

IDENTIFYING GENOMIC CHANGES BETWEEN INDEPENDENT PAIRS OF WILD/DOMESTIC ATLANTIC SALMON POPULATIONS USING A HIGH DENSITY SNP ARRAY

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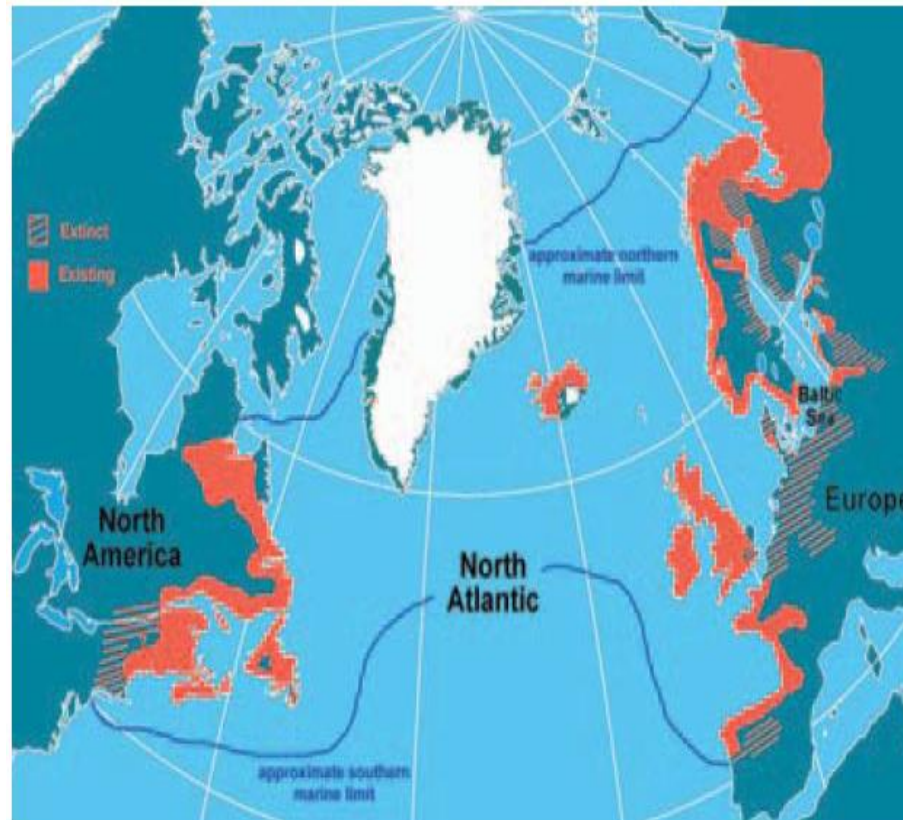
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Distribution of populations of Atlantic salmon

North America

Quebec, Canada to Southern New England (USA).



Europe

North Western Russia to Portugal. United Kingdom (UK), Iceland and Greenland.

