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# Genome-centric resolution of anaerobic digestion microbiome in biogas reactors fed with Long Chain Fatty Acids

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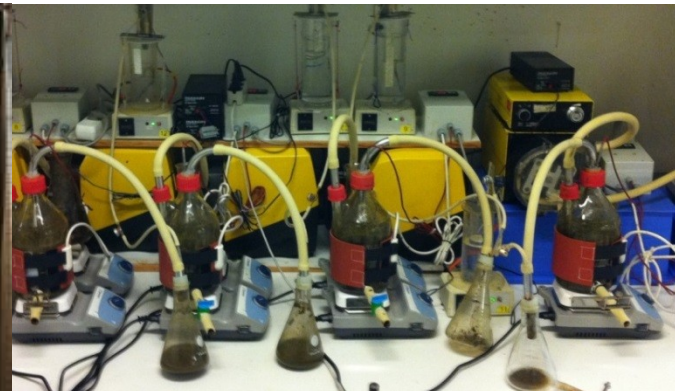
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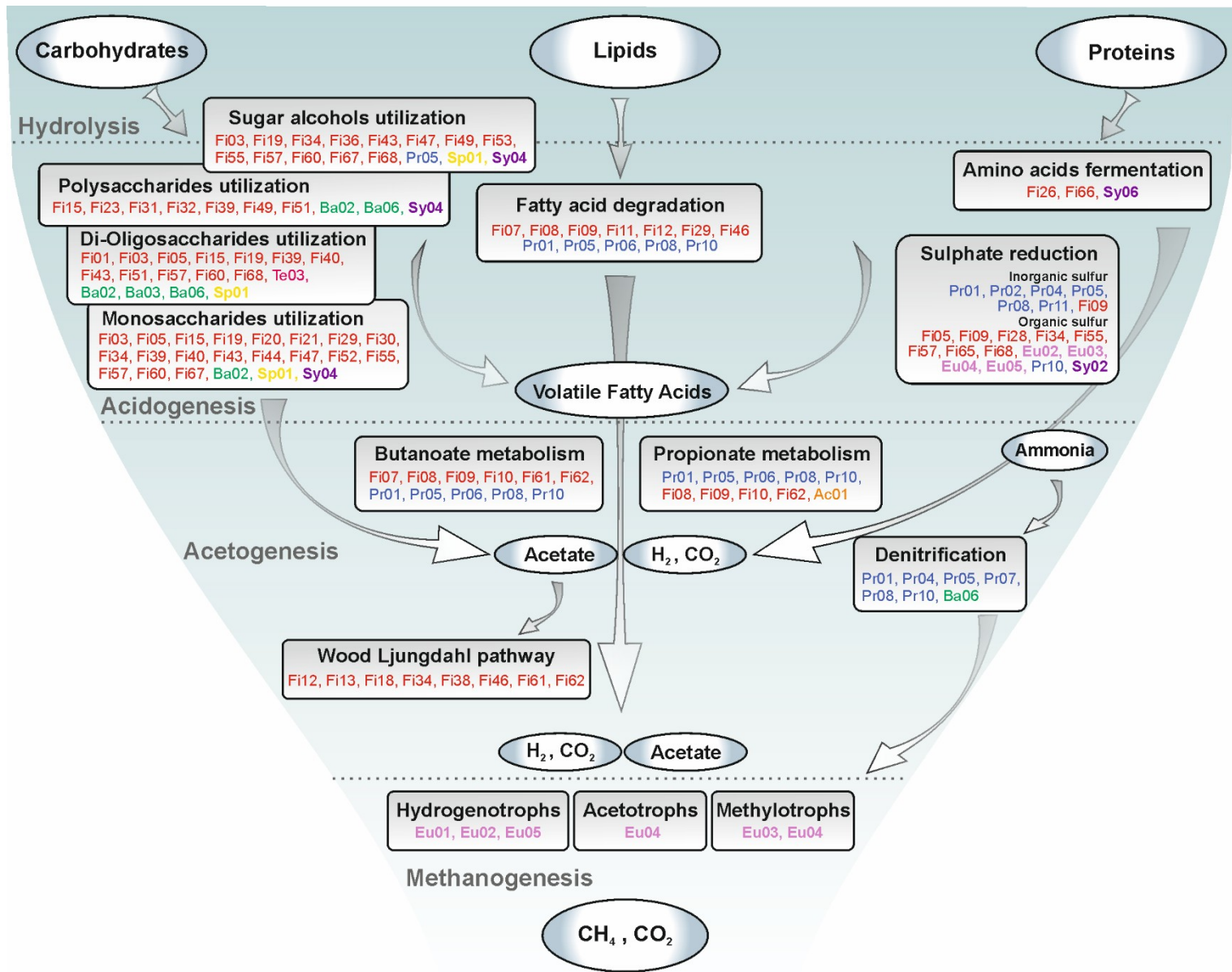


