**Supplementary material**

**Fig. S1.** Growth of culture 1MN with 30 mM Fe(OH)3 as electron acceptor in medium reduced with 0.7 mM Na2S in the absence of an organic carbon source. A) Time series of Fe(II) (circles) and SO42- (triangles) in active incubations (filled symbols) compared to abiotic controls (open symbols). Error bars represent standard deviations of two biological replicates. B) Electropherogram of FAM-labelled 16S rRNA gene amplicons from DNA extracts of one replicate culture shown in A) digested with the restriction enzyme MSPI.



**Fig. S2 (A)** total ion chromatogram of metabolites (derivatized with BSTFA) extracted from culture 1-MN cultivated with 1-methylnaphthalene dissolved in HMN. Mass spectra profiles of **(B)** 1-naphthoic acid; **(C)** 3,4-dihydroxybutanoic acid; and **(D)** benzophenone.



**Fig. S3.** Bacterial 16S rRNA gene T-RFLP fingerprint of enrichment culture 1MN cultivated with naphthalene (upper panel), 2-methylnaphthalene (middle panel), and 1-methylnaphthalene (lower panel) expressed as relative abundance, measured as a percentage of total peak height of a given restriction fragment. Time of culture cultivation is indicated in brackets.



Relative abundance, %

**Supplementary Table S1.**

Specifications of assembled 16S rRNA gene contigs from amplicon sequencing via Seqman II software 

**Assembled 16S rRNA gene sequences from amplicon sequencing of enrichment 1MN**

>Seq1

TACTCTCGTGAGAGTTTGATCMTGGCTCAGGACGAACGCTGGCGGCGTGCCTAACACATGCAAGTCGCACGGTTCTGGGGGCTGGAAGCTAGGGGCTAGAGGCTGGAAAAAGGGCAGGTATTGGCAAAGCCGATGCCAACGAGGAATCCAGCATCAAG

CATCCRGCTTCCAGCTTCCAGGGCAGTGGCGGACGGGTGAGTAACACGTGGATAACCTACCCTTCAGACCGGGATAACCCTGGGAAACCGGGGCTAATACCGGATACGTTCCTGTTGGGGCATCCTGACGGGAAGGAAGGCGGCCTCTGGGAAACCAA

GCTGTCGCTGAAGGATGGGTCCGCGGCCCATTAGCTAGTTGGTGAGGTAAAGGCTCACCAAGGCGACGATGGGTAGCCGGCCTGAGAGGGTGGCCGGCCACACTGGGACTGAGATACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATCTTGCG

CAATGGGGGAAACCCTGACGCAGCGACGCCGCGTGGGTGAAGAAGGCCTTCGGGTTGTAAAGCCCTGTCATAGGGGACGAAGTCTGTAGGGTGAATAGCGCTACAGGTGACGGTACTCTAAGAGGAAGCCCCGGCTAACTACGTGCCAGCMGCCGCGG

TAATACACGAGAGTA

>Seq3

TACTCTCGTGAGAGTTTGATCCTGGCTCAGGACGAACGCTGGCGGCGTGCCTAACACATGCAAGTCGCACGGTTCTGGG

GGCTGGAAGCTAGGGGCTAGAGGCTGGAAAAAGGGCAGGTATTGGCAAAGCCGATGCCAACGAGGAATCCAGCATCAAG

CATCCGGCTTCCAGCTTCCAGGGCAGTGGCGGACGGGTGAGTAACACGTGGATAACCTACCCTTCAGACCGGGATAACC

CTGGGAAACCcGGGGCTAATACCcGGATACGTTCCTGTTGGGGCATCCTGACGGGAaGgAAGGCGGCcTCTGGGAACCA

GCTGTCGCTGAAGGATGGGTCCGcGGCCCATTAGCTAGTTGGTGAGGTAAAGGCTCACCAAGGCGAcGaTGGGTAGCCG

GCCTGAGAGGGTGGCCGGCCACACTGGGACTGAGATACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATCTTGCG

CAATGGGGGAAACCCTGACGCAGCGACGCCGCGTGGGTGAAGAAGGCCTTCGGGTTGTAAAGCCCTGTCATAGGGGACG

AAGTCTGTAGGGTGAATAGCGCTACAGGTGACGGTACTCTAAGAGGAAGCCCCYGGCTAACTACGTGCCAGCMGCCGCG

GTAATACACGAGAGTA

>Seq4

TACTCTCGTGAGARTTTGATCCTGGCTCAGGACGAACGCTGGCGGCGTGCCTAACACATGCAAGTCGCACGGTTCTGGG

GGCTGGAAGCTAGGGGCTAGAGGCTGGAAAAAGGGCAGGTATTGGCAAAGCCGATGCCAACGAGGAATCCAGCATCAAG

CATCCGGCTTCCAGCTTCCAGGGCAGTGGCGGACGGGTGAGTAACACGTGGATAACCTACCCTTCAGACCcGGGATAAC

CCcTGGGAAAaCCcGGGGCTAATACCGGATACGTTCCTGTTGGGGCATCCTGACGGGAAGGAAGGCGGCCTCTGGGAAA

CCAAGCTGTCGCTGAAGGATGGGTCCGCGGCCCATTAGCTAGTTGGTGAGGTAAAGGCTCACCAAGGCGACGATGGGTA

GCCGGCCTGAGAGGGTGGCCGGCCACACTGGGACTGAGATACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATCT

TGCGCAATGGGGGAAACCCTGACGCAGCGACGCCGCGTGGGTGAAGAAGGCCTTCGGGTTGTAAAGCCCTGTCATAGGG

GACGAAGTCTGTAGGGTGAATAGCGCTACAGGTGACGGTACTCTAAGAGGAAGCCCCGGCTAACTACGTGCCAGCCGCC

GCGGTAATACACGAGAGTA

>Seq7

TACTCTCGTGAGAGTTTGATCCTGGCTCAGATTGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGAGAAAGGG

ACTTCGGTCCTGAGTAGAGTGGCGCACGGGTGAGTAACGCGTAGGTAATCTACCTCTGCATCTGGGATAACACTTCGAA

AGGGGTGCTAATACCGGATACACTTATGGATCGCAAGGTCTATAAGGAAAGGAGACGATCCGCAAGGAGTTTCTGTGTA

GAGATGAGCCTGCGTCCCATTAGCTAGTTGGTAGGGTAAAGGCCTACCAAGGCGACGATGGGTAGCGGGTCTGAGAGGA

TGATCCGCCACACTGGAACTGAAACACGGACCAGACTCCTACGGGAGGCAGCAGTGAGGAATATTGGACAATGGGCGCA

AGCCTGATCCAGCGACGCCGCGTGAGTGATGAAGGCCTTTGGGTCGTAAAGCTCTGTCAGCAGGGAAGAACGGCCGTGT

GGTTAATACCCATGCGGATTGACGGTACCTGCAGAGGAAGCACCGGCTAACTCCGTGCCAGCMGCCGCGGTAATACACG

AGAGTA

**Figure S4:** Neighbor-Joining dendrogram of putatitve NmsA sequences from 1MN culture grown on 13C10- naphthalene after 97 days of incubations. NmsA-like sequences (labelled with solid circle) were aligned with the AssA/BssA/NmsA sequences of reference strains. The dendrogram was rooted with pyruvate formate lyase (PFL) as outgroup. The accession numbers are given next to representative sequences. Abbreviations: Ass; alkylsuccinate synthase, Mas; methylalkylsuccinate synthase, Bss; benzylsuccinate synthase, and Nms; naphthylmethylsuccinate synthase. The scale bar represents 10% sequence divergence. Bootstrap test (1000 replicates) is shown next to the branches. The scale bar represents 10% sequence divergence.



