



# Tackling methane emissions through a (pheno, geno and metageno)-omics approach

**O. González-Recio**, I. Goiri, R. Atxaerandio, E. Ugarte, R. Ruiz, R. Alenda, J.A. Jiménez-Montero, A. García-Rodríguez

## How cattle produce methane

**FACT CARD**

Cattle can eat grasses and shrubs that other animals can't digest...

They regurgitate the food as "cud" and rechew it

bacteria in stomach breaks down the cud, producing methane in the process

**#GOODMEAT**

## The Beef Burden: the real cost of America's steak obsession

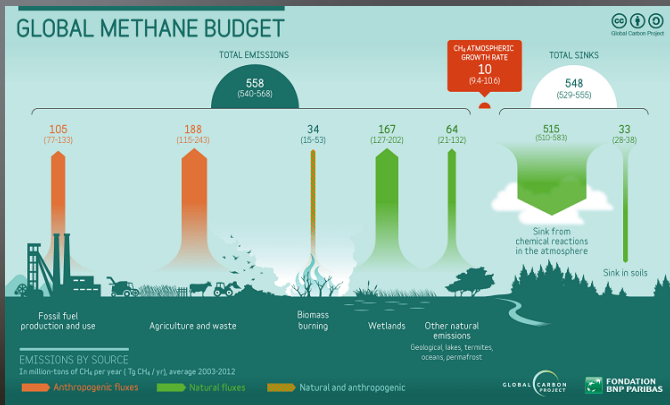
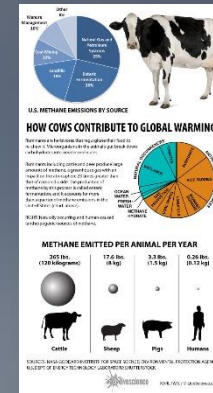
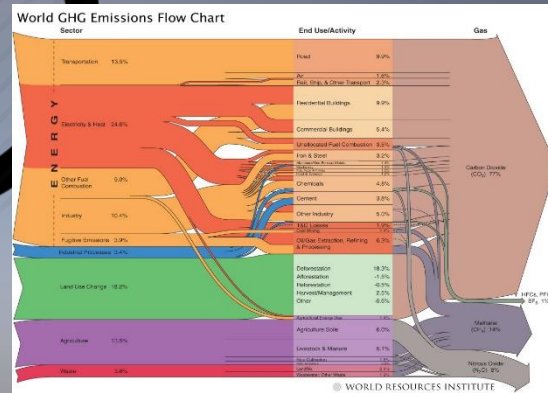
32 Million produced in 2013

**POLLUTION CREATED**

- 1.5 of beef's methane emissions (10% of world's)
- 18% of U.S. methane emissions
- 6% of total greenhouse gas emissions (10% of U.S.)

**FEED PRODUCTION**

- 27% water footprint
- 60% nitrogen footprint
- 40% land footprint



## GRASS-FED BEEF THE CARBON FARMPRINT

FARM CARBON OUTPUT FROM BEEF: 80 Tons (produced by 50 mother cows and 80 young calves)

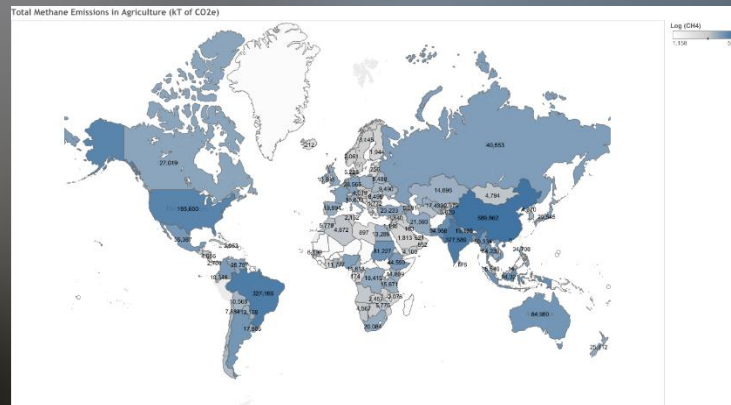
CARBON SEQUESTERED IN SOIL BY PASTURES: 32 Tons (produced by Tractor/Equipment Processing/Distribution)

500 Tons (removed by 150 Acres of Pasture)

**Total Output: 112 Tons of Carbon**

**Total Sequestration: 500 Tons of Carbon**

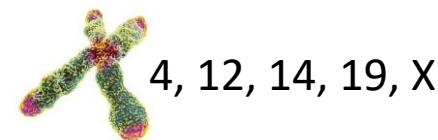
**388 Tons From the Atmosphere Annually** (Net Removal)



[J Anim Sci](#). 2016 Oct;94(10):4151-4166. doi: 10.2527/jas.2016-0431. [Paperpile](#)

## Genomewide association study of methane emissions in Angus beef cattle with validation in dairy cattle.

[Manzanilla-Pech CI](#), [De Haas Y](#), [Hayes BJ](#), [Veerkamp RF](#), [Khansefid M](#), [Donoghue KA](#), [Arthur PF](#), [Pryce JE](#).



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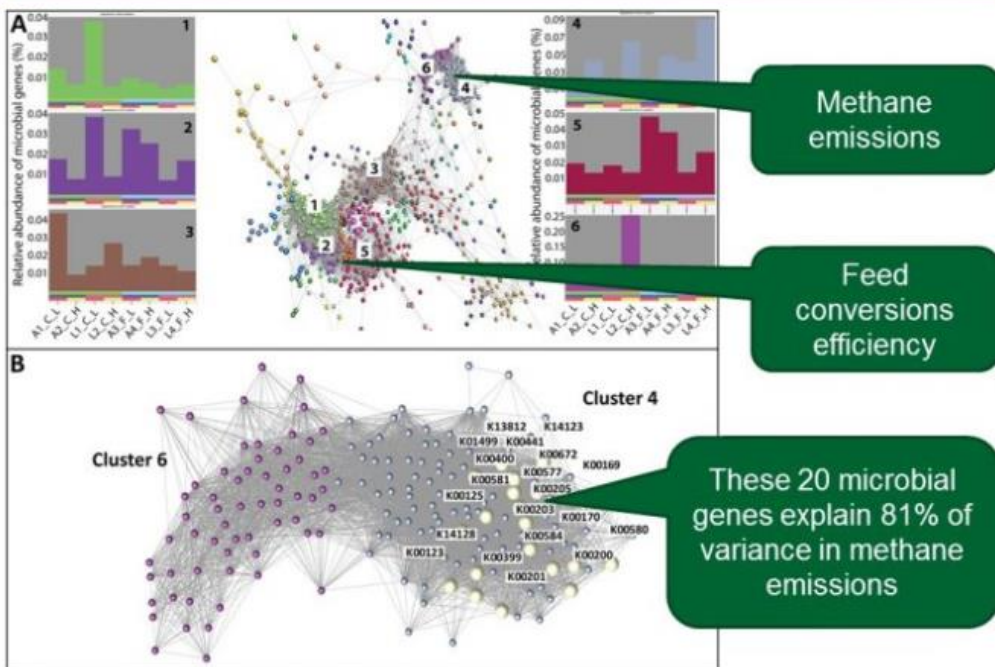
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Meta-analysis of heritability estimates for methane emission indicator traits in cattle and sheep

$$h^2 = 0.25$$

[Luiz Fernando Brito](#), [Flavio Schenkel](#), [Hinayah Rojas de Oliveira](#), [Angela Canovas](#), [Filippo Miglior](#)

## Networks of rumen microbial genes are related to traits



Genetics and microbiome of cattle methane production: 2017 PLOS Genetics Research Prize Winning Research

