

The Impact of Selection on the Genome

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Introduction

- Historically pedigree used to manage genetic diversity
 - Assumes selection-free, neutral loci
- Loci close to QTL will have higher loss of diversity

Roughsedge et al. (2008) *Genetics Research*, 90:199-208

Sonesson et al. (2012) *Genetics Selection Evolution*, 44:27

- With high density data we can:
 1. Identify regional variations in selection
 2. Examine level of conformity with pedigree model

Materials & Methods

- Line A
 - Reproductive traits & growth rate
 - 1,551 genotyped individuals over 6 generations
 - 39,377 SNPs
- Line B
 - Reproductive traits
 - 4,889 genotyped individuals over 6 generations
 - 40,396 SNPs
- Illumina PorcineSNP60 Beadchip

- Fit a regression for each SNP :

$$\ln(H_{ij}) = \alpha_j + \beta_j \ln(1-F_i) + \mu_{ij}$$

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Where,

H = Observed heterozygosity

1-F = Expected heterozygosity

\pm = Intercept

μ = Error term

β = Slope of the regression

Model

- Fit a regression for each SNP :

$$\ln(H_{ij}) = \alpha_j + \beta_j \ln(1-F_i) + \mu_{ij}$$

Where,

H = Observed heterozygosity

1-F = Expected heterozygosity

α_j = Intercept

μ = Error term

β_j = Slope of the regression

- Fit a regression for each SNP :

$$\ln(H_{ij}) = \pm_j + 2_j \ln(1-F_i) + \mu_{ij}$$

Where,

H = Observed heterozygosity

1-F = Expected heterozygosity

\pm = Intercept

μ = Error term

2 = Slope of the regression

Regression slope, 2

- Fit a regression for each SNP :

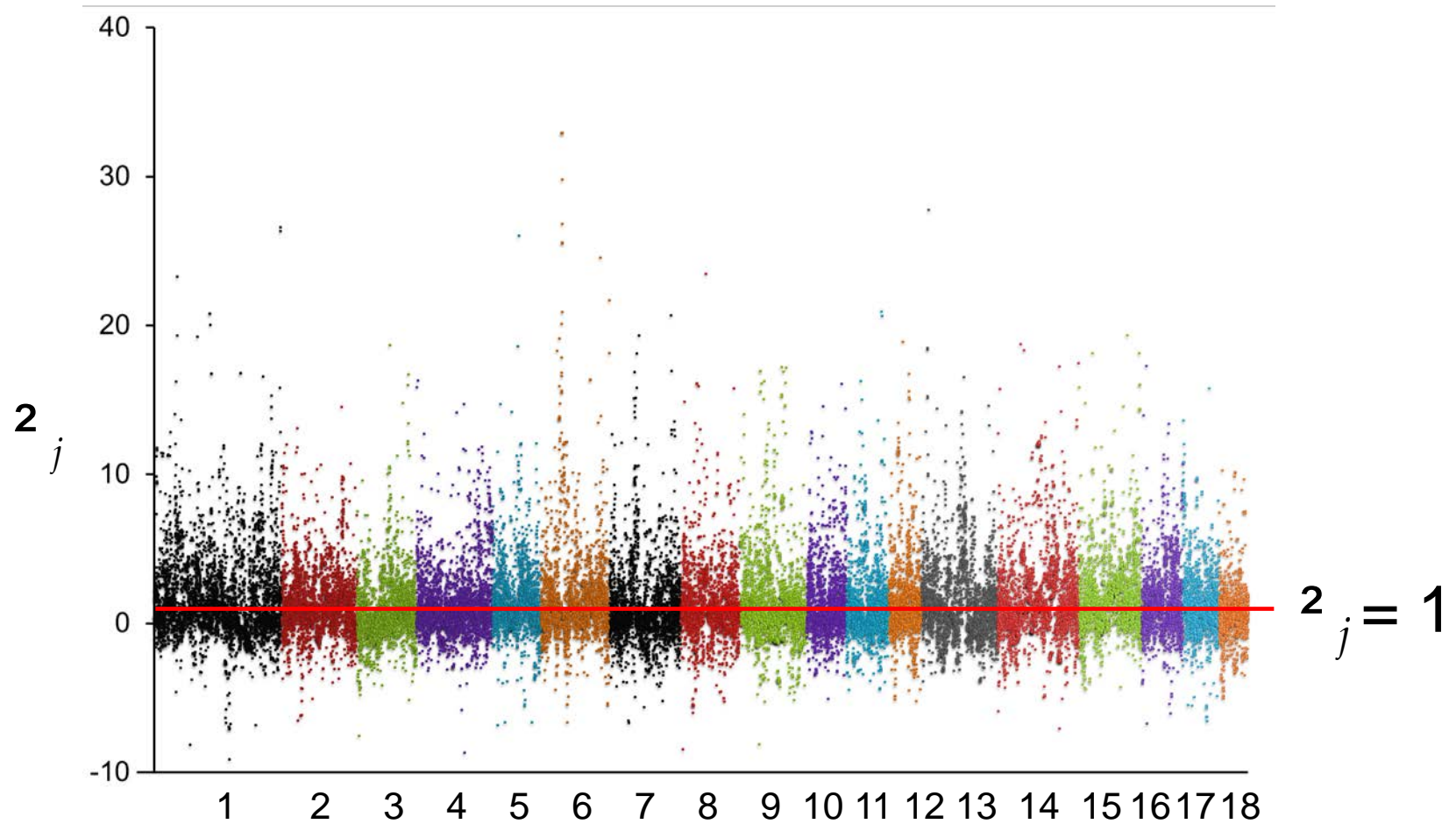
$$\ln(H_{ij}) = \pm_j + \mathbf{^2_j} \ln(1-F_i) + \mu_{ij}$$