**Table S2.**

**Sequences of two putative fumarate addition genes encoding proteins**

>NODE\_28\_length\_131Kb\_cov\_148.143\_77; putative fumarate-adding enzyme

MTTPDFKPGPWQEEINVRDFIITNYTPYLGDSSFLTGPTPRTSKLWNKCLELLQEEHRRGGVYKVDARTPITITSHPPGYIDRDLEIIVGLQTDEPLKRAVNPFGGLRMARSACAEFGEDVDPEVCRIFTEYRTTHNDGVFAVYTDEMLALRRSGVITGLPDAYGRGRIIGDYRRVPLYGVDRLIAAKVADIRELPVLQRITRDTIQLREEIRQQVNSLEDLKKMAAGYGFDLSRPAADARDAIQWLYLAYLGAIKQQNGAAMSLGRVSTFLDIYLERDLHAGRLTEEQAQQLIDDFVIKLRLTRHLRTRSYNELFAGDPNWVTEALGGMALDGRPLVTRTTYRFLQTLYNLGPAPEPNMTVLWAADLPRPFKEYCARVSIDTSAVQYENDDLMRPIFGDDYAIACCVSAMRLGKQMQFFGARCNVPKALLLTLNQGVDELTGEKIAPVFYLPRGREEVLDYREVWPAFRRVLDWLASKYVEVMNIIHYMHDKYAYESLQMALHDSLVGRFMAFGLAGLSVTADSLAAMKYARVRARRDDRGIAREFSIEGAYPAFGNNDDRVDRLAVELVQTFMEALRRYPTYRNAVHTLSVLTITSNVVYGHKTGATPDGRQAGEPFAPGANPMHGRDRKGALAALSSVAKIPYQDALDGISYTFSITPRALGPDPQARVDNLIALLDGYFKQGGHHKNVNVFDREILQEAMEHPEKYPQLTIRVSGYAVHFIKLSREQQEEVIARTIF\*

>NODE\_30\_length\_127013\_cov\_150.652\_6; putative fumarate-adding enzyme

MSIAEVKLGEMRLSFQYGKVPKEVTDREIRKEPSKRAKKLRDDYLNAKISLDIEFPYWYTRKWIEEEGQHPLIRRALALKCGFEHLTPMIRAGELLVMQKTRYIRGAFVMPWTANRYPLSIEERMEHEAEEASKMSLEEVVVLAKGGGNVTQSAGNVLSISGRFGIRREEFPMLVEVCRYWKNKSSEDTCFMWAAMHPKYDQYLNMKKAVLMHVDLEYSLRHGRNVVNYQLPLQIGFKGMIDACTEKINANIKEGNADKIAFWKATIIVIEGVQAWIRNYAKEAKRLAAKEKNVKQKQEFEEIAGRLEWIAENPPRTFIEALQLCWTCHIAVVNELQISGLSPGRLGQVLYPFWKQDIKEGRITREQTLEILECMRVKFTEIEIAQSVGTIGLTGGSTFNNLCIGGVNPDGTSAENELEELIIESAMTCATPQPTLTVLYDGKLSEKFLLKAIECNKIGTGYPAWVNNRVAMEYLMKTFKDEGITLEDARAWTIGGCLEIQPGALVNGRLGAGSYSSTGVGFINMPKVLELVLWDGVDPRTKVRVFPPHGSKLETYEELYRAWQQYFYEVVTVFEEMYNLKAAAMFNIDNPIFYSALMADCIEKGLDMDRGGCRYNRTLTTWITGQVNLANSLASIKKNVYEERNFTLDELKNALINNFGYRSALETSQFSLLDQKRETDEWARIHSLCVNAPKYGNDDPYVDEIYKDVIEYWRDVVPQVKDVFGRPWVPCQLSVASHGPLGQACIASADGRLAGLTLADAAQSPYPGTDLNGPYAVLNSAVIIDHSDYQNTQLNLKVHPSCIKGTQGSRKLLELIKAYMDKGGYHIQFNVVDTRMLRDAQDHPENYRDLLVRVAGFTAYWVELSKPIQDEIIARTEYGEI

**Figure S5**

**(A)** Maximum likelihood tree of putative naphthalene carboxylases in 1MN (filled symbols) and N47 (open symbols), and related UbiD family carboxylases selected from NCBI´s non-redundant protein database. The tree represents a consensus tree of 100 bootstrap replicates. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test are shown next to the branches. (**B)** Gene organisation of 1MN genes in comparison to respective blastp hits (same shading) within the naphthalene carboxylase gene cluster in culture N47. The symbols represent the corresponding sequences in (A).



**Table S3.** Gene annotations of scaffold 66 (excerpt) and blastp hits against putative naphthalene carboxylases in enrichment culture N47

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **ORF** | **Uniref\_100** | **Length(aa)** | **Identity(%)** | **Bit-score** | **Annotation** | **Organism** | **Hits in putative naphthalene carboxylation cluster of culture N47** |
|  |  |  |  |  |  |  | NCBI (nr) | Identity (%) | Bit-score |
| 21 | A0A1F9BPN9 | 494 | 55.5 | 545.8 | Phenylphosphate carboxylase subunit beta | Deltaproteobacteria bacterium  | CBX30510 | 32 | 138 |
| 22 | A0A1F9BT12 | 186 | 73.5 | 295.4 | Uncharacterized protein | Deltaproteobacteria bacterium  |  |  |  |
| 23 | A0A1F9BVE3 | 184 | 77.9 | 274.2 | Uncharacterized protein | Deltaproteobacteria bacterium  |  |  |  |
| 24 | UPI00046D15DA | 478 | 61.5 | 622.1 | Phenylphosphate carboxylase subunit alpha | Deferrisoma camini | CBX30514 | 51 | 465 |
| 25 | A0A1F9BV94 | 83 | 45.2 | 69.7 | Uncharacterized protein | Deltaproteobacteria bacterium  |  |  |  |
| 26 | A0A0U2L5W7 | 464 | 43.8 | 388.7 | Phenylacetate-coenzyme A ligase | Paenibacillus naphthalenovorans |  |  |  |
| 27 | D8WWD5 | 202 | 70.5 | 268.9 | Putative UbiX-like carboxylase subunit  | Clostridia bacterium, culture BF |  |  |  |
| 28 | A0A0K1J7B3 | 454 | 43.9 | 350.5 | UbiD-like carboxylase subunit | Azoarcus sp. CIB | CBX30506;CBX30499 | 36; 42 | 303, 318 |
| 29 | A0A1F8TBK2 | 631 | 47.9 | 584.3 | Aldehyde ferredoxin oxidoreductase | Chloroflexi bacterium |  |  |  |
| 30 | A0A1F9BZJ5 | 143 | 54.5 | 148.7 | Uncharacterized protein | Deltaproteobacteria bacterium  |  |  |  |
| 32 | A0A1M5B1M8 | 402 | 35.3 | 211.1 | Glycosyltransferase | Desulfotomaculum australicum  |  |  |  |
| 33 | A0A0M2U3X0 | 732 | 41.0 | 436.0 | Uncharacterized protein | Clostridiales bacterium  |  |  |  |
| 34 | UPI0005550B90 | 126 | 73.6 | 198.4 | S-adenosylmethionine decarboxylase proenzyme | Clostridiales bacterium  |  |  |  |
| 35 | A0A0M2TZA5 | 242 | 35.5 | 134.0 | Uncharacterized protein | Clostridiales bacterium  |  |  |  |
| 36 | F6DRR2 | 272 | 51.1 | 243.8 | Demethylmenaquinone methyltransferase | Desulfotomaculum ruminis  |  |  |  |
| 37 | A0A1F8RSF7 | 337 | 47.1 | 318.9 | Uncharacterized protein | Chloroflexi bacterium  |  |  |  |
| 38 | A0A0M2U4A7 | 313 | 63.6 | 378.6 | UTP--glucose-1-phosphate uridylyltransferase | Clostridiales bacterium  |  |  |  |
| 39 | D3FBQ7 | 388 | 51.2 | 357.5 | Putative glutamate--cysteine ligase 2  | Conexibacter woesei  |  |  |  |
| 40 | A0A0M2U3G3 | 842 | 39.4 | 508.1 | Uncharacterized protein | Clostridiales bacterium  |  |  |  |
| 41 | A0A101ECR7 | 572 | 73.4 | 865.1 | Fumarate reductase, flavoprotein subunit | Moorella sp.  |  |  |  |
| 42 | A0A0T6ARF9 | 144 | 53.4 | 166.4 | Uncharacterized protein | Armatimonadetes bacterium  |  |  |  |
| 43 | A0A0M2U3S6 | 121 | 51.7 | 117.1 | Uncharacterized protein | Clostridiales bacterium  |  |  |  |
| 44 | A0A1F8M755 | 287 | 61.7 | 365.2 | Succinate dehydrogenase iron-sulfur subunit | Chloroflexi bacterium  |  |  |  |
| 45 | A0A1J4WUH9 | 276 | 51.6 | 272.3 | Short-chain dehydrogenase | Parcubacteria group  |  |  |  |
| 46 | UPI0004712E7E | 210 | 45.2 | 185.3 | Transcriptional regulator | Caldicoprobacter oshimai |  |  |  |

