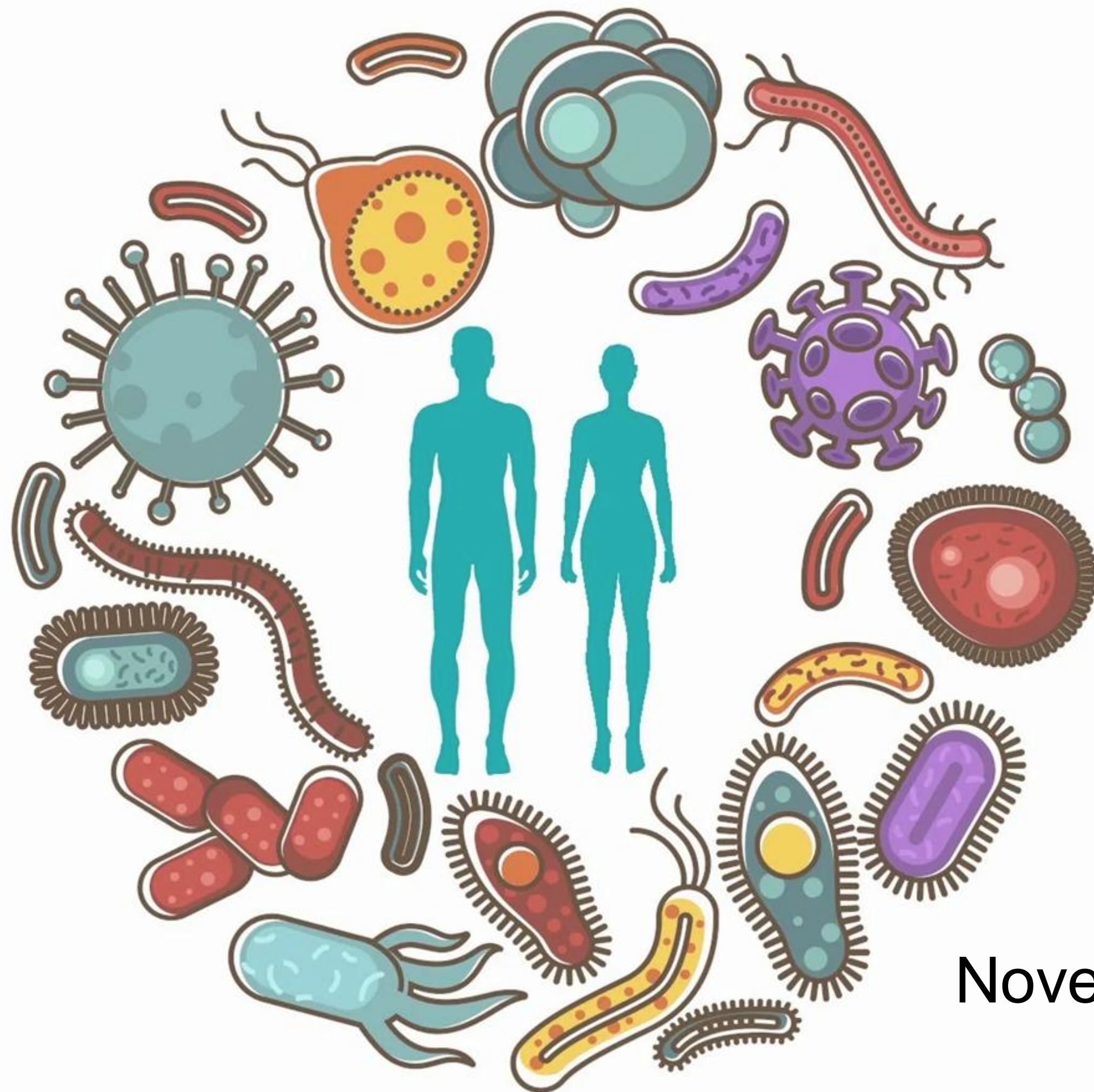


Practical II



Ece Kartal

Postdoctoral Fellow, @psecekartal
Saez-Rodriguez Lab, Heidelberg University

November 23, 2023

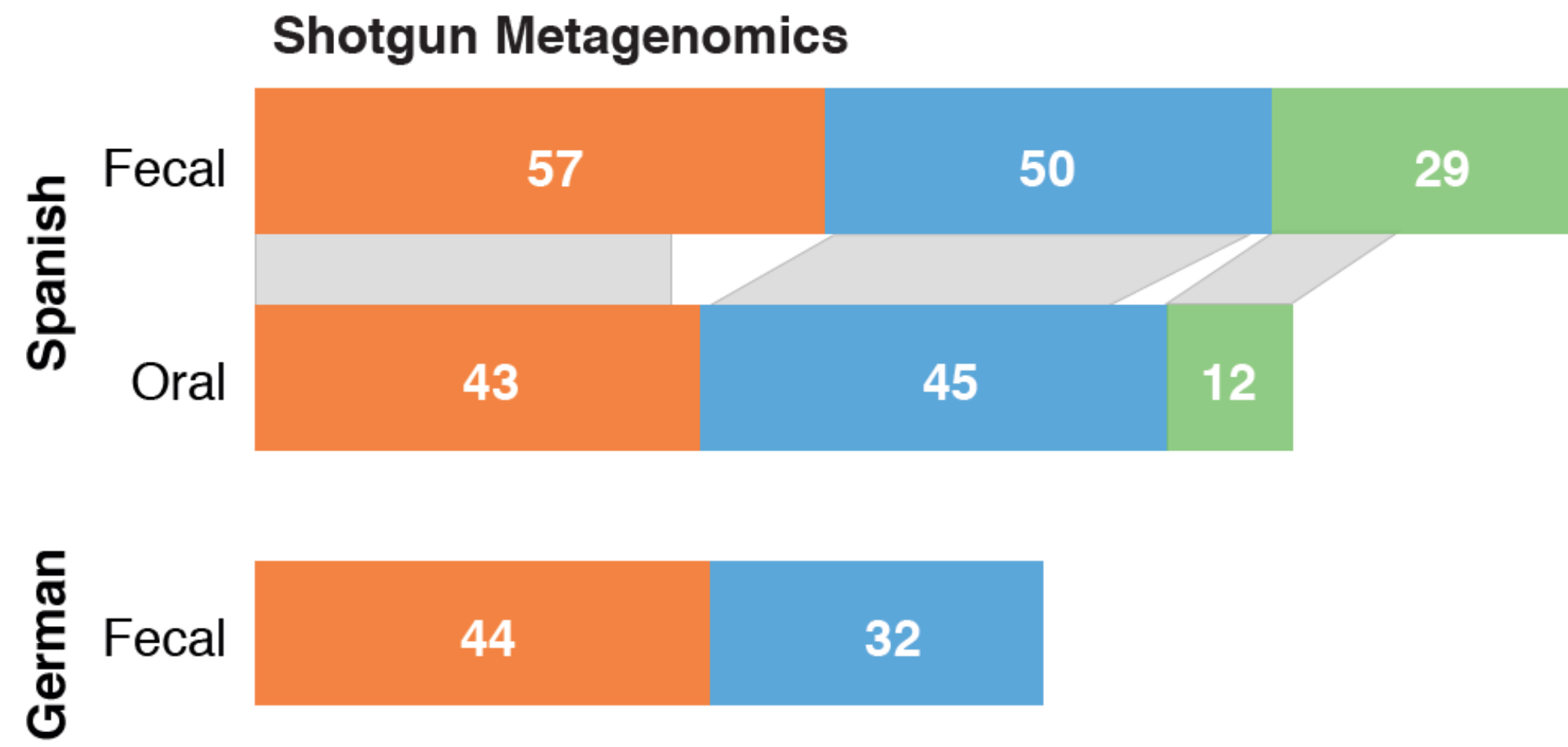
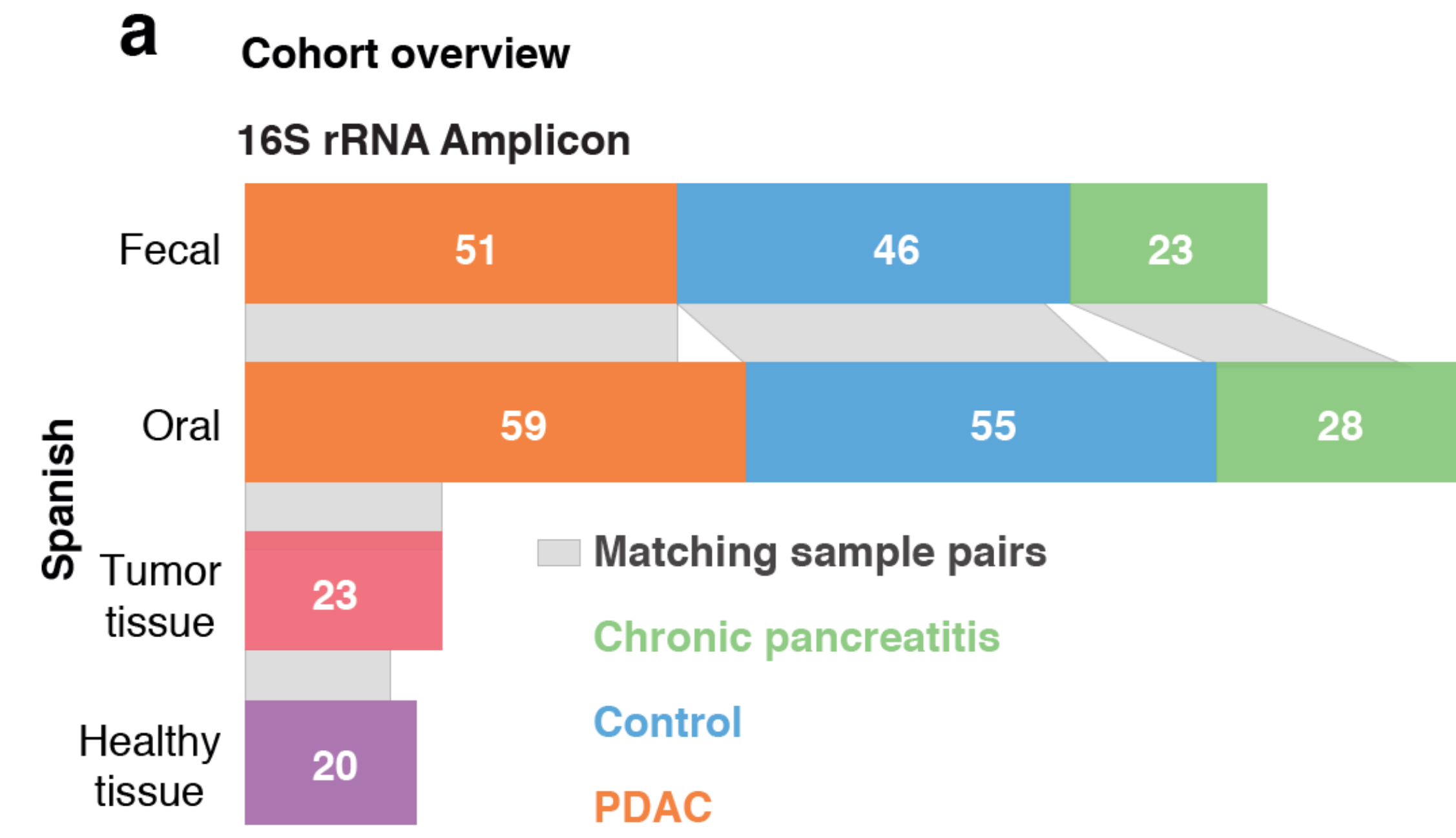
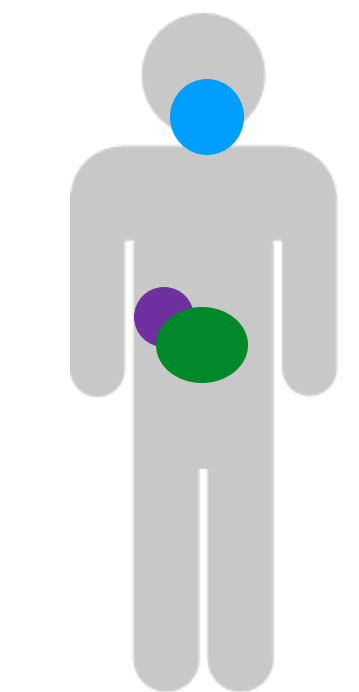