Posted September 21, 2017 by Jessica Miller in Uncategorized

The *PLOS Genetics* Editors-in-Chief and Senior Editors would like to congratulate: **Rainer Roehle, Richard J. Dewhurst, Carol-Anne Duthie, John A. Rooke, Nest McKain, Dave W. Ross, Jimmy J. Hyslop, Anthony Waterhouse, Tom C. Freeman, Mick Watson and R. John Wallace**, authors of the article chosen as the recipient of the 2017 *PLOS Genetics* Research Prize: 'Bovine Host Genetic Variation Influences Rumen Microbial Methane Production with Best Selection Criterion for Low Methane Emitting and Efficiently Feed Converting Hosts Based on Metagenomic Gene Abundance'

<http://blogs.plos.org/blog/2017/09/21/genetics-and-microbiome-of-cattle-methane-production-2017-plos-genetics-research-prize-winning-research/>



J. Dairy Sci. 93:5902–5912

doi:10.3168/jds.2010-3500

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## Host specificity of the ruminal bacterial community in the dairy cow following near-total exchange of ruminal contents<sup>1</sup>

P. J. Weimer,<sup>\*†2</sup> D. M. Stevenson,<sup>\* H. C. Mantovani,‡</sup> and S. L. C. Mant<sup>†</sup>

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<sup>‡</sup>Departamento de Microbiologia, Universidade Federal de Viçosa, Viçosa-MG, 36571-000, Brazil

## Host Genome Influence on Gut Microbial Composition and Microbial Prediction of Complex Traits in Pigs

Amelia Camarinha-Silva, Maria Maushammer, Robin Wellmann, Marius Vital, Siegfried Preuss and Jörn Bennewitz

GENETICS *Early online May 3, 2017; https://doi.org/10.1534/genetics.117.200782*

### Resource

## Genetic Determinants of the Gut Microbiome in UK Twins

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<http://dx.doi.org/10.1016/j.chom.2016.04.017>



RESEARCH ARTICLE

## Bovine Host Genetic Variation Influences Rumen Microbial Methane Production with Best Selection Criterion for Low Methane Emitting and Efficiently Feed Converting Hosts Based on Metagenomic Gene Abundance

Rainer Roehe<sup>1\*</sup>, Richard J. Dewhurst<sup>1</sup>, Carol-Anne Duthie<sup>1</sup>, John A. Rooke<sup>1</sup>, Nest McKain<sup>2</sup>, Dave W. Ross<sup>1</sup>, Jimmy J. Hyslop<sup>1</sup>, Anthony Waterhouse<sup>1</sup>, Tom C. Freeman<sup>3</sup>, Mick Watson<sup>4\*</sup>, R. John Wallace<sup>5\*</sup>

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J. Dairy Sci. TBC:1–8

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JDS13179

## Short communication: Signs of host genetic regulation in the microbiome composition in 2 dairy breeds: Holstein and Brown Swiss

O. Gonzalez-Reco,<sup>\*†1</sup> I. Zubiria,<sup>‡</sup> A. García-Rodríguez,<sup>‡</sup> A. Hurtado,<sup>§</sup> and R. Atxaerandio<sup>‡</sup>

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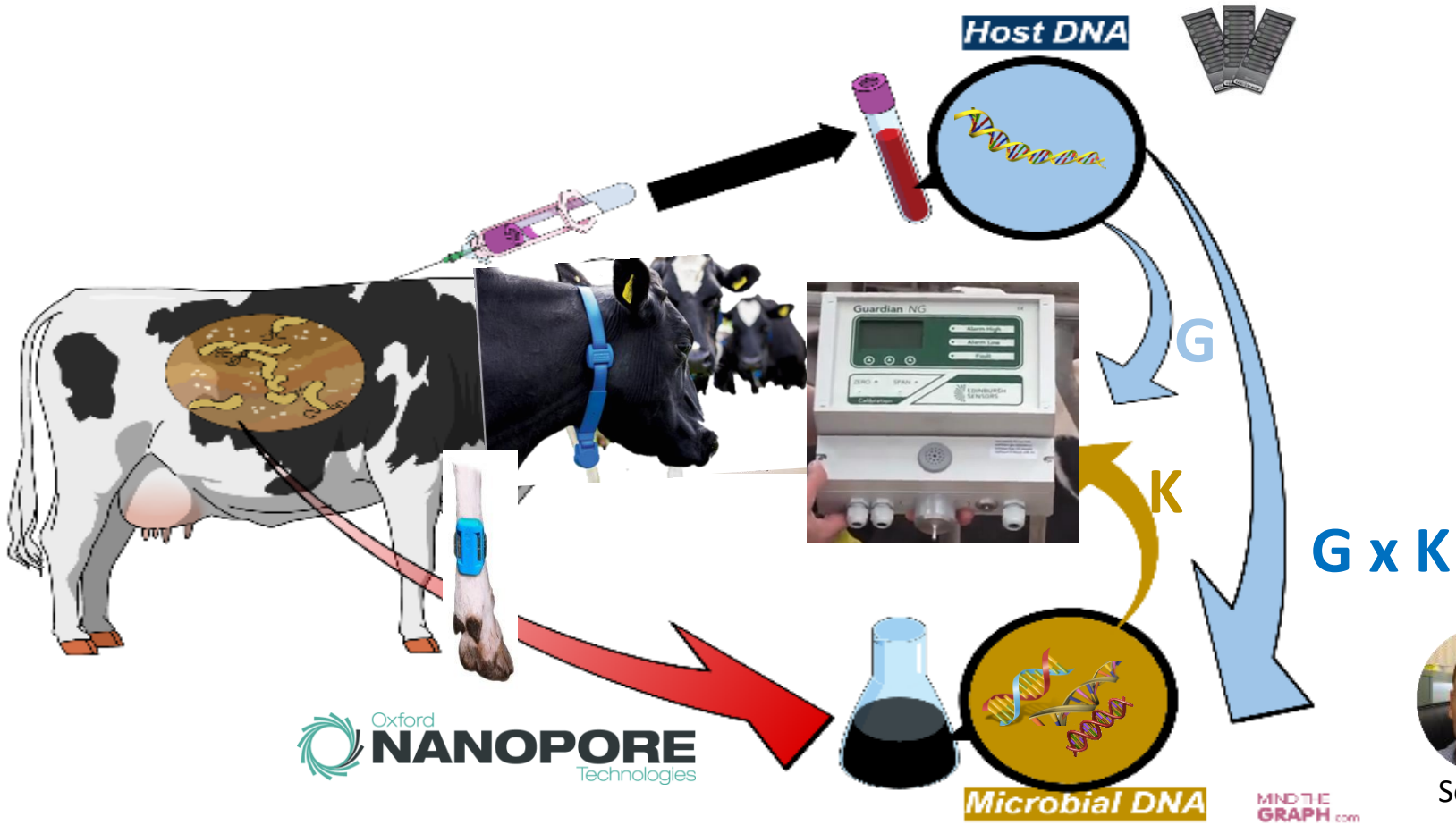
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- 1) Study and compare most favourable non-invasive techniques for measuring methane gas production in cattle, to apply them in a large number of animals
- 2) Determine the relationship between the microbiome and the host genotype
- 3) Estimate the genetic correlations between the microbiome, feed efficiency and methane emissions
- 4) Propose strategies to incorporate these traits in the Spanish breeding program

