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ORIGINAL ARTICLE

Stool consistency is strongly associated with gut microbiota richness and composition, enterotypes and bacterial growth rates

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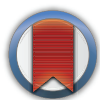
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ABSTRACT

Objective The assessment of potentially confounding factors affecting colon microbiota composition is essential to the identification of robust microbiome based disease markers. Here, we investigate the link between gut microbiota variation and stool consistency using Bristol Stool Scale classification, which reflects faecal water content and activity, and is considered a proxy for intestinal colon transit time.

Design Through 16S rDNA Illumina profiling of faecal samples of 53 healthy women, we evaluated associations between microbiome richness, Bacteroidetes:Firmicutes ratio, enterotypes, and genus abundance with self-reported, Bristol Stool Scale-based stool consistency. Each sample's microbiota growth potential was calculated to test whether transit time acts as a selective force on gut bacterial growth rates.

Results Stool consistency strongly correlates with all known major microbiome markers. It is negatively correlated with species richness, positively associated to the Bacteroidetes:Firmicutes ratio, and linked to *Akkermansia* and *Methanobrevibacter* abundance. Enterotypes are distinctly distributed over the BSS-scores. Based on the correlations between microbiota growth potential and stool consistency scores within both enterotypes, we hypothesise that accelerated transit contributes to colon ecosystem differentiation. While shorter transit times can be linked to increased abundance of fast growing species in Ruminococcaceae-*Bacteroides* samples, hinting to a washout avoidance strategy of faster replication, this trend is absent in *Prevotella*-enterotyped individuals. Within this enterotype adherence to host tissue therefore appears to be a more likely bacterial strategy to cope with washout.

Conclusions The strength of the associations between stool consistency and species richness, enterotypes and community composition emphasises the crucial importance of stool consistency assessment in gut metagenome-wide association studies.

Significance of this study

What is already known on this subject?

- Stool consistency, measured by the Bristol Stool Scale (BSS), reflects differences in water content and activity in the colon ecosystem and is correlated with colon transit time. (low scores: firm stool and slow transit, high scores: loose stool and fast transit).
- Species richness is proposed to be a major marker for gut health because of the idea that high bacterial richness and diversity often reflect ecosystem stability and resilience together with the consistent association between disease and a reduction in the number of species in a faecal sample.
- Faecal metagenomes have been shown to stratify into enterotypes, splitting the human population around three possible constellations in terms of their gut microbial ecosystem; likewise Firmicutes:Bacteroidetes and Prevotellaceae:Bacteroidetes ratios have been put forward as important stratifiers for gut microbiomes.

What are the new findings?

- Observed species richness declines with higher BSS scores reaching its minimum in individuals with loose stool.
- Enterotypes are distinctly distributed over the BSS scores: the *Prevotella* (P) enterotype is more abundant in subjects with loose stool while the Ruminococcaceae-*Bacteroides* (RB) enterotype completely dominates the harder stool samples.
- Within the RB enterotype, *Methanobrevibacter* and *Akkermansia* are positively correlated with colon transit time. A similar observation can be made for *Oxalobacter* and *Butyricimonas*, while *Bacteroides* is more abundant in loose stool.
- Microbiota growth potential is positively correlated with BSS scores in the RB enterotype, hinting to transit time as a selective force on microbial life-strategies.

INTRODUCTION

Despite recent efforts undertaken to characterise the healthy colon microbiota,[1–4] many parameters potentially affecting microbial composition and metabolic capacity remain underexplored. The identification of such confounding factors, including diet,[5 6] history of antibiotics intake,[7] and inflammation status,[8 9] is essential to define the boundaries of a healthy gut ecosystem and, hence, to identify robust disease markers in clinical microbiome association studies.

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Significance of this study

How might it impact on clinical practice in the foreseeable future?

- Here we show that major alterations in species richness or community composition could partially be reflecting variation in stool consistency, hampering the identification, but especially robustness and reproducibility of disease markers. Proper confounder analysis is thus impossible without stool consistency measurements. This study therefore stresses the urgent necessity of these measurements in gut microbiota research and clinical studies.

