Status of Yukon River Salmon Genetic Baselines

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GENE CONSERVATION LABORATORY
Alaska Department of Fish & Game

ALASKA DEPARTMENT OF FISH AND GAME

Outline

- ADF&G Gene Conservation Laboratory
- Overview of genetic mixed stock analysis and genetic baselines
- Yukon River Chinook salmon baseline
- Yukon River coho salmon baseline
- Questions

Gene Conservation Laboratory

- The mission of the Gene Conservation Laboratory is to protect genetic resources and provide genetic information and advice to department staff, policy makers, and the public to support management of resources consistent with the mission of Alaska Department of Fish and Game.

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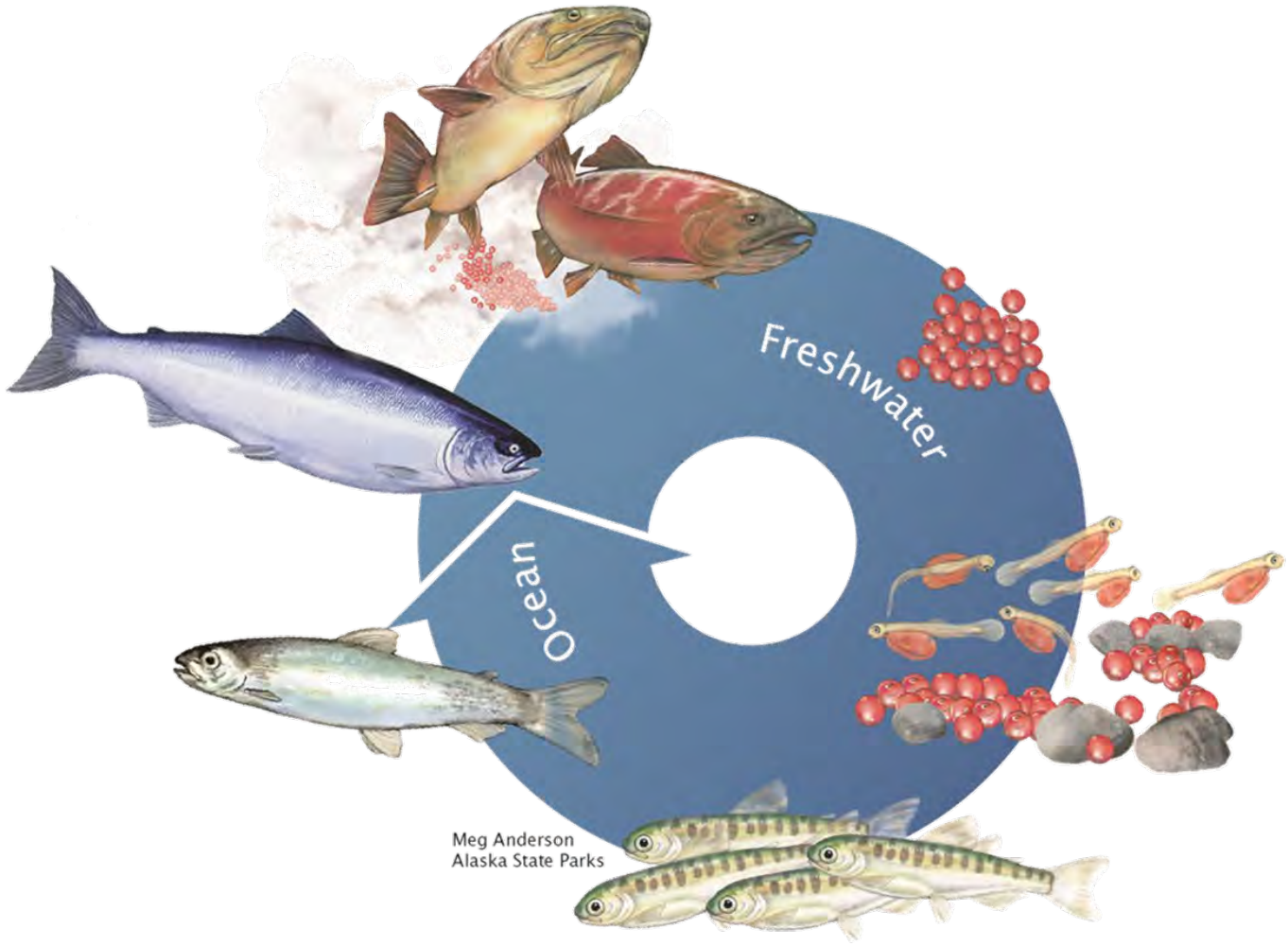
  - Through our extensive sampling efforts over a broad geography, **we maintain and develop improved genetic baselines** for species, which are then used to understand the structure of populations, estimate the composition of mixed stock fishery harvests, and provide advice on the potential genetic effect of human activities on fish populations.

How can we use Genetic Tools?

Salmon return to their natal stream to spawn



How can we use Genetic Tools?

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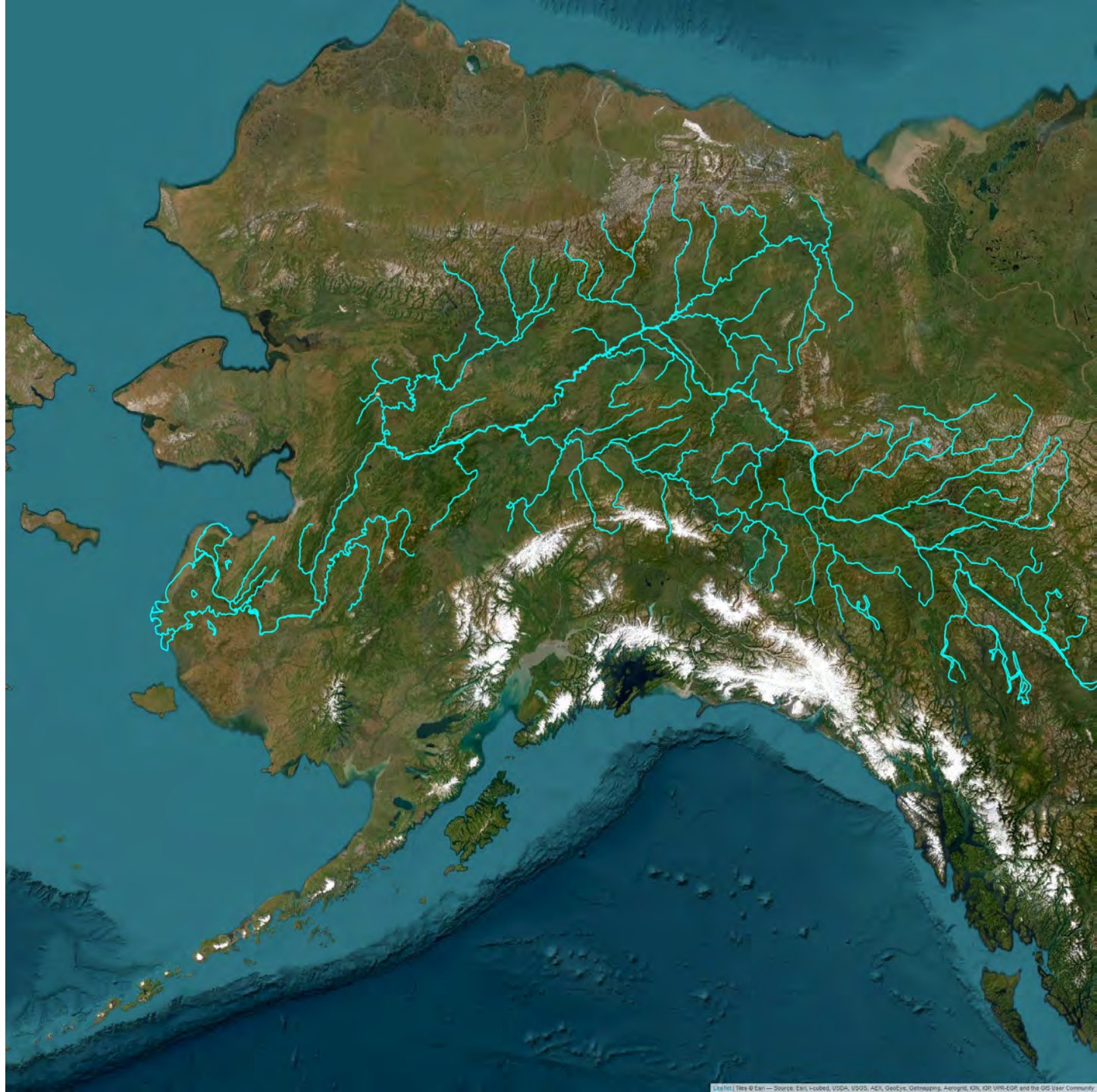

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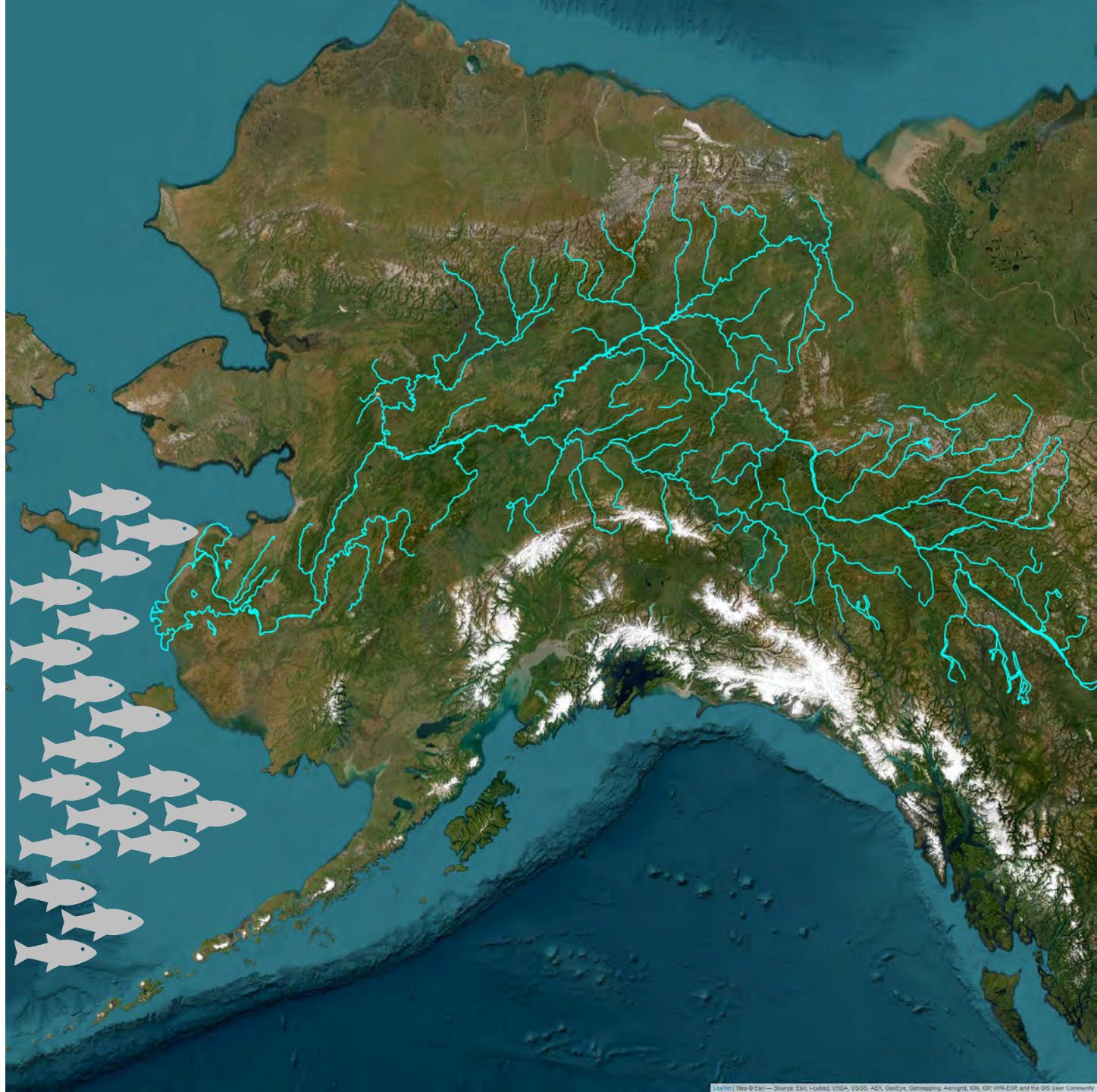

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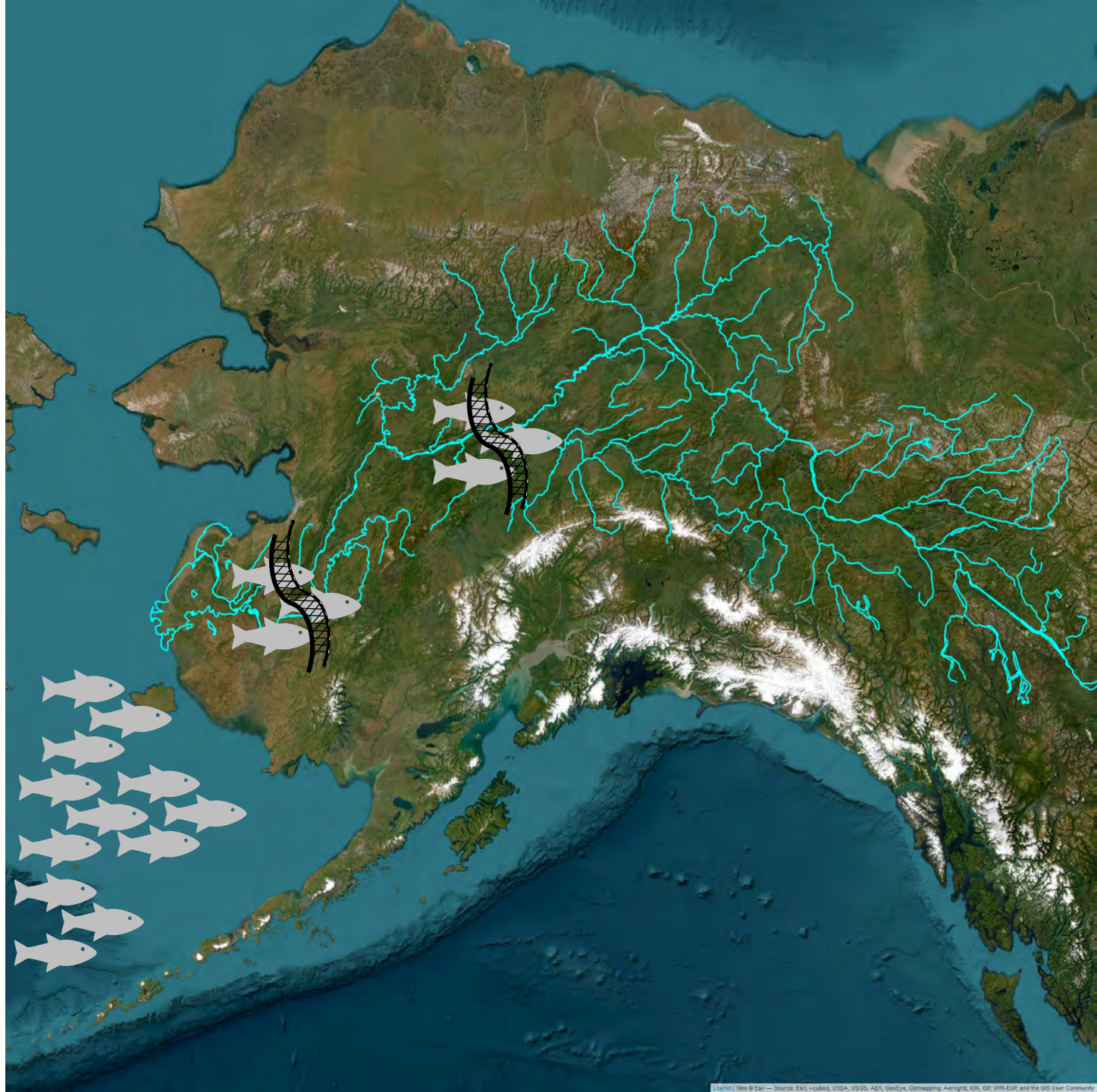

How can we use Genetic Tools?

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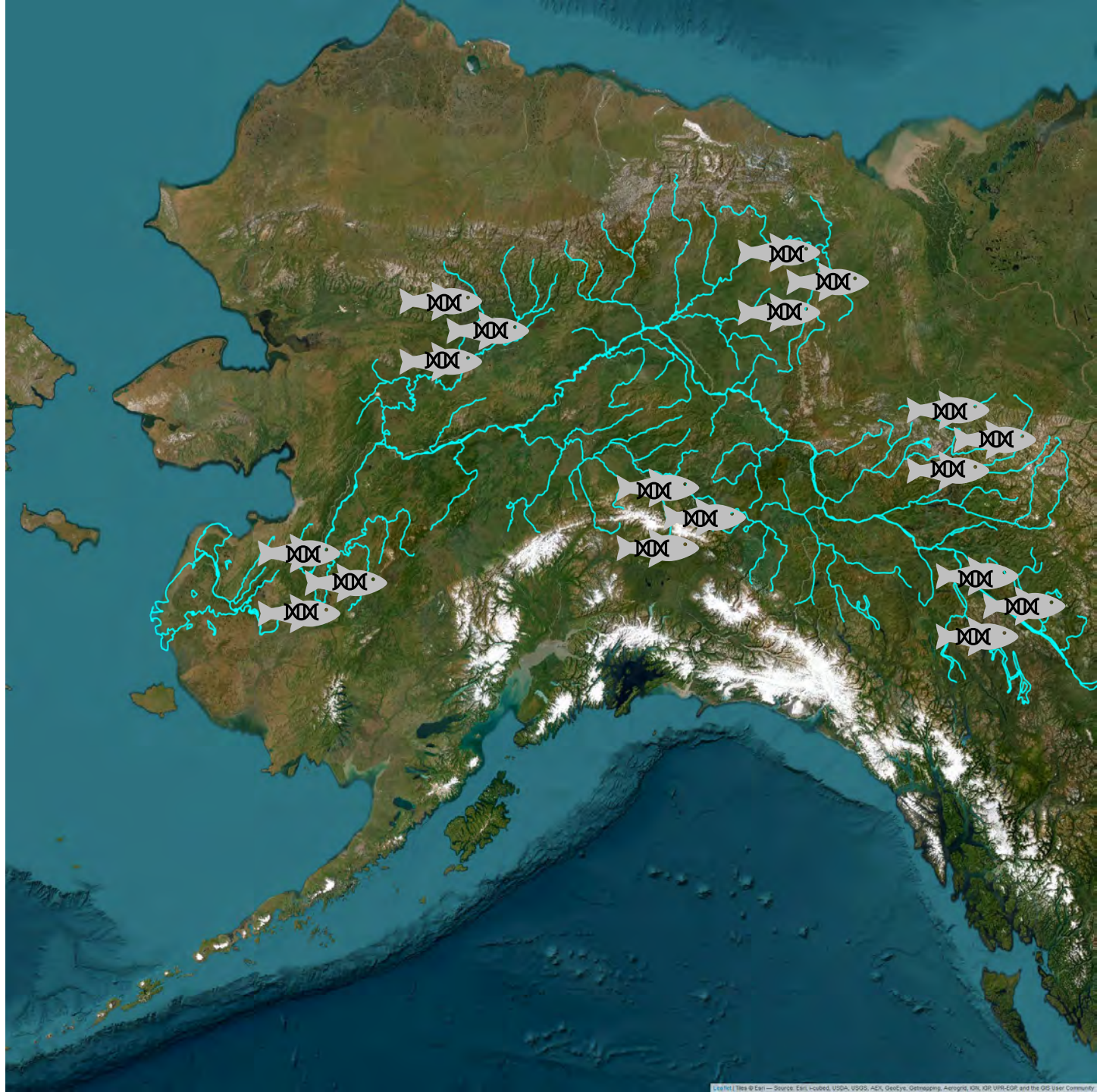
Genetic Baselines



Genetic Baselines

1. Populations
2. Genetic markers

Genetic Baselines

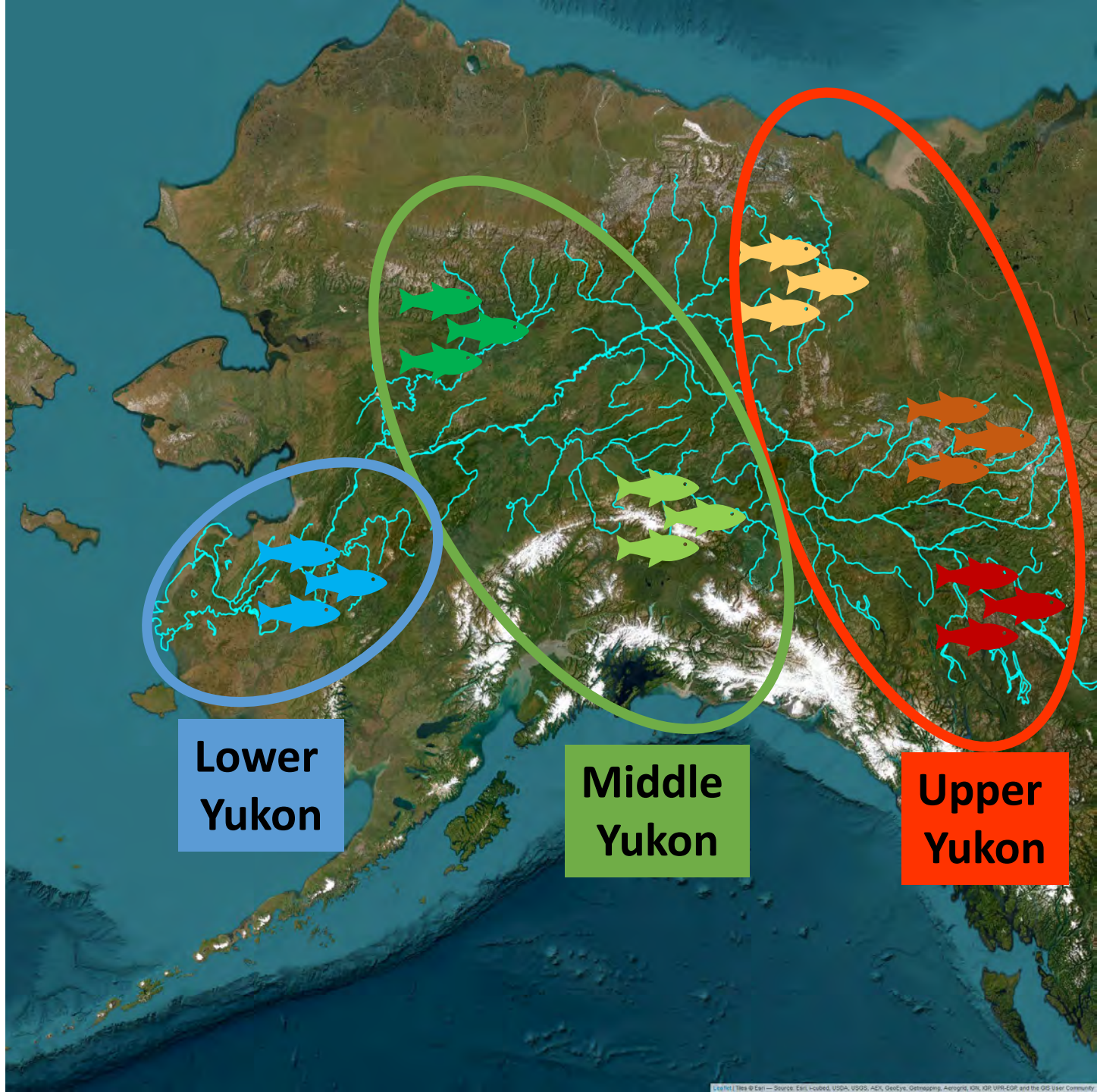
1. Populations
   - Pops
   - Baseline collections
   - Spawning aggregates
2. Genetic markers
   - Loci, locus
   - SNPs, SNP, “snip”
   - Microsatellite, uSAT
   - Marker set, panel

Genetic Baselines

1. Populations
2. Genetic markers

Genetic Baselines

Reporting groups (“stocks”)



How can we use Genetic Tools?