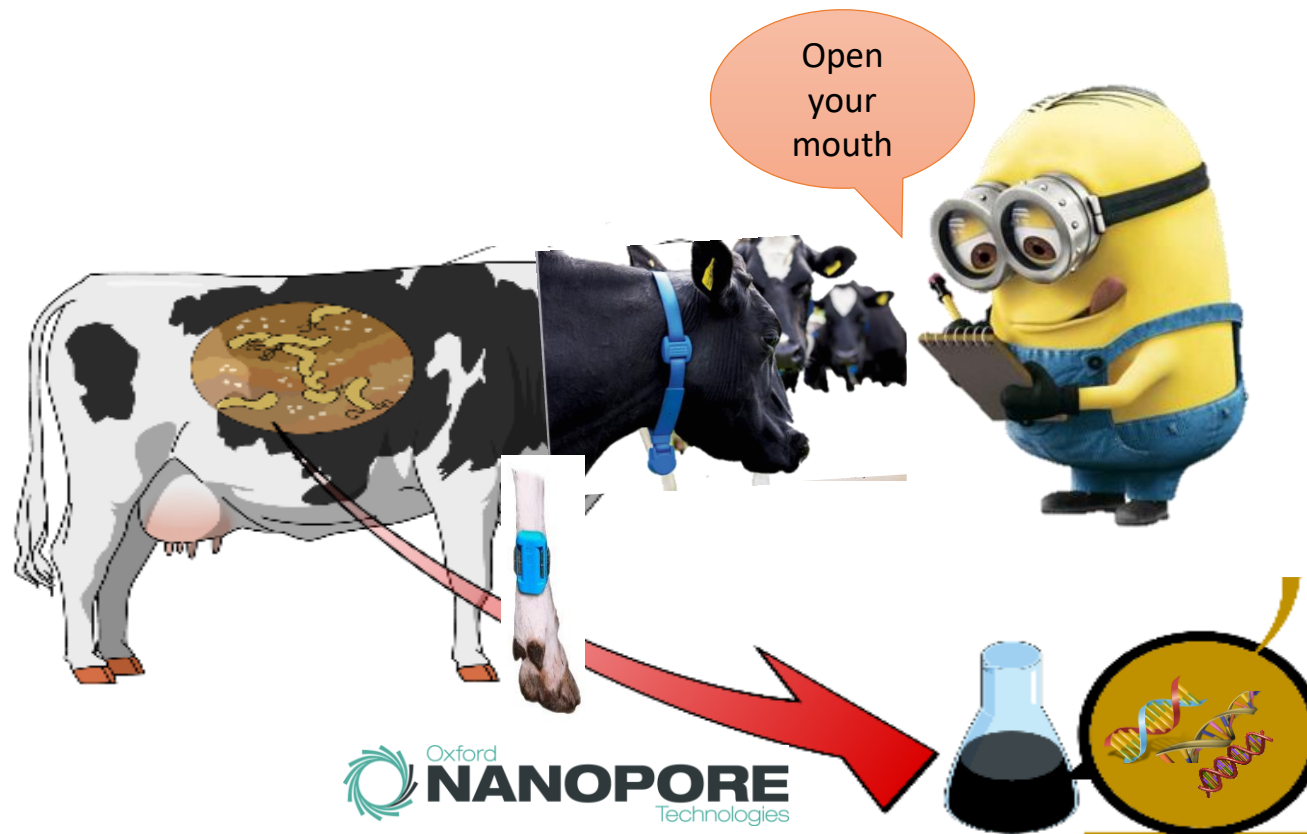






Session 42





MINDTE  
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## 14 Herds



AMS  
2-3 weeks



## >4000 cows



>30.000.000 CH<sub>4</sub> records  
Genotypes - Imputed to WG (1000 bulls)  
500 Metagenomes

# Preliminary Analyses

## 439 COWS

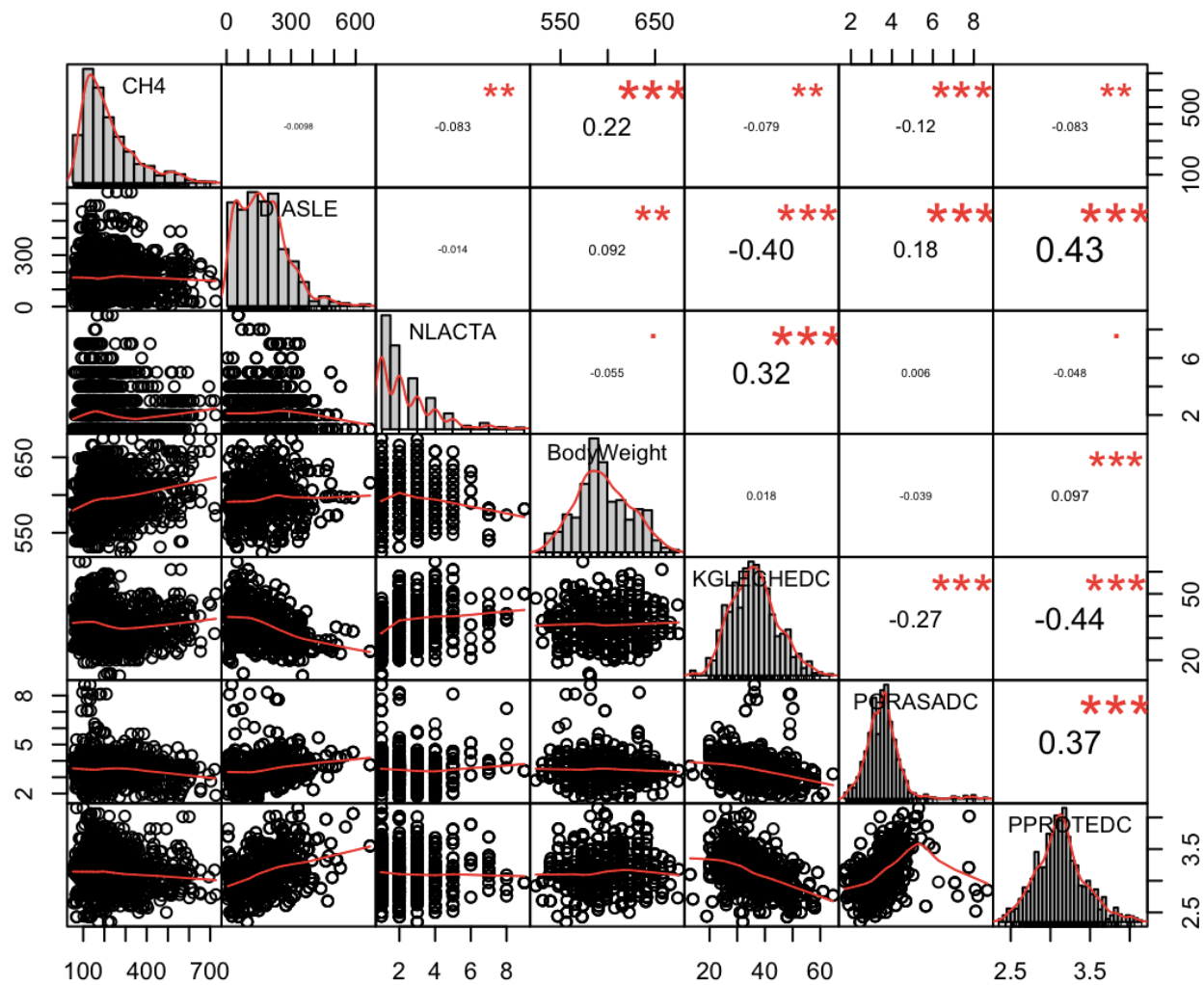
After QC:

1386 weekly averages for CH<sub>4</sub>

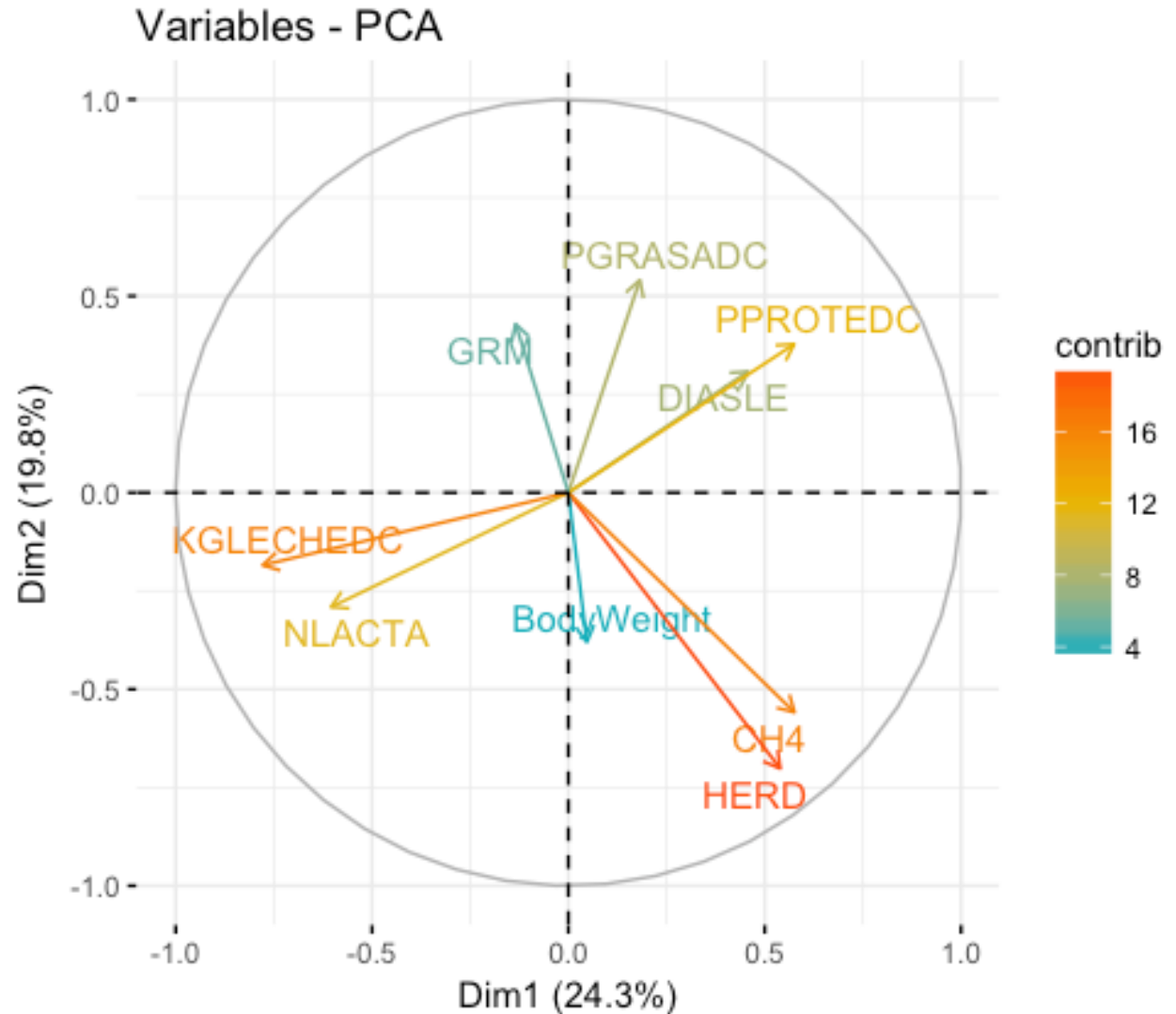
13 records/cow/week

Production traits from test-days

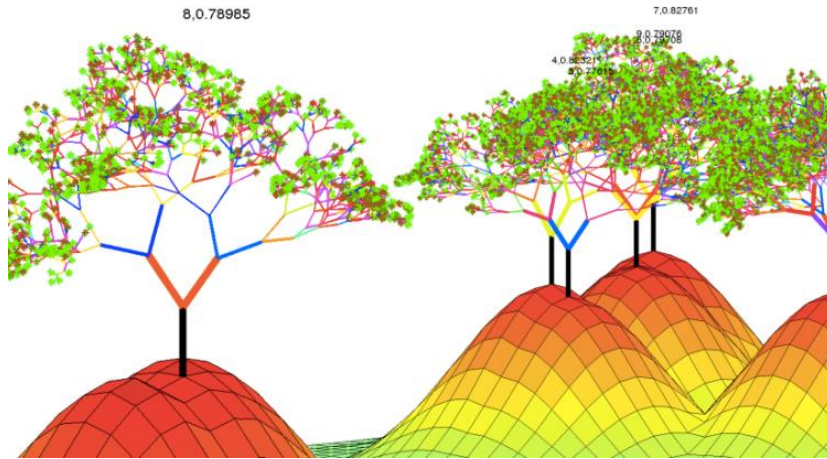
Body Weight from type traits



# Preliminary Analyses: Principal Components



# Random Forest: Variable Importance



HERD

PROT %

FAT %

GRM

Kg Milk

DIM

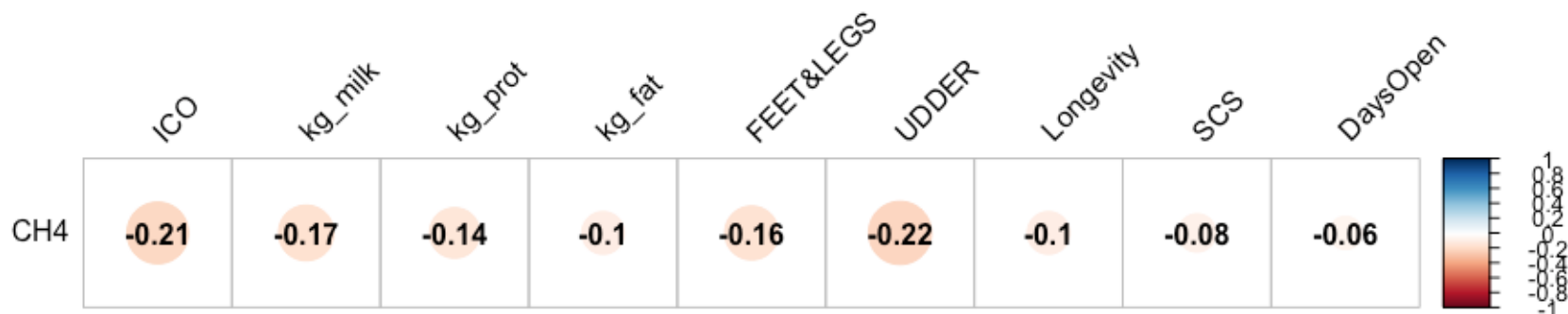
BodyWeight

NLACTA



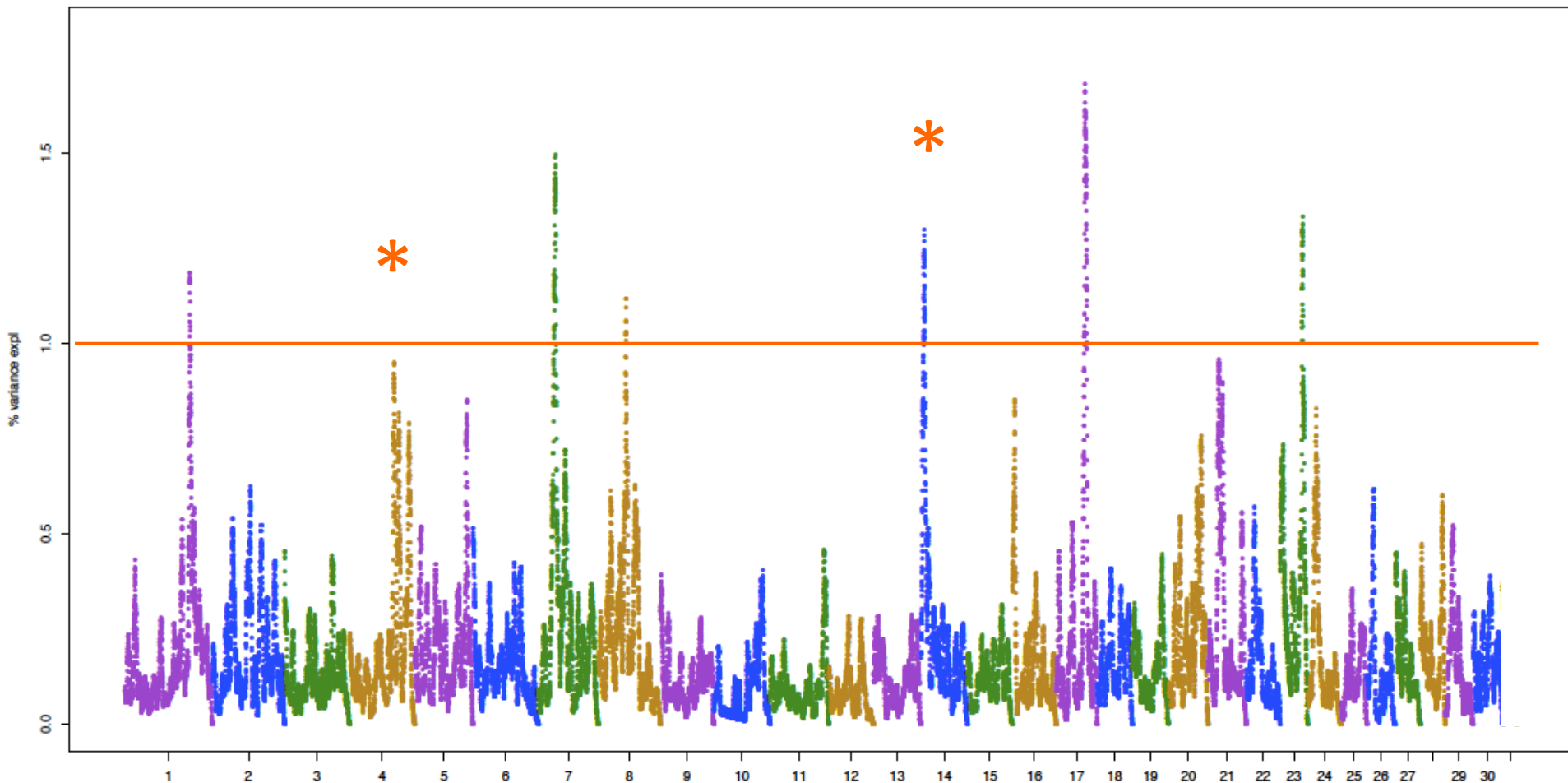
## • Genetic correlations from EBVs

- 15,379 animals in pedigree (Bayesian analysis, TM)
- Herd\*Robot, Parity, Lactation stage, Permanent, Genetic, Residual
- $h^2=0.37$  (0.16)



# Single-Step. Variance explained (100 adjacent SNPs)

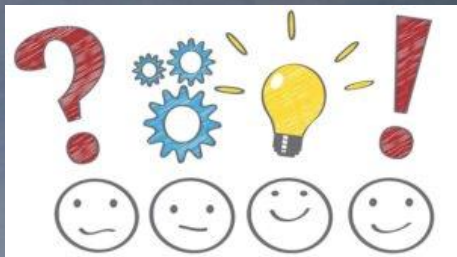
