Genetic Stock Composition the Commercial Harvest of Sockeye Salmon in Bristol Bay, Alaska, 2006-2008

**Tyler H. Dann,
Christopher Habicht,
Jim R. Jasper,
Heather A. Hoyt,
Andrew W. Barclay,
William D. Templin,
Timothy T. Baker,
Frederick W. West,
and
Lowell F. Fair**

**Oral Report:
RC3 notebook
White Tab 5**

**Written Report:
Color Tab 5**

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Genetics analyses

- Genetics overview
- Baseline development
- Mixed stock analysis

What is DNA?

- Composed of individual units called "nucleotides" (A, T, G, C)

- A "gene" is made up of a sequence of nucleotides that contains instructions for making a single protein

- A "chromosome" is made up of millions of nucleotides that are coiled together

- Chromosomes come in pairs – one from the mother and one from the father

Father

Chromosome

Mother

Gene

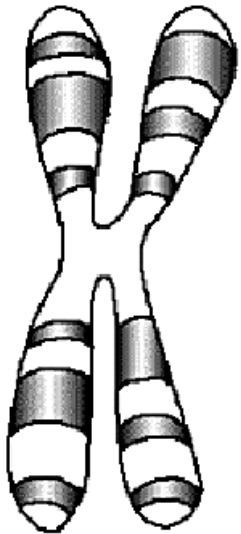*Protein*

3
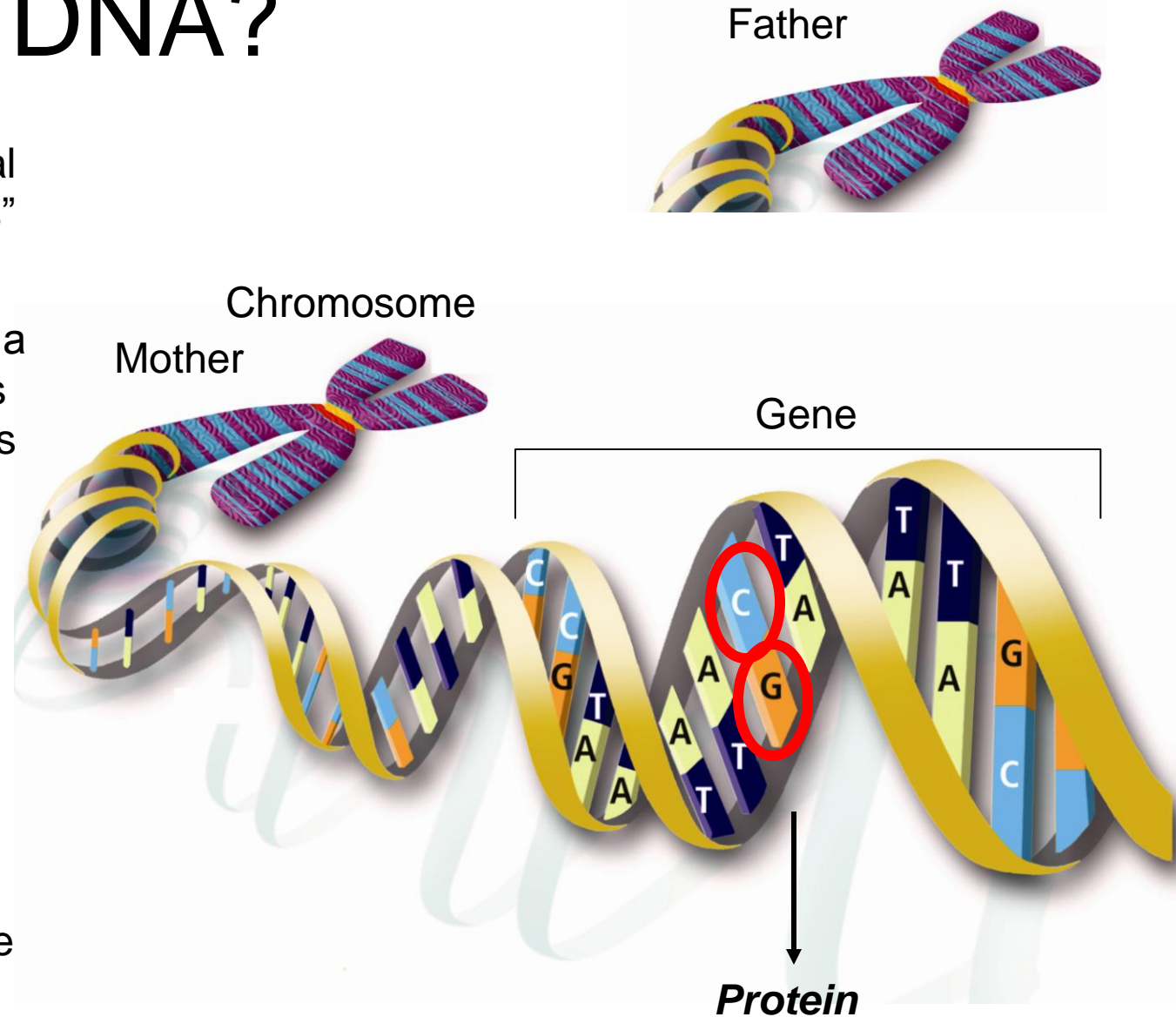
Pacific Salmon DNA

60-80 chromosomes

~2.5 billion DNA
nucleotides
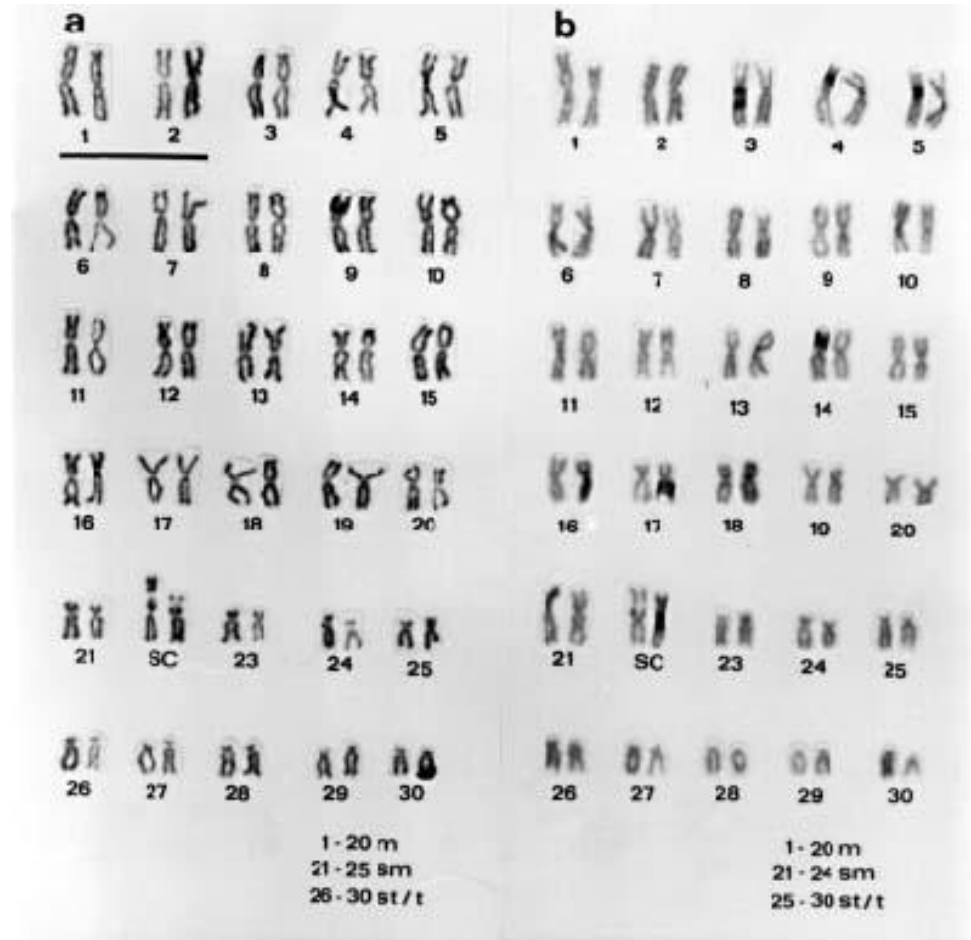
Some terminology…

Locus - Allele

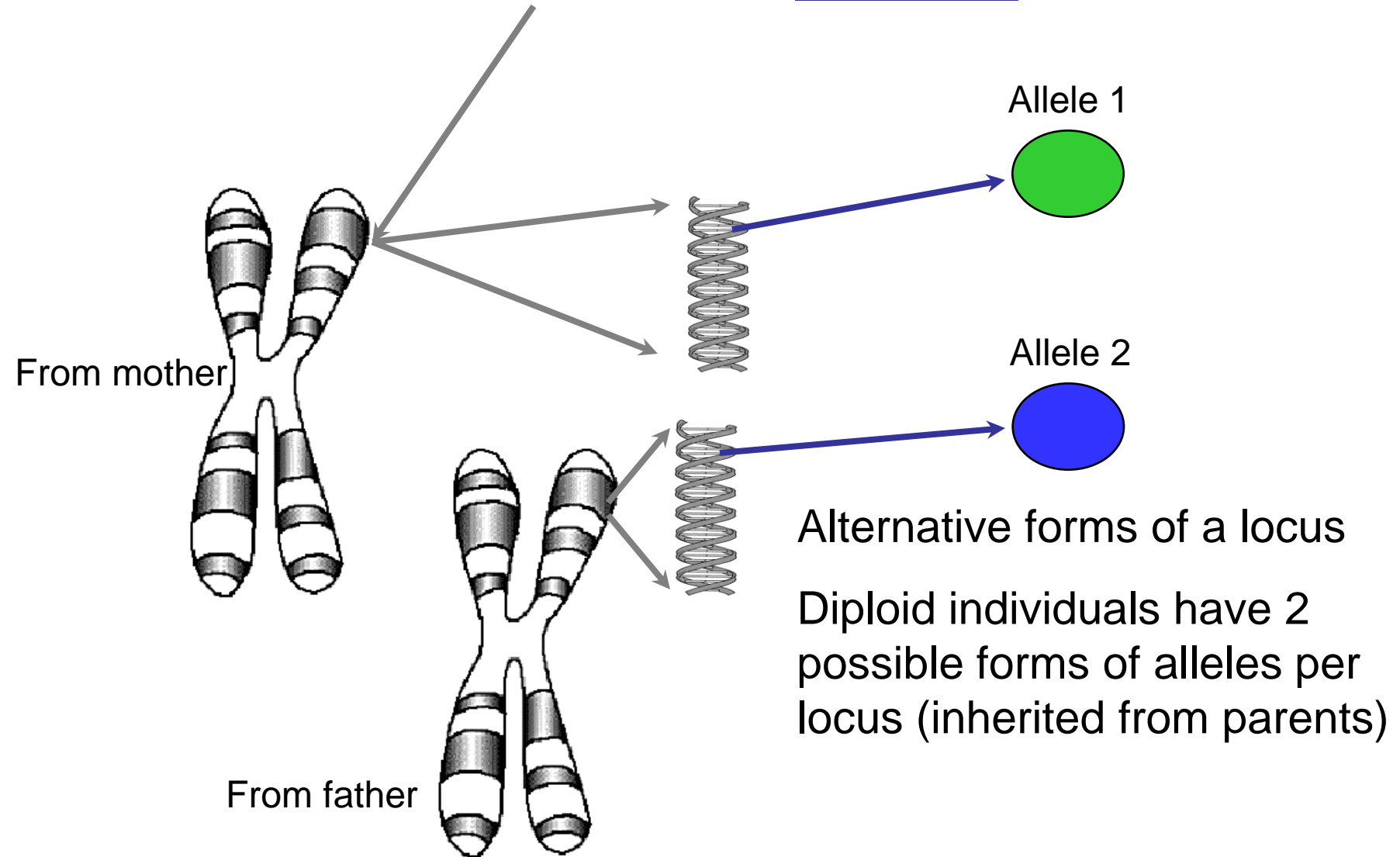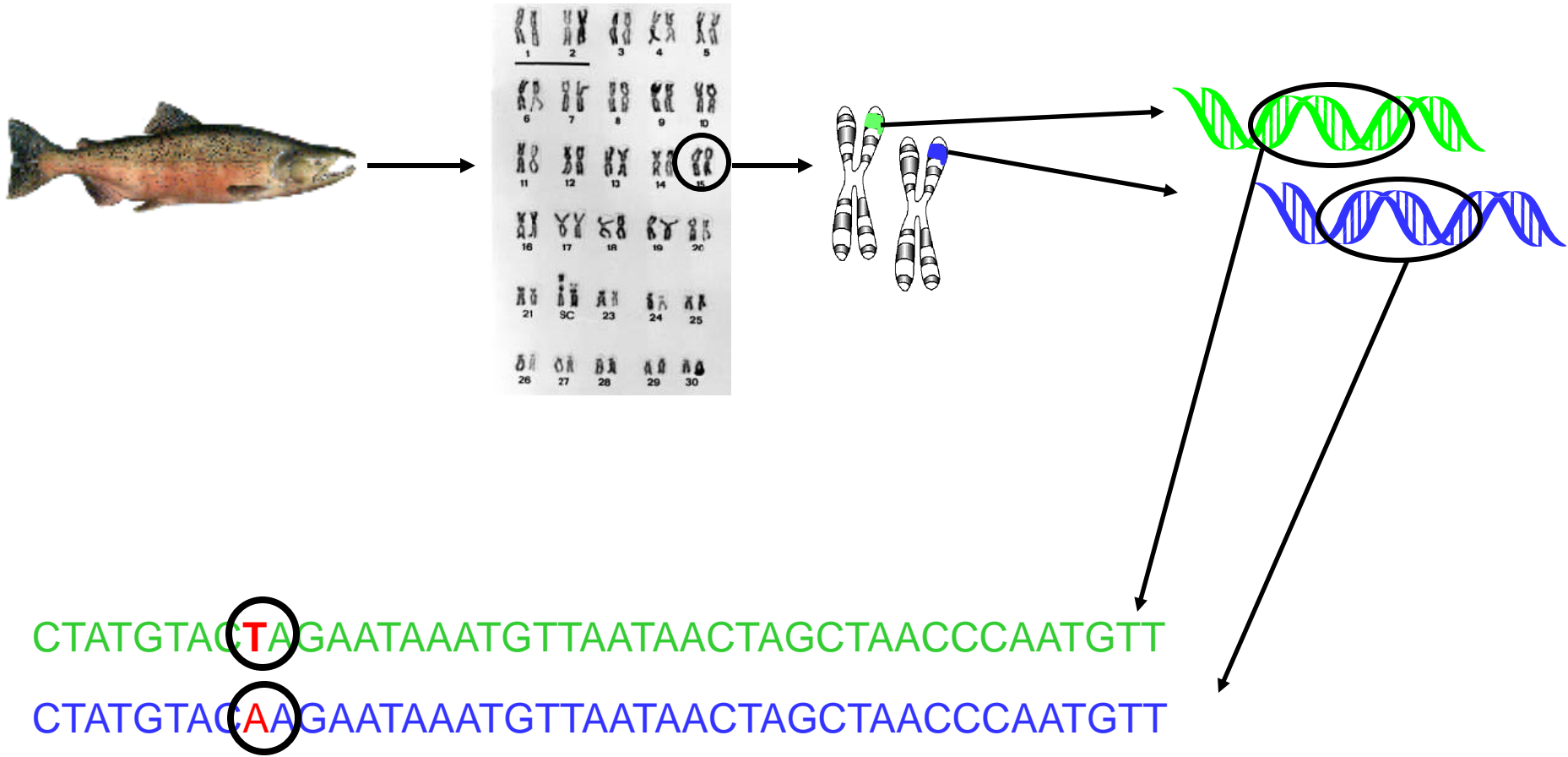Position on a chromosome where a gene or a particular DNA sequence is occupied.

Some terminology…

Locus - Allele

Allele 1

From mother

Allele 2

Alternative forms of a locus

Diploid individuals have 2 possible forms of alleles per locus (inherited from parents)

From father

Forms of a locus (alleles)

CTATGTAC**T**AGAATAAATGTTAATAACTAGCTAACCCAATGTT

CTATGTAC**A**AGAATAAATGTTAATAACTAGCTAACCCAATGTT

"SNPs" = Single Nucleotide Polymorphisms

SNP variation

Fish A
CTATGTA**T**TAAATGTTAATAATAATAACTAGCTAACC   *T genotype*
CTATGTA**A**TAAATGTTAATAATAATAACTAGCTAACC   *A genotype*

Fish B
CTATGTA**A**TAAATGTTAATAATAATAACTAGCTAACC   *A genotype*
CTATGTA**A**TAAATGTTAATAATAATAACTAGCTAACC   *A genotype*

Fish C
CTATGTA**A**TAAATGTTAATAATAATAACTAGCTAACC   *A genotype*
CTATGTA**T**TAAATGTTAATAATAATAACTAGCTAACC   *T genotype*

Fish D
CTATGTA**T**TAAATGTTAATAATAATAACTAGCTAACC   *T genotype*
CTATGTA**T**TAAATGTTAATAATAATAACTAGCTAACC   *T genotype*

Green genotype came from the mother, blue from the father

Sockeye salmon home: Allele frequencies diverge

- Drift: luck of the draw
  - Straying
  - Population size
- Selection: different forces among habitats

DNA Markers

- Alleles of a locus that differ ("DNA polymorphisms") are used as natural tags.

