# GWAS for feed intake and methane emission across cattle populations

**Birgit Gredler-Grandl and co-authors**

BovReg Final Conference, February 15th, 2024

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BovReg
Understanding cattle genomes

EuroFAANG

# Thank you to all co-authors (BovReg & gDMI)

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# Introduction

- BovReg: Providing a catalogue of functionally active genomic features in cattle

- Key traits: Biological & environmental efficiency
  - → Feed efficiency
  - → Methane emission

- Large scale recording of methane & feed intake difficult
  - → size of reference populations for GWAS & genomic selection limited
  - → accuracy is limited

https://hokofarmgroup.com

# Objective

Combine resources across-countries to identify relevant genome regions related to **dry matter intake** (**DMI**) and **methane production** (**CH4 g/day**)

Meta-GWAS across dairy and beef cattle populations

# Meta-GWAS for DMI and CH4 g/day

BovReg

- Phenotypes recorded
- DMI
  - Feed bins
  - Dairy cows, beef cattle, dairyxbeef cross
  - Different lactation stages
- CH4:
  - GreenFeed, sniffer and SF6
  - Dairy cows and beef cattle
  - Different lactation stages

**Dairy**

**Beef**

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# Meta-GWAS for DMI and CH4 g/day

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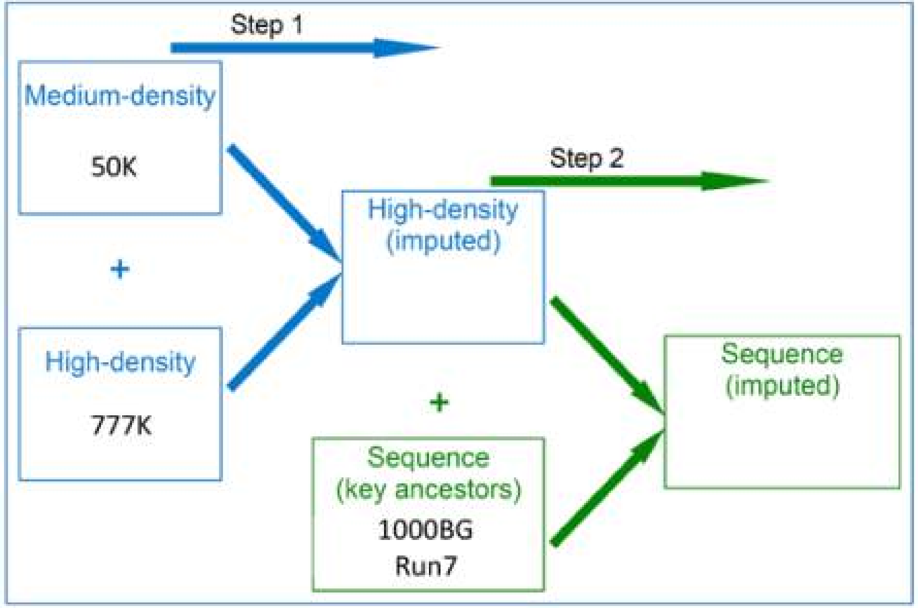
- Imputation to sequence level


Step 1

Medium-density
50K

+

High-density
777K

Step 2

High-density
(imputed)

+

Sequence
(key ancestors)
1000BG
Run7

Sequence
(imputed)

Pausch et al, 2020

**Dairy**

**Beef**

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# Animals and variants local GWAS

| Population | Dry matter intake | | Methane production | |
|---|---|---|---|---|
| | N | N variants imp. $r^2 > 0.6$ | N | N variants imp. $r^2 > 0.6$ |
| AU | 495 | 17,158,878 | 495 | 17,158,878 |
| AgVIC | 584 | 17,597,583 | 354 | 17,030,121 |
| FBN dairy | 140 | 14,016,930 | | |
| FBN beef | 253 | 16,057,514 | | |
| INIA | 561 | 12,829,538 | 971 | 13,308,847 |
| LUKE | 366 | 18,392,101 | | |
| UAL | 7,552 | 30,381,524 | 602 | 28,483,478 |
| UoG | 588 | 11,694,898 | 346 | 11,329,136 |
| WUR | 2,565 | 17,817,916 | 460 | 13,489,734 |

