

# Ecology and physiology of planktonic archaea

Alyson Santoro

Horn Point Laboratory

University of Maryland Center for Environmental Science

C-MORE Microbial Oceanography Course 2014

# Talk outline

Who are the marine archaea?

Tracking down the MGI archaea

Taming wild archaea to investigate their  
physiology

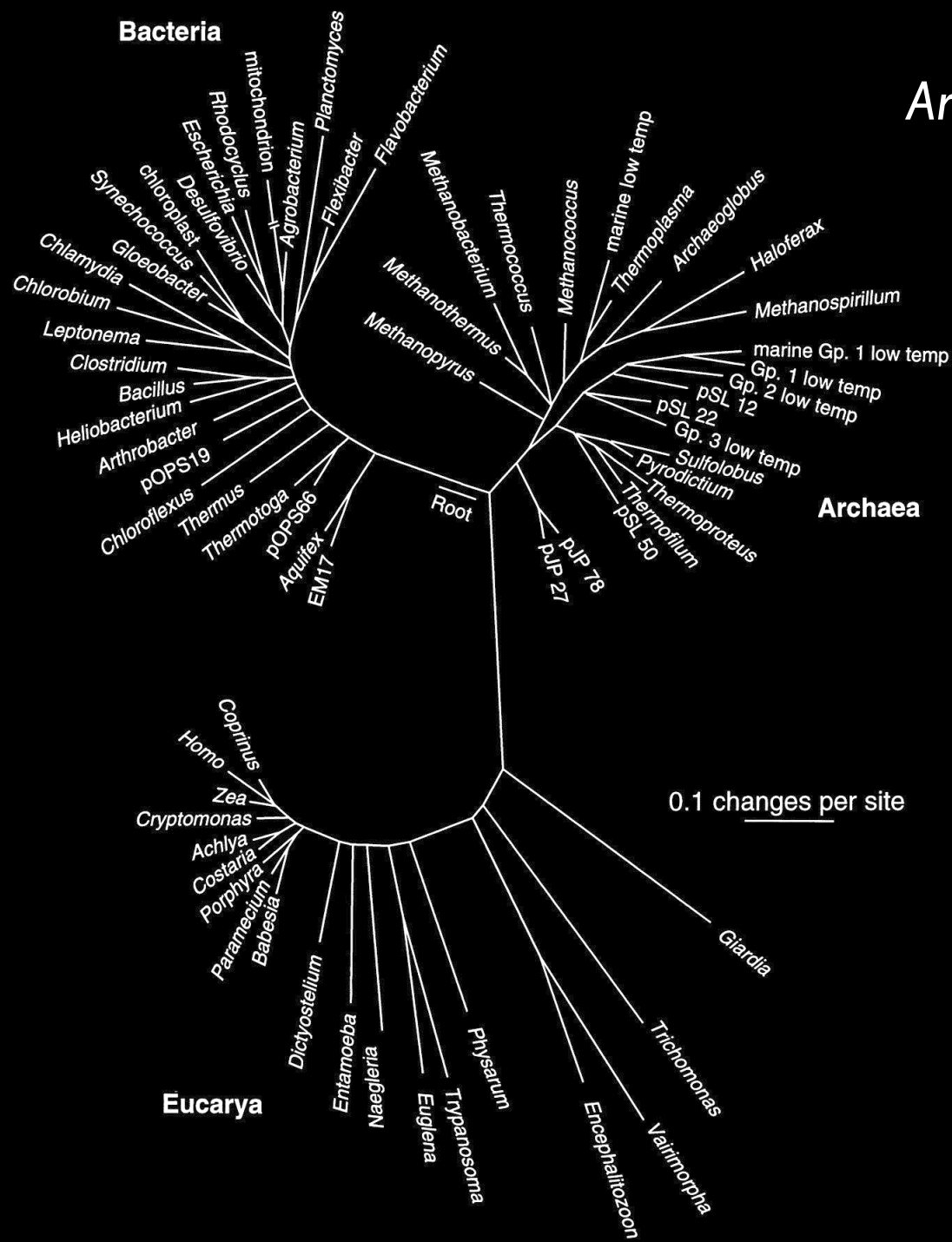
The elusive Euryarchaeota

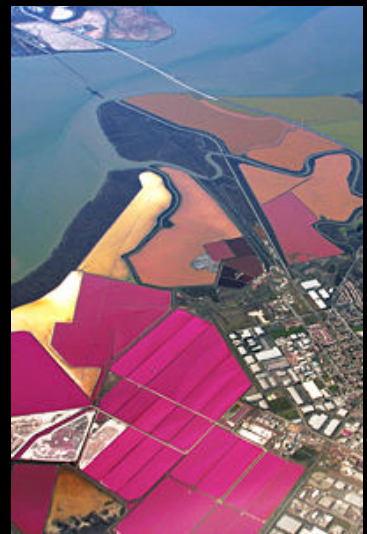
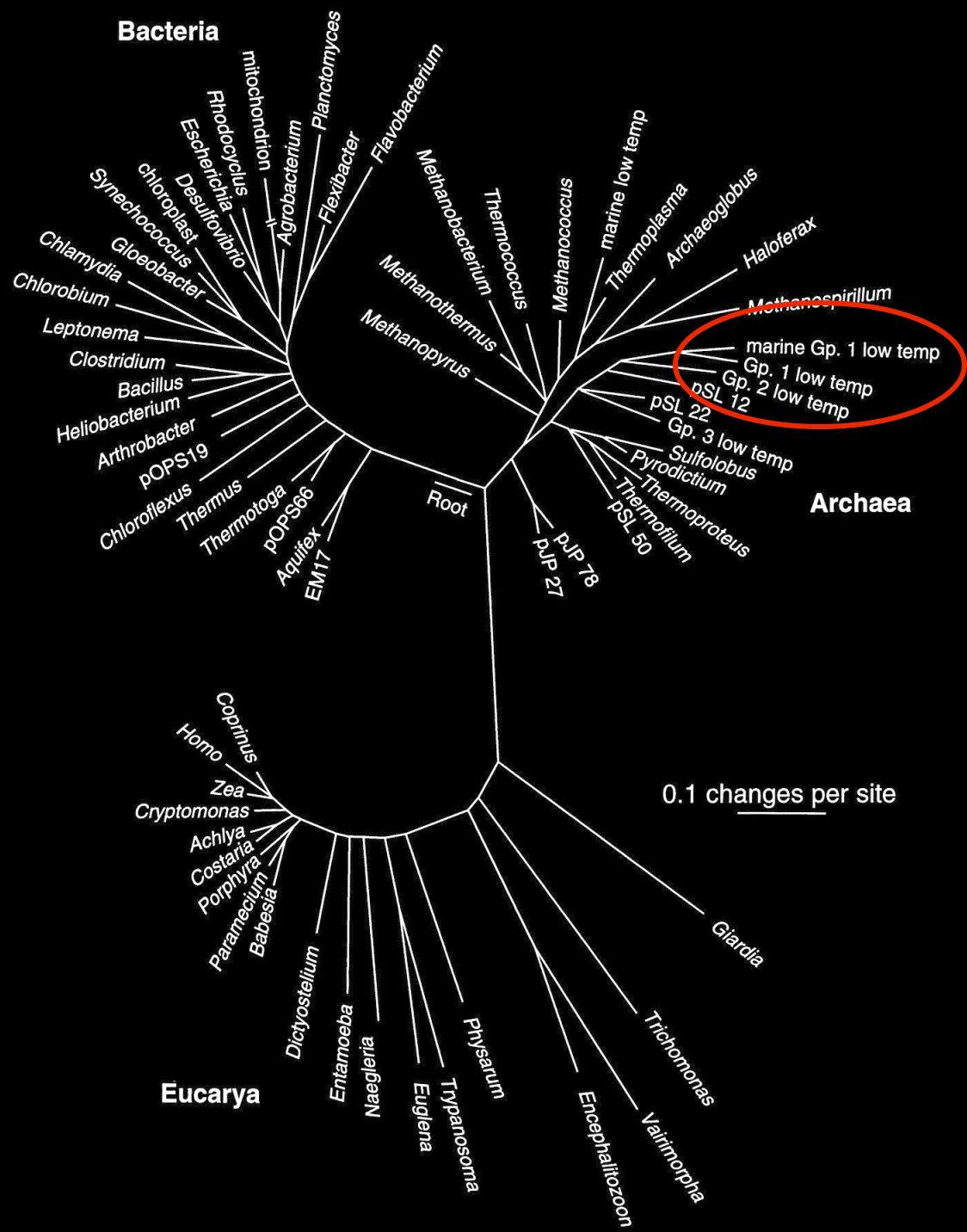
Who are the marine archaea?

# Eucarya

# Bacteria

# Archaea

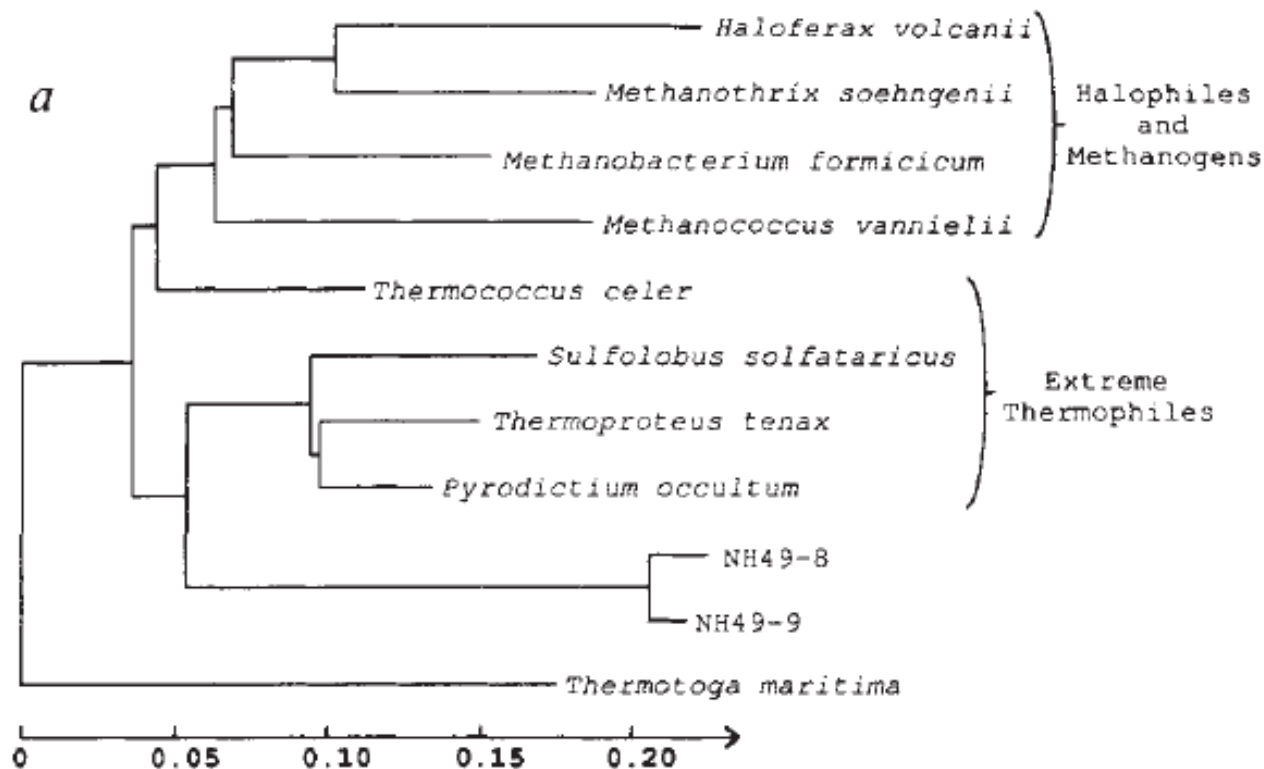




# Novel major archaeobacterial group from marine plankton

Jed A. Fuhrman, Kirk McCallum\* & Alison A. Davis

Department of Biological Sciences, University of Southern California,  
Los Angeles, California

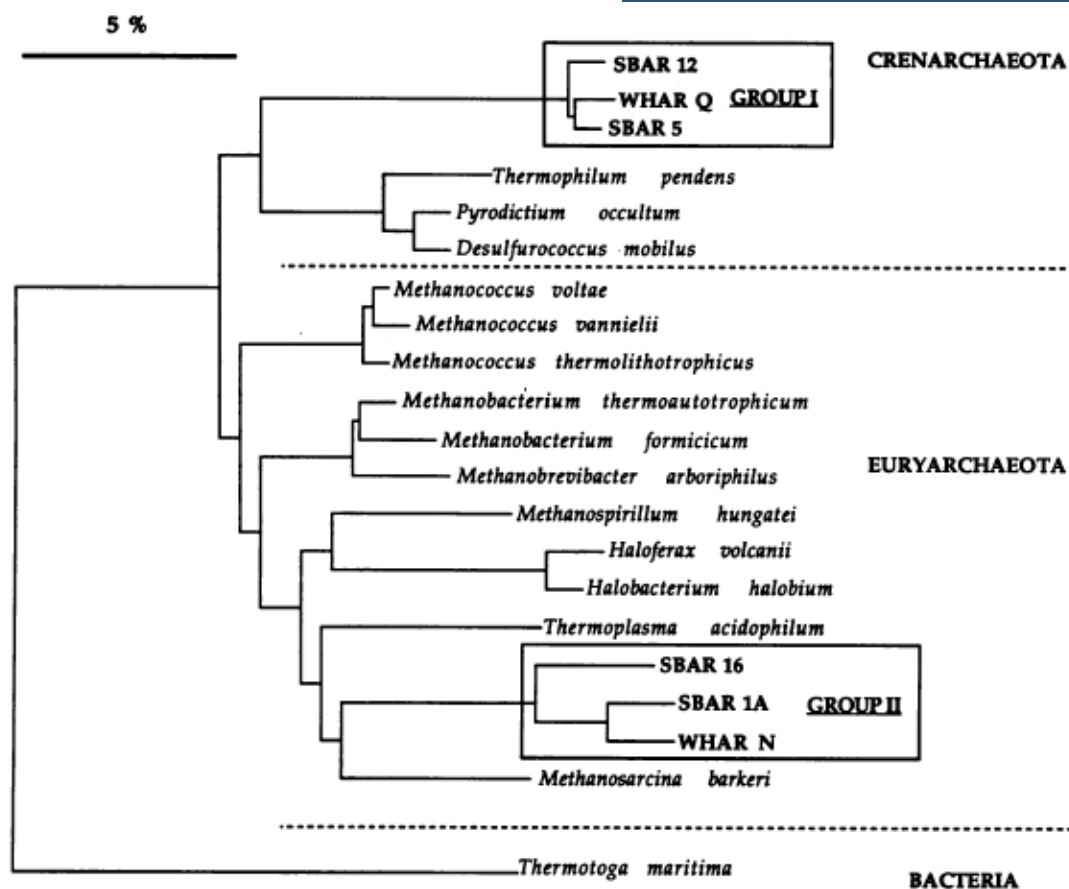


# Archaea in coastal marine environments

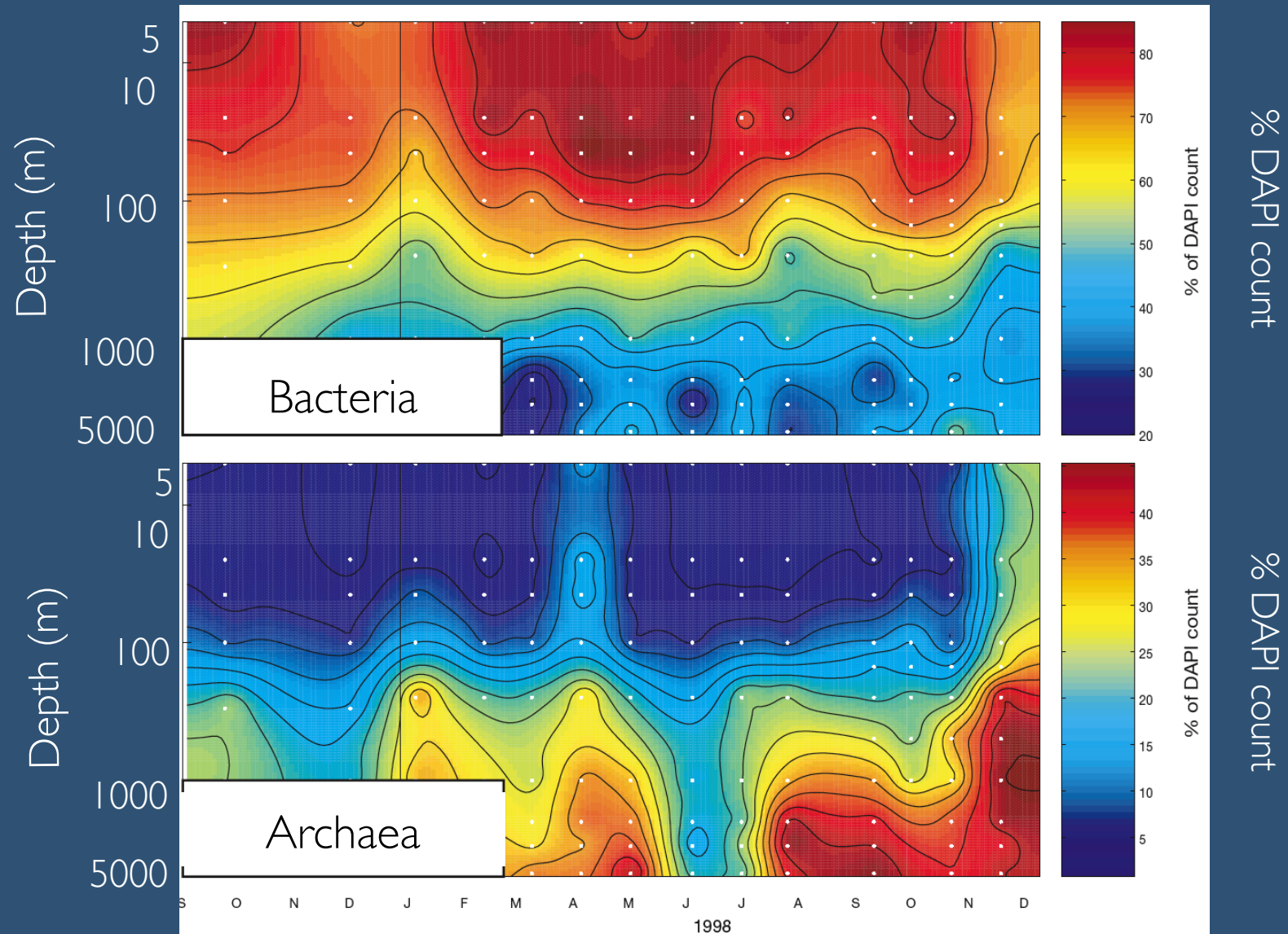
(archaeobacteria/phylogeny/bacterioplankton/molecular ecology)

EDWARD F. DeLONG\*

Biology Department, Woods Hole Oceanographic Institution, Woods Hole, MA 02543

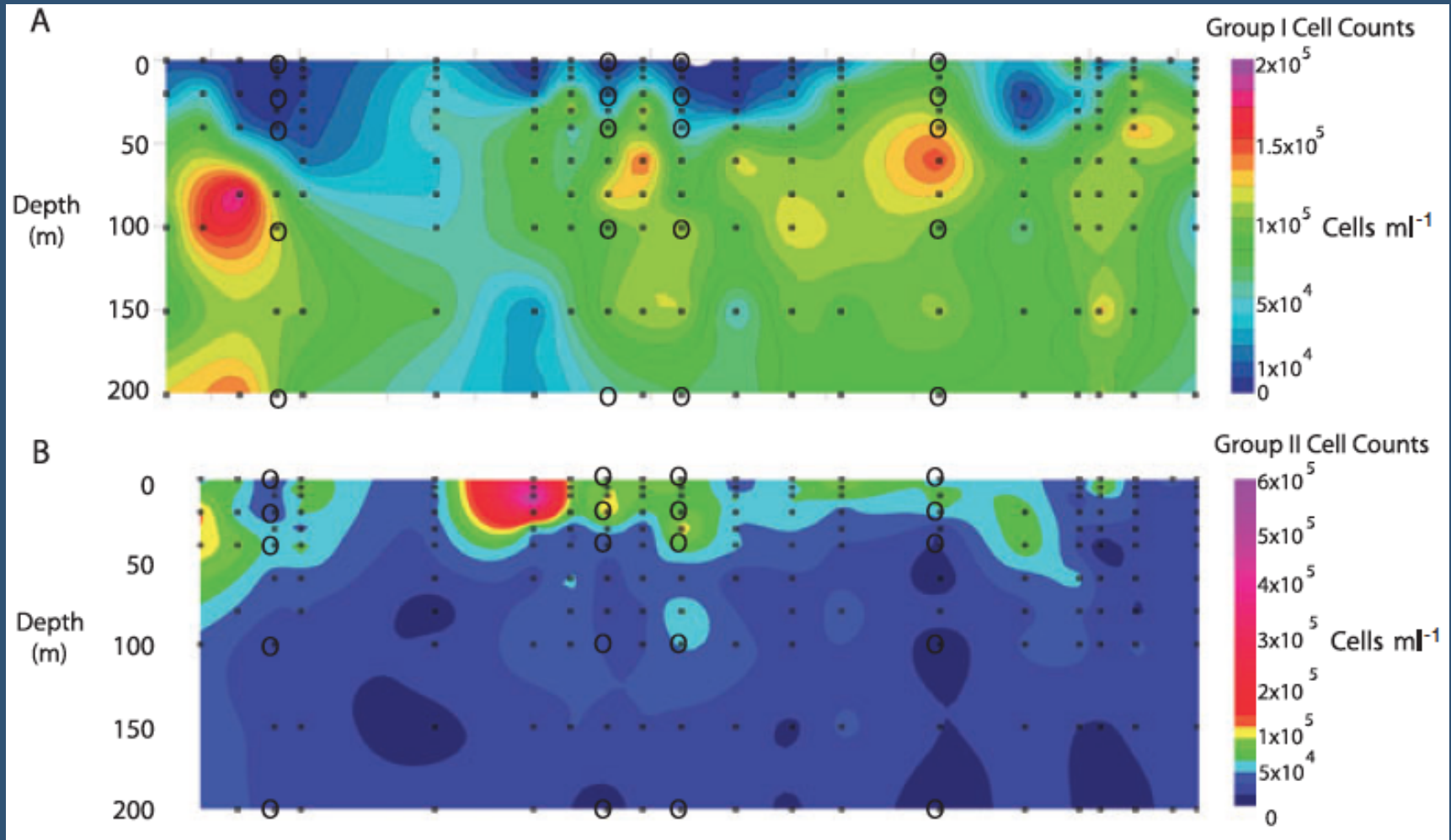


Mesophilic archaea are the most abundant cells in the deep ocean (and possibly the planet).





