


Sewers, Subways, and Space Stations: Genetic Maps of Earth's Cities & Beyond



Weill Cornell
Medicine

 @mason_lab

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The Institute for Computational Biomedicine (ICB),
Meyer Cancer Center, Feil Family Brain and Mind Research Institute,
at Weill Cornell Medicine,
Affiliate, New York Genome Center (NYGC)

November 21st, 2022

Free!

1) GeoSeq Sequencing

2) Phase Genomics cross-linked WGS

3) Books (more today)

August 26-28, 2023,
Cusco, Perú

THE HOTEL



MONAS
A BELMON
CUSCO





Ken McGrath





Scott Tighe







Latest



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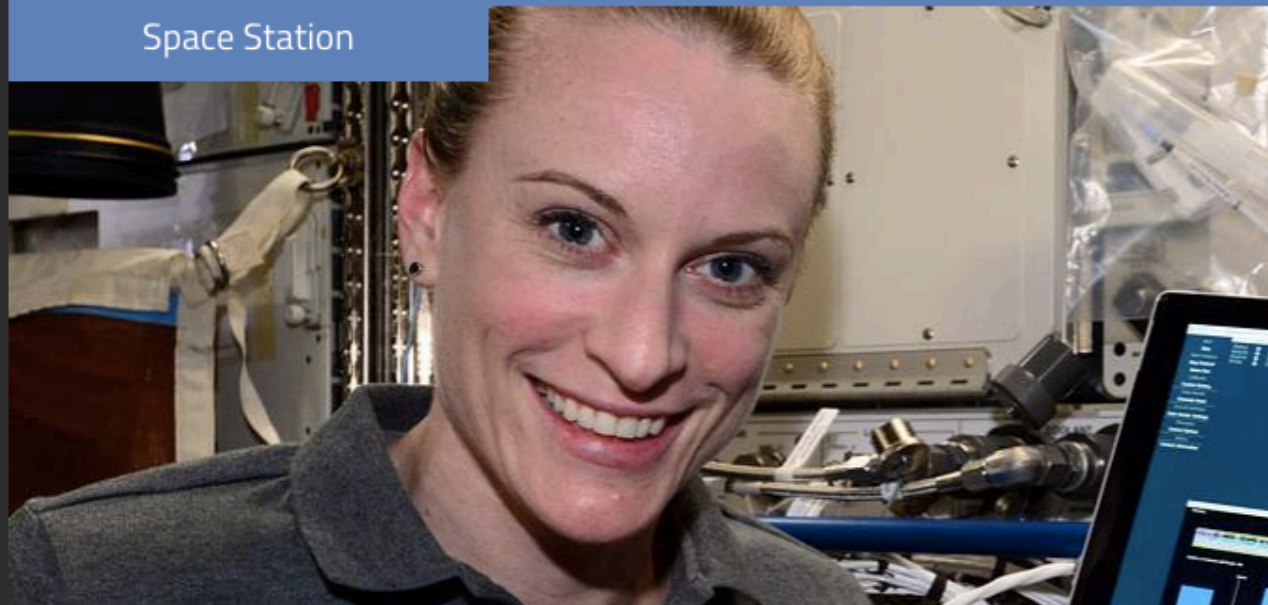
24 days ago



[Weekly Recap From the Expedition Lead Scientist](#)

a month ago

Space Station



Aug. 29, 2016

First DNA Sequencing in Space a Game Changer

For the first time ever, DNA was successfully sequenced in microgravity as part of the [Biomolecule Sequencer](#) experiment performed by NASA astronaut Kate Rubins this weekend aboard the [International Space Station](#). The ability to sequence the DNA of living organisms in space opens a whole new world of scientific and medical possibilities. Scientists consider it a game changer.

DNA, or deoxyribonucleic acid, contains the instructions each cell in an organism on Earth needs to live. These instructions are represented by the letters A, G, C and T, which stand for the four chemical bases of DNA, adenine, guanine, cytosine, and thymine. Both the number and arrangement of these bases differ among organisms, so their order, or sequence, can be used to identify a specific organism.



spasmunkey

@spasmunkey



Following

Great to see this team at work from training to operations at "the dawn of genomics...in space" #AstroKate



RETWEETS 4 LIKES 12



9:40 PM - 29 Aug 2016

Houston, TX

You, Aaron Burton, Kristen John and 3 others



4

12



The first genome sequence and assembly off Earth


SCIENTIFIC REPORTS

Altmetric: 171

[More detail >>](#)

Article | [OPEN](#)

Nanopore DNA Sequencing and Genome Assembly on the International Space Station

Sarah L. Castro-Wallace, Charles Y. Chiu, Kristen K. John, Sarah E. Stahl, Kathleen H. Rubins, Alexa B. R. McIntyre, Jason P. Dworkin, Mark L. Lupisella, David J. Smith, Douglas J. Botkin, Timothy A. Stephenson, Sissel Juul, Daniel J. Turner, Fernando Izquierdo, Scot Federman, Doug Stryke, Sneha Somasekar, Noah Alexander, Guixia Yu, Christopher E. Mason & Aaron S. Burton 

Scientific Reports **7**, Article number: 18022
(2017)

doi:10.1038/s41598-017-18364-0

Received: 01 August 2017

Accepted: 11 December 2017

Published online: 21 December 2017

<https://www.nature.com/articles/s41598-017-18364-0>

The first space epigenome



nature
COMMUNICATIONS

Article | **OPEN** | Published: 04 February 2019

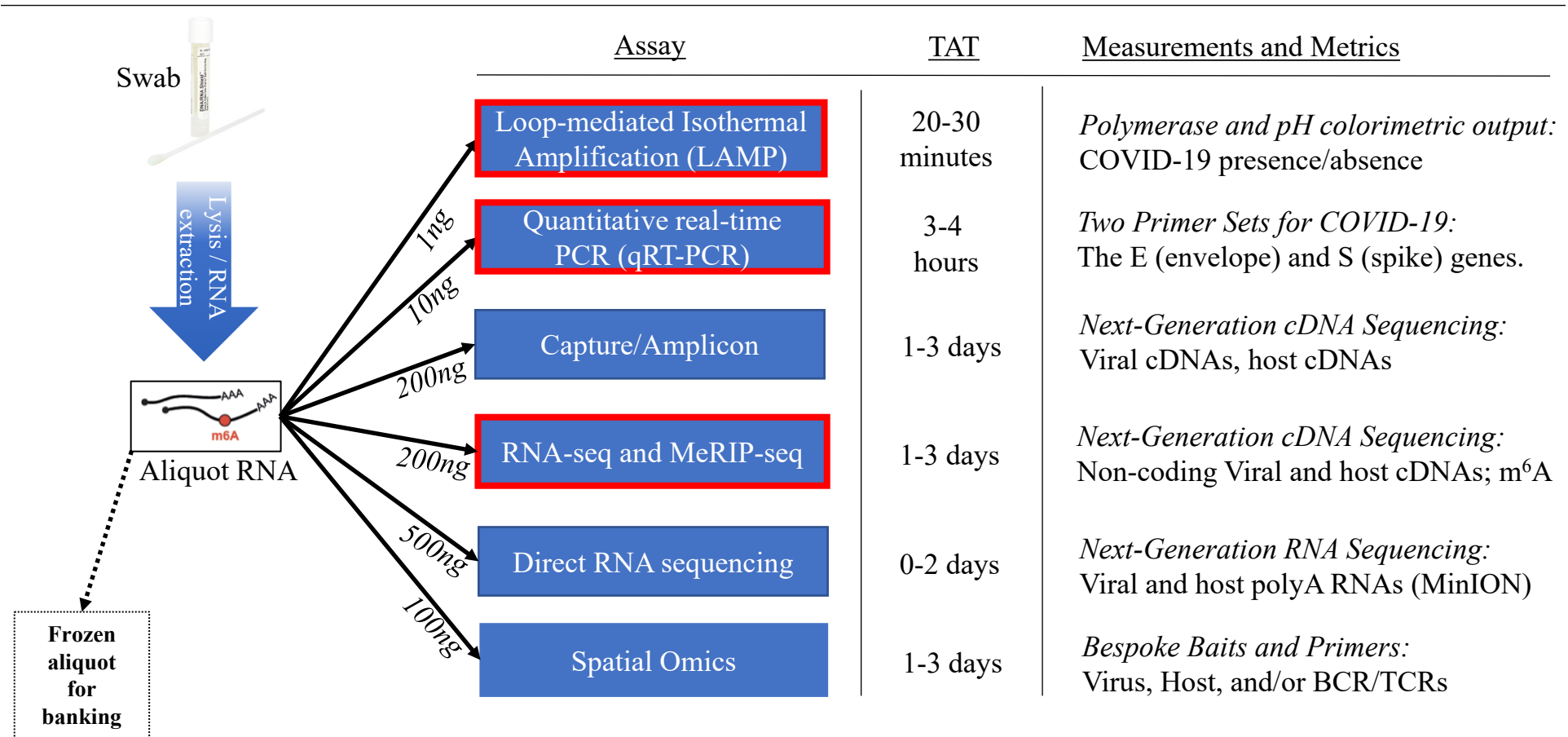
Single-molecule sequencing detection of N6-methyladenine in microbial reference materials

Alexa B. R. McIntyre, Noah Alexander, Kirill Grigorev, Daniela Bezdán, Heike Sichtig, Charles Y. Chiu & Christopher E. Mason 

<https://www.nature.com/articles/s41467-019-08289-9> <https://github.com/al-mcintyre/mCaller>

Where on Earth can we use all these tools?

Battery of methods to learn about a new virus & host response



857 COVID-19 samples' total RNA-seq (63.2M 150x150 PE reads)

857 clinical specimens from
735 NYP-WCMC patients
with known or suspected
SARS-CoV-2 infection



86 NYC
Subway
Specimens

Swab

RNA
extraction

1ng

10ng

10ng



Assay

Time

Reagents

Result

Loop-mediated
Isothermal
Amplification
(LAMP)

30-40 minutes

One primer sextet
for SARS-CoV-2

Color change representing
level of SARS-CoV-2
E (envelope) and N (nucleocapsid)
gene in specimen

qRT-PCR

3-4 hours

Two primer sets
for SARS-CoV-2

Ct representing
level of SARS-Cov2 E (envelope)
and S (Spike) gene in specimen

Total RNA-seq

8 hours -
2 days

Random Hexamers

Shotgun metatranscriptomes
of all host and species
RNA sequences in specimen

1) 735 suspected COVID-19 patients:

COVID-19-POS, n=216

COVID-19-NEG, n=519

2) 86 Environmental (54 sites)

Grand Central

Times Square

3) 36 Controls

CP (Vero E6 Cells w/ SARS-CoV-2)

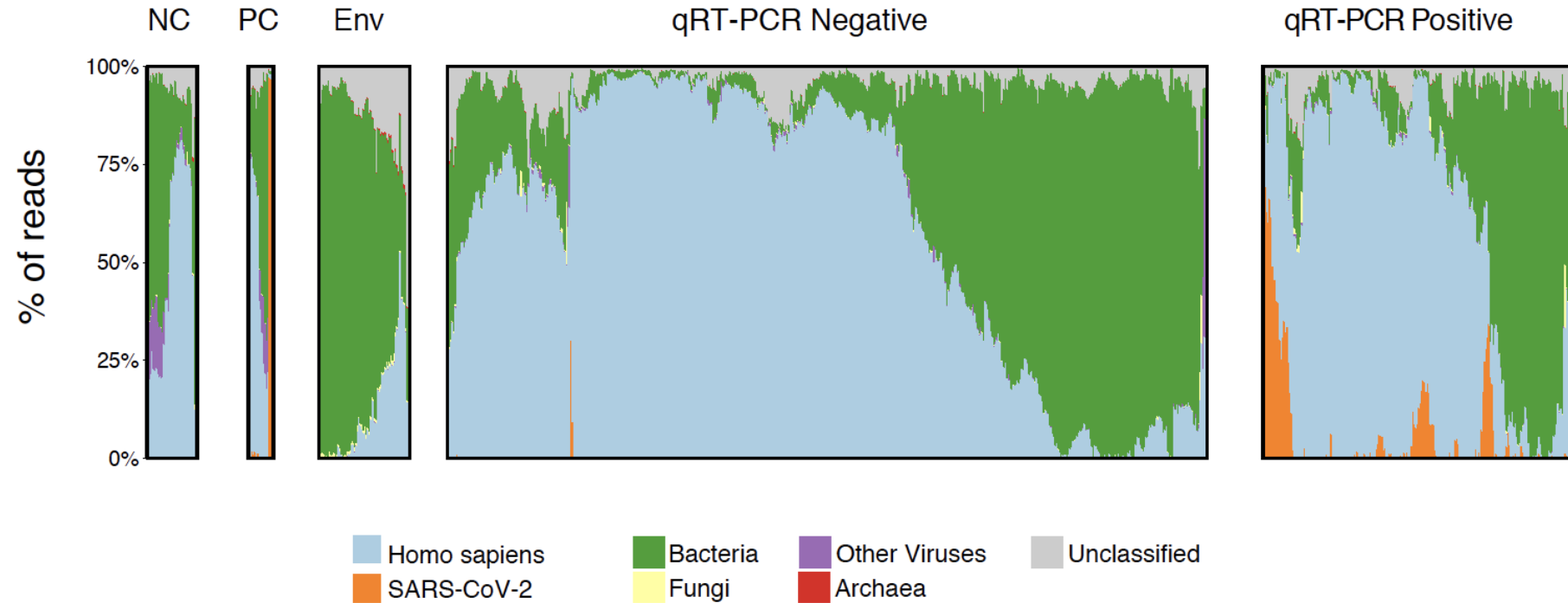
Twist Synthetic RNA (2 strains)

Negative Controls (TE buffer)

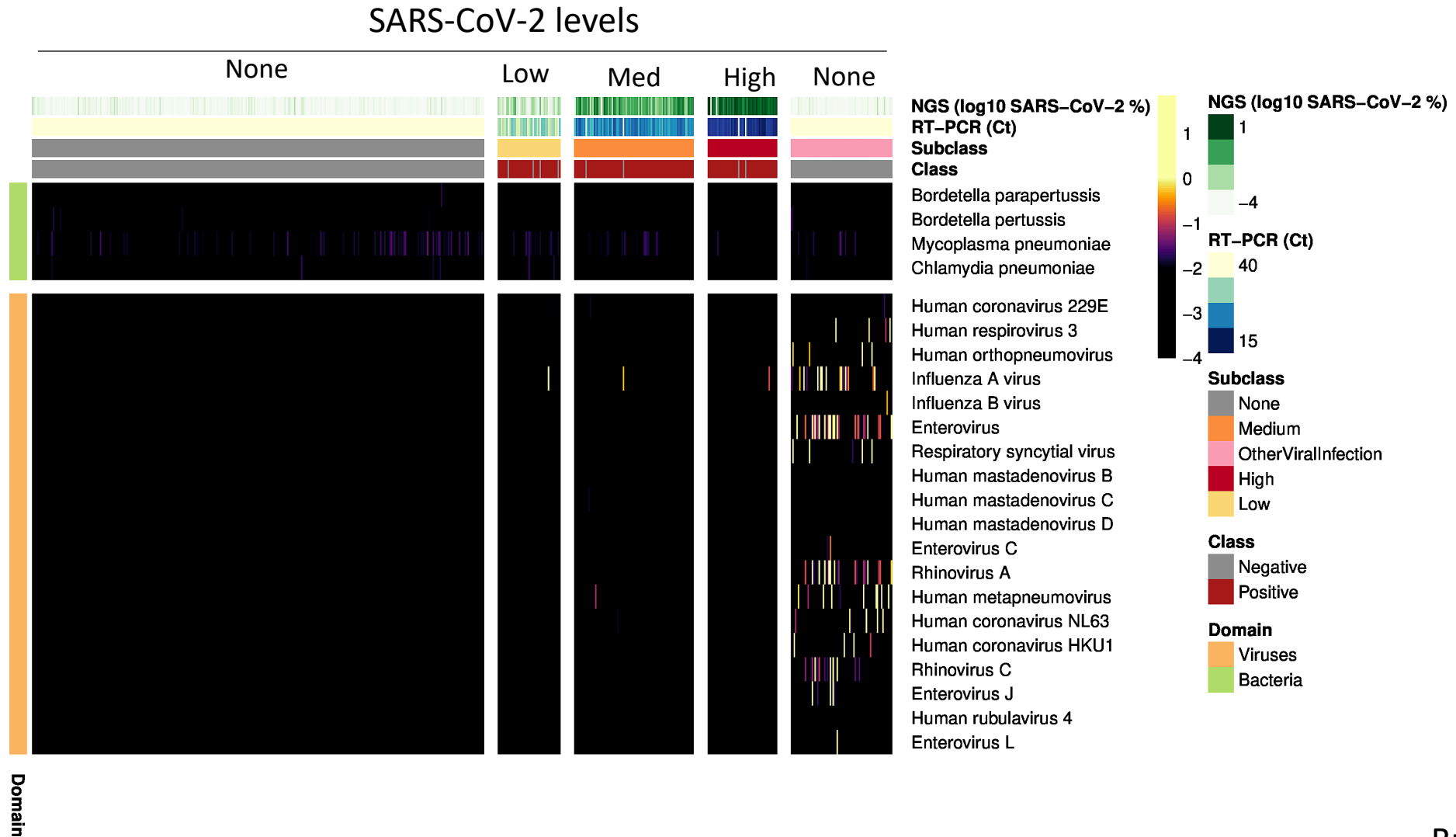
Butler *et al.*, 2021,

<https://www.nature.com/articles/s41467-021-21361-7>

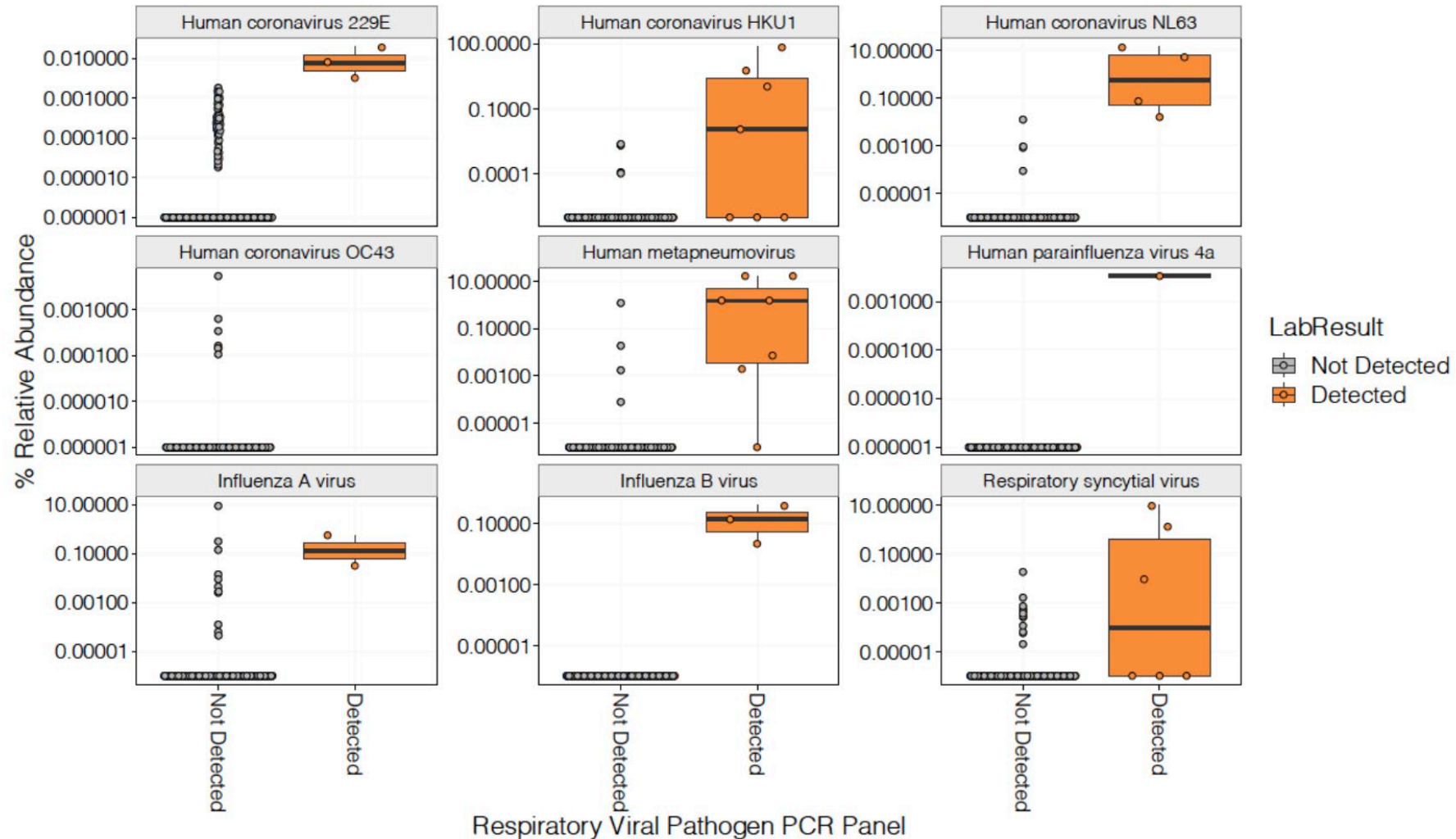
Mostly human, bacterial, viral RNA in the NP swabs



Co-infection is rare



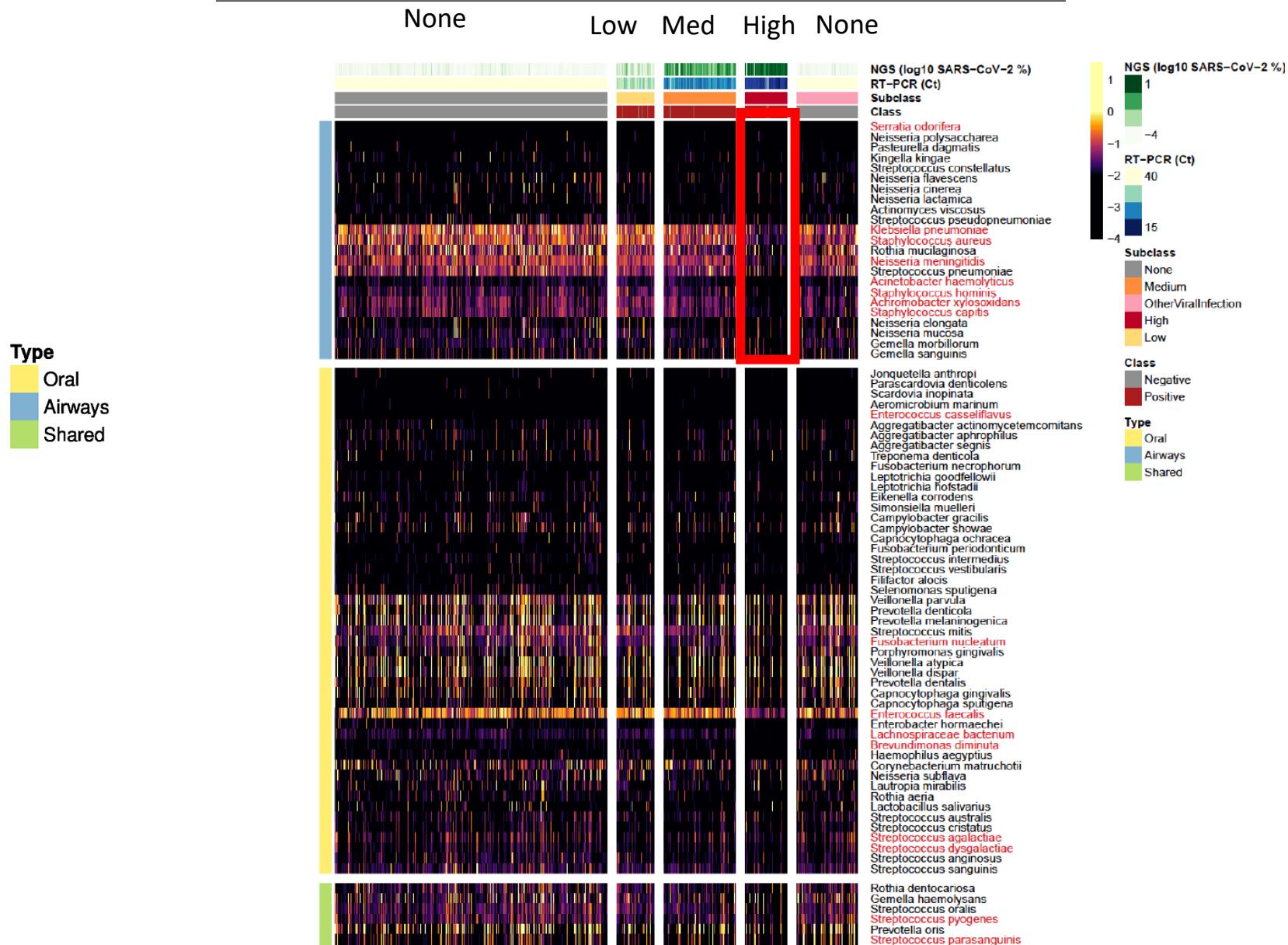
Confirmed by BioFire



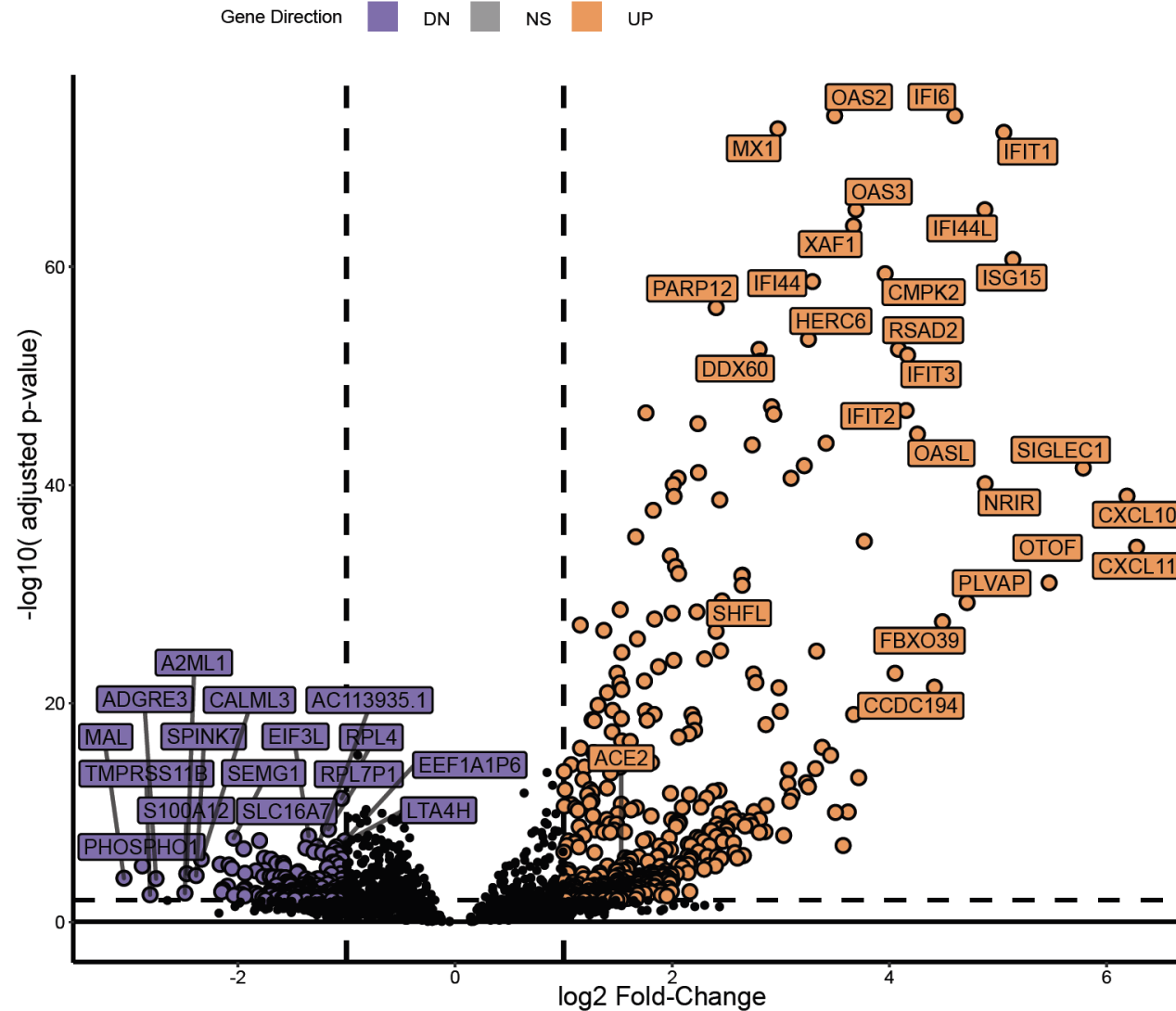
AUROC = 0.89;
Accuracy = 0.99;
Sensitivity = 0.76;
Specificity = 0.98,

Microbiome Disruption in High Titer Patients

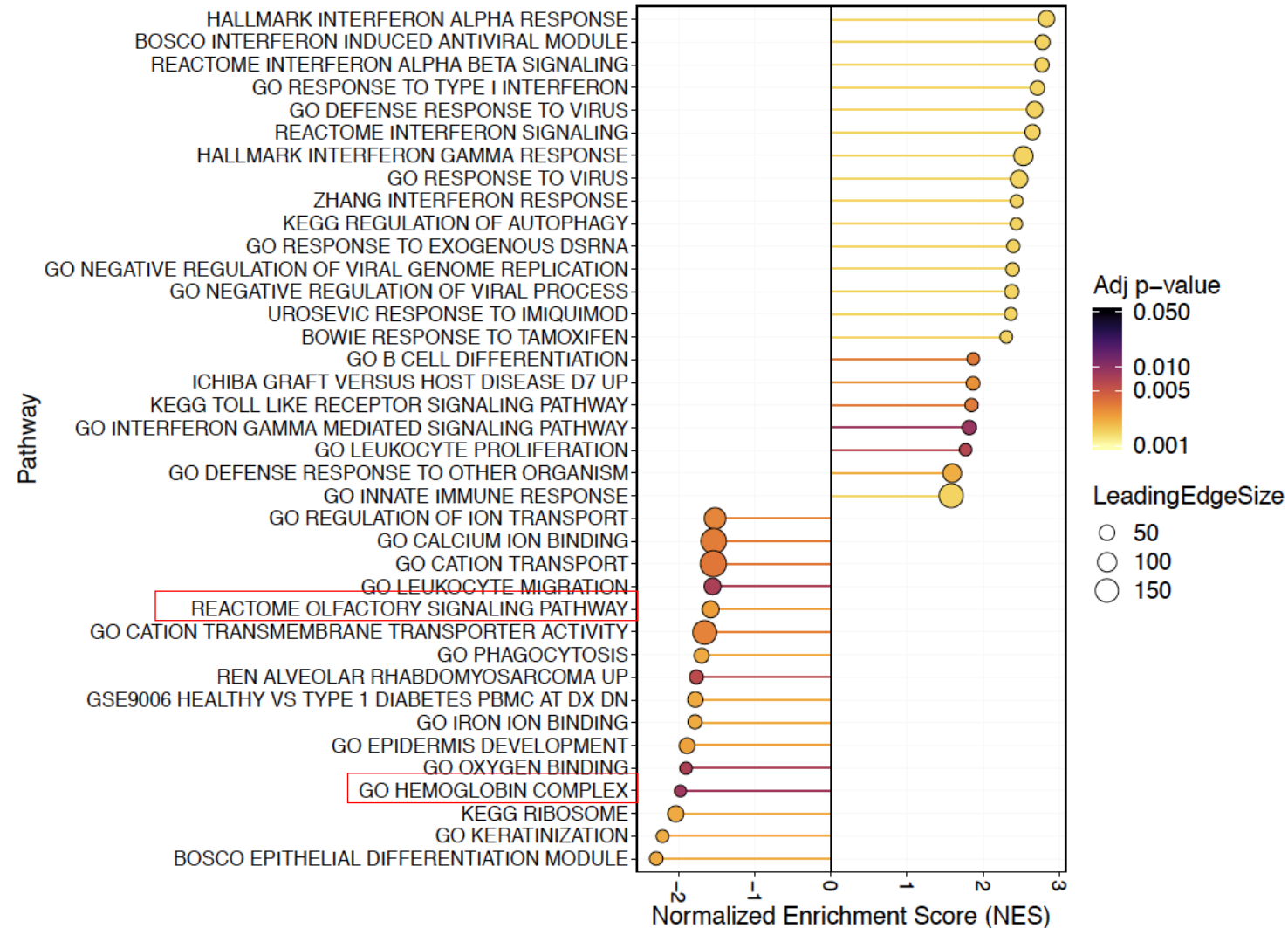
SARS-CoV-2 levels



The human response: Host DEGs ($q < 0.01$, > 1.5 -fold)



Biological pathways feature familiar, and some new networks (including heme, olfaction)





i Information

📊 Single Gene Plot <

📈 Multi Gene Heatmap <

Enter/Paste gene symbols (comma, space, new line separated)

IFIT3 ACE2 SHFL IL6

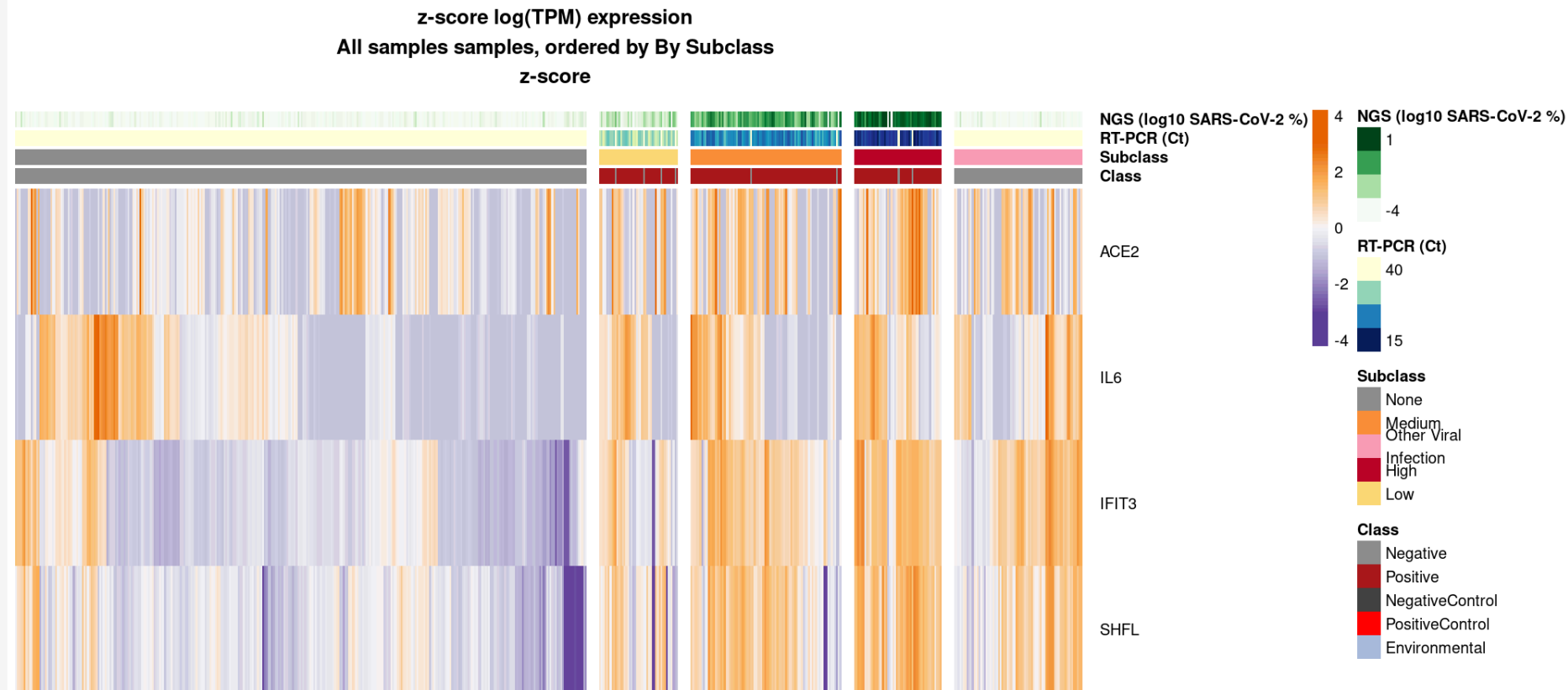
Plot

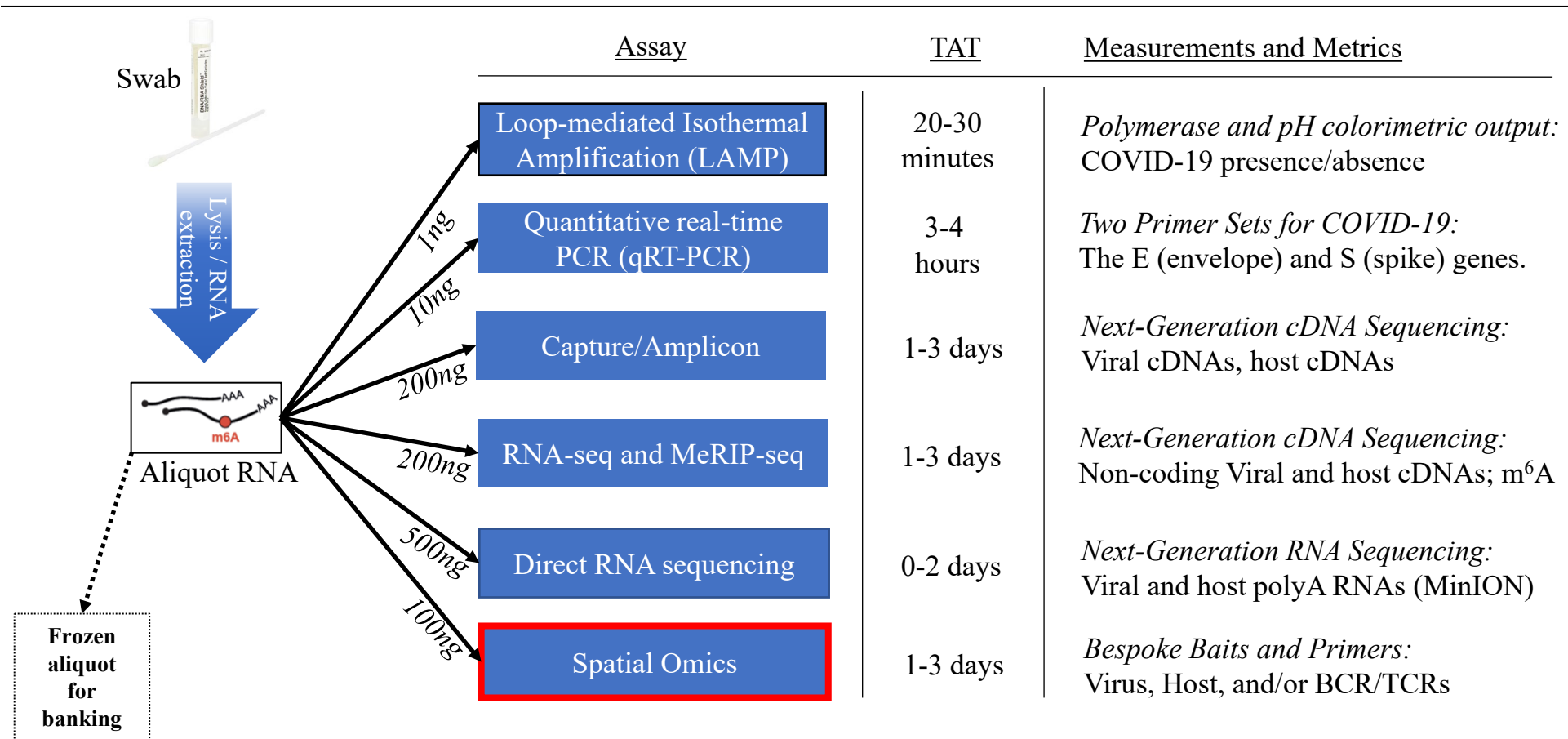
🔗 Pathway Enrichment <

⚙️ Settings <

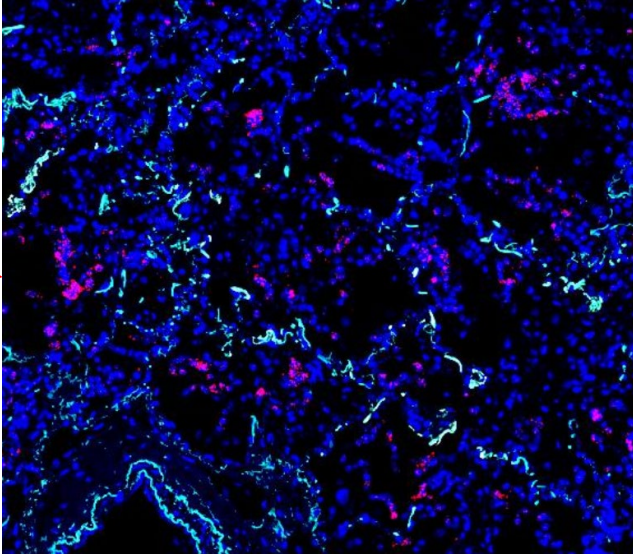
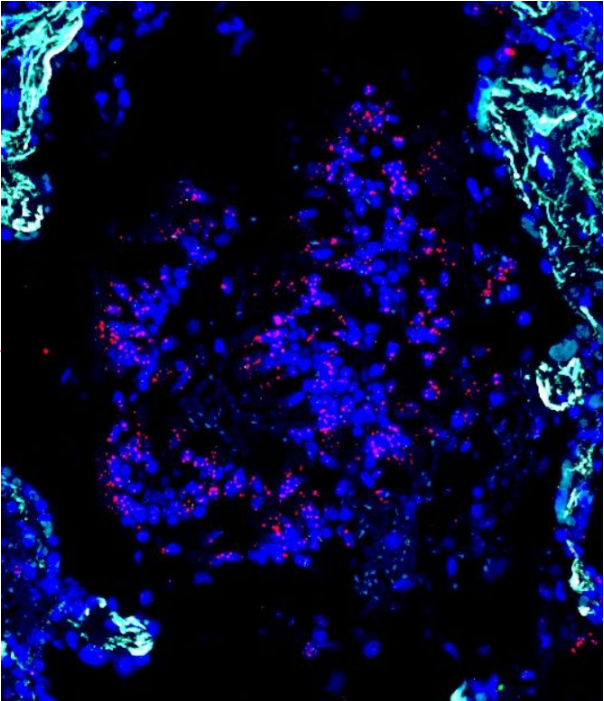
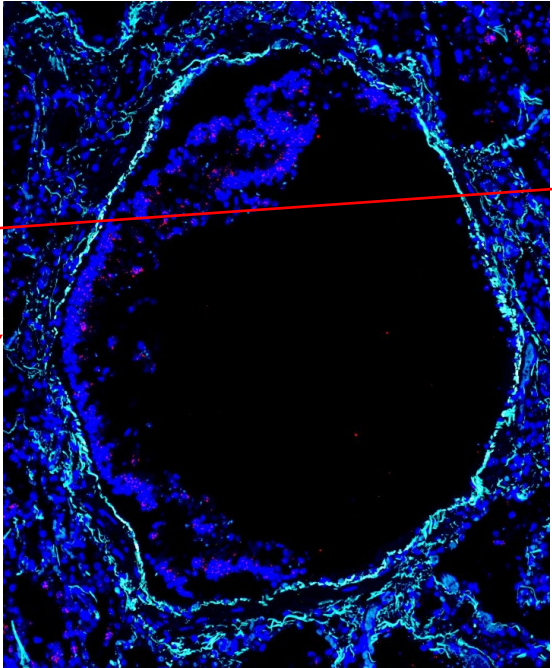
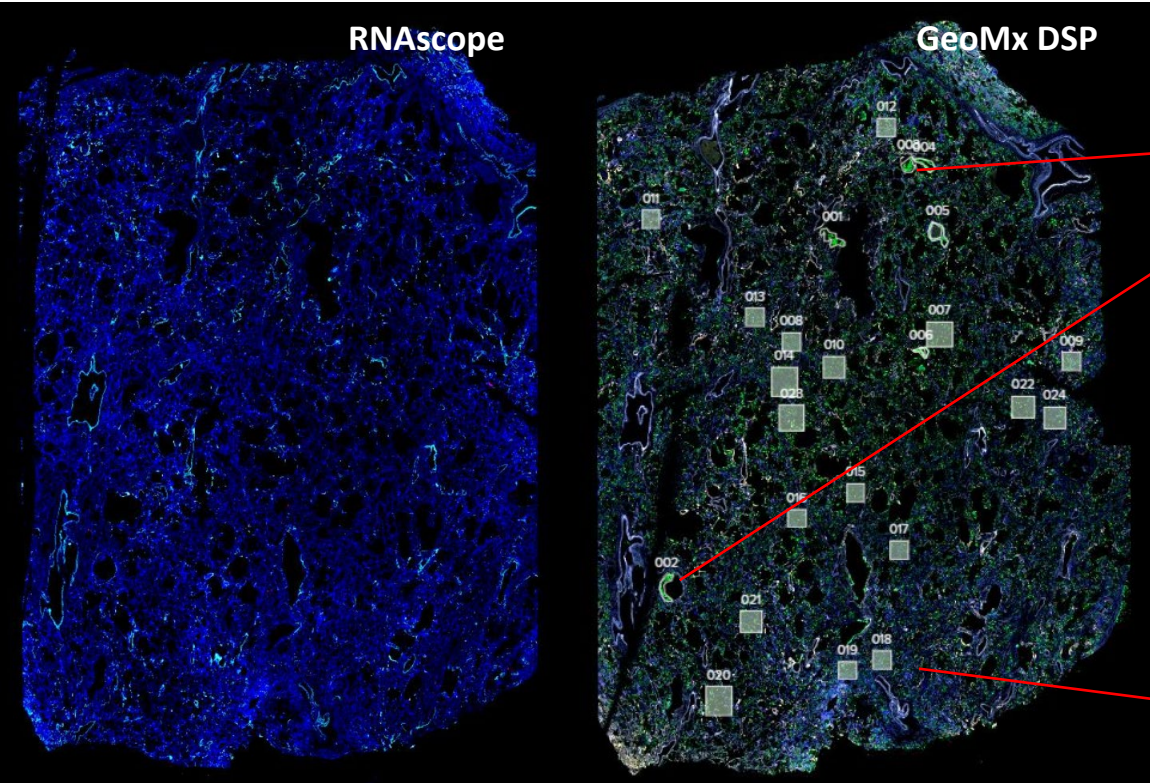
Multi gene heatmap

Heatmap



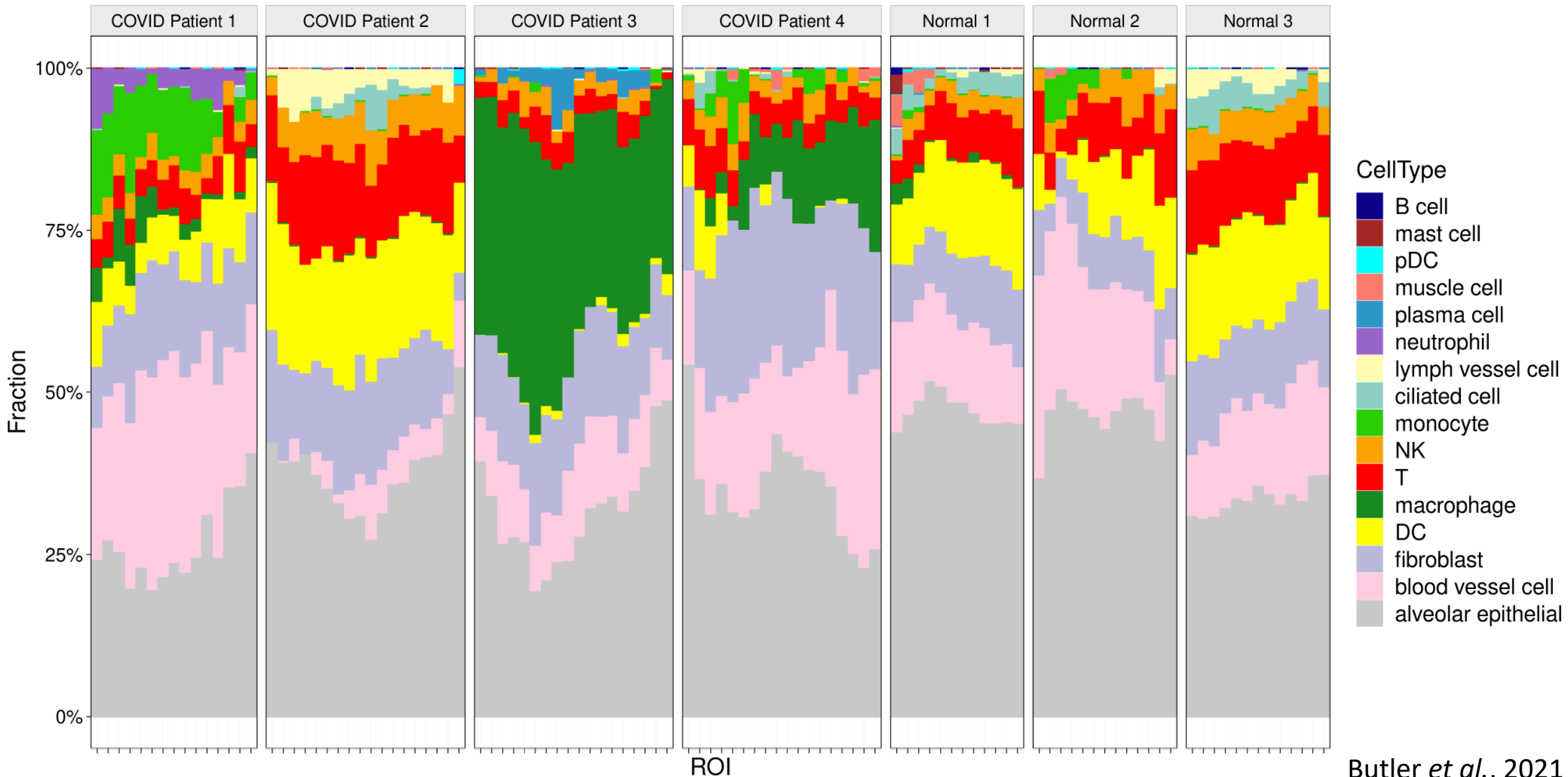


Covid21_ High TMPRSS2 in both large airway and Alveoli

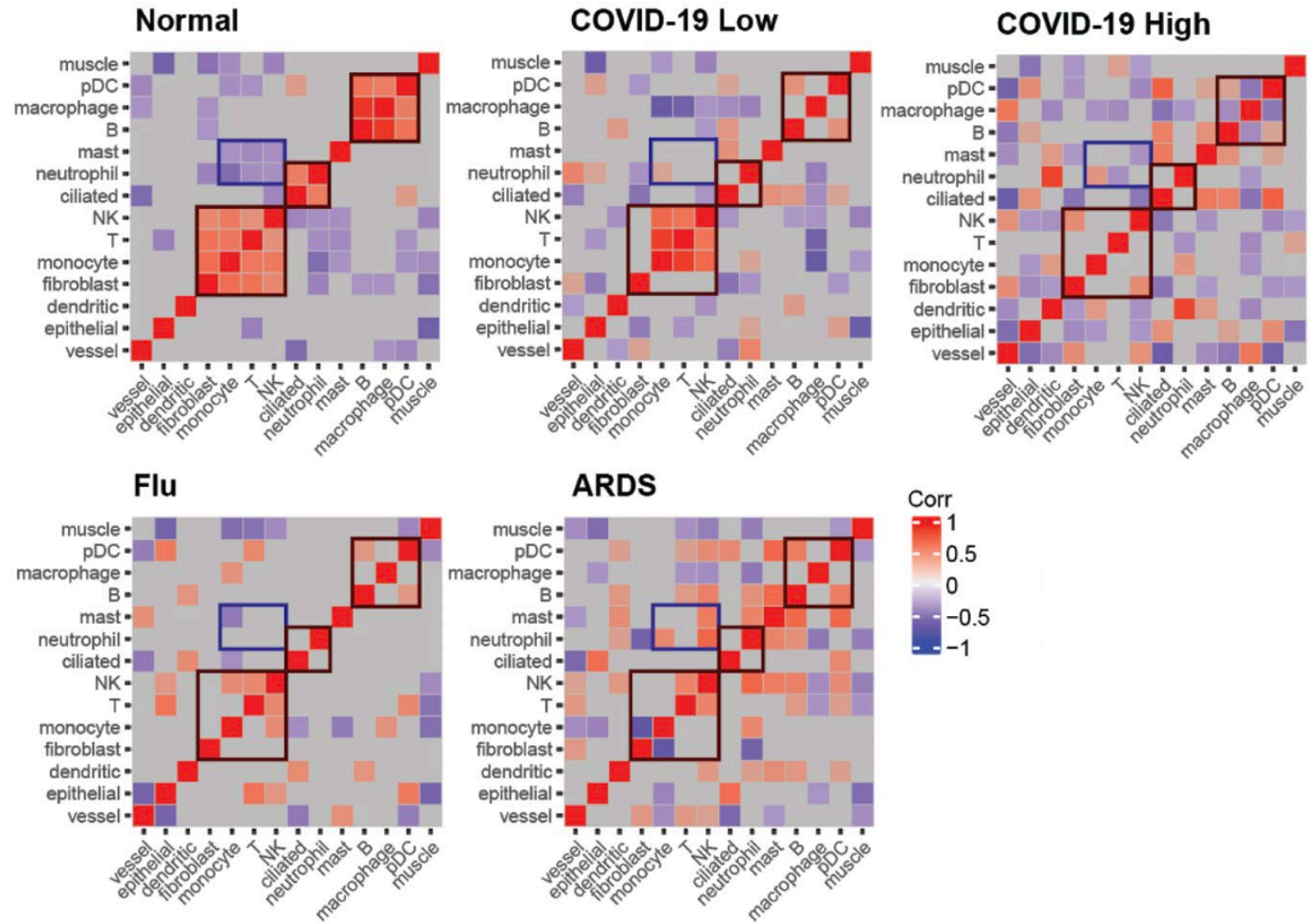


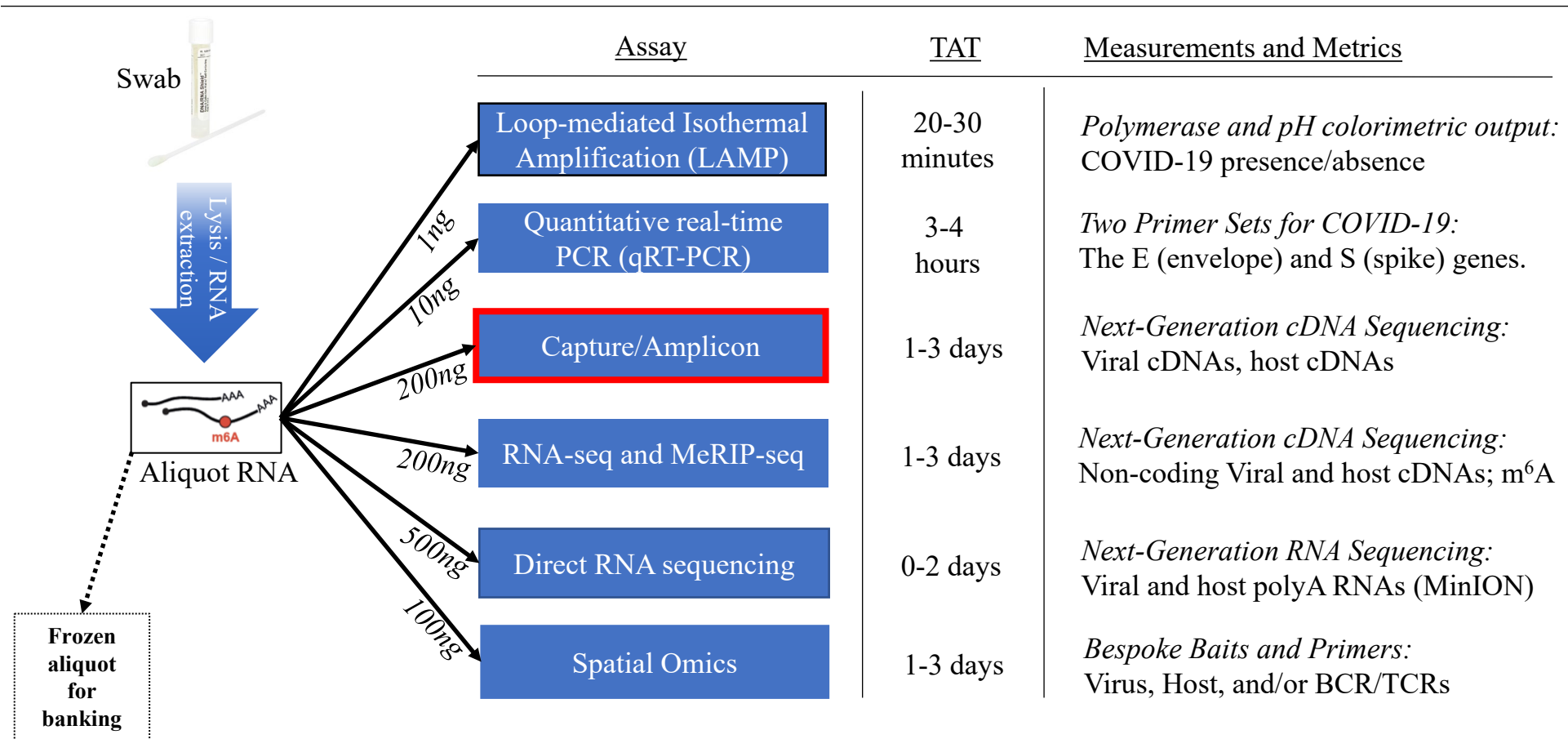
DNA
V-nCoV2019-S
Hs-ACE2
Hs-TMPRSS2

Spatial mapping of cell types within ROIs reveals immune infiltration



Co-cellular organization map is also disrupted





B.1.17 variant (alpha)

Cell

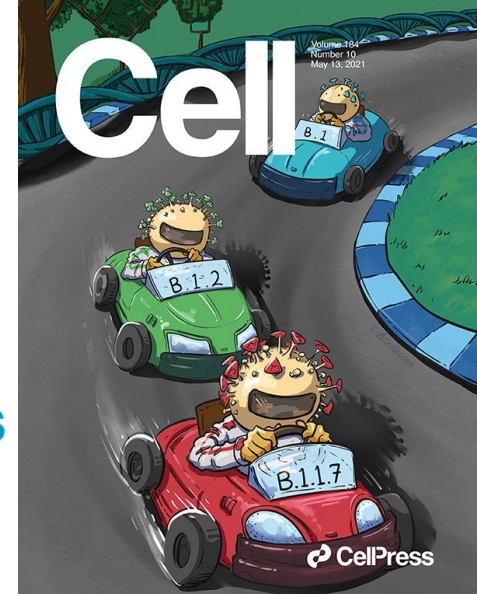
CellPress

Article

Early introductions and transmission of SARS-CoV-2 variant B.1.1.7 in the United States

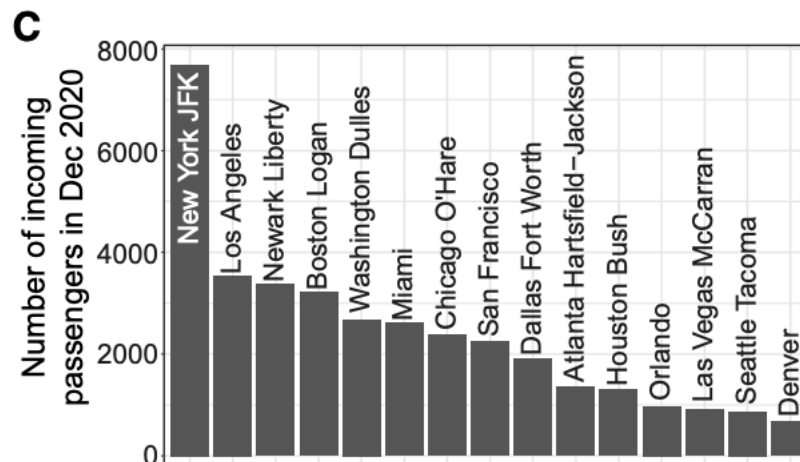
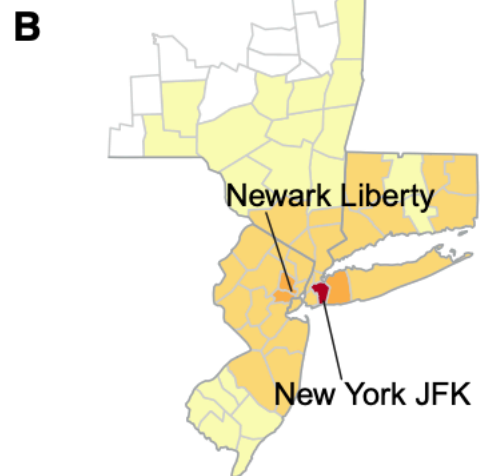
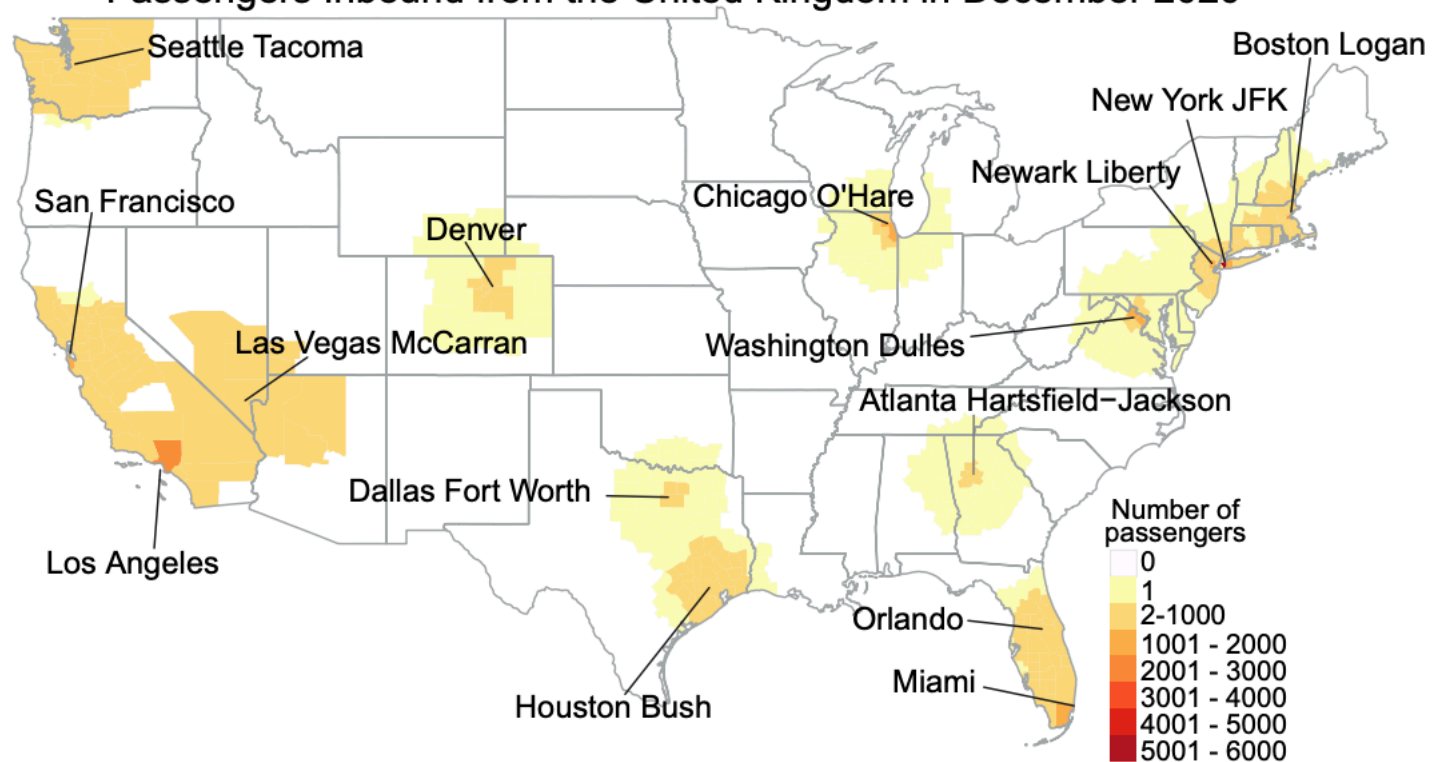
Tara Alpert,^{1,15} Anderson F. Brito,^{1,15} Erica Lasek-Nesselquist,^{2,3,15} Jessica Rothman,^{1,15} Andrew L. Valesano,^{4,15} Matthew J. MacKay,^{5,15} Mary E. Petrone,¹ Mallery I. Breban,¹ Anne E. Watkins,¹ Chantal B.F. Vogels,¹ Chaney C. Kalinich,¹ Simon Dellicour,^{6,7} Alexis Russell,² John P. Kelly,² Matthew Shudt,^{2,3} Jonathan Plitnick,^{2,3} Erasmus Schneider,^{2,3} William J. Fitzsimmons,⁴ Gaurav Khullar,⁵ Jessica Metti,⁵ Joel T. Dudley,⁵ Megan Nash,⁵ Nike Beaubier,⁵ Jianhui Wang,⁸ Chen Liu,⁸ Pei Hui,⁸ Anthony Muyombwe,⁹ Randy Downing,⁹ Jafar Razeq,⁹ Stephen M. Bart,^{9,10} Ardath Grills,¹⁰ Stephanie M. Morrison,¹⁰ Steven Murphy,¹¹ Caleb Neal,¹¹ Eva Laszlo,¹¹ Hanna Rennert,¹² Melissa Cushing,¹² Lars Westblade,¹² Priya Velu,¹² Arryn Craney,¹² Lin Cong,¹² David R. Peaper,¹³ Marie L. Landry,¹³ Peter W. Cook,¹⁰ Joseph R. Fauver,^{1,16} Christopher E. Mason,^{5,12,16} Adam S. Lauring,^{4,16} Kirsten St. George,^{2,3,16,*} Duncan R. MacCannell,^{10,16,*} and Nathan D. Grubaugh^{1,14,16,17,*}

[https://www.cell.com/cell/pdf/S0092-8674\(21\)00434-7.pdf](https://www.cell.com/cell/pdf/S0092-8674(21)00434-7.pdf)



May 13, 2021

A Passengers Inbound from the United Kingdom in December 2020



FDA EUA Granted for SARS-CoV-2 NGS Assay & COVID-DX



Q Search

Bloomberg

Business

Twist Bioscience and Biotia Receive U.S. FDA Emergency Use Authorization for First Hybridization Capture-Based Next-Generation

March 24, 2021, 8:00 AM EDT

SHARE THIS ARTICLE

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Twist Bioscience First Hybridization Assay

- Ability to se
- Enables bat

Business Wire

SOUTH SAN FRANCISCO

Twist Bioscience succeed through platform, and Biotia software for information Authorization (EUA) for SARS-CoV-2 Next-Generation

This press release is available at: <https://www.businesswire.com>

Biotia BIOTIA RUO TEST REPORT SARS-CoV-2 NGS Assay

ORDERING	SAMPLE	PATIENT
Institution: Test Institution Physician: Jane Doe Address: 77 Brackton Avenue, Abington MA 2351 Phone Number: 612-345-6789 Email: test@twist.com	Specimen Type: Specimen Collection Date: 04/01/2020 Received By Lab: 04/02/2020 Run Date: 04/05/2020 Report Date: 04/10/2020	Name: Joe Doe DOB: 10/28/1981 Sex: Male ID#I/HN/MRN: XX

THIS REPORT IS FOR RESEARCH USE ONLY

DISCLAIMER: The research use only (RUO) section of this report is only intended to be used for research and is not intended to guide treatment of patients. This RUO report is generated based on the SARS-CoV-2 NGS Assay, which is a qualitative, viral capture plus next-generation sequencing-based, in-vitro diagnostic test built by Twist Bioscience and powered by Biotia COVID-DX (G1.0) software. This test was developed and its performance characteristics determined by Twist and Biotia. The RUO section of this test has not been cleared or approved by the FDA, nor is it required to be. The Biotia Laboratory is certified under the Clinical Laboratory Improvement Amendments of 1988 (CLIA '88) and is accredited to perform high-complexity clinical laboratory testing.