Transit time is a key determinant of the gut microbial habitat, affecting nutrient and water absorption along the intestine as well as setting the pace of luminal microbial population clearance during egestion.[10] As direct measurement of transit time is often impractical or mildly invasive, it has generally been neglected in microbiome studies so far. However, stool consistency as categorised by the Bristol Stool Scale (BSS) scores has been put forward as a proxy for colonic transit rate,[10–12] allowing assessment of its impact even when applying home-based sampling protocols. The use of the BSS is widespread in clinical studies and has been advised for the assessment of constipation and diarrhoea in functional bowel disorders.[13–15] The BSS classifies human faeces into seven consistency categories, with highest scores corresponding to loose stools and fast transit, while lower scores stand for hard stools and longer colon transit times.[10–12 16] Each consistency category reflects differences in moisture content of faecal material, with decreased water activity—associated with prolonged intestinal transit—limiting microbial growth through reduced nutrient mobility and hampered enzymatic activity.[17] Hence, BSS categorisation summarises the impact of two major—and obviously related—selective forces shaping the gut ecosystem: rate of intestinal transit and water activity.

Here, we used self-reported BSS scores combined with 16S rDNA Illumina amplicon profiles of faecal samples of 53 healthy volunteers to assess potential associations between microbiota composition and stool consistency. In a healthy Western population, more than half of the stools passed are predicted to belong to the central BSS categories 3 and 4.[11] However, increased occurrence of harder stools has been reported to be more common among women.[11 12 18] Hence, in order to increase chances of sampling a more uniform distribution of stools over all BSS categories, we limited inclusion to female volunteers.

METHODS

Sample data

Fifty-three healthy women, aged 20–55 years (median 42.5), were recruited as part of the Flemish Gut Flora Project. None were diagnosed with cancer or IBD, or had taken diarrhoea inhibitors, laxatives or prebiotics in the week before sampling, nor antibiotics within 3 months before sampling (see online supplementary table S1). The aims of the project and the commitments required were explained by means of an information brochure and all participants signed a statement of informed consent. The participants' general practitioner recorded their medical history, together with height, weight, and waist and hip circumferences. Volunteers recorded time of defaecation and BSS and reported this information together with information about general diet and health status in a questionnaire.

Characterisation of the bacterial component of the gut microbiota by variable region 4 rDNA sequencing

Faecal samples were frozen at −20°C immediately after collection by the participants. After frozen transport to a collection point in their neighbourhood and subsequent transport on dry ice, samples were stored at −80°C within 72 h after delivery at the collection point until DNA extraction. DNA extraction was performed according to Godon *et al*.[19] To amplify the variable region 4 of the 16S rRNA gene, we used the 515F and 806R primers (GTGCCAGCMGCCGCGGTAA and GGACTACHVGGGTWTCTAAT, respectively) modified to contain Illumina adapters and barcode sequences to allow for directional sequencing. Amplifications were performed in triplicate as 25 µL reactions containing 2 µL of diluted template (1:10), 2.5 µL of 10X AccuPrime PCR Buffer I, 0.1 µL of AccuPrime Taq High Fidelity (5 U/µL), and 0.5 µL of 515F and 1.0 µL of 806R primer (10 µM of each primer). Thermal cycling consisted of an initial denaturation step (3 min at 94°C), followed by 30 cycles of denaturation (45 s at 94°C), annealing (60 s at 50°C) and 90 s extension at 72°C. Final extension consisted of 5 min at 72°C. Amplicons were quantified on the Agilent 2100 Bioanalyzer (Agilent Technologies, Santa Clara, California, USA) and pooled in equimolar concentrations. Fragment size was selected (~400 bp) by cutting the main band from the agarose gel to reduce non-specific products of amplification. A final library size and quantification was also conducted with the Agilent Bioanalyzer. Sequencing was performed on the Illumina MiSeq platform (MiSeq Reagent Kit V.2, 500 cycles) according to the manufacturer's specifications to generate paired-end reads of 250 bases in length in each direction. The overlapping paired-end reads were merged using fastq-join[20] and processed with MacQIIME V.1.8. Only Illumina reads with a length >250 bp and an average quality score above 30, were retained for further analysis. Reads were assigned to operational taxonomic units (OTUs) by de novo OTU picking through the QIIME pipeline. This way 99.6%, 87.6%, 53.4% and 12.5% of the reads were assigned to order, family, genus and species levels, respectively. Closed OTU picking with QIIME against the Greengenes 2013 database was performed in addition for a more stringent taxonomic assignment. From OTU abundance and their respective taxonomic classifications, feature abundance matrices were calculated at different taxonomic levels, representing OTU and taxa abundance per sample. To compare the different samples, sample counts were rarefied to 26 260 reads for the de novo OTU picking data set and 26 024 reads for closed OTU picking and trimmed for the consequently absent OTUs with the phyloseq package based on the minimum of the sum of taxa abundances in RV.3.0.1.

