

Loci associated with adult stature also affect calf birth survival in cattle

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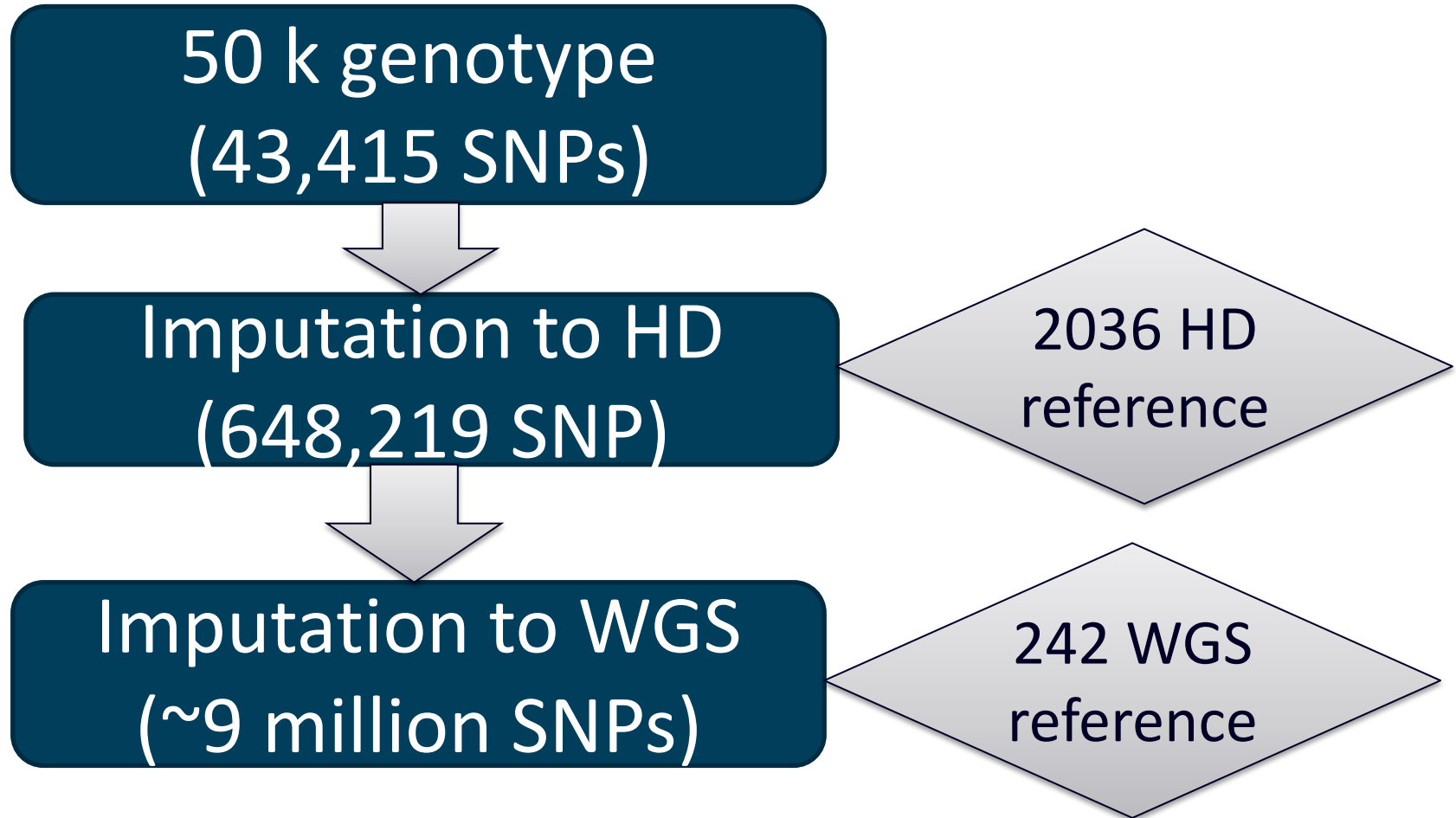
Background

- Genome scan in Nordic Red cattle population
- A QTL at ~39 Mb on chromosome 6 with a large effect on
 - Birth index
 - Body conformation index
- Objectives
 - Fine-map
 - Pleiotropy or linkage?

Animals and traits

- Nordic Red Cattle (~4,500)
- Birth index
 - Calving ease
 - Stillbirth
 - Calf size
- Body conformation index
 - 7 traits
 - Stature (correlation with the index = 0.80)

