



Identification of a Gut Microbial Signature Linked to Severity of Irritable Bowel Syndrome

Julien Tap, Lena Ohman, Hans Törnblom, Boris Le Nevé, Remi Brazeilles,
Joël Doré, Muriel Derrien, Magnus Simren

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Identification of a Gut Microbial Signature Linked to Severity of Irritable Bowel Syndrome

Julien Tap

Lena Öhman, Hans Törnblom, Boris Le Névé,
Rémi Brazeilles, Joël Doré, Muriel Derrien, Magnus Simrén



UNIVERSITY OF
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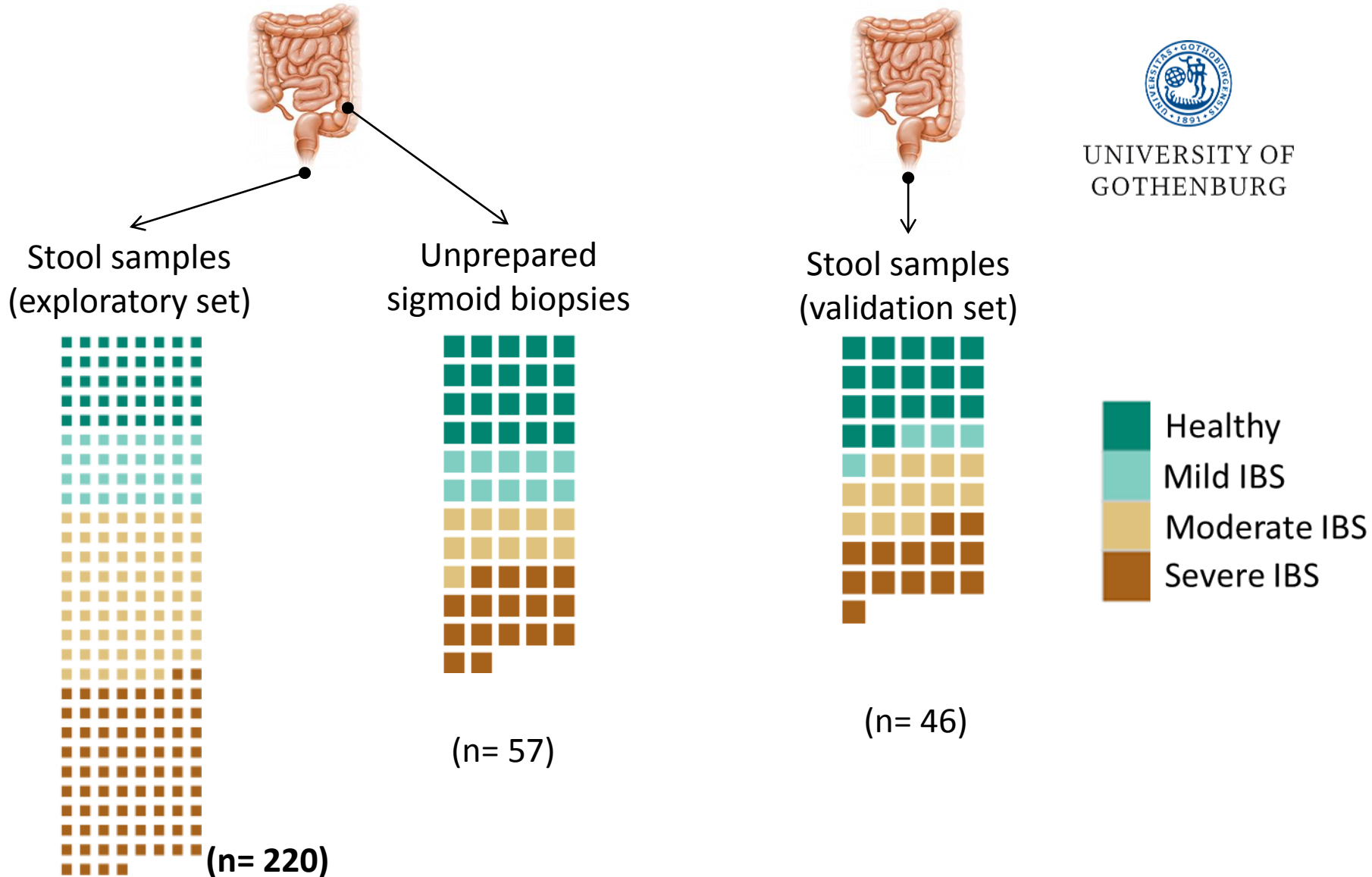
#DDW15
@julientap

IBS and Gut Microbiota hypothesis

- Irritable Bowel Syndrome (IBS) : most common GI disorder (10-15% western pop.)
- Symptom severity and pattern are used to stratify IBS patients (IBS-SSS, ROME III)
- Gut microbiota might play a role in IBS pathophysiology
- Gut microbiota studies on IBS vs healthy showed differences but **low sample size ($n < 50$)** may explain heterogeneity of outcomes

Aim: to explore gut microbiota in a larger IBS cohort and to establish a potential link with symptom severity.