Potential of fecal microbiota for specific detection of PDAC

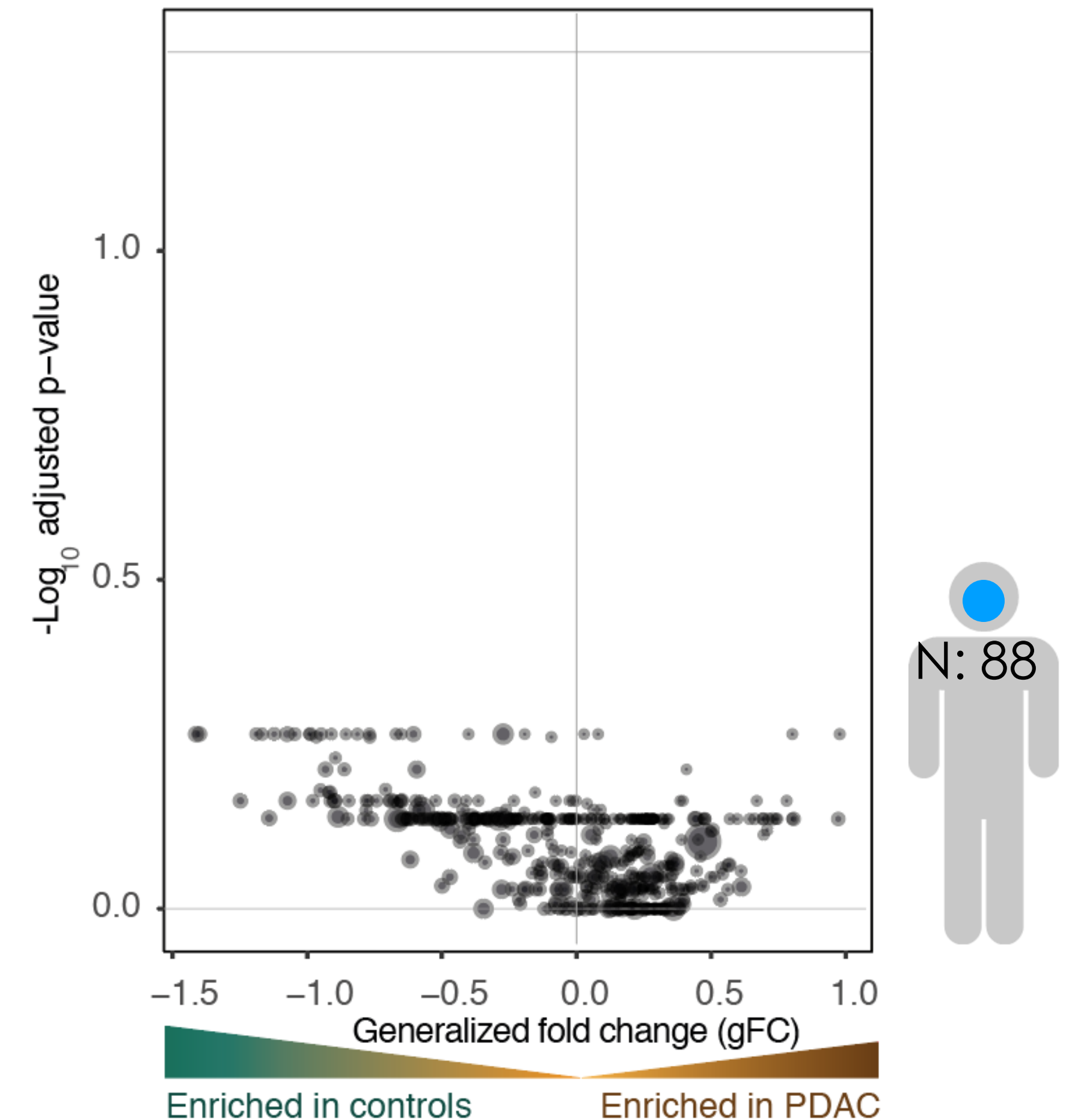
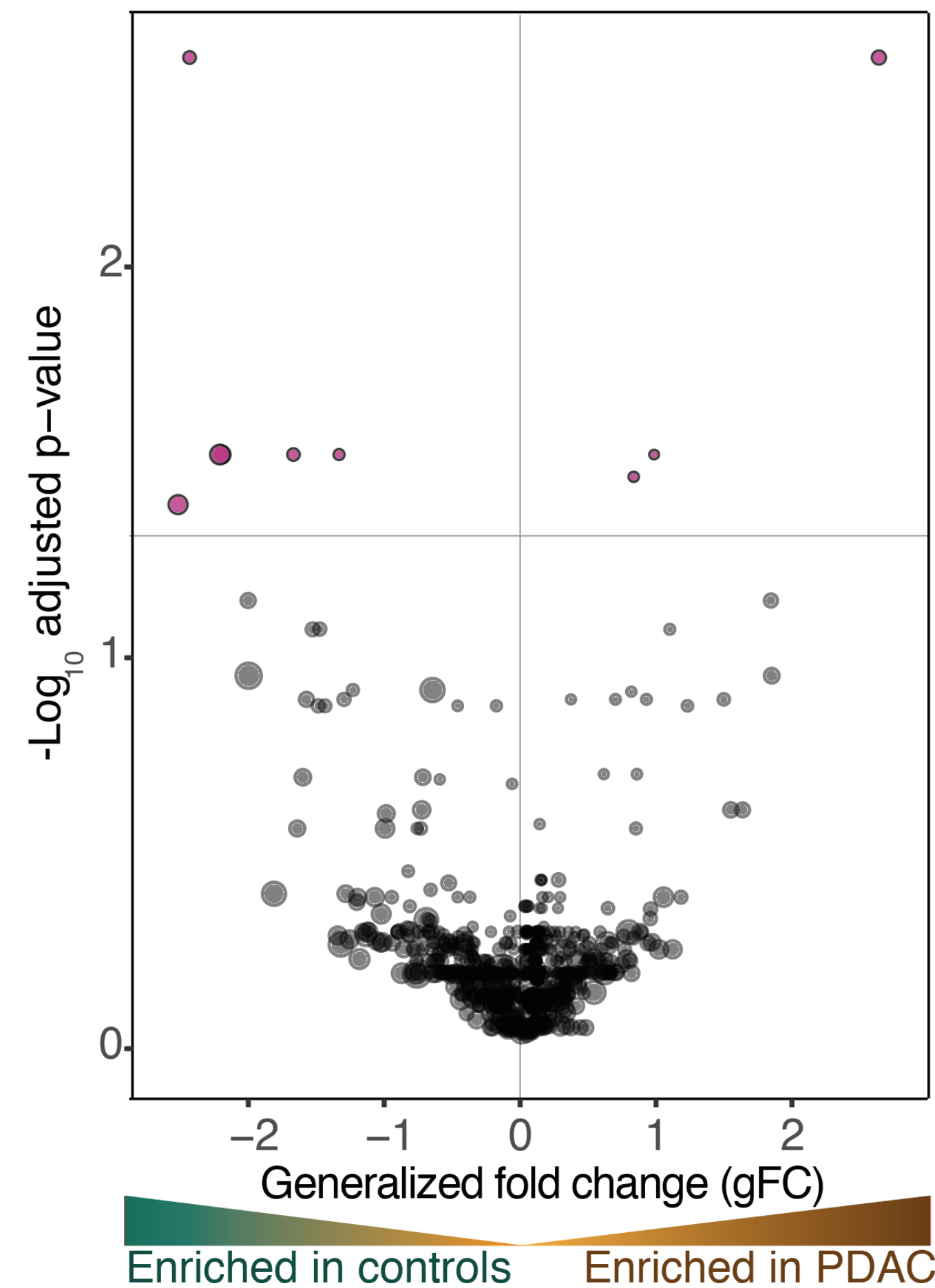
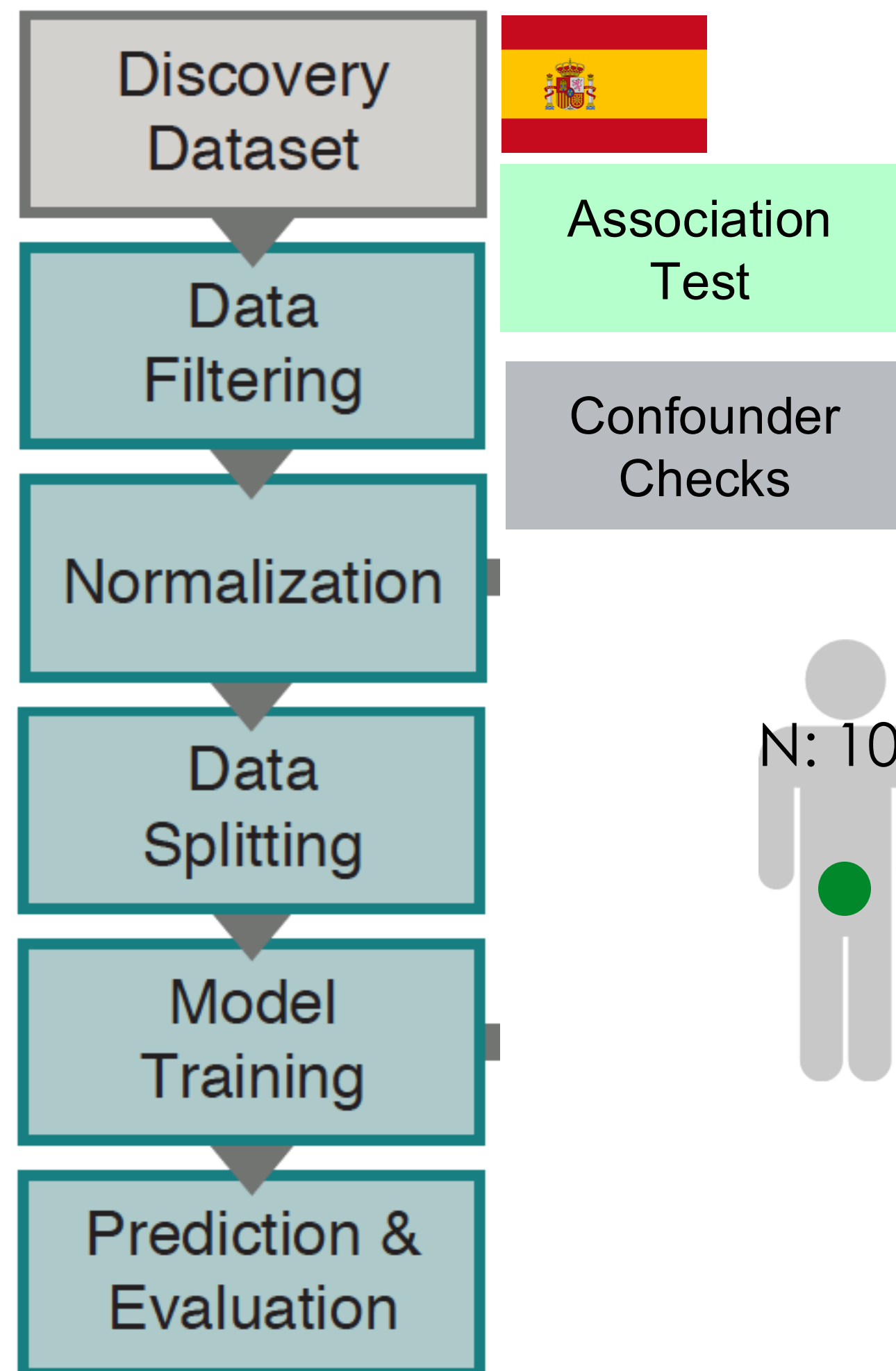
PanGen & MAGIC Consortiums

