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# **Multivariate and network analysis identified microbial biomarkers linked to methane emission**

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## I. Motivation

- The ruminant holobiont

## II. Description of $\mu$ Ficient project

- Phenotyping and sampling
- Initial results:
  - Structural and functional analysis
  - Microbial biomarkers linked to  $\text{CH}_4$  (CH<sub>4</sub>/DMI)
  - Microbial network analysis

## III. Future directions



# Rumen symbionts

## PROVIDE

- **Energy**  
VFA can provide up to 80% of the energy needs
- **Protein**  
microbes convert NPN into high quality protein
- **Vitamins**  
synthesis of B-complex and K vitamins
- ....

## PRODUCE

- Toxic products
- **Methane**  
~14.5% of total global GHG emissions



# Phenotyping and sampling

2016



n=65



Sep

Nov



n=68



Jan

Mar

2017



GreenFeed



Calan gate syst



Methane emission

Digestibility

Body weight

Residual feed intake

Milk production

Average daily gain



## From raw sequencing to OTU

- OTU picking
- Taxonomic assignment
- Phylogenetic tree

## Ruminal ecosystem

- Diversity index (alpha, beta, richness)
- Ruminotype like-cluster
- Functional analysis (**whole-metagenome**)
- Microbial network inference

## Multivariate Analysis

- sPLS-DA ( X=OTU, Y= CH<sub>4</sub>y classification)
- sPLS-DA ( X=OTU, Y= Ruminotype cluster)
- sPLS (regression mode: X=OTU, Y= CH<sub>4</sub>y)

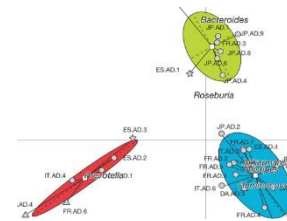
# Analytic workflow



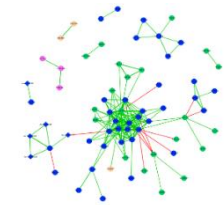
Schloss et al., 2009



Quast et al., 2013



Arumugam et al., 2011



Ramayo-Caldas et al., 2016



Rohart et al., 2017

# ade4

Dray et al., 2007



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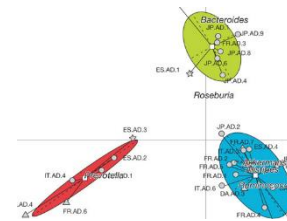
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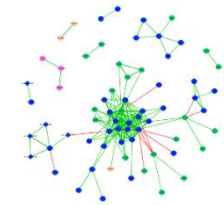
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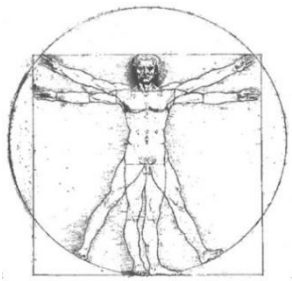
Ramayo-Caldas et al., 2016



