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May 1, 2018

### MEMORANDUM

**TO: Council Members**

**FROM: Jeff Allen**

**SUBJECT: Update on Genetic Monitoring Program**

### BACKGROUND:

**Presenters:** Dr. Shawn Narum, Lead Geneticist, CRITFC  
Matt Campbell, Fisheries Genetics Program Coordinator, IDFG

**Summary:** In 2009, the CRITFC and IDFG first presented to NWPCC the concept of using genetic tools to monitor distinct stocks of salmonids in the Columbia River Basin. The overarching goal was to monitor stock specific abundance, run-timing, and harvest to contribute to fisheries management and recovery in the Columbia River Basin. Three BPA funded projects (CRITFC 2008-907-00; IDFG 2010-026-00; IDFG 2010-031-00) enabled this concept to be developed into ongoing studies to identify stock of origin of salmonids at fixed locations (Bonneville Dam and Lower Granite Dam) and intercepted in mainstem fisheries (commercial, sport, tribal). An update on progress was delivered to the NWPCC Tagging Forum in February of 2012 that summarized the development of genetic resources, empirical testing/demonstration, and results for long-term status and trend monitoring of steelhead and Chinook Salmon stocks. Now in 2018, we provide an update on this broadly implemented genetic monitoring program of salmonids in the Columbia River Basin. This includes use of two powerful approaches to identify hatchery origin fish with Parentage Based Tagging (PBT) and natural origin fish with Genetic Stock Identification (GSI). We summarize how these technologies work, the status of genetic baselines, and provide examples of how these

studies inform fisheries management and recovery. Finally, we highlight recent advances that have led to improvements in assignment accuracy of stocks, cost efficiency, and better understanding of variable life histories of salmonids. We also discuss directions for further improvements in upcoming years.

# Update on Genetic Monitoring throughout the Columbia River Basin

Matthew Campbell (IDFG) and Shawn Narum (CRITFC)

NWPCC Meeting  
Wednesday, May 9<sup>th</sup>, 2018  
8:30 – 9:00 a.m.



Idaho Department of Fish and Game



Columbia River Inter-Tribal Fish Commission

# Talk Outline

## I. Background

- Why these projects were initiated
- What these genetic technologies are and how they work
- The major objectives achieved during proof-of-concept period

## II. Current Status

- Review projects that provide status and trend monitoring of ESA-listed stocks in the CRB
- These contribute directly to ESA status reviews and BiOp reporting requirements
  - ✓ Campbell-Snake River Basin
  - ✓ Narum- Columbia River Basin

# Why these genetic projects were initiated?

## 1. RPAs in the 2008 FCRPS BiOp:

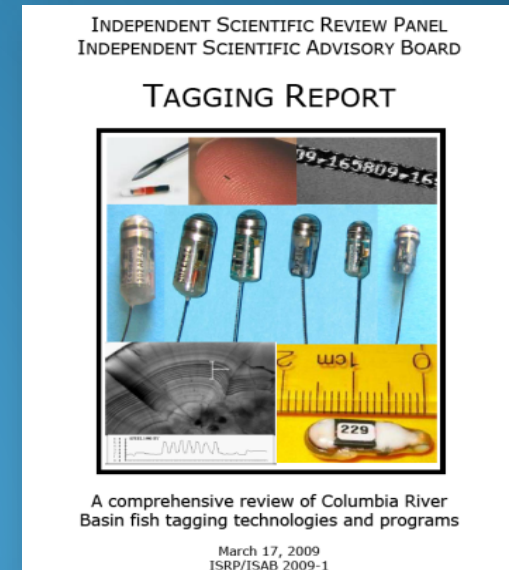
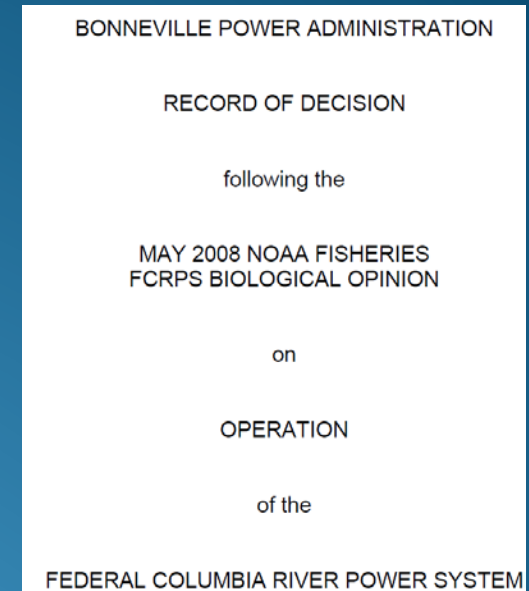
RPAs (*reasonable and prudent alternatives*) are required mitigation actions to prevent jeopardy of these species

- ✓ RPA 62.5
- ✓ RPA 50.5
- ✓ RPA 50.7
- ✓ RPA 64.2

← BiOp says genetic tools can address these!

## 2. The ISAB/ISRP “Tagging Report”:

- They endorsed proof-of-concept trials for these genetic methods!!!!



# What these genetic technologies are and how they work

## Parentage-based genetic tagging - PBT (Hatchery Fish)

- Genetic-based fish tagging method that involves genotyping hatchery broodstock
- By genetically sampling the parents, all offspring are genetically “tagged”
- ‘Tag’ recovery is non-lethal, and possible at all life stages

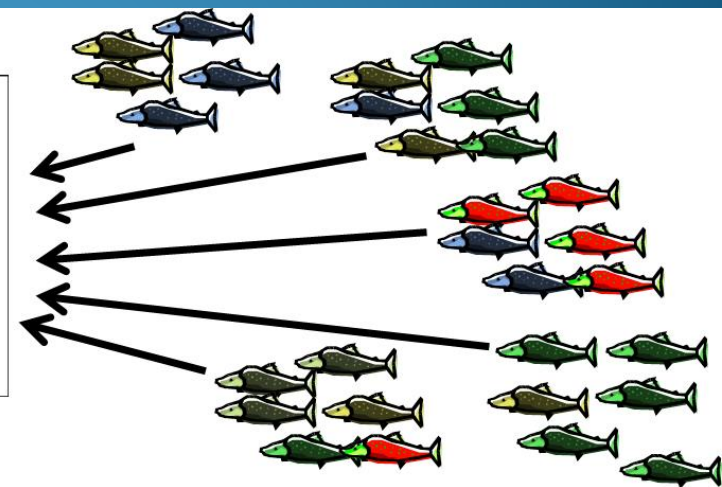
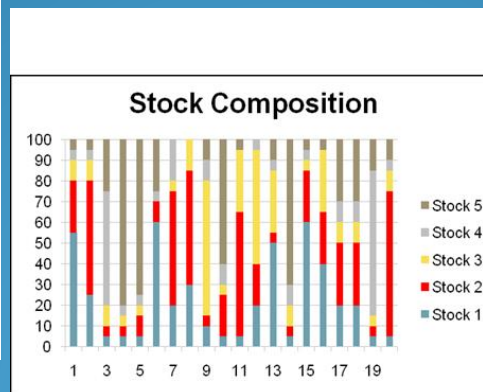
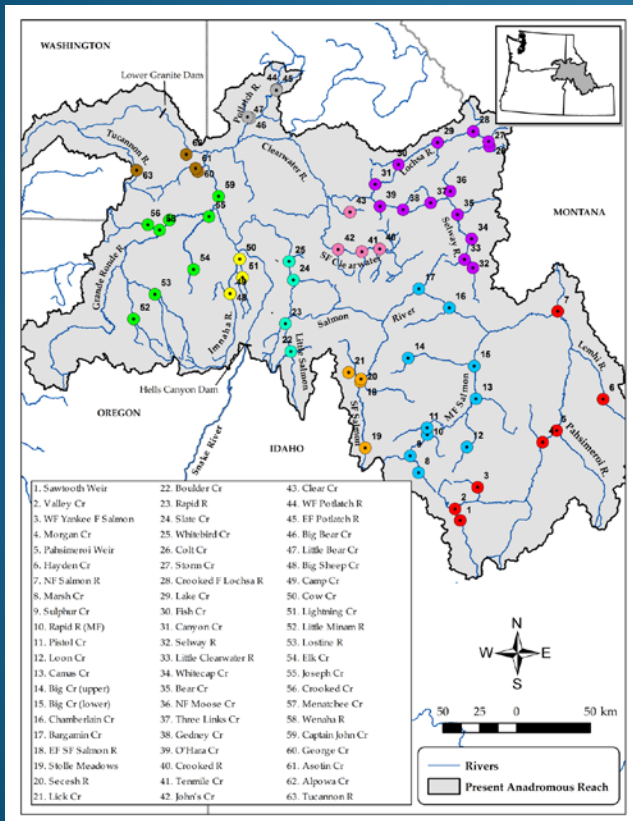
2 = 6,000!!!!



