

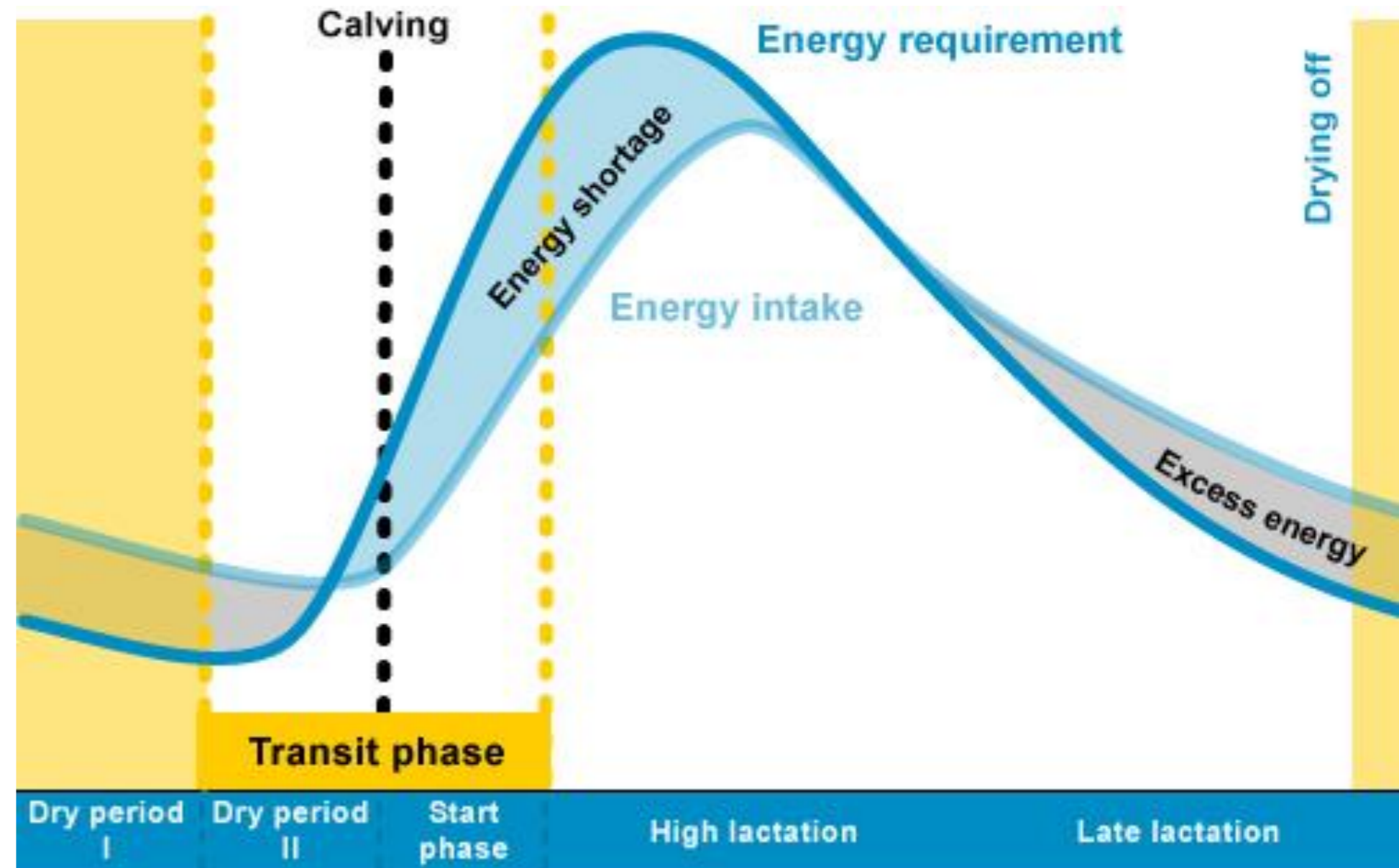
GENOME WIDE ASSOCIATION FOR METABOLIC ADAPTATION IN EARLY LACTATION DAIRY COWS

Matthieu Salamone - 28.08.2019

INTRODUCTION

THE TRANSITION PERIOD

- -3/+3 weeks around calving
- Pregnant – Non milking → Non-pregnant – Milking
- DMI ↑ ↔ Energy demand ↑↑↑
- Lipid mobilization ↑↑↑ → Uncontrolled mobilization → metabolic & infectious disorders ↑↑↑ & reproductive performance ↓↓↓