Verspoor et al 2007

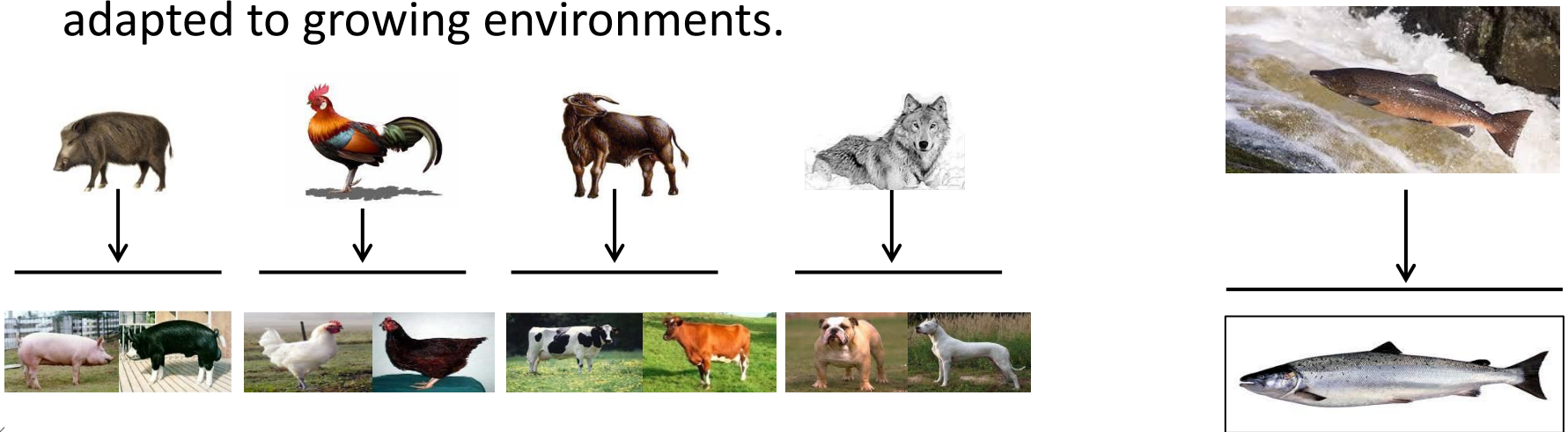
Domestication

Domestication is the process by which a population of plant or animal becomes adapted to a captive environment by genetic changes occurring over generations.

Phenotypic changes: morphology, physiology and behavior.

Genotypic changes: Produced by selective changes and bottlenecks.

The populations of Atlantic salmon farmed in Chile and the world, correspond to populations that have recently been domesticated and adapted to growing environments.



Background of the study populations

Canadian wild population from Gaspé Bay, Quebec, Canada

Scottish wild population from East coast of Scotland



Canadian domestic population
-High growth
-Late sexual maturity.

Scottish domestic population
-High growth.
-Early sexual maturity.



OBJECTIVE

To detect genomic signatures of selection between farmed and wild populations of the same geographical origin (Scotland and Canada).



METHODOLOGY

Samples

	CANADA		SCOTLAND
Wild	(n=44)	Wild	(n=41)
Domestic	(n=37)	Domestic	(n=43)

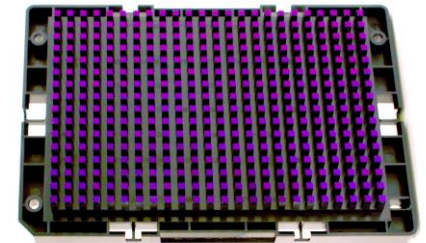
Development of 200K Array.

Whole genome sequencing (WGS) of 20 fish from 7 populations (Illumina HiSeq2000).