Genetic Stock Identification (GSI)

- Mixed stock analysis (MSA)
- Individual Assignment (IA)

How can we use Genetic Tools?

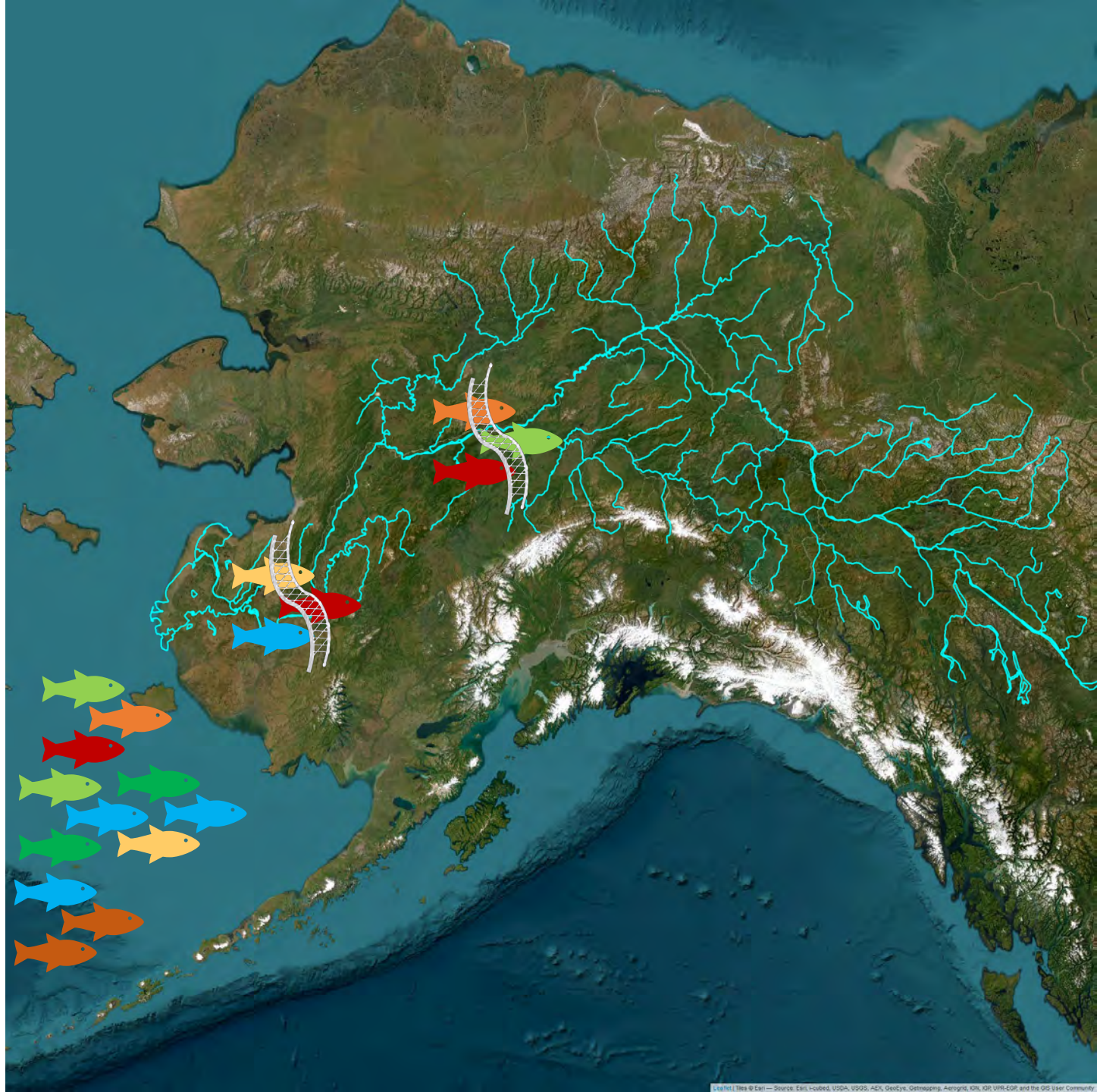
Mixed stock analysis

- Stock composition estimates are produced by comparing the genetic composition of a set of samples to the known genetic compositions of populations within the drainage (i.e., “genetic baseline”)

How can we use Genetic Tools?

Mixed stock analysis

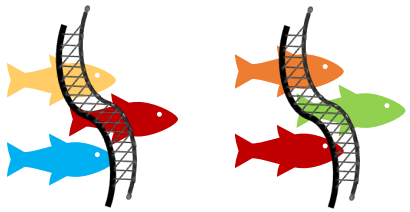
1. Sample

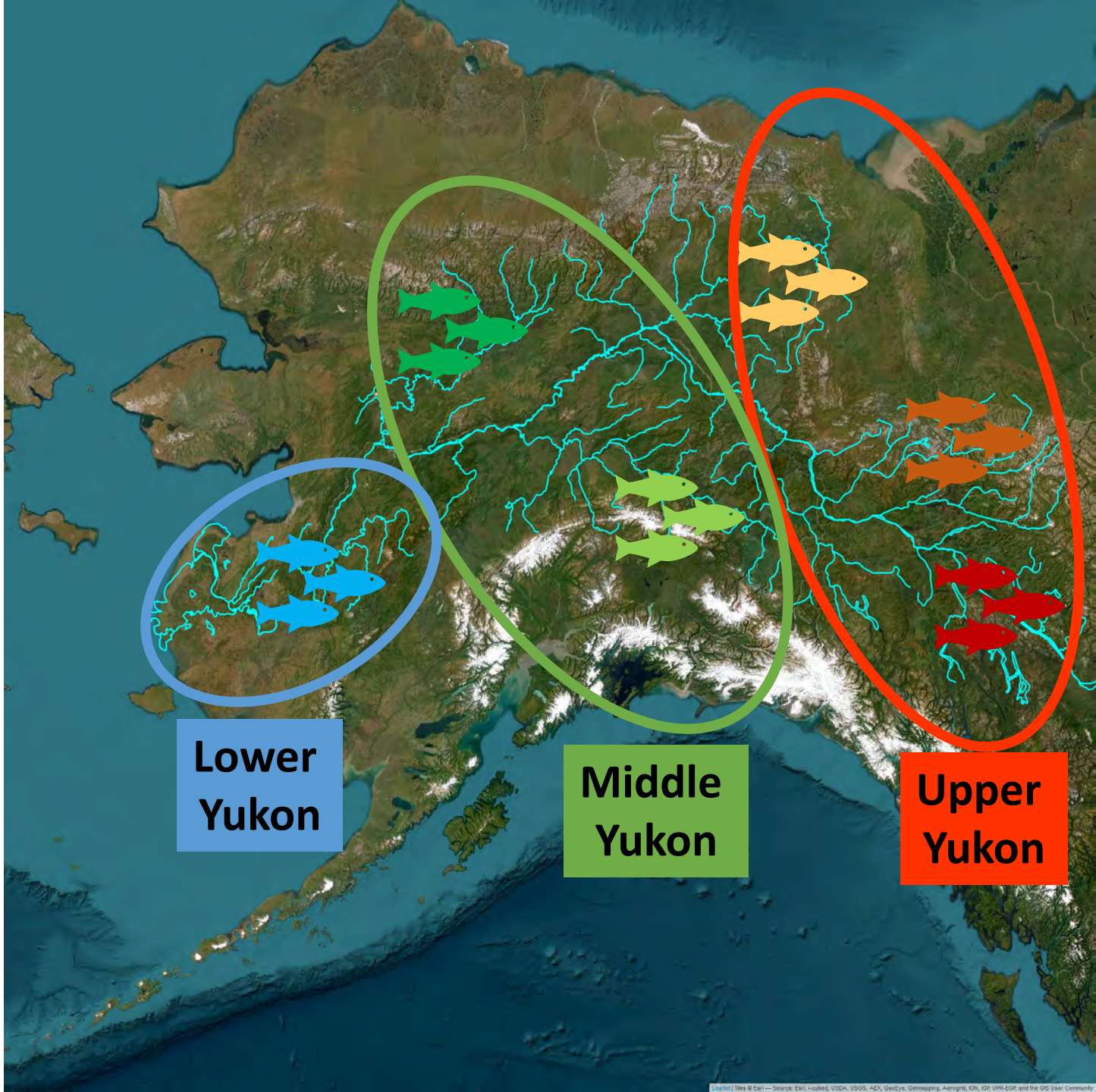


Genetic Baselines

Mixed stock analysis

1. Sample
2. Compare





How can we use Genetic Tools?

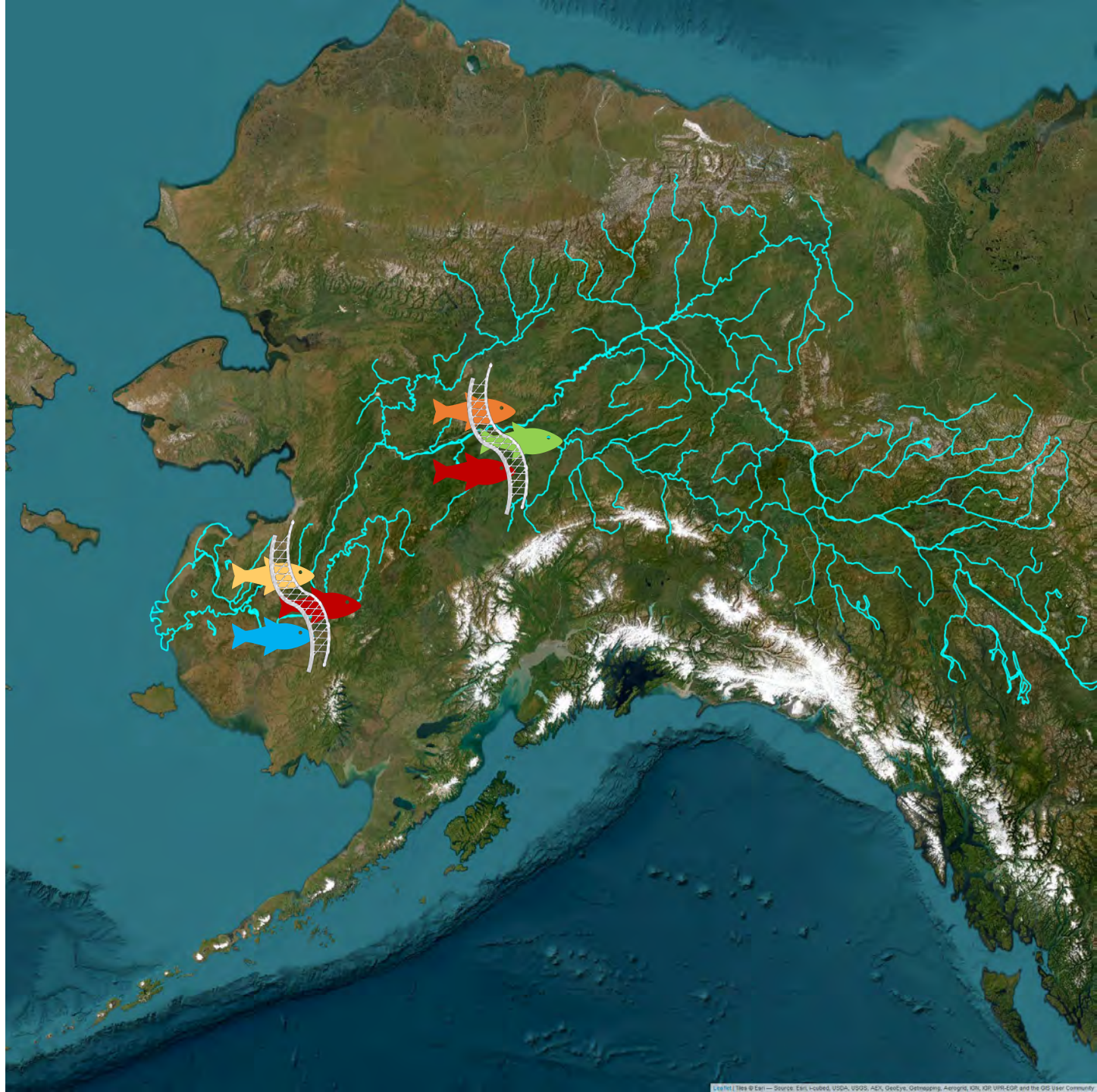
Mixed stock analysis

1. Sample
2. Compare
3. Report

Lower Yukon = 17%

Middle Yukon = 17%

Upper Yukon = 66%



How can we use Genetic Tools?

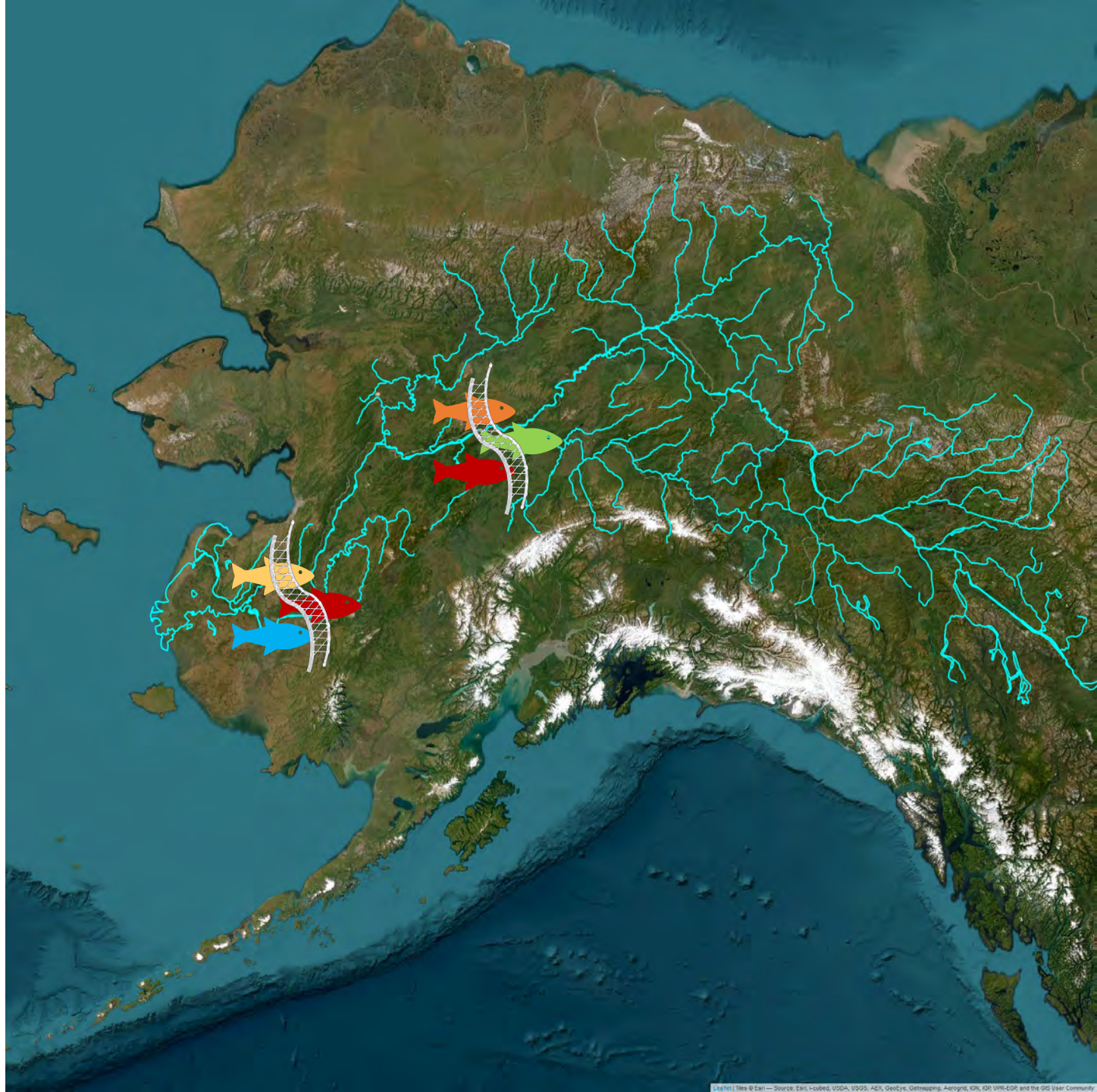
Mixed stock analysis

1. Sample
2. Compare
3. Report

Lower Yukon = 17% (CI: 12-21%)

Middle Yukon = 17% (CI: 14-20%)

Upper Yukon = 66% (CI: 61-68%)



Genetic Baselines

Yukon River (in-river projects)

- Chinook salmon
  - ADF&G Update
- Coho salmon
  - ADF&G Update
- Chum salmon
  - USFWS

Why Update Genetic Baselines?

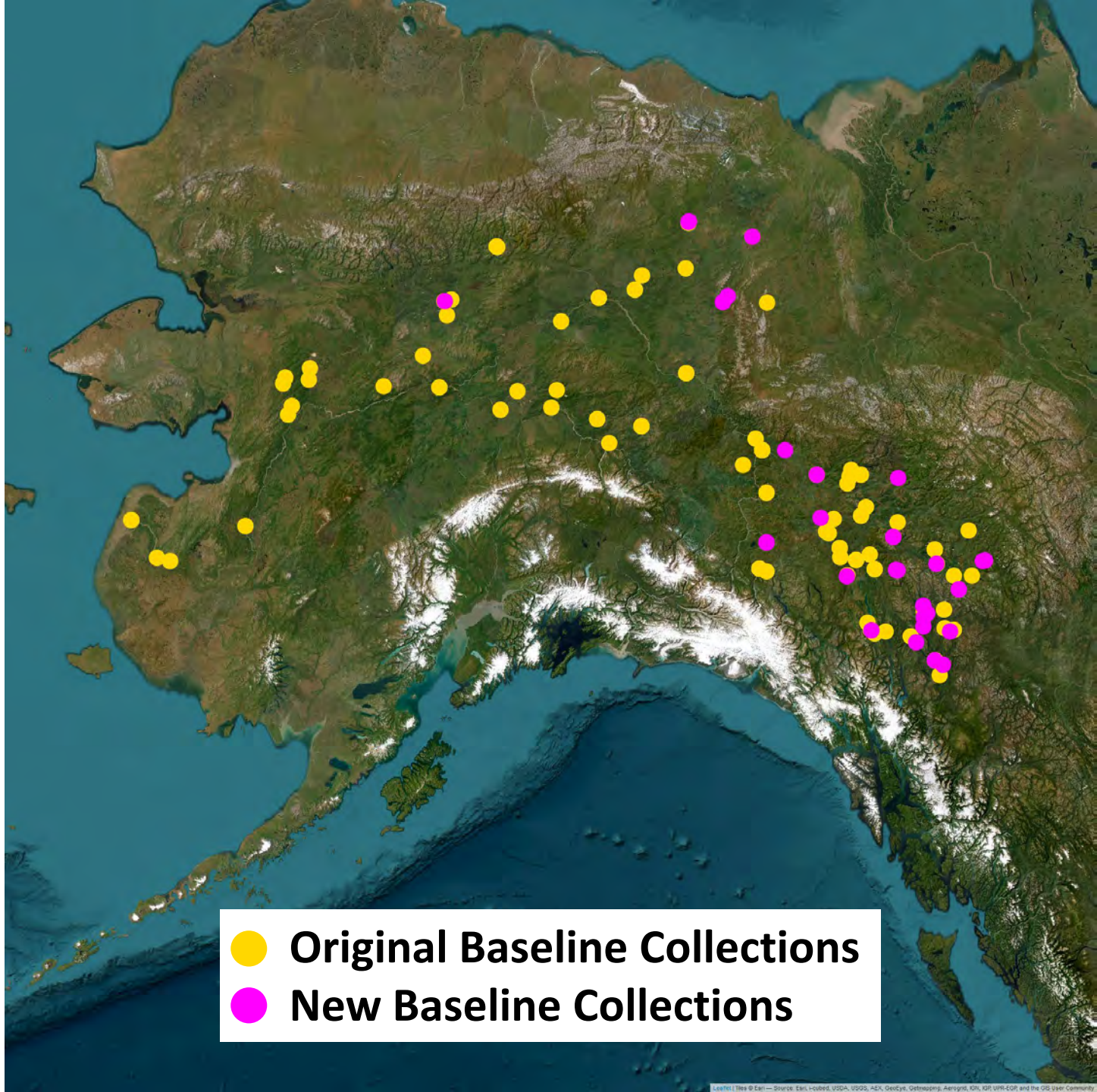
Yukon River salmon

Genetic stock estimates are only as good as the baseline used for analysis

Technology and efficiency

Chinook Salmon: Baseline Improvements

1. Populations



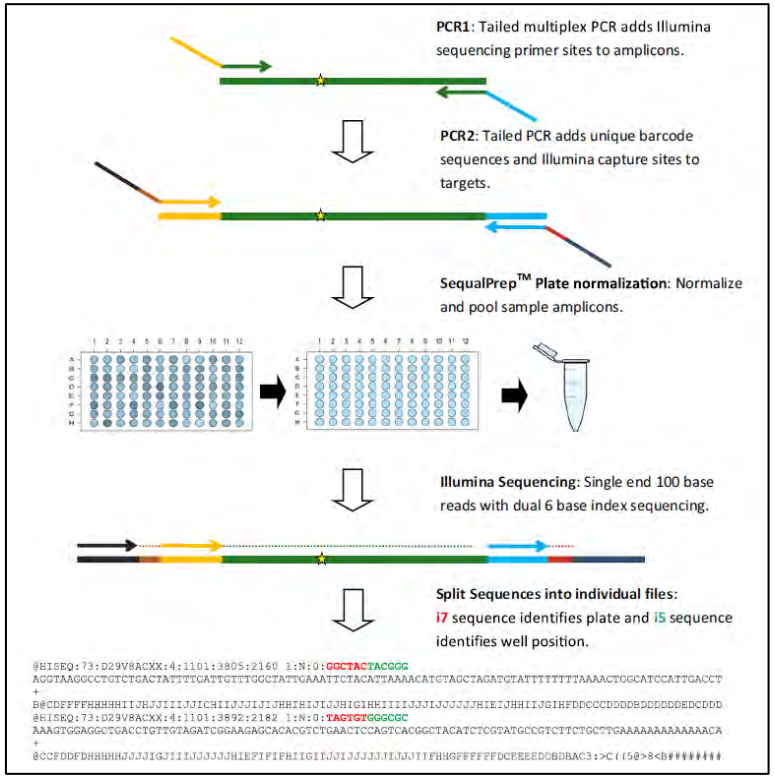
Chinook Salmon: Baseline Improvements

1. Populations
2. Genetic Markers

MOLECULAR ECOLOGY
RESOURCES
Molecular Ecology Resources (2015) 15, 855–867 doi: 10.1111/1755-0998.12357

