



UNIVERSITÀ DEGLI STUDI DI MILANO

DIPARTIMENTO DI
SCIENZE DELLA SALUTE

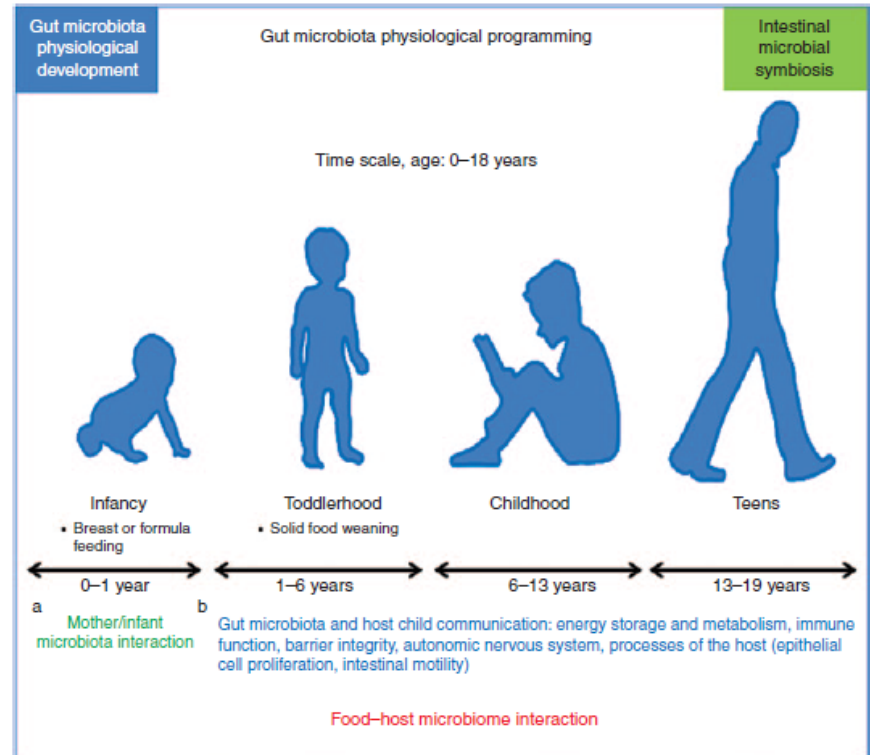
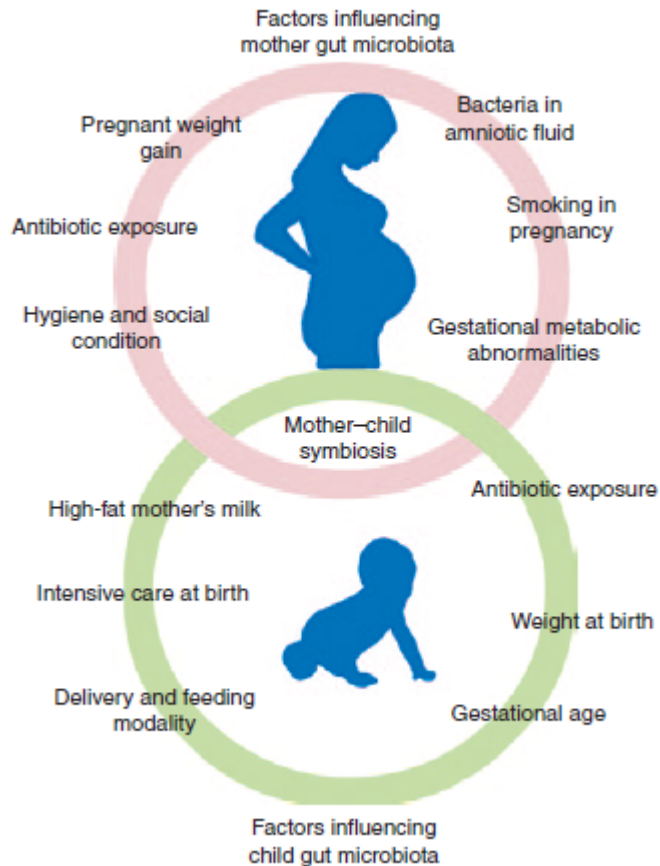
“Pediatric obesity is associated with altered gut microbiota communities”

