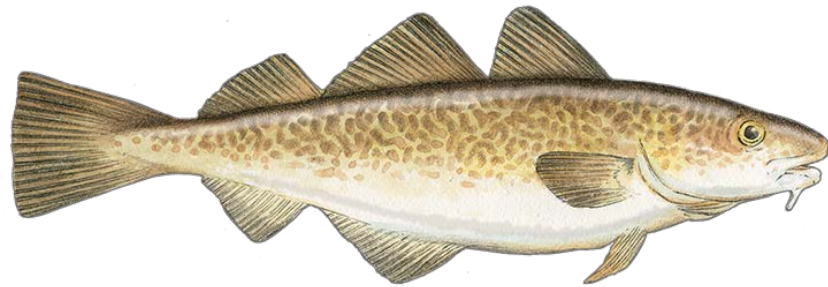


Pacific cod genomics

Sara Michele Schaal¹, Ingrid Spies¹, Wes Larson²

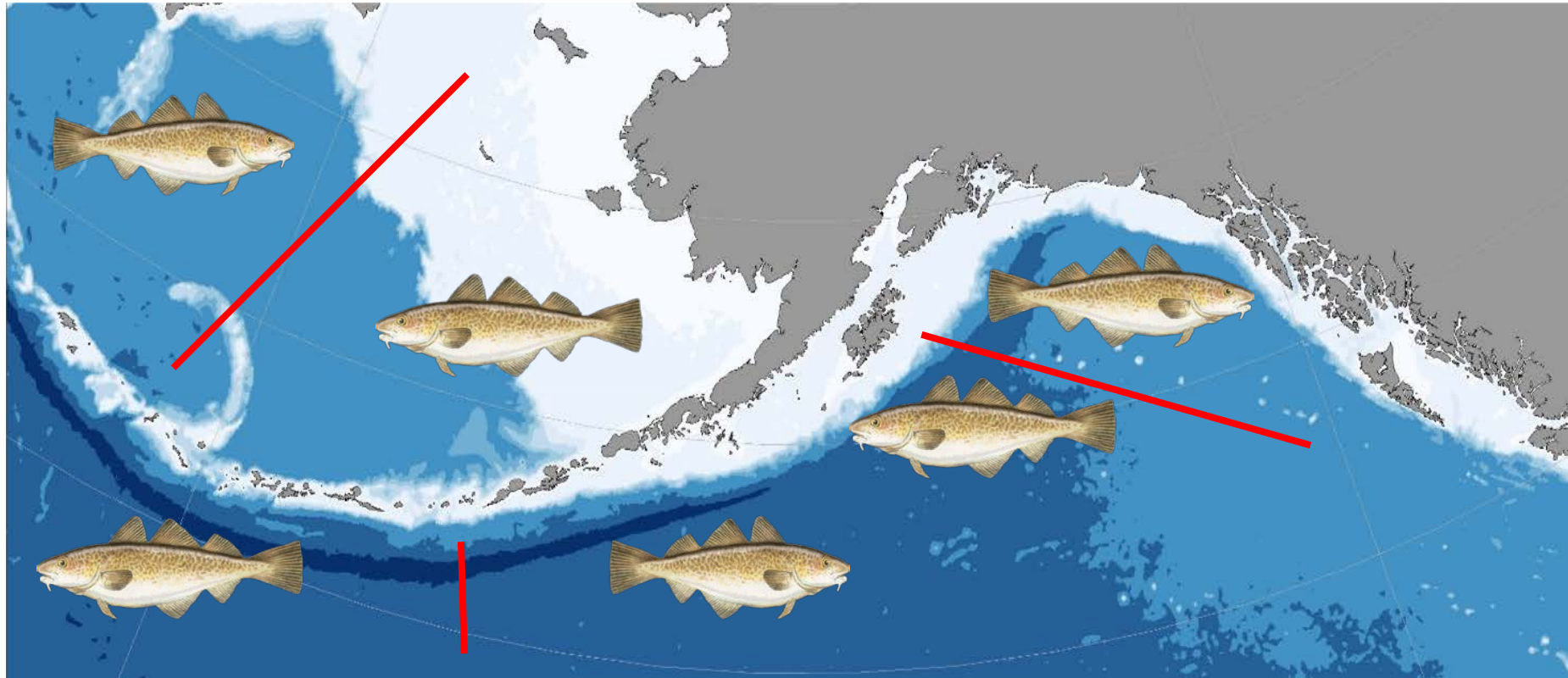
¹Alaska Fisheries Science Center, Seattle, WA

²Alaska Fisheries Science Center, Auke Bay Laboratory, Juneau, AK



Major Goal of Management

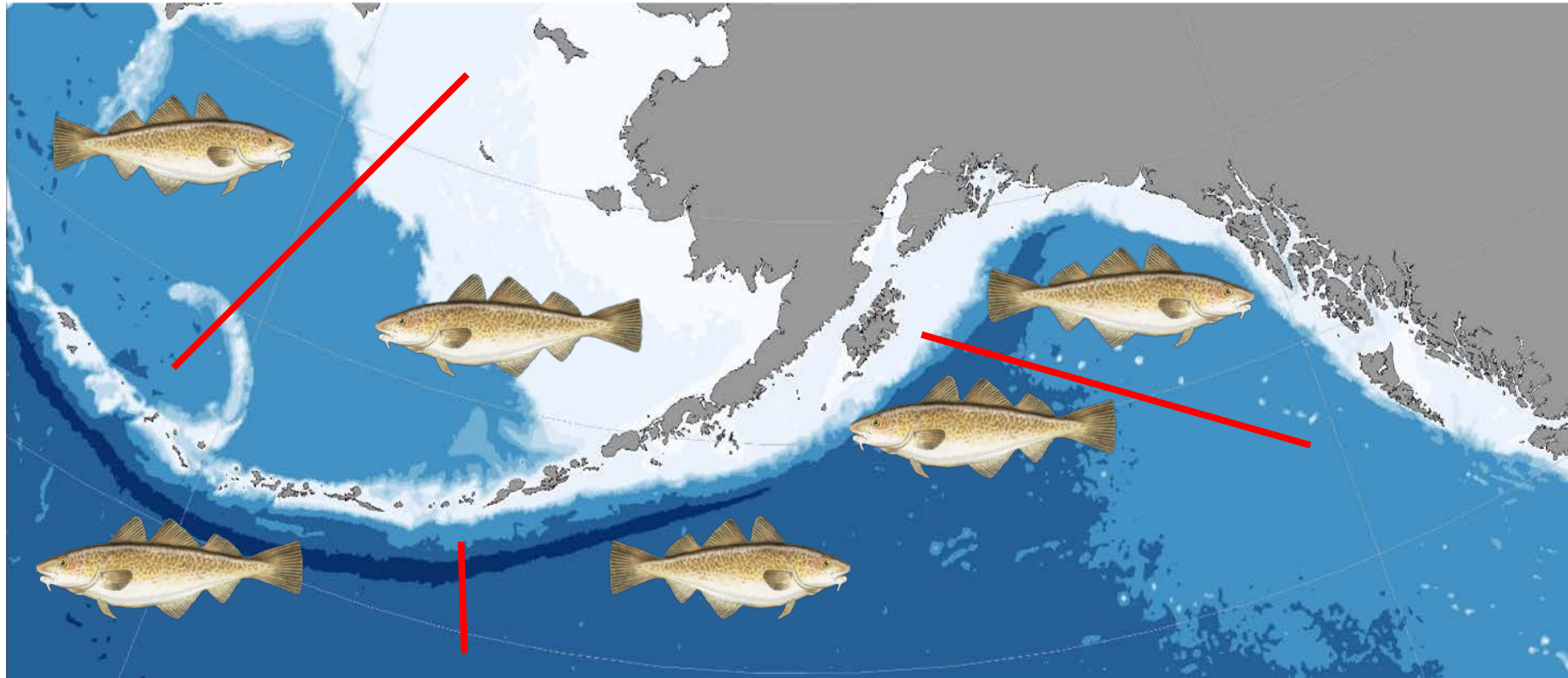
Identify population boundaries



Major Goal of Management

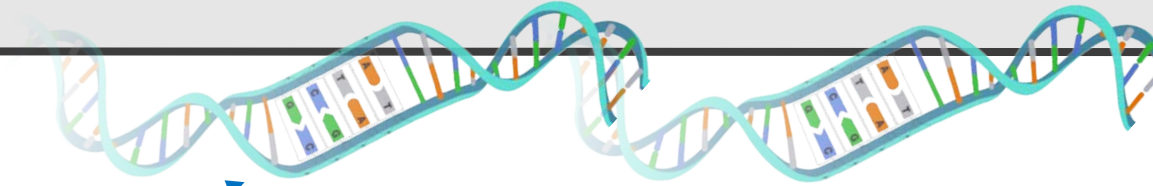
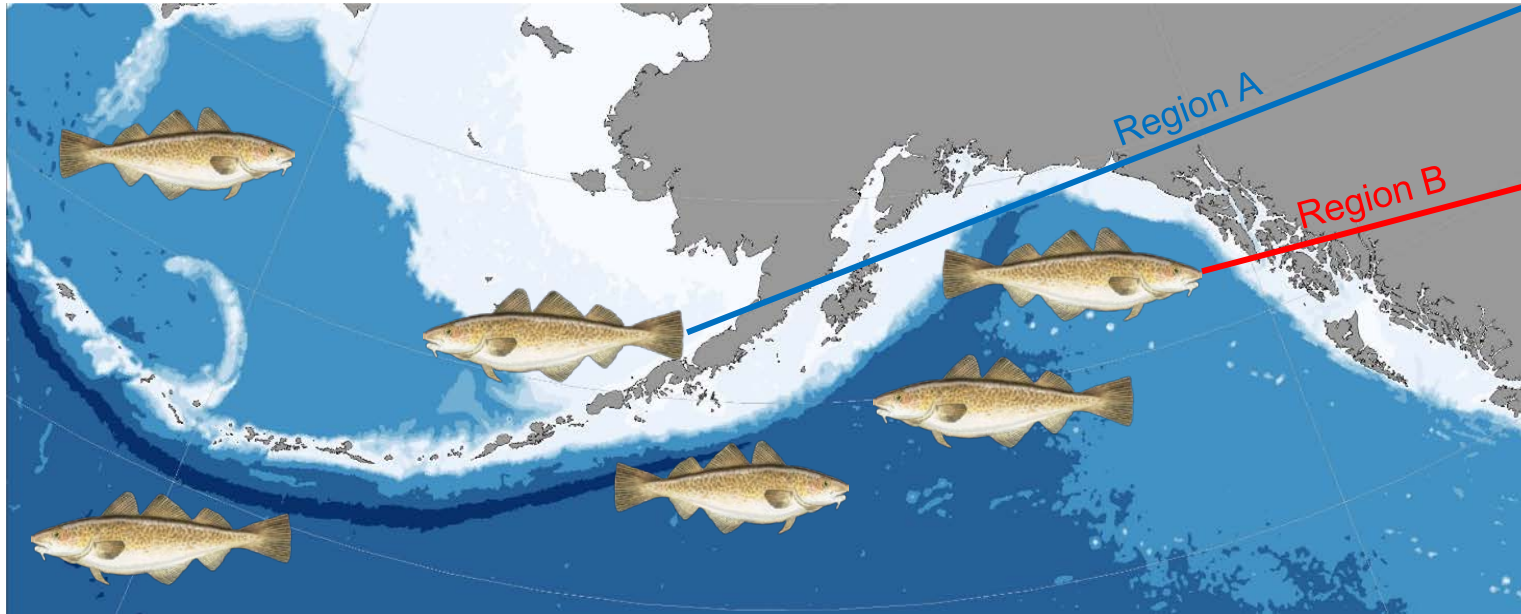
Identify population boundaries

Highly mobile species make this difficult



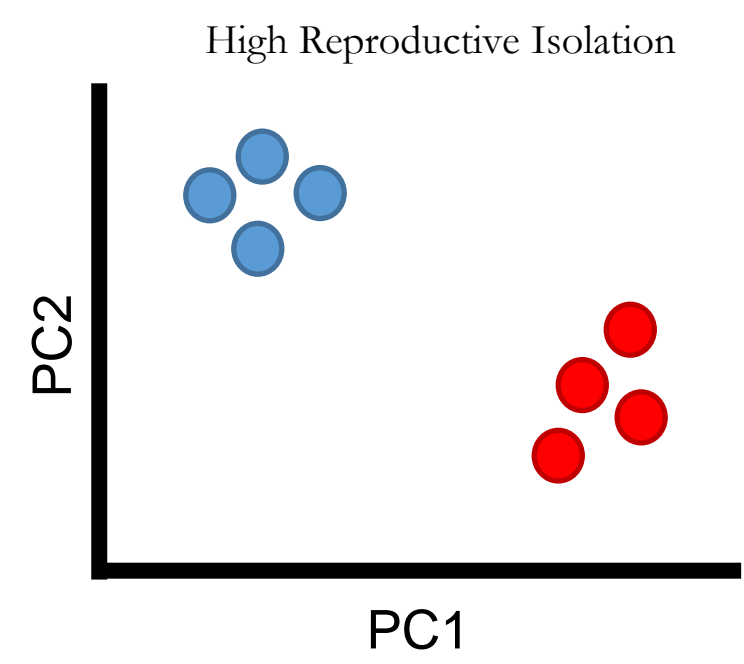
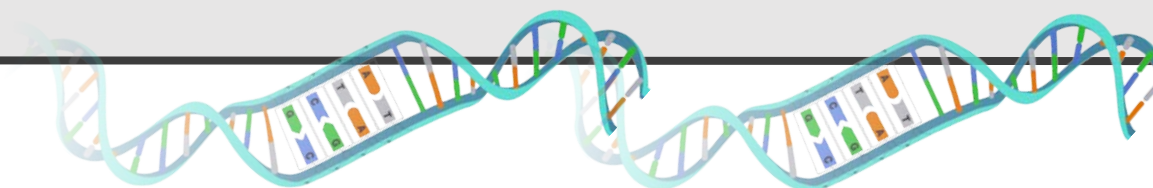
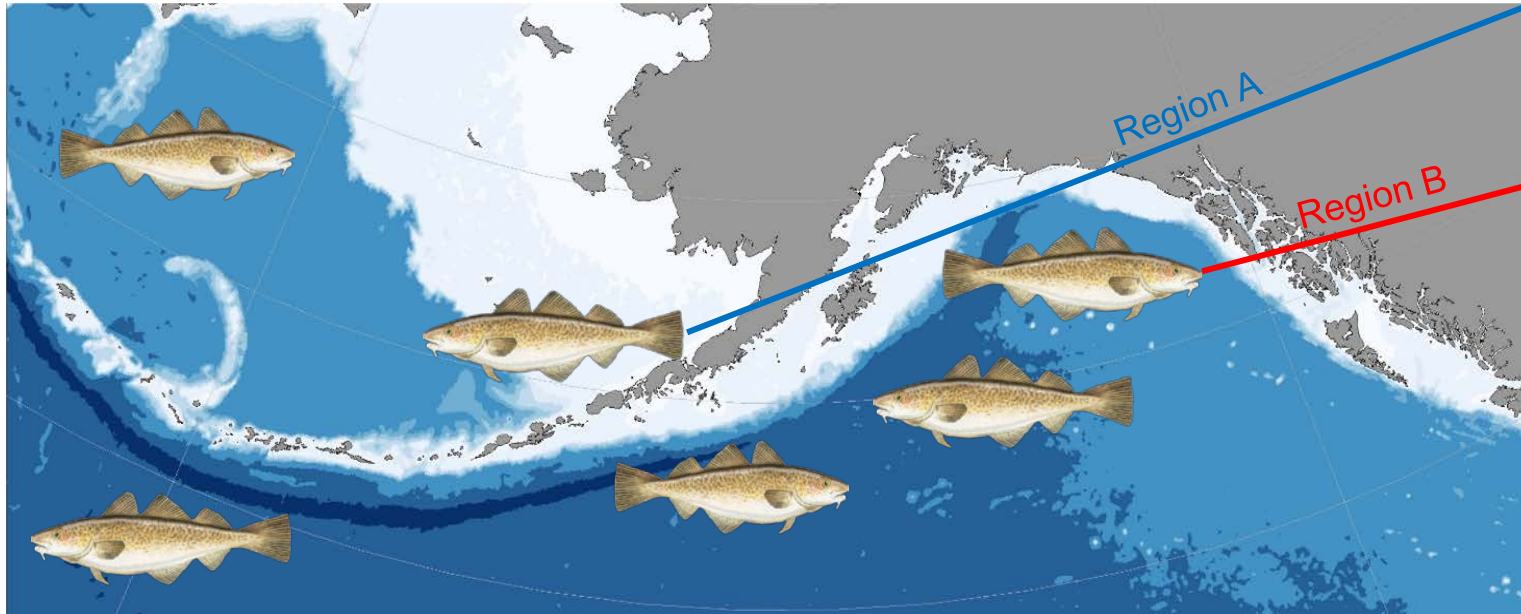
What can genomics tell us?

Populations that are reproductively isolated



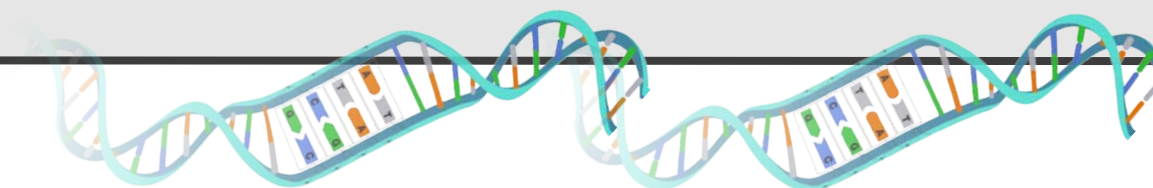
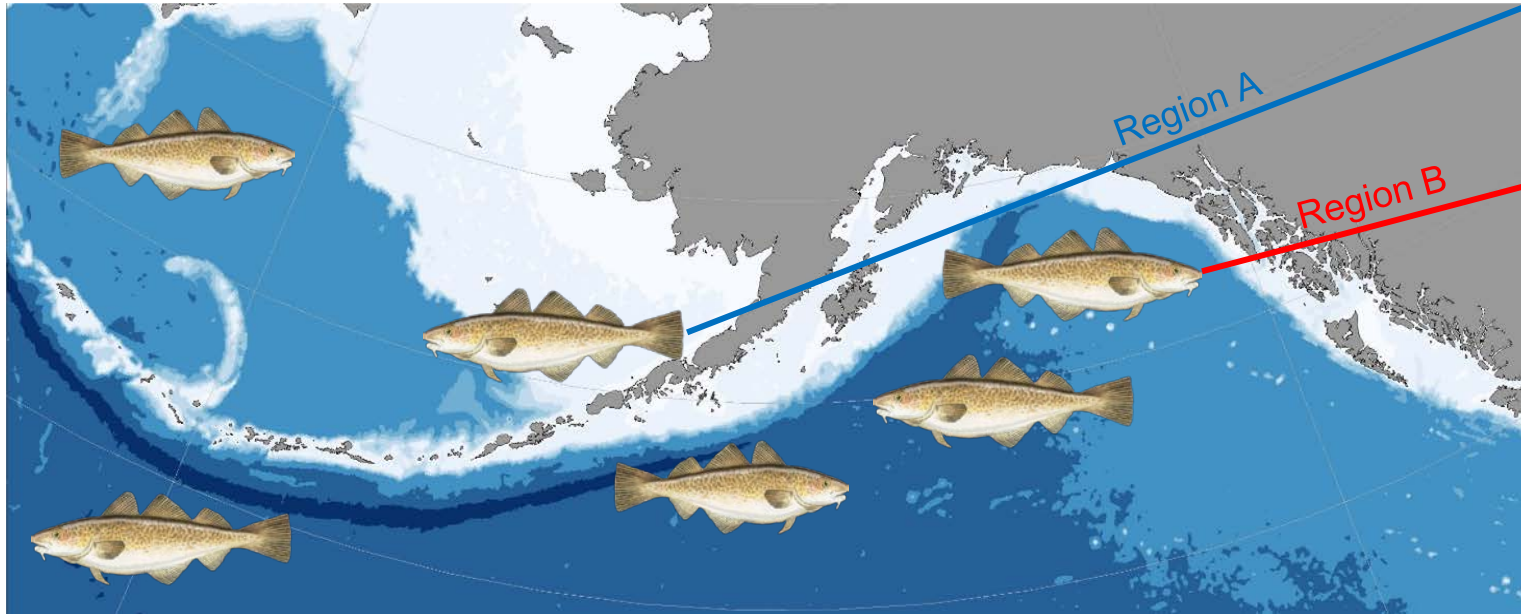
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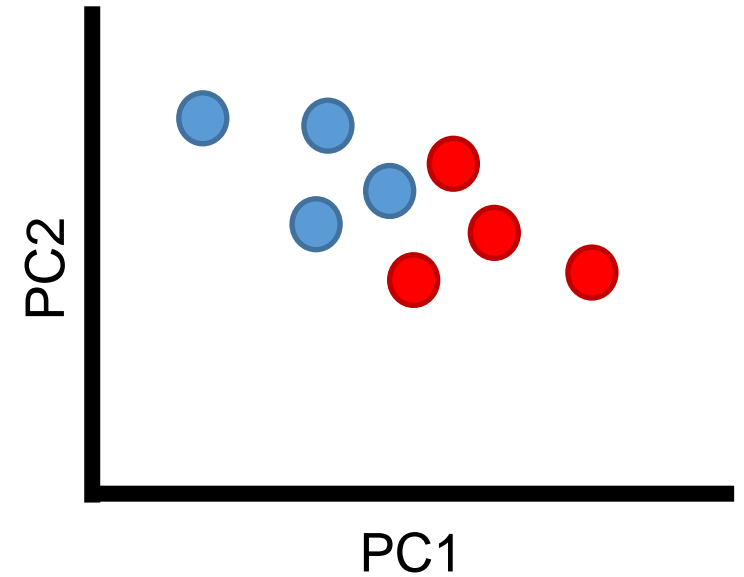


What can genomics tell us?

