Distribution of genetic variation underlying adult migration timing in steelhead of the Columbia River basin

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2020 Ecology & Evolution

Background

Fish migrations

- temporal and spatial availability of resources
- cultural, economic, and ecological resource

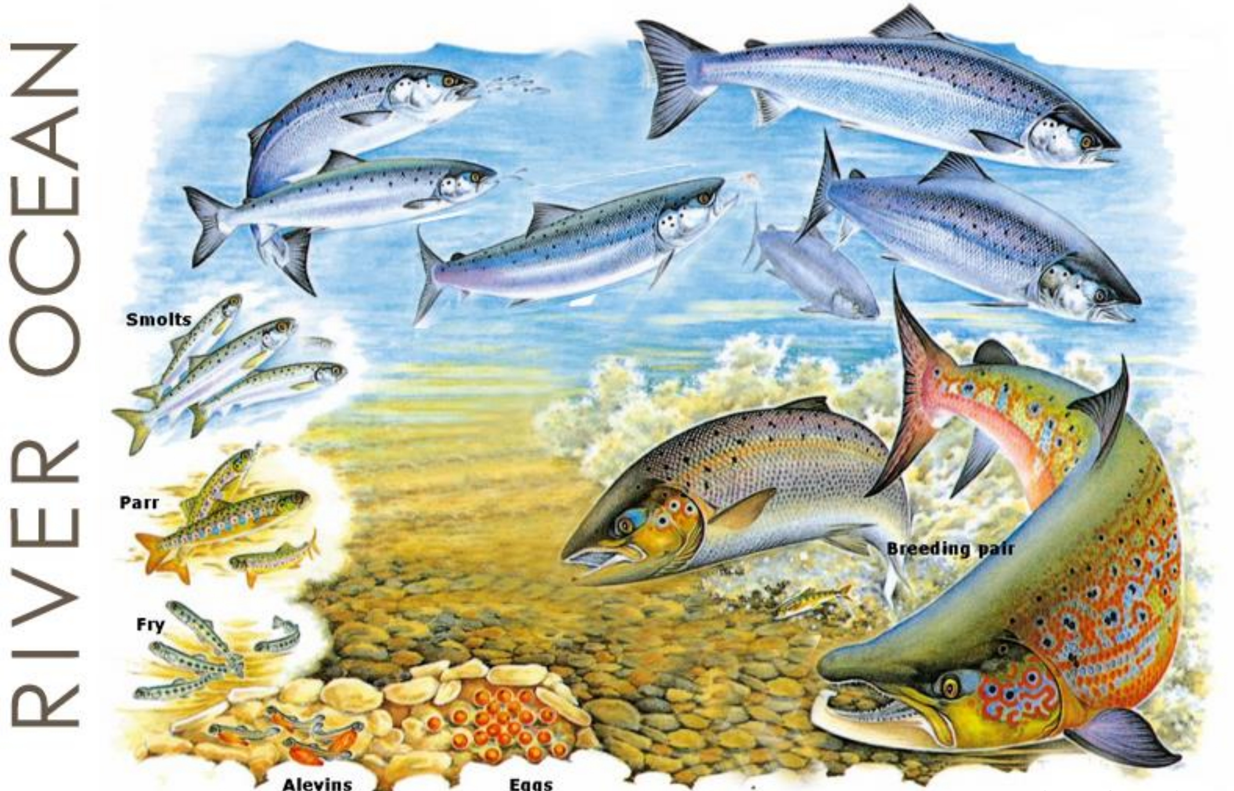


Image credit: Robin Ade

Management

Causes of decline:

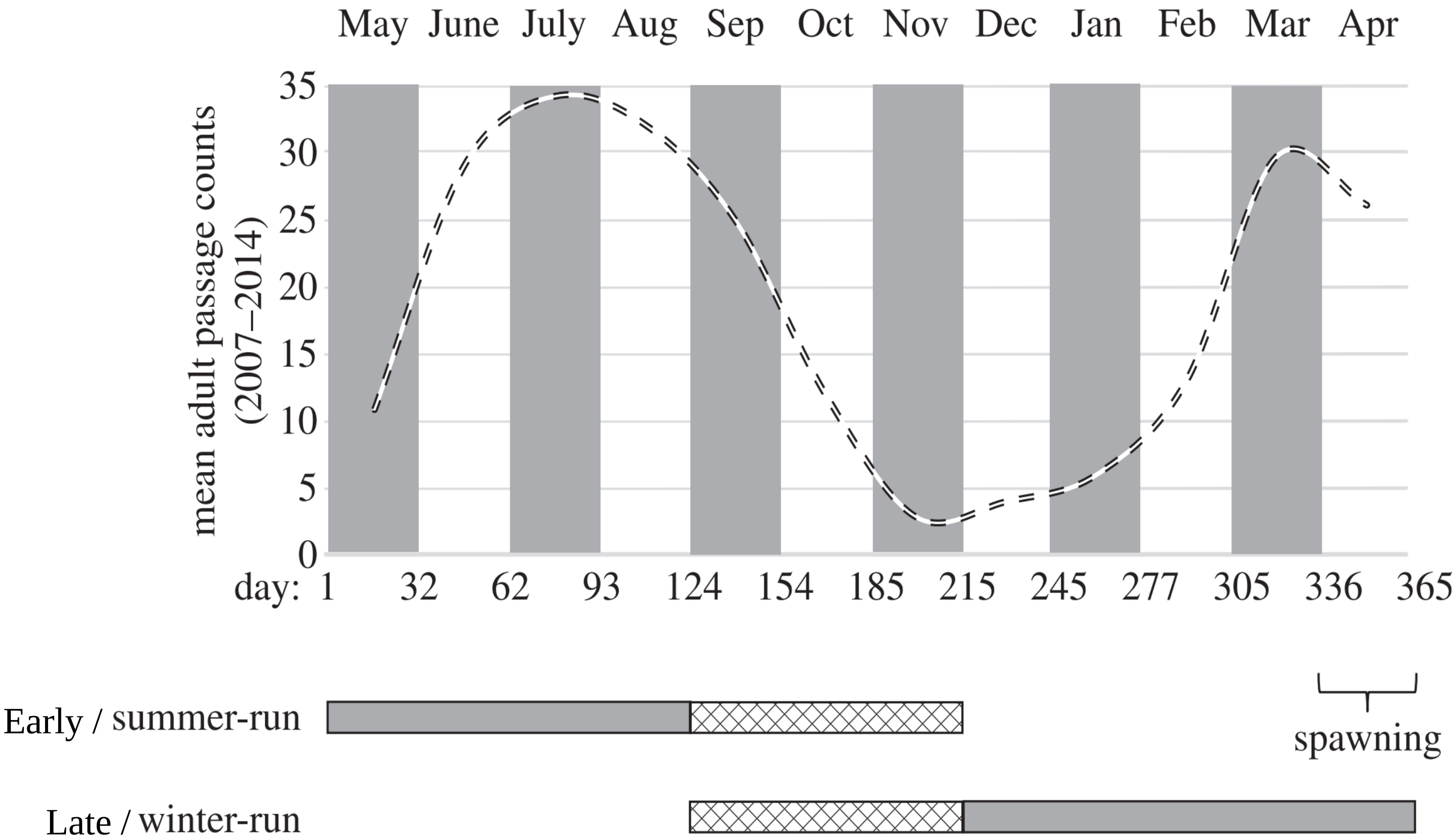
- overharvest, habitat degradation, hydroelectric dams, climate change, other anthropogenic development

Solutions:

- Identify evolutionarily significant units (ESU)
- maintain phenotypic and genetic variation of distinct populations, such as migration timing

Background

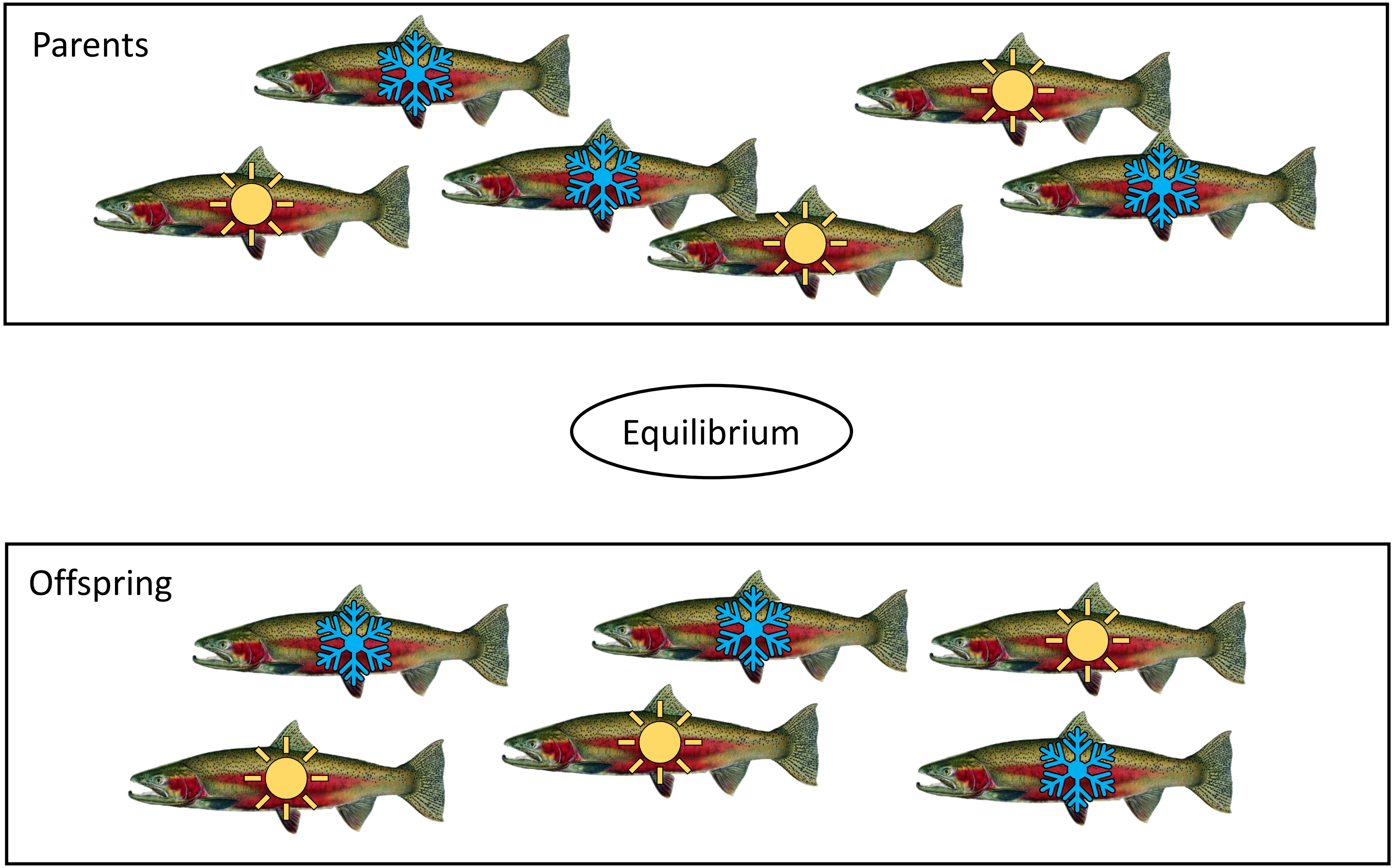
- Bimodal migration timing in steelhead
- Early / summer-run mature in streams and late / winter-run mature in ocean, both spawn at the same time



