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# Genetic analysis of Northern Bering Sea Pacific cod

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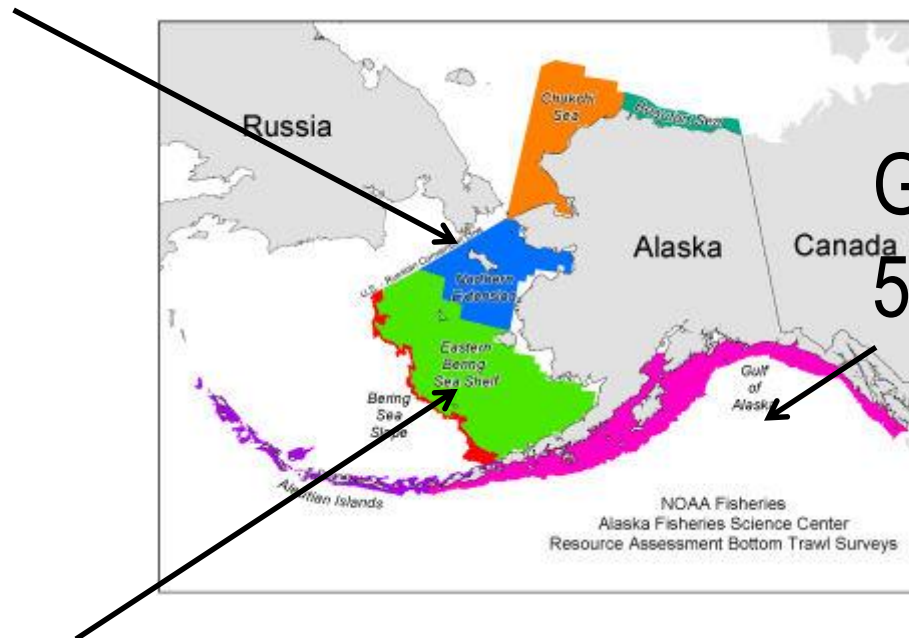
Lorenz Hauser (UW), Carolyn Tarpey (UW, PSMFC),  
Mike Canino (AFSC)

August 20, 2018



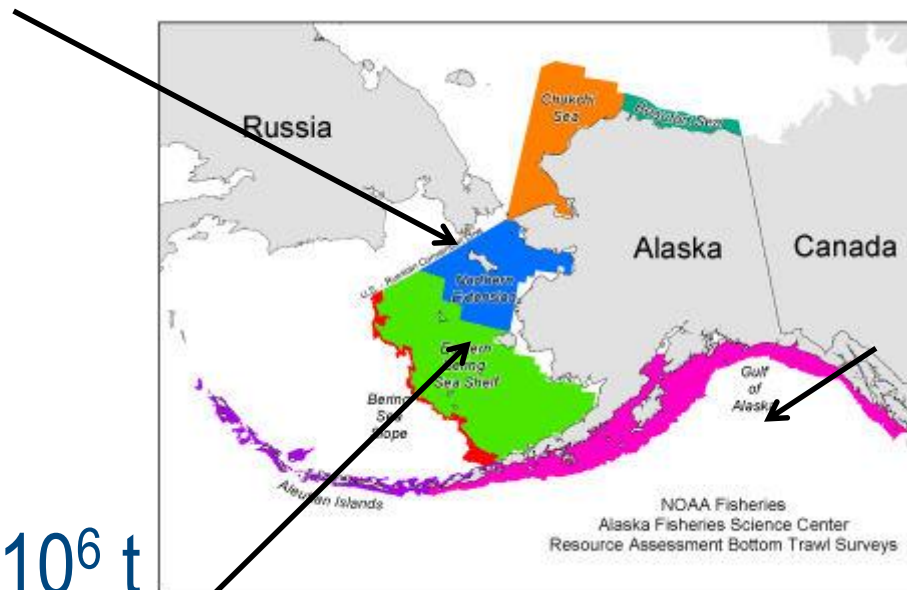
# 2017: shifts in distribution of Pacific cod

Pacific cod in the NBS increased from 28,425 t to 286,310 t between 2010 and 2017,



# 2017: we observed more walleye pollock in the Northern Bering Sea

- 2010: 11,000 t.
- 2017: 1.3 million t.



