

Gut microbiome in horses: the sprint towards endurance fitness

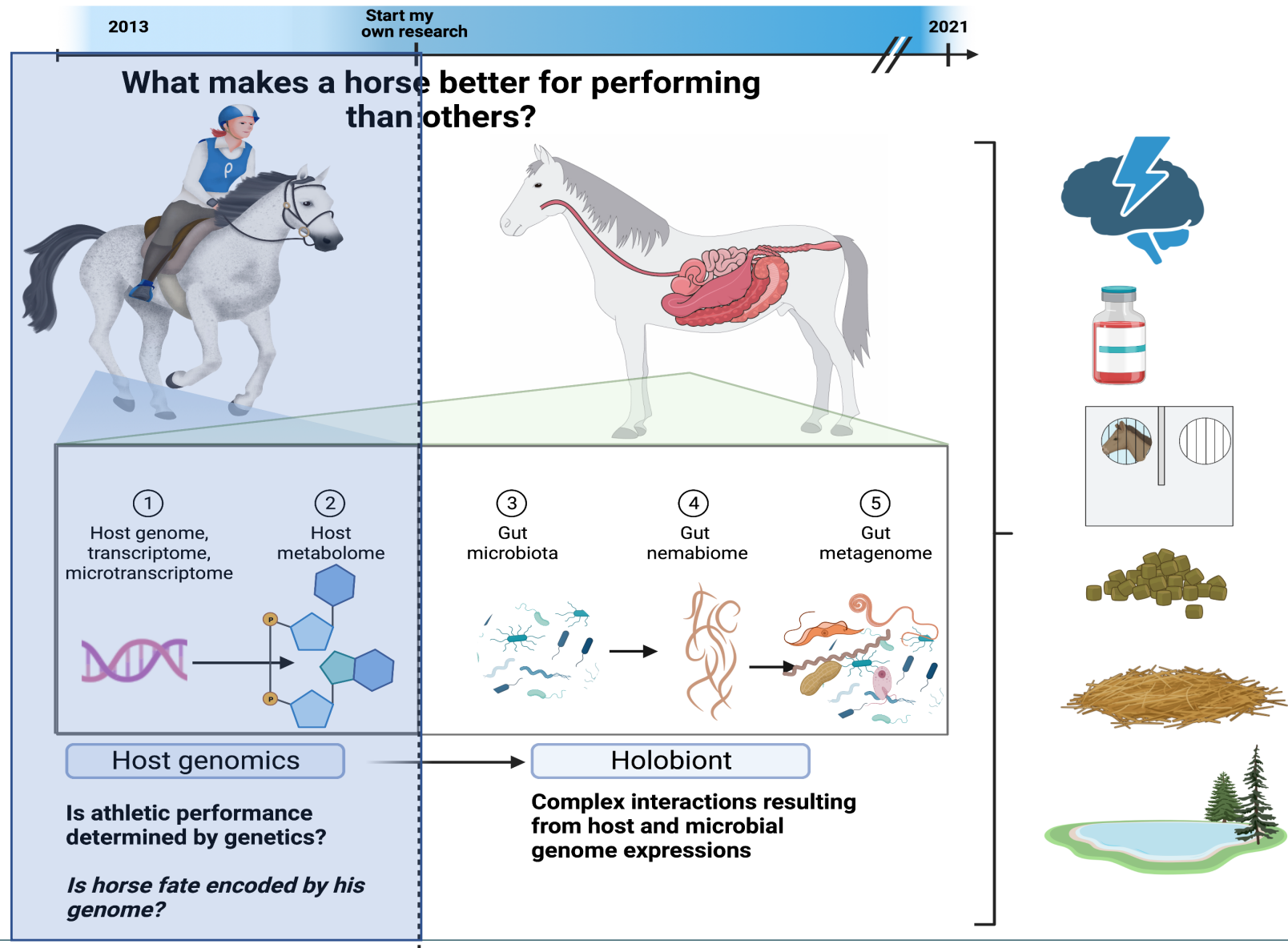
Núria MACH, PhD

UMR, INRAE, ENVT, Interactions Hôtes-Agents Pathogènes

Biopuces, FEBRUARY, 9TH, 2023



➤ OVERVIEW: MY IMPRINT AS A RESEARCHER AT GABI



➤ RESEARCH AXIS: THE GUT MICROBIOME IN HORSES; THE SPRINT TOWARDS ENDURANCE FITNESS



Allison Clark

Dolors Fuster-
Botella
Jesús María López
Alizé Nevot



Dr. Eric Barrey

➤ RESEARCH AXIS 2: THE ENDURANCE HORSES

Endurance exercise: prolonged cardiovascular efforts —such as running, cross-country skiing, cycling, aerobic exercise, or swimming —performed for an extended period

Joyner et al. 2008. J Physiol

| Endurance horses



Who are they?

- Arabian breed (oldest horse breeds)
- Bedouin people in the desert
- Small horses
- Large cardio-respiratory system
- Higher proportion of slow-twitch muscle fibers
- Run 160 km/day

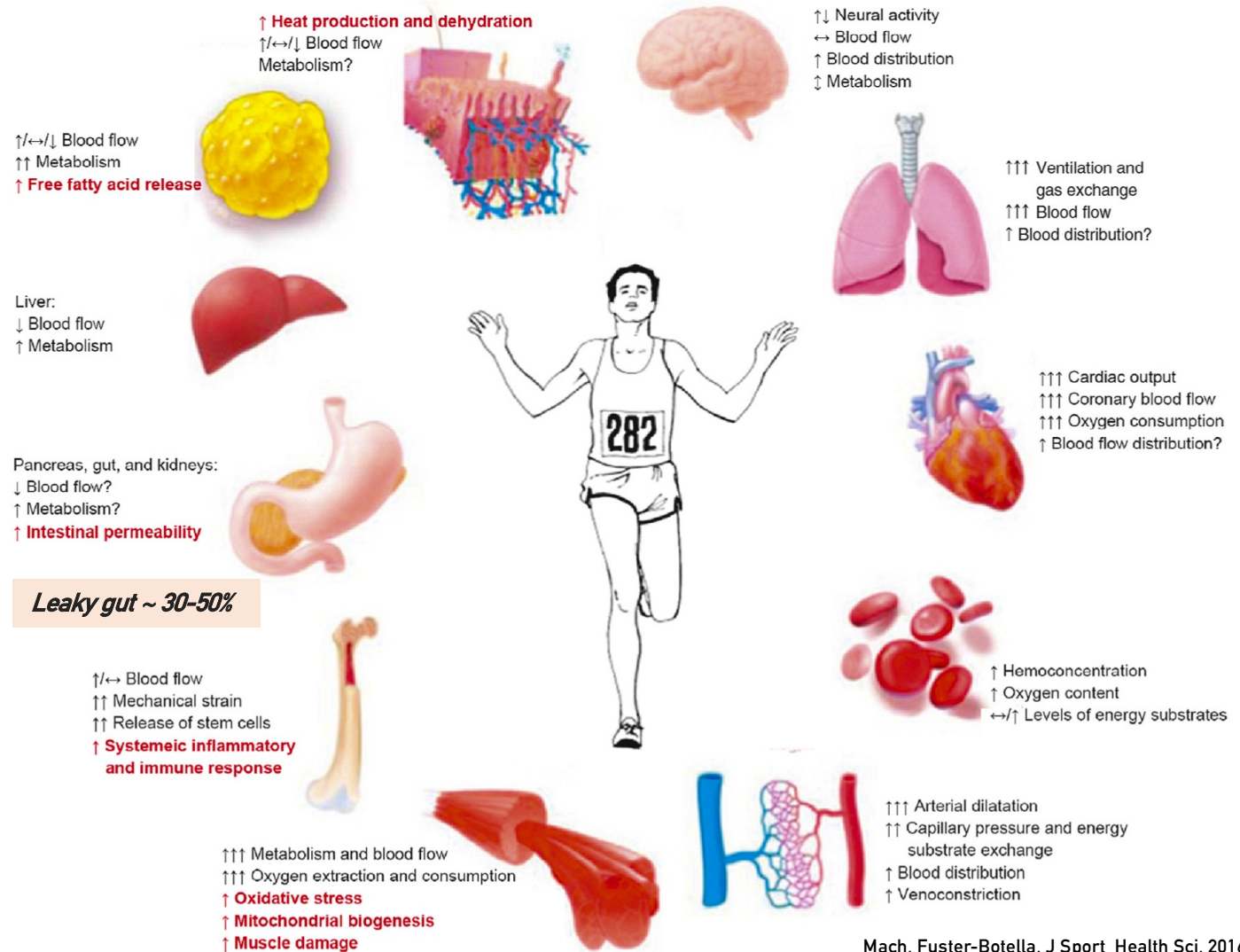
➤ RESEARCH AXIS 2: THE ENDURANCE HORSES



➤ RESEARCH AXIS 2: THE ENDURANCE ADAPTATION

*Complex interplay:
musculoskeletal-
cardiovascular-
respiratory system
+ motivation*

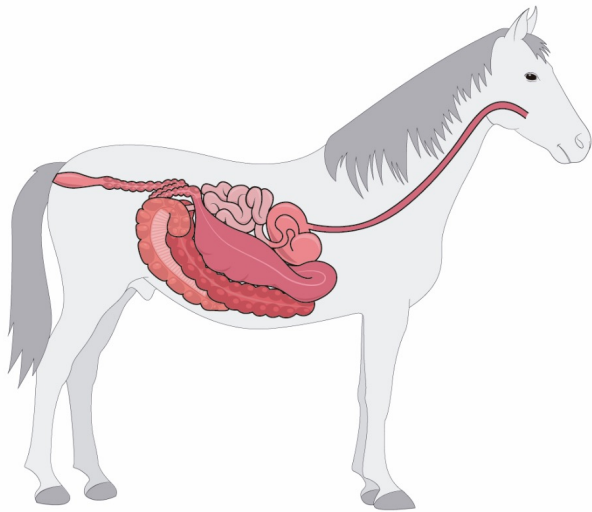
(Dohnalová et al 2021)



Mach, Fuster-Botella, J Sport Health Sci, 2016.

