

Lawrence Berkeley National Laboratory

LBL Publications

Title

Energy and carbon metabolisms in a deep terrestrial subsurface fluid microbial community.

Permalink

<https://escholarship.org/uc/item/6vr16087>

Journal

The ISME Journal, 11(10)

Authors

Momper, Lily
Lee, Michael
Amend, Jan
et al.

Publication Date

2017-10-01

DOI

10.1038/ismej.2017.94

Peer reviewed

ORIGINAL ARTICLE

Energy and carbon metabolisms in a deep terrestrial subsurface fluid microbial community

Lily Momper¹, Sean P Jungbluth^{2,3}, Michael D Lee⁴ and Jan P Amend^{2,4,5}

¹Department of Earth, Atmospheric and Planetary Sciences, The Massachusetts Institute of Technology, Cambridge, MA, USA; ²Center for Dark Energy Biosphere Investigations, University of Southern California, Los Angeles, CA, USA; ³Department of Energy, Joint Genome Institute, Walnut Creek, CA, USA; ⁴Department of Biological Sciences, Marine Environmental Biology Section, University of Southern California, Los Angeles, CA, USA and ⁵Department of Earth Sciences, University of Southern California, Los Angeles, CA, USA

The terrestrial deep subsurface is a huge repository of microbial biomass, but in relation to its size and physical heterogeneity, few sites have been investigated in detail. Here, we applied a culture-independent metagenomic approach to characterize the microbial community composition in deep (1500 meters below surface) terrestrial fluids. Samples were collected from a former gold mine in Lead, South Dakota, USA, now Sanford Underground Research Facility (SURF). We reconstructed 74 genomes from metagenomes (MAGs), enabling the identification of common metabolic pathways. Sulfate and nitrate/nitrite reduction were the most common putative energy metabolisms. Complete pathways for autotrophic carbon fixation were found in more than half of the MAGs, with the reductive acetyl-CoA pathway by far the most common. Nearly 40% (29 of 74) of the recovered MAGs belong to bacterial phyla without any cultivated members—microbial dark matter. Three of our MAGs constitute two novel phyla previously only identified in 16 S rRNA gene surveys. The uniqueness of this data set—its physical depth in the terrestrial subsurface, the relative abundance and completeness of microbial dark matter genomes and the overall diversity of this physically deep, dark, community—make it an invaluable addition to our knowledge of deep subsurface microbial ecology.

The ISME Journal (2017) 11, 2319–2333; doi:10.1038/ismej.2017.94; published online 23 June 2017

Introduction

Most of the Earth's deep subsurface biosphere (DSB) is energy-starved and functionally defined by the exclusive presence of microbial life and the lack of light or light-derived biomass. The DSB, in particular the terrestrial component, has only recently been appreciated as dynamic, populated, metabolically active, interacting with and perhaps controlling global elemental cycles. In terrestrial environments, a functional definition mandates that the DSB be independent from photosynthetically derived organic matter and reliant on endogenous sources of energy (Fredrickson and Onstott, 1996; Stevens, 1997). However, it is impossible to know definitively that a subsurface environment is truly independent from surface-derived products without significant study. In this study, we define deep similar to Orcutt *et al.* (2011) and Lovely and Chapelle (1995): the DSB is an environment absent of photosynthesis and isolated from direct contact with surface waters.

It has also been shown recently that the terrestrial DSB harbors a great abundance and diversity of microorganisms (for example, Chivian *et al.*, 2008; Rinke *et al.*, 2013; Dong *et al.*, 2014; Lau *et al.*, 2014; Nyysönen *et al.*, 2014; Magnabosco *et al.*, 2015; Baker *et al.*, 2016). Early estimates of terrestrial subsurface cells were on the order of $0.25\text{--}2.5 \times 10^{30}$ (Whitman *et al.*, 1998). More recent estimates put the total deep subsurface biomass at 16–157 Pg C, with the terrestrial part accounting for 14–135 Pg C (Kallmeyer *et al.*, 2012; McMahan and Parnell, 2014). However, the microbial physiologies, corresponding metabolisms and their reaction energetics remain almost completely unmapped.

The carbon sources and cycling processes in the vast terrestrial DSB are of particular interest (McMahan and Parnell, 2014). Due in large part to limited global samples, these sources and processes remain poorly constrained (Onstott *et al.*, 1998; Piffner *et al.*, 2006; Simkus *et al.*, 2016). Metagenomic and single cell genomic sequencing studies in shallow (≤ 100 m) terrestrial systems provided insight into metabolic capabilities of microbial dark matter (Rinke *et al.*, 2013) and genomic expansion of the domain Archaea (Tyson *et al.*, 2004; Castelle *et al.*, 2015; Youssef *et al.*, 2015a; Baker *et al.*, 2016; Seitz *et al.*, 2016). However, metagenomic analyses

Correspondence: L Momper, Department of Earth, Atmospheric and Planetary Sciences, The Massachusetts Institute of Technology, 45 Carleton Street, Cambridge, MA 02139, USA.
E-mail: momper@mit.edu

Received 4 December 2016; revised 8 May 2017; accepted 12 May 2017; published online 23 June 2017

Table 1 Sample metadata and shotgun sequencing results

	<i>SURF-B</i>	<i>SURF-D</i>	<i>Co-assembly</i>
Longitude	-103.765784	-103.765784	-103.765784
Latitude	44.350967	44.350967	44.350967
Depth (km)	1.5	1.5	1.5
Temperature	23	18	
Reads	147 742 812	137 946 268	285 689 080
Contigs	276 553	442 676	637 833
Max contig (bp)	476 530	293 691	576 430
ORFs	478 845	816 244	1 187 179

Abbreviations: bp, base pairs; ORF, open reading frame. Temperature is recorded in degrees Celsius.

of samples from the deeper terrestrial biosphere remain rare (see Edwards *et al.*, 2006; Chivian *et al.*, 2008; Dong *et al.*, 2014; Lau *et al.*, 2014; Nyssönen *et al.*, 2014; Magnabosco *et al.*, 2015).

In an effort to understand the metabolic capabilities of microbial communities in the terrestrial DSB, we performed random shotgun metagenomic sequencing on whole genomic DNA extracted from two separate fluid samples collected 1.5 kilometers below surface (kmbs). Genomes from the two metagenomes were binned and phylogenomic and 16 S rRNA sequence analyses were used to taxonomically classify them. These curated metagenome assembled genomes (MAGs) were interrogated for metabolic capabilities including electron donor and acceptor usage, and heterotrophic and autotrophic carbon utilization. In addition, genomes from two new candidate phyla were identified. Two genomes, SURF_5 and SURF_17 are the first members of a new candidate phylum, designated SURF-CP-1 and named Abyssbacteria, Latin prefix meaning deep, owing to their collection 1.5 km below surface. One genome, SURF_26, is the first member of a new candidate phylum, initially designated SURF-CP-2 and named Aureabacteria, Latin prefix meaning gold, to represent its collection in the former Homestake gold mine.

Materials and methods

Field sampling

All fluid samples and corresponding geochemical data were collected in the former Homestake gold mine (now Sanford Underground Research Facility, SURF) near Lead, South Dakota, USA (44°21' N 103° 45' W) in October 2013. Both samples are deep subsurface fracture fluids from legacy boreholes drilled ~1.5 kmbs, and 600 and 900 horizontal feet (180 and 270 m) into host rock. The SURF archive names, given to these boreholes in 2001 at the time of drilling, are DUSEL-B and DUSEL-D, but for the sake of simplicity, we will hereafter refer to the borehole fluid samples as SURF-B and SURF-D, respectively. A comprehensive description of sampling methods for geochemistry can be found in Osburn *et al.*

(2014). Details of samples and sample locations are provided in Table 1.

DNA extraction and sequencing

Total microbial cells were collected from borehole fluids on 47 mm, 0.2 µm Supor filters (Pall Corporation, Port Washington, NY, USA), which were then stored on dry ice, transported to the University of Southern California, and frozen at -80 °C. Whole genomic DNA was extracted using a modified phenol-chloroform method with ethanol precipitation as previously described in Momper *et al.* (2015). DNA concentration was checked on a Qubit 2.0 fluorometer (Thermo Fisher Scientific, Chino, CA, USA), and purity was measured on a NanoDrop 2000 spectrophotometer (Thermo Fisher Scientific) before samples were sent for sequencing. Sequencing was performed at the University of Southern California's Genome and Cytometry Core Facility (Los Angeles, CA, USA). Illumina sequencing libraries were prepared according to Dunham and Friesen (2013) with the exception that DNA was sheared with dsDNA Shearase Plus (Zymo: Irvine, CA, USA) and cleaned using Agencourt AMPure XP beads (Beckman-Coulter: Indianapolis, IN, USA). Fragment size selection was also carried out using beads instead of gel electrophoresis. Libraries were quantified using the Qubit 2.0 Fluorometer (Thermo Fisher Scientific), and the fragment size distribution was determined with an Agilent Bioanalyzer 2100. The libraries were then pooled in equimolar concentrations, quantified via qPCR using the Kapa Biosystems Library Quantification Kit and paired-end sequenced on an Illumina HiSeq 2500 platform. The libraries preparation, pooling, quality control and sequencing were all performed at the University Park Campus Genome Core (University of Southern California, Los Angeles, CA, USA).

De novo assembly and read mapping

Quality control was performed using Trimmomatic 0.36 with default parameter and a minimum sequence length of 36 base pairs (Bolger *et al.*, 2014). Reads were assembled using IDBA-UD v1.1.1 (Peng *et al.*, 2012) with a 5000 bp minimum contig

length. Sequences from each of the two borehole fluids were assembled individually, and together as a co-assembly. All downstream analyses reported here were performed on the co-assembly because (a) the co-assembly produced a longer maximum contig length, (b) a larger number of contigs were produced and (c) preliminary 16S data (Osburn *et al.*, 2014) indicated highly similar community composition between the two fluids, and initial metabolic and phylogenetic analyses from the individual assemblies were producing redundant results (data not shown). Coverage depth information was then generated for scaffolds greater than 5000 base pairs by mapping the 150 base pair paired-end reads of each of the two samples to the co-assembled scaffolds using Bowtie2 v2.2.6 (Langmead and Salzberg, 2012) with the BWA-SAMPLE algorithm and default parameters. SAMtools v0.1.17 (Li *et al.*, 2009) was then used to convert files to binary format for downstream analysis.

