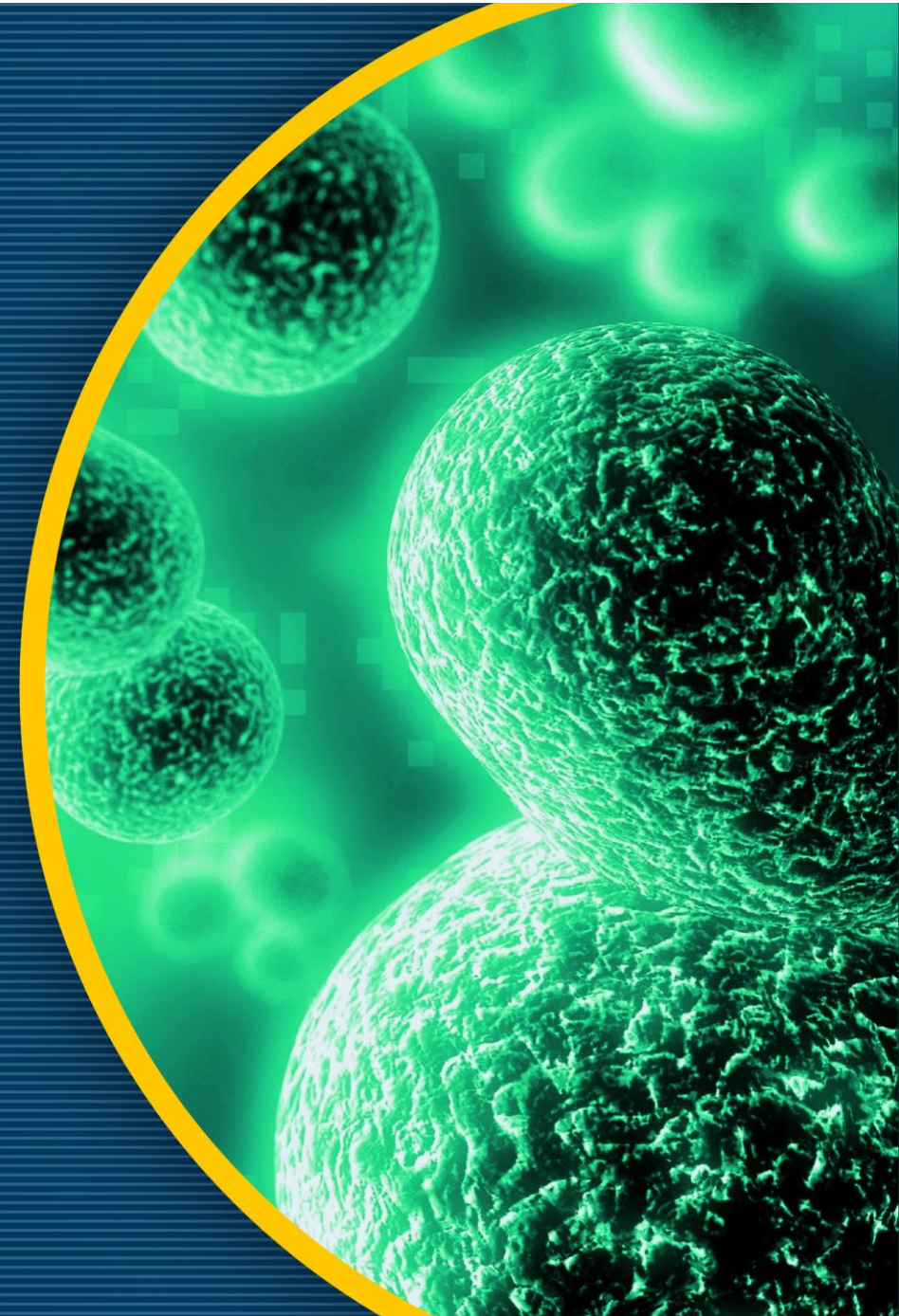




NIH Common Fund  
**Human Virome Program**

Yvonne L. Hernandez-Kapila, DDS, PhD

May 20, 2026



# • The Human Microbiome

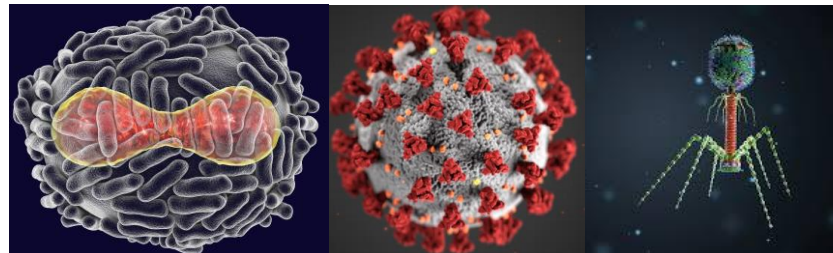
## Human Microbiome

- Viruses 380 trillion
- Bacterial 38 trillion
- Archaea 3.8 trillion
- Fungi 3.8 trillion



## The Human Virome

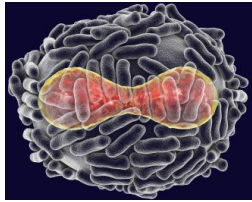
all human viruses



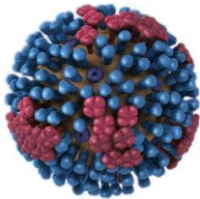
HUMAN  
VIROME  
PROGRAM

# Historical Context- Impact of Viral Outbreaks

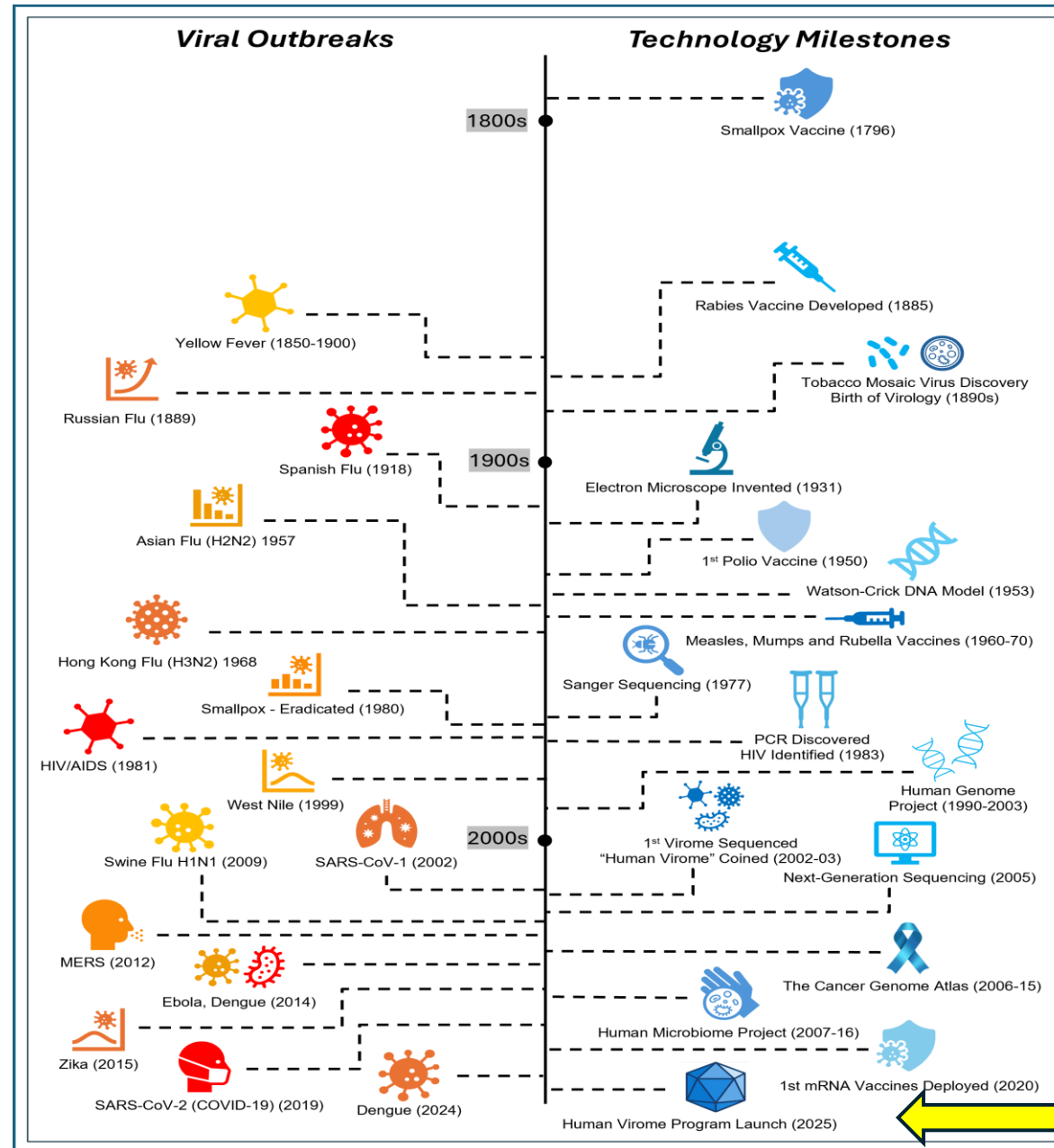
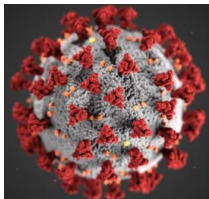
Smallpox  
dsDNA



Influenza  
ssRNA

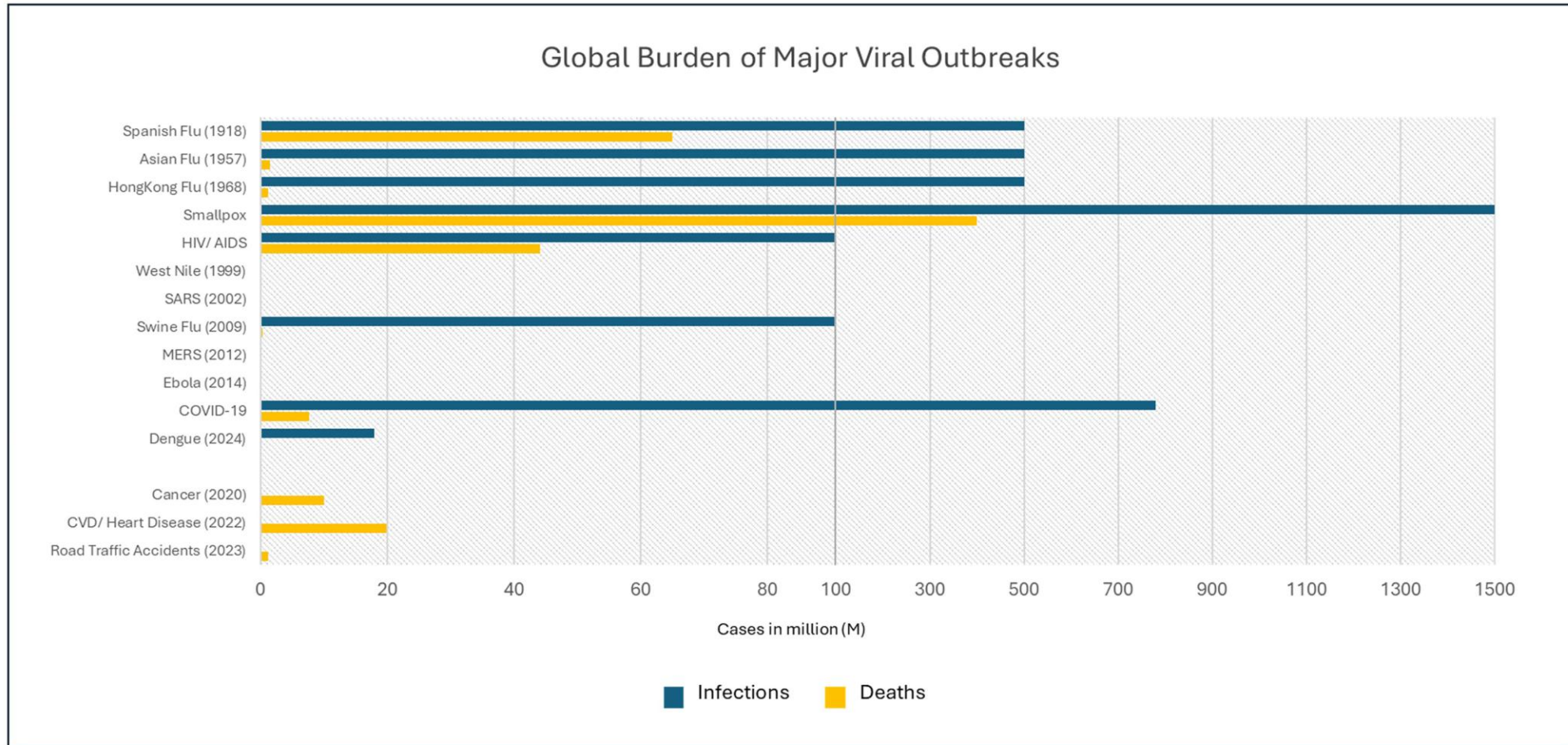


SARS-CoV-2  
(COVID-19)  
ssRNA



# Historical Context- Impact of Viral Outbreaks

Deaths from Cancer, Heart Disease, and Traffic Accidents Combined are Surpassed by Deaths due to Viral Outbreaks



The estimated number of infections and deaths (in millions) from significant viral outbreaks in the 20<sup>th</sup> and 21<sup>st</sup> centuries, compared with deaths due to cancer, cardiovascular disease and road traffic accidents (X-axis not to scale- axis break has been used to improve visualization).  
Data estimates drawn from Bloom and Cadarette (2019), the Centers for Disease Control and Prevention and the World Health Organization (accessed November 2025).





