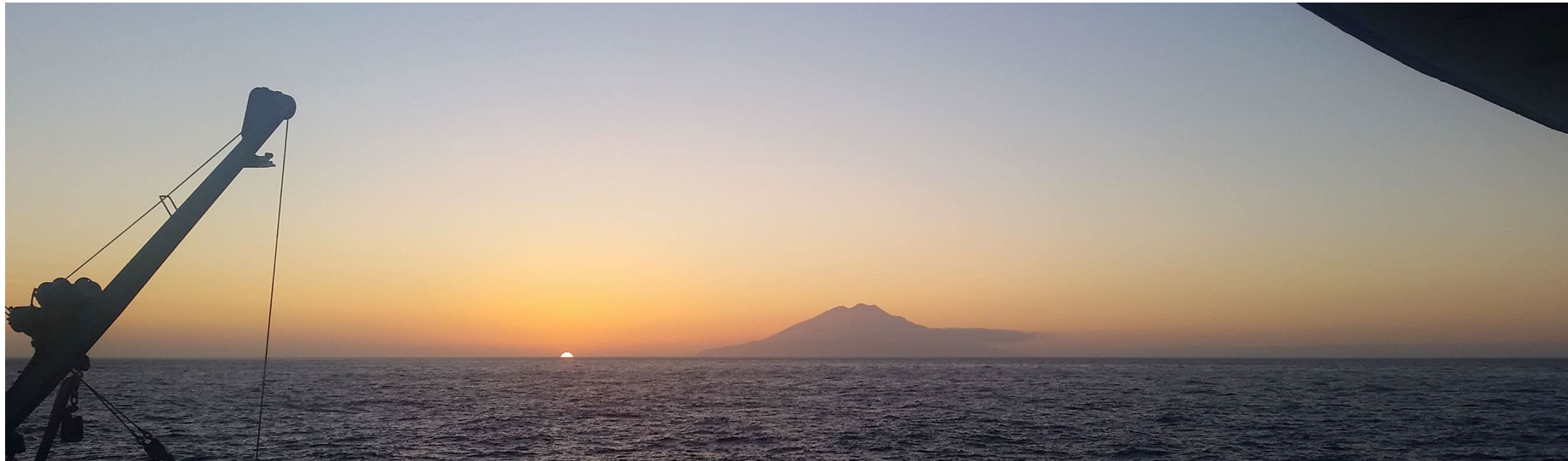
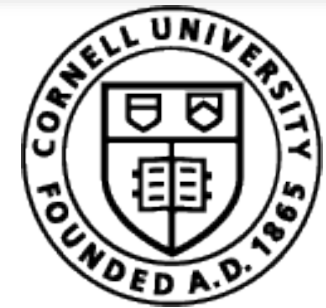
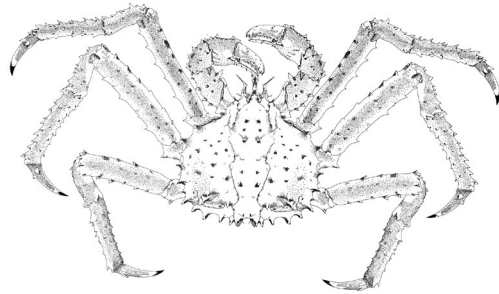


Whole genome sequencing reveals substantial genetic structure and local adaptation in Alaskan Red King Crab

Carl St. John¹, Laura Timm², Wesley A. Larson²

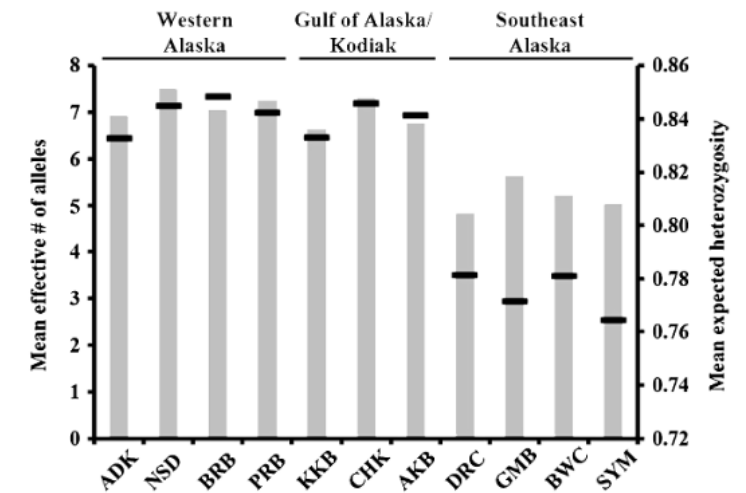
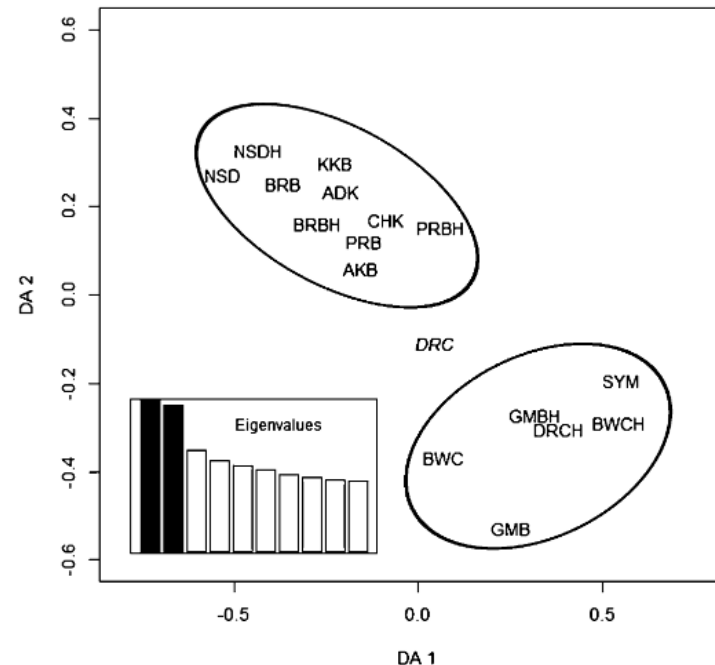
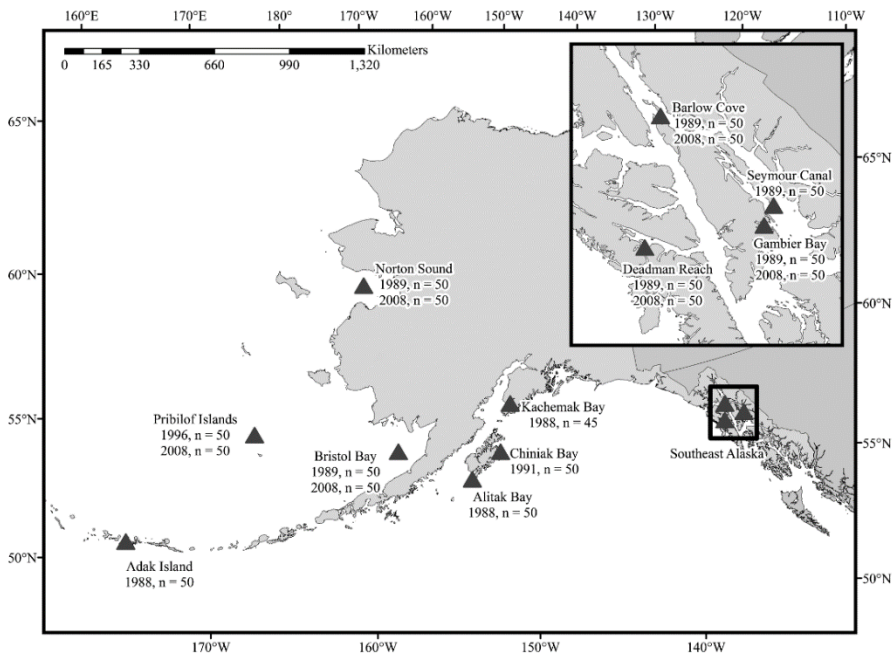
¹Cornell University, Dept. Natural Resources & the Environment

²NOAA ABL, Genetics Program



Past research finds broad scale structure: Vulstek et al. (2013)

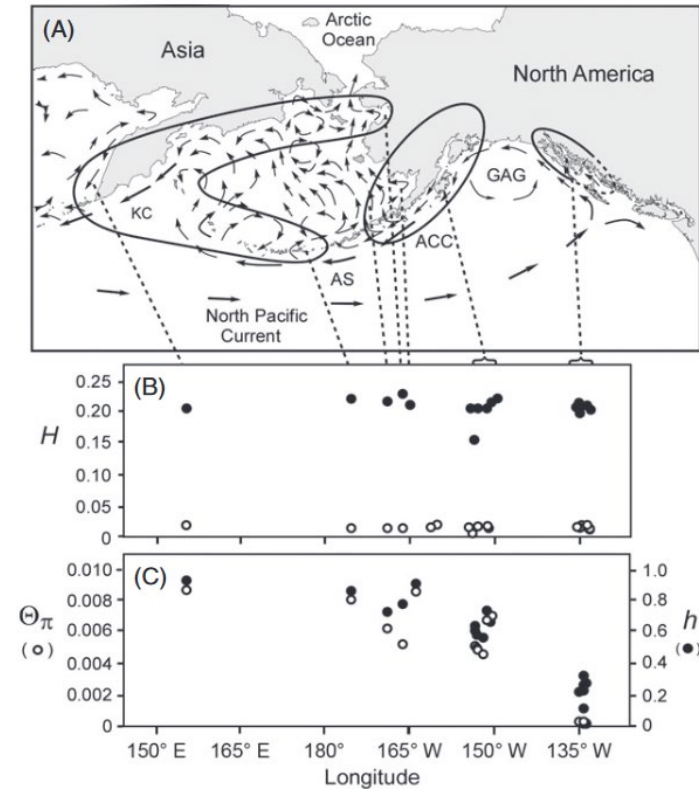
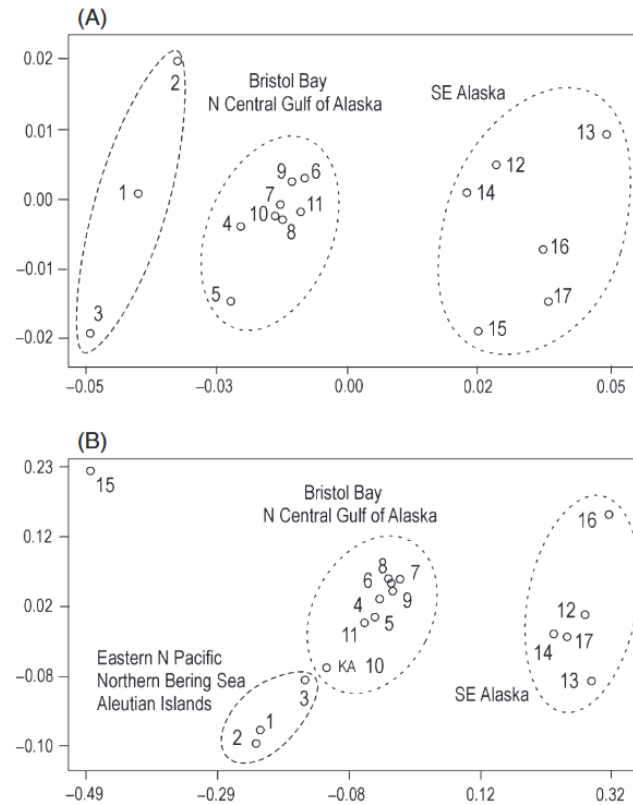
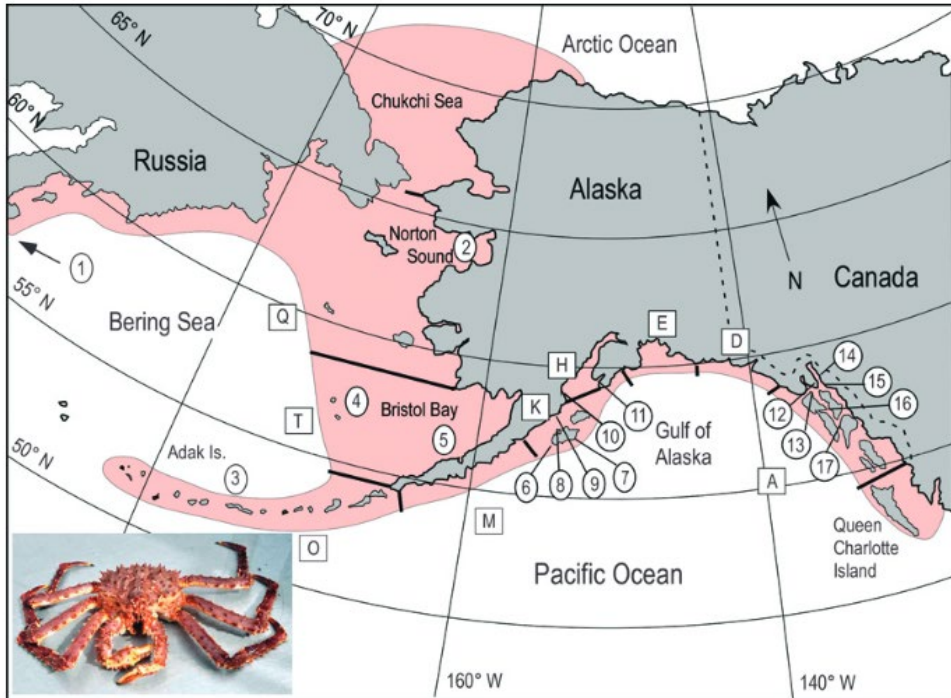
- Six microsatellite loci
- 11 sampling locations, N = 50 for each location except for Kachemak Bay (N = 45)