RESULTS SUMMARY	Controls: Passed	Reference Value: Not Detected
Detected: SARS-CoV-2		

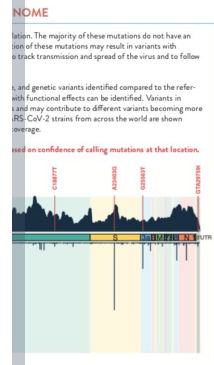
GENETIC VARIANTS DETECTED

Detected	Gene	Site (bp)	Alteration	Reference Value
+	ORF1ab	241	T	Not Detected
+	ORF1ab	478	T	Not Detected
+	ORF1ab	3037	T	Not Detected
+	ORF1ab	14408	T	Not Detected
+	ORF1ab	18877	T	Not Detected
+	S	23403	G	Not Detected
+	3a	25583	T	Not Detected
+	3'UTR	29759	C	Not Detected

Details	Variant Literature Notes (if available)	References
14408	Corresponds to P232L mutation in the RdRp, ORF1ab gene. RdRp enzymes are binding targets for several drugs and studies indicate a mutation may affect drug efficacy.	Pachetti et al. 2020

Report Status: Final - Page 1 of 6
© Biotia Inc. • Castle Oaks, PA, Lab Director • CLIA ID: 330280921 • PFI 9518 • 140 5th Street Building A Suite 81, Brooklyn, NY 11220, NY
Contact: clinicalsupport@biotia.io

Patient: Joe Doe Accession Number: 123456-789-123



Page 2 of 6

8 • 140 5th Street Building A Suite 81, Brooklyn, NY 11220, NY

© Biotia

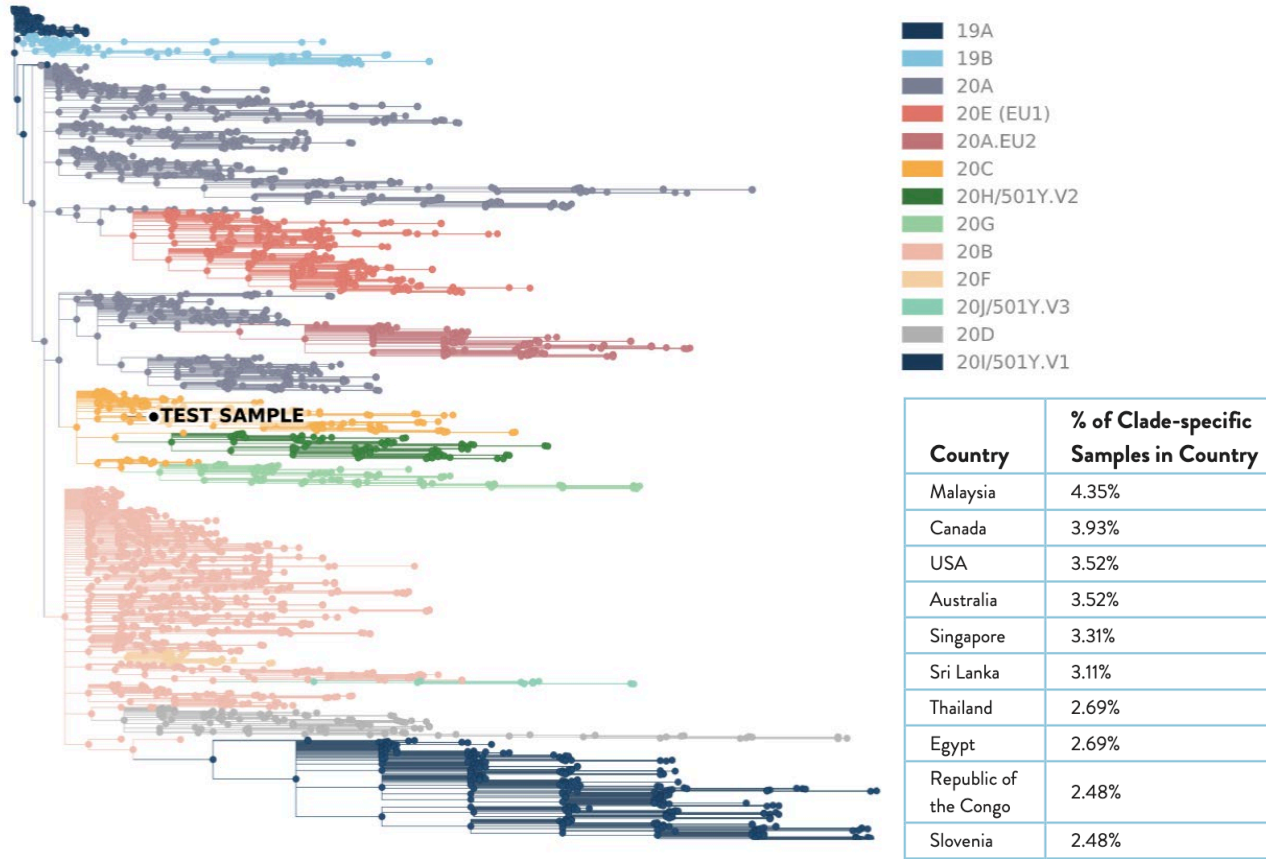
LAUNCHED

LAUNCHED

- Deep insight into virus and genetic variants
- User portal built and connected to LIMS with automated NY reporting

- Agile team responded to COVID-19 pandemic, in 4 months partnered with Twist Bioscience, optimized kit, validated on clinical samples, built COVID-DX software, and co-submitted to FDA for EUA
- Built and launched RUO version of the product (launched Nov 2020). Being used across Europe and in US labs to profile and track genetic variants
- FDA EUA Granted (March 2021): 1st hybrid capture-based NGS FDA EUA test; has both diagnostic and research applications

Placement and frequency report:



Patient: POS-016 Accession Number: 14924

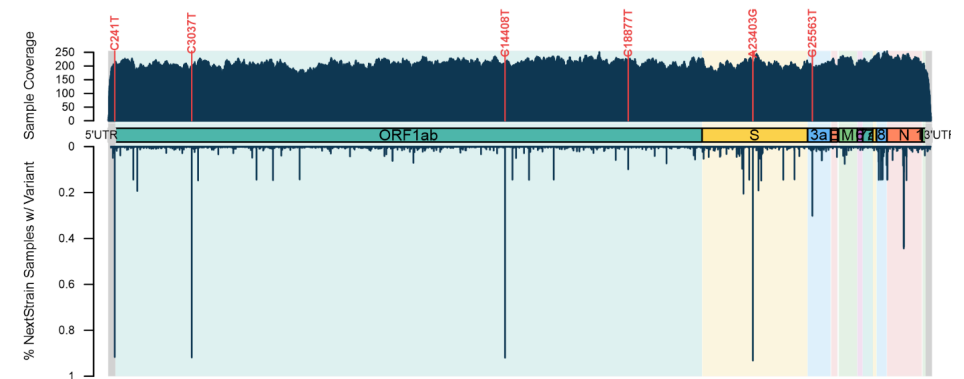
BIOTIA RUO TEST REPORT SARS-CoV-2 NGS Assay

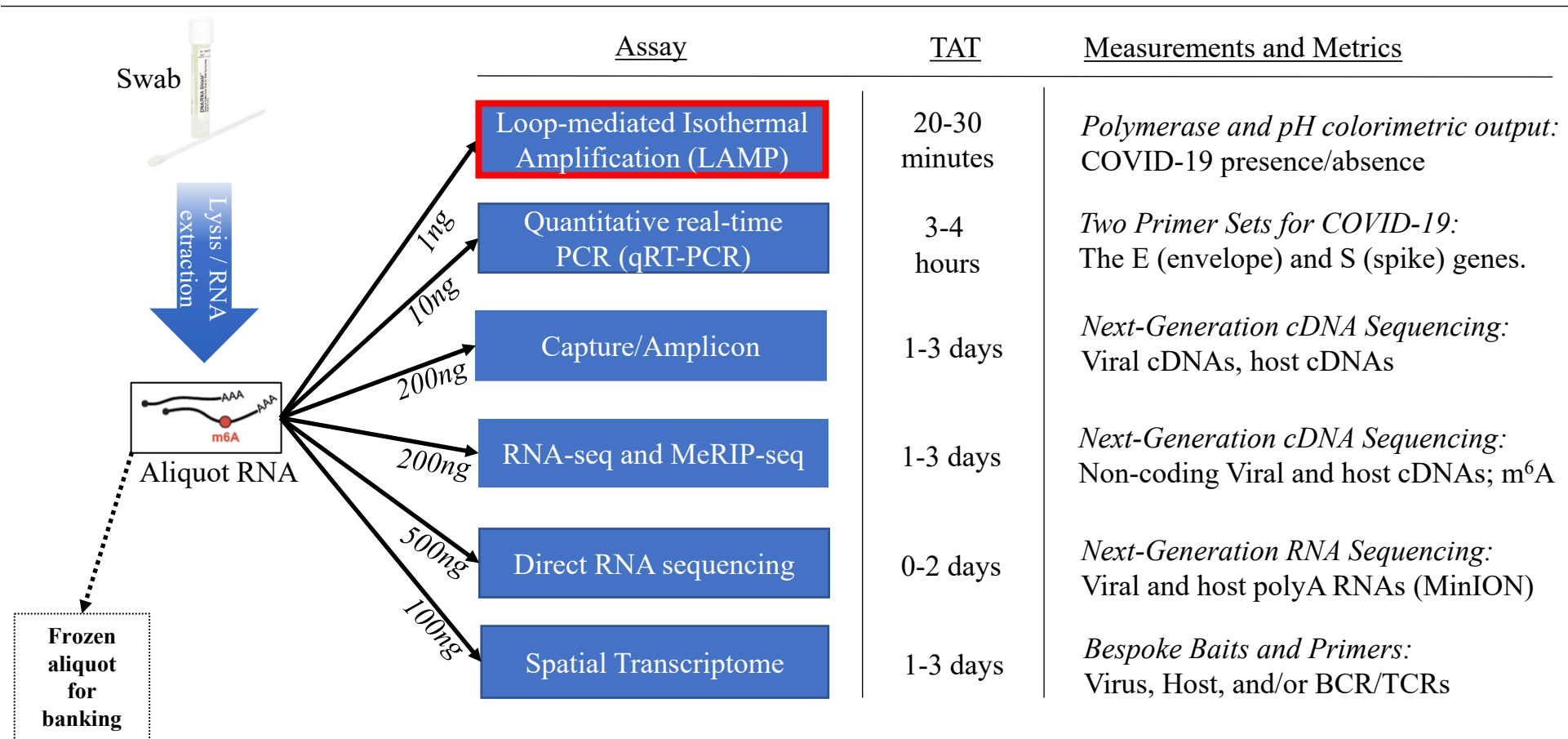
ORDERING	SAMPLE	PATIENT
Institution: Johns Hopkins Medical Center Name: Joseph Barrows Address: 9601 Medical Center Drive Rockville MD 20850 Phone Number: 2406784510 Email: jbarrow6@jhu.edu	ID: POS016 Specimen Type: Nasopharyngeal swab Collection Date: 12/07/2020 Received By Lab: 12/07/2020 Run Date: 04/28/2021 Report Date: 04/28/2021	Name: POS-016 DOB: 12/07/2020 Sex: Female ID#/HN/MRN: 12345678

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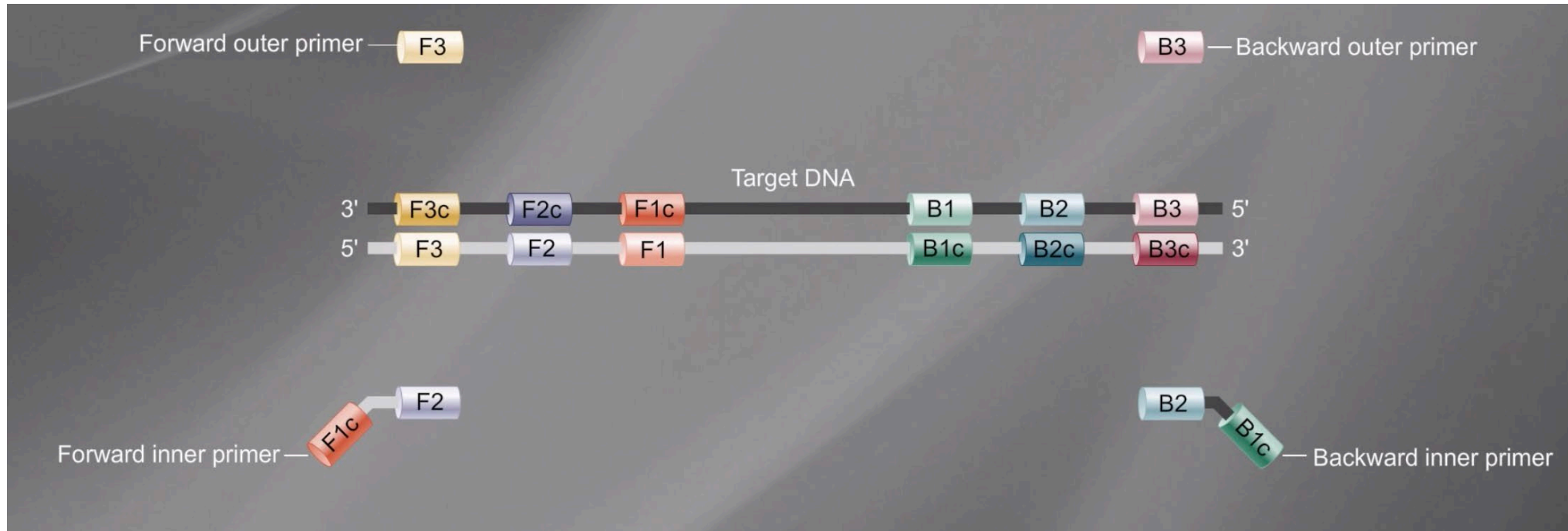


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Loop-Mediated Isothermal Amplification (LAMP)



A fast (30-40min) and inexpensive (<\$5) RT-PCR assay for targeted amplification of COVID-19 genes:

RNA → cDNA → dsDNA
with Bst strand-displacing polymerase

Loop Mediated Isothermal Amplification (LAMP) from New England BioLabs: <https://www.youtube.com/watch?v=L5zi2P4lggw> | <https://www.neb.com/protocols/2014/06/17/loop-mediated-isothermal-amplification-lamp>

Colorimetric LAMP led to FDA-approval in partnership with
Color/Broad/Weill Cornell



FierceBiotech

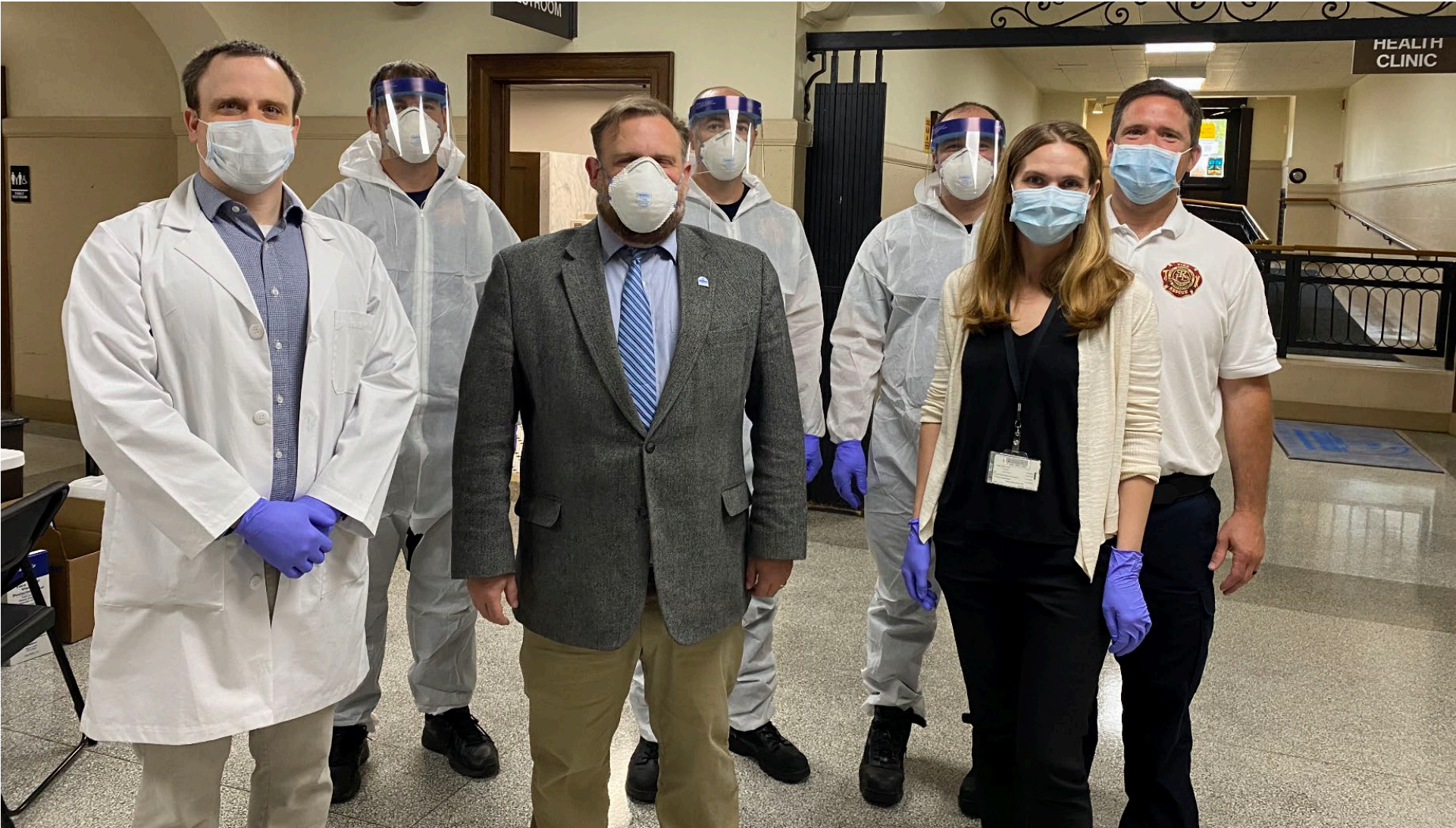
Color gets green light for LAMP-based COVID-19 screening test

by [Conor Hale](#) | May 20, 2020 11:00am

To develop its tests for the pandemic, Color has been working with the Broad Institute of MIT and Harvard as well as Weill Cornell Medicine. The company is also publishing its LAMP [protocol](#) (PDF) for use by other laboratories.

<https://www.fda.gov/media/138249/download>

Racine City Hall On-site Testing



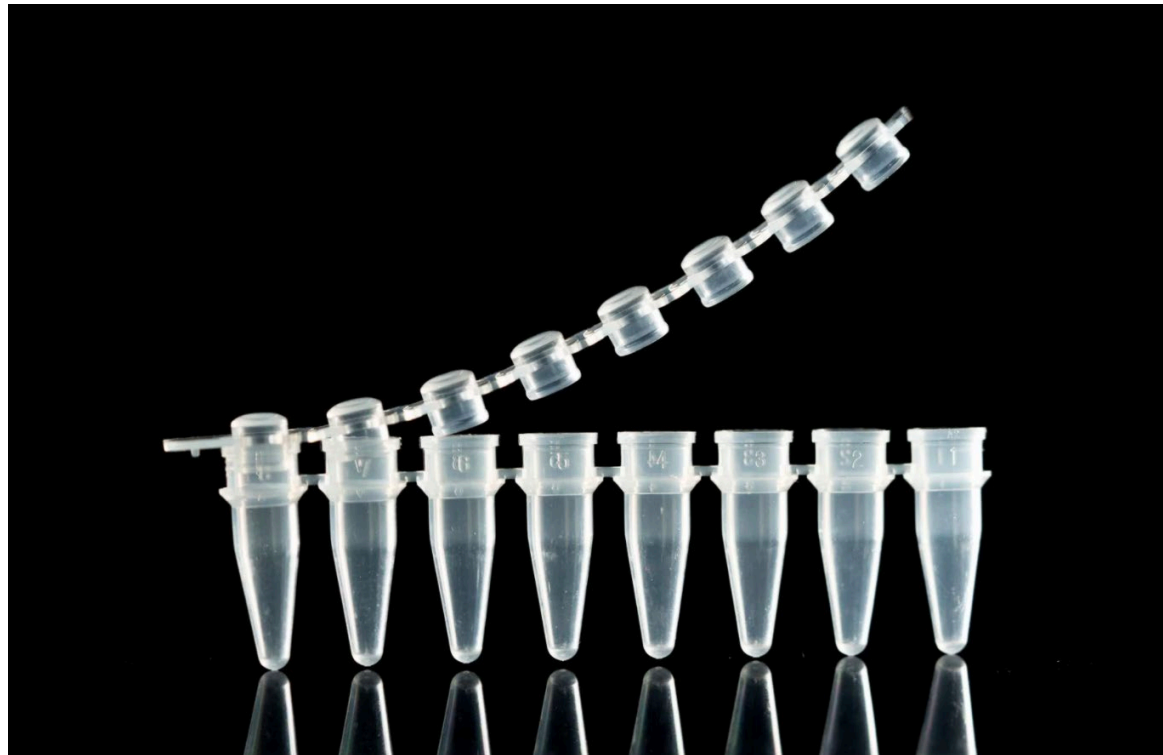


GREGORY BARBER

SCIENCE 07.23.2020 07:00 AM

A Wisconsin City Experiments With a Faster, DIY Covid-19 Test

In a former boxing gym in Racine, firefighters are trying out a spit test that's simpler and cheaper than PCR. Could it change how we screen for the virus?



<https://www.wired.com/story/a-wisconsin-city-experiments-with-a-faster-diy-covid-19-test/>



What if we had been looking all along?

What if every lab could be a meth lab?

NGS on sewage in FL, WI, and NY

DEVELOPMENT AND PROOF-OF-CONCEPT IMPLEMENTATION OF THE SOUTH FLORIDA MIAMI RADX-RAD SARS-COV-2 WASTEWATER-BASED SURVEILLANCE INFRASTRUCTURE

Award Number: U01DA053941

ORGANIZATION: NATIONAL INSTITUTE ON DRUG ABUSE

OPDIV: NIH

AWARD CLASS: COOPERATIVE AGREEMENT

AWARD ACTIVITY TYPE: SCIENTIFIC/HEALTH RESEARCH (INCLUDES SURVEYS)

Group Awards By Issue Date FY or Funding FY: Issue Date FY Funding FY

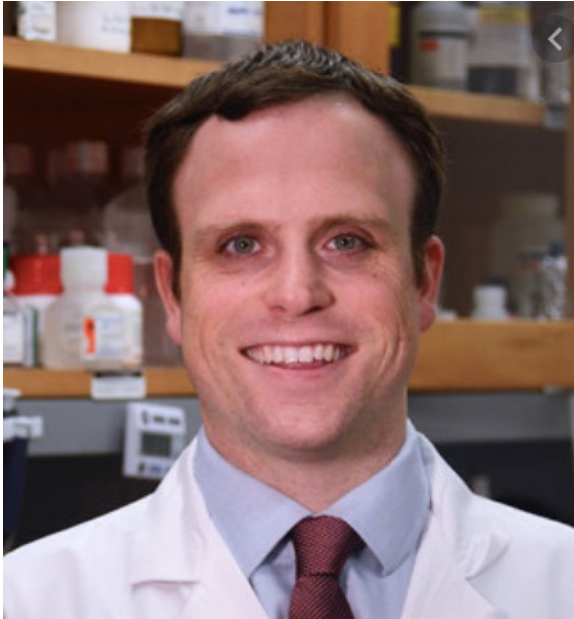
HIDE AWARD ABSTRACT

PROJECT SUMMARY The University of Miami (UM), with three primary campuses in Miami, Florida, is geographically spread within one of the worst current COVID-19 hotbeds. UM has deployed an elaborate human surveillance testing, tracking and tracing (3T) system to monitor the student body, faculty, and staff. This 3T system includes a major hospital that is part of UM and that treats COVID-19 patients. To augment this COVID-19 monitoring system, UM has deployed a pilot wastewater surveillance program for detecting SARS-CoV-2 from clusters of buildings on campus. Weill Cornell Medicine (WCM) is located in New York City, NY, an area that until recently had one of the worst outbreaks of COVID-19. WCM has established an international consortium for SARS-CoV-2 environmental surveillance, including in NYC and globally with the [MetaSUB Consortium](#), which is creating metagenomic and metatranscriptomic maps of the world's sewage. Based on this work at both UM and WCM, this proposal aims to develop, implement, and demonstrate effective and predictive wastewater surveillance by optimizing sampling, concentration, and detection strategies. Working closely with the RADx-rad Data Coordination Center (DCC), this application (SF-RAD) will

https://taggs.hhs.gov/Detail/AwardDetail?arg_AwardNum=U01DA053941&arg_ProgOfficeCode=114

SF-RAD: SARS-CoV-2 Wastewater-Based Surveillance

Project Leaders



Chris



Stephan



Helena

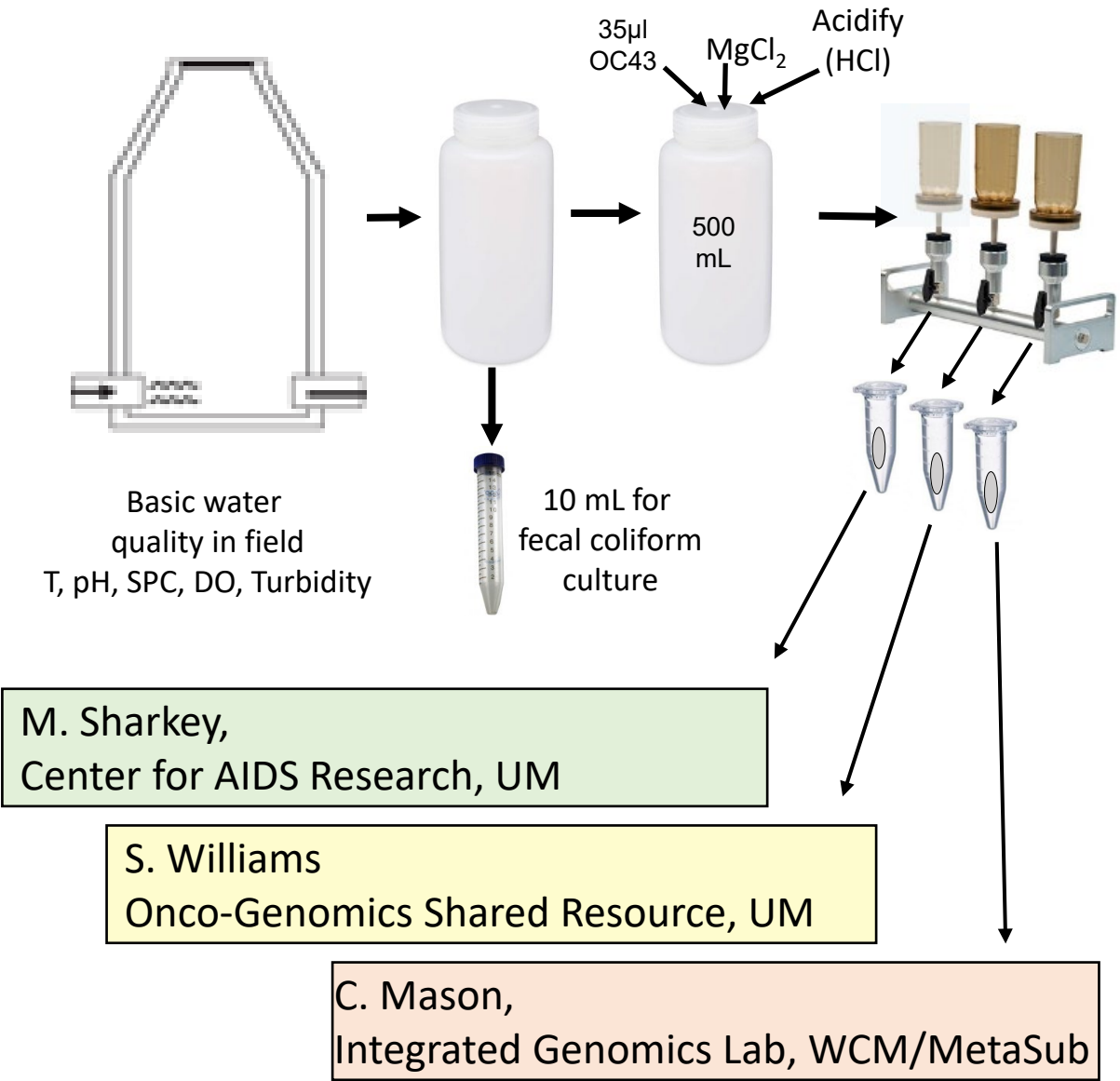


George

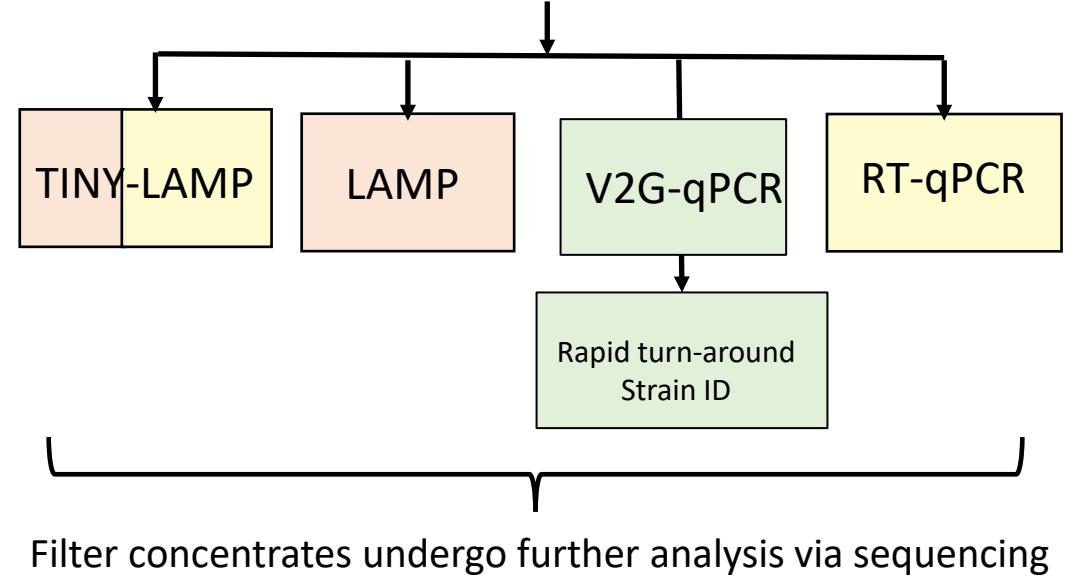
PIs: Chris Mason, Stephan Schürer, Helena Solo-Gabriele*
Administrative Core: George Grills (co-I)

