



Footprints and Fingerprints: Microbiome on the Moon

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Pediatrics, Bioengineering and
Computer Science & Engineering
University of California San Diego

Error-correcting barcoded primers for pyrosequencing hundreds of samples in multiplex

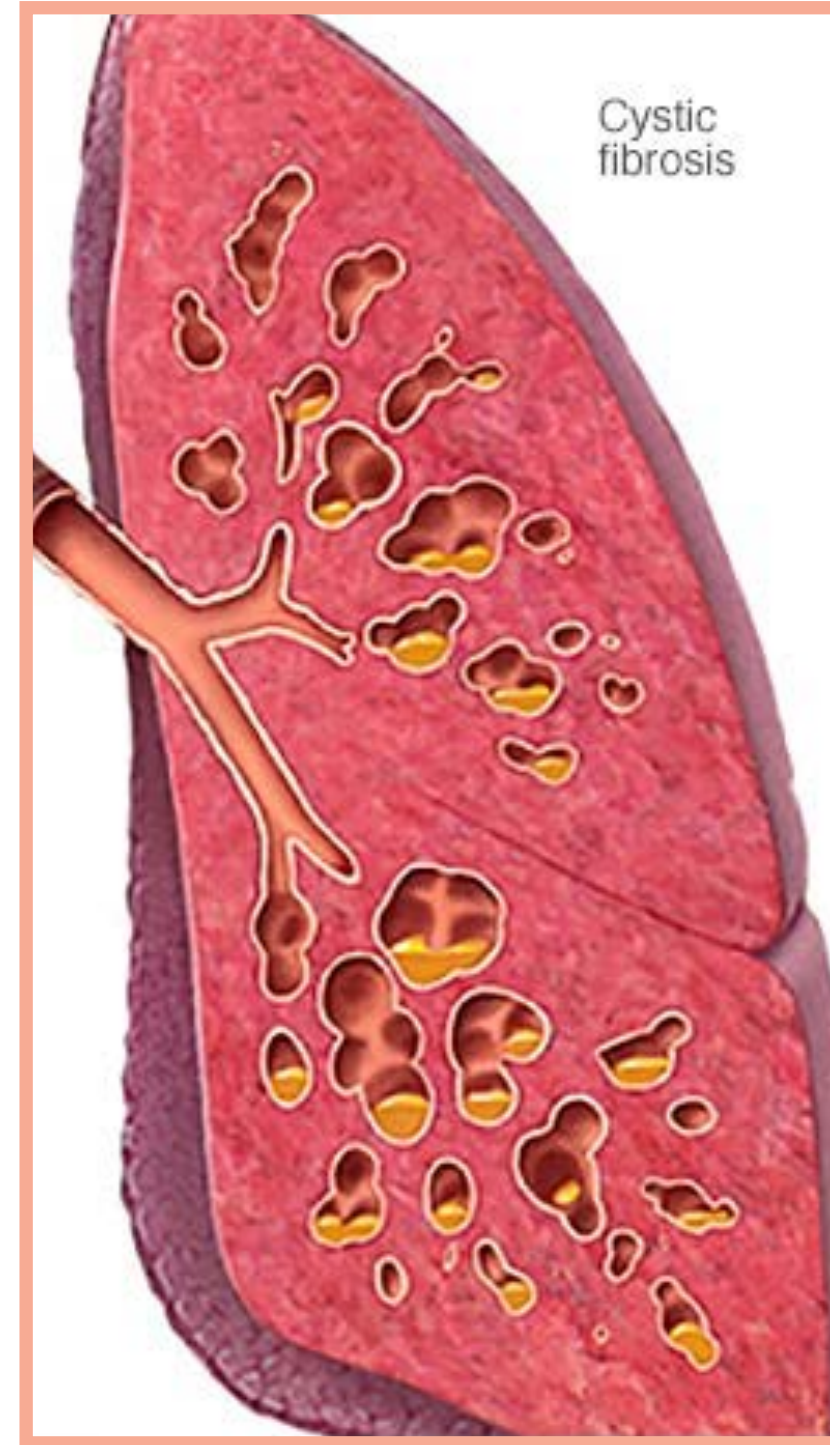
Micah Hamady¹, Jeffrey J Walker², J Kirk Harris³,
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NATURE METHODS | VOL.5 NO.3 | MARCH 2008 | 235

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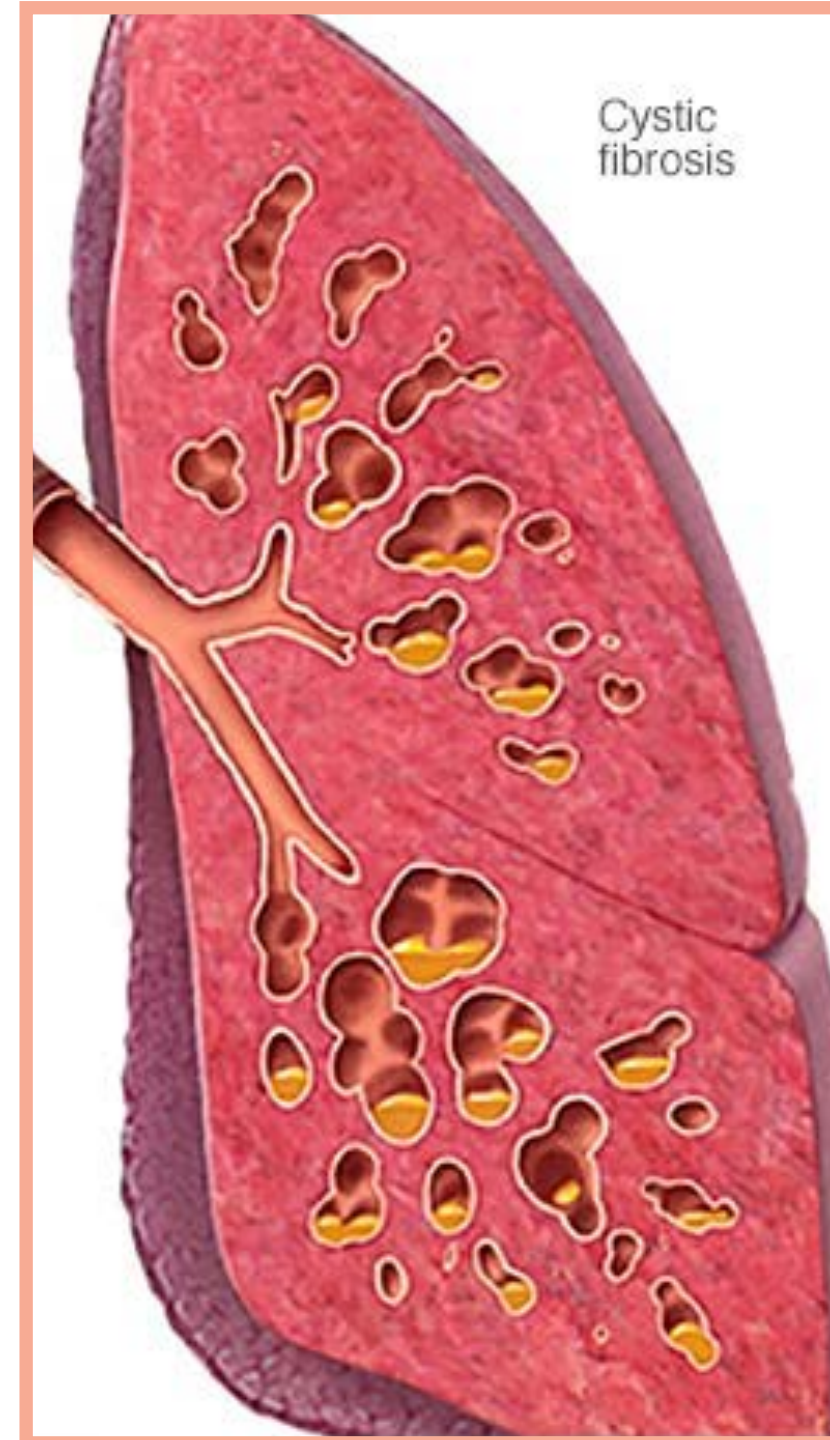
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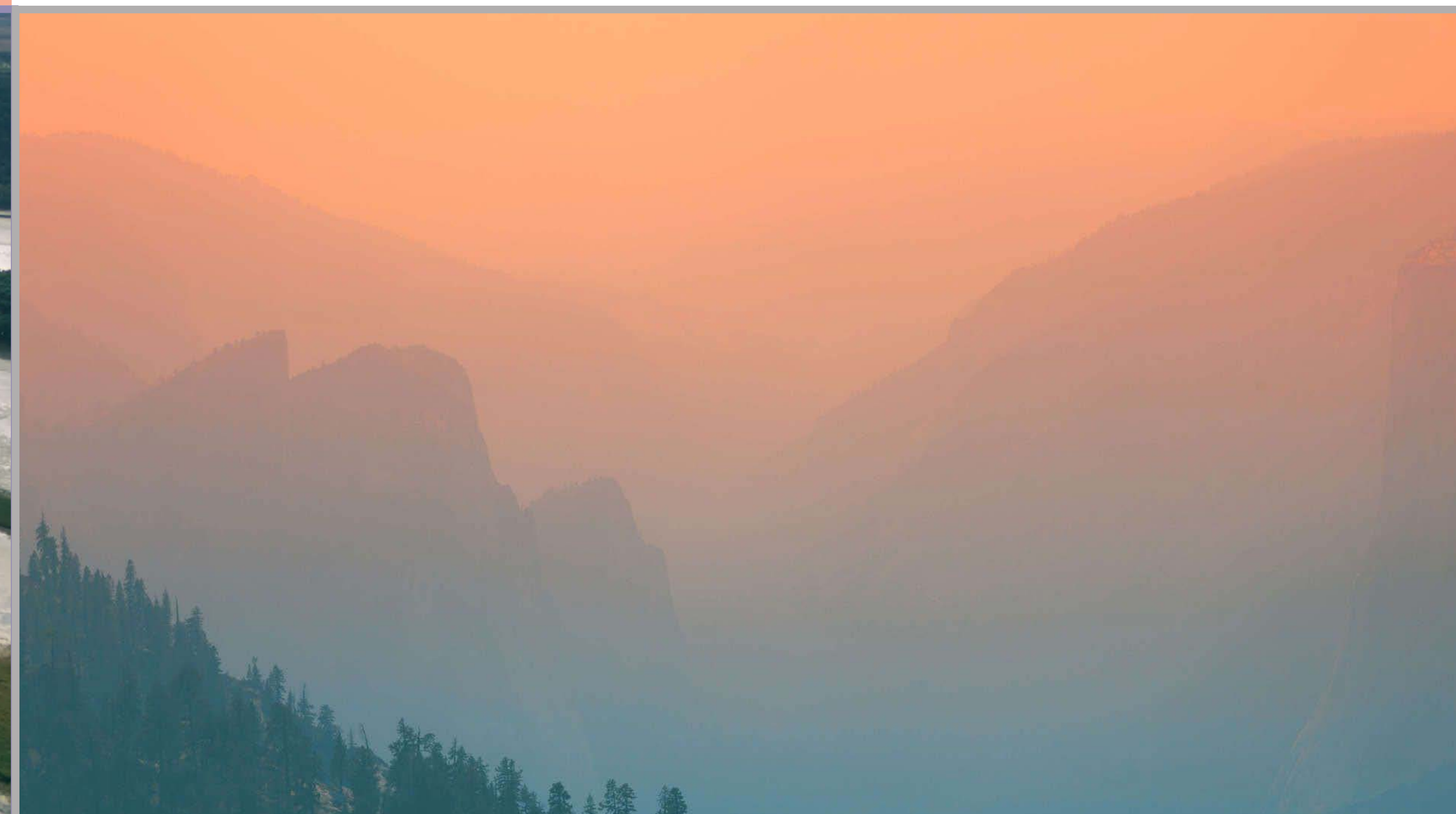
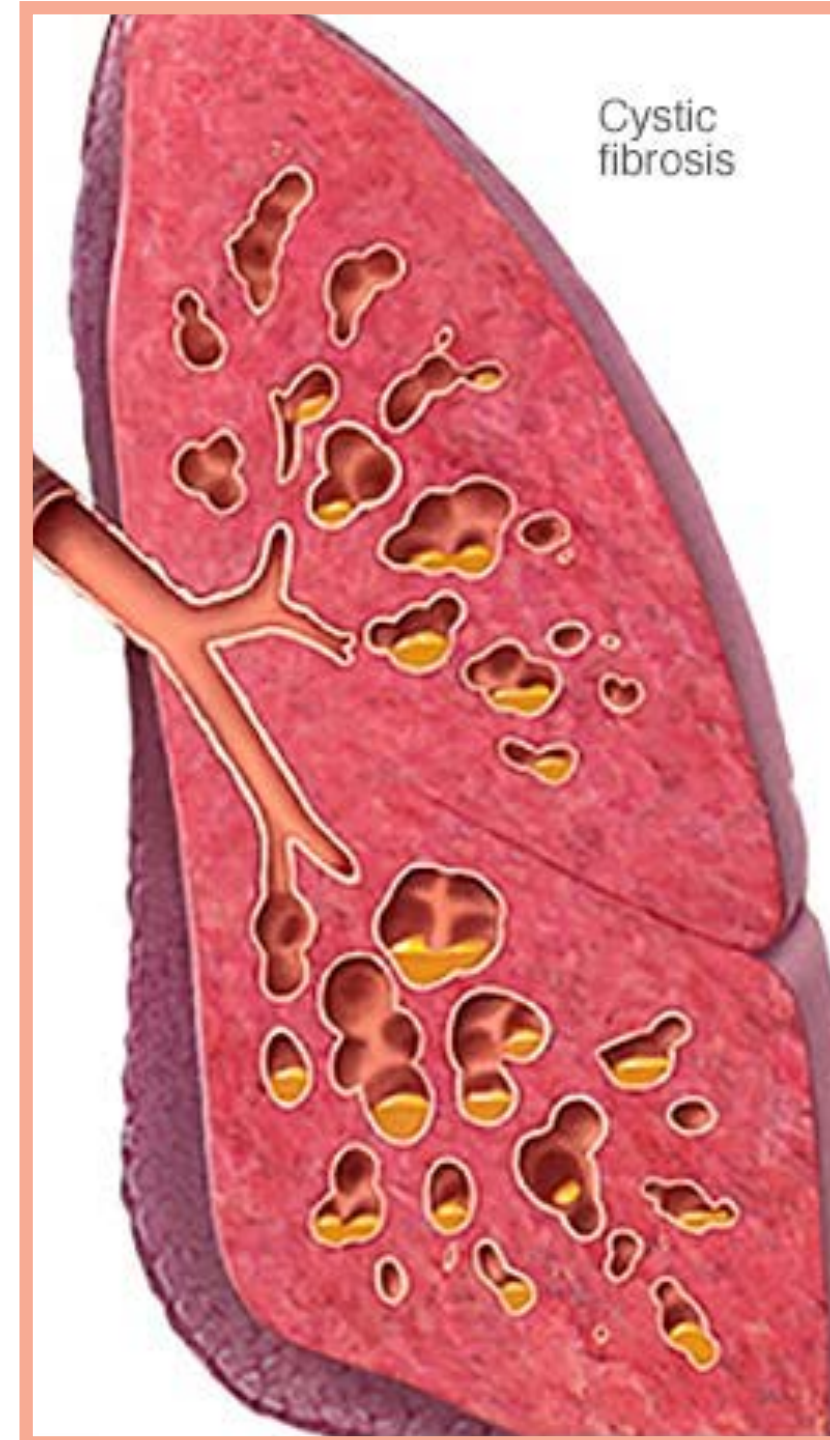
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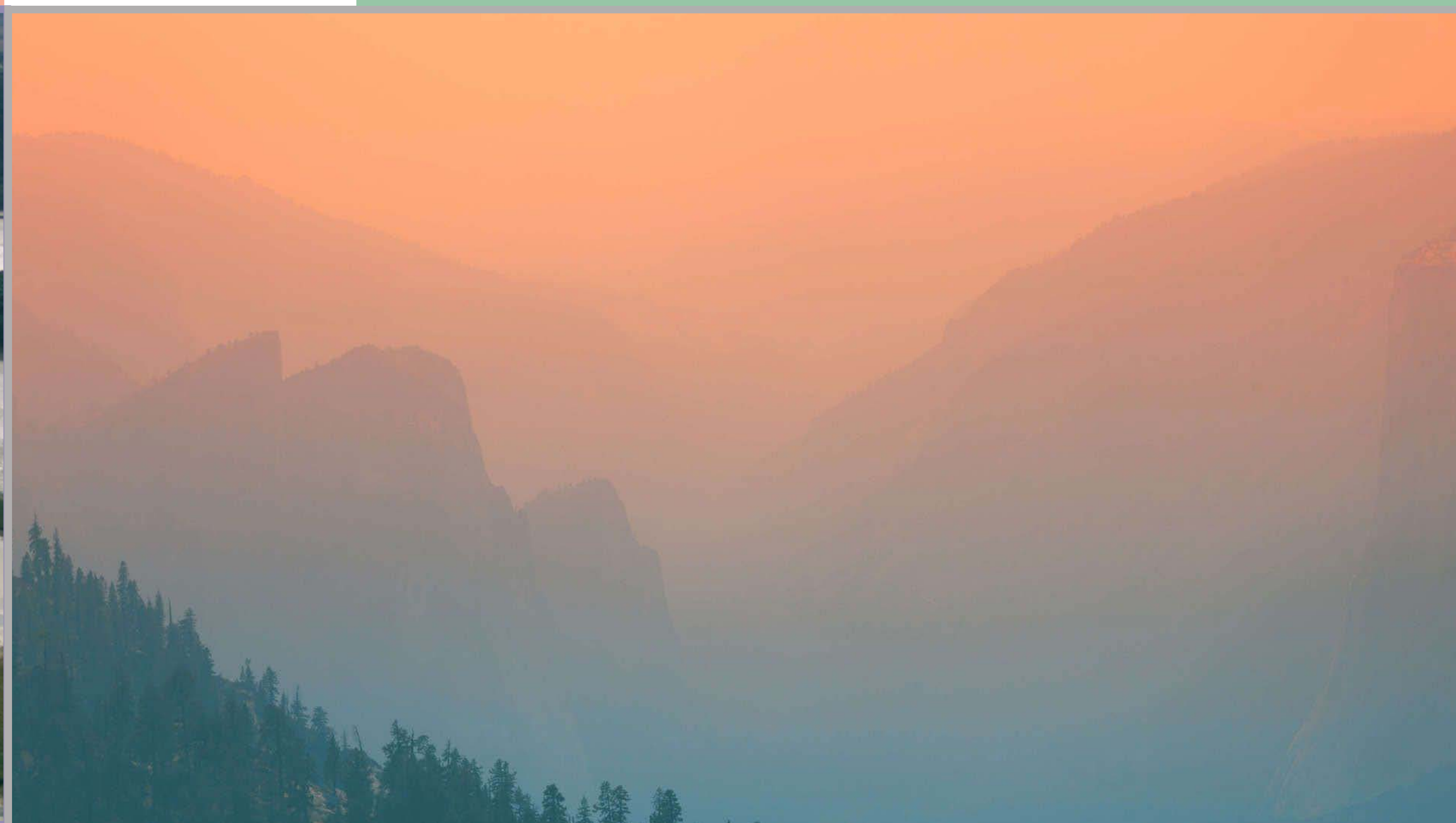
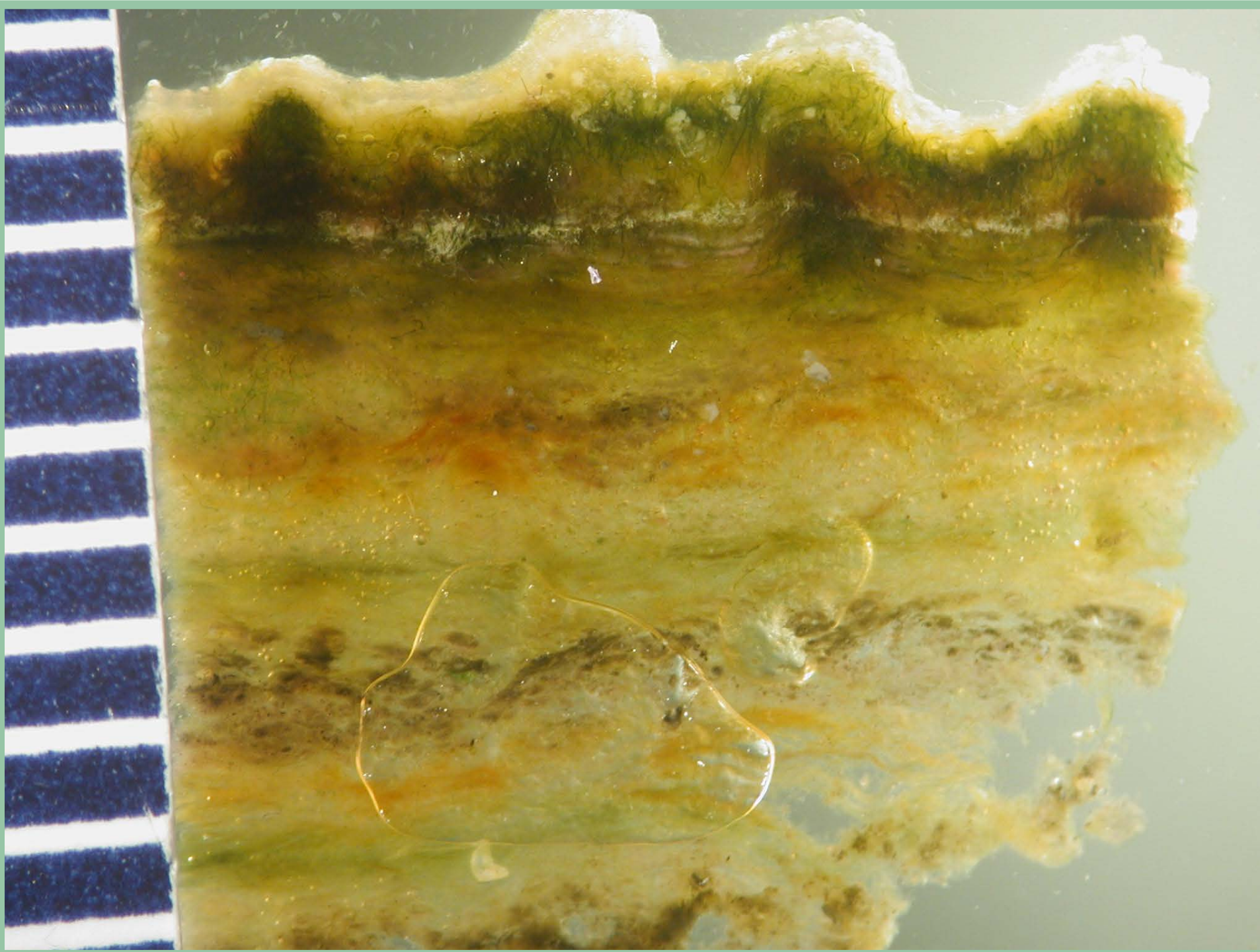
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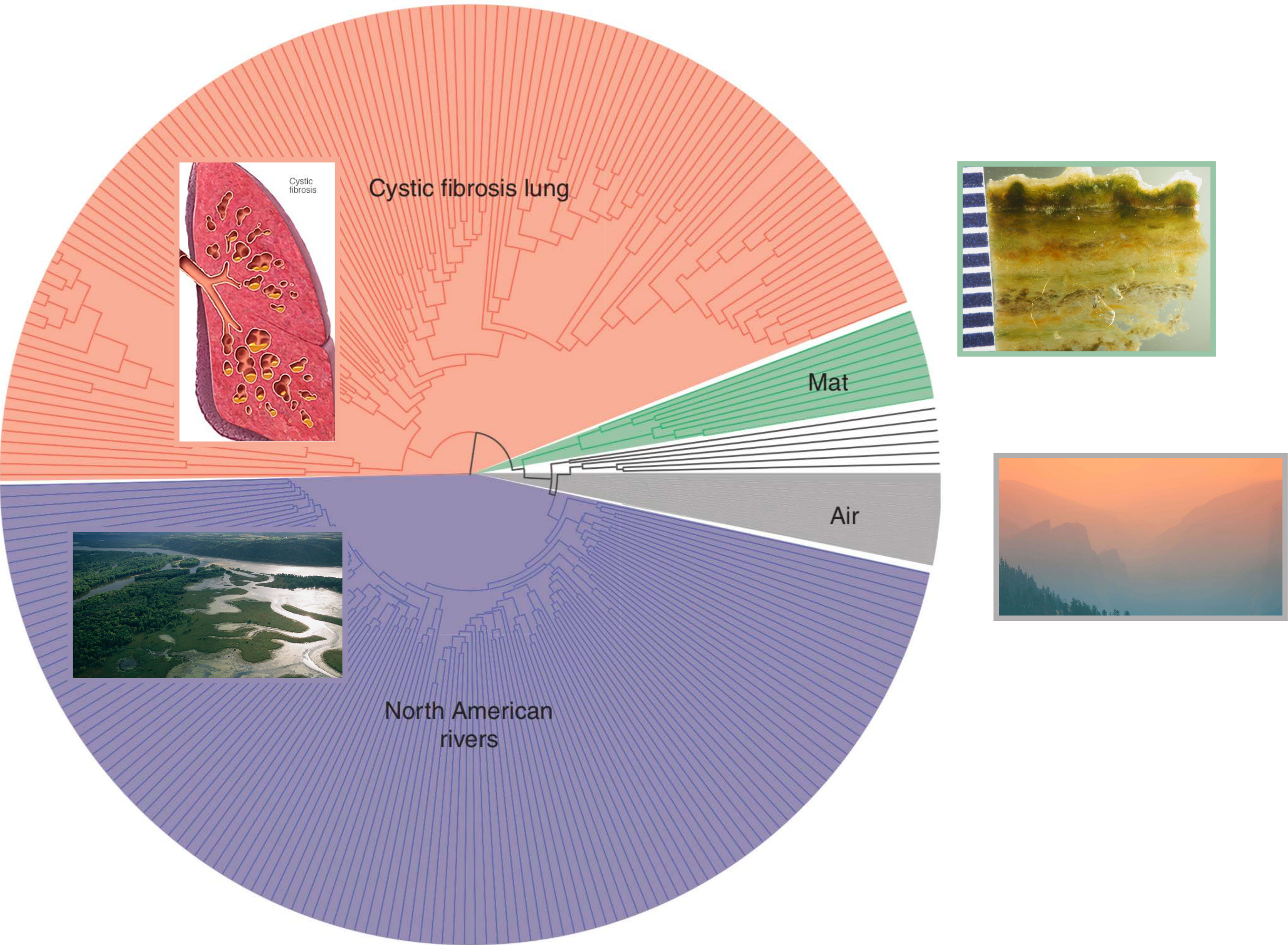