➤ RESEARCH AXIS 2: OBJECTIVES

Objectives

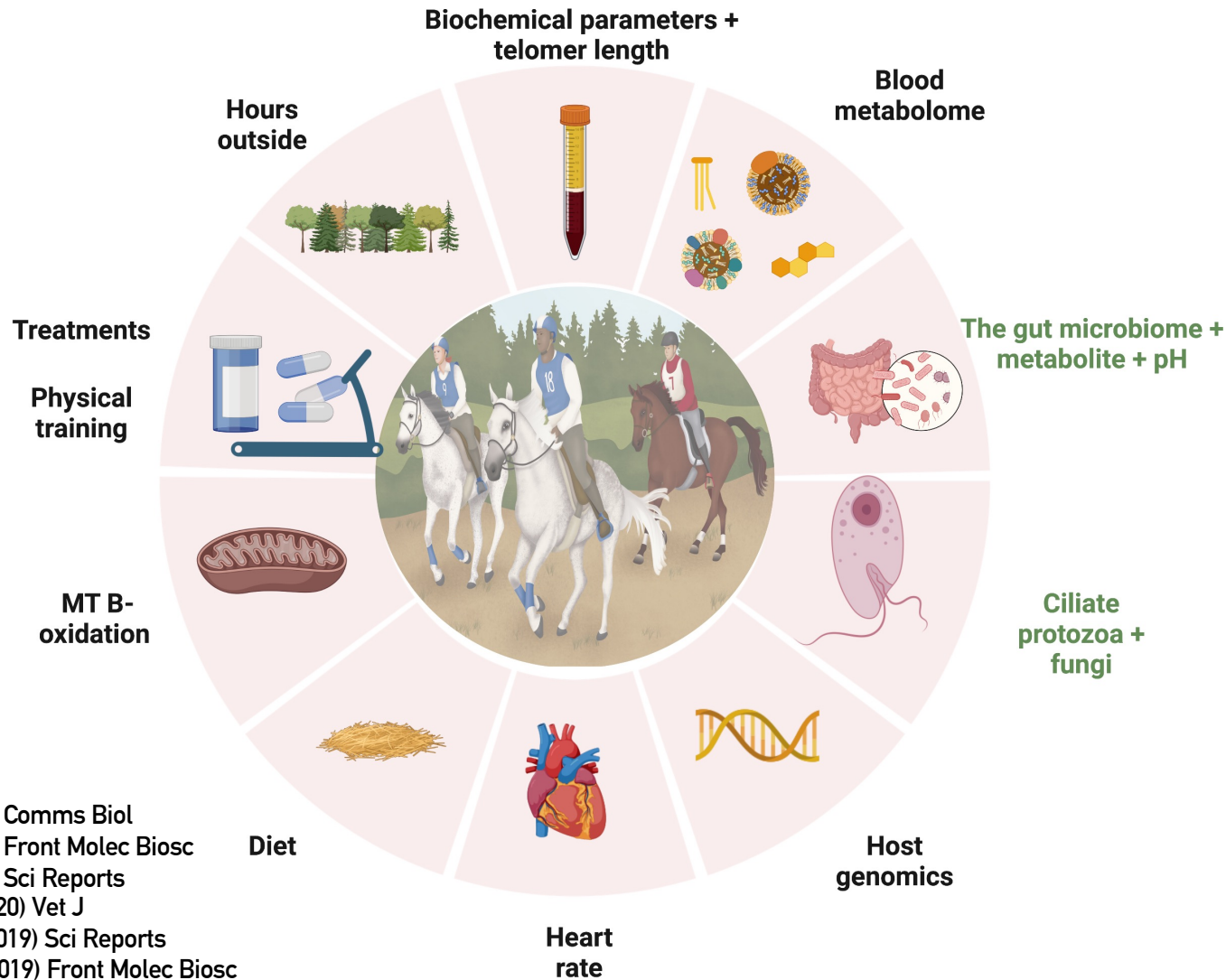


To identify the relationship between host exercise adaptation and the gut microbiome

To reveal biomarkers of athletic performance

➤ RESEARCH AXIS 2: THE COHORT AND DESIGN

150 ENDURANCE HORSES TO ➤ 52 ENDURANCE HORSES AFTER RACE



Mach et al (2022) Comms Biol
 Mach et al (2021) Front Molec Biosc
 Mach et al (2021) Sci Reports
 Van der Kolk (2020) Vet J
 Plancade et al (2019) Sci Reports
 Le Moyec et al (2019) Front Molec Biosc

➤ RESEARCH AXIS 2: CROSS-LINKED METHODS

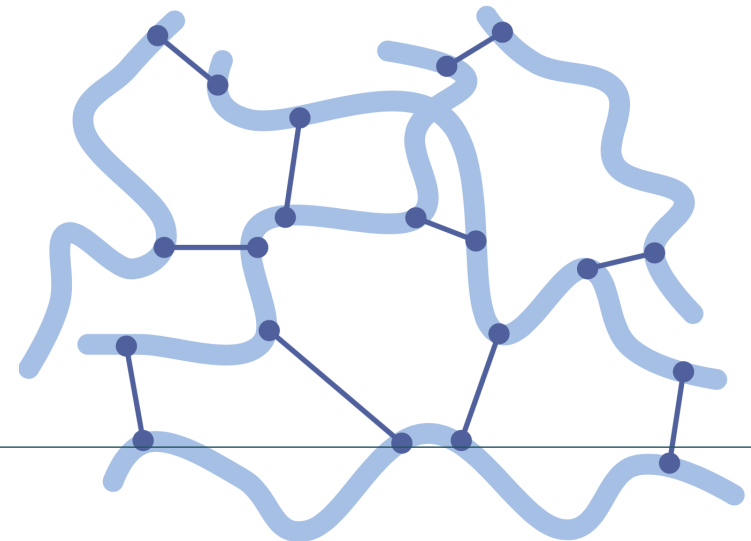
Techniques

- Transcriptome and μ transcriptome analysis
- Metabolomic analysis: ^1H NMR
- Acylcarnitine profiling: ESI-MS-MS
- Biochemical assays: photometric tests
- SCFA: gas chromatography
- Fecal metagenome + resistome : 16S rRNA gene amplicon + shotgun

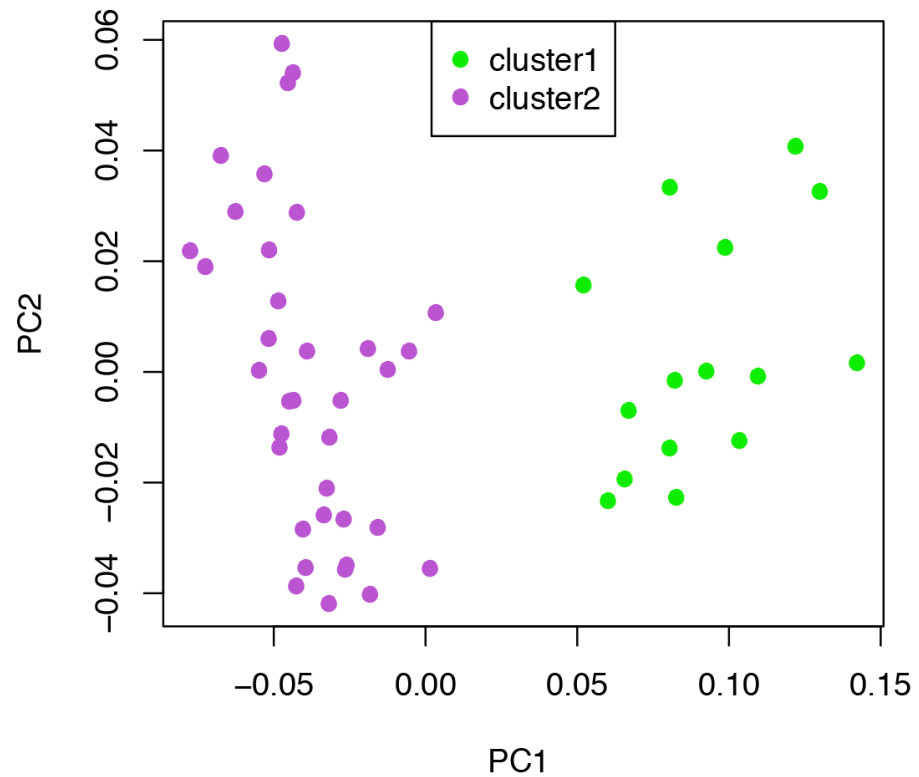
Statistical methods

- Multiple testing: ANOSIM, PERMANOVA, DESeq2
- Mixed models (multiple time points): GLMM, MaAslin
- Unsupervised and supervised machine learning methods: oPLS, sPLS-DA, dbRDA forward sel; sCCA; N -integration algorithm DIABLO
- Network inference: SPIEC-EASI; PCIT