Genotypes and imputation



Association analyses

Genome scan using a sire model



LMM for the targeted region



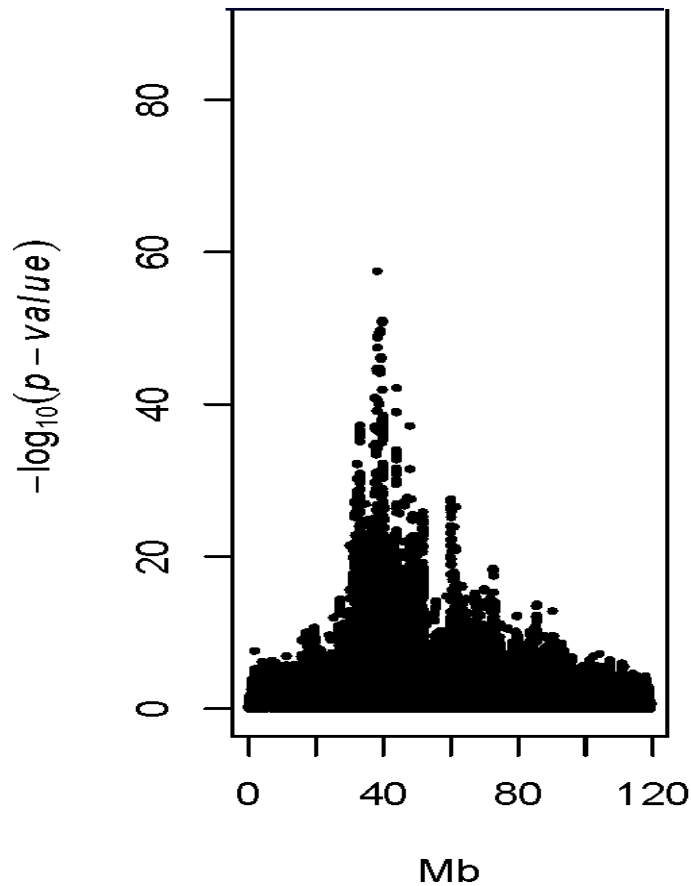
Construction of haplotypes



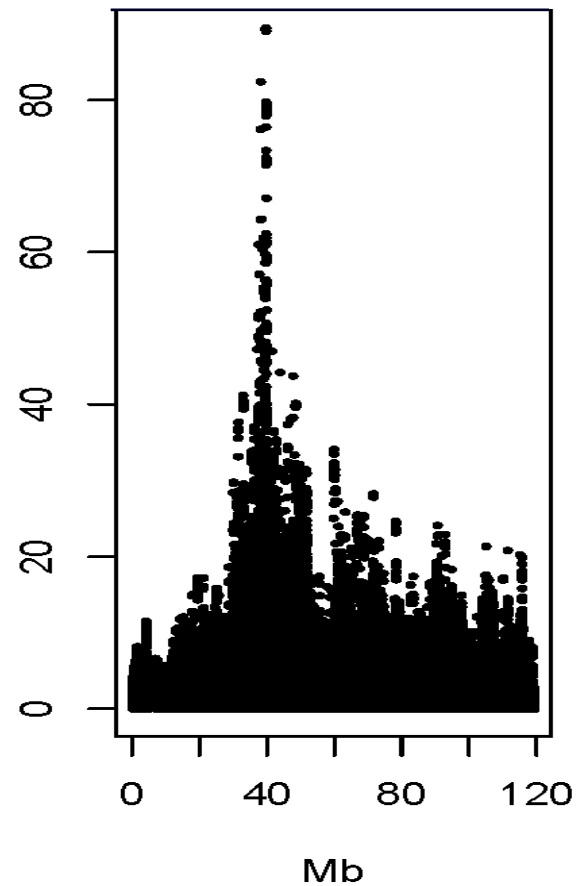
Haplotype-based analyses

Genome scan: QTL at the same location

Birth index



Body conformation index

