

Development of a SNP marker set for selection against left-sided displacement of the abomasum in German Holstein cattle

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Introduction

- Left-sided displacement of the abomasum (LDA)
 - Mainly dairy cattle
 - 90% of all cases left-sided
 - Prevalence in German Holsteins at about 3.6%
 - Polygenic disease, $h^2=0.2-0.5$
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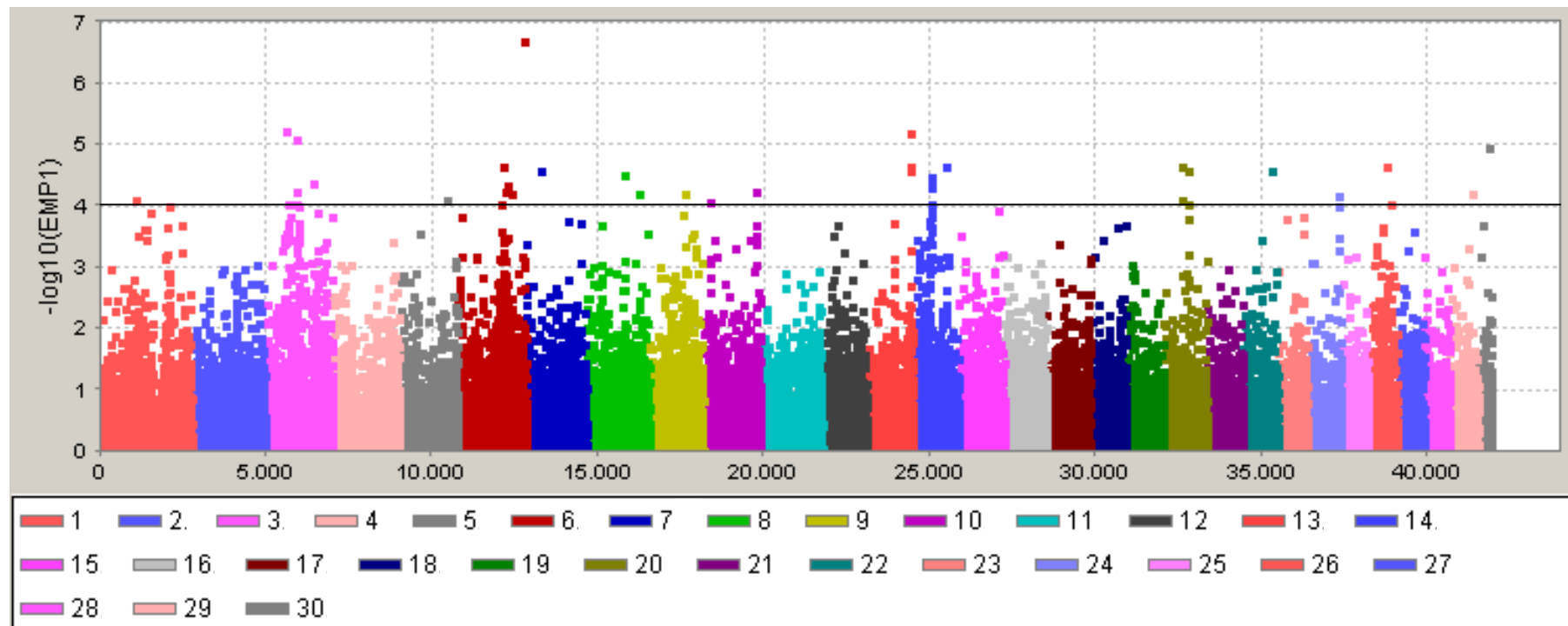
Introduction