2016: 4.9 x10<sup>6</sup> t

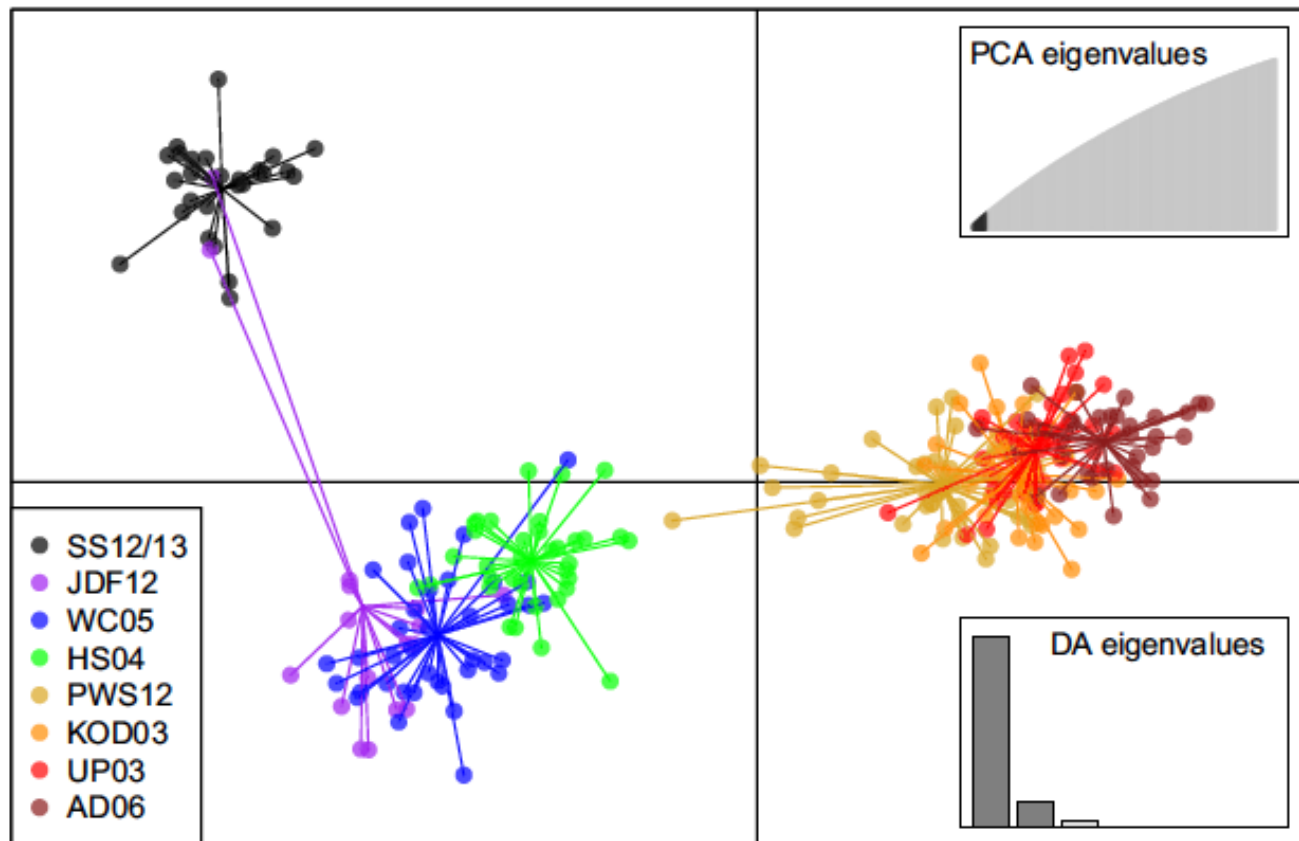
2017: 4.8 x10<sup>6</sup> t

BSAI SAFE Introduction, 2017

# Could genetics be used to identify origins of NBS P.cod?

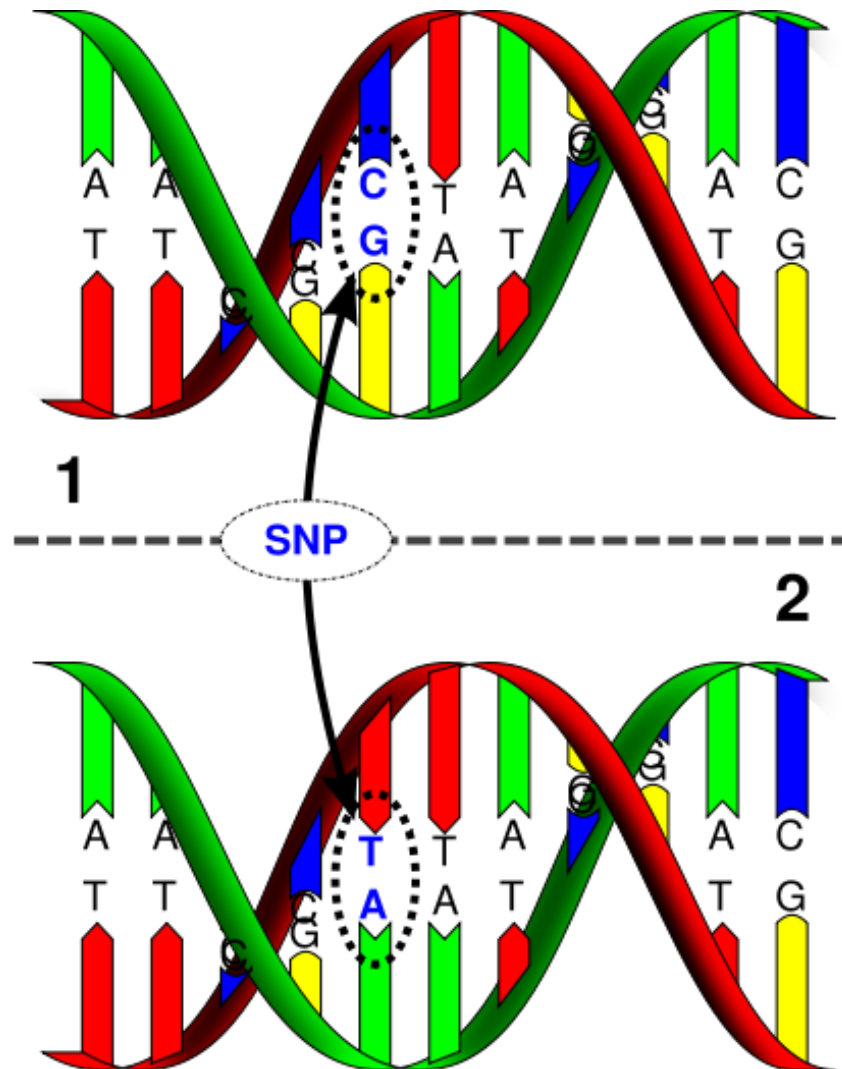
- Recent work indicated that this might be possible (Drinan et al. 2018).

# Drinan et al.: 6,425 SNP loci characterized differences among spawning groups



Drinan et al. 2018

# What is a SNP? Single Nucleotide Polymorphism



# What is RAD sequencing?

## Many DNA sequences throughout the genome.

### RAD (restriction-site associated DNA) sequencing

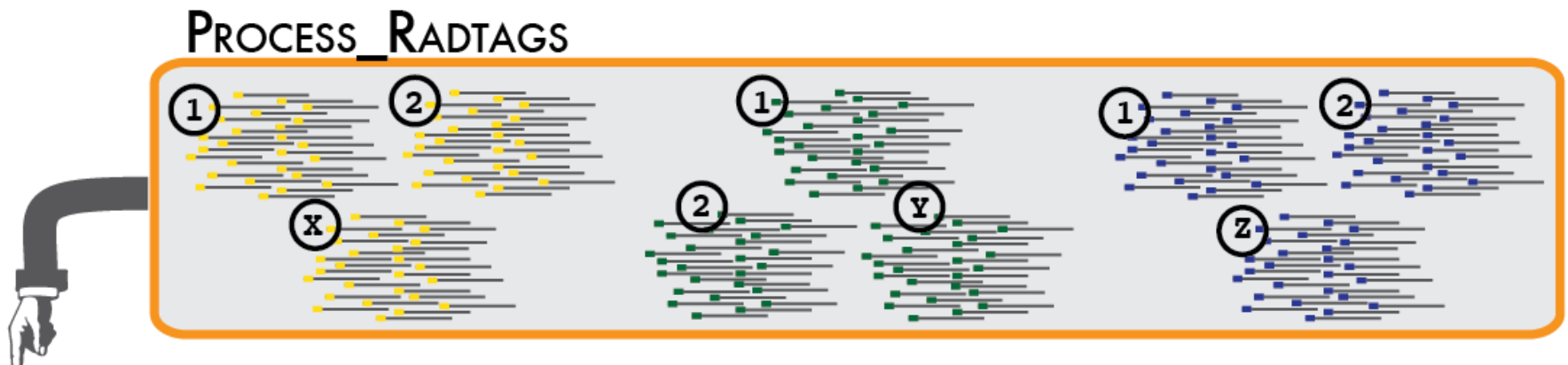
SbfI



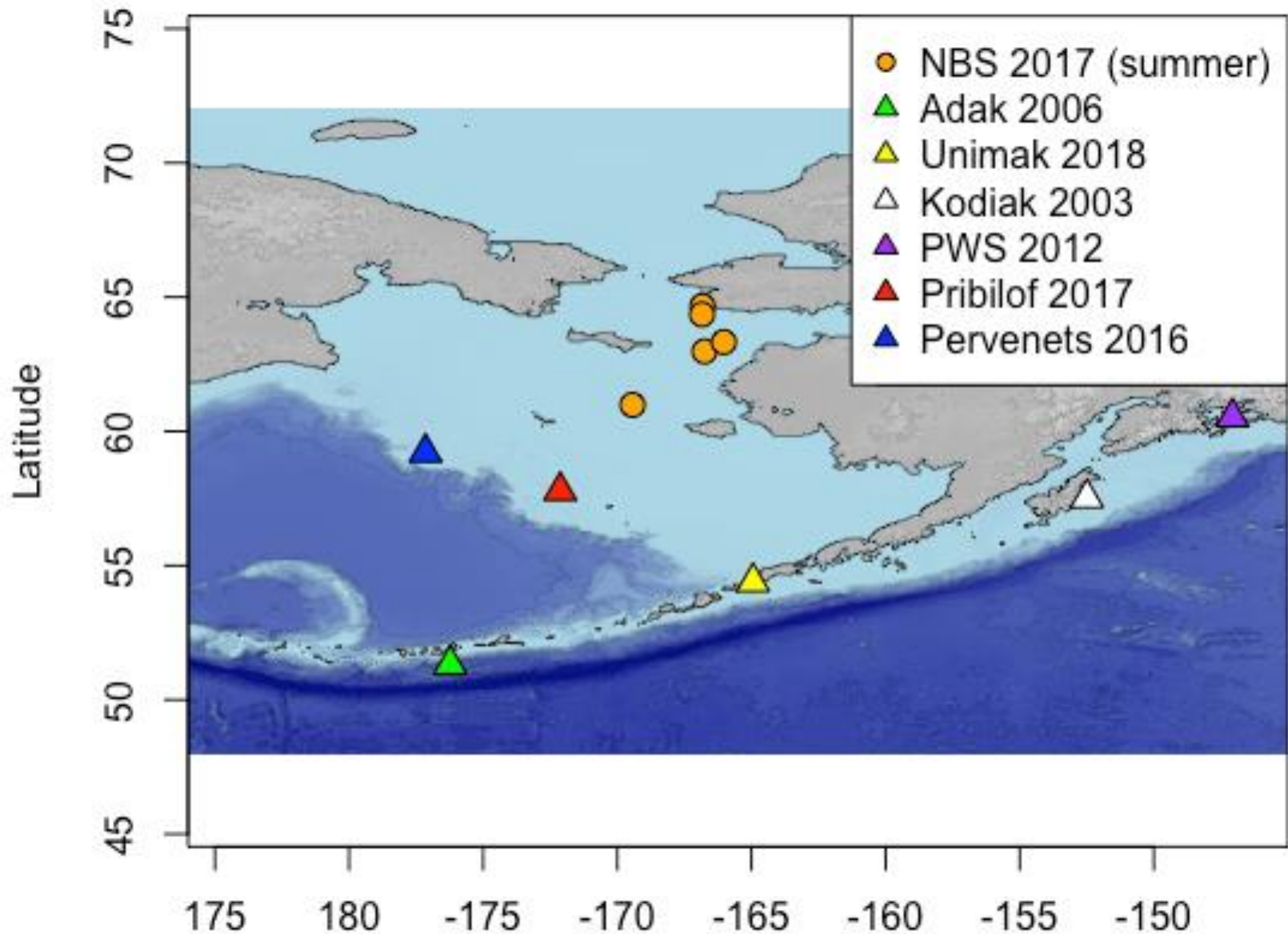
5'... CCTGCAGG... 3'  
3'... GGACGTCC... 5'