Manhattan Plot SNP Variance explained by 100adjacents SNP window – Trait: 1 Effect: 4





- There is little linkage disequilibrium between genomic regions for milk yield and methane production
- ...or if it exists, favourable variants for milk yield are linked with positive and negative variants for methane production





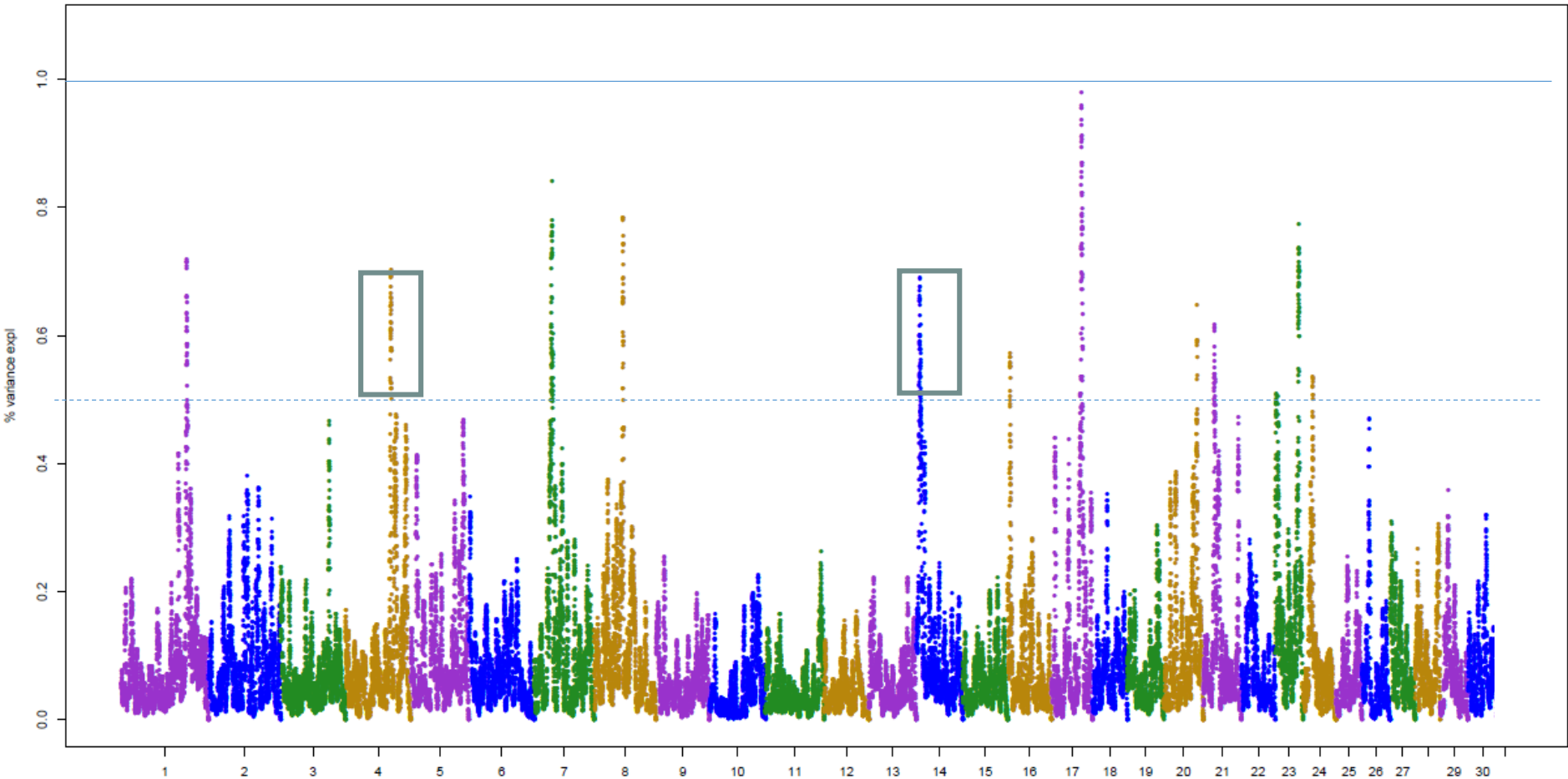


# Take home message

- Important herd effect (feeding, management, device)
- Genetic component for methane production ( $h^2=0.36$ )
- High emitter cows are less efficient, lower milk, less profit
- Some genomic regions explained more than 1% of genetic variance of methane production

