

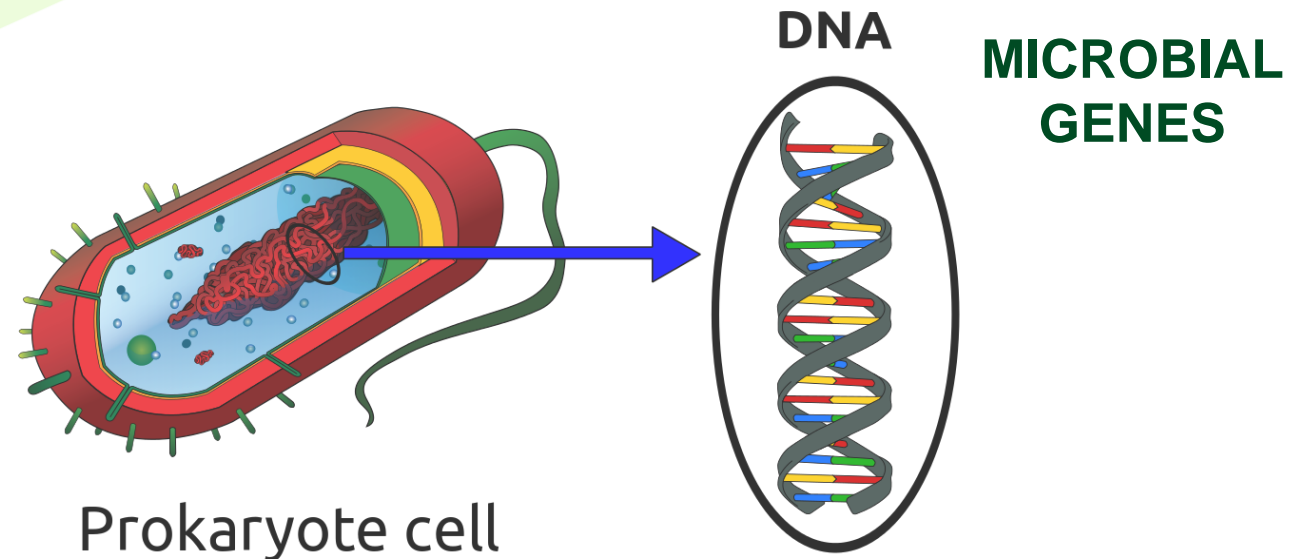
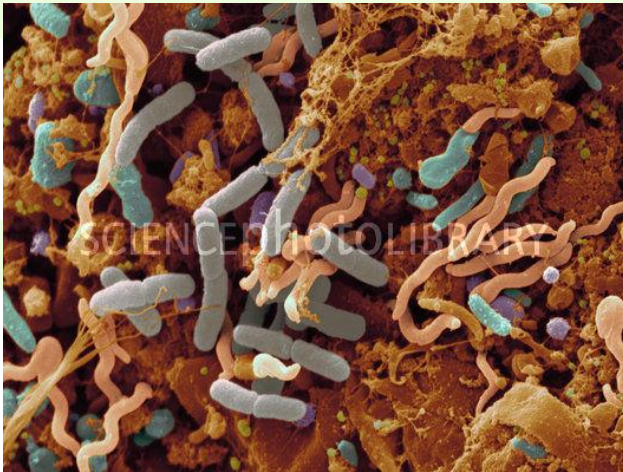
# METHANE EMISSIONS EXPLAINED BY INTERACTIONS IN RUMEN MICROBIOME

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Freeman TC, Blasco A, Watson M, Roehe R

Overall aim:

Interactions between rumen **microbial community** and **microbial genes** to explain methane emissions

