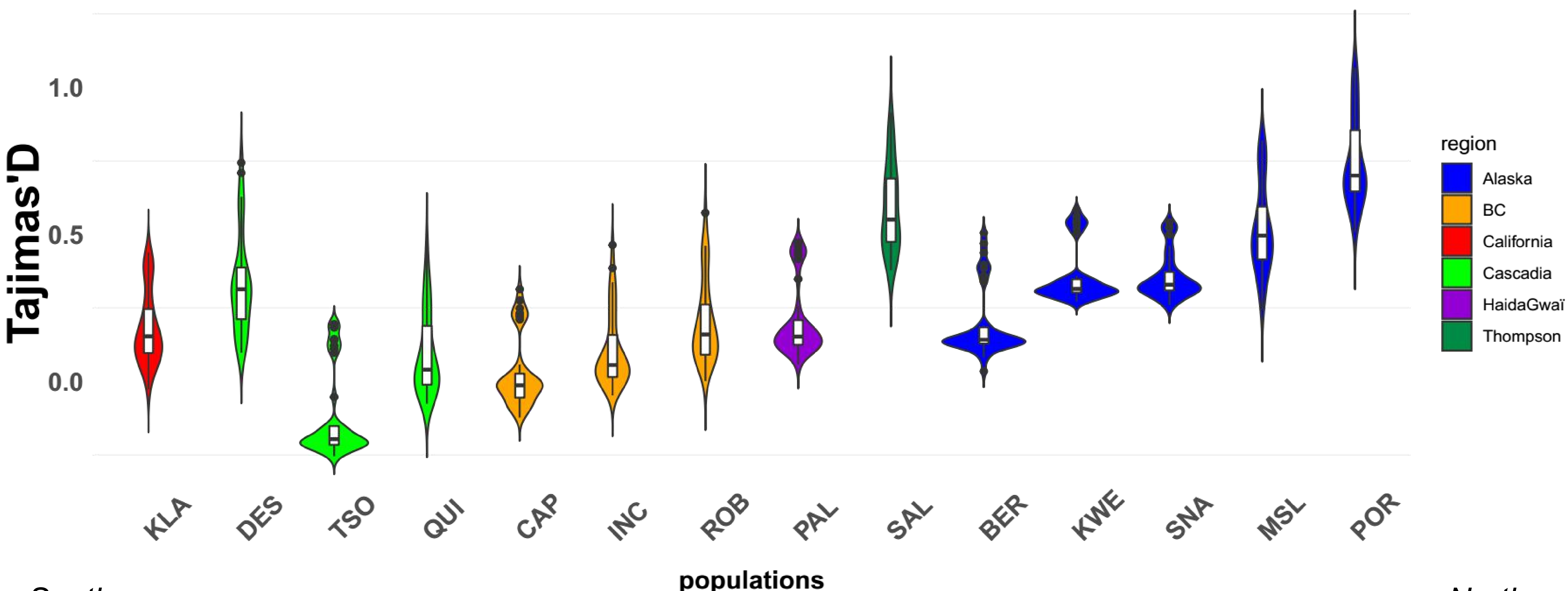
WGS data :

- Genetic differentiation follows a pattern of IBD
- Ancestral population located in Southern Areas



Population bottleneck toward the north

WGS data :



South → *North*

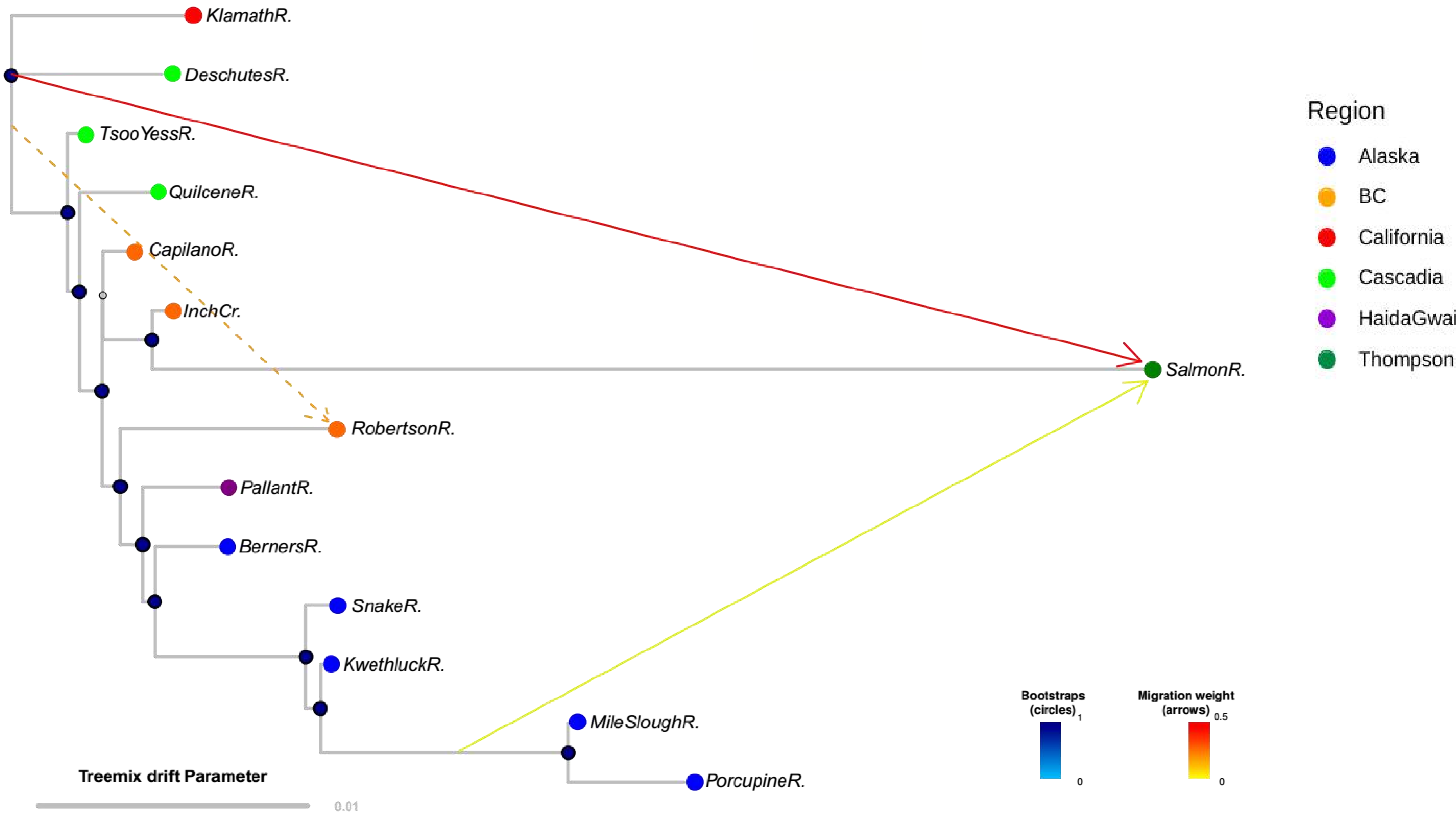
→

→

→ **Strong founder event during upstream post-glacial recolonization**

Support for the south-north topology

WGS data :

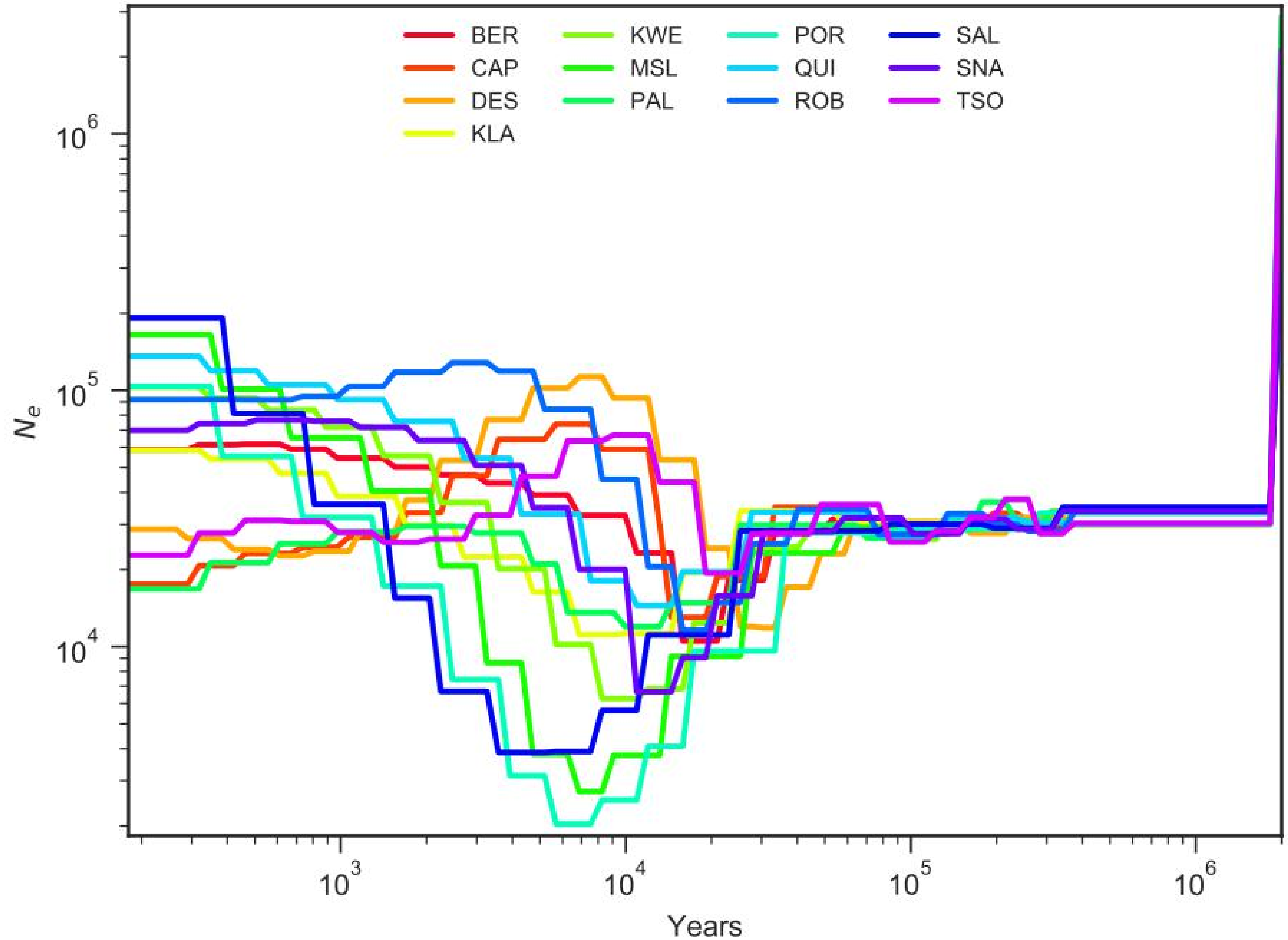


Whole genomes demography

WGS data :

- Rapid demographic expansion after deglaciation
- Bottleneck intensity ~ follows geography

Sequentially Markovian Coalescent (SMC++)

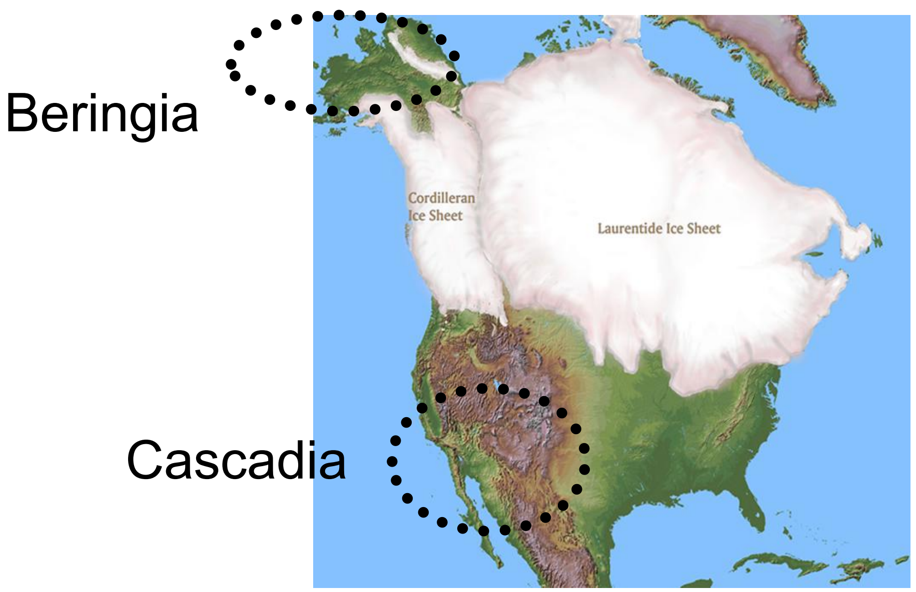


Present *Past*

Formal testing of gene flow from a second refugial population

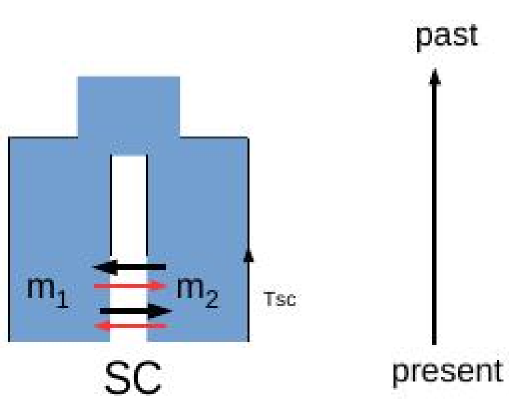
Hypothesis :