Atlantic cod genome: 25 million base pairs.

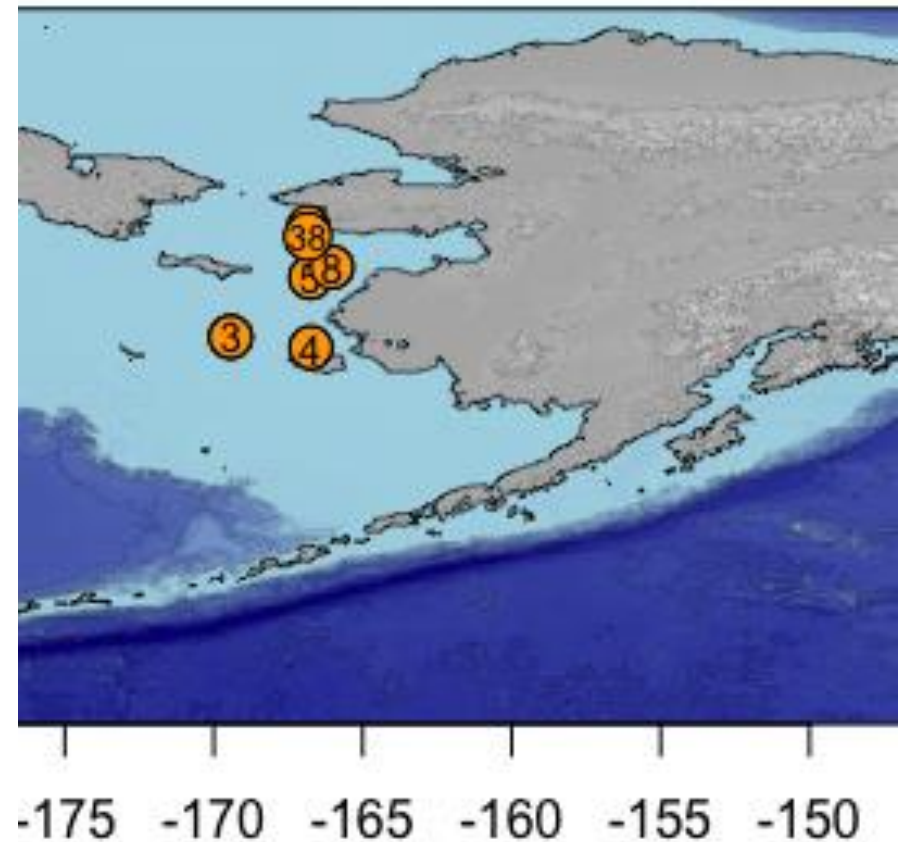
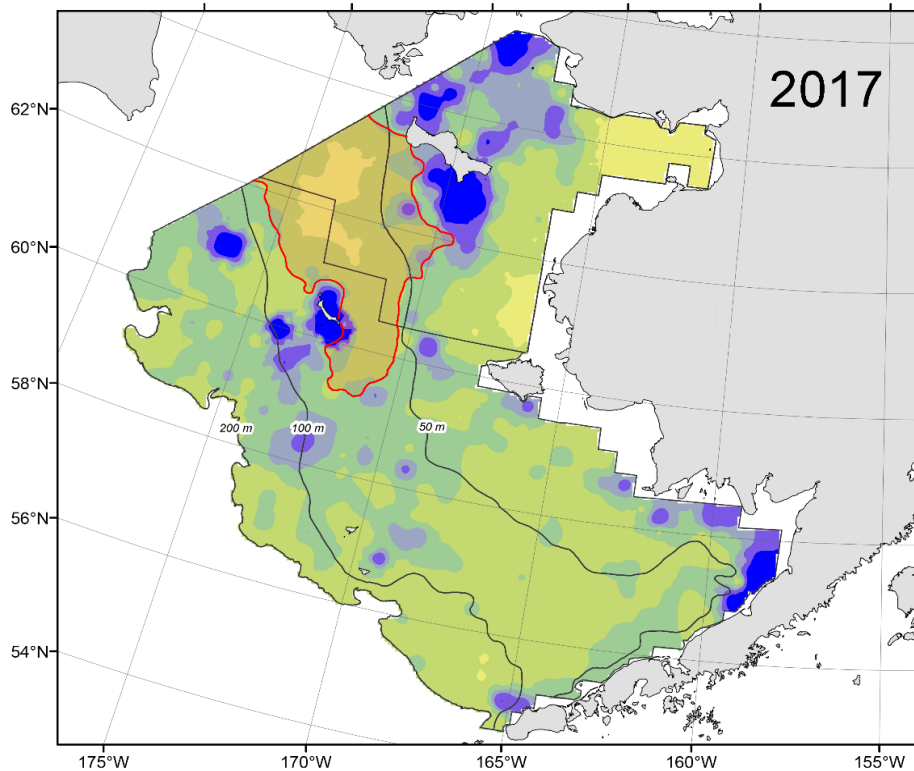
# RAD sequencing – many sequences aligned



