# Population genomics of Pacific cod

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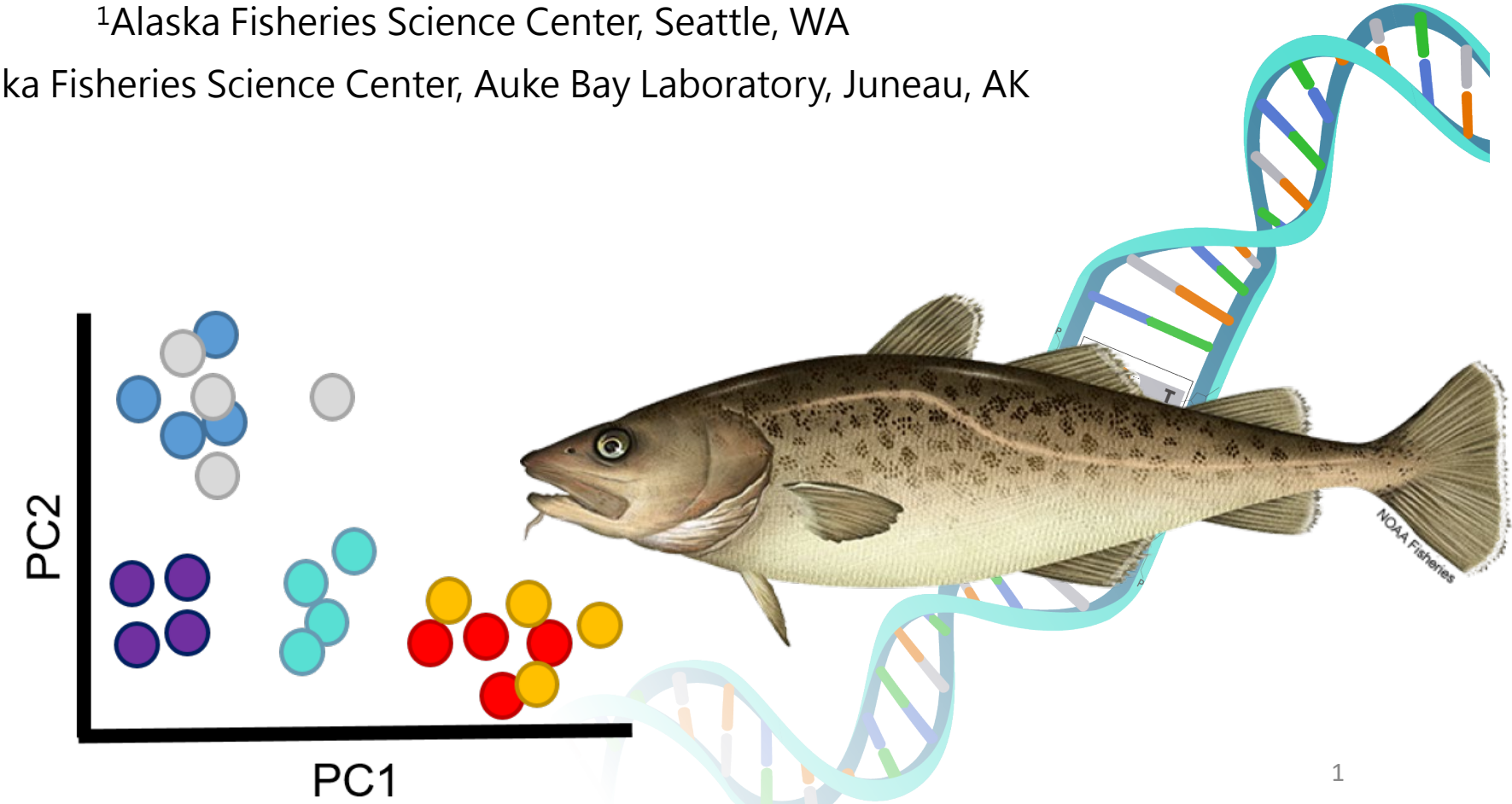
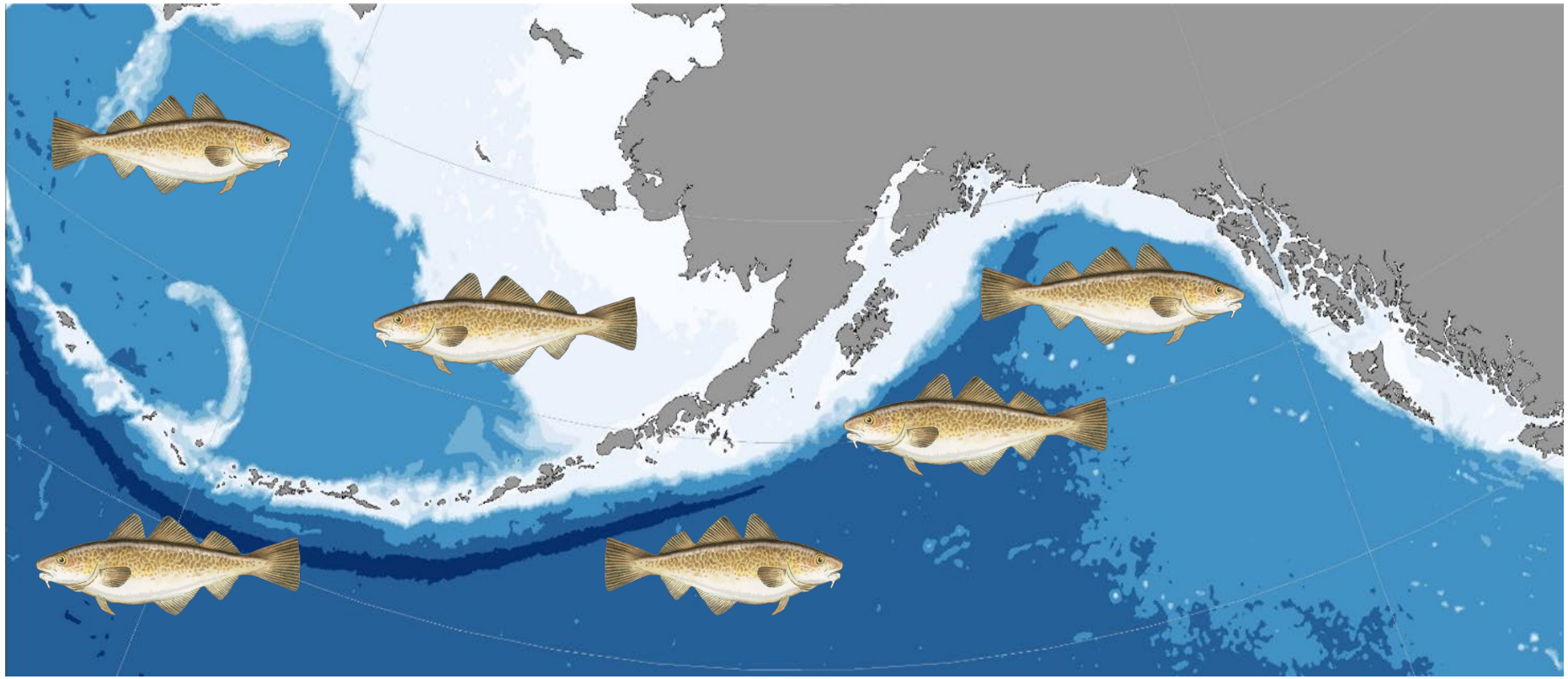


# Major goal of management

Identify Population Boundaries



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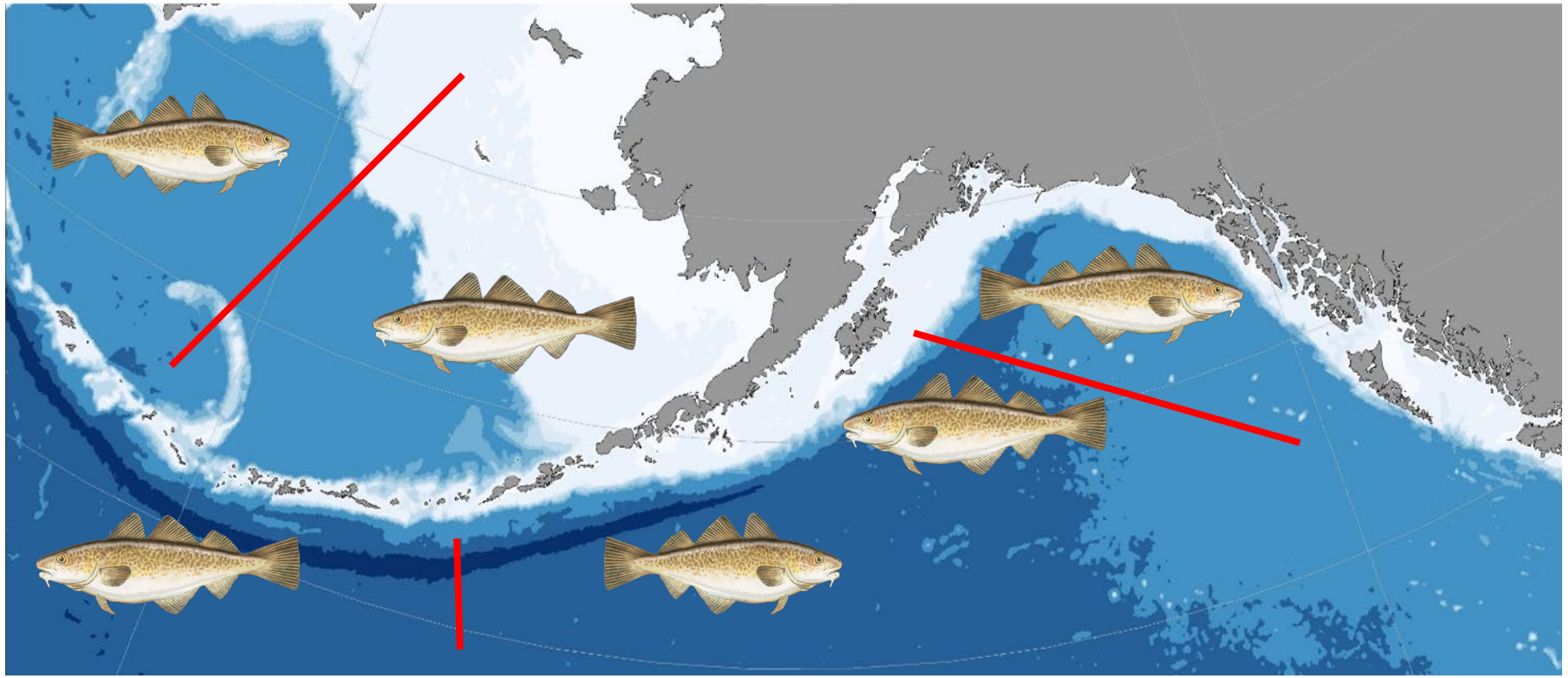
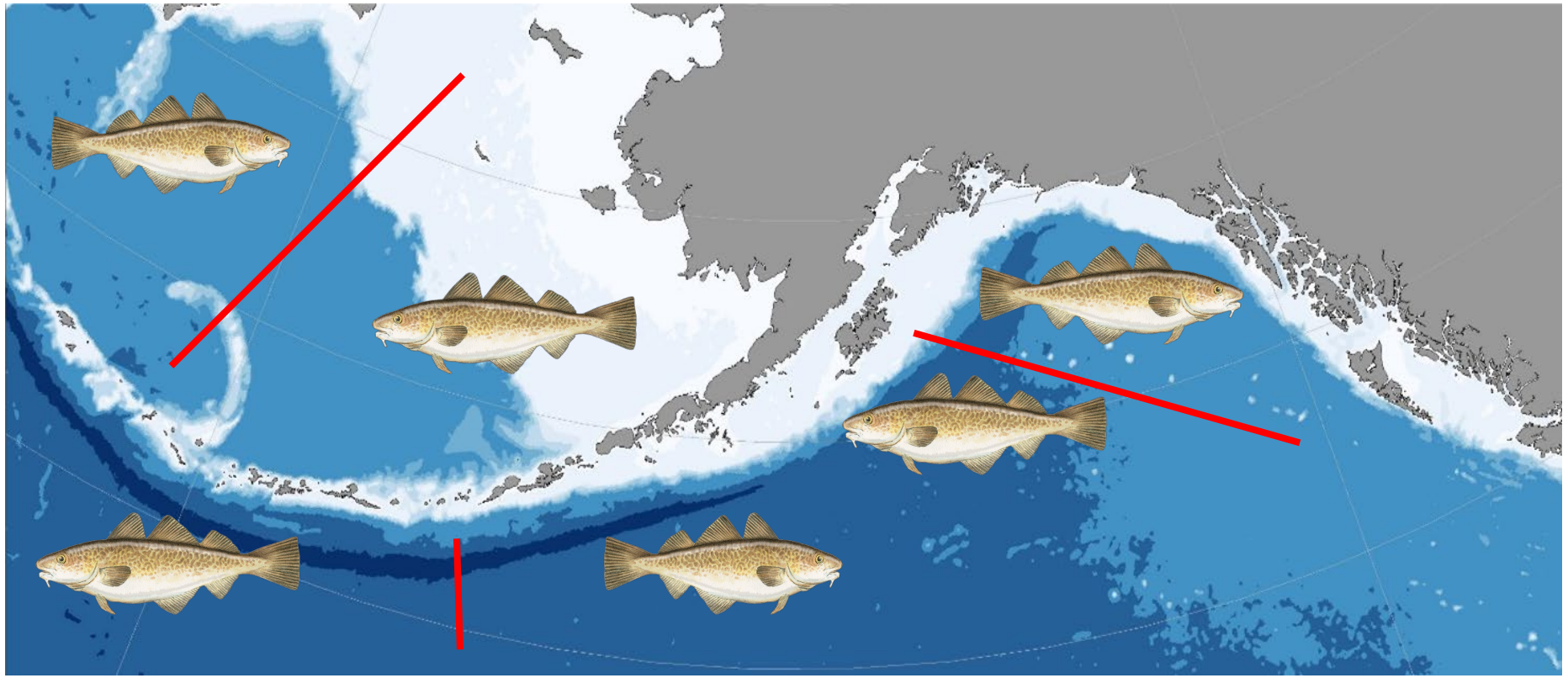


# Major goal of management

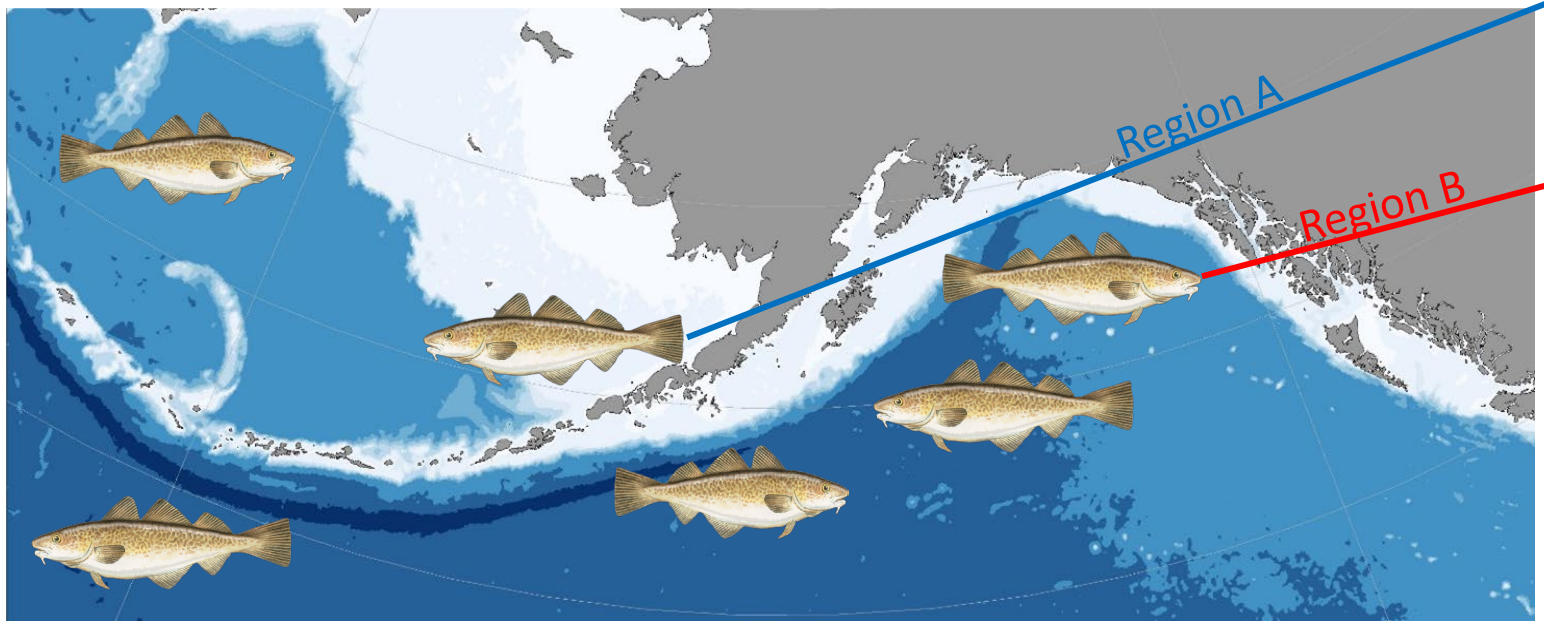
Identify Population Boundaries

Highly mobile species make this difficult



# What can genomics tell us?

Populations that reproductively isolated



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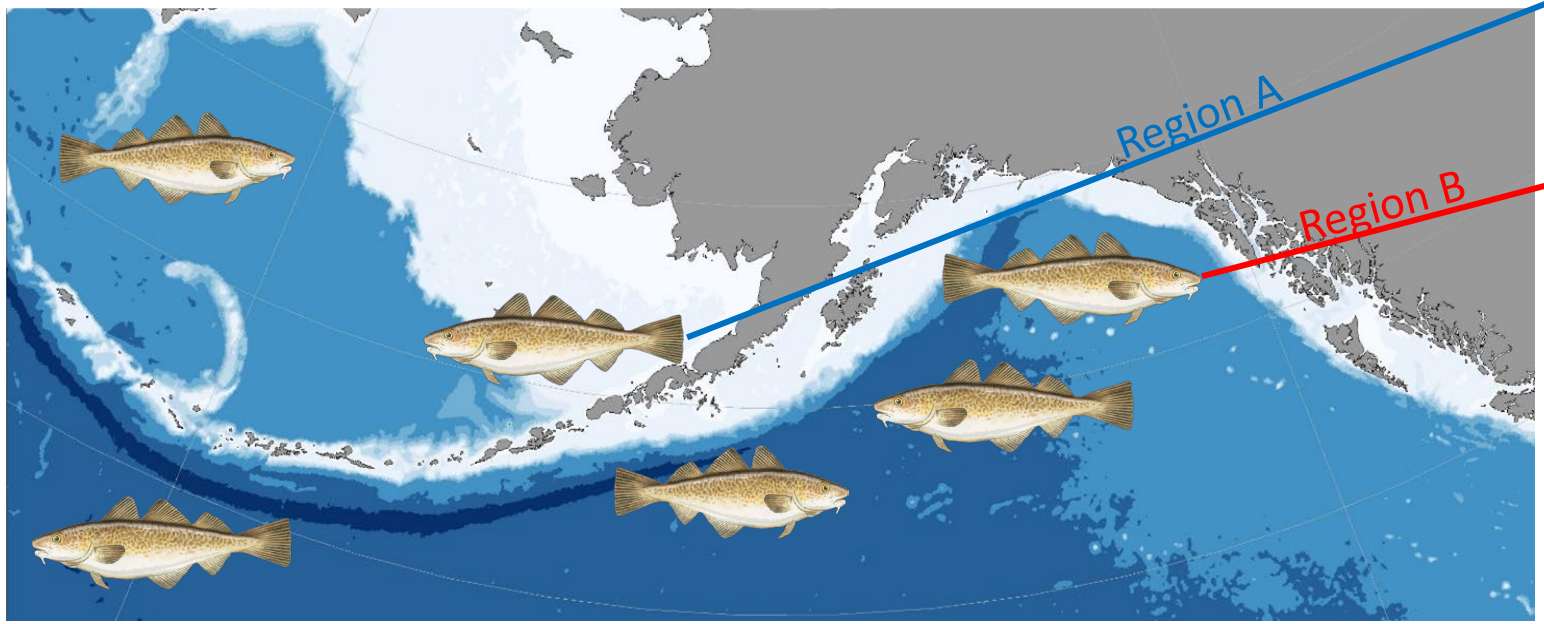


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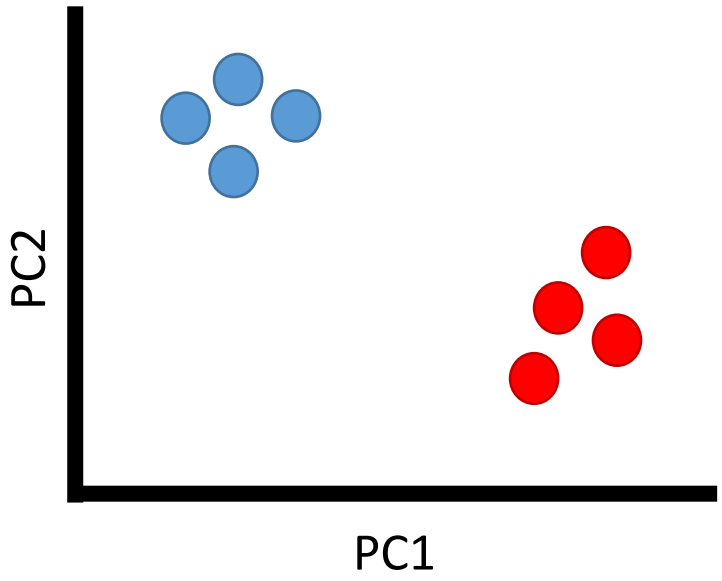

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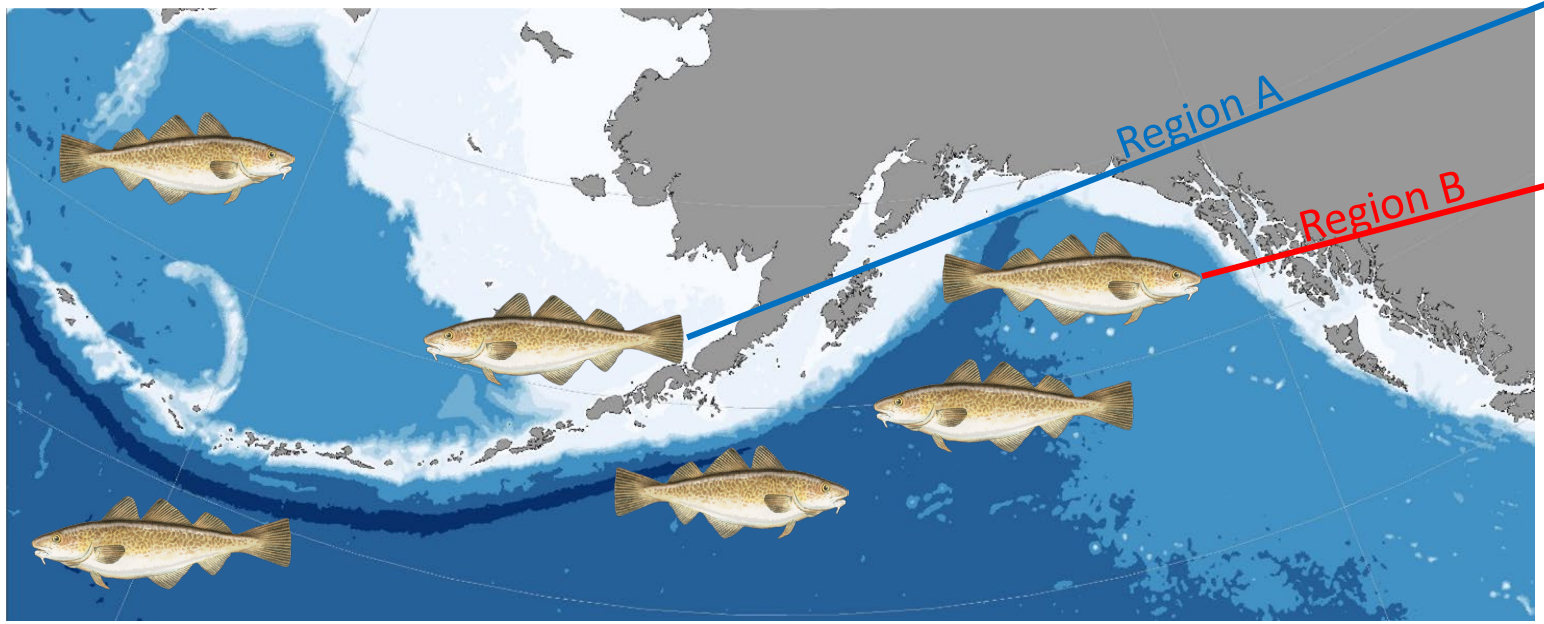
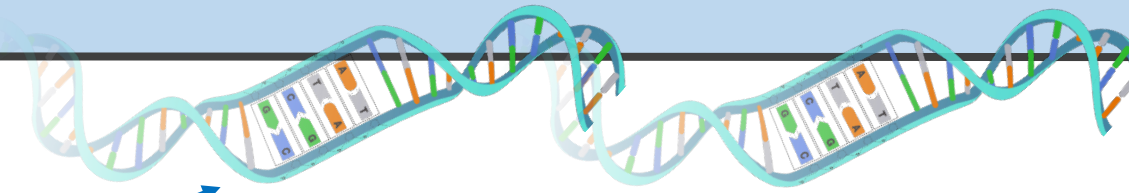
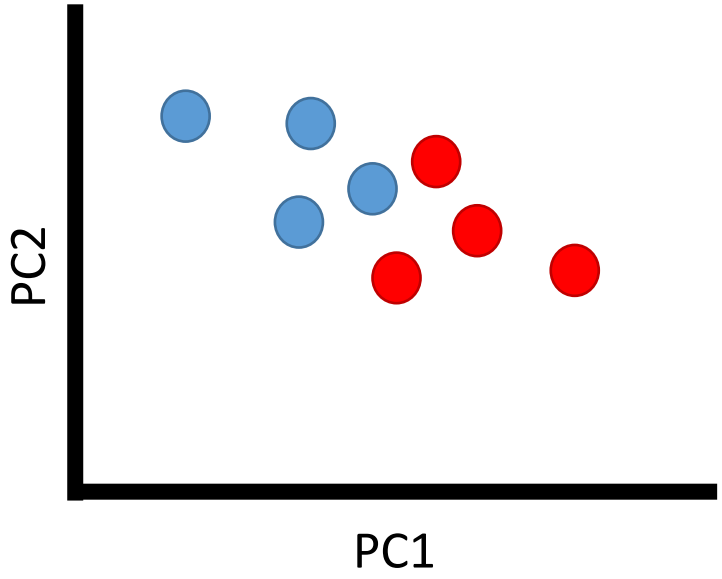


Some Genetic Overlap

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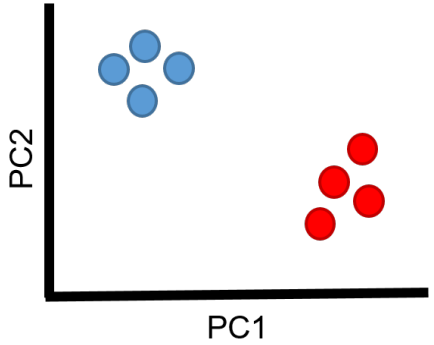

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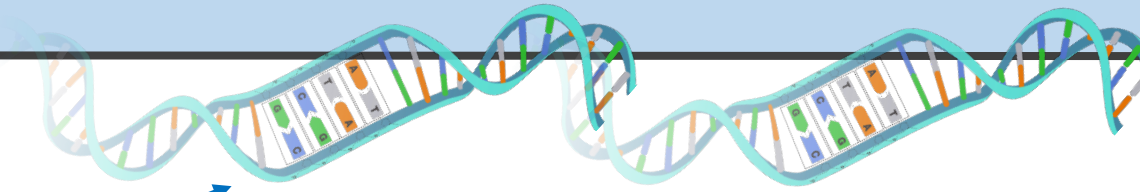