More than one refugia existed during the last glacial period



Prediction :

Secondary-Contact models should be favoured



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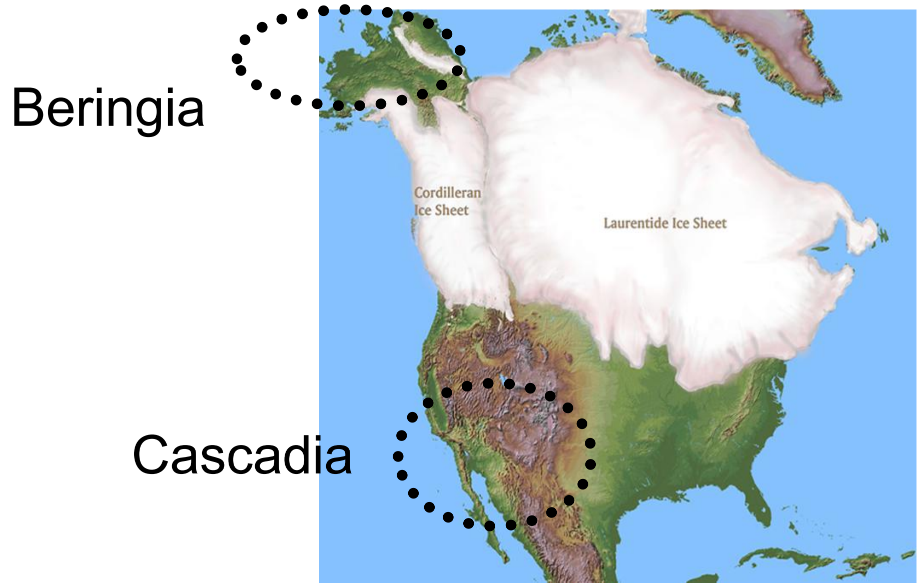

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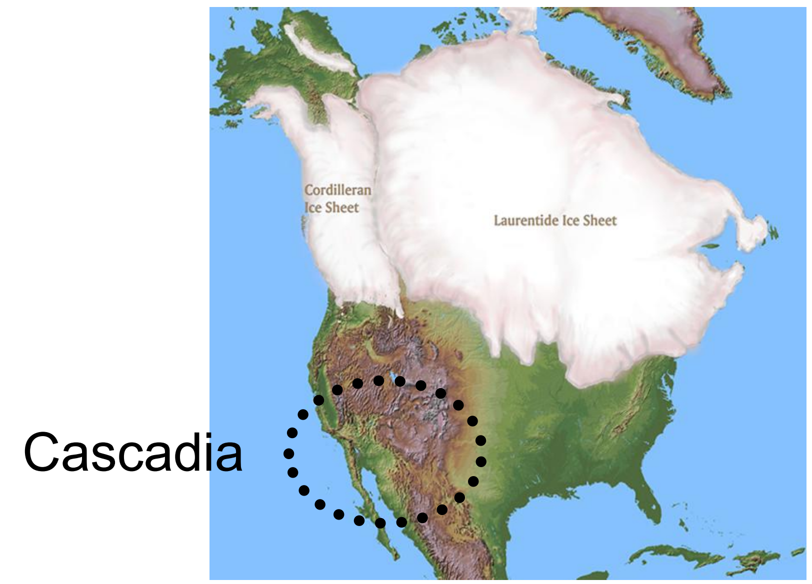

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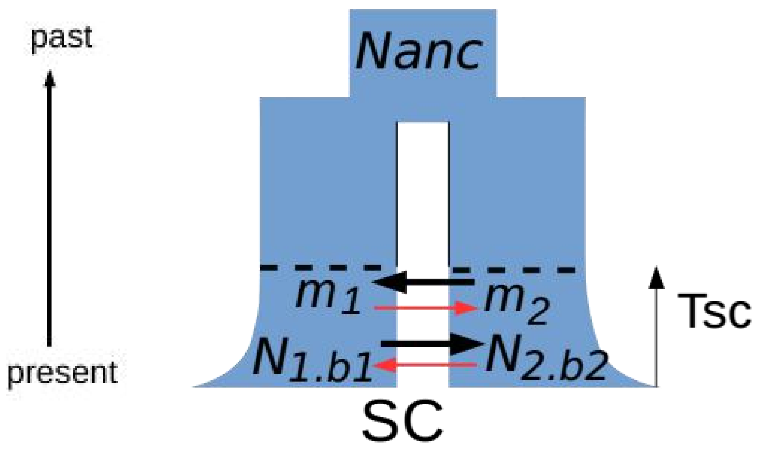
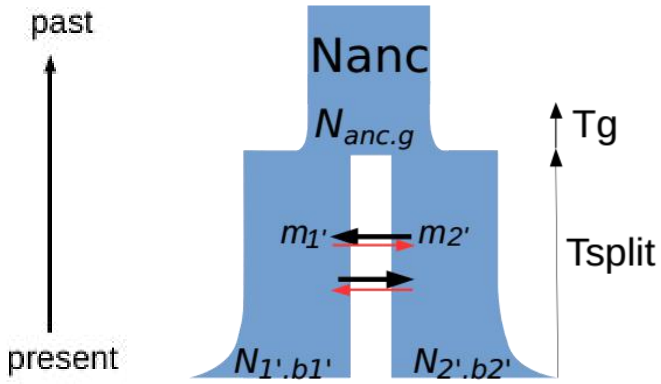


Isolation w. Migration models should be favoured
Population expansions



Formal testing of gene flow from a second refugial population

migration : homogeneous *vs* heterogeneous (*m*)
Barriers to gene flow

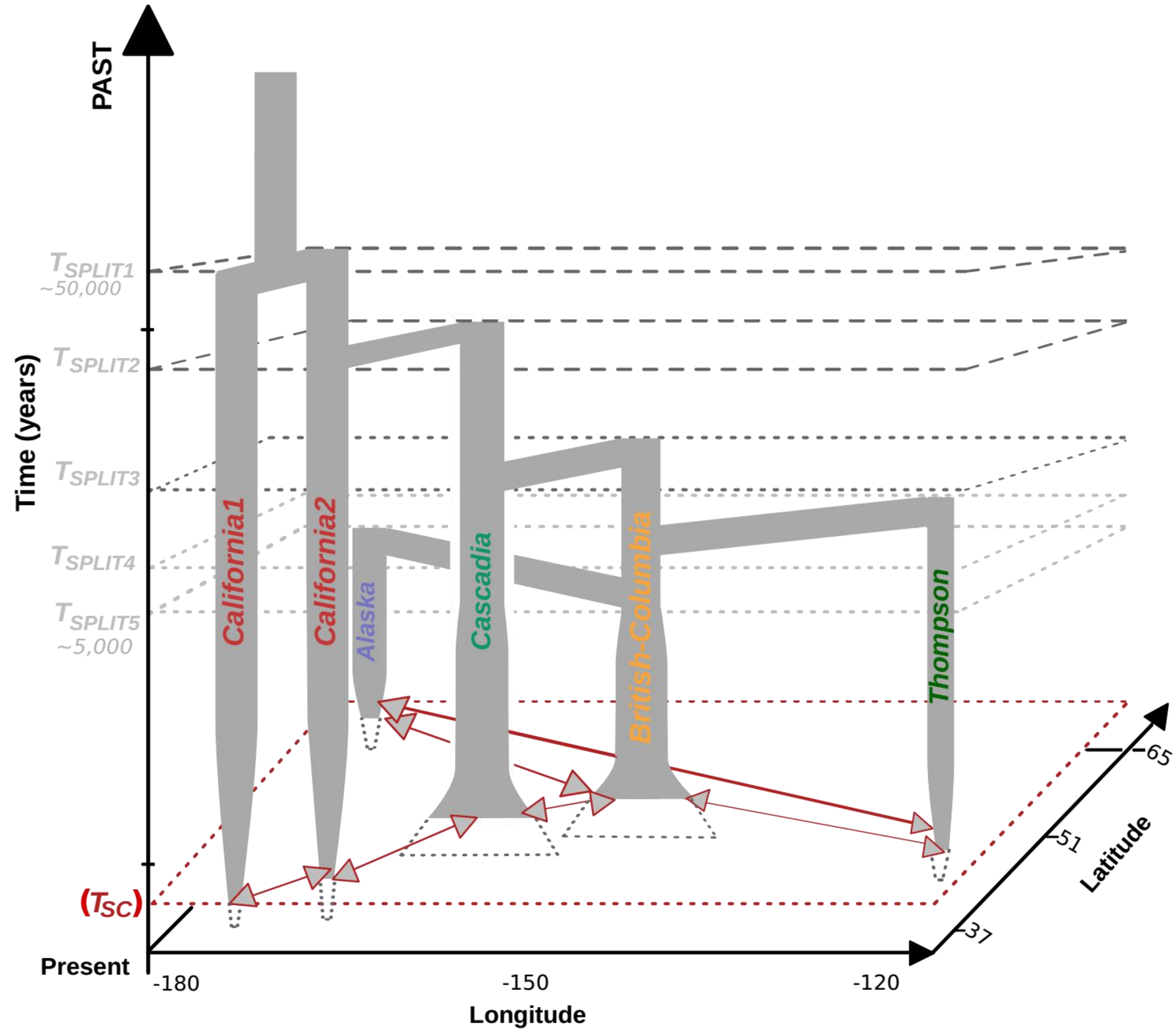
Genetic drift : homogeneous *vs* heterogeneous *Ne* **(Linked selection)**

- With/Without Growth **(expansion/contraction)** in daughter and ancestral populations
- 3 outgroups
- Comparison between: Southern pop vs Alaska
  Southern pop vs Thompson
  Alaska vs Thompson
- ***δaδi :*** 28 scenario * 20-30 replicates

Roux et al. 2013, 2014 ; 2016
Tine et al. 2014

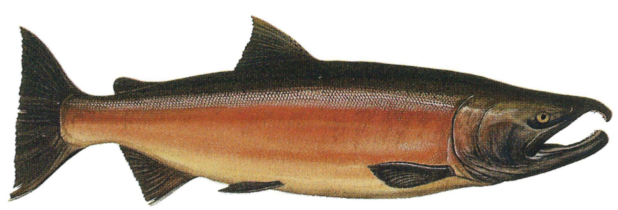
Demographic history – Summary **v2**

GBS data :



Demographic modelling suggest a role for linked selection

Demography and **recombination** may influence the **deleterious load**



Coho salmon

Rainbow trout

sockeye/kokanee
salmon

Demography and **recombination** may influence the **deleterious load**

WGS data :

Prediction : Increased load in bottlenecked populations

Increased load at range margins

Deleterious mutations ~f(**recombination**)

Demography and **recombination** may influence the **deleterious load**

WGS data :

Measuring load :

$\pi N/\pi S$ (e.g. Chen et al. 2017)

Selection efficacy : (e.g. Galtier, 2016)

Rate of (non)-adaptative non-synonymous amino-acid substitutions :

ω & ω

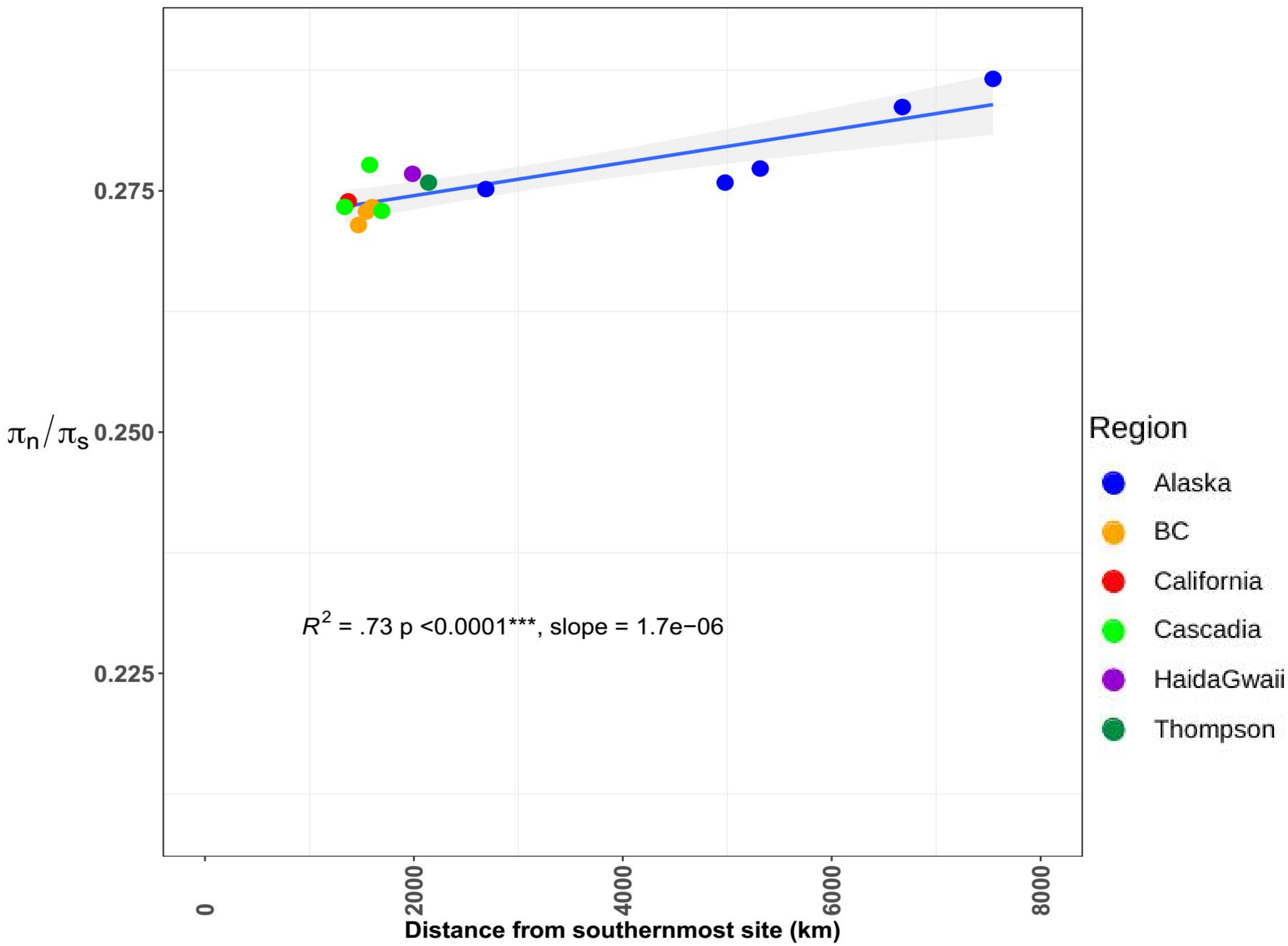
Proportion of adaptative non-synonymous amino-acid substitutions :

α = ω /(dN/dS)

3 outgroups + whole genome reseq. from available sp.