Administrative Support: Maria Robertson

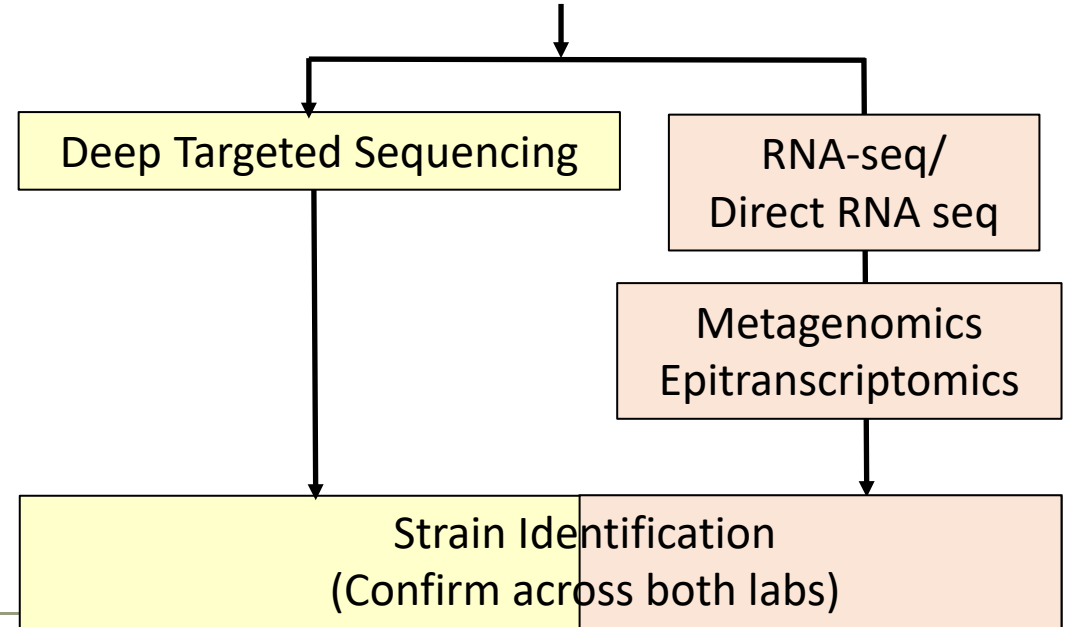
Sample Analysis



Rapid Detection

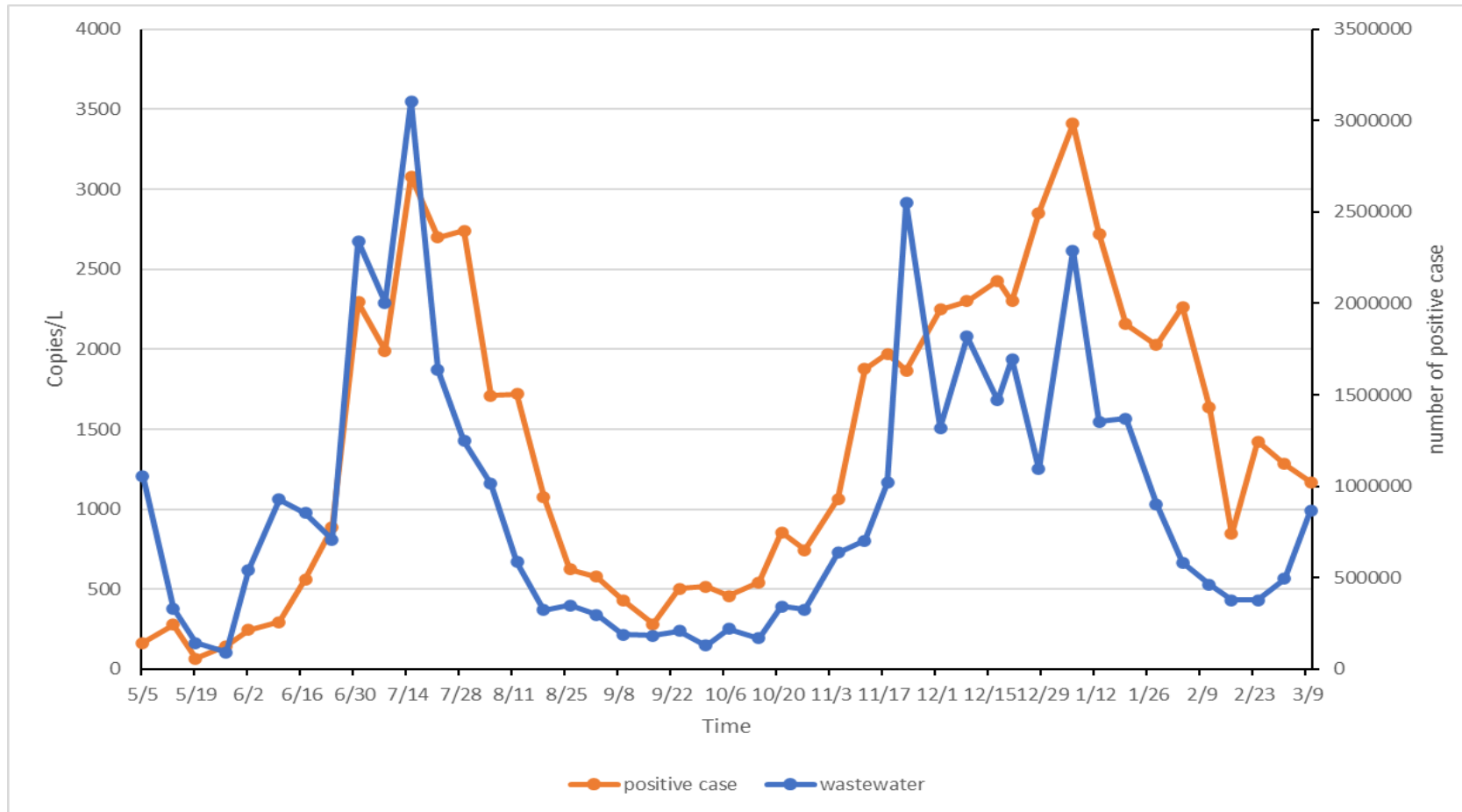


Genomic Analysis



SARS-CoV-2 Wastewater-Based Surveillance

Close correlation between the sewage and population metrics

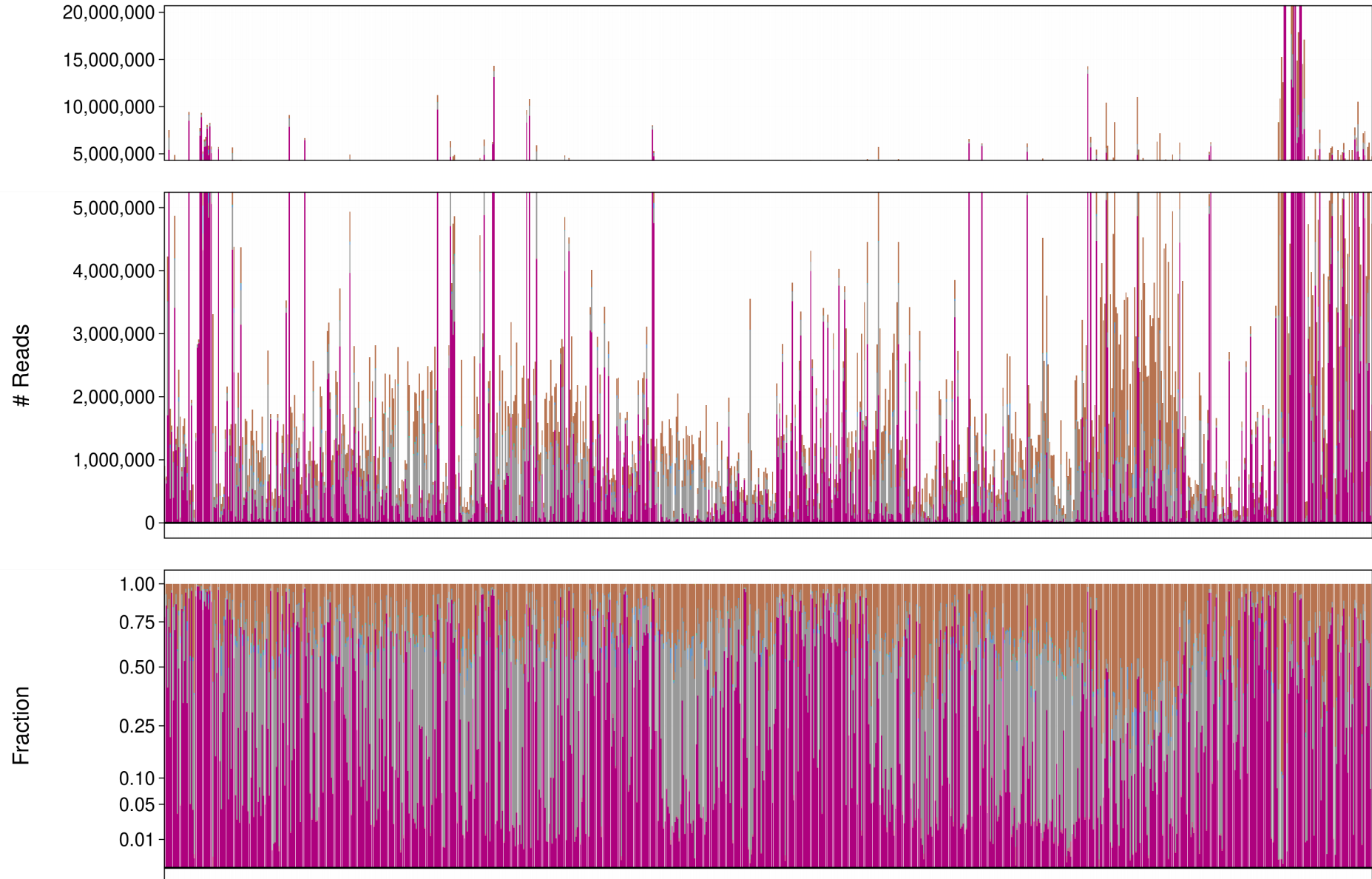


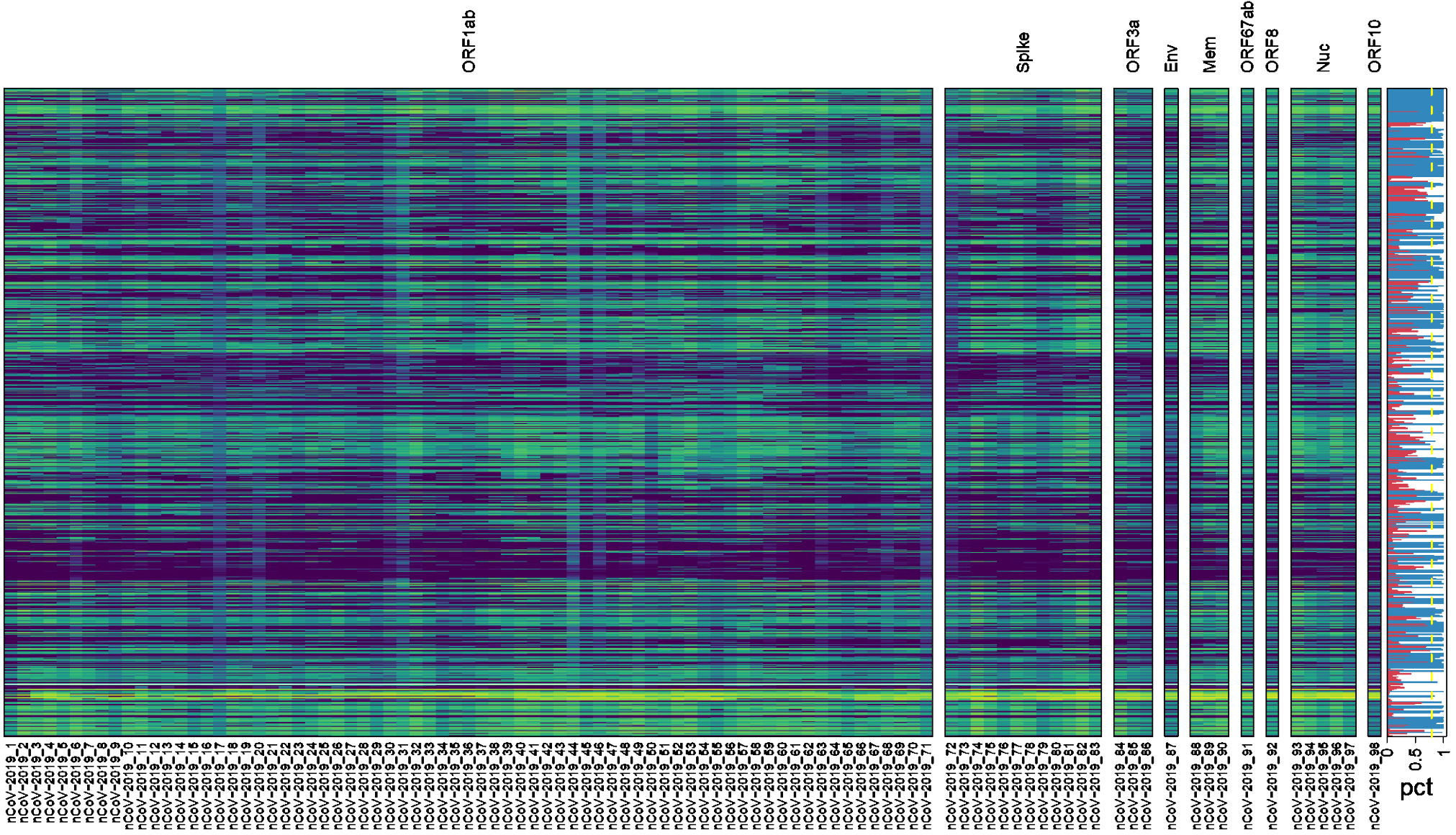
Wastewater VOC Detection Methodology

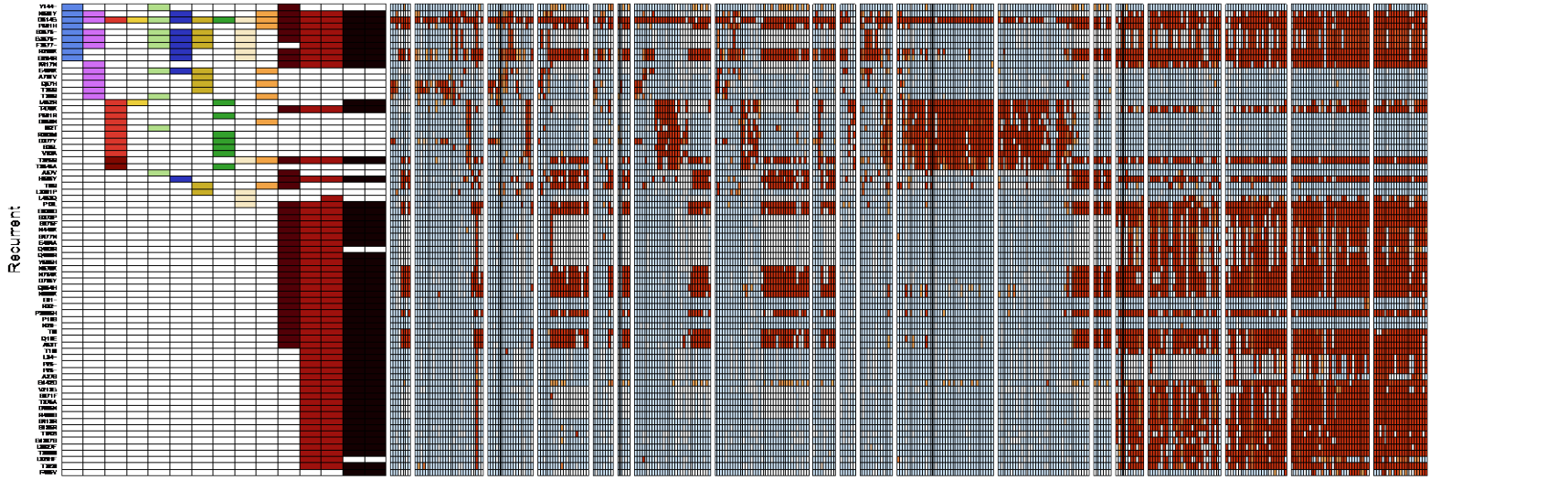
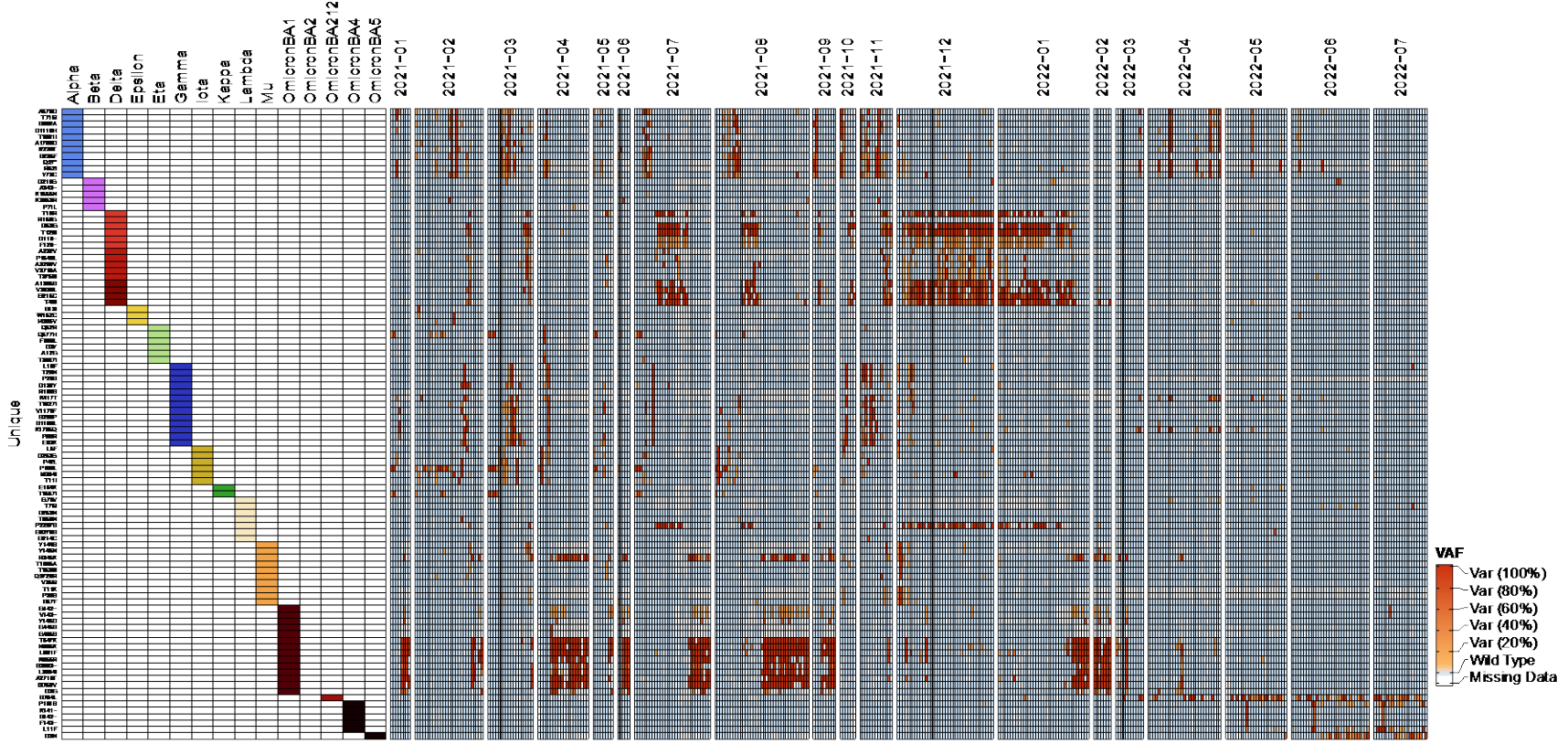
1. Assign taxonomy to all reads and filter SARS-CoV-2 matches with **kraken2**
 - Run using custom pan-kingdom DB
 - Generate SARS-CoV-2 FASTQs leveraging **seqtk**
2. Align to Wuhan reference with **bwa mem**
 - Sort and index alignment with **sambamba**
3. Trim primers with **ivar trim** using version-specific ARTIC BED file
 - Get coverage statistics on trimmed BAMs
 - **bedtools genomecov** for per-base coverage
 - **mosdepth** for per-amplicon coverage
4. Call variants using hybrid approach with **lofreq** and **ivar**
 - Take union of calls to avoid FNs and use mean DP/VAF per mutation call
5. Annotate mutations (assign gene, impact, amino acid substitutions) with **VEP**
6. Estimate relative VOC lineage abundances with **Freyja**

Classification

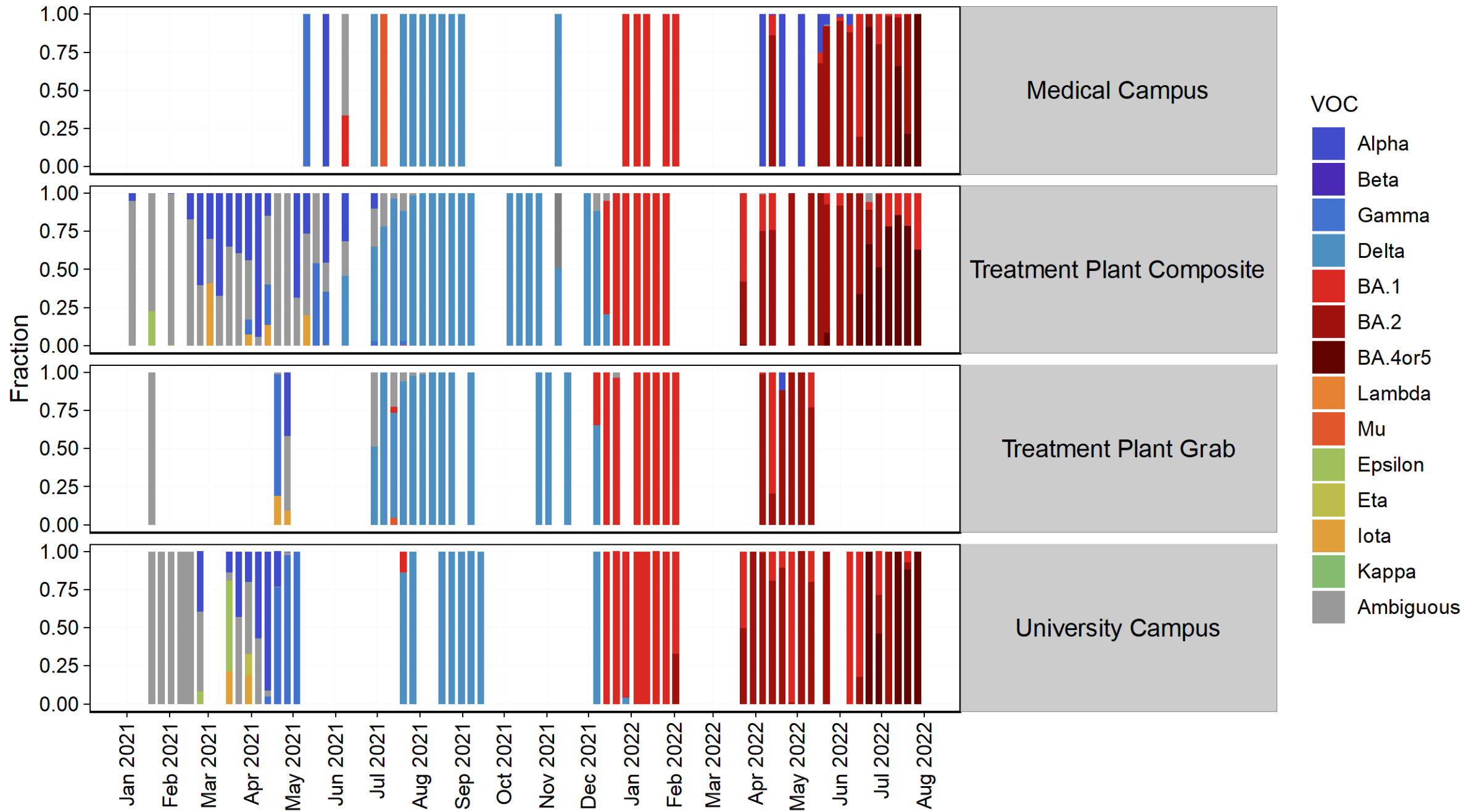
sars_cov2	fungi	archaea	not in database
human	bacteria	other_viruses	



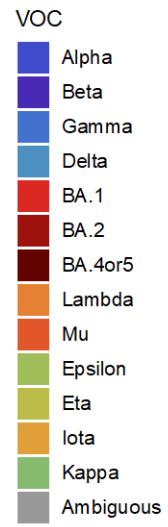
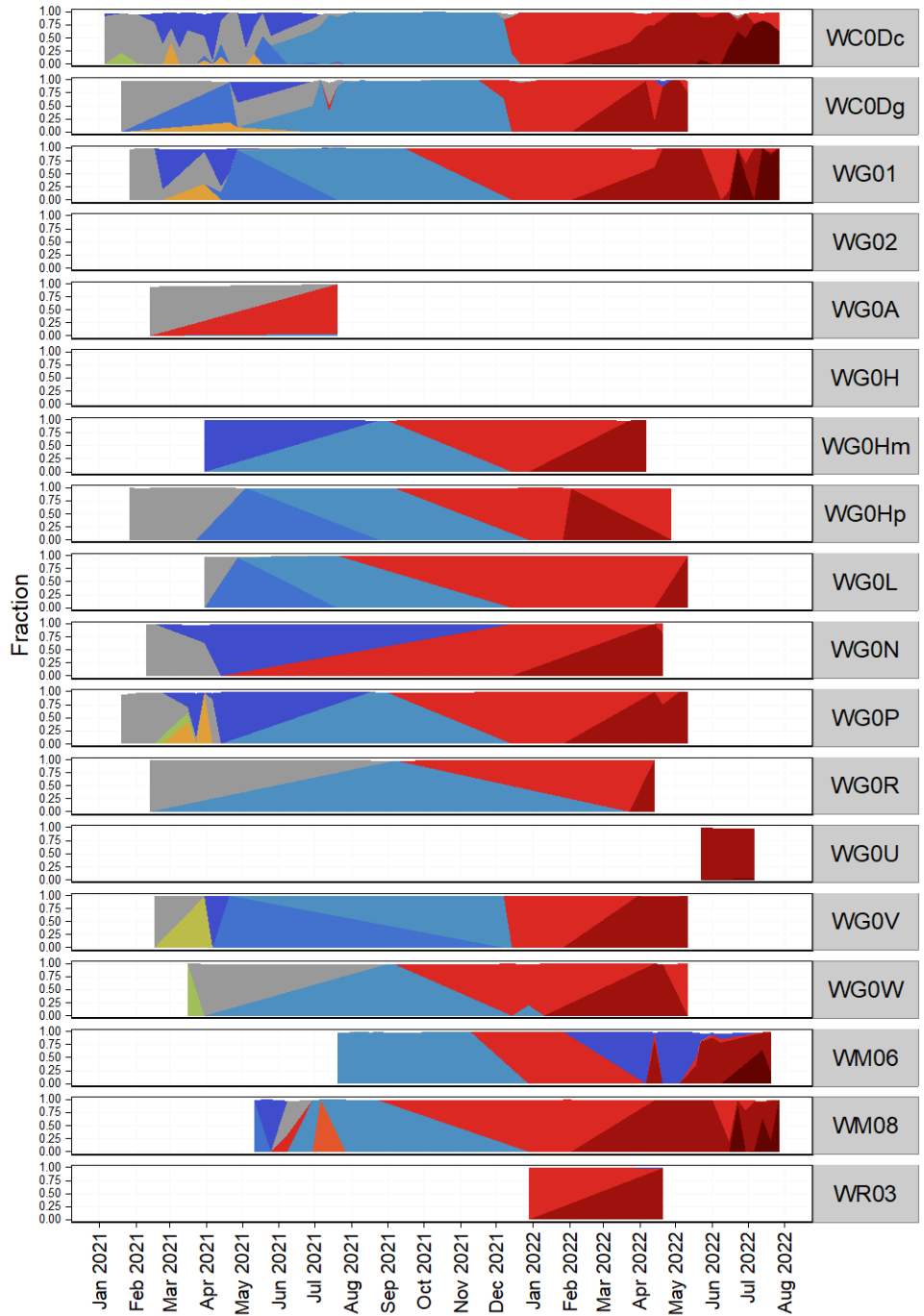




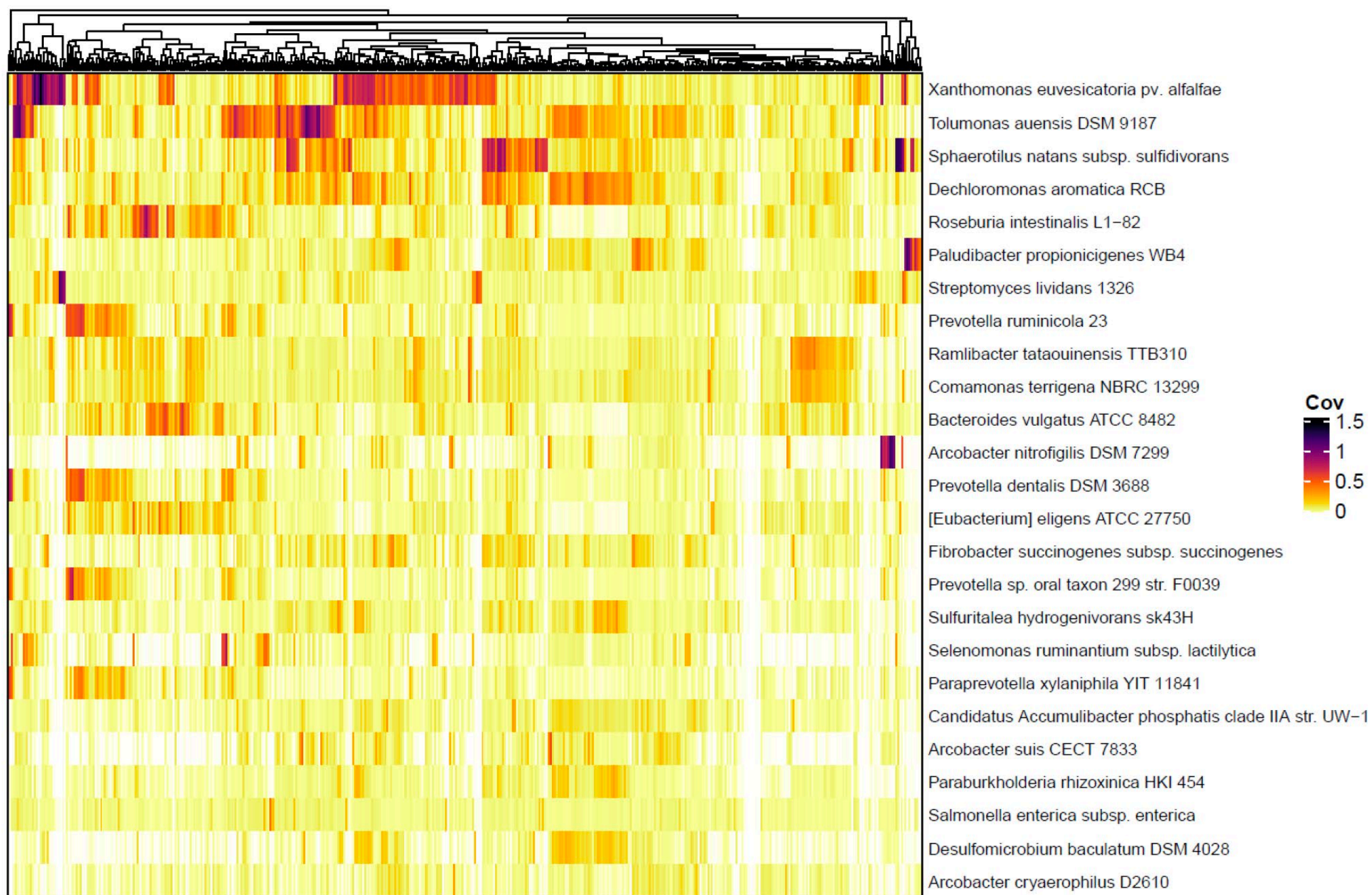
Wastewater Variant Abundance



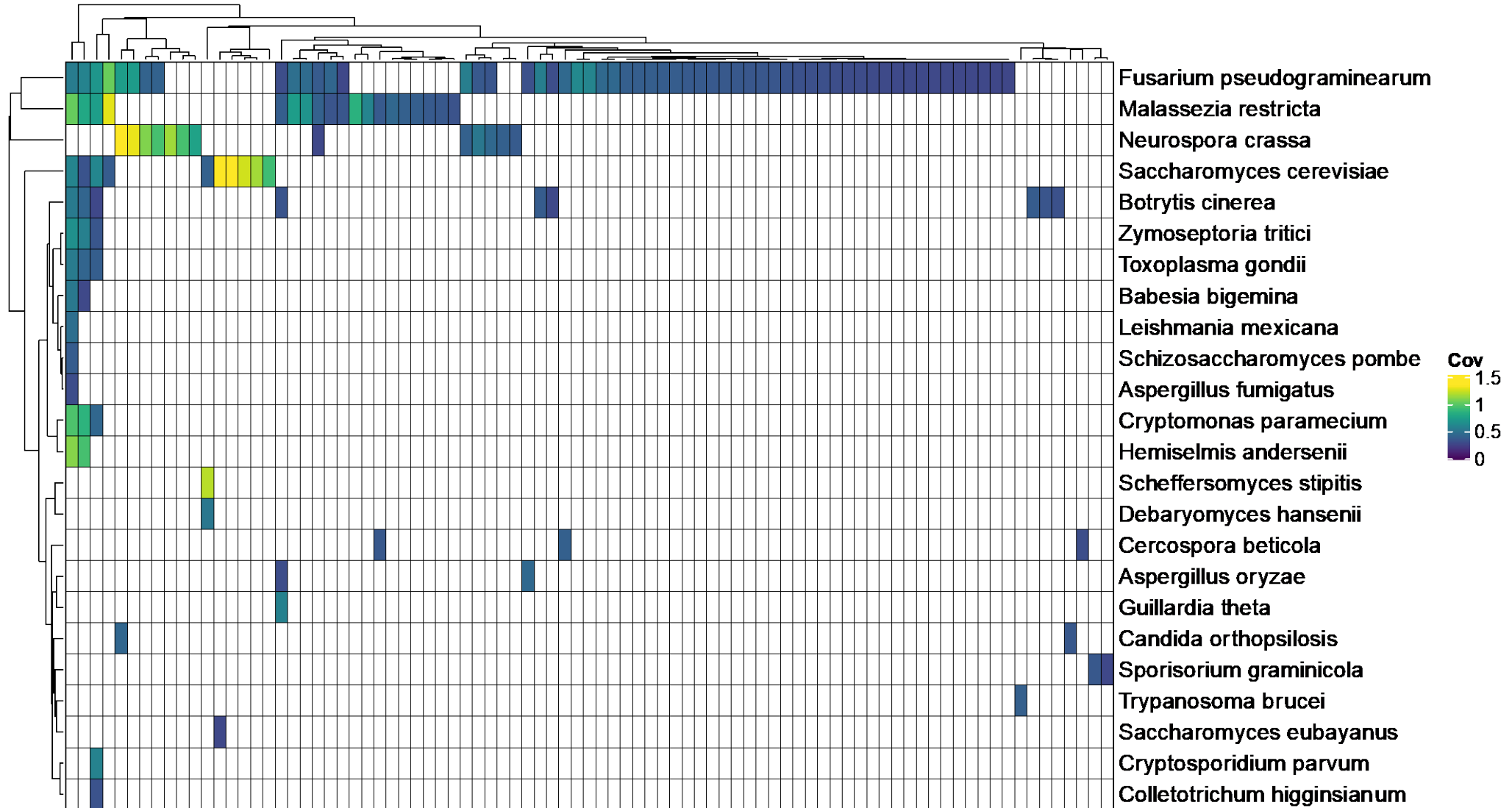
Wastewater Variant Abundance

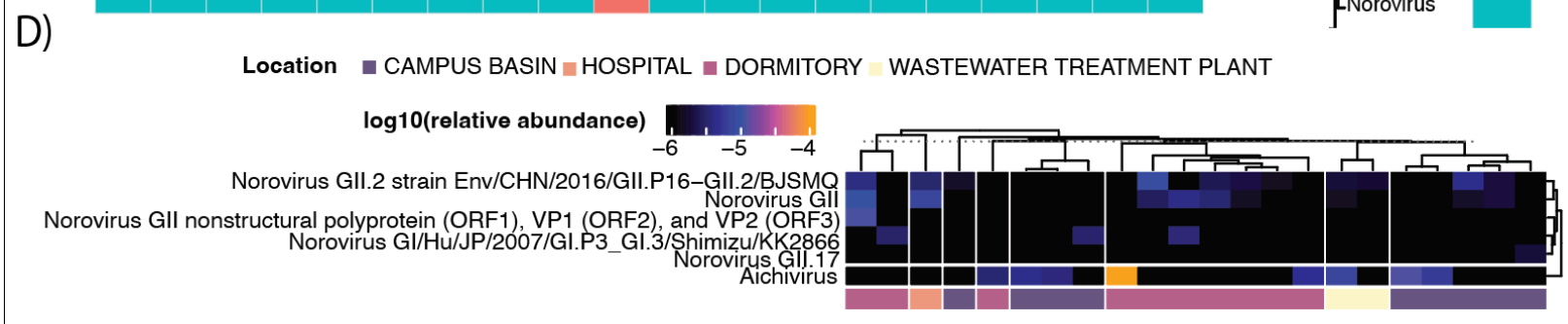
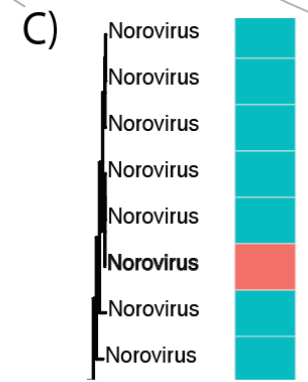
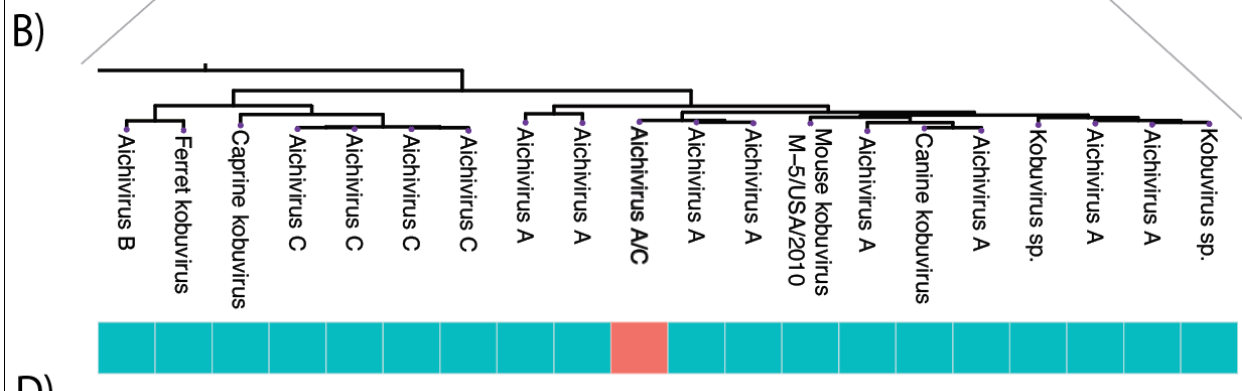
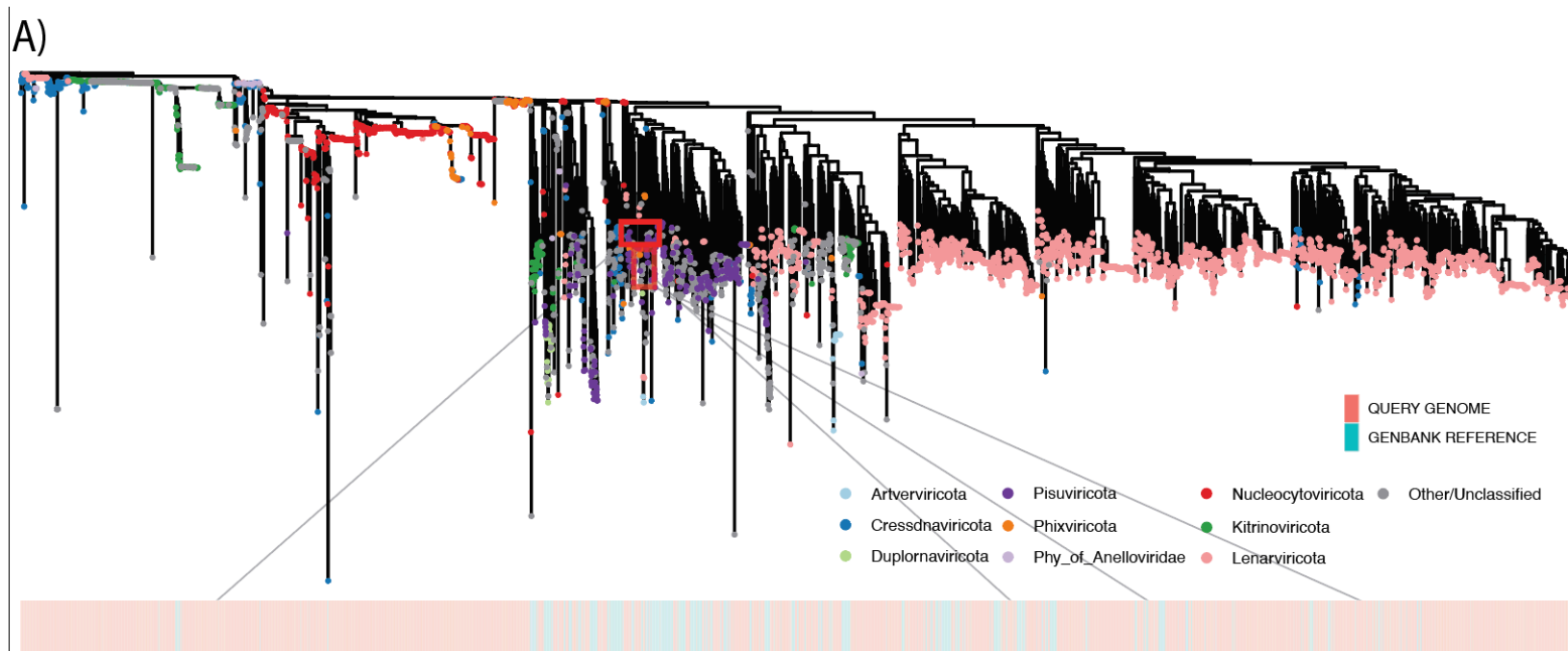


