

Clinical Gut Health: Microbiome Science, Functional Assessment and Personalised Interventions

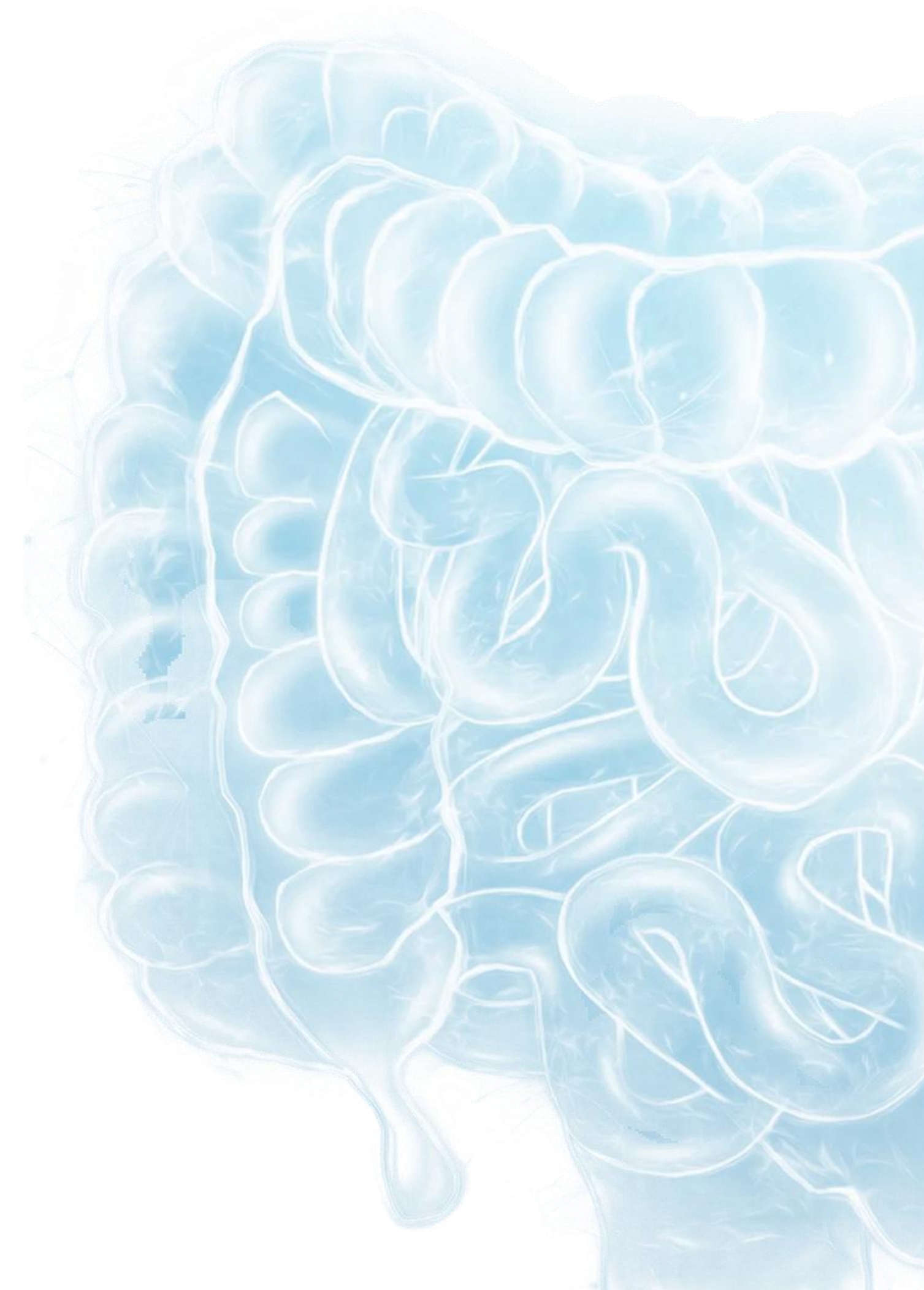
Dr. Federica Amati PHD, MPH, RNUTR

Head Nutritionist, ZOE · Research Fellow & Nutrition Lead, Imperial College London · IPM Congress London · 18 June 2026 · 14:15–14:45

Your patients are asking about their gut. The science finally has answers.

Roughly 1 in 5 global deaths linked to diet—the #1 modifiable risk factor worldwide, yet clinical translation of gut microbiome science remains the missing link.

GBD 2017 diet collaborators, lancet 2019
(PMID 30954305)



Microbiome composition tracks with habitual diet — and independently predicts cardiometabolic markers.

1,098 PREDICT 1 participants: microbiome species significantly associated with specific nutrients, foods, and postprandial cardiometabolic markers.

>34,000 participants: 50 favourable species, 50 adverse — and favourable species shift with dietary intervention.

Asnicar et al., Nat Med 2021 (PMID 33432175) Nature 2025 (DOI 10.1038/s41586-025-09854-7)



Why We Start With The Gut

75% of the Immune System Lives in the Gut

Early aging begins with gut permeability. When dysbiosis takes hold, systemic cytokines trigger nervous system hyperactivation, creating a cascade that impacts every major system.

If the gut is inflamed, the whole system is inflamed.

CRITICAL INFLUENCES

- Brain function & cognition
- Mood regulation
- Hormone signaling pathways
- Insulin sensitivity
- Cardiovascular inflammation



Assessment → Interpretation → Intervention → Reassess

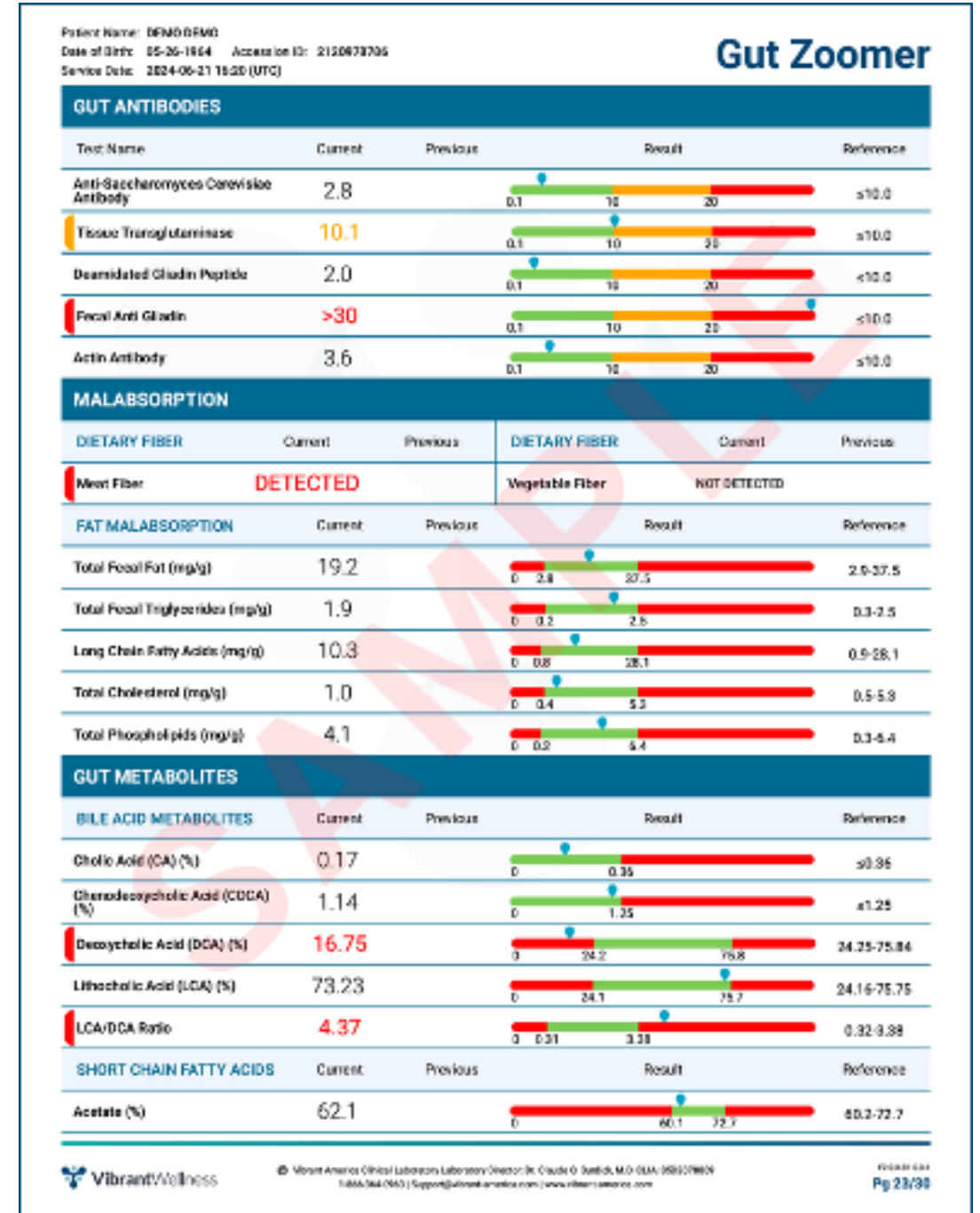
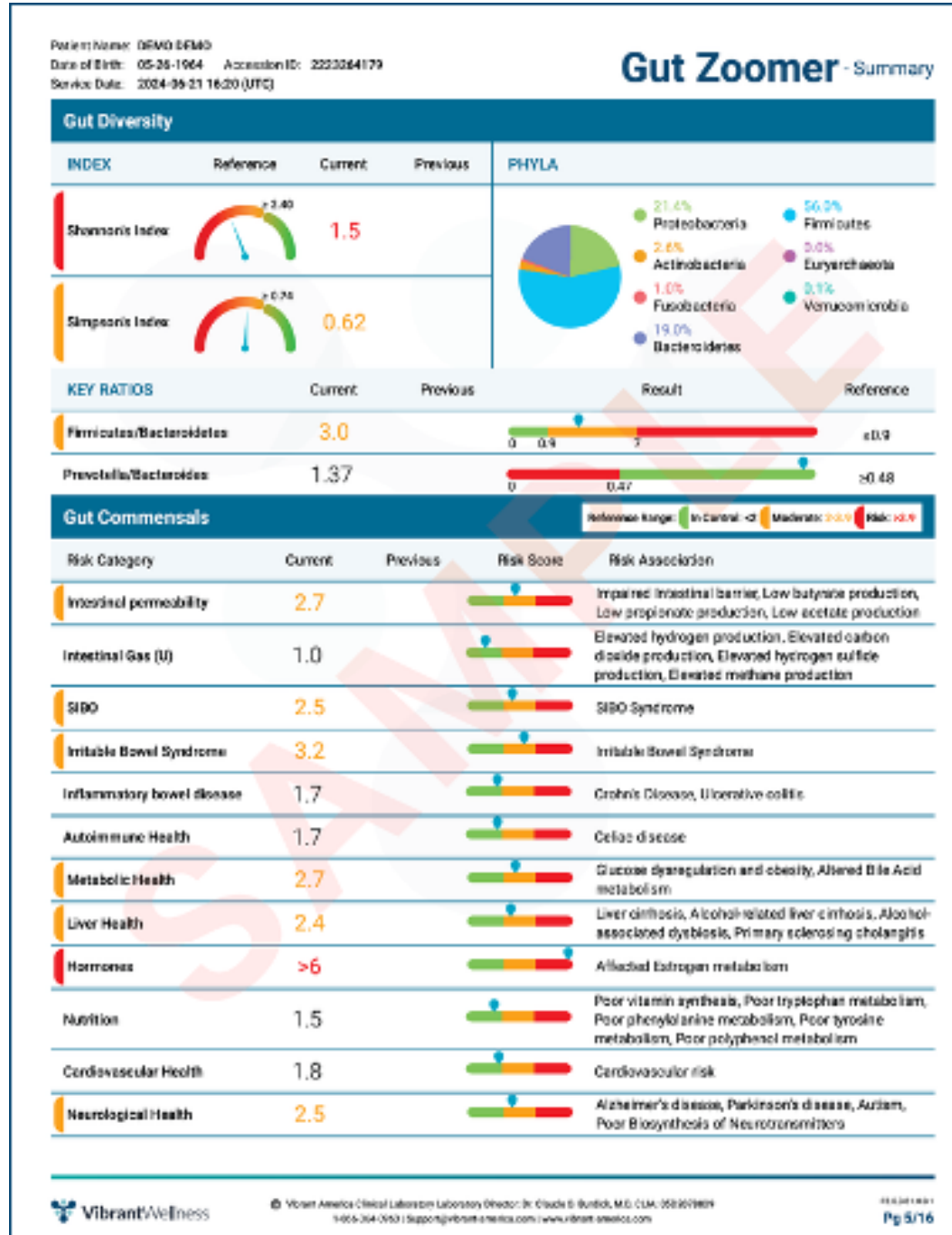
1. ASSESS • Gut Zoomer and/or additional functional panel Clinical history + dietary recall • Cardiometabolic biomarkers: lipids, HbA1c, hsCRP	1. INTERVENE (DIET-FIRST) • Mediterranean foundation for all Fermented foods daily • 30+ plant species/week • Minimise UPFs • Targeted support for barrier/immune clusters
1. INTERPRET • Dysbiosis / barrier disruption / immune activation / combined • Note severity • Exclude organic disease first	1. REASSESS • Repeat testing at 3–6 months • Track clinical markers in parallel • Adjust — the microbiome responds, but not uniformly

For most patients: the prescription is MORE, not less. Add diversity, fermentation, and colour. The test shows us where to focus.