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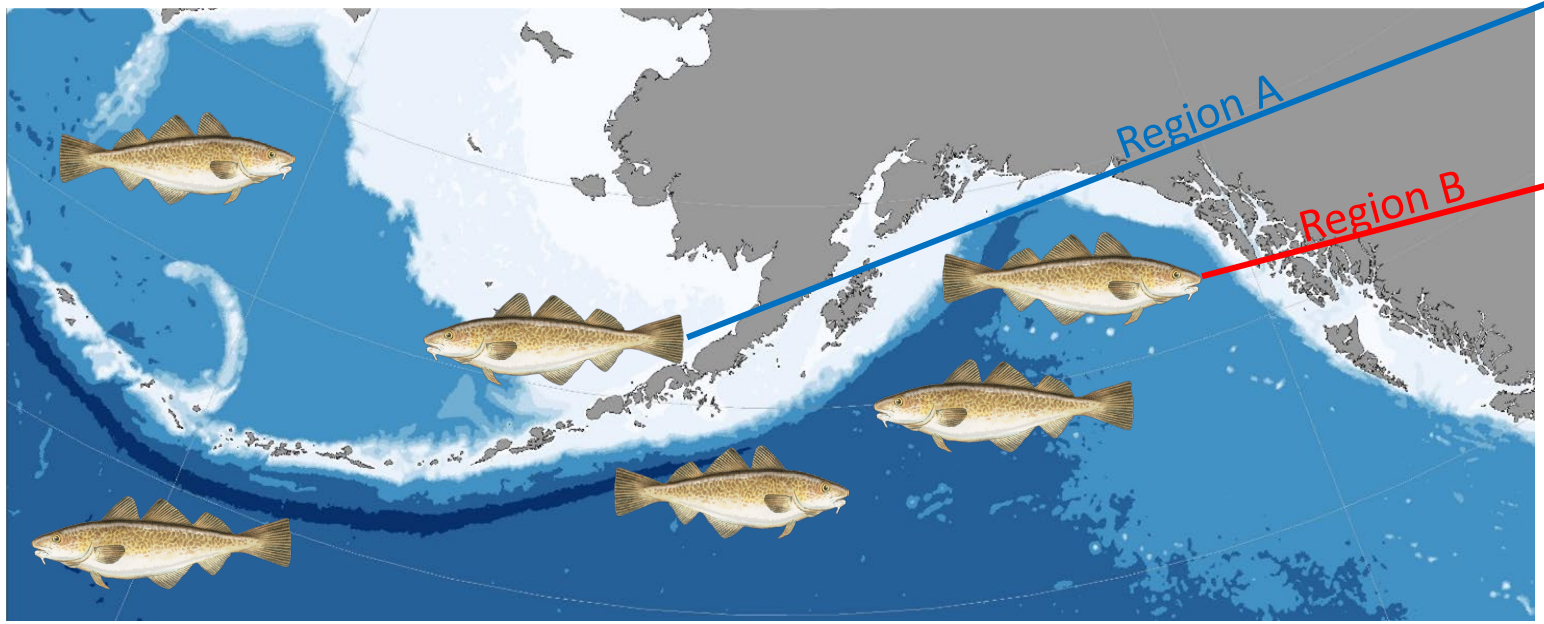
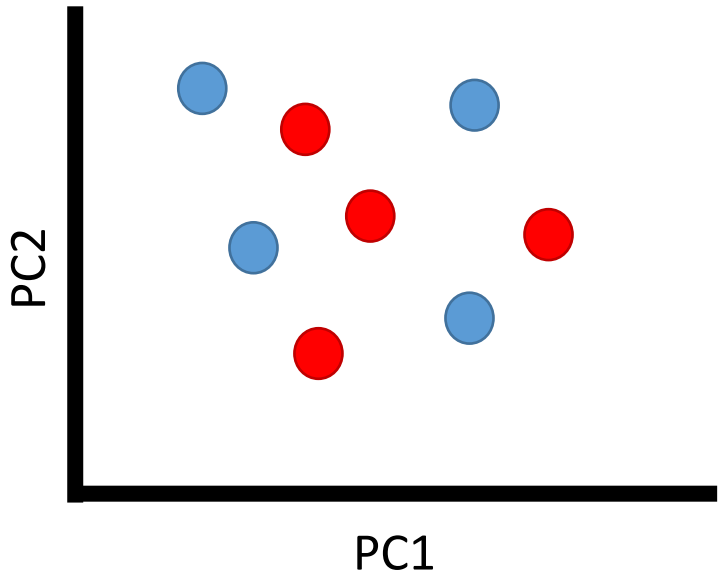



Fully Interbreeding Regions

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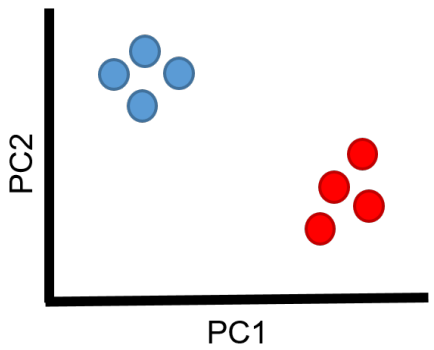


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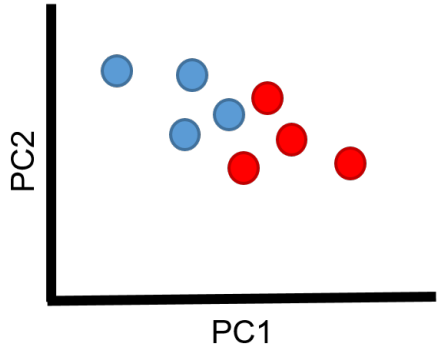

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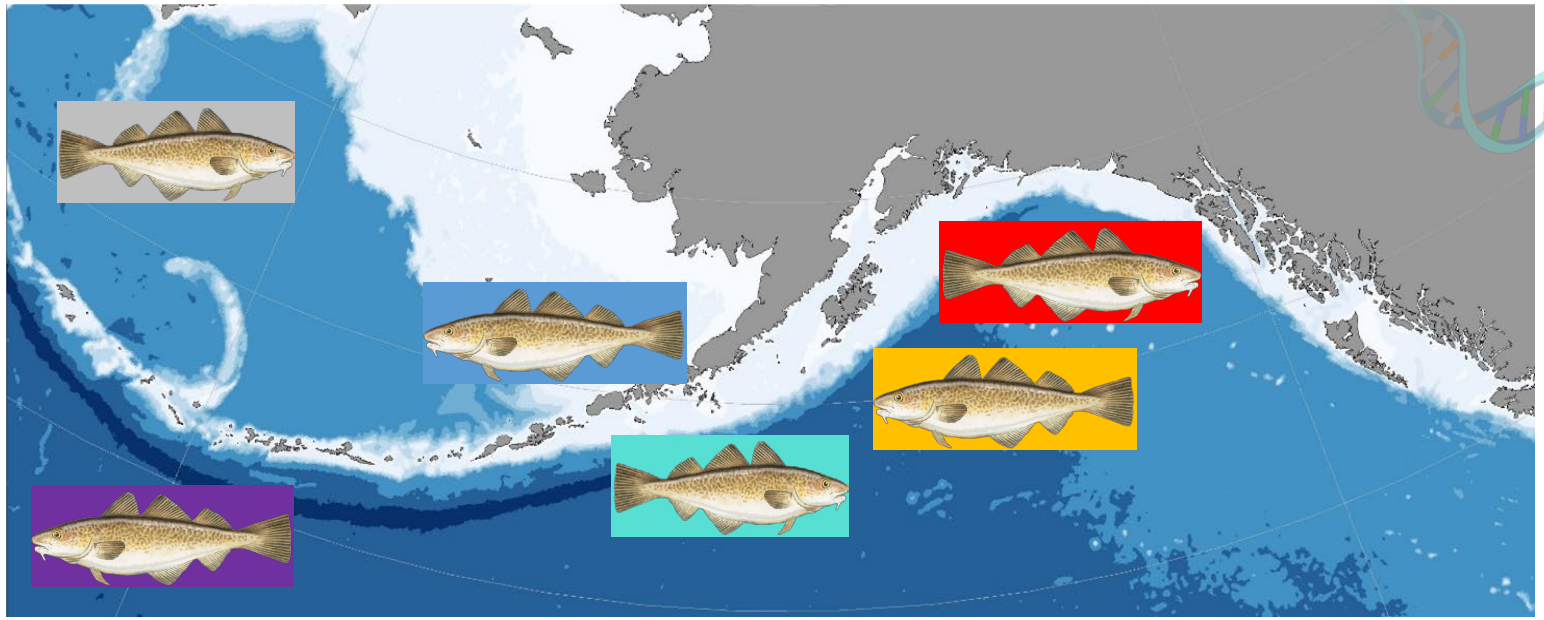
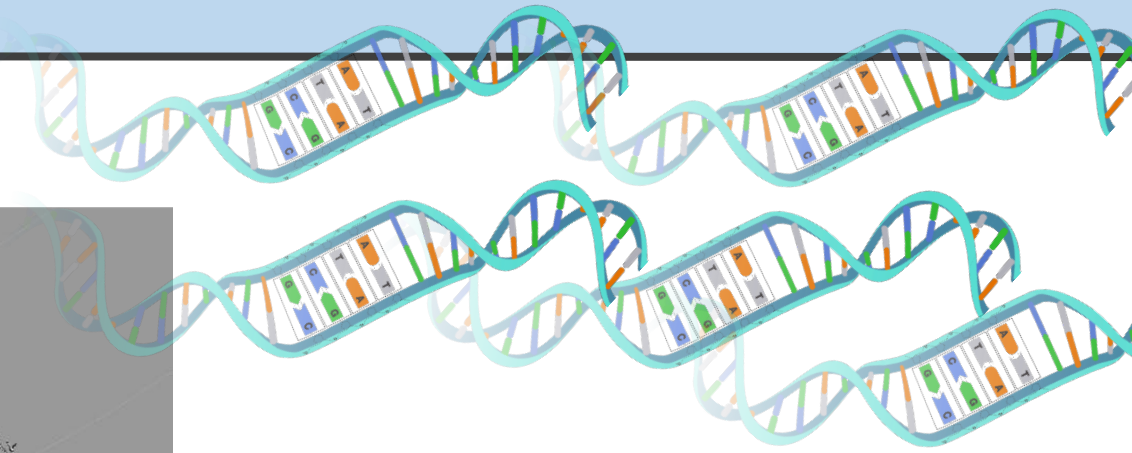
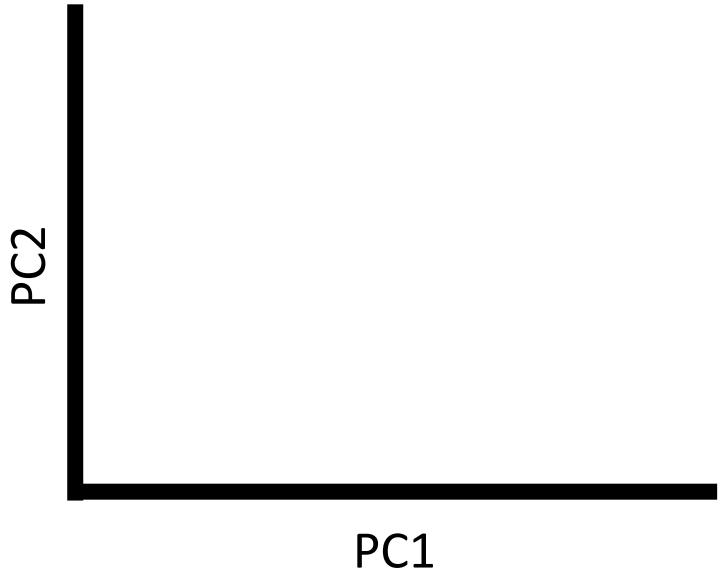




Many Regions

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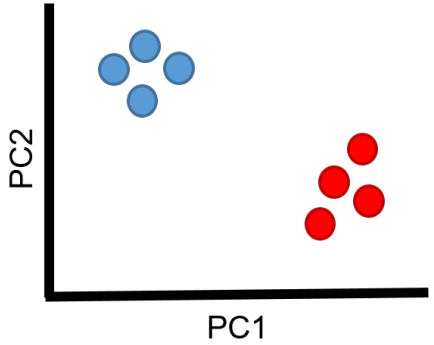


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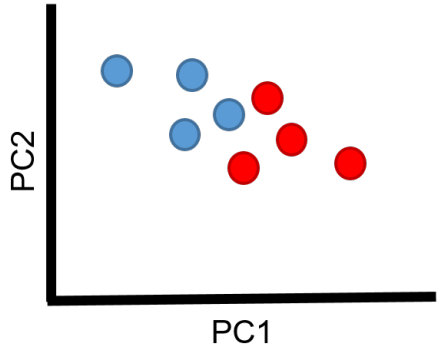


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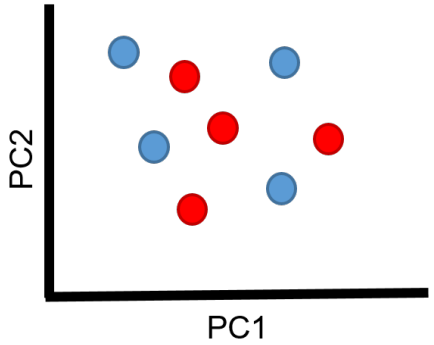

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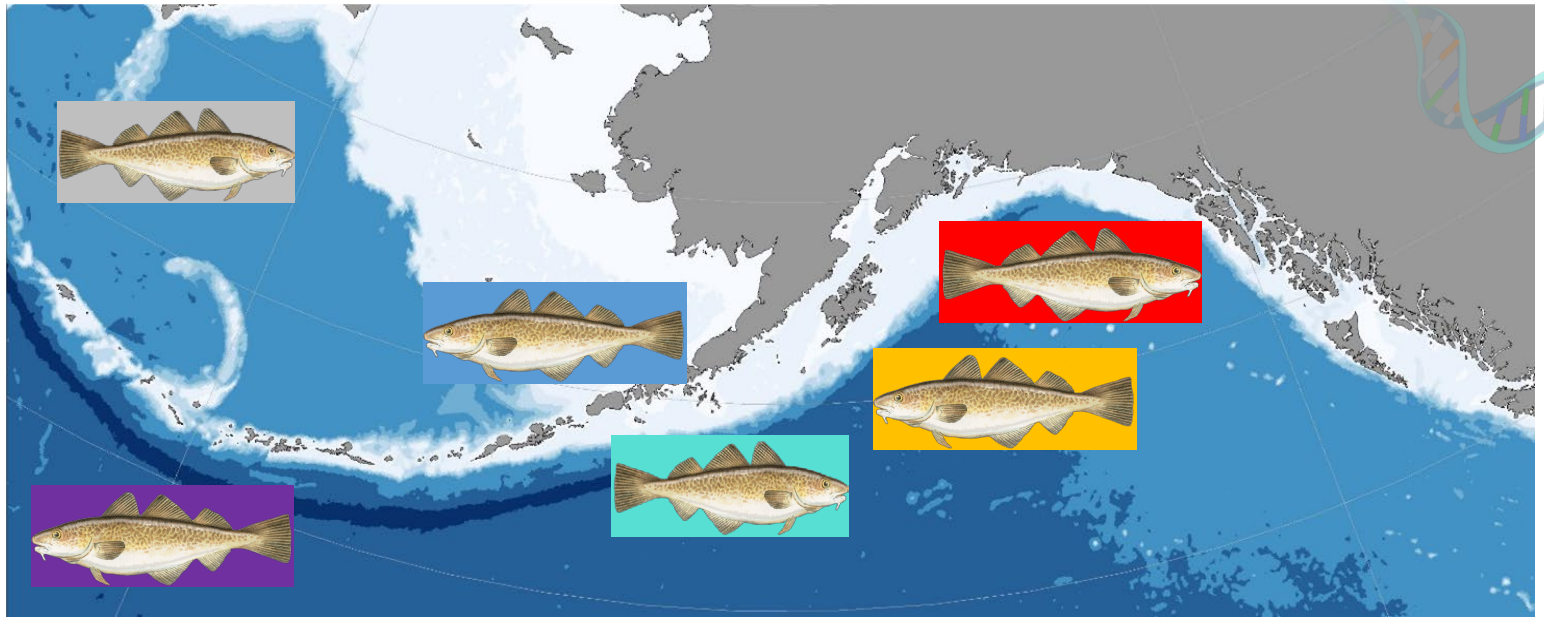

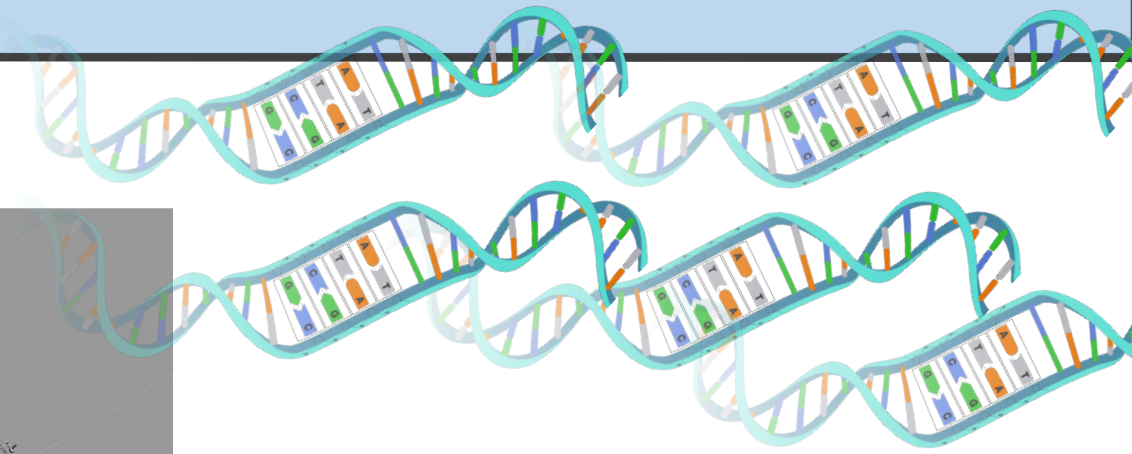

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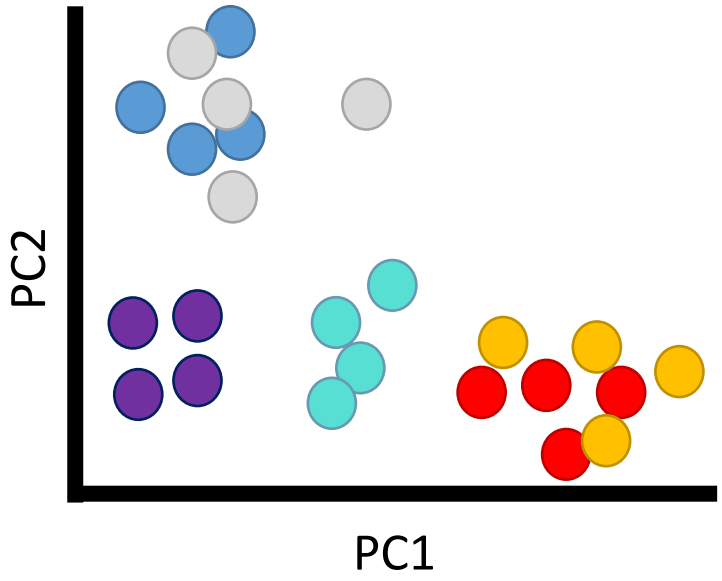


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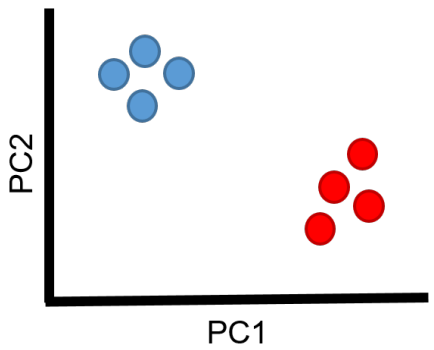


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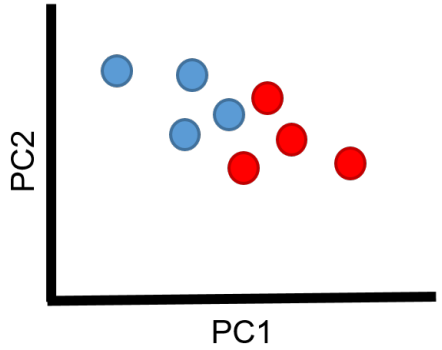


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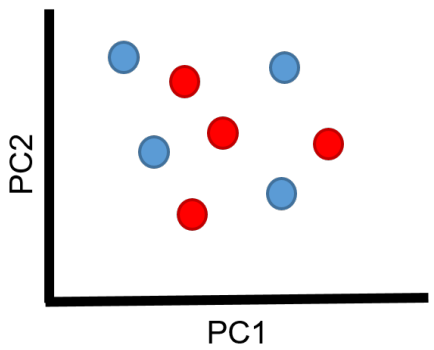
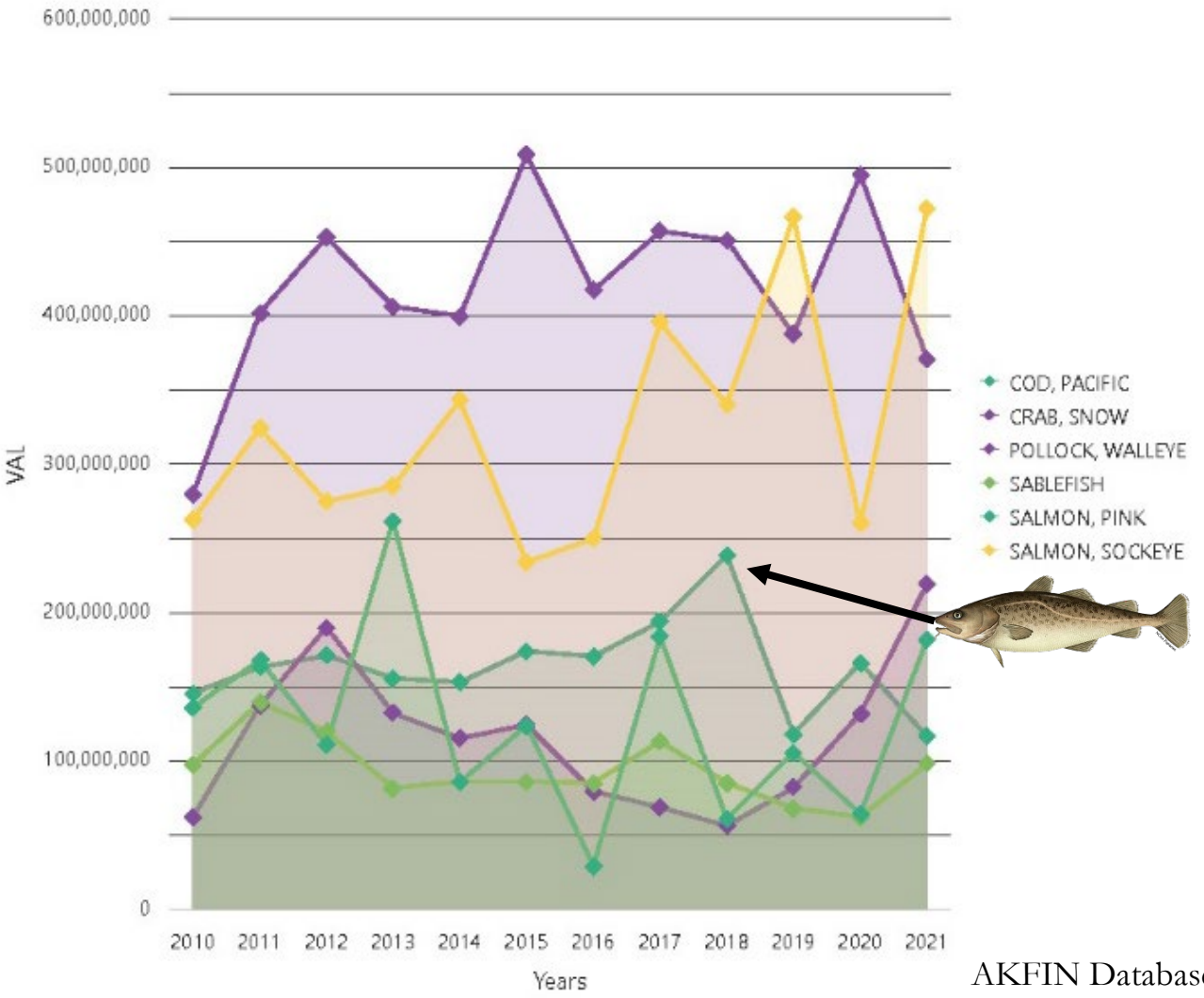


# Pacific cod

**One of the largest and most valuable groundfish fisheries in the Alaska.**

- Pacific cod worth $116 million in 2021




AKFIN Database

# Pacific cod Research Questions

**Is there genetic stock structure in Pacific cod?**

**Does the genetic stock structure match the management areas?**

# Pacific cod sampling

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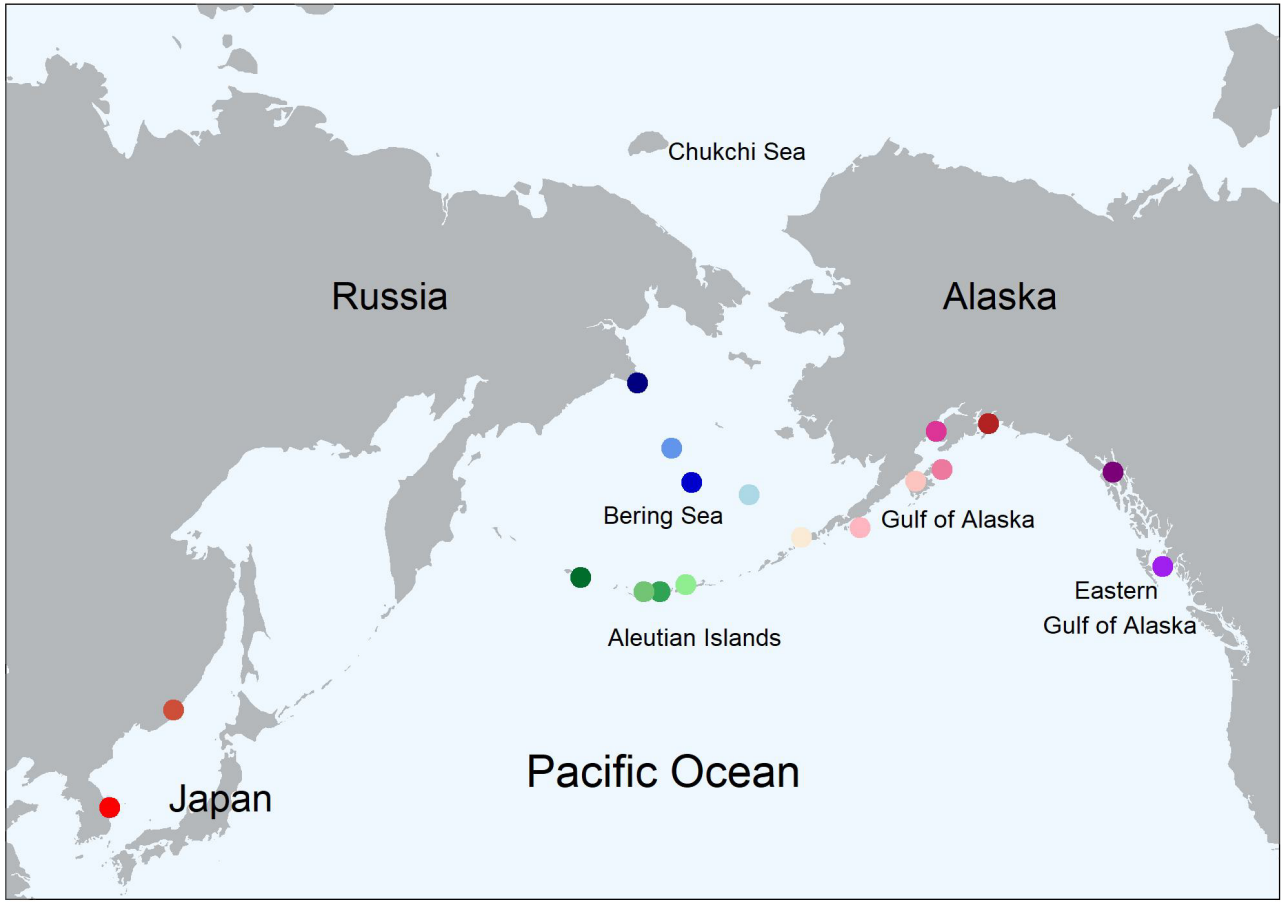
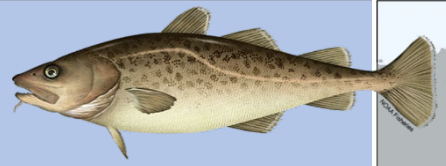
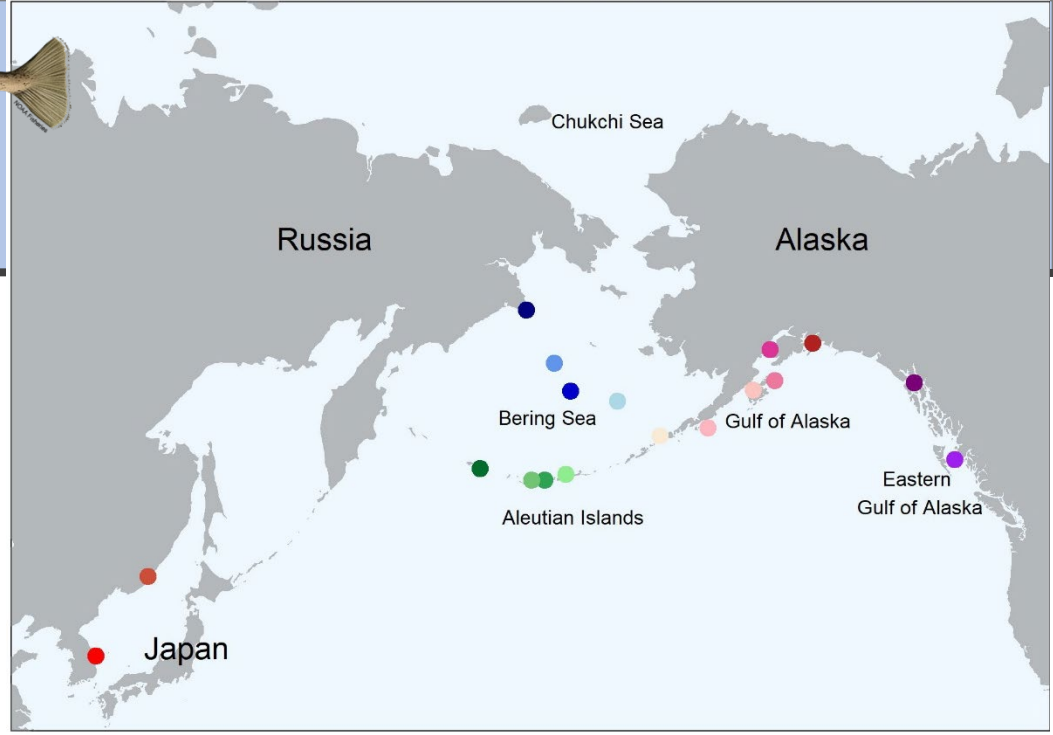


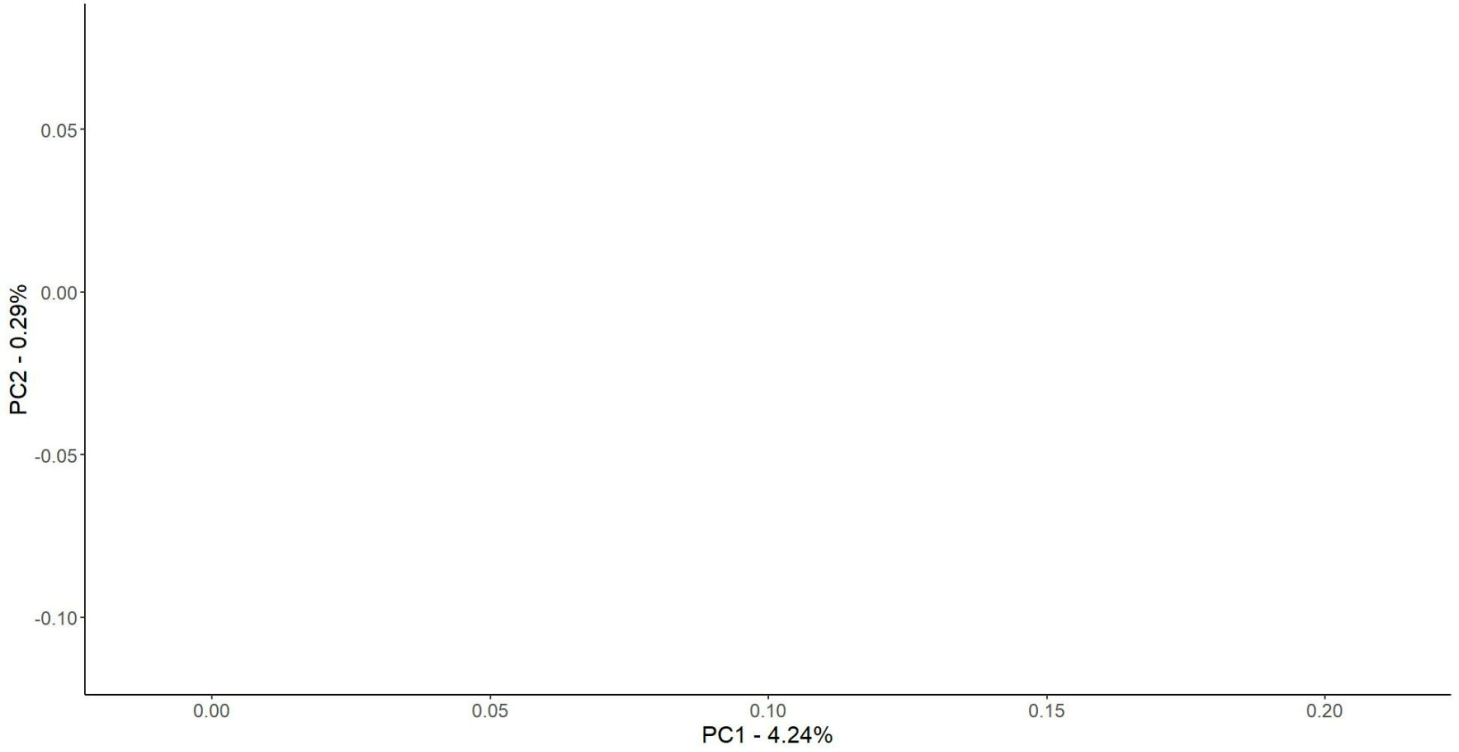
# Pacific cod population structure

# Low-coverage whole genome sequencing (lcWGS)



~3 million markers from throughout the genome (aligned to ***new*** Pacific cod genome!)




