

An evaluation of selection across four generations within a Chinook salmon supportive breeding program



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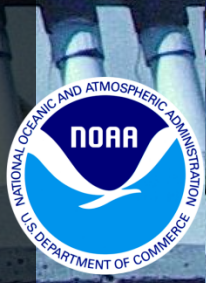
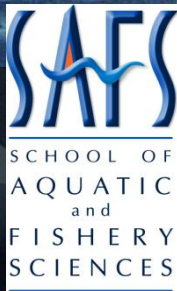
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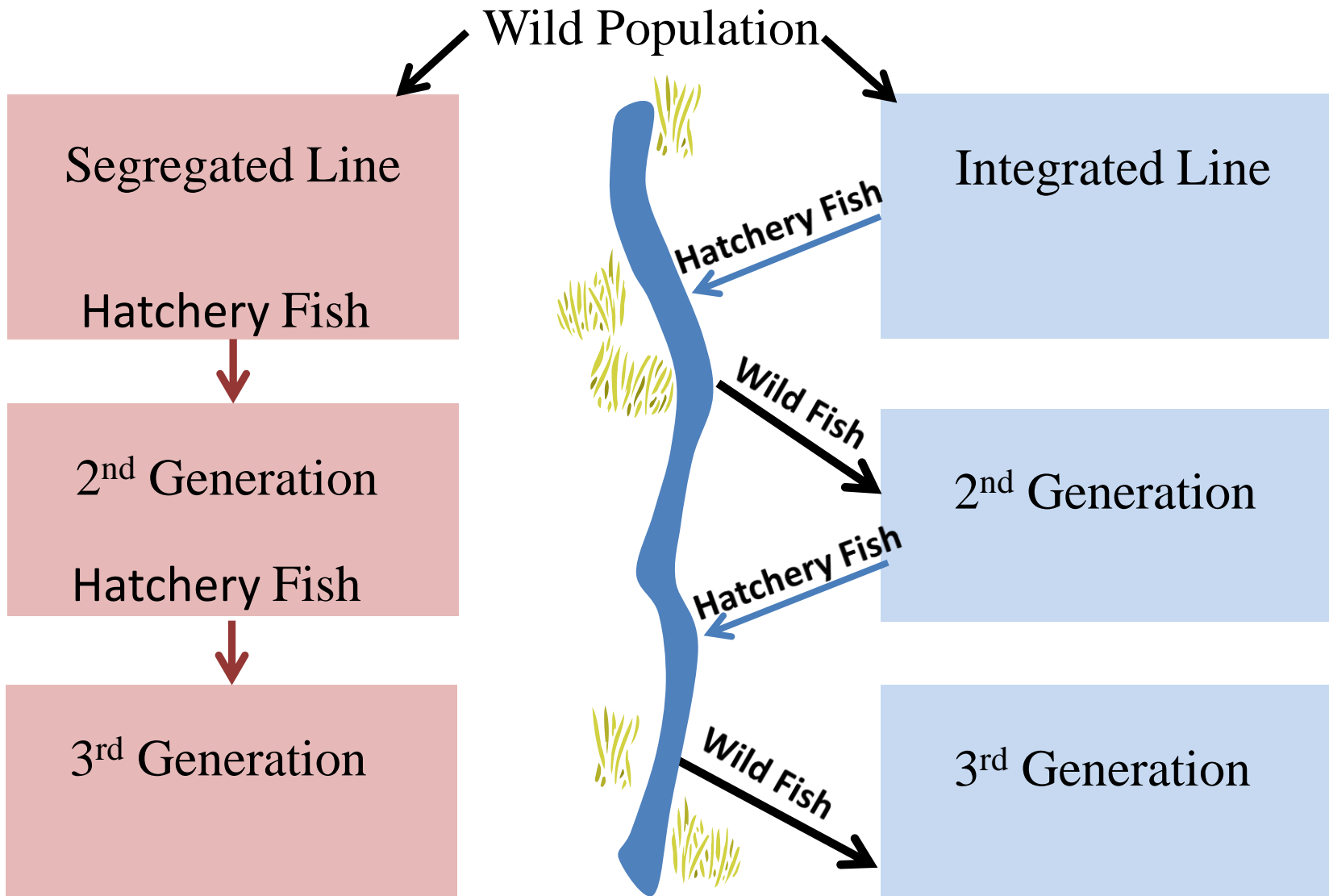
Outline

- 1) Quick review of the study system
- 2) Updated results of genetic divergence with the 4th hatchery generation
- 3) Preliminary results for identifying loci that are associated with phenotypic traits of adult spawners
- 4) Ongoing research

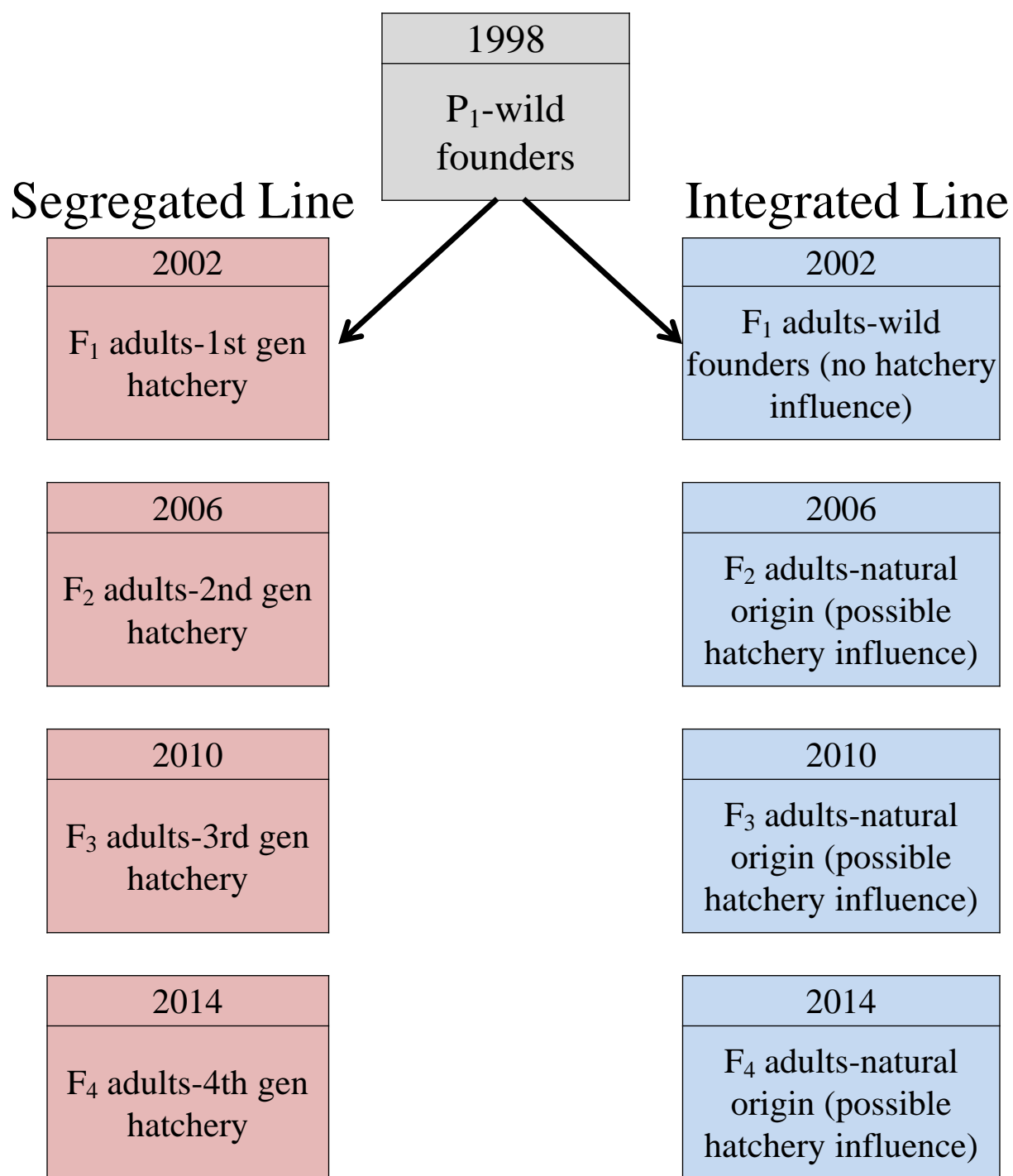
Segregated

vs.