Rohart et al., 2017

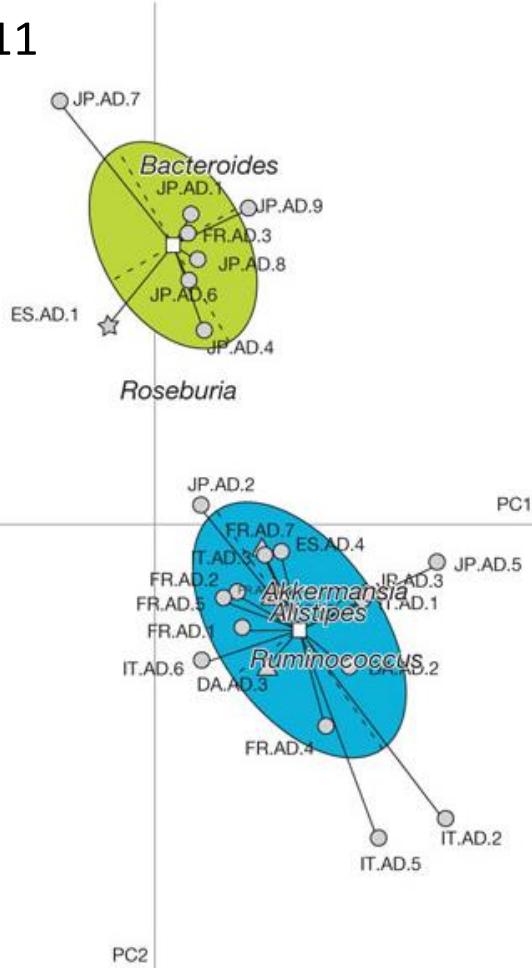
ade4

Dray et al., 2007



# Structure of bacterial gut ecosystem

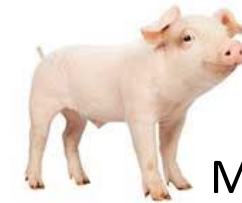
Arumugam et al, 2011