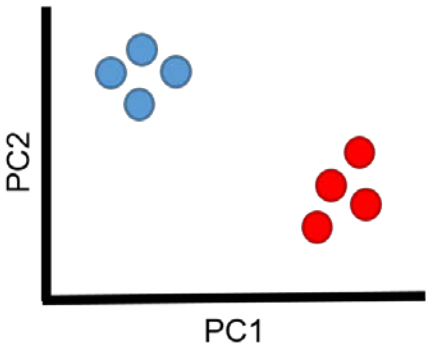
Populations that are reproductively isolated



Some Genetic Overlap

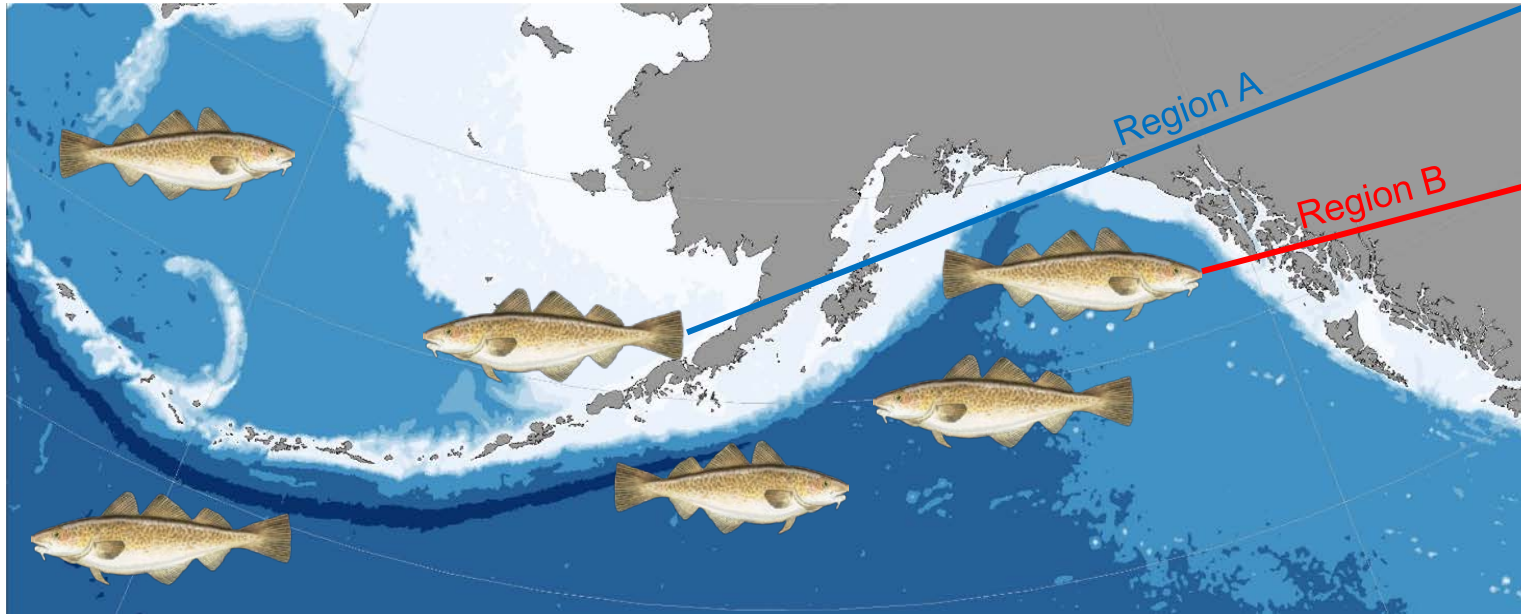


High Reproductive Isolation

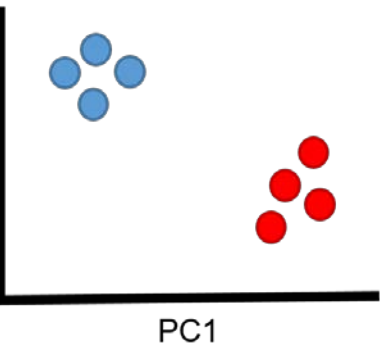


What can genomics tell us?

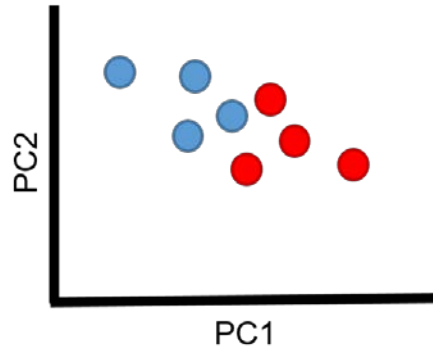
Populations that are reproductively isolated



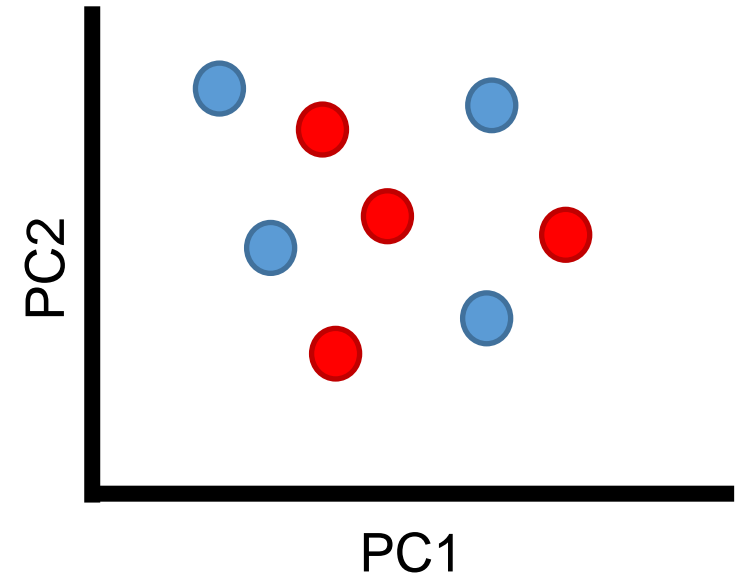
High Reproductive Isolation



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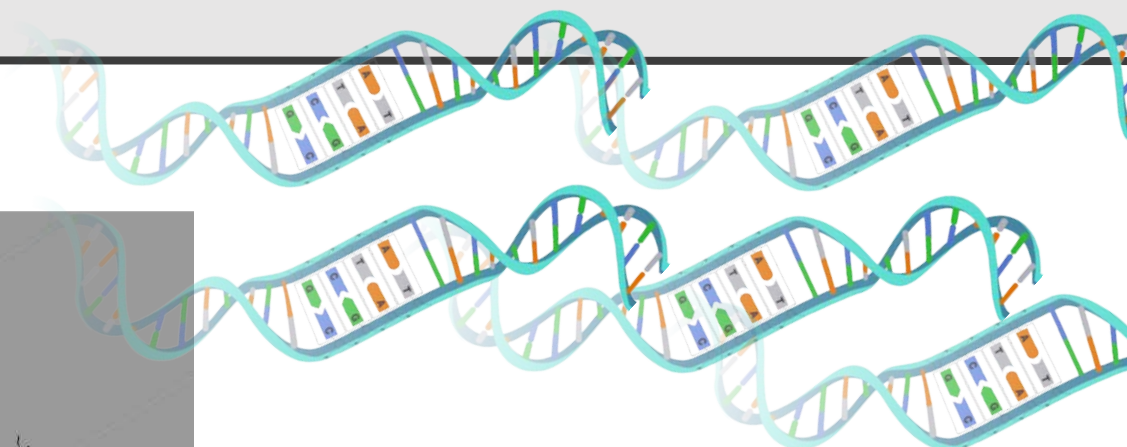
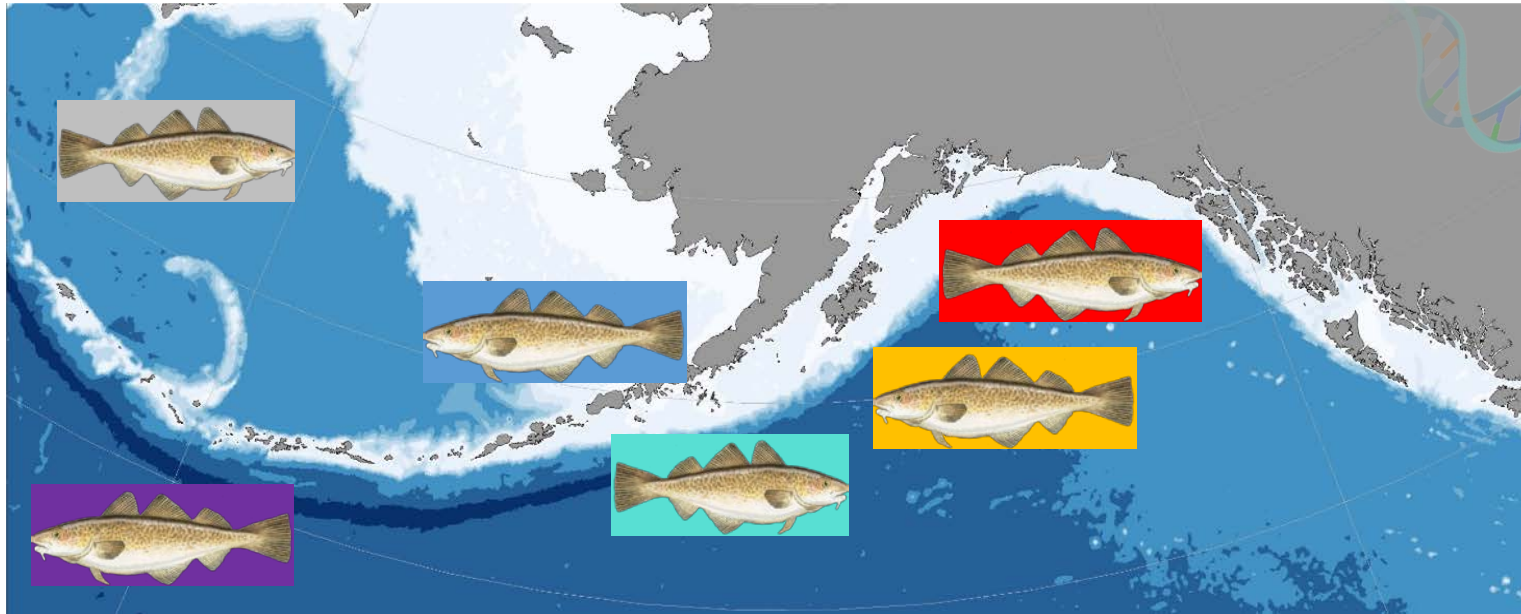


Fully Interbreeding Regions

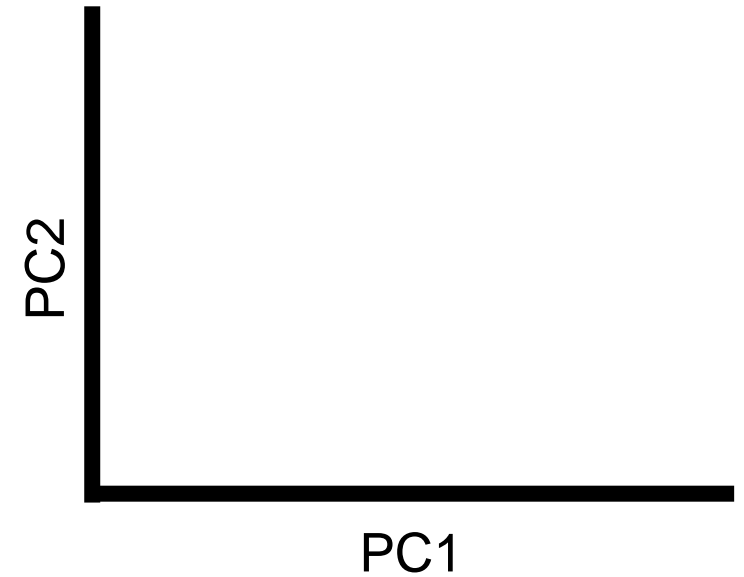


What can genomics tell us?

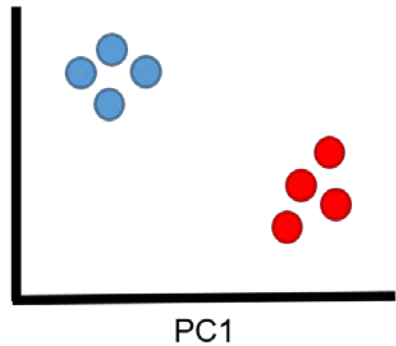
Populations that are reproductively isolated



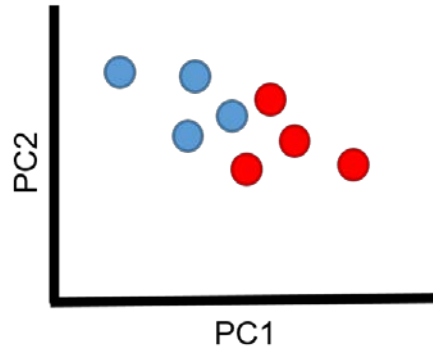
Many Populations



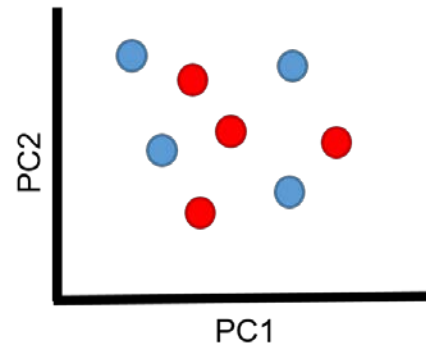
High Reproductive Isolation



Some Genetic Overlap

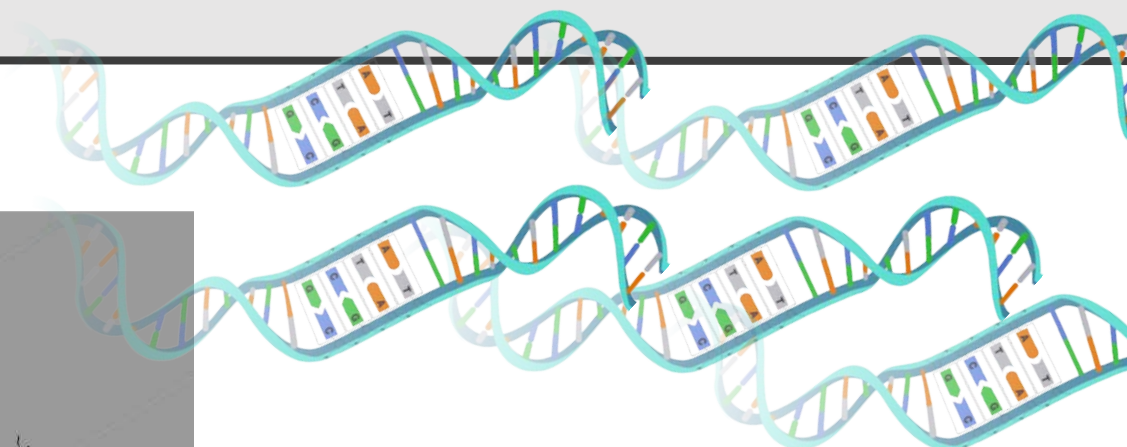
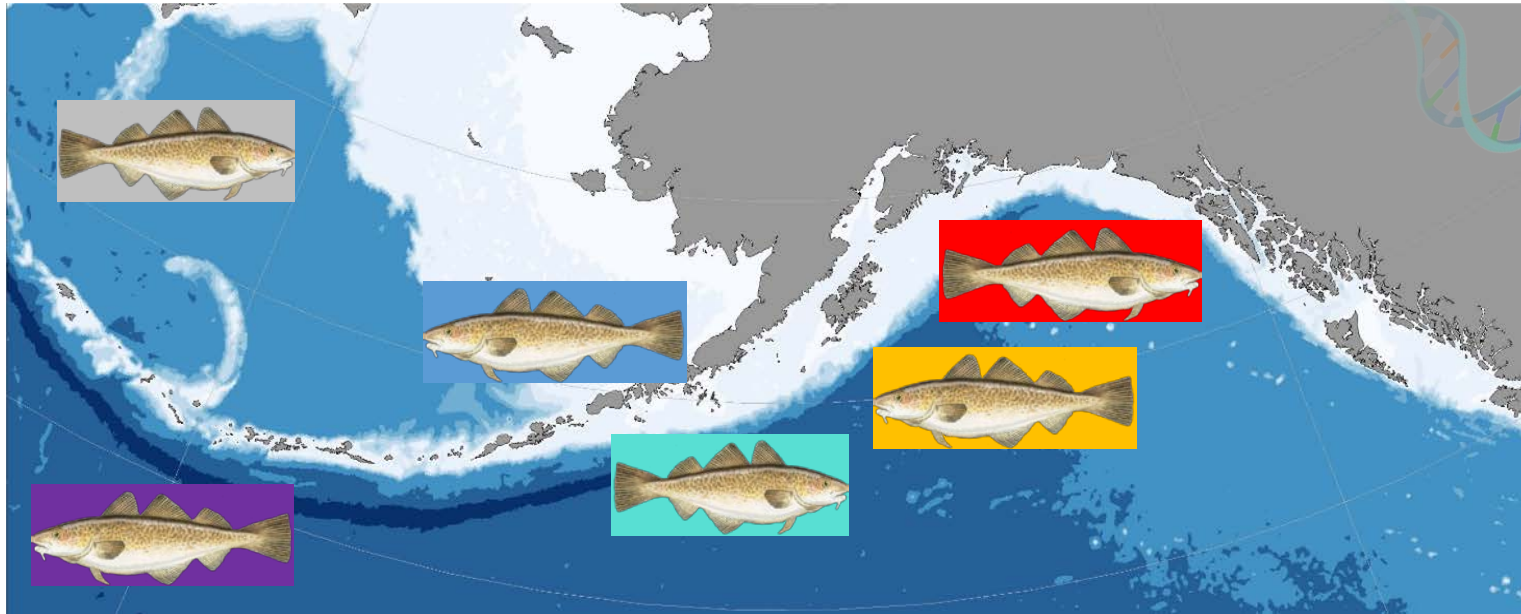


