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Fine Mapping a QTL for Somatic Cell Score in the German Holstein

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Introduction

Somatic Cell Score (SCS)

- indicator trait for mastitis
- $h^2 = 16 - 17\%$
- marker assisted selection

☺ Over 50 QTL for SCS reported

☹ Large confidence intervals

Objectives

- Investigate chromosomal region on BTA27 affecting SCS:
    - ↑ marker density
    - ↑ number of families
    - linkage disequilibrium
- Identify haplotypes associated with increases or decreases in SCS

Experimental Design

Pedigree

- GDD (6 families)
- 492 sires → **492 DYD for SCS**
- 4,622 animals

Linkage Map

- 19 Microsatellites (~95 SNP) spanning 33.8 cM
- 6.84 alleles / marker
- Marker interval: 1.78 cM
- Putative QTL at midpoint of every marker interval

$\mathbf{y}_{i\,(m\times1)}$

Observations for sire *i*
(DYD for SCS)

$\mathbf{X}_{(m\times k)}\mathbf{Z}_{(m\times n)}\mathbf{W}_{(m\times gam)}$

Design matrices

$$\mathbf{y}_i = \mathbf{X}\boldsymbol{ß} + \mathbf{Zu} + \mathbf{Wv} + \mathbf{e}$$

$\boldsymbol{ß}_{(k\times1)}$

Fixed
Average

$\mathbf{u}_{(n\times1)}$

Random polygenic effects
which have nothing
to do with the QTL

$\mathbf{v}_{(gam\times1)}$

Random gametic
(QTL) effects

$\mathbf{e}$

Random
residual

Analysis

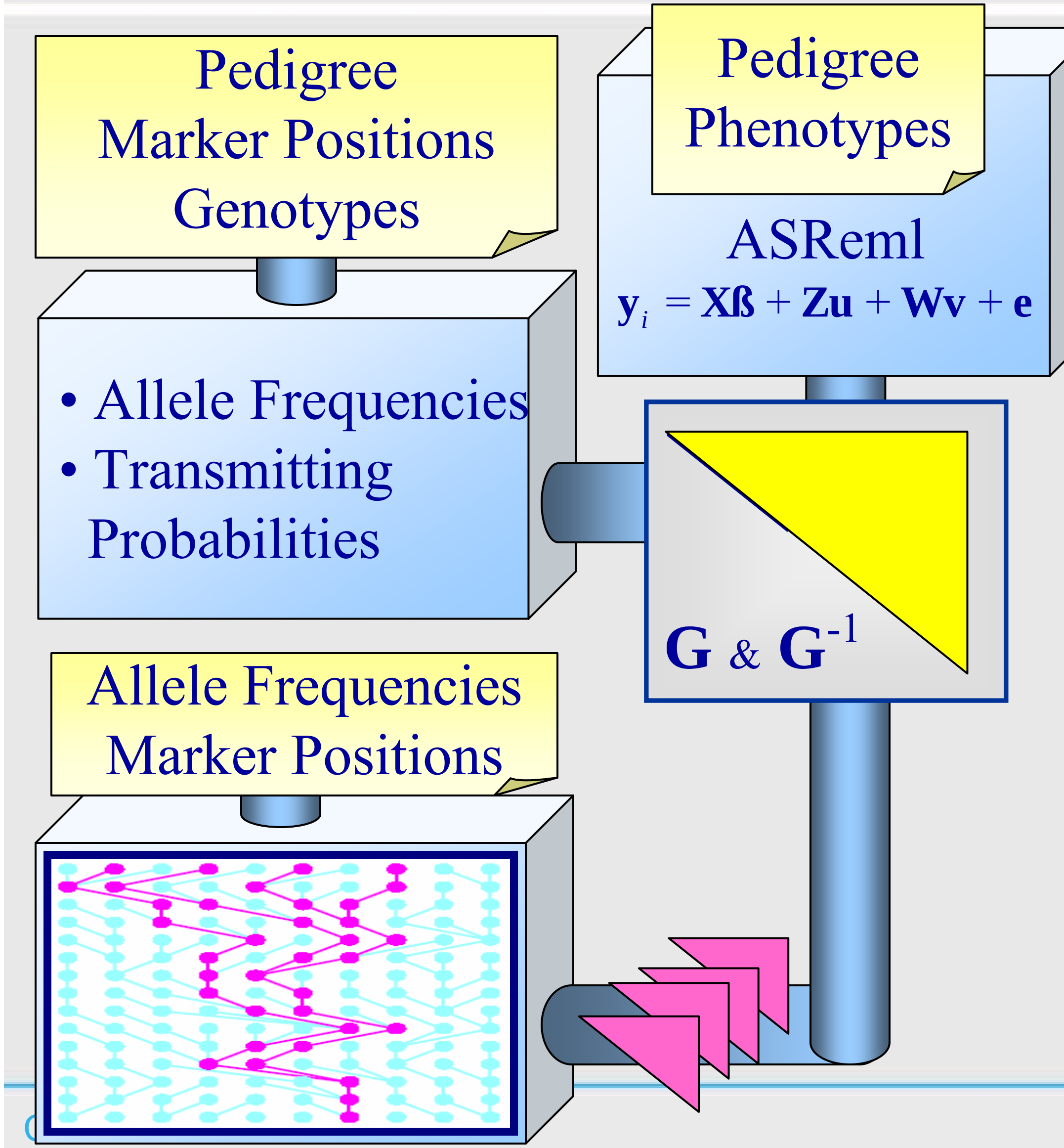
Restricted log likelihood ratio test statistic for all QTL positions (*pos*=1-18):