Bork & Zeller Groups





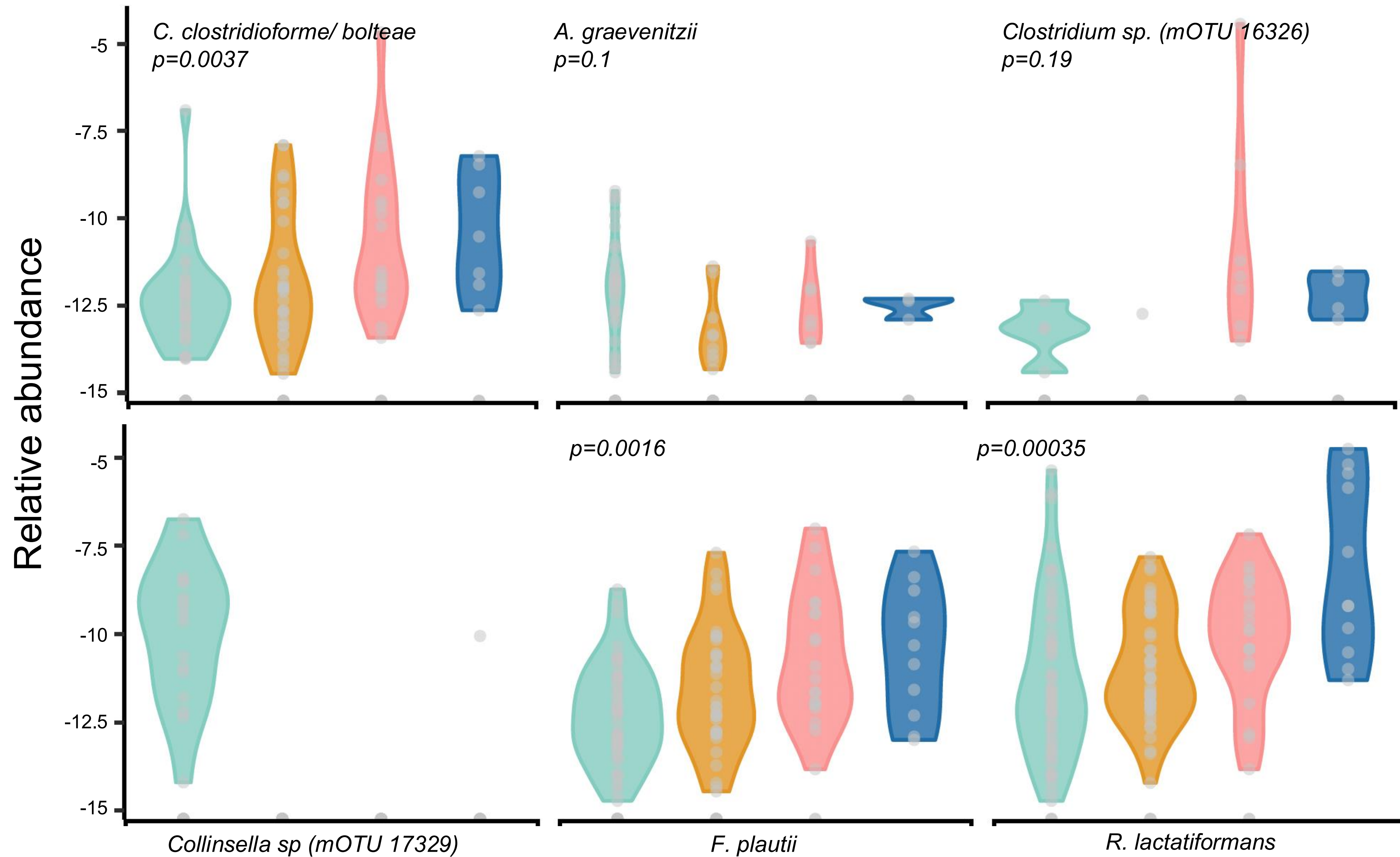
Differential abundant species between PDAC & CTR



- Not significant
- Adjusted p-value < 0.05
- Relative abundance ● 0.01 ● 0.03 ● 0.05

