

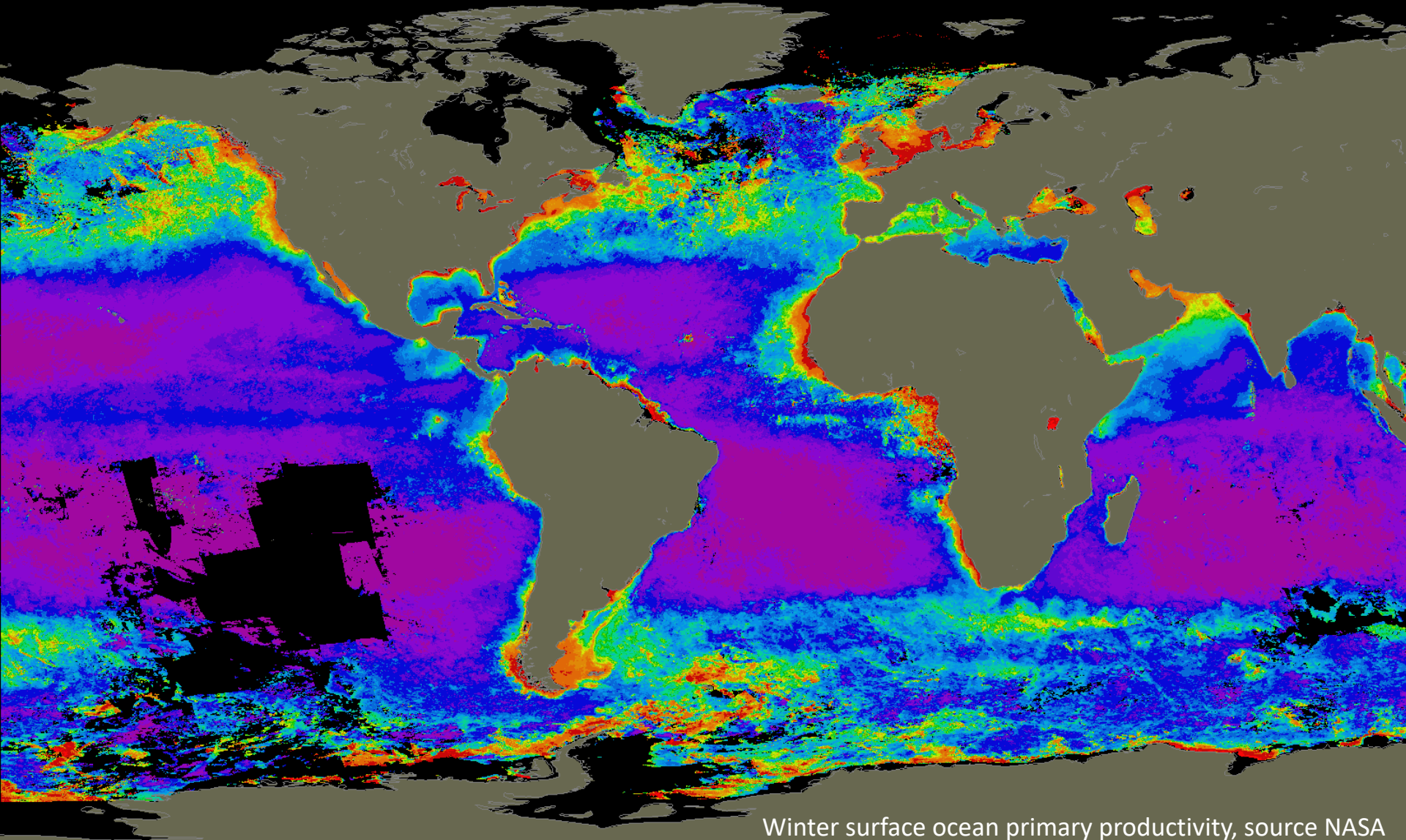
Exploring new branches on the tree of life

Brett Baker
@archaeal



Microbes are small but mighty!

For example – Microbes in the ocean's create half of the oxygen you are breathing right now



Winter surface ocean primary productivity, source NASA

Microbes get energy from lots of sources

“Edible”

CH_2O

(organic carbon)

“Breatheable”

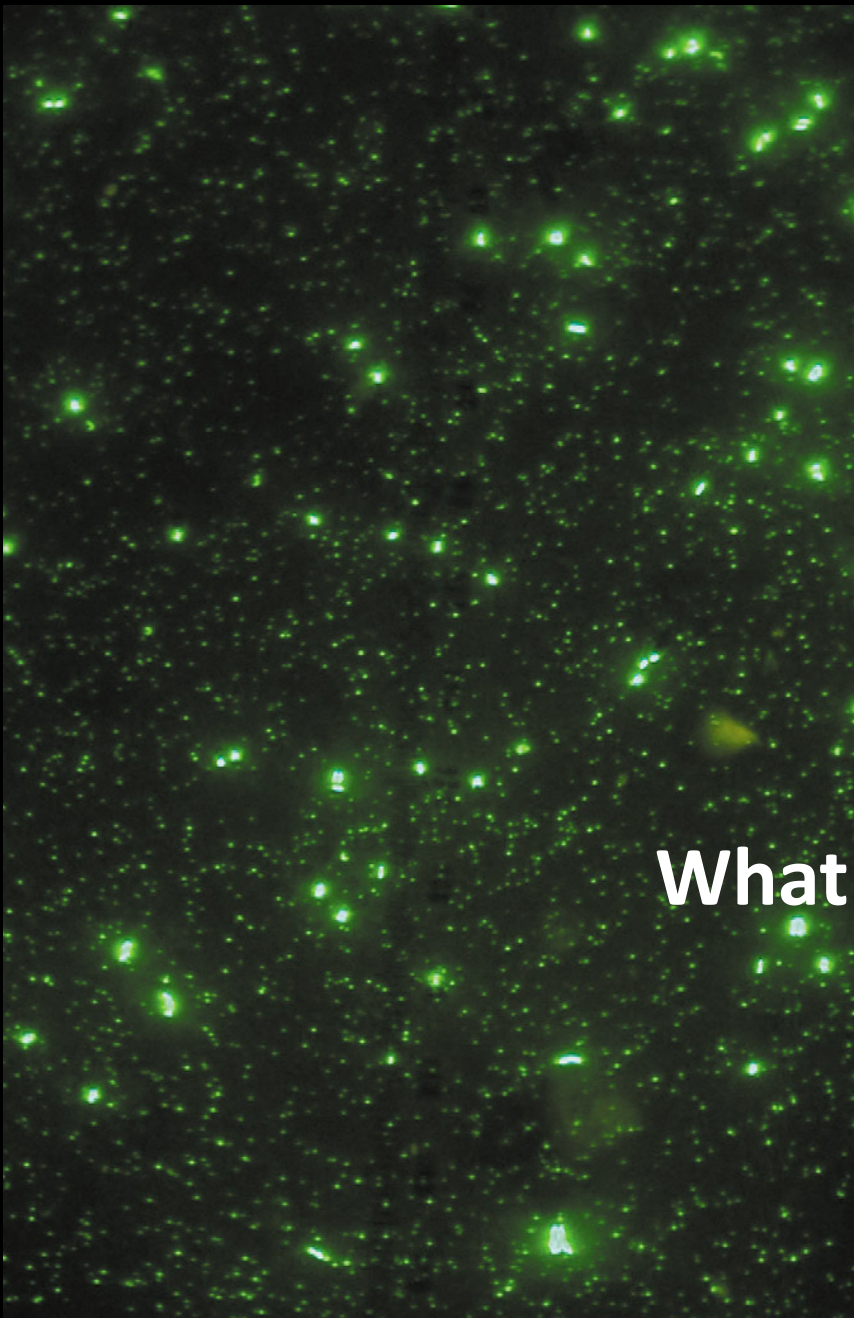
O_2

Process

Heterotrophy

ALL ANIMALS!

Microbes are the most abundant life on the planet



Microbes in the oceans =

118,100,000,000,000,000,000,000,000

Stars in the universe =

70,000,000,000,000,000,000,000



What is out there?

How do we investigate the microbes in nature?



Photo by Greg Dick

Culturing



Microbial dark matter

Growth in the lab

Natural community



≠



At best 0.1% of what is present in nature can be grown in the laboratory

How do we investigate the microbes in nature?



Photo by Greg Dick

Culturing



DNA sequencing



Metagenomic characterization of microbial communities



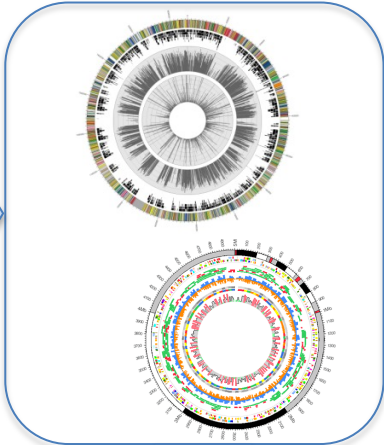
Extract DNA



Sequence DNA



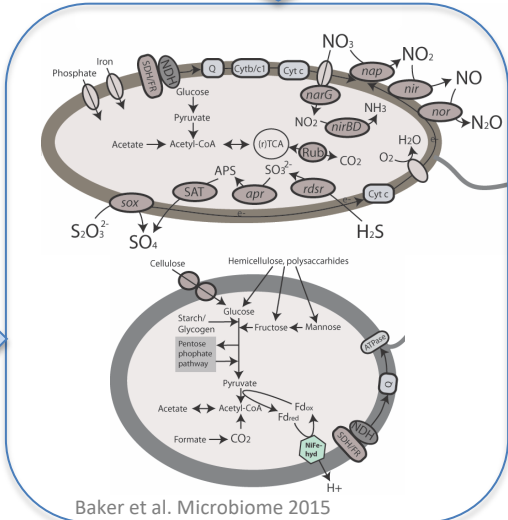
Genome assembly



In house pipeline overview:

1. Illumina HiSeq4000
2. Genomic assembly optimized with IDBA-UD MetaSpades
3. Genomes binned using coverage and TNF CONCOT, Metabat, ESOM (in-house pipeline)
4. Bins were refined using DASTool and mmgenome
5. Functional predictions – KEGG, InterProScan, COG, phylogeny, and structural models

**BONCAT
DNA-SIP**



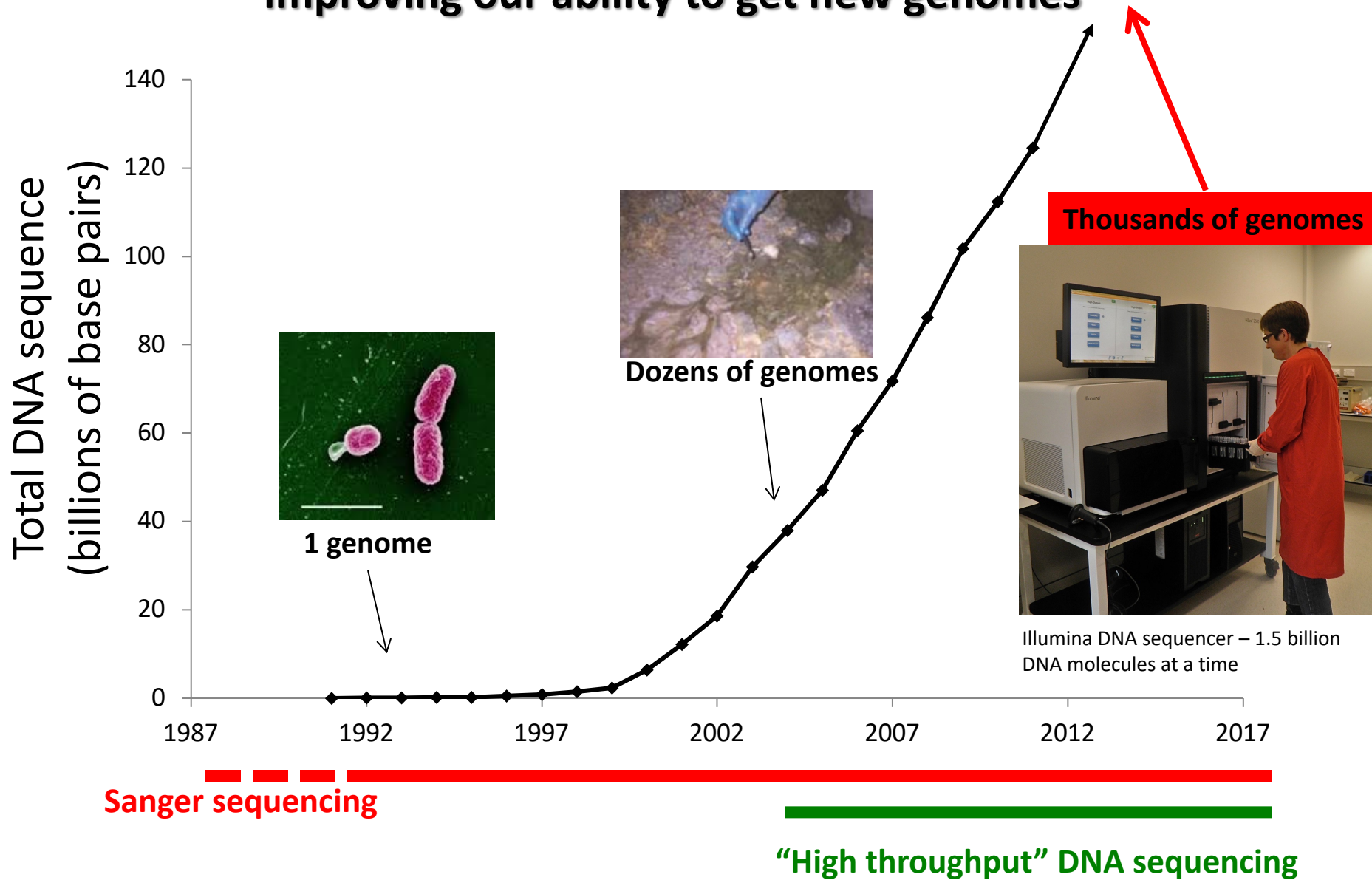
Baker et al. Microbiome 2015

Reconstruct metabolisms of all the microbes

Constructing genomes from nature is challenging



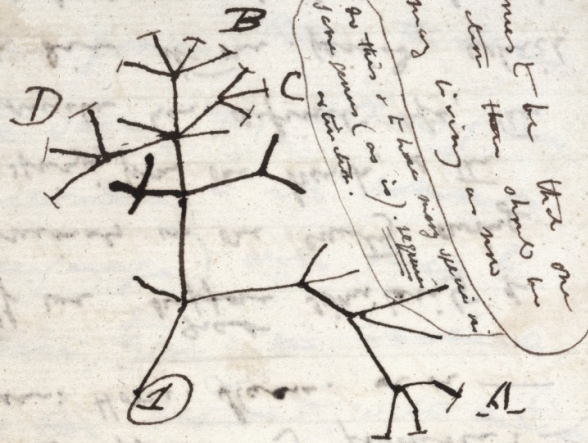
New DNA technologies and computational approaches are improving our ability to get new genomes



1837

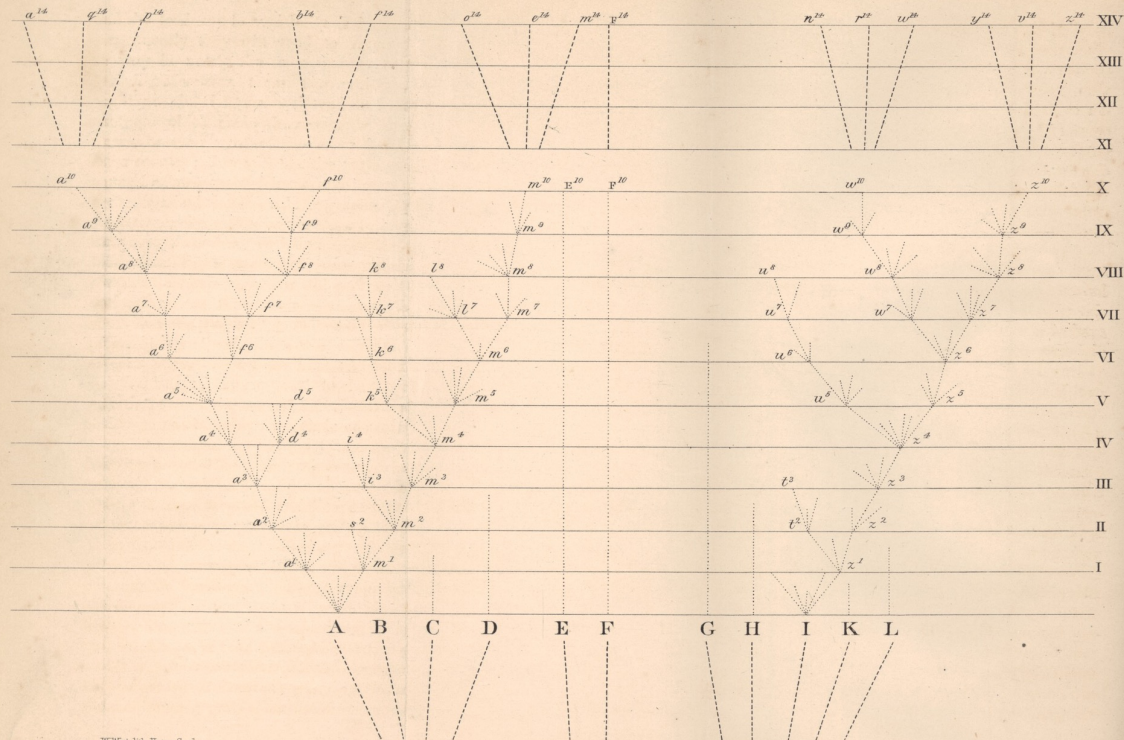
Darwin's tree of life

I think



There between A & B. various
 sort of relation. C + B. The
 finest gradation, B & D
 rather greater distinction
 than genus would be
 formed. - bearing relation

Origin of Life, 1859

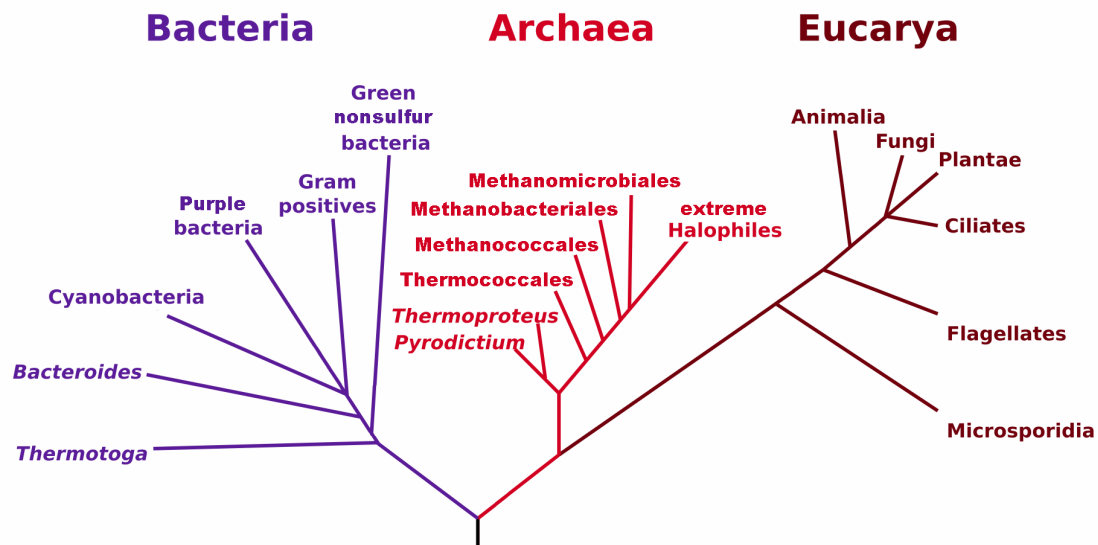


Evolutionary analysis through comparison of gene sequences

Human ... GTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTAAGTTGCTGCAGTTAAAAAG ...
 Brewer' Yeast ... GTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTAAGTTGTTGCAGTTAAAAAG ...
 Corn ... GTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAG ...
 Intestinal Bacterium ... GTGCCAGCAGCCGCGGTAATACGGAGGGTGAAGCGTTAATCGGAATTACTGGGGGTAAAGCG ...
 Environmental Bacterium ... GTGCCAGCAGCCGCGGTAATACGGGAGAGGCAAGCGTTATCCGGAATTATTGGGGGTAAAGCG ...
 Deep Ocean Bacterium ... GTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTACCCGGATTACTGGGGGTAAAGGG ...
 Methane Producer ... GTGCCAGCAGCCGCGGTAATACCGACGGCCCGAGTGGTAGCCACTGTTATTGGGGCTAAAGCG ...
 "Bacterium" 1 ... GTGGCAGCCGCGCGGTAATACCGGCGGCGGAGTGGTGGGGGCTATTATTGGGGCTAAAGCG ...
 "Bacterium" 2 ... GTGTCAGCCGCGCGGTAATACCAGCTCCGCGAGTGGTGGGGTGATTACTGCAGTTAAAGCG ...



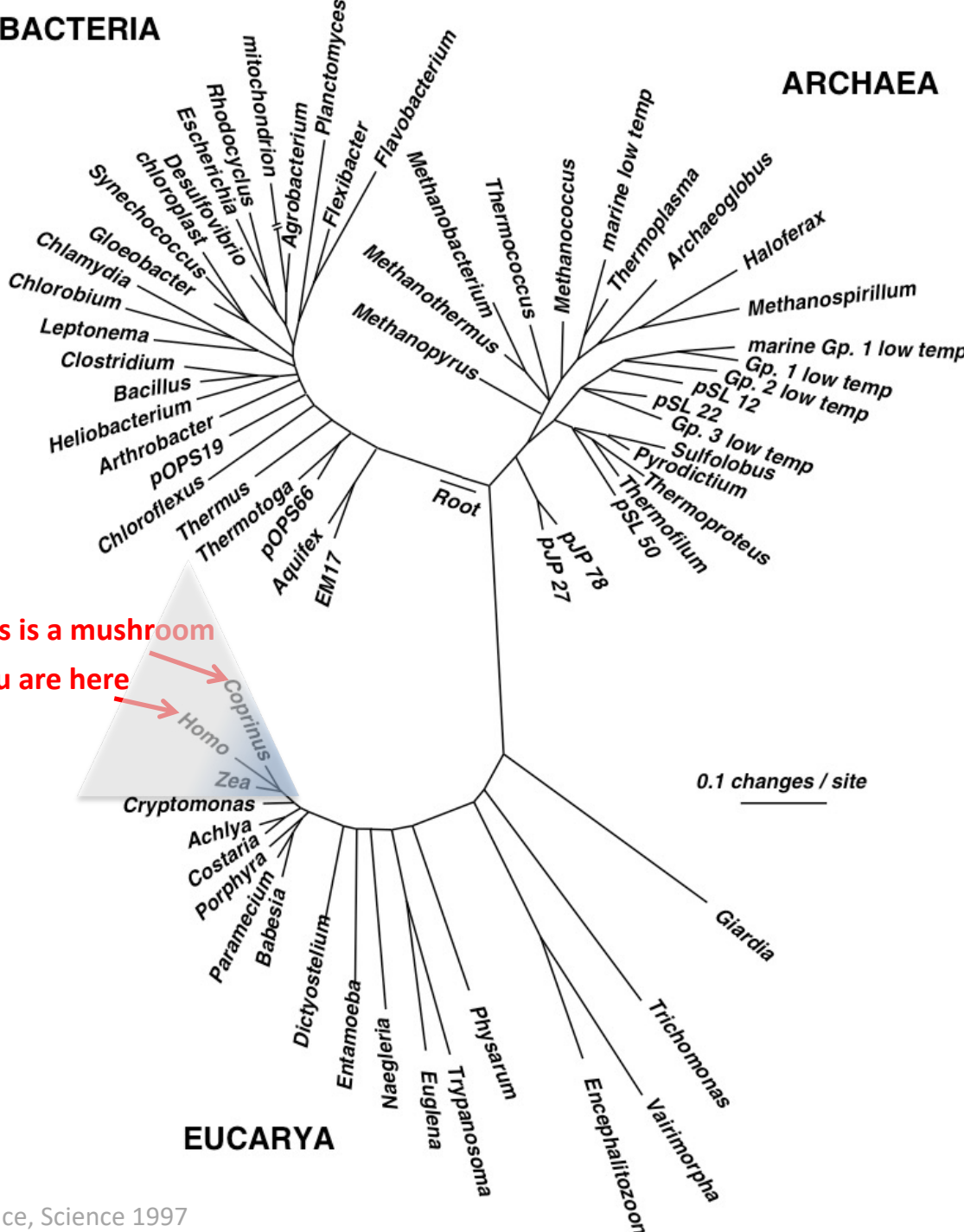
Carl Woese



BACTERIA

ARCHAEA

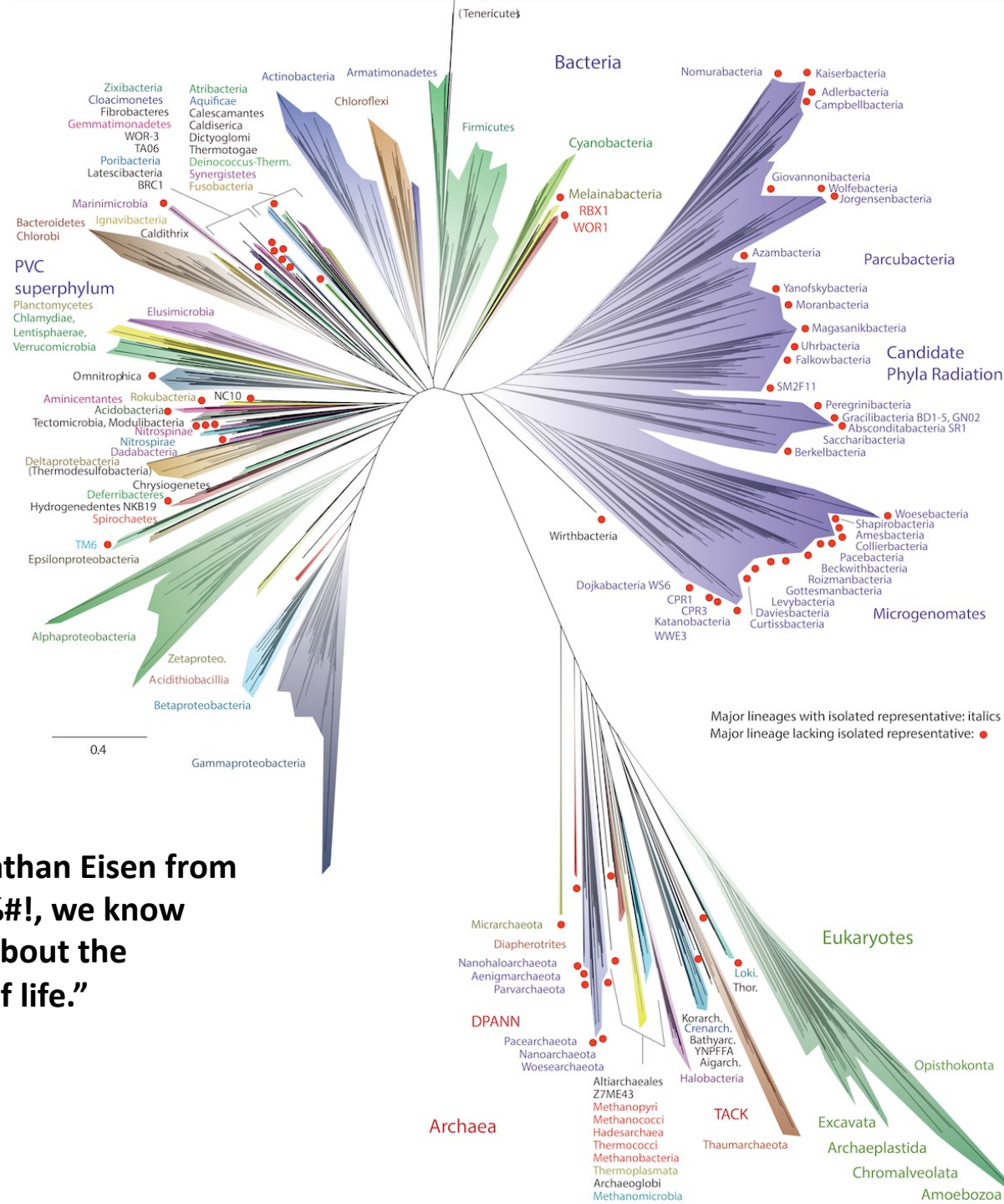
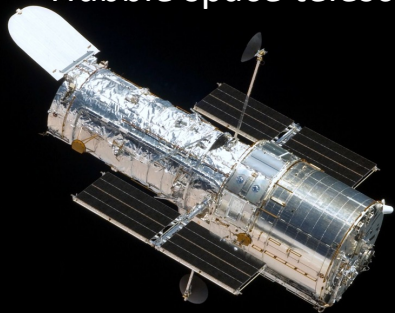
1997 tree of life



Based on 1 gene - 16S rRNA gene

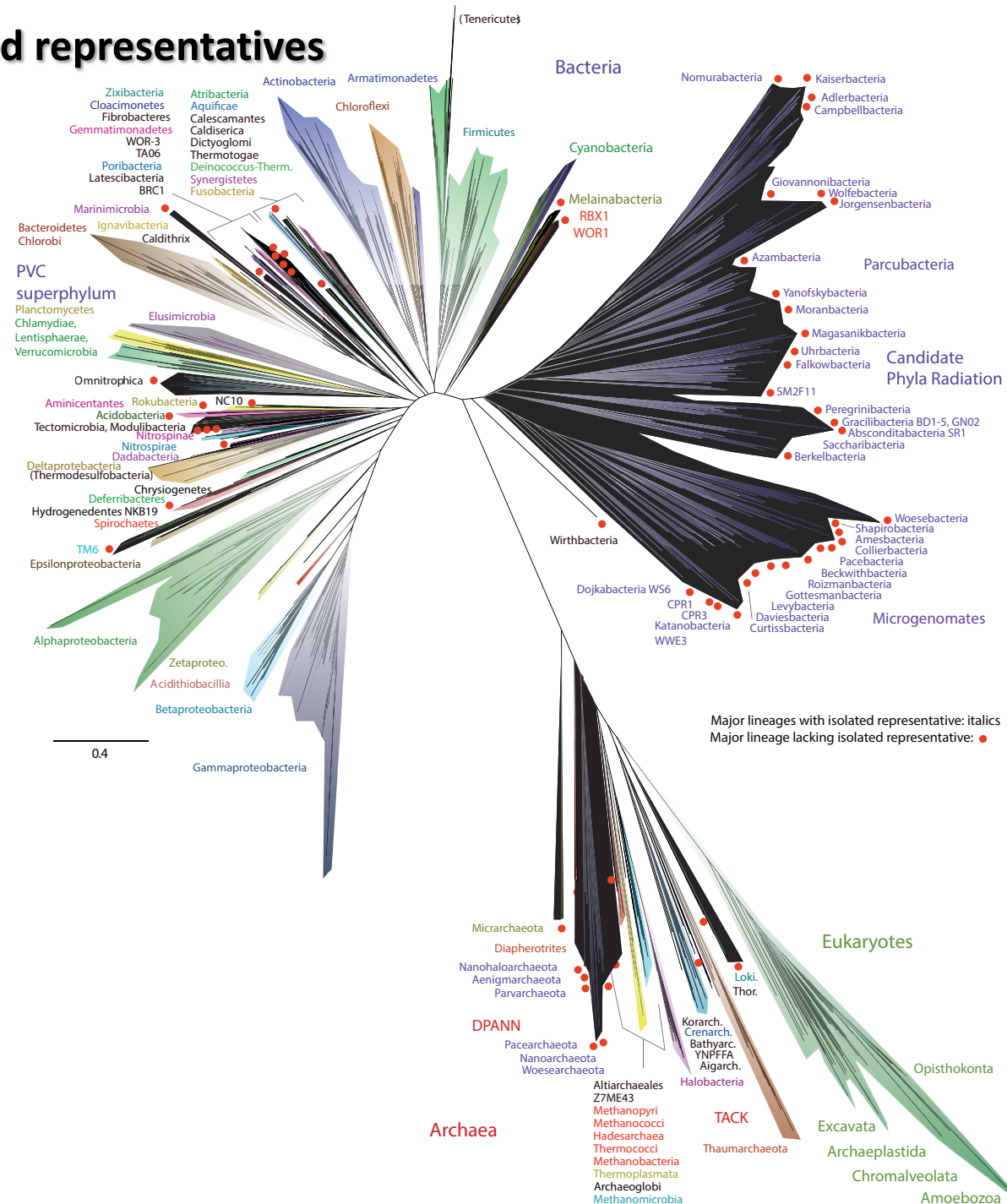
EUCARYA

Hubble space telescope



“This is humbling,” says Jonathan Eisen from UC Davis, “because holy **%#!, we know virtually nothing right now about the biology of most of the tree of life.”

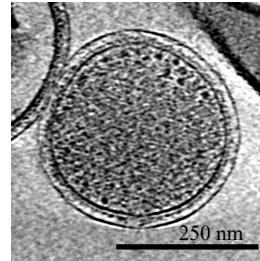
Phyla that lack cultured representatives



Genomic era – Tree of Life



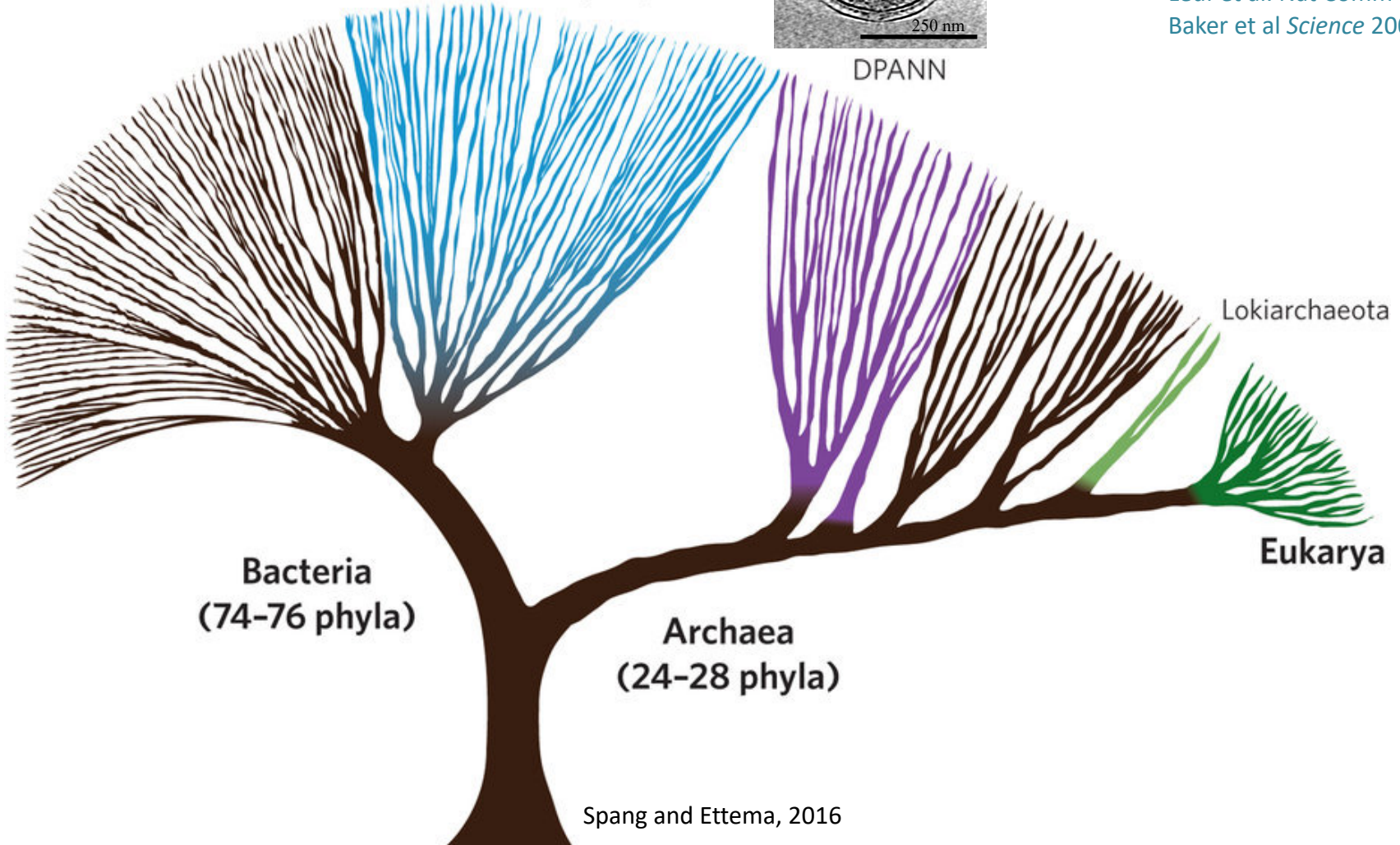
Candidate Phyla Radiation (CPR)



DPANN

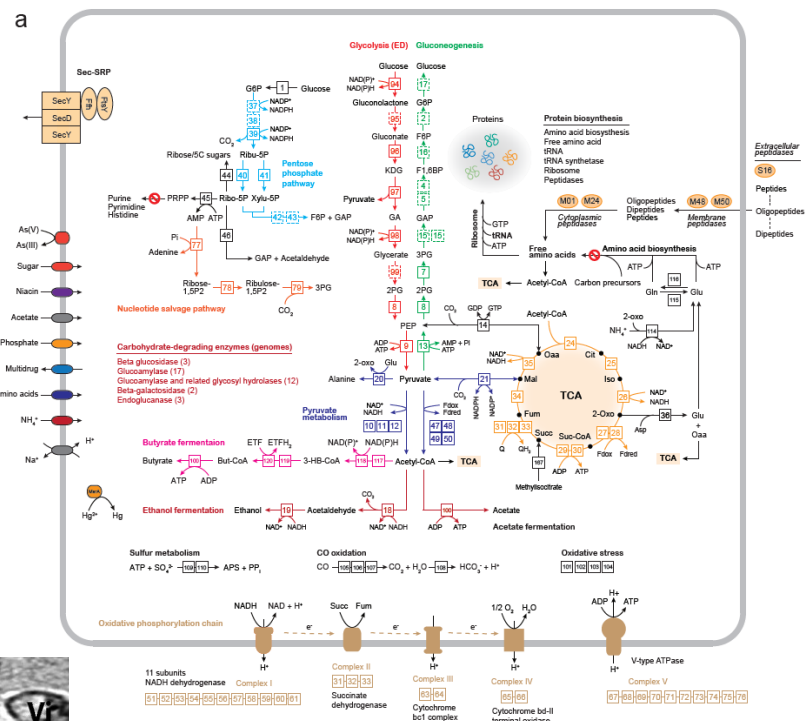
Small cells <400 nm and small genomes <0.8-1.2 Mb

Leuf et al. *Nat Comm* 2015
Baker et al *Science* 2006

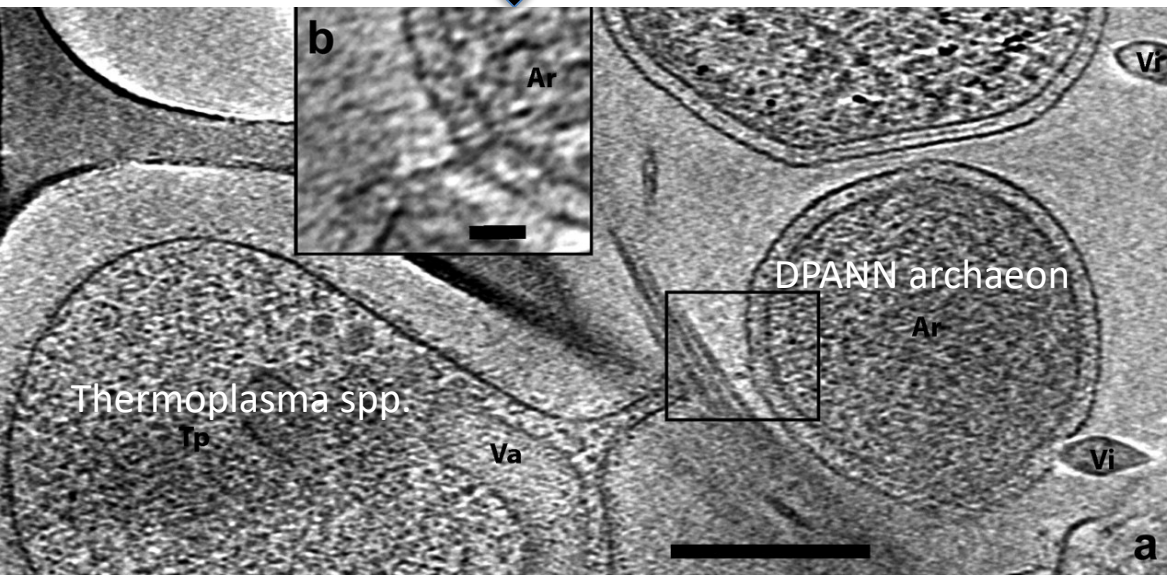


DPANN and CPR are metabolically limited and have associations with other species in nature

- Little/no respiratory pathways, appear to be fermenters
- Lacking many core biosynthetic pathways (eg. nucleotide, amino acids, and membranes)
- Many have been shown to be associated with other cells in nature

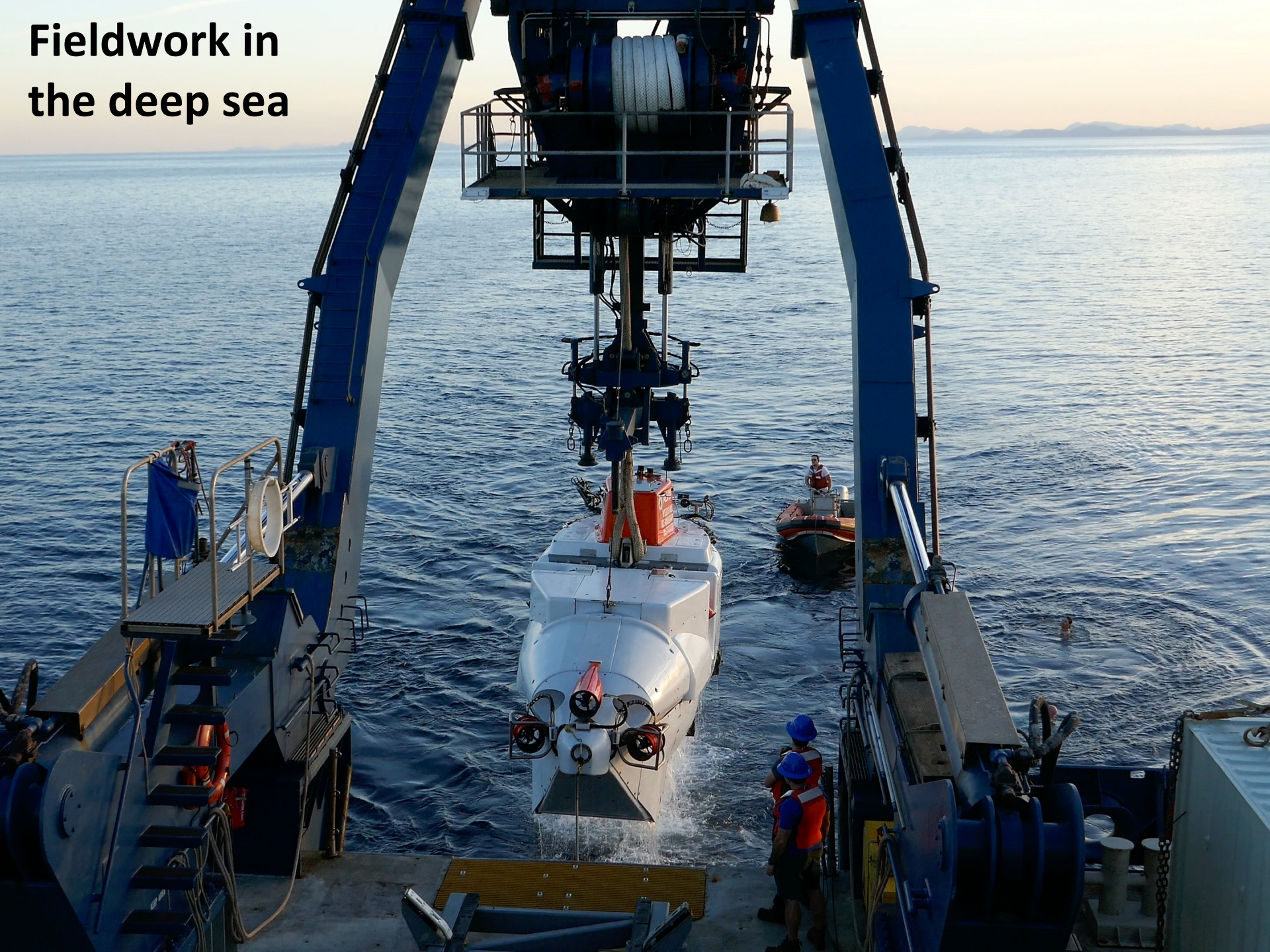


Chen, Baker et al. 2018 *ISME J.*

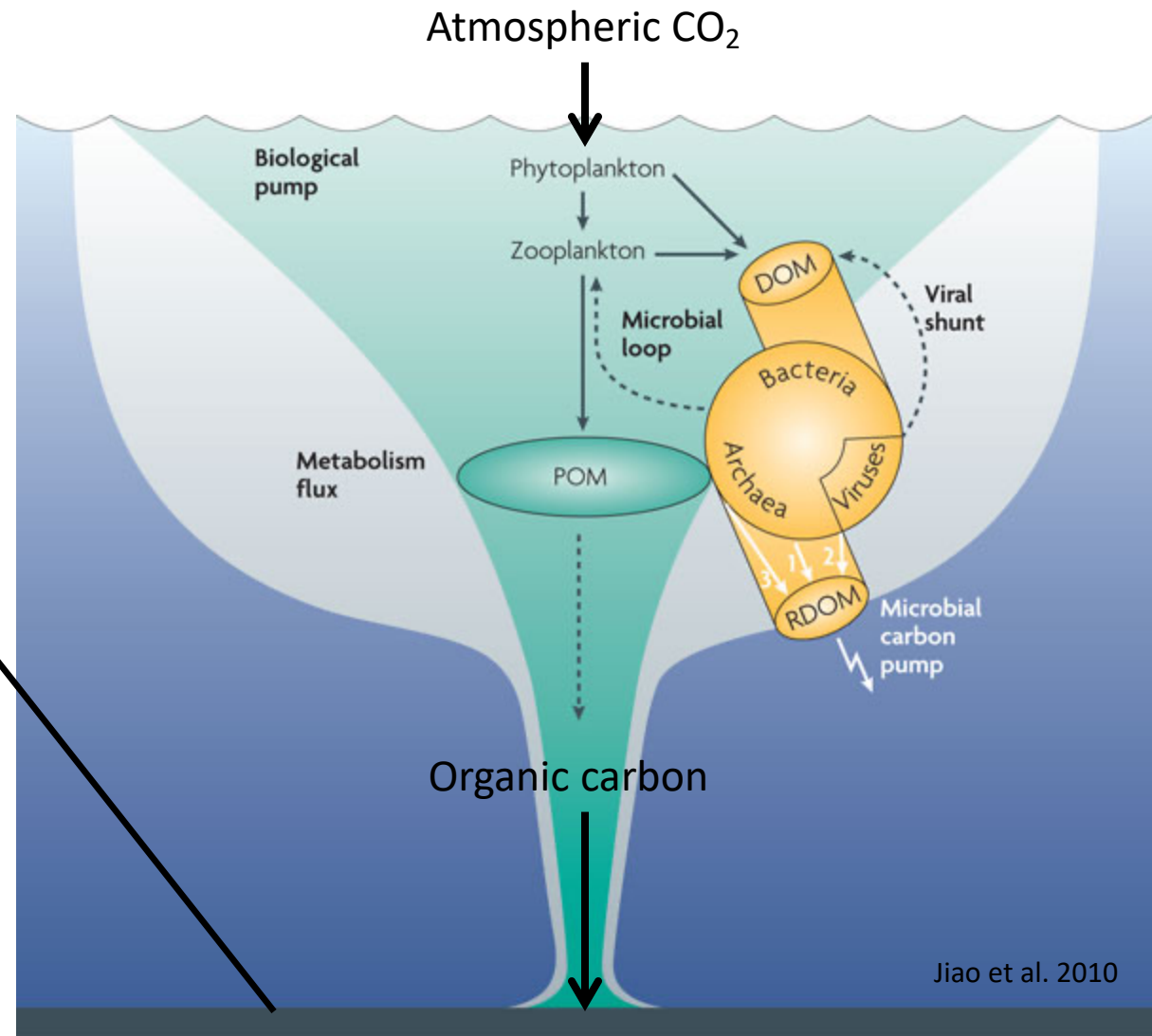


Baker et al. *PNAS* 2010

Fieldwork in the deep sea



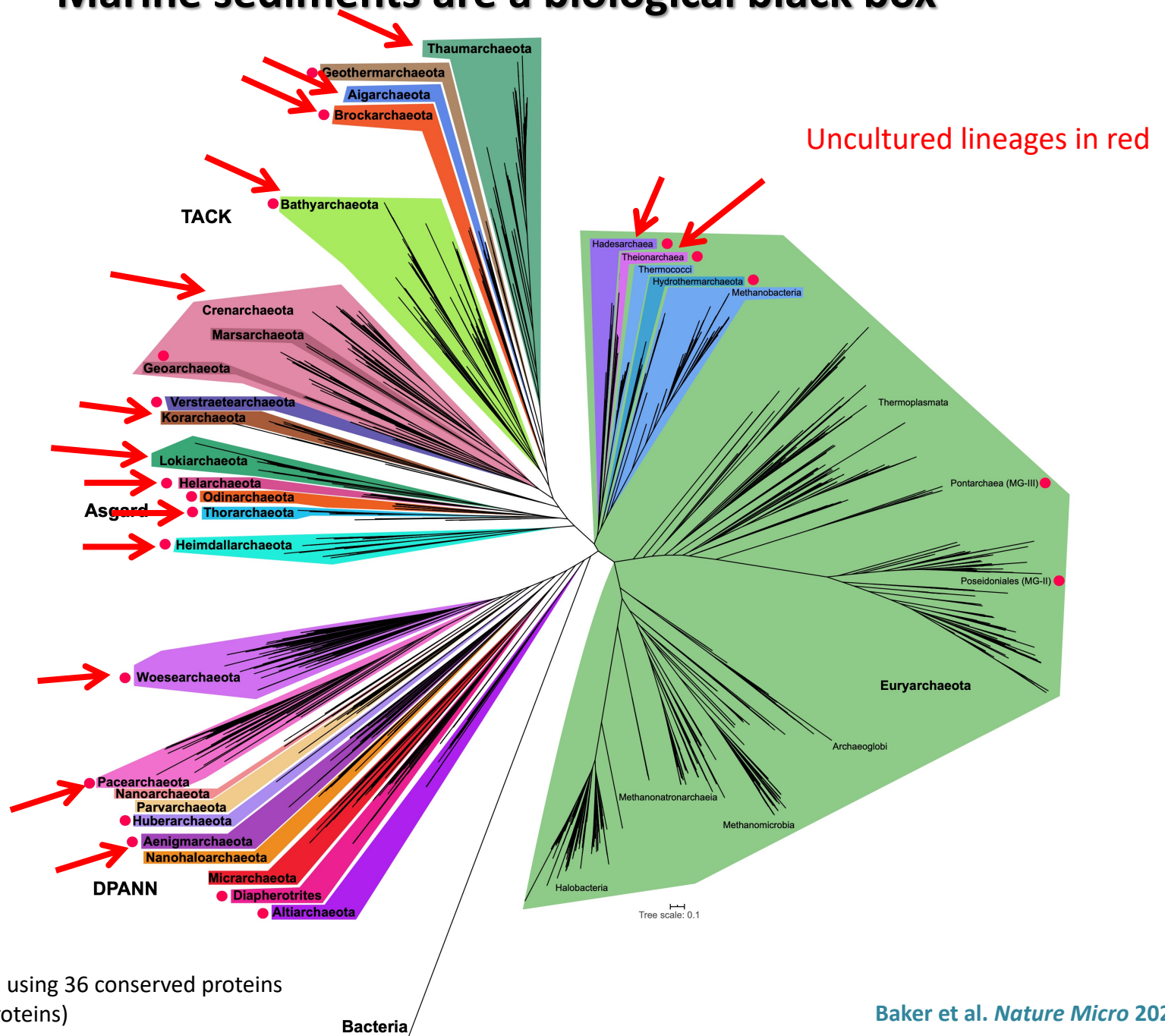
Sediments are the final resting place for detrital matter in the oceans



Marine sediments contain the largest pool of organic carbon on the planet

Jiao et al. 2010

Marine sediments are a biological black box



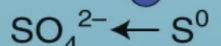
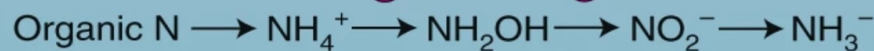
Phylogeny generated using 36 conserved proteins
(30 are ribosomal proteins)

Oxic environments

- | | |
|-----------------------|----------------------|
| ● Aigarchaeota | ● Bathyarchaeota |
| ● Geothermarchaeota | ● DPANN |
| ● Hydrothermarchaeota | ● Helarchaeota |
| ● Brockarchaeota | ● Thorarchaeota |
| ● Theionarchaeae | ● Heimdallarchaeota |
| ● Hadesarchaeae | ● Korarchaeota |
| ● Nezhaarchaeota | ● Vestraetearchaeota |
| ● Thaumarchaeota | ● Heimdallarchaeota |
| ● Euryarchaeota | ● Crenarchaeota |

Organic carbon Inorganic carbon

Deep sea biomass



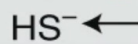
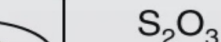
Organic carbon



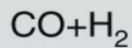
Methylamines



Short-chain alkanes



Fermentation byproducts

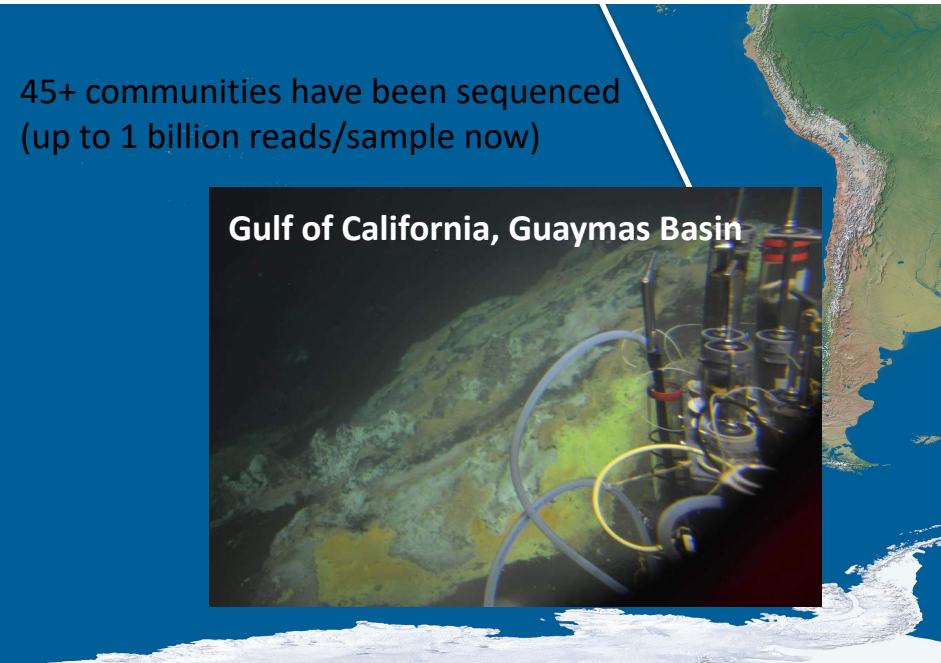
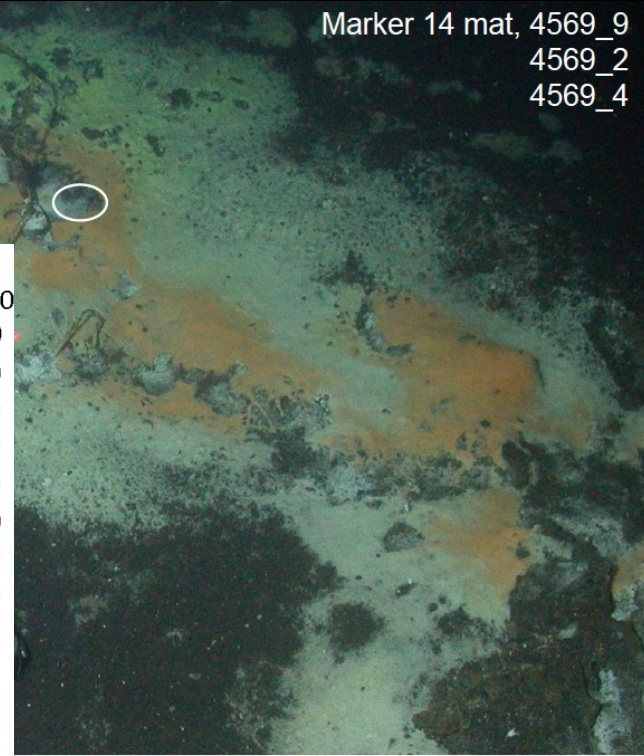
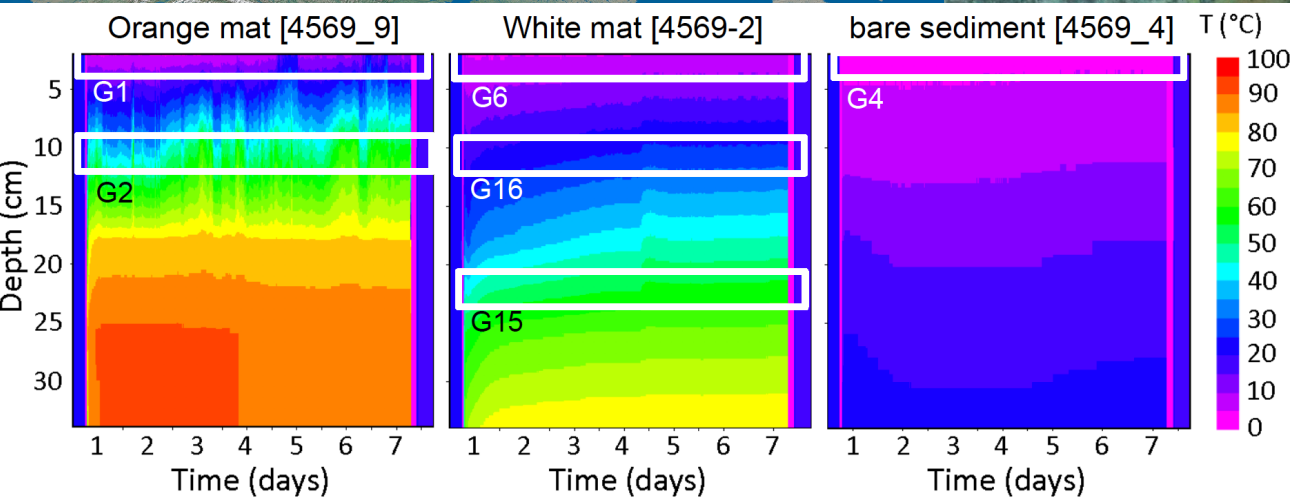


Anoxic environments

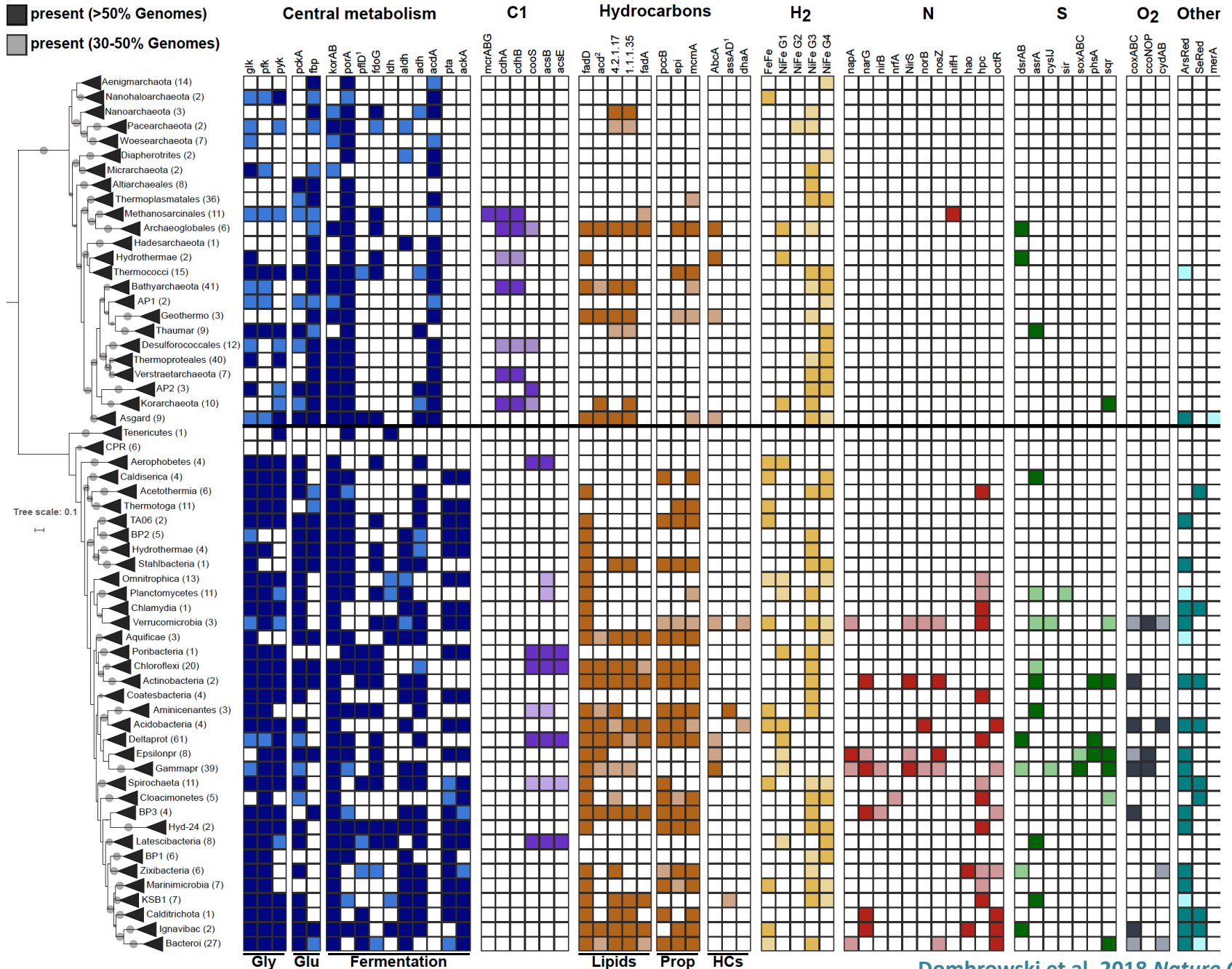
- Aigarchaeota
- Bathyarchaeota
- Geothermarchaeota
- DPANN
- Helarchaeota
- Thorarchaeota
- Heimdallarchaeota
- Korarchaeota
- Vestraetearchaeota
- Heimdallarchaeota
- Crenarchaeota
- Hadesarchaeae
- Nezhaarchaeota
- Thaumarchaeota
- Euryarchaeota

Guaymas Basin deep sea hydrothermal sediments

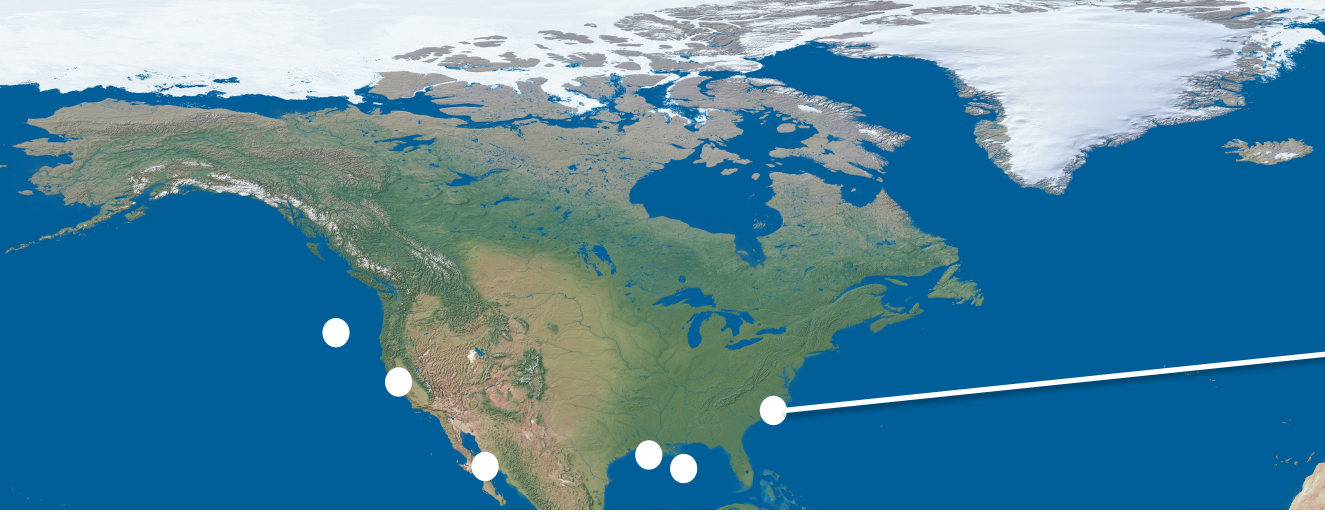
Marker 14 mat, 4569_9
4569_2
4569_4



Guaymas sediments contain considerable metabolic diversity

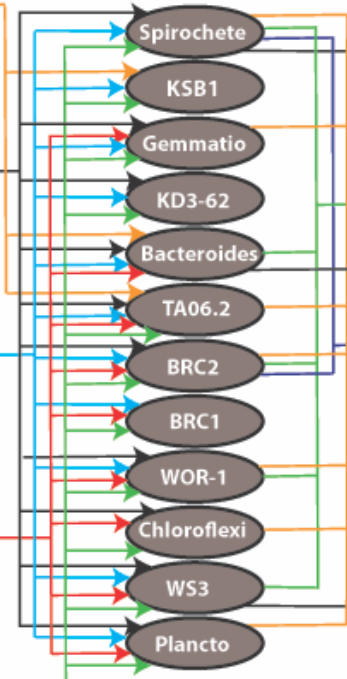


Mapping the flow of carbon and energy through the community

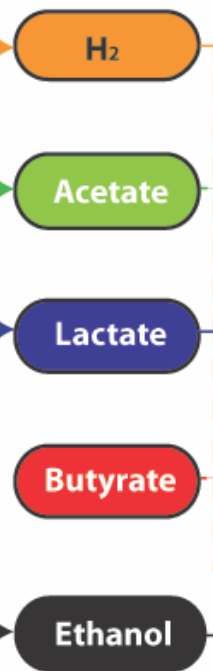


White Oak River Estuary

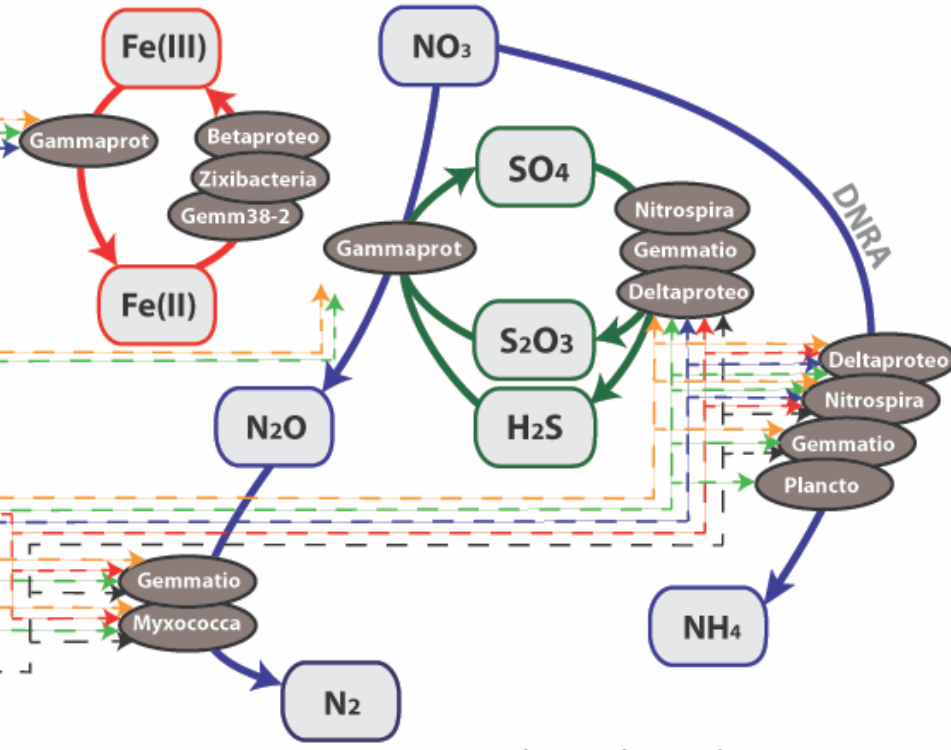
Carbon sources



Electron donors



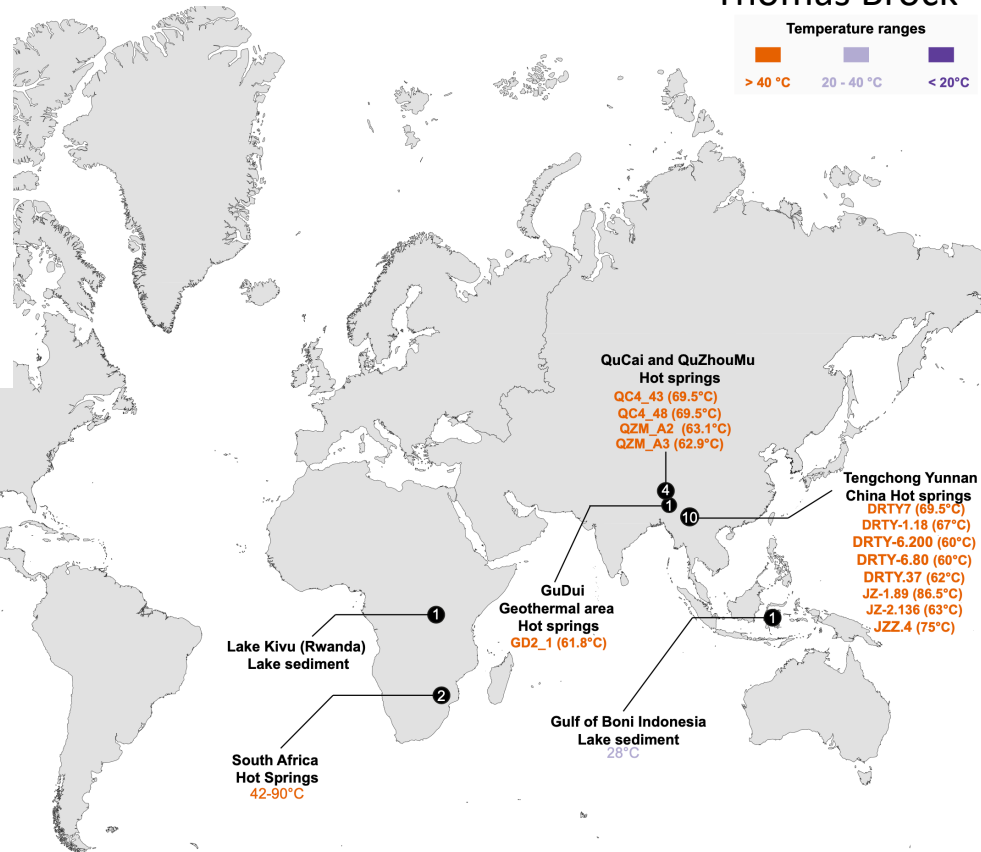
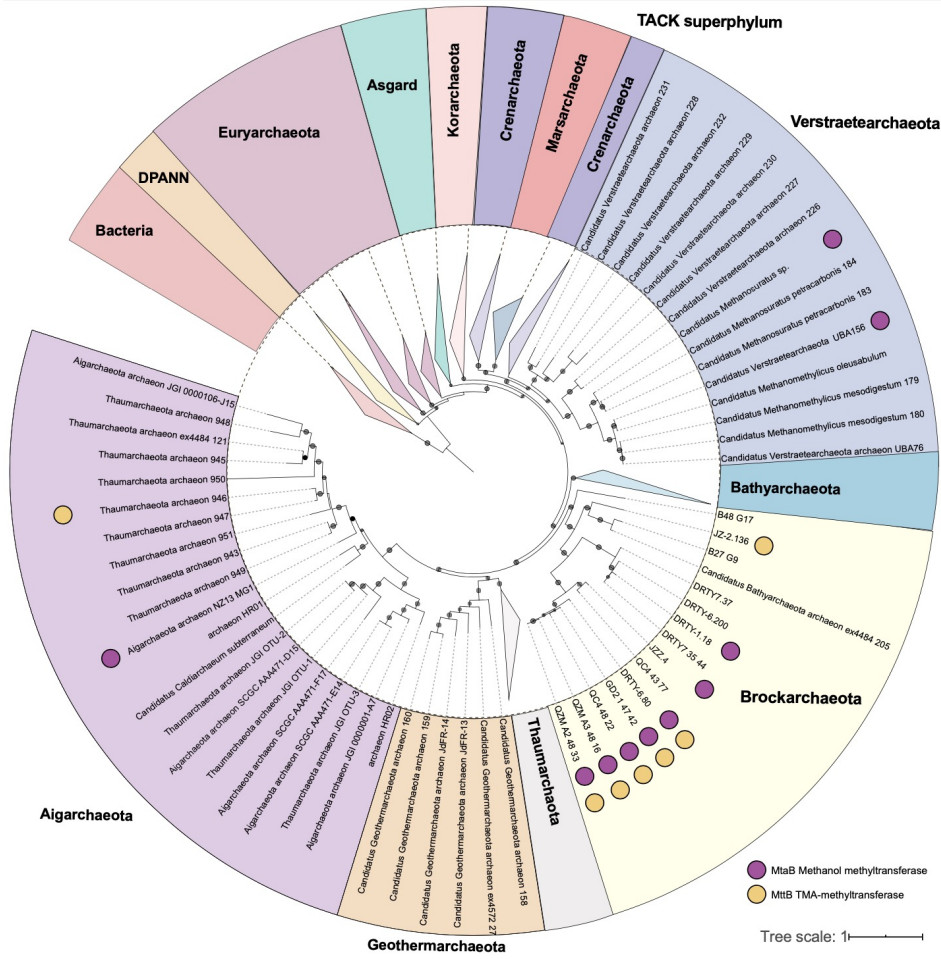
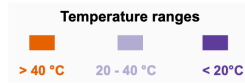
Respiratory geochemical processes



Brockarchaeota – an overlooked, widespread archaeal phylum



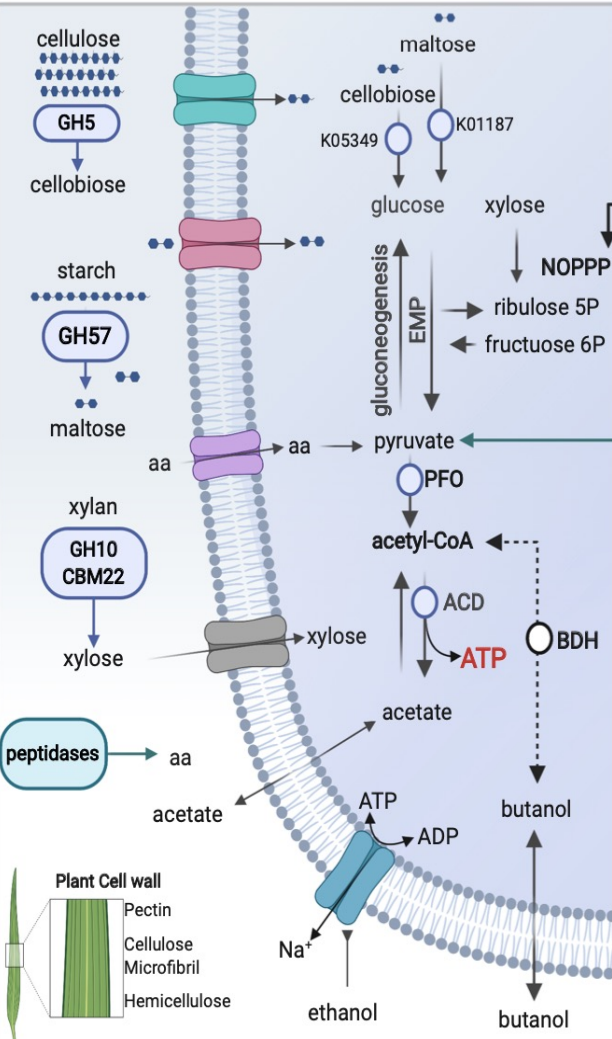
Thomas Brock



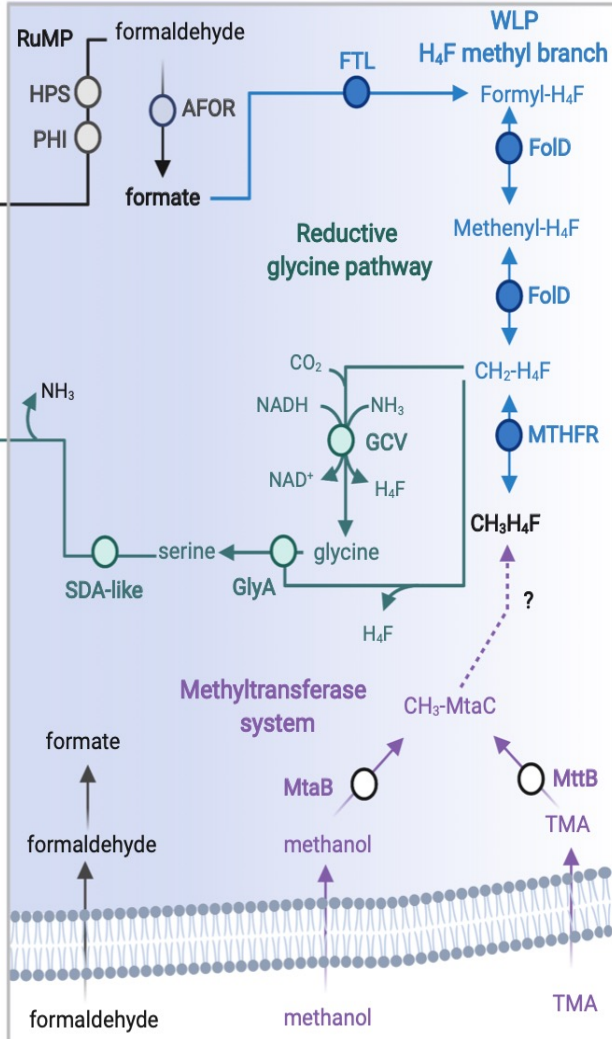
Brockarchaeota are non-methanogenic methylotrophs