~10 Million of SNPs

~**200K best SNPs**

200,000 SNPs array



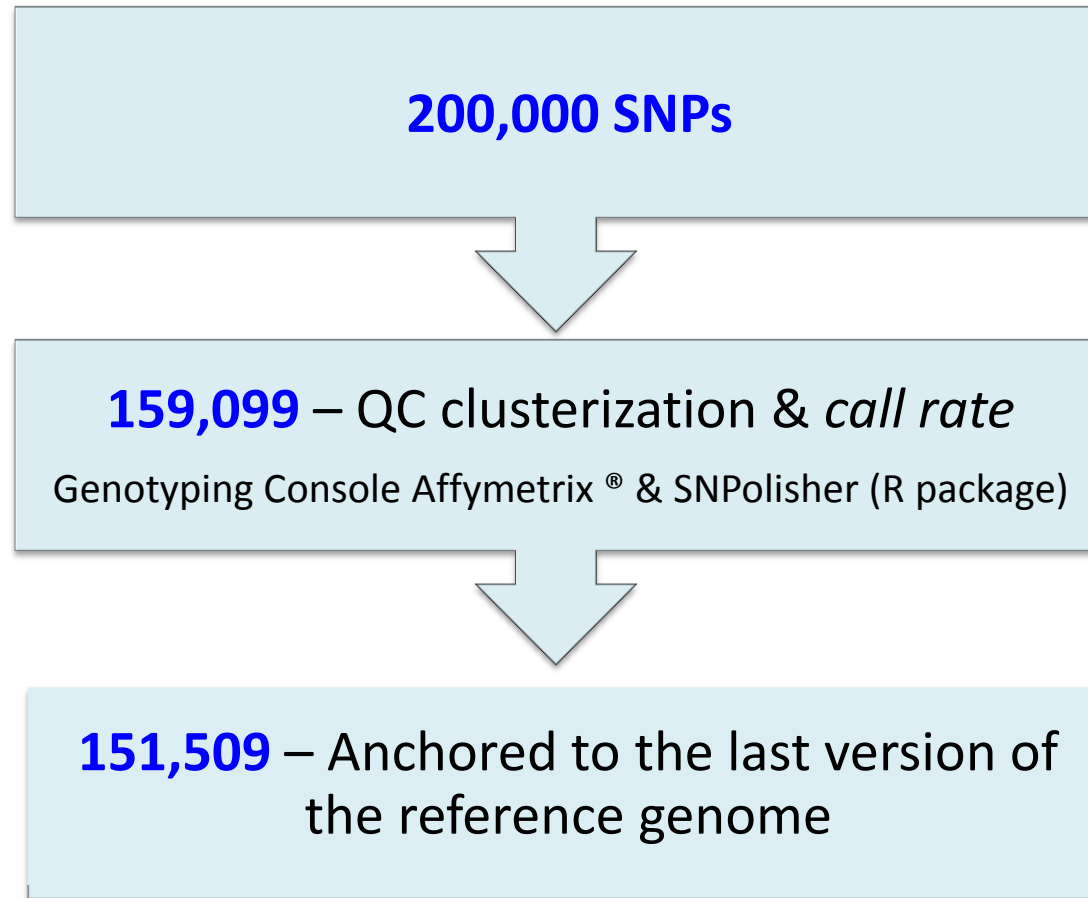
SNP Genotyping

200K SNP Axiom[®] myDesign[™] Genotyping Array

(UGGA-FAVET-University of Chile, Aquainnovo and Affymetrix)