Generation of MAGs

MAGs were generated using sequence composition, differential coverage and read-pair linkage through the CONCOCT program within the Anvi'o software (Alneberg *et al.*, 2014; Eren *et al.*, 2015). MAGs were manually refined and curated using an interactive interface in the Anvi'o program (Eren *et al.*, 2015). After refinement, MAG completeness (reported as percentage of the set of single-copy marker genes present) and contamination (calculated as multiple occurrence of a single-copy marker gene) were recalculated using five different standard marker gene suites (Creevey *et al.*, 2011; Dupont *et al.*, 2012; Wu and Scott, 2012; Campbell *et al.*, 2013; Alneberg *et al.*, 2014) (Supplementary Figure 1).

Assignment of putative taxonomies

MAGs were assigned putative taxonomic identities according to their placement in a phylogenome tree using the 'tree' command in CheckM (Parks *et al.*, 2015). CheckM employs pplacer (Matsen *et al.*, 2010) to place concatenated amino-acid alignments into an Integrated Microbial Genomes (IMG) database of complete genomes (CheckM database v1.0.4). Phylogenetic identities of MAGs were further refined according to information from 16S rRNA and other conserved single-copy marker genes, as described below.

16S rRNA tree construction

Small subunit ribosomal RNA genes (>300 nucleotides) were extracted from the MAGs using the 'ssu_finder' tool integrated within CheckM (Parks *et al.*, 2015) and their three closest neighbors identified via a BLAST (Basic Local Alignment Search Tool) query against the non-redundant NCBI database. All sequences were pooled and aligned

using the online SINA tool v1.2.11 (Pruesse *et al.*, 2012). For comparison, additional SSU rRNA sequences from Kantor *et al.* (2013), Rinke *et al.* (2013) and Castelle *et al.* (2015) were aligned in a similar fashion. All aligned sequences were imported ARB v6.0.3 (Ludwig *et al.*, 2004), and additional closest relatives to the MAG SSU rRNA genes were identified within the SSUR-ef_NR99_123_SILVA_12_07_15 and LTPs123_SSU databases (Pruesse *et al.*, 2007; Yarza *et al.*, 2008; Quast *et al.*, 2013). A maximum-likelihood phylogenetic analysis was performed using RAXML v8.2.8 with the GTR model of nucleotide substitution under the gamma—and invariable—models of rate heterogeneity (Stamatakis, 2006).

Phylogenomic analyses

From all SURF MAGs described here with completeness >50% and relevant MAGs and SAGs (single-amplified genomes) from IMG (Markowitz *et al.*, 2014), ggKbase and National Center for Biotechnology Information (NCBI) GenBank databases, phylogenetically-informative marker genes were identified and extracted using the 'tree' command in CheckM. In CheckM, open reading frames were called using prodigal v2.6.1 (Hyatt *et al.*, 2012) and a set of 43 lineage-specific marker genes, similar to the universal set used by PhyloSift (Darling *et al.*, 2014), were identified and aligned using HMMER v3.1b1 (Eddy, 2011). The 75 MAGs with >50% completeness were given taxonomic identifications through analysis of a concatenated marker gene alignment (6988 amino-acid positions) and placement in a phylogenomic tree with closest related MAGs and SAGs found in the NCBI, IMG and ggKbase databases. The phylogeny was produced using FastTree v2.1.9 (Price *et al.*, 2010) with the WAG amino-acid substitution model and 'fastest' mode and bootstrap values reported by FastTree analysis indicate local support values (Figure 1).

Metabolic pathway analysis

Co-assembled metagenomes and individual genomes were submitted for gene calling and annotations through the DOE Joint Genome IMG-MER (Institute Integrated Microbial Genomes metagenomics expert review) pipeline (Markowitz *et al.*, 2008; Huntemann *et al.*, 2015). Genes of encoding metabolic and other functions of particular interest were queried in IMG-MER and associated to the previously described MAGs using common scaffold ID identifiers. Functional genes that were found in candidate phyla bins in this study that had not been reported previously in those phyla were scrutinized using additional methods; specifically, the coding region for each gene of interest was extracted, translated and used to perform a BLASTp search for nearest neighbors. Alignments were examined and, if the alignment was of poor quality (for example, large gaps and/or low

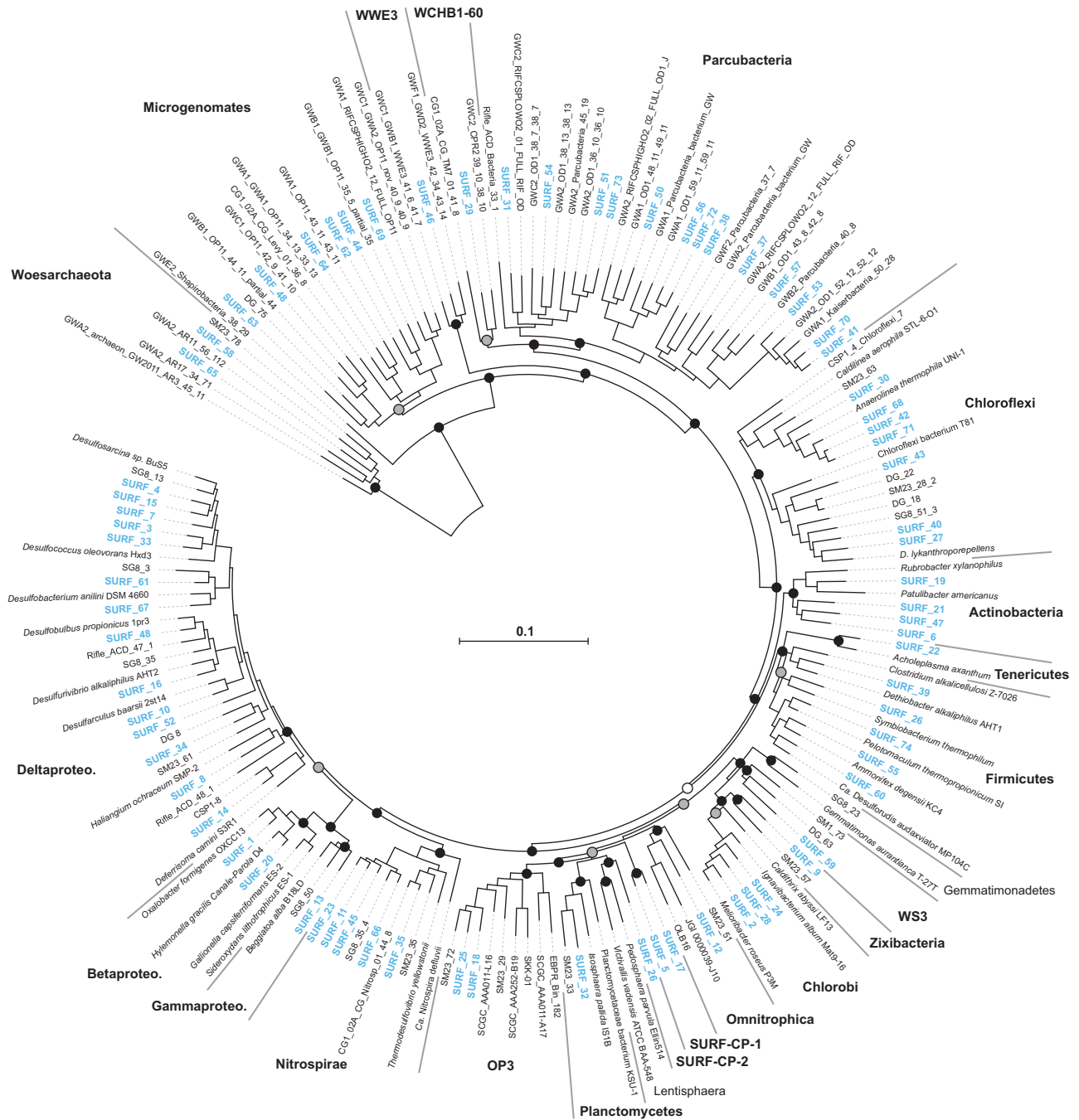


Figure 1 Diversity of organisms from which genomes from metagenomes (MAGs) were reconstructed from the Sanford Underground Research Facility fluids. Maximum-likelihood phylogenomic analysis of all MAGs > 50% complete and select genomes, MAGs and single cell amplified genomes from IMG, NCBI and ggKbase. The scale bar corresponds to 1 substitution per amino-acid position. Each numbered and blue-colored branch represents one MAG identified here. The names of major lineages with MAGs found in SURF fluids are indicated with bold-face font. MAGs belonging to novel phyla for which no reference genomes identified (SURF-CP-1 and SURF-CP-2) are indicated. Black (100%), gray ($\geq 75\%$) and white ($\geq 50\%$) circles indicate nodes with high local support values, from 1000 replicates.

identity), the gene was deemed a false hit and was not included in our results and discussion. A complete list of metabolic genes of interest that were queried in this study can be found in Supplementary Table 1.

Possible autotrophy was investigated in all MAGs. We examined KEGG (Kyoto Encyclopedia for Genes and Genomes) biochemical maps for the

six known carbon fixation pathways in each MAG, but only genes that are known to code for enzymes unique to carbon fixation were included (for example, genes involved in glycolysis were not included in the gene suite for the reductive citric acid cycle). A complete list of the KEGG identifiers for each of the six pathways can be found in Supplementary Table 2.