Integrated



Has managed gene flow reduced divergence from founder population?



Experimental Approach

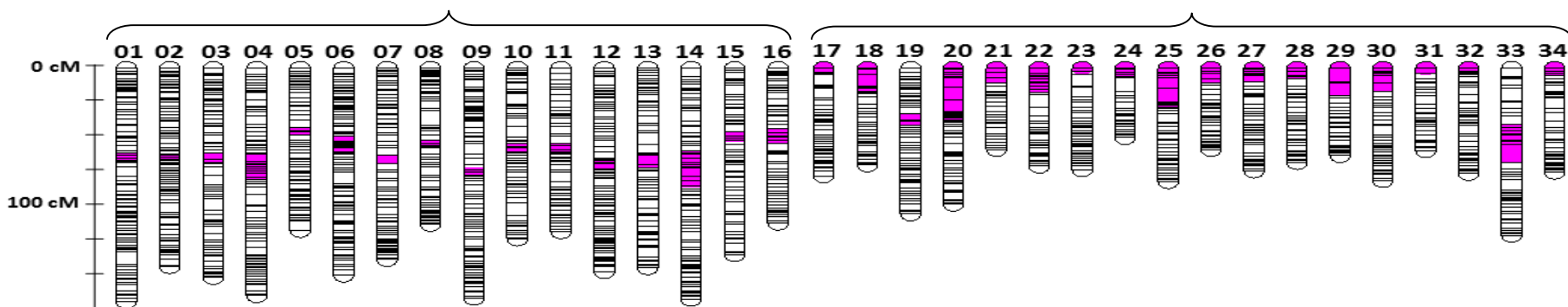
Chinook Map (Brieuc et al. 2014), 7146 markers