Adapted from: Hess et al. 2016

Background

- Migration timing has genetic basis and is heritable



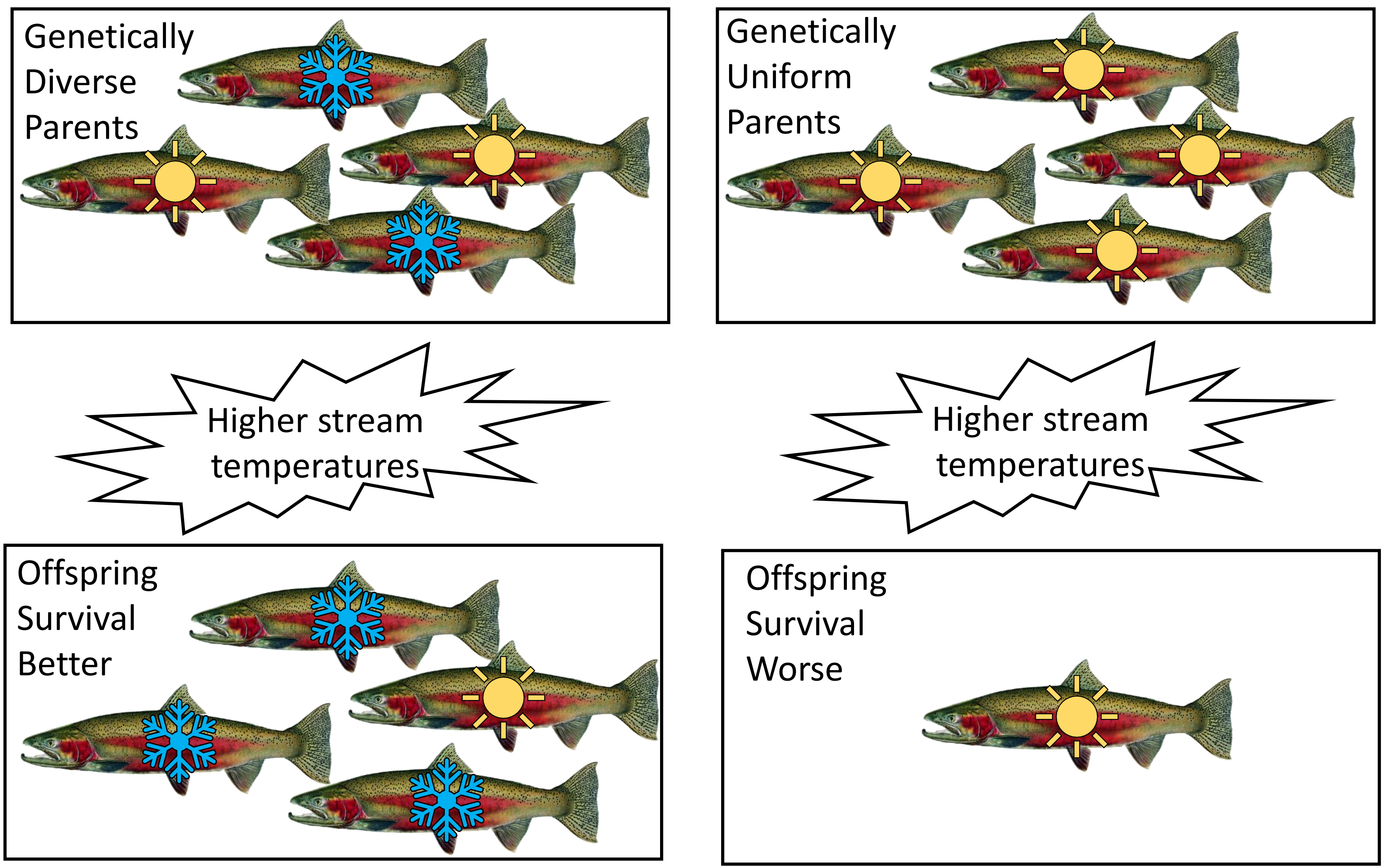
Parents

Equilibrium

Offspring

Background

- Genetic diversity and conservation



Genetically Diverse Parents

Higher stream temperatures

Offspring Survival Better

Genetically Uniform Parents

Higher stream temperatures

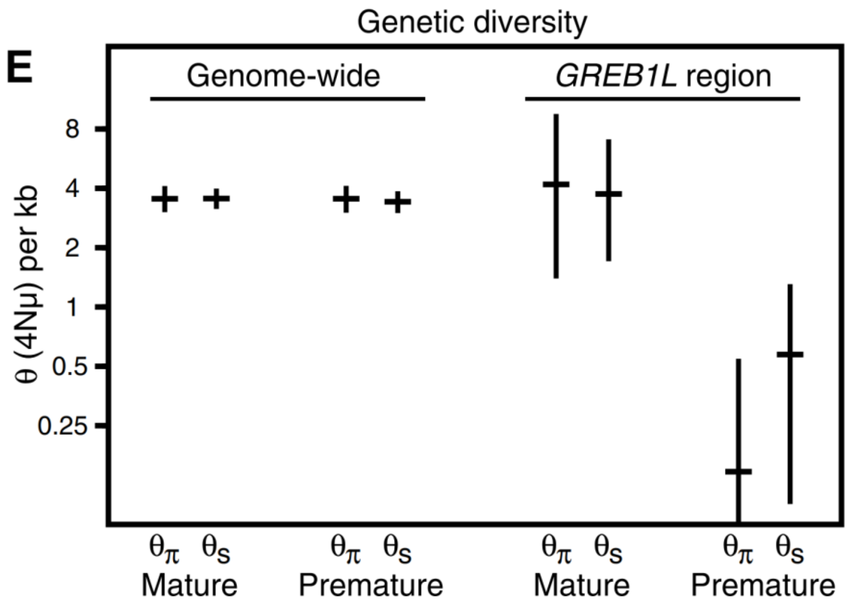
Offspring Survival Worse

Background

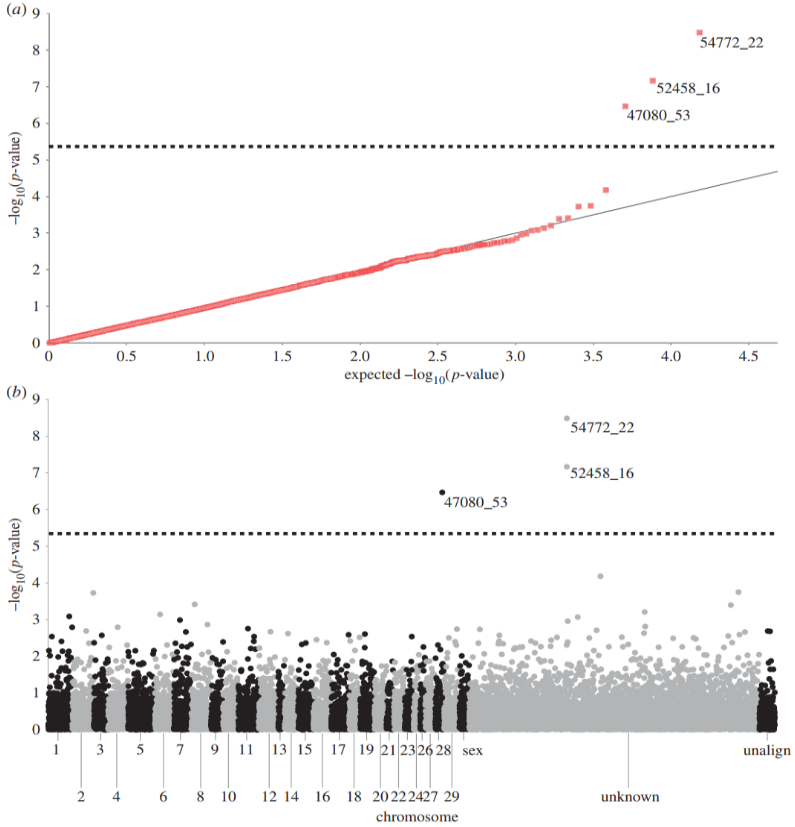
- Neutral vs. adaptive genetic markers
  - Neutral genetic markers differentiate between genetic lineages
    - coastal or inland
    - distinct populations
  - Adaptive markers can differentiate between phenotypic traits
    - migration-timing
    - sex
    - thermal-tolerances
    - age
    - etc.
- Within Populations
  - Low variation at neutral genetic markers
  - Greater variation in adaptive markers

Background

- Previous studies



Adapted from: Prince et al. 2018



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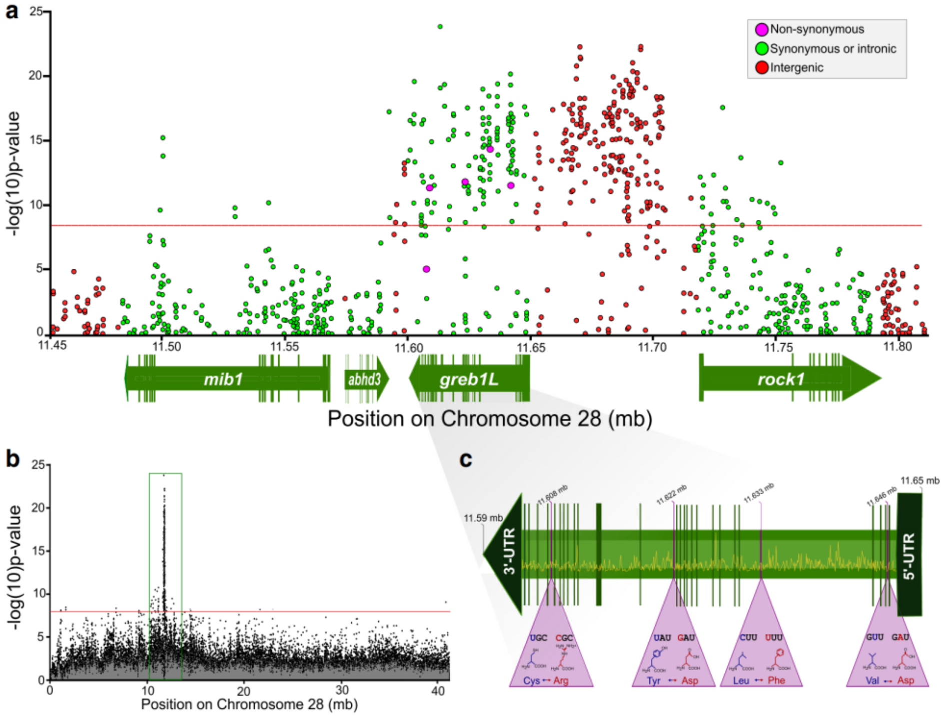
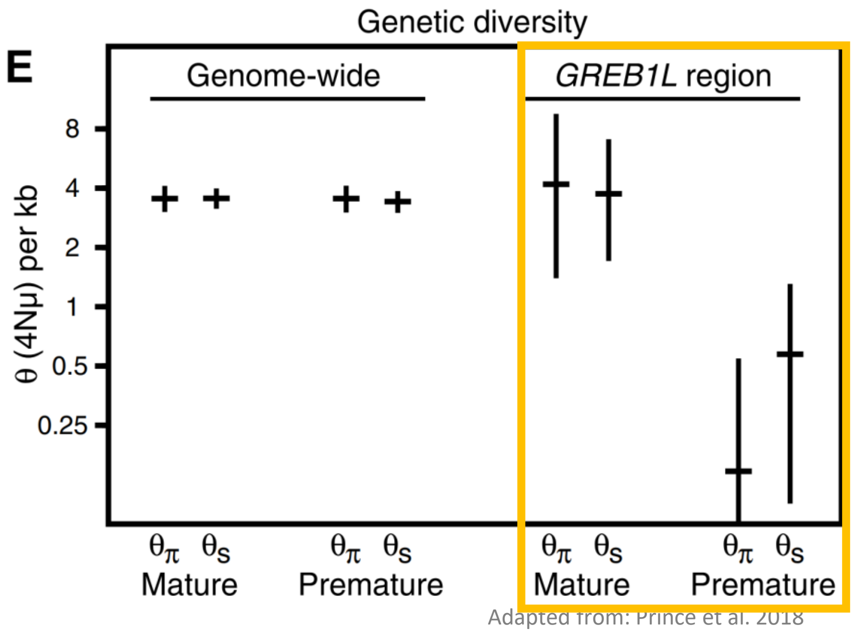


Adapted from: Micheletti et al. 2018

Background

- Previous studies



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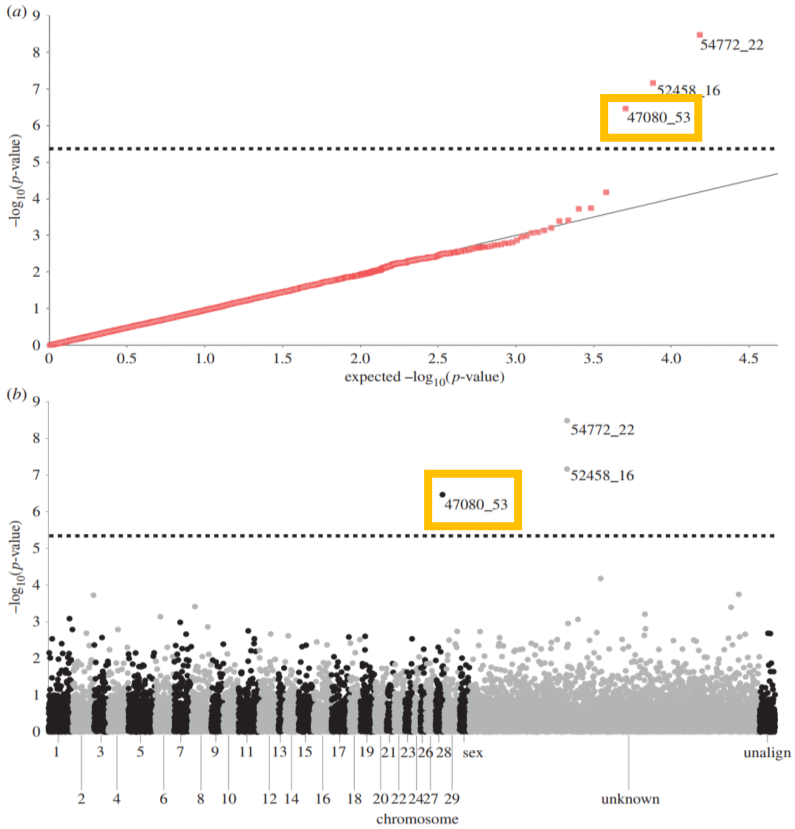

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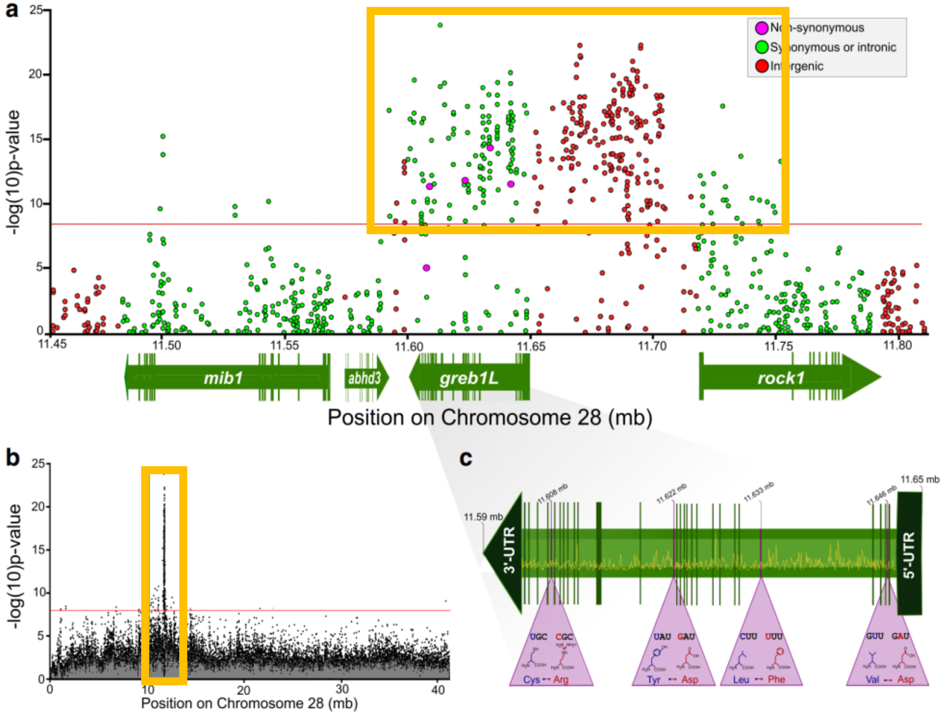
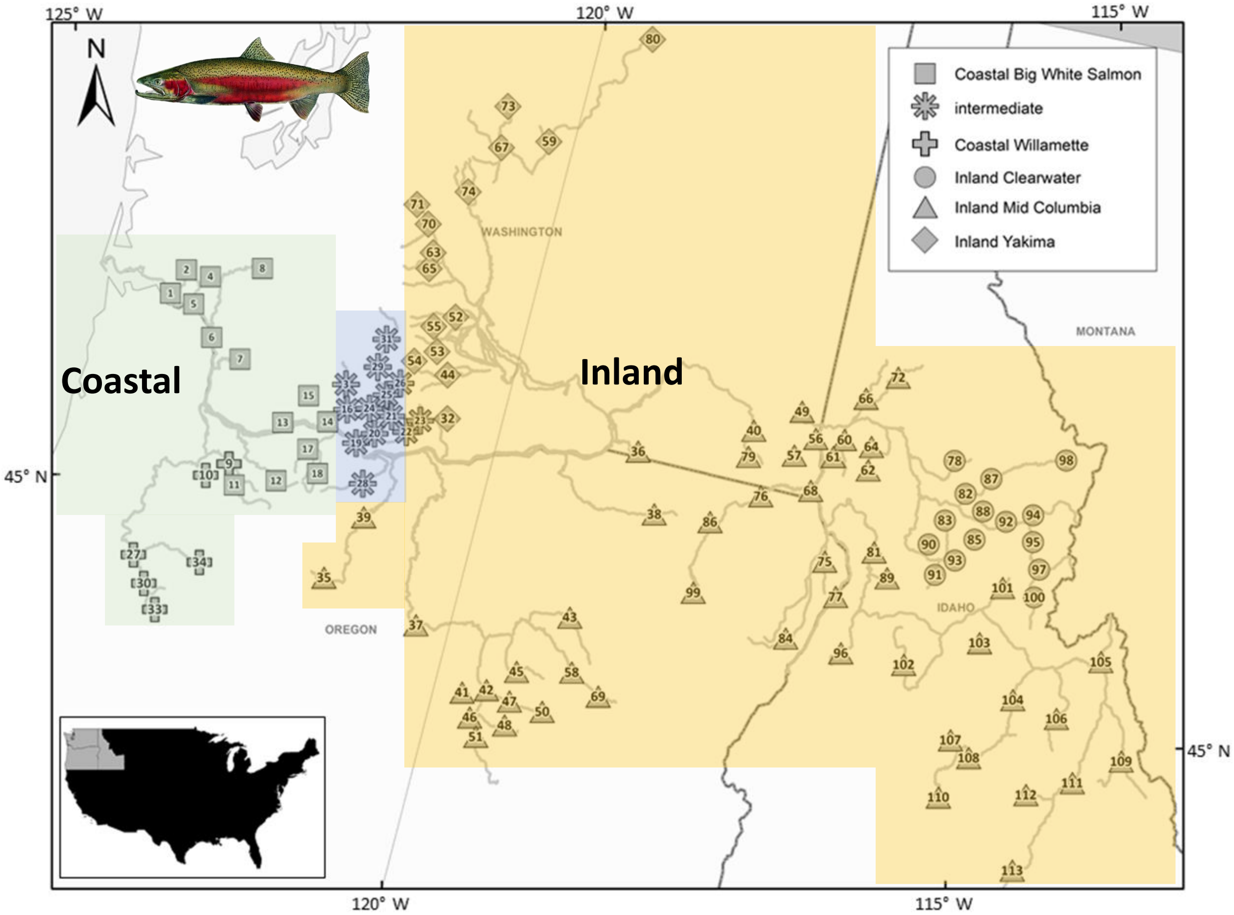