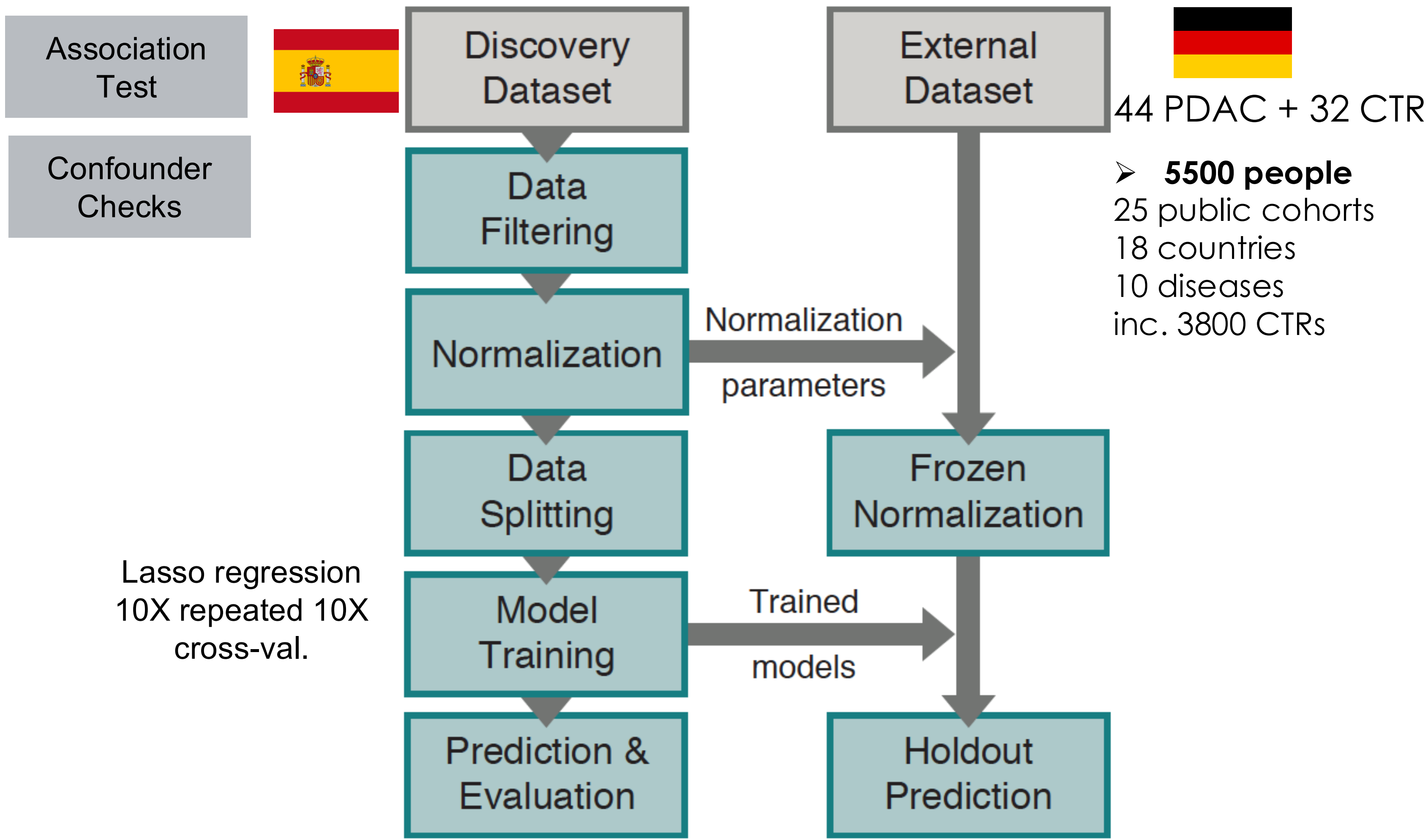


Differentially abundant species between timepoints



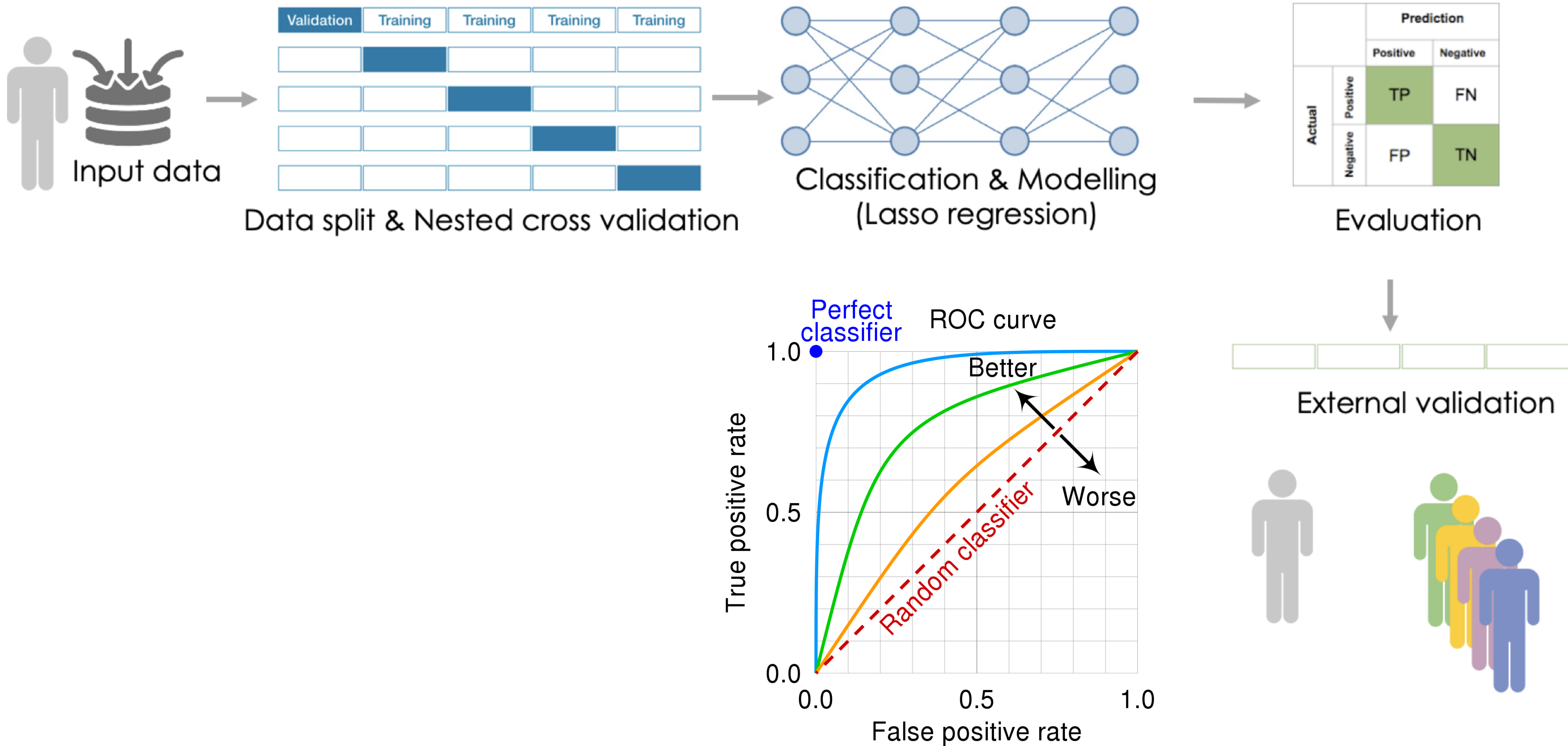


Model building steps for classification problems



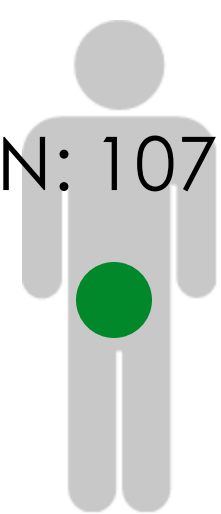
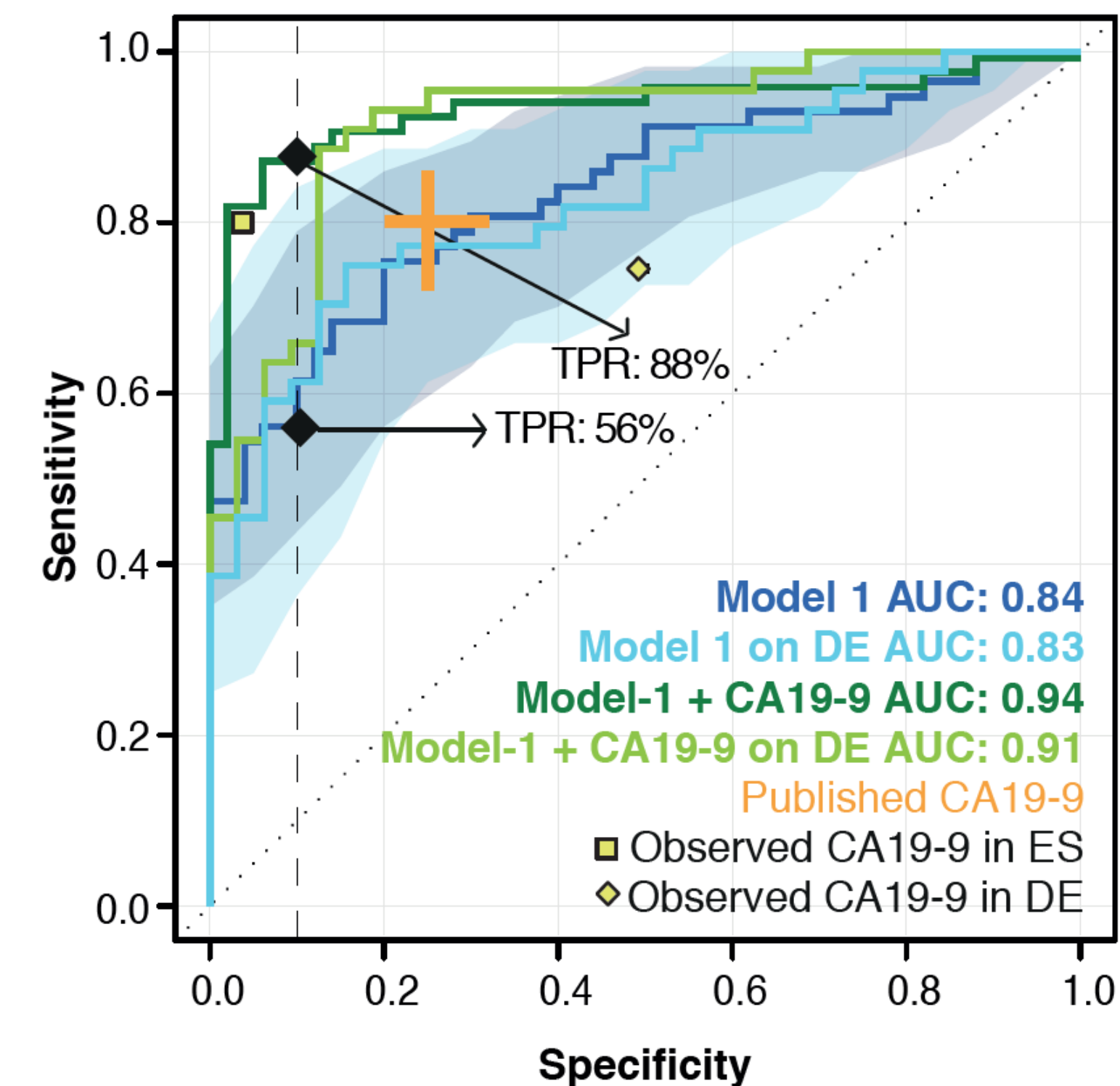
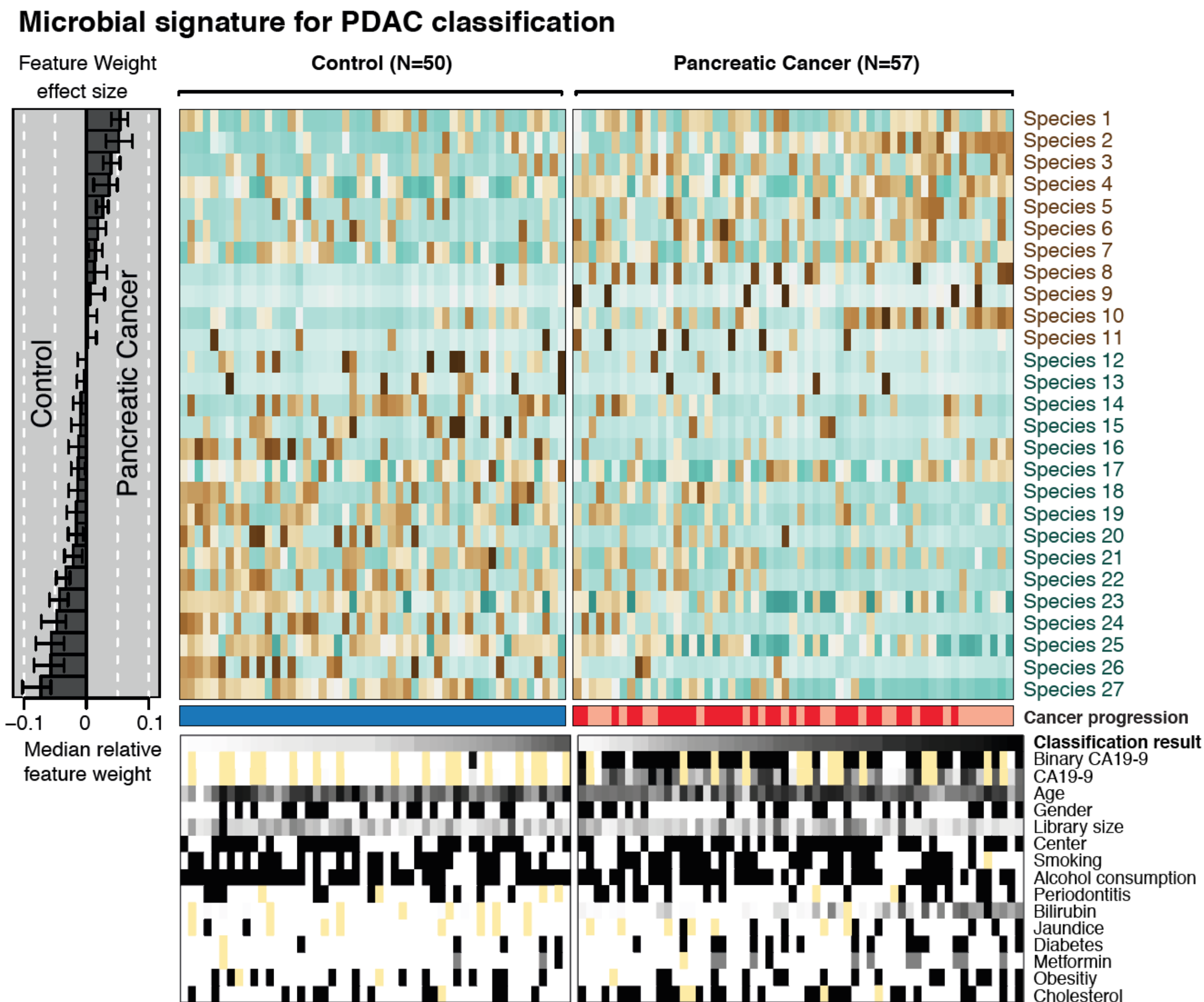
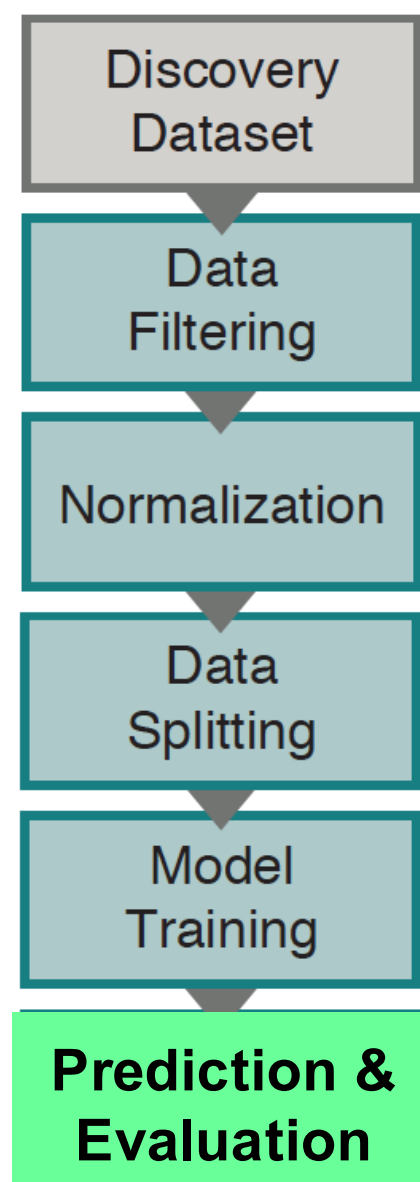