# National Institutes of Health

## 27 Institutes & Centers

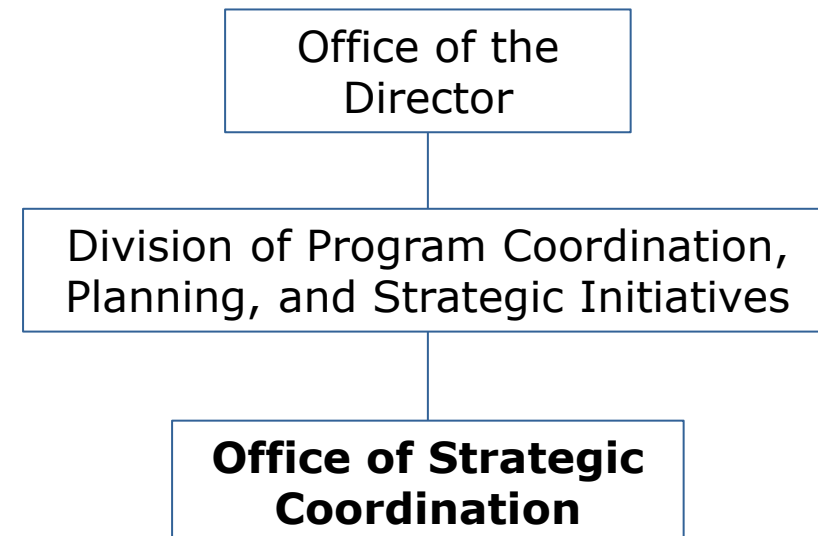
- Center for Information Technology
- Center for Scientific Review
- Clinical Center
- *Eunice Kennedy Shriver* National Institute of Child Health and Human Development
- Fogarty International Center
- National Cancer Institute
- National Center for Advancing Translational Sciences
- National Center for Complementary and Integrative Health
- National Eye Institute
- National Heart, Lung, and Blood Institute
- National Human Genome Research Institute
- National Institute of Allergy and Infectious Diseases
- National Institute of Arthritis and Musculoskeletal and Skin Diseases
- National Institute of Biomedical Imaging and Bioengineering
- National Institute of Dental and Craniofacial Research
- National Institute of Diabetes and Digestive and Kidney Diseases
- National Institute of Environmental Health Sciences
- National Institute of General Medical Sciences
- National Institute of Mental Health
- National Institute of Neurological Disorders and Stroke
- National Institute of Nursing Research
- National Institute on Aging
- National Institute on Alcohol Abuse and Alcoholism
- National Institute on Deafness and Other Communication Disorders
- National Institute on Drug Abuse
- National Institute on Minority Health and Health Disparities
- National Library of Medicine

And the Office of the Director!

# The Common Fund

## Office of the Director

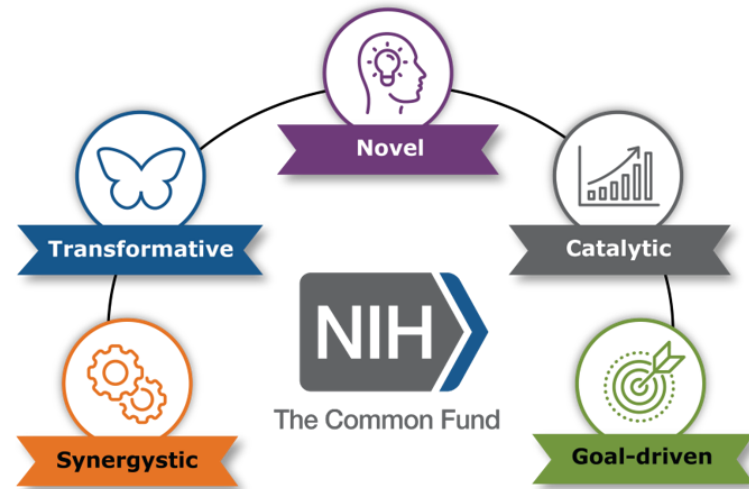
- 2003: **NIH Roadmap for Medical Research** created
- 2006: **Common Fund** created by Congress through 2006 NIH Reform Act
  - Separate appropriation



# The NIH Common Fund

## Mission:

To support **bold scientific programs that catalyze discovery** across all biomedical and behavioral research. Investigators and **multiple NIH Institutes, Centers, and Offices** collaborate on **innovative research** expected to address high priority challenges for the NIH as a whole and make a **broader impact in the scientific community**.



**COMMON FUND = Uncommon Approaches + Research**

# Common Fund Science and Management are Collaborative



Scientists from diverse disciplines provide input as we plan new programs.



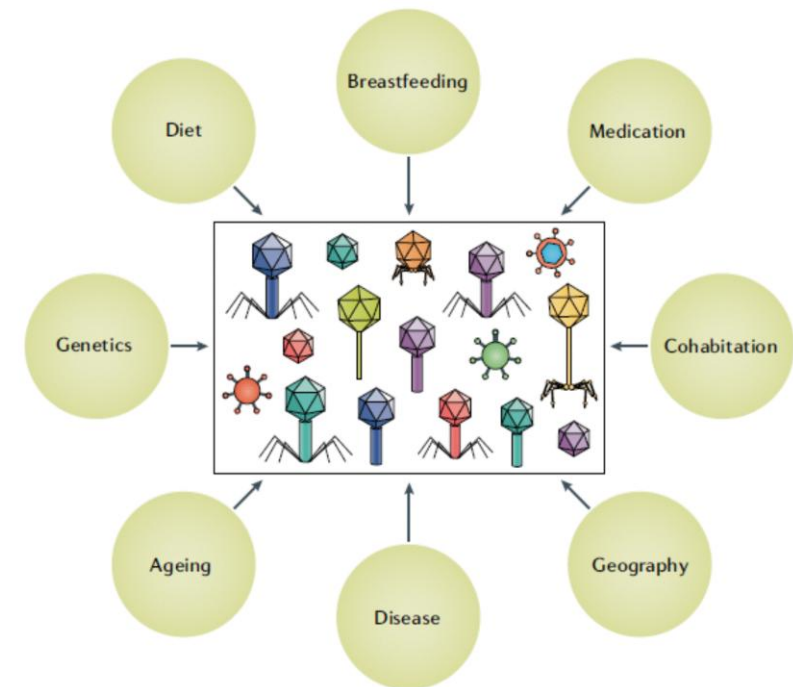
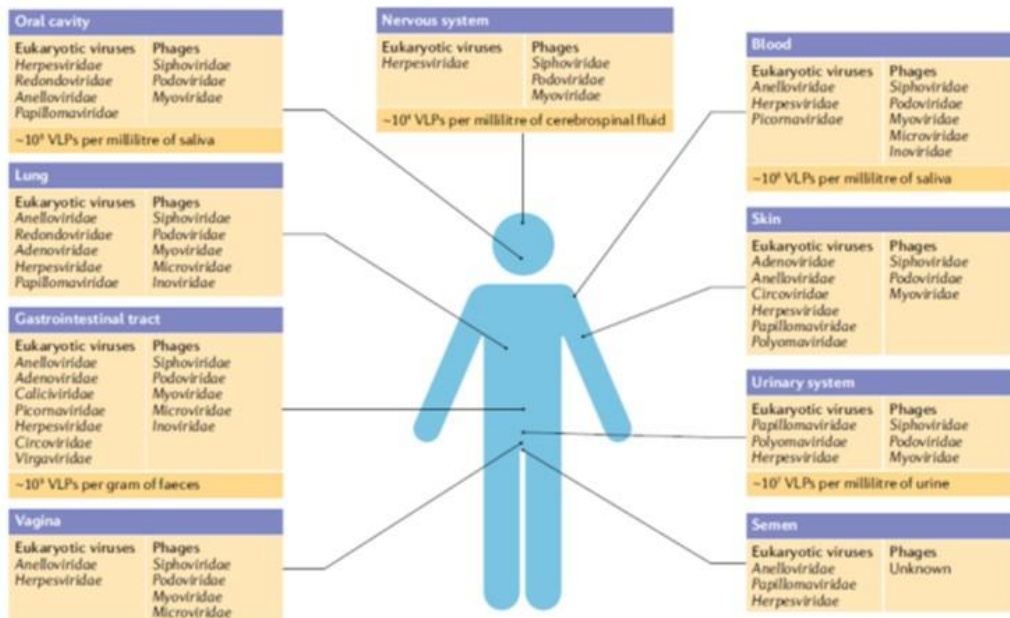
Researchers participate in interdisciplinary consortia to tackle shared goals.



Leadership and staff from Institutes, Centers, and the Office of the Director work together to design funding opportunities and oversee the projects.

# Program Background

- The human virome is large and diverse with  $>10^{13}$  particles per person
- The commensal virome is largely understudied and its interactions with the human body and long-term impacts on health and disease are unknown

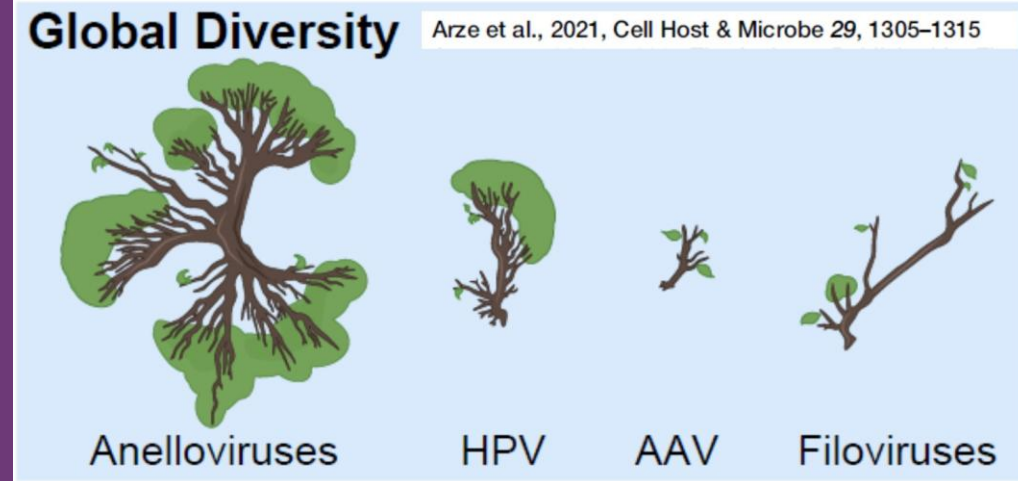
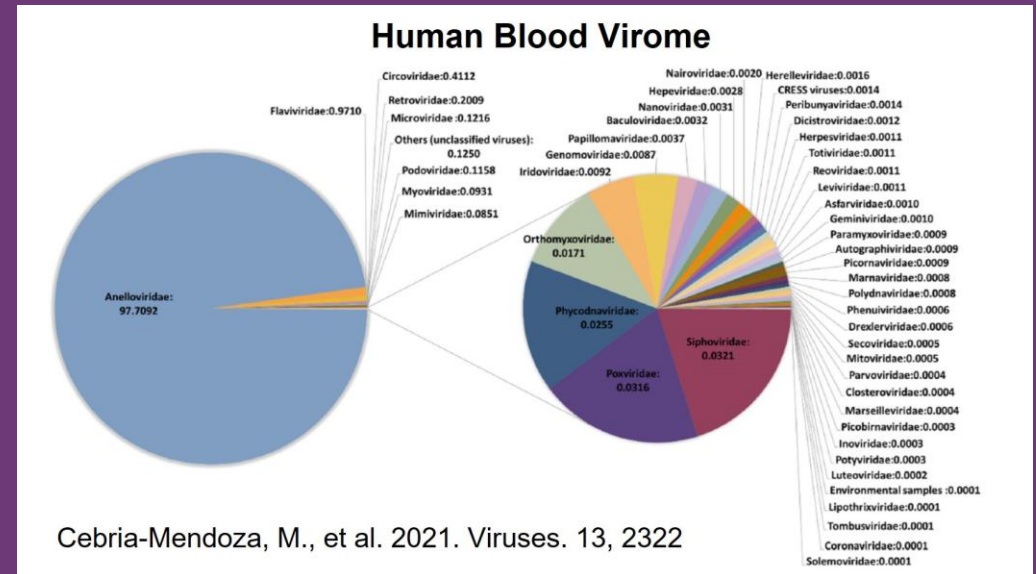


Liang, G., Bushman, F.D. *Nat Rev Microbiol* **19**, 514–527 (2021)

# Program Scope

- ❖ The primary focus is on the commensal human virome
- ❖ Example: Anelloviruses
- ❖ Humans across the globe are infected for their lifetimes

- ❖ What is the source of initial infection?
- ❖ Are they beneficial or do they cause disease?
- ❖ What host cells support Anellovirus replication?