# What these genetic technologies are and how they work

## Genetic Stock Identification- GSI (Wild fish)

- Uses genetic profiles from all contributing wild populations to identify the stock of origin of any unknown fish



# PBT achievements during proof-of-concept period:

## What we demonstrated:

- PBT accurate and matched CWT assignments (Steele et al 2014)
- PBT/GSI genetic marker panels combined (efficient), multiple labs = same data
- High Snake River genetic tagging annually for each species (>95%) (2009- present)
  - ✓ ~9 million hatchery steelhead
  - ✓ ~14 million hatchery Chinook Salmon
- Now expanded throughout CRB

## It's all in the genes—including the tracking device

June 24, 2013, Canadian Science Publishing (NRC Research Press)



1046



ARTICLE

## A validation of parentage-based tagging using hatchery steelhead in the Snake River basin

Craig A. Steele, Eric C. Anderson, Michael W. Ackerman, Maureen A. Hess, Nathan R. Campbell, Shawn R. Narum, and Matthew R. Campbell

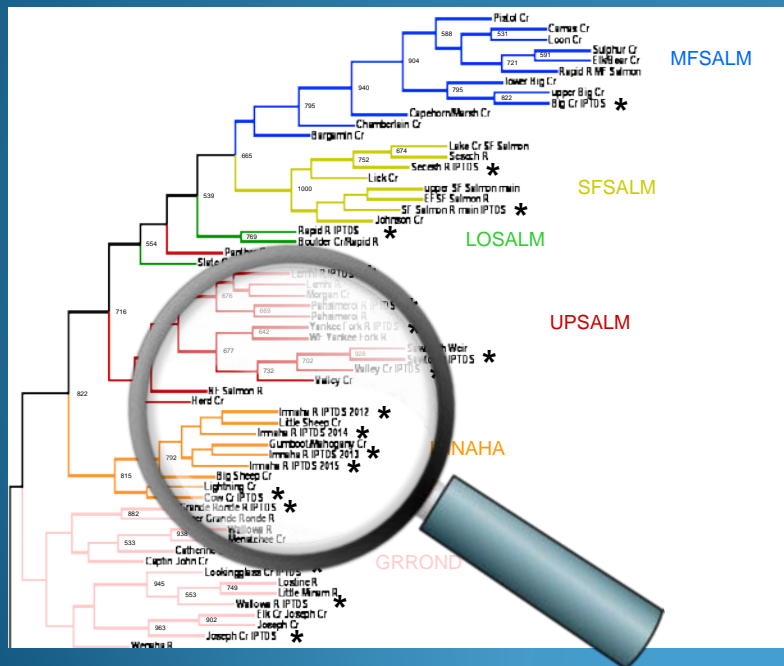
**Abstract:** Parentage-based tagging (PBT) is a promising alternative to traditional coded-wire tag (CWT) methodologies for monitoring and evaluating hatchery stocks. This approach involves the genotyping of hatchery broodstock and uses parentage assignments to identify the origin and brood year of their progeny. In this study we empirically confirmed that fewer than 100 single nucleotide polymorphisms (SNPs) were needed to accurately conduct PBT, we demonstrated that our selected panel of SNPs was comparable in accuracy to a panel of microsatellites, and we verified that stock assignments made with this panel matched those made using CWTs. We also demonstrated that when sampling of spawners was incomplete, an estimated PBT rate for the offspring could also be predicted with fewer than 100 SNPs. This study in the Snake River basin is one of the first large-scale implementations of PBT in salmonids and lays the foundation for adopting this technology more broadly in the region, thereby allowing the unprecedented ability to mark millions of smolts and an opportunity to address a variety of parentage-based research and management questions.



# GSI achievements during proof-of-concept period:

## What we demonstrated:

- Can monitor these species at the ESU and MPG level
- Stock abundance estimates using GSI baselines exhibit low bias (Powell et al 2018) and high precision (Steinhorst et al 2016)

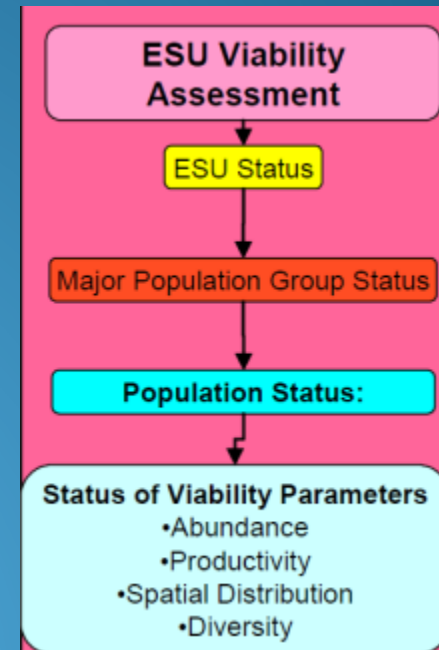
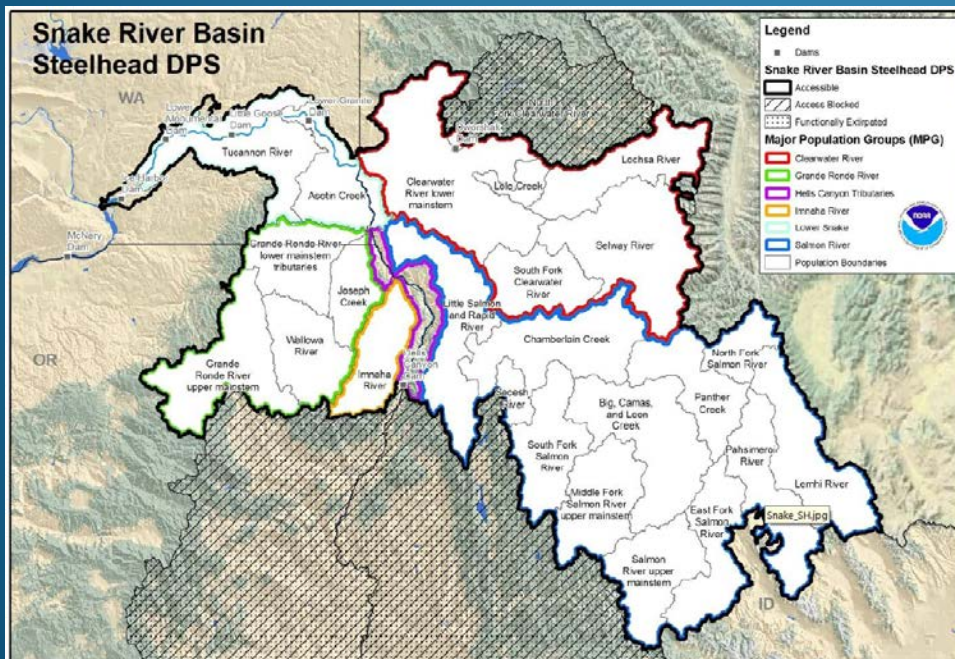


# Transition from proof-of-concept to Status and Trend Monitoring Programs

Example: Steelhead VSP  
Monitoring in the Snake River  
Basin

# VSP: Viable Salmonid Population Monitoring

- **ABUNDANCE** is one of the primary metrics NOAA uses to evaluate a population's viability
- Estimates of abundance (combined with age and sex data) over time allows estimation of population growth and productivity parameters
- Estimates of these metrics provide indicators of the resiliency and viability of populations and allows assessment of extinction risk



Are these populations recovering?

# Before GSI/PBT: Steelhead Monitoring Difficulties

- Viability assessments for the Snake River steelhead ESU **were impossible** due to...
  - Wide distribution
  - Winter/Spring spawning
- Most Snake River steelhead MPGs and populations had little or no abundance/productivity information



These parameters can be estimated annually for the entire Snake River basin using a comprehensive sampling and genetic program at Lower Granite Dam

# Lower Granite Dam

- Facilities and programs in place to representatively sample fish during adult and juvenile migrations
- 3,500 – 4,500 adults sampled annually
- 1,500 – 2,500 juveniles sampled annually

Adult Trapping Facility

Counting Window



Adult Fish Ladder



Juvenile sampling facility



# LGR Bio-sampling

Tissue (Genetic profile and Sex)



PIT Tag



Scale (Age)



Length



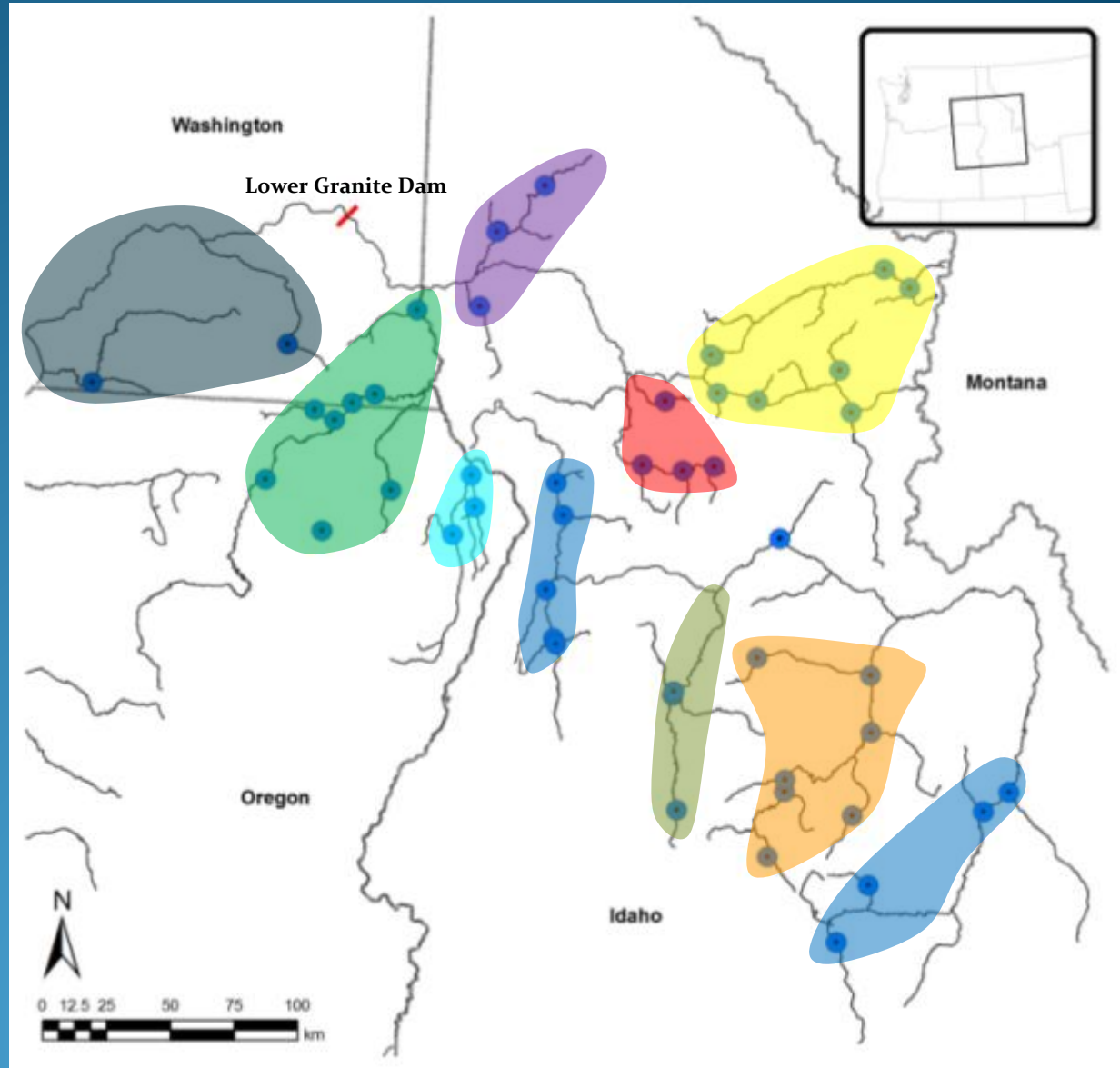
\*Trapping date also recorded

# Wild Abundance by Genetic Stock



What genetic stock am I from?