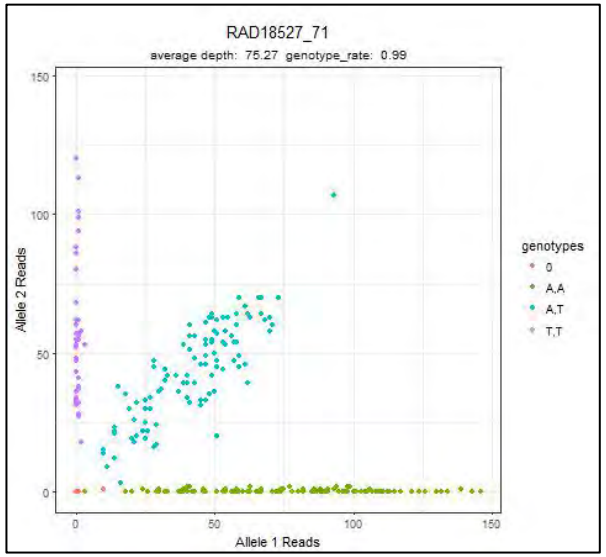
Genotyping-in-Thousands by sequencing (GT-seq): A cost effective SNP genotyping method based on custom amplicon sequencing

NATHAN R. CAMPBELL, STEPHANIE A. HARMON and SHAWN R. NARUM
Columbia River Inter-Tribal Fish Commission, 3059F National Fish Hatchery Road, Hagerman, ID 83332,USA



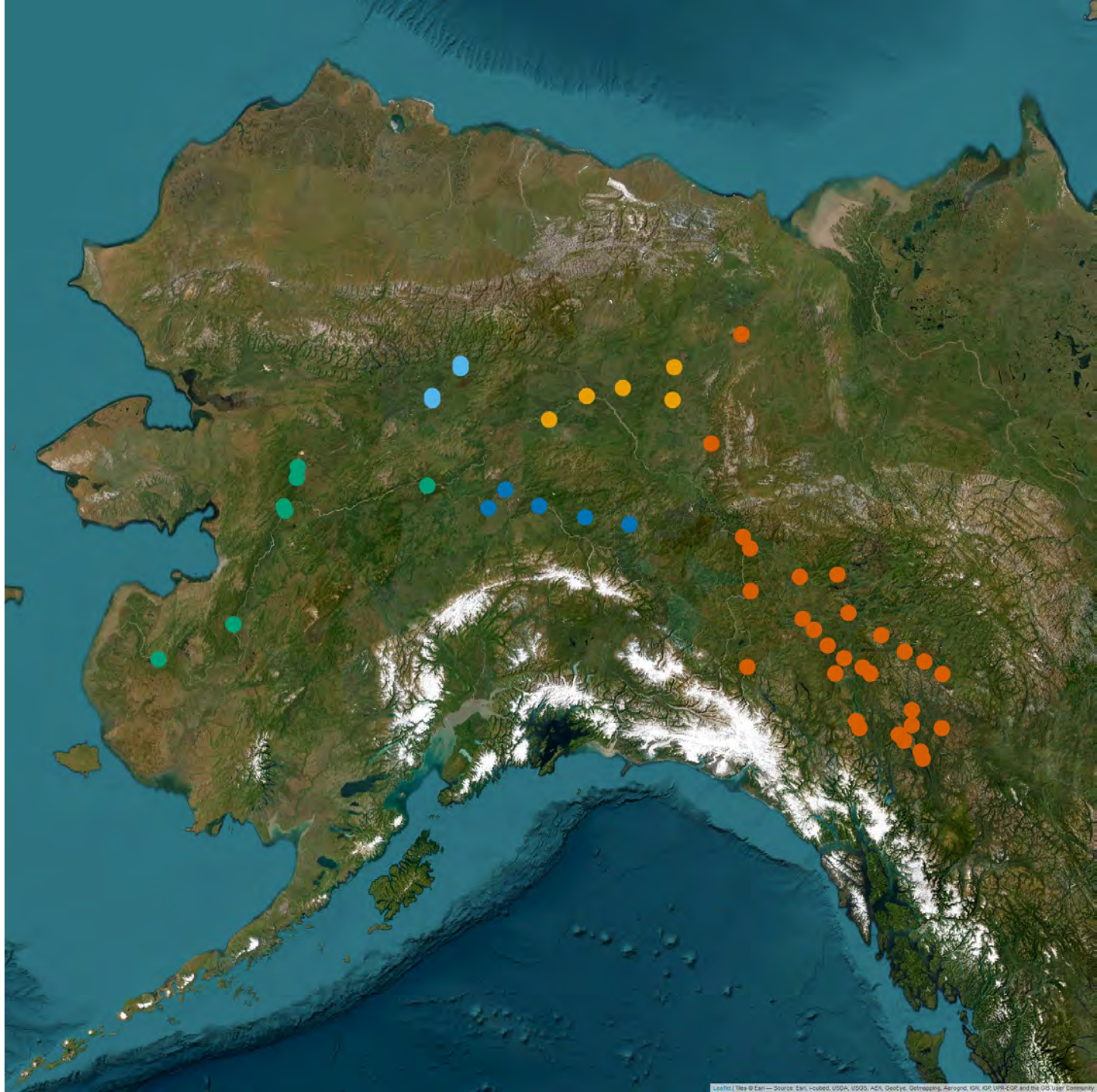
GT-score: Pipeline for genotyping and troubleshooting amplicon sequencing data

Garrett McKinney 6/23/2020



Chinook Salmon: Baseline Improvements

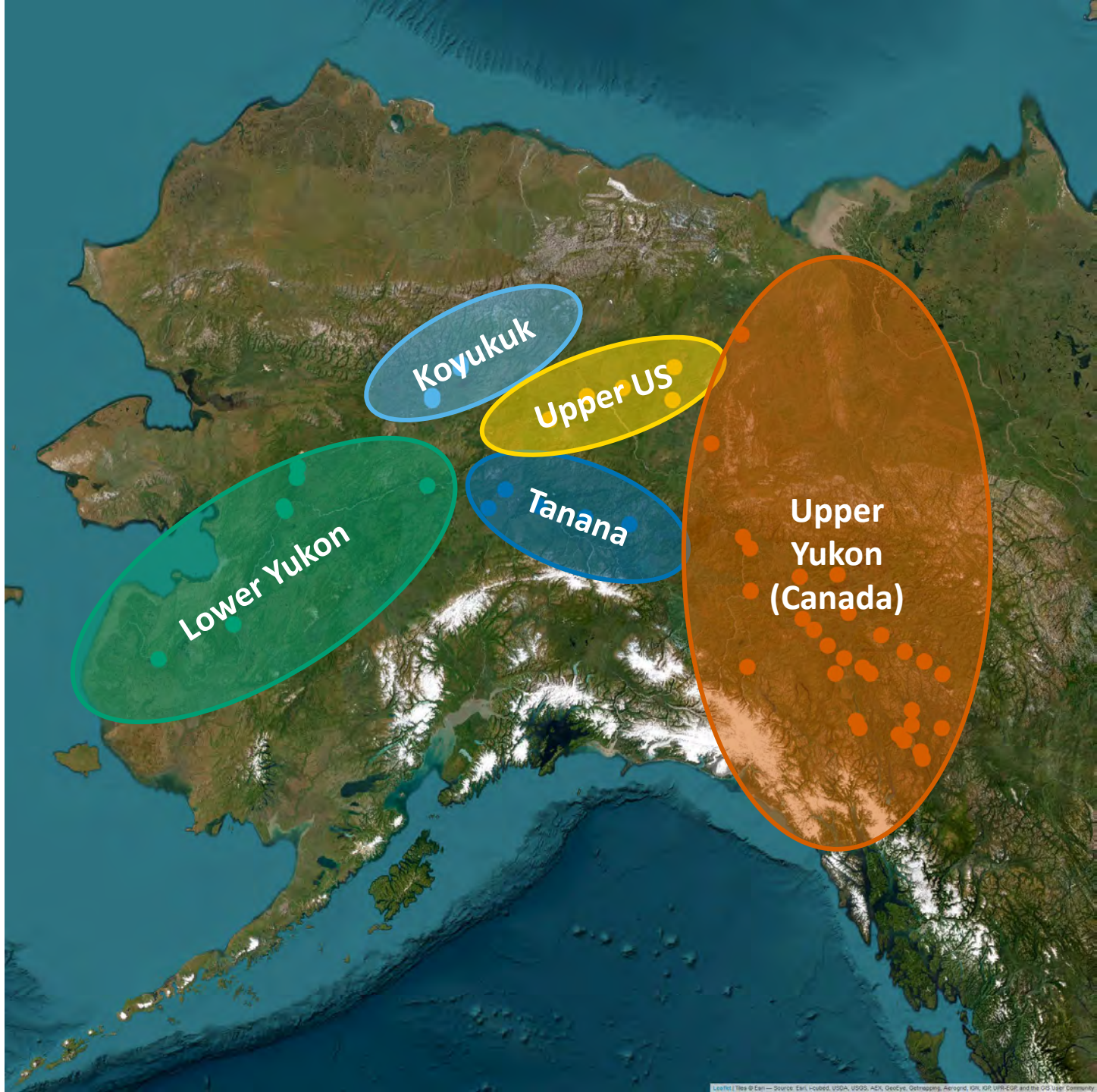
1. Populations
   - 36 → 50
2. Genetic Markers
   - 41 → 380



Chinook Salmon Baseline

Reporting groups:

- Lower Yukon (US)
- Middle Yukon (US)
  - Koyukuk
  - Tanana
  - Upper US
- Upper Yukon (Canada)



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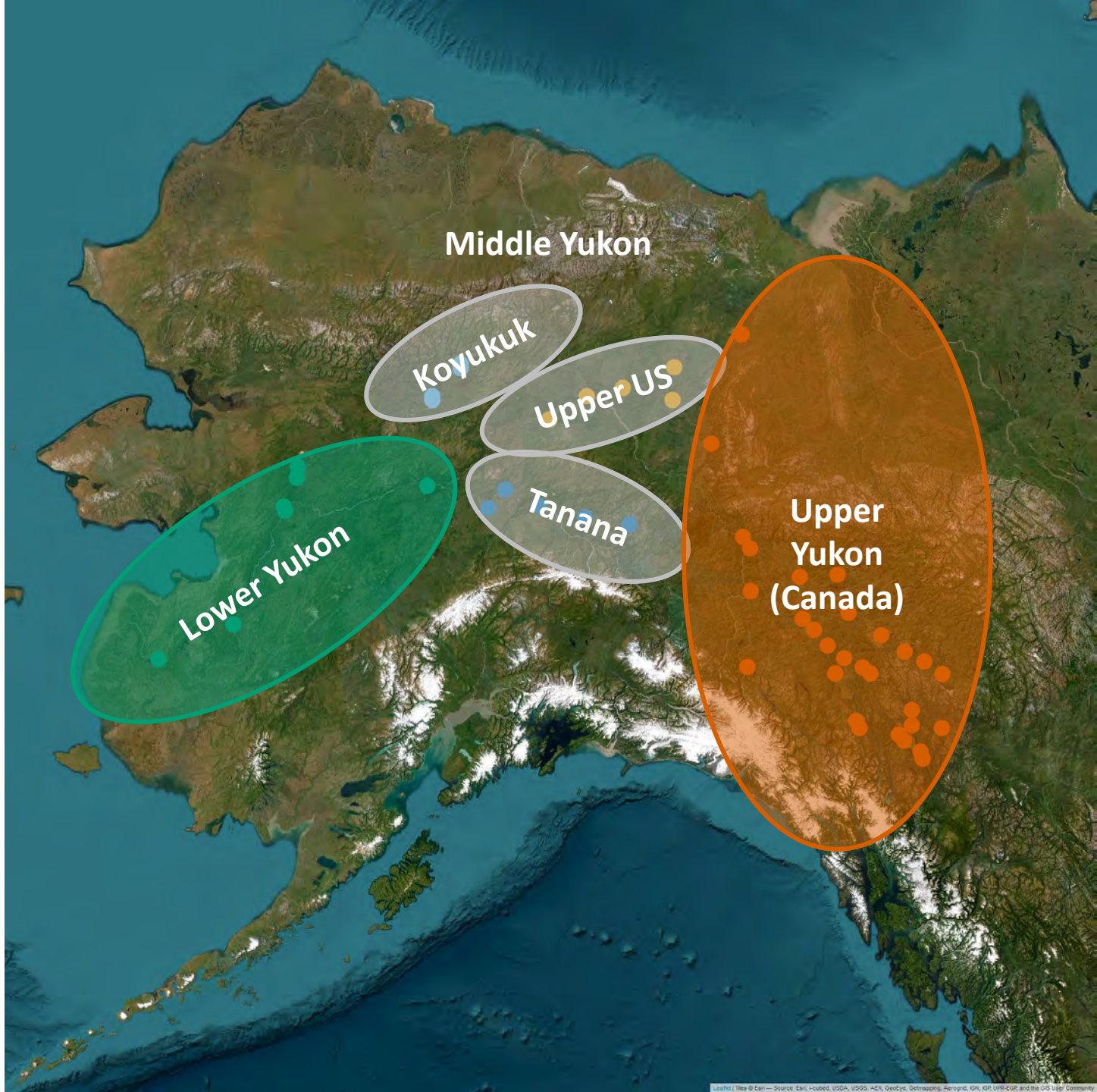

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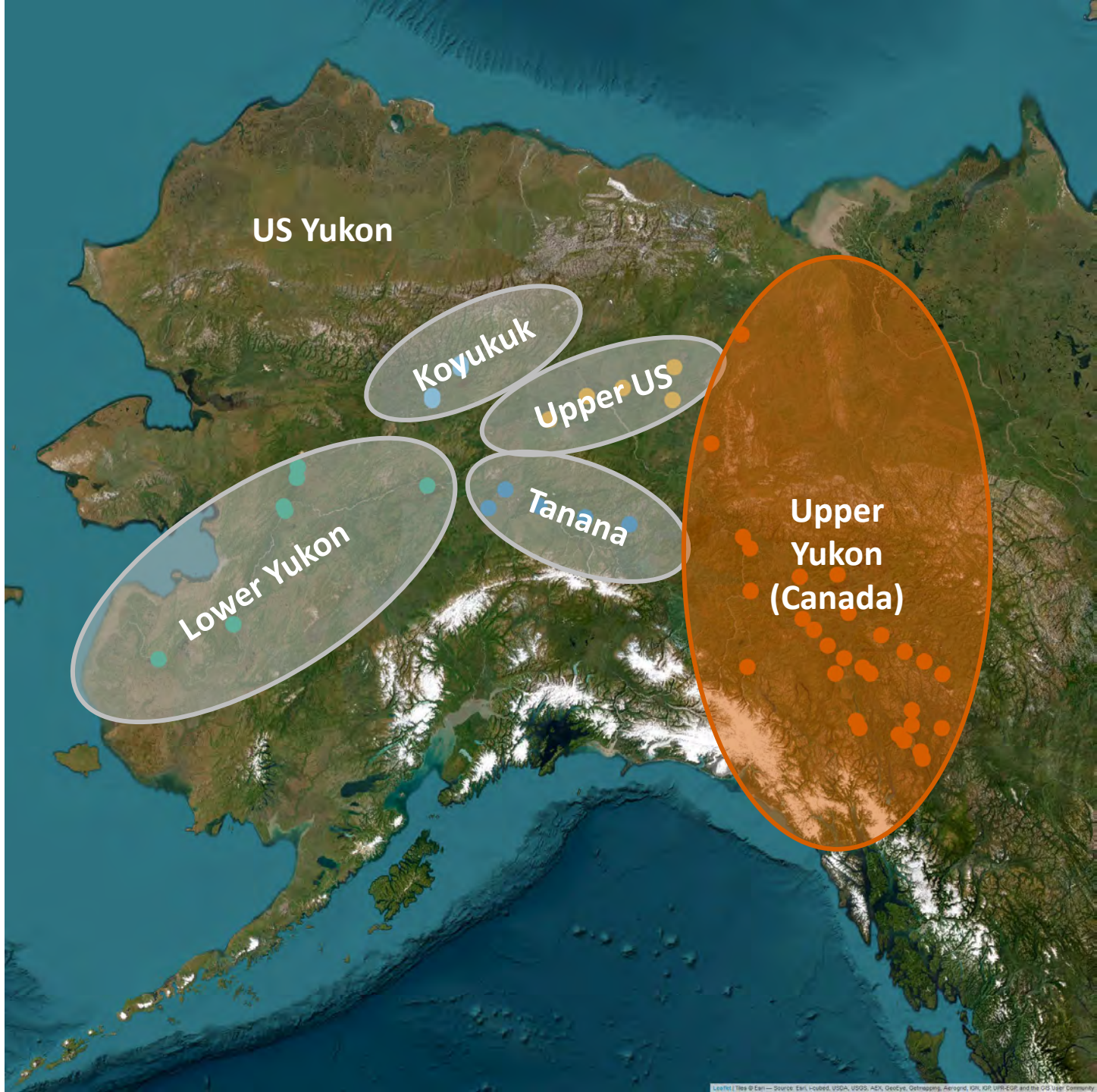

Chinook Salmon Baseline

Reporting groups:

- Lower Yukon (US)
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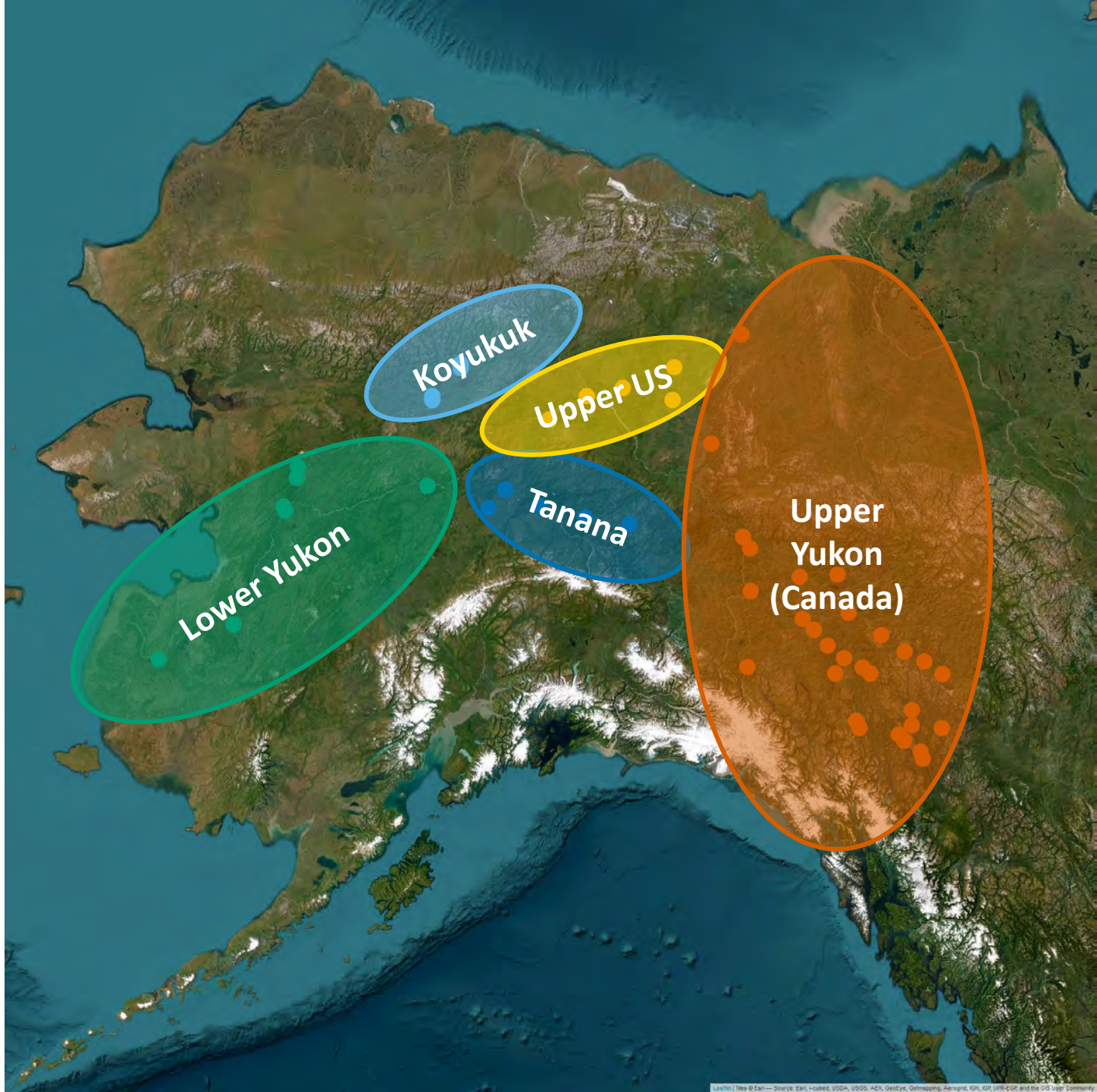
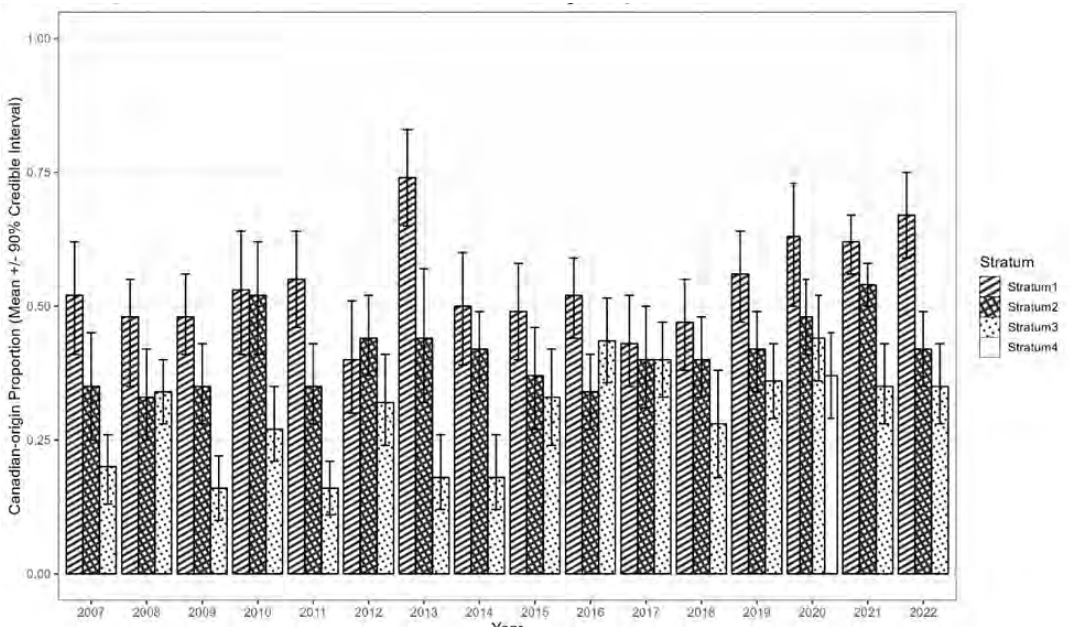
  - Koyukuk
  - Tanana
  - Upper US
- Upper Yukon (Canada)

Chinook Salmon Baseline: Applications

- Pilot Station inseason and postseason
  - Brood tables, total run, escapement, harvest, treaty obligations
- Radiotelemetry (tagging)
- Fish health and condition
- Bering Sea juveniles

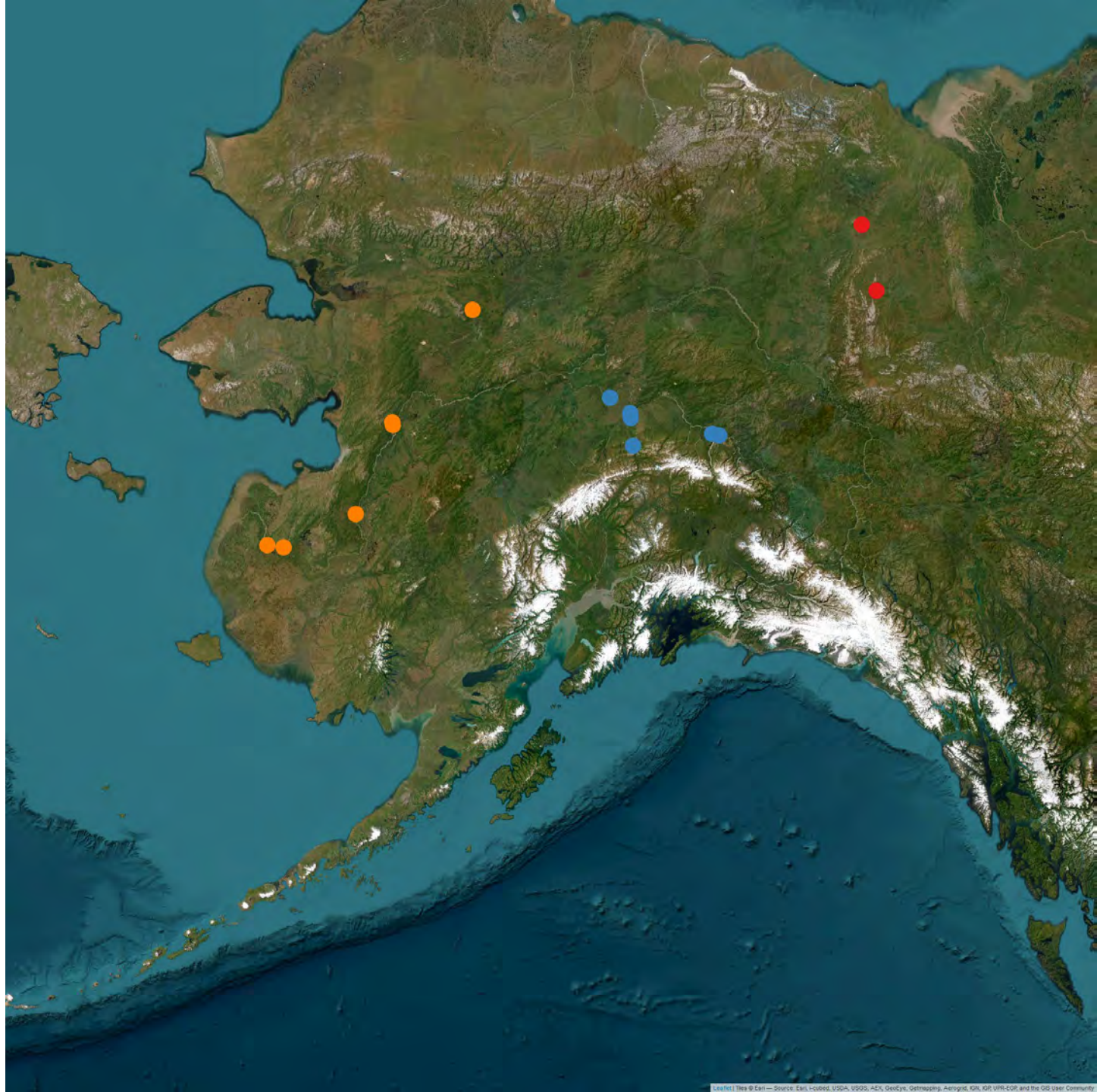


Chinook Salmon: Pilot Station GSI



Coho Salmon: Baseline Development

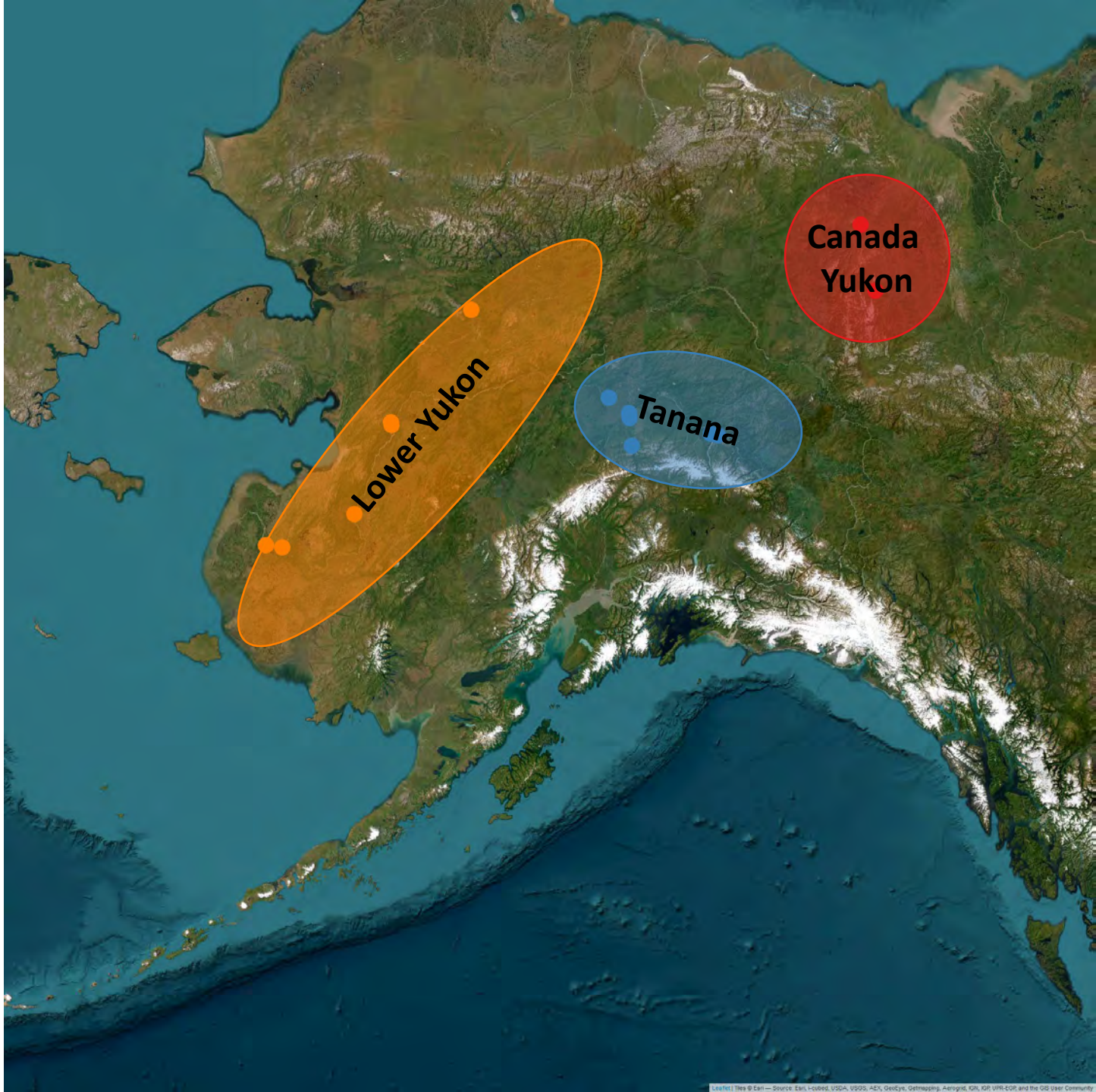
1. Populations: 17
2. Genetic Markers: 234



Baseline Improvements

Reporting Groups:

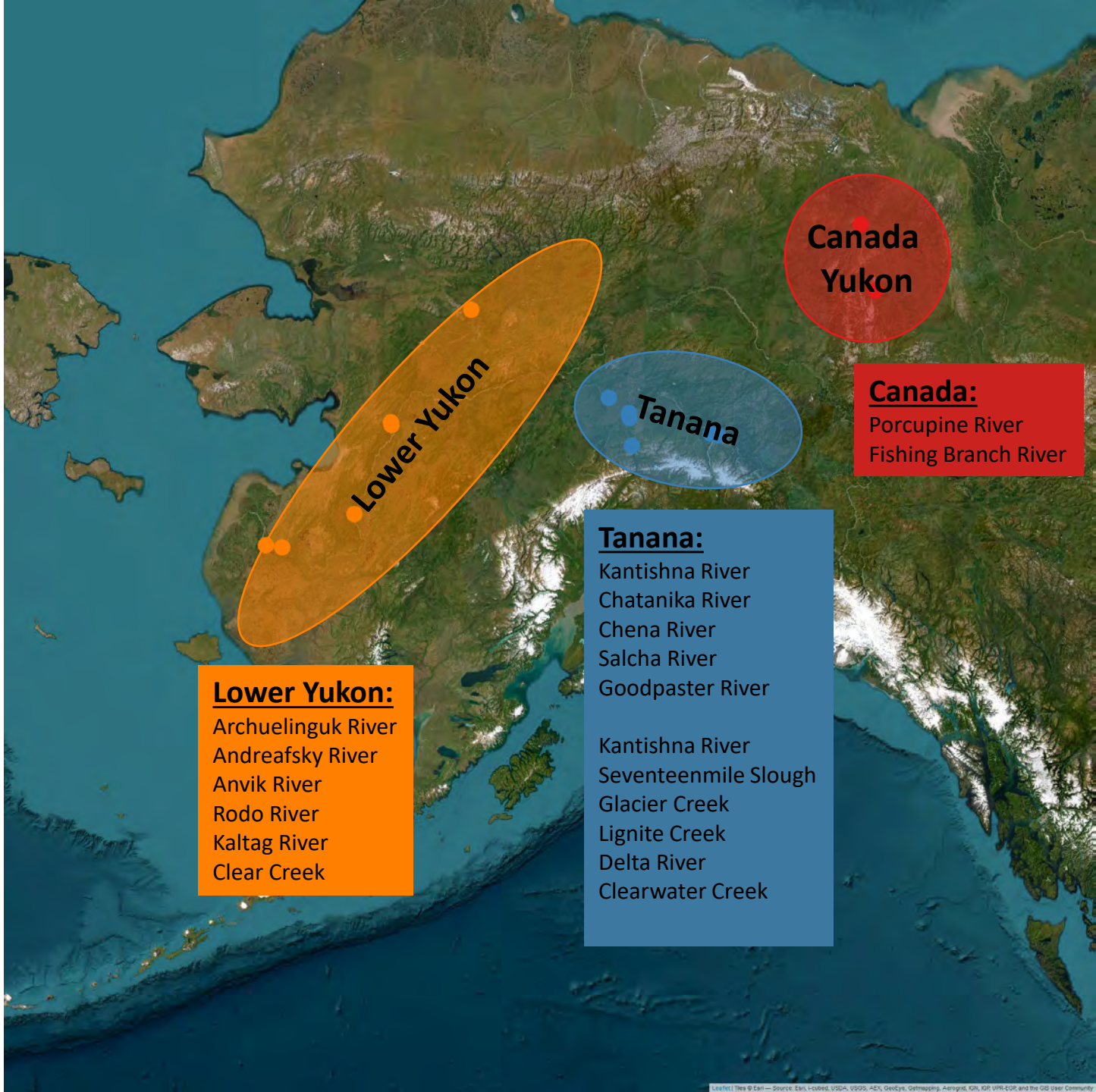
- Lower Yukon (US)
- Tanana (US)
- Upper Yukon (Canada)



Baseline Improvements

Reporting Groups:

- Lower Yukon (US)
- Tanana (US)
- Upper Yukon (Canada)



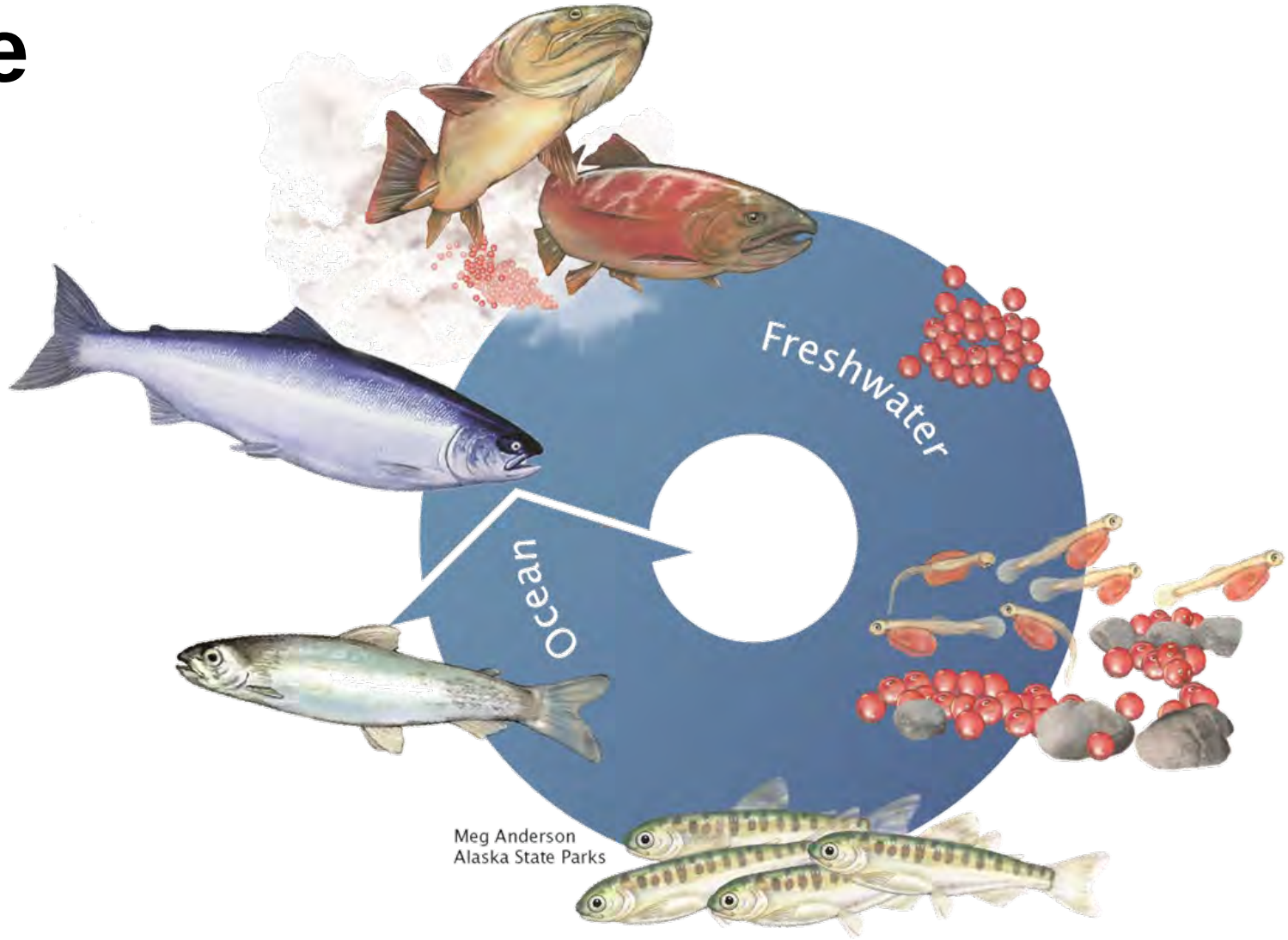
Summary of Genetic Baseline Improvements

Greater representation of major salmon systems

More genetic markers to capture genetic variation

Improved genetic stock identification accuracy and precision

Improved performance for research and management applications



Acknowledgements

Funding provided by Saltonstall-Kennedy Program Grant, Yukon River Panel Restoration and Enhancement Fund, Yukon River Treaty Implementation Funds, and the Alaska Department of Fish and Game.

Samples provided by Alaska Department of Fish and Game, National Oceanic and Atmospheric Administration, Fisheries and Oceans Canada, U.S. Fish and Wildlife Service, Norton Sound Economic Development Corporation, Tanana Chiefs Conference, and other partners within Alaska.

Questions: elizabeth.lee@alaska.gov

Extra slides....

Chum salmon (in-river): USFWS

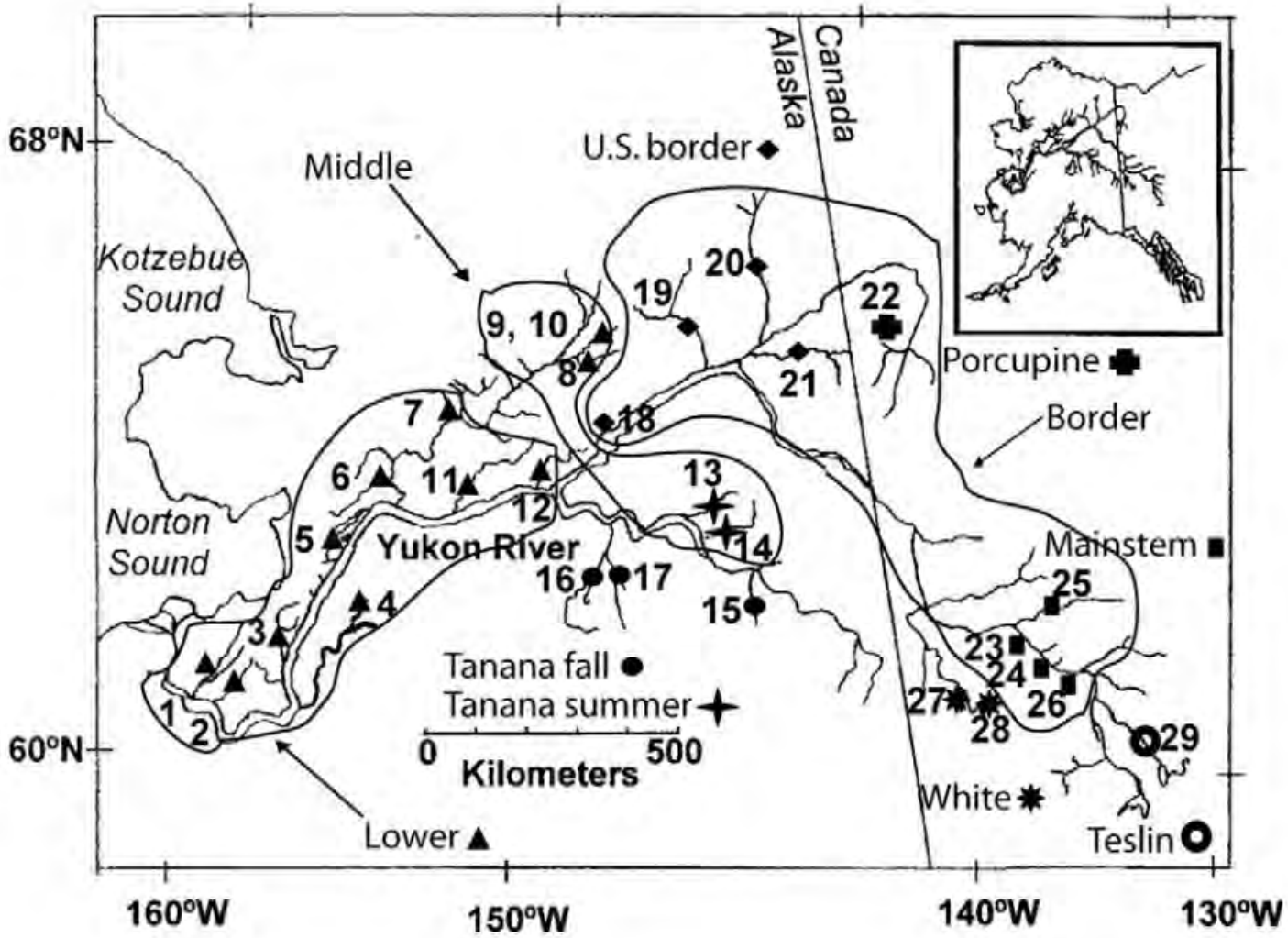


TABLE 1.—Yukon River chum salmon baseline, identifying stock location, stock label, seasonal race, management region, country, sample collection years, and number of fish sampled (*N*) from 29 putative stocks.