Japan
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Russia
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Pervenets Canyon
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region
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eGOA
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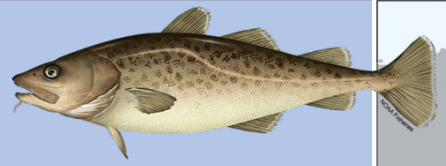

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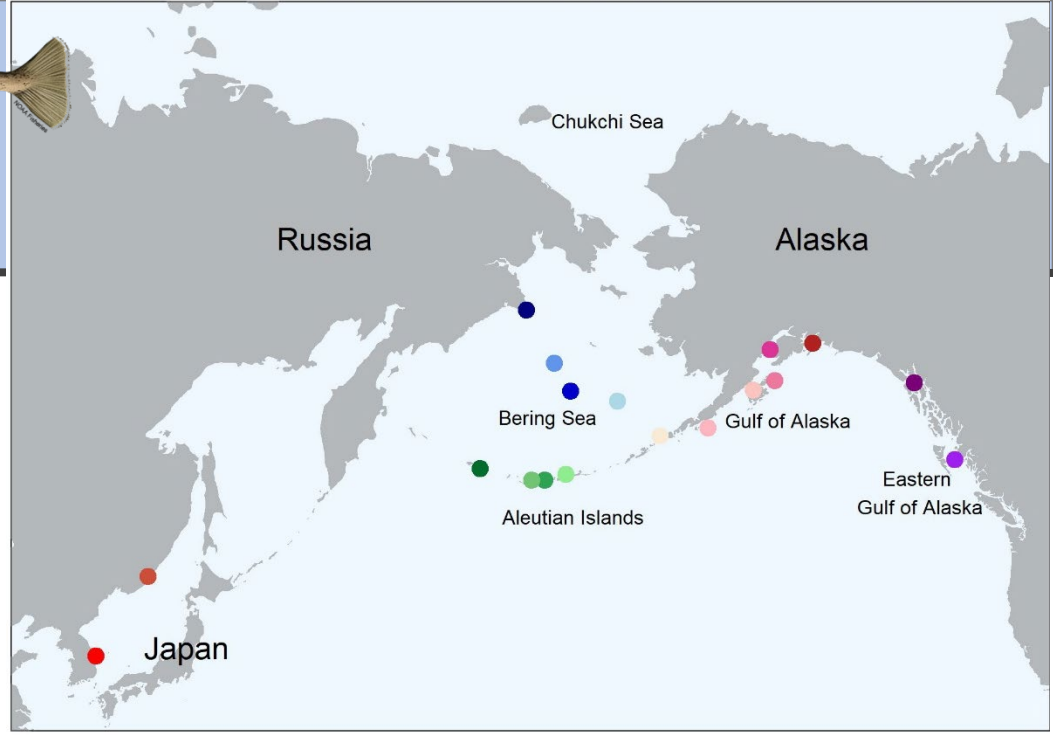


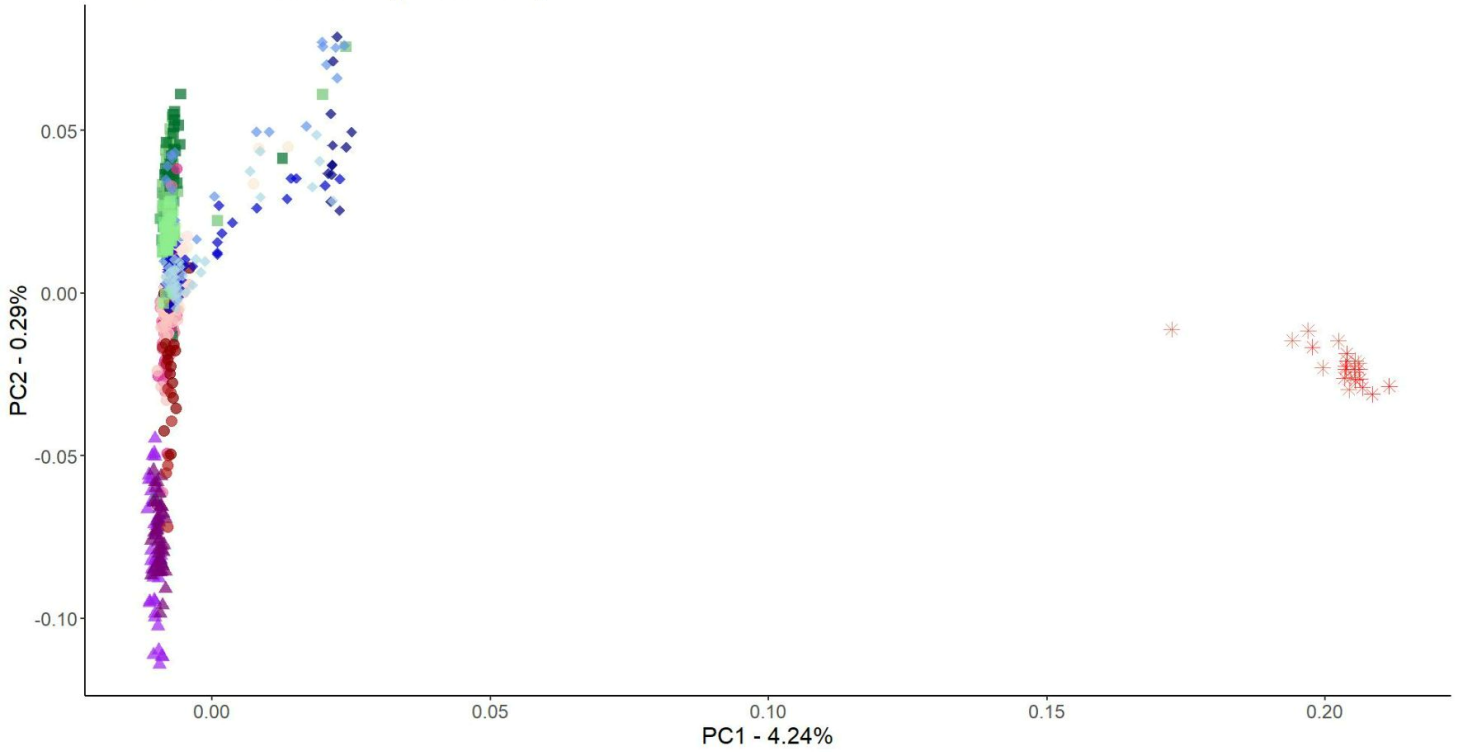


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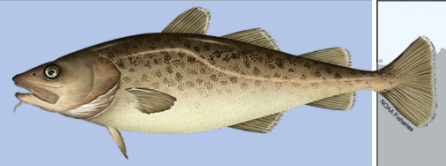

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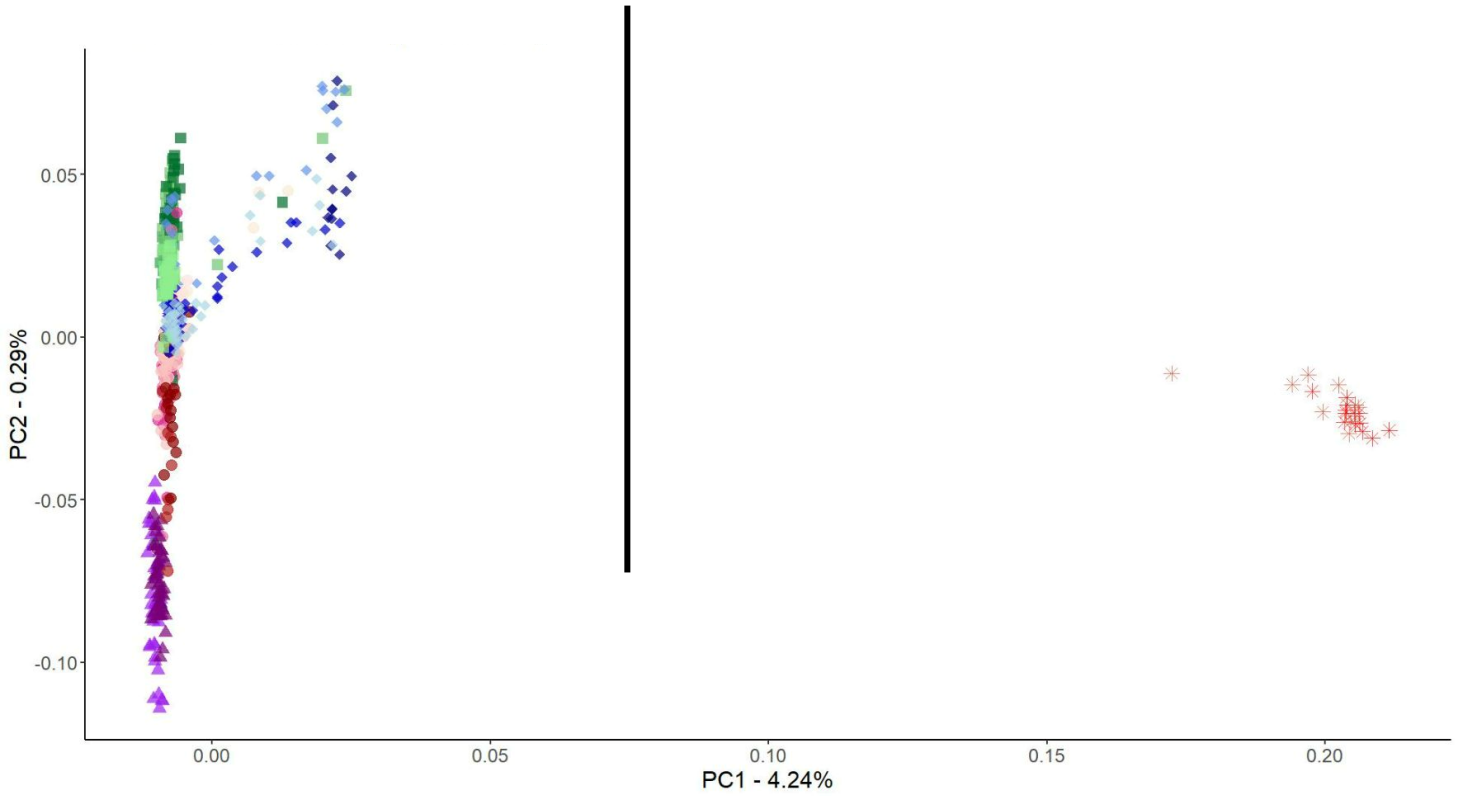
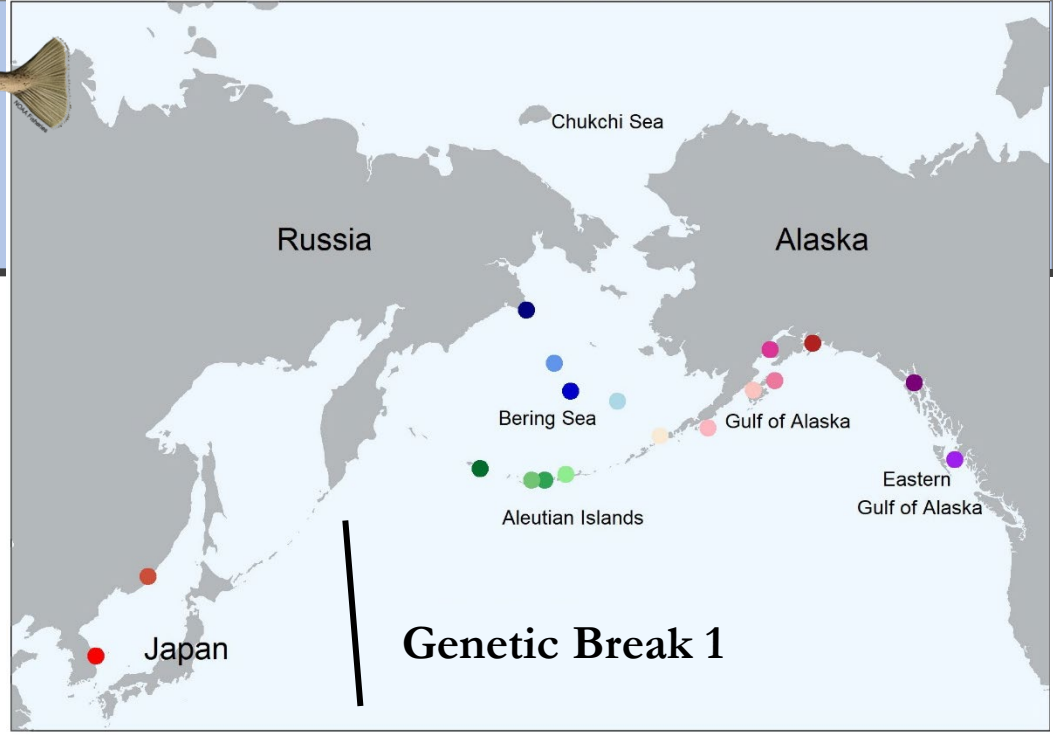
**Major genetic break between the Eastern and Western Pacific.**

**Genetic Break 1**

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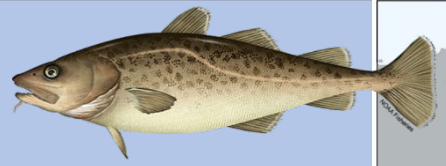

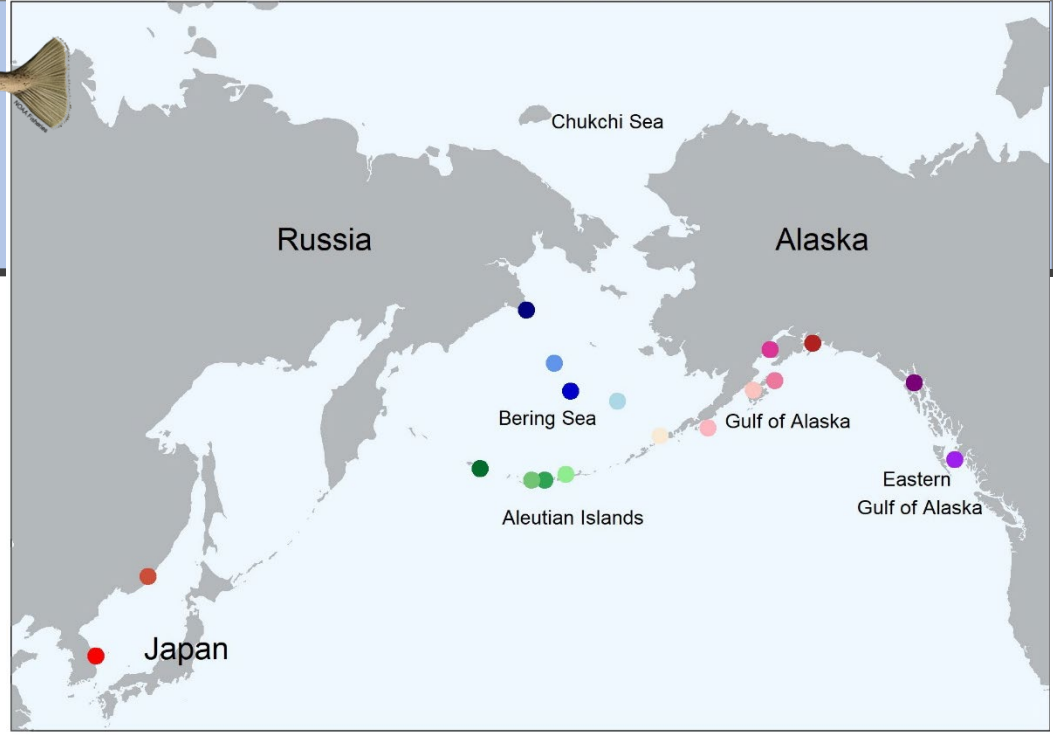


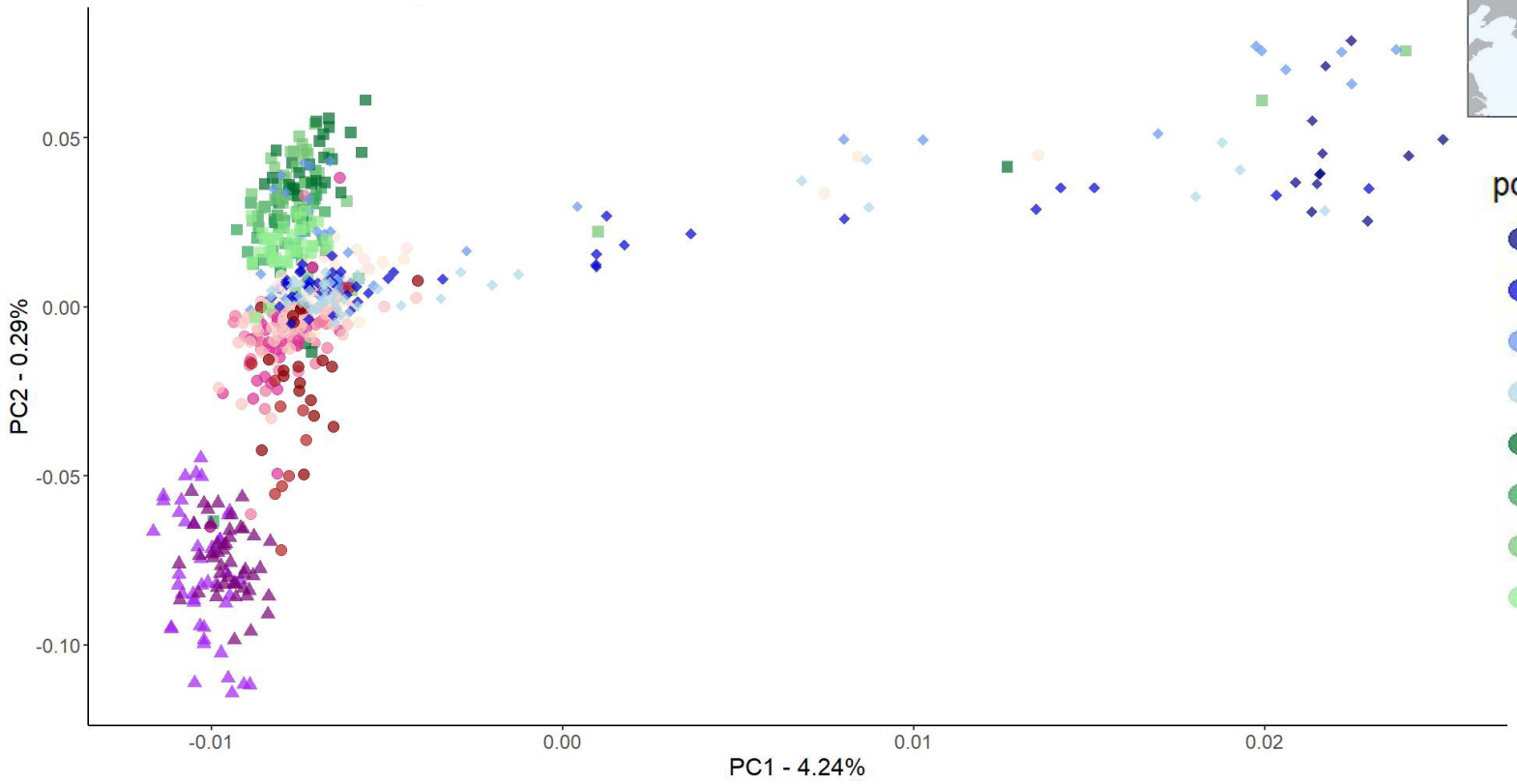


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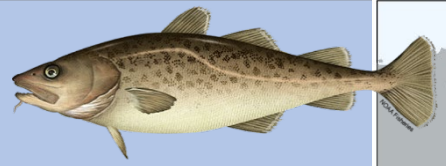
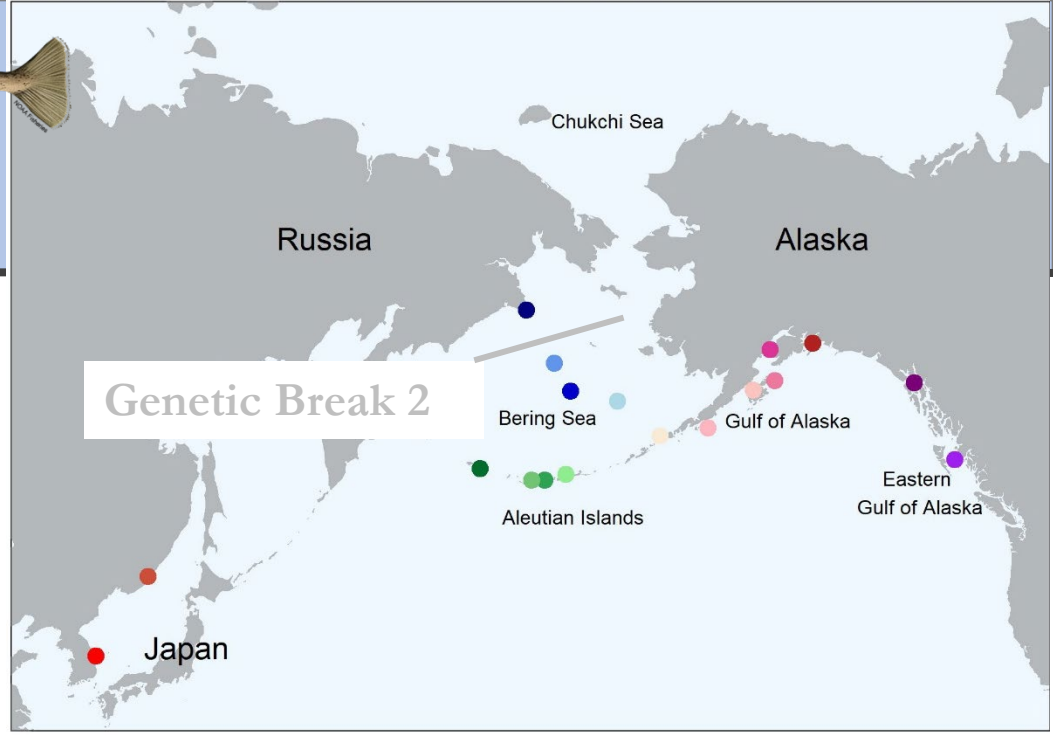
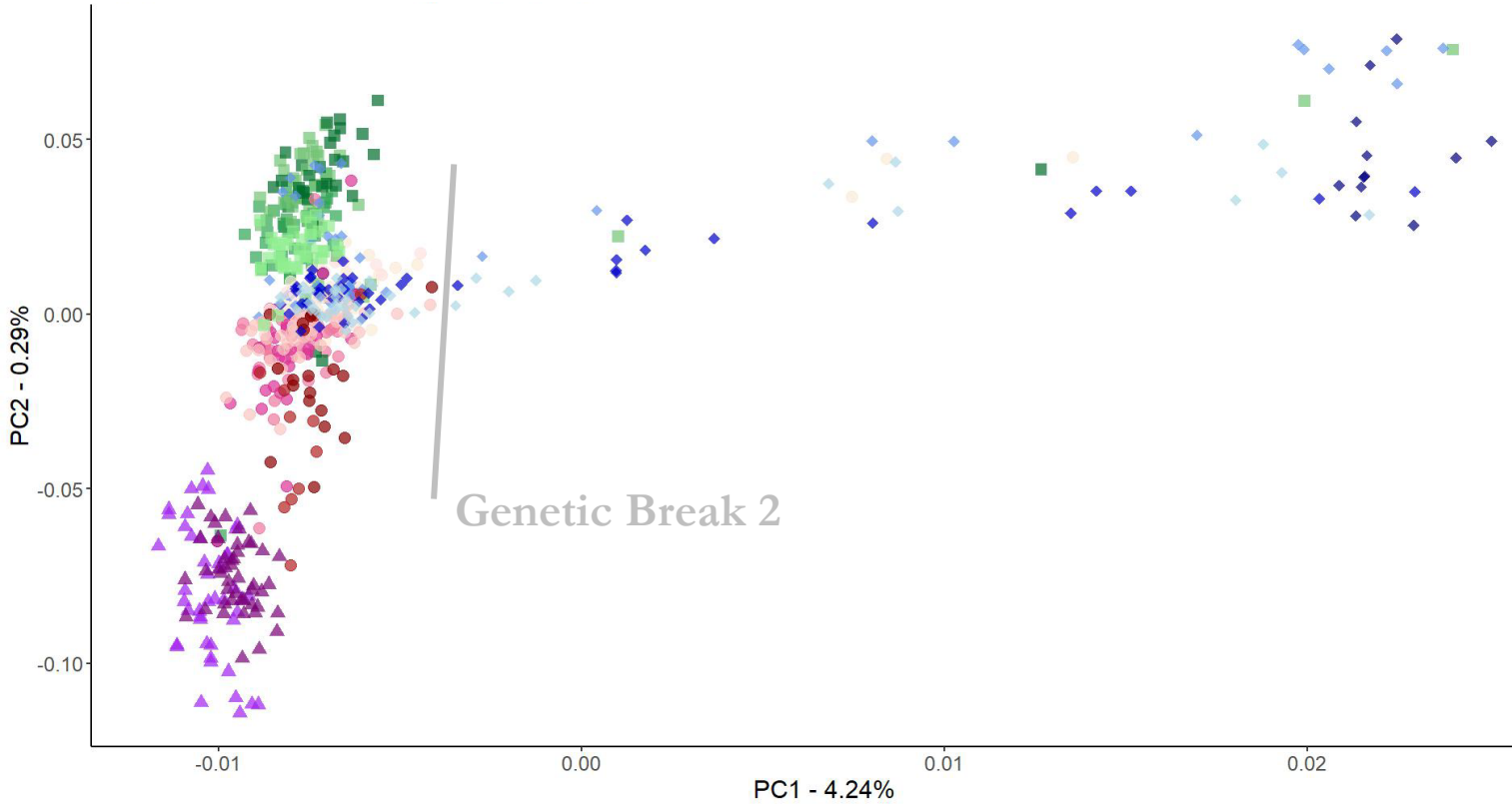


**A second genetic break between the Northern Bering Sea and Eastern Bering Sea**

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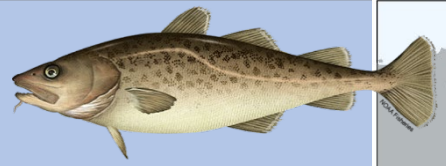

