Corrigendum: Genomic inference of the metabolism of cosmopolitan subsurface Archaea, Hadesarchaea

Brett J. Baker, Jimmy H. Saw, Anders E. Lind, Cassandre Sara Lazar, Kai-Uwe Hinrichs, Andreas P. Teske and Thijs J. G. Ettema

Nature Microbiology **1,** 16002 (2016); published online 15 February 2016; corrected 7 March 2016.

Subsequent to this work being published it was discovered that 3 (out of 67) of the scaffolds (totaling 93 kb) in one of the Hadesarchaea bins (YNP_45) are actually contaminants. Table 1 has been modified to reflect the removal of these scaffolds. The presence of these contaminating sequences does not alter the major conclusions drawn; the carbon fixation, hydrogen and CO oxidation pathways as well as proteins used for phylogenetic analyses are not included in the contaminants. However, one of the nitrite reductases (c552) mentioned in the paper is on one of them (the other nitrite reductase (in bin YNP_N21) is not). Accordingly, the main text and Figure 3 have been modified to remove reference to c552 and Supplementary Figure 7 has been removed. The relevant sequences have been removed from Genbank.

nature microbiology

SUPPLEMENTARY INFORMATION

ARTICLE NUMBER: 16002 | DOI: 10.1038/NMICROBIOL.2016.2

Genomic inference of the metabolism of cosmopolitan subsurface Archaea, Hadesarchaea

Brett J. Baker[1]*, Jimmy H. Saw[2], Anders E. Lind[2], Cassandre Sara Lazar[3], Kai-Uwe Hinrichs[3], Andreas P. Teske[4], and Thijs J. G. Ettema[2]

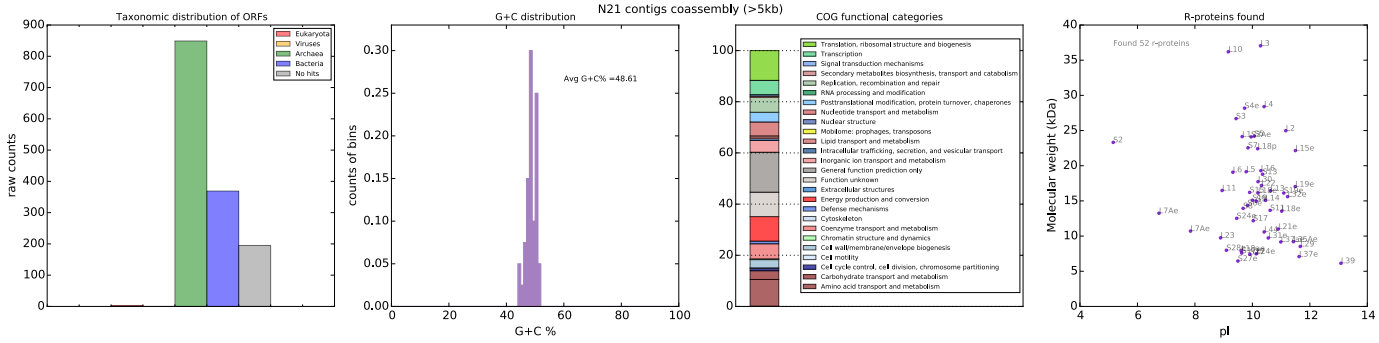
1 Dept. of Marine Science, University of Texas Austin, Marine Science Institute, Port Aransas, TX 78373, USA; 2 Department of Cell and Molecular Biology, Science for Life Laboratory, Uppsala University, SE-75123 Uppsala, Sweden; 3 MARUM Center for Marine Environmental Sciences, University of Bremen, Bremen, Germany; 4 Department of Marine Sciences, University of North Carolina, Chapel Hill, NC, USA

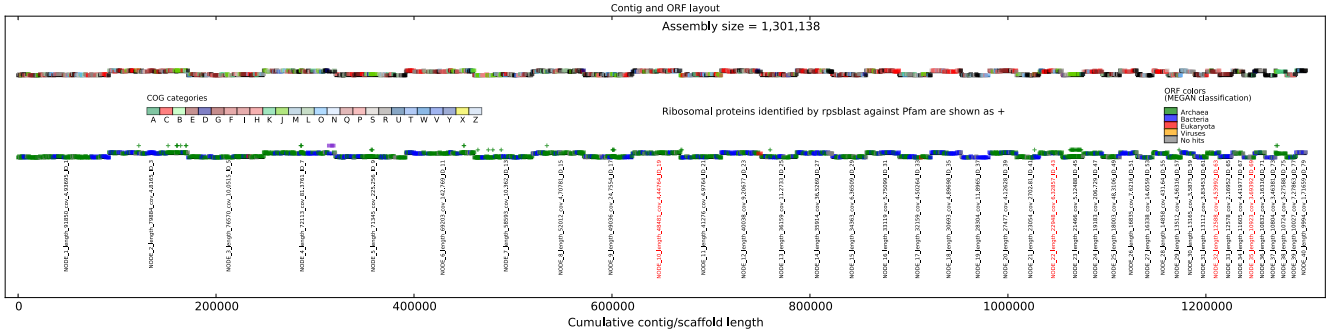
*email acidophile@gmail.com, phone +1-361-749-6774. To whom correspondence should be addressed.

