The genetic and evolutionary basis of summer run timing in coastal steelhead

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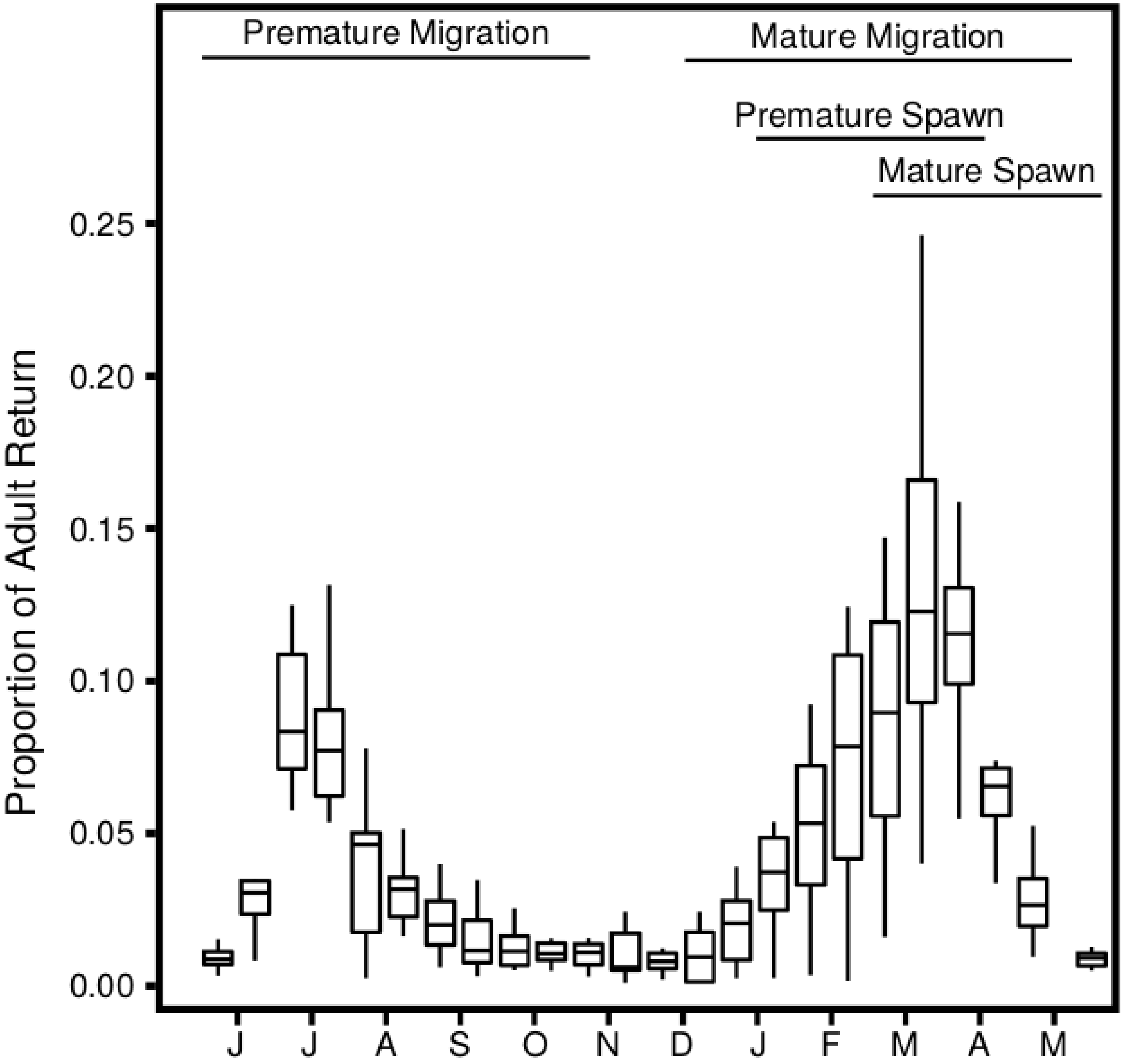
Summer run timing (aka premature migration) likely evolved in response to seasonal variation in water flow and temperature.

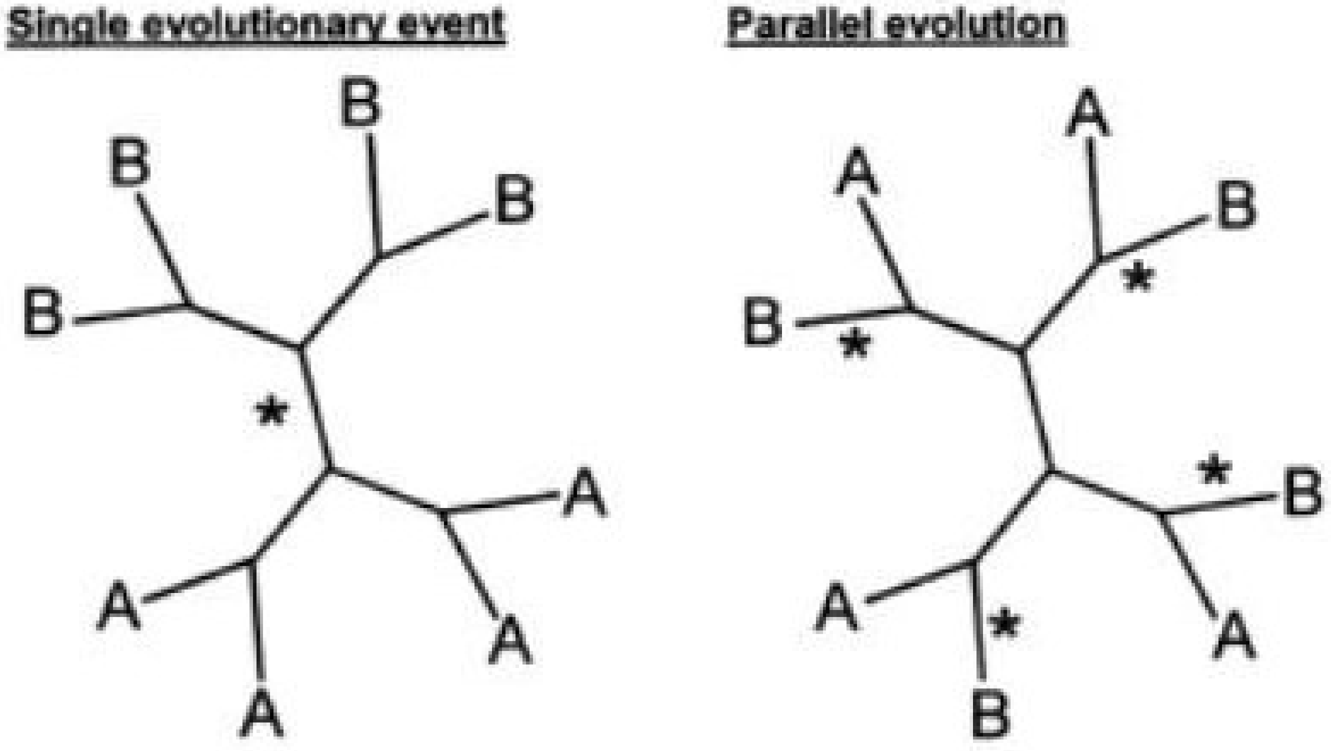


Prince *et al.* 2017

Premature migrating individuals have a dramatically different behavior and physiology.

*Store excess fat to uncouple migration and spawning behavior

Many studies have investigated the genetic and evolutionary basis of premature migration.



A = Mature
B = Premature

Allendorf 1975
Chilcote *et al.* 1980
Thorgaard 1983
Nielsen *et al.* 1999
Waples *et al.* 2004
Kinziger *et al.* 2013
Arciniega *et al.* 2015

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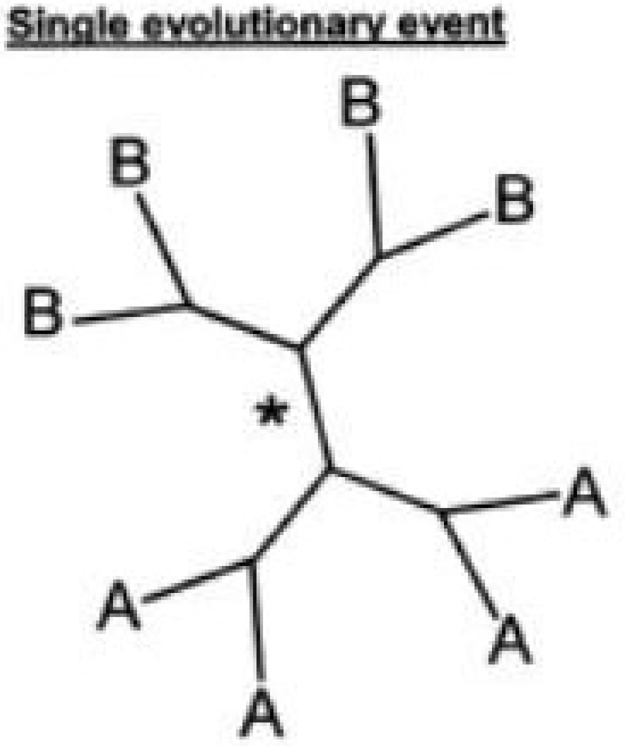
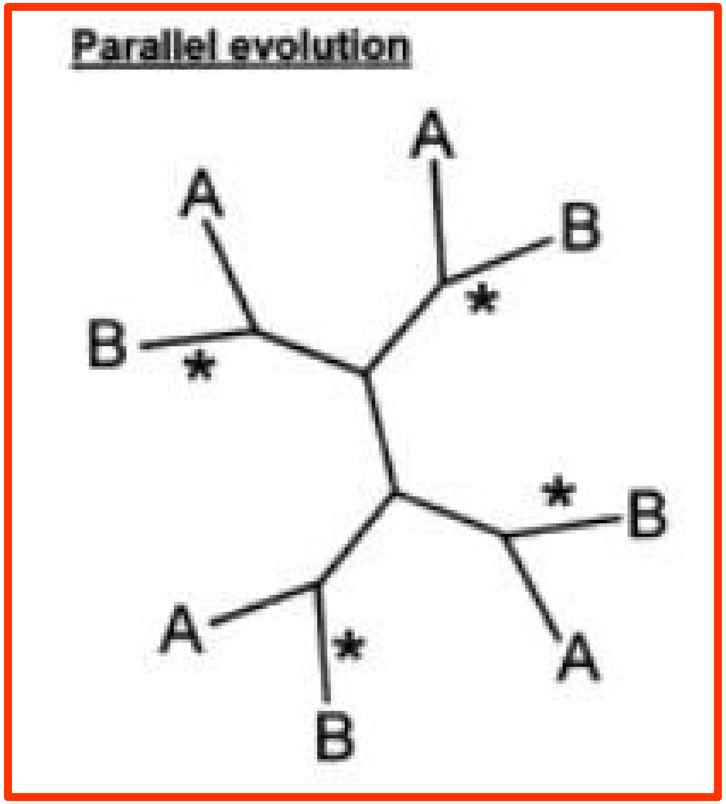

Single evolutionary event


Parallel evolution

A = Mature
B = Premature

Allendorf 1975
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All studies have supported a scenario of independent parallel evolution and evolutionary plasticity.

