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# Genome Screens Identify Chromosomal Regions Under Divergent Selection in Steelhead/Rainbow Trout

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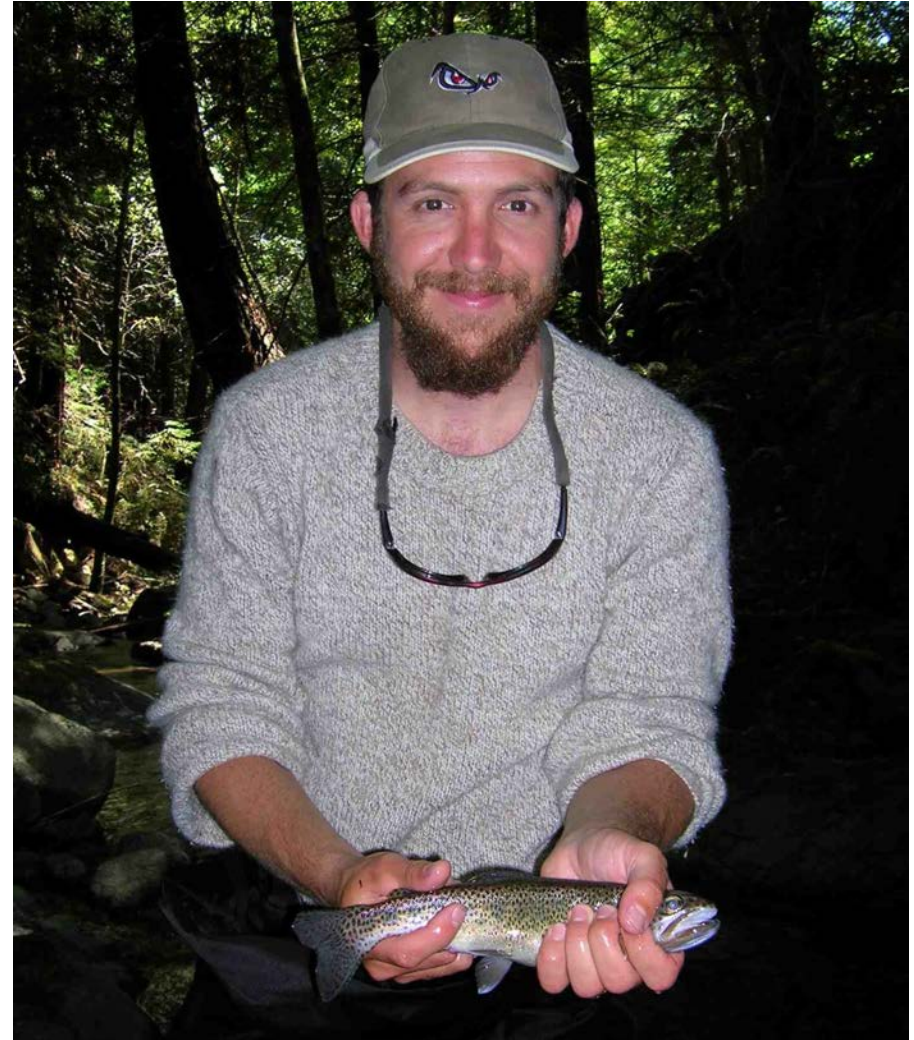
*and*

University of California, Santa Cruz  
Dept. of Ocean Science and Dept. of Ecology and Evolutionary Biology

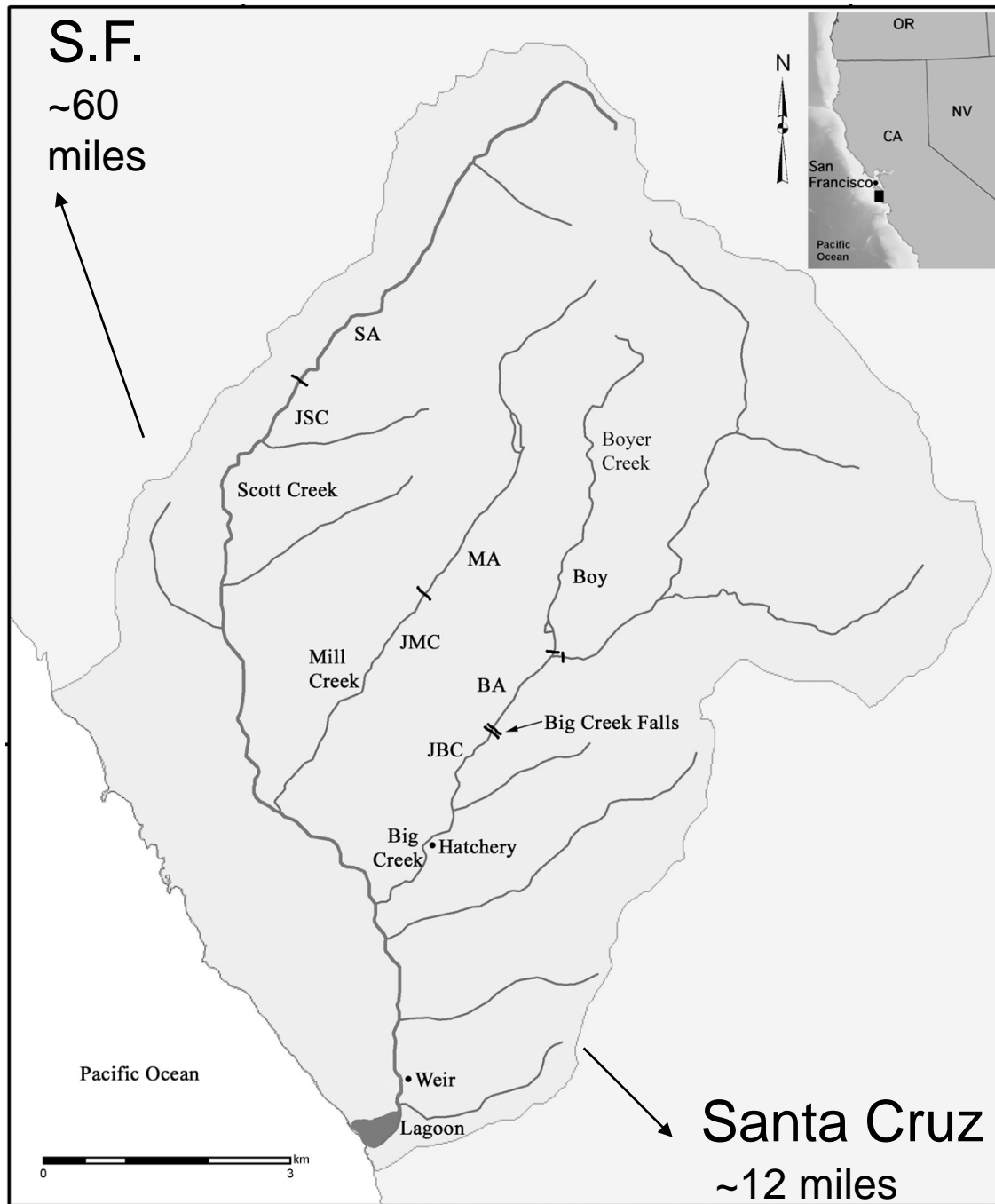
*AFS Meeting, Seattle, WA, Sept. 7, 2011*



- Steelhead: Anadromous, spend 1-2 years in freshwater and 1-4 years in salt water prior to spawning. Iteroparous.



