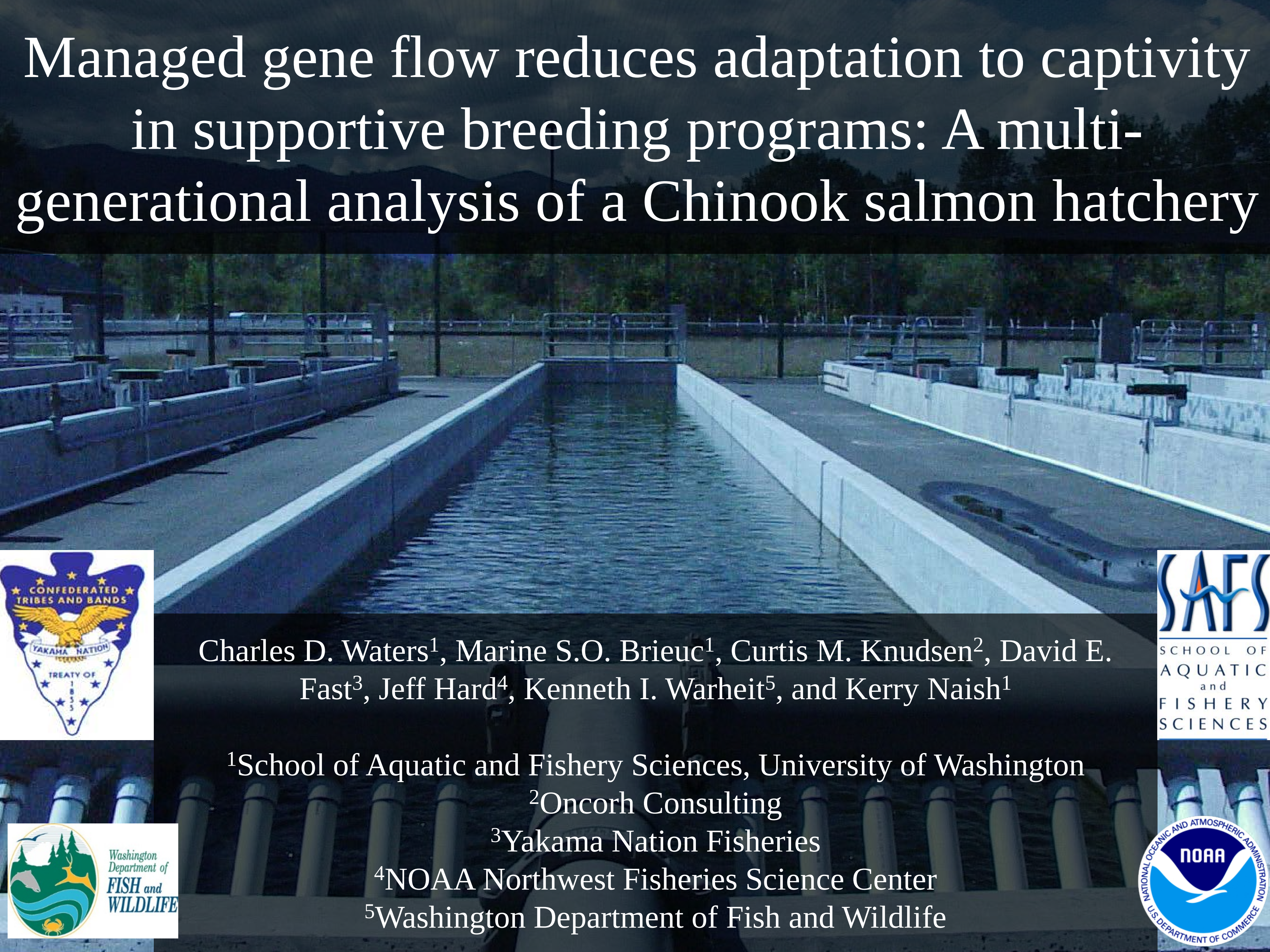

Managed gene flow reduces adaptation to captivity in supportive breeding programs: A multi-generational analysis of a Chinook salmon hatchery

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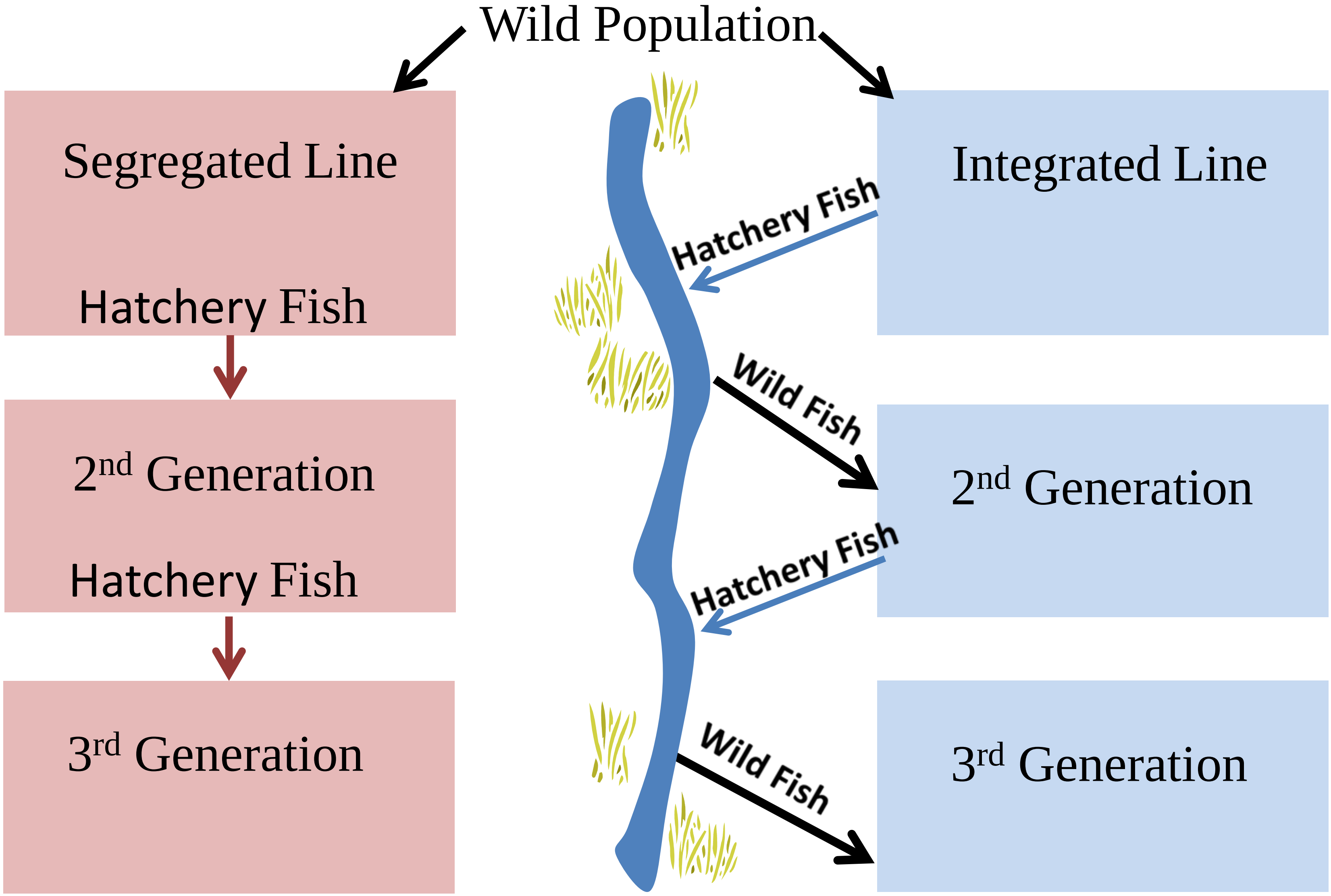
[5]Washington Department of Fish and Wildlife

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



Wild Population

Segregated Line

Hatchery Fish

2nd Generation

Hatchery Fish

3rd Generation

Integrated Line

Hatchery Fish

Wild Fish

2nd Generation

Hatchery Fish

Wild Fish

3rd Generation

Has managed gene flow reduced divergence from founder population?