# Single-Step- Variance explained

Manhattan Plot SNP Variance explained by 50adjacents SNP window – Trait: 1 Effect: 4



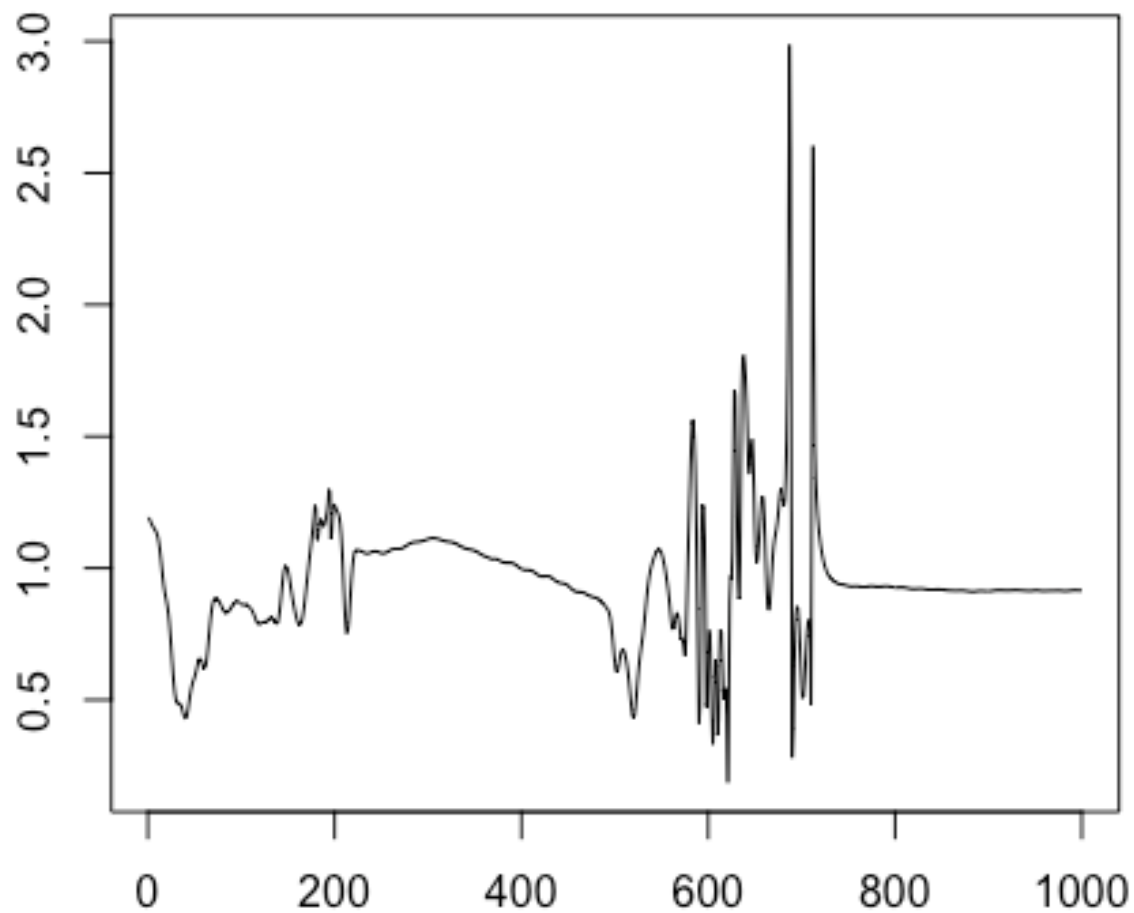
# Single-Step. Variance explained (100 adjacent SNPs)

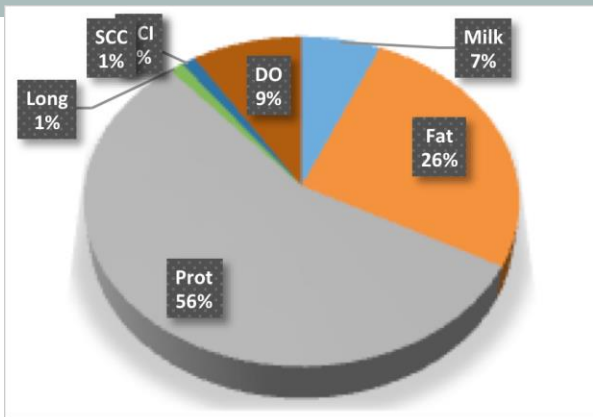
$$\begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{X} & \mathbf{X}'\mathbf{R}^{-1}\mathbf{Z} \\ \mathbf{Z}'\mathbf{R}^{-1}\mathbf{X} & \mathbf{Z}'\mathbf{R}^{-1}\mathbf{Z} + \mathbf{H}^{-1} \otimes \boldsymbol{\Sigma}_g^{-1} \end{bmatrix} \begin{bmatrix} \hat{\mathbf{b}} \\ \hat{\mathbf{u}} \end{bmatrix} = \begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{y} \\ \mathbf{Z}'\mathbf{R}^{-1}\mathbf{y} \end{bmatrix}$$

$$\mathbf{H}^{-1} = \mathbf{A}^{-1} + \begin{bmatrix} 0 & 0 \\ 0 & \mathbf{G}^{-1} - \omega \mathbf{A}_{22}^{-1} \end{bmatrix} \quad \text{Aguilar et al. (2010)}$$

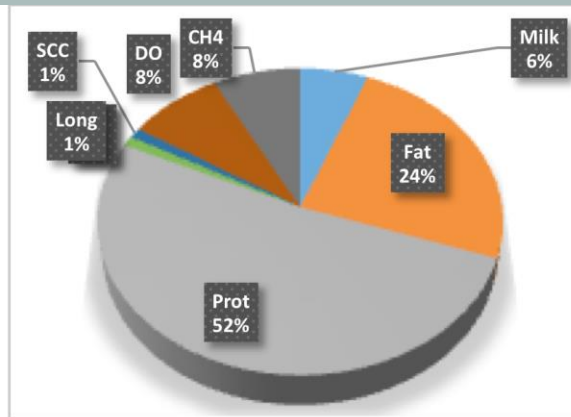
Herd\*Robot, Parity, Lactation stage, Permanent, Genetic, Residual

$h^2=0.19$  (0.11)