ADK (Adak Island), NSD (Norton Sound), BRB (Bristol Bay), PRB (Pribilof Islands), KKB (Kachemak Bay), CHK (Chiniak Bay), AKB (Alitak Bay), DRC (Deadman Reach), GMB (Gambier Bay), BWC (Barlow Cove), SYM (Seymour Canal). Four letter abbreviations ending in "H" denote historic samples.

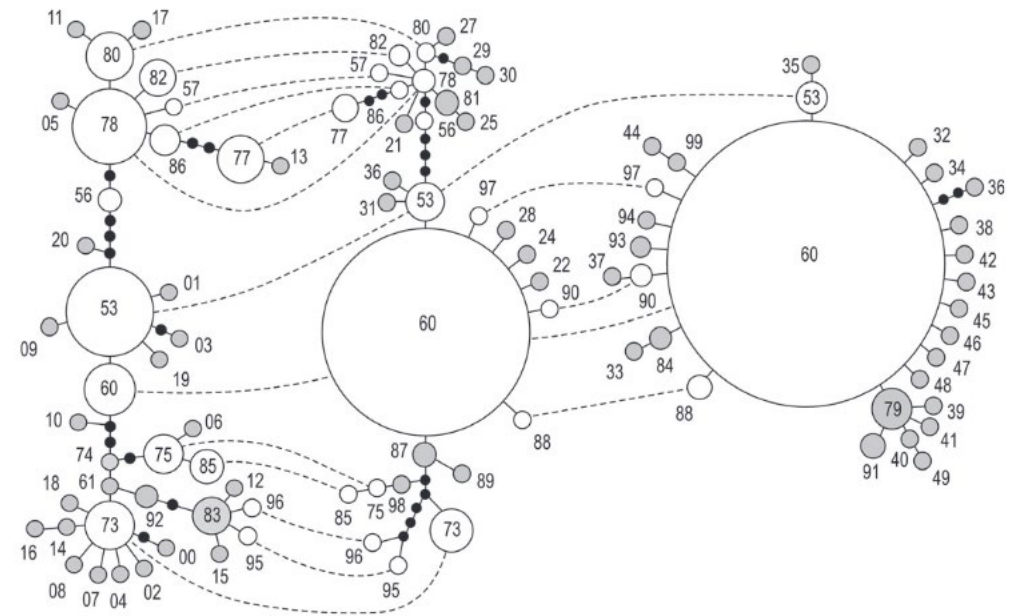
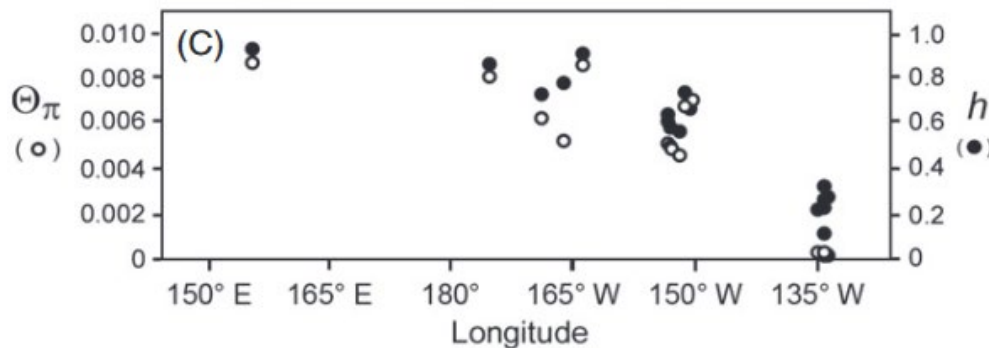
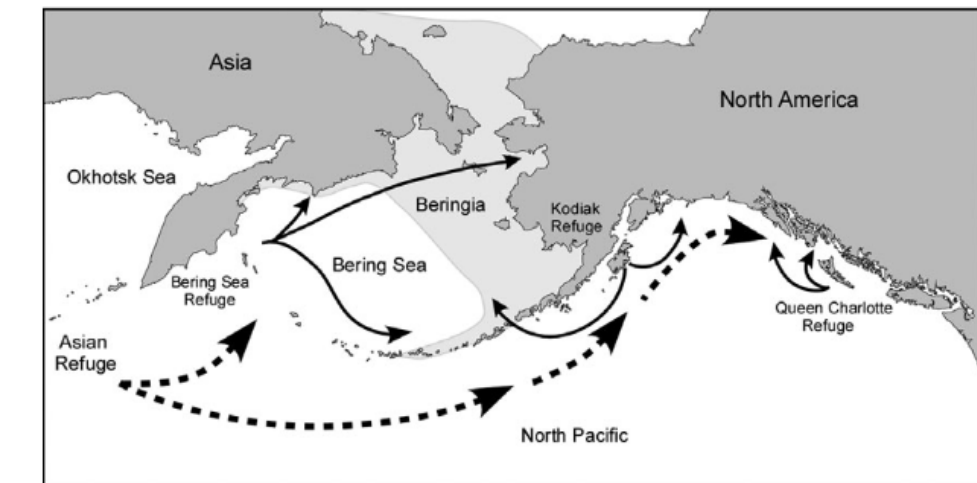
Past research finds broad scale structure: Grant and Cheng (2012)

- 665-bp fragment of mitochondrial gene COI
- 15 SNP loci
- 17 locations, N = 1501 mean N = 94



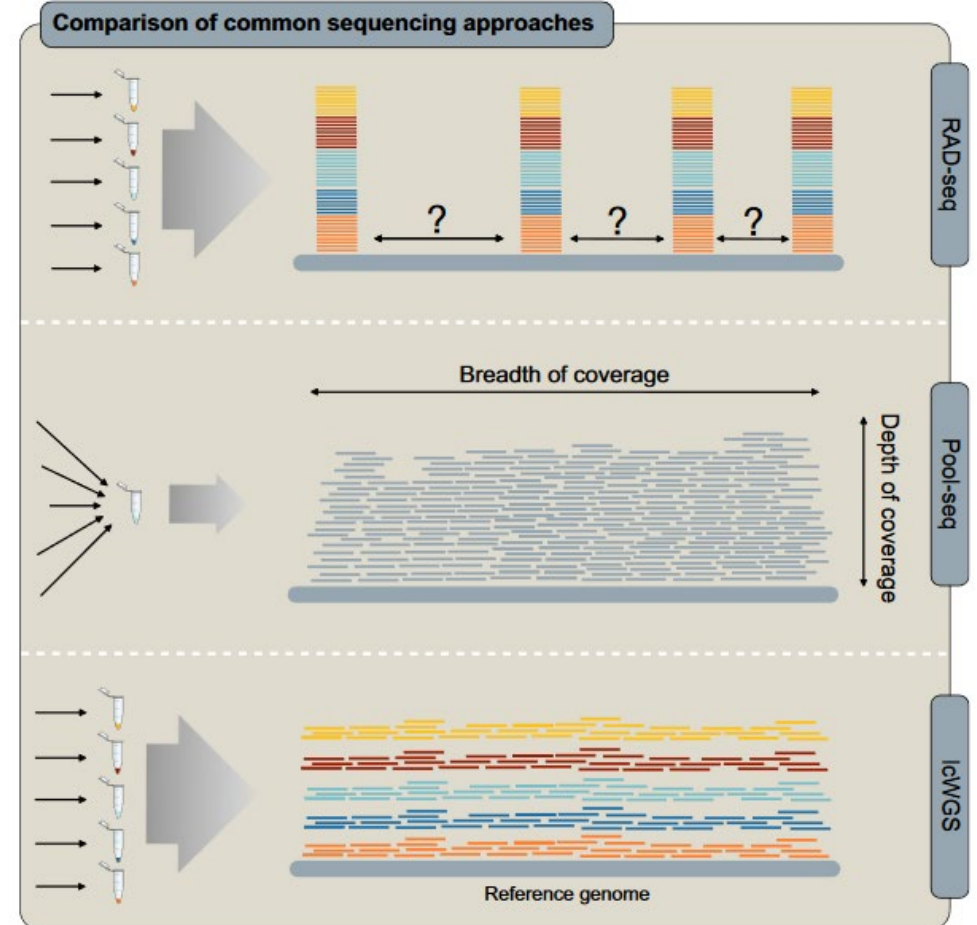
Past research finds broad scale structure: Grant and Cheng (2012)

- Differences likely result of low population size in glacial refugia, not overharvest