- Rainbow Trout: Stay in stream entire life (Resident).



## Scott Creek watershed

- Hayes et al. 2004
- Bond et al. 2008
- Hayes et al. 2008
- Pearse et al. 2009
- Martinez et al. 2011
- Hayes et al. submitted
- Charrier et al. in prep



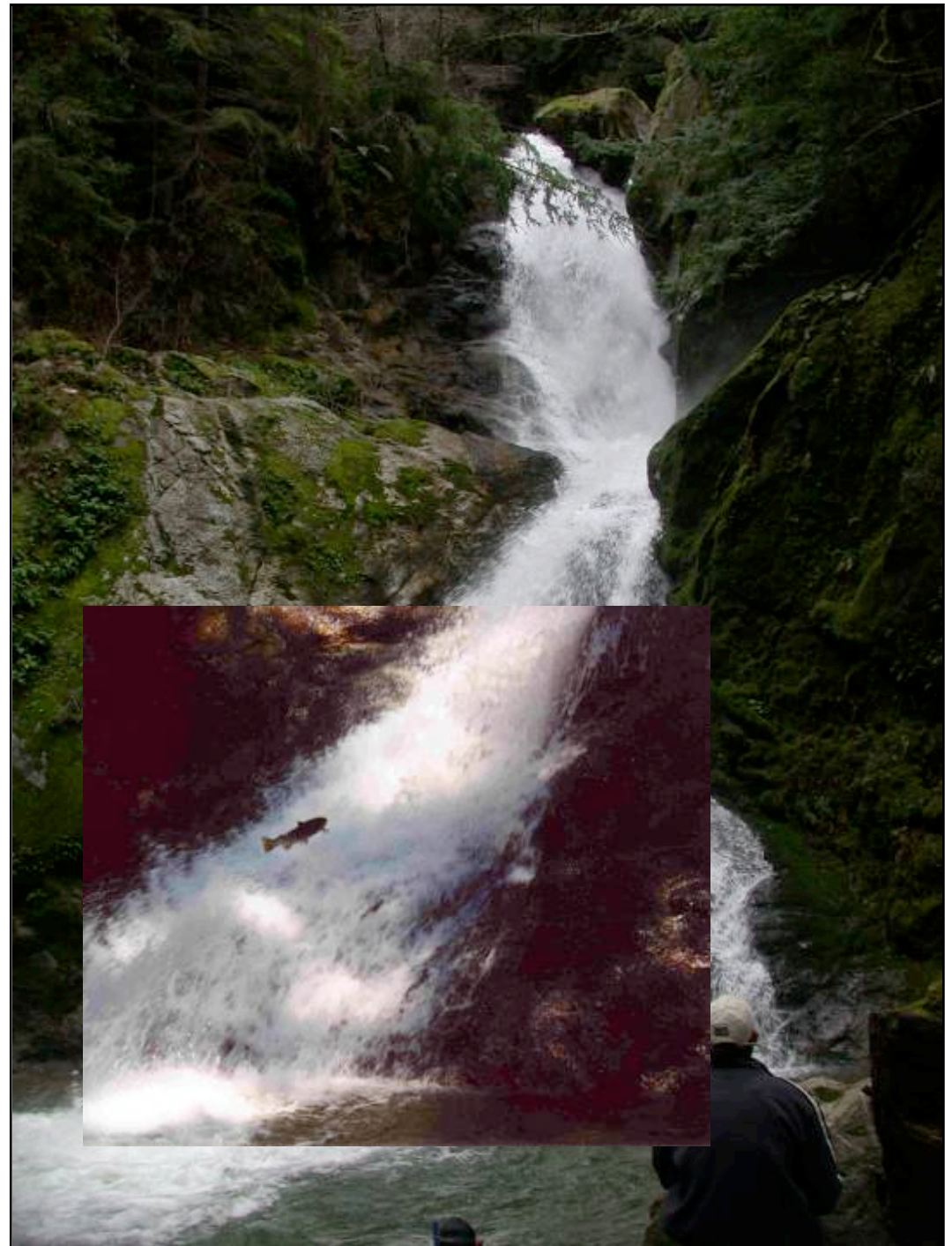
## Over the Falls?

- *O. Mykiss* introduced above Big Creek Falls c. 1910
- Surveyed 18 microsatellite loci in fish throughout watershed.  
(Pearse et al. 2009)
- Low pairwise  $F_{st}$  at Big Creek Falls (0.018), supporting within-basin origin.
- Although above barrier habit is limited, bottleneck/founder effects do not appear to be significant.  
(Anderson & Slatkin 2007)
- Hatchery stocking may have occurred above other barriers.



## Over the Falls?

- Regardless of source, there must be strong, continuing selection on above-falls fish not to move downstream.





Caught as YOY in Fall 2007  
Photos Spring 2009.

Above Barrier, ~100%



Below Barrier, >90%

In 2010, spawned 10 females to create 28 pure and mixed families to assess variation in growth and development in a common growth environment.