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13,104 animals

3,228 animals

# GWAS for CH4 g/day and DMI

- Local GWAS (GCTA, Yang et al. 2011) by each partner

$$y=1\mu+xb+u+e$$

- Phenotypes: de-regressed BV, direct phenotypes corrected for fixed effects

- Local GWAS summary statistics to WUR

**Dairy**

**Beef**

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# Meta-GWAS for CH4 g/day and DMI @WUR

- Standardisation of variant effects by genetic standard deviation
- Variants effect size +/- 5 s.d.
- MAF >0.005
- Software METAL (Willer et al., 2010)
  - STDERR method
  - Genomic control
- Scenarios: ALL – HOL - BEEF

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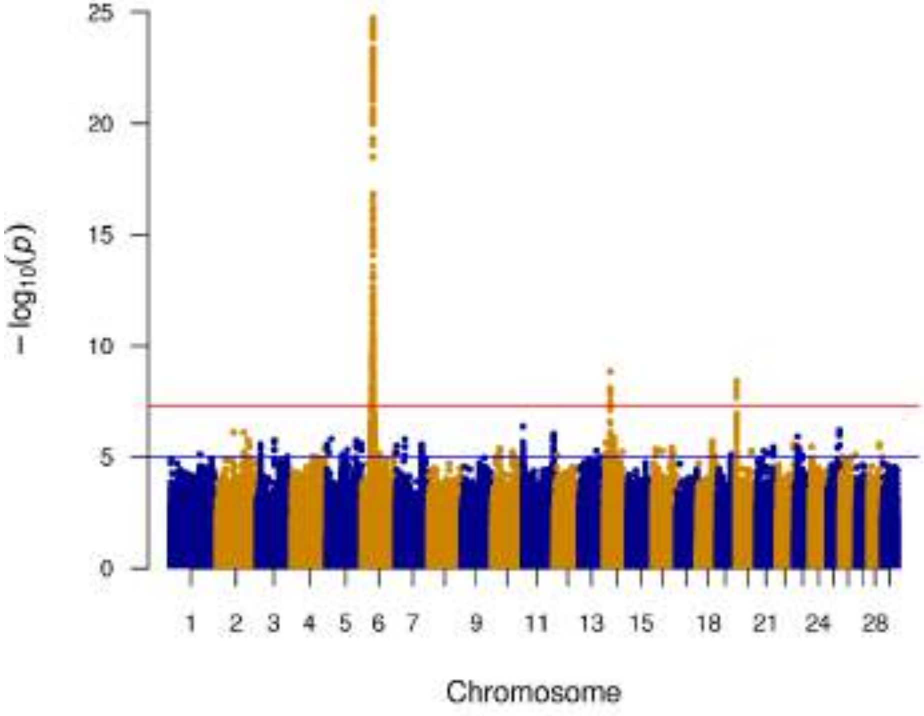
# Gene-based GWAS @WUR