# Program Planning

## Identify current state of knowledge and critical gaps

- Public input through Request for Information ([NOT-RM-22-010](#))
- Portfolio analysis
- [Human virome workshop](#)

Request for Information (RFI): Challenges and Opportunities in Elucidating the Human Virome

Notice Number:  
NOT-RM-22-010

Key Dates

Release Date: \_\_\_\_\_ March 16, 2022

Response Date: \_\_\_\_\_ April 29, 2022



**NIH Common Fund's  
Human Virome Virtual Workshop**

**April 29, 2022  
1:00-5:00 PM EDT**

 National Institutes of Health  
Office of Strategic Coordination—The Common Fund

## NIH Portfolio Analysis



# NIH Common Fund: Human Virome Program

Define "Healthy" Virome- Across the Healthspan and Lifespan in Diverse Human Cohorts

## Funded Research

<a href="#">Human Virome Characterization Centers (U54 Clinical Trial Not Allowed) RFA-RM-23-019</a>		
PI Name	Institution Name	Title
COLLMAN, RONALD G (contact) BUSHMAN, FREDERIC D	UNIVERSITY OF PENNSYLVANIA	The Oro-Respiratory-Gut Virome Axis Over Space and Time
DAS, SUMAN RANJAN (contact) FISHER-HOCH, SUSAN P NORTH, KARI E SHAH, RAVI	VANDERBILT UNIVERSITY MEDICAL CENTER	Vanderbilt-coordinated human Virome Collaborative Center (V2C2)
KAPILA, YVONNE L (contact) CERHAN, JAMES R LAJONCHERE, CLARA M LEE, JANICE S PETROSINO, JOSEPH FRANK	UNIVERSITY OF CALIFORNIA LOS ANGELES	Human Virome Characterization Center for the Oral-Gut-Brain Axis
SABETI, PARDIS CHRISTINE (contact) WANG, DONG	BROAD INSTITUTE, INC.	Virome Investigation in Diverse Human Populations
SNYDER, MICHAEL P (contact) BHATT, AMI SIDDHARTH MASON, CHRISTOPHER EDWARD	STANFORD UNIVERSITY	VAST Center: Viromes Across Space(s) and Time

<a href="#">Consortium Organization and Data Collaboration Center (CODCC) for the Human Virome Program (HVP) (U24 Clinical Trial Not Allowed) RFA-RM-23-016</a>		
PI Name	Institution Name	Title
WHITE, OWEN R (contact) HUTTENHOWER, CURTIS	UNIVERSITY OF MARYLAND BALTIMORE	A consortium facilitation, coordination, and data management center for the HVP

<a href="#">Human Virome Program: Characterization of functional interactions between viruses and human and microbial hosts (U01 Clinical Trial Not Allowed) RFA-RM-23-017</a>		
PI Name	Institution Name	Title
DANTAS, GAUTAM (contact) BALDRIDGE, MEGAN T	WASHINGTON UNIVERSITY	Functional characterization of viral-bacterial-human interactions during antimicrobial and inflammatory perturbations across different lifespans
HENRICH, TIMOTHY JENSEN (contact) TSENG, ZIAN H	UNIVERSITY OF CALIFORNIA, SAN FRANCISCO	Whole Body Deep Tissue Characterization of the Human Virome
LAREAU, CALEB ANDREW	SLOAN-KETTERING INST CAN RESEARCH	The Human DNA virome: from petabase scale to single-cell resolution
ROUND, JUNE LOUISE (contact) STEPHENS, W ZAC	UNIVERSITY OF UTAH	Antibody targeting of the virome
WYLIE, KRISTINE M (contact) ERNST, LINDA M STOUT.	WASHINGTON UNIVERSITY	Dynamic changes in virome-host interactions during pregnancy and postpartum

<a href="#">Human Virome Program: Developing novel and innovative tools to interrogate and annotate the human virome (U01 Clinical Trial Not Allowed) (RFA-RM-23-018)</a>		
PI Name	Institution Name	Title
DITTMER, DIRK P	UNIVERSITY OF NORTH CAROLINA CHAPEL HILL	Concentration and single virion analysis of the virome
EMERSON, JOANNE	UNIVERSITY OF CALIFORNIA AT DAVIS	Establishing laboratory methods for quantitative recovery of diverse DNA and RNA viral sequences from human biosamples
ISMAGILOV, RUSTEM	CALIFORNIA INSTITUTE OF TECHNOLOGY	Viral MEM: Viral Enrichment and Precise Stochastic Quantification with Microbial Context Preservation for Rigorous Virome Analysis of Challenging Human Samples
KYRPIDES, NIKOS C	UNIVERSITY OF CALIFORNIA-LAWRENCE BERKELEY NATIONAL LABORATORY	Advanced analytics for uncovering virus dynamics and functional potential
MCDERMOTT, JASON EDWARD (contact) WHEELER, TRAVIS JOHN	BATTELLE PACIFIC NORTHWEST LABORATORIES	Computational tools for illuminating the dark matter of the human virome

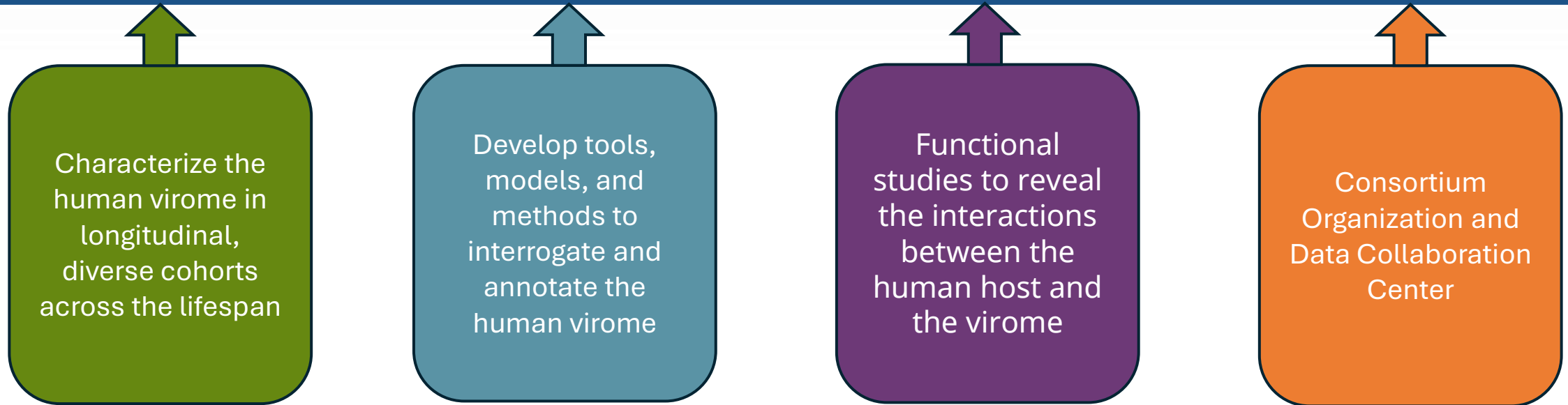


# Critical Knowledge Gaps Identified

- Diversity and dynamics (across tissues, time, populations, and lifespan)
- Establishment (timing and mechanisms)
- Host immune system interactions
- Functional and multi-omic studies
- Impacts of ‘exposome’
- Isolation, quantification, and propagation
- Animal models
- Standardized protocols
- Reference sequence database
- Annotation and contamination detection tools

# Program Goal & Initiatives

**Overall Goal: To characterize the human virome and define its role in health and disease**



***Four initiatives will work synergistically as a consortium of multidisciplinary and innovative teams who will collaborate to achieve the goals of the program.***

# Program Overview

**Objective:** To characterize the human virome and define its role in health and disease

*The Human Virome program consists of four initiatives that will work synergistically as a consortium of multidisciplinary and innovative teams who will collaborate to achieve the goals of the program.*

## Initiatives:

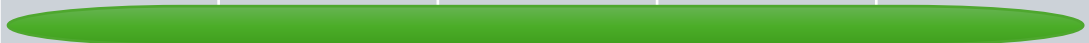






1. Characterize the human virome in longitudinal, diverse cohorts across the lifespan ([RFA-RM-23-019](#))
2. Develop tools, models, and methods to interrogate and annotate the human virome ([RFA-RM-23-018](#); [RFA-RM-24-009](#))
3. Functional studies to reveal the interactions between the human host and the virome ([RFA-RM-23-017](#))
4. Consortium Organization and Data Collaboration Center ([RFA-RM-23-016](#))
5. Pilot Projects to Enhance the Human Virome Program ([RFA-RM-25-006](#))

**Program Duration:** 5 years, FY2025-FY2029

**Total Available Program Funds :** \$173M



# Activities

	Activity Code	# of Awards	FY24	FY25	FY26	FY27	FY28	FY29
VCCs	U54	5						
Tools 1	U01	5						
Tools 2	U01	5						
Functional	U01	5						
CODCC	U24	1						
Pilot Projects 1	R03	(6)						
Pilot Projects 2	R03	(6)						

(anticipated)

# Virome Characterization Centers

- Diverse U.S. cohorts with no overt disease
  - Well-characterized and phenotyped cohorts
- Biospecimens from various anatomic sites
  - Blood, respiratory tract, gastrointestinal and urogenital tracts, oral cavity, central nervous system, and skin
- Collect, process, and analyze biospecimens
- Categorize virus taxonomy and characterize new viruses
- Determine factors that influence virome composition and host dynamics
- Set-aside funds for consortium collaboration pilot projects

# Virome Characterization Centers

- Cores:
  - Administrative
  - Biospecimen collection
  - Biospecimen analysis
  - Data analysis and submission
  - Ethical, legal, and social implications
- Coordinate with Consortium Organization and Data Coordination Center
  - Develop standards for sample collection, processing, and storage; defining appropriate cohort characteristics; and data acquisition procedures and system interoperability

# Virome Characterization Centers

## 1. Ronald Collman & Frederic Bushman, University of Pennsylvania

“The Oro-Respiratory-Gut Virome Axis Over Space and Time”

- Longitudinal oral/dental, gut (fecal), respiratory tract, and blood specimens from biobanks and new subjects
- Healthy children, adolescents, adults and elderly individuals from the mid-Atlantic region
- Describe and quantify virome, including viruses of humans, bacteria, and human eukaryotic commensals, and identify host cells for novel viruses and characterization of viral DNA modification
- Define the commonalities and differences of virome communities over time within individuals and between age groups
- Adhere to ethical norms and regulatory requirements
- Collaborate, harmonize, and integrate with other VCCs and openly share data
- Ensure representation of traditionally under-studied populations

# Virome Characterization Centers

## 1. Ronald Collman & Frederic Bushman, University of Pennsylvania

“The Oro-Respiratory-Gut Virome Axis Over Space and Time”