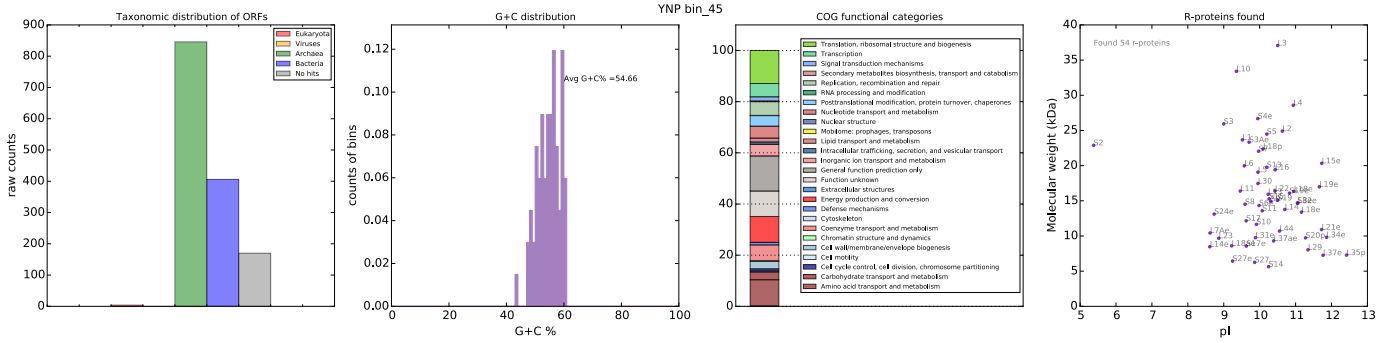
DOI: 10.1038/NMICROBIOL.2016.2

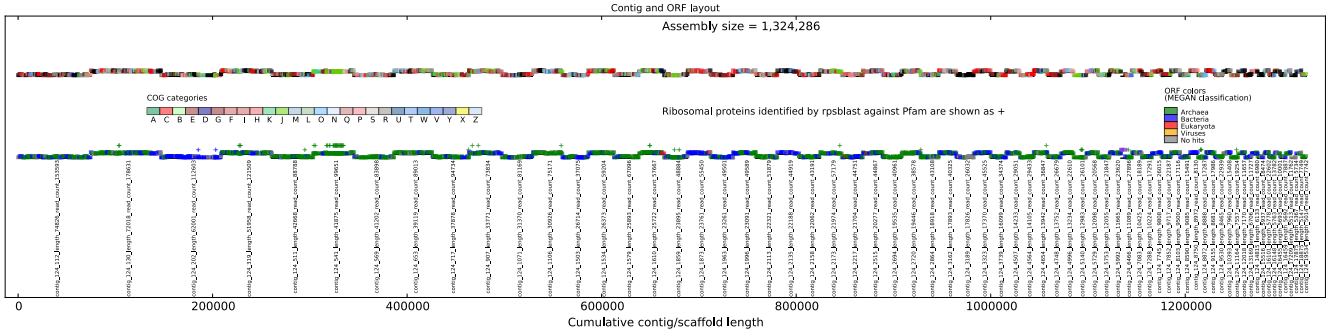
Supplementary Table 1. Assembly statistics for N21 SAG alone, metagenomic bin, and co-assembly. Completeness, contamination, and strain heterogeneity are based on checkM outputs[1].

Assembly	N21 SAG	N21 metagenomic bin	Co-assembly	Co-assembly (manually checked)
Contigs (>5 kbp)	24	108	64	40
Total assembly size (bp)	271,966	1,572,974	1,467,263	1,301,138
Largest contig	27,345	83,223	91,850	91,850
Average G+C%	48.63	48.64	48.72	48.61
Number of markers identified	56	189	189	189
Completeness	8.33	84.13	84.92	80.6
Contamination	0.00	21.83	10.79	10
Strain heterogeneity	0.00	21.74	8.82	9.09