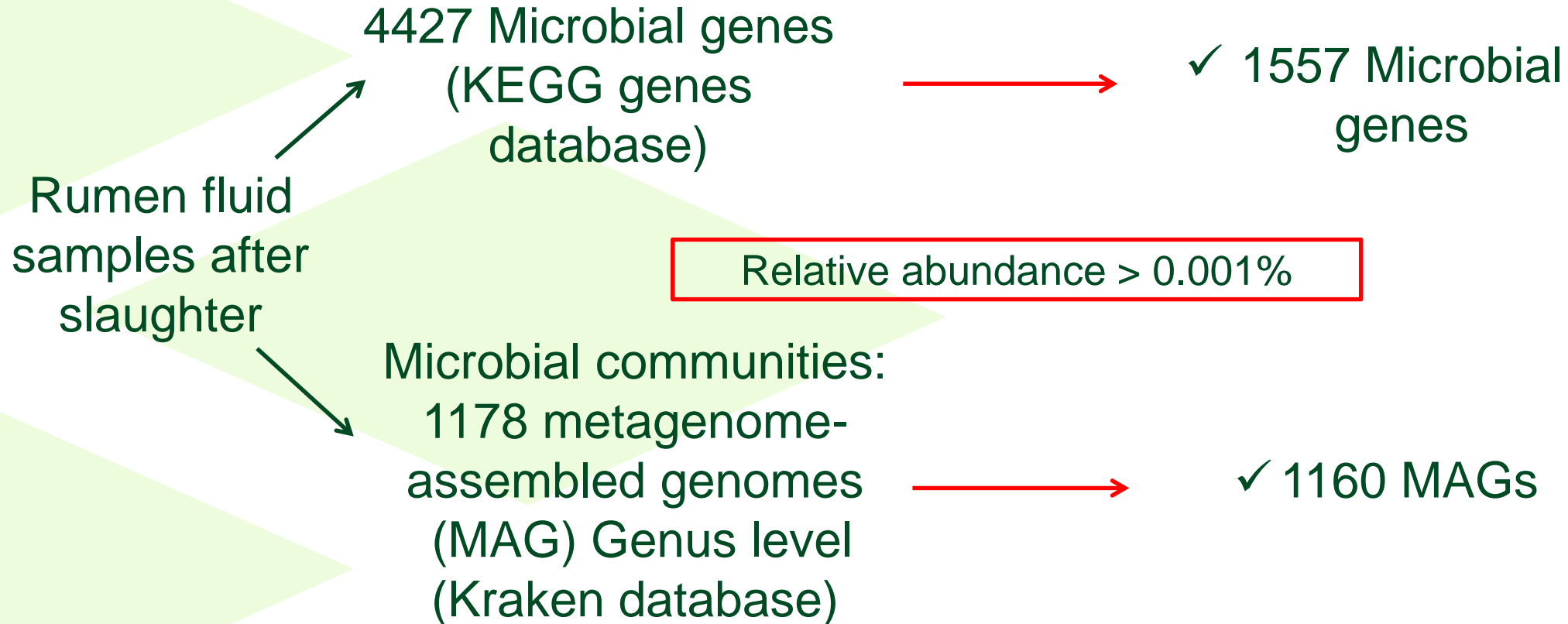
MICROBIAL  
COMMUNITIES



# Data from 63 animals with different breeds and diets