Modelling





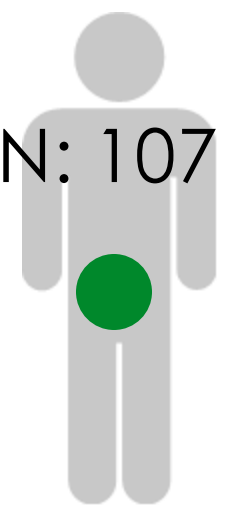
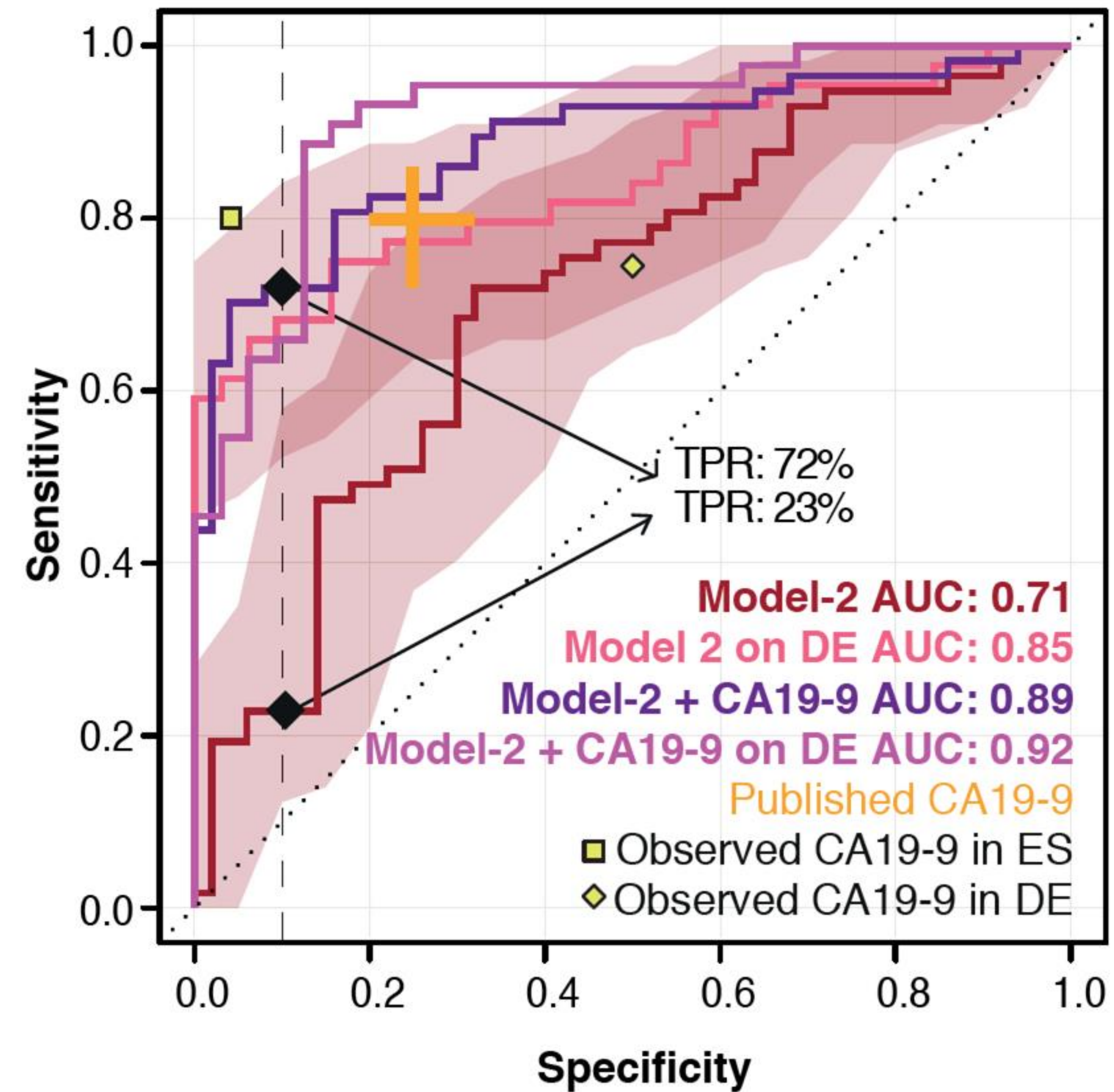
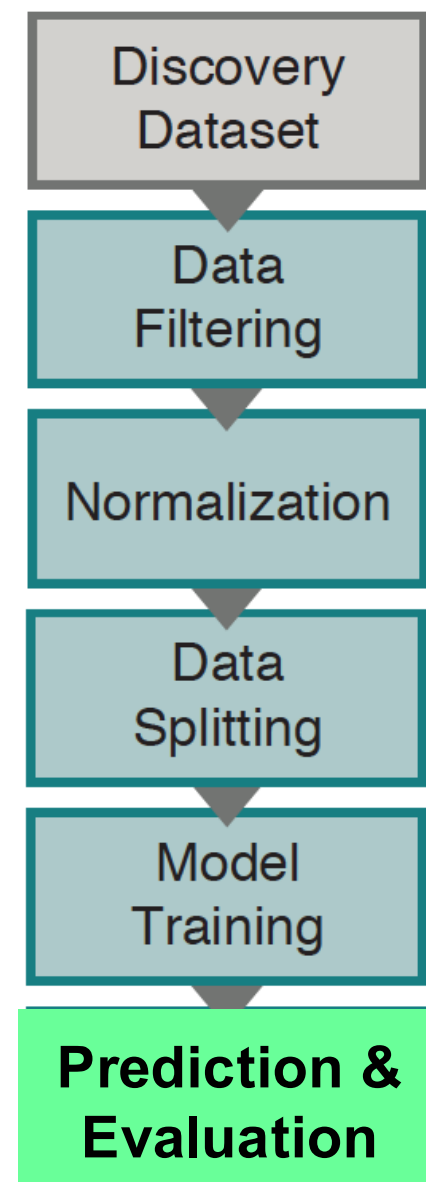
Model 1: PDAC-associated fecal microbiome signatures



N: 107



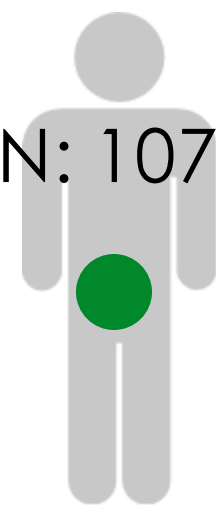
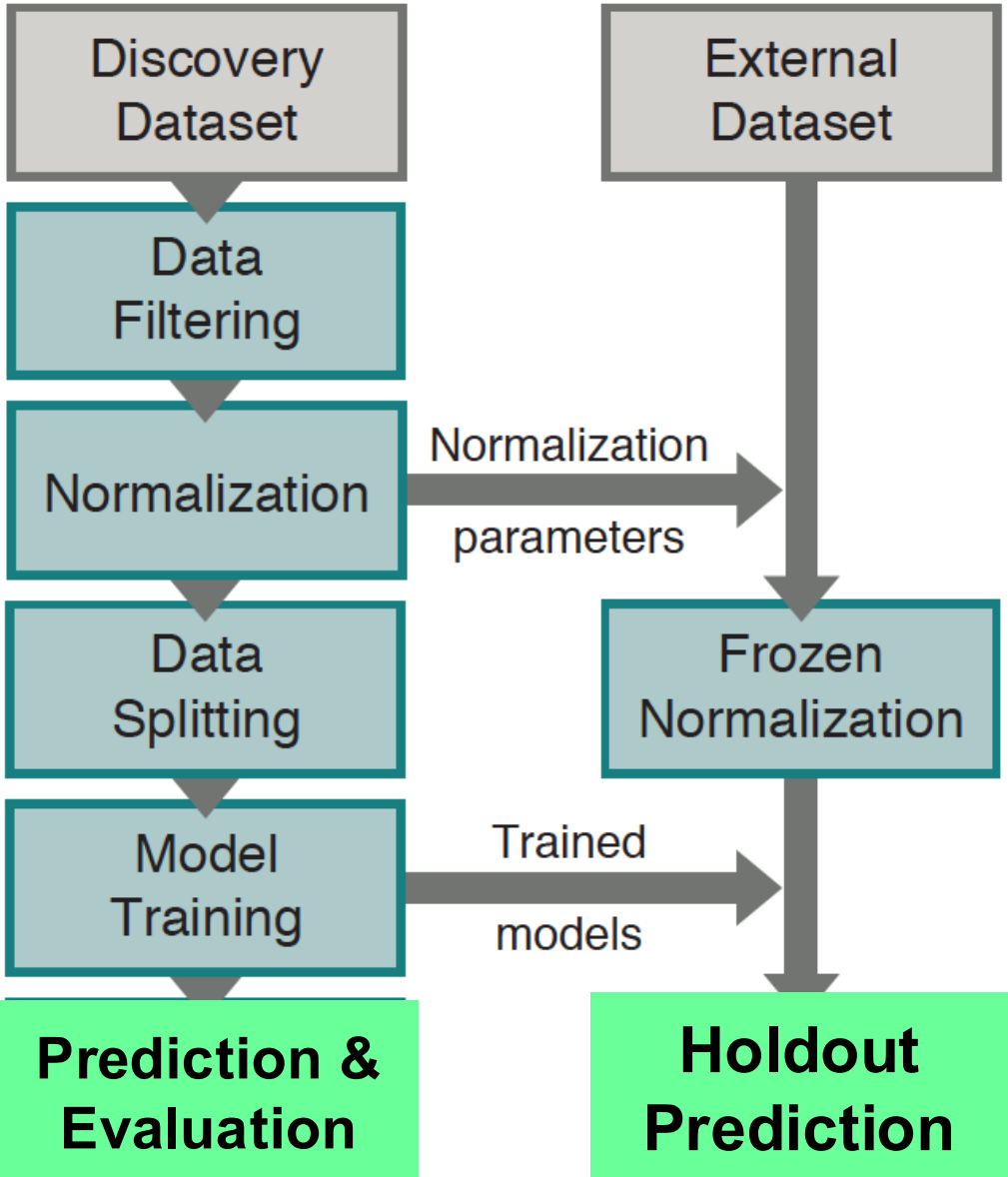
Model 2: PDAC-enriched fecal microbiome based classifiers



