

The Human Microbiome: a New Frontier in Health

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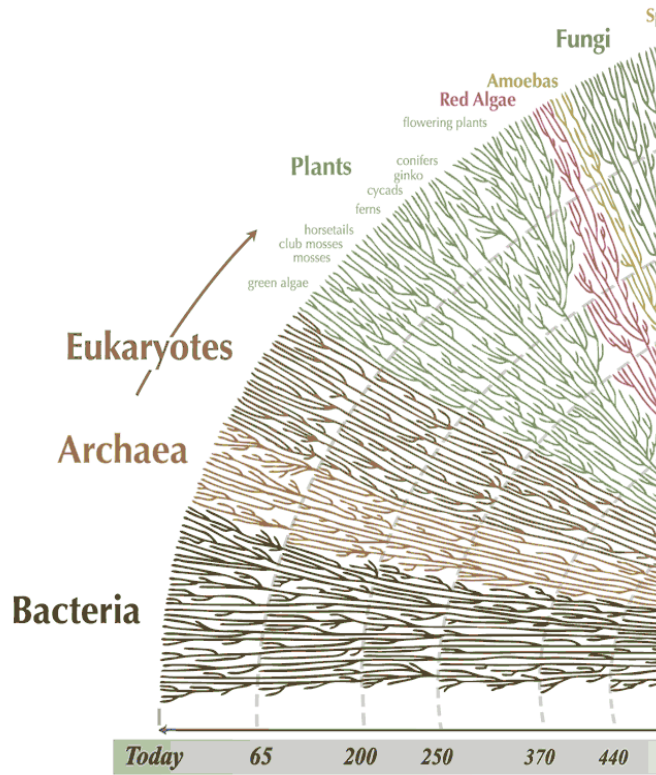
<https://microbiome.ucsf.edu>

What We'll Cover Tonight.....

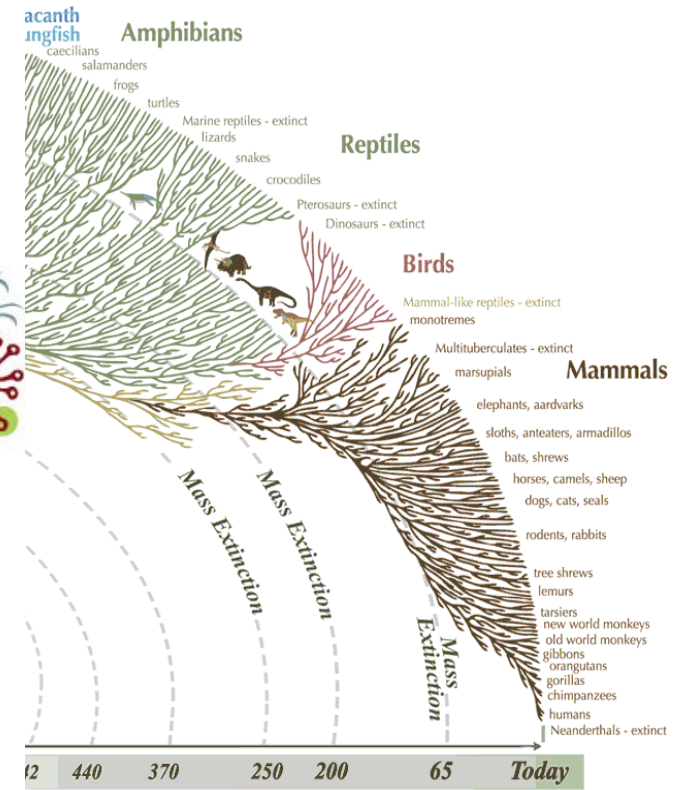
- How do you study entire populations of microbes?
- Human microbiome 101!
- Case study – leveraging the early life gut microbiome to predict and treat childhood allergic asthma
- What's next?

Microbes Pre-date Earth's Biodiversity

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All the



Dinosaurs - extinct

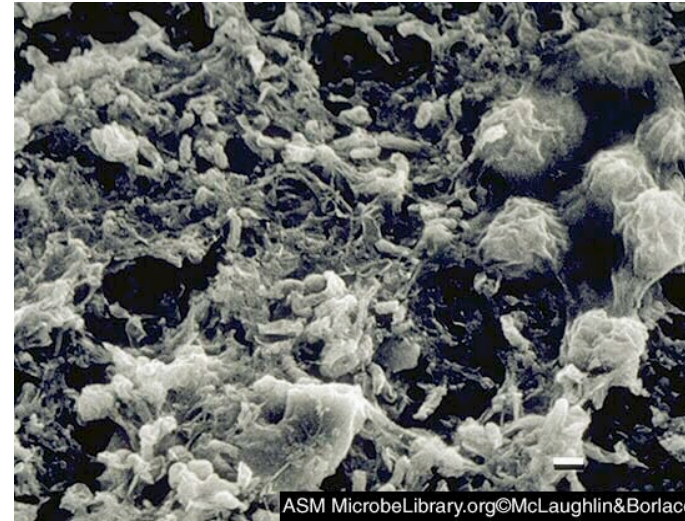
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Tree of life – Leonard Eisenberg

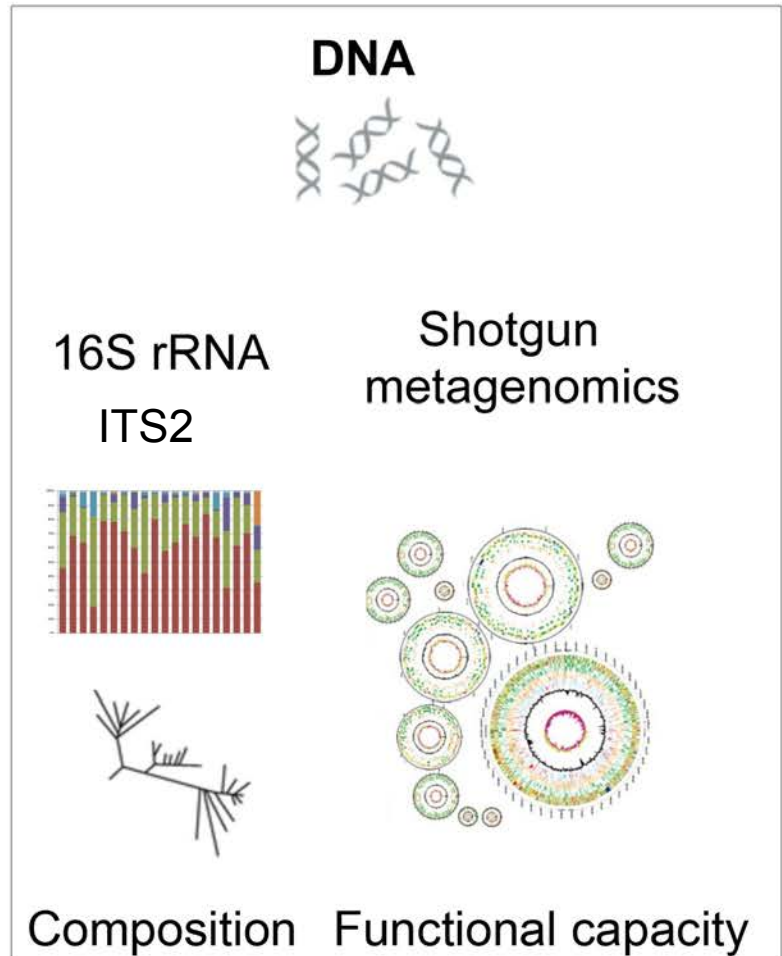
Culture-based Approaches do not Reflect the True Diversity or Physiology of Microorganisms



≠



Enabling Tools to Interrogate Microbial Dark Matter

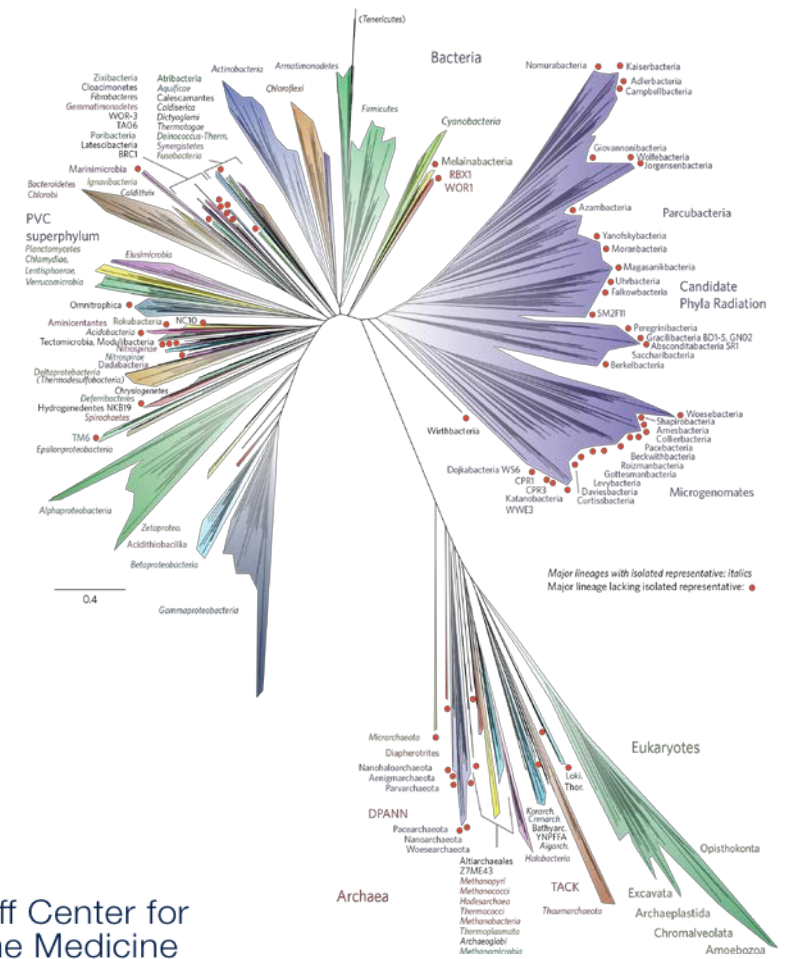


Next-generation sequencing platforms

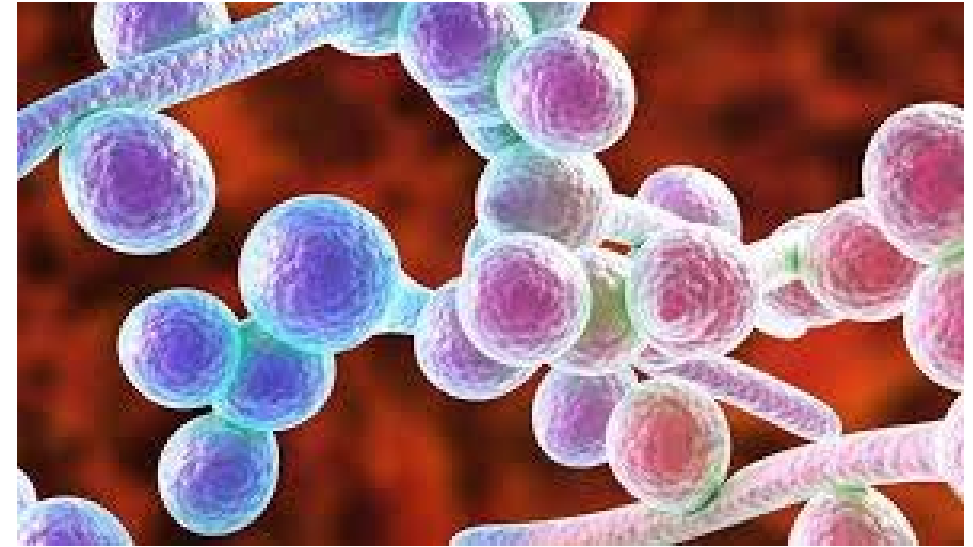
A new view of the tree of life

Laura A. Hug^{1†}, Brett J. Baker², Karthik Anantharaman¹, Christopher T. Brown³, Alexander J. Probst¹, Cindy J. Castelle¹, Cristina N. Butterfield¹, Alex W. Hermsdorf³, Yuki Amano⁴, Kotaro Ise⁴, Yohey Suzuki⁵, Natasha Dudek⁶, David A. Relman^{7,8}, Kari M. Finstad⁹, Ronald Amundson⁹, Brian C. Thomas¹ and Jillian F. Banfield^{1,9*}

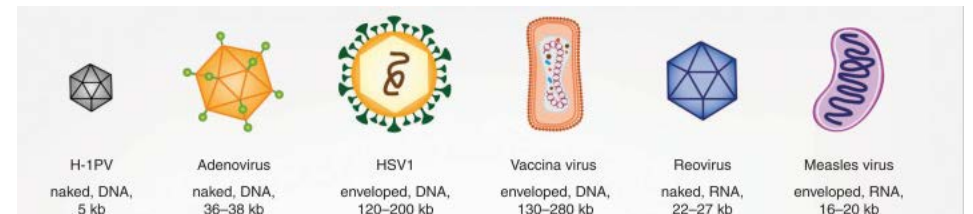
LETTERS NATURE MICROBIOLOGY DOI: 10.1038/NMICROBIOL.2016.48









Fungi



Viruses



A human gut bacterial genome and culture collection for improved metagenomic analyses

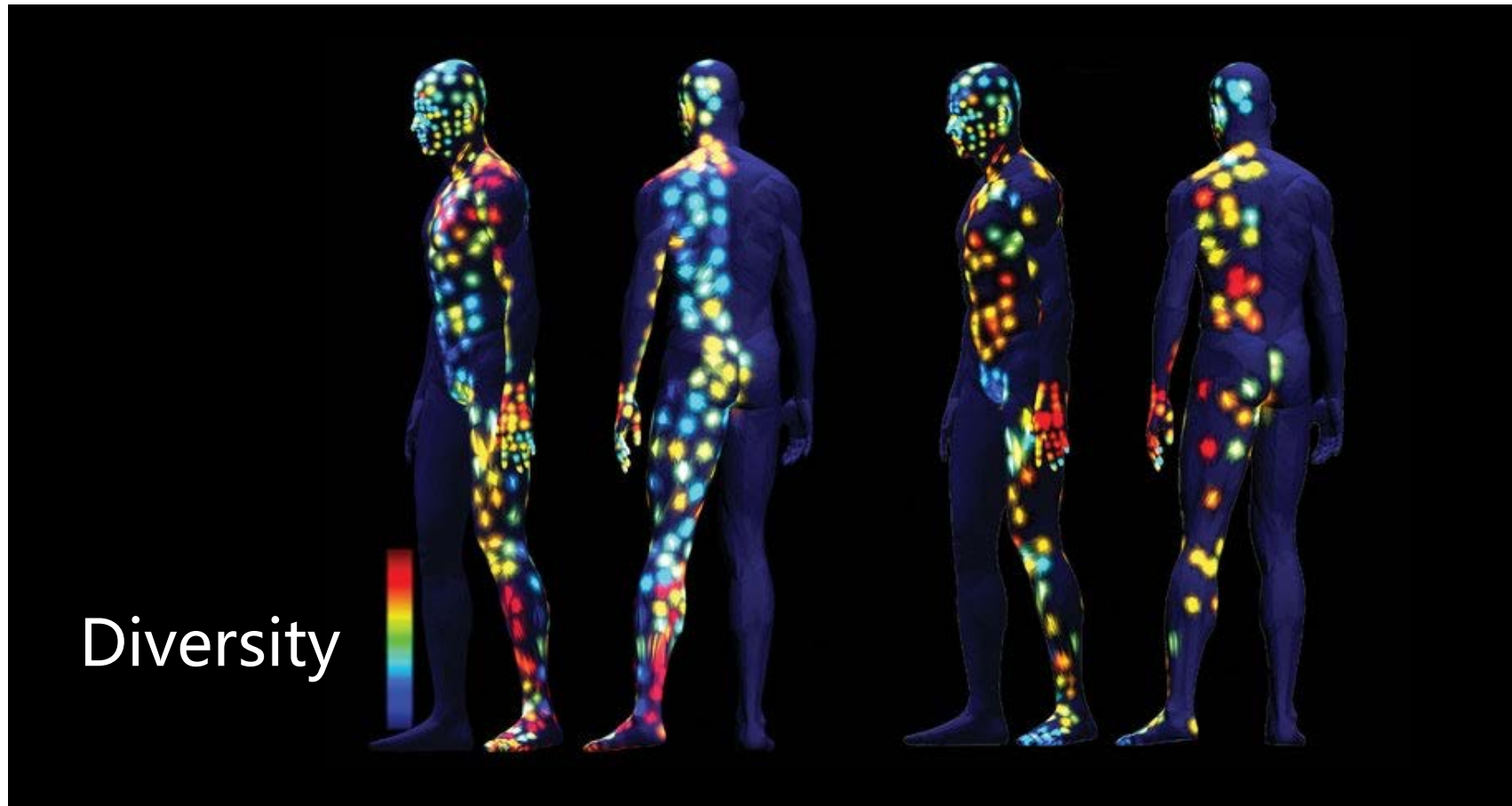
Samuel C. Forster ^{1,2,3,8*}, Nitin Kumar^{1,8}, Blessing O. Anonye ^{1,7}, Alexandre Almeida ^{4,5}, Elisa Viciani¹, Mark D. Stares¹, Matthew Dunn¹, Tapoka T. Mkandawire¹, Ana Zhu¹, Yan Shao ¹, Lindsay J. Pike¹, Thomas Louie⁶, Hilary P. Browne ¹, Alex L. Mitchell⁴, B. Anne Neville¹, Robert D. Finn ⁴ and Trevor D. Lawley^{1*}

- Human Gastrointestinal Bacteria Culture Collection (HBC)
- Set of 737 whole-genome-sequenced bacterial isolates
 - 273 species (105 novel species)
 - 31 families in the human gastrointestinal microbiota

