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Birthdate	
Analysis	

Average 

Unusual 

PHYLUM	FAMILY	GENUS	% of total	Ref.
Firmicutes (gram +)	Lachnospiraceae	Anaerostipes	 0,01	<1
		Coproccoccus	 7,68	<10
		Dorea	 5,55	<15
		Moryella	 0	<1
		Roseburia	 0,57	<50
		Sporobacterium	 0	<1
		Syntrophococcus	 0	<1
	Ruminococcaceae	Acetanaerobacterium	 0	<5
		Acetivibrio	 0	<1
		Ethanoligenens	 0,56	<1
		Faecalibacterium	 1,16	<25
		Papillibacter	 0	<1
		Ruminococcus	 0,09	>2
		Sporobacter	 0,01	<1
		Subdoligranulum	 0,01	<25
	Clostridiaceae	Butyricicoccus	 0,07	<5
		Clostridium Senu Stric.	 0,02	<5
		Lactonifactor	 0	0
	Eubacteriaceae	Anaerofustis	 0,01	<0,5
		Eubacterium	 0,07	0
	Blautia	Blautia	 12,31	<50
	Howardella	Howardella	 0	<1
	Lactobacillaceae	Lactobacillus	 0,08	<1
	Enterococcaceae	Enterococcus	 0,05	0
	Streptococcaceae	Lactococcus	 5,89	<1
		Streptococcus	 27,25	<5
	Leuconostoc	Leuconostoc	 0,01	<0,3
	Erysipelotrichaceae	Catenibacterium	 0	<0,3
		Coproccoccus	 0	<1
		Holdemania	 0,04	<1
		Turicibacter	 0	>0,5
	Veillonellaceae	Dialister	 0	0-1
		Megamonas	 0	0
		Megasphaera	 0	0
	Oscillospiraceae	Oscillibacter	 3,46	<4
	Staphylococcus	Staphylococcus	 0	<0,05
Bacteroidetes (gram-)	Bacteroidaceae	Bacteroides	 25,99	<10
	Rikenellaceae	Alistipes	 4,91	<3
	Porphyromonadaceae	Barnesiella	 0,54	<2
		Odoribacter	 0,26	<0,5
		Parabacteroides	 0,49	<3
	Prevotellaceae	Prevotella	 0,01	<5
		Xylanibacter	 0	<1
Actinobacteria (gram+)	Bifidobacteriaceae	Bifidobacterium	 0,17	>5
	Actinomycineae	Actinomyces	 0	<1
	Micrococcineae	Rothia	 0,01	<0,2
	Coriobacterineae	Asaccharobacter	 0	>0,1
		Collinsella	 0	<25
		Olsenella	 0	0
		Slackia	 0	<1
Proteobacteria (gram-)	Enterobacteriaceae	Escherichia/Shigella	 0	<0,5
		Klebsiella	 0	<0,5
	Sutterellaceae	Sutterella	 0	<1
	Desulfovibrionaceae	Lawsonia	 0	<0,5

	Value	Ref.
Total Lachnospiraceae	 13,81	>5
Total Ruminococcaceae	 1,83	>5
Total Clostridiaceae	 0,09	<5
Enterococcus	 0,05	0
Streptococcus	 27,25	<5
Ruminococcus	 0,09	>2
Lactonifactor	 0	0
Turicibacter	 0	>0,5
Bacteroides	 25,99	<10
Prevotella	 0,01	<5
Bifidobacterium	 0,17	>5
Asaccharobacter	 0	>0,1


Firmicutes	64,9 %
Bacteroidetes	32,2 %
Actinobacteria	0,18 %
Proteobacteria	0 %
Other	2,72 %

Range of Firmicutes % in European population: 50-85%

Firmicutes/Bacteroidetes ratio	
High	
Average	
Low	2,02

Low ratio may be associated with gut inflammation

Gram+ / Gram- ratio	
High	
Average	
Low	2,02

Diversity Index	 3,58
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Low <4, Average 4-5, High >5

Dysbiosis associated with low diversity

Electronically validated on:

Requesting physician:

Observations:

Others:



Clostridium IV	1,53
Clostridium XI	0
Clostridium XIX	0
Clostridium XIVa	0,12
Clostridium XIVb	0
Clostridium XVIII	0,22
Acidaminococcus	0
Anaerofilum	0
Anaerotruncus	0
Anaerovorax	0,01
Carnobacterium	0
Corynebacterium	0
Eggerthella	0,03
Flavobacterium	0
Gemella	0,22
Gordonibacter	0
Granulicatella	0,03
Lachnobacterium	0
Lutispora	0
Methanobrevibacter	0
Methylobacterium	0
Mitsuokella	0
Mogibacterium	0
Paraprevotella	0
Parasutterella	0,5
Pediococcus	0
Peptoniphilus	0,01
Peptostreptococcus	0,01
Phascolarctobacterium	0
Porphyromonas	0
Propionibacterium	0
Ralstonia	0
Robinsoniella	0
Sporacetigenium	0
Varibaculum	0
Victivallis	0
Weissella	0,01
Akkermansia	0
Hallella	0
Hydrogenoanaerobacterium	0,01
Neisseria	0

Electronically validated on:

Requesting physician:

Observations: