

Conventional biogas production process

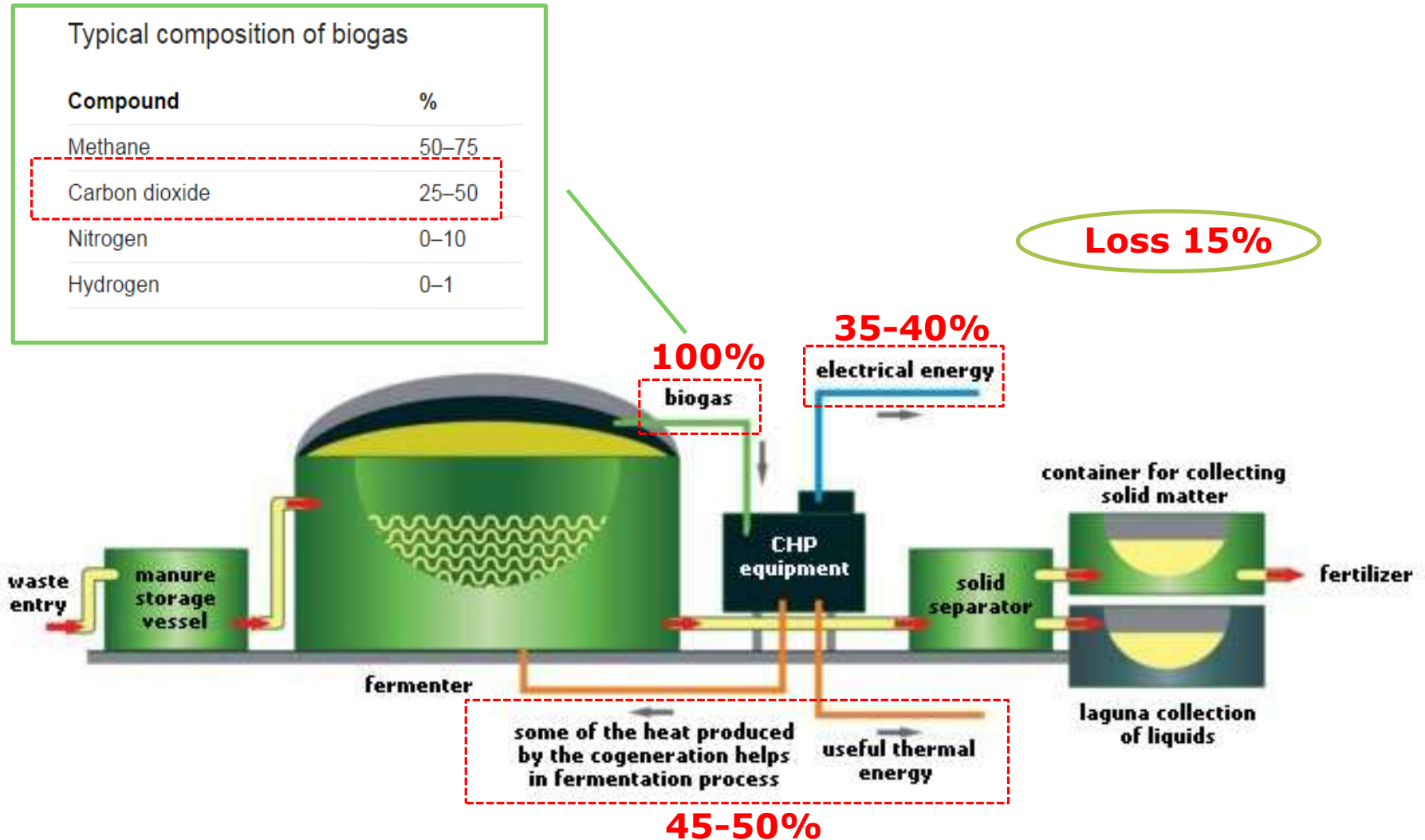


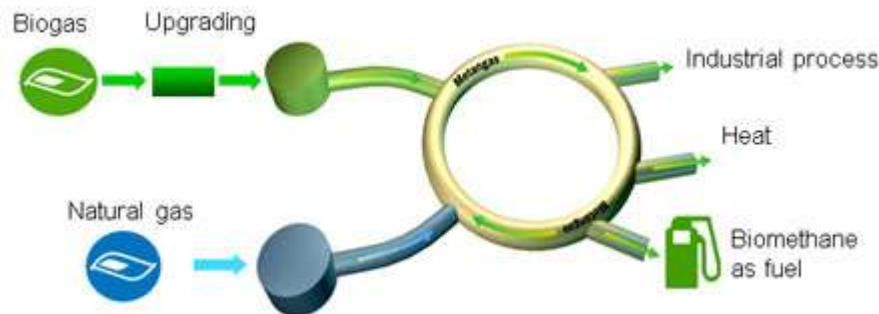
Figure obtained by <http://www.bteam-energy.ro/en/information/biogas> (last access 07/09/2017)

Biogas upgrading

“The process in which the final output gas consists of higher methane concentration compared to raw biogas, mainly due to removal or transformation of carbon dioxide”

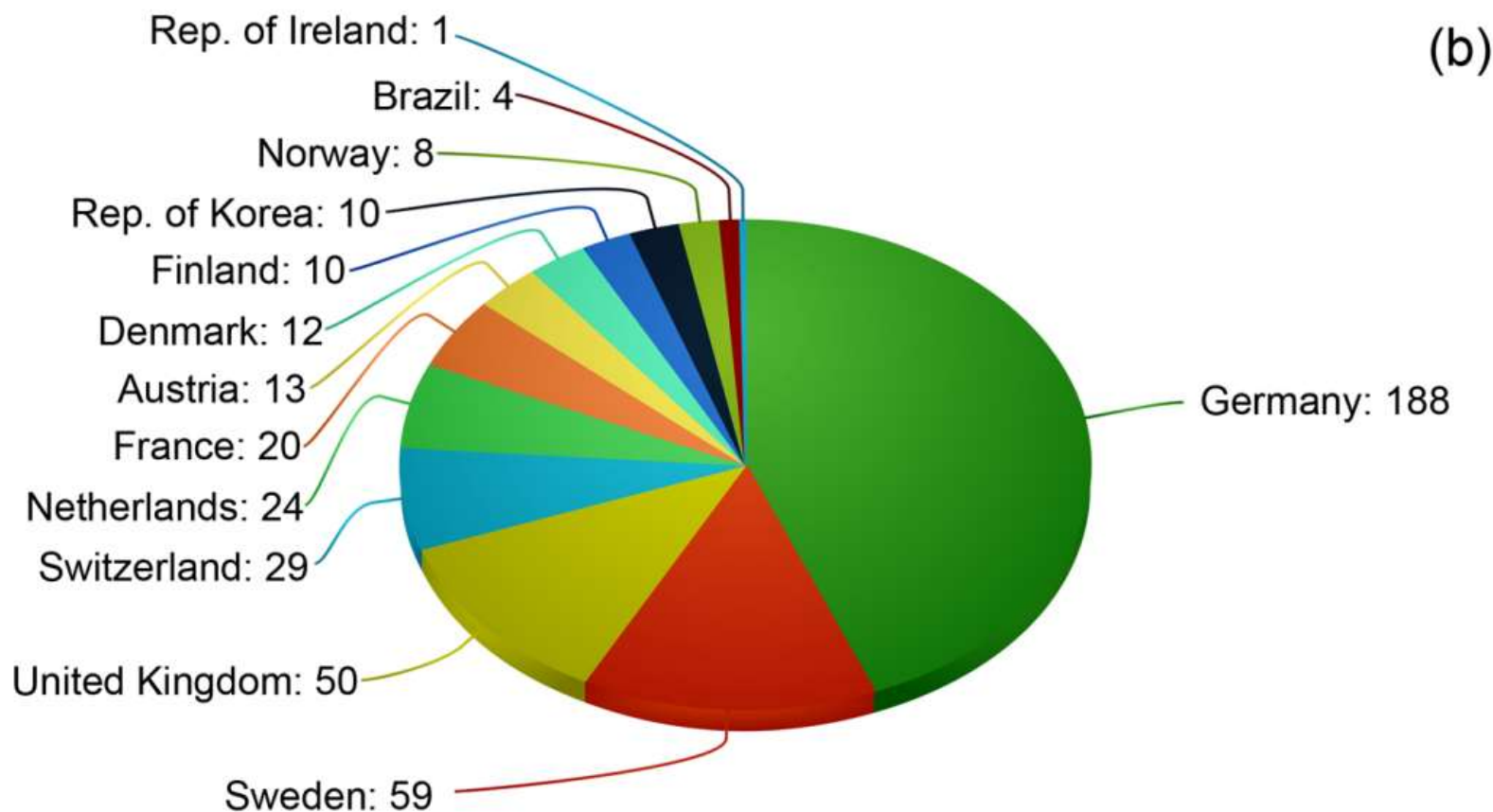
Applications?

Can be used as a **substitute for transport fuels**, to produce **combined heat and power (CHP)**, **heat alone** or serve as **feedstock for the chemical sector**. It can be transported and stored in the facilities and infrastructure available for natural gas.



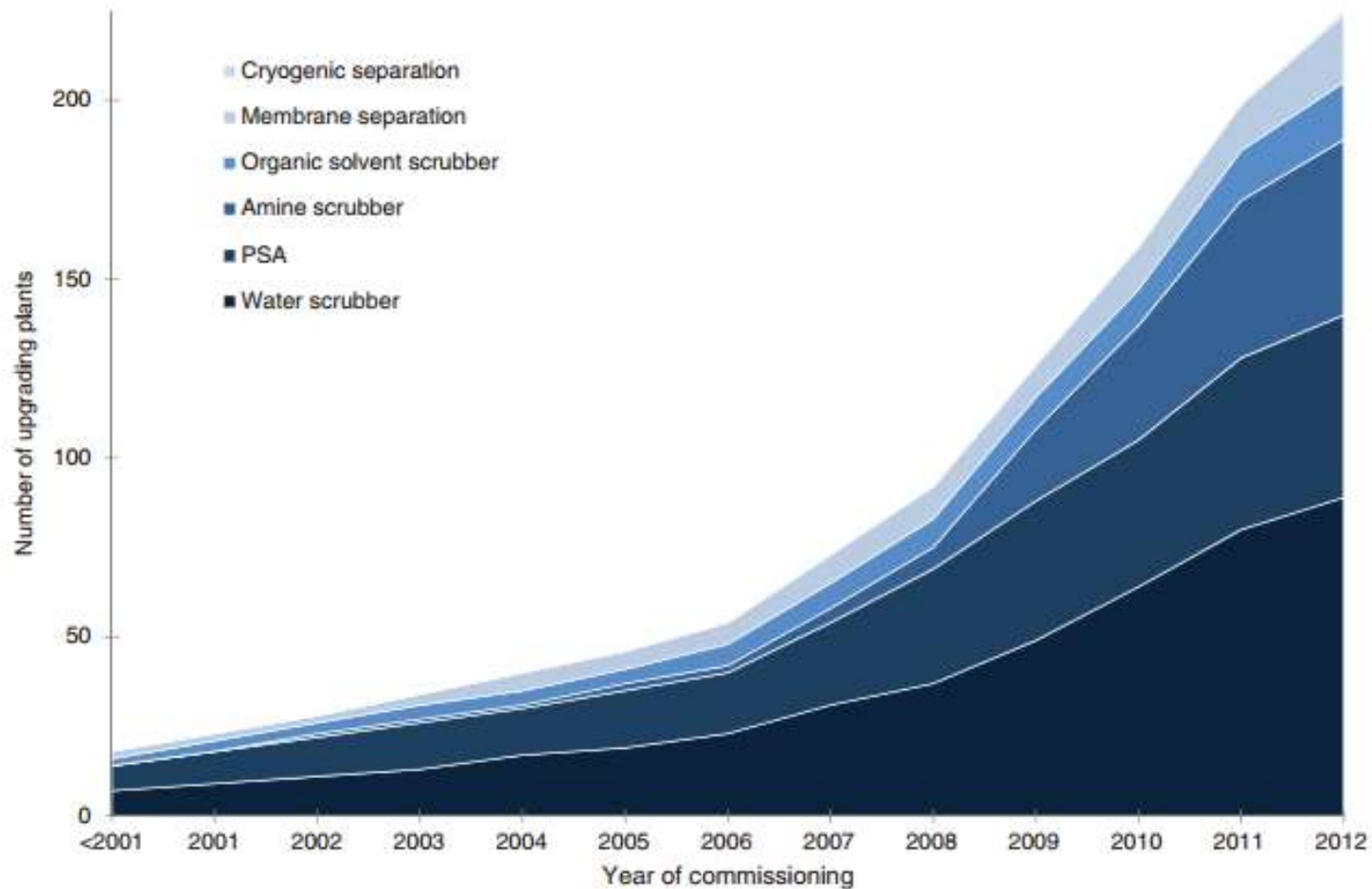
Source: IEA Bioenergy 2014, Joint Study by IEA Bioenergy Task 40 and Task 37

Biogas upgrading



IEA Bioenergy Task 37 as reported in Hoyer et al. (2016) and European Biogas Association
Hoyer, K., Hulteberg, C., Svensson, M., Jernberg, J., Nørregård, Ø., 2016. Biogas Upgrading – Technical Review. ISBN: 978-91-7673-275-5.

Biogas upgrading



Source: Bauer, F., Persson, T., Hulteberg, C., & Tamm, D. (2013). Biogas upgrading—technology overview, comparison and perspectives for the future. *Biofuels, Bioproducts and Biorefining*, 7(5), 499-511.

Biogas upgrading

Parameter	Water scrubber	PSA	Membrane (2-4 stages)	Chemical scrubber (amine)	Organic physical scrubber
CH ₄ in product gas	96 – 98 %	96 – 98 %	96 – 98 %	96 - 99 %	96 – 98 %
Availability	95 - 98%	95 – 98 %	95 - 98%	95 - 98%	95 – 98 %
Annual maintenance cost (% of investment cost)	2 - 3%	2 – 3 %	3 – 4 %	2 – 3 %	2 – 3 %
H ₂ S removal	Yes	External	External	External/Yes	External
H ₂ O removal	External	Yes	Yes	External	External
N ₂ and O ₂ separation	No	No/partly	Partly (O ₂)	No	No
Electricity consumption (product gas > 4 bar(g)) (kWh/Nm ³ raw biogas)	0.2 – 0.3	0.2 – 0.3	0.2 – 0.3	0.10 – 0.15	0.2 – 0.3
Heat (kWh/Nm ³ raw biogas)	None	None	None	0.5 – 0.6	Internal
Pure CO ₂	No	Yes	Yes	Yes	No

Source: Bauer F, Persson T, Hulteberg C, Tamm D (2013) Biogas upgrading – Review of commercial technologies. Swedisch Gas Technology Centre (SGC), Malmö

Surplus Energy/Energy Storage?



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Environment

Scotland's wind turbines provided more electricity than the country needed four days in a row

Two new records for Scottish wind power 'underline the massive progress Scotland is making in securing an ever increasing proportion of its electricity needs from wind power and other clean renewable sources', says WWF Scotland director Lang Banks

Ian Johnston Environment Correspondent | @montaukian | Monday 9 January 2017 11:30 GMT | 154 comments