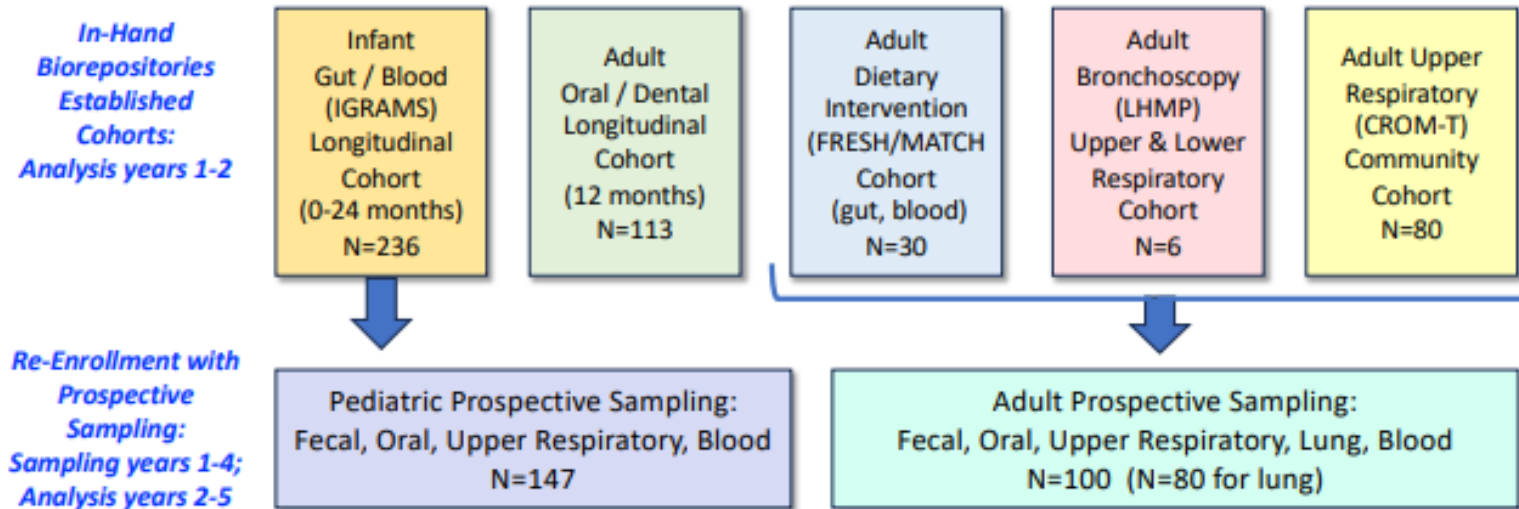


Figure 4. Overview of in-hand biobanks samples (top row) to be analyzed in years 1-2, and prospective collections from re-enrolled participants (bottom row) to enable broad and long-term longitudinal understanding of the respiratory tract, oral, gut and blood virome.

# Virome Characterization Centers

## 2. Suman Das, Susan Fisher-Hoch, Kari North, & Ravi Shah, Vanderbilt University

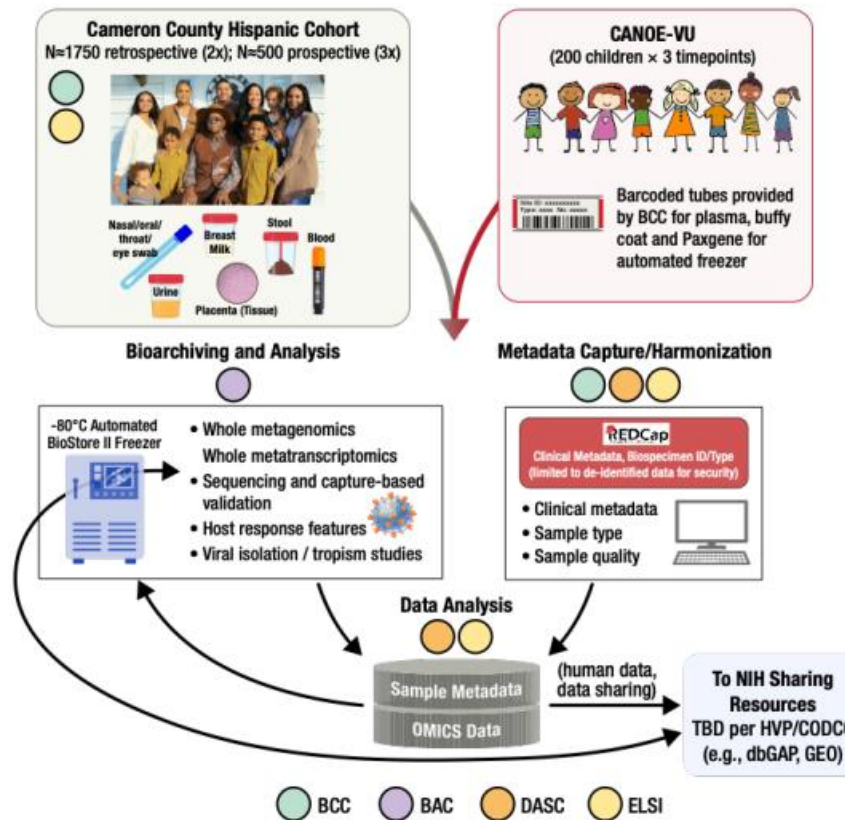
“Vanderbilt-coordinated human Virome Collaborative Center (V2C2)”

- Ocular, nasal, oropharyngeal, plasma, blood (extracellular vesicles, PBMCs, platelets), urine, and stool samples, and accompanying placental and breast milk samples
- 2,250 Hispanic/Latinx individuals at the US-Mexico border (ages 8-90)
- Examine interactions of host biology and flora, viral persistence, and variation in biologically relevant phenotypes in healthy individuals
- Viral whole metagenomic/metatranscriptomic sequencing
- Study host-viral interactions via (1) host genomics, (2) viral tropism studies, and (3) host response characterization (at the cellular and organism-wide level with proteomics/transcriptomics)
- Establish and manage ethically-responsible repository of harmonized metadata and molecular information for data sharing that allows multi-omic connections between longitudinal phenotypes and host-viral characteristics

# Virome Characterization Centers

## 2. Suman Das, Susan Fisher-Hoch, Kari North, & Ravi Shah, Vanderbilt University

“Vanderbilt-coordinated human Virome Collaborative Center (V2C2)”



# Virome Characterization Centers

## 3. Yvonne Kapila, James Cerhan, Clara Lajonchere, Janice Lee, & Joseph Petrosino, UCLA

“Human Virome Characterization Center for the Oral-Gut-Brain Axis”

- Access to hundreds of thousands of patients across the U.S. with saliva, nasopharyngeal, dental plaque, gingiva, teeth, crevicular fluid, bone, muscle, buccal/tongue swabs, blood, stool, colon biopsies, CSF, brain tissue, and fecal samples
- Sequence 5,000 different samples per year, including approximately 2,250 oral/nasopharyngeal (800 teeth, 500 dental plaque, 750 nasopharyngeal, 100 gingival tissues, 100 saliva), 2,250 brain (1,500 CSF, 500 saliva, 240 blood, 10 brain tissues), and 500 GI (125 each of stool/urine/saliva/GI biopsy) samples
- Characterize virome of the oral–gut–brain axis and estimate its richness and complexity in health across the lifespan
- Use next-generation sequencing and shotgun metagenomic sequencing

# Virome Characterization Centers

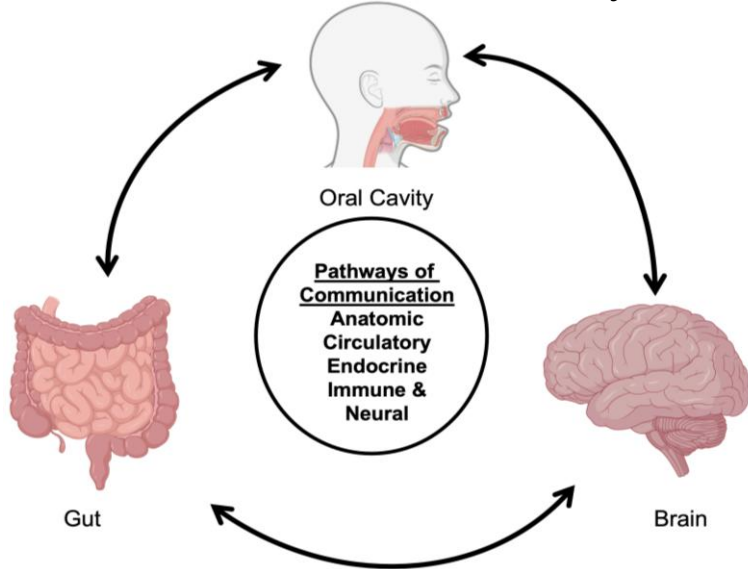
## 3. Yvonne Kapila, James Cerhan, Clara Lajonchere, Janice Lee, & Joseph Petrosino, UCLA

“Human Virome Characterization Center for the Oral-Gut-Brain Axis”

- UCLA Biospecimen Bank
- UCLA BrainSPORT
- UCLA Clinical Microbiology Lab
- UCLA Dentistry
- UCLA Institute for Precision Health
- UCLA Microbiome Center
- UCLA Neuropathology
- UCLA Oral and Public Health
- UCLA Oral Surgery
- UCLA Pediatric Dentistry
- UCLA Periodontics
- UCLA Psychiatry
- UCLA Visiting Scholar Dentistry
- All India Institute for Medical Sciences
- CARE Consortium
- Concussion Assessment Research & Education for Kids
- Mayo Clinic
- NIH/NIDCR
- Together for CHANGE

# Human Virome Characterization Center for the Oral-Gut-Brain Axis

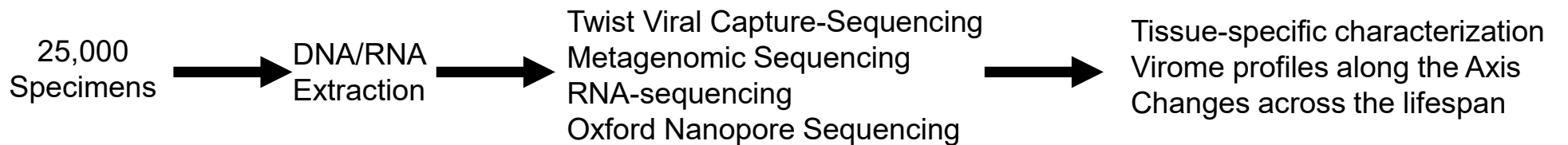
## Oral-Gut-Brain Axis Communication Pathways