- Use frequency differences to distinguish between populations.

- These tags can be used to identify where groups of fish were spawned ("fingerprint").

Genetics analyses

- Genetics overview
- Baseline development

Baseline Stocks

Legend

- 🔴 North Peninsula
- ⚪ Ugashik
- 🔵 Egegik
- 🟡 Naknek
- 🟠 Alagnak
- 🟣 Kvichak
- 🔴 Nushagak
- ⚪ Wood
- 🟣 Igushik
- 🔵 Togiak
- 🟢 Kuskokwim

14,236 individuals
144 collections
96 populations

0   125 250   500   750   1,000
Kilometers
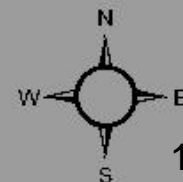
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Baseline Development

- Collecting tissues from spawning aggregations
- Screen loci in the lab

Laboratory analysis

- 45 SNP loci

- Automated Methods

- Re-analysis of 8%
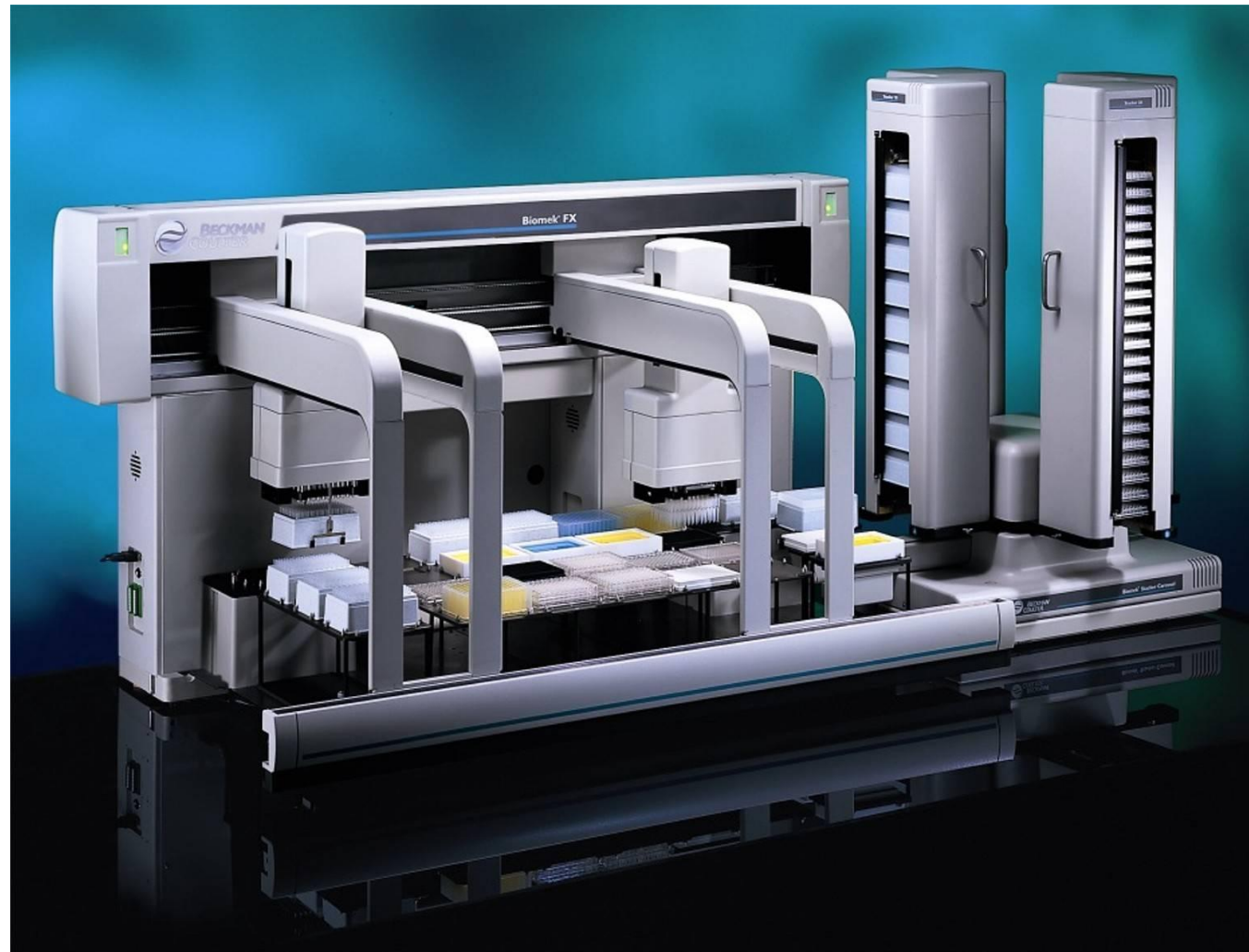
Microfluidics:
low error, high throughput
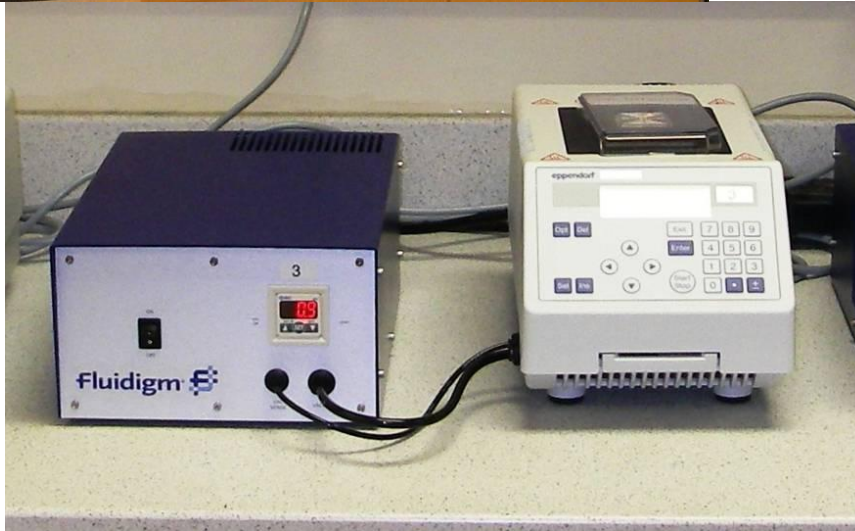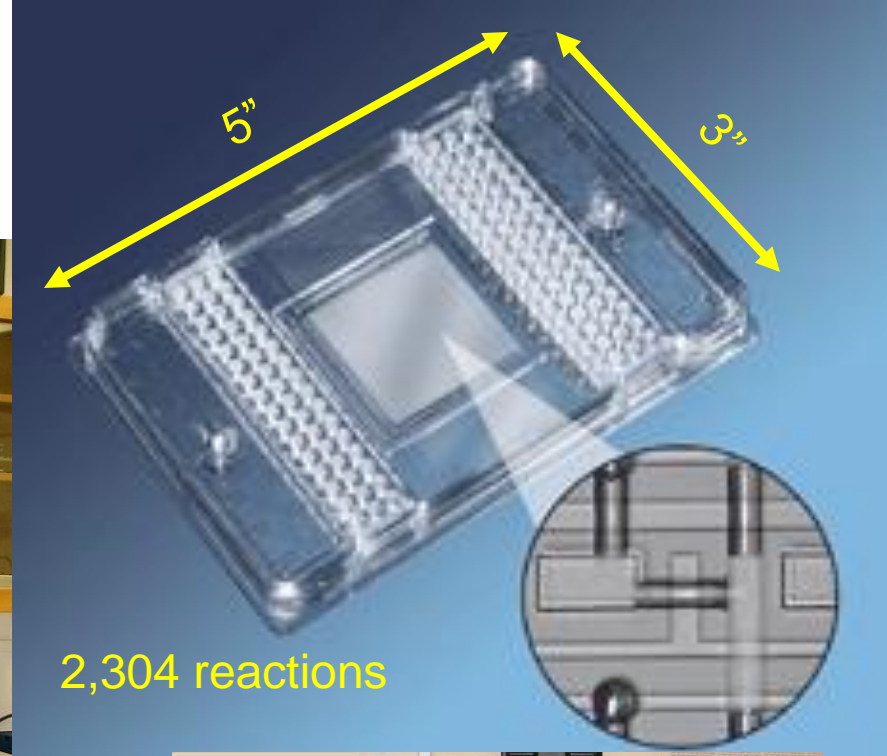
5"

3"

2,304 reactions

15

Baseline Development

- Collecting tissues from spawning aggregations
- Screen loci in the lab
- HW and Linkage
  - Verify that markers meet assumptions
- Pooling collections
  - Populations
  - Pooling nearby collections
- Baseline evaluation
  - Proof tests
  - Escapement tests

Proof tests - methods

Baseline:

Use all the baseline except for 200 fish from one reporting group.

Mixture:

Use the 200 fish taken out of the baseline.

17
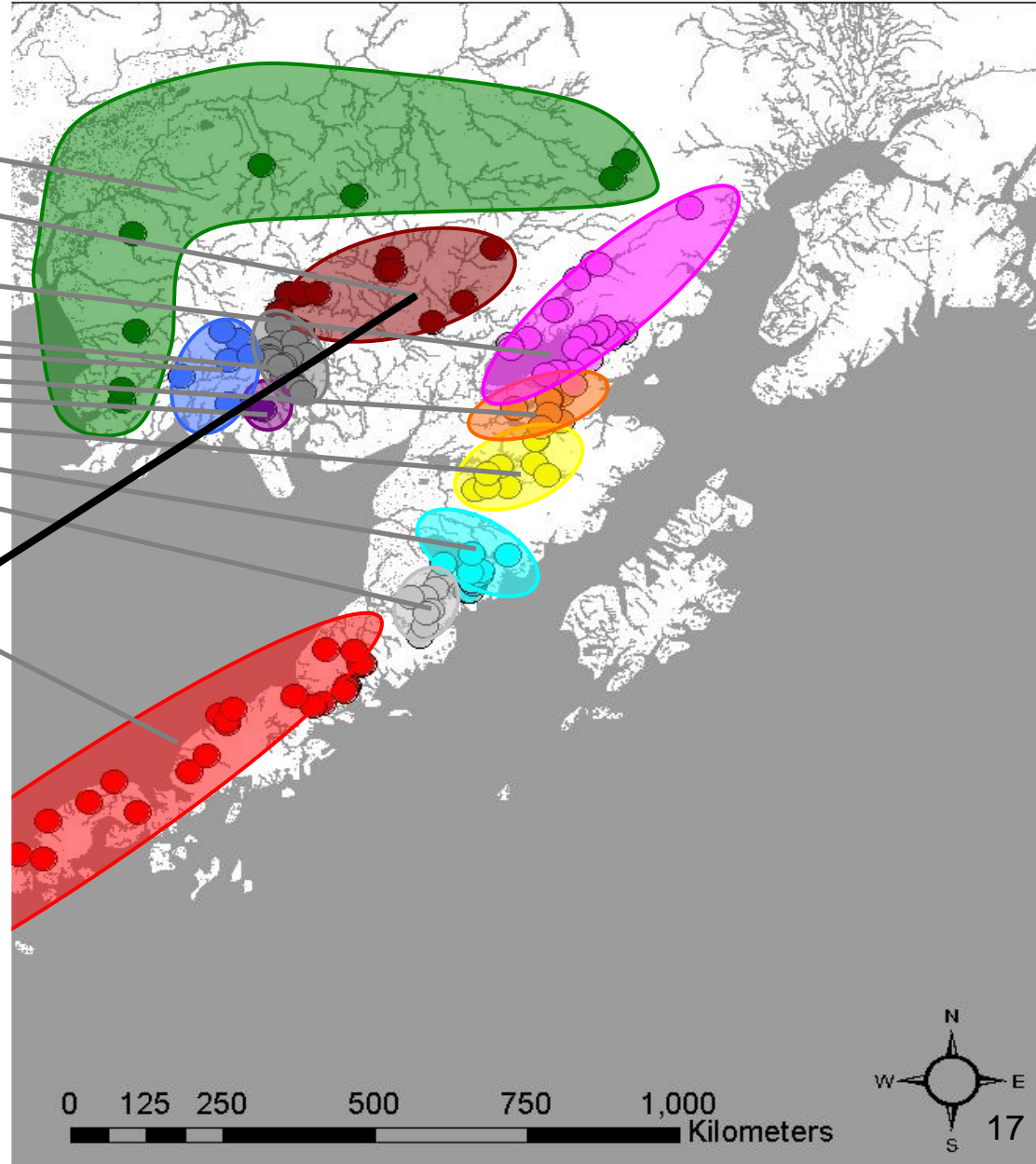
Nushagak proof test

Proportion correctly allocated
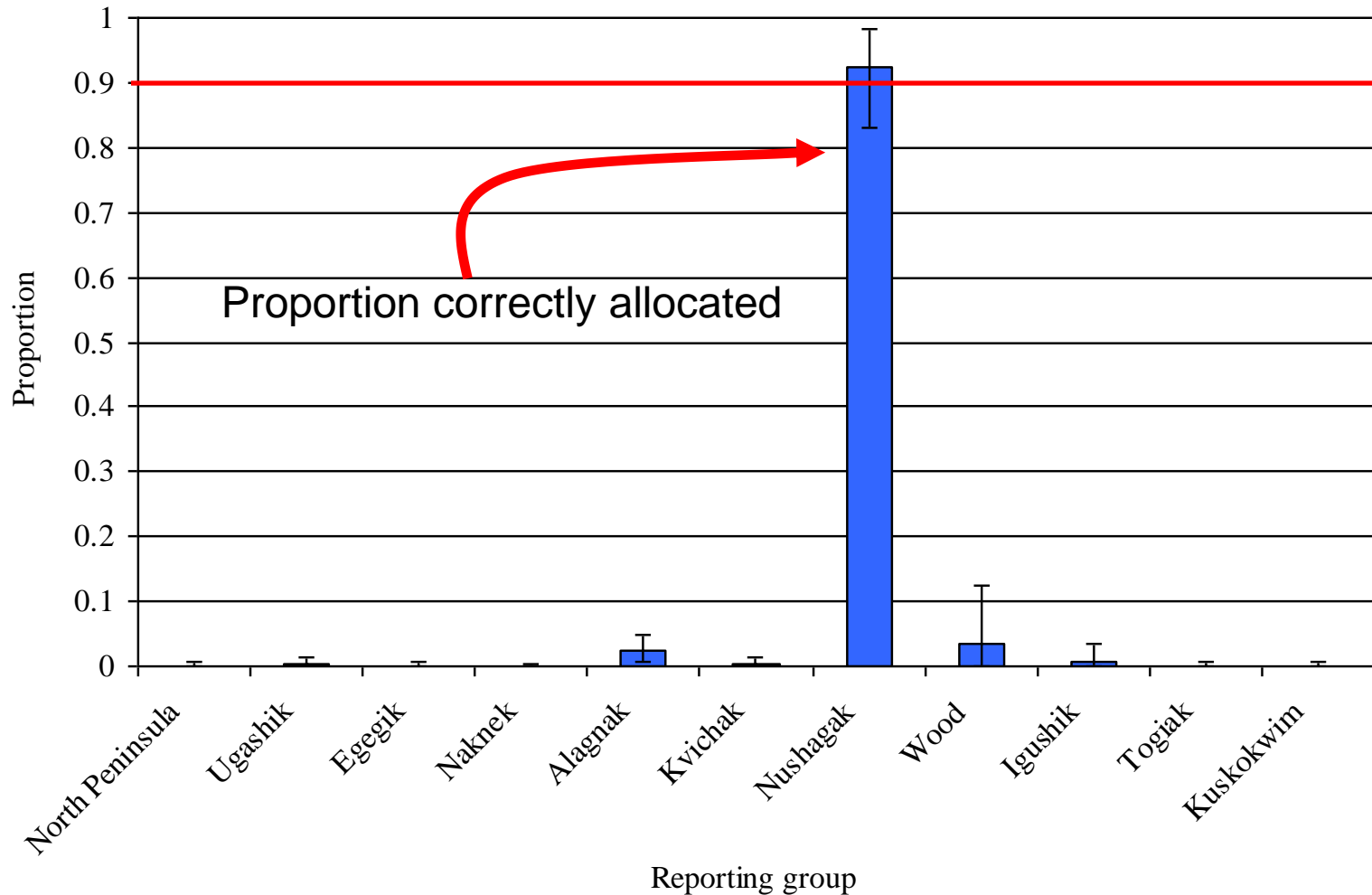
All stocks - proof tests
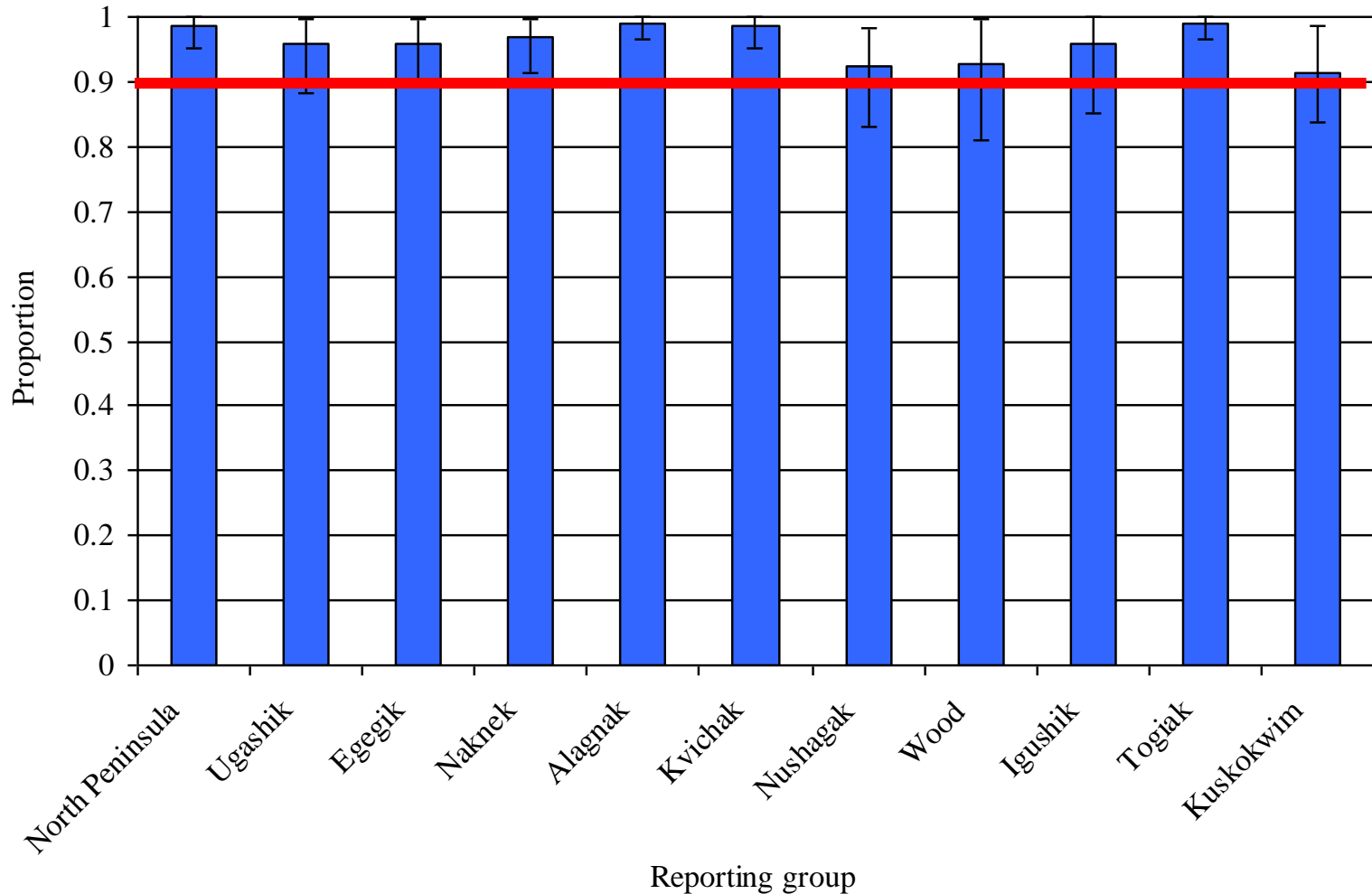
Figure 4 in report

