

Syngas Fermentation to Ethanol: CODH/AdhE1 genes expression and Microbial community dynamics

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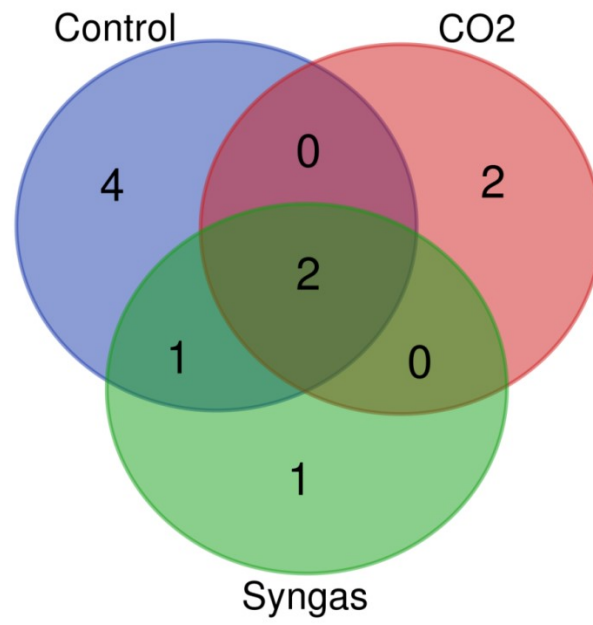
Supplementary Table 1: Taxonomic affiliation of different bands excised from DGGE gel based on V3 region sequence.

DGGE Band	Closed Relative	Phylum	Accession number
Control (C)			
CNTSVM1	<i>Phaeospirillumtilakii</i>	Proteobacteria	NR_108482.1
	<i>Microvirga aerilata</i>	Proteobacteria	NR_114298.1
	<i>Ferrovibrio xuzhouensis</i>	Proteobacteria	NR_145543.1
CNTSVM2	<i>Reyranella terrae</i>	Proteobacteria	NR_157018.1
	<i>Hyphomicrobium methylovorum</i>	Proteobacteria	NR_113655.1
	<i>Clostridium polynesiense</i>	Firmicutes	NR_144690.1
CNTSVM3	<i>Enhydrobacteraerosaccus</i>	Proteobacteria	NR_113385.1
	<i>Reyranella massiliensis</i>	Proteobacteria	NR_116005.1
	<i>Niveispirillum fermenti</i>	Proteobacteria	NR_126263.1
CNTSVM4	<i>Chitinimonas taiwanensis</i>	Proteobacteria	NR_029099.2
	<i>Lysobacter rhizophilus</i>	Proteobacteria	NR_152715.1
	<i>Silanimonas lenta</i>	Proteobacteria	NR_025815.1

CNTSVM6	<i>Xanthomonas albilineans</i>	Proteobacteria	NR_112570.1
	<i>Pseudoxanthomonaskalamensis</i>	Proteobacteria	NR_043110.1
	<i>Lysobacter</i>	Proteobacteria	NR_156843.1
CNTSVM7	<i>Acinetobacter baylyi</i>	Proteobacteria	NR_115042.2
	<i>Marinomonasvaga</i>	Proteobacteria	NR_114183.1
	<i>Prolinoborus fasciculus</i>	Proteobacteria	NR_104948.1
CNTSVM8	<i>Thermovenabulumgondwanense</i>	Firmicutes	NR_104554.1
	<i>Fimbriimonasginsengisoli</i>	Armatimonadetes	NR_121726.1
CNTSVM10	<i>Azospirarestricta</i>	Proteobacteria	NR_044023.1
	<i>Nitrosomonas nitrosa</i>	Proteobacteria	NR_104819.1
	<i>Nitrosomonas communis</i>	Proteobacteria	NR_119314.1
CNTSVM11	<i>Aminobacteriumcolombiense</i>	Synergistetes	NR_074624.1
	<i>Desulfothermobacteracidiphilus</i>	Firmicutes	NR_159908.1
	<i>Aminobacteriumcolombiense</i>	Synergistetes	NR_027531.2
CNTSVM12	<i>Xanthobacter flavus</i>	Proteobacteria	NR_113665.1
	<i>Azorhizobiumcaulinodans</i>	Proteobacteria	NR_119216.1
	<i>Methylophilacapsulata</i>	Proteobacteria	NR_024843.1
CNTSVM13	<i>Mobilicoccusaccae</i>	Actinobacteria	NR_157612.1
	<i>Parvibaculumlavamentivorans</i>	Proteobacteria	NR_074262.1
	<i>Ferrovibriodenitrificans</i>	Proteobacteria	NR_117302.1
CNTSVM14	<i>Fudaniajinshanensis</i>	Actinobacteria	NR_164622.1
	<i>Actinotignumschaalii</i>	Actinobacteria	NR_119244.1
	<i>Desulfotomaculumruminis</i>	Firmicutes	NR_074605.1