Post-glacial recolonization explains variation in **deleterious load**

WGS data :



→ Load slightly increases with distance

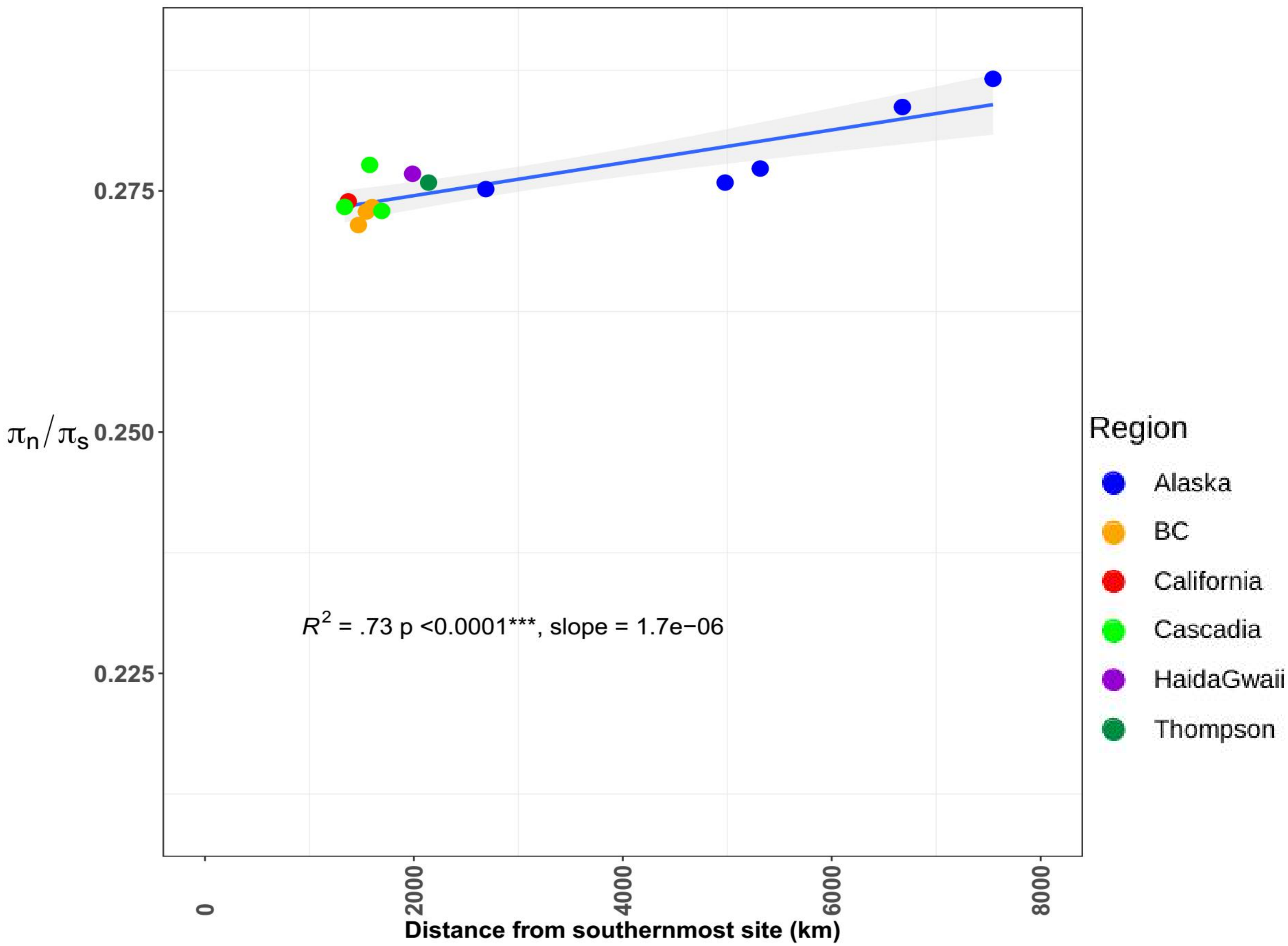
Post-glacial recolonization explains variation in **deleterious load**

WGS data :


Sockeye (n=10)


Kokanee (n=11)


Rainbow (n = 19)



→ **Load slightly increases with distance**

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WGS data :


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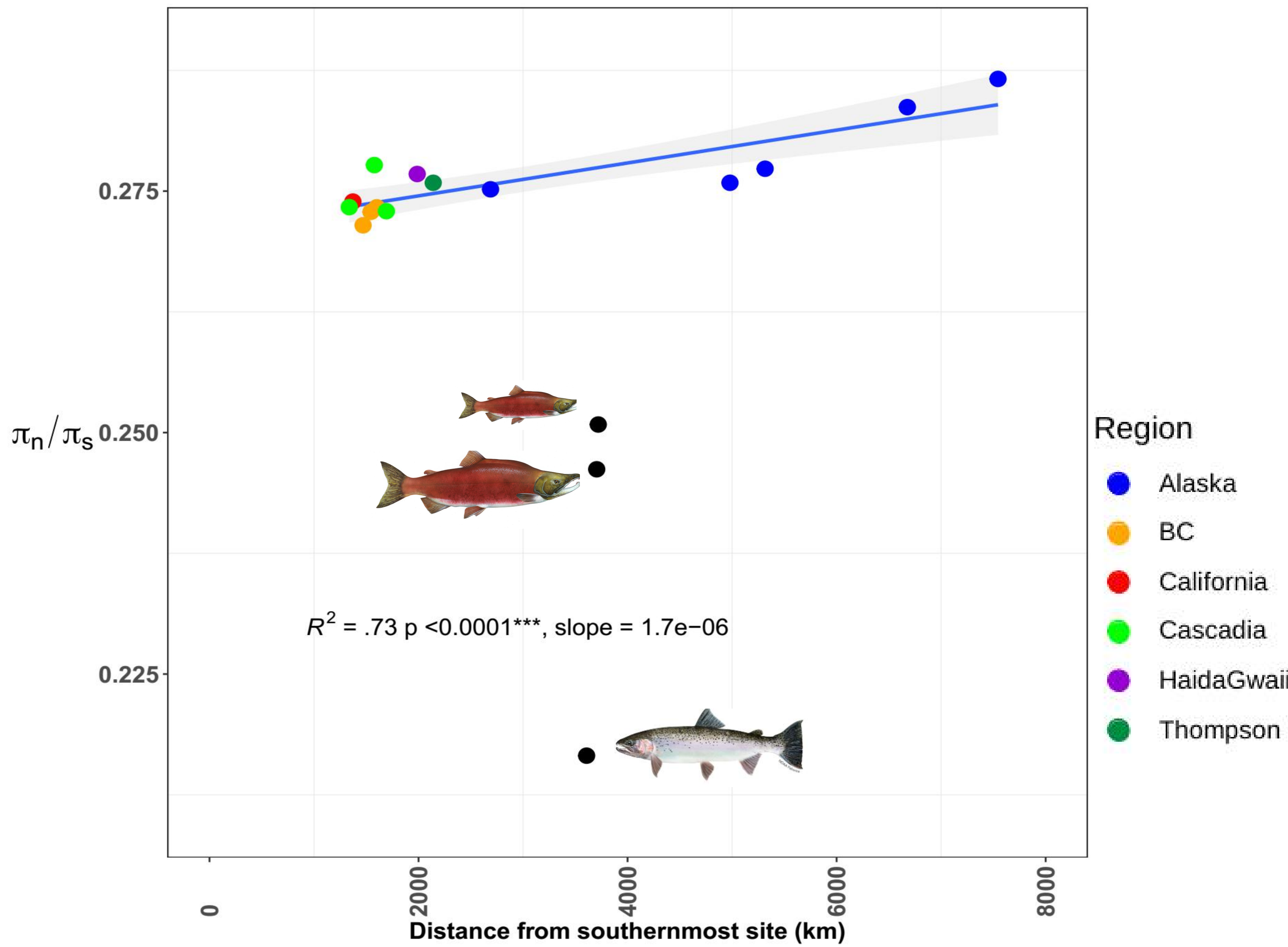
Kokanee (n=11)


Rainbow (n = 19)