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INNOVATION

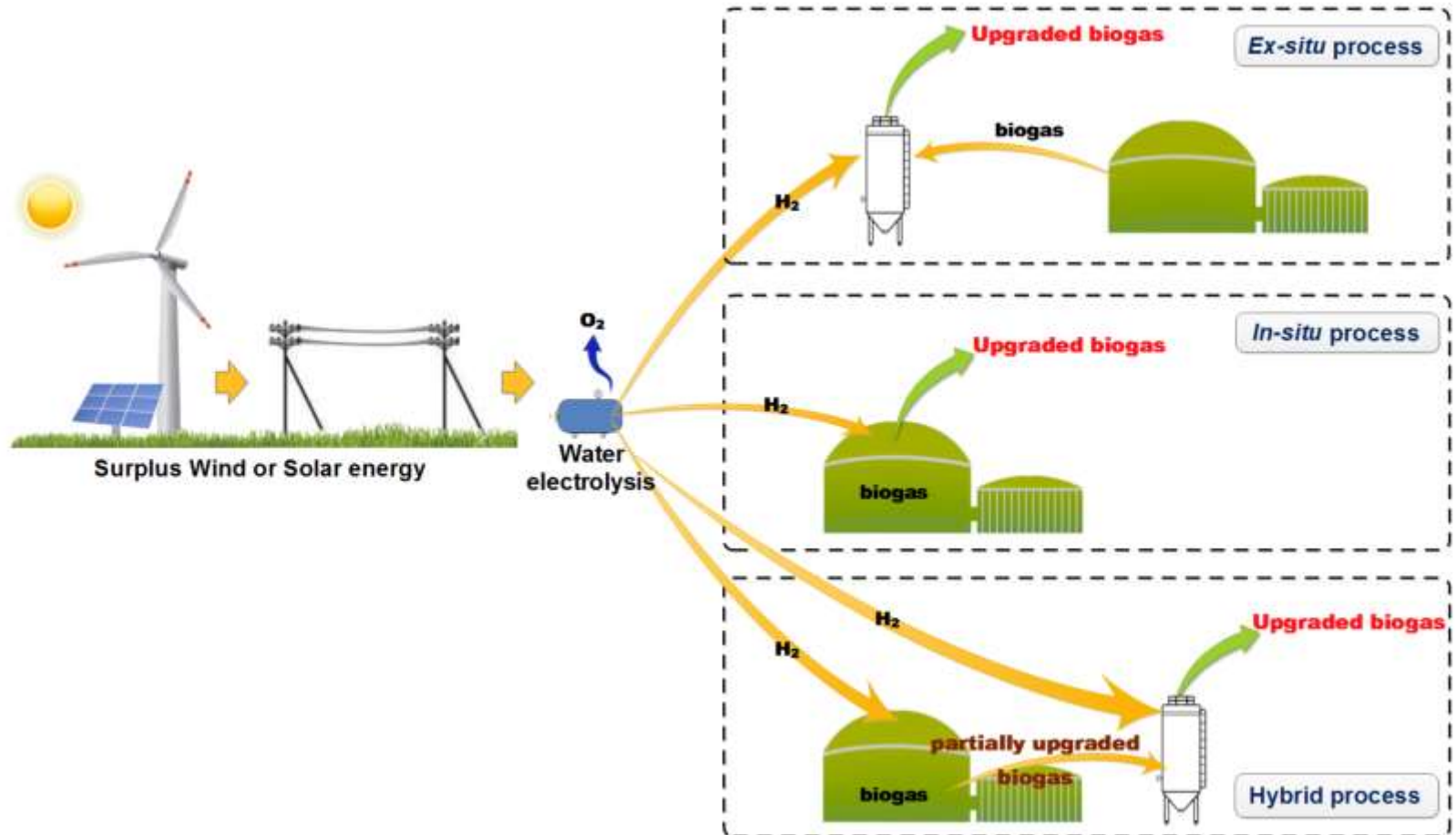
Germany basically had to pay people to use electricity Sunday

By Michael Harthorne · Published May 12, 2016 · Newser

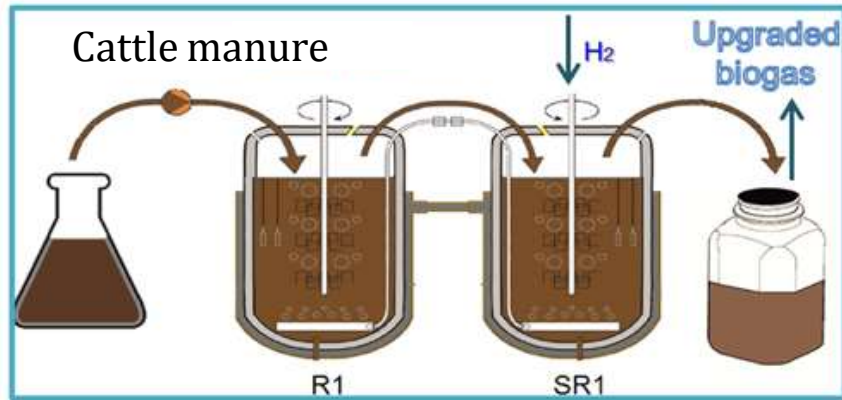
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Biological biogas upgrading

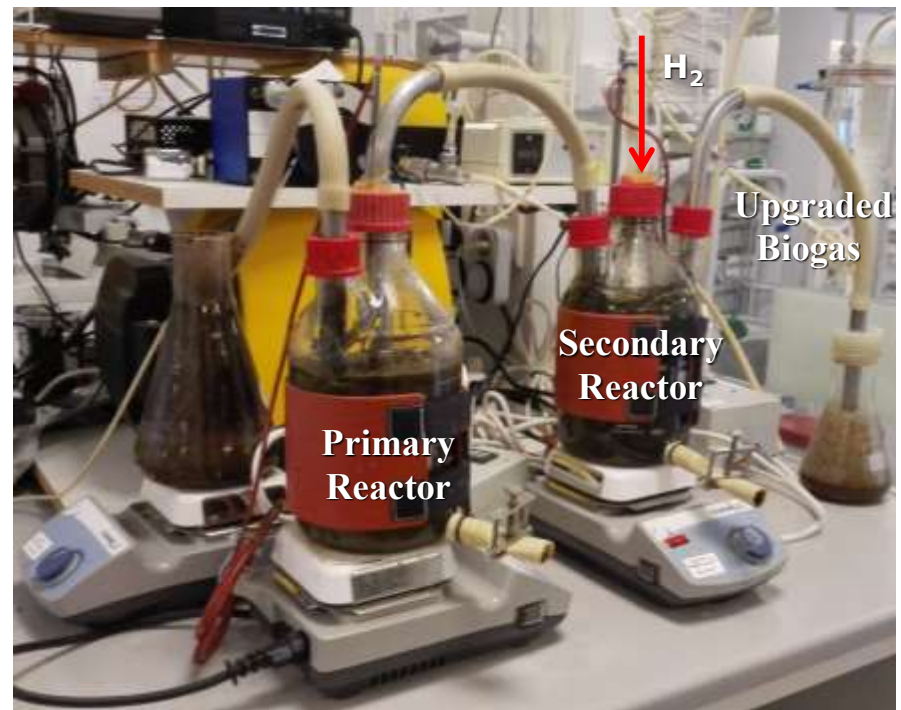


Example 1: Serial configuration



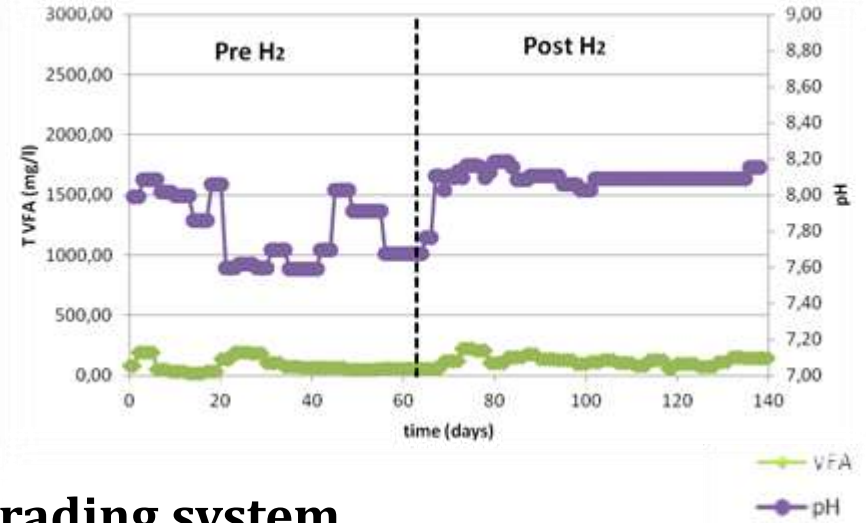
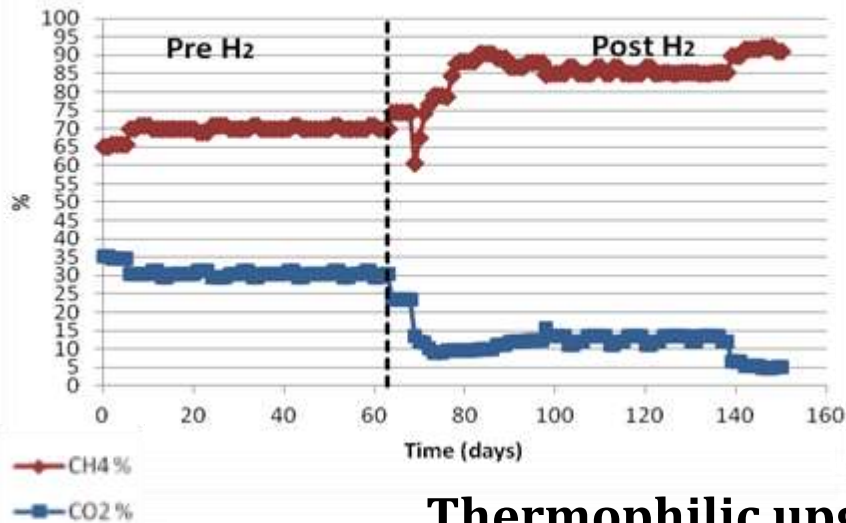
Reactor	Working volume (L)	Temp. (°C)	HRT (days)
R1	1.5	35±1	25
SR1	2.0	35±1	33
R2	1.5	55±1	15
SR2	2.0	55±1	20