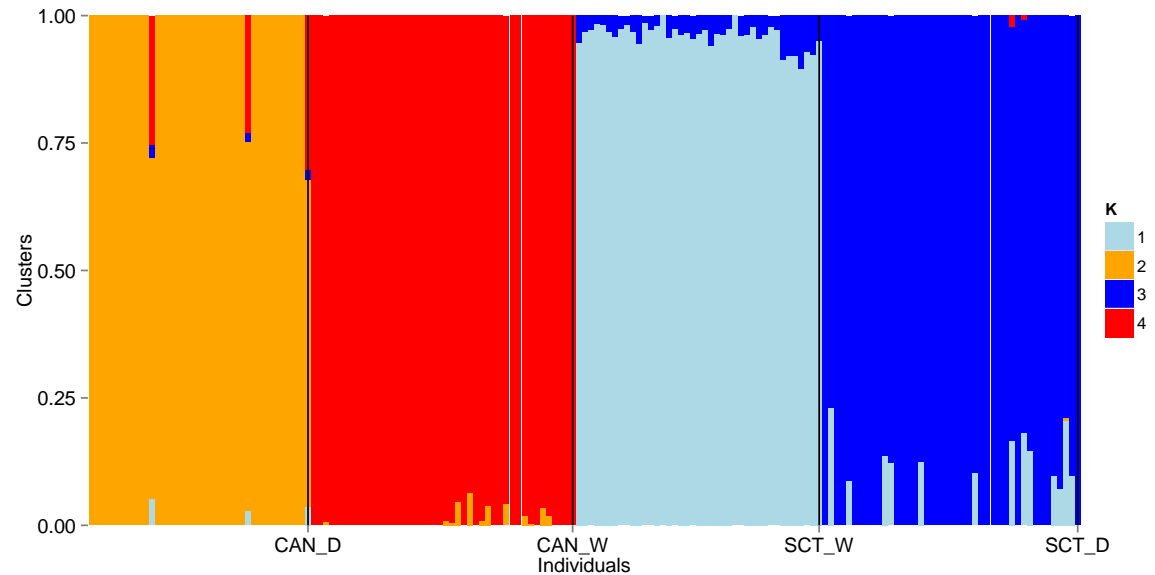
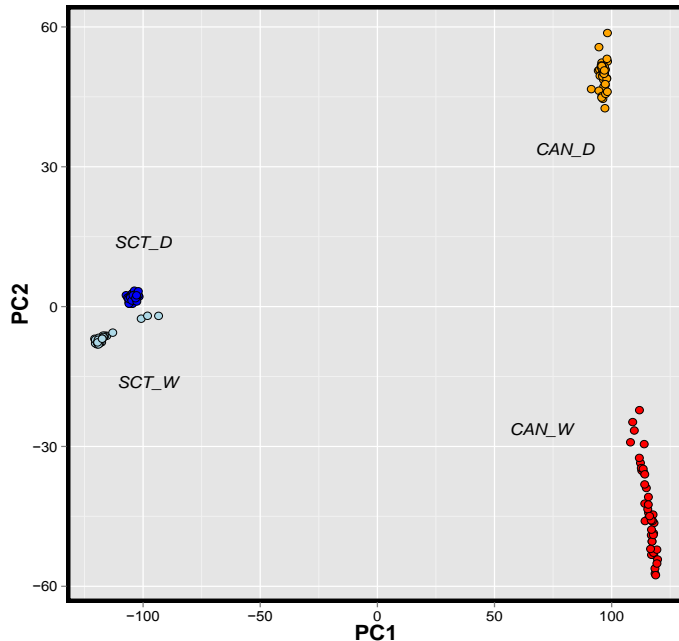
METHODOLOGY AND RESULTS