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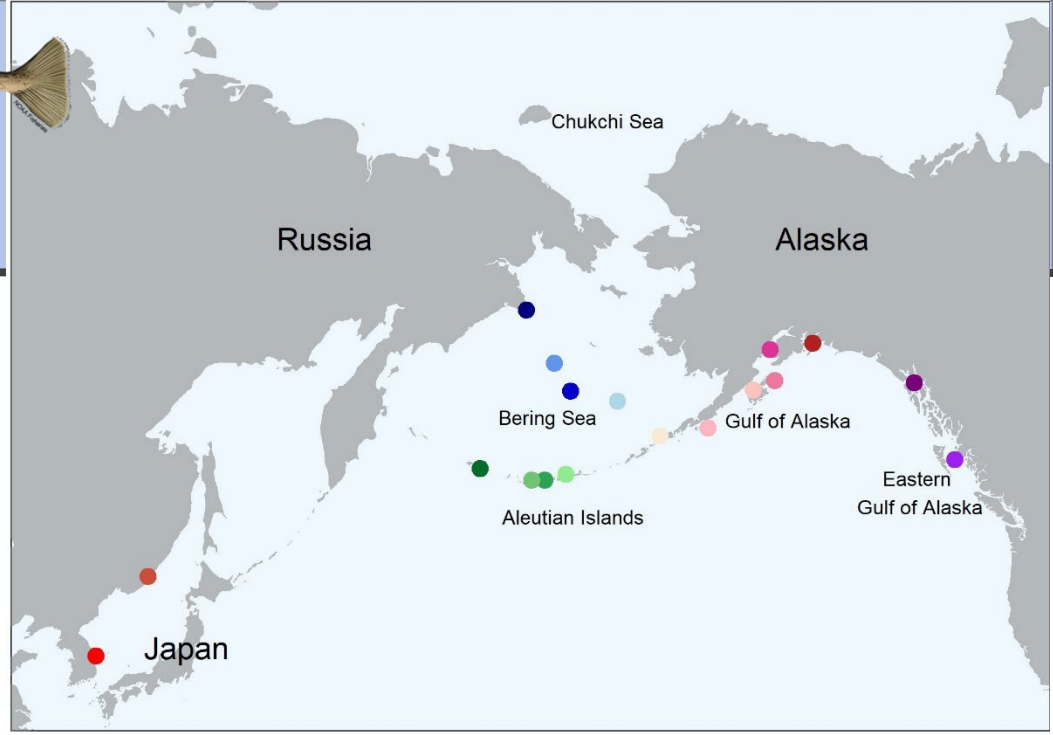


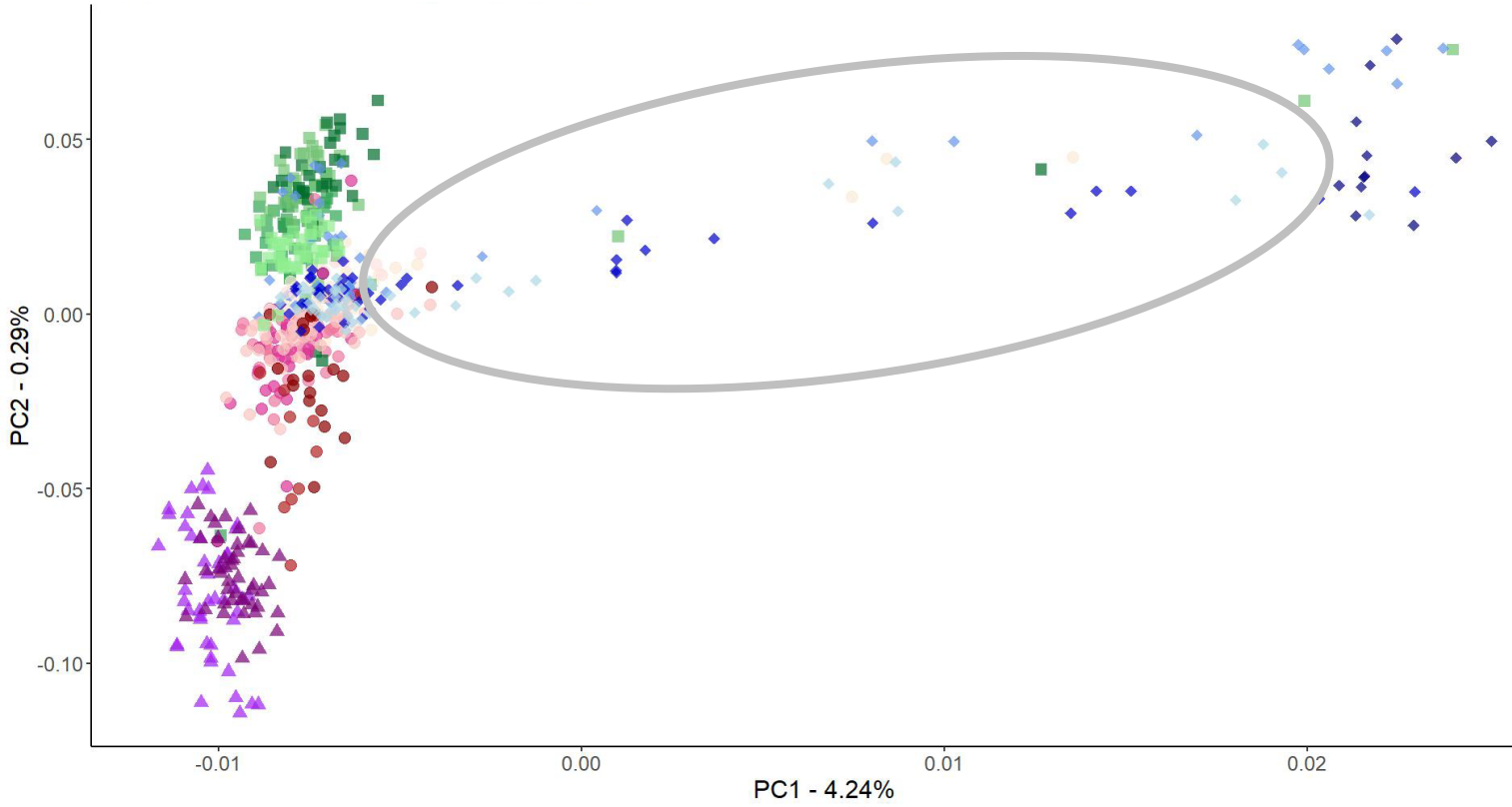


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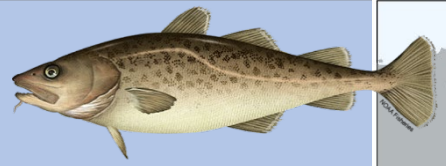

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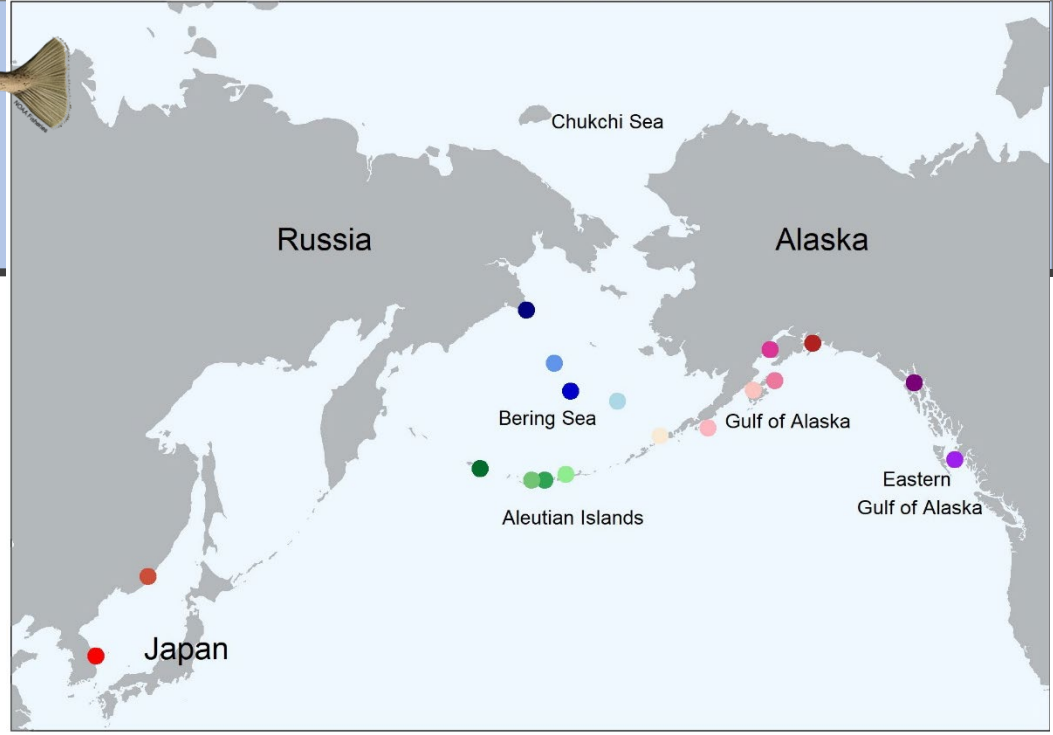


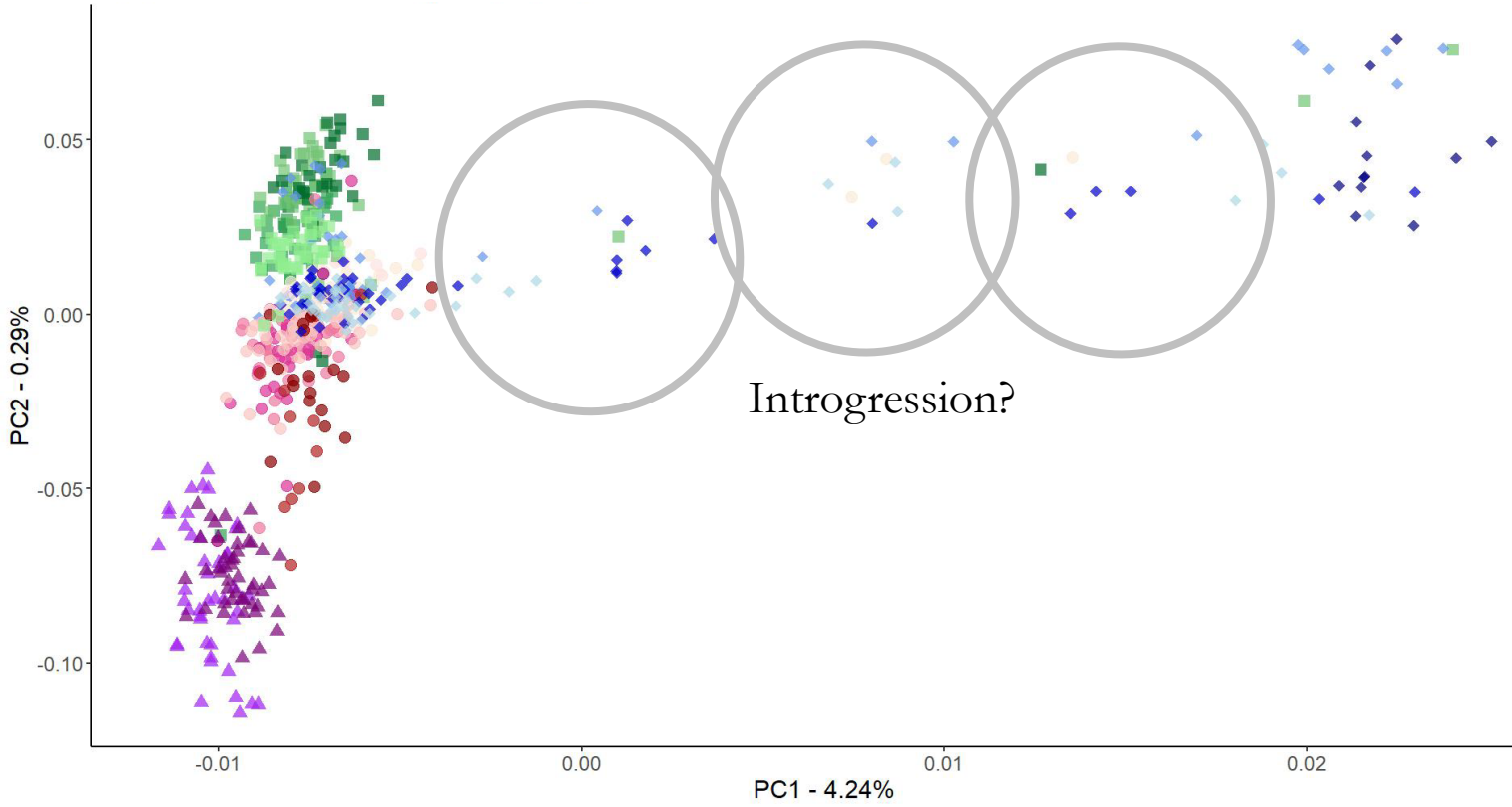


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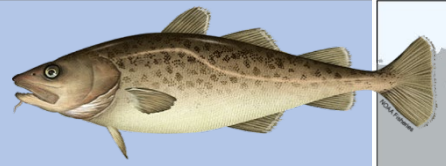
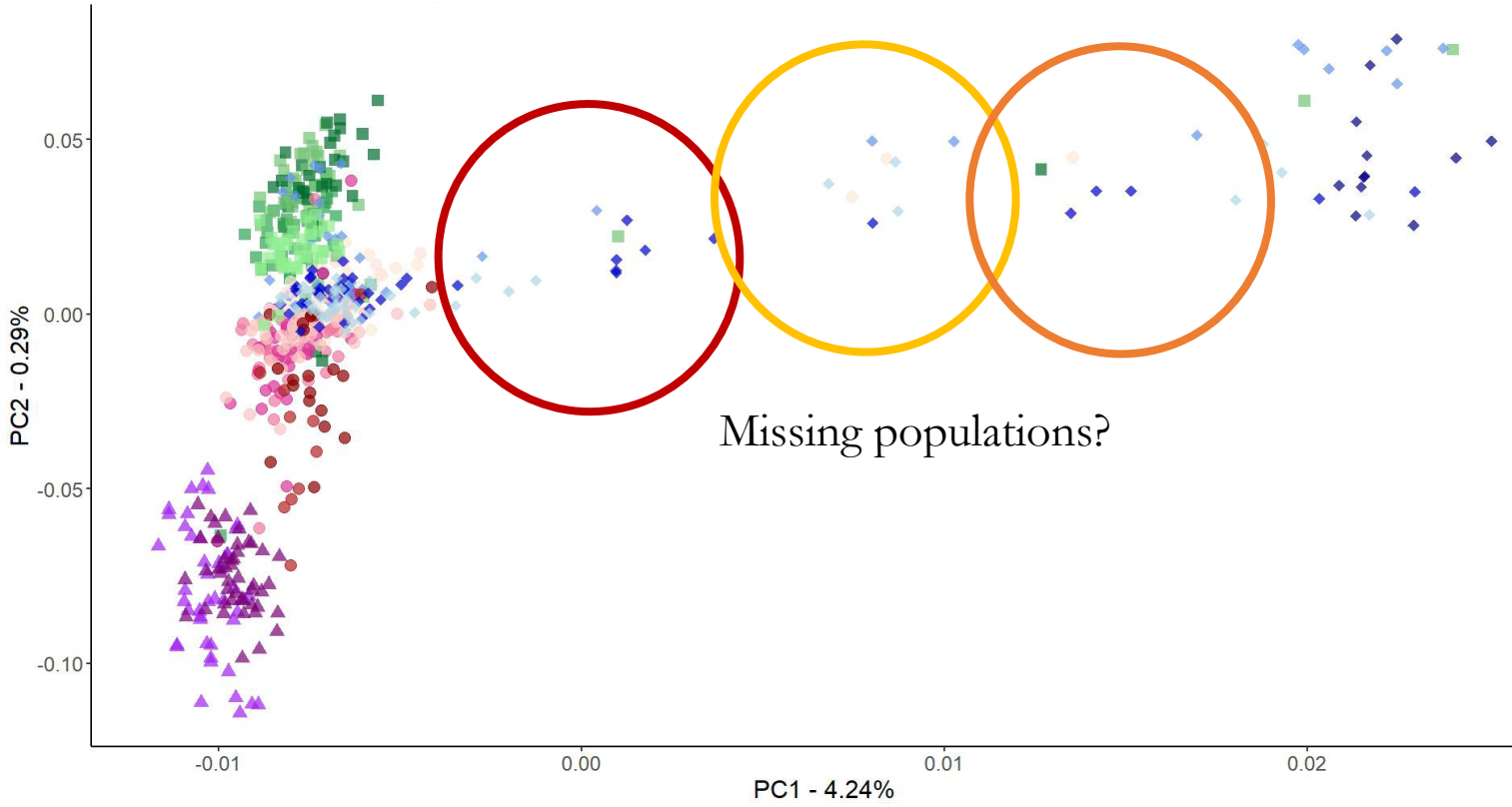
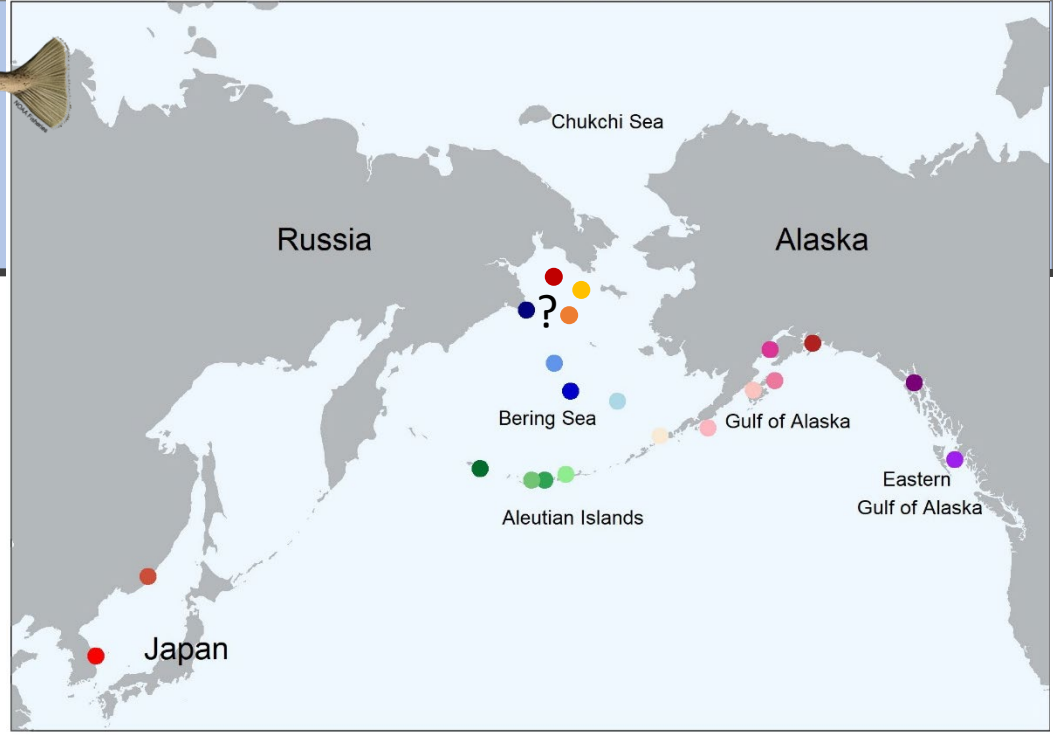
# Low-coverage whole genome sequencing (lcWGS)



**A second genetic break between the Northern Bering Sea and Eastern Bering Sea**

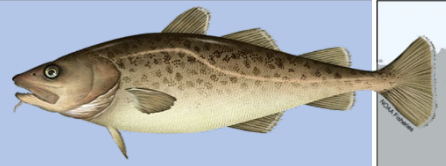


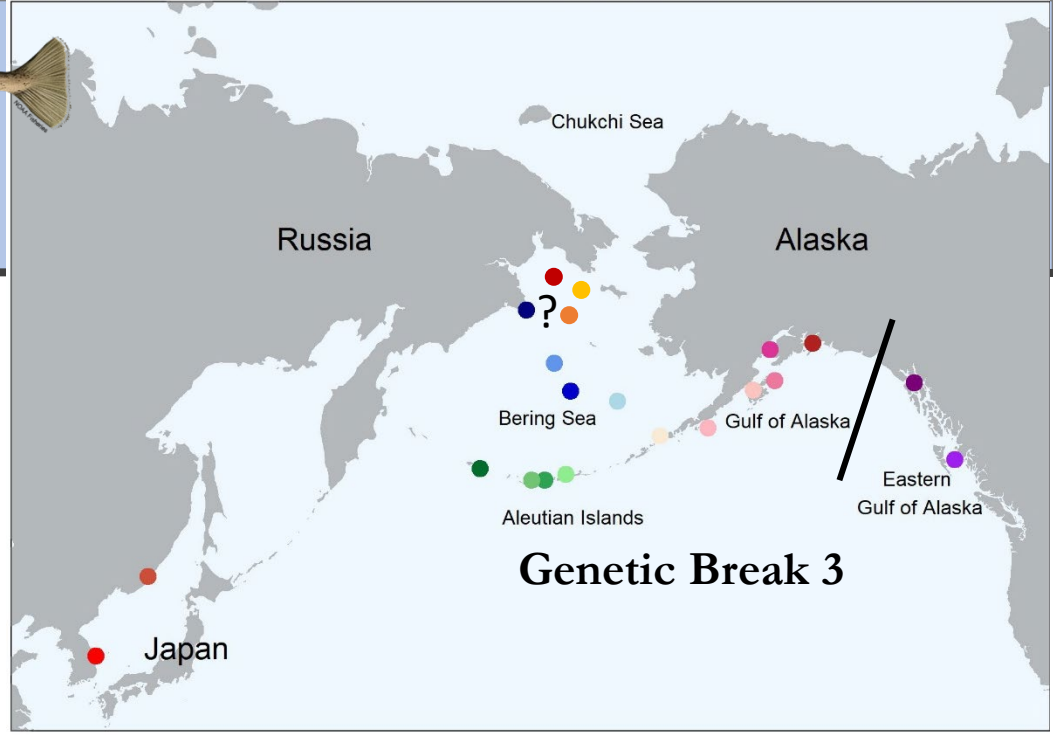

pop
- Russia
- Zhemchug Canyon
- Pervenets Canyon
- Pribilof
- Near Islands
- Tanaga Island
- Amchitka Pass
- Adak
- Unimak
- Shumagins
- West Kodiak
- Kodiak
- Cook Inlet
- PWS
- Lynn Canal
- Hecate Strait

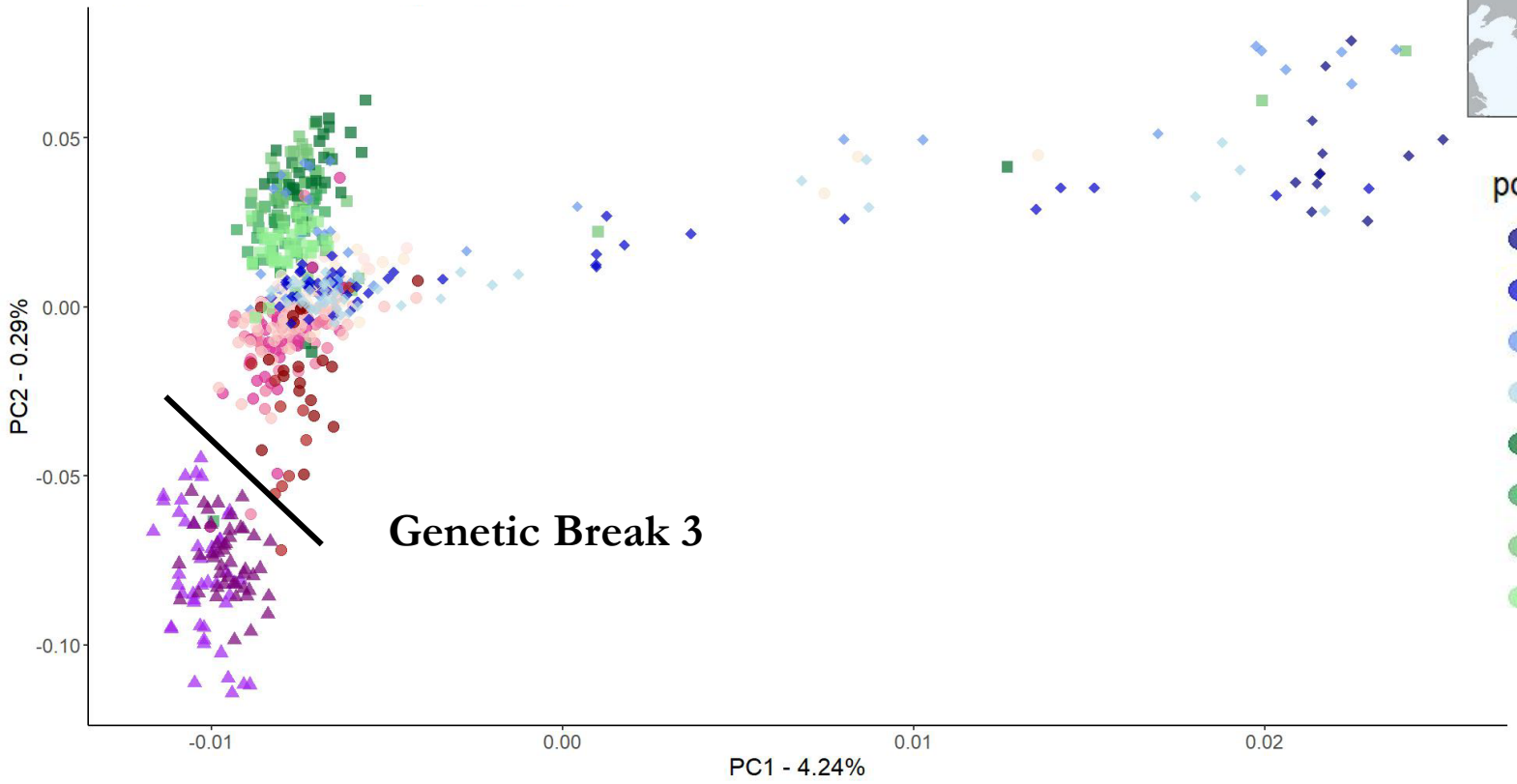
region
- Aleutians
- Bering Sea
- eGOA
- wGOA