Figure 2 | UniFrac clustering by community was essentially perfect with sequences from pyrosequencing. Samples from cystic fibrosis lung, Guerrero Negro microbial mat, air and North American rivers cluster by environment type.

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\$4,000,000

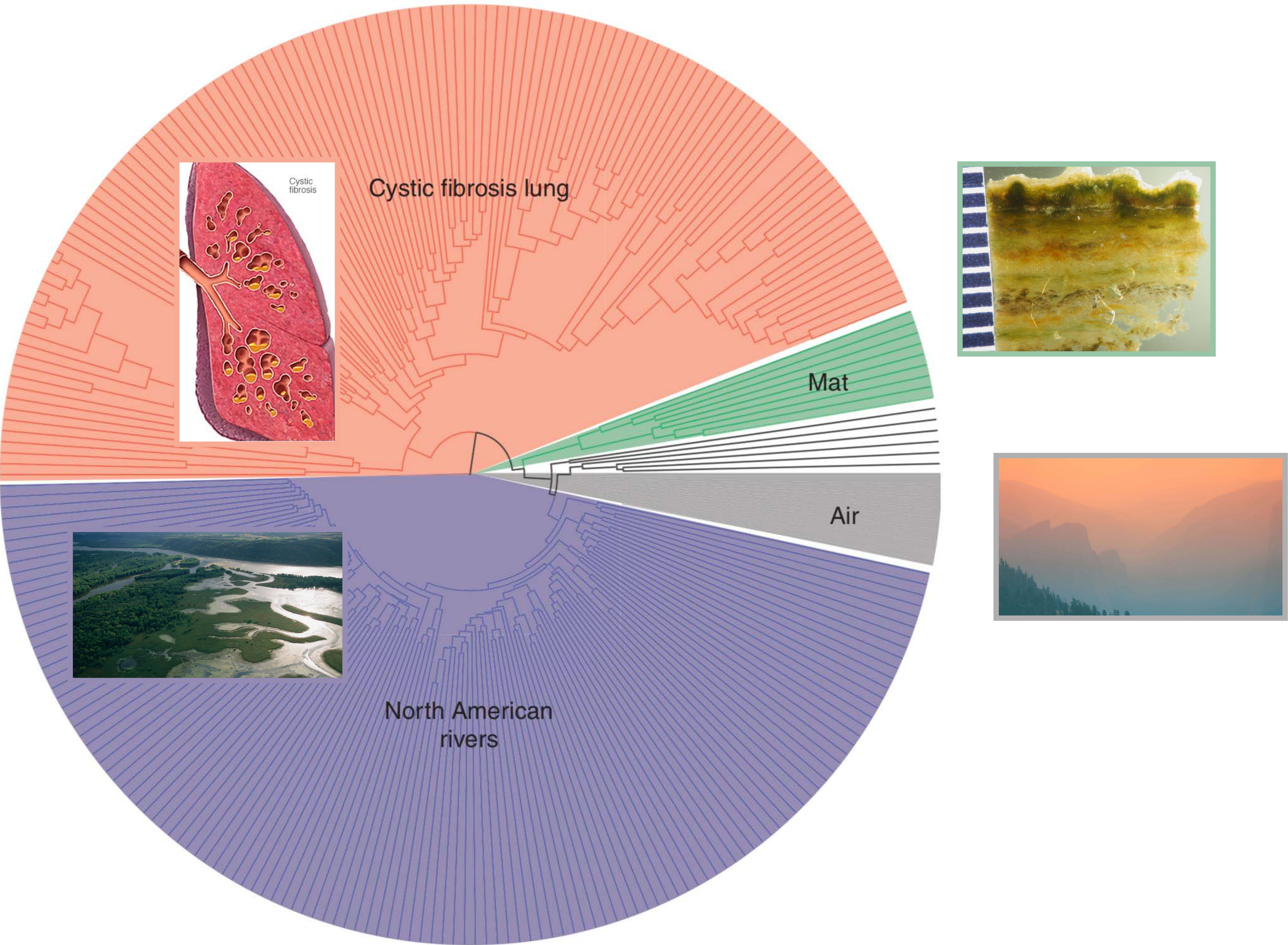


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\$12,000

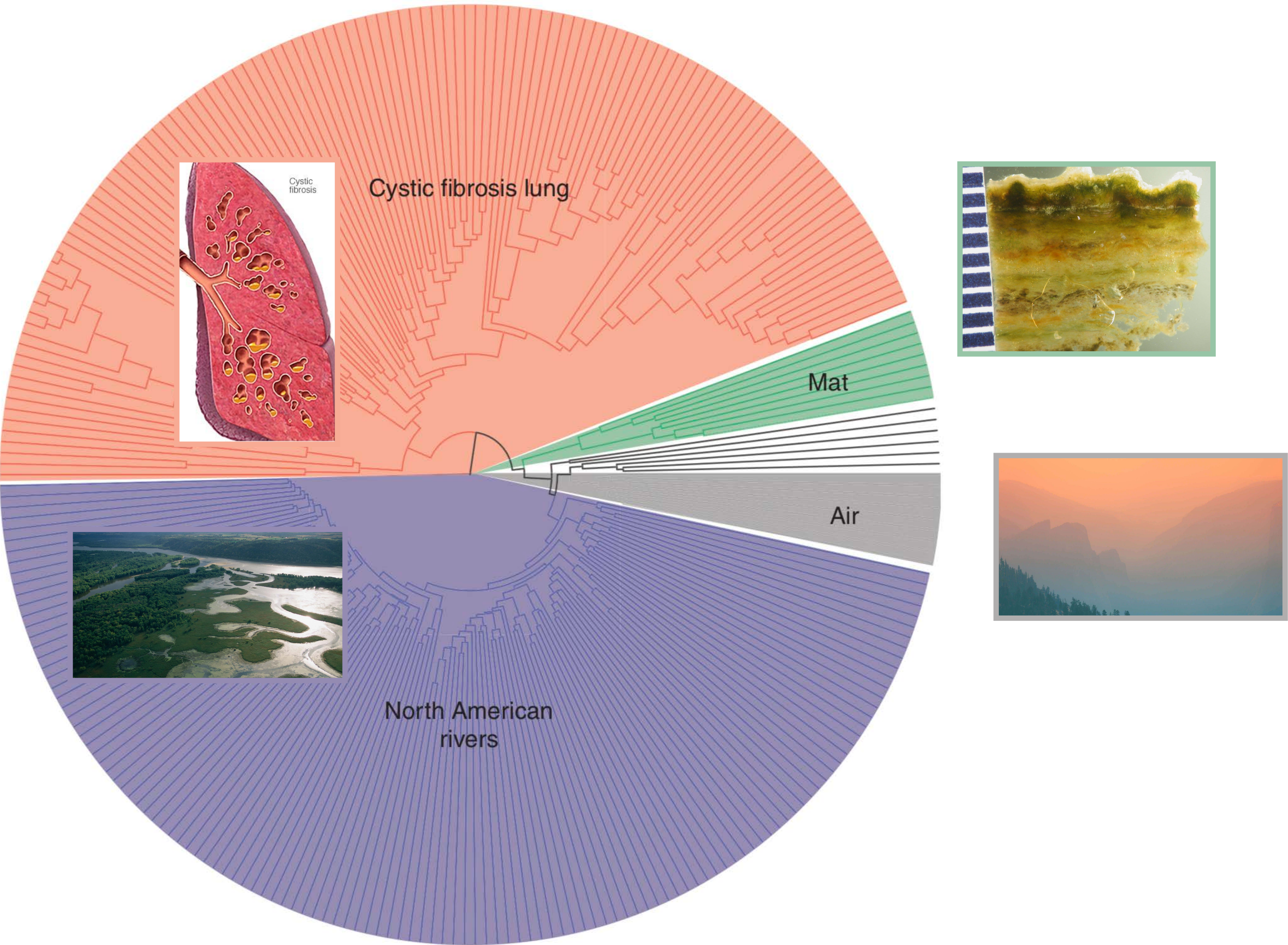


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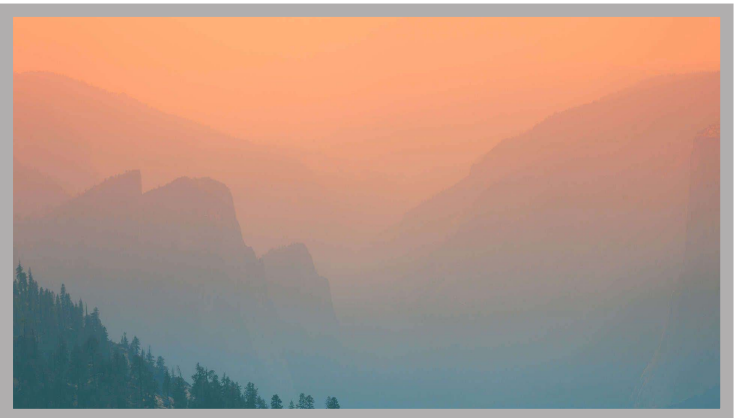
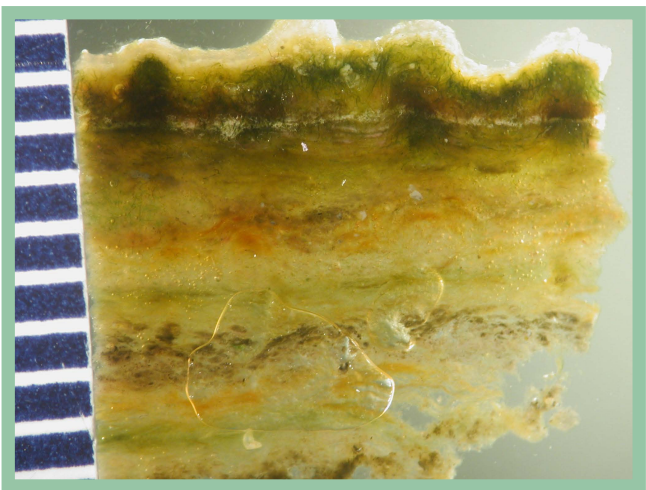
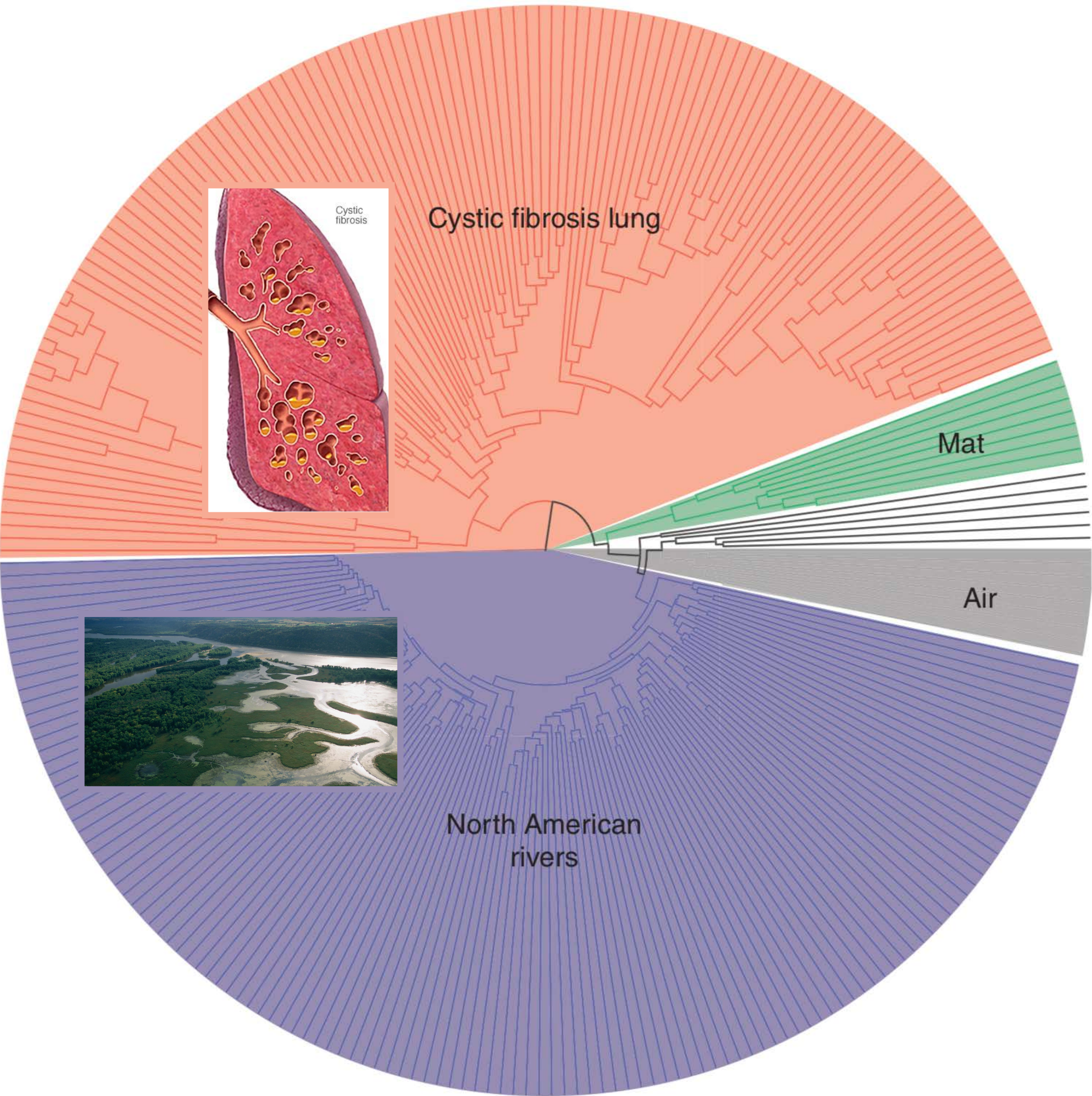
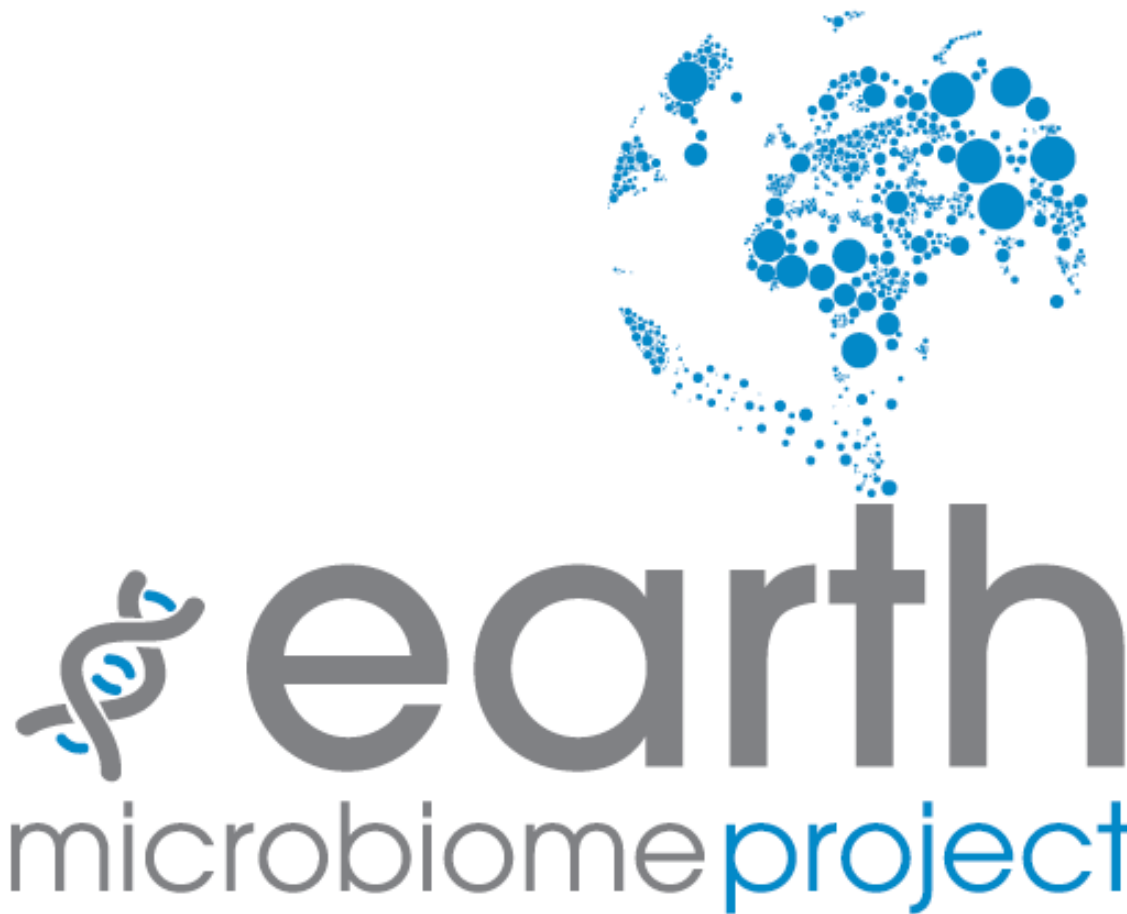


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Thompson et al. 2017 *Nature*