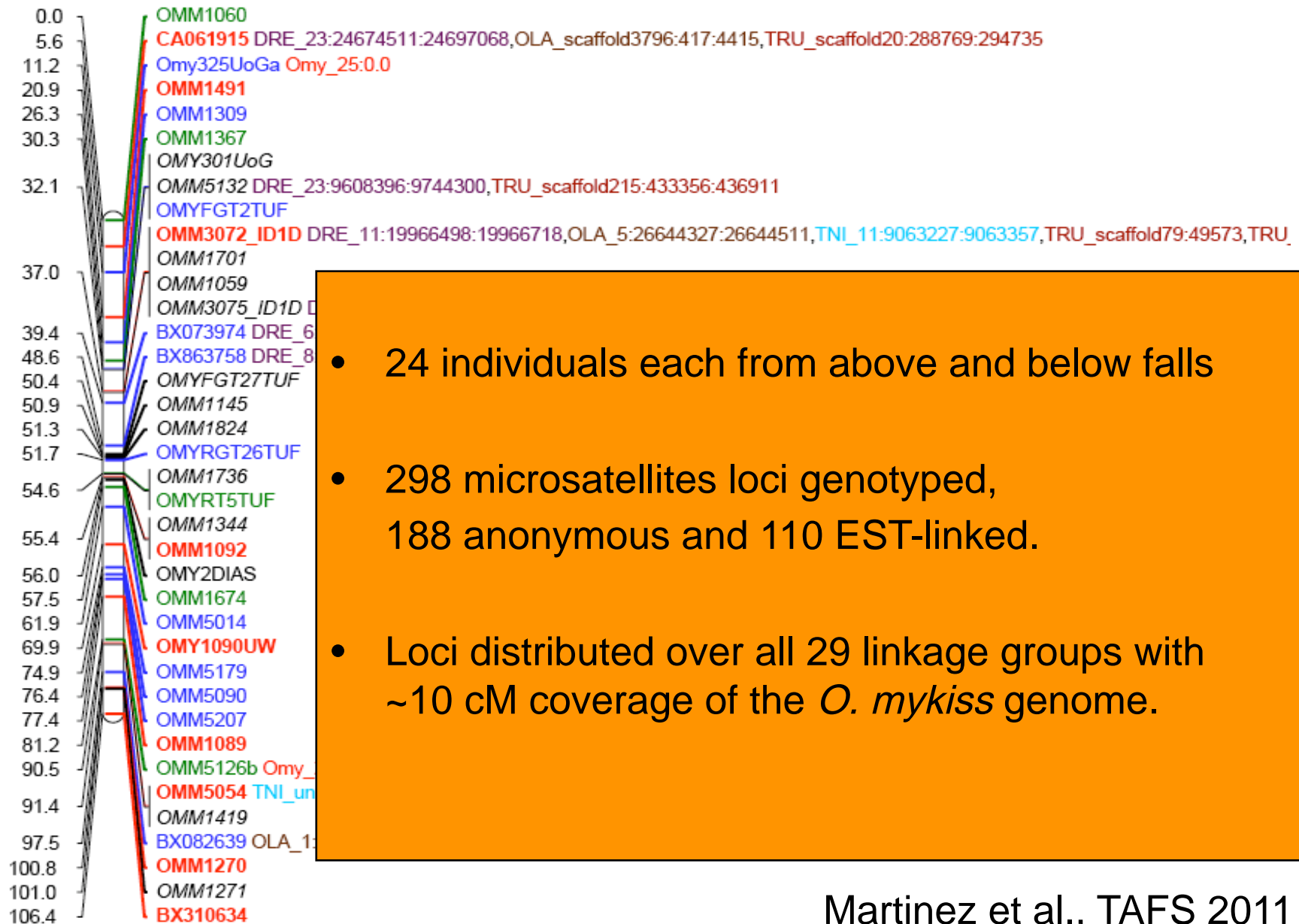
**Growth,  
development,  
and  
ecological  
impacts:**

**Corey Phillis  
Thurs 10:30am,  
Rm 607**



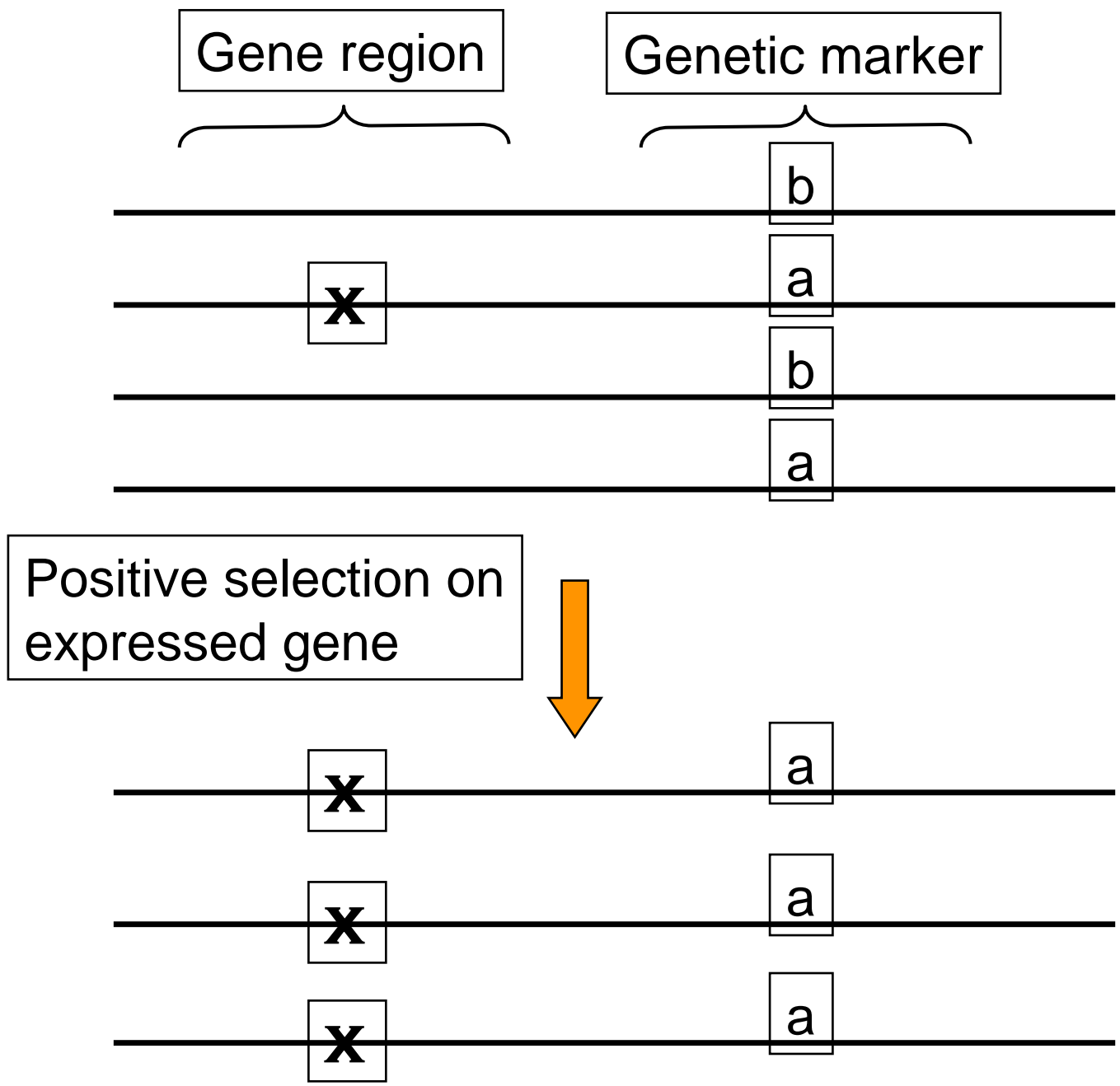


# Genome Screen



- 24 individuals each from above and below falls
- 298 microsatellites loci genotyped, 188 anonymous and 110 EST-linked.
- Loci distributed over all 29 linkage groups with ~10 cM coverage of the *O. mykiss* genome.





## Genome Screen: methods of outlier detection

### ➤ **Differentiation**

Fdist; Beaumont & Nichols 1996.

DetSel; Vitalis et al. 2003.