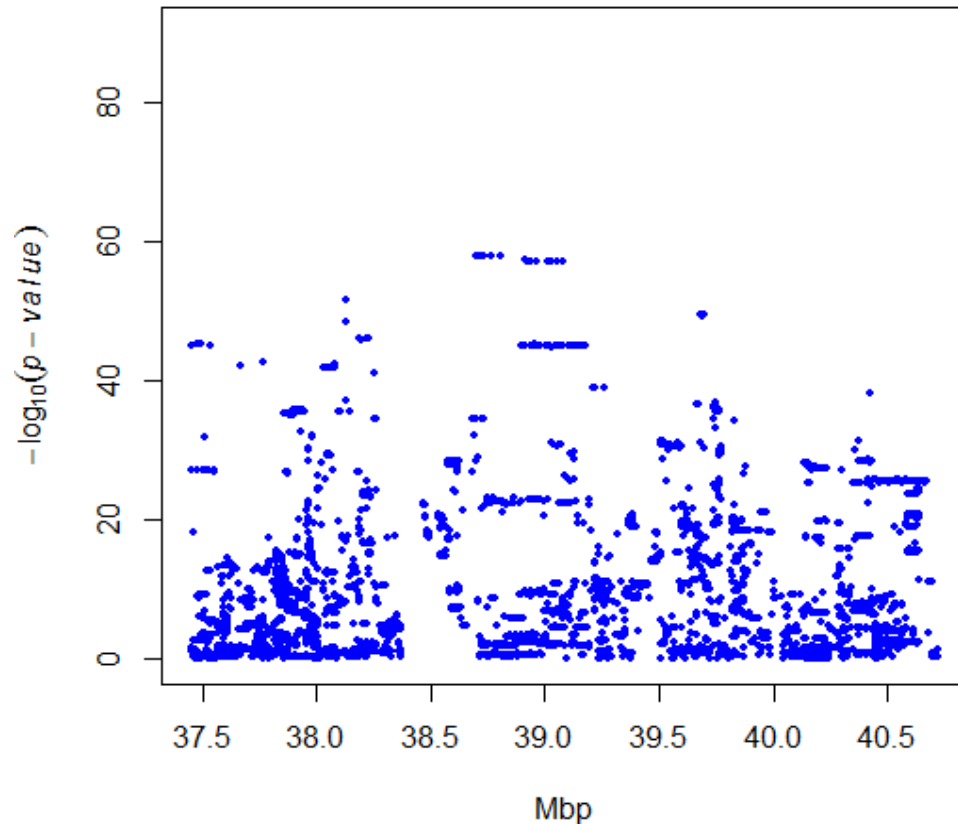


Top SNPs for two indices

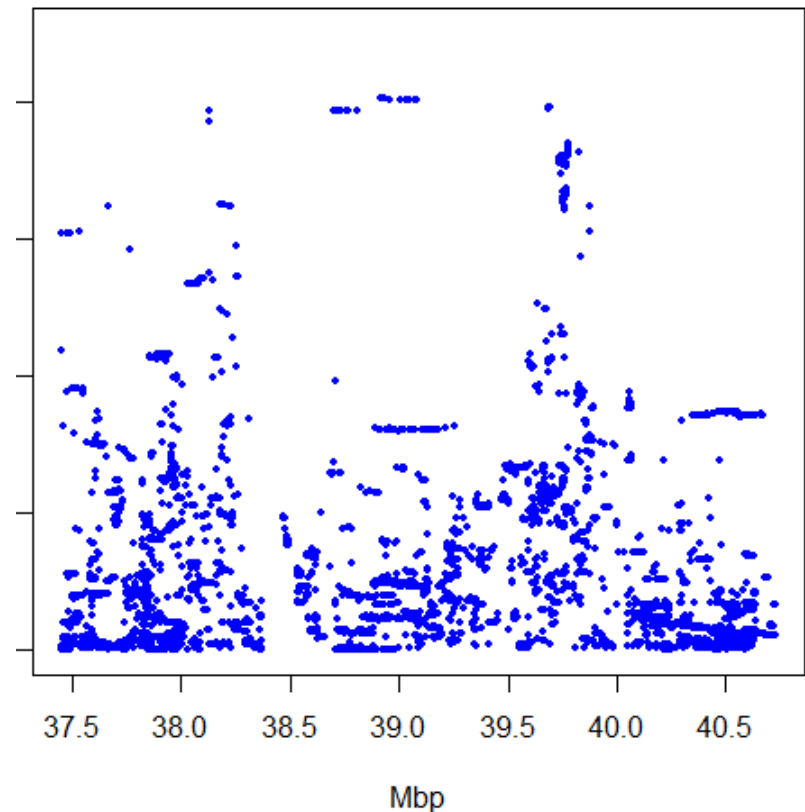
	Birth index	Body conformation index
Location	38,127,504 bp	39,685,188 bp
$-\log_{10}(P)$	57.5	89.4
MAF	0.31	0.40
Effect size	0.4% of V_A	0.5% of V_A
Annotation	5' UTR	intergenic
Top 20 SNPs	38.127-39.750 Mb	38.127-39.697 Mb

