SUPPLEMENTARY MATERIAL

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Anaerobic degradation of the plant sugar sulfoquinovose concomitant with H_2S production: *Escherichia coli* K-12 and *Desulfovibrio sp.* strain DF1 as co-culture model

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Table S1. Stoichiometry of fermentation of glucose and of SQ by *E. coli* K-12

	Fermentative growth in 10 ml 6 mM glucose medium	**Fermentative growth in 10 ml 12 mM SQ medium**
Total protein [mg]	0.724	0.556
Total cell dry mass [mg]	1.45	1.11
Assimilation equation	17 $C_6H_{12}O_6$ → 24 <$C_4H_7O_3$> + 6 CO_2 + 18 H_2O	17 $C_6H_{11}O_8S^-$ + H_2O → 10 <$C_4H_7O_3$> + 17 $C_3H_7O_5S^-$ + 11 CO_2
Substrate assimilation [mol/g dry mass]	6.9	16.6
Total substrate used [µmol]	44	117
Assimilated substrate [µmol]	10.0	18.5
Dissimilated substrate [µmol]	34.0	98.5
Succinate produced [µmol]	6	12
Formate produced [µmol]	58	44
Acetate produced [µmol]	31	51
Ethanol produced [µmol]	11	0
DHPS produced [µmol]	0	96
dissimilation equation	34.0 glucose → 6 succinate + 58 formiate + 31 acetate + 11 ethanol	98.5 SQ → 95.9 DHPS + 12 succinate + 44 formiate + 51 acetate
total carbon in dissimilated substrate [µmol]	204.1	591.2
total carbon in fermentation products [µmol]	166.0	482.0
Carbon recovery [%]	**81**	**82**
Molar growth yield for dissimilated substrate [g dry mass/mol diss. substrate]	**42.6**	**11.3**
Electrons gained by carbon oxidation	1 glucose → 6 CO_2 + 24 e^- 1 SQ → 6 CO_2 + 24 e^-	1 formate → 1 CO_2 + 2 e^- 1 ethanol → 2 CO_2 + 12 e^- 1 DHPS → 3 CO_2 + 14 e^-
Electrons in dissimilated substrate	816	2365
Electrons in fermentation products	580	2008
Electron recovery [%]	**71**	**85**

Table S2: PCR primers used for cloning

Enzyme	Gene (IMG locus tag)	forward Primer (restriction: NdeI)	reverse primer (restriction: XhoI)
DHPS dehydrogenase	Ga0134130_130620	*CGT***CATATG**CAGATCGGATTTATCGGC	*ATT***CTCGAG**ATCCGGCTCTTCCACCTCAA
SLA dehydrogenase	Ga0134130_130623	*CGT***CATATG**TTGACAACATTCGAACTCATGCG	*ATT***CTCGAG**GGTTGCCCTATCCTTATCCGTTTTG
SuyA	Ga0134130_10402	*CGT***CATATG**TCTATCCAATTTATTGTCCACGAA	*ATT***CTCGAG**GTCCATTCTCACGCCGATACC
SuyB	Ga0134130_10403	*CGT***CATATG**AAGACCAAGTTCATGGGGTATCG	*ATT***CTCGAG**AACCGCCGGCCCGACTAC

Letters in bold, restriction enzyme recognition site;
letters in italic, base pairs added for restriction efficiency.

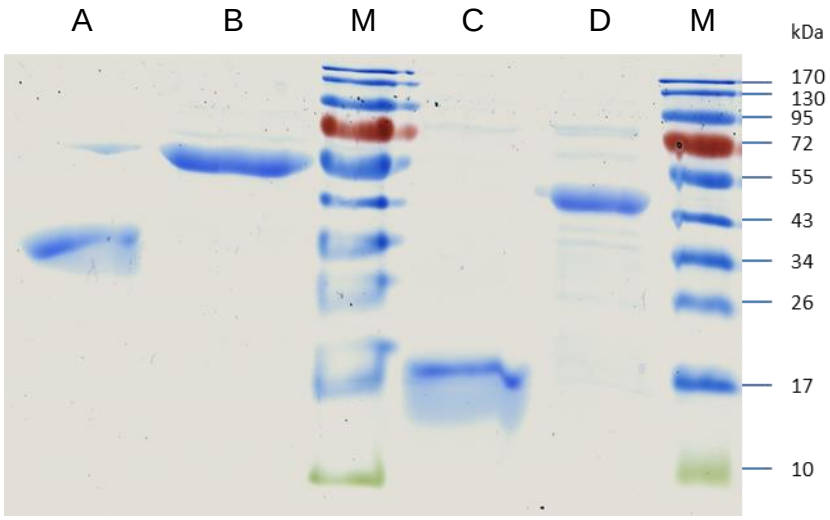

Fig S1: Evaluation of the purity of recombinant His-tagged proteins by SDS-PAGE
(A) DHPS dehydrogenase (locus tag Ga0134130_130620, calculated mass 33.3 kDa);
(B) SLA dehydrogenase (Ga0134130_130623, 54.9 kDa);
(C) SuyA (Ga0134130_10402, 14.5 kDa);
(D) SuyB (Ga0134130_10403, 45.9 kDa);
(M) molecular mass marker.