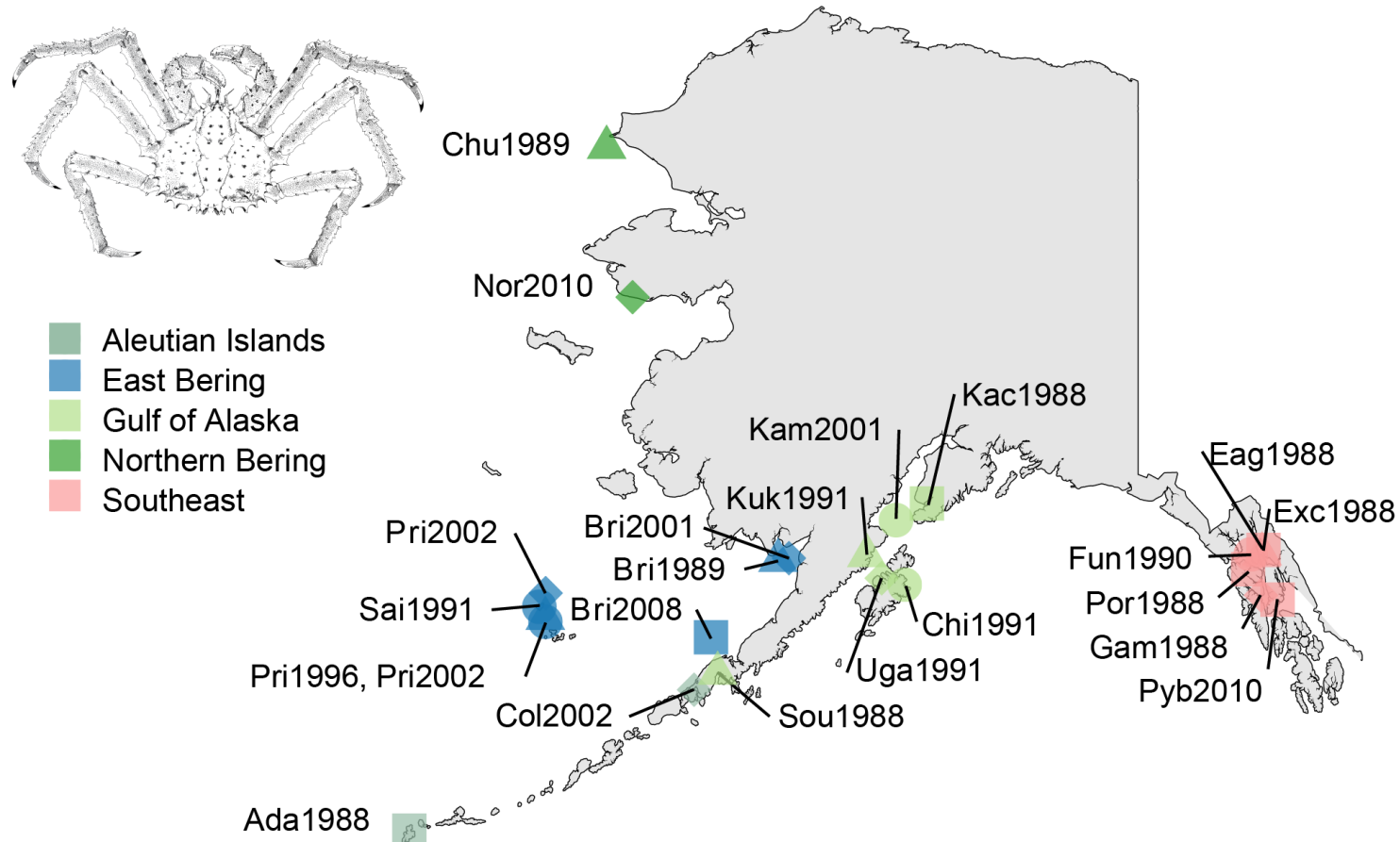


Innovations of this study

- Use low coverage whole genome sequencing (lcWGS) to add more genetic information
 - better resolution of population structure
 - Potential to detect local adaptation using genome scans
 - Comparison of wgs data to past microsat and mtDNA data

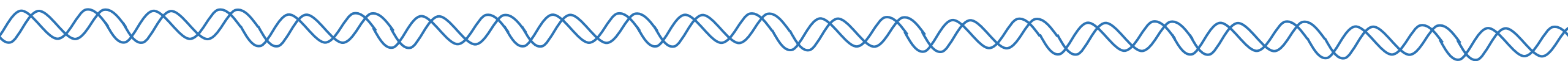


Geographic sampling

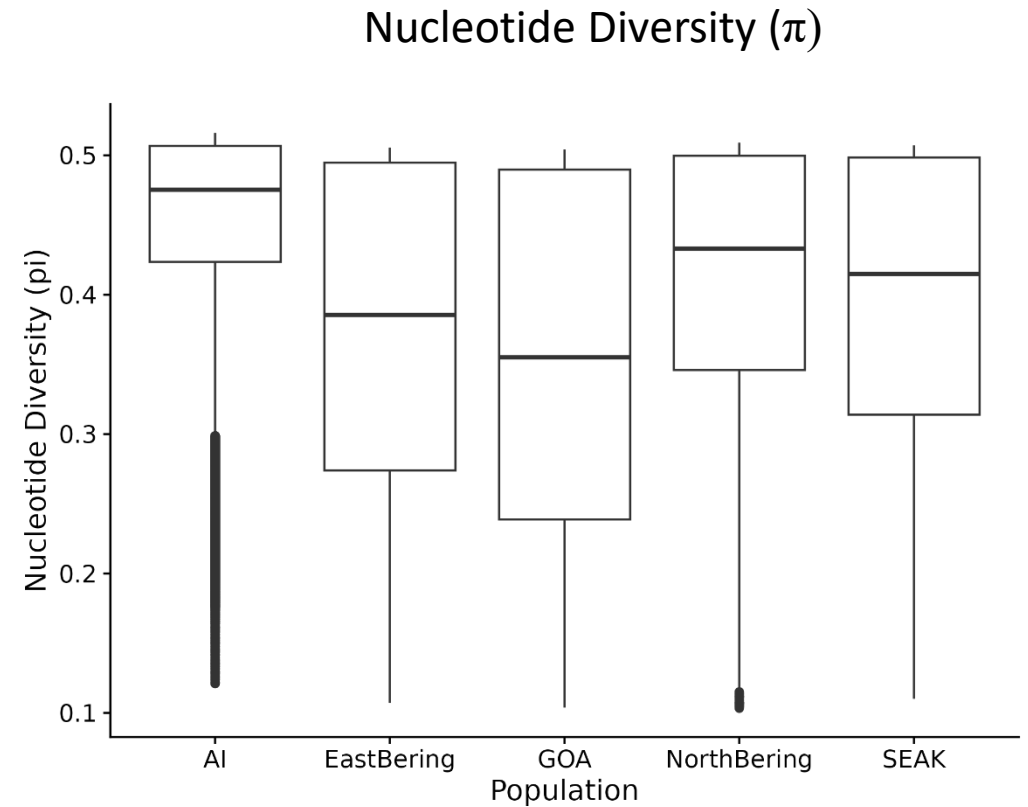
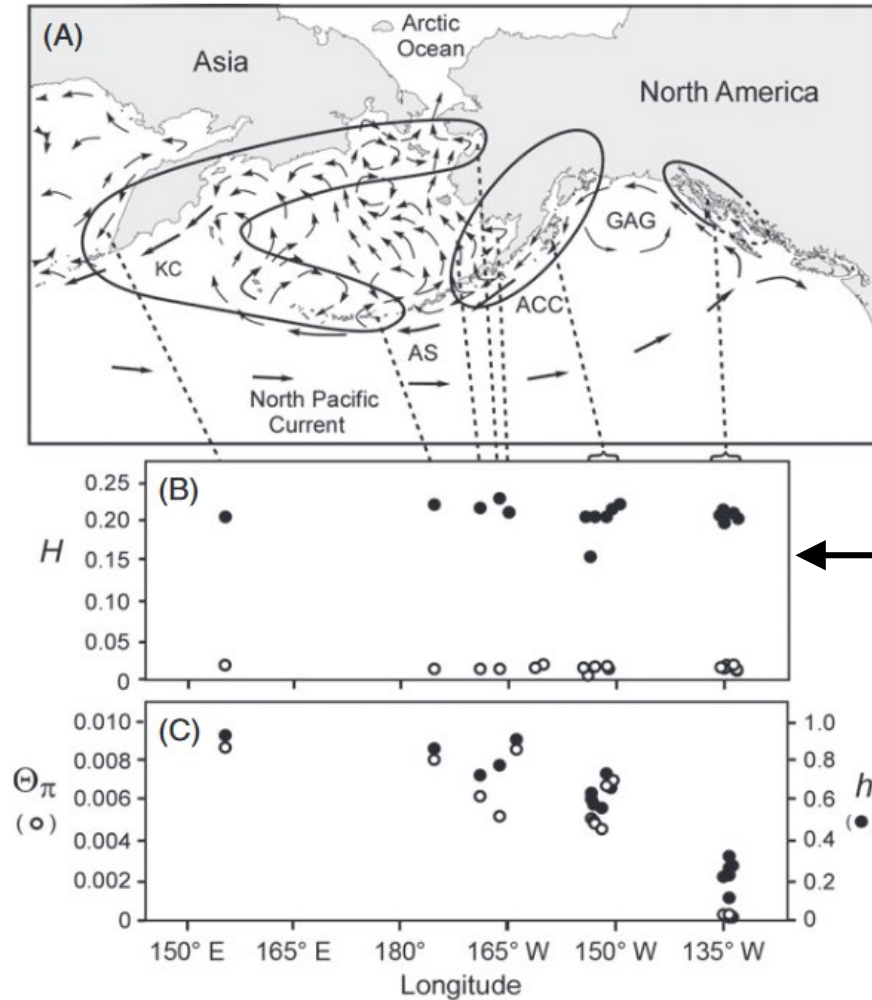


- Region abbreviations will be used on subsequent figures: AI = Aleutian Islands, East Bering = East Bering Sea, GOA = Gulf of Alaska, North Bering = North Bering Sea, SEAK = Southeast Alaska

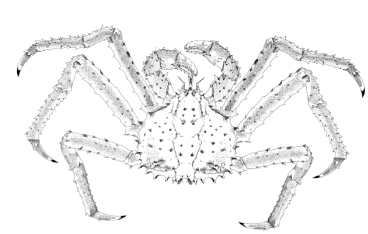
IcWGS results

- 
- 192 individuals and retained 173 after quality filtering
 - 9 excluded for low sequencing quality. 11 excluded for ambiguous metadata
 - Mean sequencing depth = 2.07351 (standard deviation = 0.637345)
 - 8973301 SNPs retained for downstream analysis