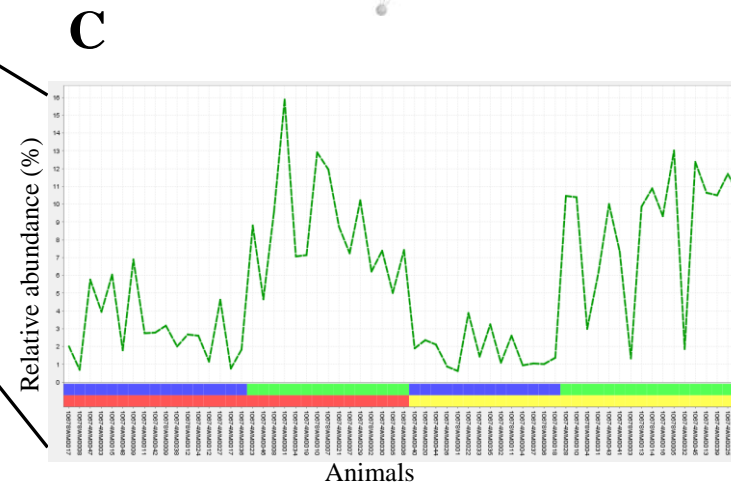
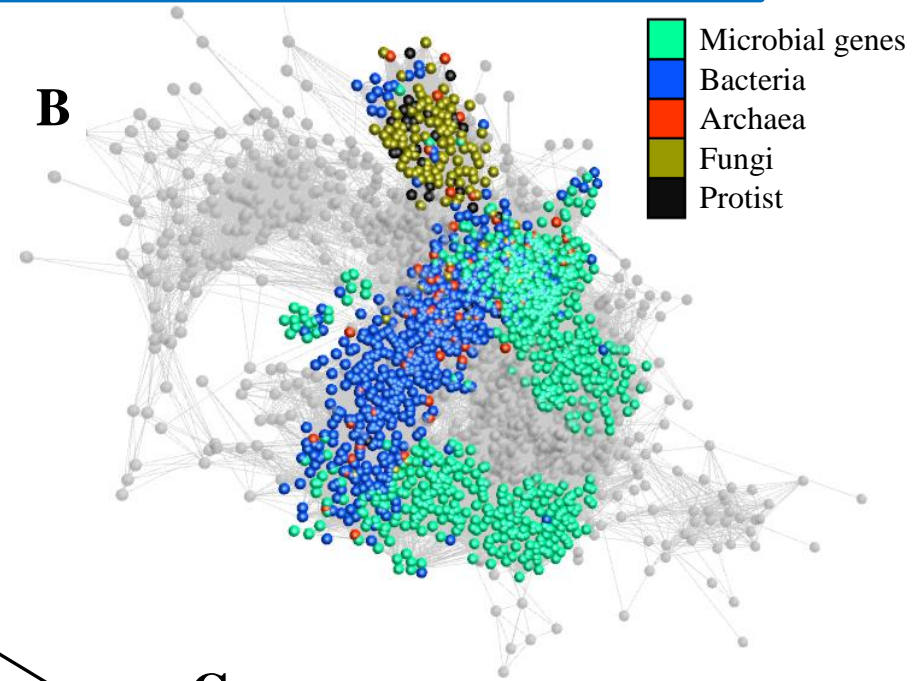
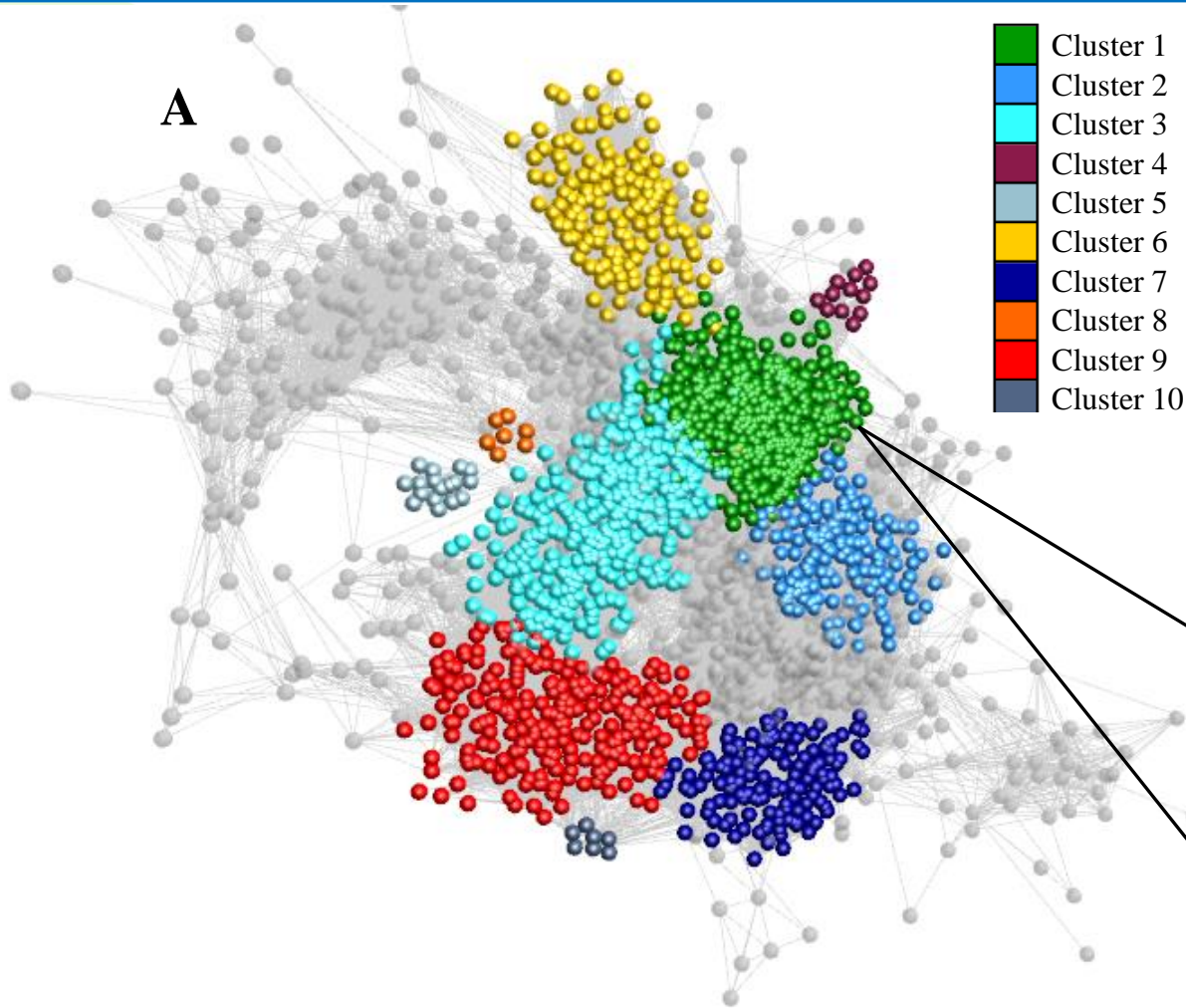