Metacentric

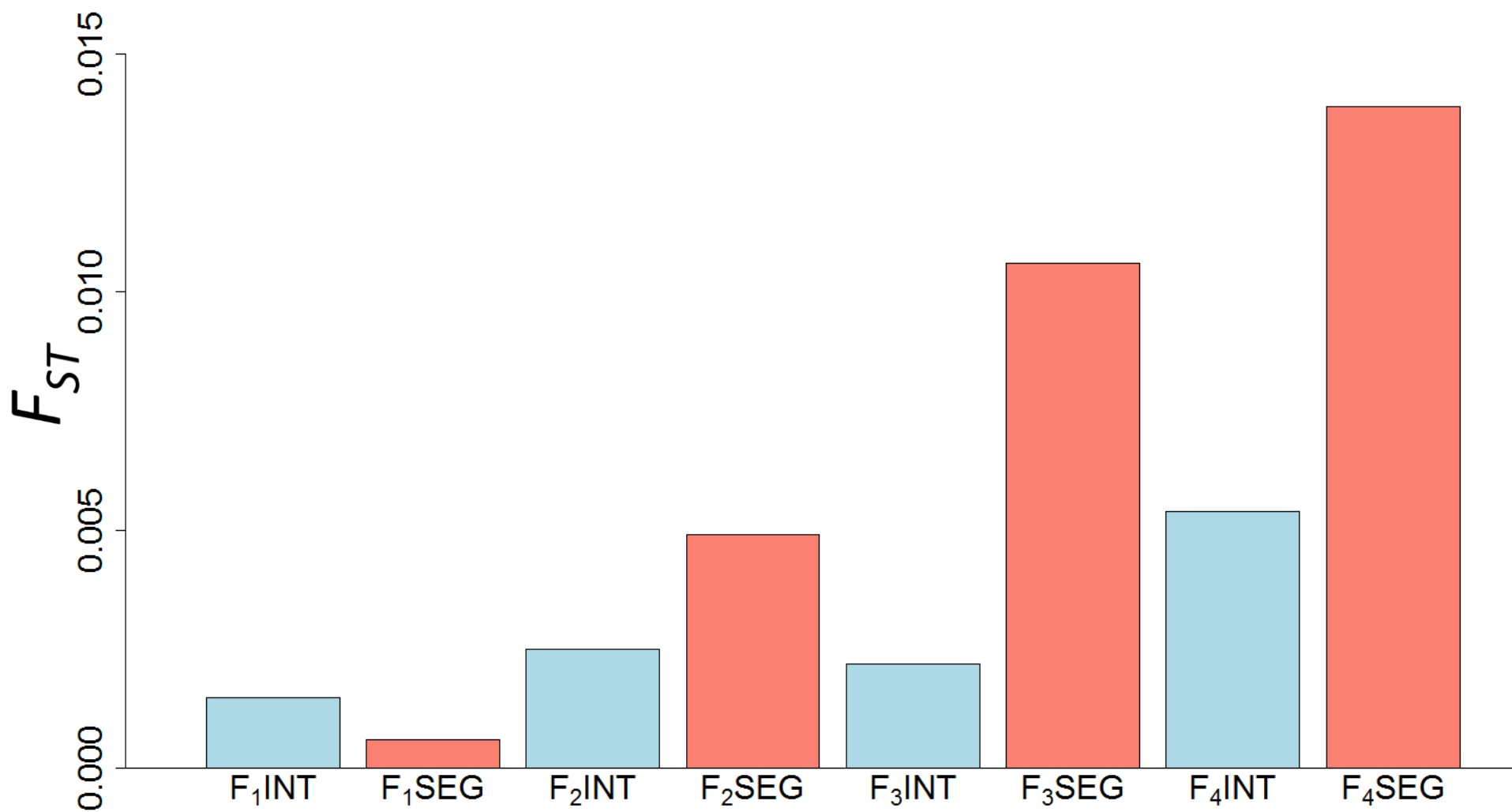
Acrocentric

Joseph R.
Tomelleri

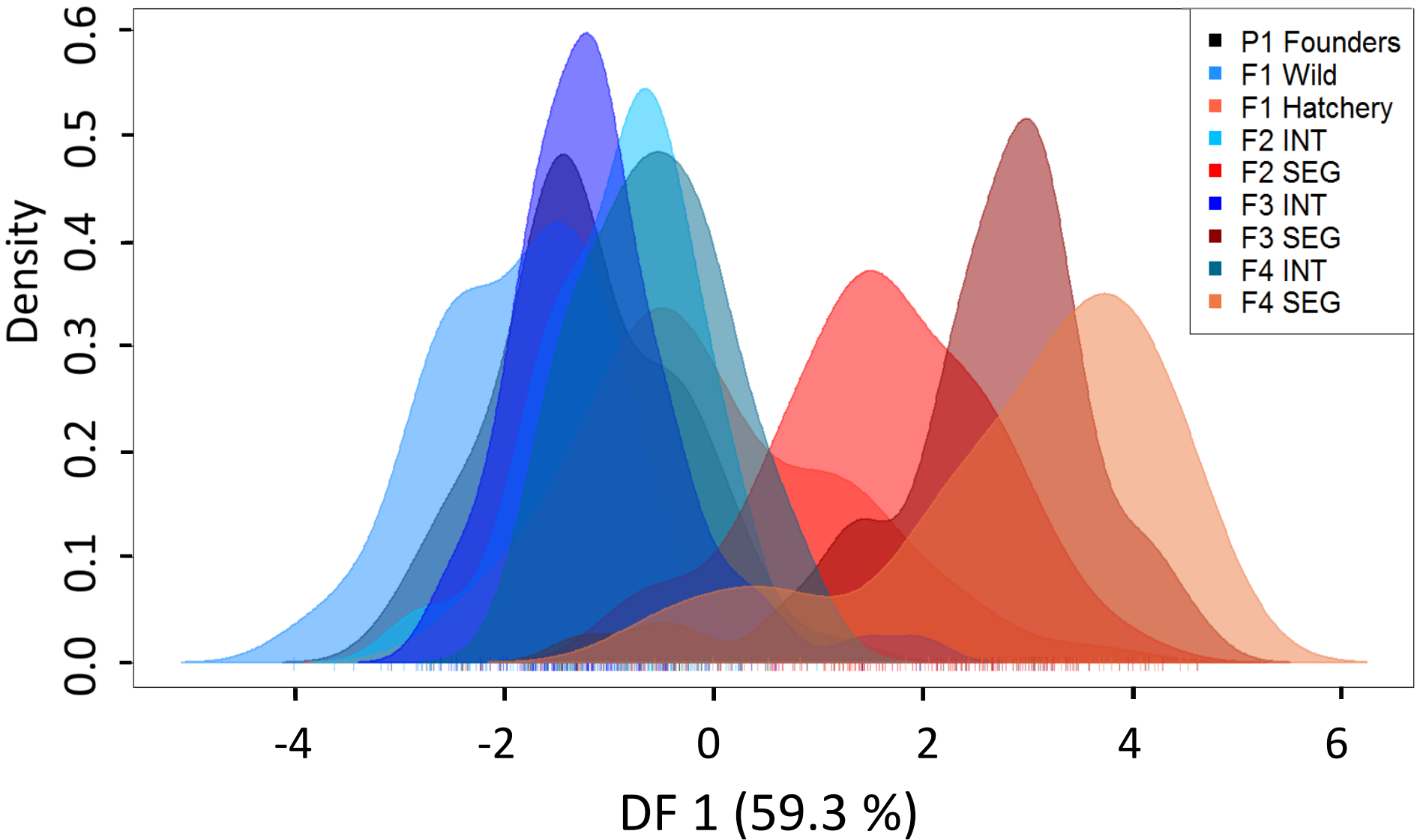


Number of loci = 8,872 RAD loci (4,178 are mapped)