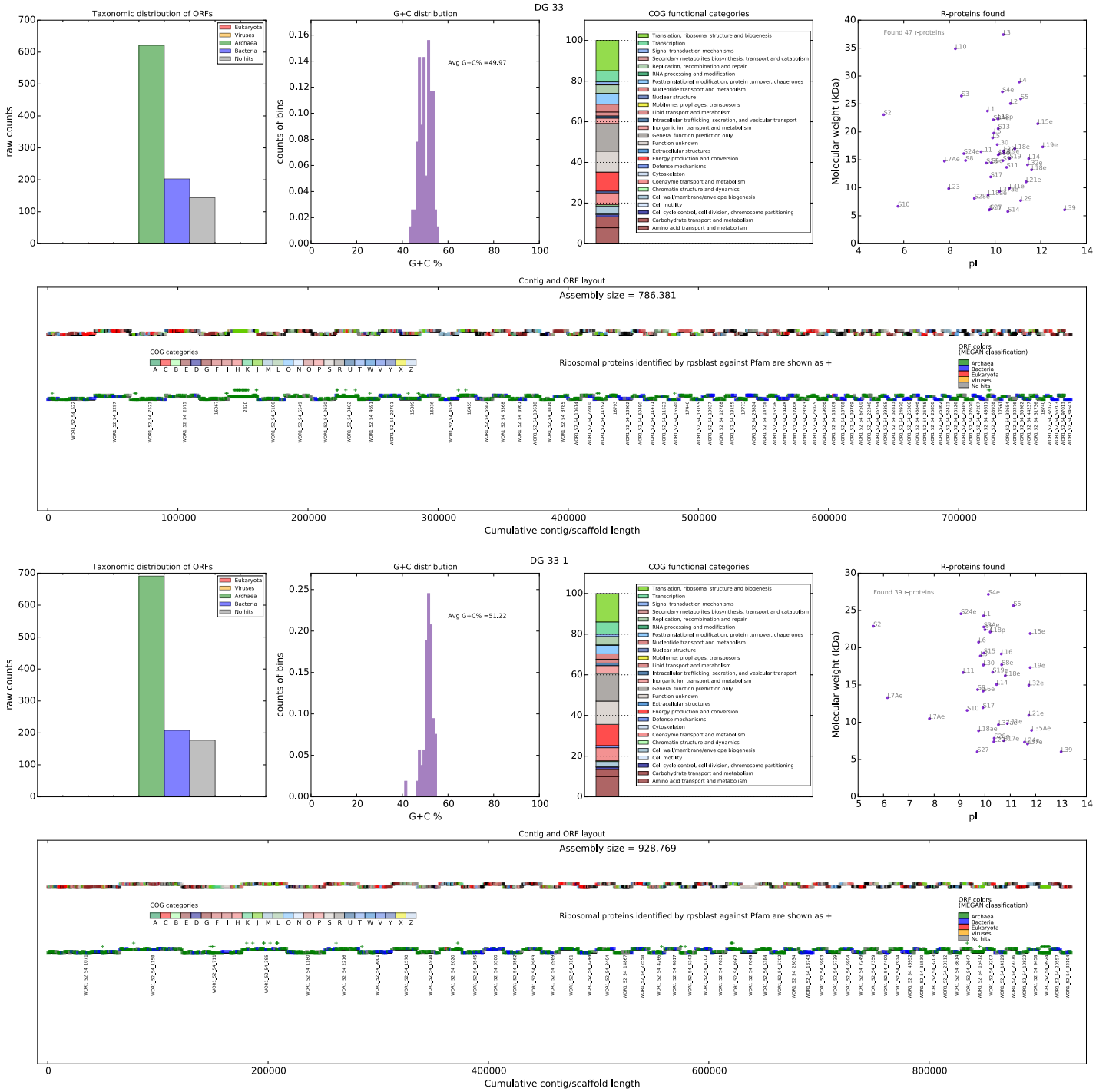




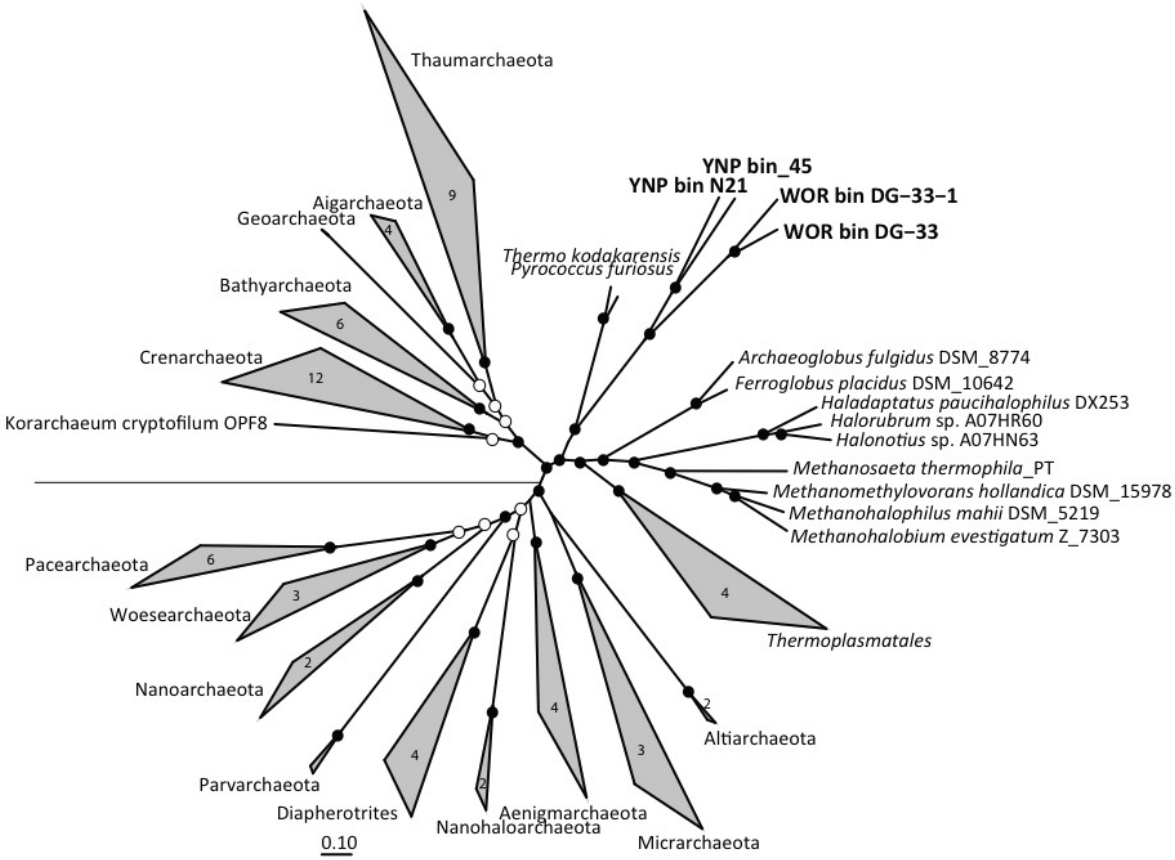




DOI: 10.1038/NMICROBIOL.2016.2

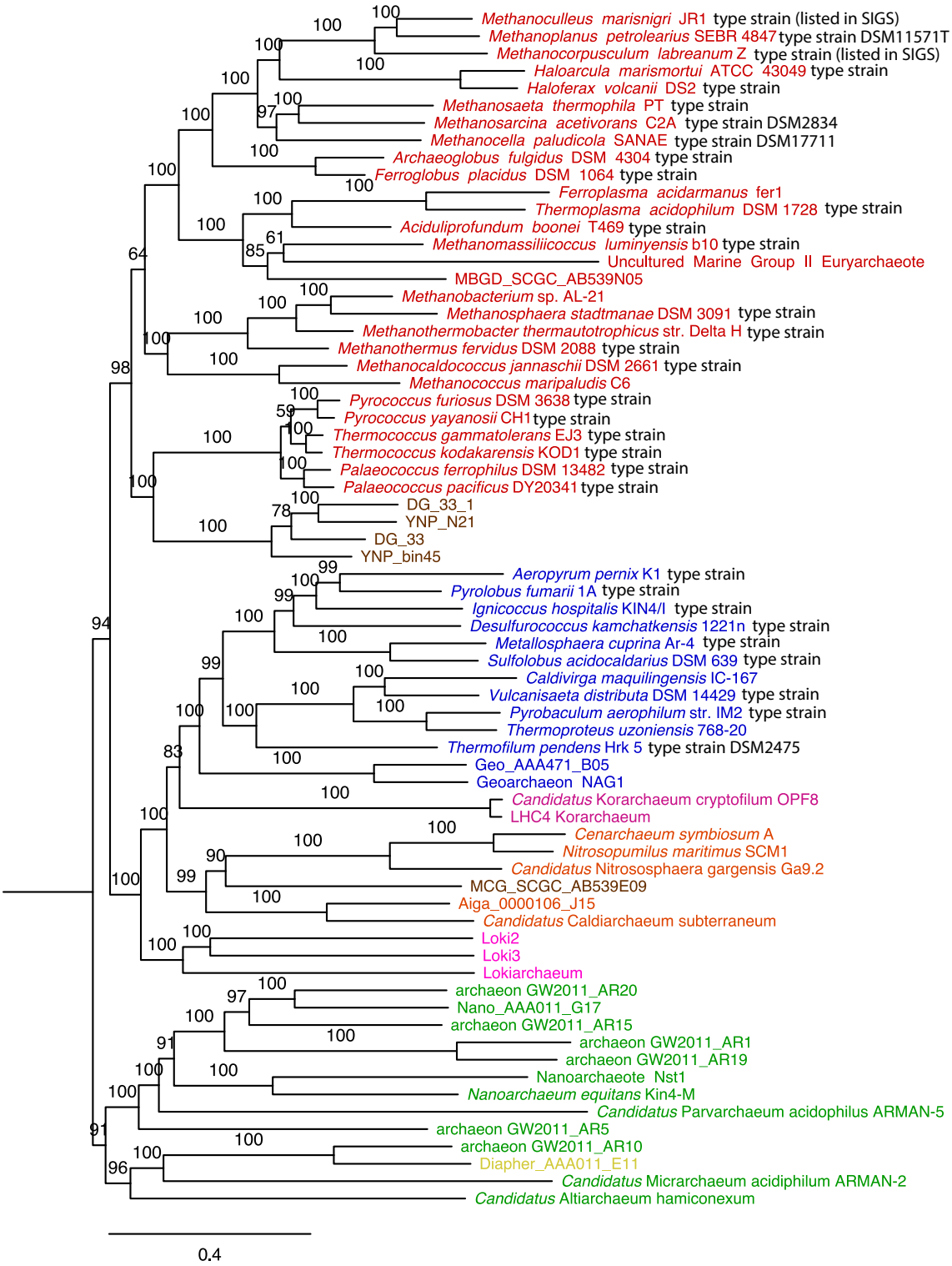


Supplementary Figure 1. Overview of the four Hadesarchaea genomic bins reconstructed in this study. Domain-level taxonomic top hits of ORFS, GC distribution, percentage of COG functional categories, and the molecular weight (kDa) vs pI plots are shown on the top. All of the contigs that makeup the bins are shown on the bottom and the locations of the ribosomal proteins are marked with "+" symbols.