Table 2 Overview of all genome bins >50% complete and with <10% contamination

<i>SURF Bin</i>	<i>Taxon</i>	<i>Number scaffolds</i>	<i>Number genes</i>	<i>Genome size (Mbp)</i>	<i>Average completeness</i>	<i>s.d. of completeness</i>	<i>Contamination</i>
SURF_1	Proteobacteria; Oxalobacter	17	2253	2.32	97.6	2.1	3.5
SURF_2	Ignavibacteriales	114	3654	4.06	97.3	3.4	4.5
SURF_3	Proteobacteria; Desulfobacteraceae	90	4281	4.51	96.9	3.8	5.4
SURF_4	Proteobacteria; Desulfobacteraceae	197	5969	6.45	95.9	3.4	7.2
SURF_5	SURF-CP-1	145	4482	5.10	95.7	3.0	4.3
SURF_6	Actinobacteria	58	2812	2.81	95.4	4.3	8.3
SURF_7	Proteobacteria; Desulfobacteraceae	100	4680	5.01	95.1	3.8	3.9
SURF_8	Proteobacteria; Myxococcales	183	4450	5.40	94.0	5.4	5.8
SURF_9	Zixibacteria	140	3190	3.77	93.9	4.0	4.4
SURF_10	Proteobacteria; Desulfarculus	78	3539	3.60	93.5	3.2	5
SURF_11	Nitrospirae; Nitrospiraceae	87	2653	2.64	93.6	1.8	4.2
SURF_12	Omnitrophica	192	3357	6.88	93.3	2.4	4.7
SURF_13	Gammaproteobacteria	50	1774	1.69	92.6	3.7	3.4
SURF_14	Proteobacteria; Deltaproteobacteria	105	3075	3.08	91.7	1.5	6.6
SURF_15	Proteobacteria; Desulfobacteraceae	268	5070	5.29	91.5	8.9	3.6
SURF_16	Proteobacteria; Desulfurivibrio	118	3854	1.14	91.5	3.3	5.2
SURF_17	SURF-CP-1	144	4105	4.64	90.9	4.7	3.7
SURF_18	OP3	10	1696	1.69	90.8	3.3	1.3
SURF_19	Actinobacteria; Gaiellales	77	2392	2.35	90.8	5.6	3.8
SURF_20	Proteobacteria; Commomonadacea	106	4253	4.29	90.8	2.5	4.6
SURF_21	Actinobacteria; OPB41	104	3392	3.79	90.2	4.3	2.8
SURF_22	Tenericutes; Achleplasma	46	1705	1.72	90.0	2.3	4.5
SURF_23	Nitrospirae; Nitrospiraceae	106	2771	2.90	88.8	5.3	2.9
SURF_24	Ignavibacteriales	173	4163	5.04	87.8	3.5	6.1
SURF_25	OP3	36	1480	1.46	87.8	4.3	1.4
SURF_26	SURF-CP-2	105	2775	3.54	87.7	3.7	5.4
SURF_27	Chloroflexi; Dehalococcoidia	71	2067	1.80	86.8	2.4	1.9
SURF_28	Ignavibacteriales	117	2337	2.45	85.9	10.0	3
SURF_29	WCHB1-60	61	1573	1.55	85.6	9.5	6
SURF_30	Chloroflexi; Anaerolineaceae	84	2238	2.26	85.5	2.3	2.2
SURF_31	Parcubacteria	21	1047	0.99	84.0	11.5	0.6
SURF_32	Planctomycetes; Phycisphaerales	155	3489	4.31	82.7	12.8	4.4
SURF_33	Proteobacteria; Desulfobacteraceae	137	3507	3.72	82.3	3.0	3.2
SURF_34	Proteobacteria; Deltaproteobacteria	108	2002	1.92	80.6	7.9	3.8
SURF_35	Nitrospirae; Nitrospiraceae	63	1502	1.40	80.4	7.3	1.3
SURF_36	Firmicutes	101	2261	2.32	80.3	5.6	2
SURF_37	Parcubacteria	13	1017	0.93	79.0	9.9	0.7
SURF_38	Parcubacteria	14	774	0.69	78.8	11.3	0.6
SURF_39	Firmicutes; Dethiobacter	79	2434	2.34	78.5	9.6	4
SURF_40	Chloroflexi; Dehalococcoidia	74	1662	1.56	76.8	14.0	3.9
SURF_41	Parcubacteria	18	804	0.72	76.4	9.7	0.9
SURF_42	Chloroflexi; Anaerolineaceae	143	2257	2.78	76.3	8.6	2.8
SURF_43	Chloroflexi; Dehalococcoidia	82	2131	2.01	76.3	8.8	2.2
SURF_44	Microgenomates	34	1343	1.28	75.9	8.4	9.6
SURF_45	Nitrospirae; Nitrospiraceae	74	3041	3.05	75.3	10.7	6.5
SURF_46	WWE3	25	1169	1.10	74.8	12.2	2
SURF_47	Actinobacteria	22	1501	1.52	74.7	10.8	2.9
SURF_48	Proteobacteria; Desulfobulbus	108	2395	2.64	74.7	6.8	2.8
SURF_49	Microgenomates	29	1300	1.15	74.7	16.3	5.7
SURF_50	Parcubacteria	104	2242	2.04	73.2	9.7	3
SURF_51	Parcubacteria	34	769	0.72	71.8	10.9	1.3
SURF_52	Proteobacteria; Deltaproteobacteria	179	3873	3.93	72.0	3.7	4.8
SURF_53	Parcubacteria	40	1043	0.92	71.4	13.5	0.6
SURF_54	Parcubacteria	19	885	0.78	70.1	13.6	2.1
SURF_55	Firmicutes; Ammonifex	89	1892	1.82	70.2	5.5	3.8
SURF_56	Parcubacteria	24	810	0.70	68.4	11.3	1.7
SURF_57	Parcubacteria	35	931	0.91	68.4	7.5	2.1
SURF_58	Woesearchaeota	6	1515	1.31	68.1	28.3	3.7
SURF_59	WS3	99	1631	1.85	68.1	10.7	1.1
SURF_60	Firmicutes; Desulfurudis	75	3205	3.14	74.1	20.8	7.4
SURF_61	Proteobacteria; Desulfobacteraceae	316	7377	8.09	67.2	11.7	7.7
SURF_62	Parcubacteria	64	1121	1.40	64.2	7.3	2.6
SURF_63	Microgenomates	27	874	0.76	63.5	15.1	0.8
SURF_64	Microgenomates	32	991	0.93	63.3	13.3	0.6
SURF_65	Woesearchaeota	26	1363	1.15	62.5	24.5	3.4
SURF_66	Nitrospirae; Nitrospiraceae	120	2914	3.13	62.4	11.5	2.6
SURF_67	Proteobacteria; Desulfobacteraceae	149	2911	3.01	62.0	9.0	3.4
SURF_68	Chloroflexi; Anaerolineaceae	149	4034	1.01	60.9	16.9	3.2

Table 2 (Continued)

<i>SURF</i> <i>Bin</i>	<i>Taxon</i>	<i>Number</i> <i>scaffolds</i>	<i>Number</i> <i>genes</i>	<i>Genome size</i> <i>(Mbp)</i>	<i>Average</i> <i>completeness</i>	<i>s.d. of</i> <i>completeness</i>	<i>Contamination</i>
SURF_69	Armatimonadetes	28	597	0.54	55.8	20.8	2.4
SURF_70	Parcubacteria	29	747	0.65	53.1	8.3	0.6
SURF_71	Chloroflexi; Anaerolineaceae	111	2053	1.95	52.3	9.0	0
SURF_72	Parcubacteria	28	637	0.52	52.3	11.0	0.8
SURF_73	Parcubacteria	107	1705	1.54	50.8	16.5	2.5
SURF_74	Firmicutes; Peptococcaceae	120	2020	2.40	50.3	15.0	16

Abbreviations: Mbp, million base pairs; SURF, Sanford Underground Research Facility; s.d., standard deviation.

Results

Sequencing and assembly

Shotgun sequencing of total community genomic DNA produced 147 742 812 and 137 946 268 150 base pair (bp) paired-end reads for SURF-B and -D fluids, respectively. After quality filtering, 94.68% of reads were retained for assembly. *De novo* assemblies of quality-filtered reads generated a total of 637 833 contigs for the co-assembly. Maximum contig length was 576 430 bp. Prediction of open reading frames resulted in 1 187 179 putative genes in the co-assembly (Table 1).

MAGs

A total of 74 MAGs with >50% completeness and <10% contamination were recovered from the co-assembled metagenomes. Genome statistics including number of scaffolds, genes, genome size, average completeness and contamination are listed in Table 2. Bins were assigned numerical identifiers in order of decreasing completeness. Of the 74 individual MAGs, 22 were >90% complete and 15 were 80–90% complete. Completeness and contamination was averaged from five sets of widely accepted single-copy marker genes (Supplementary Figure 1; Creevey *et al.*, 2011; Dupont *et al.*, 2012; Wu and Scott, 2012; Campbell *et al.*, 2013; Alneberg *et al.*, 2014). Standard deviation of these values is reported in Table 2.

MAG phylogenetic identification

The majority of the SURF MAGs (72 of 74) were from the domain Bacteria; only two were from the domain Archaea, specifically the phylum Woesearchaeota (Figure 1). Within the Bacteria, members of the class *Deltaproteobacteria* are highly represented (16 MAGs) in both SURF-B and -D fluids. Recruitment of the MAGs found in SURF fluid indicates similar coverage values for most genomes investigated (data not shown). The exceptions included numerous members (SURF 49, 50, 63, 73) of the *Patescibacteria* superphylum, *Microgenomates* (formerly OP11) and *Parcubacteria* (formerly OD1), which have relatively higher coverage in SURF-D fluids. We note that the MAGs for these two phyla

are 50–75% complete and comprise many of our MAGs that are <80% complete (Table 2, Figure 2 and Supplementary Figure 1).

Candidate phyla make up almost 40% (29 of 74) of the MAGs in deep fluids at SURF. MAGs belonging to the bacterial candidate phyla *Zixibacteria* (formerly RBG-1), *Omnitrophica* (formerly OP3), *WCHB1-60*, *Parcubacteria* (formerly OD1), *Microgenomates* (formerly OP11), *WWE3* and *Latescibacteria* (formerly WS3) were recovered from SURF fluids. One MAG (SURF_60) is most closely related to candidate phylum *Candidatus Desulforudis audaxviator*, a member of the phylum *Firmicutes* that has been found globally in deep subsurface environments (Baker *et al.*, 2003; Cowen *et al.*, 2003; Chivian *et al.*, 2008; Aüllo *et al.*, 2013; Tiago and Veríssimo, 2013; Magnobosco *et al.*, 2015; Jungbluth *et al.*, 2016). At last, two of our MAGs (SURF_58 and SURF_65) are affiliated with the recently named archaeal candidate phylum *Woesearchaeota* (Castelle *et al.*, 2015).