Adapted from: Micheletti et al. 2018

Methods

Sample Collection

- Inland and coastal sampled
- 1996-2018
- Electrofishing, smolt traps, weirs
- Non-lethal fin tissue



Adapted from: Collins et al. 2020

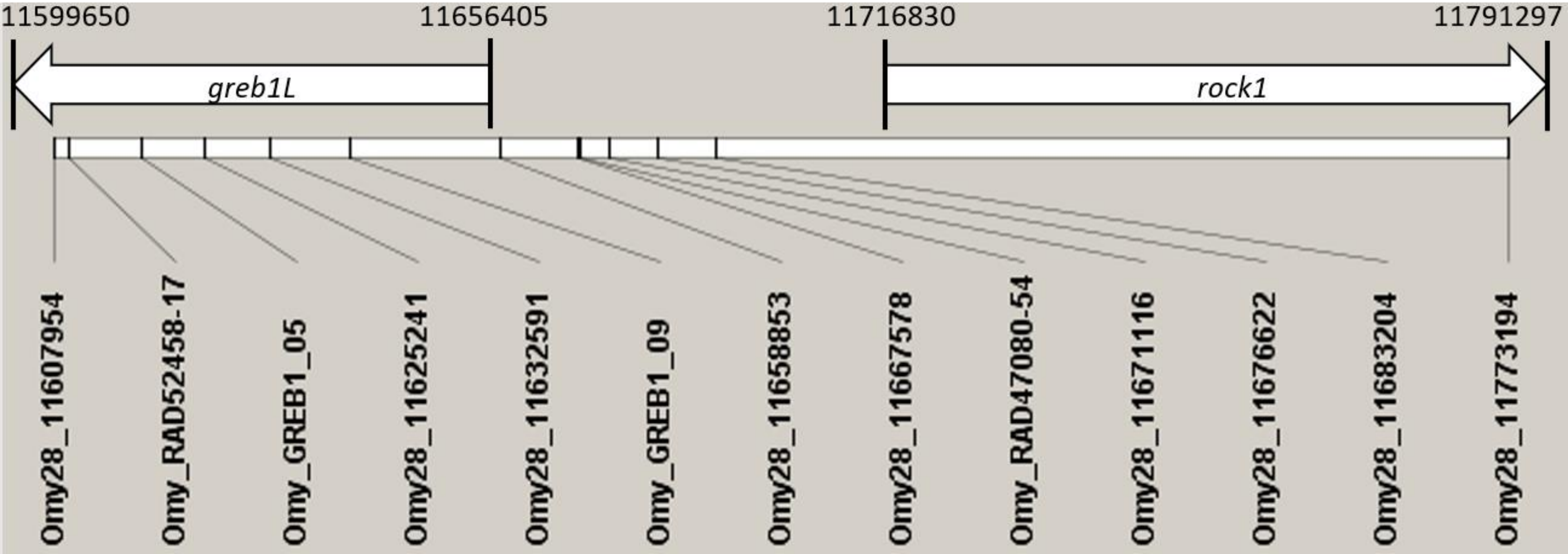
Analyses

- Neutral marker PCA
- Migration timing genotype proportions were assessed across all collection locations
- Linkage disequilibrium (LD) within the adaptive markers to identify haplotype blocks
- Redundancy analyses (RDA) were conducted for all Columbia River basin collections to model the degree to which the variation in environmental variables explained the variation in allele frequencies of adaptive markers

Methods

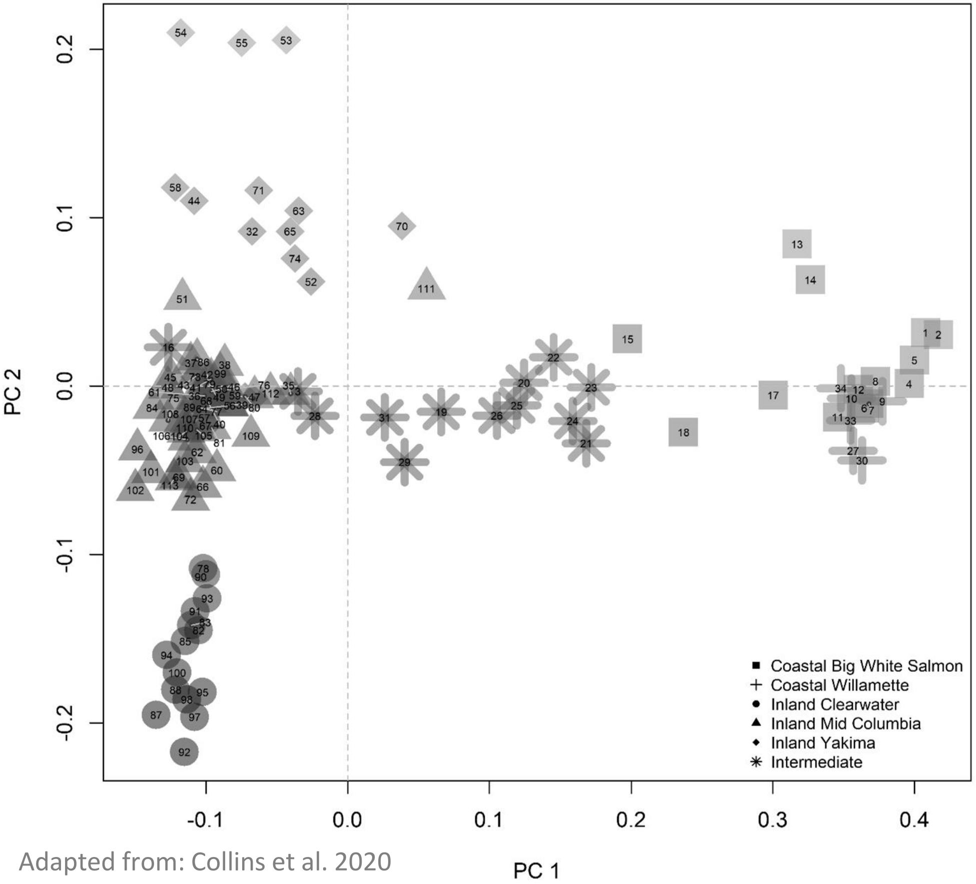
- Migration timing is heritable – genomic region of major effect
- *greb1L* – initial SNPs identified with RAD-seq methods
- More SNPs identified on *greb1L*, intergenic, *rock1* with Pool-seq methods

Adapted from: Collins et al. 2020



Results

- 9,471 steelhead from 113 populations
- 226 neutral markers



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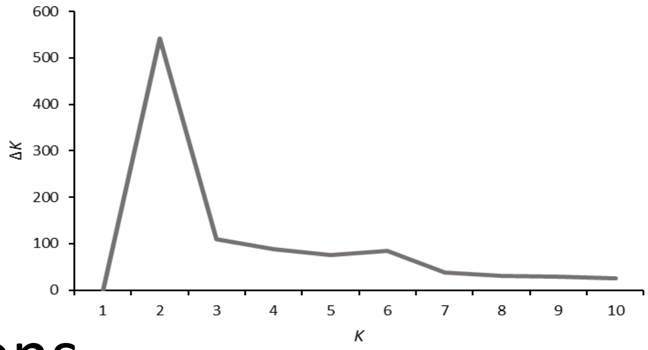

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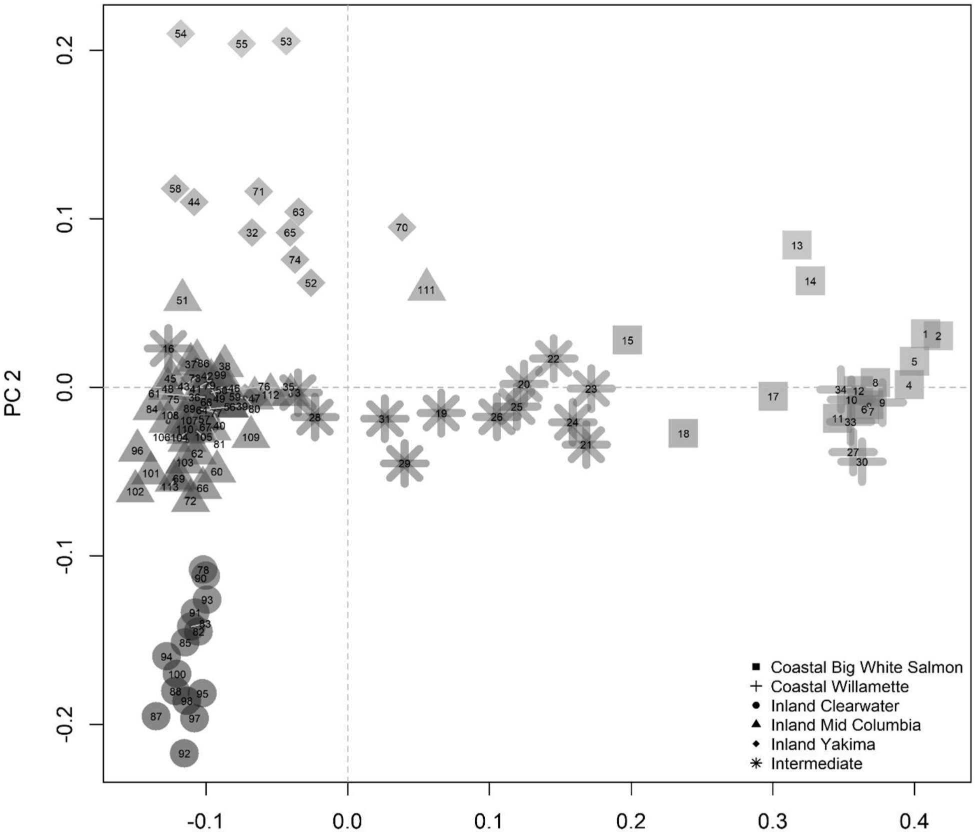

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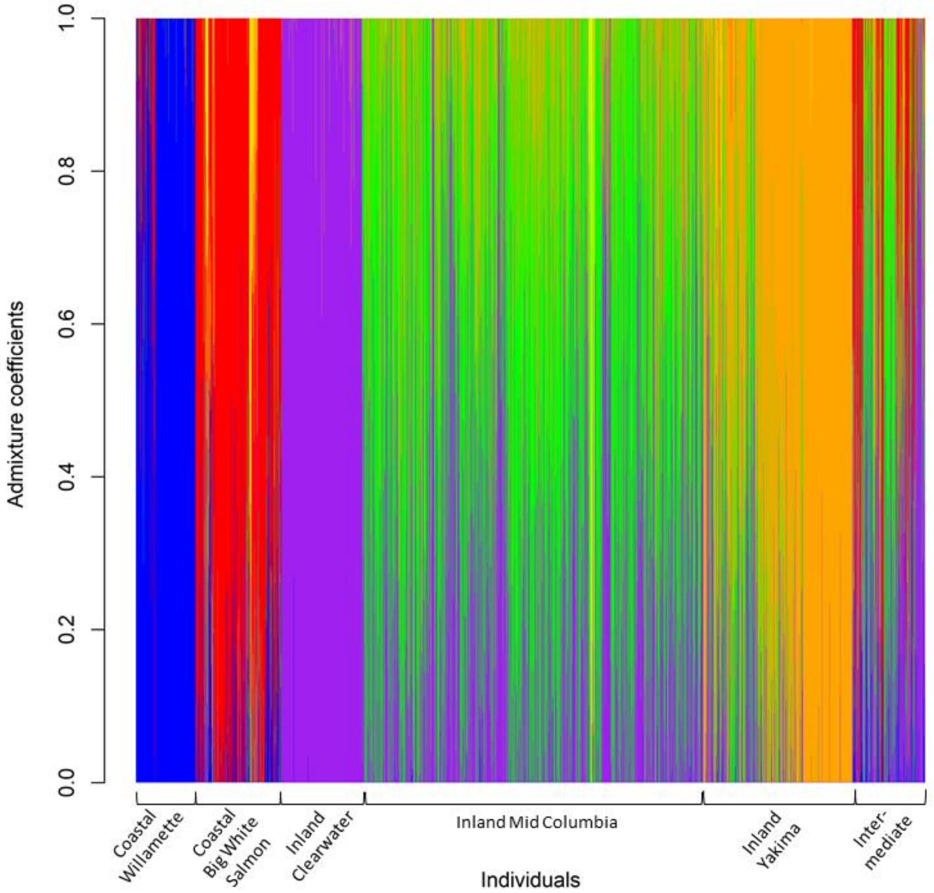