Targeted QTL region: Mixed model analysis with polygenic component

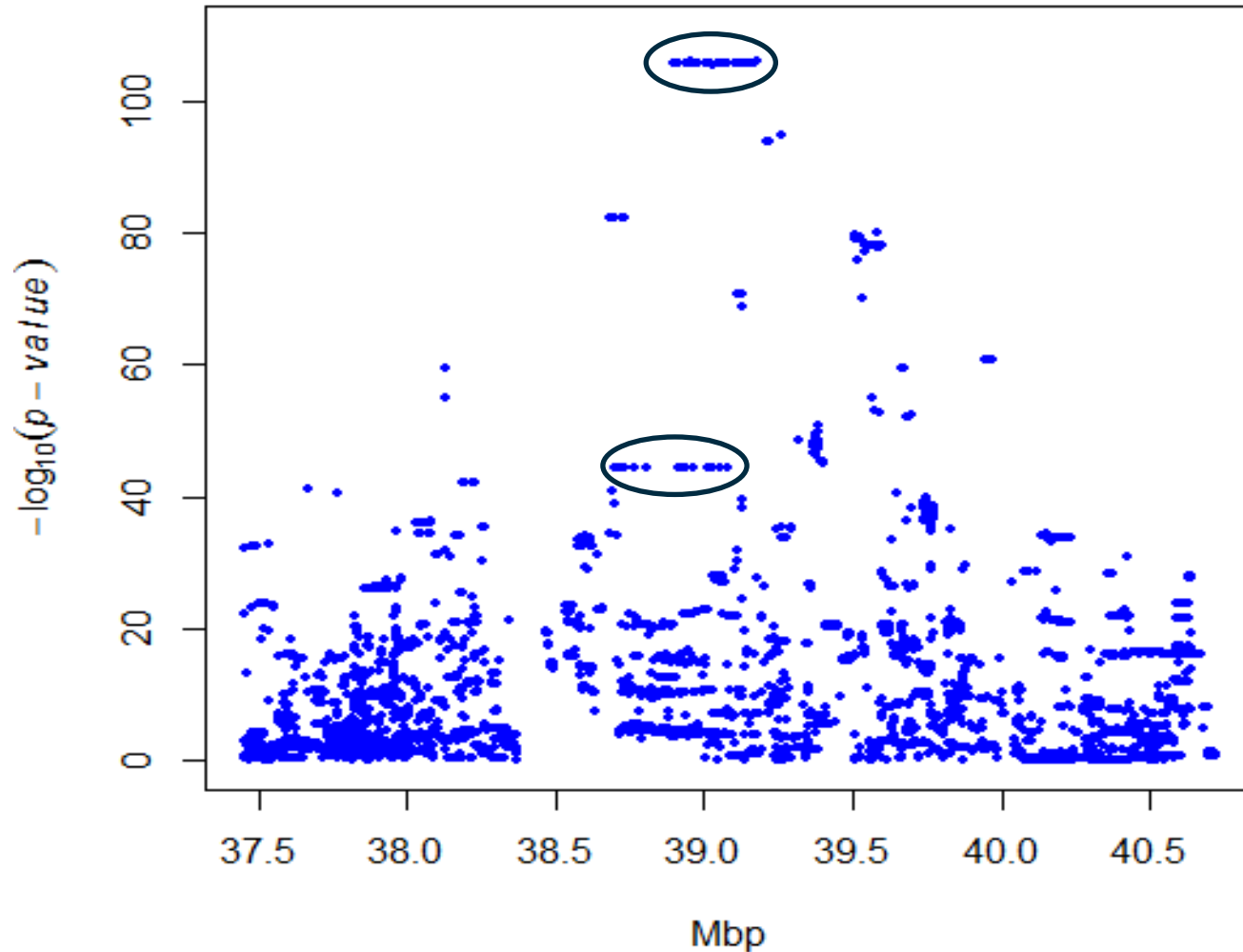
Birth Index



Body Conformation Index



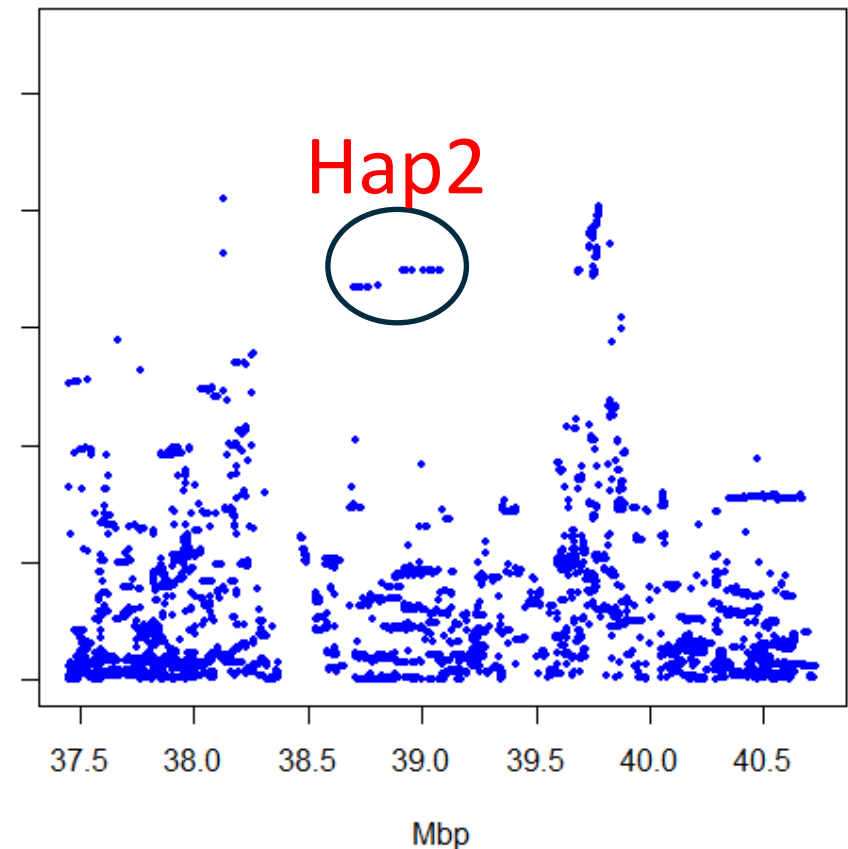
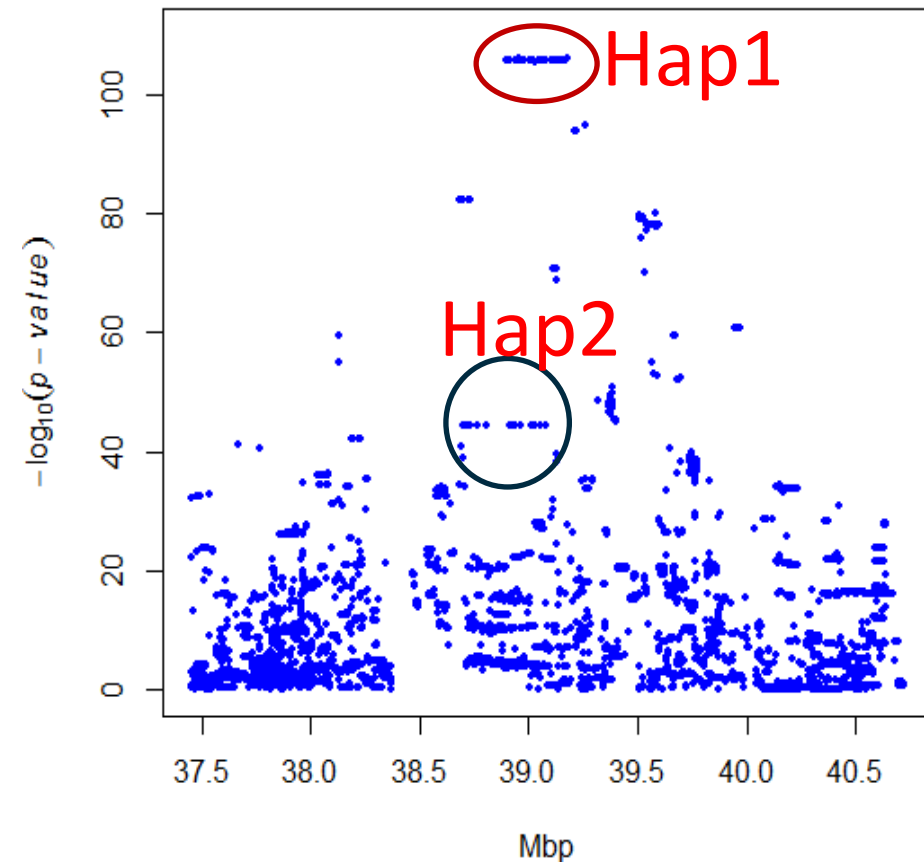
Strongest signal was for calf size



