

SUPPLEMENTAL INFORMATION

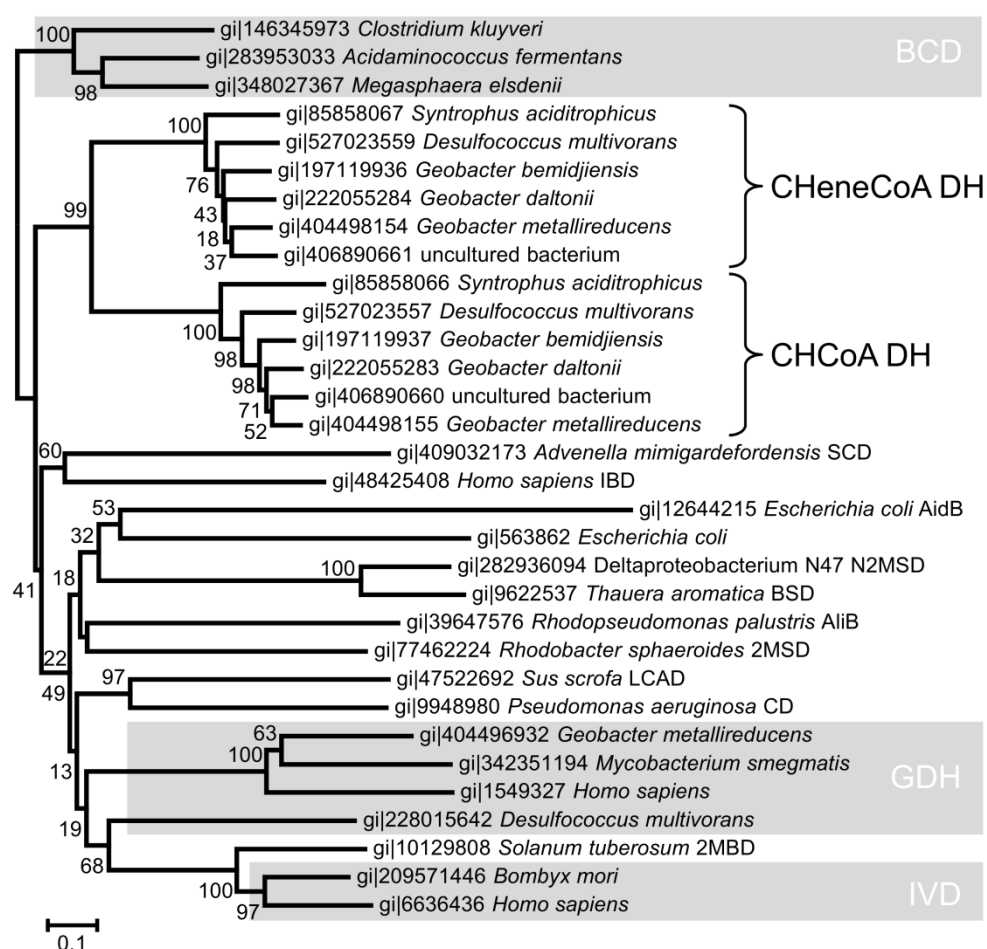


Figure S1. Neighbour-joining phylogenetic tree of a representative selection of biochemically characterized acyl-CoA dehydrogenases including the two acyl-CoA dehydrogenases involved in the cyclohexanecarboxylic acid fermentation of axenically growing *Syntrophus aciditrophicus*. The putative CHCoA and CHeneCoA dehydrogenases show sequence similarities of >60 % compared to the ChCoA and Ch1enCoA dehydrogenase, respectively. The subbranch of well described butyryl-CoA dehydrogenases was used as outgroup. Abbreviations: BCD, butyryl-CoA dehydrogenase; SCD, 3-Sulfinopropionyl-CoA desulfonase; IBDH, Isobutyryl-CoA dehydrogenase; IVD, Isovaleryl-CoA dehydrogenase; 2MBD, 2-Methylbutyryl-CoA dehydrogenase; GDH, Glutaryl-CoA dehydrogenase; CD, Citronellyl-CoA dehydrogenase; LCAD, Long chain acyl-CoA dehydrogenase; 2MSD, 2-Methylsuccinyl-CoA dehydrogenase; AliB, ChCoA dehydrogenase; BSD, Benzylsuccinyl-CoA dehydrogenase; N2MSD, Naphthyl-2-Methylsuccinyl-CoA dehydrogenase; CBD, Crotonobetainyl-CoA dehydrogenase; AidB, Catalytically inefficient acyl-CoA dehydrogenase homolog involved in DNA repair. Bootstrap values are given for 1000 repetitions are given.