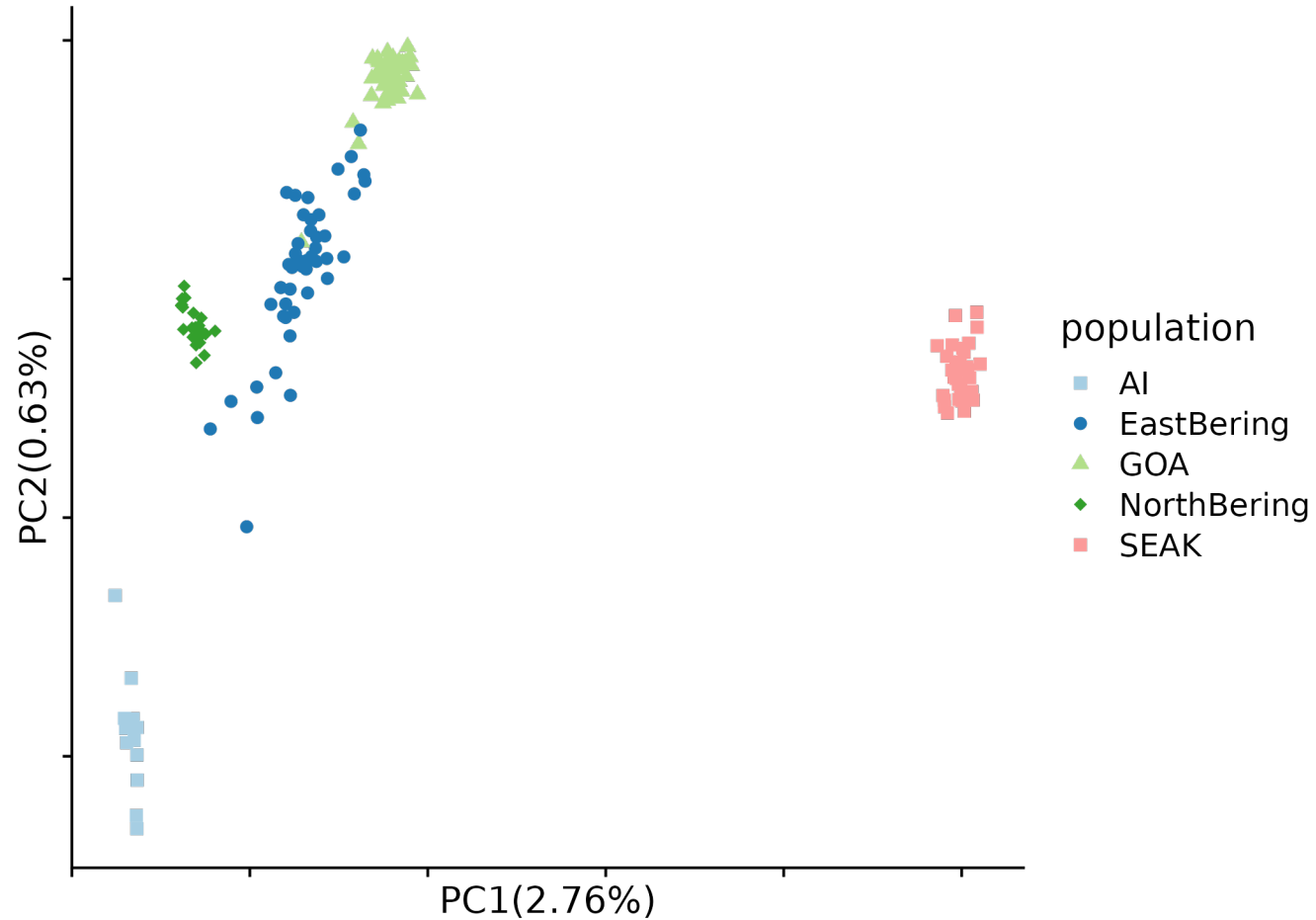
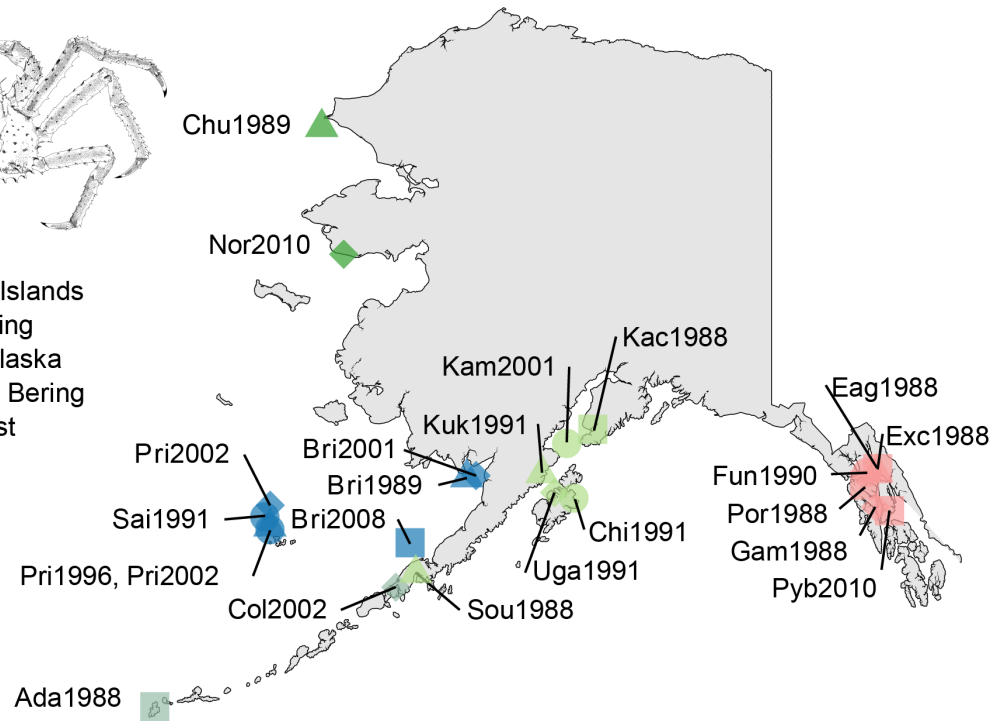
Nuclear diversity is similar across populations



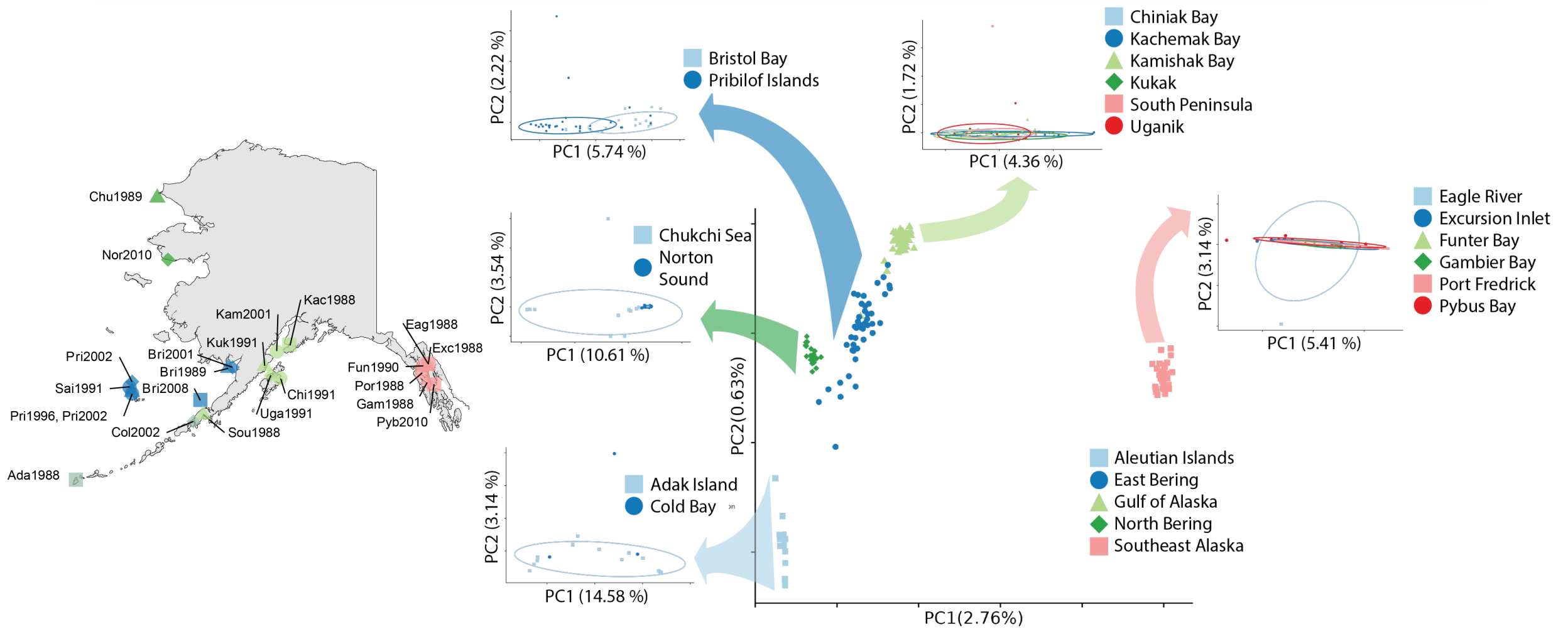
IcWGS resolves more fine scale population structure