Technical challenge: limitations in injection of H₂ using metal diffusers

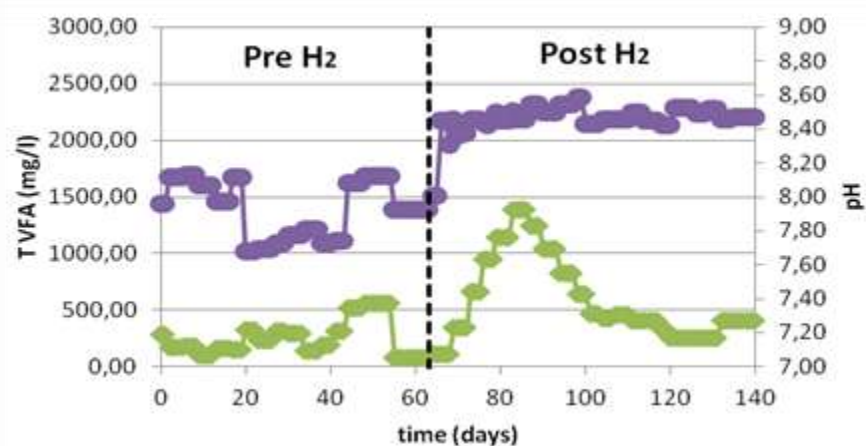
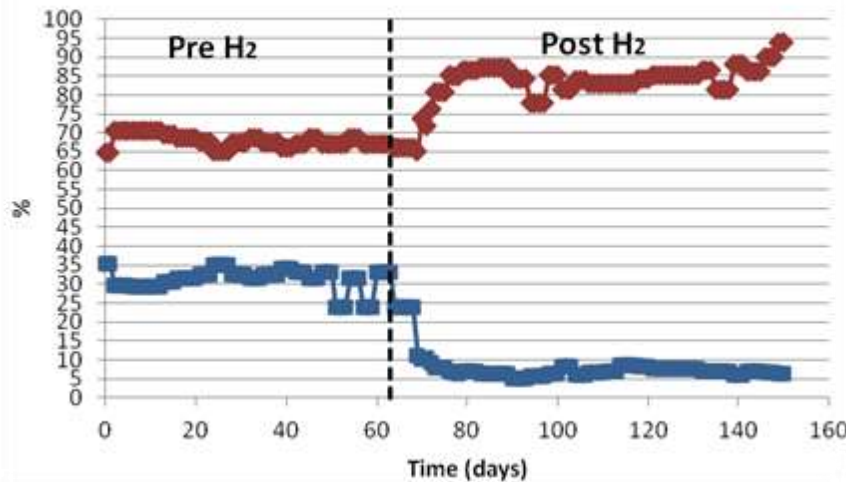