✓ Methane emissions (g CH<sub>4</sub>/kg DMI)



# Network analysis with functional genes and microbiota

Statistics: Network analysis using MCL algorithm in Miru software (Corr =0.70)



# Division of animals in high (HME) & low (LME) methane emitters

## HIGH METHANE EMITTERS (HME)

	LIM	Aax
FOR	7	9
CONC	7	8

	LIM	Aax
FOR	15	17
CONC	14	17

## LOW METHANE EMITTERS (LME)

	LIM	Aax
FOR	8	8
CONC	7	9

Grouping within

- ✓ Breed (Limousin / Aberdeen Angus)
- ✓ Diet (Forage: 500 forage to 500 concentrate)
- ✓ or Concentrate: 80 forage to 920 g/kg DM concentrate)

# HME - LME

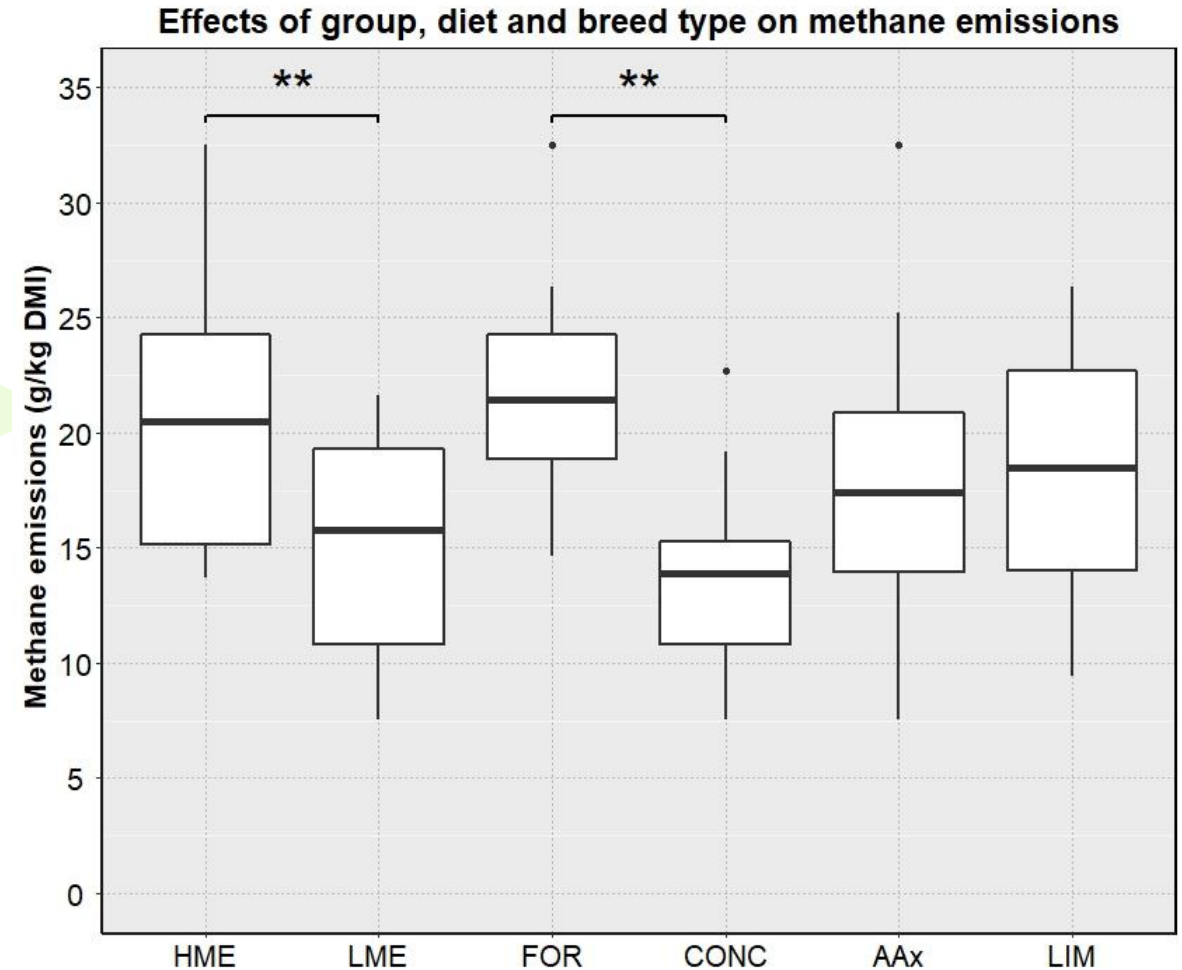


Statistics: GLM in R software. Model  $y = \text{group} + \text{breed} + \text{diet} + e$

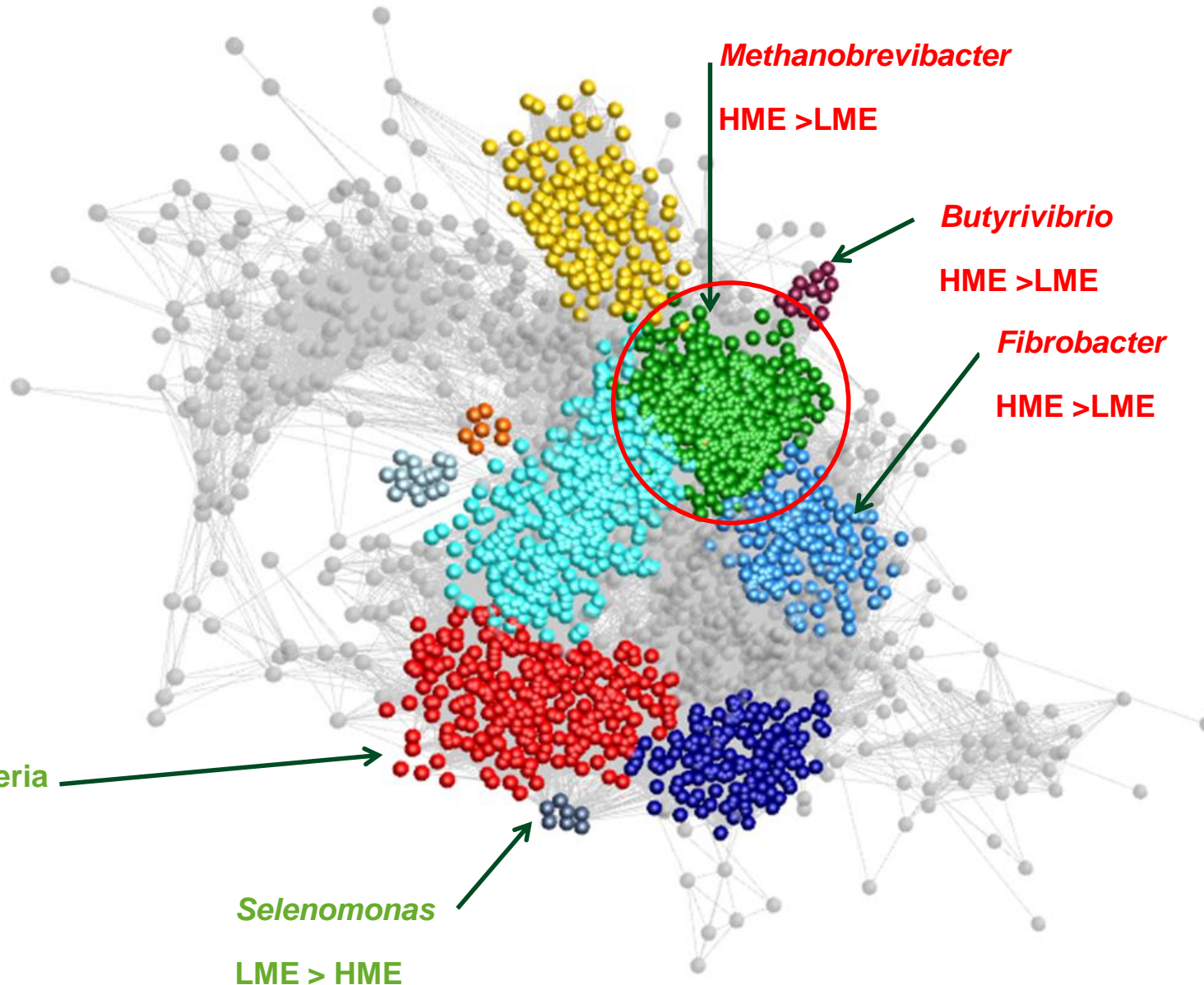
Methane emissions (g/kg DMI)				
MEAN	SD	CV	HME-LME	P-val
17.75	5.39	30.53	5.73	3.04E-15