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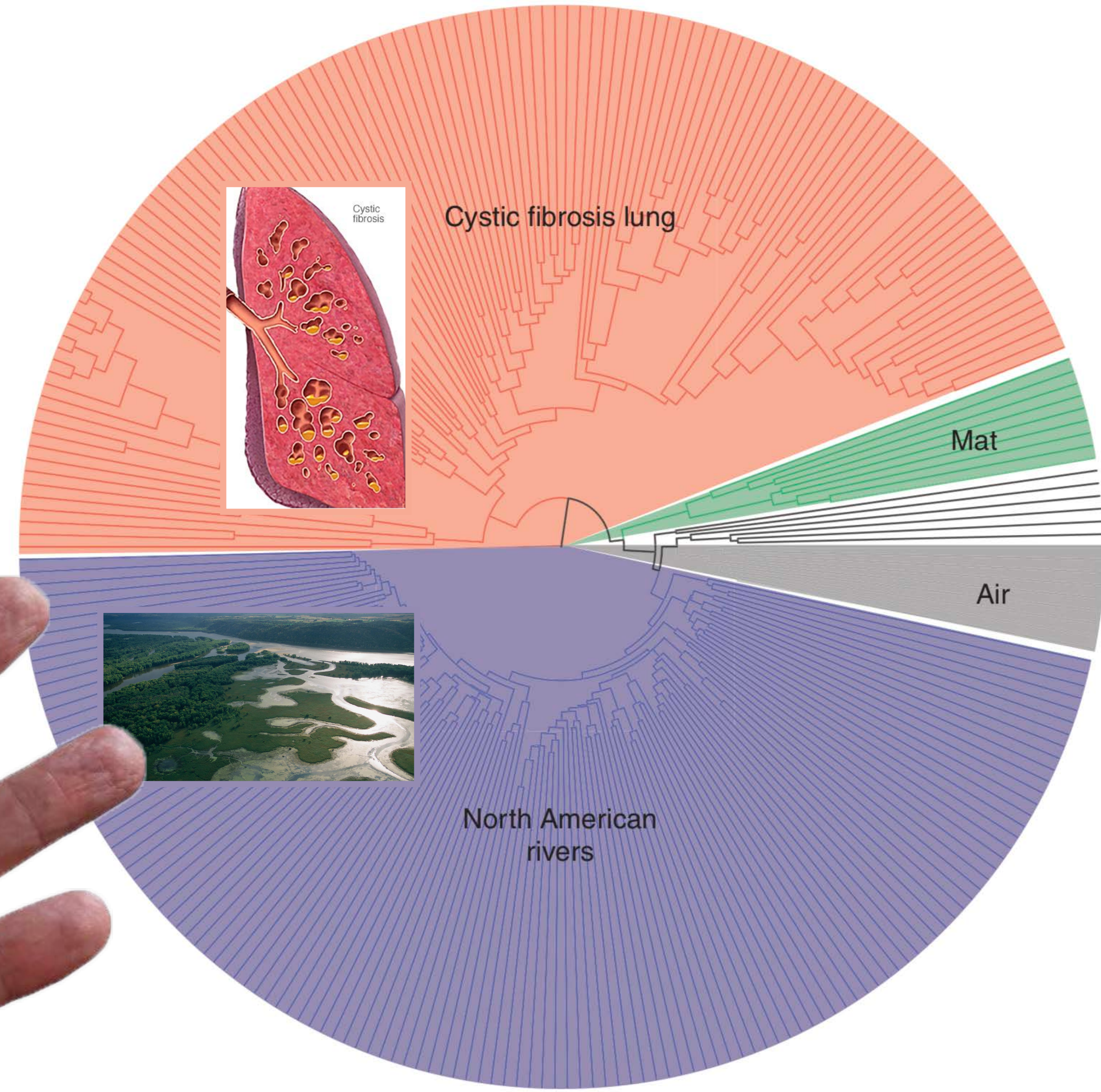
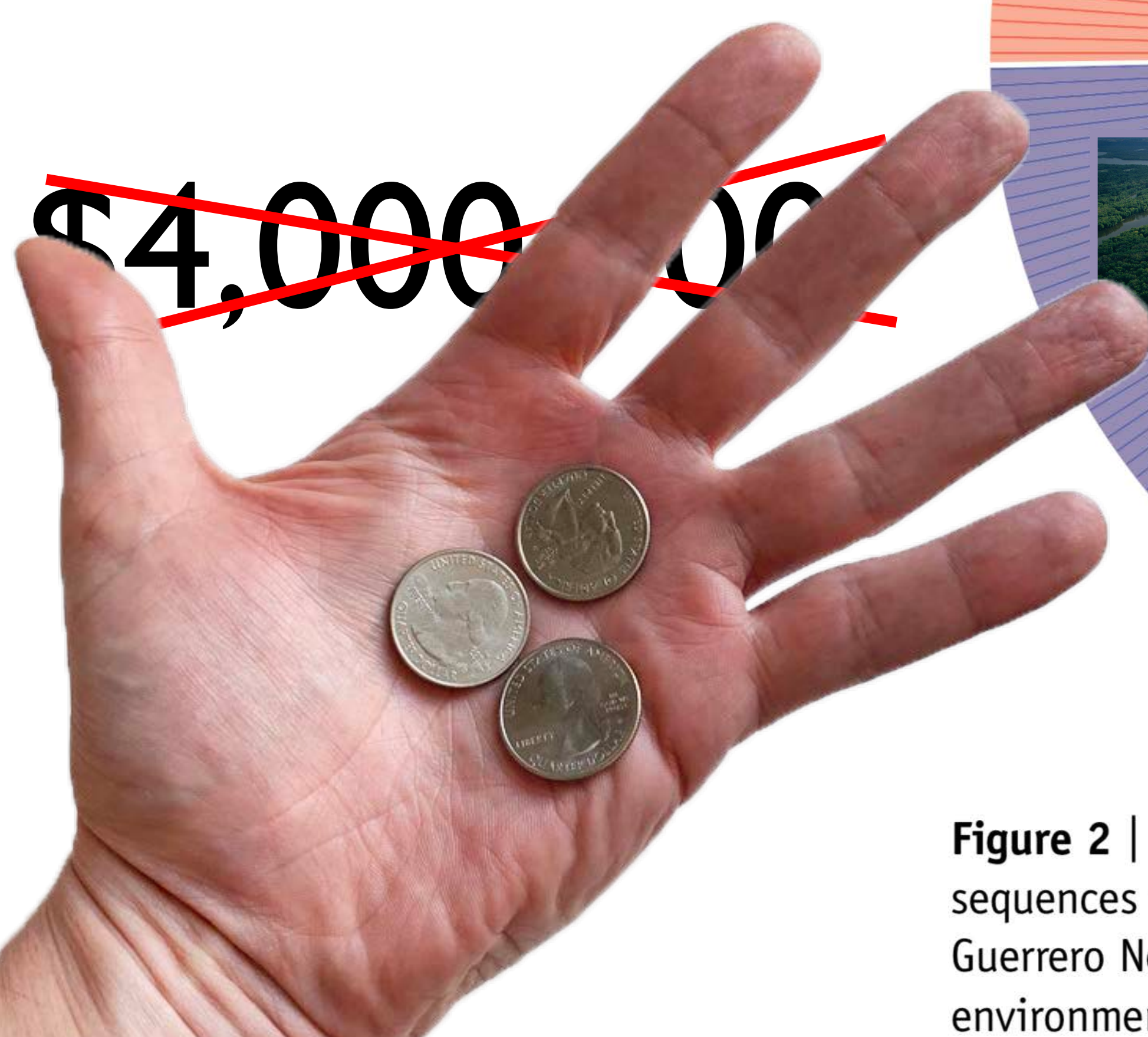
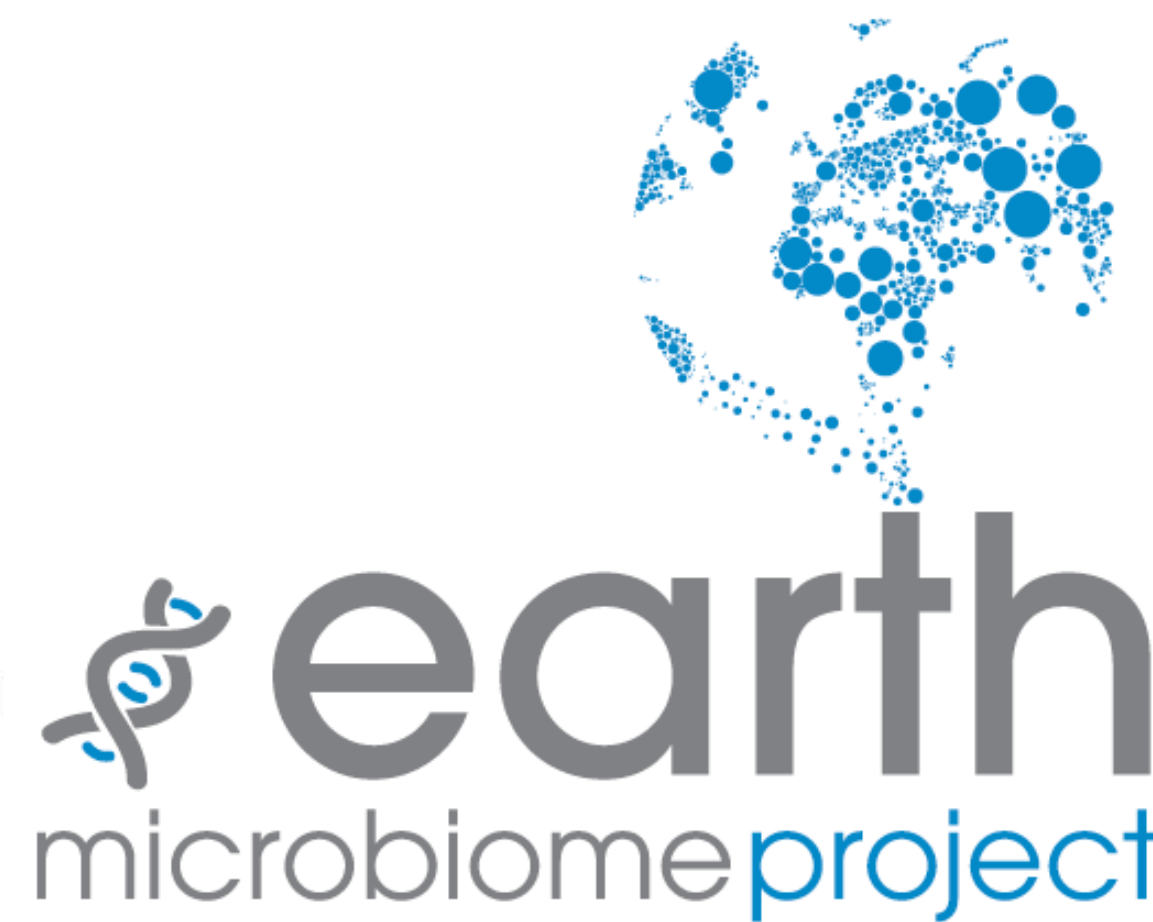


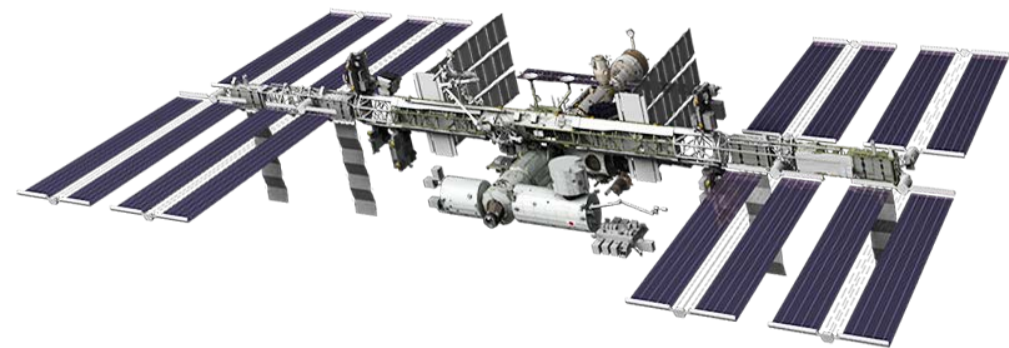
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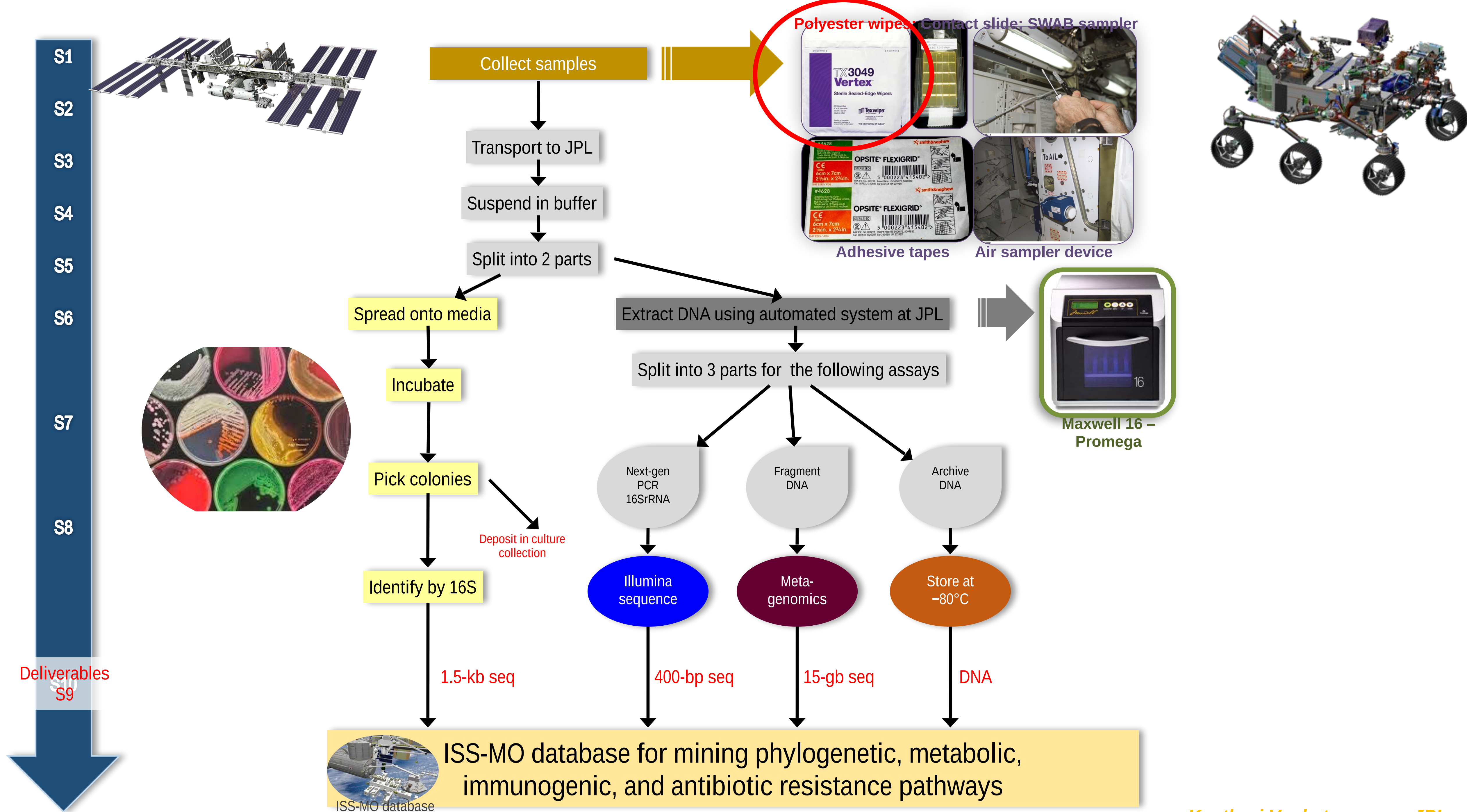


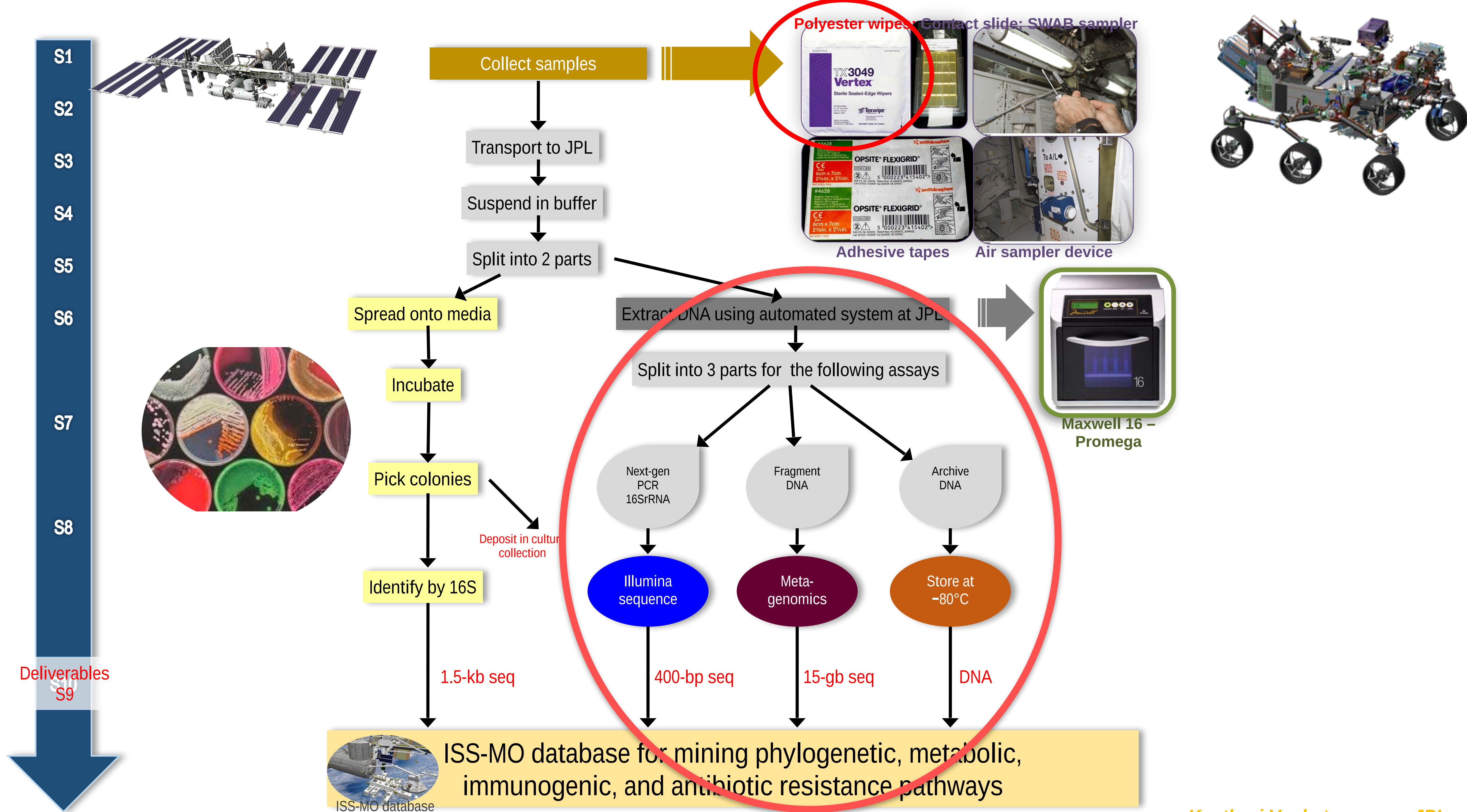
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What does the microbiome have
to do with lunar exploration?

I. Planetary protection: let's not
find life that we put there





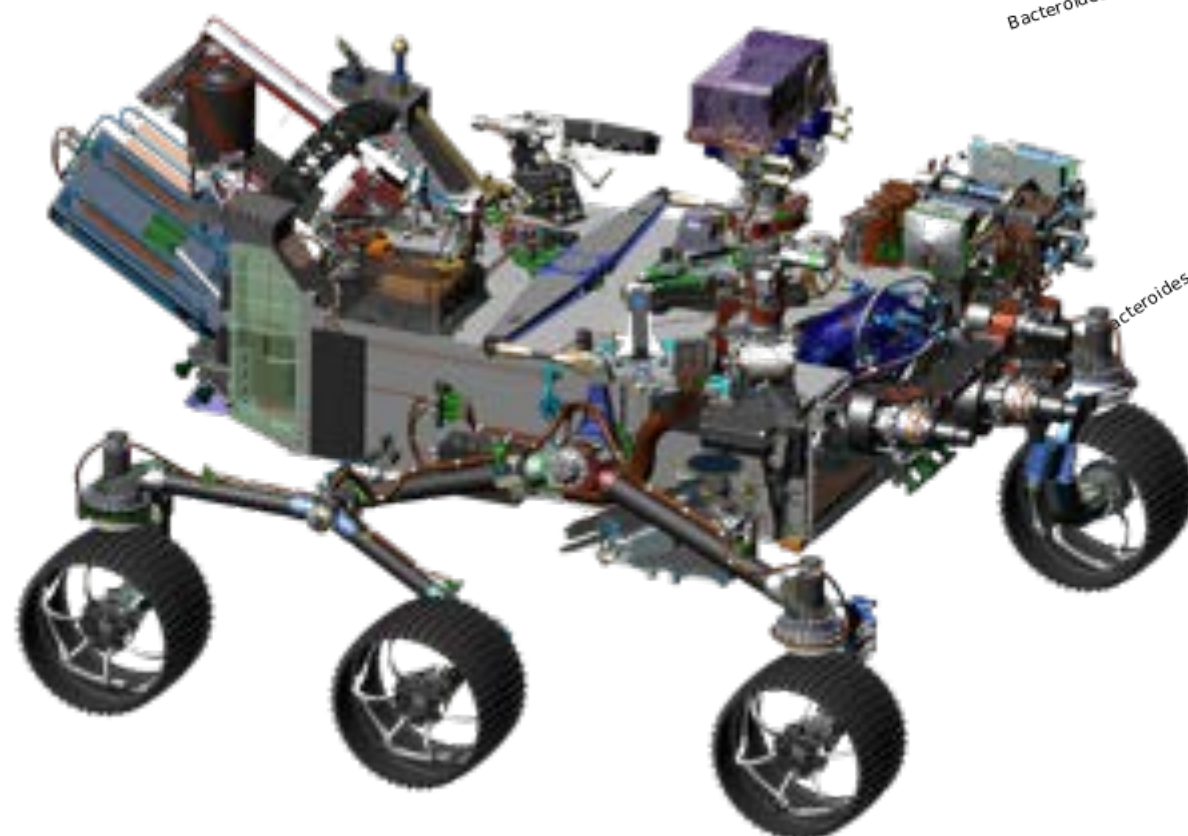
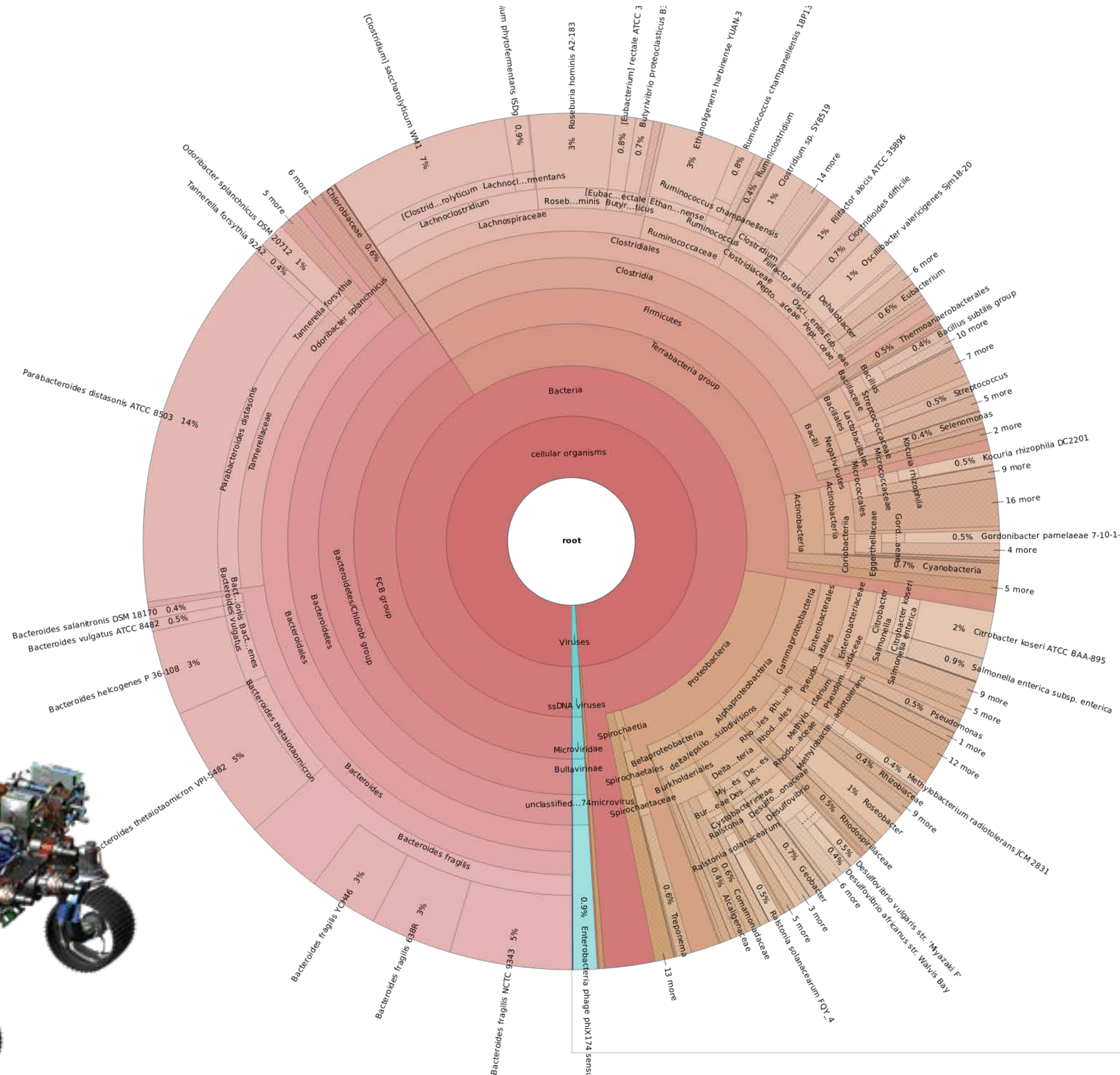