Our 16 S rRNA gene phylogenetic analysis showed that four MAGs (SURF_12, 18, 25 and 26) are related to the *Omnitrophica*/OP3, but they were polyphyletic relative to the OP3/*Omnitrophica* group (Supplementary Figure 2). In-depth phylogenomic analysis using concatenated ribosomal proteins of publicly available genomes from both SAGs and MAGs revealed a distinction between the *Omnitrophica* and OP3, and the existence of two phyla, not one (Figure 1 and Supplementary Figure 2). MAGs SURF_12, 18, 25 and 26 were further investigated by a BLAST search of all coding regions within the genomes against all publicly available genomes (BLAST2GO, v1.3, BioBam, Valencia Spain). Results revealed that MAGs SURF_12 is a member of the candidate phylum *Omnitrophica*; MAGs SURF_18 and SURF_25 are members of the candidate phylum OP3 (Supplementary Figure 3), phyla that were previously grouped together as a single phylum, but with inclusion of new additional data appear to be two distinct phyla. MAG SURF_26 is the first member of a new candidate phylum, here named SURF-CP-2 (Figure 1 and Supplementary Figure 4). Similar phylogenetic classification obstacles were encountered with genomes SURF_5 and SURF_17. Genes were translated into amino-acid sequences and phylogenomic analysis of concatenated marker

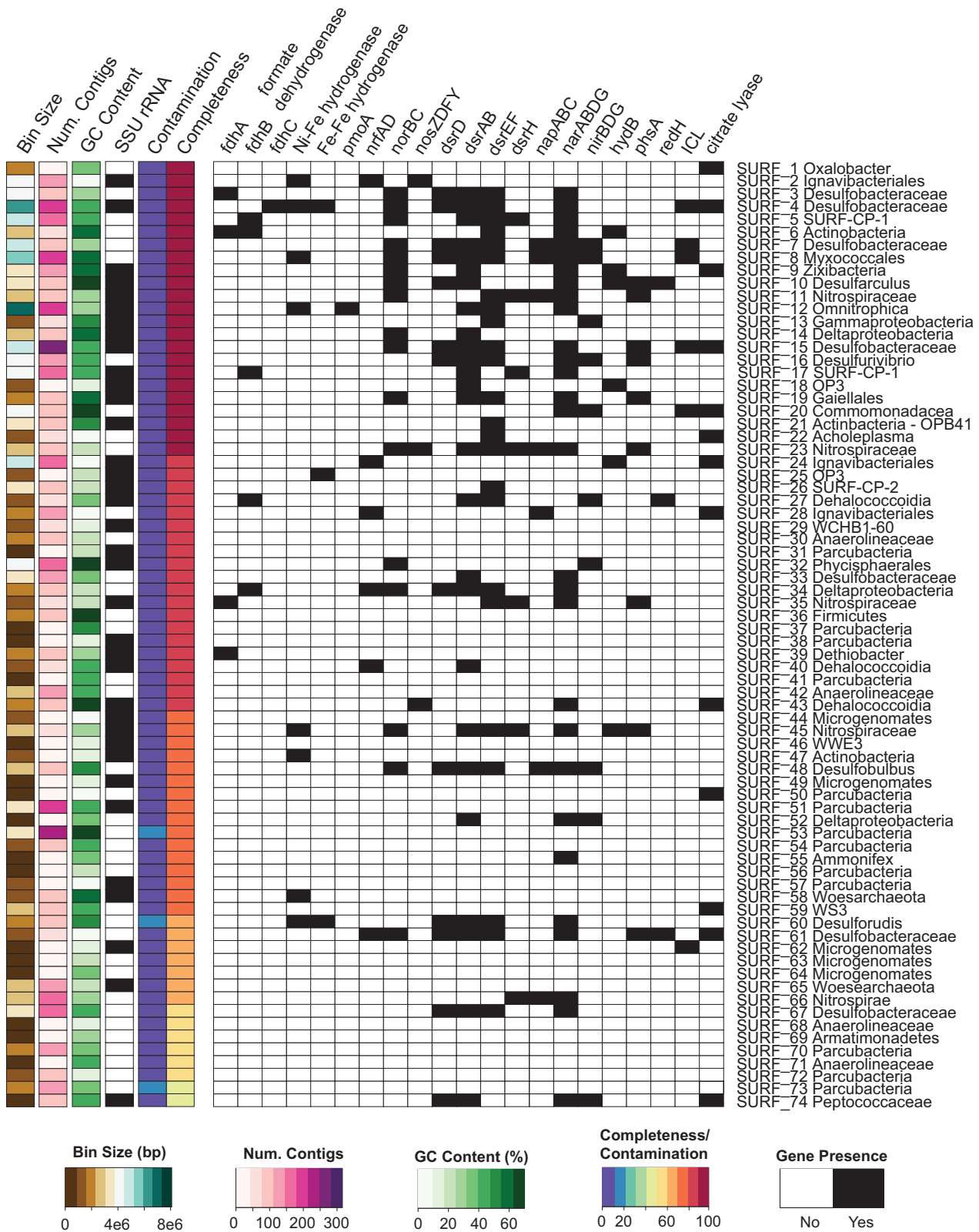


Figure 2 Functional genes, genome size, GC content and small subunit 16S rRNA presence in MAGs. Heat maps indicate total MAG scaffold size, number of contigs, GC content, completeness and contamination. Presence and absence of all SSU rRNA genes > 300 bp and presence of genes encoding functional genes are indicated by black boxes: pmoA, particulate methane monooxygenase; nrfAD, nitrite reductase; norBC, nitric oxide reductase; nosZDFY, nitrous oxide reductase; dsrAB, dissimilatory sulfite reductase; napABC, periplasmic nitrate reductase; narABDG, nitrate reductase; nirBDG, nitrite reductase; hydB, sulfur reductase; phsA, thiosulfate reductase; redH, reductive dehalogenase; ICL, isocitrate lyase.

genes and single-copy marker genes and review of top species hits results indicate that these MAGs constitute the first members of a novel candidate phylum, here designated SURF-CP-1, which is phylogenetically related to the Omnitrophica and *Planctomycetes* (Figure 1 and Supplementary Figure 5).

Metabolic capabilities in MAGs: inferred electron donors

Presence of functional genes was queried in MAGs and all results can be found in Figure 2. Particulate methane (*pmoA*) monooxygenase was identified in candidate phylum Omnitrophica MAG SURF_12 only. To our knowledge this is the first report of putative methanotrophic capability in the candidate phylum Omnitrophica. Nickel-Iron (Ni-Fe) and (Fe-Fe) hydrogenases were present in >10% of all MAGs (9 of 74), possibly indicating a widespread ability to utilize hydrogen as an electron donor. Homologs of formate dehydrogenase (*fdhABC*) were queried in all genomes, but no single genome contained genes for all three subunits (*ABC*) for this multimeric protein (Figure 2). Similarly, genes involved in carbon monoxide oxidation (*coxMLS*) were searched for but only homologs for *coxS* were identified (Supplementary Table 1). Canonical genes involved in thiosulfate, sulfur or sulfide oxidation, respectively (*soxBCY*, *sor*, *sqr*, *fcc*) were queried in the MAGs as well as in all of the scaffolds from both metagenomes, but none were found. Genes indicative of sulfur oxidation via the reverse dissimilatory sulfate reduction pathway (*dsrEFH*) (Ghosh and Dam, 2009) were found in three genomes that also contained a homolog for dissimilatory sulfite reductase (*dsrAB*). However, *dsrL*, which is considered the essential enzyme for sulfur oxidation in this pathway (Sander *et al.*, 2006; Grimm *et al.*, 2008; Ghosh and Dam, 2009) is not present in any genomes (Figure 2). Genes encoding enzymes involved in ferrous iron oxidation (Supplementary Table 1) were not found in any genome recovered from these fluids.

Metabolic capabilities in MAGs: inferred electron acceptors

Putative sulfate/sulfite reducing microorganisms are relatively abundant among the 74 reconstructed MAGs in this study, with 20% (13 of 74, Figure 2) containing the genes for dissimilatory sulfite reductase (*dsrAB*) and the necessary accessory protein *dsrD*. The genes encoding for cytoplasmic nitrate reductase (*nar*, all enzyme subunits) were identified in 35% (27 of 74) of the MAGs. All subunits of the *nar* operon (*ABDG*) were found in MAG SURF_12, belonging to the candidate phylum Omnitrophica. Conversely, putative periplasmic nitrate reduction ability (*napABC*) was less common, found in only seven MAGs. Nitrite reductase (*nirBDG*) and nitric oxide reductase (*norBC*) were present in 10 and 19

MAGs, respectively, but nitrous oxide reductase (*nosZDFY*) was only found in three MAGs.

It should be noted that genes for enzymes and co-factors involved in methane transformation (*mcrA*, coenzyme F420) and cellulose degradation (*cel5*, *cel48*) were found on scaffolds in the assembled metagenomes but were not found on scaffolds in the MAGs. In addition, genes involved in extracellular iron reduction (*mtrA*), and tetrahydromethanopterin-linked C1 transfer (*fae* and *fhcD*) were queried but not found in MAGs or the full assembled metagenomes as a whole (Supplementary Table 1).

Modes of carbon fixation in MAGs

Carbon fixation capability was examined in each of the 74 MAGs (Figure 3). The reductive Acetyl-CoA (Wood-Ljungdahl) pathway was the most common; 33 MAGs contained at least 75% of the necessary genes involved in this pathway (essential genes are listed in Supplementary Table 2). The corresponding lineages were diverse and included *Ammonifex*, *Ca. Desulforudis*, *Dehalococcoidia*, *Dethiobacter*, numerous *Deltaproteobacteria*, *Actinobacteria*, *Firmicutes* and *Chloroflexi*, as well as members of the candidate phyla Omnitrophica and Hydrogenedentes. Only one MAG contained the gene encoding for RuBisCO and phosphoribulokinase, the canonical enzymes involved in carbon fixation via the reductive pentose phosphate (Calvin) cycle. This MAG was a member of the *Gammaproteobacteria*. The sequences were homologous with known Type II RuBisCO, which catalyzes the carboxylation and oxygenation of ribulose 1,5-bisphosphate (Tabita *et al.*, 2008). The four other carbon fixation pathways (3-hydroxypropionate bi-cycle, 3-hydroxypropionate/4-hydroxybutyrate, dicarboxylate/4-hydroxybutyrate, reductive citric acid cycle) were far less common in MAGs (Figure 3) and in general less complete. No MAG contained all of the known genes involved in any of these pathways, but numerous members of the *Deltaproteobacteria* contained >80% of the necessary genes for the reductive citric acid, 3-hydroxypropionate bi-cycle, 3-hydroxypropionate/4-hydroxybutyrate and dicarboxylate/4-hydroxybutyrate cycles (Figure 3).