In 2717 variables...

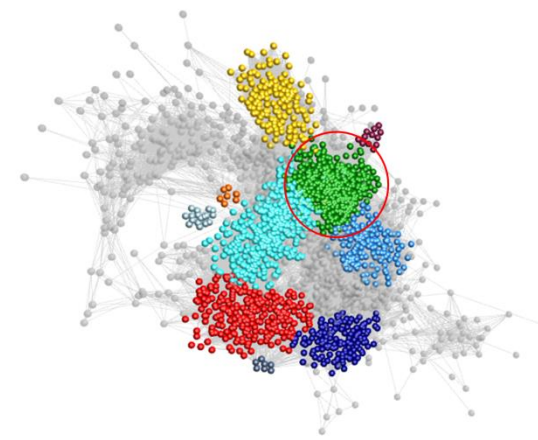
	P-val<0.05	P-val<0.1
Microbial Genes	22	71
Microbial Communities	34	97
Total	56	168



# Where are the variables with different relative abundance in HME and LME?



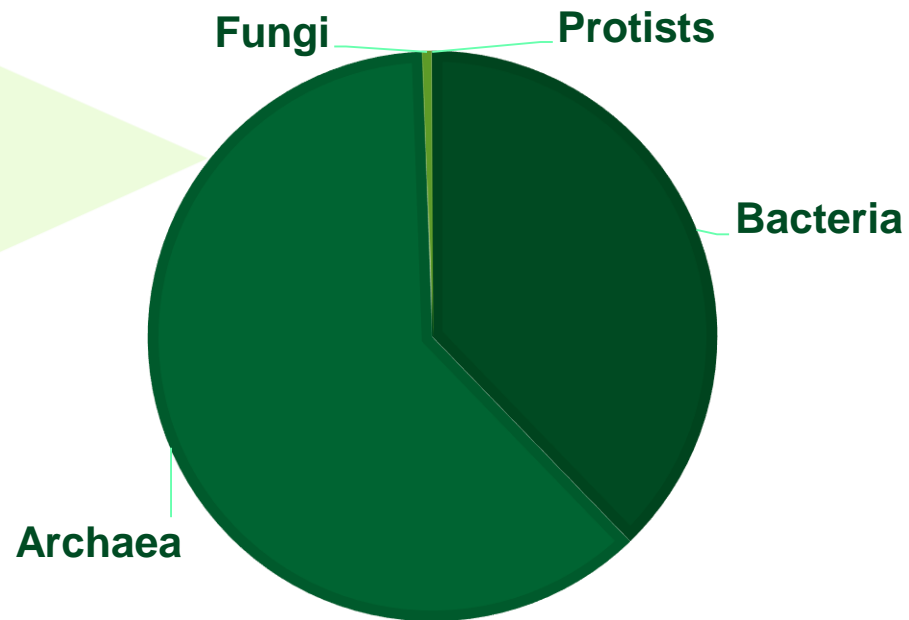
# Cluster with main methanogens



## Cluster description

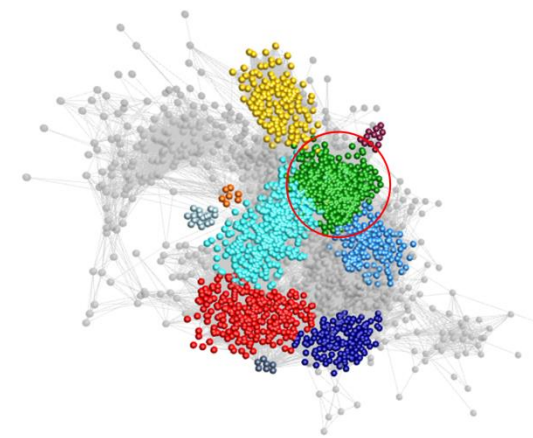
Variable	Connections
Microbial genes	329
Archaea	15
Bacteria	69
Fungi	13
Protists	1
Total variables	427