Gut Zoomer Test

Identifying over 200 species of bacteria and gut pathogens along with diversity indices and a broad array of gut health markers:

- Gut Inflammatory Markers
- Digestion and Immune Balance
- Malabsorption Markers
- Gut Antibodies
- Gut Metabolites
- Gut Pathogens
- Gut Commensals
- Urine Neurotransmitters



Gut Zoomer Markers List

Gut Pathogens		
28 Bacteria <i>Aeromonas</i> spp. <i>Bacillus cereus</i> <i>Campylobacter coli</i> <i>Campylobacter jejuni</i> <i>Campylobacter</i> spp. <i>Campylobacter upsaliensis</i> <i>Clostridium difficile</i> <i>Clostridium difficile</i> Toxin A <i>Clostridium difficile</i> Toxin B <i>Clostridium perfringens</i> <i>E. coli</i> O157 <i>Edwardsiella tarda</i> - Enteroaggregative <i>E. coli</i> (EAEC) - Enteropathogenic <i>E. coli</i> (EPEC) - Enterotoxigenic <i>E. coli</i> (ETEC) LT/ST <i>Helicobacter pylori</i> <i>Klebsiella pneumoniae</i> <i>Listeria</i> - Non-<i>pylori</i> <i>Helicobacter</i> spp. <i>Plesiomonas shigelloides</i> <i>Salmonella</i> - Shiga-like toxin-producing <i>E. coli</i> (STEC) Stx1/Stx2 <i>Shigella</i>/EIEC <i>Staphylococcus aureus</i> <i>Vibrio cholerae</i> <i>Vibrio parahaemolyticus</i> <i>Vibrio vulnificus</i> <i>Yersinia enterocolitica</i>	14 Protozoans <i>Balantidium coli</i> <i>Blastocystis hominis</i> <i>Chilomastix mesnili</i> <i>Cryptosporidium</i> <i>Cyclospora cayentanensis</i> <i>Cyclospora</i> spp. <i>Dientamoeba fragilis</i> <i>Endolimax nana</i> <i>Entamoeba coli</i> <i>Entamoeba histolytica</i> <i>Giardia lamblia</i> <i>Isospora belli</i> <i>Pentatrichomonas hominis</i> <i>Trichomonas hominis</i>	6 Fungi <i>Candida albicans</i> <i>Candida glabrata</i> <i>Candida</i> spp. <i>Geotrichum</i> spp. <i>Microsporidium</i> spp. <i>Rodotorula</i> spp.
	13 Viruses - Adenovirus F40/41 - Astrovirus - Cytomegalovirus - Enterovirus - Epstein Barr virus - Human Bocavirus - Norovirus GI Virus - Norovirus GII Virus - Rotavirus A - Sapovirus I - Sapovirus II - Sapovirus IV - Sapovirus V	
		Gut Diversity Indices - Shannon's Diversity Index - Simpson's Diversity Index - Firmicutes/Bacteroidetes - Prevotella /Bacteroidetes (P/B)

Gut Inflammatory Markers
- Beta defensin 2 (ng/mL) - Calprotectin (mcg/g) - Fecal Eosinophil Protein X (mcg/g) - Fecal lactoferrin (mcg/ml) - Lysozyme (ng/mL) - MMP 9 (ng/mL) - S100A12 (mcg/ml)
Gut Antibodies
- Tissue transglutaminase (tTg) - Deamidated gliadin peptide (DGP) - Fecal Anti Gliadin - Actin antibody - Lipopolysaccharide (LPS) antibody - Anti-Saccharomyces cerevisiae antibody (ASCA)
Malabsorption
- Meat fiber - Vegetable fiber Fat Malabsorption - Total Fecal Fat (mg/g) - Total Fecal Triglycerides (mg/g) - Long chain fatty acids (mg/g) - Total Cholesterol (mg/g) - Total Phospholipids (mg/g)

Digestion & Immune
- Fecal Immunochemical Test (FIT) - Fecal Zonulin (ng/mL) - Pancreatic elastase 1 (mcg/g) - pH - Secretory IgA (mcg/g)
Gut Metabolites
- β-glucuronidase (U/mL) Bile Acids - Cholic acid (CA) (%) - Chenodeoxycholic acid (CDCA) (%) - Deoxycholic acid (DCA) (%) - Lithocholic acid (LCA) (%) - LCA/DCA ratio Short Chain Fatty Acids - Acetate (%) - Butyrate (%) - Propionate (%) - Valerate (%) - Total SCFA (mmol/g)

Gut Zoomer Commensals

Gut Commensals - Probiotic Organisms

- *Bacillus coagulans*
- *Bifidobacterium bifidum*
- *Bifidobacterium breve*
- *Bifidobacterium dentium*
- *Bifidobacterium infantis*
- *Bifidobacterium longum*
- *Escherichia coli* Nissle
- *Lactobacillus acidophilus*
- *Lactobacillus brevis*
- *Lactobacillus bulgaricus*
- *Lactobacillus casei*
- *Lactobacillus fermentum*
- *Lactobacillus paracasei*
- *Lactobacillus plantarum*
- *Lactobacillus reuteri*
- *Lactobacillus rhamnosus*
- *Lactobacillus rhamnosus* GG
- *Lactobacillus salivarius*
- *Saccharomyces boulardii*
- *Streptococcus*
- *Streptococcus thermophilus*

- *Prevotella*
- *Prevotella copri*
- *Propionibacterium freudenreichii*
- *Proteus mirabilis*
- *Pseudobutyrvibrio*
- *Pseudomonas*
- *Roseburia*
- *Roseburia intestinalis*
- *Ruminococcaceae*
- *Ruminococcus*
- *Ruminococcus bromii*
- *Ruminococcus gnavus*
- *Ruminococcus obeum*
- *Solobacterium moorei*
- *Staphylococcaceae*
- *Staphylococcus epidermidis*
- *Staphylococcus pasteurii*
- *Staphylococcus species*
- *Tyzzereella*
- *Tyzzereella 4*
- *Veillonella*
- *Veillonellaceae*
- *β-galactosidase producing bacteria*
- *β-glucuronidase producing bacteria*

- *Acinetobacter*
- *Actinomyces*
- *Akkermansia muciniphila*
- *Alistipes*
- *Alloprevotella*
- *Atopobium*
- *Atopobium parvulum*
- *Bacillus subtilis*
- *Bacteroidales*
- *Bacteroides*
- *Bacteroides caccae*
- *Bacteroides vulgatus*
- *Bifidobacterium*
- *Bifidobacterium adolescentis*
- *Bifidobacterium animalis*
- *Bifidobacterium animalis subspecies lactis*
- *Bifidobacterium catenulatum*
- *Blautia*
- *Blautia hydrogenotrophica*
- *Bradyrhizobiaceae*
- *Butyricimonas*
- *Butyrvibrio*
- *Catenibacterium*
- *Christensenella minuta*
- *Clostridia cluster IV*
- *Clostridia cluster XIVa*
- *Clostridia cluster XVIII*
- *Clostridiales Family XIV Incertae sedis*
- *Clostridiales Incertae Sedis IV*
- *Clostridium*
- *Clostridium hathewayi*
- *Clostridium ramosum*
- *Clostridium symbiosum*
- *Collinsella*

- *Coprococcus*
- *Desulfovibrio*
- *Desulfovibrio piger*
- *Dialister invisus*
- *Dorea*
- *Eggerthella lenta*
- *Enterobacter aerogenes*
- *Enterobacteria*
- *Enterobacteriaceae*
- *Enterococcus*
- *Enterococcus gallinarum*
- *Escherichia coli*
- *Eubacterium*
- *Eubacterium rectale*
- *Faecalibacterium prausnitzii*
- *Fusobacterium*
- *Haemophilus*
- *Hafnia*
- *Holdemania*
- *Lachnospiraceae*
- *Lactobacillaceae*
- *Lactobacillus*
- *Lactobacillus animalis*
- *Lactobacillus ruminis*
- *Lactobacillus sakei*
- *Lactococcus*
- *Leuconostoc*
- *Marvinbryantia*
- *Methanobrevibacter smithii*
- *Mycoplasma*
- *Oscillospira*
- *Parabacteroides*
- *Pediococcus*
- *Peptostreptococcus*
- *Phascolarctobacterium*
- *Porphyromonas ainovalis*

Gut Zoomer - Urine Neurotransmitters

Dopaminergic Pathway	Other Pathways	Serotonergic Pathway	Resistance Genes	
• PEA (Phenylethylamine) • Dopamine • DOPAC • HVA • Normetanephrine • VMA • 3-Methoxy-tyramine • Metanephrine • Tyrosine • Tyramine • L-DOPA • HVA / VMA Ratio • HVA / DOPAC Ratio	• Glycine • Taurine • Acetylcholine • Aspartate • Serine • Oxytocin	• Serotonin • 5-HIAA • 5-HTP • Tryptophan	• Helicobacter - Clarithromycin • Helicobacter - Fluoroquinolones • Fluoroquinolones • Vancomycin • b-lactamase	• Macrolides • Tetracycline • Aminoglycoside • Bactrim • Carbapenem • Rifampin • Polymyxins
	Kynurenine Pathway	GABAergic Pathway	Gut Phyla	
	• Xanthurenic acid • Quinolinic acid • Kynurenic acid • Quinolinic Acid / 5-HIAA Ratio	• GABA • Glutamate		
		Histaminergic Pathway	• Proteobacteria • Actinobacteria • Fusobacteria • Bacteroidetes	• Firmicutes • Euryarchaeota • Verrucomicrobia
Tryptamine Pathway				
• Tryptamine				

Five Things To Take Back To Your Clinic Tomorrow

- 1 The microbiome is modifiable. Diet — especially **plant diversity** and **fermented foods** — is its most powerful driver, not genetics.
- 2 For low diversity: start with **fermented foods**. Build fibre gradually. Sequence matters.
- 3 **Mediterranean diet**: best-evidenced foundation for all patients. Personalisation refines it; it does not replace it.
- 4 Use **functional assessment** with clinical judgement and honest communication about validation status.
- 5 Microbiome responds within **2–4 weeks**. Reassess at 3–6 months. The relationship is what makes patients follow through.

The Mediterranean pattern is the foundation.

ASSESSMENT TELLS US WHAT TO BUILD ON TOP.

For All The Patients

- 30+ plant species/week
- Fermented foods daily
- Legumes 3–5×/week
- Oily fish 2–3×/week
- EVOO daily
- Minimise UPFs

MEDITERRANEAN FOUNDATION

Low Diversity

Emphasise fermented foods first.
Build fibre gradually.
Review antibiotics and PPIs.

FERMENTATION FIRST

Elevated Zolulin

Trial gluten/casein 4–6 weeks.
Zinc carnosine + L-glutamine.
Omega-3 and stress management.

BARRIER REPAIR

High TMAO / Butyrate

Reduce red meat.
Add dietary polyphenols.
Targeted prebiotic support (inulin, FOS, PHGG).

PERSONALISED LAYER

Personalised Microbiome-Informed Dietary Advice Outperforms Standard Guidance

Study Overview

Bermingham et al., Nature Medicine 2024

18-week RCT · n=347

- **ZOE arm:** TG -0.13 mmol/L (p=0.016)
- HbA1c, BMI, waist circumference, and diet quality all improved vs control
- Significant improvement in microbiome beta-diversity vs control (PMID 38714898)

The Intervention

vs standard USDA dietary advice

Personalised dietary recommendations

Data Inputs:

- Continuous Glucose Monitoring (CGM)
- Microbiome profiling
- Blood biomarker input

Three Clinical Clusters —

AND WHAT TO DO WITH EACH.

Dysbiosis

MARKERS

- Low diversity
- Elevated pathobionts
- Low butyrate-producing species

INTERVENTION

- Fermented foods first (kefir, yoghurt, kimchi)
- Gradual plant diversity
- Review antibiotics/PPIs

Barrier Disruption

MARKERS

- Elevated zonulin
- Low sIgA
- Elevated Fecal Eosinophil Protein X
- Anti-gliadin IgG+

INTERVENTION

- Trial gluten/casein 4–6 wks
- Zinc carnosine · L-glutamine
- Omega-3
- Stress management

Immune Activation

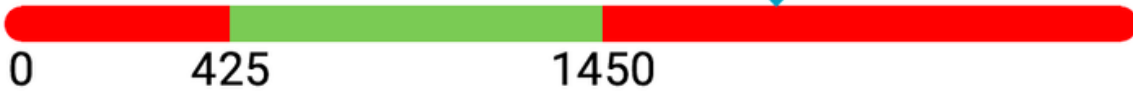
⚠ HIGH CALPROTECTIN

- REFER for colonoscopy (>250 µg/g)

CLINICAL ACTIONS

- Exclude IBD before any gut protocol
- Anti-inflammatory diet alongside clinical investigation

Digestion And Immune Balance

DIGESTION AND IMMUNE BALANCE				
Test Name	Current	Previous	Result	Reference
Pancreatic Elastase 1 (mcg/g)	331.9			≥200.0
Fecal Immunochemical Test (FIT) (mcg/g)	5.3			≤10.0
 Fecal Zonulin (ng/mL)	221.6			25.1-160.8
pH	6.8			6.1-7.8
 sIgA (mcg/g)	1973.5			426.0-1450.0

Trillions Of Microbes. One Profoundly Modifiable Organ System.

Microbial Scale

~38 trillion microbial cells — approximately equal to human cell count

(Sender et al., Cell 2016 · PMID 27541692)

Immune Interaction

Estimated 70–80% of the body's immune cells are found in or associated with the gut mucosa (GALT)

(Mann et al., Nat Rev Immunol 2024 · PMID 38565643)

Clinical Impact

In type 2 diabetes: microbiome measurably different — depleted in butyrate-producing bacteria, enriched in opportunistic pathogens

(Qin et al., Nature 2012 · PMID 23023125)

30 Different Plant Foods Per Week.

A MOTIVATING TARGET WITH STRIKING SCIENCE.

The Core Finding

People eating 30+ plant types/week: significantly greater microbiome diversity vs ≤ 10 /week — regardless of dietary pattern (vegan, vegetarian, or omnivore).