Genetic Divergence from Founders

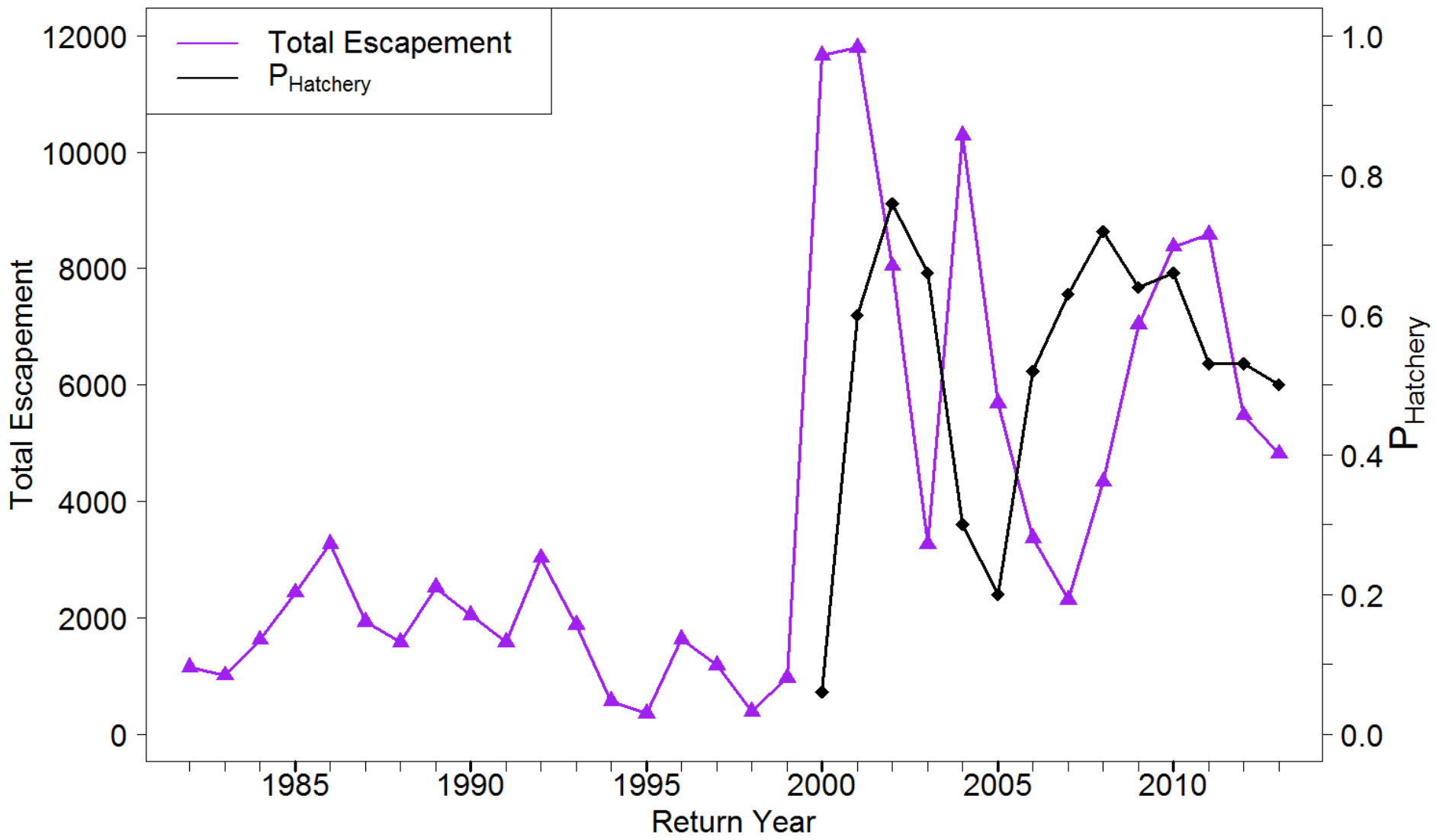


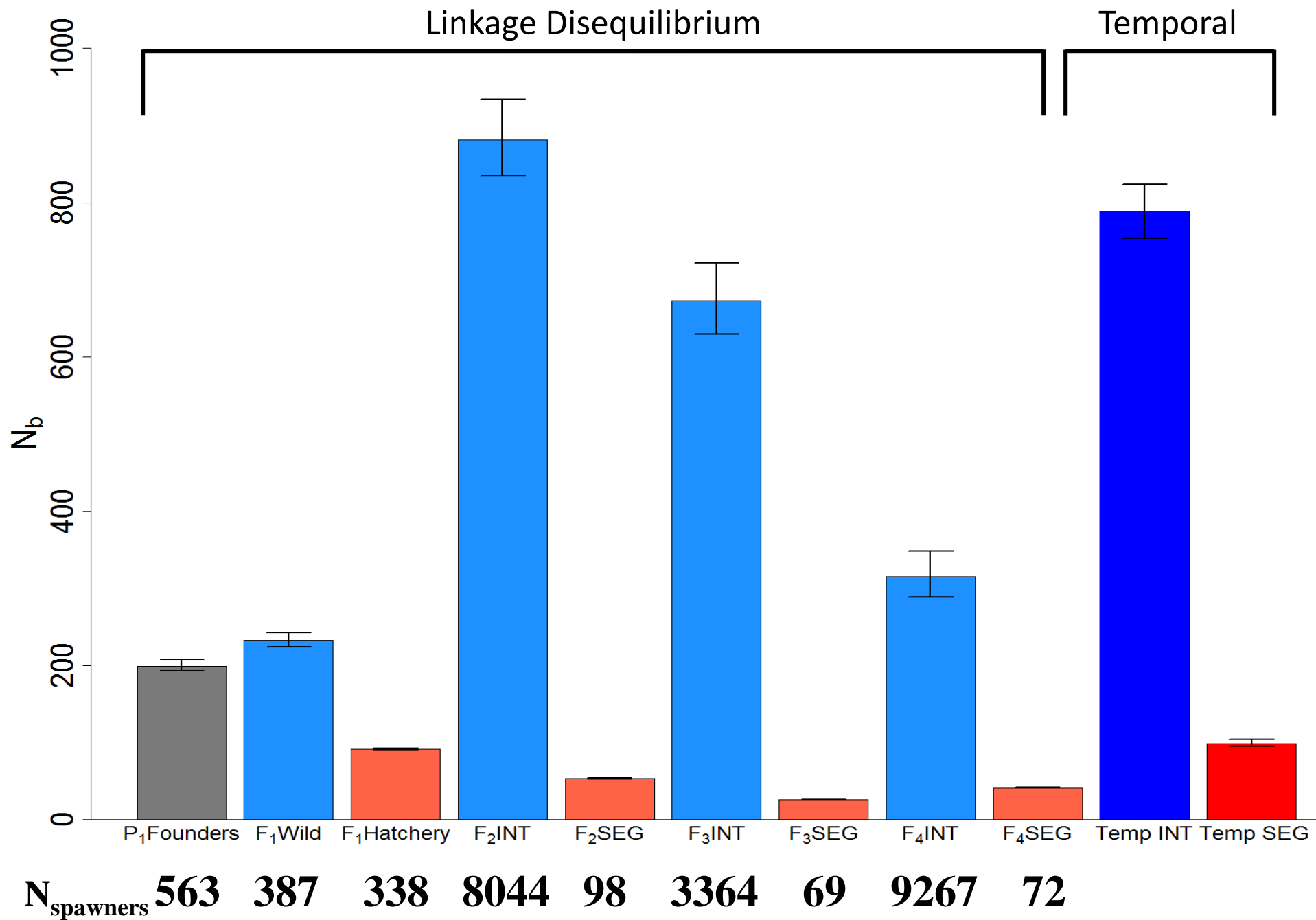
Discriminant Analysis of Principal Components