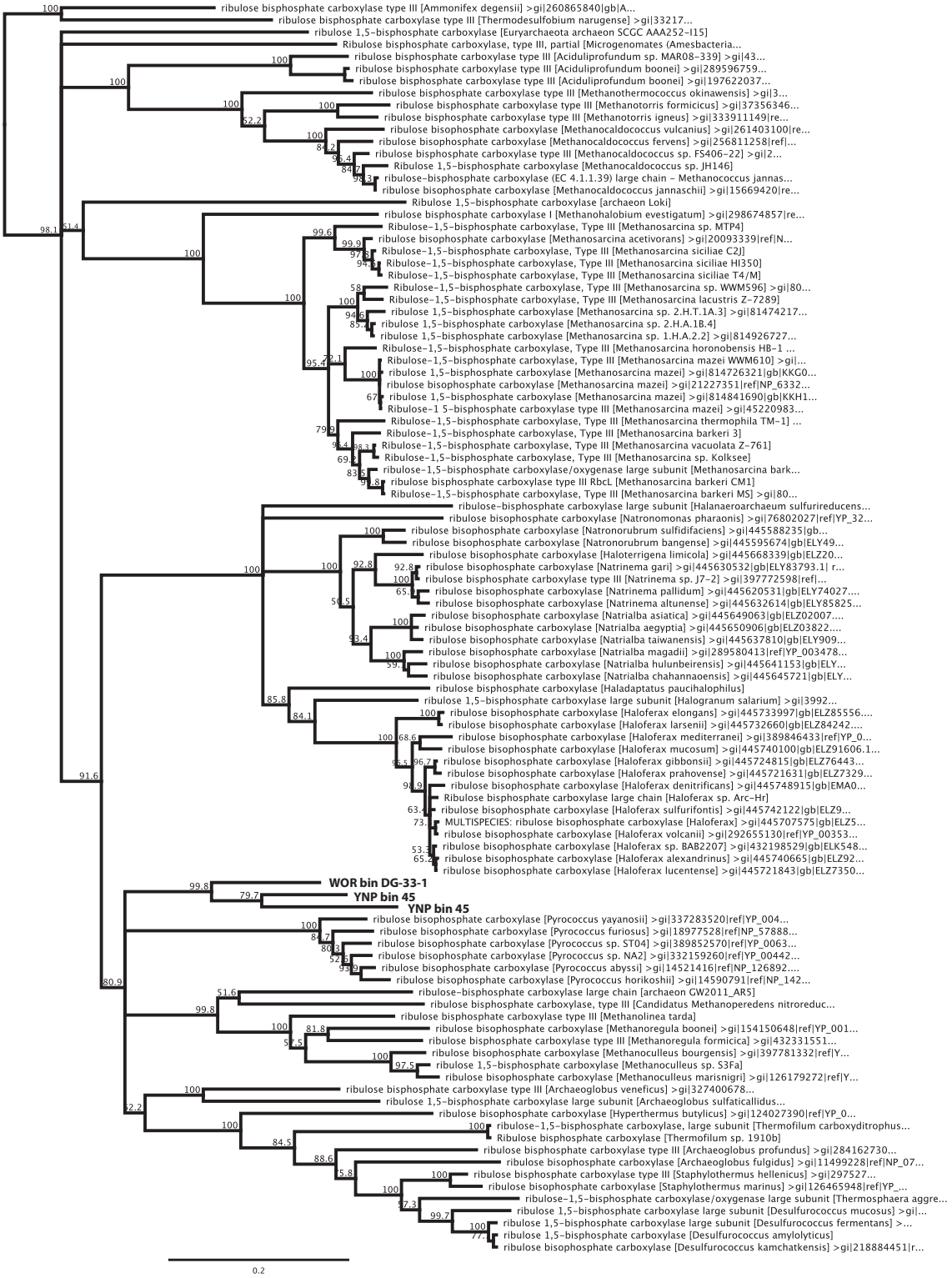


Supplementary Figure 2. Phylogenetic analysis of 16 concatenated ribosomal proteins (rpL2, 3, 4, 5, 6, 14, 15, 16, 18, 22, 24 and rpS3, 8, 10, 17, 19) generated from 3298 unambiguous characters using RAxML in the ARB software package. Closed circles represent bootstrap values were generated using UFBoot[2] with 1000 replicates, those that are >98 are shown with closed circles and those >75 are open circles. Bacteria were used as the outgroup (not shown). The numbers of sequences present in the collapsed wedges are labeled.