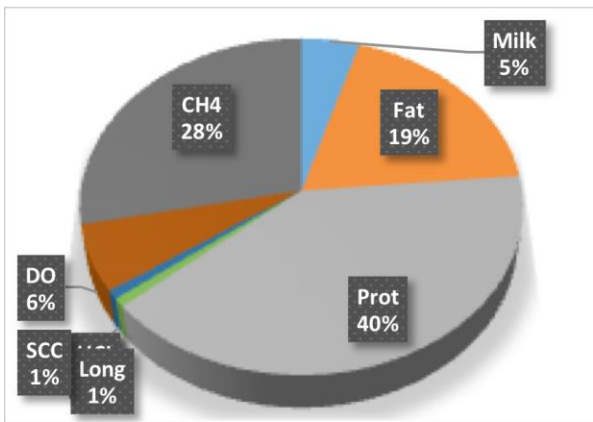




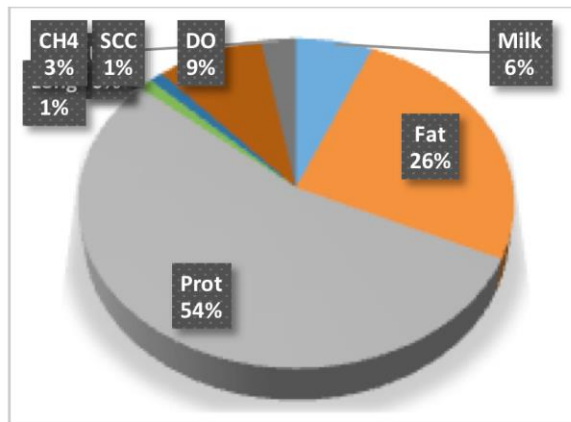
Scenario 1



Scenario 2

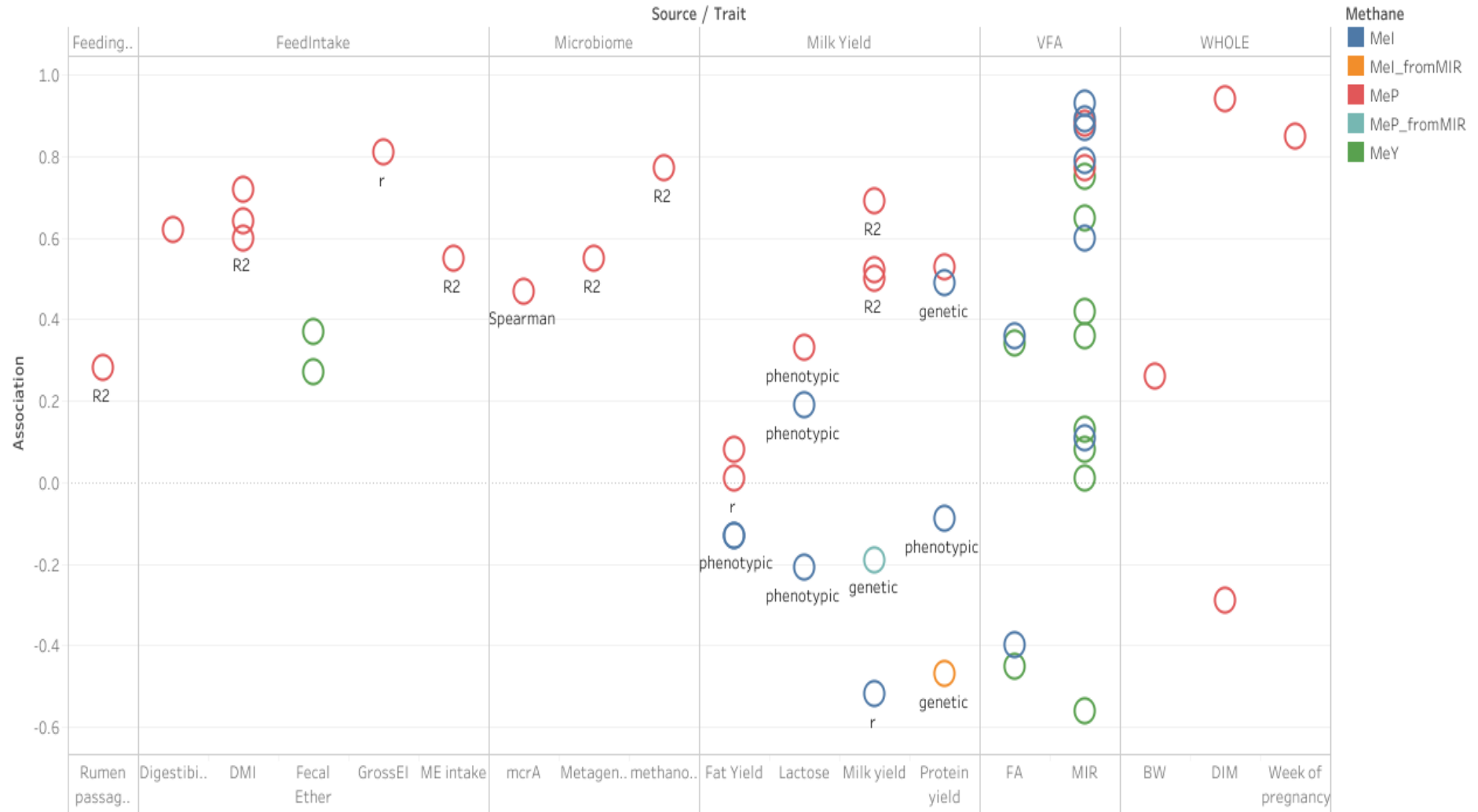


Scenario 3



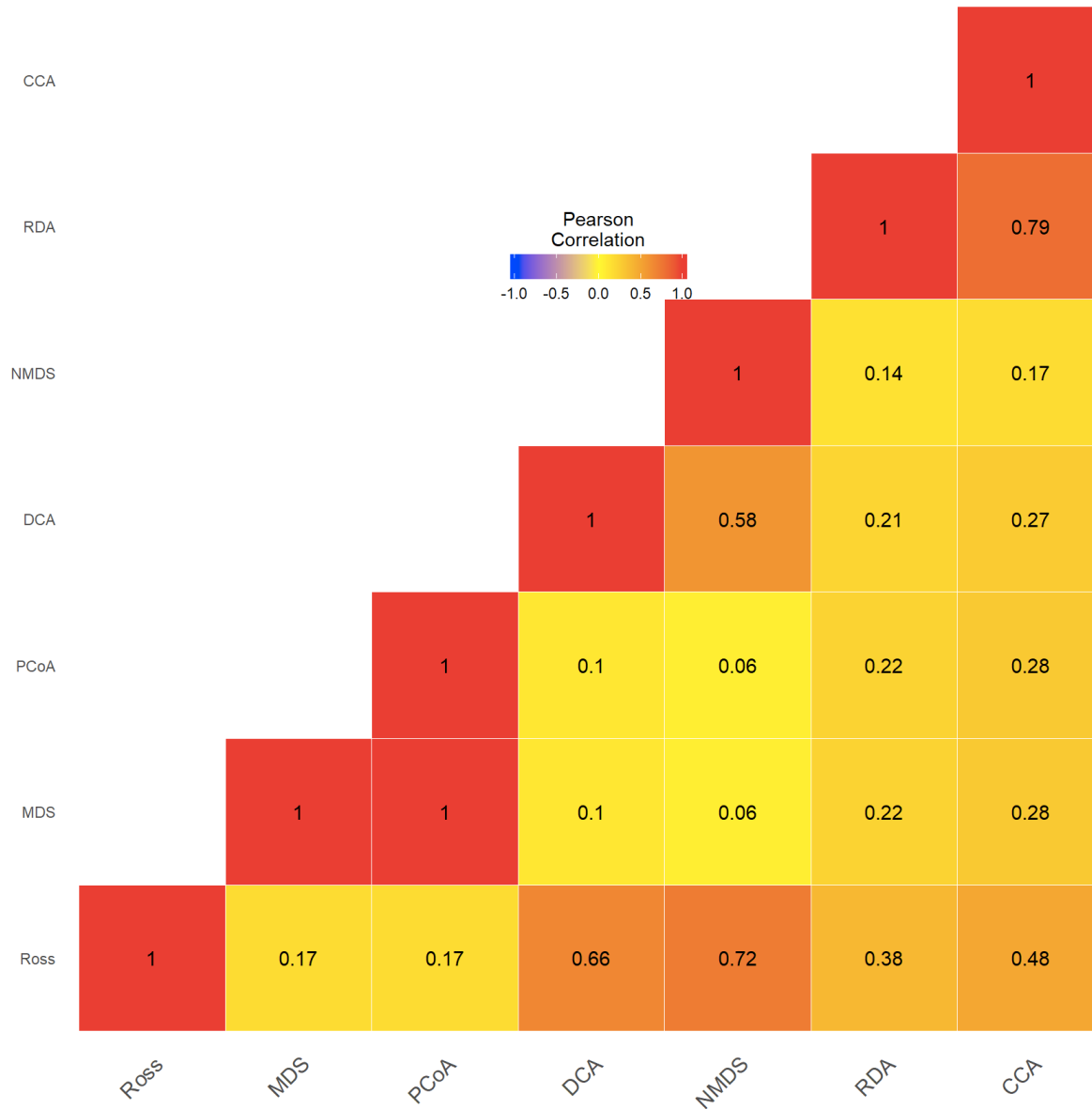
Scenario 4

Sheet 1

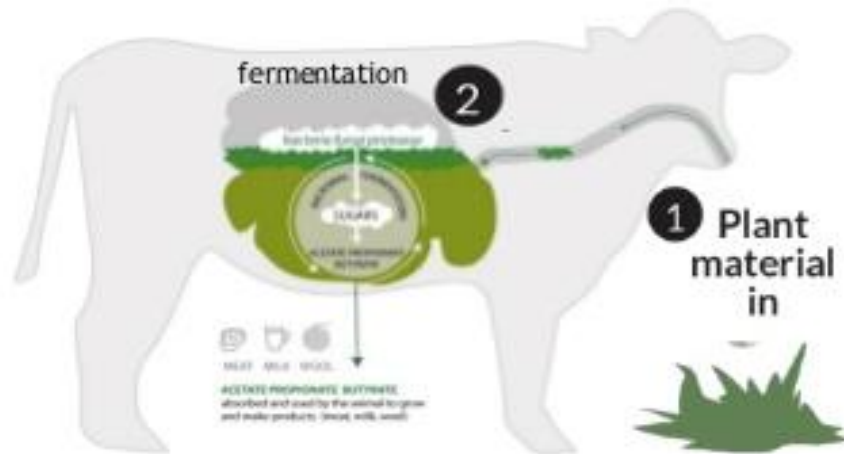




# Metrics for metagenome matrices

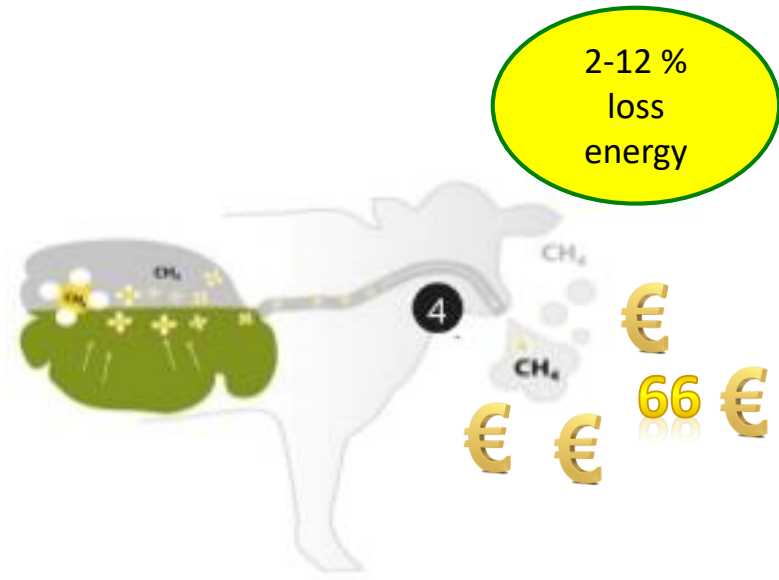


## THE RUMEN: MICROBIAL FERMENTATION



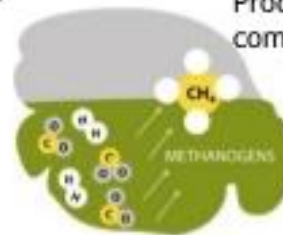
### Rumen microorganisms and their roles

- **Bacteria:** ferment fiber, starch, sugar in feed to VFA, H<sub>2</sub>, CO<sub>2</sub>
- **Protozoa:** consume and ferment bacteria to VFA and NH<sub>3</sub>, ferment starch, recycle N
- **Funghi:** assist in fibre digestion



### 3 Methanogens

Produce CH<sub>4</sub>, but allows for more complete feed utilization