BayeScan; Foll & Gaggiotti 2008.

### ➤ **Variation**

$\ln(RV)$ ,  $\ln(RH)$ ; Schlötterer 2002; Kauer et al. 2002.

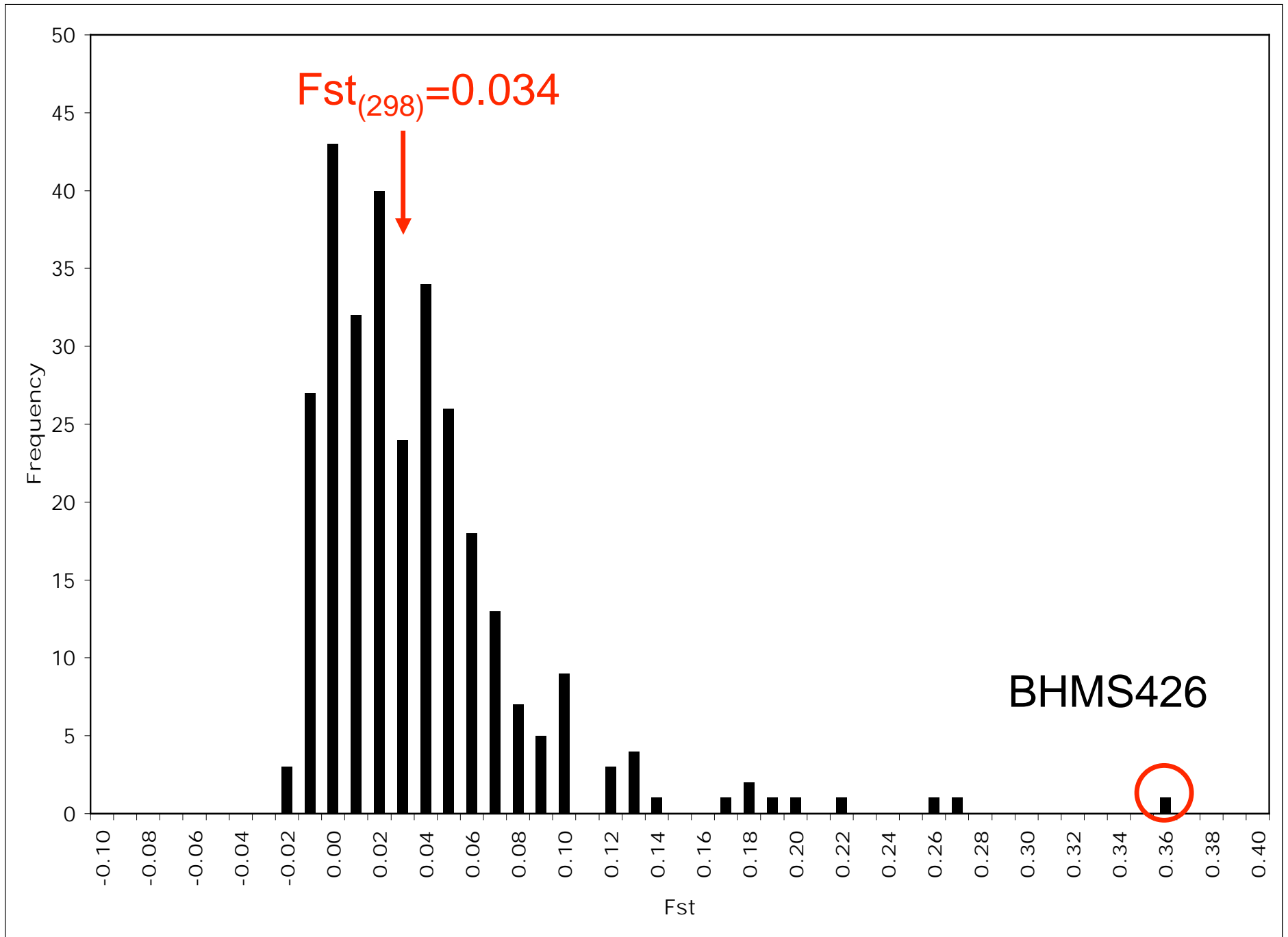


## Summary

Marker	$F_{ST}$	Fdist2	DetSel	ln(RH)	Chromosome	Linkage Group	Position
OMM1120	0.111	X	X	X	10	20	80.5
OMM5011	0.214	X	X	X	23	30	24.2
OMM1289	0.183	X	X	X	21	15	32.4
OMM3067	0.196	X	X	X	19	14	39.3
OMM1409	0.180	X	X	X	15	7	93.4
OMM1009	0.097	X	X	X	5	8	76.7
BHMS426	0.358	X	X		5	8	76.7
OMM3090 <sup>1</sup>	0.127	X	X		18	16	62.7
OMM1213	0.166	X	X		6	10	74.4
OMM5229	0.258	X	X		sex	1	48.3
OMM5195	0.267	X	X		10	20	104.4
BX873238	0.179	X	X		18	16	110.2
OMM1292	0.115	X	X		22	5	26.4
OMM5136	0.092		X	X	sex	1	35.6
OMM3024 <sup>1</sup>	0.096		X	X	17	29	0
OMM5008	0.092	X			12	9	30.1
OMM5166	0.090		X		-	-	-
OMM5117	0.121		X		-	-	-
OMM5014	0.057		X		9	21	61.9
CA361411	0.130		X		22	5	45.4
OMM5038	0.079		X		20	17	43
CA054538	0.118		X		6	10	51.9
OMM1756	0.099		X		24	26	9.6
OMM1000	0.044		X		sex	1	21.1
OMM5060	0.131		X		5	8	60.5
BX310634	0.095		X		9	21	106.4
OMM1386	0.020		X		22	5	19.8
OMM3097	0.124		X		11	19	51.6
OMM1231	0.099		X		1	6	96.8
OMM1581	0.048		X		11	19	22.8
OMM1036	0.037			X	21	15	52.4
OKI23	0.048			X	-	-	-
OMM5109	0.045			X	3	31	120.4
OMM5124	0.047			X	18	16	76
OMM1762	0.025			X	28	13	5.3
BX076085	0.062			X	sex	1	35.6
OMM1241	0.074			X	19	14	29

- Total of 37 outliers.
- 20 anonymous,  
17 EST-linked  
--elevated proportion of  
EST-linked loci
- 9 with two methods.
- 6 outlier loci identified  
by all three methods

