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# NEW INSIGHTS ON RELATIONSHIPS BETWEEN FODMAPS INTAKE, GUT MICROBIOTA AND SEVERITY OF SYMPTOMS IN IRRITABLE BOWEL SYNDROME

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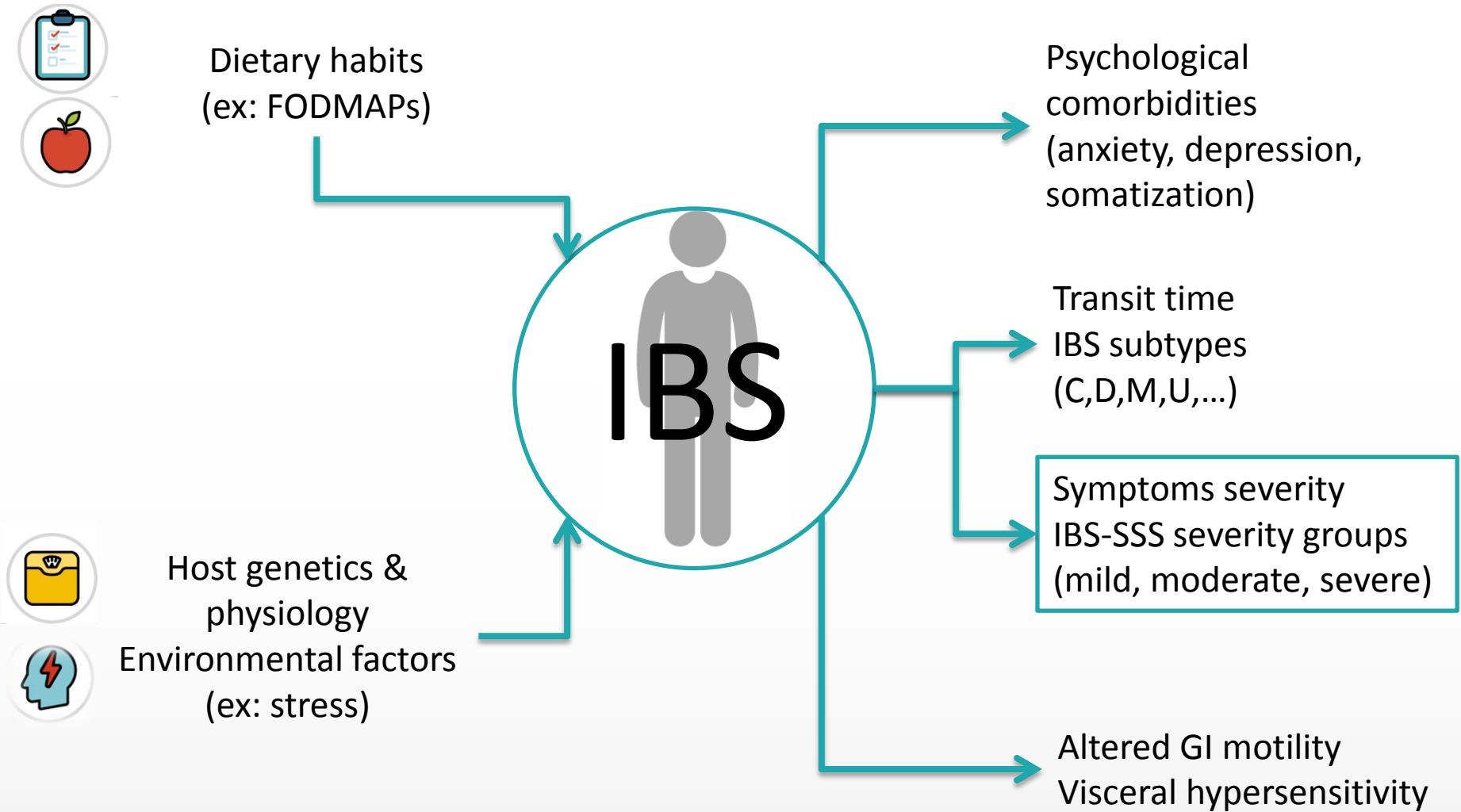
# NEW INSIGHTS ON RELATIONSHIPS BETWEEN FODMAPS INTAKE, GUT MICROBIOTA AND SEVERITY OF SYMPTOMS IN IRRITABLE BOWEL SYNDROME