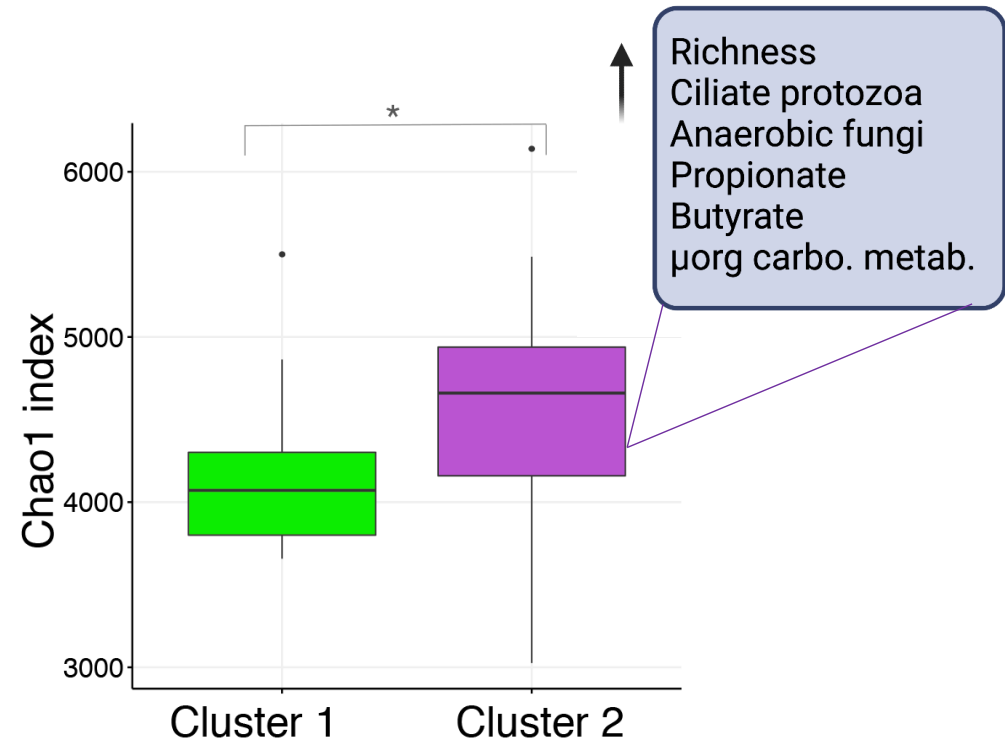
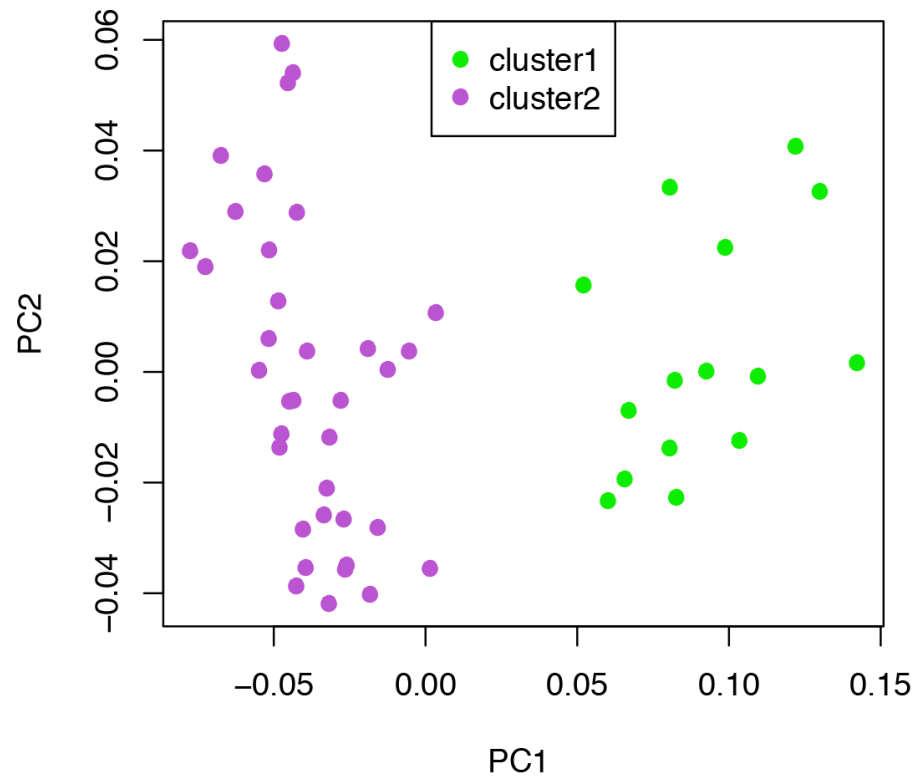
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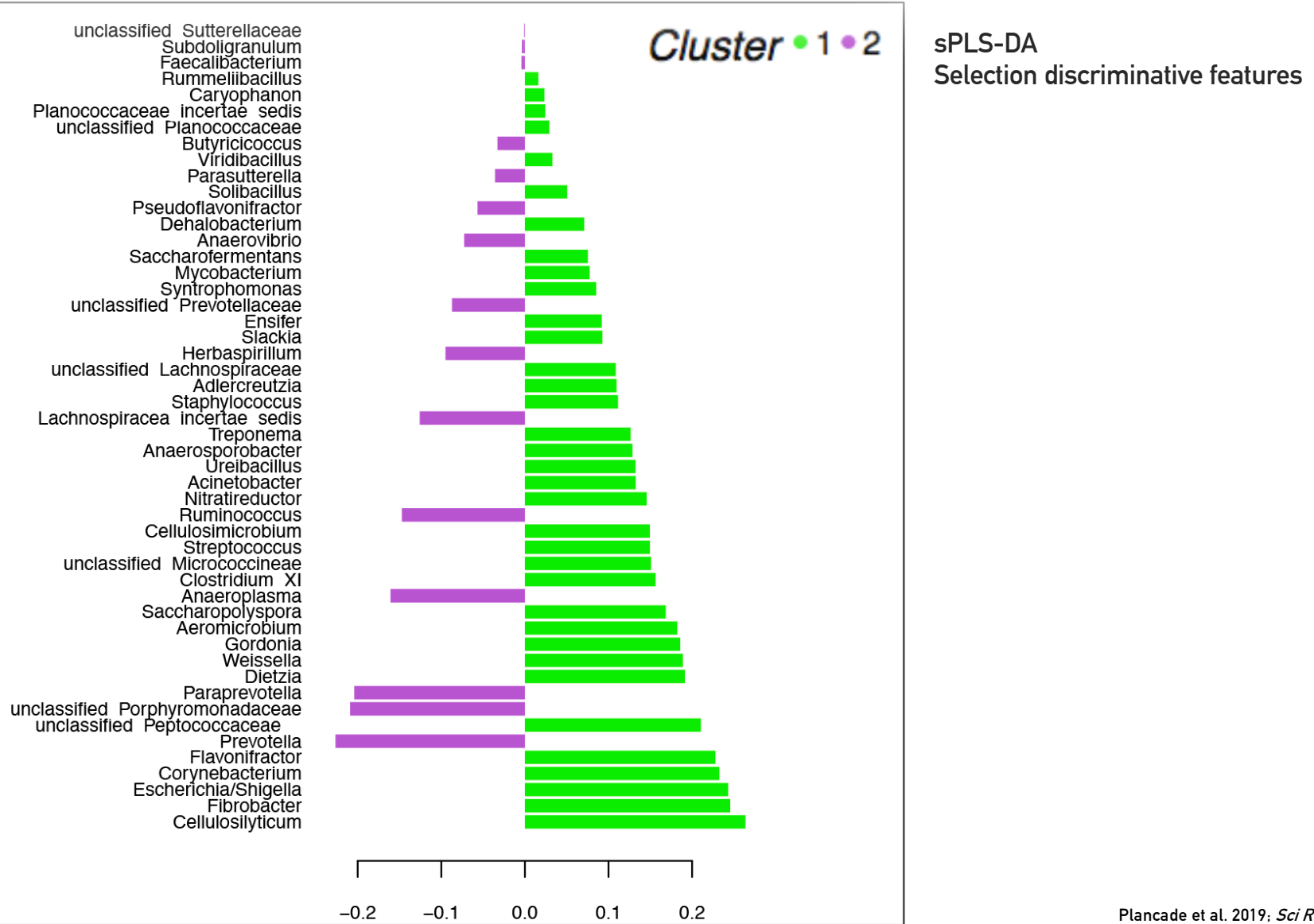
➤ RESEARCH AXIS 2: TWO MICROBIOTA CLUSTERS 16S rRNA



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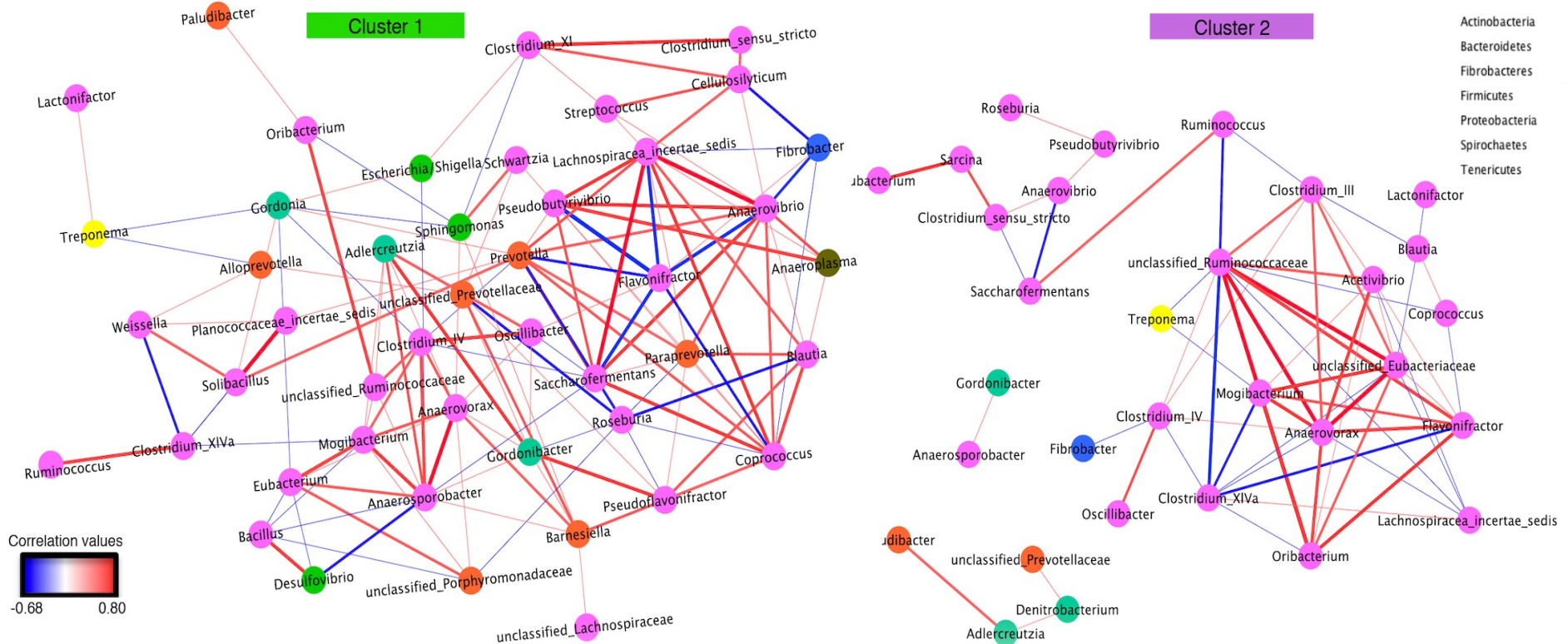
RESEARCH AXIS 2: TWO MICROBIOTA CLUSTERS 16S rRNA



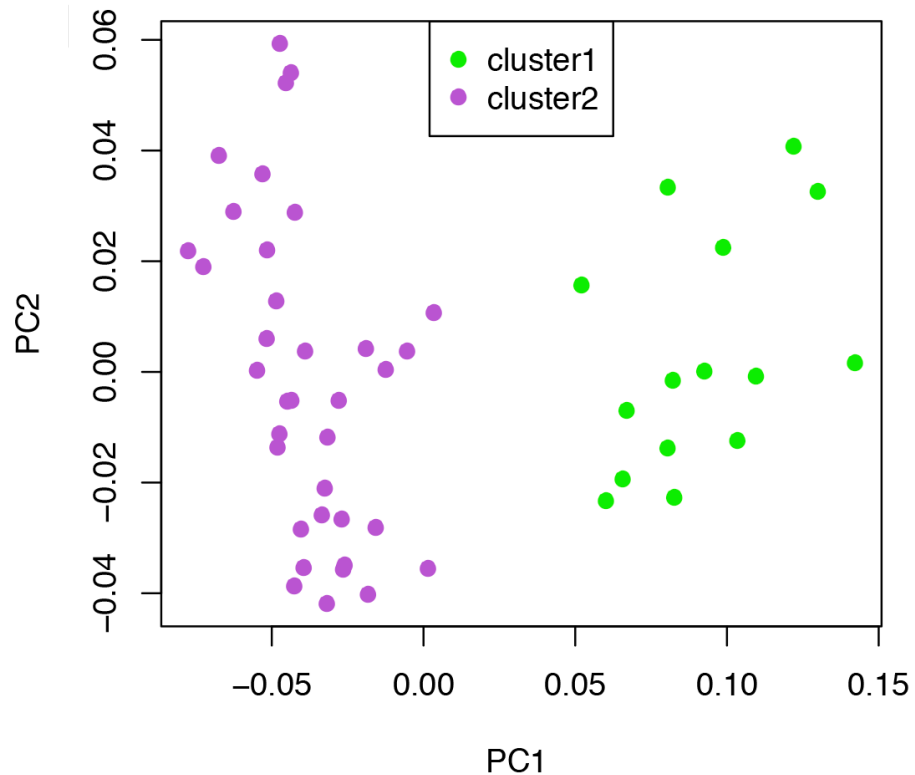
Plancade et al. 2019; *Sci Reports*

RESEARCH AXIS 2: TWO MICROBIOTA CLUSTERS 16S rRNA

PCIT: co-occurrence based on partial correlation



➤ RESEARCH AXIS 2: TWO MICROBIOTA CLUSTERS 16S rRNA



Host kinship

Age, Breed

Distance

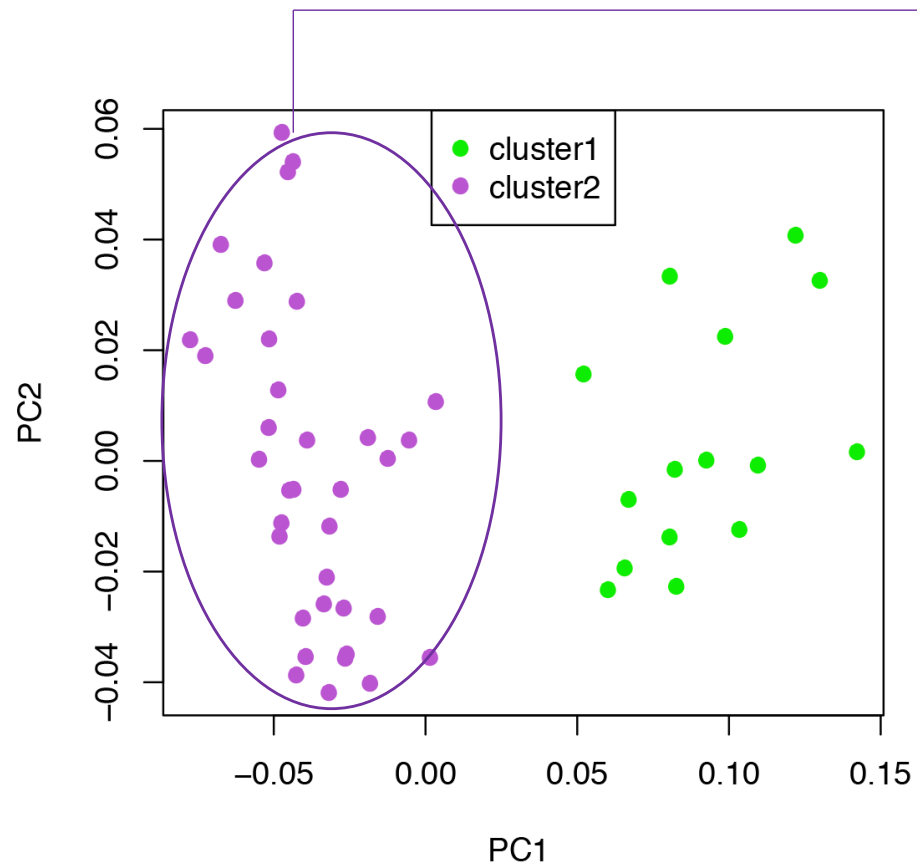
Gut environment

Performance



Post hoc power analysis

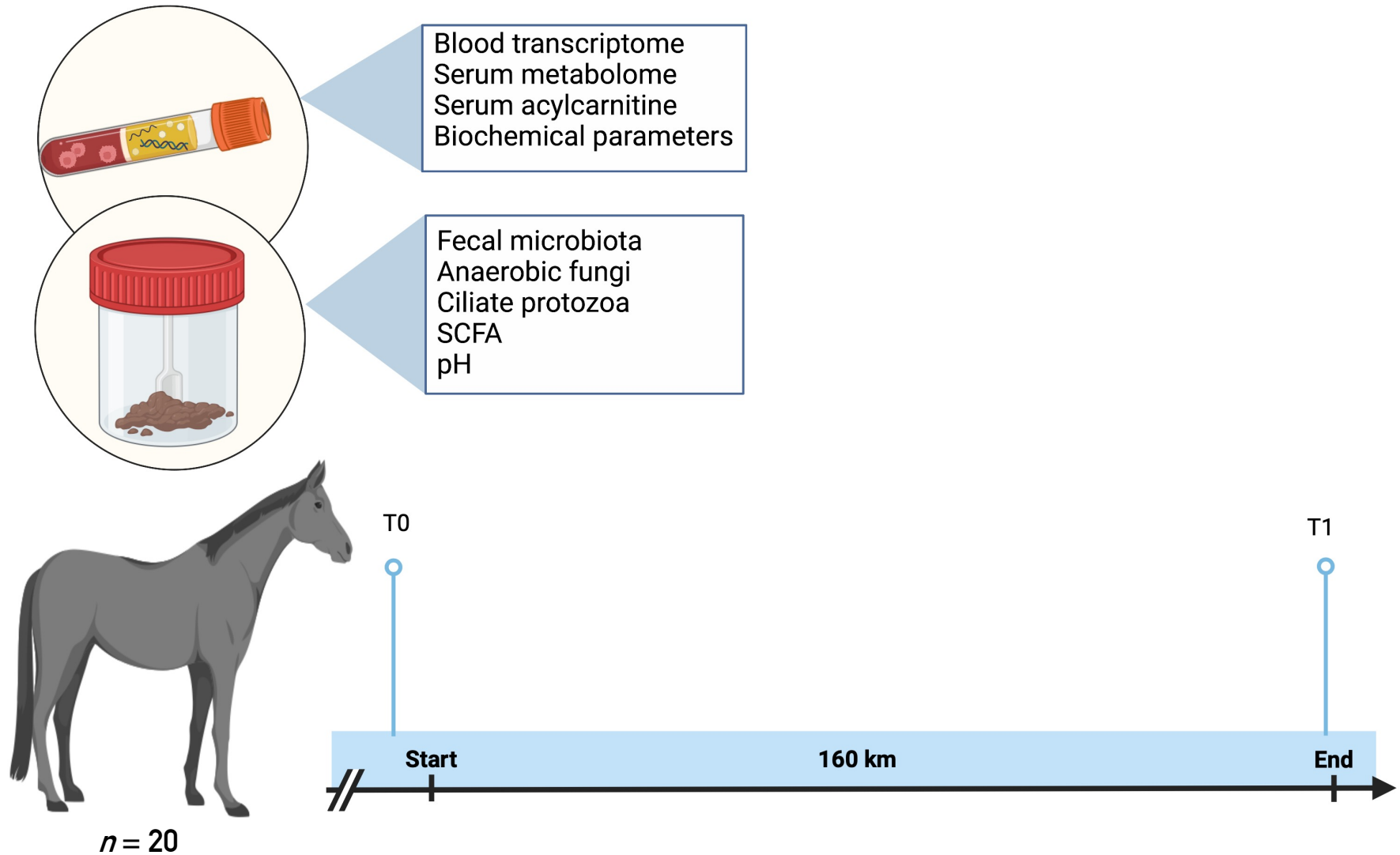
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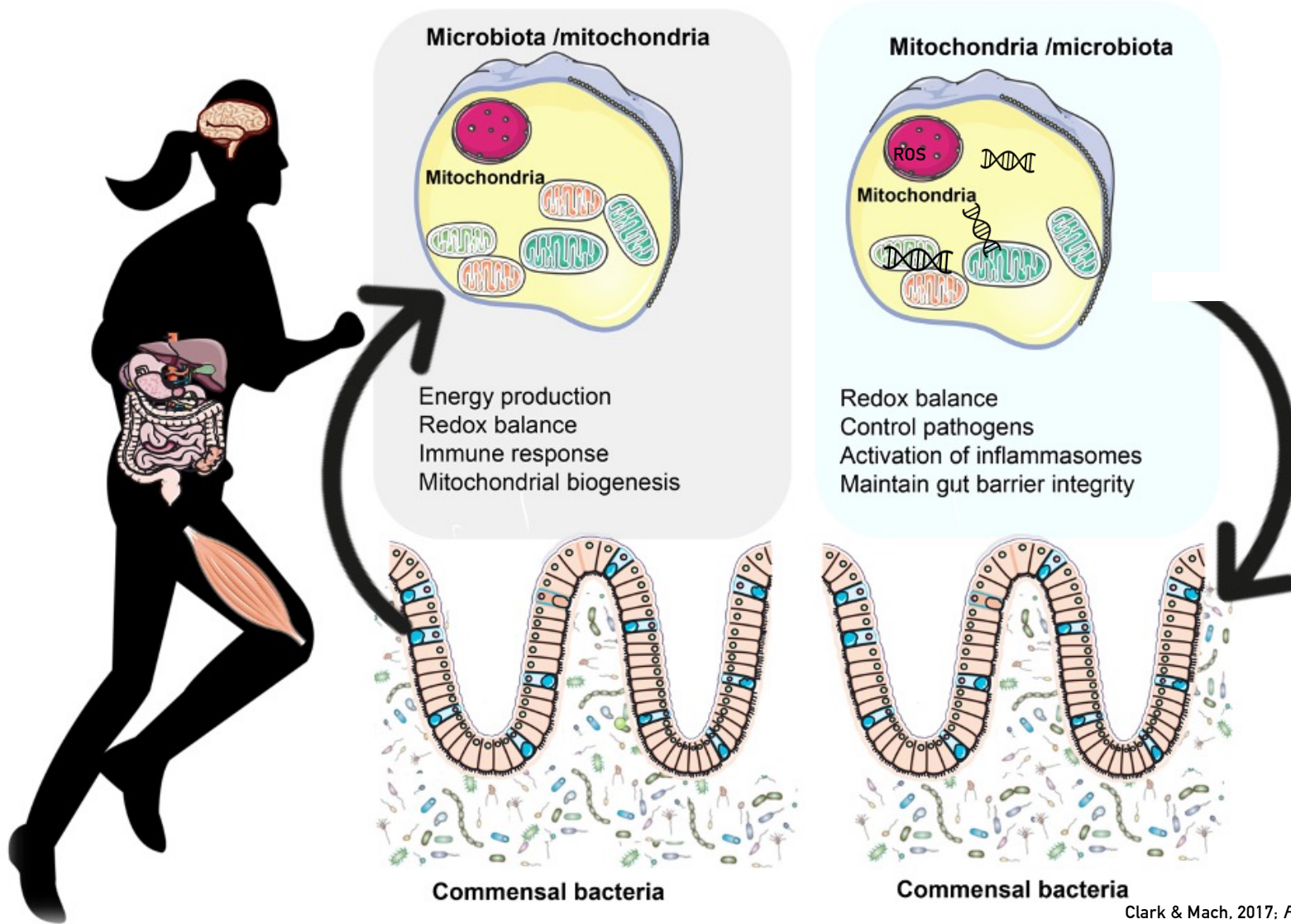
↑
Richness
Ciliate protozoa
Anaerobic fungi
Propionate
Butyrate
μorg carbo. metab.