## Oral-Gut-Brain Axis Sampling



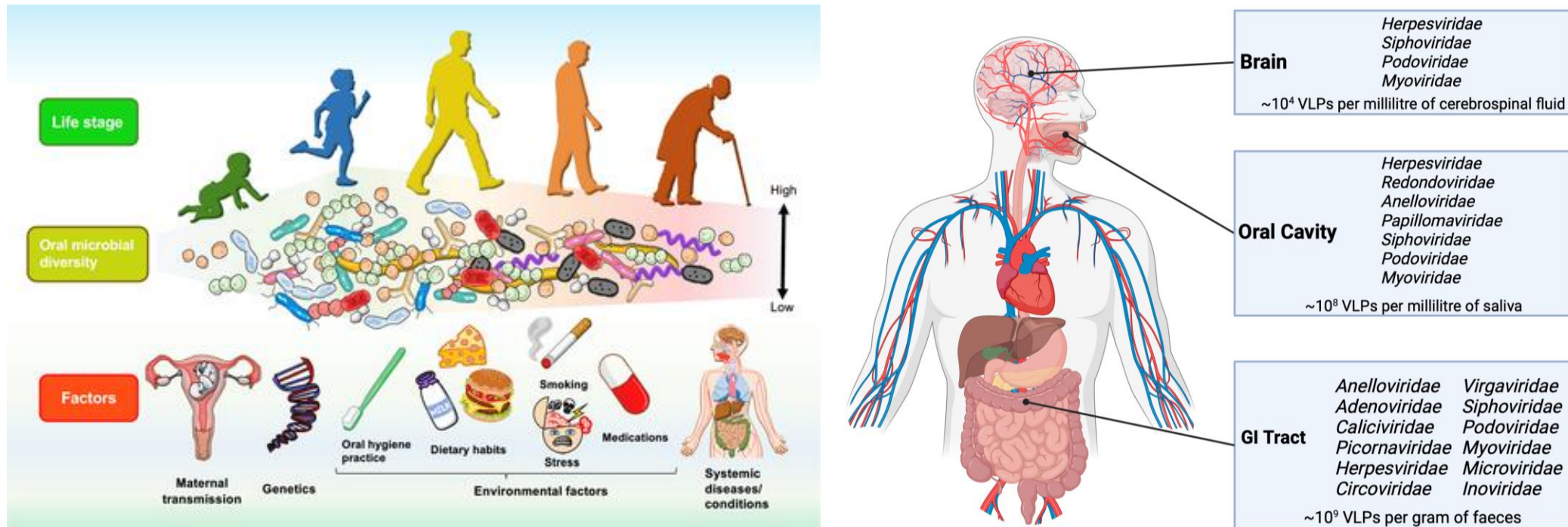
## Virome Characterization



# NIH Human Virome Program (HVP) 2025

## Human Virome Characterization Centers

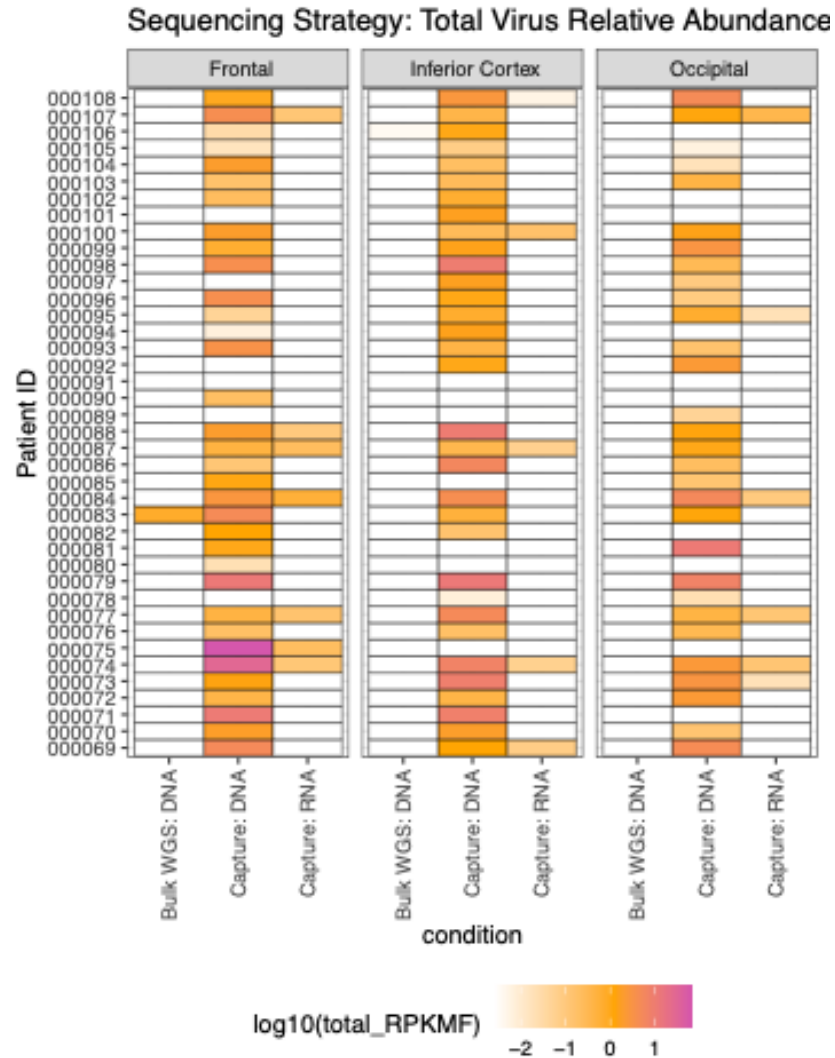
### UCLA-Oral-Gut-Brain Axis



# Human Virome-Across the Oral-Gut-Brain Axis

## Twist Capture and Whole Genome Sequencing Pilots

Sequencing strategy matters:  
Hybrid capture of DNA yields most  
abundant human-tropic viromes



Human Brain Specimens

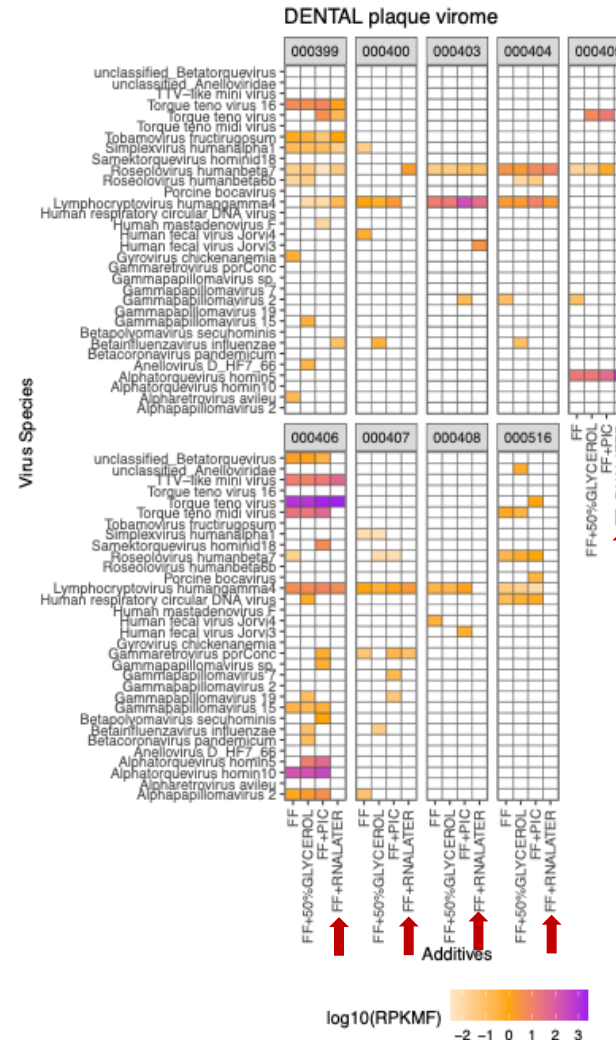
# Human Virome-Across the Oral-Gut-Brain Axis

## Twist Capture and Shotgun Metagenomic Sequencing - Storage Solution Pilots

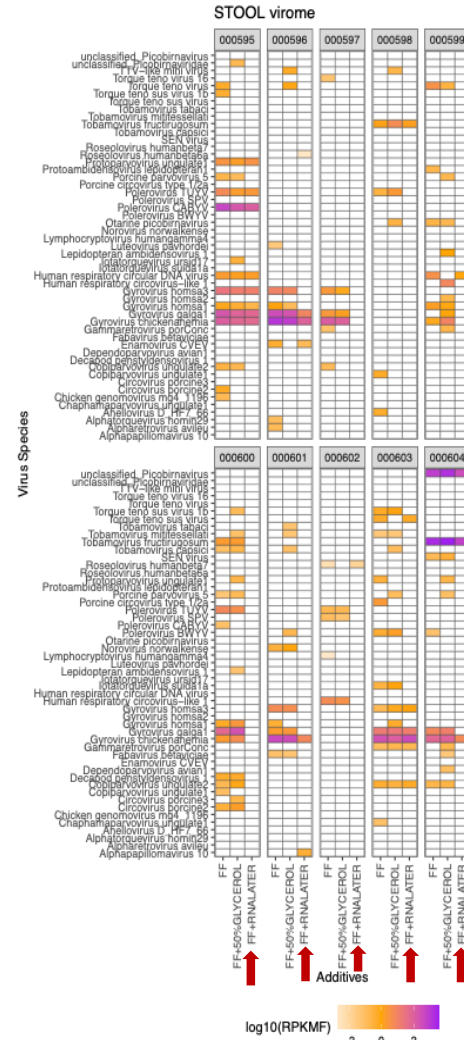
### Viral abundance by patient, additive type- Dental Plaque, Stool

- RNALater may decrease virus yield
- Stool: some instances of FF + 50% glycerol out-performing FF (patient 00601)
- Some instances of a clear patient-specific signal for certain viruses

### Dental Plaque



### Stool

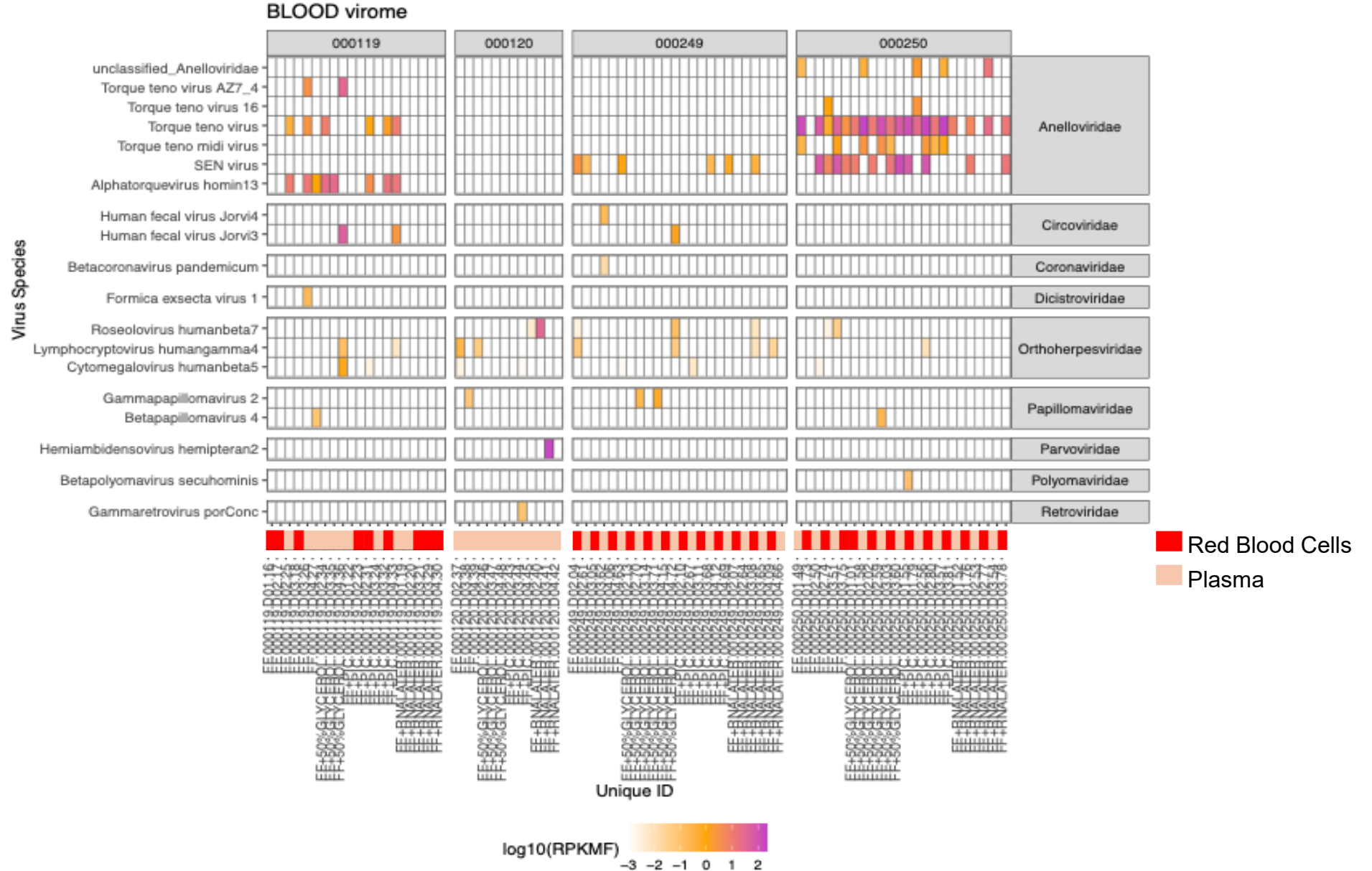


# Human Virome-Across the Oral-Gut-Brain Axis

## Twist Capture and Shotgun Metagenomic Sequencing - Storage Solution Pilots

Blood

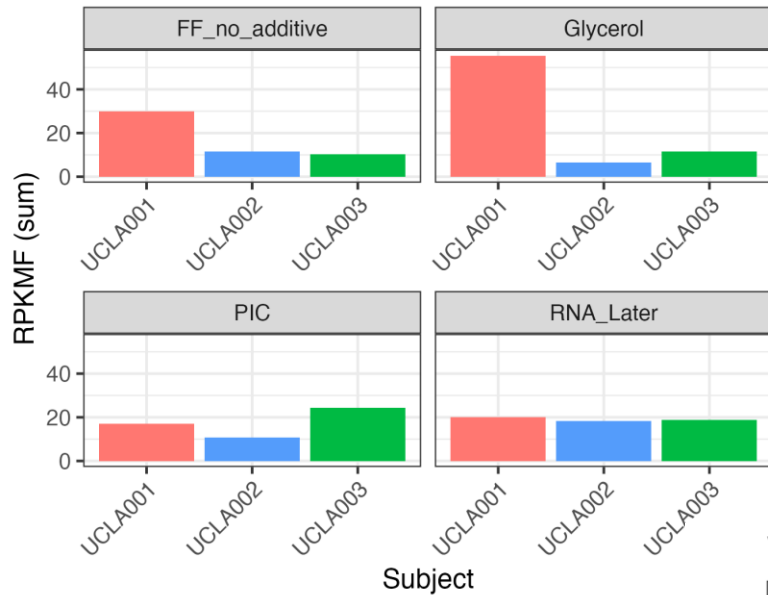
Plasma higher  
virome levels than  
RBCs



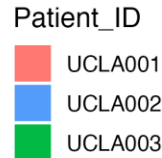
# Human Virome-Across the Oral-Gut-Brain Axis