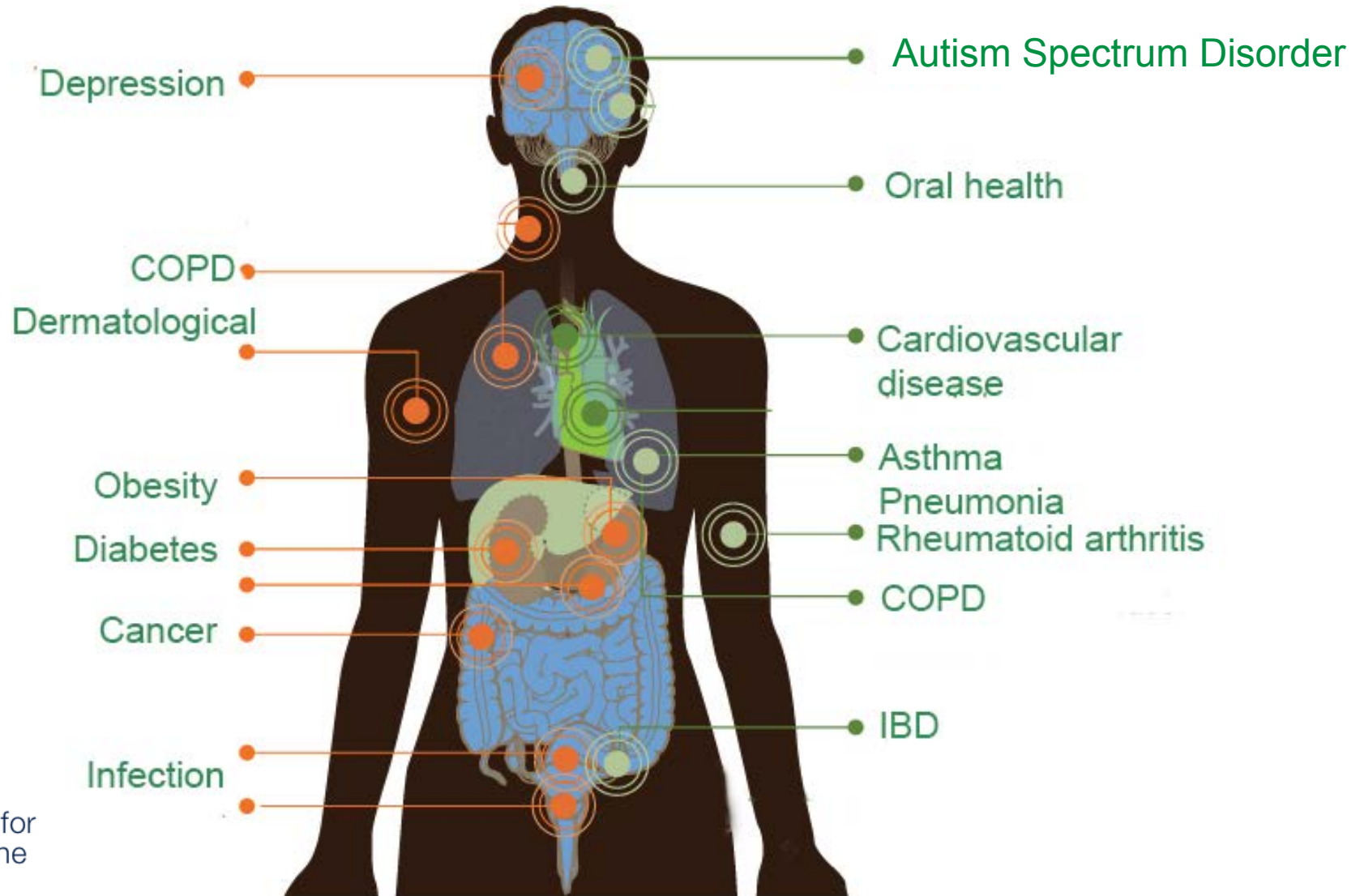
Humans are Superorganisms

Microbial

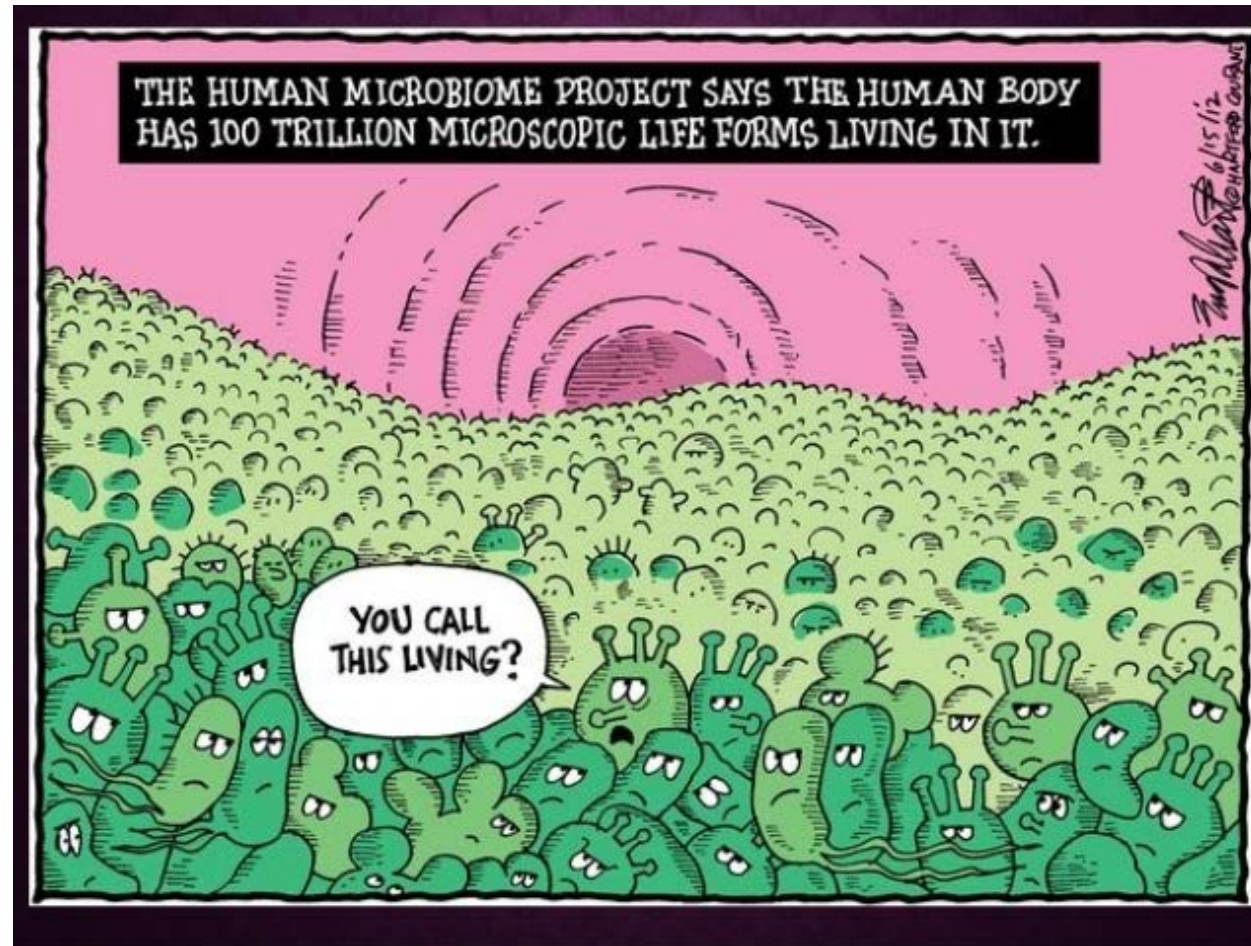
Biochemical



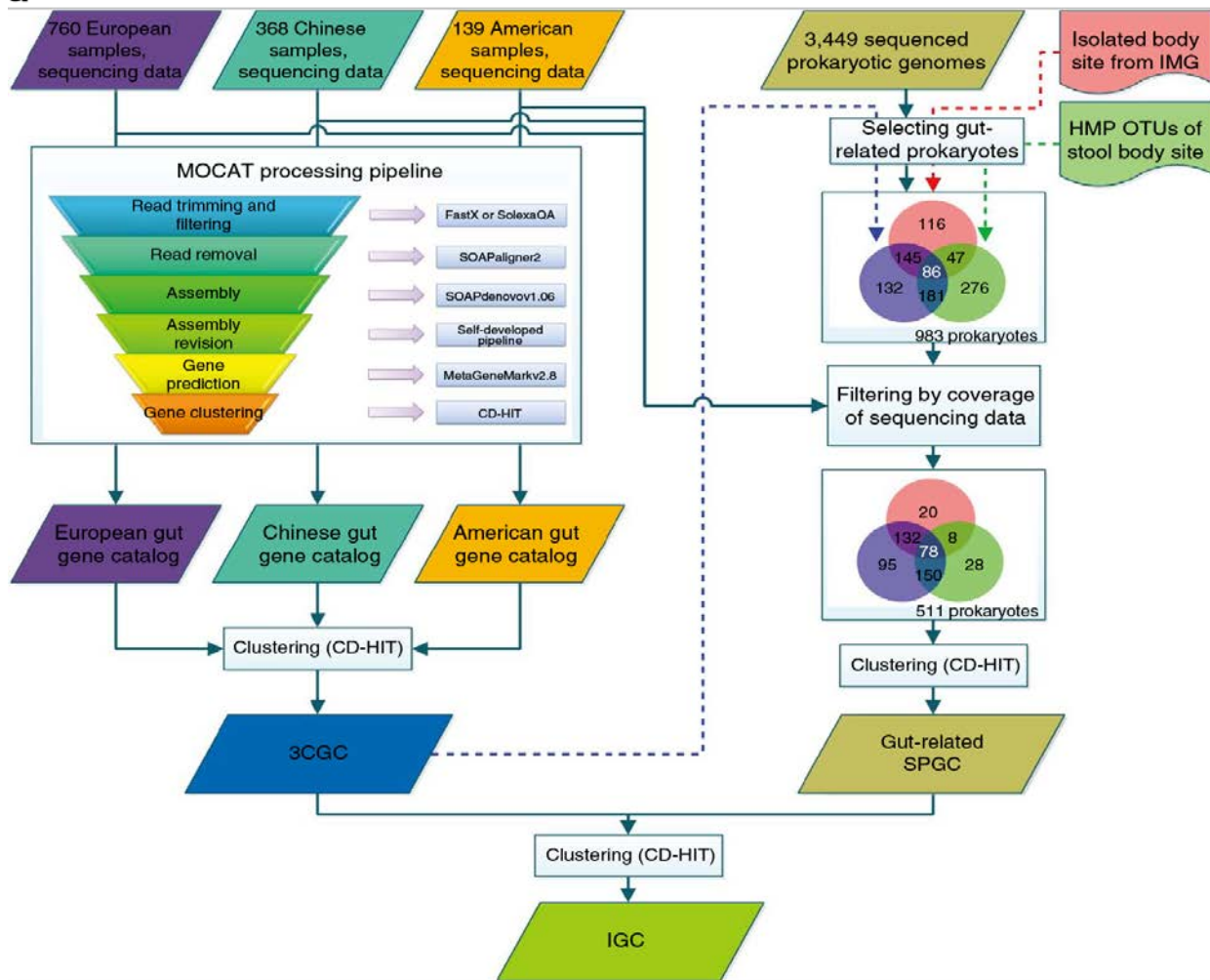
MICROBIOME PERTURBATION ASSOCIATES WITH DISEASE



The Gut Microbiome is Home to Several Trillion Microbes



Genetic Capacity of the Gut Microbiome Dwarfs that of the Human Host



nature
biotechnology

An integrated catalog of reference genes in the human gut microbiome

Junhua Li^{1-3,19}, Huijue Jia^{1,19}, Xianghang Cai^{1,19}, Huanzi Zhong^{1,19}, Qiang Feng^{1,4,19}, Shinichi Sunagawa⁵, Manimozhiyan Arumugam^{1,5,6}, Jens Roat Kultima⁵, Edi Prifti⁷, Trine Nielsen⁶, Agnieszka Sierakowska Juncker⁸, Chaysavanh Manichanh⁹, Bing Chen¹, Wenwei Zhang¹, Florence Levenez⁷, Juan Wang¹, Xun Xu¹, Liang Xiao¹, Suisha Liang¹, Dongya Zhang¹, Zhaoxi Zhang¹, Weineng Chen¹, Hailong Zhao¹, Jumana Yousuf Al-Aama^{10,11}, Sherif Edris^{11,12}, Huanming Yang^{1,11,13}, Jian Wang^{1,13}, Torben Hansen⁶, Henrik Bjørn Nielsen⁸, Søren Brunak⁸, Karsten Kristiansen⁴, Francisco Guarner⁹, Oluf Pedersen⁶, Joel Doré^{7,14}, S Dusko Ehrlich^{7,15}, MetaHIT Consortium¹⁶, Peer Bork^{5,17} & Jun Wang^{1,4,6,11,18}

9,879,896 genes
(n=1,267 adult participants)

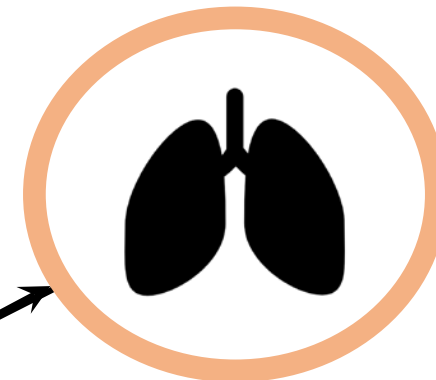
The Gut Microbiome Influences Remote Organ and Immune Responses

Neurological



Hsiao, E et al.
Cell 2015
Dae-Wook Kang et al
Microbiome. 2017

Respiratory



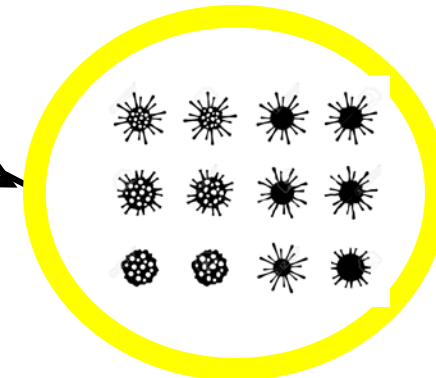
Arietta, C.E. et al, Sci.
Transl. Med 2015
Fujimura, K.E., et al,
Nature Medicine 2016

Cardiovascular

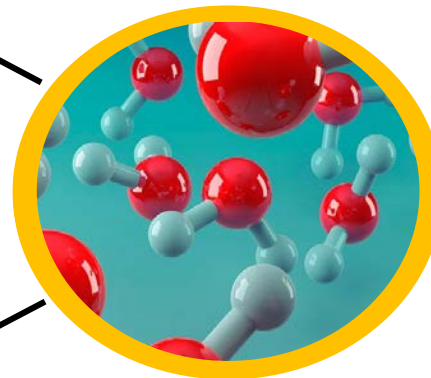


Koeth et al Nat.
Med. 19(5):576. 2013
Tang et al NEJM
2013
Wang et al Nature
2011