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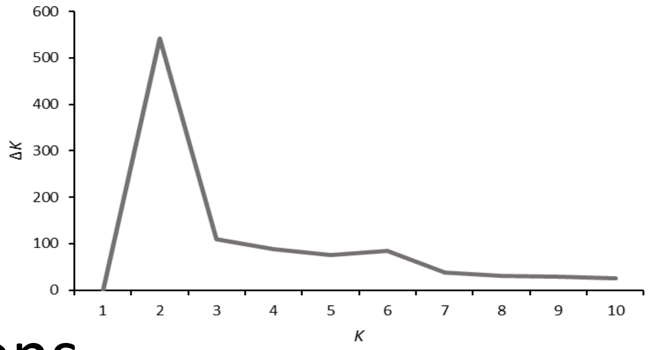

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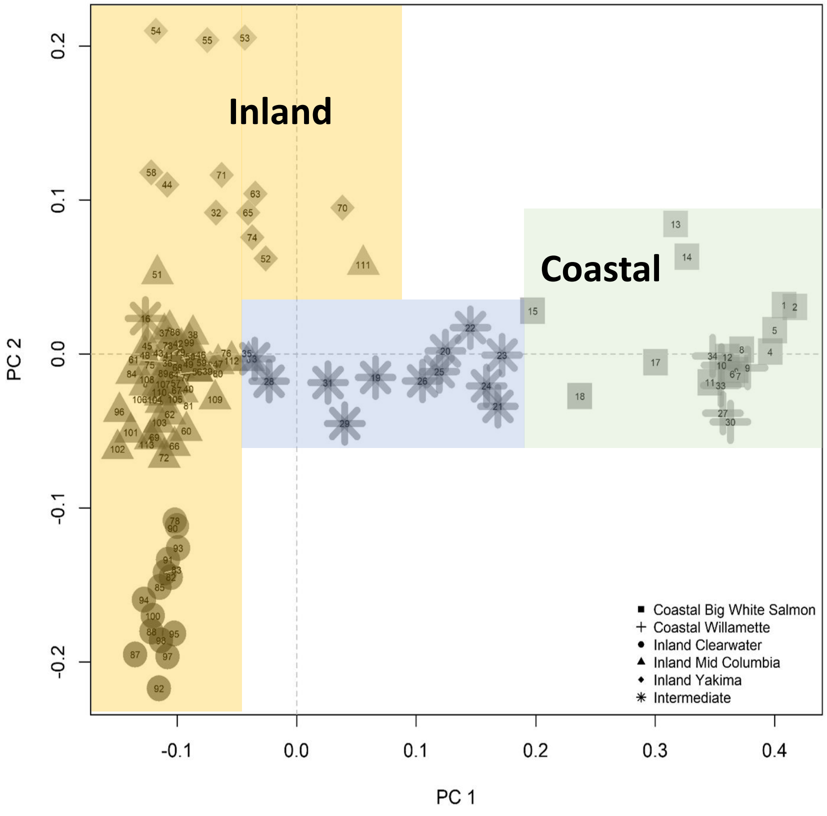

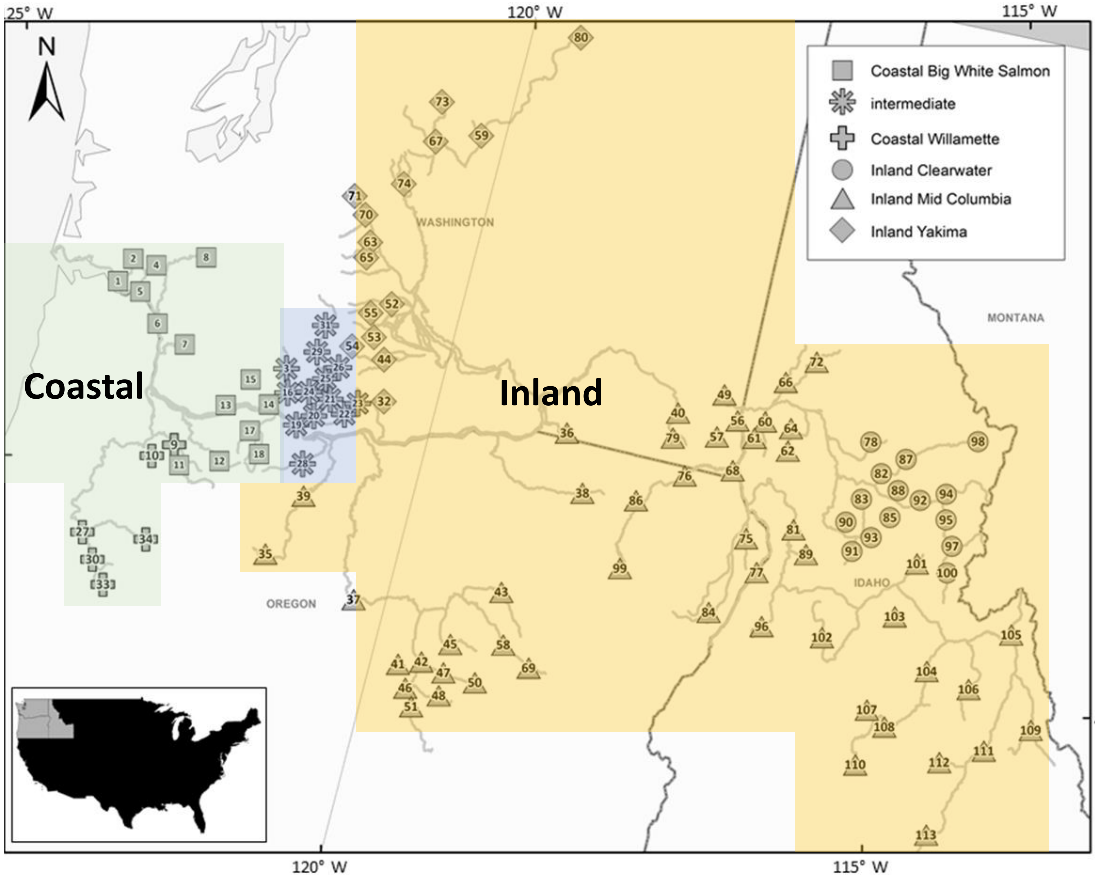

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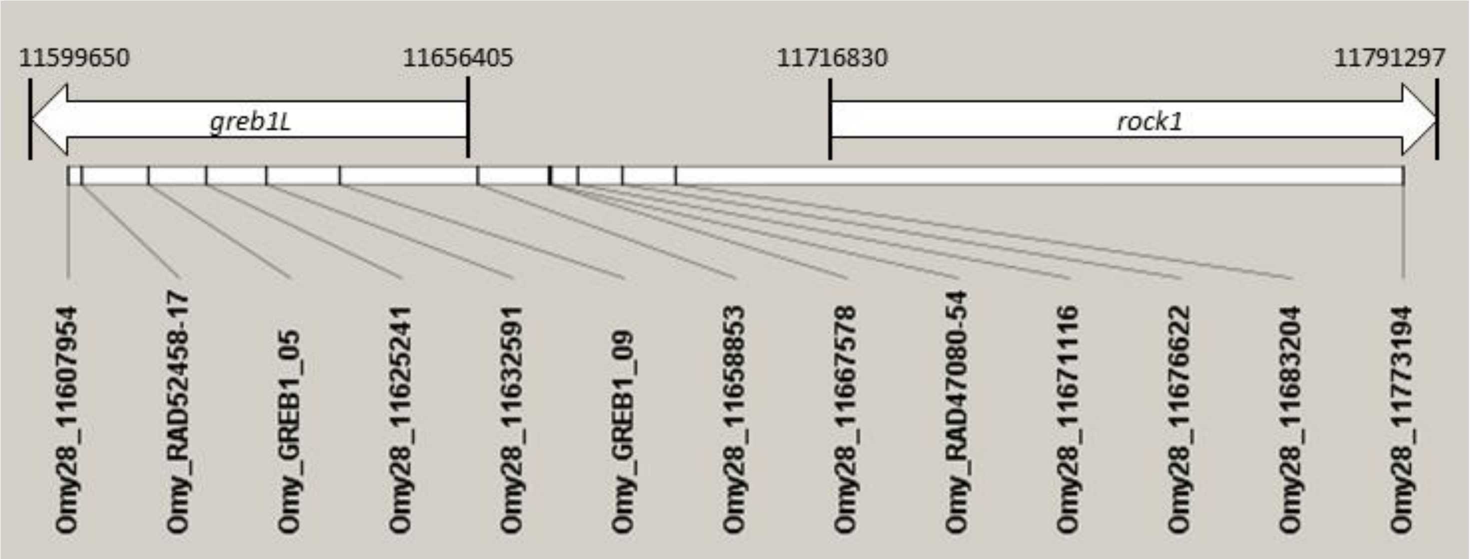
Results



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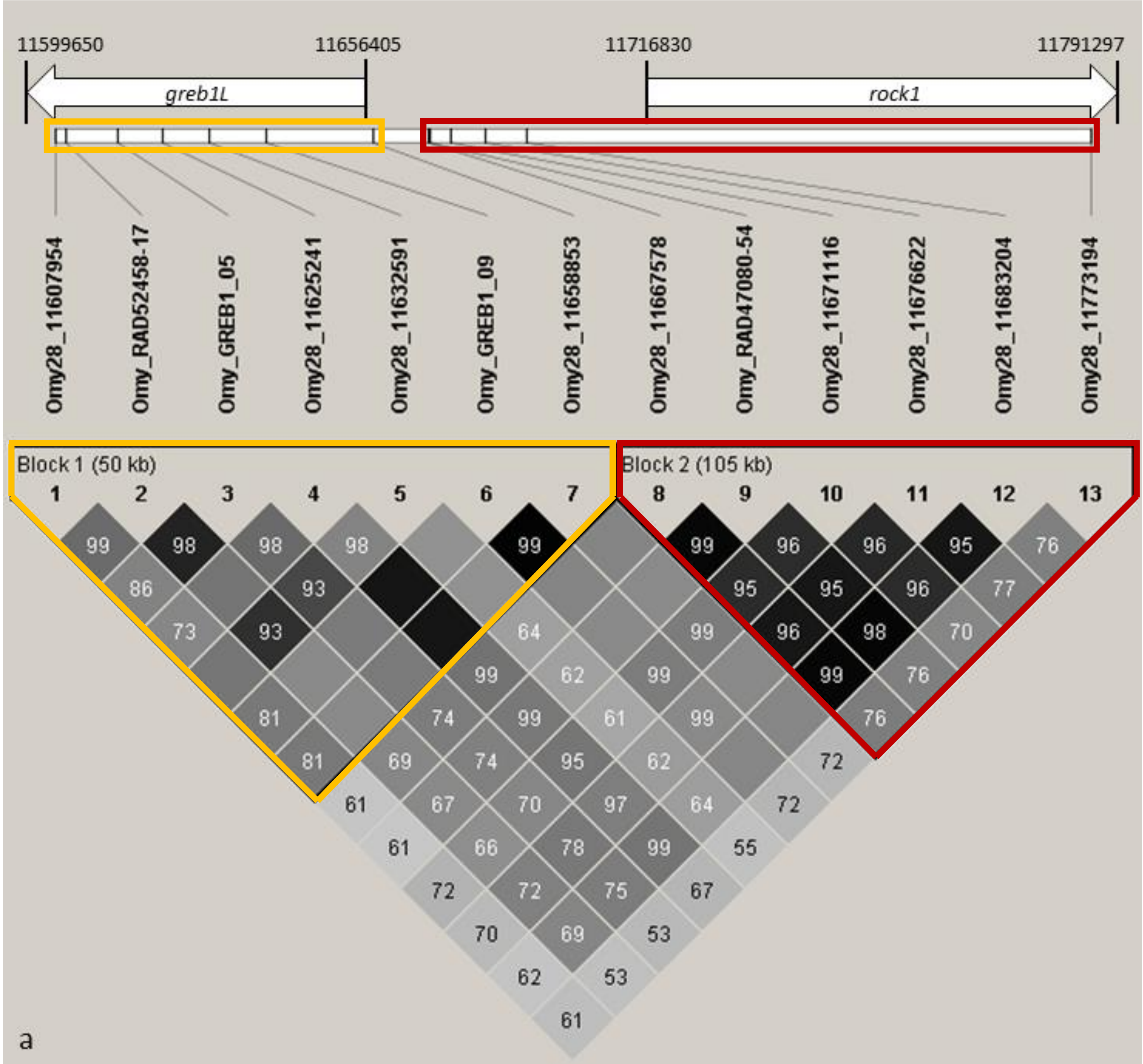
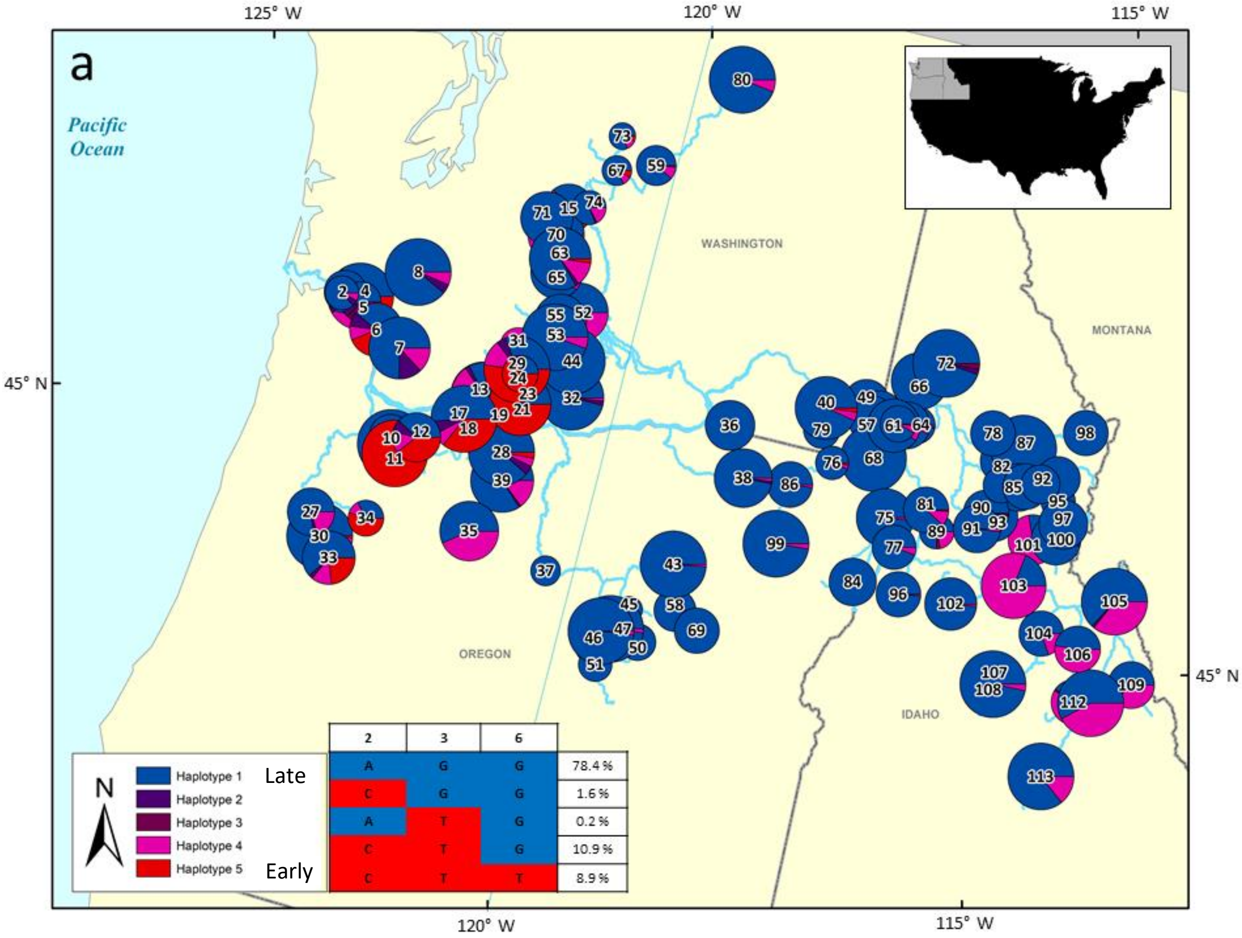