**Julien Tap**

Muriel Derrien, Hans Törnblom, Nicolas Pons, Stéphanie Cools,  
Joël Doré, Boris Le Nevé, Lena Öhman, Magnus Simrén



# COMPLEXITY OF IRRITABLE BOWEL SYNDROME (IBS)

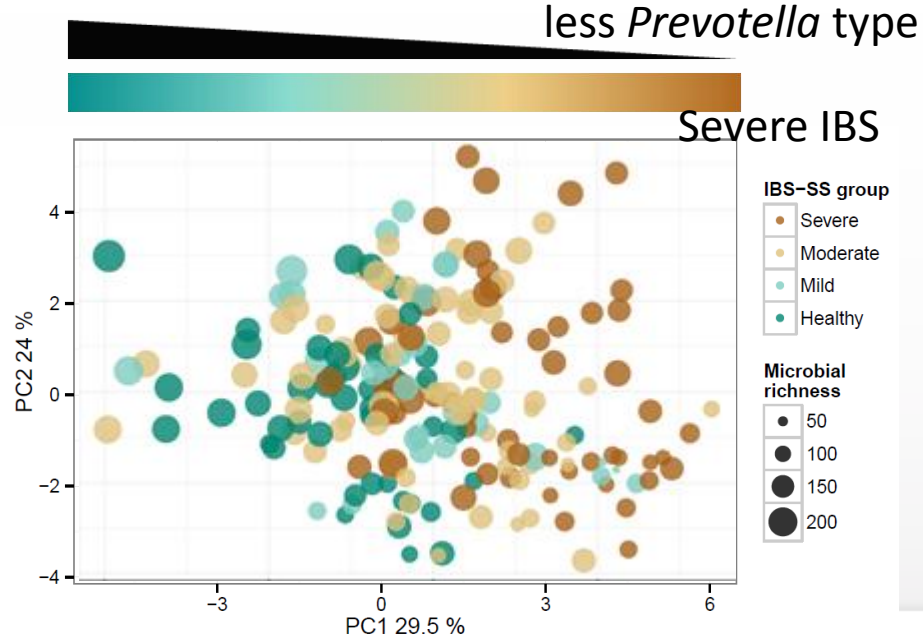
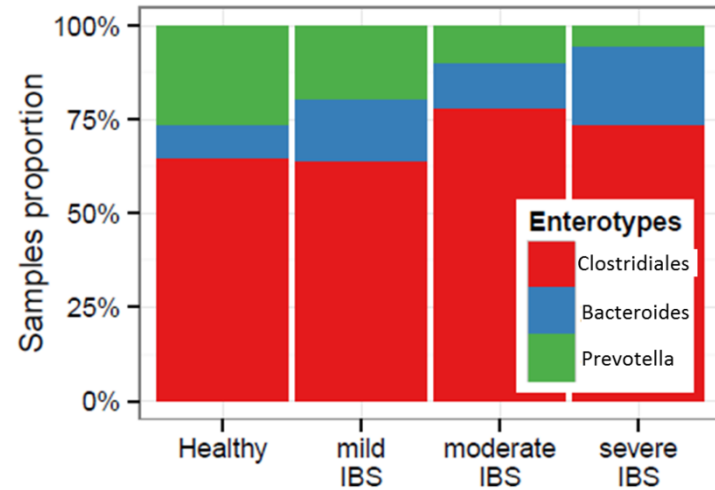
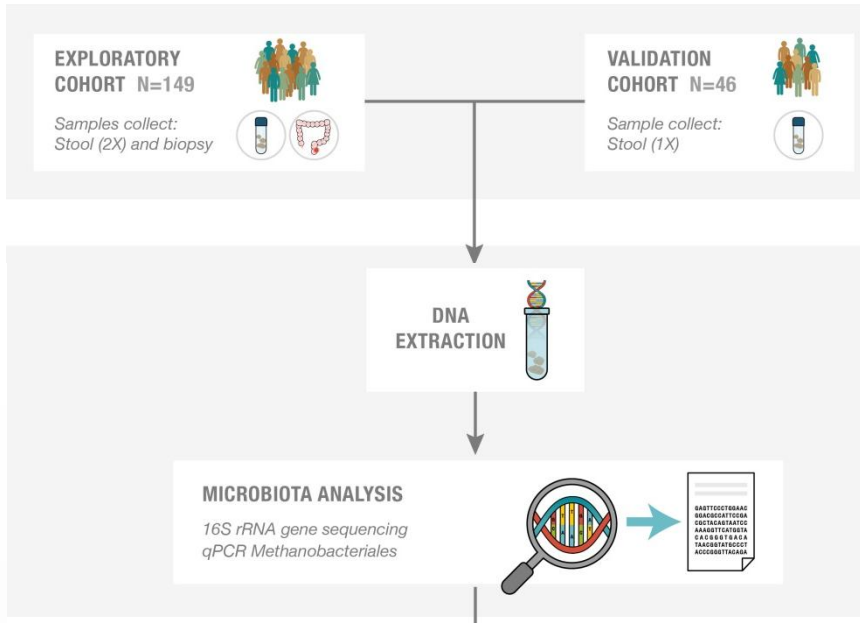