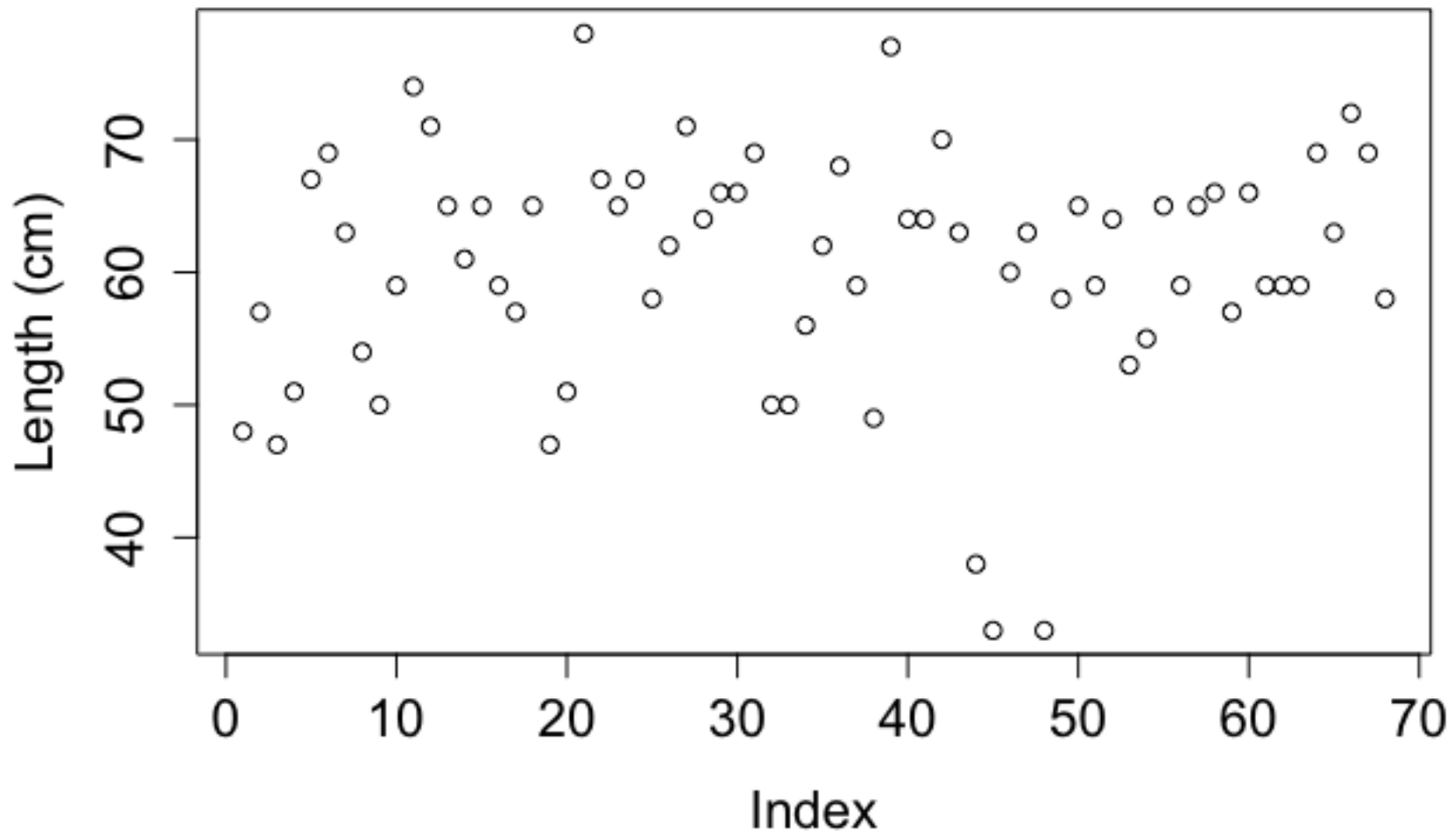
# Genetic baselines from six spawning populations



# Samples were obtained from the Northern Bering Sea in 2017



Northern Bering Sea sample ranged from 33-78 cm  
(as young as 2 years old)



# Samples

Location	Month / Year	Abbr.	Lat.	Long.	N
Prince William Sound*	Mar. 2012	PWS12	60° 32' N	147° 4' W	47
Kodiak Island*	Mar. 2003	KOD03	57° 48' N	152° 31' W	45
Adak Island*	Mar. 2006	AD06	51° 40' N	176° 36' W	45
Northern Bering Sea	Aug. 4, 2017		60° 59' N	169° 26' W	3
	Aug. 18, 2017		60° 37.8' N	166° 44.8' W	4
	Aug. 18, 2017		62° 59' N	166° 45' W	5
	Aug. 18, 2017		63° 19' N	166° 02' W	8
	Aug. 23, 2017		64° 40' N	166° 50' W	10
	Aug. 23, 2017		64° 21' N	166° 50' W	38
					<hr/> 68
Pribilof Canyon	Apr. 10 2017		57° 47' W	172° 8' W	48
Pervenets Canyon	Mar. 28 2016		59° 21' W	177° 13' W	48
Unimak Pass	Feb. 7 2018		54° 35' N	165° 15' W	47

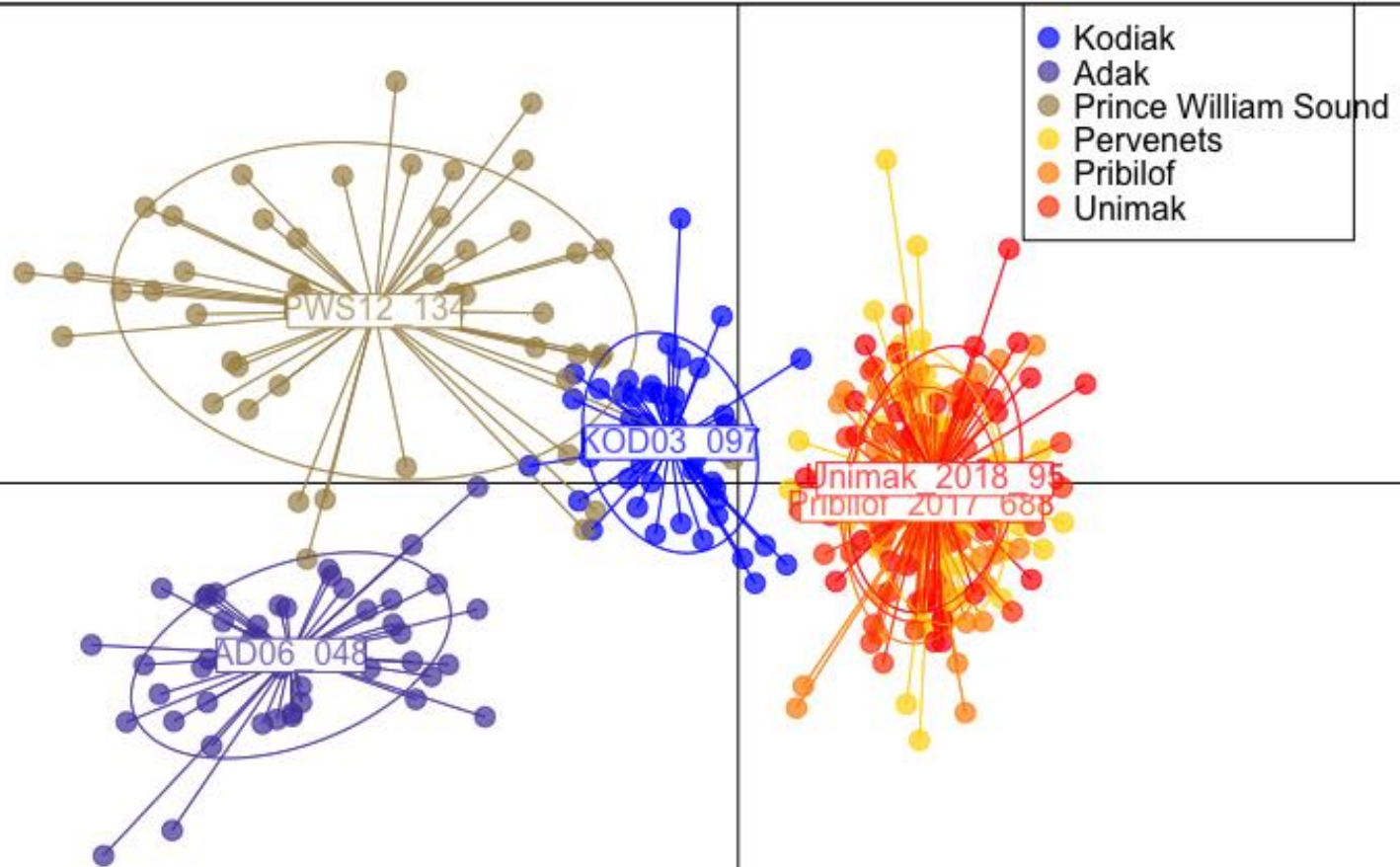
# We obtained 3,599 SNP loci.