### MICROBIAL COMPOSITION IN ABUNDANCES (%)





# Cluster with main methanogens



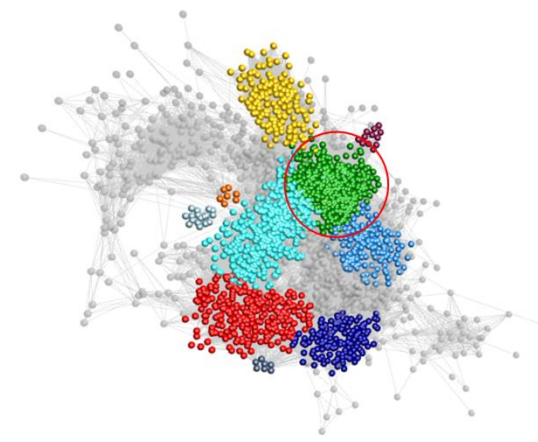
## HME - LME

Variable	Description	HME - LME	P- val
<i>Candidatus.Azobacteroides</i>	<i>Bacteria Bacteroidetes</i>	0.0009	<0.050
<i>Endomicrobium</i>	<i>Bacteria Elusimicrobia</i>	0.0015	<0.050
<i>Endozoicomonas</i>	<i>Bacteria Proteobacteria</i>	0.0004	<0.050
<i>Pirellula</i>	<i>Bacteria Plantomycetes</i>	0.0007	<0.1
<i>Anthracocestis</i>	<i>Fungi Basidiomycota</i>	0.0006	<0.1
K00091	dihydroflavonol-4-reductase	0.0015	<0.050
K00639	glycine C-acetyltransferase	0.0045	<0.005
K07072	(4-(4-[2-(gamma-L-glutamylamino)ethyl]phenoxy)methyl)furan-2-yl)methanamine synthase	0.0009	<0.1
K05884	(R)-2-hydroxyacid dehydrogenase	0.0023	<0.1

# Cluster with main methanogens

## Explaining CH<sub>4</sub>

Statistics: PLS Regression in R (mixOmics Package)



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Final PLS

CH<sub>4</sub> = X  
X = 5 variables

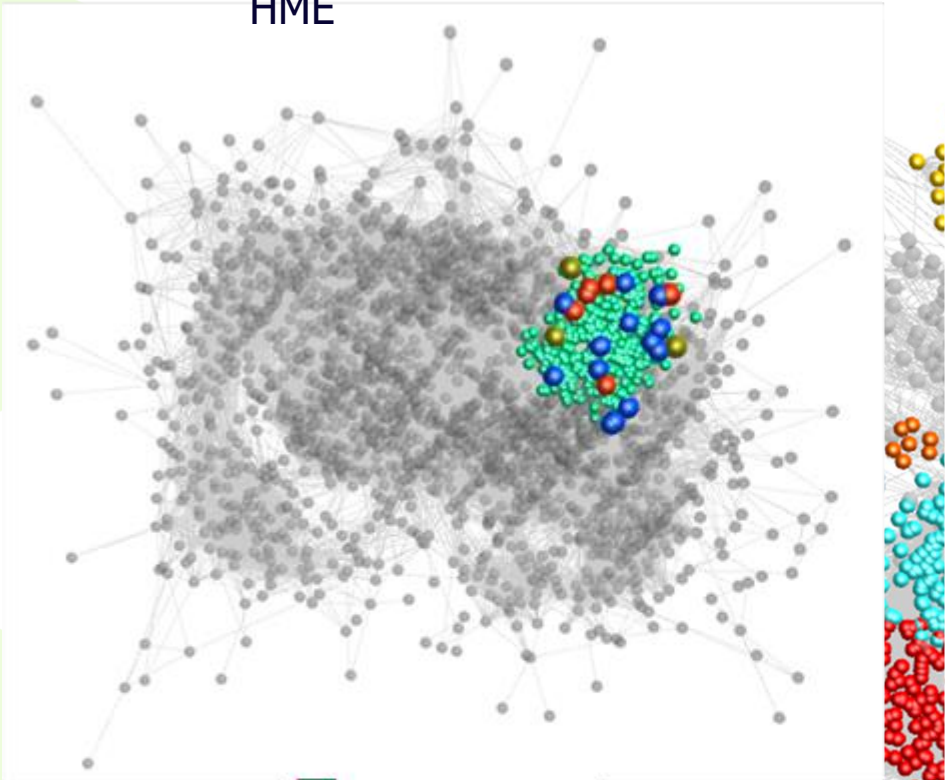
Factors	%Variability X	%Variability of CH <sub>4</sub>
1	78.1%	<b>57.3%</b>