**Table S4. Scaffold of sequences of putative naphthalene carboxylase.**

>NODE\_66\_length\_50651\_cov\_165.733\_1

MPILMSLILVSYGIAASVLVSVTRGNGNASLGAWFTAAGMFVTIGVMVTGELLKRIKSQNDKL\*

>NODE\_66\_length\_50651\_cov\_165.733\_2 UniRef100\_M0C2K4 Na+/solute symporter Taxonomy=Archaea; Euryarchaeota; Halobacteria; Natrialbales; Natrialbaceae; Haloterrigena

MMTTVGIISTAFIILYVIIGIWSARTARKSIDEYLAAGRRIGMLVGGFALYAAFCSAMVYVGLPGMTYSLGLNATWQITLGAALGFGLLYFLLAEPVRRFAQFTLVDYLAARYNHLAIRILVALFICGIFTFAIVPQIIGAGLMIGNTFGVSLRTGEIIFAVVLLLYVSIGGMRAVTFSDAFQGIIMFIPLMVVGLLAIAYFGGITPMIAQAAQNNPKIVEPTLPLVSYLGLVFGIALGQSSAAHIIMRISSAASPPVARTTVVVGVVLAVLMYFLASNILGIAAWAVSPGLSKPDNALWAVMEKIIPQWLFGWIIAGLVAAAISTASAMLMGSVASLVSDIYYRVLNPNASPGELYWRGIVITWALGVAAVLVSLFASQQVSWFVAIQSQALGATFFFPLVLGIWWKRTTTAGAISGMVGGLGSFILFTALKILPLYGPVVPAIIISLCLTVLISLLTQPPPVEVVEACCTKLHQRE\*

> NODE\_66\_length\_50651\_cov\_165.733\_3 UniRef100\_A0A0M2U9E6 Uncharacterized protein Taxonomy=Bacteria; Firmicutes; Clostridia; Clostridiales

MDGEGTQLLFGRDFTEAELALVREVVALFPRLSSKELAATLCEHLGWATSAGRLKVESCLKLLLKLEAKGEIKLLPKARKAKRKESAPLLSKRTDPPSQELAGELWEFEPVWVLVQDKEGMWLWNEYIQRYHPLGYQRPFGAHQRYFIVCGGGELLGCISFAASAWAVEARDRWIGWSQSDRSRRLHLVANNNRFLIFPWVKVKNLASRVLALVVRRIREDWQARYGYGPVLLETFVDLEYACTCYRAANWIKLGQTAGRGRMDRDTQYLSTPKRIYVYPLVREFRAVLCGKEKGGSG\*

> NODE\_66\_length\_50651\_cov\_165.733\_4 UniRef100\_A0A0M2U7Z0 Uncharacterized protein Taxonomy=Bacteria; Firmicutes; Clostridia; Clostridiales

MKESLLLNRRLMWRELRAKQKEKGIKPRPRASLTNGKAGWQTVEEERAGRWQVVEECHKVWRVVLPVLLKRLAKIPDPRNPRSSKHKLQRPEKPLTFPGWERNSGTRIGLSCGMRIYWLVPGPAGAE\*

>NODE\_66\_length\_50651\_cov\_165.733\_5

MPLNIPEAAAPVDLRLAGPDSPCRFLSPRPAILPTFAPWSRTPVPLRRSSCRVHGTSETEIRNCAQLNSCTPPRFPPPPQTWKPSRHKASITGKSYLFRKHCVHRHAPRQEEALPSLPPPPAQRSRAMGLLSAPRTPCIAVVALALGSHAGAQPGRPLKGPASRTPSAAGTCPQRGPLLRAAVPLFFHPGP\*

>NODE\_66\_length\_50651\_cov\_165.733\_6

MGRQCFYRQKIVTQARSVEAKTLVSYLVGEIRSRRELAPEEAALVAEDALEYLMHLADRGPGQIDFPAILGLDAHWGAPGGTSPSR\*

>NODE\_66\_length\_50651\_cov\_165.733\_7

MLEEFGVVAMQVGRMARCIEEAYFQGCLLDWPRLGVLFPYNHQALRQRLEPLFGRREHSCPWRA\*

>NODE\_66\_length\_50651\_cov\_165.733\_8 UniRef100\_A0A0C7NNL1 Uncharacterized protein Taxonomy=Bacteria; Firmicutes; Clostridia; Thermoanaerobacterales; Thermoanaerobacteraceae; Moorella\_group; Moorella

MELYLRGEDLTSVRKKLCCSRTAWRRWWQLFCQVGGLGEEDPEEAARRLGQPVVLVRGFAELWAEVRENTRLSEKVKREGLWALAAPPGGGPRQAFRQRLLERHRYTPAAADQFEQELRELASRLSSRGRSAGQIVWTGVAQDQPPAAAWETAAWFPPYWTTWCRGLGRKEYK\*

>NODE\_66\_length\_50651\_cov\_165.733\_9 UniRef100\_A0A174LI01 4-hydroxyphenylacetate decarboxylase activating enzyme Taxonomy=Bacteria; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae

MSSSQERALIFDIQGFSVHDGPGGRTLVFFKGCPLRCYWCCNPEGQNQYREVMYRRSKCQMCYRCMDSCPNGAIHVKNKGDFIAIDRSKCGYCNNLDCVKGCYNGALKVVGKYMTIDELMMKIERDRRFWGTGGGVTLGGGEVMLQYKFAARLLEECHASYIHTAIETSGYAPWSHYQEVLKNVDWLFVDIKHMDPDIHRKGTGVSNVSNLENIERMASHQKDYQMVIRIPVIPGYNDNTENIVATAKFMKRIGVHVINILPFHRLATSKYEQLDRKYACKNMESPRLGDMYQIQNIFHNYGLMCYVGSDTPF\*