> “These results suggest that the different times of return may have evolved independently in the different river systems.”
>
> Thorgaard 1983

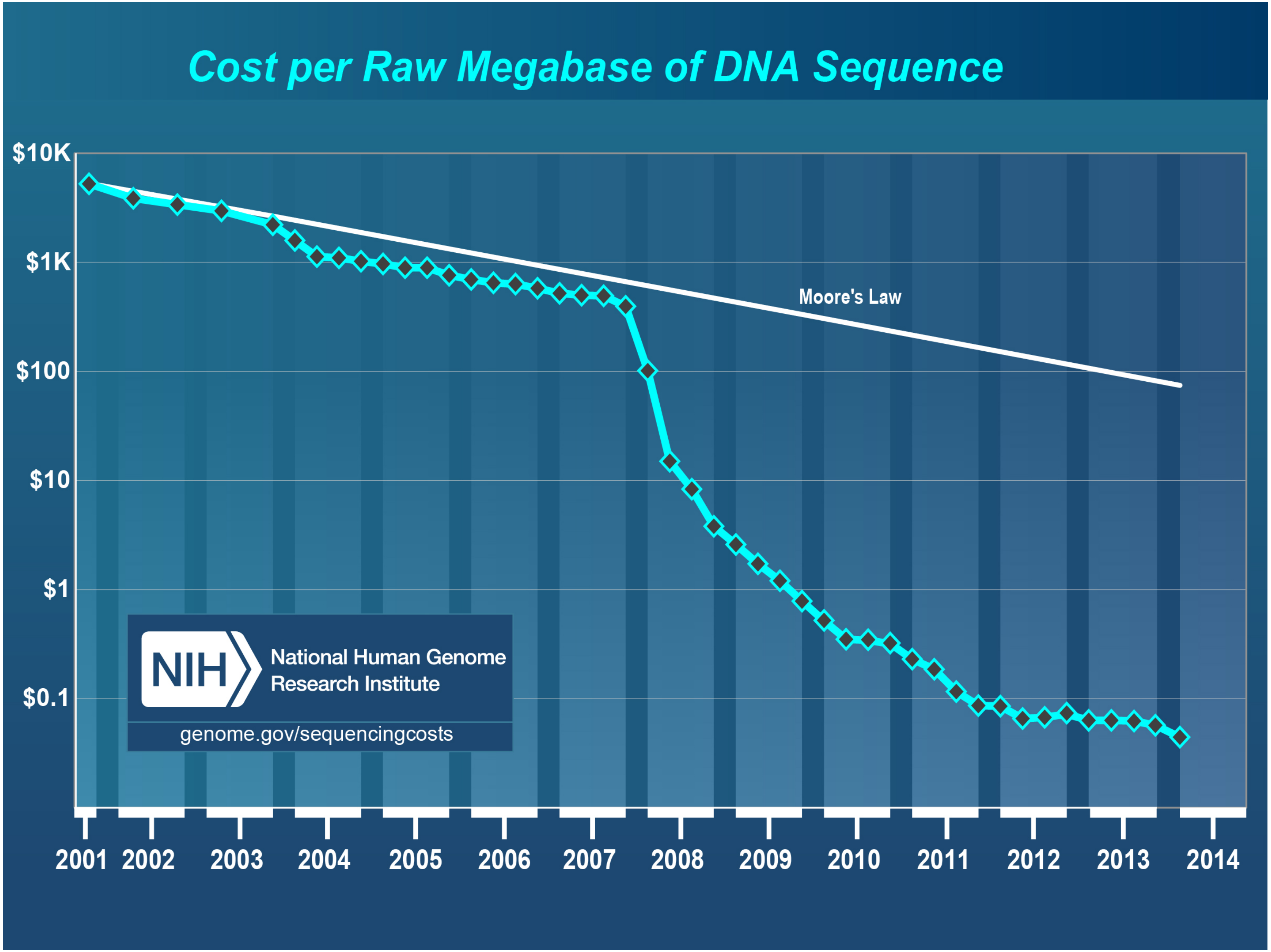
> “These results indicate that run-timing diversity has developed independently by a process of parallel evolution in many different coastal areas.”
>
> Waples *et al.* 2004

All studies have supported a scenario of independent parallel evolution and evolutionary plasticity.

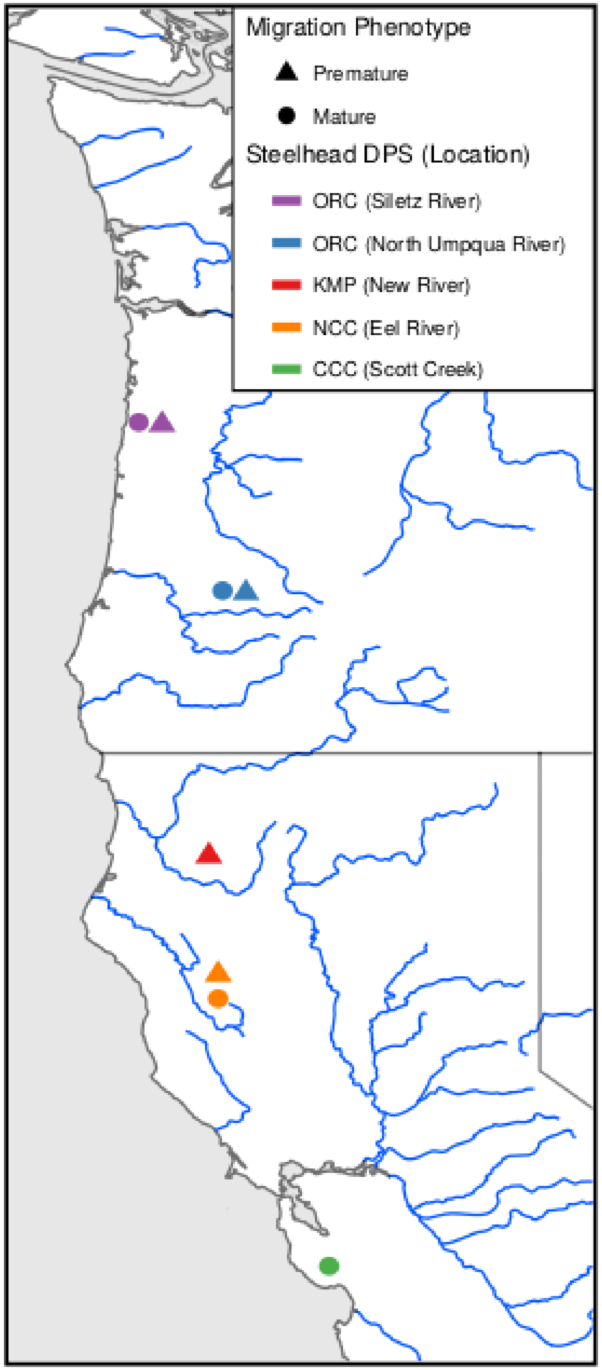
> “… at least some patterns of Chinook salmon life-history diversity appear to be evolutionarily replaceable, perhaps over time frames of a century or so. The evidence for repeated parallel evolution of run timing in Chinook salmon indicates that such a process is likely, provided that habitats capable of supporting alternative life-history trajectories are present and sufficient, robust source populations are maintained.”

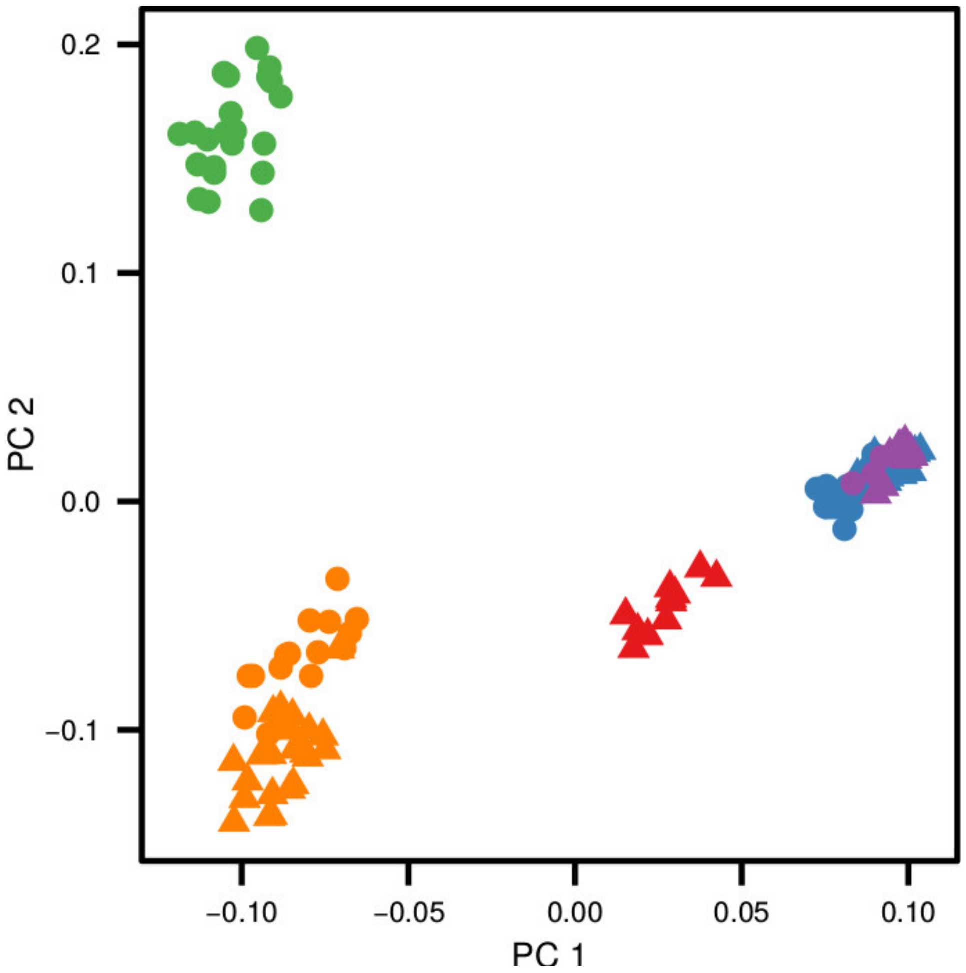
Waples *et al.* 2004

New sequencing technologies enable high resolution genetic analyses in any species.



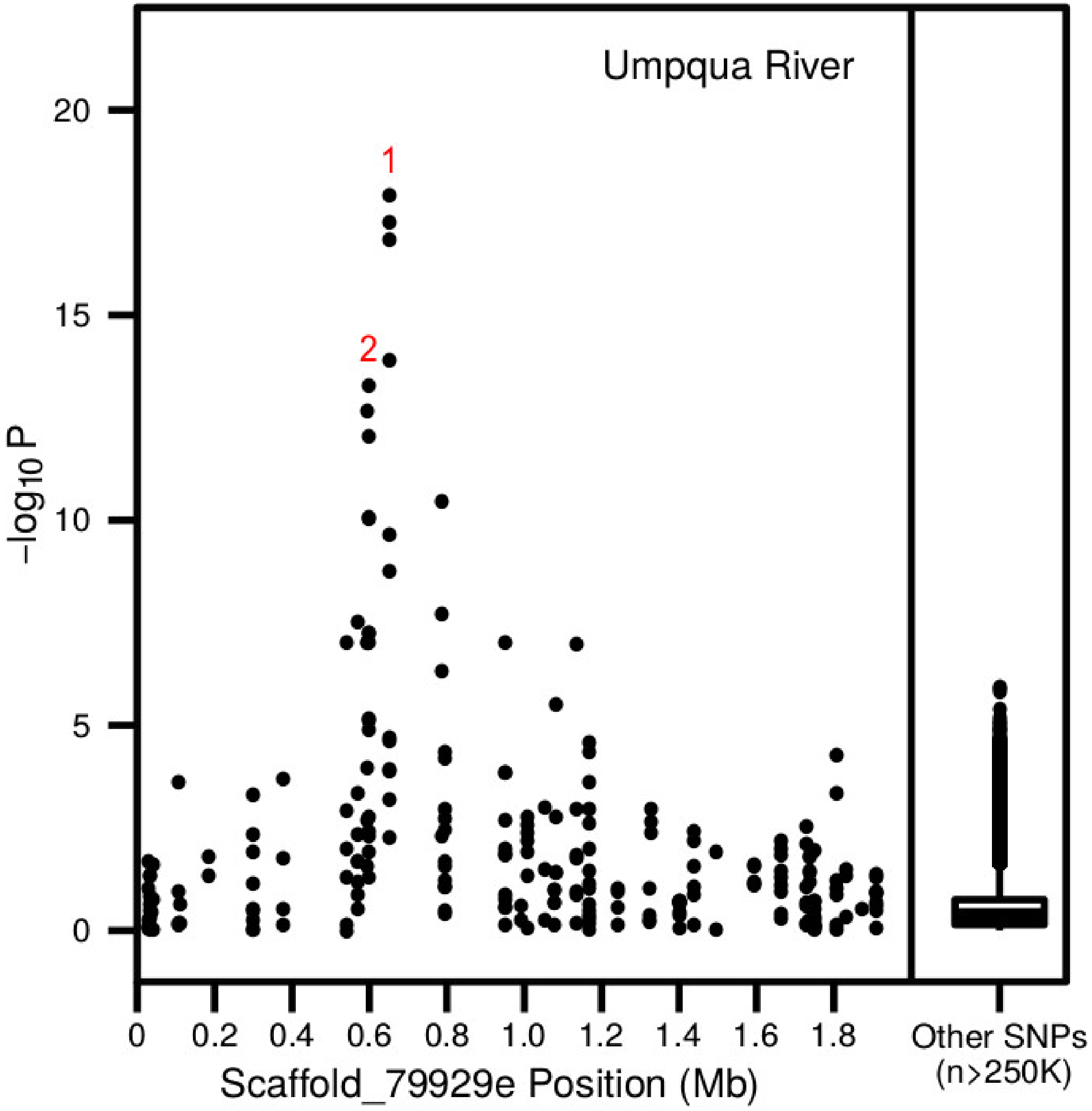
RAD sequencing confirms that overall genetic structure relates to geography and mirrors current DPS designations.