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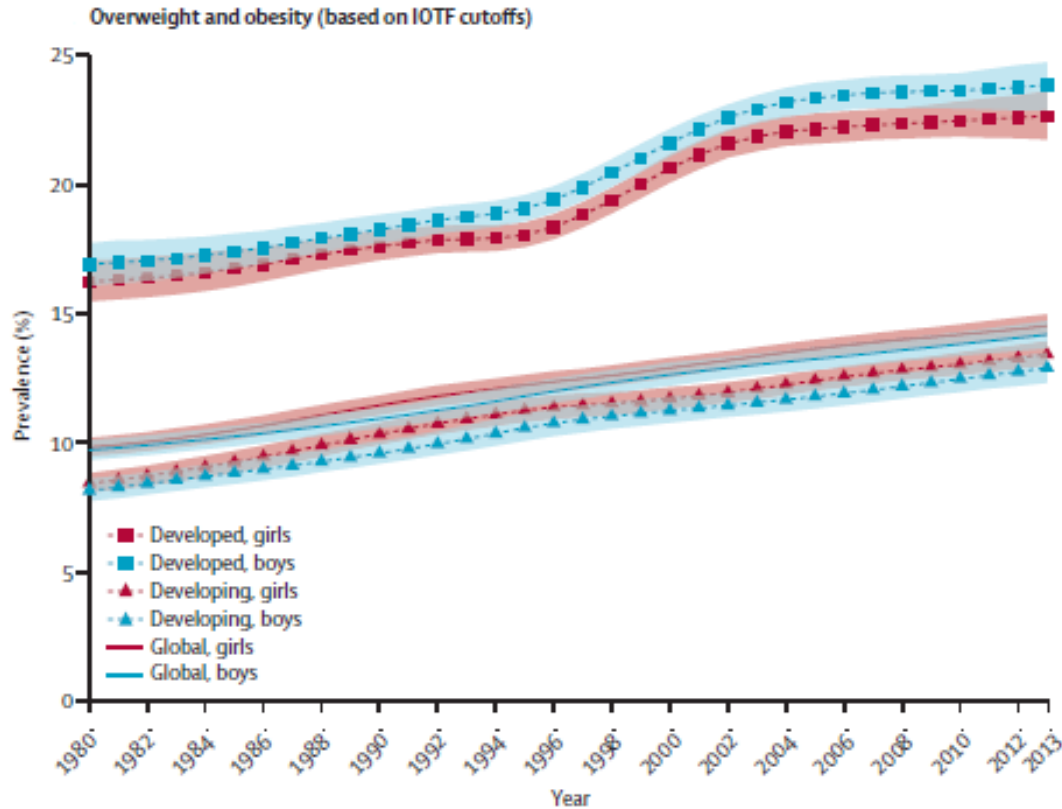
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Munich, 13-15 October 2016

The human gut microbiota: a dynamic interplay with the host from birth to senescence settled during childhood



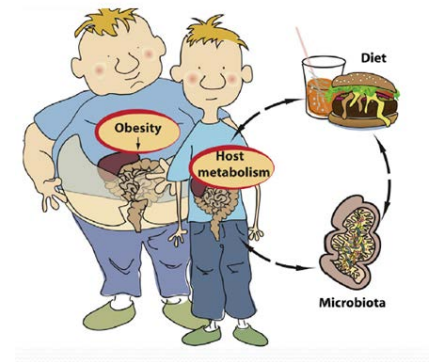
Pediatric obesity: a growing problem



Since 1980, the prevalence of overweight and obesity has increased remarkably in developed countries

	1980	2013
Female	16.2%	22.6%
Male	16.9%	23.8 %

The gut microbiota in obese and normal-weight children

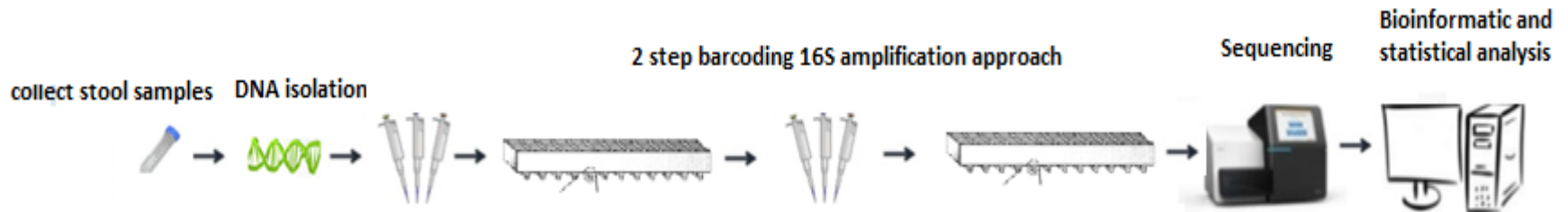


	N (n=36)	O(n=42)
Age (years)	11±0.33	11±1.99
Sex (male:female)	17:19	21:21
BMI z-score (kg/m²)	0.3±0.82	3.0±0.7
Delivery type (vaginal: caesarean)	28:8	22:18
Infant diet (breast-fed: formula-fed)	14:22	18:21