> NODE\_66\_length\_50651\_cov\_165.733\_10 UniRef100\_K4LX65 Transposase, IS4 family Taxonomy=Bacteria; Firmicutes; Clostridia; Thermoanaerobacterales; Thermoanaerobacteraceae; Thermacetogenium

MYIRTIQRKNKDGSVVRYVQLAQNEWDPQARCAKARVLYSFGREEEVDREALKRLIRSINRFLGPEEMLRYEAETTGQNLLRFLSSRPLGGAWALNQLWEELGIKEVLLKLLKKRQFKAPVERAIFAMVANRALDPTSKRGVQEWVEEDVVIPDLDQIPLQQLYRAMDFLLENEAEMQKQVYYALANLLNLQVDLLYFDTTSVYFETEEEDEDGLRRRGHSKDHRPDLPQAVIGLAVTRDGLPVRCWVWPGNTADMSVVEQVKKDLIGWKLGRVITVLDRGFNSEDNLRYLQRAGGHYIVGEKMRSGRENTVKALSRPGRFQTVRDNLEVKEIVVGEGEARERYILVRNPQEAQRDKAKREAVIKELEEQLPKIRSHAKAVCELMAHPVYGRYLKLDSRGLPKIDRAKIKEEEKLDGKYLLRTSDDTLSSEDVALGYKQLLLVEDAFRTLKSRLEPRPVYHRLEDRIRAHVLLCWLALLLIRVAENKTGQTWKNLRSTLERMHLGEFSGECGQVW\*

>NODE\_66\_length\_50651\_cov\_165.733\_11

MTISVHMATMALVLWLKQCSKFQFCFKSLKQLFSMSHLRWAIRQITSALVLDLGAVVTR\*

> NODE\_66\_length\_50651\_cov\_165.733\_12 UniRef100\_A0A0B7MER2 Uncharacterized protein Taxonomy=Bacteria; Firmicutes; Clostridia; Thermoanaerobacterales; Thermoanaerobacterales\_Family\_III.\_Incertae\_Sedis; Syntrophaceticus

MAGRTKKYAEPGRLDPKNDFIFRKLFSSPGNEDLLTDLLNSILQPTPEKTICQVNILNPIKPRDHRADKEAVMDILARTNDGTLVTIEIQVADEHNMAQRAVYYWSVVFTSQMVTGMTYAEIKKTISINILDYVFLKQTARYHTVFHLCEETEGFQLTDVEEIRFVDLPKMLDKWRKSELIRETEPLTKWFLLLEANEDQEIAKELEAMAMSDAALQKAIREWERLSRDPETIAQYISRMKGKMDRLSALKTAEERGMAKGRAEGMAEGRAEGRAEAKQEAICTLLDKRFQPVAGELQEKVRQMTAEKVLDRIYEELLEAETVEQAKQIISRAGKTKPR\*

>NODE\_66\_length\_50651\_cov\_165.733\_13 UniRef100\_UPI00083023C5 UPI00083023C5 related cluster Taxonomy=unknown

MPDIFVEVVPDLGARWVDKSFCYRVPPVLKEKVAPGCLVQVPLGRRMVYGFVVRRVEEPPAVAIKDIAGVSGLRPLGPDLLDLARWMGRRYFYPLGAVLGMMVPSPAREGTGRQRRYAVLDVPAEAAAAEAERFQARAPAQARVLRGLVTANGLAMEELGPARRSLAALVSRGLVRVEDYPVYREGYSGVEEMADRAGPPALSAEQQEAVARIMGAVEGAGFAPFLLHGVAASGKTEVNLRLVEEVIRRGRHCLFLVPEIALVPQVLAQLRRRLGSEHVVVWHSSLSPGQRHDAWEMAASGRAGVVVGTRSAIFAPVPRLGLVVLDEEQEPAYKEDQGCRYHAREVALKRCQLARAVLVMGSATPSLETYSRARSGVYRLVRLQQRVTGTGPPRICLVDMREEVKAGNTGILSRLLVRRLQEVLEAGRQALVFINRRGFYPYVYCGNCRFVWRCPHCDVGLTYHRAREELRCHYCGYALPYPQPCPACGATRVWQGRGAGTQQVEAELTRLFPAVEVLRVDLDTTRSSW\*

>NODE\_66\_length\_50651\_cov\_165.733\_14 UniRef100\_UPI0005CAF0E5 hypothetical protein Taxonomy=Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus

MTEPIQGVIFVNPEVRDDLFYWQAARRYPWDEFTDIAQQFLQARYQELKRRLPQVEGQAELFKDAVDLDSSCGSGERKSPRGRKGIPFWPLFRAFSLARLMRVEDSARDVYFLLKNNPTFARACGFEAVPSYRVTARFDHIMTHHGLWAKARIKAVQLNLDKQVFFPLRGNSSGYHPRRGRGNSSSKG\*

> NODE\_66\_length\_50651\_cov\_165.733\_15 UniRef100\_F7Z2V8 Transposase IS4 family protein Taxonomy=Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus

MDTTHVEAEATAPPKDKKDDPAYQHTDDNVGVLRKSNTVTYIAHKVALVVDANEDFCYTHCTFKGNTSDPETLEGTLLKFKEEFPEVAKEVEIVLADGIYQSANNQKVSKEVLEAKLYAPINPRNRKSVKLENVRGITEIDPYGRPKCLSGRCLDLVGRDQKQQQYIWGCPVFGIRHQETLDCPEANHLQCCNLNAGGRYYRTNRTDFPQIDWENPQHSVRFGLHYNREVPLNG\*

> NODE\_66\_length\_50651\_cov\_165.733\_16 UniRef100\_A0A1M5ACZ3 Transposase IS116/IS110/IS902 family protein Taxonomy=Bacteria; Firmicutes; Clostridia; Clostridiales; Peptococcaceae; Desulfotomaculum

MQDILEICCGLDVHKETVVACLLKGDTDGEPKTTIRIFSTLLAGLDELRAWLEAENCRHVAMESTGVYWQPVYSVLEEAFDGSMVLTVTNARHMKNVPGKKTDMKDAEWIATLLRAGLLQGSFIPVKPIRELRNLTRYRKSIMEEITAQKNRIEKHMQSCGFKLSTFLTDIFGVSGRAIMDHLCRHGKISAWEVDALVKGRAKSKLHEIKQAVNGKMDLHQREFLKLLLVWLDQHYEHLRQVEQKLEEKMAQYQRQLEQLDGIPGIDKTAAAAILAEIGIDMSHFKTAEHICSWAGLSPGNNESAGKKVHSHHQW\*

> NODE\_66\_length\_50651\_cov\_165.733\_17 UniRef100\_Q39TT7 Metal-dependent phosphohydrolase Taxonomy=Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales; Geobacteraceae; Geobacter

MQRAKIREVYSLARPFLNTRHNDIHTVISYGYALRLLRDEGGDRETVIPAILLHDVGWSSVPEHLQLTAFGPNPTNPALNRVHEVEGARLARDILRQATYDEQKIEEIAEIIVGHDSRLEALSLNDMVVKDADKLYRFSRWGFAIDVKRFRRDPVVHLQWLGQQIDRWFFTARAMALARGRILAEQSDNLF\*