- Aleutian Islands
- East Bering
- Gulf of Alaska
- Northern Bering
- Southeast

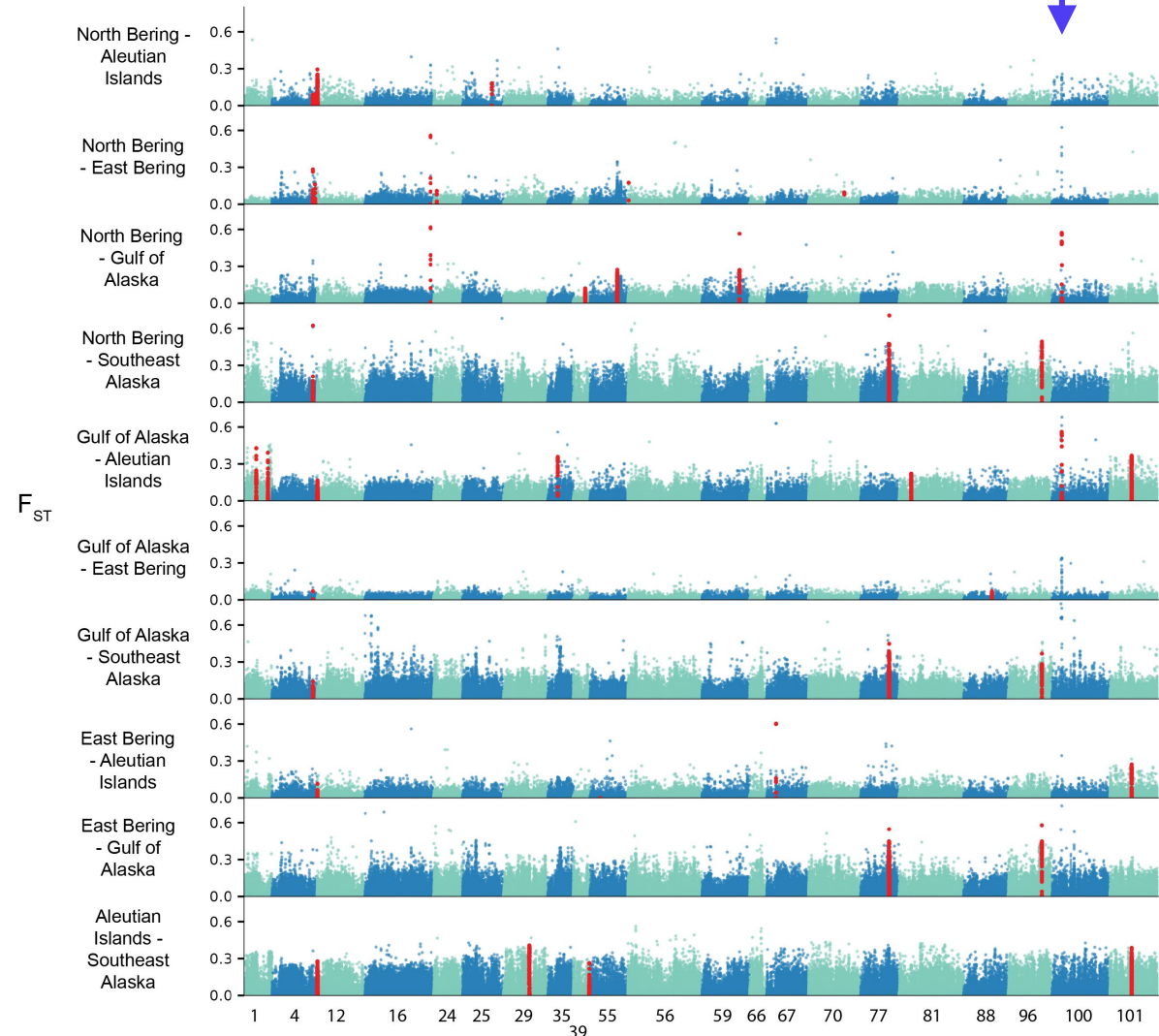


Pribilof Islands and Bristol Bay can be genetically separated



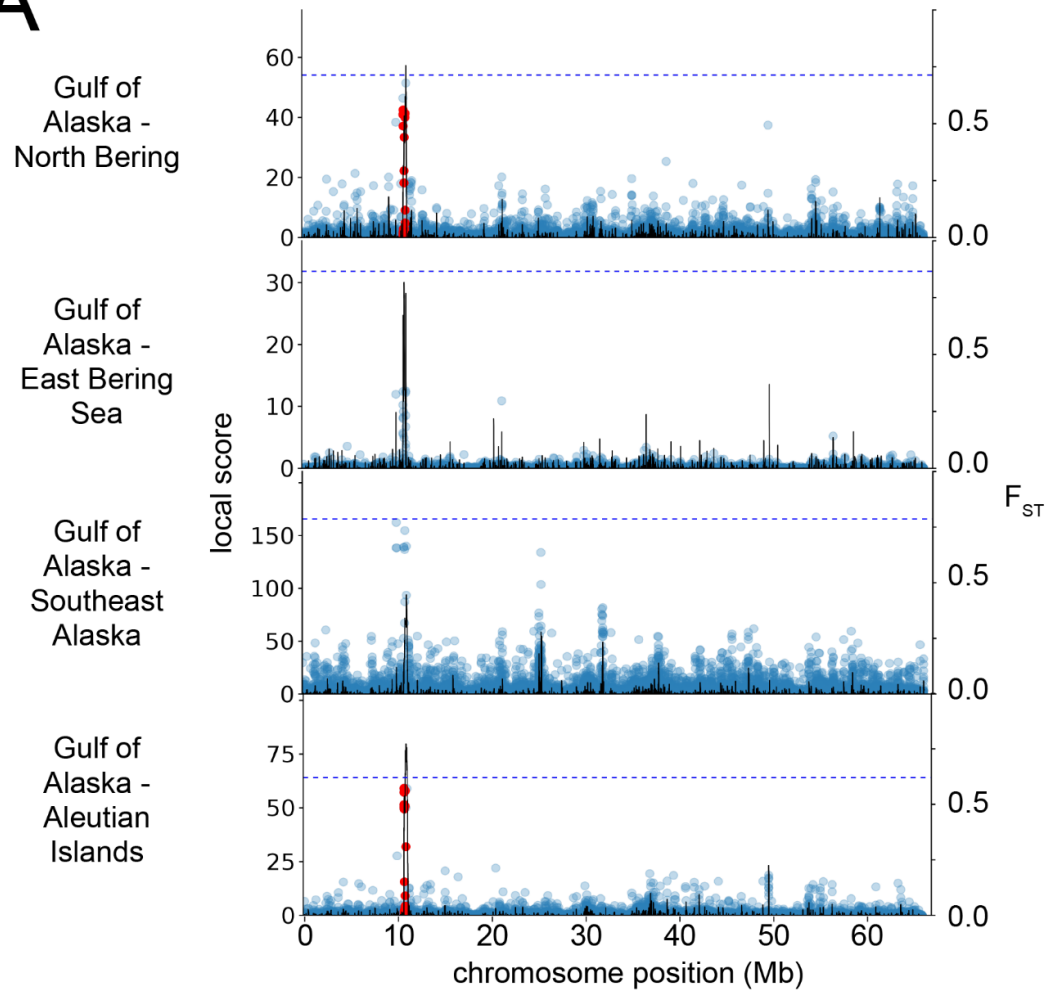
Genome scans identify regions of high differentiation

- PCAs show genomic differences between populations but not across difference parts of the genome
- Genome scans can locate parts of the genome that differ more than others
- With more analyses, these differentiated regions (candidates) may be associated with local adaptation

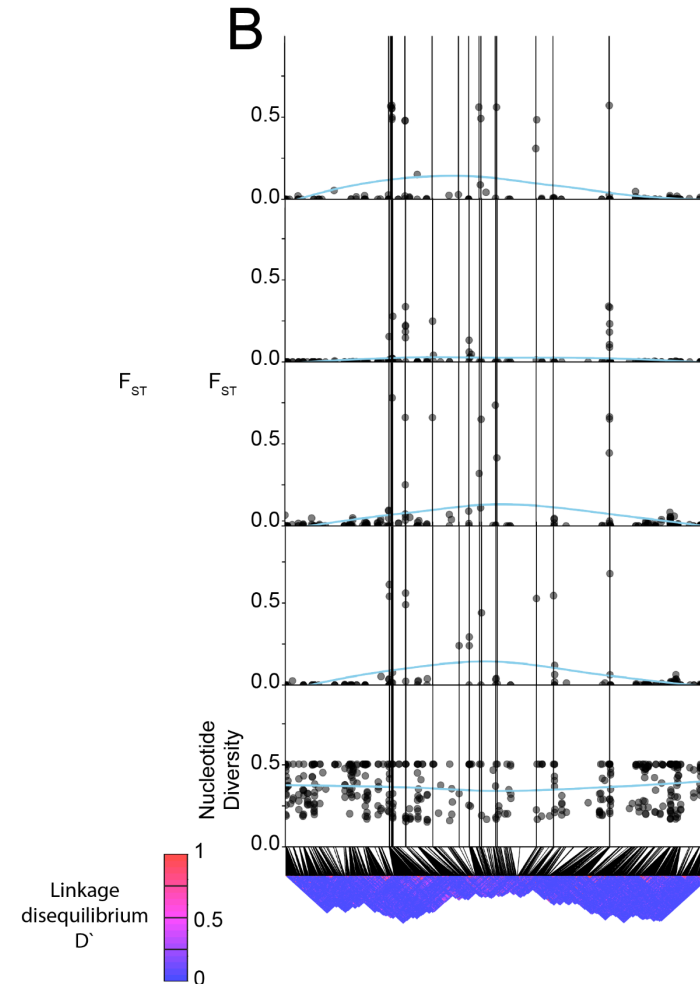


Evidence supporting local adaptation on chromosome 100

A

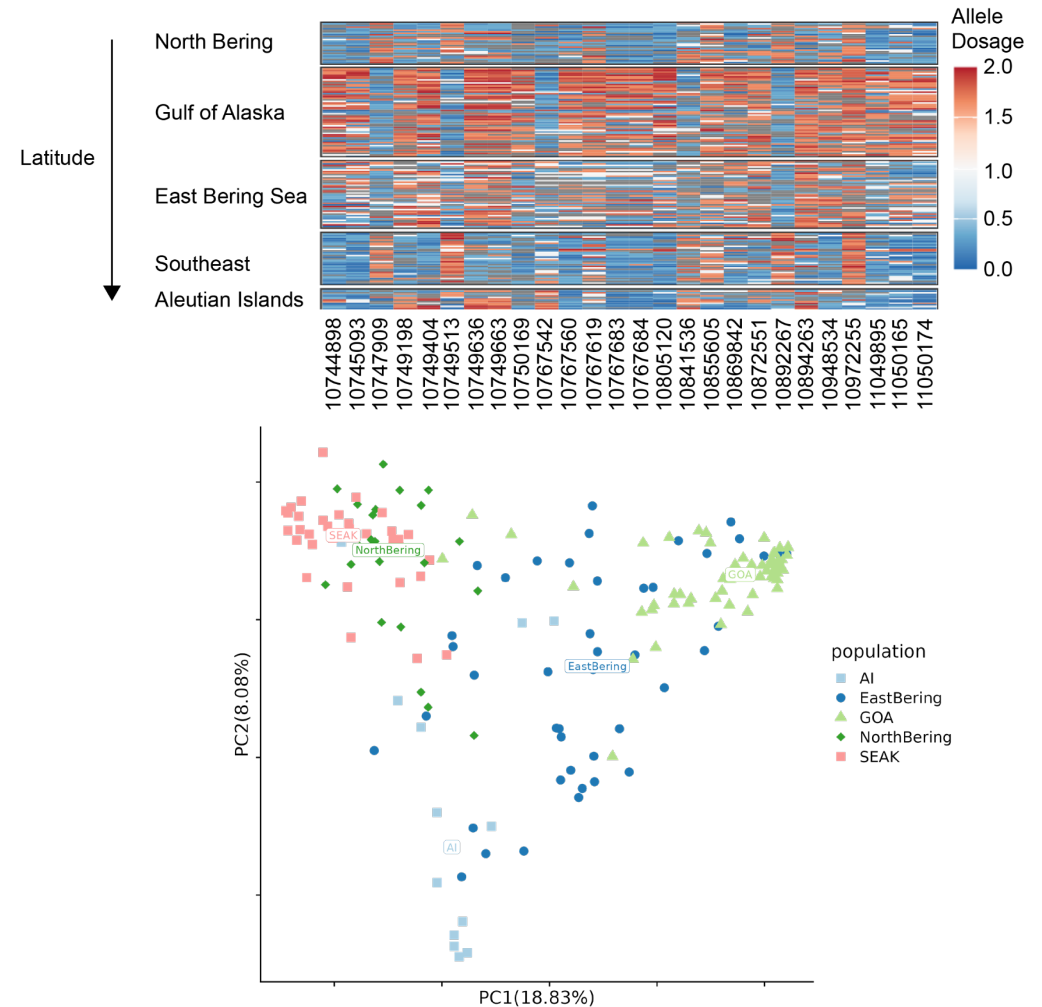
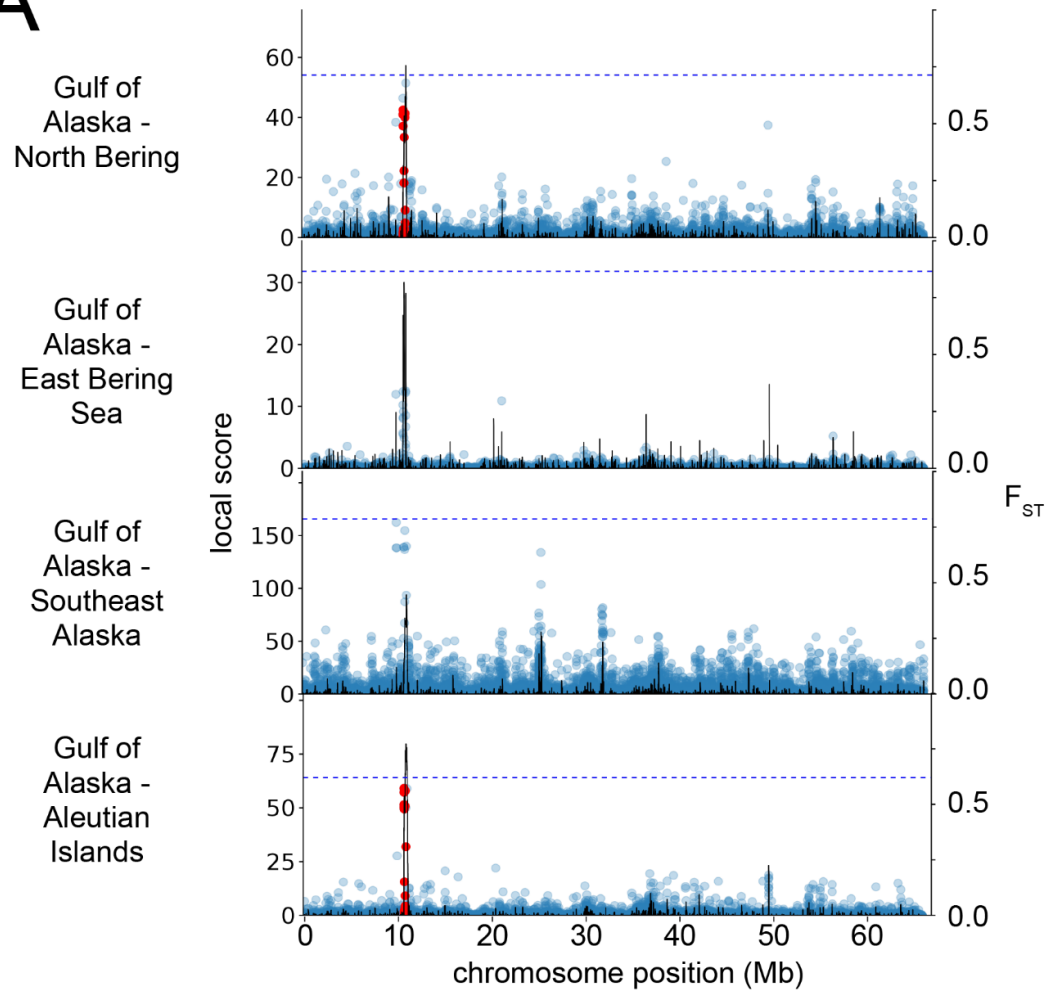