# STUDY SCHEME

Je rajouterai une slide sur le process utilisé en terme analytique

- Nombre échantillons
- Analyses faites ...

# SEVERITY OF IBS SYMPTOMS IS LINKED WITH GUT MICROBIOTA



90 bacterial OTUs selected



Gastroenterology

Available online 7 October 2016

In Press, Accepted Manuscript — Note to users



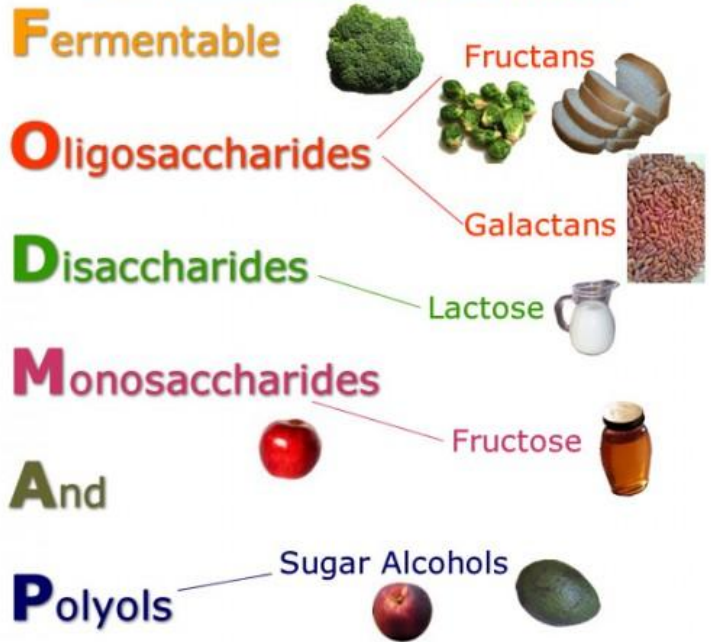
## Identification of an Intestinal Microbiota Signature Associated With Severity of Irritable Bowel Syndrome

Julien Tap<sup>1,2,\*</sup>, Muriel Derrien<sup>1</sup>, Hans Törnblom<sup>3,4</sup>, Rémi Brazeilles<sup>1</sup>, Stéphanie Cools-Portier<sup>1</sup>, Joël Doré<sup>2</sup>, Stine Störsrud<sup>3</sup>, Boris Le Nevé<sup>1</sup>, Lena Öhman<sup>3,5,6,#</sup>, Magnus Simrén<sup>3,4,7</sup>

