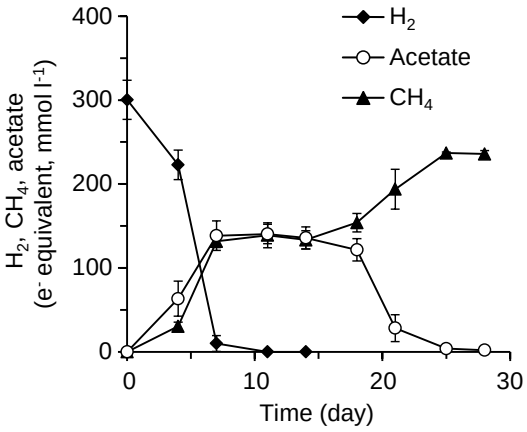

Fig. S1 Metabolic profiles of the H_2-enrichments with H_2 gas as the sole electron donor. The amount of each metabolite was normalized to electron equivalents in the unit of mmol e^- per liter of culture medium. Data are presented as the means of three independent cultures, and error bars represent standard deviations.

Table S1. The bacterial phylotypes detected in the enrichment cultures.

Phylogenetic group (Phylum)	Phylotype	Closest relative (Similarity, %)	Number of clones		
			H_2	Fe^0	Fe^0+BES
Firmicutes	CB01	NR_025417 *Sporomusa sphaeroides* strain DSM 2875(99)	9	4	10
	CB02	NR_026322 *Clostridium pascui* strain DSM 10365 (99)		3	2
	CB03	AF295656 *Desulfotomaculum* sp. 175 (99)	4		
	CB04	AB538430 *Clostridium subterminale* strain JCM 1417 (99)		2	2
	CB05	Y11575 *Desulfotomaculum thermosapovorans* (97)	2		
	CB06	AB490809 *Christensenella minuta* (91)	2		
	CB07	HF546400 *Oxobacter pfennigii* DSM 3222^T (96)	2		
	CB08	EU887828 *Clostridium lituseburense* strain H17 (99)		1	1
	CB09	HQ646364 *Turicibacter sanguinis* strain 111732/2010 (88)	1		
	CB10	DQ117468 *Gracilibacter thermotolerans* strain JW/YJL-S1 (93)	1		
	CB11	CP003629 *Desulfosporosinus meridiei* DSM 13257 (89)	1		
	CB12	AY571338 *Sedimentibacter hongkongensis* strain KI (99)	1		
	CB13	NR_074793 *Oscillibacter valericigenes* Sjm18-20 (99)	1		
	CB14	NR_041236 *Lutispora thermophila* strain EBR46 (97)	1		
	CB15	NR_043579 *Desulfotomaculum arcticum* strain 15 (96)	1		
	CB16	AB298768 *Clostridiaceae* bacterium FH052 (96)	1		
	CB17	NR_026409 *Desulfotomaculum guttoideum* strain DSM 4024 (99)			1

Table S1. Continued.

Phylogenetic group (Phylum)	Phylotype	Closest relative (Similarity, %)	Number of clones		
			H_2	Fe^0	Fe^0+BES
Proteobacteria	CB18	NR_029118 *Desulfovibrio putealis* strain B7-43 (97)		34	9
	CB19	NR_043620 Desulfovibrio carbinoliphilus strain D41 (98)	1		
	CB20	AJ582758 *Desulfovibrio idahonensis* strain CY2 (99)	1		
Bacteroidetes	CB21	AB623230 *Bacteroidetes* bacterium 4F6B (90)	3		
	CB22	AB787271 *Bacteroides* sp. UasXn-3 (98)	2		
	CB23	AJ229237 Bacteria from anoxic bulk soil (strain XB45) (96)	2		
	CB24	AB239481 Rumen bacterium R-7 (95)	1		
	CB25	AB611036 *Bacteroidetes* bacterium RL-C (91)	1		
	CB26	AB078043 *Flavobacterium johnsoniae* IFO 15970 (99)		1	
Total			39	45	24

Table S2. The archaeal phylotypes detected in the enrichment cultures.

Phylogenetic group (Family)	Phylotype	Closest relative (Similarity, %)	Number of clones	
			H_2	Fe^0
Methanosarcinaceae	CA01	CP000099 *Methanosarcina barkeri* strain Fusaro (99)	26	7
Methanomicrobiaceae	CA02	NR_074174 *Methanoculleus marisnigri* JR1 (97)		17
	CA03	NR_074174 *Methanoculleus marisnigri* JR1 (99)	2	7
Methanobacteriaceae	CA04	AF028688 *Methanobacterium bryantii* strain RiH2 (99)	4	
Total			32	31