Bacteria

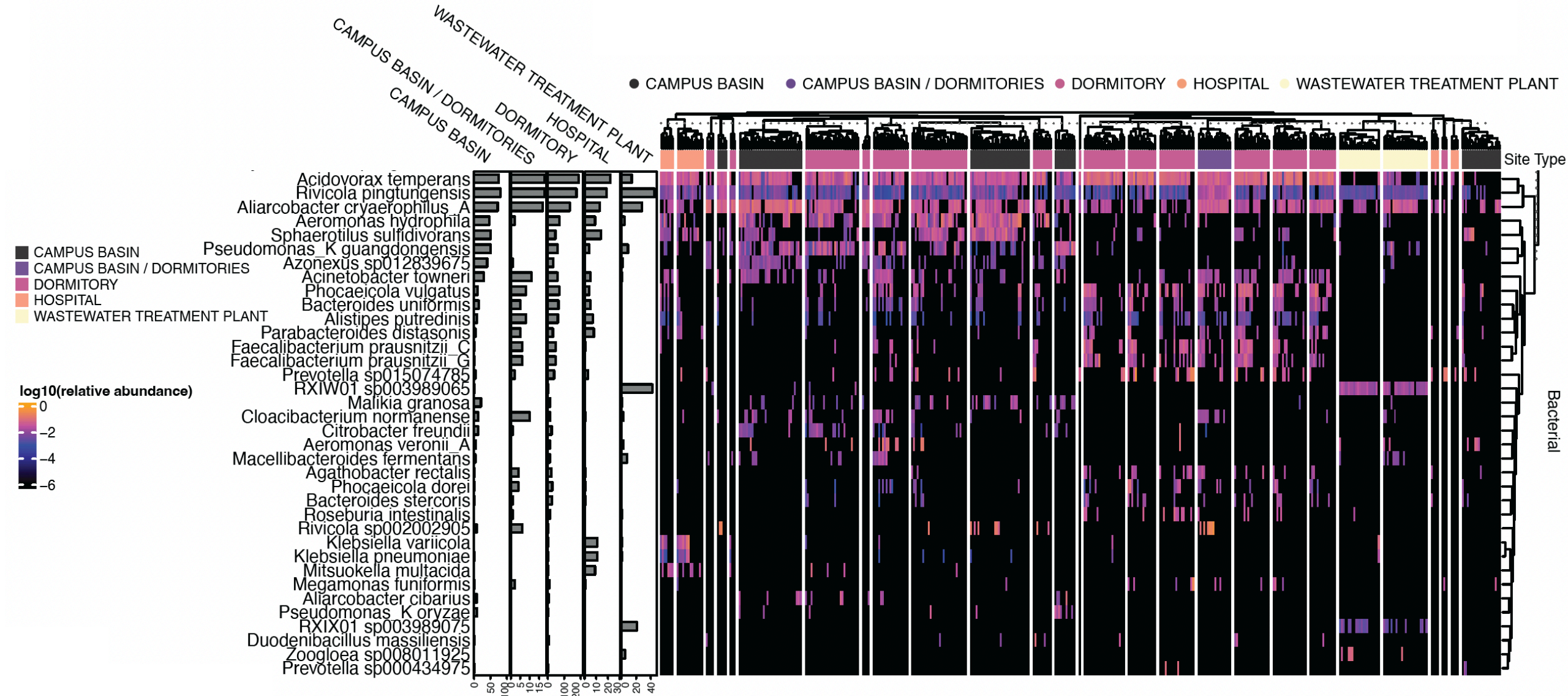


Top Fungi observed in shotgun RNA-seq

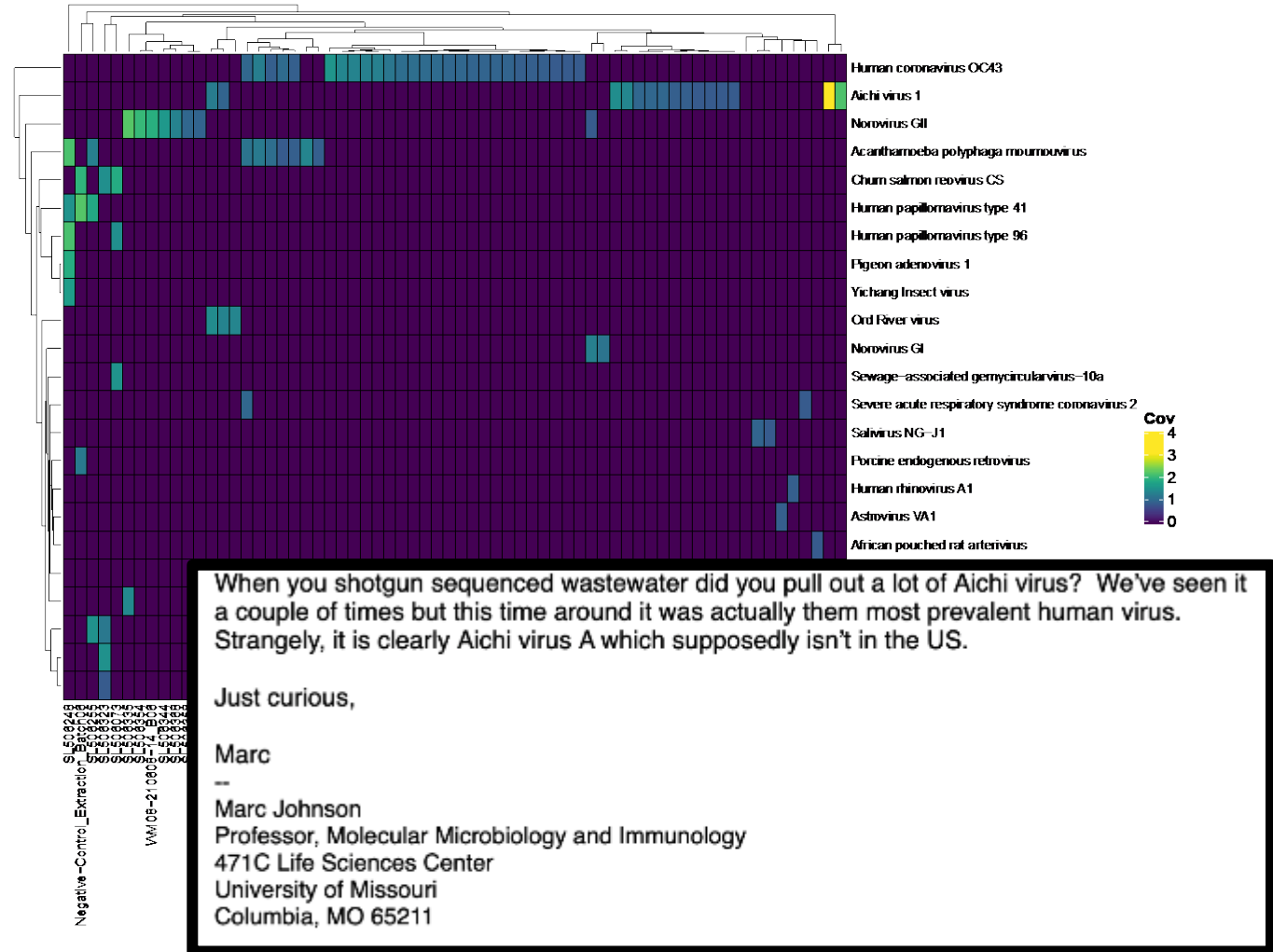
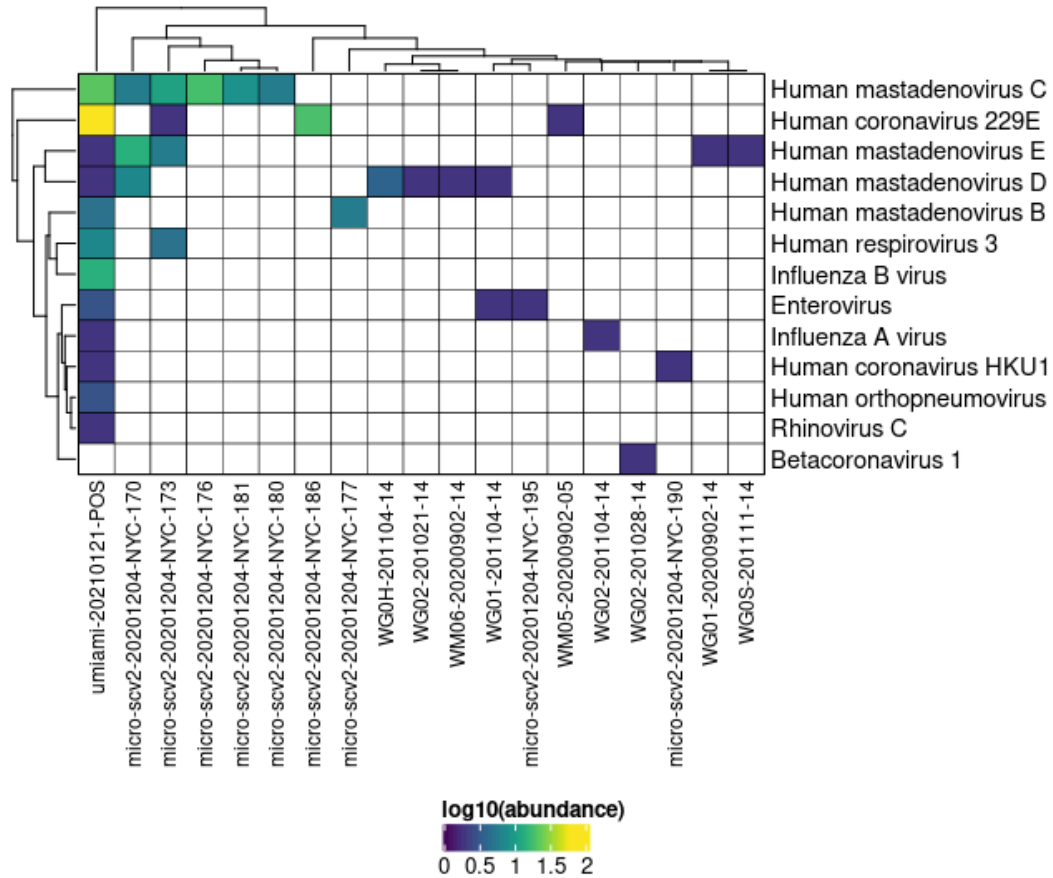




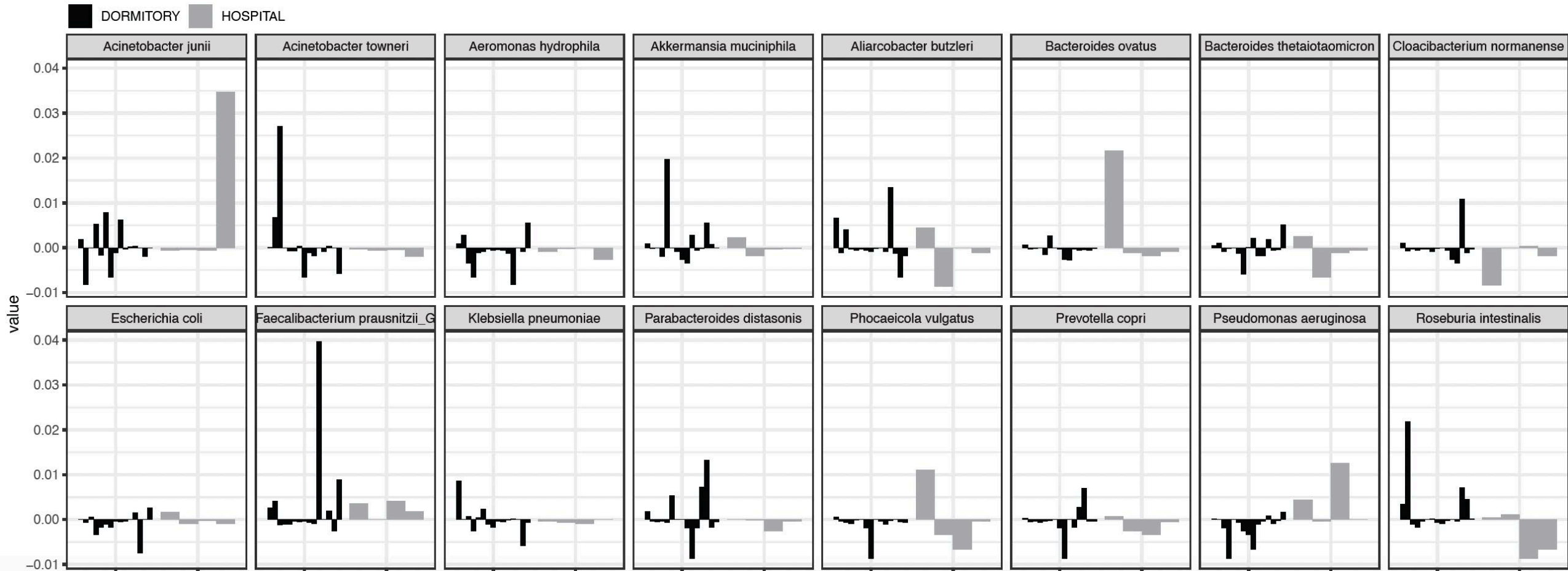
Details: regional microbial movement on campus



Targeted search for respiratory pathogens



Dorm vs. Hospital environments each shows unique enrichments



Now for planes at JFK!



Andrew Franklin with Ginkgo Bioworks

Not the first time...

New fields lead to new lessons: 2013

What Microbes Live In YOUR Subway Station?

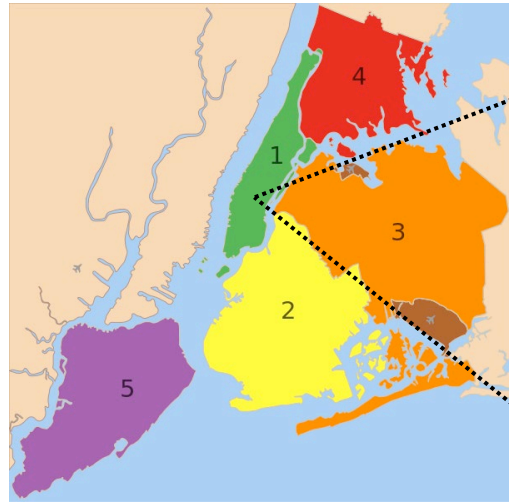
BY [LAUREN EVANS](#)

NOV. 4, 2013 4:40 P.M. • [10 COMMENTS](#)



[TWITTER](#)

We can presume that the man who licked his shoe on the subway dropped dead moments after [the last frame of this video](#), but plenty of daily straphangers forget



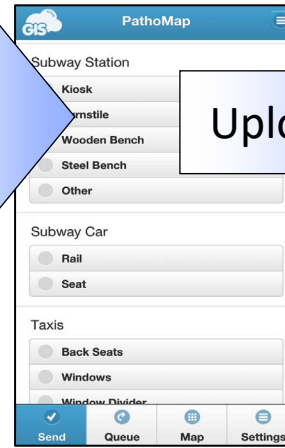
1. Swab (3 min)

2. Annotate

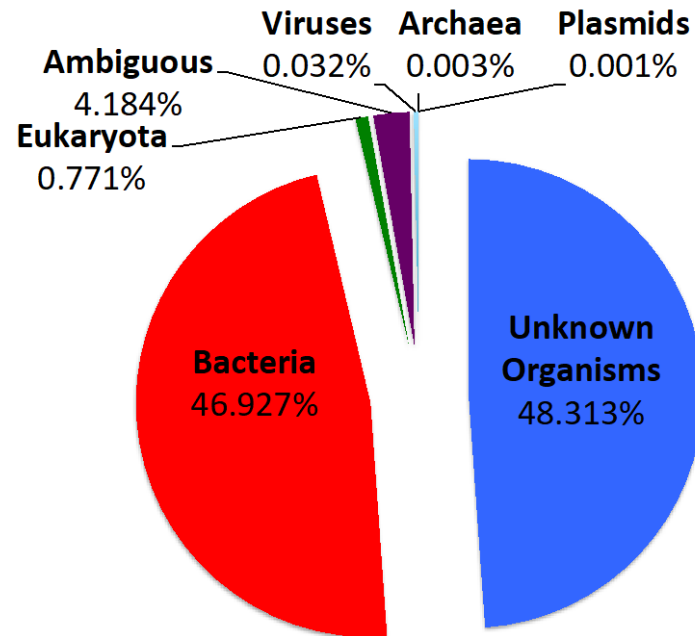
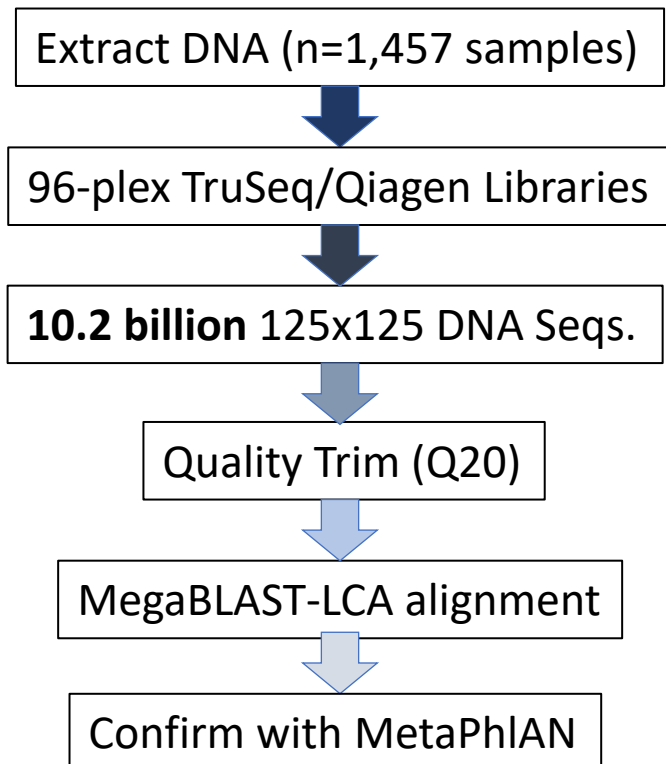
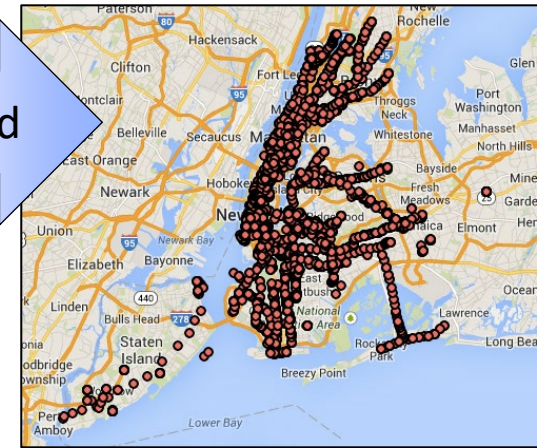
3. GPS-tag/timestamp



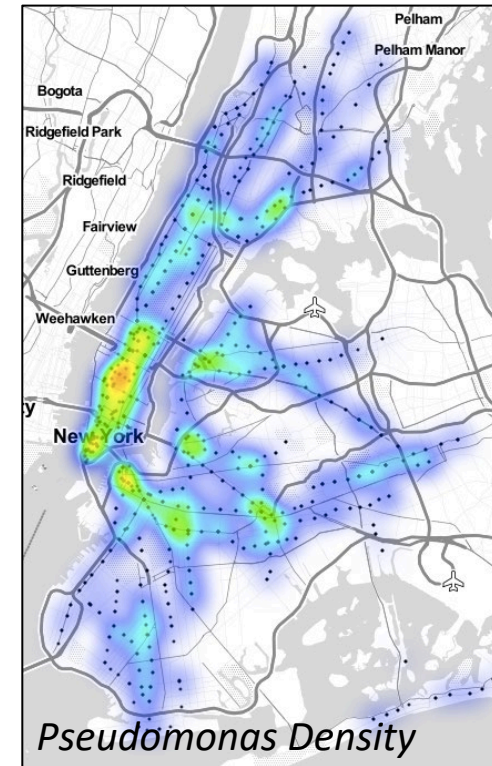
Data Entry



Upload



Half of the world under our fingertips is unknown



THE WALL STREET JOURNAL.

Big Data and Bacteria: Mapping the New York Subway's DNA

Scientists in 18-Month Project Gather DNA Throughout Transit System to Identify Germs, Study Urban Microbiology

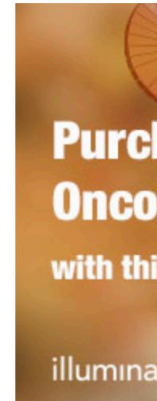


Mapping the Bacteria in the NYC Subway

Researcher Christopher Mason from Weill Cornell Medical College collecting DNA samples at the 68th Street subway station in New York City last summer. The scientists identified hundreds of types of bacteria, most harmless, in the transit system as a way to study the microbiology of urban environments. Photo: Katie Orlinsky for The Wall Street Journal

By *Robert Lee Hotz*

Feb. 5, 2015 1:07 pm ET



RECOMMEND

1. Iraqi Parli to Expel U
2. 2020 Gold Winners
3. Soleimani Unites Ira Inflames / Mood
4. The Debat Buybacks,

Media is not the place for nuance


ARTS & ENTERTAINMENT

Licking Subway Poles "Probably Fine," Says Expert

BY [REBECCA FISHBEIN](#)

PUBLISHED FEBRUARY 5, 2015 | MODIFIED FEBRUARY 5, 2015 |  43 COMMENTS



 No scary germs here! RYAN QUINN/GOTHAMIST

Expert: If You Lick a Bunch of Subway Poles You'll "Probably be Fine"



Hudson Hongo

02/05/15 11:10PM Filed to: PUBLIC SERVICE ANNOUNCEMENTS



13.50K



[HOME](#) > [SCIENCE](#)

A geneticist says any new parent should 'roll their child on floor of the New York subway' — here's why

Erin Brodwin Aug 15, 2015, 10:45 AM

A team of geneticists made headlines a few months ago after its mission to document all the bacteria on the New York City subway turned up nearly 600 different species of microbes crawling around on all those greasy rails.



REUTERS/Carlo Allegri

“Traces of species” becomes...



The image is a screenshot of a CBS News website article. At the top, the navigation bar includes the CBS News logo, menu items for NEWS, SHOWS, LIVE, and LOCAL, a search icon, and a Login button. The main content area features a large background image of a subway map with a heatmap overlay. The heatmap shows various colored zones (red, orange, yellow, green, blue) and numbered markers (1, 2, 3, 4, 5) along the subway lines, indicating the presence of pathogens. The article title is "Dangerous pathogens and mystery microbes ride the subway" in a large, bold, white font. Below the title, the text "HEALTH >" is visible. At the bottom of the article preview, there is a date and time stamp: "FEBRUARY 6, 2015 / 10:42 AM / CBS NEWS" and social media sharing icons for Facebook, Twitter, and a square icon.

CBS NEWS NEWS ▾ SHOWS ▾ LIVE ▾ LOCAL ▾ Login

HEALTH >

Dangerous pathogens and mystery microbes ride the subway

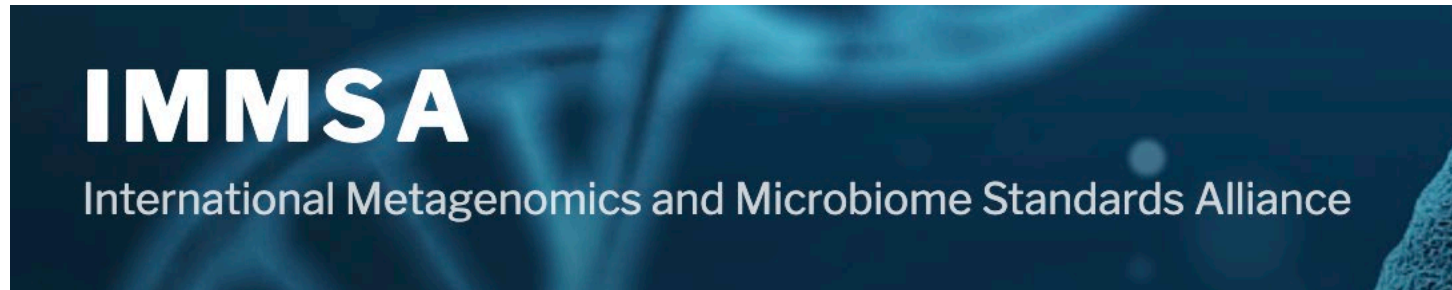
FEBRUARY 6, 2015 / 10:42 AM / CBS NEWS

f t

Letting the
molecules
speak for
themselves
is
not enough

Running multiple
algorithms
is
not enough

How to learn and fix it?



<https://genomebiology.biomedcentral.com> › articles

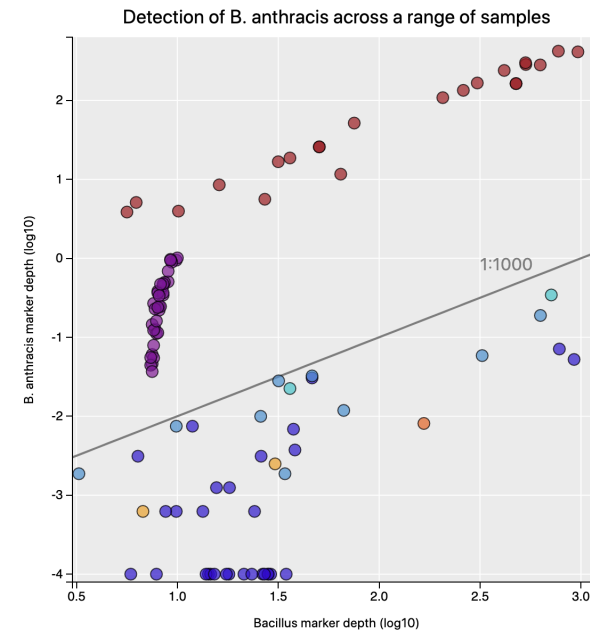
Comprehensive benchmarking and ensemble approaches for ...

by ABR McIntyre · 2017 · Cited by 233 — In this study, we use the largest-to-date set of laboratory-generated and simulated controls across 846 species to evaluate the performance...

<https://genomebiology.biomedcentral.com/articles/10.1186/s13059-017-1299-7>

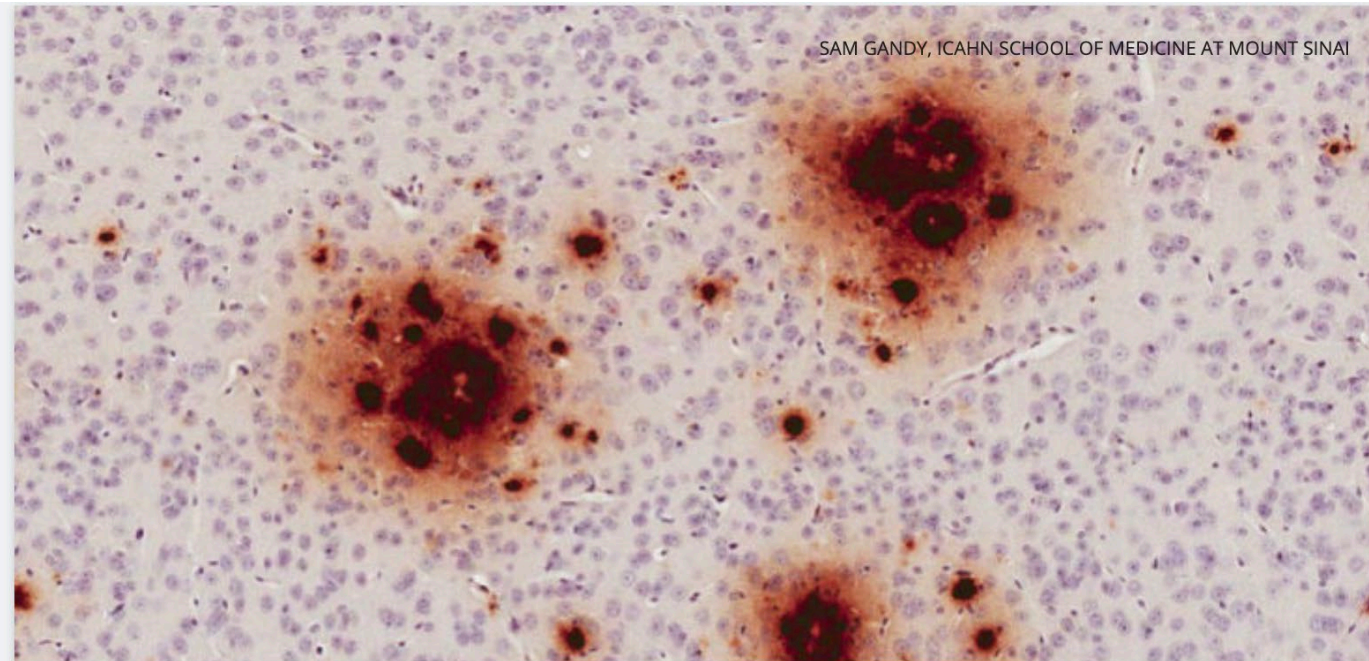
New methods

Detection of *Bacillus anthracis* using a targeted gene panel



More eyes, more critique,
and more open data

Herpes?



SAM GANDY, ICAHN SCHOOL OF MEDICINE AT MOUNT SINAI

Home / News & Opinion

Herpes Viruses Implicated in Alzheimer's Disease

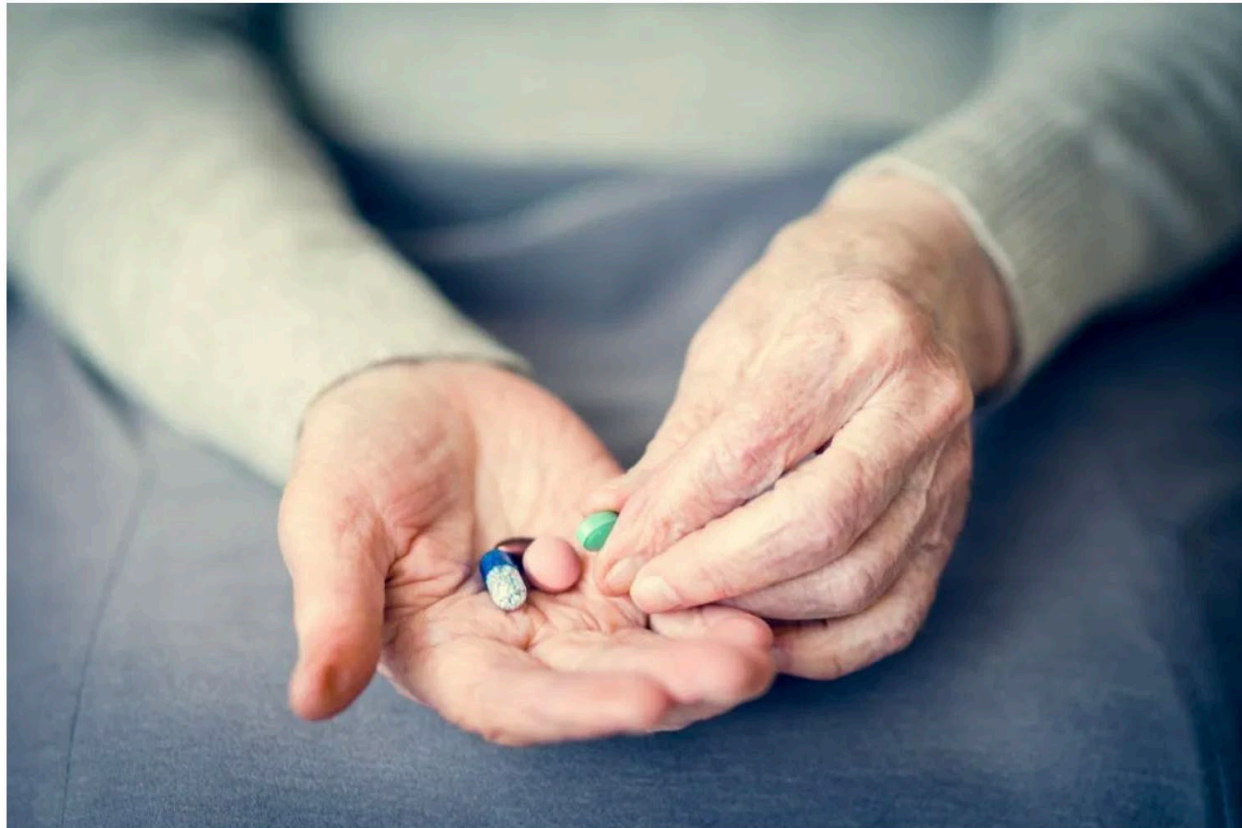
A new study shows that the brains of Alzheimer's disease patients have a greater viral load, while another study in mice shows infection leads to amyloid- β build up.