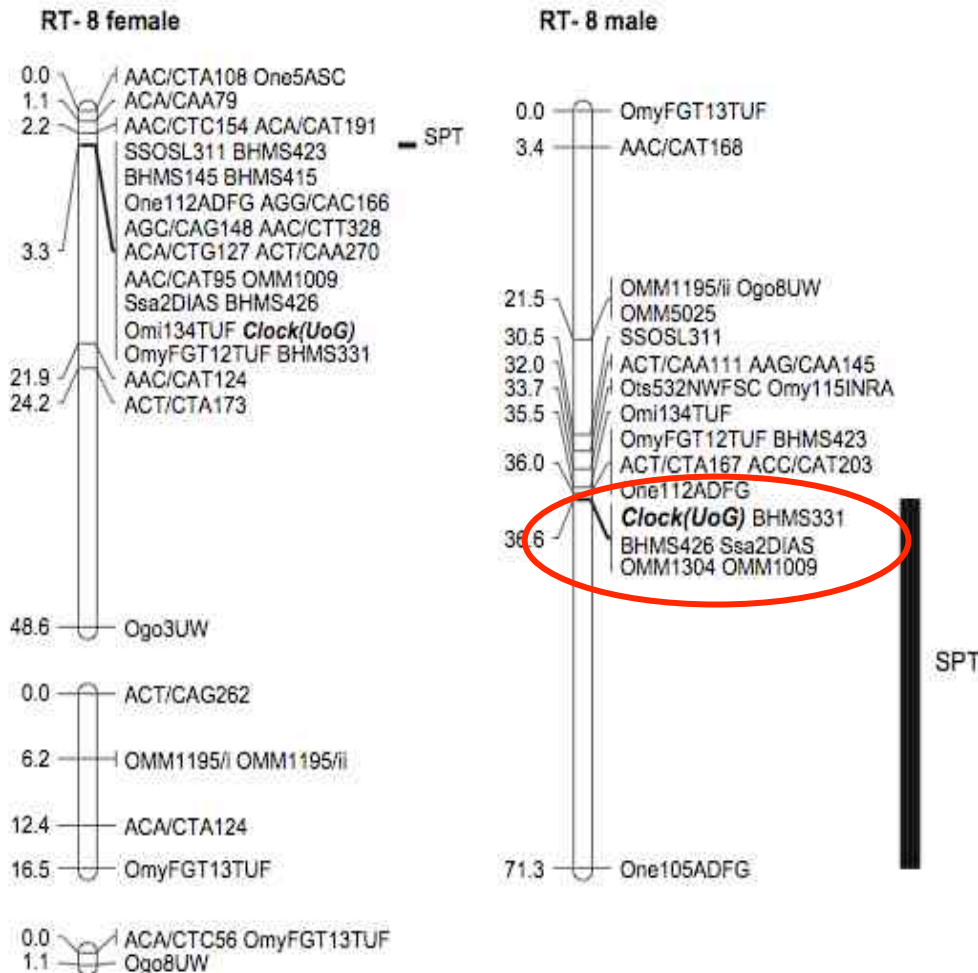
from Martinez et al. 2011





*BHMS426* & *OMM1009* map to same genomic region identified as a QTL for spawn timing, as well as the *Clock* gene.

(O'Malley et al. 2003; Leder et al. 2006)



Nichols et al. 2008, Genetics

OC8= Chromosome Omy5  
Rexroad et al. 2008

from Leder et al. 2006

**Now What?**



- - **More Loci:**
    - Random loci
    - Targeted loci
  - **More Populations.**