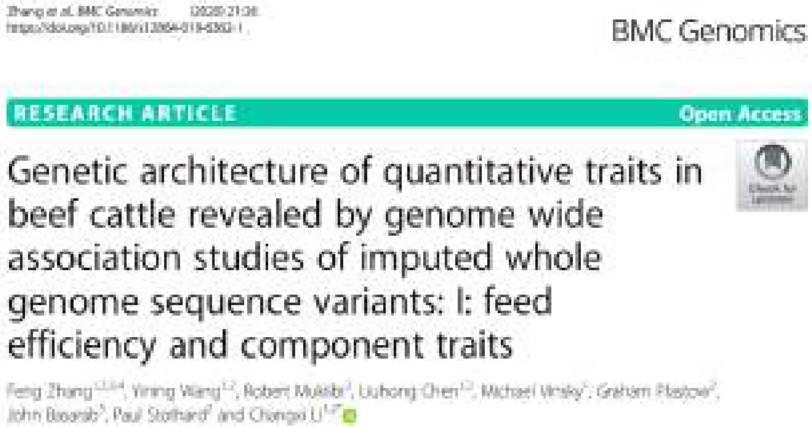
- GCTA-fastBAT (Bakshi et al., 2016)
- Genes downloaded from Ensemble (cow genes ARS-UCD1.2)
- LD calculation based on 1000 Bull Genomes data
- Bonferroni corrected sign. level $PfastBAT < 1.92 \times 10-6$ (0.05/26,101)
- Number of genes tested per trait and scenario

| **DMI** | | | **CH4** | | |
|---|---|---|---|---|---|
| ALL | HOL | BEEF | ALL | HOL | BEEF |
| 26,056 | 26,083 | 26,067 | 26,045 | 26,054 | 25,971 |

# Results Meta-GWAS DMI - ALL

13,104 animals
25,617,425 variants



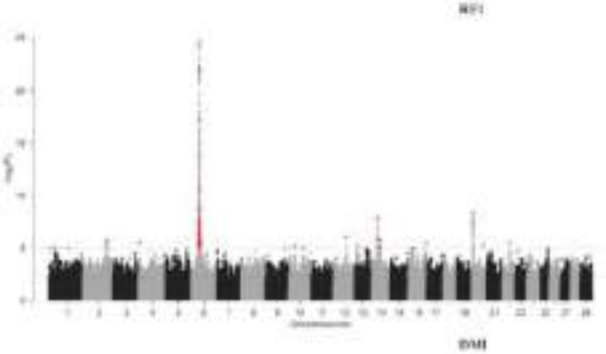

Zhang et al. BMC Genomics (2020) 21:36
https://doi.org/10.1186/s12864-019-6362-1

BMC Genomics

RESEARCH ARTICLE Open Access

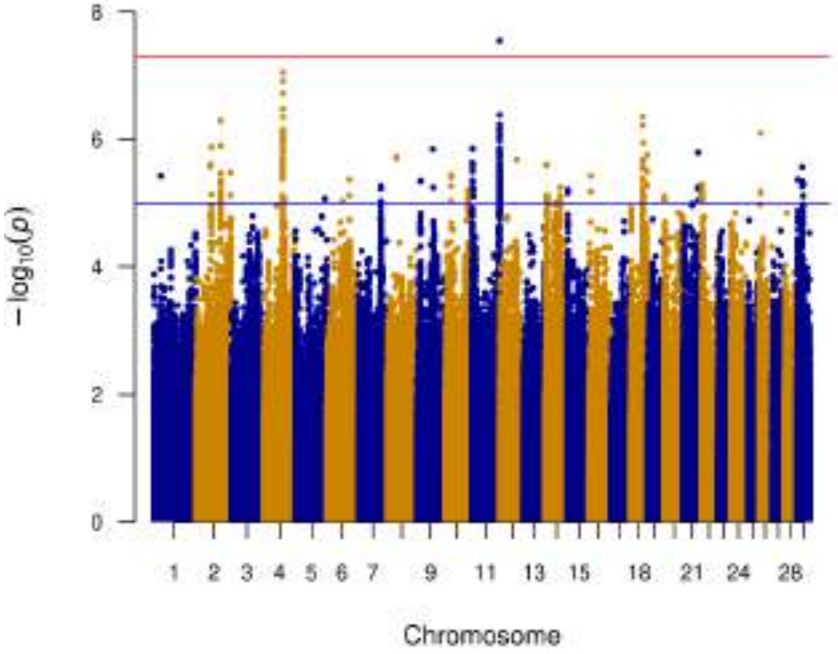
Genetic architecture of quantitative traits in beef cattle revealed by genome wide association studies of imputed whole genome sequence variants: I: feed efficiency and component traits