B



Evidence supporting local adaptation on chromosome 100

A



Takeaways

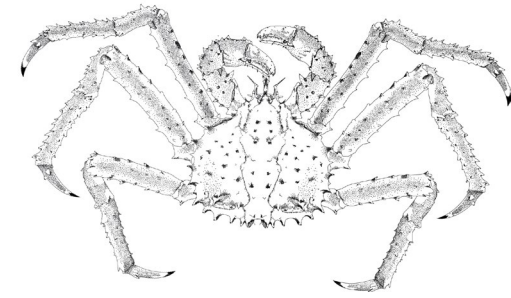
- New evidence finds the Aleutian Islands, Bristol Bay, Pribilof Islands, Gulf of Alaska, North Bering, and Southeast Alaska all form separate genetic stocks
- Gulf of Alaska likely harbors locally adapted alleles derived from standing genetic variation
- If stock enhancement is ever considered, genetic evidence supports sourcing broodstock from the population to be stocked (same as guidelines for salmon stocking)

Limitations

- Sample sizes varied from 16 to 59 among regional populations
 - Sample sizes were considerably smaller for local populations limited our power to separate them (some stock structure may be found in SEAK and the North Bering, and East Bering with larger sample sizes)
- No trait data was collected with samples limiting our ability to associate locally adapted traits with genetic differences
- We mapped our Red King Crab genetic data to a Blue King Crab genome as there is no assembled Red King Crab genome
 - Assembly of a Red King Crab genome would greatly improve future genetic studies

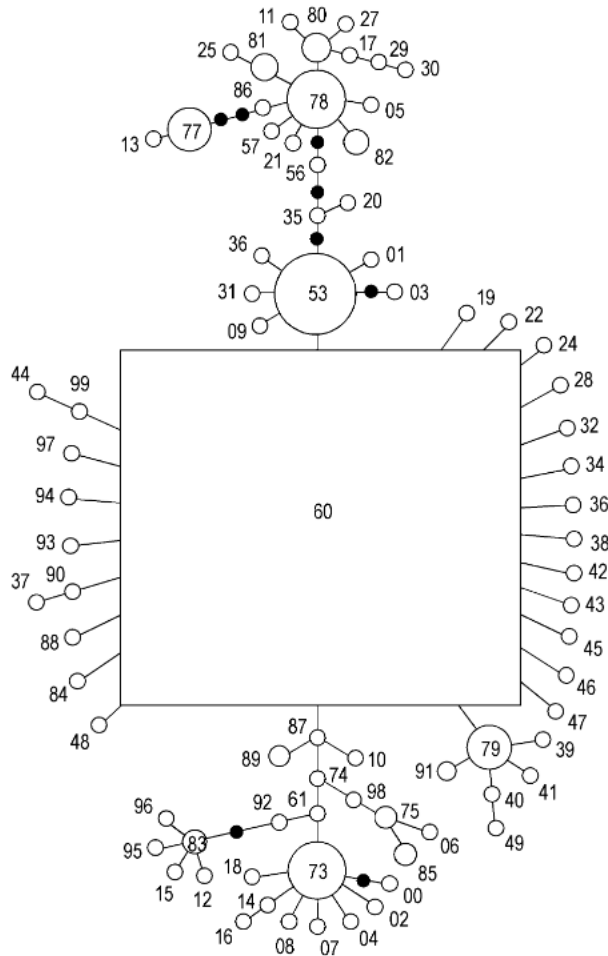
Questions?

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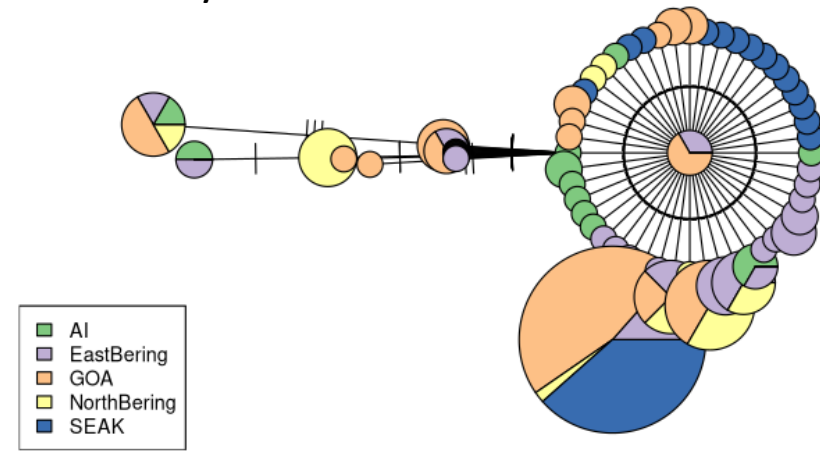


Haplotype network comparisons

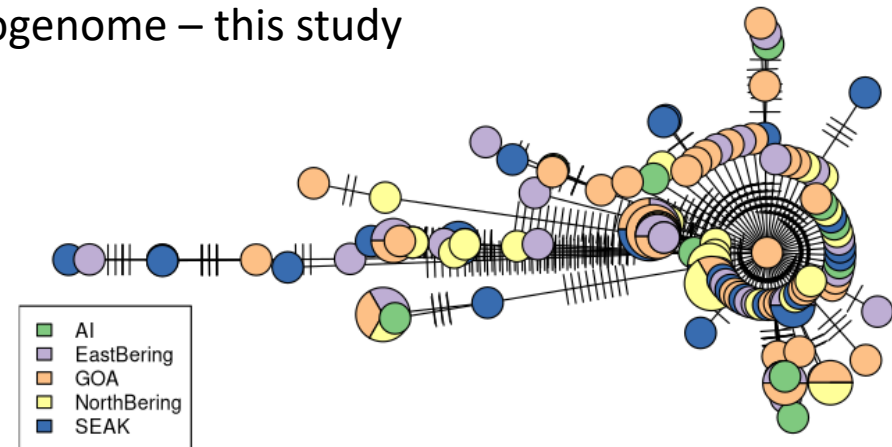
COI - Grant and Cheng (2012)



COI – this study



Mitogenome – this study



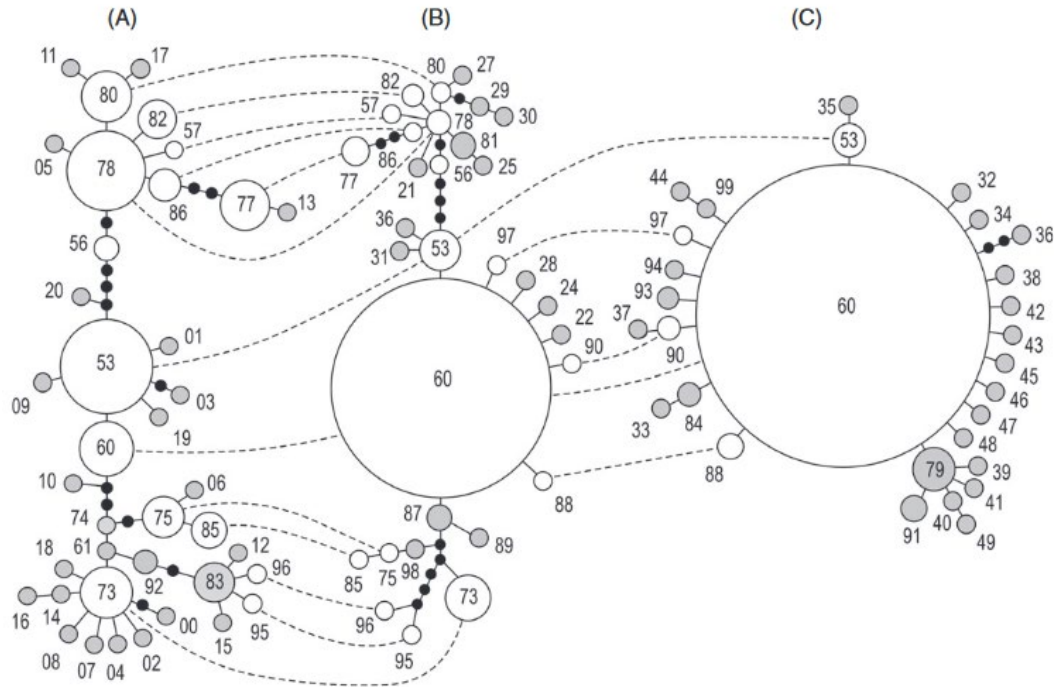
Haplotype network comparisons

COI - Grant and Cheng (2012)

