GWAS for Robustness traits

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ROBUSTMILK

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SEVENTH FRAMEWORK PROGRAMME

Develop innovative and practical breeding tools for improved dairy products from more robust dairy cows

SAC

SLU

gembloux agro bio tech

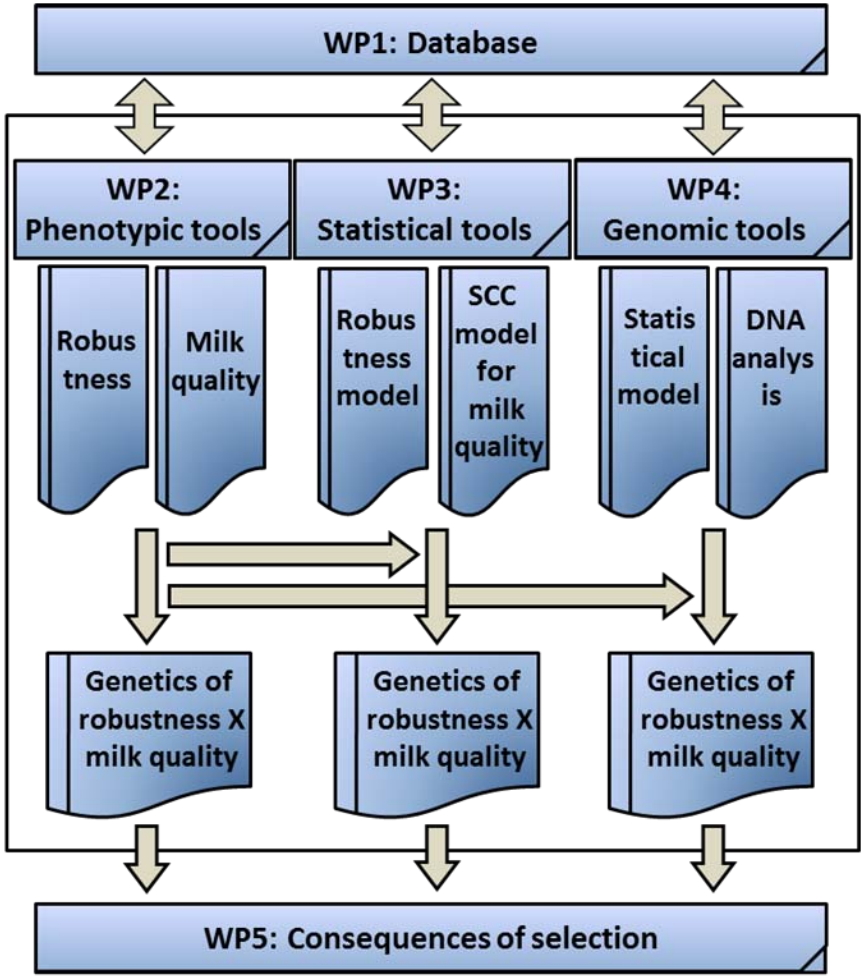
Université de Liège

WAGENINGEN UNIVERSITY WAGENINGEN UR

ANIMAL SCIENCES GROUP WAGENINGEN UR

eatasc

www.robustmilk.eu



Robustmilk - GWAS

Moorepark
Ireland
- Donagh Berry
- Linda Giblin

WUR Livestock Research
The Netherlands
- Roel Veerkamp
- Mario Calus
- Yvette de Haas

SAC
United Kingdom
- Eileen Wall
- Mike Coffey

SLU
Sweden
- Erling Strandberg
- Anne Lunden

WU
The Netherlands
- John Bastiaansen
- Susan Wijga
- Henk Bovenhuis

Introduction

"Traditional" selection strongly depends upon phenotypic observations $\Rightarrow$ drawbacks

- Traits with low heritability.
- Sex limited traits (e.g. milk production).
- Traits that are expressed late in the animal's life.
- Traits that can not be measured easily (e.g. milk fatty acid composition).

Genomic information is expected to contribute to selection for these “difficult” traits.