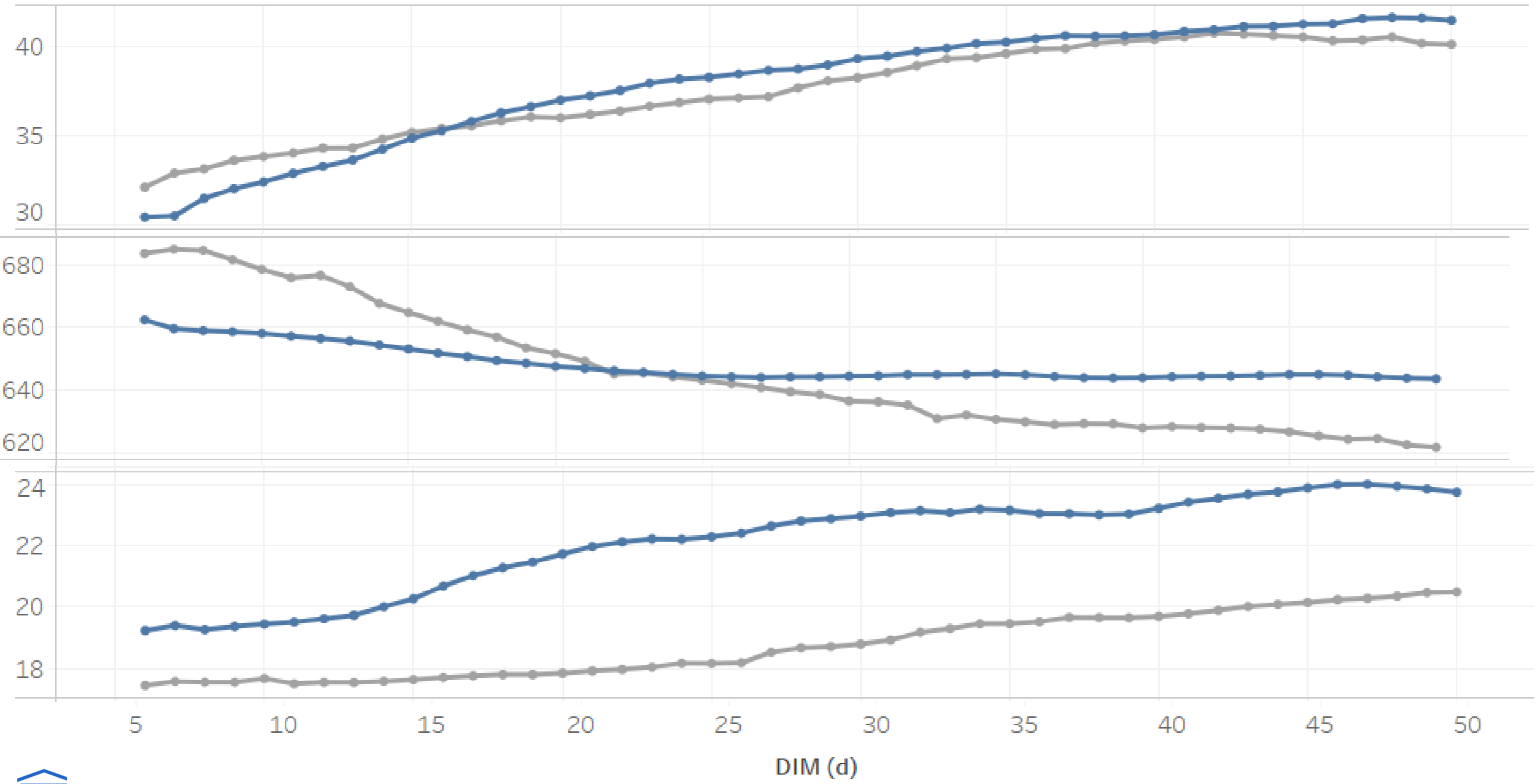


METABOLIC DISORDERS DURING TRANSITION

- Variance in metabolic disorders → Partly explained by Genetic background
- Heritability estimates: Ketosis → 0.01 – 0.16, Displaced Abomasum → 0 – 0.32 & Milk fever → 0.01 – 0.35
- Possible genetic selection for healthy cows during transition.