- QTL on BTA1, 3, 21, 23, 24
 - Genome wide association analysis (Illumina 50K bovine SNP Chip)
 - Candidate gene analysis
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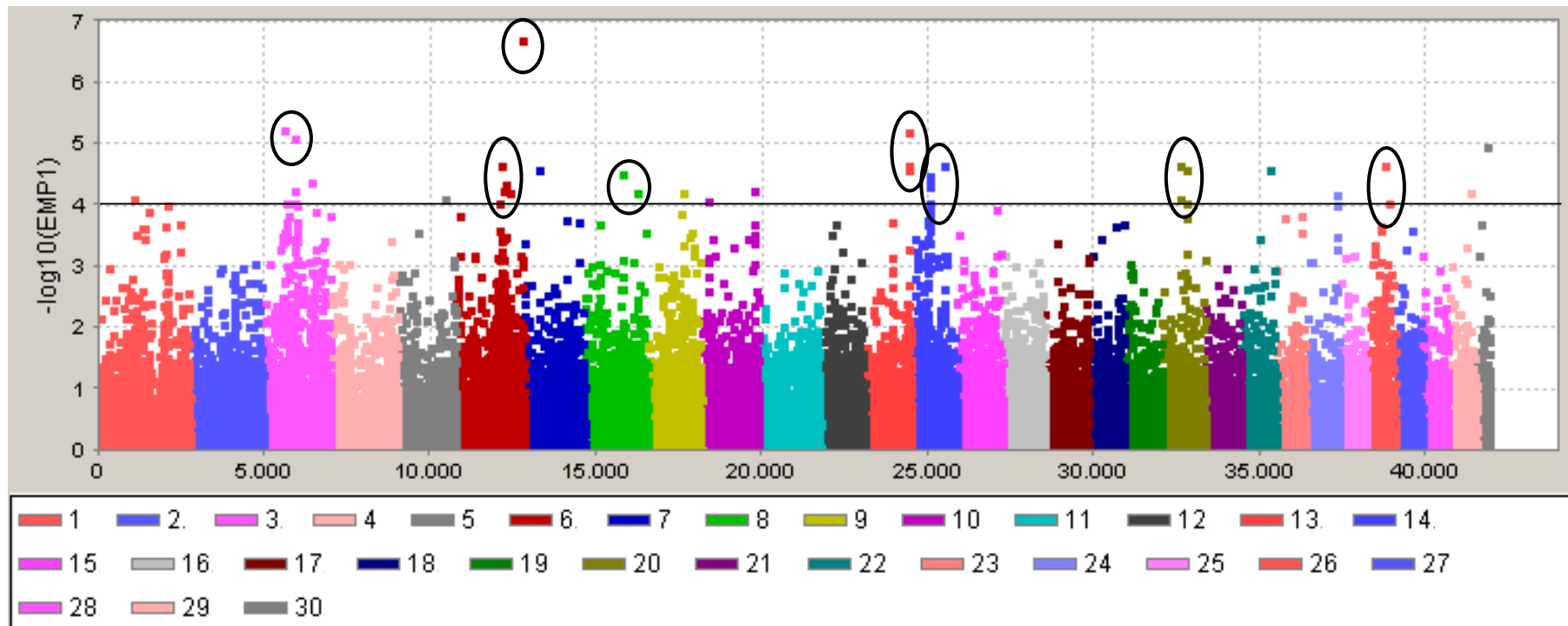
Genome wide association study