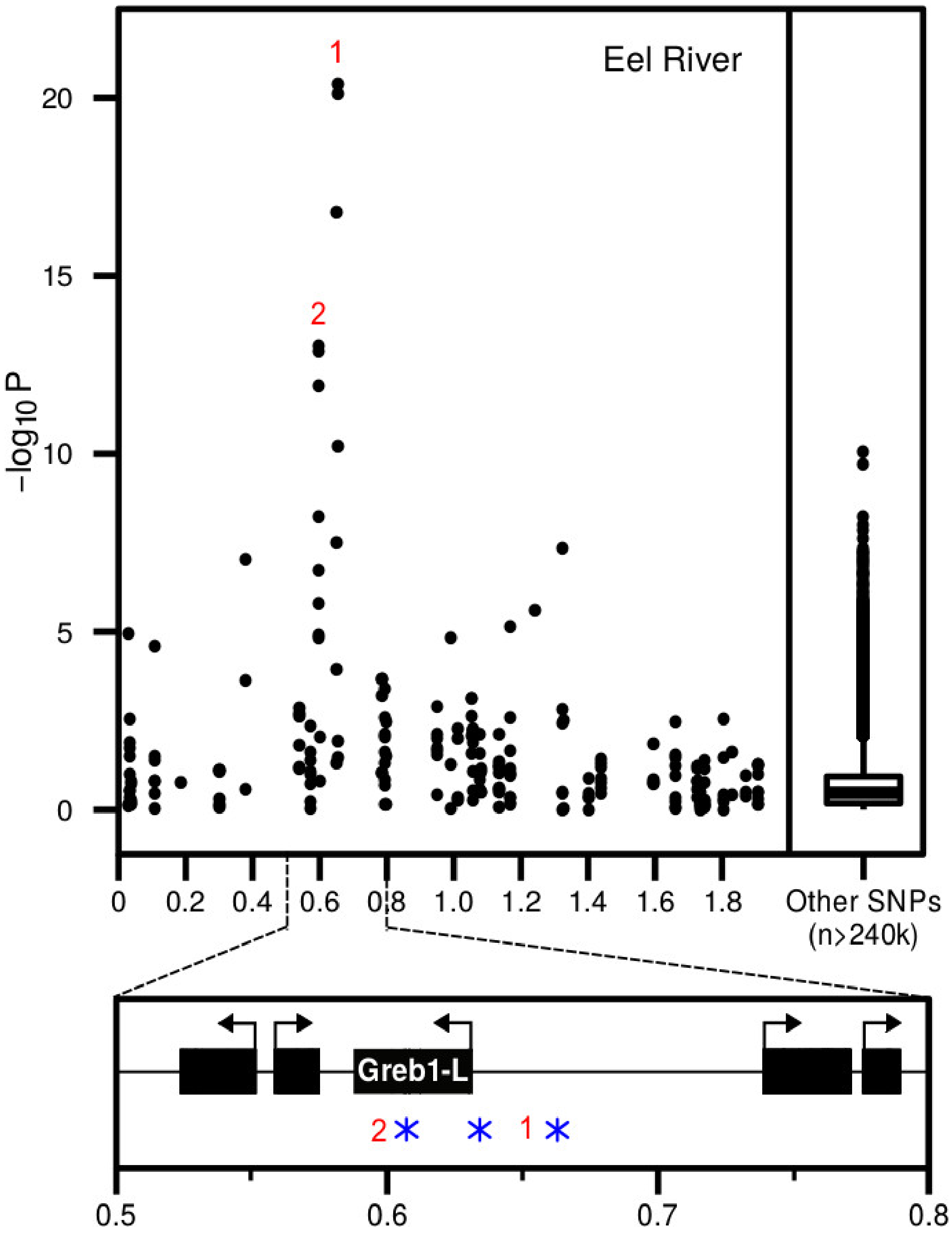
Prince *et al.* 2017

A single genetic locus associated with premature migration in North Umpqua steelhead.



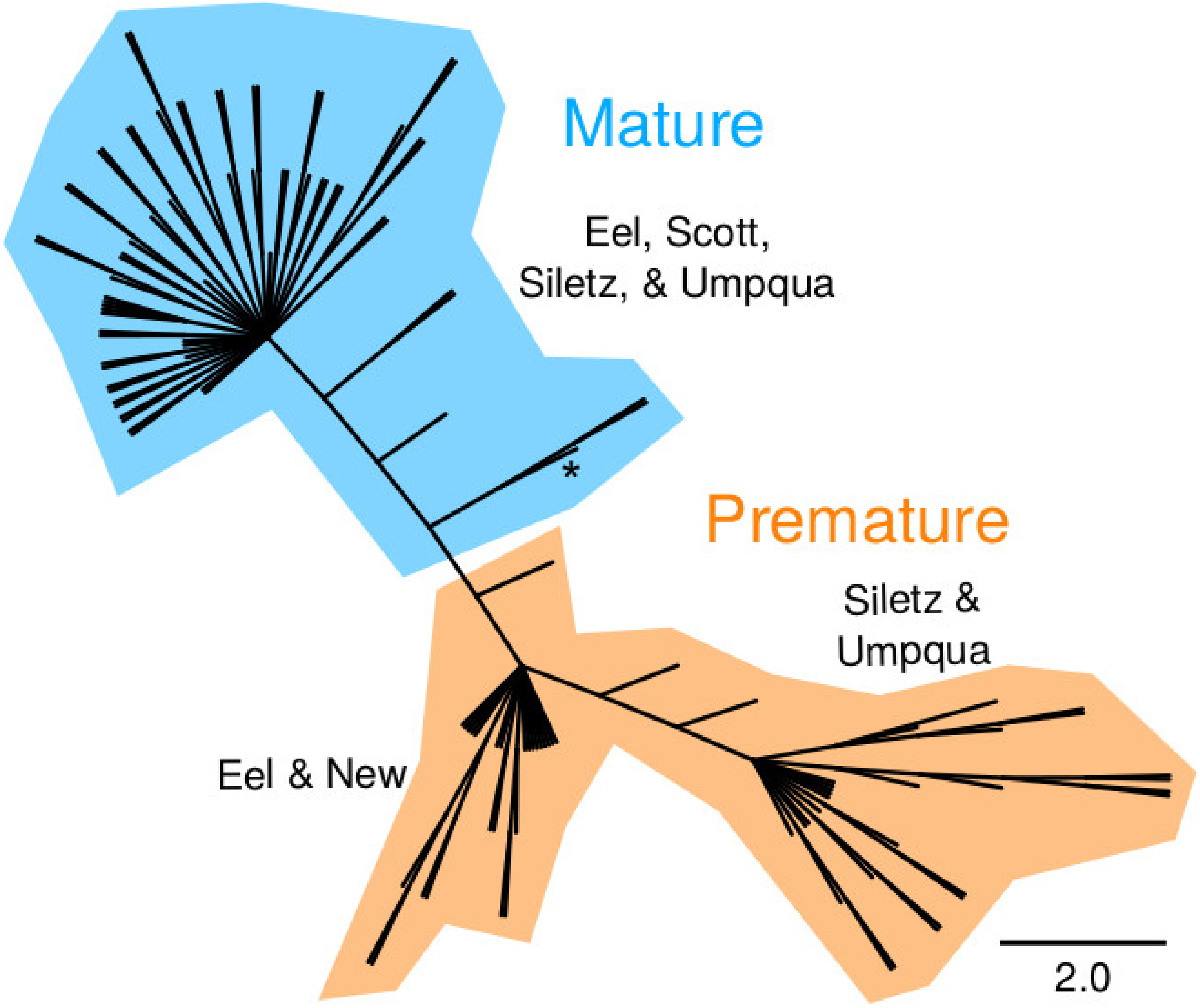
Prince *et al.* 2017

The same genetic locus associated with premature migration in Eel River steelhead.



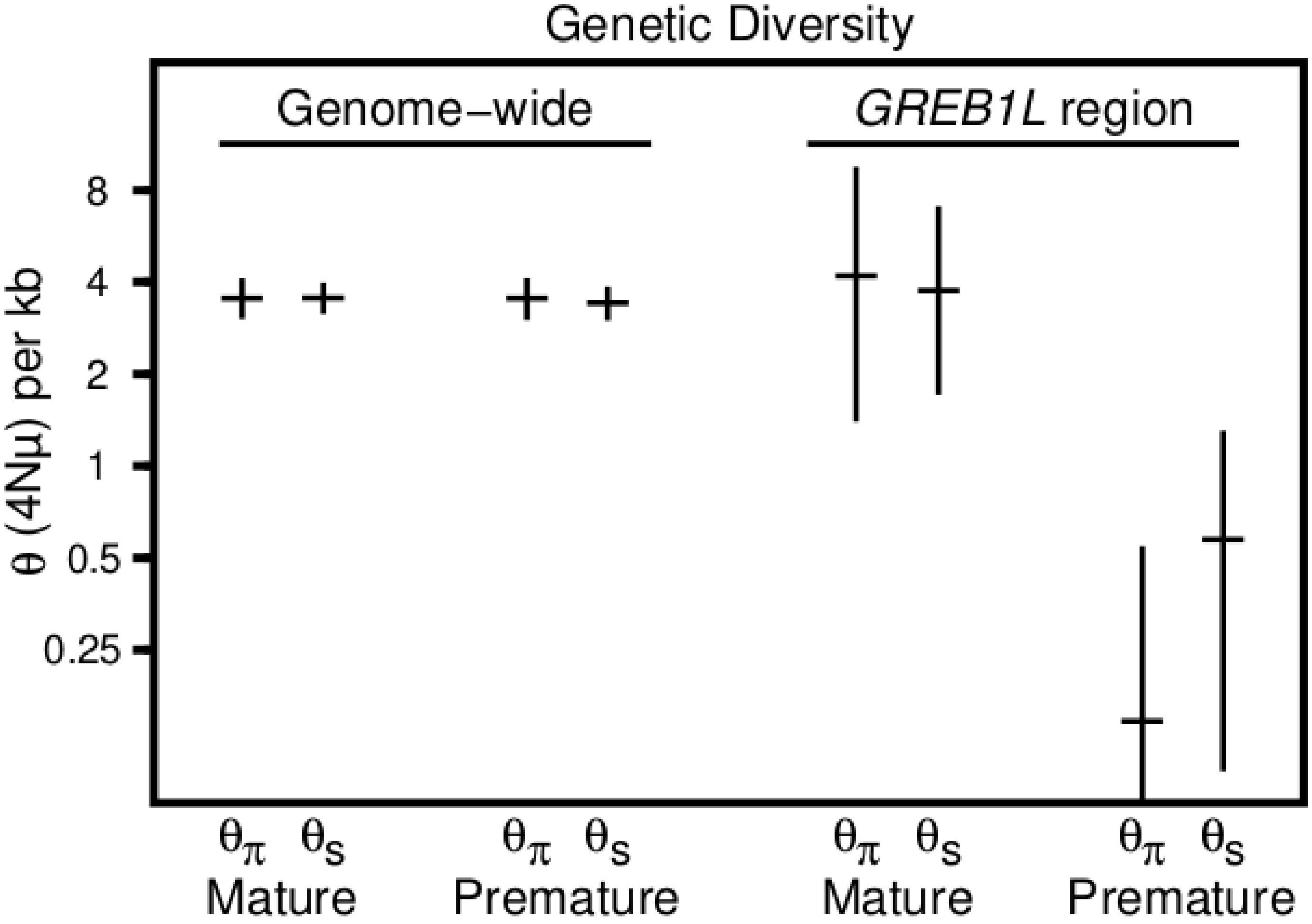
Prince *et al.* 2017

A single ancient genetic evolutionary event is the ultimate source of all premature migration alleles.



Prince *et al.* 2017

Strong positive selection allowed premature migration to spread around the West Coast.