# Contrasting distribution of MGI and MGII



MGI archaea: Tracking down the most abundant cells in the deep ocean

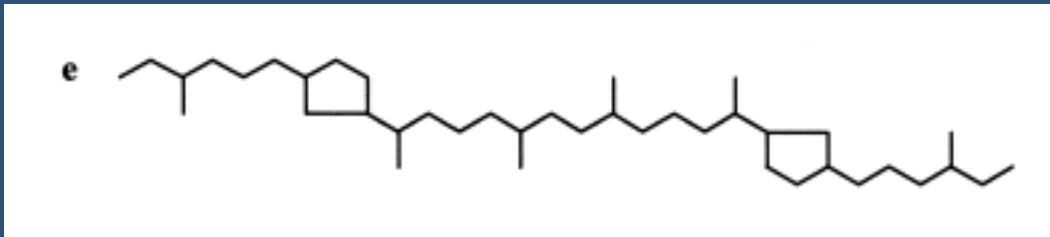
# MGI archaea are autotrophic?

## Origins of lipid biomarkers in Santa Monica Basin surface sediment: A case study using compound-specific $\Delta^{14}\text{C}$ analysis

A. PEARSON,<sup>1,\*</sup> A. P. McNICHOL,<sup>2</sup> B. C. BENTEZ-NELSON,<sup>1,†</sup> J. M. HAYES,<sup>2</sup> and T. I. EGLINTON<sup>1</sup>

<sup>1</sup>Department of Marine Chemistry and Geochemistry, Woods Hole Oceanographic Institution, Woods Hole, MA 02543 USA

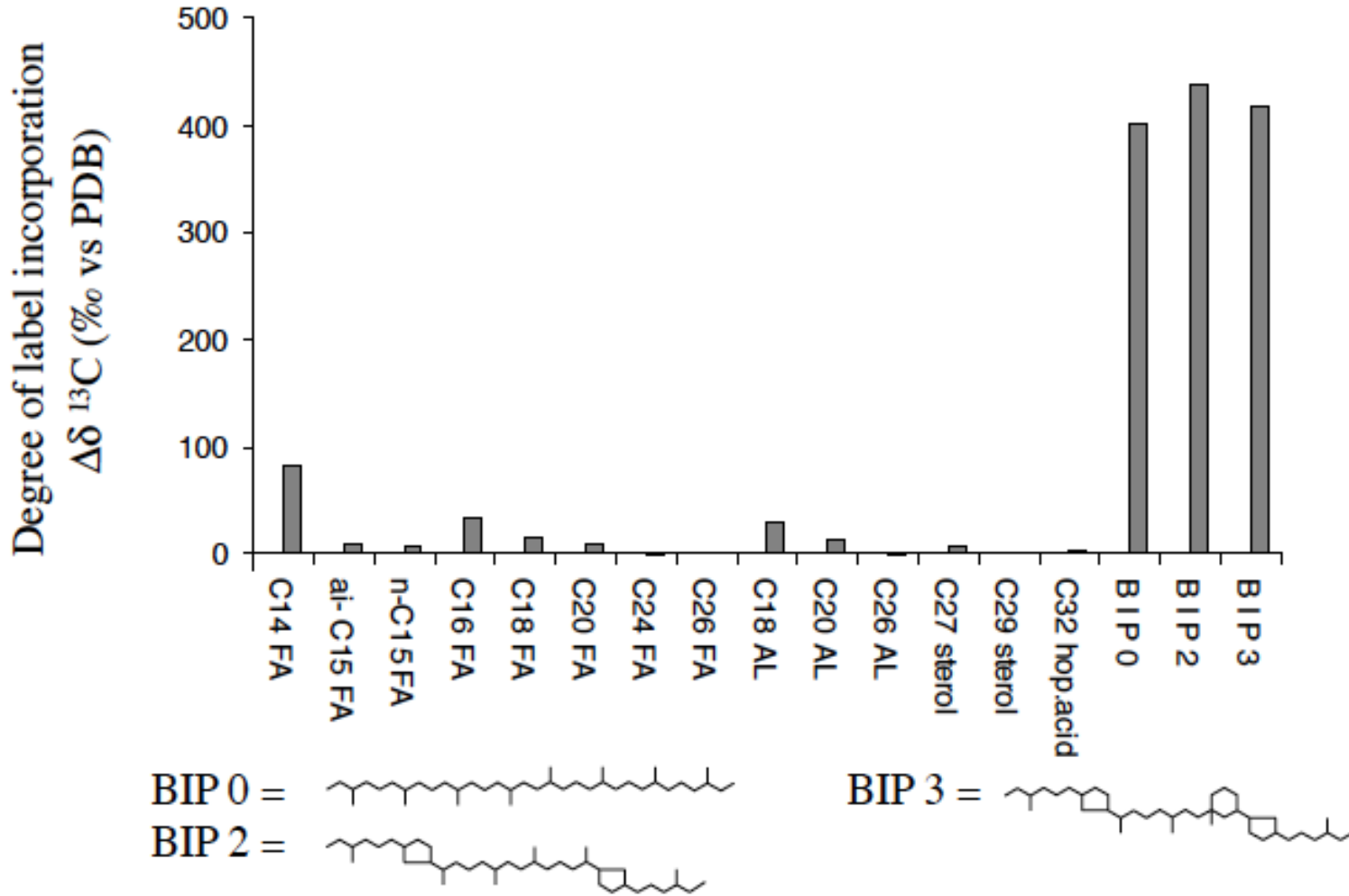
<sup>2</sup>National Ocean Sciences Accelerator Mass Spectrometry (NOSAMS) Facility, Department of Marine Geology and Geophysics, Woods Hole Oceanographic Institution, Woods Hole, MA 02543, USA



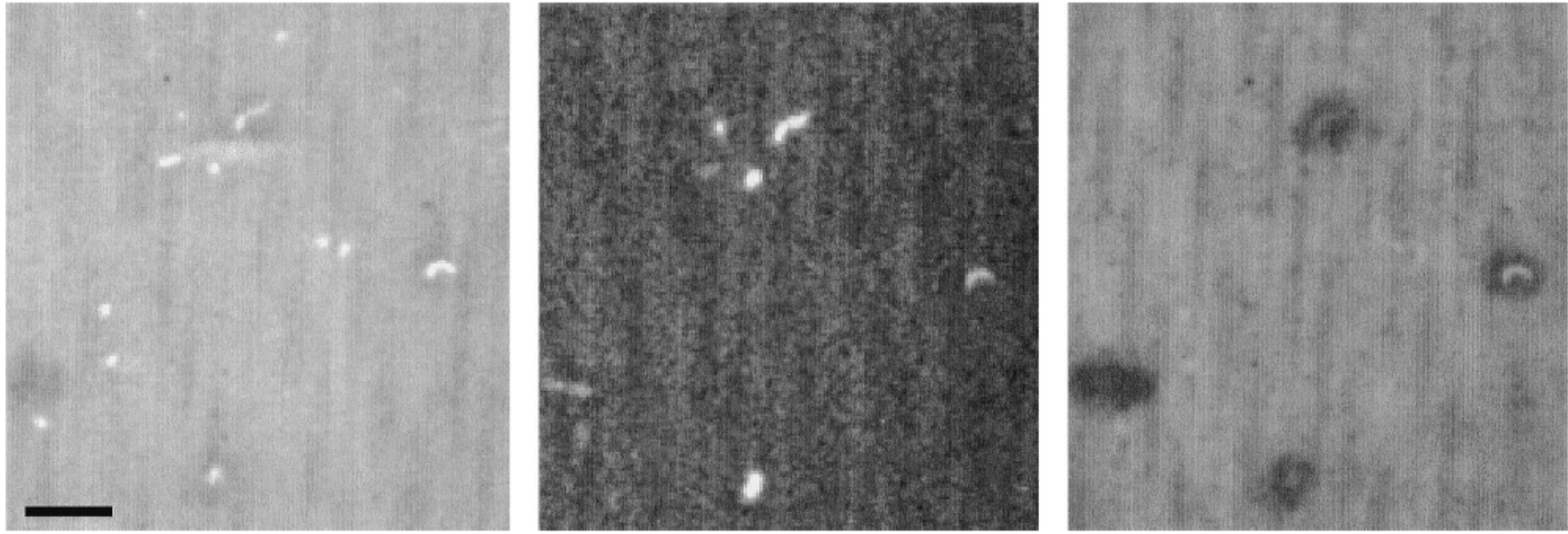
“The  $\Delta^{14}\text{C}$  data are consistent with chemoautotrophic growth below the euphotic zone.”

Pearson et al. 2001

# MGI archaea are autotrophic?



# MGI archaea are heterotrophic?

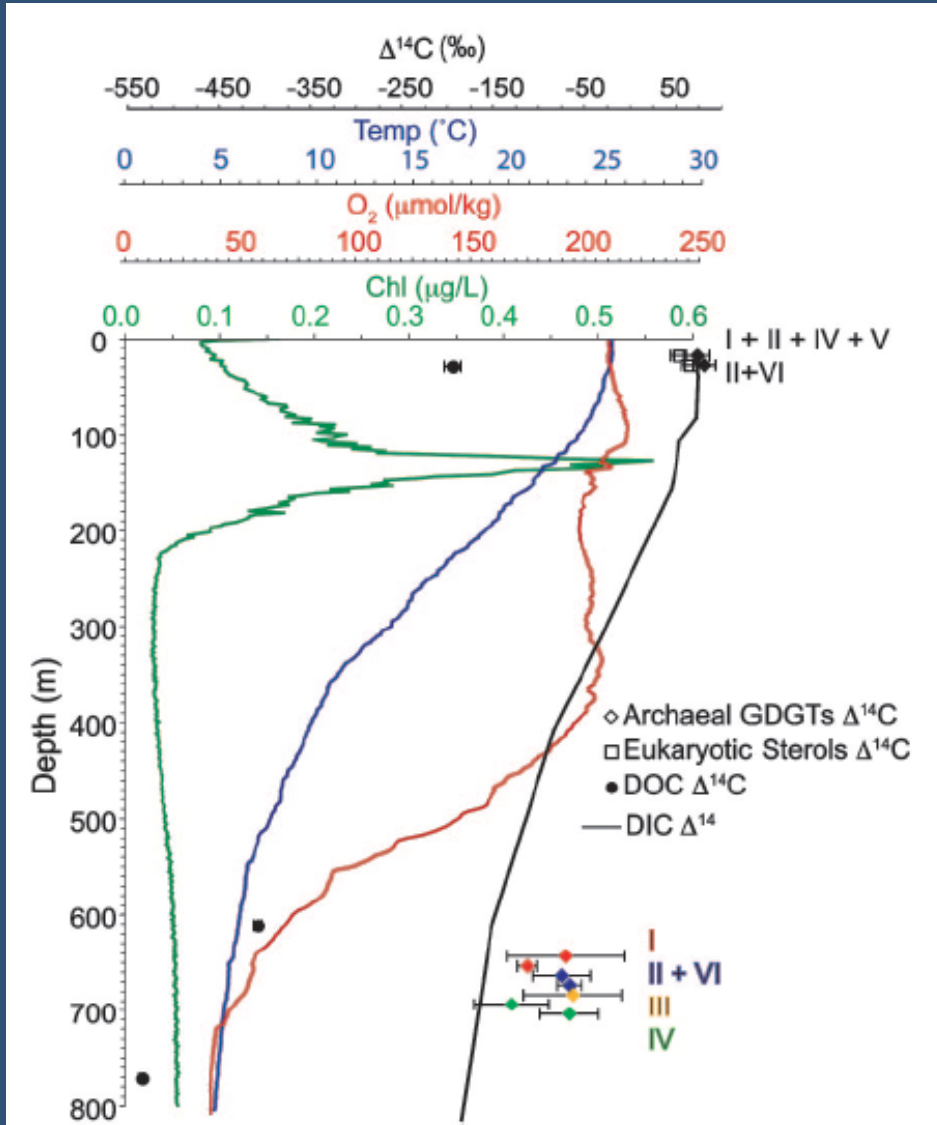


Uptake of  $^{14}\text{C}$  labeled amino acids into archaeal cells.

Ouverney and Fuhrman 2000

# MGI archaea are mixotrophic?

Suggests ~80% of C is coming from autotrophy, 20% from heterotrophy.



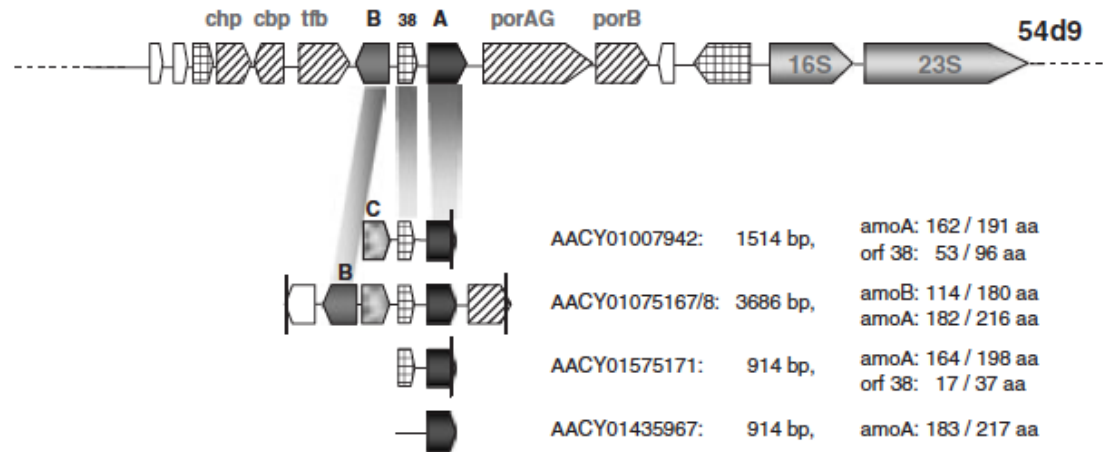
Ingalls et al. 2006

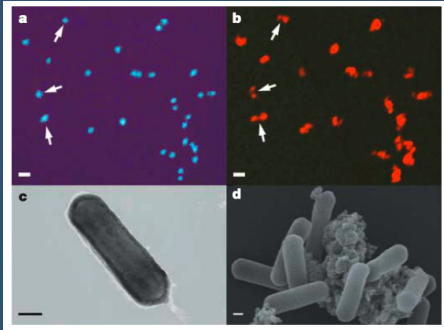
## Environmental Genome Shows Sequencing of the Sargasso

J. Craig Venter,<sup>1\*</sup> Karin Remington,<sup>1</sup> John F. Heidelberg

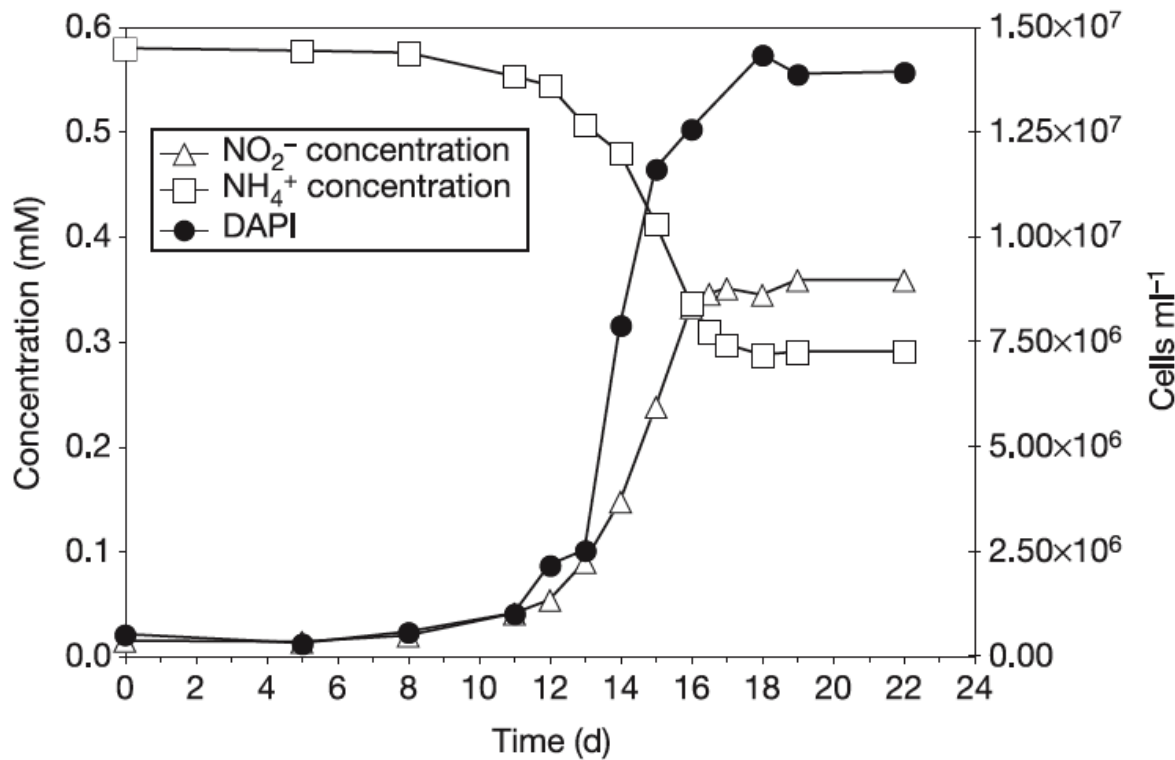
We are a long way from a full understanding of the biology of the organisms here, but this relatively small genome demonstrates areas where important insights may be gained. For example, because it has been believed that only members of the bacterial domain were capable of oceanic nitrification, it is interesting to note that an ammonium monooxygenase gene was found on an archaeal-associated scaffold within our data set. Though ultraviolet (UV) light in the

B





The first culture of a marine group I archaea, isolated from gravel at the Seattle Aquarium, *Nitrosopumilus maritimus*.