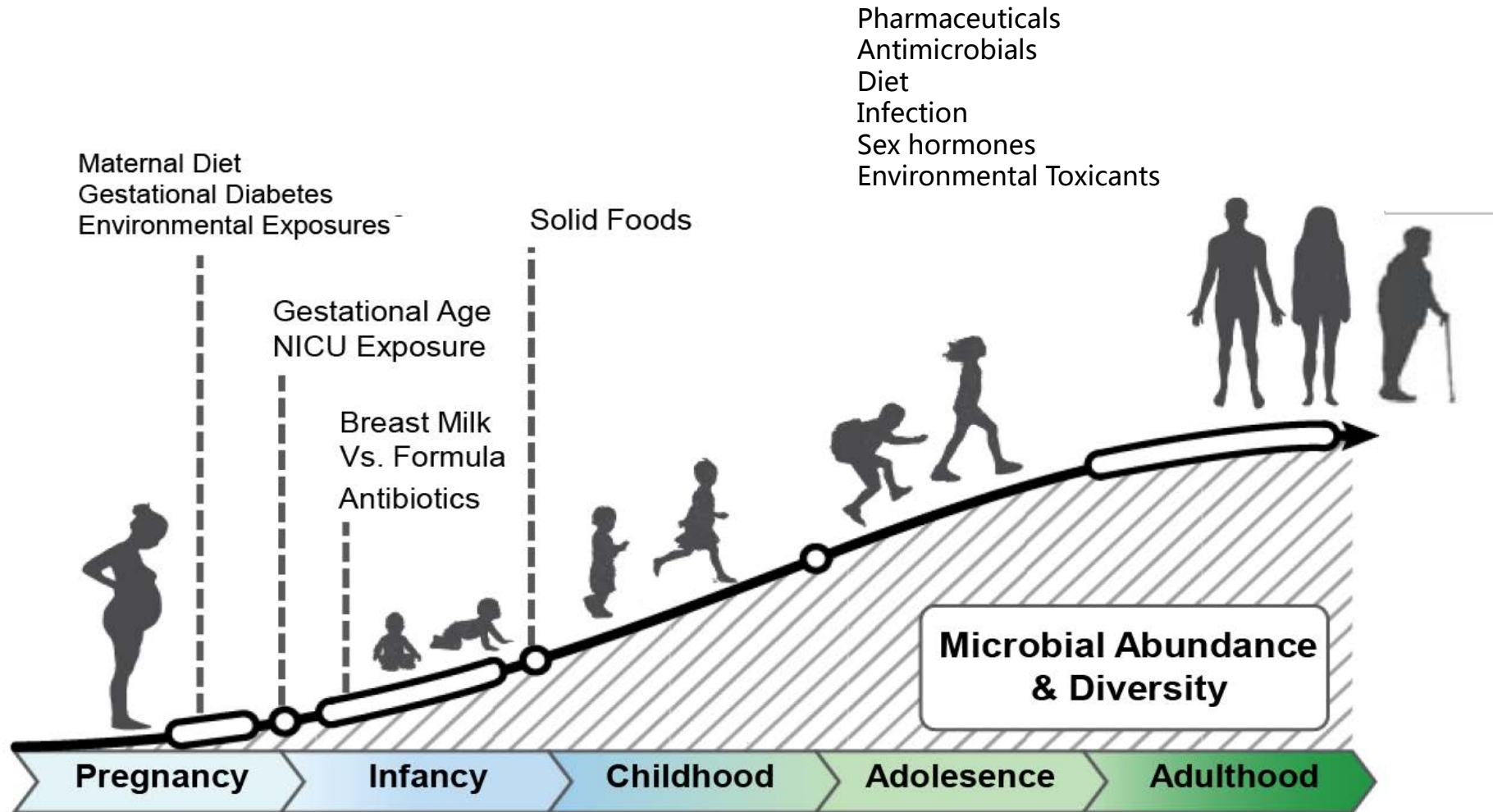
Immunity



Trompette et al
Nature Medicine,
2014
Fonseca et al,
Mucosal
Immunity 2017



The Gut Microbiome Evolves Over Human Lifespan

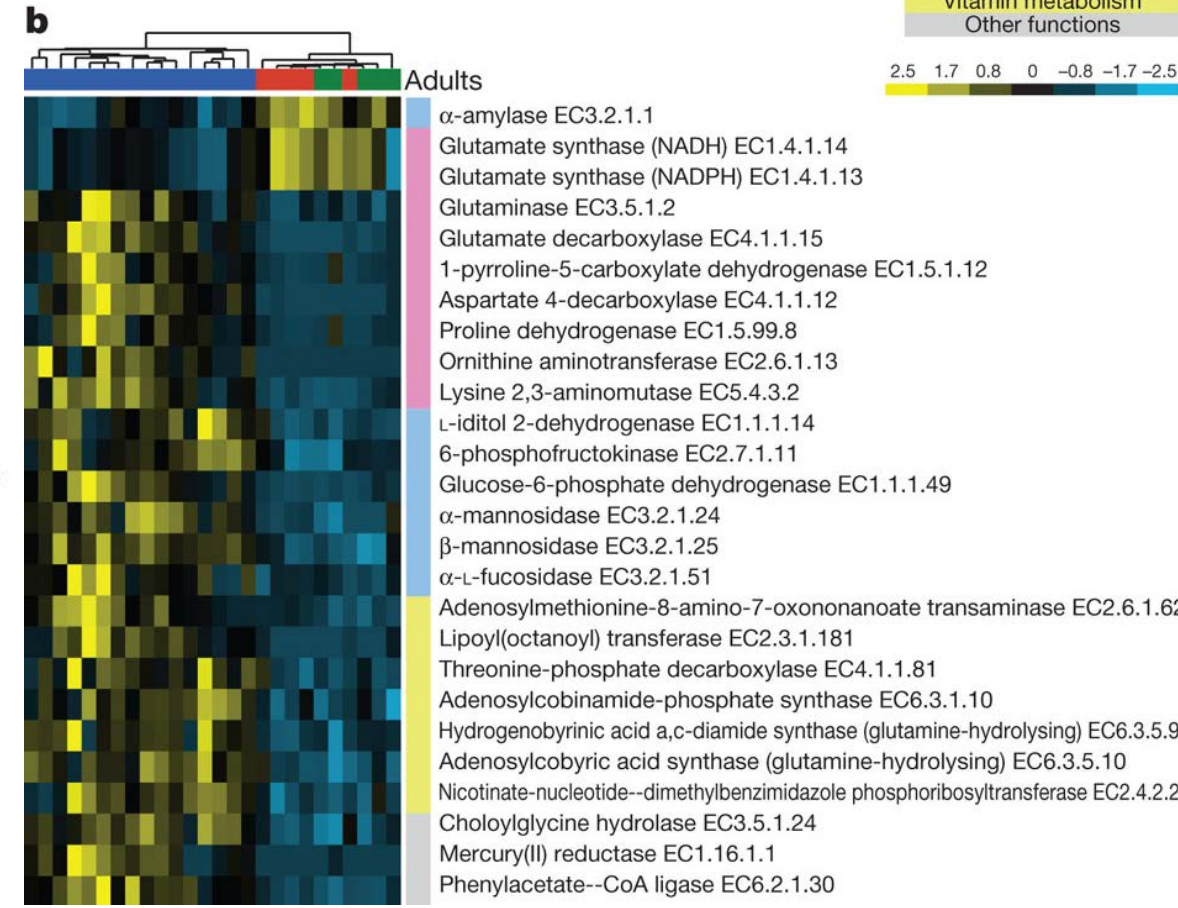
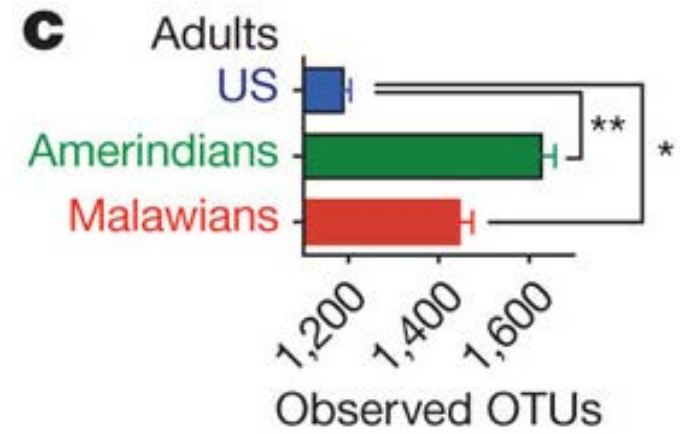
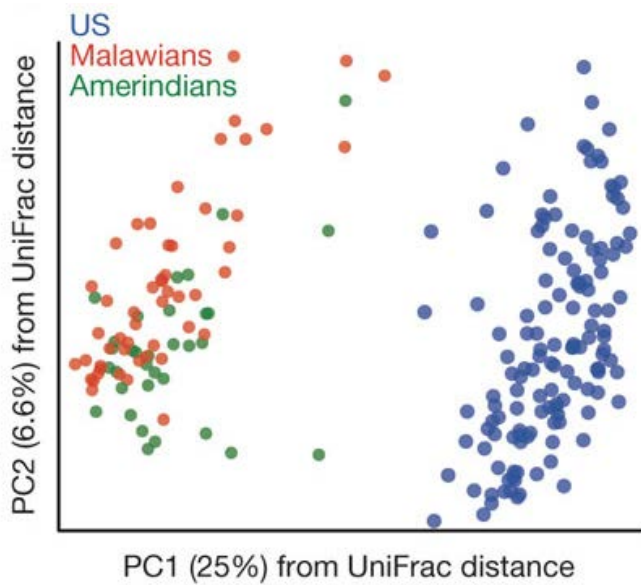


Human gut microbiome viewed across age and geography

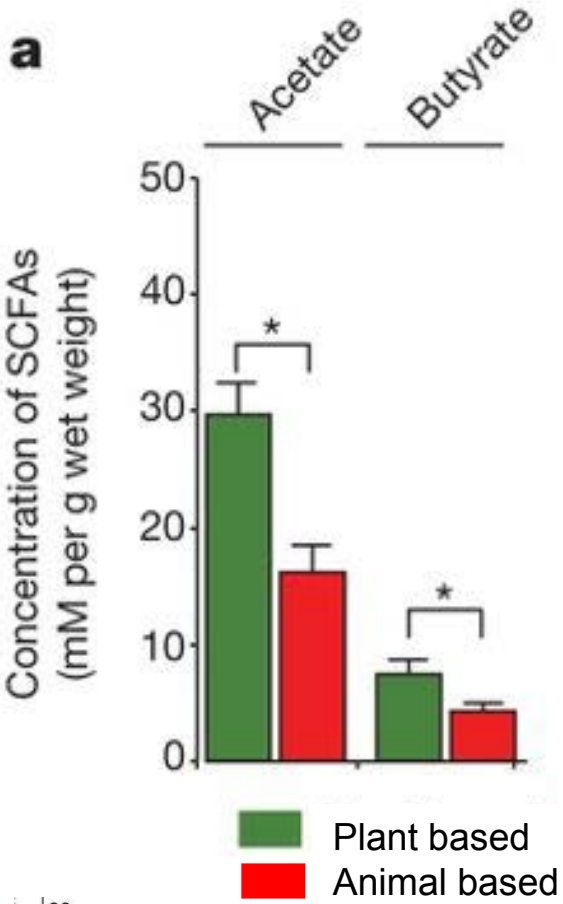
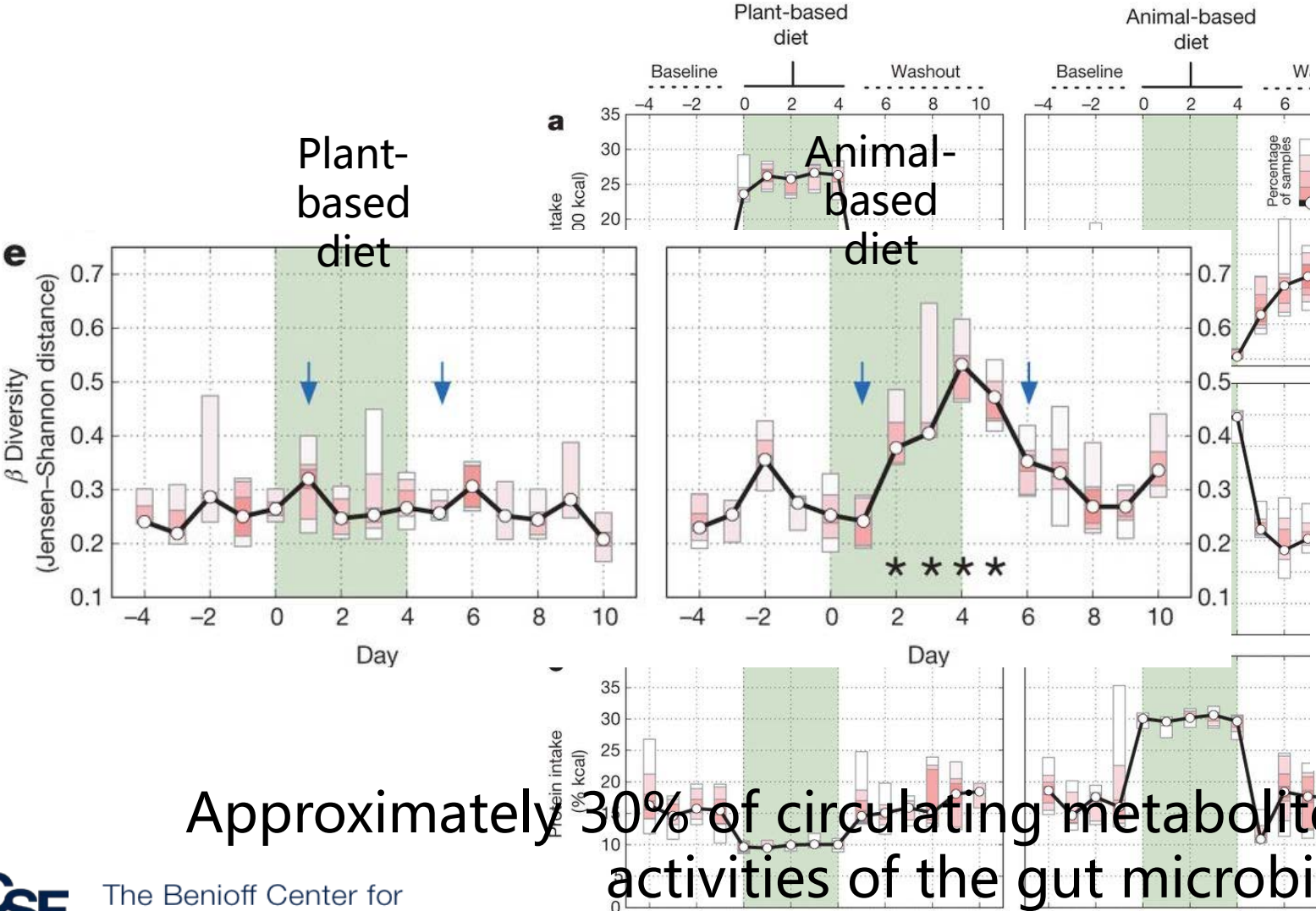
Tanya Yatsunenکو¹, Federico E. Rey¹, Mark J. Manary^{2,3}, Indi Trehan^{2,4}, Maria Gloria Dominguez-Bello⁵, Monica Contreras⁶, Magda Magris⁷, Glida Hidalgo⁷, Robert N. Baldassano⁸, Andrey P. Anokhin⁹, Andrew C. Heath⁹, Barbara Warner², Jens Reeder¹⁰, Justin Kuczynski¹⁰, J. Gregory Caporaso¹¹, Catherine A. Lozupone¹⁰, Christian Lauber¹⁰, Jose Carlos Clemente¹⁰, Dan Knights¹⁰, Rob Knight^{10,12} & Jeffrey I. Gordon¹

US
Malawians
Amerindians

Amino acid metabolism
Carbohydrate metabolism
Vitamin metabolism
Other functions



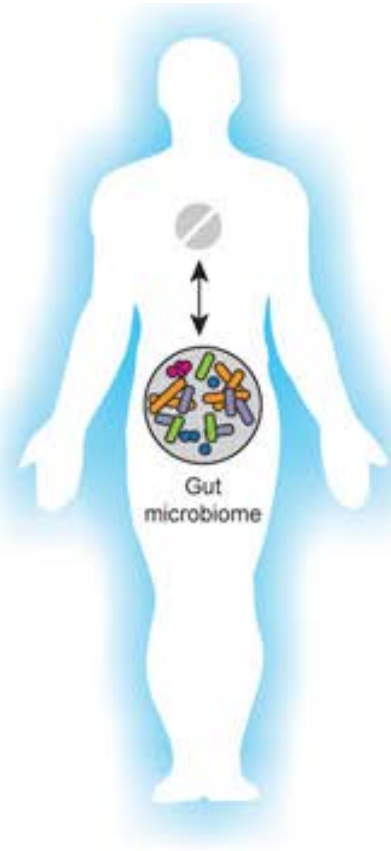
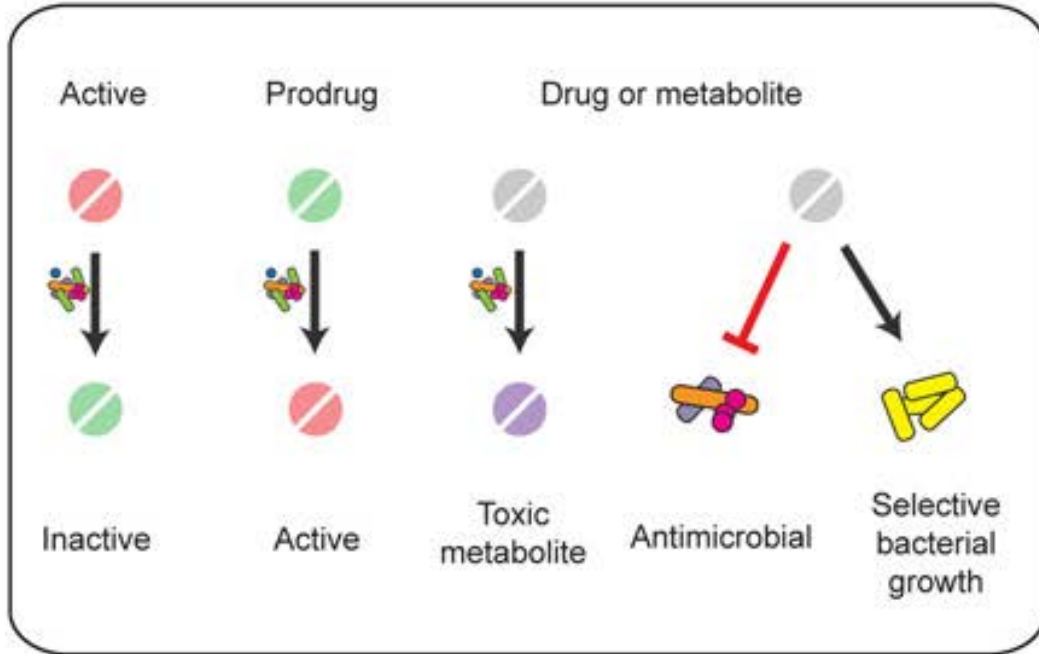
Diet Rapidly and Reproducibly Alters the Gut Microbiome



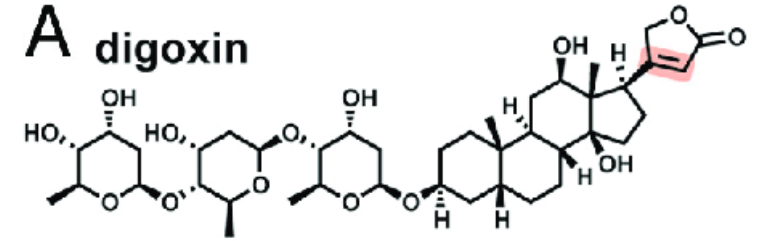
Approximately 30% of circulating metabolites are attributable to activities of the gut microbiome