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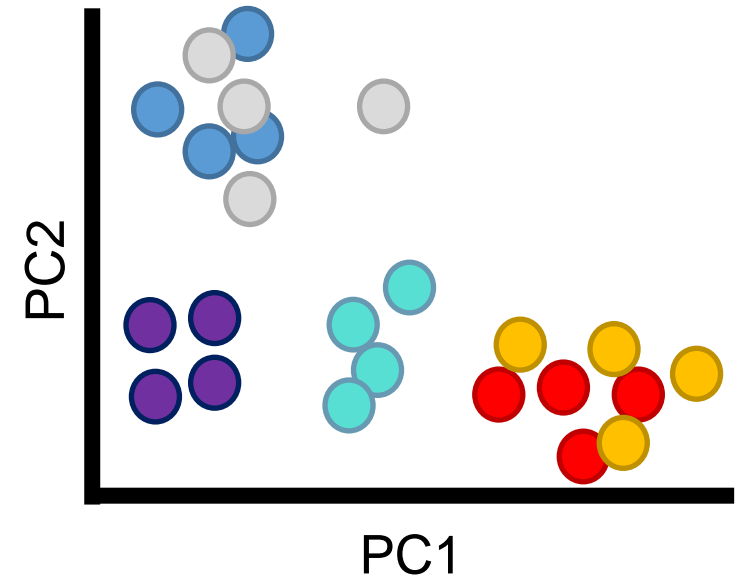


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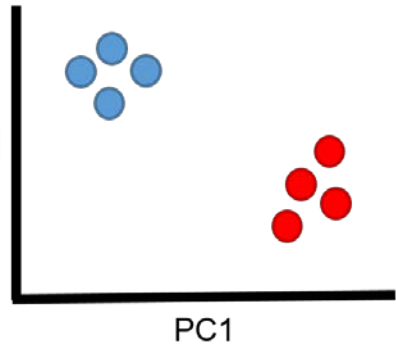
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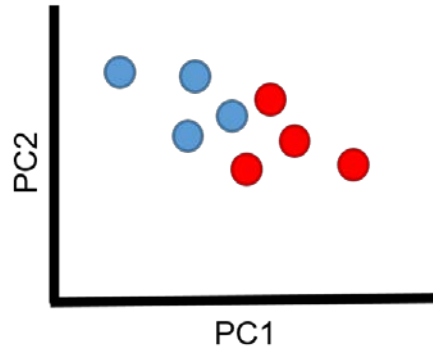
Many Populations



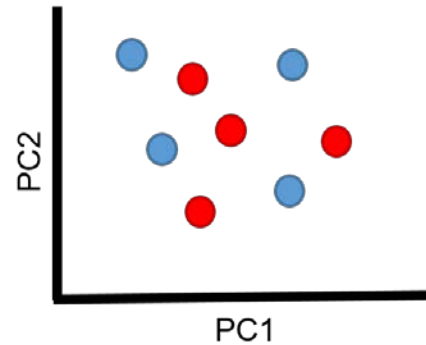
High Reproductive Isolation



Some Genetic Overlap



Fully Interbreeding Regions

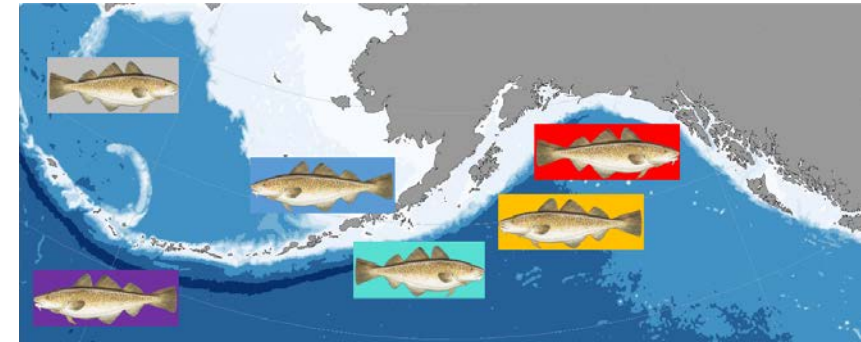
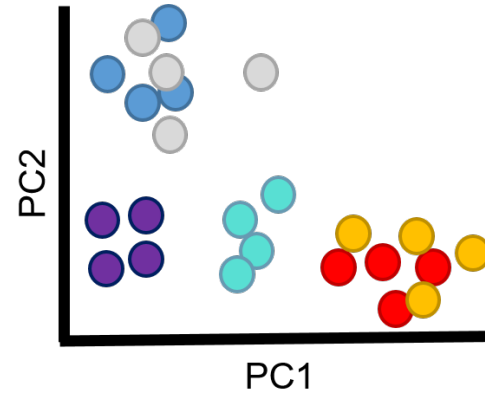


What can genomics tell us?

Populations that are reproductively isolated

Neutral Genetic Markers

- Historic patterns of gene flow, reproductive isolation

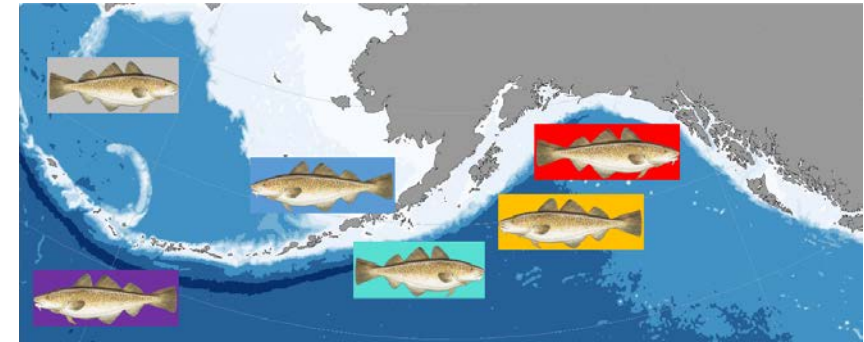
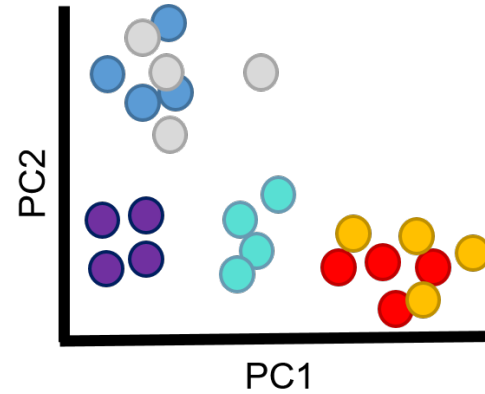


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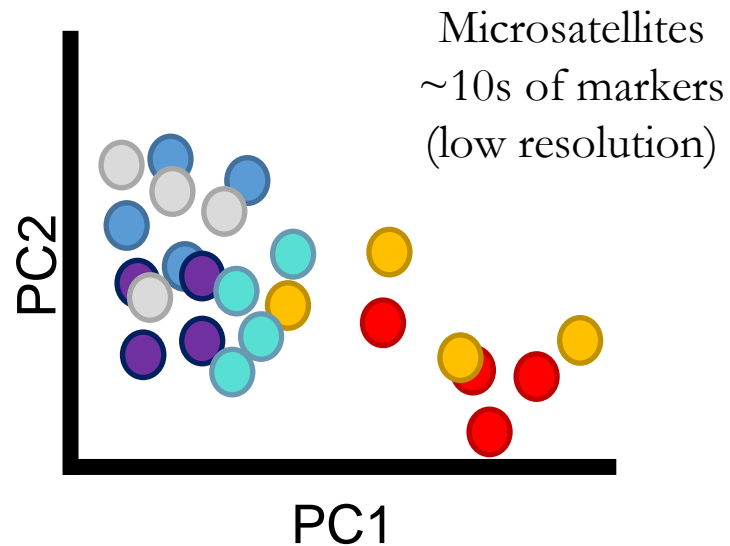
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Genomic Resolution

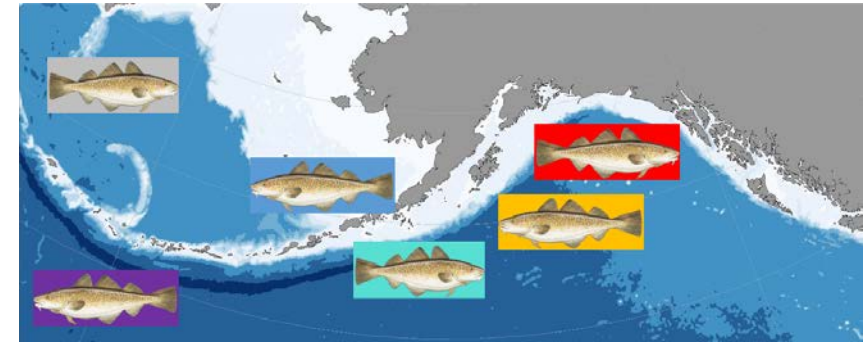
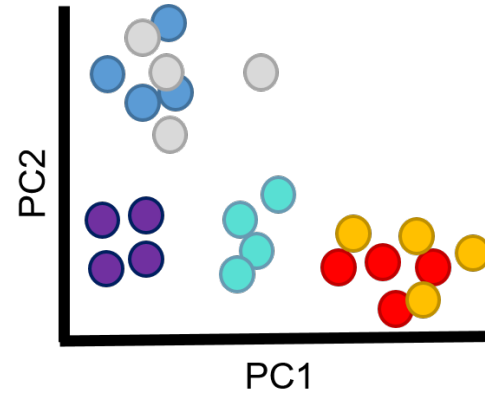


What can genomics tell us?

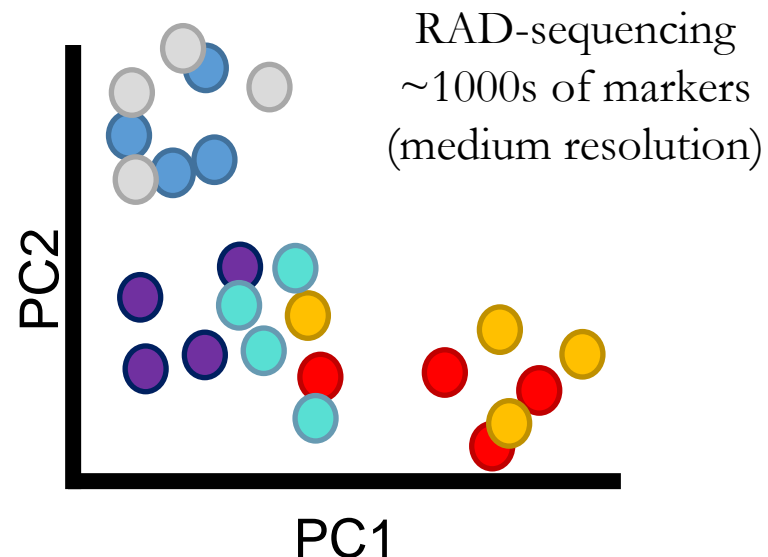
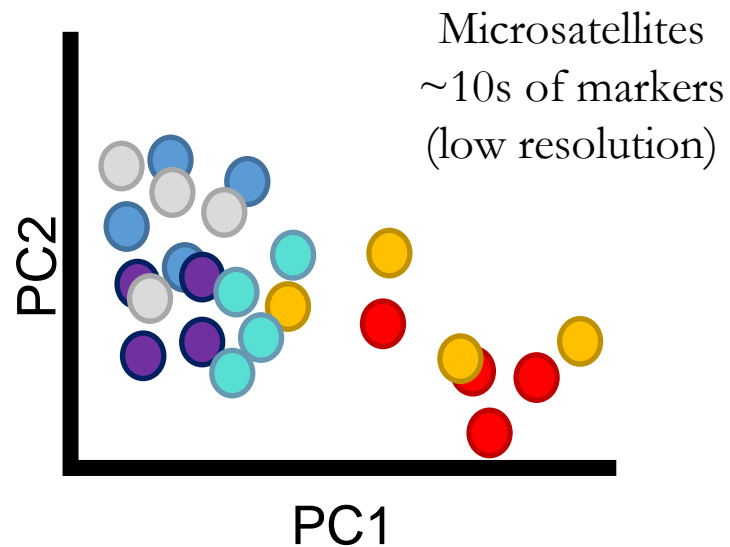
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Genomic Resolution

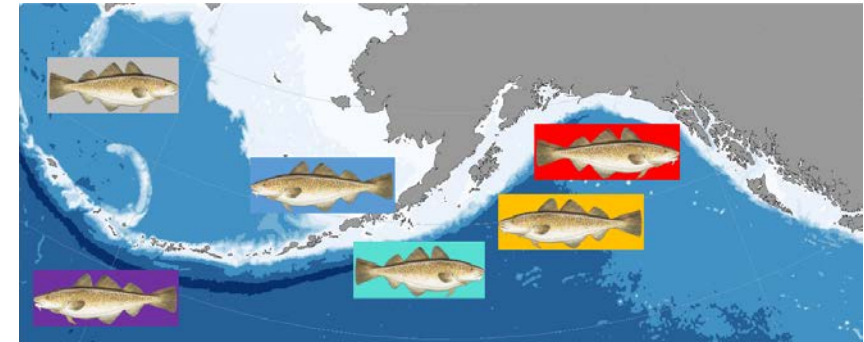
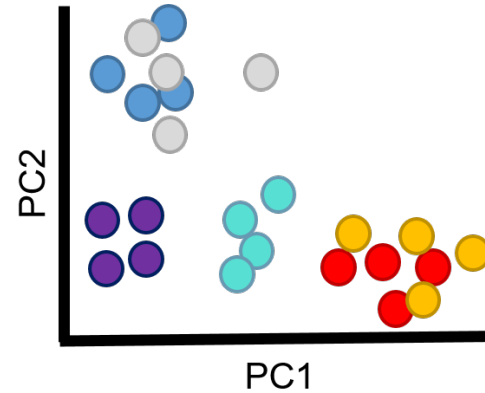


What can genomics tell us?

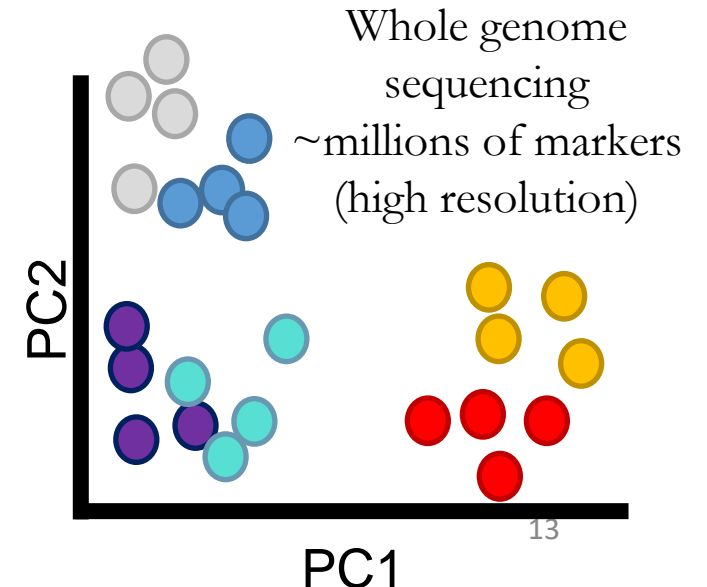
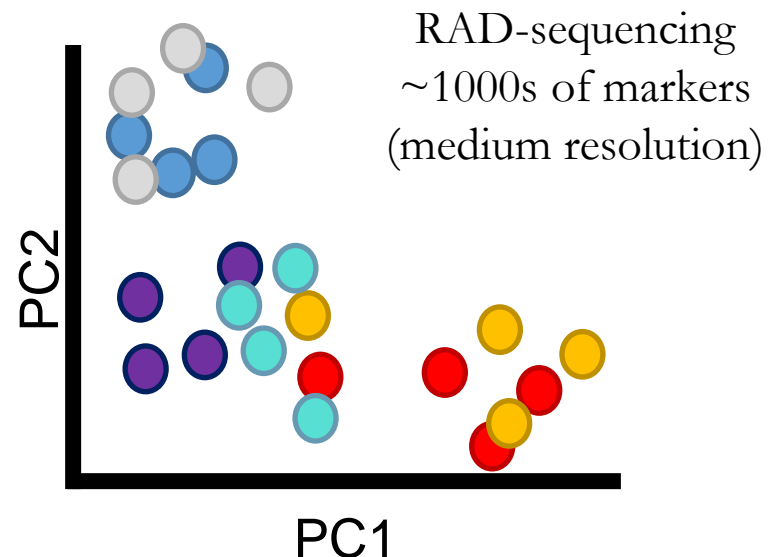
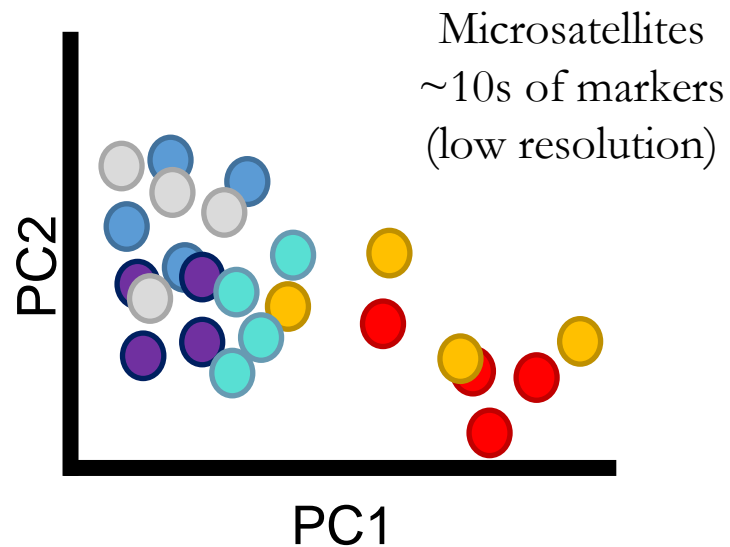
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Genomic Resolution