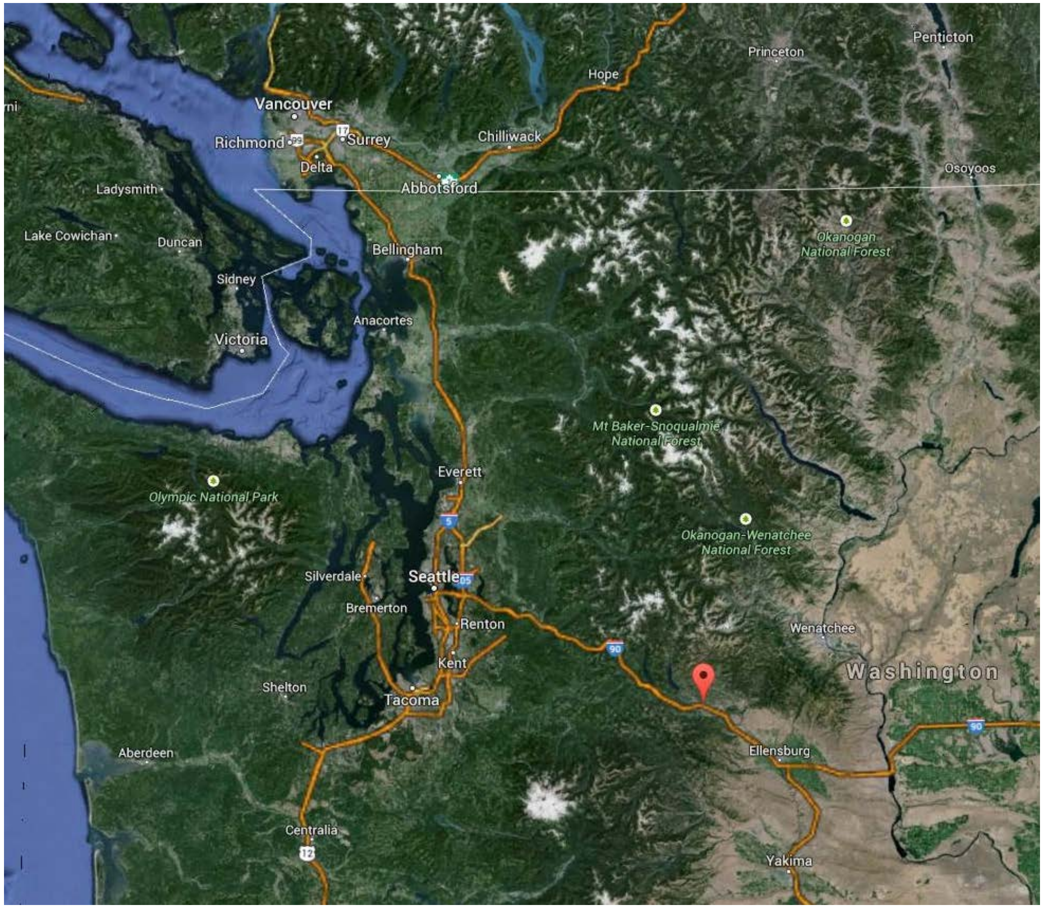
Cle Elum Supplementation and Research Facility

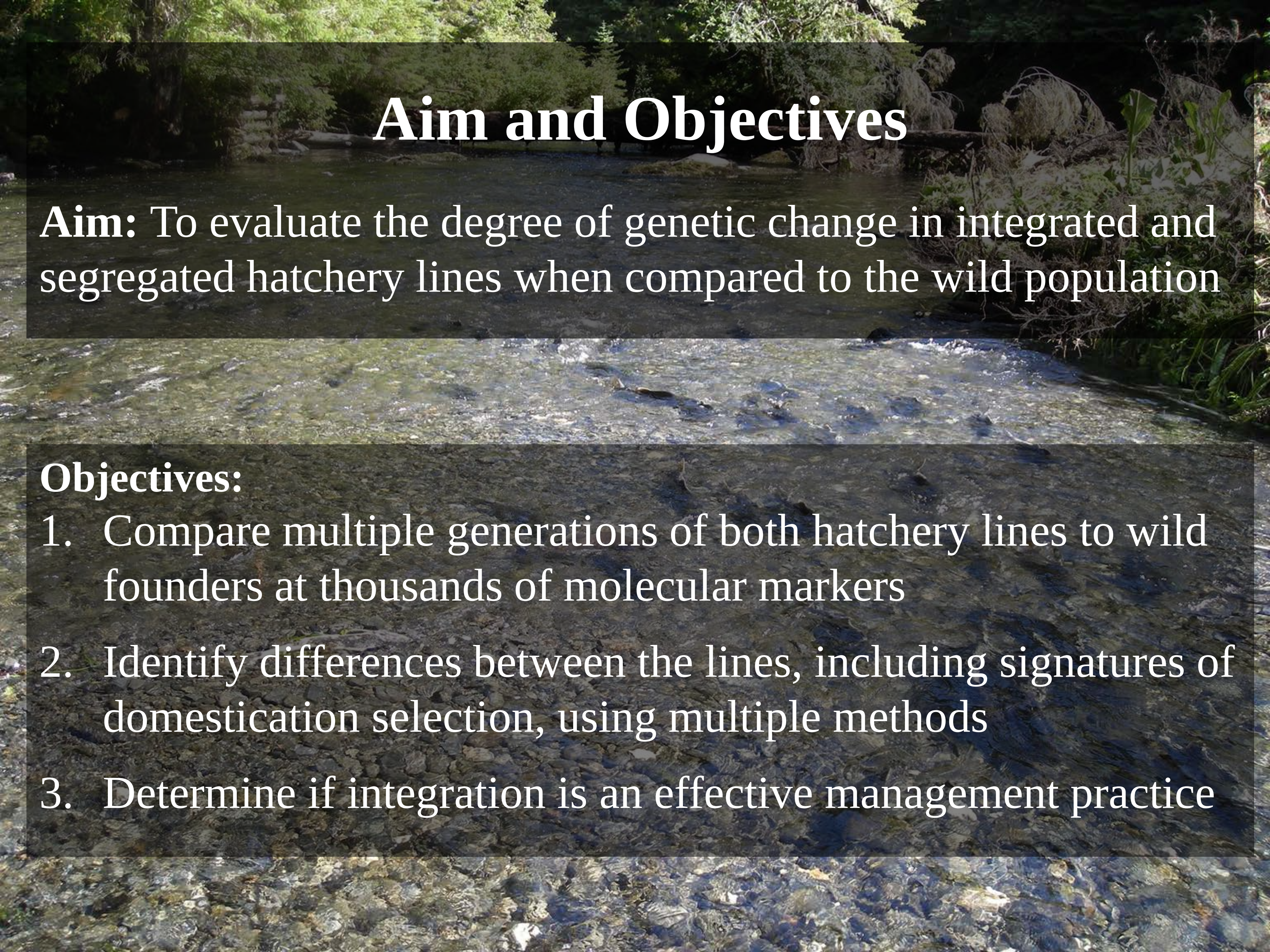
- Model system – Started Chinook salmon hatchery line in 1997; segregated and integrated hatchery lines diverged in 2002

- Collect DNA and phenotypic data from every fish

- Ideal for tracking genetic changes over time

Photo: www.nwcouncil.org





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 both hatchery lines to wild founders at thousands of molecular markers
2. Identify differences between the lines, including signatures of domestication selection, using multiple methods
3. Determine if integration is an effective management practice

Experimental Approach

- Collected tissue samples (N=642)

Segregated Line

1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010
P_1-wild founders N=116				F_0 adults-1st gen hatchery N=87				F_1 adults-2nd gen hatchery N=68				F_2 adults-3rd gen hatchery N=76

Integrated Line

2002	2003	2004	2005	2006	2007	2008	2009	2010
F_0 adults-wild founders (no hatchery influence) N=113				F_1 adults-natural origin (possible hatchery influence) N=89				F_2 adults-natural origin (possible hatchery influence) N=93