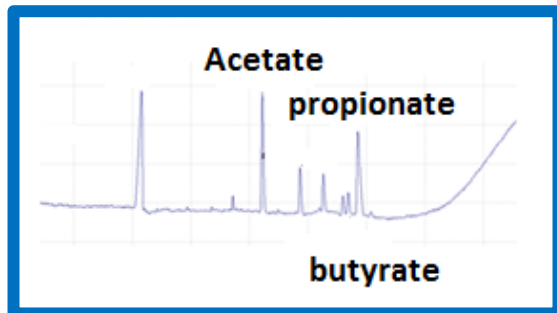


Materials and Methods

1- Is there a correlation between gut microbiota and weight?

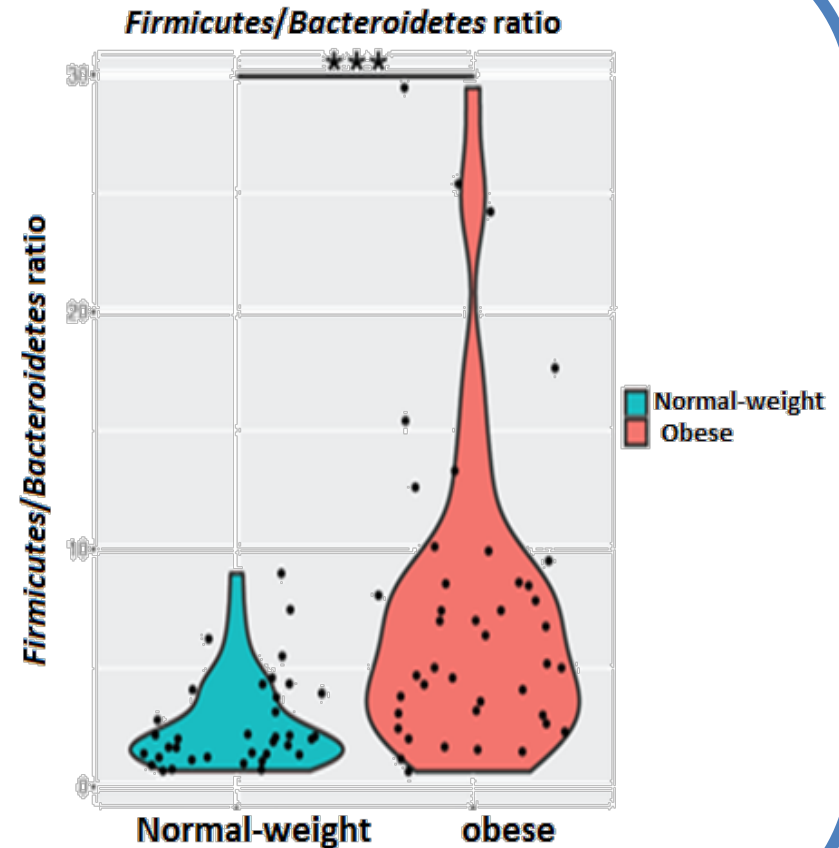
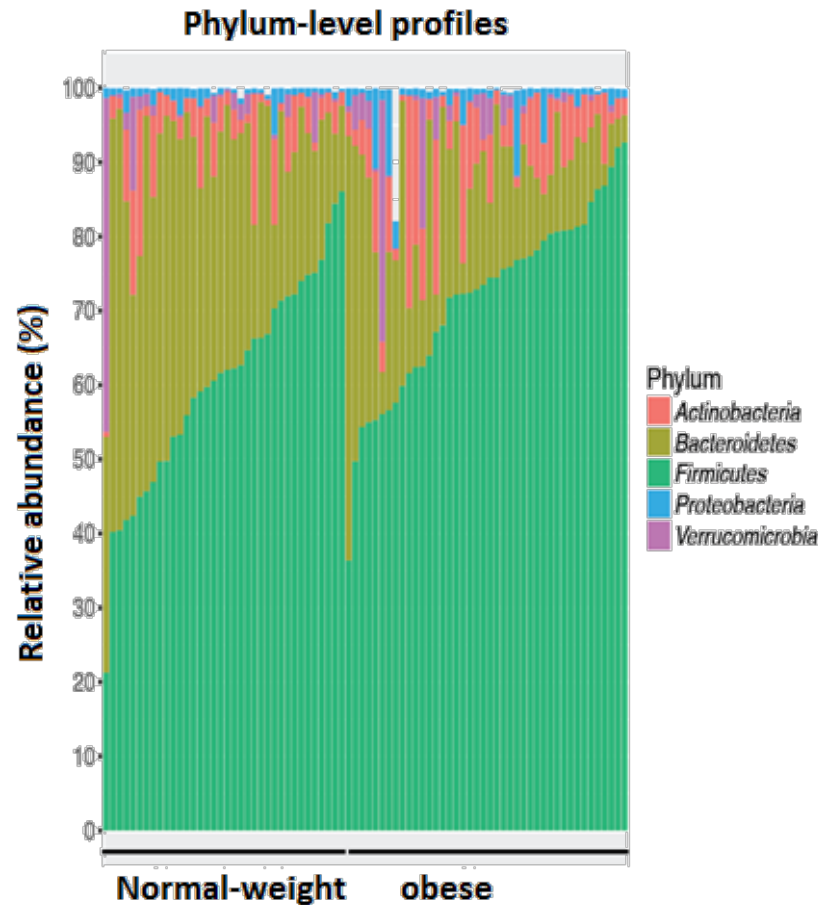