# Anaerobic digestion: State of the art

Many different aspects and problems affecting biogas reactors are directly connected with microbial activity:

- Ammonia rich substrates
- Biogas upgrade
- Foaming
- Temperature disturbances
- Cellulosic and lignocellulosic feedstocks





# Experimental design



## Case Study 1

Cattle manure



Cattle manure



Shock Load

## Case Study 2

Cattle manure

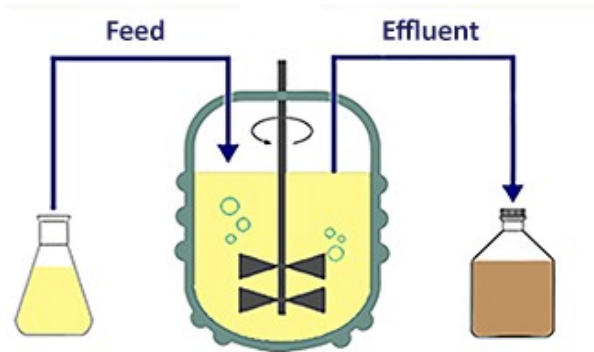


Cattle manure +  
LCFA

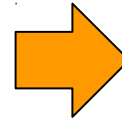


Change of influent composition

# Approach and methodology



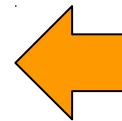
**1. Biogas Reactors**



**2. DNA extraction**



**3. Shotgun Sequencing**

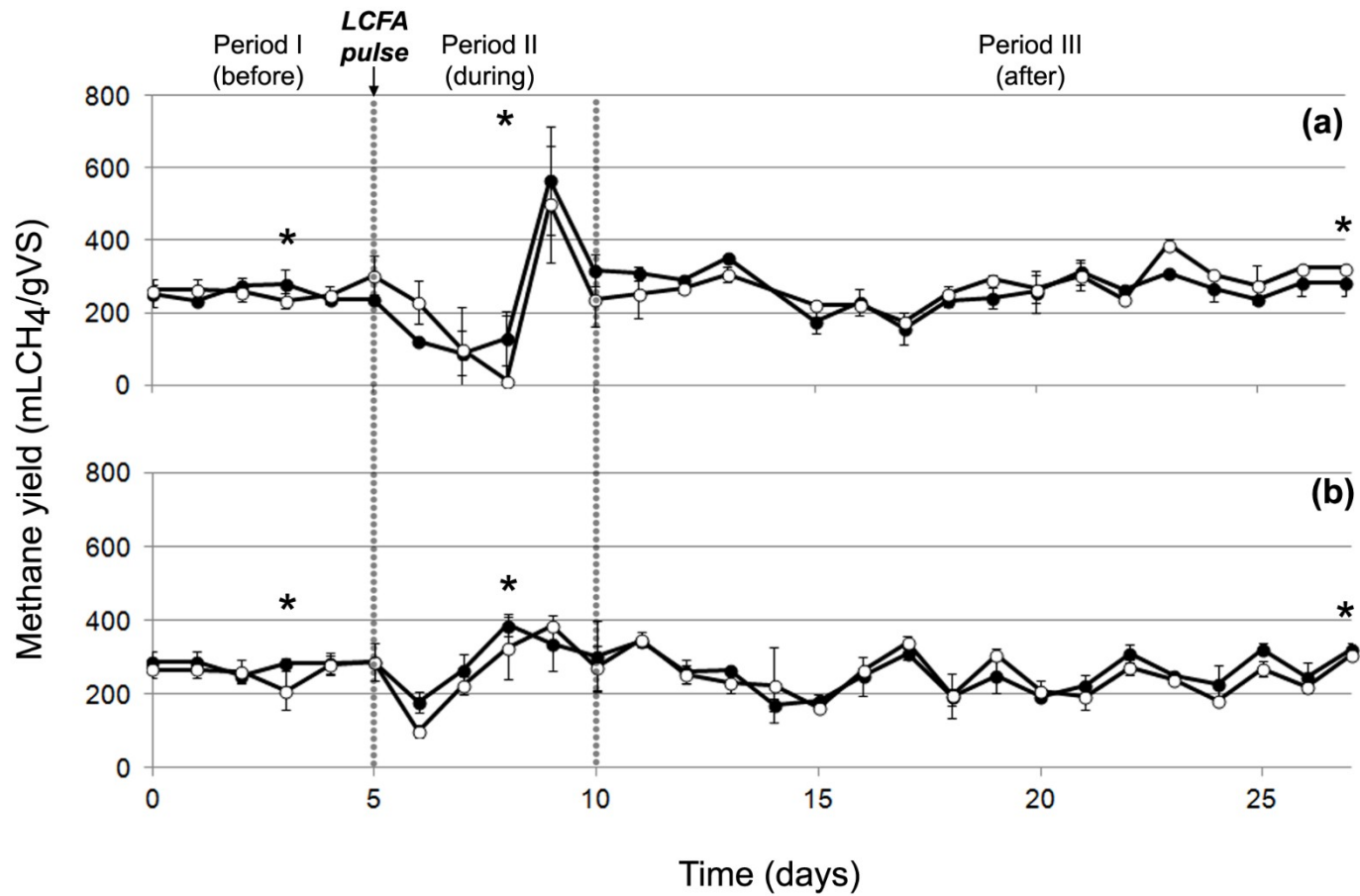


**4. Bioinformatic Analyses**

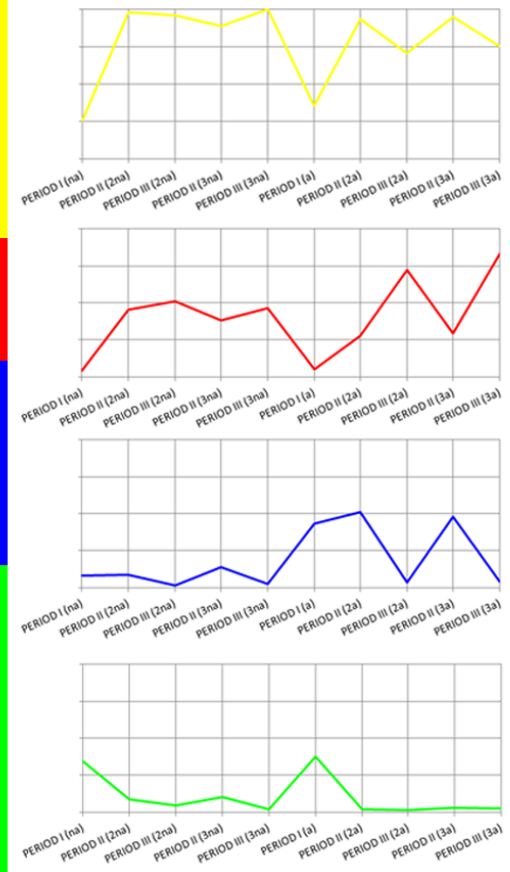
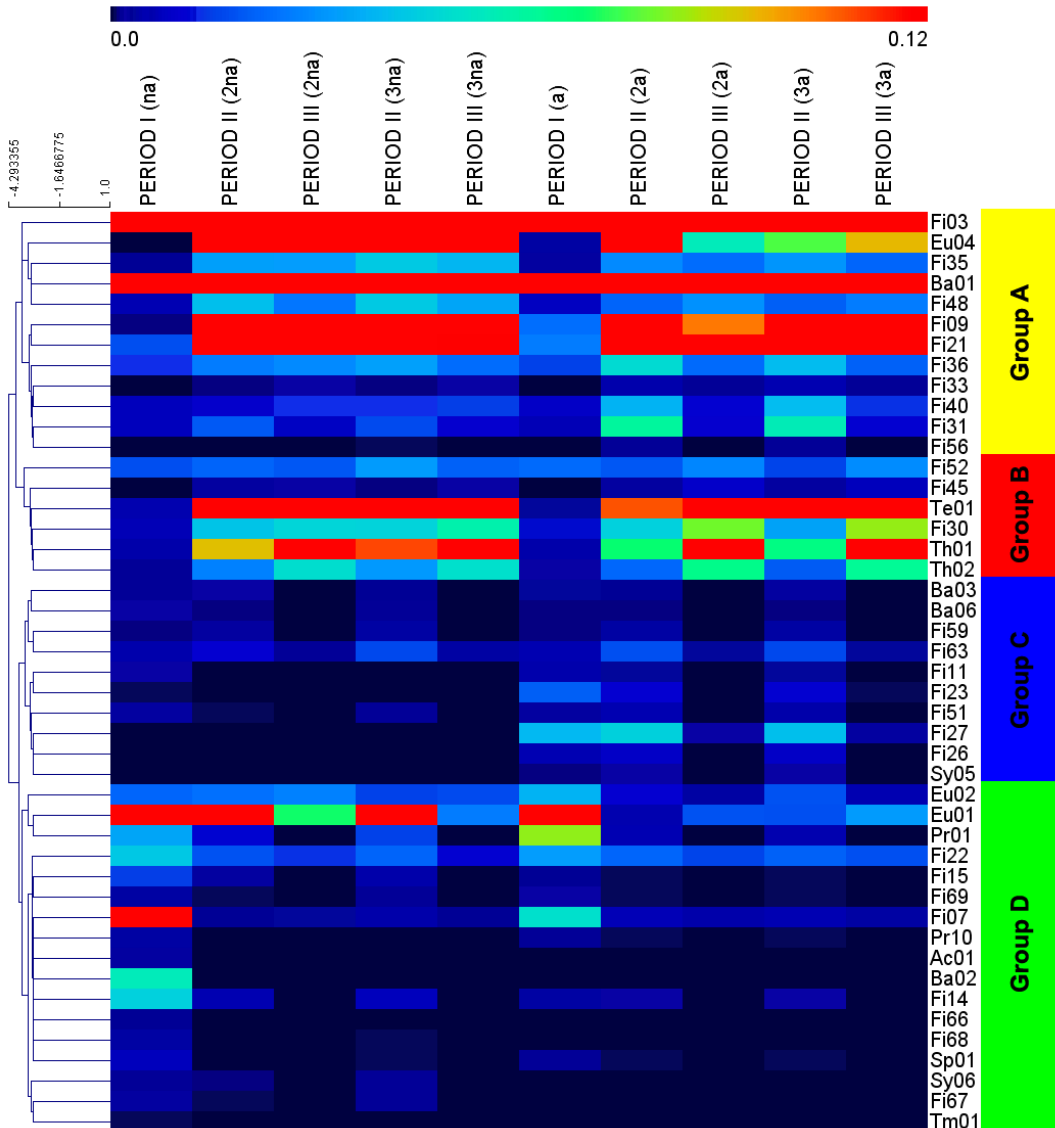




