

# Evaluating the effectiveness of managed gene flow to reduce adaptation to captivity in supportive breeding programs



Charlie Waters<sup>1</sup>, Marine Briec<sup>1</sup>, Curtis Knudsen<sup>2</sup>, Dave Fast<sup>3</sup>, Jeff Hard<sup>4</sup>,  
Ken Warheit<sup>5</sup>, and Kerry Naish<sup>1</sup>

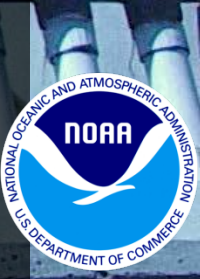
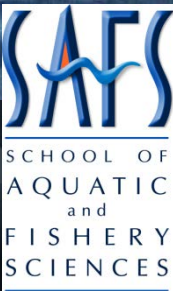
<sup>1</sup>School of Aquatic and Fishery Sciences, University of Washington

<sup>2</sup>Oncorh Consulting

<sup>3</sup>Yakama Nation

<sup>4</sup>NOAA Northwest Fisheries Science Center

<sup>5</sup>Washington Department of Fish and Wildlife



# Risk: Domestication

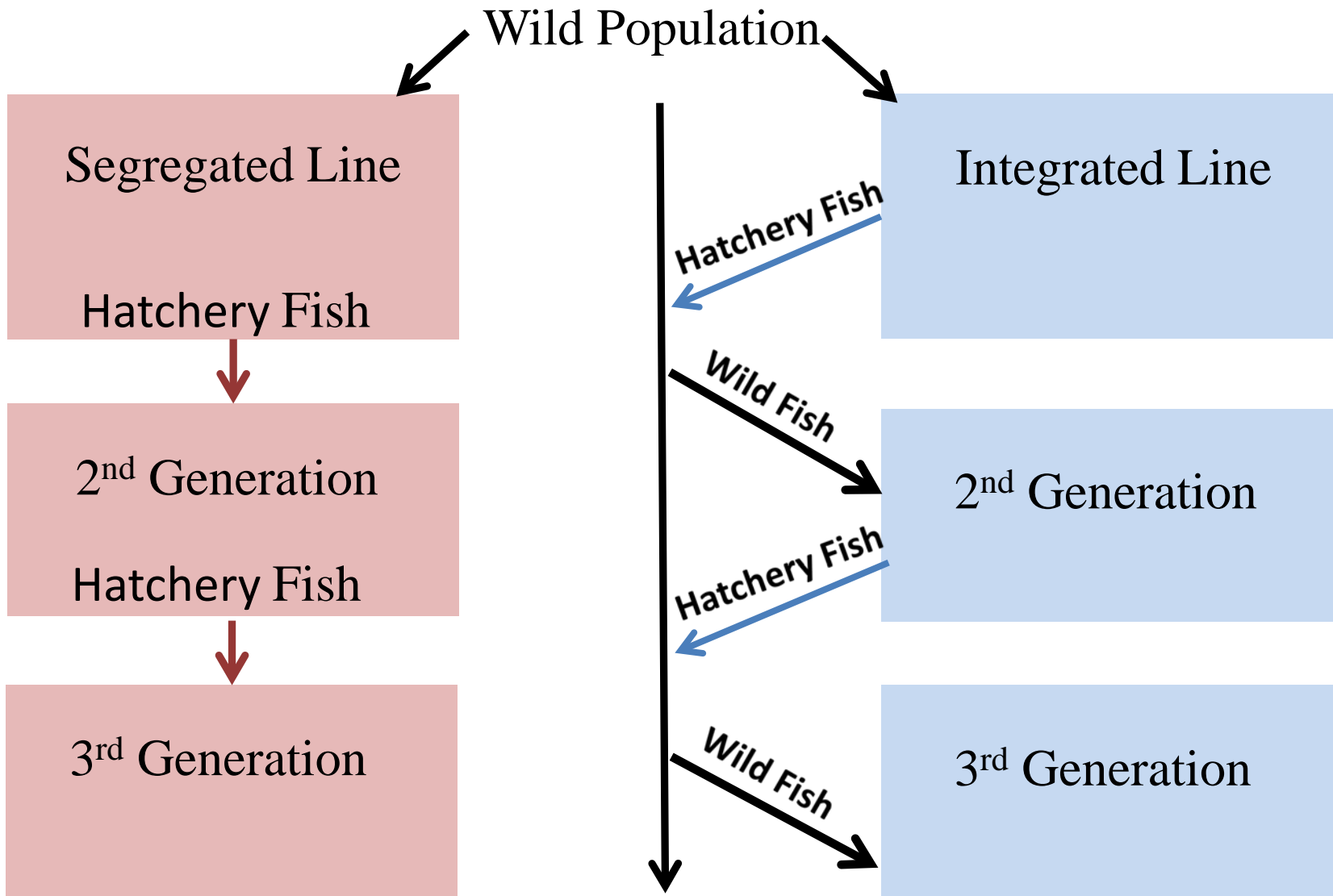
- Captive conditions are different from the natural environment
- Selection imposed by captive environment
- Relaxation of natural selective pressures
- Reduce fitness in wild and thus entire population through interbreeding



# Segregated

vs.

# Integrated



Has managed gene flow reduced divergence from founder population?

# Aim and Objectives

**Aim:** To evaluate the degree of genetic change in integrated and segregated hatchery lines when compared to the wild population

## **Objectives:**

1. Compare multiple generations of segregated and integrated hatchery lines to the wild founders at thousands of molecular markers and identify differences between the lines
2. Quantify the rate at which divergence can occur
3. Determine if integration is an effective management practice

# Cle Elum Supplementation and Research Facility

- Model system – Started Chinook salmon hatchery line in 1997; segregated and integrated hatchery lines diverged in 2002
- Collect DNA and phenotypic data from every fish
- Ideal for tracking genetic changes over time



Photo: [www.nwcouncil.org](http://www.nwcouncil.org)