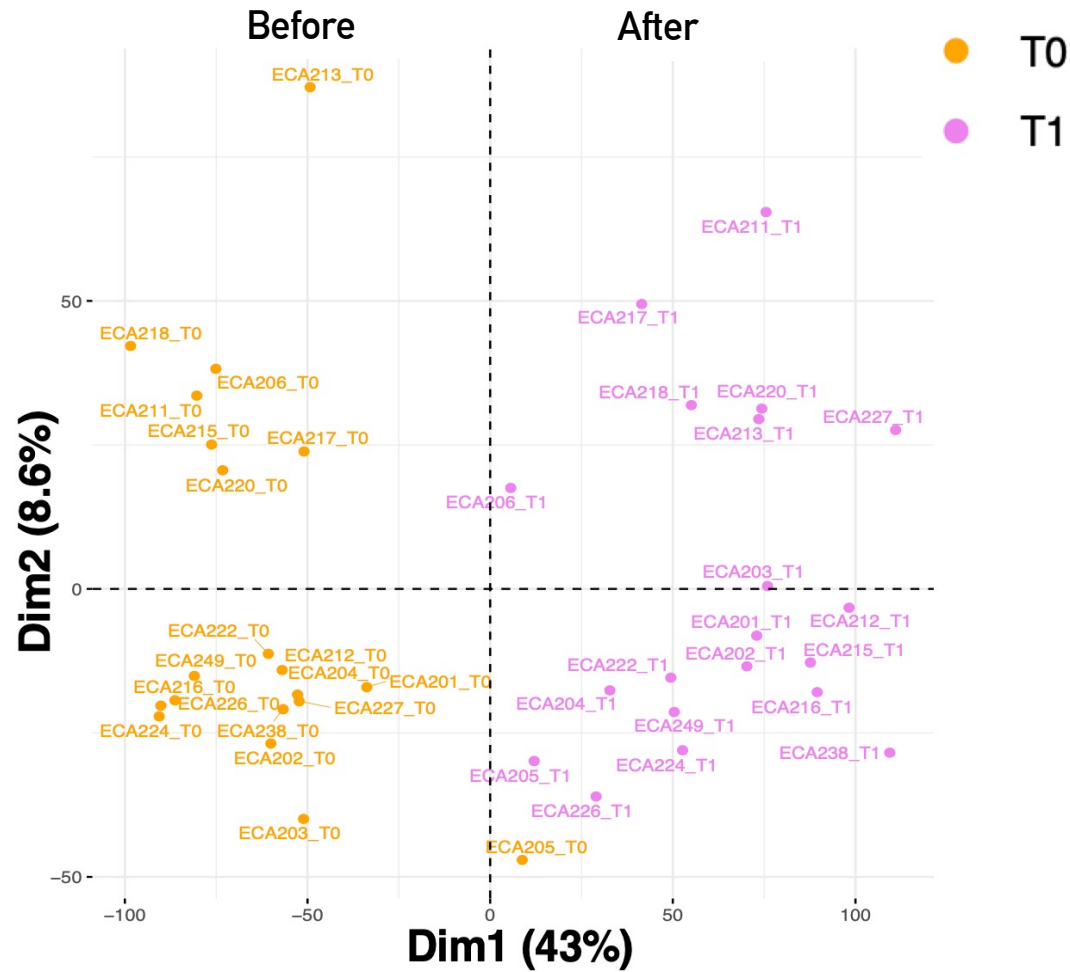
➤ RESEARCH AXIS 2: DOES HOST-MICROBIOTA INTERPLAY AFFECT THE ENDURANCE ADAPTATION?