Our goal with this sampling is to partition the returning wild run over LGR into their genetic stocks



# Wild versus Hatchery Determination



Am I hatchery or wild?

Some hatchery fish are unclipped/marked:

- Intentionally released
- Miss-clipped
- CWT/PIT shed
- CWT/PIT undetected

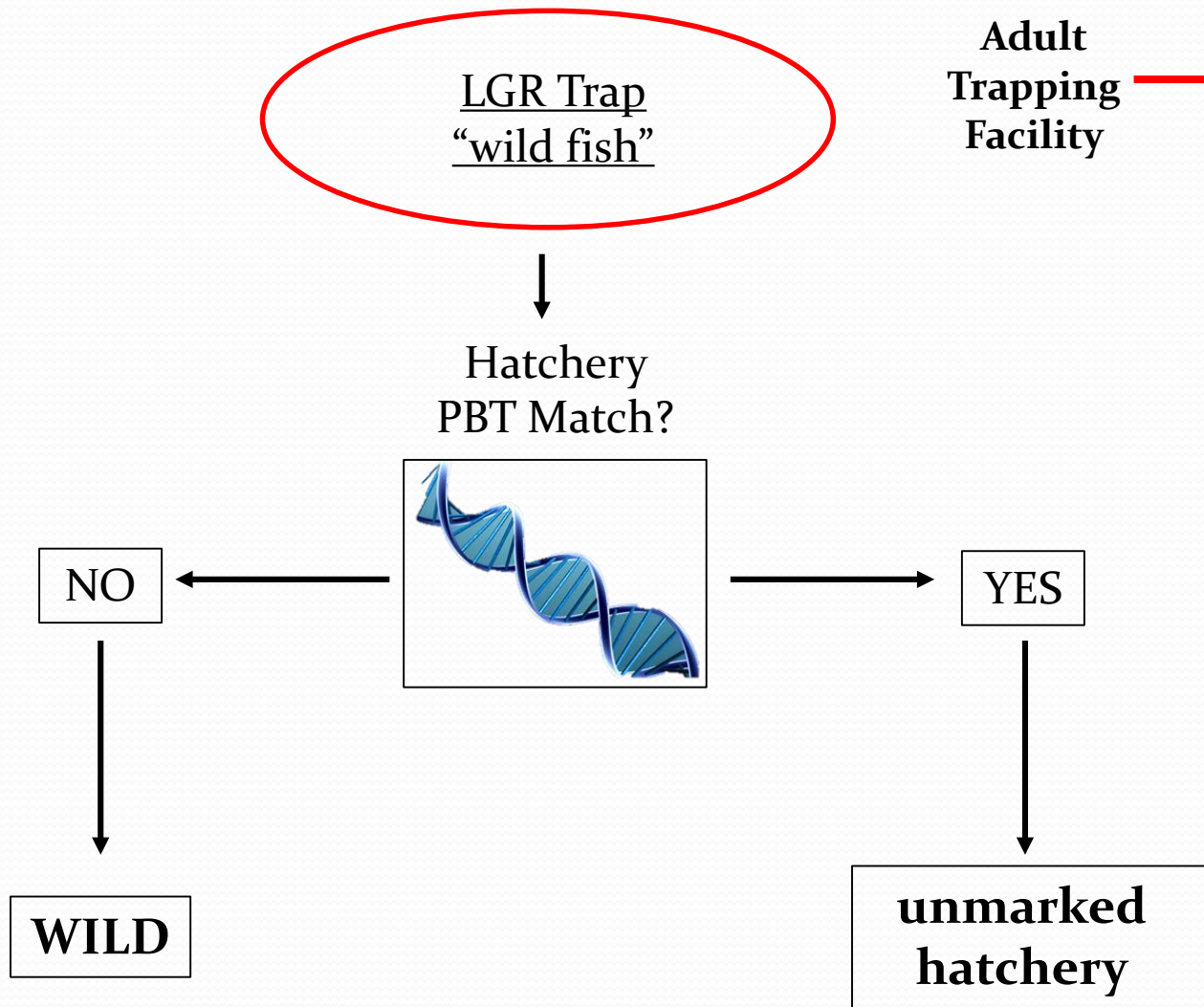


**NOAA FISHERIES**  
National Oceanic and Atmospheric Administration

NOAA Requires  
accurate estimates  
of wild  
abundance!!!!



# Wild versus Hatchery Determination

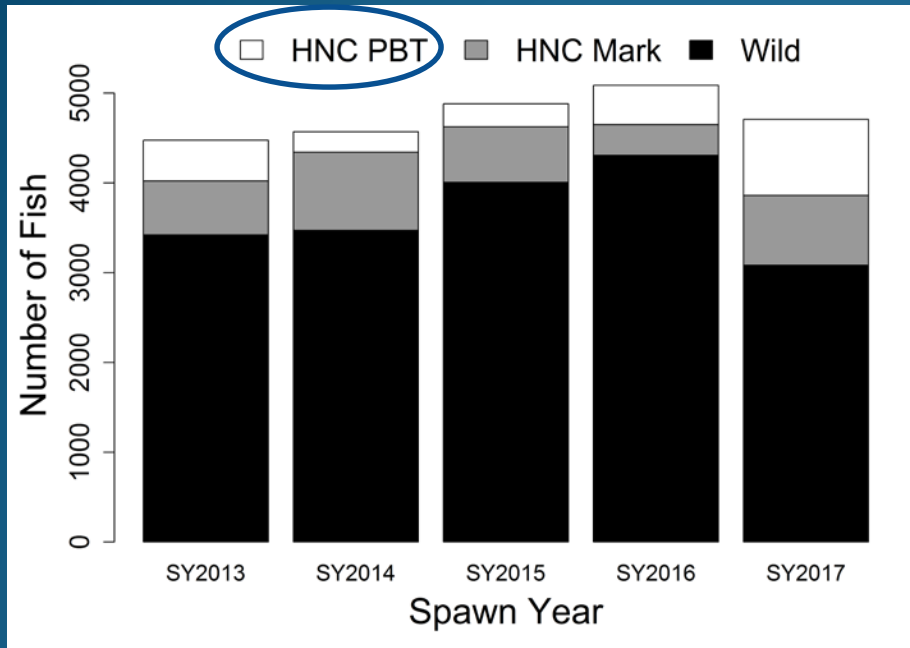


Adult  
Trapping  
Facility

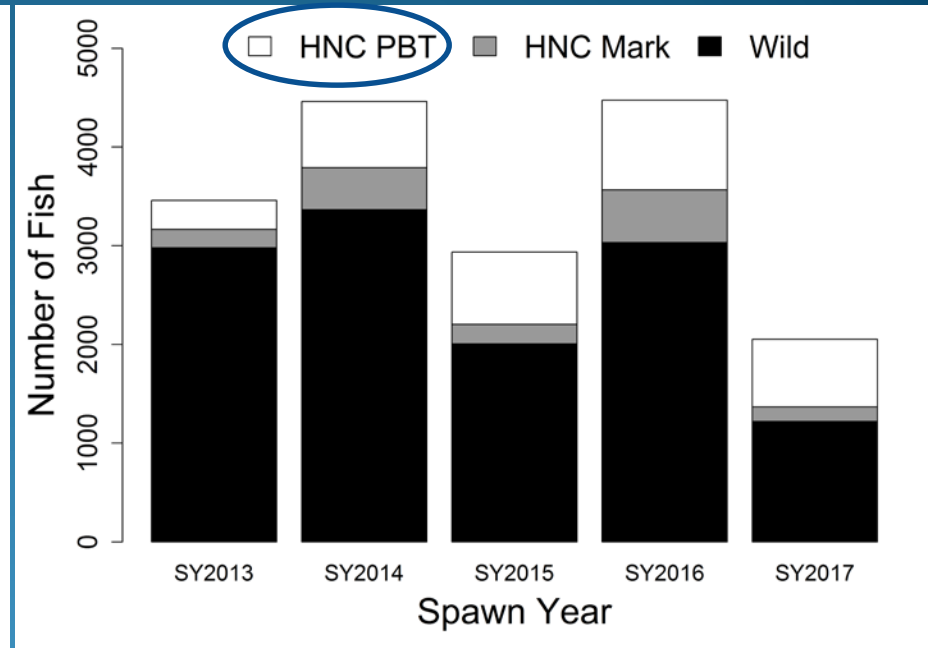


# Removing unclipped hatchery fish critical!

PBT makes the difference!!!!!!