# Experimental Approach

- Collected tissue samples

## Segregated Line

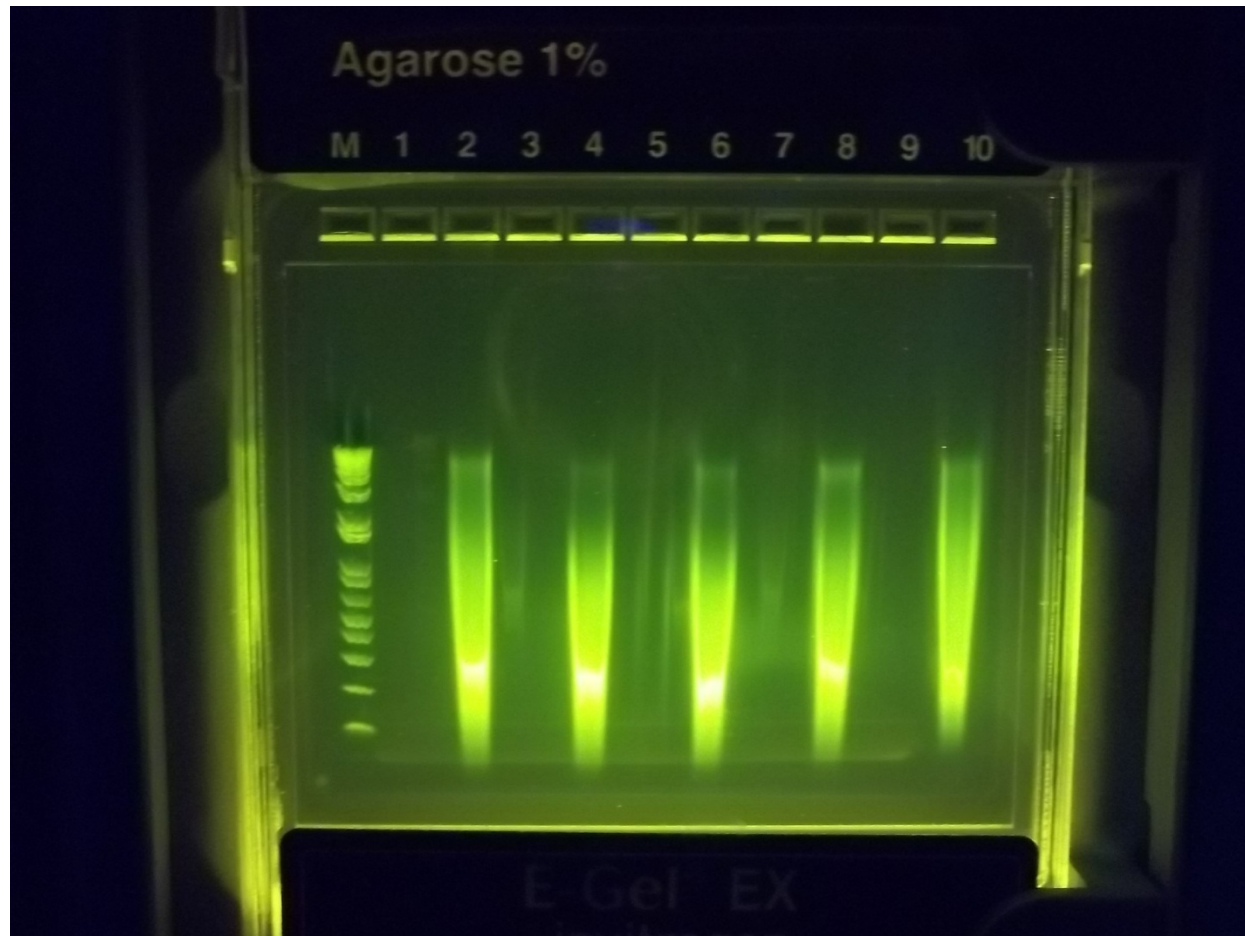
<b>1998</b>	1999	2000	2001	<b>2002</b>	2003	2004	2005	<b>2006</b>	2007	2008	2009	<b>2010</b>
P <sub>1</sub> -wild founders N=74				F <sub>0</sub> adults-1 <sup>st</sup> gen hatchery N=58				F <sub>1</sub> adults-2 <sup>nd</sup> gen hatchery N=65				F <sub>2</sub> adults-3 <sup>rd</sup> gen hatchery N=75

## Integrated Line

<b>2002</b>	2003	2004	2005	<b>2006</b>	2007	2008	2009	<b>2010</b>
F <sub>0</sub> adults-wild founders (no hatchery influence) N=71				F <sub>1</sub> adults-natural origin (possible hatchery influence) N=89				F <sub>2</sub> adults-natural origin (possible hatchery influence) N=92

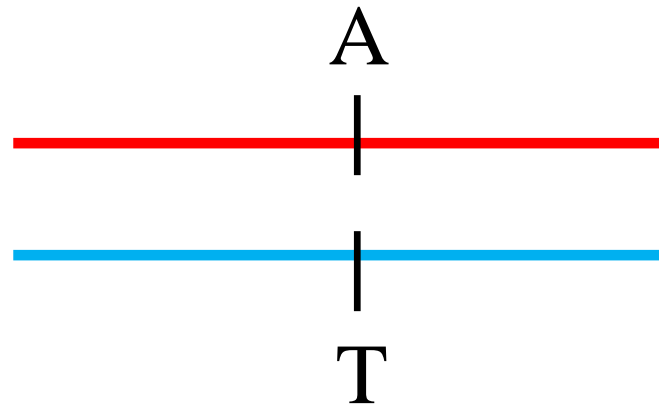
# Experimental Approach

- Sequenced hundreds of thousands DNA fragments per individual using restriction site-associated (RAD) sequencing