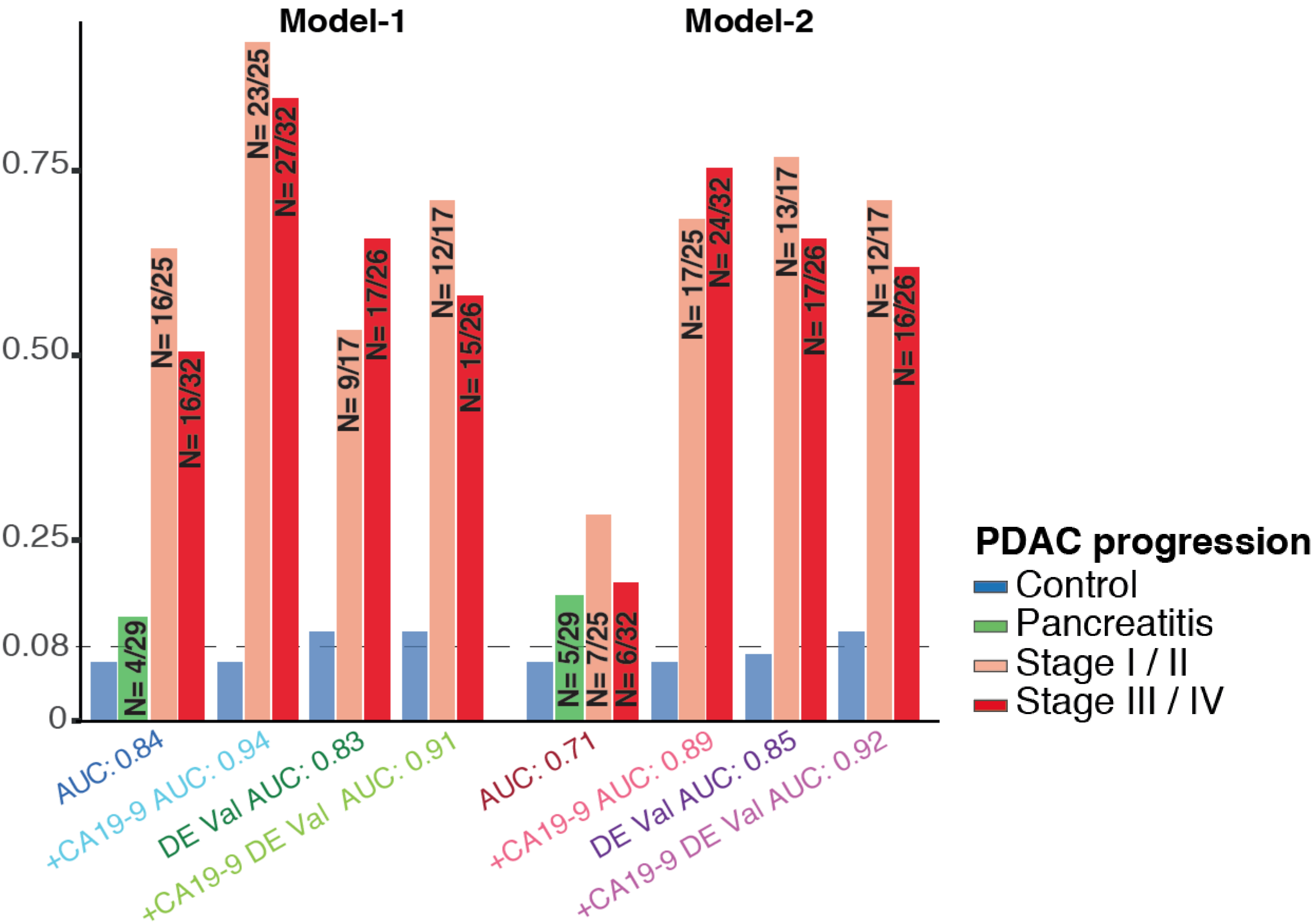
N: 107



PDAC prediction rate

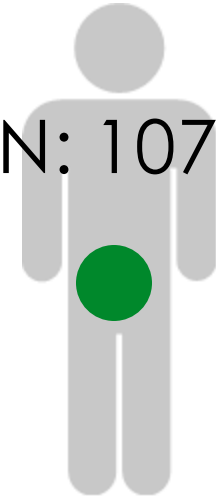
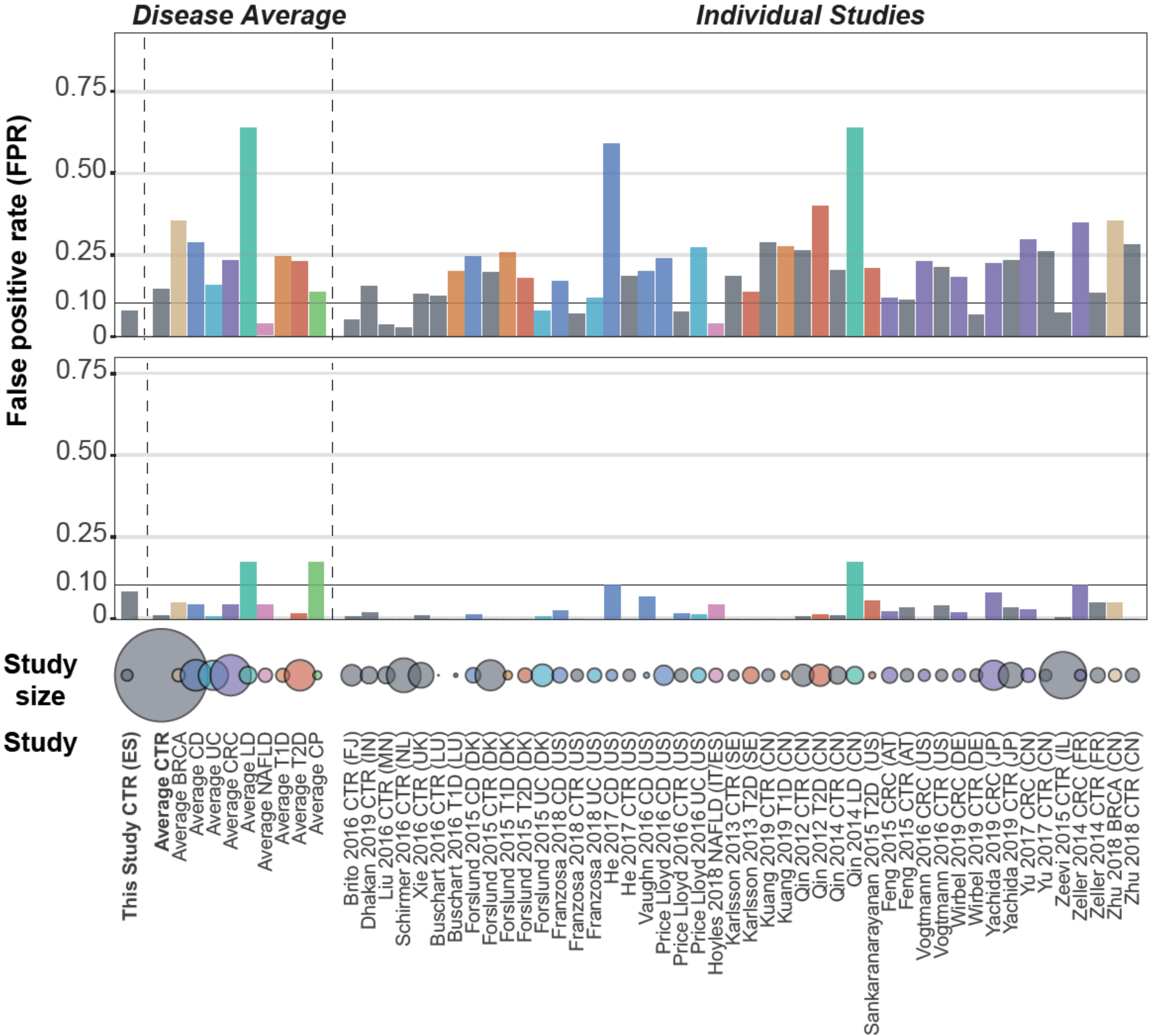


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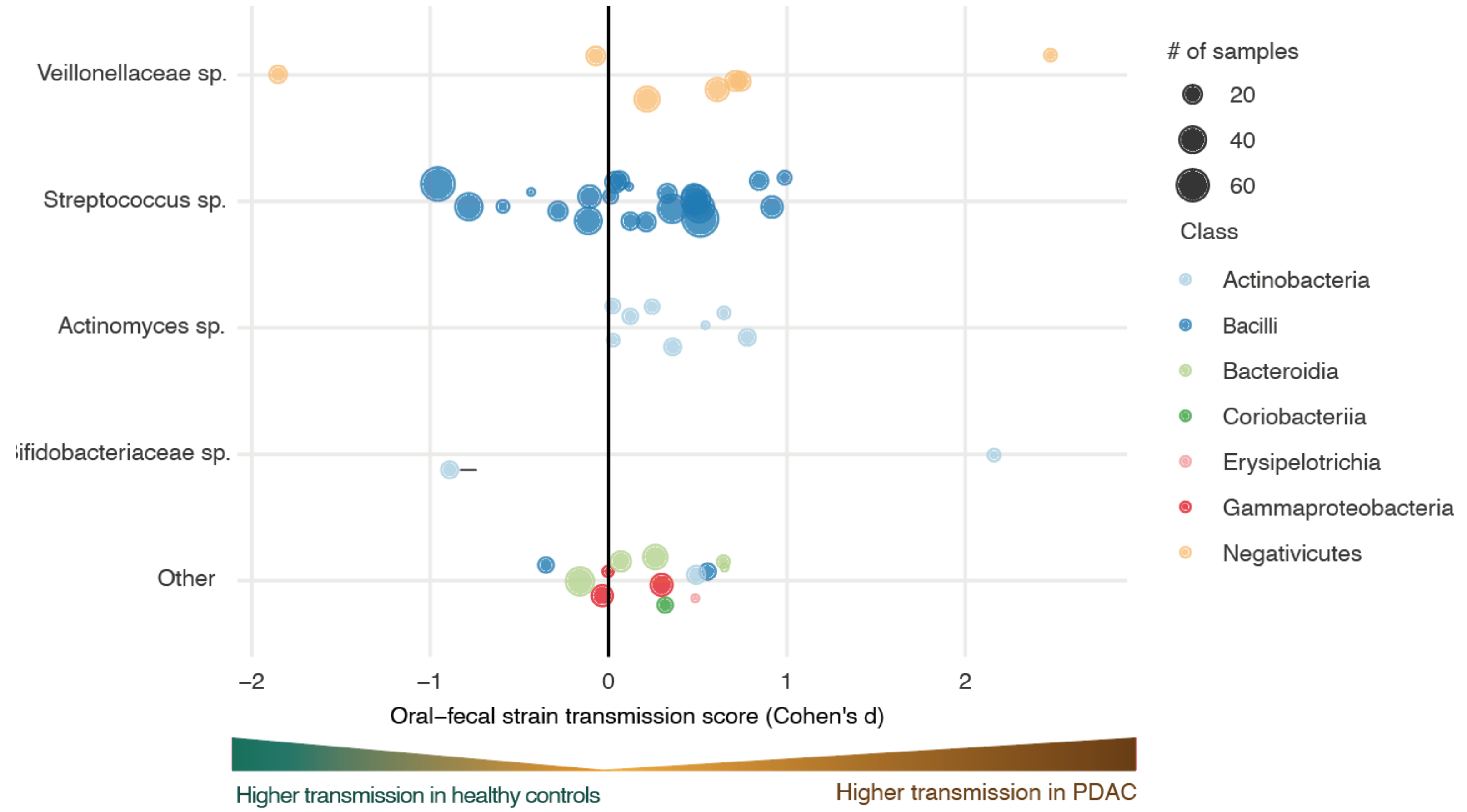
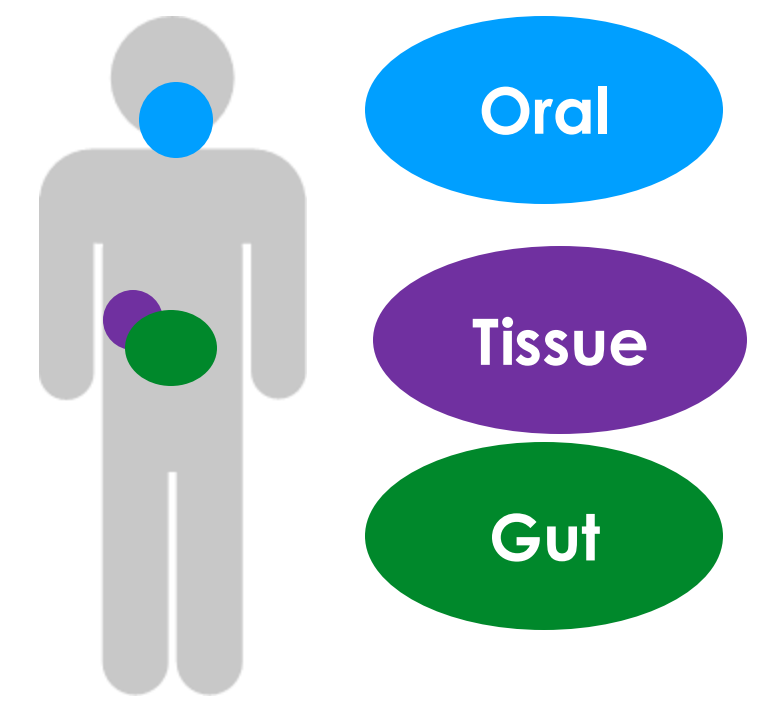