Variable	Information	VIP	Regression Coefficient
<i>Candidatus Azobacteroides</i> *	Bacteria Bacteroidetes	1.03	0.177
<i>Tremella</i>	Fungi Basidiomycota	1.01	0.174
K02585	nitrogen fixation protein NifB	0.99	0.171
K00639*	glycine C-acetyltransferase	0.99	0.170
K00091*	dihydroflavonol-4-reductase	0.98	0.169

# Different interactions in HME and LME

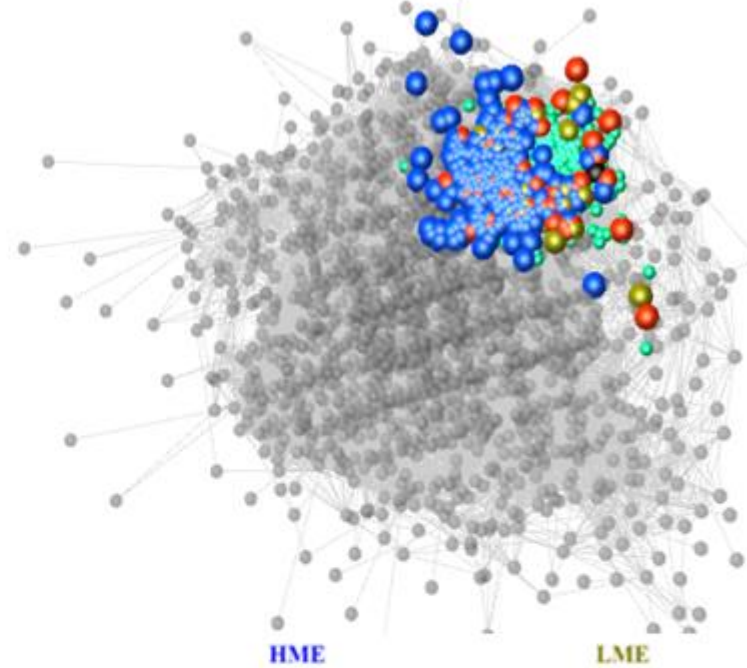
## Network analysis within group

HME



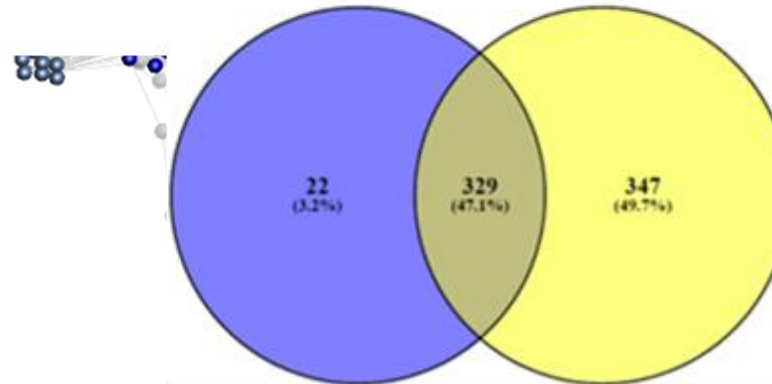
Microbial genes  
Bacteria  
Archaea  
Fungi  
Protist

LME



HME

LME



Statistics: Network analysis using MCL algorithm in Miru software (Corr = 0.70)

# Conclusions

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- Bacteria (n=14) and Fungi (n=3) MAGs and microbial genes associated with carbohydrate degradation explain most of the differences between low and high methane emitters but not archaea and microbial gene associated with methane metabolism
- These bacteria and fungi communities are therefore highly important for prediction of methane emissions from rumen samples



Thank you for your attention



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