# Experimental Approach

- Identified loci with single nucleotide polymorphisms (SNPs) for comparisons



Number of loci = 2,803 that are mapped to genome  
= 1,774 that are not mapped



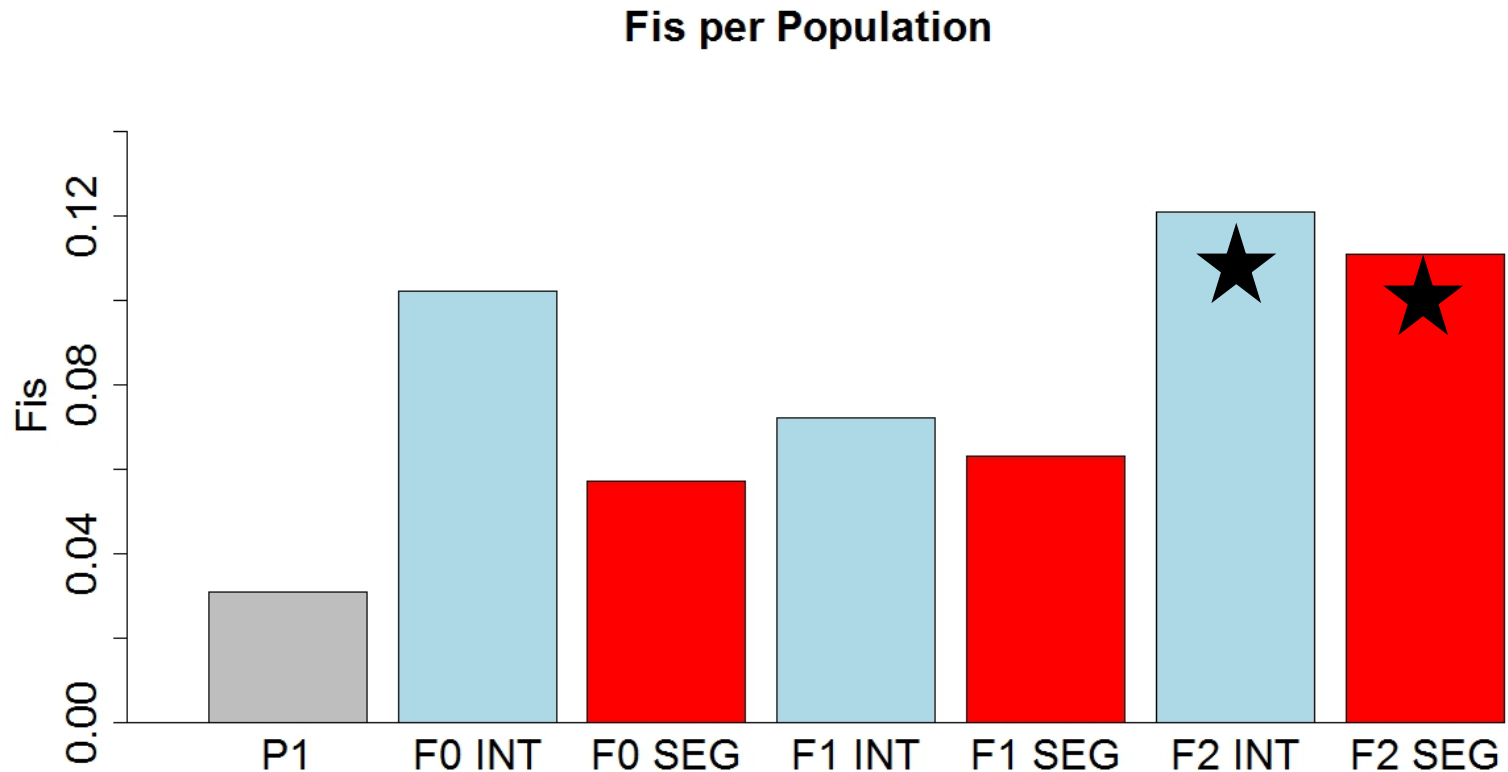
# Individuals with more than 2 million sequences

<b>Population</b>	<b>N</b>	<b>Avg. Proportion of Loci Scored per Individual</b>
1998 founders ( $P_1$ )	20	0.90
2002 wild adults ( $F_0$ INT)	13	0.90
2002 marked adults ( $F_0$ SEG)	12	0.94
2006 natural adults ( $F_1$ INT)	41	0.92
2006 marked adults ( $F_1$ SEG)	27	0.91
2010 natural adults ( $F_2$ INT)	57	0.92
2010 marked adults ( $F_2$ SEG)	43	0.91