Wang et al. 2015



Moeller et al. 2012



Mach et al. 2014



Ramayo-Caldas et al. 2018

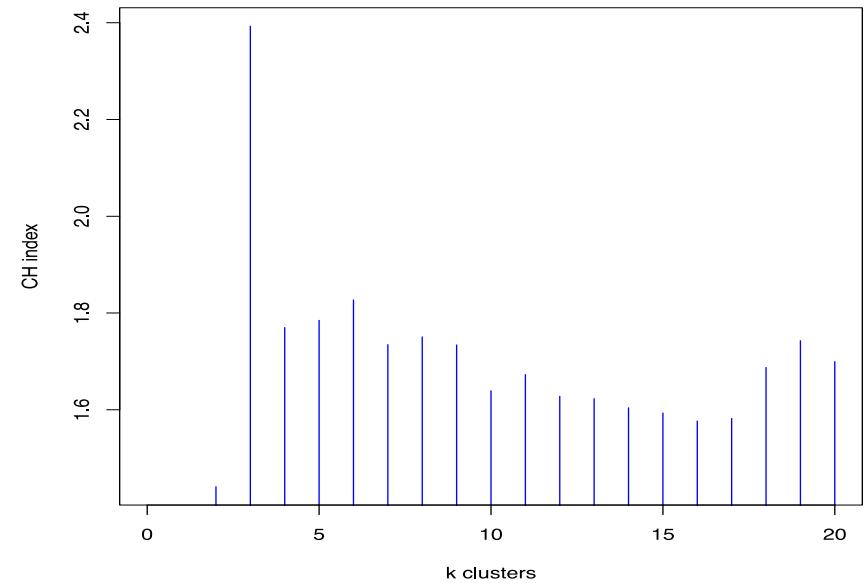
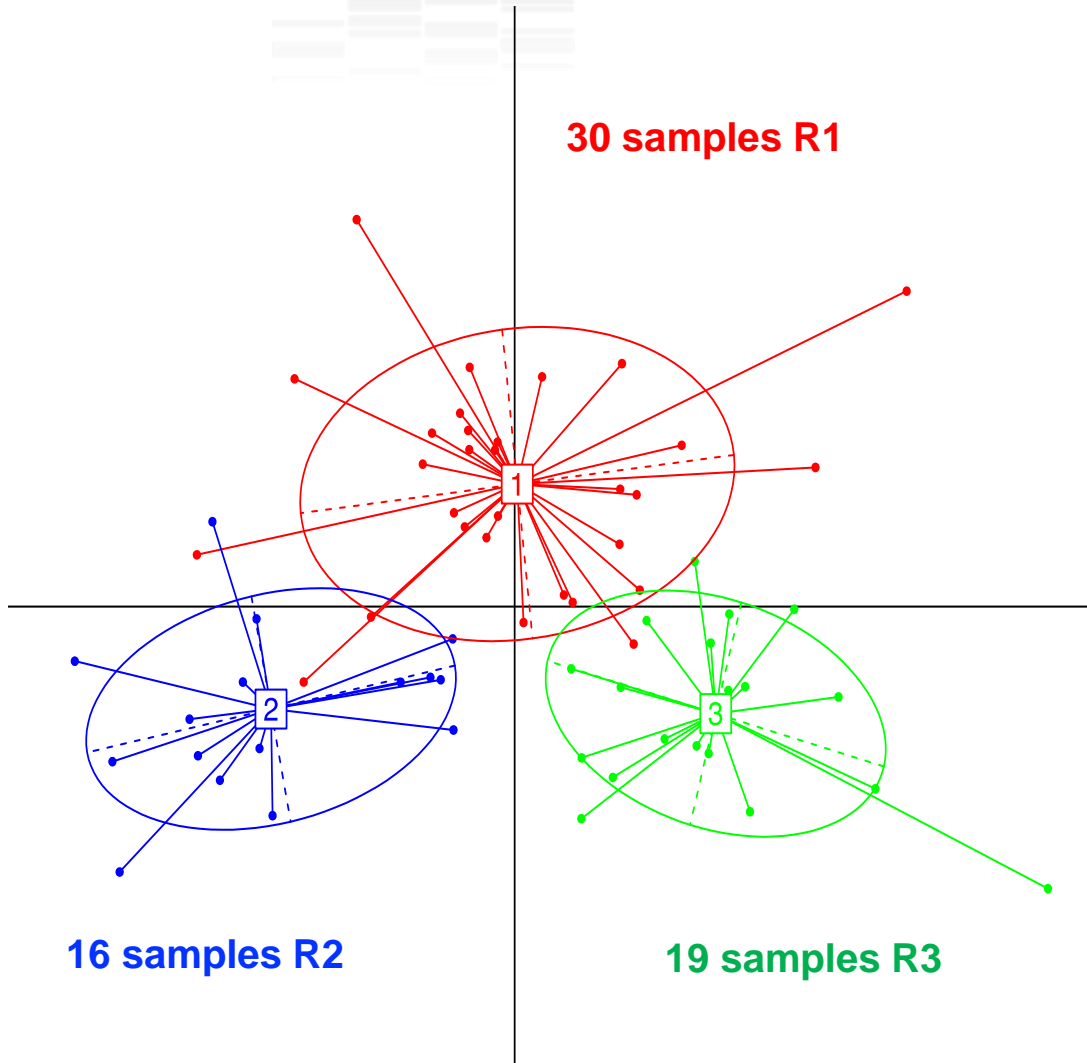