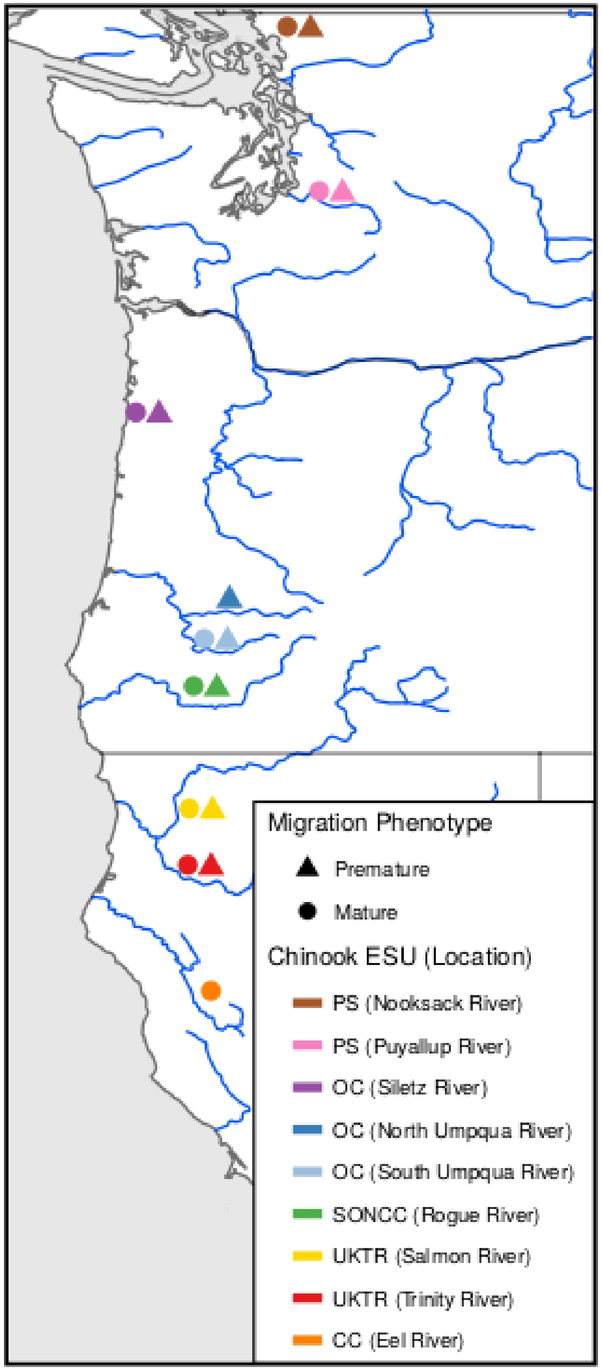


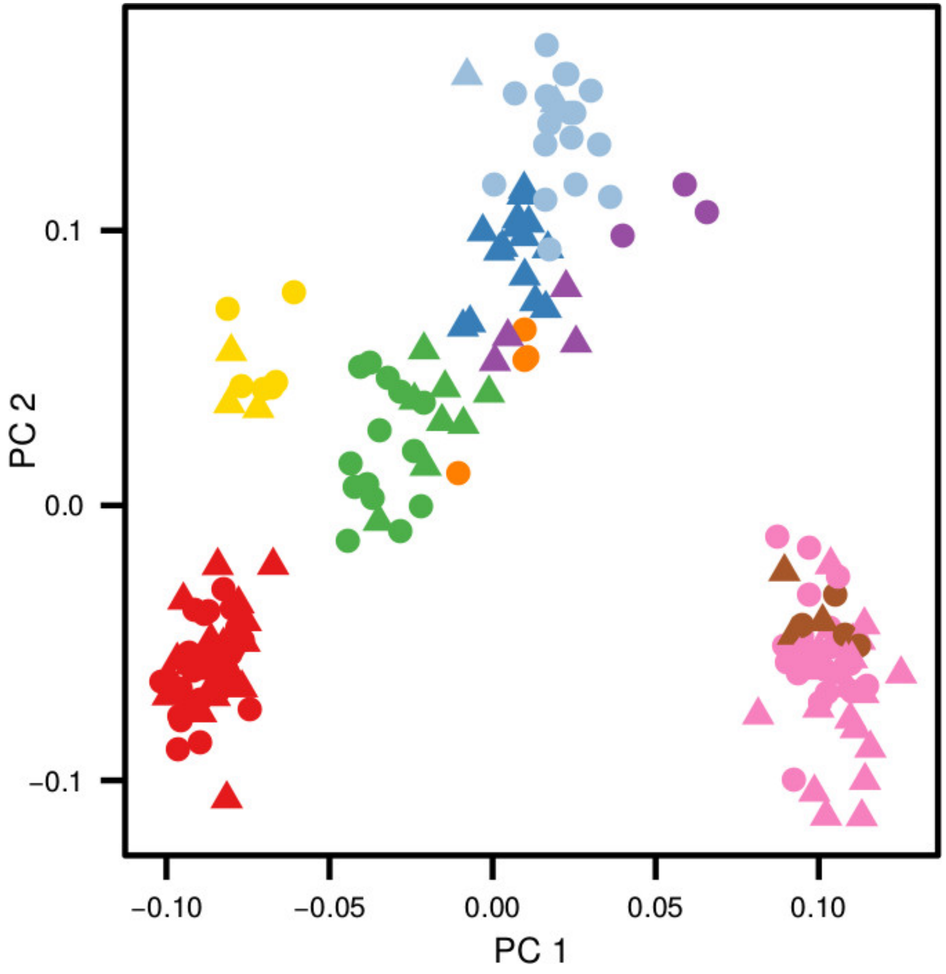
Prince *et al.* 2017

Greb1L is expressed in AgRP neurons which modulate diverse behavior and metabolic processes.

Greb1L expression in mice

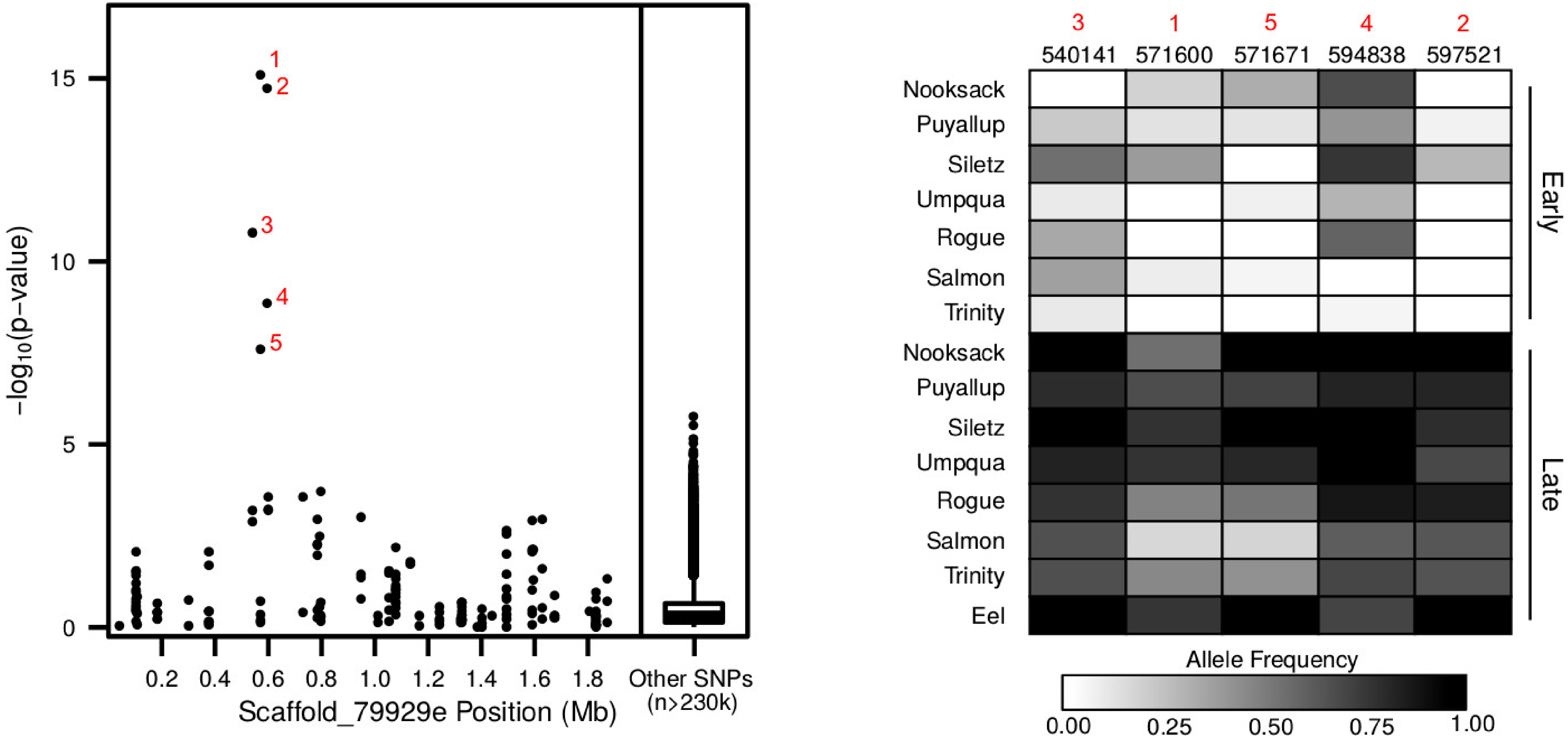
Chinook overall genetic structure relates to geography and mirrors current ESU designations.





Prince *et al.* 2017

The same genetic and evolutionary mechanism explains premature migration in Chinook too.



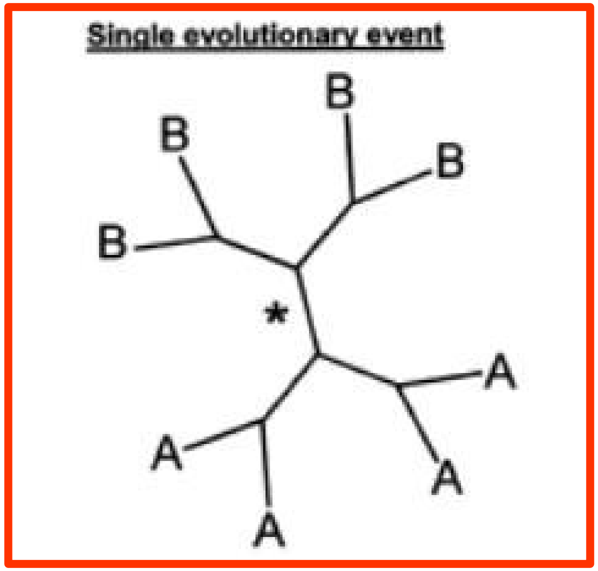
Prince *et al.* 2017

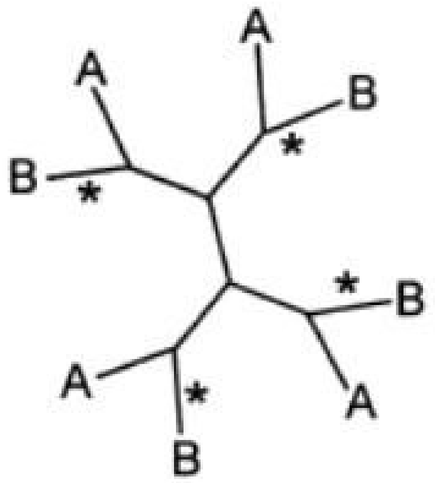
Previous genetic studies were correct with respect to phenotypic evolution but not allelic evolution.

> "... at least some patterns of Chinook salmon life-history diversity appear to be evolutionarily replaceable, perhaps over time frames of a century or so. The evidence for repeated parallel phenotypic evolution of run timing in Chinook salmon indicates that such a process is likely, provided that habitats capable of supporting alternative life-history trajectories are present and sufficient, robust source populations that contain the necessary, pre-existing allele are maintained."

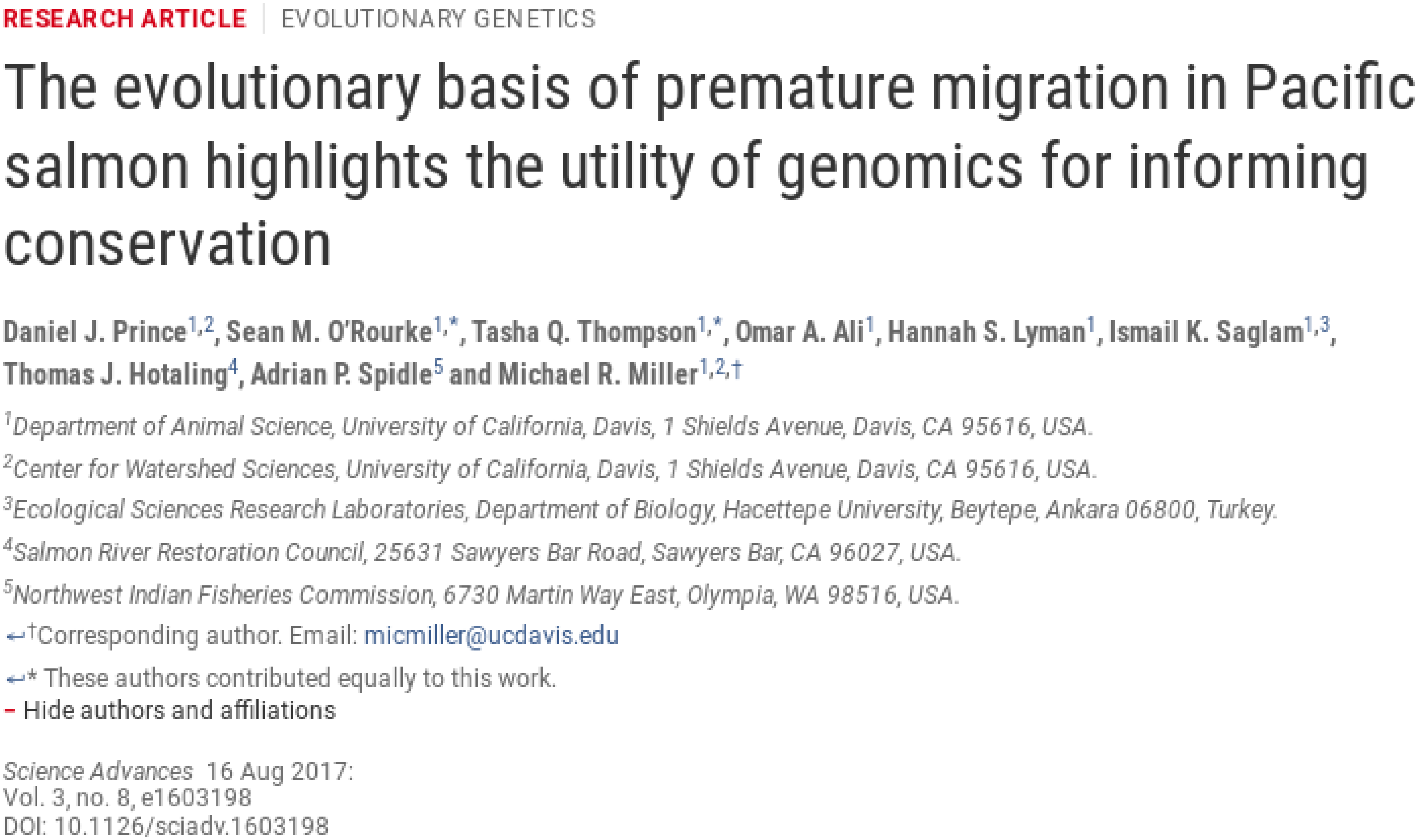
Waples *et al.* 2004*

Identifying the run-timing locus led to opposite conclusions about the evolutionary basis and conservation priority of run timing variation.