# Level of Inbreeding

$F_{IS}$  is a common measure of inbreeding

- Higher values indicate reduced heterozygosity

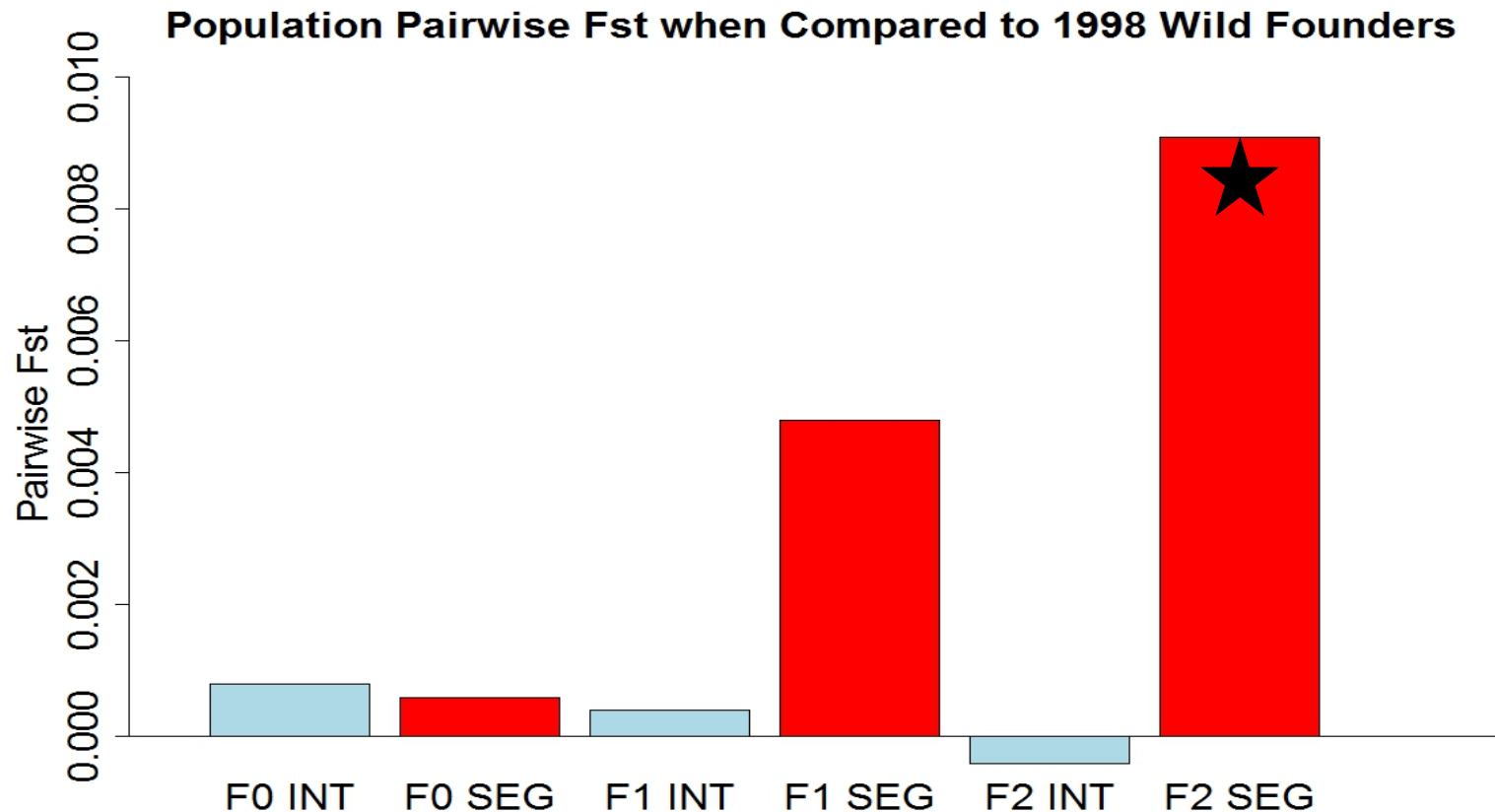


Increased level of inbreeding over time for both hatchery lines

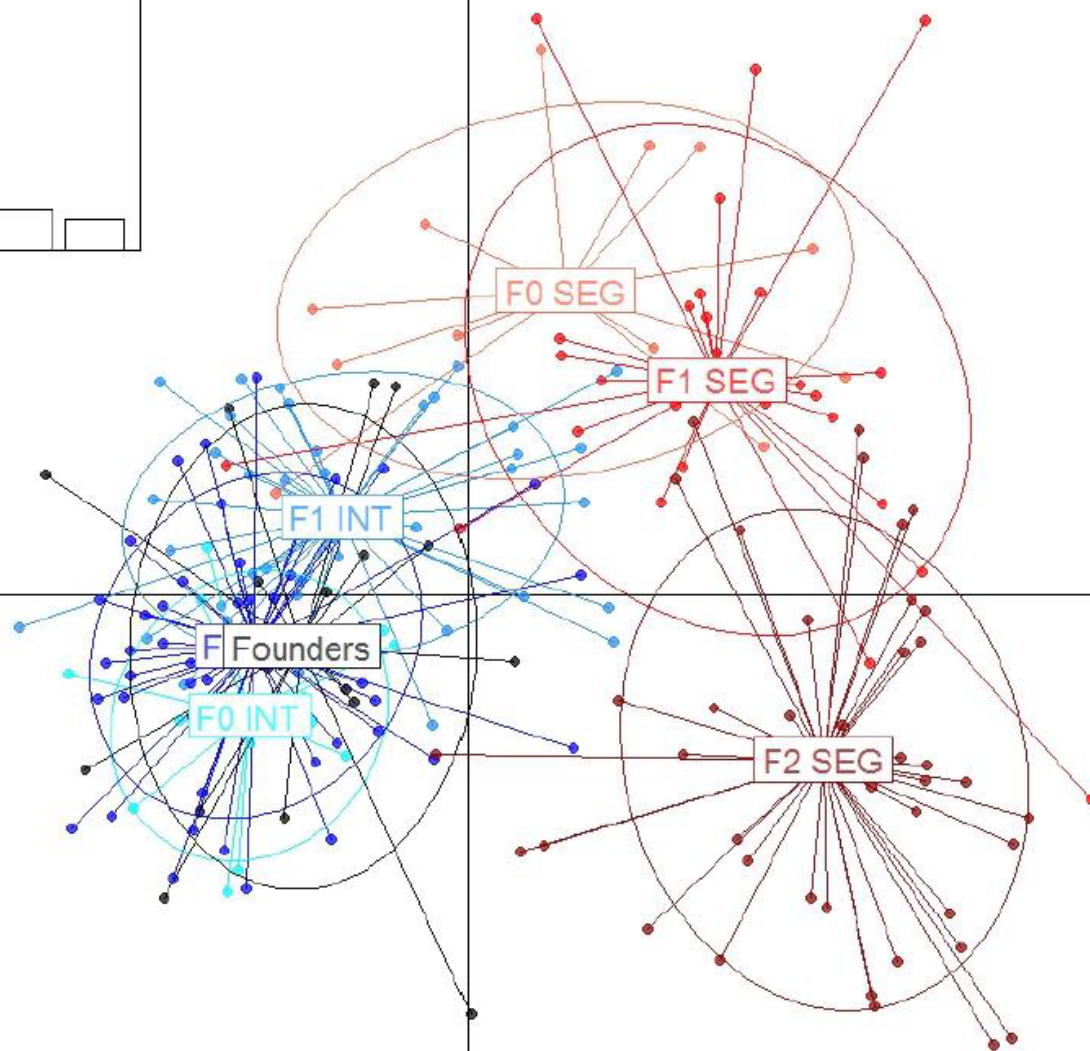
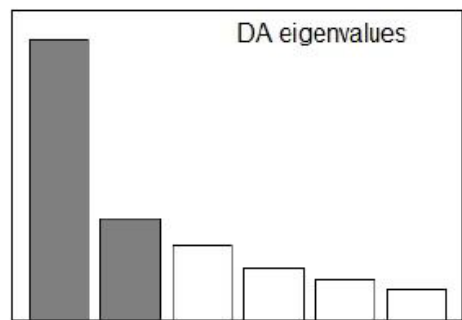
# Genetic Differentiation

$F_{st}$  is a common measure of genetic differentiation

- Higher  $F_{st}$  means more differentiation
- $F_{st}$  of 0.05-0.1 common among salmon populations