McDonald et al., mSystems 2018 · $n > 10,000$ · PMID 29795809



Dysbiosis Drives Systemic Inflammation

Healthy State

- Diverse microbiome → Abundant SCFAs
- Intact epithelial tight junctions
- Regulated mucosal immunity → Low systemic LPS

Dysbiosis State

- Low diversity → Reduced butyrate → Impaired junctions
- LPS translocation → TLR4 → NFκB activation
- Metabolic endotoxaemia → Chronic systemic inflammation

Examples from Gut Zoomer:

- **Enterobacteriaceae:** Produces high LPS → brain fog, anxiety
- **Prevotella:** Associated with joint inflammation
- **Fusobacterium:** Linked to cardiometabolic risk
- **Low butyrate producers:** Poor gut lining repair and immune regulation
- **Candida/yeast:** Gas, bloating, fatigue, and systemic symptoms

ASSOCIATED CONDITIONS:

- | | |
|----------------------|--------------|
| • T2D | • Depression |
| • Metabolic syndrome | • Autoimmune |
| • Atherosclerosis | • CRC risk |

(Mann et al., Nat Rev Immunol 2024 · PMID 38565643)

Gut Inflammatory Markers

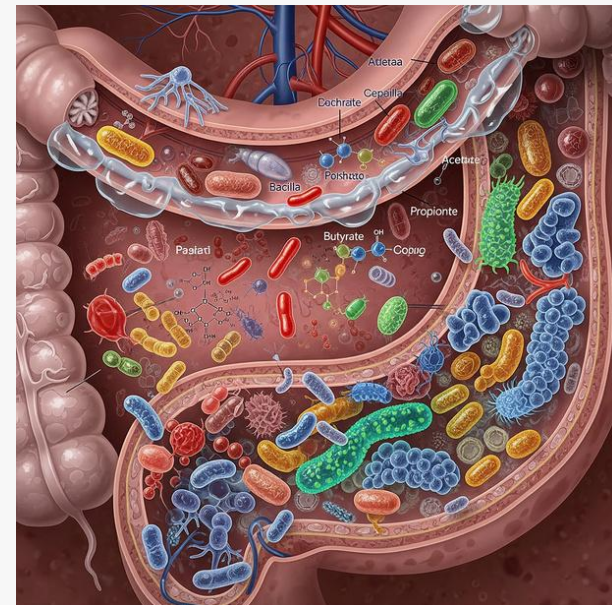
GUT INFLAMMATORY MARKERS				
Test Name	Current	Previous	Result	Reference
 Beta Defensin 2 (ng/mL)	51.0			≤34.9
Lysozyme (ng/mL)	463.1			≤575.0
MMP 9 (ng/mL)	0.2			≤0.2
S100A12 (mcg/ml)	30.0			≤50.0
 Calprotectin (mcg/g)	81.7			≤50.0
Fecal Lactoferrin (mcg/ml)	2.1			≤6.4
 Fecal Eosinophil Protein X (mcg/g)	9.4			≤4.8

Fermented Foods Increased Microbiome Diversity.

HIGH-FIBRE ALONE DID NOT.

High Fermented Food Diet

- ↑ Microbiome diversity
- ↓ 19 inflammatory proteins
- (incl. IL-6, IL-12p70, CXCL10)



High Fiber Diet

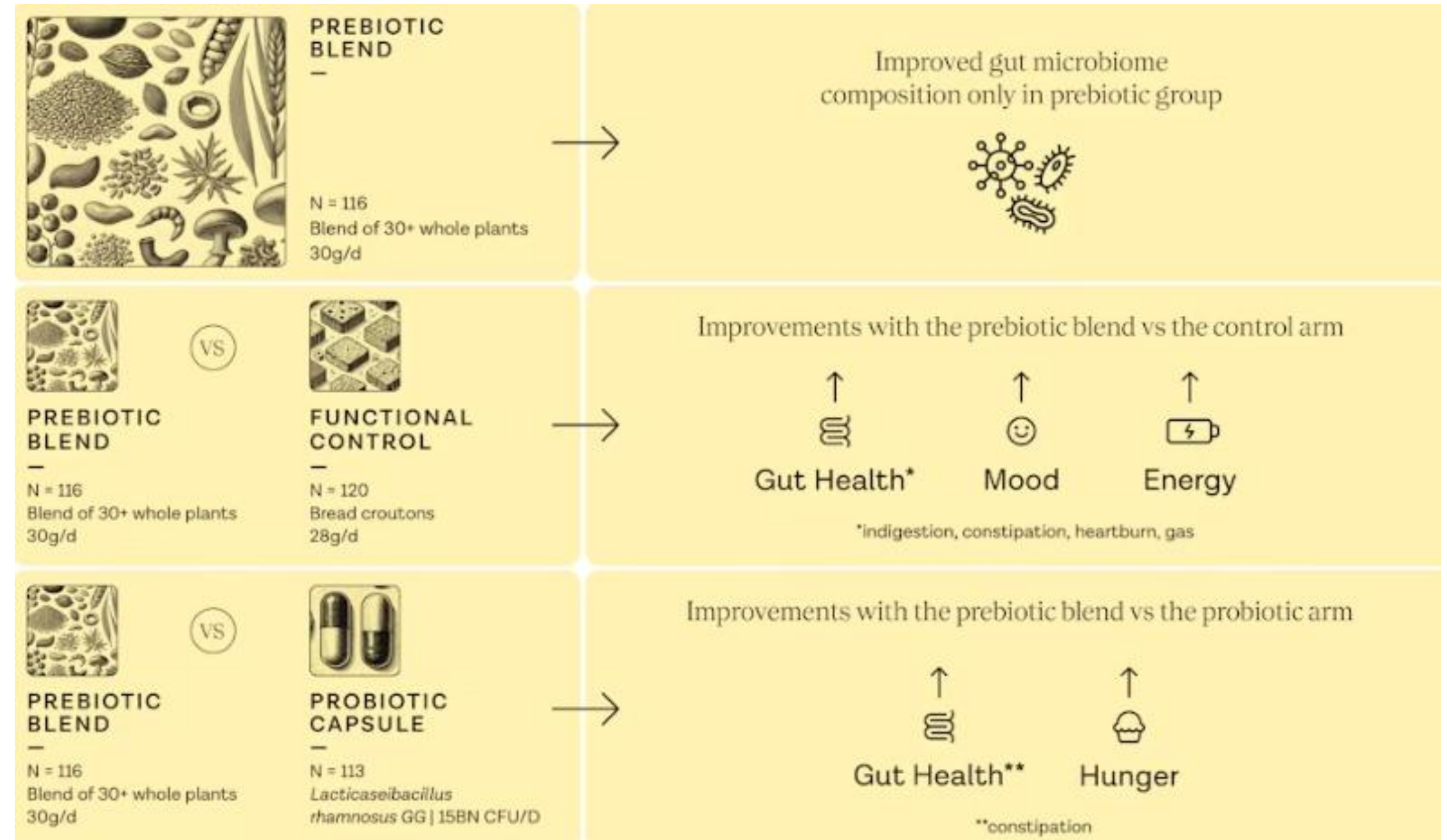
- Diversity did NOT increase
- Response depended on baseline microbiome diversity
- 3 distinct immune trajectories observed

WASTYK ET AL., CELL 2021 — 17-week RCT, Stanford · n=36 (n=18 per arm) · PMID 34256014



Daily30+ / The BIOME Study RCT

Creedon et al., in review 2024



Same Meal. Completely Different Responses.

WHY?

103%

TRIGLYCERIDES

Variation between individuals eating
identical meals

68%

GLUCOSE

Variation between individuals

59%

INSULIN

Variation between individuals

PREDICT 1 · Berry et al., Nat Med 2020 · n=1,002 · PMID 32528151

“Good” bugs

E. eligens
B. animalis
F. prausnitzii
H. parainfluenzae
Oscillibacter sp. 57 20
Oscillibacter sp. PC13
Firmicutes bacterium CAG:95
Firmicutes bacterium CAG:170
Roseburia sp. CAG:182
Clostridium sp. CAG:167
Romboutsia ilealis
Veillonella atypica
V. infantium
V. dispar
P. copri

Microbiome signature

+

Healthy measures of health

- Good blood fat & blood sugar control
- Good blood lipids
- Lower inflammation
- Lower levels of body fat
- Lower CVD & type 2 diabetes risk

and diet

- Healthy dietary patterns
- Healthy plant-based foods
- Healthy oils/fats

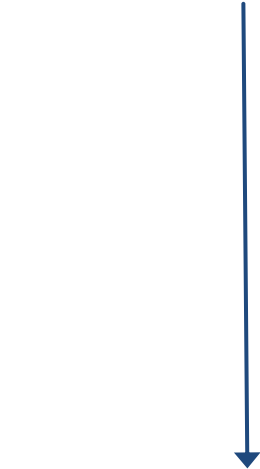
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“Bad” bugs

E. lenta
C. leptum
F. plautii
C. bolteae
Escherichia coli
R. lactatiformans
Collinsella intestinalis
Blautia hydrogenotrophica
Clostridium sp. CAG:58
C. symbiosum
C. bolteae CAG 59
A. colihominis
C. innocuum
C. spiroforme
R. gnavus

The same microbes are associated with favourable or unfavourable measures of diet

Can we personalise the microbiome?



Elicit changes in health?

Gut Commensals

Test Name	Current	Previous	Result	Reference
Akkermansia muciniphila ⁺				
Butyrivibrio				
Alloprevotella ⁺				
Roseburia intestinalis				
Bacteroides vulgatus ⁺				
Prevotella ⁺				
Faecalibacterium				
Ruminococcaceae				
Dialister invisus ⁺				
Veillonella ⁺				
Haemophilus ⁺				
Bacteroidales ⁺				
Bacteroides caccae ⁺				
Bifidobacterium animalis				
Christensenella minuta				
Pseudomonas				
Blautia hydrogenotrophica				
Clostridia clusters XVIII				
Clotridiales Incertae Sedis IV				
Enterobacter aerogenes ⁺				
Peptostreptococcus				
Propionibacterium freudenreichii				
Ruminococcus obeum				
β-galactosidase producing bacteria				
β-glucuronidase producing bacteria				
Gut Commensals - Probiotic Organisms				
Test Name	Current	Previous	Result	Reference
Streptococcus	28.4			
Lactobacillus bulgaricus	24.2			
Lactobacillus plantarum	0.9			
Gut Commensals - Gut Microbiome				
Test Name	Current	Previous	Result	Reference
Clostridium hathewayi ⁺	13.1			
Clostridium ramosum	2			
Clostridium symbiosum ⁺	1			
Eggerthella lenta	1			
Oscillospira ⁺	2			
Collinsella	5			
Phascolarctobacterium ⁺	1			
Hafnia	1			
Parabacteroides	1			
Ruminococcus bromii	1			
Eubacterium	2			
Ruminococcus gnavus	1			
Marvinbryantia	1			
Bifidobacterium catenulatum	8			
Dorea	1			
Enterobacteriaceae ⁺	2			
Ruminococcus	2			
Bifidobacterium adolescentis	2			
Enterococcus	2			
Desulfovibrio piger ⁺	4			
Roseburia	2			
Eubacterium rectale	1			
Atopobium parvulum	1			
Gut Commensals - Probiotic Organisms				
Test Name	Current	Previous	Result	Reference
Staphylococcus species	5.4			
Fusobacterium ⁺	25.0			
Methanobrevibacter smithii	>30			
Clostridium	6.4			
Porphyromonas gingivalis ⁺	1.9			
Proteus mirabilis ⁺	11.0			
Pseudobutyrvibrio ⁺	25.0			
Bifidobacterium	15.7			
Staphylococcaceae	15.5			
Staphylococcus epidermidis	4.0			
Staphylococcus pasteurii	13.6			
Clostridia clusters IV	23.1			
Clostridia clusters XIVa	28.0			
Enterococcus gallinarum	1.4			
Actinomyces	19.6			
Bacteroides ⁺	20.8			
Bifidobacterium animalis subspecies lactis	29.6			
Lactobacillus animalis	21.8			
Clostridiales Family XIV Incertae Sedis	17.2			
Enterobacteria ⁺	14.0			
Faecalibacterium prausnitzii	14.6			
Lactobacillus	6.4			
Lactococcus	22.7			
Gut Commensals - Probiotic Organisms				
Test Name	Current	Previous	Result	Reference
Bifidobacterium breve	11.6			≥10.0
Bifidobacterium infantis	1.6			≥10.0
Bifidobacterium longum	28.9			≥10.0
Escherichia coli Nissle ⁺	27.6			≥10.0
Lactobacillus acidophilus	23.6			≥10.0
Lactobacillus brevis	11.5			≥10.0
Lactobacillus casei	26.4			≥10.0
Lactobacillus fermentum	10.0			≥10.0
Lactobacillus paracasei	1.2			≥10.0
Lactobacillus reuteri	17.0			≥10.0
Lactobacillus rhamnosus	5.3			≥10.0
Lactobacillus rhamnosus GG	12.8			≥10.0
Lactobacillus salivarius	1.6			≥10.0
Enterobacter aerogenes ⁺	13.9			≤20.0
Peptostreptococcus	6.2			≤20.0
Propionibacterium freudenreichii	19.6			≥10.0
Ruminococcus obeum	13.7			≤20.0
β-galactosidase producing bacteria	20.7			≤20.0
β-glucuronidase producing bacteria	9.6			≤20.0

Clinically Significant Bacteria

Test Name	Current
Akkermansia muciniphila ⁺	11.2
Clostridium hathewayi ⁺	13.1
Ruminococcaceae	28.6
Dialister invisus ⁺	21.6
Veillonella ⁺	23.4
Faecalibacterium prausnitzii	14.6

The Microbiome Is Far More Environment Than Genetics.

Diet & Plants

PRIMARY DRIVER

Microbiome responds to dietary change within days.
Target **30+ plant species** per week.
Focus on diversity, not just quantity.

Lifestyle

MEDICATIONS & STRESS

Antibiotics: Strong disruptor.
PPIs: Alter mucosal pH.
Sleep and physical activity are key secondary modulators.

Genetics

SMALL & FIXED

Twin studies show genetics explains a small, fixed proportion of variance.
Crucially, your patients can change their outcome through choice.

The Microbiome Speaks To Every System — Through Metabolites.

SCFA (Beneficial)

Butyrate, propionate, acetate from dietary fibre fermentation.

- Fuel colonocytes
- Maintain epithelial barrier
- Regulate T-regulatory cells
- Suppress NFκB-driven inflammation

Mann et al., Nat Rev Immunol 2024

Bile Acids

Double-edged: Primary bile acids modified by gut bacteria to secondary bile acids.