Introduction

- However, before we can utilize genomic information in selection we first need phenotypes....
  - Estimate GEBVs
  - Identify genes
- Experimental farms
  - Accurate/unique phenotypes
  - Limited in size
  - Phenotypes on cows
- Combine data across countries = Robustmilk

Material & Methods

- Genotypes Illumina BovineSNP50 BeadChip
- Holstein Friesian cows

The Netherlands, WUR:	696 cows
Ireland, Moorepark:	577 cows
Sweden, SLU:	243 cows
United Kingdom, SAC:	452 cows (+318 cows)

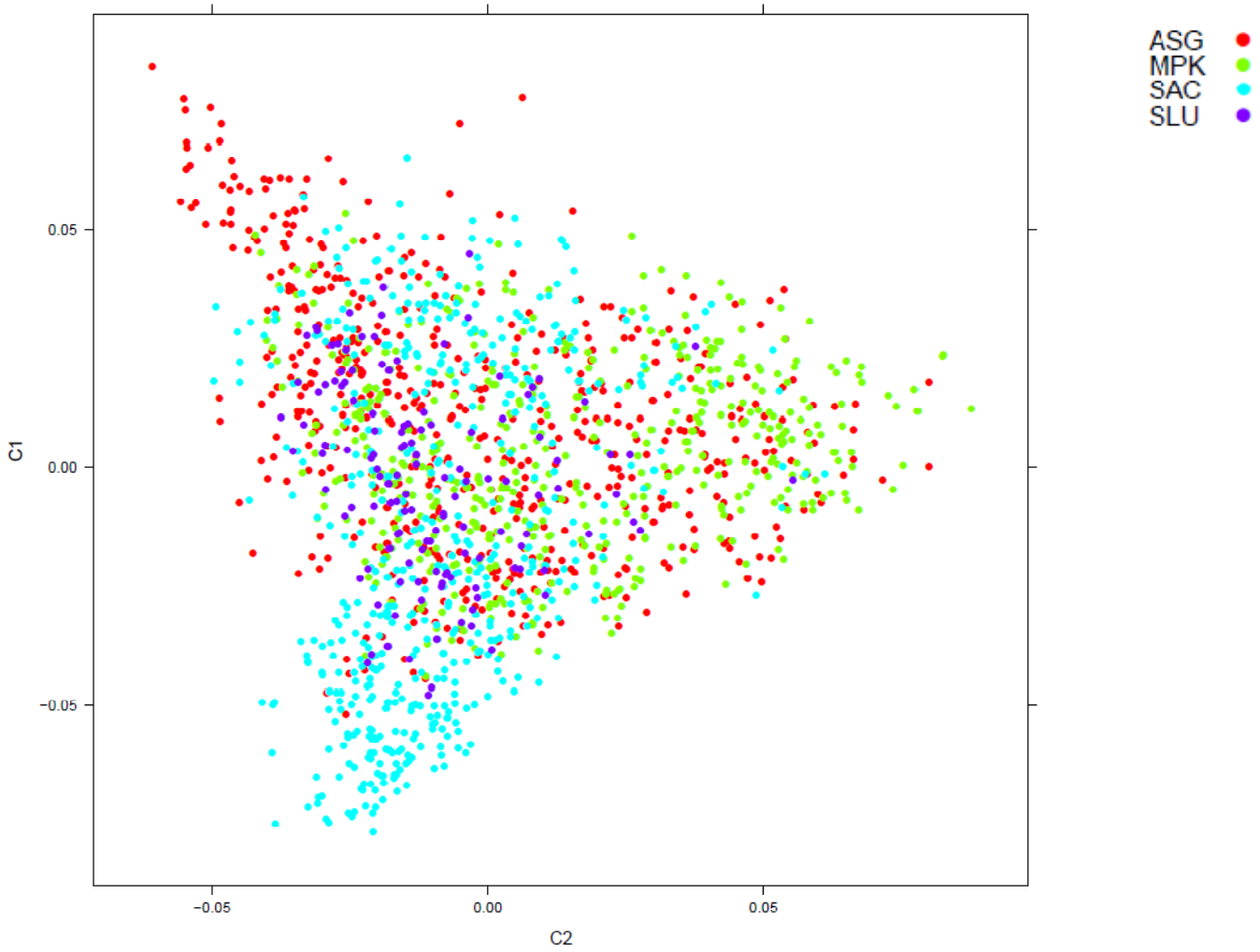
- HF Sires: 58 (+154 sires - Moorepark)
- Check for pedigree inconsistencies + SNP quality control (37,590 SNP used in association studies)