Escapement tests: Sample fish at counting sites
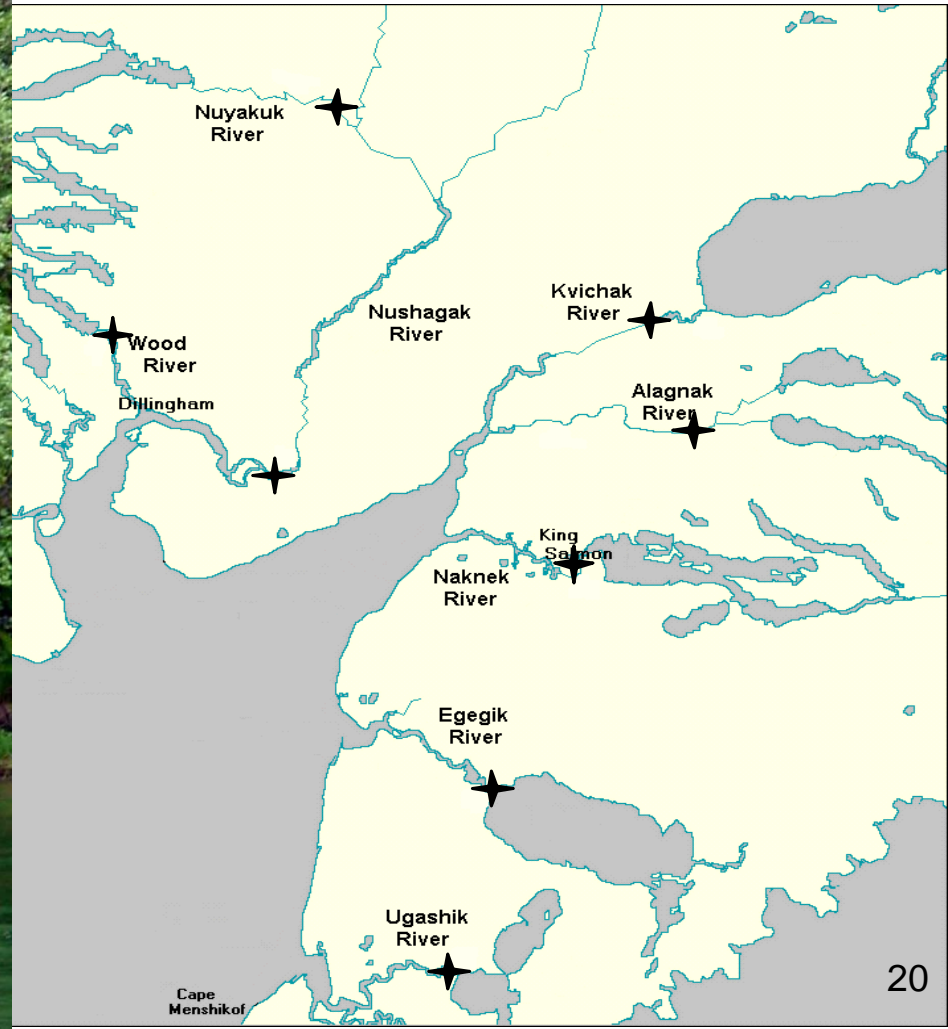
Baseline evaluation – escapement tests
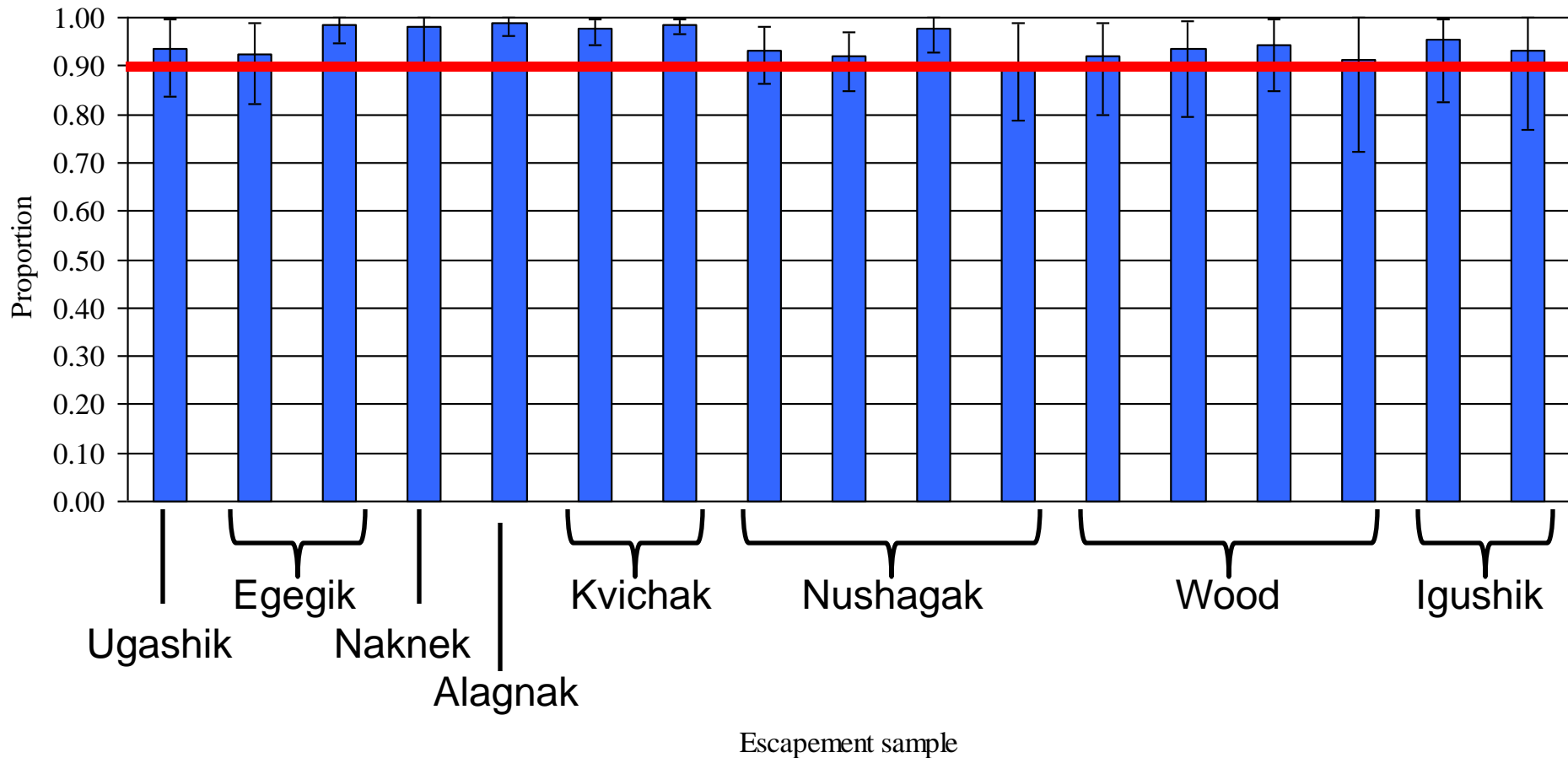
Note that Togiak River is not here.

Genetics analyses

- Genetics overview
- Baseline development
- **Mixed stock analysis (MSA)**

Methods

- Mixed stock analysis of district catch
  - Strata were within districts across time and fishing areas
  - Sample size goals were 190 fish per strata
  - Stock proportions were multiplied by strata catch to calculate stock-specific catch

Ugashik District

Number of fish harvested
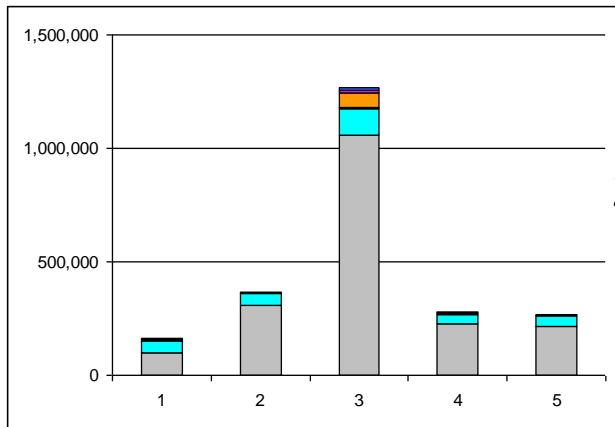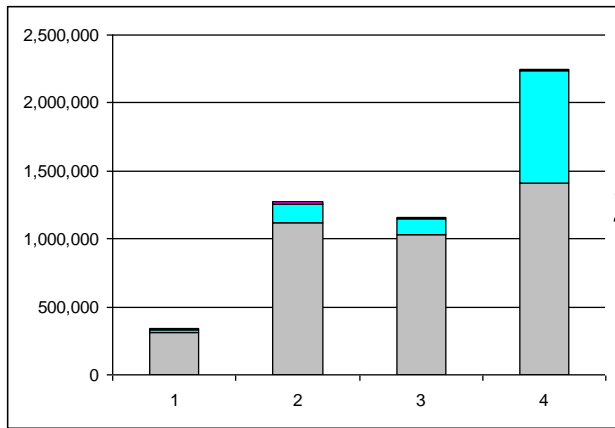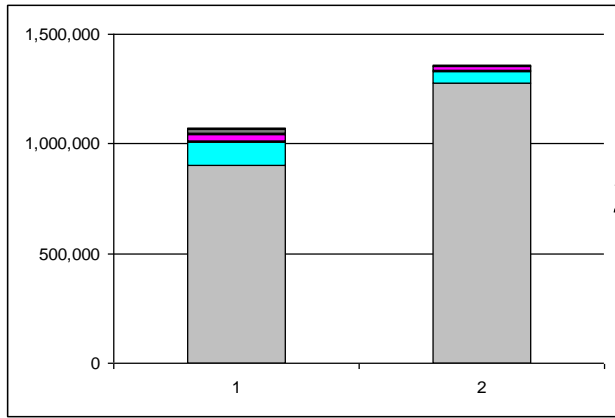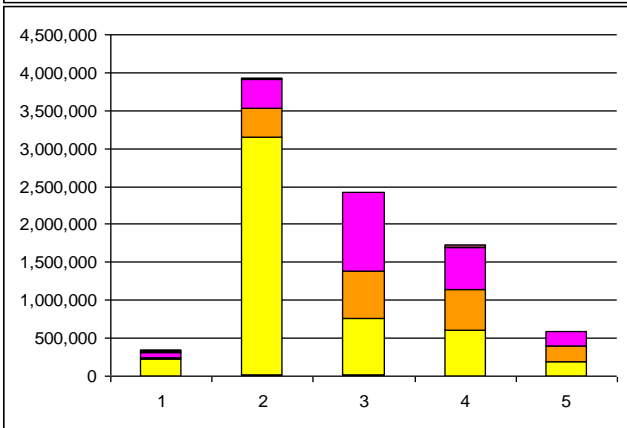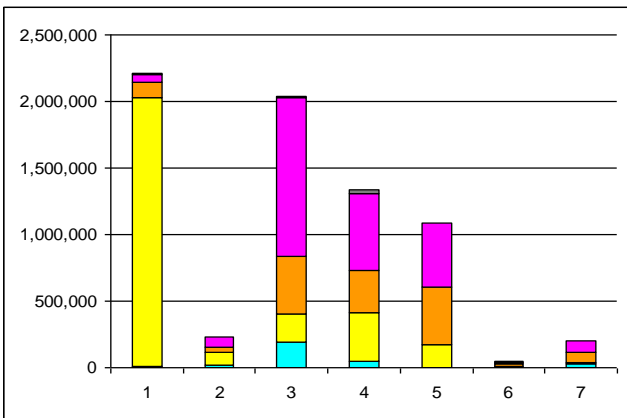
Time strata
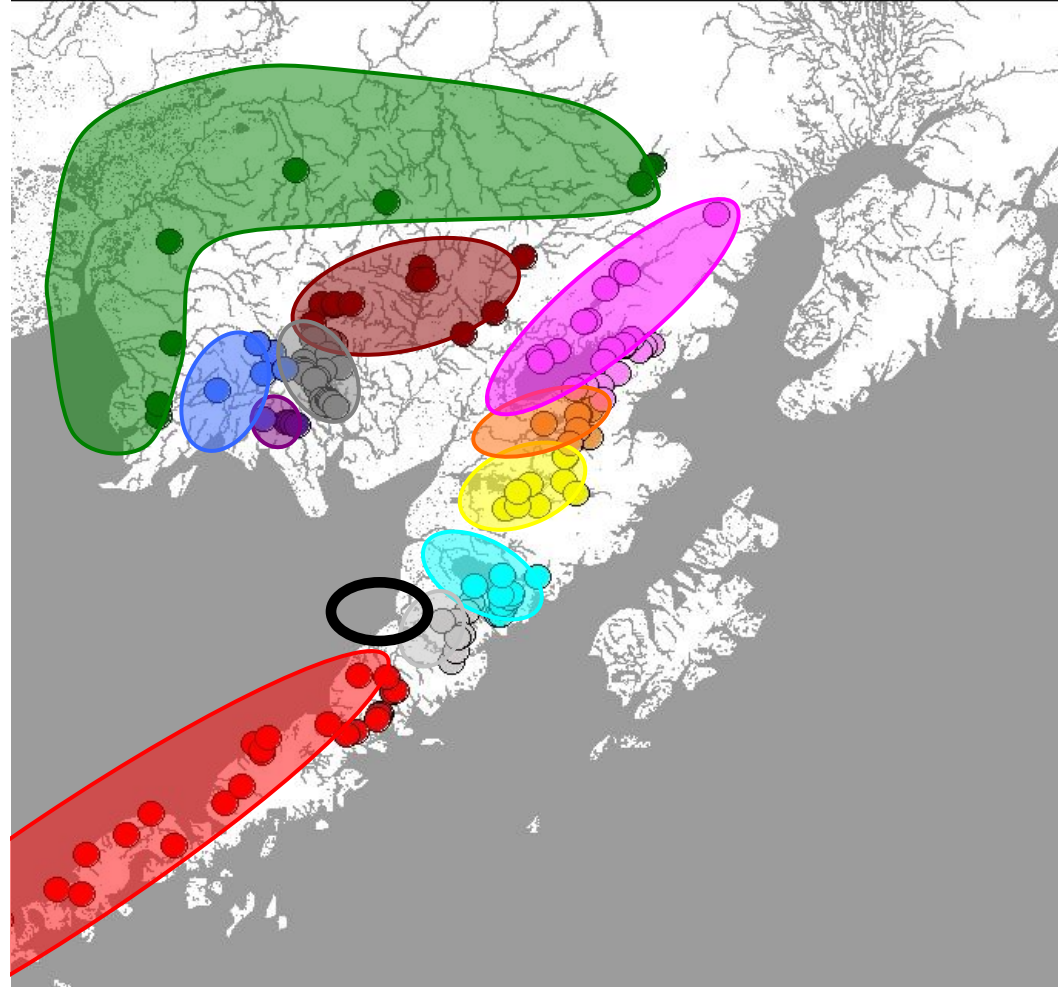
2006