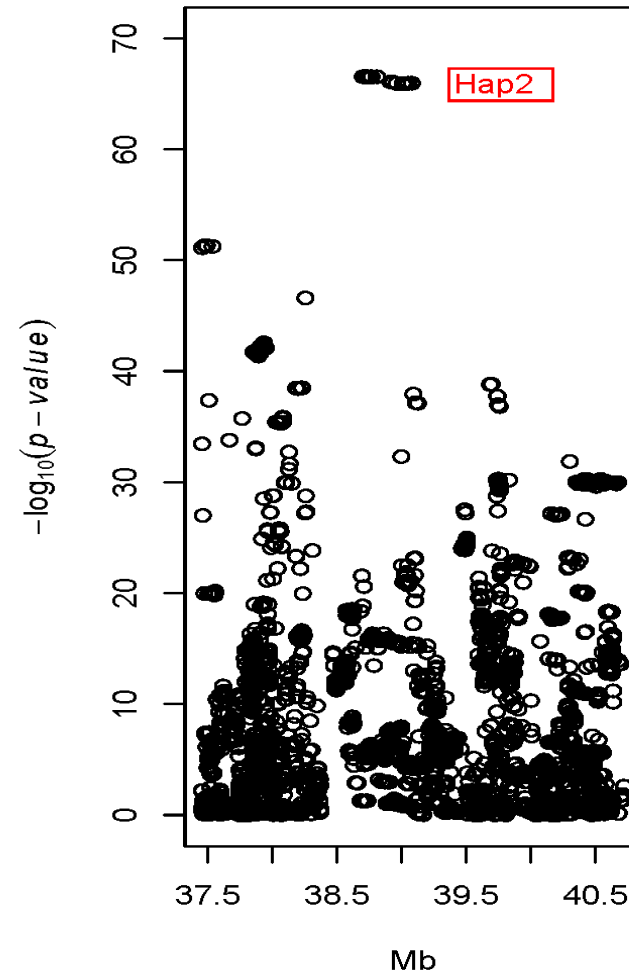
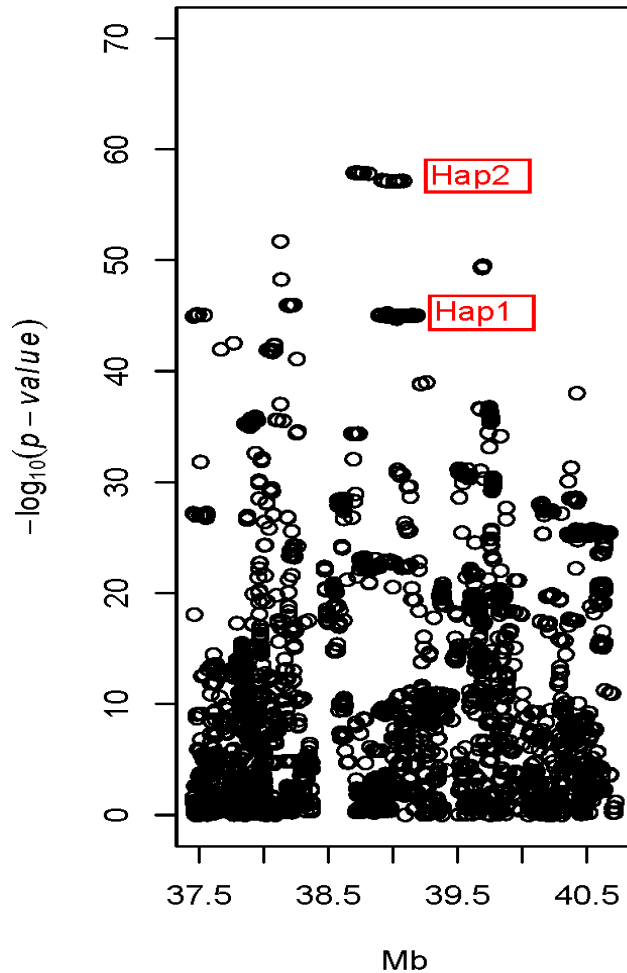
Subset of markers affecting size at birth and at adult