Material & Methods

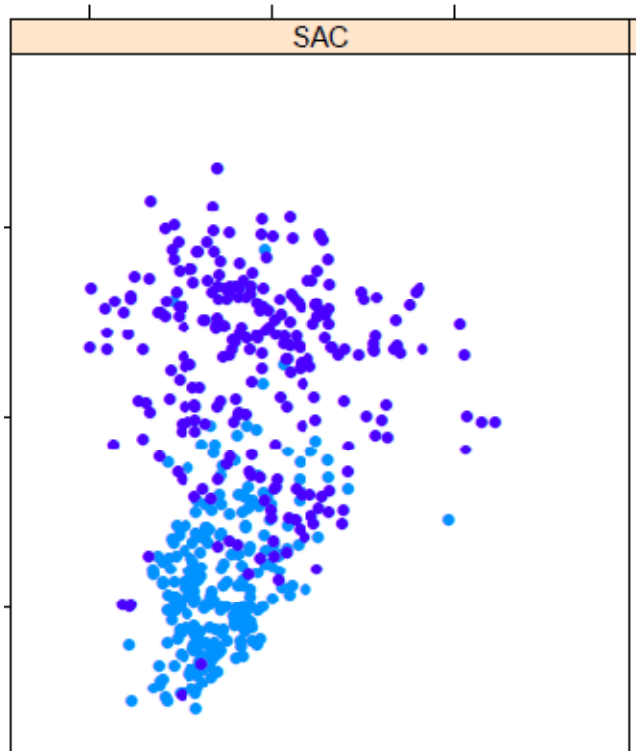
Traits

- Milk production
- Feed Utilisation (e.g. feed intake)
- Fertility (e.g. milk progesterone)
- Health (e.g. mastitis)
- Milk quality (e.g. Fatty acids)