Jun 21, 2018
ANNA AZVOLINSKY



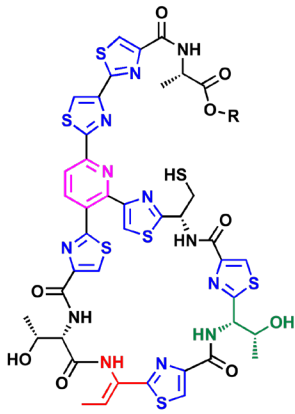
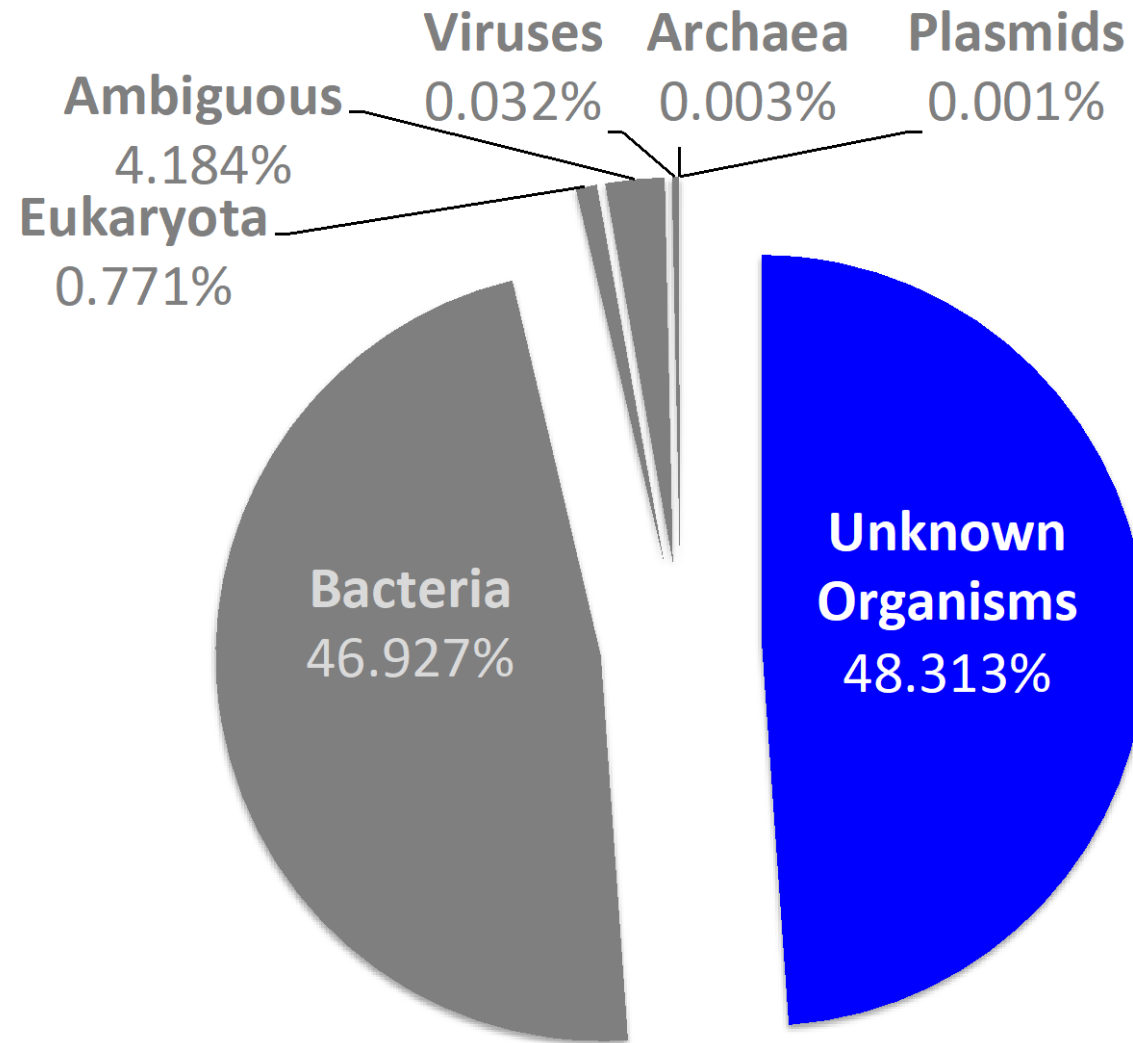
Alzheimer's risk 10 times lower with herpes medication

New results could change the face of Alzheimer's treatment; the herpes simplex virus is found to play a vital role in the condition, and antiherpetic medication is shown to have a dramatic effect on dementia risk.

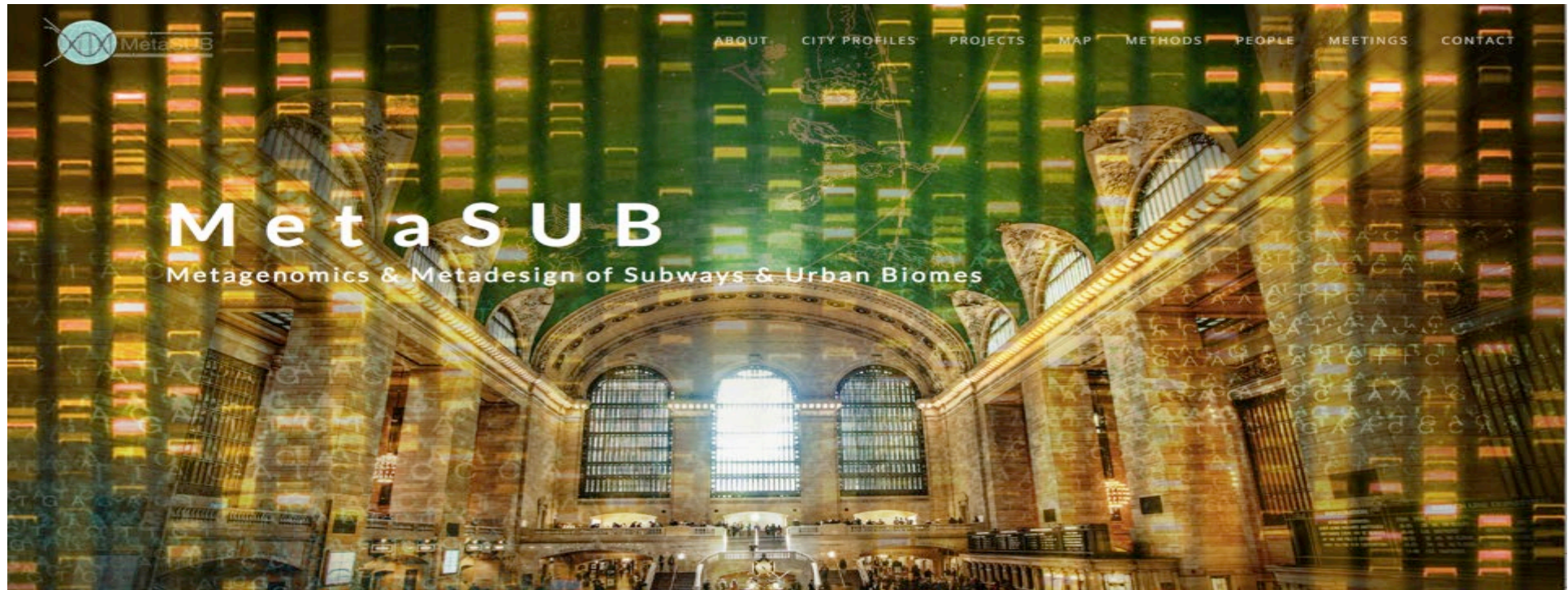


Alzheimer's disease may soon be treated with antiviral medication.

Who is there, and what are they making?



Global teams



3 Goals:

1. Geospatial Metagenomic and Forensic Maps
2. Anti-microbial resistance (AMR) marker tracking by genetics and epigenetics
3. New Biosynthetic Gene Clusters (BGCs); new drugs

www.metasub.org





You Retweeted

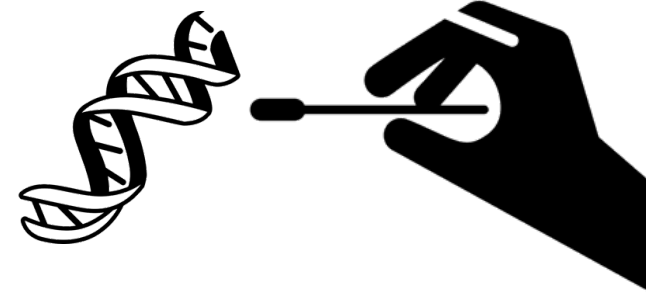


Niranjan Nagarajan @NiranjanTW · Jun 21

The Swab action team in Singapore as part of [#metasub2019](#) @metasub



MetaSUB



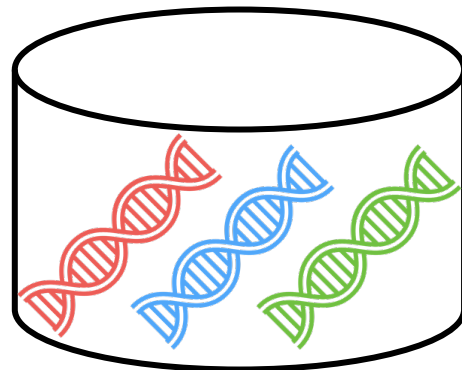
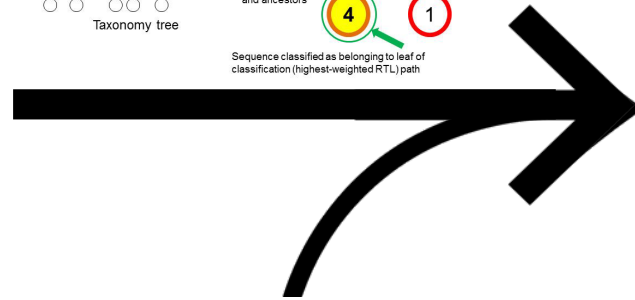
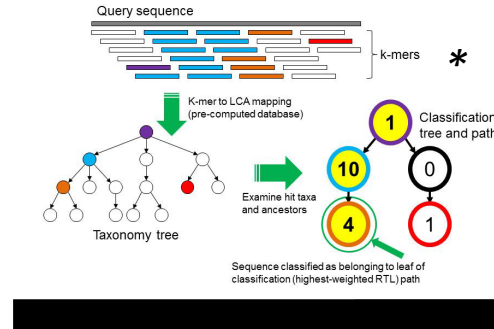
ATCGAGTAGA...GATCGATCGT

AGCTGAGCTT...GATAAGTCGT

Paired End 150bp Reads
~6 Million Reads per Sample

Reference Based Metagenomic Analysis and *de novo* assembly

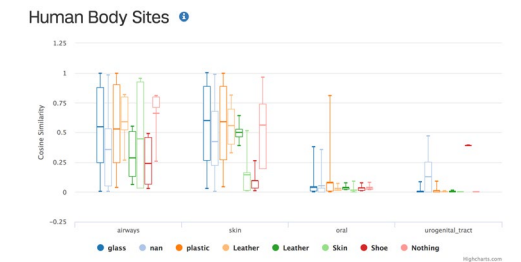
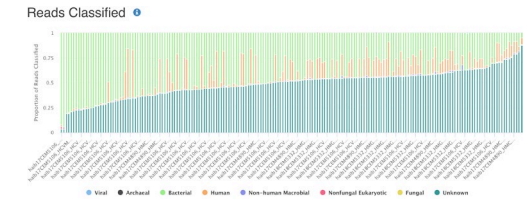
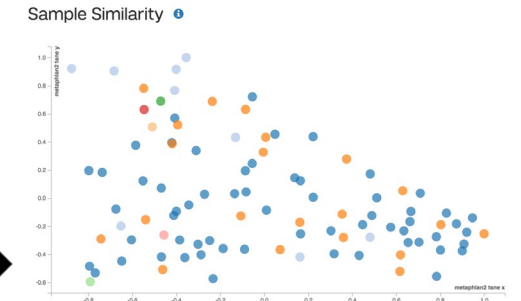
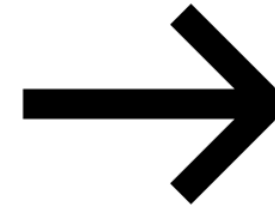
>1
ATGCGTACGAT
>2
GCGATAGAGAG
>3
TTTTTAATATT
>4
ATAGCGAGCTG
>5
TTTTTAATATT
>6
GCGGGGAGCTG
>7
TGTAGTCNTCC
>8
TGAGGAGGAGT



UniRef90, RefSeq,
NCBI-NR, etc



Assembly



*Kraken Salzberg, 2014

Danko, Bezdán et al., Cell, 2021

The MetaSUB Core Analysis Modular Pipeline (CAMP)



Open Science for Life in Space

Core modules

QUALITY CONTROL

- Summary statistics
- FASTQC
- Deduplication
- Adapter trimming
- Host read removal
- Error correction

SHORT READ

- Taxonomic abundances
- Pathway/functional abundances
- GT-Pro/SNP abundances
- Wastewater analysis

ASSEMBLY

- Multiple long/short/co-assembly methods
- Contig quality control

A modular git ecosystem
as an alternative to one—
click pipelines

GENE CATALOG

- Open-Reading-Frame prediction/annotation
- Non-redundant clustering at different percent identities
- Abundance quantification

CONSENSUS BINNING

- Multiple binning approaches
- Dereplication
- Quality control
- Metapangenomic analysis
- Functional annotation

PHAGE HUNTING

- Identification
- Taxonomic annotation
- Dereplication
- Functional analysis
- Host-matching
- Abundance quantification

COMPARATIVE GENOMICS

- Functional annotation
- SNP identification
- Doubling rate estimation
- GWAS + statistical analysis

Sustainable, long-term development

Clear teams and module ownership + accountability

Adaptable to new software/methods

Standardized documentation and development practices

Support modules

Canopy clustering

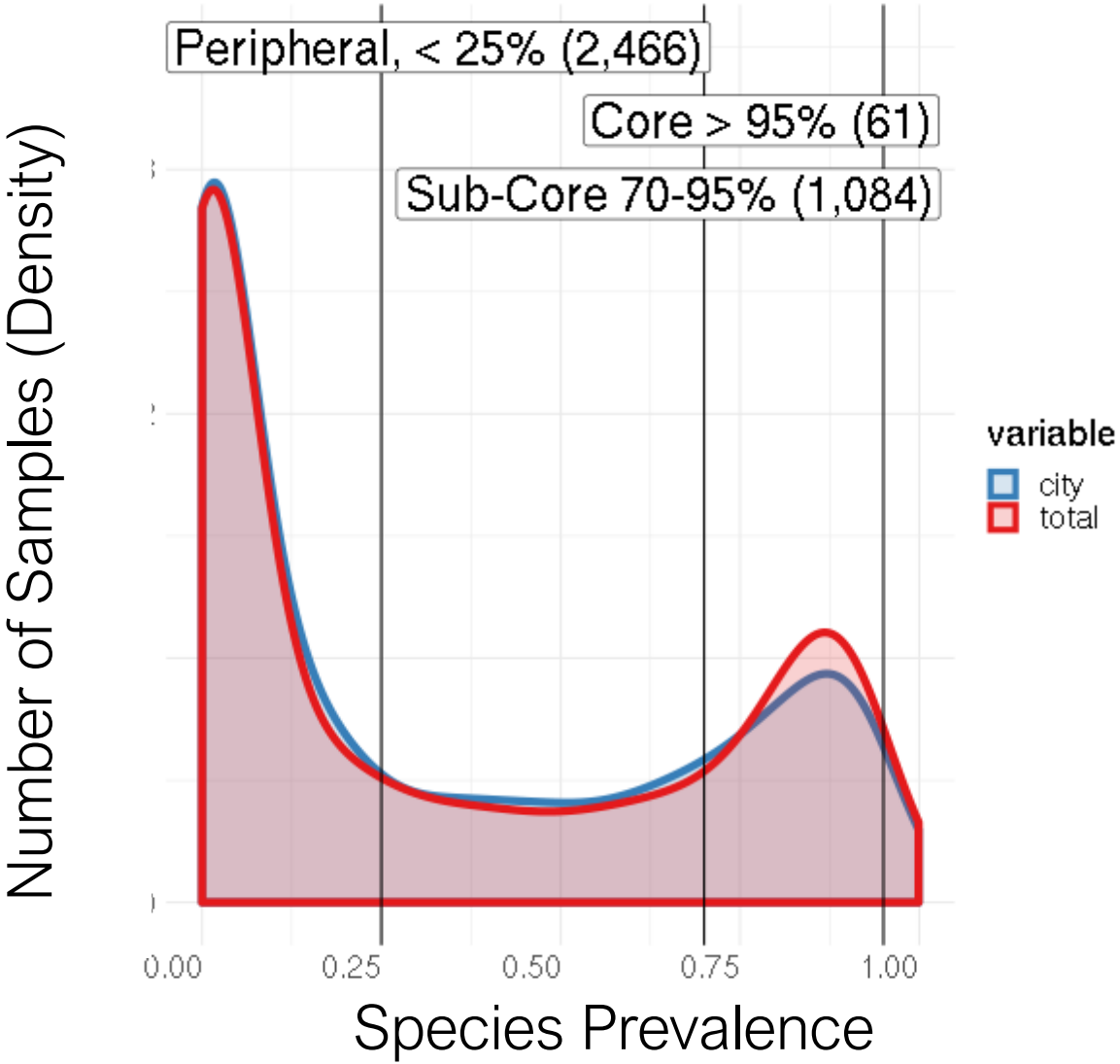
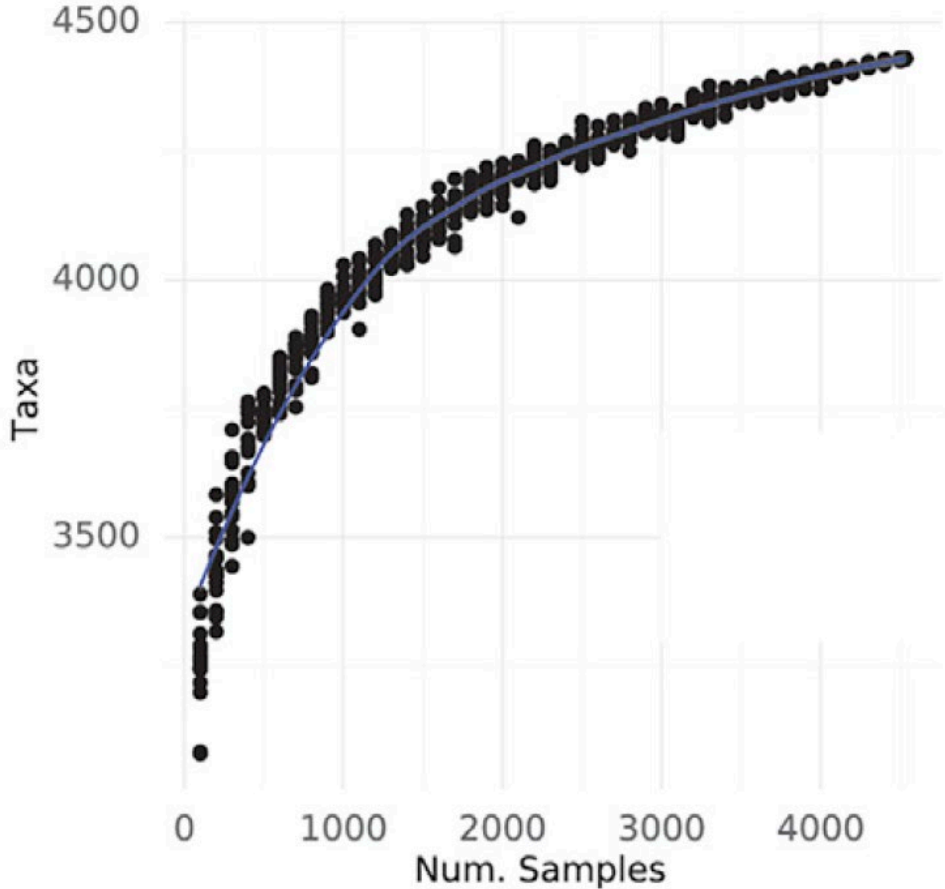
MAS/GWAS/SWAS

Statistical model evaluation

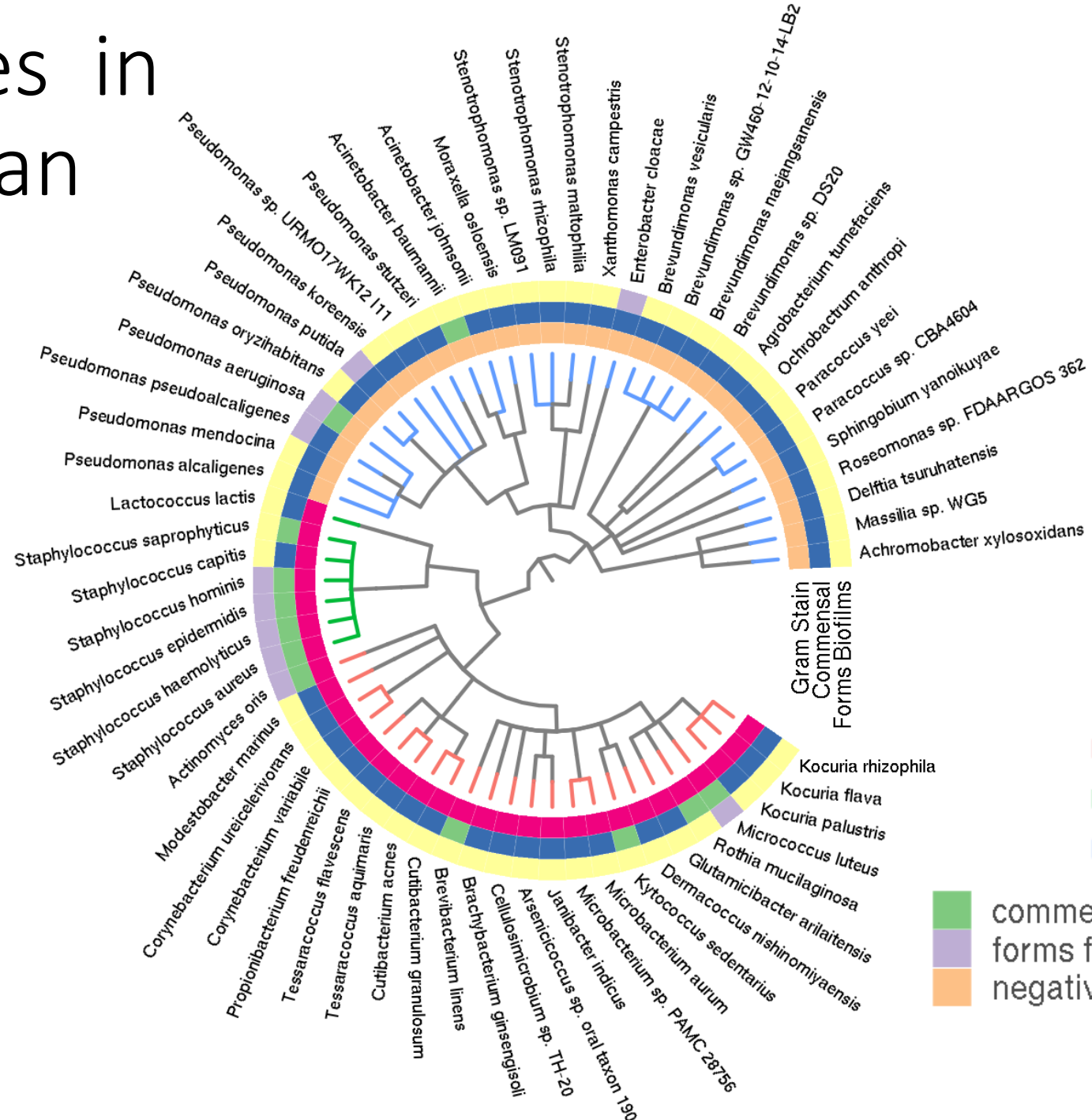
Colab/Alphafold2

Braden Tierney

A Core Urban Microbiome found across 4,728 samples and 60 cities



31 species in the Urban Core

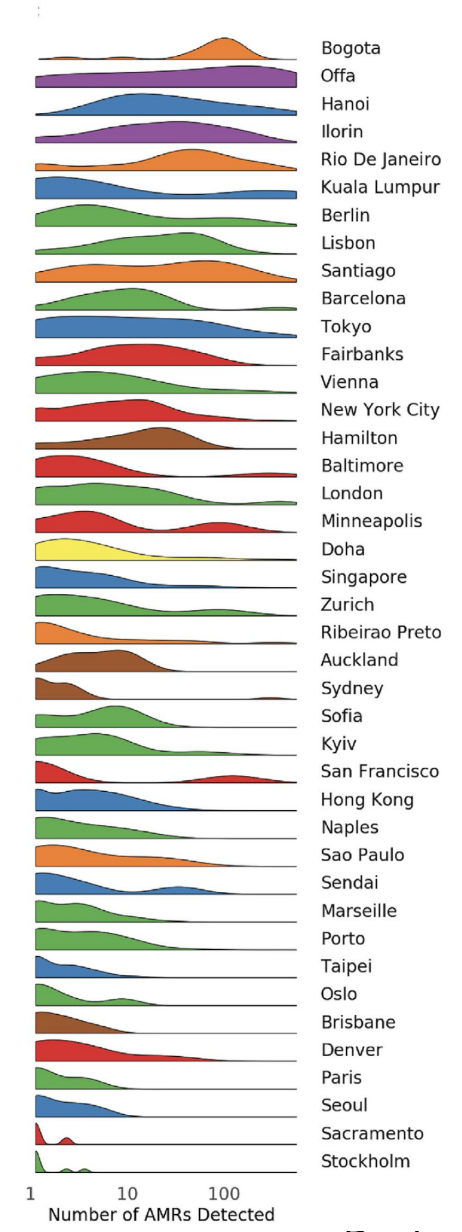
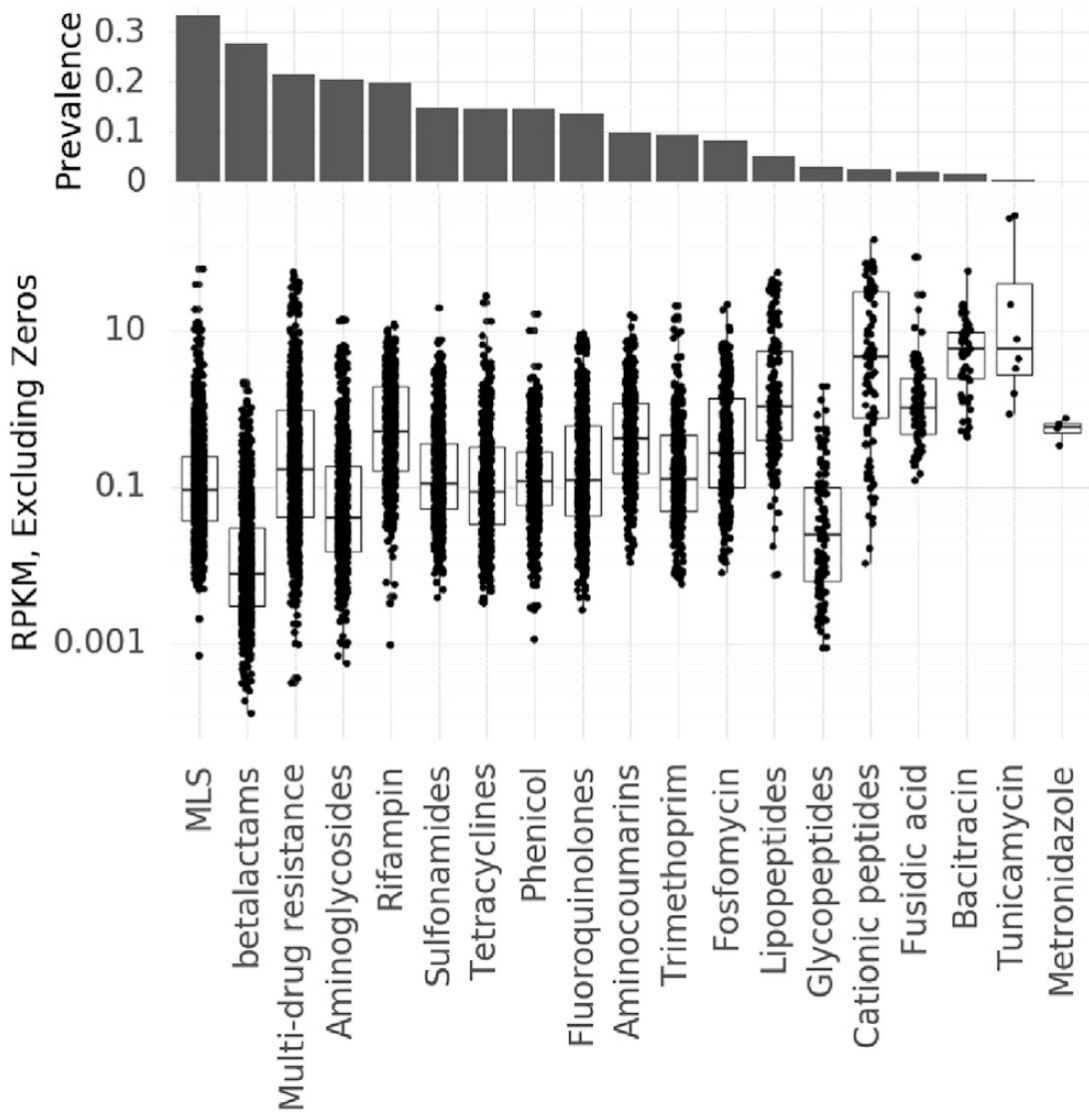


Phylum

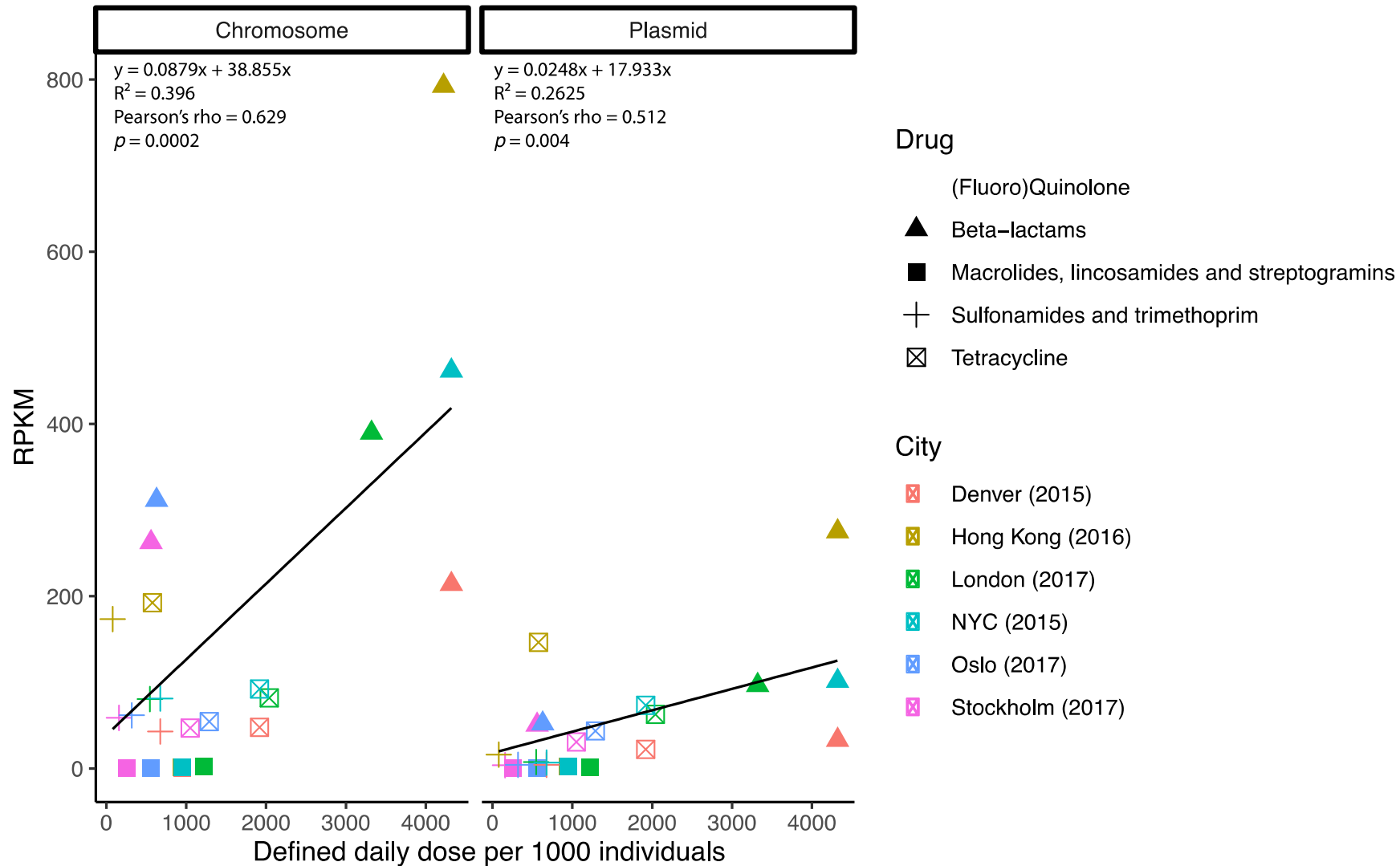
- Actinobacteria
- Firmicutes
- Proteobacteria

- commensal
- forms films
- negative
- no films
- not commensal
- positive

Wide diversity of AMRs across the world's cities



OTC Antibiotic use can be derived from the cities themselves



10-100x less than what is seen in gut or soil

Current Biology

Volume 24, Issue 10, 19 May 2014, Pages 1096-1100



Report

Large-Scale Metagenomic-Based Study of Antibiotic Resistance in the Environment

Overall, the percentage of different ARGD sequences detected ranged from 0.97% in cow gut (4441680.3) to 32.78% in Rothamsted soil E41.