Mars 2020 JPL SAF associated microbiome (a shotgun metagenome approach)

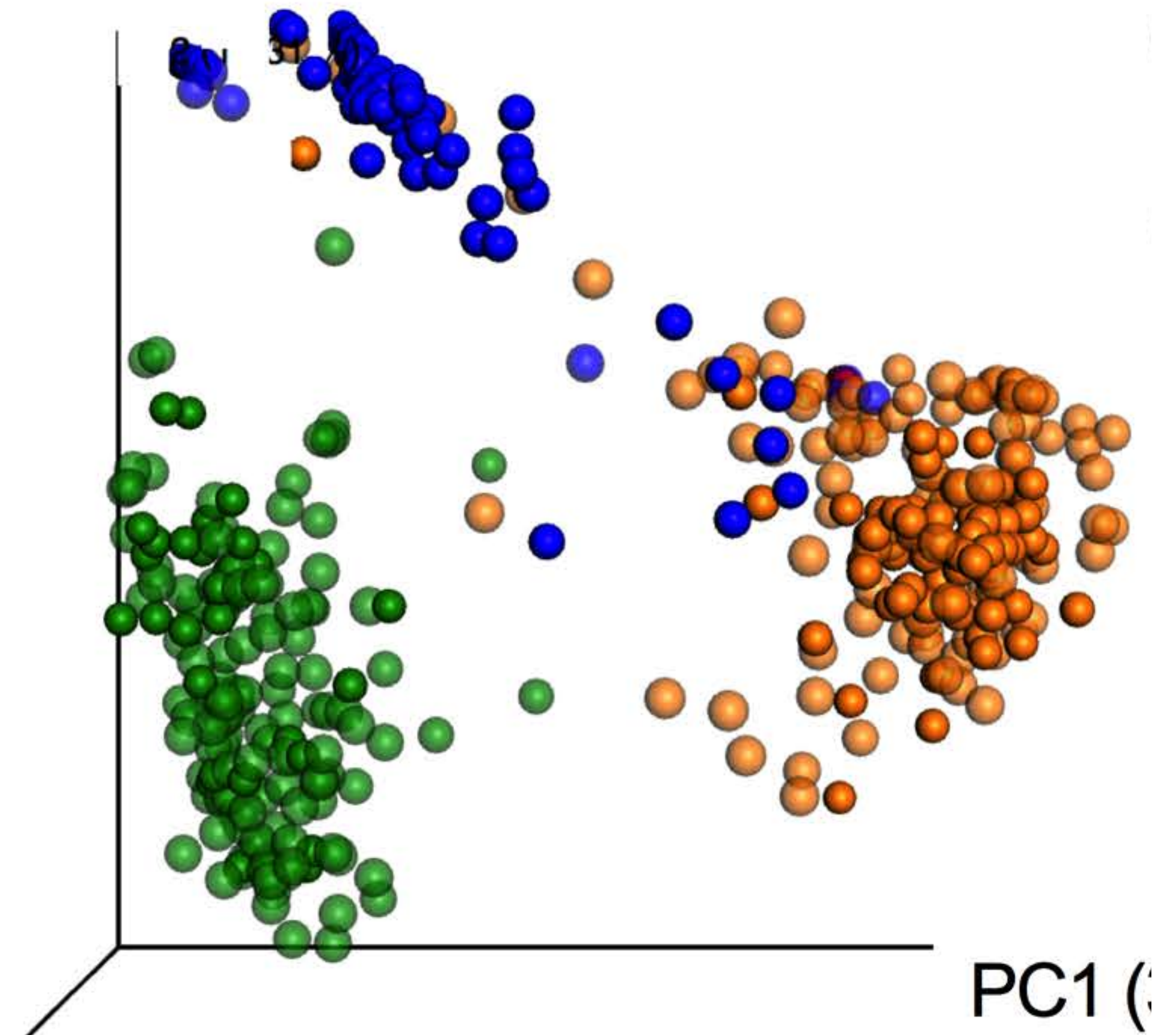
**A bird eye view of SAF
Microbiome. Red – Brown
portion represents Bacteria
while blue represent Fungi,
Archaea and Viruses.**

Bacteria:	5194
Fungi:	282
Archaea:	38
Viruses:	63

PP relevant Group
Firmicutes: 891

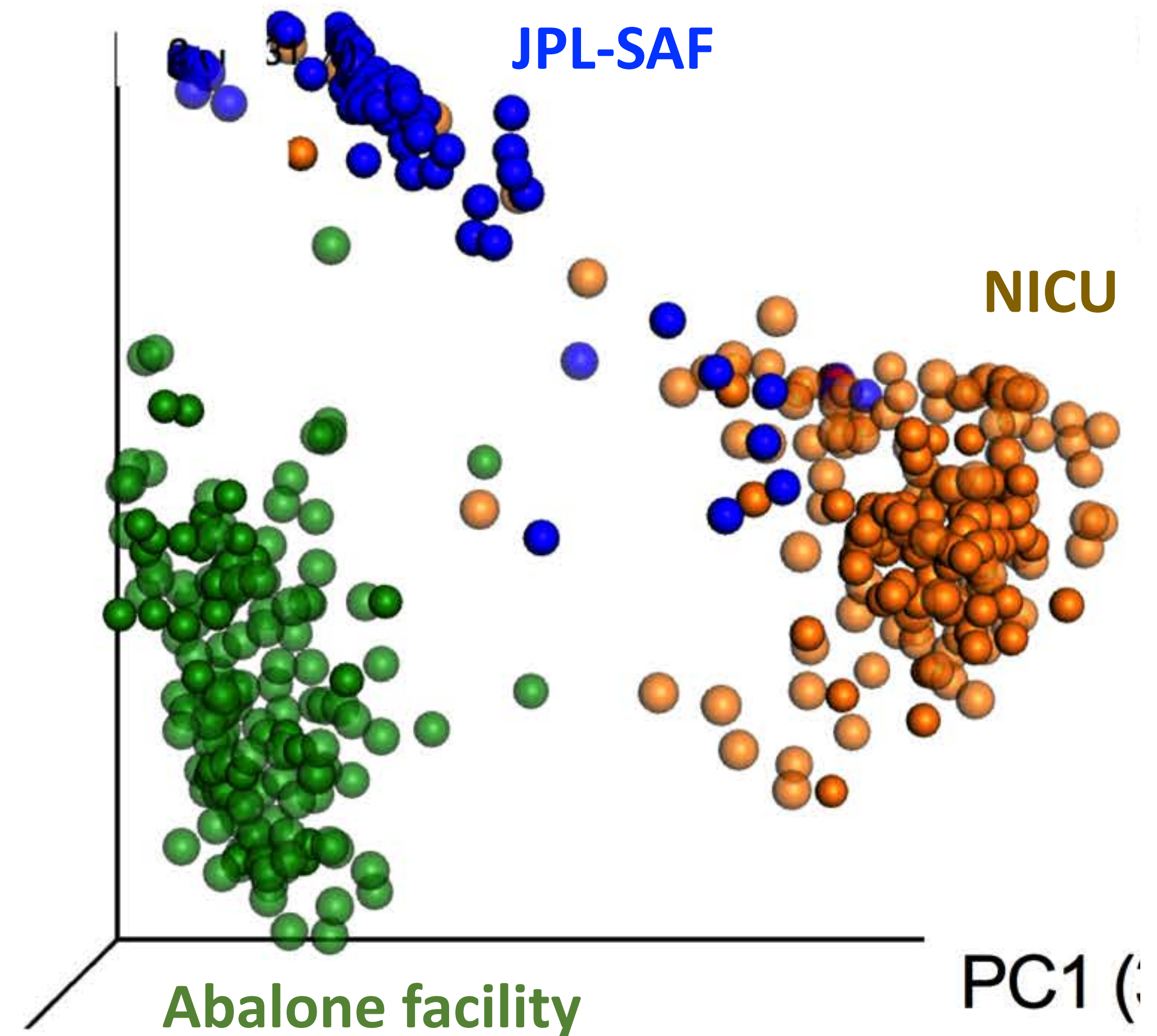


Mars 2020 spacecraft assembly facility microbiome



Minich JJ, Zhu Q, Janssen S, Hendrickson R, Amir A, Vetter R, Hyde J, Doty MM, Stillwell K, Benardini J, Kim, J. H., Allen, E. E., [Venkateswaran, K.](#), Knight, R.: **KatharoSeq Enables High-Throughput Microbiome Analysis from Low-Biomass Samples.** *mSystems* 2018, **3**(3).

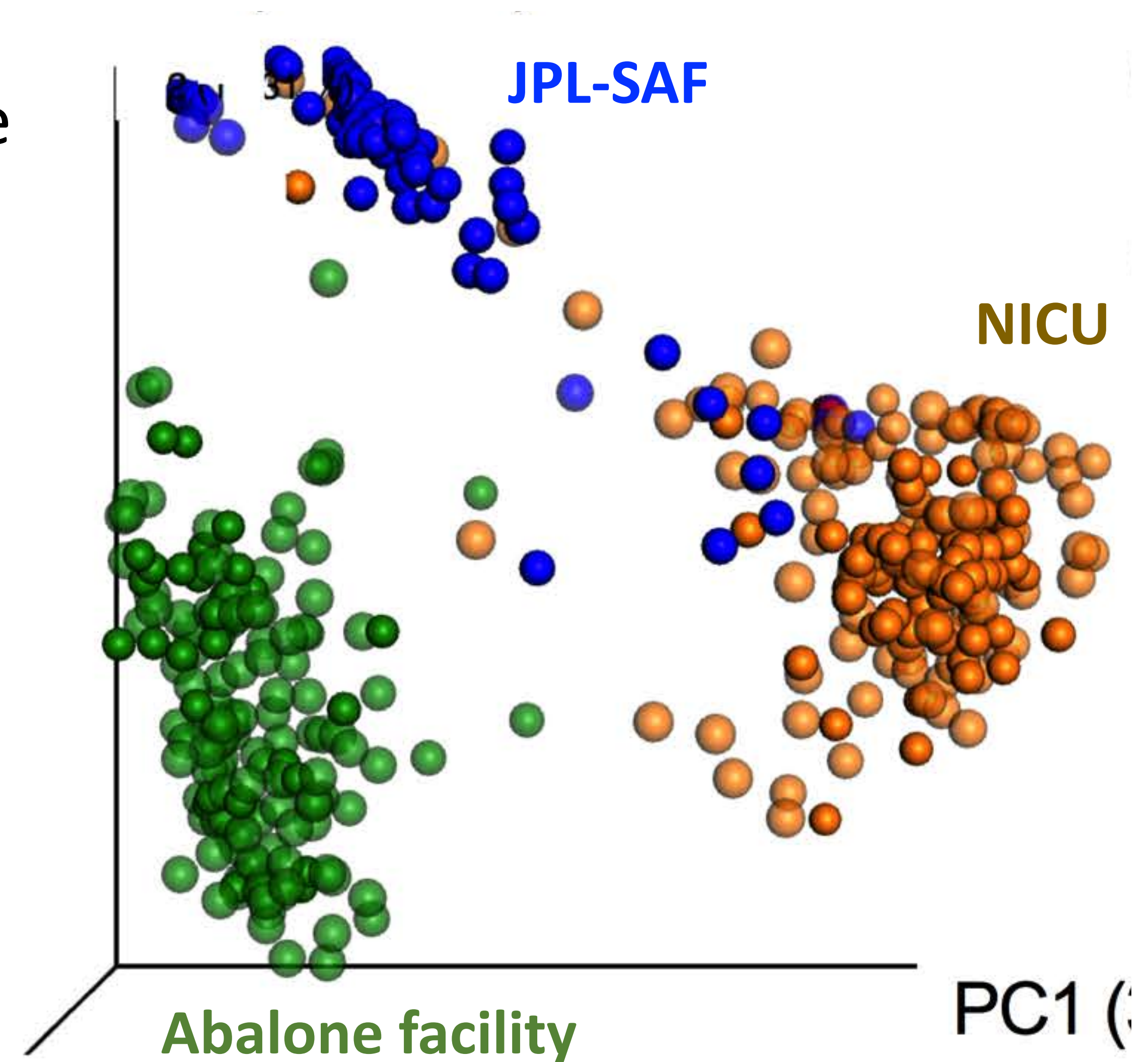
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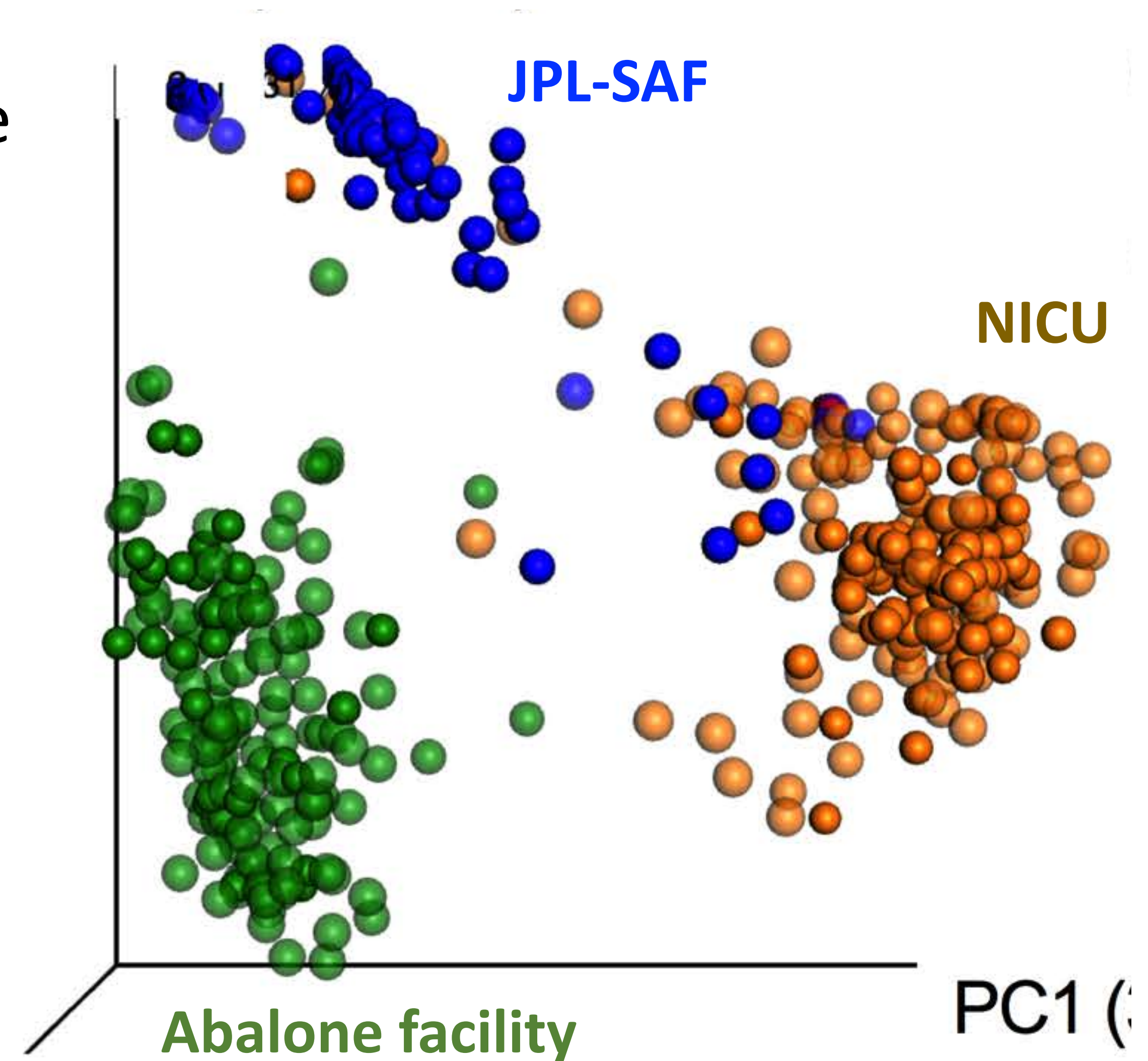
Mars 2020 spacecraft assembly facility microbiome