Kittelman et al. 2014

Danielsson et al. 2017



# Structure of ruminal ecosystem



## Cluster stability

Clusterwise Jaccard 100 bootstrap

$K2 = (0.61, 0.44)$

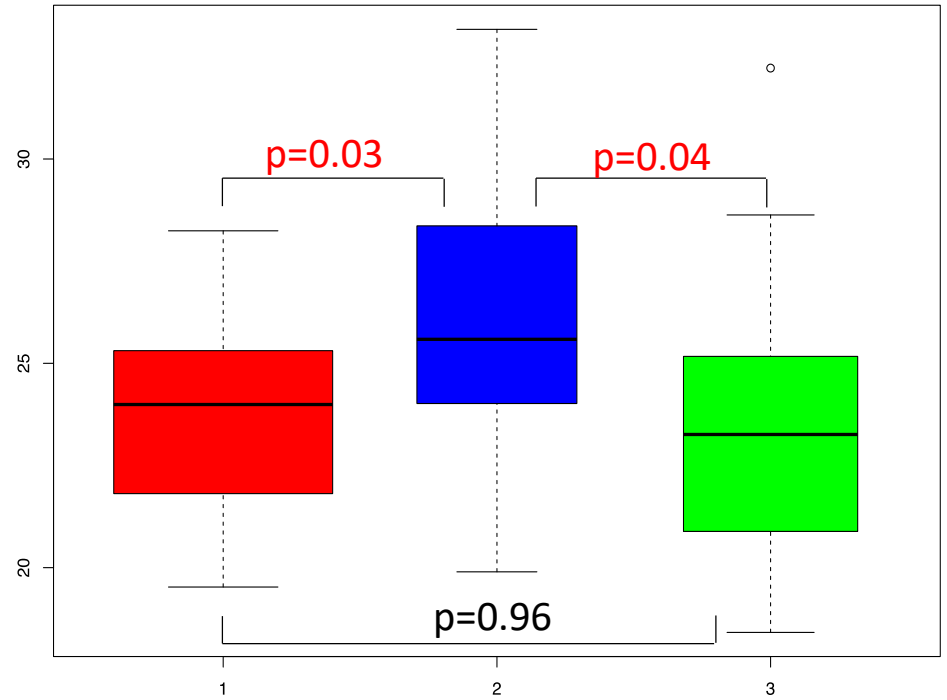
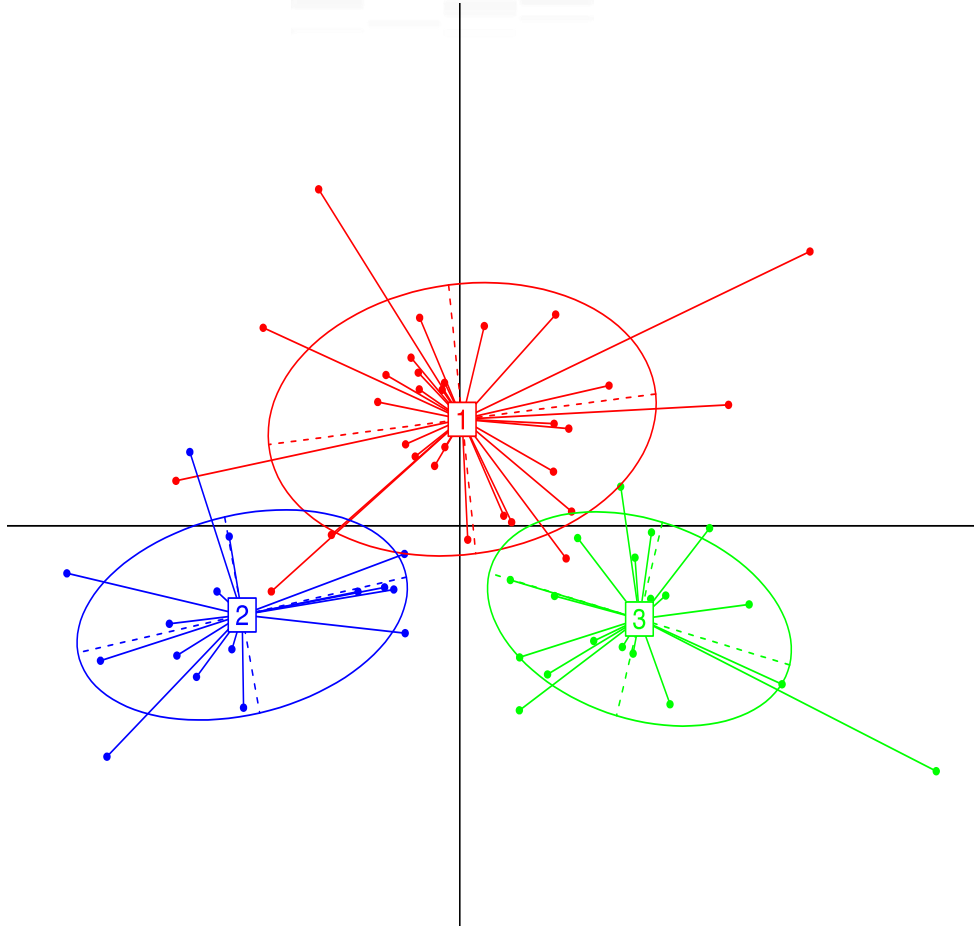
$K3 = (0.63, 0.64, 0.63)$