2- Is there a correlation between microbial metabolites and obesity?



Short chain fatty acids (SCFAs) quantification with capillary electrophoresis

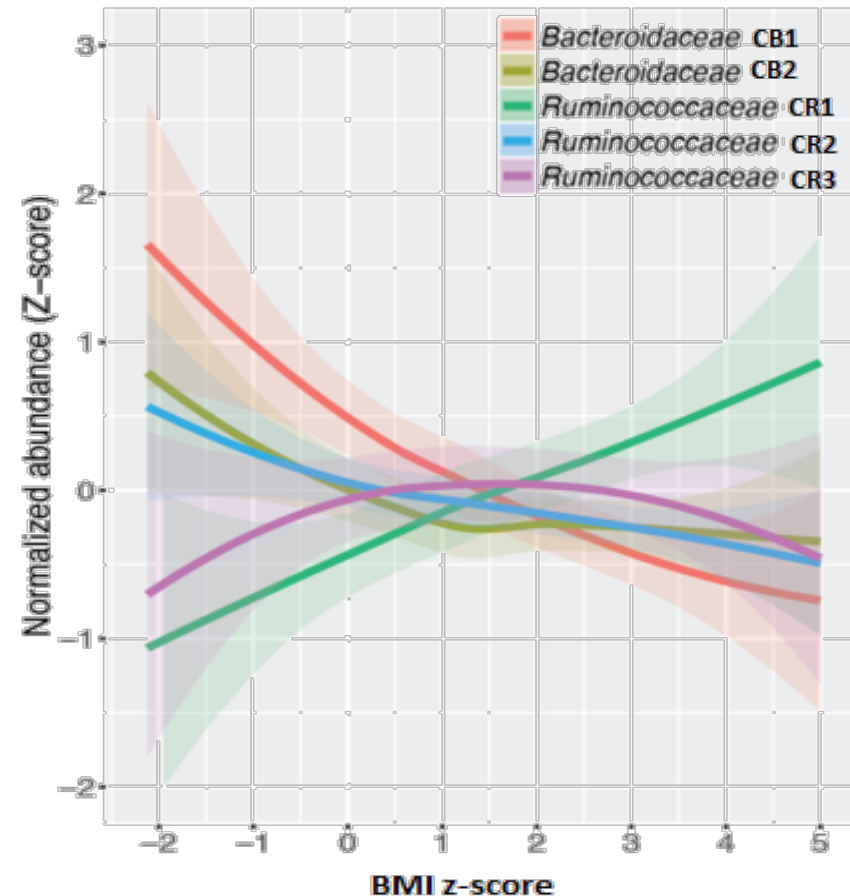
Can *Firmicutes/Bacteroidetes* ratio explain the pathophysiology of obesity?