DOI: 10.1038/NMICROBIOL.2016.2

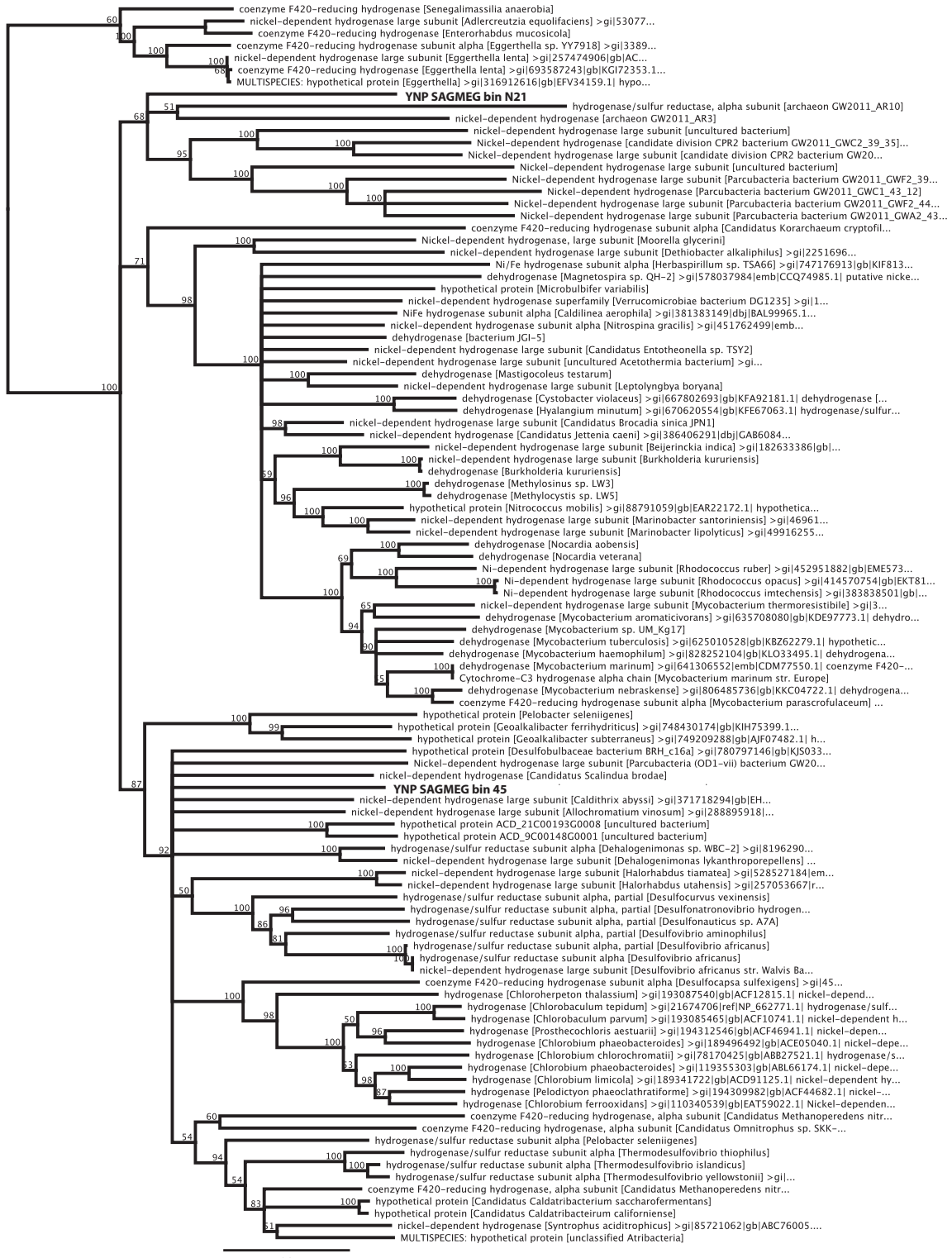


Supplementary Figure 3. Maximum Likelihood phylogeny using 48 concatenated arCOGs. These are the same sequences that were used to generate Figure 2 (main text). The maximum likelihood phylogeny was inferred by IQ-TREE with C60+LG mixture model and using 1000 rapid bootstraps. "Loki2", "Loki3", and "Lokiarchaeum" are Lokiarchaeota genomes from Spang et al[3]. Branches with "archaeon GW…" are DPANN genomes from Castelle et al.[4].



Supplementary Figure 4. Phylogenetic analysis of type III RubisCO proteins. We did not identify this gene in bin DG-33.