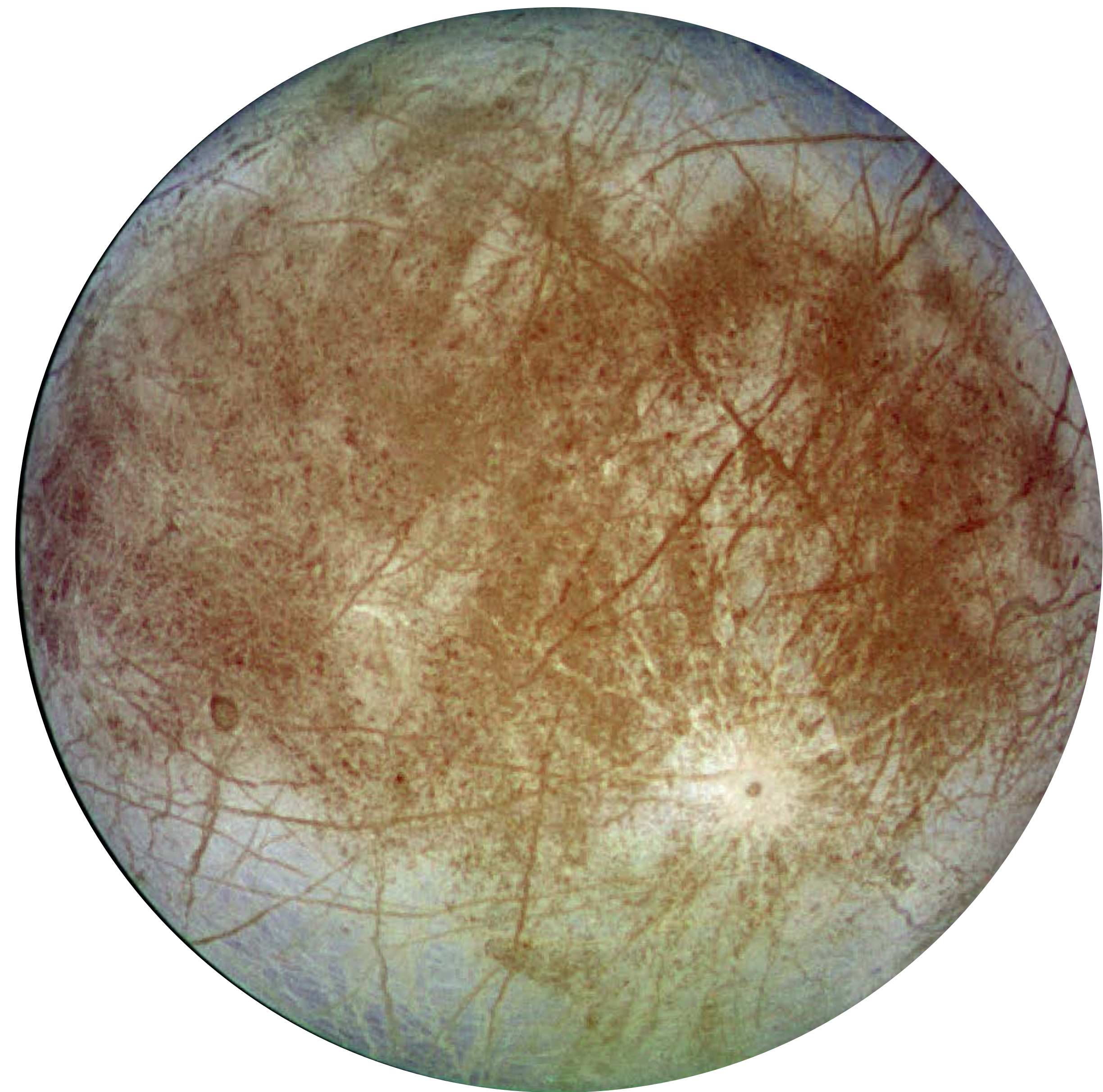
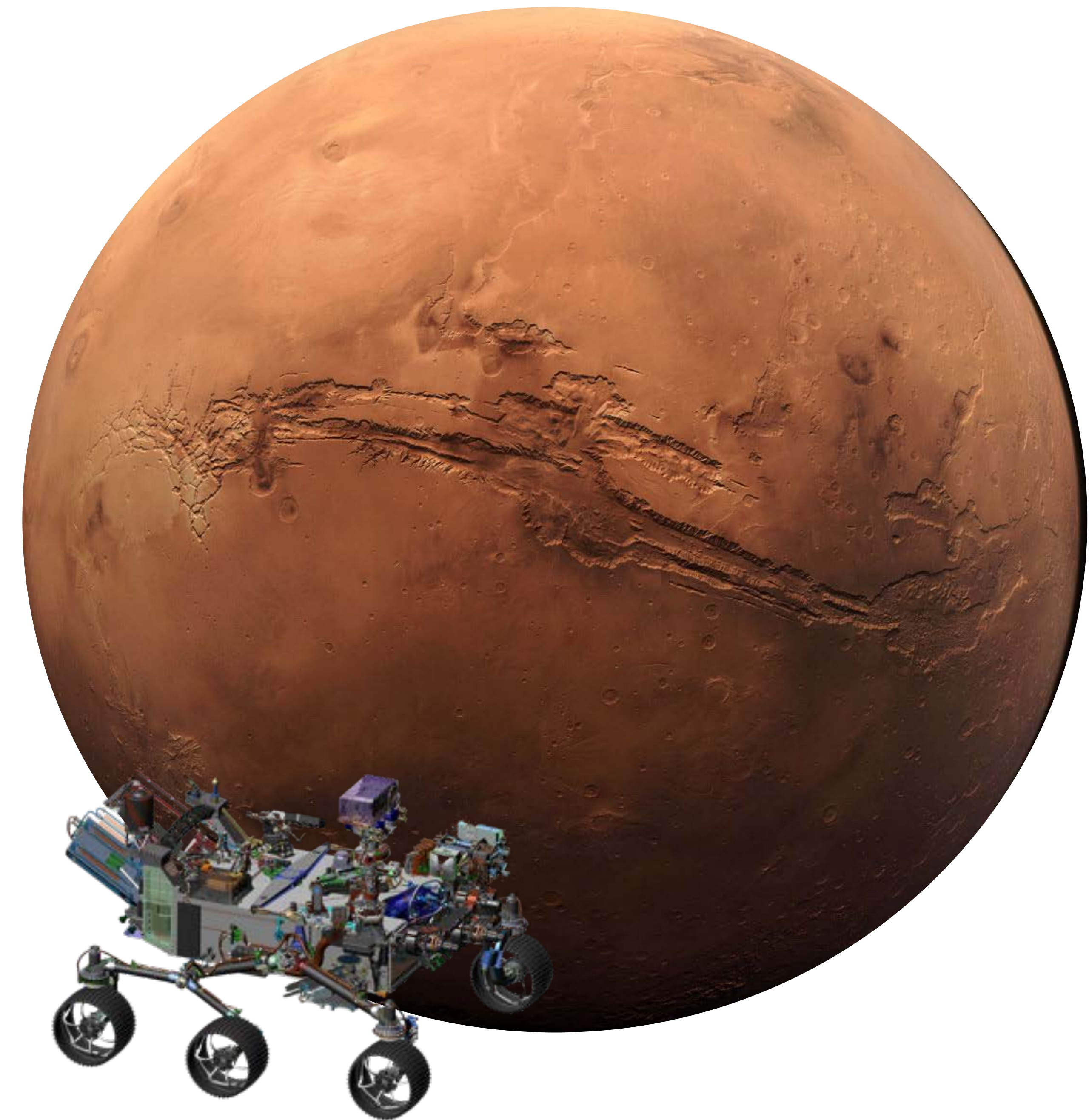
- Among the built environments of neonatal **ICU** and **JPL-SAF** cleanrooms, the alpha diversity measured by microbial taxon richness was highest in the **NICU** than the **JPL-SAF** cleanroom floors.



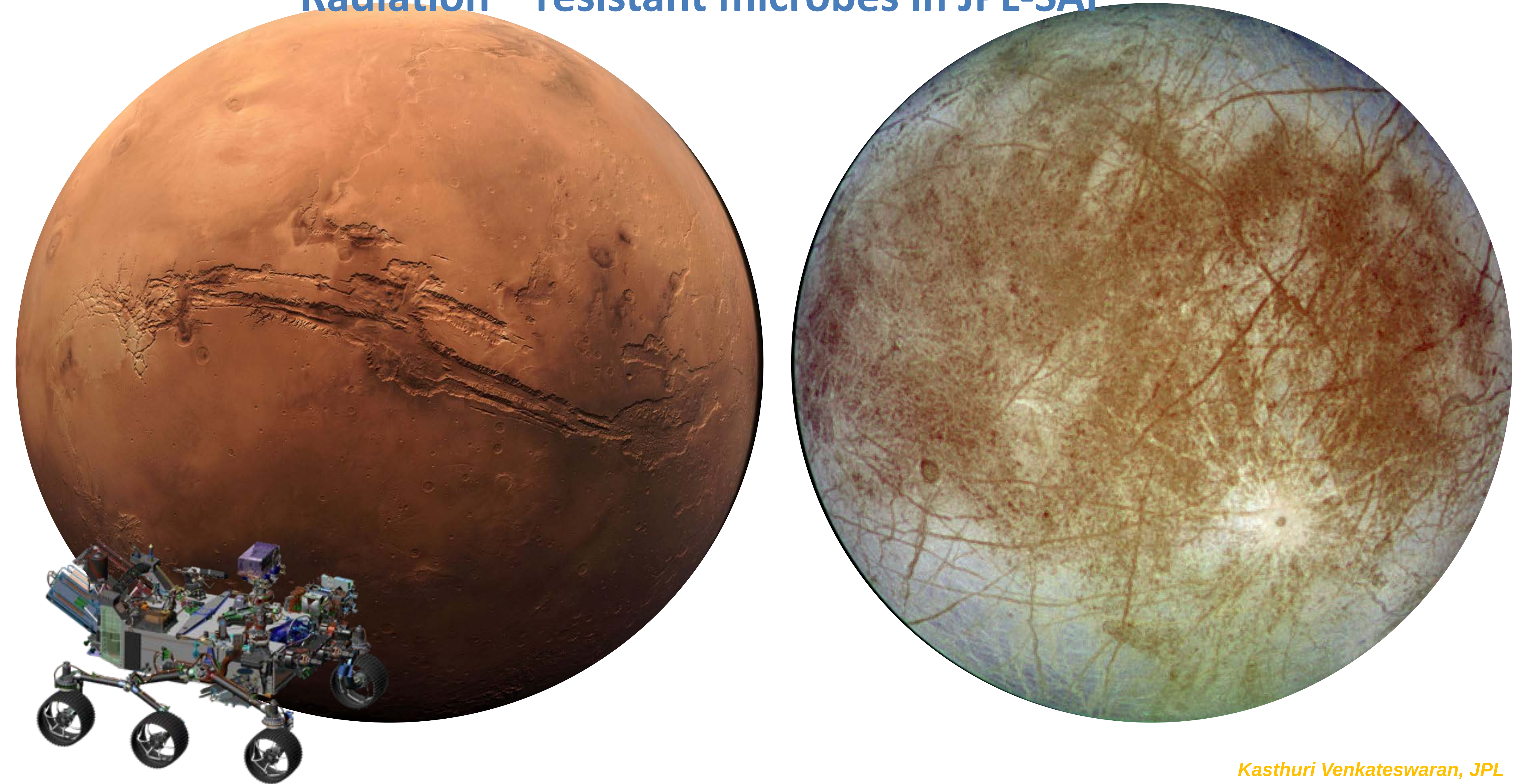
Mars 2020 spacecraft assembly facility microbiome

- Among the built environments of neonatal **ICU** and **JPL-SAF** cleanrooms, the alpha diversity measured by microbial taxon richness was highest in the **NICU** than the **JPL-SAF** cleanroom floors.
- Human exposure was associated with microbial taxon richness, although some of the details differed among the environments.
 - *Klebsiella* and *Staphylococcus* with NICU
 - *Acinetobacter baumannii*, *Acinetobacter equi*, and *Acinetobacter johnsonii* in JPL-SAF floors

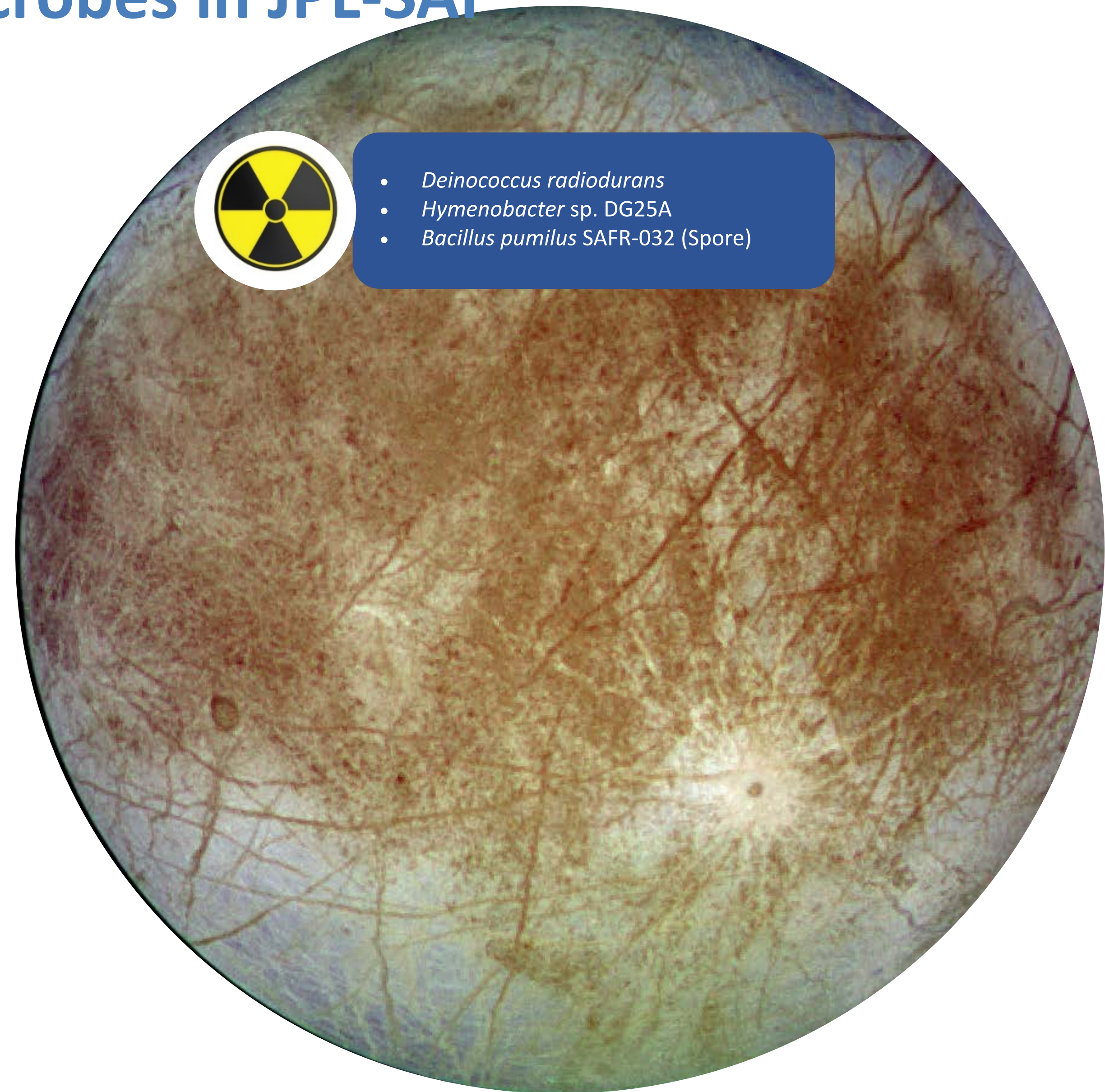
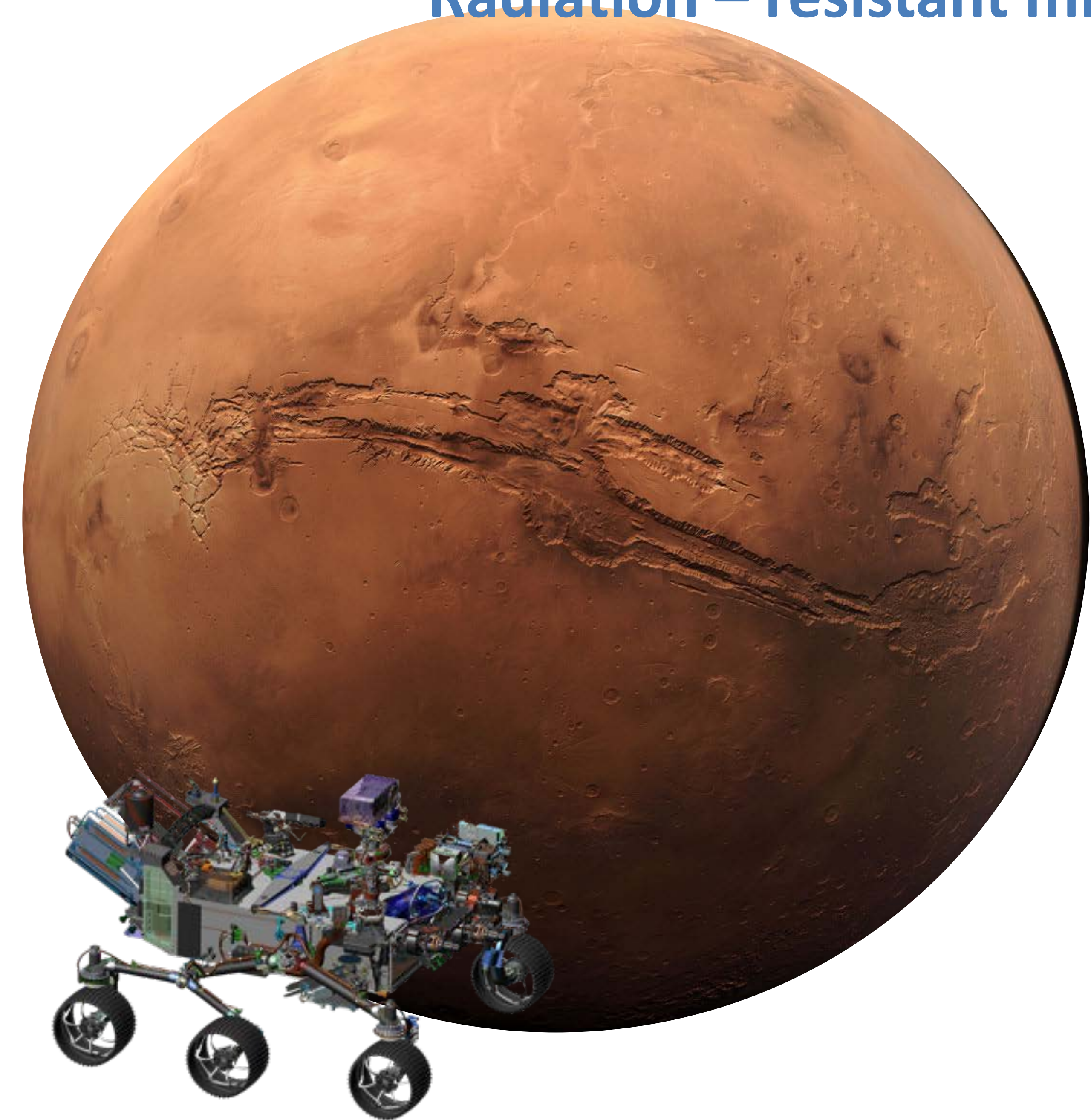




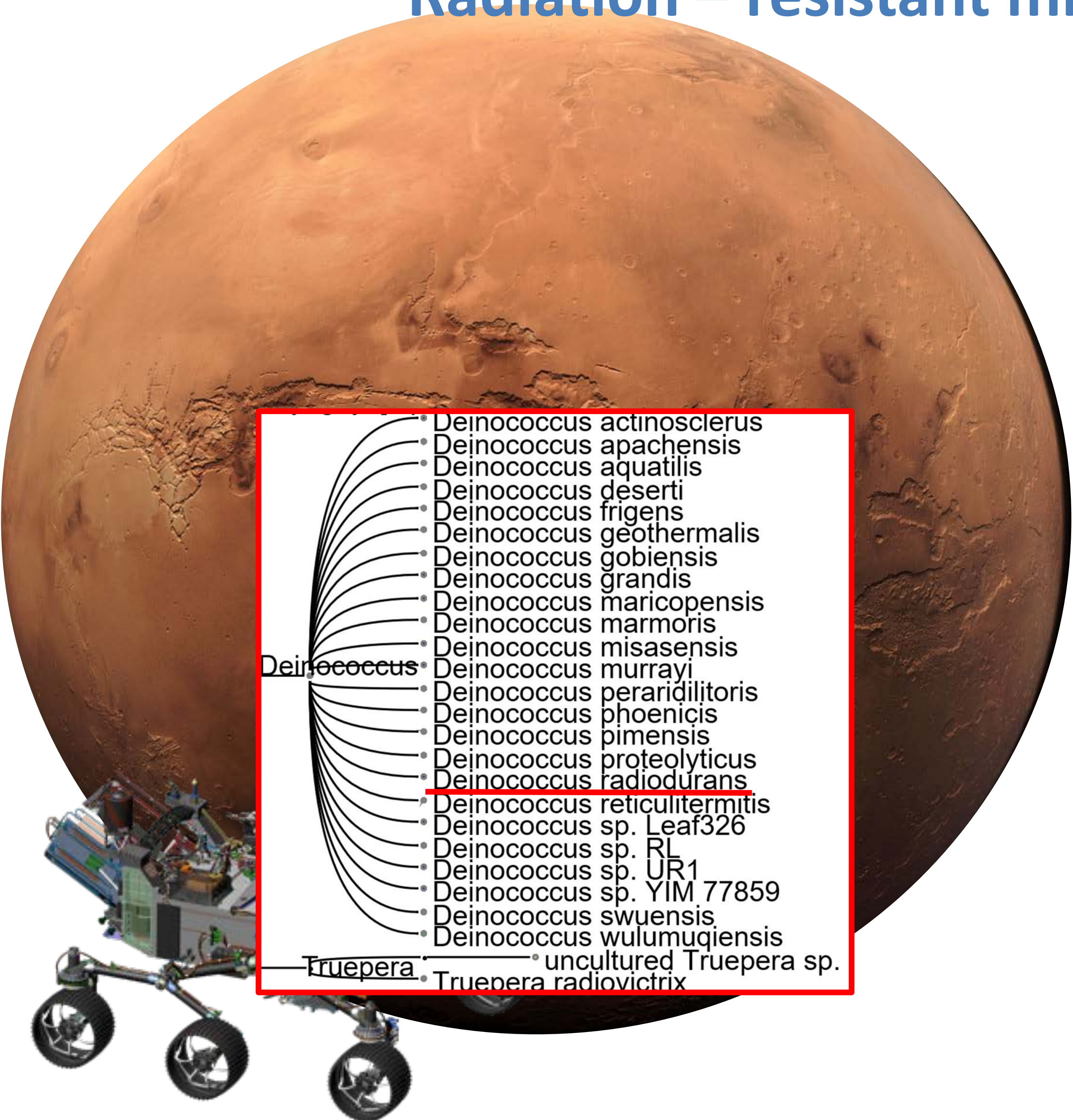
Radiation – resistant microbes in JPL-SAF



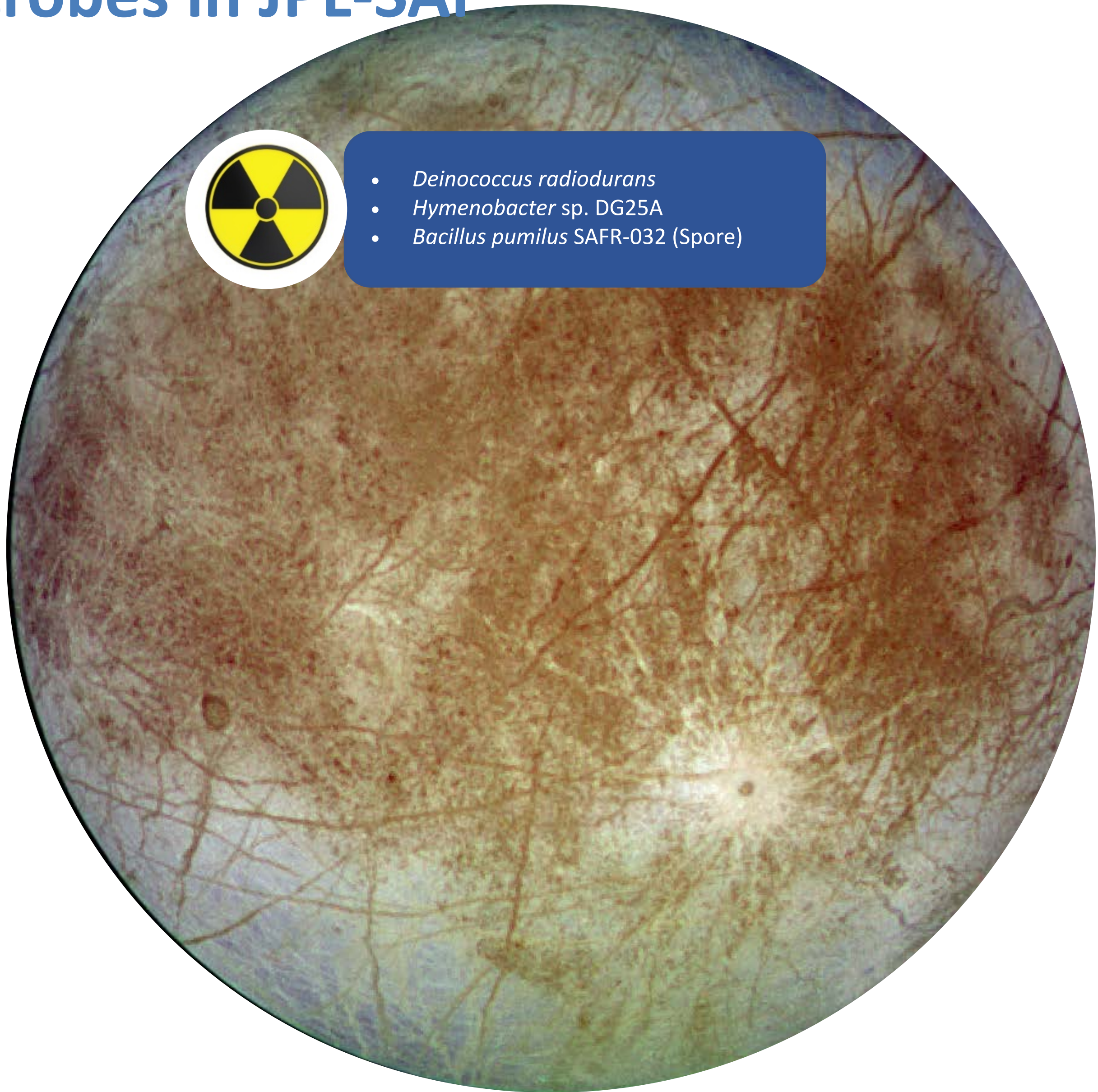
Radiation – resistant microbes in JPL-SAF