$^2_j = 1$, Loss of heterozygosity equals expectation

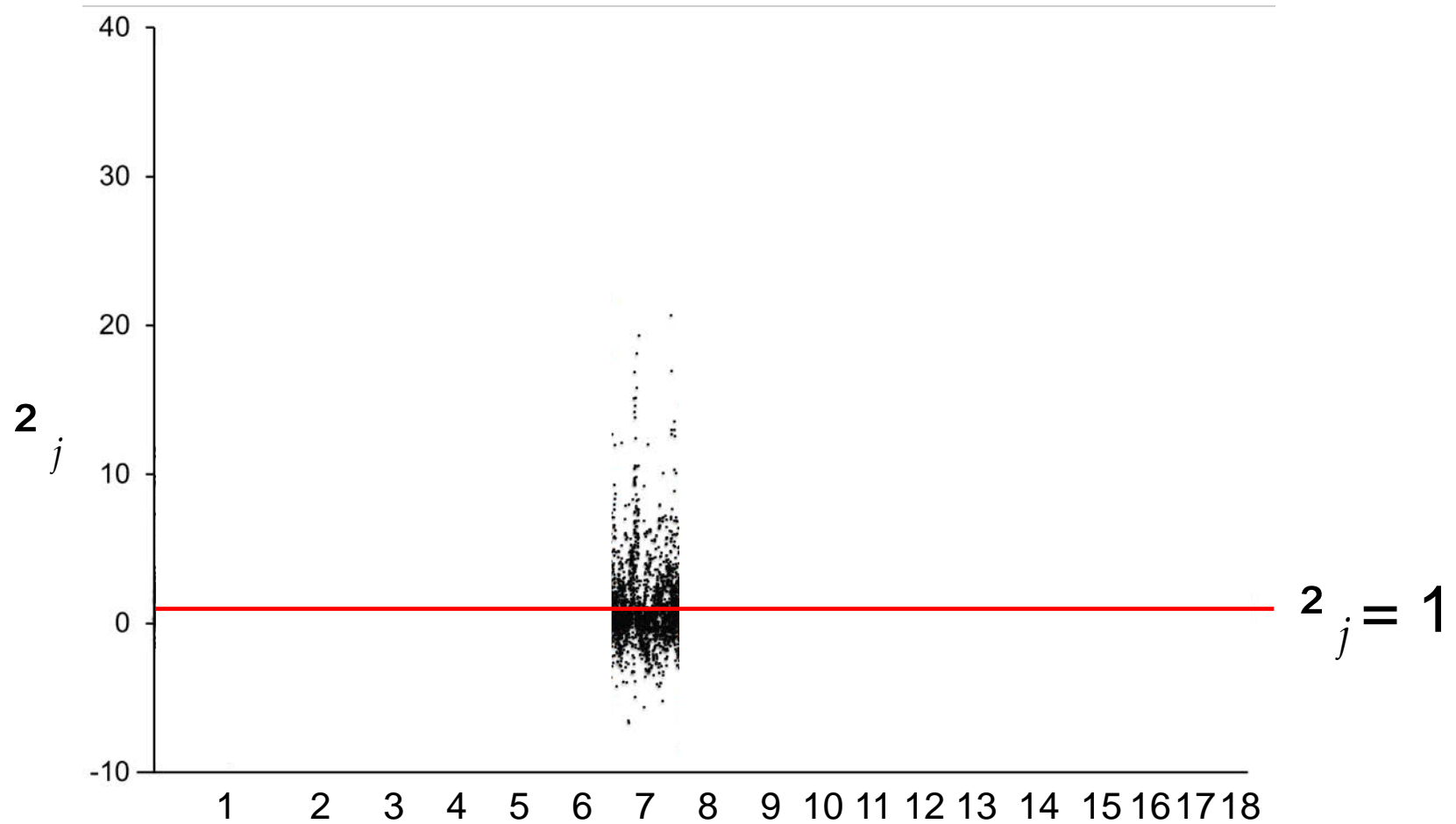
$^2_j > 1$, Loss is greater than expected