**most stable solution at K=3**



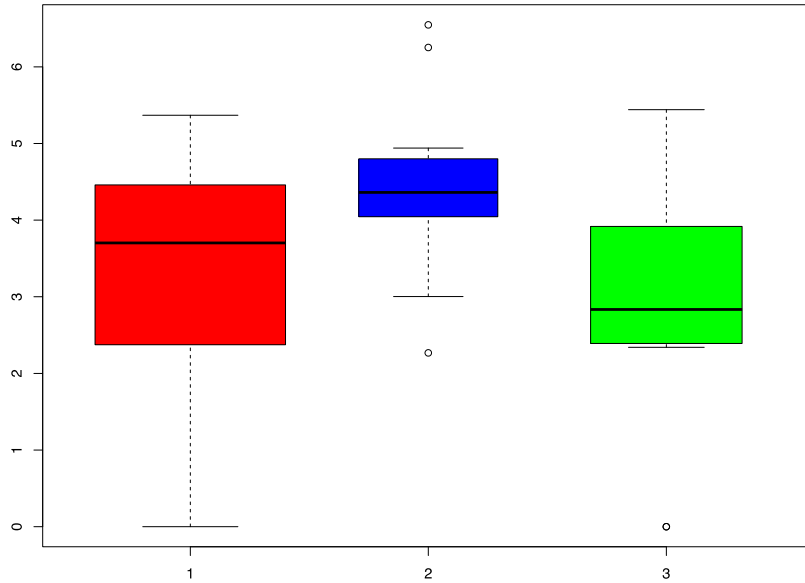


# Ruminotype-like cluster is linked to CH<sub>4</sub>y





## Ruminococcaceae



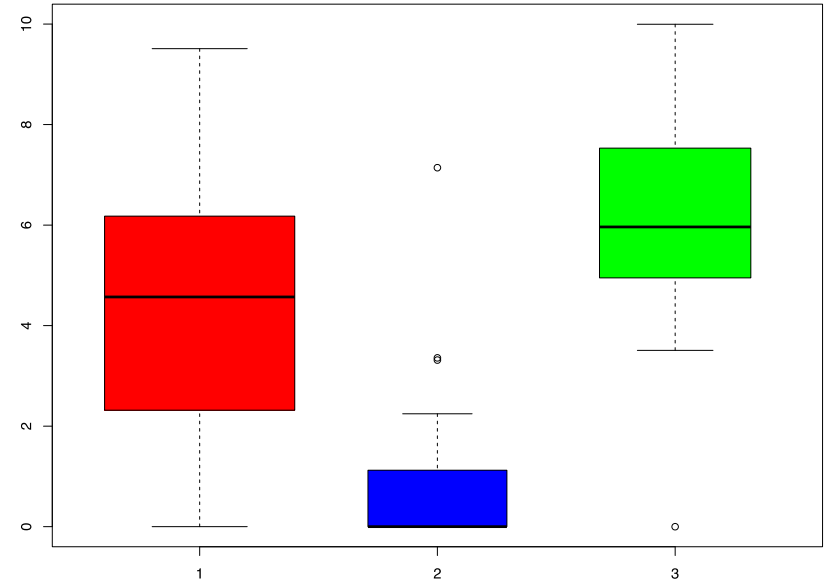
### Linked to High CH<sub>4</sub>y

Kittelmann et al. (2014)

Danielsson et al. (2017)

# Taxonomic composition

## Succinivibrionaceae

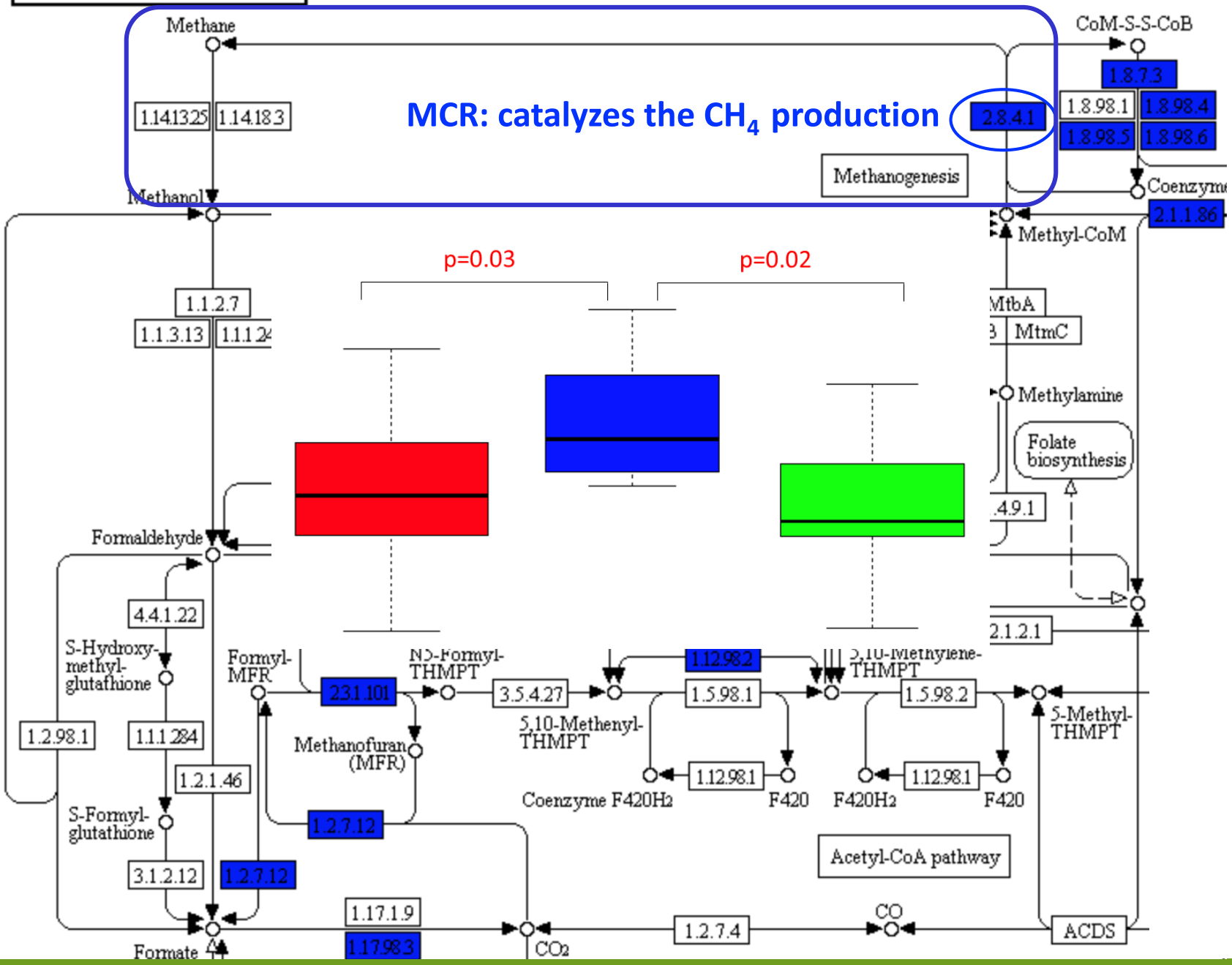


### Linked to Low CH<sub>4</sub>y

Wallace et al. (2015)