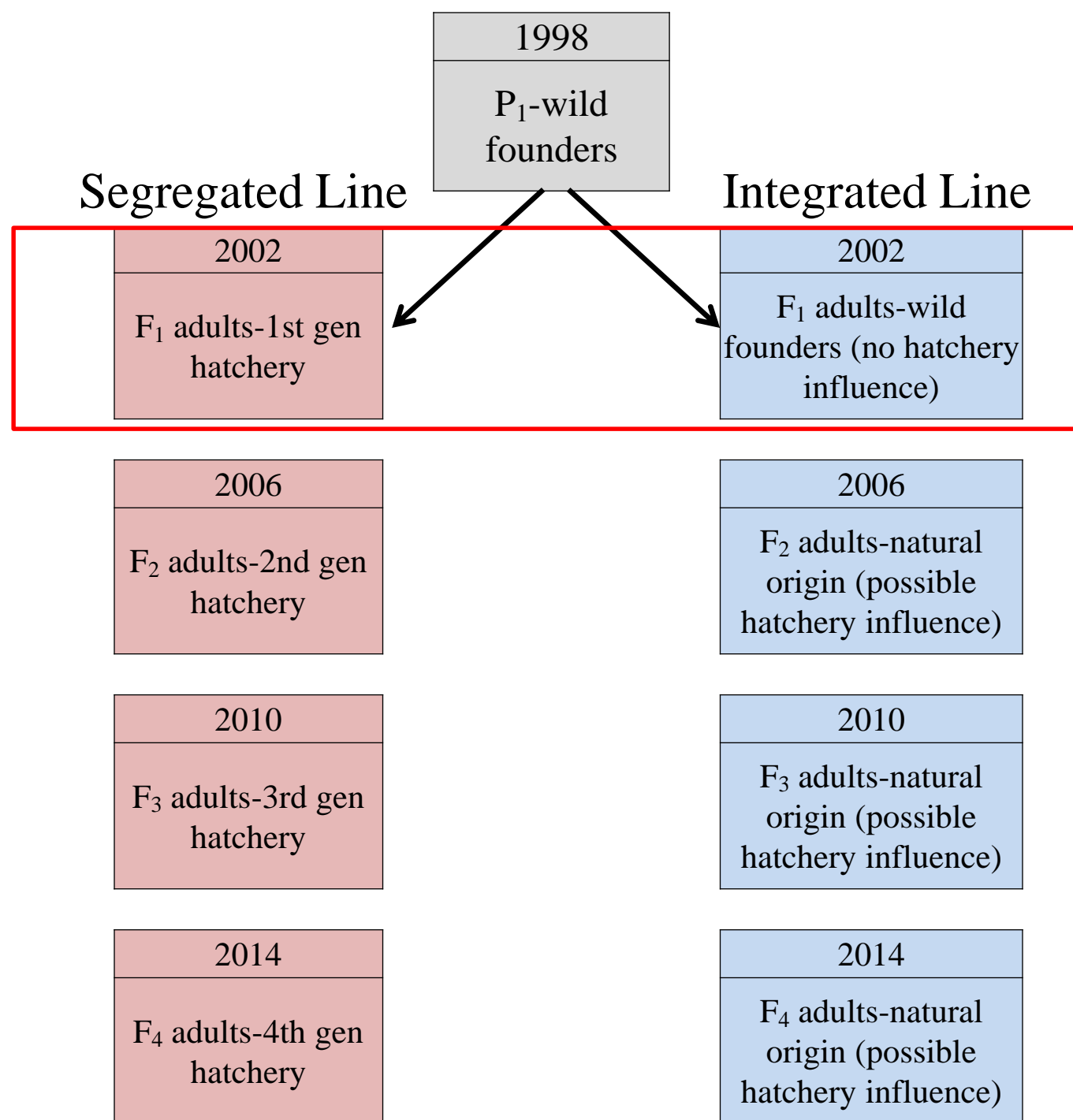


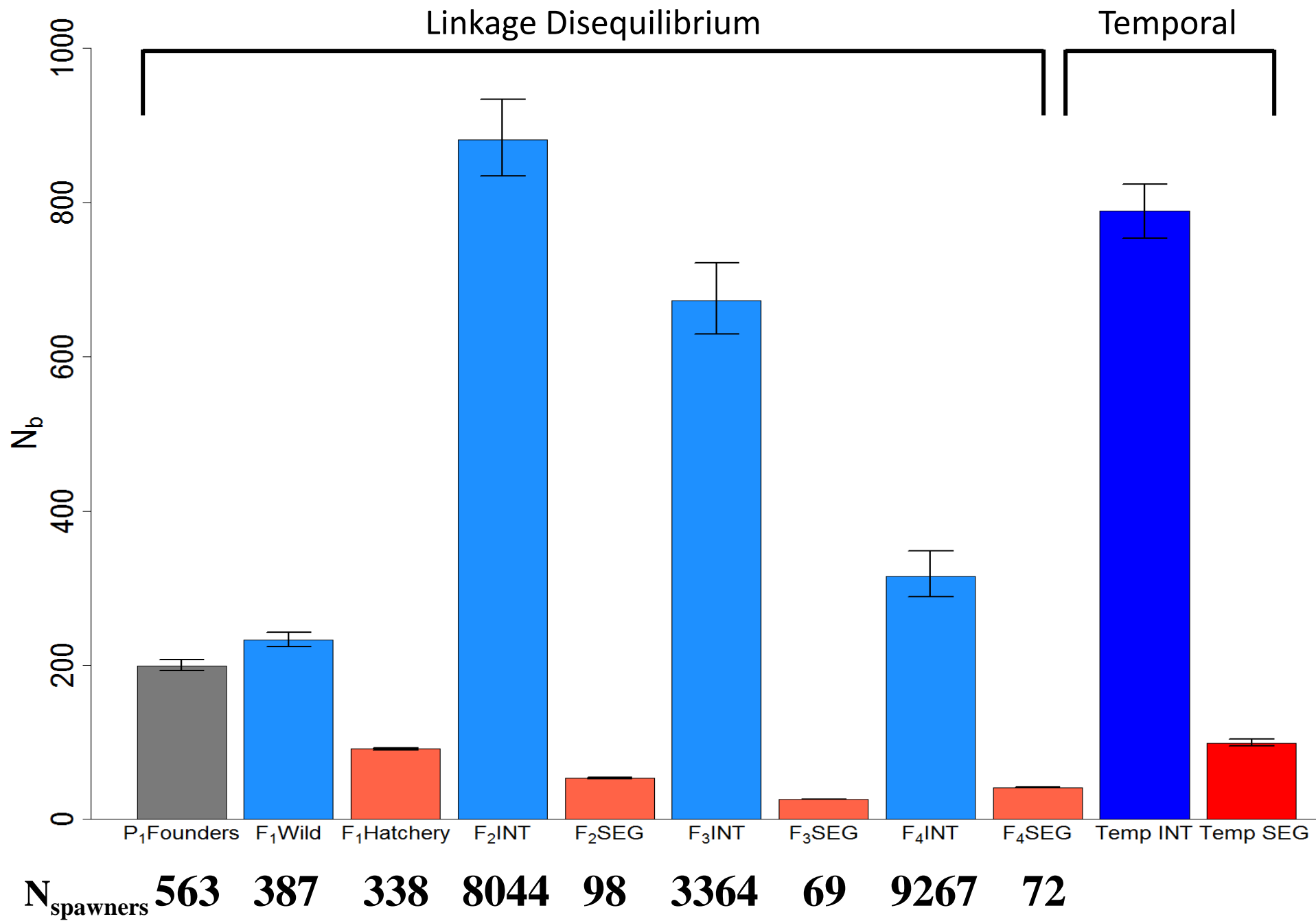
Effective Number of Breeders

- Used to examine divergence due to genetic drift
 - Genetic drift is the dominant evolutionary process in small populations (loss of genetic variation; inbreeding)
 - Avg. # broodstock: INT=363; SEG=85
- Estimated effective number of breeders using the linkage disequilibrium and temporal methods