3X increase in size of the tree of life,
including 10,928 new viruses
(vs. JGI/NCVBI)



Altmetric: 499

More detail >>

Article | OPEN

Recovery of nearly 8,000 metagenome-assembled genomes substantially expands the tree of life



ARTICLE | ONLINE NOW

A global metagenomic map of urban microbiomes and antimicrobial resistance

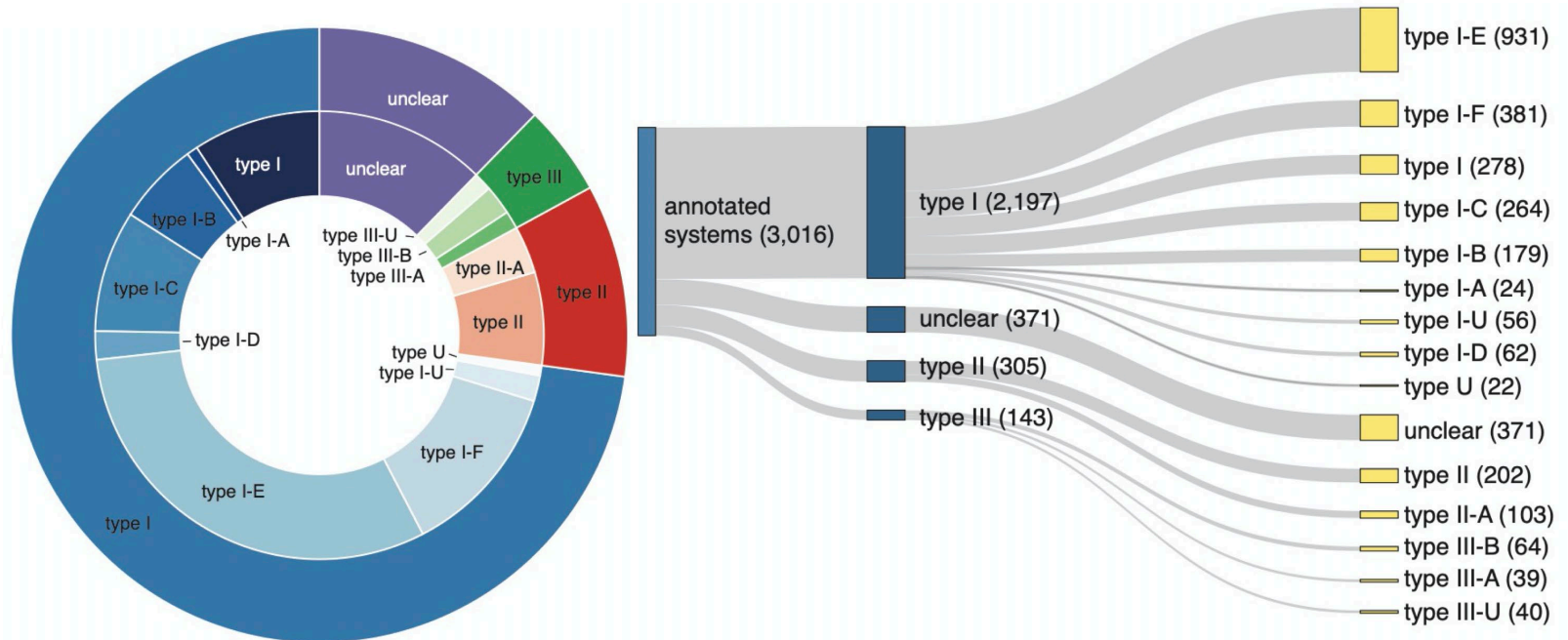
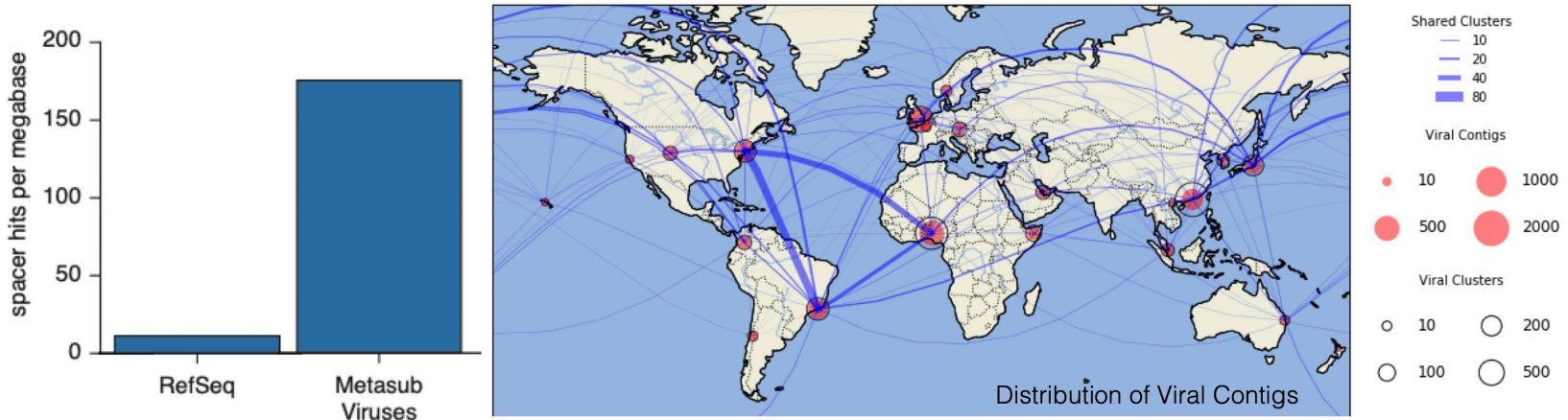
David Danko ⁶⁸ • Daniela Bezdán ⁶⁸ • Evan E. Afshin • ... Sibó Zhu • Christopher E. Mason ⁶⁹ 

The International MetaSUB Consortium • [Show all authors](#) • [Show footnotes](#)

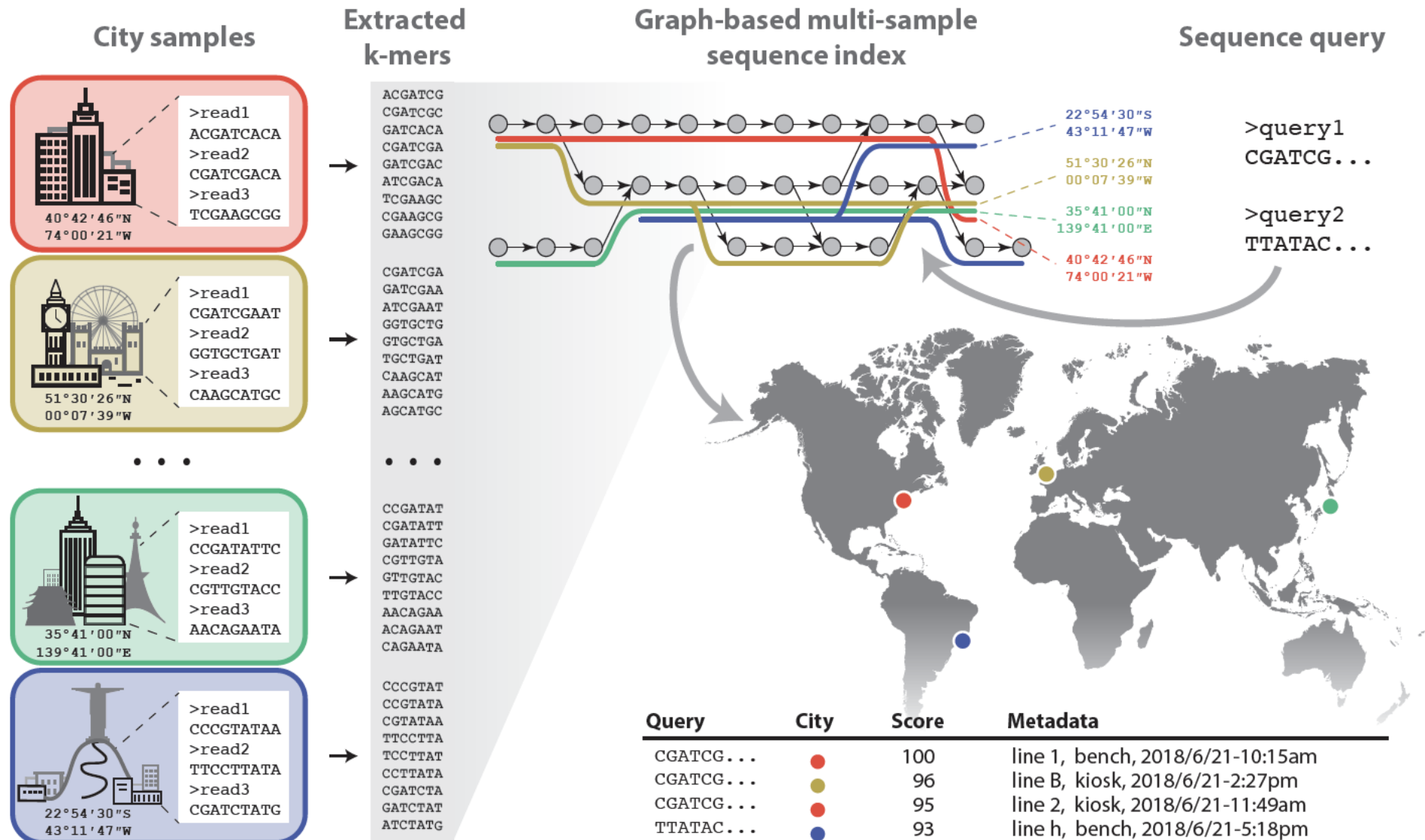
Open Access • Published: May 26, 2021 • DOI: <https://doi.org/10.1016/j.cell.2021.05.002>

<https://www.nature.com/articles/s41564-017-0012-7>
[https://www.cell.com/cell/fulltext/S0092-8674\(21\)00585-7](https://www.cell.com/cell/fulltext/S0092-8674(21)00585-7)

and >800K new CRISPR arrays



Global K-mer index



www.metasub.org

<https://metagraph.ethz.ch/graphs>

Andre Kahles, Gunnar Rätsch

Also found in space...

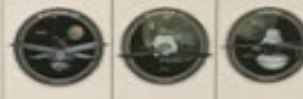
Sneaky New Bacteria on the ISS Could Build a Future on Mars

NASA tracks the microbes that live on the space station, and sometimes it discovers new ones. Those hardy bugs may offer clues about surviving long missions.



<https://www.wired.com/story/sneaky-new-bacteria-on-the-iss-could-build-a-future-on-mars/>

Dr. Kasthuri J Venkateswaran



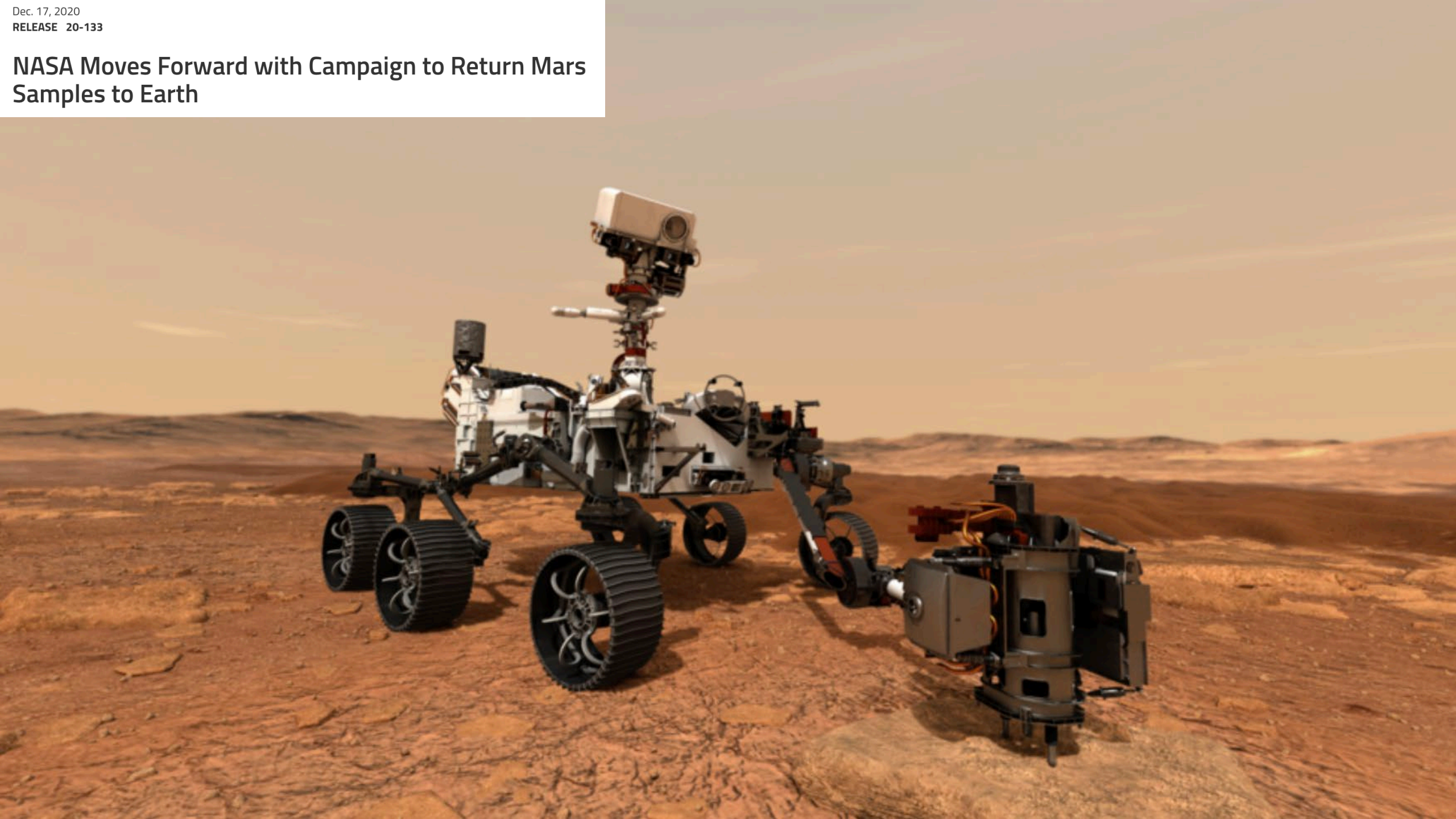


S

WARNING
NO OPEN FLAMES



NASA Moves Forward with Campaign to Return Mars Samples to Earth










A New View

 Earth

View from Curiosity rover, evening of January 31, 2014 (Mars year 32, late spring)

Earth-Mars distance: 180 million km (112 million mi)

JPL

Mars Sample Return

MSR

Mars Sample Return is a proposed mission to return samples from the surface of Mars to Earth.

ETA: 2032



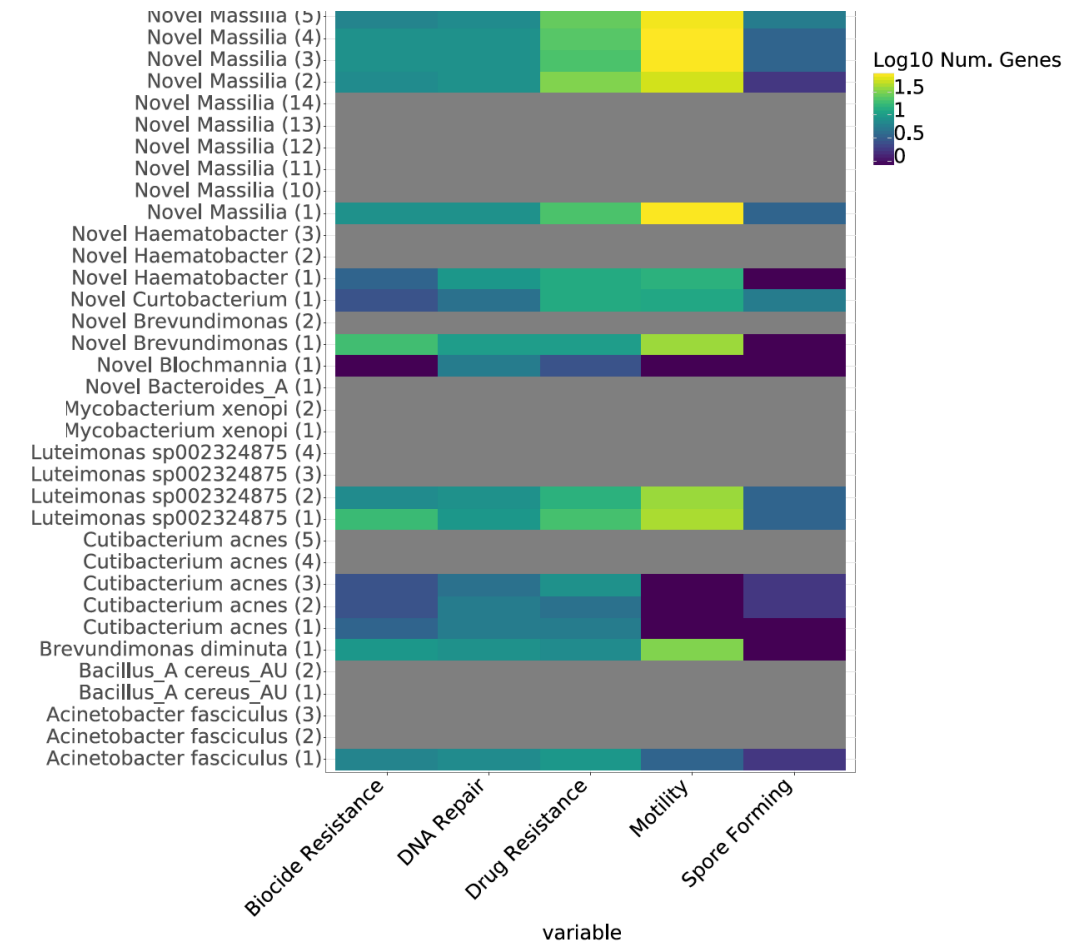
Planetary Genomics

Research | [Open Access](#) | [Published: 01 April 2021](#)

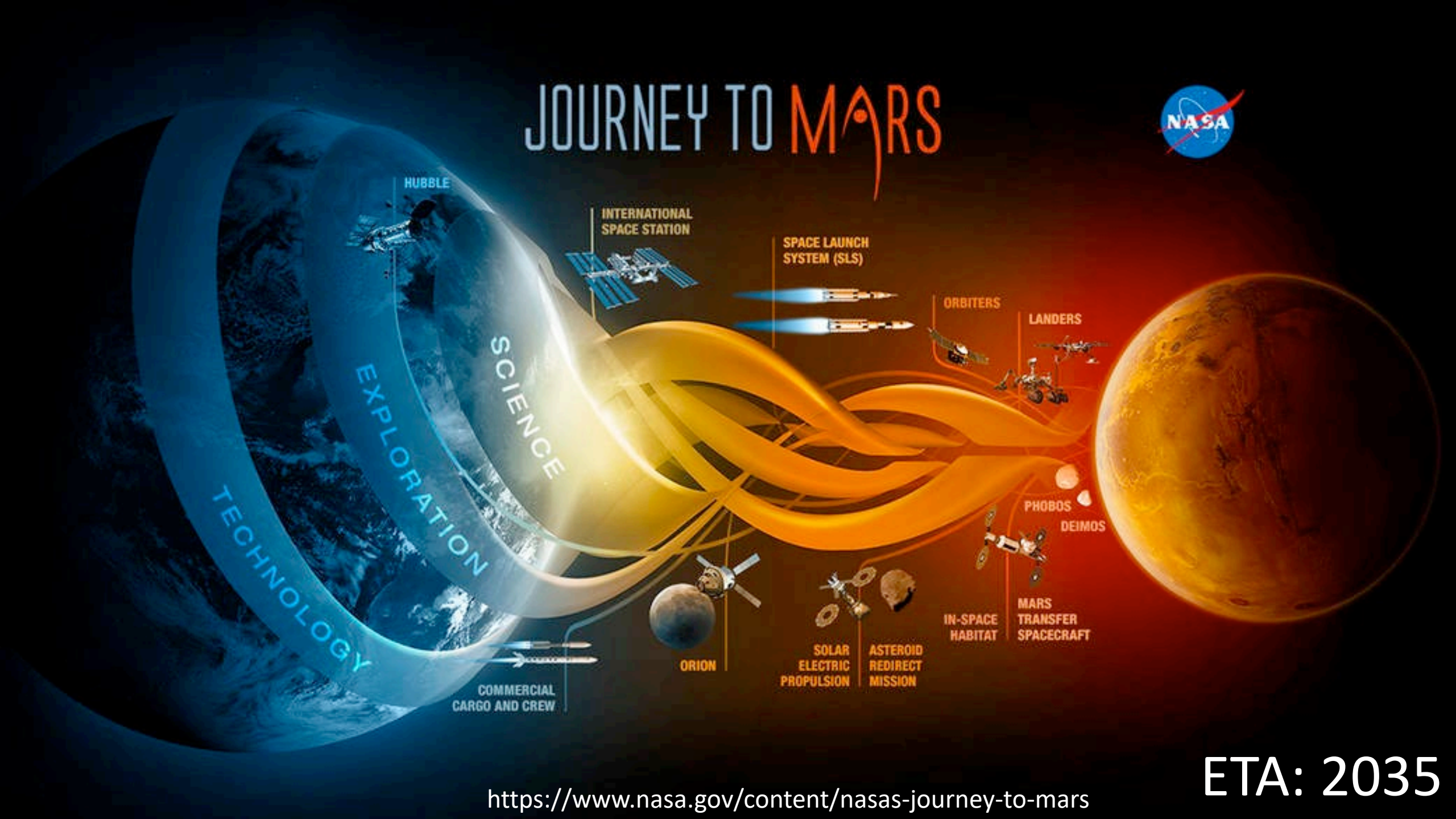
A comprehensive metagenomics framework to characterize organisms relevant for planetary protection

[David C. Danko](#), [Maria A. Sierra](#), [James N. Bernardini](#), [Lisa Guan](#), [Jason M. Wood](#), [Nitin Singh](#), [Arman Seuylemezian](#), [Daniel J. Butler](#), [Krista Ryon](#), [Katerina Kuchin](#), [Dmitry Meleshko](#), [Chandrima Bhattacharya](#), [Kasthuri J. Venkateswaran](#) ✉ & [Christopher E. Mason](#) ✉

Microbiome **9**, Article number: 82 (2021) | [Cite this article](#)

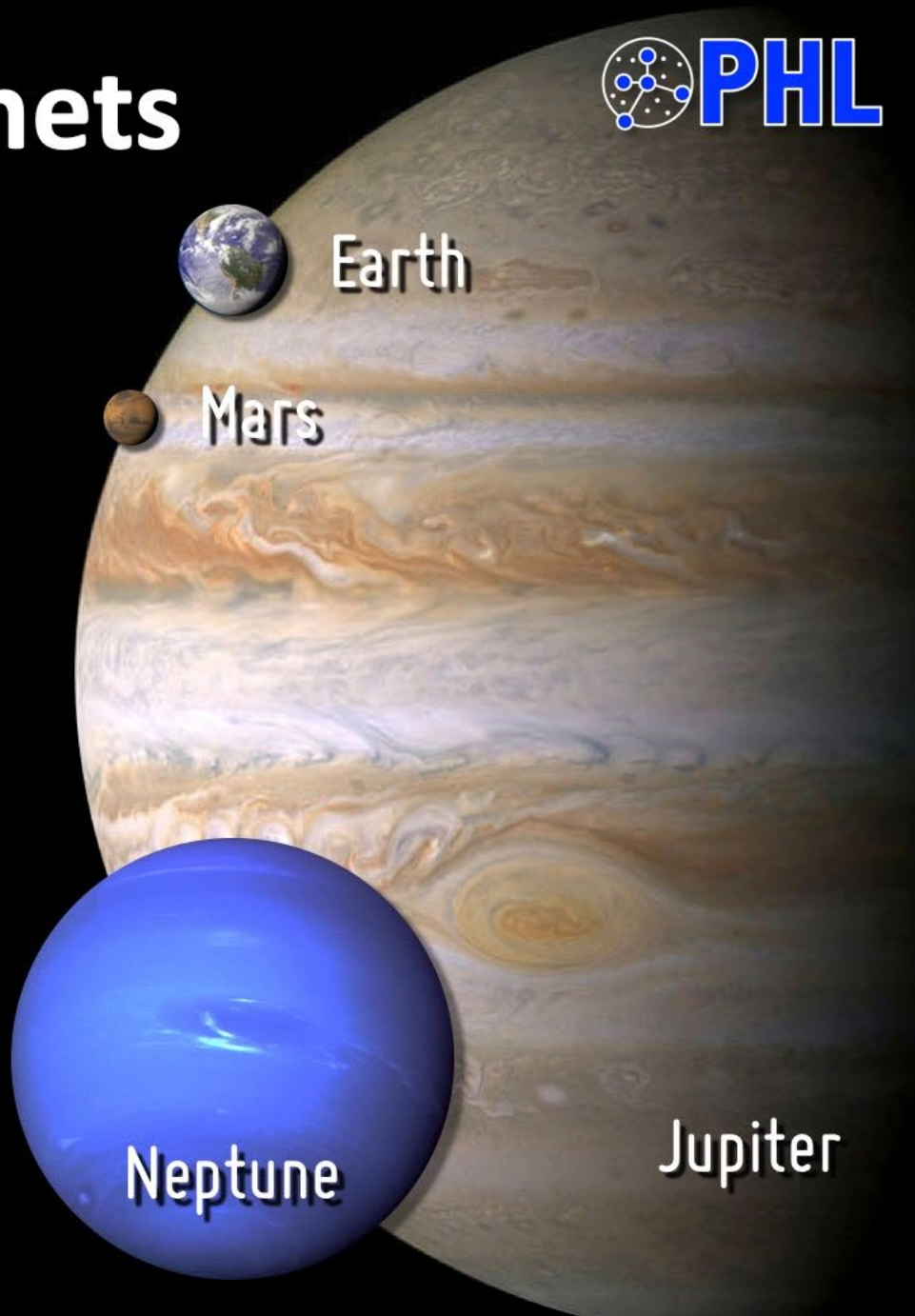
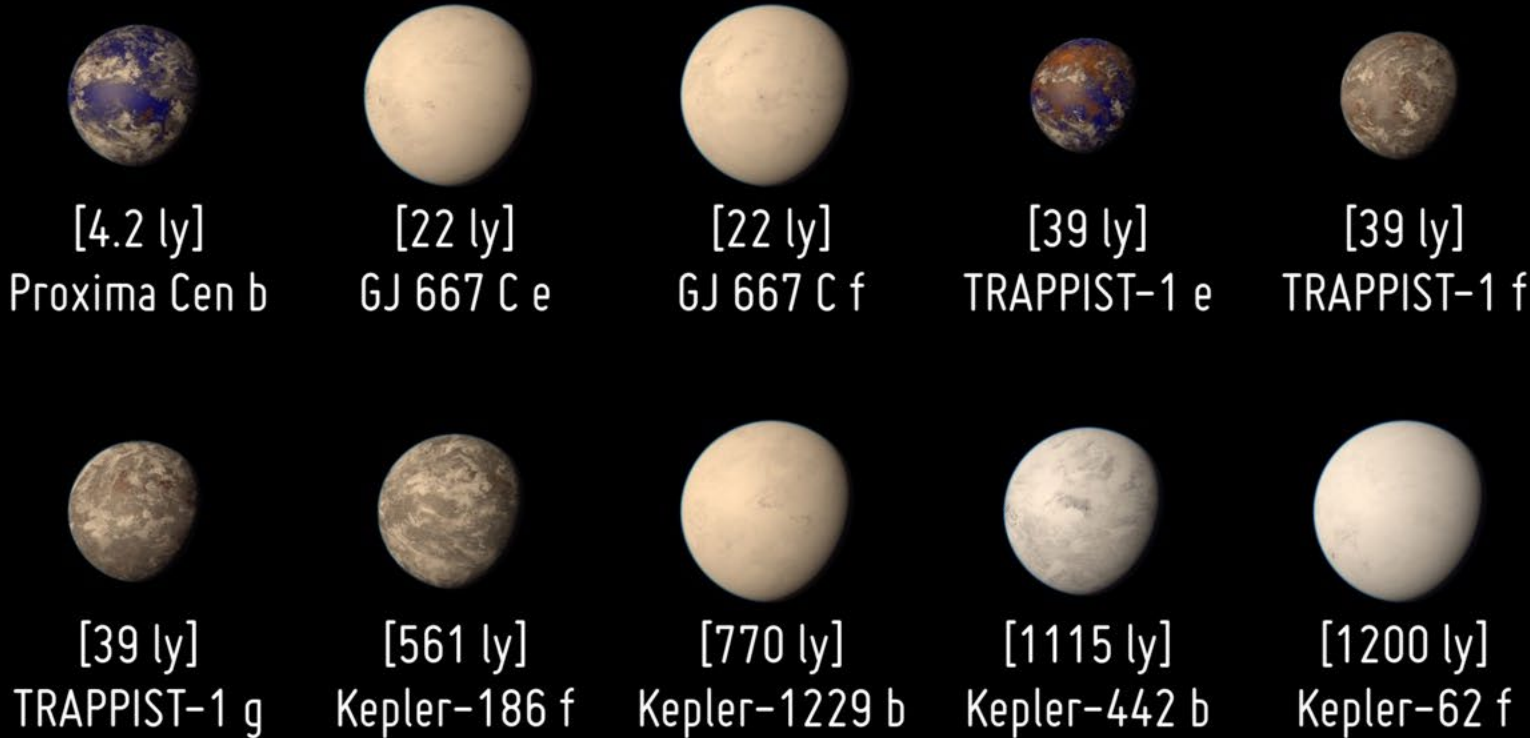


JOURNEY TO MARS



Potentially Habitable Exoplanets

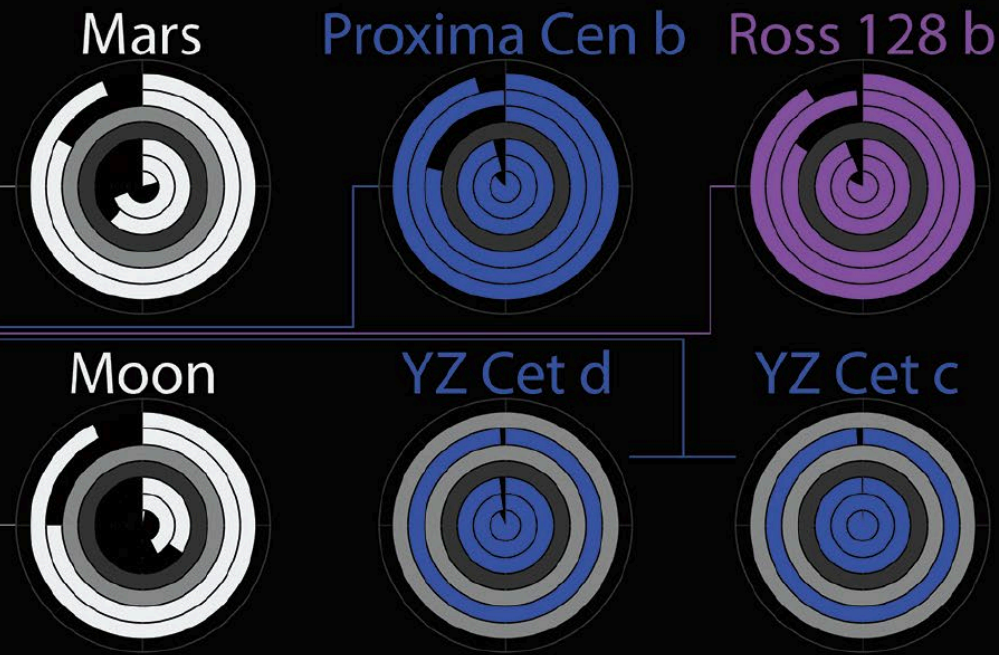
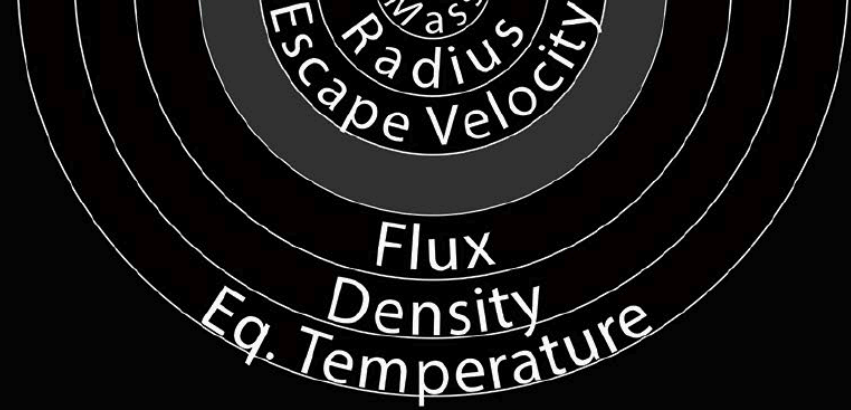
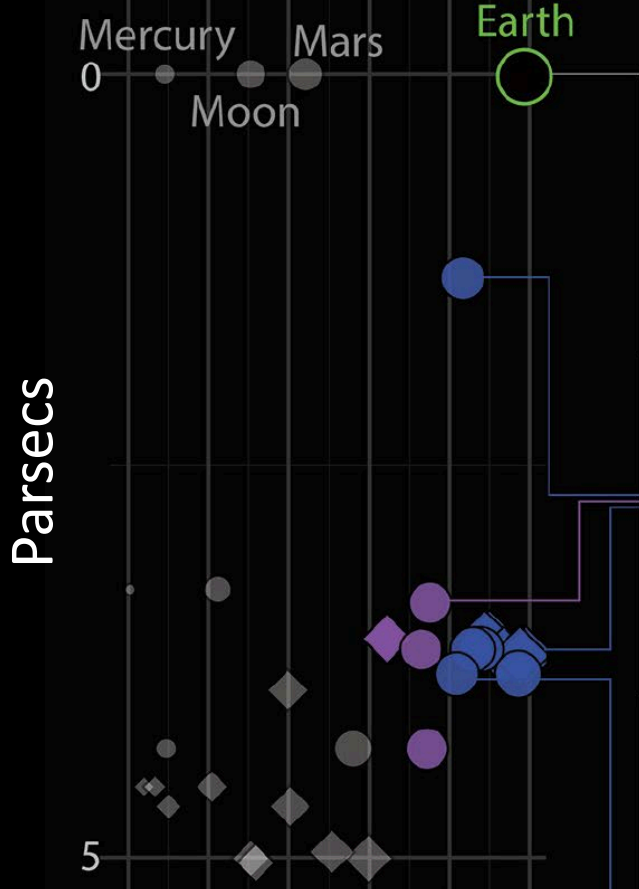
Ranked by Distance from Earth (light years)



Candidate Planets

Earth Similarity Index (ESI)

0.5 0.6 0.7 0.8 0.9 1



b



Candidate Planets

Earth Similarity Index (ESI)
0.5 0.6 0.7 0.8 0.9 1

Mercury Mars Earth

0 Moon

5

10

15

Distance (pc)