Single evolutionary event


Parallel evolution

- Premature migration explained by a single locus
- Single ancient evolutionary event in each species
- New allele spread through positive selection and straying
- Can only evolve through limited genetic mechanisms
- Allele will not soon re-evolve if lost
- Higher conservation priority than previously thought
- Genomics powerful tool for prioritizing conservation



RESEARCH ARTICLE | EVOLUTIONARY GENETICS

The evolutionary basis of premature migration in Pacific salmon highlights the utility of genomics for informing conservation

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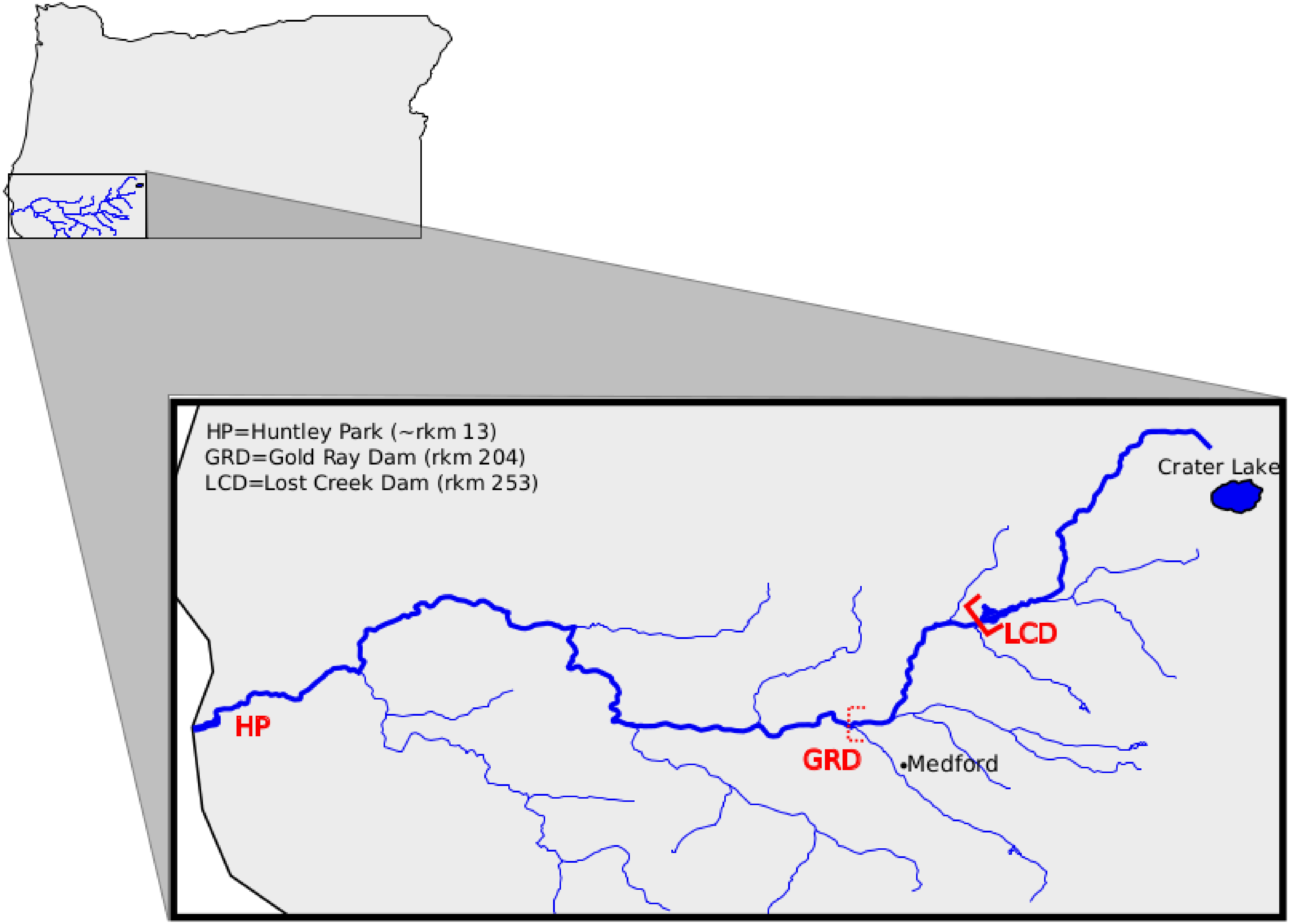
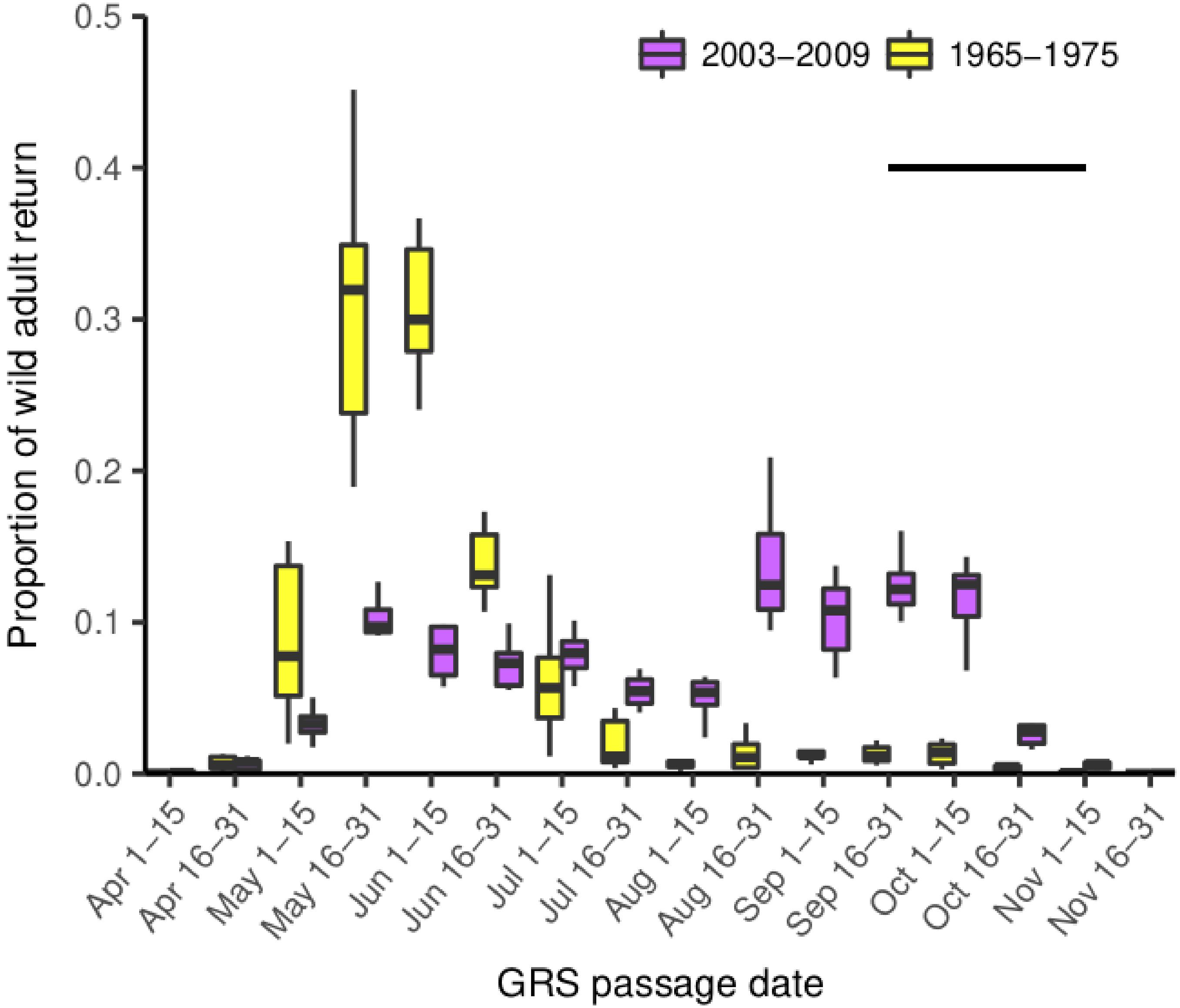
The Rogue River provides a unique opportunity to further investigate the conservation genetics of premature migrating (aka spring-run) Chinook.

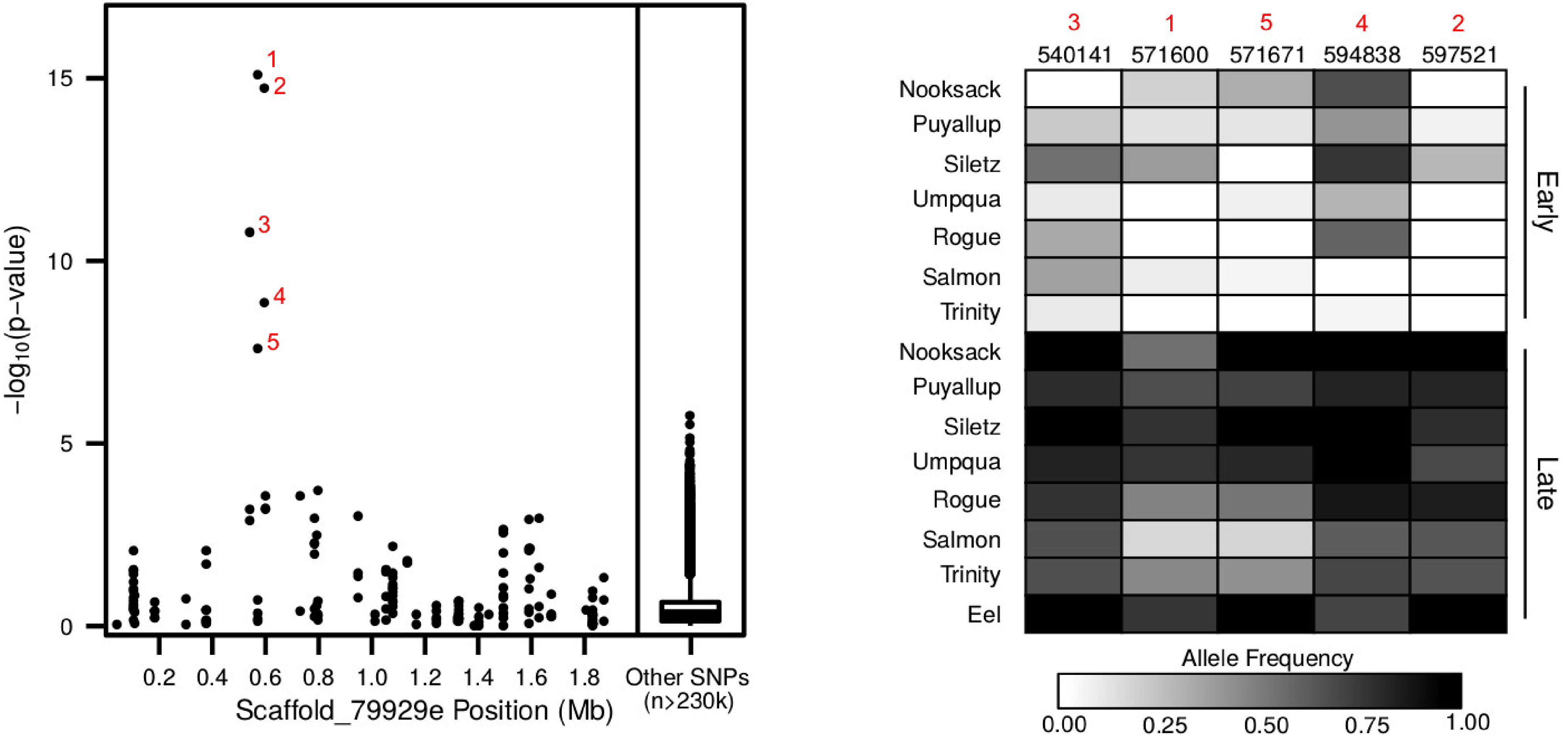


Rogue Chinook have experienced a dramatic shift in migration timing since the Lost Creek Dam was built.