Calf Size

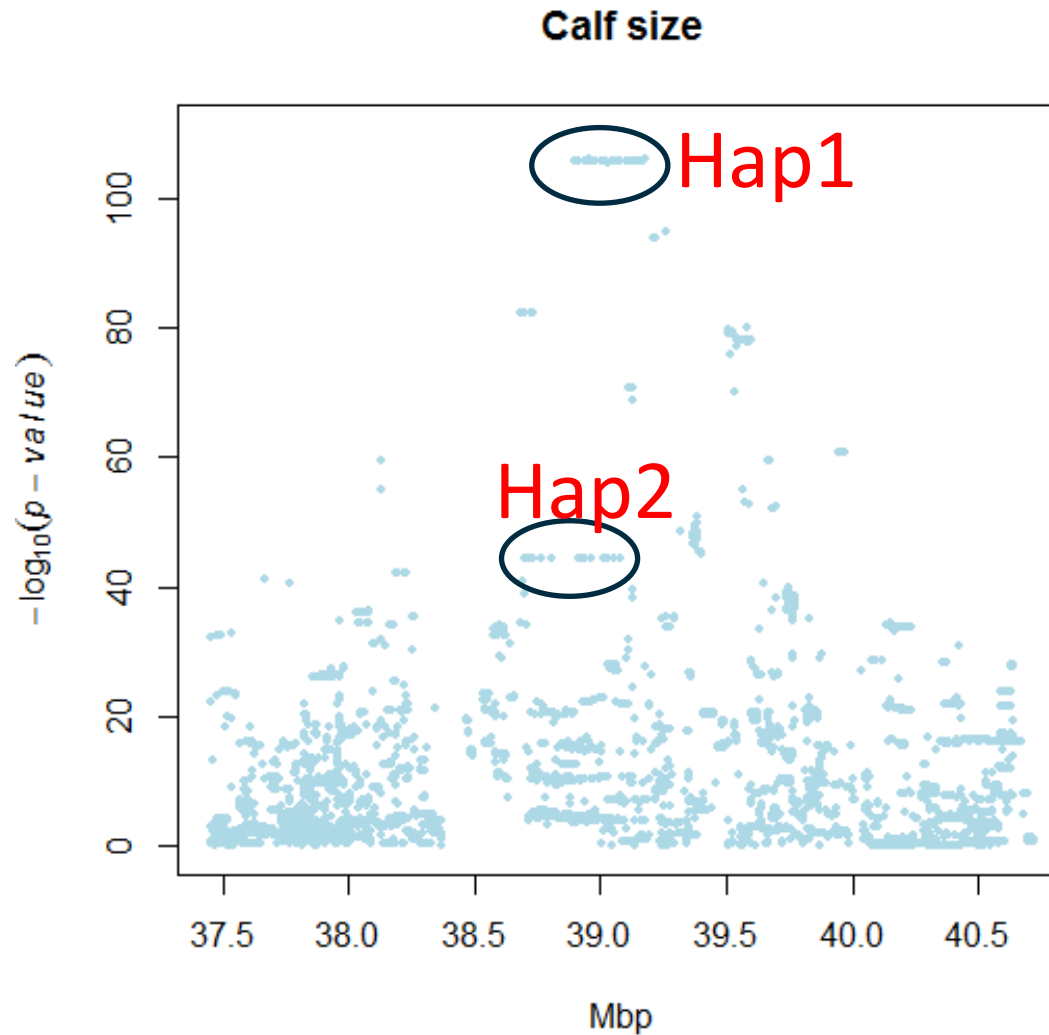
Stature



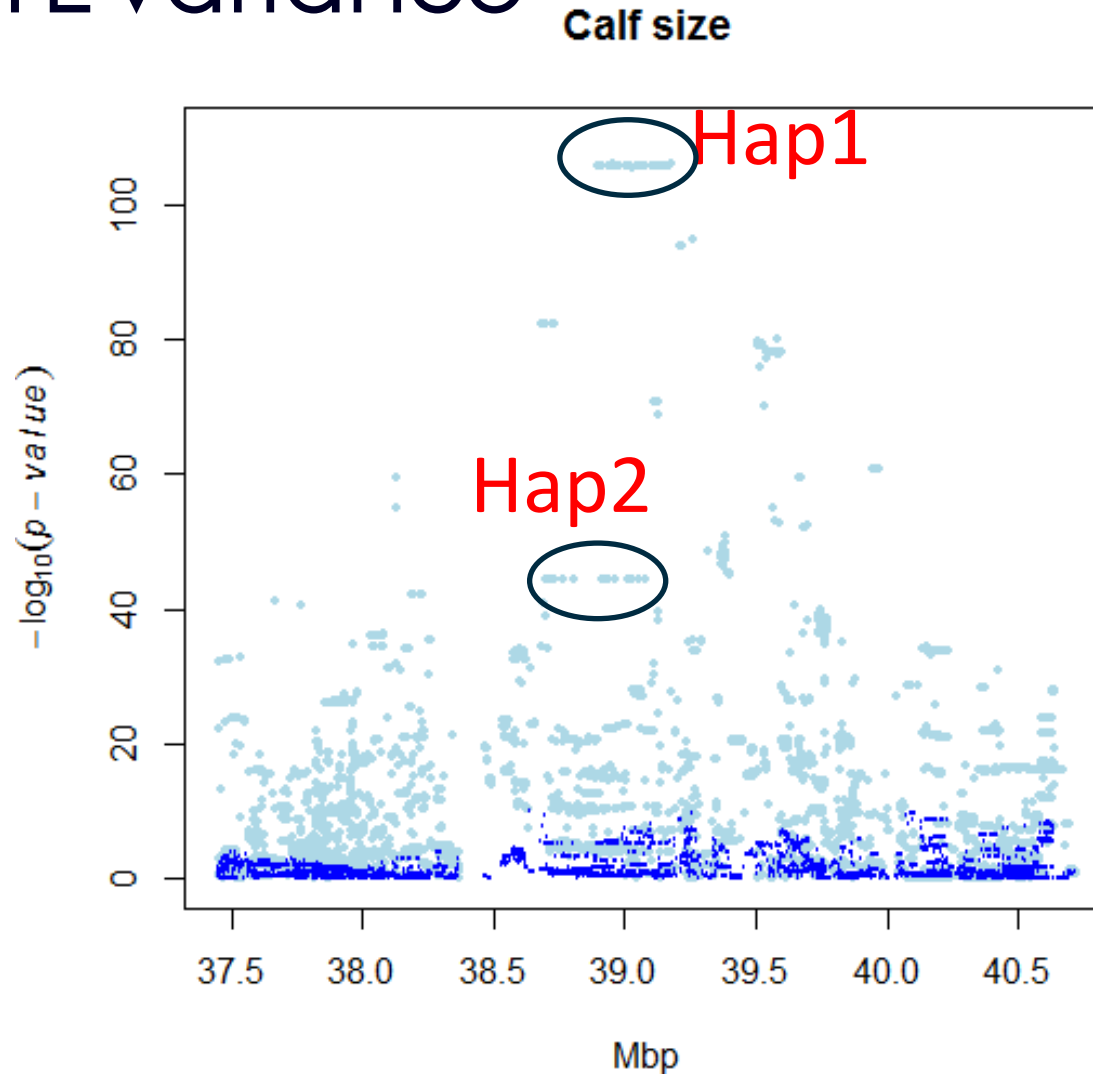
One haplotype does not explain QTL variance for birth index