Discussion

Next-generation Illumina sequencing technology has only been used in a few terrestrial deep biosphere studies to explore microbial community composition and metabolic capabilities. Dong *et al.* (2014) showed that one bacterial species, *Halomonas sulfidaeris*, dominated the community in a 1.8 km-deep Cambrian Sandstone reservoir. Similarly, Chivian *et al.* (2008) found a mono-species community in 2.8 km-deep fracture fluids in a South African gold mine. In contrast to the Dong *et al.* (2014) and Chivian *et al.* (2008) studies, the present study of

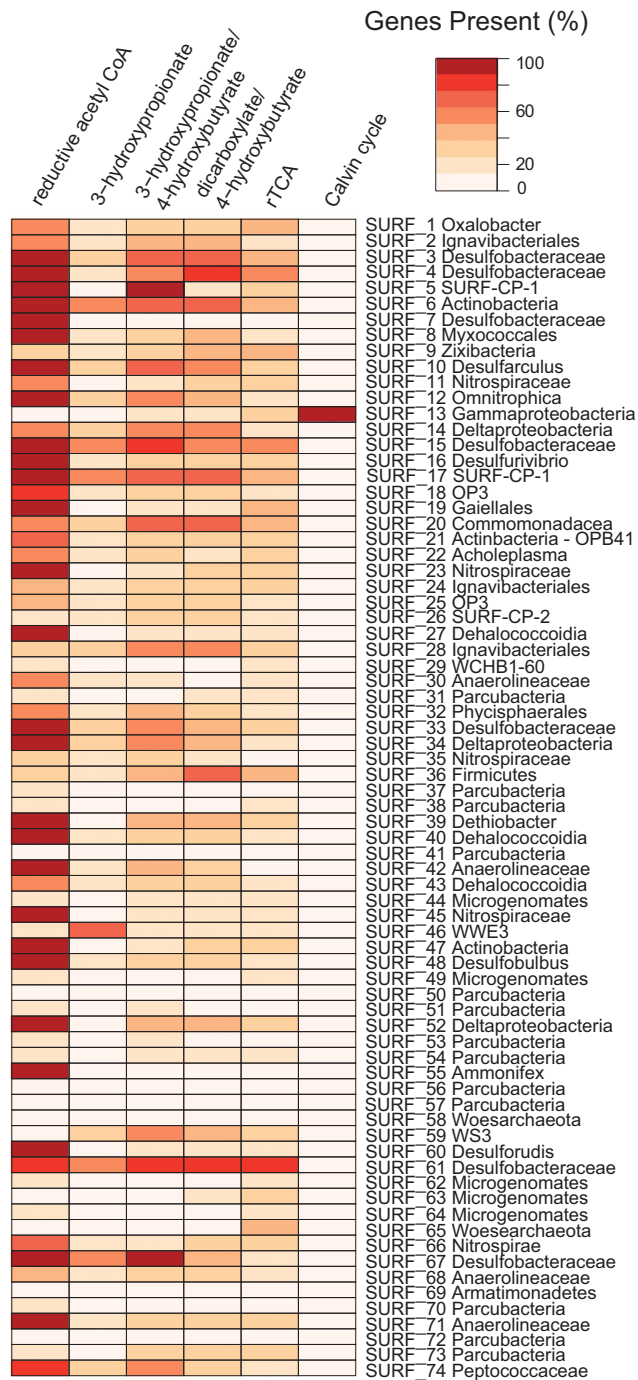


Figure 3 Identification of carbon fixation capabilities in all MAGs >50% complete. Heat map indicates the percent of signature genes present in six well-characterized carbon fixation pathways. A full list of genes queried is described in Supplementary Table 2.

fluids from the 1.5 km-deep Paleoproterozoic meta-sedimentary units at SURF, found a diverse subsurface community residing in the terrestrial DSB. This is more in line with similar studies by Lau *et al.* (2014), Nyssönen *et al.* (2014) and Maganbosco *et al.* (2015). This highlights the microbial variability, both in terms of cell density and diversity within terrestrial subsurface fluids. In this study, we

found similar phylogenetic diversity as that reported in Magnabosco *et al.* (2015) from 3 km-deep Precambrian continental crust in the Witwatersrand Basin of South Africa. In both studies ~25 bacterial phyla were identified in the community. The major difference in phylogeny was the large proportion of candidate phyla identified in this study and almost complete absence of candidate phyla in the other—a mere four groups could only be identified on the domain level (Magnabosco *et al.*, 2015). This study recovered a total of 74 MAGs, 22 of which are high quality genomes, meaning >90% complete and <5% contaminated by recent standards (Bowers *et al.*, 2017). The remaining 52 MAGs are >50% complete and <10% contaminated, deemed medium quality by current standards (Bowers *et al.*, 2017). Here, we discuss trends in metabolic capability among these 74 MAGs from SURF fluids, with a particular focus on subsurface microbial dark matter represented by near-complete candidate phyla genomes. Given the *in situ* geochemical conditions and calculations of redox reaction energetics (Osburn *et al.*, 2014), particular interest was paid to energy metabolisms involving cycling of hydrogen, nitrogen, sulfur and methane.

Biological transformation of nitrogen, sulfur and hydrogen

Evidence of denitrification (*nar*, *nap*, *nir*, *nor*, *nos* and/or *nrf*) was found in 38 MAGs. The commonality of both cytoplasmic (*narABDC*) and periplasmic (*napABC*) nitrate reductases and all other enzymes that perform steps in the complete denitrification ($\text{NO}_3^- \rightarrow \text{N}_2$) process suggests that dissimilatory nitrogen-transforming metabolisms are common and there is likely a dynamic nitrogen cycle occurring within SURF fluids. Note that although nitrite levels were below detection limit, nitrate measured 10.3 and 23.7 μM in SURF-D and -B fluids, respectively at the time these samples were collected (Osburn *et al.*, 2014). Thermodynamic calculations indicate that nitrate reduction (especially with hydrogen as an electron donor) is highly exergonic in SURF-B and -D fluids (Osburn *et al.*, 2014).

Genes for putative hydrogen-oxidizing enzymes (Ni-Fe and Fe-Fe hydrogenases) were common (10 of 74 genomes), however dissolved molecular hydrogen was detected in only nanomolar levels in SURF fluids. Despite the extremely low measured concentrations, hydrogen is still an energetically favorable electron donor for most redox couples considered here (Osburn *et al.*, 2014). The common occurrence of Ni-Fe and Fe-Fe hydrogenases and discrepancy with measured hydrogen could be due to multiple factors. First, these genes may not be expressed and could be turned on opportunistically if hydrogen concentrations increase. Second, the low solubility and rapid escapes of hydrogen make it an extremely difficult gas to measure accurately *in situ*. Concentrations experienced by microbes *in situ* may very well be higher than laboratory-measured

concentrations. Forthcoming metatranscriptomics should shed light on the active use of hydrogen as an electron donor in these deep fluids.

Putative sulfate reducers are abundant among the MAGs in this study, with ~20% of all bins containing the *dsrABD* genes (Figure 2). Interestingly, the genes for *dsrABD* and Ni-Fe, Fe-Fe hydrogenases were present in SURF_60, a phylogenetic relative to *Ca. Desulforudis audaxviator*, a member of the *Firmicutes* that has been found in other terrestrial and marine subsurface environments (Baker *et al.*, 2003; Jungbluth *et al.*, 2013; Magnabosco *et al.*, 2015). For example, in fracture water in South Africa it was found to dominate (>99%) the microbial community (Lin *et al.*, 2006; Chivian *et al.*, 2008). Genome analysis of that lineage revealed an almost self-sufficient chemolithoautotrophic bacterium, putatively capable of carbon and nitrogen fixation and sulfate reduction using hydrogen as an electron donor (Chivian *et al.*, 2008).

Note that canonical genes involved in thiosulfate oxidation, sulfur oxidation or sulfide oxidation (*soxB*, *soxBCY*, *sor*, *sqr*, *fcc*) were not detected in any of our SURF MAGs, nor were they found when all scaffolds in the metagenomes were queried (Supplementary Table 1). This could indicate that sulfur species are rarely, if ever, used as an electron donor in SURF fluids. This may seem counter-intuitive given the relatively high total sulfide levels (83–130 $\mu\text{g l}^{-1}$) in SURF-B and -D fluids (Osburn *et al.*, 2014). However, thermodynamic calculations demonstrate that when considering energy density ($\text{J kg}^{-1} \text{H}_2\text{O}$), sulfide oxidation with either oxygen or nitrate as the oxidant is not favorable (that is, endergonic) (Osburn *et al.*, 2014). Using a combination of metagenomic, geochemical and thermodynamic data, we conclude that sulfate reduction to elemental sulfur or sulfide is likely an important energy metabolism in these subsurface fluids. However, the oxidation of reduced sulfur back to sulfate appears to be a rare metabolic strategy, most likely because other electron donors (example, methane, carbon monoxide, hydrogen, ferrous iron) have a higher energy density than reduced sulfur species such as elemental sulfur and sulfide (Osburn *et al.*, 2014). This highlights the importance of considering energy density, not only Joules per mole of electrons transferred, when modeling *in situ* thermodynamic yields of dissimilatory metabolisms.

Carbon fixation in deep subsurface fluids

Although photosynthetically derived organic carbon can be found in Earth's subsurface, it is often recalcitrant and a limiting nutrient for heterotrophs (Pedersen, 2000). Bioavailable, surface-derived organic carbon is likely limited at the deep sites in SURF, and hence, many resident heterotrophs must rely on *in situ* production of fixed carbon by chemolithoautotrophs, including nitrate reducers, methanogens, acetogens, sulfate reducers and iron reducers (Stevens and McKinley, 1995; Stevens, 1997;

Pedersen, 2000; Lollar *et al.*, 2006; Chivian *et al.*, 2008; Beal *et al.*, 2009; Magnabosco *et al.*, 2015). As noted above, the most common mode of carbon fixation in the 74 MAGs was the reductive acetyl-CoA pathway. This ancient pathway is the only one known to be used by both Archaea and Bacteria (Hügler and Sievert, 2010). The predominance of this pathway was also documented in the metagenomic analysis of another terrestrial deep subsurface environment, the Witwatersrand Basin in South Africa (Magnabosco *et al.*, 2015). That study concluded that the preference for the reductive acetyl-CoA pathway was in response to energy limitation, it being energetically inexpensive compared with the other five pathways (Berg, 2011; Hügler and Sievert, 2010) and hence ideal for organisms operating near the thermodynamic limit of life. Furthermore, the acetyl-CoA pathway requires anoxic conditions, as some of its enzymes, especially the crucial acetyl-CoA synthase, are highly oxygen sensitive (Berg, 2011). This pathway's requirement for high levels of metals with low solubility under oxic or sulfidic conditions (Mo, Co, Ni, Fe) (Berg, 2011) also points to anoxic environments. Because of energetic efficiency and the necessity for anoxia, the acetyl-CoA pathway is the ideal mode of inorganic carbon fixation in highly reducing, aphotic and energy-deplete deep subsurface fluids, including those encountered at SURF, where the oxidation-reduction potential measured -235 to -276 mV (Osburn *et al.*, 2014). Certainly, the relative dominance of the reductive acetyl-CoA pathway is, in part, because of the wide variety of organisms that have been reported to use this pathway, spanning both the Archaeal and Bacterial domains (Berg, 2011). Such organisms include acetogens, sulfate reducing bacteria, ammonia-oxidizing *Planctomycetes* and anaerobic facultative autotrophs (Schauder *et al.*, 1988). Recently, the pathway was also shown to be run in reverse, with heterotrophs using carbon monoxide dehydrogenase and acetyl-CoA synthase to oxidize acetyl-CoA (Rabus *et al.*, 2006), so it cannot be ruled out that some of the Bacteria found in SURF fluids are employing the reductive acetyl-CoA pathway heterotrophically.

Members of the phylum *Chloroflexi* commonly use the 3-hydroxypropionate bi-cycle for carbon fixation (Hügler and Sievert, 2010). In our seven *Chloroflexi* MAGs, however, evidence for this pathway was rare, limited to only one to two genes out of the 14 key genes in that cycle (Figure 3 and Supplementary Table 2). These results may be explained by the high energetic costs of this pathway; it requires seven ATP equivalents for the synthesis of pyruvate and three additional ATPs for the formation of triose phosphate (Berg, 2011). In many lineages of *Chloroflexi*, this high energy cost is offset by phototrophy, which is not possible in the dark subsurface at SURF. Instead, five *Chloroflexi* genomes contain the complete or near-complete reductive acetyl-CoA pathway (85–100% of genes) (Figure 3), which in contrast requires only 1 ATP and 2 NADPH reducing equivalents (Hügler and Sievert, 2010).

The canonical genes encoding enzymes requisite for the reduction of CO₂ via the Calvin cycle, RuBisCo and phosphoribulokinase, were found in only one of our 74 MAGs (Figure 3). This MAG belongs to the phylum *Proteobacteria*. These translated genes were further investigated using BLASTp analysis and found to be closely related (93% identity over 99% query coverage) to the Type II RuBisCo found in typical *Proteobacteria* lineages (Hanson and Tabita, 2001; Tabita, *et al.*, 2008). This would indicate that the *Proteobacteria* found in SURF fluids is likely capable of carbon fixation via the Calvin cycle and the *cbbL* annotation was not a false hit nor are these genes related to the Type IV Rubisco-like protein that has been shown not to fix carbon (Tabita *et al.*, 2008).

Expansion of the predicted metabolic capabilities of the microbial dark matter and identification of two novel candidate phyla

In this study, we added four nearly complete (88–94%) MAGs to the repository of analyzed genomes in the candidate phylum Omnitrophica/OP3 (Rinke *et al.*, 2013; Kolinko *et al.*, 2015; Speth *et al.*, 2016). This phylum was originally identified in a terrestrial hot spring, Obsidian Pool, in Yellowstone National Park, USA, leading to its designation 'OP3' (Hugenholtz *et al.*, 1998). Since then, this phylum has been detected globally in environments such as flooded paddy soil (Derakshani *et al.*, 2001), freshwater lakes and marine estuaries (Rinke *et al.*, 2013), lake sediments (Kolinko *et al.*, 2015), wastewater bioreactors (Speth *et al.*, 2016), and the terrestrial subsurface (Rinke *et al.*, 2013 and this study). Without cultured members, and with previously very little genetic sequence data to analyze, OP3 was placed within the *Planctomycetes-Verrucomicrobia-Chlamydiae* superphylum, along with *Lentisphaerae* (added later) (Wagner and Horn, 2006; Pilhofer *et al.*, 2008). Our Omnitrophica and OP3 MAGs (SURF_12, 18, 26), include one of the most complete *Ca. Omnitrophica* genomes to date (93%, SURF_12). Similar to Rinke *et al.* (2013), we found genes for carbon fixation via the reductive acetyl-CoA pathway in all three MAGs.

In our 16 S rRNA and phylogenomic analyses, we observed incompatible polyphyly for MAGs SURF_12, 18, 25 and 26 with respect to the phyla OP3 and Omnitrophica. Previously, the phylum Omnitrophica was named on the basis of SAGs loosely related to OP3 16 S rRNA gene sequences from targeted gene surveys (Rinke *et al.*, 2013). More recent studies have also grouped OP3 and Omnitrophica as a single phylum (Baker *et al.*, 2015; Kolinko *et al.*, 2015; Speth *et al.*, 2016). However, after comparing all publically available OP3/Omnitrophica genomes, we conclude that OP3 and Omnitrophica are divergent. Based on extremely low (<30%) pairwise average amino-acid identity (data not shown) and phylogenomic analysis of

concatenated single-copy genes (Figure 1), we propose that they be split into two separate phyla.

Based on our phylogenomic analysis using a concatenated alignment of single-copy marker genes (Figure 1), phylogenetic analysis of 16 S rRNA gene sequences (Supplementary Figure 2), and average amino-acid identity analyses, three MAGs did not fall within any previously described phylum. We propose that one MAG (SURF_26) represents the first genome of a novel phylum. With time, more related genomes from environmental datasets will likely become available, and we should then be able to better describe and name this phylum. The two other MAGs (SURF_5 and SURF_17) do not identify with any known phylum, either, and we propose that these belong to a newly described phylum within the domain Bacteria, here named SURF-CP-1.

The Zixibacteria (formerly RBG-1) were recently defined as a novel candidate phylum (Castelle *et al.*, 2013). Sequences corresponding to this phylum have been identified in 16 S rRNA targeted surveys and metagenomic studies in global subsurface environments (Lin *et al.*, 2012; Castelle *et al.*, 2013; Baker *et al.*, 2015). Most recently, numerous lineages within this phylum were found in the sulfate-methane transition zone in anoxic sediments of the eastern United States (Baker *et al.*, 2015). Similar to previous studies (Castelle *et al.*, 2013), we failed to identify a complete carbon fixation pathway in bin SURF_9, although the MAG is near (94%) complete. We consequently suggest that this candidate phylum heterotrophically scavenges reduced carbon for biomass synthesis (anabolism), and is capable of nitrate (*narG*), nitric oxide (*norB*) or sulfate (*dsrAB*) reduction, and possibly thiosulfate (sulfhydrogenase) disproportionation, as catabolic strategies (Figure 2).

Putative metabolisms in newly identified candidate phyla, SURF-CP-1 and -2

SURF-CP-1, the newly identified candidate phylum named Abyssubacteria, is composed of two genomes in this study, SURF_5 and SURF_17. These genomes are 96% and 91% complete, respectively. They contain homologs of cytoplasmic nitrate reductase (*narABDG*) (Figure 2). In addition, SURF_5 contains a putative nitric oxide reductase (*norBC*). We hypothesize that these Bacteria can use, nitrate or nitric oxide as electron acceptors. Interestingly, the two genomes have different profiles with respect to putative carbon fixation (Figure 3). SURF_5 contains 90% of the genes unique to the 3-hydroxypropionate/4-hydroxybutyrate bi-cycle and all genes necessary for the reductive Acetyl-CoA (Wood-Ljungdahl) pathway, whereas SURF_17 has only a complete reductive Acetyl-CoA pathway (Figure 3 and Supplementary Figure 1). This could be indicative of a highly versatile lifestyle, as the reductive Acetyl-CoA pathway can be utilized as both an autotrophic assimilatory metabolism and in reverse as a heterotrophic dissimilatory metabolism, as

discussed above (Schauder *et al.*, 1988; Rabus *et al.*, 2006). SURF-CP-1 may even be using carbon monoxide as an electron donor for nitrate or sulfate reduction, redox couples that were predicted to be highly exergonic in these fluids by Osburn *et al.* (2014). SURF-CP-2 has a more cryptic lifestyle. The SURF_26 genome does not encode for any metabolic genes queried (Figure 2) nor does it have a complete carbon fixation pathway. It does not seem to be capable of a chemolithotrophic or autotrophic lifestyle, but could be heterotrophic or fermentative, metabolisms that were not as heavily investigated in this study.

Concluding remarks

This study used high-throughput Illumina sequencing to investigate a microbial ecosystem in the terrestrial DSB. Here, we find that *Deltaproteobacteria* and candidate phyla bacterial lineages are most abundant, with putative sulfate/sulfur reduction and nitrate/nitrite reduction likely being the most common energy metabolisms employed. This is consistent with previously calculated reaction energetics for deep subsurface fluids at SURF (Osburn *et al.*, 2014). We also identified a surprisingly high relative abundance of candidate phyla in these deep subsurface fluids and identified two novel putative candidate phyla bacterial lineages (SURF-CP1 and SURF-CP-2). SURF-CP-1 has been given the name Abyssobacteria, the Latin prefix meaning 'deep,' as it was collected in the deep subsurface, and its closest relatives according to 16S rRNA gene identity (98%) were found in the Nankai Trough and the world's largest sink hole, located in central Mexico. SURF-CP-2 has been named Aureobacteria, Latin prefix meaning 'gold' in recognition that it was collected in the former Homestake gold mine.