Large dataset



Clinical data

- Age, BMI, gender
- Symptom severity and pattern :
 - IBS-SSS,
 - ROME III subtypes
- Psychological symptoms
- Quality of Life
- Exhaled gas : CH₄, H₂

Gut microbiota analysis

16S rRNA gene targeted metagenomics
Quantitative PCR targeted on Archaea



Sample (stool, biopsy)



Extract

DNA



Sequence

Reads



Denoising & clustering

Numerical Data



Ecological and statistical data analysis



Numerical Data

Richness and beta-diversity assessment

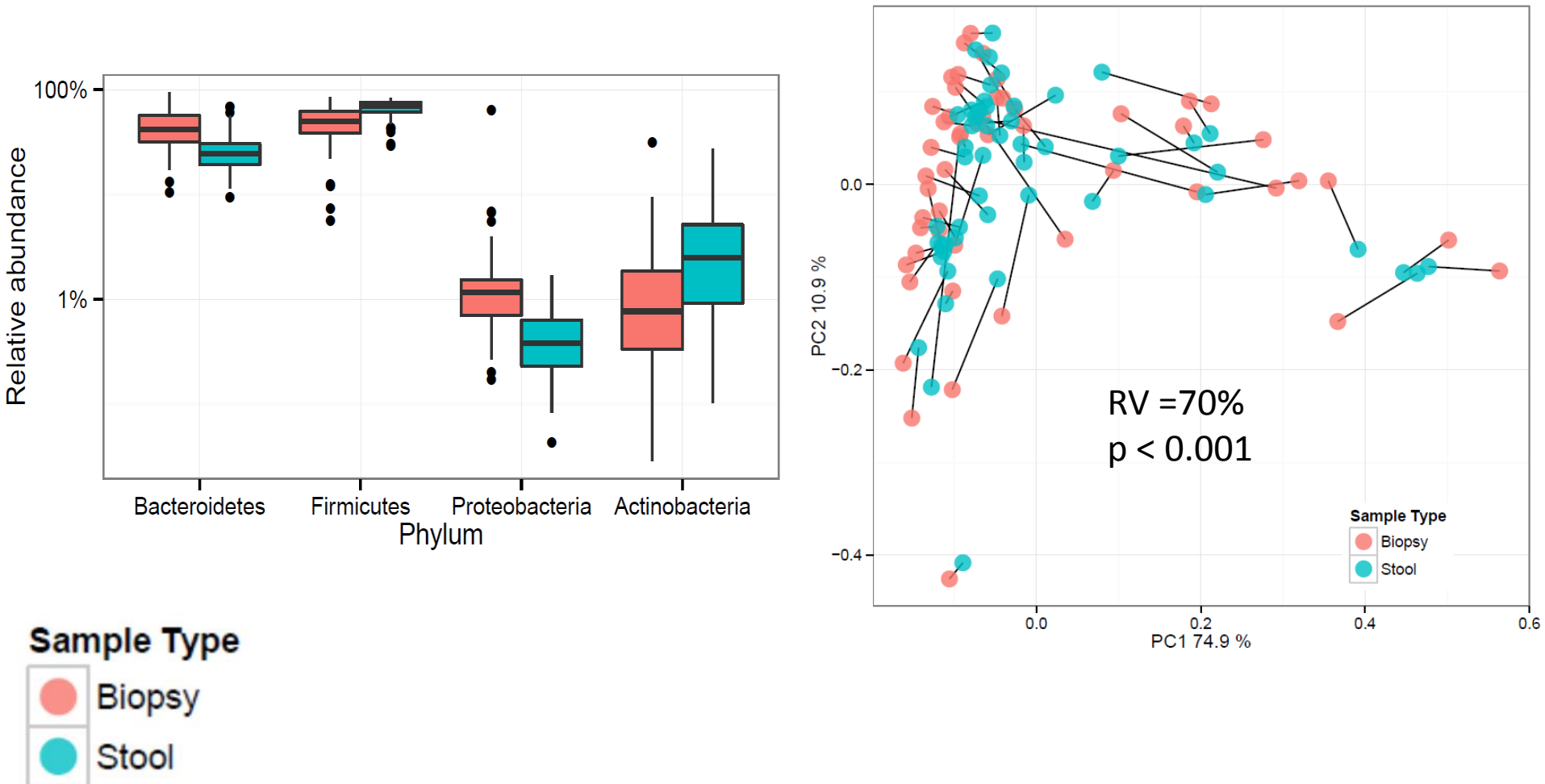
Unsupervised enterotyping

Univariate and multivariate analysis

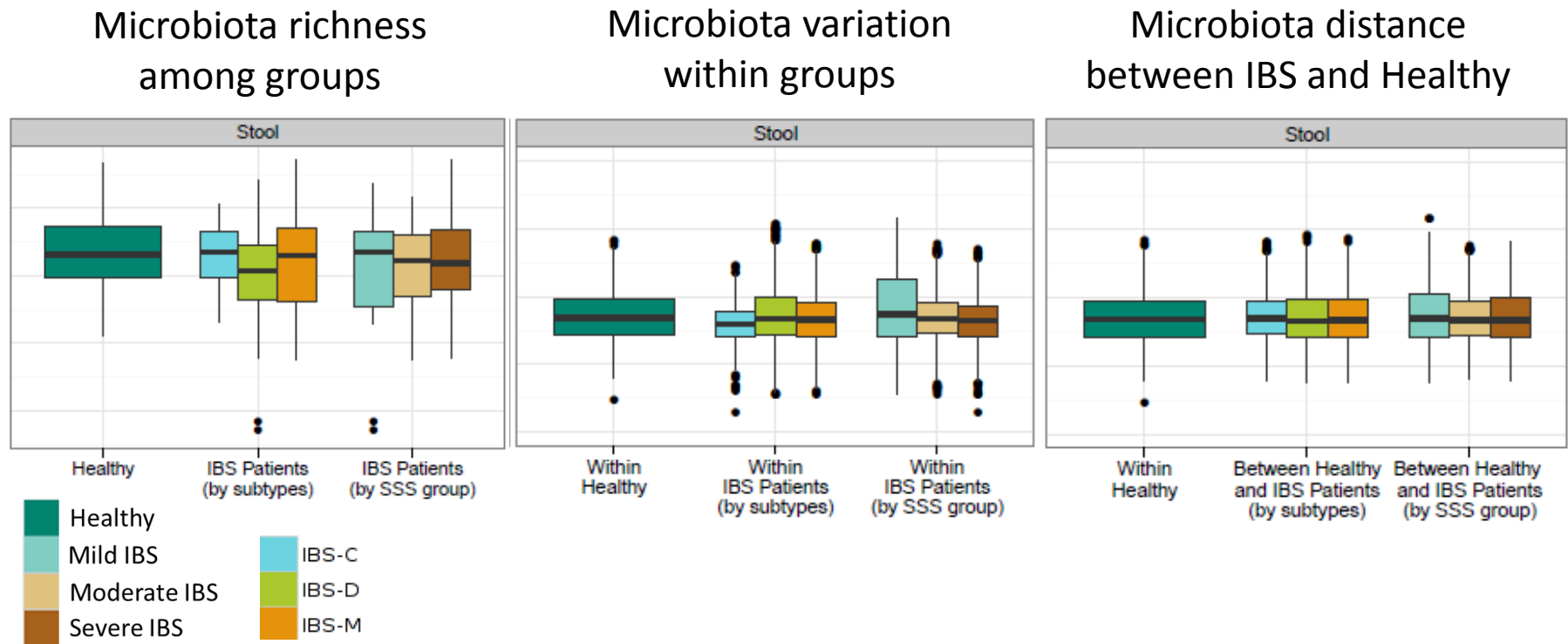
Machine learning procedure

Gut Microbial Signature for IBS Severity

Fecal microbiota is a good proxy for mucosal microbiota