- Data were quality checked for Hardy-Weinberg Equilibrium, linkage disequilibrium.
- Loci were only selected if they were represented in 6 of 7 populations.
- Total genotyping rate was 96%.

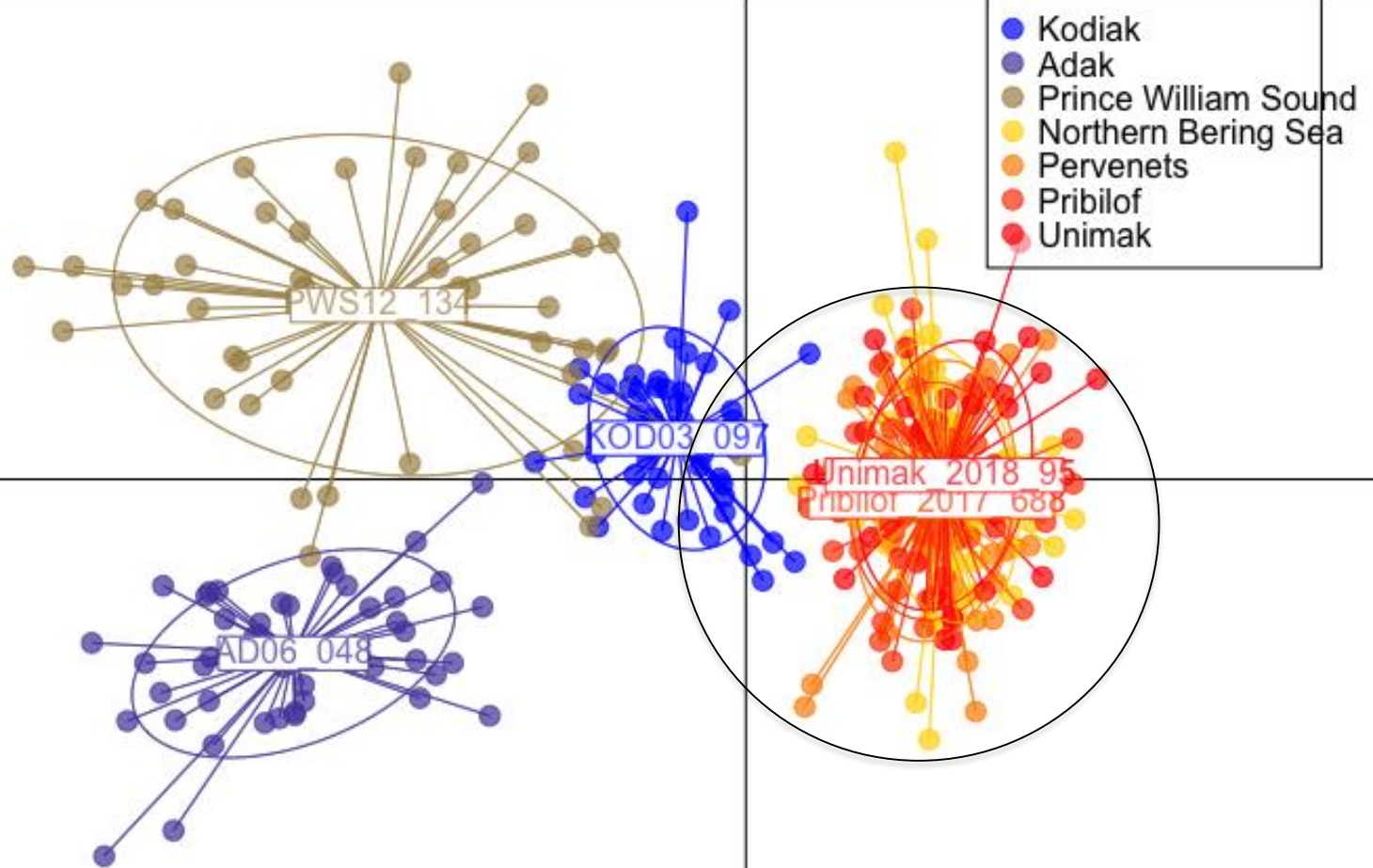
# Discriminant analysis by principal component

- Used to visualize spatial relationships in the data.
- Data transformed using a principal components analysis (PCA) and subsequently clusters are identified using discriminant analysis (DA).
- Sample is partitioned into a between-group and within- group component, in an effort to maximize discrimination between groups.
- Number of principal components were optimized.

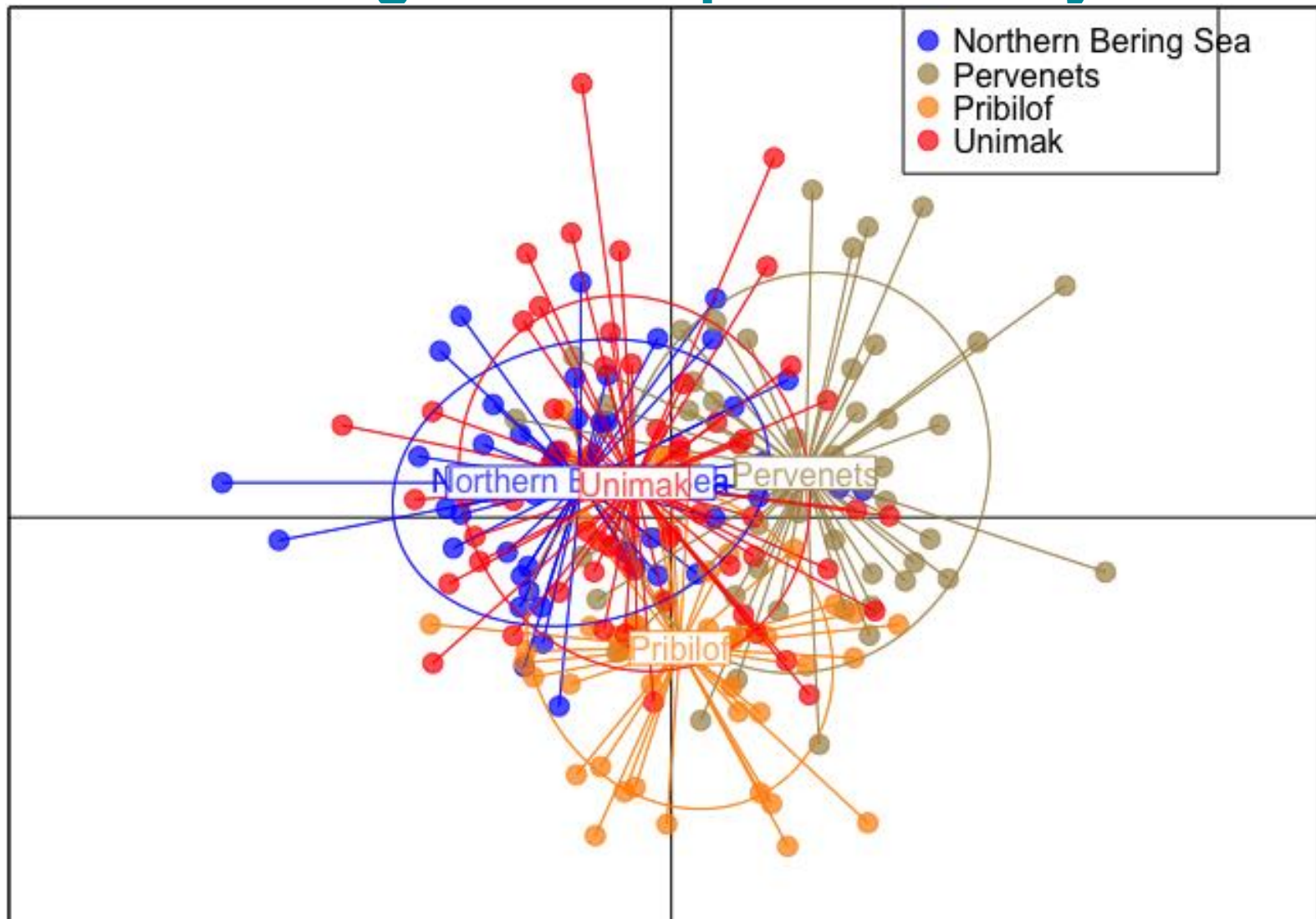
# Eastern Bering Sea samples cluster together, separate from Kodiak, Prince William Sound, Adak