Danielsson et al. (2017)

## METHANE METABOLISM





# Multivariate analysis

## Ch<sub>4</sub><sub>y</sub> classification

(X=OTU, Y= H<sub>Ch4y</sub>, L<sub>Ch4y</sub>, Int<sub>Ch4y</sub>)

## ruminotypes assignation

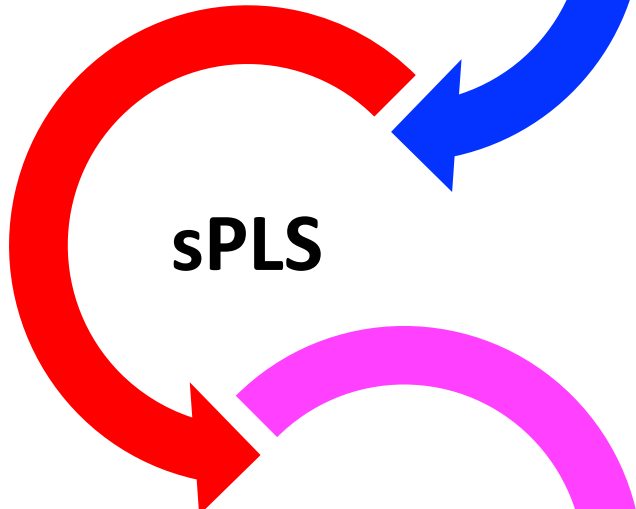
(X=OTU, Y= R1, R2, R3)



sPLS-DA

## regression model

(X=OTU, Y=CH<sub>4</sub>y)



sPLS

Common  
OTUs?

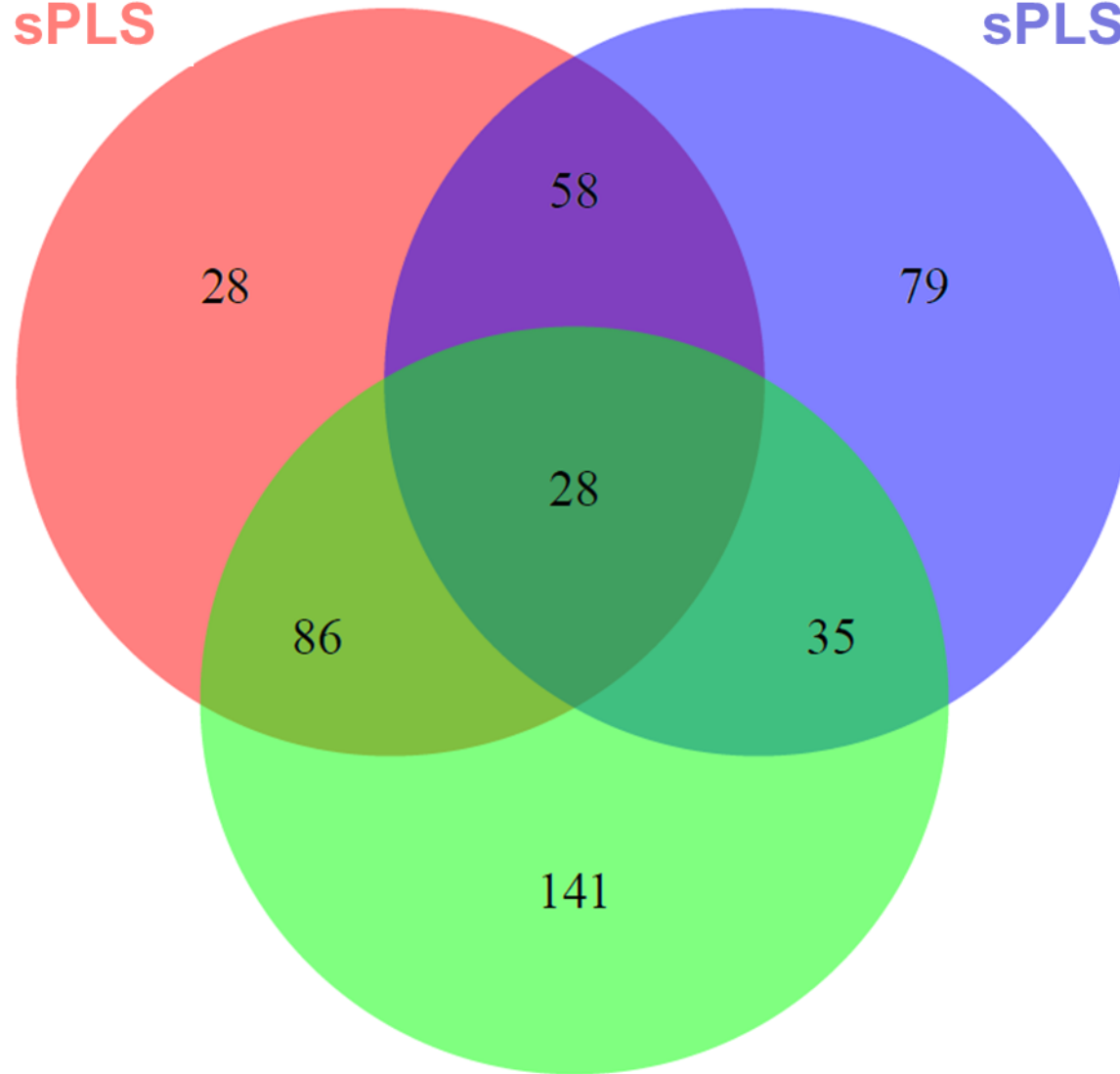
OTU jointly associated  
with CH<sub>4</sub>y and sample  
classification