Steelhead



Chinook Salmon

Species	Without PBT	With PBT	Difference	%
Steelhead	19,592	15,576	4,016	20.4%
Chinook	9,049	5,793	3,256	35.9%

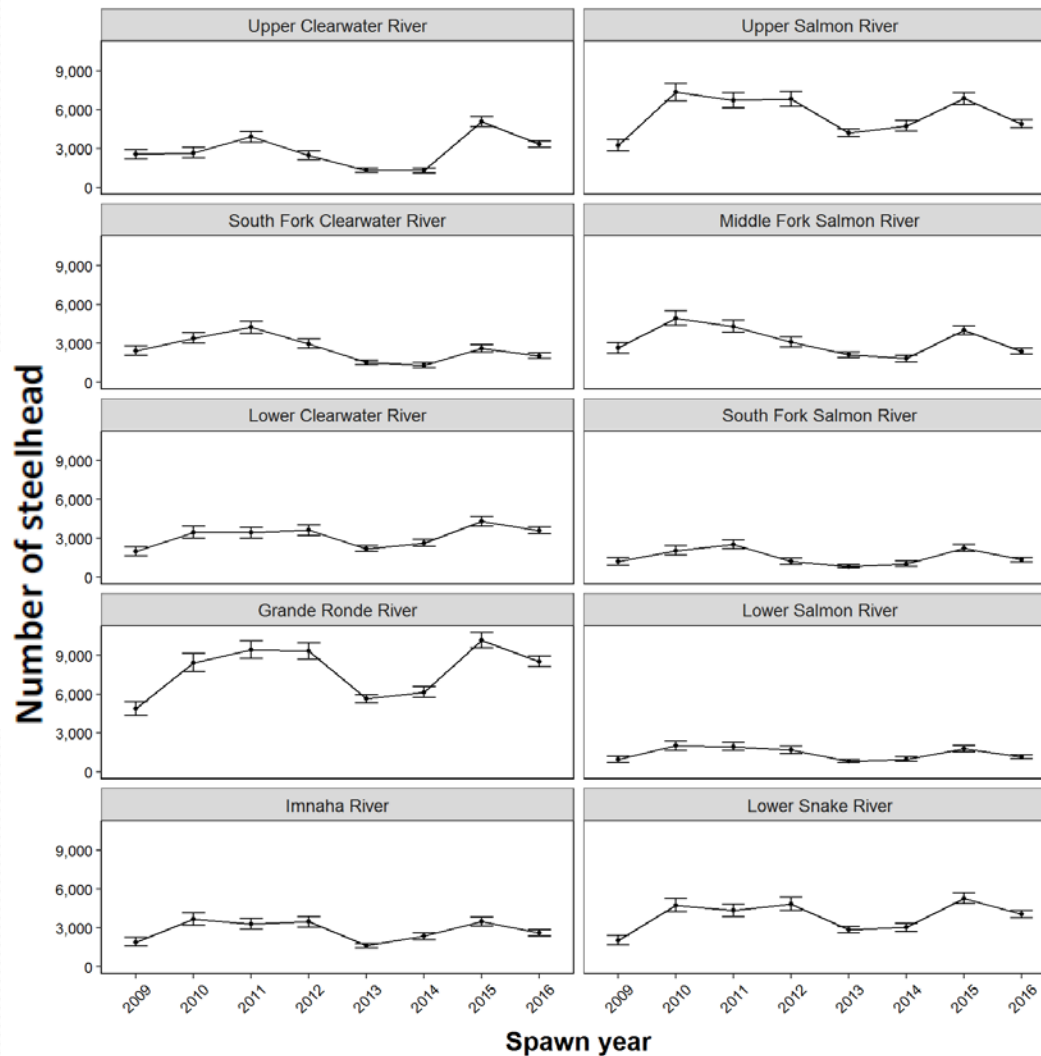
Only now can we get accurate estimates of wild abundance back to the Snake River!!!



# Wild Escapement - Genetic Stock



Steelhead



- Annual estimates of wild abundance needed to determine recovery status are now available annually!!!!
- Same estimates available for Snake River Chinook ESU
- Same technology used throughout the CRB

Escapement above Lower Granite Dam of STHD by stock from spawn years 2009 to 2016

I have provided VSP example in  
the Snake River

Other programs throughout the  
Columbia River Basin uses these  
genetic technologies for status  
and recovery monitoring...

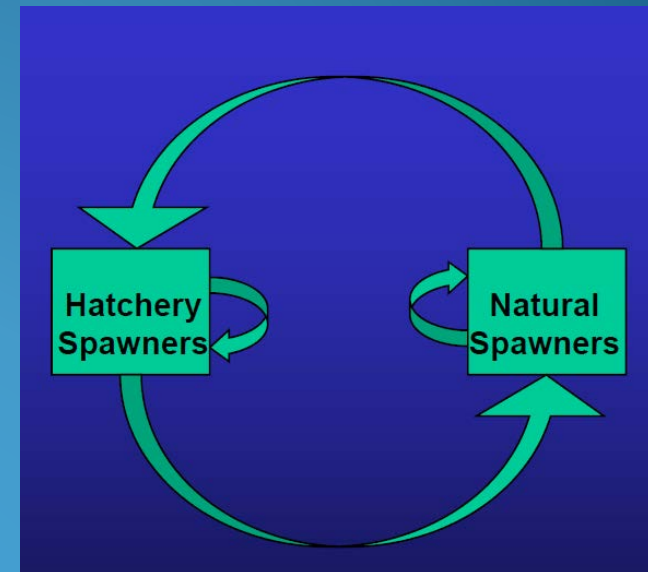
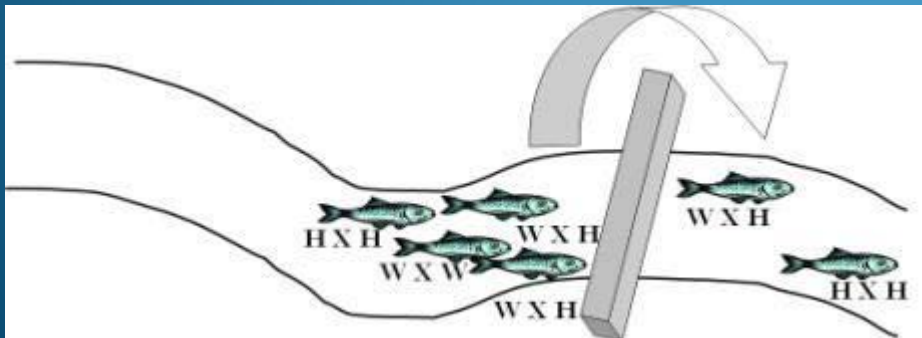
# Other status and trend monitoring programs: HATCHERY REFORM

- ✓ BPA funds many hatchery programs
- ✓ Committed to ensuring these programs do not impede recovery!!!!!!

HOW?

- ✓ HSRG-Hatchery Reform!!!!!! **All** hatchery programs must manage broodstocks to achieve proper genetic integration with, or segregation from, wild populations
- ✓ Our projects provide annual monitoring of HGMP goals for the entire Snake River Fall Chinook ESU (includes monitoring natural production areas, necessary for recovery and ESA Delisting)
- ✓ On a smaller scale projects provide annual monitoring of HGMP goals for Integrated hatchery programs at Sawtooth, Pashimeroi and McCall

## HATCHERY AND GENETIC MANAGEMENT PLAN (HGMP)




## Other status and trend monitoring programs: Predation Monitoring

Standardized, secured, accessible genetic data are important!!!!

Some examples: (sea lion and bird predation on ESA listed stocks)

- ✓ Rub et al 2017- NOAA researchers showed 24% mortality of spring/summer Chinook and concluded that “about 68% of the Chinook Salmon tagged and sampled near Astoria were destined for the river and tributaries **above Bonneville** based on genetic testing”...
- ✓ Kuligowski et al 2014-NOAA researchers concluded that “PBT analysis suggests Snake River steelhead and Chinook Salmon are a larger proportion of the birds diets”...



**Survival of adult spring/summer Chinook salmon through the estuary and lower Columbia River amid a rapidly changing predator population**

A. Michelle Wargo Rub, Ben Sandford, Don Van Doornik, Matthew Nesbit, Samuel Rambo, Jesse Lamb, Louis Tullos, Gordon Axel, Brian Burke, Kinsey Frick, Mark Sorel, David Huff, & Rich Zabel  
NOAA Fisheries Northwest Fisheries Science Center (NWFSC)

Genetic Analysis of Caspian Tern (*Hydroprogne caspia*) and Double Crested Cormorant (*Phalacrocorax auritus*) Salmonid depredation in the Columbia River Estuary 2006-2013

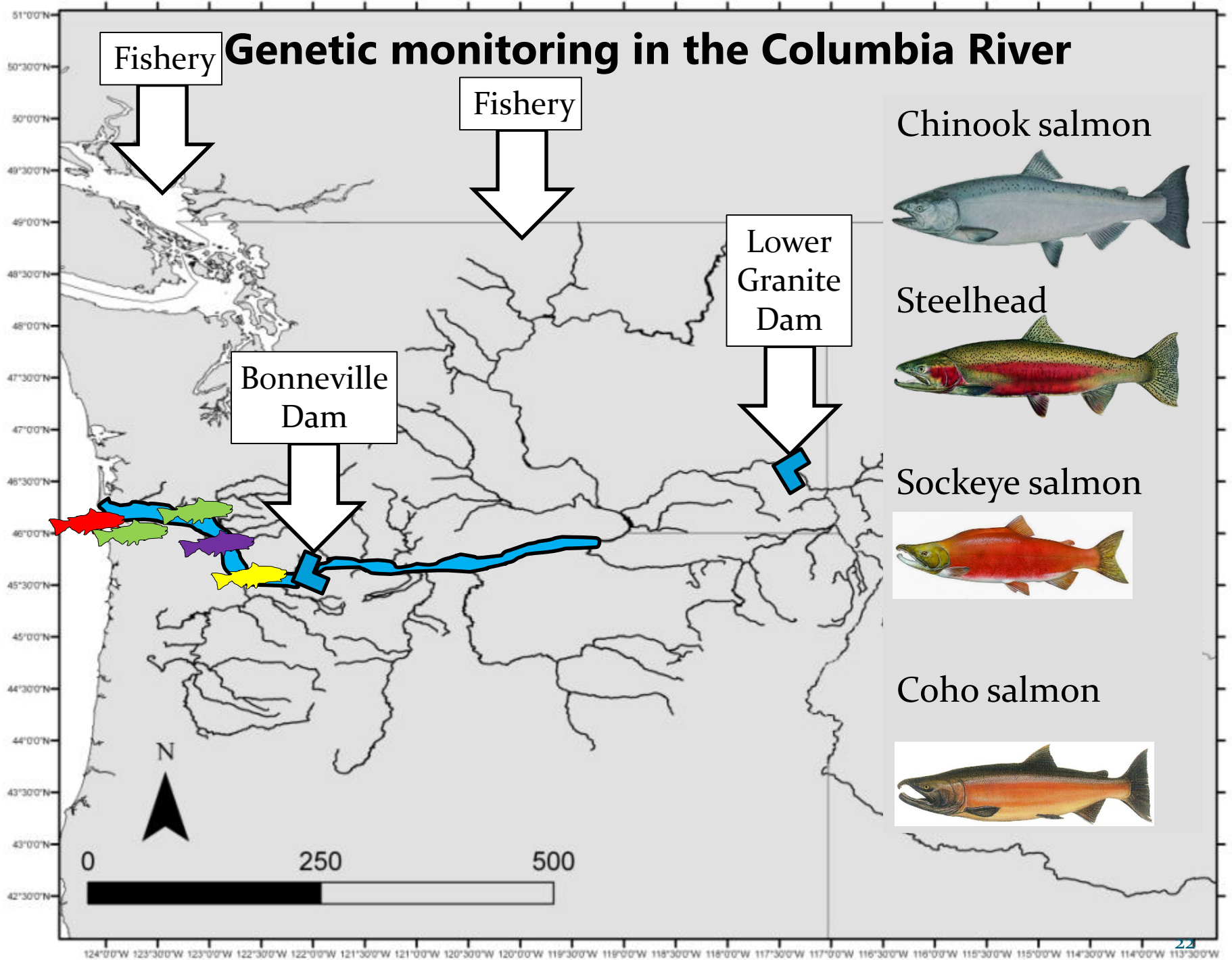
David Kuligowski<sup>1</sup>, Laurie Weitkamp<sup>1</sup>, Curtis Roegner<sup>1</sup>, Daniel Roby<sup>2</sup>, Ken Collis<sup>3</sup>, Donald Lyons<sup>4</sup>, Donald Van Doornik<sup>1</sup>, Lauren Reinalda<sup>4</sup>, Allen Evans<sup>3</sup>, Tim Marcella<sup>4</sup>, Peter Loschl<sup>4</sup>, and David Teel<sup>1</sup>.