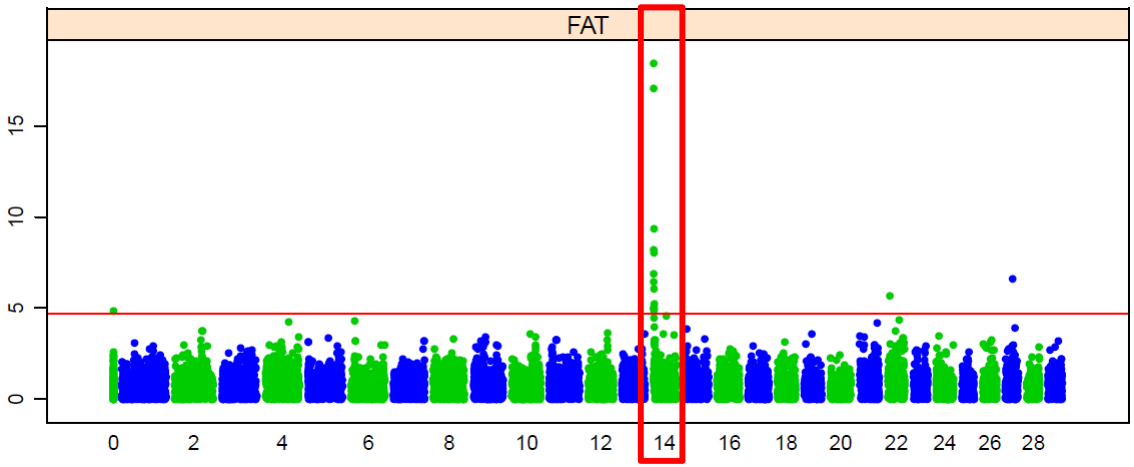
Results - relations

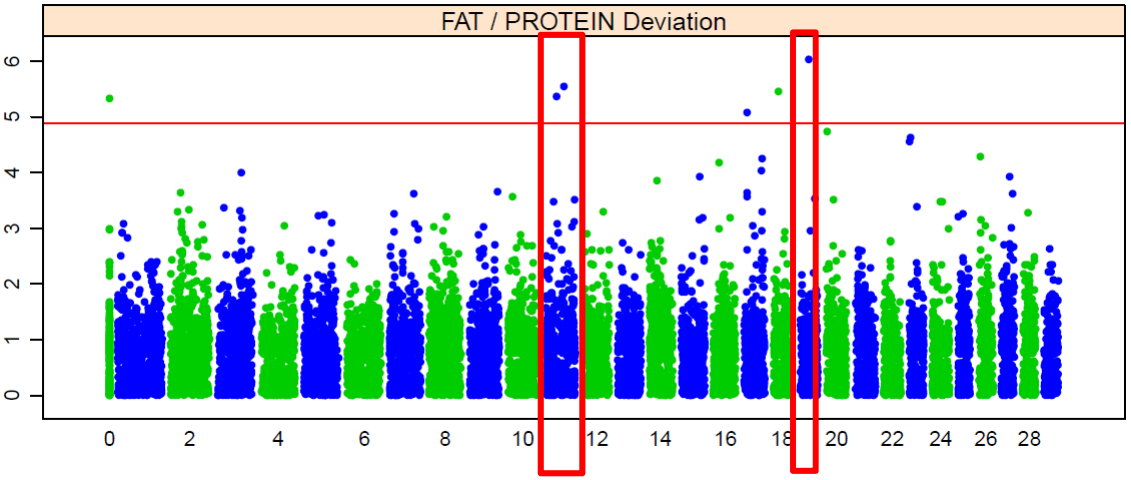


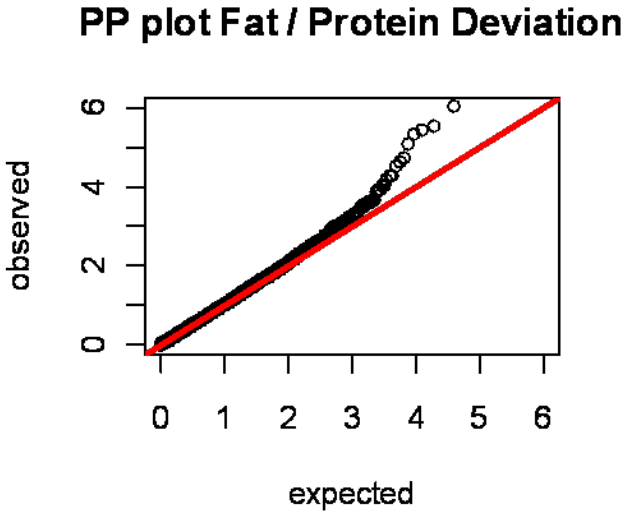
Results - relations



Bastiaansen et al. – Milk



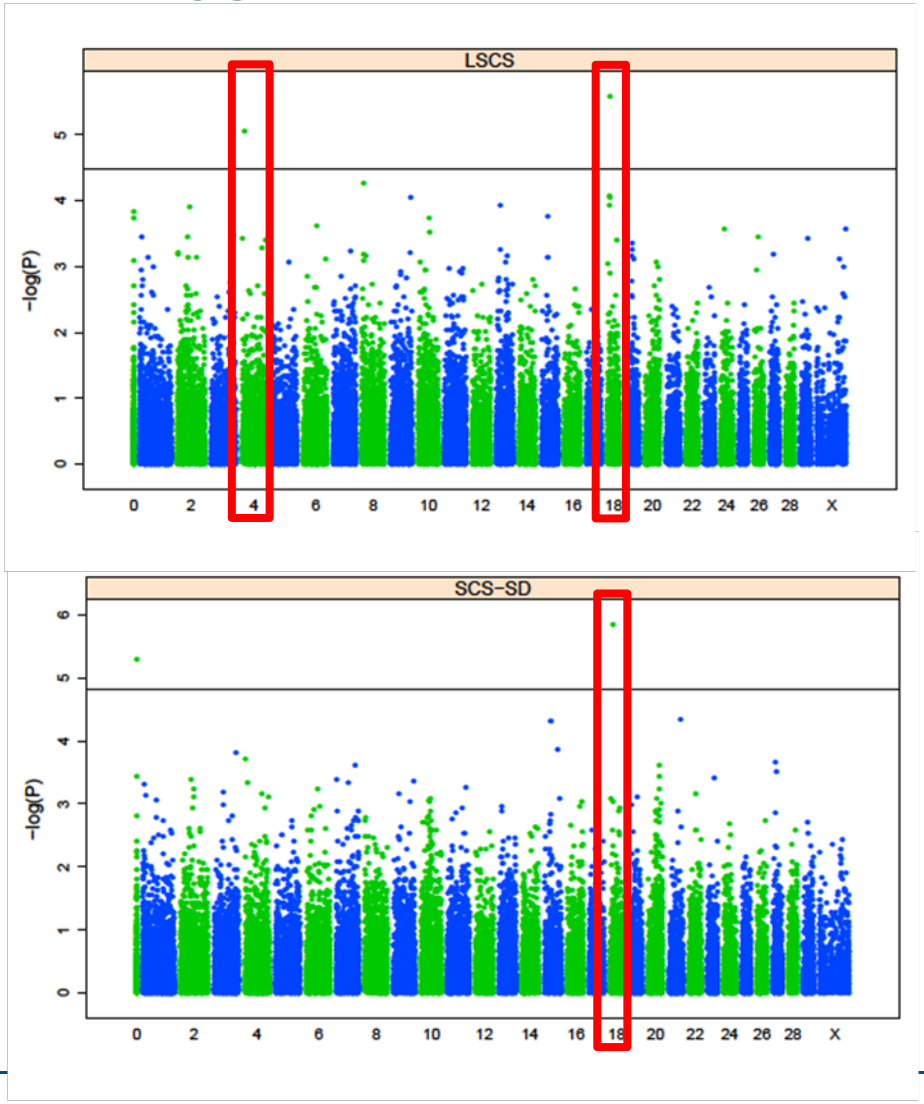




Wijga et al – mastitis

- On average 31 SCC test-day records per cow!!
  - Accurate estimates of lactation average SCS (LSCSC) and standard deviation of SCS (SCS-SD)
  - SCS-SD – see presentation Urioste et al
  - Higher probability of detecting deviations in SCC
- Part of the animals have data on Clinical Mastitis

Wijga et al – mastitis



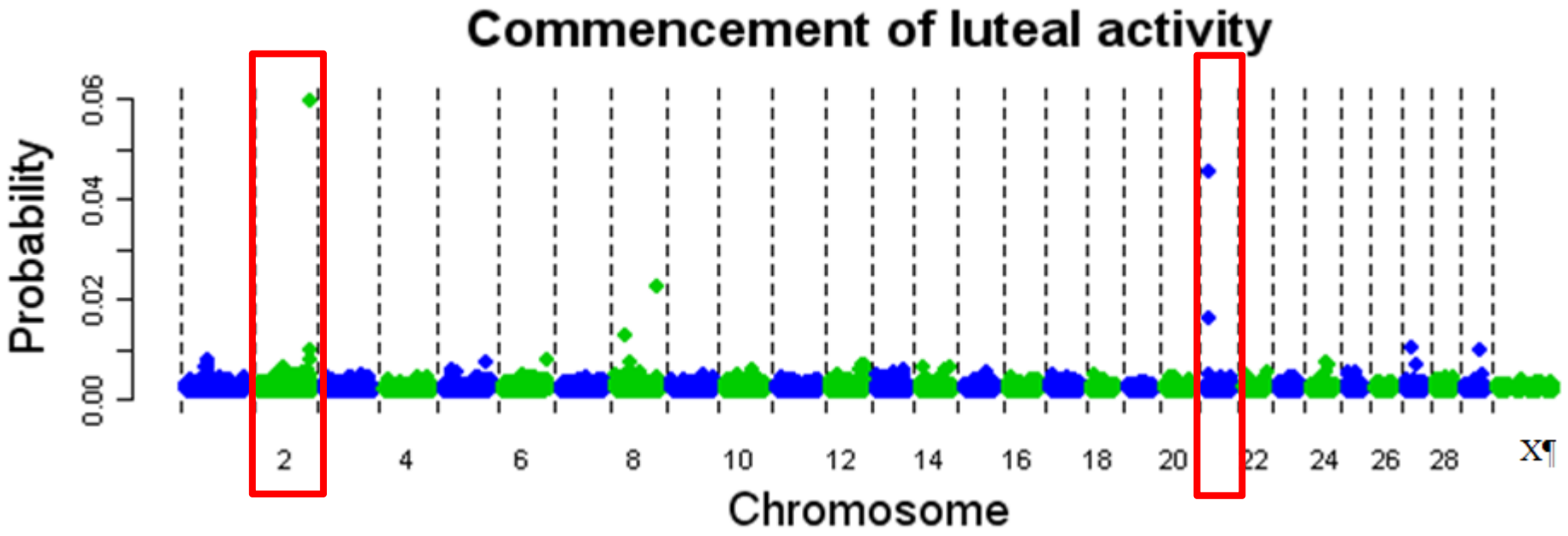
- Heritabilities
  - LSCS: 0.17
  - SCS-SD: 0.14
- No regions with large effects on SCC-derived traits were detected.
- Significant effects on
  - BTA4 – LSCS
  - BTA18 – LSCS, SCS-SD
- No effects on Clinical Mastitis

Berry et al – Fertility

- Fertility is a typical trait with substantial genetic variation but low heritability – difficult to obtain accurate phenotypes
- Hormonal profiles are more accurate
  - less missed fertility events
  - less noise due to management decisions
- Post-partum commencement of luteal activity quantified using milk progesterone concentration
- In addition traditional fertility traits