BALANCED ~ PRODUCTION

Most stable metabolism
BALANCED
Other



Milk (kg/day)

Weight (kg)






DMI (kg/day)

AIMS

Using GWAS to identify genetic markers linked with metabolic adaptation based blood metabolite in early lactation
Holstein dairy cows

MATERIAL & METHODS

ANIMALS & PHENOTYPES

- 105 animals → 4 research herds → ,  , , 
- K-means clustering → BHB, IGF-1, FFA, Glucose →
DIM 14 & 35

GENOTYPE & GENOTYPE QUALITY CONTROL

- Genotyped → Illumina BovineHD Beadchip → 777K SNP
- QC
 - No position information
 - < 95% call rate
 - MAF < 5%
 - HWE P-value < 5.0×10^{-6}

GENOME-WIDE ASSOCIATION STUDY

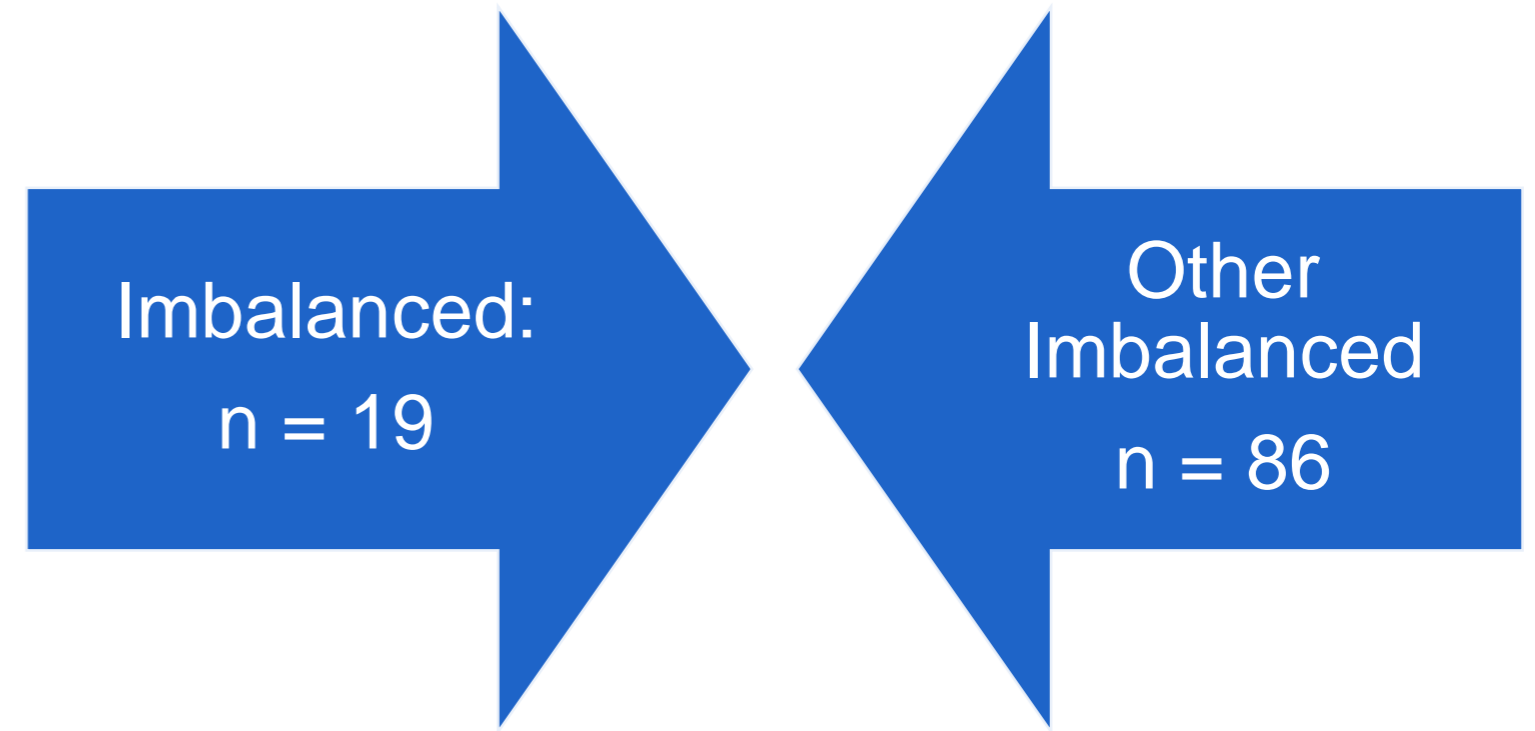
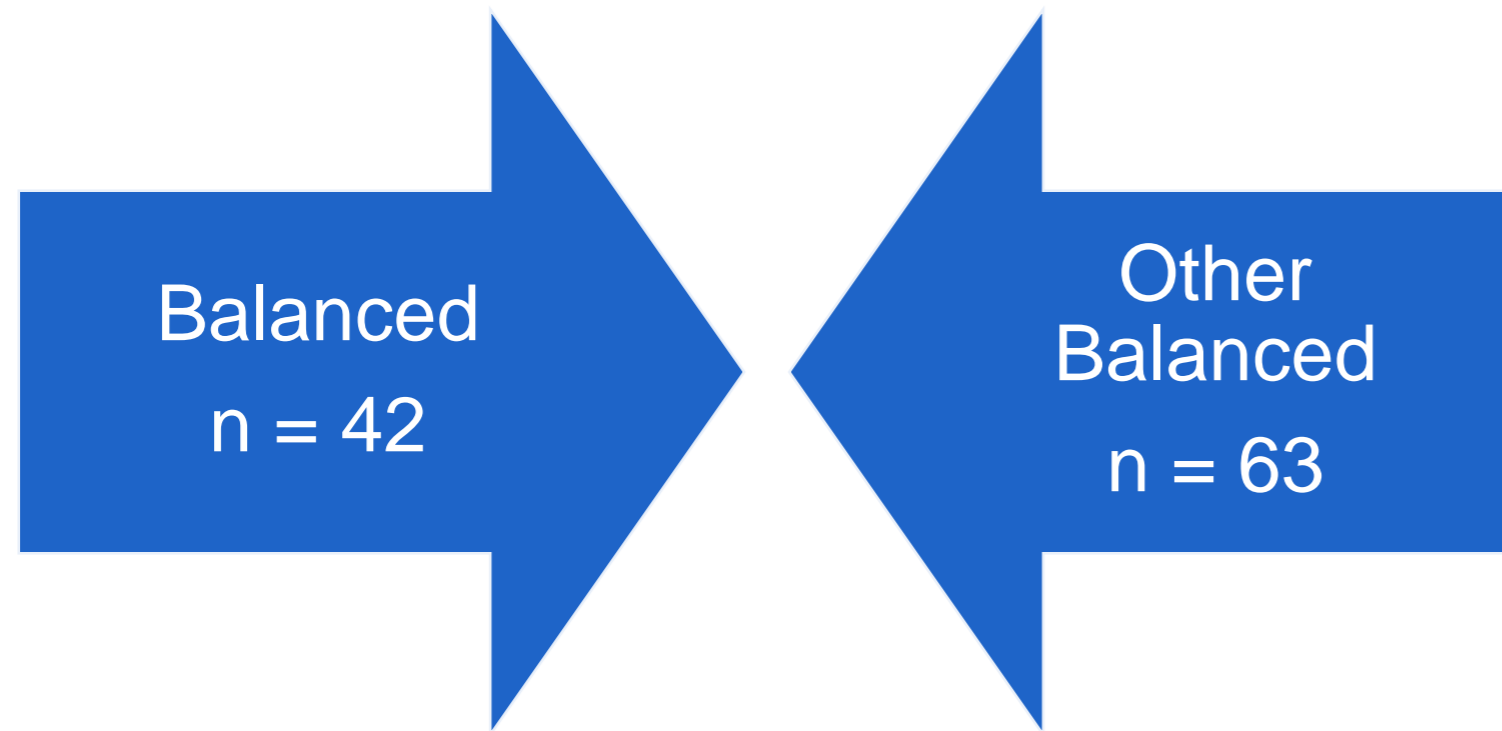
- Single SNP association ← GEMMA software
 - SNP → As covariate → Wald test
 - Threshold P value : 6.6×10^{-7}

GENE MAPPING & ENRICHMENT ANALYSIS

- Candidate genes → Genes 1Mbp up or downstream from significant SNP
- Gene Enrichment Analysis
 - List of candidate genes → uploaded to Enrichr Software