Sea Lion Photo: U.S. Army Corps of Engineers

# Columbia River Basin

# Genetic monitoring in the Columbia River

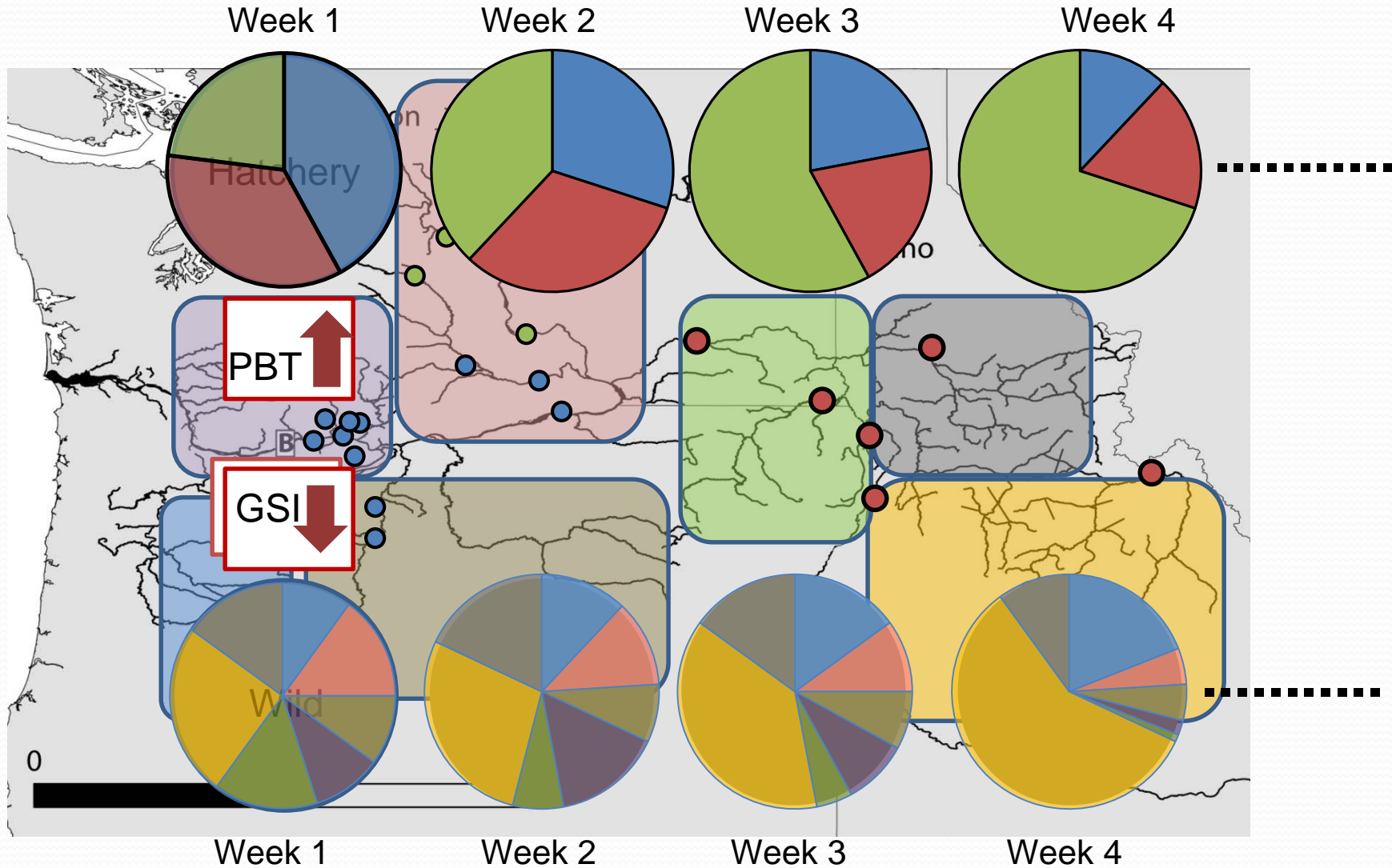




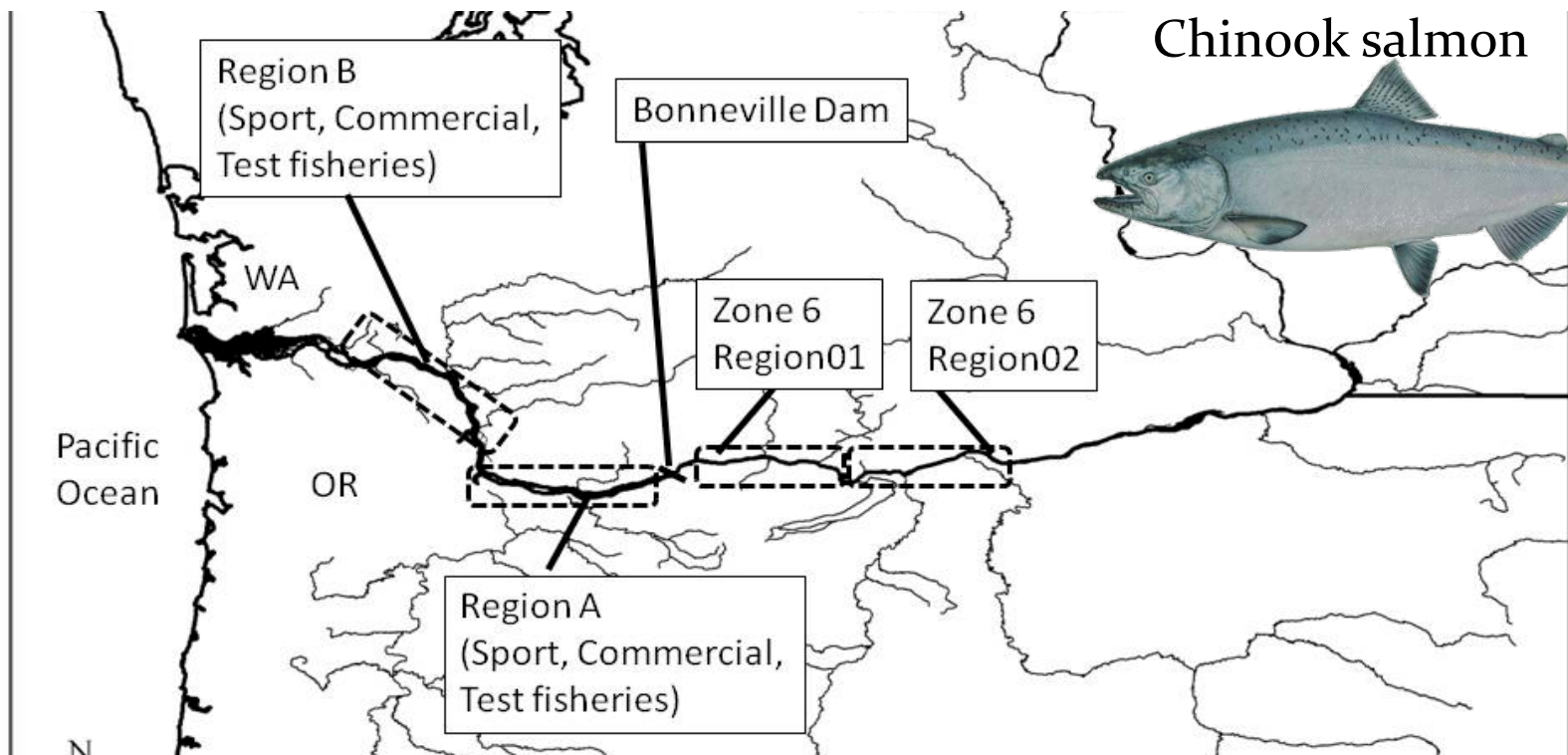
# Bonneville Dam:

-Weekly sampling April - October

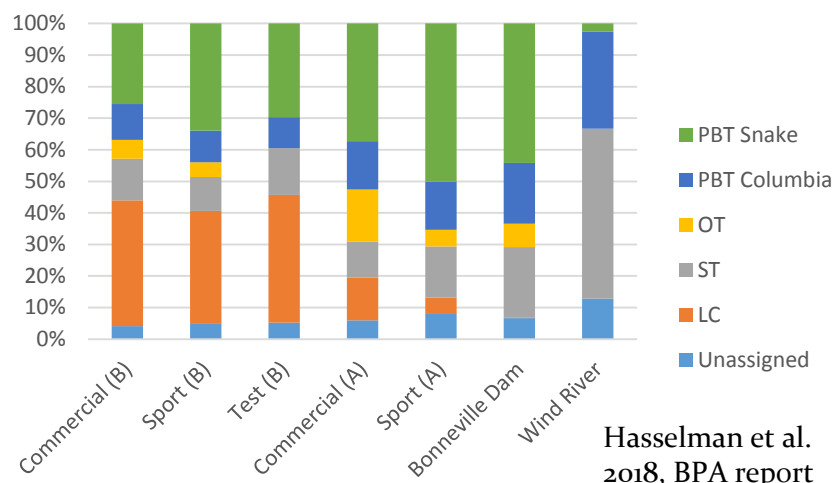
-In-season analysis



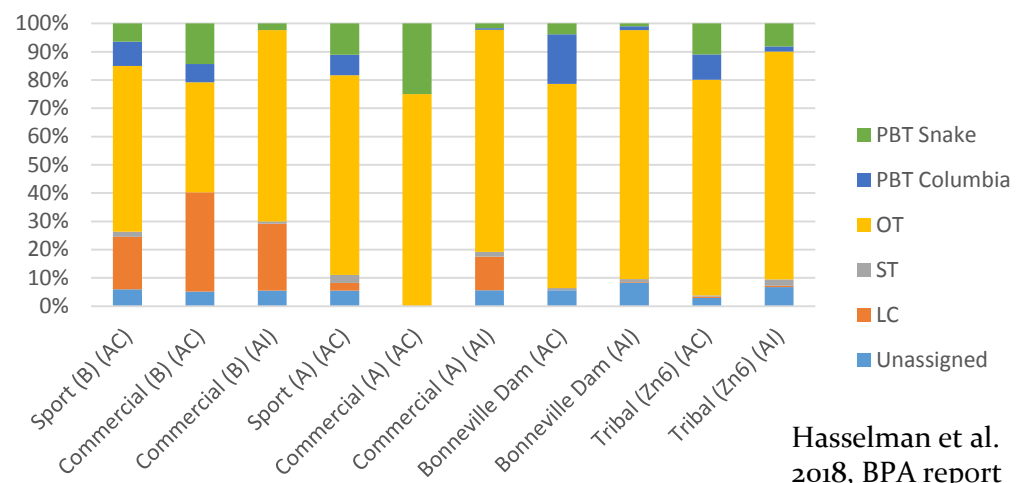
# Monitor Harvest in mainstem Columbia River



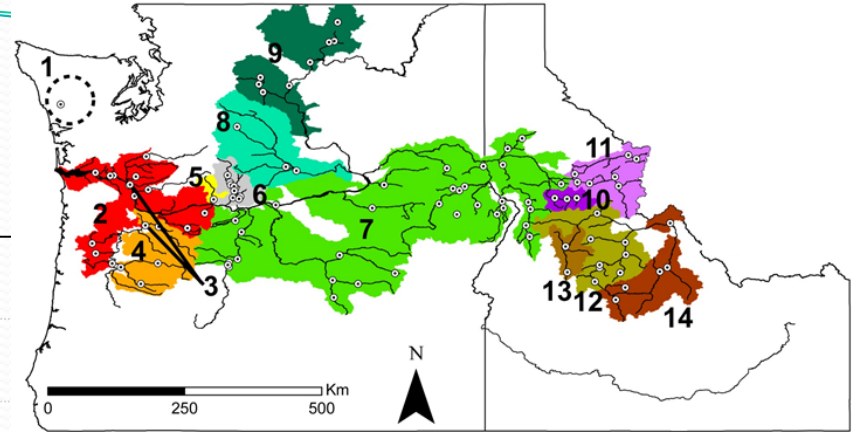
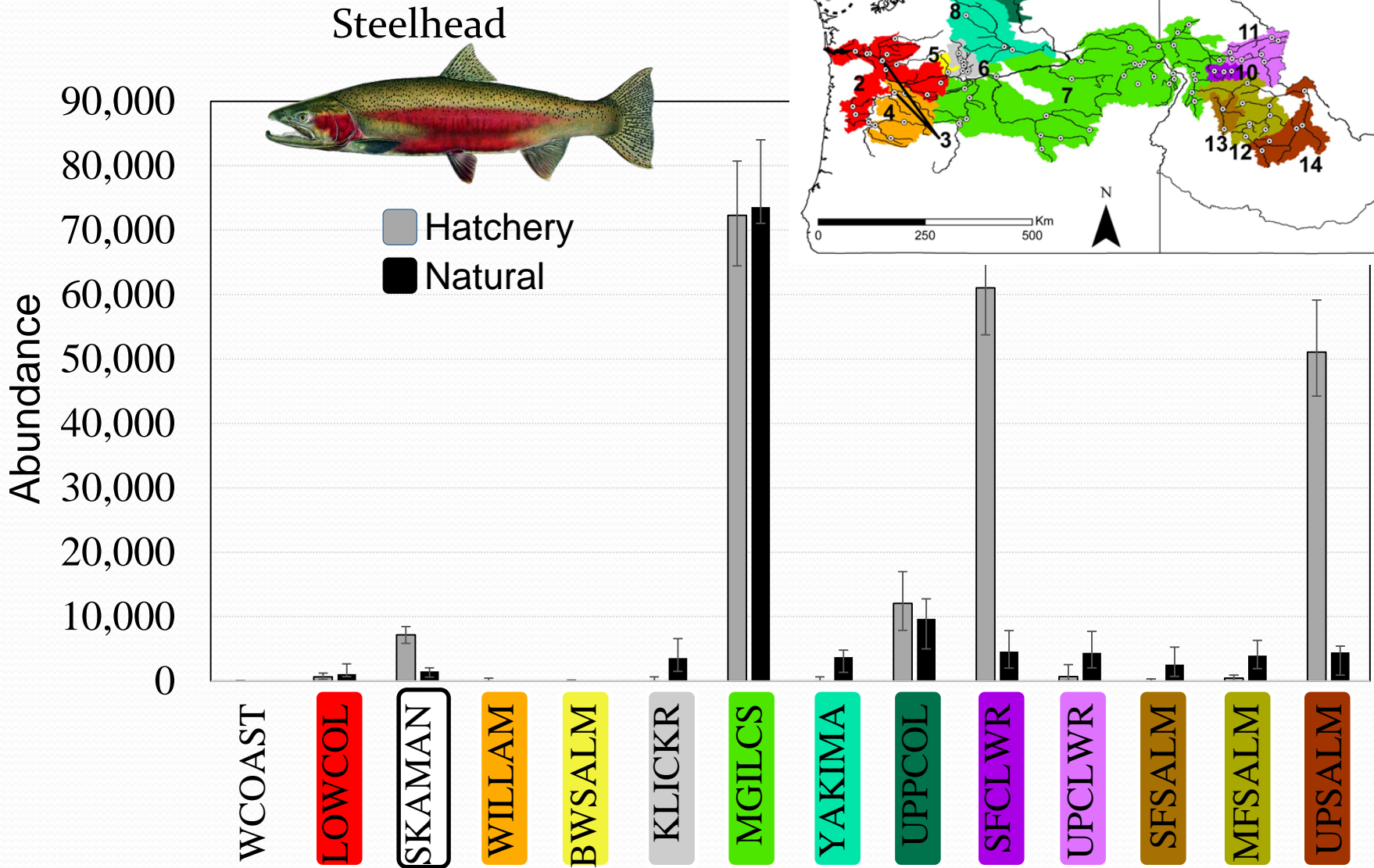
## Harvest during **spring** mgmt period



## Harvest during **summer** mgmt period



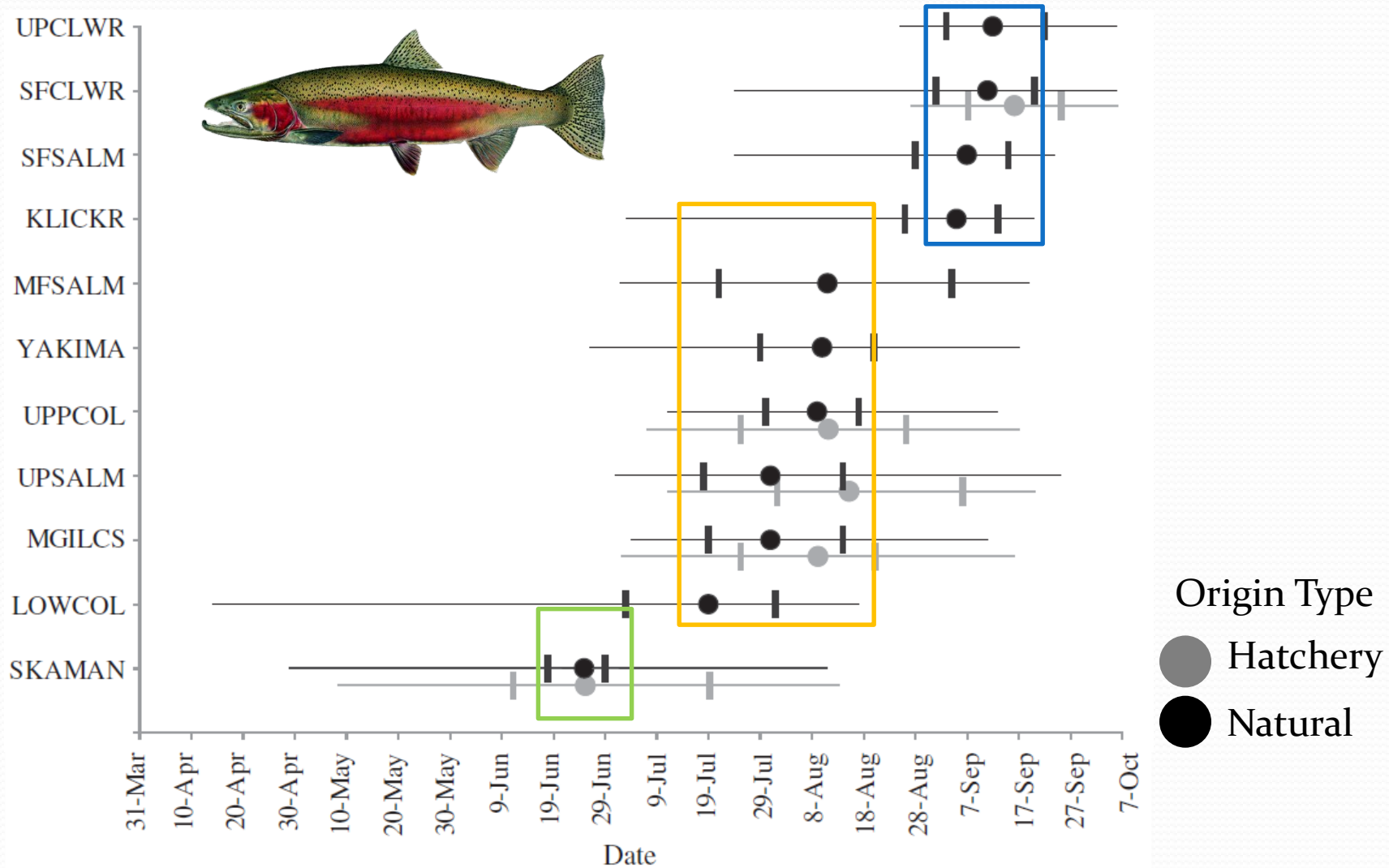
# Stock-specific abundance at Bonneville Dam