The Gut Microbiome Influences Drug Metabolism

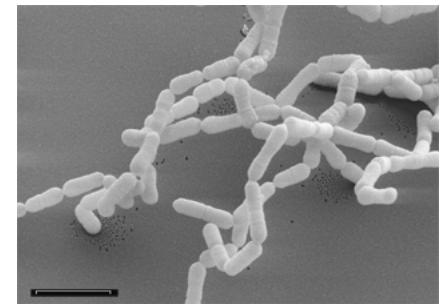
Direct mechanisms



A digoxin



B dihydrodigoxin

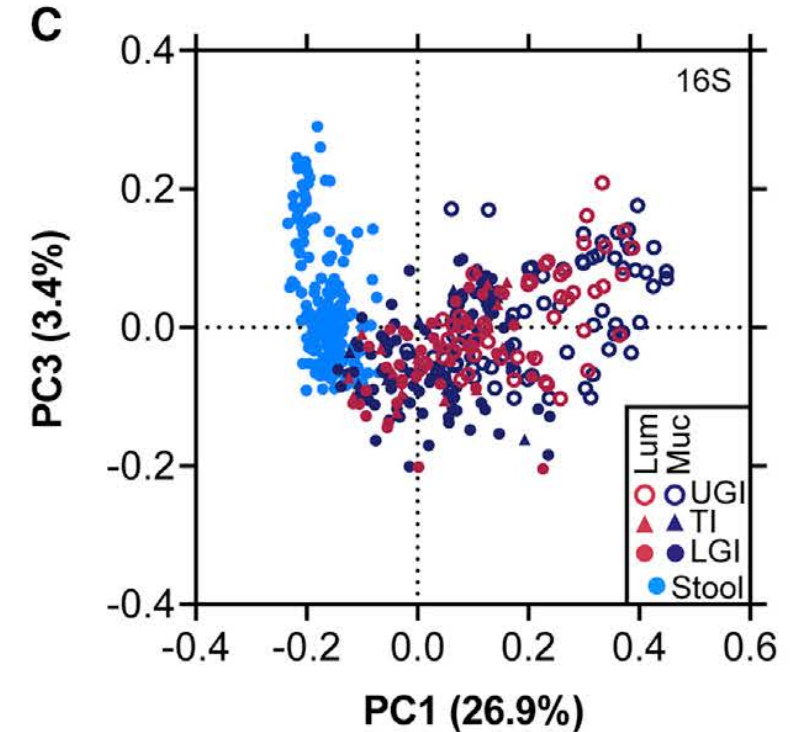
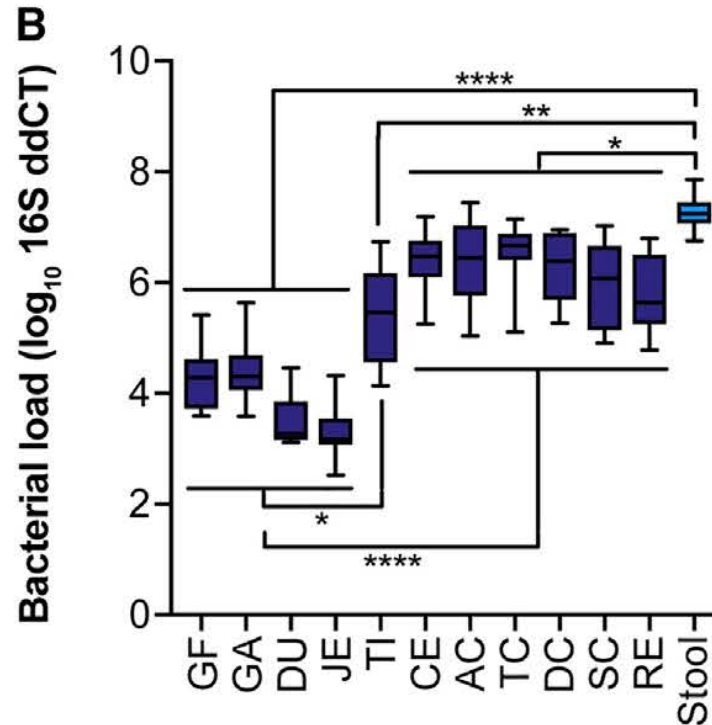
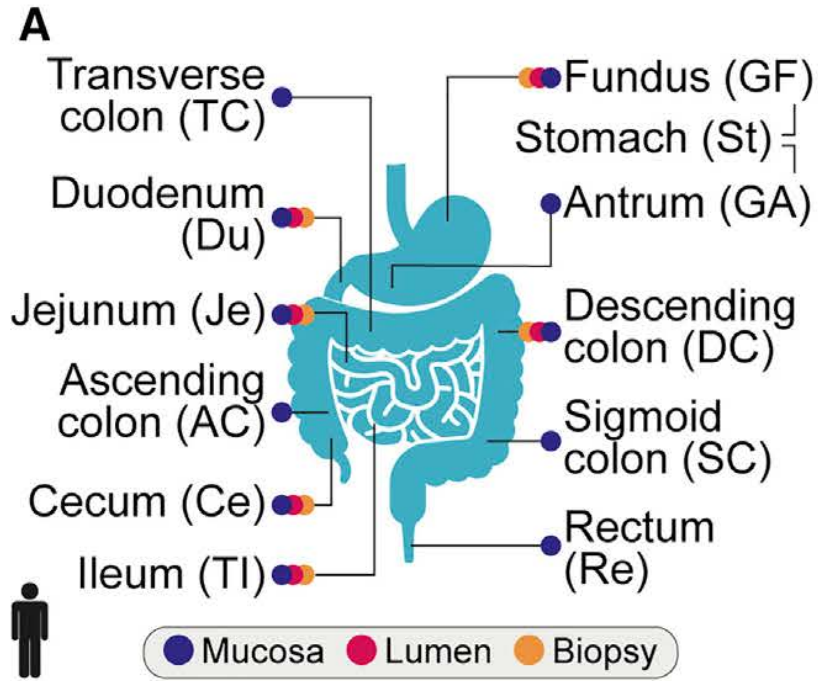


Eggertella lenta

Spanogiannopoulos, P et al Nat Rev Microbiol. 2016 14(5): 273–287.

Hasier, H. et al [Science](#). 2013 Jul 19; 341(6143): 295–298.

Niche-specific Microbiomes Exist Along the Length of the Gastrointestinal Tract



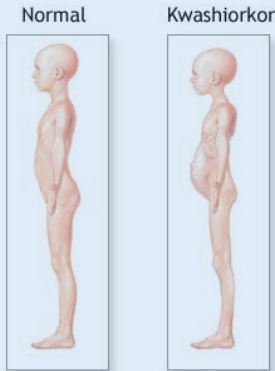
Zmora et al., 2018, Cell 174, 1388–1405
 September 6, 2018 © 2018 Elsevier Inc.
<https://doi.org/10.1016/j.cell.2018.08.041>

Human Microbiome – a Lever on Host Physiology.

OBESITY



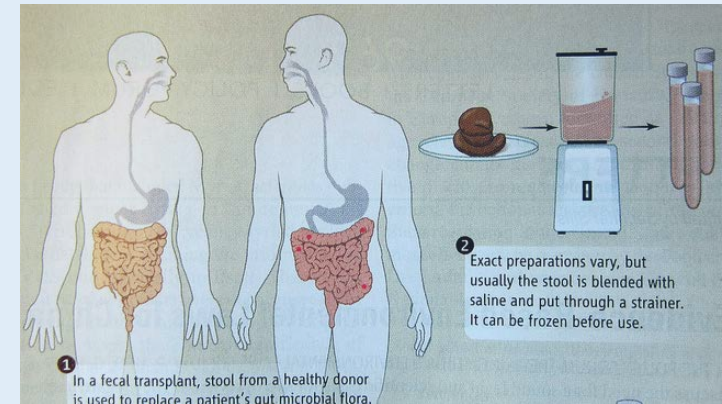
KWASHIKOR



AUTISM SPECTRUM
DISORDER

C. difficile
INFECTION

PEDIATRIC
AUTISM SPECTRUM
DISORDER



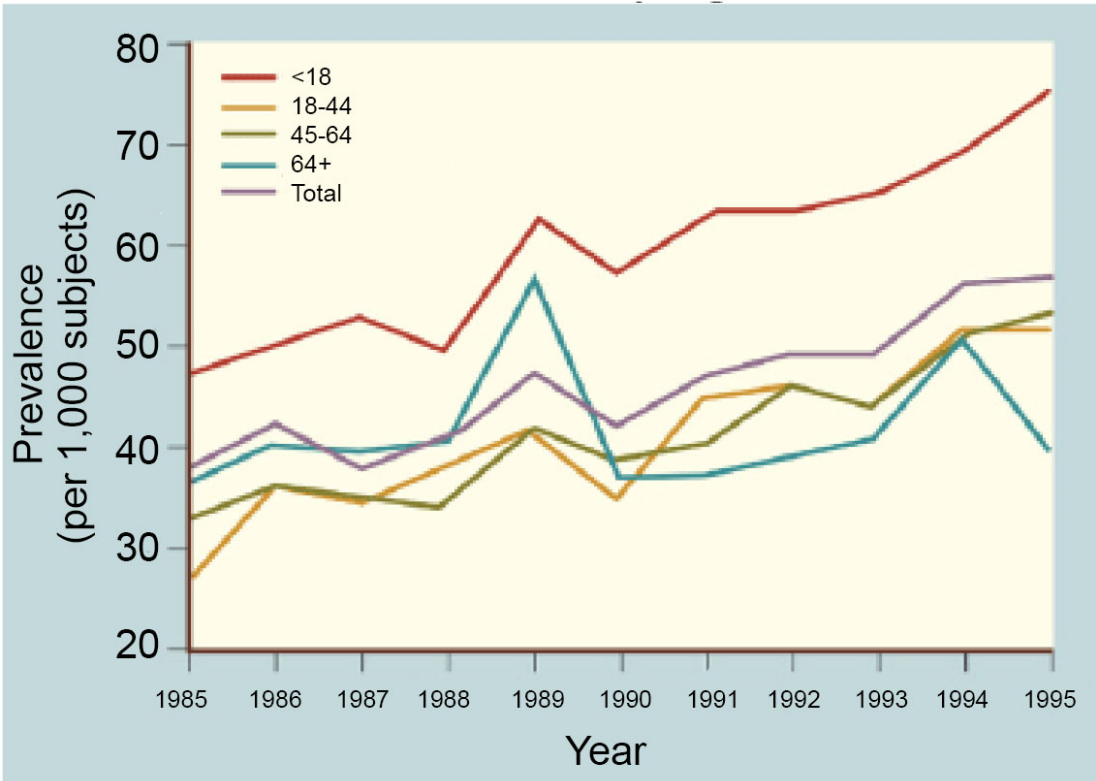
IBD

A Watershed Moment in Human Biology



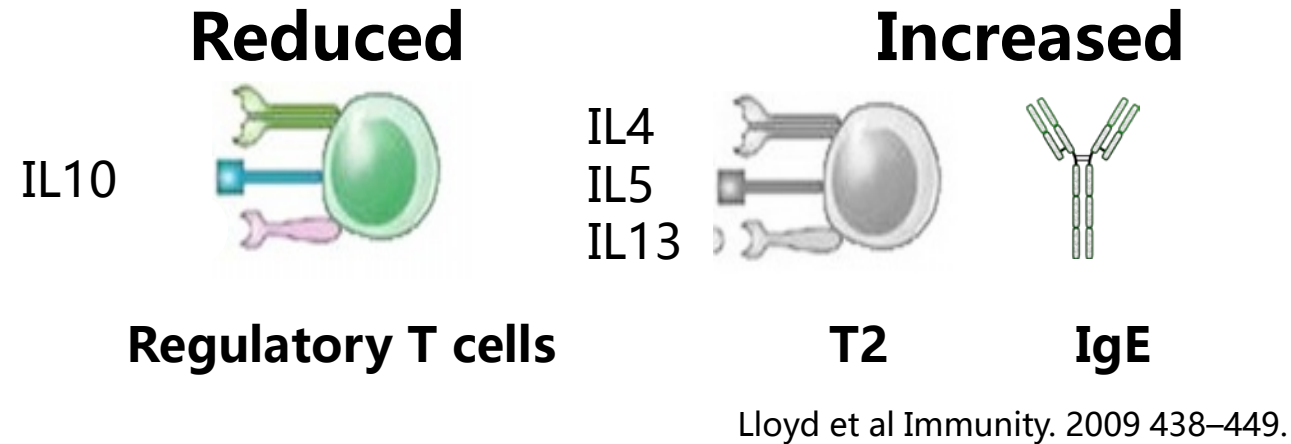
Asthma is Prevalent in Westernized Nations

ASTHMA AROUND THE WORLD



Global Initiative for Asthma

Allergic Asthma

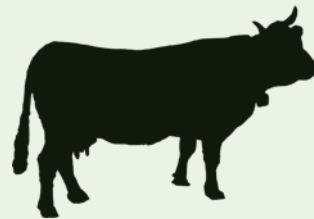


NO CURE > PREVENTION

INCREASED RISK FOR ALLERGY and ASTHMA

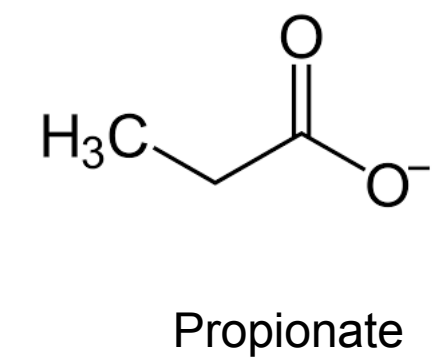
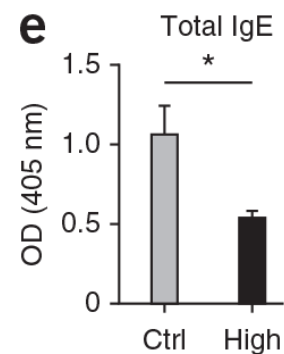
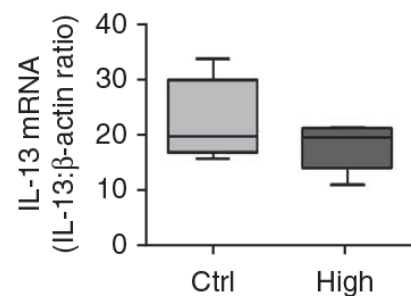
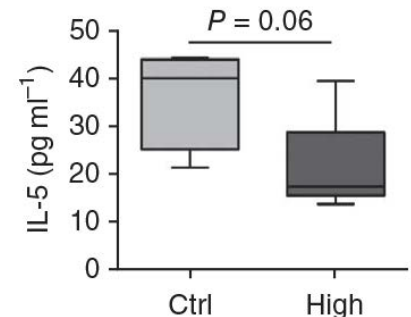
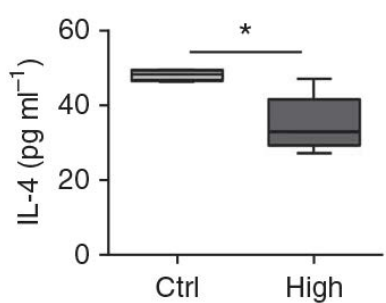
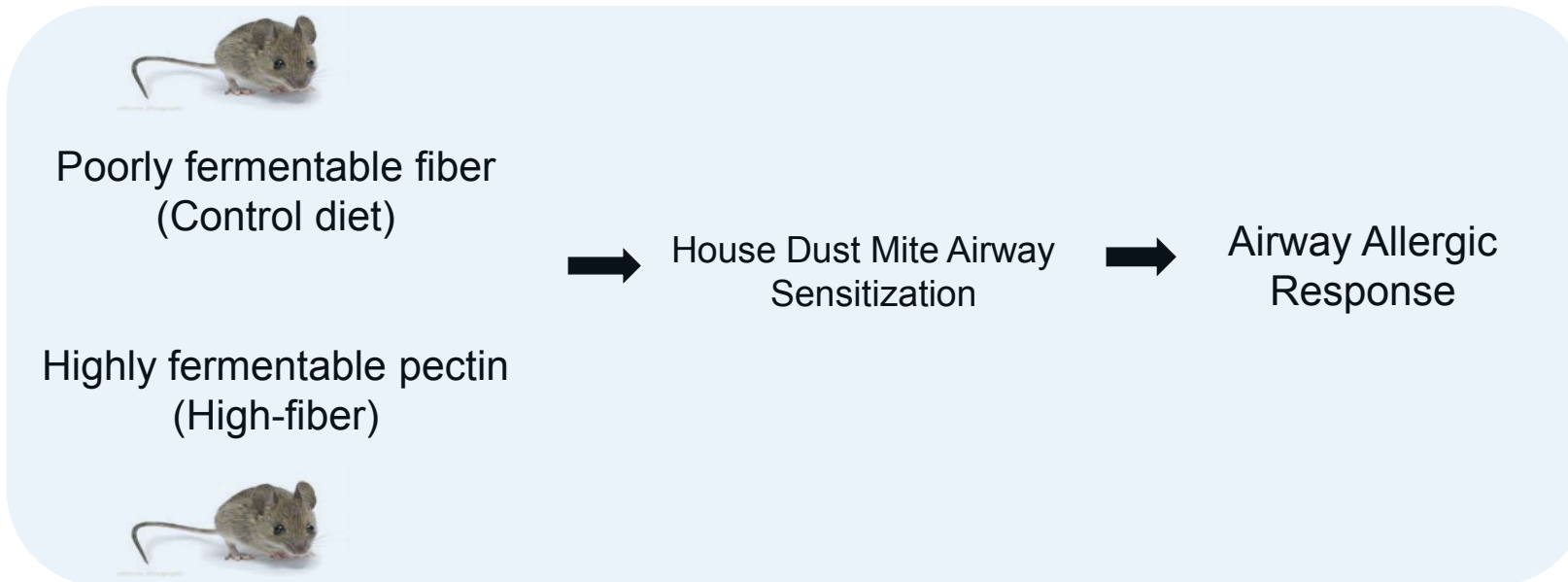