Adapted from: Collins et al. 2020

Results

- Late returning (blue) steelhead are the most common
- Early returning (red) are rarer: Only 9 out of 113 (8%) populations had higher frequency for early migration
- More genetic diversity in coastal populations than inland
- Corresponds with observations that early returning fish have experienced the greatest decline over time
- Concerns over loss of variation over time



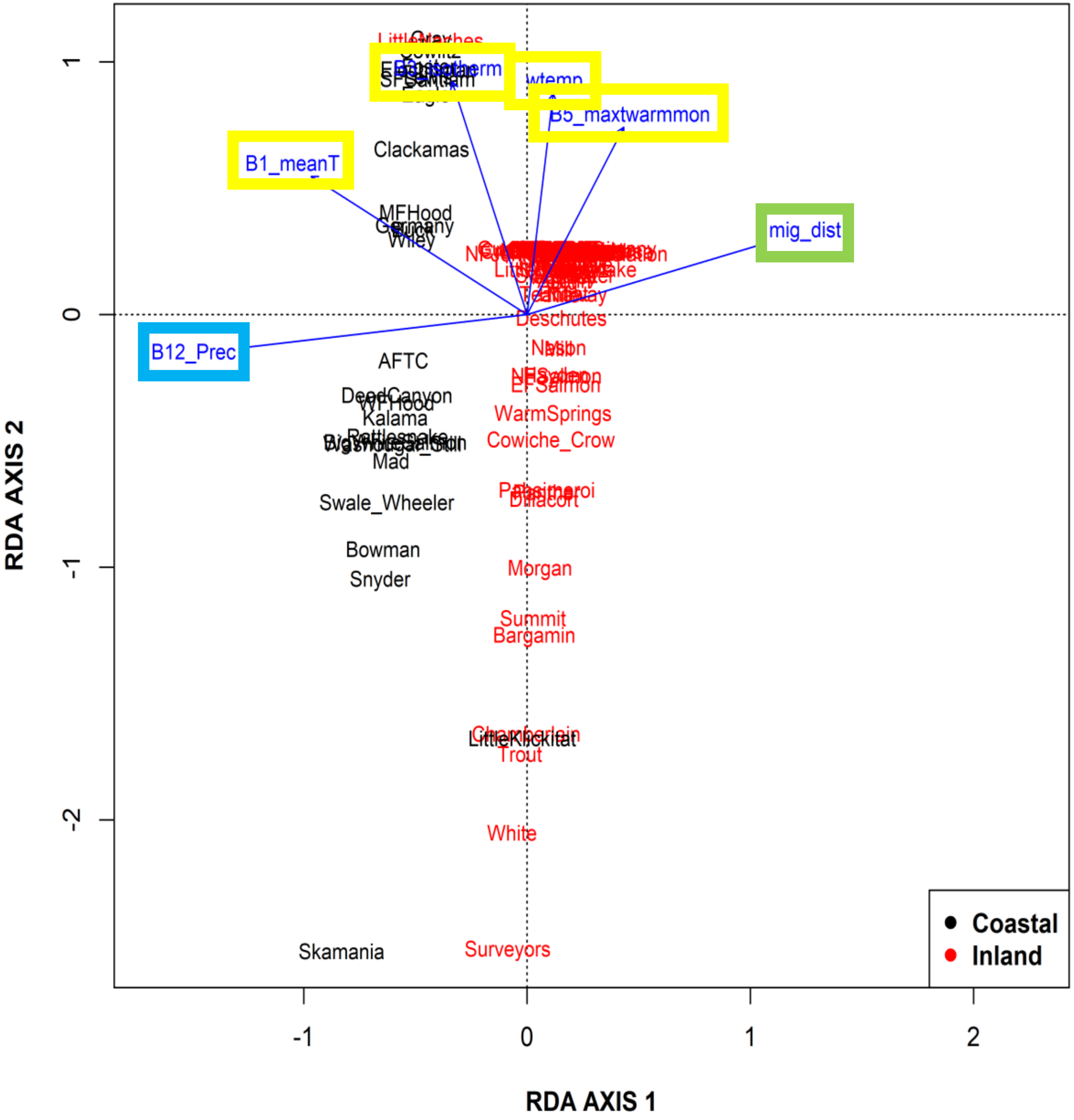
	2	3	6	
Haplotype 1	A	G	G	78.4 %
Haplotype 2	C	G	G	1.6 %
Haplotype 3	A	T	G	0.2 %
Haplotype 4	C	T	G	10.9 %
Haplotype 5	C	T	T	8.9 %

Adapted from: Collins et al. 2020

Results

- Analysis to find environmental factors that drive genetic variation associated with migration timing:
  - Migration distance
  - Temperature
  - Precipitation

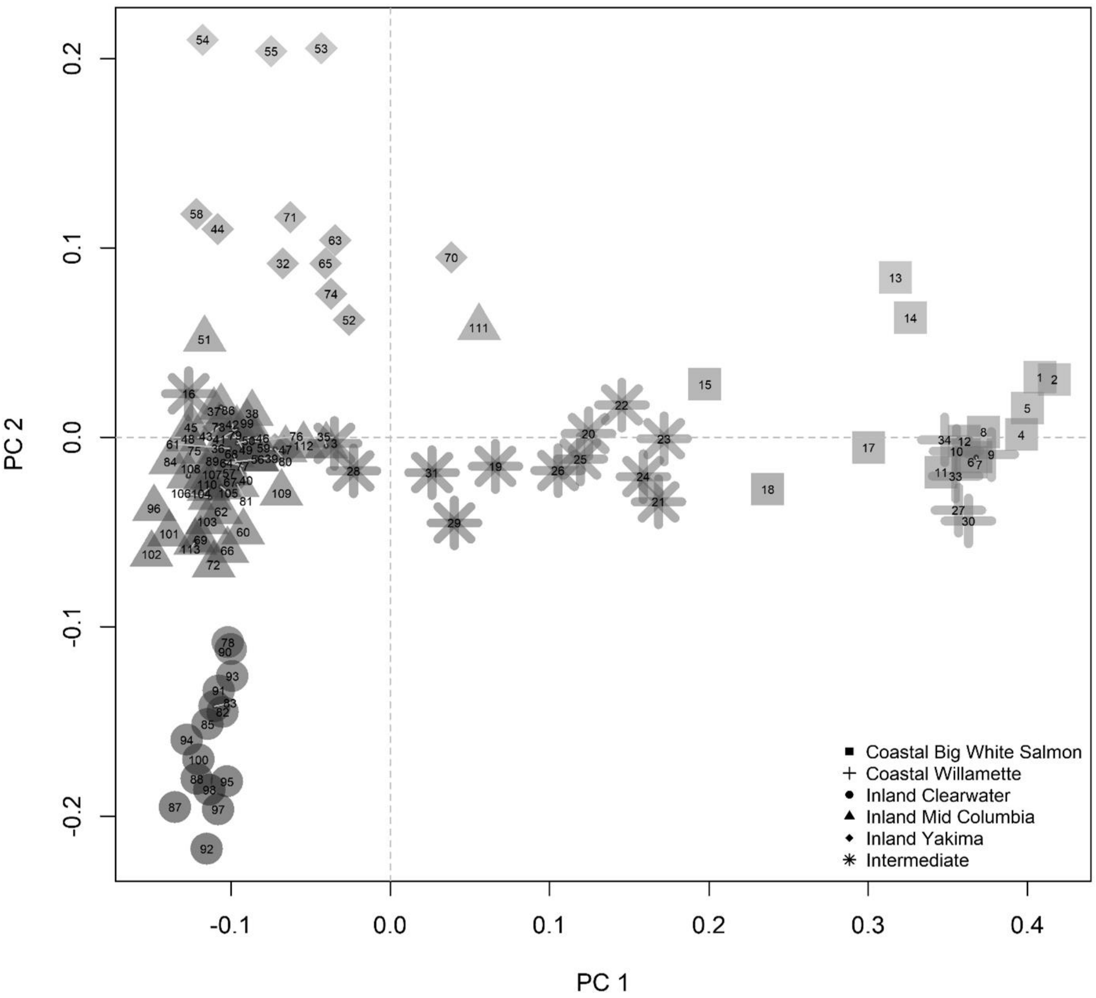
- Significant relationships between environmental variables and genetics suggest that these may be environmental drivers leading to local adaptation among populations.



Adapted from: Collins et al. 2020

Conclusions

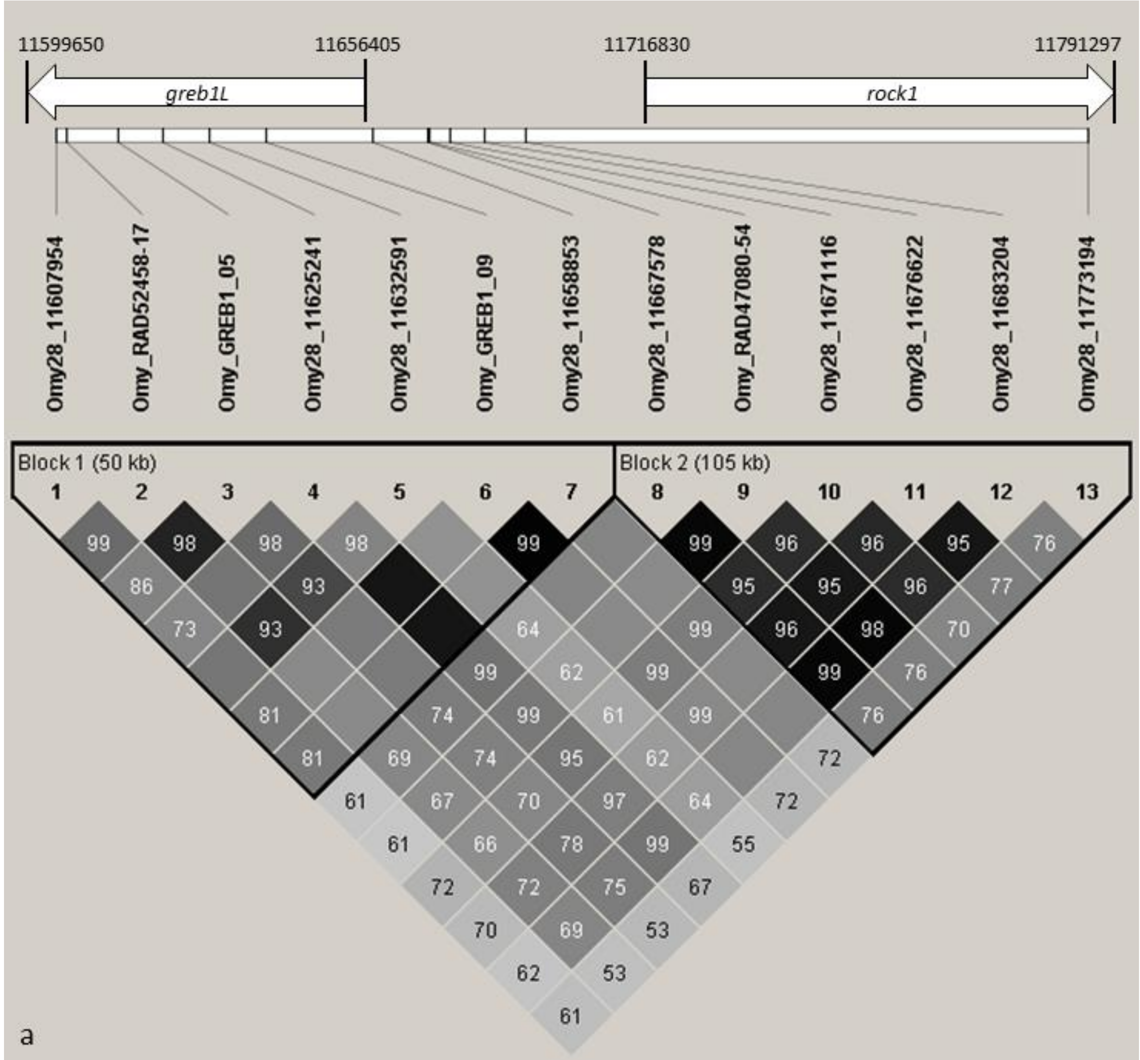
- Neutral marker analyses of population structure, supported and improved upon previous findings