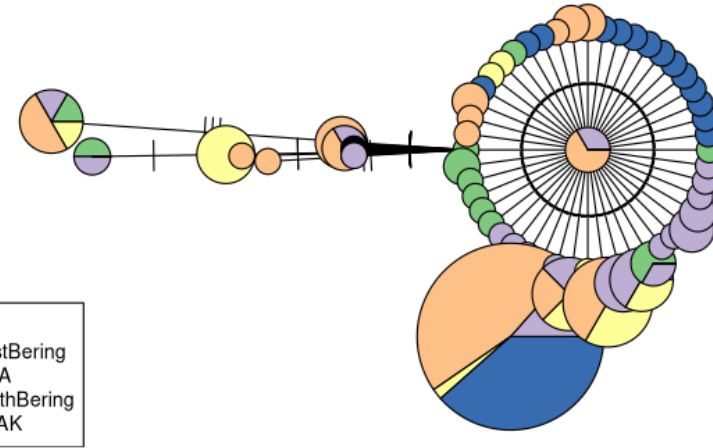
North Bering-AI

East Bering-GOA

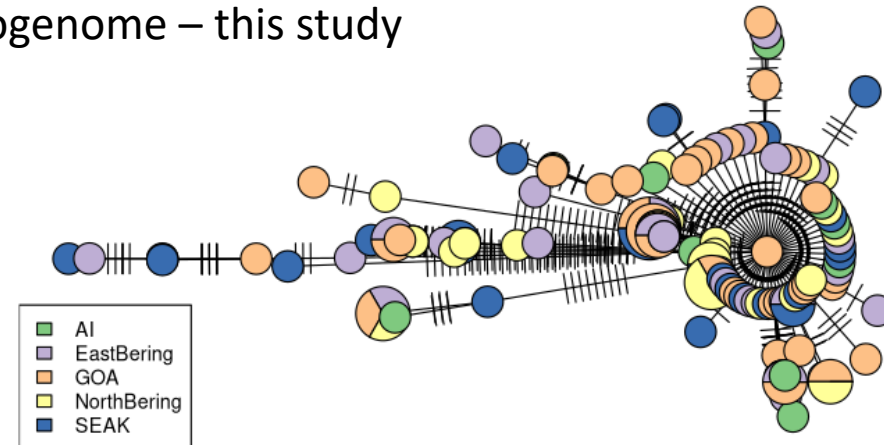
SEAK



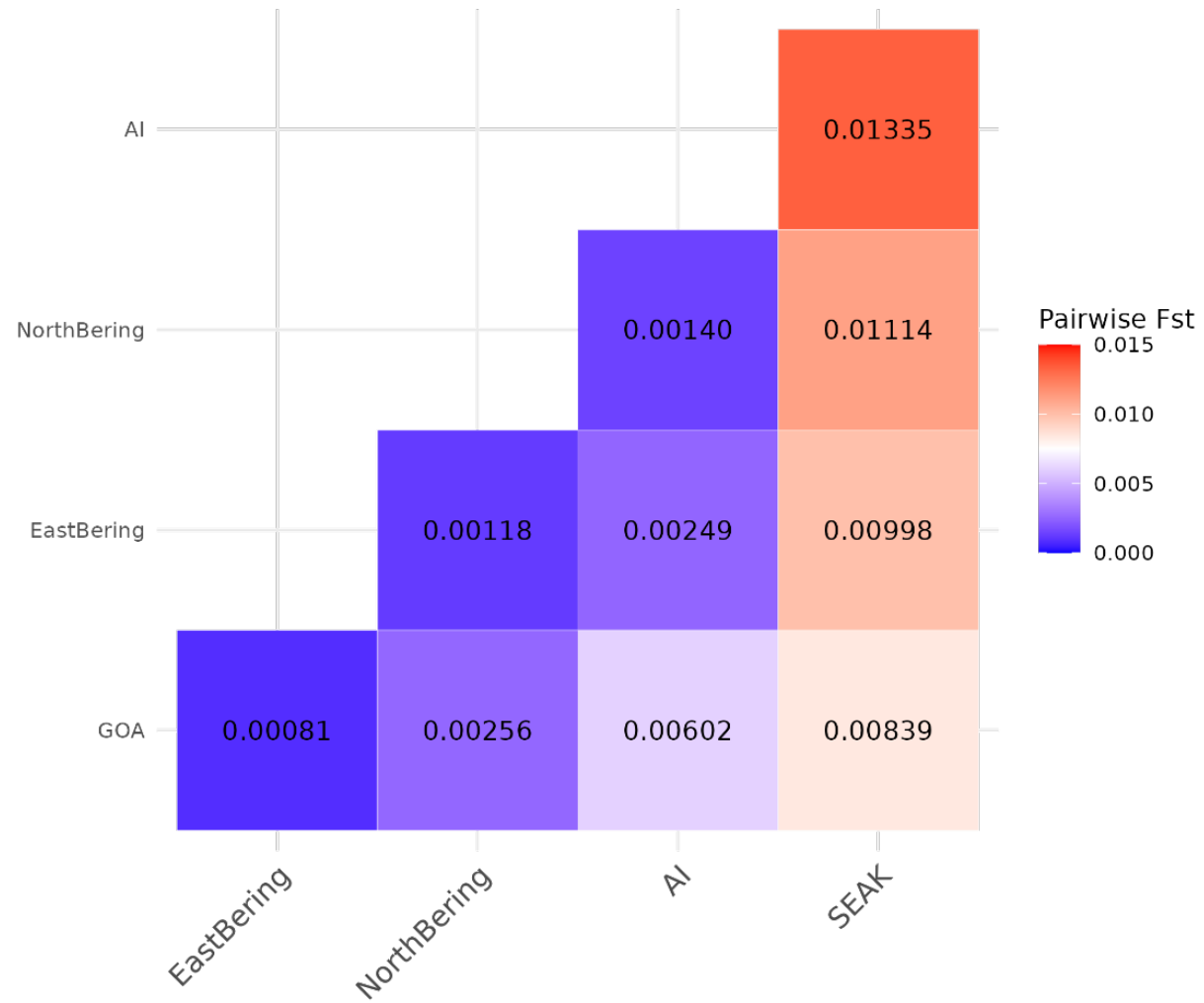
COI – this study



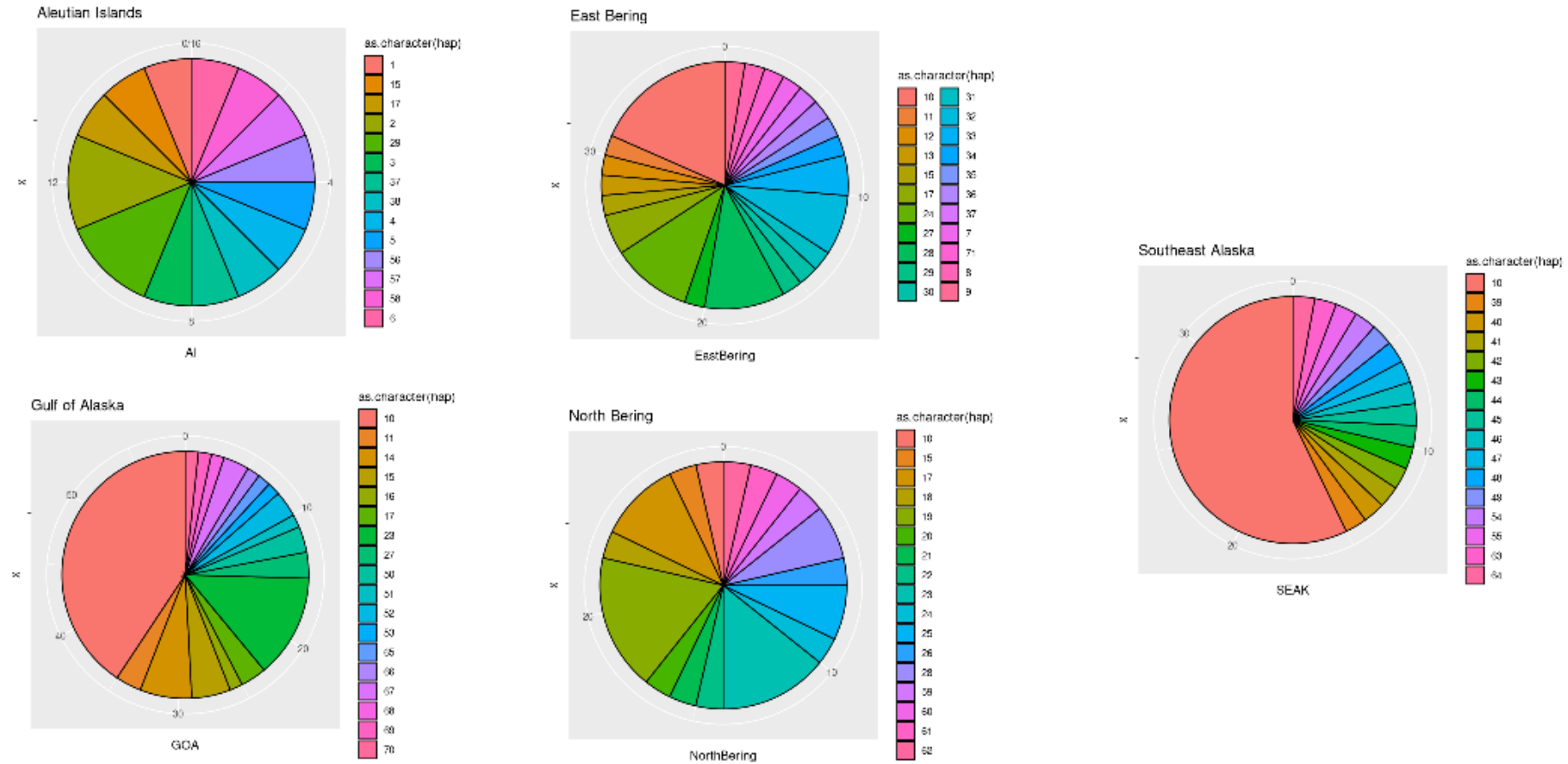
Mitogenome – this study



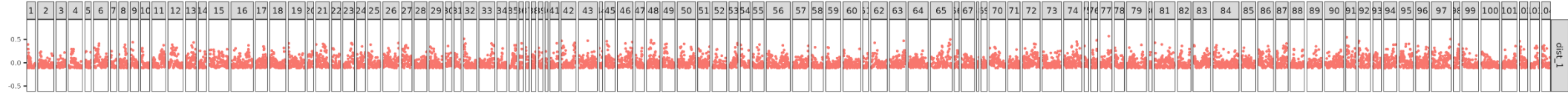
Global Fst



Mitochondrial Haplotypes

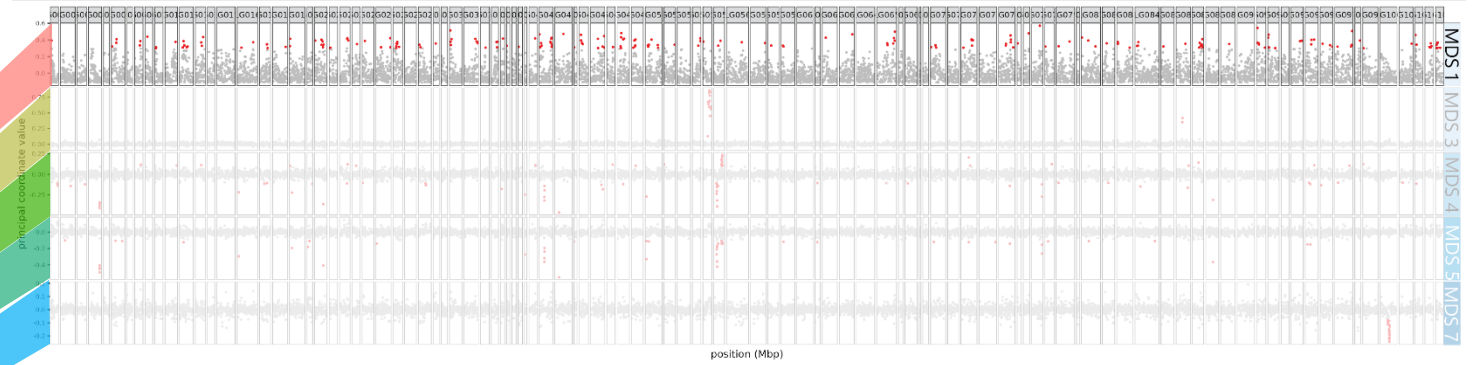


Local PCA reveals variation localized to parts of the genome

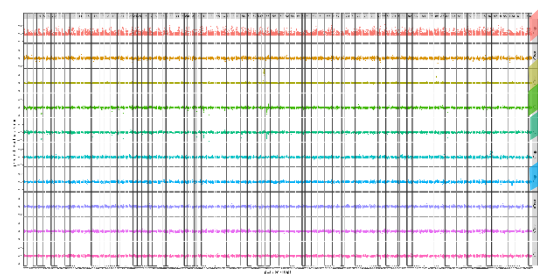
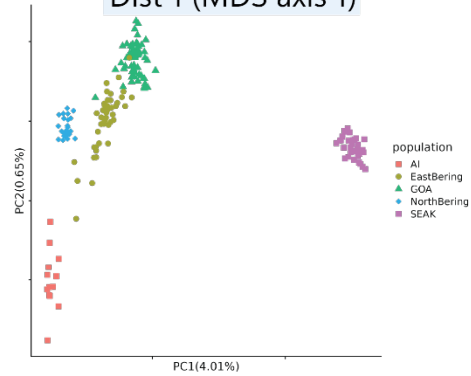


Local PCA reveals variation localized to parts of the genome