Radiation – resistant microbes in JPL-SAF



- Deinococcus actinosclerus
- Deinococcus apachensis
- Deinococcus aquatilis
- Deinococcus deserti
- Deinococcus frigens
- Deinococcus geothermalis
- Deinococcus gobiensis
- Deinococcus grandis
- Deinococcus maricopensis
- Deinococcus marmoris
- Deinococcus misasensis
- Deinococcus murrayi
- Deinococcus peraridilitoris
- Deinococcus phoenicis
- Deinococcus pimensis
- Deinococcus proteolyticus
- Deinococcus radiodurans
- Deinococcus reticulitermitis
- Deinococcus sp. Leaf326
- Deinococcus sp. RL
- Deinococcus sp. UR1
- Deinococcus sp. YIM 77859
- Deinococcus swuensis
- Deinococcus wulumuqiensis
- Trueperera uncultured Trueperera sp.
- Trueperera radiovictrix



- *Deinococcus radiodurans*
- *Hymenobacter* sp. DG25A
- *Bacillus pumilus* SAFR-032 (Spore)

Radiation – resistant microbes in JPL-SAF



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Deinococcus

- *Deinococcus actinosclerus*
- *Deinococcus apachensis*
- *Deinococcus aquatilis*
- *Deinococcus deserti*
- *Deinococcus frigens*
- *Deinococcus geothermalis*
- *Deinococcus gobiensis*
- *Deinococcus grandis*
- *Deinococcus maricopensis*
- *Deinococcus marmoris*
- *Deinococcus misasensis*
- *Deinococcus murrayi*
- *Deinococcus peraridilitoris*
- *Deinococcus phoenicis*
- *Deinococcus pimensis*
- *Deinococcus proteolyticus*
- *Deinococcus radiodurans*
- *Deinococcus reticulitermitis*
- *Deinococcus* sp. Leaf326
- *Deinococcus* sp. RL
- *Deinococcus* sp. UR1
- *Deinococcus* sp. YIM 77859
- *Deinococcus swuensis*
- *Deinococcus wulumuqiensis*

Truepera

- *uncultured Truepera* sp.
- *Truepera radiovictrix*

Hymenobacteraceae

Hymenobacter

- *Hymenobacter actinosclerus*
- *Hymenobacter aerophilus*
- *Hymenobacter norwichensis*
- *Hymenobacter psychrophilus*
- *Hymenobacter sedentarius*
- *Hymenobacter* sp. APR13
- *Hymenobacter* sp. AT01-02
- *Hymenobacter* sp. DG25A
- *Hymenobacter* sp. DG25B
- *Hymenobacter* sp. IS2118
- *Hymenobacter* sp. PAMC 26554
- *Hymenobacter* sp. PAMC 26628
- *Hymenobacter* sp. unc380mfsha3.1
- *Hymenobacter swuensis*
- *Hymenobacter terrenus*

Pontibacter

- *Pontibacter actiniarum*
- *Pontibacter akesuensis*
- *Pontibacter chinhatensis*

Rufibacter

- *Rufibacter roseus*
- *Rufibacter ruber*
- *Rufibacter* sp. DG15C
- *Rufibacter* sp. DG31D
- *Rufibacter tibetensis*

Siccationidurans arizonensis

Radiation – resistant microbes in JPL-SAF

Deinococcus actinotransformans
Deinococcus apacheyensis
Deinococcus aquatilis
Deinococcus deserti
Deinococcus frigida
Deinococcus geothermophilus
Deinococcus gobiensis
Deinococcus grandis
Deinococcus maricopaensis
Deinococcus marmarissinus
Deinococcus misasensis
Deinococcus murrayi
Deinococcus perarabius
Deinococcus phoenicis
Deinococcus pimerianus
Deinococcus proteolyticus
Deinococcus radiodurans
Deinococcus reticulatus
Deinococcus sp. Leptotrichia
Deinococcus sp. R1
Deinococcus sp. U1
Deinococcus sp. Y1
Deinococcus swuensis
Deinococcus wulumensis
Trueperia uncultured
Trueperia radiovictriculata

Bacillus circulans
Bacillus clausii
Bacillus coagulans
Bacillus dielmoensis
Bacillus eiseniae
Bacillus endophyticus
Bacillus firmus
Bacillus flexus
Bacillus fordii
Bacillus fumarioli
Bacillus humi
Bacillus krulwichiae
Bacillus mannanolyticus
Bacillus marisnigellus
Bacillus massiliogorillae
Bacillus megaterium
Bacillus mesonae
Bacillus niacini
Bacillus okhensis
Bacillus persicus
Bacillus pumilus
Bacillus simplex
Bacillus smithii
Bacillus soli
Bacillus sp. 103mf
Bacillus sp. 105MF
Bacillus sp. 123MFChir2
Bacillus sp. 171095_106
Bacillus sp. 1NLA3E
Bacillus sp. 2_A_57_CT2
Bacillus sp. 95MFCvi2.1
Bacillus sp. Aph1
Bacillus sp. EB01
Bacillus sp. ES3
Bacillus sp. FJAT-14578
Bacillus sp. FJAT-21351
Bacillus sp. FJAT-27225
Bacillus sp. FJAT-27916
Bacillus sp. FJAT-27986
Bacillus sp. FJAT-28004
Bacillus sp. FJAT-29814
Bacillus sp. GeD10
Bacillus sp. H1a
Bacillus sp. HMSC76G11
Bacillus sp. J37
Bacillus sp. L27
Bacillus sp. Leaf75
Bacillus sp. MUM_13
Bacillus sp. OV194
Bacillus sp. Root147
Bacillus sp. Root239
Bacillus sp. Soil531
Bacillus sp. Soil745
Bacillus sp. UNC41MES5



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Siccationidurans arizonensis

2. Creating a healthy built environment on the moon

Sloan Program on Microbiology of the Built Environment

microBEnet is funded by a grant from the Alfred P. Sloan Foundation as part of their [program on the Microbiology of the Built Environment](#).

A conversation with Paula Olsiewski, program director, Alfred P. Sloan Foundation program on the Microbiology of the Built Environment

What is the Foundation's program on the Microbiology of the Built Environment?

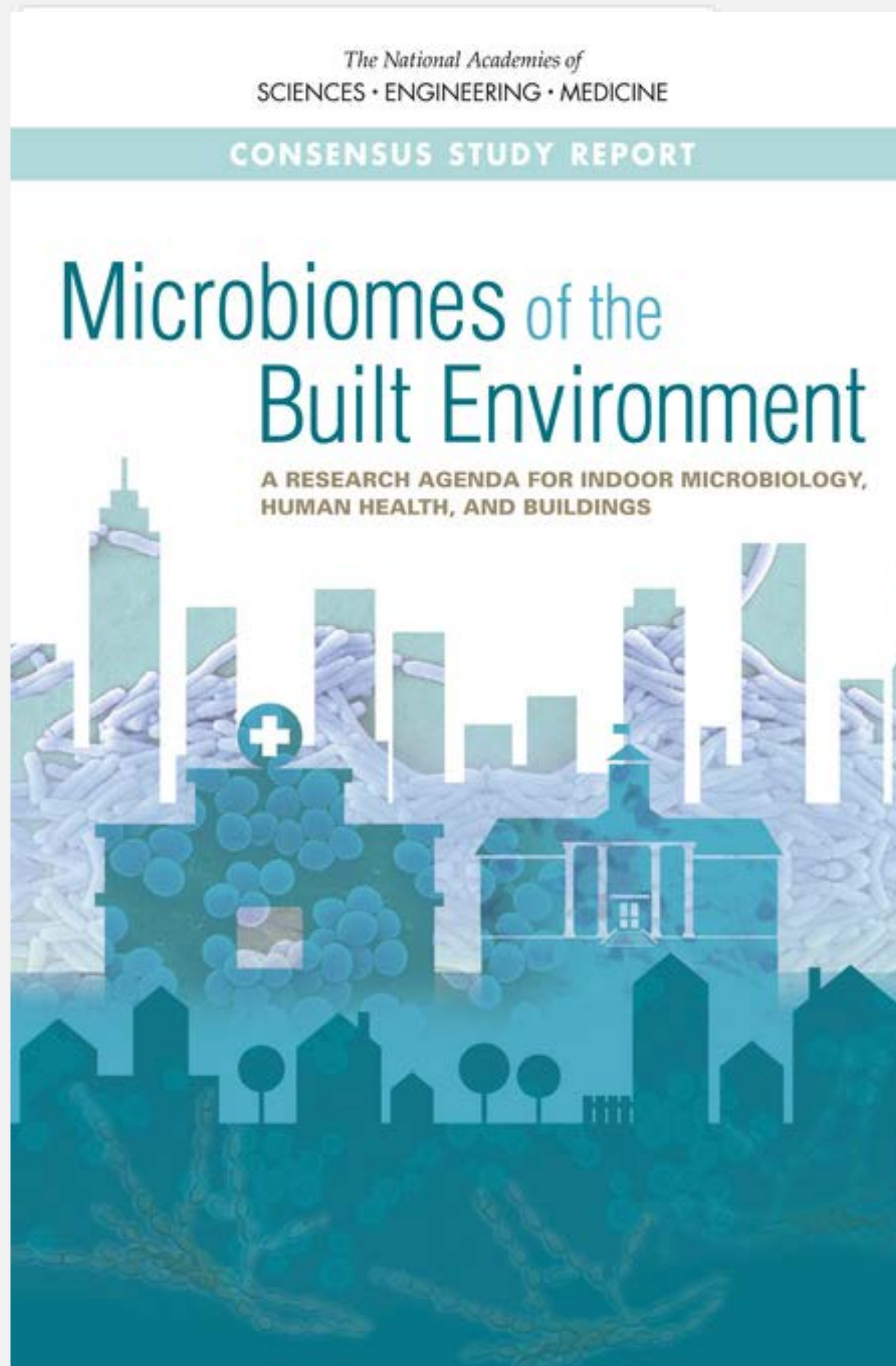
The Alfred P. Sloan Foundation is funding an emerging field of scientific inquiry — the microbiology of the built environment. Science knows a lot about microbiology in the natural environment, but we know next to nothing about the complex microbial ecosystems found in the built environment.

The Sloan Foundation is funding basic science to better understand the trillions of life forms invisible to the naked eye in our homes and workplaces, hospitals and schools — any form of built environment — office buildings, airplanes, subways systems, you name it.

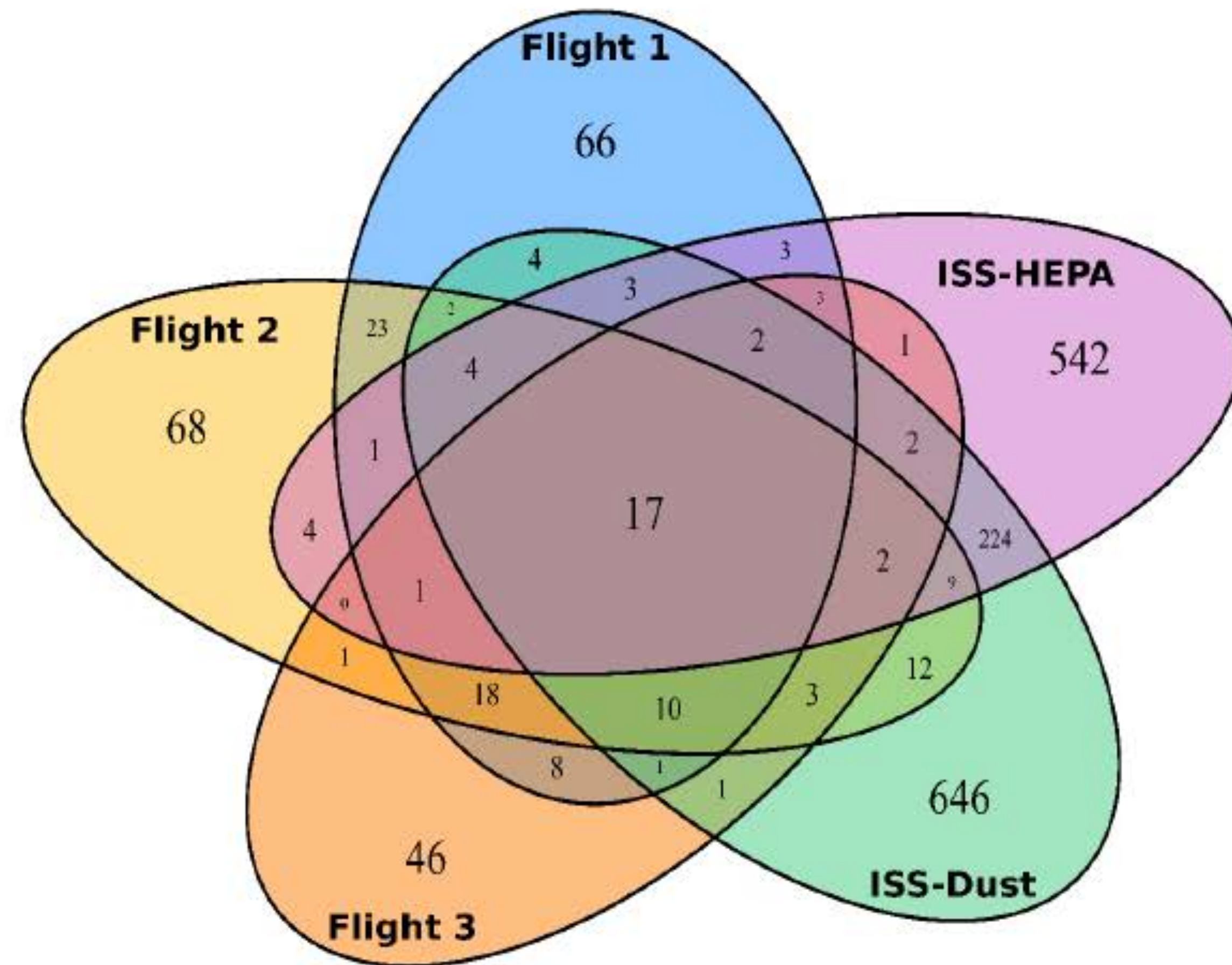
Why study the built environment?

People spend more than 90% of their time indoors, where we breathe in and come in contact with trillions of microorganisms – life forms invisible to the naked eye. These tiny creatures live inside and have probably been there from the beginning of construction. But they also come in through windows and mechanical systems such as heating and air-conditioning systems, and are brought inside by humans and other creatures, which are constantly shedding microbes.

Our homes and workplaces, hospitals and schools are quite literally complex ecosystems filled with a variety of microbes. Given the amount of time we spend indoors it's important to understand what is living in these environments, how these microorganisms interact, what the potential implications are for human health, both positive and negative. We may also learn things that could influence building construction practices and inform other industrial processes.

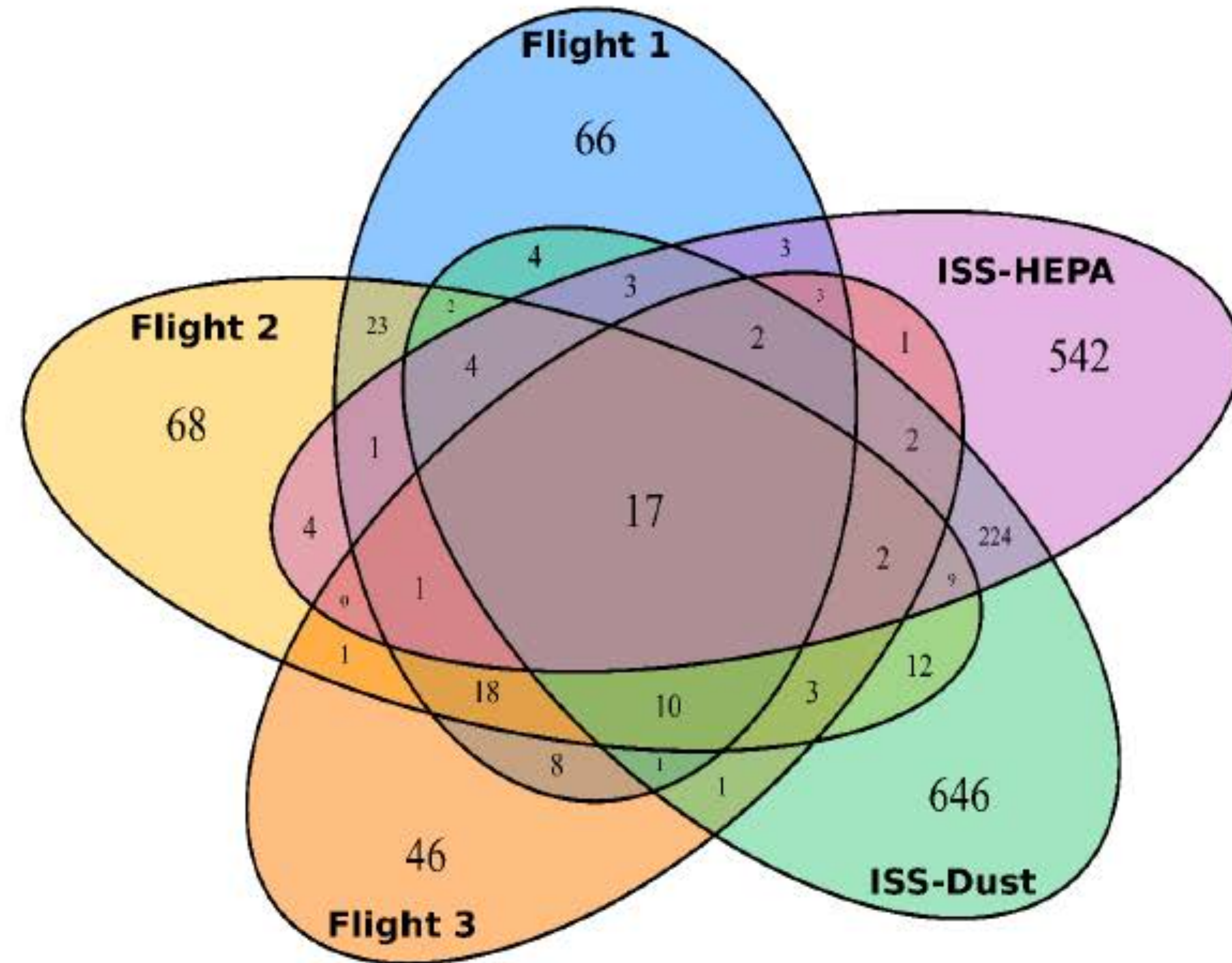


Core microbiome of ISS (metagenome sequencing)

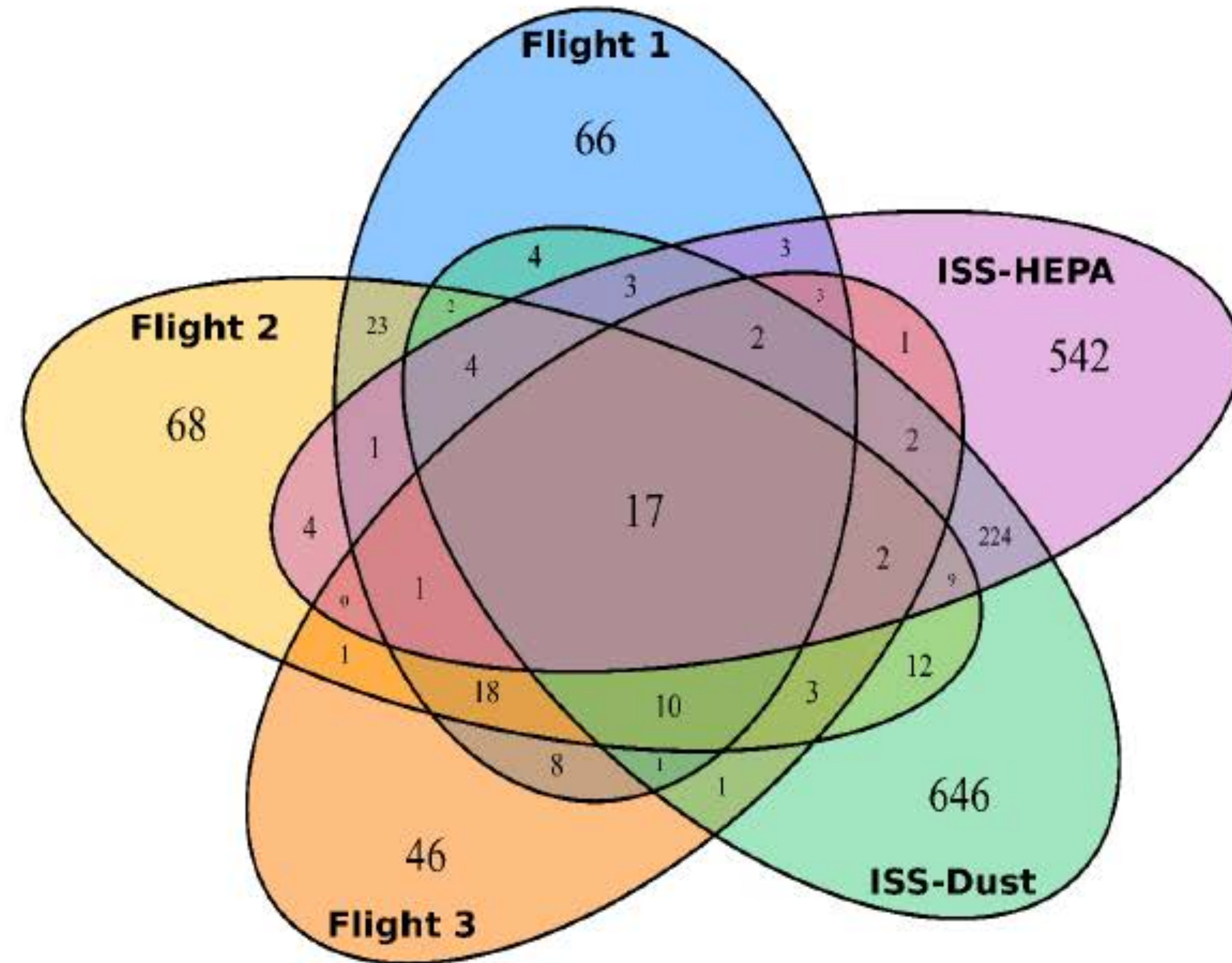


Core microbiome of ISS (metagenome sequencing)

- The ISS microbiome is unique to a particular subsystem but also some microbial species are common (core microbiome; 17 species).