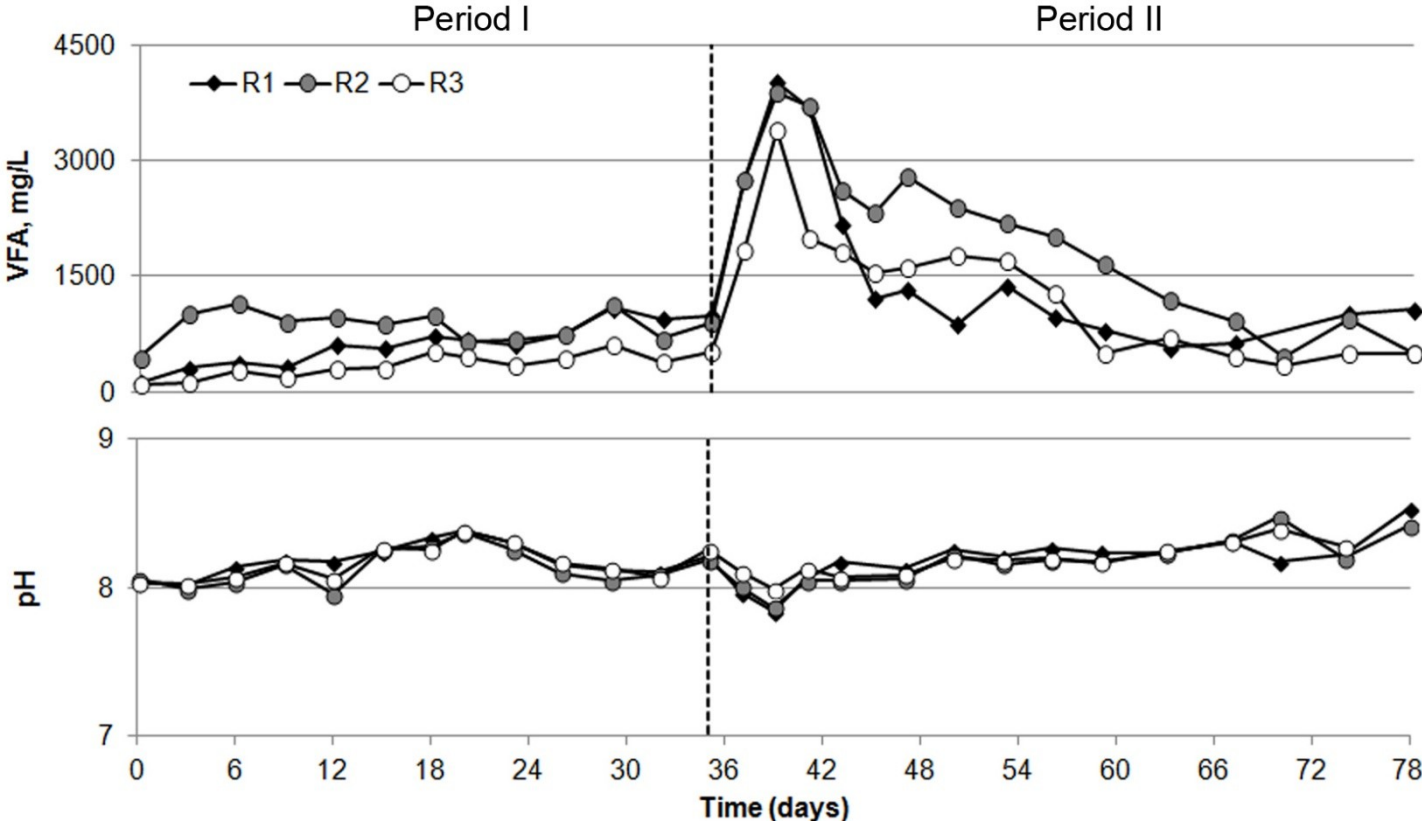
# Results



# Results

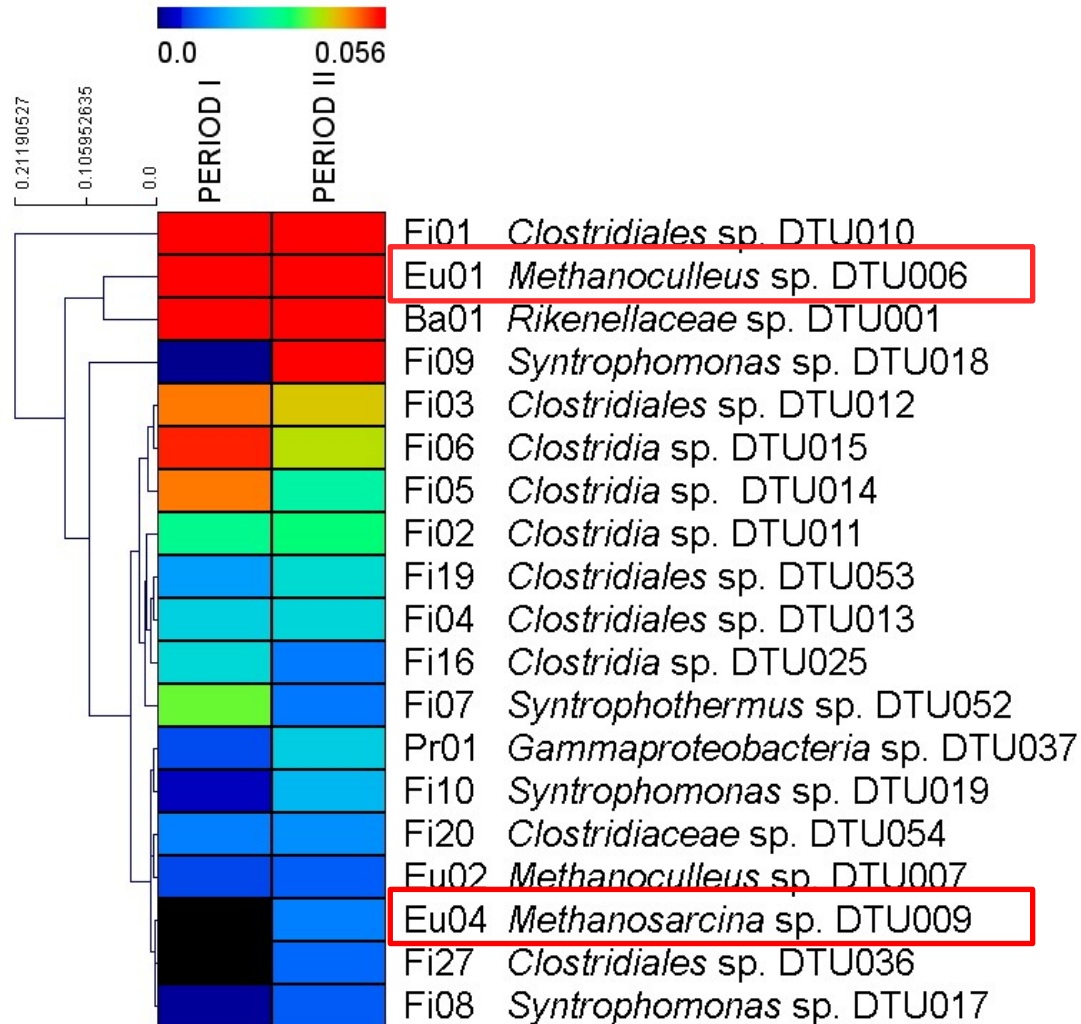


# Results



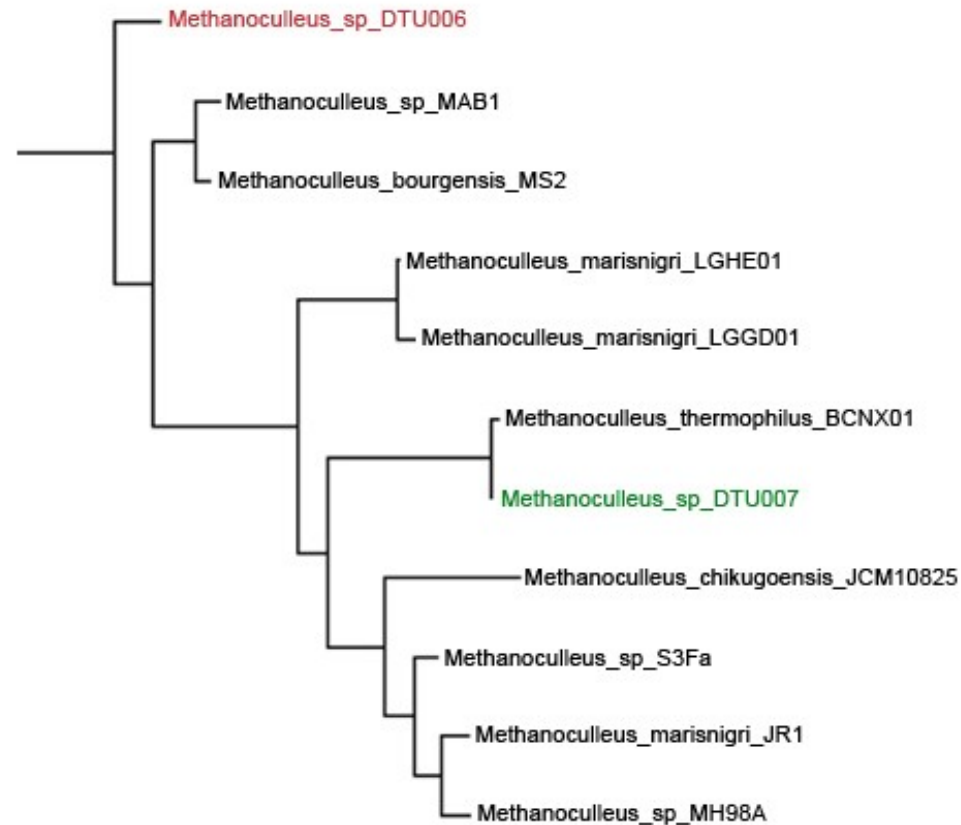


# Results

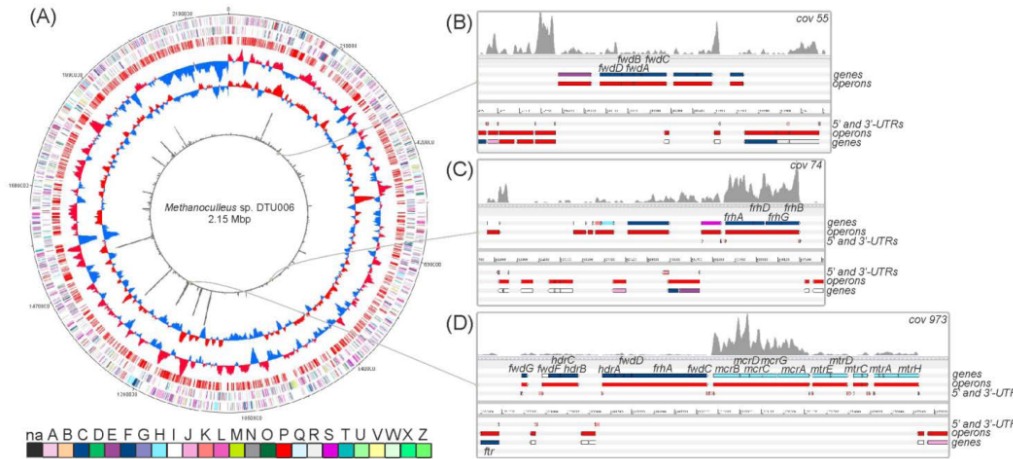


# Results

- Genomes belonging to *Methanoculleus* genus were downloaded from NCBI microbial genome database and were compared using PhyloPhlAn.

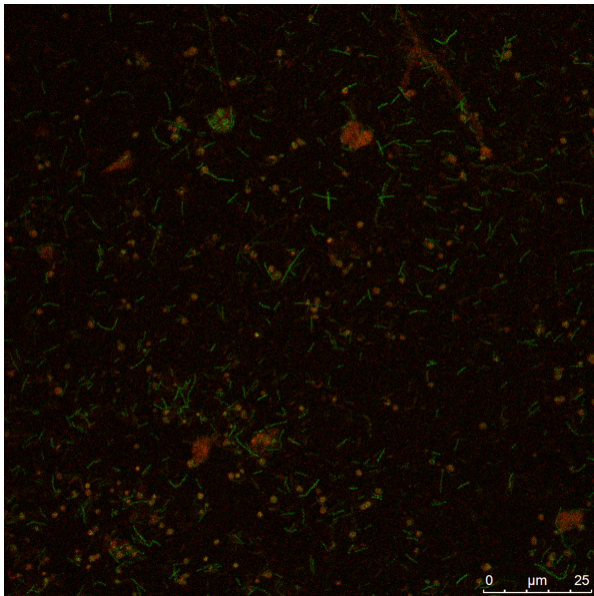


# Results (novel species)



## *Candidatus Methanoculleus thermohydrogenotrophicum*

GENOME CHARACTERISTICS	
Genome size [bp]	2.15 Mbp
GC content	59.20%
Scaffold N50 [bp]	17,178
Number of contigs	503
Number of protein-encoding genes	2,297
Total number of essential genes	32
Estimated completeness % (CheckM)	92.70%
Estimated contamination level % (CheckM)	2.30%



# Conclusions



**LCFA inhibition is a reversible phenomenon**

**Biogas microbiome unveiled**

**Syntrophic interactions**

**Novel species were identified**

**New opportunities for microbial resource management**

## what is biogasmicrobiome.com

Biogasmicrobiome. decipher the microbi shotgun sequencing, were extracted using

In our first work, the achieved. Annotation for the first time a cl reference collection genomic studies.

### Background

Metagenomic as derived from dif is the process o the operational binning procedu from microbial c clones.

From this proj

Binning p



Search

### New Results

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## The anaerobic digestion microbiome: a collection of 1600 metagenome-assembled genomes shows high species diversity related to methane production

Stefano Campanaro, Laura Treu, Luis M Rodriguez-R, Adam Kovalovszki, Ryan M Ziels, Irena Maus, Xinyu Zhu, Panagiotis G. Kougias, Arianna Basile, Gang Luo, Andreas Schlüter, Konstantinos T. Konstantinidis, Irimi Angelidaki

doi: <https://doi.org/10.1101/680553>

[www.b](http://www.b)

**Released this week!**



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# Teamwork



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