$\Delta\pi N/\pi S$ coho = 0.015

$\Delta\pi N/\pi S$ sockeye-kokanee = 0.005



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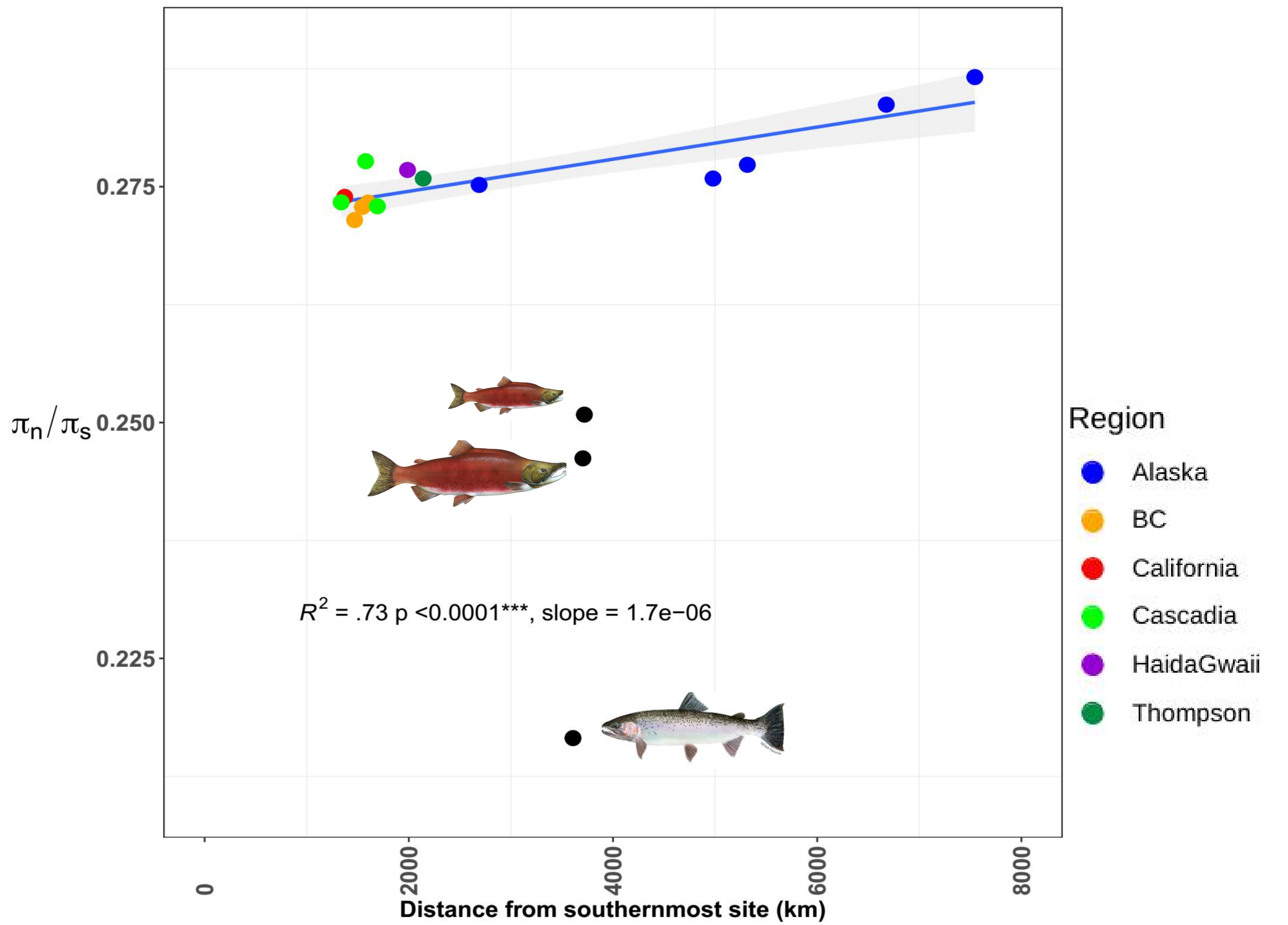
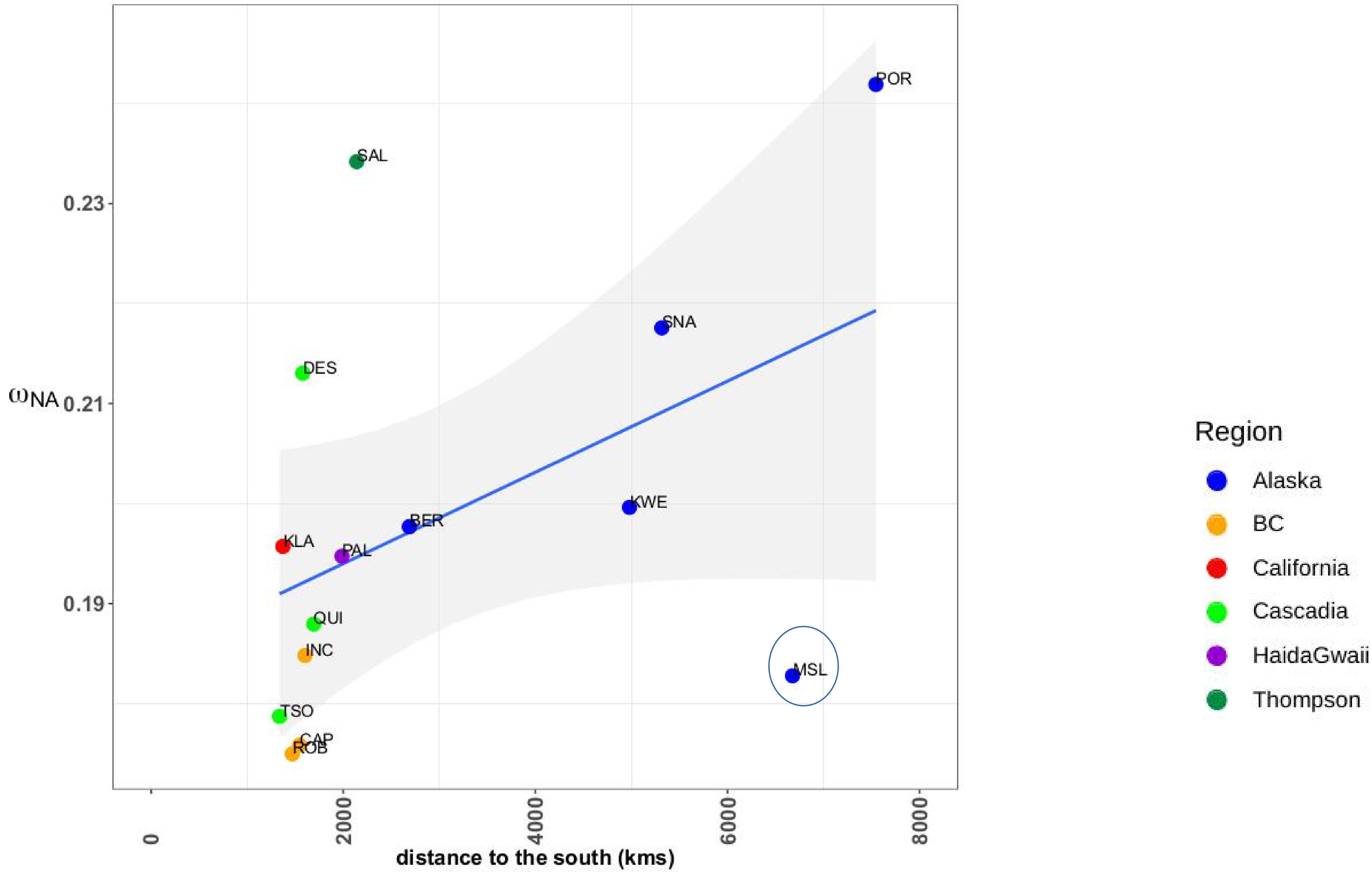


→ **Load also associated to loss of anadromy**

→ **Large variation among species**

Post-glacial recolonization explains variation in **deleterious load**

WGS data :

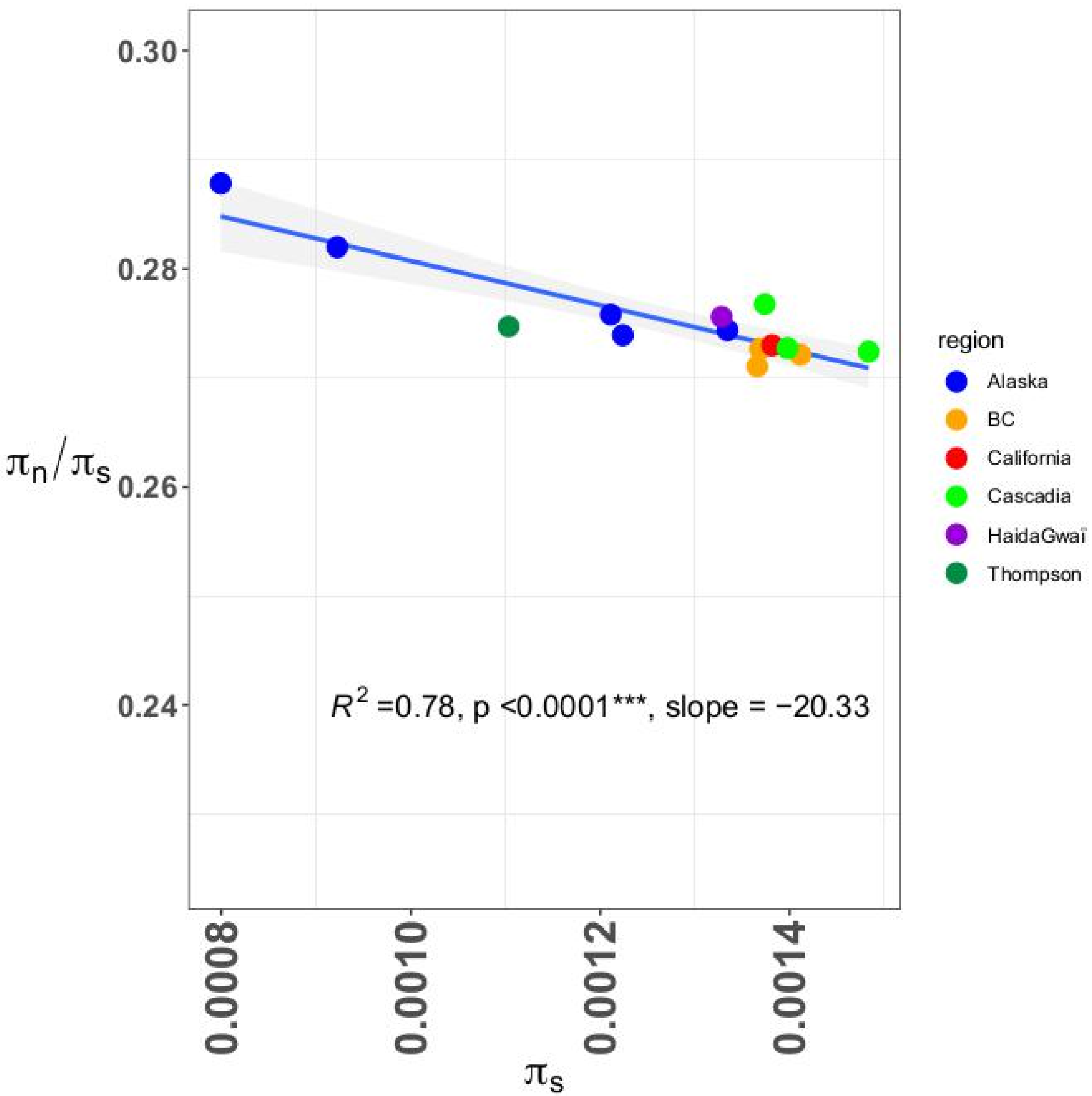


Lower rate of adaptation in the North

Lower rate of adaptation in bottlenecked populations

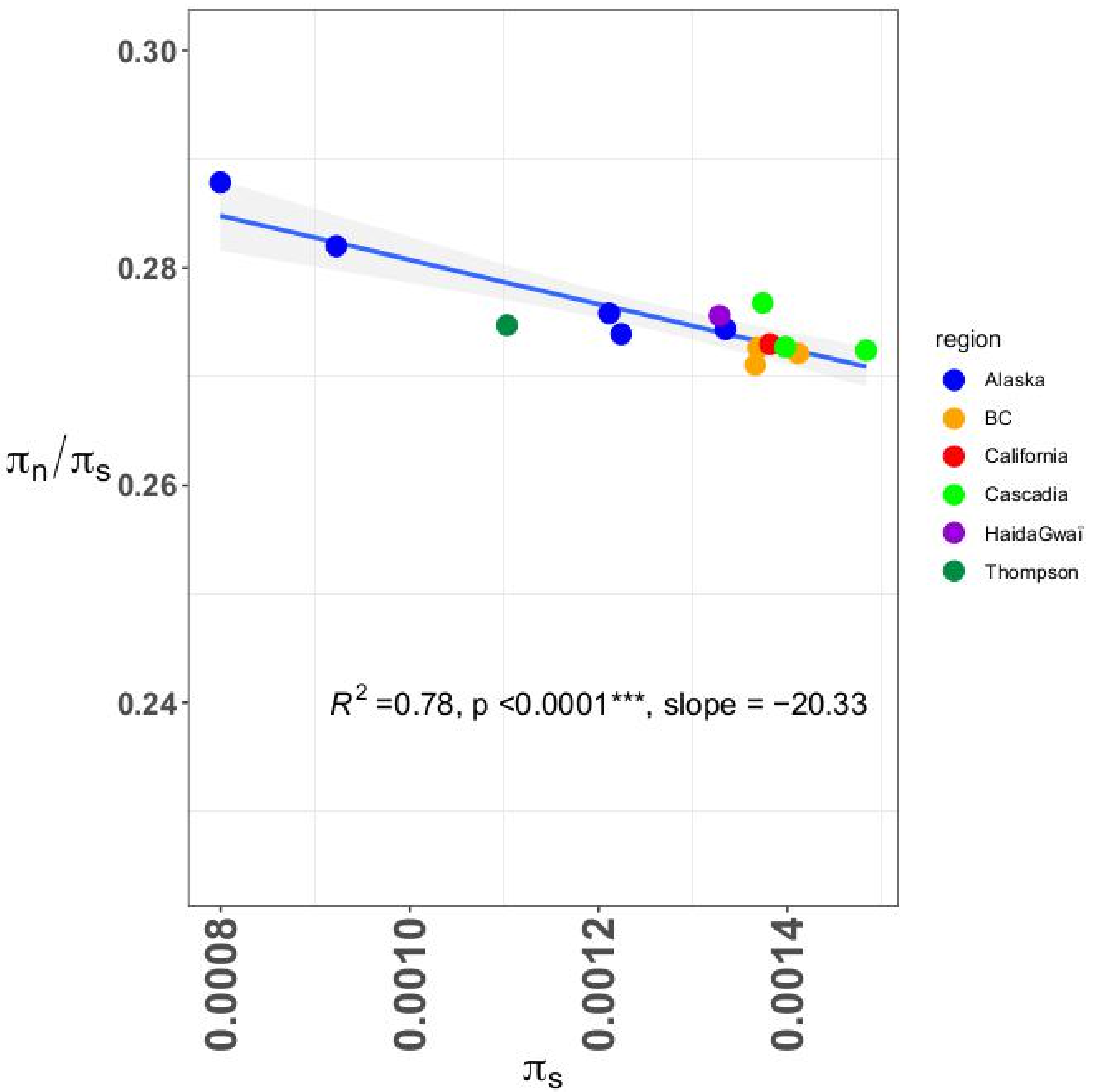
Effective pop. size explains variation in deleterious **mutation load**

WGS data :