Data deposit

Sequence data for metagenomic reads, contigs and genes were submitted to the JGI-IMG under accession numbers IMG_3300007354, 3300007352 and 3300007351 for SURF-B and -D fluids, and the combined assembly, respectively. Sample metadata can be accessed using the BioProject identifier PRJNA355136. The NCBI BioSamples used here are SAMN06064269 (SURF-B fluid), SAMN06064270 (SURF-D fluid), and SAMN06064271 (SURF fluid_coassembly). FASTA files containing the contigs of all 74 MAGs can be accessed at doi: 10.6084/m9.figshare.4284578. A FASTA file containing 44 SSU rRNA genes with length >300 base pairs, including 40 extracted from the 74 MAGs, plus 4 additional SSU rRNA genes identified in preliminary (that is, non-reported) MAGs can be accessed at doi: 10.6084/m9.figshare.4284584. IMG/M-relevant files needed to isolate scaffold sets for all 74 genomes from metagenomes can be accessed at doi: 10.6084/m9.figshare.4284587.

Conflict of Interest

The authors declare no conflict of interest.

Acknowledgements

This work was supported by the NASA Astrobiology Institute under cooperative agreement NNA13AA92A. Many thanks to John Heidelberg and Rohan Sachdeva at USC for use of their servers and help in metagenomic analysis. We would also like to recognize A Murat Eren for his invaluable help in utilizing the Anvi'o interface. We want to thank especially staff and personnel at SURF for access to the deep subsurface and repeated access to samples used in this study. This work was funded by the NASA Astrobiology Institute under cooperative agreement NNA13AA92A.

References

- Alneberg J, Bjarnason BS, de Bruijn I, Schirmer M, Quick J, Ijaz UZ *et al.* (2014). Binning metagenomic contigs by coverage and composition. *Nat Methods* **11**: 1144–1146.
- Aülo T, Ranchou-Peyruse A, Ollivier B, Magot M. (2013). *Desulfotomaculum* spp. and related gram-positive sulfate-reducing bacteria in deep subsurface environments. *Front Microbiol* **4**: 362.
- Baker BJ, Moser DP, MacGregor BJ, Fishbain S, Wagner M, Fry NK *et al.* (2003). Related assemblages of sulphate-reducing bacteria associated with ultradeep gold mines of South Africa and deep basalt aquifers of Washington State. *Environ Microbiol* **5**: 267–277.
- Baker BJ, Lazar CS, Teske AP, Dick GJ. (2015). Genomic resolution of linkages in carbon, nitrogen, and sulfur cycling among widespread estuary sediment bacteria. *Microbiome* **3**: 14.
- Baker BJ, Saw JH, Lind AE, Lazar CS, Hinrichs K-U, Teske AP *et al.* (2016). Genomic inference of the metabolism of cosmopolitan subsurface Archaea, Hadesarchaea. *Nat Microbiol* **1**: 16002.
- Beal EJ, House CJ, Orphan VJ. (2009). Manganese- and iron-dependent marine methane oxidation. *Science* **325**: 184–187.
- Berg IA. (2011). Ecological aspects of the distribution of different autotrophic CO₂ fixation pathways. *Appl Environ Microbiol* **77**: 1925–1936.
- Bolger AM, Lohse M, Usadel B. (2014). Trimmomatic: a flexible trimmer for Illumina sequence data. *Bioinformatics* **30**: 2114–2120.
- Bowers RM, Kyrpides NC, Stepanauskas R, Harmon-Smith M, Schulz F, Doud D *et al.* (2017). Genome standards for single amplified genomes and genomes from metagenomes of Bacteria and Archaea. *Nat Biotechnol* in press.
- Campbell JH, O'Donoghue P, Campbell AG, Schwientek P, Sczyrba A, Woyke T *et al.* (2013). UGA is an additional glycine codon in uncultured SR1 bacteria from the human microbiota. *Proc Natl Acad Sci USA* **110**: 5540–5545.
- Castelle CJ, Hug LA, Wrighton KC, Thomas BC, Williams KH, Wu D *et al.* (2013). Extraordinary phylogenetic diversity and metabolic versatility in aquifer sediment. *Nat Commun* **4**: 2120.

- Castelle CJ, Wrighton KC, Thomas BC, Hug LA, Brown CT, Wilkins MJ. (2015). Genomic expansion of domain archaea highlights roles for organisms from new phyla in anaerobic carbon cycling. *Curr Biol* **25**: 690–701.
- Chivian D, Brodie EL, Alm EJ, Culley DE. (2008). Environmental genomics reveals a single-species ecosystem deep within Earth. *Science* **322**: 275–278.
- Cowen JP, Giovannoni SJ, Kenig F, Johnson HP, Butterfield D, Rappé MS *et al.* (2003). Fluids from aging ocean crust that support microbial life. *Science* **299**: 120–123.
- Creevey CJ, Doerks T, Fitzpatrick DA, Raes J, Bork P. (2011). Universally distributed single-copy genes indicate a constant rate of horizontal transfer. *PLoS One* **6**: e22099.
- Darling AE, Jospin G, Lowe E, Matsen FA IV, Bik HM, Eisen JA. (2014). PhyloSift: phylogenetic analysis of genomes and metagenomes. *PeerJ* **9**: e243.
- Derakshani M, Lukow T, Liesack W. (2001). Novel bacterial lineages at the (sub)division level as detected by signature nucleotide-targeted recovery of 16 S rRNA genes from bulk soil and rice roots of flooded rice microcosms. *Appl Environ Microbiol* **67**: 623–631.
- Grimm F, Franz B, Dahl C. (2008) Thiosulfate and sulfur oxidation in purple sulfur bacteria. In *Microbial Sulfur Metabolism*. Springer: Berlin, Heidelberg, 101–116.
- Dong Y, Kumar CG, Chia N, Kim PJ, Miller PA, Price ND *et al.* (2014). *Halomonas sulfidaeris*-dominated microbial community inhabits a 1.8 km-deep subsurface Cambrian Sandstone reservoir. *Environ Microbiol* **16**: 1695–1708.
- Dunham JP, Friesen ML. (2013). A cost-effective method for high-throughput construction of Illumina sequencing libraries. *Cold Spring Harbor Protocols* **2013**: 820–834.
- Dupont C, Rusch DB, Yooseph S, Lombardo MJ, Richter RA, Valas R *et al.* (2012). Genomic insights to SAR86, an abundant and uncultivated marine bacterial lineage. *ISME J* **6**: 1186–1199.
- Eddy SR. (2011). Accelerated profile HMM searches. *PLoS Comput Biol* **10**: e1002195.
- Edwards RA, Rodriguez-Brito B, Wegley L, Haynes M, Breitbart M, Peterson DM *et al.* (2006). Using pyrosequencing to shed light on deep mine microbial ecology. *BMC Genomics* **7**: 57.
- Eren AM, Esen ÖC, Quince C, Vineis JH, Morrison HG, Sogin ML *et al.* (2015). Anvi'o: an advanced analysis and visualization platform for 'omics data. *PeerJ* **3**: e1319.
- Fredrickson JK, Onstott TC. (1996). Microbes deep inside the earth. *Sci Am* **275**: 68–73.
- Ghosh W, Dam B. (2009). Biochemistry and molecular biology of lithotrophic sulfur oxidation by taxonomically and ecologically diverse bacteria and archaea. *FEMS Microbiol Rev* **33**: 999–1043.
- Hanson TE, Tabita FR. (2001). A ribulose-1, 5-bisphosphate carboxylase/oxygenase (RubisCO)-like protein from *Chlorobium tepidum* that is involved with sulfur metabolism and the response to oxidative stress. *Proc Natl Acad Sci* **8**: 4397–4402.
- Hugenholtz P, Pitulle C, Hershberger KL, Pace NR. (1998). Novel division level bacterial diversity in a Yellowstone hot spring. *Journal of Bacteriology* **180**: 366–376.
- Hügler M, Sievert SM. (2010). Beyond the Calvin cycle: autotrophic carbon fixation in the ocean. *Marine Sci* **3**: 261–289.
- Huntmann M, Ivanova NN, Mavromatis K, Tripp HJ, Paez-Espino D, Palaniappan K *et al.* (2015). The standard operating procedure of the DOE-JGI Microbial Genome Annotation Pipeline (MGAP v. 4). *Stand Genomic Sci* **10**: 86.
- Hyatt D, LoCascio PF, Hauser LJ, Uberbacher EC. (2012). Gene and translation initiation site prediction in metagenomic sequences. *Bioinformatics* **28**: 2223–2230.
- Jungbluth SP, Grote J, Lin HT, Cowen JP, Rappé MS. (2013). Microbial diversity within basement fluids of the sediment-buried Juan de Fuca Ridge flank. *ISME J* **7**: 161–172.
- Jungbluth SP, Glavina del Rio T, Tringe SG, Stepanauskas R, Rappé MS. (2017). Genomic comparisons of a bacterial lineage that inhabits both marine and terrestrial deep subsurface systems. *PeerJ* **5**: e3134.
- Kallmeyer J, Pockalny R, Adhikari RR. (2012). Global distribution of microbial abundance and biomass in subseafloor sediment. *Proc Natl Acad Sci USA* **109**: 16213–16216.
- Kantor RS, Wrighton KC, Handley KM, Sharon I, Hug LA, Castelle CJ *et al.* (2013). Small genomes and sparse metabolisms of sediment-associated bacteria from four candidate phyla. *MBio* **4**: e708–e713.
- Kolinko S, Richter M, Glöckner FO, Brachmann A, Schüler D. (2015). Single-cell genomics of uncultivated deep-branching magnetotactic bacteria reveals a conserved set of magnetosome genes. *Environ Microbiol* **18**: 21–37.
- Langmead B, Salzberg SL. (2012). Fast gapped-read alignment with Bowtie 2. *Nat Methods* **9**: 357–359.
- Lau MCY, Cameron C, Magnabosco C, Brown CT, Schilkey F, Grim S *et al.* (2014). Phylogeny and phylogeography of functional genes shared among seven terrestrial subsurface metagenomes reveal N-cycling and microbial evolutionary relationships. *Front Microbiol* **5**: 531.
- Lin LH, Wang PL, Rumble D, Lippmann-Pipke J, Boice E, Pratt LM *et al.* (2006). Long-term sustainability of a high-energy, low-diversity crustal biome. *Science* **314**: 479–482.
- Lin X, Kennedy D, Fredrickson J, Bjornstad B, Konopka A. (2012). Vertical stratification of subsurface microbial community composition across geological formations at the Hanford Site. *Environ Microbiol* **14**: 414–425.
- Lollar BS, Larampe-Couloume G, Slater GF, Ward J, Moser DP, Gihring TM *et al.* (2006). Unravelling abiogenic and biogenic sources of methane in the Earth's deep subsurface. *Chem Geol* **22**: 328–339.
- Lovley DR, Chapelle FH. (1995). Deep subsurface microbial processes. *Rev Geophys* **33**: 365–381.
- Loy A, Duller S, Baranyi C, Mußmann M, Ott J, Sharon I *et al.* (2009). Reverse dissimilatory sulfite reductase as phylogenetic marker for a subgroup of sulfur-oxidizing prokaryotes. *Environ Microbiol* **11**: 289–299.
- Ludwig W, Strunk O, Westram R, Richter L, Meier H, Buchner A *et al.* (2004). ARB: a software environment for sequence data. *Nucleic Acids Res* **32**: 1363–1371.
- McMahon S, Parnell J. (2014). Weighing the deep continental biosphere. *FEMS Microbiol Ecol* **87**: 113–120.
- Magnabosco C, Ryan K, Lau MC, Kuloyo O, Lollar BS, Kieft TL *et al.* (2015). A metagenomic window into carbon metabolism at 3 km depth in Precambrian continental crust. *ISME J* **10**: 730–741.
- Matsen FA, Kodner RB, Armbrust EV. (2010). pplacer: linear time maximum-likelihood and Bayesian