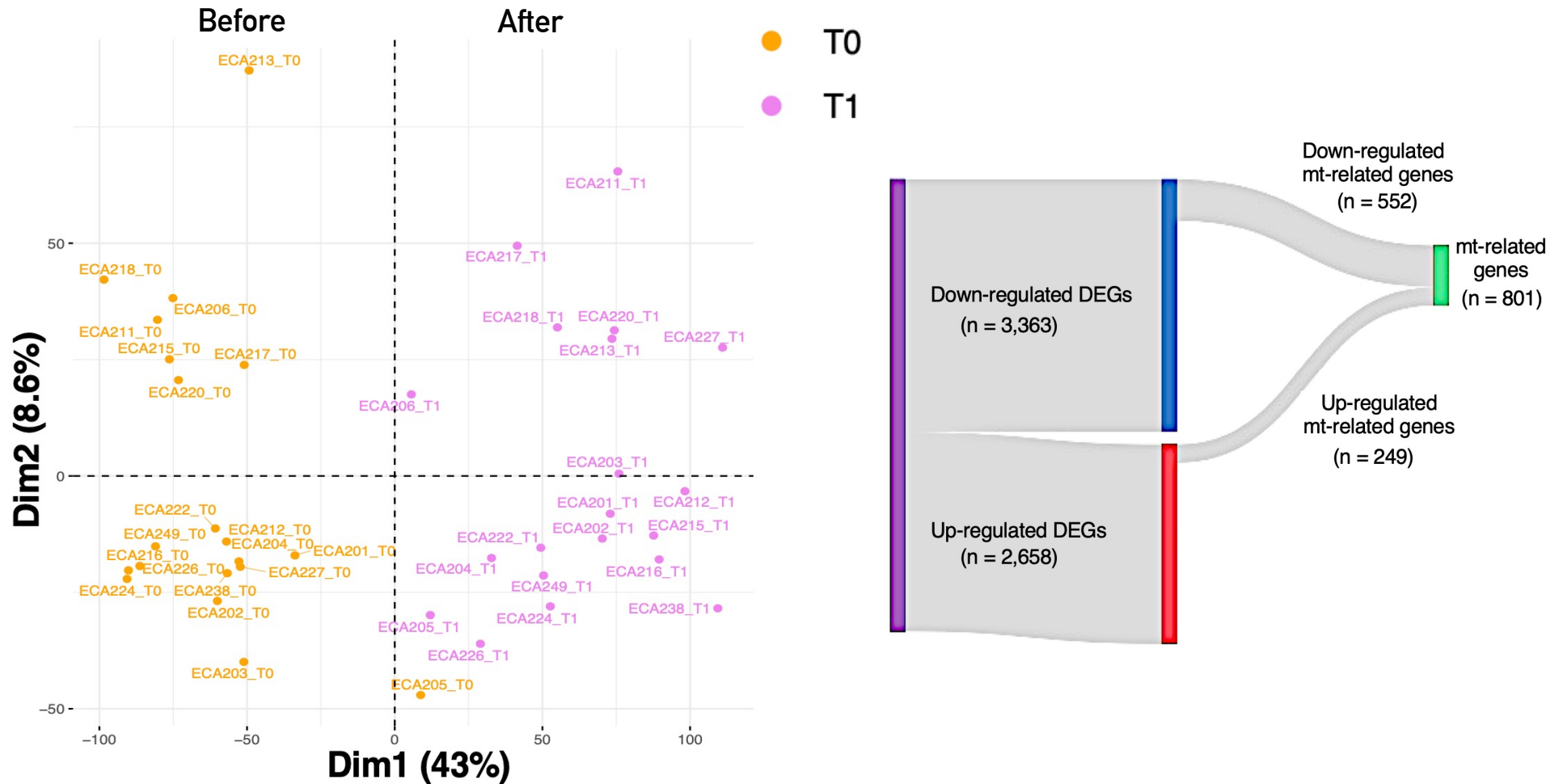
➤ RESEARCH AXIS 2: FOCUS ON THE MITOCHONDRIA-MICROBIOTA RESPONSE TO EXERCISE



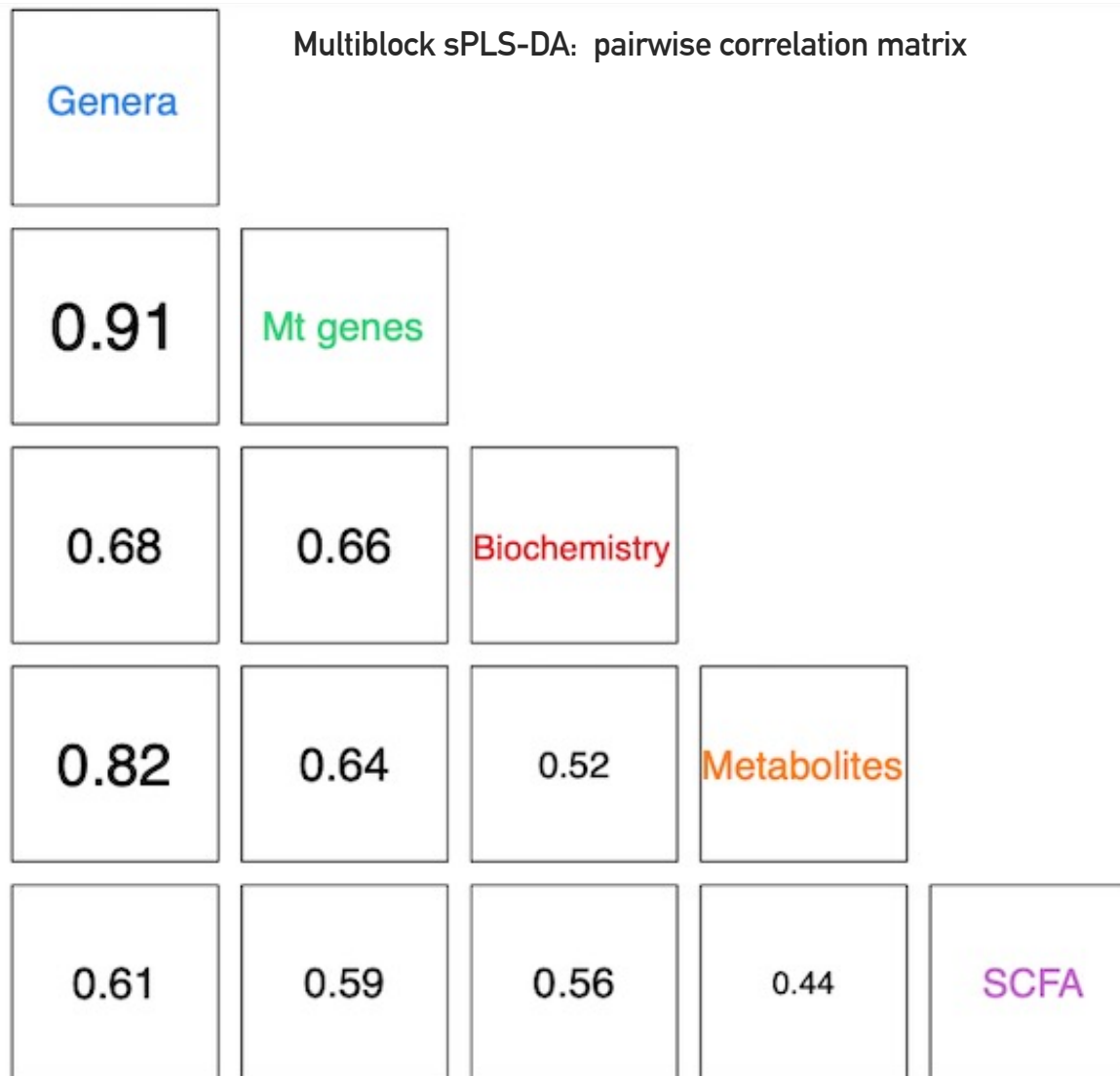
➤ RESEARCH AXIS 2: SIGNIFICANT TRANSCRIPTOME RESPONSE TO ENDURANCE



➤ RESEARCH AXIS 2: SIGNIFICANT MITOCHONDRIAL GENE RESPONSE TO EXERCISE

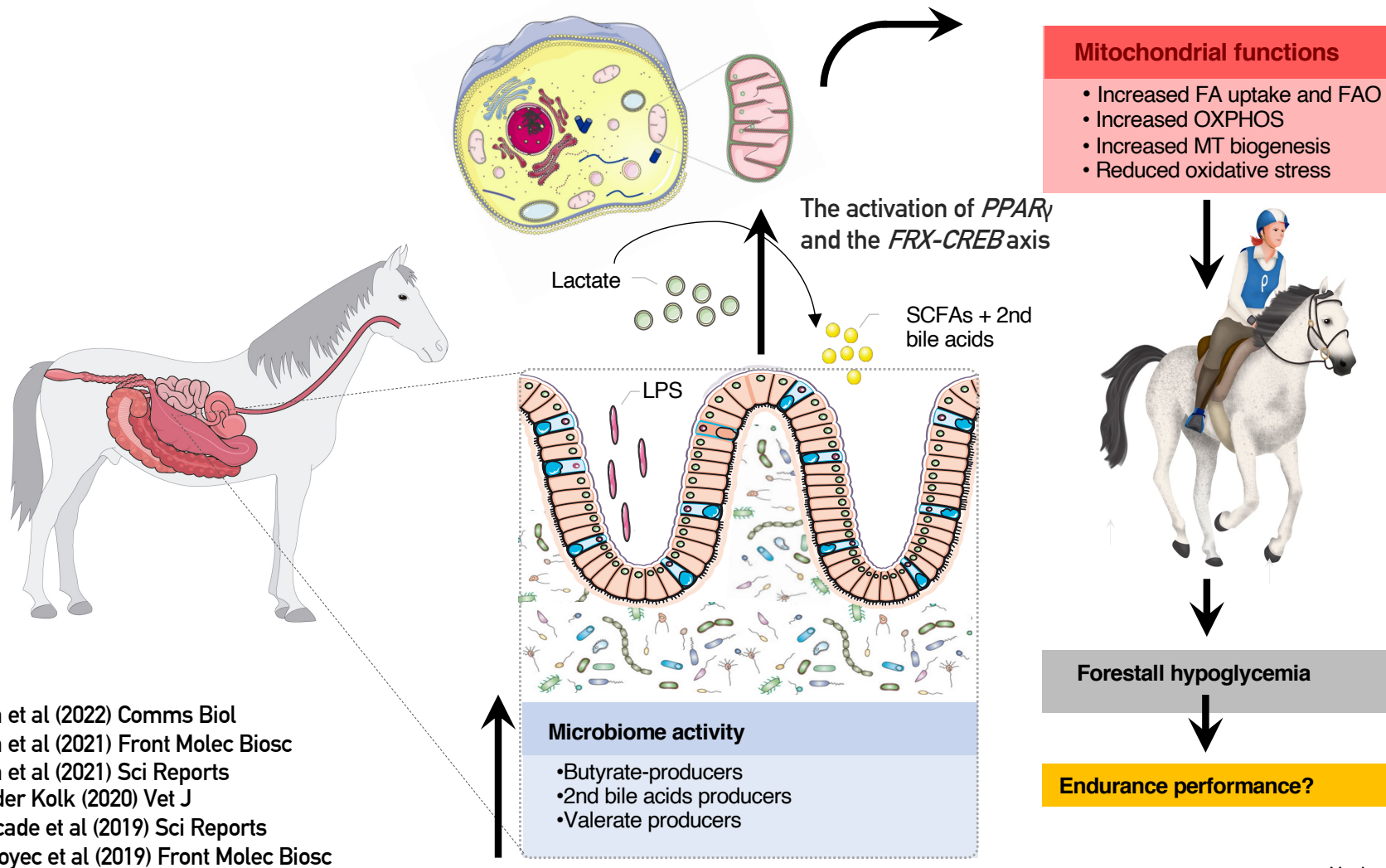


➤ RESEARCH AXIS 2: MITOCHONDRIAL GENES RELATE TO MICROBIOTA



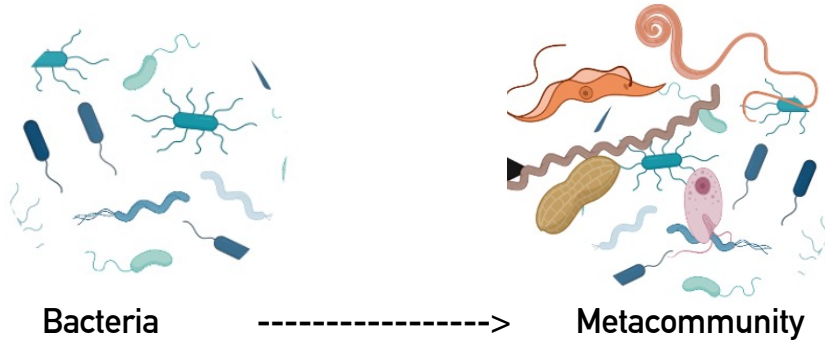
Mach et al. 2021; Front Molec Biosc

➤ RESEARCH AXIS 2: THE MICROBIOTA CROSSTALK WITH THE MT

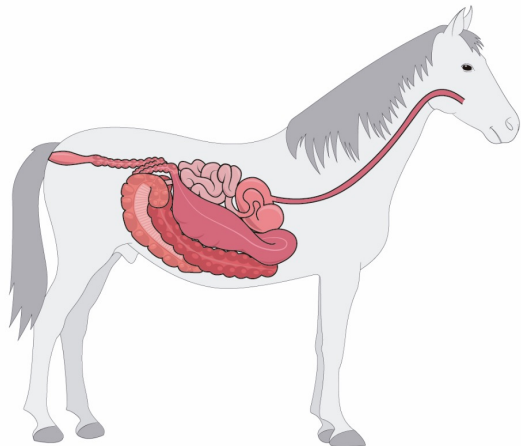