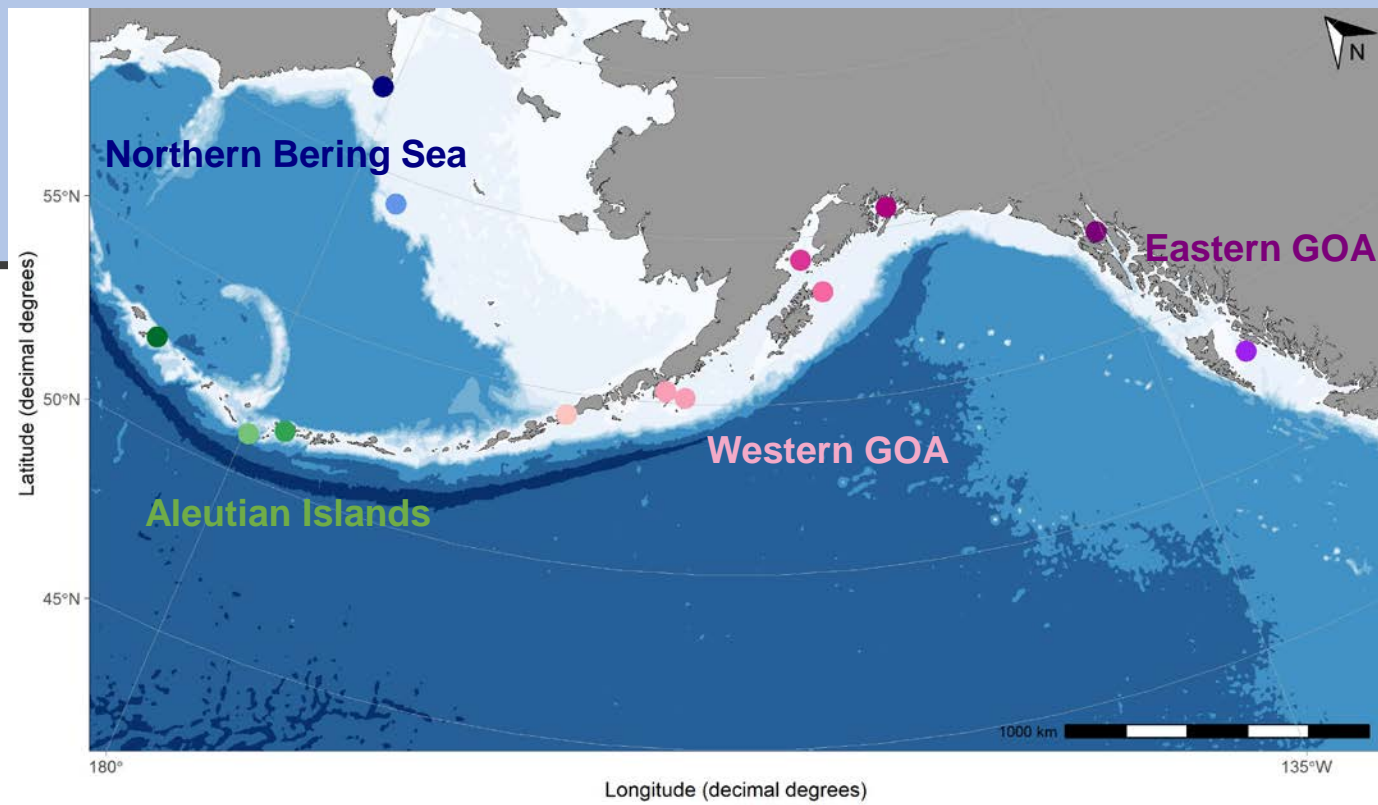
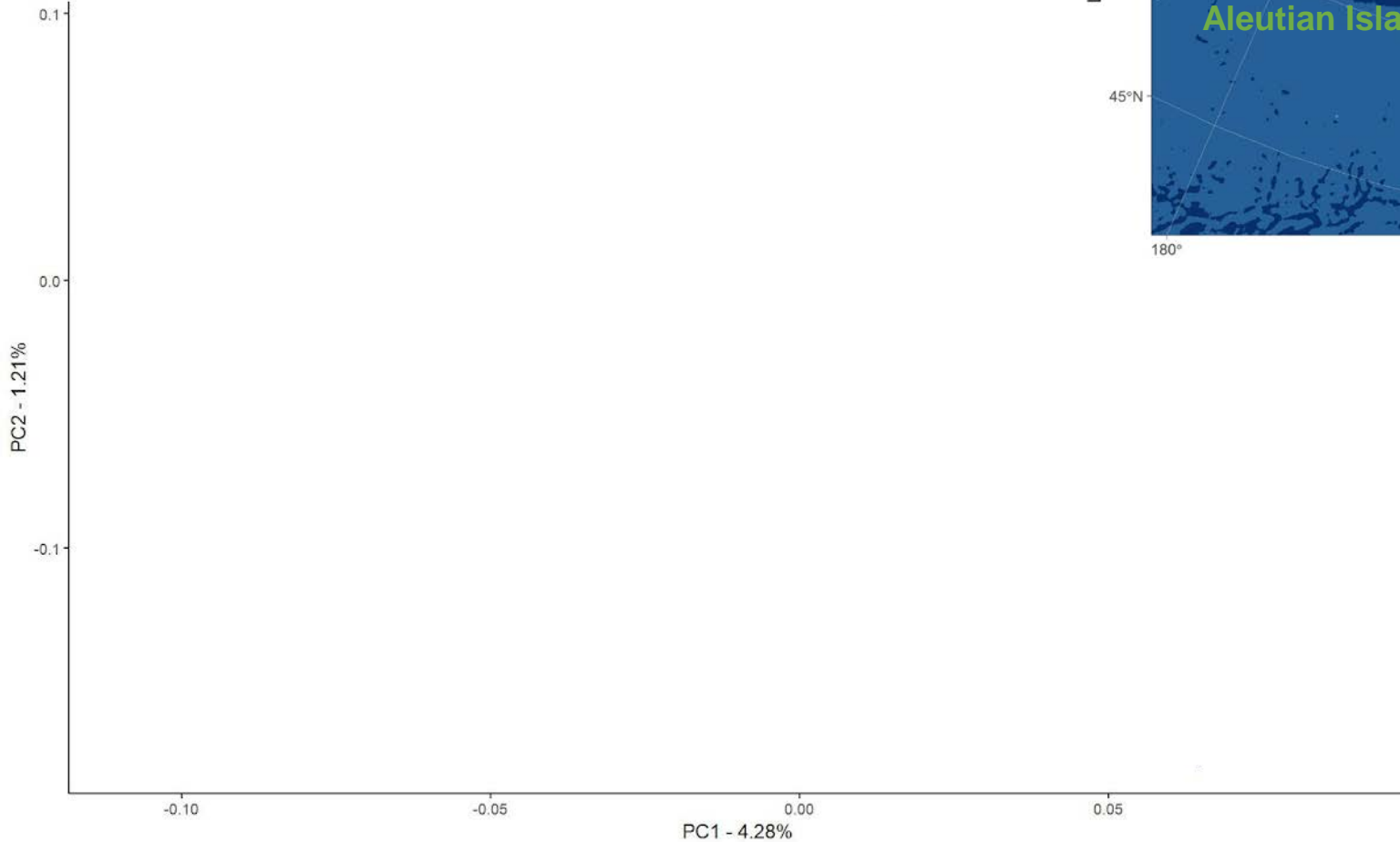


Pacific cod population structure

Whole genome sequencing

> a million markers from throughout the genome

Pacific cod Genome-wide PCA



pop

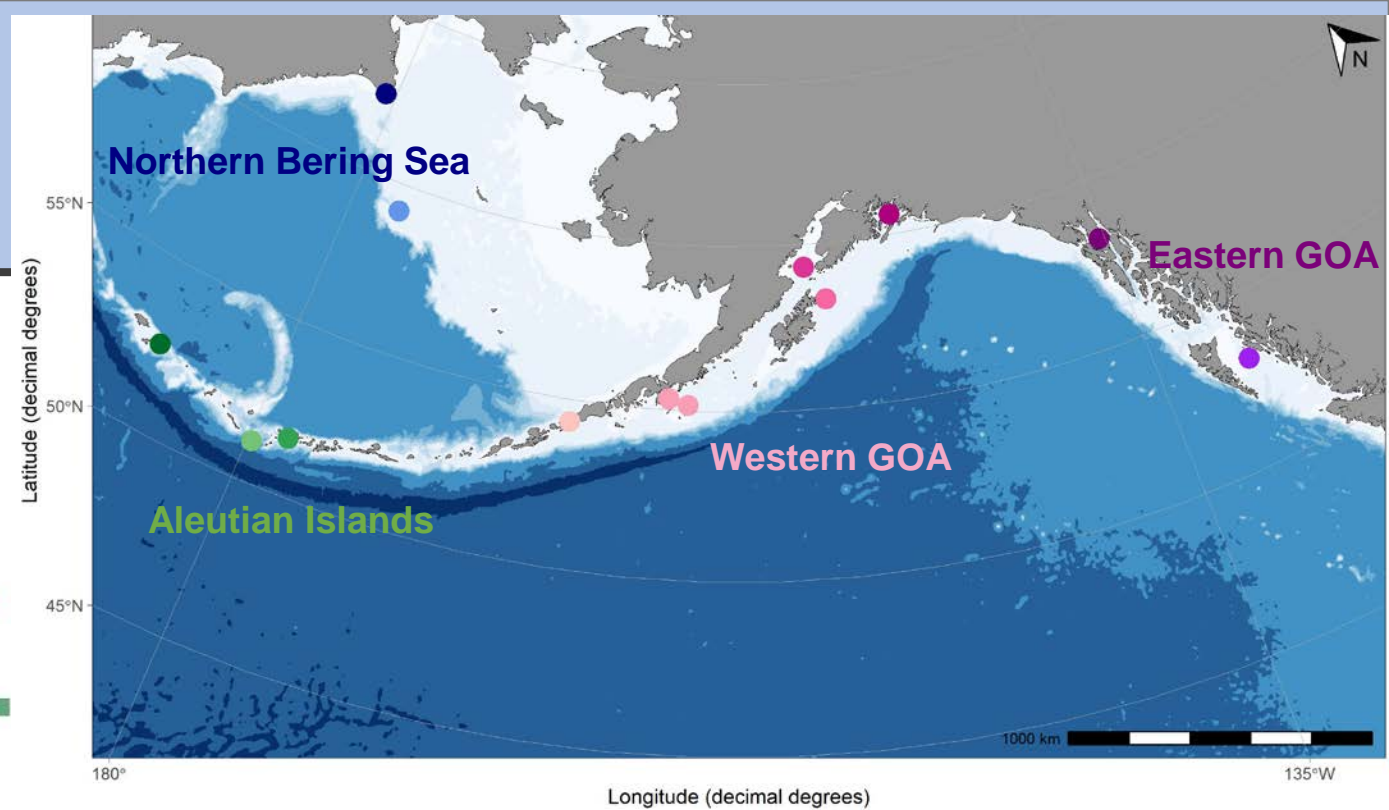
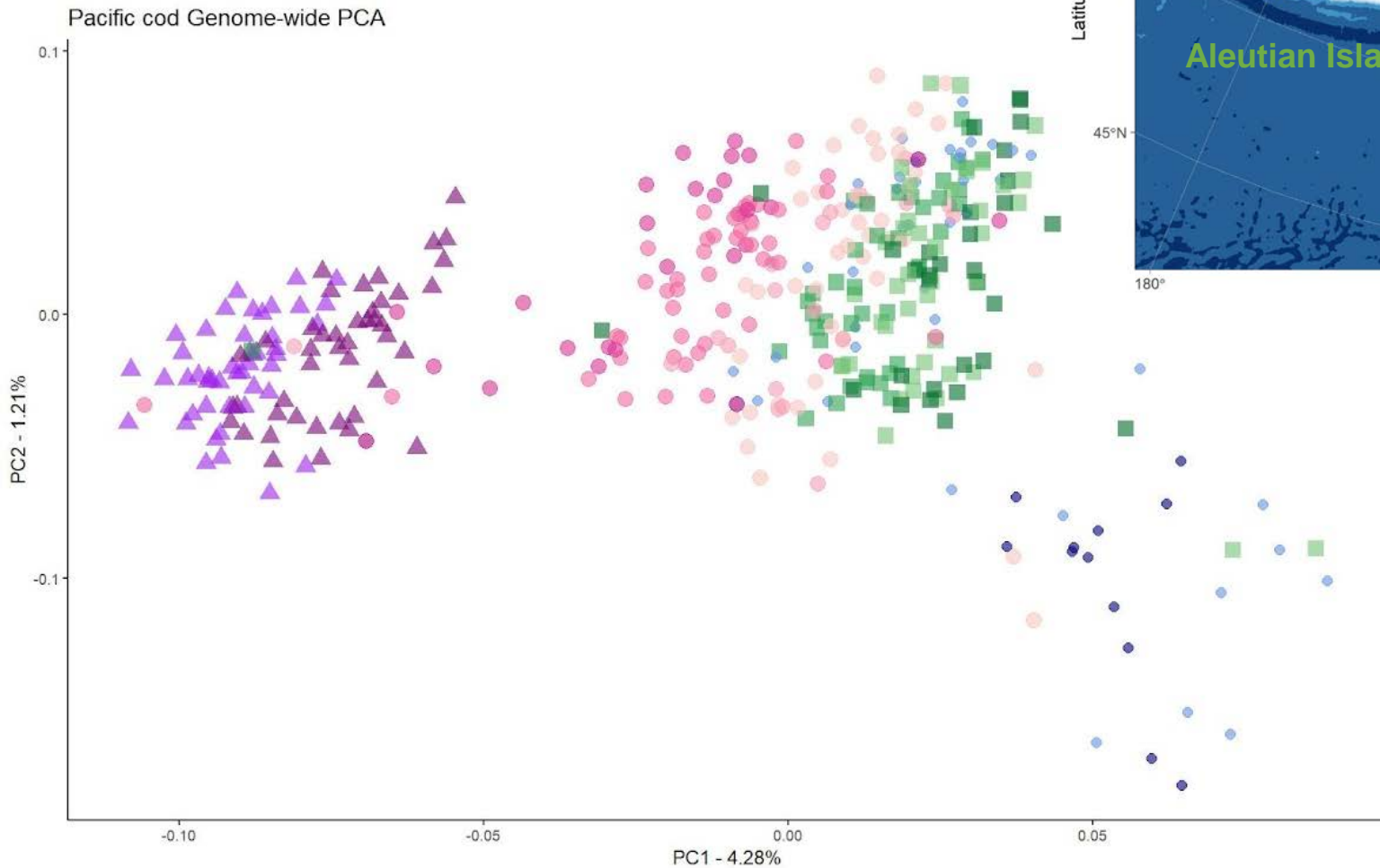
- Russia
- Pervenets Canyon
- Near Islands
- Tanaga Island
- Amchitka Pass
- Unimak
- Shumagins
- Kodiak
- Cook Inlet
- PWS Inside
- Lynn Canal
- Hecate Strait

region

- ▲ Alaska Panhandle
- Aleutians
- Bering Sea
- GOA

Whole genome sequencing

> a million markers from throughout the genome



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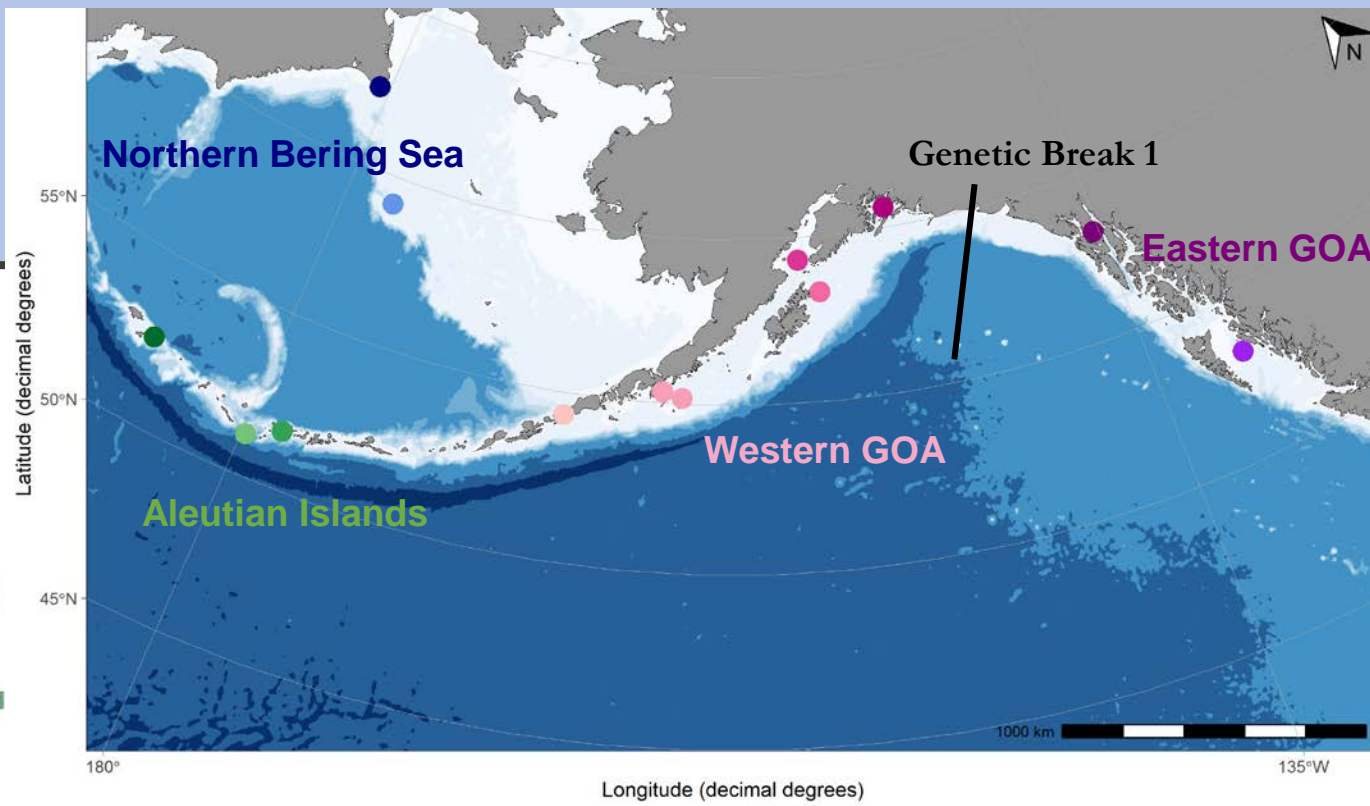
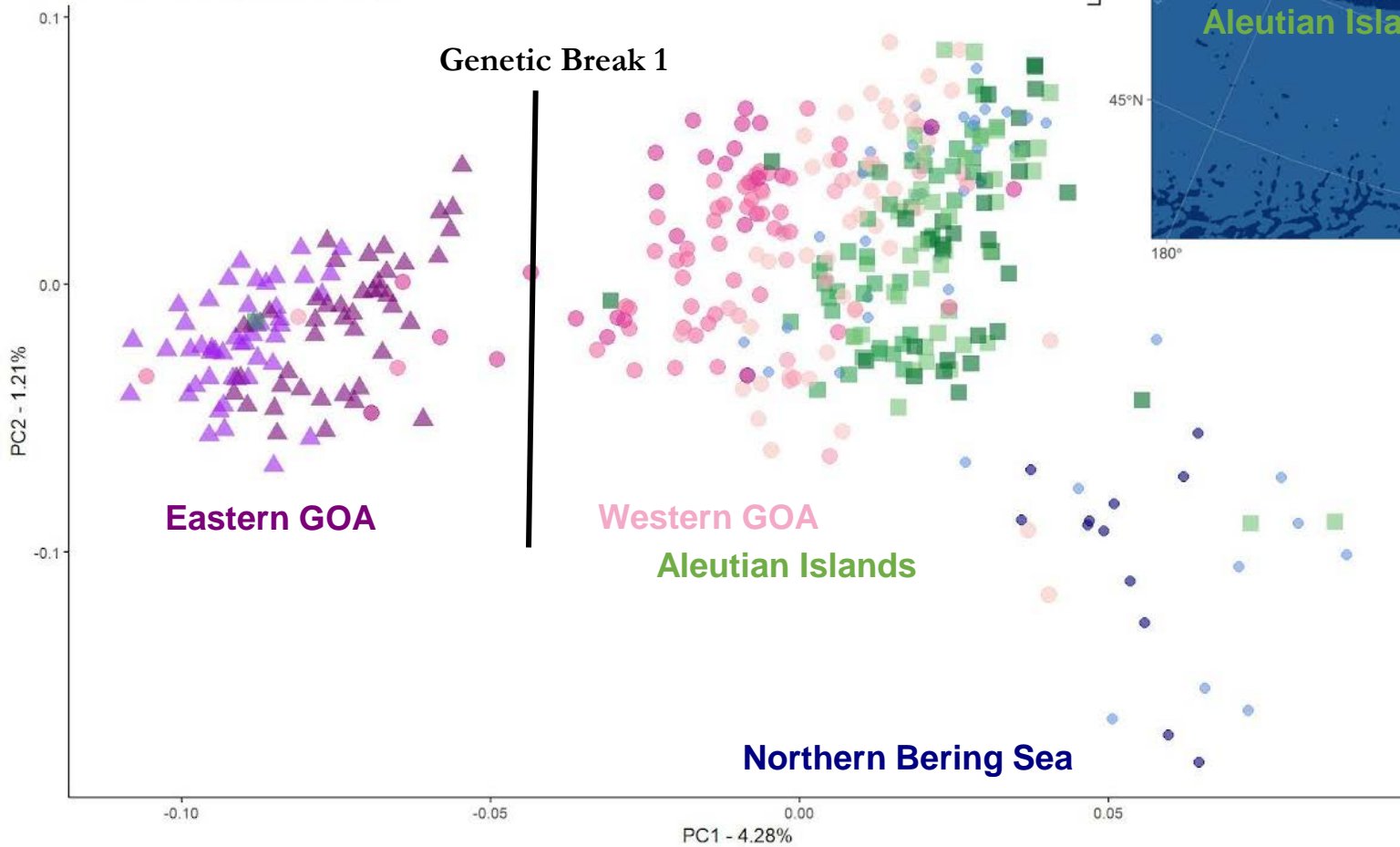
region

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Whole genome sequencing

Two major genetic breaks representing reduced gene flow.