2007

2008

Ugashik District
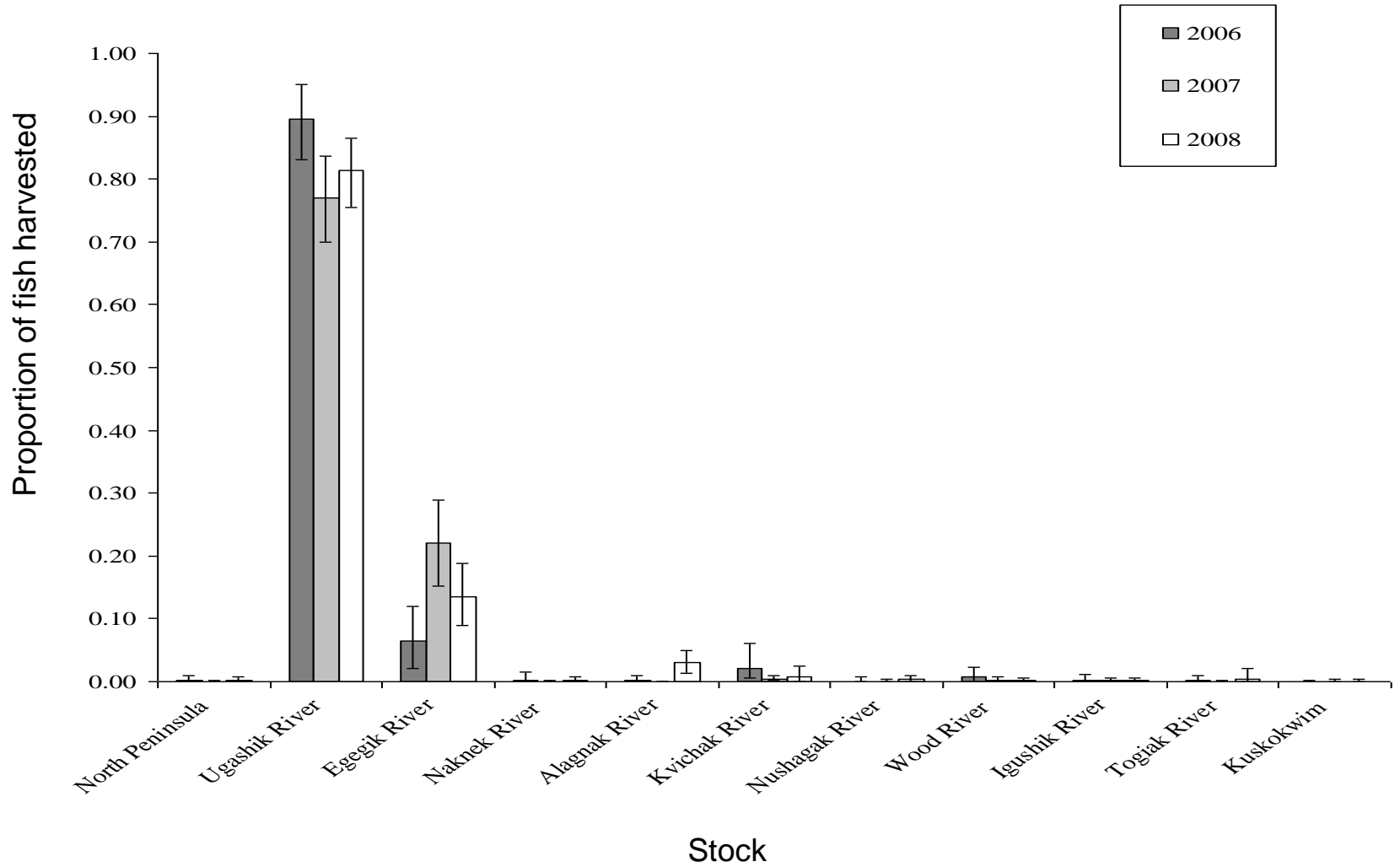
Figure 7 in report

Egegik District

Number of fish harvested
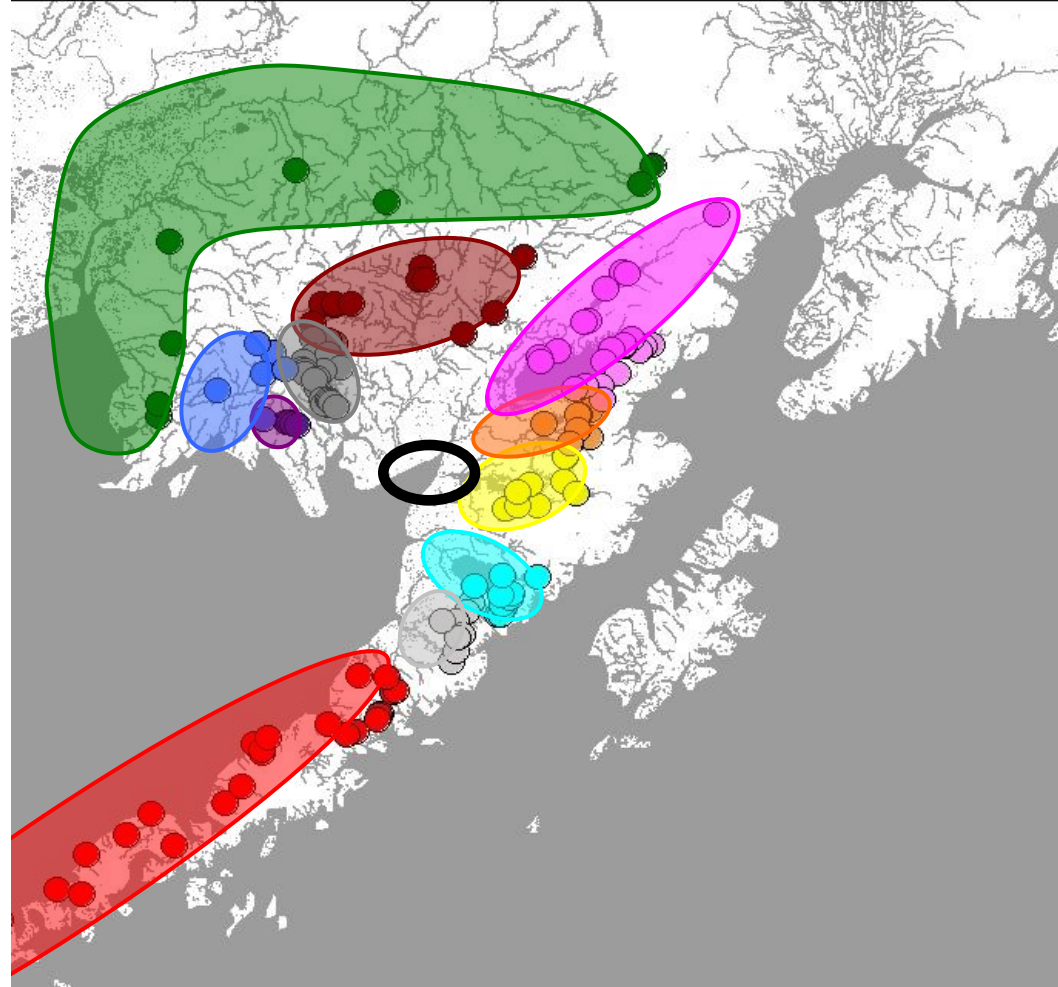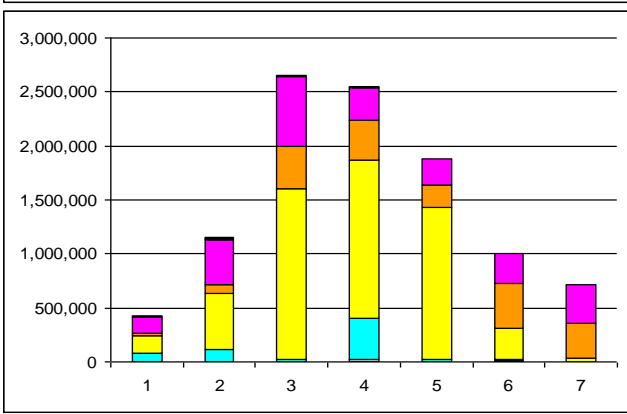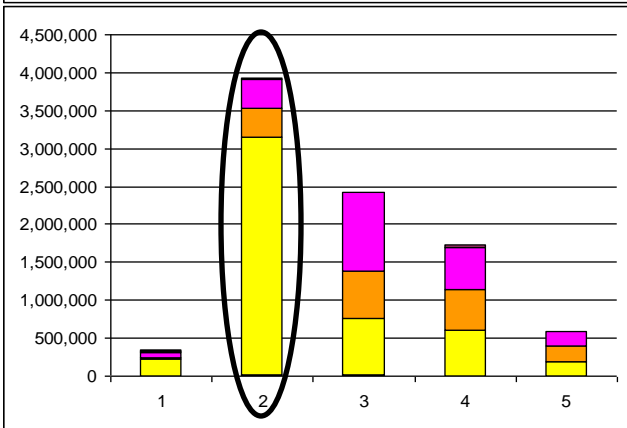
Time strata

2006
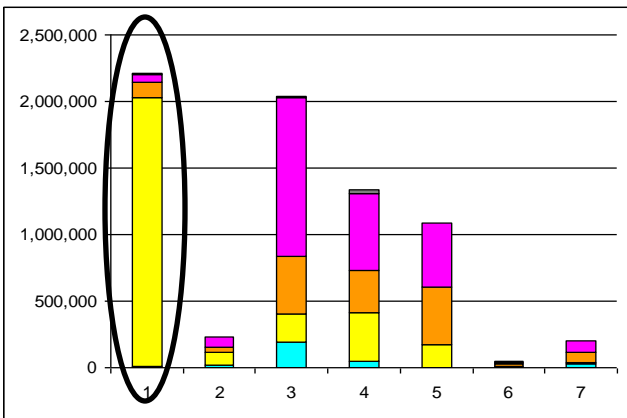
2007

2008

Egegik District

Number of fish harvested

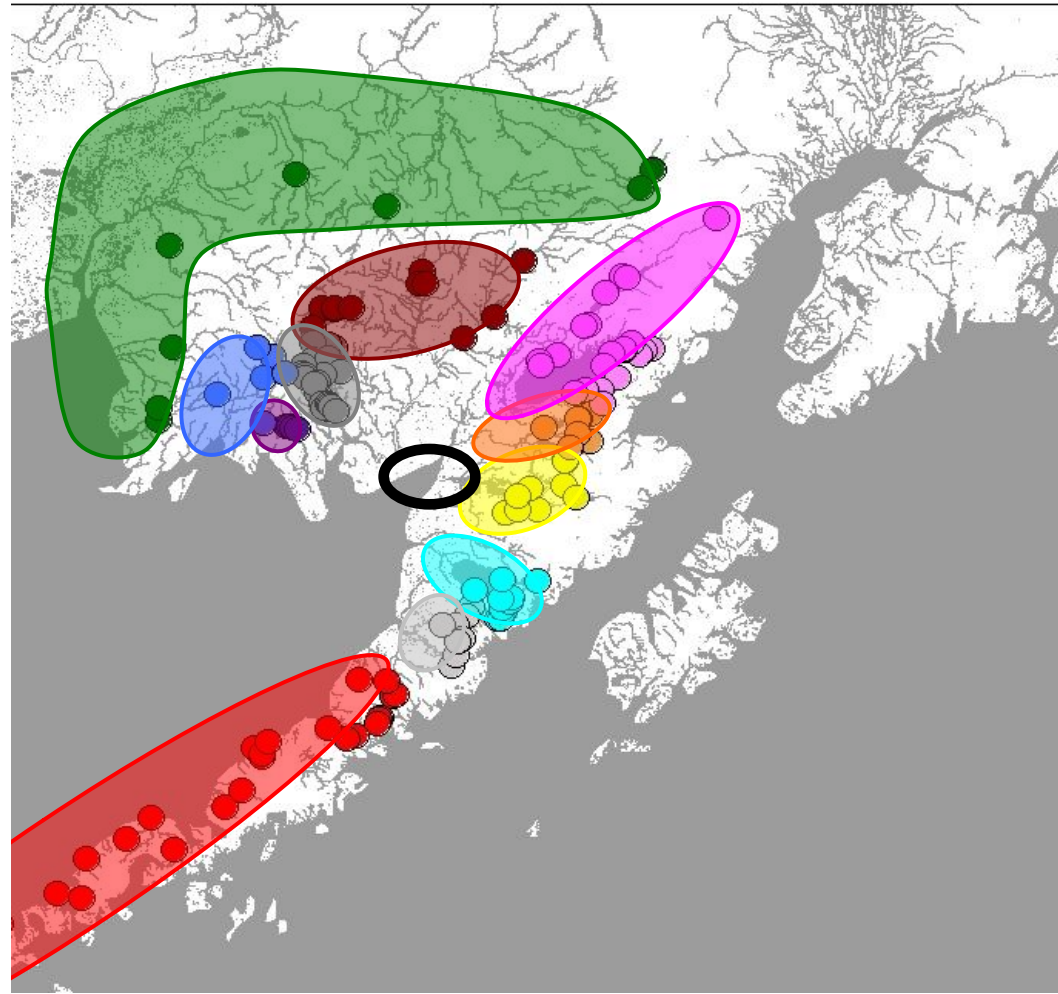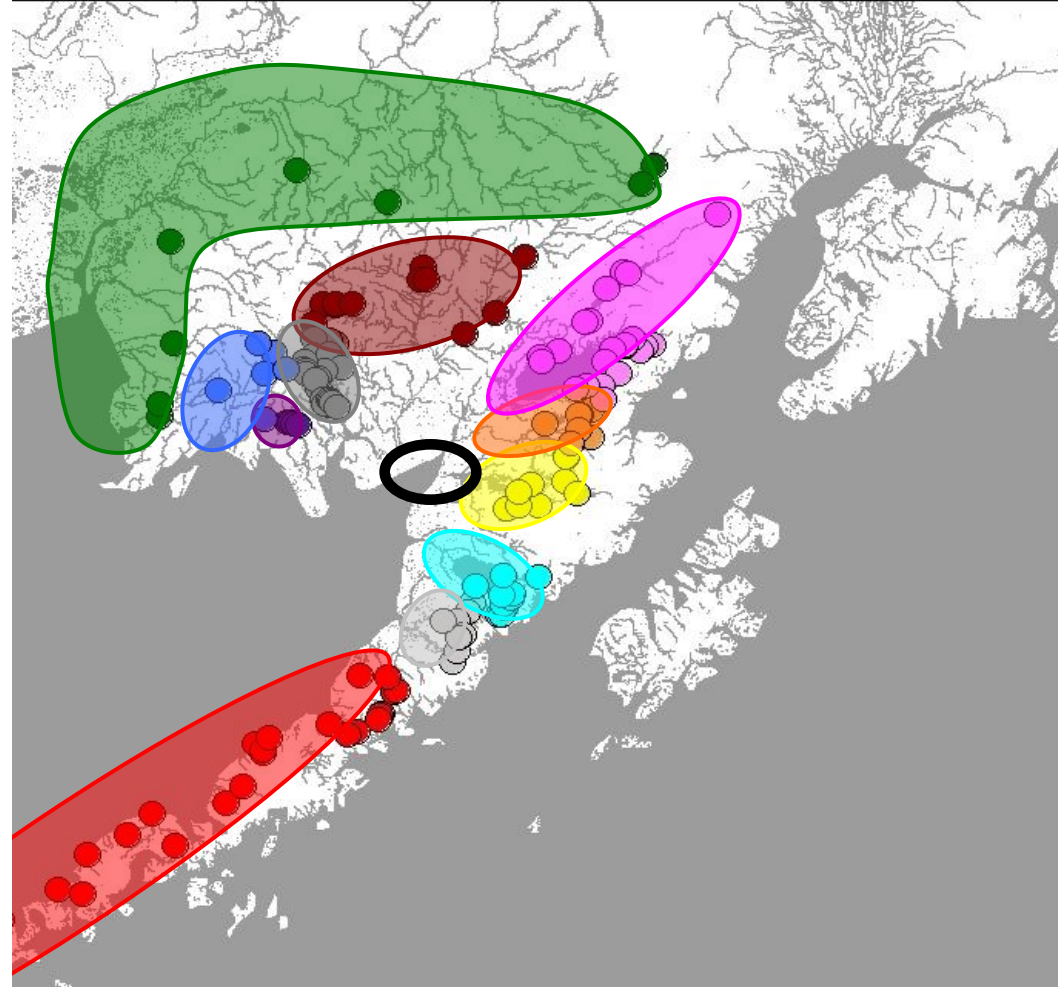Time strata