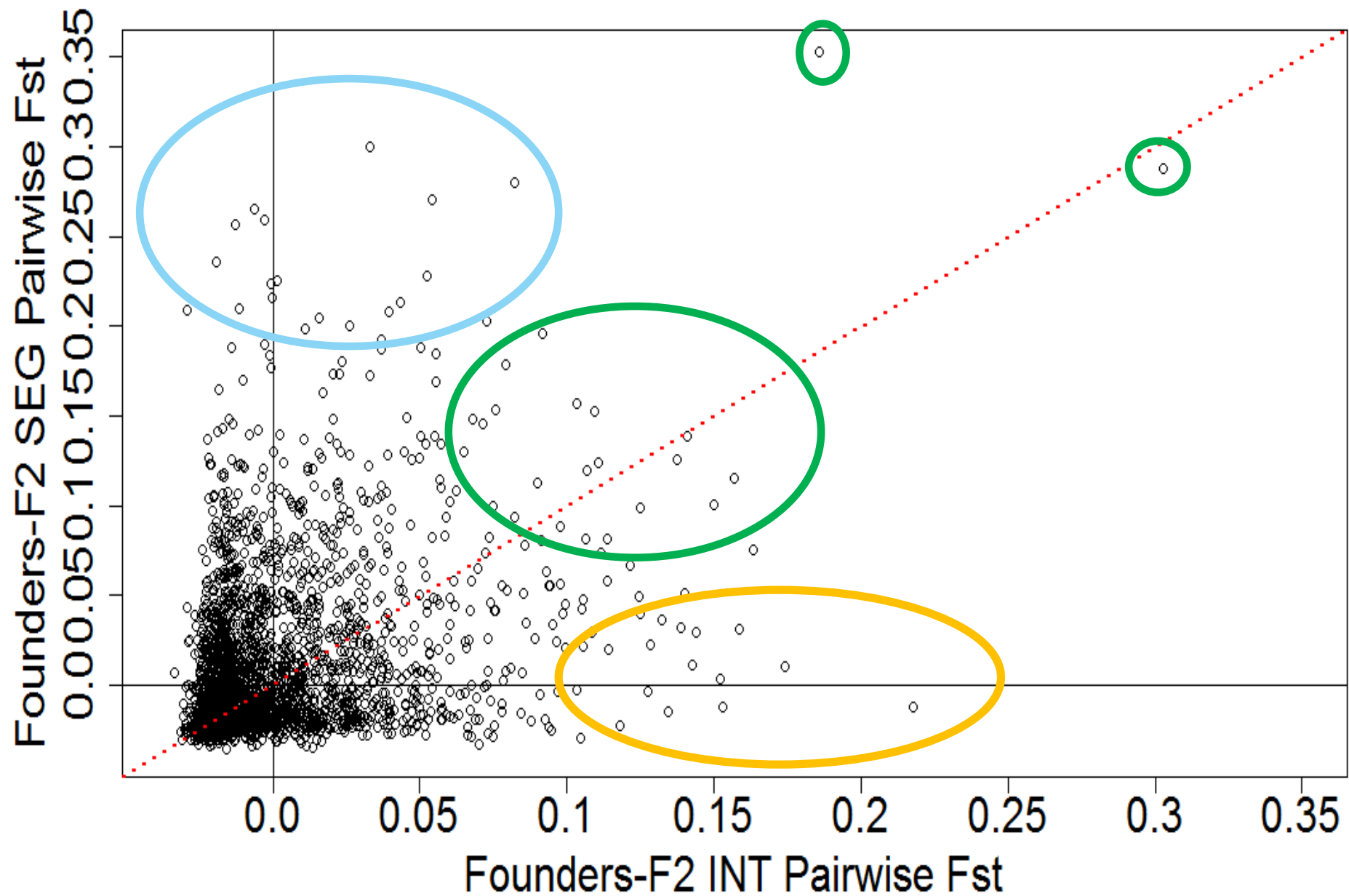


DAPC 2 (17.4%)



DAPC 1 (48.4%)

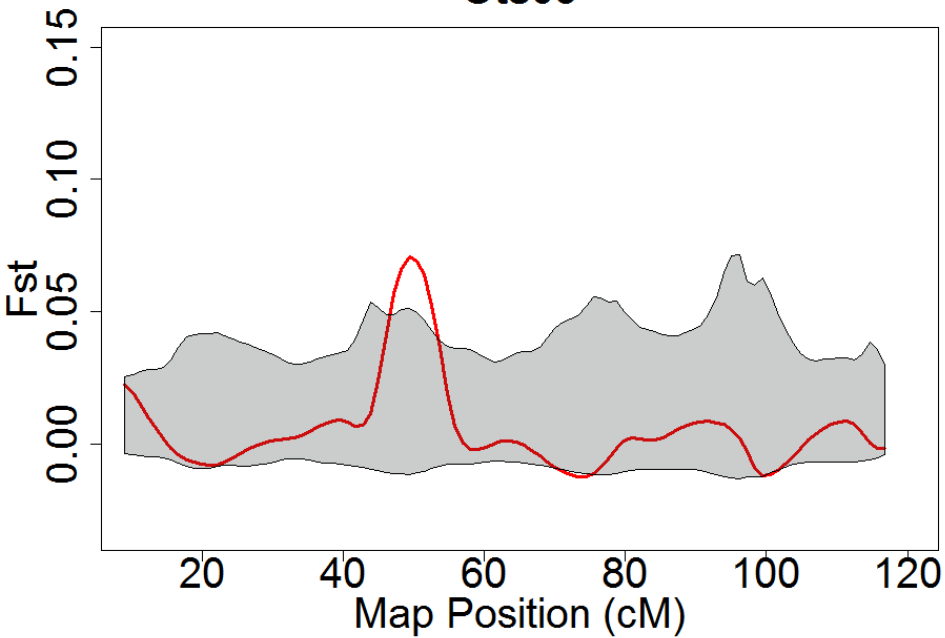
# Pairwise Fst Comparison of F2 Hatchery Lines with 1998 Founders