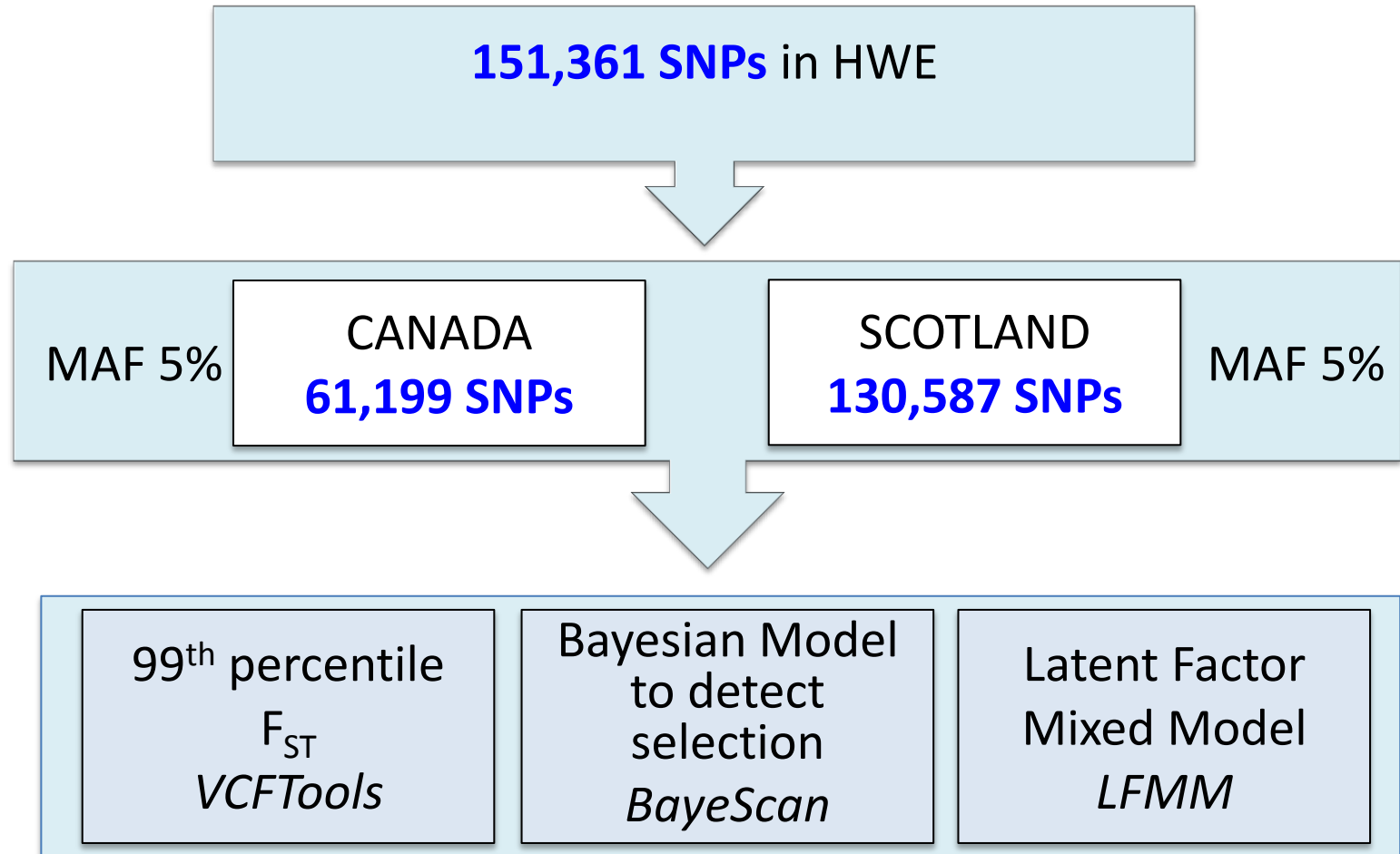
METHODOLOGY AND RESULTS

151,361 SNPs in HWE

Population structure

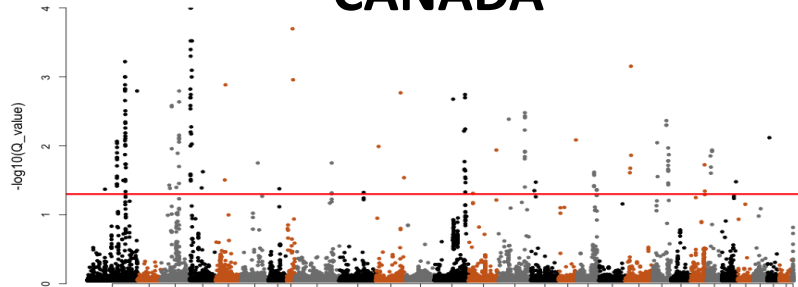


METHODOLOGY AND RESULTS

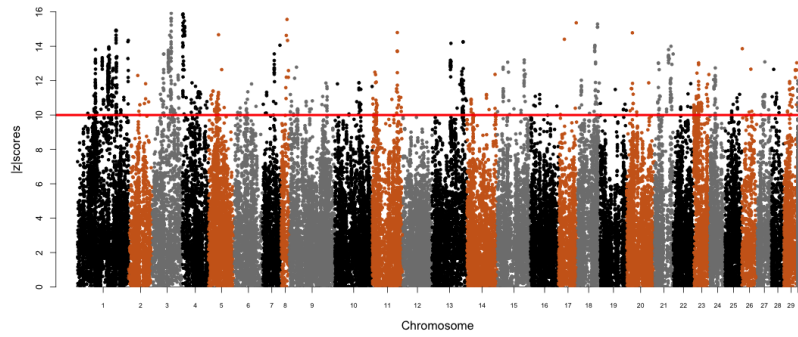


RESULTS

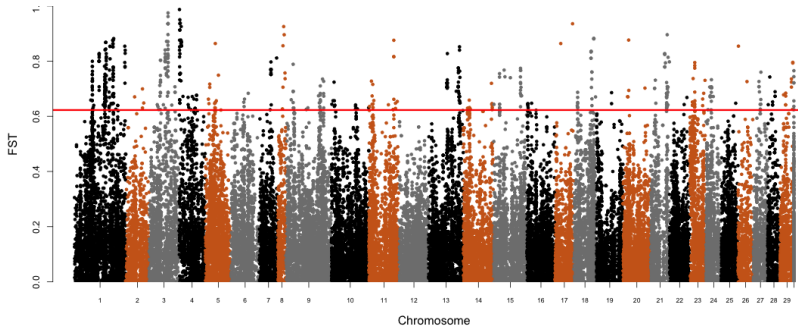
CANADA



BayeScan



LFMM

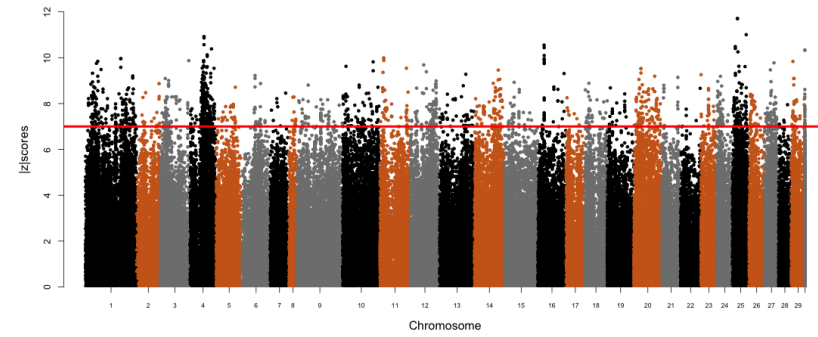


99th Percentile

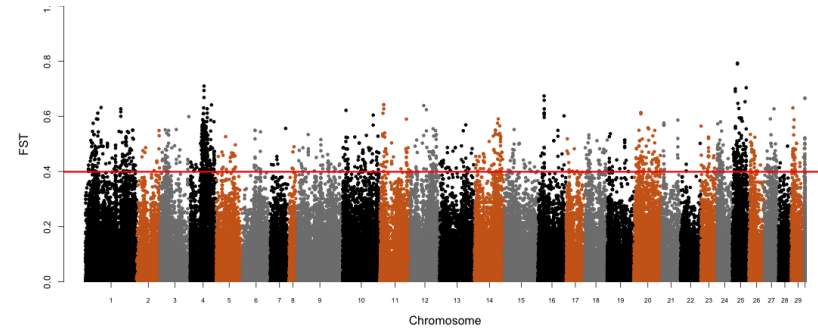
SCOTLAND



BayeScan



LFMM



99th Percentile



RESULTS