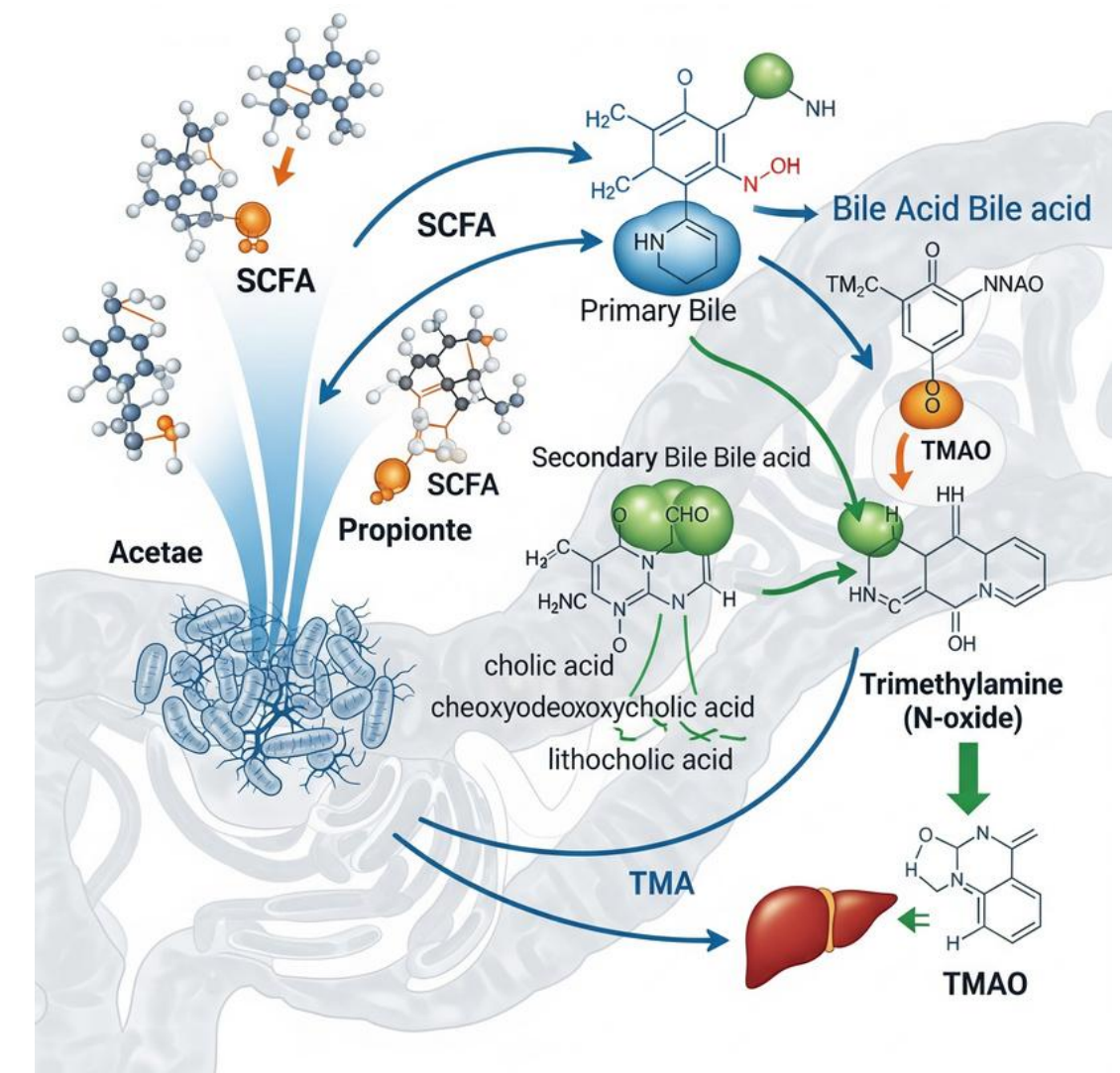
- Profile shapes metabolic risk
- Highly diet-responsive

TMAO (Harmful)

Harmful at high levels: Derived from red meat/eggs via specific bacteria.

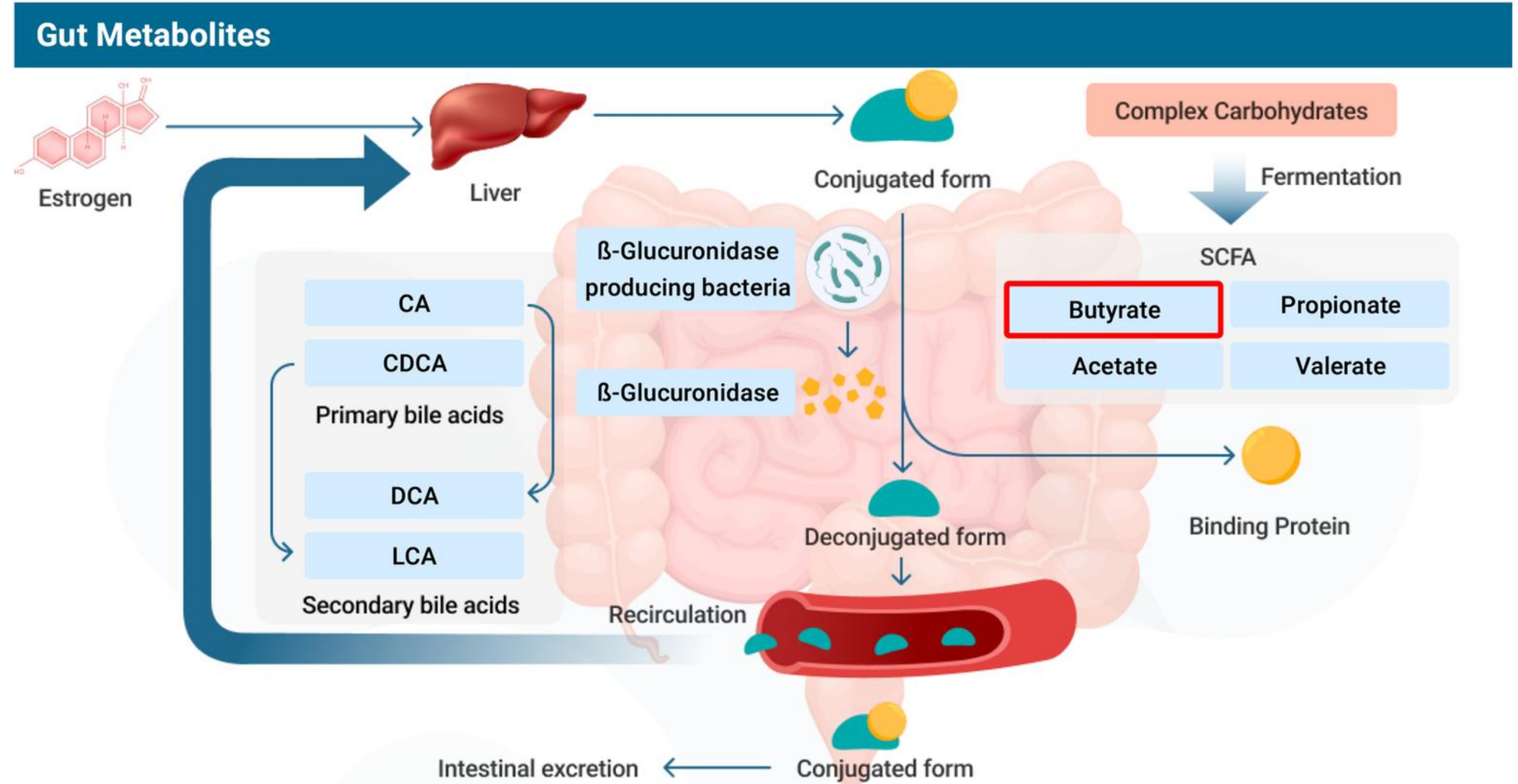
- Converted hepatically
- Linked to hypertension
- Cardiometabolic risk factor

Farhangi, Nutrition Reviews 2021



Gut Metabolites Infographic

BILE ACID METABOLITES		Current
Cholic Acid (CA) (%)		0.17
Chenodeoxycholic Acid (CDCA) (%)		1.14
Deoxycholic Acid (DCA) (%)		16.75
Lithocholic Acid (LCA) (%)		73.23
LCA/DCA Ratio		4.37
SHORT CHAIN FATTY ACIDS		Current
Acetate (%)		62.1
Propionate (%)		30.5
Butyrate (%)		1.5
Valerate (%)		2.0
Total Short Chain Fatty Acids (micromol/g)		176.4
ESTROGEN METABOLISM		Current



Case Study: Addition Over Restriction



Patient Profile

47-year-old perimenopausal woman with fatigue, bloating, and weight gain. No benefit from FODMAP diet.

Intervention & Assessment

Found low diversity and elevated zonulin. Shifted from restriction to a **Mediterranean foundation** + 30-plant protocol, kefir, and targeted supplements.

3-Month Outcome

Significant symptom improvement, increased microbial diversity, and improved inflammatory markers (TGs and hsCRP).

Microbiome & Mediterranean Diet Research



The Paradigm Shift

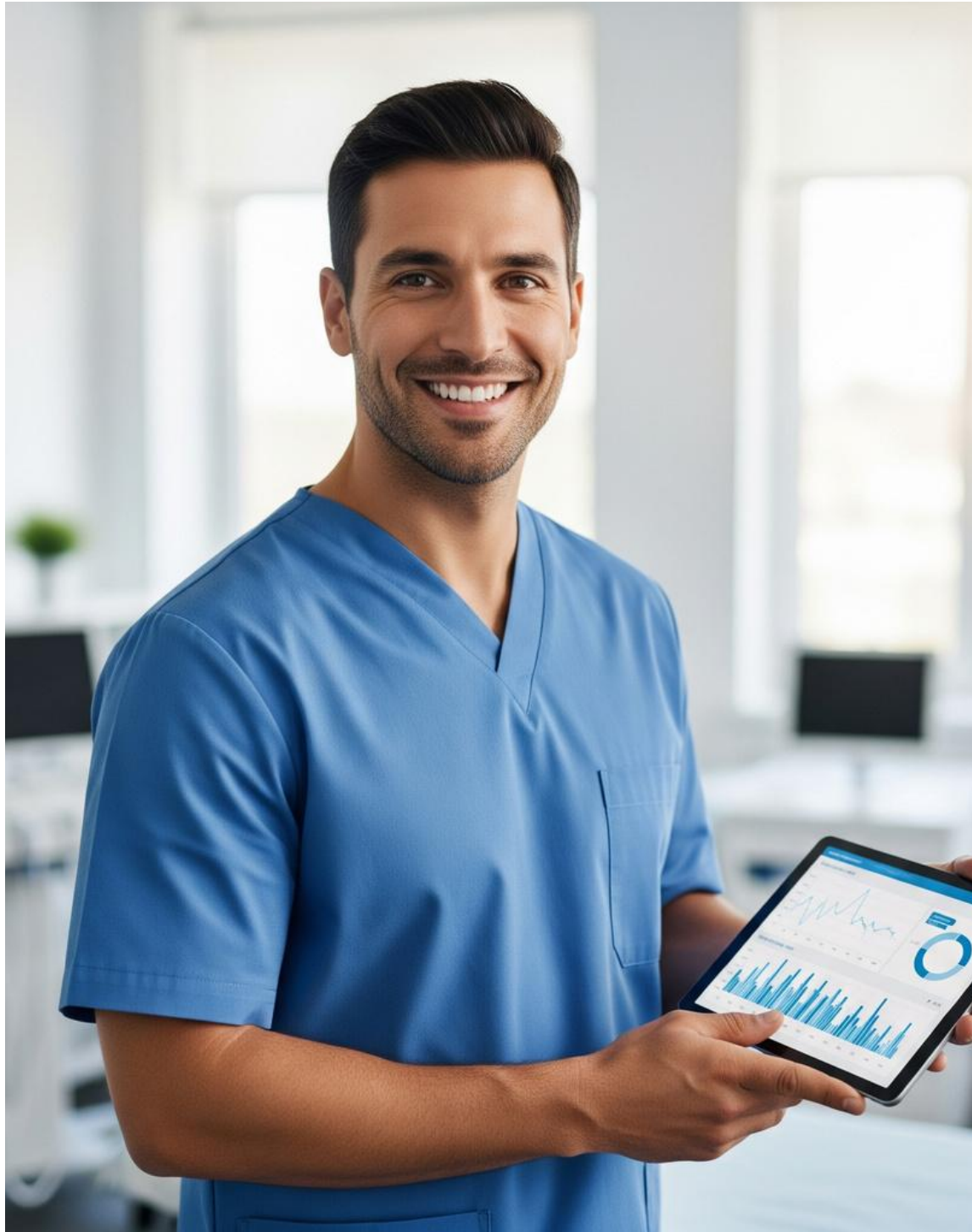
"The Mediterranean diet is not a weight loss plan. It is a **microbiome maintenance programme.**"

Ghosh et al., Gut 2020 · PMID 32066625

12-Month RCT Findings (n=612)

- **Shifted Microbiome:** Mediated by increased SCFA production and reduced secondary bile acids.
- **Reduced Inflammation:** Significant decrease in CRP and IL-17 markers.
- **Clinical Improvement:** Improved frailty scores and enhanced cognitive function.

Standard Stool Tests: A Different Question.