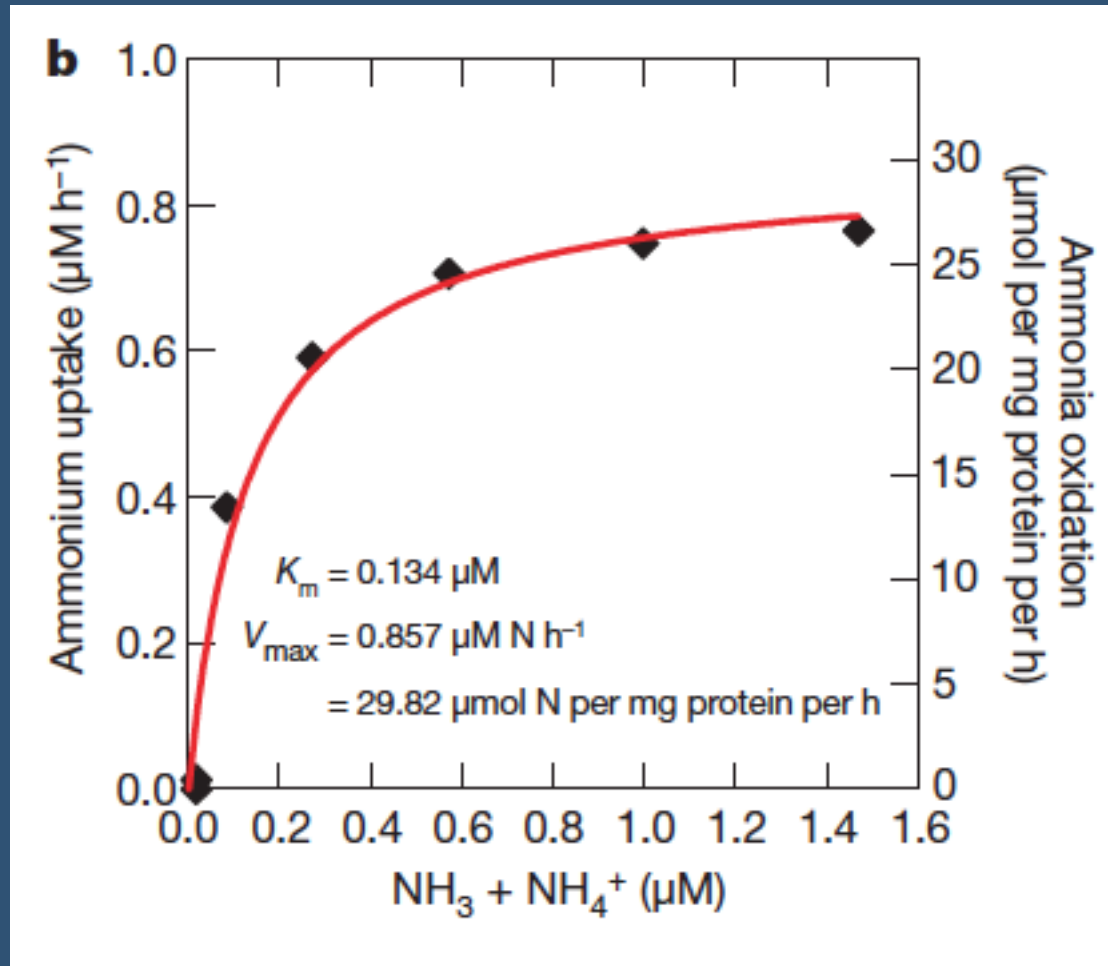


Showed that MGI archaea can oxidize NH<sub>3</sub>

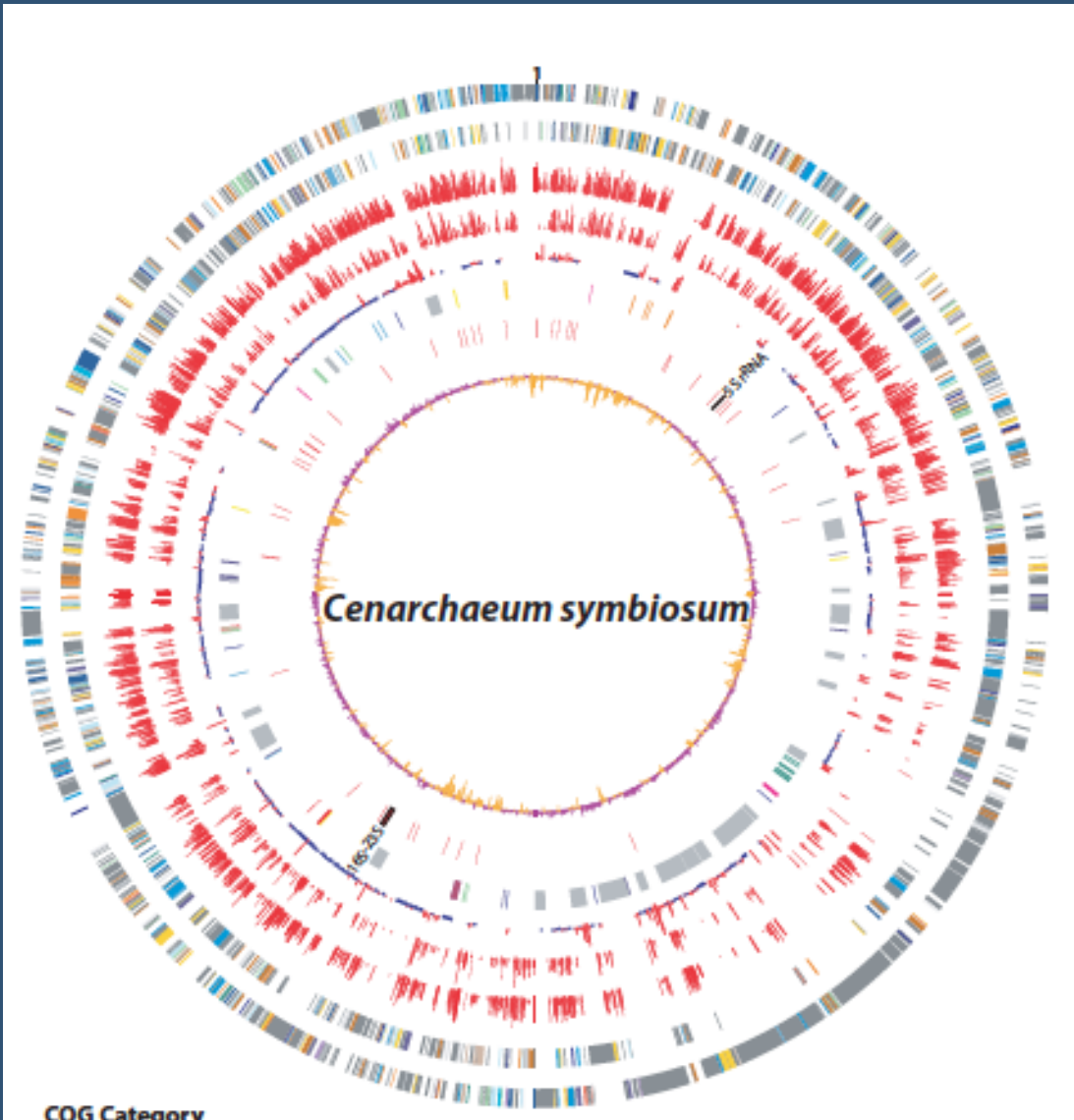
Grow as chemolithoautotrophs



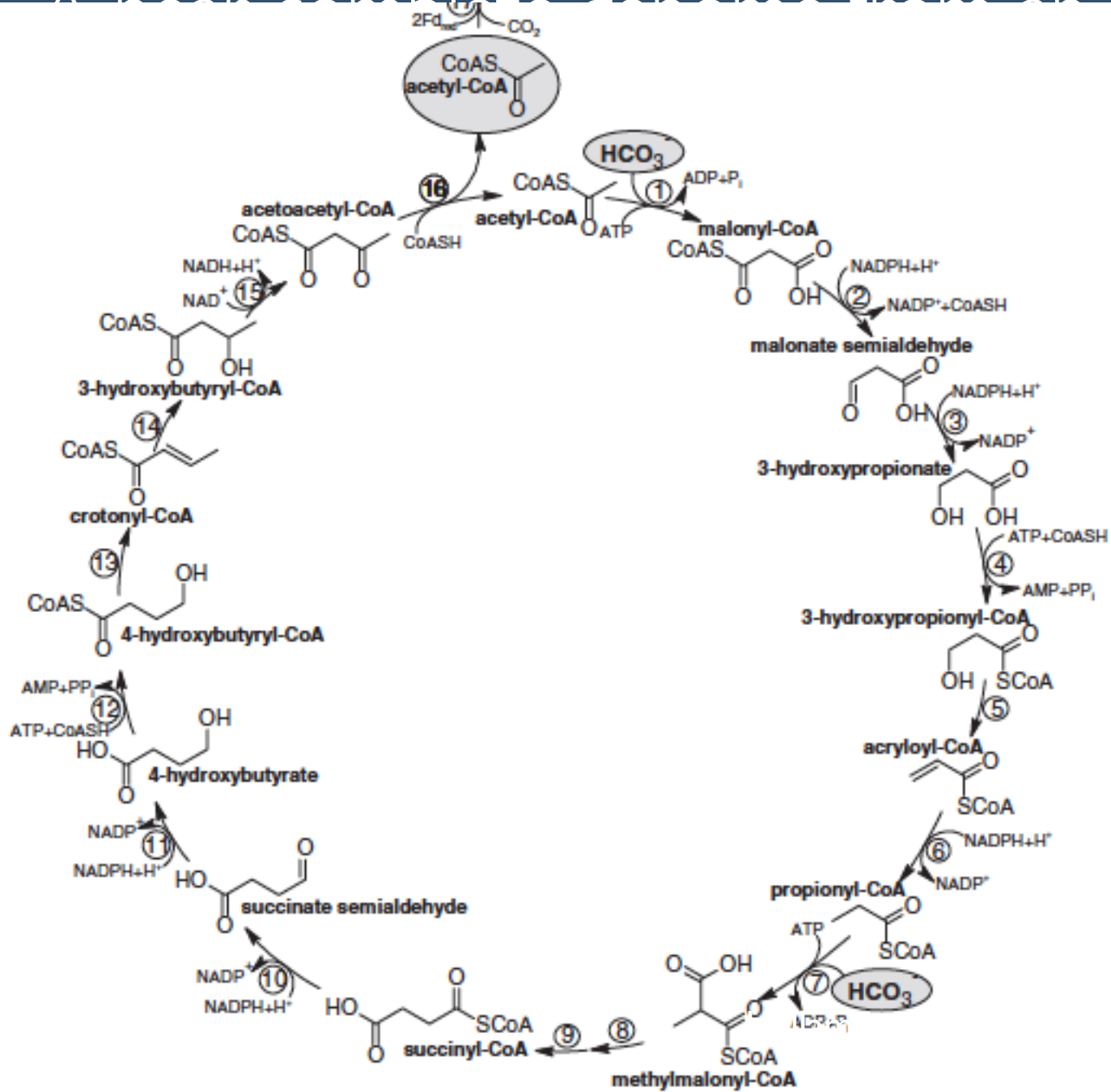
# *N. maritimus* has a high affinity for ammonium



# A near-complete genome from an uncultivated archaea



Hallam et al. 2006; Berg et al. 2007



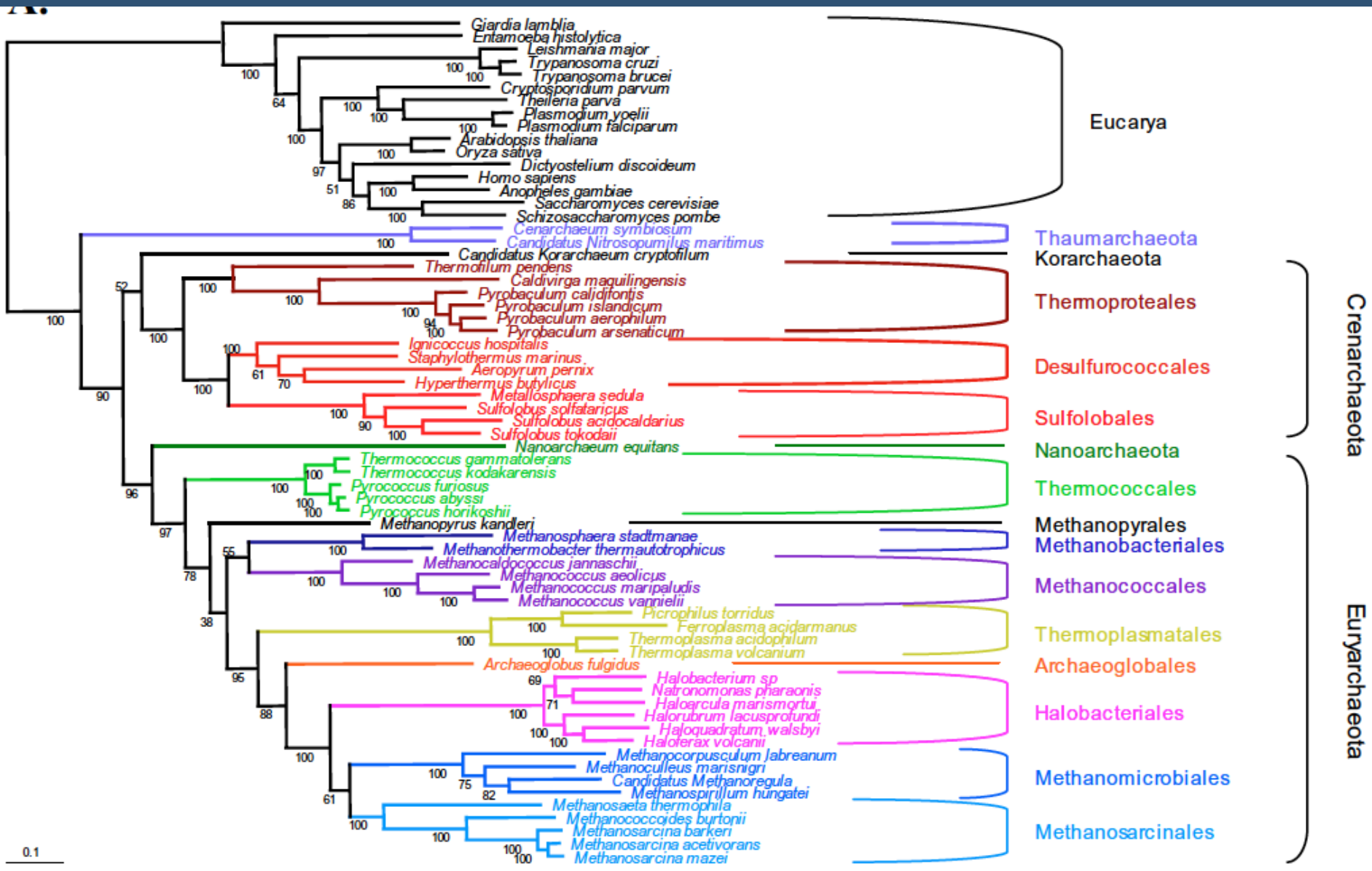
et al. 2007

# Thaumarchaea fix carbon using an extremely energy efficient pathway

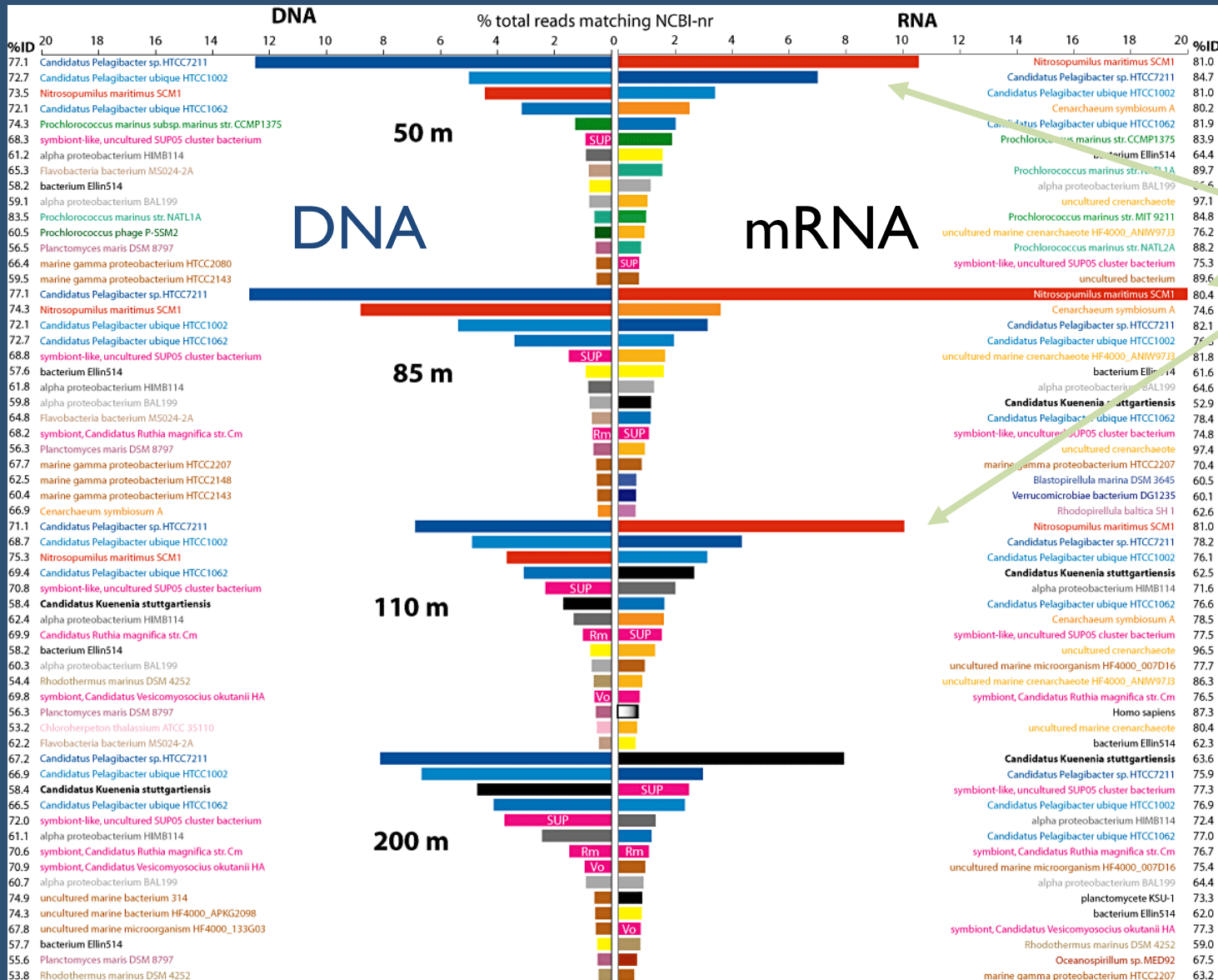
**Table 4. Comparison of the energy efficiency of aerobic autotrophic CO<sub>2</sub> fixation cycles**

1 mole precursor or 1 g biomass	Calvin–Benson cycle*	3-Hydroxypropionate bicycle	Crenarchaeal HP/HB cycle	Thaumarchaeal HP/HB cycle
Acetyl-CoA	7	7	6	4
Pyruvate	7	7	9–10 <sup>†</sup>	5
Phosphoenolpyruvate	8	9	10–11 <sup>†</sup>	7
Oxaloacetate	8	9	9–10 <sup>†</sup>	6
2-Oxoglutarate	15	16	15–16 <sup>†</sup>	10
Biomass (1 g)	0.12*	0.13	0.13–0.15 <sup>†</sup>	0.09

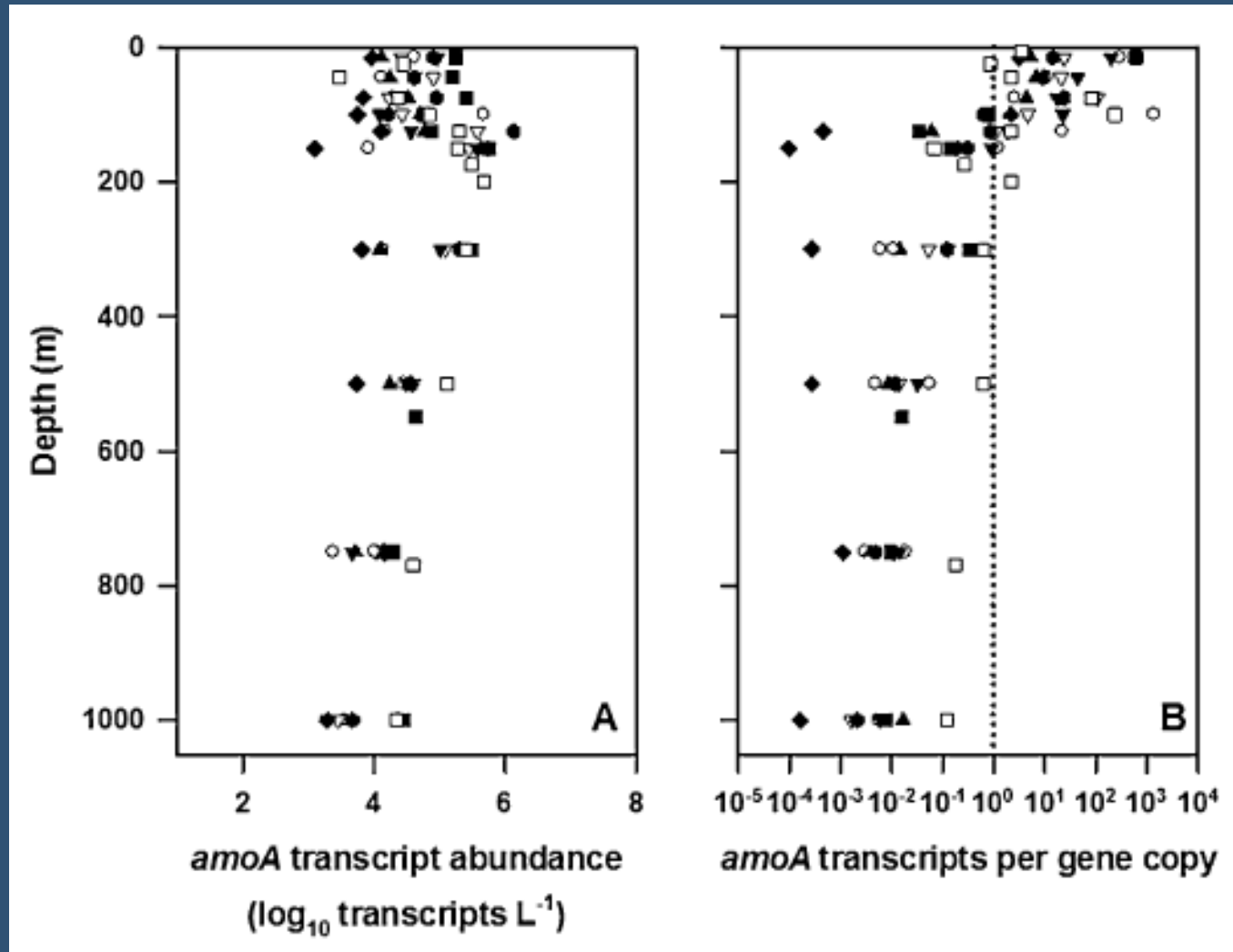
The numbers represent moles of high-energy anhydride bonds of ATP required to form 1 mole of central precursor metabolite or of the main precursors for the synthesis of 1 g of dry biomass. For the details of calculations, see [SI Appendix, SI Text](#). The estimated amount of the central metabolic precursors