- phylogenetic placement of sequences onto a fixed reference tree. *BMC Bioinformatics* **11**: 1–16.
- Markowitz VM, Ivanova NN, Szeto E, Palaniappan K, Chu K, Dalevi D *et al.* (2008). IMG/M: a data management and analysis system for metagenomes. *Nucleic Acids Res* **36**: 534–538.
- Markowitz VM, Chen IM, Chu K, Szeto E, Palaniappan K, Pillay M *et al.* (2014). IMG/M 4 version of the integrated metagenome comparative analysis system. *Nucleic Acids Res* **42**: 568–573.
- Momper LM, Reese BK, Carvalho G, Lee P, Webb EA. (2015). A novel cohabitation between two diazotrophic cyanobacteria in the oligotrophic ocean. *ISME J* **4**: 882–893.
- Nyysönen M, Hultman J, Ahonen L, Kukkonen I, Paulin L, Laine P *et al.* (2014). Taxonomically and functionally diverse microbial communities in deep crystalline rocks of the Fennoscandian shield. *ISME J* **8**: 126–138.
- Onstott TC, Phelps TJ, Colwell FS, Ringelberg D, White DC, Boone DR *et al.* (1998). Observations pertaining to the origin and ecology of microorganisms recovered from the deep subsurface of Taylorsville Basin, Virginia. *Geomicrobiol J* **15**: 353–585.
- Orcutt BN, Sylvan JB, Knab NJ, Edwards KJ. (2011). Microbial ecology of the dark ocean above, at, and below the seafloor. *Microbiol Mol Biol Rev* **75**: 361–422.
- Osburn MR, LaRowe DE, Momper L, Amend JP. (2014). Chemolithotrophy in the continental deep subsurface: Sanford Underground Research Facility (SURF), USA. *Front Extr Microbiol* **5**: 610.
- Parks DH, Imelfort M, Skennerton CT, Hugenholtz P, Tyson GW. (2015). CheckM: assessing the quality of microbial genomes recovered from isolates, single cells, and metagenomes. *Gen Res* **25**: 1043–1055.
- Peng Y, Leung HC, Yiu SM, Chin FY. (2012). IDBA-UD: a de novo assembler for single-cell and metagenomic sequencing data with highly uneven depth. *Bioinformatics* **28**: 1420–1428.
- Pedersen K. (2000). Exploration of deep intraterrestrial microbial life: current perspectives. *FEMS Microbiol Lett* **185**: 9–16.
- Pfiffner SM, Cantu JM, Smithgall A, Peacock AD, White DC, Moser DP *et al.* (2006). Deep subsurface microbial biomass and community structure in Witwatersrand Basin mines. *Geomicrobiol J* **23**: 431–442.
- Pilhofer M, Rappl K, Eckl C, Bauer AP, Ludwig W, Schleifer KH *et al.* (2008). Characterization and evolution of cell division and cell wall synthesis genes in the bacterial phyla *Verrucomicrobia*, *Lentisphaerae*, *Chlamydiae*, and *Planctomycetes* and phylogenetic comparison with rRNA genes. *J Bacteriol* **190**: 3192–3202.
- Price MN, Dehal PS, Arkin AP. (2010). FastTree 2—approximately maximum-likelihood trees for large alignments. *PLoS One* **5**: e9490.
- Pruesse E, Queast C, Knittel K, Fuchs BM, Ludwig W, Peplies J *et al.* (2007). SILVA: a comprehensive online resource for quality checked and aligned ribosomal RNA sequence data compatible with ARB. *Nucleic Acids Res* **35**: 7188–7196.
- Pruesse E, Peplies J, Glöckner FO. (2012). SINA: accurate high-throughput multiple sequence alignment of ribosomal RNA genes. *Bioinformatics* **28**: 1823–1829.
- Quast C, Pruesse E, Yilmaz P, Gerken J, Schweer T, Yarza P *et al.* (2013). The SILVA ribosomal RNA gene database project: improved data processing and web-based tools. *Nucleic Acids Res* **41**: 590–596.
- Rabus R, Hansen TA, Widdel F. (2006). Dissimilatory sulfate- and sulfur-reducing prokaryotes. *The Prokaryotes*. Springer: New York, NY, USA, pp 659–768.
- Reed AJ, Lutz RA, Vetrani C. (2006). Vertical distribution and diversity of bacteria and archaea in sulfide and methane-rich cold seep sediments located at the base of the Florida Escarpment. *Extremophiles* **10**: 199–211.
- Rinke C, Schwientek P, Sczyrba A, Ivanova NN, Anderson IJ, Cheng JF *et al.* (2013). Insights into the phylogeny and coding potential of microbial dark matter. *Nature* **499**: 431–437.
- Sander J, Engels-Schwarzlose S, Dahl C. (2006). Importance of the DsrMKJOP complex for sulfur oxidation in *Allochromatium vinosum* and phylogenetic analysis of related complexes in other prokaryotes. *Arch Microbiol* **186**: 357–366.
- Schauder R, Preuß A, Jetten M, Fuchs G. (1988). Oxidative and reductive acetyl CoA/carbon monoxide dehydrogenase pathway in *Desulfobacterium autotrophicum*. *Arch Microbiol* **151**: 84–89.
- Seitz KW, Lazar CS, Hinrichs K-U, Teske AP, Baker BJ. (2016). Genomic reconstruction of a novel, deeply branched sediment archaeal phylum with pathways for acetogenesis and sulfur reduction. *ISME J* **10**: 1696–1705.
- Simkus DN, Slater GF, Lollar BS, Wilkie K, Kieft TL, Magnabosco C *et al.* (2016). Variations in microbial carbon sources and cycling in the deep continental subsurface. *Geochimica et Cosmochimica Acta* **173**: 264–283.
- Speth DR, Guerrero-Cruz S, Dutilh BE, Jetten MS. (2016). Genome-based microbial ecology of anammox granules in a full-scale wastewater treatment system. *Nature Communications* **7**: 1–10.
- Stamatakis A. (2006). RAxML-VI-HPC: maximum likelihood-based phylogenetic analyses with thousands of taxa and mixed models. *Bioinformatics* **22**: 2688–2690.
- Stevens T. (1997). Lithoautotrophy in the subsurface. *FEMS Microbiol Rev* **20**: 327–337.
- Stevens TO, McKinley JP. (1995). Lithoautotrophic microbial ecosystems in deep basalt aquifers. *Science* **270**: 450–454.
- Tabita FR, Satagopan S, Hanson TE, Kreel NE, Scott SS. (2008). Distinct form I, II, III, and IV RuBisCo proteins from the three kingdoms of life provide clues about RuBisCo evolution and structure/function relationships. *J Exp Botany* **59**: 1515–1524.
- Tiago I, Verissimo A. (2013). Microbial and functional diversity of a subterrestrial high pH groundwater associated to serpentinization. *Environ Microbiol* **15**: 1687–1706.
- Tyson GW, Chapman J, Hugenholtz P, Allen EE, Ram RJ, Richardson PM *et al.* (2004). Community structure and metabolism through reconstruction of microbial genomes from the environment. *Nature* **428**: 37–43.
- Wagner M, Horn M. (2006). The *Planctomycetes*, *Verrucomicrobia*, *Chlamydiae* and sister phyla comprise a superphylum with biotechnological and medical relevance. *Curr Opin Biotechnol* **17**: 241–249.
- Whitman WB, Coleman DC, Wiebe WJ. (1998). Prokaryotes: the unseen majority. *Proc Natl Acad Sci USA* **95**: 6578–6583.
- Wu M, Scott AJ. (2012). Phylogenomic analysis of bacterial and archaeal sequences with AMPHORA2. *Bioinformatics* **28**: 1033–1034.

Yarza P, Richter M, Peplies J, Euzéby J, Amann R, Schleifer KH *et al.* (2008). The All-Species Living Tree project: A 16 S rRNA-based phylogenetic tree of all sequenced type strains. *Syst Appl Microbiol* **31**: 241–250.

Youssef NH, Rinke C, Stepanauskas R, Farag I, Woyke T, Elshahed MS. (2015a). Insights into the metabolism, lifestyle and putative evolutionary history of the novel archaeal phylum 'Diapherotrites'. *ISME J* **9**: 447–460.

Supplementary Information accompanies this paper on The ISME Journal website (<http://www.nature.com/ismej>)