Feng Zhang[1,2,3,4], Yining Wang[1,2], Robert Mukiibi[2], Liuhong Chen[1,2], Michael Vinsky[5], Graham Plastow[2], John Basarab[3], Paul Stothard[2] and Changxi Li[1,2*]

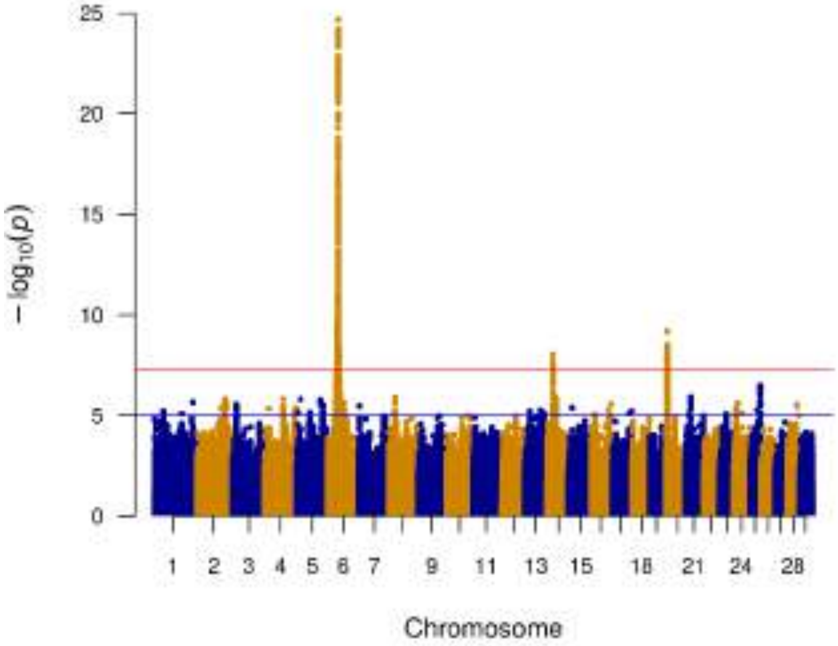


# Results Meta-GWAS DMI – HOL & BEEF

**HOL** 4,933 animals
19,457,738 variants

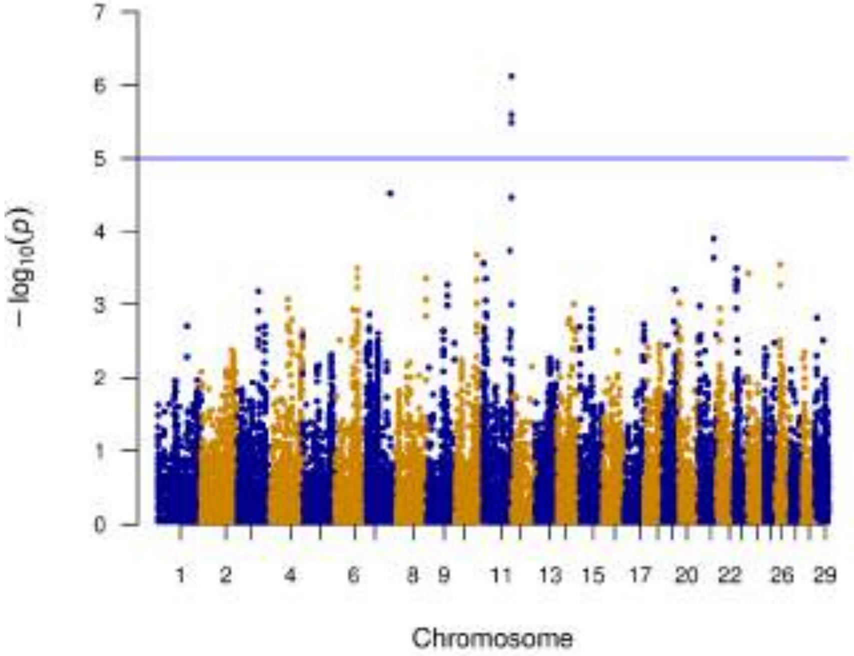


**BEEF** 7,805 animals
22,646,101 variants