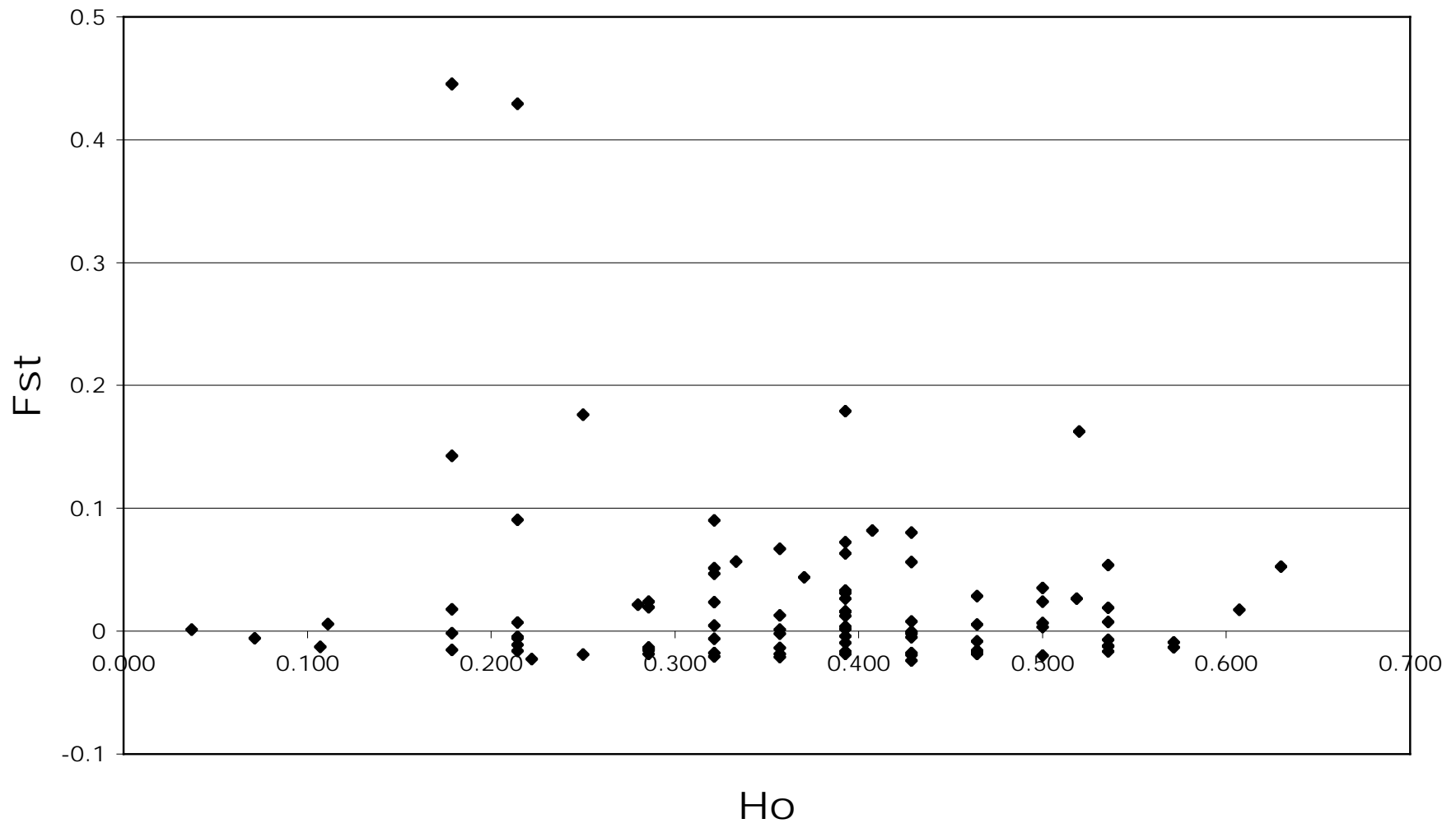


## More Loci: SNP genome scan

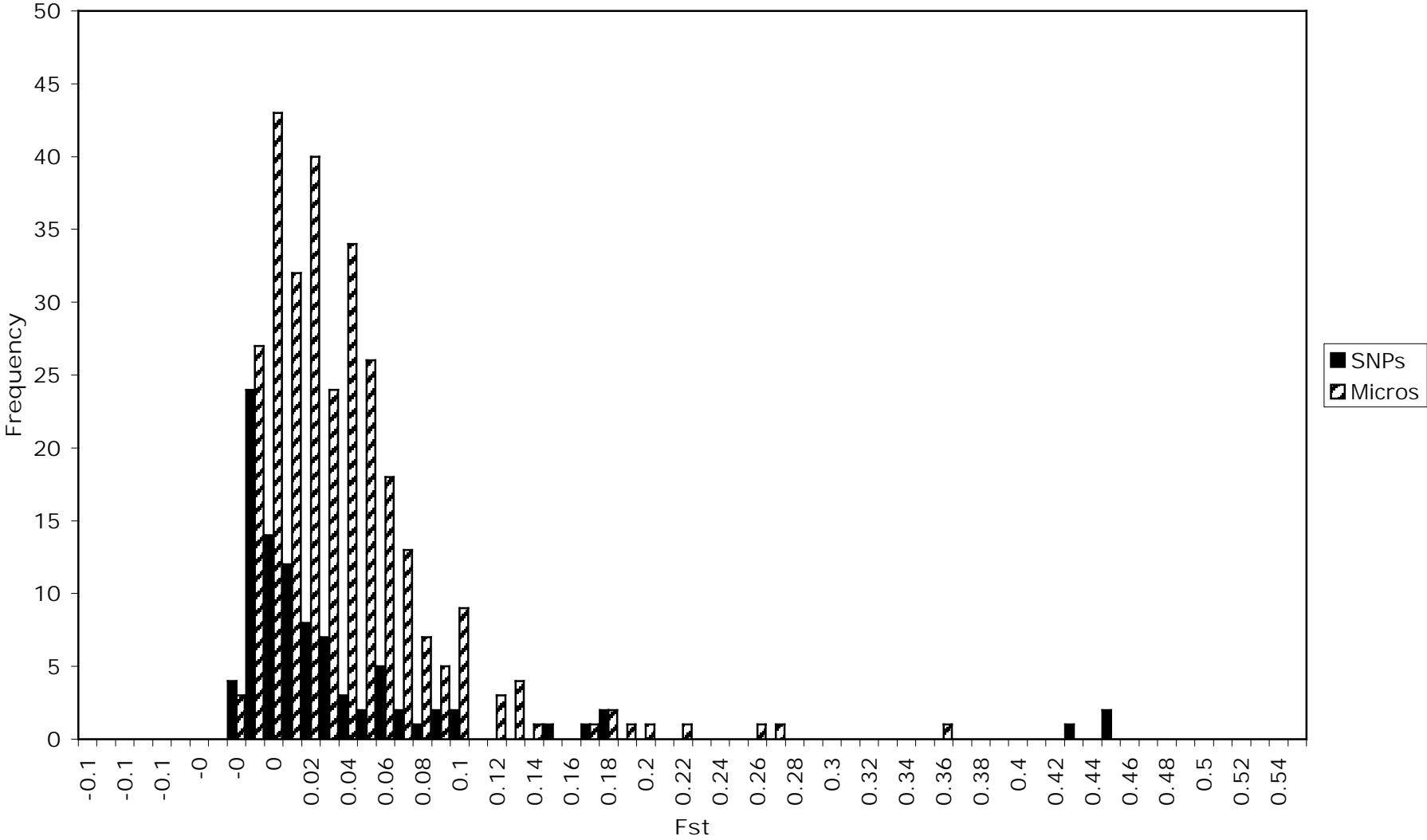
>>Abadía-Cardoso et al. (2011) developed a panel of 96 SNP loci from *O. mykiss* ESTs.

>>Genotyped these loci on a sample of individuals from the same populations above and below Big Creek Falls.