~ 11M annual target release  
 ~ 88% from Snake R. hatcheries

\* Target release #'s from *US v Oregon* production table B6 and non-*USvOR* table

# Estimate Run-timing of Distinct Stocks

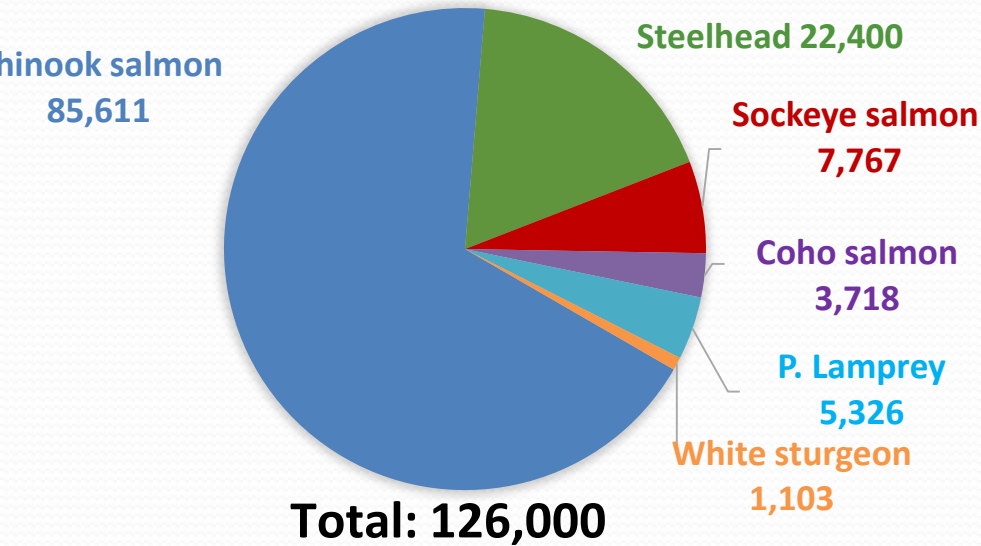


Hess and Narum 2016,  
 ICES Journal of Marine Science

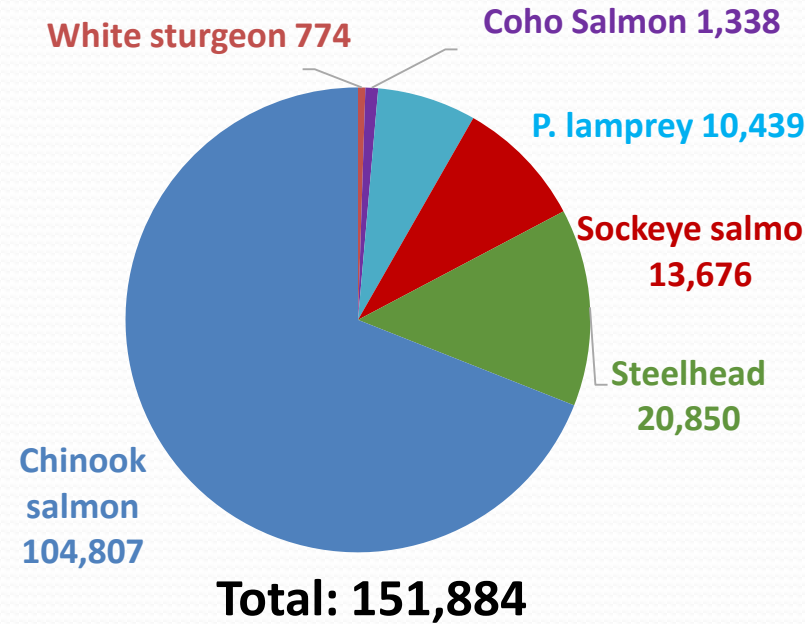
# Requires High Genotyping Capacity

CRITFC – Hagerman Genetics Lab

2016

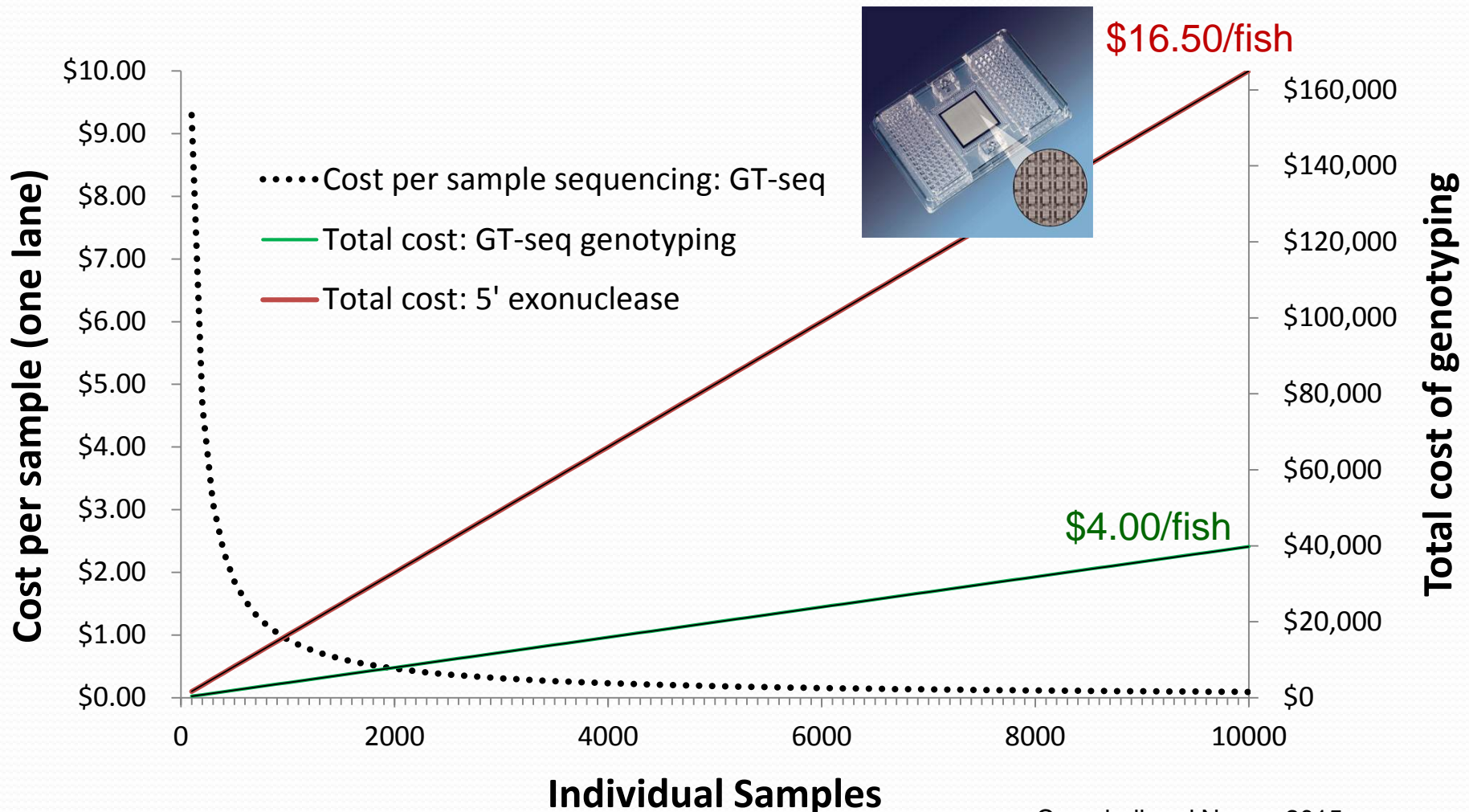


2017



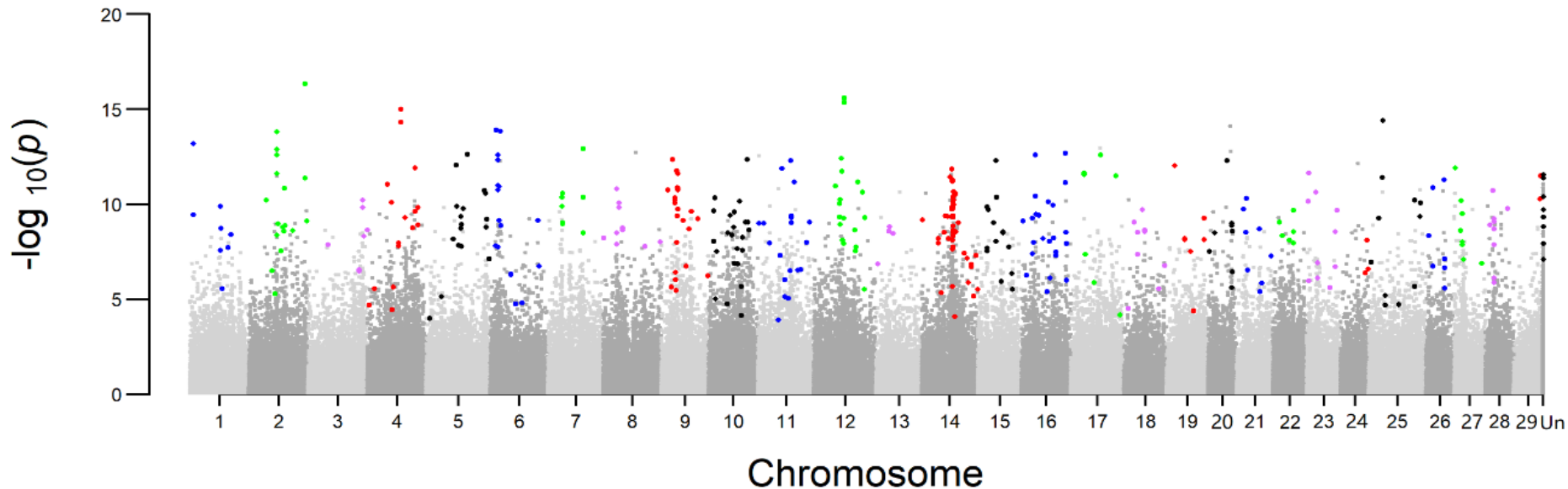
# Improved Cost Efficiency

## GT-seq – Genotyping-in-thousands by sequencing



# Advances in Genomic Methods

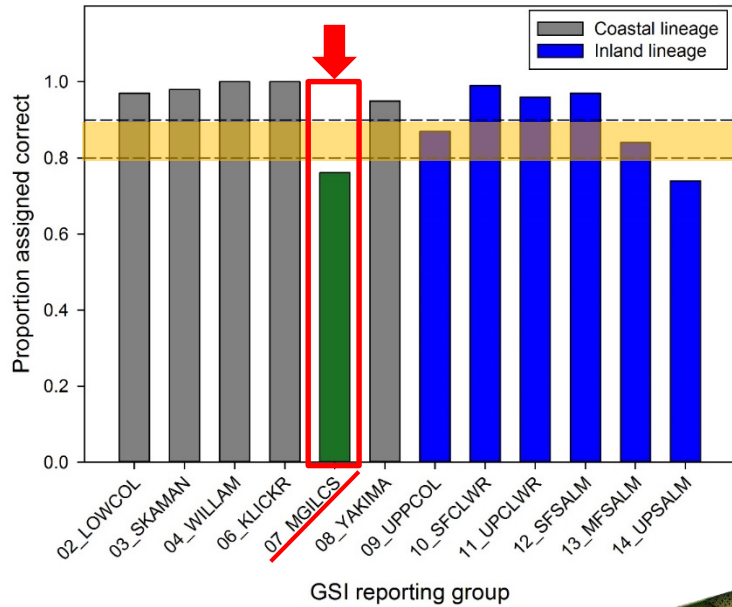