Most ESI Measurements Available

Missing Important ESI Measurements

Shape: ● ◆

Color: Earth ESI >= 0.9 ESI >= 0.8 ESI < 0.8 NA



Mars Proxima Cen b Ross 128 b



Moon YZ Cet d YZ Cet c



Mercury Teegarden c Teegarden b



GJ 273 c GJ 273 b Trappist-1 c



GJ 667 C e Trappist-1 f Trappist-1 d



GJ 667 C f Trappist-1 g Trappist-1 e



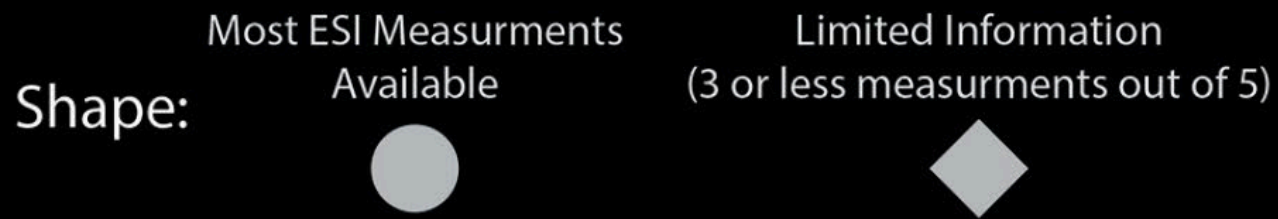
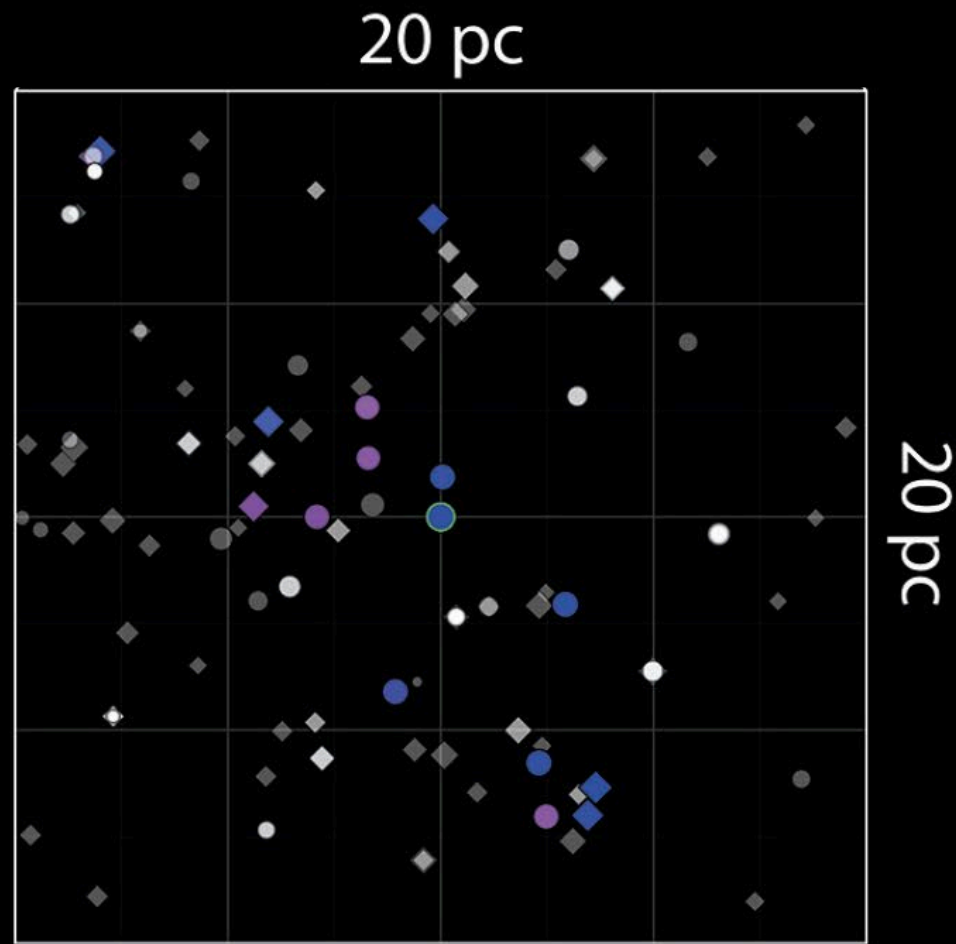
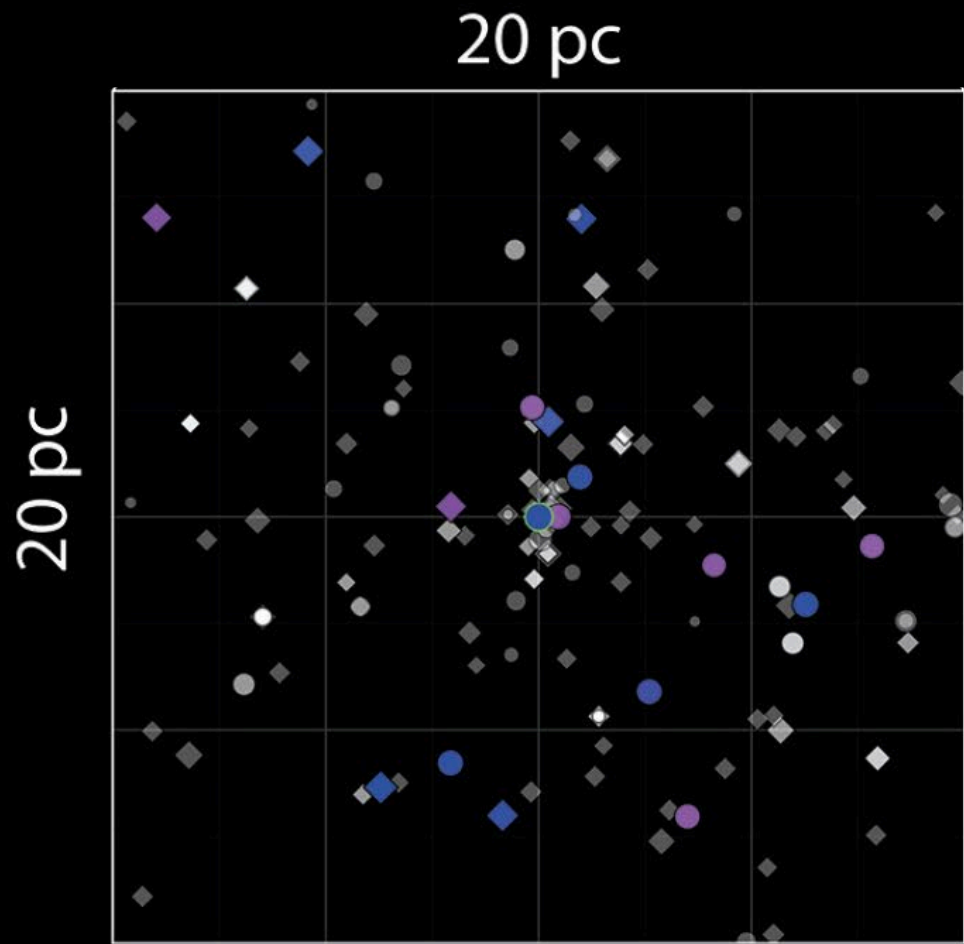
GJ 1132 c LHS 1140 b

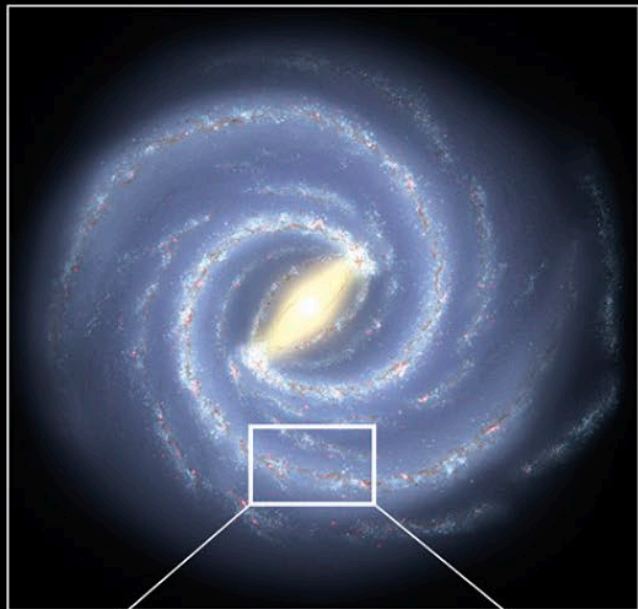


Distance (pc)

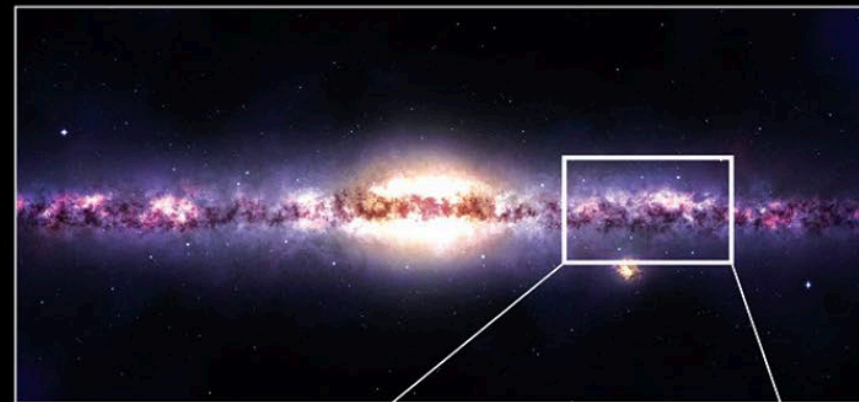
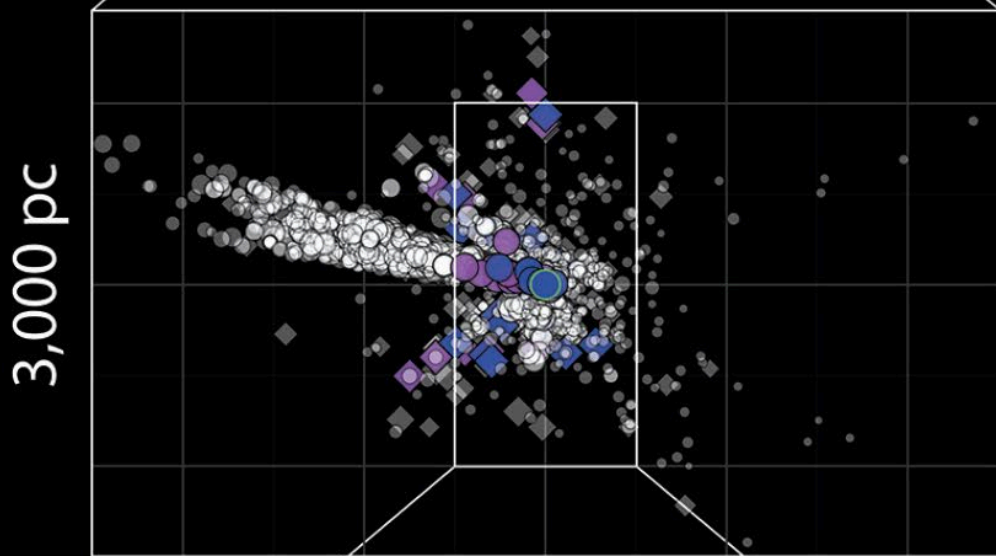
0 5 10 15

Shape: ● ◆ Color: Earth ESI >= 0.9 ESI >= 0.8 ESI < 0.8 NA

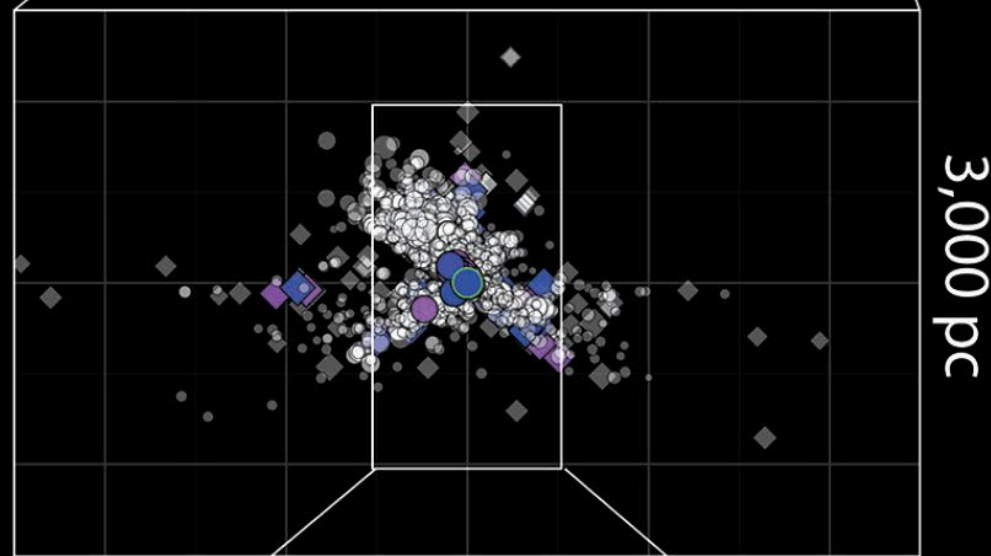




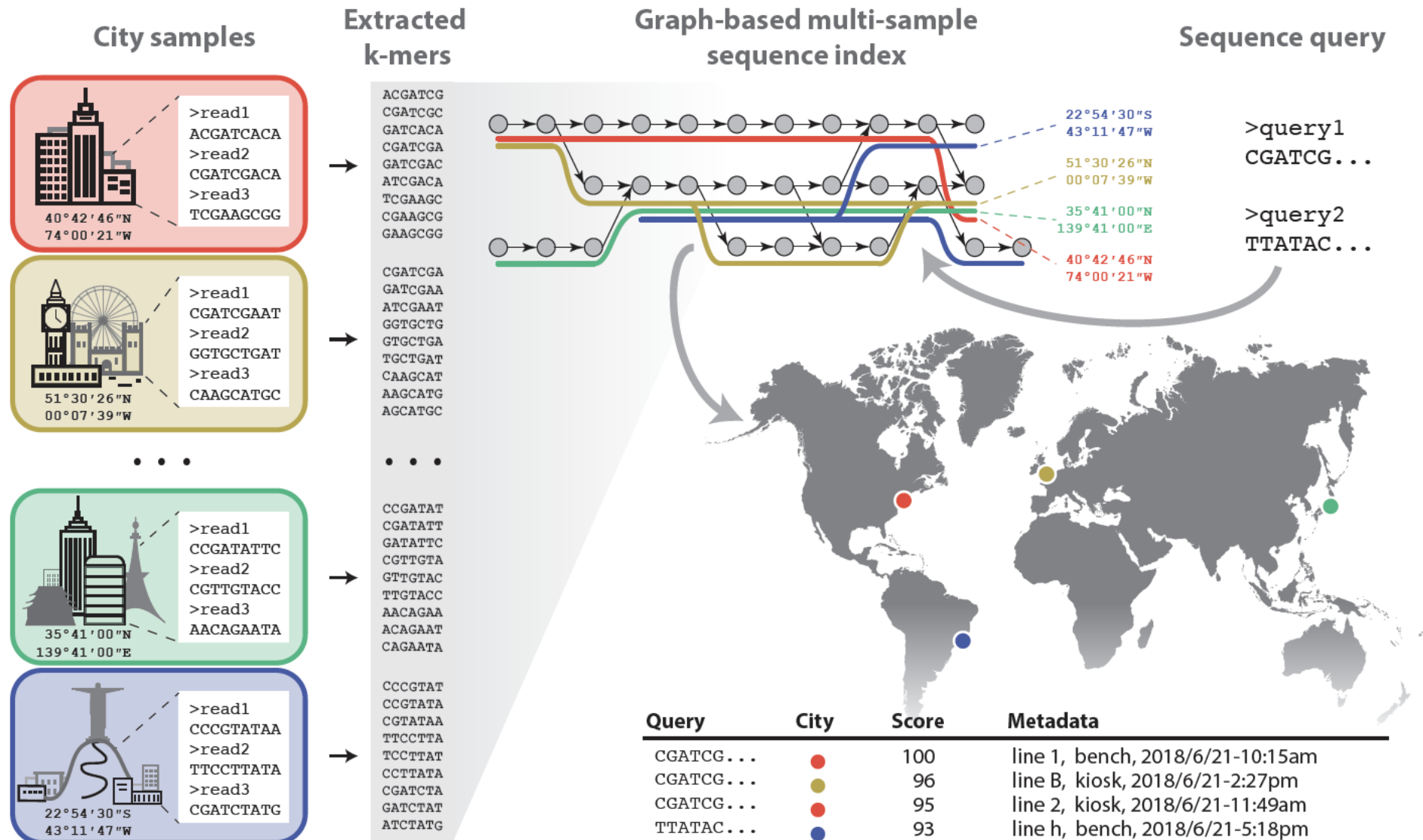
5,000 pc



5,000 pc



Global K-mer index



www.metasub.org

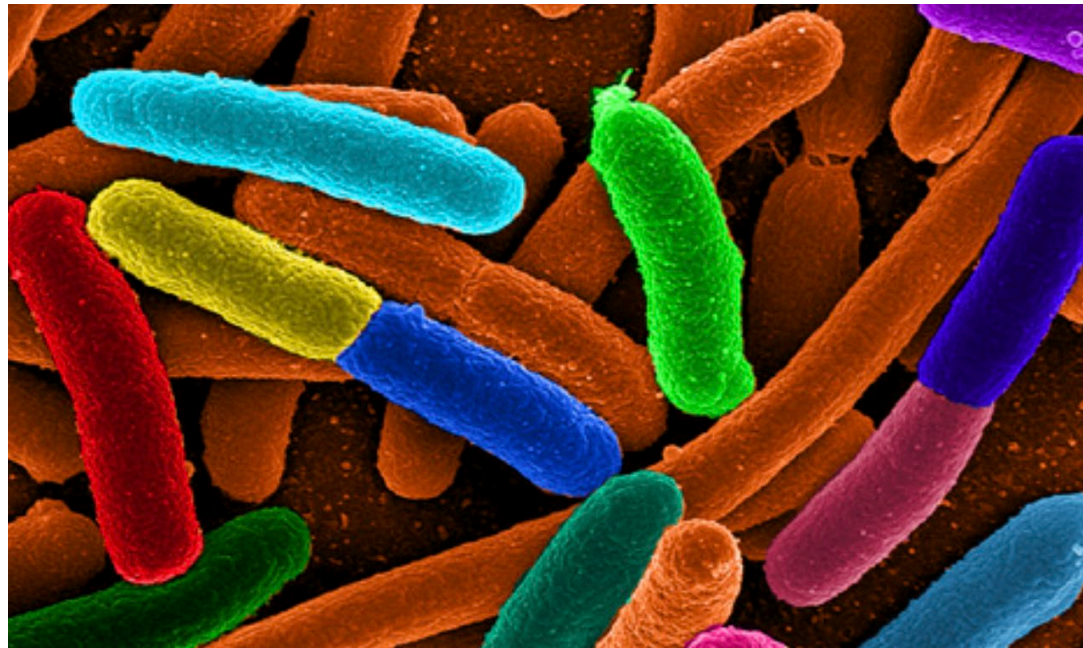
<https://metagraph.ethz.ch/graphs>

Andre Kahles, Gunnar Rätsch

Our Modern Lifestyle May Be Destroying Microbiome Diversity

Samples from an "untouched civilization" show dramatic differences

BY SARAH FECHT | PUBLISHED APR 17, 2015 10:10 PM



<https://www.popsci.com/modern-lifestyles-may-dramatically-reduce-diversity-human-microbiome/>

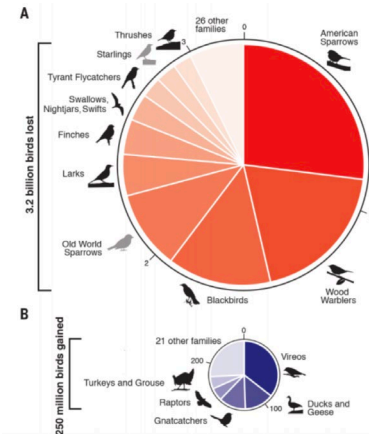
1 / 4
birds
are gone



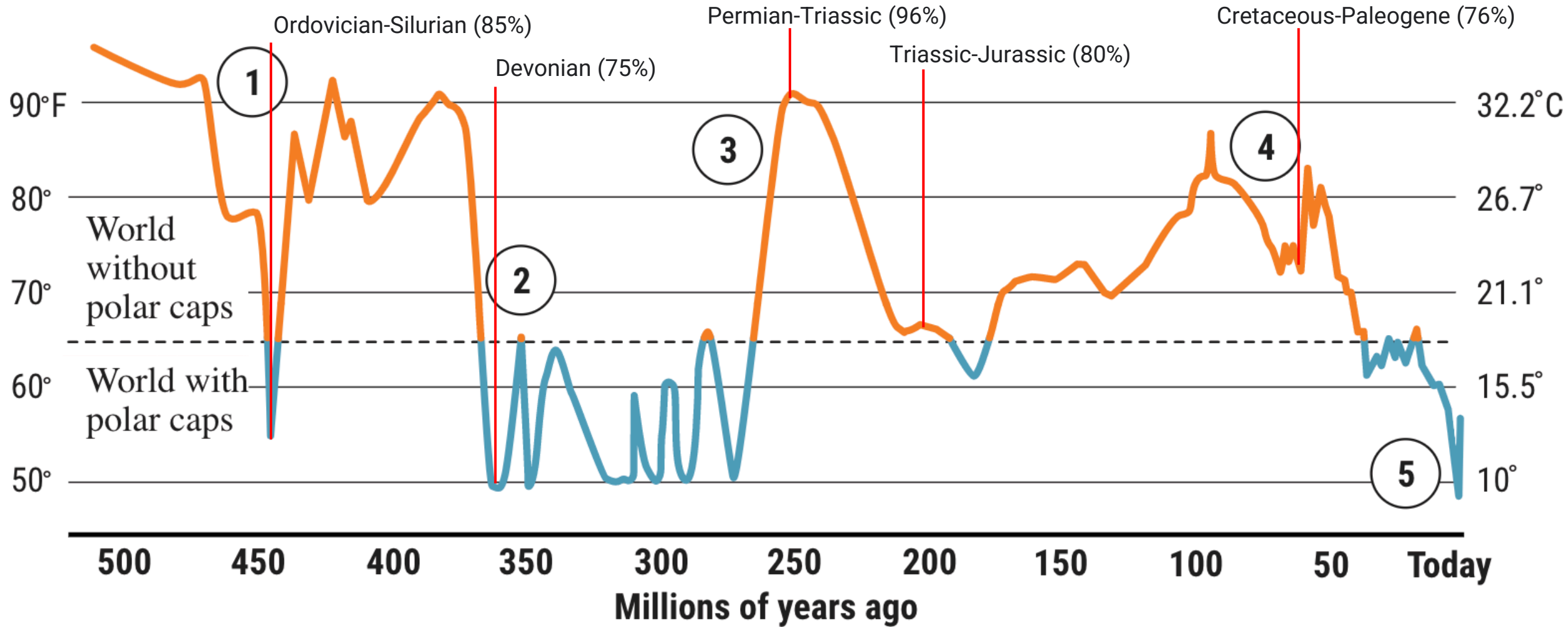
Shorebirds such as sanderlings may be dwindling because of habitat loss. TIM GRAHAM/GETTY IMAGES

Three billion North American birds have vanished since 1970, surveys show

<https://www.sciencemag.org/news/2019/09/three-billion-north-american-birds-have-vanished-1970-surveys-show>

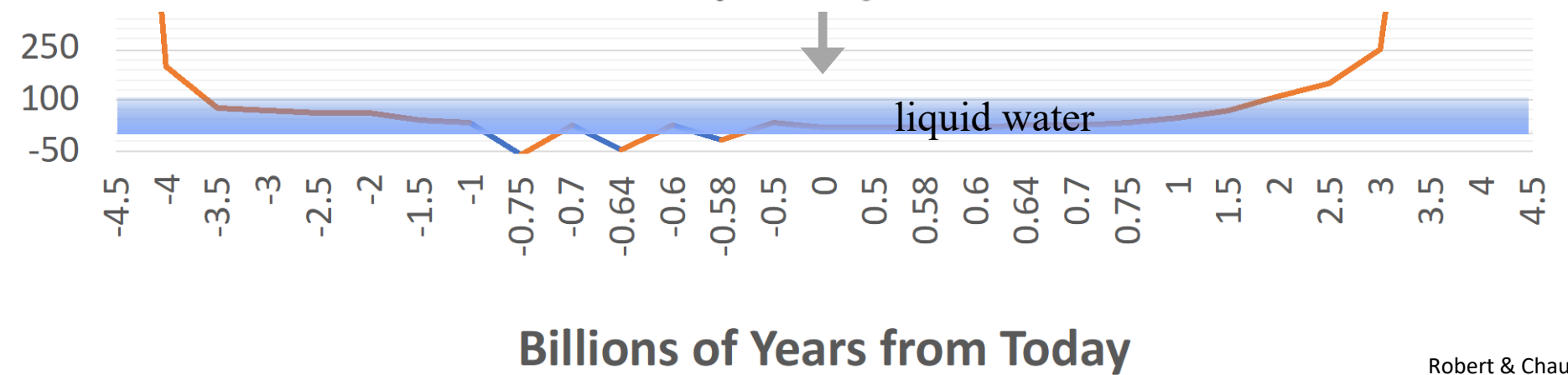
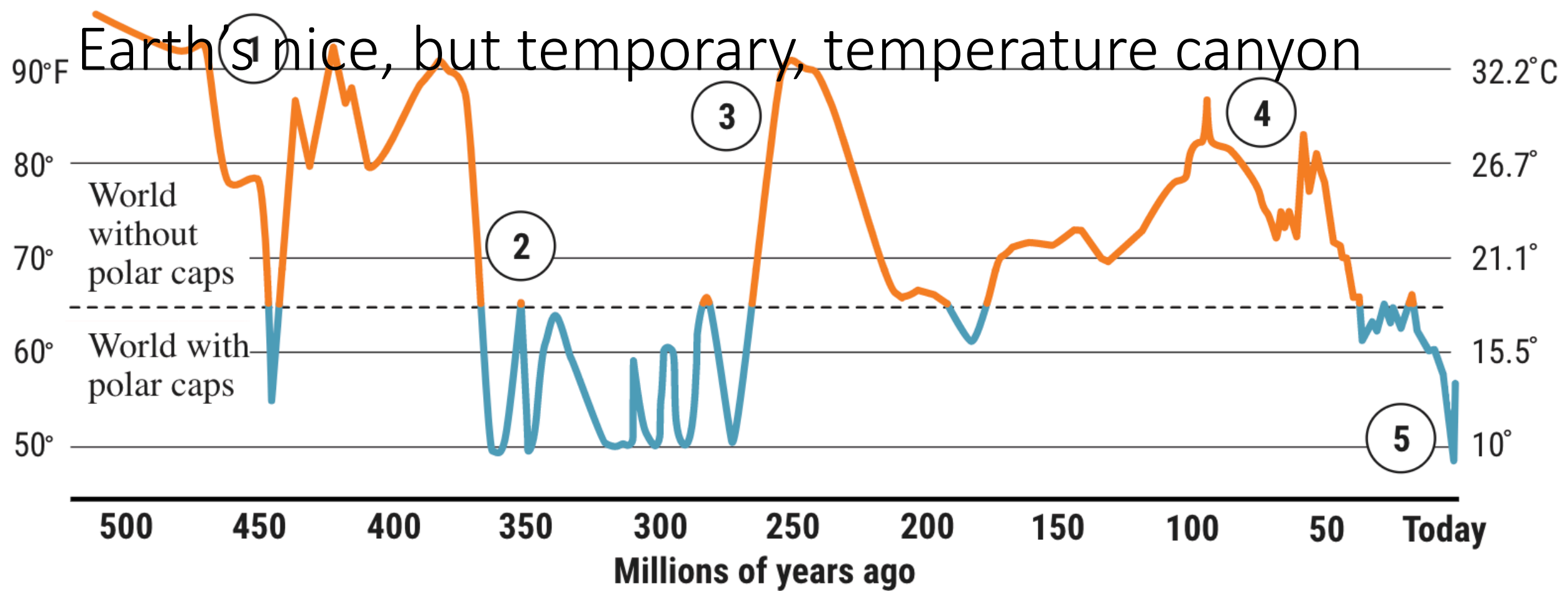


Not the first time: Earth's Temperature History and Mass Extinctions





Earth's nice, but temporary, temperature canyon





Food Chain



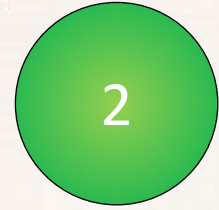
Producer



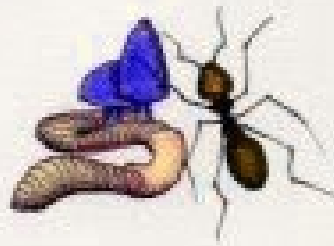
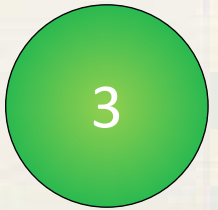
Primary Consumer



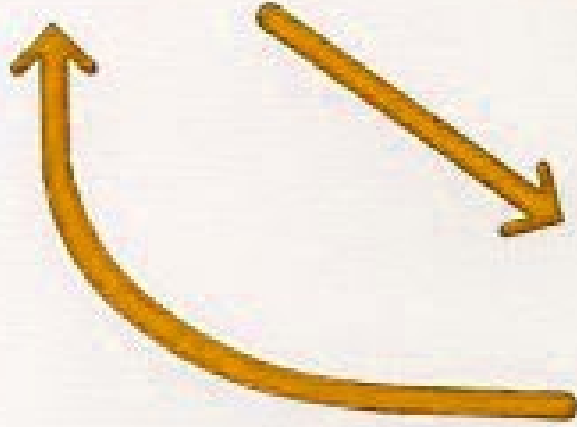
Secondary Consumer



Tertiary Consumer



Decomposers



The birth of the 4th kind of organism:

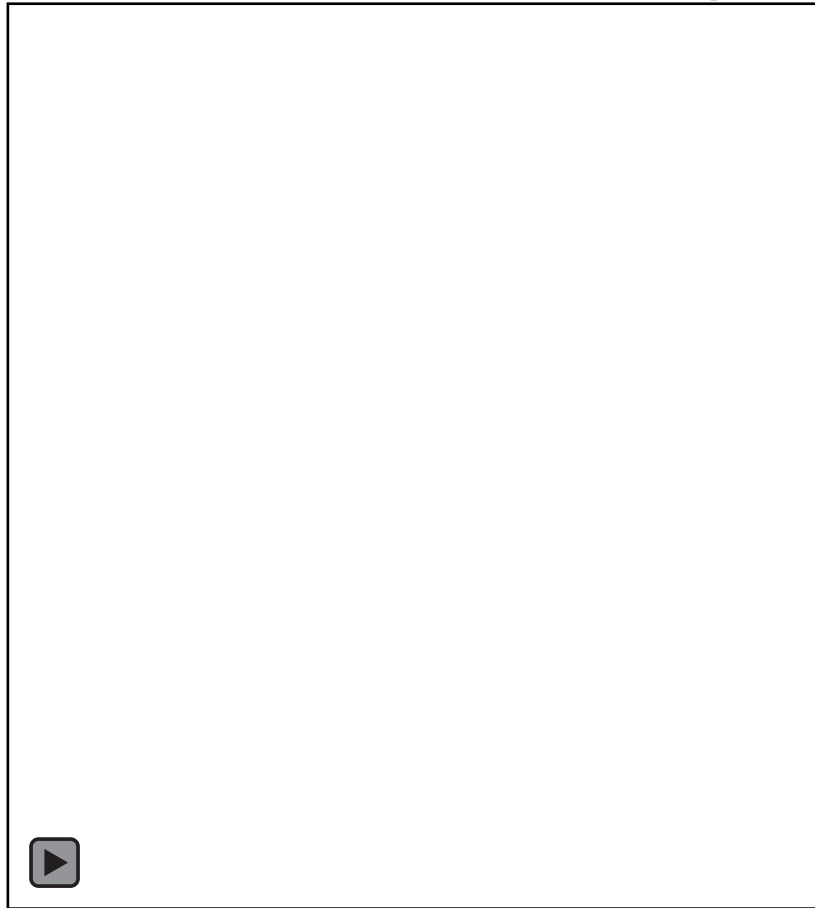
Guardians

Only humans

are

“extinction aware”

After 32 years in storage, cells were cloned,
donor gestated, and born



Ben Novak, Revive & Restore

MATTER

A New Company With a Wild Mission: Bring Back the Woolly Mammoth

With \$15 million in private funding, Colossal aims to bring thousands of woolly mammoths back to Siberia. Some scientists are deeply skeptical that will happen.



The biologist George Church unearthing woolly mammoth remains in Siberia. Eriona Hysolli

Cloning to protect and revive other species

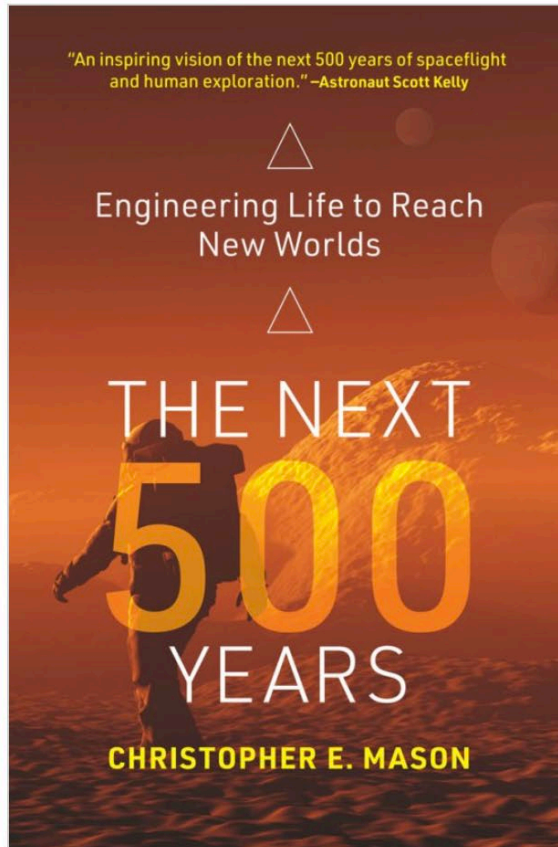


colossal 



Duty to all Life:
Past, Present, and Future

Preserving and mapping genetics for helping this planet and eventually others...



The Next 500 Years

Engineering Life to Reach New Worlds

By Christopher E. Mason

An argument that we have a moral duty to explore other planets and solar systems – because human life on Earth has an expiration date.

<https://mitpress.mit.edu/books/next-500-years>

Deep Gratitude to Many People:

Mason Lab

Ebrahim Afshinnekoo
Yared Bayleyen
Chandrima Bhattacharya
Daniel Butler
Chris Chin
Rafael Colon
David Danko
Namita Damle
Ceyda Durmaz
Radwa Elshafey
Jonathan Foox
Sebastian Garcia-Medina
Kirill Grigorev
Hannah Kelly
JangKeun Kim
JJ Hastings
Matthew MacKay
Lauren Mak
Cem Meyden
Deena Najjar
Eliah Overbey
Jiwoon Park
Krista Ryon
Maria Sierra
Braden Tierney
Delia Tomoiaga
Craig Westover
WorldQuant Fellows

Cornell/WCM

Alain Borczuk
David Erickson
Selina Chen-Kiang
Iwijn De Vlaminck
Olivier Elemento
Samie Jaffrey
Iman Hajirasouliha
Marcin Imielinski
Ari Melnick (Melnick Lab)
Margaret Ross
Rob Schwartz

MetaSUB Global

Biotia

Niamh O'Hara
Dorottya Nagy-Szakai

NYU

Martin Blaser
Jef Boeke
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Chris Park
Elizabeth Hénaff

Rockefeller

Jeanne Garbarino
Charles Rice

Nanostring

Tyler Hether
Joe Beechem
Sarah Warren

New England Biolabs

Eileen Dimalanta
Nathan Tanner
Ted Davis
Fiona Stewart

NASA/JPL/Ames/ISSOP

Afshin Beheshti
Kate Rubins
Craig Kundrot
Stefania Giacomello
David Smith
Kasthuri Venkateswaran

Univ. Chicago

Yoav Gilad

UCSF

Charles Chiu

UKT /UNI/NCCT TUEBINGEN

Daniela Bezdán,
Stephan Ossowski,
Thirumalaisamy P. Velavan

Icahn/MSSM

Eric Schadt
Joel Dudley
Bobby Sebra

UVA

Francine Garrett-Bakelman

Illumina

Gary Schroth

Duke

Stacy Horner

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Sheng Li

Baylor

Fritz Sedlazeck
Jeff Rogers

MSKCC

Alex Kentsis
Christina Leslie
Ross Levine

AMNH

George Amato
Cheryl Hiyashi

HudsonAlpha

Shawn Levy



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Nicolas Robine
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Northwell Hospital

Lance Becker
Peter Gregersen

Miami / UM

George Grills
Helena Solo-Gabriele
Maria E Figueroa
Stephan Schürer

MIT Media Lab

Kevin Slavin
Devora Najjar

FDA/SEQC/Fudan.

Leming Shi

ABRF/Vermont

Scott Tighe
Don Baldwin

The Biggest Thanks

to

the patients, their families,

and what they leave behind