# Eastern Bering Sea and Northern Bering Sea samples cluster together



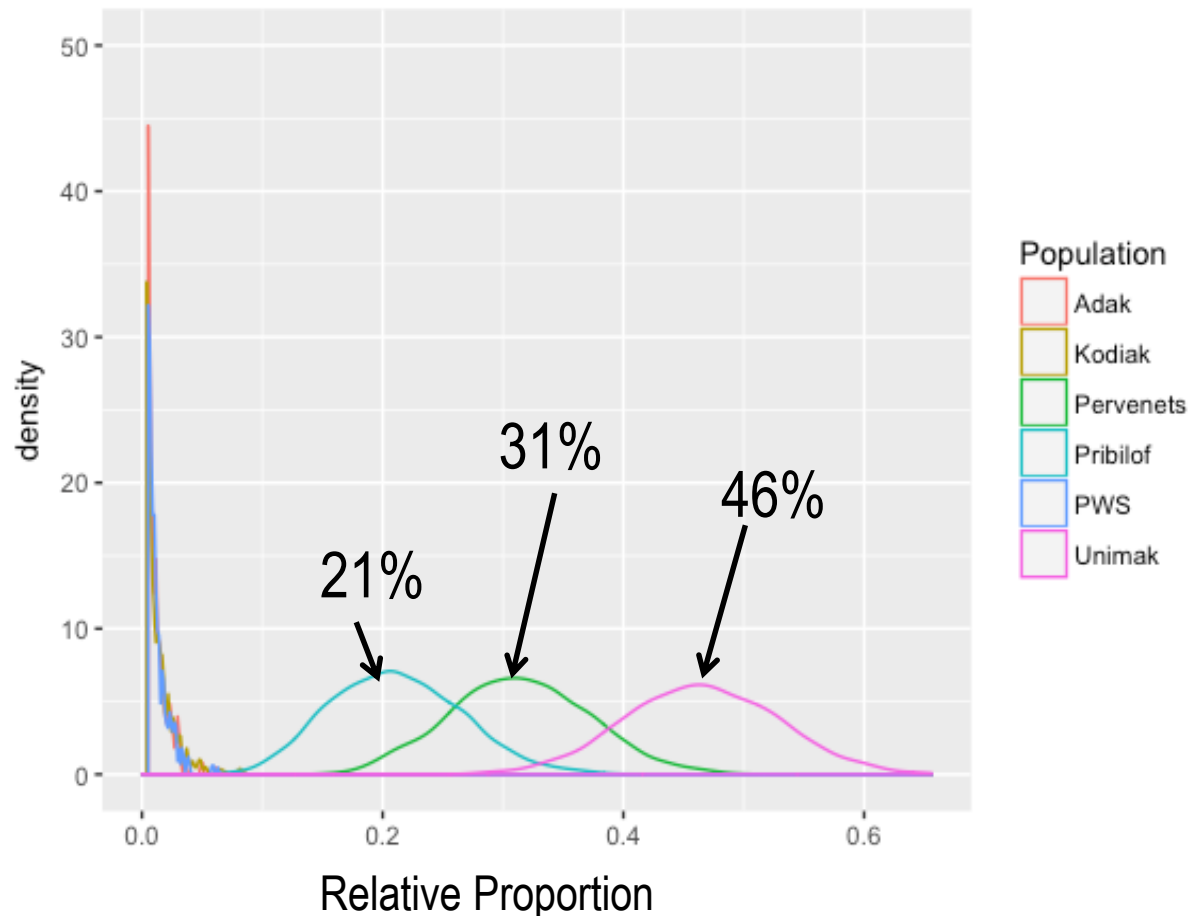
# Eastern Bering Sea samples are very similar.



# Assignment testing

- Rubias (Eric Anderson, SWFSC).
- Use spawning stocks as “reference populations”.
- Northern Bering Sea sample as “unknown”.
- Statistical finite mixture model for genetic stock ID (GSI\_SIM).
- Also a simulation mode to predict the accuracy of assignment test.

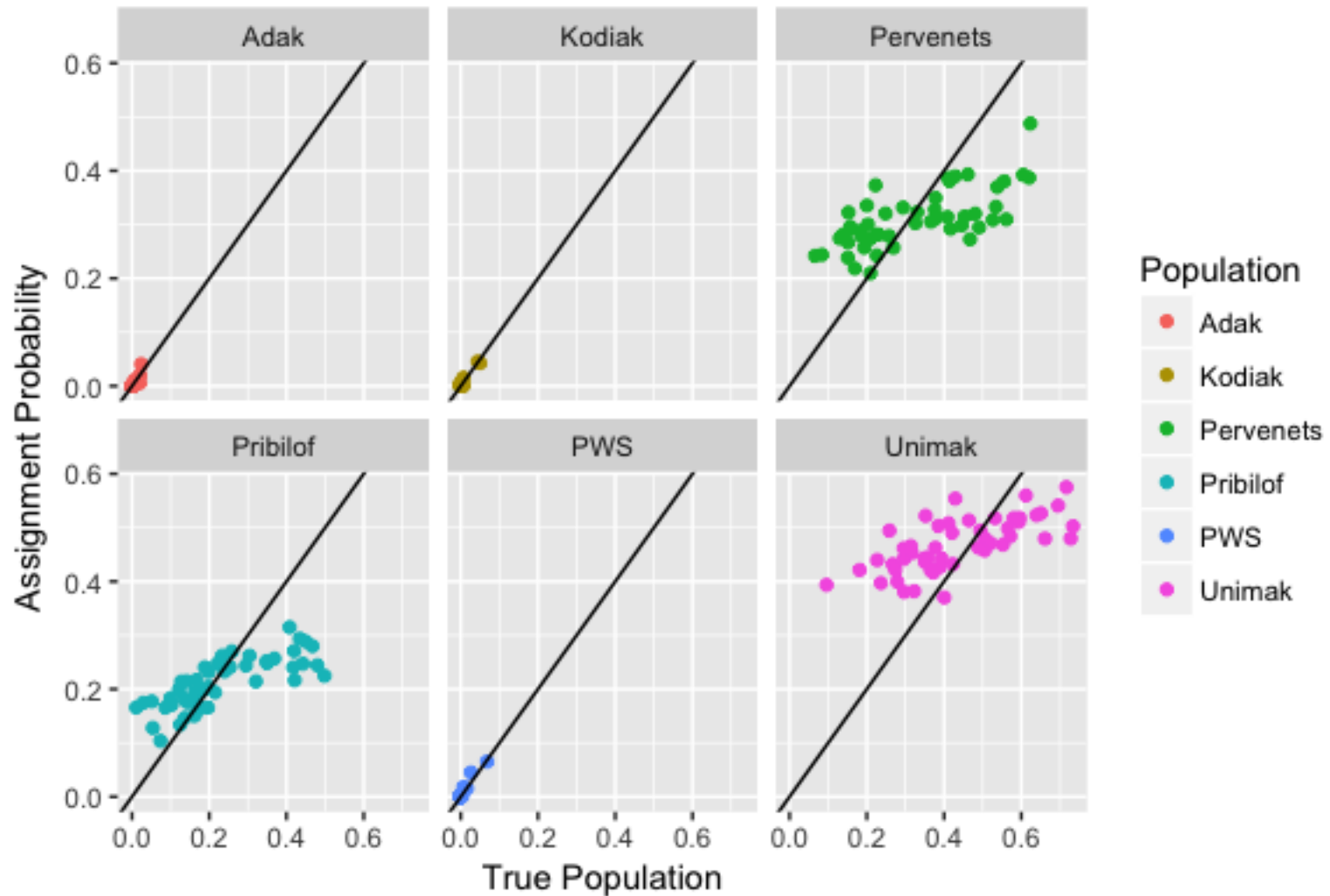
# Northern Bering Sea sample assigns to Southern Bering Sea samples