$$\mathrm{RLRT}^{Pos} = -2\left[\ln(L_0) - \ln(L_1^{Pos})\right]$$

$$L_0 \longrightarrow \mathbf{y}_i = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}\mathbf{u} + \mathbf{e}$$

$$L_1^{Pos} \longrightarrow \mathbf{y}_i = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}\mathbf{u} + \mathbf{W}\mathbf{v} + \mathbf{e}$$

Analysis



Pedigree
Marker Positions
Genotypes

- Allele Frequencies
- Transmitting Probabilities

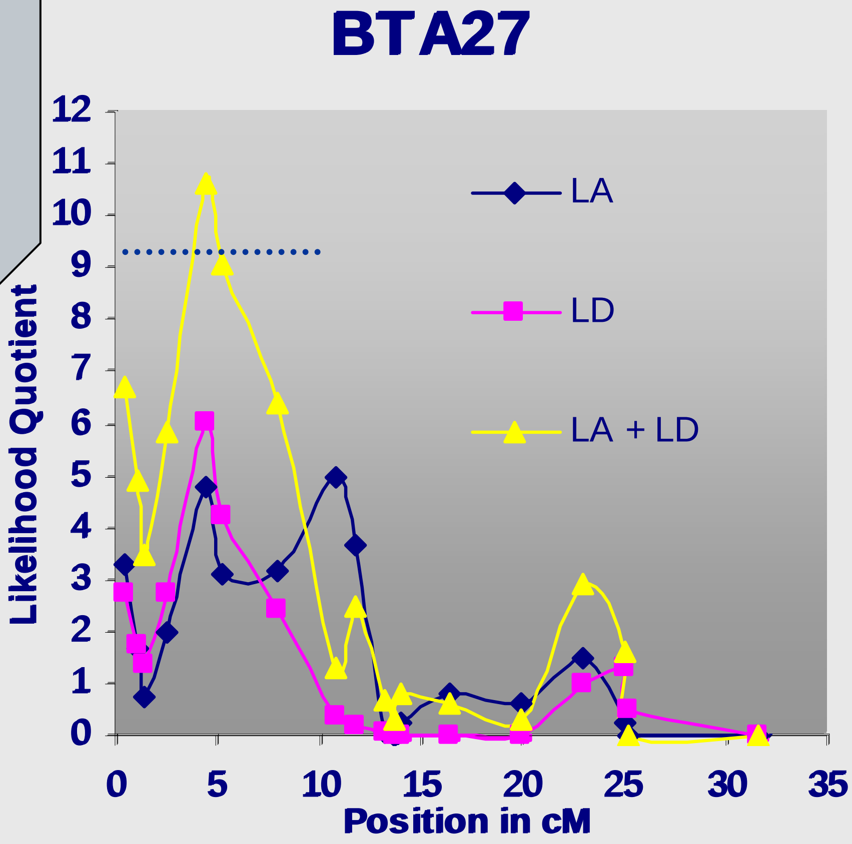
Allele Frequencies
Marker Positions

Pedigree
Phenotypes

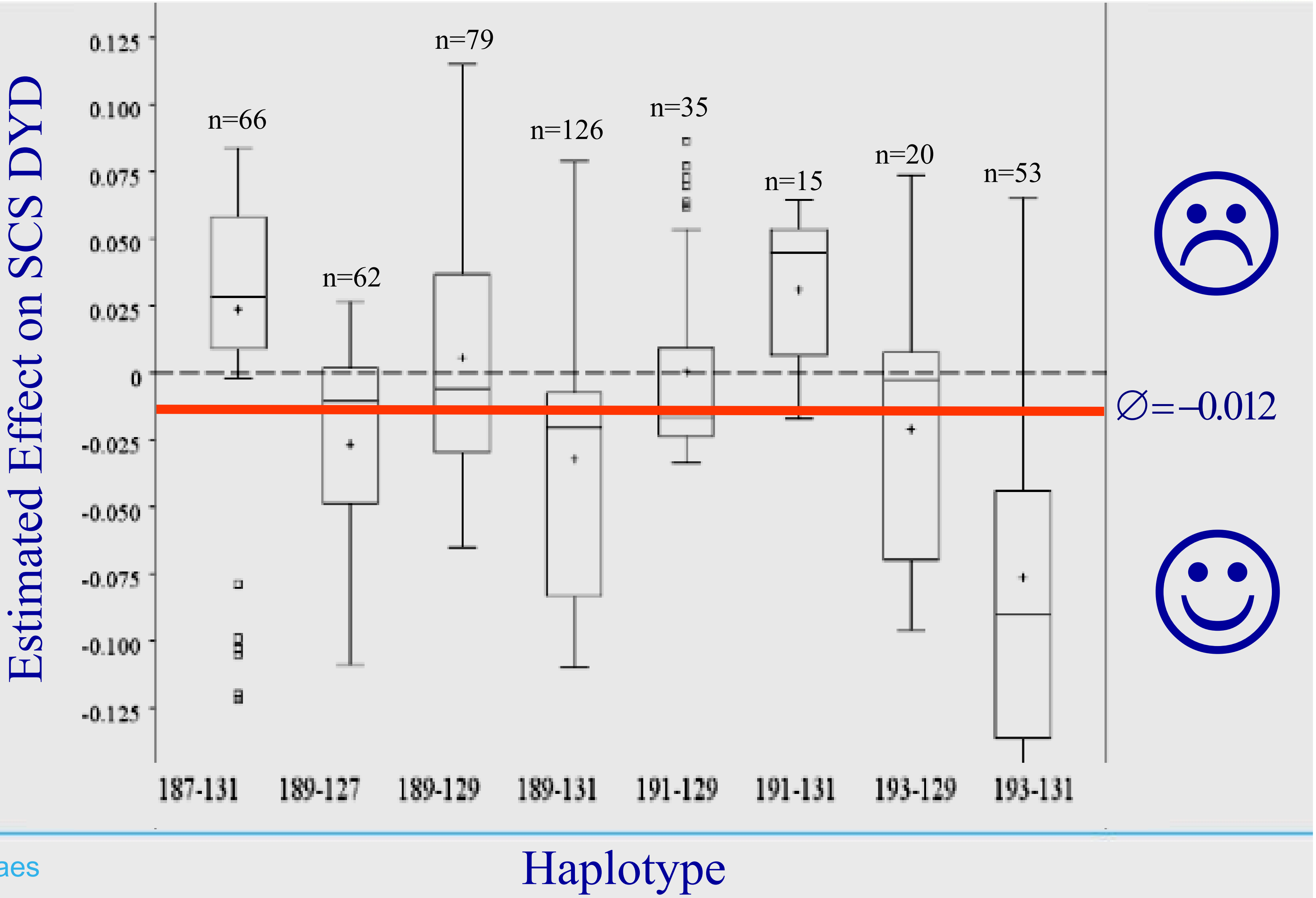
ASReml

$y_i = X\beta + Zu + Wv + e$