>NODE\_66\_length\_50651\_cov\_165.733\_18

MLMLSAKEDHAQTLISRDMIEAIDRVRTIVGVQVAGVALYDAAQVVFE\*

> NODE\_66\_length\_50651\_cov\_165.733\_19 UniRef100\_A0A1F9DPQ6 Uncharacterized protein Taxonomy=Bacteria; Proteobacteria; Deltaproteobacteria

MTEKLIYWLEELGVEDNDLVGKKCANLGELTKAGVRVPPGFALAVQAYERFLATTGAREEMQRFLETFKADPNDPKDLAKFEKASEVLREIVDSKEMPSDMADIISAHYDKLCQRTGISDVPVAVRSAGPVSRPGQYETYLWVIGQKDLMKKIIRVWSSTFNHRSMVYRAQNGLPMEFDPIGCAVIQMVDAKVSGVMFTLHPANGDVSKIVIEANWGLGESVVSGRLSPDFYVVDKQTLNIVEKRVSDKTYEYLLDPATGATDFFEVPQERRNIPCLTDEELVELAKLGLFVEKHYGKPQDTEWTISKDLPFPQNIFMVQSRPVTAKMSKKKTATDTILDMMMSRLYQL\*

> NODE\_66\_length\_50651\_cov\_165.733\_20 UniRef100\_UPI0005597D8B hypothetical protein Taxonomy=Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacterales; Desulfobacteraceae; Desulfatiglans

MPYGYYHYDWRGEPDLDPQYYDCWVCNVAHSVPAWTPLFTSEWYRLIPYAMQYANDYICEPTSKGWDWRIYNGYAYITSIKVPESEVEGRKQVYREQLASIIDDPWGYSERLFSRLMEKYDYYKPLNVKEMRDCELVQHLWDMAELDRLMWEVHMLGWDGLLGGLRLWREMLVDLFGITPYDVRYAKLLSGFDNALFKLNSDLTHVAARAVELNVESNFSLPDEEVIPAMEQTEAGREWLGEFDKFLNEHGYRSDRMLEFTRPTWLEKPTLAIPDIRRIISAGVSHAPDILRHQLRKEGEEIERELLAKLPSDQREWFHKLTQCAQAAHSWSESHDYWCEFQTYGLRRRAIKELSERLYRKDIIDDPEDTAYLLHQDLIYAAVIQEKVGKKYFRDLIKRNKEEFEYYKSIPPGGDTTPLFLGDPSKLPLVAGRDTLFGVVAAPPAEDAAKVGAVAVGCAGAPGIVEGTARVIASASEWDQIKPGDILVCPMTDATWTPLFALLKGVVTDSGGLLAHPAIVCREYGIPAVCGTFDASKKIKTGDRIRVDGNLLRVYKLDQ\*

> NODE\_66\_length\_50651\_cov\_165.733\_21 UniRef100\_A0A1F9BPN9 Phenylphosphate carboxylase subunit beta Taxonomy=Bacteria; Proteobacteria; Deltaproteobacteria\_**putative\_naphthalene\_carboxylase**

MSTVETATDQKTMGGMVLMKPIRNLRDYIEVCEAEGEVKRVKAEVDWDLELSHIAKINEEQGGPALLFENVKGCLGSVLIGVFSSPKRMAIALGMPPEYTMCQMADEWRRIGSRKPIPSVEVNTGPIMENIVEEKDIDLTKFPAPKYFPLDGGRFMGTSAFRITRDPETGELEIGMGRMQLYDEKNVGLYLSPGRGGDKIRAKYEKLGKPAPFALVFGCDPALALASVMFIKGASKYDIAGTLRGIPVETVVSDFTGLPIPAEAELVVEGFMDHDDLRPEGPFGDVTGLYTSELQKPIPKRFVKAKRVLYRNDPIMLANSSGRPVSDVQMMISLPRTAALWQELEAMKIPGIKSVYIPPQMAGRFWAIVSVKTQYPGHANQVAHAVISTTTGHLGIKGVIVVDDDIAADDMDRVLWALATRYLPDRDTEIIKRGRSSPLDPAVPPETGYVEIISKILIDATVPYEWPQKPVVAALDEEVVKKVKSRWKEYGLD\*

> NODE\_66\_length\_50651\_cov\_165.733\_22 UniRef100\_A0A1F9BT12 Uncharacterized protein Taxonomy=Bacteria; Proteobacteria; Deltaproteobacteria

MGLKKDRETAVEKATKVKLFAHDVHGVLTSSAFFCDIEGRRQYSFWHMDGFGDLSLSANGIRIAFLDTTSVDGEGLYRAKELKLDQYYYKVSDKVAKIRELEQELGISDENVGYIGSEITDAAAMRICGFRVATADAVDEIKELADYVTTAPGGRGAIREVCEFILGSMGLWEAWTEKVMRMGYK\*

> NODE\_66\_length\_50651\_cov\_165.733\_23 UniRef100\_A0A1F9BVE3 Uncharacterized protein Taxonomy=Bacteria; Proteobacteria; Deltaproteobacteria

MGNGKSREAAVEKAKRTKFVILDIHGVLTDNTLYYTDDGKKSERFSLRDRLGCLALMEGGISVAFLTSKISRADEQVGKIYNIPTEYLWGSSAKMARLDEFEKDSGLKDEDFCYVGDEMIDLGIMKRVGFSVAPADAASEVKEIADYISSAGGGQGVVRELAEFILTAQGKWEAIKEKISASG\*

> NODE\_66\_length\_50651\_cov\_165.733\_24 UniRef100\_UPI00046D15DA phenylphosphate carboxylase subunit alpha Taxonomy=Bacteria; Proteobacteria; Deltaproteobacteria; Deferrisoma\_**putative\_naphthalene\_carboxylase**

MAFRDNREFFEALLRTGDGIRVAREVDWDLEMGAIVRRVCEMGGPAPLFESIRDYPGWRALGAPLATFRRLAVALGLPAHASVREISEVYIEKTRAPGPEPKLVSTGPCKENVVVGDEVDLFMLPAPMVHEGDGGRYLSTWHMVVSKDPDTAEVNWGMYRQMVIDEHTMVGPLLPVSDTGRVFHNKYKPKNKPMPFATVIGADPTSSIAAAAGVPWQEPVFASALSGEPVELVKCETVDLEVPATAEVVLEGEILPGKELPEGPFGEYPGYRTSLREPRTVYRVNAITYRNNPILPGANMGVPVDEGQLLRAFTLGLEARRILASQGLPVSEVFMPPCSAHHLMIVSVKSAVTNIAVQVAHALFGSKLAPWFYYVVVVDADVDIYNLEEVIHAICTGCHPGRGIRIYEDDIGSFATPFLSLEERRQGRGAKAVFDCTFPPDWDPKTELPIKVSFETNYPKEVKERVIANWKDYGFPQ\*

> NODE\_66\_length\_50651\_cov\_165.733\_25 UniRef100\_A0A1F9BV94 Uncharacterized protein Taxonomy=Bacteria; Proteobacteria; Deltaproteobacteria

MEFEIYVSRLEELPVEQECELLIRALTPSDRRKKYKYQKVRALISQQKDRYPDLLWVRFLKGQLHTDPYSIRIANTKGATDE\*

> NODE\_66\_length\_50651\_cov\_165.733\_26 UniRef100\_A0A0U2L5W7 Phenylacetate-coenzyme A ligase Taxonomy=Bacteria; Firmicutes; Bacilli; Bacillales; Paenibacillaceae; Paenibacillus