2006

2007

2008

Egegik Special Harvest Area

27
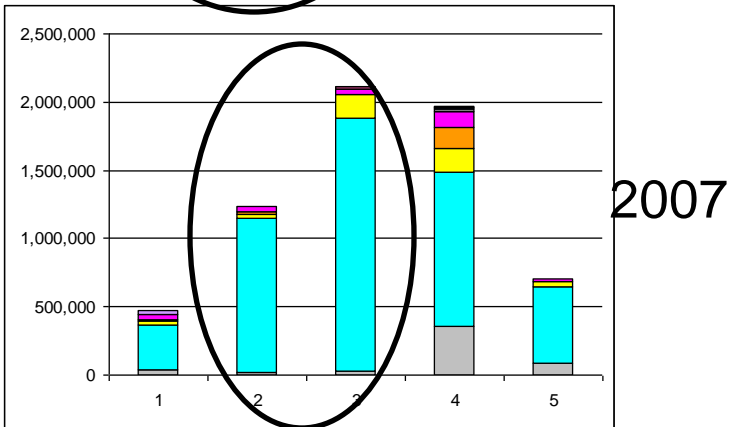
Egegik District

Figure 8 in report

Naknek-Kvichak District
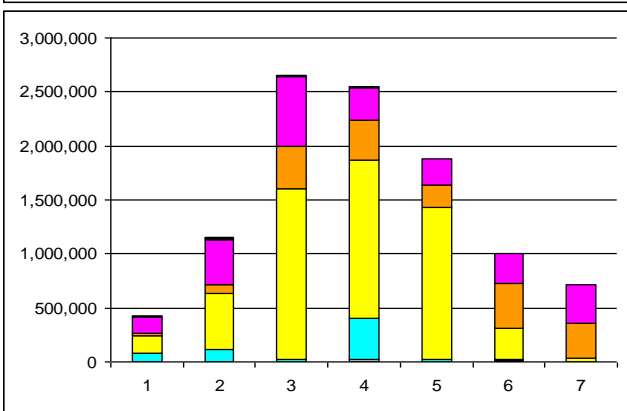
Naknek-Kvichak District

2006

2007

2008

Number of fish harvested

Time strata

Naknek Special Harvest Area

Naknek-Kvichak District
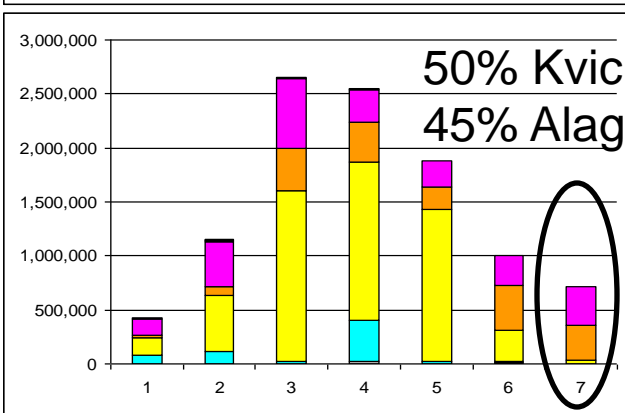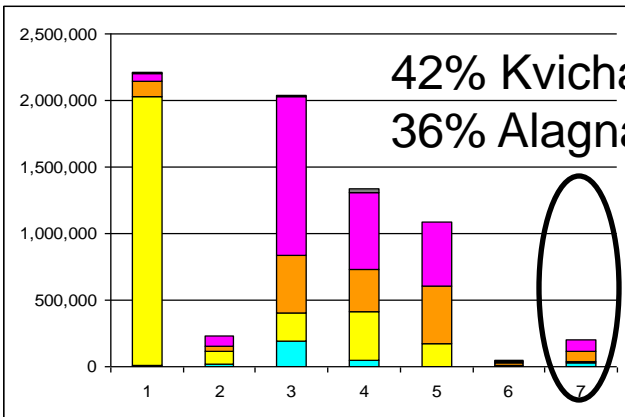
Kvichak Section set gillnet

Number of fish harvested

Time strata

42% Kvichak
36% Alagnak
2006

2007

50% Kvichak
45% Alagnak
2008

31

Naknek-Kvichak District
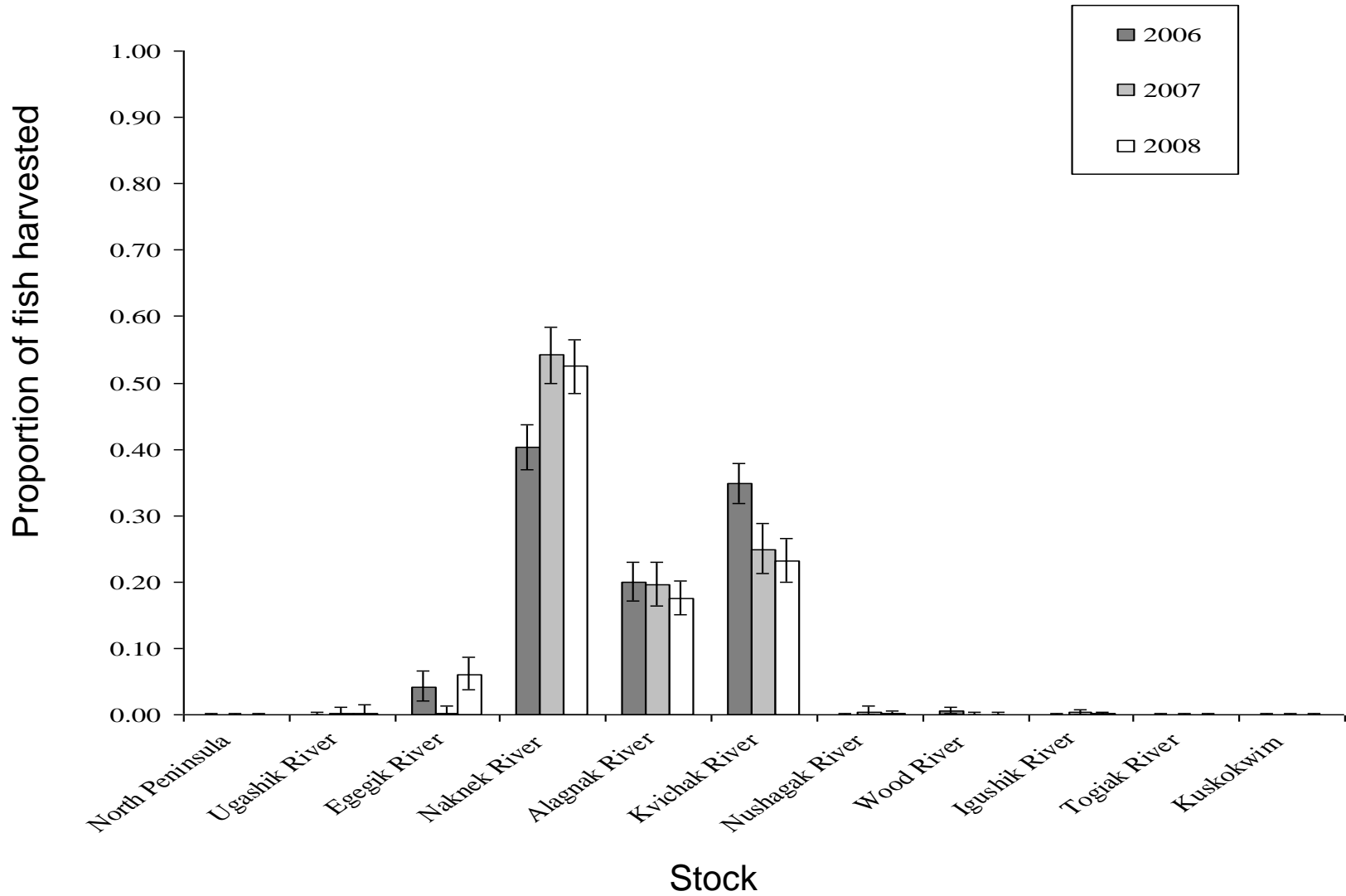
Figure 9 in report
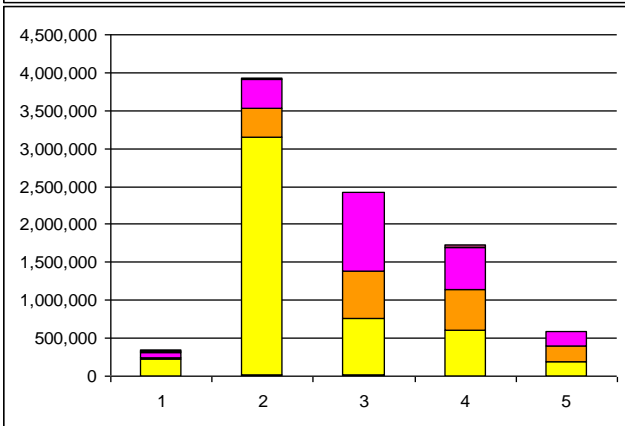
Nushagak District

Number of fish harvested

Time strata

2006

2007
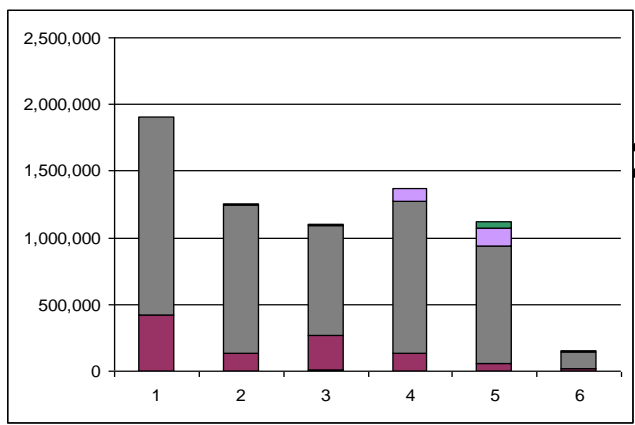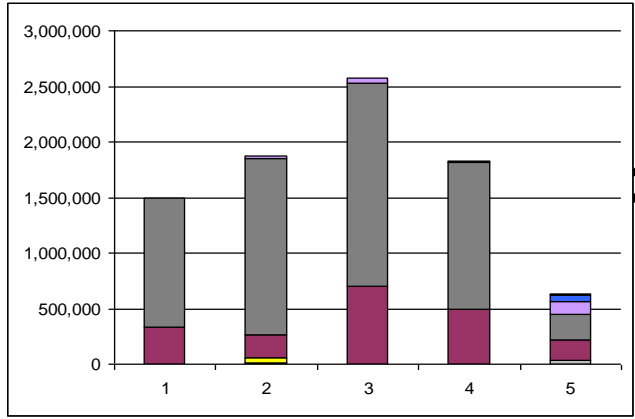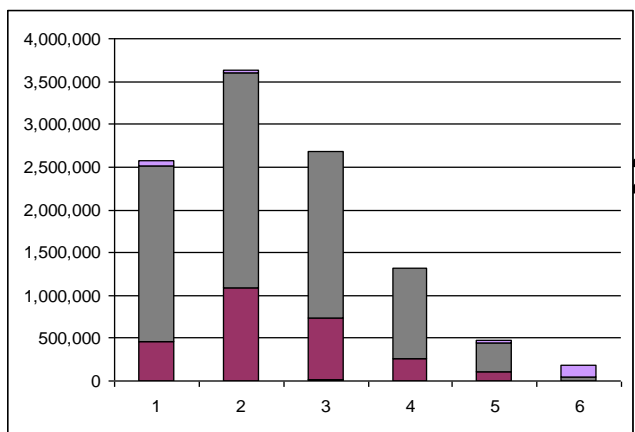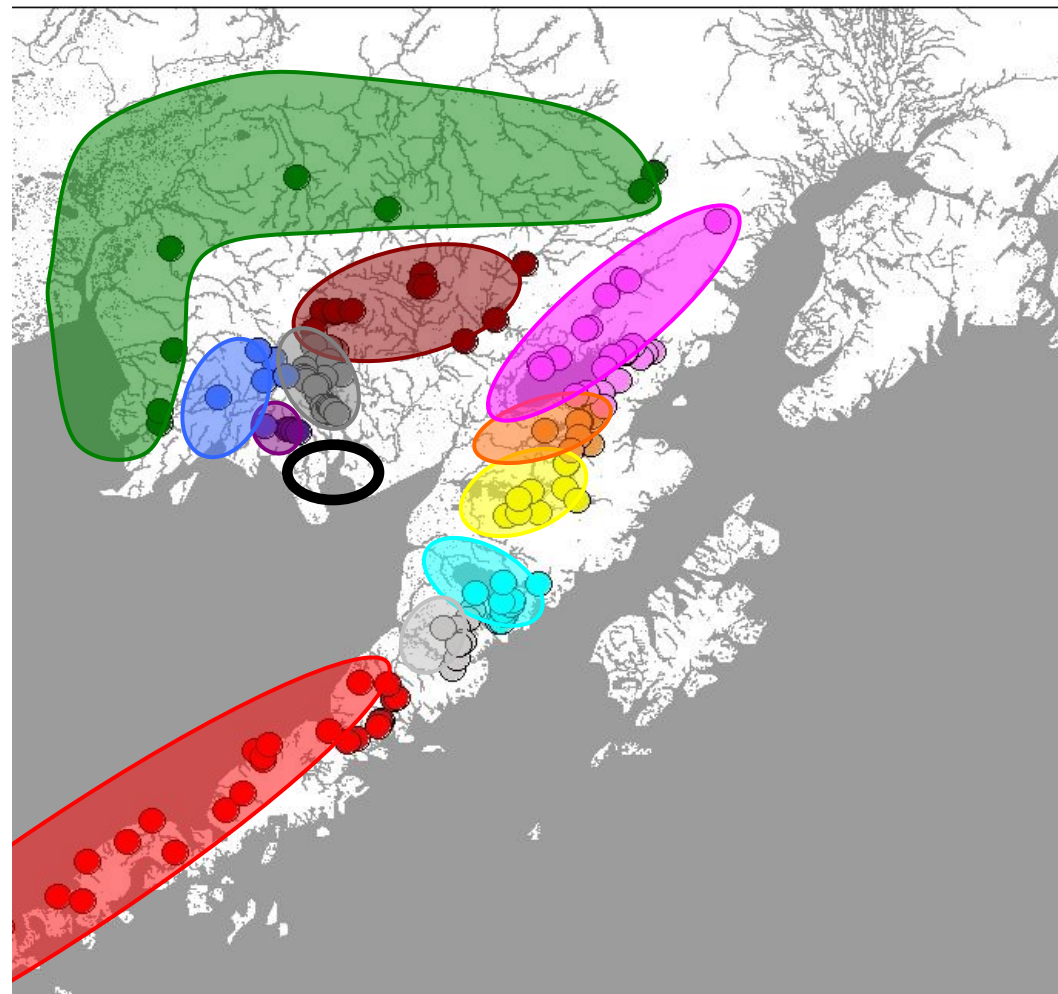
2008

Nushagak District
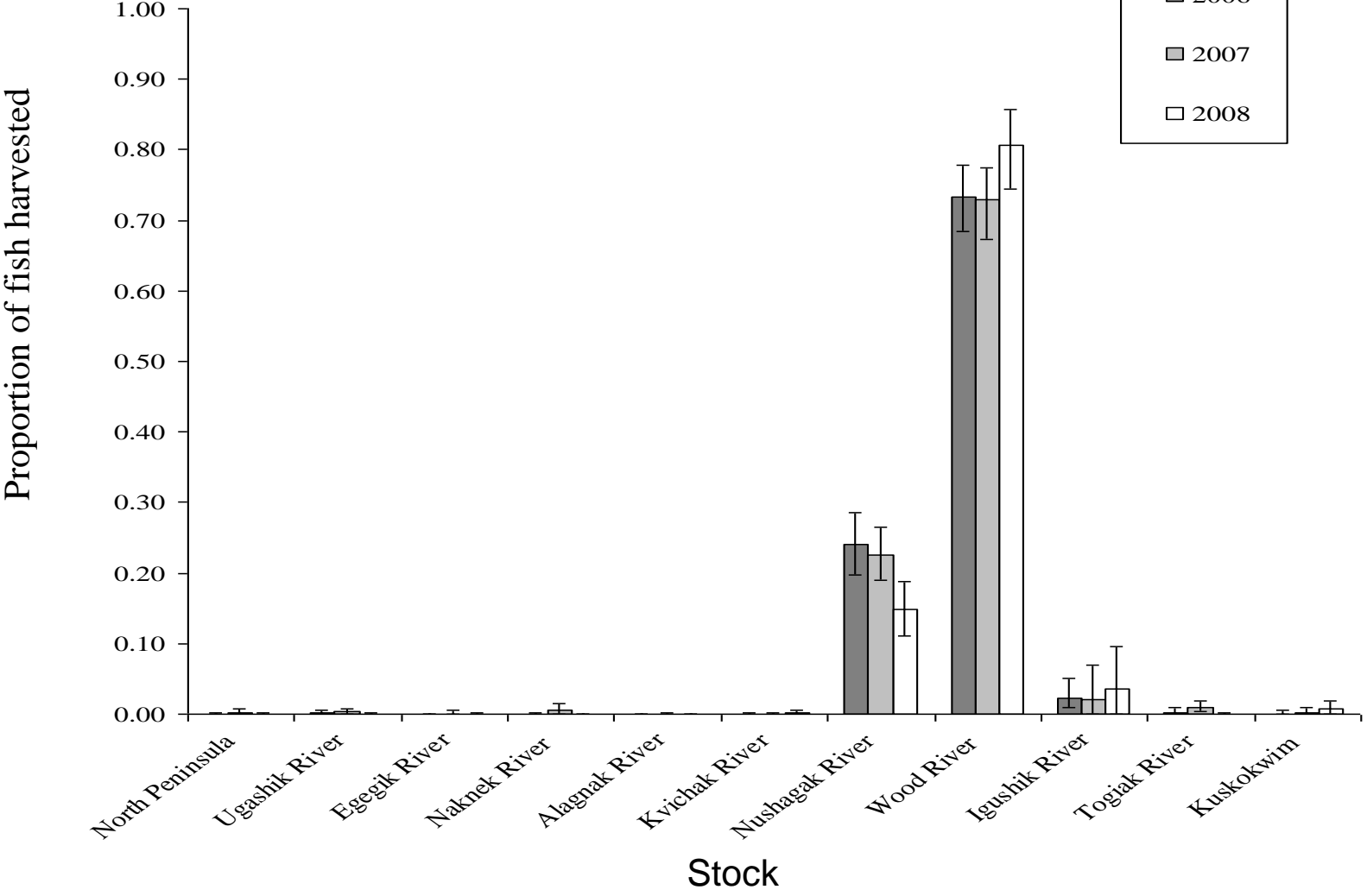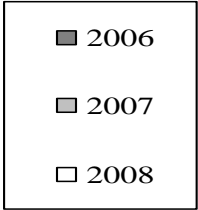
Figure 10 in report