C-section

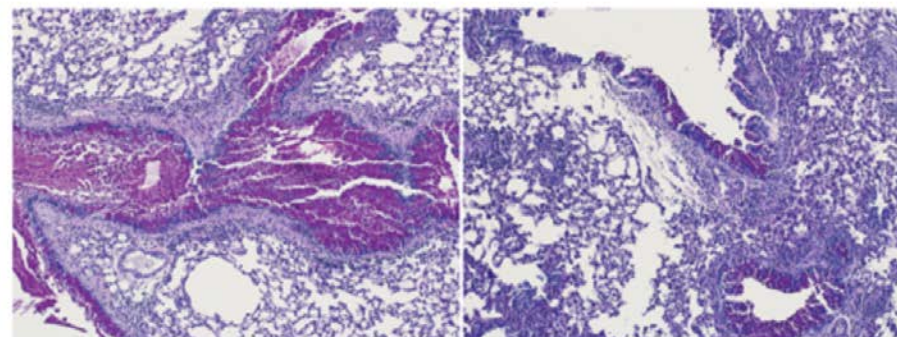
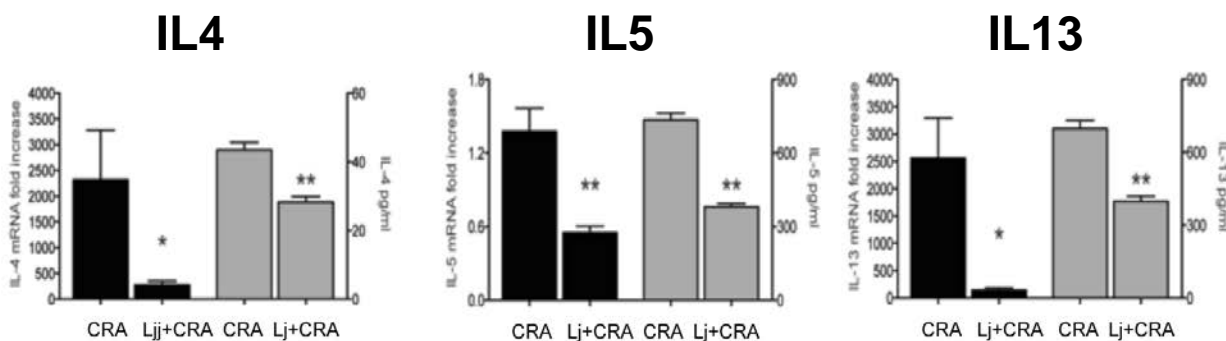
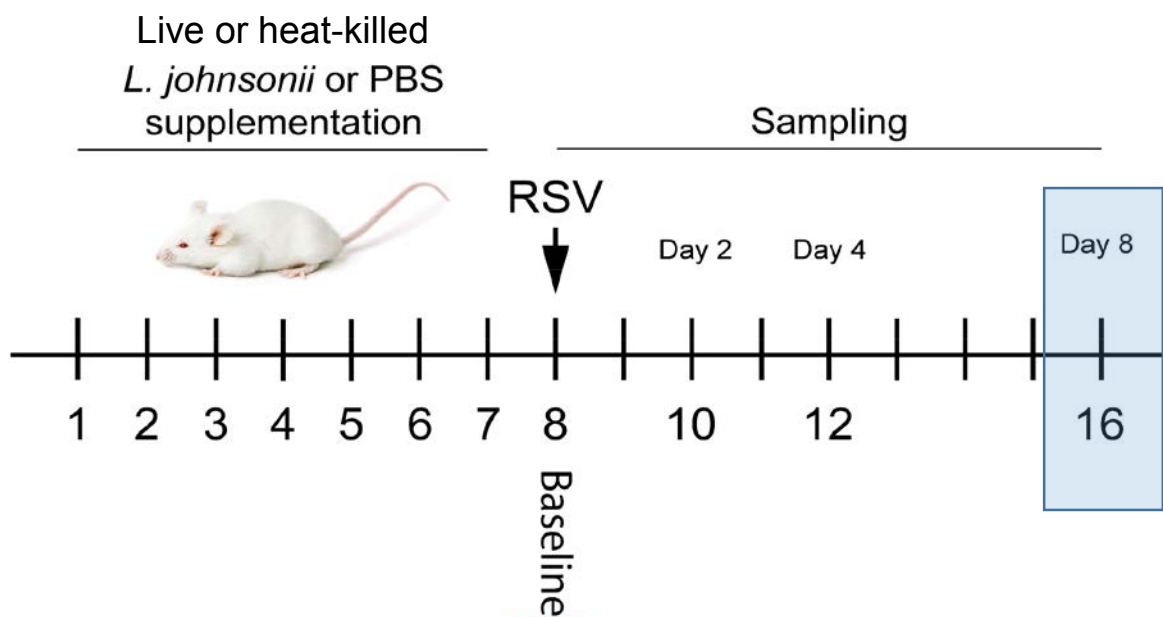


DECREASED RISK FOR ALLERGY and ASTHMA

Gut Microbial-derived Metabolites Influence Airway Immunity

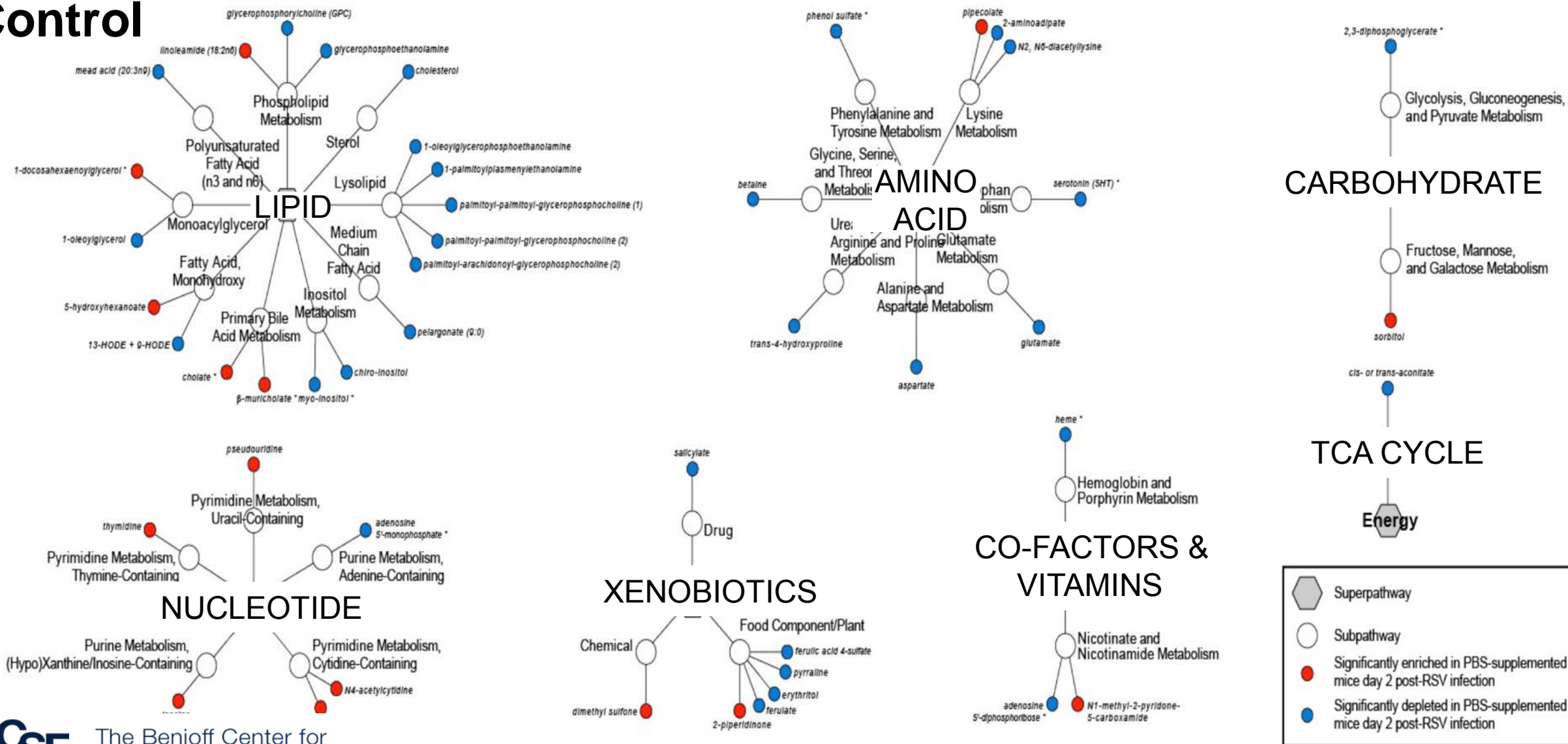


Gut Microbiome Manipulation Alters Airway Mucosal Response to Allergen Challenge or Viral Infection



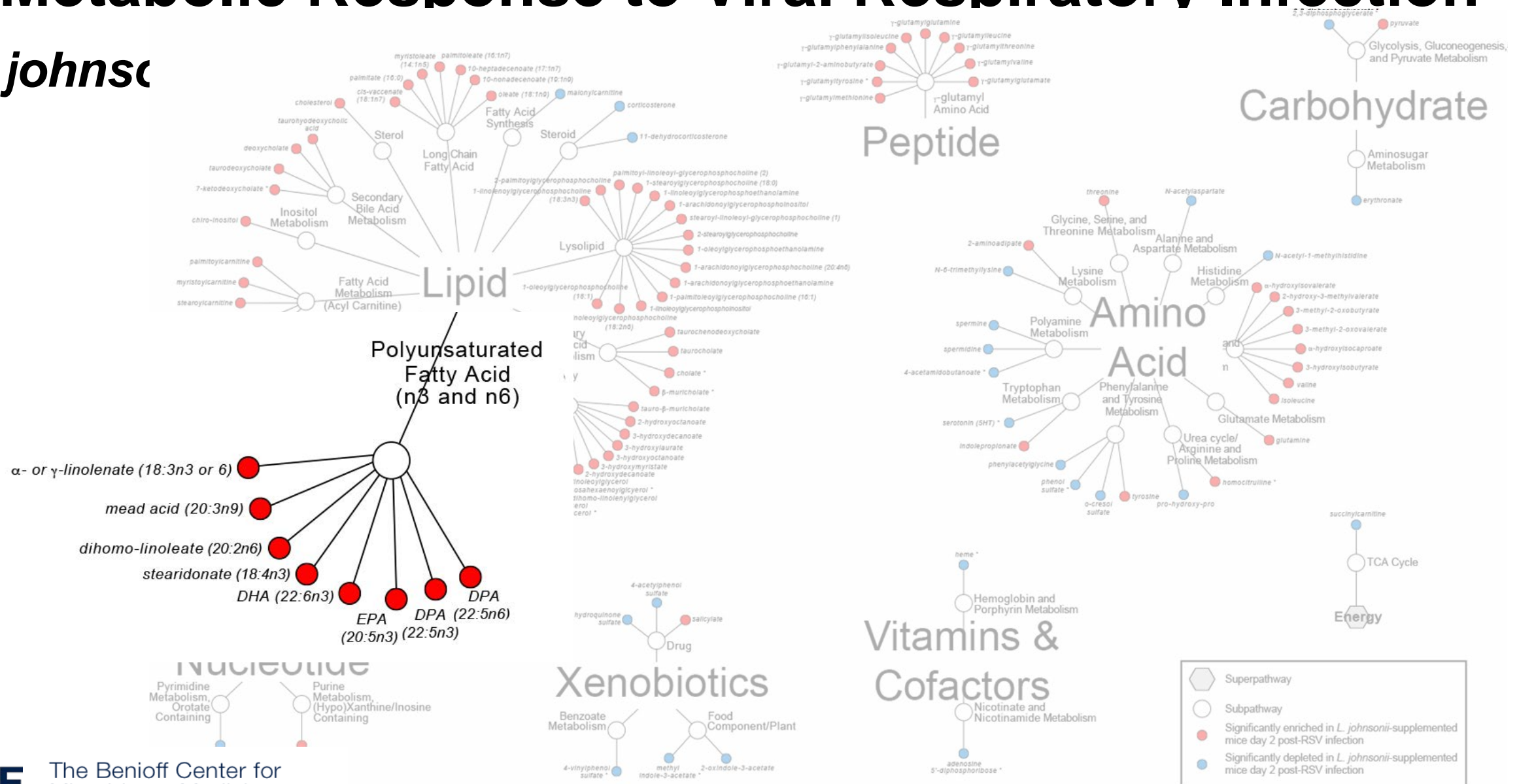
Gut Microbiome Manipulation Alters Serum Metabolic Response to Viral Respiratory Infection

Control

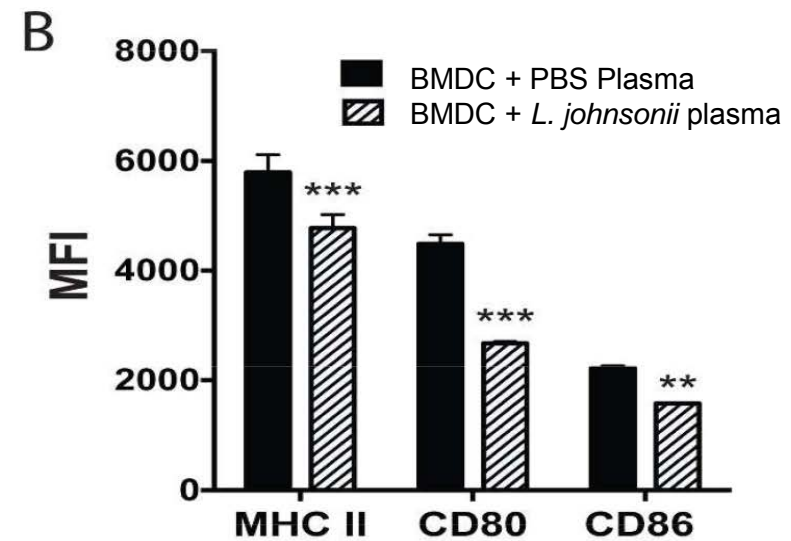
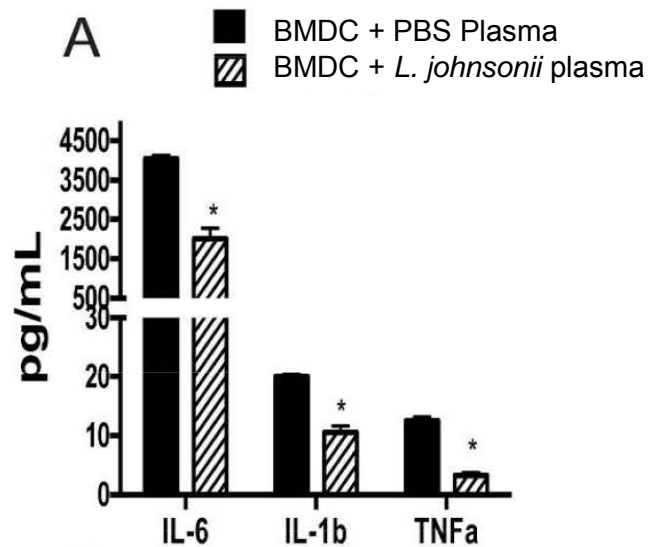


Gut Microbiome Manipulation Alters Peripheral Metabolic Response to Viral Respiratory Infection

L. johnsonii

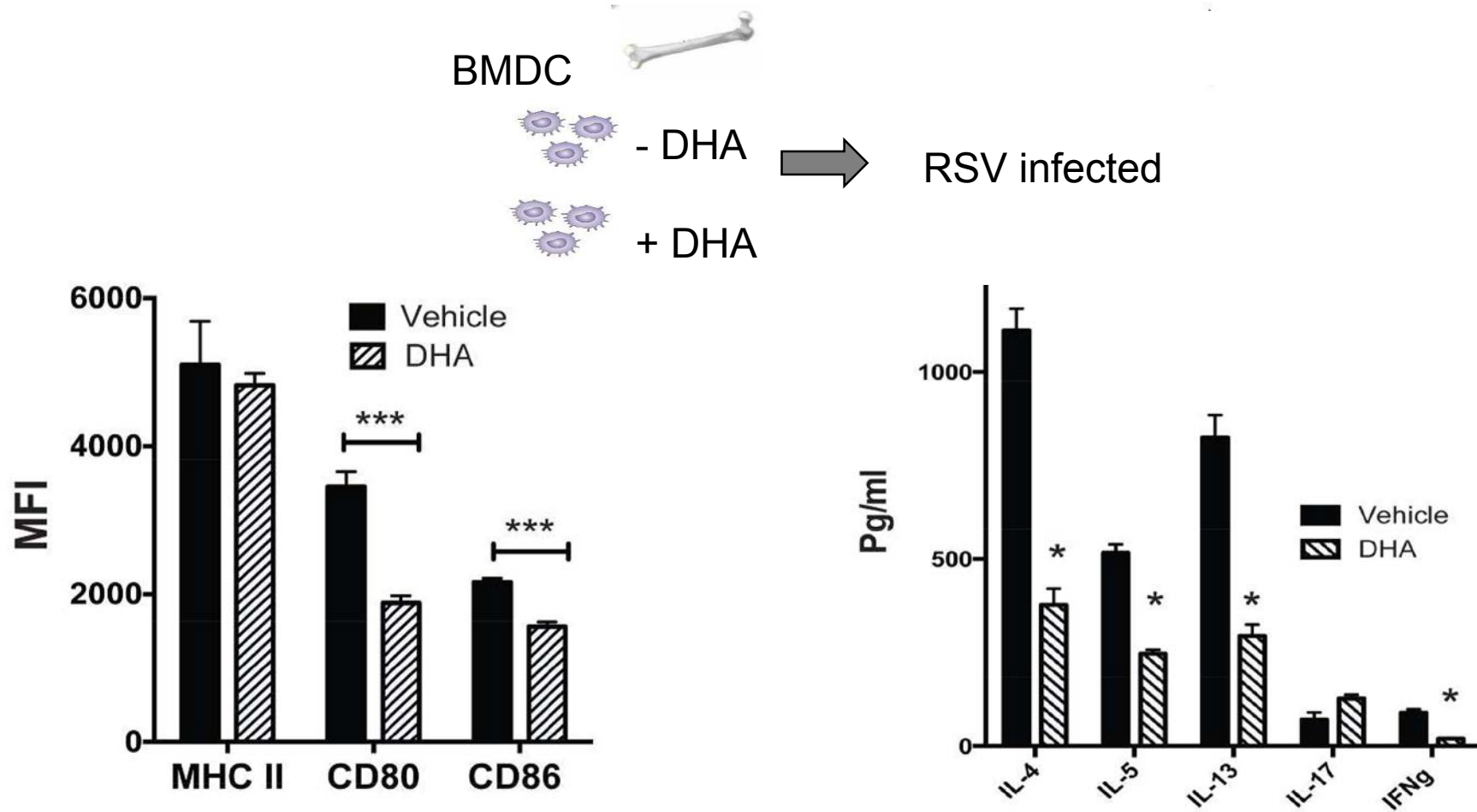


Gut Microbiome Influences Hematopoietic Cell Programming via Plasma-associated Mediators



BMDC: Bone marrow derived dendritic cells

Docosahexanoic Acid (DHA) inhibits RSV activation of BMDCs



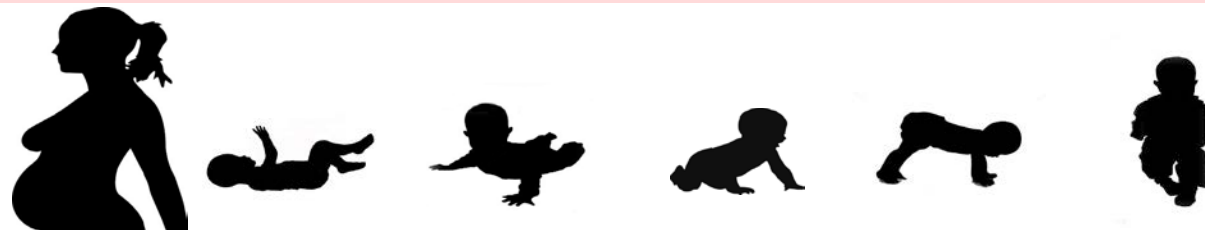
Circulating Products of the *L. johnsonii*-supplemented Gut Microbiome Down-regulate Pro-inflammatory Responses

Could Early-life Gut Microbiome Perturbation and Metabolic Dysfunction Relate to Childhood Atopy and Asthma?