Experimental Approach

Chinook Map (Brieuc et al. 2014), 7146 markers

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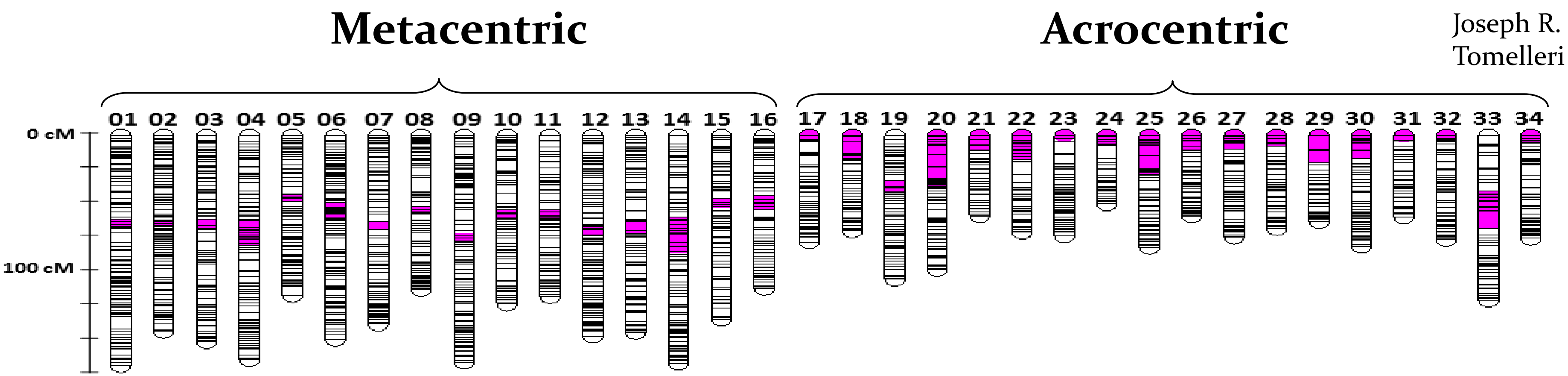
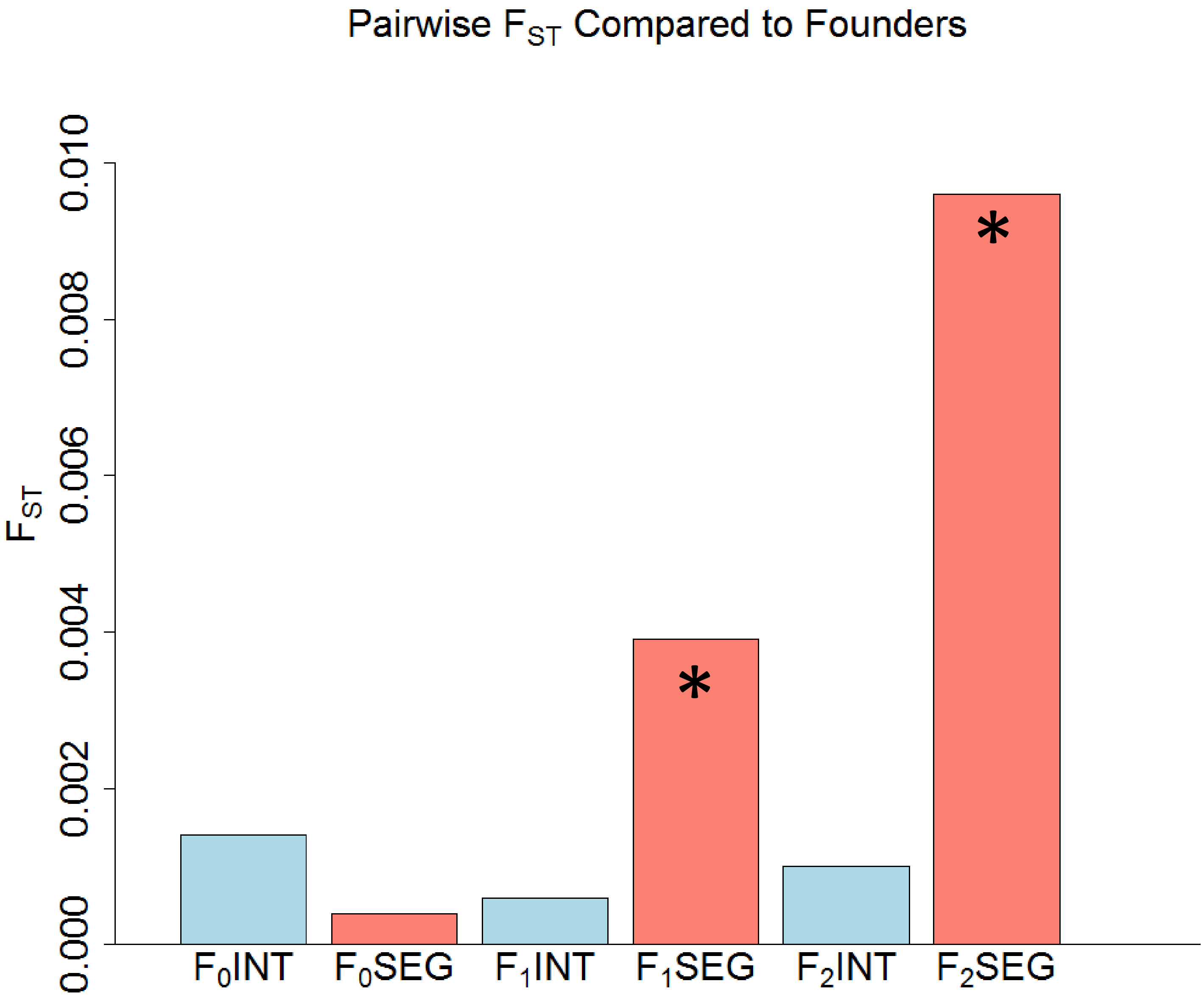


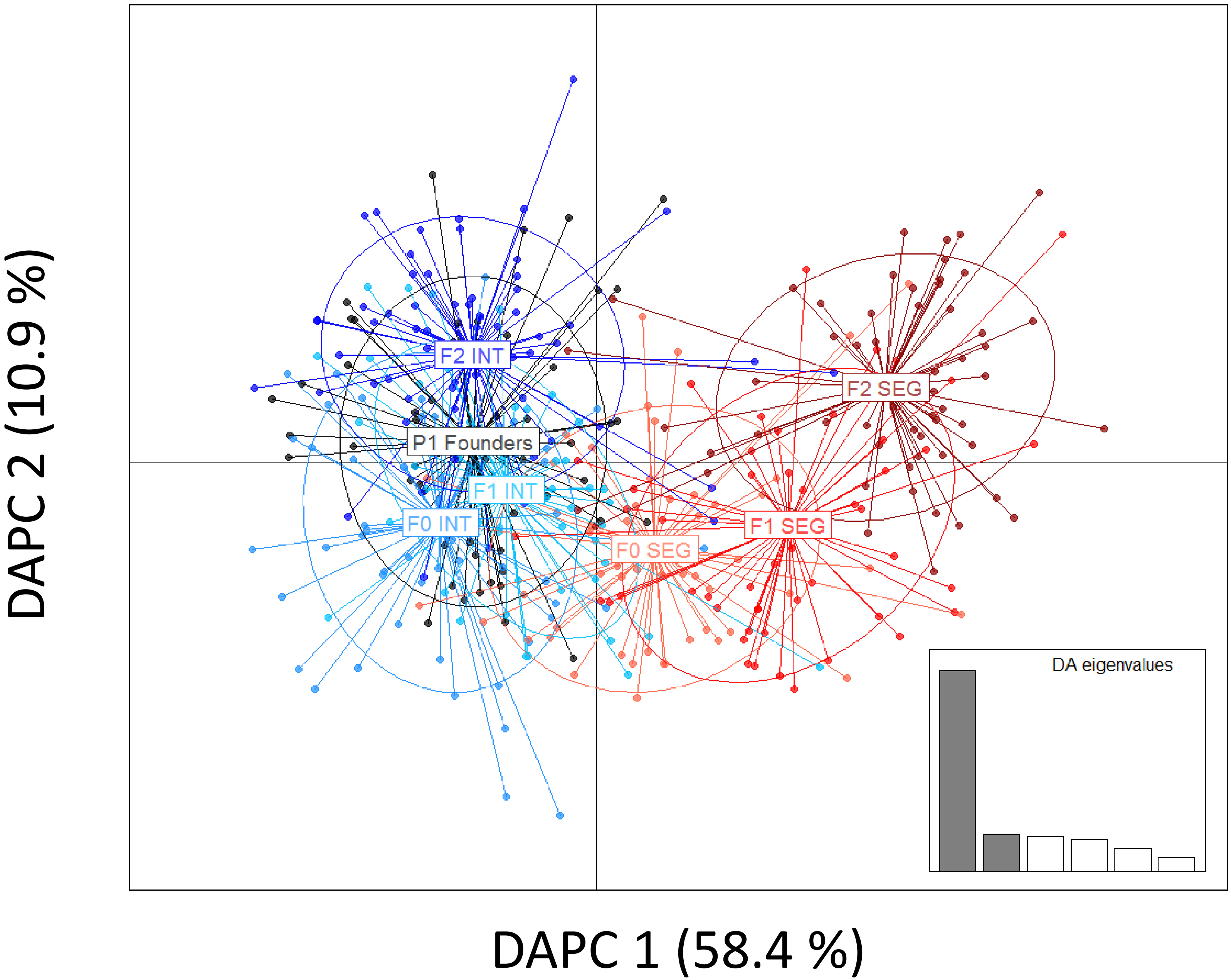
Number of loci = 9,479 RAD loci (4,405 are mapped)