Togiak District

Number of fish harvested

2006

2007

2008

Time strata

35
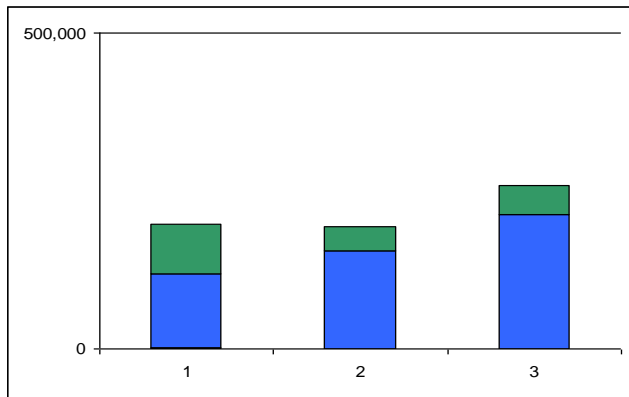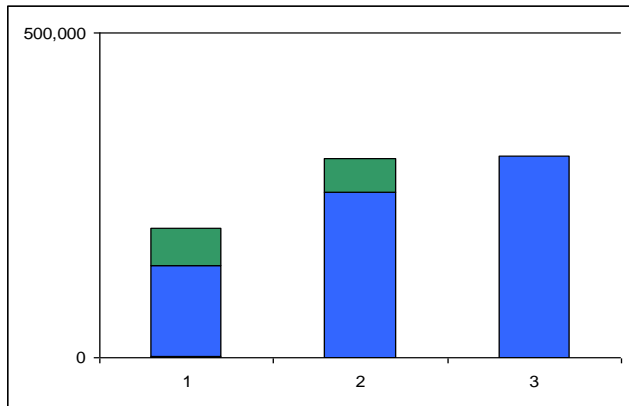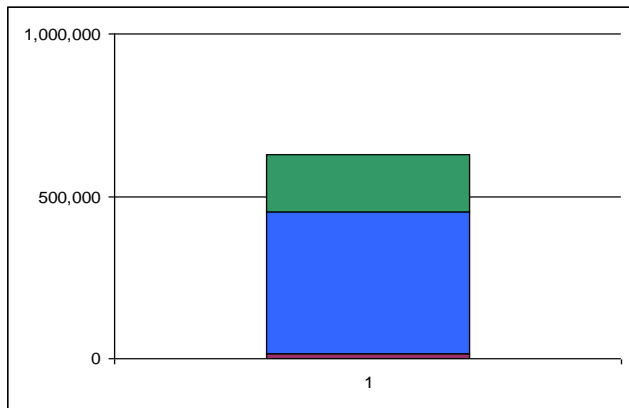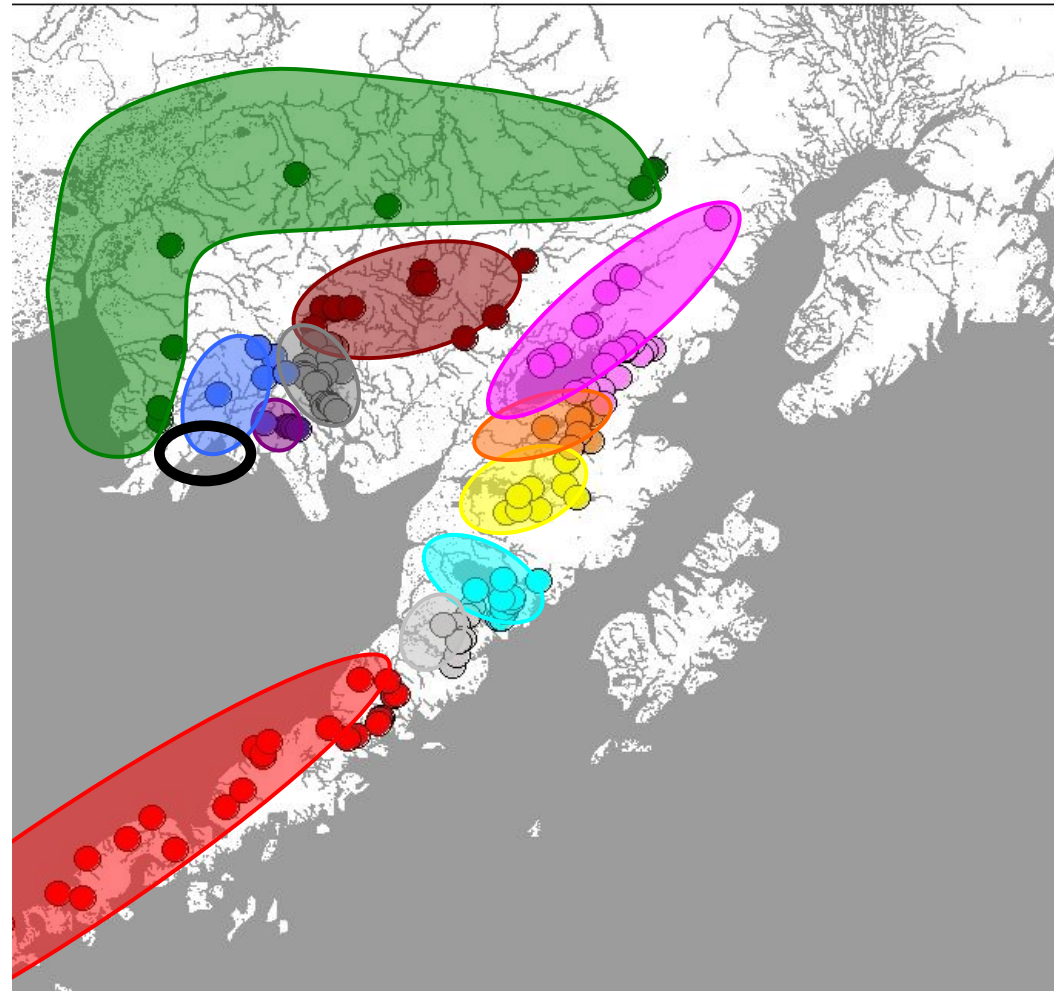
Togiak District
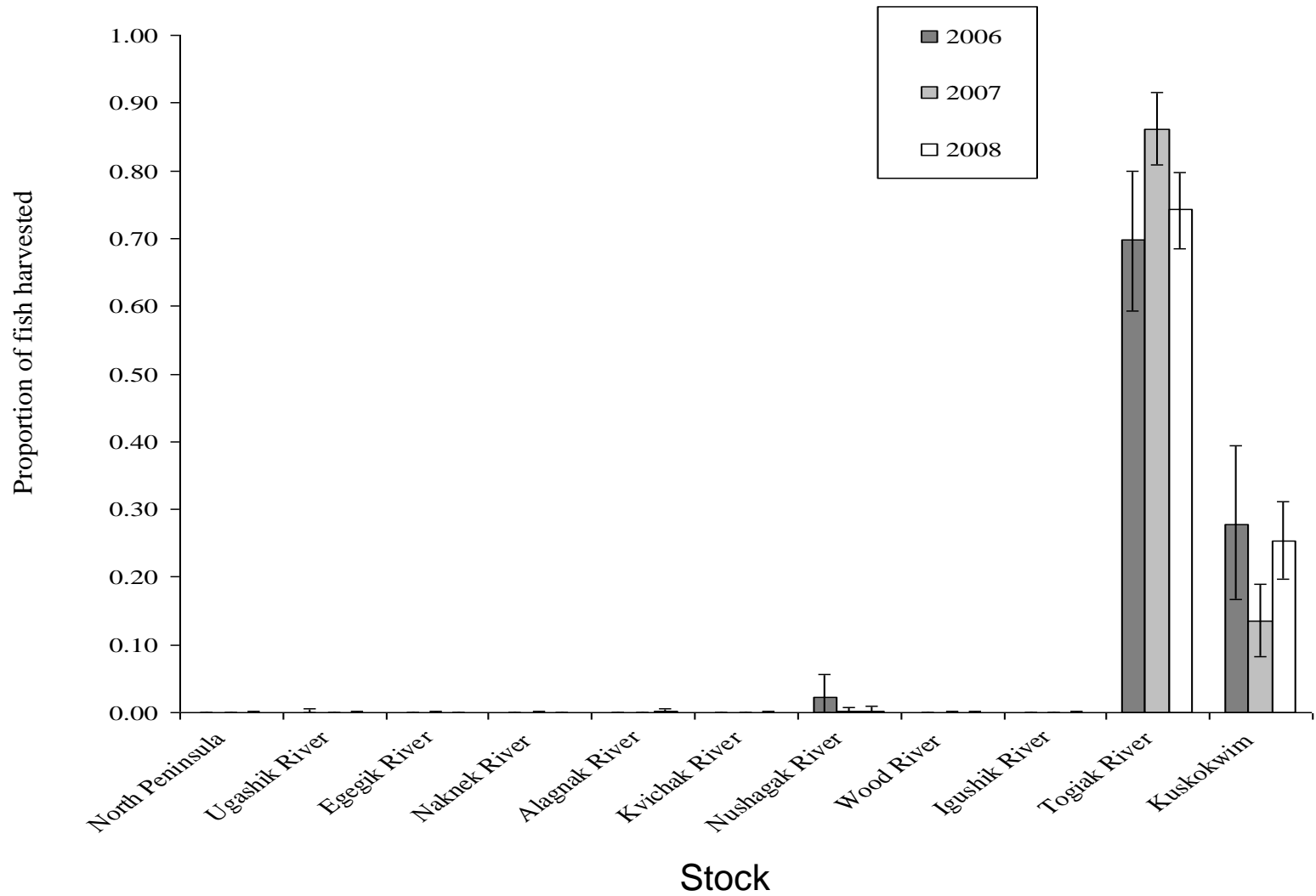
Figure 11 in report

Genetics analyses

- Genetics overview

- Baseline development

- Mixed stock analysis

  – Districts among years

  – Within Districts

– Comparisons with current methods

  - Traditional age-based

  - MSA genetics-based

Comparison of traditional and genetics methods
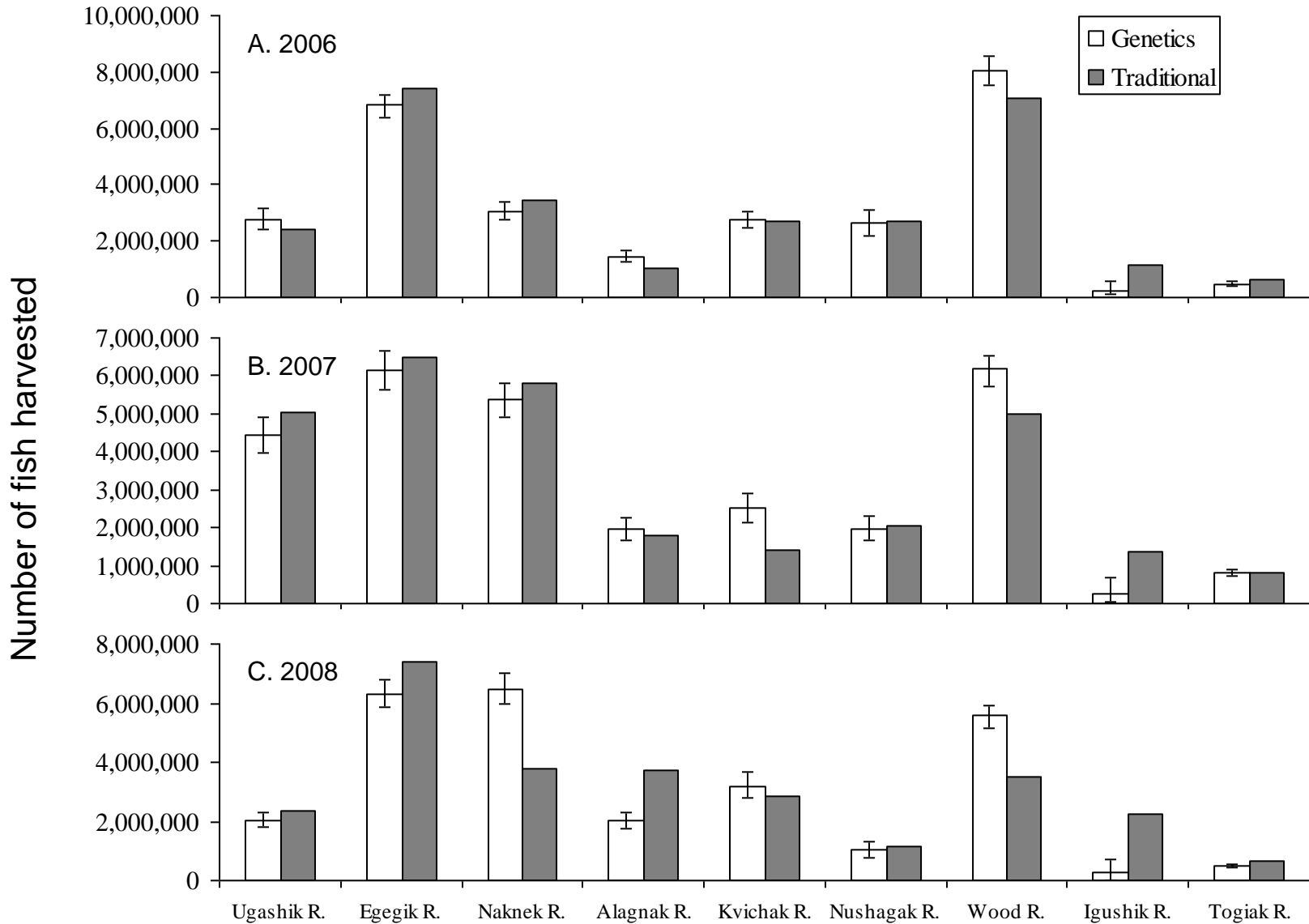
Number of fish harvested

Stock

Figure 12 in report

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Comparison of traditional and genetics methods