Stock	Label	Seasonal race	Management region	Country	Year(s)	*N*
Andreafsky River	1	Summer	Lower	USA	1987, 2004	261
Chulinak River	2	Summer	Lower	USA	1989	100
Anvik River	3	Summer	Lower	USA	1988	100
California Creek	4	Summer	Lower	USA	1997	50
Nulato River	5	Summer	Lower	USA	2003	100
Gisasa River	6	Summer	Lower	USA	2003	200
Henshaw Creek	7	Summer	Lower	USA	2003	200
Jim River	8	Summer	Lower	USA	2002	160
South Fork Koyukuk River early	9	Summer	Lower	USA	1996	100
South Fork Koyukuk River late	10	Summer	Lower	USA	1996	100
Melozitna River	11	Summer	Lower	USA	2003	146
Tozitna River	12	Summer	Lower	USA	2002	200
Chena River	13	Summer	Tanana River	USA	1992, 1994	186
Salcha River	14	Summer	Tanana River	USA	1994, 2001	185
Delta River	15	Fall	Tanana River	USA	1990	80
Kantishna River	16	Fall	Tanana River	USA	2001	161
Toklat River	17	Fall	Tanana River	USA	1990, 1994	250
Big Salt River	18	Fall	U.S. border	USA	2001	71
Chandalar River	19	Fall	U.S. border	USA	1989, 2001	338
Sheenjek River	20	Fall	U.S. border	USA	1987, 1988, 1989	263
Black River	21	Fall	U.S. border	USA	1995, 2001	112
Fishing Branch River	22	Fall	Porcupine River	Canada	1987, 1989, 1992, 1994, 1997	481
Big Creek	23	Fall	Main stem	Canada	1992, 1995	200
Minto Slough	24	Fall	Main stem	Canada	1989, 2002	166
Pelly River	25	Fall	Main stem	Canada	1993	84
Tatchun Creek	26	Fall	Main stem	Canada	1987, 1992	175
Donjek River	27	Fall	White River	Canada	1994	72
Kluane River	28	Fall	White River	Canada	1987, 1992, 2001	462
Teslin River	29	Fall	Teslin River	Canada	1992, 2001	143

Mixed Stock Analysis vs Individual Assignment

- Mixed stock analysis (MSA):
  - Proportional assignment
  - Every fish assigned
  - Appropriate for finer-scale groups
  - Assigns best fit of full mixture
- Individual assignment (IA):
  - Assigns each fish individually to group with highest likelihood
  - Only fish above likelihood cut-off are assigned (we use 80%)
  - May not be appropriate for finer-scale groups

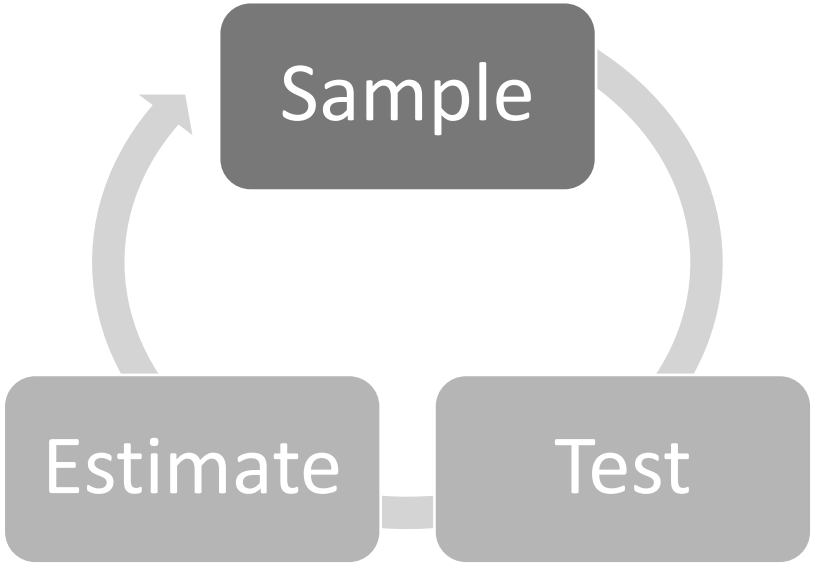
Considerations for Genetic Stock ID

- What are the research questions that could use genetic data?
  - Stock-specific abundance
  - Linking diet, condition factor, environmental data, otolith information, etc.
- Defining appropriate reporting groups
  - Importance of stakeholder input
  - What is in the baseline? Is representation adequate?
  - Fine-scale vs broad-scale (balancing accuracy with level of detail)
- How well do reporting groups perform for:
  - Mixed stock analysis?
  - Individual assignment?

Baseline evaluation testing

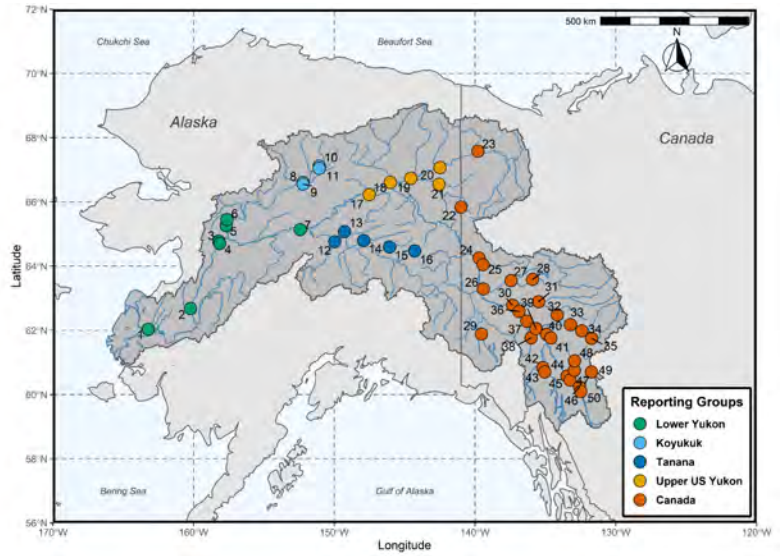
Describe **accuracy** and **precision** with four measures:

1. root mean square error
2. mean bias
3. maximum percentage from the true proportion where 90% of mean point estimates occurred
4. percentage of observations where the estimated 90% credible interval contains the true proportion

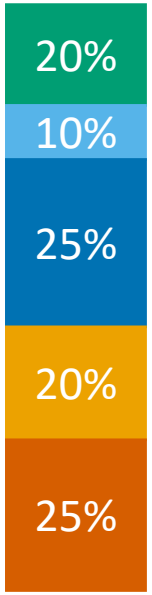


Baseline evaluation testing

Sample 200 baseline fish:
Test mixture

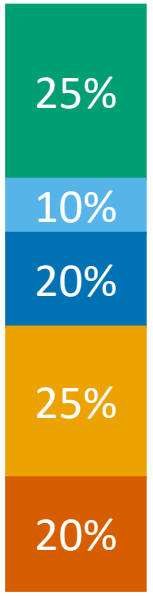


Known proportions



Conduct MSA on test mixture

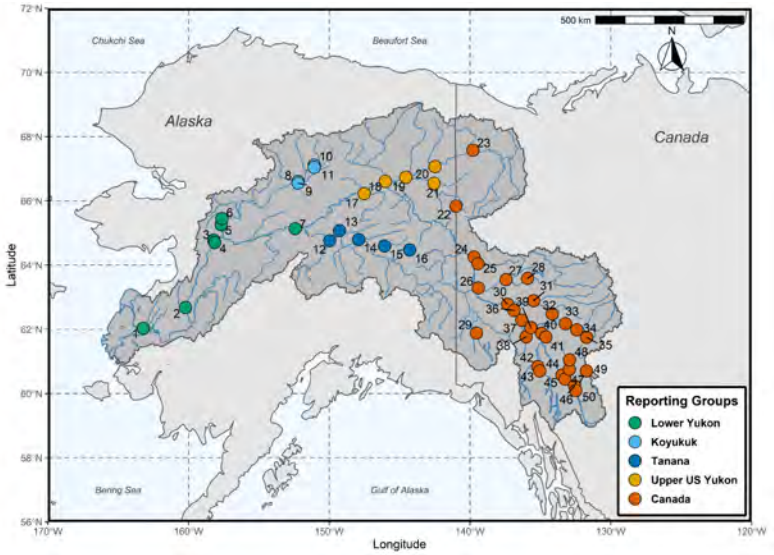
Estimated proportions



How different are the true proportions from the estimated proportions?

Baseline evaluation testing

Sample 200 baseline fish:
Test mixture



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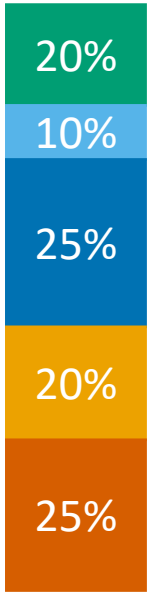

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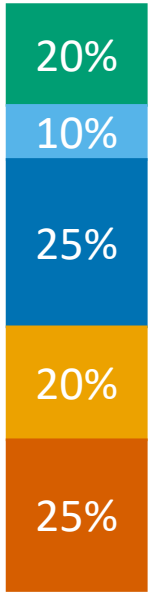

How different are the true proportions from the estimated proportions?

Baseline evaluation testing

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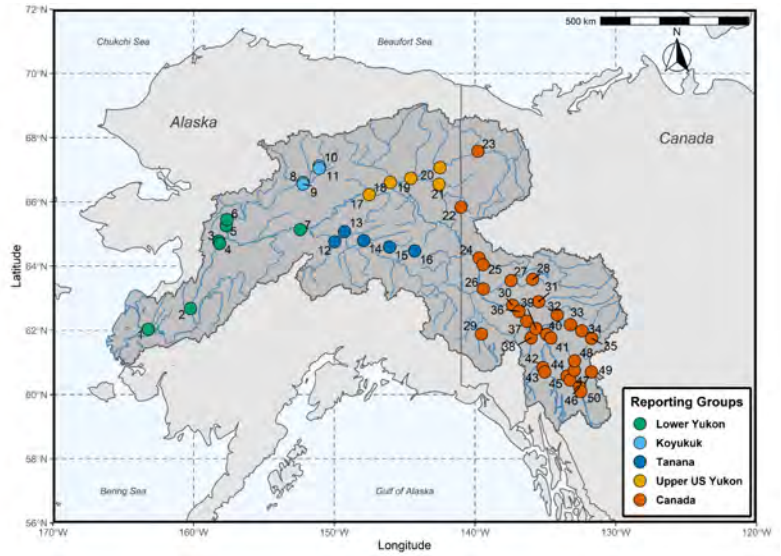

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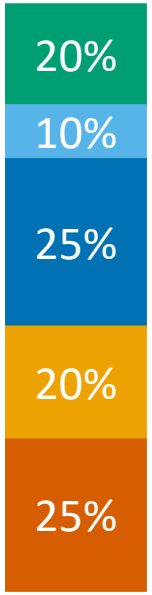
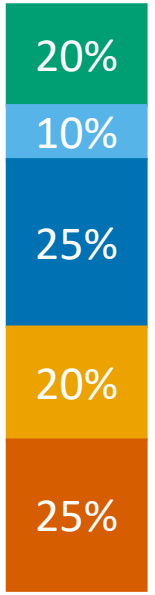


Conduct MSA on test mixture

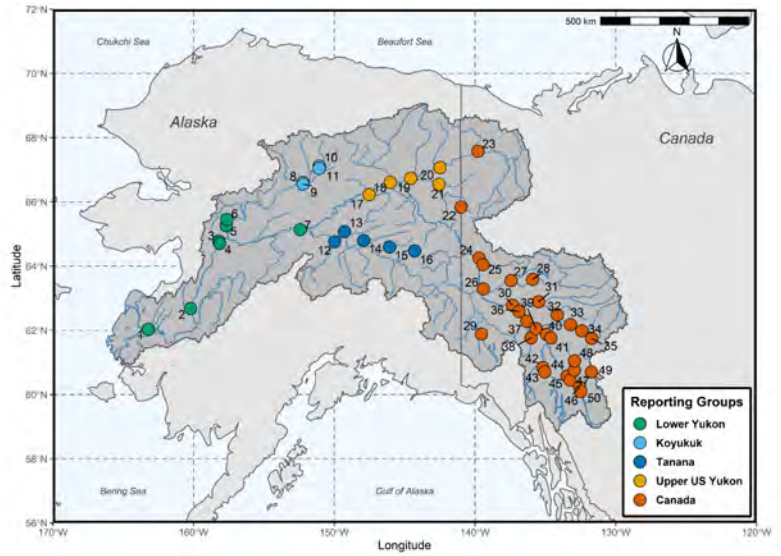
Estimated proportions



At least 90% of the estimates should be within ±10% of the true proportion

Baseline evaluation testing

Sample 200 baseline fish:
Test mixture



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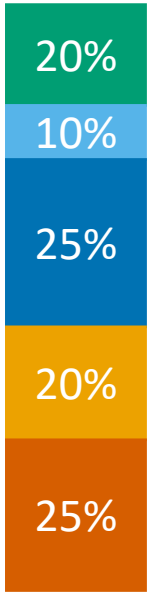

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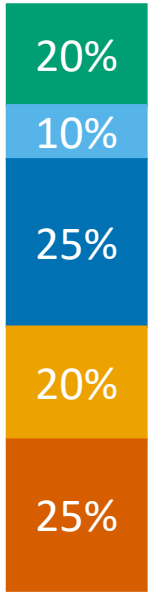

90% of the test mixtures had estimated proportions **within 2.6% of the true proportion**

Baseline evaluation testing

Describe **accuracy** and **precision** with four measures:

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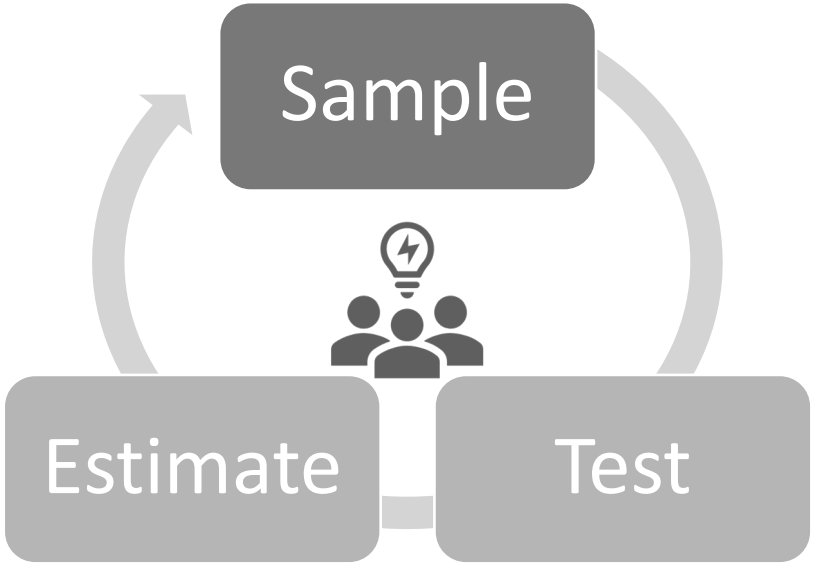


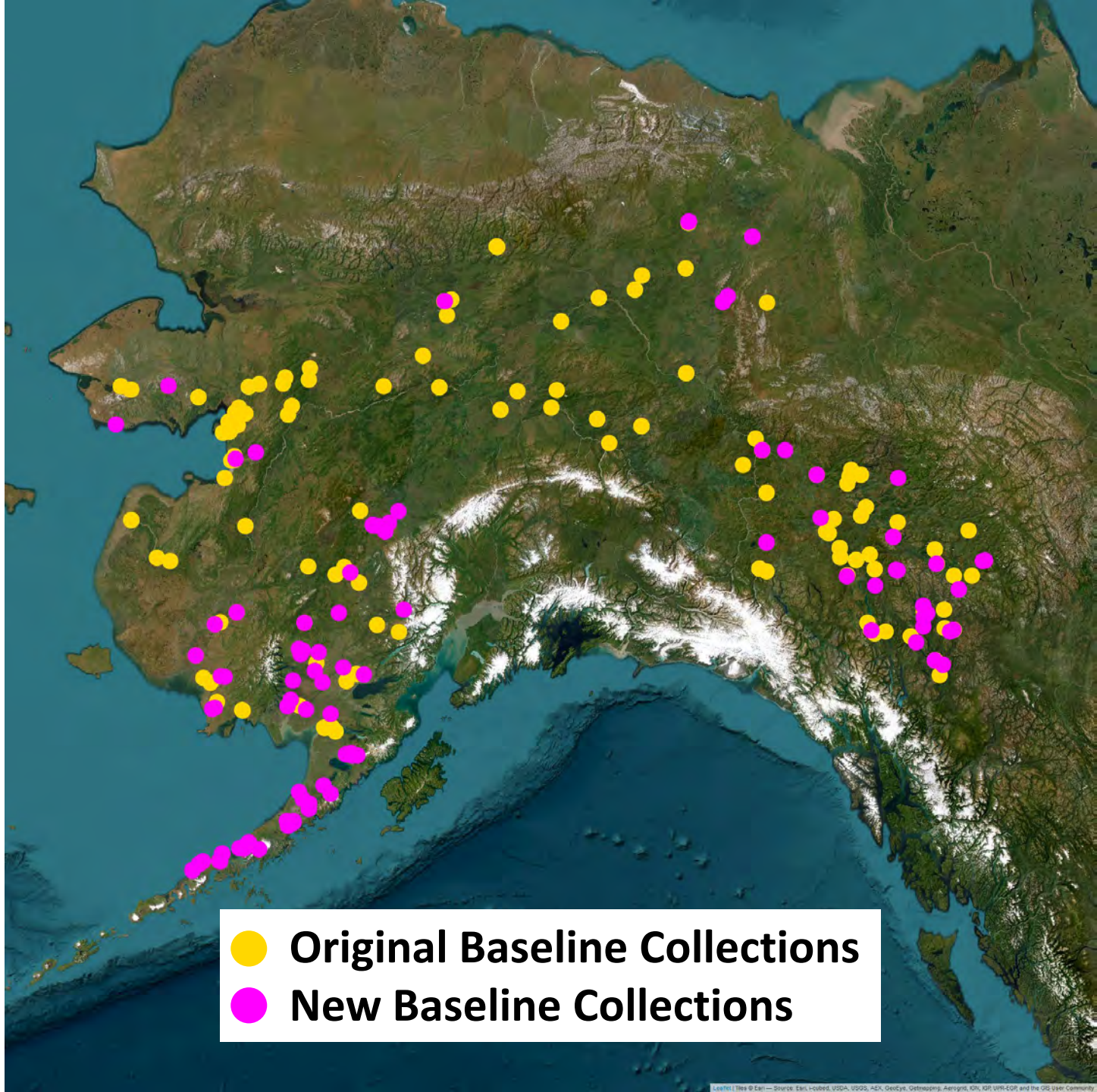
WAK Chinook Baseline Improvements

Comparison to previous Western Alaska Chinook salmon baseline:

6,327 individuals	→	11,806 individuals
60 populations	→	117 populations
80 genetic markers	→	447 genetic markers
506,160 genotypes	→	5,277,282 genotypes
4 reporting groups	→	9 reporting groups