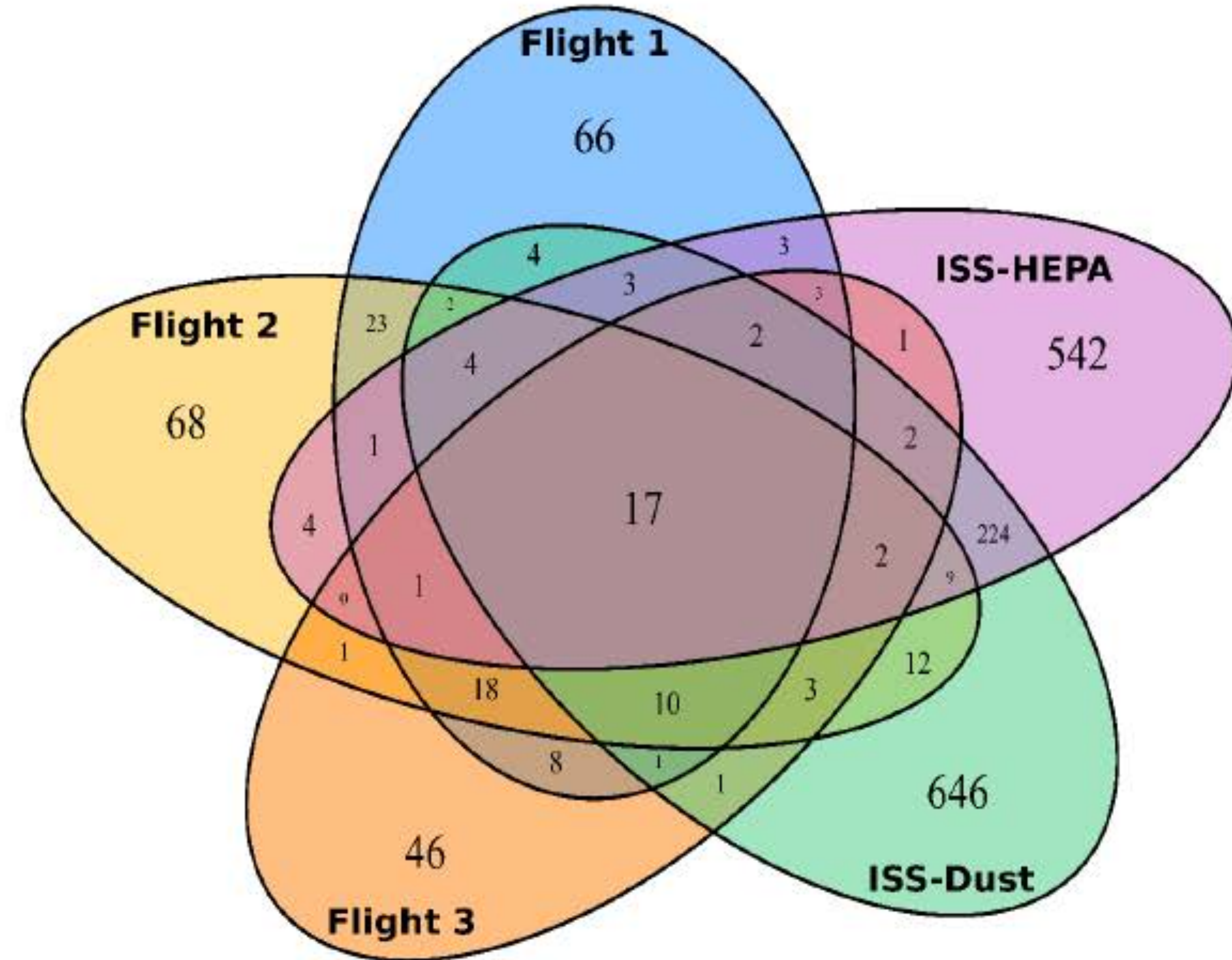


Core microbiome of ISS (metagenome sequencing)



- The ISS microbiome is unique to a particular subsystem but also some microbial species are common (core microbiome; 17 species).
- Dominant ISS core microbiome:
 - Fungi (*P. brasilianum*, *P. chrysogenum*, *P. digitatum*, *P. expansum*, *P. freii*, *P. griseofulvum*, *P. roqueforti*, *P. rubens*, *A. calidoustus*, and *A. niger*).
 - Bacteria (*E. cloacae*, *E. coli*, *P. ananatis*, *S. enterica*, *S. aureus*, and *S. epidermidis*).

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 - Bacteria (*E. cloacae*, *E. coli*, *P. ananatis*, *S. enterica*, *S. aureus*, and *S. epidermidis*).
- Compare with other microbiome studies:
 - The ISS microbiome represents a "minimal core" human model in which all the human subjects shared few microbial species, large overlaps were found in subsets but a very little was common between all the sets.

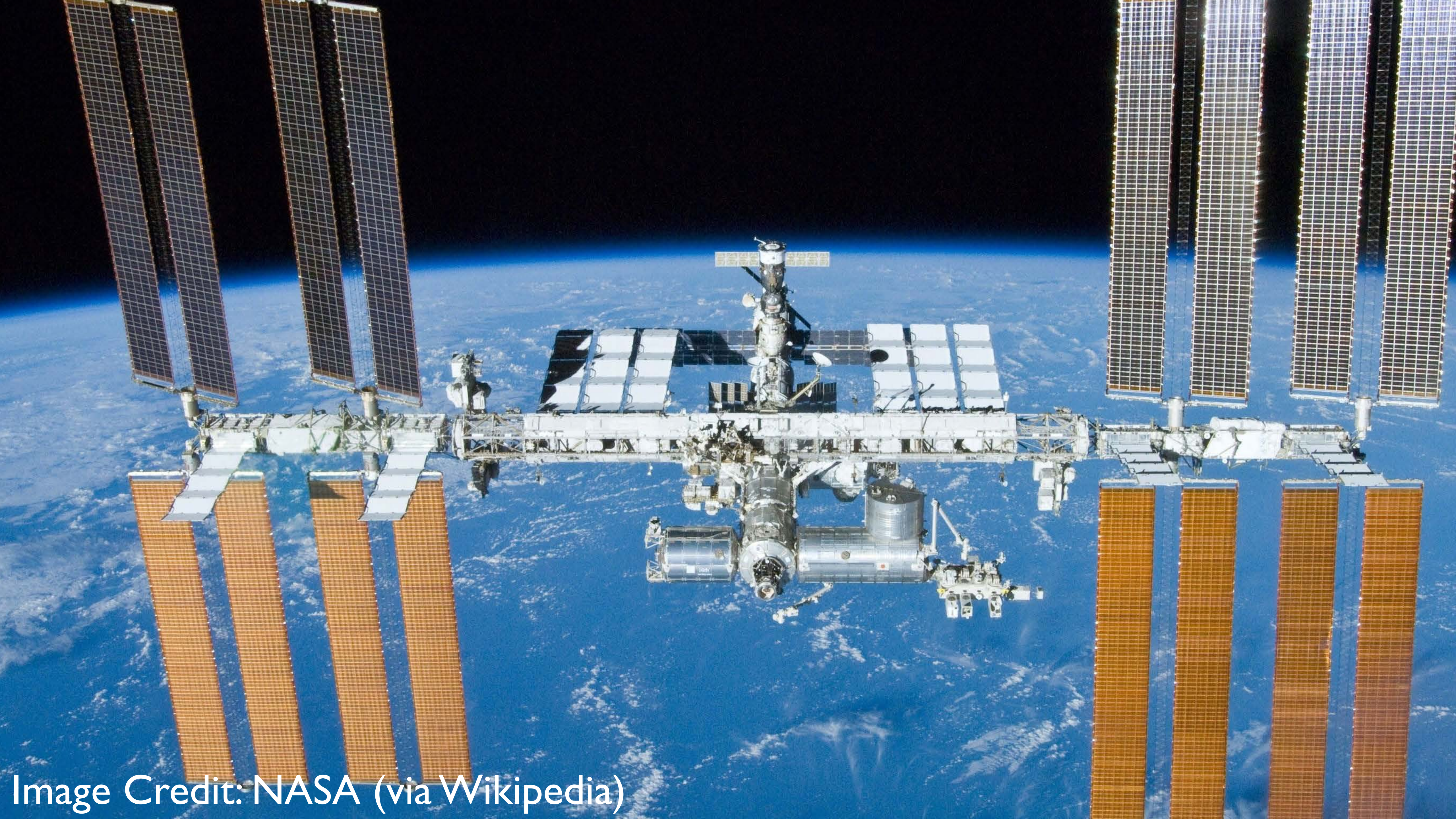


Image Credit: NASA (via Wikipedia)

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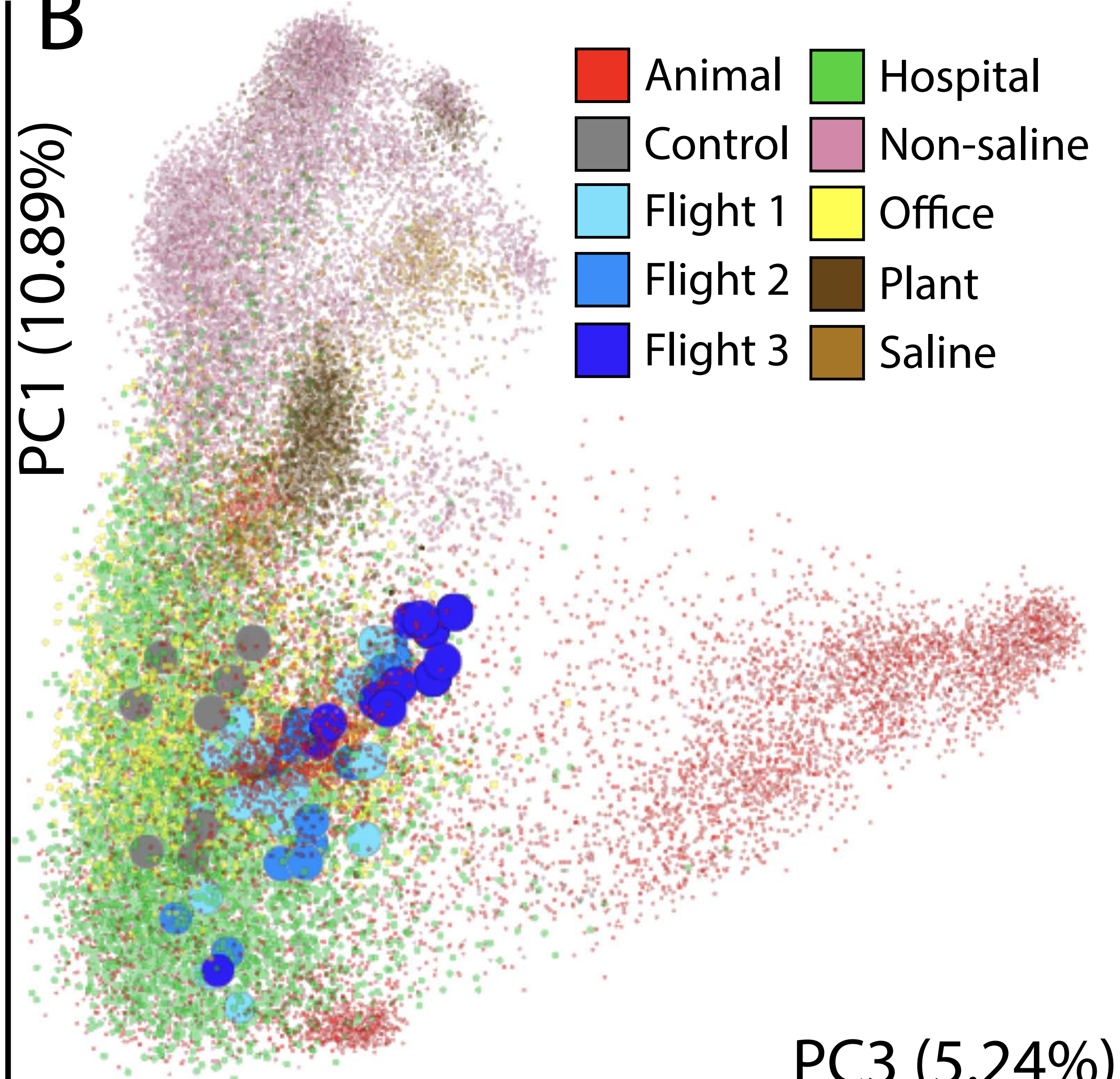
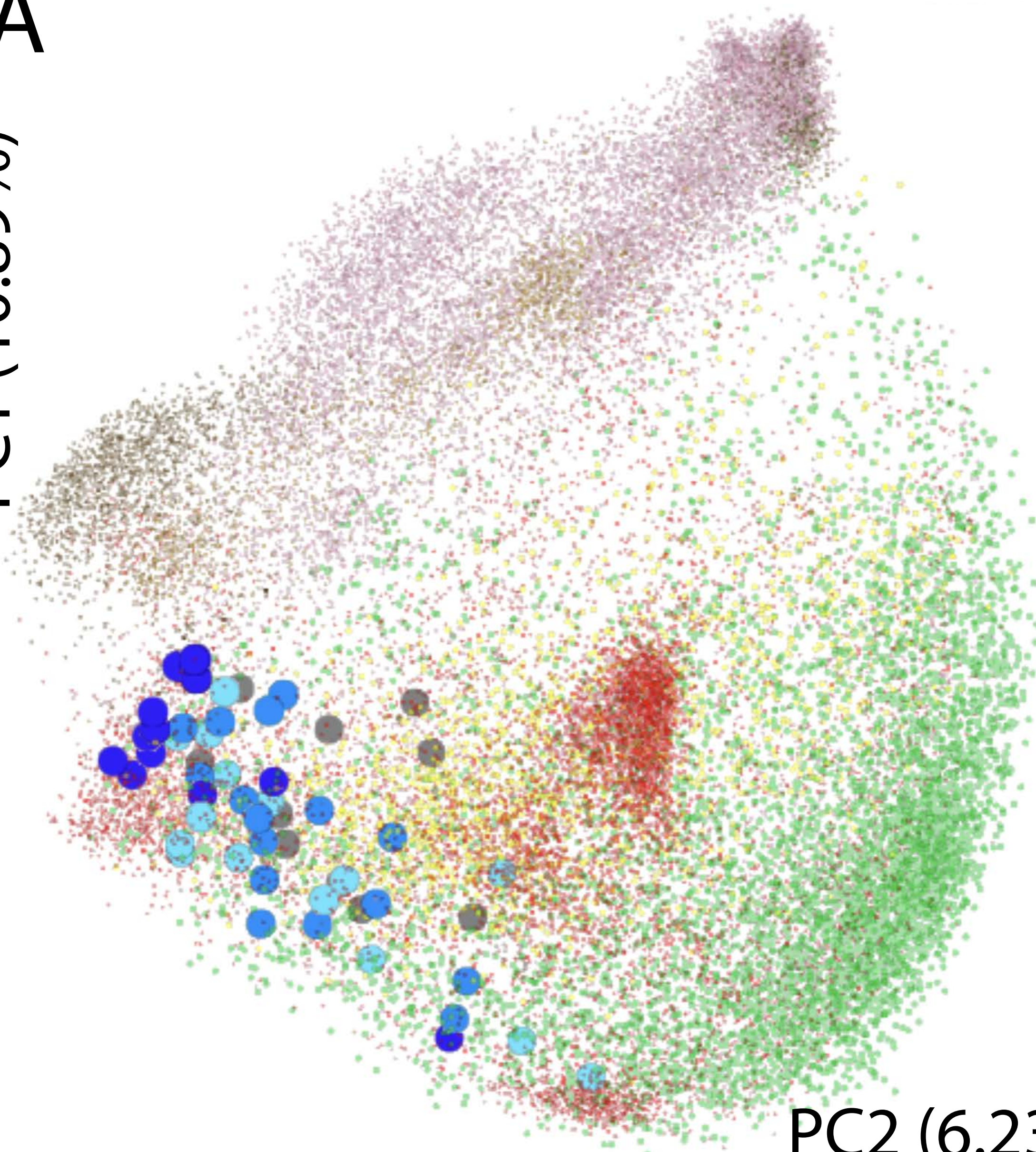
PC1 (10.89%)

PC2 (6.23%)

B

PC1 (10.89%)

PC3 (5.24%)



Growing up on an Amish farm protects children against asthma by reprogramming immune cells

August 3, 2016

Written By
John Easton

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Immunology →



By probing the differences between two farming communities -- the Amish of Indiana and the Hutterites of South Dakota -- an interdisciplinary team of researchers found that specific aspects of the Amish environment are associated with changes to immune cells that appear to protect children from developing asthma.

3. Precision medicine and nutrition for lunar explorers



A troubling surge in
right whale deaths *p. 740*

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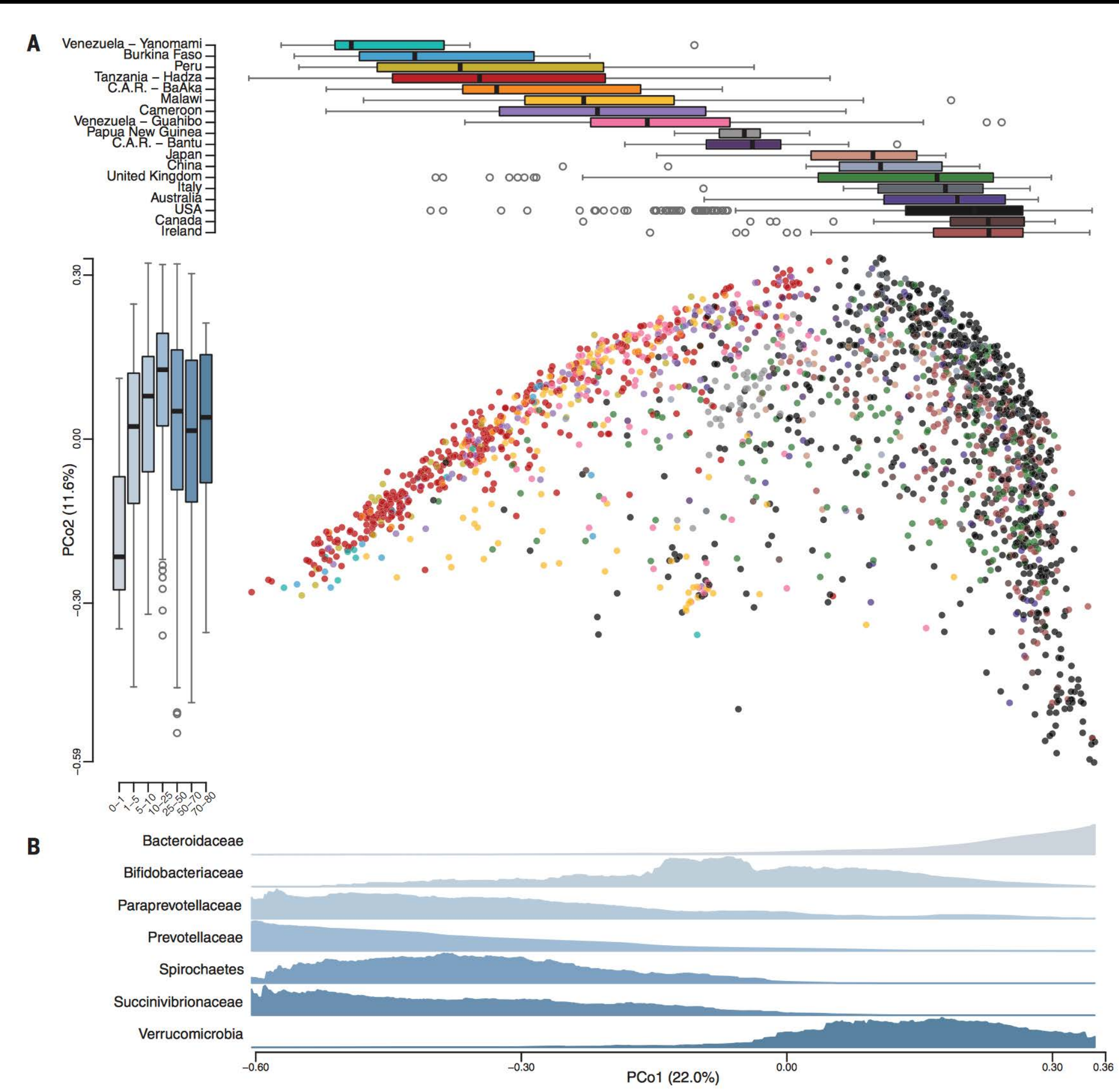
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Seasonal cycling in the gut microbiome of the Hadza hunter-gatherers of Tanzania