Two distinct haplotypes



Two distinct haplotypes – explain the QTL variance

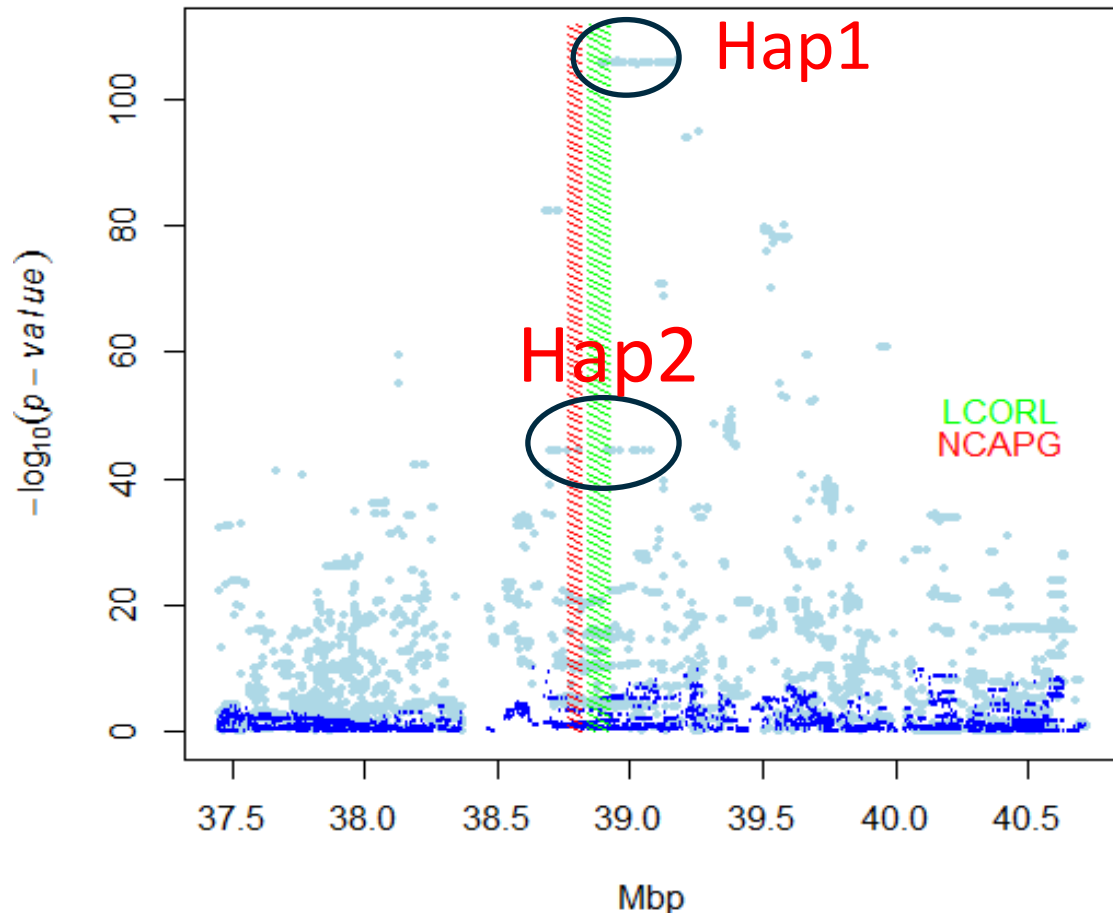


Two distinct haplotypes: effect estimates

Model: $y = \text{mean} + \text{population} + \text{haplotype (s)} + \text{animal} + \text{error}$

Trait	M ₁ : Hap1	M ₂ : Hap2	M ₃ : Hap1 + Hap2	
Body index	4.79 ± 0.41	4.36 ± 0.24	5.66 ± 0.39	4.65 ± 0.24
Stature	5.09 ± 0.40	3.84 ± 0.22	5.89 ± 0.39	4.10 ± 0.22
Birth index	-6.78 ± 0.49	-3.78 ± 0.25	-7.54 ± 0.48	-4.05 ± 0.24
Calf size	5.74 ± 0.29	2.07 ± 0.14	6.23 ± 0.28	2.30 ± 0.14
Calving ease	-5.97 ± 0.32	-2.60 ± 0.16	-6.54 ± 0.31	-2.84 ± 0.15
Stillbirth	-5.86 ± 0.48	-3.66 ± 0.24	-6.58 ± 0.47	-3.90 ± 0.24

Candidate genes

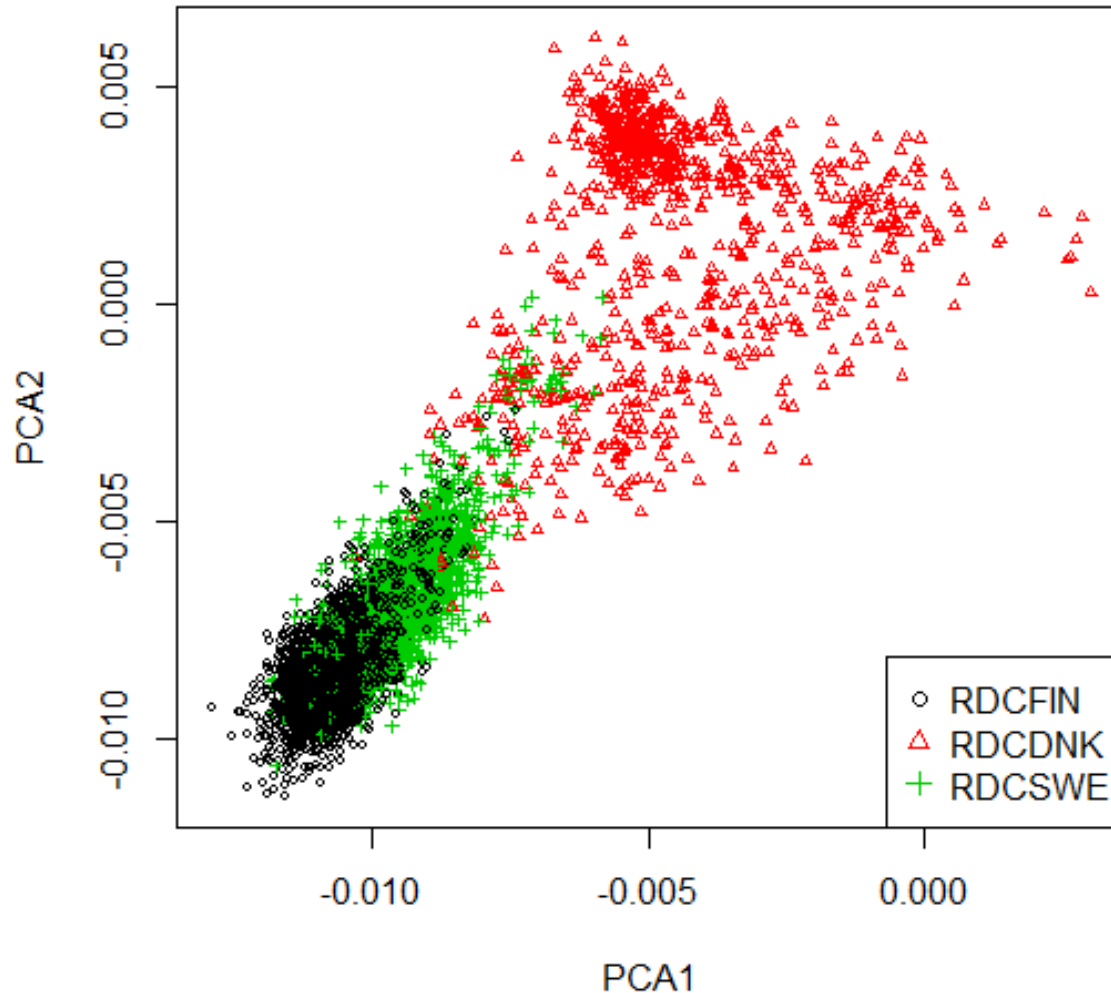


NCAPG (6:38.76-38.81)