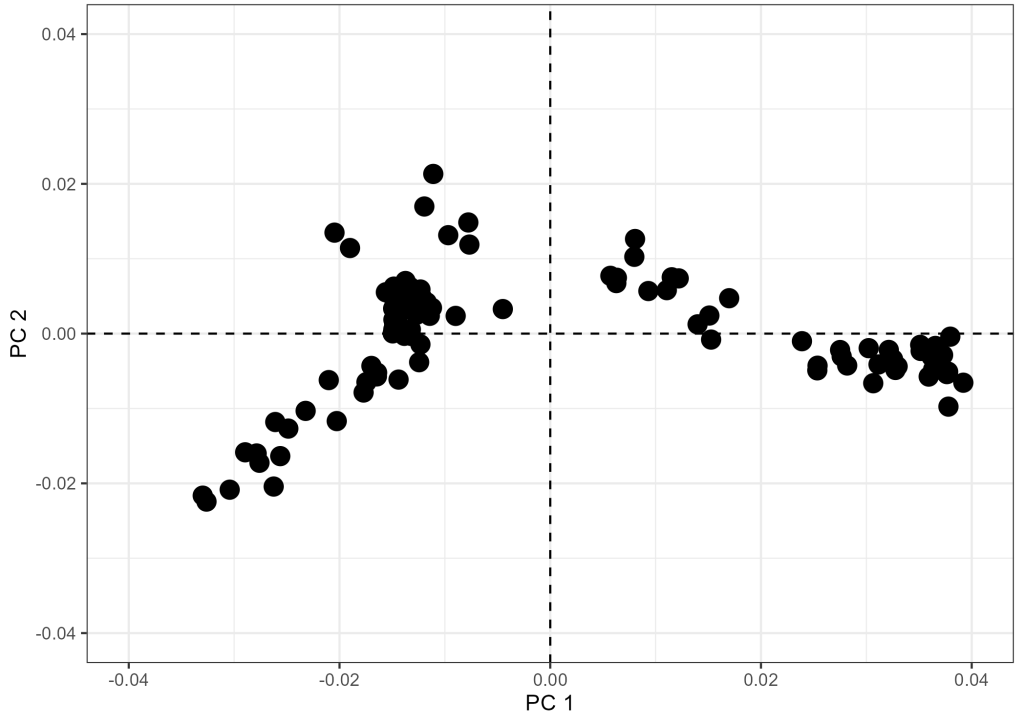
Baseline Improvements

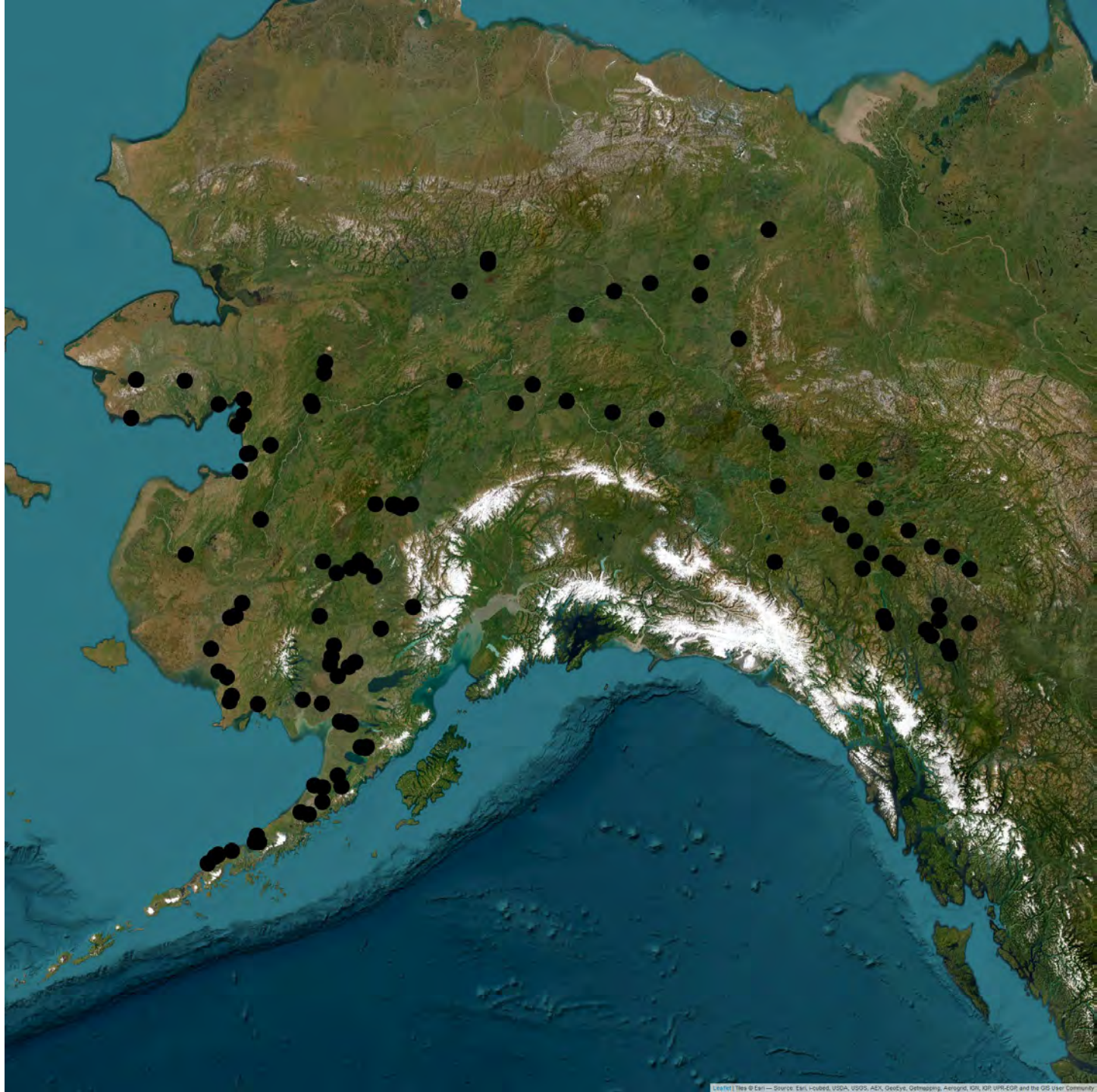
1. Populations



Baseline Improvements

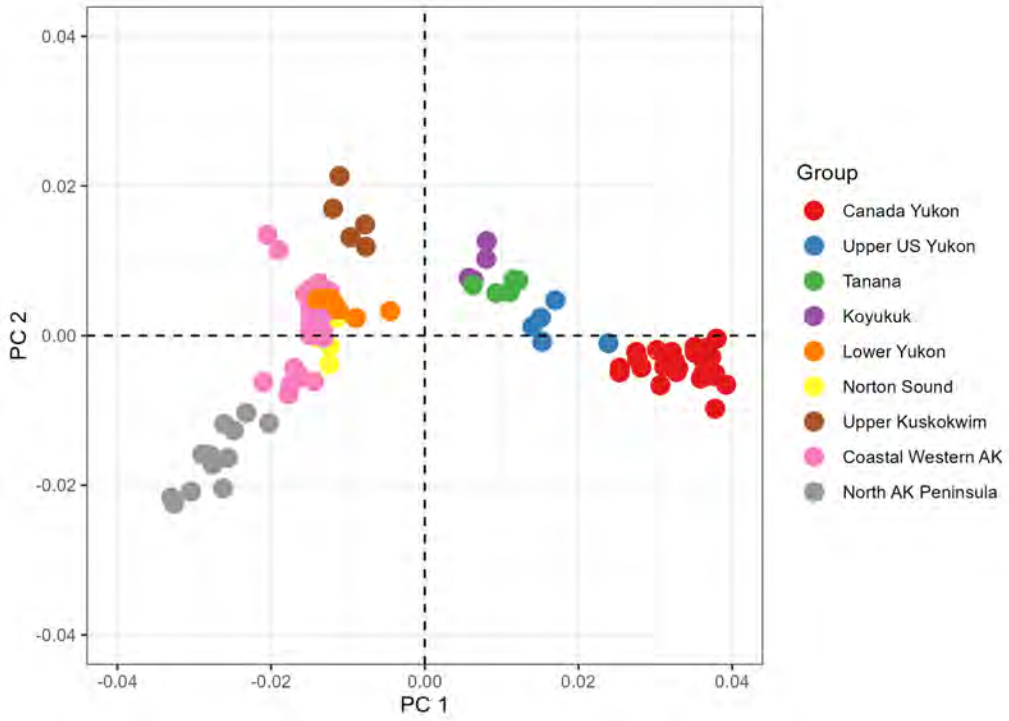
Population structure

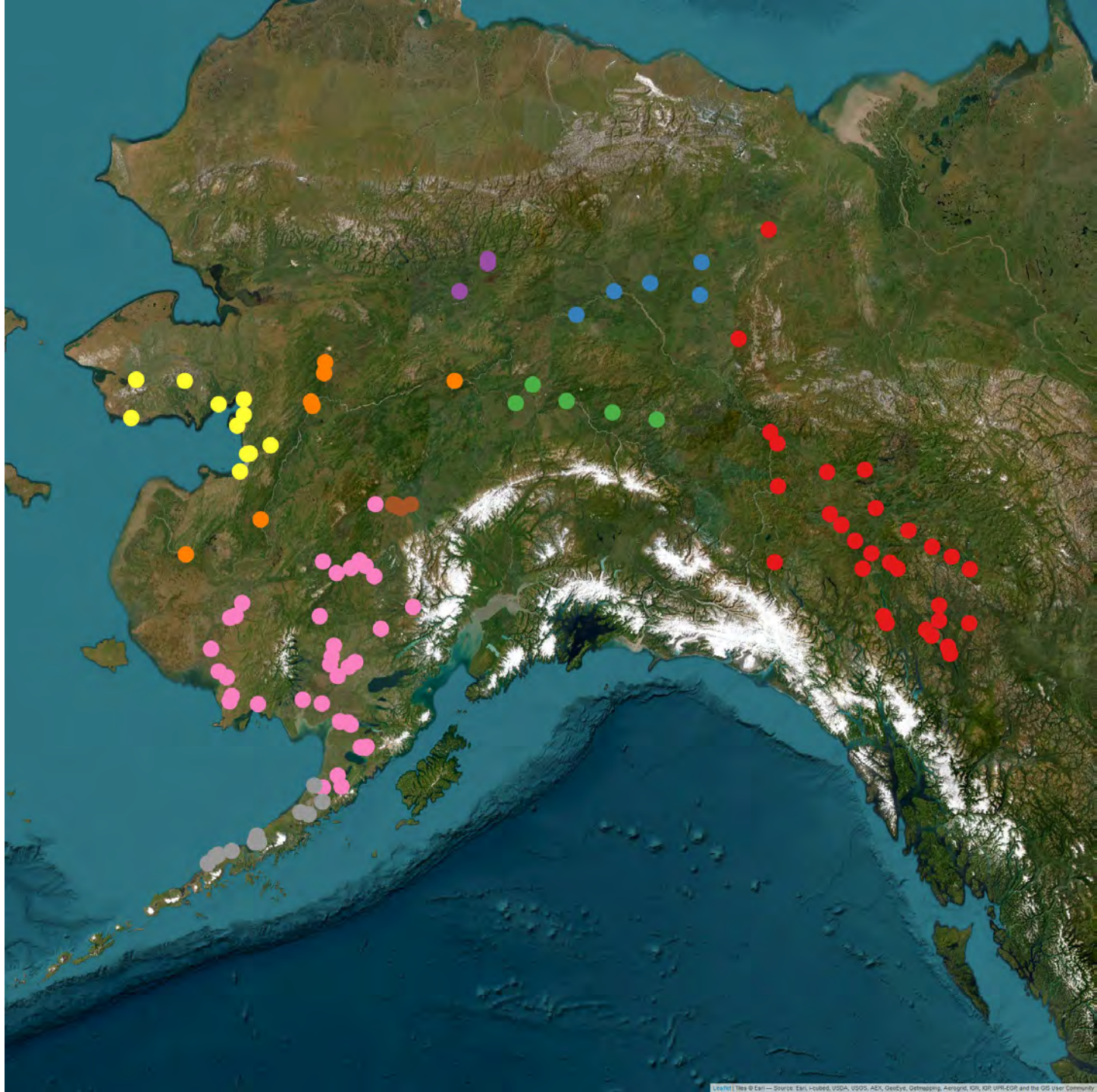




Baseline Improvements

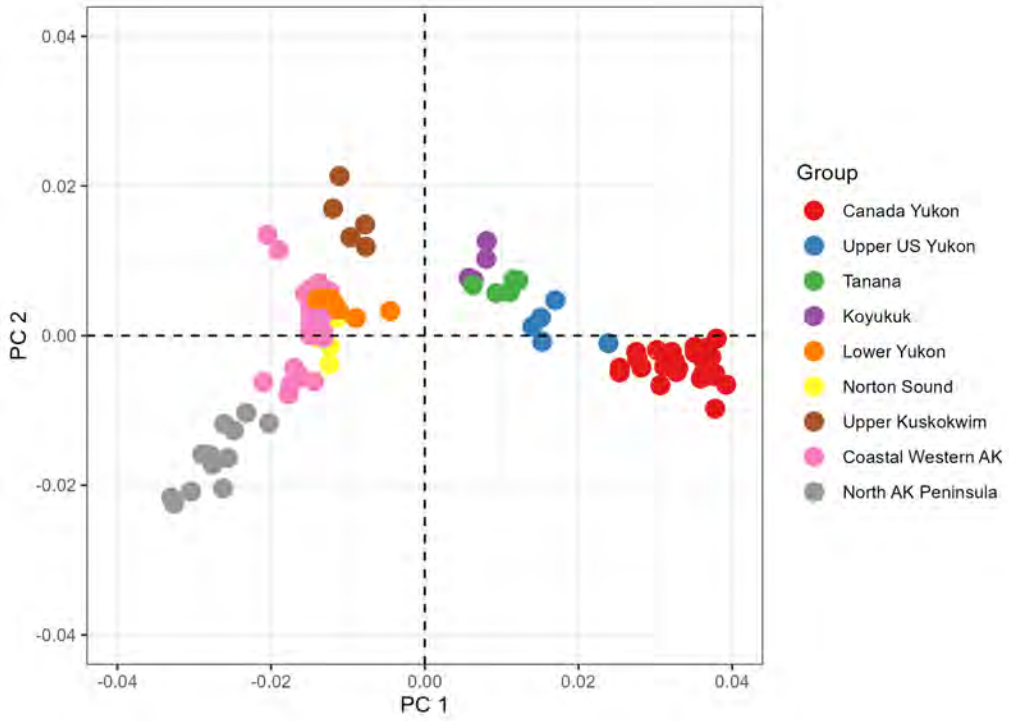
Population structure

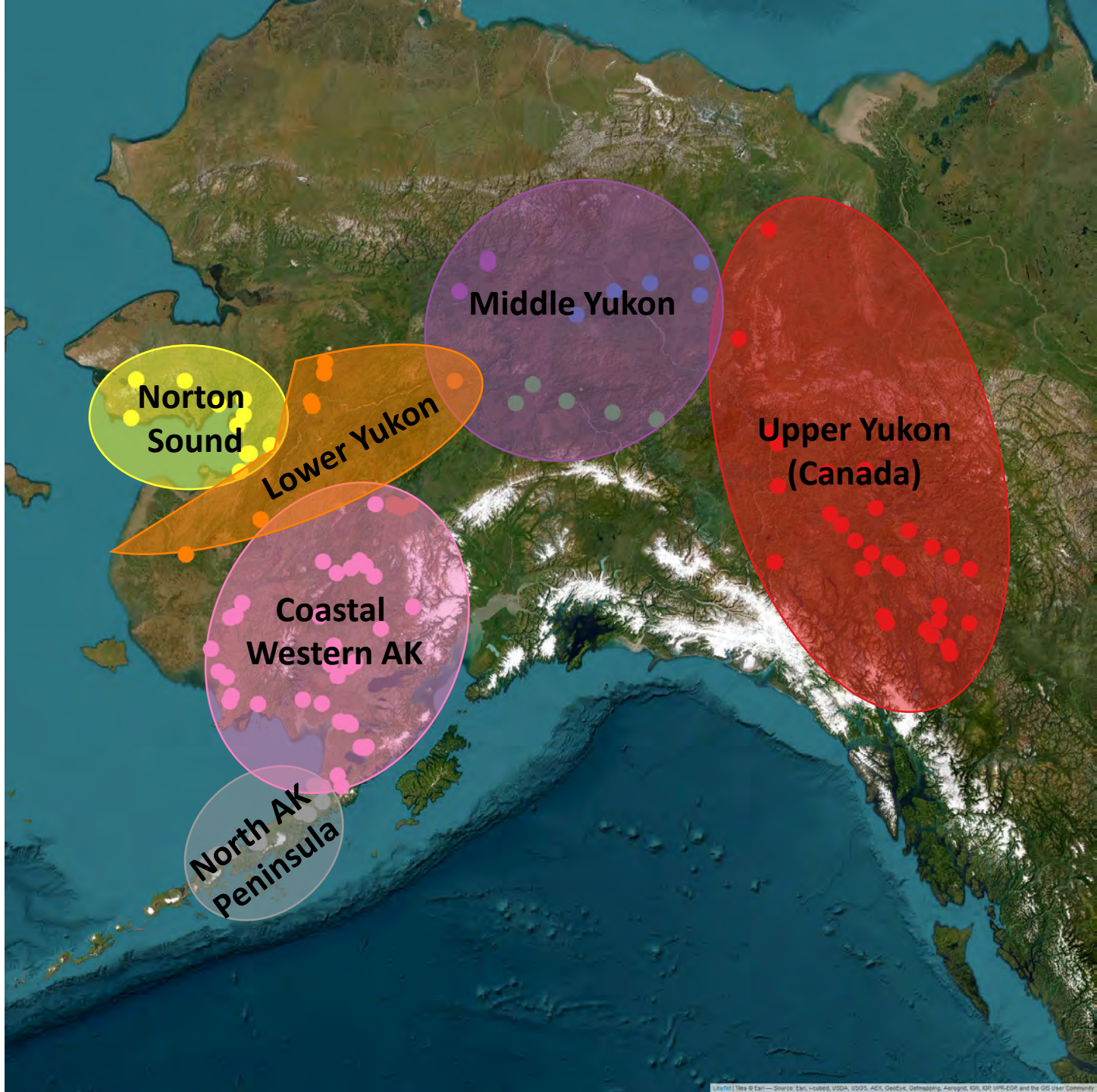




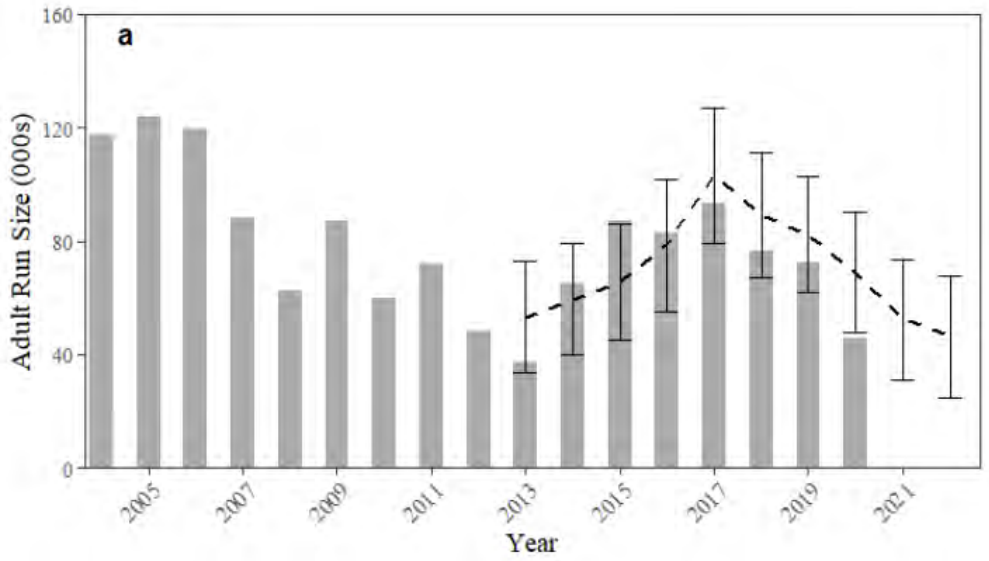
Baseline Improvements

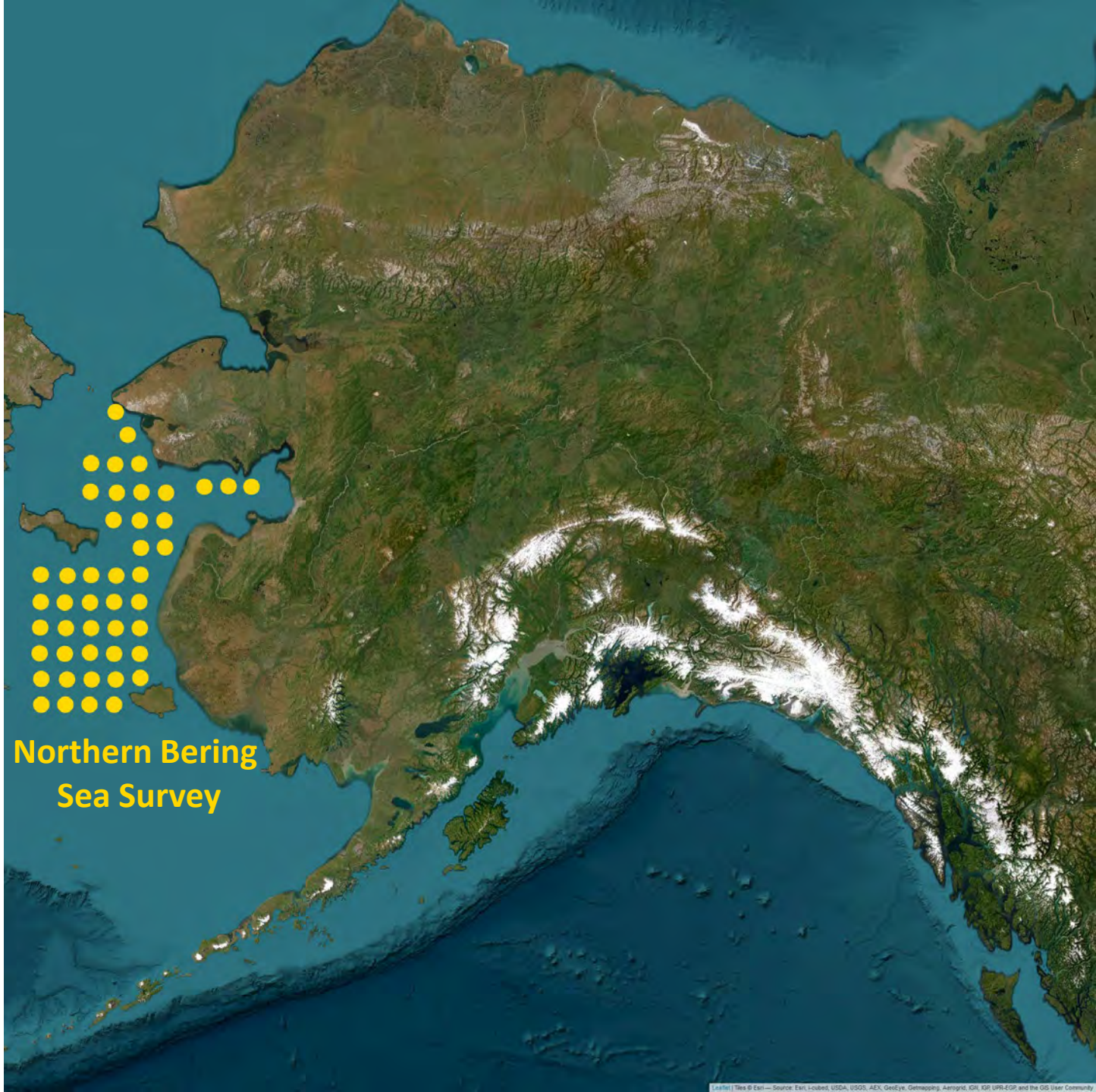
Reporting groups



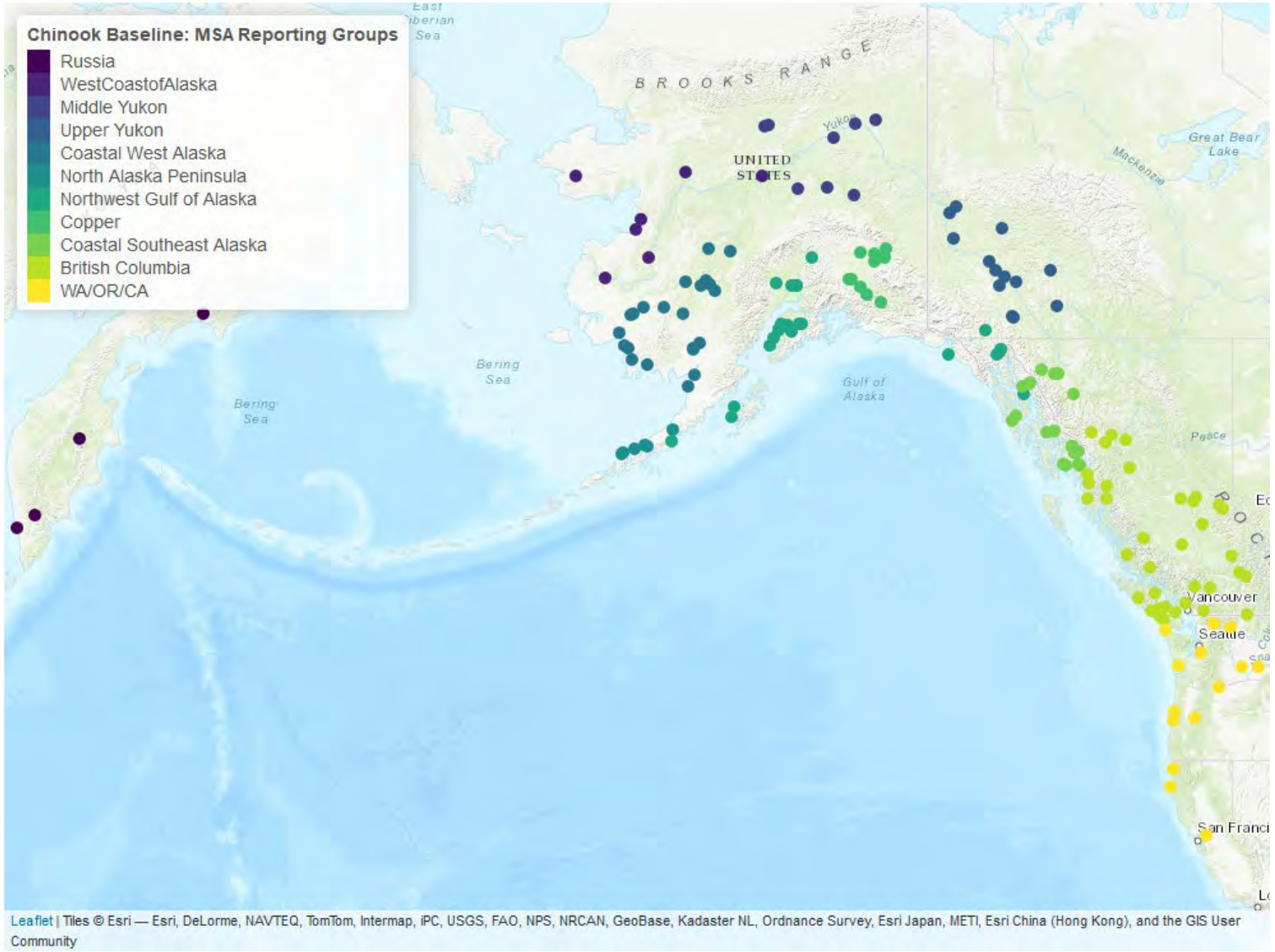


Applications in Western Alaska





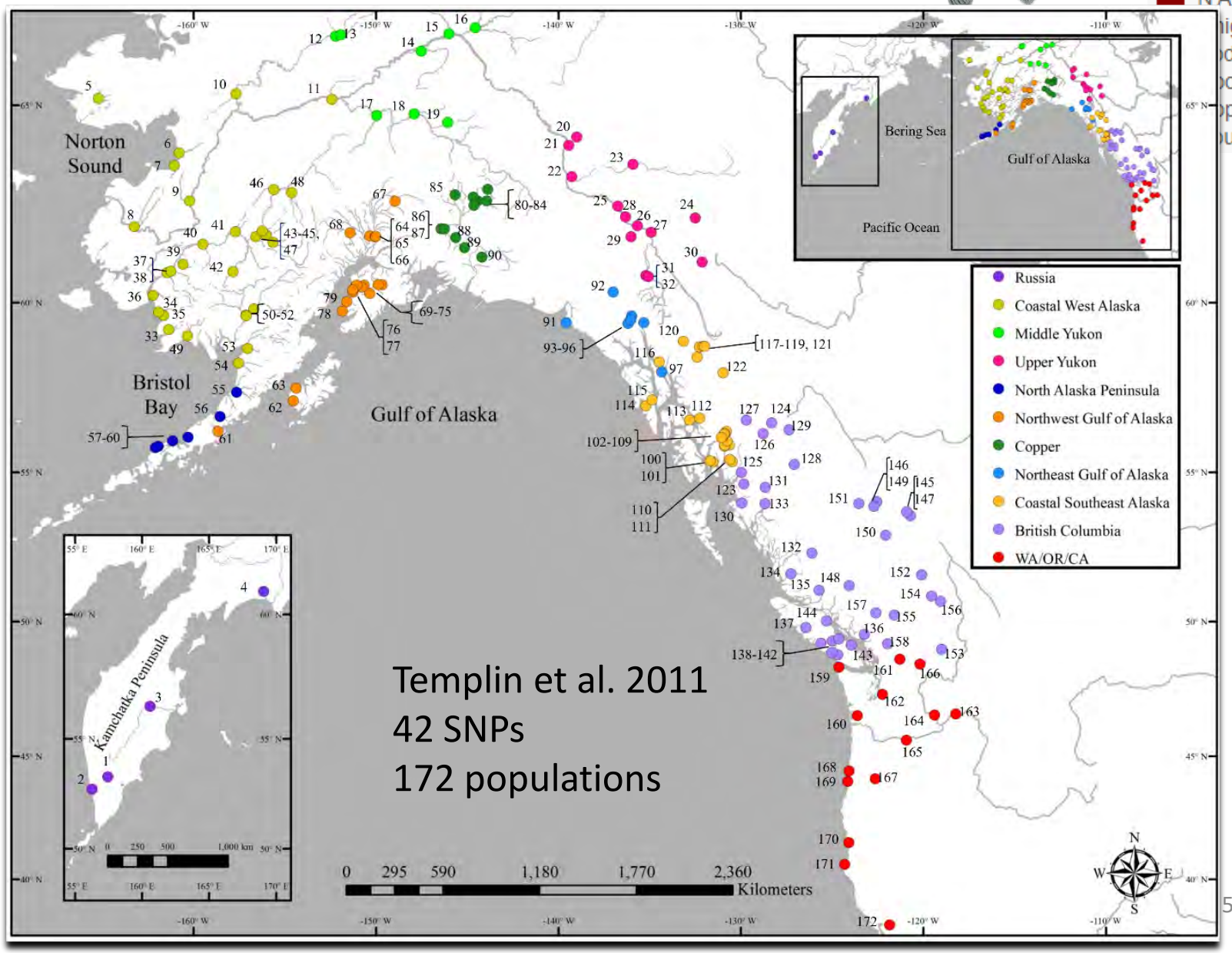
Chinook salmon baseline (Coastwide)



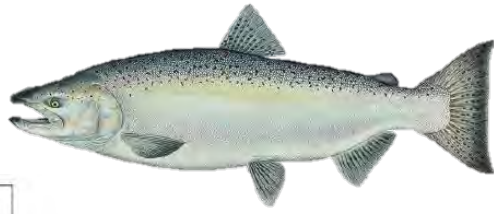
Chinook