PDAC prediction rate



Presence of key genera in pancreas

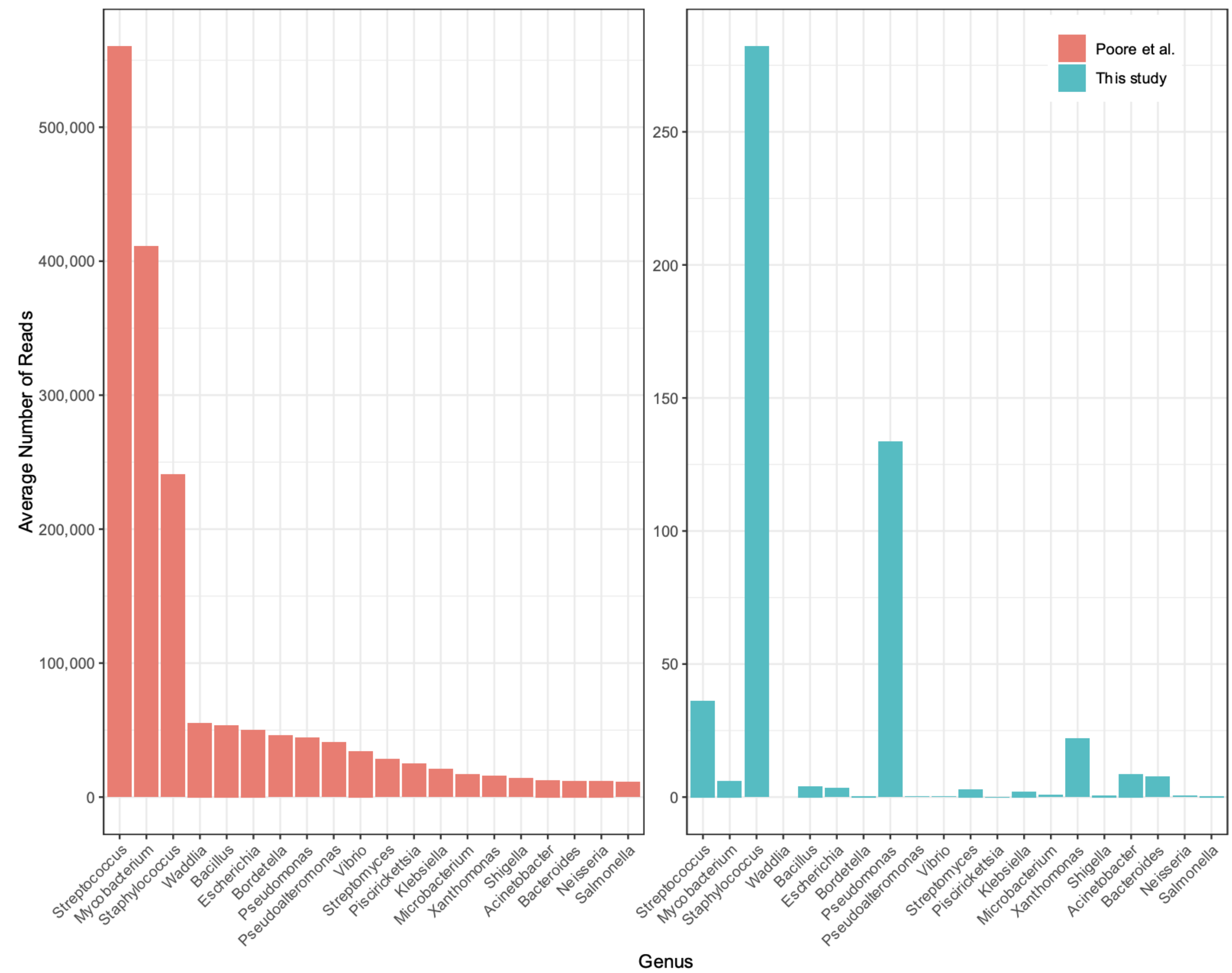
Amplicon Sequence Variants (ASVs)



Major data analysis errors invalidate cancer microbiome findings
Abraham Gihawi^{1,*}, Yuchen Ge^{2,3,*}, Jennifer Lu^{2,3,*}, Daniela Puiu^{2,3}, Amanda Xu², Colin S. Cooper¹, Daniel S. Brewer^{1,4}, Mihaela Pertea^{2,3,5}, and Steven L. Salzberg^{2,3,5,6†}

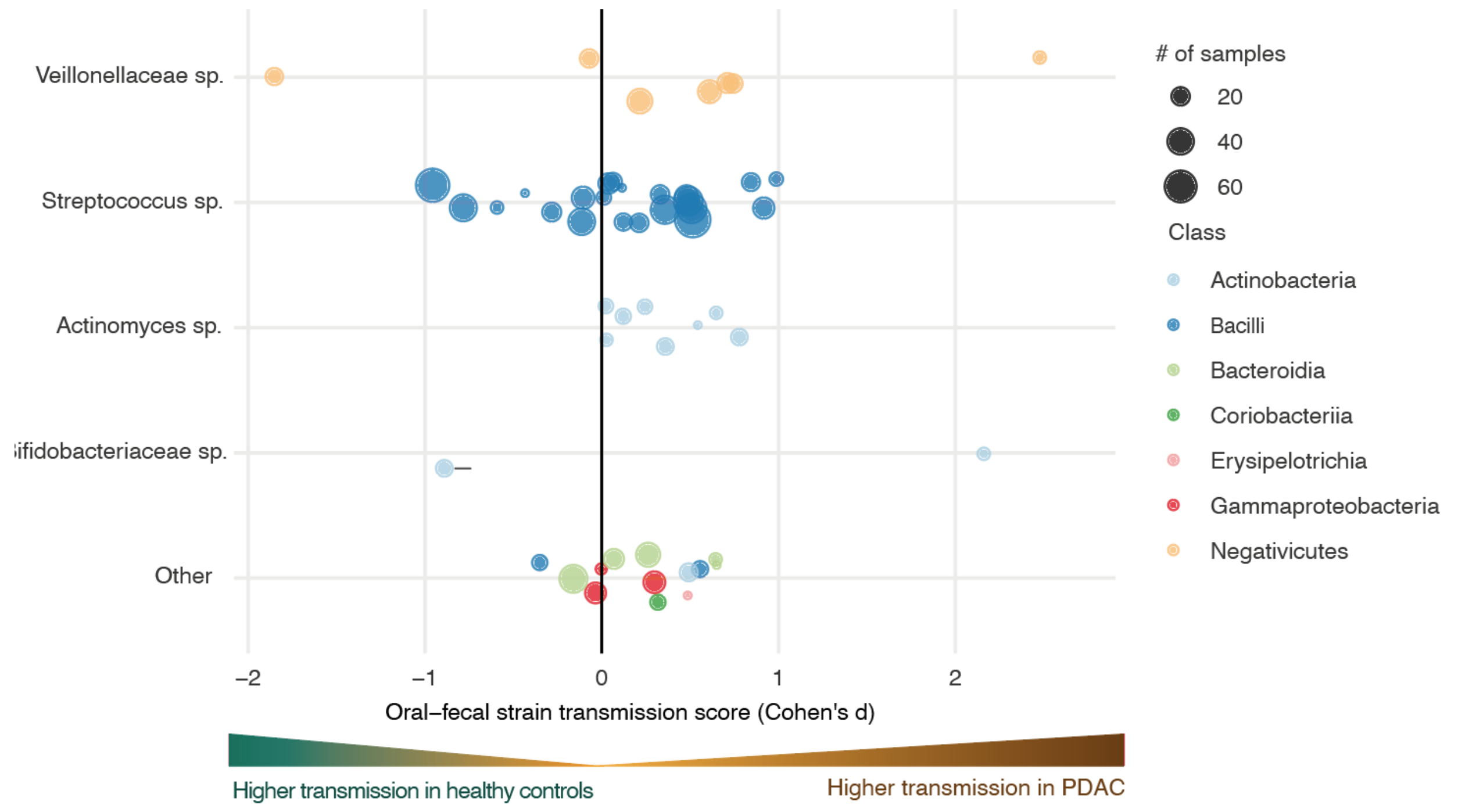
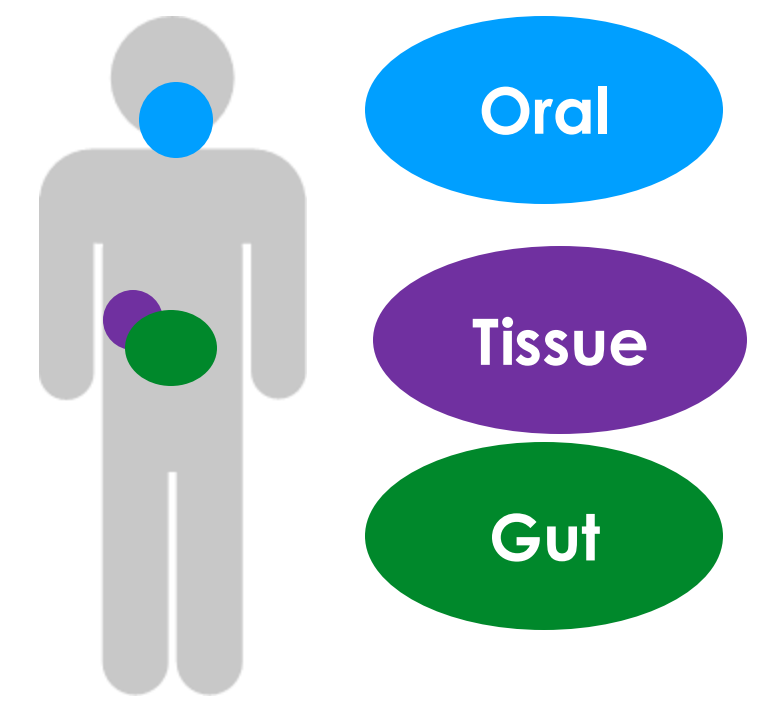
- 1. Norwich Medical School, University of East Anglia, Norwich, UK
- 2. Center for Computational Biology, Johns Hopkins University, Baltimore, Maryland, USA
- 3. Department of Biomedical Engineering, Johns Hopkins University, Baltimore, Maryland, USA
- 4. Earlham Institute, Norwich Research Park, Colney Lane, Norwich, UK
- 5. Department of Computer Science, Johns Hopkins University, Baltimore, Maryland, USA
- 6. Department of Biostatistics, Johns Hopkins University, Baltimore, Maryland, USA

*These authors contributed equally to this work.
†Corresponding author, salzberg@jhu.edu.

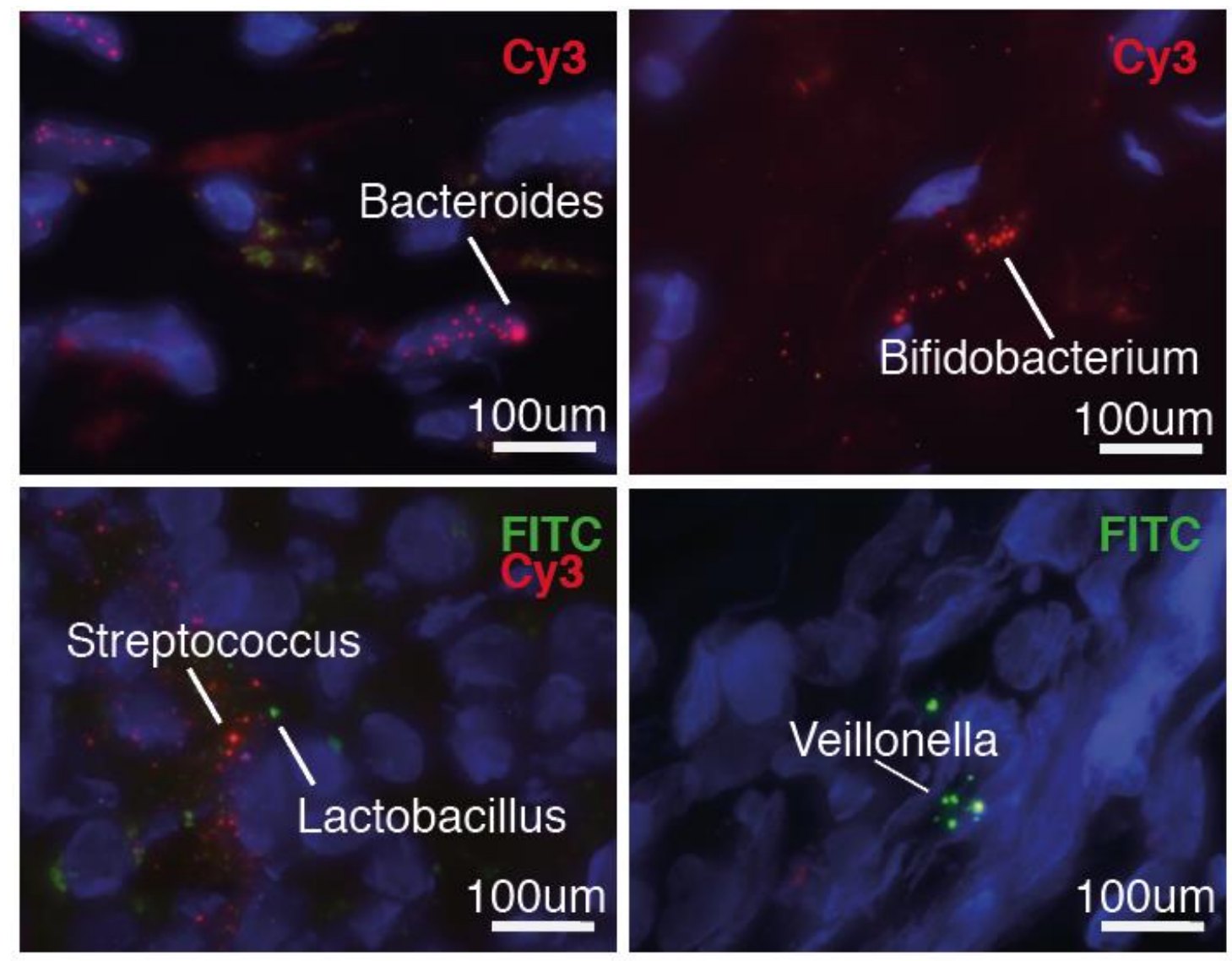


Presence of key genera in pancreas

Amplicon Sequence Variants (ASVs)