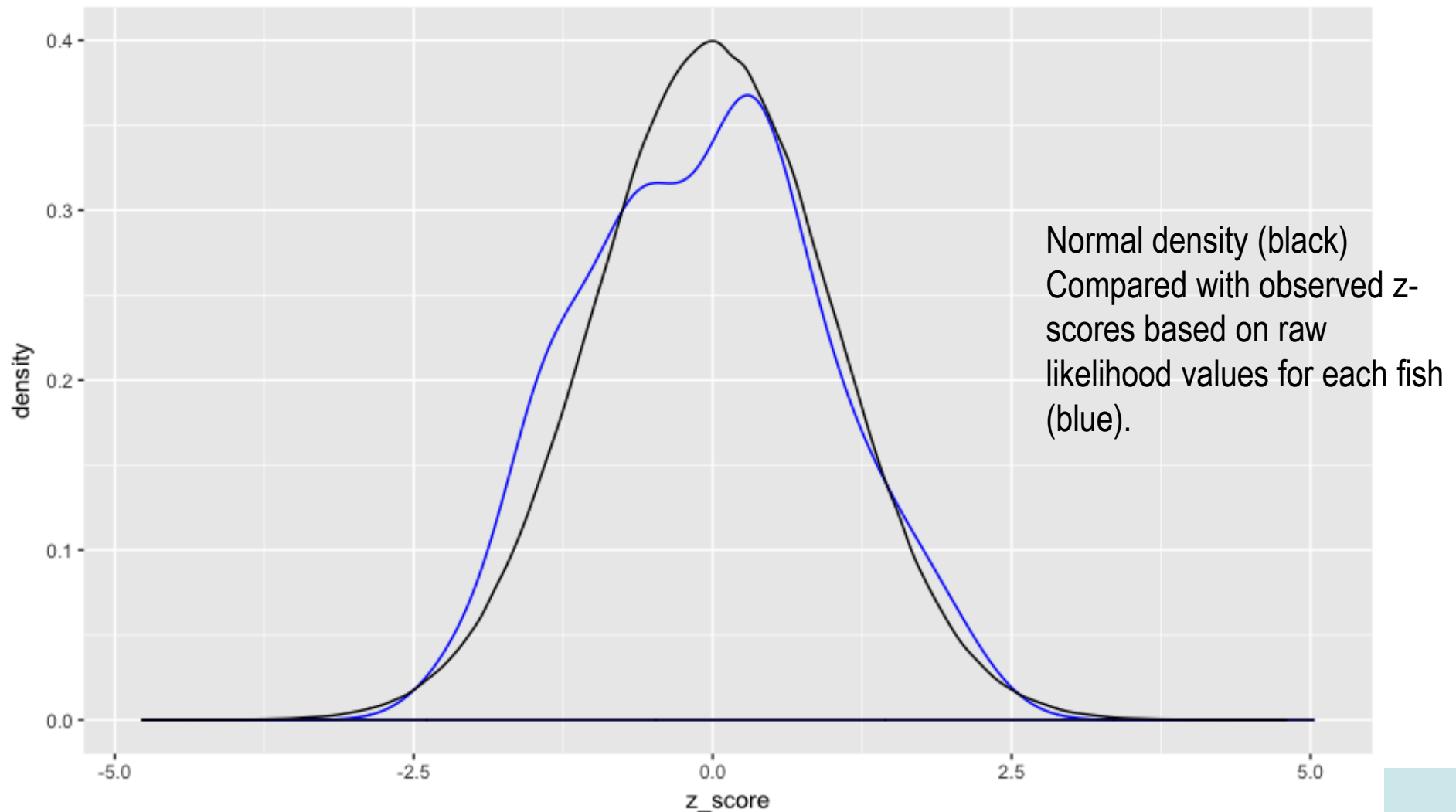
# Samples outside the Eastern Bering Sea had assignment probability close to zero.

Mixture sample	Assignment to reference	P	loCI	hiCI
NBS	Adak (2006)	0.002	5e-13	0.020
NBS	Kodiak (2003)	0.004	6e-12	0.030
NBS	Pervenets (2016)	0.314	0.2	0.443
NBS	Pribilof (2017)	0.214	0.1	0.328
NBS	PWS (2012)	0.002	1e-12	0.018
NBS	Unimak (2018)	0.464	0.3	0.586

# Simulated sample indicates accurate assignment



# Northern Bering Sea sample was not from another location (like Russia).



# $F_{ST}$ values ranged from 0.0002 to 0.0146

	Kodiak 2003	Adak 2006	PWS 2012	NBS 2017	Pervenets 2016	Pribilof 2017	Unimak 2018
Kodiak 2003							
Adak 2006	0.0094						
PWS 2012	0.0051	0.0072					
NBS 2017	0.0036	0.0139	0.0103				
Pervenets 2016	0.0041	0.0141	0.0107	0.0003			
Pribilof 2017	0.0038	0.0141	0.0109	0.0002	0.0008		
Unimak 2018	0.0037	0.0146	0.0100	0.0002	0.0009	0.0007	

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# Does the Northern Bering Sea sample show any reduction in genetic diversity?

Sampling location	N	A	$F_{IS}$
Adak	45	7,166	-0.0102
Kodiak	45	7,165	0.0275
Northern Bering Sea	68	7,142	0.0330
Pervenets	48	7,133	0.0302
PWS	47	7,186	0.0132
Pribilof	48	7,126	0.0254
Unimak 2018	47	7,135	0.0234

Positive  $F_{IS}$ : more related than you might expect by random mating.

Negative  $F_{IS}$ : less related than you might expect by random mating.

# Conclusions

- Pacific cod samples from the 2017 NBS survey were most similar to EBS spawning populations.
- Not from the GOA or from Russia.