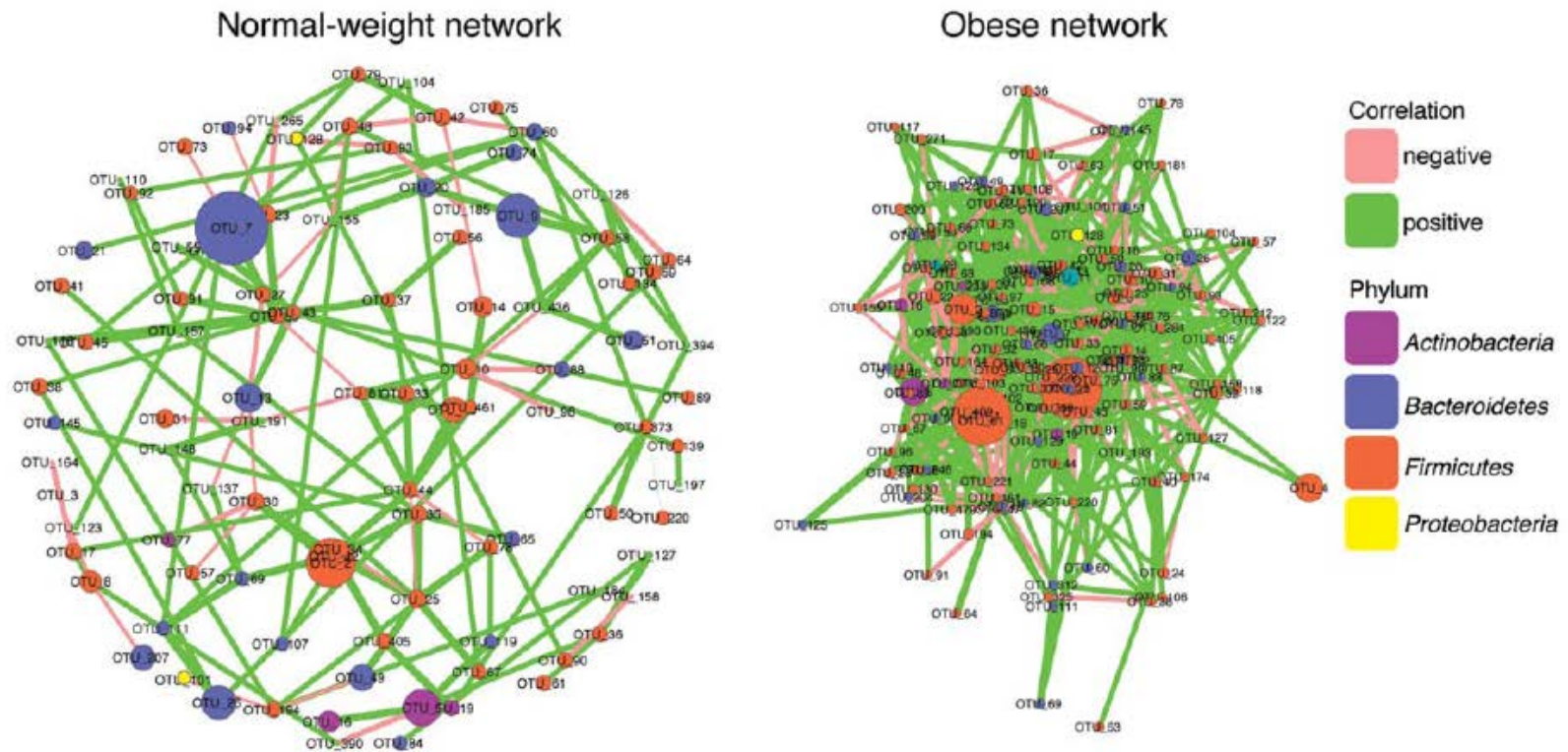
Taxa associated with BMI z-score

Taxonomic level	Taxon	r	p-value
Phylum	<i>Firmicutes</i>	0.4145	0.0001
	<i>Bacteroidetes</i>	-0.4538	<0.0001
Class	<i>Clostridia</i>	0.3688	0.0008
	<i>Bacteroidia</i>	-0.4538	<0.0001
Order	<i>Clostridiales</i>	0.3687	0.0008
	<i>Bacteroidales</i>	-0.4538	<0.0001
Family	<i>Ruminococcaceae</i>	0.3778	0.0006
	<i>Bacteroidaceae</i>	-0.4930	<0.0001
Genus	<i>Bacteroides</i>	-0.4930	<0.0001
OTU	OTU 7: <i>Bacteroides vulgatus</i>	-0.4321	<0.0001
	OTU 3: <i>Faecalibacterium prausnitzii</i>	0.3058	0.0064
	OTU 49: <i>Bacteroides stercoris</i>	-0.3252	0.003