Pacific cod Genome-wide PCA

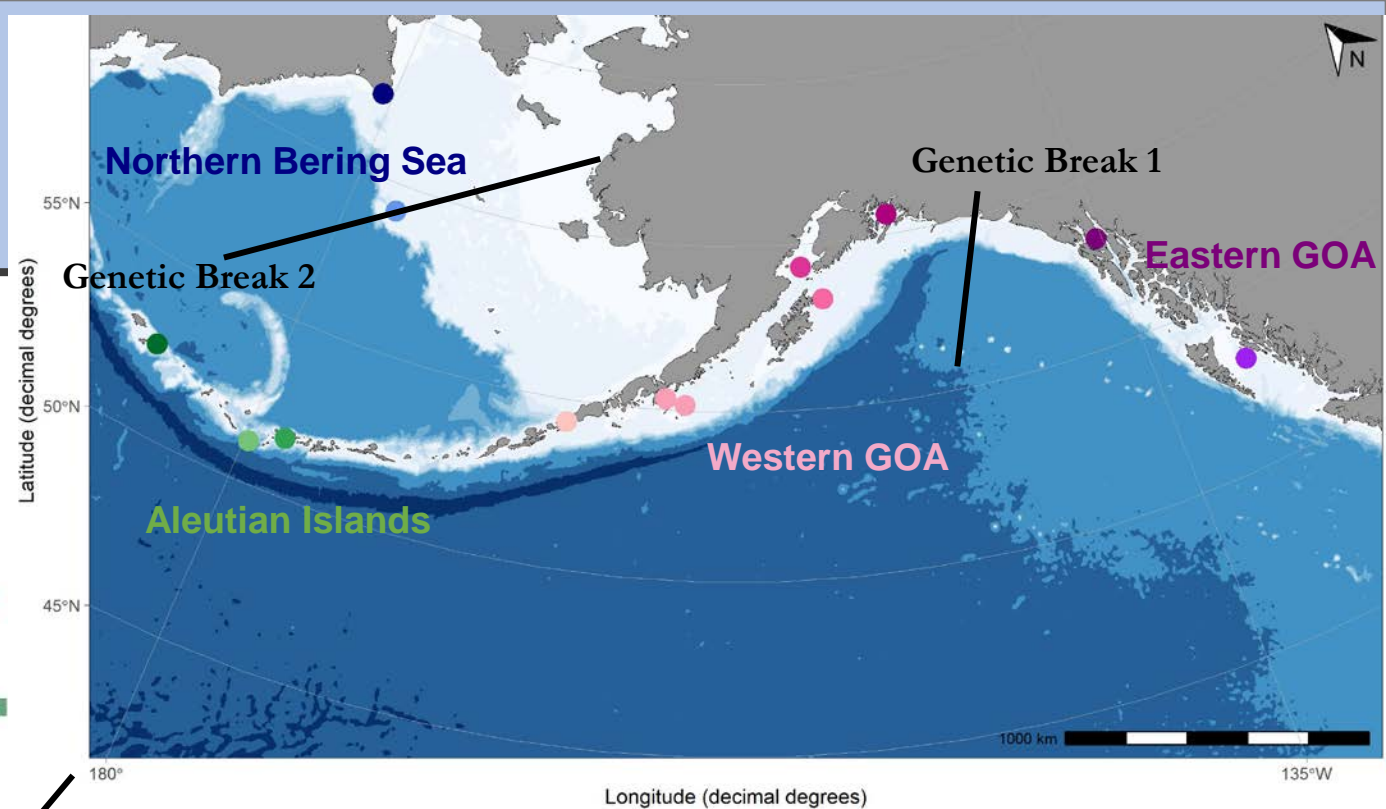
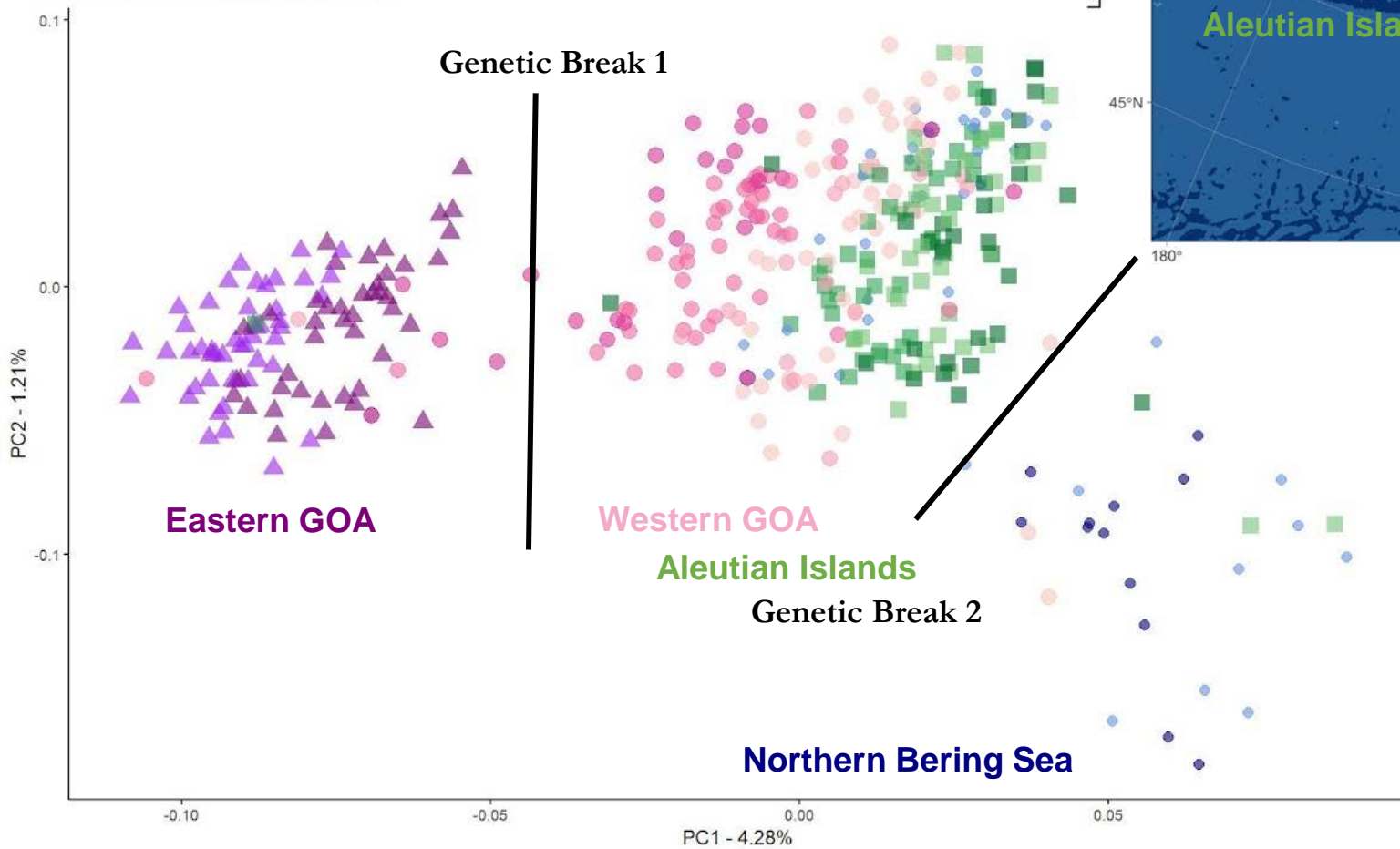


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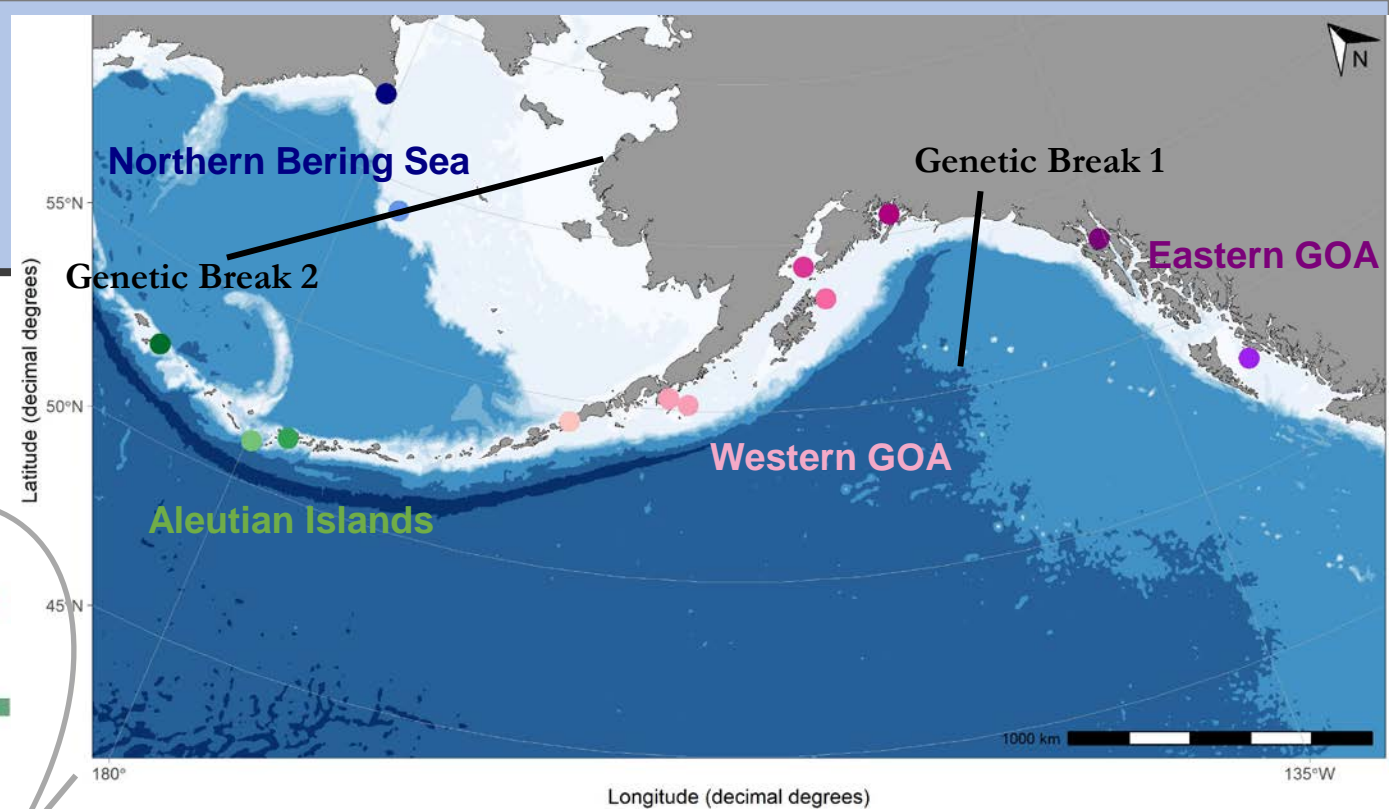
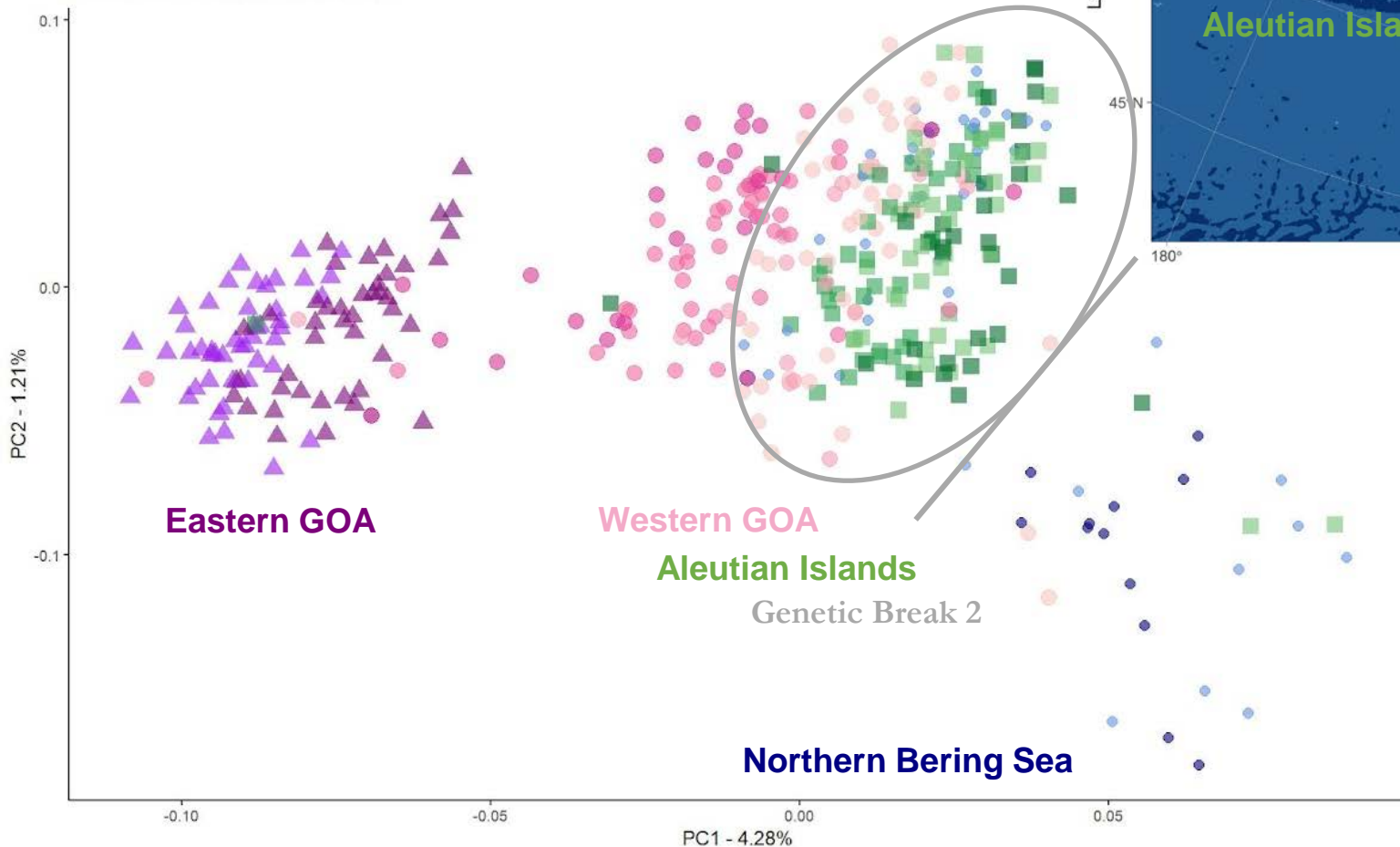
Pacific cod Genome-wide PCA



Whole genome sequencing

Second break is complex with some Pervenets samples clustering with AI cod.

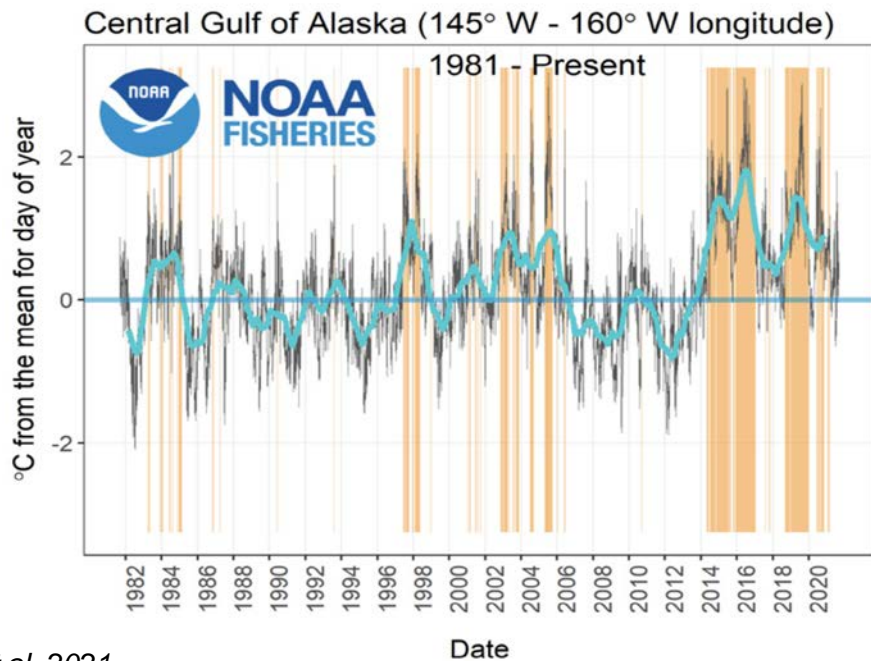
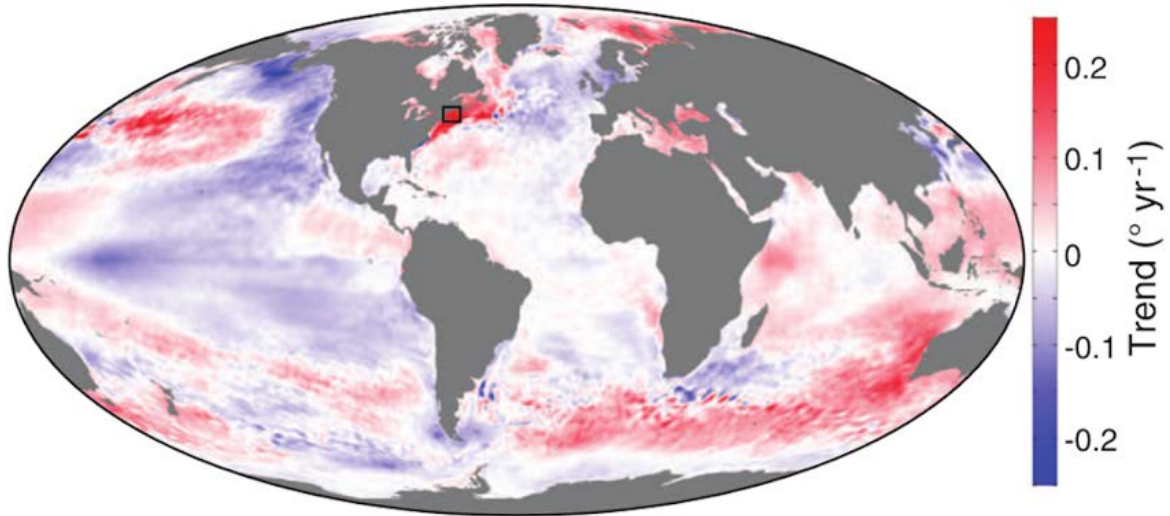
Pacific cod Genome-wide PCA



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Adaptive Genetic Markers

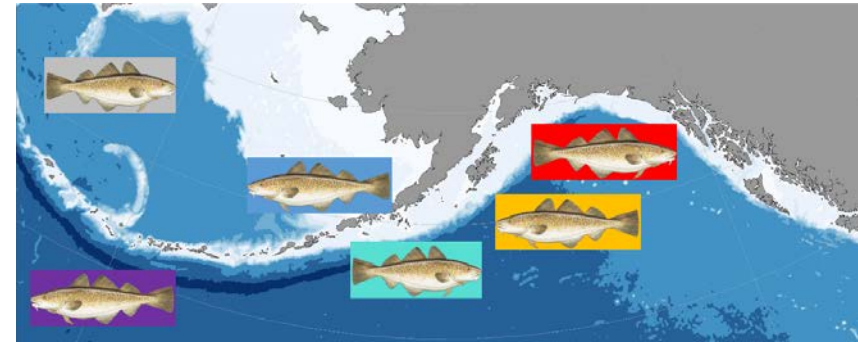
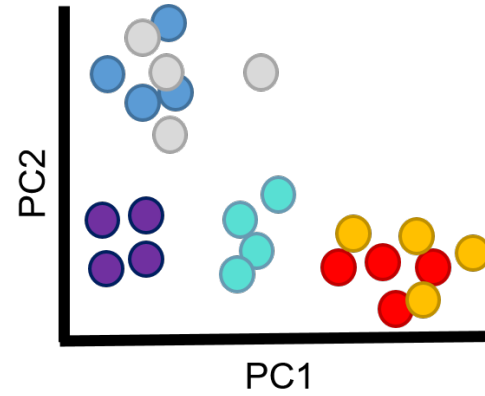
Preserving Adaptive Variation



What can genomics tell us?