$^2_j < 1$, Loss is less than expected

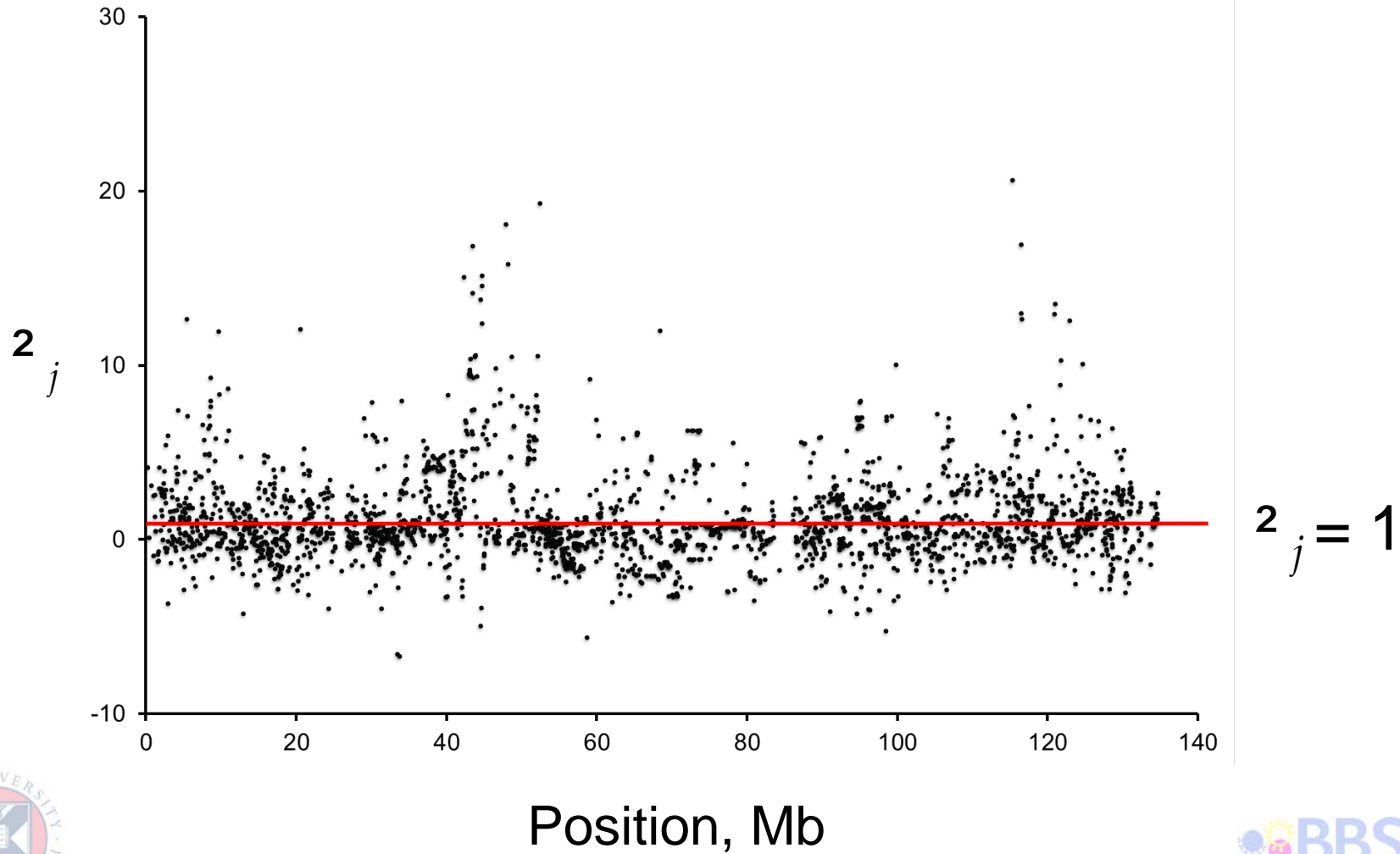
Line A, Genome Wide



Line A, Genome Wide



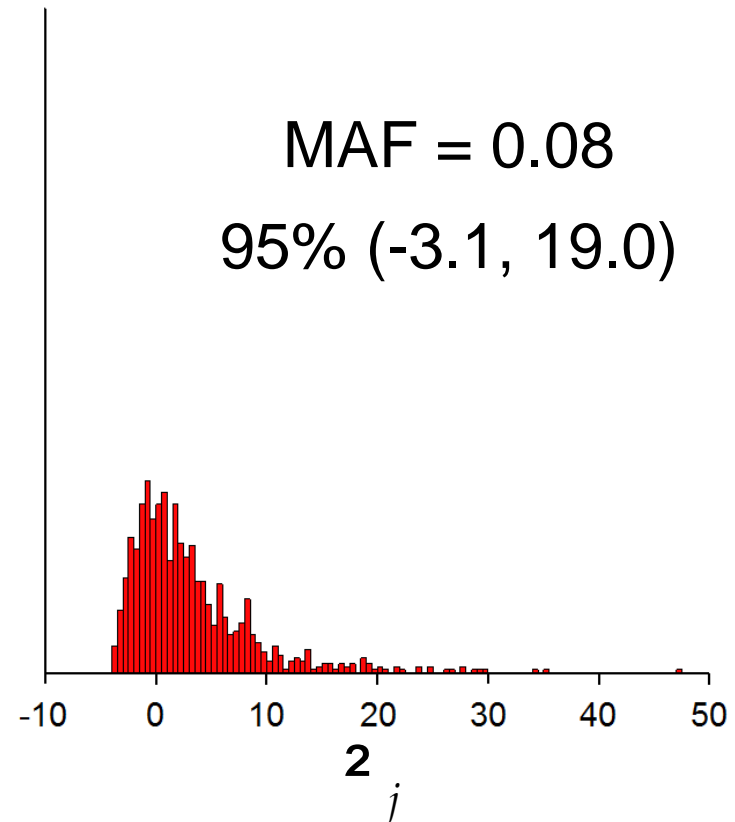
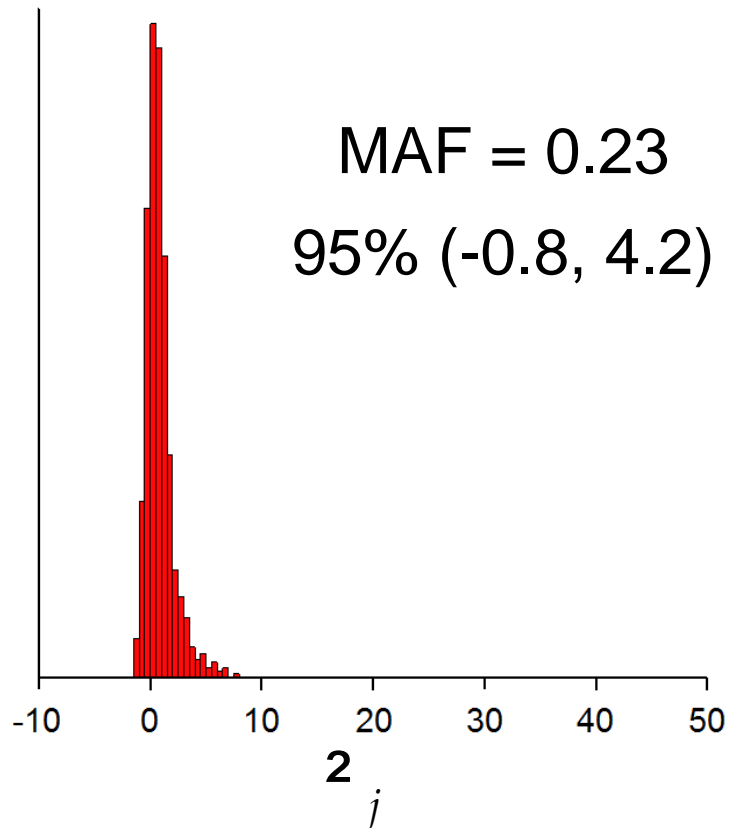
Line A, SSC07