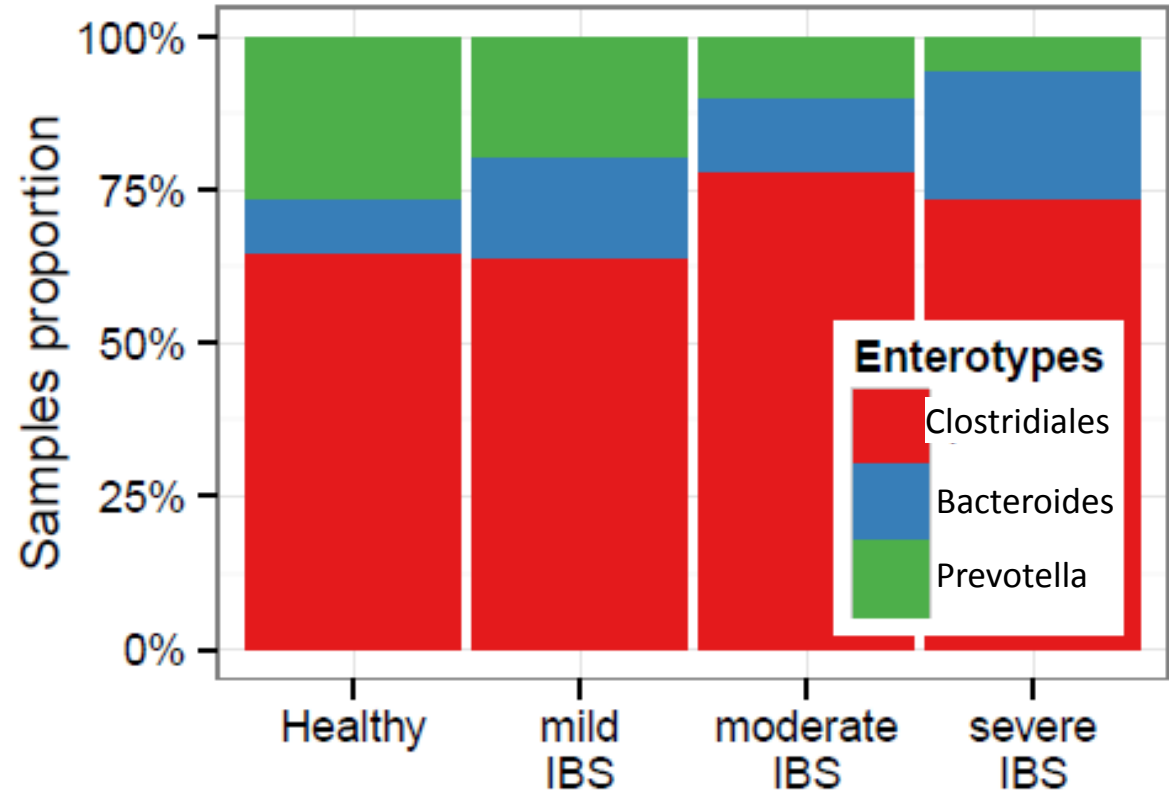
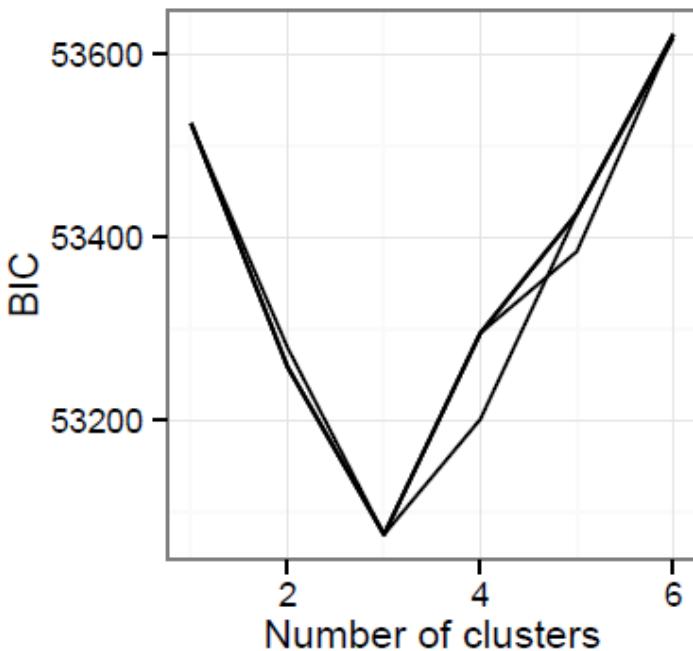


No major global microbial ecological difference between IBS and healthy



- Microbiota richness did not differ between IBS and healthy
- Gut microbiota variation was homogenous across groups
- No difference with global microbial distance between Healthy and IBS