INCREASED RISK FOR ALLERGY and ASTHMA

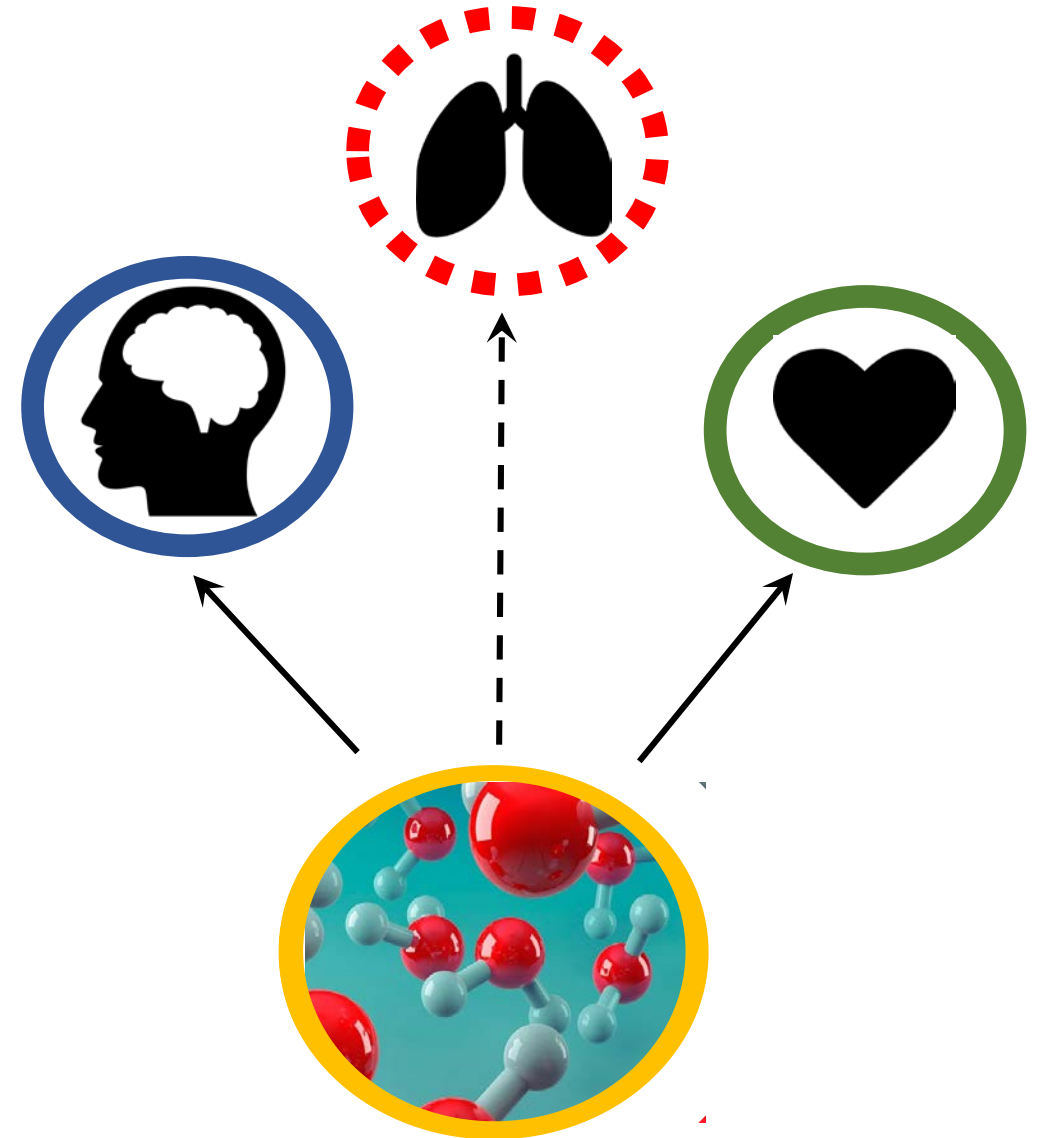
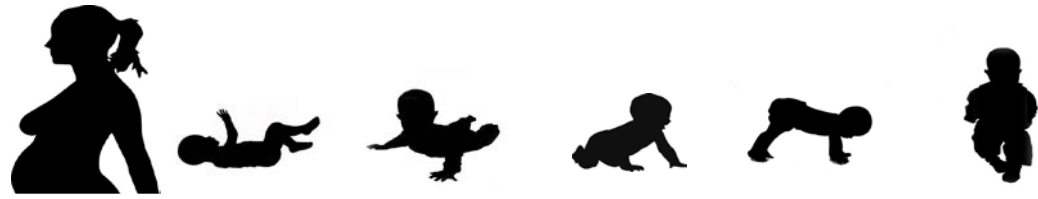


C-section



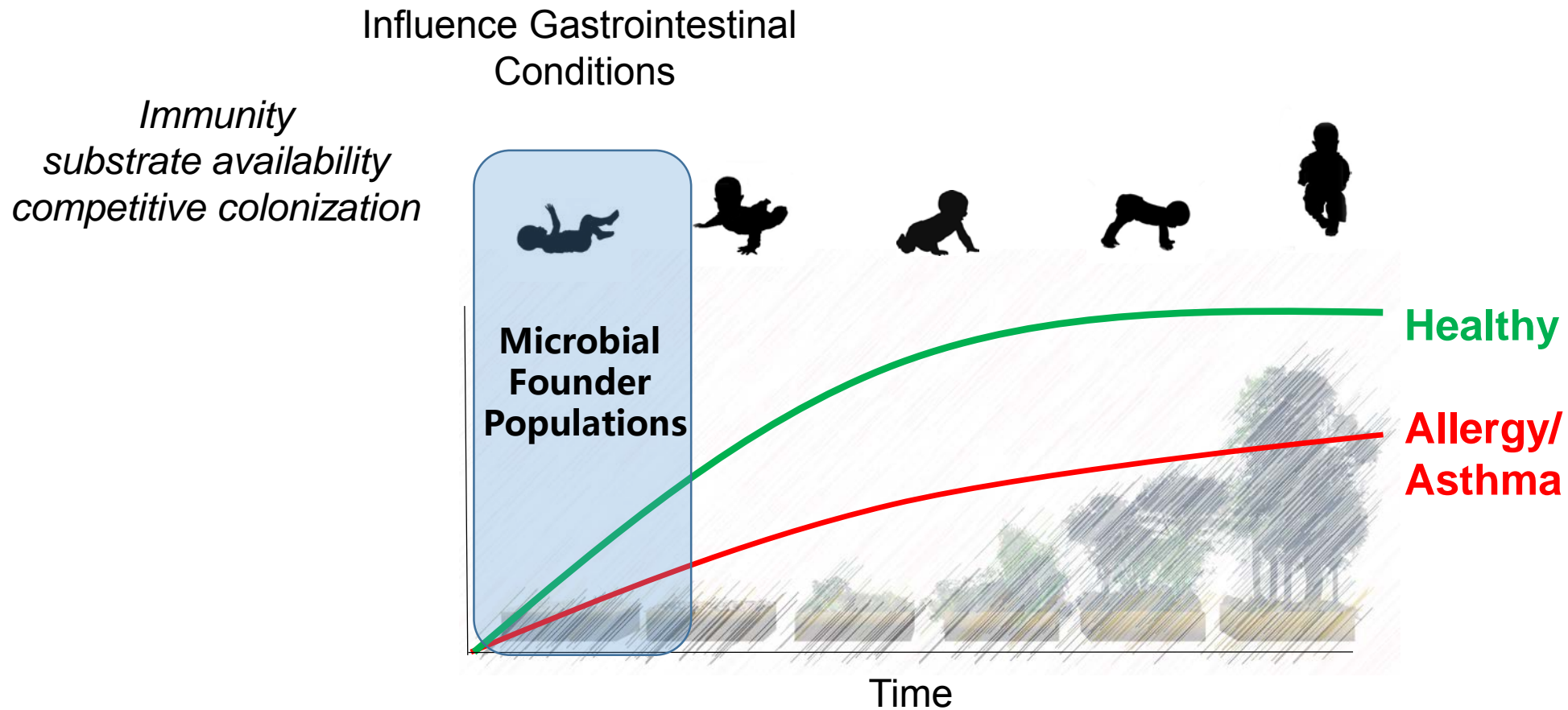
DECREASED RISK FOR ALLERGY and ASTHMA

How Could the Neonatal Gut Microbiome Influence Airway Disease Development in Childhood?

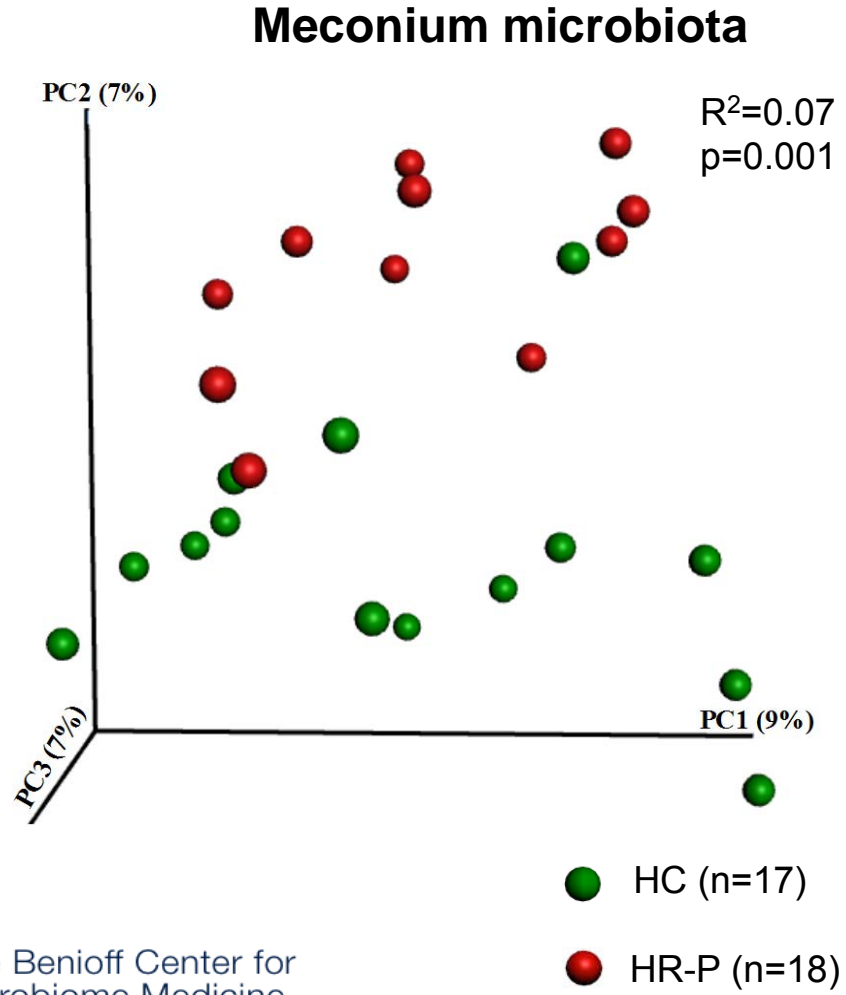


Hypothesis

Neonatal Gut Microbiome Predicts Childhood Allergy and Asthma and Offers Mechanistic Insights into the Origins of Disease



High-risk for Asthma Gut Microbiota is Distinct at Birth and Exhibits Delayed Development in Infancy



Wayne County Health, Environment, Allergy & Asthma Longitudinal Study (WHEALS)

Birth cohort



Neonates (1 month old)

N=130

Allergy at 2 years

Asthma at 4 years

16S rRNA (Bacteria) and ITS2 (Fungi) biomarker gene sequencing

Distinct Neonatal Gut Microbiota Exist and Relate to Risk of Childhood Atopy and Asthma

1 month

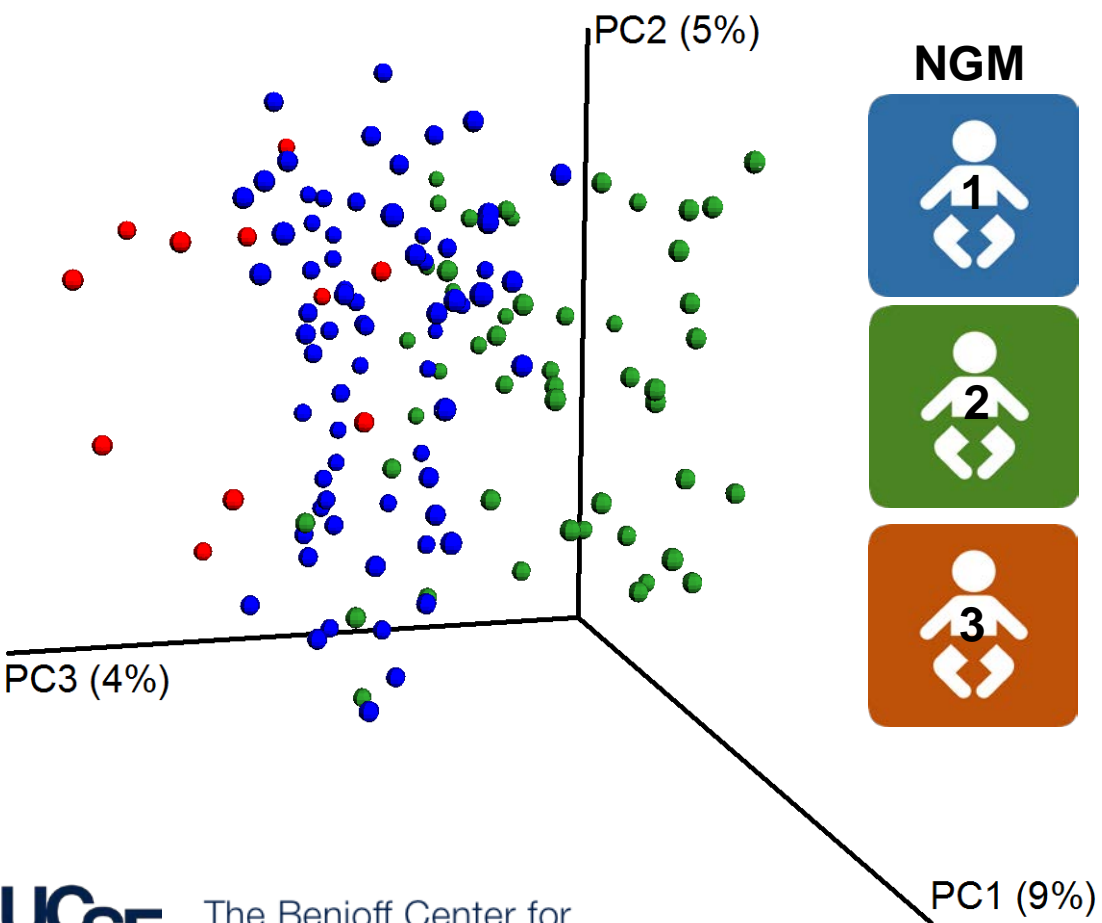


2 years
4 years



Neonatal Gut Microbiota State is Associated with Risk of Childhood Atopy and Asthma

$R^2=0.09$, $p<0.001$



	vs	vs	vs
Atopy (age 2 years)	1.43 (0.73-2.81) P=0.3	2.95 (1.42-6.09) P=0.004	2.06 (1.01-4.19) P=0.048
Asthma (age 4 years)	0.87 (0.31-2.50) P=0.87	2.95 (1.09-7.98) P=0.033	3.36 (1.10-10.3) P=0.034

NGM3

Inter-kingdom perturbation

- Depleted commensal bacteria
- Increased allergenic fungi

Metabolic dysfunction

- Reduced PUFA
- Increased 12,13 DiHOME

NGM1



NGM2



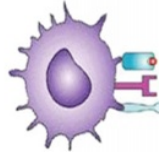
**TOLEROGENIC
GUT
MICROBIOME**

NGM3

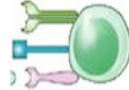


**PRO-ALLERGIC
GUT
MICROBIOME**

Human Immune Cell Assay to Assess Neonatal Gut Microbiome Immunostimulatory Capacity



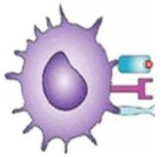
+



Healthy Adult Donors

Dendritic Cells

Naïve T-cells



+



Filter sterilized
NGM1 or NGM3
fecal water

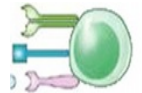
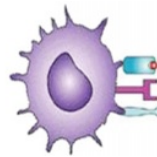
Dendritic Cell