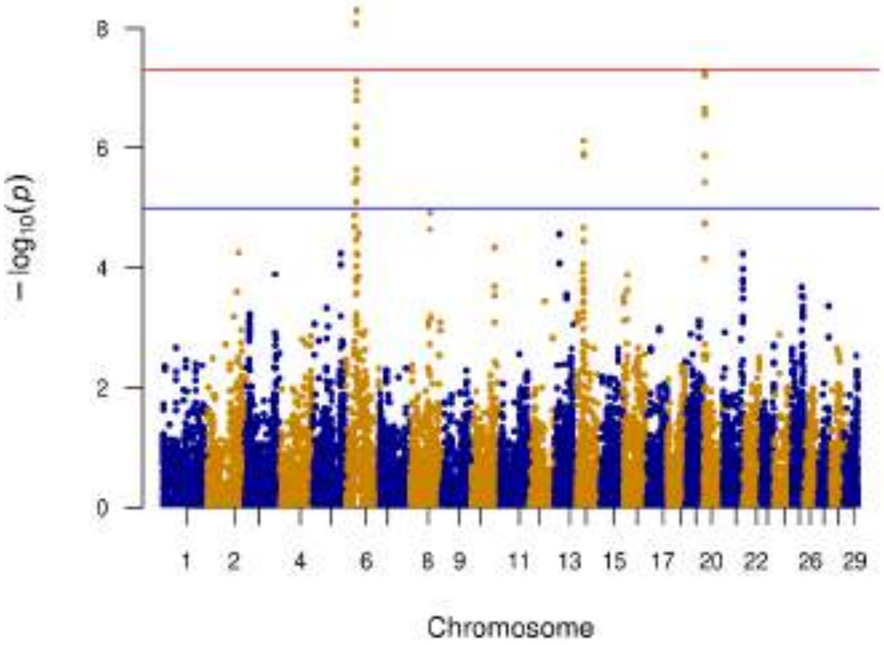


# Results genebased GWAS DMI – HOL & BEEF

HOL
26,083 genes

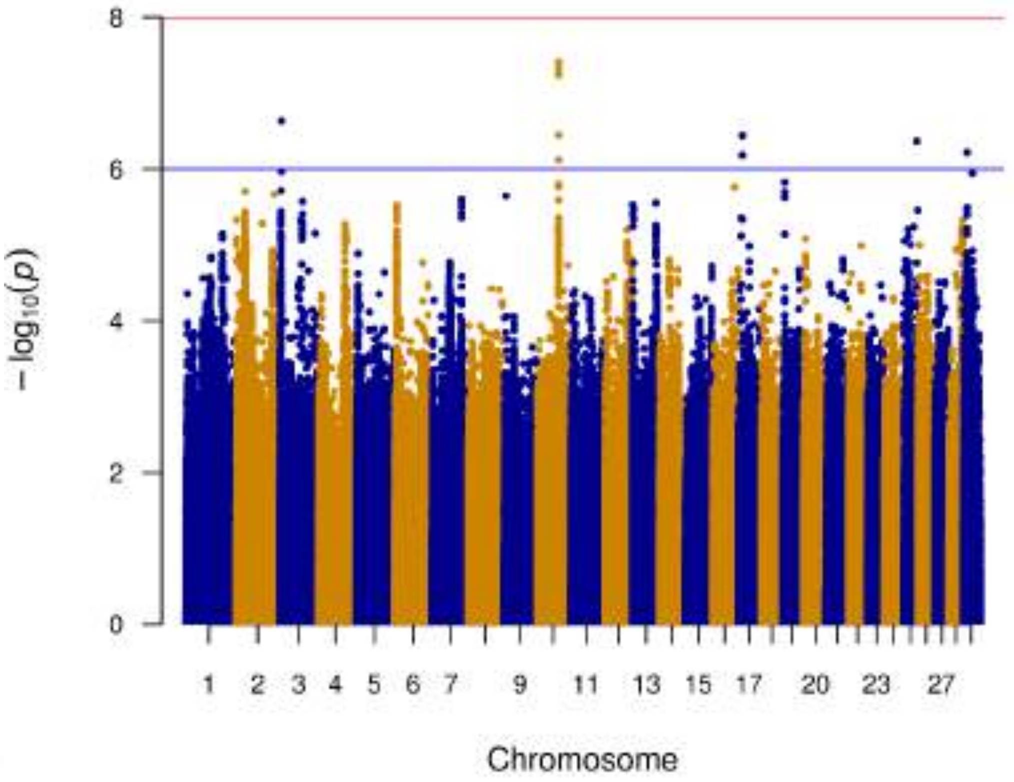


BEEF
26,067 genes



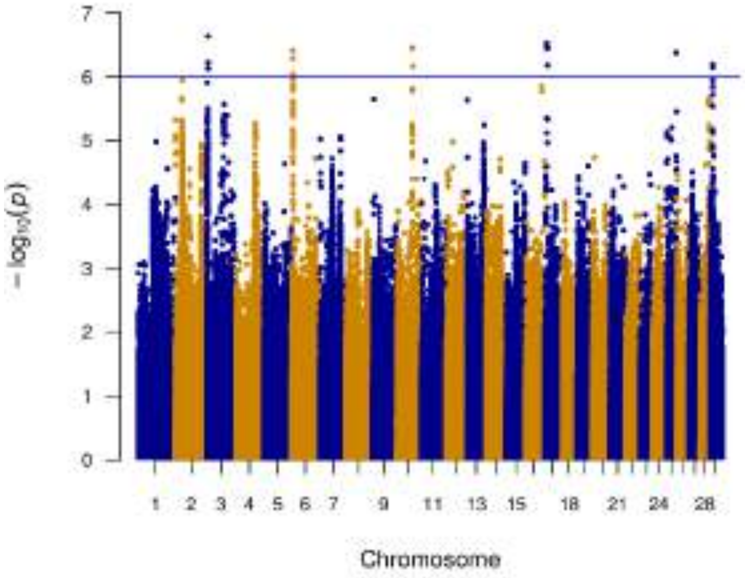
# Results Meta-GWAS CH4 - ALL

3,228 animals
22,596,906 variants

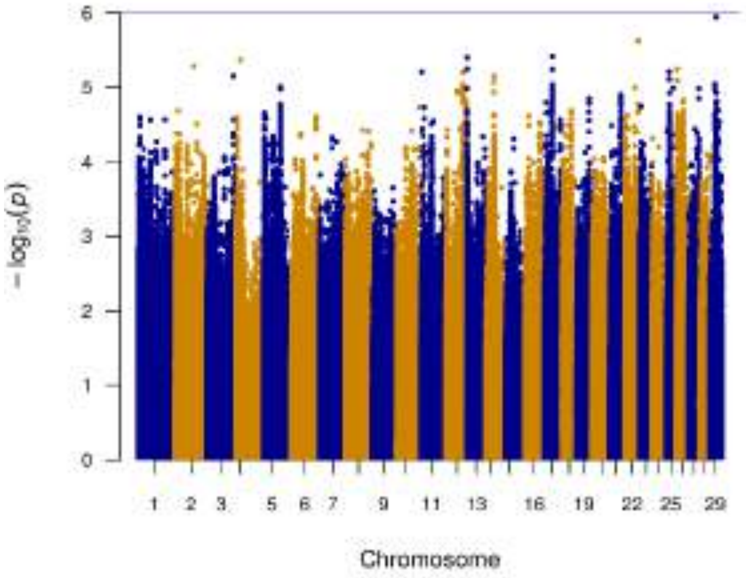


# Results Meta-GWAS CH4 – HOL & BEEF

HOL 2,626 animals
18,055,312 variants