Example 1: Serial configuration

Mesophilic upgrading system

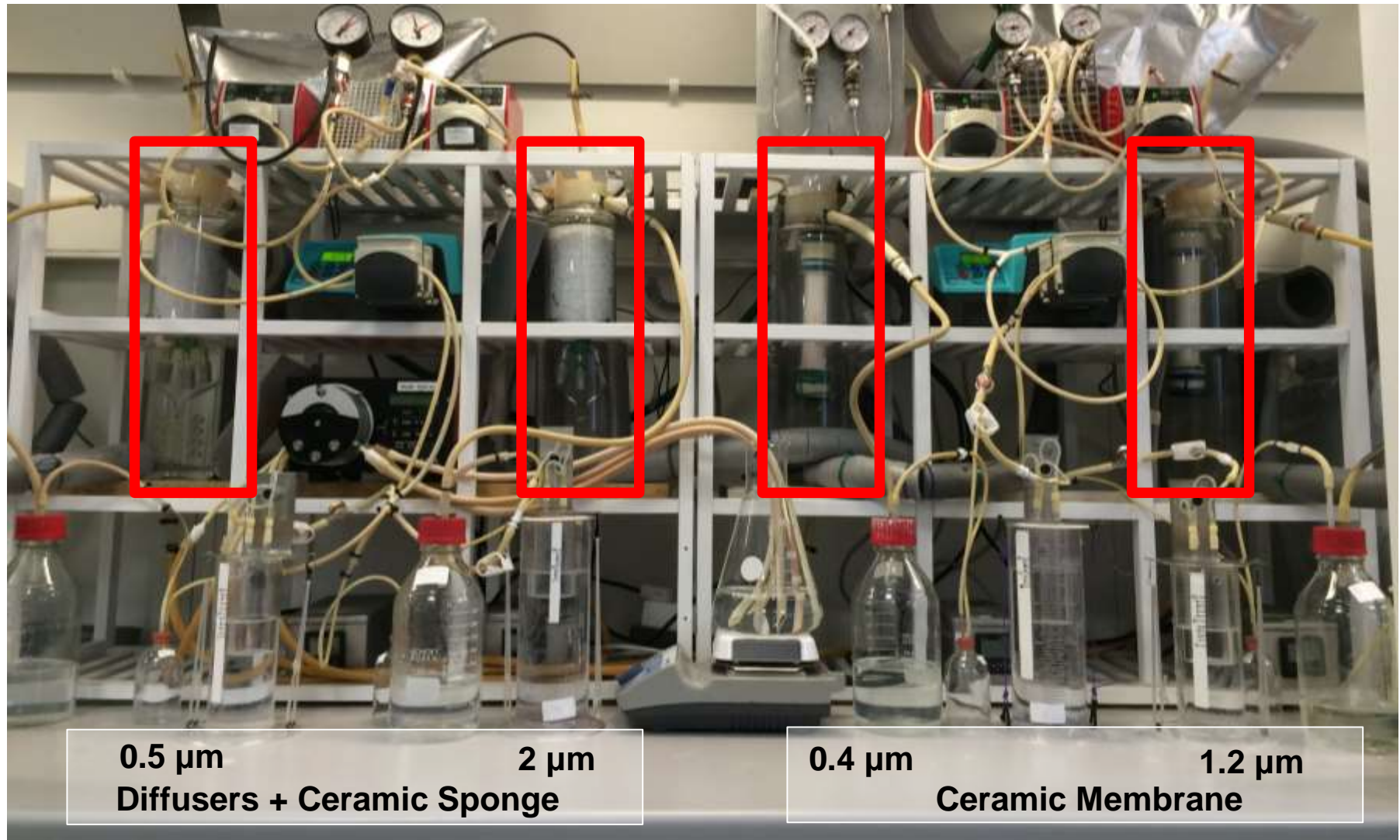


Thermophilic upgrading system



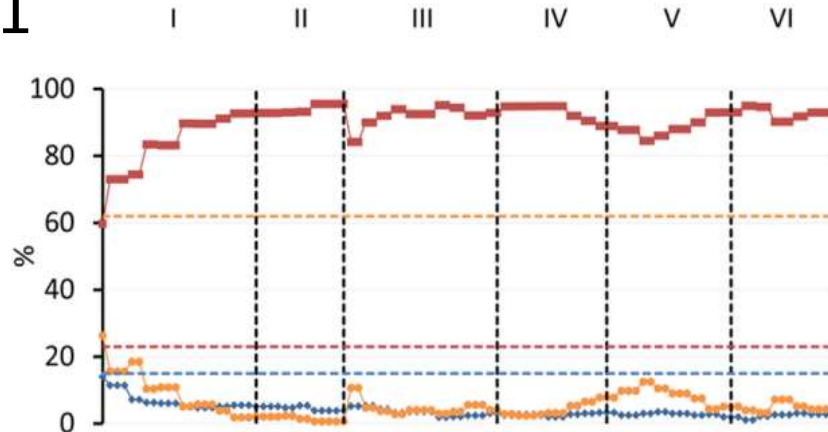
Example 2: Ex-situ biogas upgrade

62% H₂ - 23% CH₄ - 15% CO₂

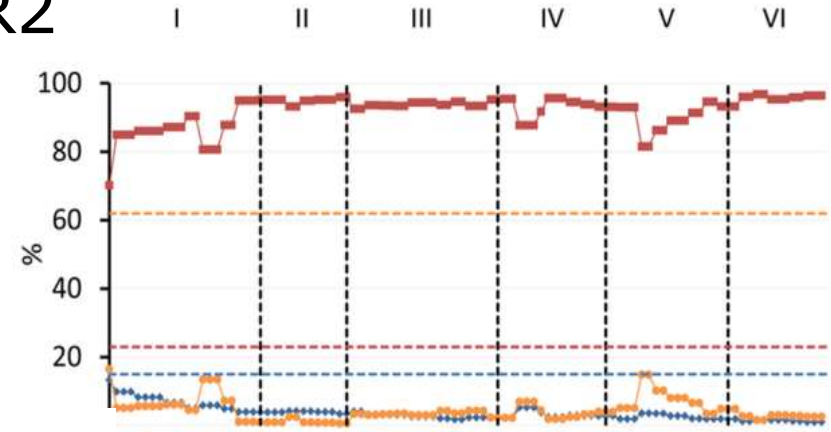


Example 2: Ex-situ biogas upgrade

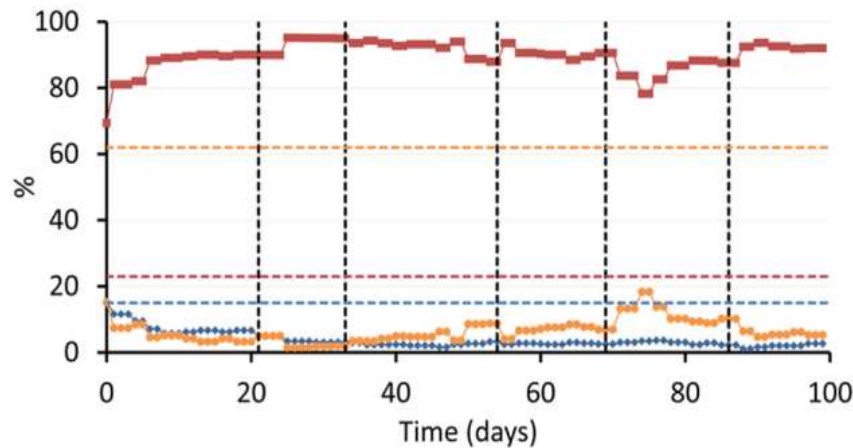
R1



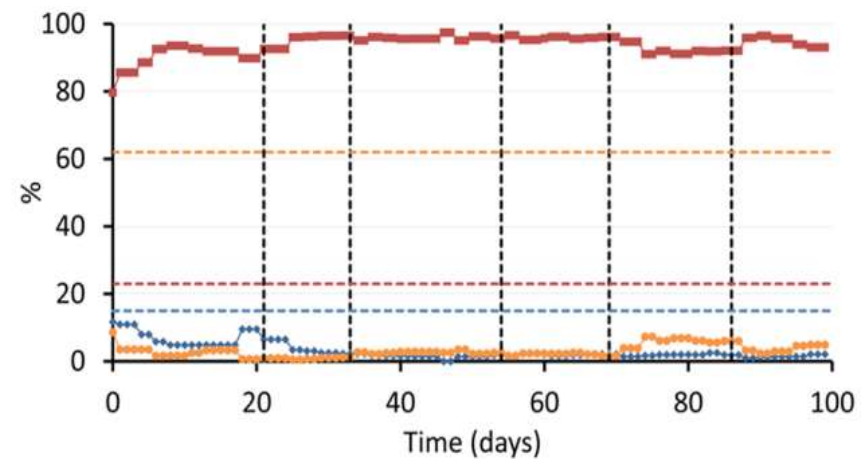
R2



R3



R4

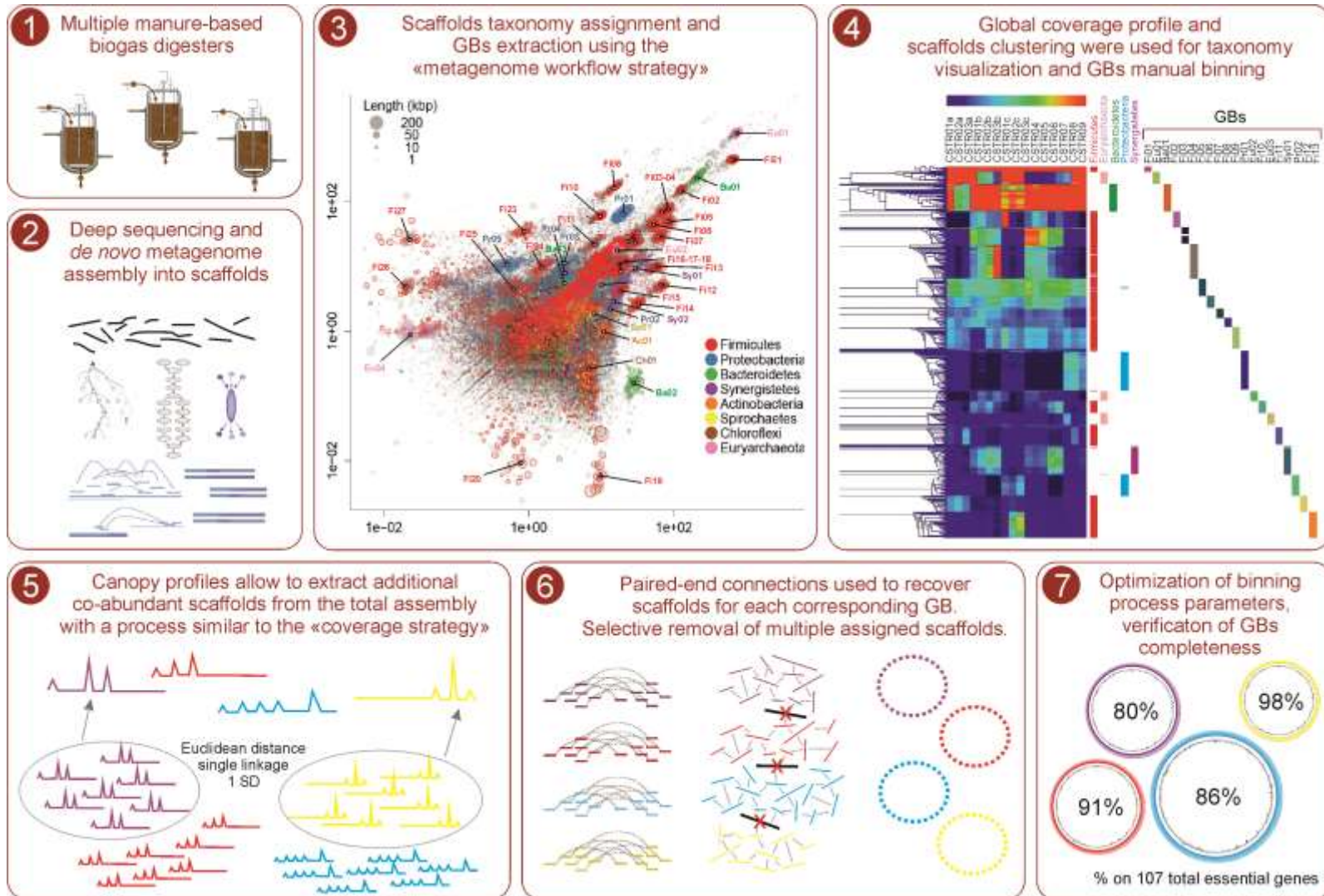


■ CH₄out
 ◆ CO₂out
 ● H₂out
 --- CH₄in
 --- CO₂in
 --- H₂in

4:1



Metagenomic approach: binning



biogasmicrobiome.com

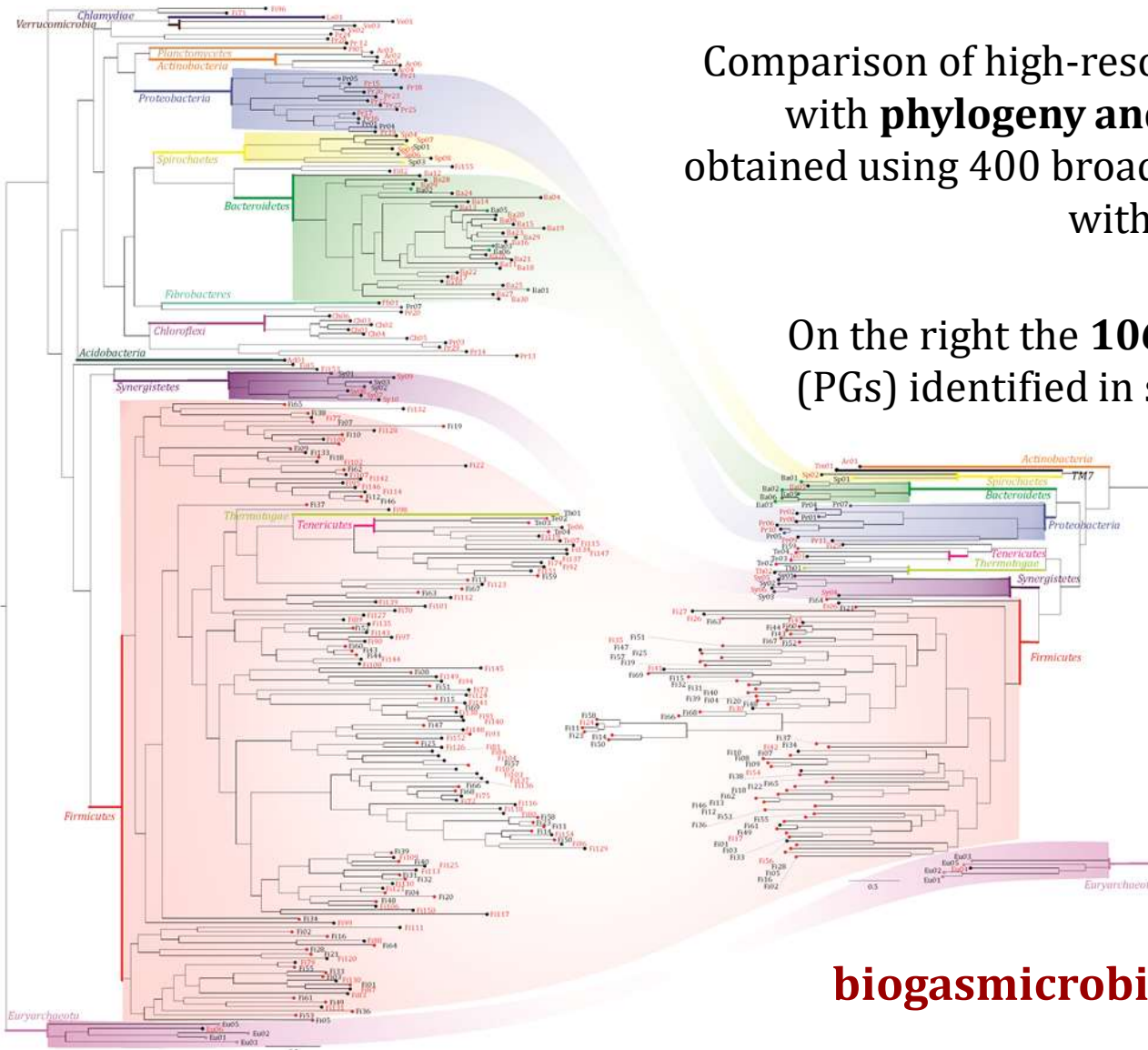
Microbial upgrading taxonomy

Comparison of high-resolution microbial trees with **phylogeny and putative taxonomy**, obtained using 400 broadly conserved proteins with PhyloPhlAn software.

On the right the **106 Population Genomes (PGs)** identified in standard thermophilic anaerobic digesters.

On the left the **236 PGs** binned from mesophilic and thermophilic **biogas upgrading reactors**.

biogasmicrobiome.com