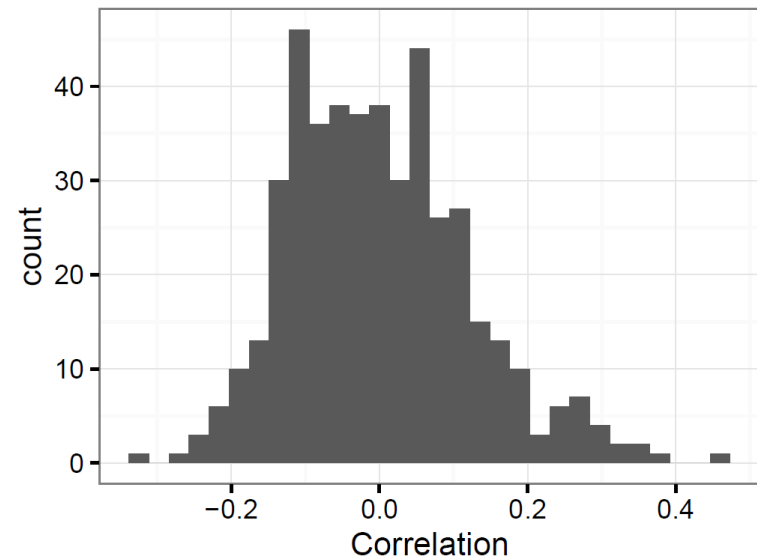


# IBS SEVERITY AND INTAKE OF FODMAPS

*IBS may be helped by keeping these FODMAPs food to a minimum*  
<http://blissfulwriter.hubpages.com/t/31f135>



... but no obvious link was found between IBS severity microbial OTU signature and intake of FODMAPs in our study

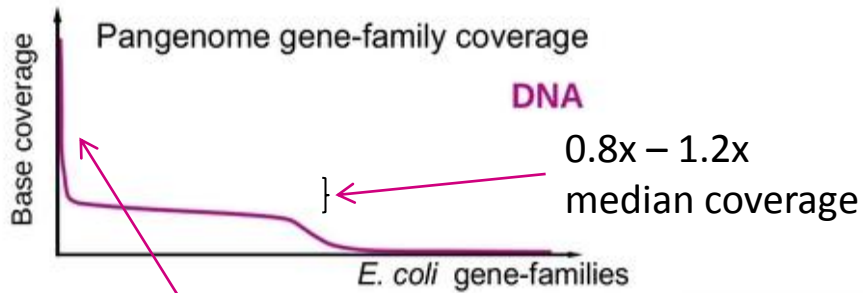


Is there a link between IBS severity, FODMAPs intake and microbiota genes content ?

# FROM BACTERIAL SPECIES TO GENOMIC DIVISIONS USING DIRECT METAGENOMICS SEQUENCING

1) Convert coverage information to presence absence matrix

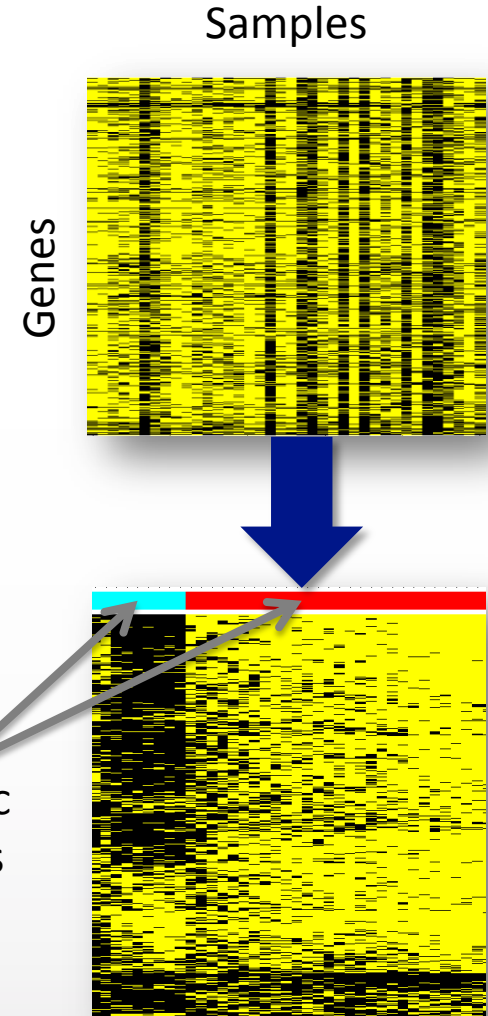
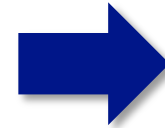
PanPhlan method adapted to SOLiD mapping data