Population	**N**	**Avg. Proportion of Loci Scored per Individual**
1998 founders (P_1)	60	0.85
2002 wild adults (F_0 INT)	60	0.82
2002 marked adults (F_0 SEG)	55	0.81
2006 natural adults (F_1 INT)	57	0.84
2006 marked adults (F_1 SEG)	53	0.80
2010 natural adults (F_2 INT)	69	0.86
2010 marked adults (F_2 SEG)	59	0.85

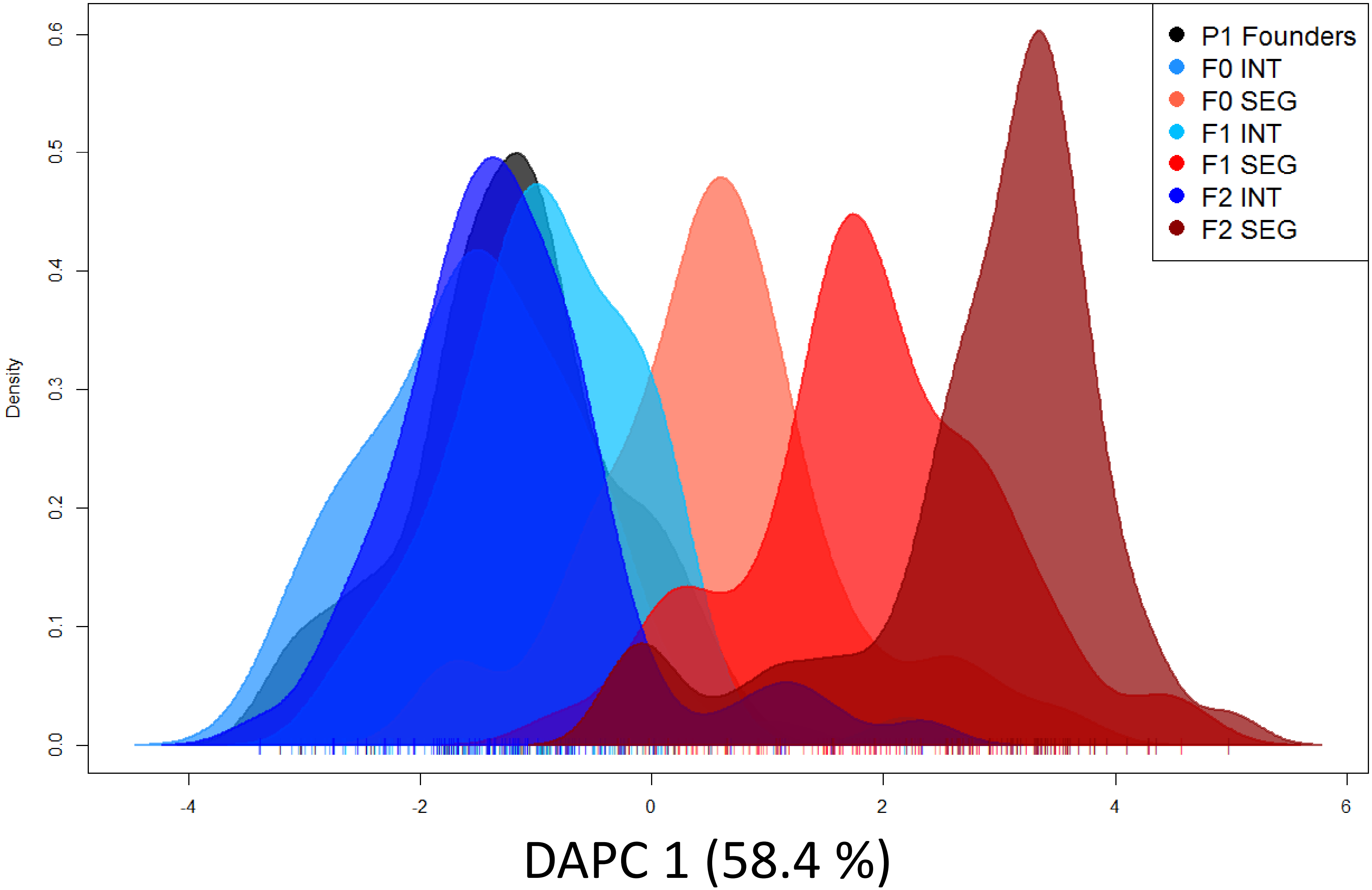


*Highly significant, test for genotypic differentiation

Discriminant Analysis of Principal Components