Effective pop. size explains variation in deleterious **mutation load**

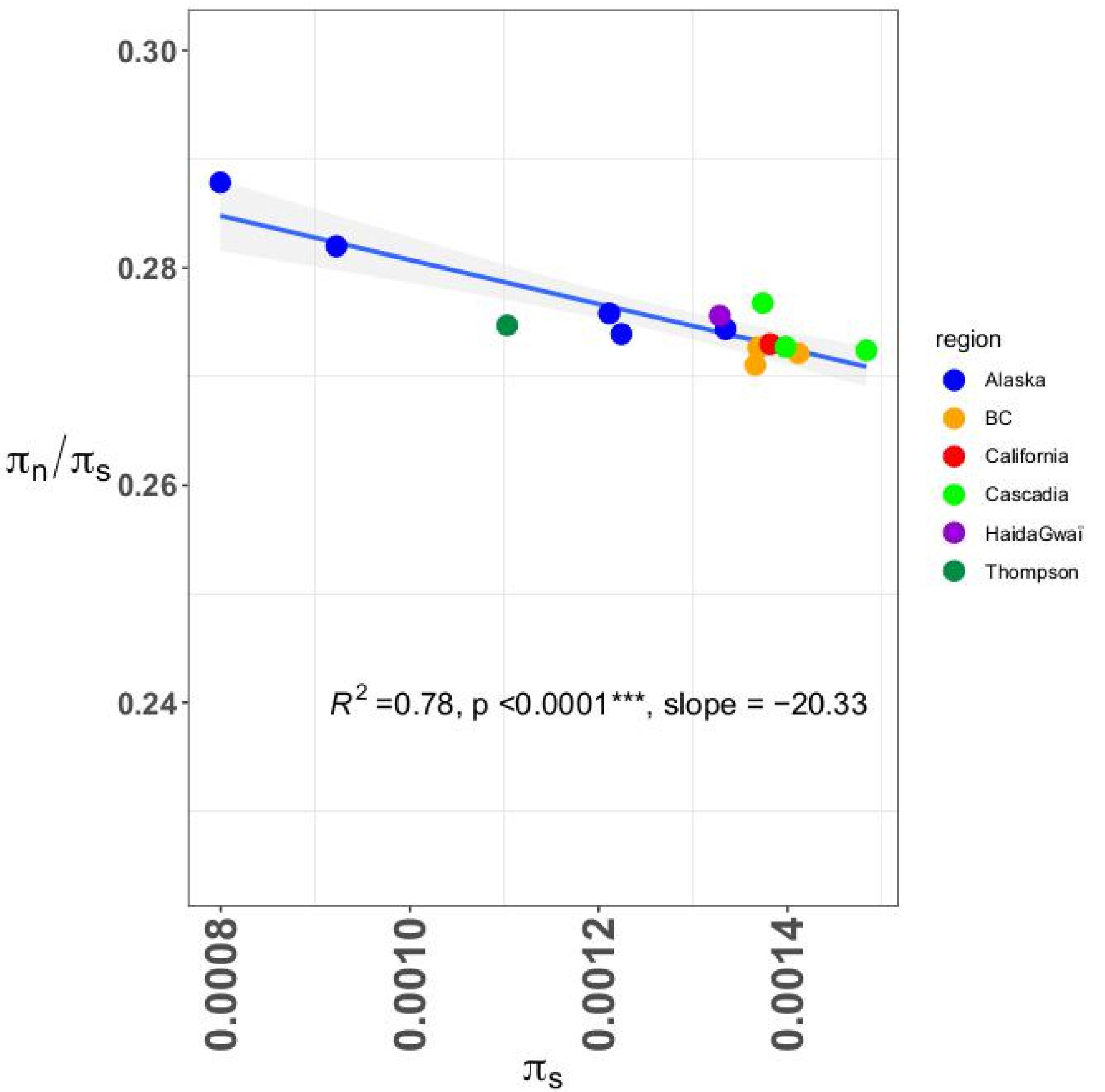
WGS data :



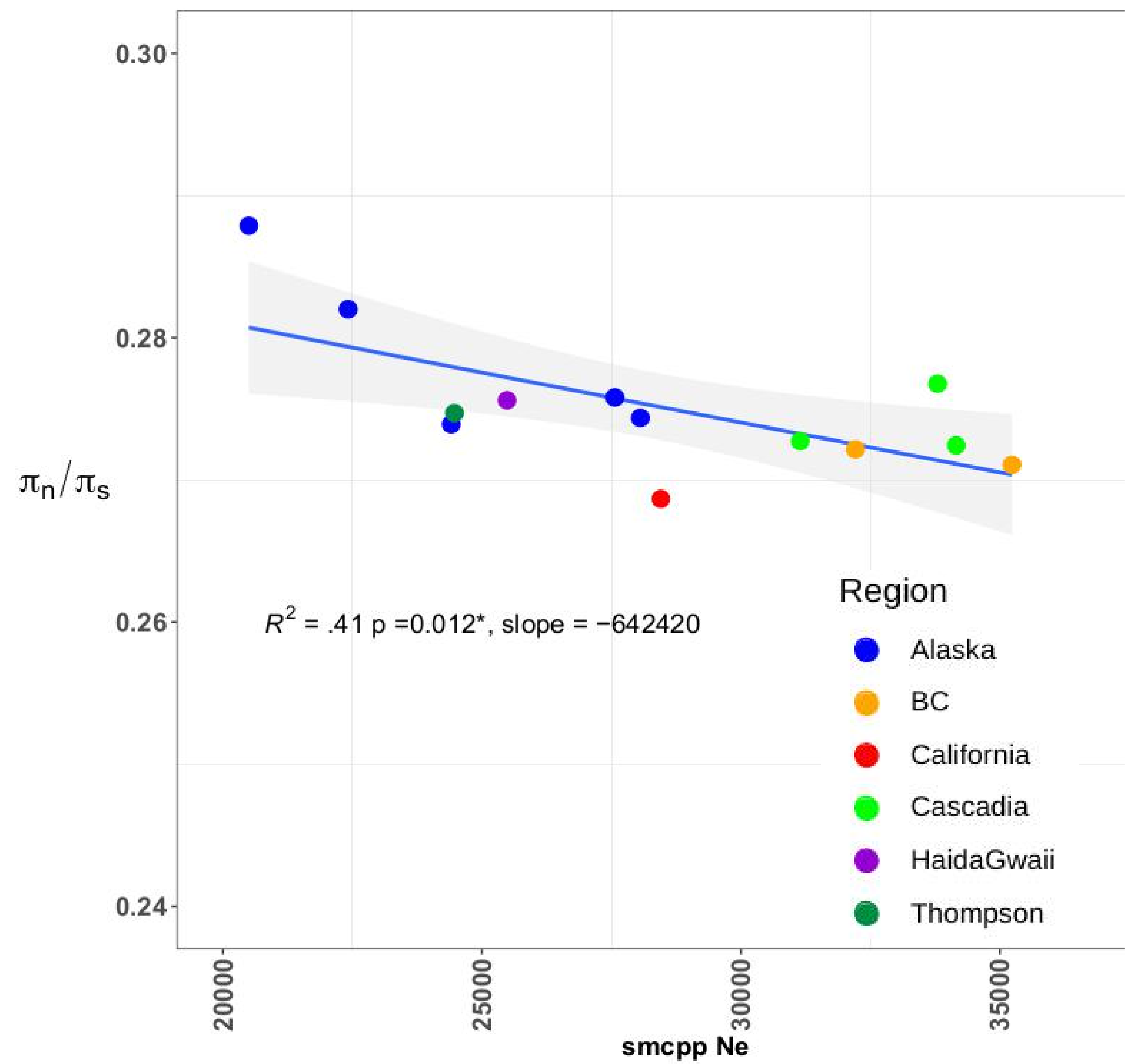
Not independent

Effective pop. size explains variation in deleterious **mutation load**

WGS data :



Not independent

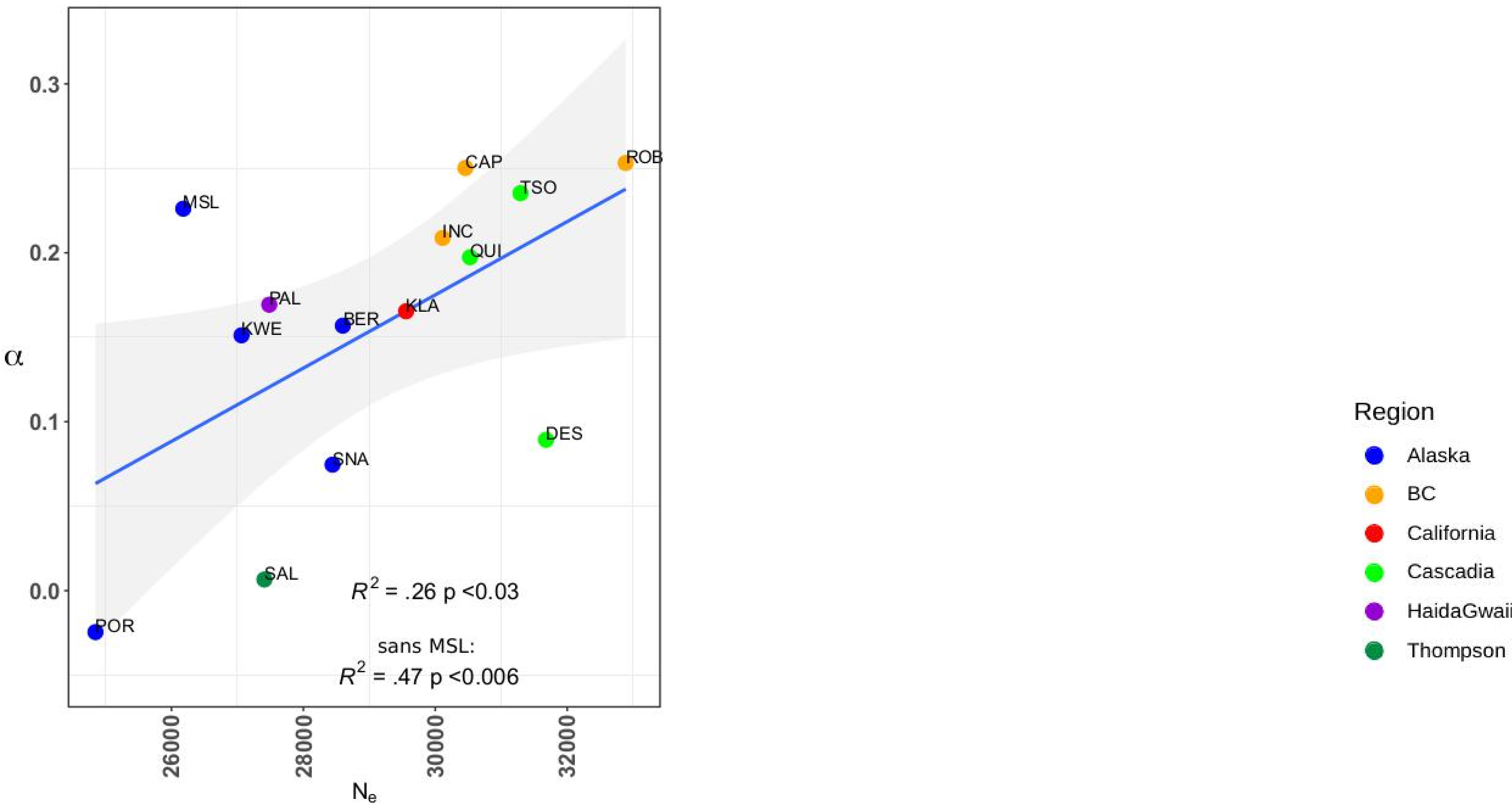


Independent!

→ **Higher load with reduced *Ne***

Effective pop. size explains variation in selection efficacy

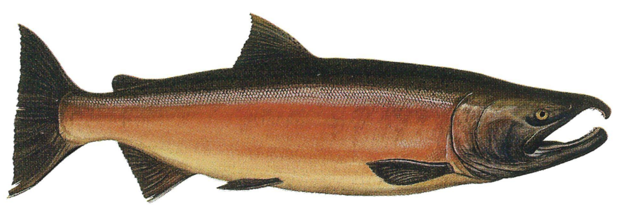
WGS data :



→ **Lower efficacy of selection with decreased *Ne***

How about recombination ??

Prediction :
Deleterious mutations are expected to be negatively correlated with **recombination**



Additional species:

Other species ongoing...