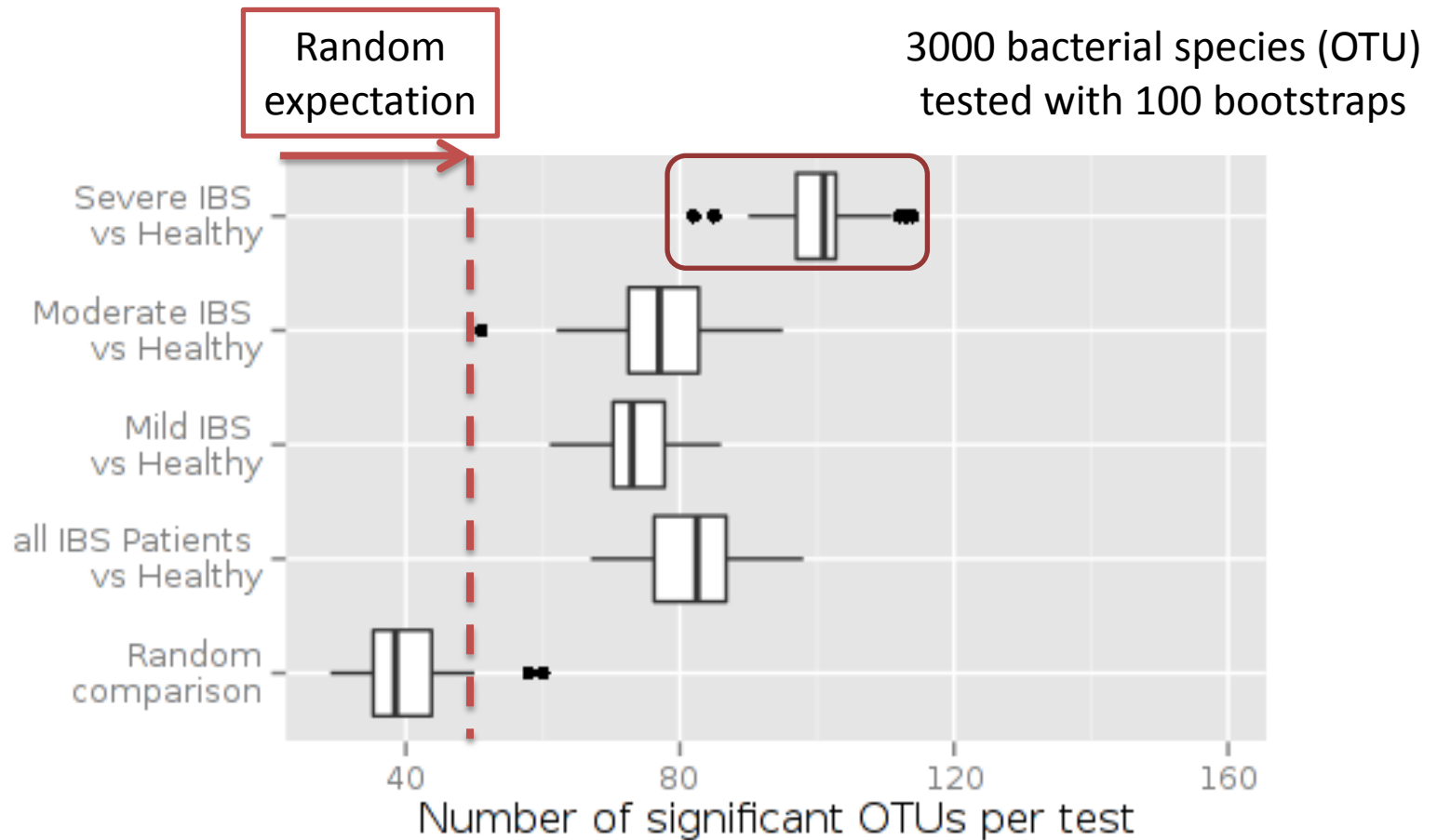
Gut microbiota enterotypes in IBS



3 enterotypes found in the stool dataset equivalent to those published elsewhere

Link between IBS severity score and enterotypes distribution

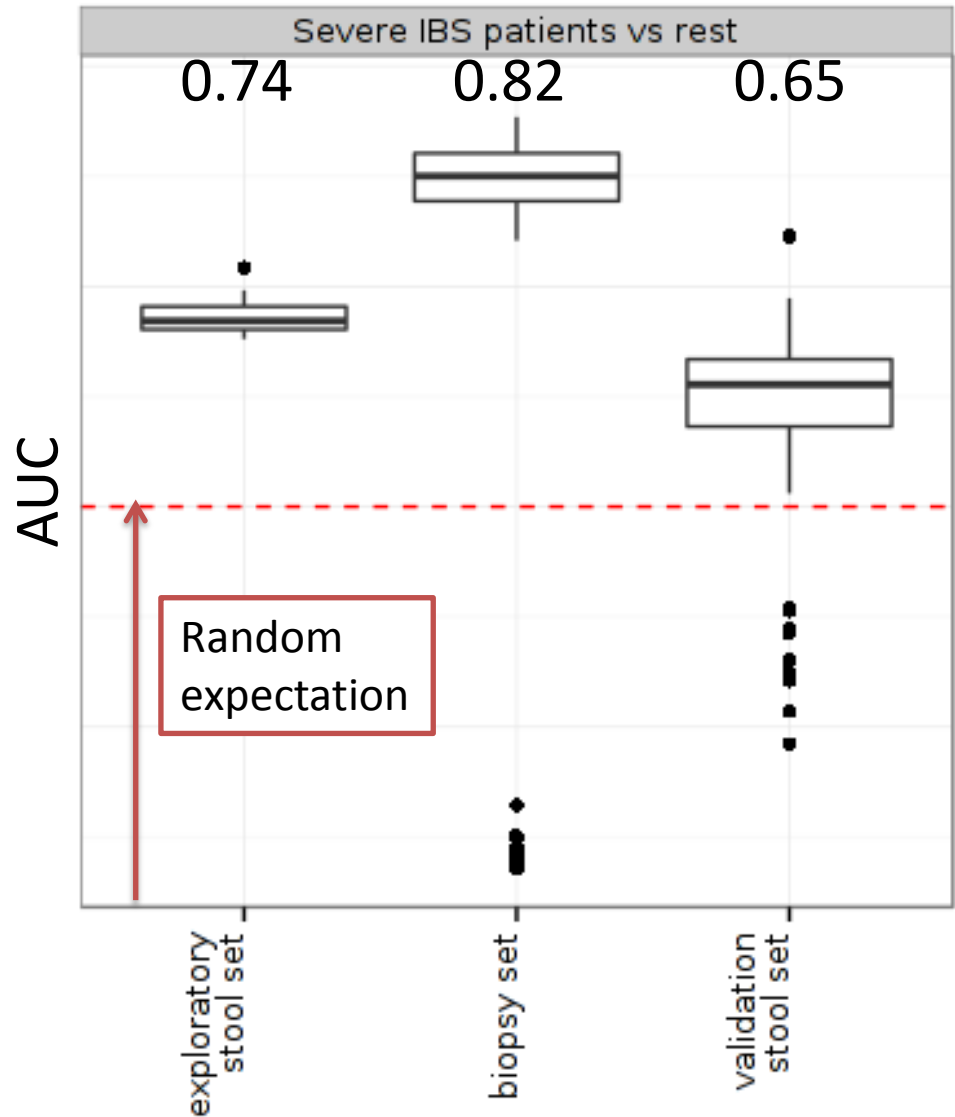
Towards a gut microbial signature for IBS severity