## Twist Capture and Shotgun Metagenomic Sequencing - Storage Solution Pilots

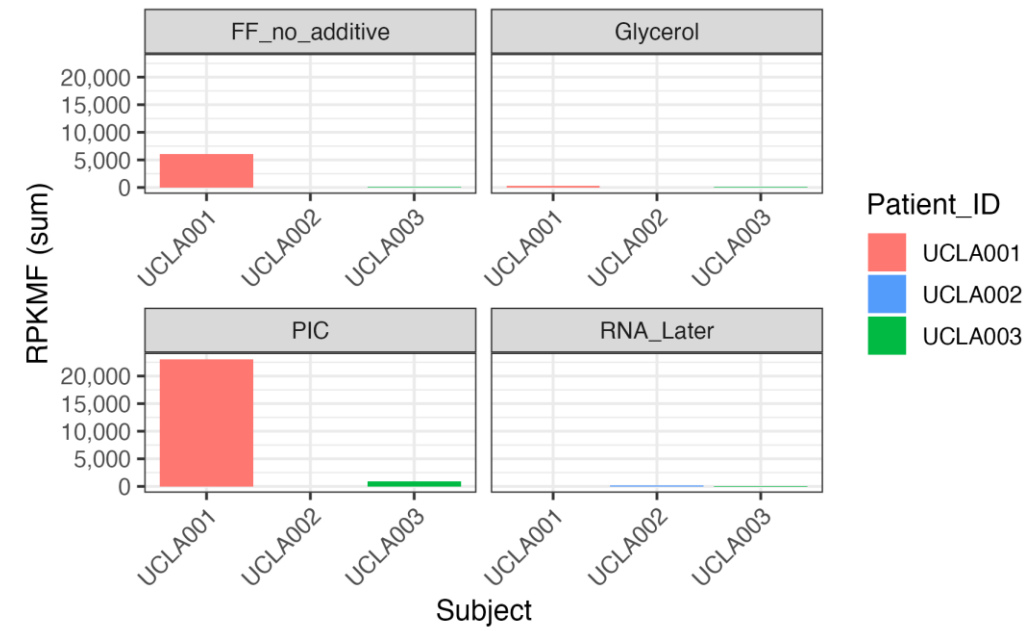
Viral RPKMF by Additive- Blood (Buffy Coat) Group



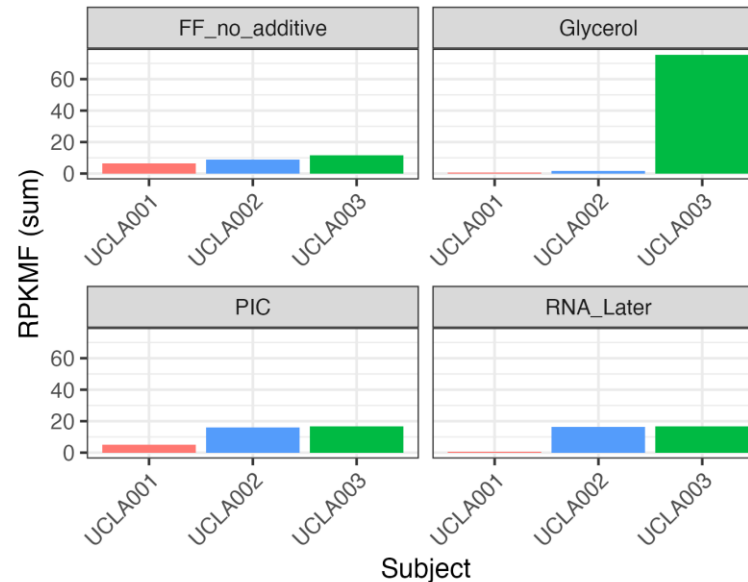
Viral RPKMF by Additive, Subject **Blood groups**



Viral RPKMF by Additive- Blood (Plasma) Group



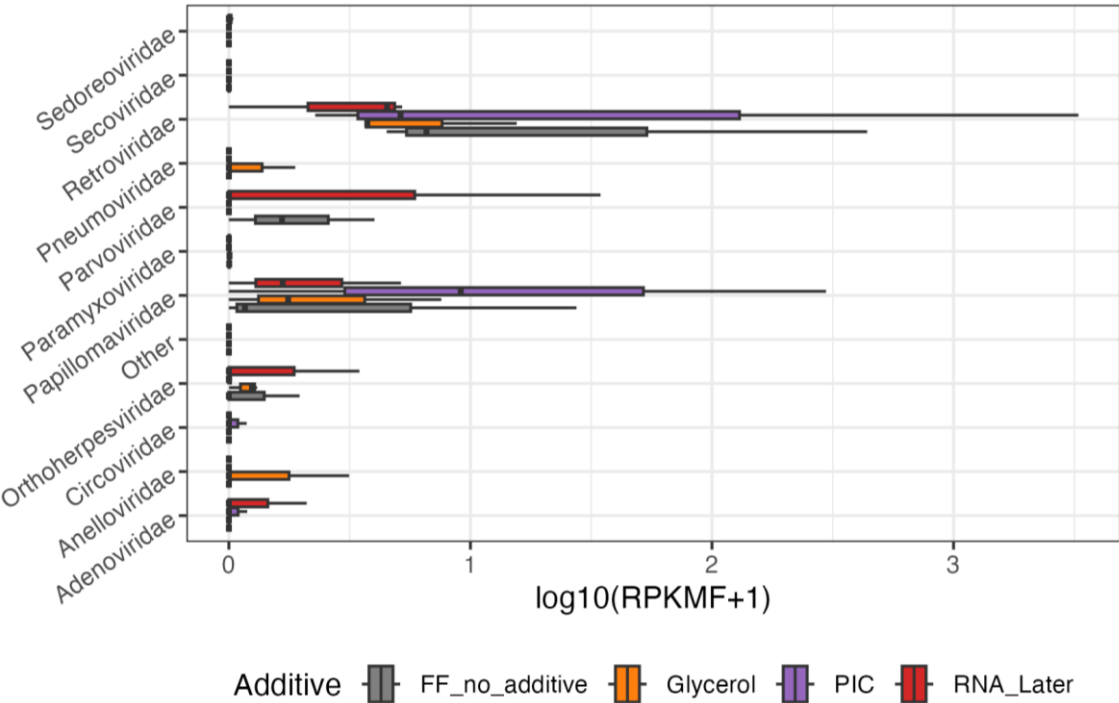
Viral RPKMF by Additive- Blood (RBC) Group



- **Patient heterogeneity**
- **Different blood fractions have different virome relative abundance**

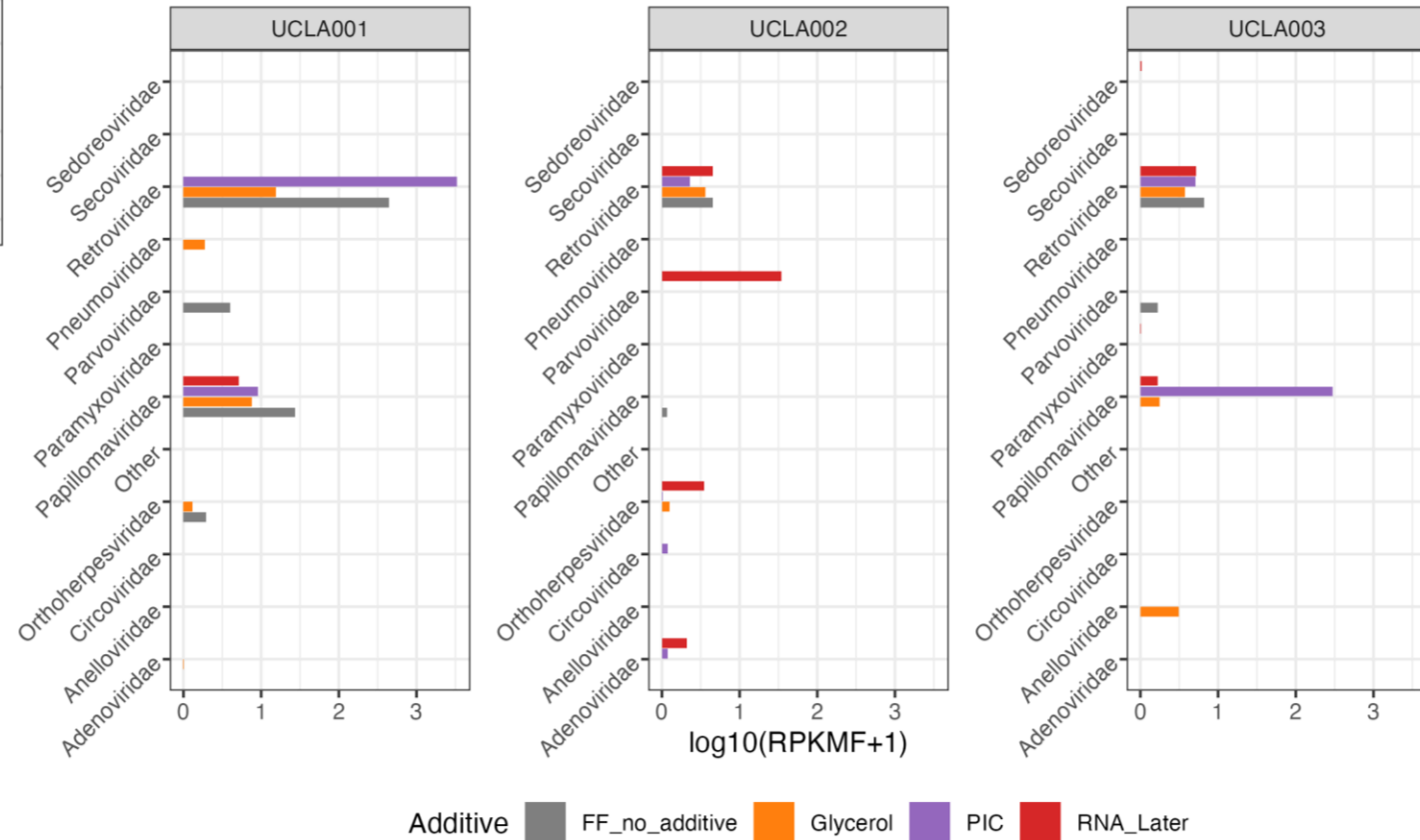
# Human Virome-Across the Oral-Gut-Brain Axis

## Twist Capture and Shotgun Metagenomic Sequencing - Storage Solution Pilots



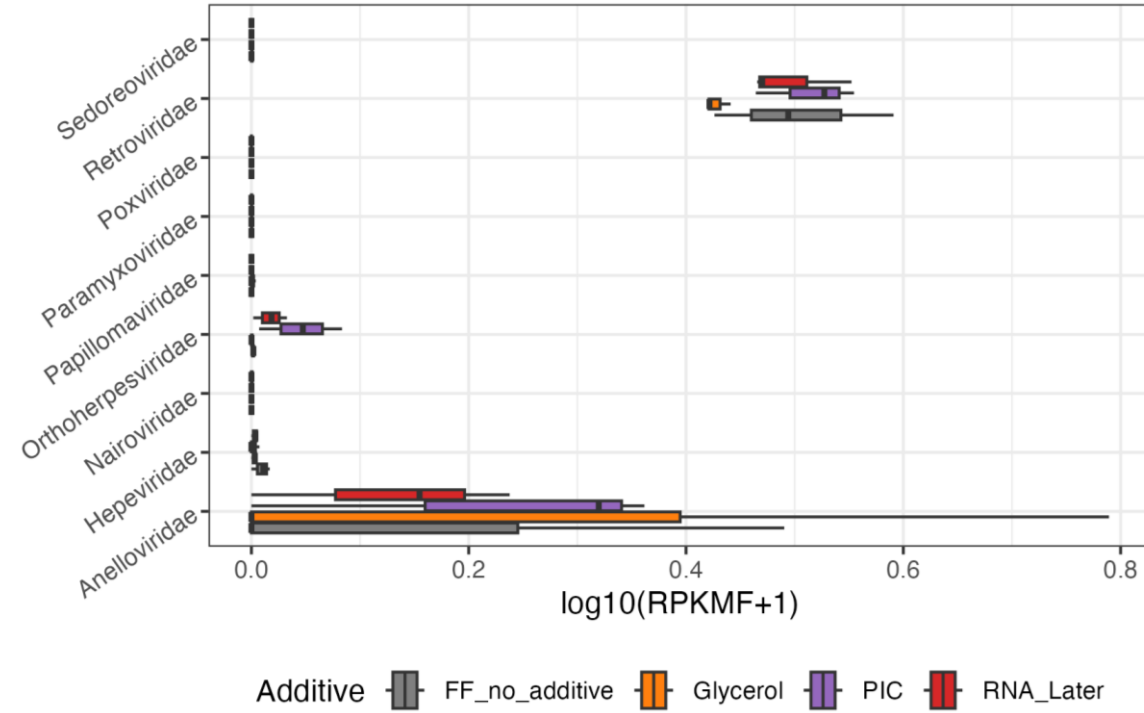
- ***Patient heterogeneity***
- ***Common virus families***