Confidence Intervals

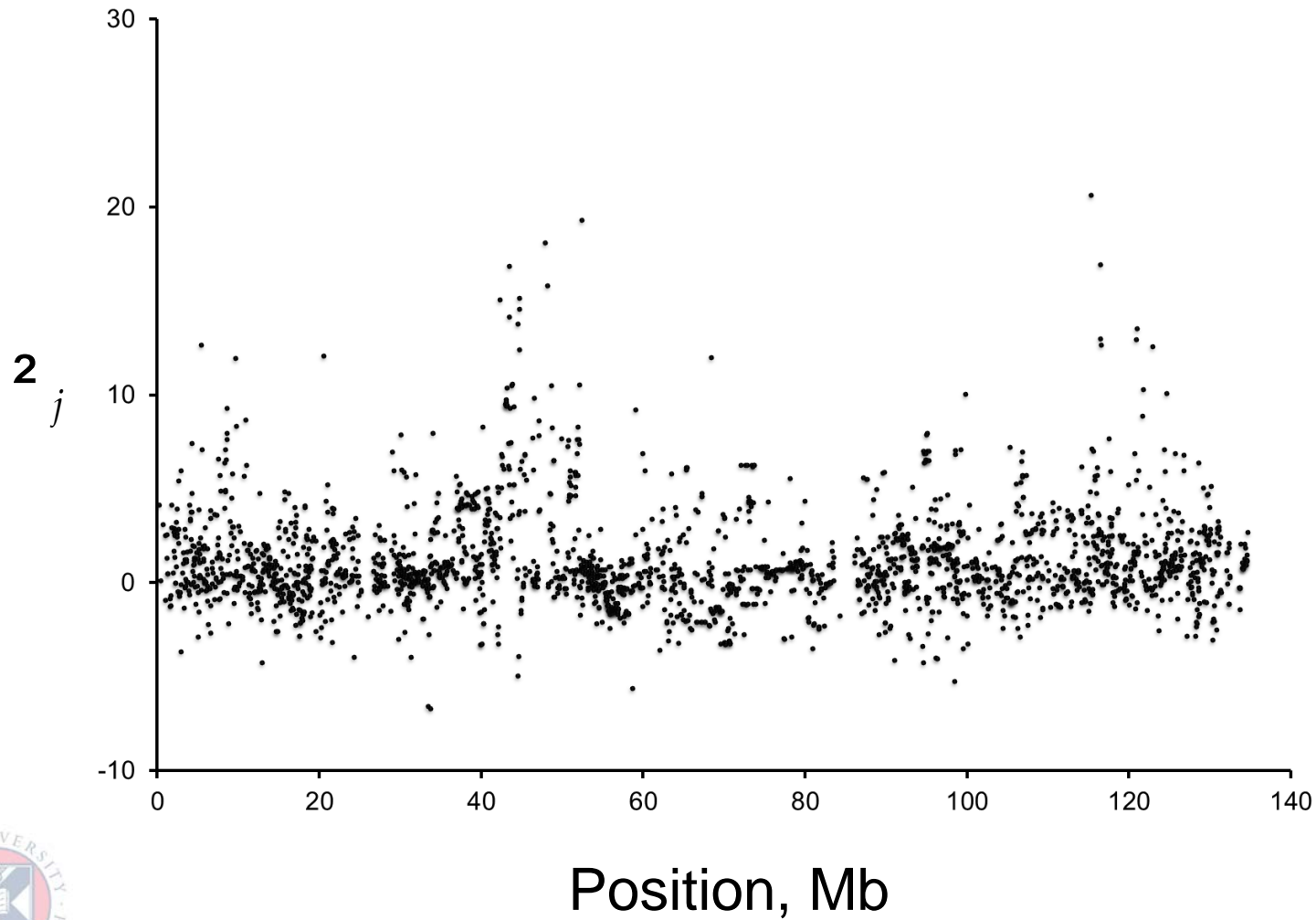


- Bootstrap using gene-dropping for every SNP
- Use distribution of iterations to form confidence intervals