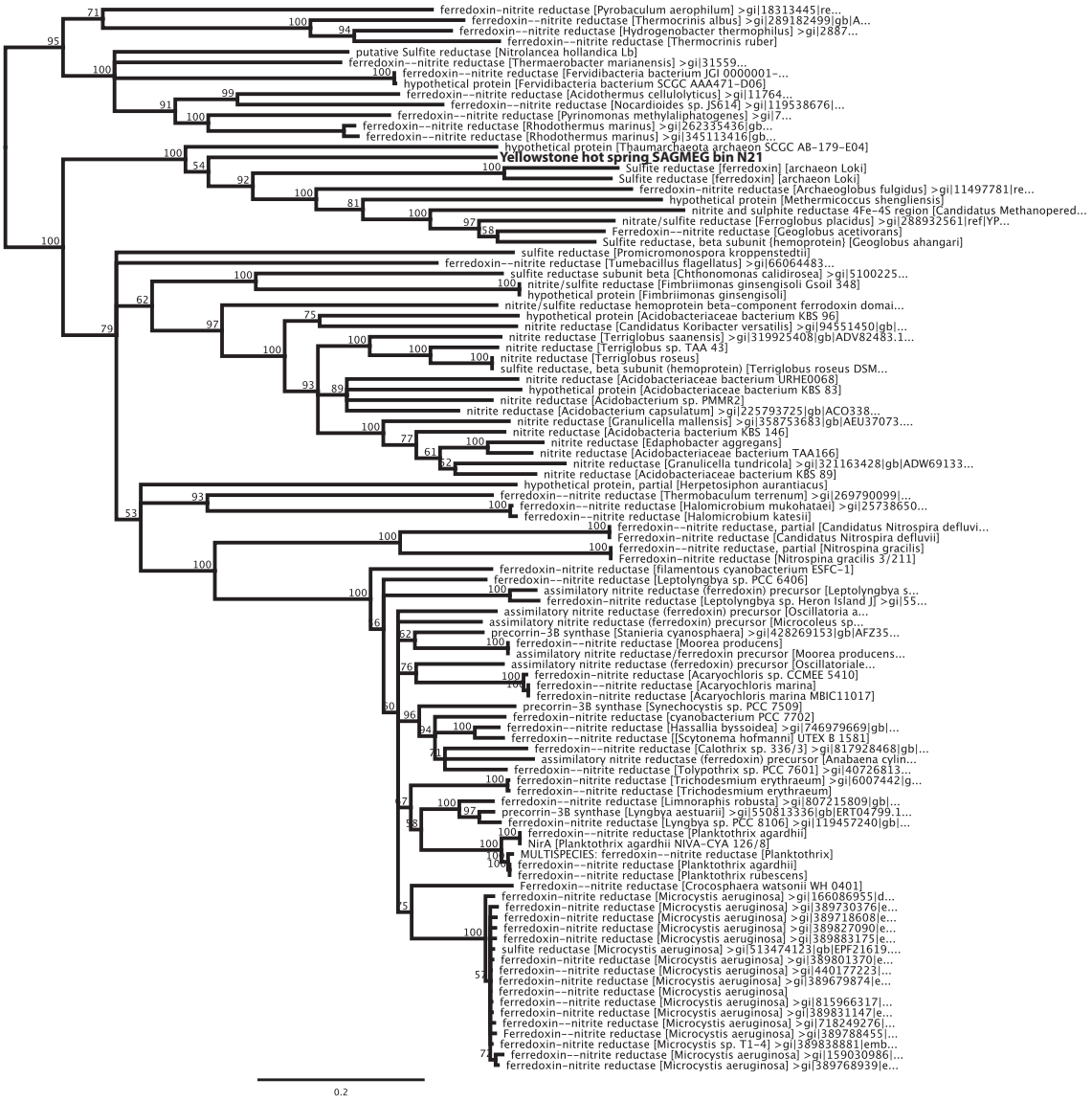
DOI: 10.1038/NMICROBIOL.2016.2



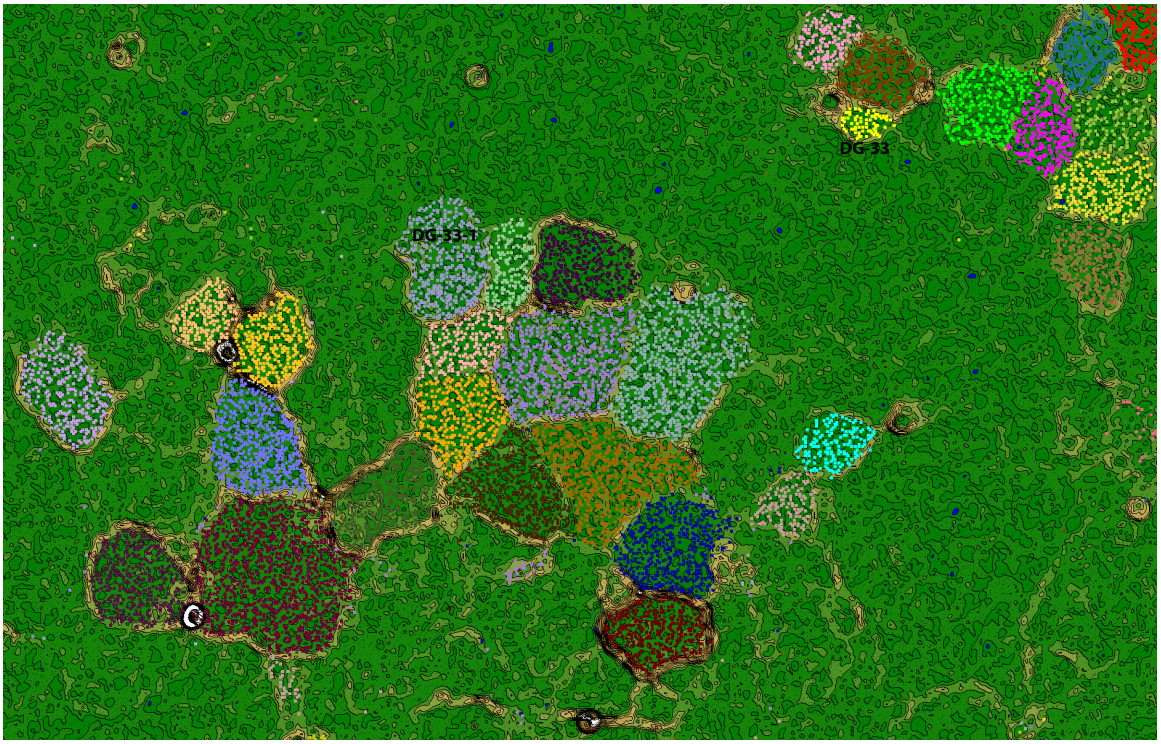
Supplementary Figure 5. Phylogenetic analysis of bins YHNP_45 and YNP_N21 type sulfohydrogenase proteins.

Supplementary Figure 6. Phylogenetic analysis of bin YNP_45 catalytic subunit (CooS) of carbon monoxide dehydrogenase protein.

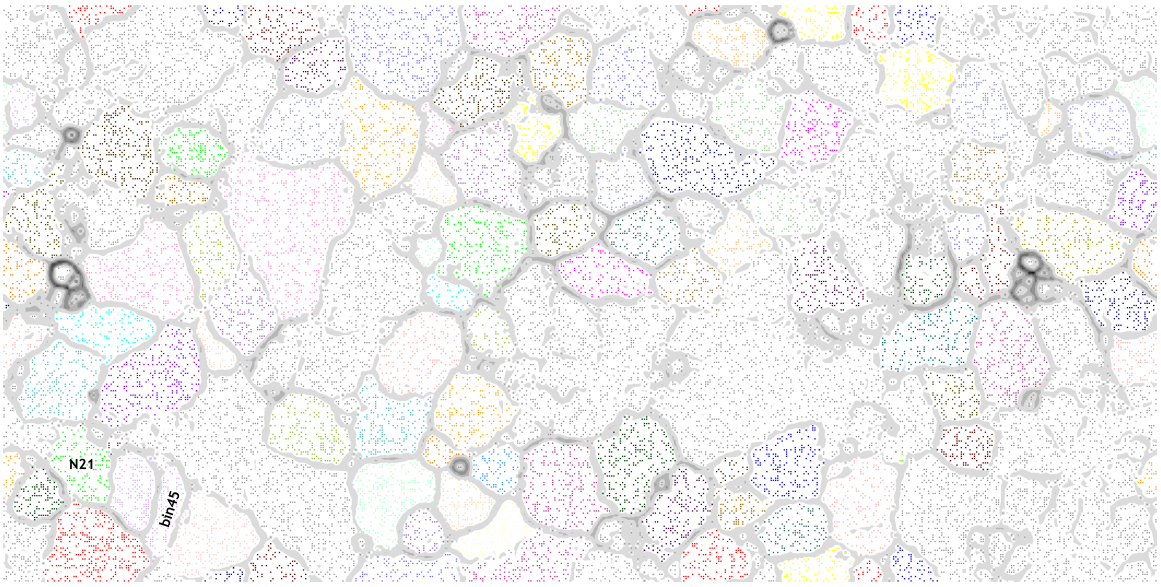
DOI: 10.1038/NMICROBIOL.2016.2



Supplementary Figure 7. Phylogenetic analysis of bin YNP_N21 type nitrite reductase proteins.