Comprehensive Markers

Intestinal health markers: zonulin, sIgA, calprotectin, EPX, lysozyme
Beyond the binary culture result

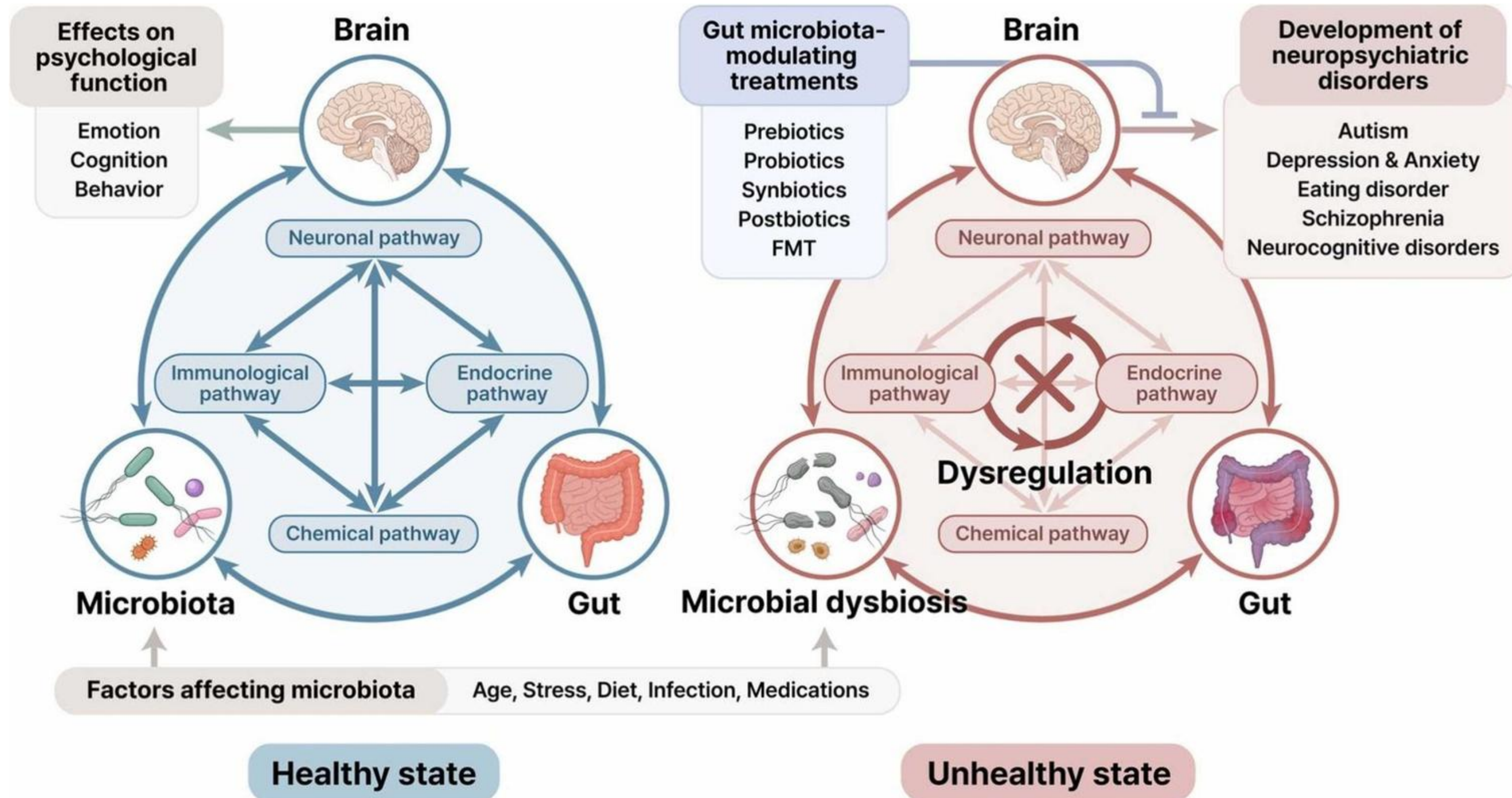
Deep Microbial Insights

PCR/sequencing: 300+ organisms detected; identifies chronic dysbiosis patterns
Quantitative (relative abundance, pathogen load)

Functional Outcomes

SCFA profiles + commensal diversity index
Actionable dietary guidance linked to findings

The Gut-Brain Axis



Seung-Hoon et al., 2025

Type 2 Diabetes And Prediabetes Are Associated With Distinct Microbiome Species

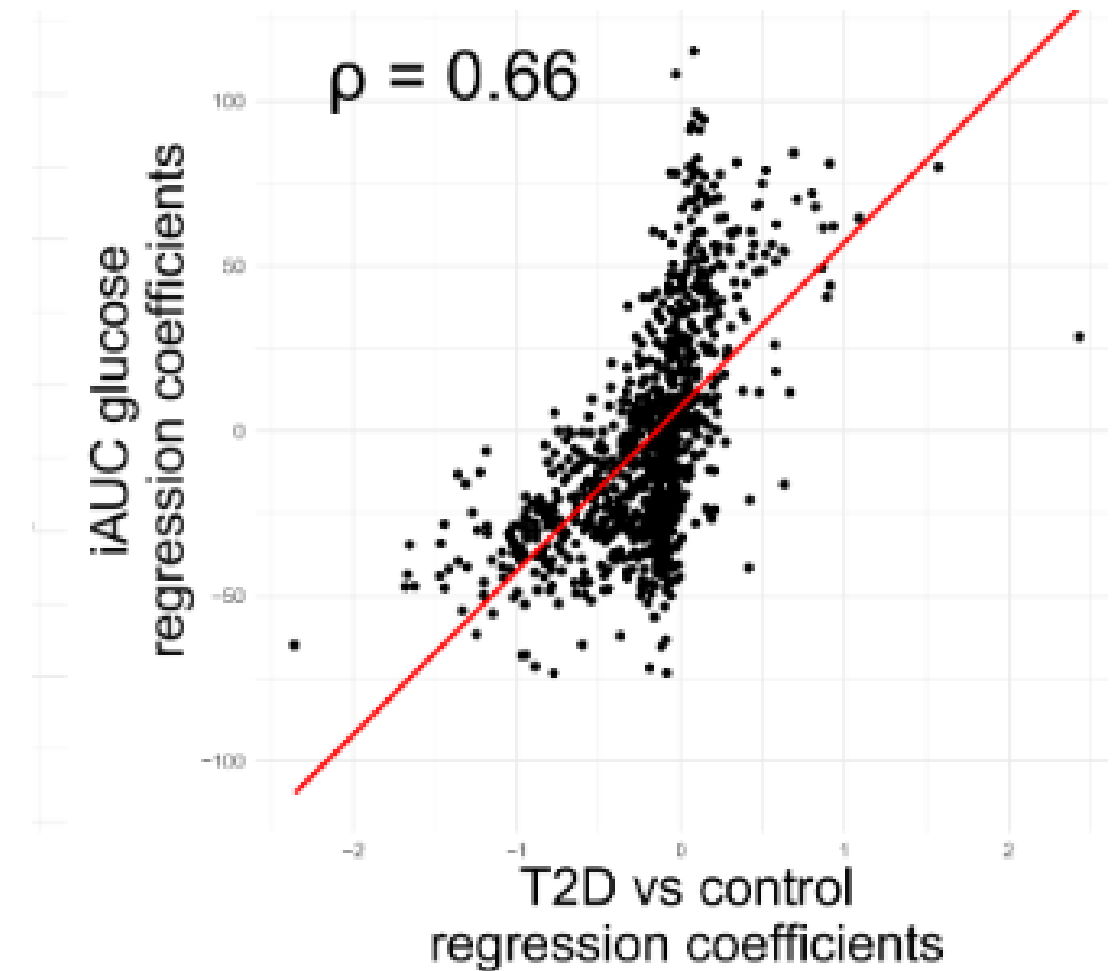
- Microbiome shifts could be due to glucose dysregulation
- Shifts occur before the onset of diabetes
- Diabetes-associated species linked to postprandial glycemia in healthy people

Baldanzi et al., Unpublished manuscript.



Gut microbiome signatures of type 2 diabetes (T2D) prediabetes and sugar spikes in 3,692 cases and > 200,000 controls

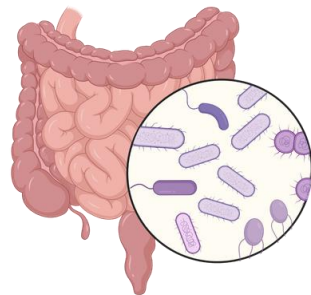
- Machine learning: microbiome signature of T2D replicated in external cohorts (AUC=0.79, replication 0.65-0.78)
- > 700 species differentially abundant in T2D (FDR 5%). Most are novel associations.
- Species linked to T2D are linked to postprandial glucose in individuals without a T2D or prediabetes diagnosis.



(Correlation between species coefficients with iAUC-glucose and with T2D)

Controls = 210,391
Prediabetes = 14,042
T2D = 3,692

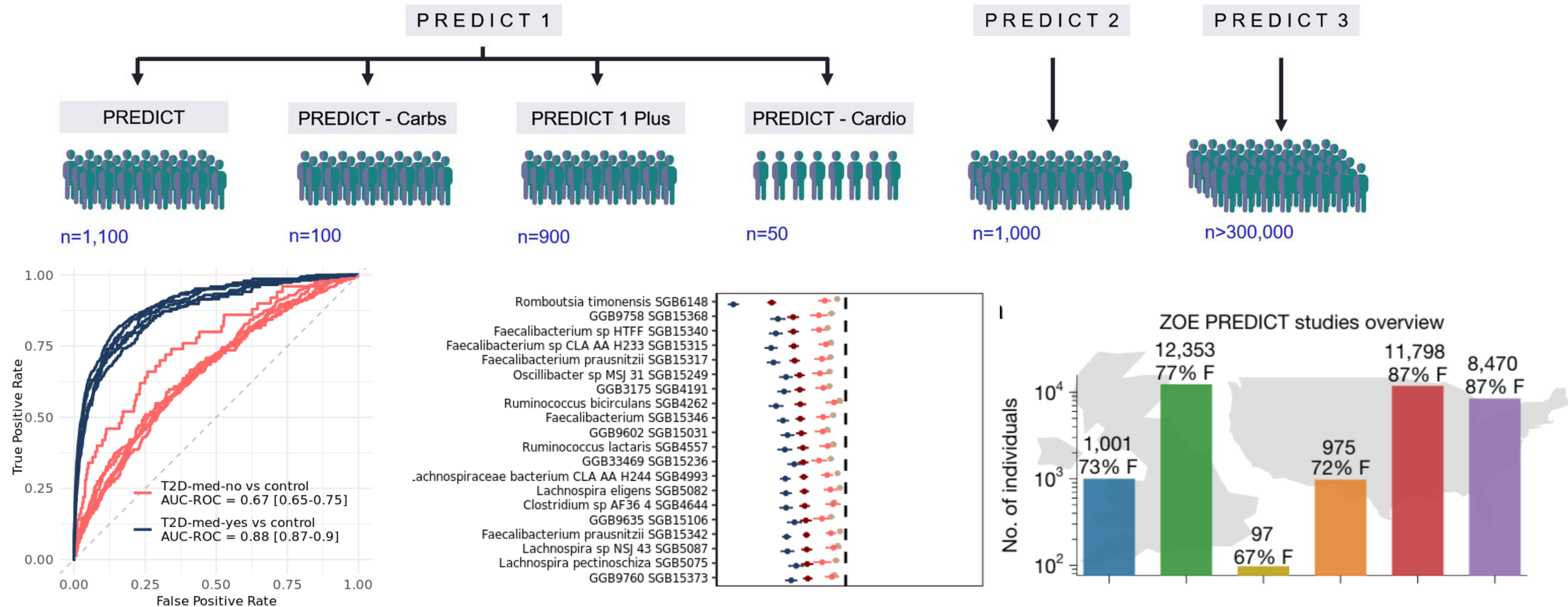
Continuous glucose monitor data in 159,340 individuals without diabetes



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Nutrition

 **VibrantWellness**

Gut microbiome signatures of type 2 diabetes (T2D) need big numbers



- Very strong microbiome signatures of type-2 diabetes

Baldanzi et al., submitted manuscript.



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VibrantWellness

Developing microbiome signatures of early onset colorectal cancer

- **PROSPECT starting point:** microbiome-CRC associations

nature
medicine

ARTICLES

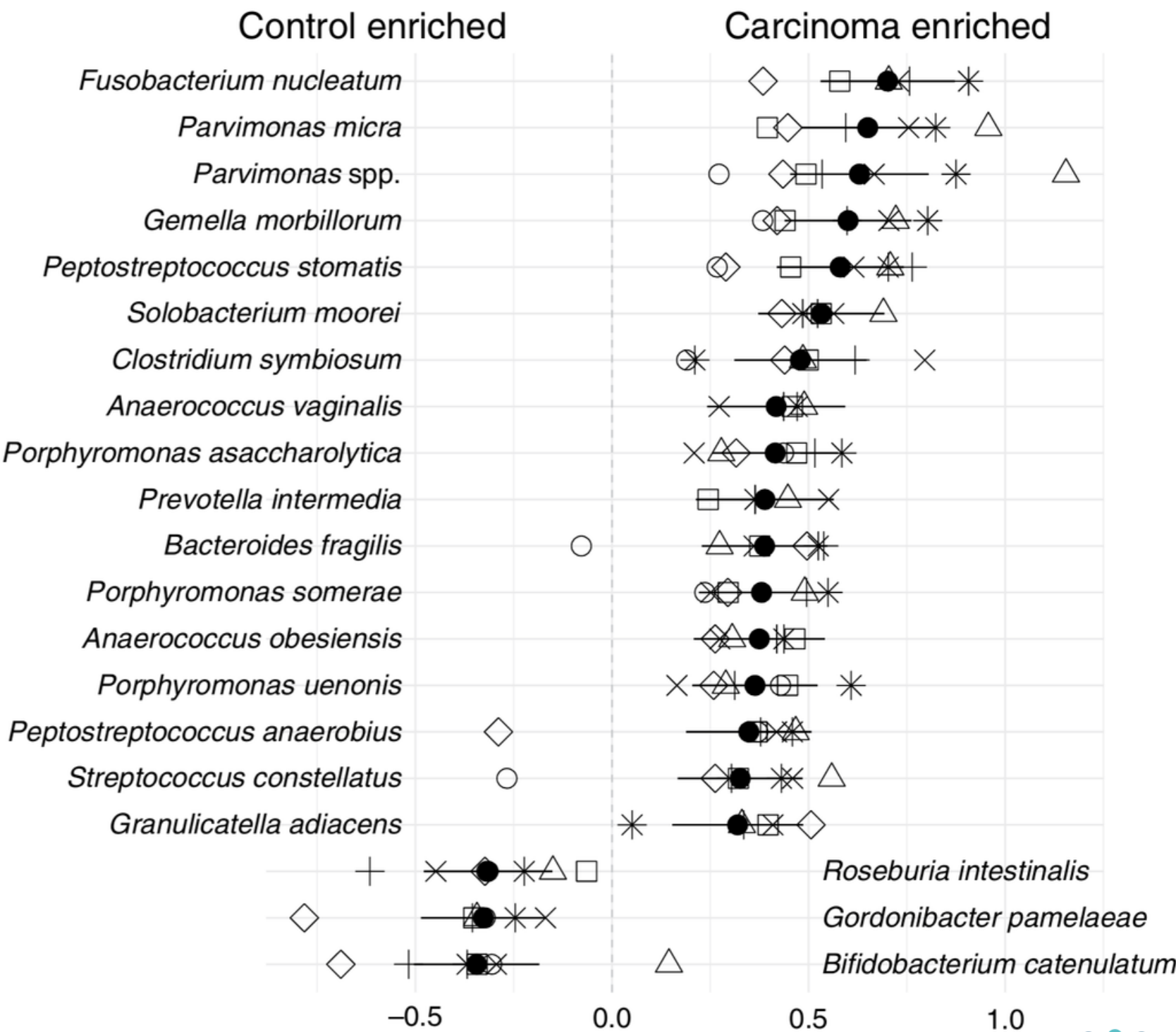
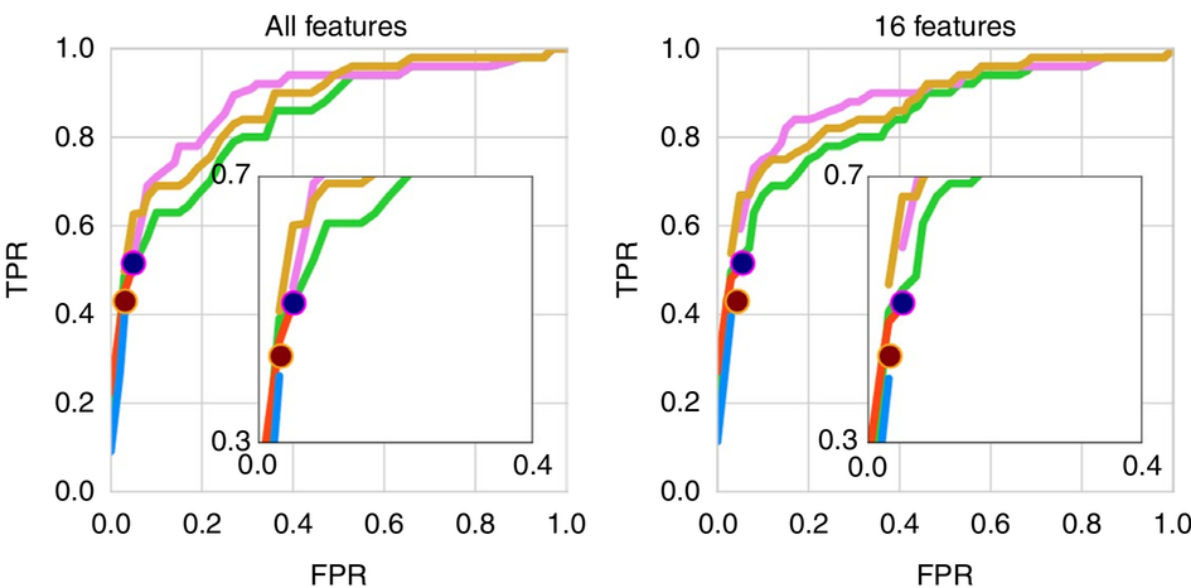
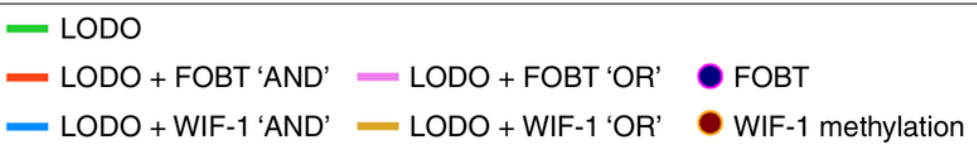
<https://doi.org/10.1038/s41591-019-0405-7>