Thompson *et al.* In prep

Capture sequencing identified better Chinook migration type markers in the GREB1L region.



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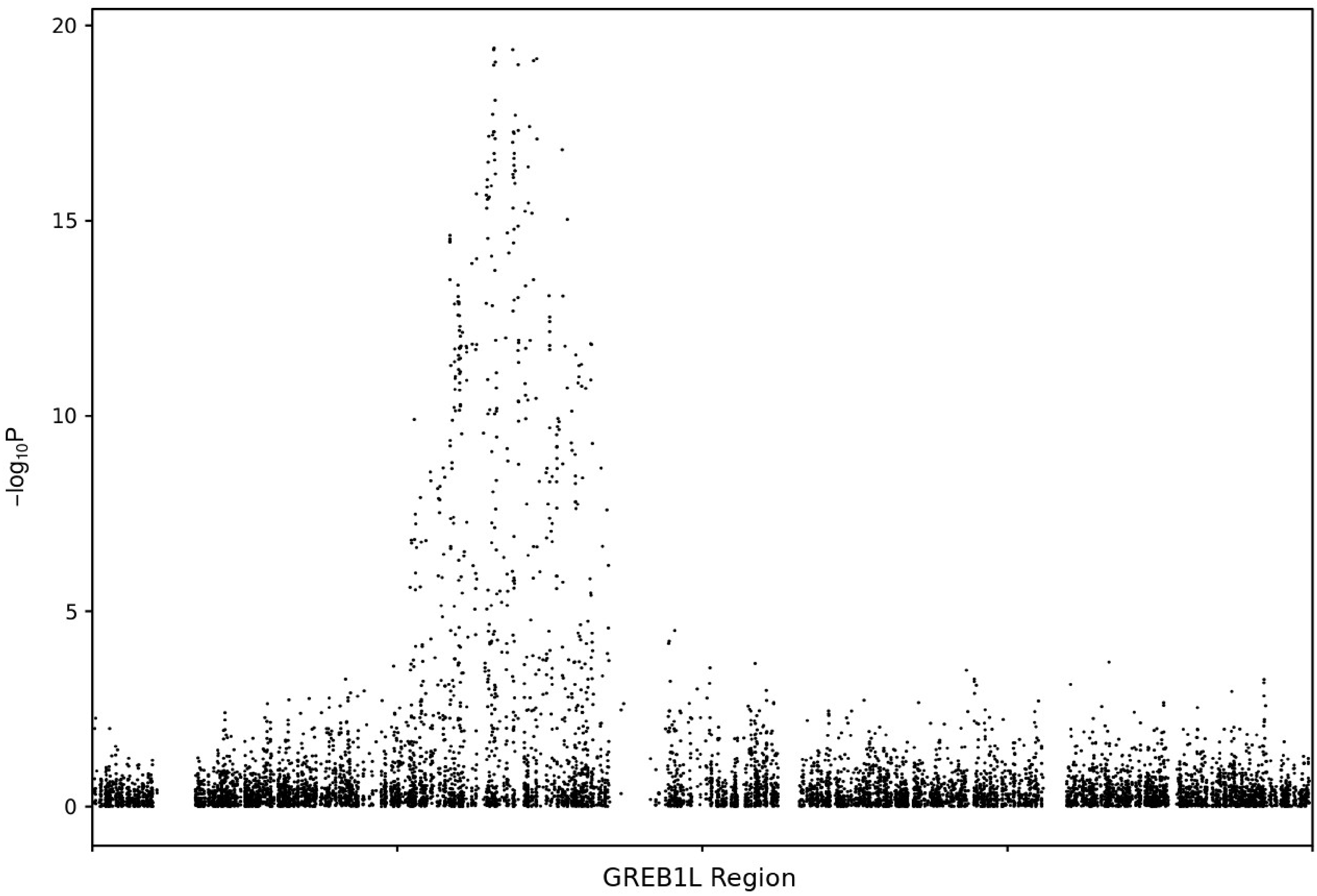
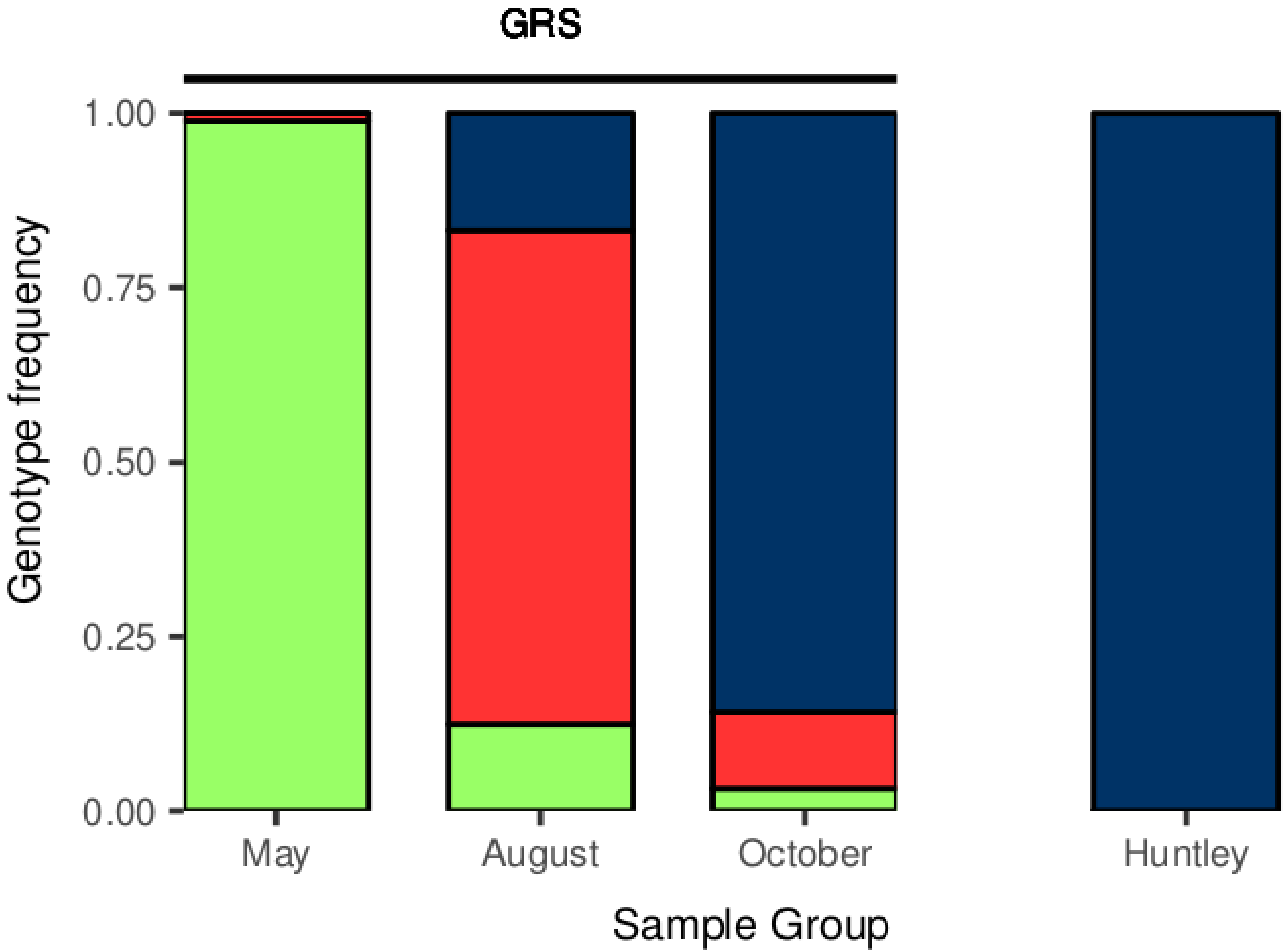


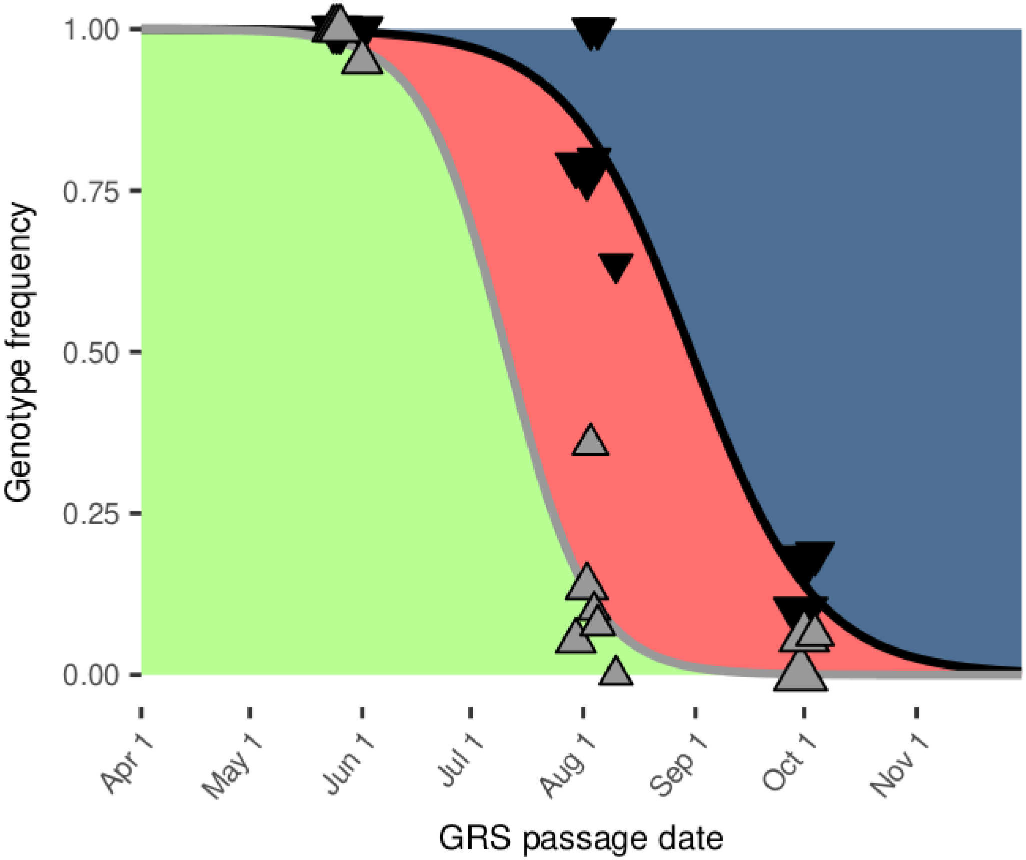
Prince *et al.* In prep

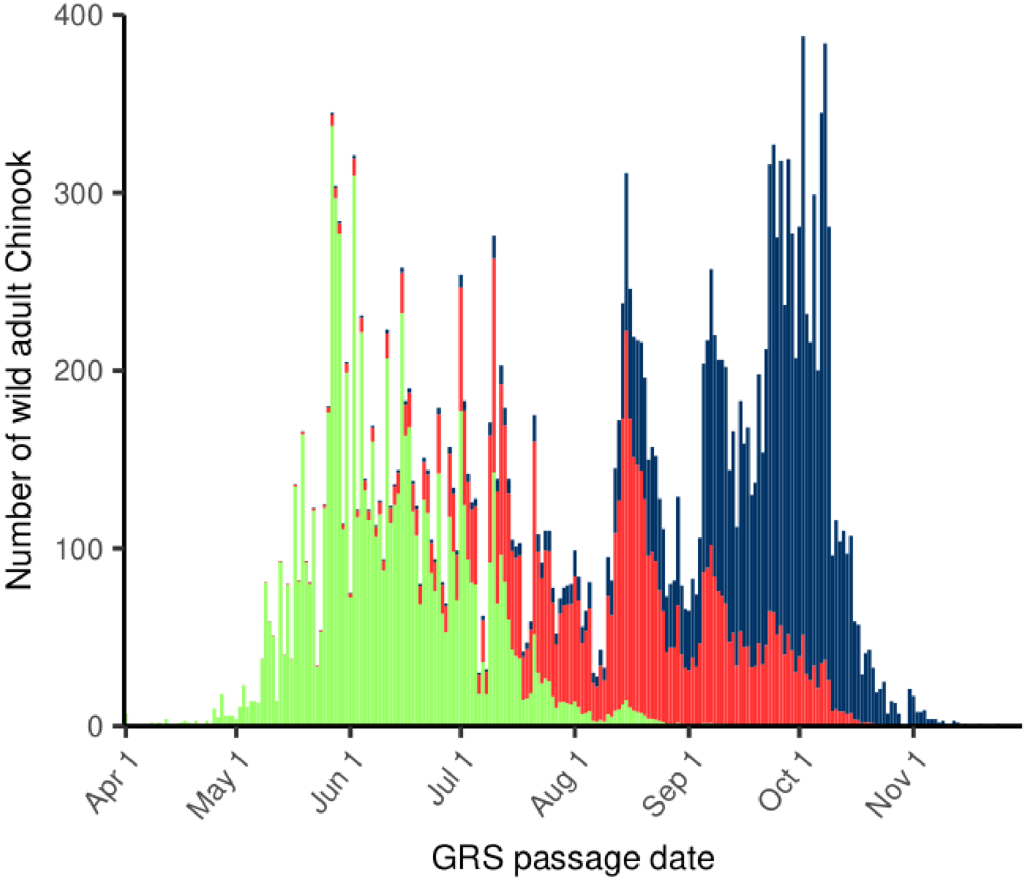
GREB1L genotype is strongly associated with migration characteristics in Rogue Chinook.