- 216 German Holstein cows:
 - ▣ 96 affected by LDA
 - ▣ 120 unaffected by LDA
-

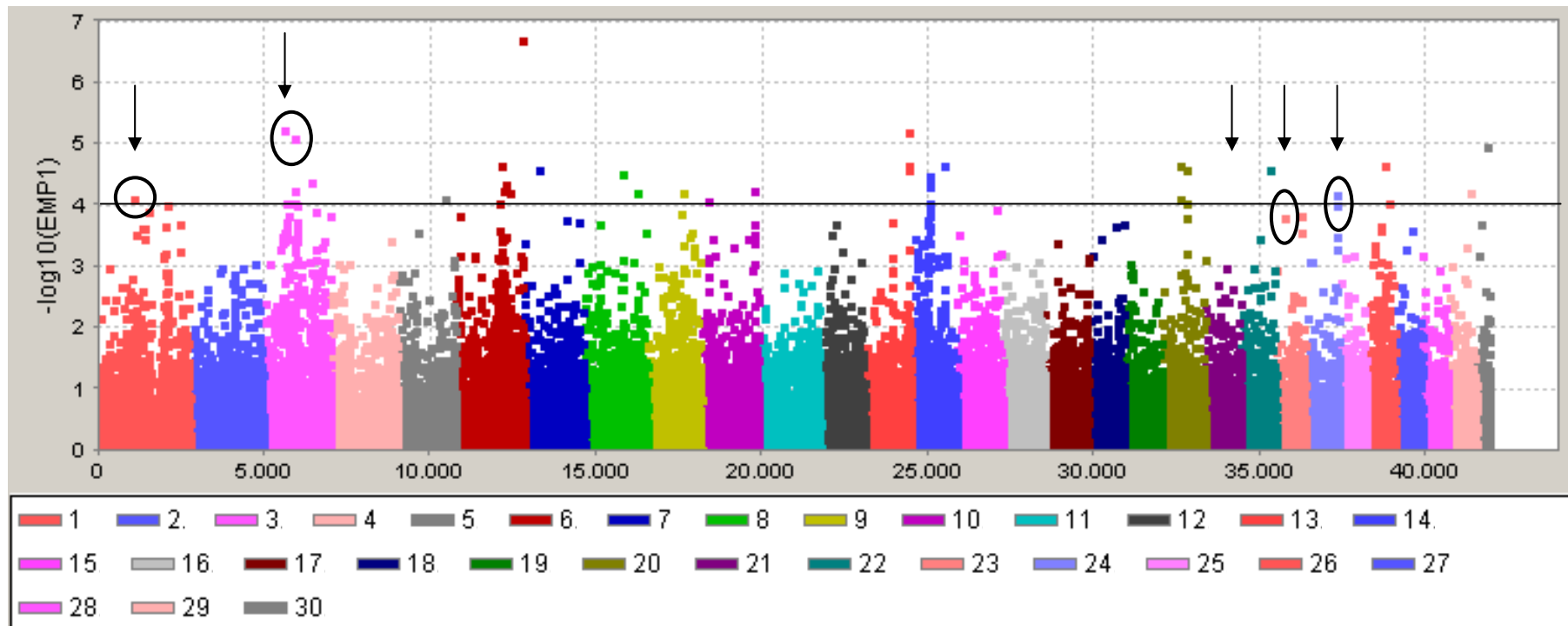
Genome wide association study



Genome wide association study



Genome wide association study



Candidate gene analysis

- *Motilin (MLN)*, proximal on BTA23
 - Comparative sequencing
 - 345 bp open reading frame
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Sequencing of bovine *MLN*

- In total 30 SNPs and 2 microsatellites
 - 11 informative polymorphisms
 - Analysed in 1,166 cows, including 646 cows affected by LDA
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Association analysis and odds ratio

Marker (FN298674)	Per Allele OR	Hom. OR	HET	<i>P</i> -value per allele (-log ₁₀)	<i>P</i> -value Hom. (-log ₁₀)
g.62G>A	0.69	0.45	0.48	4.33	9.05
g.90T>C	0.64	0.40	0.51	6.43	13.85
g.1891insG	1.75	2.98	0.47	9.65	17.73
g.2045C>G	1.59	2.40	0.44	6.41	11.60
g.4942insT	1.64	2.41	0.47	6.99	10.46
g.6689C>T	0.58	0.37	0.36	5.40	9.09
g.6728G>A	1.73	2.74	0.36	5.40	9.09