De Anda et al. Nature Comm. 2021

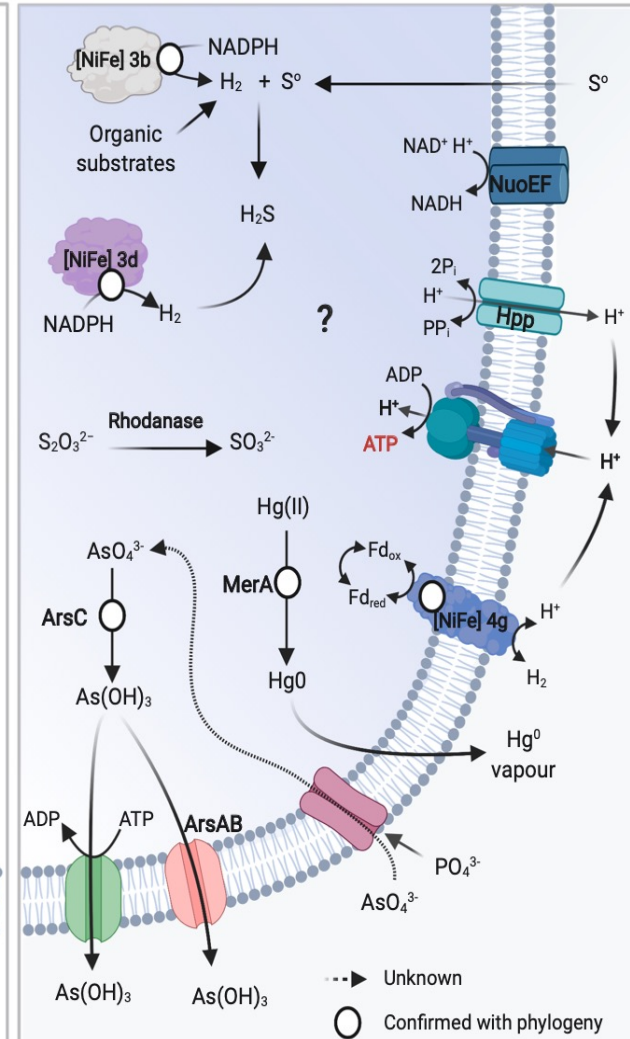
Fermentation



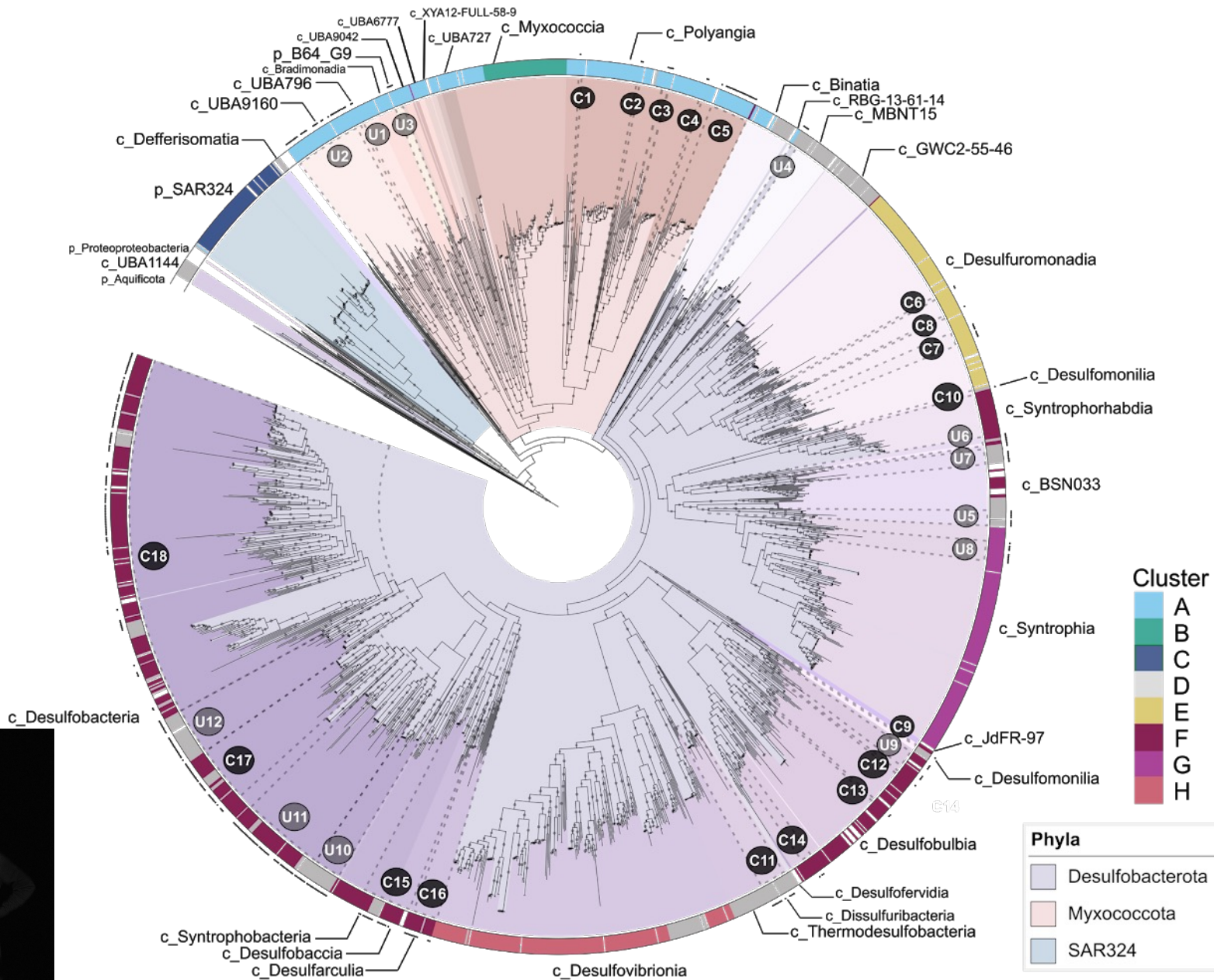
Anaerobic methylotrophy



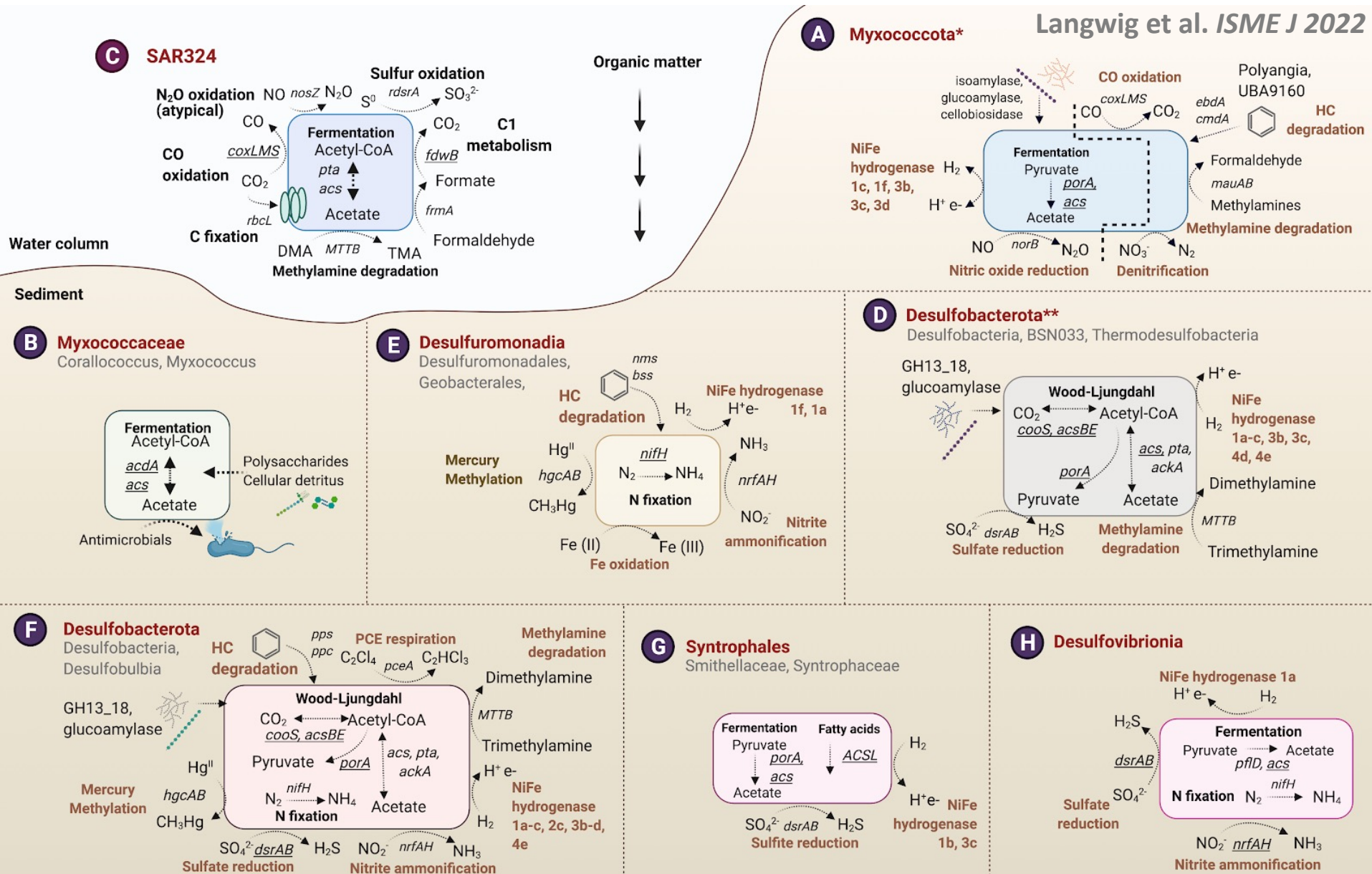
Chemolithotrophy



Protein clustering of dominant sediment bacteria



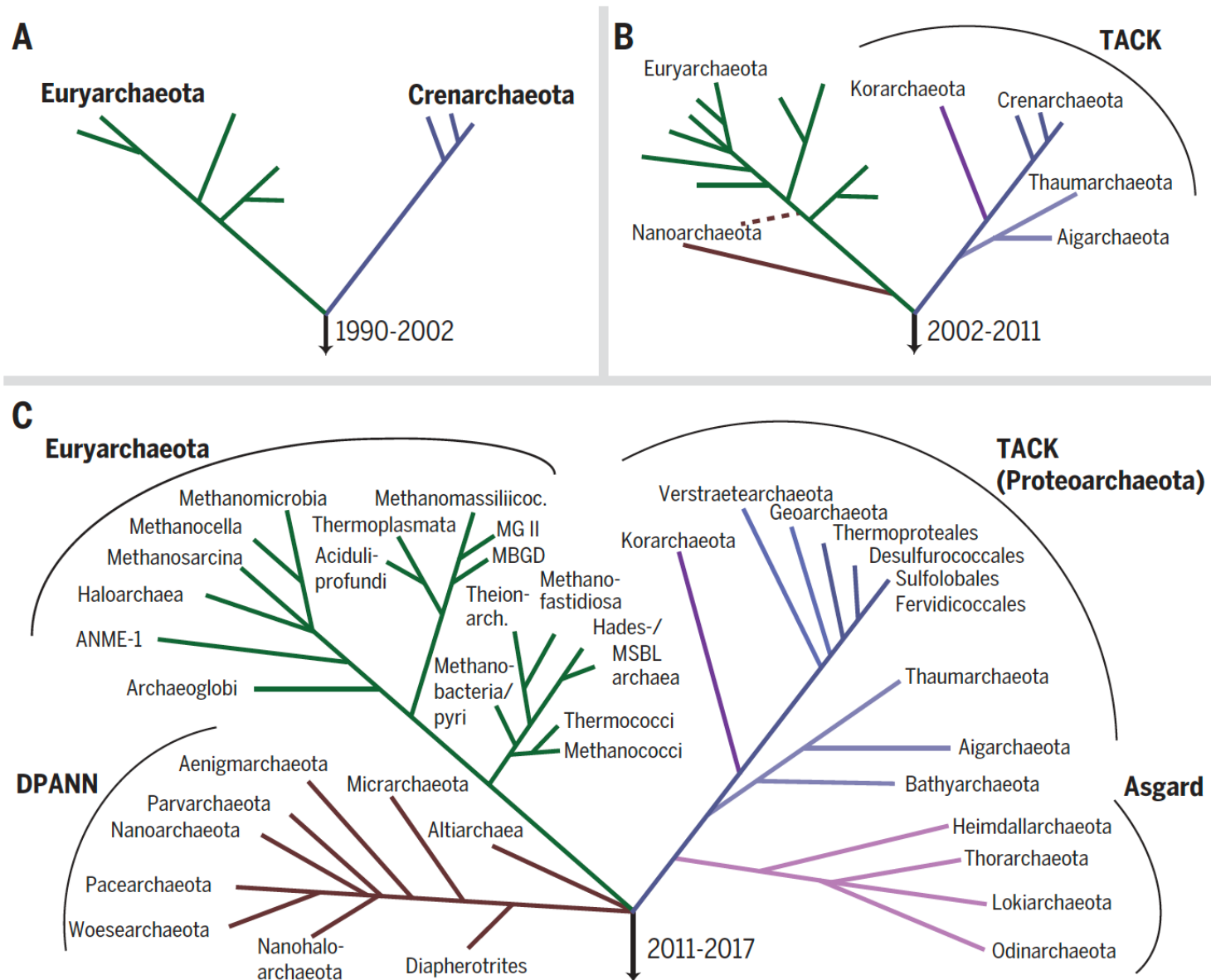
Protein clusters have distinct metabolisms



Asgard archaea

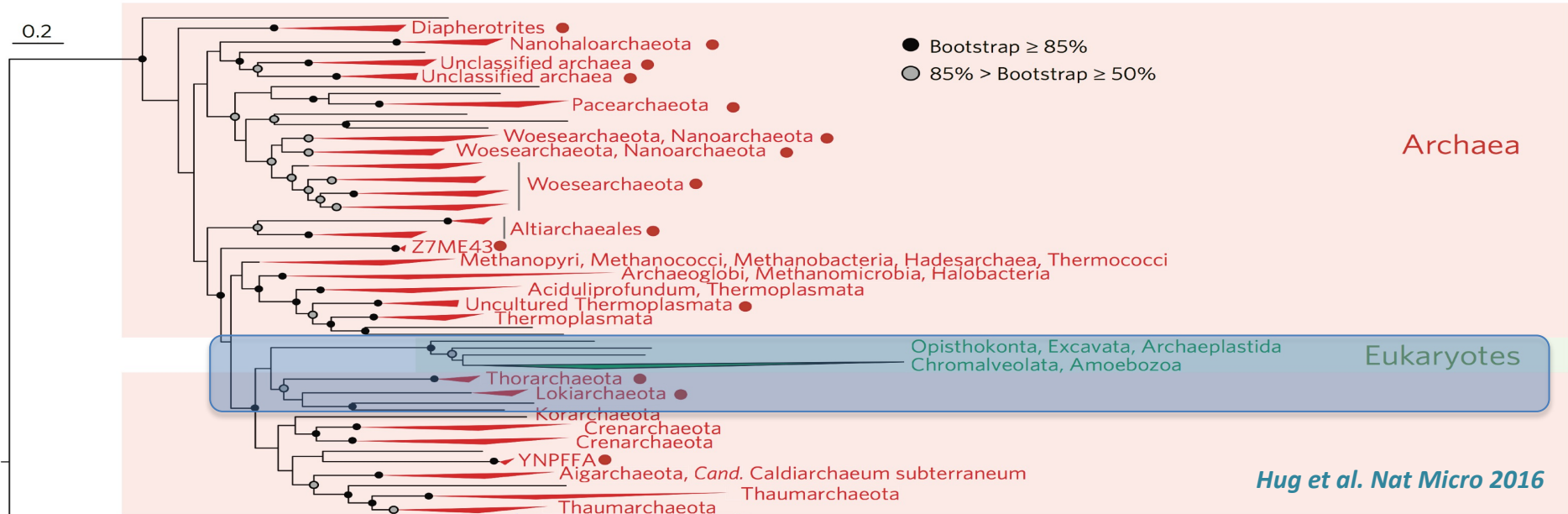


The growing tree of archaea



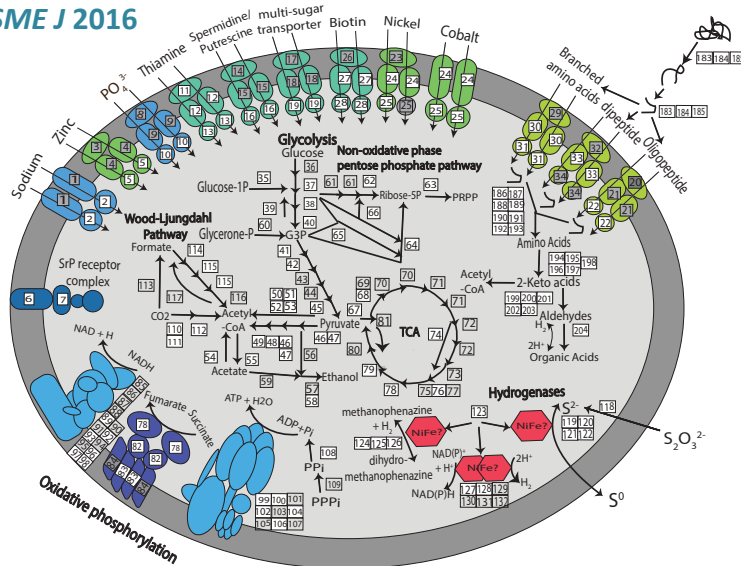
“The deepest branchings of this tree take us into uncharted evolutionary waters; the door to understanding earlier, more primitive forms of life has opened.” Carl Woese 2000

New Archaea related to eukaryotes



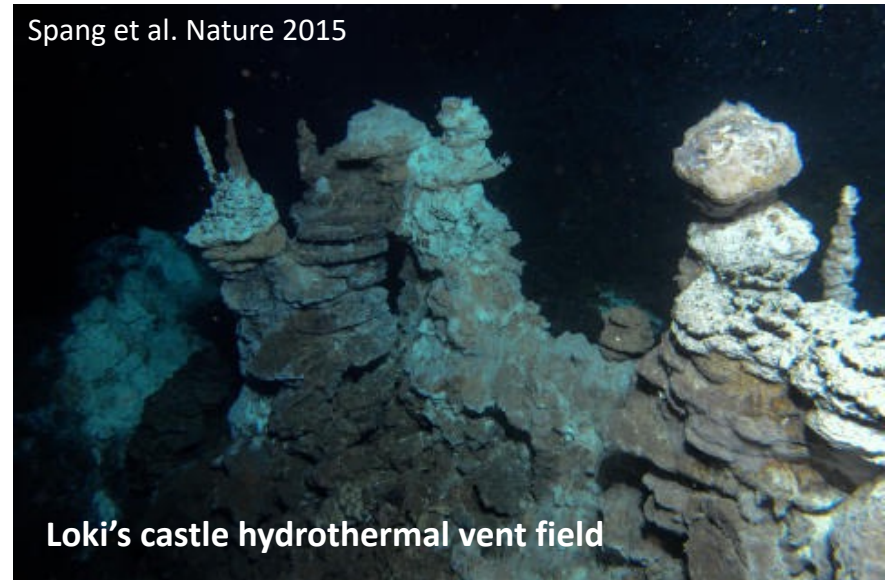
Thorarchaeota

Seitz et al *ISME J* 2016

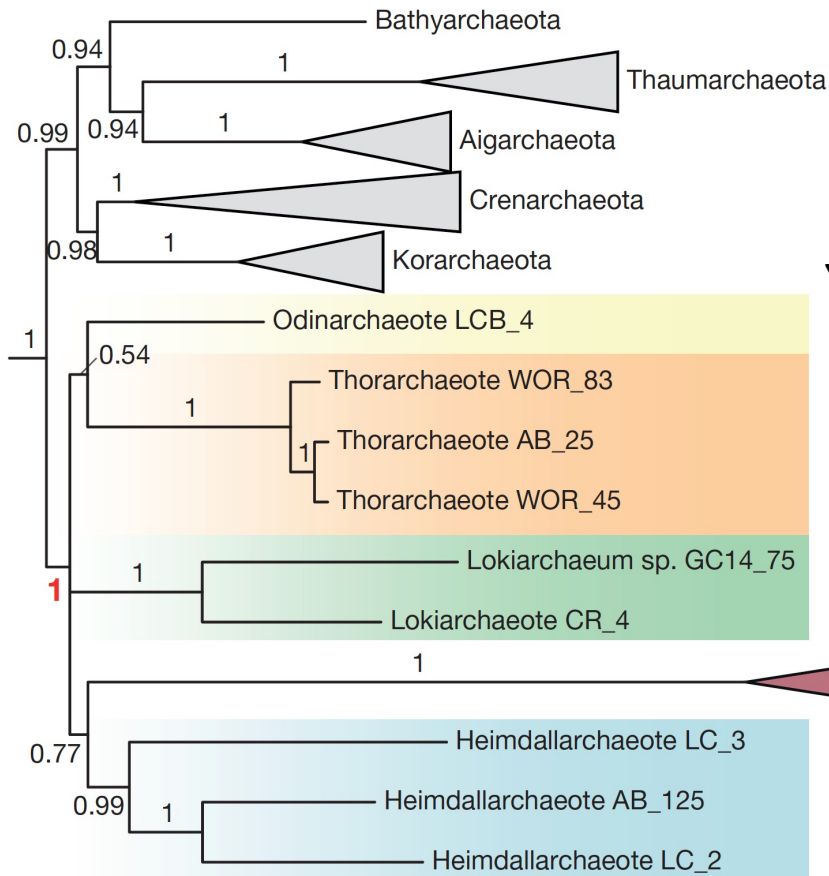
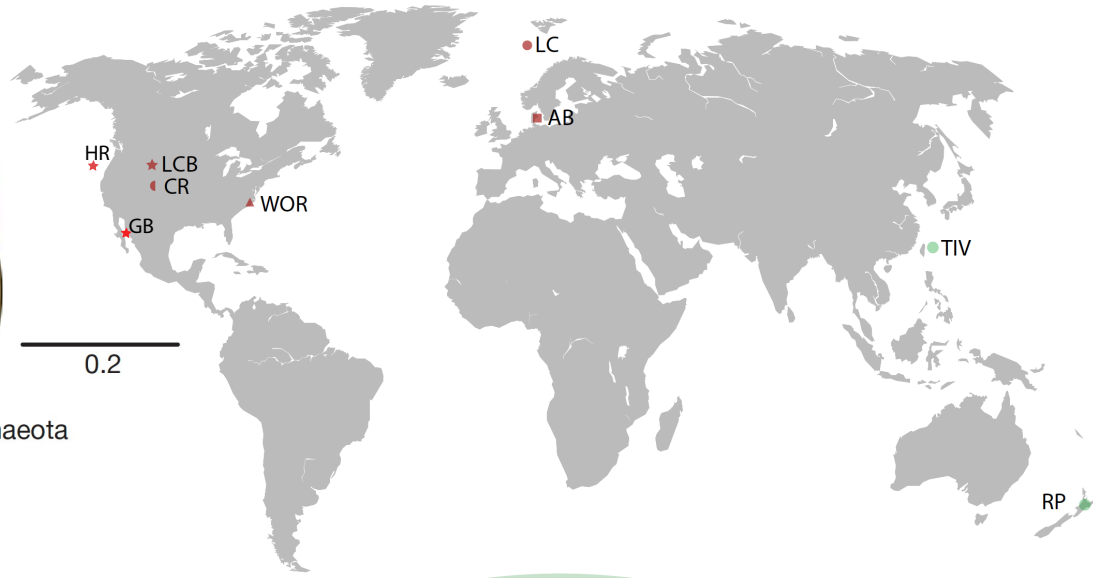