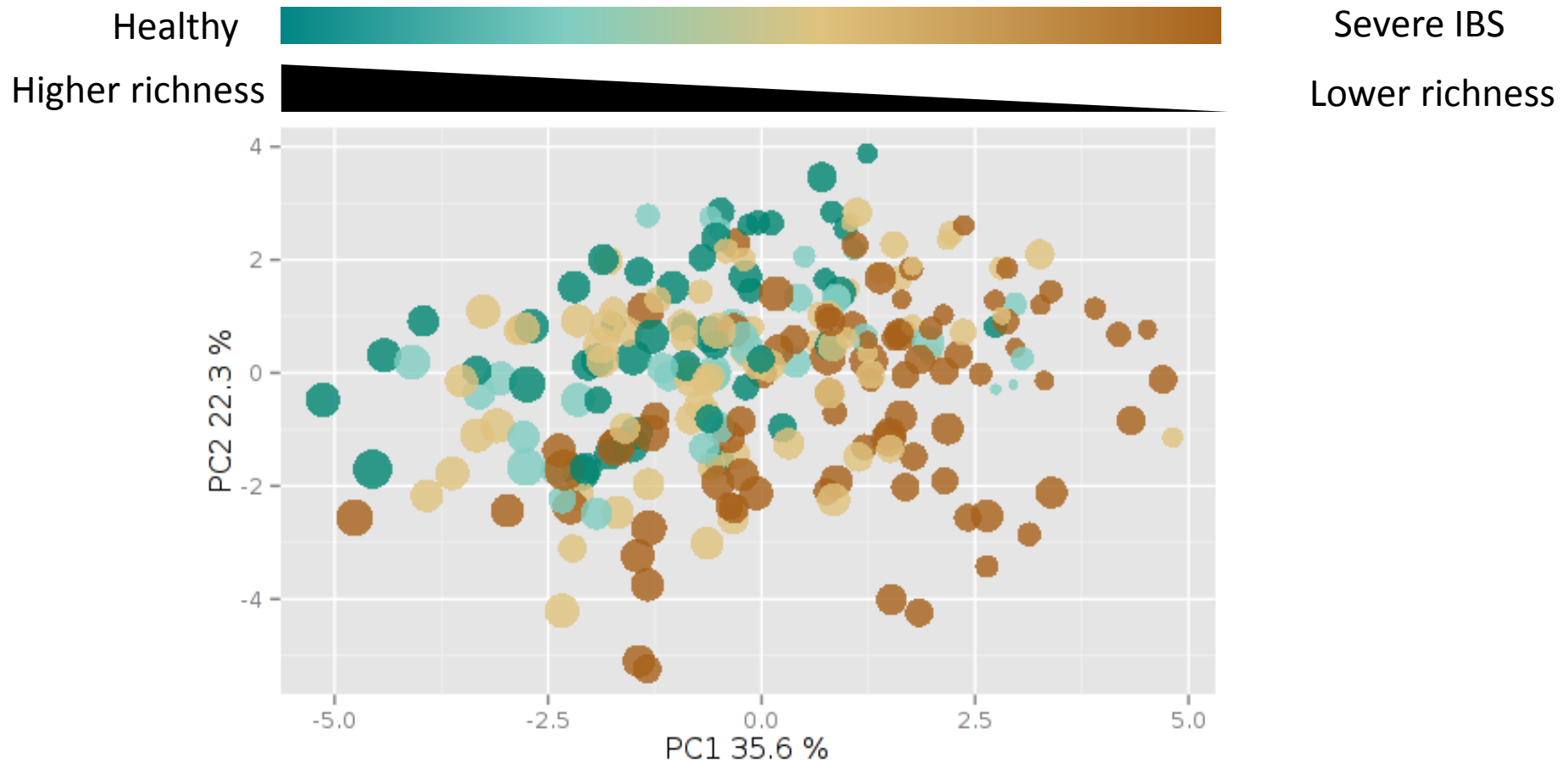
100 bacterial species might be significant for severe IBS but 50 might be just random!