Fluorescent in-situ hybridization





Summary I

- Fecal microbiome represents a PDAC-associated microbial signature
- Fecal microbiome has a potential for PDAC screening in clinics
- Pancreatic tissue harbors a unique microbiome, which differs btw tumor and non-tumor tissue





Original research

A faecal microbiota signature with high specificity for pancreatic cancer

Ece Kartal ^{1,2} Thomas S B Schmidt ¹ Esther Molina-Montes ^{3,4}
Sandra Rodríguez-Perales ^{4,5} Jakob Wirbel ^{1,2} Oleksandr M Maistrenko ¹
Wasiu A Akanni ¹ Bilal Alashkar Alhamwe ⁶ Renato J Alves ¹
Alfredo Carrato ^{4,7,8} Hans-Peter Erasmus⁹ Lidia Estudillo ^{3,4}
Fabian Finkelmeier^{9,10} Anthony Fullam ¹ Anna M Glazek¹ Paulina Gómez-Rubio^{3,4}
Rajna Hercog¹¹ Ferris Jung ¹¹ Stefanie Kandels ¹ Stephan Kersting ^{12,13}
Melanie Langheinrich ¹³ Mirari Márquez^{3,4} Xavier Molero^{14,15,16}
Askarbek Orakov ¹ Thea Van Rossum ¹ Raul Torres-Ruiz ^{4,5}
Anja Telzerow ¹¹ Konrad Zych ¹ MAGIC Study investigators, PanGenEU Study
investigators, Vladimir Benes ¹¹ Georg Zeller ¹ Jonel Trebicka ^{9,17}
Francisco X Real ^{4,18,19} Nuria Malats ^{3,4} Peer Bork ^{1,20,21,22}

► Additional supplemental material is published online only. To view, please visit the journal online (<http://dx.doi.org/10.1136/gutjnl-2021-324755>).

For numbered affiliations see end of article.

ABSTRACT

Background Recent evidence suggests a role for the microbiome in pancreatic ductal adenocarcinoma (PDAC) aetiology and progression.

Objective To explore the faecal and salivary microbiota as potential diagnostic biomarkers.

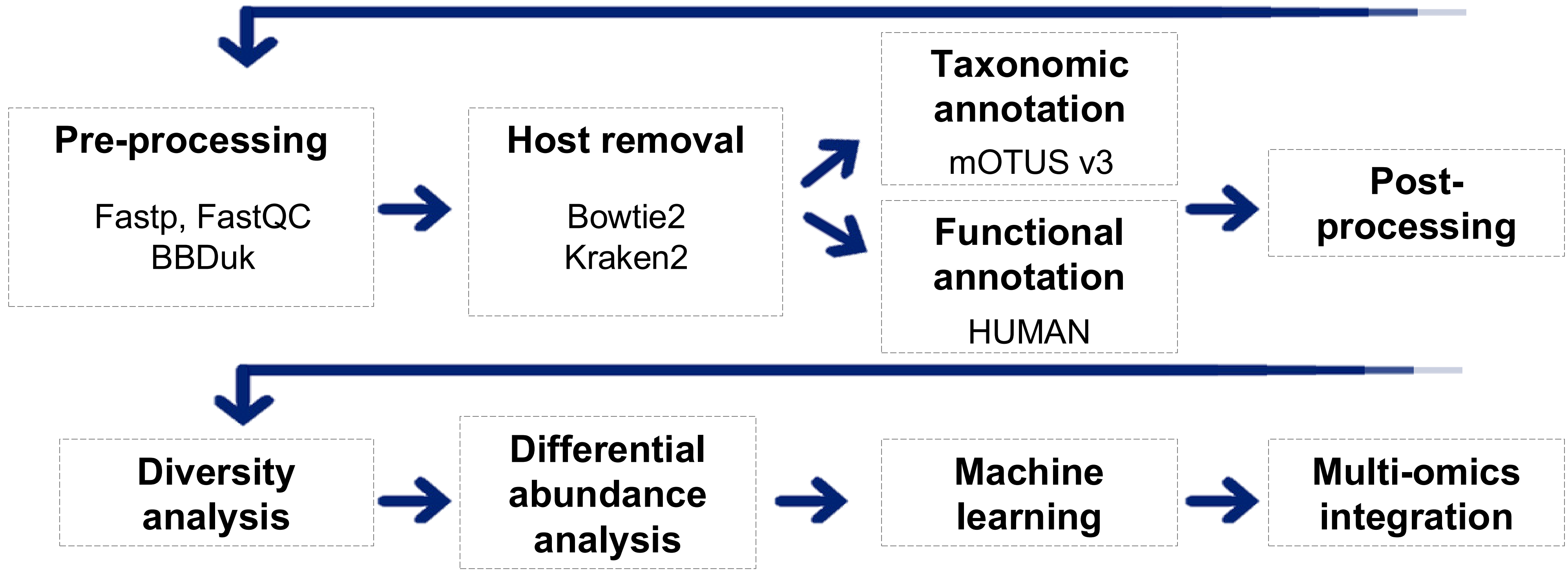
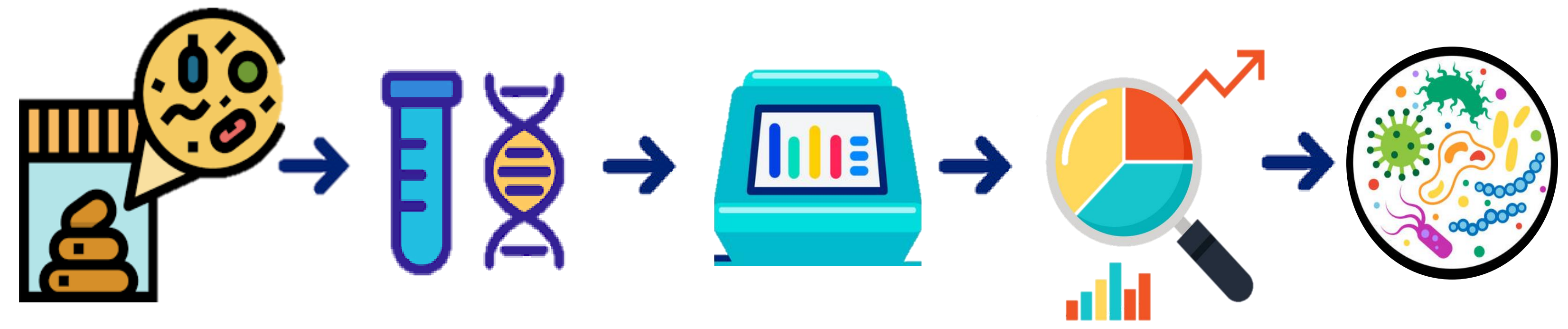
Significance of this study

What is already known about this subject?

⇒ Pancreatic ductal adenocarcinoma (PDAC) is on the rise worldwide, posing a high disease burden and

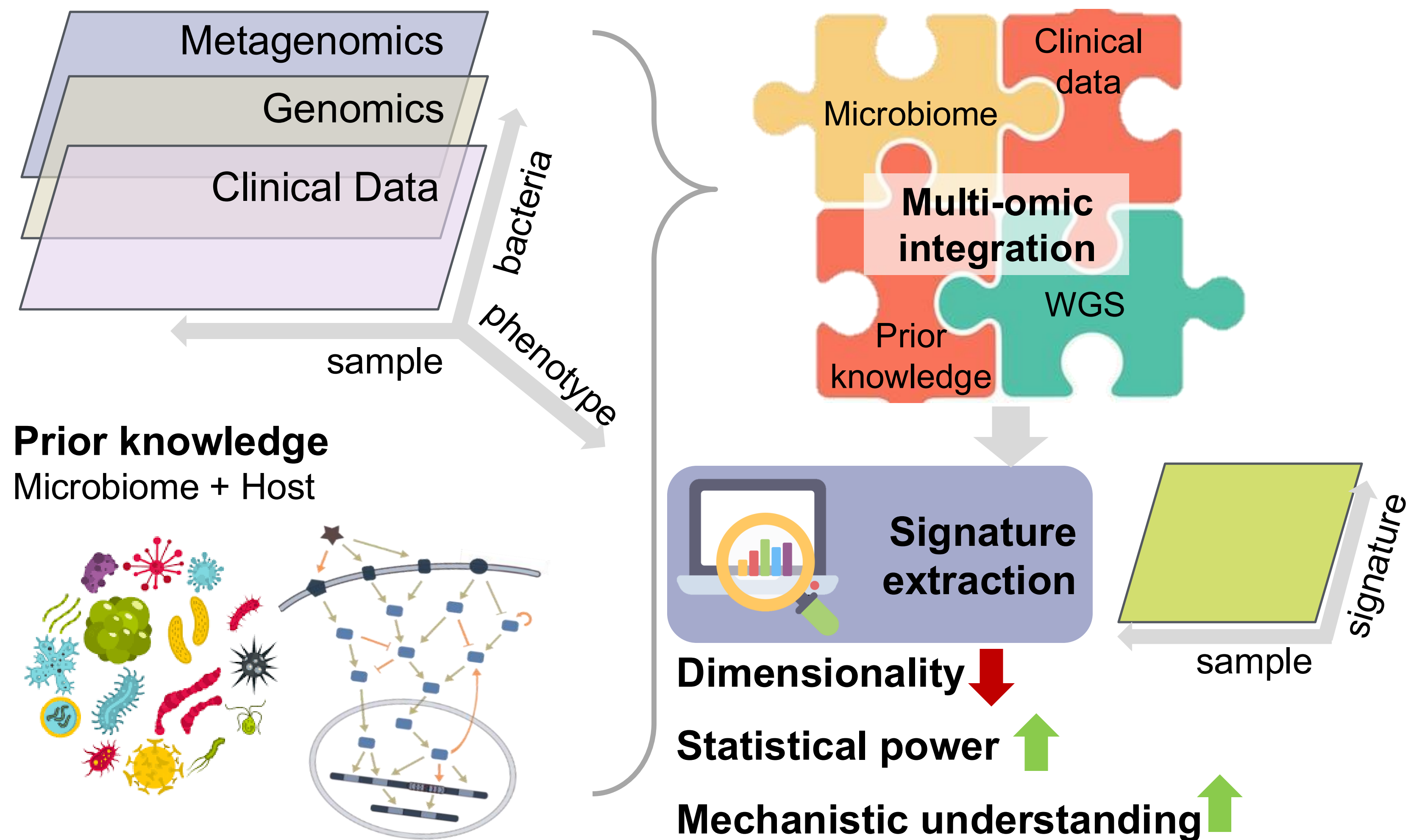


Data processing details (Snakemake workflow)





Multi-omics integration:



Lets go!