Lokiarchaeota

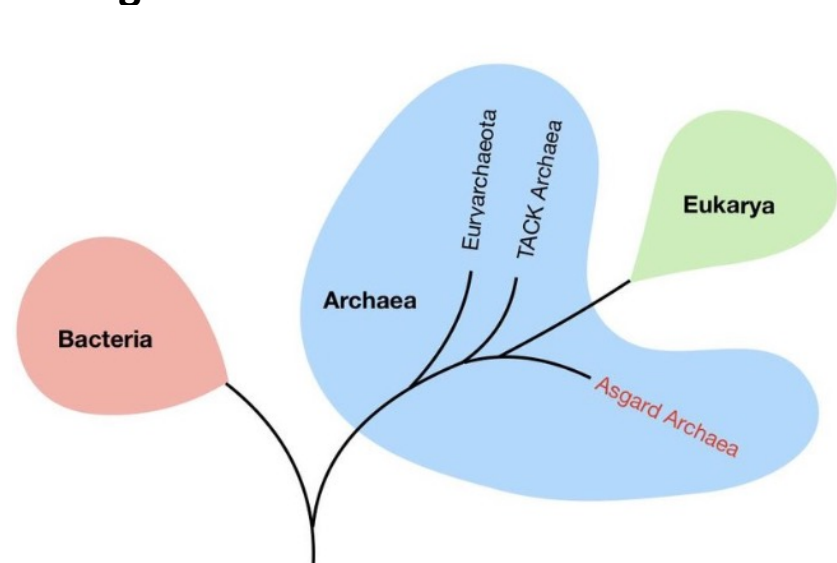
Spang et al. *Nature* 2015



Asgard archaea



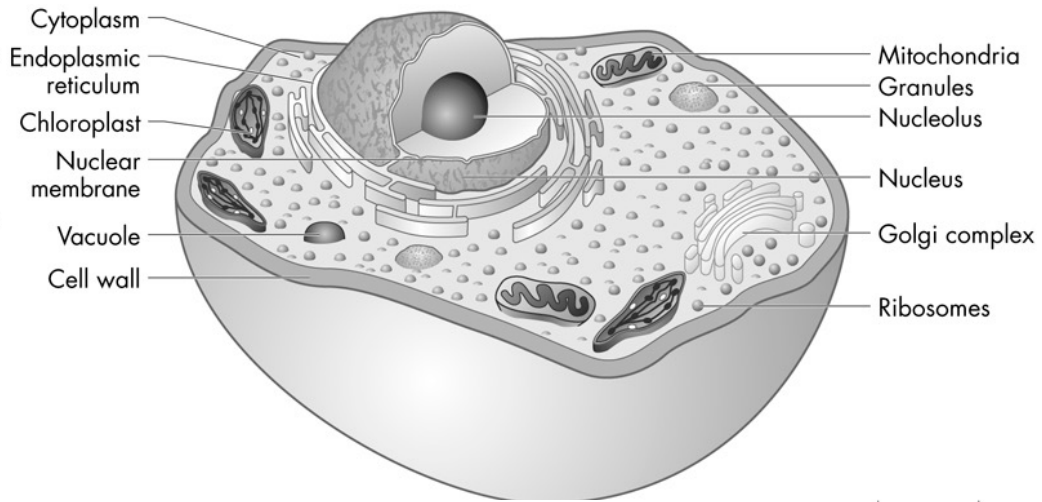
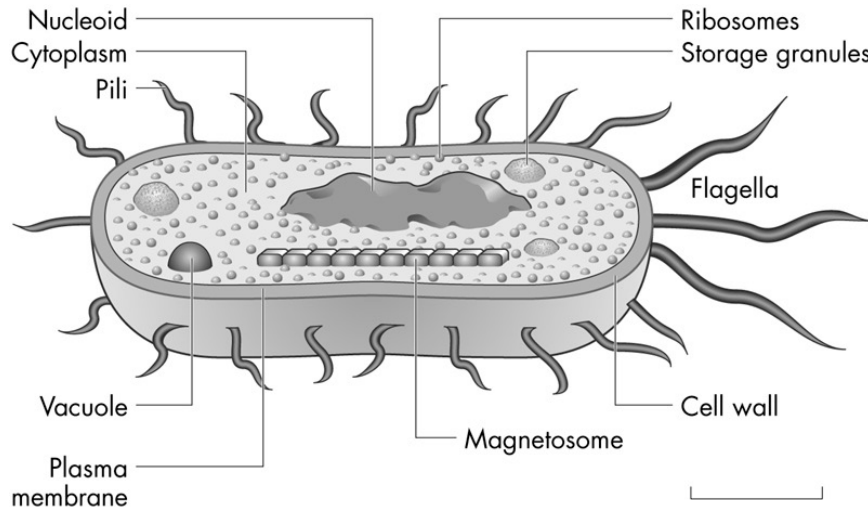
Yes, we are Asgardian!



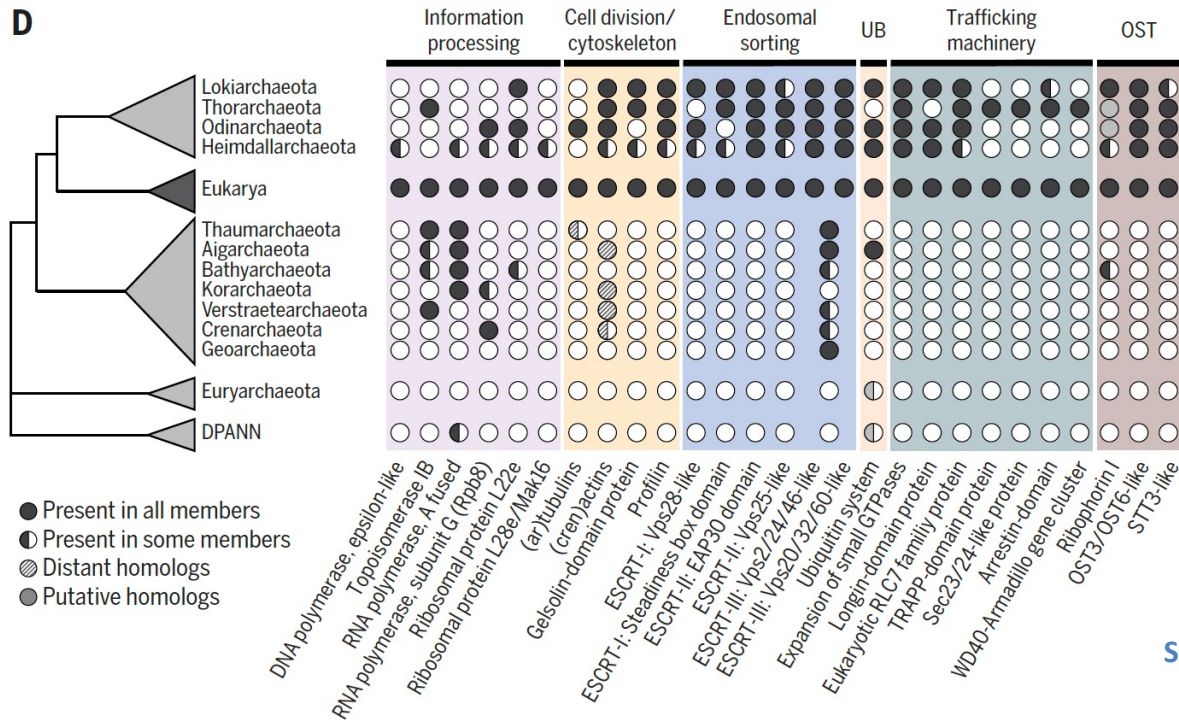
Asgard archaea contain several eukaryotic proteins

prokaryote

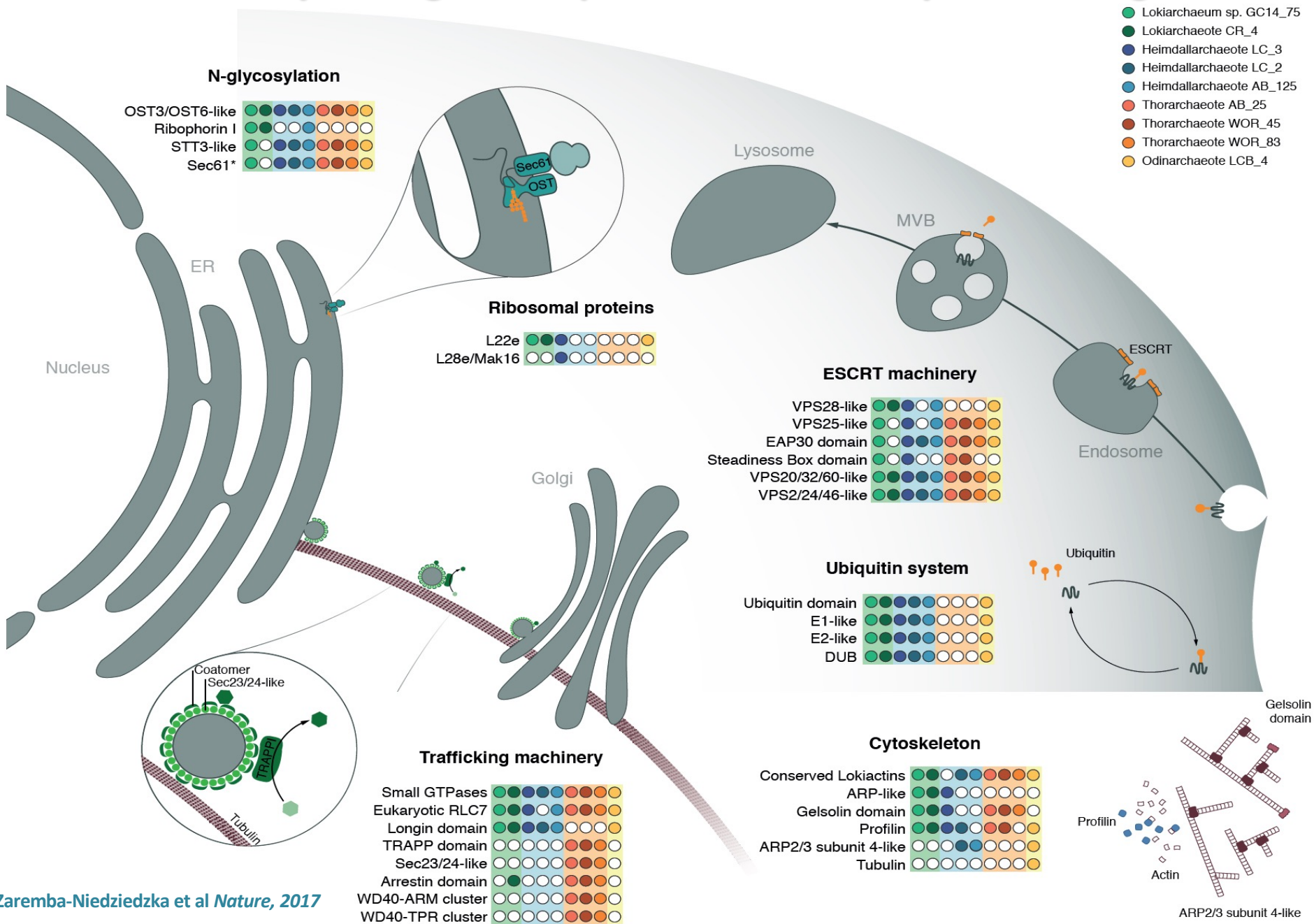
eukaryote



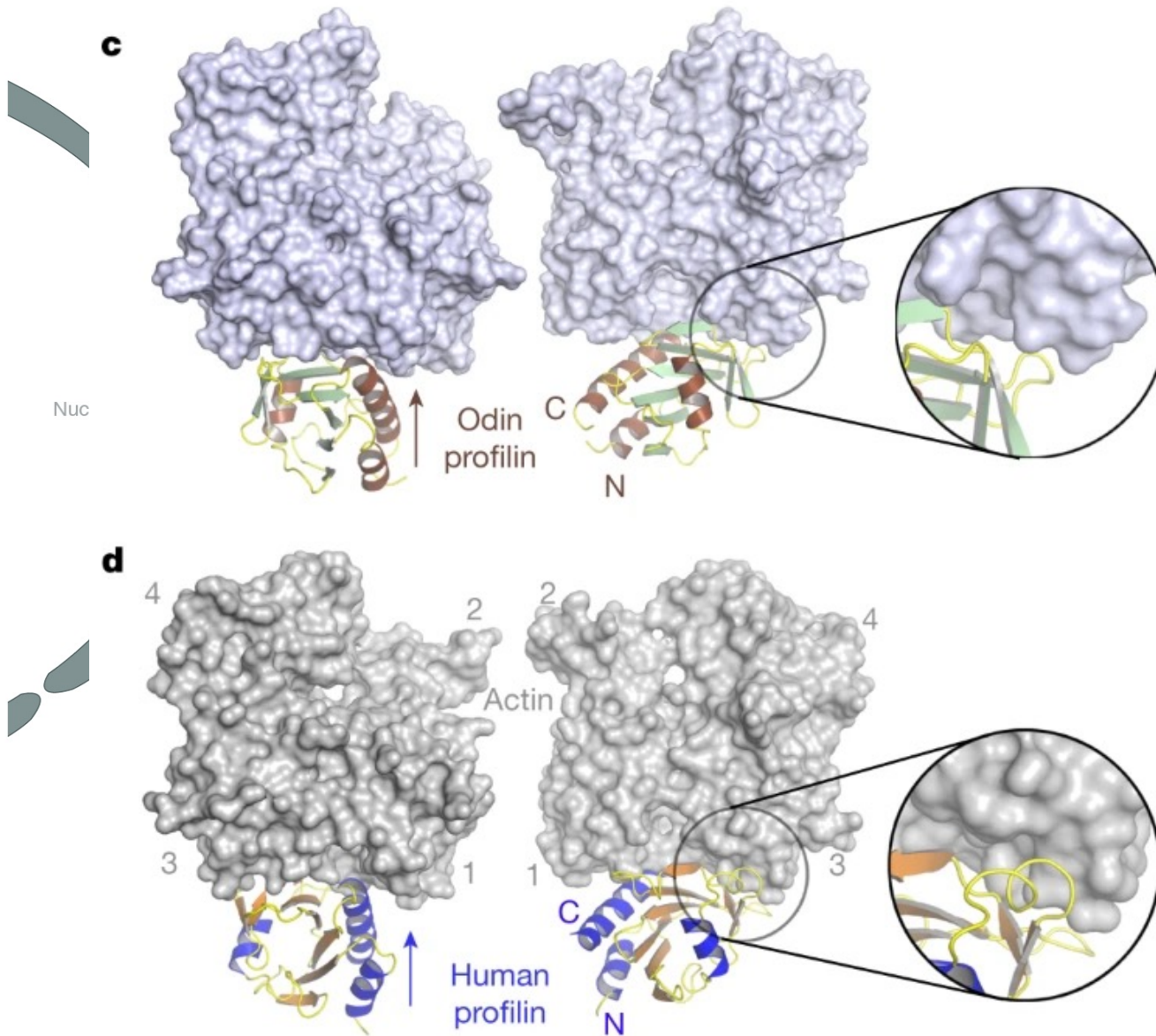
D



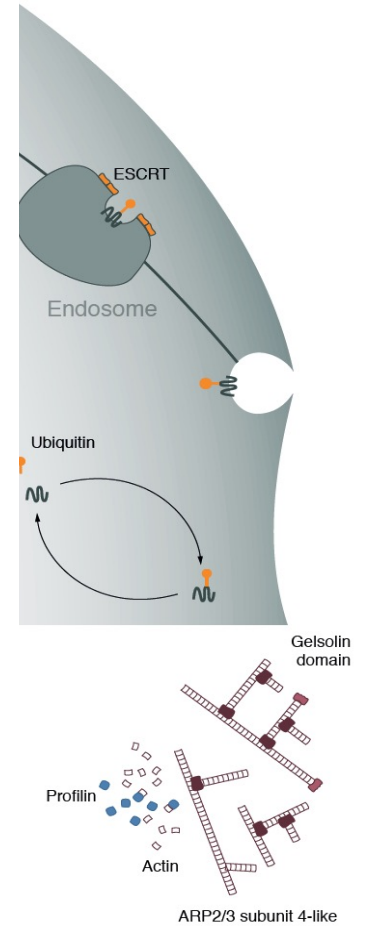
ESP = eukaryotic signature proteins are widespread in Asgard