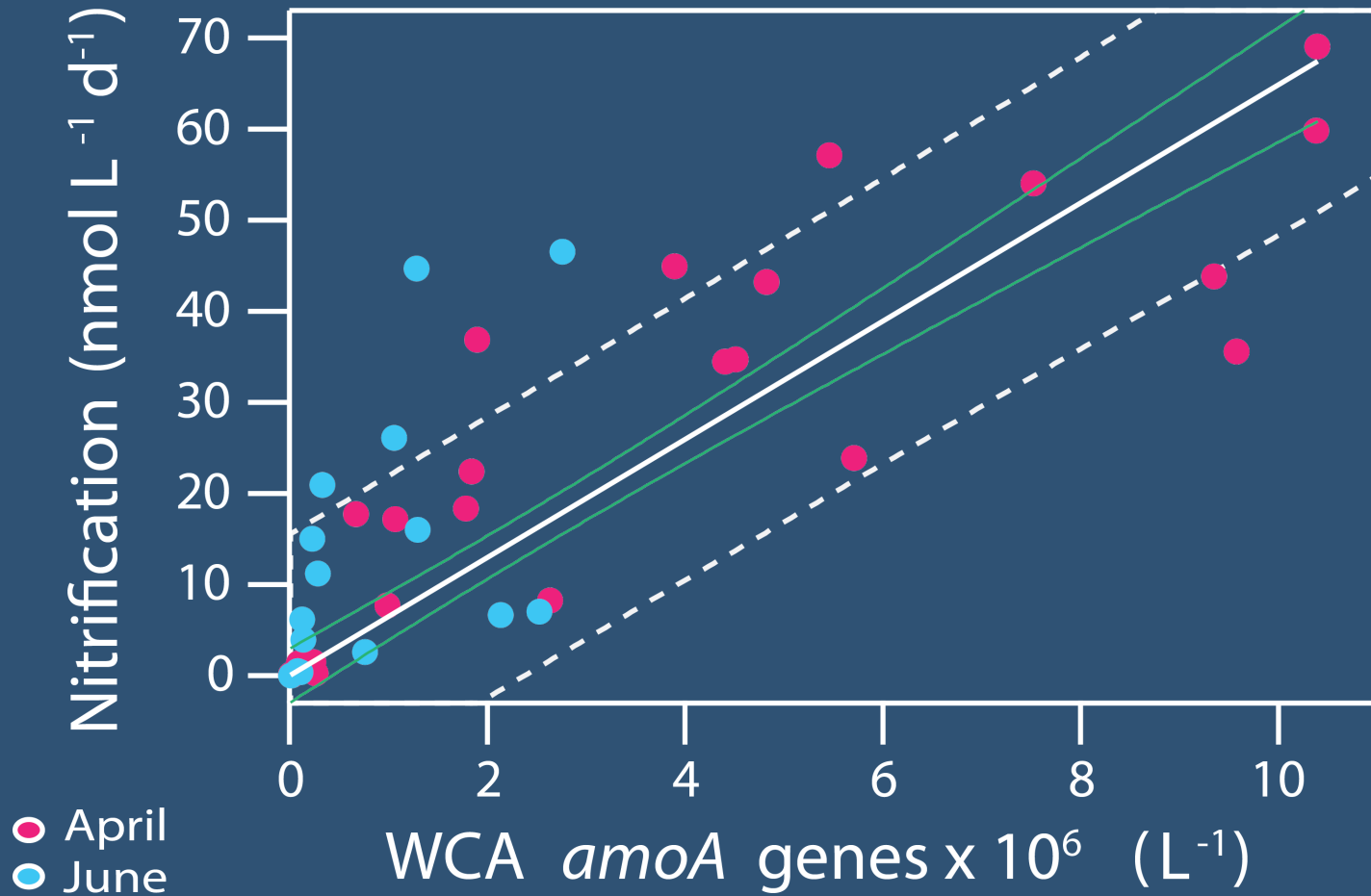
# Archaea are active in low oxygen waters



# Abundant *amoA* transcripts in surface waters at Station ALOHA



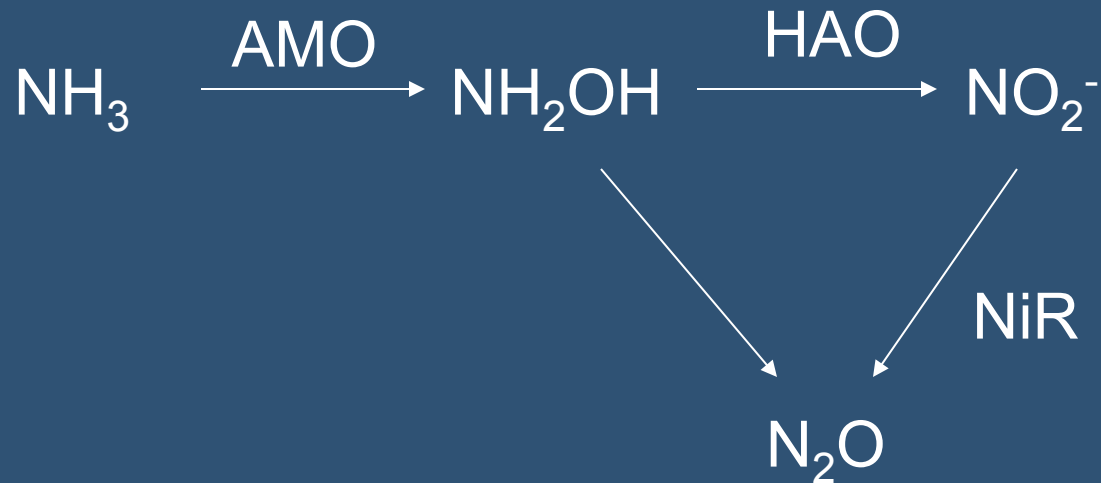
# Abundance of the shallow ecotype correlates with nitrification rates



from Smith et al. 2014, *ISMEJ*

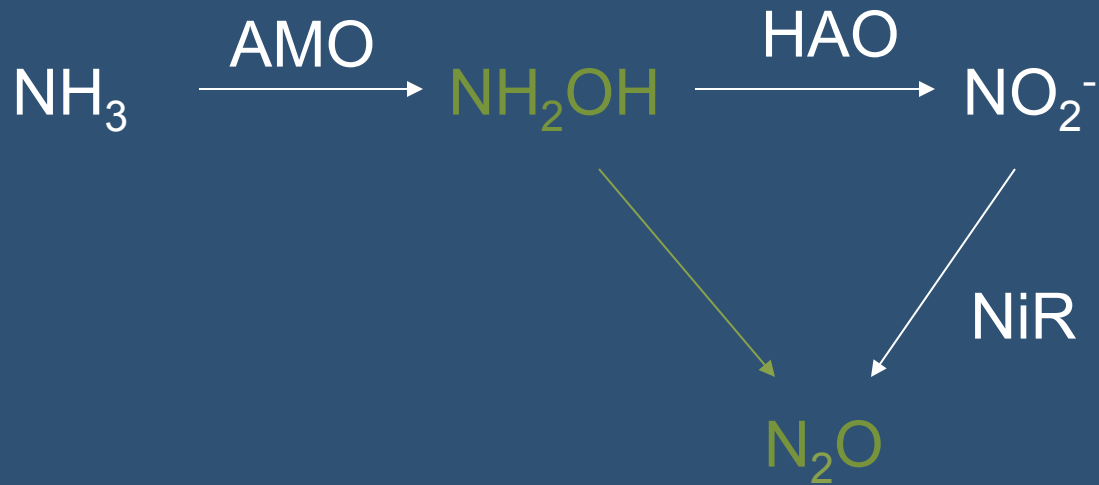


# AOB make nitrous oxide ( $\text{N}_2\text{O}$ )

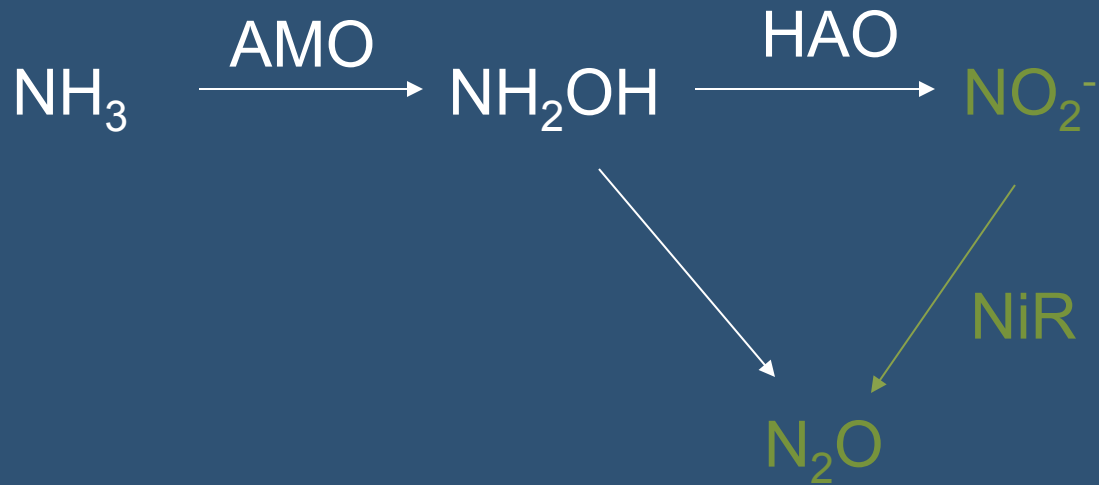


AOB = ammonia-oxidizing bacteria

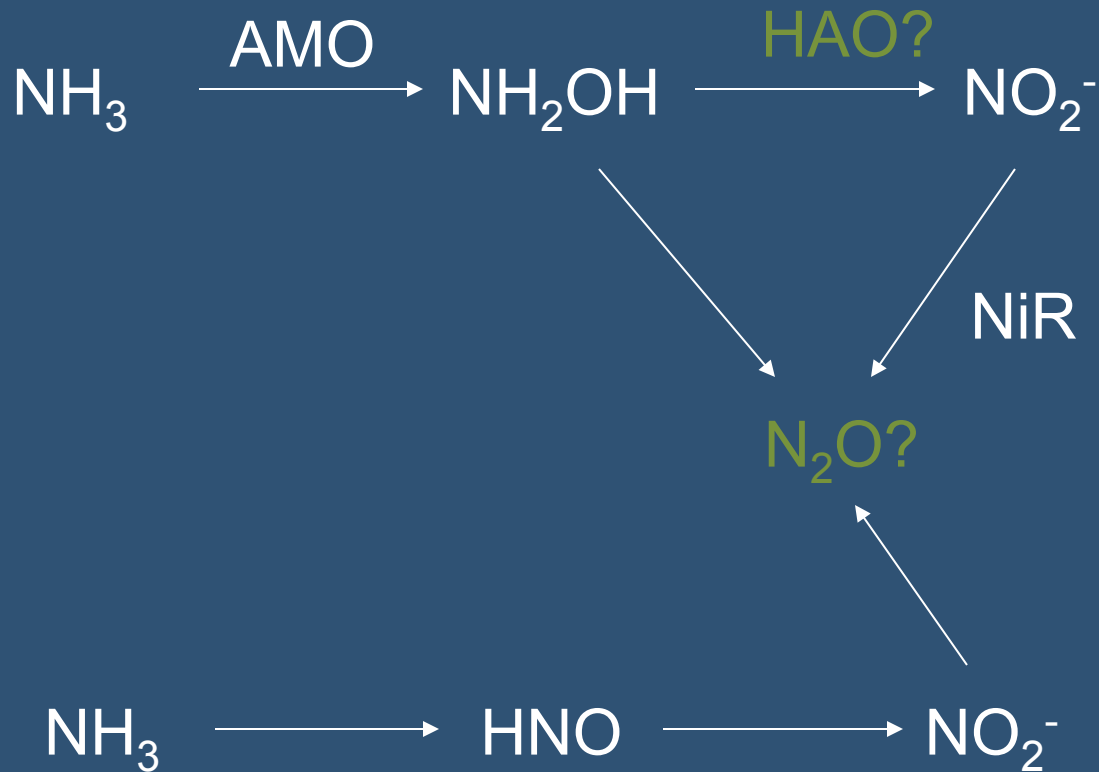
AOB can make and nitrous oxide in two ways



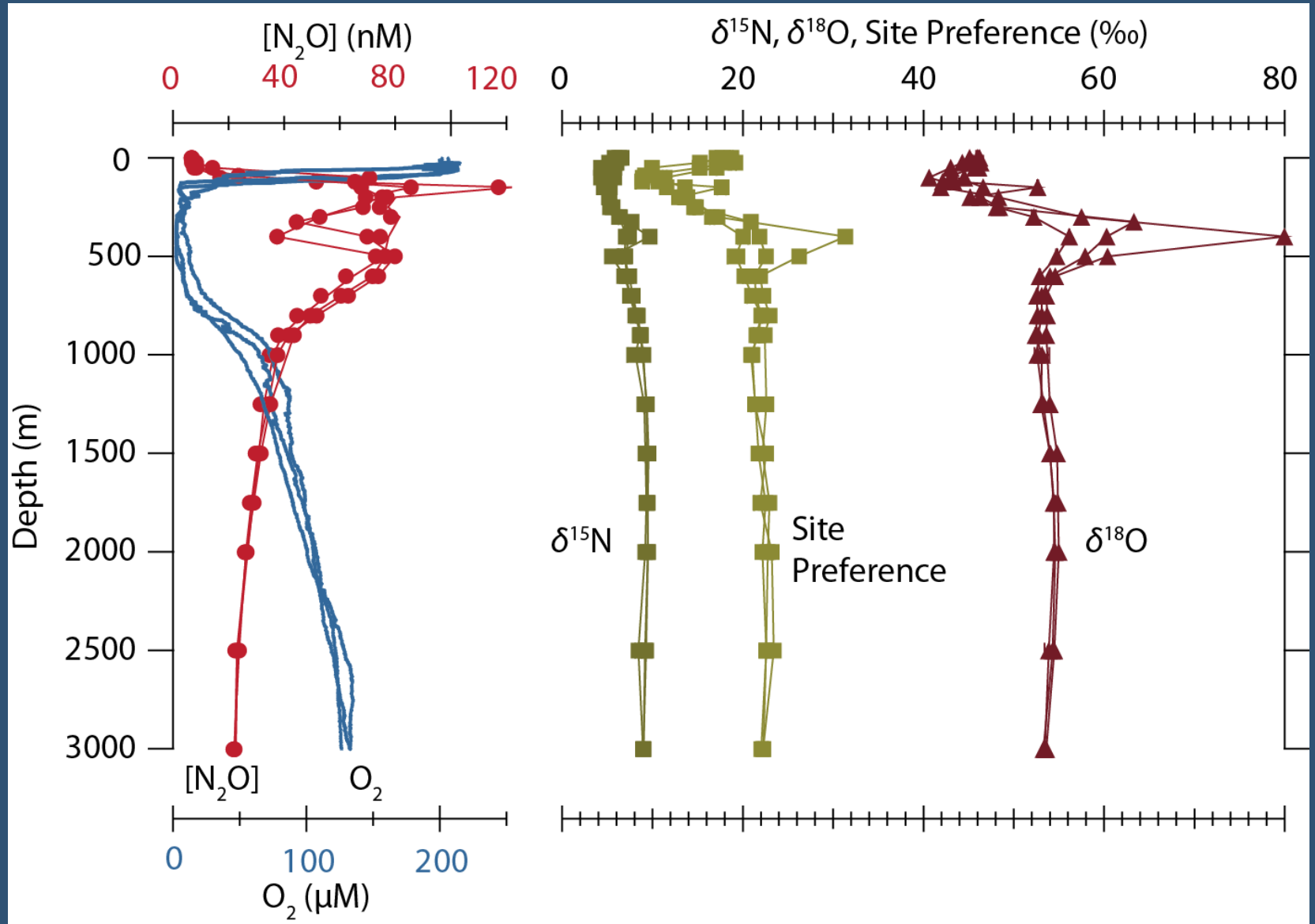
AOB can make and nitrous oxide in two ways



# Can archaea make N<sub>2</sub>O?



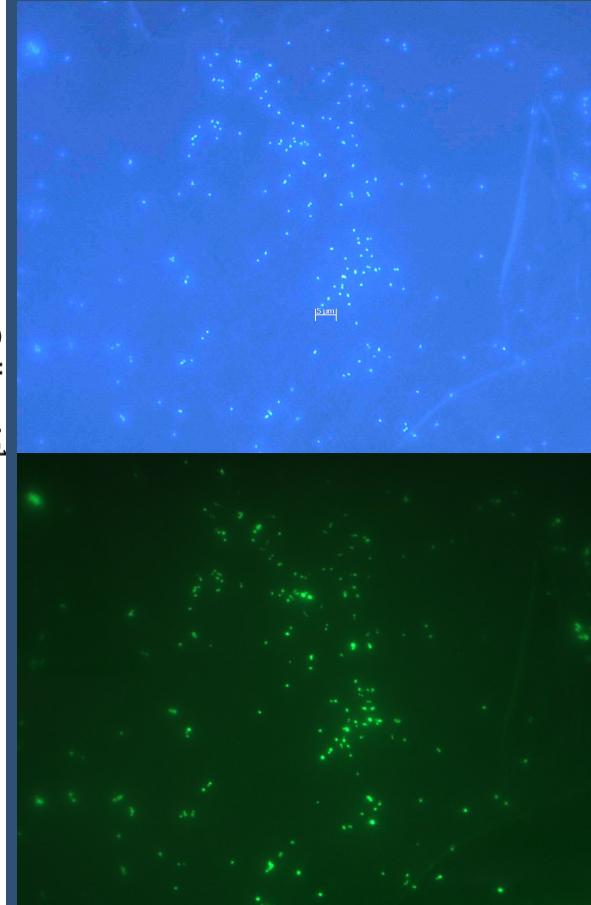
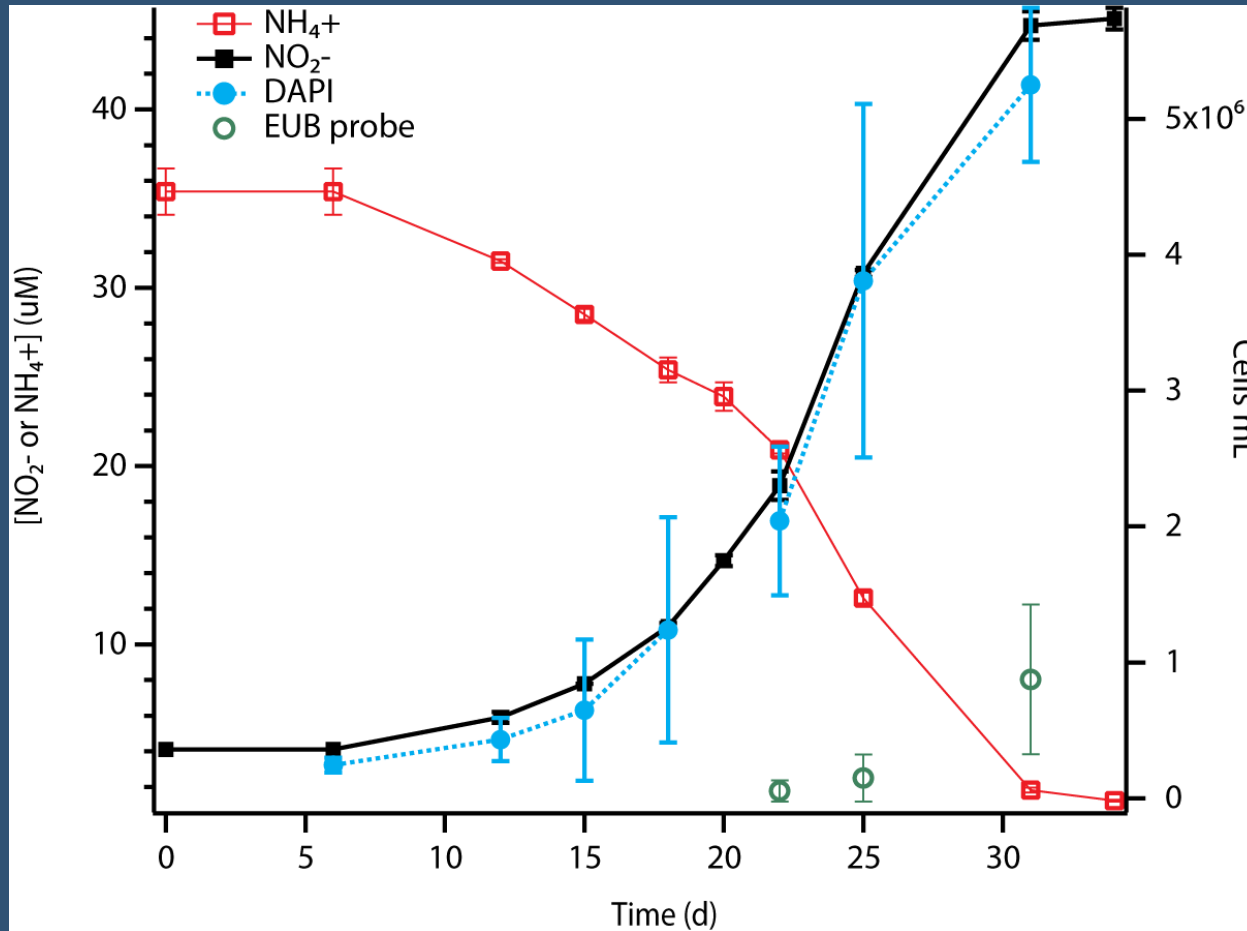
# Interpreting N<sub>2</sub>O profiles requires some information about microbial physiology