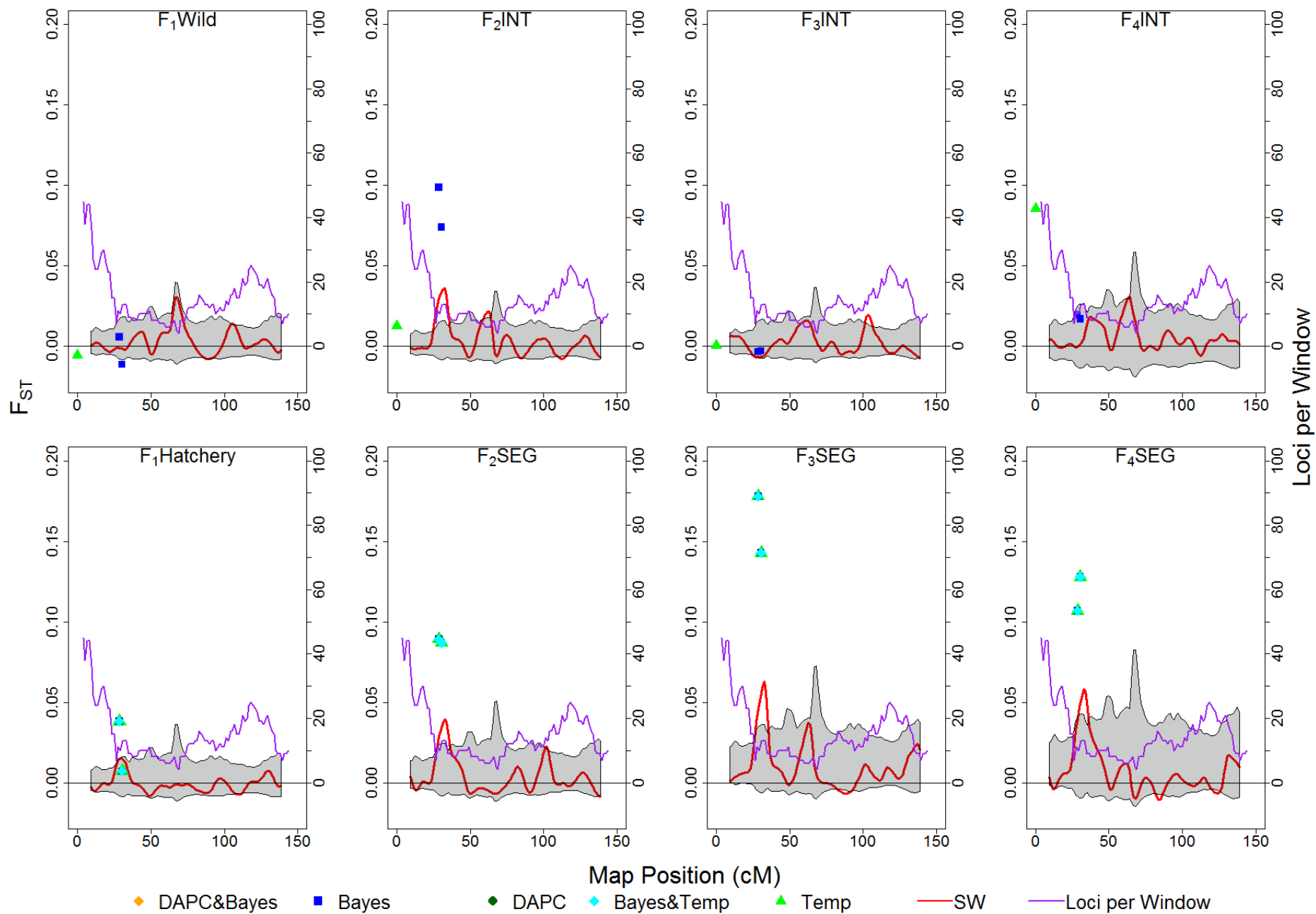








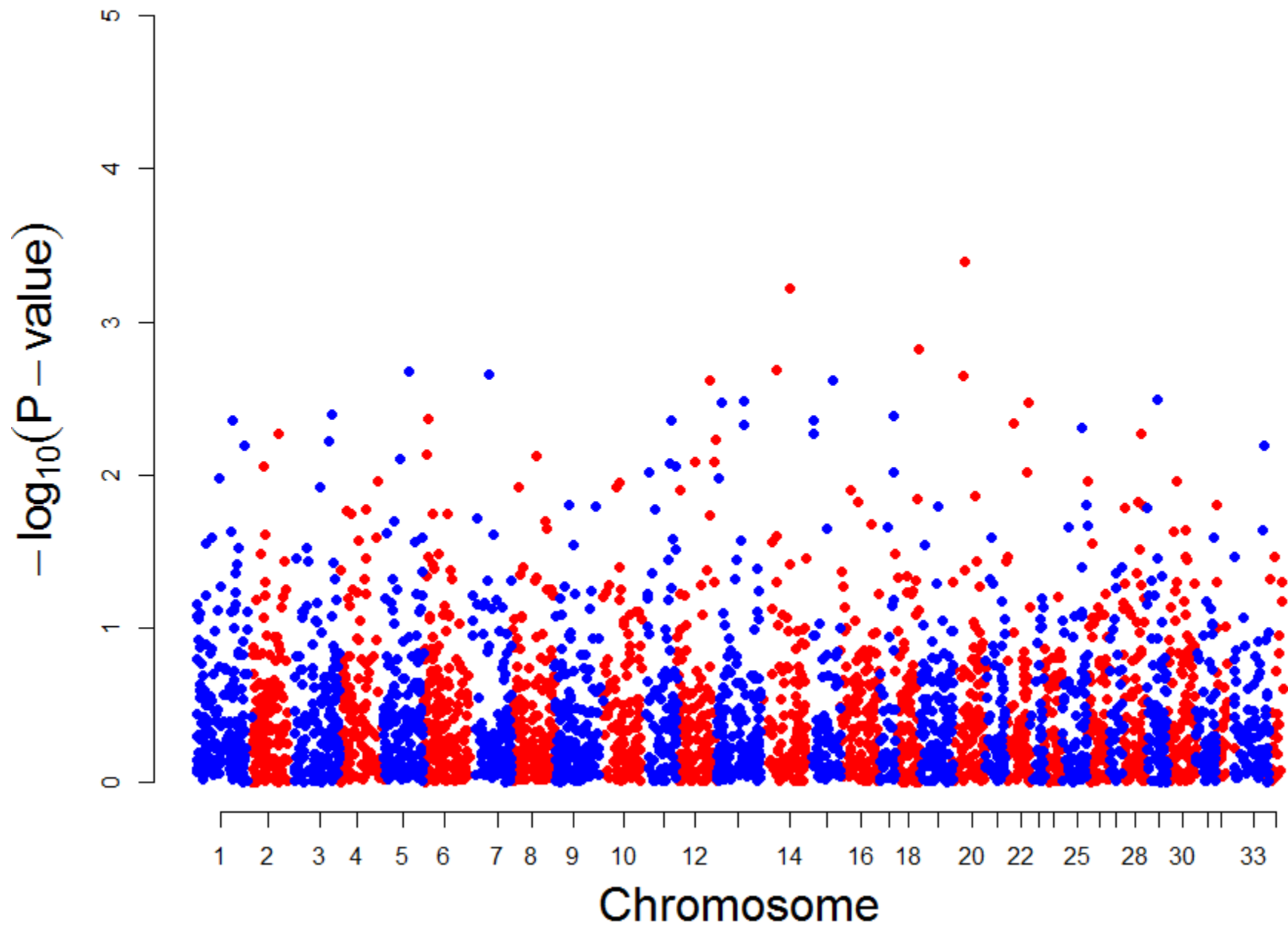
Ots12



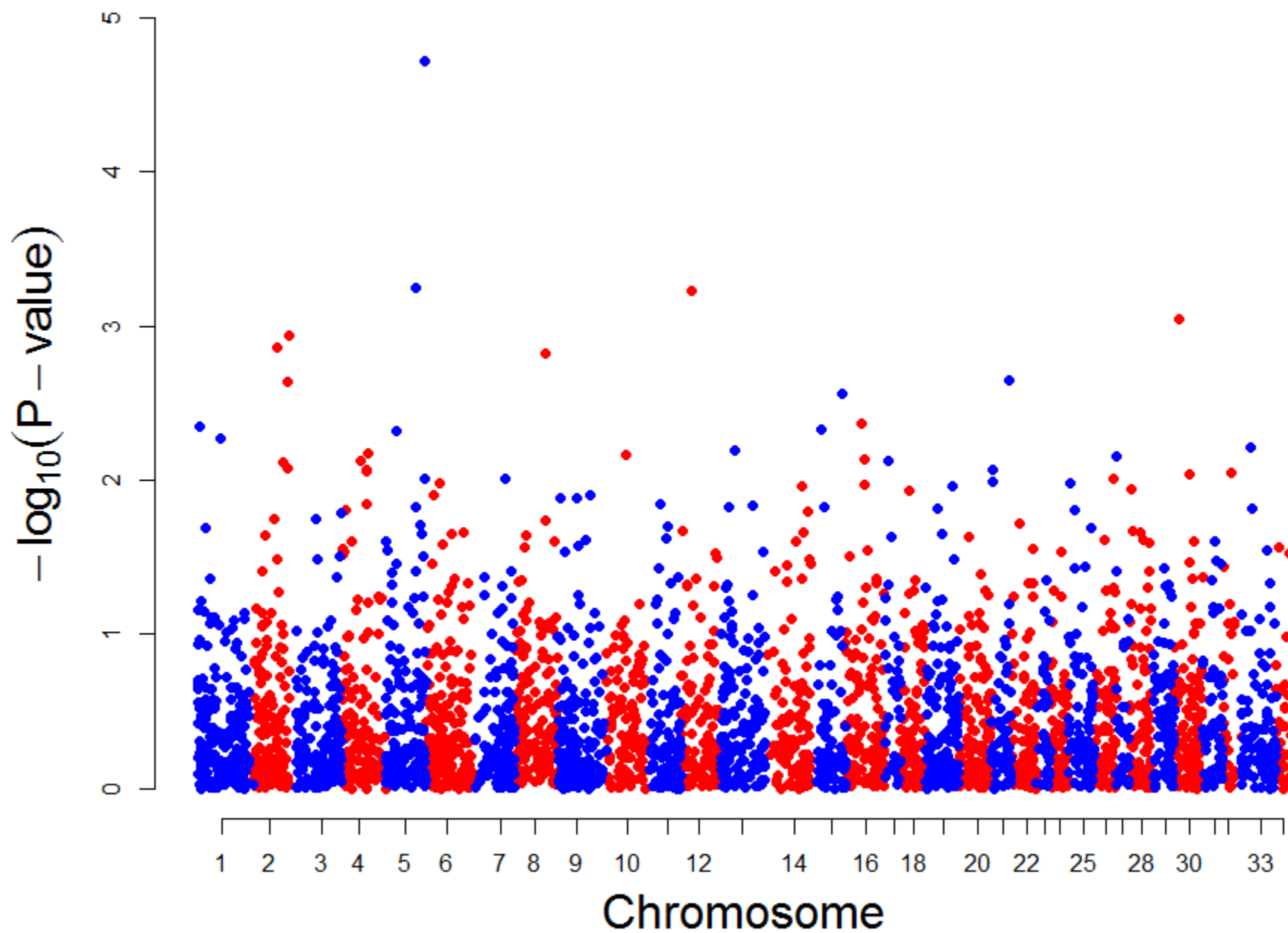
Is Selection Acting on Fitness-Related Traits?

- Look for associations between genetic markers and traits of interest using GWAS and Random Forest analyses.
- Preliminary results for GWAS on 361 individuals at 3428 loci
 - Return date to Roza
 - Age at return
 - Weights at Roza and CESRF
 - Fork length at CESRF

GWAS of Return Date



GWAS of Age at Return

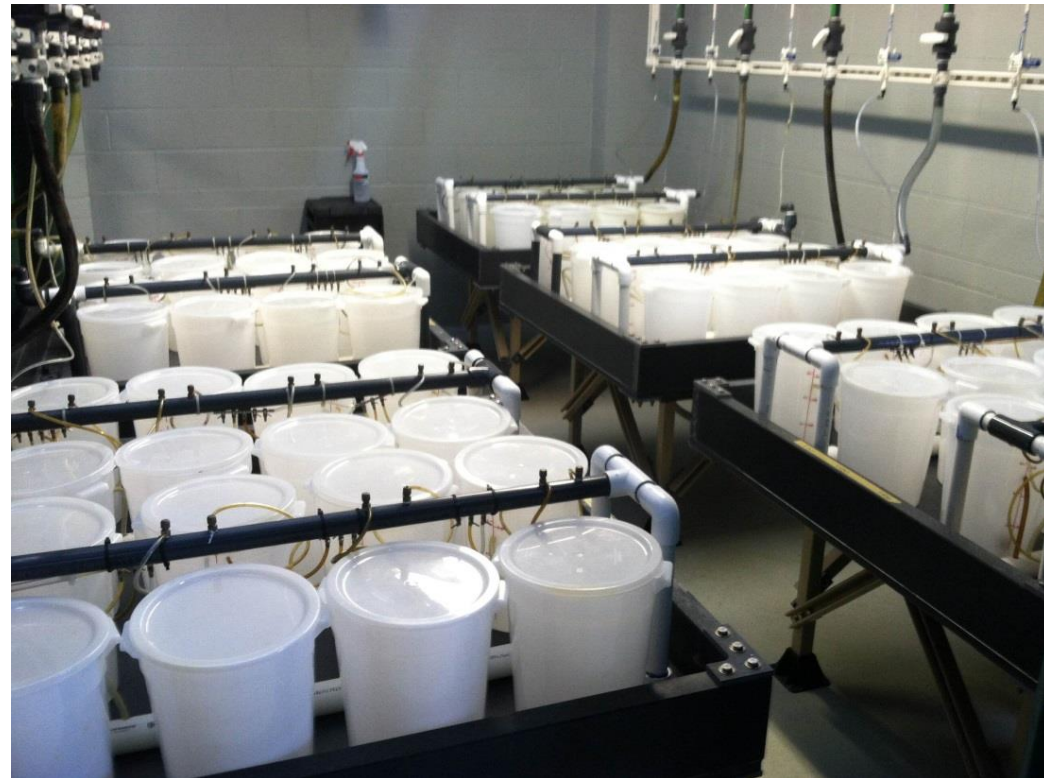


Summary of Results

- Segregated line is still slowly diverging over time
- F_{ST} also increased in F₄ INT generation
- Genetic drift is driving divergence of SEG line (broodstock size)
- Signatures of selection were identified using 3 methods with good agreement; more abundant and consistent in segregated line
- Biological significance? No links to fitness-related traits in preliminary GWAS analyses

Ongoing Research

- 1) Finalize analyses to identify loci linked fitness related traits in adults, and determine if these traits are responding to hatchery selection
- 2) Identify genomic regions associated with hatch timing, early growth rate, and disease resistance



Acknowledgments

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Questions?