Adapted from: Collins et al. 2020

Conclusions

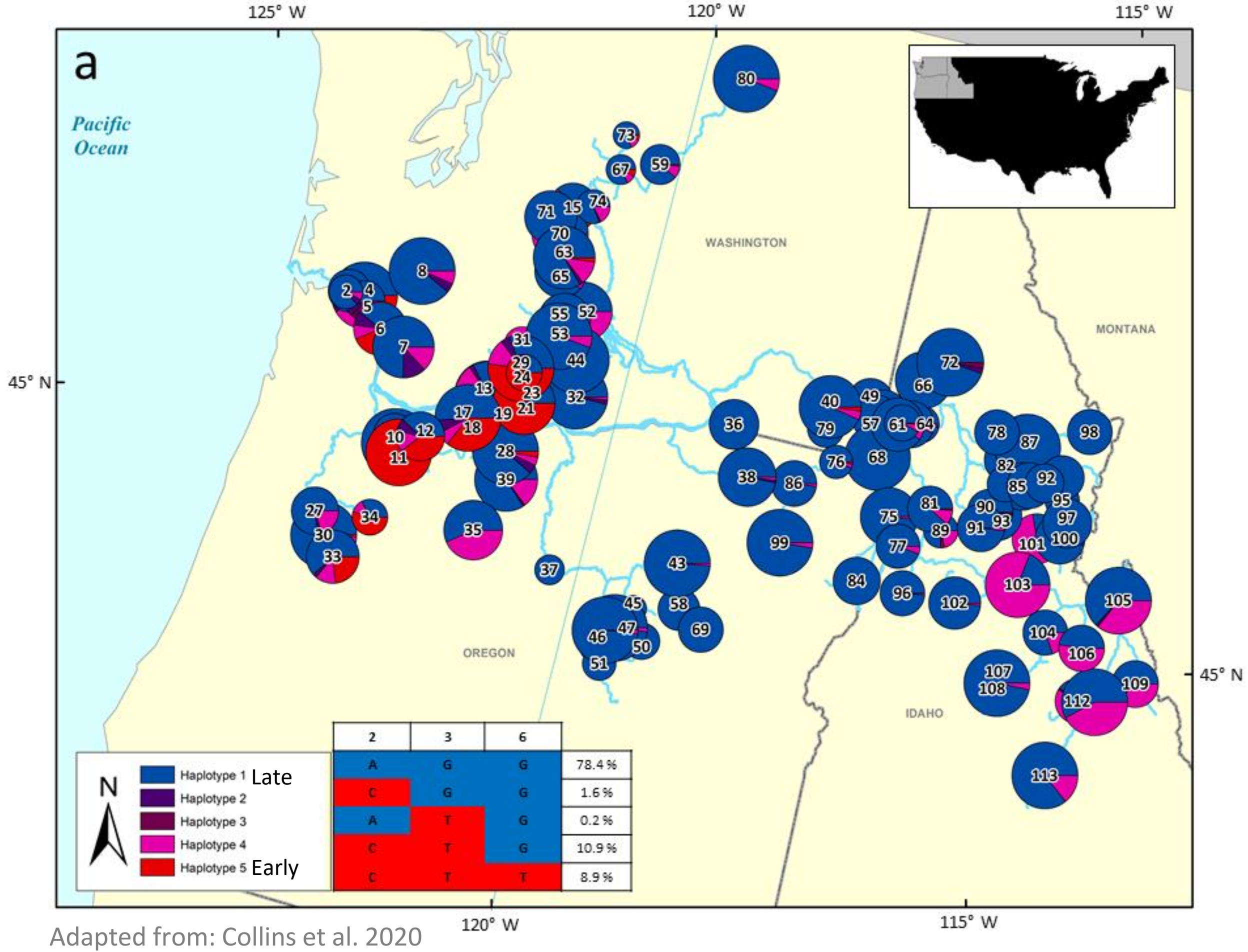
- We determined linkage blocks for 13 adaptive markers associated with migration timing



Adapted from: Collins et al. 2020

Conclusions

- Different heterozygote haplotypes were found to be predominant in coastal versus inland lineages.

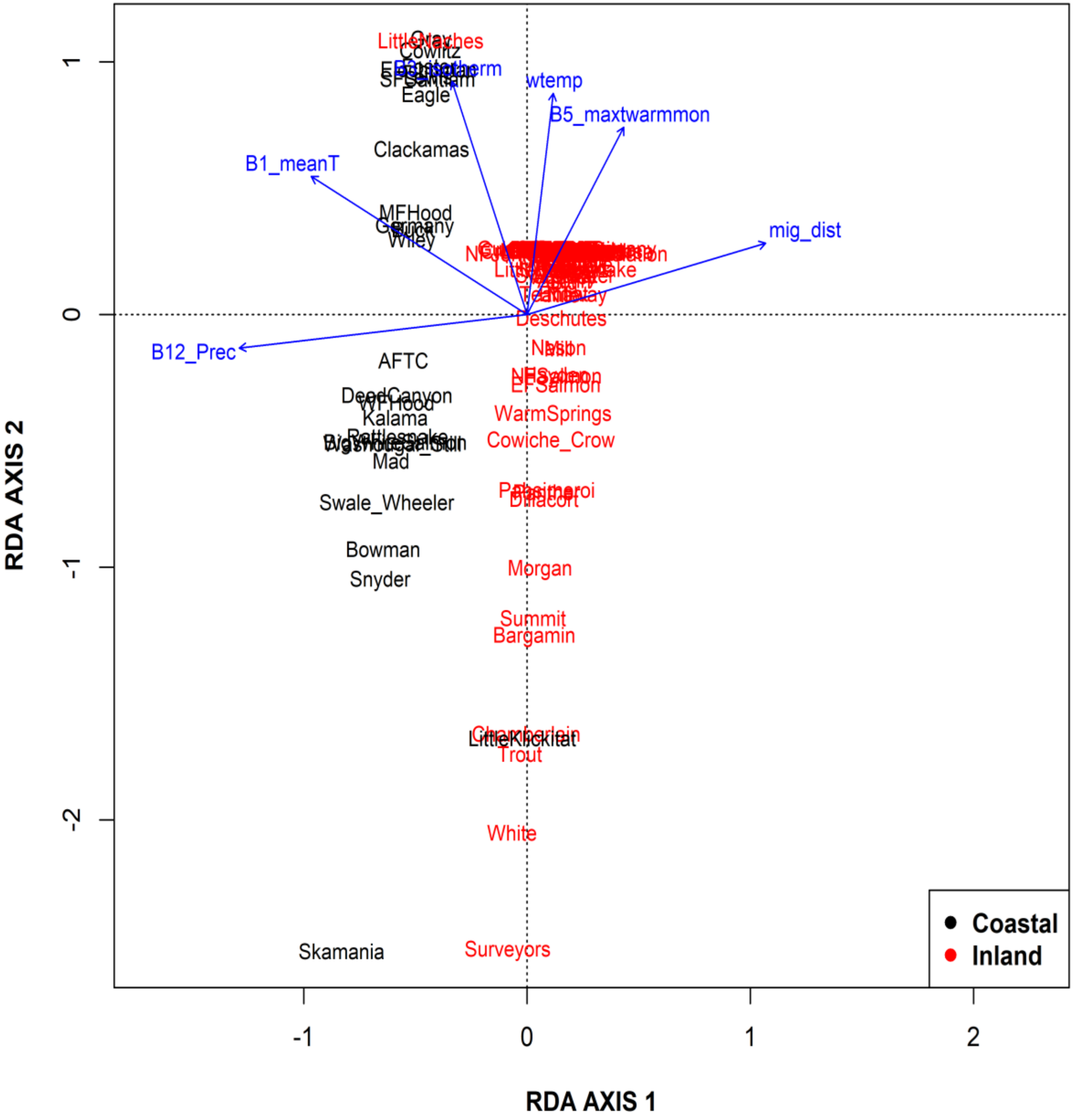


2	3	6	
A	G	G	78.4 %
C	G	G	1.6 %
A	T	G	0.2 %
C	T	G	10.9 %
C	T	T	8.9 %

Adapted from: Collins et al. 2020

Conclusions

- Candidate adaptive marker variation revealed the importance of temperature and precipitation

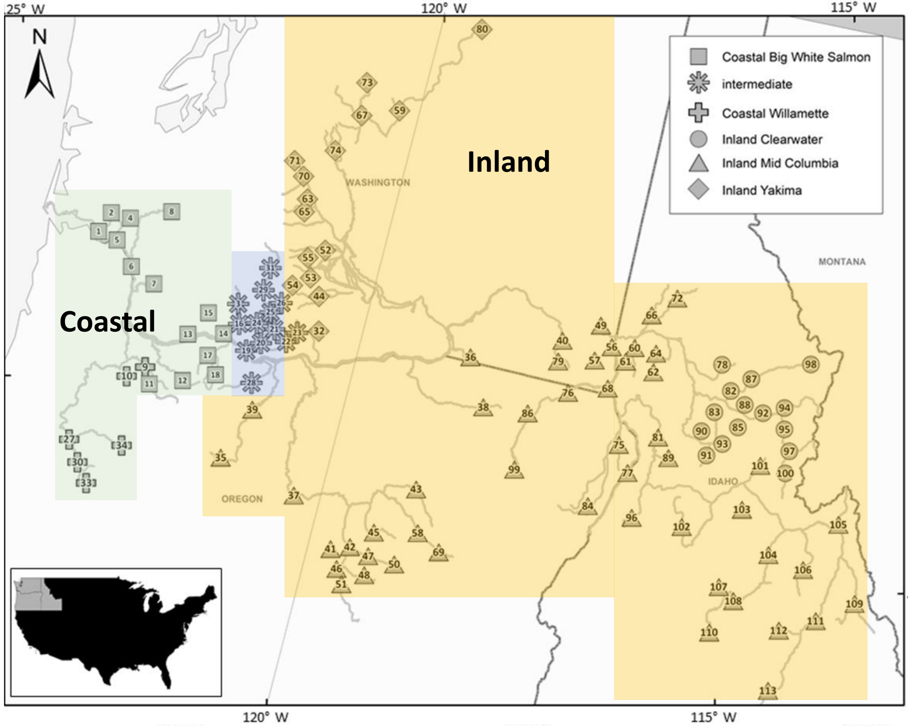


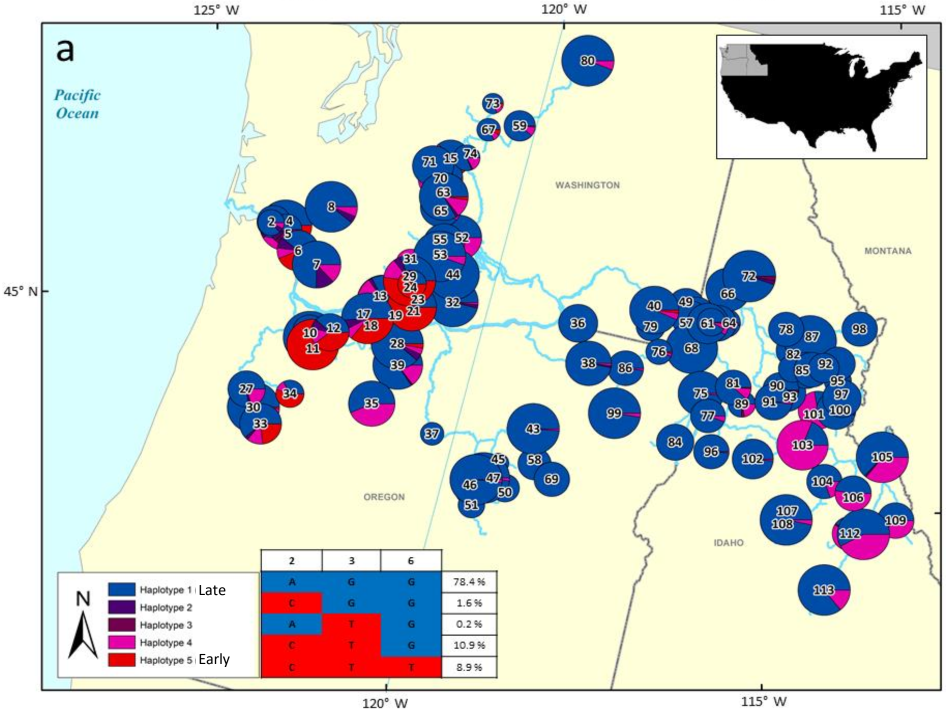
Adapted from: Collins et al. 2020

Conclusions

Monitor Genetic Diversity

- Maintain or improve underlying genetic variation for native fish species in Columbia River to provide broader life history diversity for populations to endure stochastic environments
- Combination of genetic markers
    - Monitor distinct populations
    - Specific migration related traits (timing, age, sex, thermal-tolerance)





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A	T	G	0.2 %
C	T	G	10.9 %
C	T	T	8.9 %

Acknowledgments

- Sample Collection Crews

  Nez Perce Tribe, Umatilla Tribes, Warm Springs Tribes, Yakama Nation, Idaho Fish and Game, Oregon Fish and Wildlife, Washington Fish and Wildlife

- Lab work

  Janae Cole, Joe Gasper, Amber Gonzales, Stephanie Harmon, Travis Jacobson, Vanessa Jacobson, Lori Maxwell, Megan Moore, Becca Sanders, Jeff Stephenson

- Co-authors

  John Hargrove, Thomas Delomas, Shawn Narum

- Funding

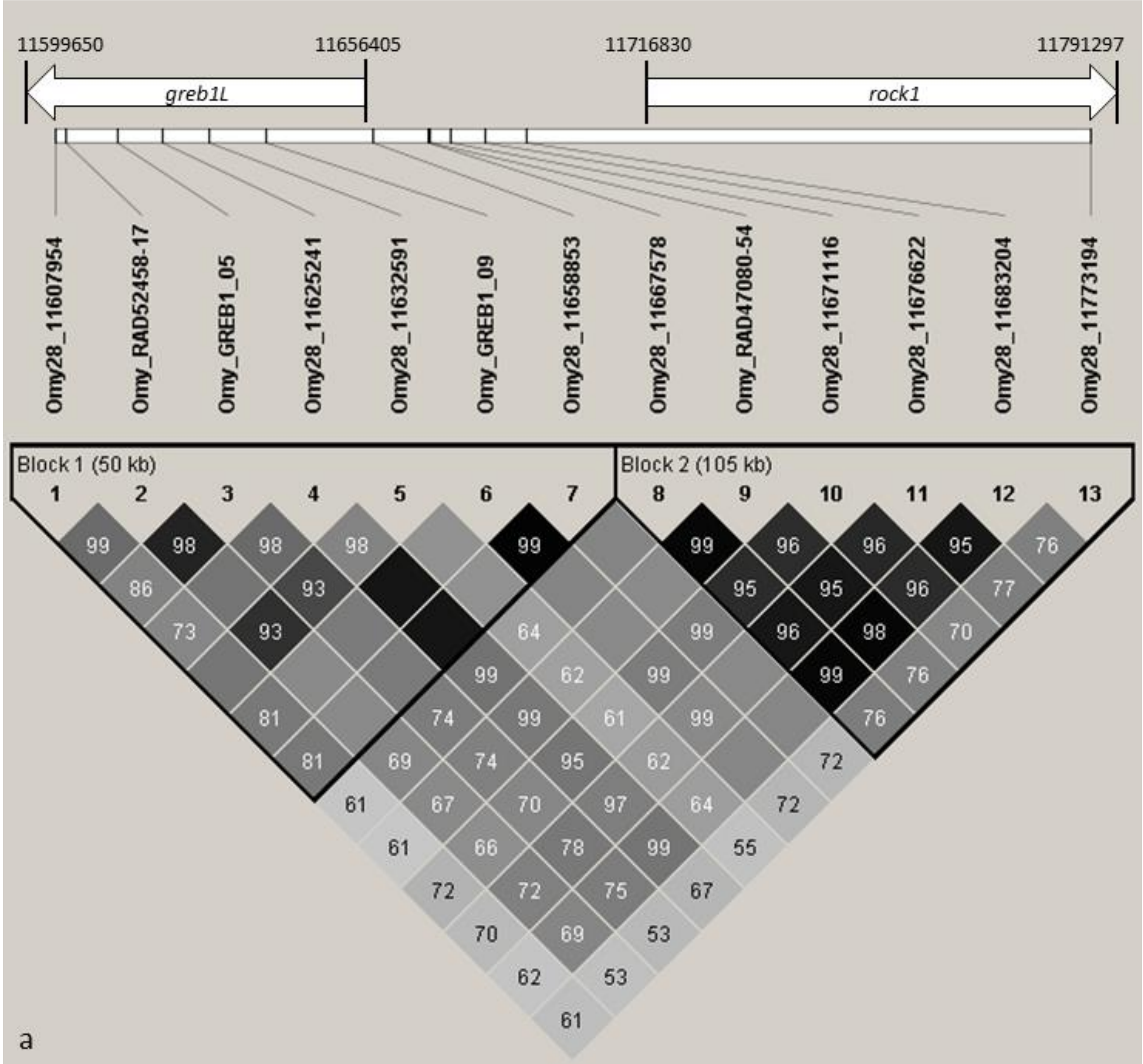
  Bonneville Power Administration

Questions?