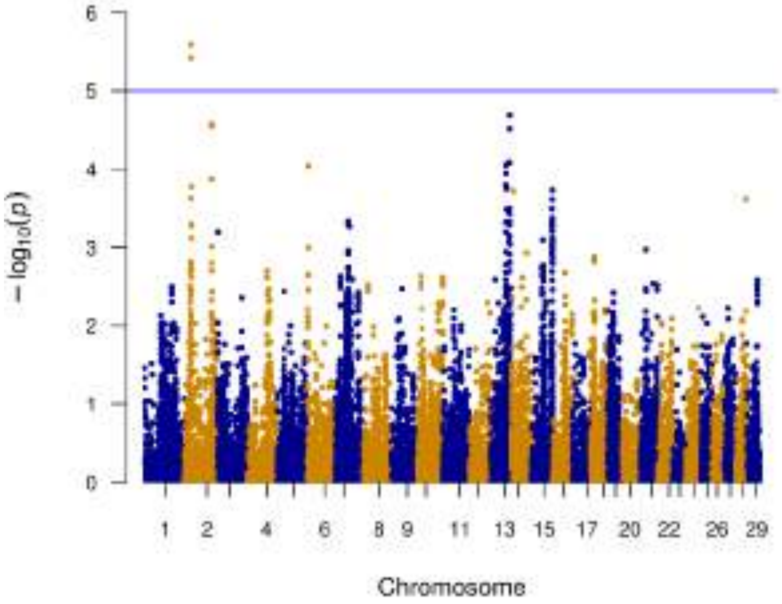


BEEF 602 animals
18,264,282 variants

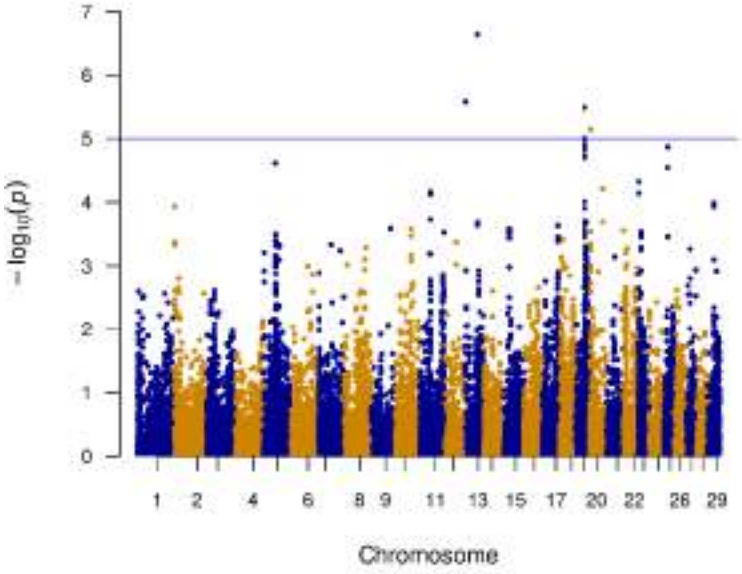


# Results genebased GWAS CH4 – HOL & BEEF

HOL
26,054 genes



BEEF
25,971 genes



# Summary

- Dry matter intake and methane emission complex traits

- **Dry matter intake**:
  - Confirmed QTL for dry matter intake in beef
  - No clear candidates in dairy breeds
  - → WP7: genomic prediction

- **Methane emission**
  - No clear candidates

- Challenge: heterogeneous data sets across-county
  - trait definition for DMI and CH4
  - Recording techniques

# Acknowledgments

The BovReg consortium

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*Thank you for your attention*

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