	Anammox	AOB	AOA
e- transport intermediate oxidase	Fe HAO/HZO	Fe HAO	Cu ?
C-fixation	acetyl-CoA	CBB	3-Hp/4-Hb
NO <sub>2</sub> <sup>-</sup> reduction	<i>nirS</i>	<i>nirK</i>	<i>nirK</i>

Taming wild archaea

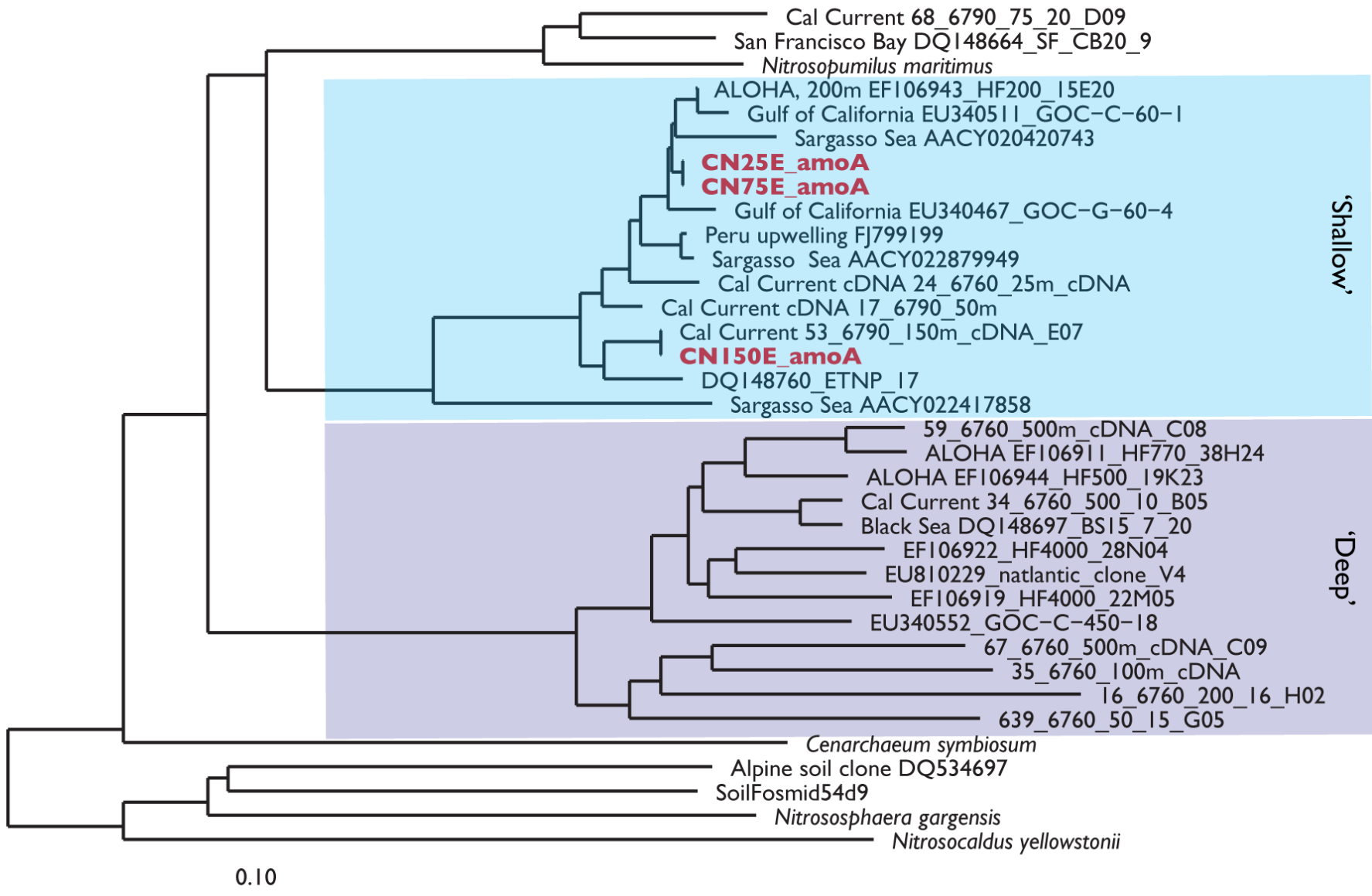
# Enrichment 'CN25' from the North Pacific



Growth rate =  $0.17 \text{ d}^{-1}$ , doubling time  $\sim 4 \text{ d}$

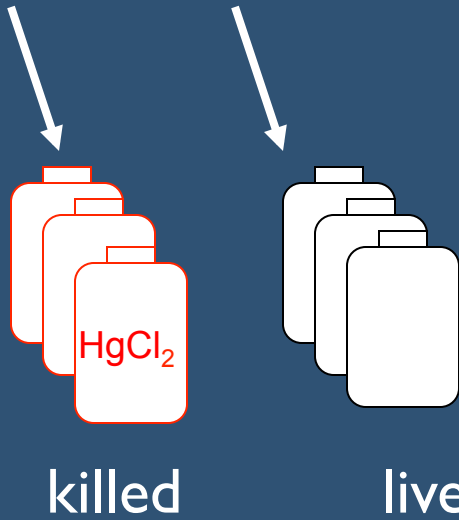
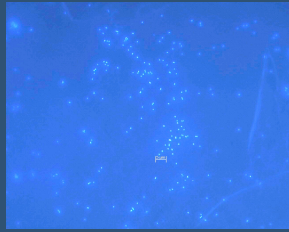


# CN25 is the 'shallow' AOA ecotype





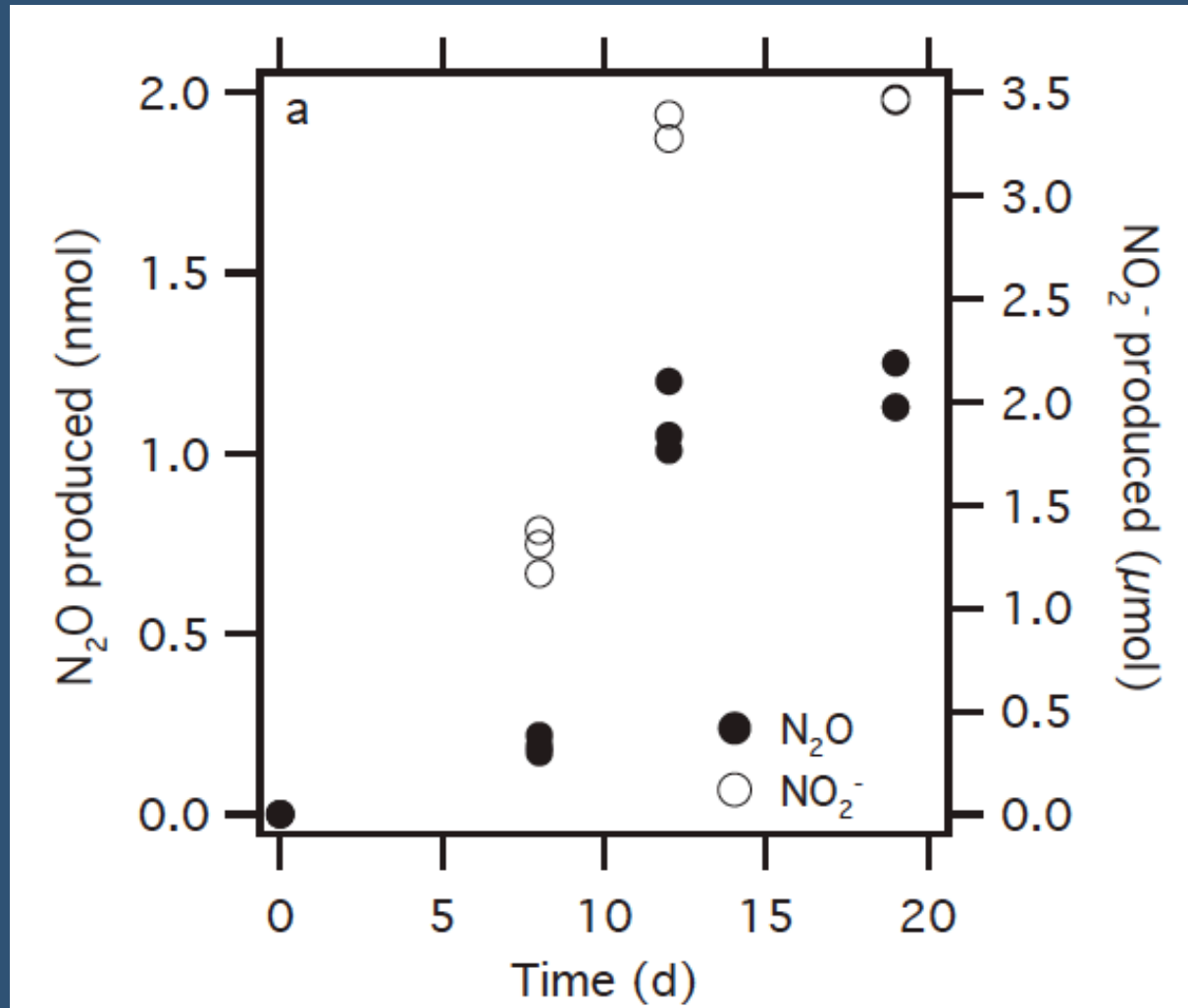
# Measuring N<sub>2</sub>O production



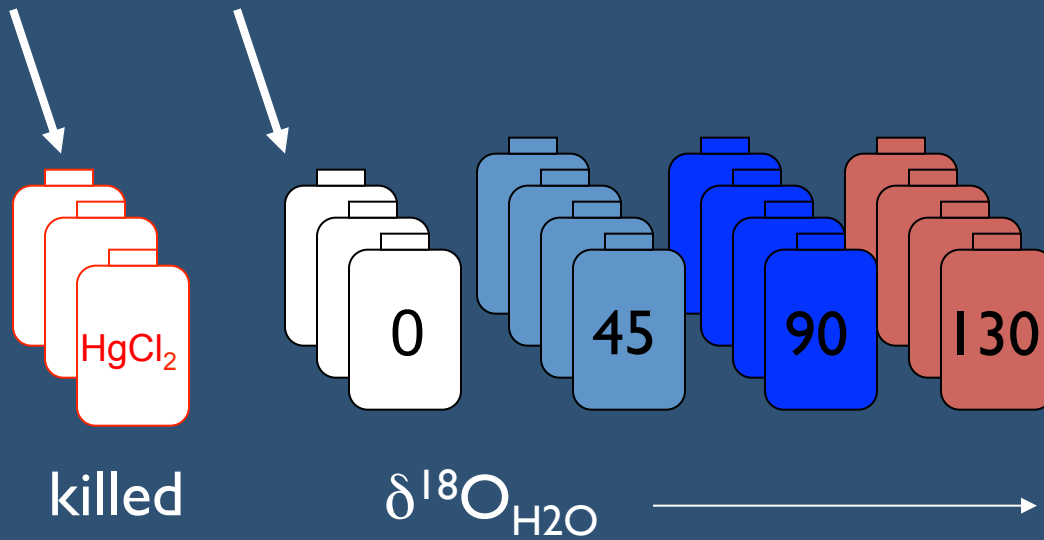
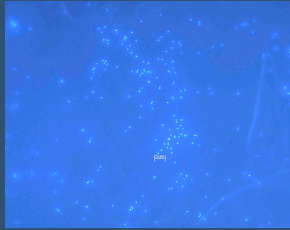
6 weeks  
→

N<sub>2</sub>O produced =  
live - killed

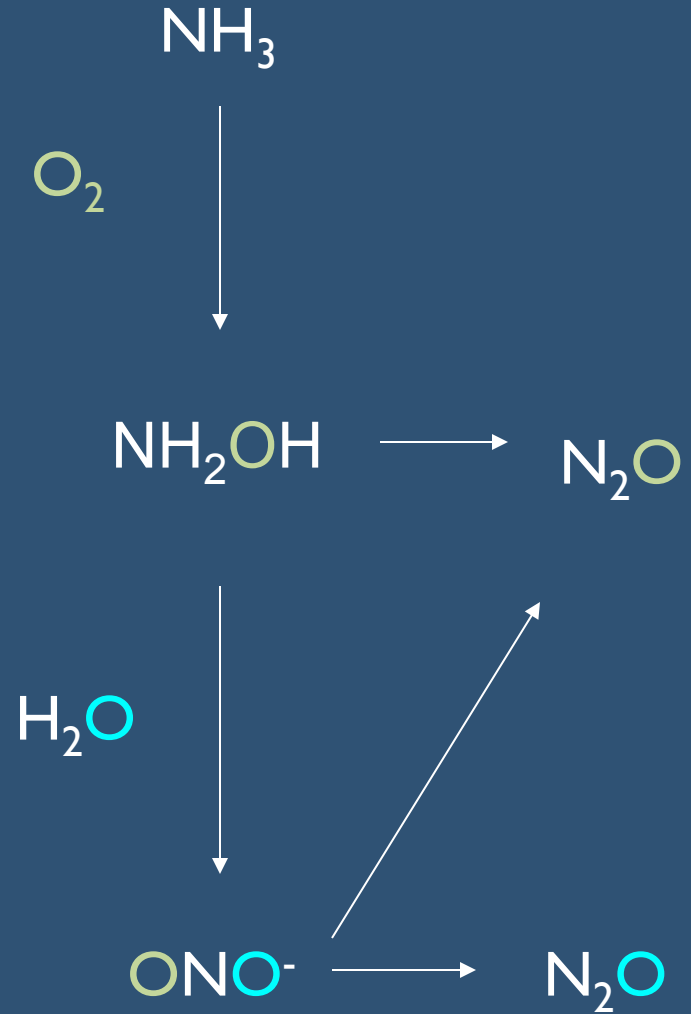
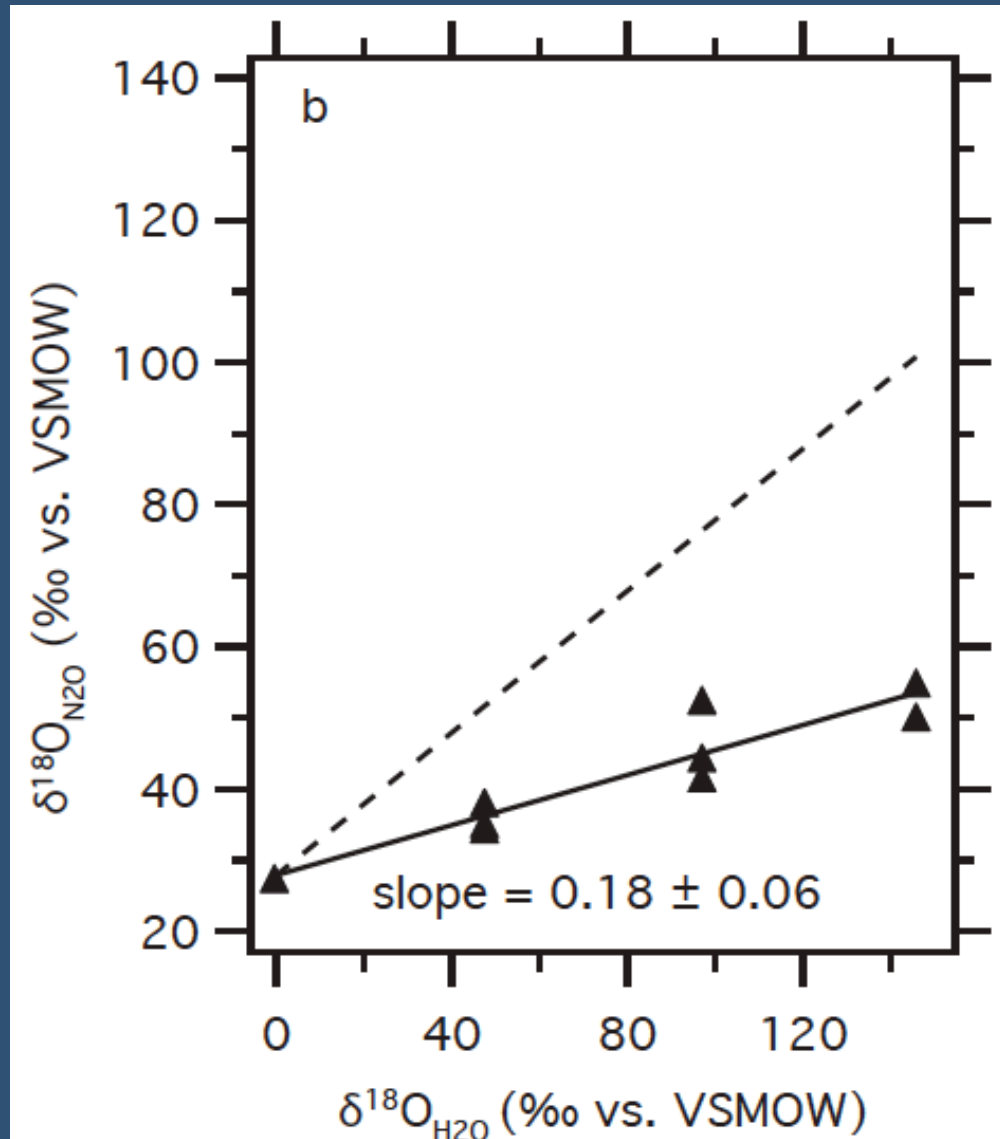
# Marine archaea do make $N_2O$