# What is next?

- Whole genome sequencing (2019).
- More complete set of Northern Bering Sea samples (2019).
- Samples:
  - NBS survey
  - Commercial fishing
  - IPHC (International Pacific Halibut Commission)
  - Volunteer fishing efforts

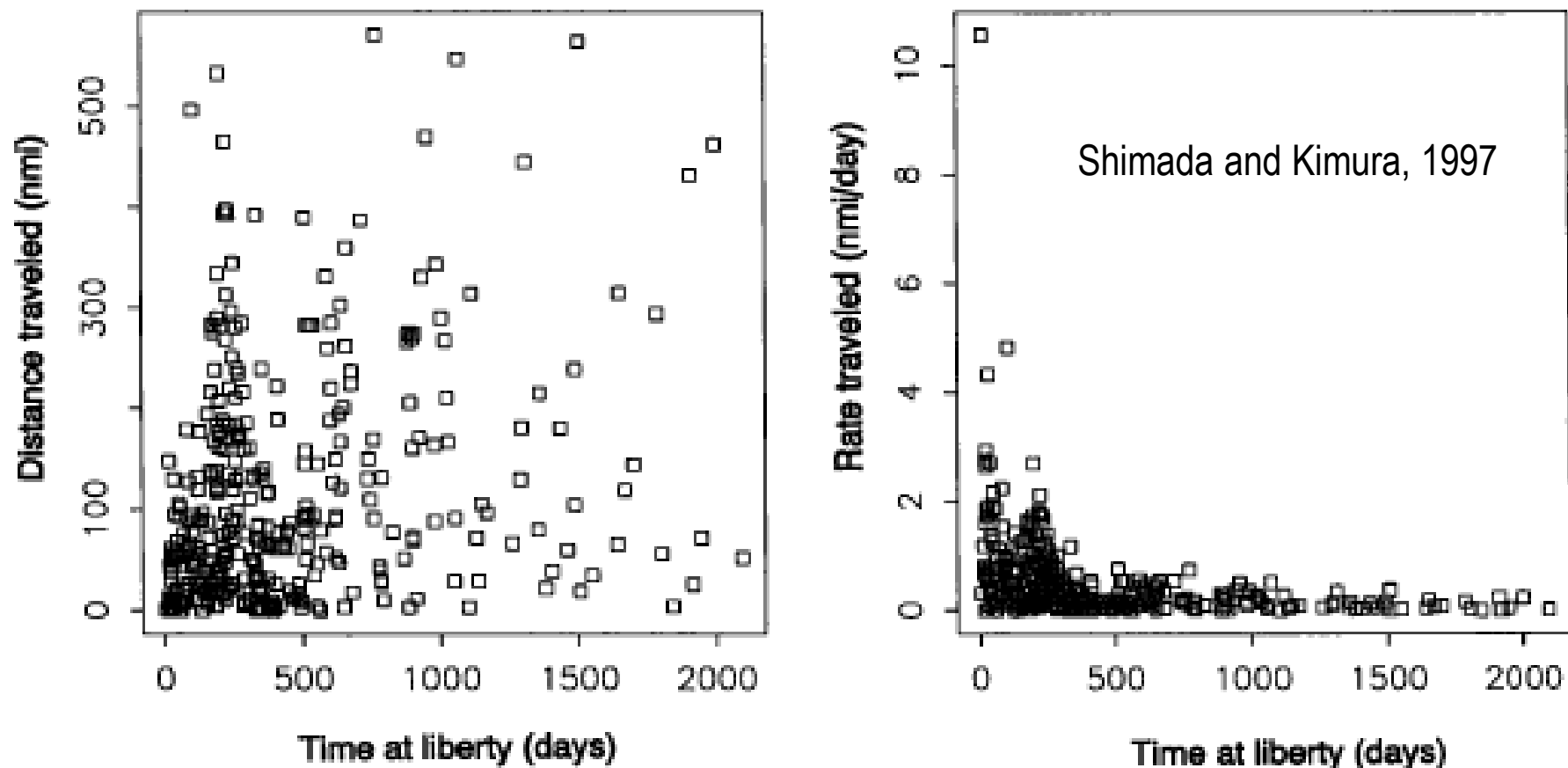
# Conclusions

- Northern Bering Sea sample (68 fish from August 2017) is most similar to spawning cod from the Southern Bering Sea.
- Not enough resolution in the data to identify to spawning stock within the EBS.
- Northern Bering Sea sample was not from Gulf of Alaska, Russia, or elsewhere.

# Movement observed may exceed typical summer feeding movements of Pacific cod.



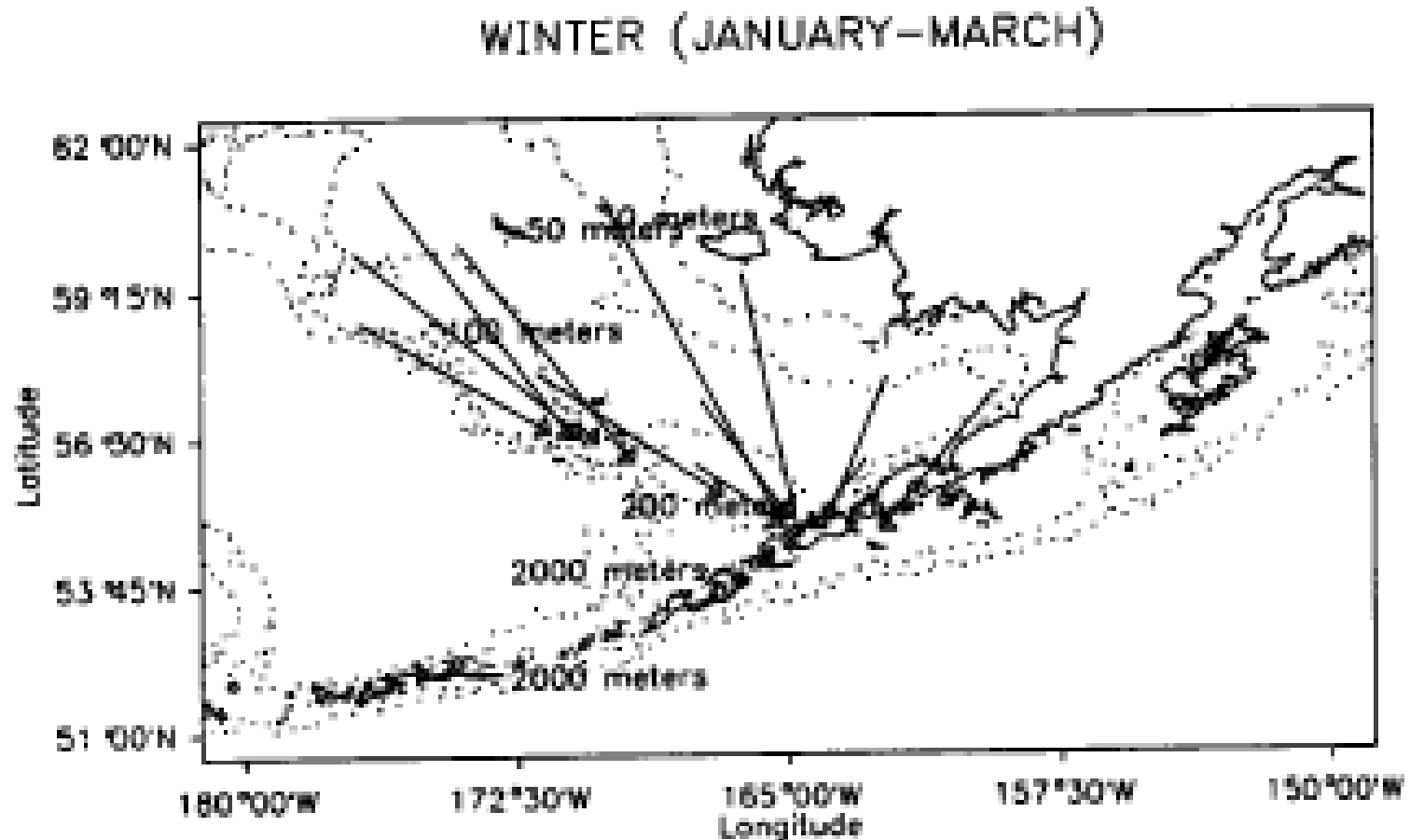
Greatest distance travelled in 1 year is  
~550 nmi = 1016 km



**Figure 9**

Scatter plots showing (left) the relationship between distance traveled (in nautical miles) and time at liberty and (right) the relationship between rate of travel and time at liberty for Pacific cod.

# Cod biology is an important part of the story



# Implications and questions

- Is a 1,000+ km feeding migration realistic?
- Will there be a change in reproduction?
- Will all cod return to spawn in their spawning area of origin?



# Thank you!

- Funding:
  - Norton Sound Fund
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