Filtering of genotype data

- Quality threshold of >90% loci successfully genotyped
- And had an estimated <0.5% genotyping error based on replicate genotyping

Results



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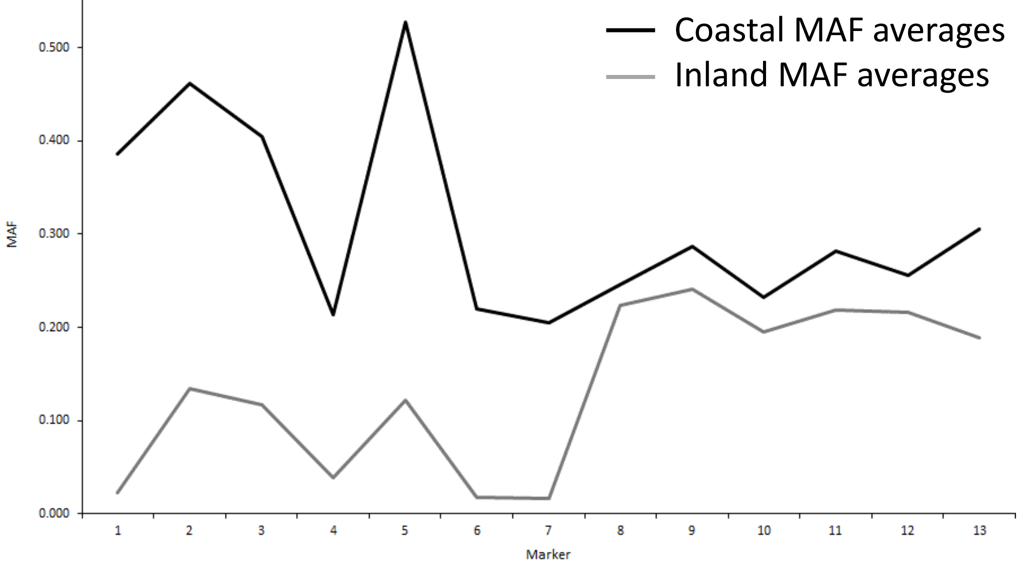
Results



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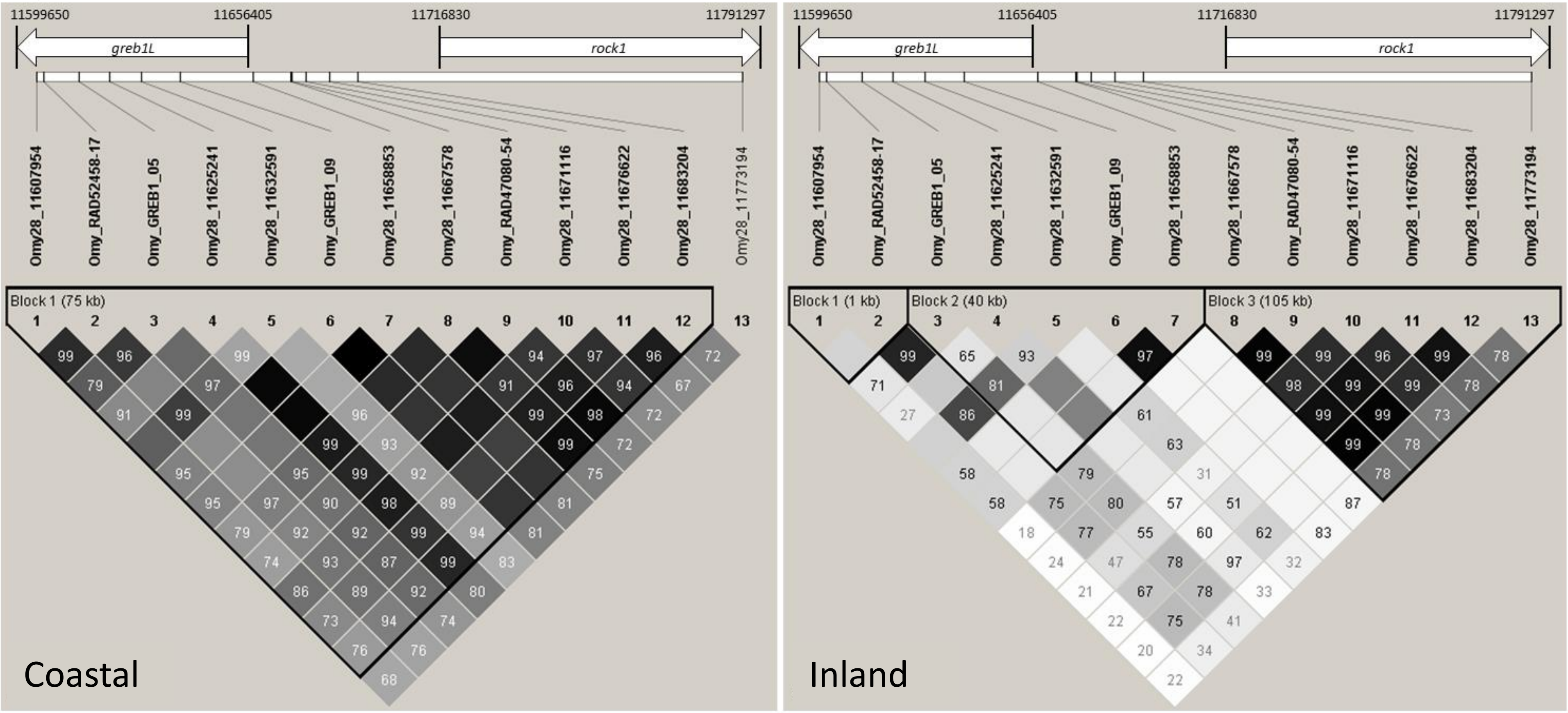
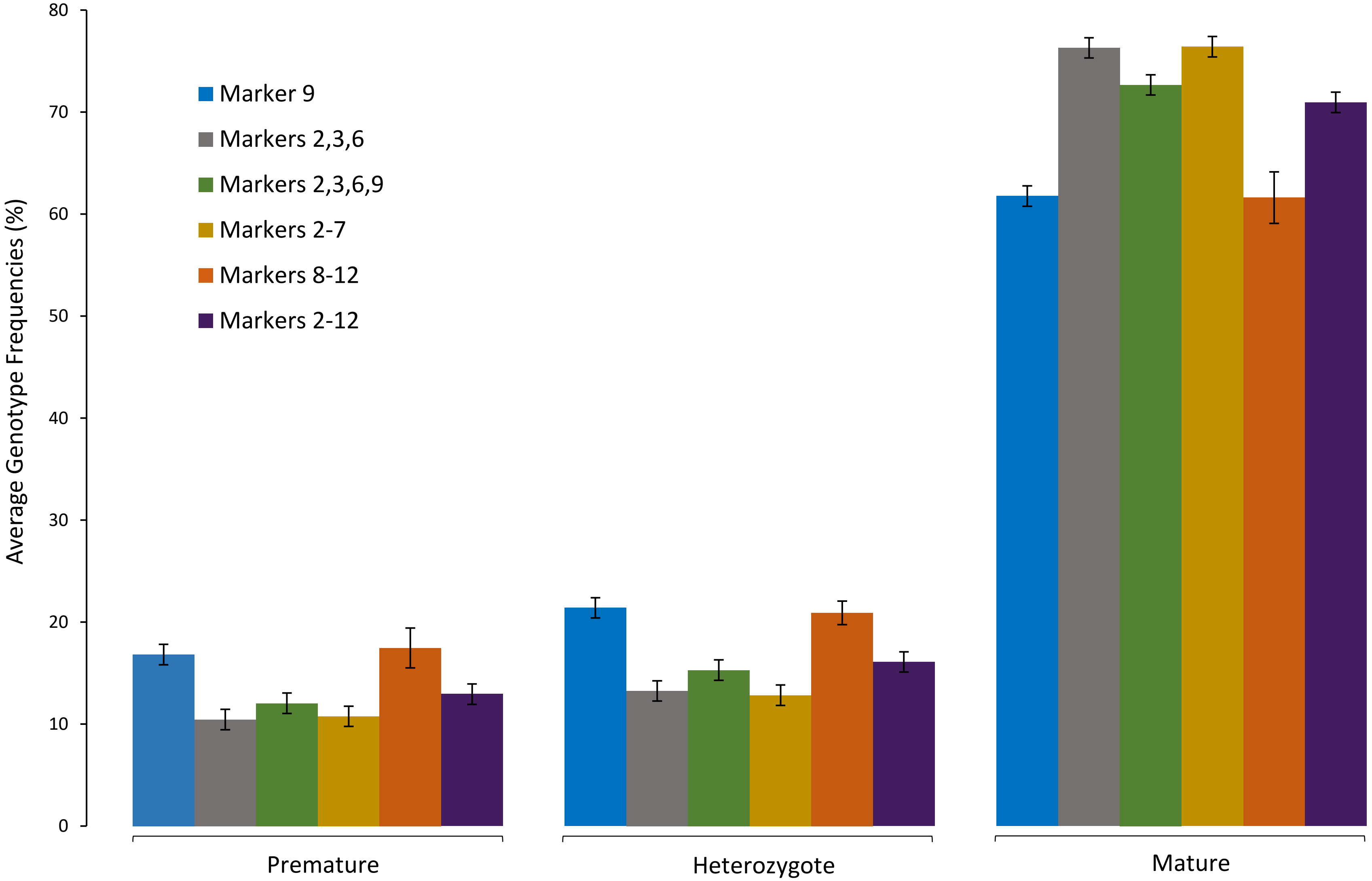