G & G^{-1}



Analysis of Haplotype Effects



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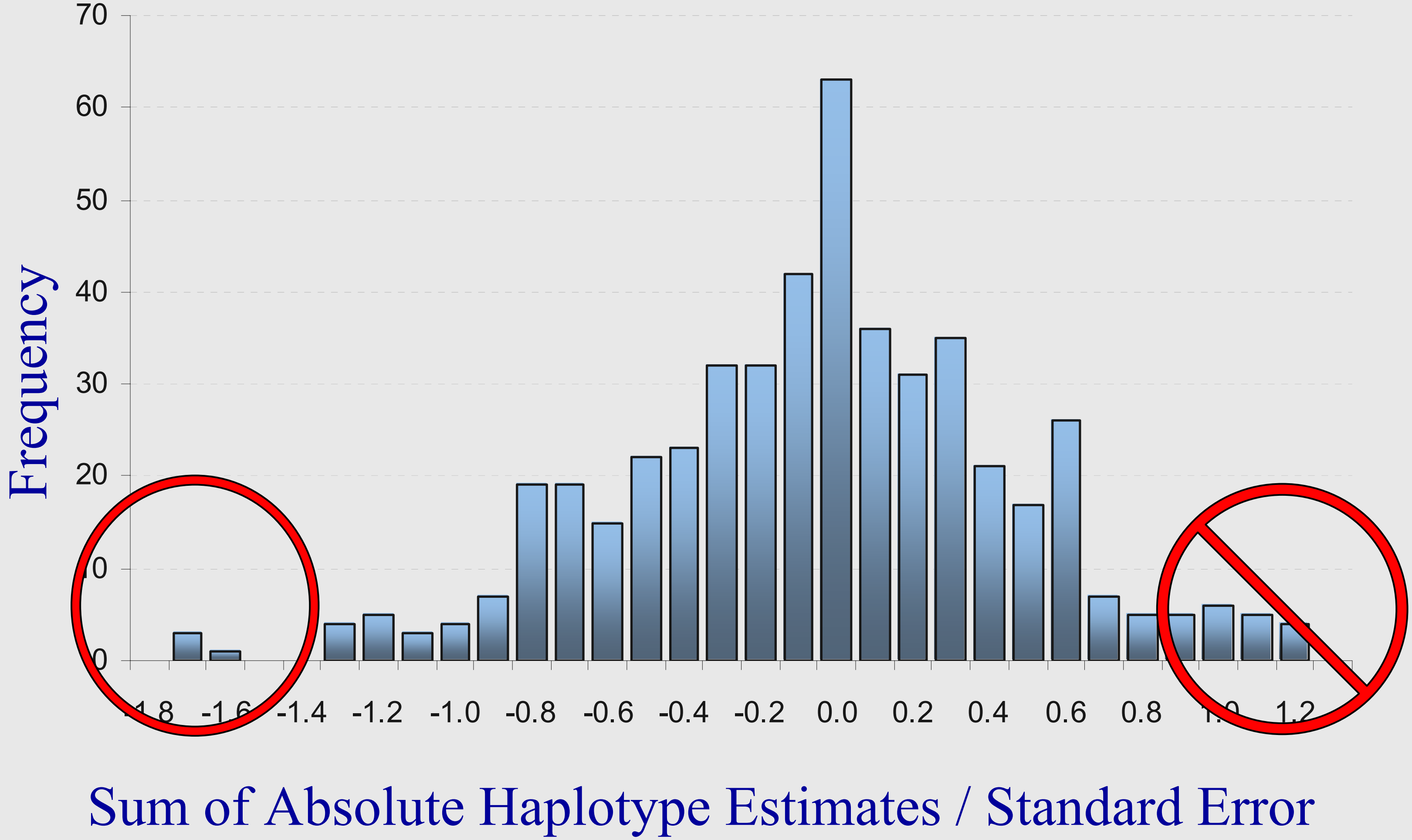
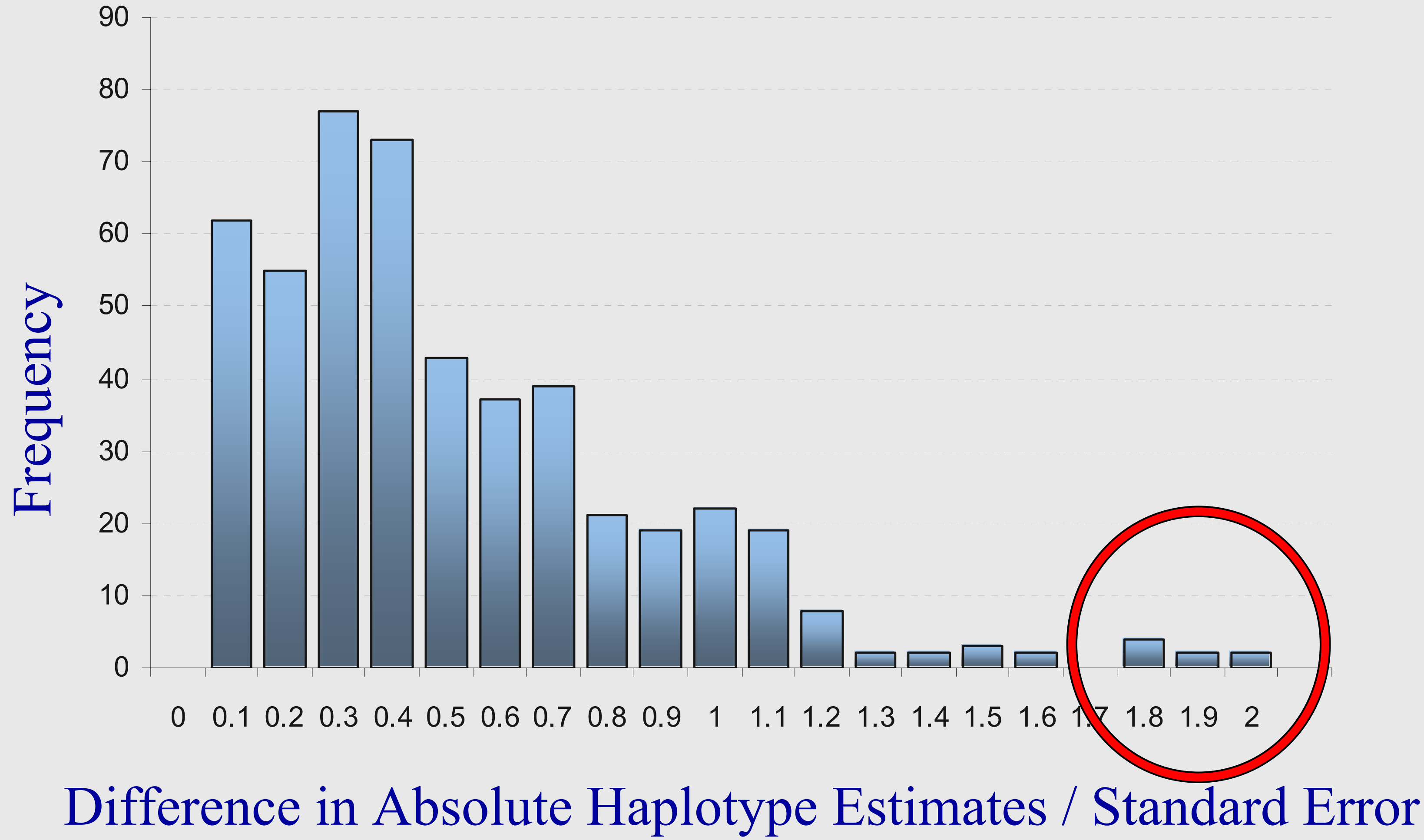