Microbial upgrading taxonomy

Some taxa were found independently from reactors operational conditions, for example several **recurrent phylotypes** are:

Methanoculleus, *Methanothermobacter*, *Syntrophomonas* and *Proteobacteria*.

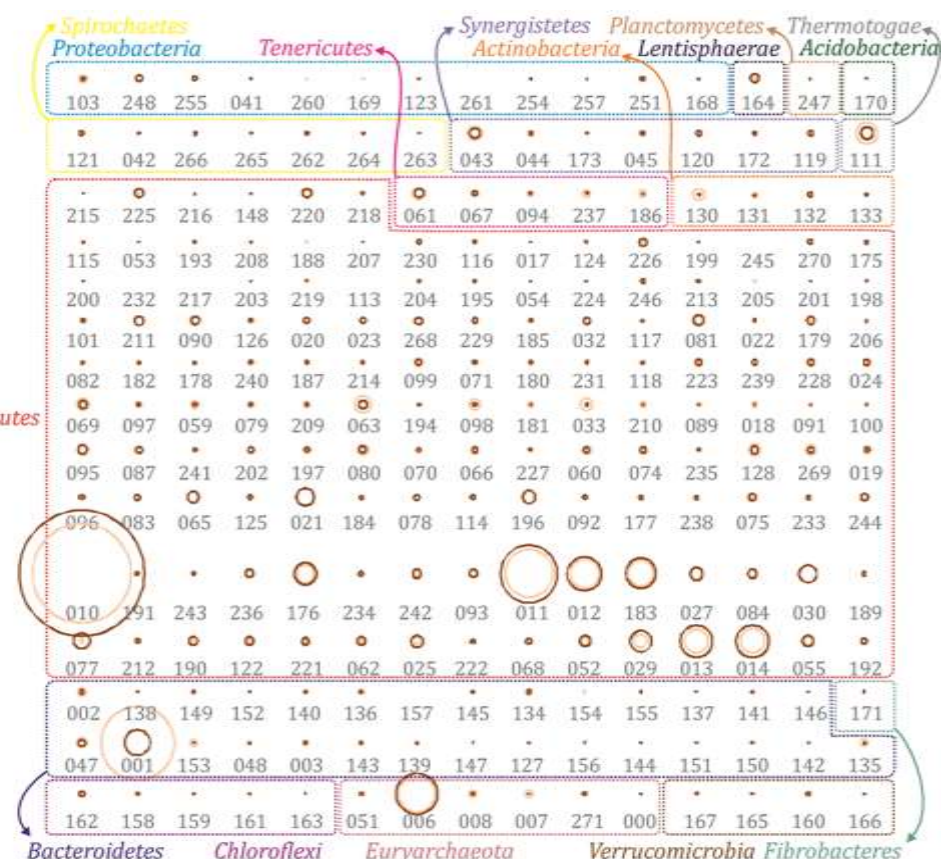
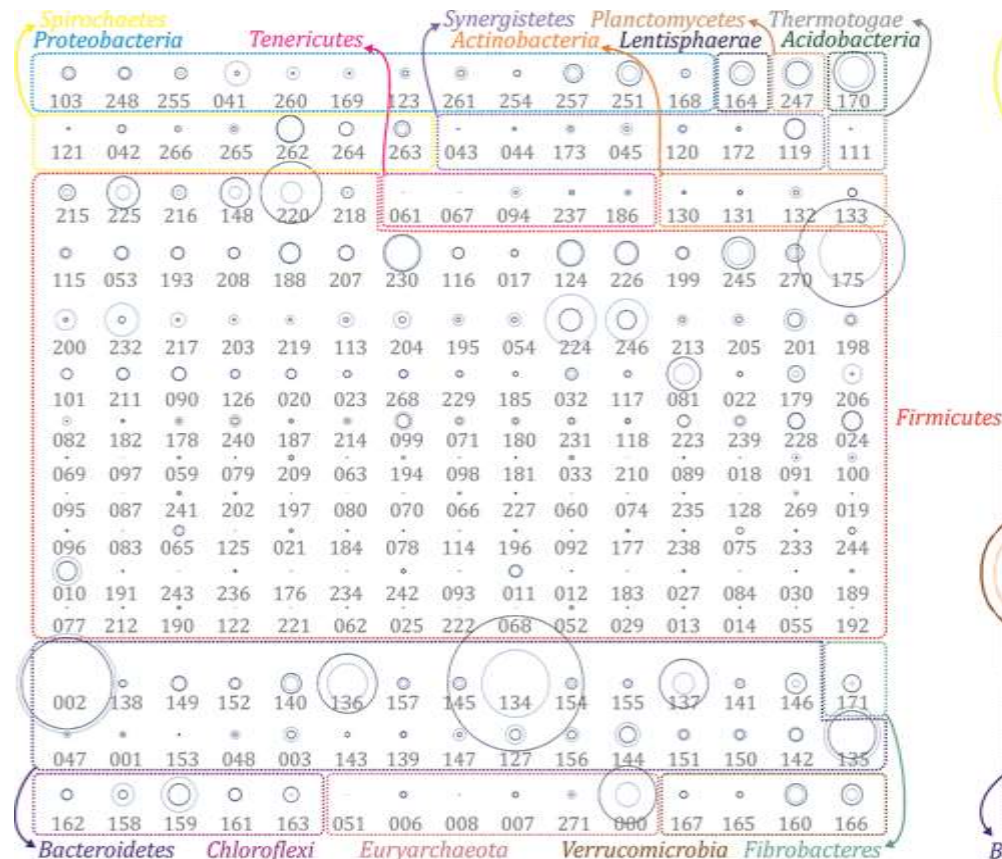
Taxon	Core microbiome		Thermophilic reactors		Upgrading reactors	
	GBs	%	GBs	%	GBs	%
<i>Firmicutes</i>	56	36%	13	8%	85	55%
<i>Syntrophomonadaceae</i>	24	50%	0	0%	24	50%
<i>Bacteroidetes</i>	5	17%	1	3%	24	80%
<i>Proteobacteria</i>	4	14%	6	21%	19	66%
<i>Synergistetes</i>	3	30%	3	30%	4	40%
<i>Spirochaetes</i>	1	13%	1	13%	6	75%
<i>Actinobacteria</i>	0	0%	1	17%	5	83%
<i>Chloroflexi</i>	0	0%	0	0%	6	100%
<i>Euryarchaeota</i>	4	67%	1	17%	1	17%
<i>Tenericutes (Firmicutes)</i>	3	50%	1	17%	2	33%
<i>Verrucomicrobia</i>	0	0%	0	0%	3	100%
<i>Thermotogae</i>	1	50%	1	50%	0	0%
<i>Fibrobactere</i>	0	0%	0	0%	1	100%
<i>Acidobacteria</i>	0	0%	0	0%	1	100%
<i>Chlamydiae</i>	0	0%	0	0%	1	100%
<i>Planctomycetes</i>	0	0%	0	0%	1	100%
<i>TM7</i>	0	0%	1	100%	0	0%