Thompson *et al.* In prep

Gold Ray fish counts reveal a dramatic decrease in spring-run allele frequency since LCD construction.





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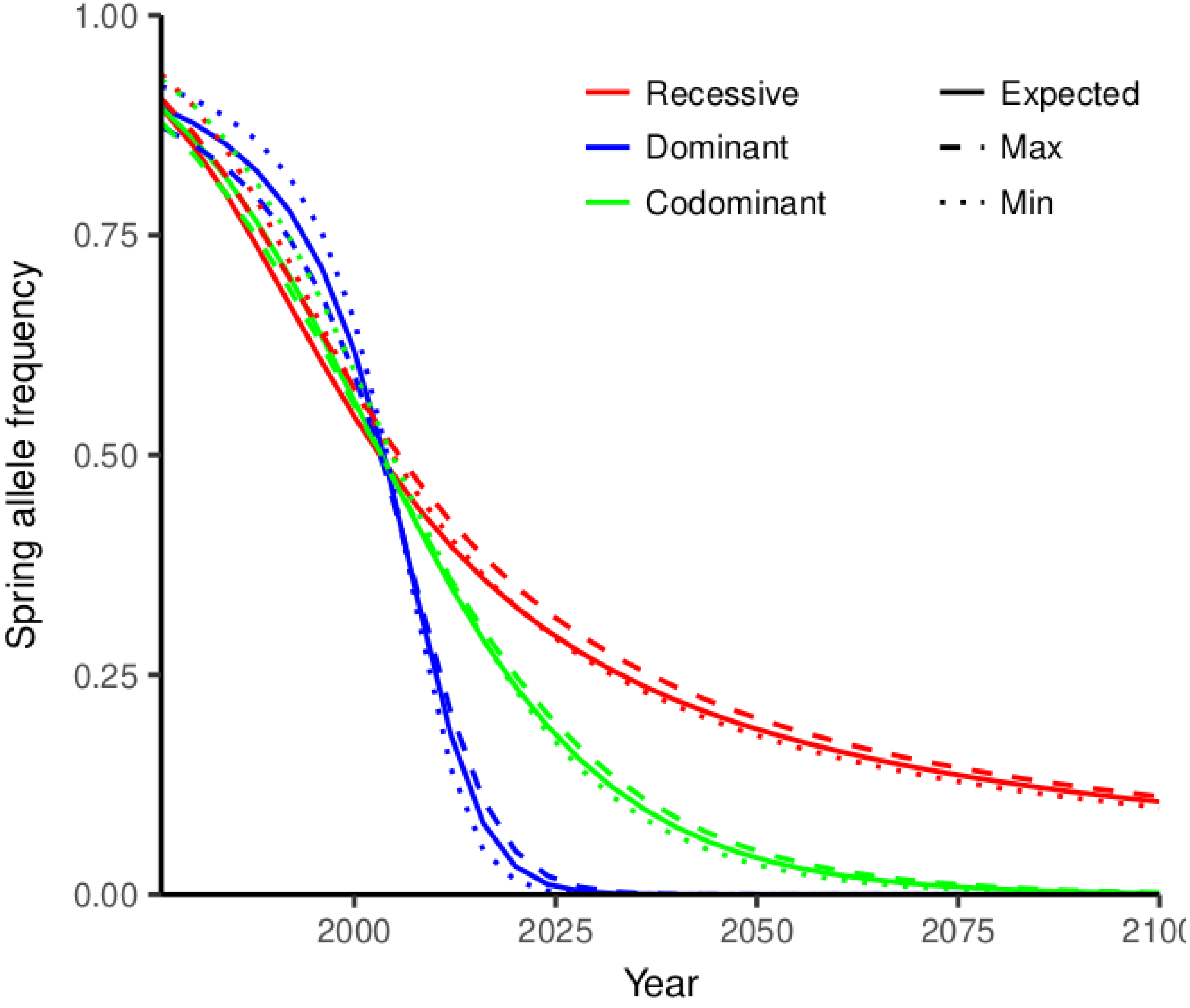
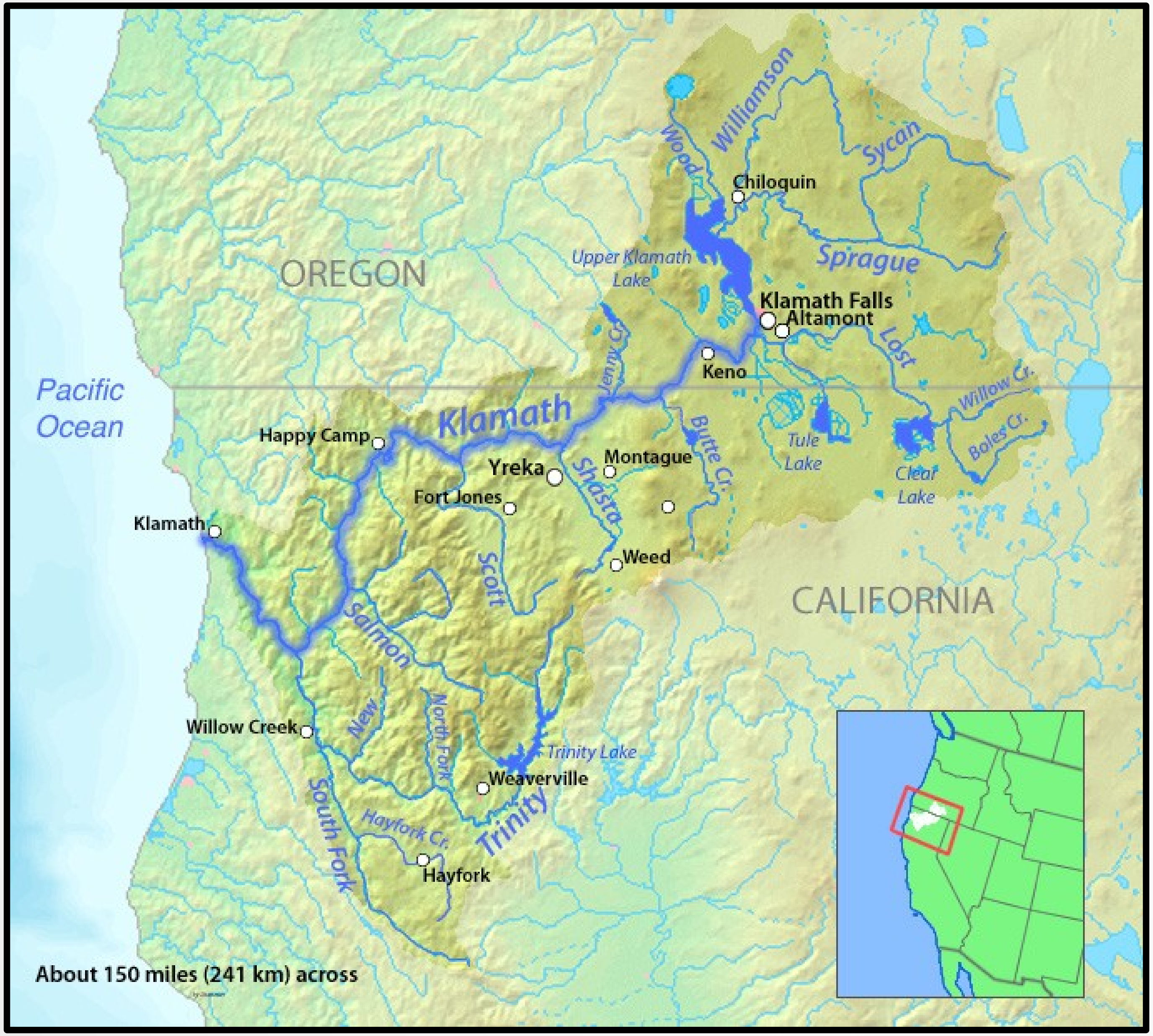
Selection modeling suggests spring-run allele will soon be lost from Rogue unless the allele is recessive with respect to fitness.