Table S1. List of primers used for cloning genes Champion pET101 directional Topo expression kit.

primer	sequence (5' to 3')	target gene	annotation
<i>Gmet_3304_For</i>	CACCATGGAAAGCGTAAAAAATGCCAAG	<i>Gmet_3304</i>	succinyl:benzoate coenzyme A transferase
<i>Gmet_3304_rev</i>	AATGCGGTTTCATCCTTCTGGC		
<i>Gmet_3306_For</i>	CACCATGAAACATCTTACCGAAGAACAG	<i>Gmet_3306</i>	short-chain acyl-CoA dehydrogenase
<i>Gmet_3306_rev</i>	CGGGAACAACAGGGCCCTCC		
<i>Gmet_3307_For</i>	CACCATGTTTAATACCAGCGAAGAAGTAC	<i>Gmet_3307</i>	short-chain acyl-CoA

<i>Gmet_3306_rev</i>	AGCGGCCTCTTTCAGGATCTC		dehydrogenase
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Table S2. List of used primers during differential transcription analysis.

primer	sequence (5' to 3')	target gene	annotation
dpcr_fwd	GGGAGACCTACGGTATTGA	<i>Gmet_0899</i>	Delta-1-pyrroline-5-carboxylate reductase
dpcr_rev	GATGGAGATGACGAGCTTCC		
mreb_fwd	AAAGTCCACAACCGCAAGAC	<i>Gmet_0918</i>	rod shape-determining protein MreB
mreb_rev	GACTCGGCAGACTCCTTGAC		
sdh_fwd	GGTTGGAGTAGACGCTCTCG	<i>Gmet_2397</i>	succinate dehydrogenase/fumarate reductase, cytochrome b558 subunit
sdh_rev	GCGGCGATATAGAGAACTGC		
atpsb_fwd	TGCCTCCCATCTACAACGCC	<i>Gmet_3406</i>	F0F1 ATP synthase subunit beta
atpsb_rev	TGGGCAACTTCGAGCACCAG		
mbptp_fwd	CCGATCCCTACATCATCGTC	<i>Gmet_3239</i>	membrane-bound proton-translocating pyrophosphatase
mbptp_rev	CCCTTGATTTACGGAAGTGC		
3305_fwd	CCACAACCTGATCGACTGTGA	<i>Gmet_3305</i>	enoyl-CoA hydratase/isomerase
3305_rev	GTTGTAGAGCCCTTCCGCC		
3306_fwd	CCGACCTCCTTGCCATGAAA	<i>Gmet_3306</i>	short-chain acyl-CoA dehydrogenase
3306_rev	GAGCCGTTGGTGATGAAGCA		
bamA_fwd	CCACAATTTGATCGACCGTGAG	<i>Gmet_2088</i>	6-oxocyclohex-1-ene-1-carbonyl-CoA hydratase
bamA_rev	CTCTGCCACACTGCCGTC		
bamB-1_fwd	CCGGGCCTTCAACATCAGAA	<i>Gmet_2087</i>	benzoyl-CoA reductase
bamB-1_rev	CCTTCTCAAGCTCGGGGAAC		
bamM_fwd	CCGAGATGGTCACCGAGATC	<i>Gmet_2075</i>	glutaryl-CoA dehydrogenase
bamM_rev	CGGAGAGTAGTTCCCCTGGT		
bamQ_fwd	TCCGCCGTCTGACAATGAAG	<i>Gmet_2151</i>	6-hydroxycyclohex-1-ene-1-carbonyl-CoA dehydrogenase
bamQ_rev	CGCCATCGTAATAGAAGCCCA		