Composition of archaeal community was found to be **resilient**, while bacterial community was more **diverse** due to higher functional variability.

Microbial upgrading populations

Mesophilic community

Thermophilic community

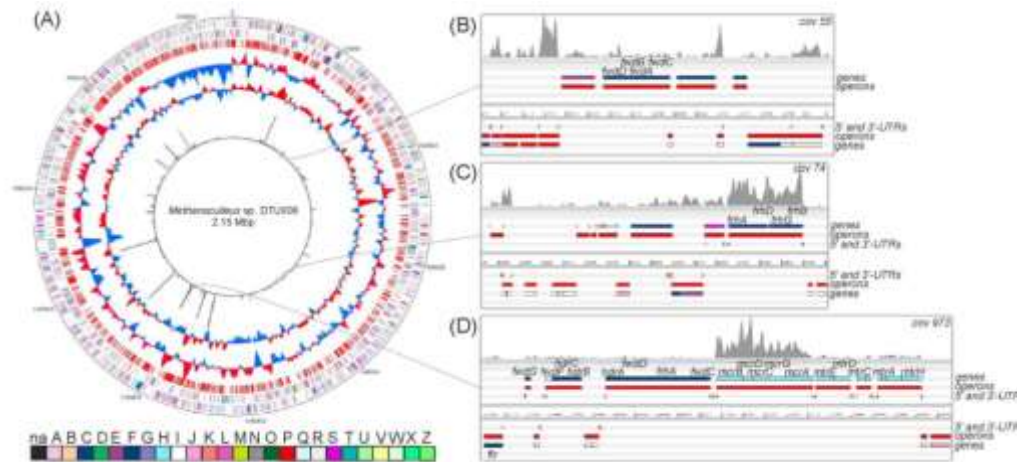


Microbial **changes in abundance** before (light) and after (dark) H_2 addition are represented as circles with areas proportional to **genome coverage**

Microbial upgrading populations

Phylum	Population genome	Taxa	16S rRNA gene	Mesophilic			Thermophilic		
				Before H ₂	After H ₂	fold change	Before H ₂	After H ₂	fold change
Bacteroidetes	DTU134	Rikenellaceae	<i>A. shahii</i> (86%)	38.8	156.6	4.04	1.0	0.5	2.24
Bacteroidetes	DTU002	Bacteroidales	<i>P. propionigenes</i> (85%)	84.0	70.8		2.0	0.4	4.40
Firmicutes	DTU175	Thermoanaerobacteraceae	<i>M. thermoacetica</i> (87%)	34.3	98.4	2.87	0.1	0.3	5.47
Bacteroidetes	DTU135	Bacteroidales	<i>O. hongkongensis</i> (86%)	27.0	19.3	1.40	1.8	0.2	9.38
Bacteroidetes	DTU136	Bacteroidaceae	<i>B. clarus</i> (87%)	13.4	29.9	2.23	0.7	0.2	3.54
Firmicutes	DTU220	Syntrophomonadaceae	nd	3.9	32.6	8.41	1.6	2.1	1.37
Firmicutes	DTU224	Erysipelotrichaceae	nd	22.1	4.2	5.26	0.0	0.0	1.88
Bacteroidetes	DTU137	Porphyromonadaceae	<i>T. forsythia</i> (83%)	3.8	20.1	5.34	0.0	0.0	1.15
Acidobacteria	DTU170	Acidobacteriales	<i>A. capsulatum</i> (86%)	7.8	14.3	1.82	0.0	0.0	1.83
Firmicutes	DTU230	Clostridiales	nd	9.5	11.6		0.1	0.5	7.30
Firmicutes	DTU246	Clostridiales	nd	14.7	3.0	4.92	0.4	0.4	1.14
Chloroflexi	DTU159	Chloroflexi	nd	10.6	3.9	2.74	0.2	0.1	3.71
Firmicutes	DTU010	Syntrophomonadaceae	nd	6.8	3.1	2.20	286.2	461.8	1.61
Bacteroidetes	DTU001	Alistipes	nd	0.3	0.1	4.13	158.2	19.5	8.10
Firmicutes	DTU011	Thermoanaerobacteraceae	<i>Th. toyohensis</i> (86%)	0.9	1.3	1.49	68.1	96.0	1.41
Euryarchaeota	DTU006	Methanoculleus	<i>M. marisnigri</i> (87%)	0.2	0.3	1.92	40.4	50.8	
Firmicutes	DTU012	Syntrophomonadaceae	nd	0.0	0.0	1.89	24.9	34.1	1.37
Firmicutes	DTU014	Clostridiales	<i>D. carboxydivorans</i> (85%)	0.0	0.0	1.05	17.3	31.2	1.81
Firmicutes	DTU013	Clostridiaceae	nd	0.0	0.0	1.09	16.4	30.7	1.87
Firmicutes	DTU183	Syntrophomonadaceae	nd	0.0	0.0	1.45	19.4	26.1	1.34
Firmicutes	DTU176	Syntrophomonadaceae	nd	0.0	0.0	1.11	9.5	14.7	1.55
Firmicutes	DTU029	Halothermothrix	nd	0.0	0.0	1.26	5.6	13.1	2.34
Firmicutes	DTU021	Syntrophomonadaceae	nd	0.1	0.1	2.08	9.5	9.0	
Firmicutes	DTU030	Syntrophomonadaceae	nd	0.0	0.0	1.98	8.6	9.3	
Thermotogae	DTU111	Defluviitoga tunisiensis	<i>D. tunisiensis</i> (98%)	0.0	0.0	1.73	12.5	4.6	2.72