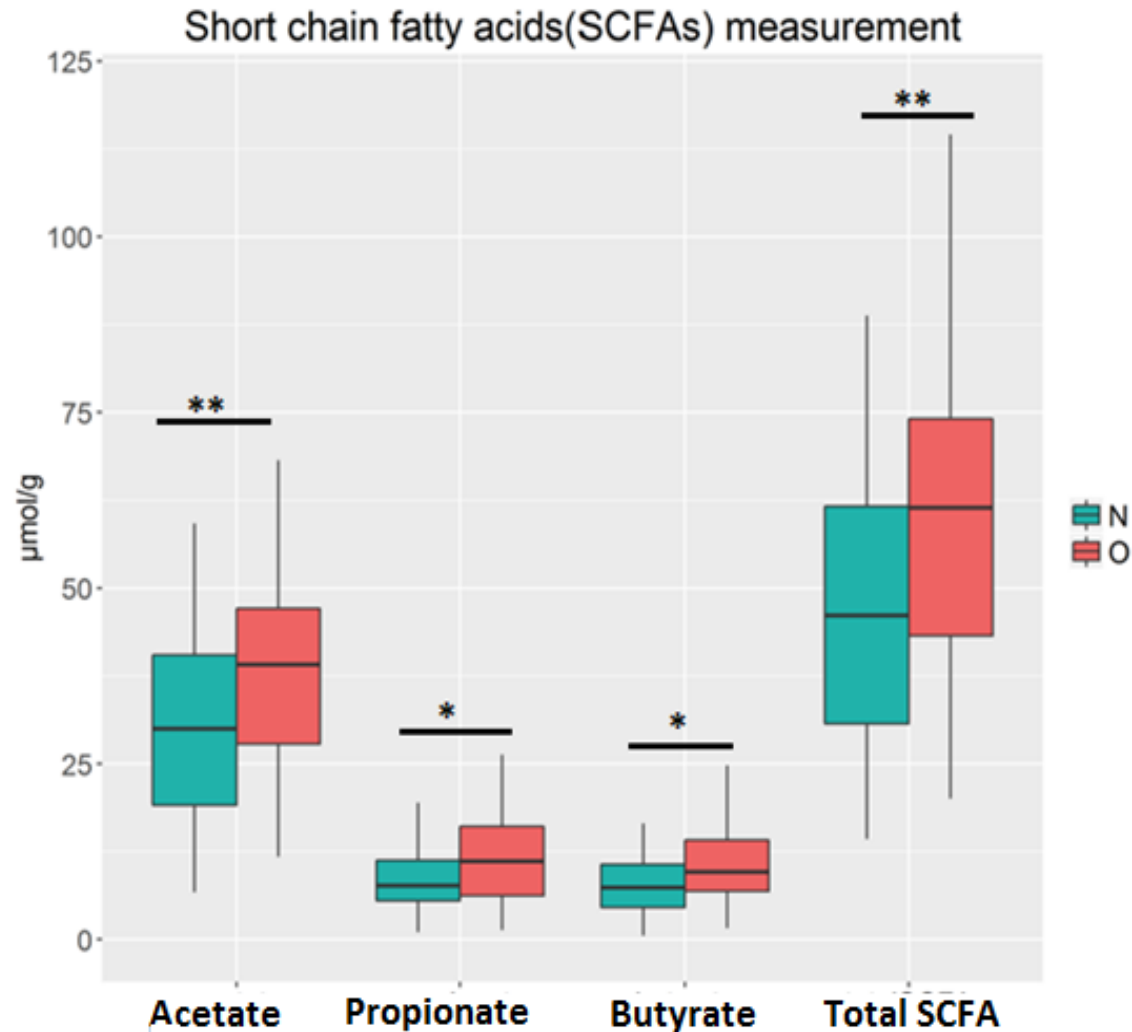
Contrasting shift for *Firmicutes* are intra-family associated