Towards a gut microbial signature for IBS severity

- Machine learning procedure allows finding a microbial signature for IBS severity
- This signature is validated in biopsies and an independent stool samples set



Gut microbial signature for IBS severity is linked with lower microbial richness

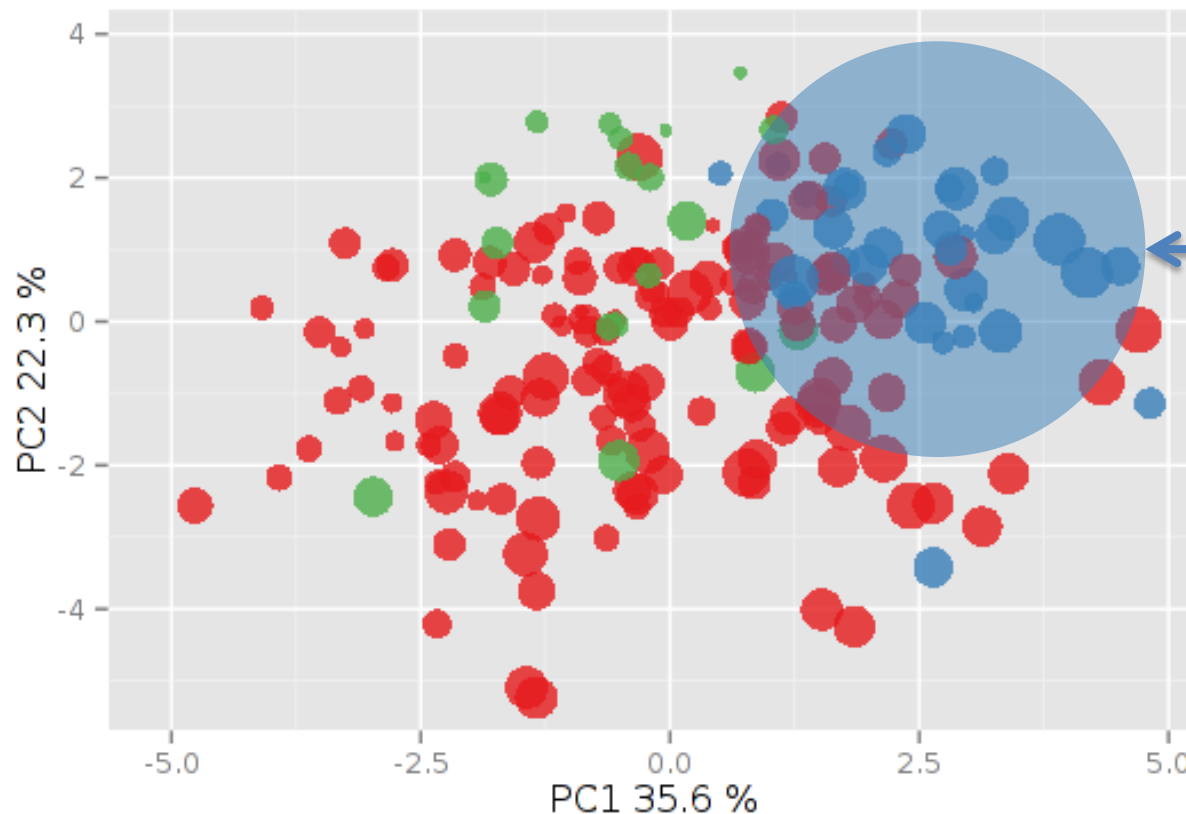


Bacterial species extracted from IBS severity signature
allowed to order samples in association with clinical metadata

Gut microbial signature for IBS severity is linked with *Bacteroides*-enriched enterotype