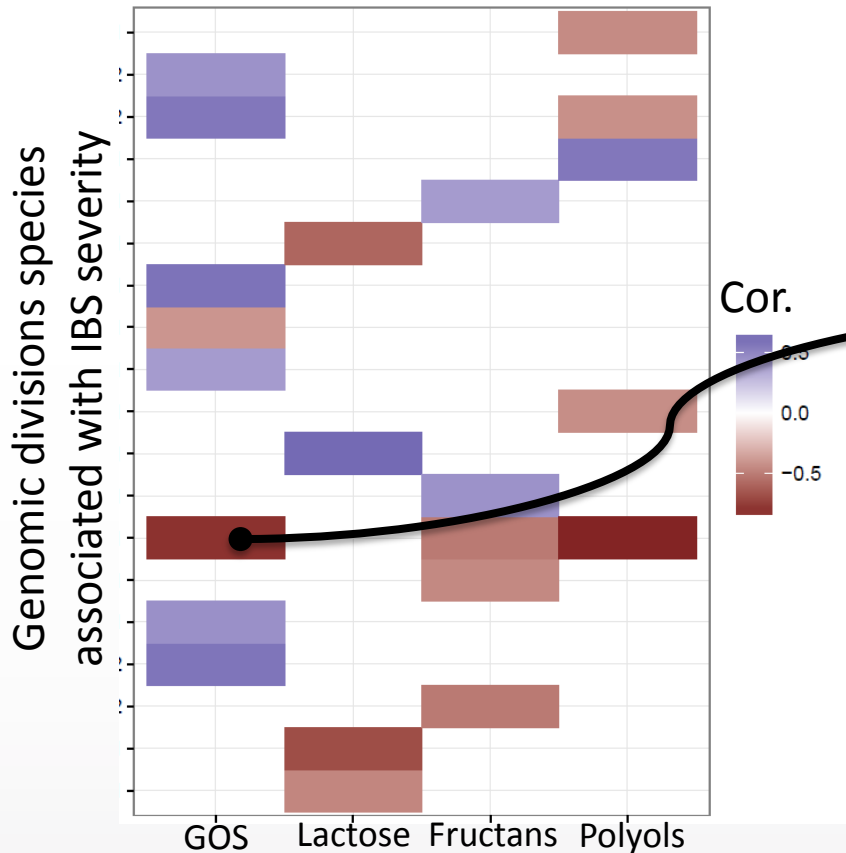
Multi copy genes

2) Detect Genomic division within metagenomics species

Bernoulli mixture model  
Block EM algorithm  
(Bhatia et al. Blockcluster.)