Gut microbiota structure is different in obese children

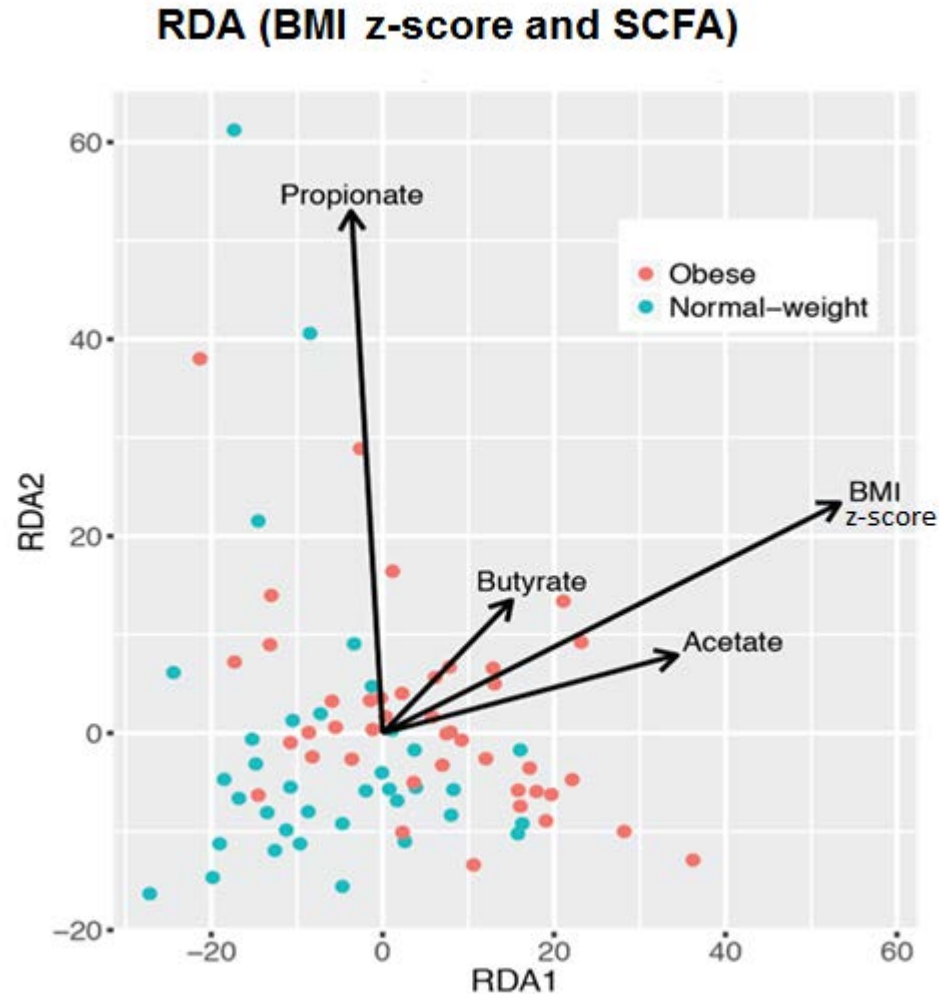


The fermentation activity of the gut microbiota is different in obese children



Several taxa are correlated with short chain fatty acids

Taxonomic level	
Phylum	
Class	
Order	
Family	Ru E Porp
Genus	Ru (P (Alistij
OTU	OTU 3 <i>prausnitzii</i> 01



p-value
0.0003
0.0005
0.0001

p value
<0.0001
<0.0001

Discussion and conclusion

- Multiple taxa are associated with SCFA levels and BMI z-score, reinforcing the tight link between the microbiota, SCFAs, and obesity.
- *Firmicutes/Bacteroidetes* ratio may not be a robust marker to explain the pathophysiology of obesity
- Correlation network analysis shows an altered structure at operational taxonomic units.
- *Bacteroidetes* taxa are generally better predictors of BMI z-score and obesity condition than *Firmicutes* taxa
- Members of the *Bacteroidetes* and certain populations of *Firmicutes* are associated with childhood obesity, though members of the *Firmicutes* exhibited contrasting shifts.

Outlook

- Additional studies are needed to better characterize and functionally categorize the members of *Firmicutes* phyla
- Future research has to include detailed analysis of metabolic activity of the gut microbiota



Acknowledgement



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