Figure 12 in report

39

Comparison of traditional and genetics methods

Figure 12 in report

40
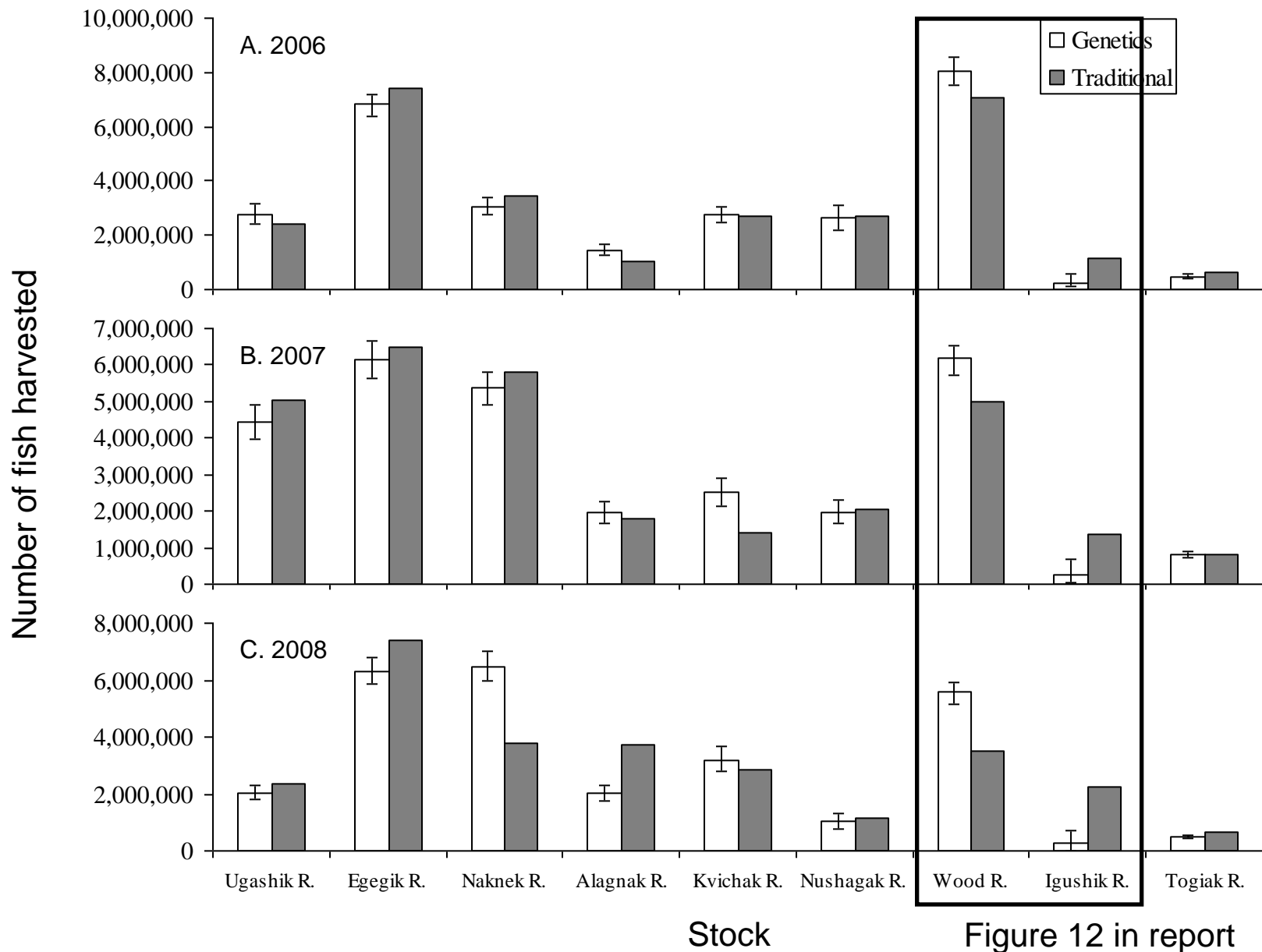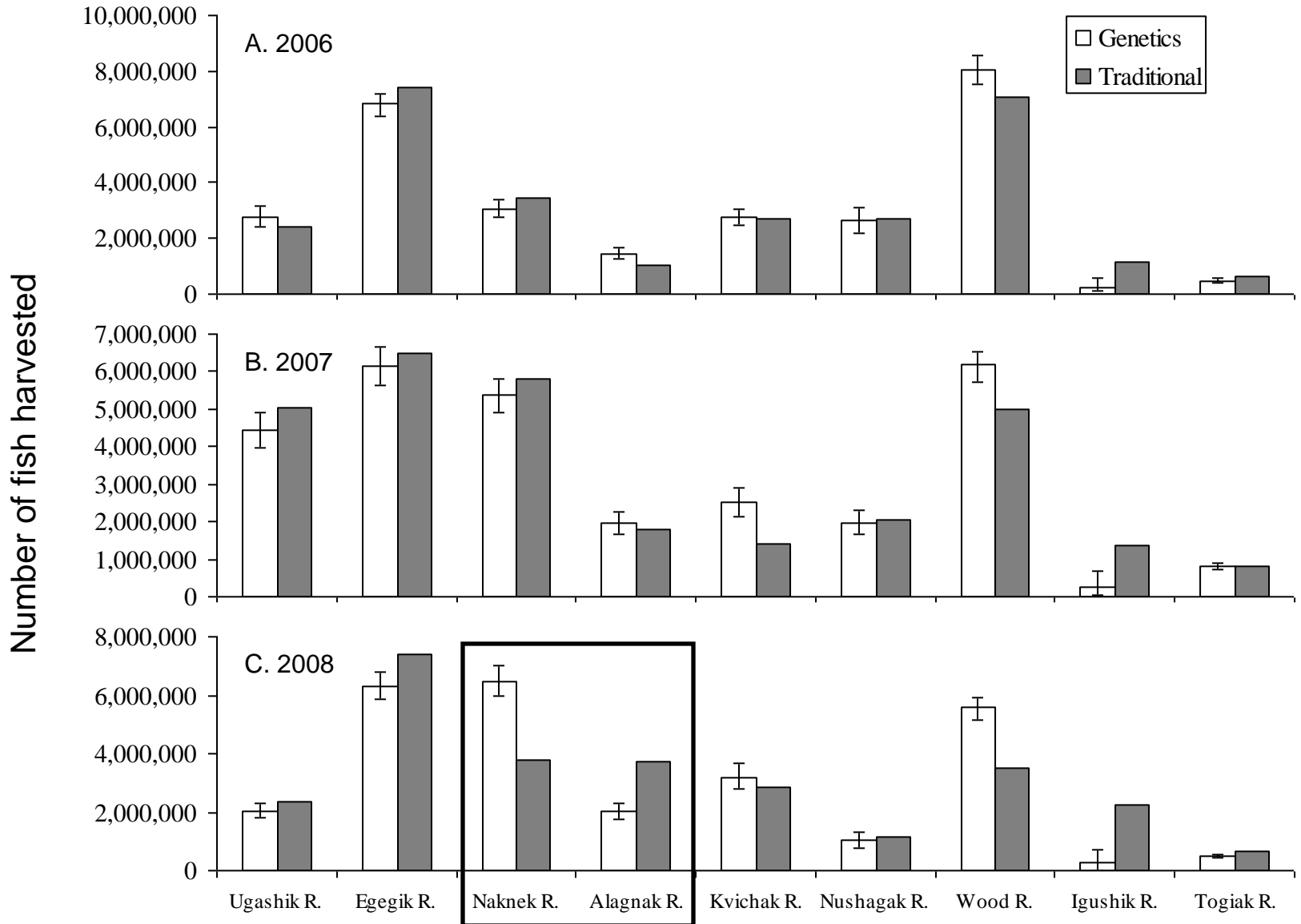
Method caveats

- Errors in sampling

Naknek-Kvichak District

2006

Number of fish harvested

Time strata

17% Wood

12% Kvichak

57% Alagnak

10% Egegik
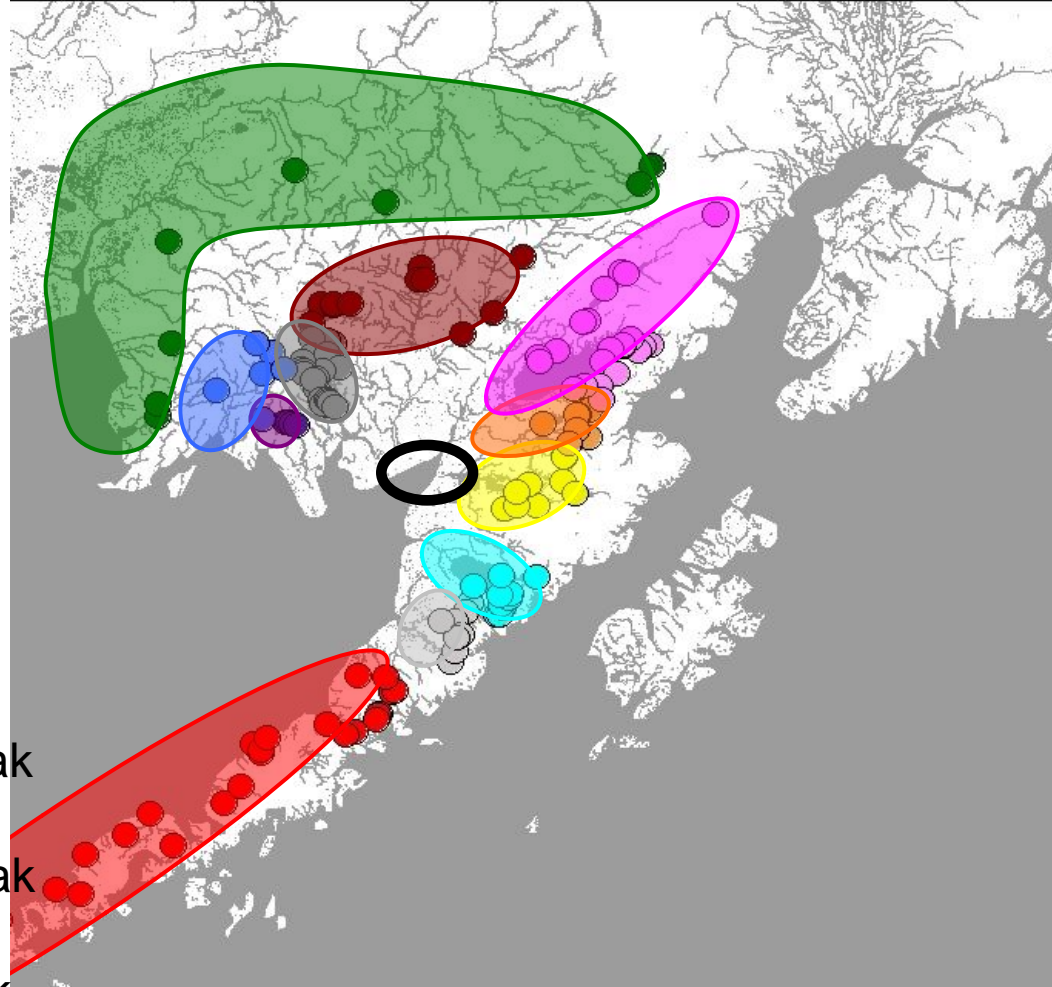
Alagnak Special Harvest Area
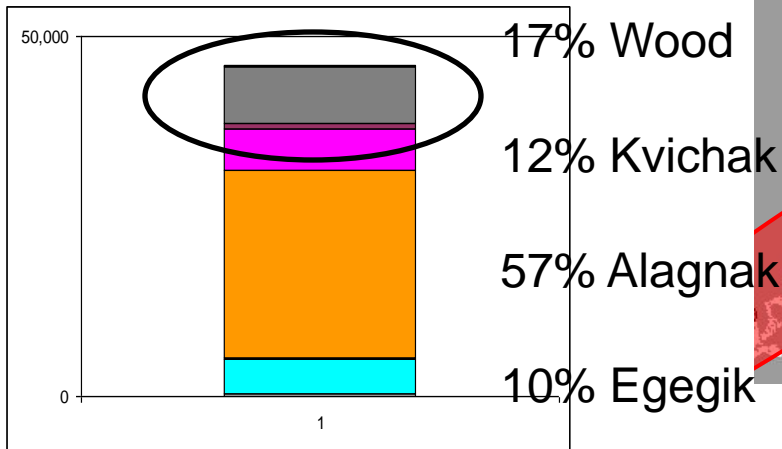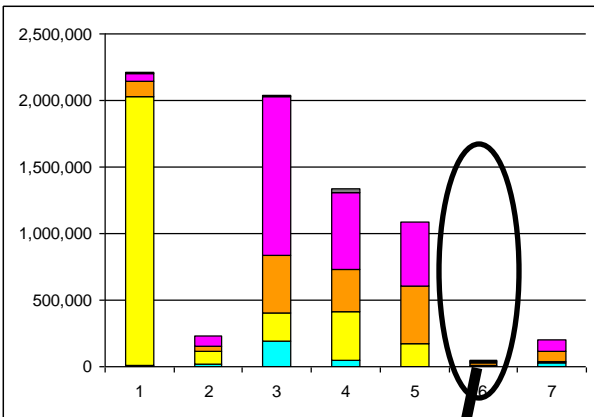
Method strengths and caveats

- Errors in sampling

- Bias in sampling

Nushagak District
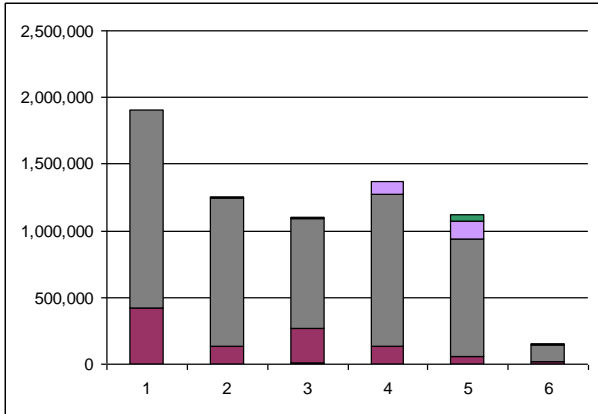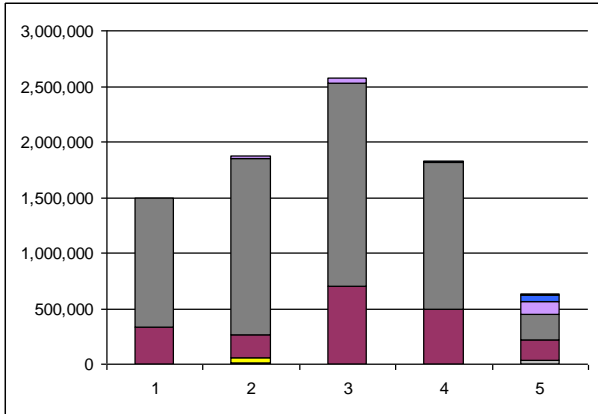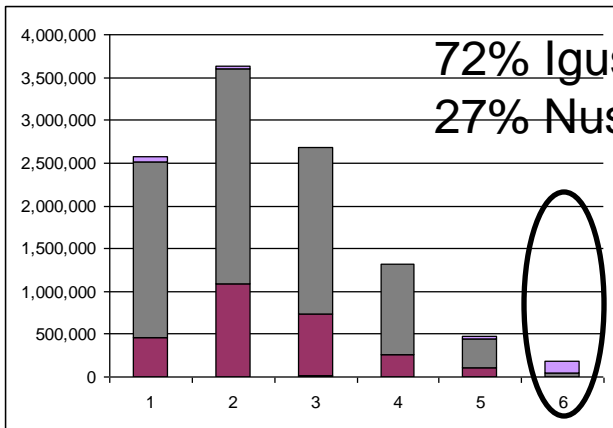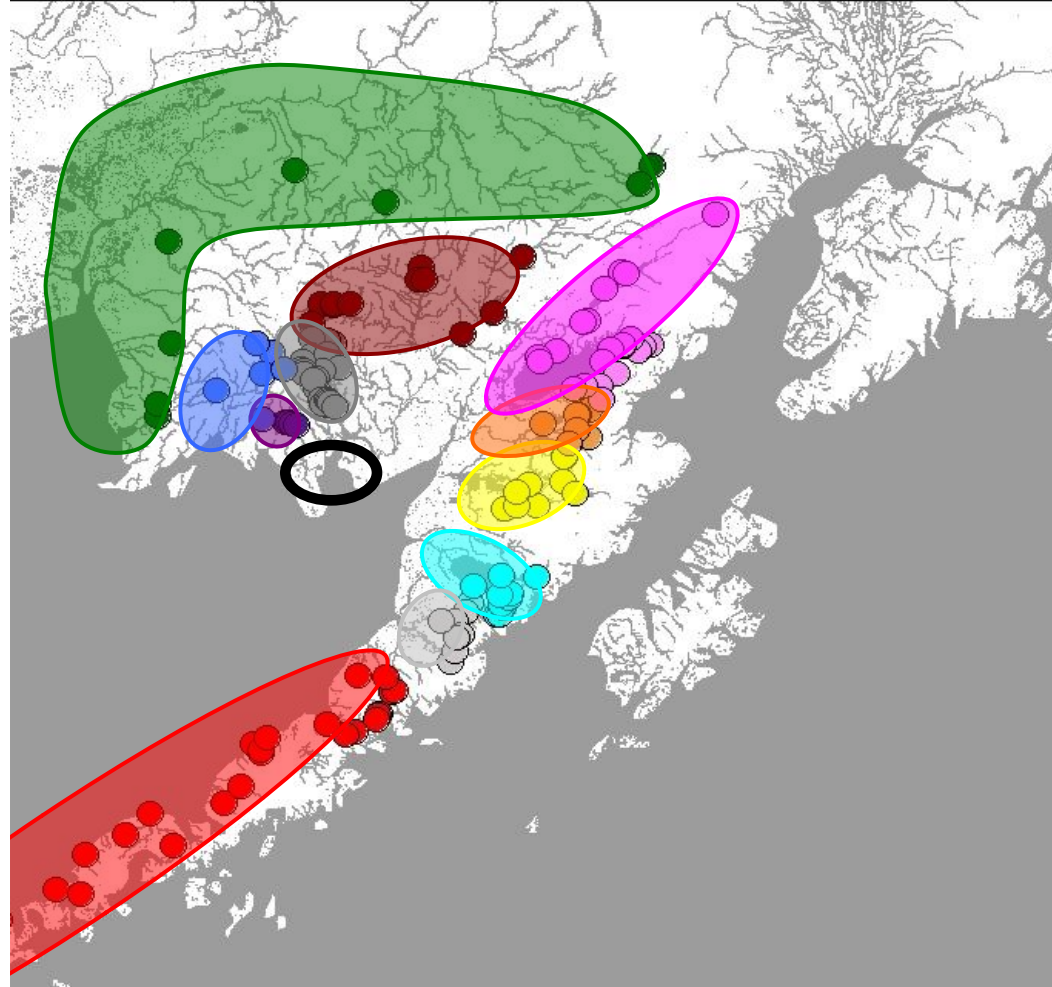
Igushik Section set gillnet