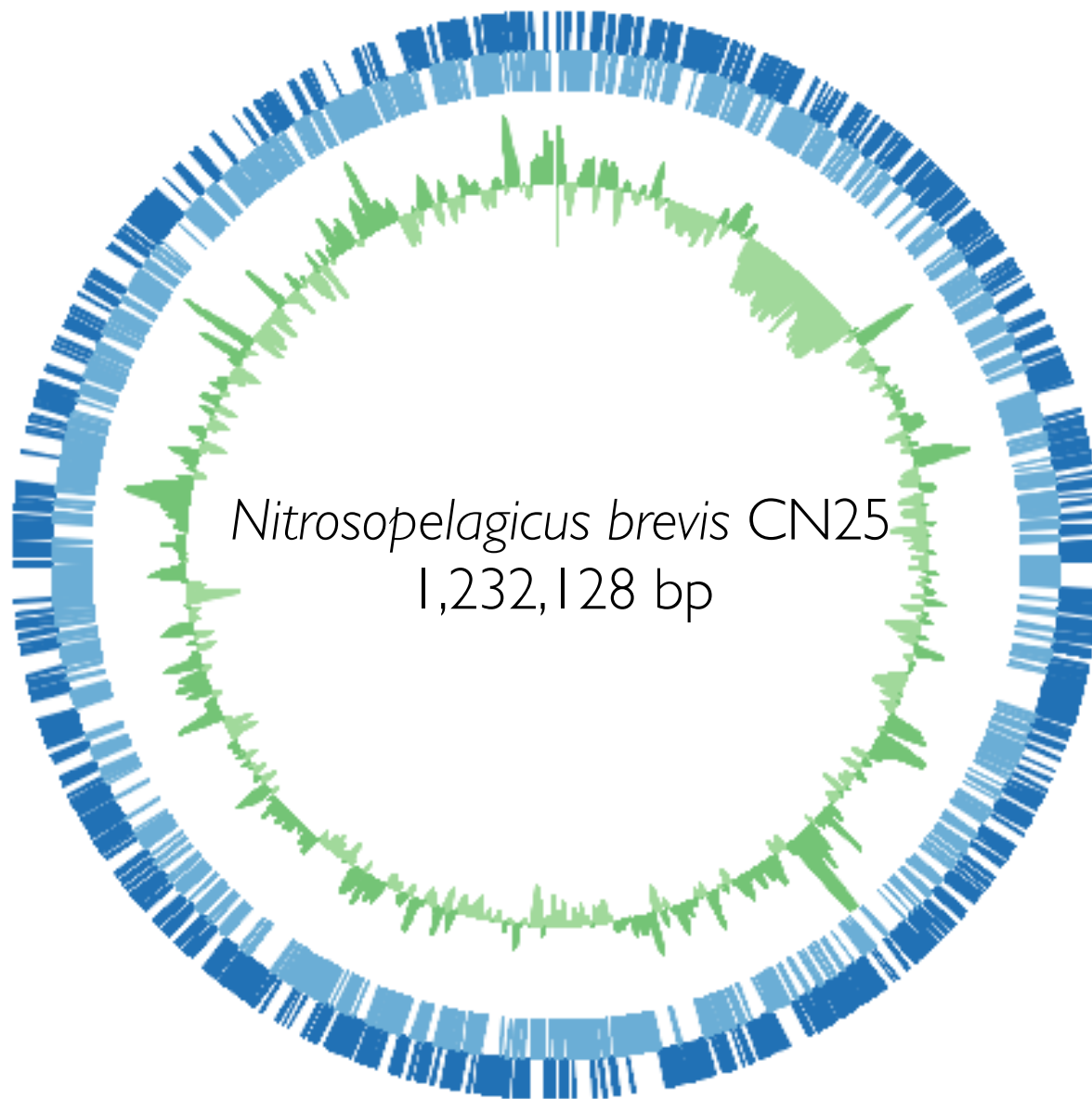
# Determining the source of O atoms



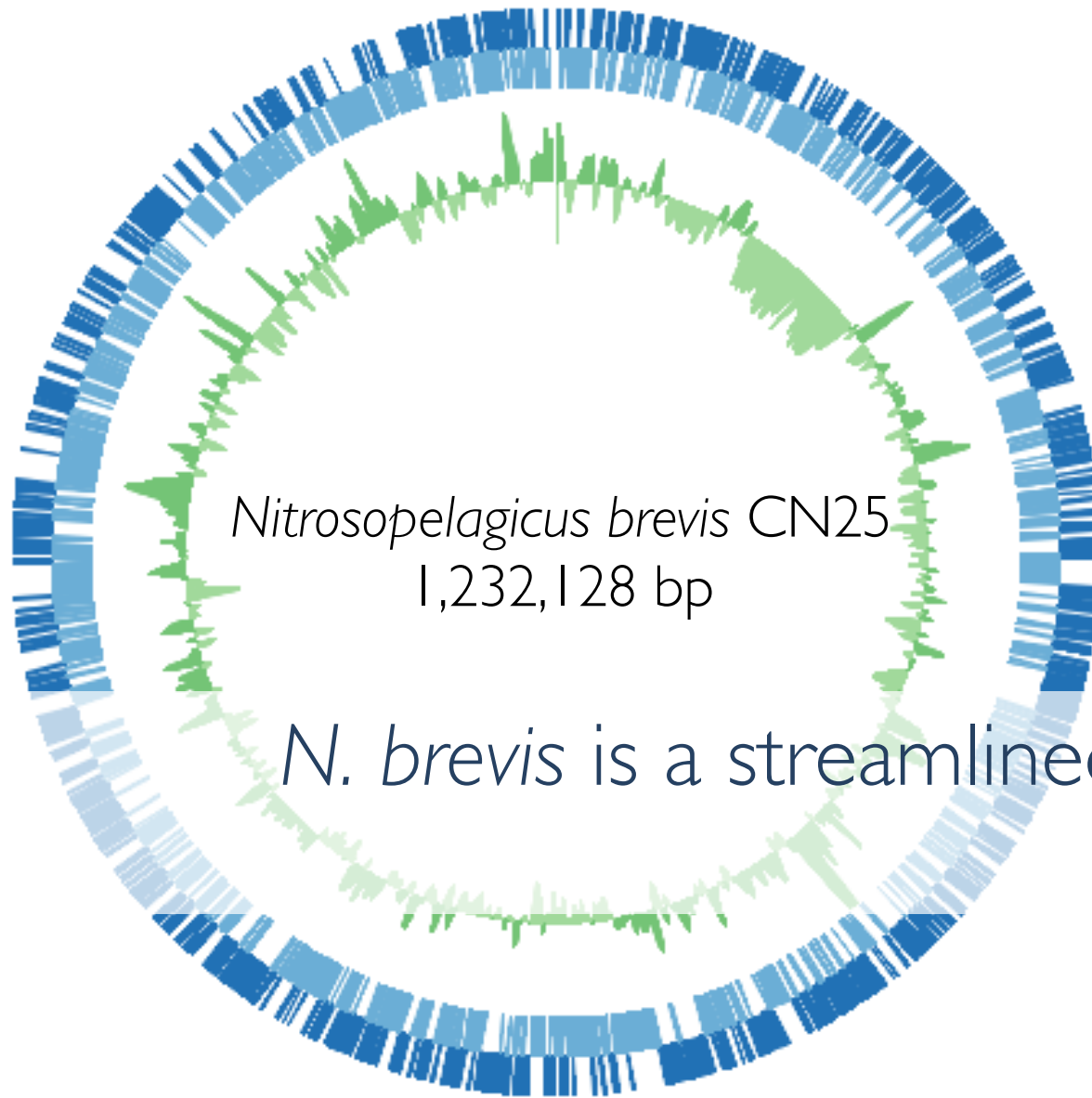
Most of the O in  $N_2O$  comes from  $O_2$











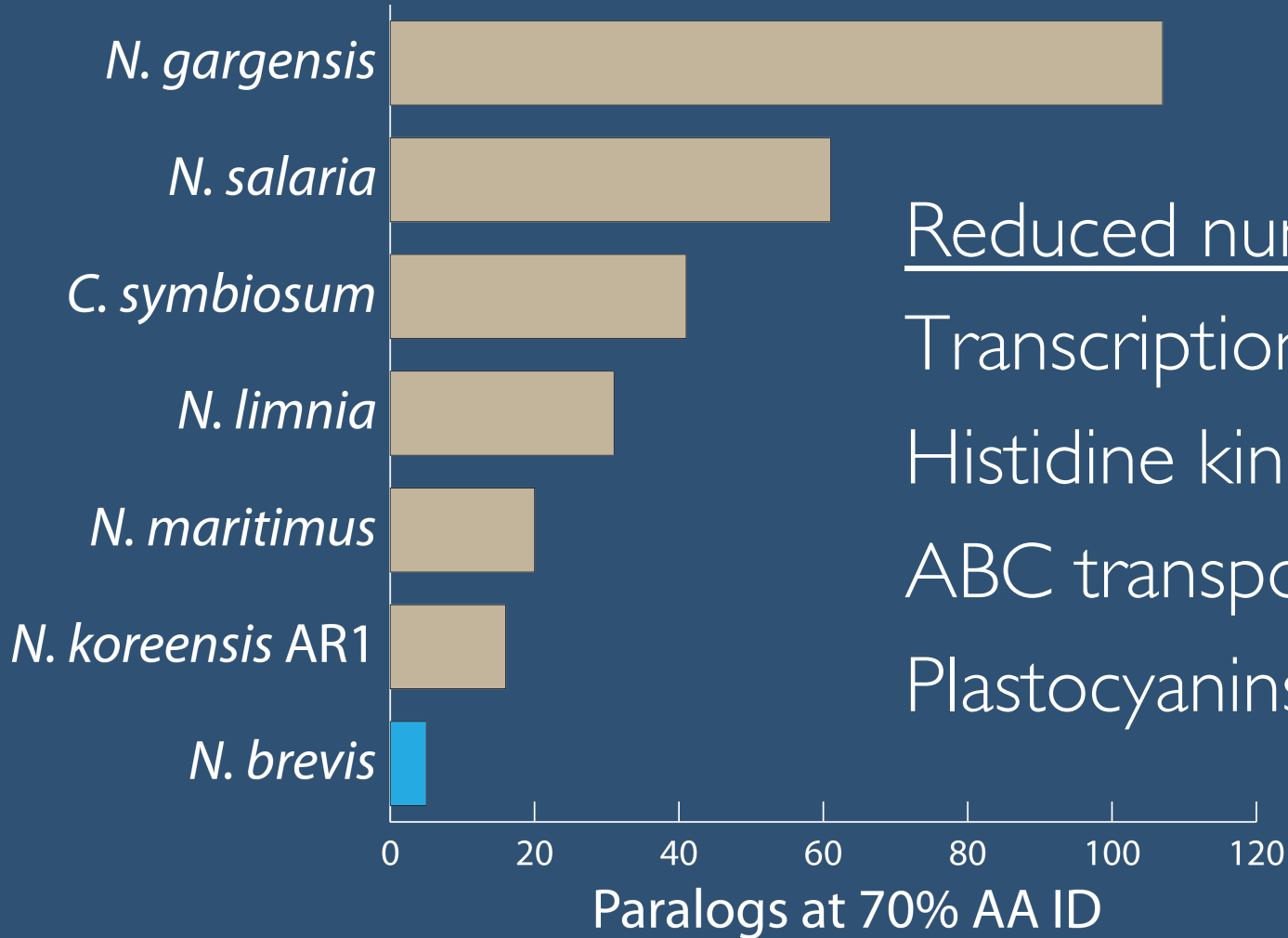
*Nitrosopelagicus brevis* CN25  
1,232,128 bp

*N. brevis* is a streamlined archaeal genome.

# Small genomes are features of other model oligotrophic microbes

	Size (Mbp)	%GC	# of genes
<i>N. brevis</i>	1.23	33	1501
<i>N. maritimus</i>	1.65	34	1842
<i>Prochlorococcus marinus</i> AS9601	1.67	31	1988
<i>Pelagibacter ubique</i> HTCC1062	1.31	30	1394
<i>Methylophilales</i> sp. HTCC2181 (OM43)	1.30	38	1377
SAR86	1.7	33	1712

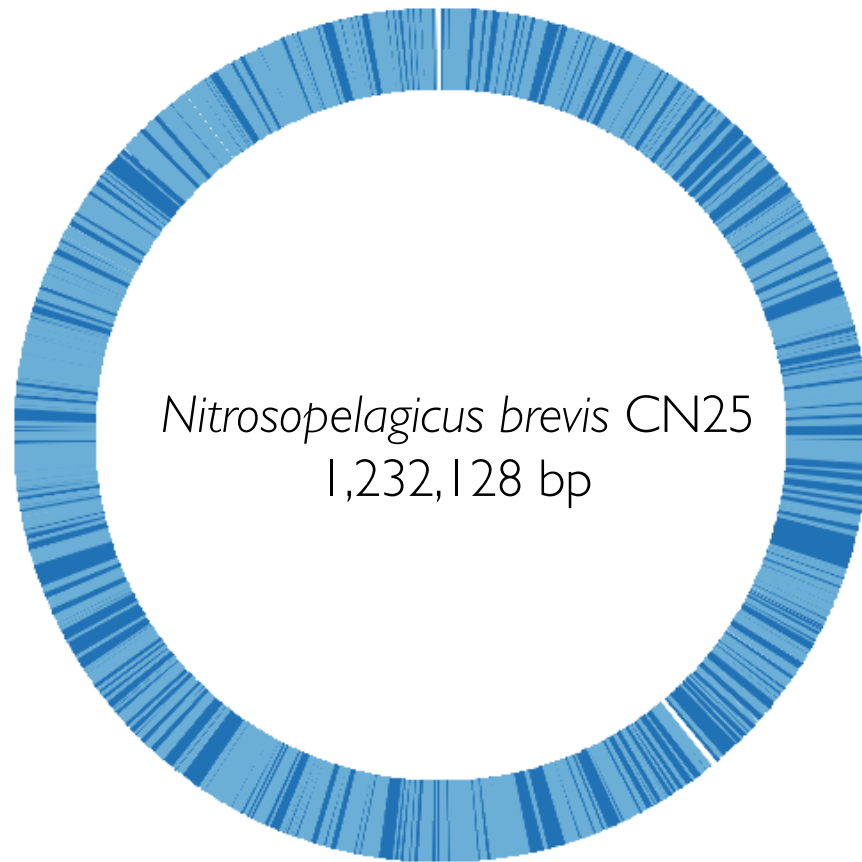
# *N. brevis* cuts out redundancy



Reduced numbers of:  
Transcriptional regulators  
Histidine kinases  
ABC transporters  
Plastocyanins/MCOs

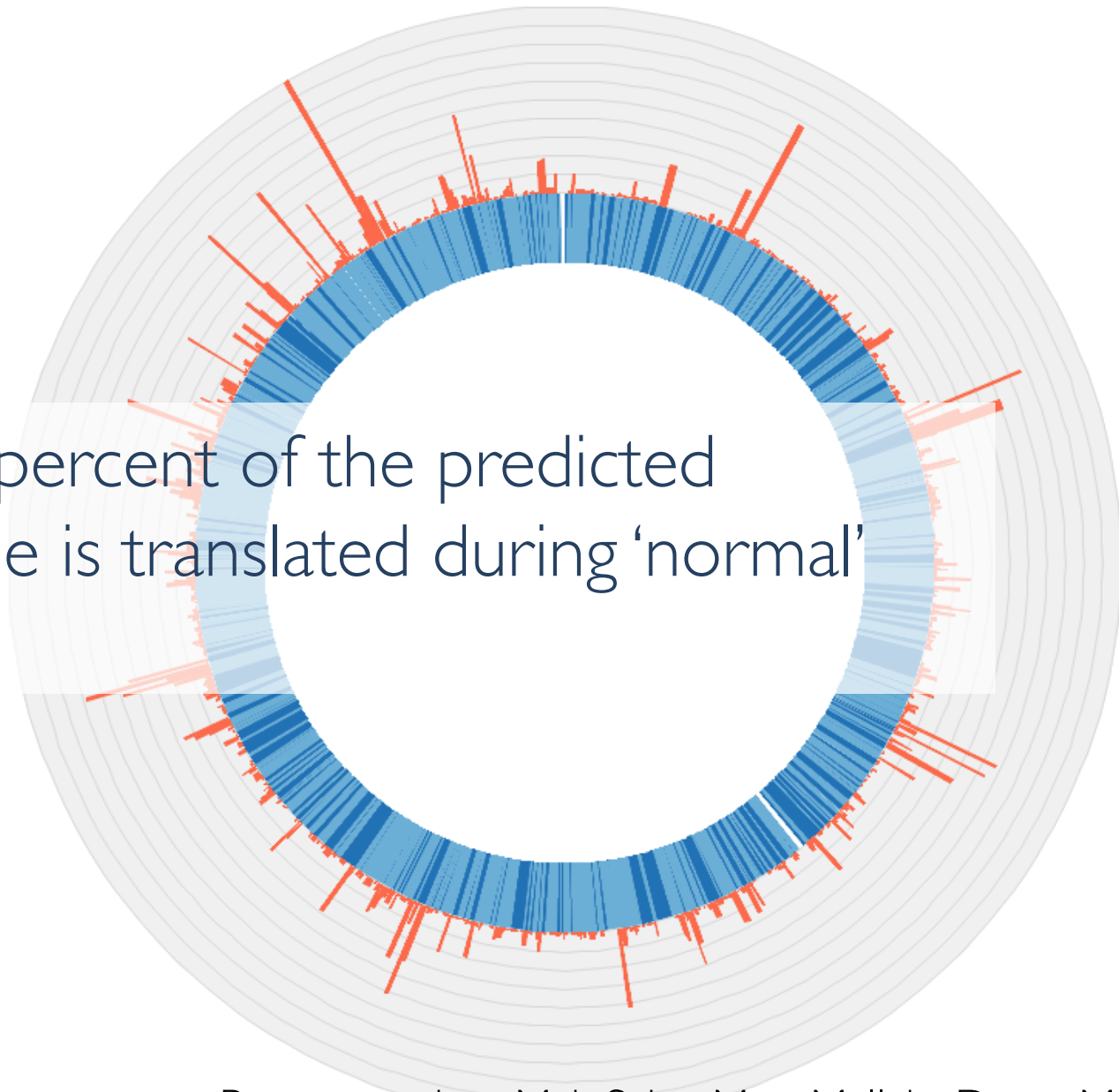
Despite its small genome, *N. brevis* makes its own vitamins and cofactors:

- Vitamin B<sub>12</sub>
- Vitamins B<sub>1</sub>, B<sub>2</sub>, B<sub>5</sub>, B<sub>7</sub>
- Cofactor F<sub>420</sub>
- All amino acids

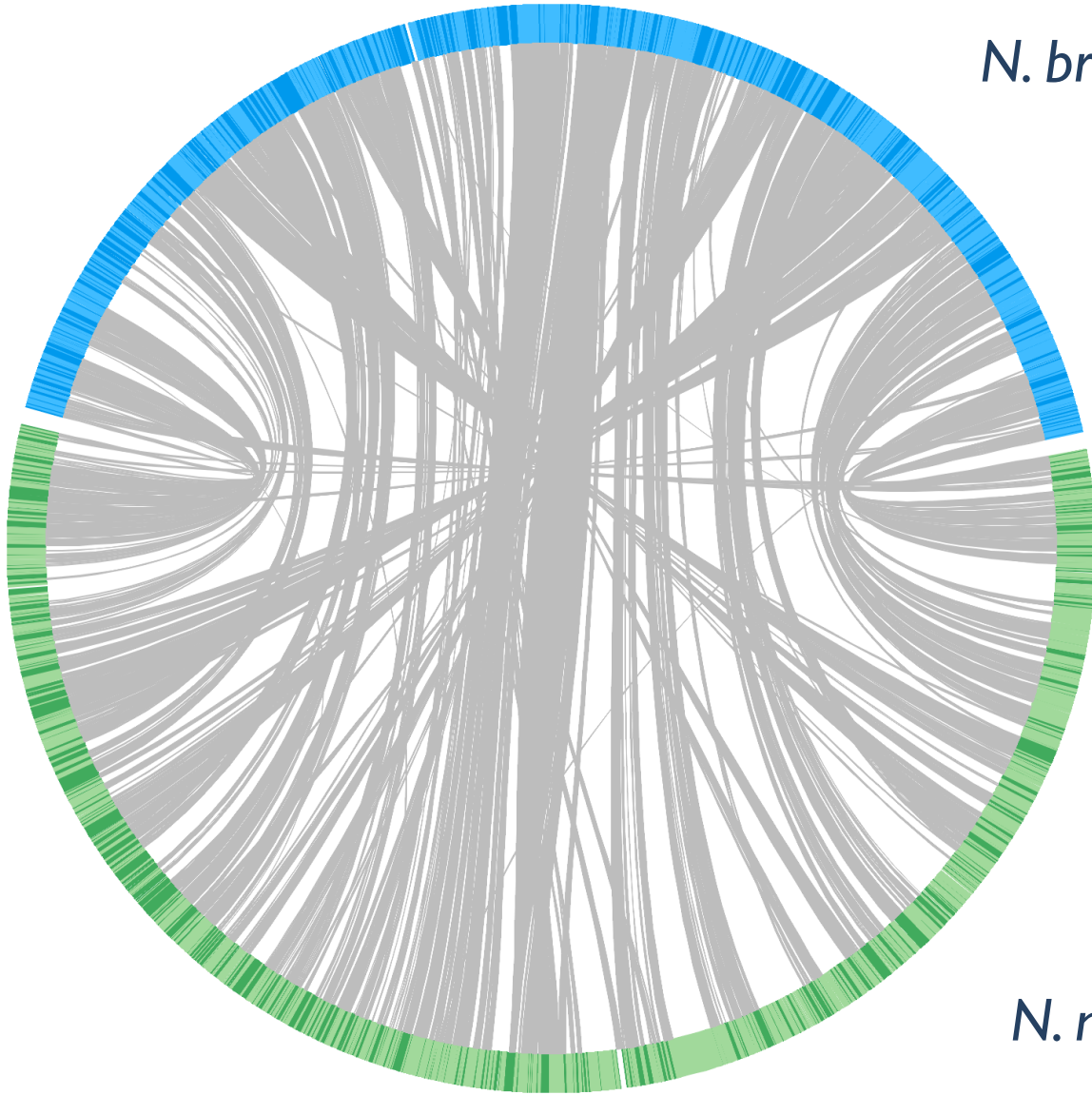


*Nitrosopelagicus brevis* CN25  
1,232,128 bp

Seventy percent of the predicted proteome is translated during 'normal' growth.