VOL 25 | APRIL 2019 | 667-678

Metagenomic analysis of colorectal cancer datasets identifies cross-cohort microbial diagnostic signatures and a link with choline degradation

Andrew Maltez Thomas^{1,2,3,32}, Paolo Manghi^{1,32}, Francesco Asnicar¹, Edoardo Pasolli¹, Federica Armanini¹, Moreno Zolfo¹, Francesco Beghini¹, Serena Manara¹, Nicolai Karcher¹, Chiara Pozzi⁴, Sara Gandini⁴, Davide Serrano⁴, Sonia Tarallo⁵, Antonio Francavilla⁵, Gaetano Gallo^{6,7}, Mario Trompetto⁷, Giulio Ferrero⁸, Sayaka Mizutani^{9,10}, Hirotugu Shiroma⁹, Satoshi Shiba¹¹, Tatsuhiro Shibata^{11,12}, Shinichi Yachida^{11,13}, Takuji Yamada^{9,14}, Jakob Wirbel¹⁵, Petra Schrotz-King¹⁶, Cornelia M. Ulrich¹⁷, Hermann Brenner^{16,18,19}, Manimozhiyan Arumugam^{20,21}, Peer Bork^{15,22,23,24}, Georg Zeller¹⁵, Francesca Cordero⁸, Emmanuel Dias-Neto^{3,25}, João Carlos Setubal^{2,26}, Adrian Tett¹, Barbara Pardini^{5,27}, Maria Rescigno²⁸, Levi Waldron^{29,30,33}, Alessio Naccarati^{5,31,33} and Nicola Segata^{1,33*}

Relationship to other non-invasive tests



Dataset	Groups (n)
ZellerG_2014 (ref. ¹⁹)	Control (61)
	Adenoma (42)
	CRC (53)
YuJ_2015 (ref. ¹⁷) ^a	Control (54)
	CRC (74)
FengQ_2015 (ref. ¹⁸)	Control (61) ^b
	Adenoma (47)
	CRC (46)
VogtmannE_2016 (ref. ²⁰)	Control (52)
	CRC (52)
HanniganGD_2018 (ref. ³¹)	Control (28)
	Adenoma (27)
	CRC (27)
Cohort1 (This study)	Control (24)
	Adenoma (27)
	CRC (29)
Cohort2 (This study)	Control (28)
	CRC (32)
Total	Control (308)
	Adenoma (143)
	CRC (313)

(Thomas et al.,
2019)

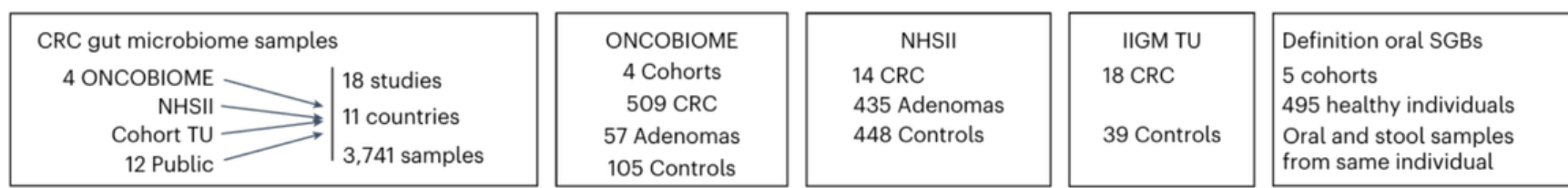
Developing microbiome signatures of early onset colorectal cancer

- PROSPECT results: largest ever CRC meta-analysis

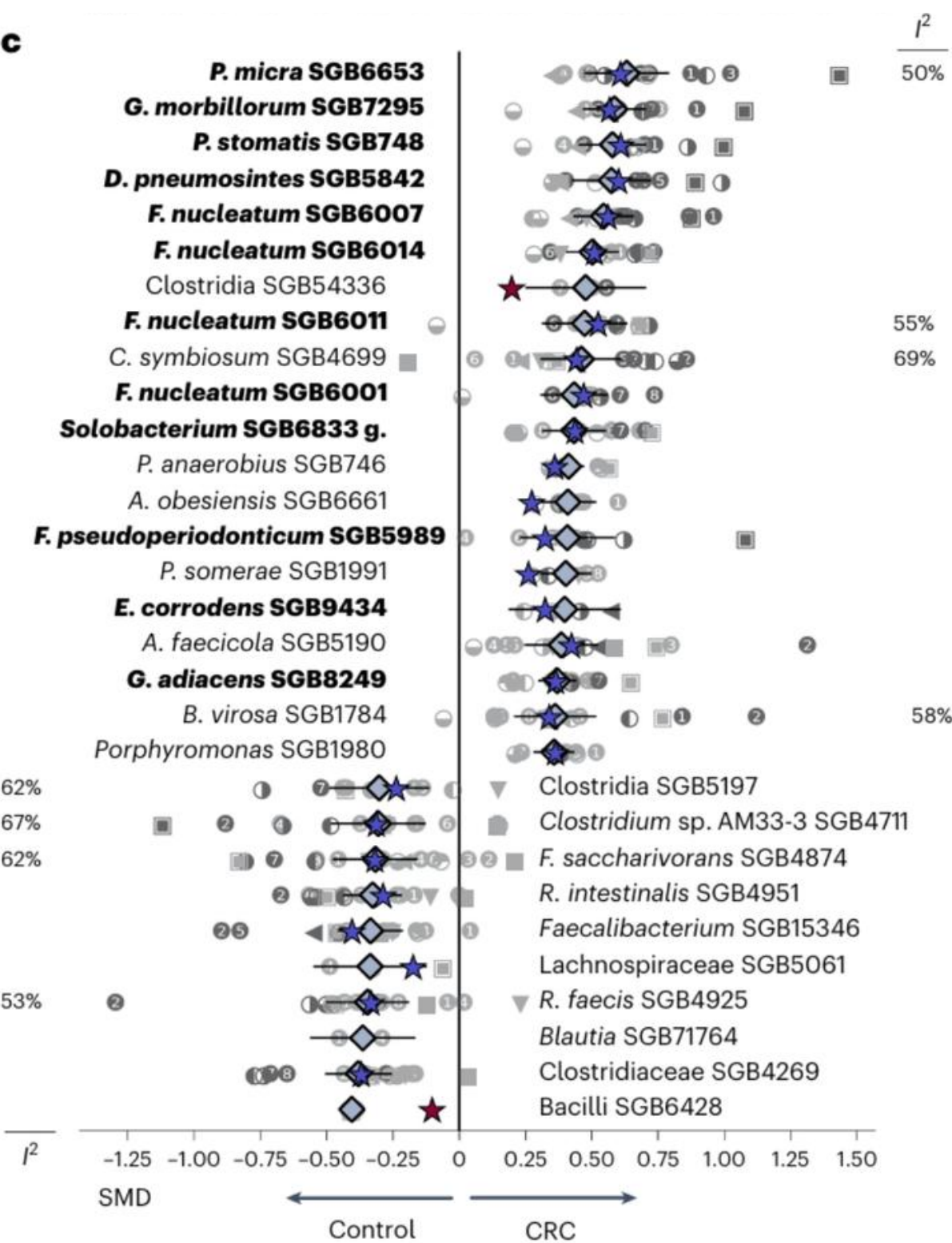
nature medicine 

Article <https://doi.org/10.1038/s41591-025-03693-9>

Pooled analysis of 3,741 stool metagenomes from 18 cohorts for cross-stage and strain-level reproducible microbial biomarkers of colorectal cancer



	Testing														
	Feng, Q. (2015)	Gupta, A. (2019)	Liu, N.N. (2022)	Obón-Santacana, M. (2022)	Thomas, A.M. (2019)	Vogtmann, E. (2016)	Wirbel, J. (2019)	Yachida, S. (2019)	Yang, J. (2019)	Yang, Y. (2020)	Yu, J. (2021)	Zeller, G. (2014)	Cohort 3	Cohort 4	Cohort 6
All SGBs	0.87	0.97	0.85	0.75	0.89	0.81	0.87	0.71	0.93	0.81	0.93	0.83	0.74	0.78	0.95
Oral SGBs	0.81	0.8	0.86	0.78	0.86	0.78	0.87	0.71	0.91	0.82	0.91	0.83	0.77	0.77	0.94
Nonoral SGBs	0.81	0.96	0.78	0.7	0.8	0.78	0.82	0.65	0.86	0.79	0.88	0.79	0.69	0.76	0.86



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- REPUBLIQUE FRANÇAISE
- INSTITUT NATIONAL DU CANCER

Lessons from metagenomics: the diet-microbiome health axis

Article

Nature | Vol 650 | 12 February 2026

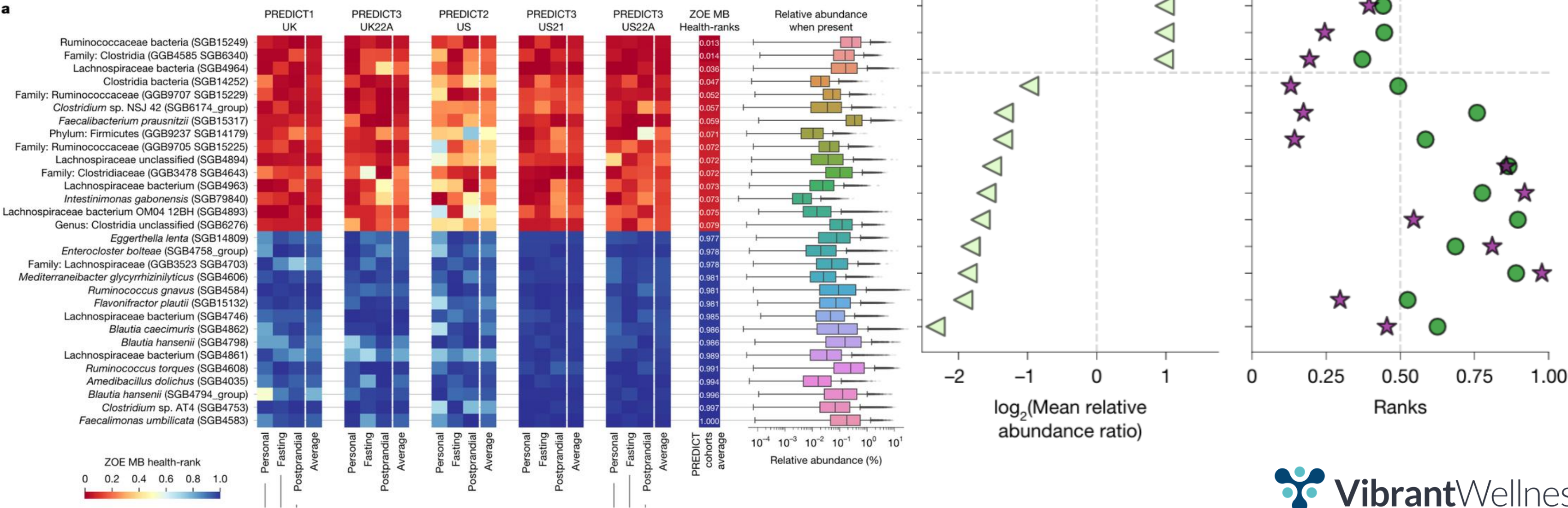
Gut micro-organisms associated with health, nutrition and dietary interventions