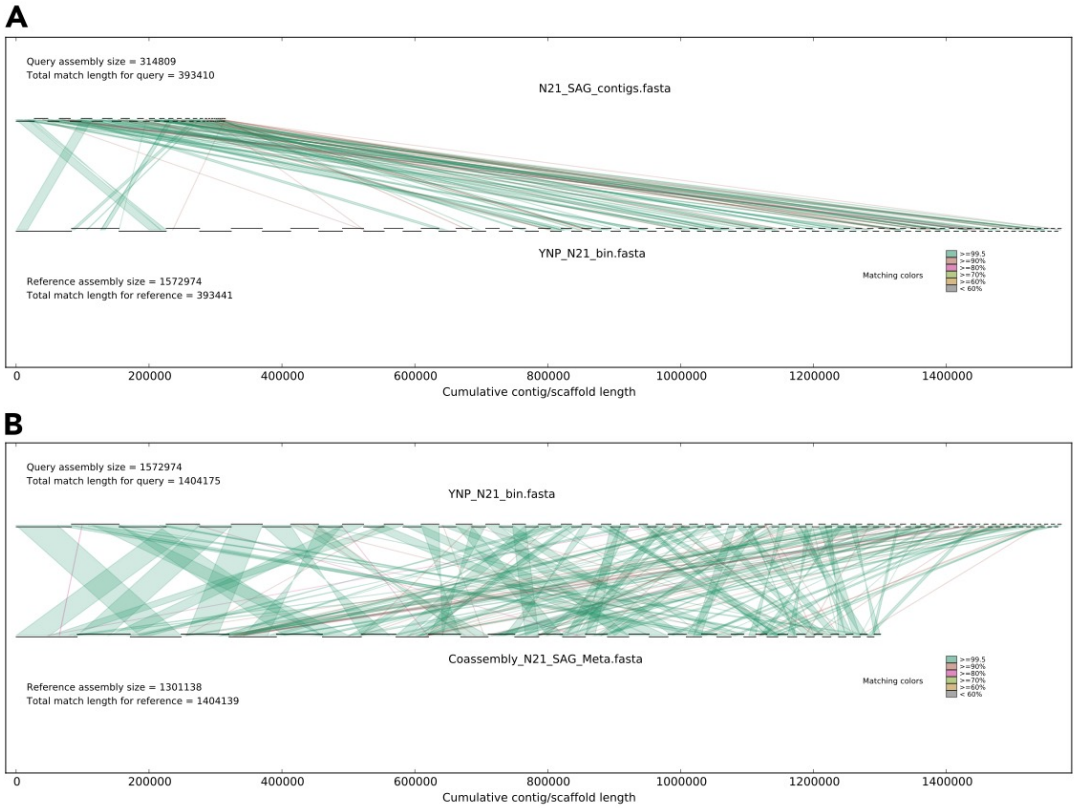


Supplementary Figure 8. Tetranucleotide-based ESOM mapping of metagenomic fragments from the methane-rich layer of White Oak River sediments. The SAGMEG genomic bins have been labeled.



Supplementary Figure 9. Emergenet Self-Organizing Map (ESOM) of Yellowstone metagenome assembly. The genomic bins presented in this study as label at their locations on the maps. Genome bins YNP_N21 and bin YNP_45 can be seen near the lower left corner of the map.

DOI: 10.1038/NMICROBIOL.2016.2



Supplementary Figure 10. Comparison of YNP_N21 assemblies before and after co-assembly with the metagenomic bin. (A) MUMMER comparison of SAG contigs and metagenomic bin. **(B)** MUMMER comparison of metagenomic bin and co-assembled contigs (after manual removal of contaminants). Contigs are ordered from largest to smallest and shown in alternating positions for improved visibility. Matching regions between contigs (MUMMER identities larger than 99.5% at the DNA level) are shown in green.

Supplementary Information References

1 Parks, D. H., Imelfort, M., Skennerton, C. T., Hugenholtz, P. & Tyson, G. W. CheckM: assessing the quality of microbial genomes recovered from isolates, single cells, and metagenomes. *PeerJ PrePrints* **2**, e554v551, doi:10.7287/peerj.preprints.554v1 (2014).

2 Minh, B. Q., Nguyen, M. A. T. & von Haeseler, A. Ultrafast Approximation for Phylogenetic Bootstrap. *Molecular Biology and Evolution* **30**, 1188-1195, doi:10.1093/molbev/mst024 (2013).

3 Spang, A. *et al.* Complex archaea that bridge the gap between prokaryotes and eukaryotes. *Nature* **521**, 173-179, doi:10.1038/nature14447 (2015).

4 Castelle, C. J., Wrighton, K. C., Thomas, B. C., Hug, L. A., Brown, C. T., Wilkins, M. J., Frischkorn, K. R., Tringe, S. G., Singh, A., Markille L. M., Taylor, R. C., Williams, K. H., Banfield, J. F. Genomic Expansion of Domain Archaea Highlights Roles for Organisms from New Phyla in Anaerobic Carbon Cycling. *Current Biol* **in press** (2015).