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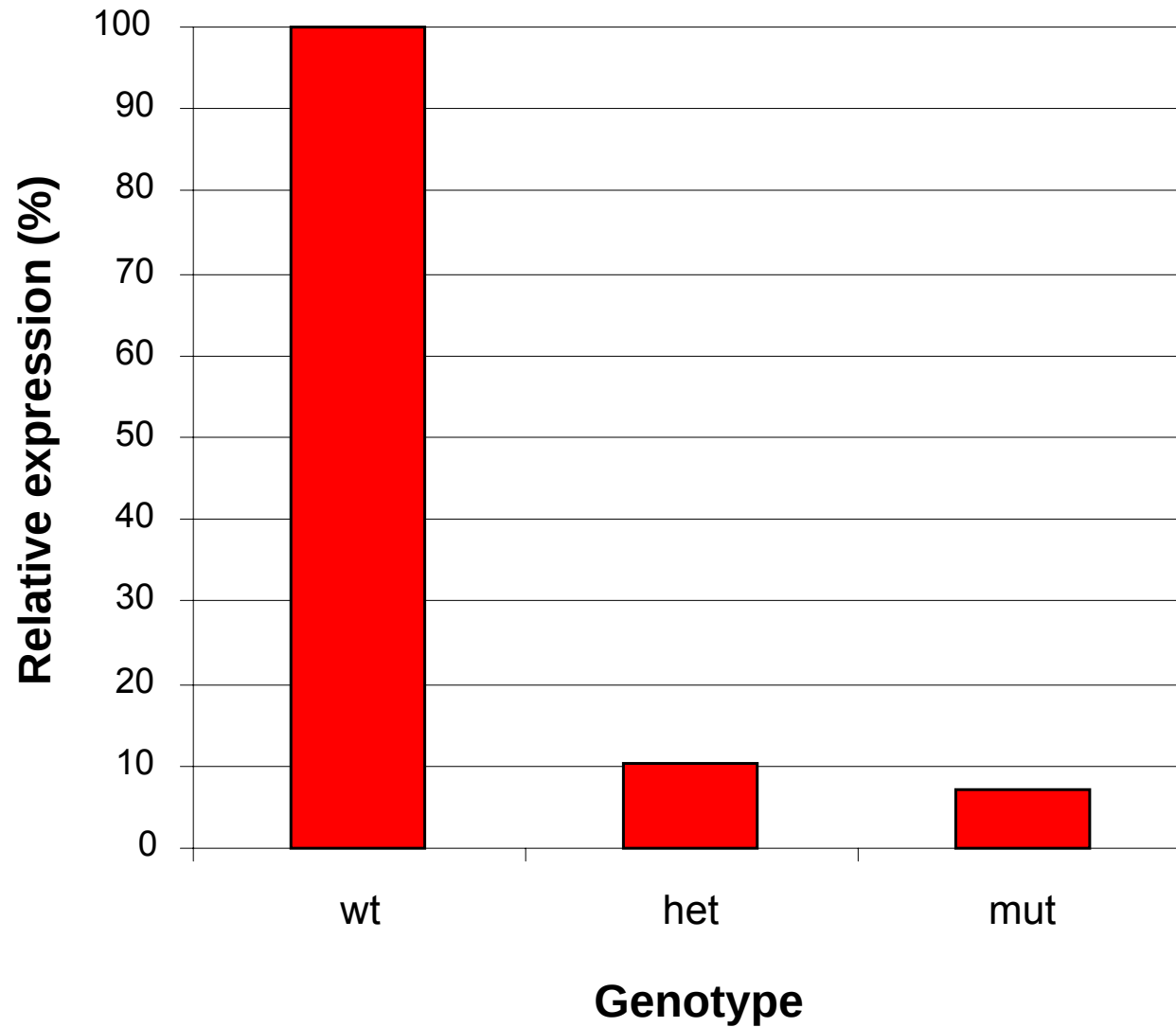
Haplotype analysis

- g.90T>C and g.1891insG
 - Most significant haplotype: C – insG
 - 55.3% of affected cows
 - 38.1% of unaffected cows
-

Expression study

- g.1891insG
 - Genotypes wt (n=14), het (n=12), mut (n=6)
 - Relative expression using qPCR
 - Housekeeping gene *RPL4*
 - $\Delta\Delta\text{CT}$ method
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Expression study



Explained variance

- SNPs within *MLN* explain 4.2% of LDA phenotypic variance
 - Combined with polymorphisms from genome wide association analysis:
36.2% of LDA phenotypic variance can be explained
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Conclusions

- Genome wide significant associations with LDA on seven chromosomes
 - Polymorphisms within *MLN* decrease expression and predispose cows for LDA
 - All SNPs combined explain 36.2% of phenotypic variance
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Thank you



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