Mach et al, 2021; Front Molec Biosc

➤ RESEARCH AXIS 2: HOW GUT MICROBIOME AFFECTS FITNESS



Objective



To identify IF and HOW microbiome functions play a role in athletic performance

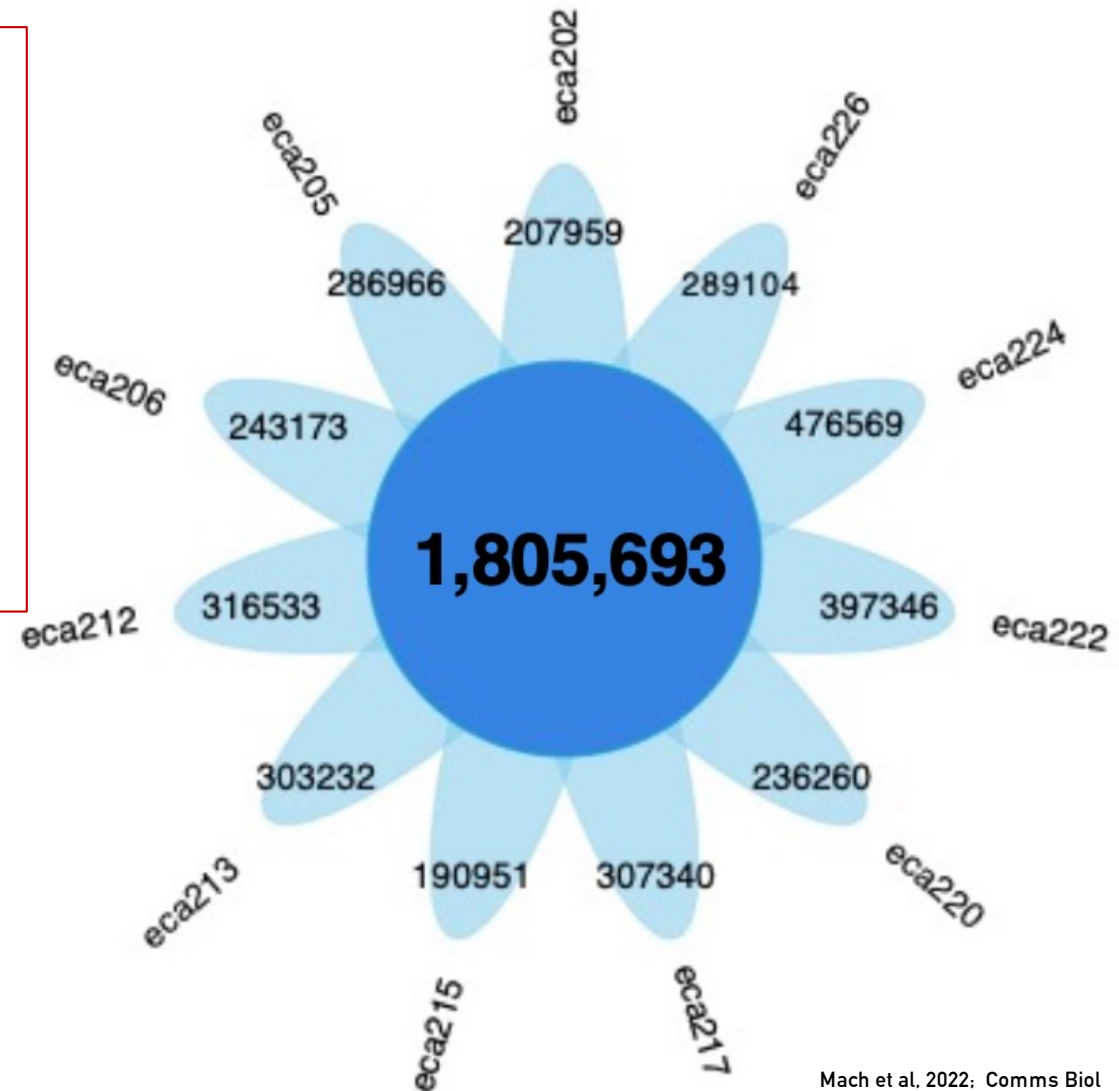
➤ RESEARCH AXIS 2: THE HORSE GUT METABIOME IS ENORMOUS

Composition rich and diverse:

- > 4,500 different taxa
- 95% bacteria
- Eukarya + virus

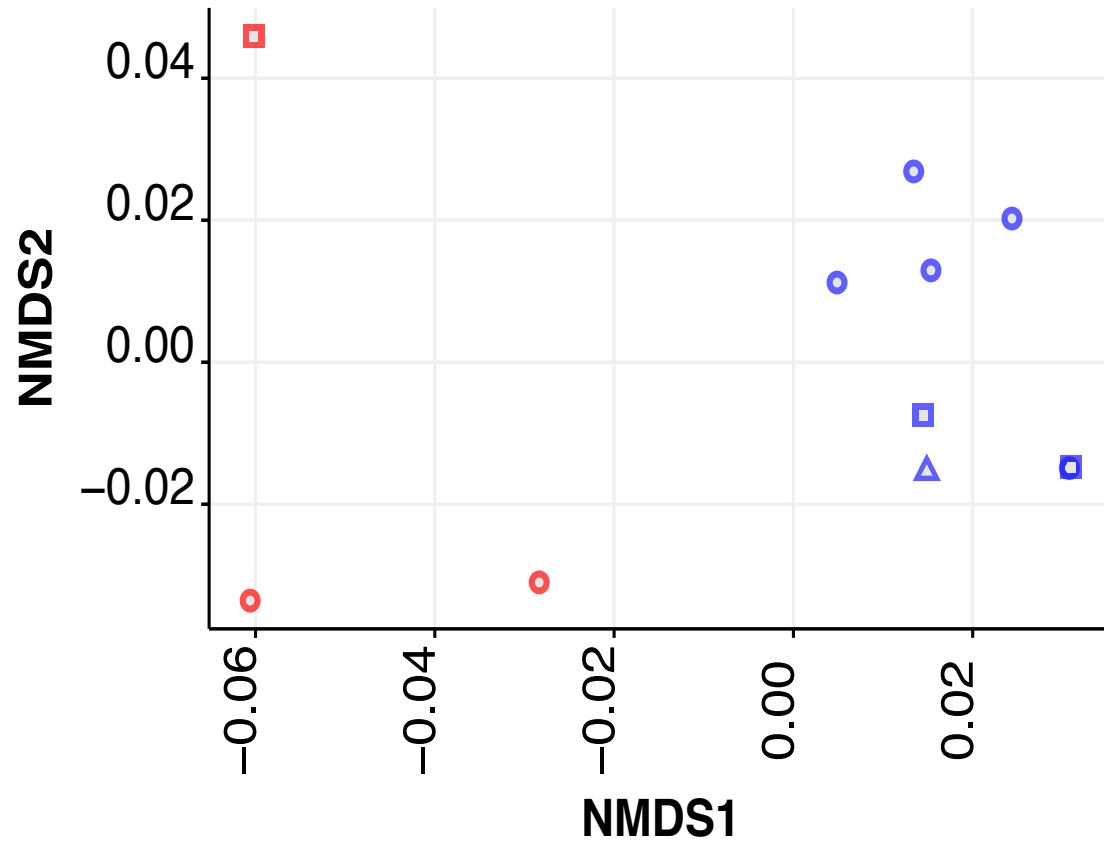
Functional redundancy

- 10 M genes/horse
- 97% of genes are shared

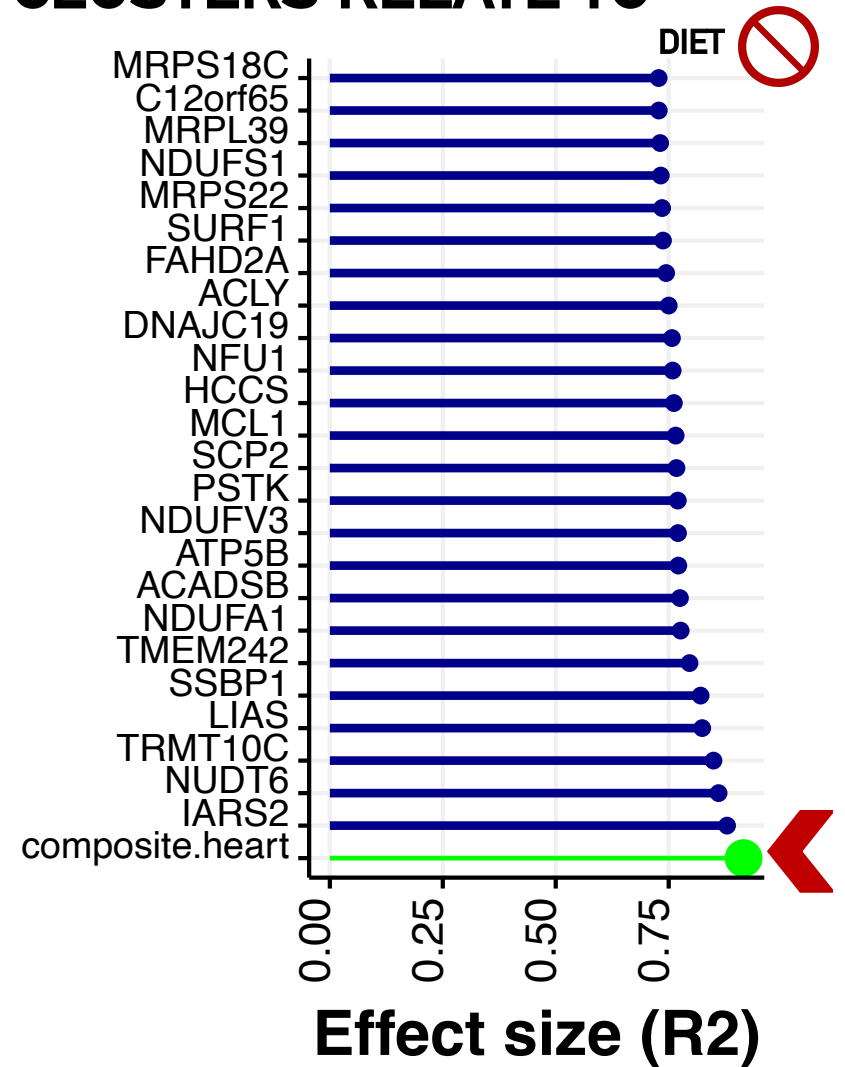
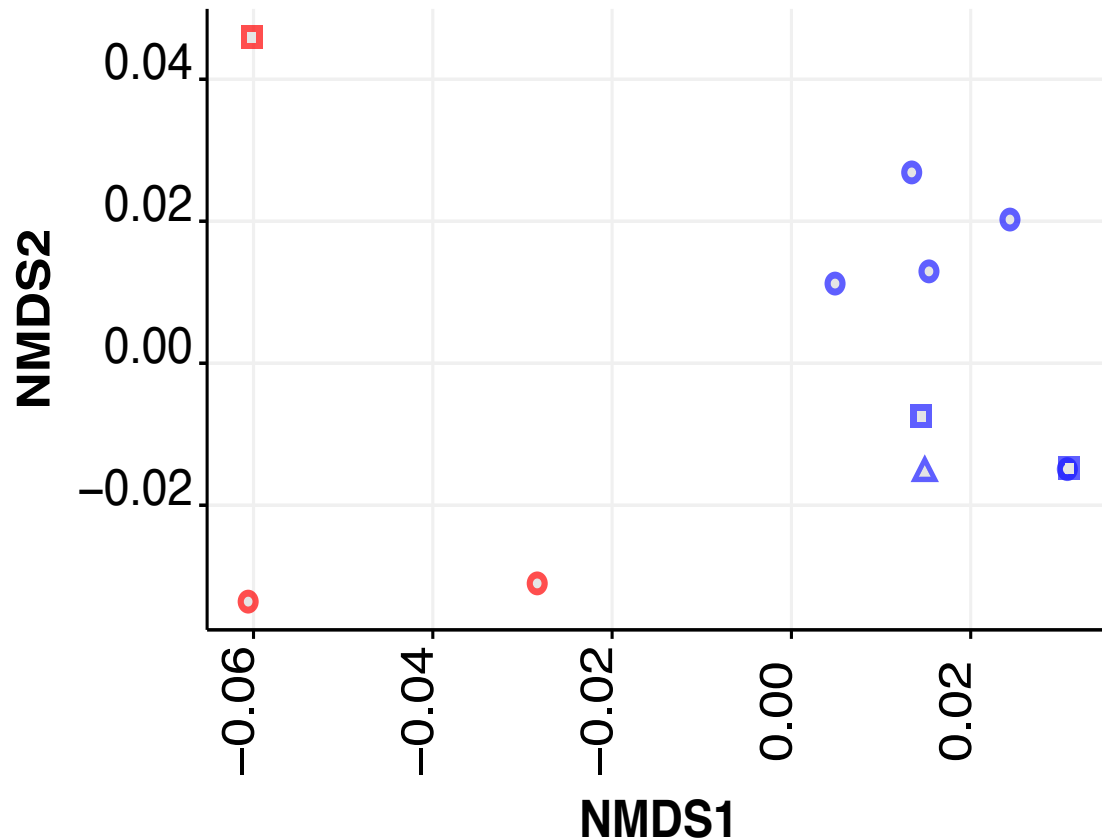