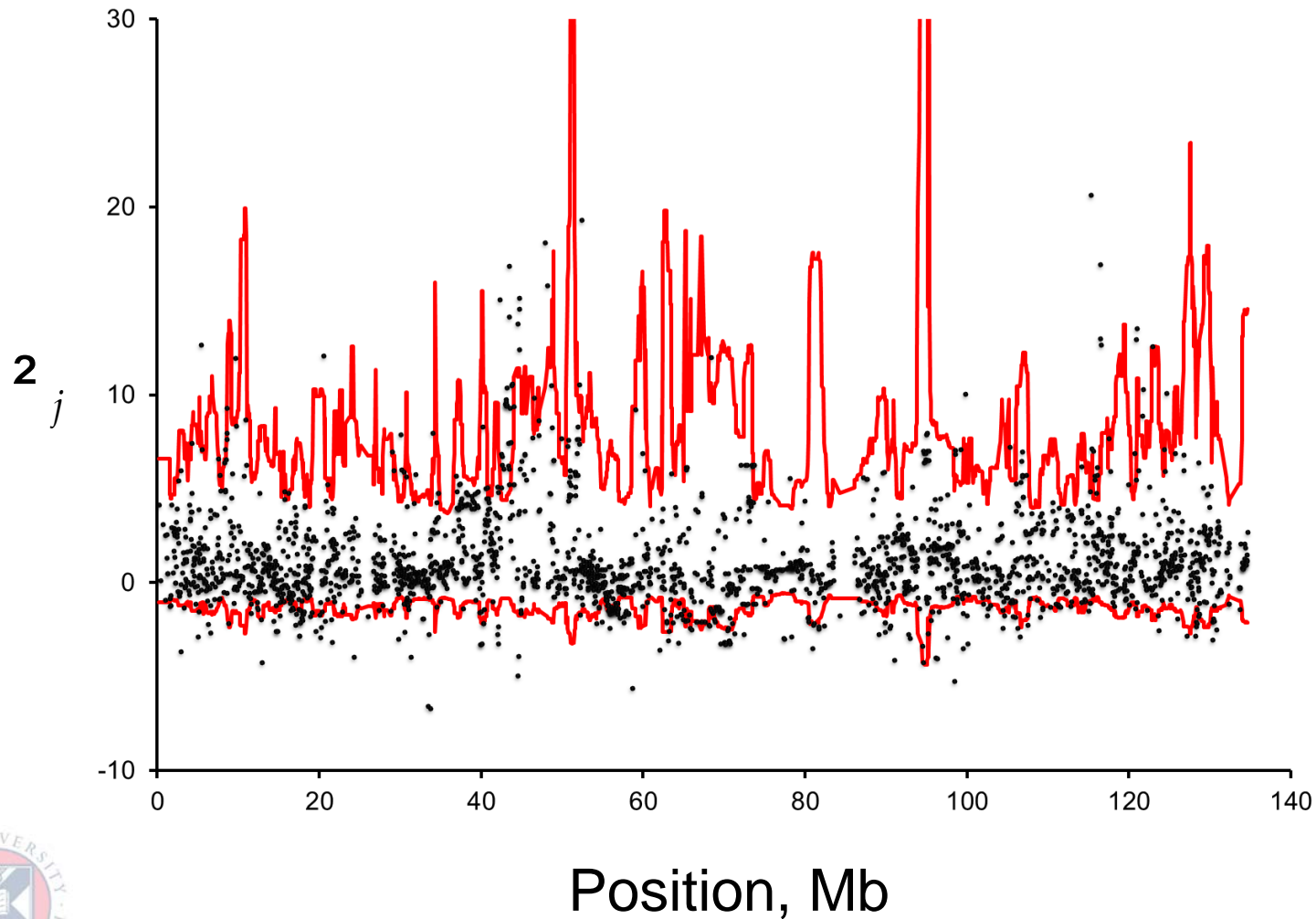


Results

Line A, SSC07



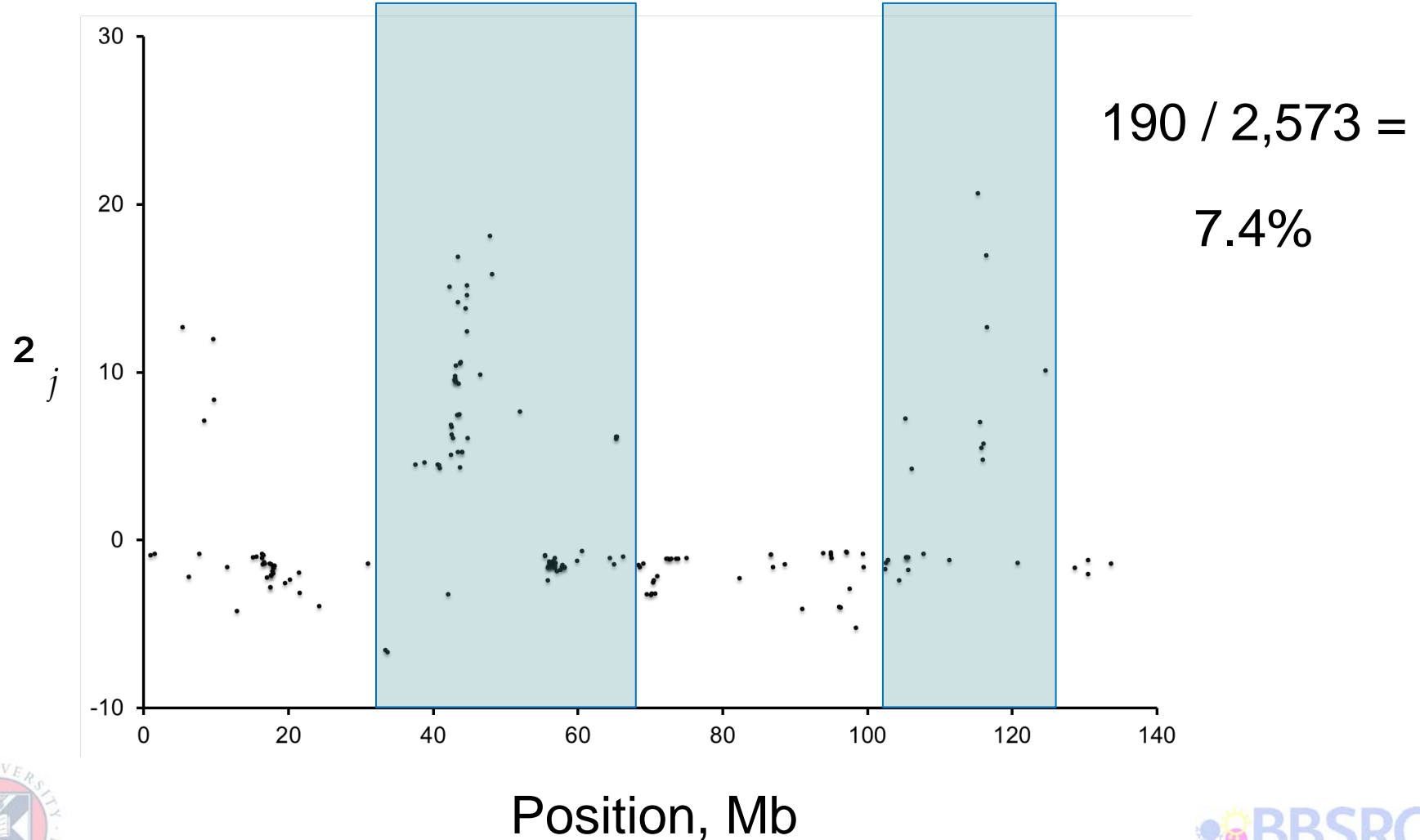
95% Confidence Interval



Line A, SSC07



Significant at 5% level



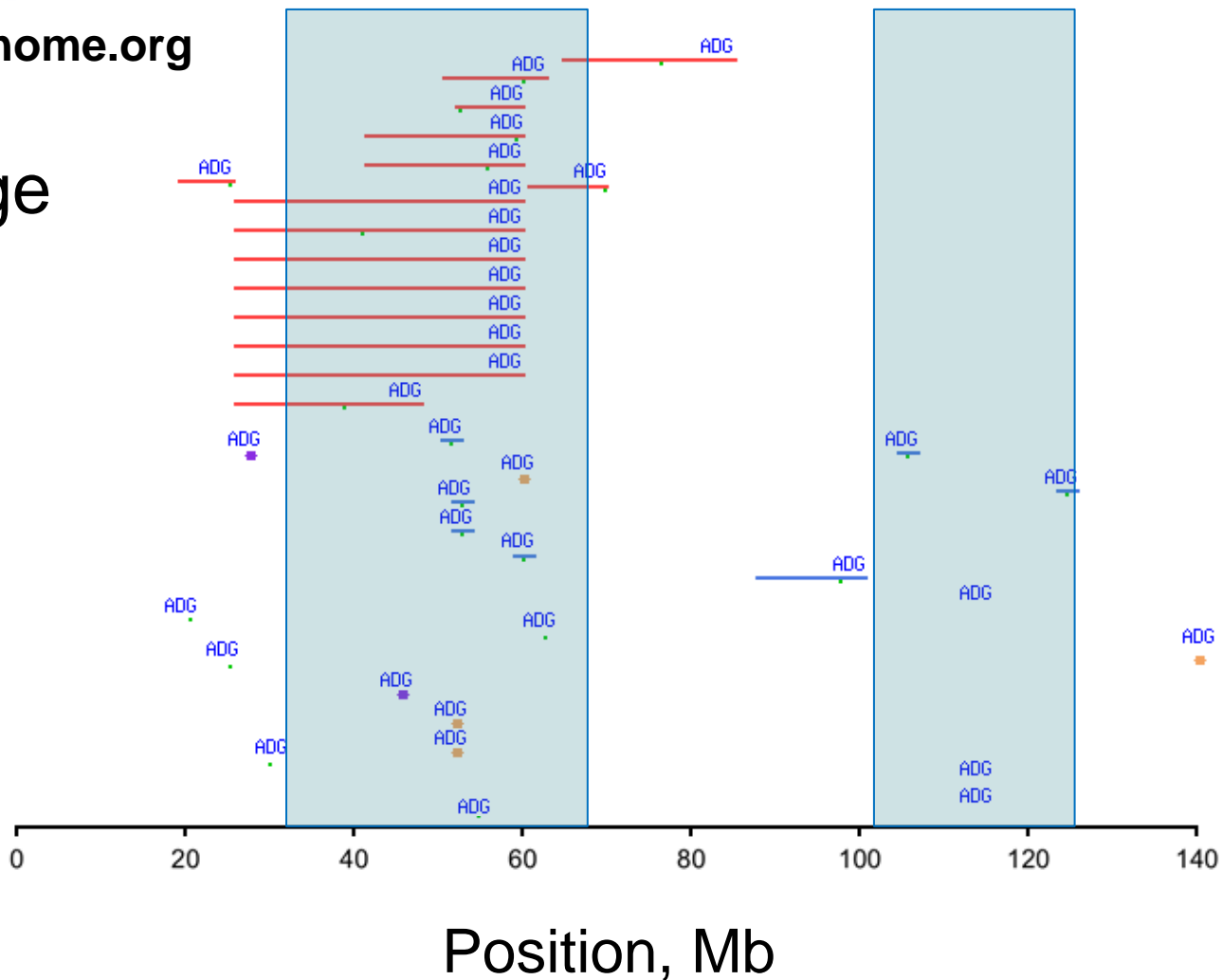
Putative QTL, SSC07



PigQTLdb

animalgenome.org

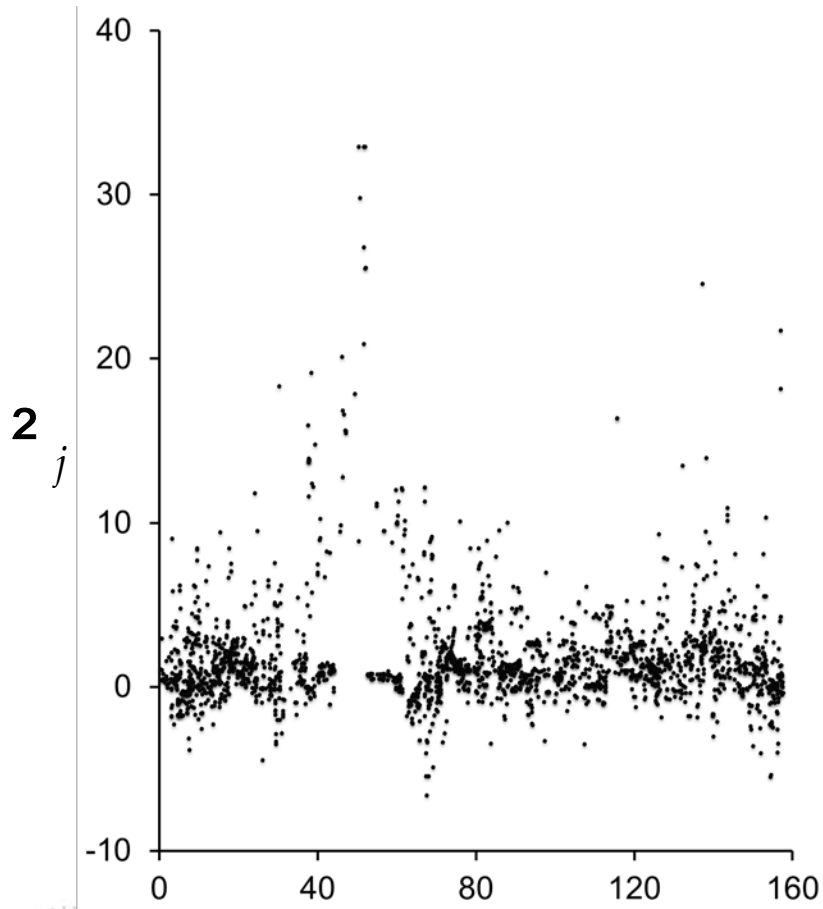
Average
Daily
Gain



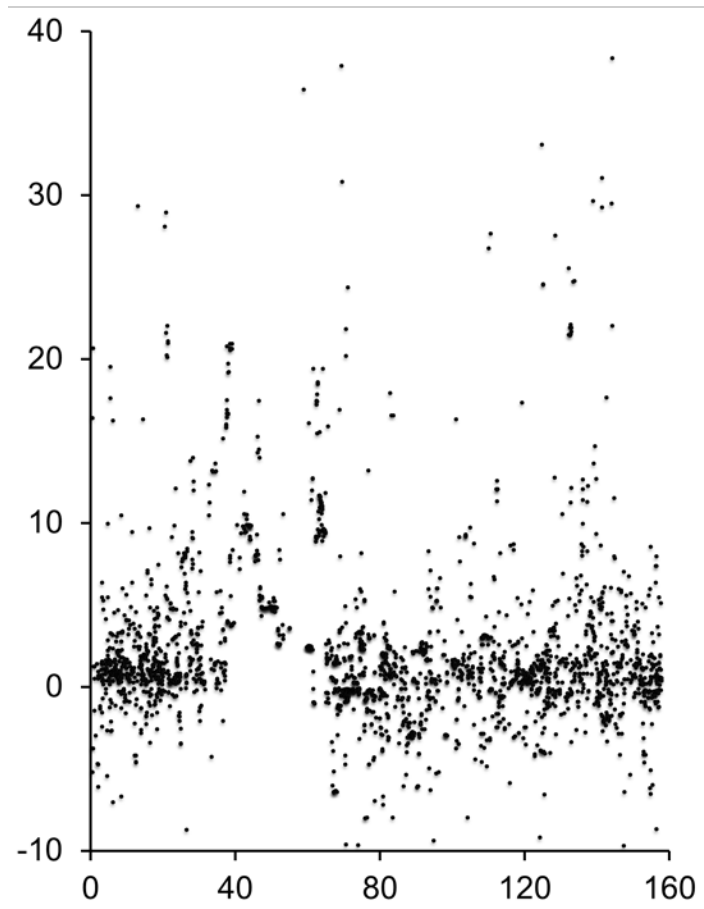
Line Comparison, SSC06



Line A



Line B



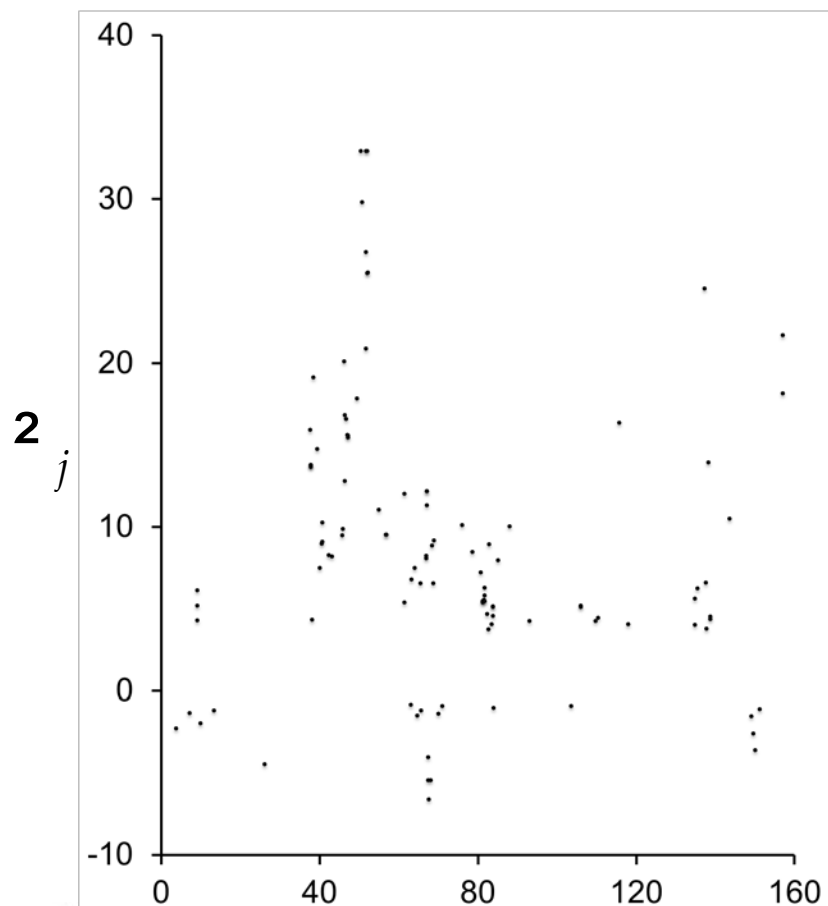
Position, Mb



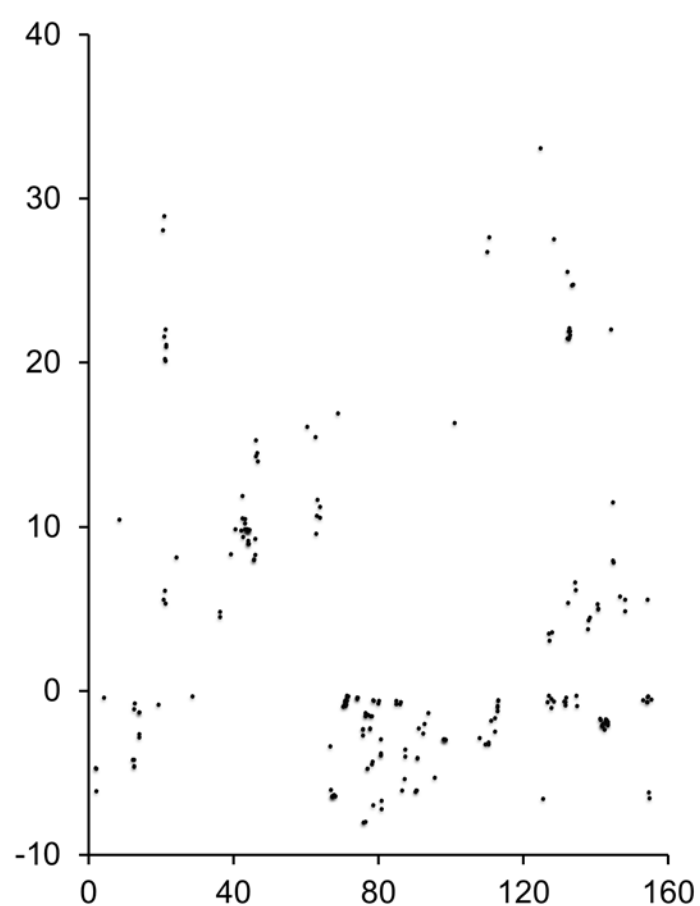