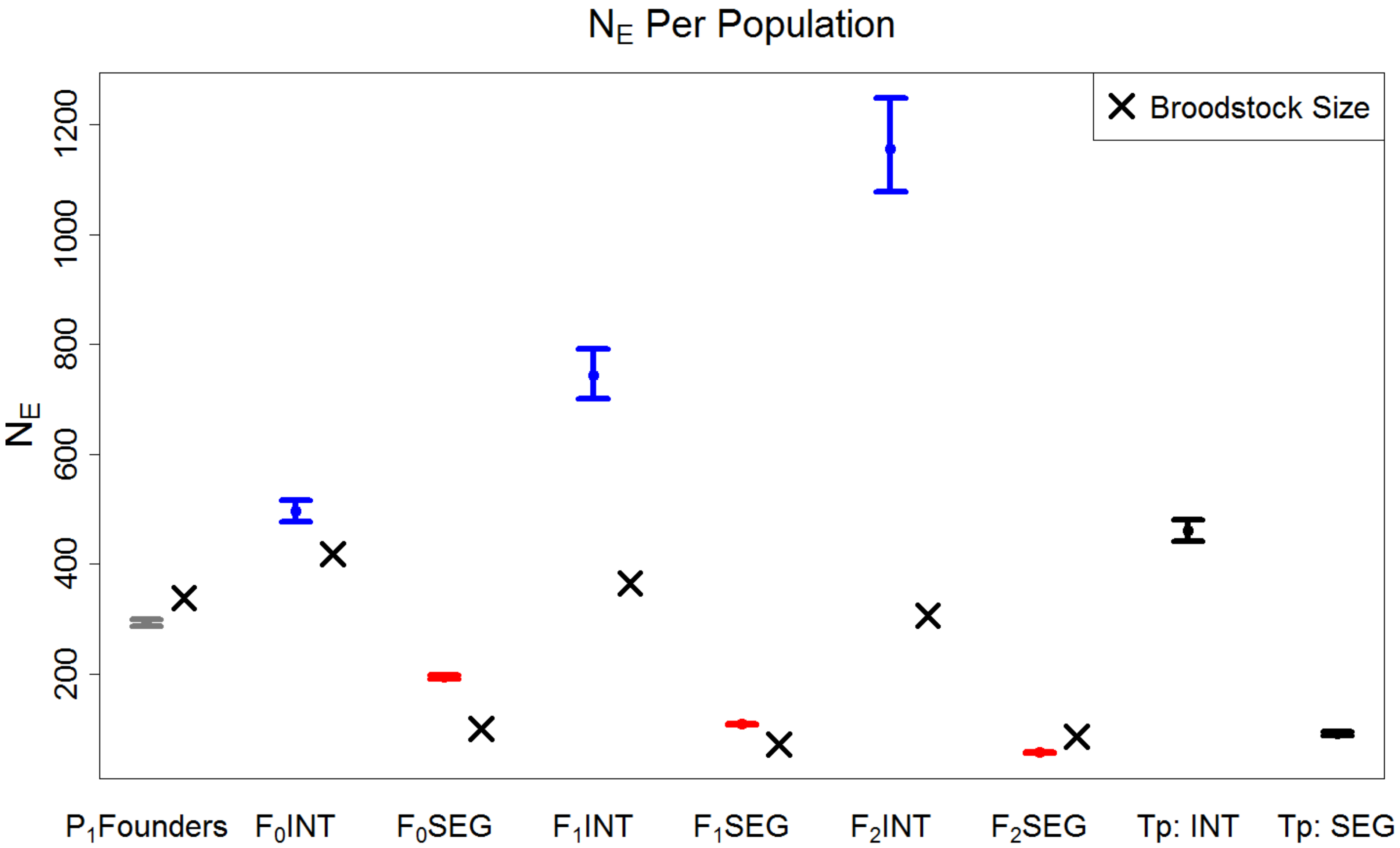
DAPC of All Individuals



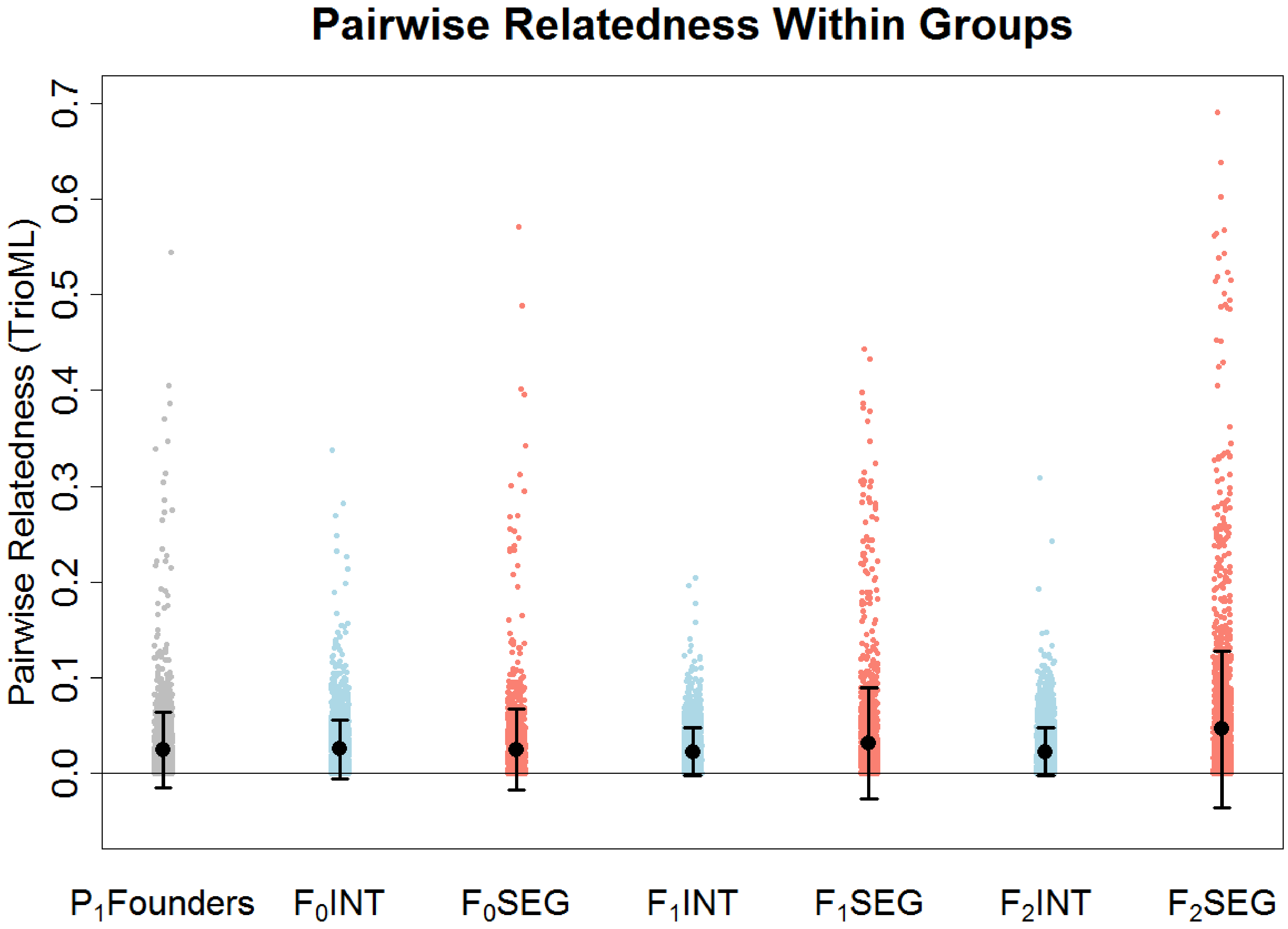
Effective Population Size

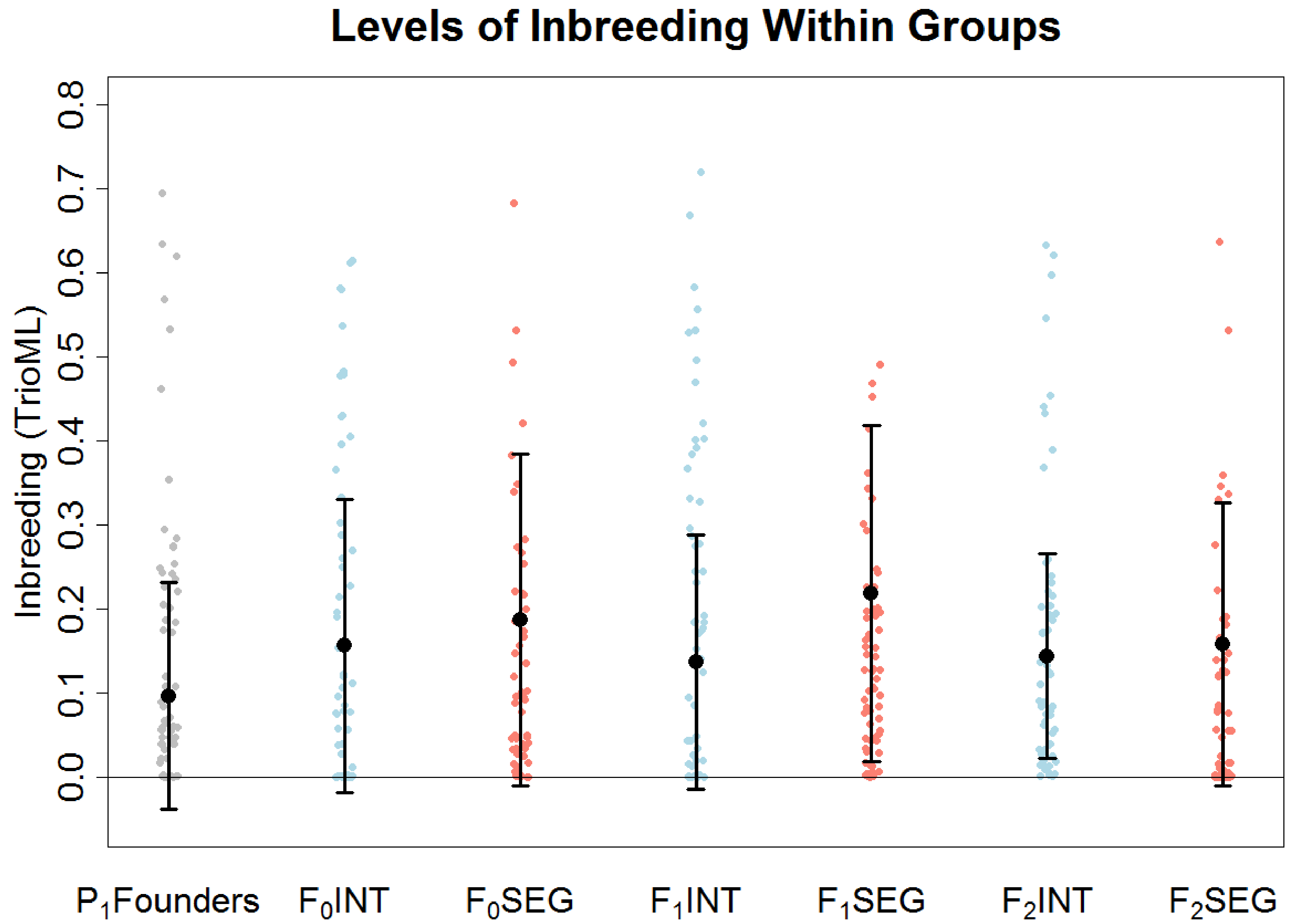
- Influences the long-term viability and adaptive potential of populations
  - Genetic drift is the dominant evolutionary process in small populations (loss of genetic variation; inbreeding)
  - Selection has a greater effect in larger populations