2 day incubation



Wash

5 day co-culture



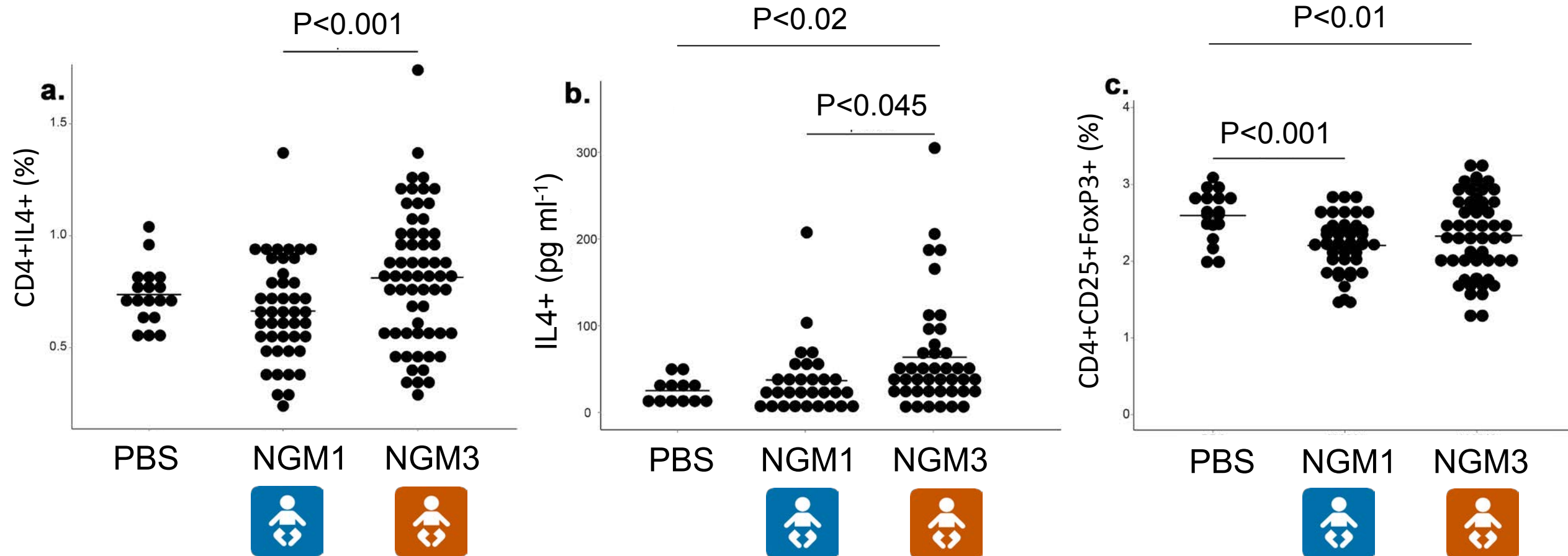
DC

Naïve
T-cell

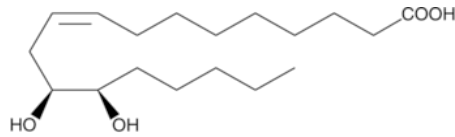
CD4+ (T-cell) phenotype:

- Th1: IFN- γ
- **Th2: IL-4**
- Th17: IL-17
- **Treg: CD25, Foxp3**

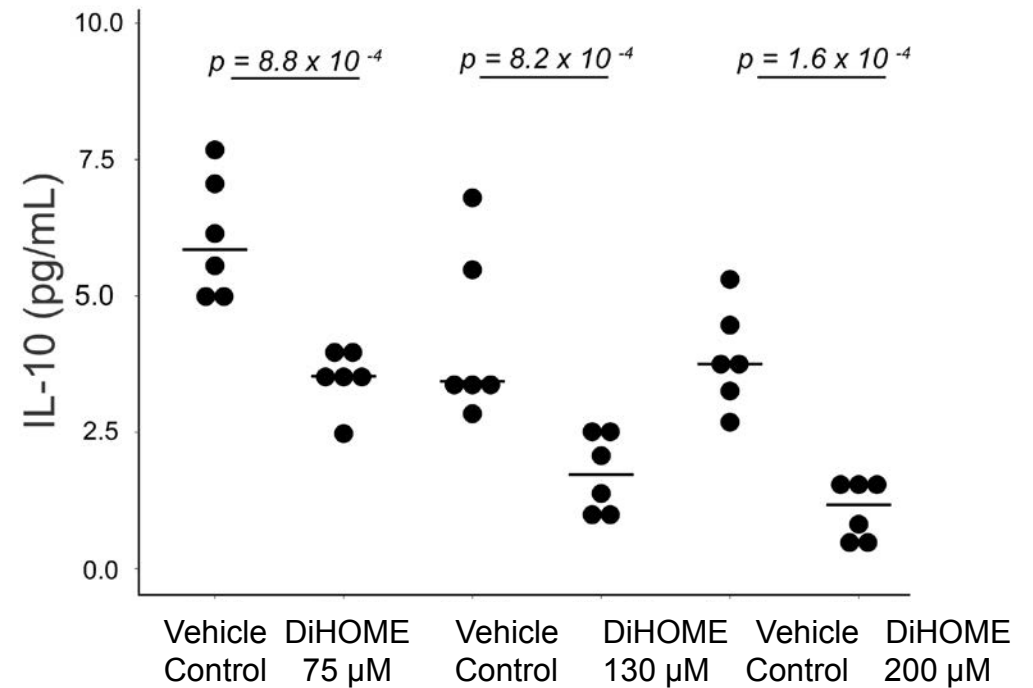
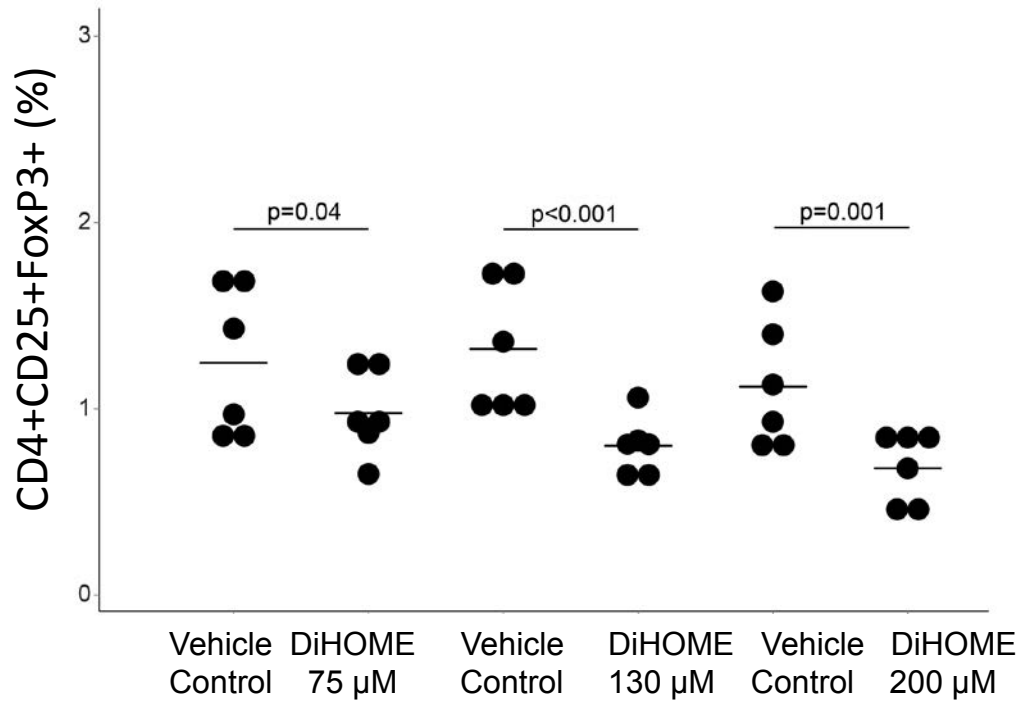
High-risk Neonatal Gut Microbiome Induces Allergic Inflammation and Suppresses T-regulatory Cells



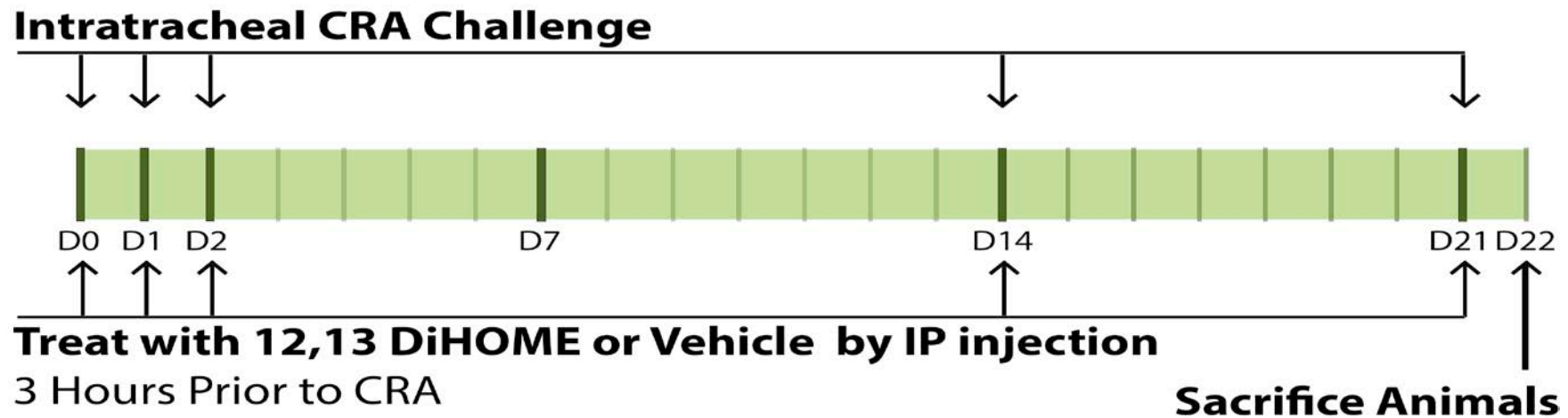
12,13 DiHOME Suppresses T-regulatory cell Populations *ex vivo*



12,13 DiHOME

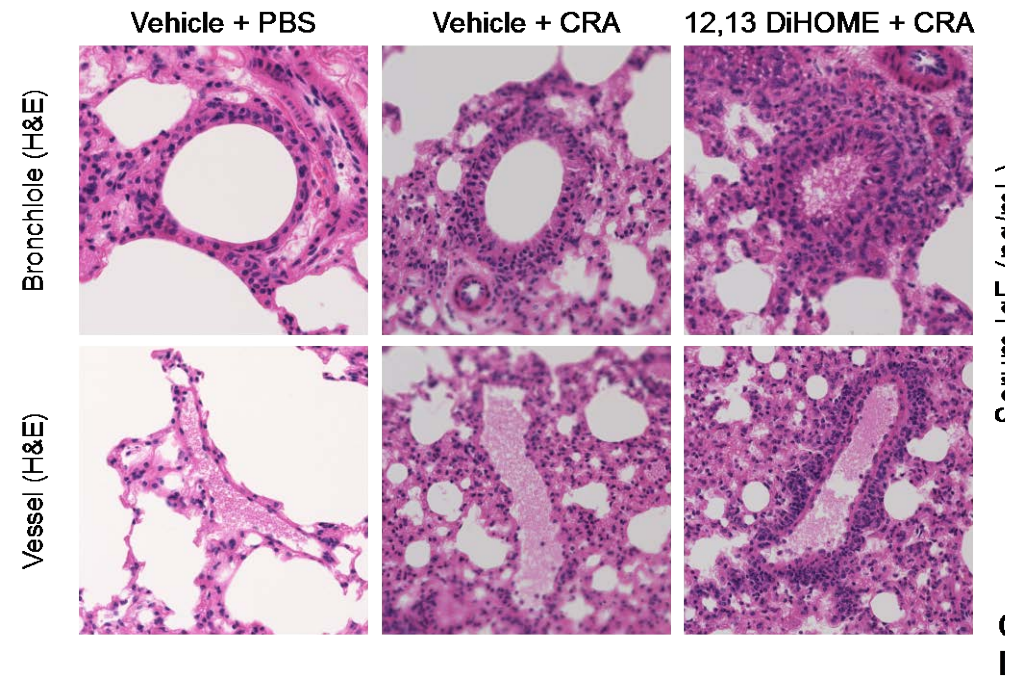


Can 12,13 DiHOME Promote Airway Allergic Sensitization in Mice?



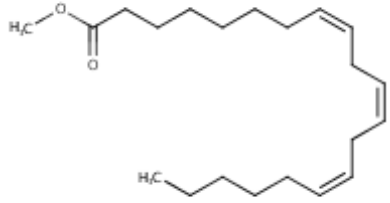
12,13 DiHOME Promotes Airway Allergic Sensitization and Increased Circulating IgE in Mice

k

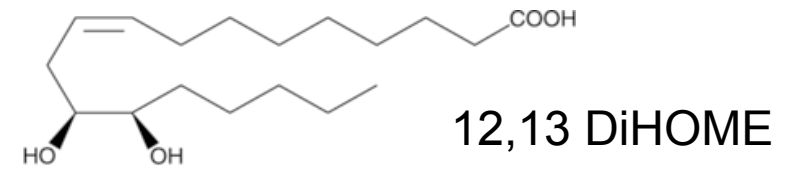
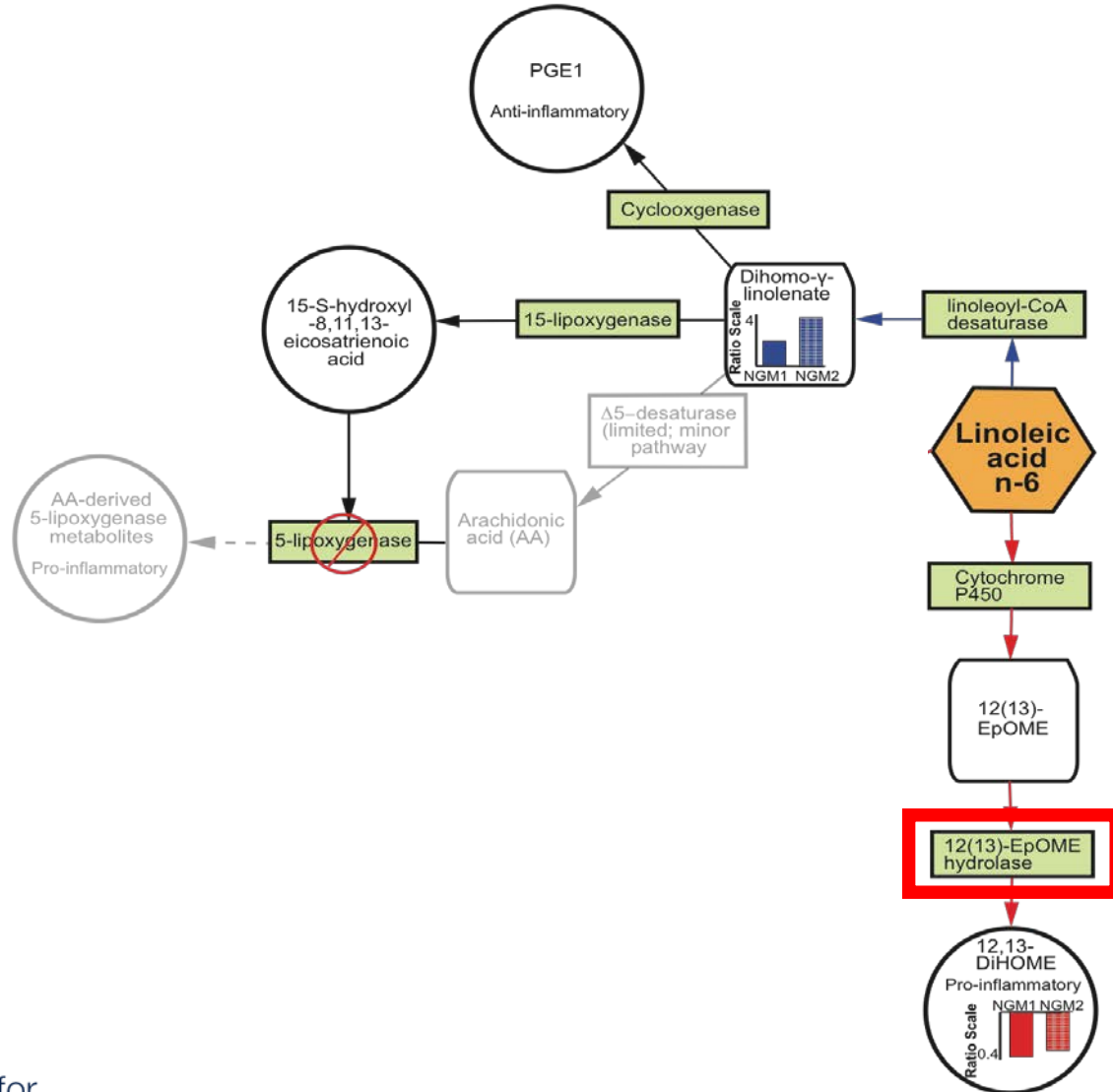


Elevated concentrations of 12,13 DiHOME in the neonatal gut may promote allergic inflammation via reduction of T-reg frequency and activity

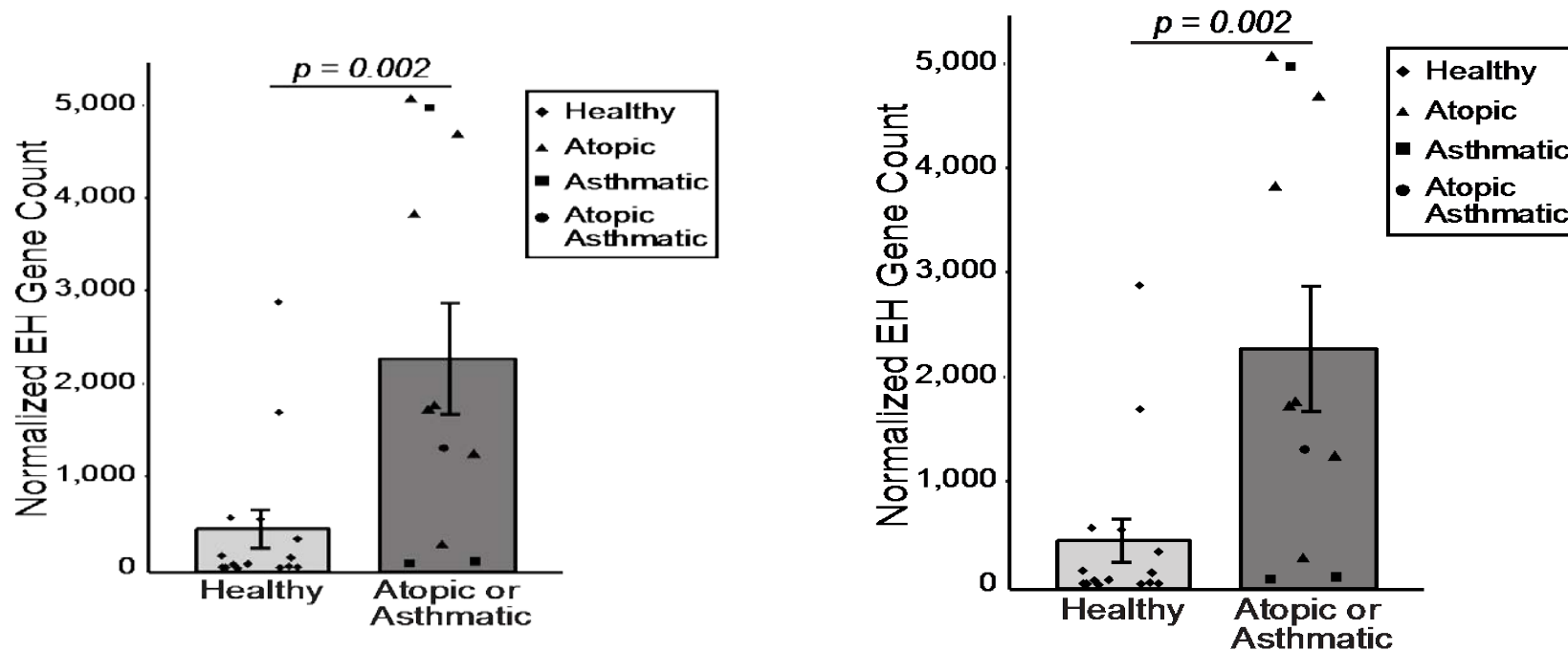
Altered Linoleic Acid Metabolism Characterizes High-risk Gut Microbiota



DiHomo- γ -linoleate



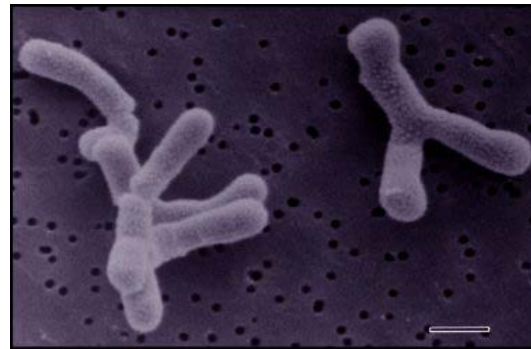
Is the H₂O₂-risk Neonatal Gut Microbiome Enriched for 12,13 DiHOME Production?