## Viral Family RPKMF by Specimen Type *Blood- Plasma* (top 12 families)



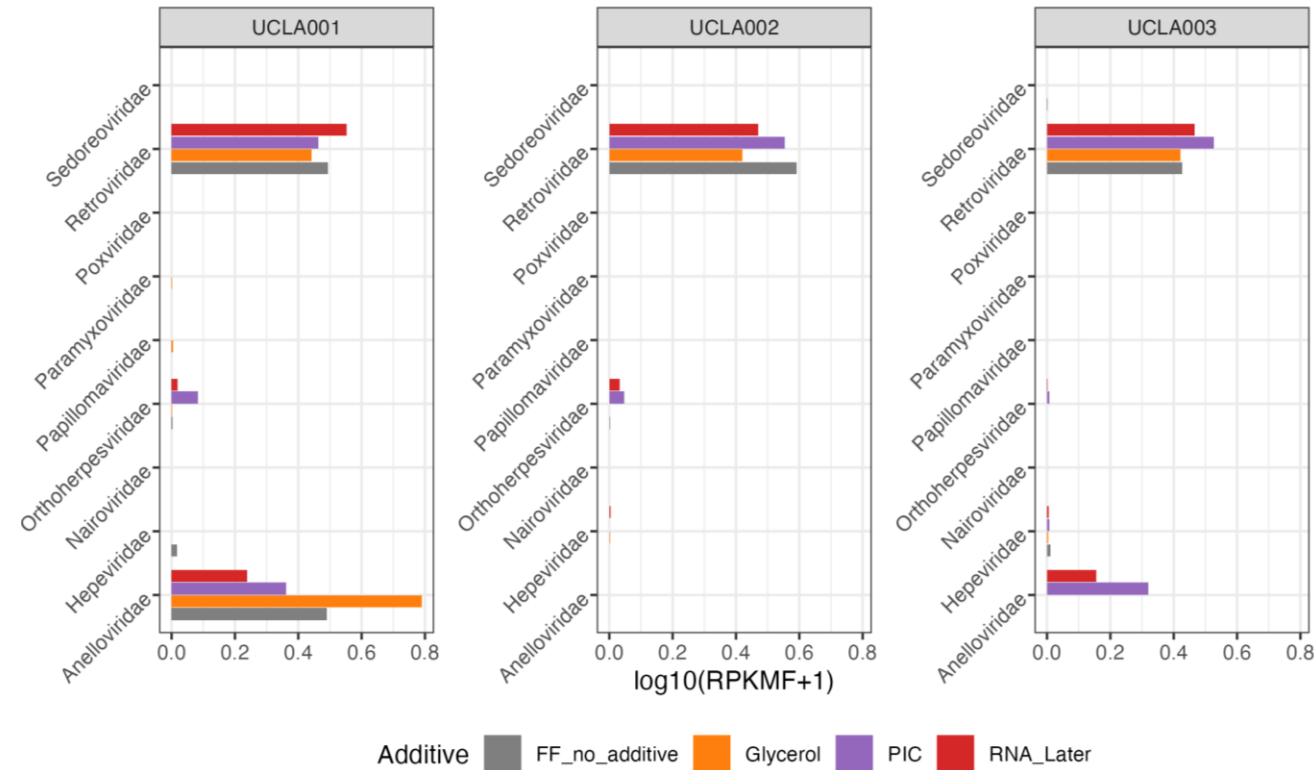
# Human Virome-Across the Oral-Gut-Brain Axis

Twist Capture and Shotgun Metagenomic Sequencing - Storage Solution Pilots



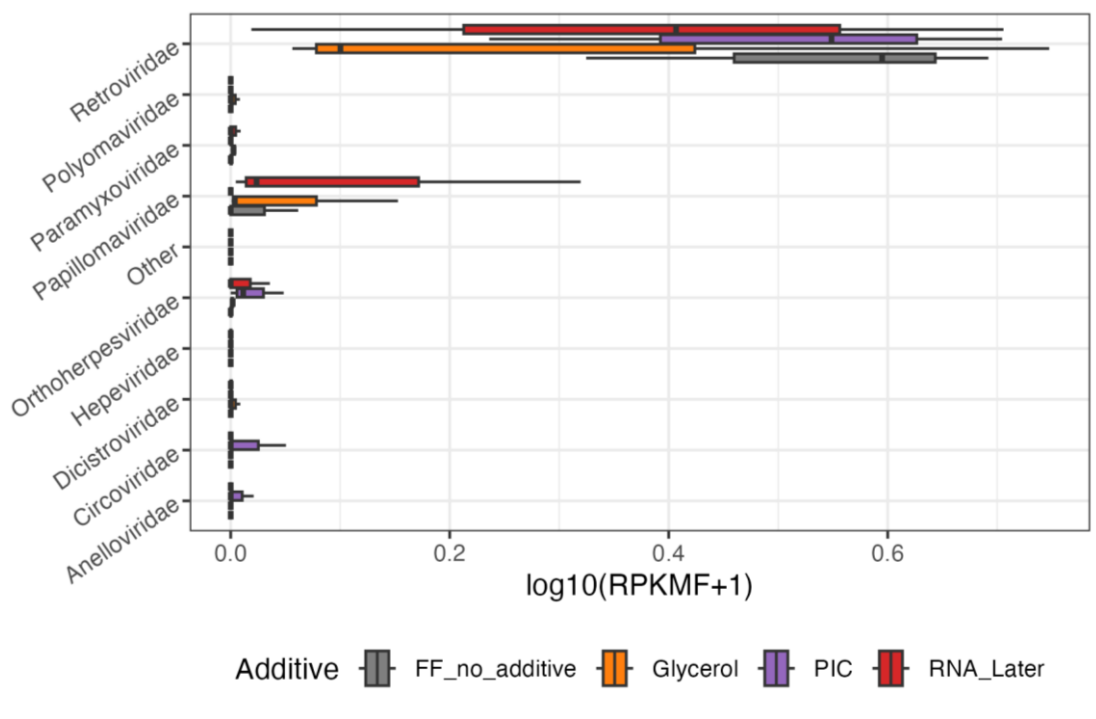
- ***Patient heterogeneity***
- ***Common virus families***

## Viral Family RPKMF by Specimen Type *Blood- Buffy Coat*

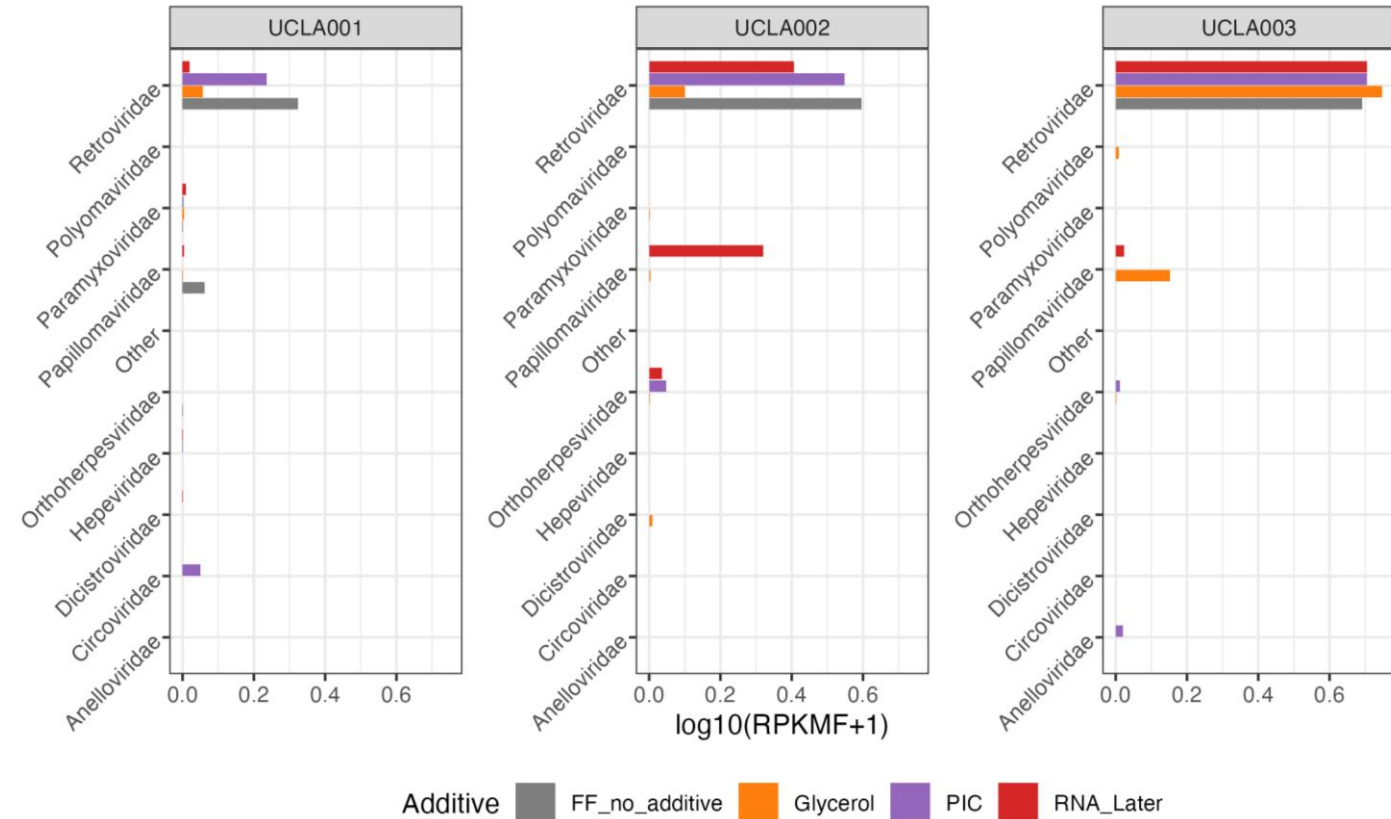


# Human Virome-Across the Oral-Gut-Brain Axis

Twist Capture and Shotgun Metagenomic Sequencing - Storage Solution Pilots



## Viral Family RPKMF by Specimen Type *Blood- RBCs*(top 12 families)



- ***Patient heterogeneity***
- ***Common virus families***

# Distinct Ethical, Legal, and Social Implications (ELSI) issues in HVP Research

Distinctive ELSI Issues	ELSI issues in HVP	Considerations
<b>Human genomic data in virome datasets</b>	Human data may need to be filtered to protect privacy when sharing data	Tradeoff: filtering limits study of host-virus interactions
<b>Reporting obligations</b>	Virome findings may raise questions about: <ul style="list-style-type: none"> <li>● Communicable disease reporting</li> <li>● Possible child and elder abuse reporting</li> </ul>	Connections to public health/legal reporting compared to similar research (Human Genome Project, Human Microbiome Project)
<b>Return of results</b>	<ul style="list-style-type: none"> <li>● No framework to guide return of results</li> <li>● Uncertain actionability thresholds</li> <li>● Historically stigmatization of some viral infections</li> </ul>	<ul style="list-style-type: none"> <li>● Less established guidance than genomics</li> <li>● Potentially more socially sensitive than microbiome results</li> </ul>
<b>Common ELSI Issues</b>	<ul style="list-style-type: none"> <li>● Privacy and data governance</li> <li>● Potential for 3rd party harms (e.g., stigma or discrimination risks for groups)</li> <li>● Concern about downstream applications (e.g., misuse, individual and community access to benefits such as new virome-based diagnostics or therapies)</li> </ul>	

# Example VCC ELSI Project: “Healthy” Virome



*\*AI-generated image*

## Research Questions

- How are researchers defining the “healthy” human virome?
- What influences the health status of a virome?

## Step 1: Systematic Literature Review

- 1466 articles imported from PubMed.
- 954 studies undergoing full-text screening.