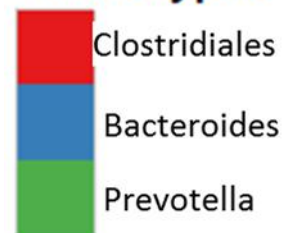
Lower severity

Higher Severity

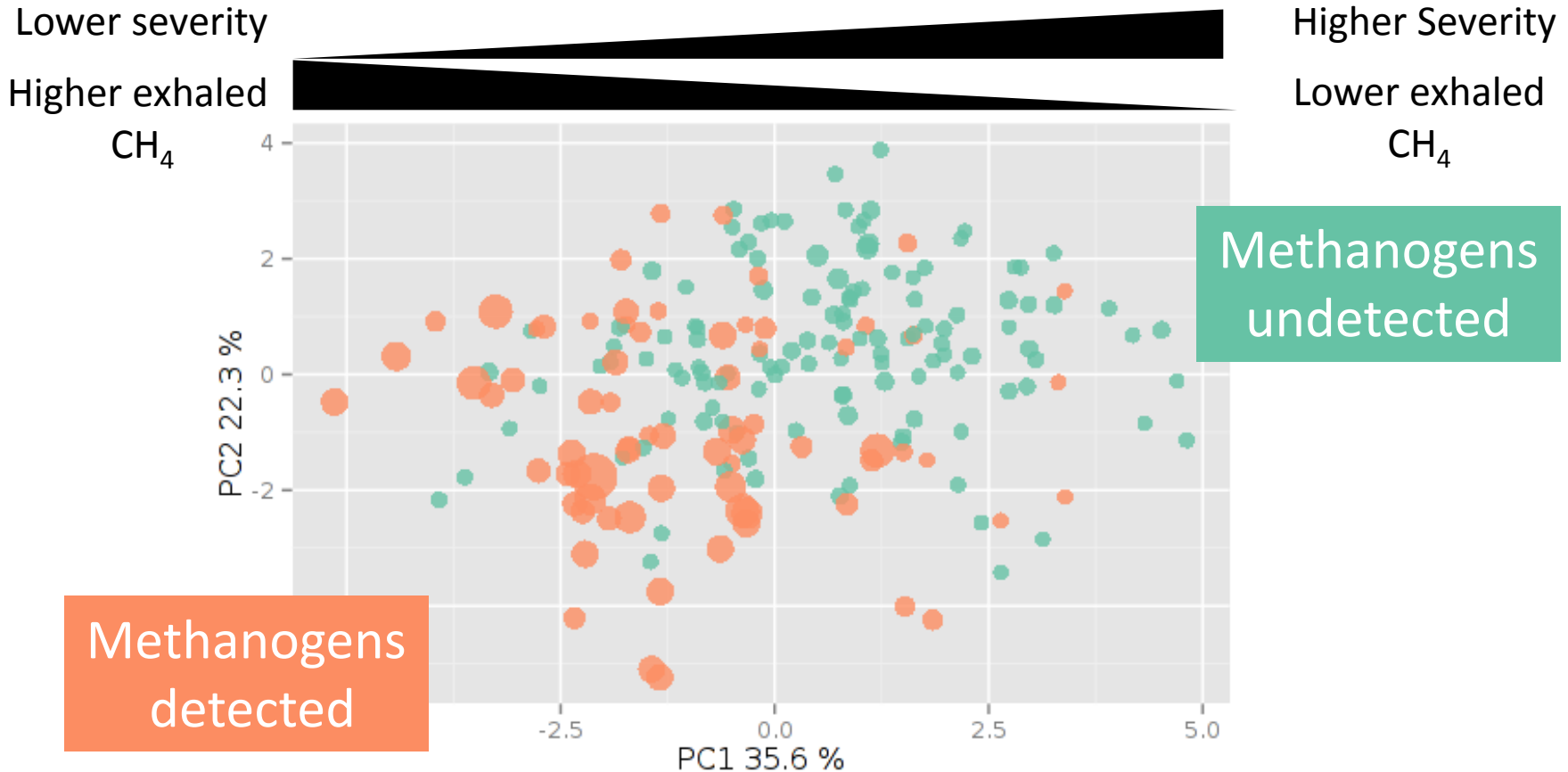


Higher IBS severity scores were found in ***Bacteroides*** enriched enterotype

Enterotypes



Gut microbial signature for IBS severity is linked with lower exhaled CH_4



Take home messages

- A larger cohort of IBS patients ($n > 200$) allows finding gut microbiota alteration **over random expectation**
- IBS symptom severity is associated with a distinct signature at fecal microbiota level
- Gut microbial signature for IBS severity is linked with
 - low microbial richness
 - *Bacteroides* enriched enterotype
 - low Archea methanogens and exhaled CH_4

The role of gut microbiota alterations
in the genesis of IBS remains to be investigated

Acknowledgments



UNIVERSITY OF
GOTHENBURG

M. Simrén
H. Törnblom
L. Öhman



INRA
SCIENCE & IMPACT

J. Doré



**DANONE
NUTRICIA
RESEARCH**

B. Le Nevé
M. Derrien
R. Brazeilles
S. Cools-Portier