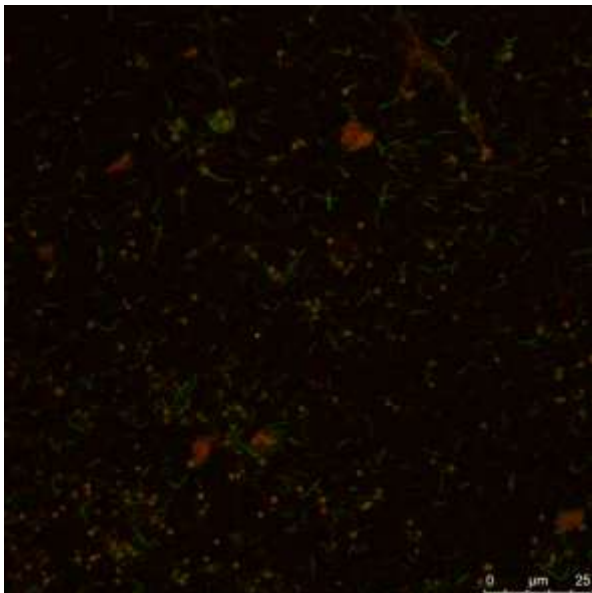
Novel microbial species



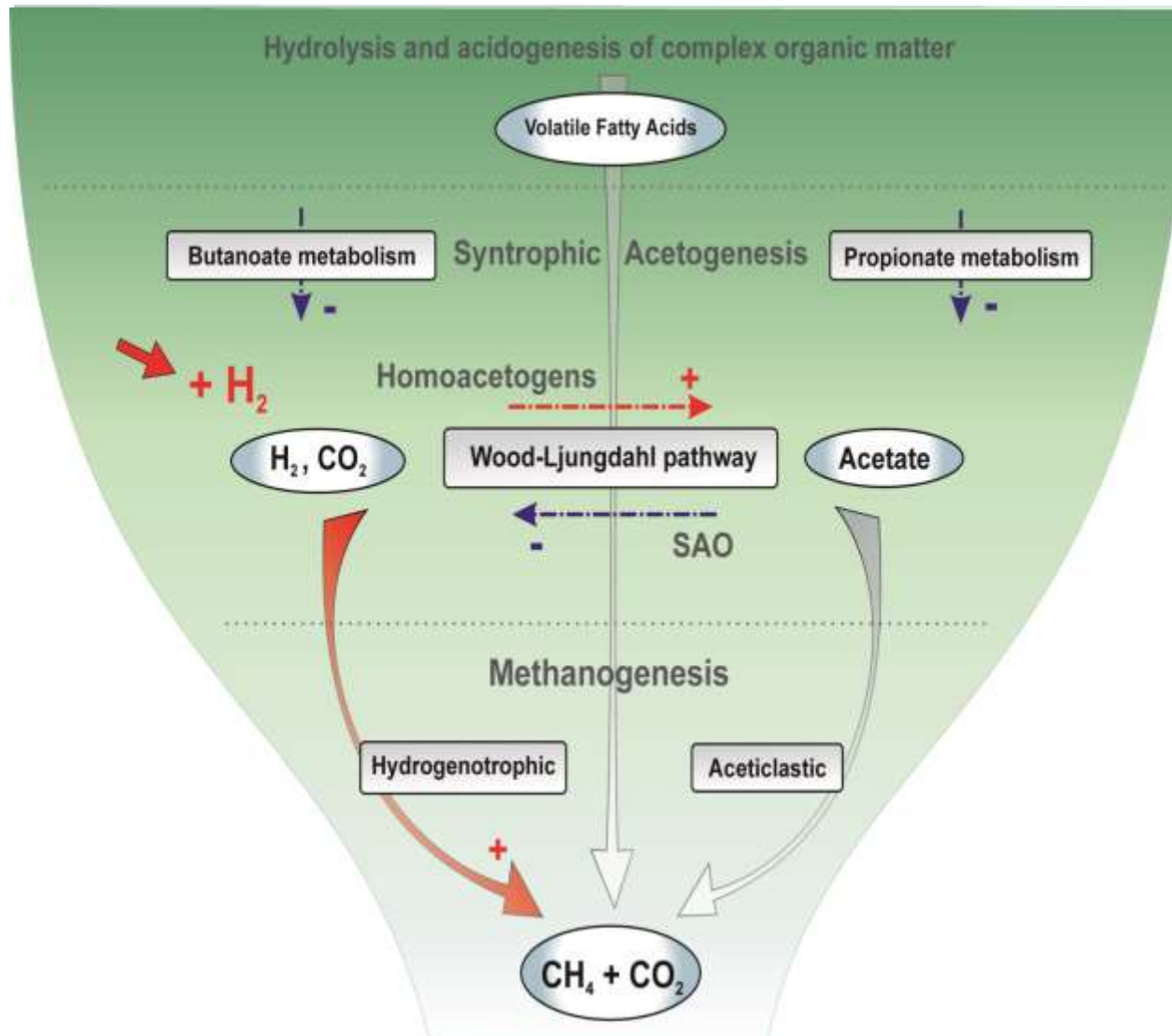
Candidatus Methanoculleus thermohydrogenotrophicum

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%



Anaerobic digestion: the funnel concept



- ✓ Functional classification
- ✓ **Generalist** GBs
- ✓ **Specialist** GBs

Some microbes are **favored** by H₂ addition some other are **inhibited**, at all levels of the funnel, but in particular at the lower levels

Effect of H₂ on syntrophic bacteria

Tentative functional reconstruction of specific population genomes with different responses to H₂ exposure

Population genome	Taxa	Mesophilic		Thermophilic		Propanoate metabolism	Butanoate metabolism	Carbon fixation	Fatty acid degradation	W-L pathway	Fdh
		Before H ₂	After H ₂	Before H ₂	After H ₂						
DTU232	Syntrophomonadaceae	9.30	0.37	0.01	0.00	15	24	28	10	8	1
DTU204	Syntrophomonadaceae	2.42	0.31	0.14	0.10	8	12	22	18	9	4
DTU223	Syntrophomonadaceae	1.26	1.12	1.52	0.76	2	4	18	0	8	3
DTU183	Syntrophomonadaceae	0.01	0.00	19.41	26.06	14	20	32	14	8	3
DTU077	Syntrophomonadaceae	0.01	0.01	0.45	7.39	4	14	23	14	10	4
DTU122	Syntrophomonadaceae	0.00	0.00	0.49	2.19	8	1	30	1	8	5
DTU063	Tepidanaerobacter	0.01	0.00	8.34	1.66	15	10	33	0	8	
DTU021	Syntrophomonadaceae	0.14	0.07	9.47	8.97	10	22	30	21	10	3
DTU236	Syntrophomonadaceae	0.01	0.06	1.17	1.83	18	24	29	5	10	2
DTU093	Syntrophomonadaceae	0.01	0.01	1.23	1.81	16	29	39	2	9	1
DTU245	Syntrophomonadaceae	4.65	8.77	0.00	0.01	20	17	32	9		
DTU190	Syntrophomonadaceae	0.11	0.06	0.46	2.26	24	45	34	25		8
DTU052	Syntrophomonadaceae	0.13	0.09	1.59	3.92	19	35	34	38		9

On average >92% completeness and < 4% contamination

Conclusions

- ✓ Biological biogas upgrading is a feasible **biomethanation technology** leading to more than 96% CH₄ content in the final gas
- ✓ Independently from the H₂ addition **distinct microbial communities** were shaped due to the operational temperature
- ✓ H₂ addition **enriched the hydrogenotrophic** methanogenic culture and promoted the formation of **syntrophic interactions**
- ✓ Novel methanogen species was identified and was proposed as ***Candidatus Methanoculleus thermohydrogenotrophicum***
- ✓ Correlation between **syntrophs response to H₂** addition and their metabolic pathways was established

Teamwork



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Thank you for your attention



SYMBIO – Integration of biomass and wind power for biogas enhancement and upgrading via hydrogen assisted anaerobic digestion -0603-00525B

ENERGINET

BioUpgrade– Ex-situ biogas upgrading through biologically mediated CO₂ reduction, 12465