Specific Gut Microbiome Bacterial Strains Encode the Capacity to produce 12,13 DiHOME



Enterococcus faecalis



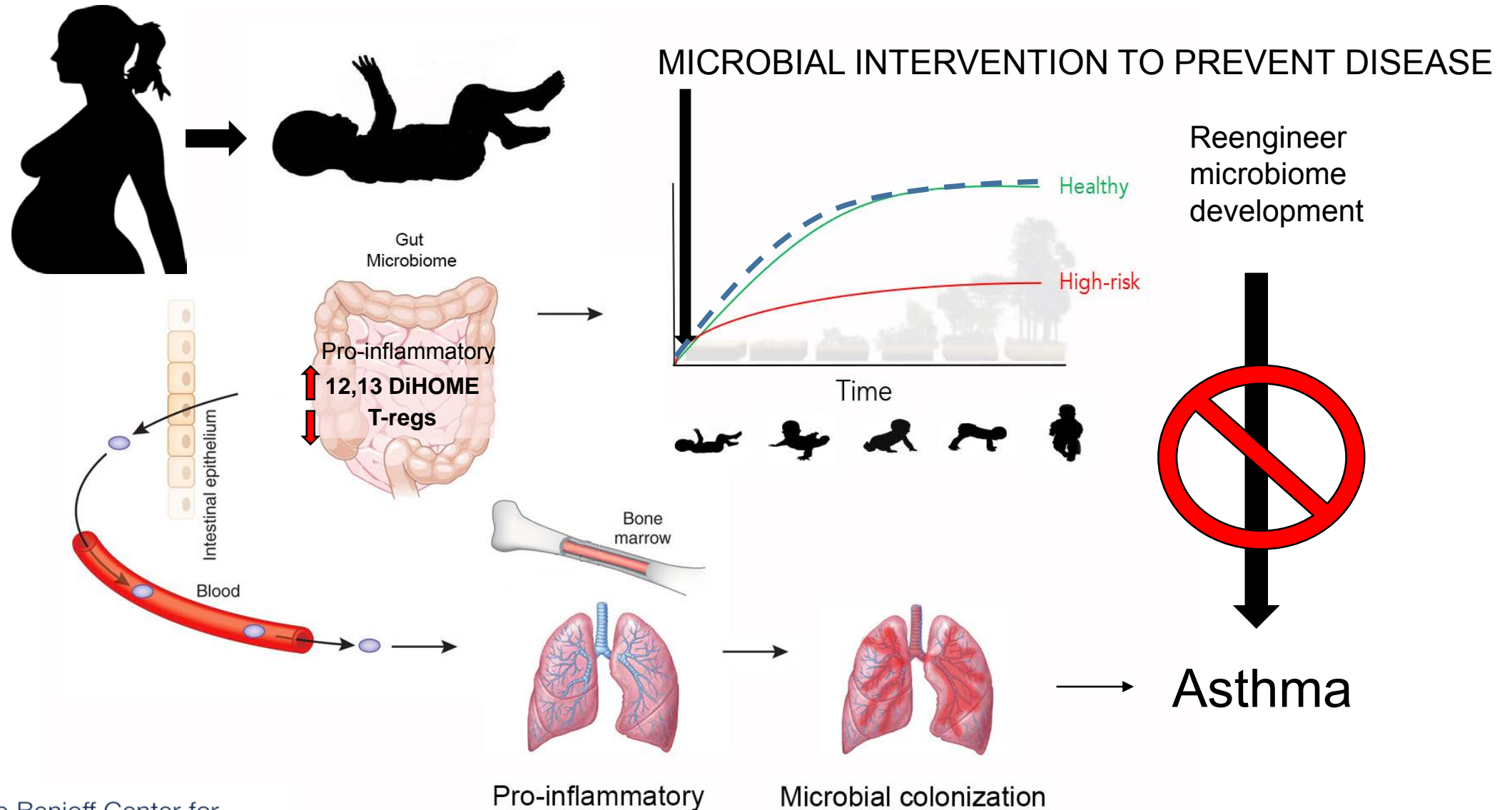
Bifidobacterium bifidium

Neonatal Fecal 3EH Copy Number and 12,13 DiHOME Concentration Predicts Childhood Atopy and Asthma

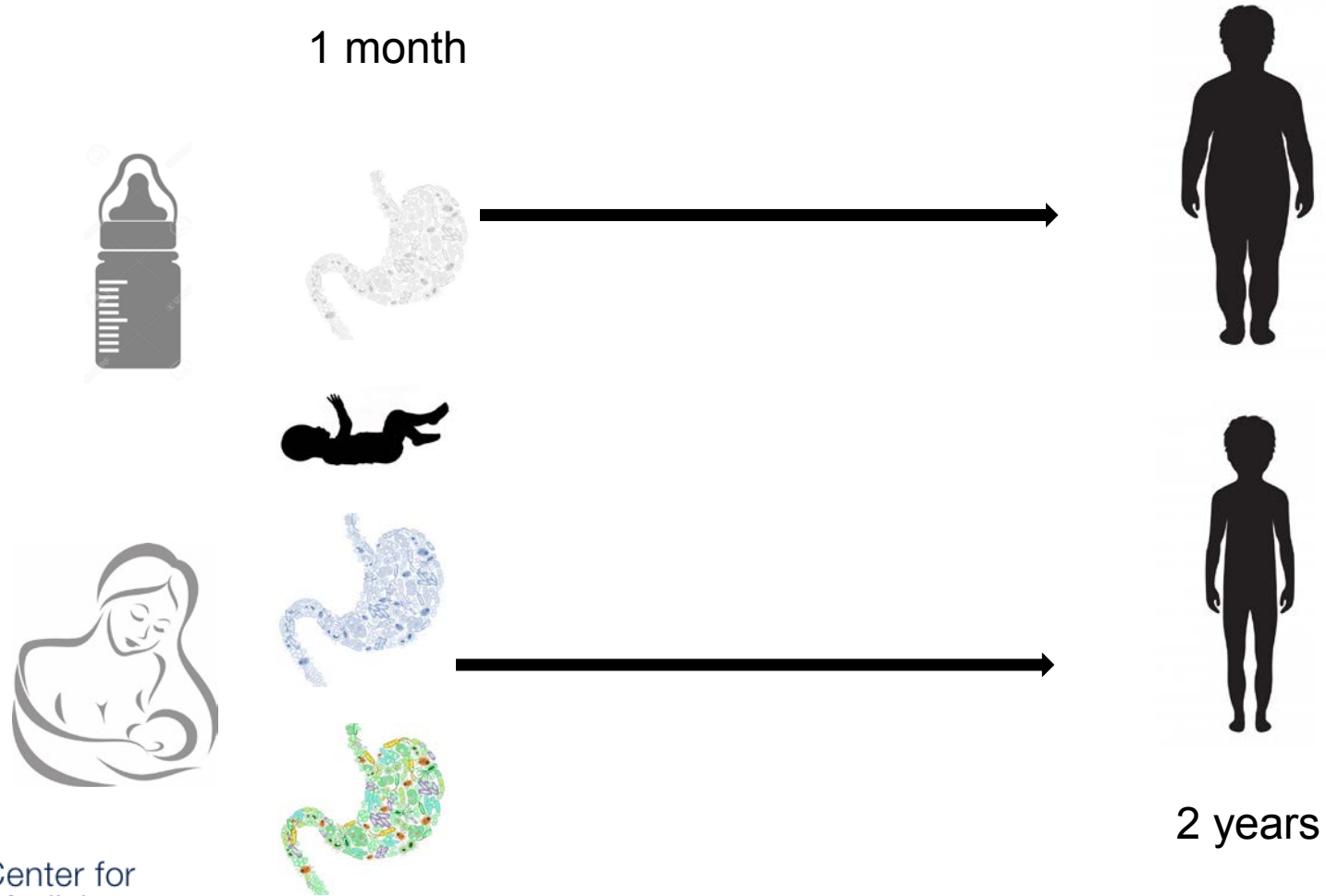
Early-life Gut *Microbial Risk Genes* Identify High-Risk neonates

Microbial-derived Molecular Mechanisms of Early-life Immune Dysfunction that Precede Childhood Disease Development

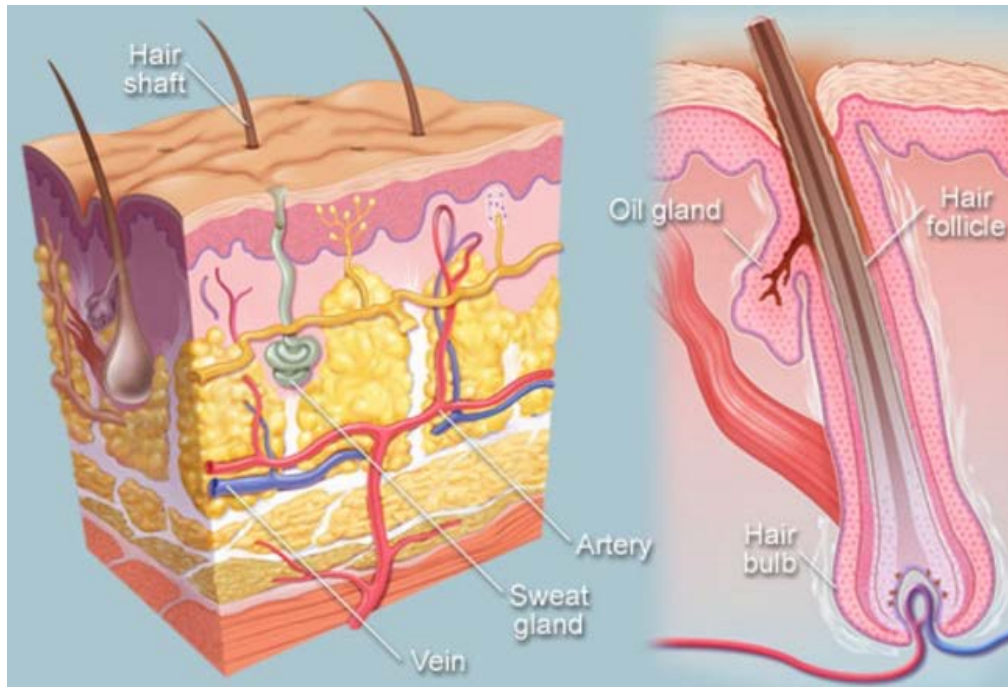
Model for Childhood Atopic Asthma Development



Early-life Gut Microbiota Relates to Childhood Obesity and Overweight Phenotypes at 2 Years

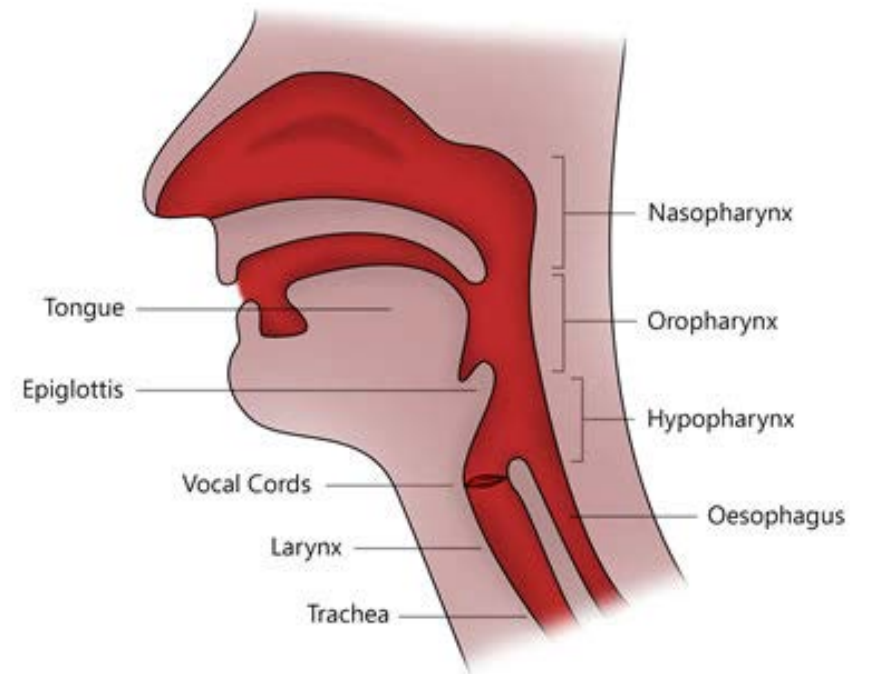


Early-life Microbial Colonization Influences Immune Status and Subsequent Microbiome Development



Scharschmidt lab

<https://scharschmidtlab.ucsf.edu>



Lynch lab

<https://www.slynchlab.com>

What Have we Learned and What's Next?

- Microbiome expands the genetic and functional capacity of its human host
- Human microbiome develops in early life
- Founder populations of gut microbes shape immune function and relate to disease outcomes in childhood
- Microbial-derived metabolites influence critical immune functions necessary for prevention of allergy and asthma
- Early-life microbial colonization relates to childhood health status



The Center is dedicated to supporting networks of multi-disciplinary investigators to accelerate microbiome-based treatment paradigms for adult and pediatric patients.

The Benioff Center for Microbiome Medicine at UCSF

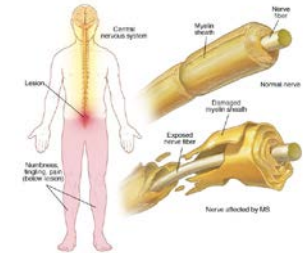
Provides a centralized home for the healthcare-based community of human microbiome researchers across the University of California, San Francisco invested in exploring the human microbiome's potential to predict, prevent and treat a wide range of diseases.

Microbiome Research @UCSF

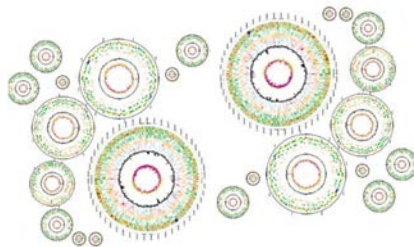
Leveraging healthy oral microbiomes to combat periodontal disease



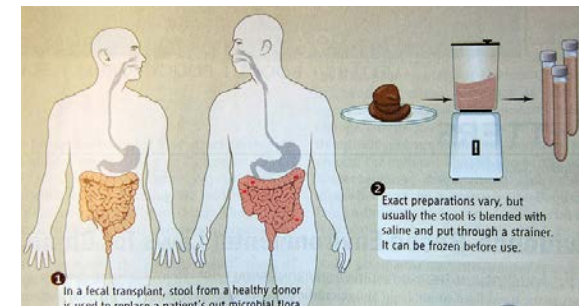
Gut Microbiome Relates to Multiple Sclerosis



Metagenomic Analysis Permitting Gene-level Associations with Disease



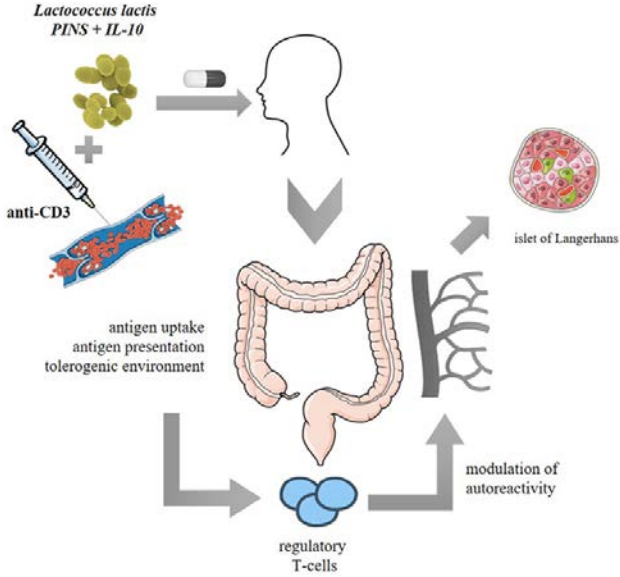
Determining the microbial basis of FMT efficacy



Next-generation Microbiome Therapeutics



PHAGE THERAPY



MICROBIAL GMOS



DIET



LIVE BIOTHERAPEUTICS

PREDICT, PREVENT, TREAT

PREDICT AND PREVENT DISEASE

TAILORED THERAPY

PRECISION MICROBIOME ENGINEERING

ACCELERATE TRANSLATIONAL DISCOVERY