# Sliding Window Analysis

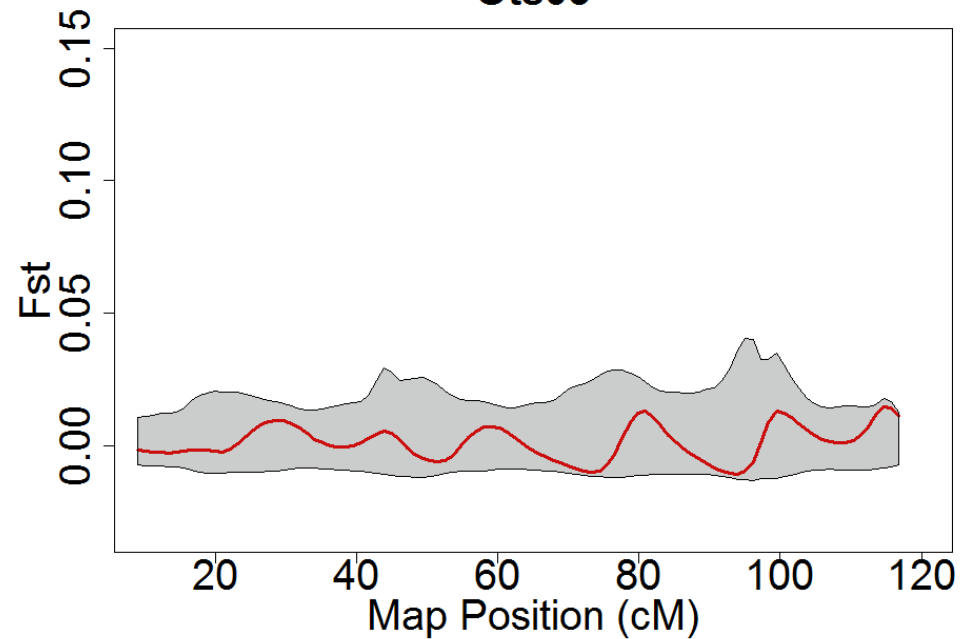
$F_2$  SEG

Ots05



$F_2$  INT

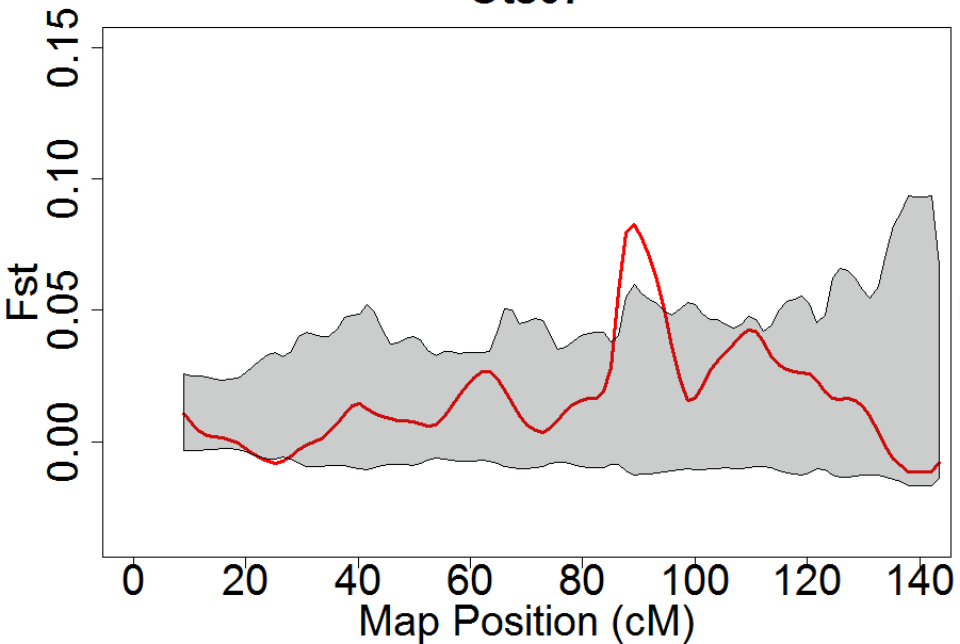
Ots05



# Sliding Window Analysis

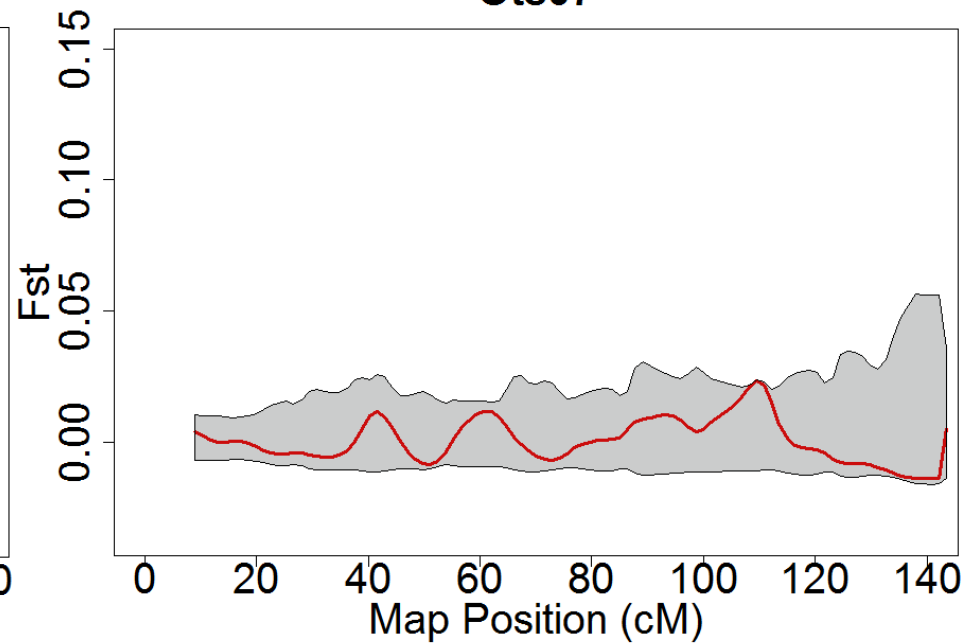
$F_2$  SEG

Ots07



$F_2$  INT

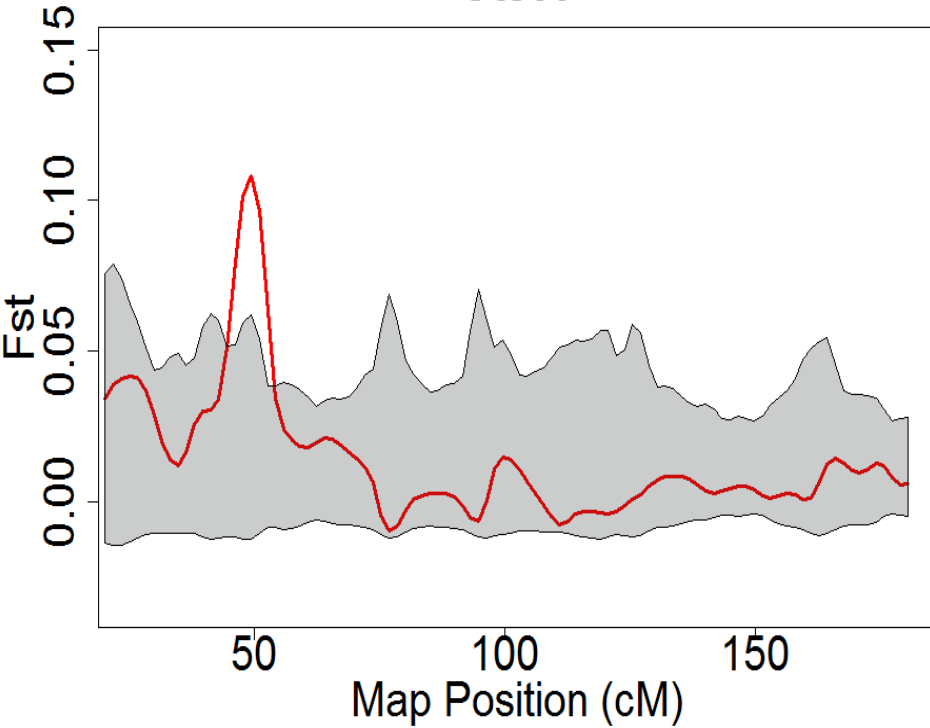
Ots07



# Sliding Window Analysis

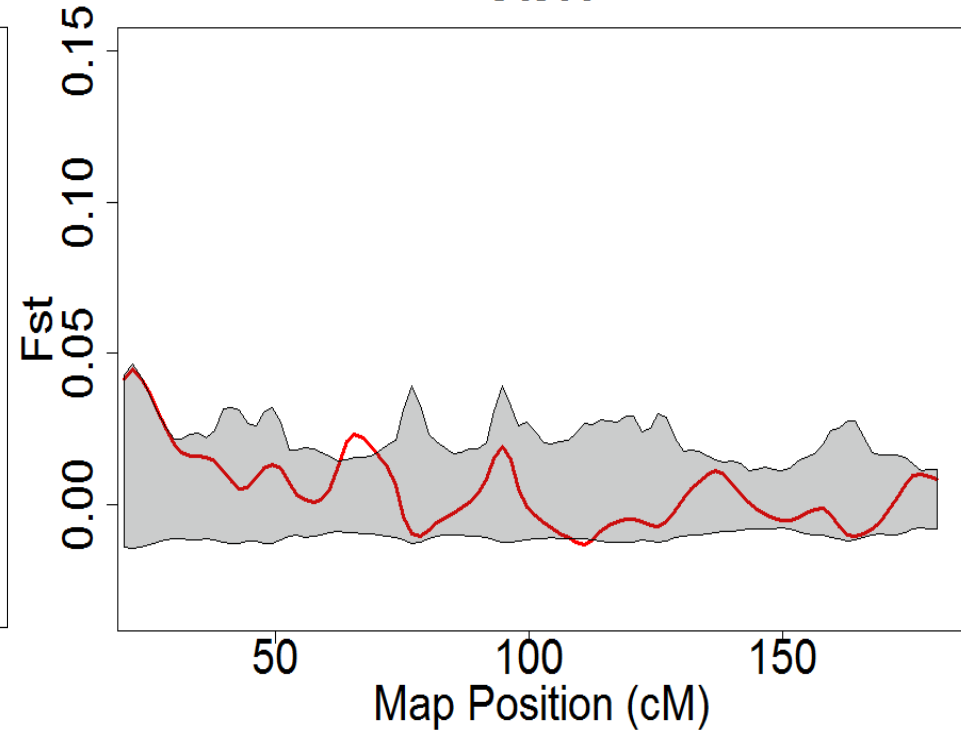
$F_2$  SEG

Ots09



$F_2$  INT

Ots09

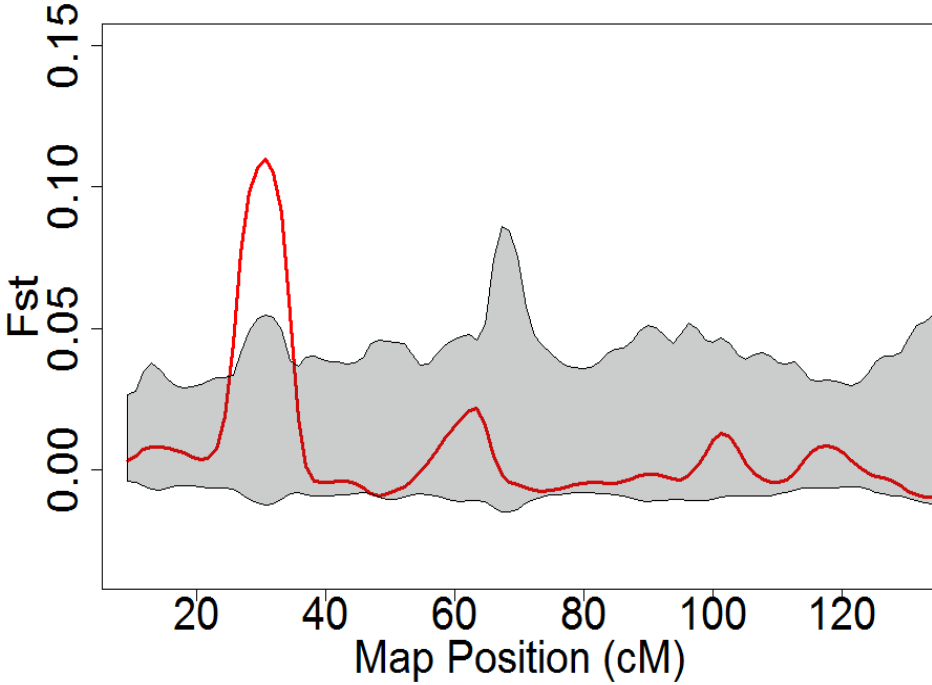




# Sliding Window Analysis

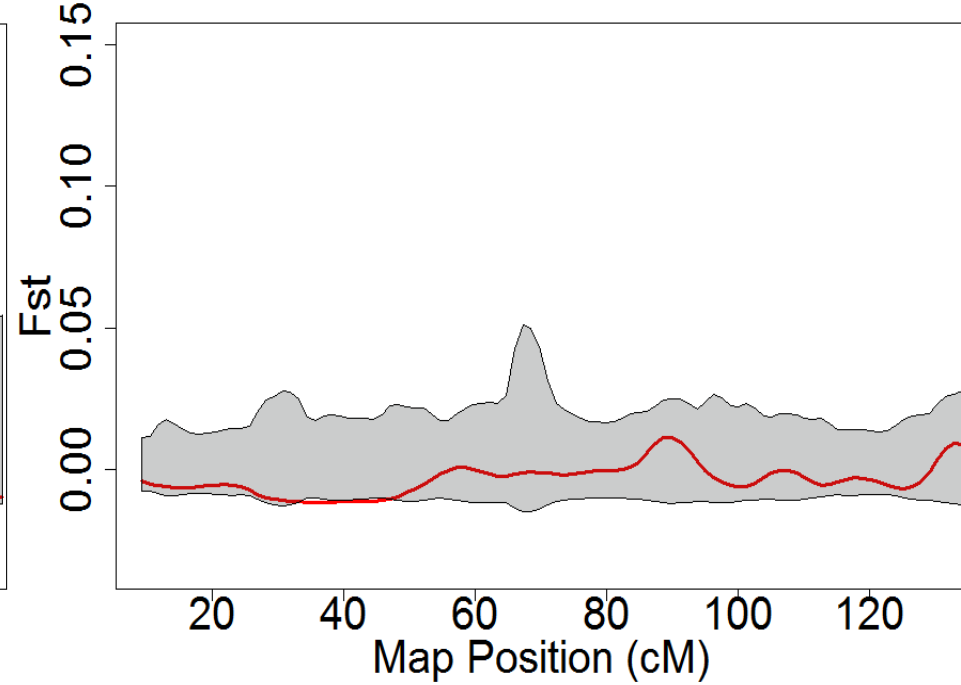
$F_2$  SEG

Ots12



$F_2$  INT

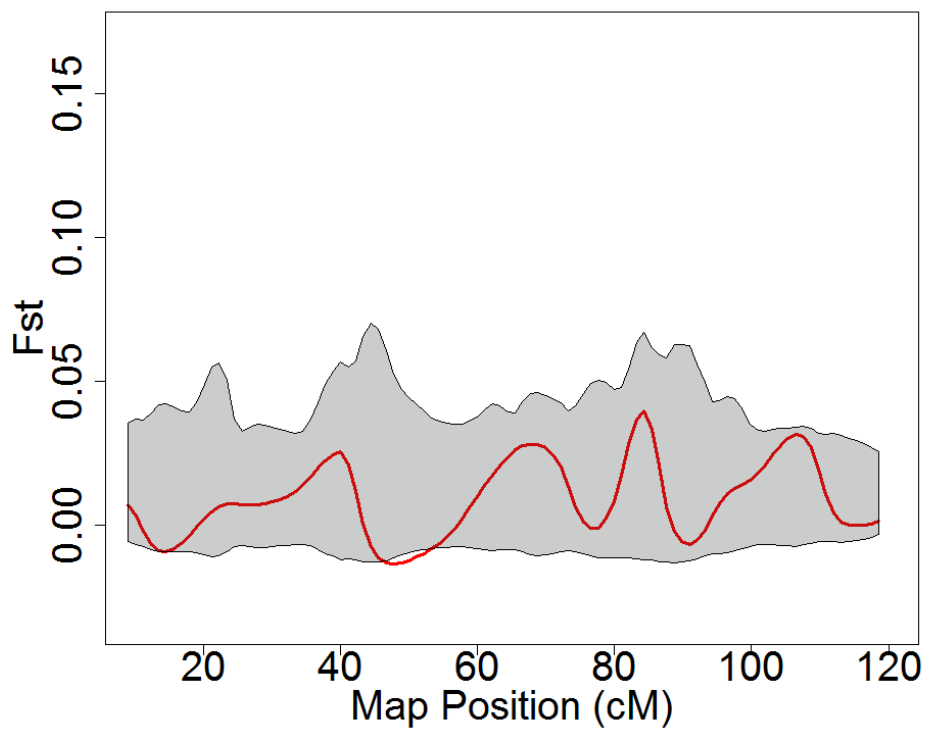
Ots12



# Sliding Window Analysis

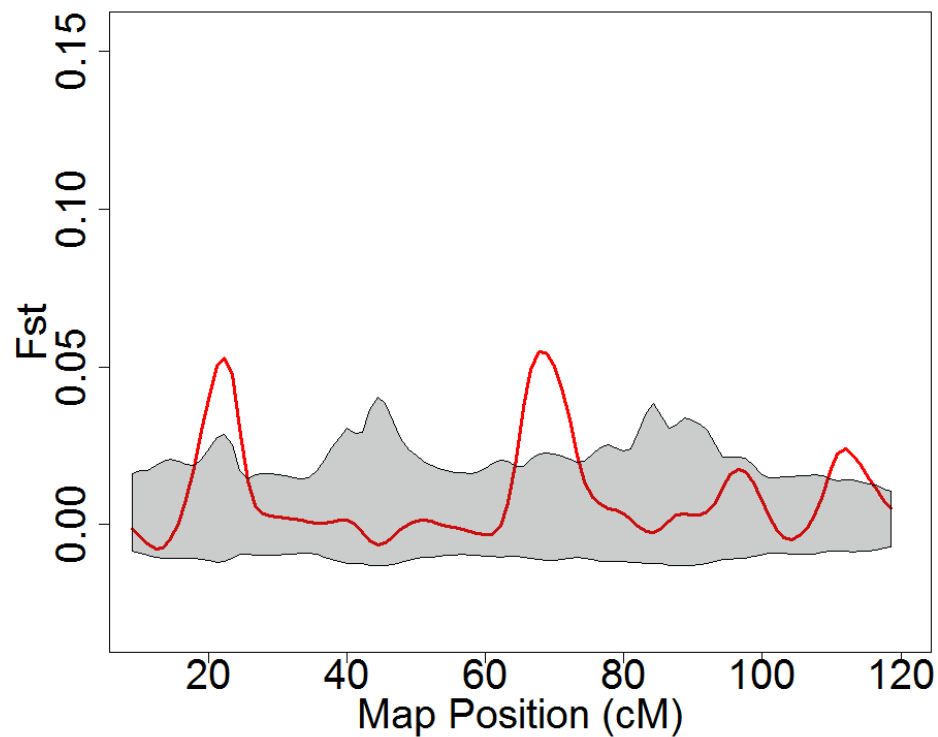
$F_2$  SEG