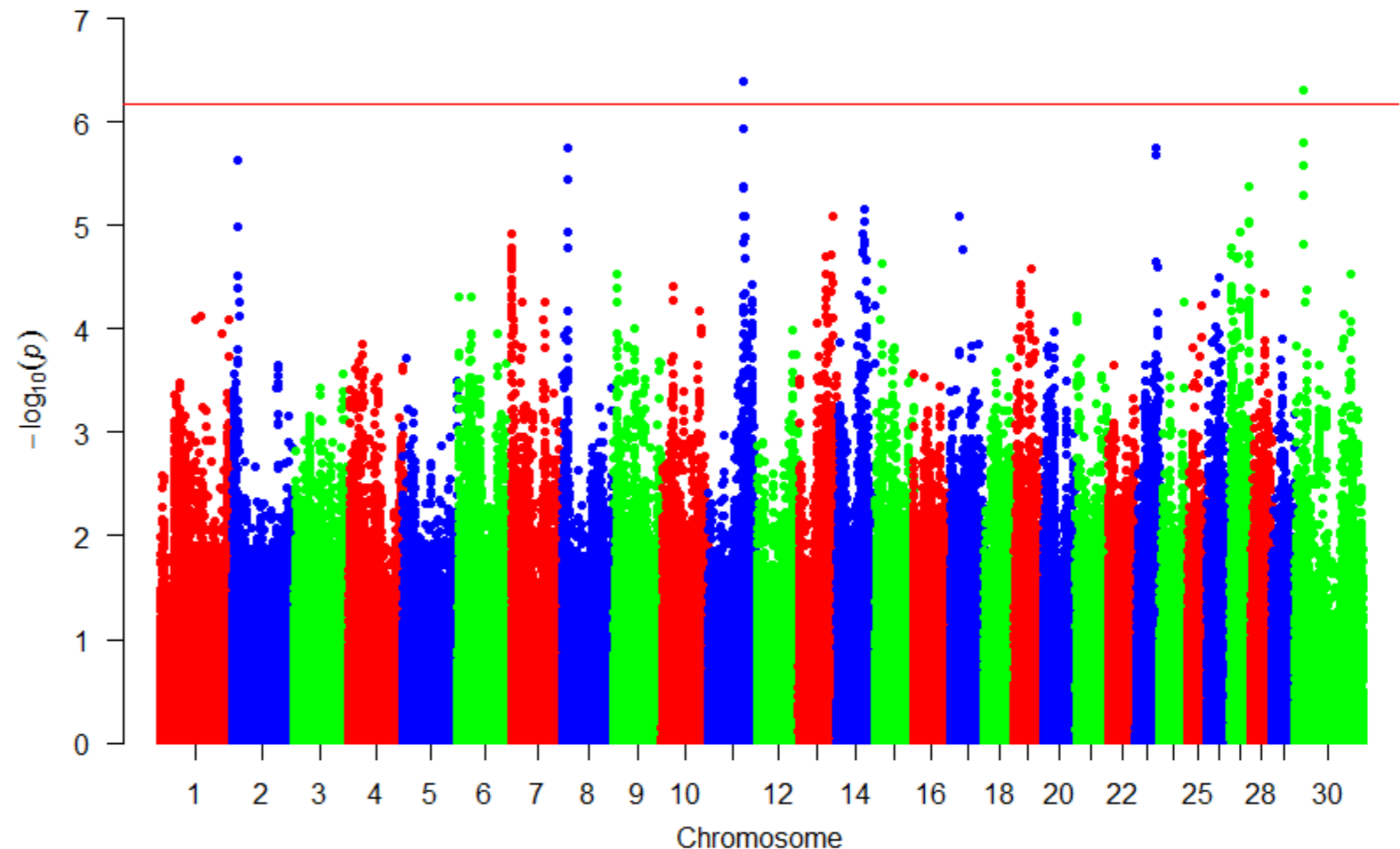
RESULTS & DISCUSSION

ANIMAL & PHENOTYPE



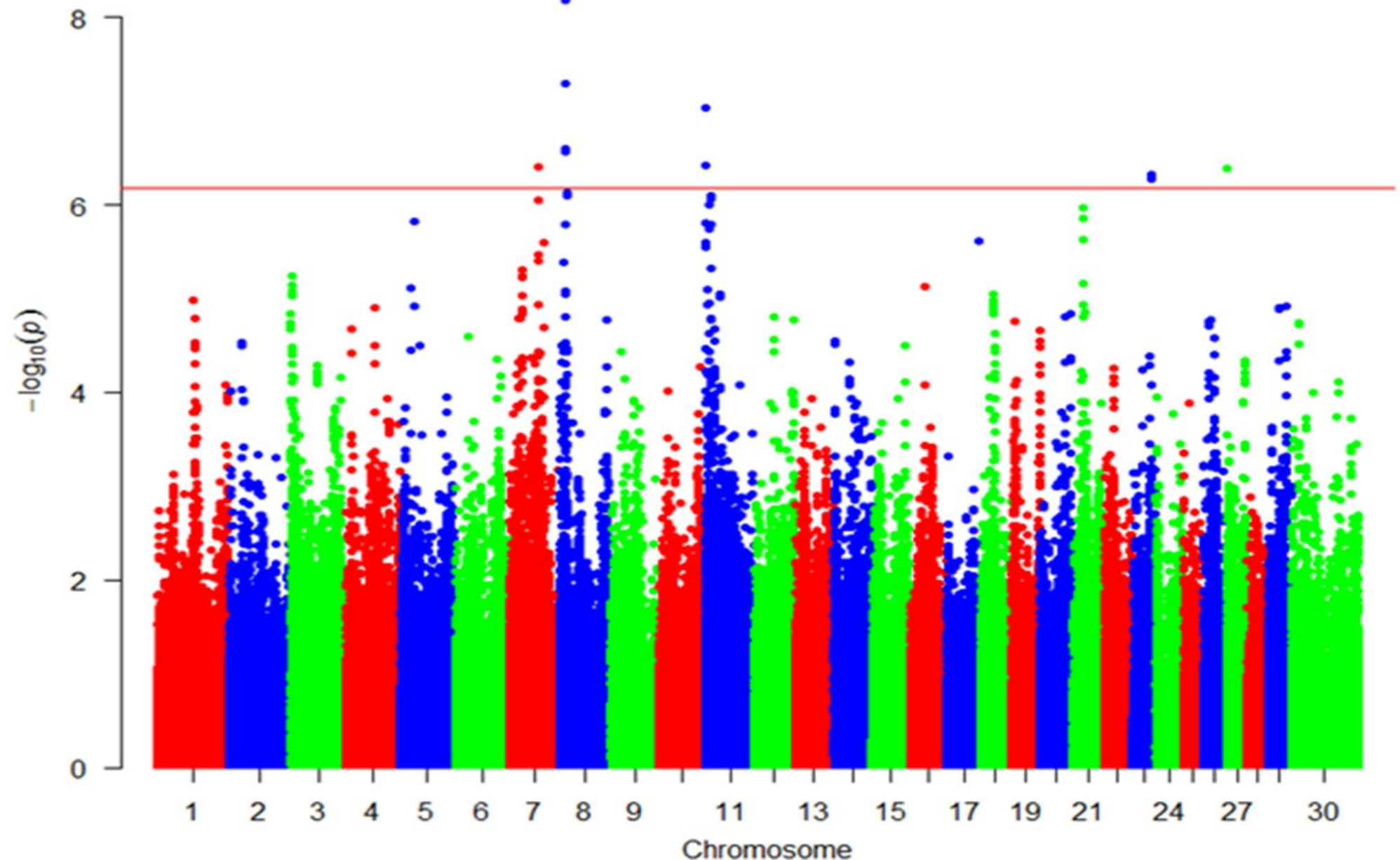
GWAS BALANCED

- 2 Significant SNP
- BTA 11
 - SNP within QTL of IgG
 - IgG ↓ in -8 w partus & recovered in +4 w partus (Herr et al., 2011)



GWAS IMBALANCED

- 12 Significant SNP
- BTA 7
 - SNP within QTL for milk yield & compositions
- BTA 8
 - SNP within QTL for Body length & protein yield
- BTA 23
 - SNP within QTL for Milk FA
- BTA 27
 - SNP within QTL for fat & protein yield



GENE MAPPING & ENRICHMENT ANALYSIS

- **Balanced**
 - Candidate genes associated with
 - **Aminoglycan:**
 - Catabolic process
 - Metabolic process
 - Biosynthetic process
 - **Glycosaminoglycan:**
 - Catabolic process



GENE MAPPING & ENRICHMENT ANALYSIS

- **Imbalanced**
 - Candidate genes associated with
 - **Transport of:**
 - L-alanine
 - Glycine
 - Proline
 - Alanine
 - Amino acid transmembrane
 - L-Amino acid



CONCLUSION

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- Genomic loci ~ metabolic adaption → identified with novel phenotype ← k-means clustering of blood metabolites
- Genetic basis of metabolic adaptation in early lactation Holstein dairy cows

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