

Organism name	% BBH ^a	% CDS in synteny ^b	Properties ^c
<i>Kuenenia stuttgartiensis</i> [CT030148, CT573074, CT573073, CT573072, CT573071]	35.7	-	Anaerobic , called anammox for "anaerobic ammonium oxidation" : The anammox reaction, which transforms ammonia and nitrites into nitrogen gas under anaerobic conditions, is a major element of the nitrogen cycle.
<i>Thermoanaerobacter tengcongensis</i> MB4 [NC_003869]	33.8	14,8	Anaerobic ; The bacterium produces acetate and ethanol from glucose and cannot degrade xylan and cellulose. Its genome has one of the most biased leading strand distributions of genes.
<i>Geobacter metallireducens</i> GS-15 [NC_007517]	33.4	14,6	Anaerobic ; couples the oxidation of organic molecules to the reduction of iron by using insoluble Fe (III) as an electron acceptor under anaerobic conditions. This bacterium plays an important part of the nutrient cycling in aquatic environments. The cell can also use uranium and plutonium
<i>Pelobacter carbinolicus</i> DSM 2380 [NC_007498]	32.8	15,6	Anaerobic ; can ferment ethanol in the presence of hydrogen-utilizing bacteria via interspecies hydrogen transfer. The utilization of hydrogen reduces the hydrogen partial pressure making ethanol fermentation by <i>Pelobacter carbinolicus</i> energetically favorable. <i>Pelobacter carbinolicus</i> is also able to grow using iron and sulfur as terminal electron acceptors.
<i>Pelobacter propionicus</i> DSM 2379 [NZ_AAJH]	32.8	14,3	Anaerobic . This species is ubiquitous in both marine and fresh water, and in anaerobic sediments. It is able to convert the unsaturated hydrocarbon acetylene to acetate and ethanol via acetylaldehyde as an intermediate. These microorganisms may survive in some sediments as an Fe(III) or elemental sulfur reducer as well as growing fermentatively as an ethanol-oxidizing acetogen.
<i>Syntrophobacter fumaroxidans</i> MPOB [NC_008554]	32.4	14,9	Anaerobic ; syntrophic propionate-oxidizing bacterium isolated from granular sludge from an anaerobic sludge bed reactor treating sugar-beet processing wastewater.
<i>Syntrophus aciditrophicus</i> SB [NC_007759]	32.1	15,2	Anaerobic ; able to ferment benzoate when grown in co-culture with hydrogen-consuming methanogens (syntrophic metabolism).
<i>Carboxydotherrmus hydrogenoformans</i> Z-2901 [NC_007503]	30.9	14,8	Anaerobic . This organism is extremely thermophilic and can utilize carbon monoxide as the sole carbon and energy source under anaerobic conditions with the production of carbon dioxide and hydrogen gas.
<i>Syntrophomonas wolfei</i> subsp, <i>wolfei</i> str, Goettingen [NC_008346]	29.8	13,8	Anaerobic . It is the only bacterium known to produce energy from anaerobic degradation of saturated four to eight carbon fatty acids with protons serving as the electron acceptor. The cells have an unusual multilayered gram-negative cell wall. <i>Syntrophomonas wolfei</i> grows in coculture with <i>Methanospirillum hungatei</i> .

Supplementary Table 2 : Similarity results between *C. acidaminovorans* and anaerobic bacteria, known or not to live in syntrophic interactions.

^a %BBH, orthologous relations between *C. acidaminovorans* and one of the 9 genomes showing the highest similarity results. They are defined as gene couples satisfying a blastP alignment threshold of at least 30% sequence identity on 80% of the length of the smallest protein.

^b % CDS in synteny, these relations are used to search for conserved gene clusters, e.g. synteny groups (syntons). All possible kinds of chromosomal rearrangements are allowed (inversion, insertion/deletion). A gap parameter, representing the maximum number of consecutive genes which are not involved in a synteny group, is set to five genes.

^c Properties, information on bacterial genomes have been found on the NCBI Web site : <http://www.ncbi.nlm.nih.gov/genomes/lproks.cgi>.