Ots16



$F_2$  INT

Ots16



# Summary

- Analyzed three generations of integrated and segregated hatchery lines and compared to founding wild population
- Increased level of inbreeding in both hatchery lines over time
- Segregated line is slowly diverging over time
- Low differentiation ( $F_{st}$ ) in all population pairwise comparisons
- Identified candidate loci and regions for further tests of selection
- Managed gene flow seems to be effective at reducing divergence

# Next Steps

- Sequence more individuals from each population
- Identify regions of genome responding to selection
- Estimate effective population size and level of inbreeding within each hatchery line
- Link molecular markers to fitness-related traits
  - Washington Sea Grant proposal submitted
  - Analyze traits measured at CESRF using GWAS
  - Measure early development and disease resistance; link to markers using QTL mapping
  - Determine which traits have responded to selection

# Acknowledgments

Curt Knudsen, Oncorh Consulting

Bill Bosch, Yakama Nation

Dave Fast, Yakama Nation

Charlie Strom, Yakama Nation

All CESRF staff

Steve Schroder, WDFW (ret.)

Ken Warheit, WDFW

Todd Kassler, WDFW

Sewall Young, WDFW

Kerry Naish, UW

Jeff Hard, NOAA

MERlab: Marine Brieuc, Dan Drinan, Miyako Kodama, Isadora

Jimenez-Hidalgo, Katrina van Raay

Funded by Federal Biop funds “Hatchery reform”