- Descriptive statistics
  - Media ppm, picos/min, etc
  - Graficos picos
  - Correlaciones
- Previous results
  - Feed efficiency and microbiome
  - Genetic background (itziar, oscar)
- Multiomics approach

- Tabla h2 y correlaciones

- GBLUP
- SStep

- Big data approach

CH4 ppm por vaca

500

400

300

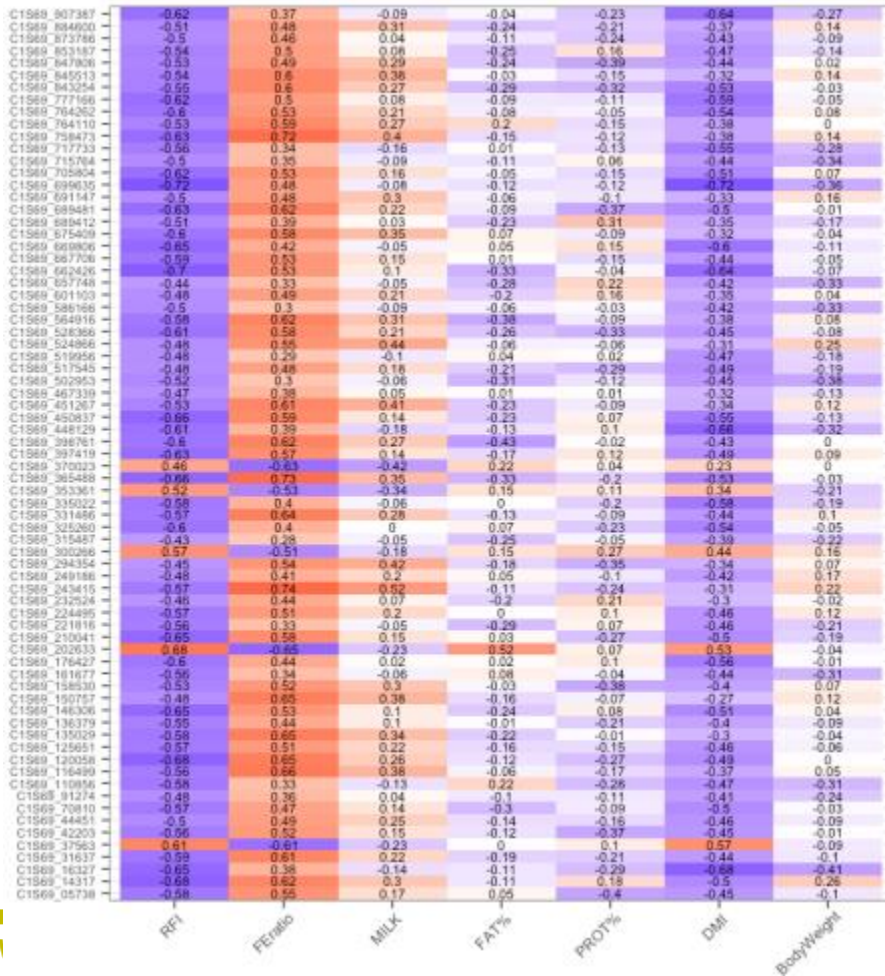
200

100

570 591 621 633 636 657 6843 6911 6928 6932 701 720 723 738 739 741 751 755 758 760 768 771 777 778 781 784 786 792 794 799 800 801 810 812 813 815 817 818 822 833 835 838 840 841 843 846 848 849 851 852 853 856 858 860 861 865 867 871 873 878 879 881 882 883 885 888 889 890 891 892 893 894 895 896 901 903 904 905 907 909 910 917 919



## Correlation analyses



## Cluster Analysis