sPLS

# Common OTUs

sPLS-DA (R)



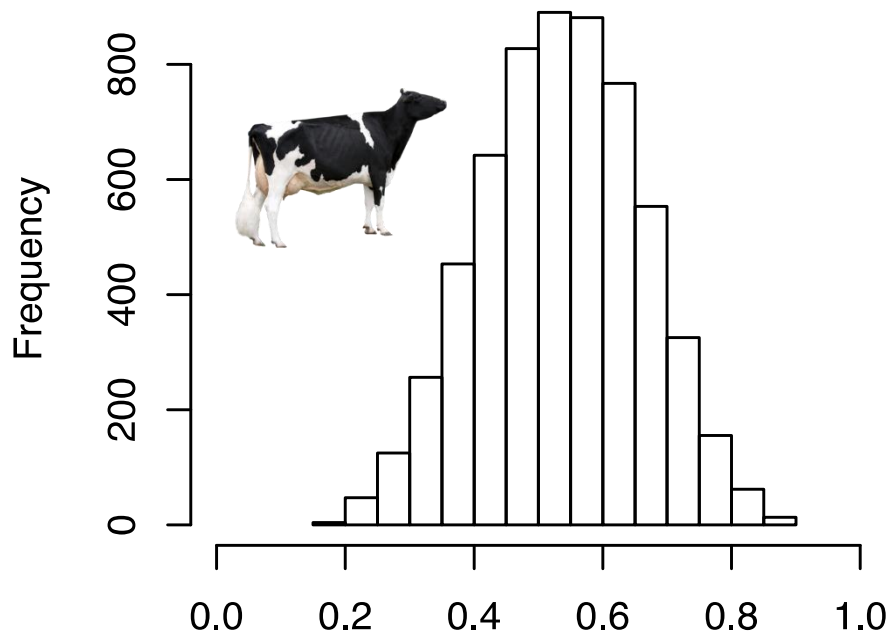
sPLS-DA (CH<sub>4</sub>)