Significant at 5% level



Line A



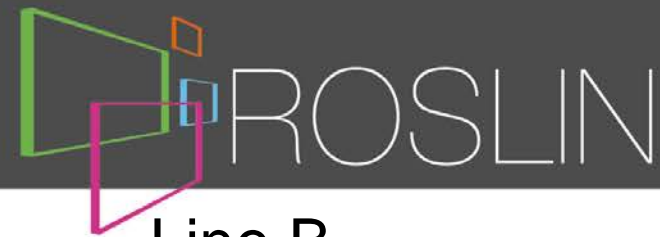
Line B



Position, Mb



Changes in Heterozygosity



Line A

	Confidence Intervals					
	1%	5%	Upper 0.5%	Upper 2.5%	Lower 0.5%	Lower 2.5%
Whole Genome	0.86%	4.05%	0.33%	1.59%	0.53%	2.46%
SSC01						
SSC02						
SSC03						
SSC04						
SSC05						
SSC06						
SSC07		7.4%				
SSC08						
SSC09						
SSC10						
SSC11						
SSC12						
SSC13						
SSC14						
SSC15						
SSC16						
SSC17						
SSC18						

Line B

	Confidence Intervals					
	1%	5%	Upper 0.5%	Upper 2.5%	Lower 0.5%	Lower 2.5%
Whole Genome	1.70%	6.14%	0.65%	2.66%	1.05%	3.48%
SSC01						
SSC02						
SSC03						
SSC04						
SSC05						
SSC06						
SSC07						
SSC08						
SSC09						
SSC10						
SSC11						
SSC12						
SSC13						
SSC14						
SSC15						
SSC16						
SSC17						
SSC18						

 = Evidence for excessive change in heterozygosity

Summation

- With high density data we can:
 1. Identify regional variations in selection
 2. Examine level of conformity with pedigree model

- Evidence of diversity loss at specific regions
 - Putative QTL identification (Line A, SSC07)
- Varying impact between lines (SSC06)
 - Trait Architecture
 - Power
 - Future - Haplotyping

- With high density data we can:
 1. Identify regional variations in selection
 2. Examine level of conformity with pedigree model

- Evidence for inadequacy of pedigree model (Line B)
- Genomic Optimal Contributions
- Precision inbreeding at SNP level
- ‘ ‘ Regional loss of diversity, provided maintained elsewhere

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