Neutral Genetic Markers

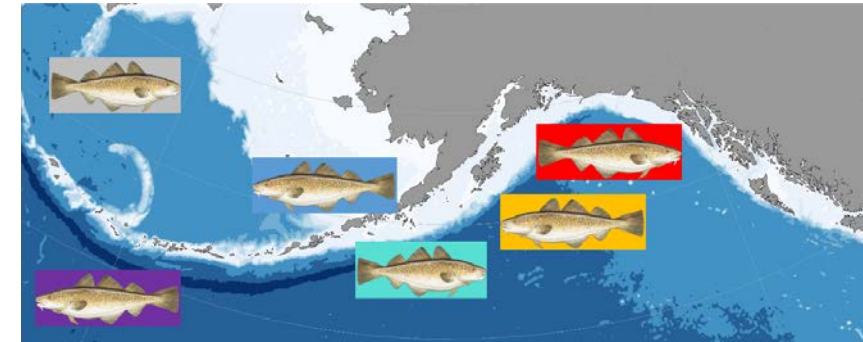
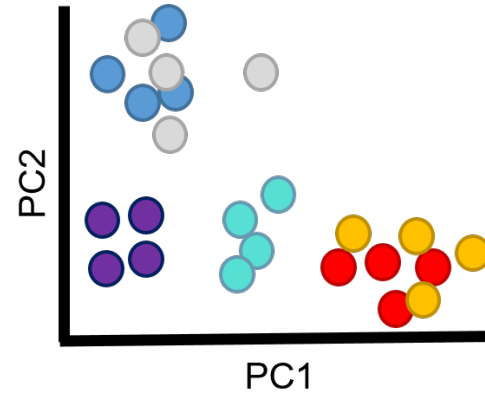
- Historic patterns of gene flow, reproductive isolation



What can genomics tell us?

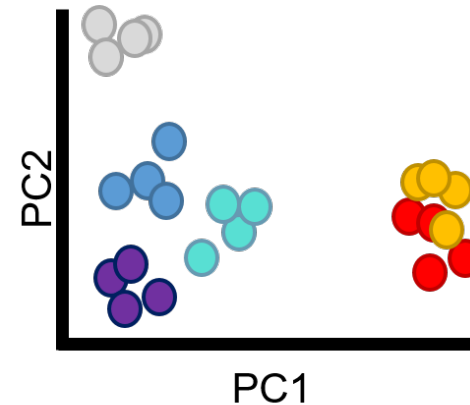
Neutral Genetic Markers

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Adaptive Genetic Markers

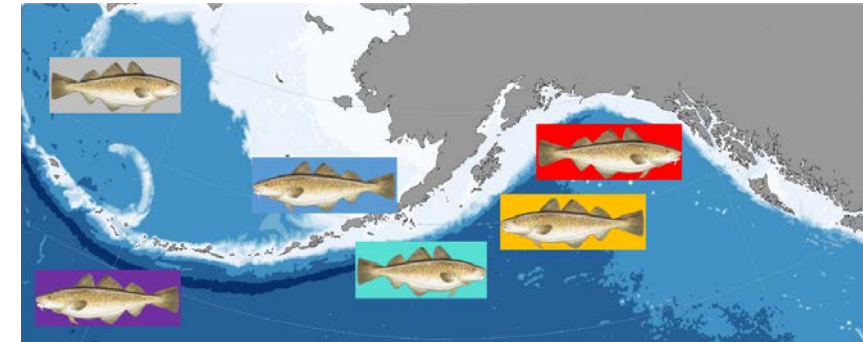
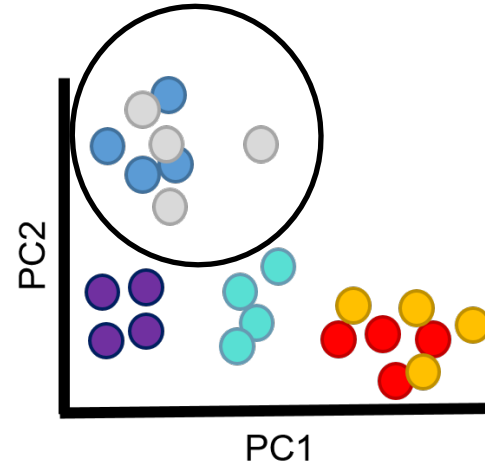
- Natural Selection
(i.e., patterns of selection to environments/stressors)



What can genomics tell us?

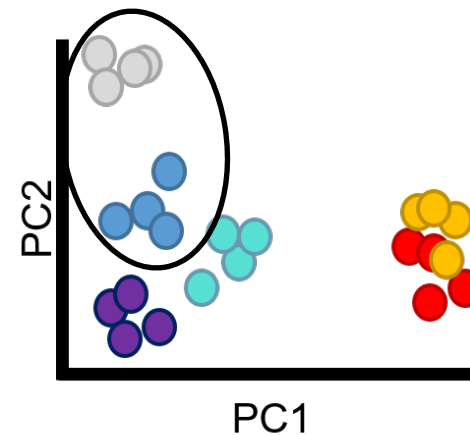
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Adaptive Genetic Markers

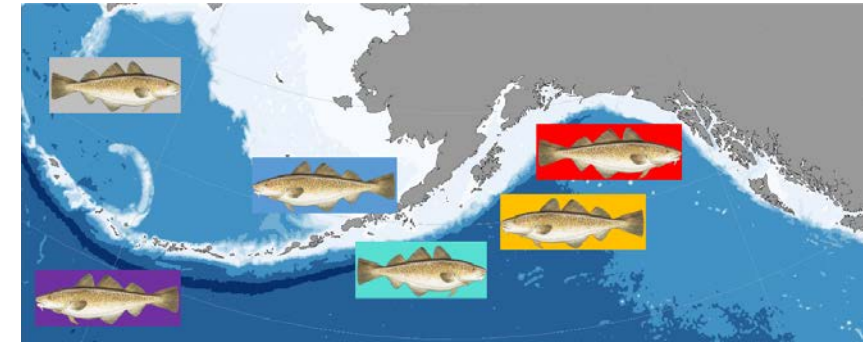
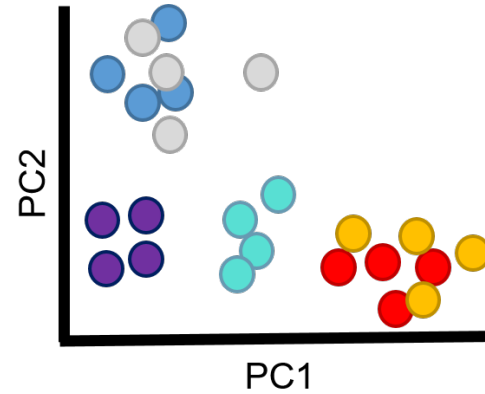
- Natural Selection (i.e., patterns of selection to environments/stressors)
- Often shows a different pattern than neutral markers



What can genomics tell us?

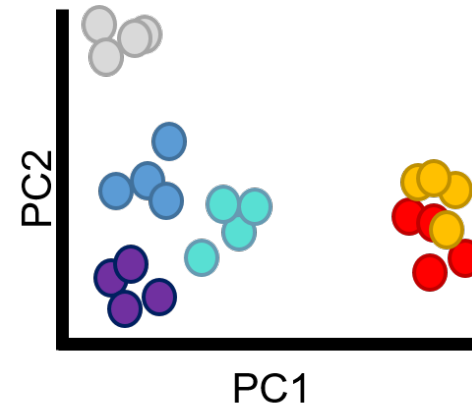
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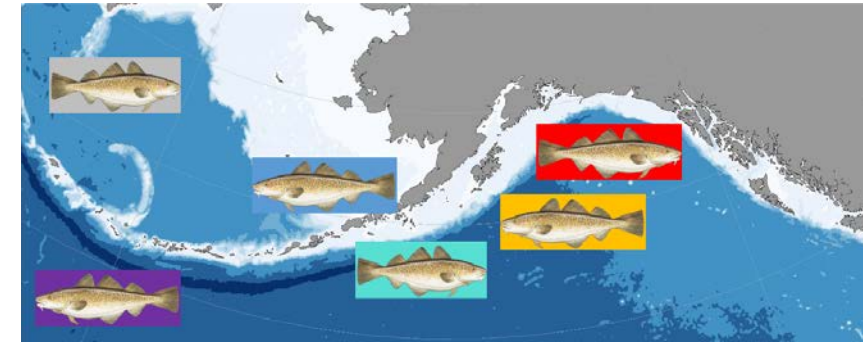
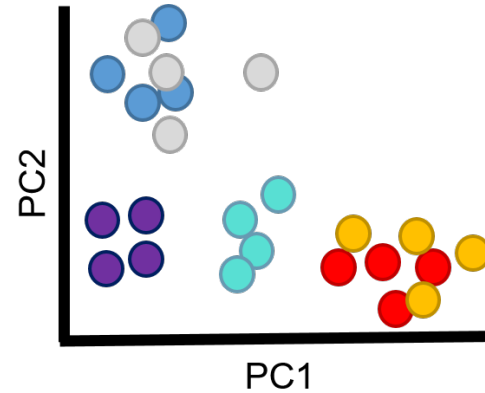
F_{ST}

Genome Position

What can genomics tell us?

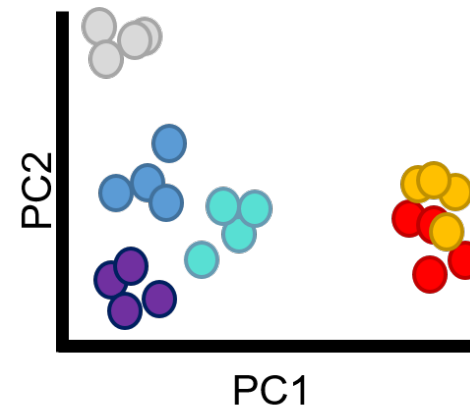
Neutral Genetic Markers

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Adaptive Genetic Markers

- Natural Selection (i.e., patterns of selection to environments/stressors)
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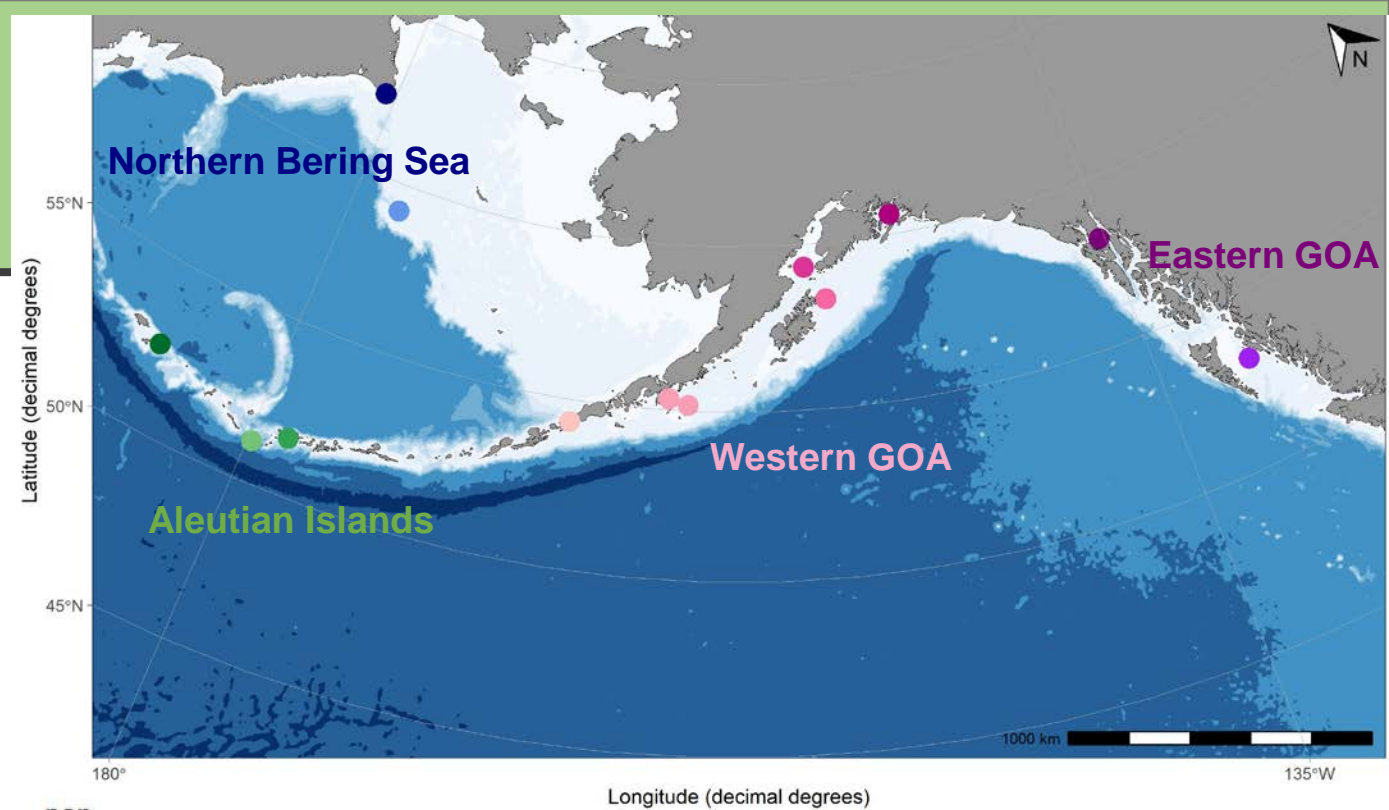
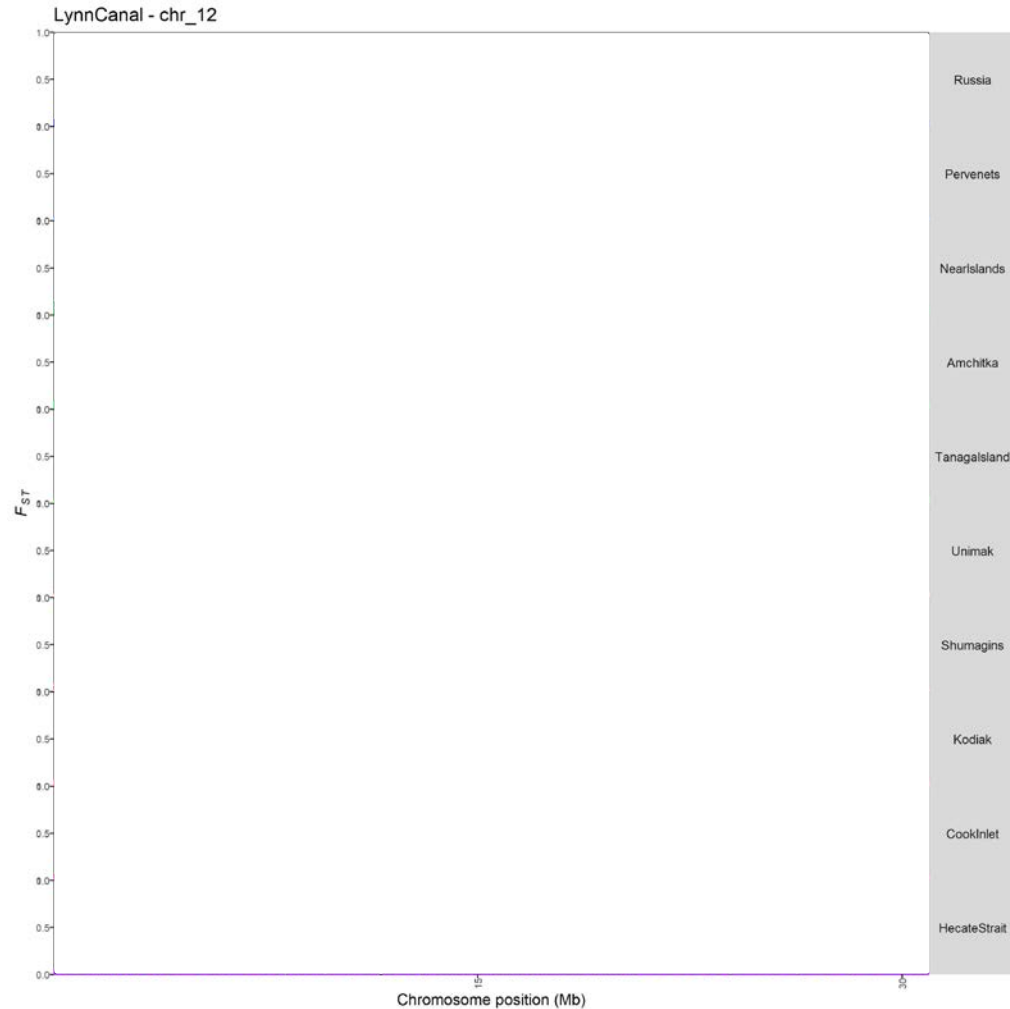
High F_{ST} more population differentiation due to putative selection