Local PCA Analysis: Red King Crab

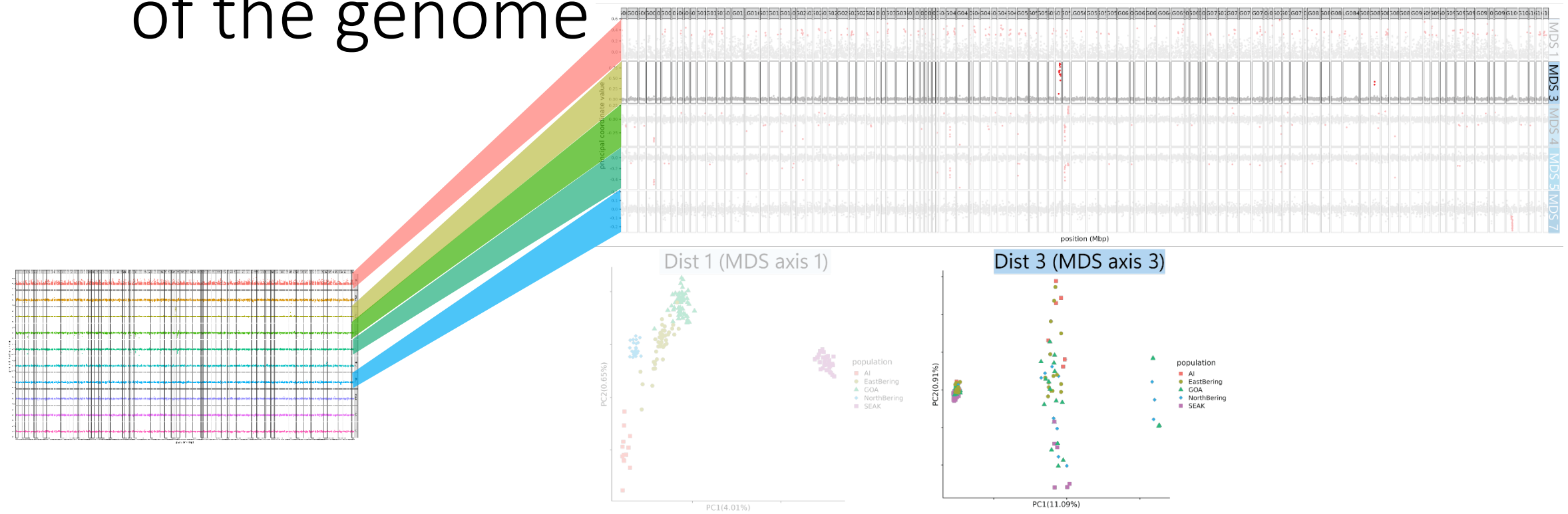


Dist 1 (MDS axis 1)



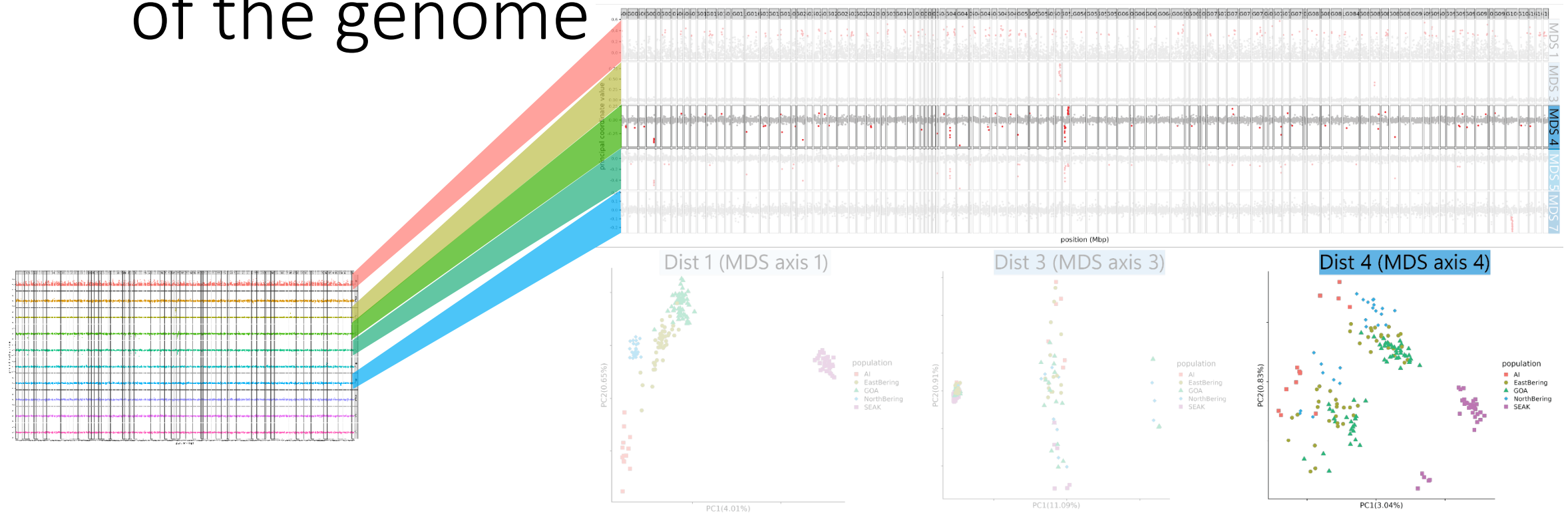
Local PCA reveals variation localized to parts of the genome

Local PCA Analysis: Red King Crab



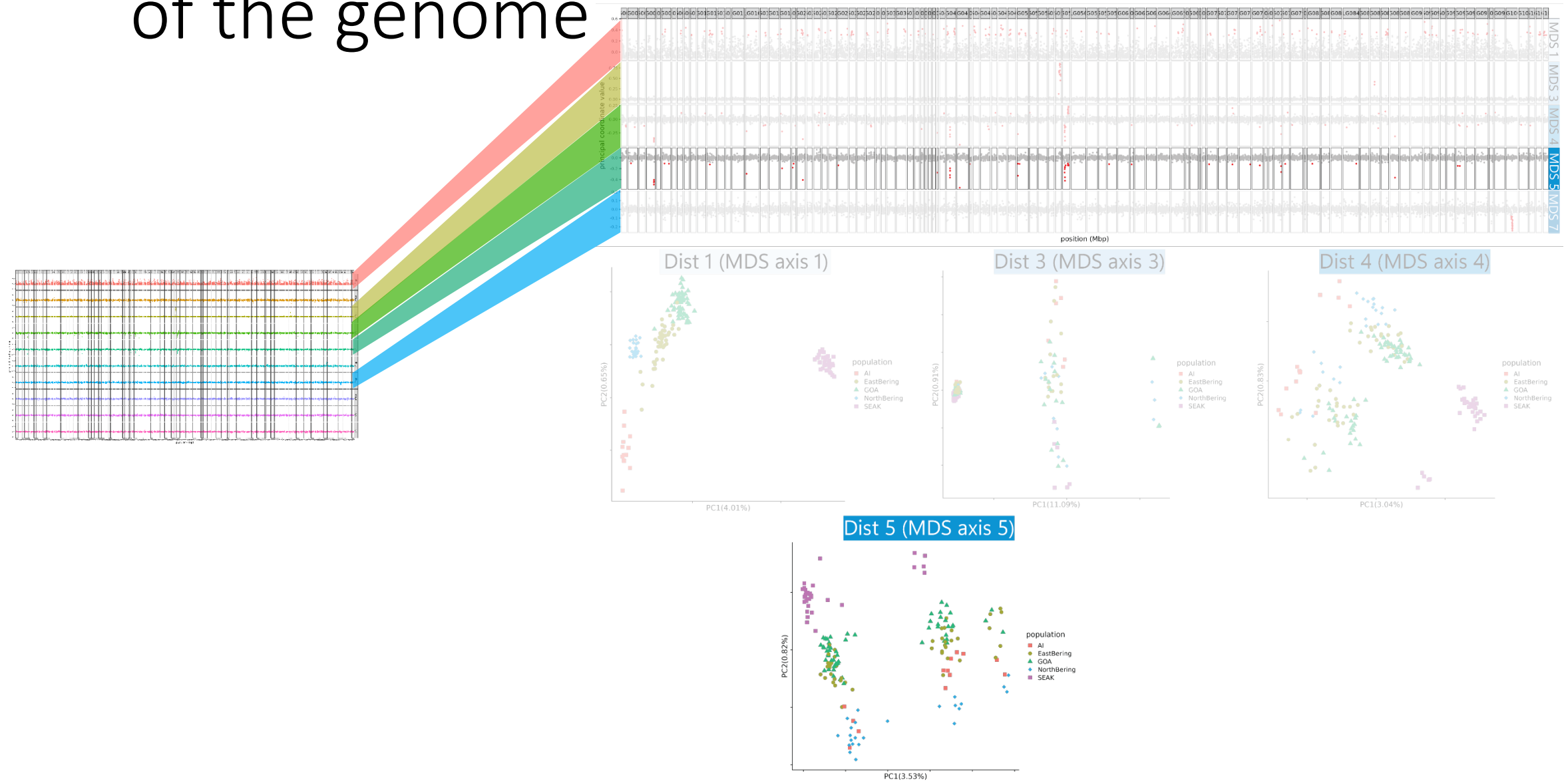
Local PCA reveals variation localized to parts of the genome

Local PCA Analysis: Red King Crab



Local PCA reveals variation localized to parts of the genome

Local PCA Analysis: Red King Crab



Local PCA reveals variation localized to parts of the genome

Local PCA Analysis: Red King Crab