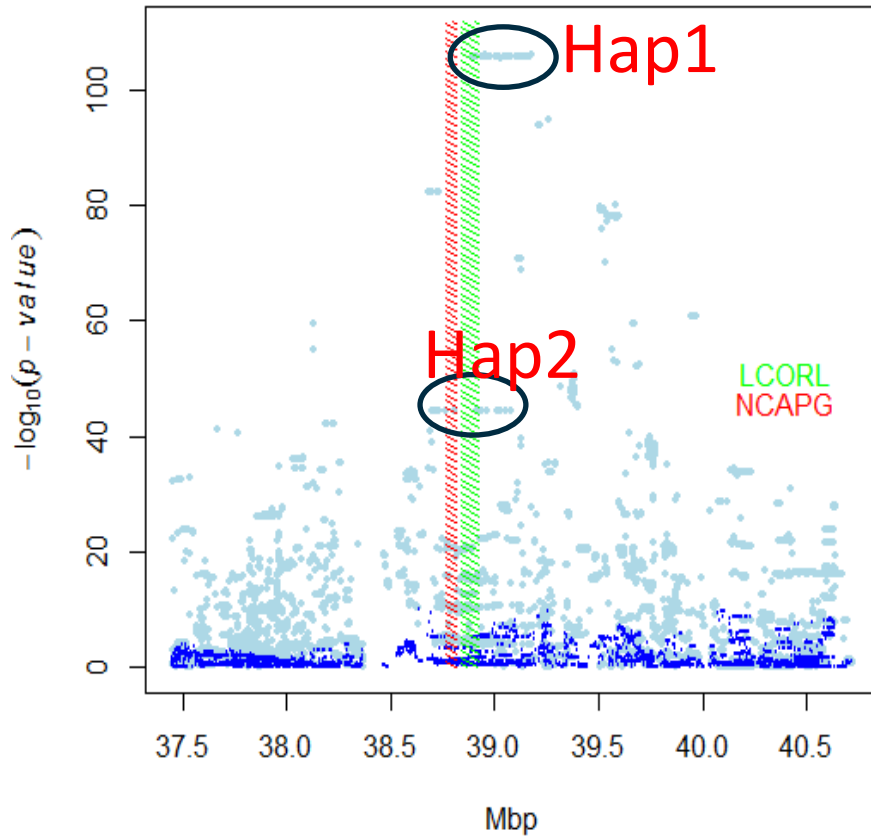
LCORL (6.38.88-38.99)

1. Bovine fetal growth
2. Height at withers in horse
3. Height and fetal growth in human

Nordic Red cattle – three sub-populations

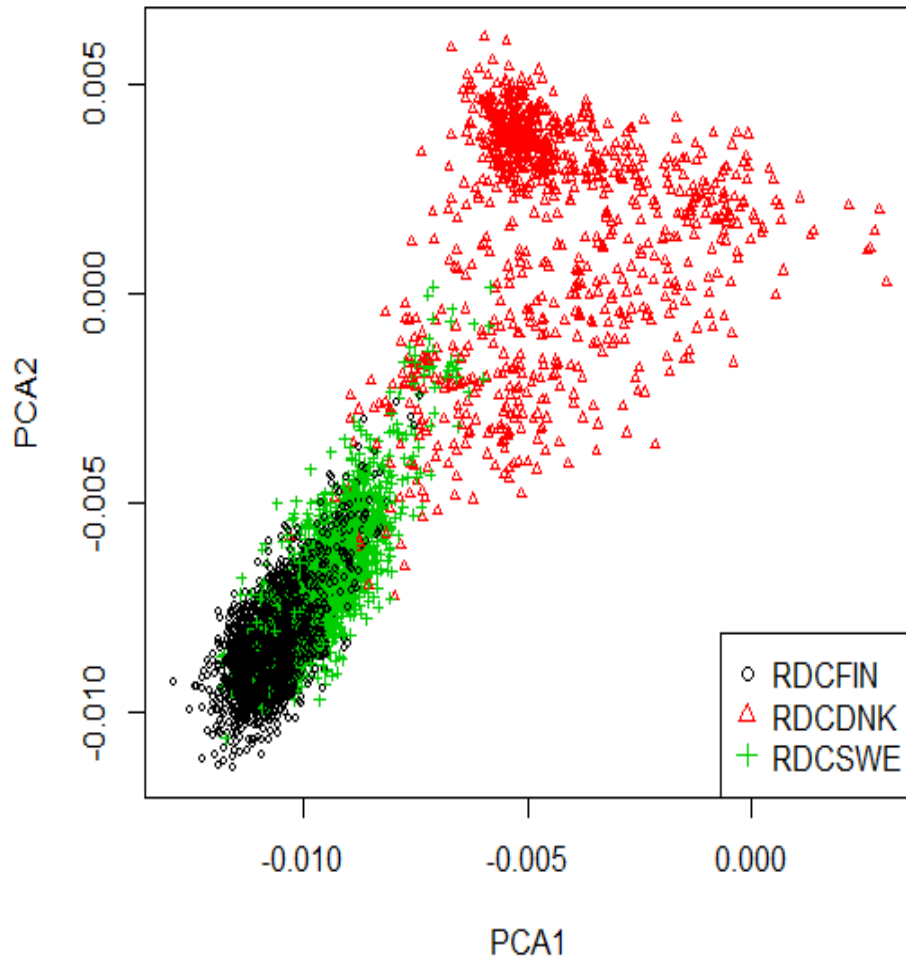


Two distinct haplotypes – two origins?



Population	Frequency	
	Hap1	Hap2
RDC	0.085	0.24
RDCDNK	0.420	0.04
RDCFIN	0.003	0.32
RDCSWE	0.019	0.21

Two distinct haplotypes – two origins?



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Conclusions

- QTL at LCORL-NCAPG genes with a large effect on calf size and stature in Nordic Red cattle
- Two haplotypes with distinct effects
- Increased calf size at birth, and favorable effect on body conformation
- BUT increased calving difficulties and stillbirth

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Abstract

Background

Methods

Results

Discussion

Conclusions

Abbreviations

Competing
interests

Authors'
contributions

Additional fi...

Acknowledgements

References

Research article

Highly accessed

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