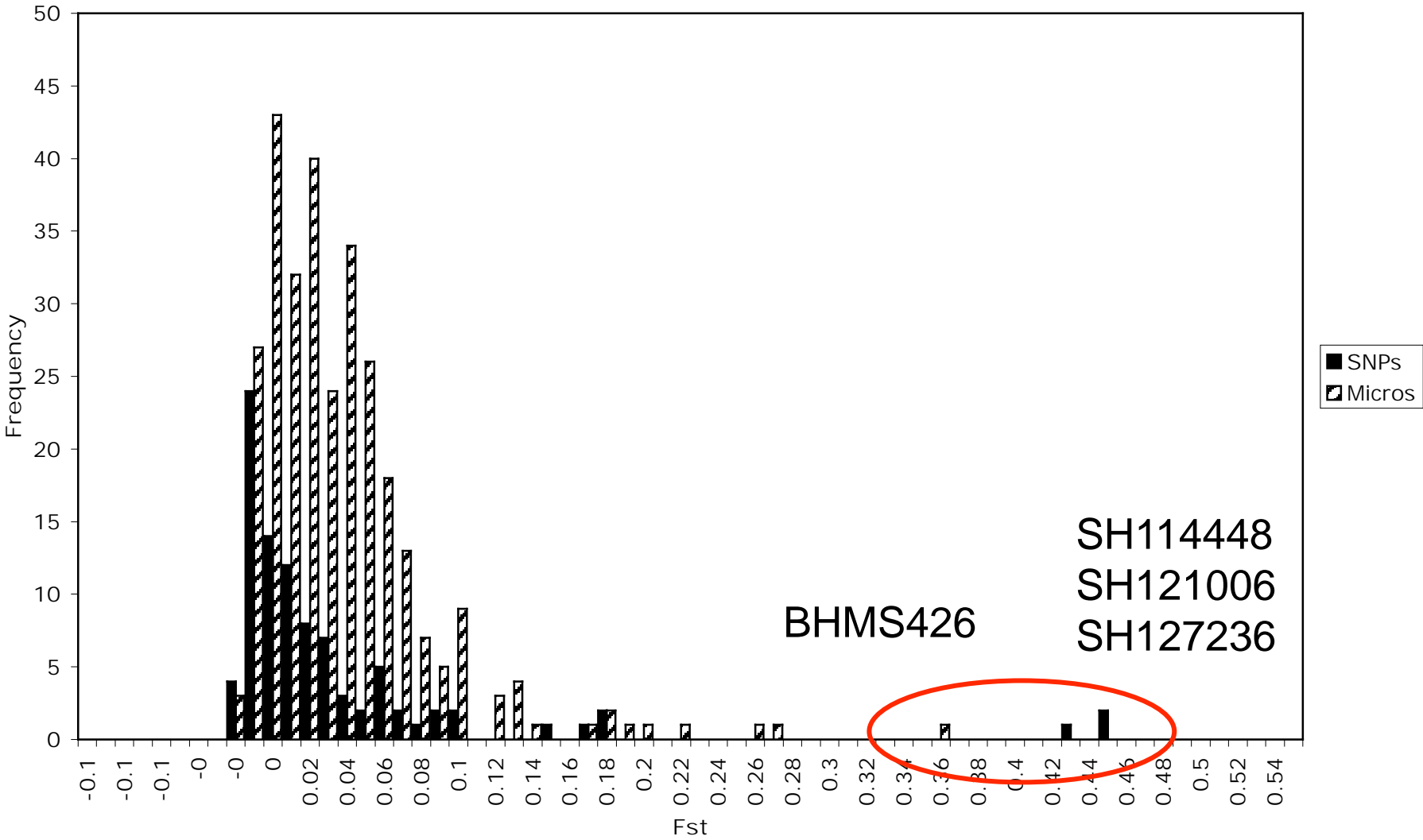
Weir vs AF SNPs



Fst Histogram Micros and SNPs



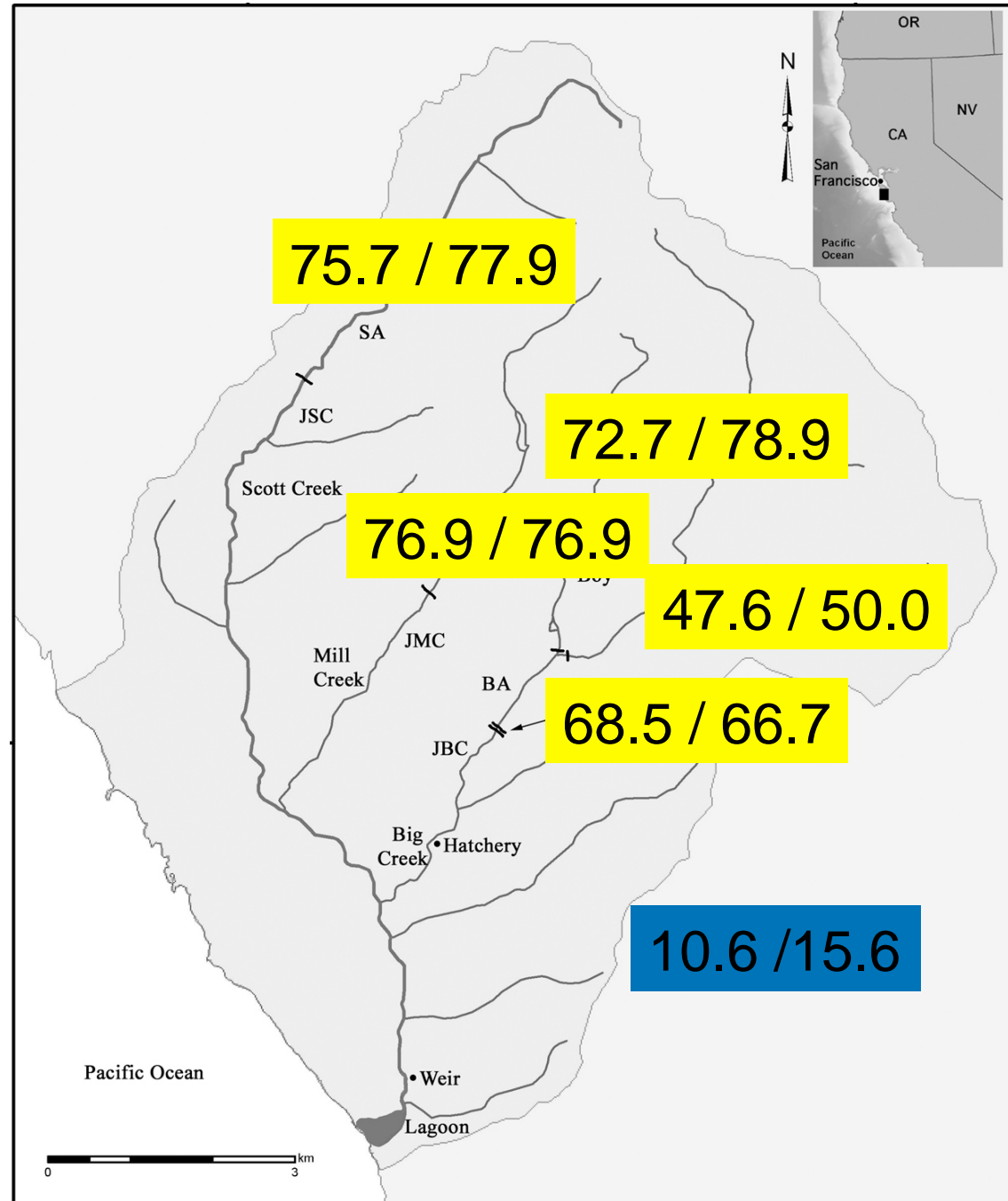
# Fst Histogram Micros and SNPs





# More Populations: Within Scott Creek

SH114448(1)  
/  
BHMS426(121)