CO ₂ Culture			
CO2SVM1	<i>Clostridium peptidivorans</i>	Firmicutes	NR_025019.1
	<i>Clostridium polynesiense</i>	Firmicutes	NR_144690.1
	<i>Caloramatorboliviensis</i>	Firmicutes	NR_108460.1
CO2SVM2	<i>Desulfotomaculumreducens</i>	Firmicutes	NR_102770.2
	<i>Caldilineatarbellica</i>	Chloroflexi	NR_117797.1
	<i>Pelotomaculumthermopropionicum</i>	Firmicutes	NR_074685.1
CO2SVM4	<i>Mycobacterium shigaense</i>	Actinobacteria	NR_146370.1
	<i>Mycobacterium parascrofulaceum</i>	Actinobacteria	NR_118110.1
	<i>Arcanobacteriumcanis</i>	Actinobacteria	NR_117199.1
CO2SVM5	<i>Clostridium magnum</i>	Firmicutes	NR_119084.1
	<i>Acetoanaerobiumsticklandii</i>	Firmicutes	NR_102880.1
	<i>Clostridium carboxidivorans</i>	Firmicutes	NR_104768.1
CO2SVM6	<i>Clostridium kogasensis</i>	Firmicutes	NR_136452.1
	<i>Clostridium tyrobutyricum</i>	Firmicutes	NR_044718.2
	<i>Clostridium aciditolerans</i>	Firmicutes	NR_043557.1
CO2SVM7	<i>Carboxydothemusferrireducens</i>	Firmicutes	NR_118851.1
	<i>Carboxydothemuspertinax</i>	Firmicutes	NR_113202.1
CO2SVM8	<i>Carboxydothemuspertinax</i>	Firmicutes	NR_113201.1
	<i>Endomicrobiumproavitum</i>	Elusimicrobia	NR_156018.1
	<i>Carboxydothemushydrogenoformans</i>	Firmicutes	NR_074395.1
Syngas Culture			
SYNSVM4	<i>Anaerococcuspaceans</i>	Firmicutes	NR_125573.1

	<i>Corynebacterium deserti</i>	Actinobacteria	NR_118005.1
	<i>Achromobacterxylosoxidans</i>	Proteobacteria	NR_118403.1
SYNSVM5	<i>Bacteroides massiliensis</i>	Bacteroidetes	NR_112938.1
	<i>Lactobacillus ginsenosidimutans</i>	Firmicutes	NR_132607.1
	<i>Bacteroides massiliensis</i>	Bacteroidetes	NR_042745.1
SYNSVM6	<i>Clostridium drakei</i>	Firmicutes	NR_044942.1
	<i>Clostridium amylolyticum</i>	Firmicutes	NR_044386.1
	<i>Sandaracinusamylolyticus</i>	Proteobacteria	NR_118001.1
SYNSVM7	<i>Clostridium beijerinckii</i>	Firmicutes	NR_113388.1
	<i>Clostridium putrefaciens</i>	Firmicutes	NR_119282.1
	<i>Clostridium butyricum</i>	Firmicutes	NR_113244.1
SYNSVM9	<i>Rhodococcuspsychrotolerans</i>	Actinobacteria	NR_164891.1
	<i>Bdellovibrioexovorus</i>	Proteobacteria	NR_102876.1
	<i>Clostridium aurantibutyricum</i>	Firmicutes	NR_044841.2
SYNSVM10	<i>Corynebacterium aurimucosum</i>	Actinobacteria	NR_028941.1
	<i>Xylanimonascellulosilytica</i>	Actinobacteria	NR_028828.1
	<i>Actinomadurakeratinilytica</i>	Actinobacteria	NR_044544.1



Supplementary Fig. 1: Venn diagram showing the unique and common OTUs

Partial sequences of expressed genes in WLP pathway

cooC2

AATAGCATTAACAGGAAAAGGTGGTGGTGGTAAAACAACCATCTCCGCAAGTTTAAGCCGATAT
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GCCGATATTCCCGAACGTTACGCAAAGGAATTTAATGGGGTCAAGCTACTAACAAATGGGAACTG
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TTTGGTATTGTACCAAAAAGATGTGGTTATCATGGATATGGAAGCTGGAATTGAACACTTGGGT
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AAATAAAATCCGGAATGACGGAGATATCGCCTTTTTTAAAAGA

Fdhl

GTTAAGGATGGAAAAATTGTAAGAGCGGAACCTGCAAATGGTGATAATAATGAAGGAAAATTAT
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AGGCT

AdhE1

TAGAAGCATACGTGTCAGTACTTGCATCAGAATATACTAATGGATTAGCACTTGAAGCAATAAG
GTTAATATTCAAGTATTTACCACAGGCATACGAGGAAGGCACAATAATGTGAAGGCAAGAGAA
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