Current

- 13 GAPS uSATs (PST)
- 42 SNPs (non-PST)
  - Templin et al. 2011



Chinook



Russia
Norton Sound
Yukon
Western AK
N AK Pen
Chignik
Kodiak
Cook Inlet
Copper River
Southeast_Alaska

Current

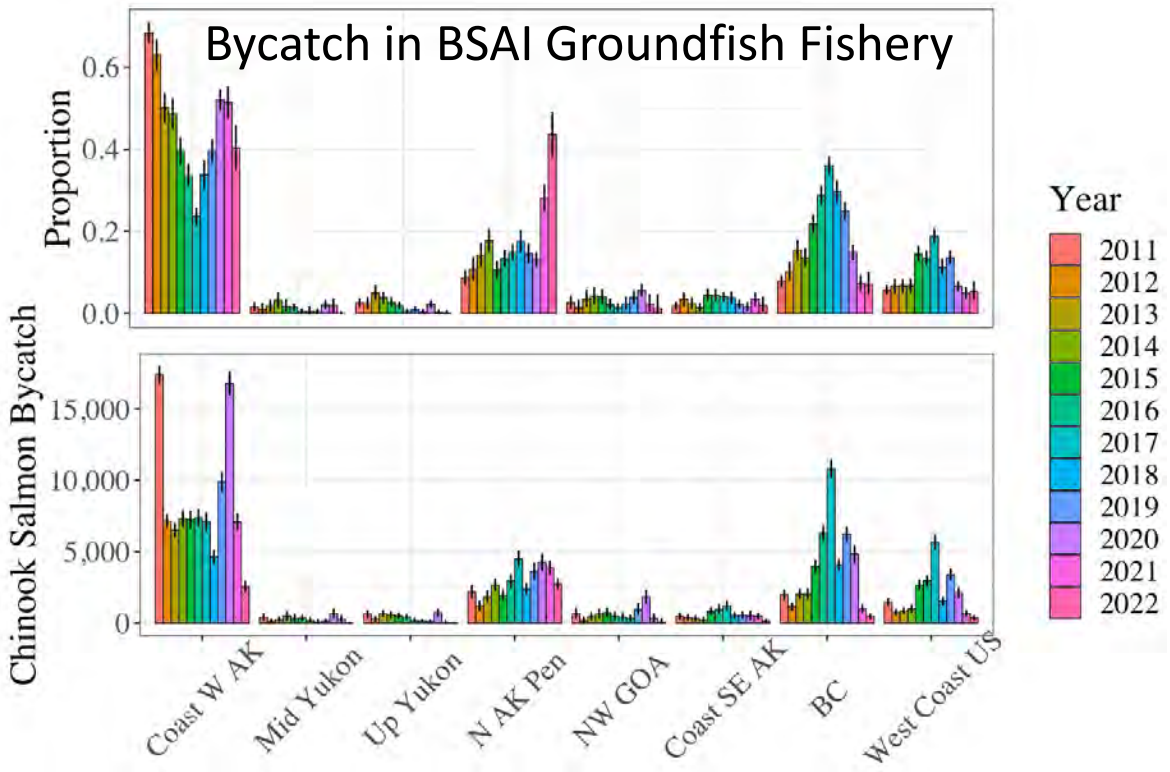
- 13 GAPS uSATs (PST)
- 43 SNPs (non-PST)
  - Templin et al. 2011
- Regional GT-seq
  - Cook Inlet + WAK

Short-term

- 299 → ~255 SNPs
- CRITFC/IDFG GT-seq v3.0
- 244 populations

Long-term

- Join existing data
- Genotype gaps (BC)



Credit: Chuck Guthrie III & Pat Barry

Applications

- IYS + Ocean Ecology
- Bycatch (replace Templin et al. 2011)

Genetic Stock Composition of Chum Salmon Harvested in Commercial Salmon Fisheries of the South Alaska Peninsula, 2022