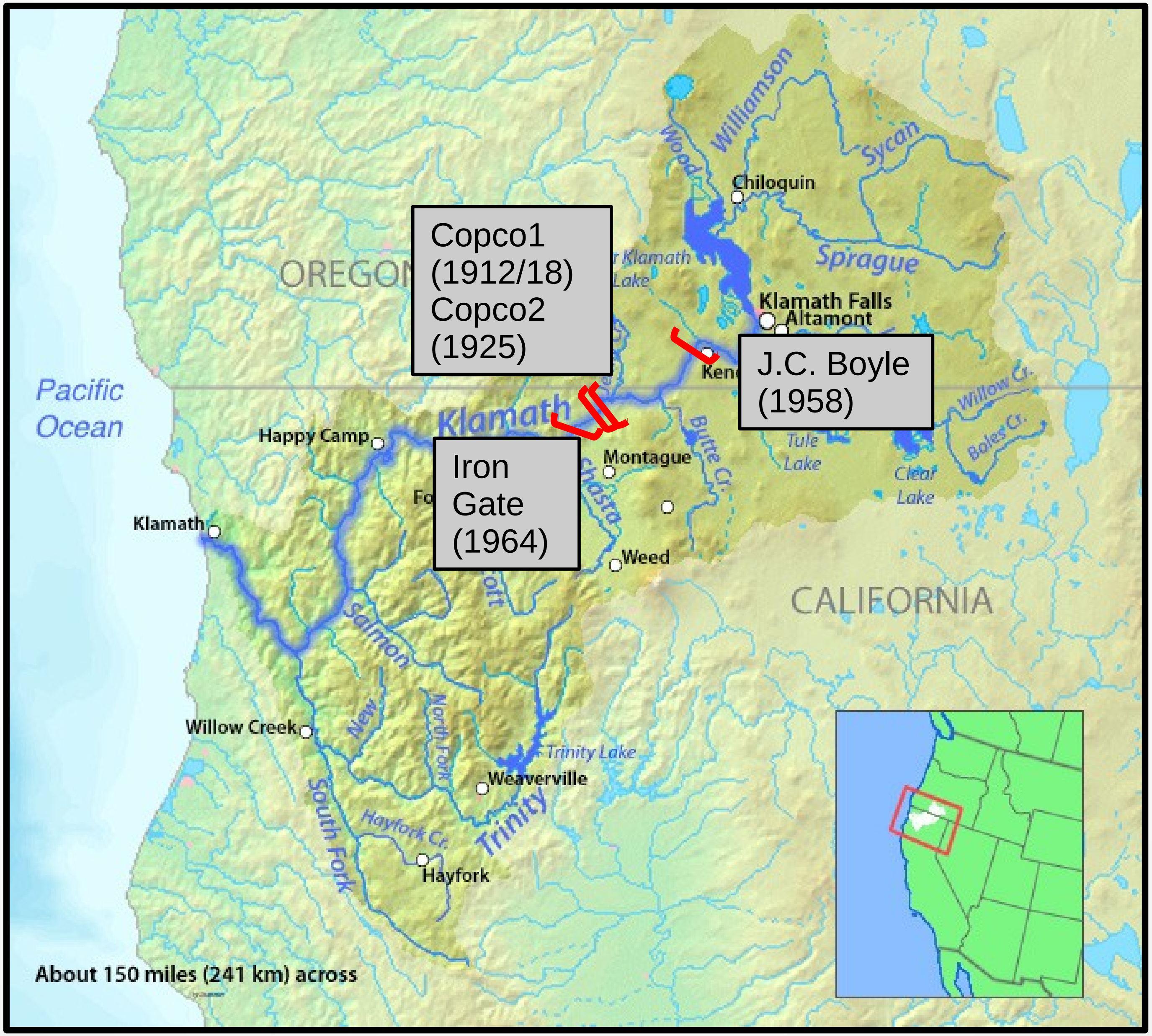
Thompson *et al.* In prep

The Klamath River used to host large numbers of spring Chinook



About 150 miles (241 km) across

Fish passage to upper Klamath blocked in 1912 but dam removal planned for 2020

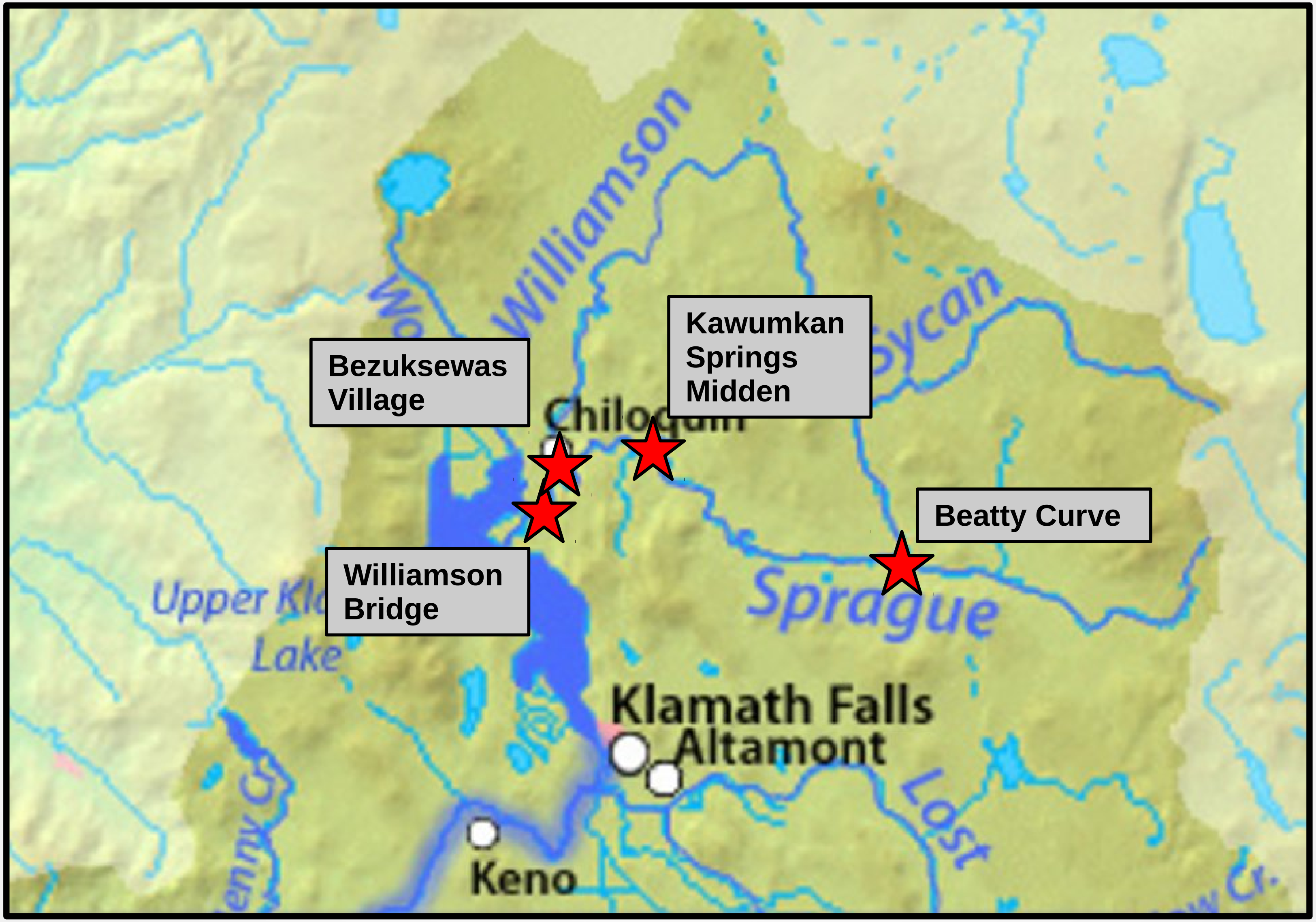


Copco1 (1912/18)
Copco2 (1925)

J.C. Boyle (1958)

Iron Gate (1964)

Nine ancient Chinook samples were analyzed from four upper Klamath archaeological sites



Spring Chinook with the same allele were present in the upper basin for thousands of years

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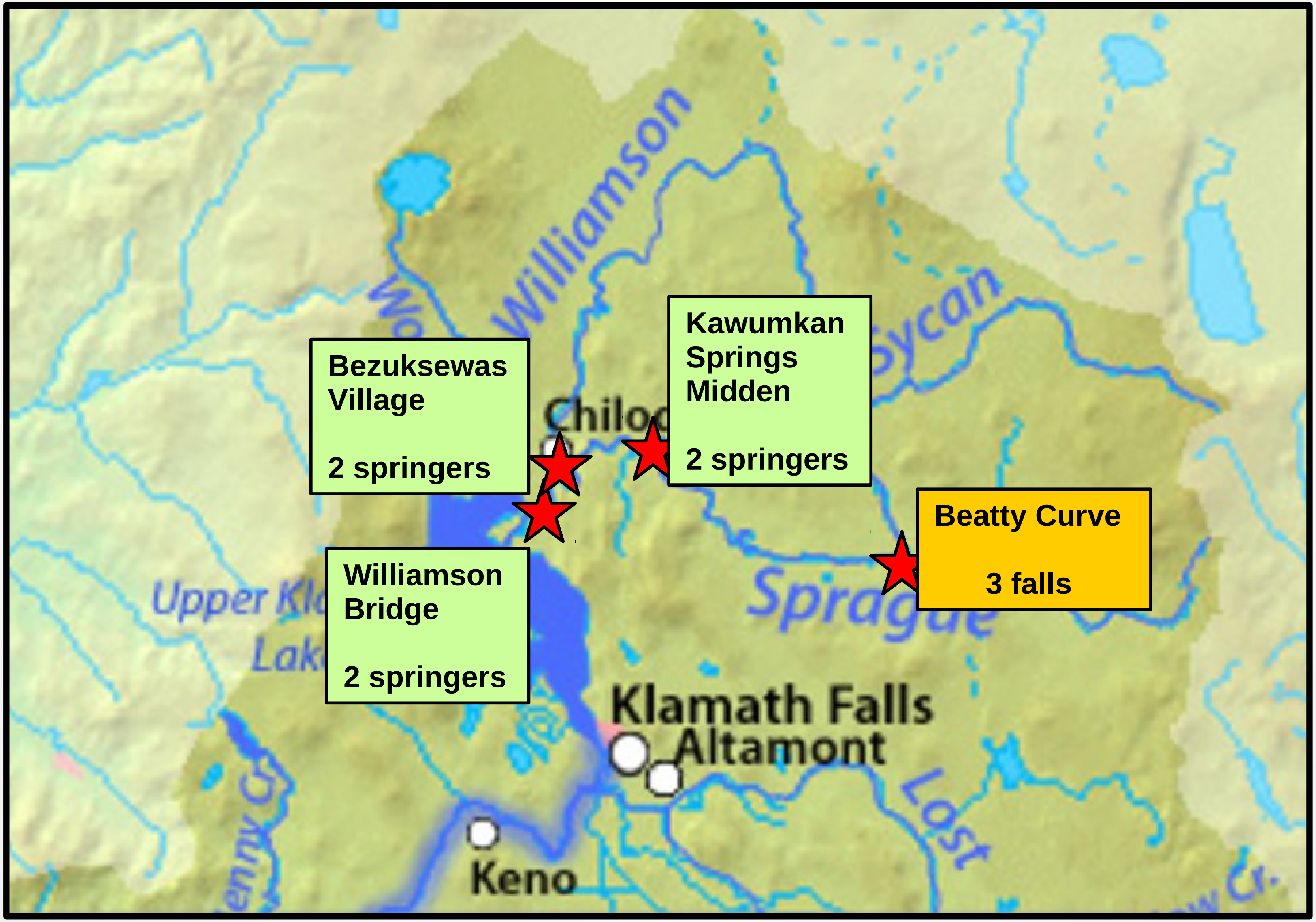


Bezuksewas Village

2 springers

Kawumkan Springs Midden

2 springers

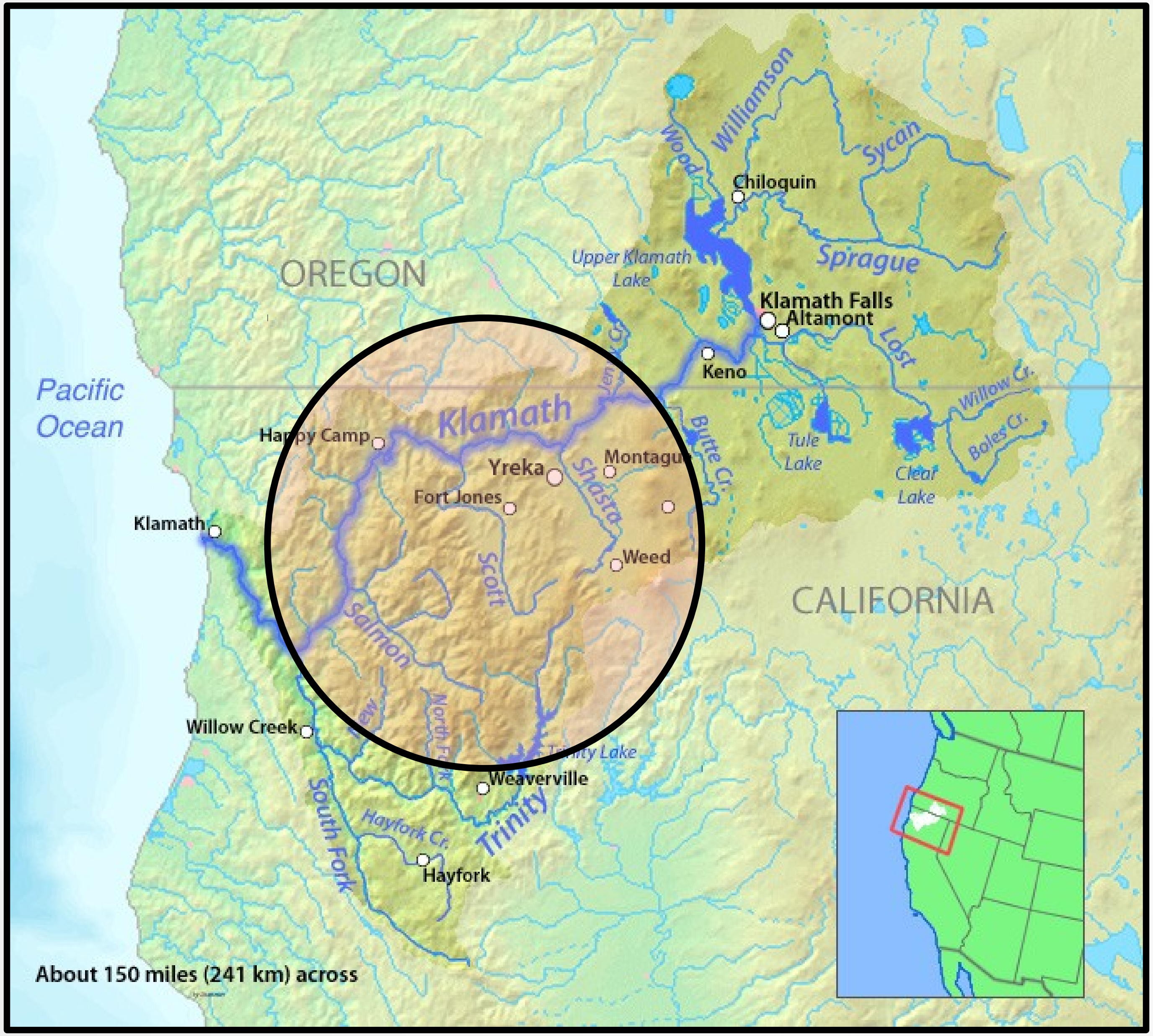
Williamson Bridge

2 springers

Beatty Curve

3 falls

Shasta likely best upper Klamath restoration source if spring-run allele is still present



Shasta: spring Chinook extirpated in 1930’s

Scott: spring Chinook extirpated in 1970’s

Salmon: spring Chinook still present

Spring-run allele not being maintained in absence of spring-run phenotype

Salmon River

- 31 juveniles

Shasta River

- ~500 juveniles

Scott River

- ~500 juveniles

Spring-run allele not being maintained in absence of spring-run phenotype

Salmon River

- 31 juveniles

- **Spring: 4**
- **Het: 6**
- **Fall: 21**

Spring allele frequency: 0.23

Shasta River

- ~500 juveniles

- **Spring: 0**
- **Het: 2**

Spring allele frequency: 0.002

Scott River

- ~500 juveniles

- **Spring: 0**
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Spring allele frequency: 0.002

Spring-run allele not being maintained in absence of spring-run phenotype

Salmon River

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- ~500 juveniles

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Scott River

- ~500 juveniles

- **Spring: 0**
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Expected spring allele frequency if NO selection against heterozygotes: >0.05

Spring allele frequency: 0.23

Spring allele frequency: 0.002

Spring allele frequency: 0.002

Anthropogenic habitat alteration leads to rapid loss of adaptive variation and restoration potential in wild salmon populations.

- Virtually perfect association between GREB1L genotype and migration type
- Heterozygotes have intermediate migration phenotype
- Historic upper Klamath Chinook used same spring-run allele as contemporary populations
- Spring-run allele not being maintained in absence of spring-run phenotype
- Spring-run allele likely not recessive with respect to fitness
- Loss of spring-run allele from lower Klamath populations may hinder restoration upon dam removal
- Reinforce the need to protect adaptive genetic variation to maintain restoration potential

Thompson *et al.* In prep acknowledgments:

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Others ...