# Low-coverage whole genome sequencing (lcWGS)

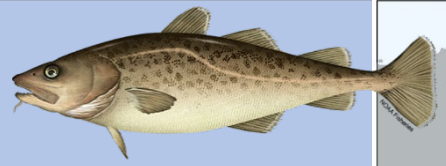


**A third genetic break between the Eastern GOA and Western GOA.**

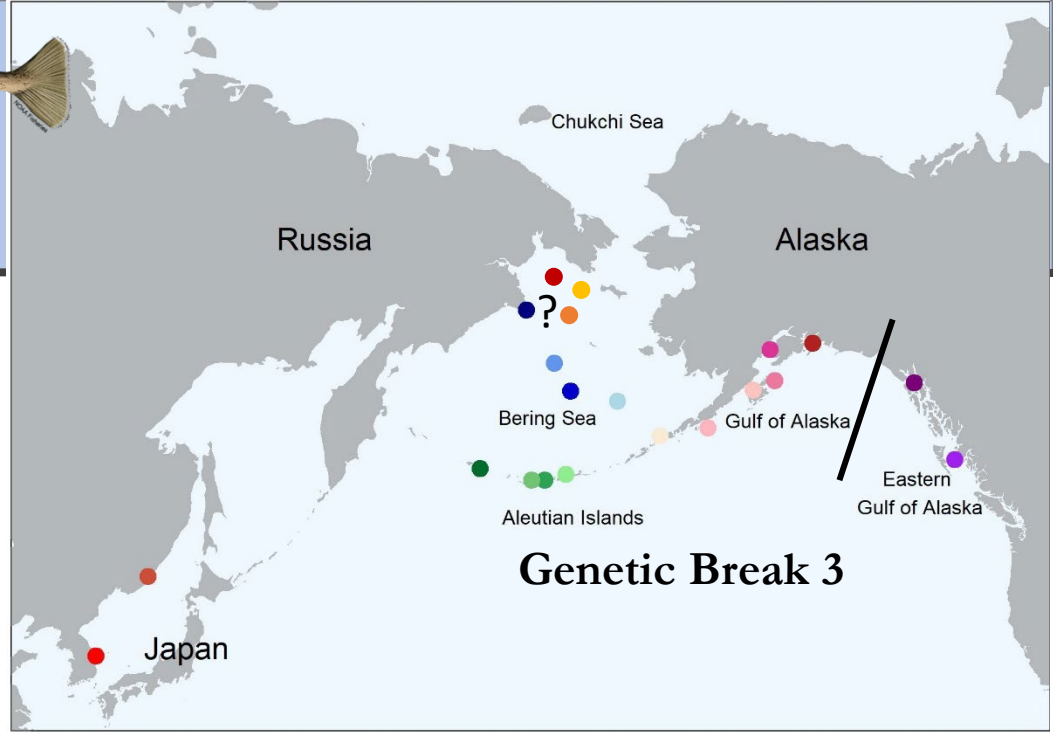


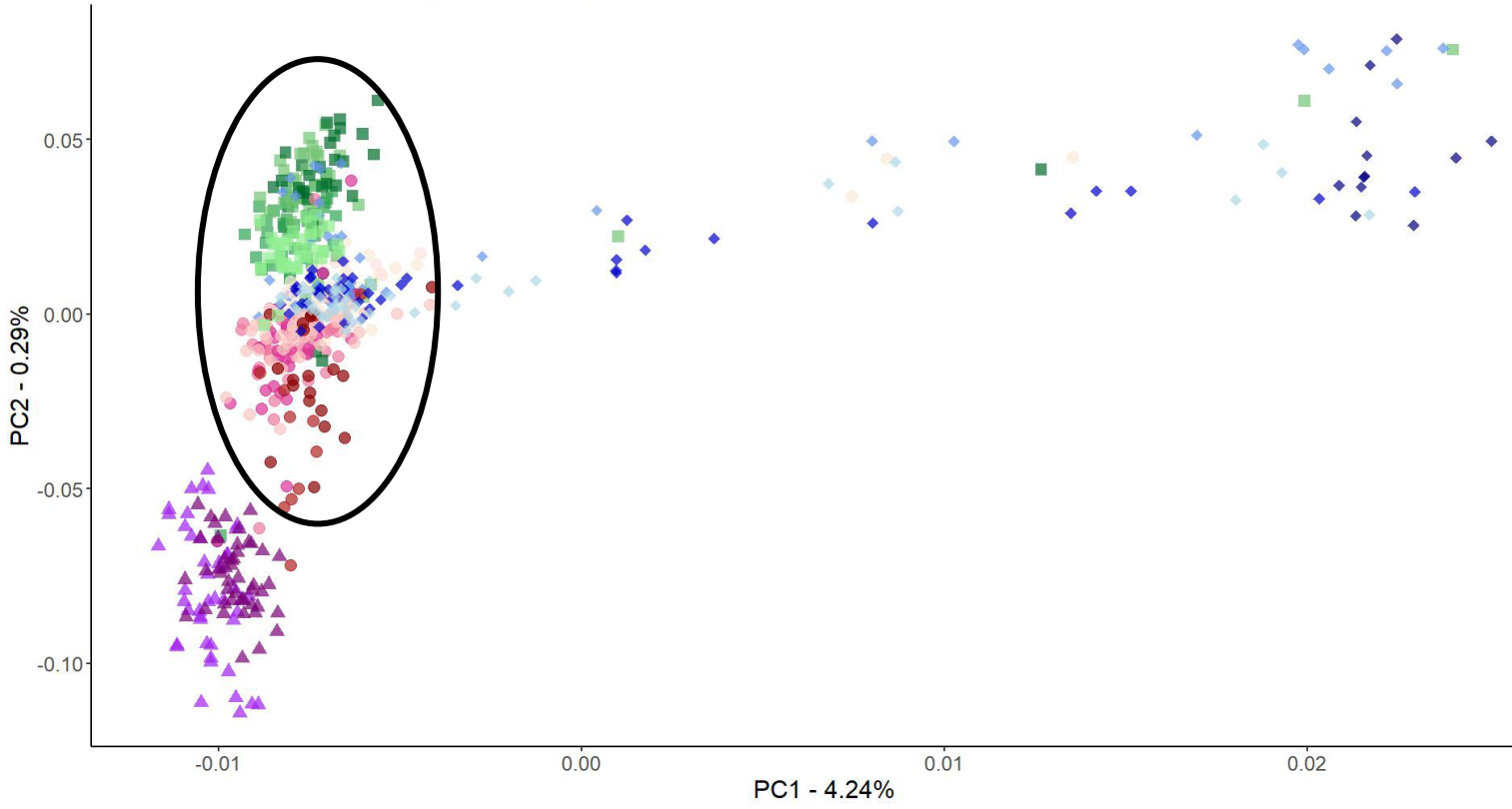




# Low-coverage whole genome sequencing (lcWGS)



**The rest being isolation by distance.**

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region
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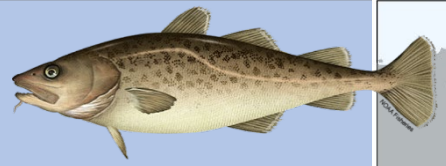
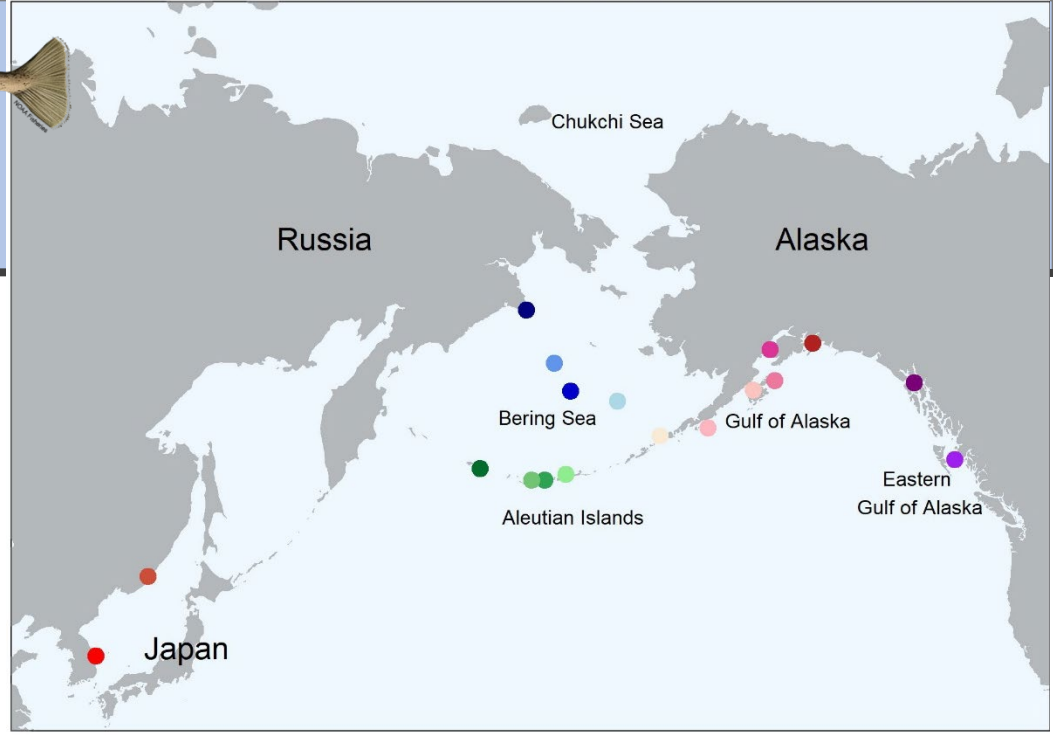
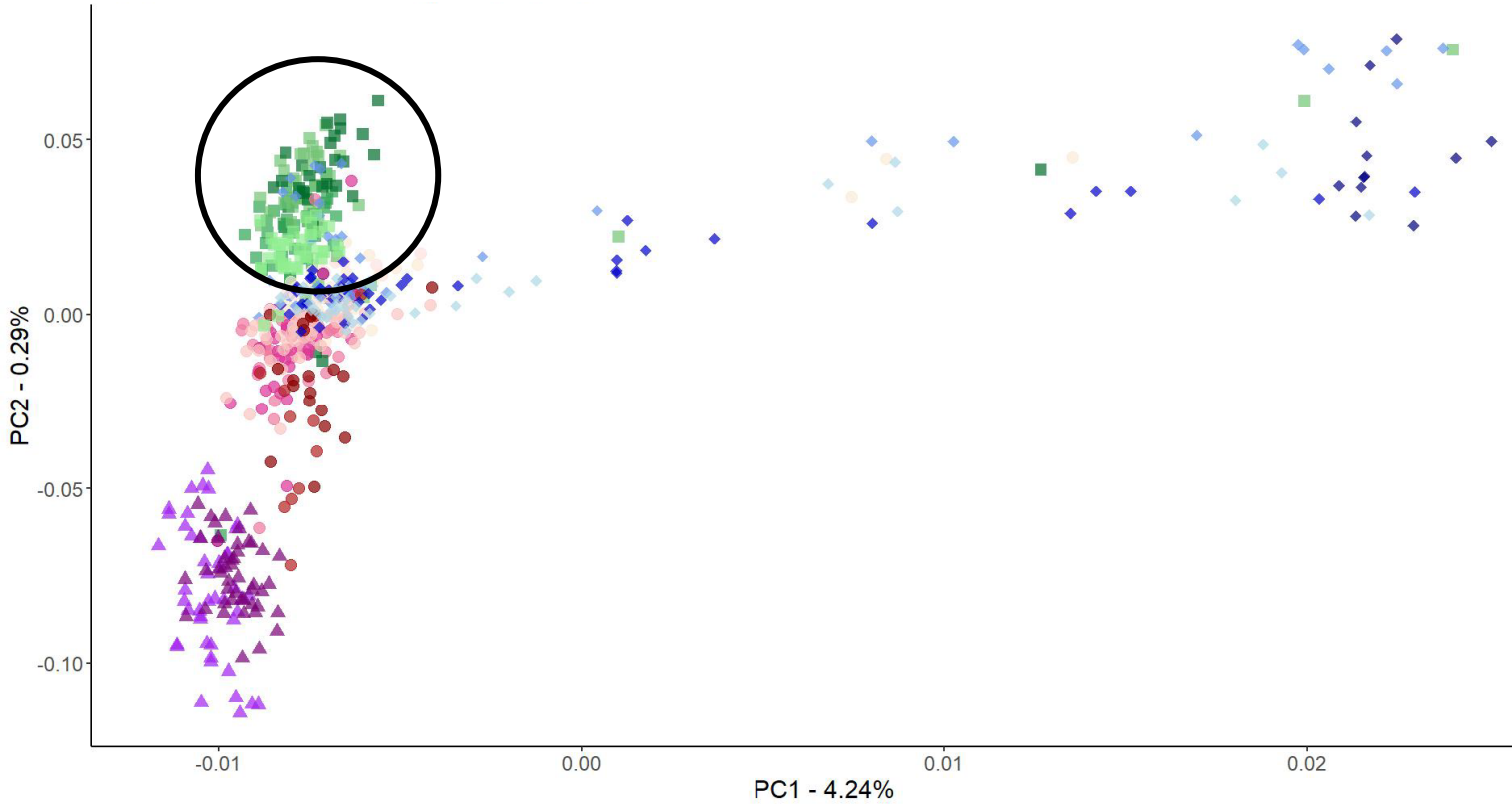
- Bering Sea
- eGOA
- wGOA

# Low-coverage whole genome sequencing (lcWGS)



**Genetic Break due to adaptive differences in the Aleutian Islands (happy to talk with anyone about this after).**

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region
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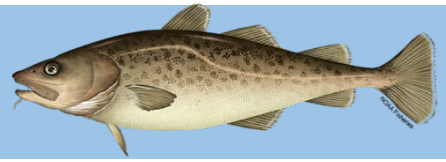
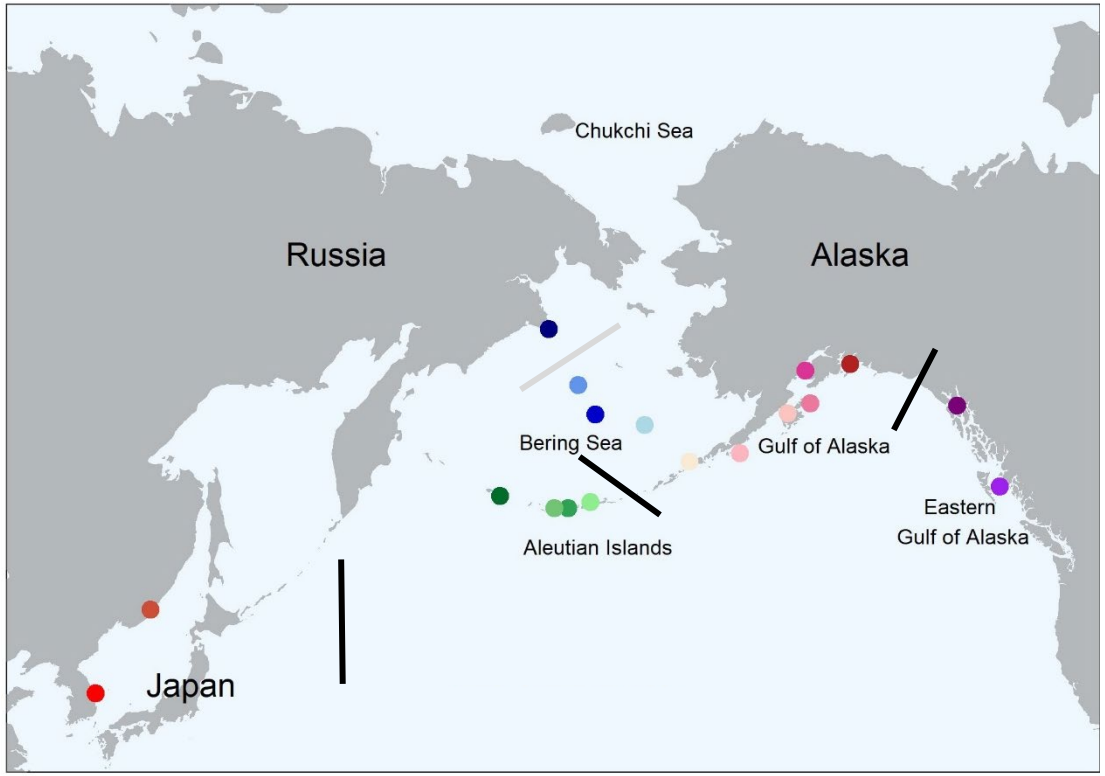
# Conclusions



## Pacific cod




### Genetic Breaks

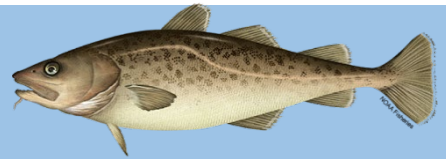
1. Eastern and Western Pacific

2. Northern Bering Sea (but messy)
Mixing with EBS

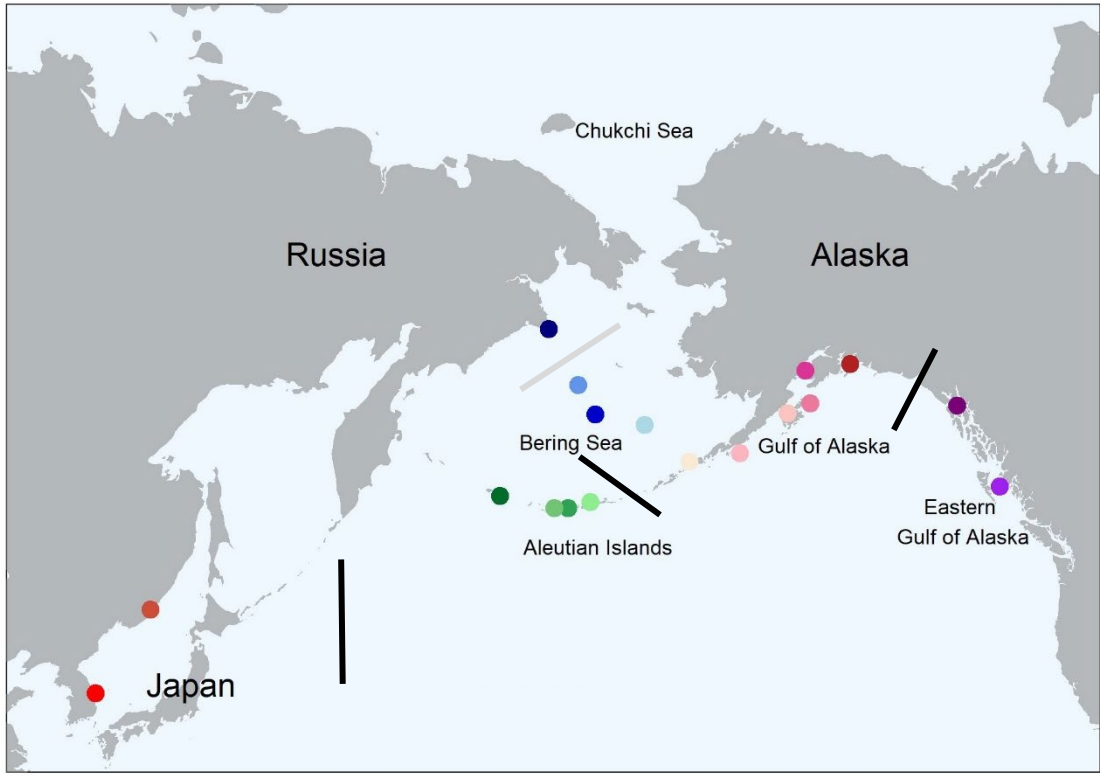
3. Aleutian Islands
Adaptive differences

4. Eastern GOA from Western GOA

# Conclusions



## Pacific cod




### Genetic Breaks

1. Eastern and Western Pacific

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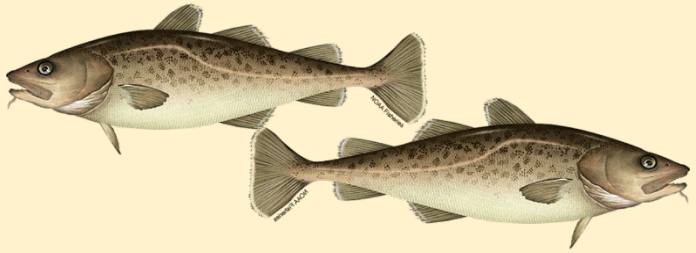
Mixing with EBS

3. Aleutian Islands
Adaptive differences

4. Eastern GOA from Western GOA

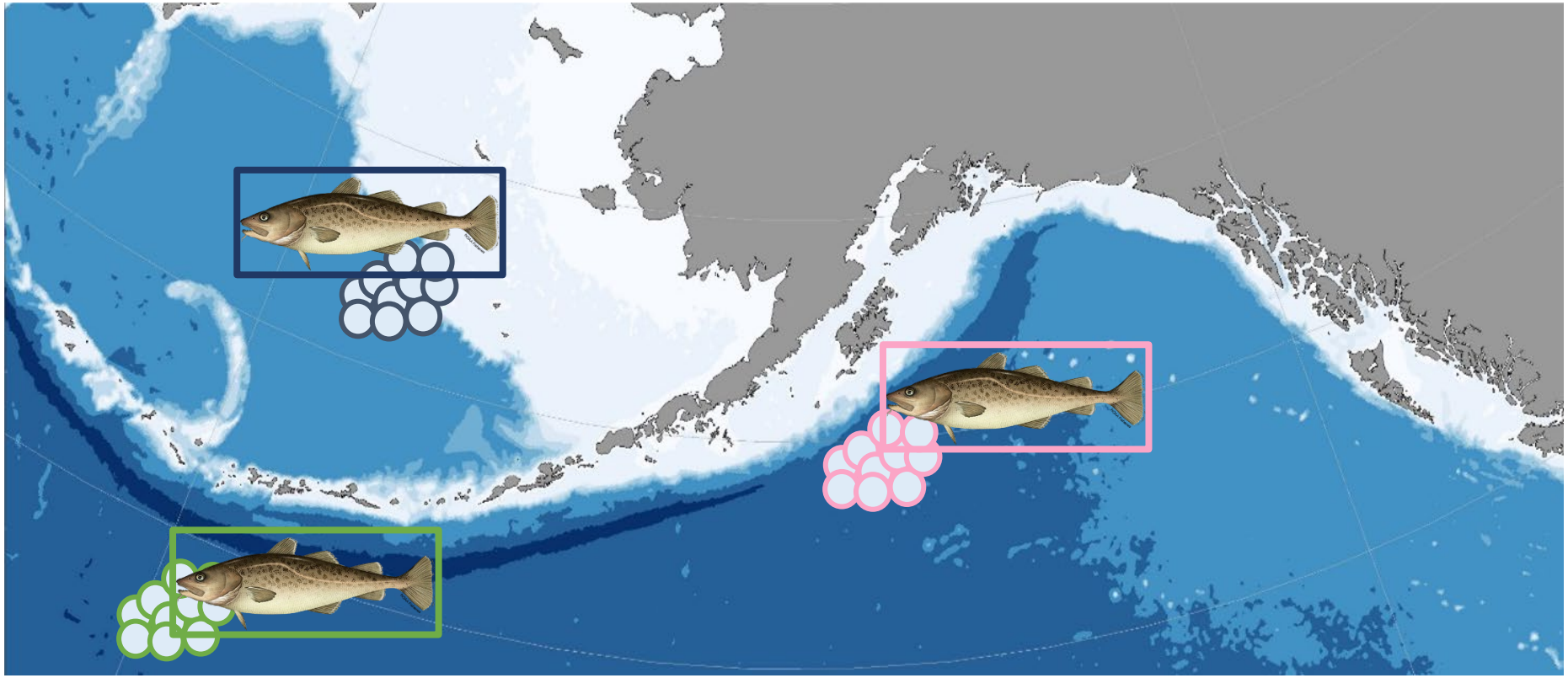
**Four Genetically distinct regions in US waters**



# Pacific cod summer stock structure

# Summer vs. Winter Distributions

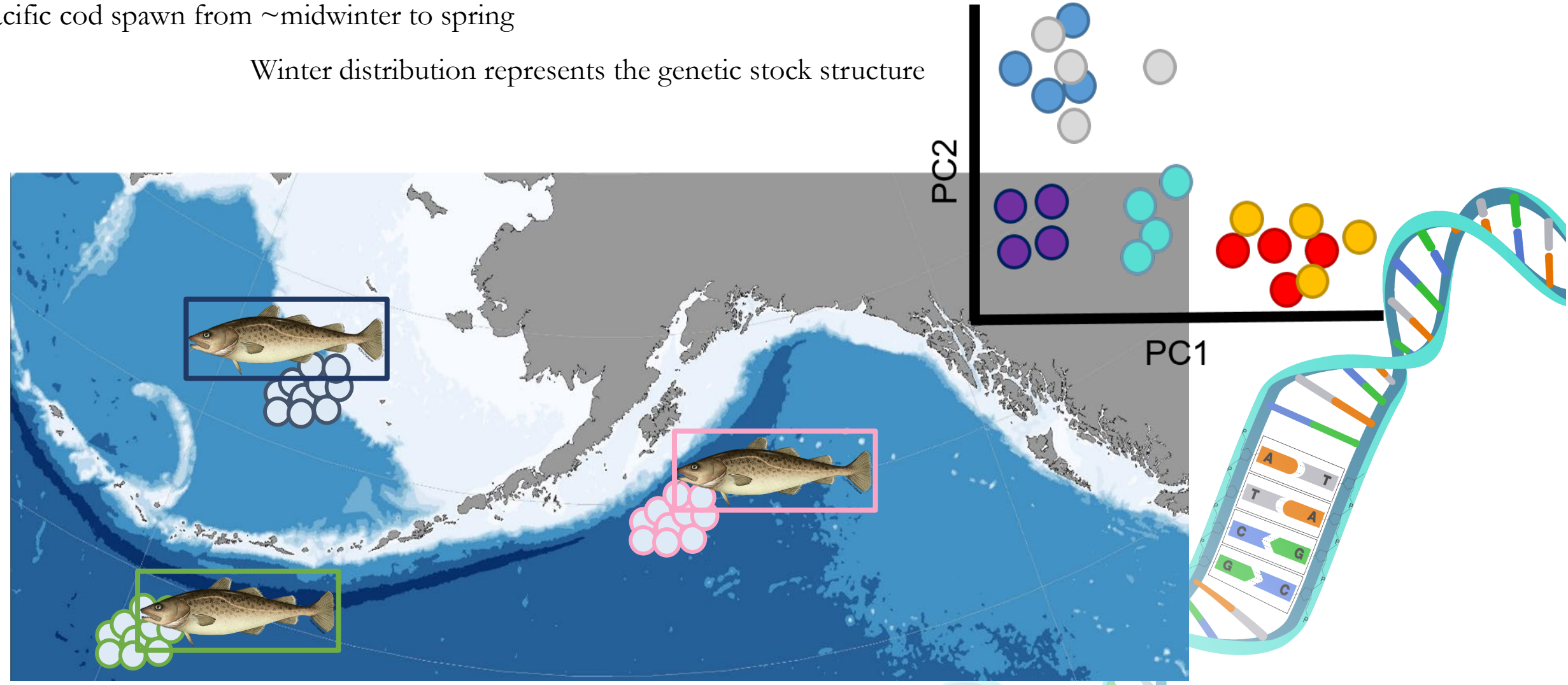
Pacific cod spawn from ~midwinter to spring



# Summer vs. Winter Distributions

Pacific cod spawn from ~midwinter to spring

Winter distribution represents the genetic stock structure

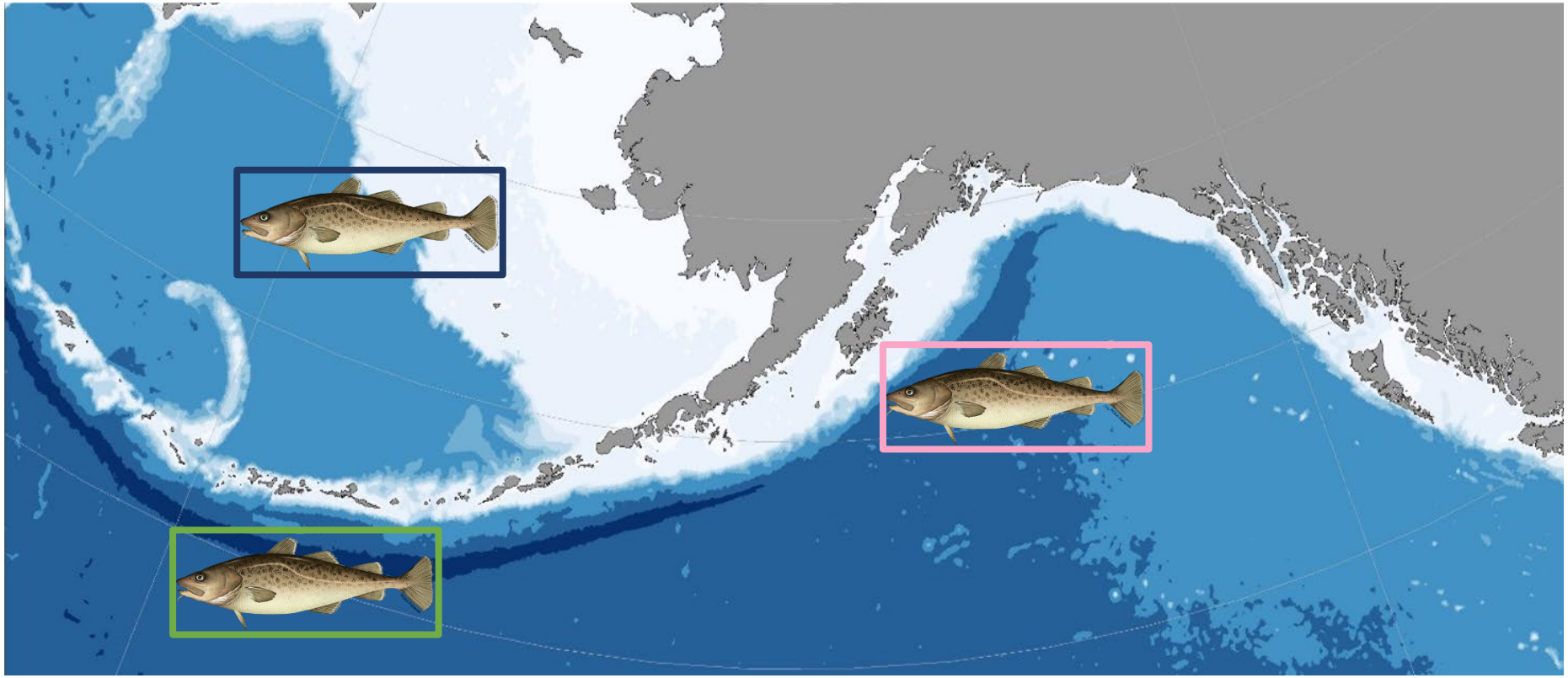


# Summer vs. Winter Distributions

Pacific cod spawn from ~midwinter to spring

Winter distribution represents the genetic stock structure

About half of the harvest and population surveys occur in the summer months



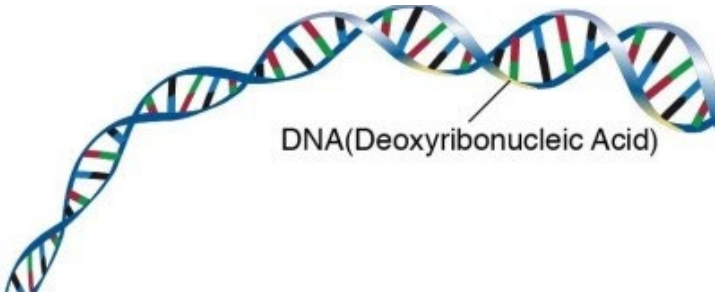
Summer movement?

Do the genetically distinct stocks mix in the summer?