- Estimated effective population size using the linkage disequilibrium and temporal methods

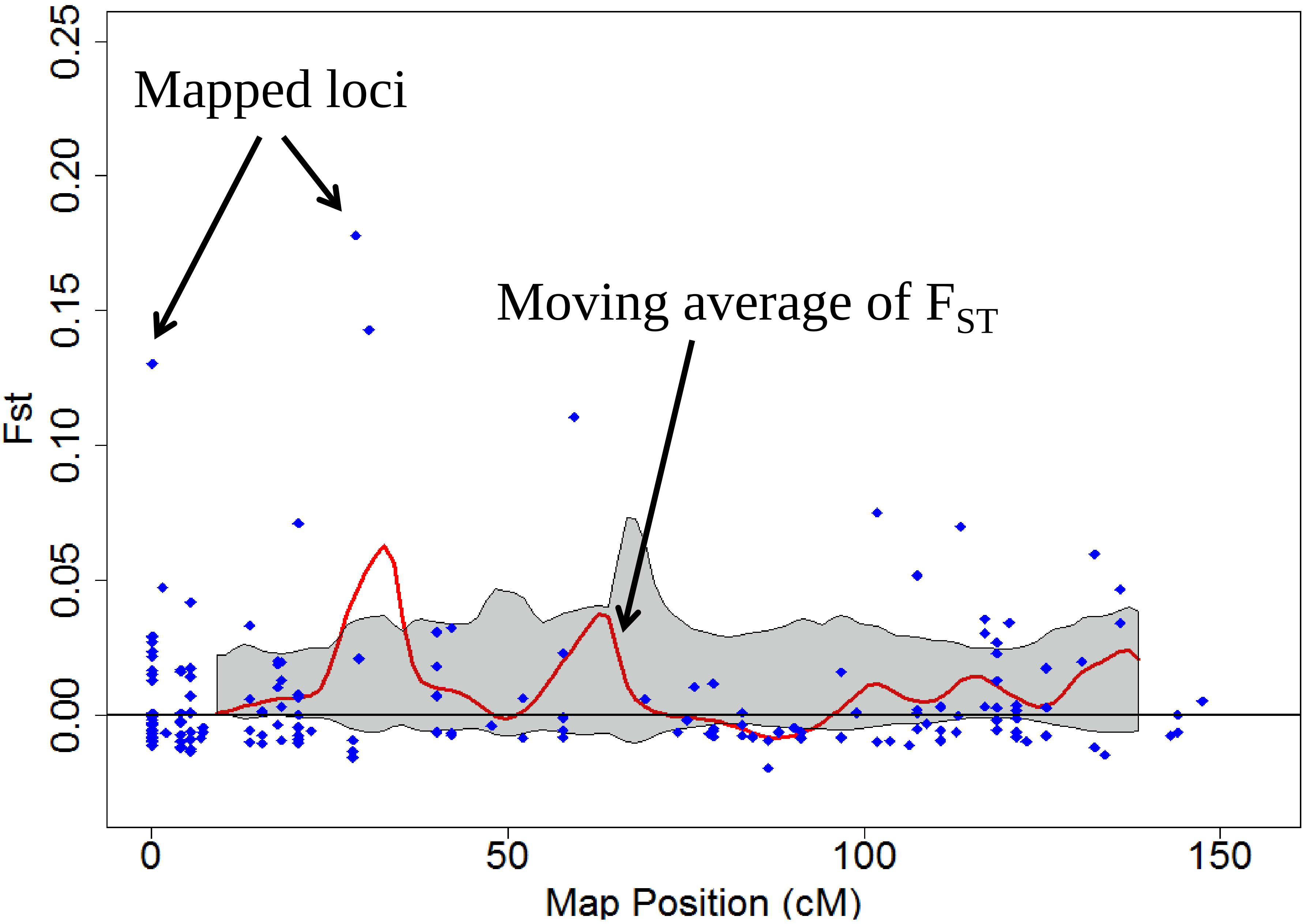


Good agreement between LD and temporal methods


Pairwise Relatedness Within Groups
Pairwise Relatedness (TrioML)
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
P1Founders
F0INT
F0SEG
F1INT
F1SEG
F2INT
F2SEG

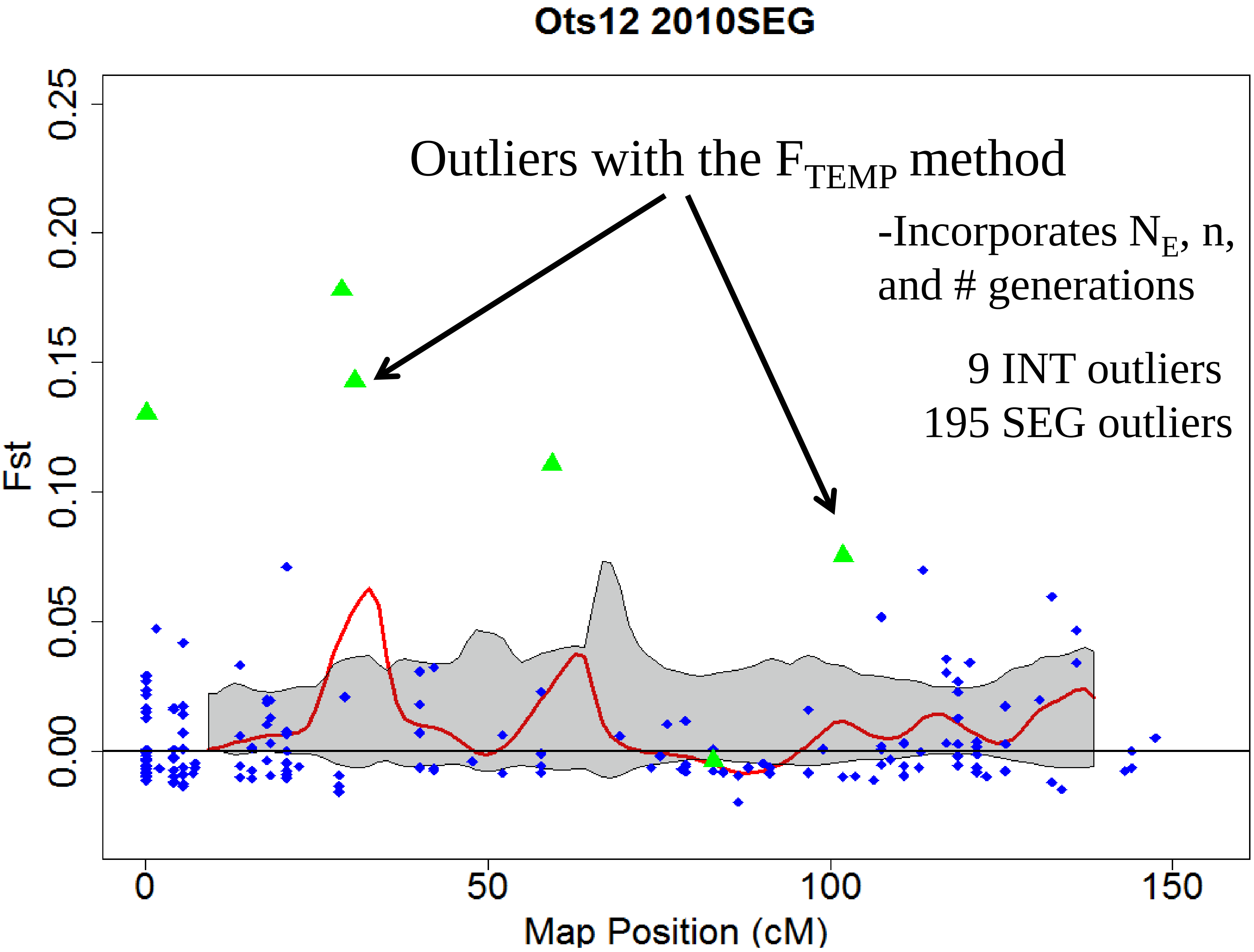

Levels of Inbreeding Within Groups
Inbreeding (TrioML)
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
P1Founders
F0INT
F0SEG
F1INT
F1SEG
F2INT
F2SEG