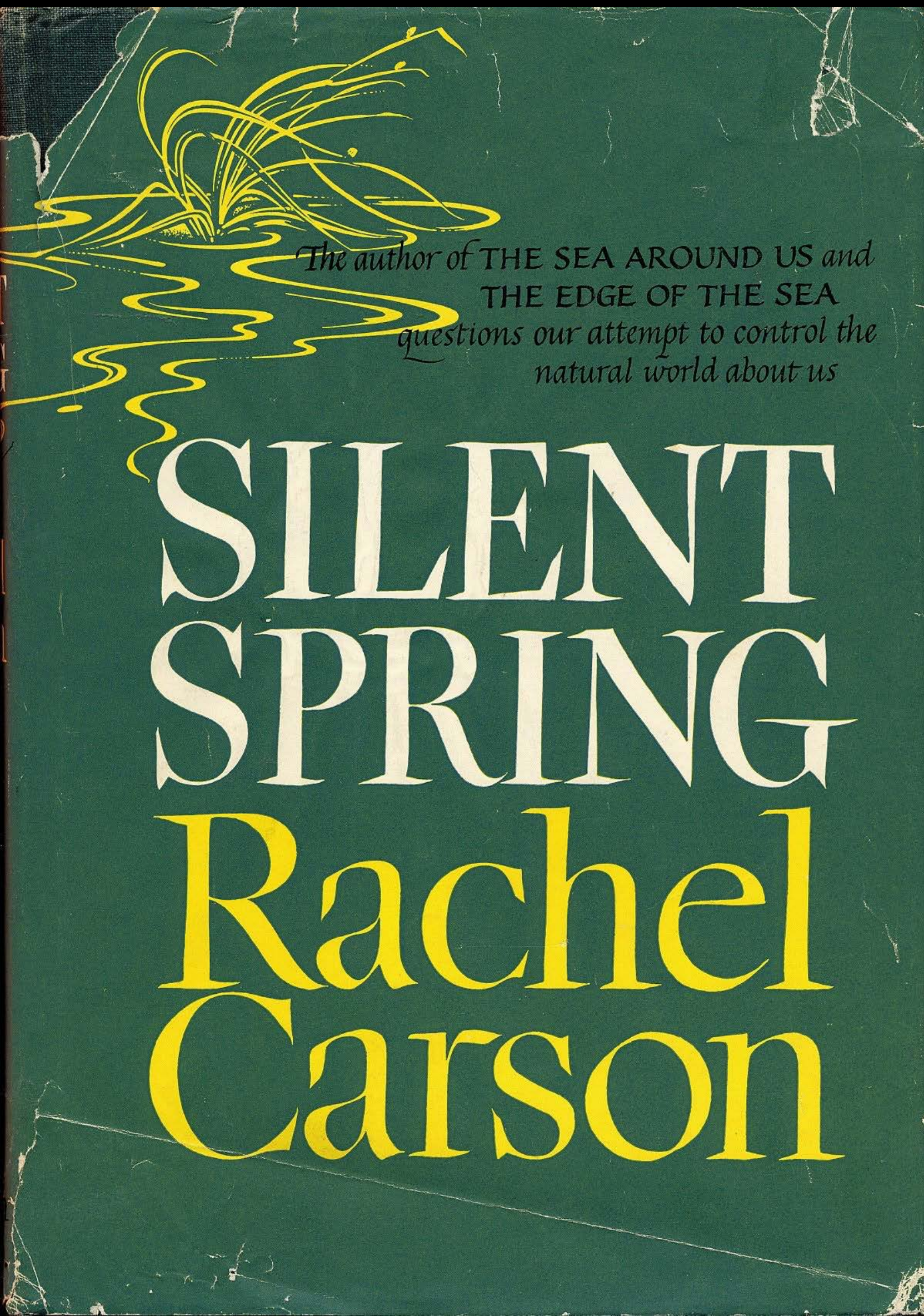
Samuel A. Smits,^{1*} Jeff Leach,^{2,3*} Erica D. Sonnenburg,¹
Carlos G. Gonzalez,⁴ Joshua S. Lichtman,⁴ Gregor Reid,⁵ Rob Knight,⁶
Alphaxard Manjurano,⁷ John Chungalucha,⁷ Joshua E. Elias,⁴
Maria Gloria Dominguez-Bello,⁸ Justin L. Sonnenburg^{1†}



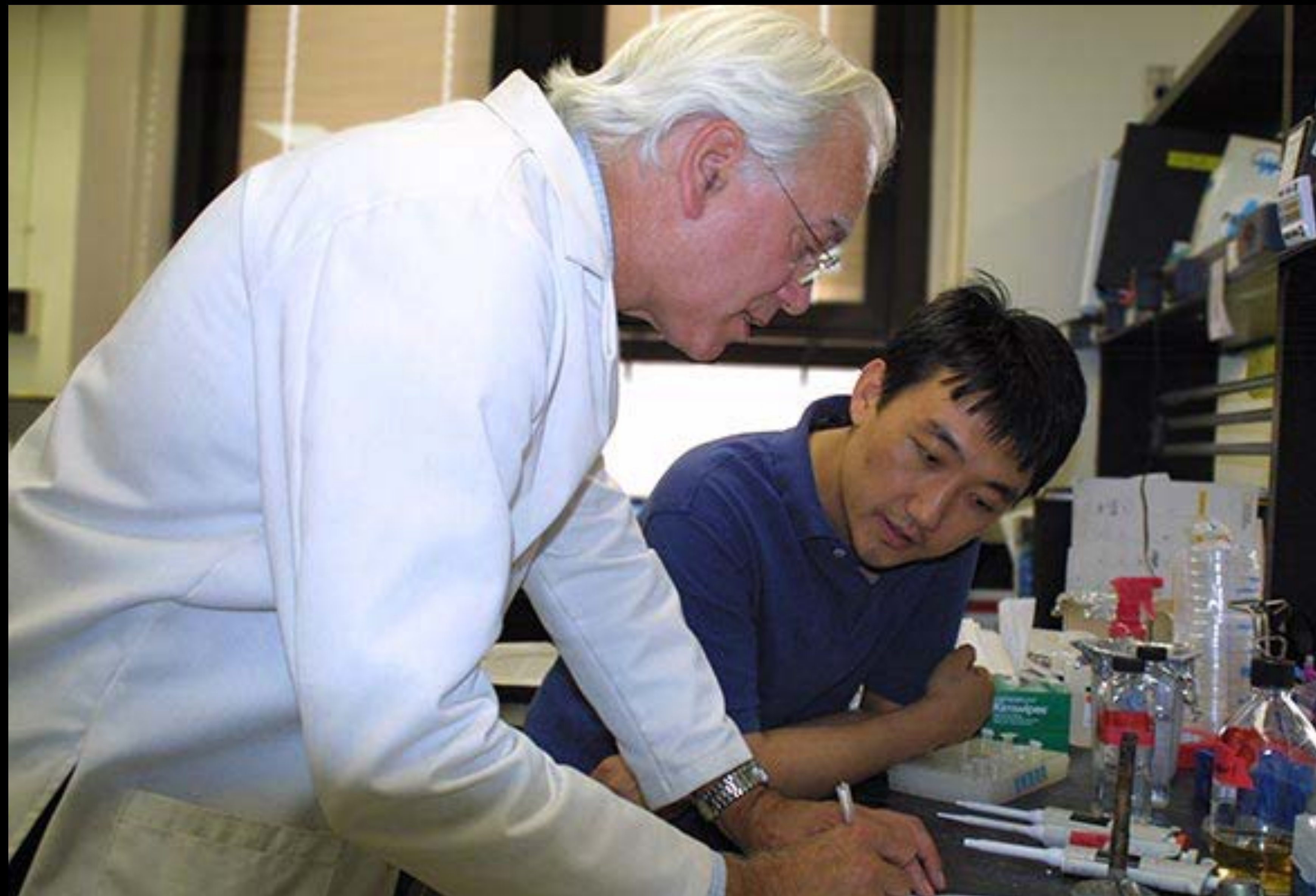
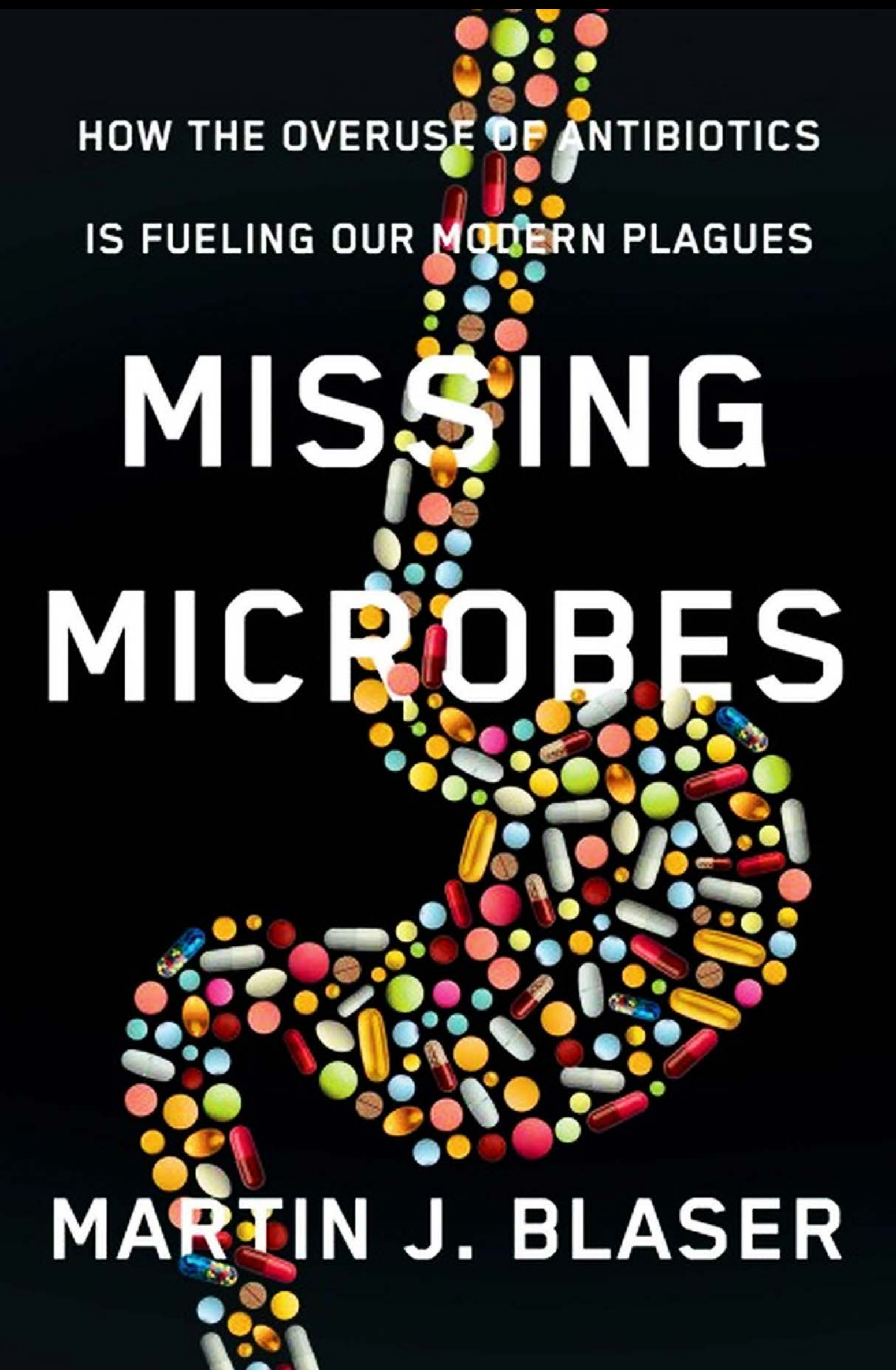




A global microbial biodiversity crisis?



A global microbial biodiversity crisis?



A global microbial biodiversity crisis?

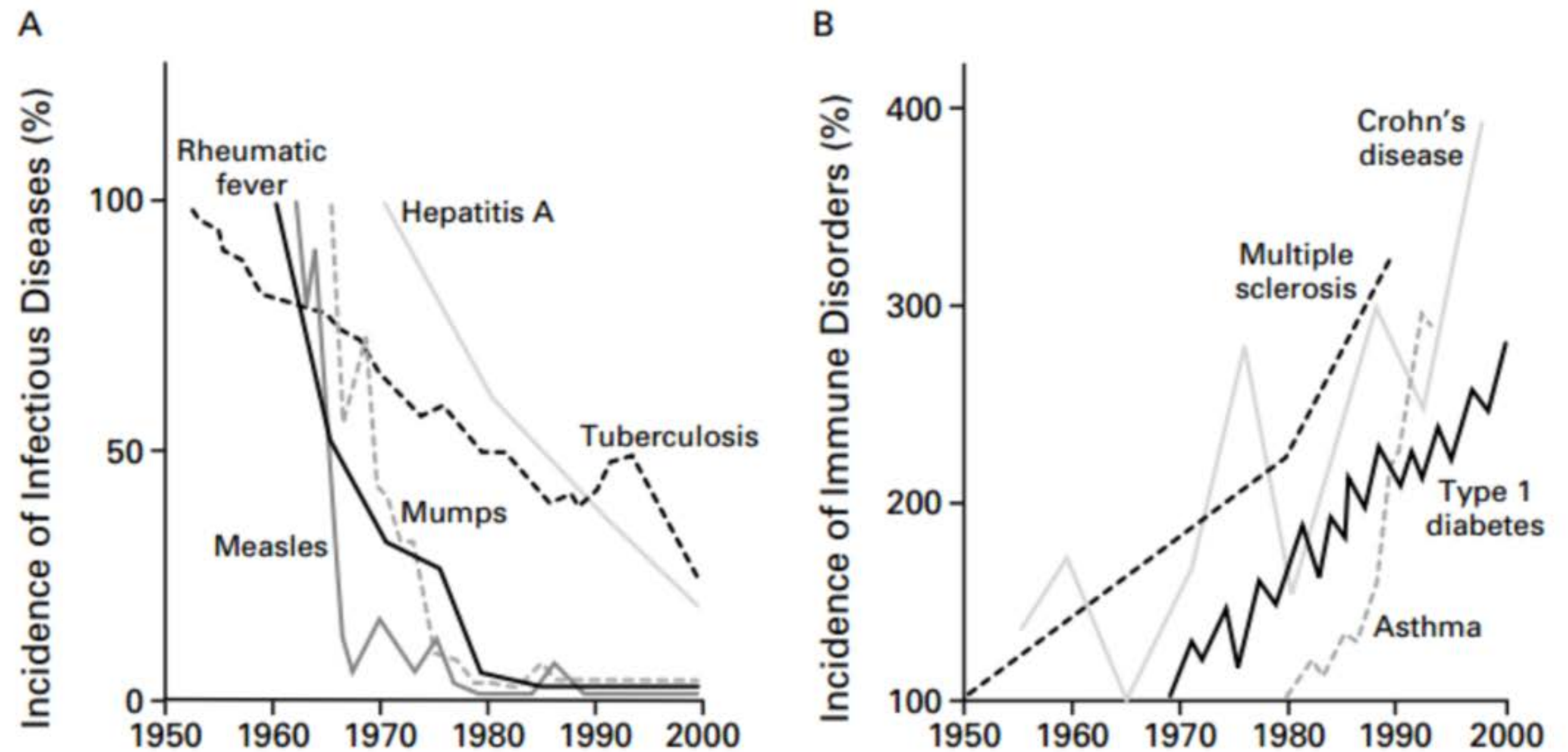
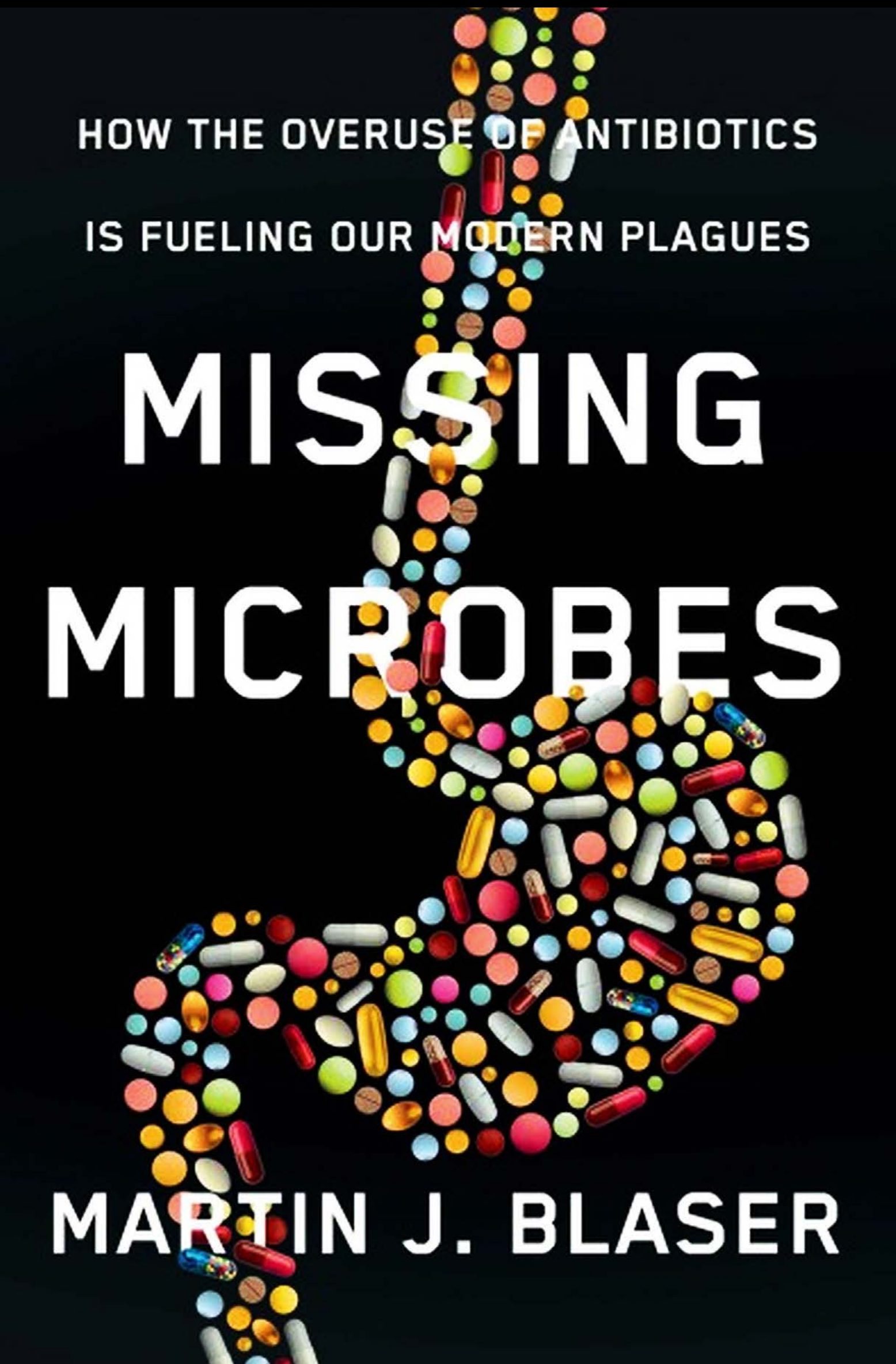
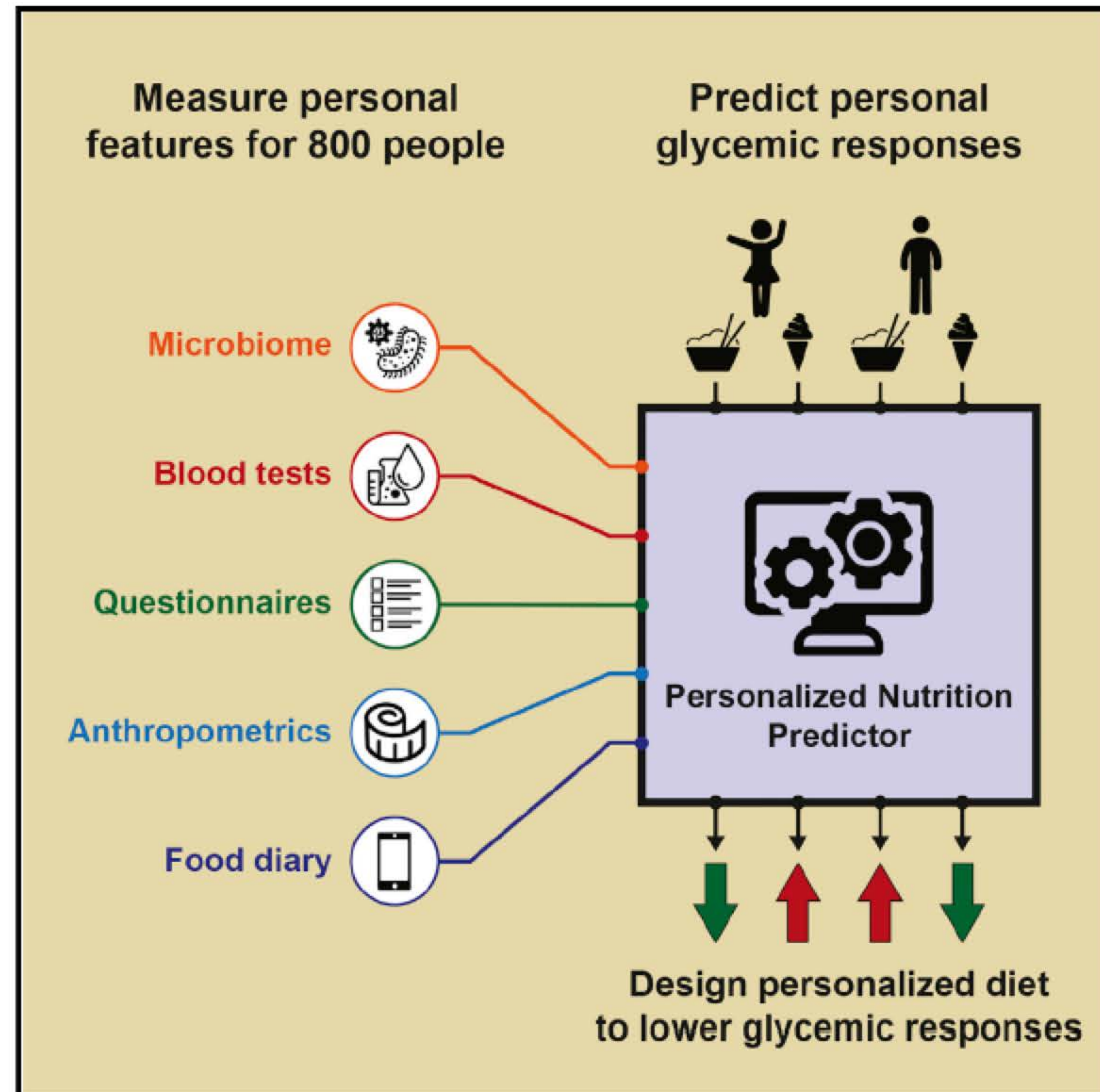


Figure 1. Inverse Relation between the Incidence of Prototypical Infectious Diseases (Panel A) and the Incidence of Immune Disorders (Panel B) from 1950 to 2000.

In Panel A, data concerning infectious diseases are derived from reports of the Centers for Disease Control and Prevention, except for the data on hepatitis A, which are derived from Joussemet et al.¹² In Panel B, data on immune disorders are derived from Swarbrick et al.,¹⁰ Dubois et al.,¹³ Tuomilehto et al.,¹⁴ and Pugliatti et al.¹⁵

Personalized Nutrition by Prediction of Glycemic Responses

Graphical Abstract



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In Brief

People eating identical meals present high variability in post-meal blood glucose response. Personalized diets created with the help of an accurate predictor of blood glucose response that integrates parameters such as dietary habits, physical activity, and gut microbiota may successfully lower post-meal blood glucose and its long-term metabolic consequences.



1 teaspoon stool =
1 ton of DVDs



Questions?

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