# GT-seq Panel Development

## Step 1

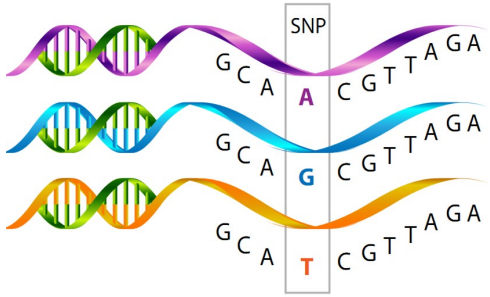
Whole-genome sequencing

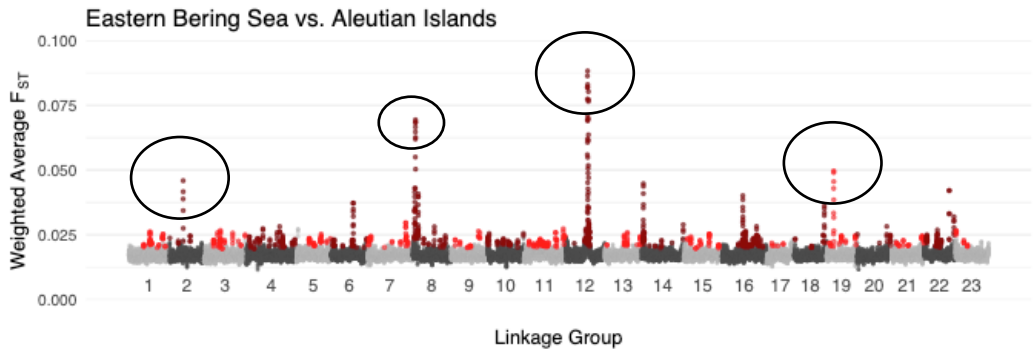



Some individuals from major spawning populations

## Step 2

Identify outlier loci




## Step 3

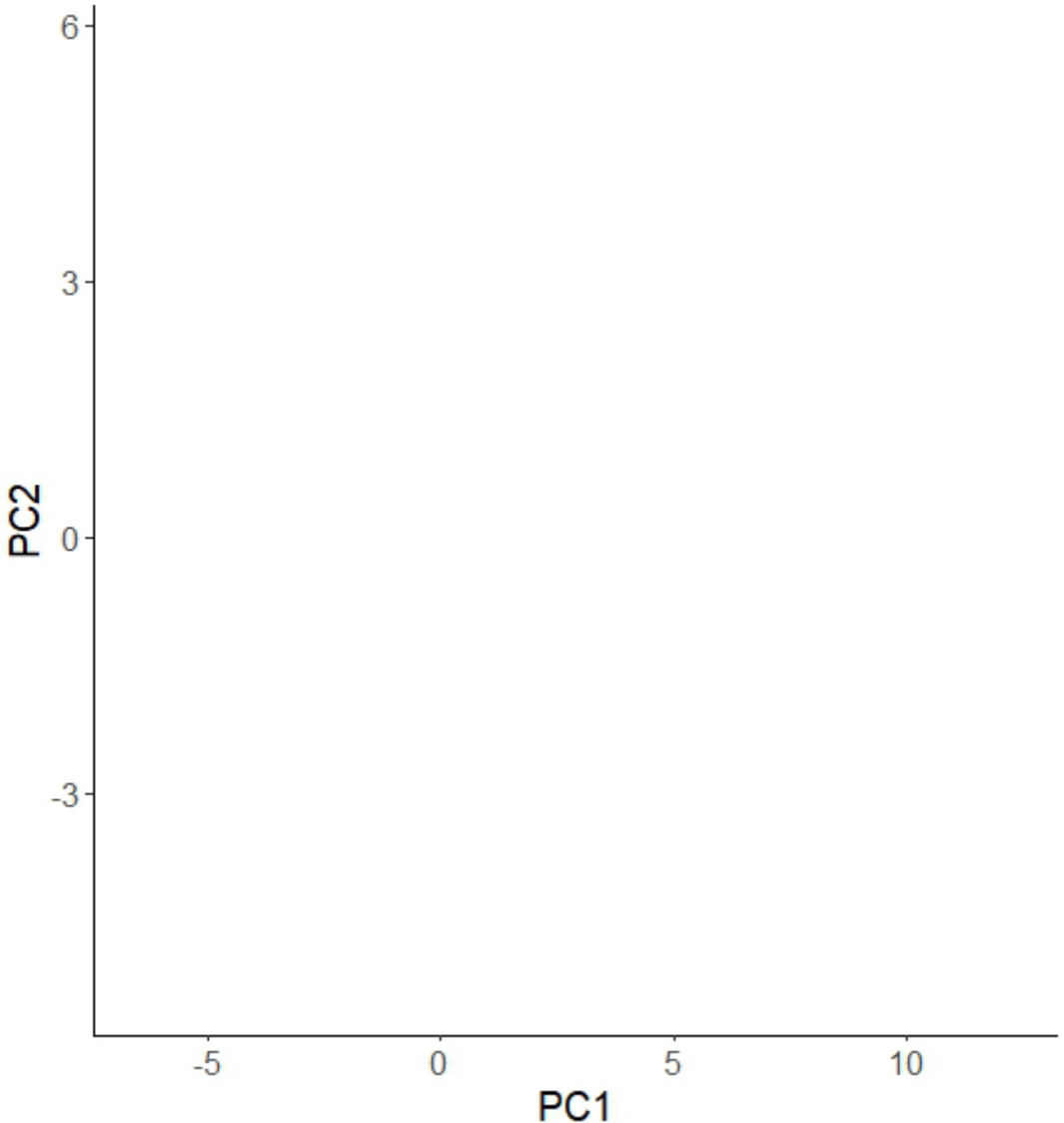
Design a panel using ~300 SNPs that maximize genetic differences

# Final GT-seq panel

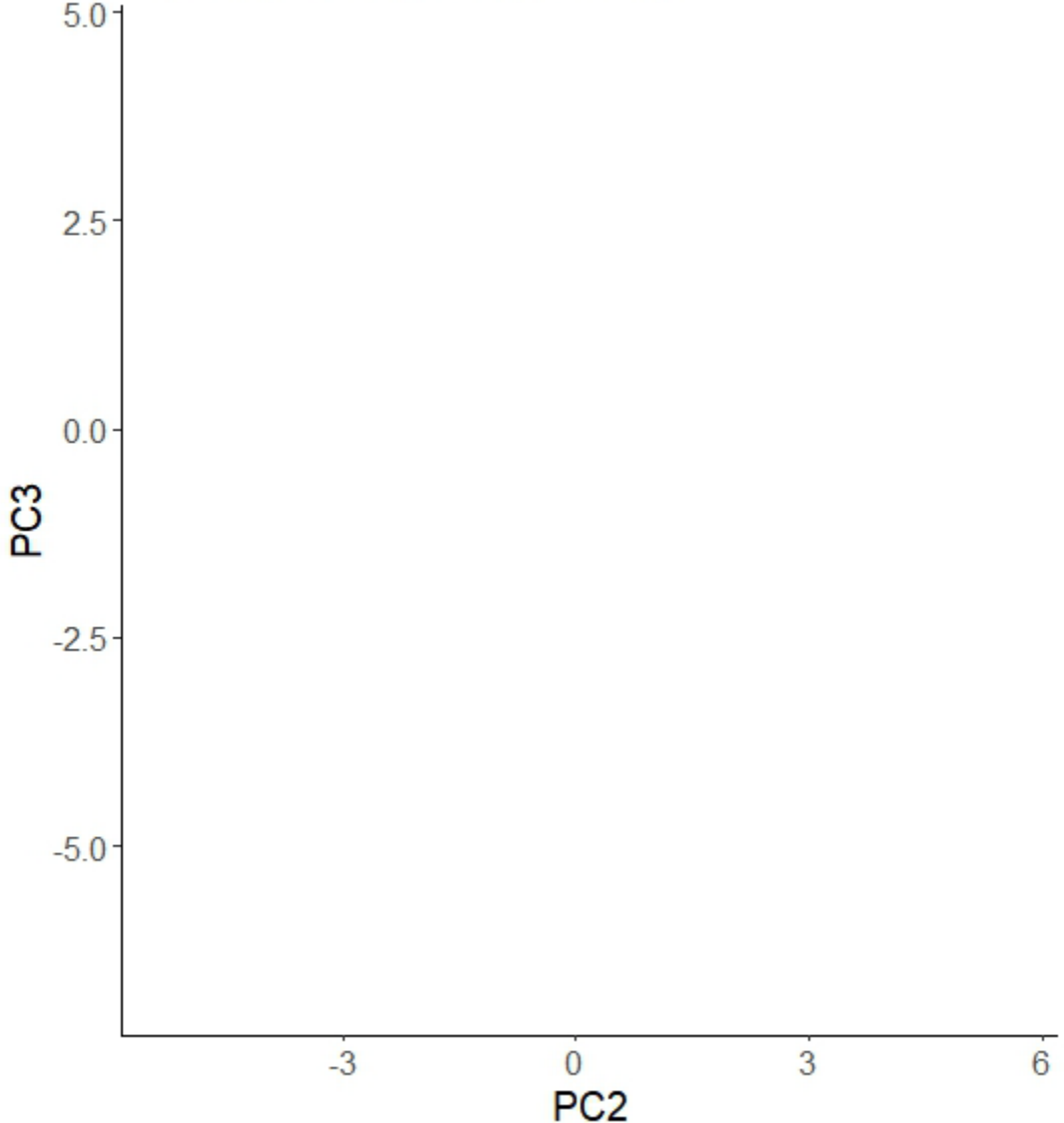
223 High $F_{ST}$ Markers

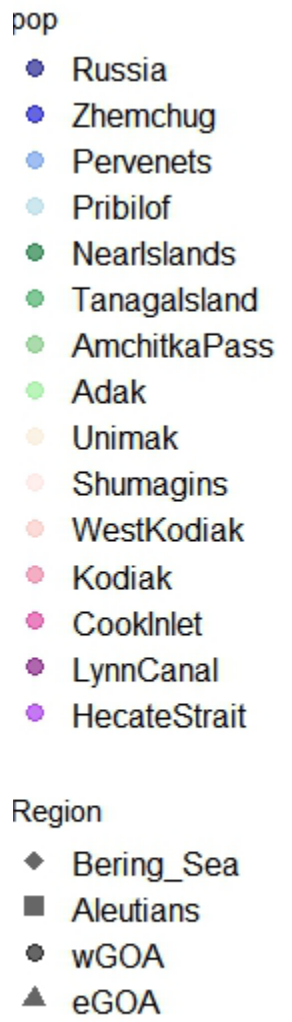
Baseline Populations of Known Spawning Origin

PC1 vs. PC2




PC2 vs. PC3



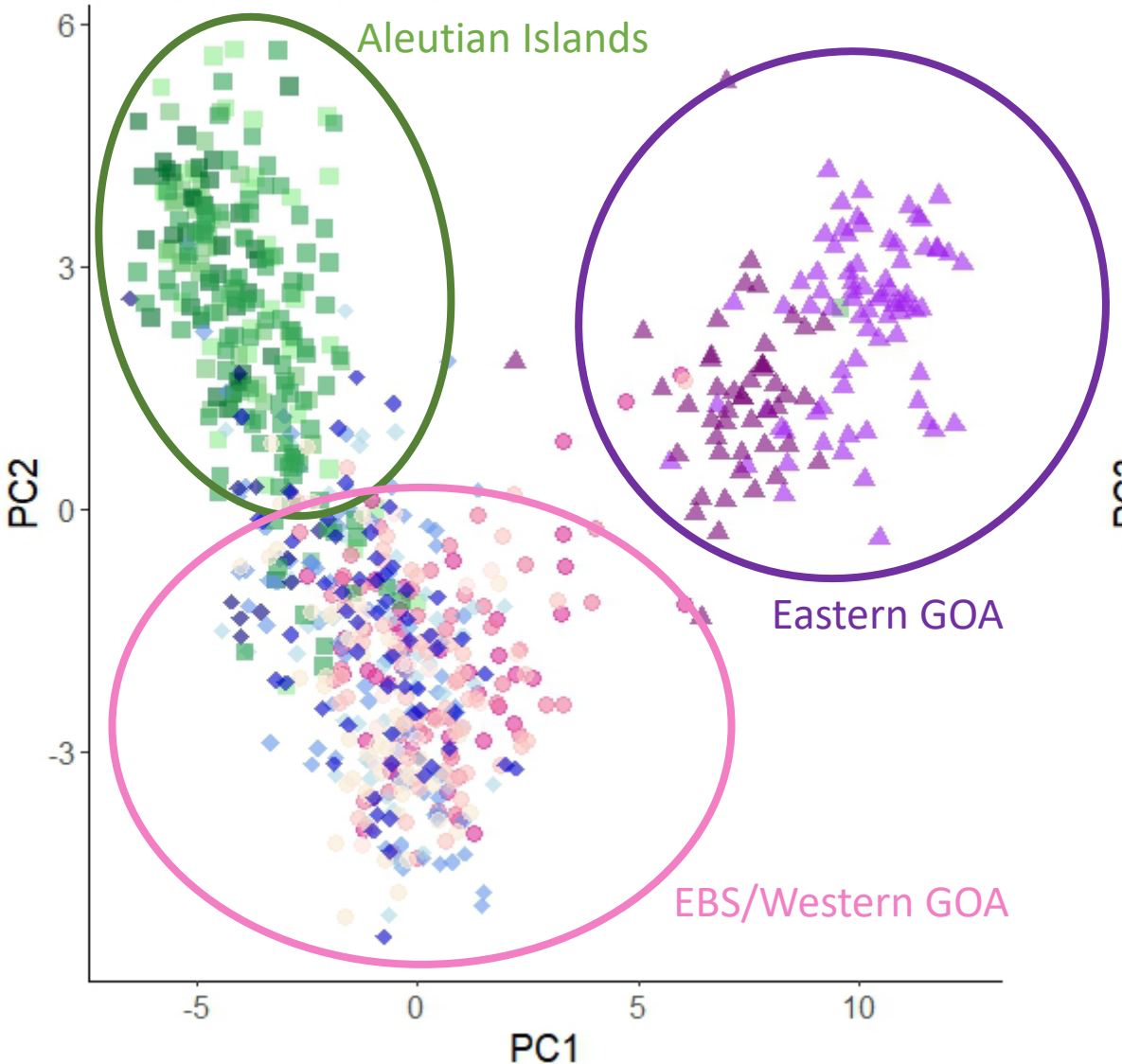



# Final GT-seq panel

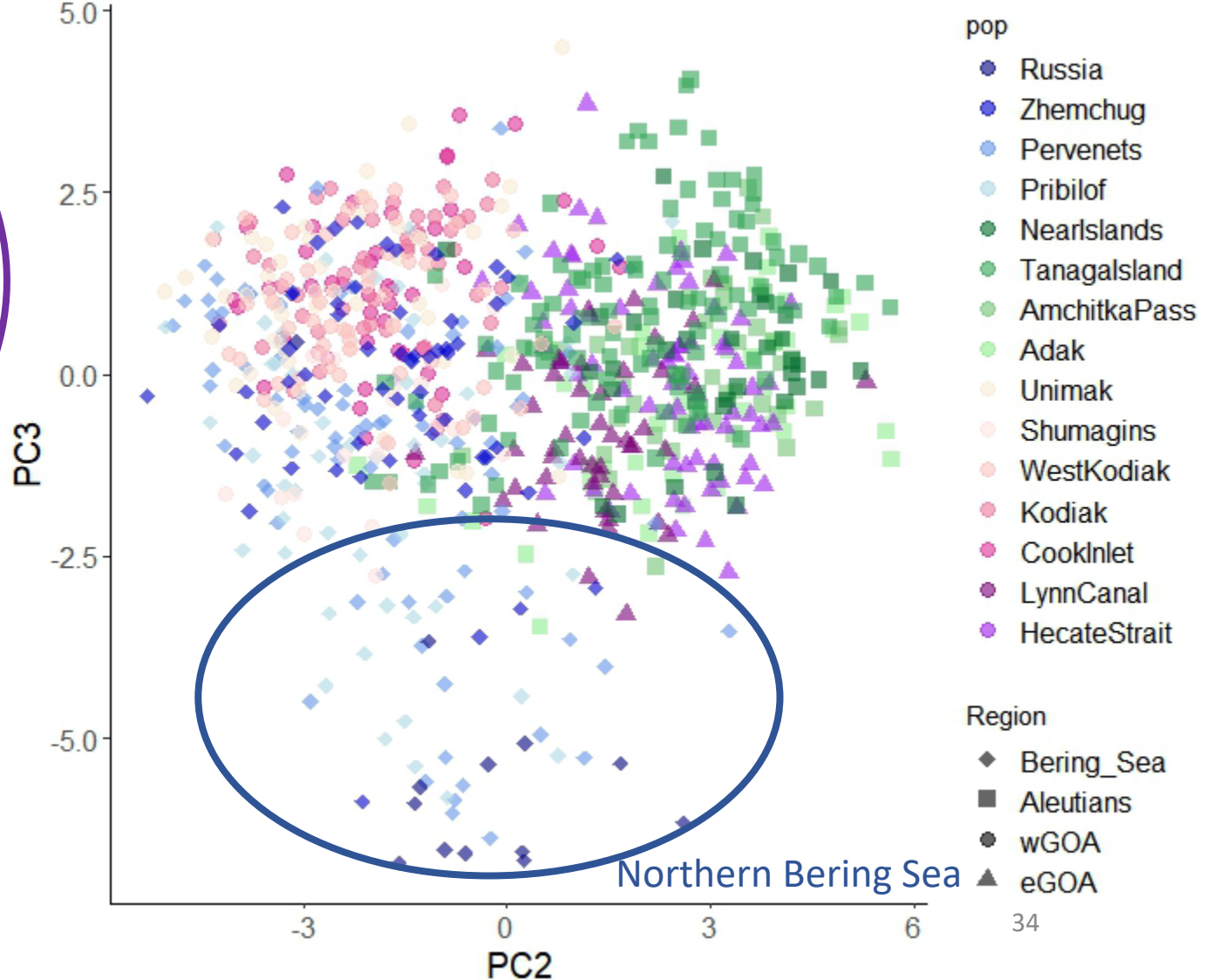
223 High $F_{ST}$ Markers

Baseline Populations of Known Spawning Origin

PC1 vs. PC2

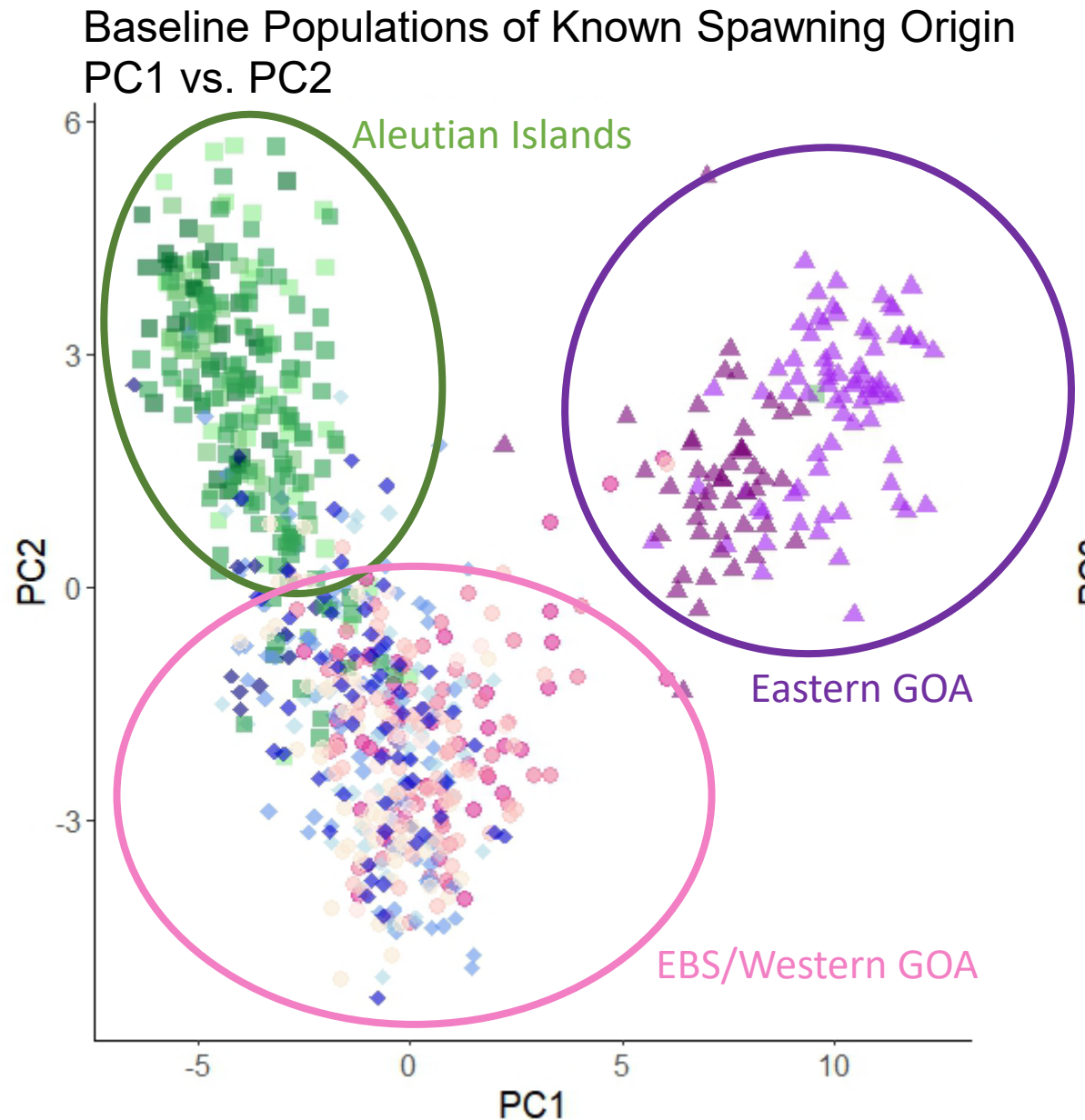


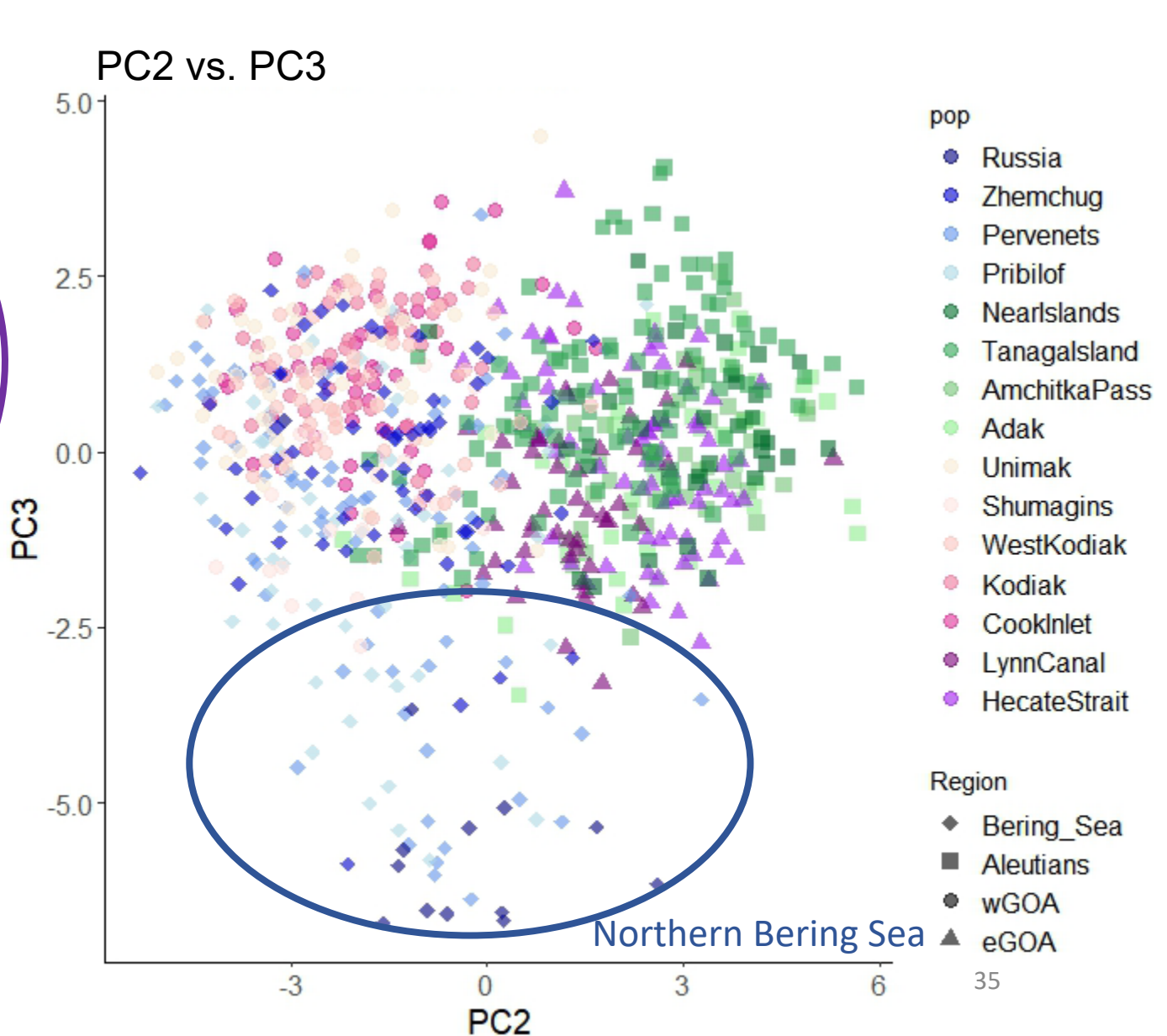

PC2 vs. PC3



# Final GT-seq panel

Four reporting groups



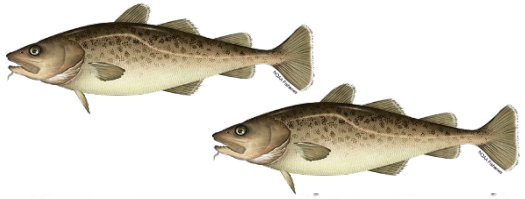
# Genetic Stock Identification – Assignment Accuracy

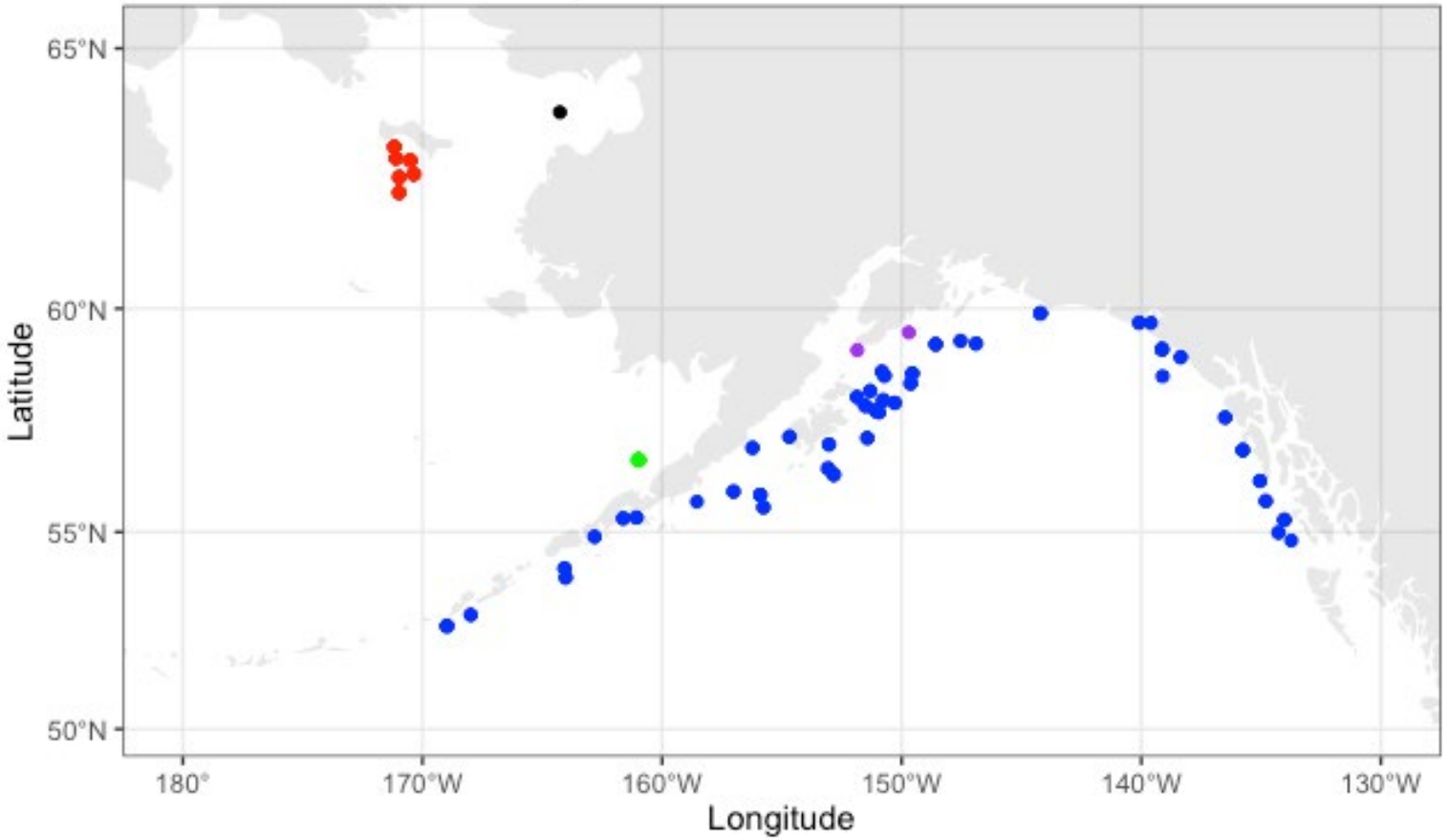
**Using baseline samples in Rubias:**

**93.1% of all samples**

| | Aleutians | eGOA | NBS | wGOA/EBS |
|---|---|---|---|---|
| **Aleutians** | 212 | 0 | 0 | 7 |
| **eGOA** | 1 | 121 | 0 | 5 |
| **NBS** | 0 | 0 | 44 | 6 |
| **wGOA/EBS** | 12 | 1 | 3 | 359 |

# Summer caught pacific cod





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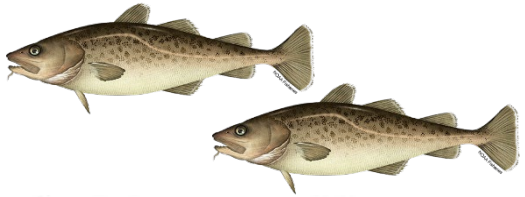

