

Zedelius et al.**Table S2.** Genome-based TBLASTN-search for genes (*bssA* and homologues) that may encode fumarate-dependent glycy radical enzymes for anaerobic alkane activation.

Query				Best TBLASTN-hit in genome of strain HdN1			
Gene name	Acc. no.	Amino acids	Predicted function, organism	Position	E-value	Identities	Positives
<i>bssA</i>	CAI07159	861	α -Subunit, benzylsuccinate synthase, denitrifying Betaproteobacterium strain EbN1	762,138 – 761,950	1.2	20/70 (29%)	30/70 (43%)
<i>masD</i>	CAO03074	839	α -Subunit, (1-methylalkyl)succinate synthase, denitrifying Betaproteobacterium strain HxN1	1,510,228 – 1,510,115	0.3	16/38 (42%)	24/38 (63%)
<i>nmsA</i>	CAO72219	828	α -Subunit, (2-naphthylmethyl)succinate synthase, sulfate-reducing Deltaproteobact. strain NaphS2	1,591,168 – 1,591,049	1.1	15/40 (38%)	20/40 (50%)
<i>dhaB1</i>	CAJ67970	790	Glycerol dehydratase, <i>Clostridium difficile</i> 630	235,877 – 235,695	4.1	22/73 (30%)	31/73 (42%)
<i>pflB</i>	P09373	760	Pyruvate formate lyase, <i>Escherichia coli</i> K12	2,685,988 – 2,686,473	0.27	41/170 (24%)	74/170 (44%)
<i>nrdD</i>	P28903	712	Anaerobic ribonucleotide reductase, <i>Escherichia coli</i> K12	1,500,318 – 1,500,040	2.1	25/95 (26%)	41/95 (43%)

TBLASTN was performed as described by Altschul, S.F., Madden, T.L., Schaffer, A.A., Zhang, J., Zhang, Z., Miller, W., and Lipman, D.J. (1997) Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. *Nucleic Acids Res* **25**: 3389–3402.