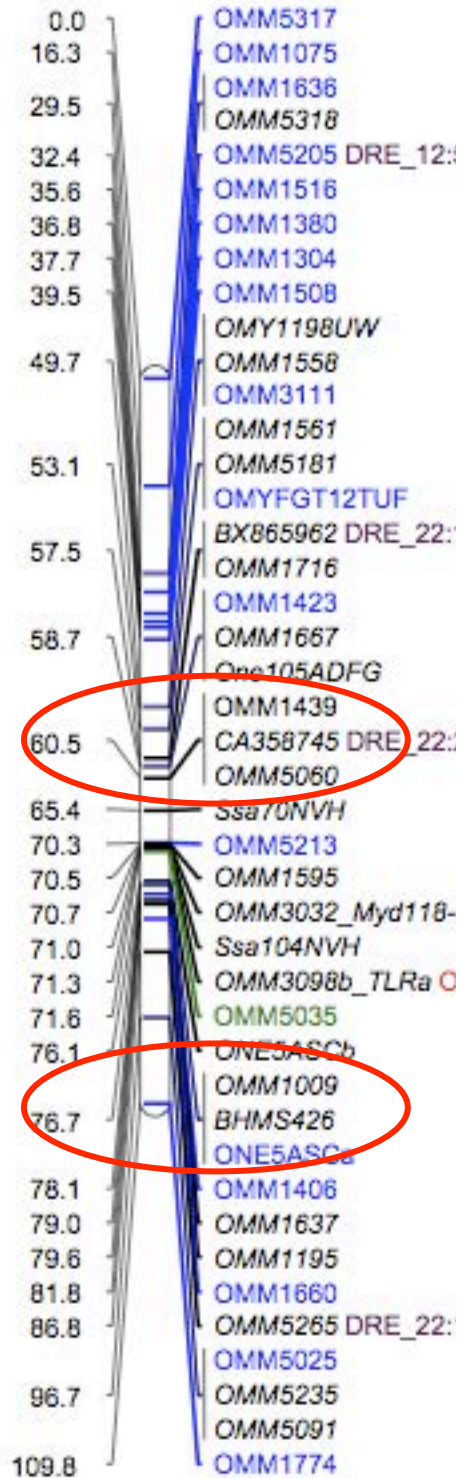


# More Populations: Fst within Scott Creek

	AF	BOY	MA	SA	TF	
BOY	0.05					
MA	0.12	0.15				All 95 loci
SA	0.07	0.12	0.20			
TF	0.01	0.09	0.14	0.08		
WEIR	0.05	0.09	0.14	0.09	0.04	
BOY	-0.01					
MA	0.00	-0.03				SH114448-87
SA	0.00	-0.02	-0.03			
TF	0.08	0.11	0.14	0.14		
→ WEIR	0.52	0.59	0.65	0.61	0.31	
BOY	-0.01					
MA	-0.01	-0.01				SH121006-131
SA	0.00	-0.02	0.00			
TF	0.06	0.10	0.03	0.12		
→ WEIR	0.52	0.60	0.54	0.61	0.34	
BOY	0.11					
MA	-0.02	0.10				SH127236-583
SA	0.00	0.17	-0.02			
TF	0.08	-0.02	0.08	0.15		
→ WEIR	0.52	0.26	0.56	0.60	0.29	
BOY	0.01					
MA	0.00	-0.03				BHMS426
SA	0.03	-0.02	-0.02			
TF	0.02	0.11	0.08	0.13		
→ WEIR	0.33	0.45	0.43	0.47	0.17	

# Omy5

## Linking it all together... literally



<--OMM5060 & SNP OMS00177\* (cM60.5)

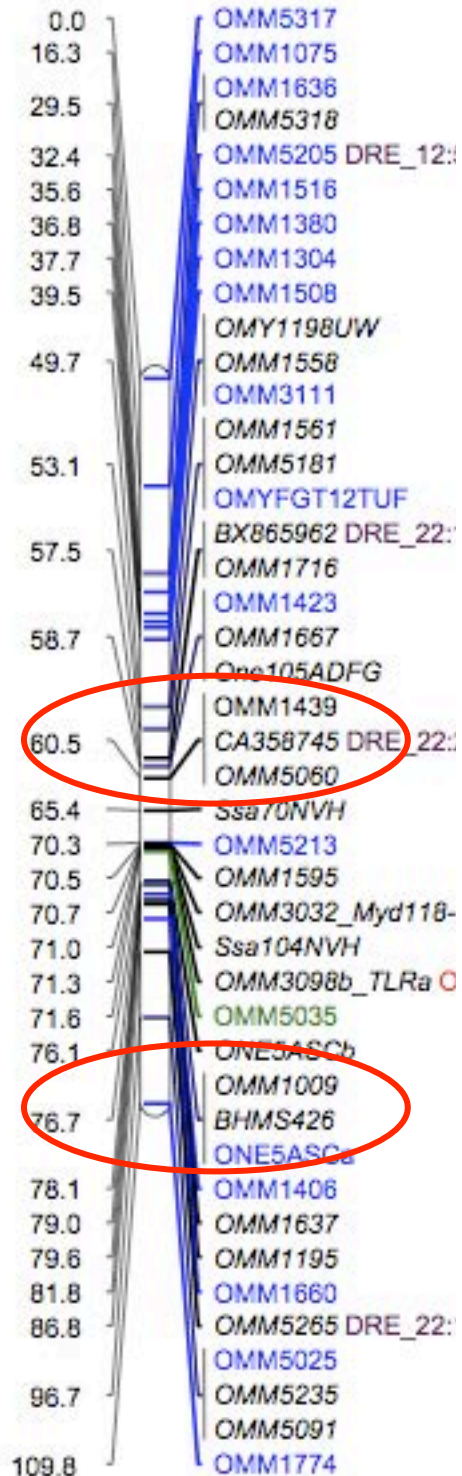
<--BHMS426, OMM1009 & SNP OMS00169\* (cM76.7)

\*OMS SNPs from Castaño Sánchez et al. 2009

# Omy5

## Linking it all together... literally

**OMS00169 and OMS00177 are in strong LD with SH114448, SH121006, and SH127236 (Thanks to Sewall Young, Morten Limborg, Lisa Seeb, and Todd Seamons).**



<--OMM5060 & SNP OMS00177\* (cM60.5)

<<SH114448, SH121006, and SH127236???

<--BHMS426, OMM1009 & SNP OMS00169\* (cM76.7)

\*OMS SNPs from Castaño Sánchez et al. 2009



In fact, these loci are not just linked, but produce identical genotypes:.

**BHMS426 SH114448 SH121006**

Above19	121	129	1	3	2	1
Above20	121	129	1	3	2	1
Above21	121	121	1	1	2	2
Above22	121	129	1	3	2	1
Above23	121	121	1	1	2	2
Above24	121	121	1	1	2	2
Below01	121	129	1	3	2	1
Below02	129	129	3	3	1	1
Below03	131	131	3	3	1	1
Below04	129	129	3	3	1	1
Below05	129	129	3	3	1	1

## Conclusions:

- Three microsatellite outliers and three SNP outliers identified in a genomic region of Chromosome 5 that also contains QTL and the *Clock* gene --Concordant signals from multiple independent analyses. (Leder et al. 2006, Nichols et al. 2008, Martinez et al. 2011, Present data.)
- These loci are in strong linkage disequilibrium, which appears to span at least 16cM.
- SNP SH121006 is a non-synonymous change in an EST; SH114448 is synonymous, but the EST sequence contains a non-synonymous substitution in complete linkage to the assayed SNP.
- But,
  - >SH121006 not identified as a candidate locus by Narum et al. 2011
  - >Linkage among these loci variable among populations

# Acknowledgements

## Molecular Ecology Team:

Alicia Abadía-Cardoso, Eric Anderson, Anthony Clemento,  
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Andres Martinez.

Sewall Young, Lisa Seeb, Morten Limborg, Todd Seamons

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## More populations: Beyond Scott Creek??

SH114448

Population	Allele 1
ARH Eagle Lake strain	0.938
Bauers Creek, Goose Lake	1.000
Buckboard Creek, Upper Klamath	1.000
FH Mt Whitney Early	0.438
HCH Owens Lake Basin, Kamloop strain	1.000
Sacramento R, McCloud R, Butcherknife Ck	1.000
Battle Creek, Sacramento River	0.587
Carmel River	0.042
Eel River, Summer	0.313
Klamath, Kelsey Ck	0.682
New Zealand	0.565
Rio Santa Cruz, Argentina	0.438
Russian River (mixed pops)	0.576
San Lorenzo	0.100
Scott Creek (Adults)	0.185
Willamette River, Columbia River	1.000