Proteome data: Mak Saito, Matt McIlvin, Dawn Moran (WHOI)



*N. brevis*

*N. maritimus*

# Full genome comparison with other thaumarchaea underscores significant differences

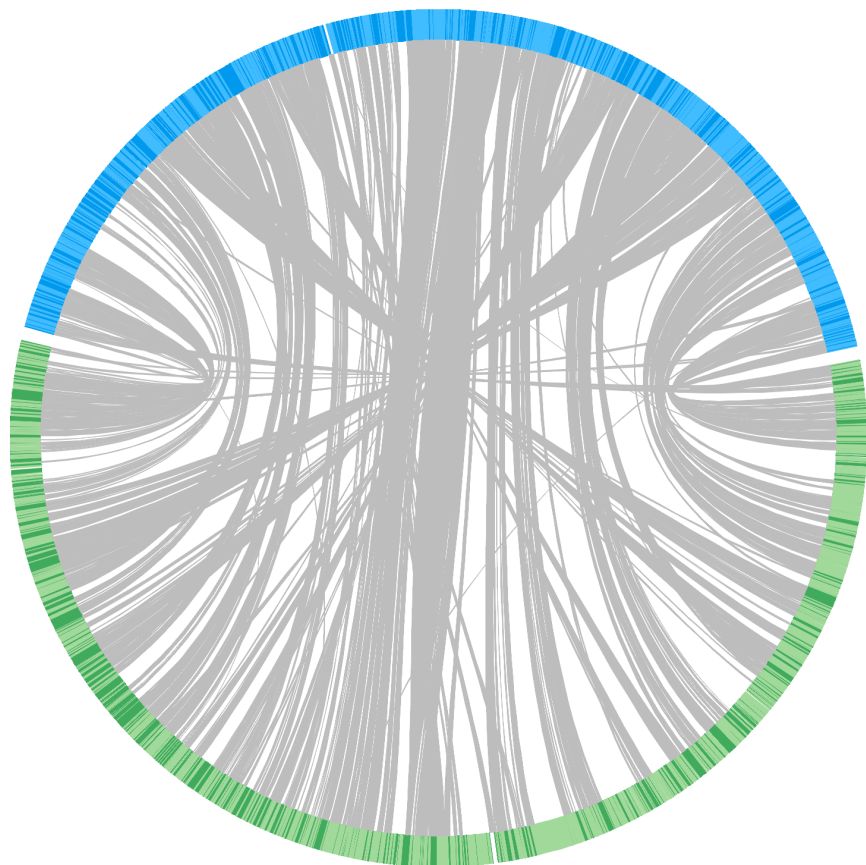
	<i>Cenarchaeum</i>	<i>N. limnia</i>	<i>N. koreensis</i>	<i>N. gargensis</i>	<i>N. maritimus</i>	<i>N. brevis</i>
<i>Cenarchaeum</i>	100					
<i>N. limnia</i>	59	99				
<i>N. koreensis</i>	58	78	99			
<i>N. gargensis</i>	53	63	62	99		
<i>N. maritimus</i>	64	76	82	38	100	
<i>N. brevis</i>	57	66	69	34	75	100

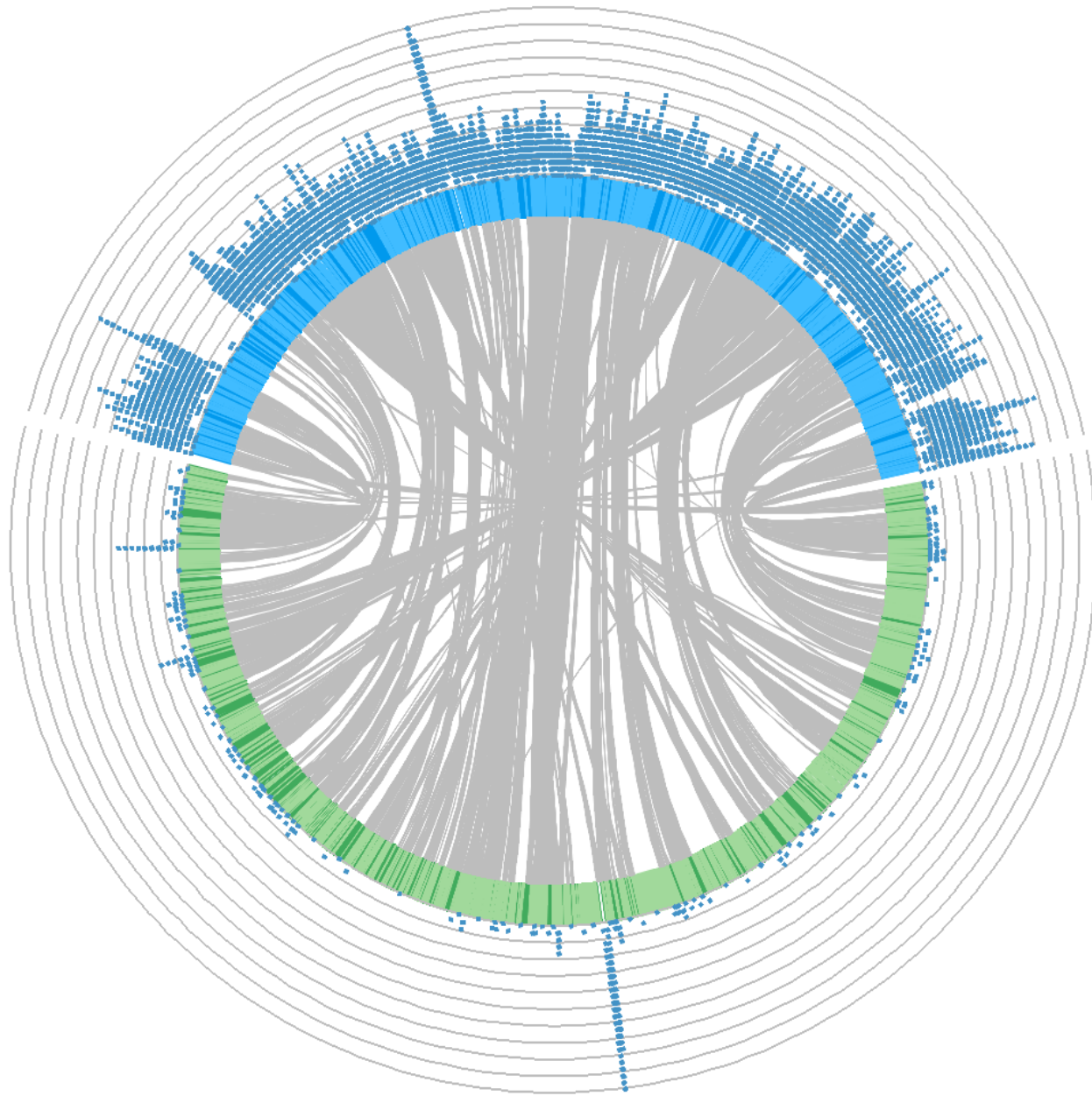


# Full genome comparison with other thaumarchaea underscores significant differences

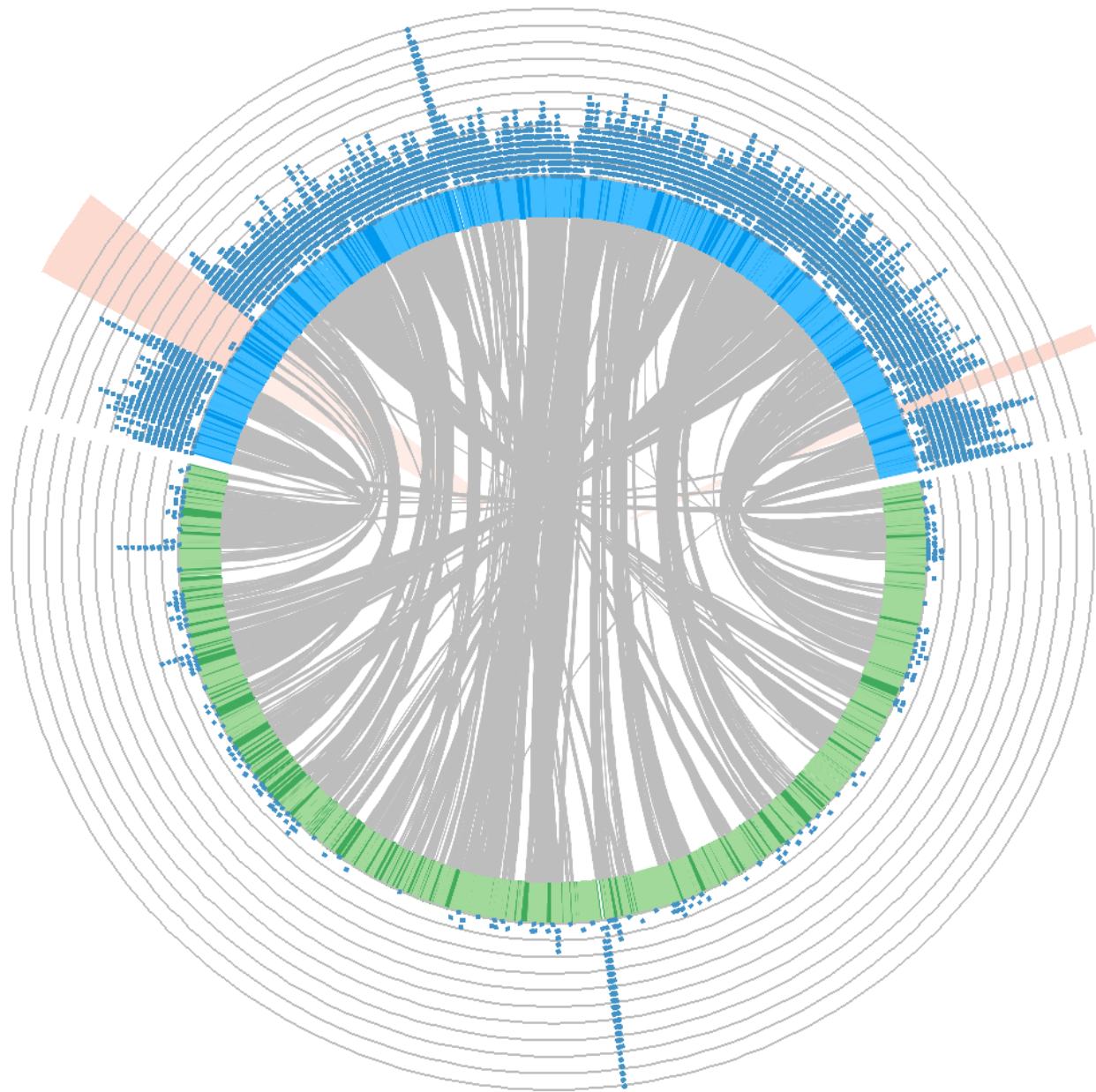
	<i>Cenarchaeum</i>	<i>N. limnia</i>	<i>N. koreensis</i>	<i>N. gargensis</i>	<i>N. maritimus</i>	<i>N. brevis</i>
<i>Cenarchaeum</i>	100					
<i>N. limnia</i>	59	99				
<i>N. koreensis</i>	58	78	99			
<i>N. gargensis</i>	53	63	62	99		
<i>N. maritimus</i>	64	76	82	38	100	
<i>N. brevis</i>	57	66	69	34	75	100

*N. brevis* averages only 75% ortholog identity with *N. maritimus*.





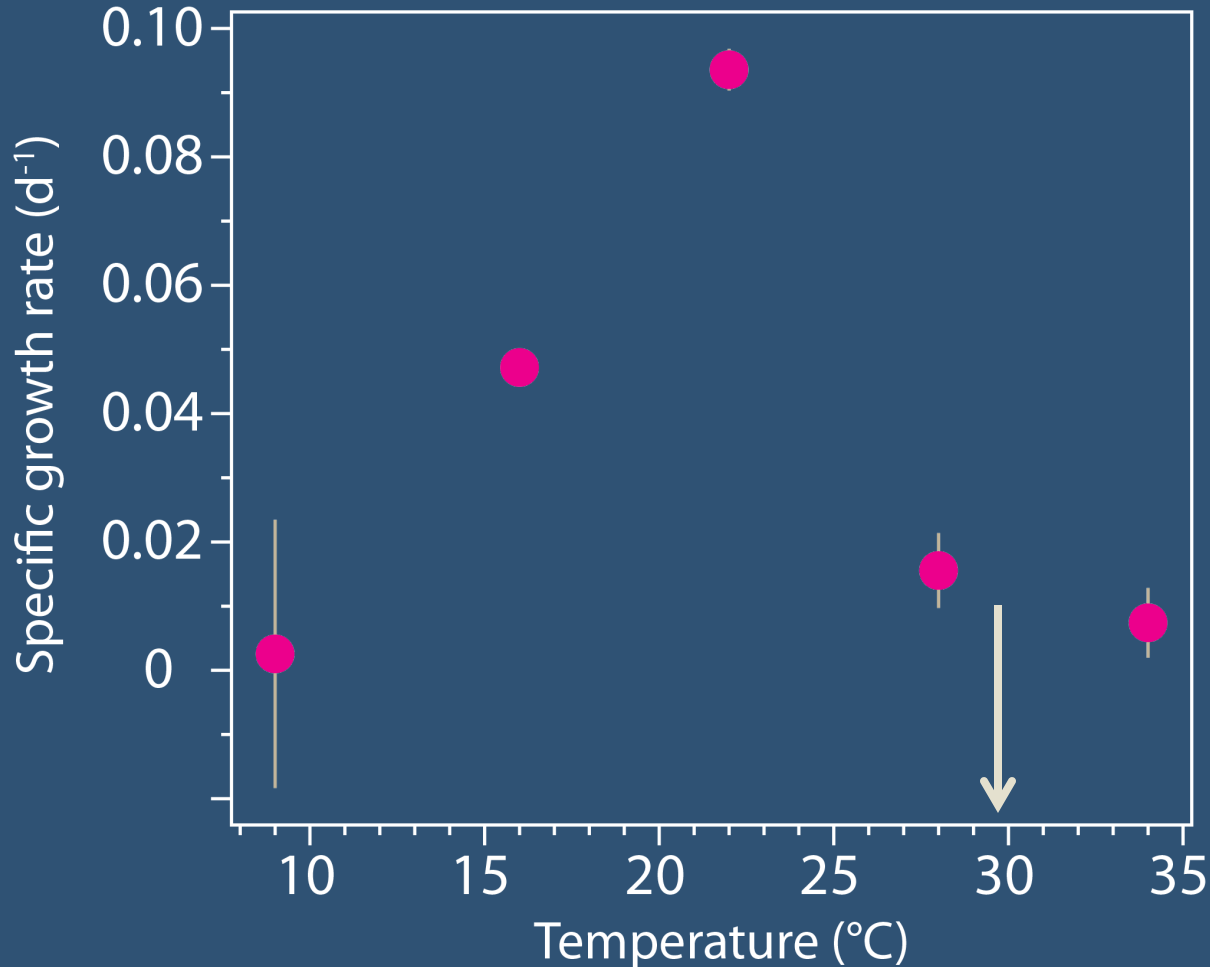
GOS data  
mapped at  
90%  
nucleotide ID



A circular genomic map of the *N. brevis* genome. The map consists of multiple concentric circles. The innermost circle is a solid grey arc. The next ring out is a blue arc with small blue dots extending outwards, representing a specific genomic track. Below the blue arc is a green arc, also with small blue dots extending outwards. Further out are several more concentric grey lines. Two orange wedge-shaped regions are positioned on the left and right sides of the map, overlapping the blue and green tracks. A semi-transparent grey rectangular box is overlaid on the right side of the map, containing text.

The *N. brevis* genome is a new tool to help us understand metagenomic and metaproteomic data from the ocean.

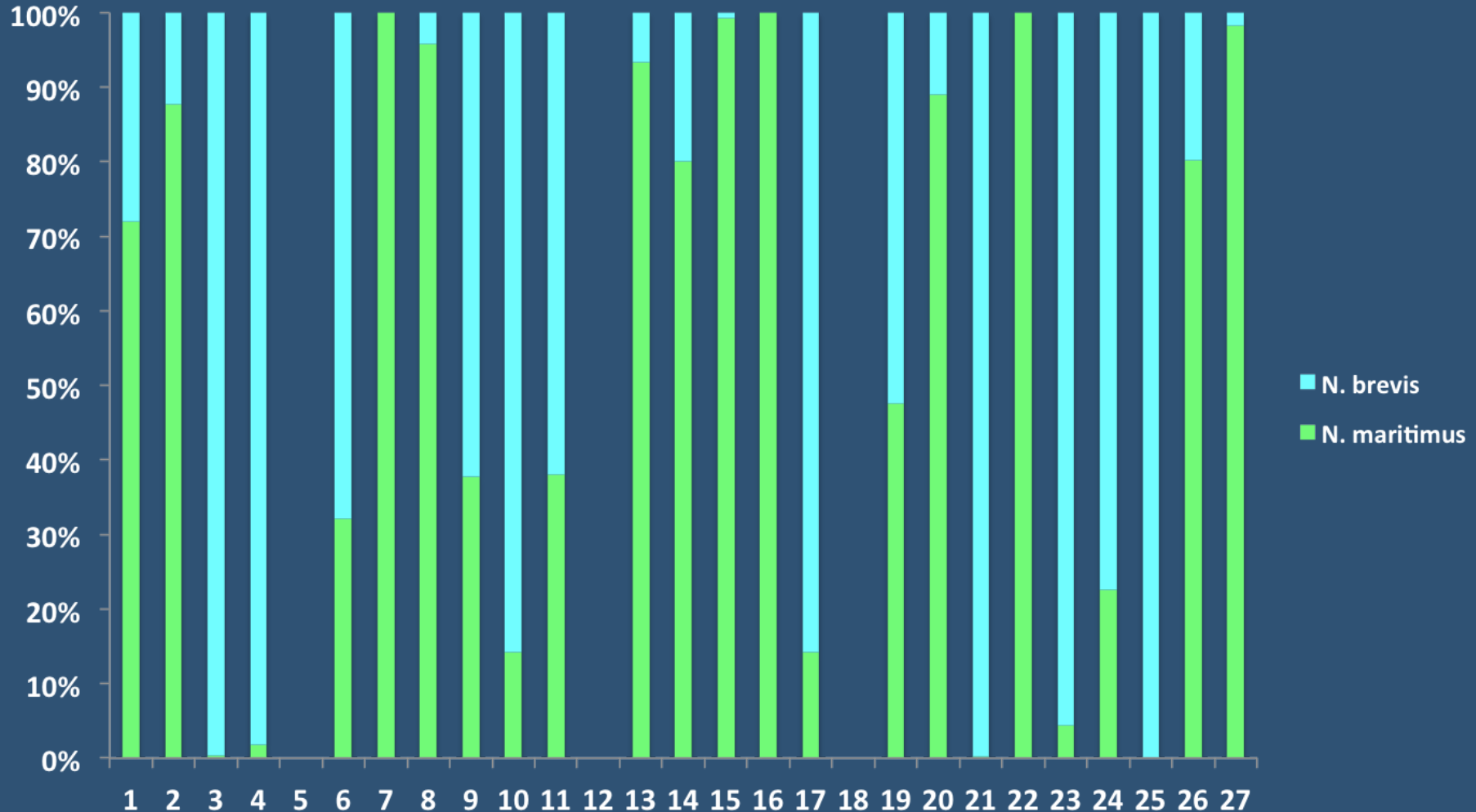
*N. brevis* temperature optimum is similar to surface ocean temperatures



Data: Paul Carini

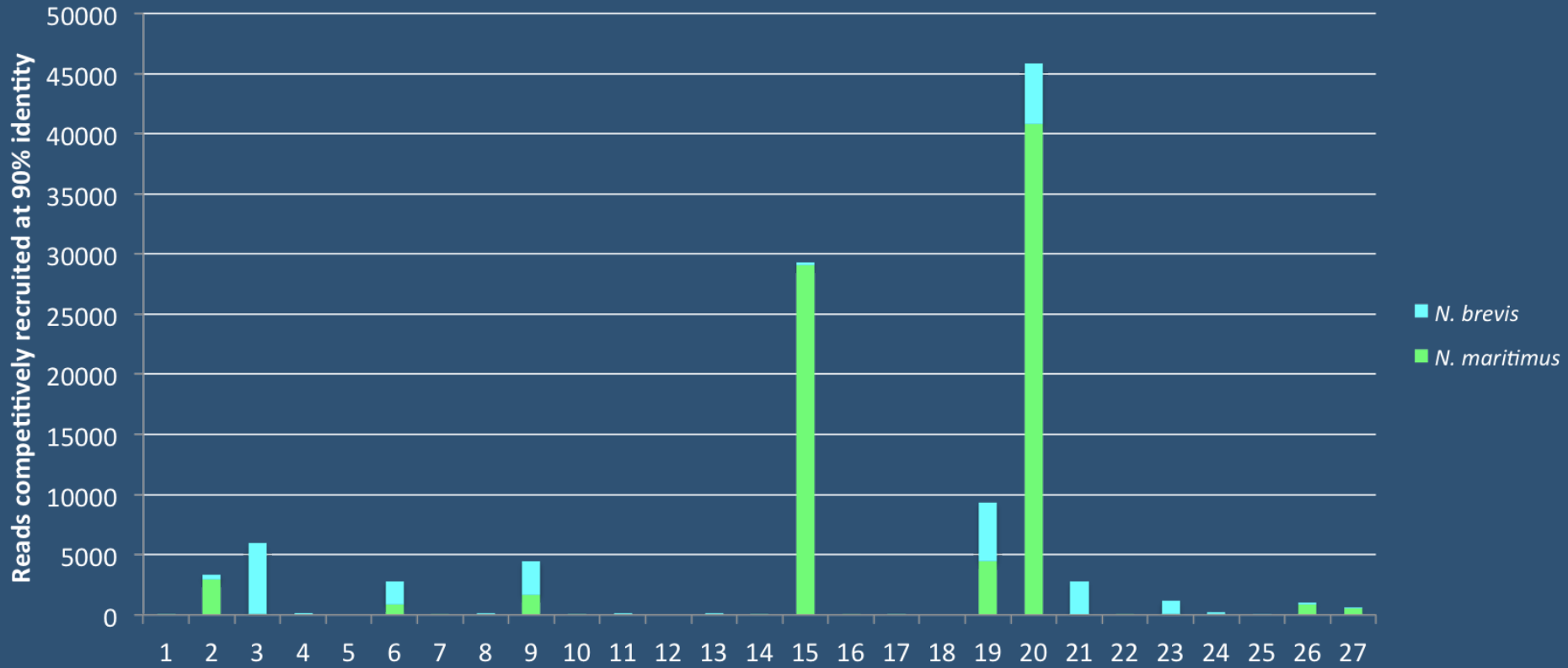
The GOS data only tell part of the story