Results

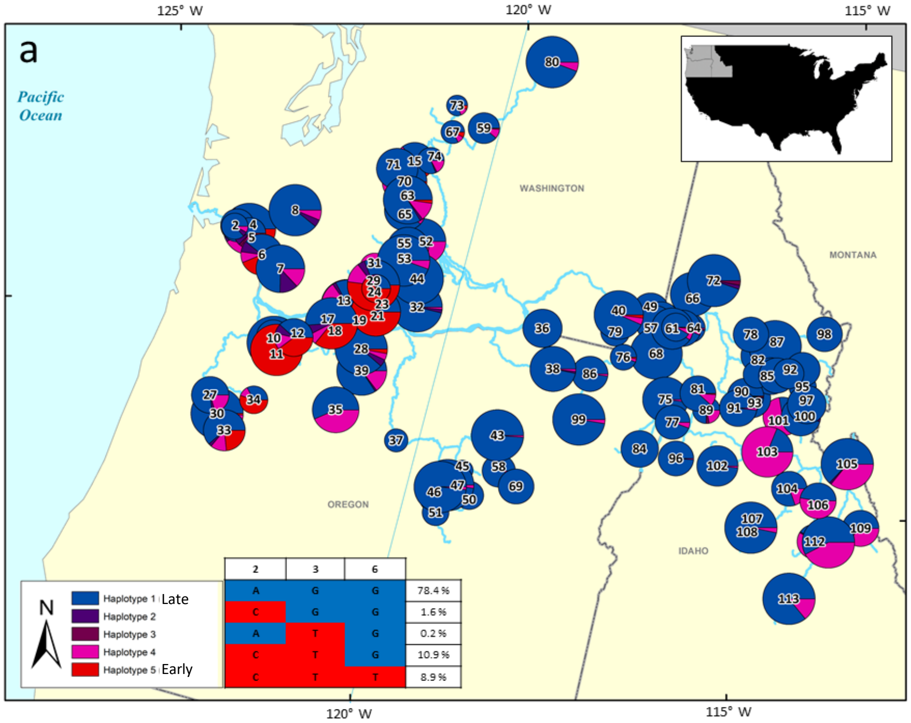


Adapted from: Collins et al. 2020

Results

- Markers 2,3,6

- Marker 9 alone



2	3	6	
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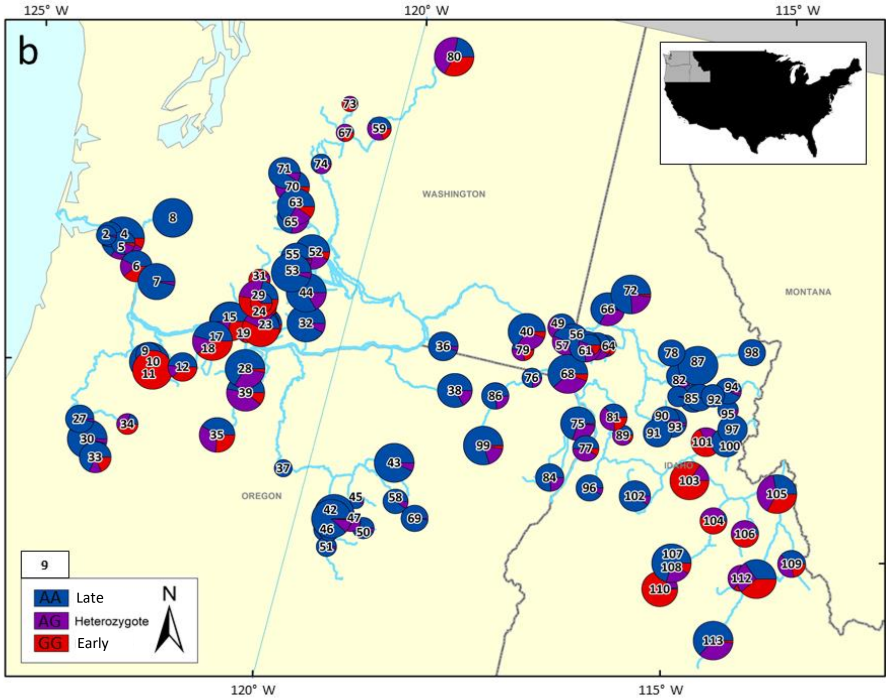
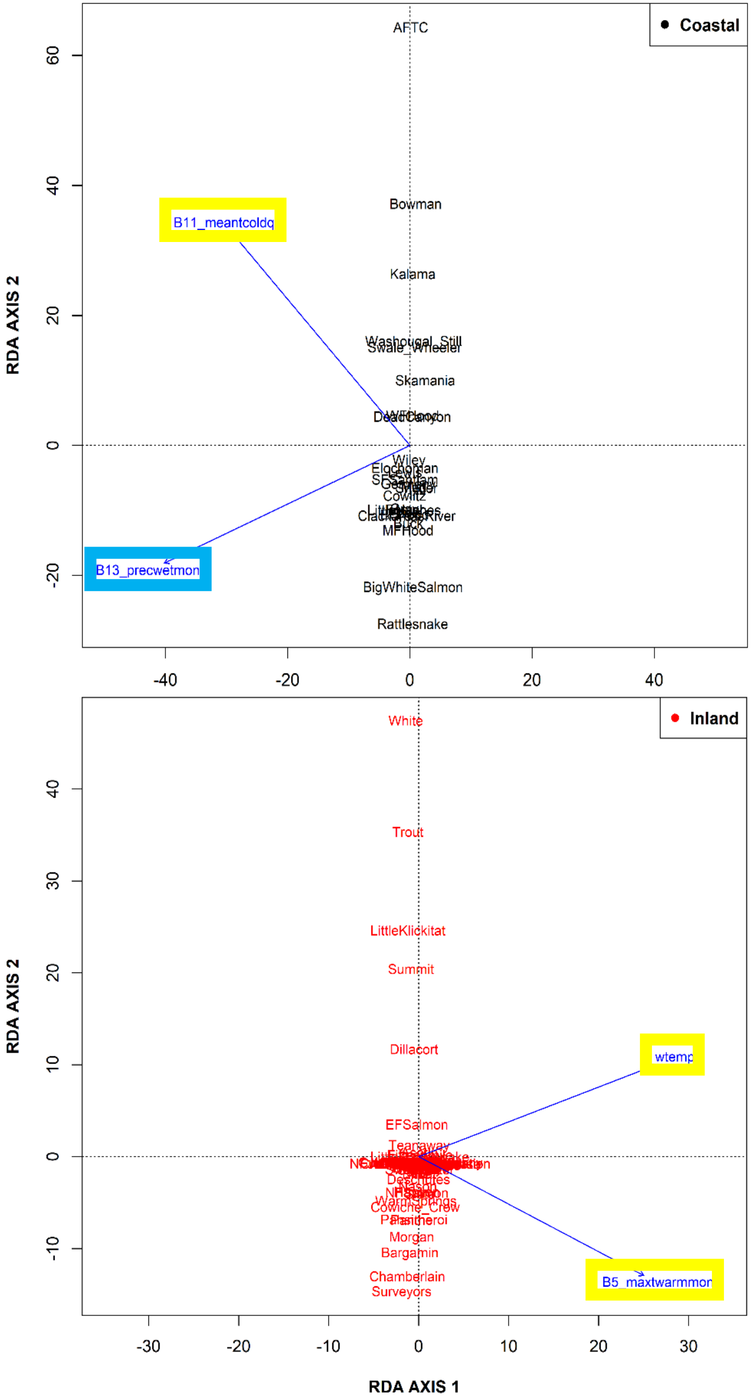
C	G	G	1.6 %
A	T	G	0.2 %
C	T	G	10.9 %
C	T	T	8.9 %



Adapted from: Collins et al. 2020

Results

- Redundancy analyses run separately for each genetic lineage
- Environmental factors assessed:
  - Migration distance
  - Temperature
  - Precipitation



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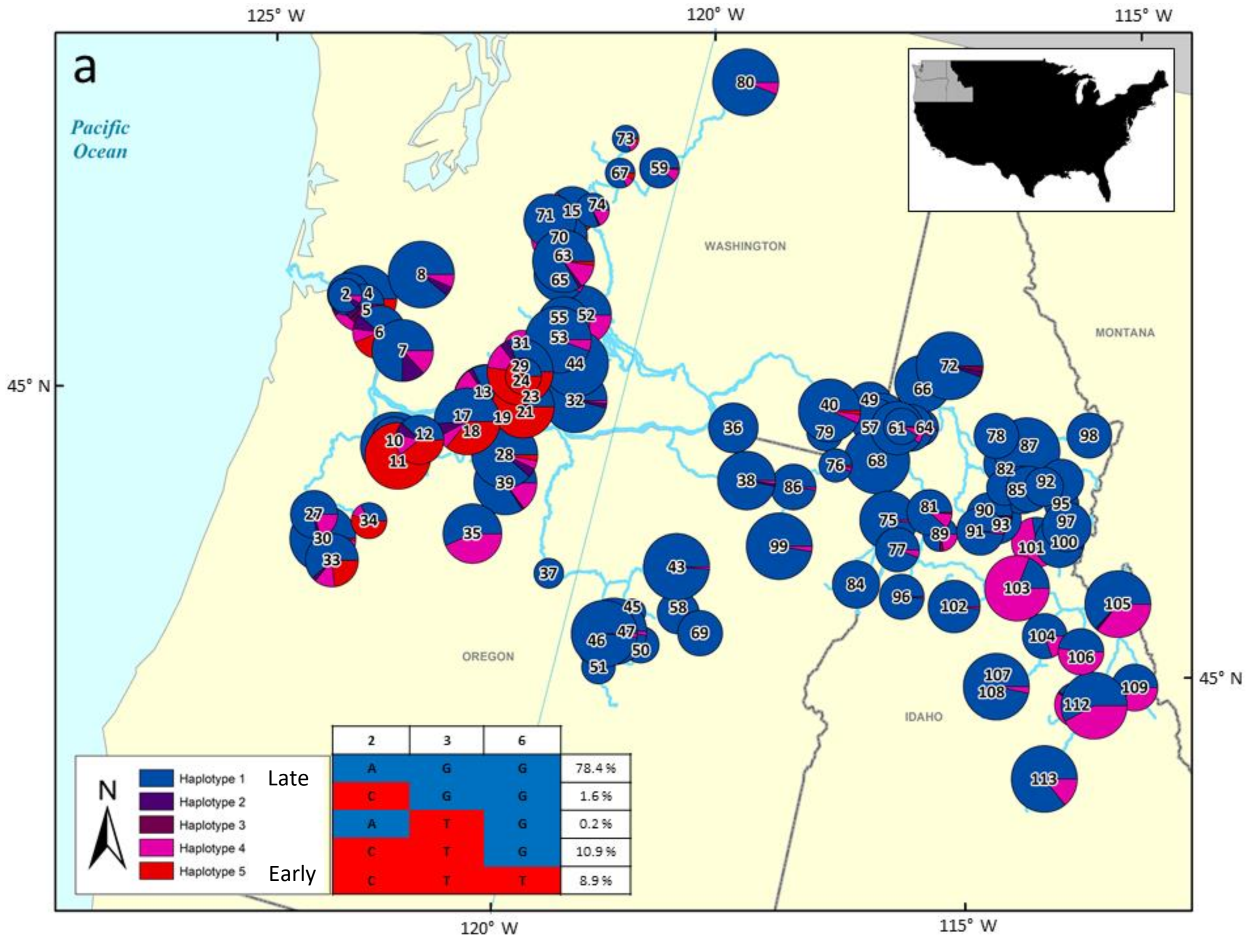
Diversity of inland lineage at adaptive markers



2	3	6	
A	G	G	78.4 %
C	G	G	1.6 %
A	T	G	0.2 %
C	T	G	10.9 %
C	T	T	8.9 %

Adapted from: Collins et al. 2020

Order ID	SNP	Chr	Position	Gene	Forward primer	Reverse primer	Probe	Orientation
1	Omy28_11607954	28	11607954	greb1L	TGACACTGATCACAATGGTGAAAT	TAAACTGGAAGGAGAGAGCAAAAT	TGTGGGCTGC[A/G]AACATACTCA	+
2	Omy_RAD52458-17	28	11609794	greb1L	ACGTGTCCCTGAGGATGGTA	AGCTCTAGGTCTGGGTCCTG	ATGGCCC[C/A][CT]AAGAACCC	-
3	Omy_GREB1_05	28	11618027	greb1L	TGGGCAGATATGGAAGAACGG	ACCTTCTAAATGGCCTCTGTGT	CGGTGGCTC[T/G]C	+
4	Omy28_11625241	28	11625241	greb1L	CAACATTTAGGGAGAGGTTGCTAT	ATCATCAAGTTTGCCTACGACAC	CCTCCTCCCT[A/G]TGGTTGTCTC	+
5	Omy28_11632591	28	11632591	greb1L	GTAGAGGCCAAAGGCTTGAG	TGCTCTTATTACCTTCCAGACTCC	TGAGAA[G/A]AACACAGAGG	+
6	Omy_GREB1_09	28	11641623	greb1L	CCAGTGGCAACCTCAGGTAG	GACTCCAGTCACCCAAGTCA	TCAA[T/G]GGAGA	+
7	Omy28_11658853	28	11658853	intergenic	CAACATATGACCACTCGAAAACTC	ATTAATCACACCGTGAGACTCCTC	TGGTACAGAC[A/C]CGCACTAGCA	+
8	Omy28_11667578	28	11667578	intergenic	ACAGTAAACCCATTCAGGCATAGT	TTATCCTCTCAATCCACATCAAGA	GTATTGATCC[T/C]GTGGGAGACA	+
9	Omy_RAD47080-54	28	11667915	intergenic	TCAAAACCTGCAGGACTTGGA	TGGTTATATCTACAGTACAGTTCGT	TGCAAG[A/G]CTTAAAACGA	+
10	Omy28_11671116	28	11671116	intergenic	AATTTCCCCAAATTTGAAACTCTT	GTGTACATTGTCAGGCAGAAACAT	CTGGTGAGAA[C/T]AGGAATTACC	+
11	Omy28_11676622	28	11676622	intergenic	CGAATGCACTGTAGCTCATTCTAA	GCAGTAGAATGTCTCGCAAATACA	ACATGTCATT[T/G]ATTGTTATCT	+
12	Omy28_11683204	28	11683204	intergenic	CAAGAAAGAAACAGATGTTGTCCA	TTGTGACTCAAATCTGCAACCTAT	ATGTAAAAAA[G/T]GGCAGAAAA	+
13	Omy28_11773194	28	11773194	rock1	AGTTTGACACCCCTGTACTAGAGC	GTCTAACAAGCTCTGGGTGATTTA	GCAATTTTTT[T/A]AAATTACCGC	+

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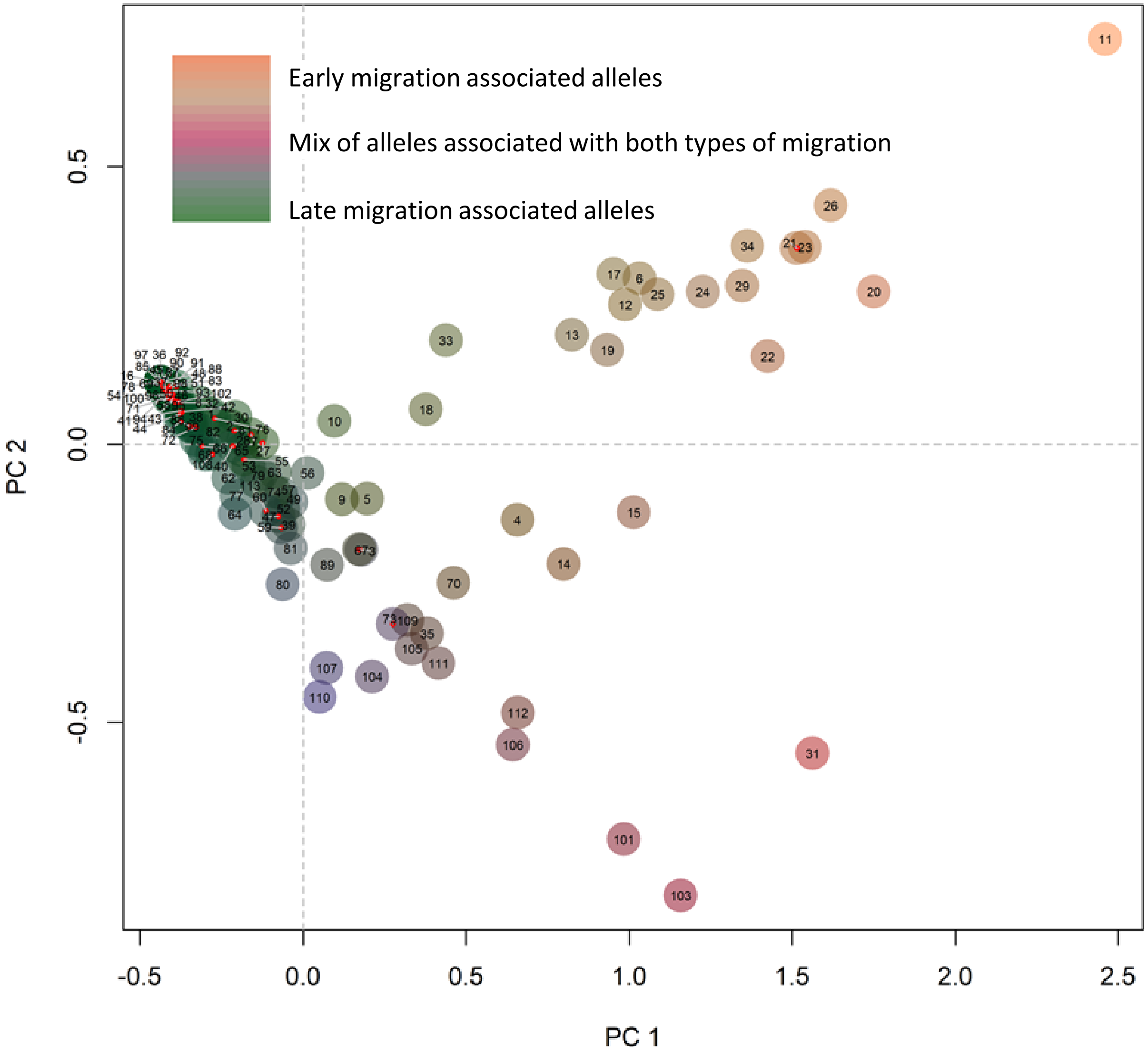
- 13 adaptive markers



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