Analysis of Haplotype Effects

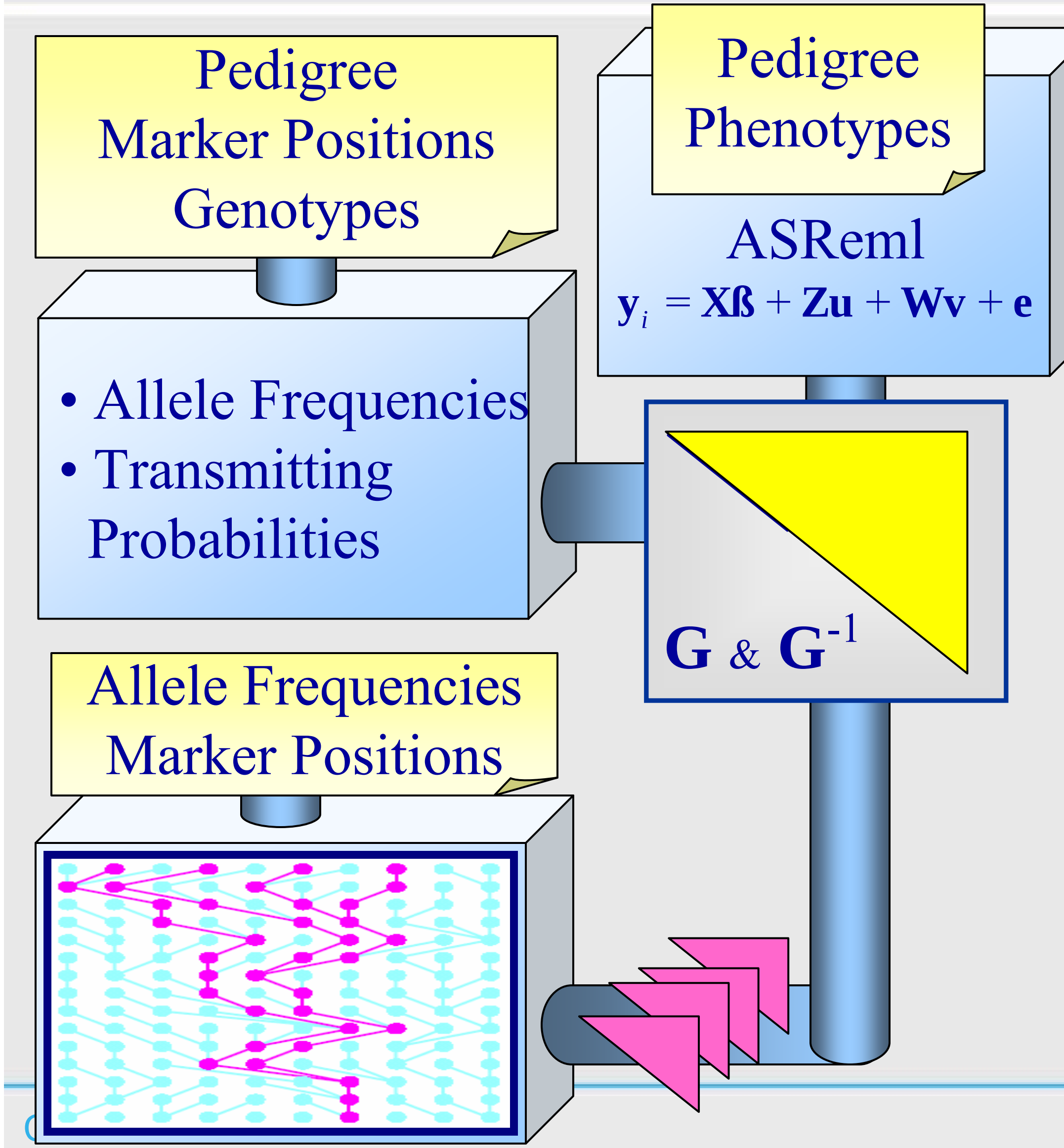


Summary

- Chromosomal region on BTA27 affecting udder health further investigated
- Sharper curves and higher peaks
- Specific haplotypes identified
- Basis for comparative sequencing

Financial support from the EAAP and the FUGATO M.A.S.-Net project is gratefully acknowledged!!!