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Overlap across Tests for Adaptive Divergence in Segregated Line

1) F_{TEMP}

- Simulates neutral genetic divergence in a single population over time
- Incorporates estimates of N_b , sample size, and # generations

2) Bayescan

- Identifies candidate loci under selection based on differences in allele frequencies between populations

3) Sliding Window Analysis

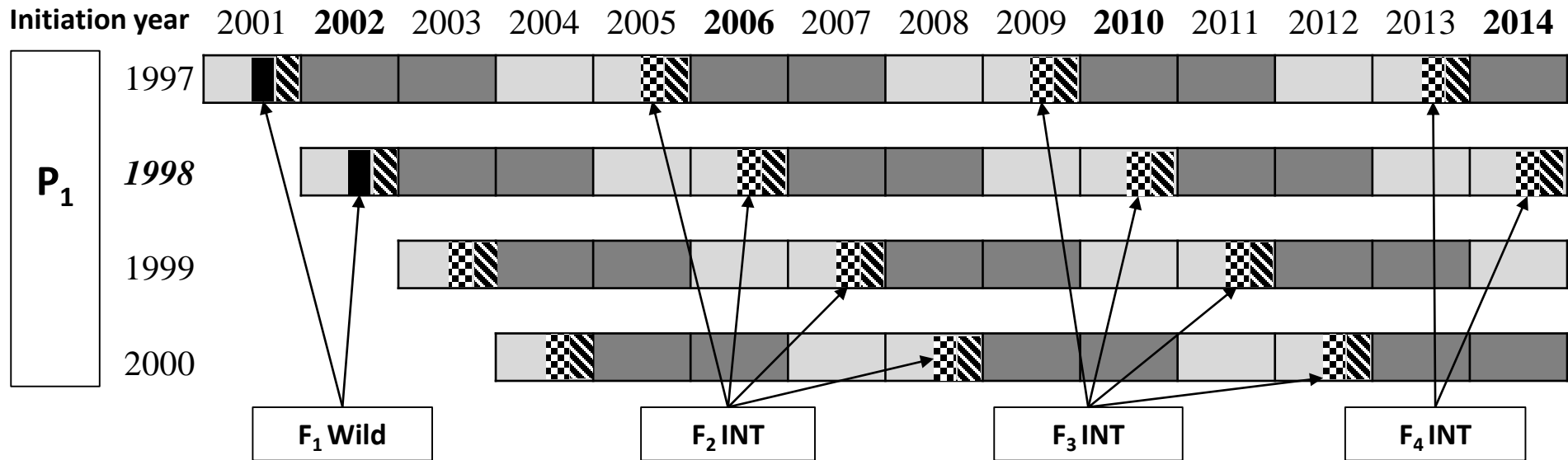
- Identifies regions of elevated divergence based on empirical genome-wide distribution of F_{ST}

Overlap across Tests for Adaptive Divergence in Segregated Line

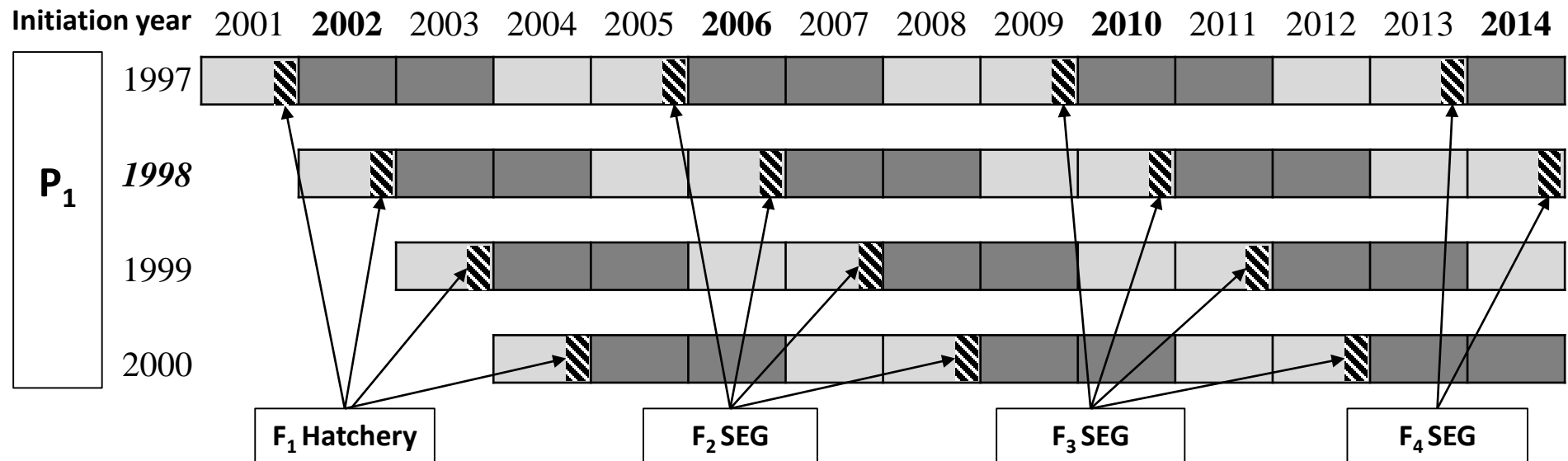
Chromosome	Map Position (cM)	# gens SW INT	# gens SW SEG	F _{TEMP} INT	F _{TEMP} SEG	Bayescan
Ots04	37.52-43.15		2		2	2
Ots05	87.43-95.05	1	3		1	1
Ots06	94.64-100.65	1	1		1	1
Ots11	57.77-71.46	2	3	1	2	1
Ots12	26.14-35.29	1	2		2	2
Ots15	132.33-139.26	1	1		1	1
Ots20	93.65-99.49	1	2		2	1

Possibly the first signatures of domestication selection identified in Pacific salmon