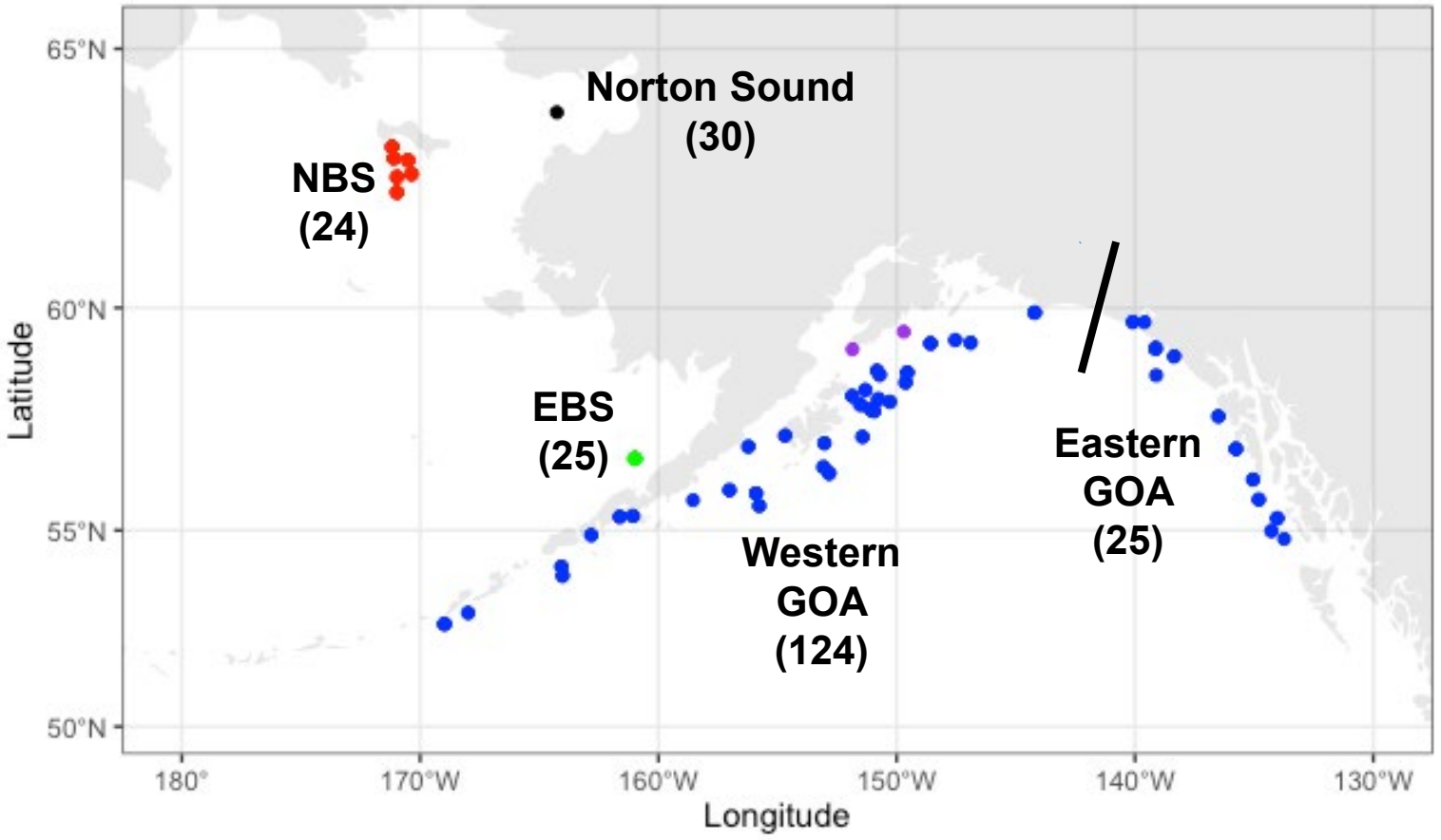

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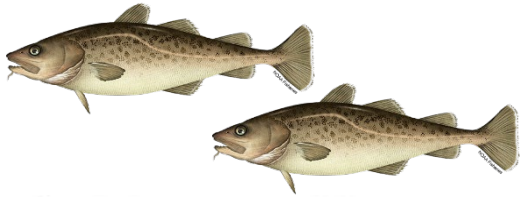
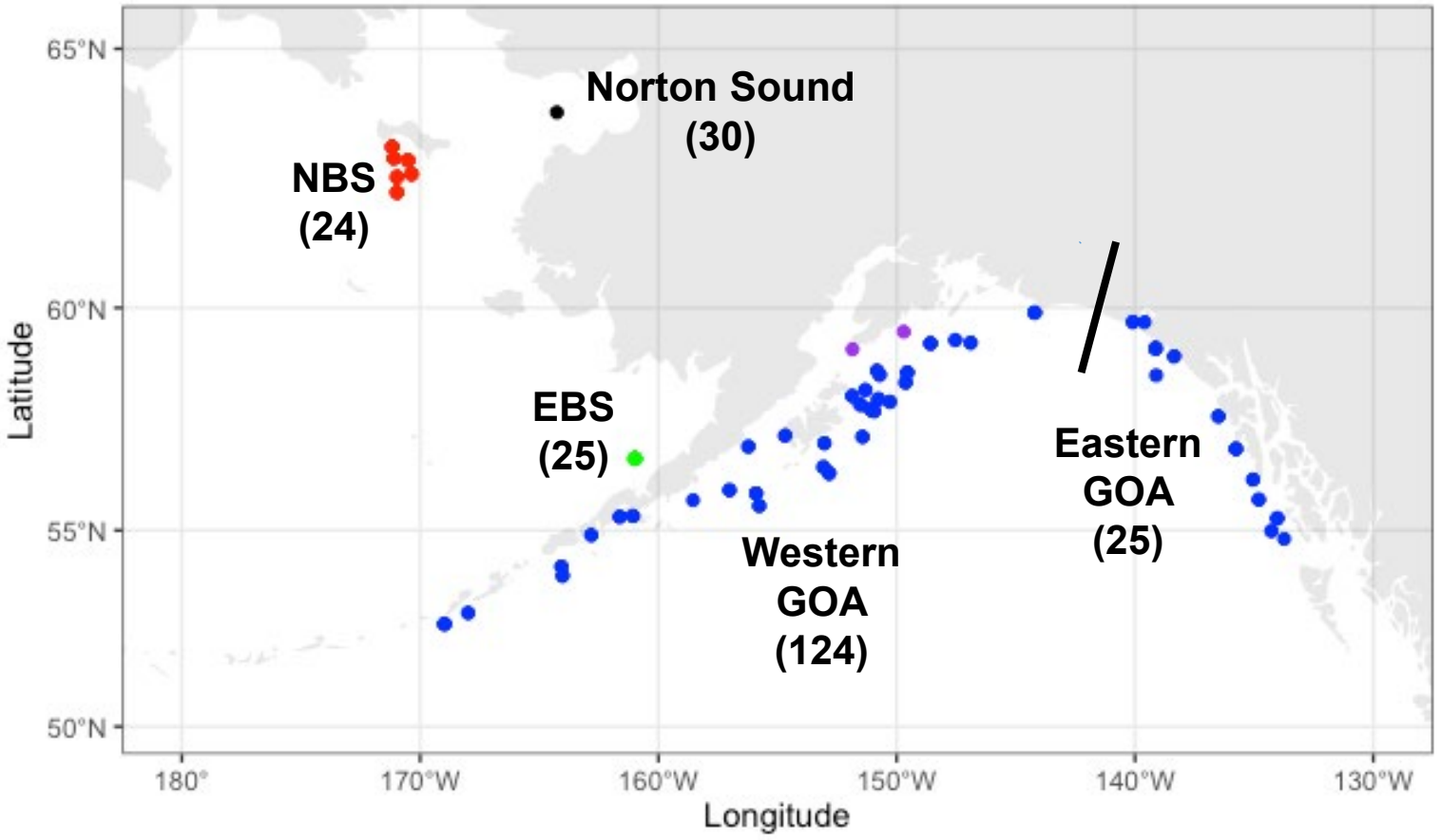
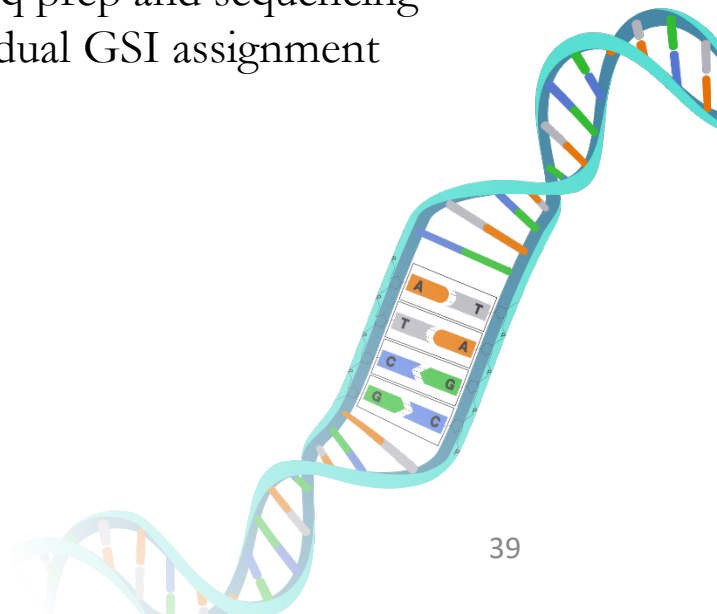


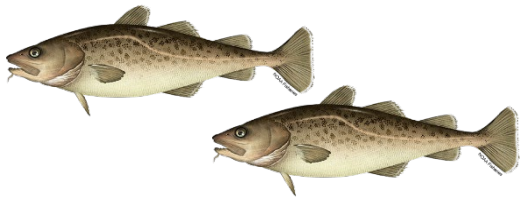


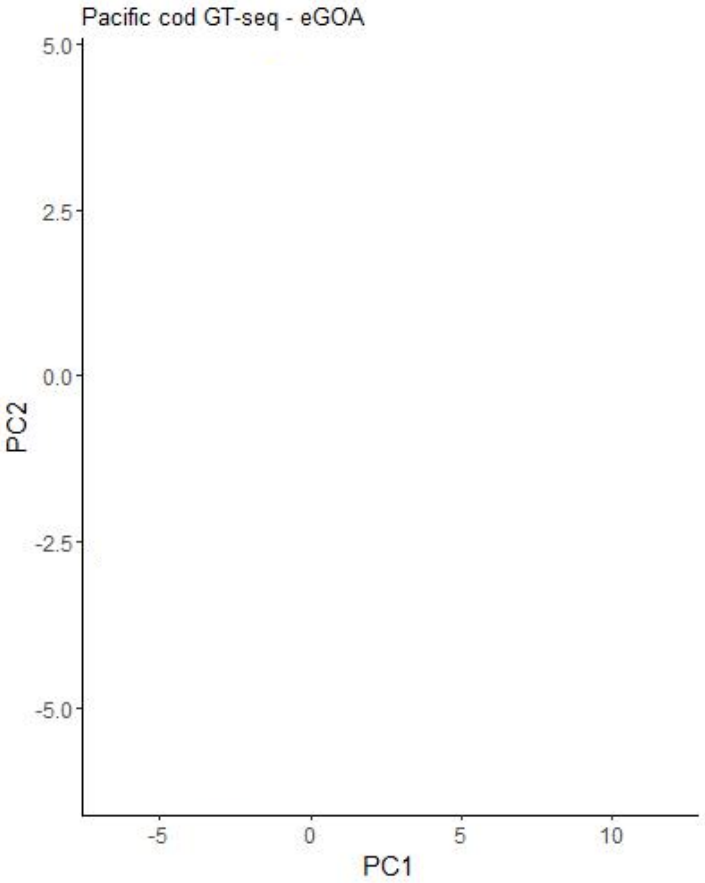

**What is the genetic stock composition of each individual?**

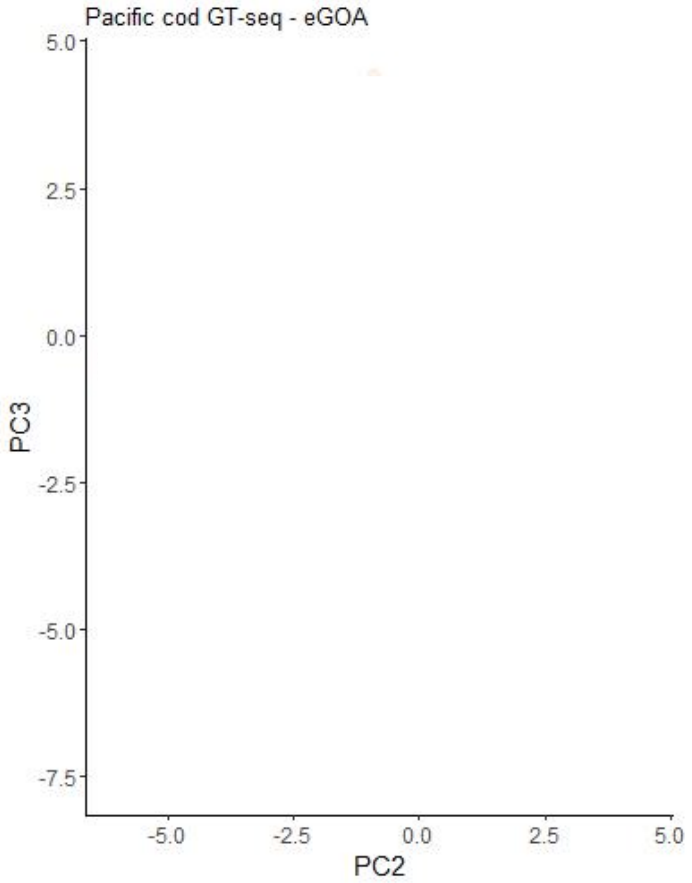
- Fin clips removed and used for DNA extraction
- GT-seq prep and sequencing
- Individual GSI assignment

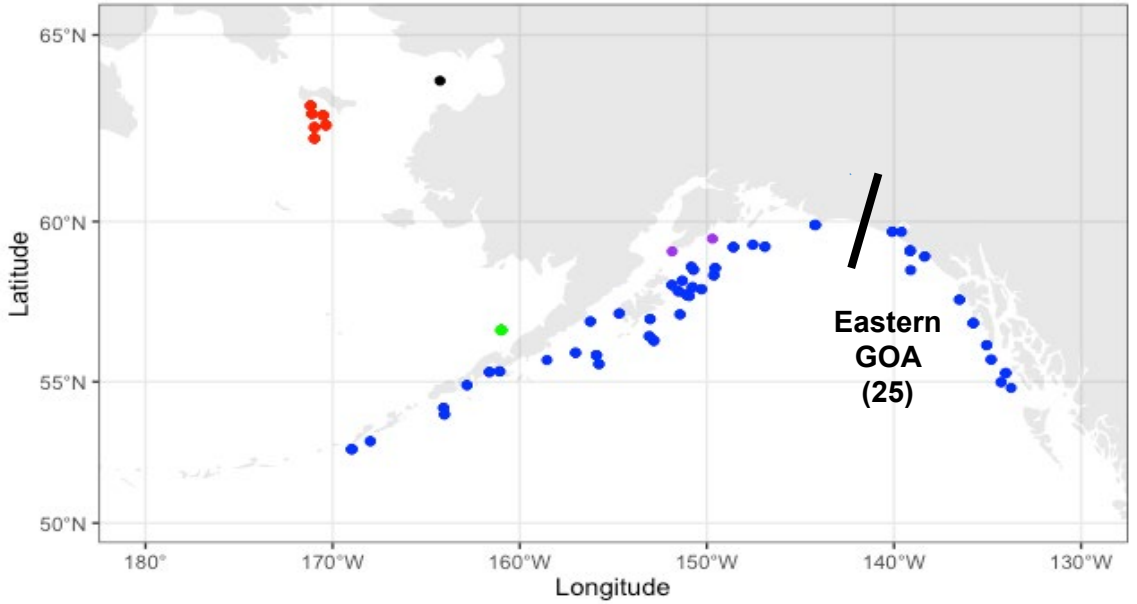


# Genetic stock identification – Eastern GOA





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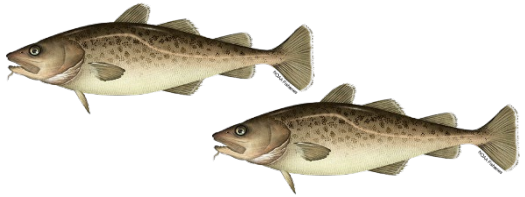
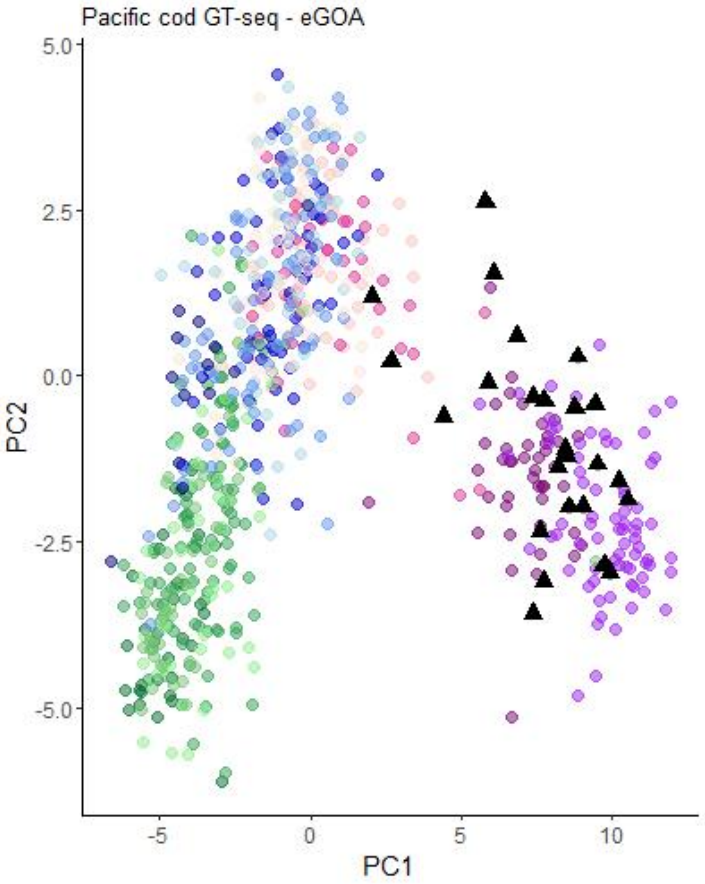
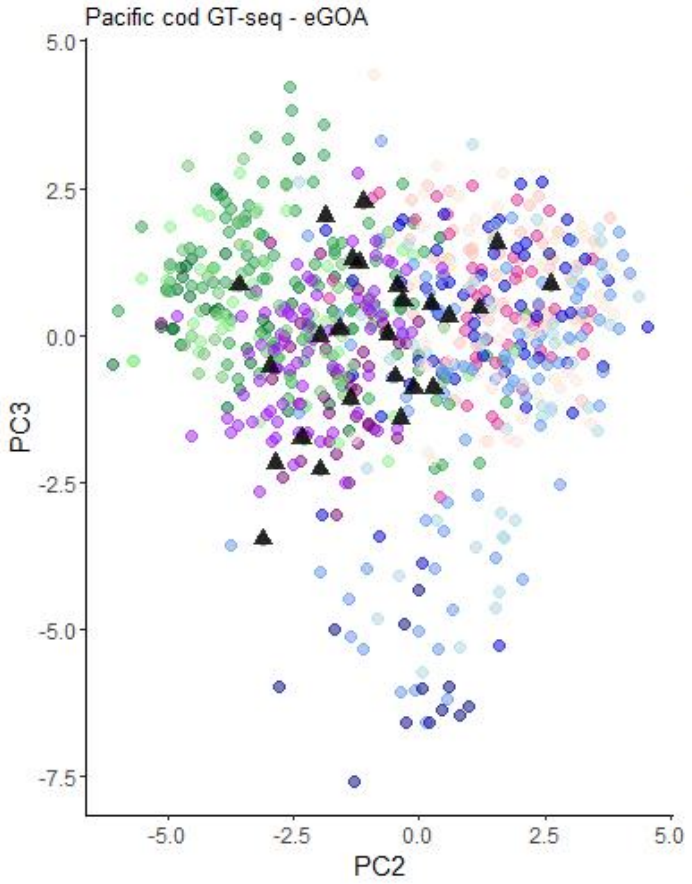
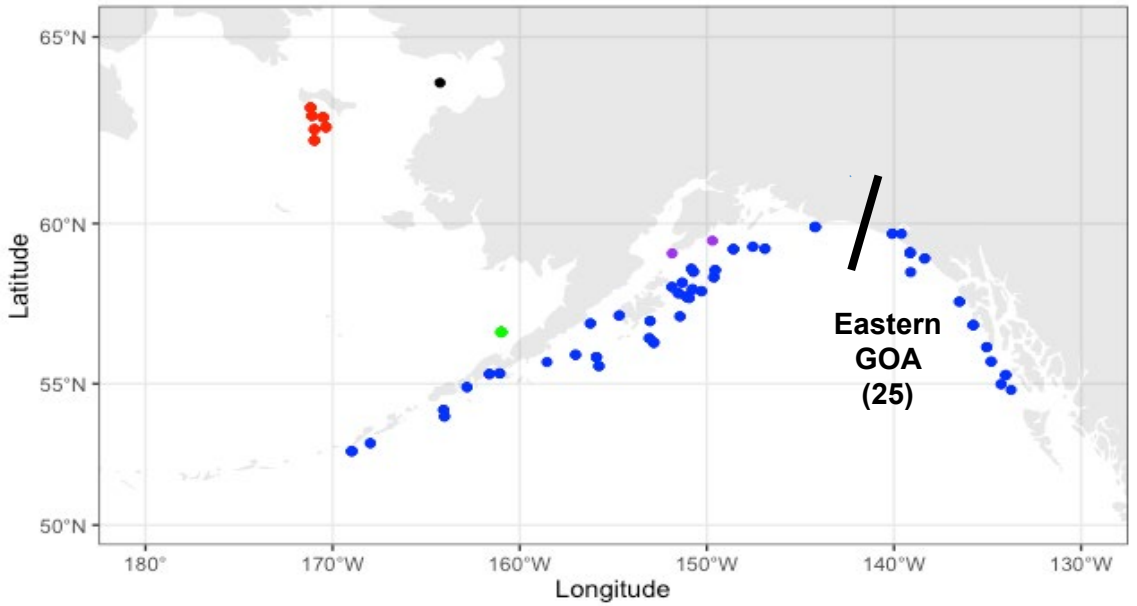


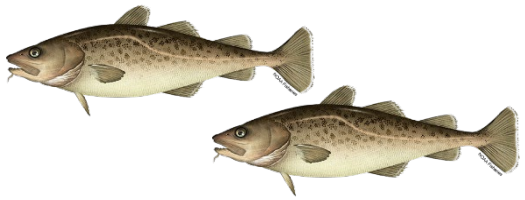


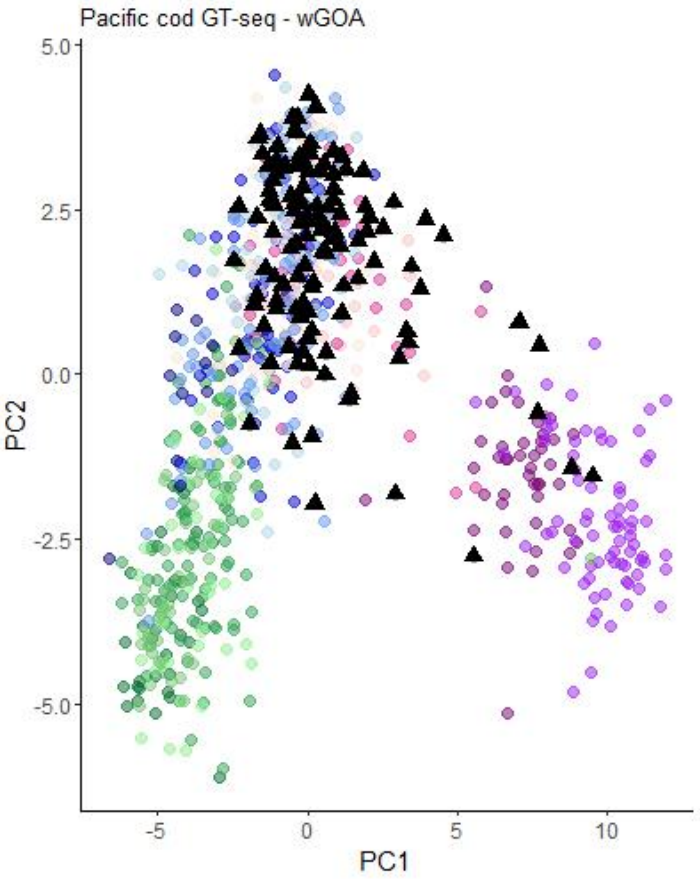



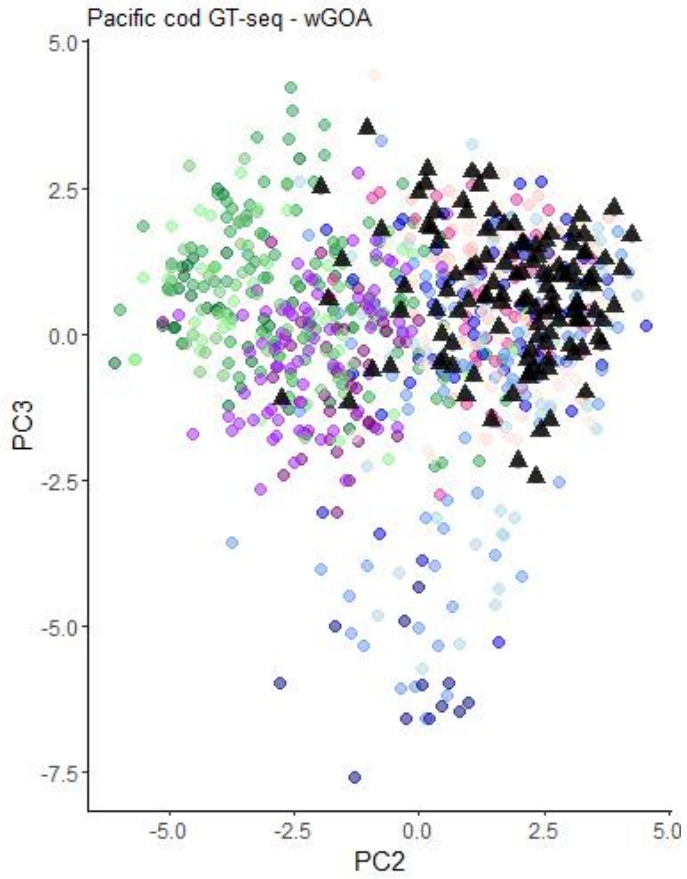



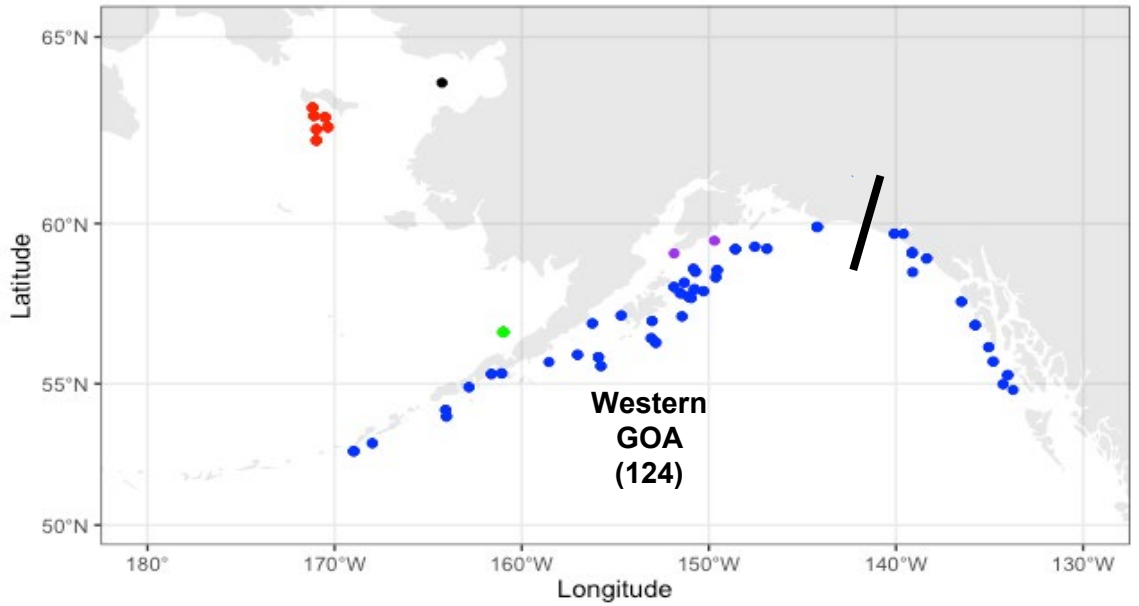

**92% assignment back to eGOA**

# Genetic stock identification – Western GOA



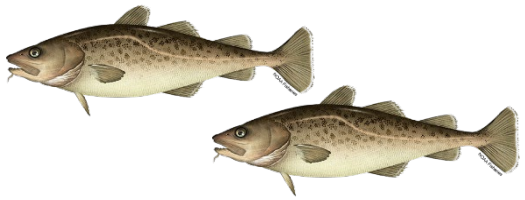


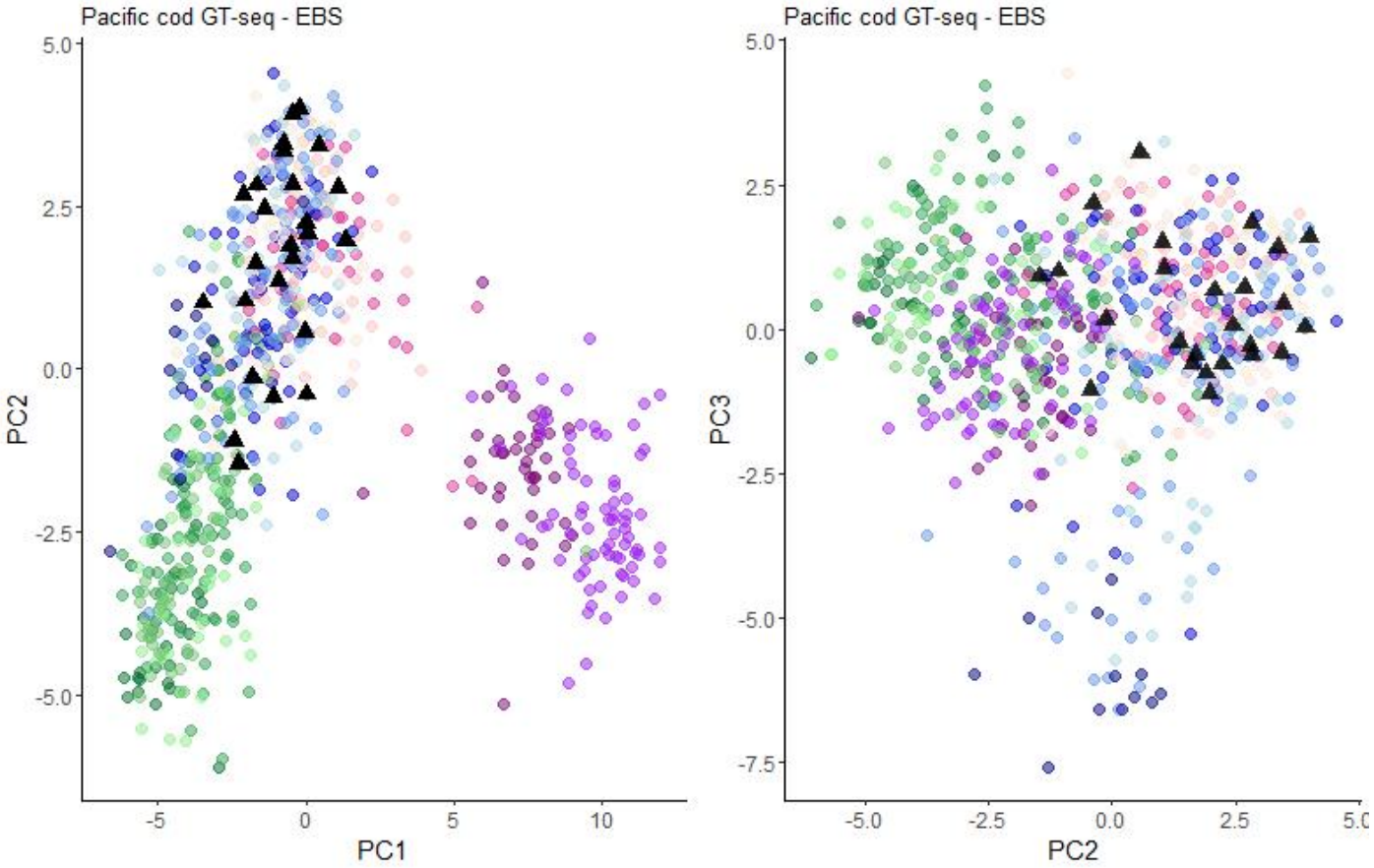




**92.7% assignment back to wGOA/EBS**

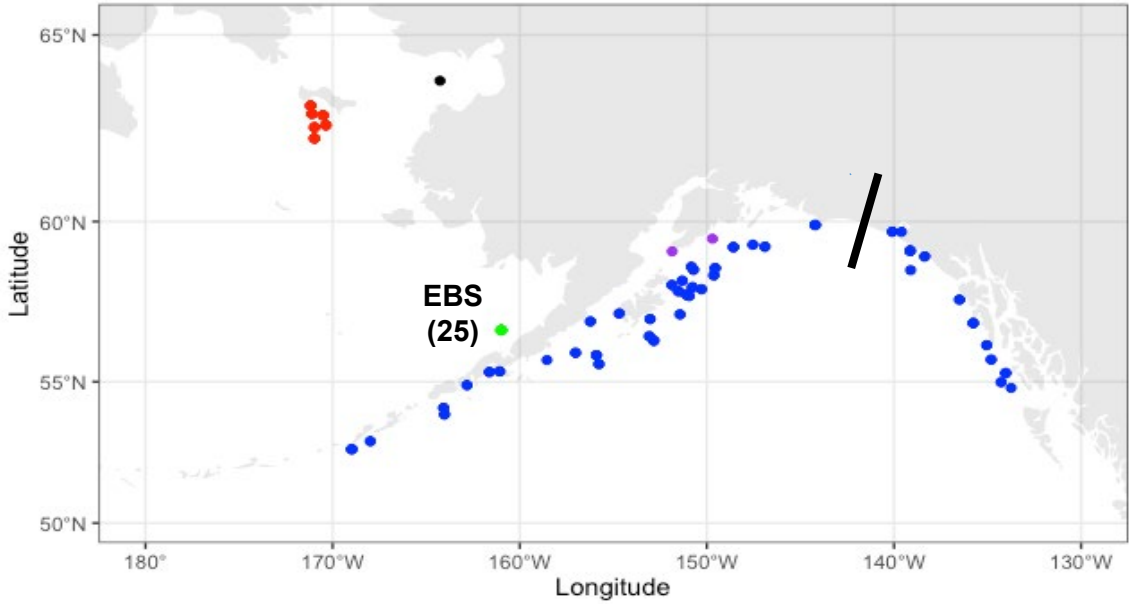
# Genetic stock identification – Eastern Bering Sea