Pacific cod adaptive diversity

Whole genome sequencing

Large island of divergence between AI and all other populations

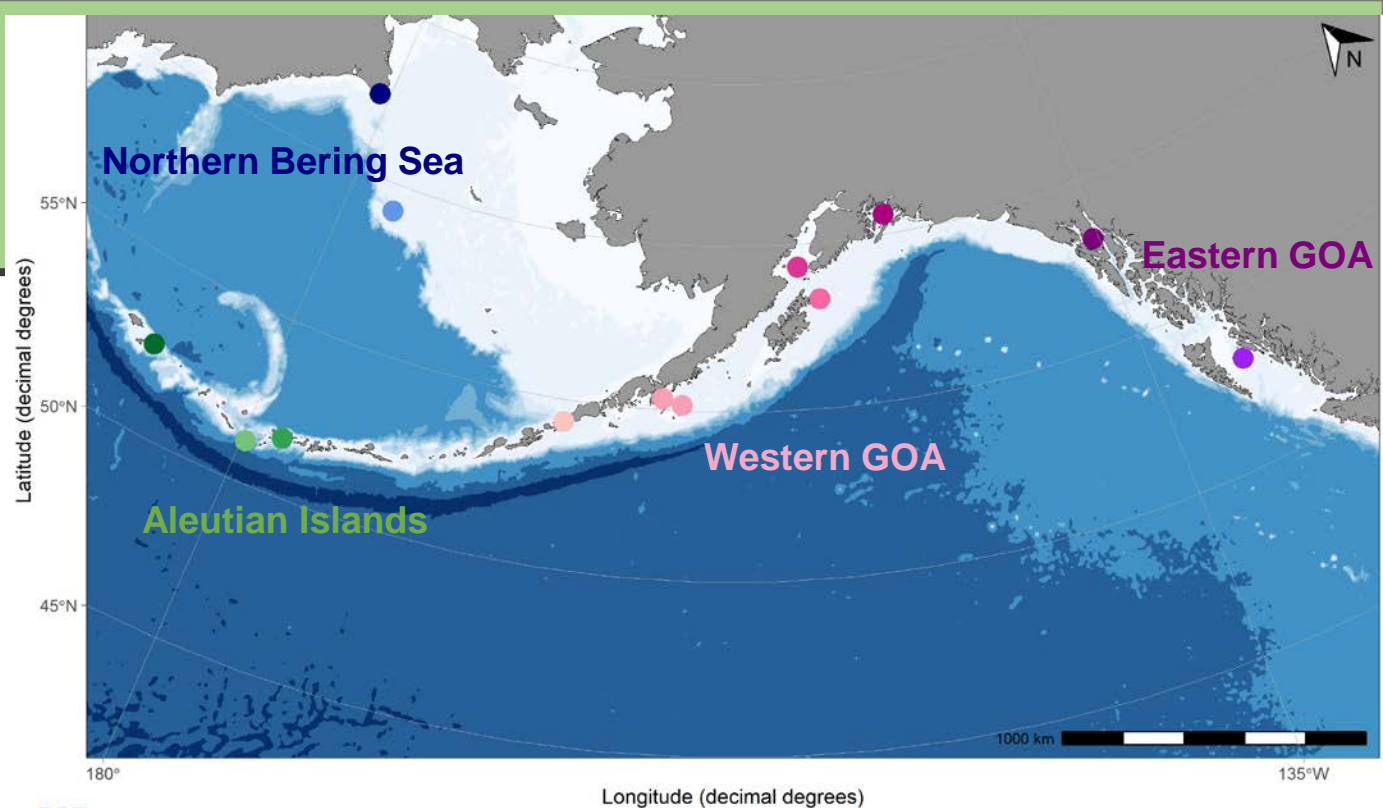
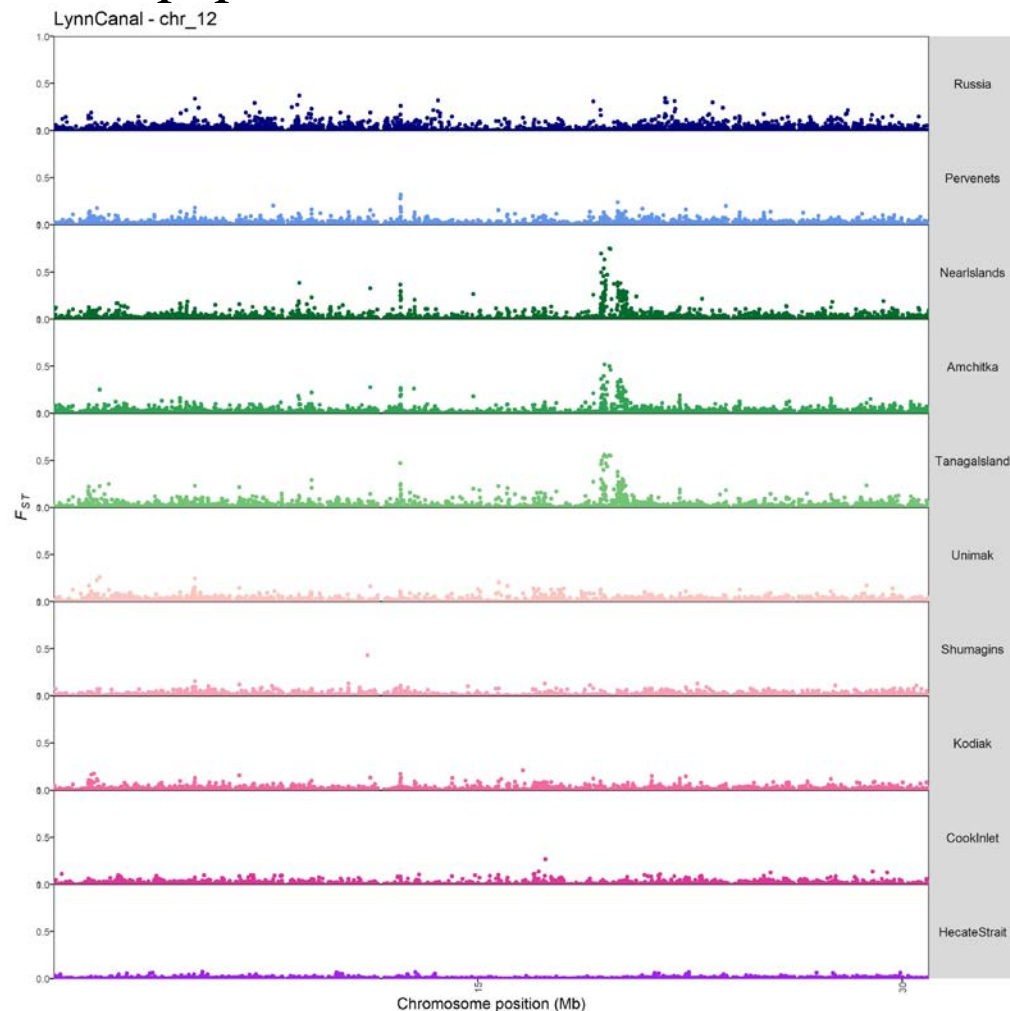


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Whole genome sequencing

Large island of divergence between AI and all other populations



pop

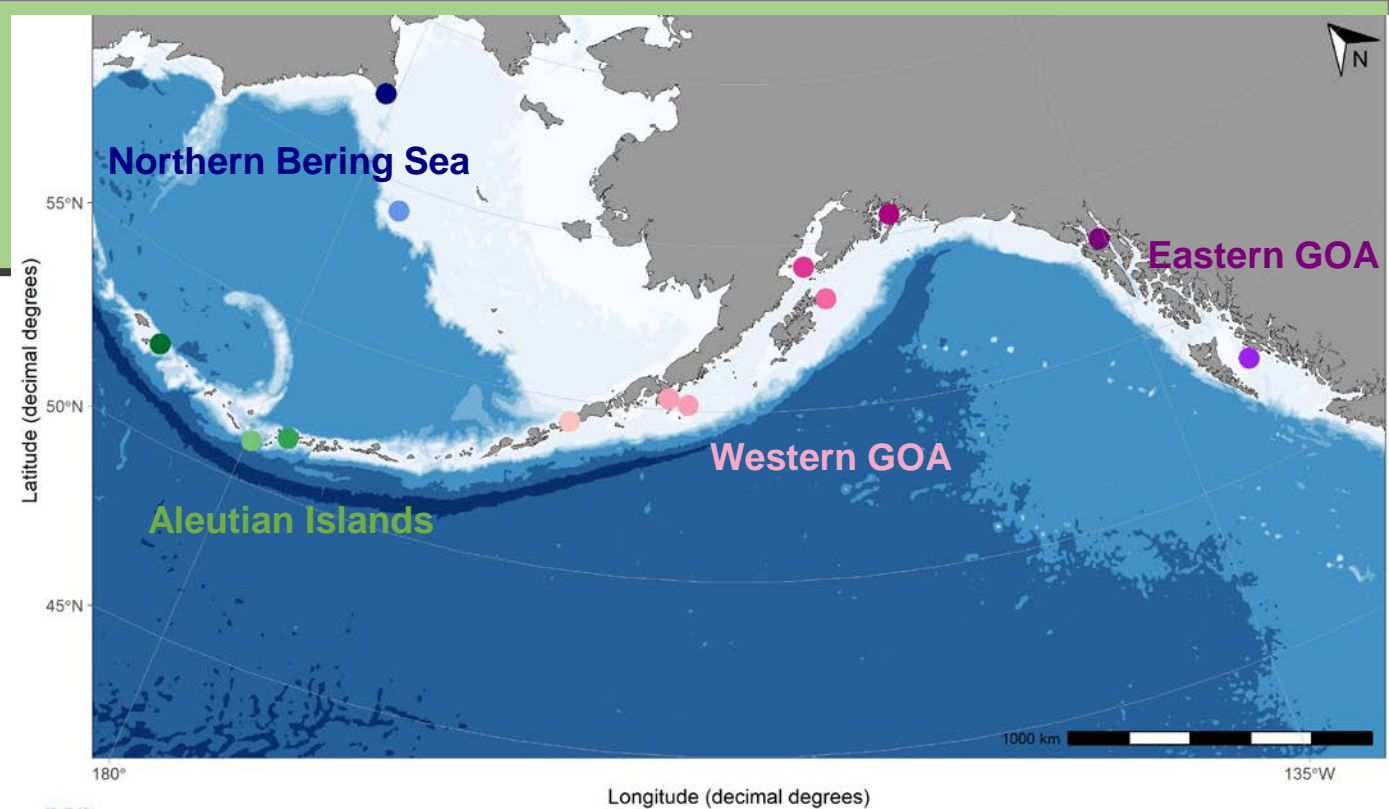
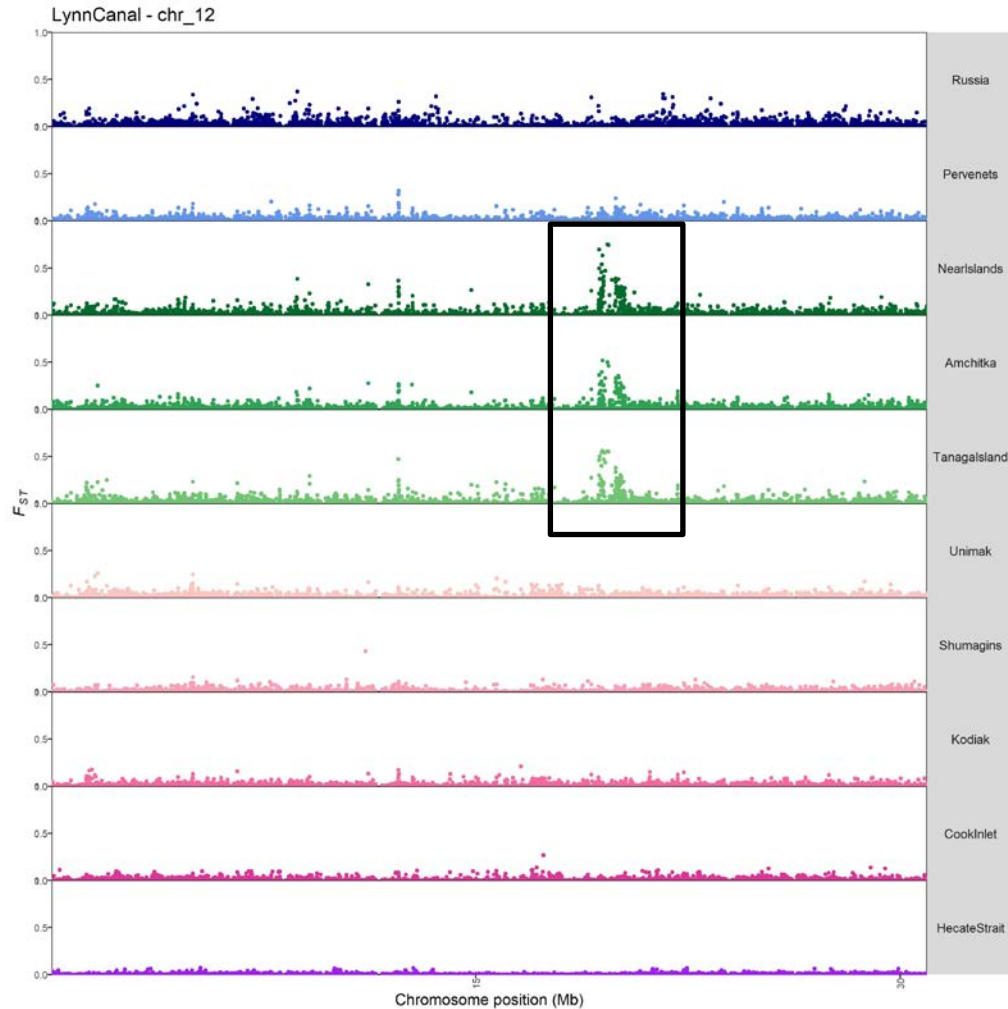
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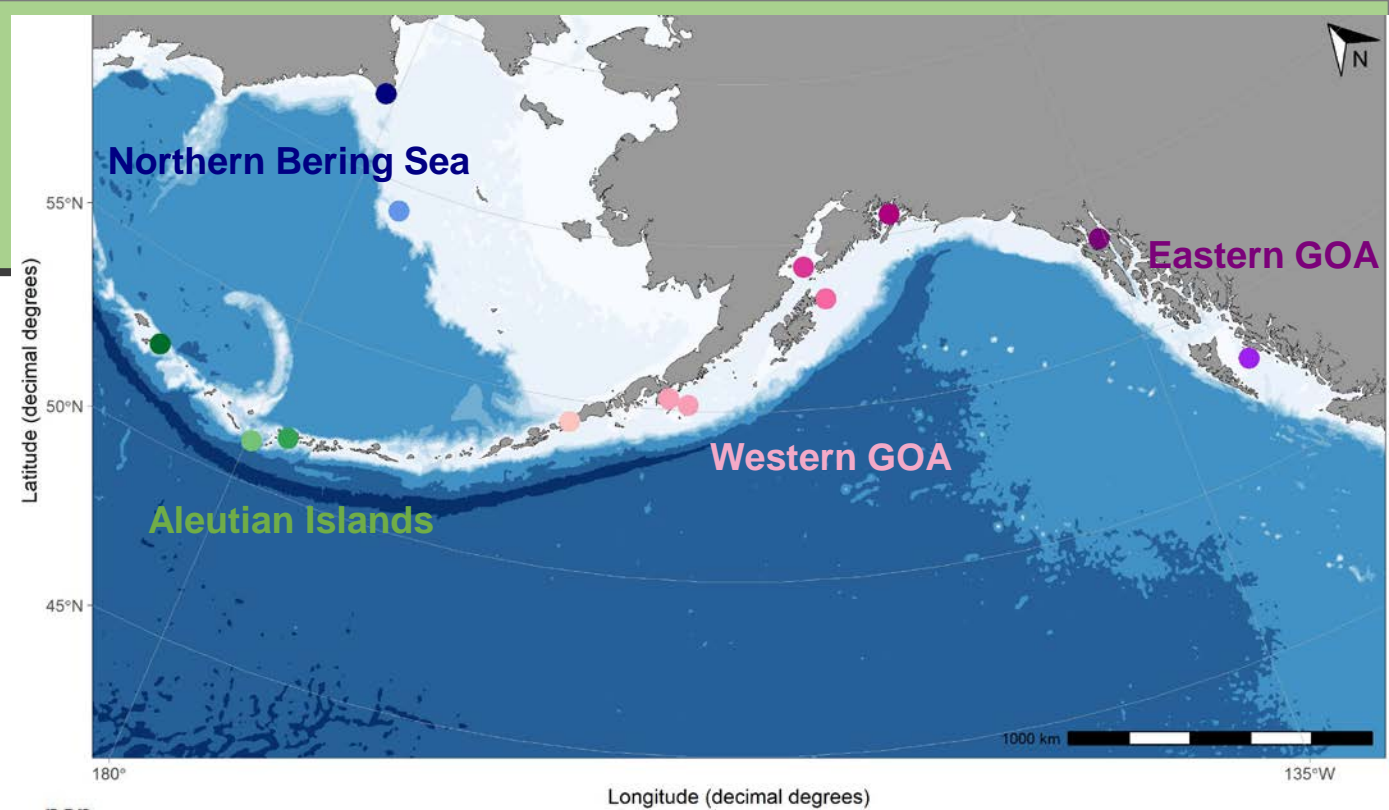
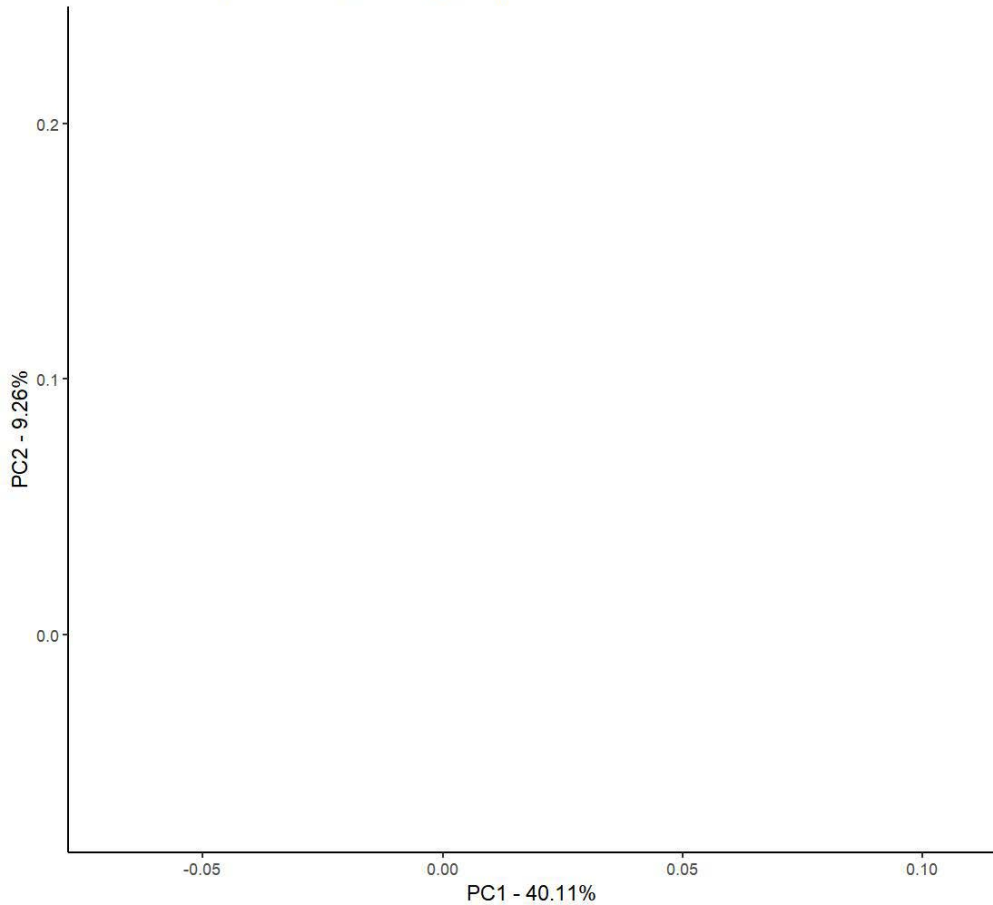
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Whole genome sequencing

Genetic break found with adaptive markers between Aleutian Islands and wGOA

Pacific cod top 0.11% high FST (8576)



pop

- Russia
- Pervenets Canyon
- Near Islands
- Tanaga Island
- Amchitka Pass
- Unimak
- Shumagins
- Kodiak
- Cook Inlet
- PWS Inside
- Lynn Canal
- Hecate Strait