## Highly Informative Regions of the Genome - Outliers



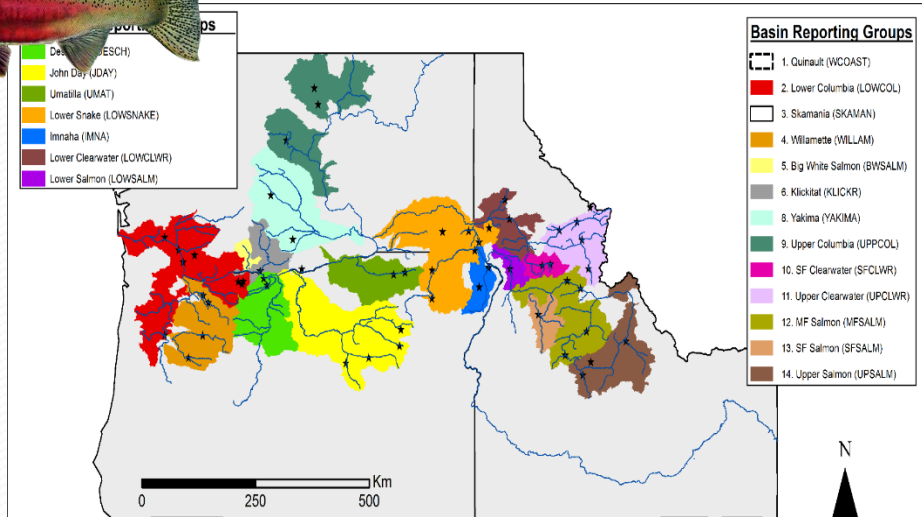
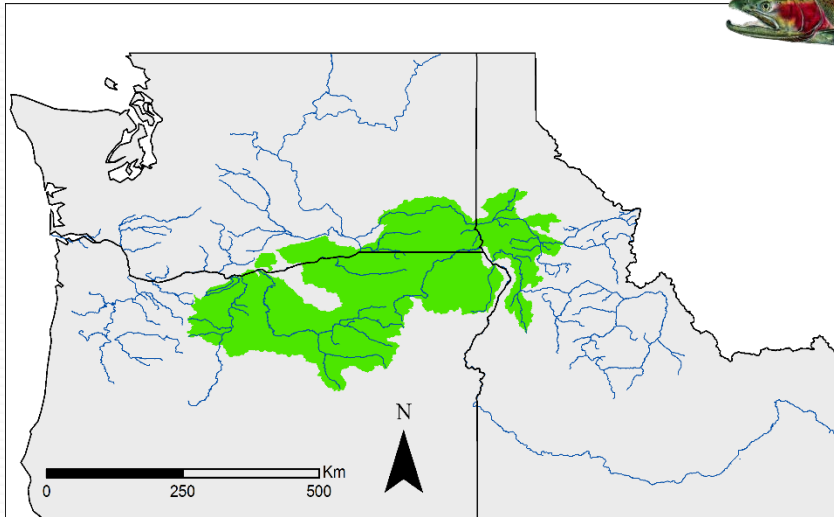
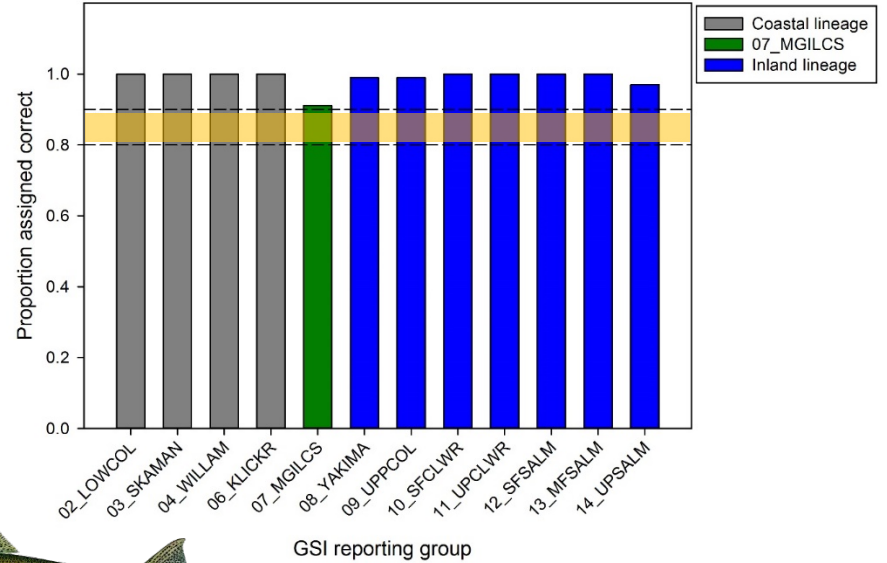
Chen et al. Narum (2018)

# Accuracy of Steelhead GSI

## Difficult stocks to resolve



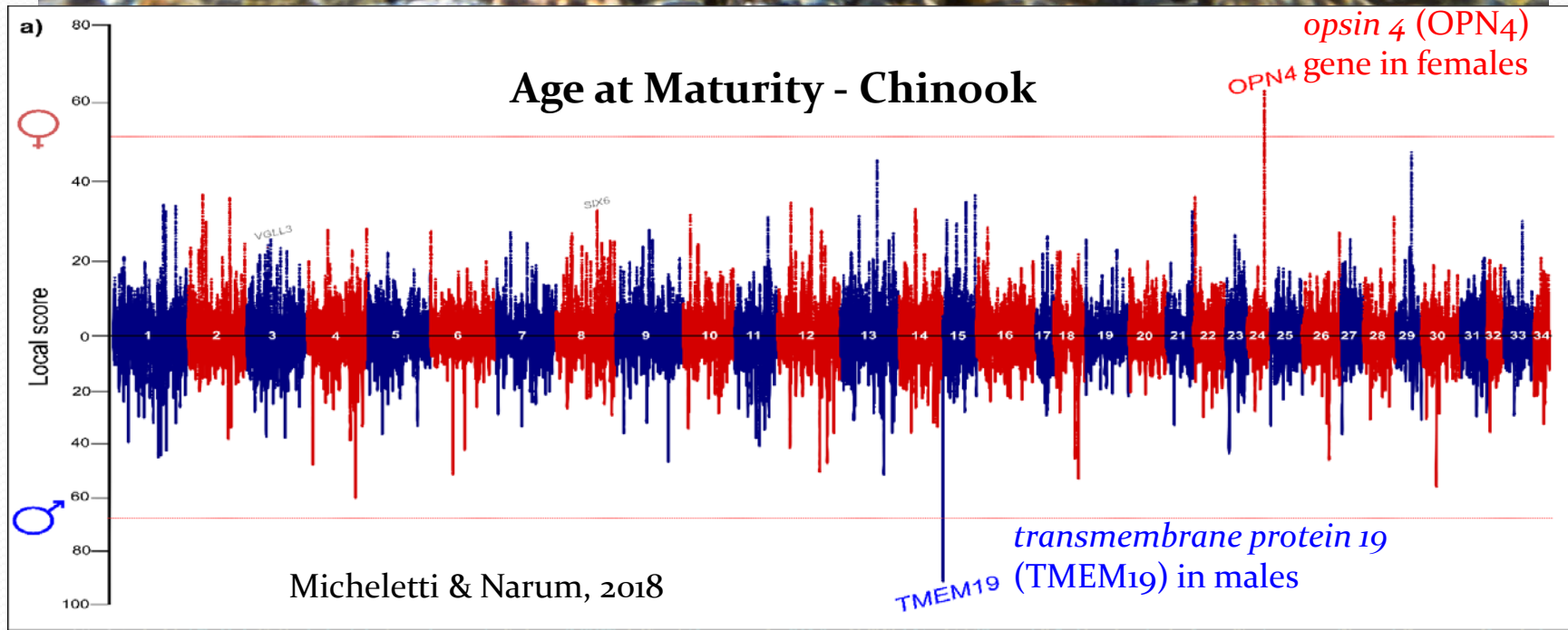
## Additional outliers improve accuracy





# Genomic Basis for Phenotypic Traits

## “Genes That Matter”



# Long-term Monitoring of Genetic Diversity in the Columbia River Basin

## Genetic Monitoring

Distinct *stocks*

+

“*Genes that matter*”

Powerful approach to monitor distinct *stocks* and phenotypic *traits* in salmonids

Questions?