Ots12 2010SEG



Mapped loci

Moving average of F_{ST}



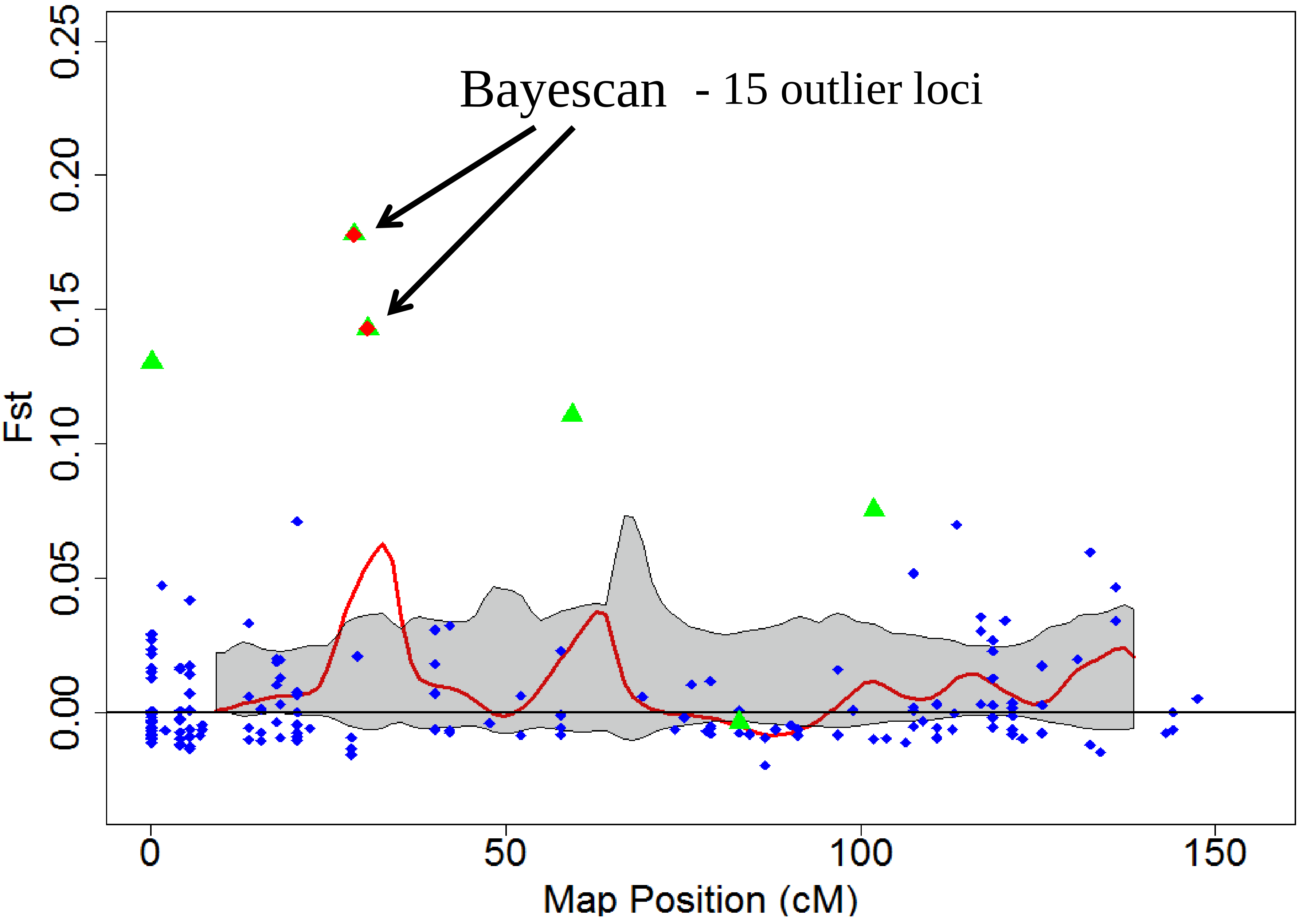
Outliers with the F_{TEMP} method

-Incorporates N_E, n, and # generations

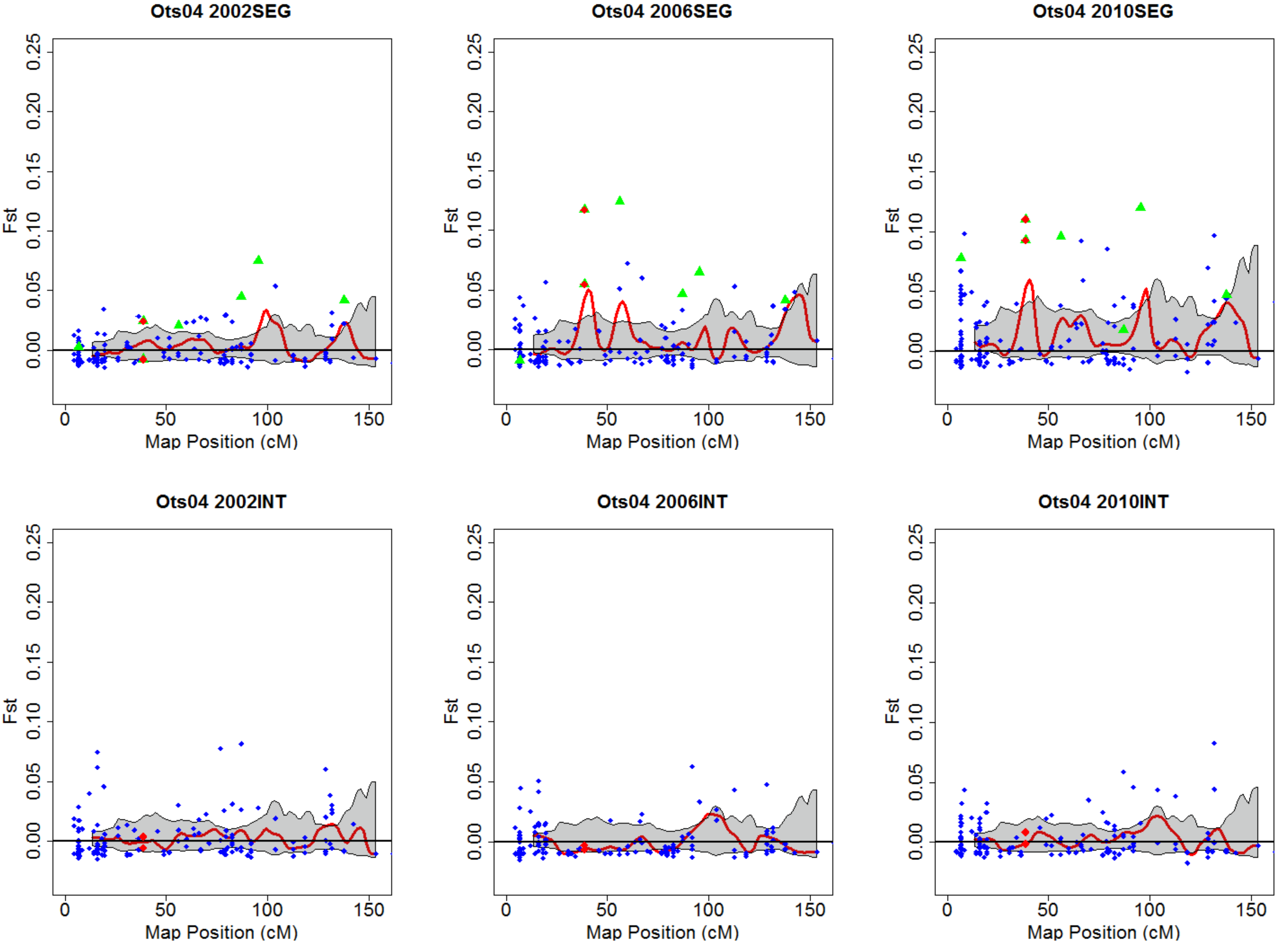
9 INT outliers

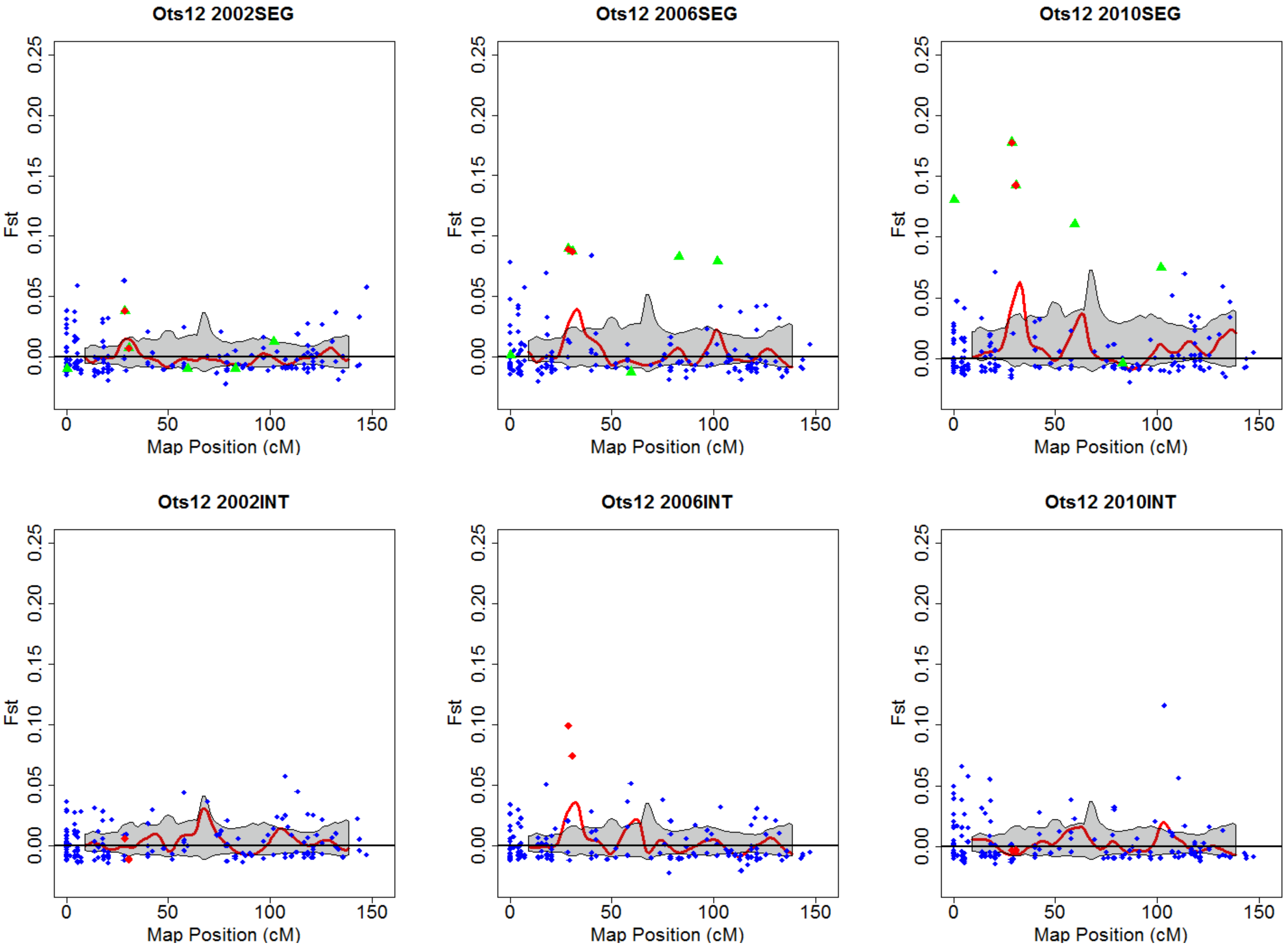
195 SEG outliers

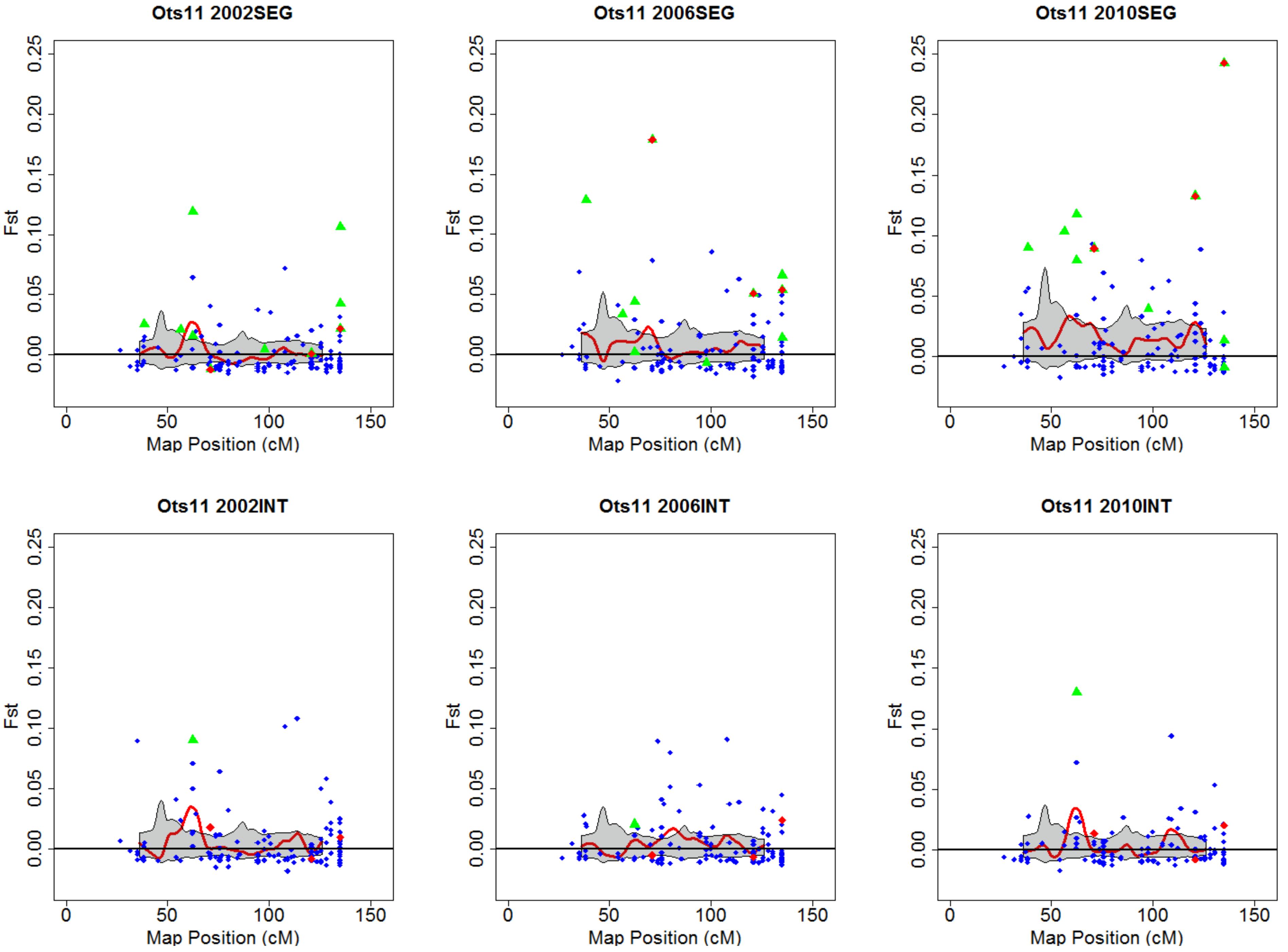
Ots12 2010SEG



Bayescan - 15 outlier loci


Ots04 2002SEG
Ots04 2006SEG
Ots04 2010SEG
Ots04 2002INT
Ots04 2006INT
Ots04 2010INT
Fst
0.00
0.05
0.10
0.15
0.20
0.25
0
50
100
150
Map Position (cM)


Ots12 2002SEG
Ots12 2006SEG
Ots12 2010SEG
Ots12 2002INT
Ots12 2006INT
Ots12 2010INT
Fst
0.00
0.05
0.10
0.15
0.20
0.25
Map Position (cM)
0
50
100
150


Ots11 2002SEG
Ots11 2006SEG
Ots11 2010SEG
Ots11 2002INT
Ots11 2006INT
Ots11 2010INT
Fst
0.00
0.05
0.10
0.15
0.20
0.25
0
50
100
150
Map Position (cM)

Summary of Results

- F_{ST} is low in all pairwise population comparisons
- Segregated line is slowly diverging over time
- Genetic drift could be a driving force in divergence of SEG line
- Signatures of selection were identified using 3 methods with good agreement; more abundant and consistent in segregated line
- Integrated management is effective at reducing adaptation to captivity

Next Steps

1) Estimate levels of inbreeding and relatedness
2) Add the 5th generation of fish to the study
3) GWAS and QTL analyses to link fitness related traits to genomic regions

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Questions?

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