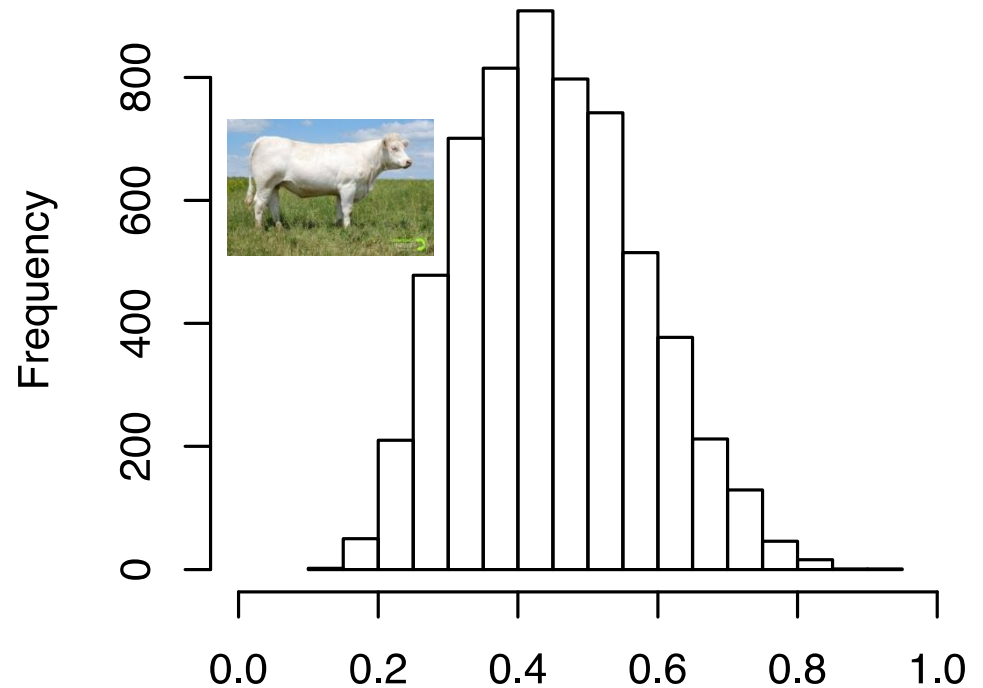
# Microbial mixed model

BGLR (de los Campos and Perez, 2013)

( $0.52 \pm 0.15$ )



( $0.45 \pm 0.19$ )



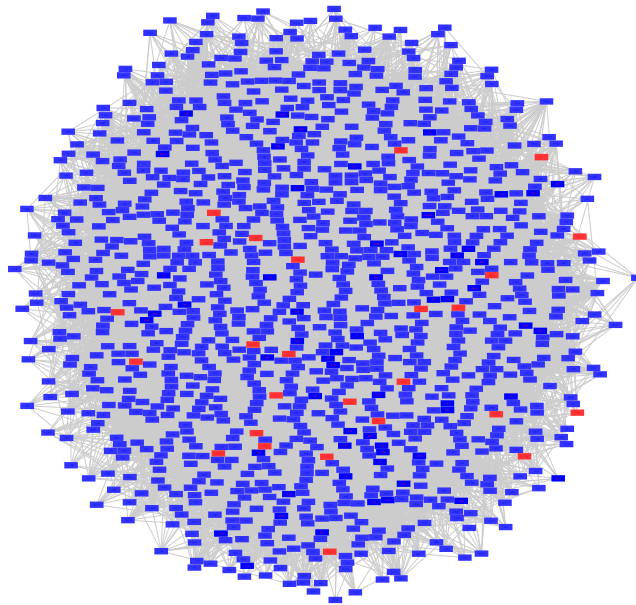
Marginal posterior distribution of CH<sub>4</sub>y microbiability



# Microbial Network

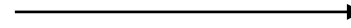
SPCIT (Ramayo-Caldas et al. 2016)

Whole network

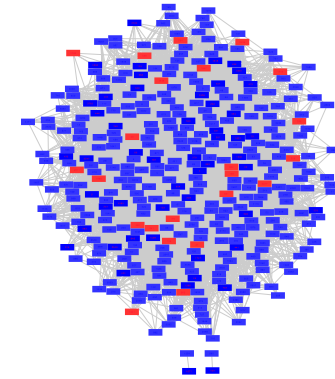


1,198 nodes (OTUs)  
&  
19,072 edges (interactions)

Cluster analyses



five modules



30% (384 OTUs)

89% (25/28)



# Conclusions

- The structure of the ruminal bacterial community is linked to CH<sub>4</sub>y emission.
- OTUs associated with CH<sub>4</sub>y emission predominantly belong to hydrogen-producing genera.
- These OTUs explained an important proportion of the CH<sub>4</sub>y phenotypic variance in Holstein and Charolaise breeds.



# Future directions



**Host genomics**  
**50K Illumina Chip**

*mQTLs and candidate genes*  
*Microbial mixed models*

*Metagenome-wide association analysis*  
*Microbial biomarkers*



**Feed efficiency**  
**Methane emission**

**Microbiota**

**16S and 18S rRNA**  
**(buccal, rumen, gut)**

Deeper analysis of rumen microbial community  
MGS and functional analysis

**Microbiome**

**Whole-metagenome**



Nature special: Interdisciplinarity 16 Sept 2015



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# Thank you for your attention



## Your



## Matters