72% Igushik
27% Nushagak

2006

2007

2008

Number of fish harvested

Time strata

44

Method caveats

- Errors in sampling
- Bias in sampling
- Precision and accuracy

2006: Not sampled in proportion to catch within strata

Egegik District as an example

Sampled in proportion to catch

Typical for 2006

Proportion of catch sampled

Typical of other years…

Date
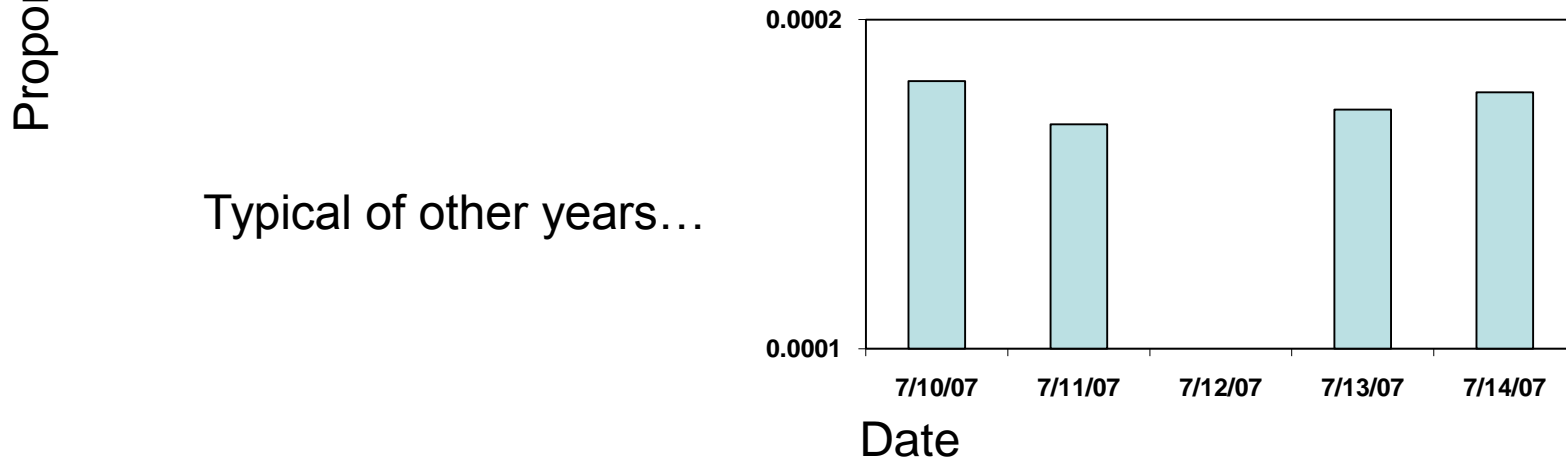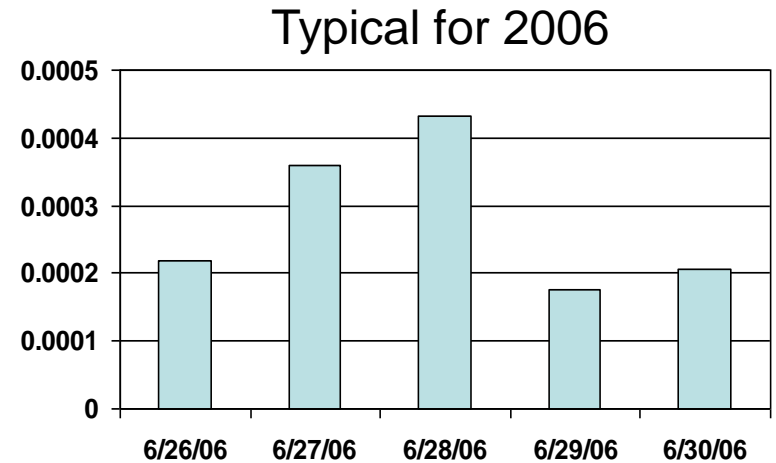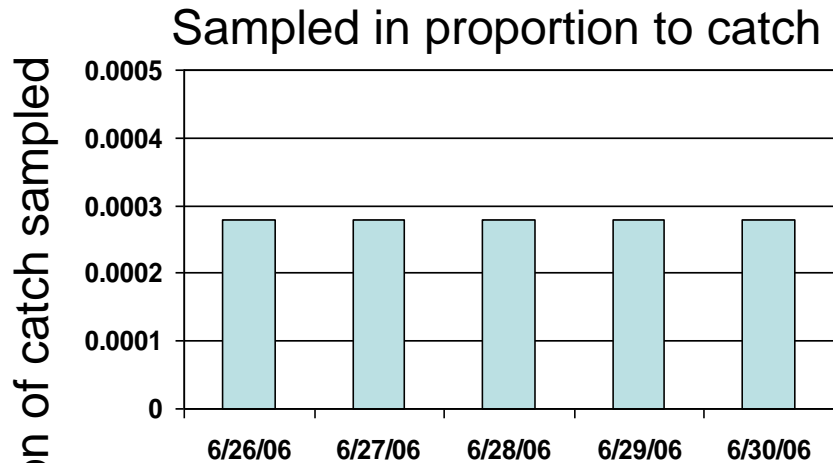
Summary

- Genetic MSA highly accurate
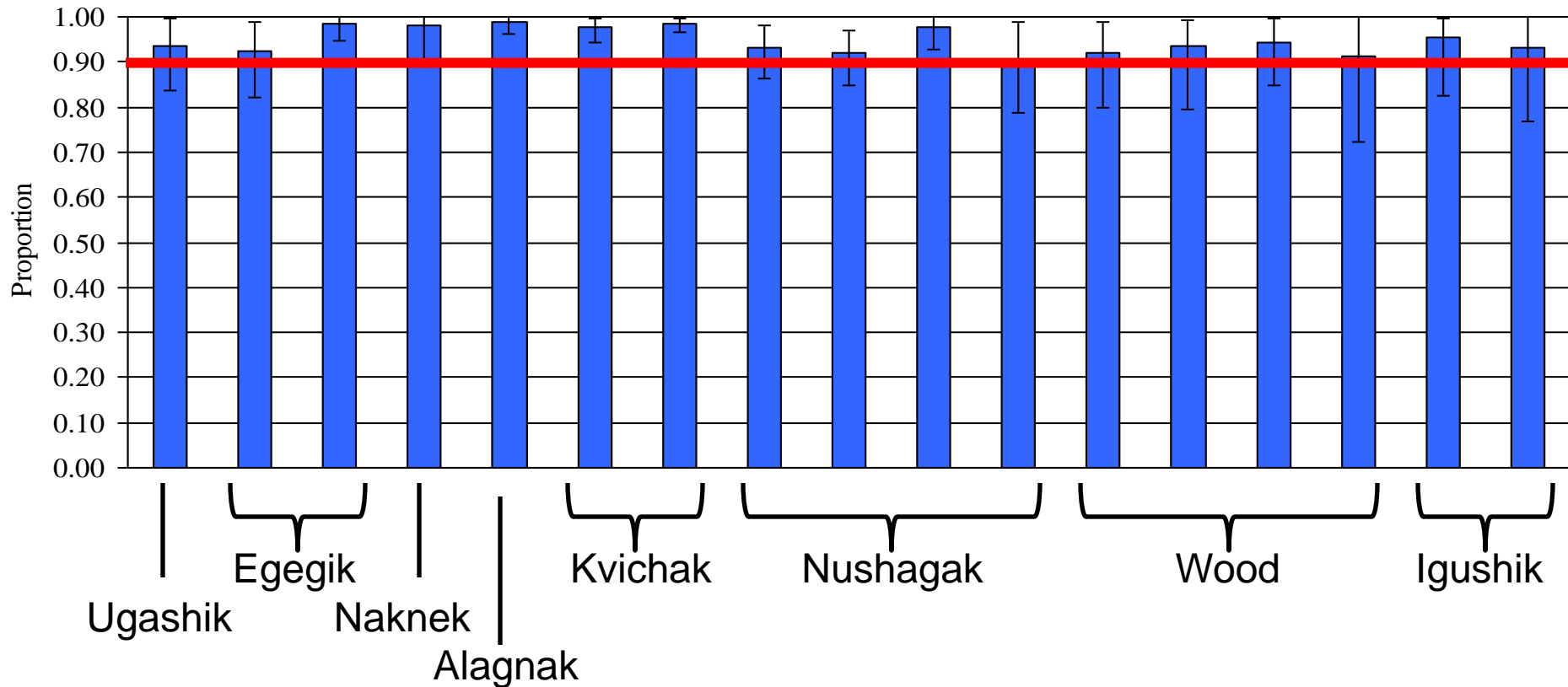
Summary

- Genetic MSA highly accurate
- Large sample sizes produce high precision
  - 190 fish per strata
    - » Sampling error +/- 7%
    - » Averaged 189 fish
    - » Ranged 143 – 278 fish
  - 380 fish per district
    - » Sampling error +/- 5%
    - » Averaged 896 fish
    - » Ranged from 278 to 1,283 fish

Summary

- Genetic MSA highly accurate
- Large sample sizes produce high precision
- Traditional and genetic method comparison
  - Similar distribution among fishing districts
  - Some differences within fishing districts
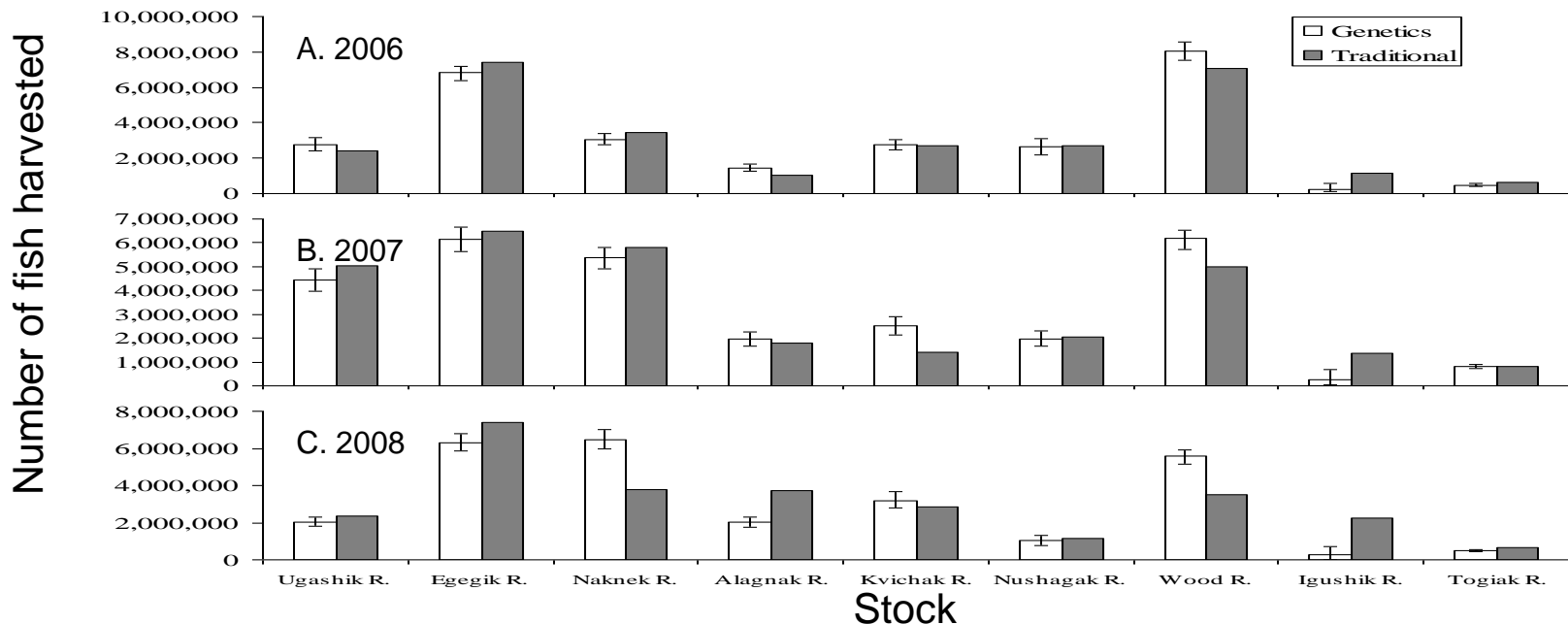
Summary

- Genetic MSA highly accurate
- Large sample sizes produce high precision
- Traditional and genetic method comparison
- **Special harvest areas are effective**

Egegik District

Egegik Special Harvest Area

Naknek-Kvichak District

Naknek Special Harvest Area

Summary

- Genetic MSA highly accurate
- Large sample sizes produce high precision
- Traditional and genetic method comparison
- Special harvest areas are effective
- Very few non-local stocks
  - 99% of fish were of Bristol Bay origin
  - Westside and Eastside fisheries segregated
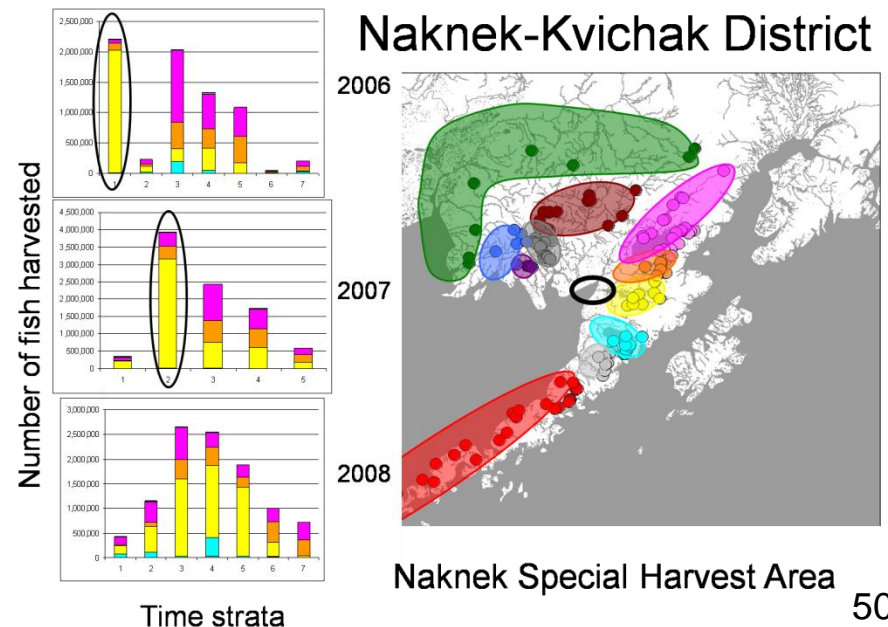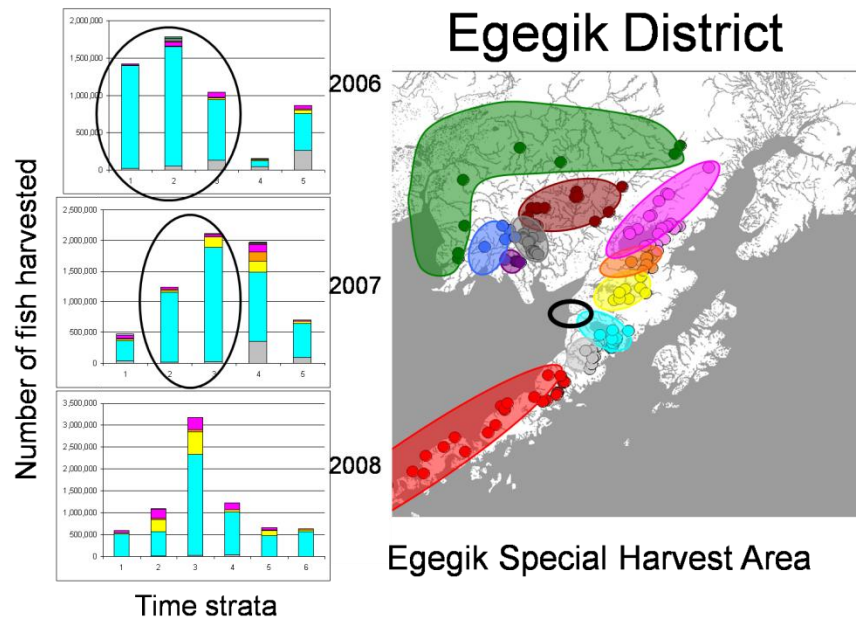 - Plan to further investigate Kuskokwim fish caught in Togiak District

Summary

- Genetic MSA highly accurate
- Large sample sizes produce high precision
- Traditional and genetic method comparison
- Special harvest areas are effective
- Very few non-local stocks
- Improves understanding of productivity by stock
  - Inshore run
  - Escapement goals
  - Forecasts

Future work

- Continued/improved sampling
  - Doubling sampling (WASSIP; 2006 – 2008)
  - Representing more variables (2010 onward)
- Improved baseline
  - Doubling loci (WASSIP)
  - Togiak River
    - Escapement samples
    - Baseline samples
- New statistical models
  - Better low proportion estimates (WASSIP)
  - Sensitivity analysis of priors
  - Incorporating more variables
    - stage of run, location within districts, tidal stage

Acknowledgements

- Jim and Lisa Seeb

- Baseline collections – Region 2, 3, and 4 staff, UW, USGS, NPS, UM, Kejulik River Lodge and Tikchik Narrows Lodge

- Baseline analysis – ADF&G, Disaster Funds, NPS, USFWS OSM, NPAFC, NPRB, NMFS, and BBSRI.

- Mixture collection and analysis – BBSRI, Gene Conservation Lab staff

- External review – Drs. R. Hilborn, J. Seeb, and D. Teel