<https://doi.org/10.1038/s41586-025-09854-7>

Received: 29 May 2024

Accepted: 4 November 2025

Francesco Asnicar^{1,2}, Paolo Manghi^{1,6}, Gloria Fackelmann¹, Gabriel Baldanzi¹, Elco Bakker², Liviana Ricci¹, Gianmarco Piccinno¹, Elisa Piperni^{1,3}, Katarina Mladenovic¹, Federica Amati^{2,4}, Alberto Arrè², Sajaysurya Ganesh², Francesca Giordano², Richard Davies², Jonathan Wolf², Kate M. Bermingham^{2,5}, Sarah E. Berry^{2,5,7}, Tim D. Spector^{2,4,7} & Nicola Segata^{1,3,4,7}



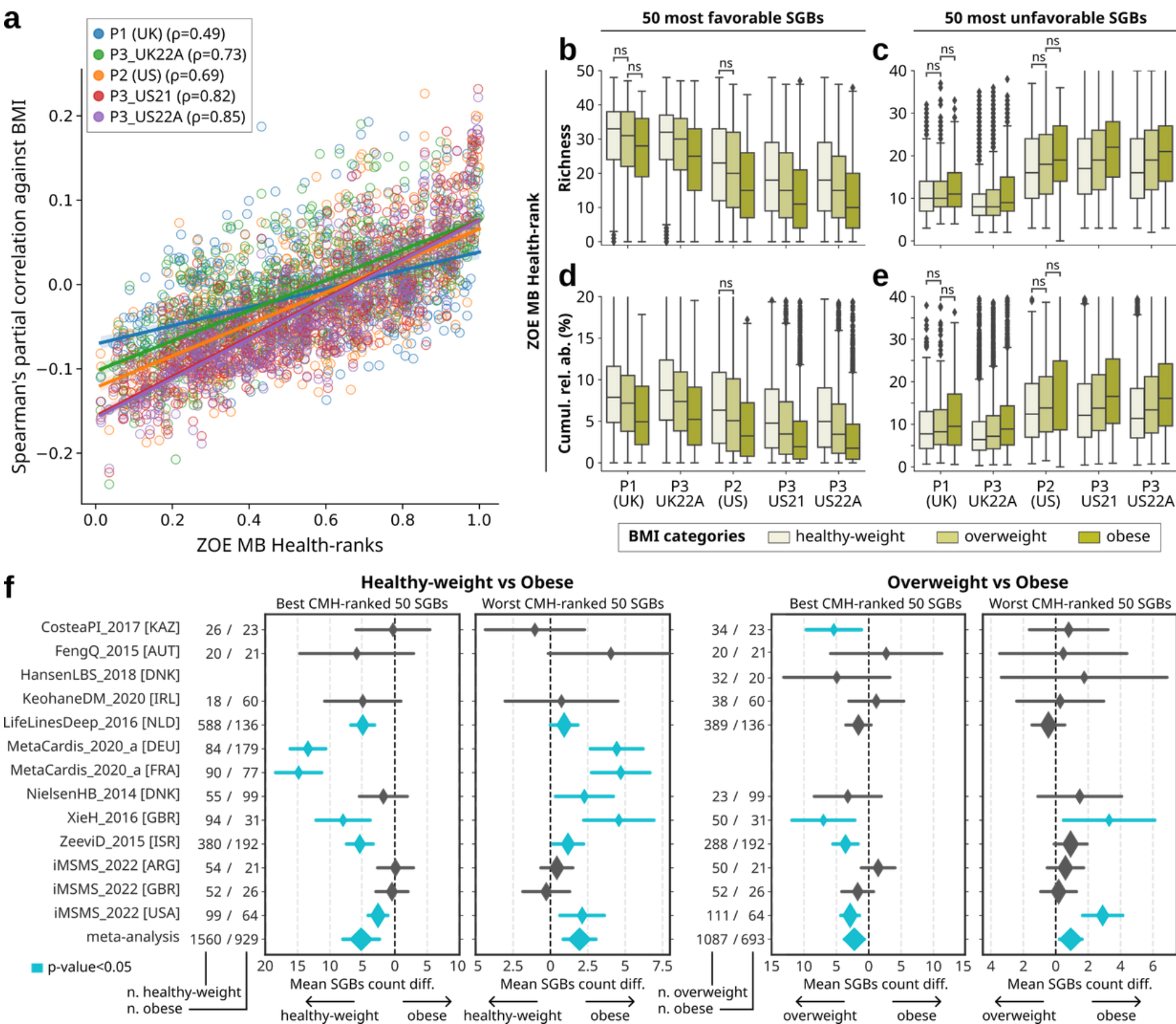
Longitudinal Microbial Testing:

82% of adherent ZOE members improve their gut
microbiome score at retest



A new ZOE Gut health score - based on 100 common microbes

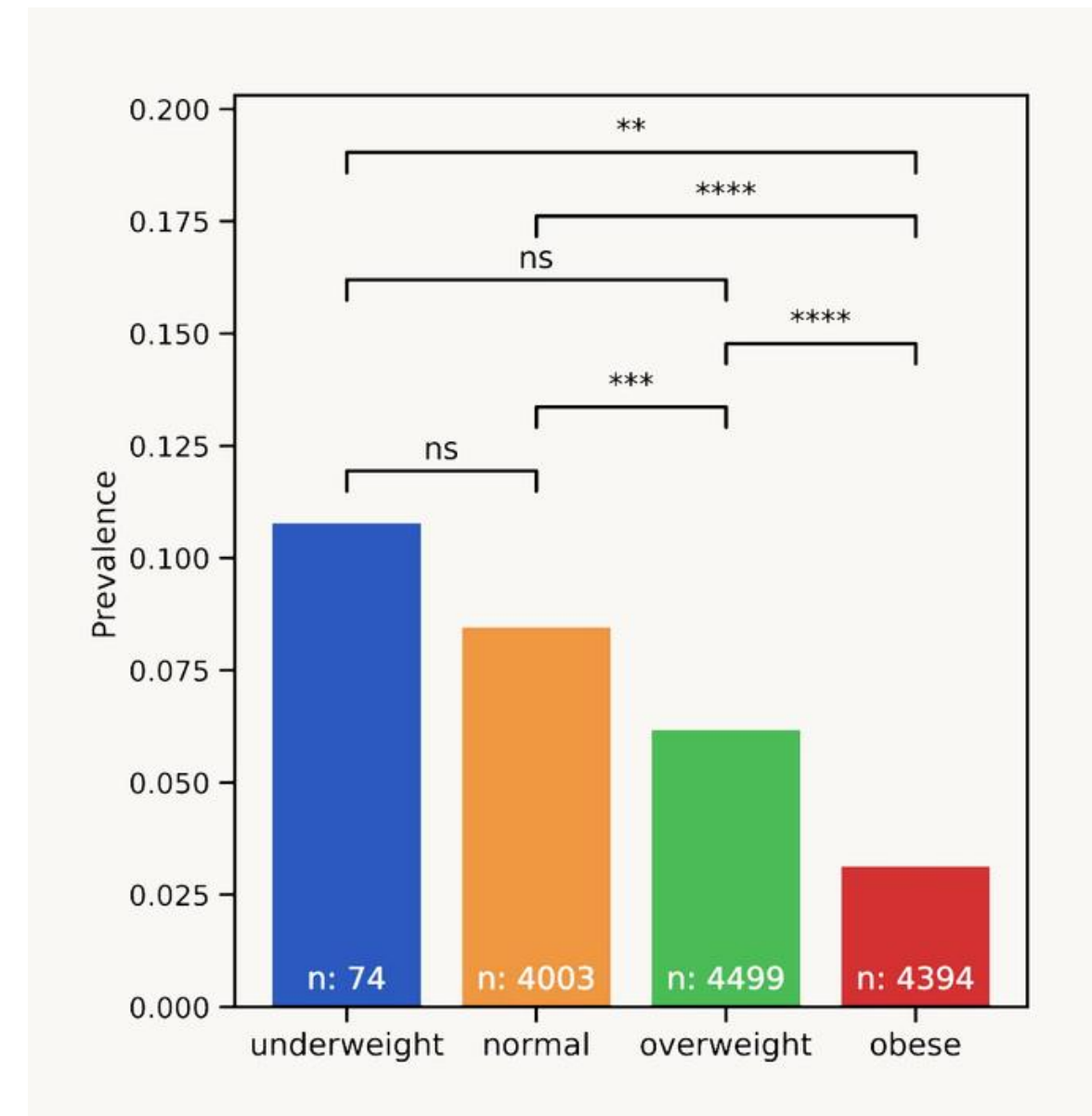
Gut microbiome species indicative of cardiometabolic health are modulated by diet in large and interventional cohorts of over 34,000 individuals



Asnicar et al Nature 2025

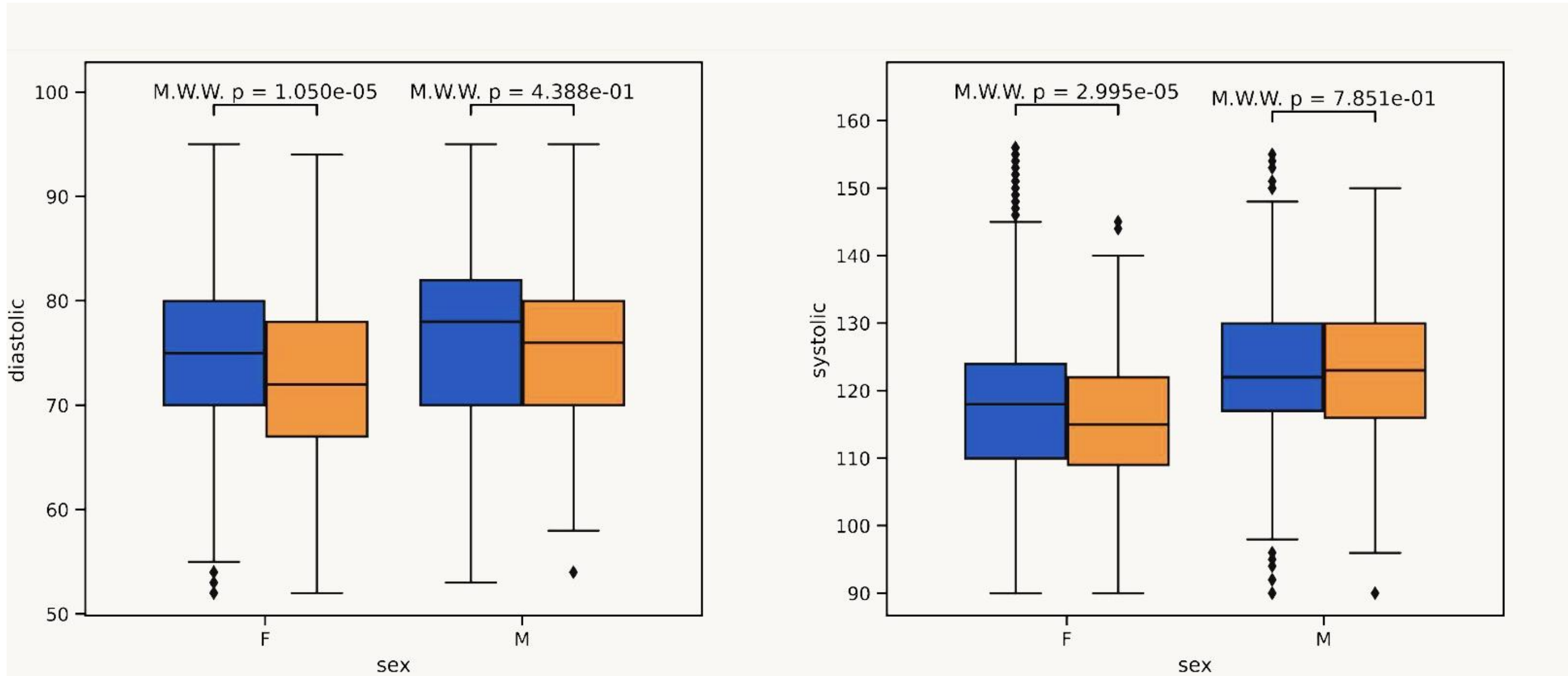
Prevalence of Blastocystis in the different BMI categories from Predict 3 ~13,000 subjects

- Prevalence in US – low 5 percent
- Prevalence in UK - mod 24 percent
- Prevalence in Non developed populations – 100%
- Prevalence in Hunter Gatherers – 100%
- Prevalence in ancient samples BC – 100%