# Virome Characterization Centers

## 4. Pardis Sabeti & Dong Wang, Broad Institute

“Virome Investigation in Diverse Human Populations”

- Uncover and curate viruses in humans and characterize key features of their biology and dynamics, including mapping viral tropism, monitoring changes over time, and identifying differences in groups of viruses
- Specimen collection from five existing large, longitudinal and diverse cohorts that share a common study design with >350,000 participants across all 55 U.S. states and territories
- Establish core sample set from diverse 4,000-participant cohort of varying ages, sex/gender, geographic origin, and racial/ethnic diversity from a range of tissues, including blood, urine, stool, oral, nasal, vaginal, skin samples, and brain and paired with phenotype data
- Metagenomic RNA, DNA, and total nucleic acid sequencing

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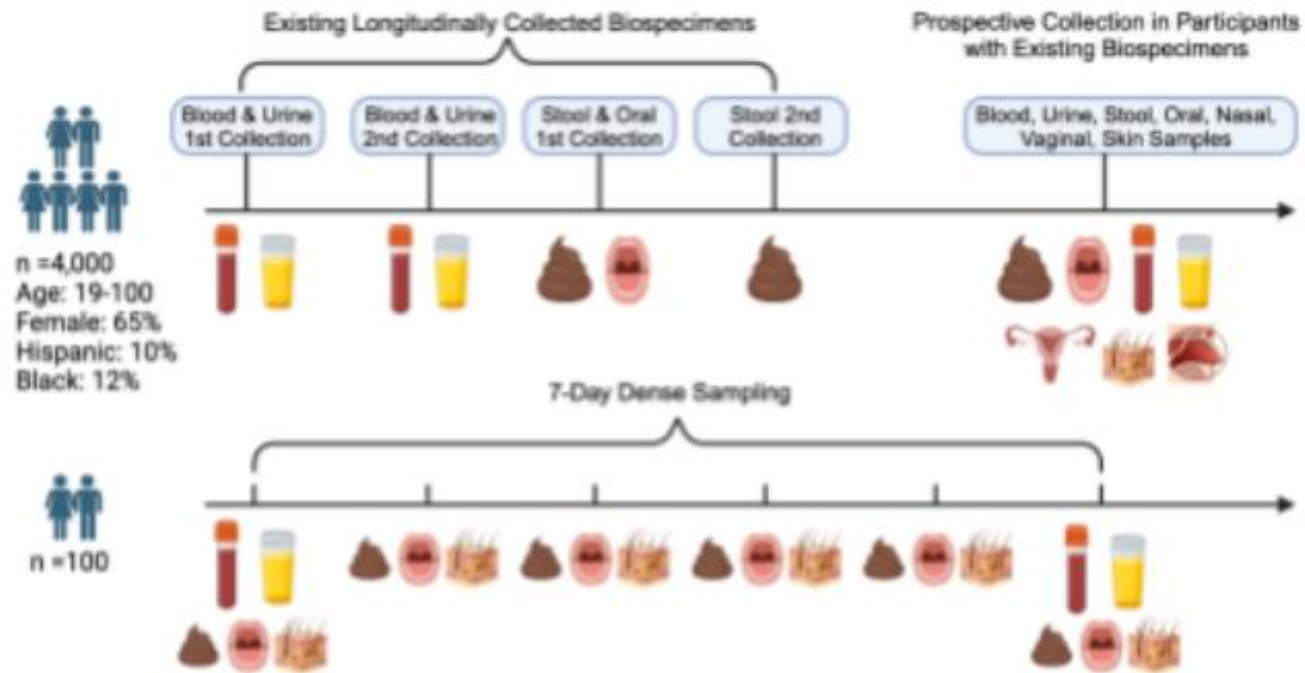


Figure 2. Availability of existing samples and planned biospecimen collection

# Virome Characterization Centers

## 5. Michael Snyder, Ami Bhatt, & Christopher Mason, Stanford University

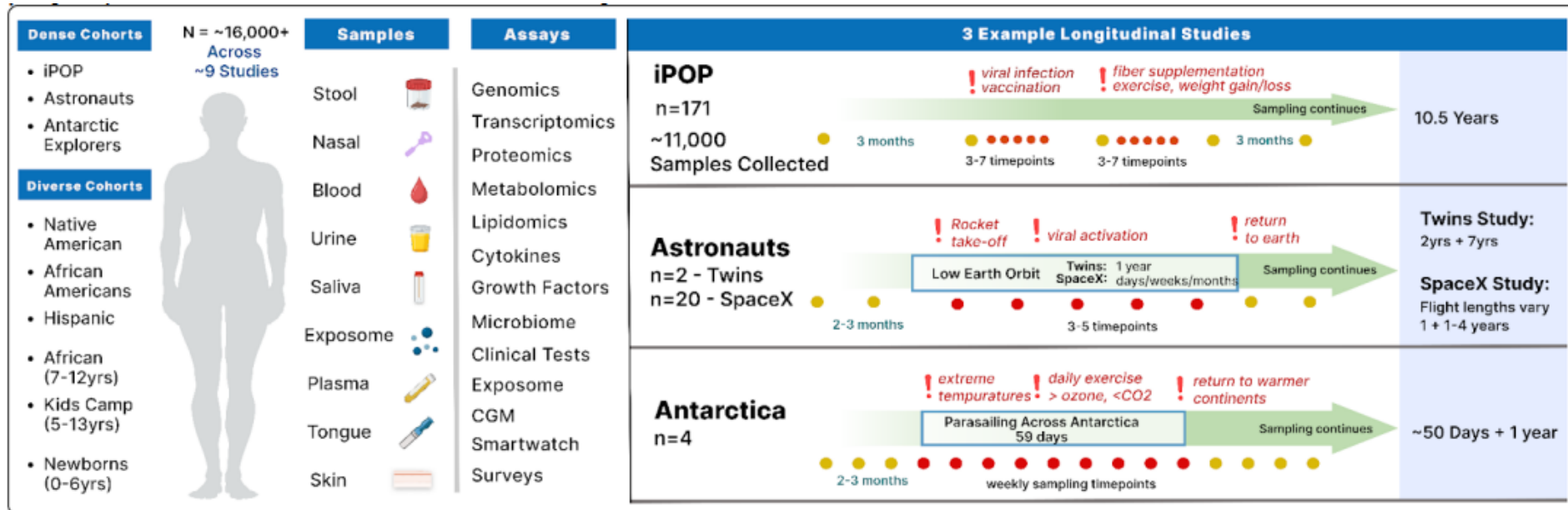
“VAST Center: Viromes Across Space(s) and Time”

- Identify human-associated virome and characterize the viral constituents through a unique set of longitudinal samples collected from healthy individuals
- Longitudinal samples from unique, well-phenotyped cohorts with diverse lifestyles, including (1) ~171 extensively characterized individuals tracked for up to 13.5 years with subsets with tracked dietary interventions and lifestyle changes; (2) individuals who have been to low earth orbit or Antarctica; (3) members of underserved groups such as Native Americans, Hispanics and African Americans; (4) children from underserved groups who have undergone exercise intervention; (5) individuals with associated airborne samples (exposome); (6) controls from clinical cohorts
- Utilize viral enrichment strategies and bulk metagenomic and metatranscriptomic deep sequencing with spatial imaging technology to delineate viral tropism at the subcellular level

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“VAST Center: Viromes Across Space(s) and Time”



**Fig.1** Summary of key cohorts, samples and assays (left). Most, but not all, assays were performed on the dense cohorts. Summary of 3 densely sampled cohorts with lifestyle or geographical perturbation (right).

**Table 1:** Breakdown VAST Center Studies and Sample Types.

# Tools & Methods Development

- Goals:
  1. Develop innovative and novel tools, models, and methods to overcome the major challenges in identifying and characterizing human viruses
  2. Develop computational biology and bioinformatics tools to enhance the analysis and visualization of the human virome
- Set-aside funds for consortium cross validation

# Tools & Methods Development

## Areas of interest:

- Viral isolation and detection
- Viral quantification
- in vitro viral propagation, replication, infectivity, and/or visualization
- Culture systems with high-throughput capacity
- Enrichment techniques for downstream sequencing
- Laboratory or in silico approaches to eliminating environmental background and contaminating sequences
- Approaches for human and animal sample procurement and storage
- in vitro assays and animal models for virome dynamics
- Host range prediction from sequence data, viral-viral interaction detection, ecology-based analysis of viral/host/population dynamics
- in silico methods and functional annotation of uncharacterized regions in viral genomes
- in silico methods to compare viromes across studies
- Identification of sequencing errors leading to false identification of viruses or variants, and lack of matches in current viral databases

# Tools & Methods Development (1)

1. **Nikos Kyrpides, University of California, Lawrence Berkeley National Laboratory:** Develop new computational tools for taxonomic classification, host prediction, and functional annotation of novel virus genomes
2. **Rustem Ismagilov, California Institute of Technology:** Develop technologies to enrich viromes, preserve microbial context, and enhance the accuracy and reproducibility of viral sequencing
3. **Dirk Dittmer, University of North Carolina Chapel Hill (aim 1 only):** Develop virus purification that can detect  $<1$  genome copy per ml and single-virion detection method to quantify viral particles
4. **Jason McDermott & Travis Wheeler, Battelle Pacific Northwest Laboratories:** Develop enhanced methods for human phage identification using graph assemblies, characterization of auxiliary genes, and annotation
5. **Joanne Emerson, University of California at Davis:** Develop methods to extract and quantify absolute abundances of DNA and RNA viruses from human biosamples by translating techniques from soil viromics

# Tools & Methods Development (2)

1. **Ami Bhatt, Stanford University:** Develop computational framework and culture platform to identify phages and their hosts and model viral-host population dynamics
2. **Ellen Foxman, Yale University:** Amplify viruses to enhance detection and map viral sequences to host cells and spatial locations in epithelial and tonsil organoid cultures
3. **Wendy Gilbert & Carson Thoreen, Yale University:** Comprehensively identify and characterize non-coding elements in the eukaryotic virome that orchestrate the translation of viral genomes
4. **Kathryn Kauffman & Libusha Kelly, University at Buffalo :** Develop computational protein language model (PLM)-based approaches to identify and characterize viral sequences in metagenomic data and deplete phages to detect previously unrecognized or undetected viruses
5. **Daniel Park, Broad Institute:** Develop platform to provide access to high-priority analytic tools, standardized benchmarking datasets, and an environment for continuous tool evaluation

# Functional Studies

- Characterize the functional interactions between the virome, microbiota, and human host
  1. Characterize tissue tropism and host reservoirs for all resident viruses
  2. Define and characterize the functional interactions of resident viruses within human host tissues and the microbiome
- Set-aside funds for consortium collaboration pilot projects

# Functional Studies

1. **Kristine Wylie, Linda Ernst, & Molly Stout, Washington University:** Examine interactions between host immune responses and virome through pregnancy and post-partum
2. **June Round & Zac Stephens, University of Utah:** Characterize and identify commensal gut viruses that interact with antibodies in humans
3. **Timothy Henrich & Zian Tseng, UCSF:** Characterize virome in deep tissues across the whole-body and determine mechanisms by which viruses persist in these tissues
4. **Caleb Lareau, Sloan-Kettering Institution for Cancer Research:** Develop new data science and experimental methods to understand why individuals respond differently to the same infections by mapping the individuals, tissues, and cells that harbor latent viruses
5. **Gautam Dantas & Megan Baldrige, Washington University:** Characterize viruses associated with microbiome shift events and their bacterial hosts, determine the effects of antibiotics and inflammation on viral activities, and define immunological causes and effects of altered viromes on mammalian host

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# Consortium Organization and Data Collaboration Center (CODCC)

- Oversee HVP Consortium administration and collaboration
  - Facilitate meetings, communication, training, logistics
- Create protocol & data standardization
  - Ensure reproducibility & rigor
- Facilitate data analysis, integration, and visualization for the broader scientific community
  - Manage software hub for analysis capabilities
  - Provide data/metadata infrastructure
  - HVP Data Portal
  - Human Virome Reference Dataset

# Consortium Organization and Data Collaboration Center (CODCC)

## **Owen White & Curtis Huttenhower, University of Maryland**

- Relationship building and social integration
- Establish stakeholders and consortia governance
- Develop administrative policies
- Maintain transparent communication
- Enable working group operations
- Create consortium-wide roadmaps
- Overseeing milestone completion
- Address technical gaps
- Data standardization, analysis, integration, and visualization

# Collaborative Pilot Projects

## **Purpose: To promote cross-initiative/project collaboration within the HVP Consortium**

- CODCC: Facilitate collaboration and shared interests among Consortium
- VCCs: Capitalize on new findings; validate new tools, methods, or approaches; determine additional functional characteristics of novel viruses
- Tools & Methods: Cross-validate developed tools, methods, and technologies
- Functional Studies: Small-scale studies relevant to broader community

# Program Deliverables



- Catalog of human commensal viruses across a diverse cohort from multiple body sites
- Tools, technologies, and methods to improve viral detection and annotation
- Functional assays interrogating interactions between the human host and virome
- International human virome consortium



# Thank you!

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 <https://human-virome.org/>