Mach et al, 2022; Comms Biol

➤ RESEARCH AXIS 2: TWO MICROBIOME CLUSTERS

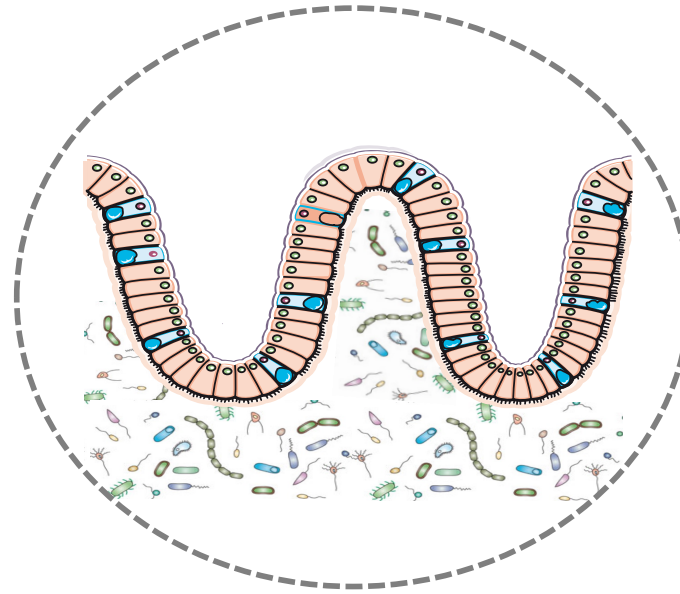
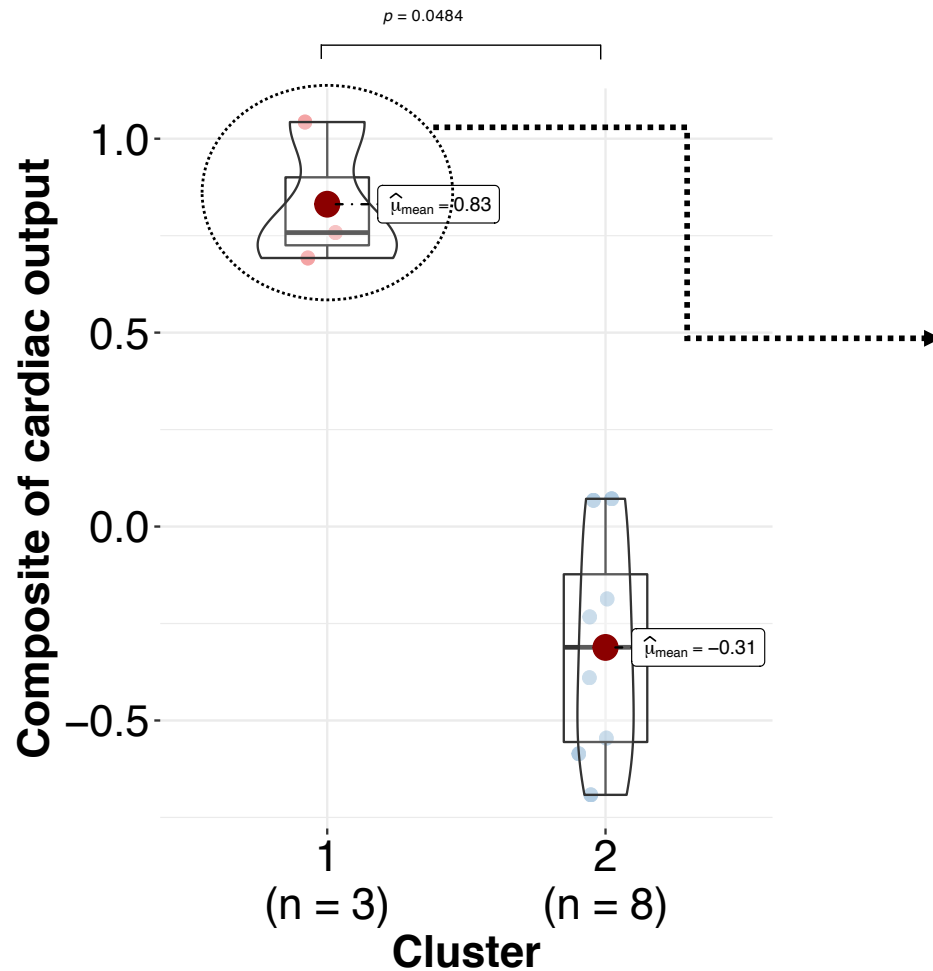


RESEARCH AXIS 2: THE MICROBIOME CLUSTERS RELATE TO CARDIAC FITNESS



Mach et al, 2022; Comms Biol

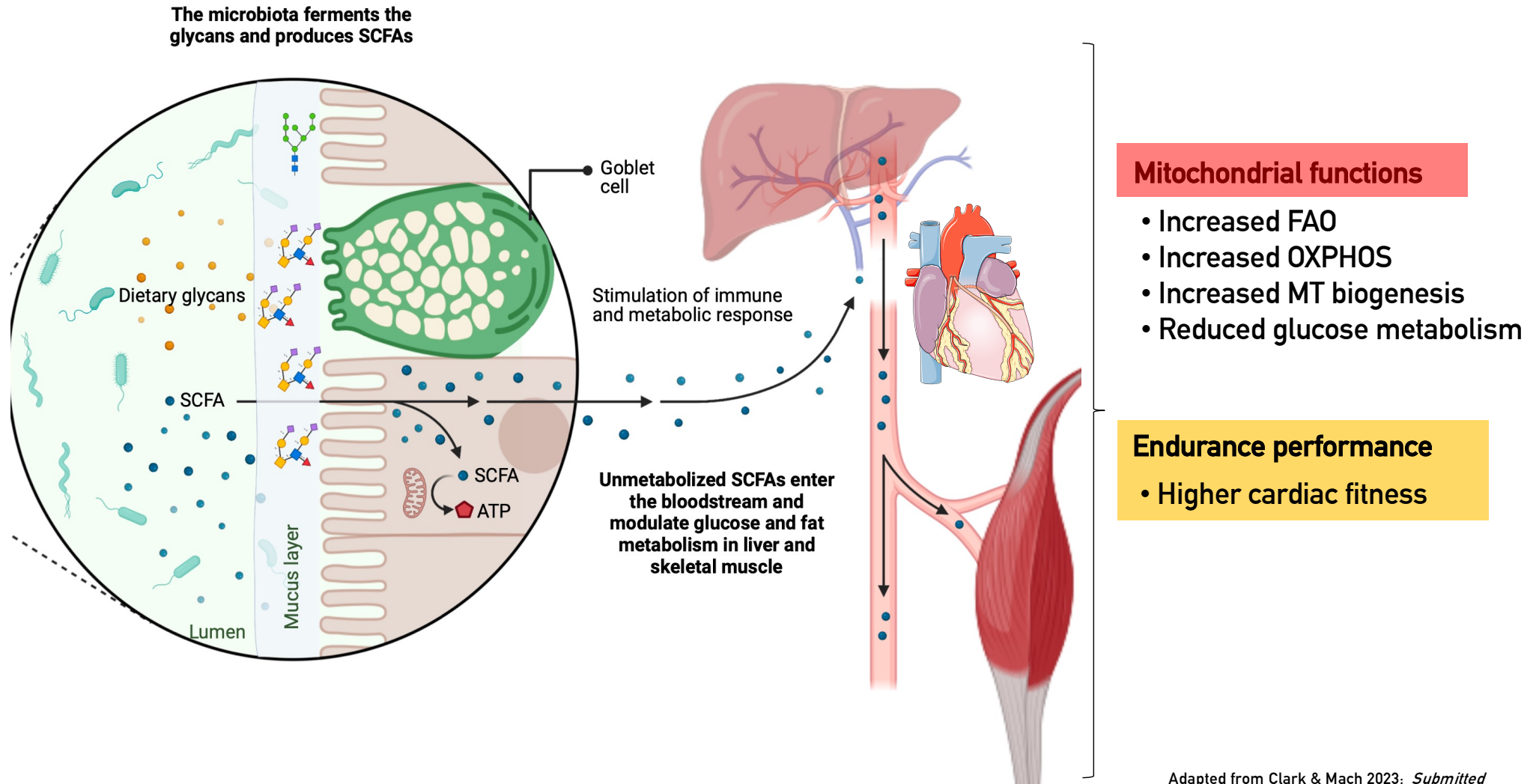
RESEARCH AXIS 2: CARDIOVASCULAR FITNESS DEPENDS ON MICROBIOME-GLYCOME AXIS



Microbiome composition and function

- Greater diversity: eukaryote
- Enrichment of rare species
- Shortage *Lachnospiraceae*
- High capacity to cleave host glycans

➤ RESEARCH AXIS 2: CARDIOVASCULAR FITNESS DEPENDS ON MICROBIOME-GLYCOME AXIS





Thank you for your attention!



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INRAE

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