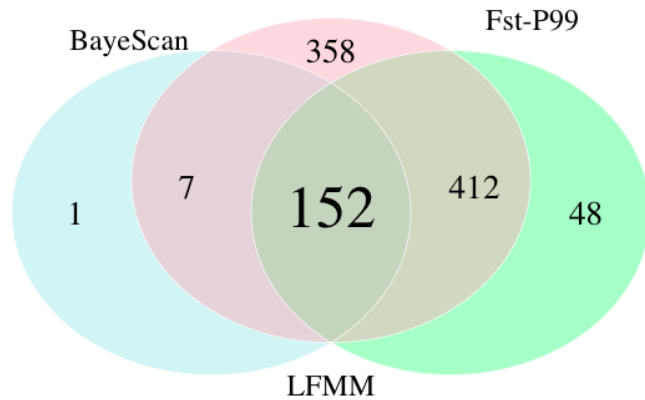
CANADA

N SNPs

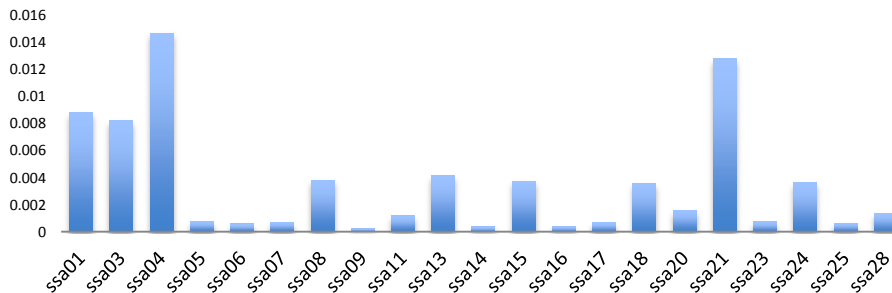
BayeSCAN 160

LFMM (p-value < 0.01) 929

99th Percentile 612



SNPs detected/ SNPs per chromosome



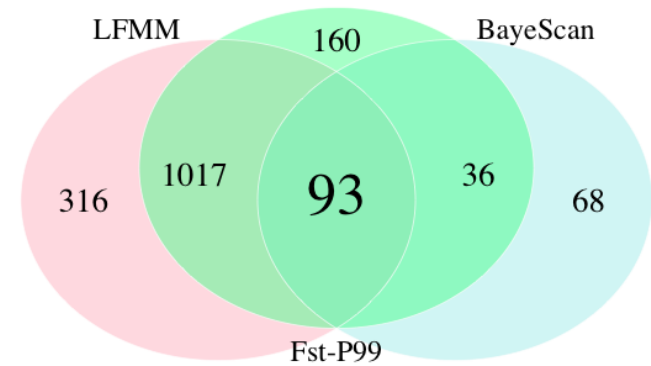
SCOTLAND

N SNPs

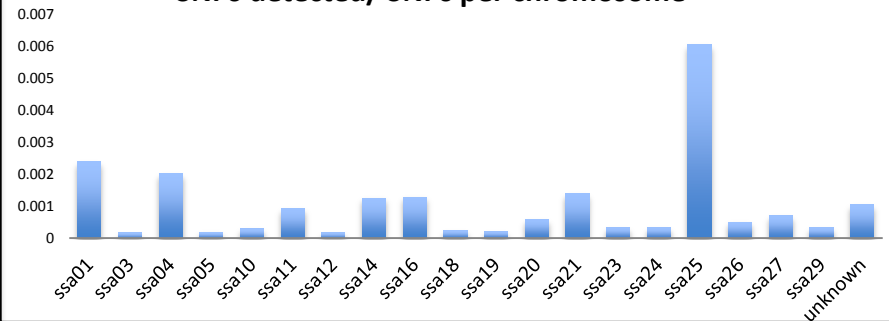
BayeSCAN 197

LFMM (p-value < 0.01) 1,426

99th Percentile 1,306



SNPs detected/ SNPs per chromosome



RESULTS: Linkage Disequilibrium Preliminary results – Chr1



RESULTS: Linkage Disequilibrium Preliminary results – Chr4



Conclusions

- 61,199 polymorphic SNPs in Canadian populations (40%).
- 130,587 polymorphic SNPs in Scottish populations (87.5%).
- 93 outliers SNPs were found in Scottish populations.
- 152 outliers SNPs were found in Canadian populations.



Acknowledgements

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UNIVERSITY OF CHILE

<http://www.favet-genstat.uchile.cl>



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