Recombination may also influence the deleterious load

WGS data :

Measuring recombination

LDhat *(Auton et al. 2005)*

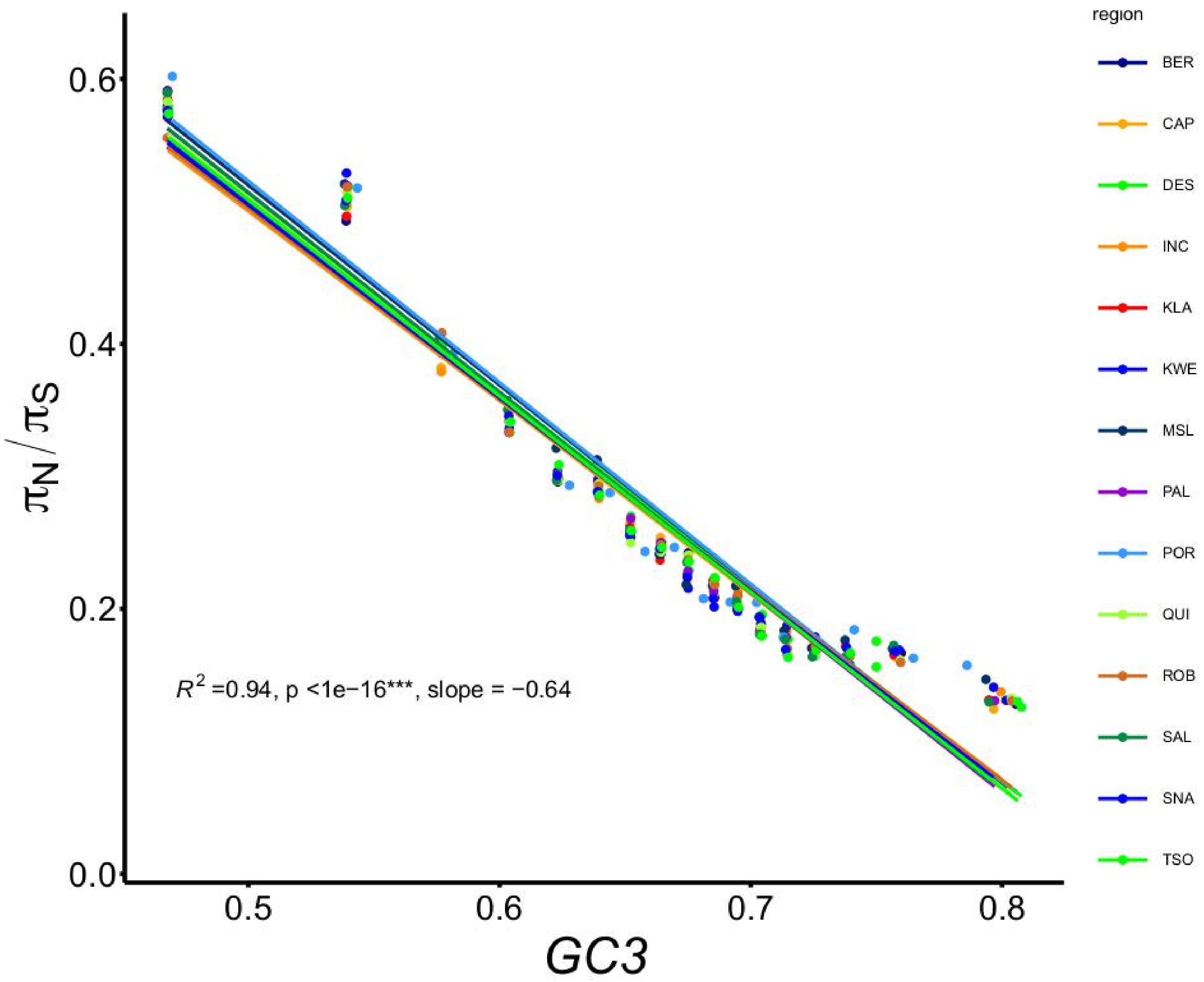
Demography aware prediction : Recurrent Neural Networks
(Adrion et al. 2020) (ongoing)

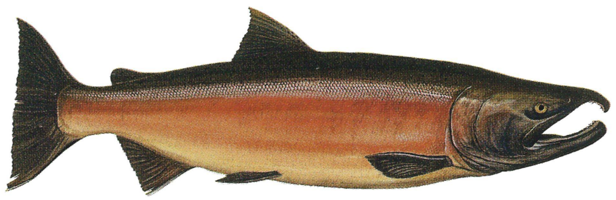
GC content at 3rd codon position (GC3) :
Recombination proxy due to gBGC favoring GC over AT
(Singhal et al. 2015 ; Leroy et al. 2021)

Regions of low recombination have elevated numbers of deleterious mutations:

WGS data :

Less efficient purging in areas of low recombination





coho

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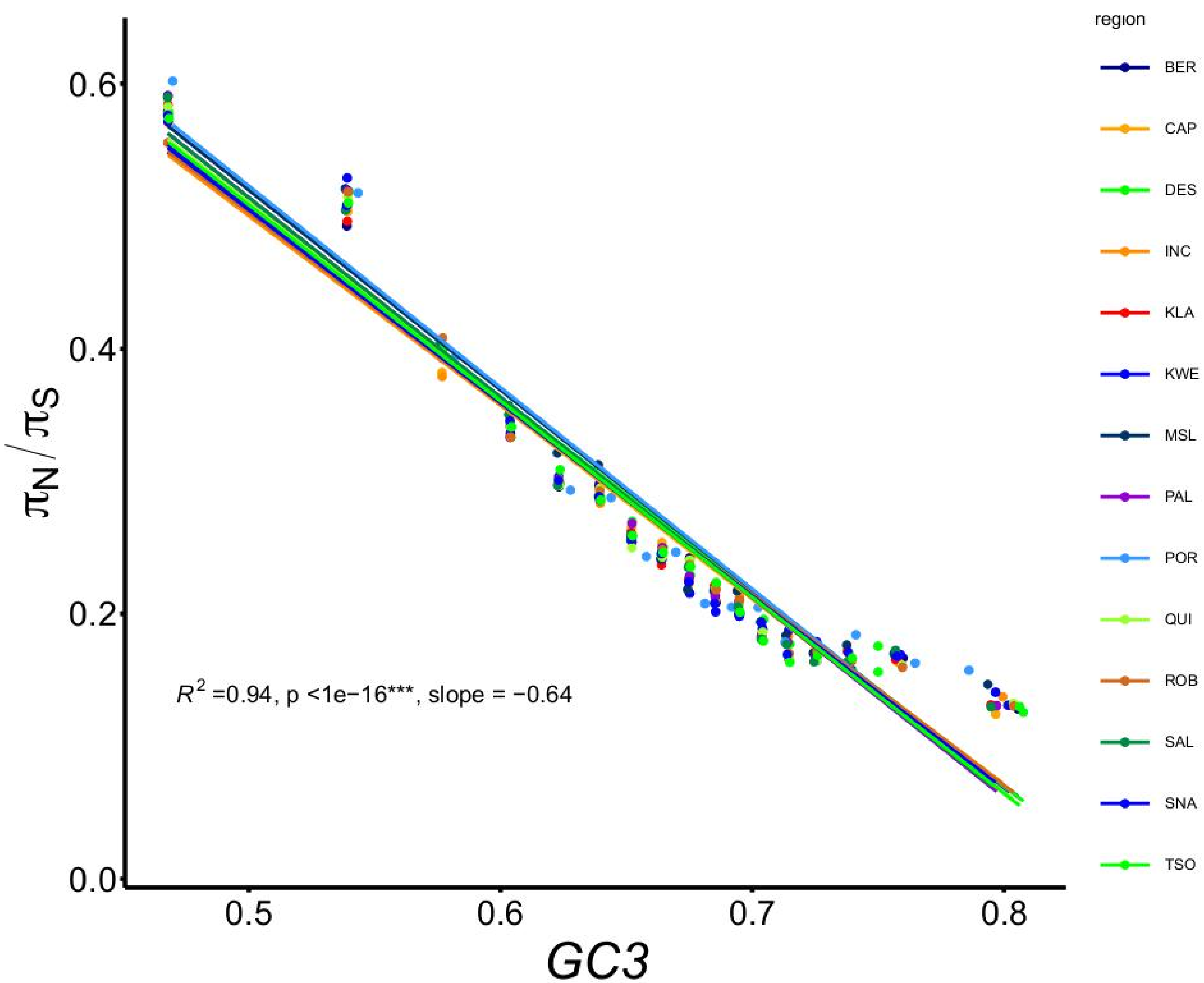
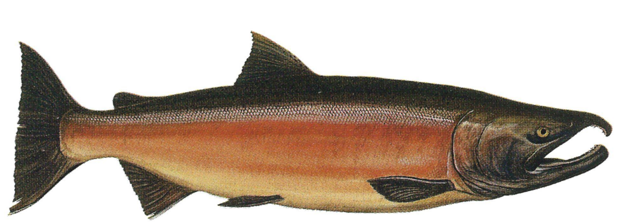


Maybe biased by gBGC?

gBGC: favors GC over AT

Solution: work on GC conservative sites (G <-> C, A <-> T) not affected By gGBC

(see Duret & Galtier 2009)



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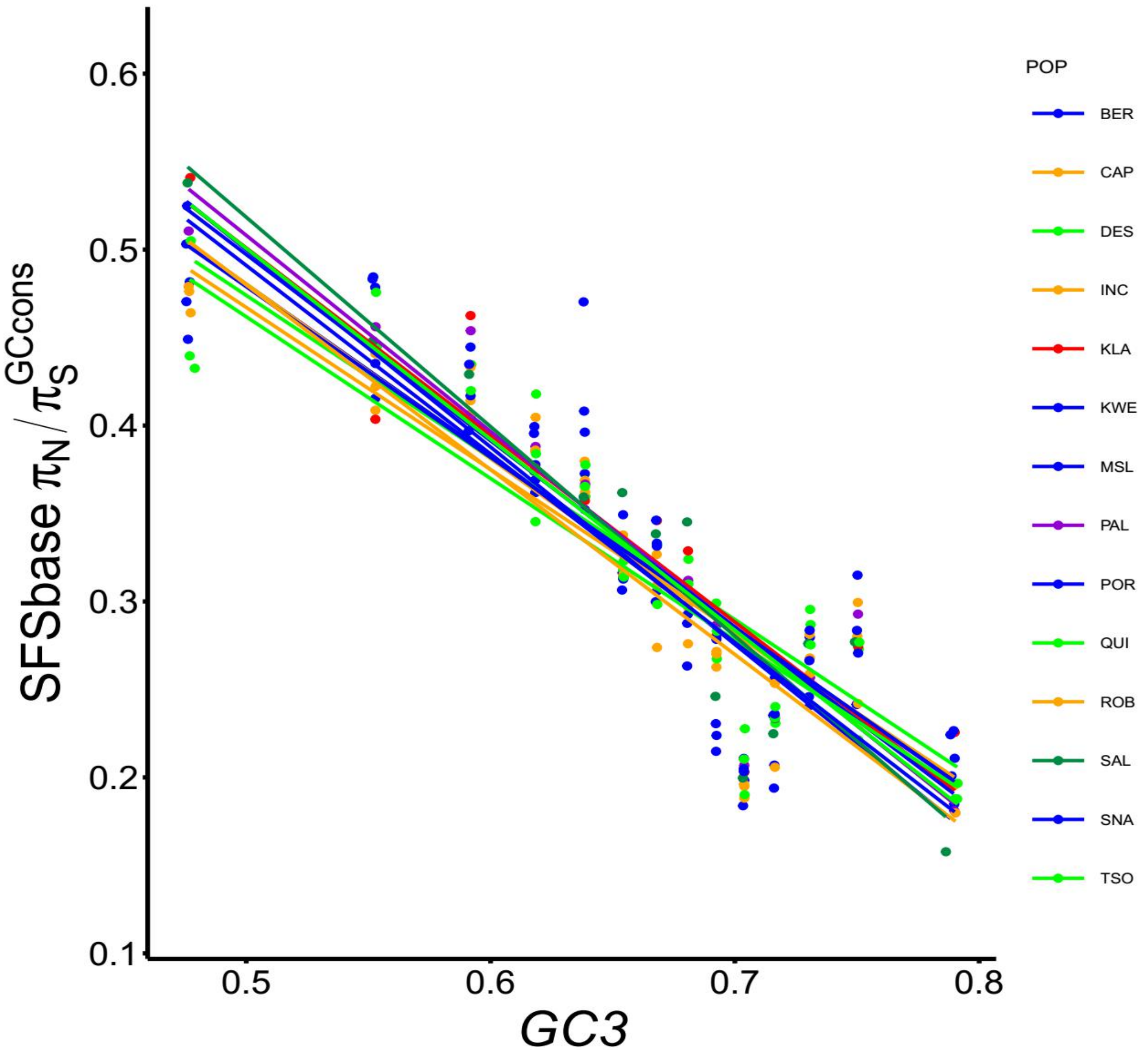
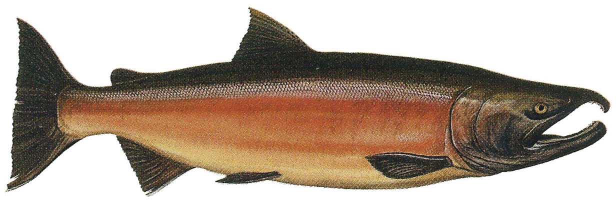