Berry et al – Fertility

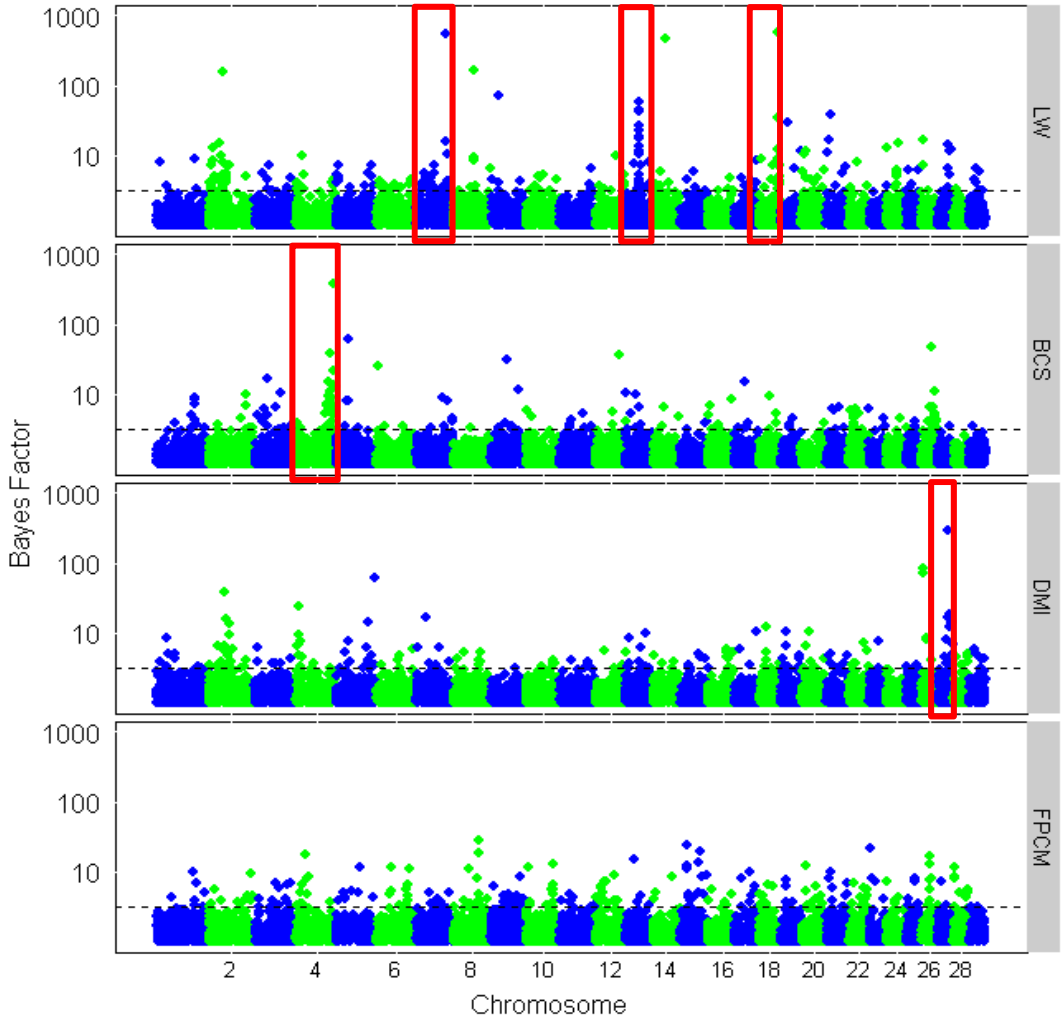
- Strongest signals for the CLA – “clean” phenotype! “Traditional fertility traits” show weak signal
- Significant evidence on BTA2 and BTA21 – SNP explain small fraction of the genetic variance



Veerkamp et al. – Feed Utilisation

- Unique data available on Live Weight (LW), Body Condition Score (BCS) and Dry Matter Intake (DMI)
- Allows studying the genomic architecture of relationships among traits Energy Balance – Fertility – Health.

Veerkamp et al. – Feed Utilisation



Conclusions

- For many years experimental herds have been collecting many unique phenotypes
- This is a valuable resource for genome wide association studies and genomic selection….if data sets are combined
- In the Robustmilk project significant associations for unique traits were detected.

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