# The GOS data only tell part of the story





# *N. maritimus* 'blooms' in hydrothermal vent plumes and coastal waters



# Does 'high' ammonium flux favor *N. maritimus*?

The ISME Journal (2012), 1–11  
© 2012 International Society for Microbial Ecology All rights reserved 1751-7362/12  
[www.nature.com/ismej](http://www.nature.com/ismej)



## ORIGINAL ARTICLE

### Genome-enabled transcriptomics reveals archaeal populations that drive nitrification in a deep-sea hydrothermal plume

Brett J Baker<sup>1</sup>, Ryan A Lesniewski<sup>1,4</sup> and Gregory J Dick<sup>1,2,3</sup>

<sup>1</sup>*Department of Earth and Environmental Sciences, University of Michigan, Ann Arbor, MI, USA;*

<sup>2</sup>*Department of Ecology and Evolutionary Biology, University of Michigan, Ann Arbor, MI, USA and*

<sup>3</sup>*Center for Computational Medicine and Bioinformatics, University of Michigan, Ann Arbor, MI, USA*

[www.nature.com/ismej](http://www.nature.com/ismej)

## ORIGINAL ARTICLE

### Metatranscriptomic analysis of ammonia-oxidizing organisms in an estuarine bacterioplankton assemblage

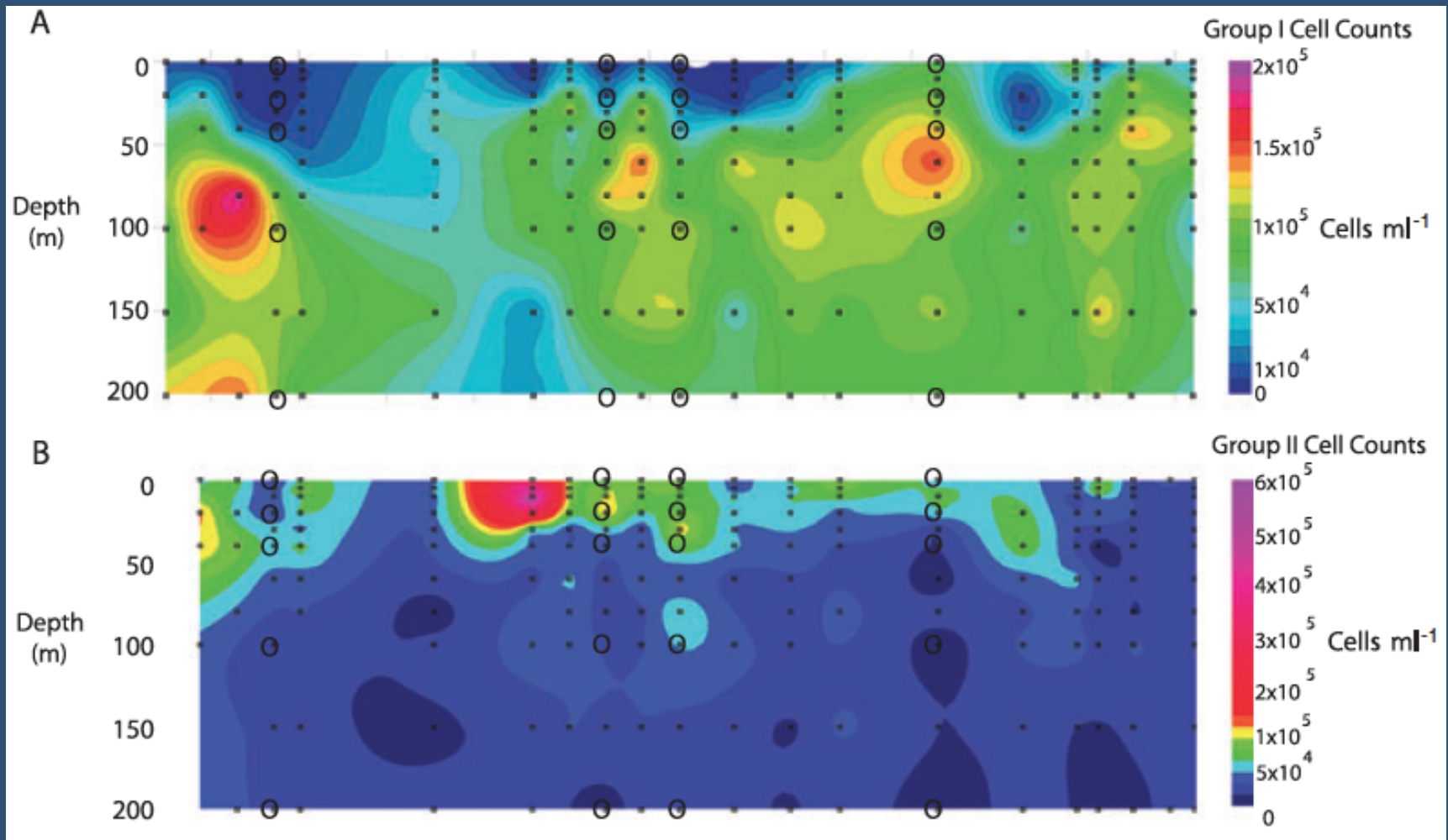
James T Hollibaugh<sup>1</sup>, Scott Gifford<sup>1</sup>, Shalabh Sharma, Nasreen Bano and Mary Ann Moran<sup>1</sup>  
*Department of Marine Sciences, University of Georgia, Athens, GA, USA*

There are a lot of thaumarchaea in the ocean that aren't *N. brevis* or *N. maritimus*

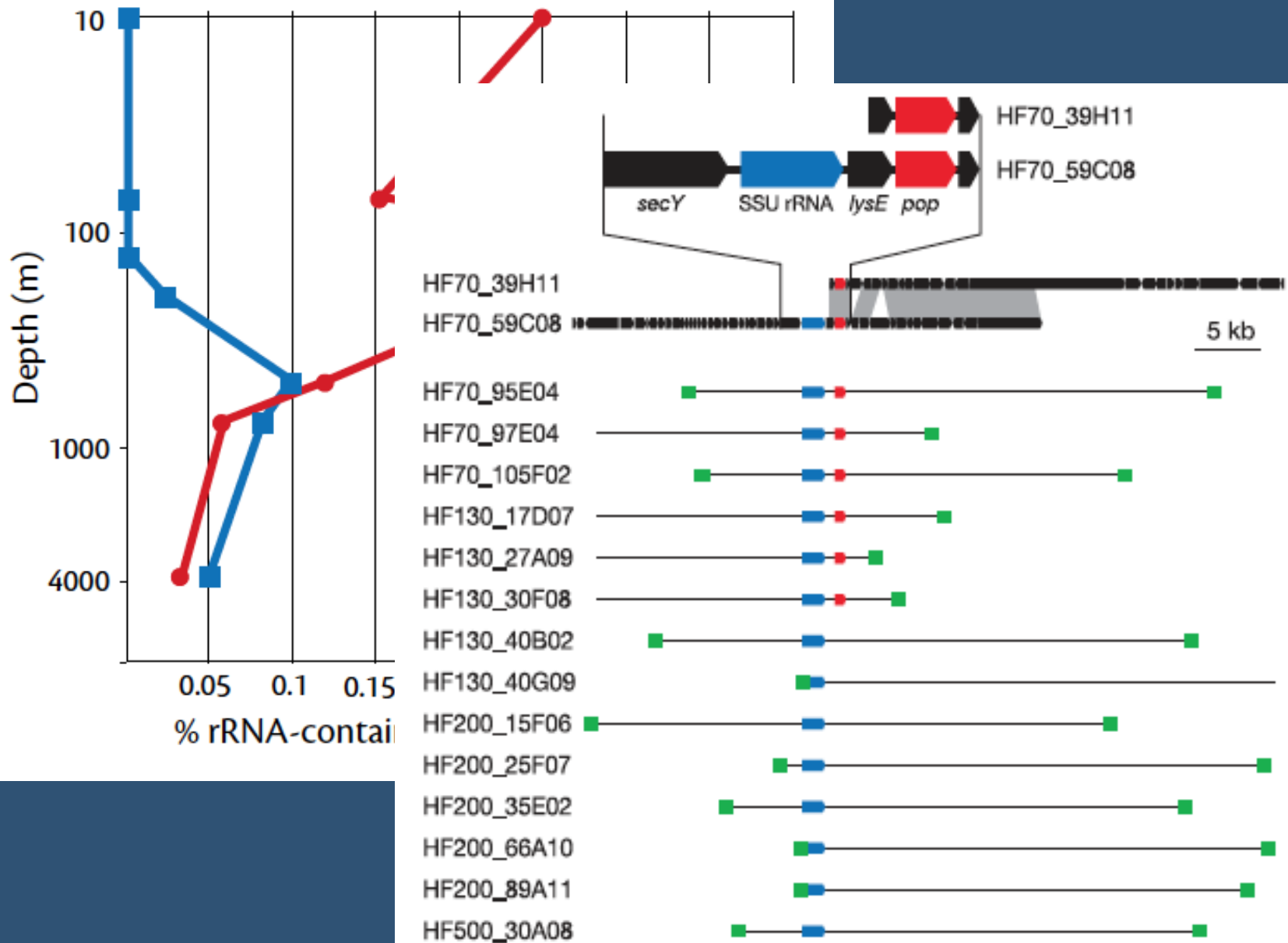


# The elusive Euryarchaeota

# Contrasting distribution of MGI and MGII

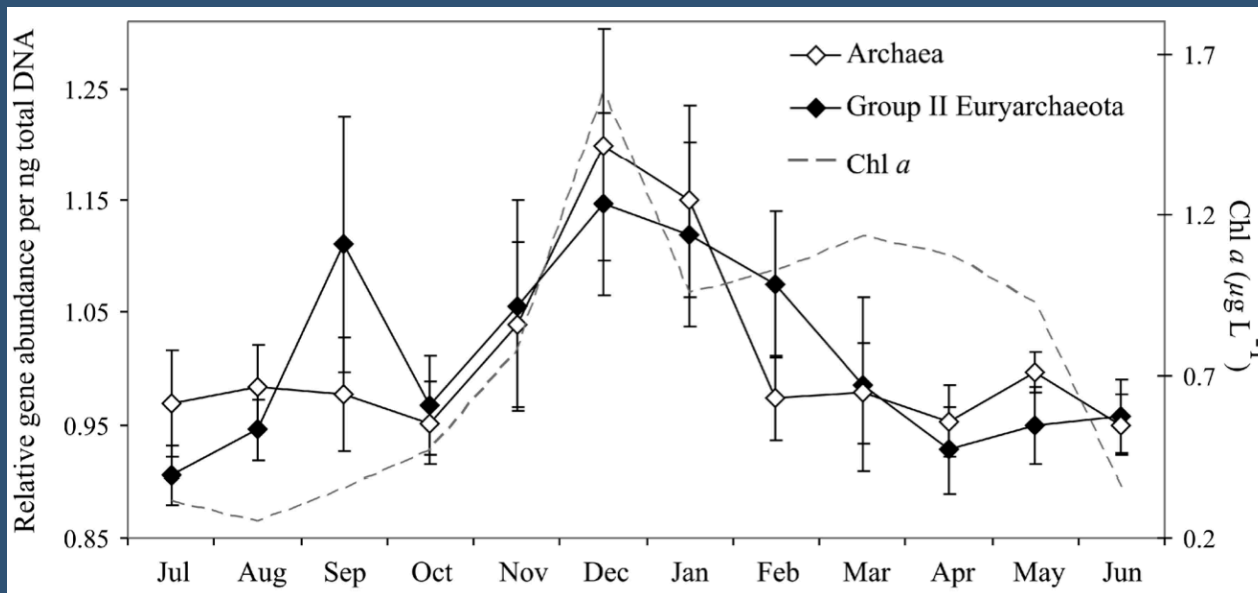


C



# Marine group II Euryarchaeota (MGII): abundant and uncultured

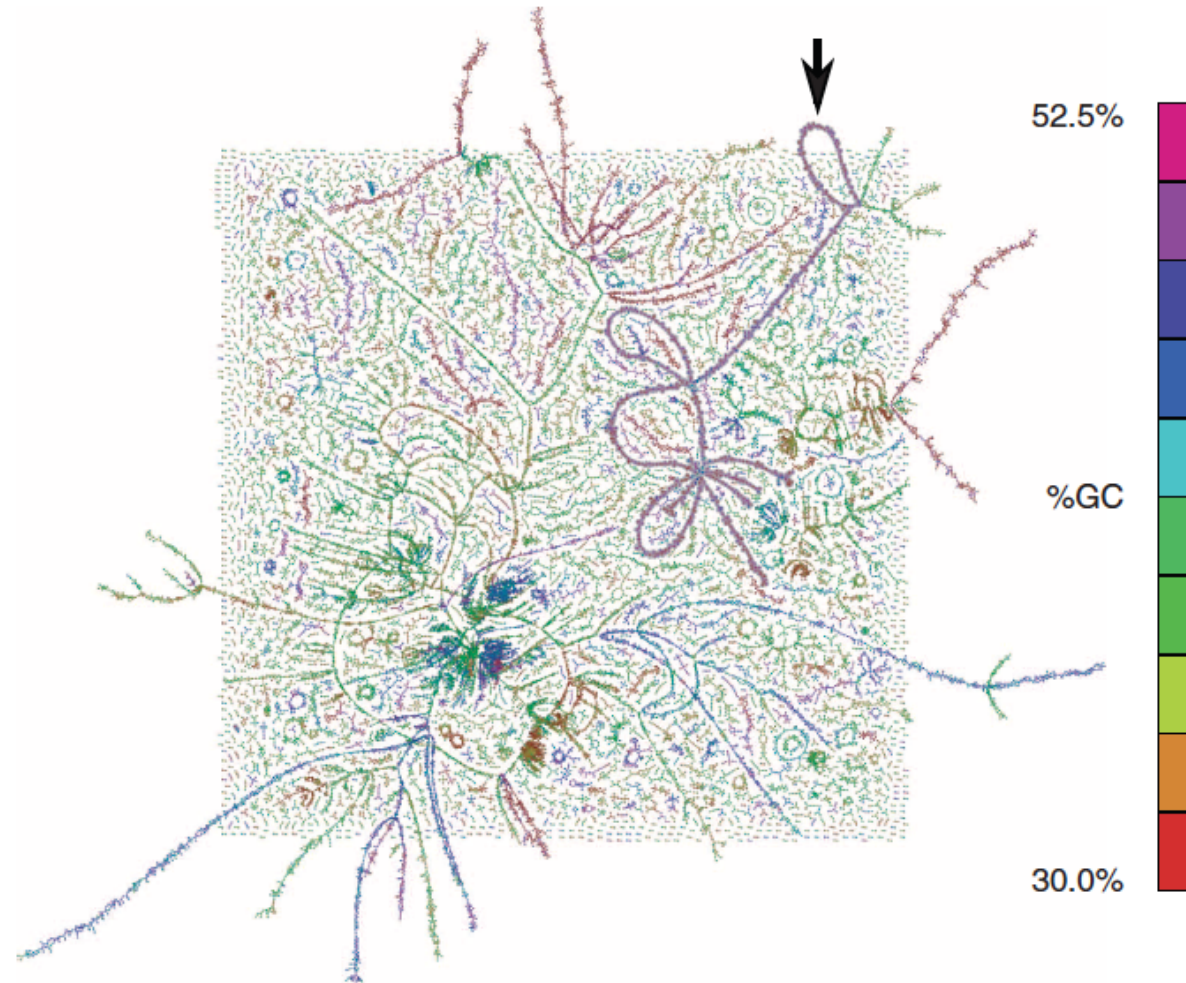
- Can reach abundances of  $> 10^4$  cells mL<sup>-1</sup>, found in coastal, open ocean, and Arctic habitats
- Contain proteorhodopsin, potential photoheterotrophs
- Have been found to correlate with Chl *a* concentrations



Galand et al. 2010

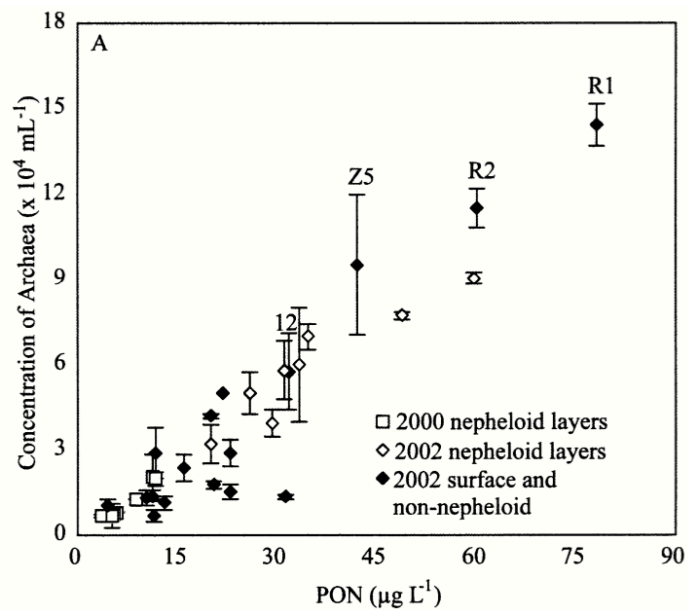
# Untangling Genomes from Metagenomes: Revealing an Uncultured Class of Marine Euryarchaeota

Vaughn Iverson, Robert M. Morris, Christian D. Frazar, Chris T. Berthiaume,  
Rhonda L. Morales, E. Virginia Armbrust\*





# Archaea have been detected on POM and PON



Wells *et al.*, 2006 L&O

## Heterogeneous archaeal communities in the particle-rich environment of an arctic shelf ecosystem

Pierre E. Galand<sup>a,\*</sup>, Connie Lovejoy<sup>a</sup>, Jérémie Pouliot<sup>a</sup>, Warwick F. Vincent<sup>b</sup>

<sup>a</sup> *Département de Biologie et Québec-Océan, Université Laval, Québec, QC G1V 0A6, Canada*

<sup>b</sup> *Département de Biologie et Centre d'Études Nordiques, Université Laval, Québec, QC G1V 0A6, Canada*

Received 10 April 2007; received in revised form 11 November 2007; accepted 7 December 2007

Available online 14 December 2007

## Archaeoplankton in the Columbia River, its estuary and the adjacent coastal ocean, USA

Byron C. Crump<sup>\*</sup>, John A. Baross

*School of Oceanography, University of Washington, Seattle, WA 98195, USA*

Received 7 September 1999; received in revised form 13 December 1999; accepted 13 December 1999

Questions:

What are MGII doing on particles?

Are there interactions between MGII and picoeukaryotes?

Is there a link between POM and MGII ecology?

Collaborators:

Mak Saito

Chris Dupont

Culture and genomic work:

NSF Bio OCE

UMCES start up funds

WHOI Ocean Life  
Institute

Proteomics and MGII:

Gordon and Betty  
Moore Foundation



# Acknowledgements

## Collaborators:

Jason Smith (MBARI)  
Jarred Swalwell (UW)  
Susanne Wilken (MBARI)  
Heather Wilcox (MBARI)  
Alexandra Worden (MBARI)  
Patrick Keeling (UBC)  
Tom Richards (U. Exeter)

## Cruise support:

Western Flyer: Captain and crew  
Tim Pennington (MBARI)  
Marguerite Blum (MBARI)  
Francisco Chavez (MBARI)  
Valeria Jimenez (UBC)  
Noriko Okamoto (UBC)



Thank you!!!