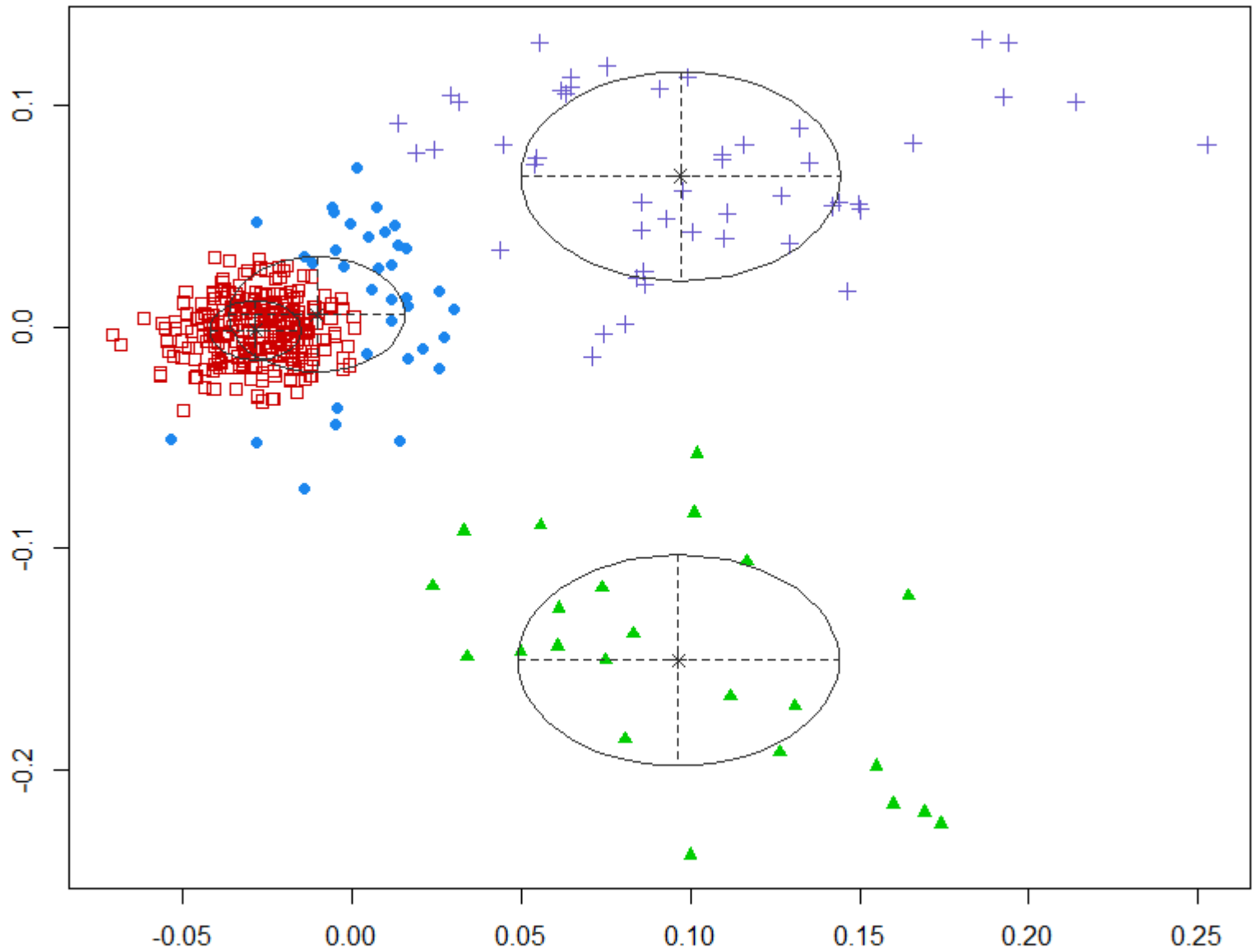
INT: Return year

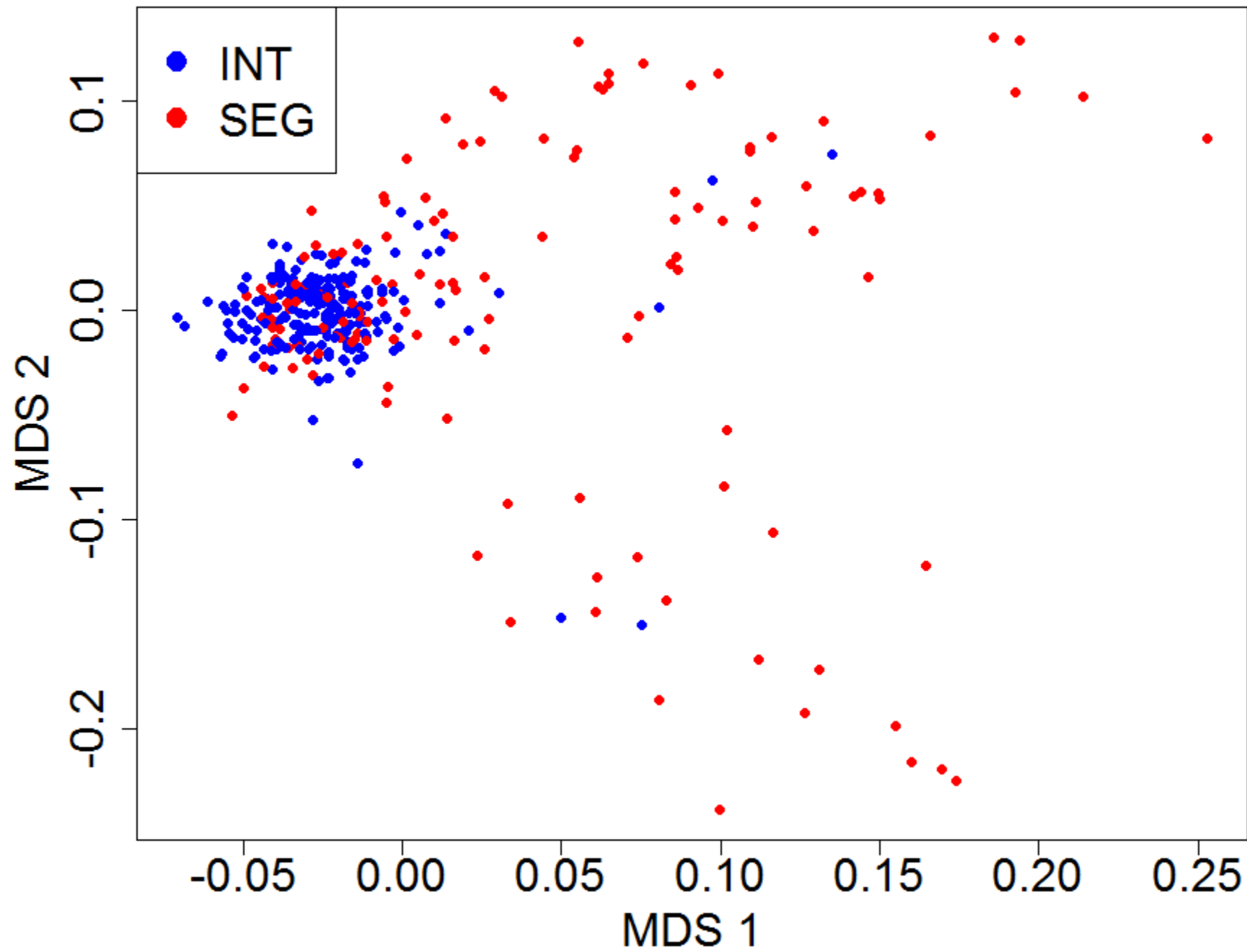


SEG: Return year

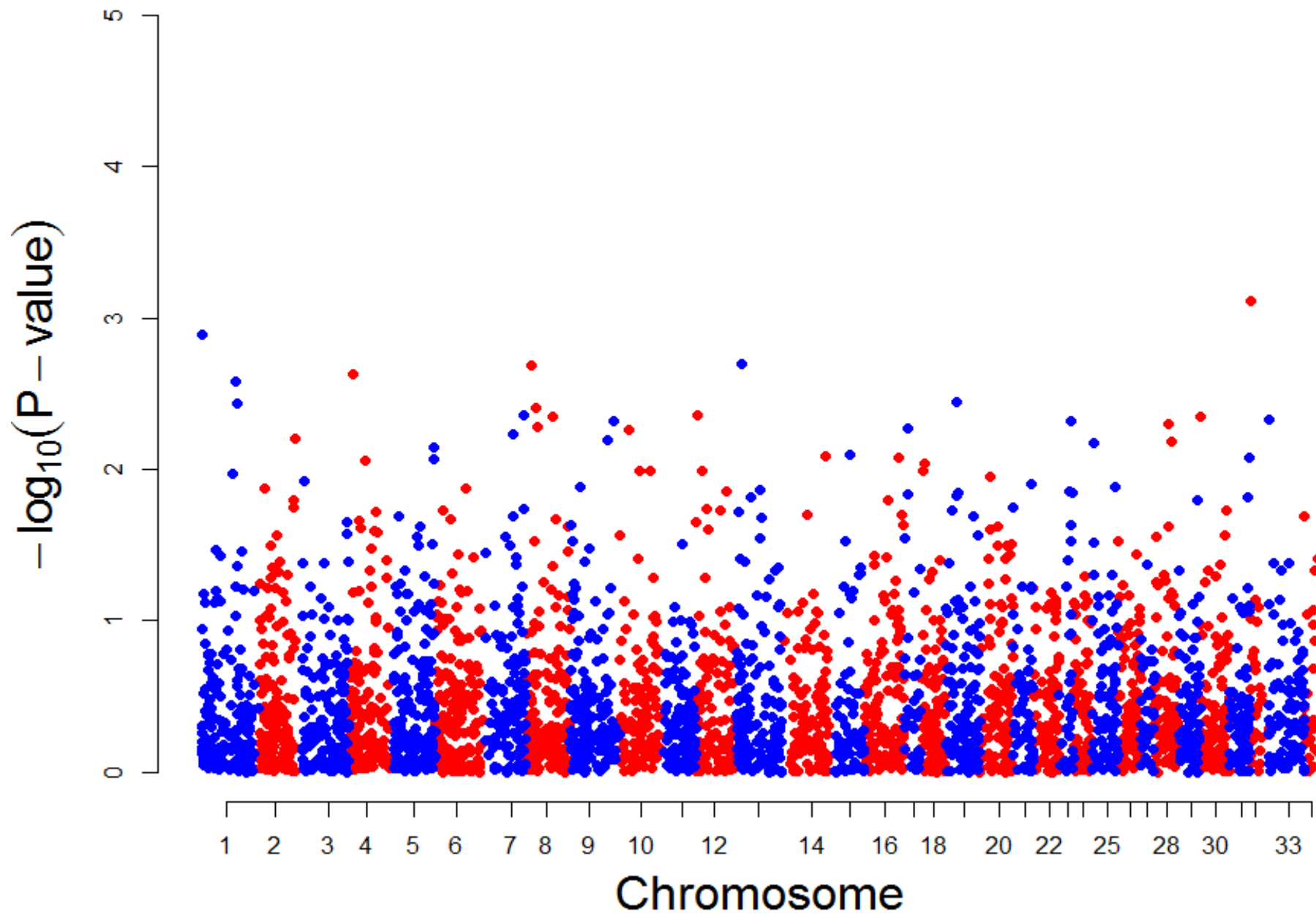


Classification





GWAS of Weight at Roza



GWAS of Fork Length at CESRF