Does not seem biased by gBGC



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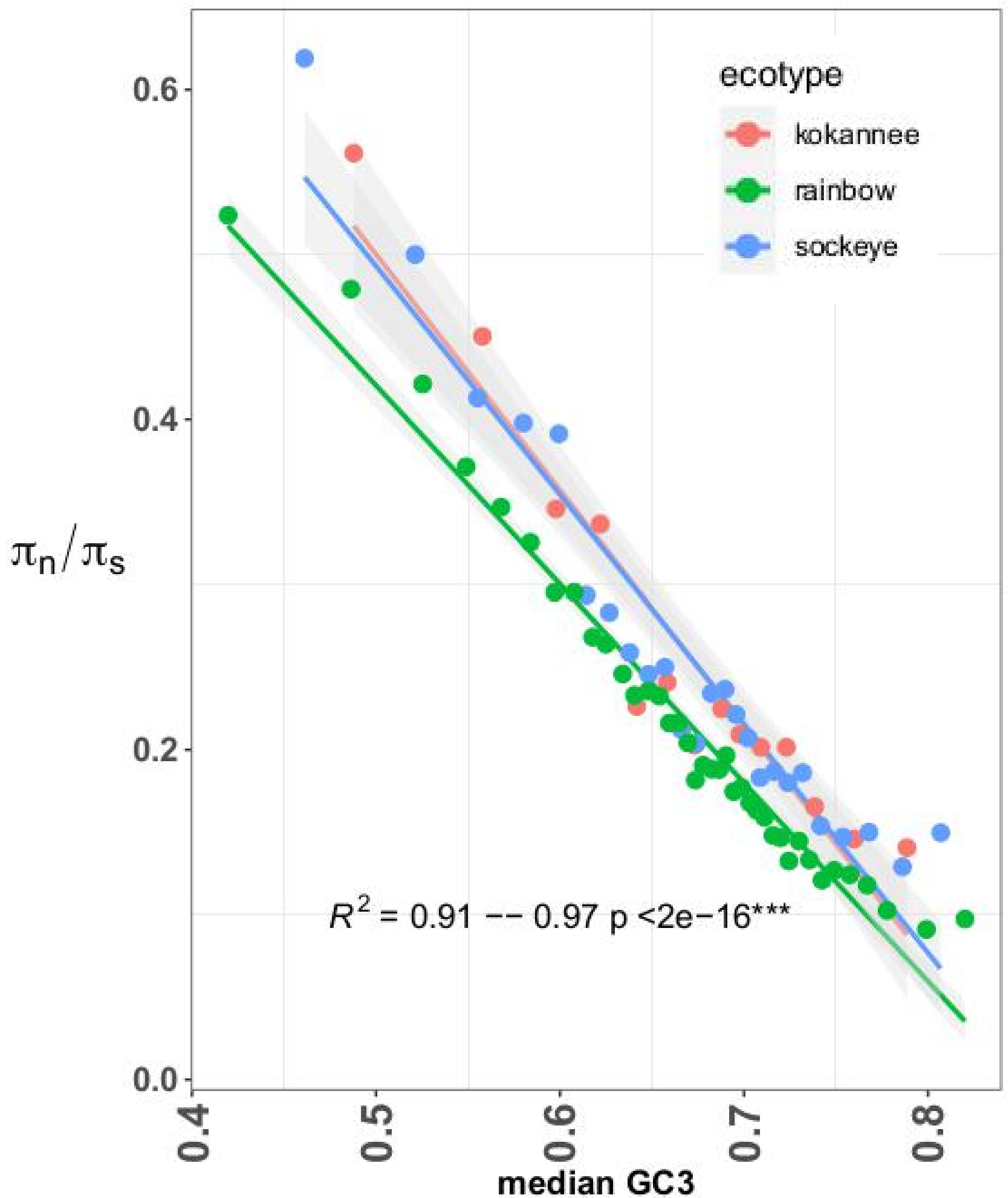
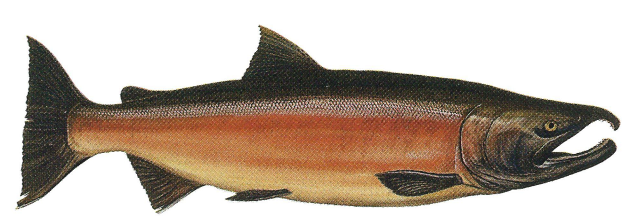


Same pattern in other species

Rainbow trout

Sockeye

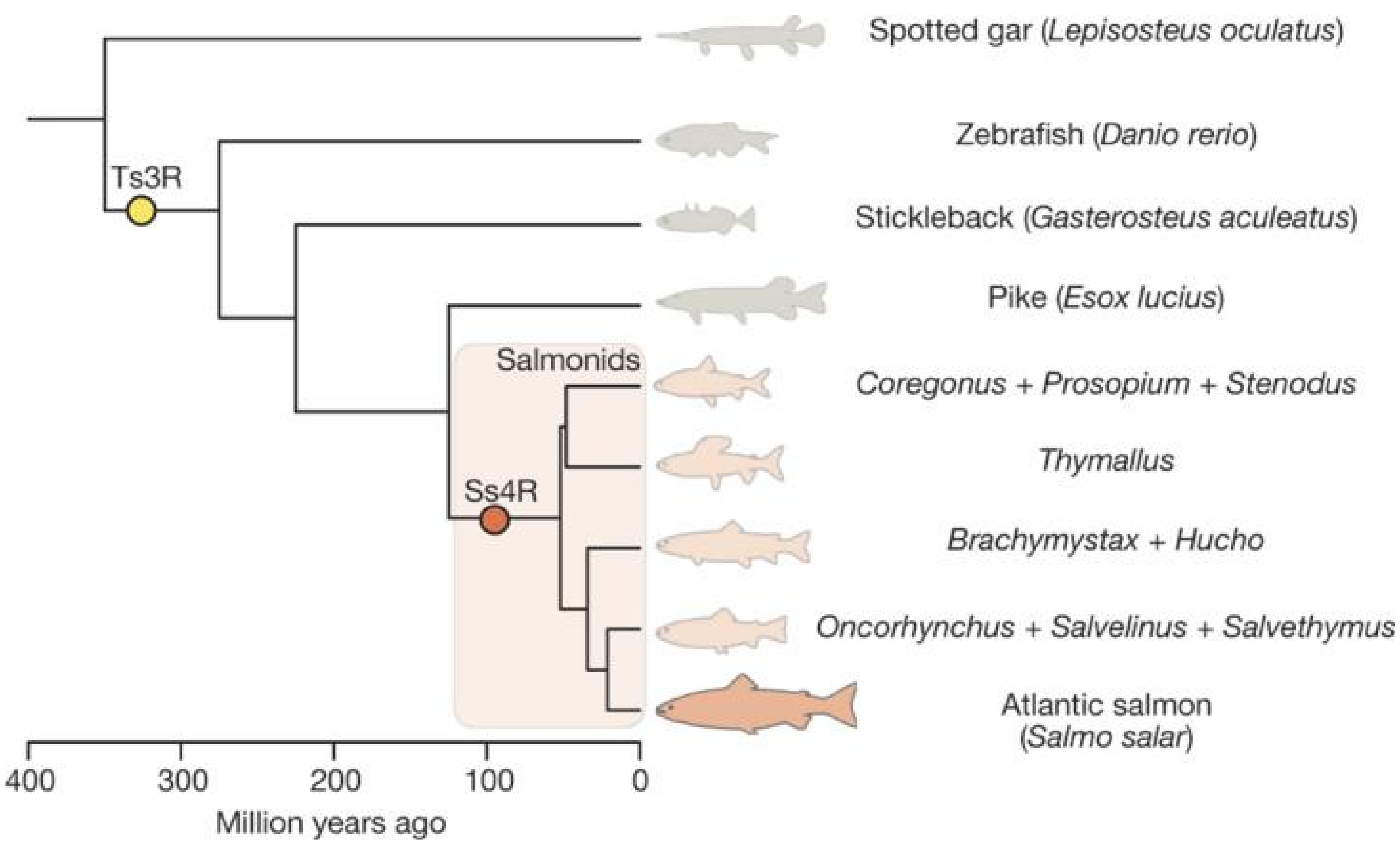
Kokannee



coho

Load in areas of residual tetraploidy

Salmon: Whole Genome Duplication ~ 80-100 My Ago. (Autotetraploidization)



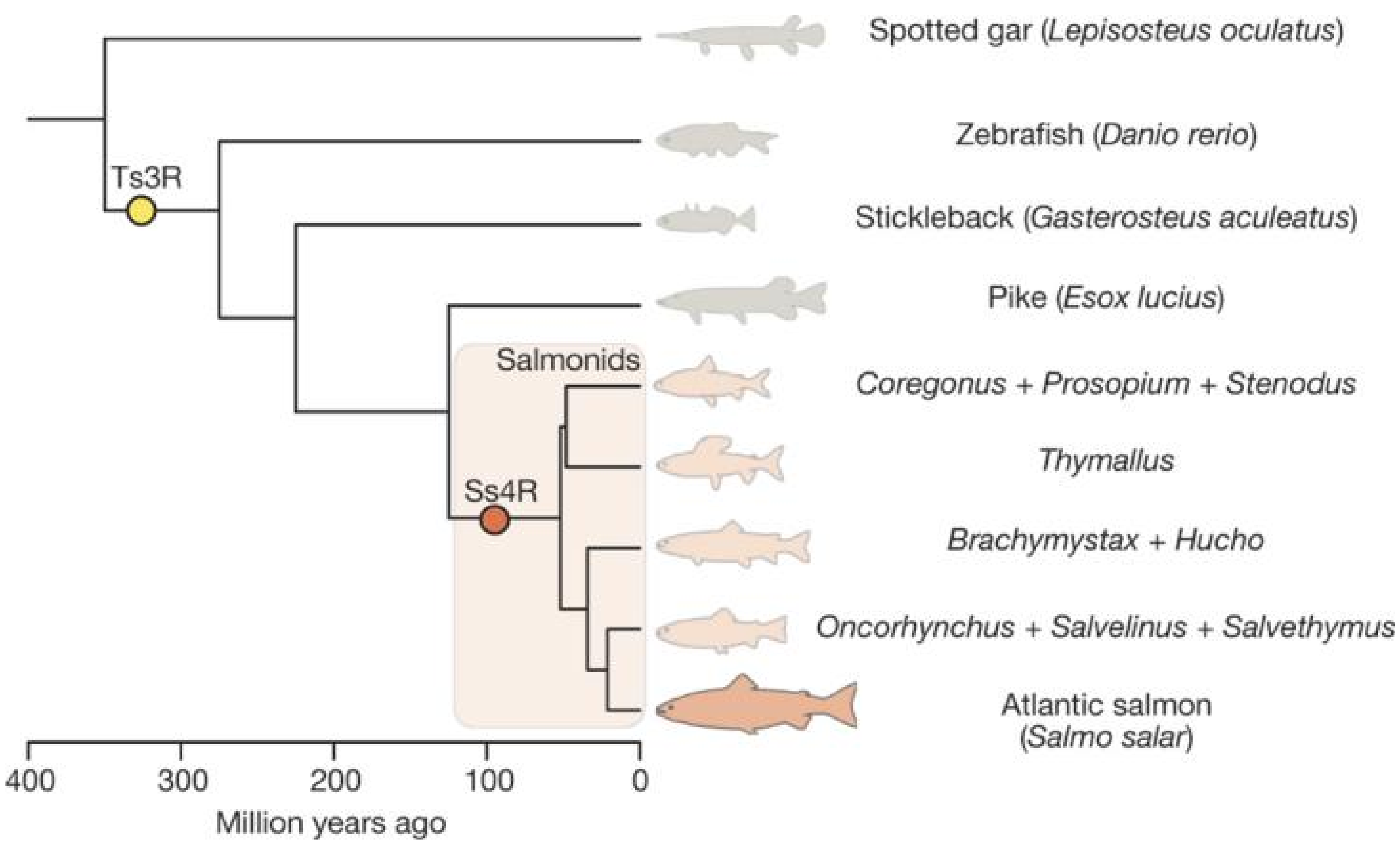
Lien et al. 2016

Rediploidization ongoing (Tetrasomic inheritance).

9 pairs of chromosome arms with residual tetraploidy (homeologuous arms)

Load in areas of residual tetraploidy

Salmon: Whole Genome Duplication ~ 80-100 My Ago. (Autotetraploidization)



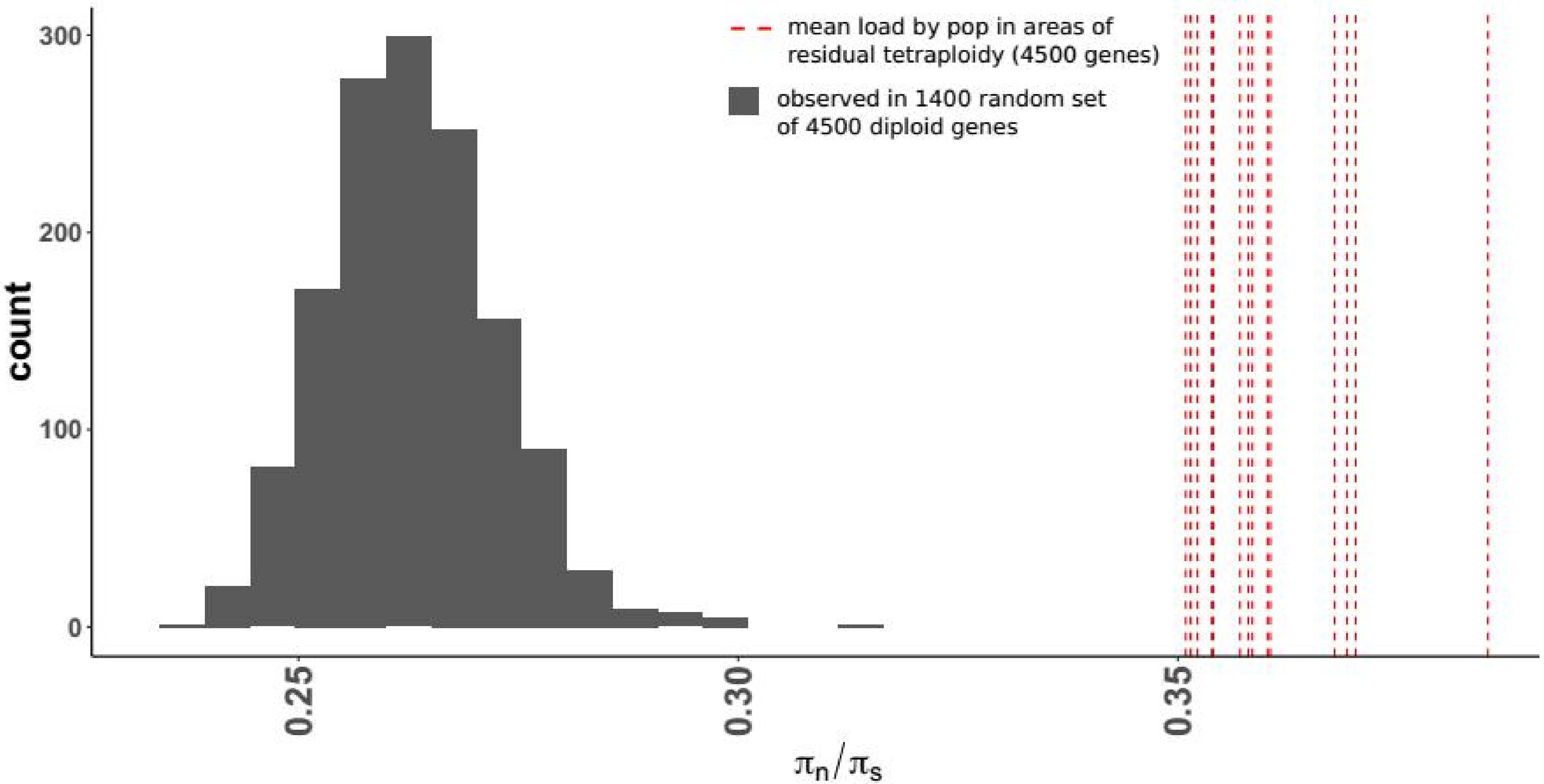
Lien et al. 2016

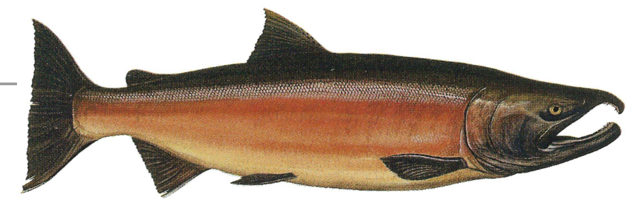
Prediction:

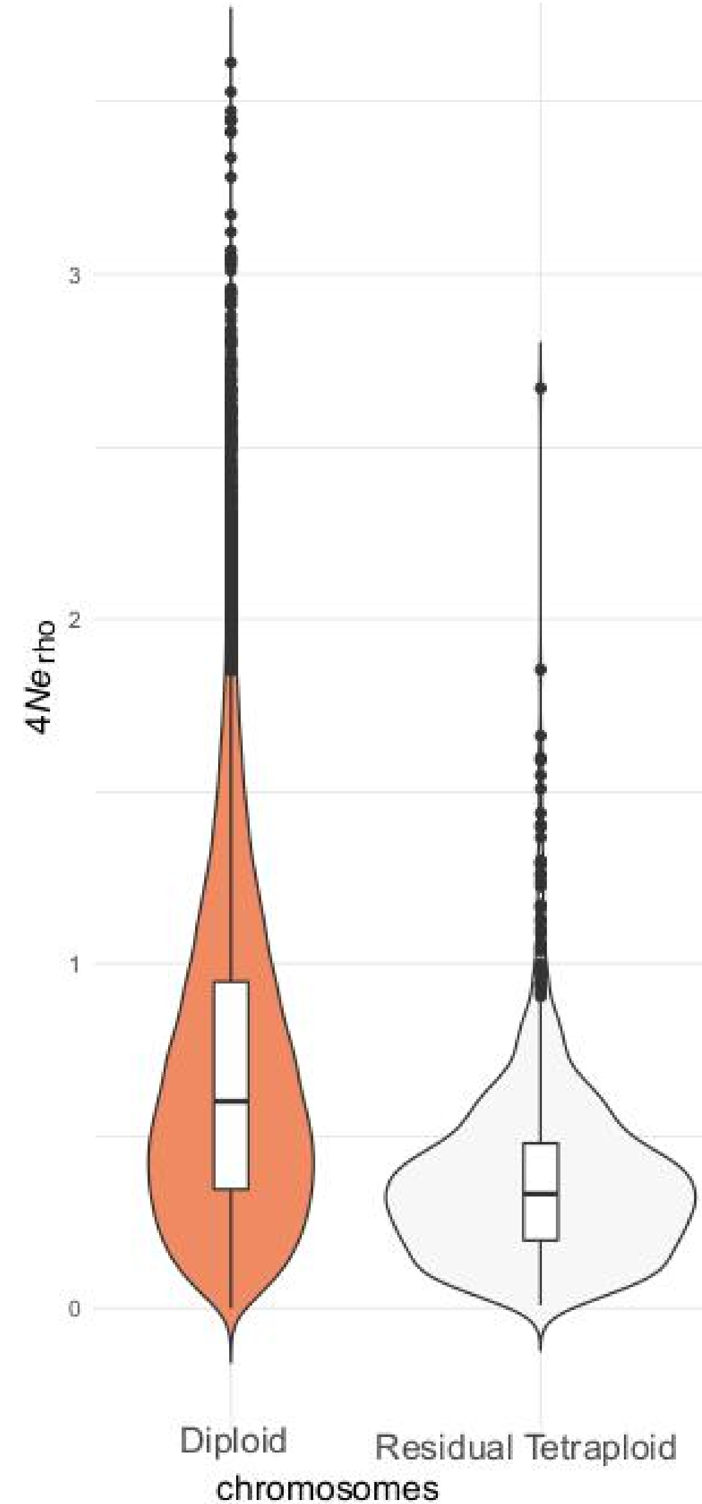
Higher *Ne* in areas of residual tetraploidy (4N) leads to more efficient purifying selection

Higher load in areas of residual tetraploidy

WGS data :







Also supported by decreased proportion of adaptive substitution

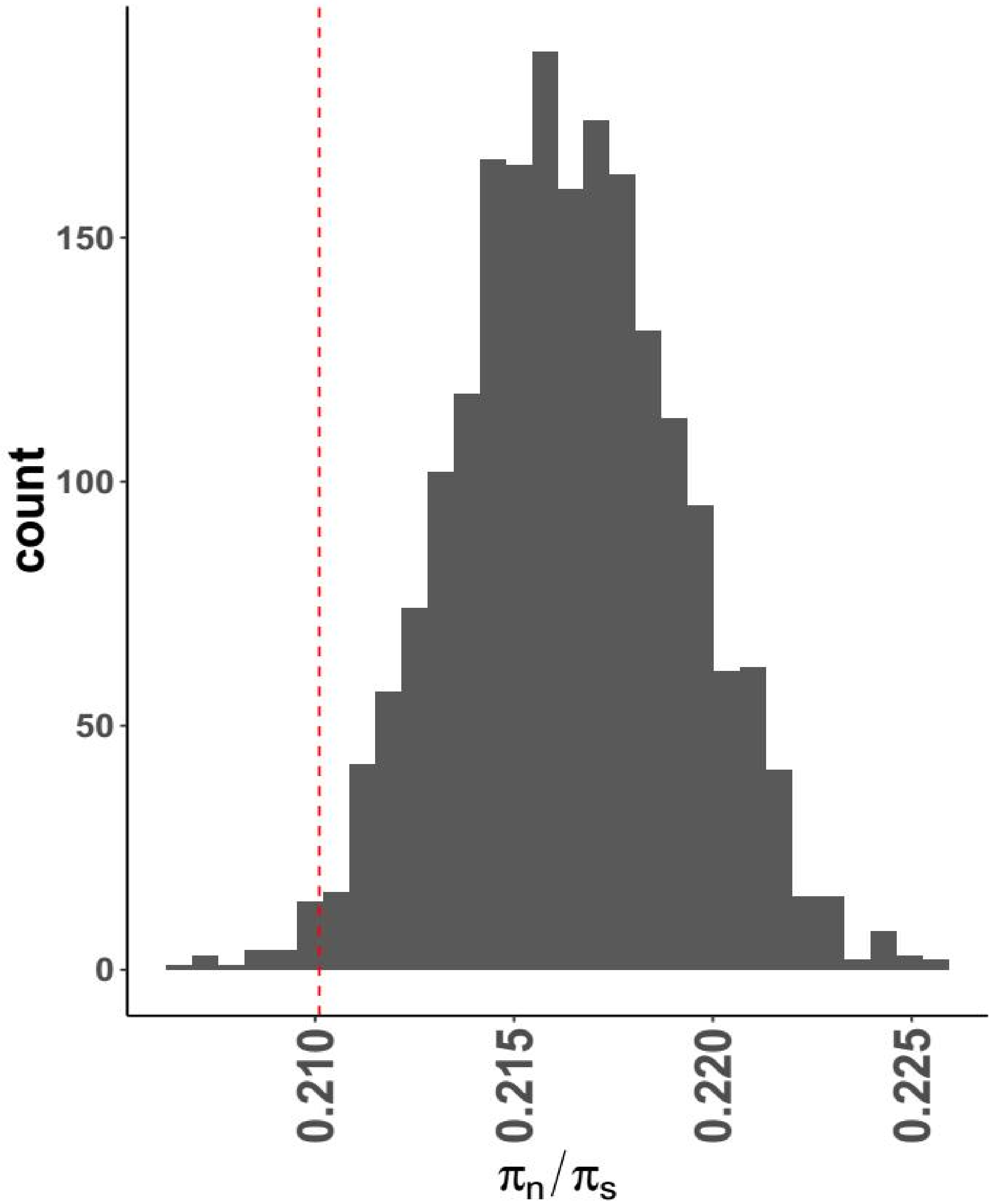
Higher load

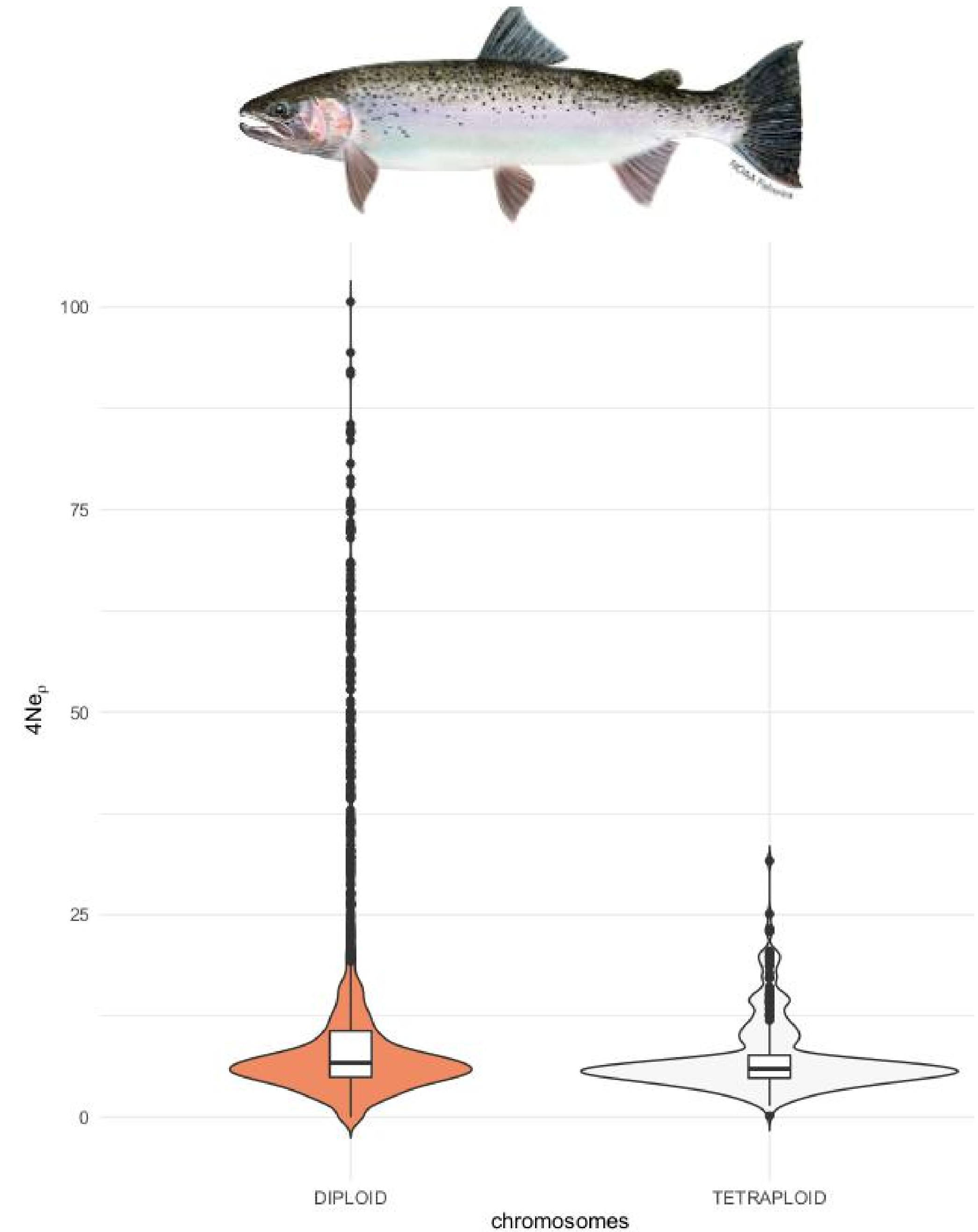
More pseudogenes?

More TE? (identification ongoing)

Not supported in Rainbow Trout ?

WGS data :





Conclusions:

- **Survival in a single refugium** south of the ice sheets explains broad scale patterns in the distribution of genetic diversity

- Post-glacial **recolonization & linked selection** had a detectable impact on the **mutation load**

- Both **Recombination and *Ne*** influence the efficacy of purifying selection and the load

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- **Survival in a single refugium** south of the ice sheets explains broad scale patterns in the distribution of genetic diversity
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★ Focusing only on local adaptation ignores the fundamental importance of deleterious mutations and a greater understanding of the historical and genomic factors driving their distribution and frequency is needed

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