MFCDFASPKAVTMTREELREYHLYHLQRLLERVYANSAFYRKLWANAGLHPEHIKTLDDFTRLVPMVTKQDFLADQNSSPPYGQRLAVSEEEICQVHLTSGTSGIGQEVYALTRDDISLEAQGWVIHLRSIGLKPGDVSIVTWPVATMAAALNVYEACREIGVNAFLVGIYDGETKIKLMQRFDMNHLVATPTYVSRLAVLCQEMGLNPSQAFGNLKAISVAAESYPANWLEEMEAVWGCPIHDVYGSTQNATALGMTCQTRRSAGEGGGTRRNMHLFEHLTFVEAIDYESGEPVSYGAEGELVLTPLFRQATPVIRFRTGDKVILYPGQTCSCGSQFDFLEAGTIARFDDMIKIKAANVWPQTVDDIIFSYKEVEEYNGVVSIDEKGRENVRVLLEFRDGVPEGTKASLMKQVGERIRQKTQVTMIVEEVPRGTLERTLFKSRRWVDRRQEGLRQVVRYLEK\*

> NODE\_66\_length\_50651\_cov\_165.733\_27 UniRef100\_D8WWD5 Putative UbiX-like carboxylase subunit (Fragment) Taxonomy=Bacteria; Firmicutes; Clostridia; environmental\_samples

MTARLIVGMSGATGSIYGIRLLEVLRDLGVETHLVMSRSAEKNISLETKWRVEDVRALATVVYPFEDIAAAISSGSFLTCGMVVAPCSIRTLSGIANSYNENLLVRAADVTLKERRRLVLLVRETPLHTGHLRLMTEVTEIGGIILPPMPAFYHHPQTIDDIINQTVGKALDMFGIEHHLFCRWSGGEAAAGVVQGPAGER\*

> NODE\_66\_length\_50651\_cov\_165.733\_28 UniRef100\_A0A0K1J7B3 UbiD-like carboxylase subunit encoded in anaerobic phenol operon Taxonomy=Bacteria; Proteobacteria; Betaproteobacteria; Rhodocyclales; Rhodocyclaceae; Azoarcus\_**putative\_naphthalene\_carboxylase**

MDMRAYLDLLQDAGEIMVIEDELDPVYEASAVLGTREVQMGPAVLFRNLKGYPGWEVLGNLFGSRRRVALYLGVHEDEAEAAFVRRQQELKPPVRVKDGPCKEVRVREPIDLLRELPILTFSEGDVAPYITAGIMVSHDPHTEERGVSVHRLRVAGPNRLGTMLMNPPLNLFMQKAEKAGTPLEVAICIGPEPAVLLATLTRWTPGIDKYEIAGGIAGSSLEVVRCETVNIEVPAASEVVIEGRILPNVREPDGPFGEHSGCYVVSNEGRIVEVTAITRRQHPIYQVIKPWTTELDLLMALGQGNSTLRRLKEVVPEVEAIHVVPLSSMLAAVIKLSSTSRARVRKAILTCLAIDPRIKQVVAVDDDIDITNPYEVAWAMVTRFQADRDVVILRDTEGTPLDPSRKAGNLTSKIGFDATSADMEGNFKKISPPATAVIRAQEVVGQYLRRYSS\*

> NODE\_66\_length\_50651\_cov\_165.733\_29 UniRef100\_A0A1F8TBK2 Aldehyde ferredoxin oxidoreductase Taxonomy=Bacteria; Chloroflexi

MPLSRQLLFVDLSSGNSQSVPIPLEVRQGFLGGRGLNMLLLYRLGLRCHDPFSSDNPLIFGAGLLTGVLGGRLNISARSPESGLLGDSNVGGDFGAELAATGYSHLVIVGRSDRPVYLIVTEDGVEIRDAGYLWGRDTLETQRMIRRELTDPEVRVACIGPAGENLVRFAGVVTGQKNIAGRTGMGAVMGSKNLKAVAVKGSRGFRISDPDGYLEAVKDVVGQVSSTRWGQALGKMGTPLLLHYSNAMGFLSVRYHQRTTLGEQGRLLEPSALEEFSTGMLACYGCPVHCRHRYAIDAGSRYAGAAGEGPEYASVASLGSHVGNLNIEAVIYMAQLCNRYGLDTISTGNYLAWAMDLYERGILTSADTSVPLEWGNEDSLIQMLHMIANRRGFGNVLAEGSRAAAELGPEAAKHLLQIKGLSMELTDERPVKSFALGLATATRGCCHMRSRPSVDVTNLPRNILAGLYGGDVGRDYTEYEGKGRMVWWHELFHAVTDAIGYCRFLSIFSSIHAVGYQEYAKLIHRATGLELDAGELQEIGERIYTTERMFLTQQGISRKDDTLPDLYFDVPVPAGPSRGKLISRTRFQEMLDEYYGLHGWNEDGIPRPETVSRLRLEEFLGGGWLAYPGS\*

> NODE\_66\_length\_50651\_cov\_165.733\_30 UniRef100\_A0A1F9BZJ5 Uncharacterized protein Taxonomy=Bacteria; Proteobacteria; Deltaproteobacteria

MGVGGLRIRVASSEVCSGCRLCEIVCSLYHLGEVNPRLAAIHVVKDDLGTSMNNPRVCLQCKDKTCLKGEEVDEKAEMSAFIWPVGRAQKCPYGALHVHNGQAYHCDLCGGDPRCVQVCTTGAIAVAGKEDGHGKVREREGS\*

>NODE\_66\_length\_50651\_cov\_165.733\_31

MGKSGNEKVVKVHLPGHLAGLAGDRRVVAGHGDTVEEVLASVREQFPGLSEALGGAGMASFSIYINDAAVEAREGLRTKVRDGDDIYLVVPLAGG\*

> NODE\_66\_length\_50651\_cov\_165.733\_32 UniRef100\_A0A1M5B1M8 Glycosyltransferase involved in cell wall bisynthesis Taxonomy=Bacteria; Firmicutes; Clostridia; Clostridiales; Peptococcaceae; Desulfotomaculum

MARRRVLLLVRPAVGGIATHVLSLALGLDRQEFSPVLVAPEGYGVLERAREQGLASYGVRFGDGLNPWQDRKAVARIREIAVREGTGLVHSHGLKADLLASLATRTGTIKHIATVHTFPVRRAGLTGFASRFLTRYVSGRVGHYIAVSQALAAELTGRYGVDPEKVSVVPNGLAREKLEDYSRQKLVRPDPAMDGPVIGSVGRLVLEKGMEDFIRAARLLRGEFPQARFWIVGDGPLRARLQALVSRLGLEGKVSLLGYQAEVAPWLAAMDVFVTCPVSEGFSLVTLEAMASGKPVVATATGGLPELIRSGVNGLLVPVRDPAALARAVSLLLRRPDVASELAVKARQHVCQRYTAESMAKQTQAVYERVLRQDSSGGGLVGFGVCAPSRTASSWGGEDRA\*

> NODE\_66\_length\_50651\_cov\_165.733\_33 UniRef100\_A0A0M2U3X0 Uncharacterized protein Taxonomy=Bacteria; Firmicutes; Clostridia; Clostridiales