Oral Report: RC #3; Tab #9

A Report to the Alaska Board of Fisheries

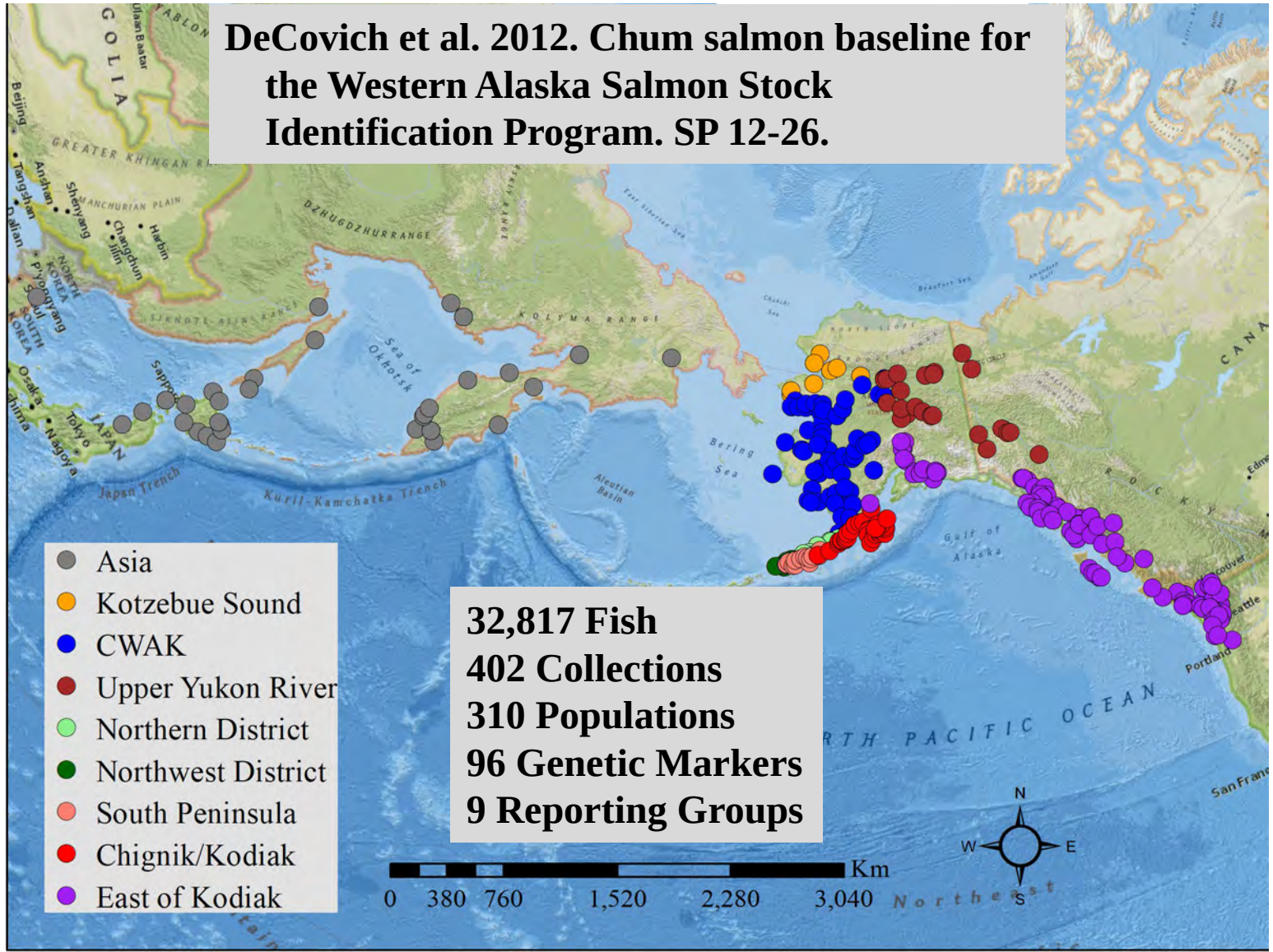
February 2023

Division of Commercial Fisheries

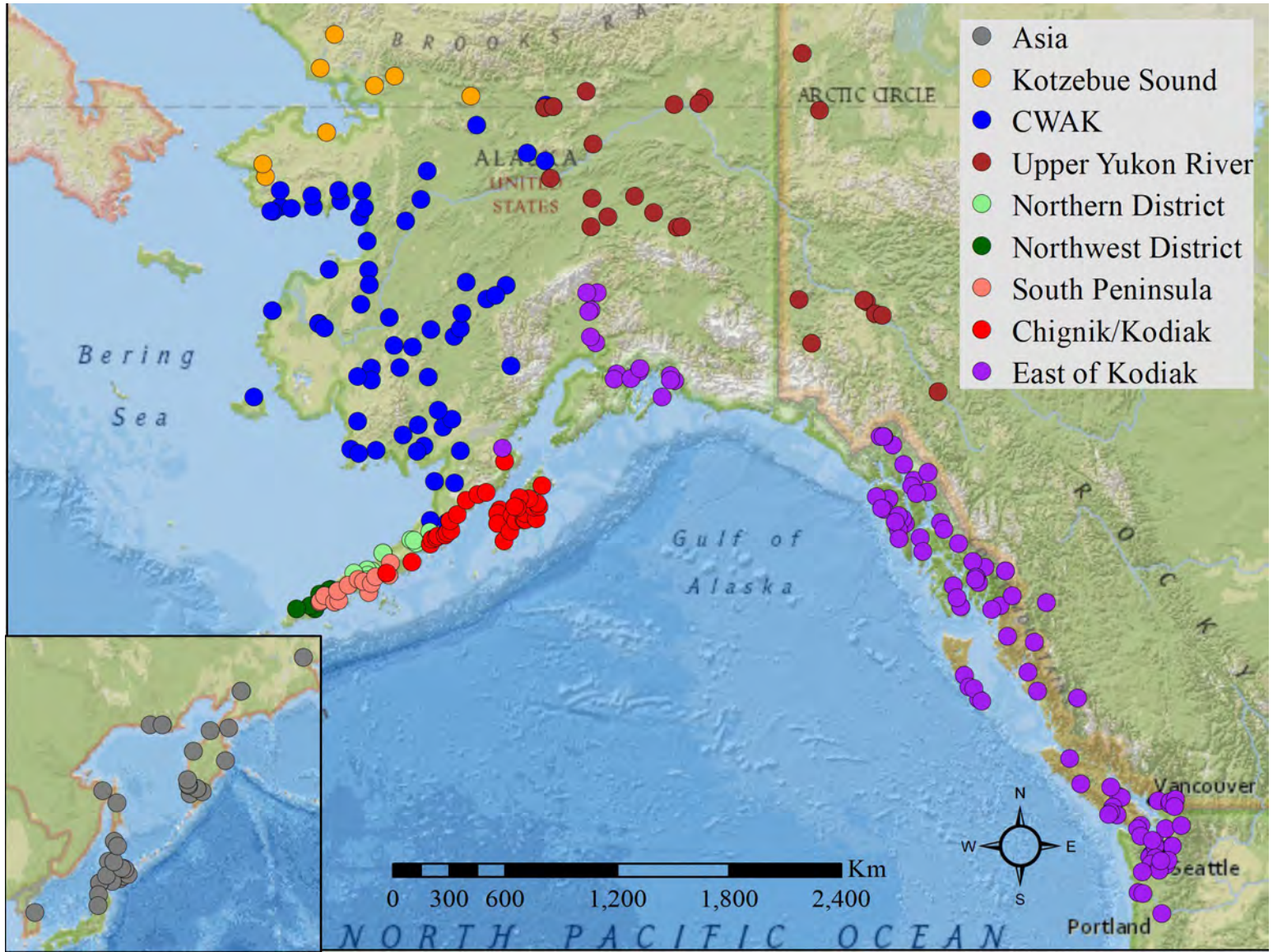
Tyler H. Dann

GENE CONSERVATION LABORATORY
Alaska Department of Fish & Game

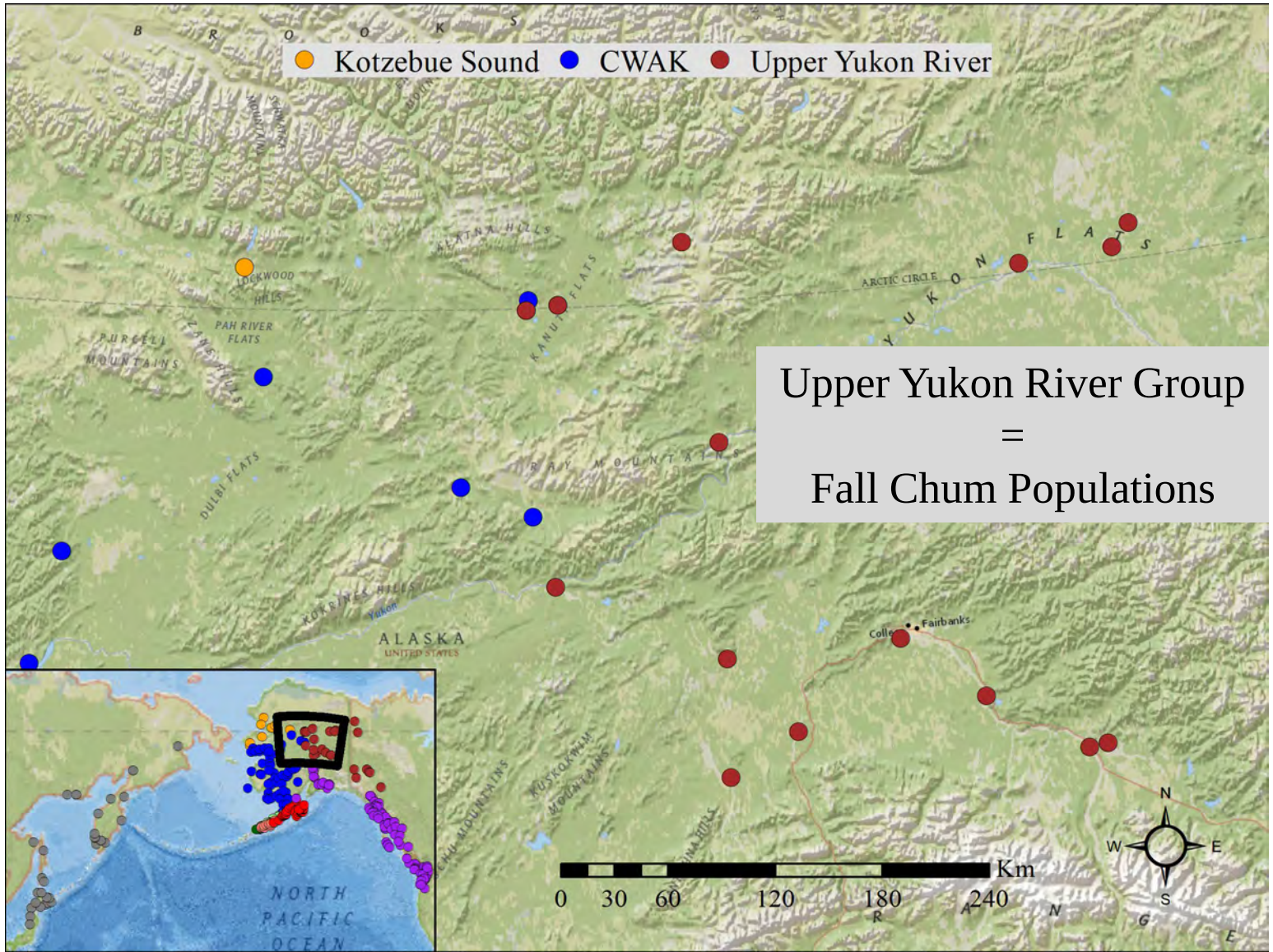
Baseline Summary



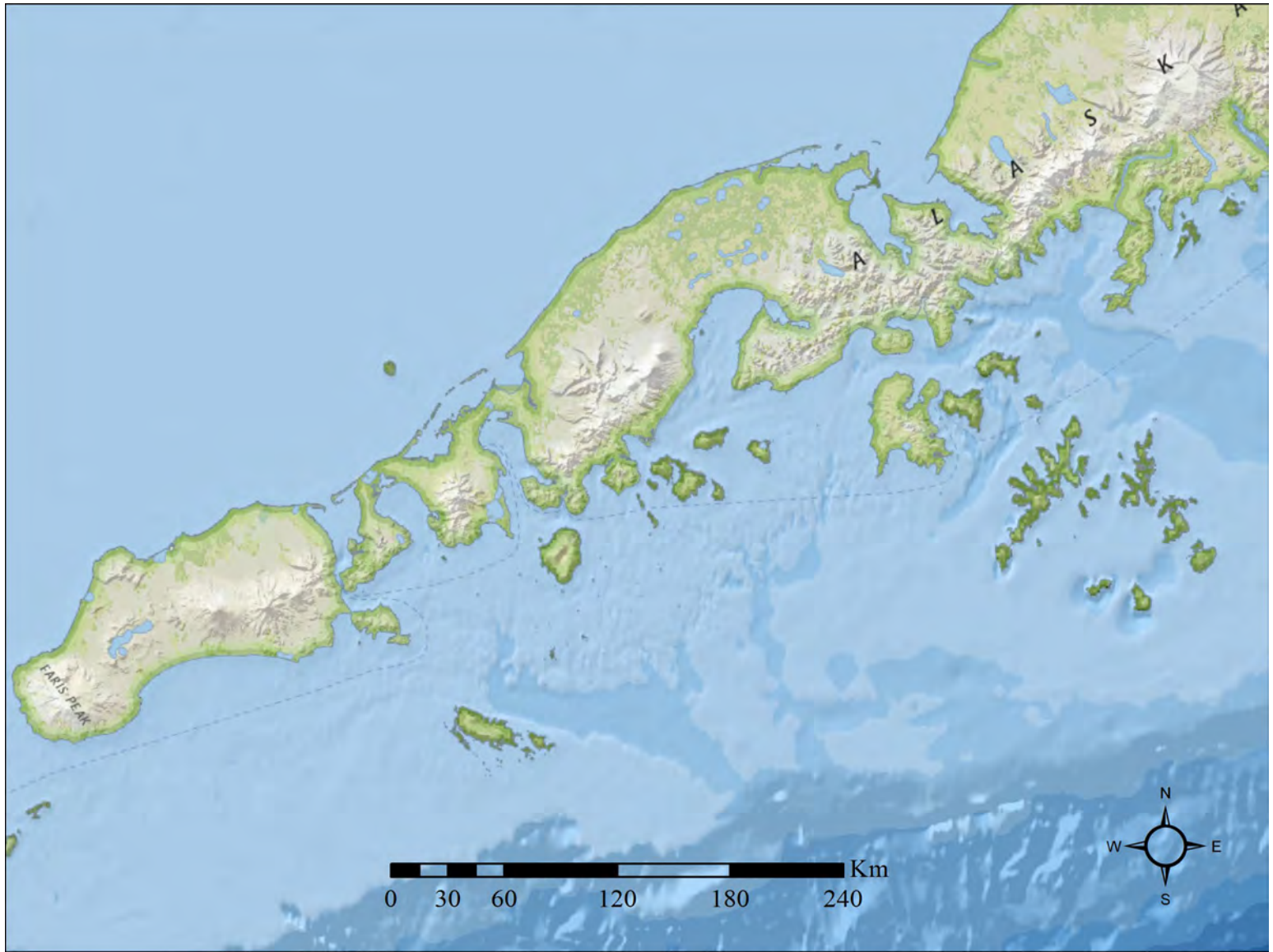
Baseline Summary



Baseline Summary



Summary of Harvests among Areas and Gear Types



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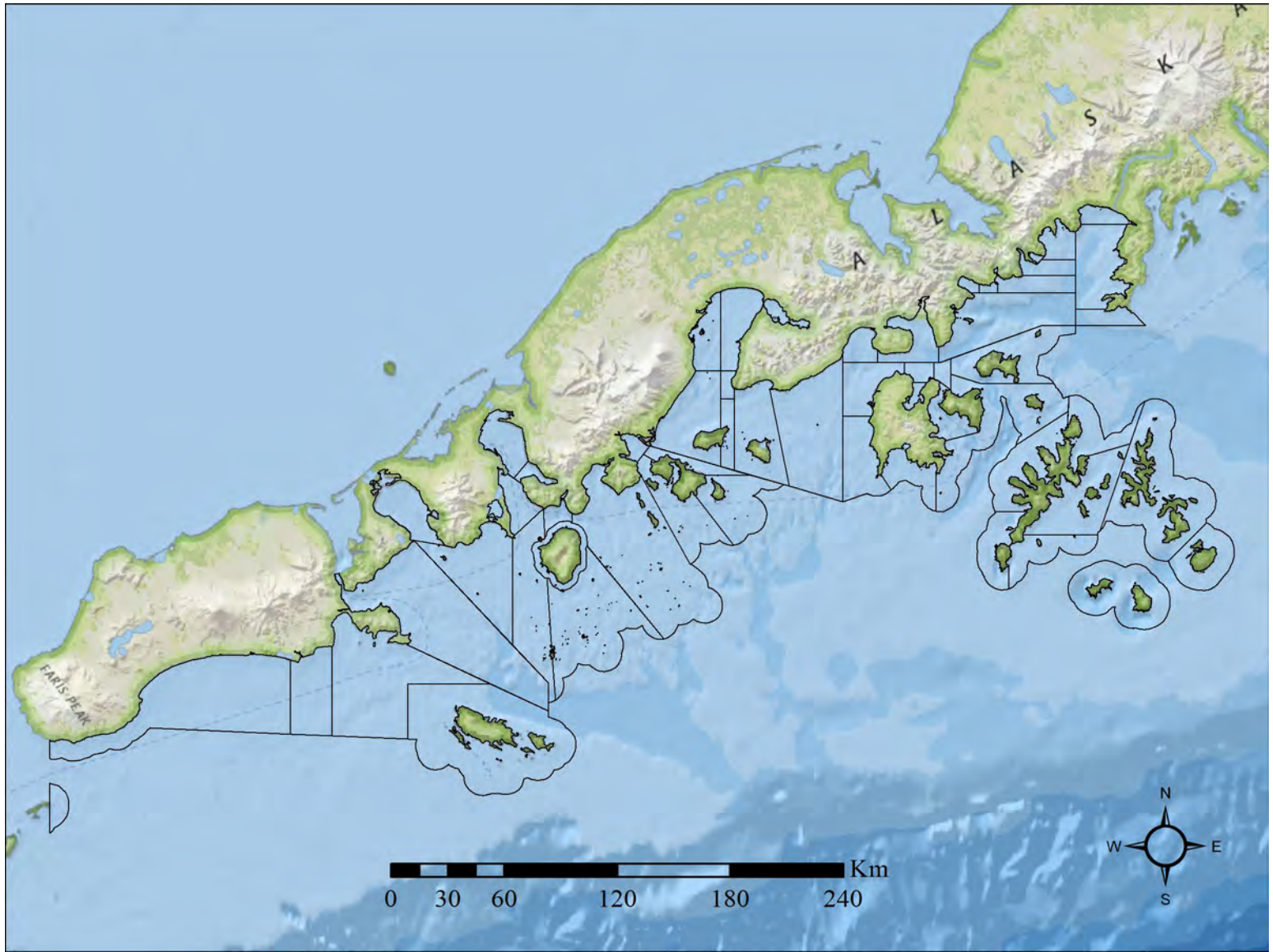
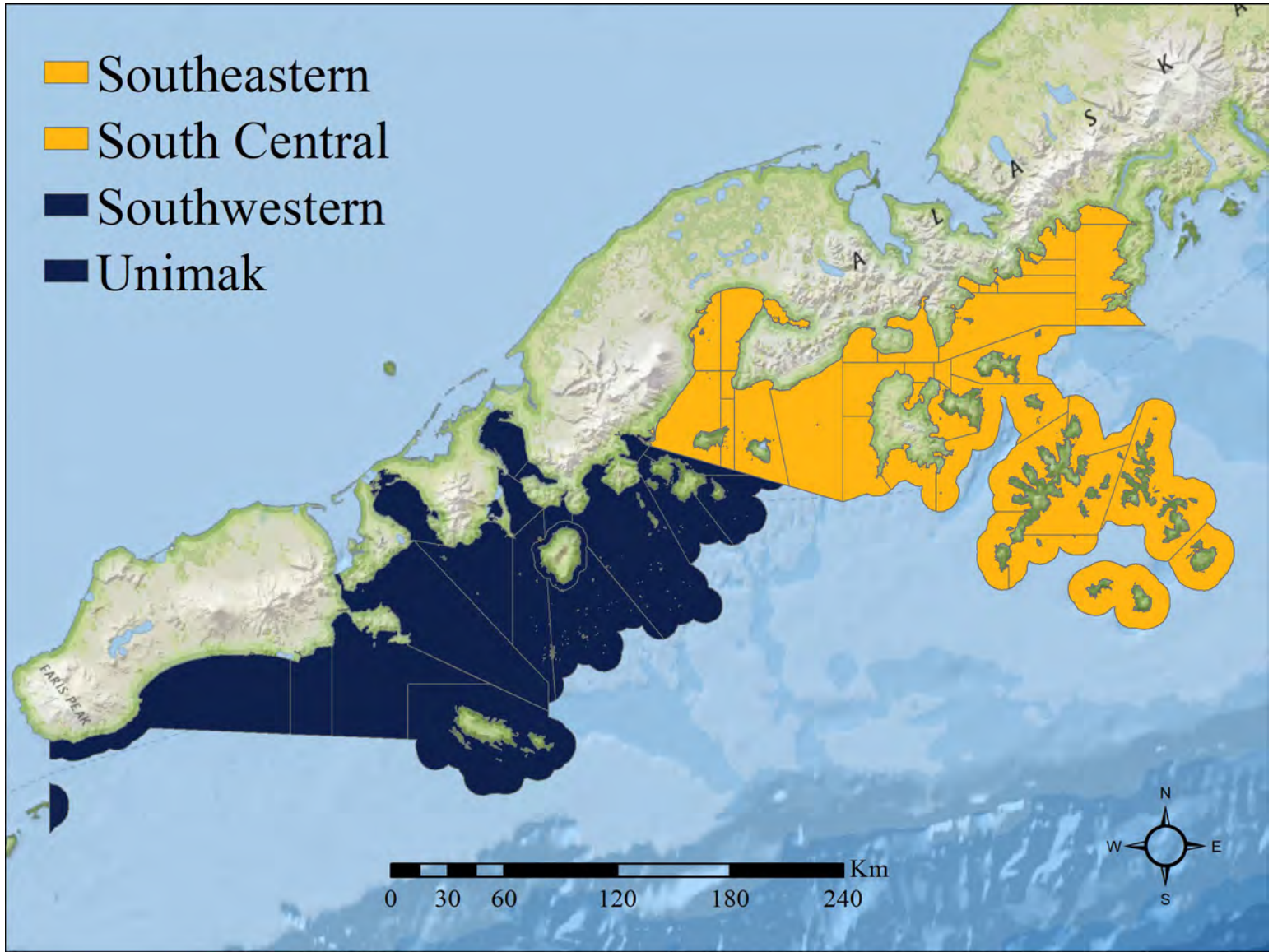
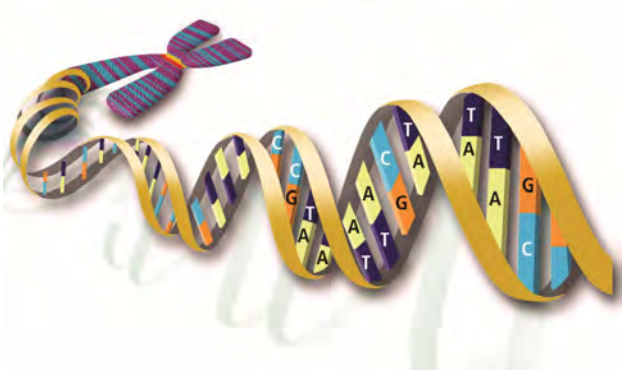
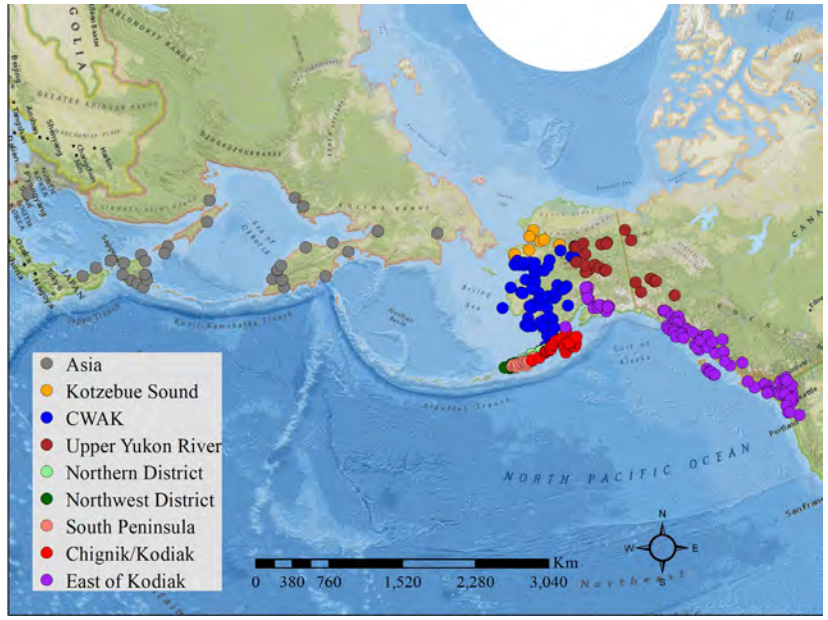


Summary of Harvests among Areas and Gear Types



Mixed Stock Analysis





Stock Composition Estimates (%)

Stock-specific Harvest (1,000s of Fish)

Harvest Represented

Stratified Estimates of Stock-Specific Harvest

- Weighted each set of stock composition estimates by represented harvest
- Summed stock-specific harvests hierarchically
- Temporal strata within gear types, areas, months
  - Gear types within areas, months
    - Areas within months
      - Months within June and post-June
        - South Alaska Peninsula as a whole

Guide to Results in Report

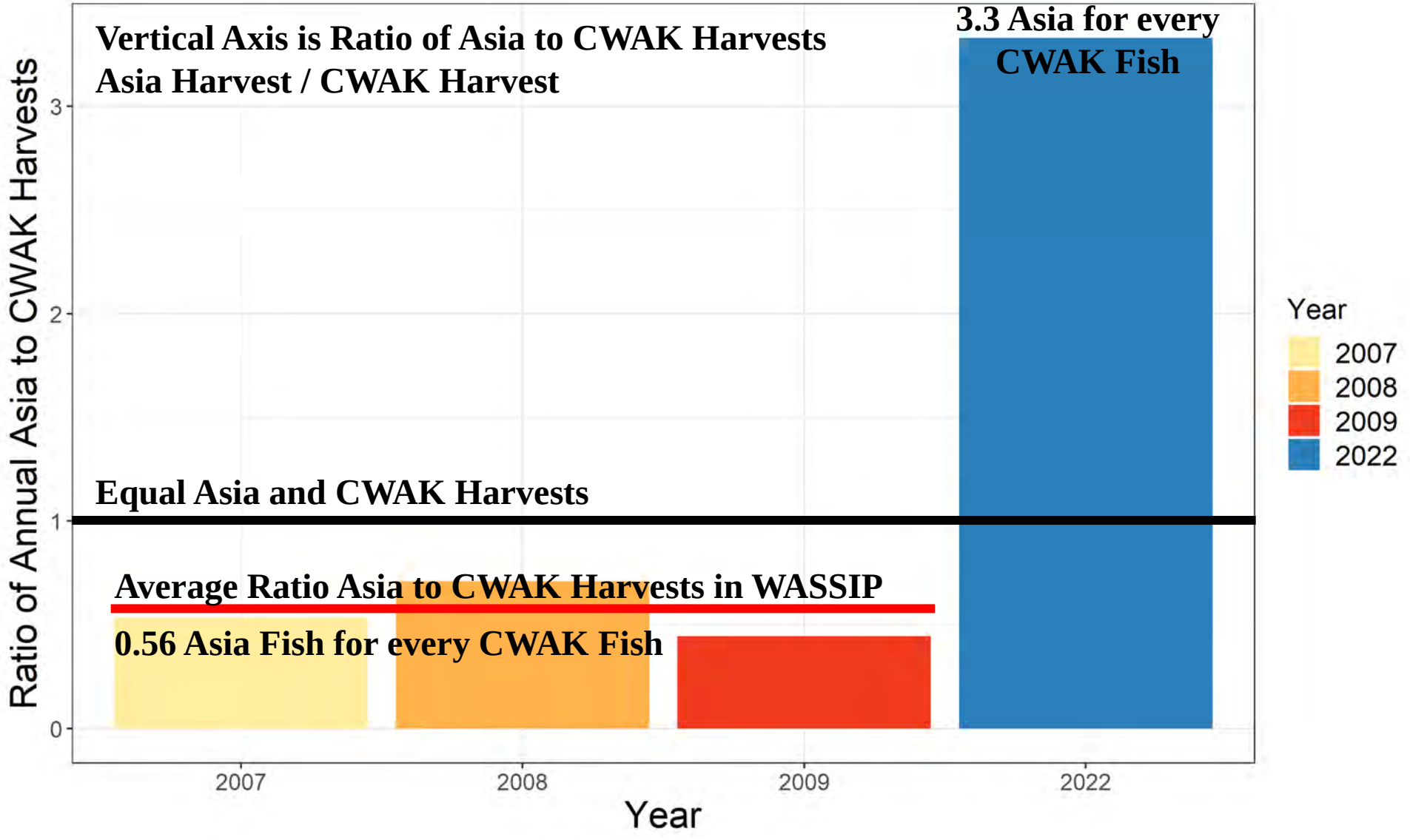
- Organizational Tables and Figures
  - Summary of Historical Harvests (Table 1)
  - Summary of WASSIP Estimates (Table 2)
  - Summary of Recent Harvests and Proposed Design (Table 3)
  - Summary of Daily Harvests and Sampling (Tables 5-6, Appendix A1-4)
  - Design of Analysis among Strata (Table 8)
  - Design of Stratified Estimates (Table 4)
  - Laboratory Results (Table 9)

Dann, T. H., H. A. Hoyt, E. M. Lee, E. K. C. Fox, and M. B. Foster. 2023. Genetic stock composition of chum salmon harvested in commercial salmon fisheries of the South Alaska Peninsula, 2022. Alaska Department of Fish and Game, Special Publication No. 23-07, Anchorage. https://www.adfg.alaska.gov/FedAidPDFs/SP23-07.pdf

Conclusions

- Total 2022 South Pen Harvest: 817,279 chum
  - 78% of 10-year average
- June: 544,137 (67% of total South Peninsula)
  - Majority in June Unimak Seine (321,875 – 40% of total)
  - Groups > 5%: Asia (315,162 – 58%), CWAK (96,466 – 18%) and East of Kodiak (72,812 – 13%)
- Post-June: 270,142 (33% of total South Peninsula)
  - Majority in July SE/SC Seine (126,102 – 15% of total)
  - Groups > 5%: South Peninsula (95,237 – 35%), East of Kodiak (65,242 – 24%), Chignik/Kodiak (60,864 – 23%), and Asia (30,674 – 11%)
- Stock-specific harvest used to inform harvest rate analysis

Key Summary Results
Asia and Coastal Western Alaska



Genotyping Output CY 2022

Species	Baseline	Mixture	Parentage	Exp/Forensic	Total
Bear				61	61
A. Grayling	190				190
N. Pike	1,026				1,026
B. Rockfish	95				95
Chinook	12,884	12,457	1,771		27,112
Chum		10,608			10,608
Coho	2,951				2,951
Pink	858	101	29,793	9,671	40,423
Sockeye	10,597	24,349			34,946
Grand Total	**28,601**	**47,515**	**31,564**	**9,671**	**117,412**

Sampling, Archiving, and Opportunistic Sampling