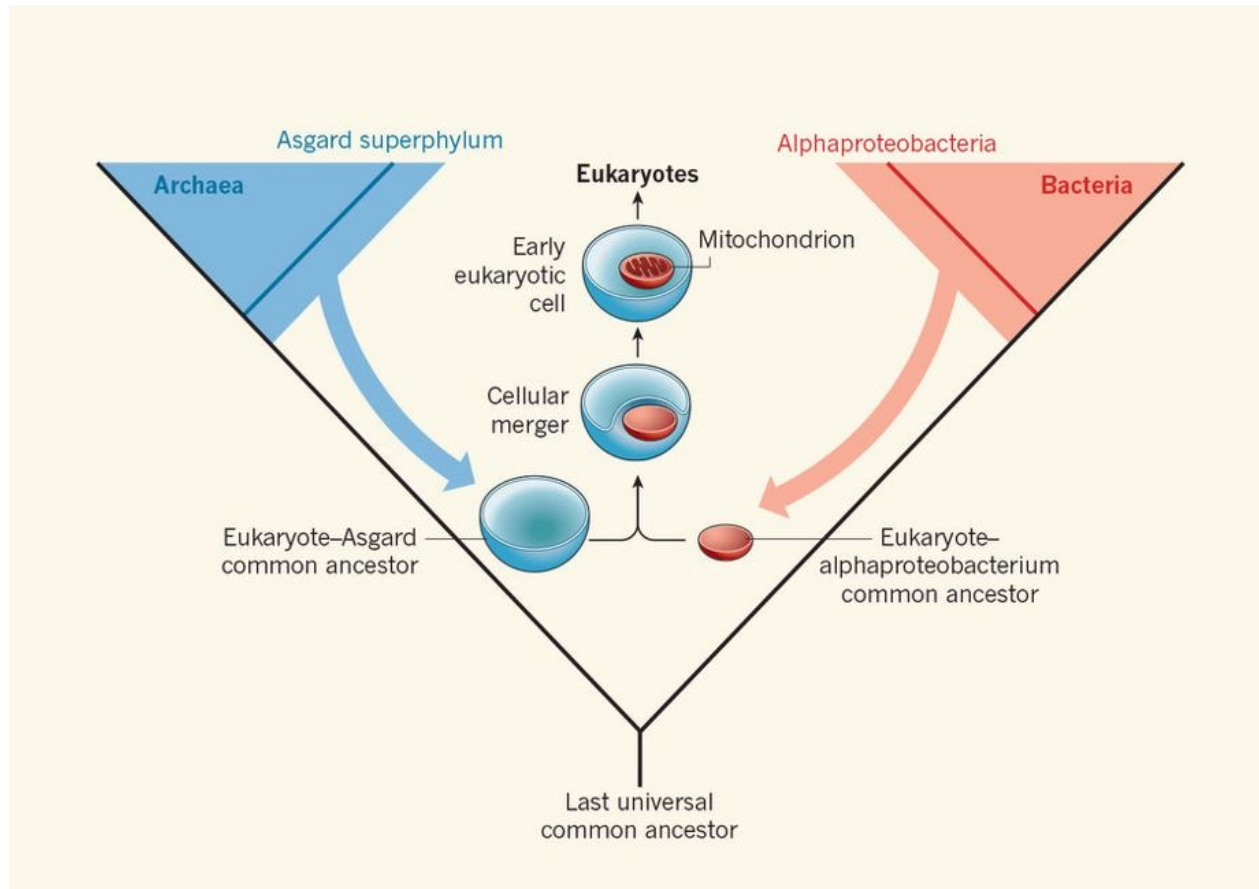
ESPs are widespread in Asgard archaea



- Lokiarchaeum sp. GC14_75
- Lokiarchaeote CR_4
- Heimdallarchaeote LC_3
- Heimdallarchaeote LC_2
- Heimdallarchaeote AB_125
- Thorarchaeote AB_25
- Thorarchaeote WOR_45
- Thorarchaeote WOR_83
- Odinararchaeote LCB_4

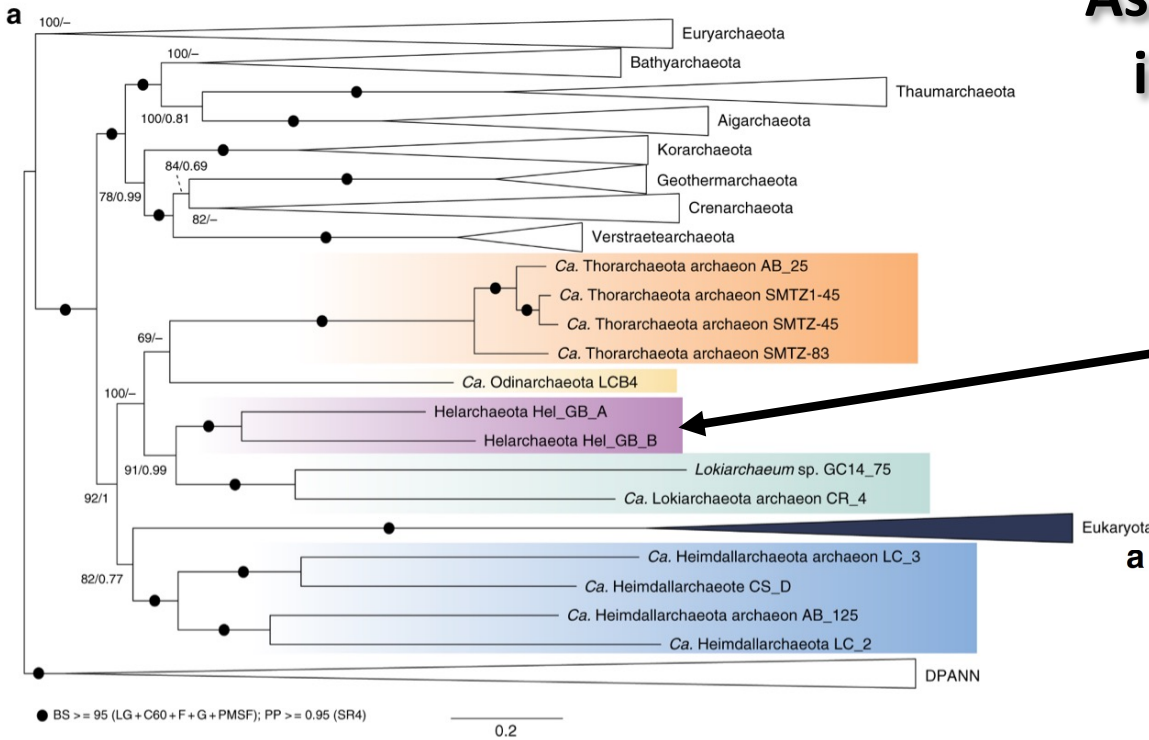


What does this mean for our understanding of eukaryotic evolution?

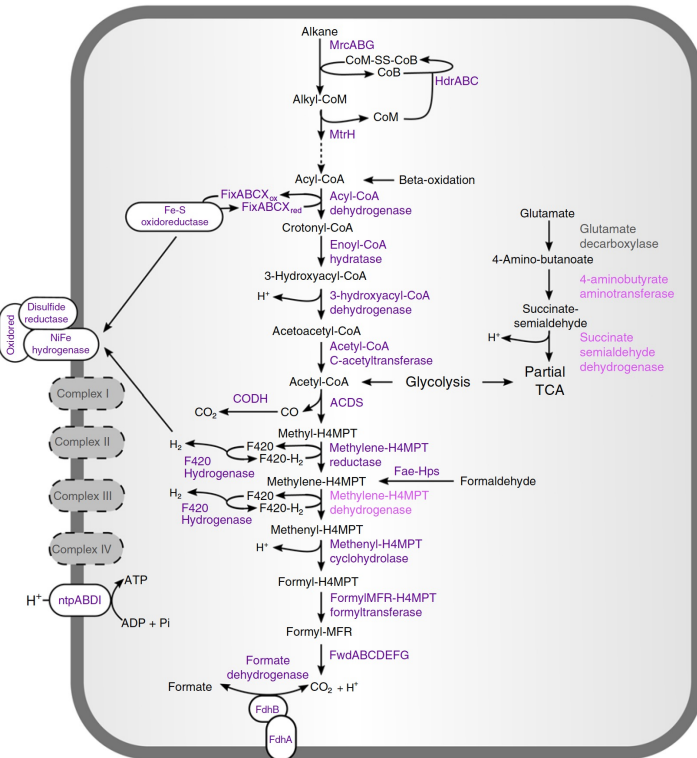


McInerney and O'Connell, Nature 2017

Asgard appear to be involved in symbiotic relationships

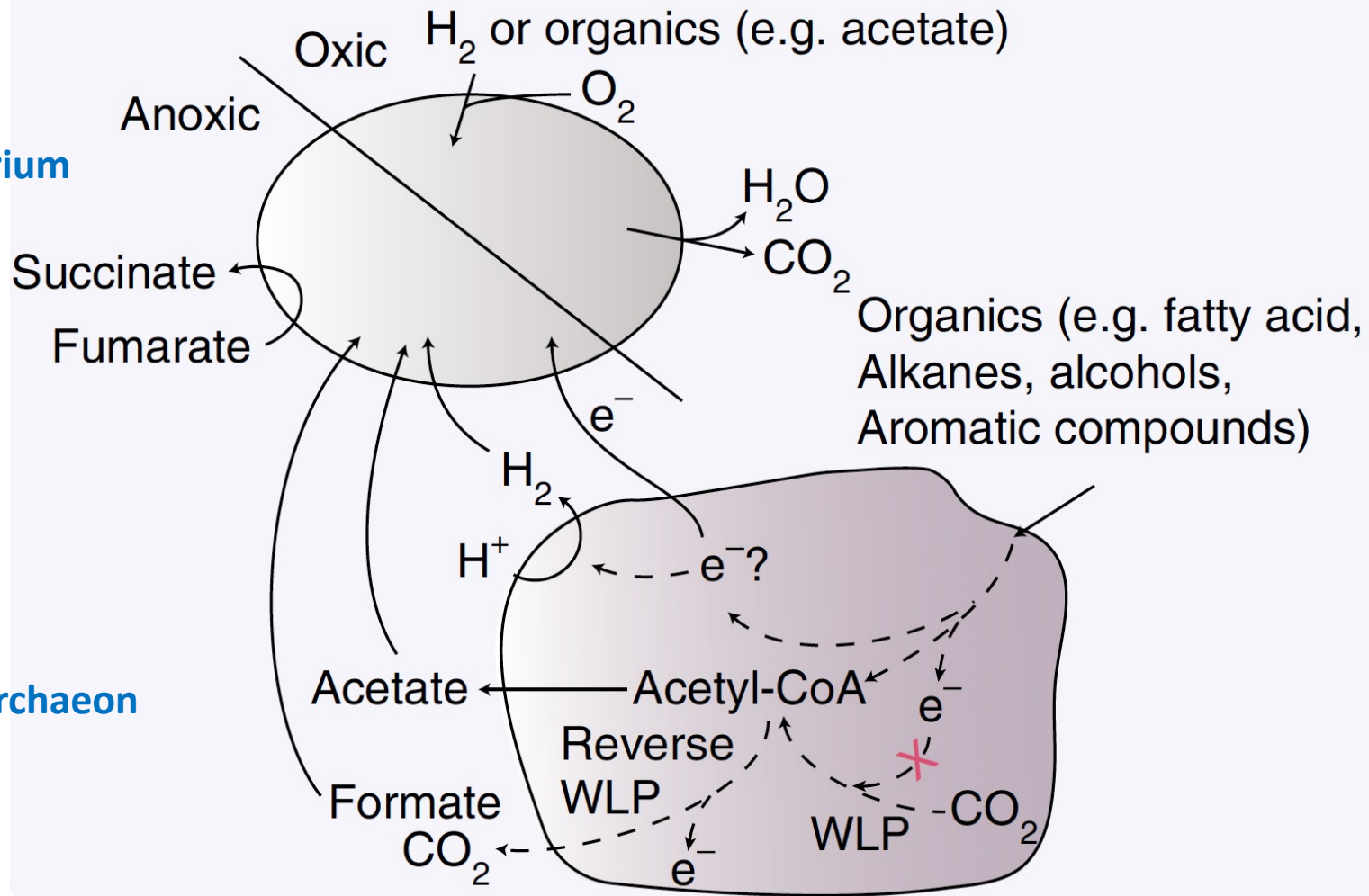


Unknown partner

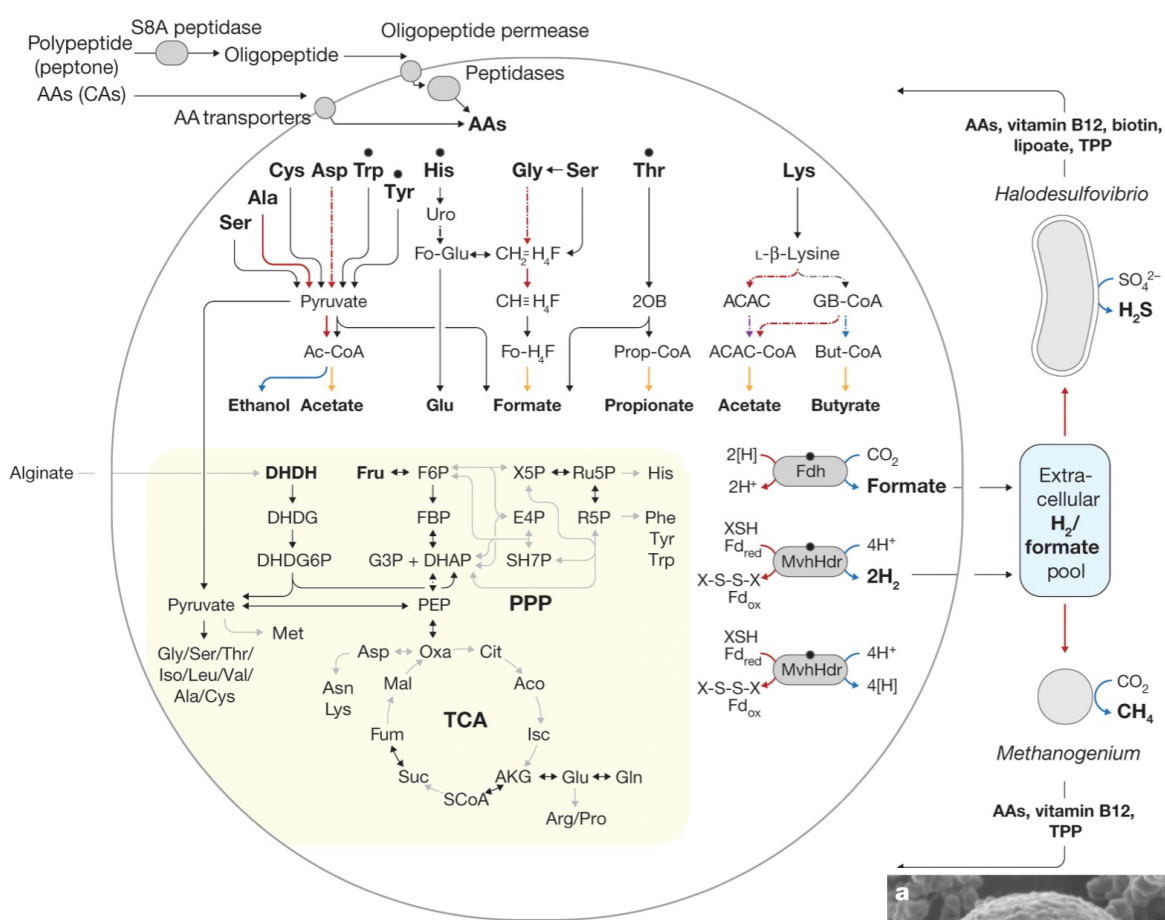


New model for interactions -> origin of eukaryotes

Alphaproteobacterium

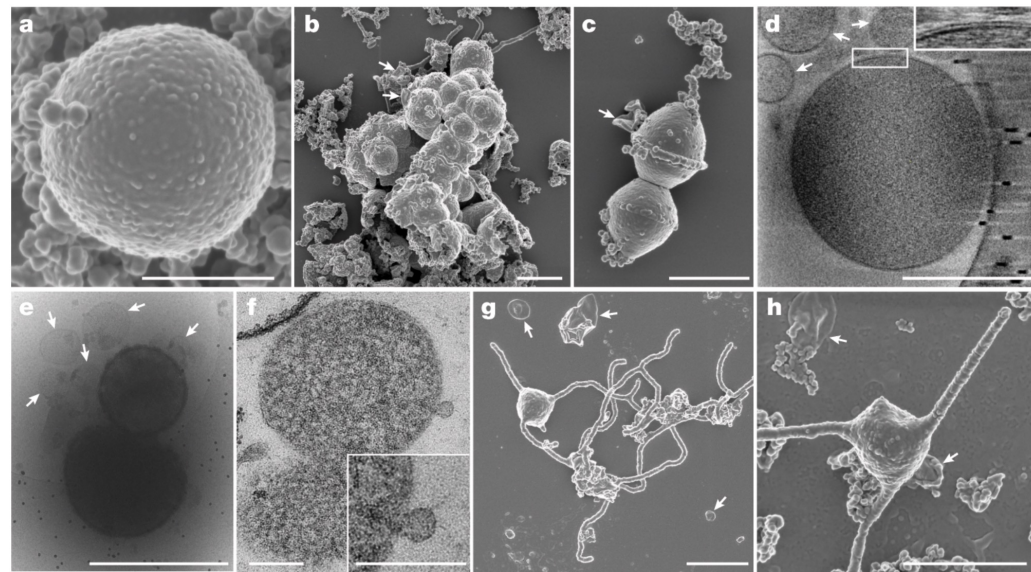


Ancestral Asgard archaeon



Cultivation of a Lokiarchaeum

Imachi et al Nature, 2020



My Lab at UT



Ian Rambo

Kiley Seitz

Valerie de Anda

Maggie Langwig

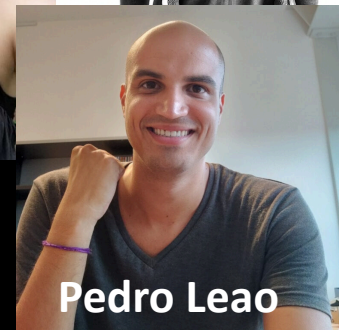
Xianzhe Gong

Mirna Vázquez



Katy Appler

JD Carlton



Pedro Leao

SIMONS FOUNDATION



GORDON AND BETTY
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Wageningen Univ.
Thijs Ettema
Anja Spang, Laura Eme
Daniel Tamari,
Eva Caceres,
Courtney Stairs

UC Berkeley
Jill Banfield



UNC-Chapel Hill
Andreas Teske