MKVWVAAAVLAIVSVGFSRPALAQSPSGRVVVVVVADRMSLADLAGADQPWPELLSRAGIALMNTNTGGGRTPENALATISAGGPAVAAPDAALAFRADEGFAGEEAGLTFTRRTGRTAAPENVVVLAWPQIAGNNRQRDGNPQPGFLGETIRRAGGKTAVLGNADMPDSPRREAALLAMDTGGIVDYGLPGKDTVTTTSQDRLLPLVTDYDRLRQAYRQLPGDANLVVIEVGDMARLDRLDSLGTAEVVAREKQTIMRDIGYFLQKLLADEPARVIFLVPTPSSPAAAEKNLLTPLLLFARDVPPASWLTSPSTRRPGLVSNVDVTATILSWLGQPLPPGLAGRPVAPAPATPPRPVEALLDFNERSVFVYALRPPLLKTYVGAQIVVIAGAVLGLLAGCSRLLGWWRPVLLALVSVPLALLLLPLLPSYGSPIFYTGIFLLLTALLTVAALRFSRSTLAAFGLLTAATWTSLIVDVFTGSNLGRQSILGYDPMAGARYYGIGNEFMGVLVGAAAMTIGIGLQLHRGREPLSSWPLAGVAVILGLTAAILAAPQYGANAGGTIAILIAACFLWAKLARGGLDWSRVALAGVAVFAVLIGMSLADARRAVEVQSHFGRTWELIGSEGVGPILDIAARKAAMNLKLIRYTIWSRVLLVALGTLVLLCYRPVNLWRHVWRSNPHFYNGFSTAVVGAVAALIFNDSGIVSAATVMTMAMAPFLYLLLQARAGPE\*

> NODE\_66\_length\_50651\_cov\_165.733\_34 UniRef100\_UPI0005550B90 S-adenosylmethionine decarboxylase proenzyme Taxonomy=Bacteria; Firmicutes; Clostridia; Clostridiales

MHALGRHVLAEIYGCEFGILNDEKKVEEIMVNAALAAGADVRESIFHKFSPQGVSGVVVISESHLAVHTWPEYGYAAVDVFTCGEKVSPWEACRYVASELGAAHLNATEVHRGLFADPHQKAVNL\*

> NODE\_66\_length\_50651\_cov\_165.733\_35 UniRef100\_A0A0M2TZA5 Uncharacterized protein Taxonomy=Bacteria; Firmicutes; Clostridia; Clostridiales

MLDILQPVQSELRLVELRMRKEFALKEGRLNELLPLHLKNPWDRLFLPAMVLLHNKLFAPIKEKTVAMACVFQFIYLATLTHRQIETNPAMVVLVGDYLYTKFFSYLCRHEALEYLDPLSRSICQIQEAGIWRQQQRSVQTDSDNLDIIDKERALLVSQACGCGAELGGAGEEQIQMSRGFGLHIGRMWALSEAEPGPRTGVERAEALKCLYRLPGGEARETLERLLLHLDSFAETVSVVG\*

> NODE\_66\_length\_50651\_cov\_165.733\_36 UniRef100\_F6DRR2 Demethylmenaquinone methyltransferase Taxonomy=Bacteria; Firmicutes; Clostridia; Clostridiales; Peptococcaceae; Desulfotomaculum

MAASDGGGGSLVAPAVDKGQMVHEVFATIARQYDRMNSLLSFGRDKGWRQRAVDILAPGAADTVLDVCCGTAMLSLEVAKRLGPQGKVIGIDFSPEMLAVGERNLRANPLGSRVELVPGDALELPFPDDSFDSAVSAFALRNLTDVVAAMAEMRRVVRPGGRIVILELAKPSATVFQRIYYFYFYHLVPLIGRVAVGRSLPYSWLPESVRIFPSQAEVQAMLSMAGLVNTSYQDLTLGTAAIYWGTKPERPRGLMEAGGDSPQAARSNTTS\*

> NODE\_66\_length\_50651\_cov\_165.733\_37 UniRef100\_A0A1F8RSF7 Uncharacterized protein Taxonomy=Bacteria; Chloroflexi

MPRLEPTEITPHVYQCPIPIPNNPLENLLAYLVQTPAGTWMIDAGWNTPEAIAAWESHLPALNLSFRDITQIIITHLHPDHYGLAGTIRERSGAPVVMSRIEAEQISSRYQDYRQLLAEVGSWLSRNGVGQGELPDLQQASLRVLNRVGPVQPDATLREGDLLEAGFTTLQVIETPGHSPGHICLFAREAGLLFAGDHVLPTISPHIGMYPQSPPNPLAVFFHSLDKVDGLKVNLVLPAHEYVFDNLRQRICQIKEHHRIRLEEILAALGDEEKTAYRVAAHISWAIGPWEQFDVWARRSALMEVVAHLEYLLGQGRVAKRCRPDLVLYRRLEVRK\*

> NODE\_66\_length\_50651\_cov\_165.733\_38 UniRef100\_A0A0M2U4A7 UTP--glucose-1-phosphate uridylyltransferase Taxonomy=Bacteria; Firmicutes; Clostridia; Clostridiales

MKQVRKAVIPAAGLGTRFLPATKAQPKEMLPVVDKPAIQYIVEEAVACGLEDILIITGRNKRAIEDHFDHSLELEAALAEKDNHEALENLRRISEMADIHYIRQKEPRGLGHAIYCARKFIGQDPFAVLLADDLIVTDGSPCLQQLLDIYETRPGNIIAIQQVLPEEVNKYGIVEGQALLPRLYQVSRLVEKPPVGSVSSNLAIVGRYILQPEIFTALAEVAPGAGGEIQLTDAIGRLLGPQPVYAYLFQGRRFDVGDKLGFLQATIEMALMRPDLRDELGAYLRGTFMTDSRLAEVVYNGGSGGFSGGQEL\*

> NODE\_66\_length\_50651\_cov\_165.733\_39 UniRef100\_D3FBQ7 Putative glutamate--cysteine ligase 2 Taxonomy=Bacteria; Actinobacteria; Thermoleophilia; Solirubrobacterales; Conexibacteraceae; Conexibacter

MEAPEAFLEGRSFENGQDLTIGLEEELQILDPRTLHLTNKFGELKKAVPADLDPWVKGELIASEIEIATVRSQDFSSAAGDFLSKHRQLVELALAHDLYLGATGVHPFSPWYDQEIIDTPHYRLVEGELRYVAWRNNTFSFHVHIGVKGRERAILVCDALRTFLPHLLALSASSPFYEGRYTYLHSVRTQLFAKNFPRCGLPDAFGSWASYRRYLEFLYRSNSIHEDTQIWWSIRPHLQWGTVEVRICDAQPWPEDTLKIASLVVALAARVLLAVDRGEPLPVYPRCYLEENFWRATRYGLGGLLVDLETEREVPAVEAIRGLLAWTRPVHDELCLKPYLEPLGEFMAAGNWARRQIRAYEAGHDLVAIHRYLAGLTMGLAVAGTCG\*

> NODE\_66\_length\_50651\_cov\_165.733\_40 UniRef100\_A0A0M2U3G3 Uncharacterized protein Taxonomy=Bacteria; Firmicutes; Clostridia; Clostridiales