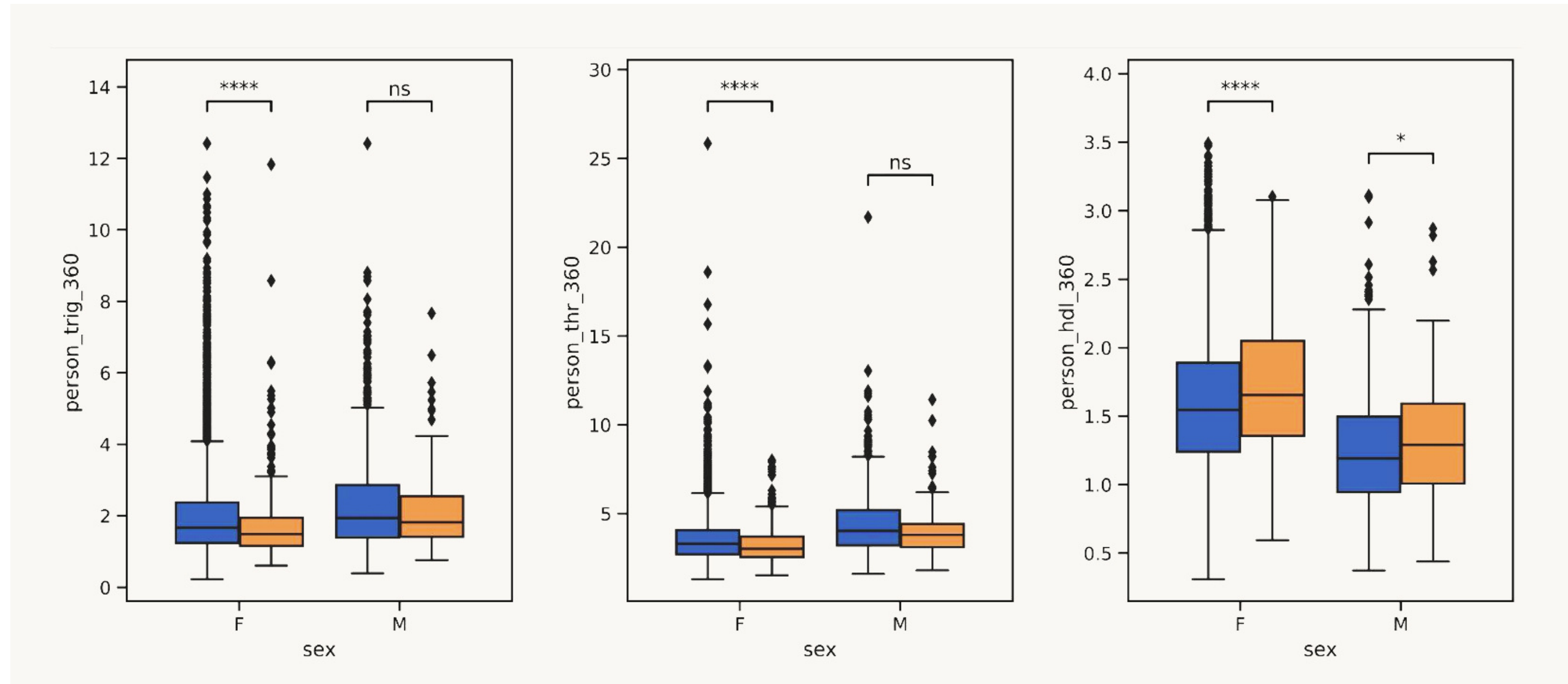
Piperni et al., In press Cell 2024

Blood pressure (diastolic and systolic) of Blastocystis presence/absence dividing by sex shows significant effect in females



Piperni et al., Cell 2024

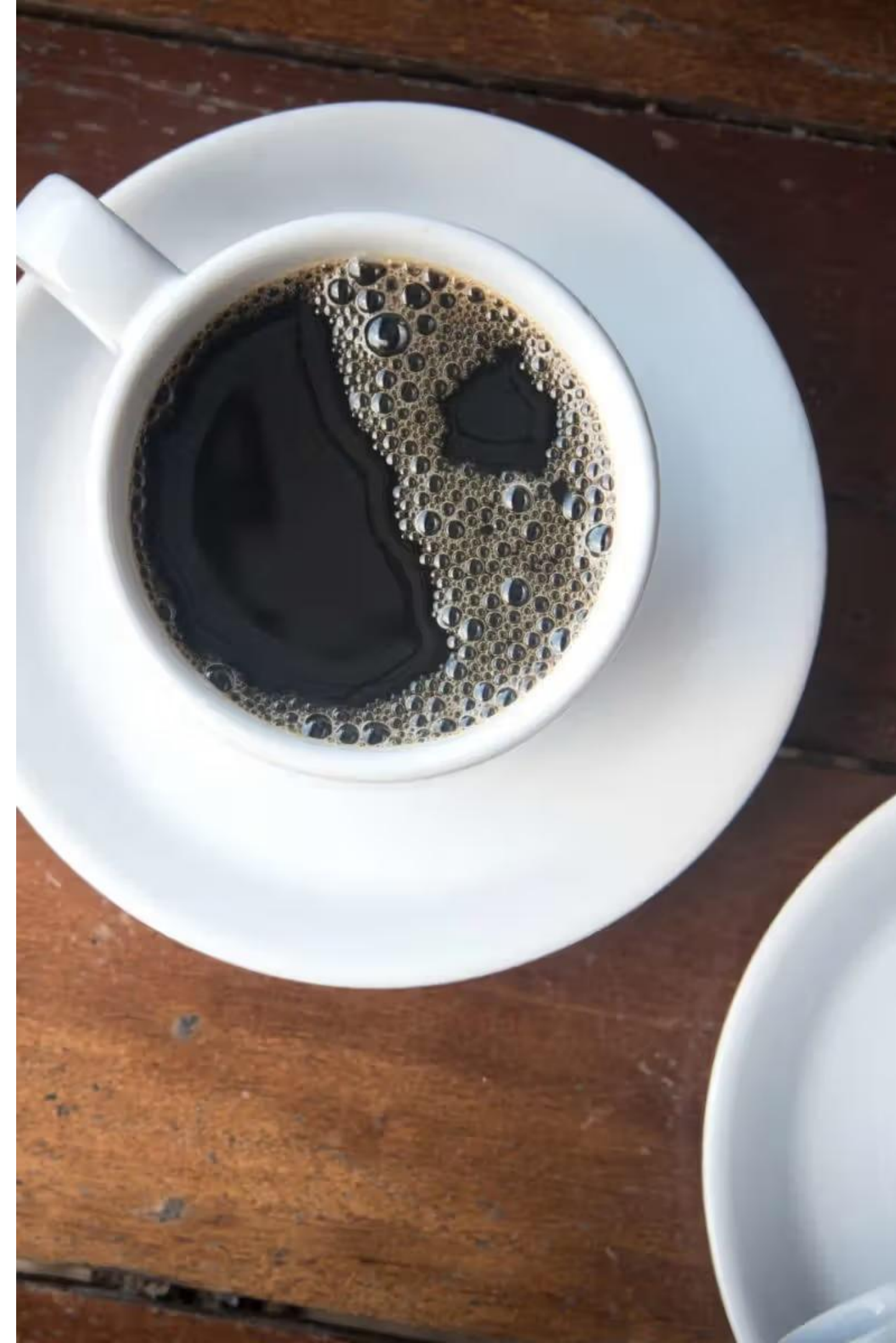
Postprandial responses (at 6h) for triglycerides, ratio of total CHOL and HDL CHOL (THR), and HDL stratifying by sex –showing main effect in females



Piperni et al., 2024

Coffee and microbes

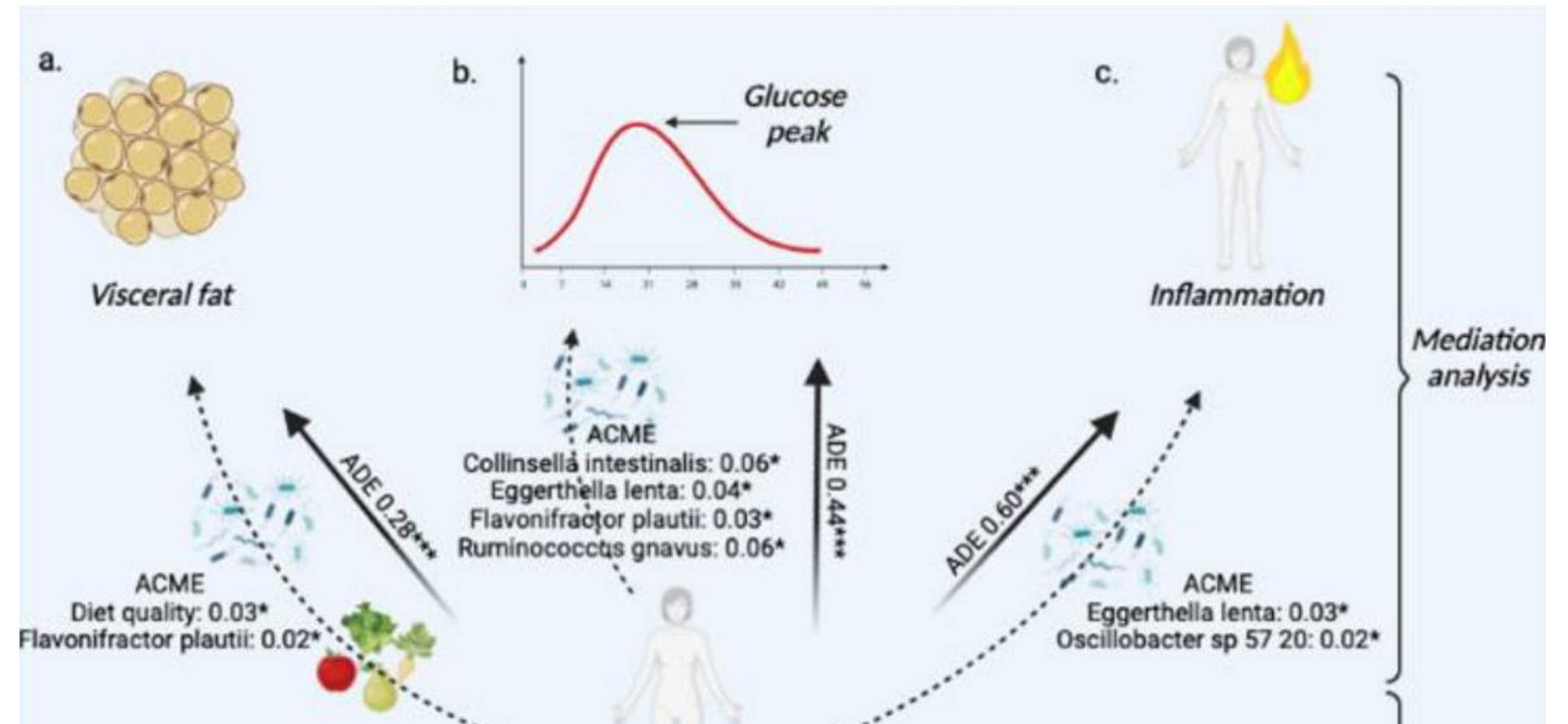
- [PREDICT 1](#) research revealed coffee had the strongest food-microbiome association, out of ~150 food and drink items
 - Unique microbiome signature related to drinking coffee.
 - ***L. asaccharolyticus*** - up to 8 times more abundant in coffee drinkers compared with non-drinkers
 - *In vitro* studies showed that coffee (and decaf coffee) stimulated the growth of *L. asaccharolyticus*
 - Analysis implicates *L. asaccharolyticus* is involved in coffee metabolism, likely via the chlorogenic acid pathway.
- (Manghi et al, 2024 Nat Micro.)



Does The Microbiome Play A Role In The Menopause Transition And Health?

Diet & microbiome mediates relationship between menopausal status and visceral fat

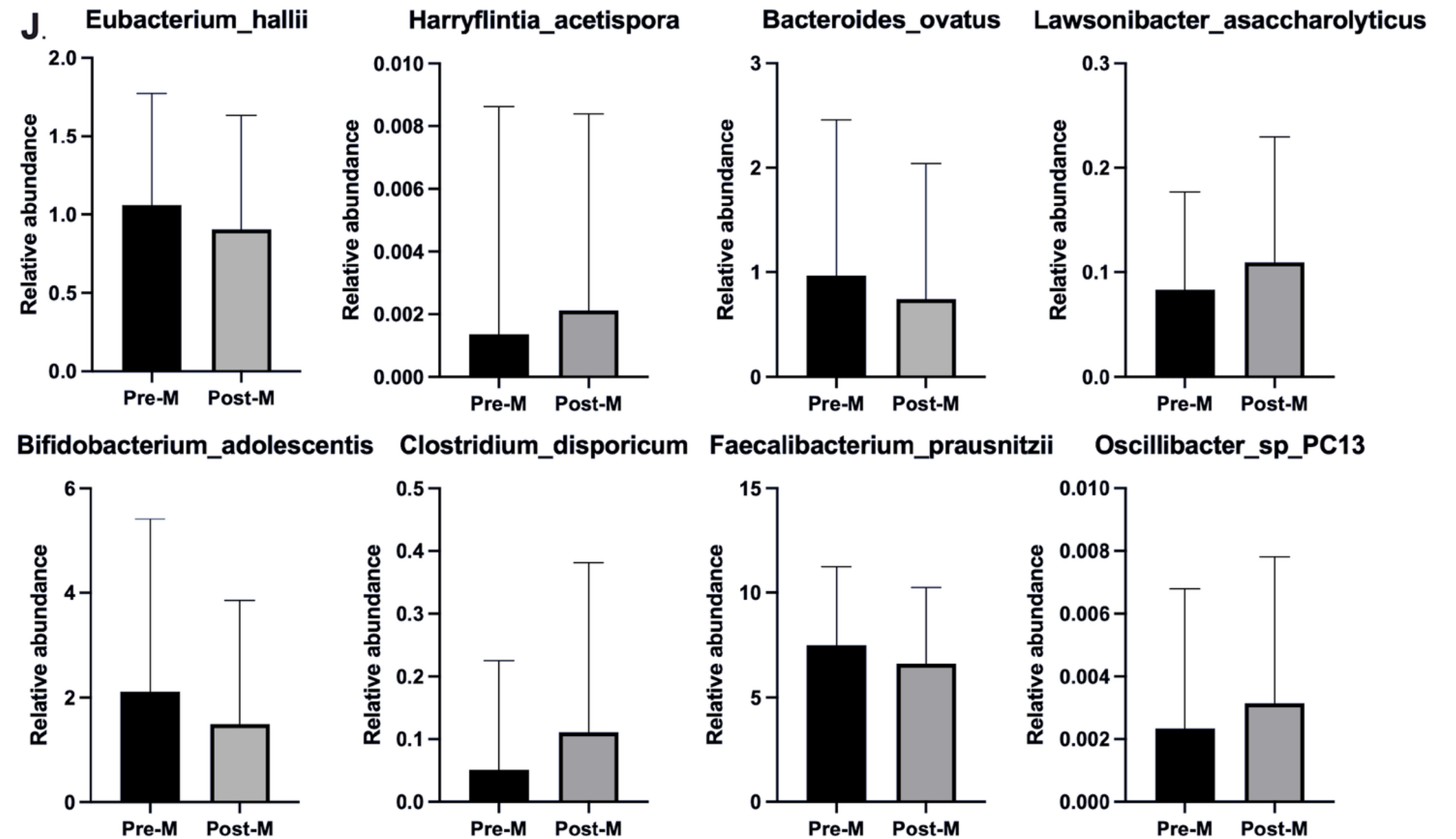
Bermingham et al., 2022



Microbes Associated With Menopausal Status

Bermingham et al., 2022

Differentially abundant taxa



PREDICT 1

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HEAD NUTRITIONIST AT ZOE &
SUNDAY TIMES BESTSELLING AUTHOR

Foreword
by Professor
Tim Spector

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