Analysis



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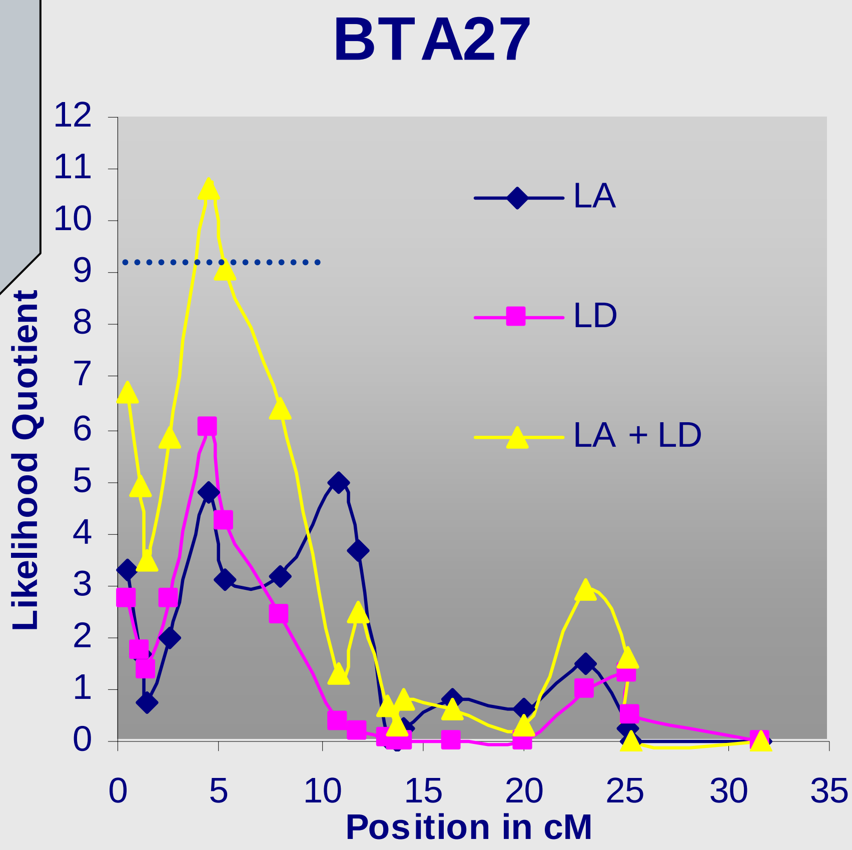
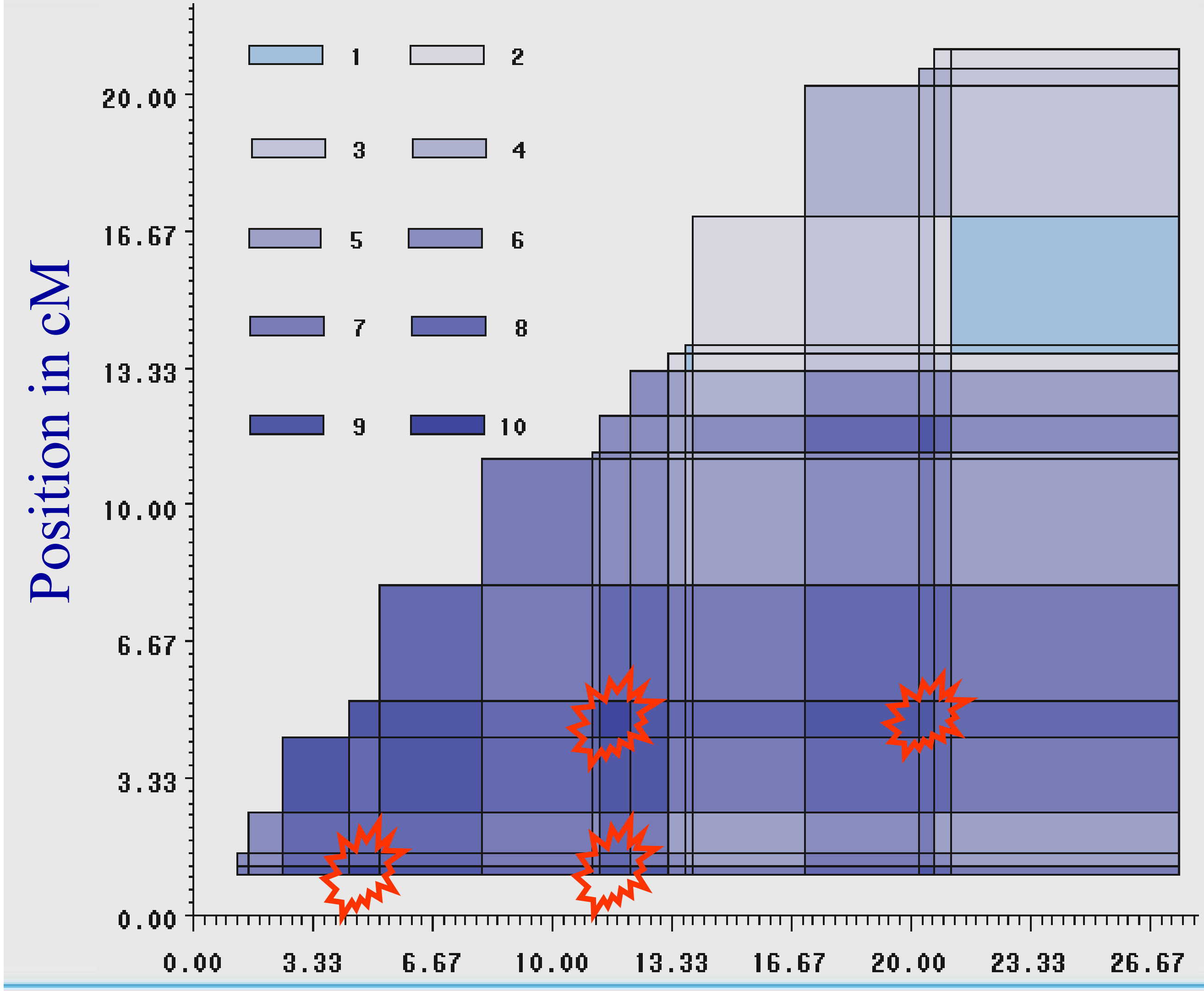


Analysis: 2-QTL Model



Position in cM

Pos1	Pos2	LogL
1.00	4.34	10.78
1.00	12.16	10.62
4.34	12.16	10.70
4.34	20.20	10.08