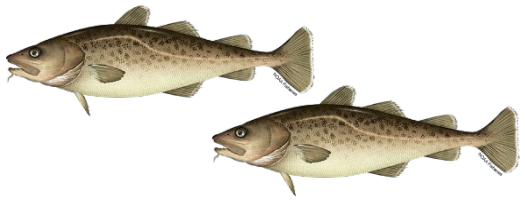


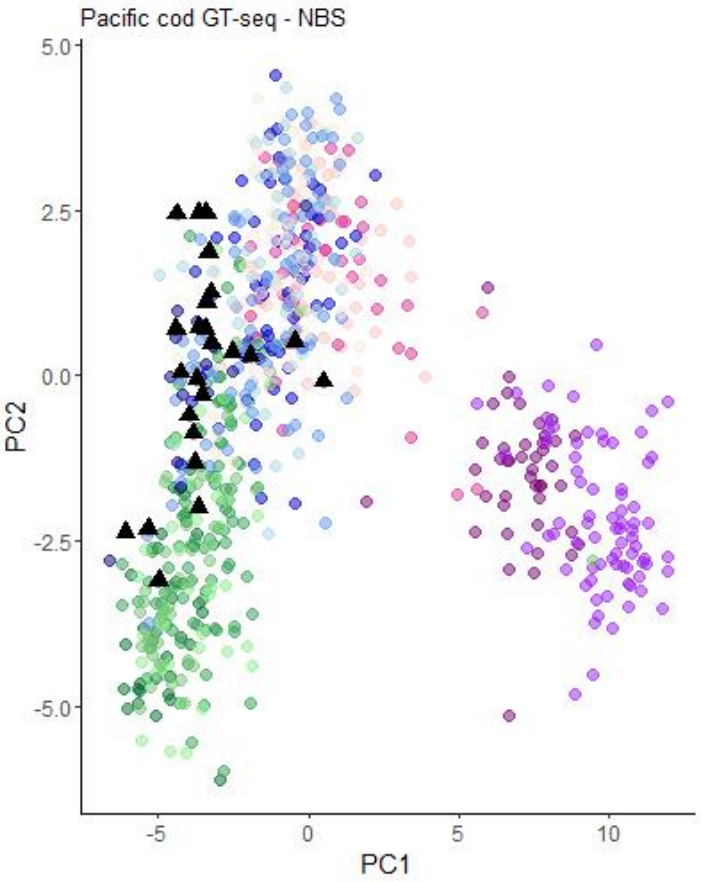


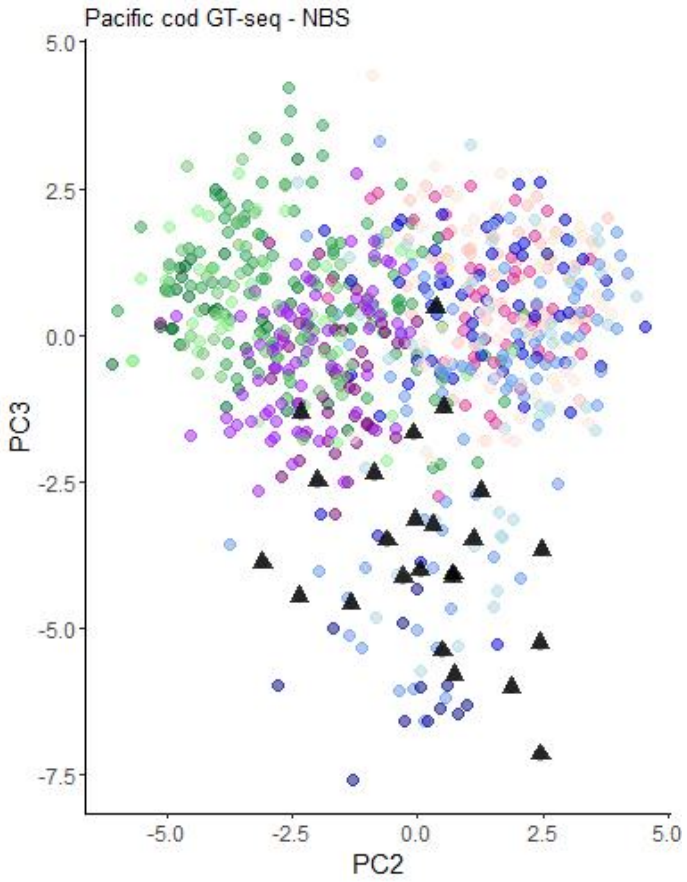


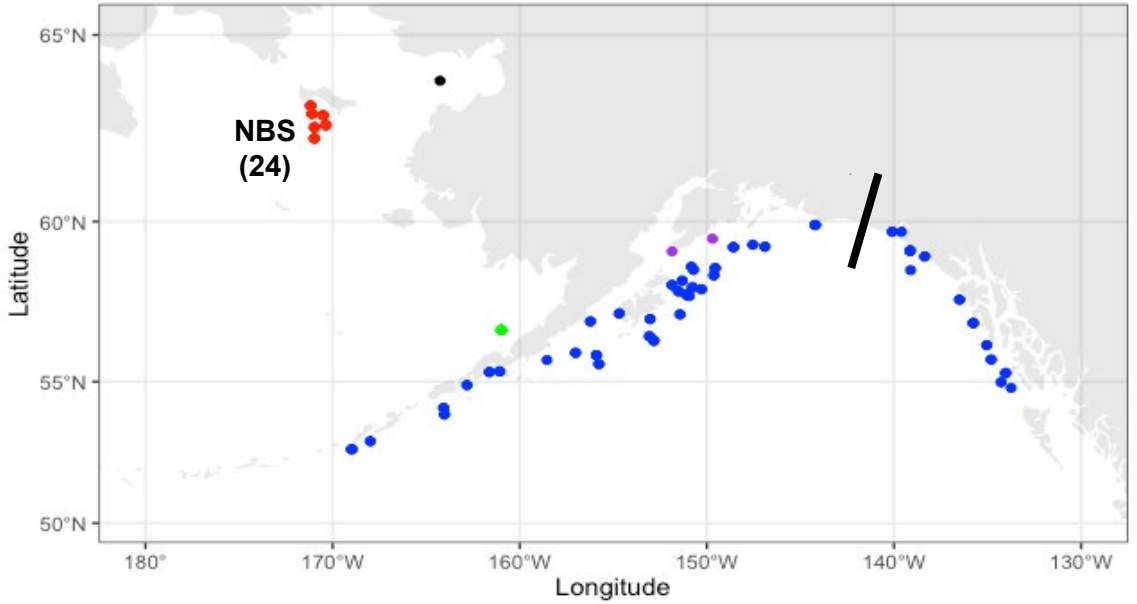

**92% assignment back to wGOA/EBS**

# Genetic stock identification – Northern Bering Sea



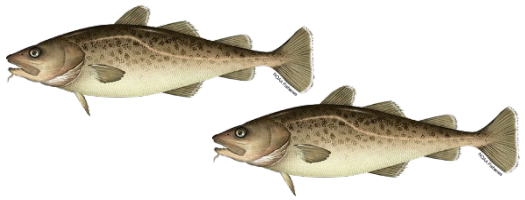


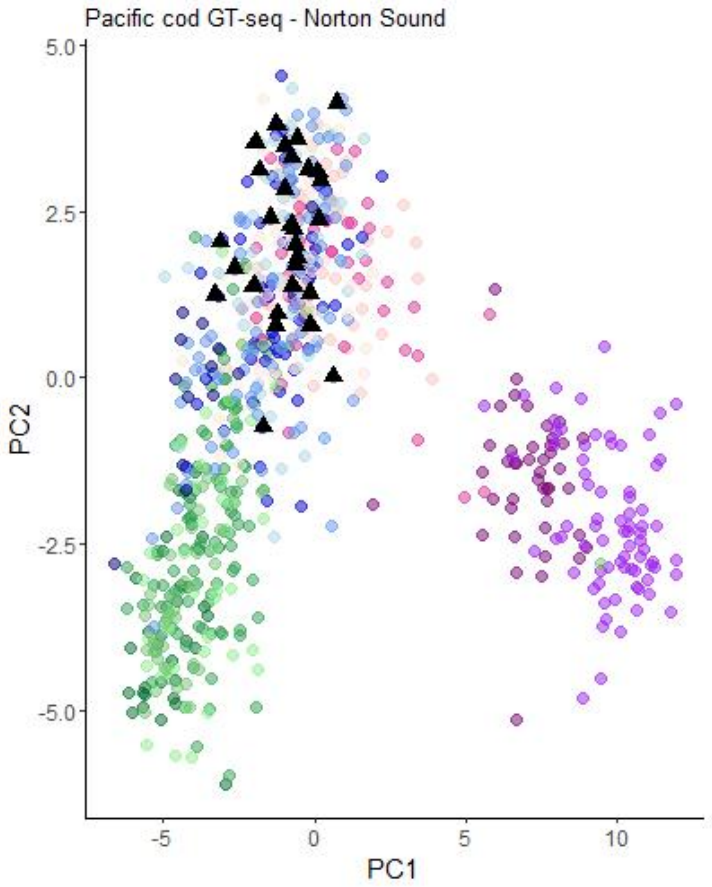



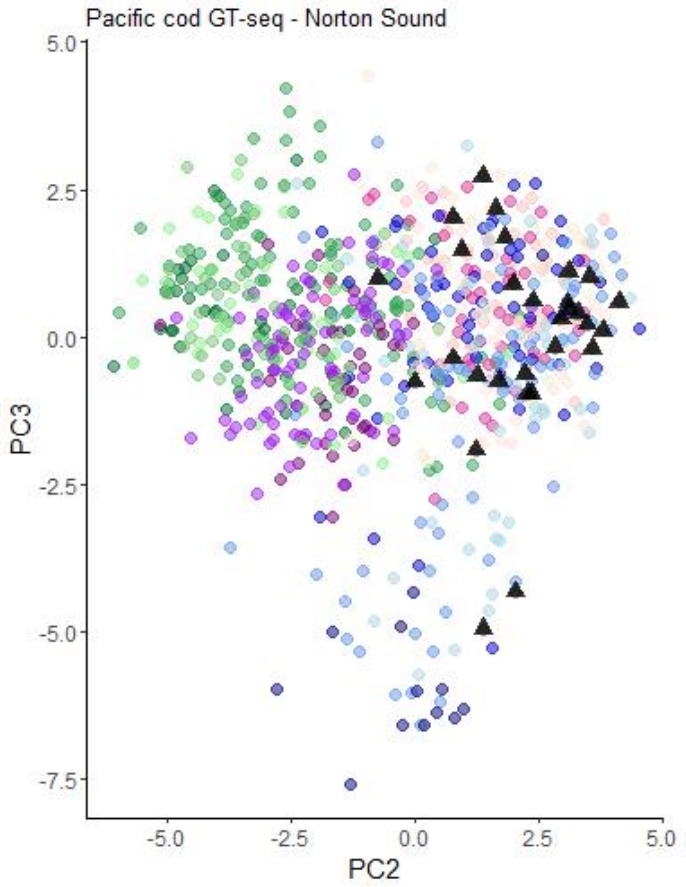



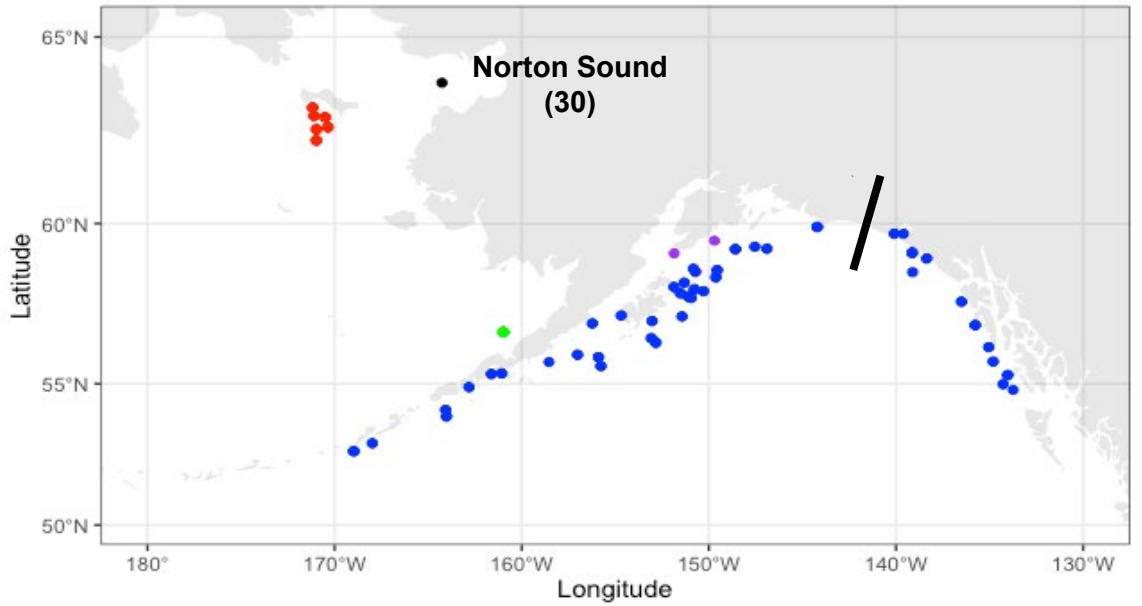

**83.3% assignment back to NBS**

# Genetic stock identification – Norton Sound





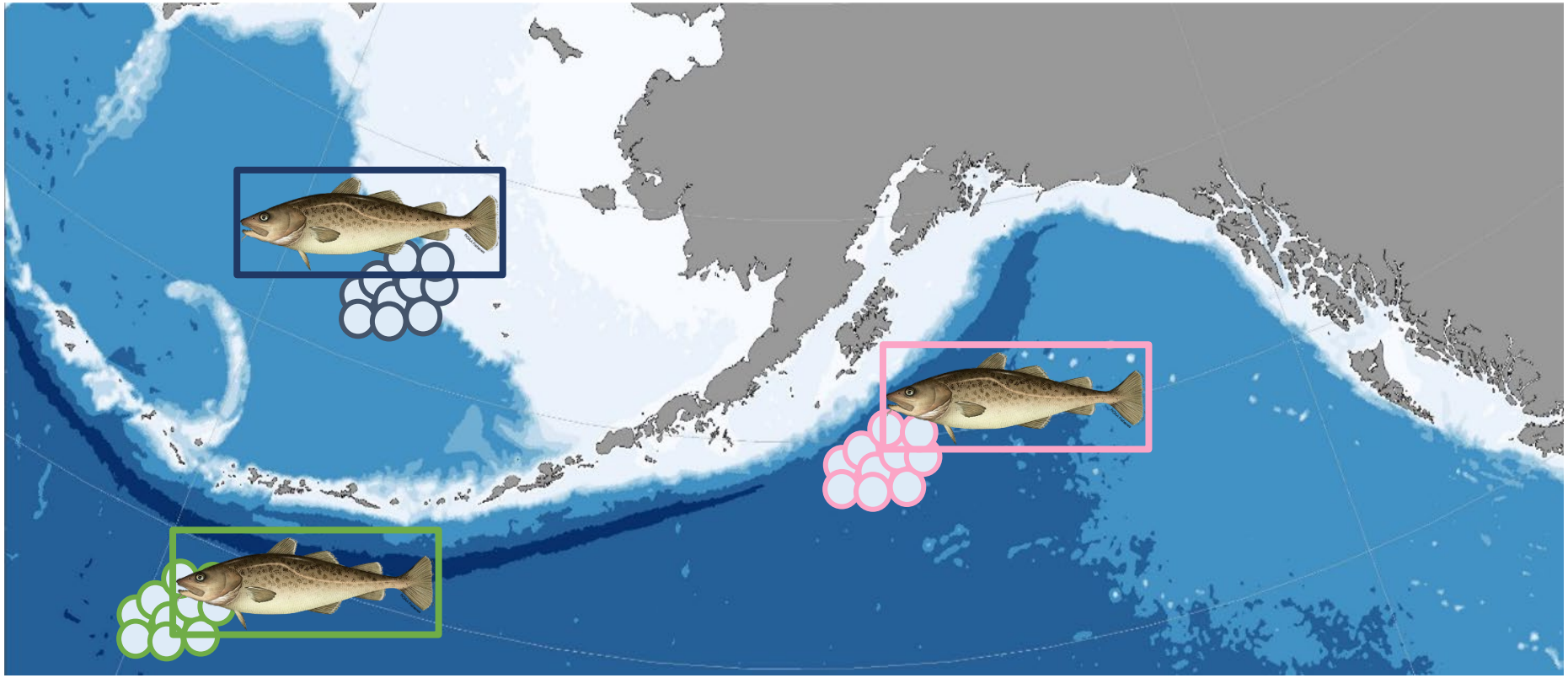




**10% assignment back to NBS**

**90% assignment back to wGOA/EBS**

# Conclusions

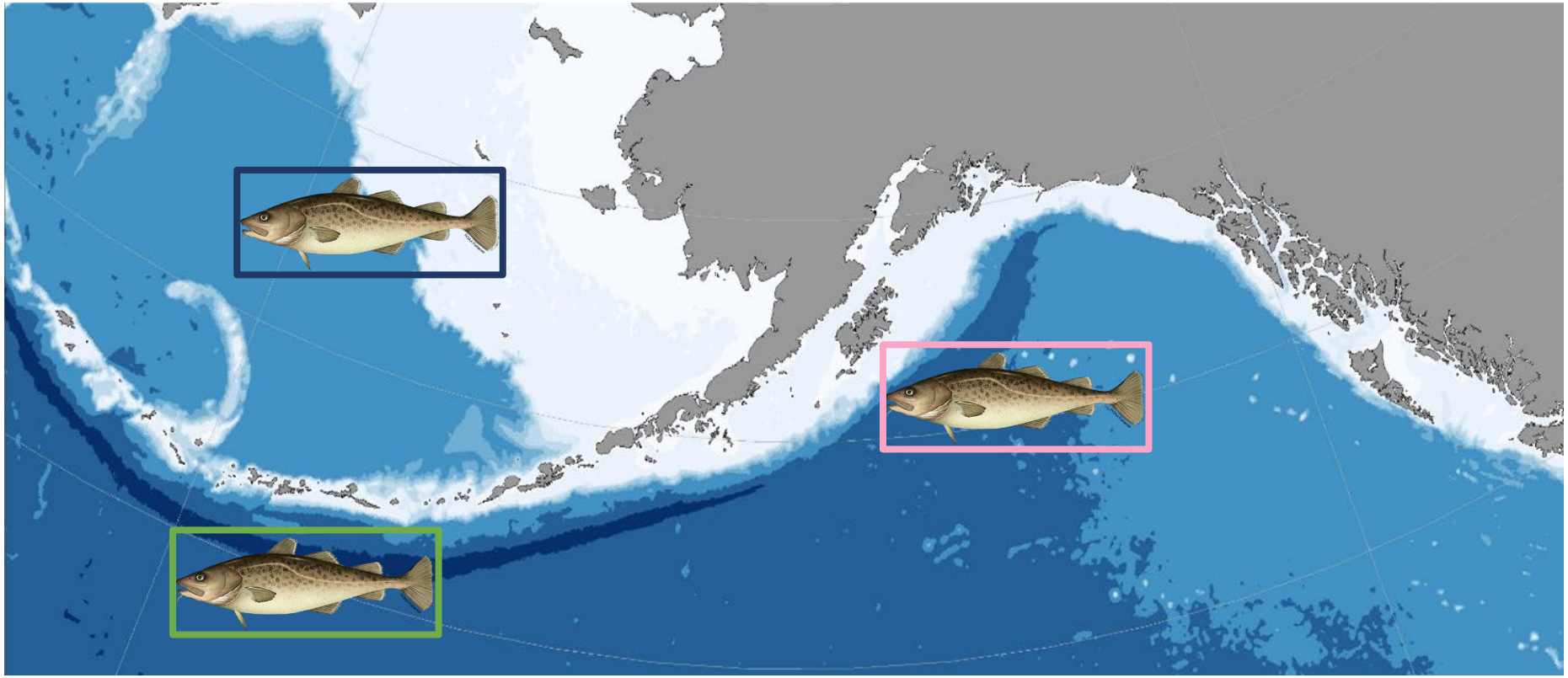
Do summer and winter distributions of Pacific cod vary?



# Conclusions

Do summer and winter distributions of Pacific cod vary?

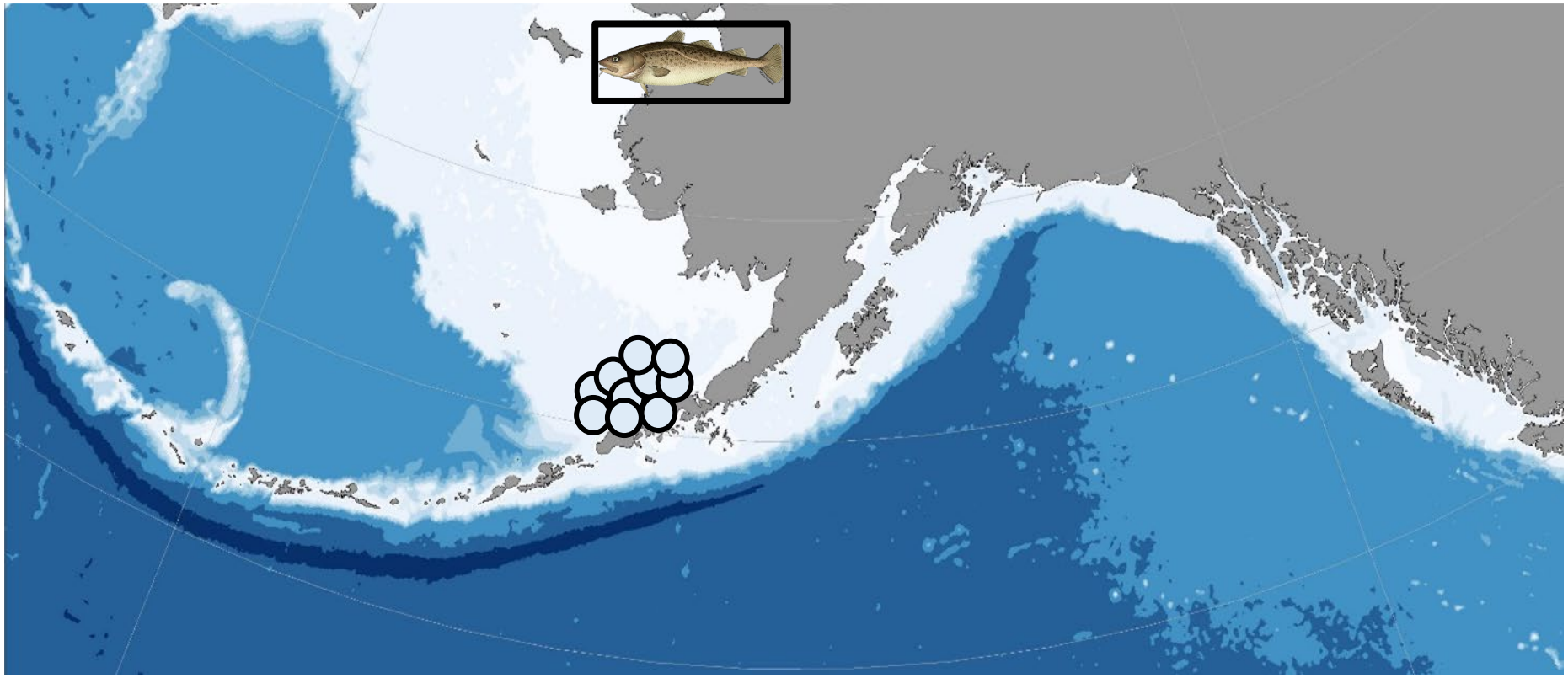
For the most part, no…



# Conclusions

Do summer and winter distributions of Pacific cod vary?

For the most part, no…but Norton Sound

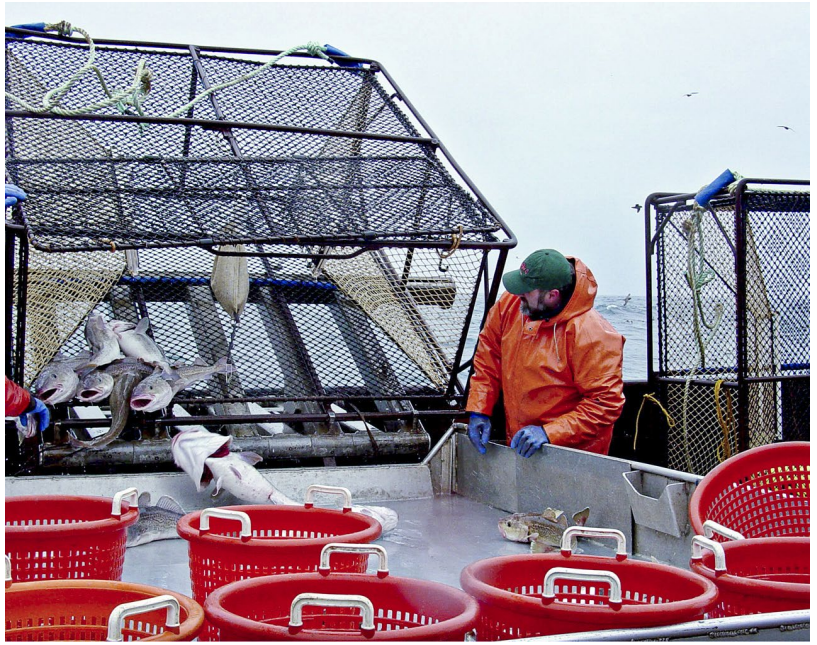


# Other GT-Seq Panel Uses

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

Knowing population of origin will:

- Investigate ontogenetic migratory behavior
- Identify origin of large cod in fishery
- Understand stock specific fishing pressure in mixed stock fisheries



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

# Acknowledgements

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Blue North Fisheries

The Freezer Longline Coalition

North Pacific Seafoods

Elisa Russ

Sonja Elmejjati

Celeste Beckgoodell

Alisa Abookire

Asia Beder

Lyle Britt

Pat Burns

Craig Cross

Dave Fraser

Elliott Hammond

Simon Kineen

Krista Milani

Sean Rooney

Chris Schaeffer

Chad See

Dawn Wehde

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