MSGKQRKQGRPEPRAGGSGAARHQTSKSNKTSTPERGKGAARPHSGGLPSRGSGGAGVRADGREKPVLPAGSPGRAWYWAAFTGVSVLLFYPPYFRGLFFQPEQLWTLLLAAGVFALVWGWKISTRDLRWLTHPFDFLALALVLVYTAATLVAANQHLAMAEVVKVALYFLVFWMVARLSQVRGQRDNLLAVLYASAAGVALAGLLTATGFIAIKDGFVAGRIYSTLQYPNALASFLVATSFTSFYLWGRLRTWPQFLLAAGNYVIVLVFLTTGSRGGYLVYPVTLILFFLLLPAGVRGKTLAHAAITFGGAFLANNFVIPAILAGNMGGAWAWFAAGLAVVEGAHVAWHLLARLTAGIPHRTRAIIGSGAVIAVLAVVAIFGAARFQAVPASTDQEGILARILPPTMLQRLQDINLETSGSAERLYWTQEAMKIVAAHPVLGAGGGAWEATYRSFQAYDYSSTQVHNHFAQIWSEIGTAGMAIWVGLWVLFLVTAAQAYRRSQGAARALPATLGVAGISLGMHAFIDFDLSLGAISLLLWSIWGLTRGLVAEKSQKSPGNRRLRLEWNWLWLVPFVAAGAIALFAASLLLGNYYARQAVAAATGGRAAEAGEYFRRASTFDPFTGSYLVDRAGLLVEKDPREAVRLARAAAEREPYNPRVLTRLGEIEWAAGHWPEAVAAMDKARDAAIWSVSGYENVGRVSALAAVNFLRQGDREQARQYAEKAAGIPAEMEERLAKVEPEARQLWQQSGRPFLAPSPGVMLNAGMAYFLLGKWDLARKSLETAAVDKGVGQEASLWLAALLEKTGDAAGAQKLLGEISRENQAWQQTYAFIHGLQVPL\*

> NODE\_66\_length\_50651\_cov\_165.733\_41 UniRef100\_A0A101ECR7 Fumarate reductase, flavoprotein subunit Taxonomy=Bacteria; Firmicutes; Clostridia; Thermoanaerobacterales; Thermoanaerobacteraceae; Moorella\_group; Moorella

MQELSHDLLILGSGLAGLRAALEAARQTKGKLDIAIISKTQLMRSHSVCAEGGTAAALRPEEGDSLELHAWDTVKGSDFLADQDVVERFAAAMPGEILQLEHWGIPWSRKPDGRIDQRPFGGHSFDRAVYAADKTGFFEMQALYDTLQKYGGVVRYDEYYVTSILIENNRFCGLTFWNLATGEFGVIRGKALIIATGGACRIYGFTTYSYTVTGDGMAMAYRAGLPLKDMEFVQFHPTGLVPSGILITEAARGEGGYLTNNRGERFMKEYAASKIELAPRDIVARSEMIEIEQGRGFAGPRGLDYVNLDLRHLGADRINERLPLIREVAIKFNDIDPITAPIPVRPAAHYSMGGIHVNIDGKTPAEGIWAAGEAACISLHGANRLGANSTAECLVWGGITGGEVVRYLQHERHLPALPADRVREEEQRVFAGFFRRKGKENLYTIRQELRDLMDNKAGVFRTARELQEAQEEIRELGQRLQEAGLTDQSRIYNTDLISAIELENMLDLAQTIVAGALTREESRGGHARRDFPERDDSNWLKHTLAYYTPQGPRLEYIPVAITMWQPVERKY\*

> NODE\_66\_length\_50651\_cov\_165.733\_42 UniRef100\_A0A0T6ARF9 Uncharacterized protein Taxonomy=Bacteria; Armatimonadetes

MAEGRKRENYLGIKGWVRAGRYGLERYLYFLQRLTGFGLIIYLLIHLYETSFRLRGEVTWEGVMGLFDQPVFAVLEYVVMAAFIFHALNGLRLVIEELGFALGKPRRPVYPYETSLQRQRPFMWAIGVLIIVFLVVSLYDFLV\*

> NODE\_66\_length\_50651\_cov\_165.733\_43 UniRef100\_A0A0M2U3S6 Uncharacterized protein Taxonomy=Bacteria; Firmicutes; Clostridia; Clostridiales

MREAHFWLLQLVTGLVLIVLLGLHMIVIHLETILGFLGLGAGGAVAYASVMERAASSPWTWFYIIFLALALYHGLYGLRTIILELTLSRTASTVVTVLLVIVGIAAFSFGTYVTWQAYAG\*

> NODE\_66\_length\_50651\_cov\_165.733\_44 UniRef100\_A0A1F8M755 Succinate dehydrogenase iron-sulfur subunit Taxonomy=Bacteria; Chloroflexi

MFTEEQIITFKVQRFDPERDQGPYLKEYHVPYTQGLTVLDGLYYIKEKLDGSLAFRASCRMAVCGSCGMFINGKPHLACHTQITELESTVLEIRPLPNYSVIKDLVCDFTPLFAKHKAIKPYIIRREAGEIDNPTREFLQSPAELESYLQFSYCMKCGLCLAACPTAATDRNFLGPQALGQAYRYCADSRDDGLAERVKEIDHAHGVWRCHLAGACSEACPKGVDPALGIQLLKRQVVLRAVGLGKGRKLAAVVPPPSGQAKPRVEAPPFTVPRAKAEIAAGDSRS\*

>NODE\_66\_length\_50651\_cov\_165.733\_45 # 47918 # 48745 # -1 # ID=6\_45; partial=00; start\_type=TTG; rbs\_motif=AGxAGG/AGGxGG; rbs\_spacer=5-10bp; gc\_cont=0.606; ORF45; UniRef100\_A0A1J4WUH9 Short-chain dehydrogenase n=1 Tax=Parcubacteria group bacterium CG1\_02\_41\_26 TaxID=1805308 RepID=A0A1J4WUH9\_9BACT

MKLDGKVAIITGAASGMGQAMALLFAREGATVVVADVNEVGGQETVRRIQEEARETSGQMERAAGAEARPTYGATDGRAEFVKVDVSQADQVKRLVDSTVNNYGKLNIMVNNAGVALLGKDGKIADVAEDTWDRVIAINLKGVYLGMKYAIPPMLKQGGGVIINTASIAGLVGFPSLAAYCASKGGIVQLTKATALDYGRDNLRVNAICPGVIRTAMTETMLADRETKEGMERTTPLPRLGEPEDIARAALYLASDEASFVTGTTLVVDGGWTAQ\*

> NODE\_66\_length\_50651\_cov\_165.733\_45 UniRef100\_A0A1J4WUH9 Short-chain dehydrogenase Taxonomy=Bacteria; unclassified\_Parcubacteria\_group

MFVRNHMSANPITVQPDDSINYAGTLMKEYGIRHLPVVSEGQLVGVVTQTDIFKVSASPATSLSIWELNYLIAKLAVKDAMTARVISVQEEAPVEEAALLMRQNKIGSLPVLNSTGKLVGIITETDLFDAILDAMGSNTATTRVVIECDDRPGELSRITGVIAEYGINIWSLVVFHPAEGIAHVVVRLQGENLEGVFEKLASEDLRLVR\*

>NODE\_66\_length\_50651\_cov\_165.733\_46 UniRef100\_UPI0004712E7E transcriptional regulator Taxonomy=Bacteria; Firmicutes; Clostridia; Clostridiales; Caldicoprobacteraceae; Caldicoprobacter

MLSEVREEMVAVIADVLSDGRARTLEQVLAELRAEYPESVETASCEYASAYGYSGCGQLMAPVNAVADALACLEGRGEAVSFFRDGLKLWQNAS\*