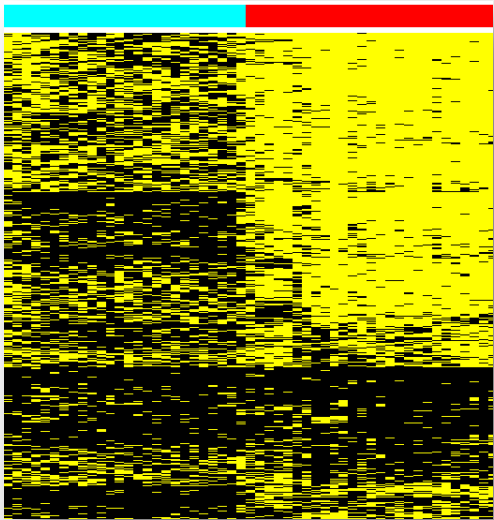


# INTAKE OF FODMAPS IS ASSOCIATED WITH SOME GENOMIC DIVISIONS OF IBS SEVERITY MICROBIOTA SIGNATURE



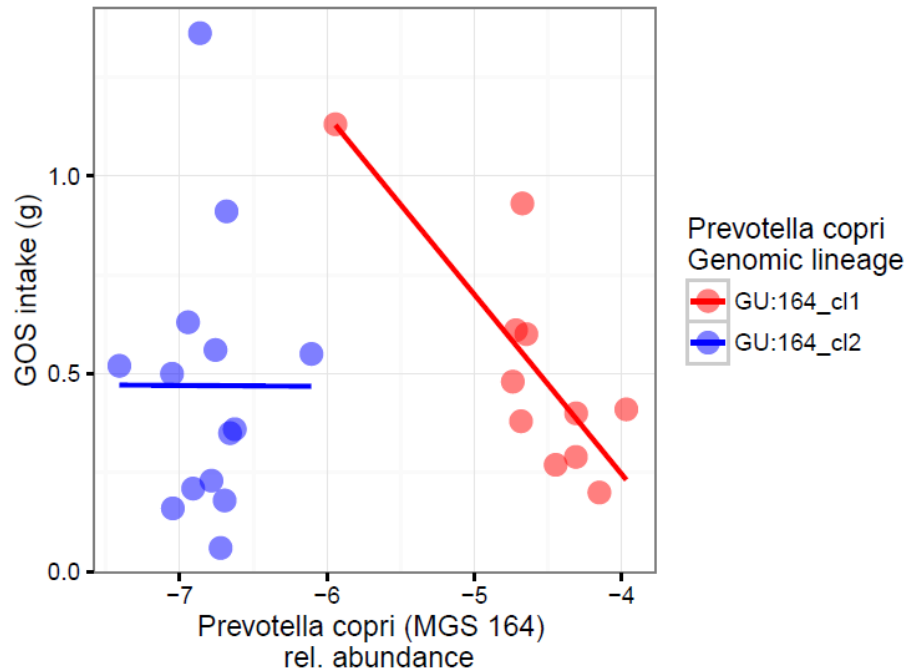
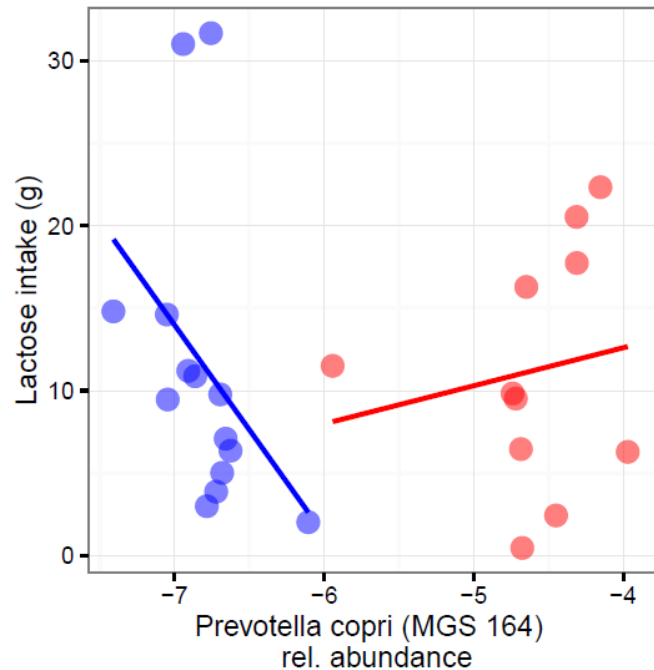
Correlation strength between FODMAPs and Genomic Division higher than bacterial OTU analysis

*Prevotella copri* genomic division





# PREVOTELLA COPRI GENOMIC DIVISIONS DIFFERENTLY ASSOCIATE WITH INTAKE OF FODMAPS



GOS and Lactose intake has been associated differently among genomic division of *Prevotella copri*

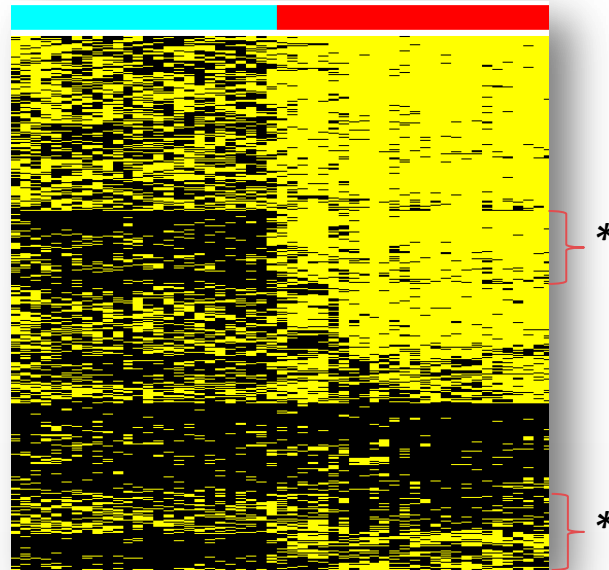
*Mettre exemple -> Clade 1 blabla*

# PREVOTELLA COPRI GENOMIC DIVISION METABOLIC PATHWAYS

*Prevotella copri*  
genomic division

*Prevotella copri* cl2

Amino acid degradation  
Succinate production  
(may promote pathogens)



*Prevotella copri* cl1

Glycolyse hydrolase  
Sucrose degradation  
Sulfate reduction

\*Different genes content was  
detected between the two  
genomic divisions

At genomic division level, links can be found between  
IBS severity, FODMAPs intake and metabolic pathway.

# ACKNOWLEDGMENTS



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