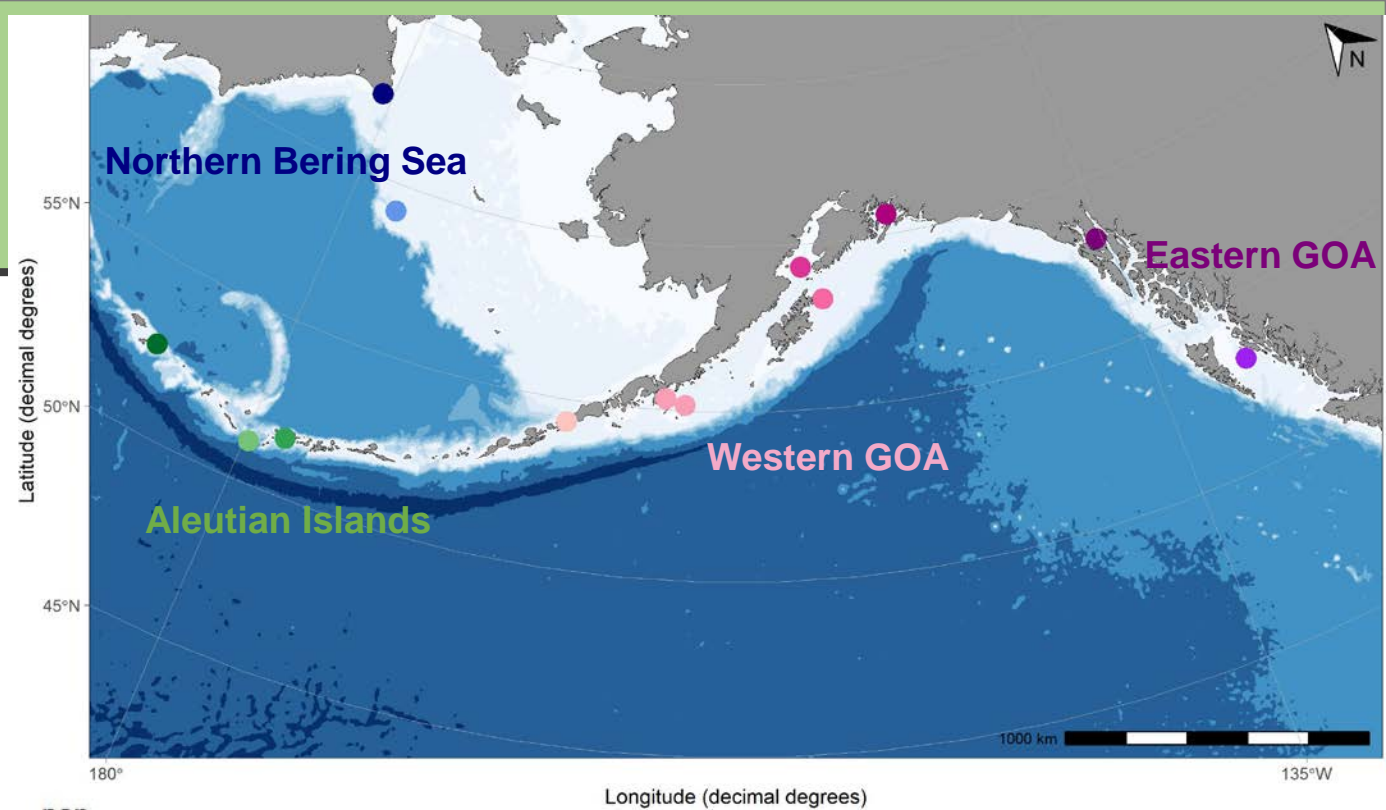
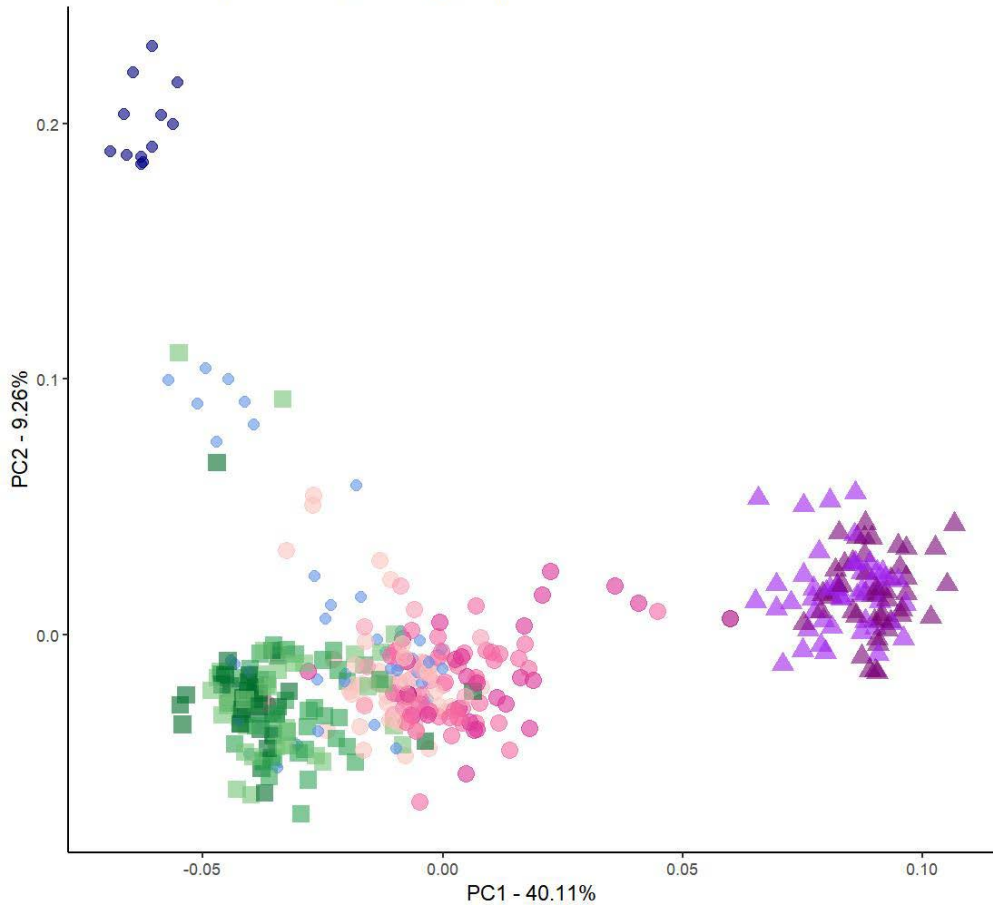
region

- Alaska Panhandle
- Aleutians
- Bering Sea
- GOA

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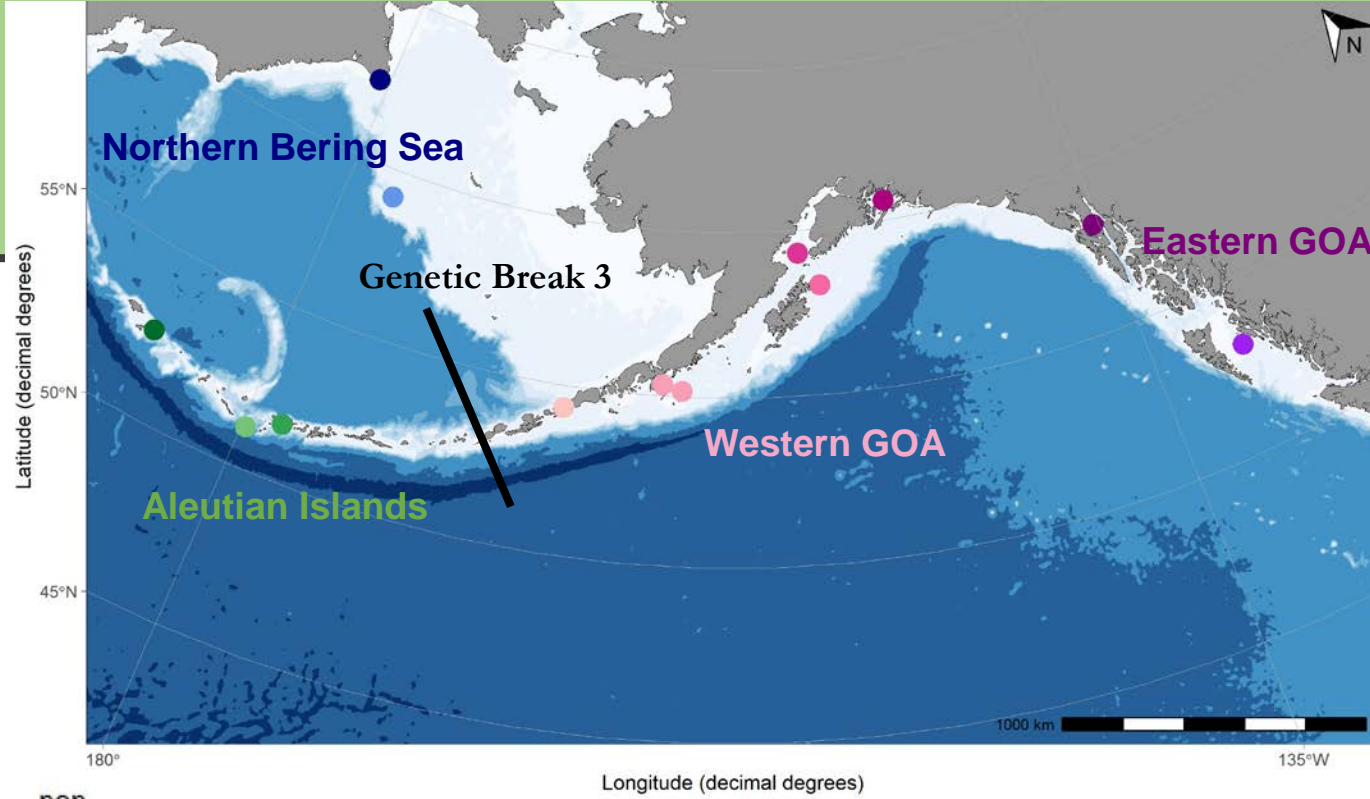
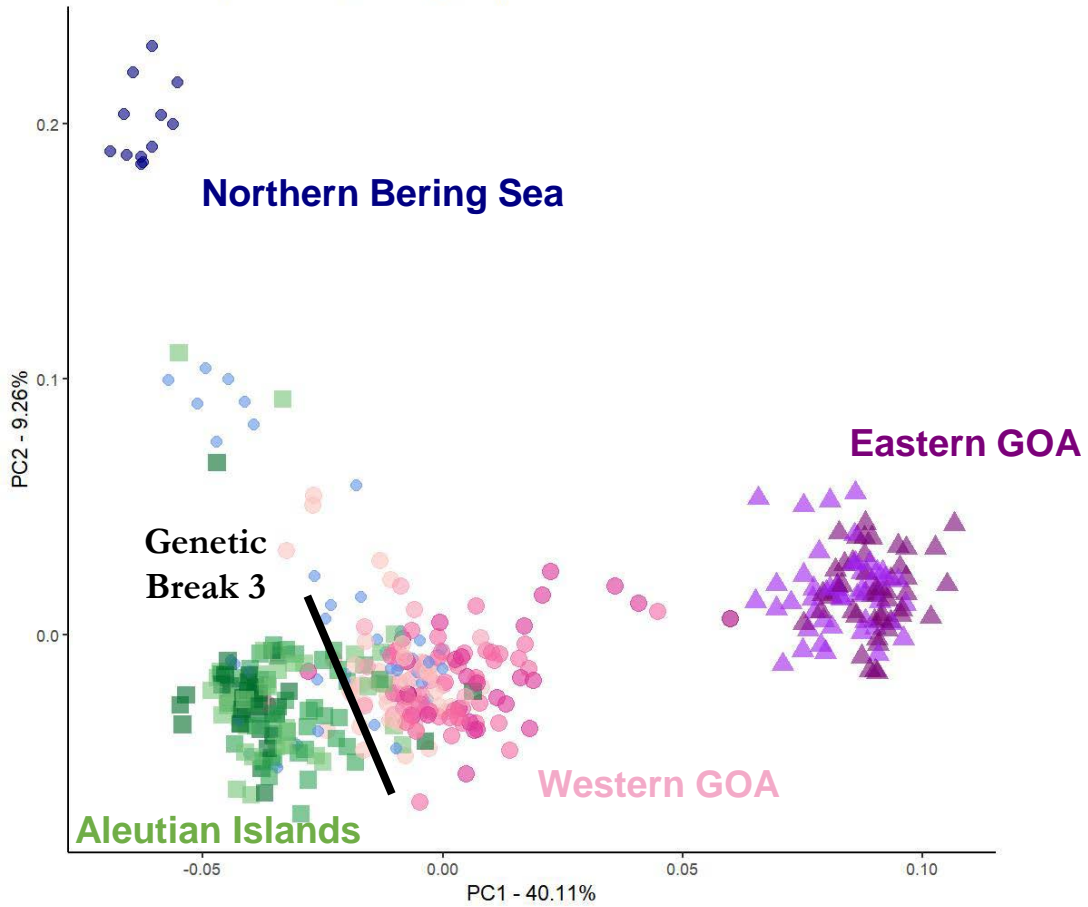
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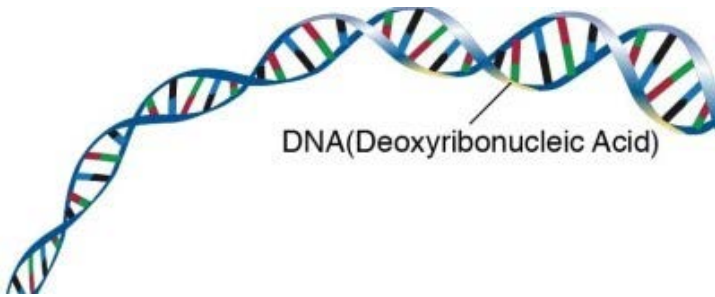


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Panel of highly informative markers

Step 1

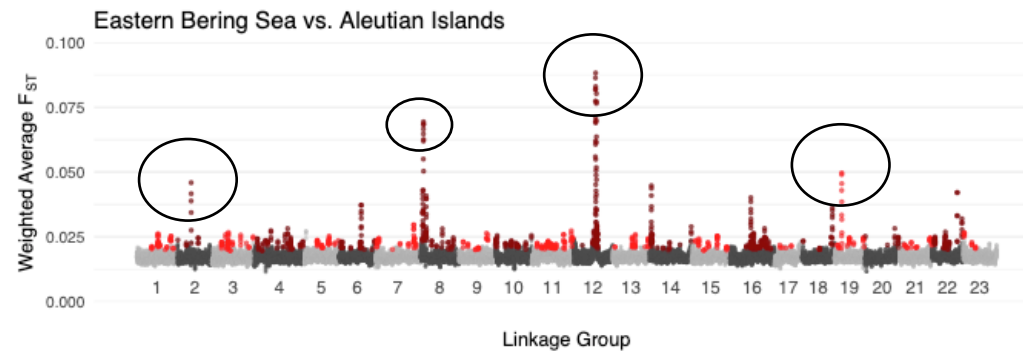
Whole-genome sequencing



Some individuals from major spawning populations

Step 2

Identify outlier loci



Step 3

Design a panel using ~300 markers that maximize genetic differences

Panel Uses

The panel will be used to determine the population origin of fish in the mixed stock fisheries.

Knowing population of origin will:

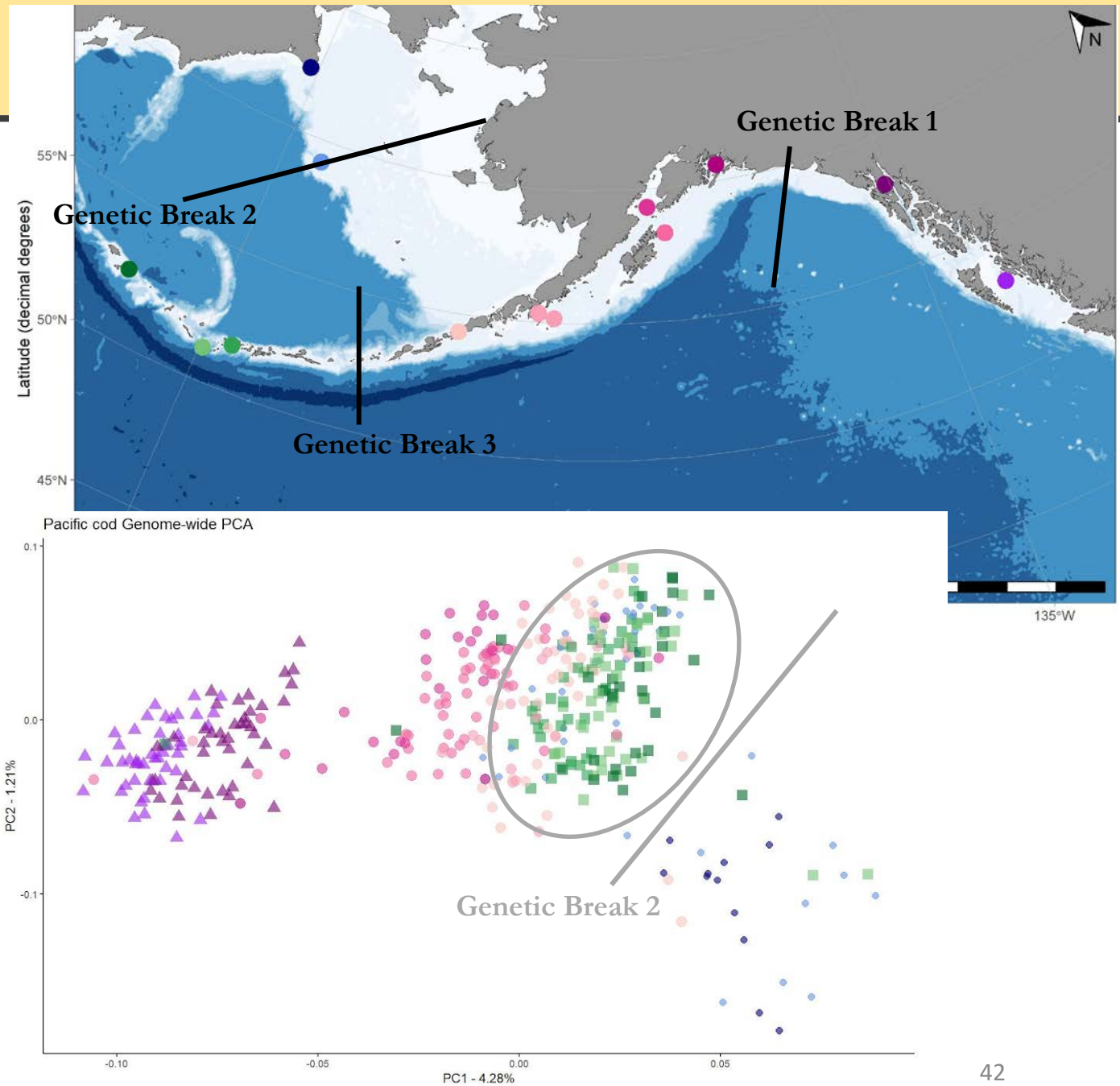
- Estimate seasonal migration rate
- Investigate ontogenetic migratory behavior
- Identify origin of large cod in fishery
- Identify summer stock boundaries



NOAA Fisheries scientists collect Pacific cod samples in the Aleutian Islands. <https://www.fisheries.noaa.gov/>

Conclusions

- Two genetic breaks due to limited migration:
 - 1) eGOA and wGOA
 - 2) Northern Bering Sea and GOA/AI
- Third genetic break due to adaptive variation:
 - 3) AI and wGOA
- The Bering Sea genetic break is complex
- Update on Pollock next time



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Lyle Britt

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Elliott Hammond

Simon Kineen

Krista Milani

Sean Rooney

Chris Schaeffer

Chad See

Dawn Wehde

Dave Fraser

Elliott Hammond

Simon Kineen

Krista Milani

Sean Rooney

Chris Schaeffer

Chad See

Dawn Wehde

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Alaska Fisheries Science Center

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Norton Sound Fund

JPA



NOAA
FISHERIES

Questions?



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