Statistical analysis

Statistical analysis was conducted on the rarefied and trimmed feature abundance matrices using RV.3.0.1. Clustering of the samples into enterotypes was done using the cluster package[21] according to instructions available on http://enterotyping.embl.de. Optimal number of clusters was determined by the Calinski-Harabasz index. In addition, enterotyping was performed with Dirichlet multinomial mixtures (DMM) using the DirichletMultinomial 1.6.0 package in R.[22] Laplace was used to determine the optimal number of clustering by penalising model complexity. Clusters were assigned the enterotype Ruminococcaceae-*Bacteroides* or *Prevotella* based on the taxa

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dominating the enterotype as in the original article of Arumugam *et al*[23] (see online supplementary table S2).

Species richness (Observed, Chao1) and α diversity measurements (Shannon) were calculated using the phyloseq package.[24]

Each sample's microbiota growth potential was estimated as the average of the maximum growth rates (maxGRs) of the genera, weighted by their abundance in the sample. The maxGRs of gut-reference species (IMG v4Ref) were estimated from genomic traits[25] and the median was assigned to the genus.

Correlations between species richness, microbiota growth potential, and relative bacterial taxa abundance with BSS were assessed by Spearman's rank order correlation, as implemented in R. p Values were corrected for multiple testing with Benjamini-Hochberg false discovery rate correction (q value). Spearman's rank order correlation was used to check the correlation between enterotype and transit time (BSS), based on the percentage of each enterotype in each BSS category. Significance of differences in microbiota growth potential between enterotypes was assessed by Wilcoxon signed rank test.

RESULTS

A healthy gut microbial ecosystem is generally thought to be characterised by high bacterial richness and diversity, presumed to reflect ecosystem stability and resilience.[26 27] Faecal microbiome analyses have revealed a seemingly consistent association between disease and a reduction in the observed or estimated number of species in a sample, suggesting bacterial richness to be a major marker for gut health.[26 27] Here, we identify stool consistency to be strongly associated to faecal microbial richness. Indeed, observed species' richness significantly declines with stool firmness (Spearman's r=−0.45, p=0.0007), reaching its minimum in diarrhoea-afflicted individuals (figure 1A). Estimation of total species richness (Chao1) confirms this negative correlation (r=−0.41, p=0.003, data not shown) and the signal remains significant with the application of a more stringent taxonomical assignment (closed reference OTU picking, see Methods; trend also confirmed in a data set excluding patients with IBS, online supplementary figure S7, and in a data set of 24 men, online supplementary figure S8). These results are in line with anecdotal reports of decreased microbial richness associated with osmotic diarrhoea.[28]

Previously, faecal metagenomes have been shown to stratify into enterotypes,[23] splitting the human population around three possible constellations in terms of their gut microbial community structure. As enterotypes have also been linked to richness gradients,[8 9] we analysed the distribution of enterotypes over stool consistency scores. Applying multiple clustering approaches, we find that our current data set optimally separates into two distinct clusters (see online supplementary table S2). Named after the dominating taxa as in the reference publication,[23] we refer to the clusters observed as the Ruminococcaceae-*Bacteroides* (RB) and the *Prevotella* (P) enterotype (77% and 23% of total samples, respectively; partitioning around medoids (PAM) clustering with Jensen-Shannon distance). The enterotypes observed are distinctly distributed over BSS scores: while the P enterotype is more abundant in individuals with loose stools (r: 0.88, p=0.019), the RB enterotype completely dominates firmer samples (r: −0.88, p=0.019; figure 1B; trend also confirmed in men, online supplementary figure S8). These observations are substantiated by the analysis of the Firmicutes:Bacteroidetes and Prevotellaceae:Bacteroidetes abundance ratios (both put forward as alternatives to enterotyping[29]) over stool score (respectively r=0.42, p=0.001 and r=−0.04, p=0.77; see online supplementary figure S1A, B). Of note, within the RB enterotype, Ruminococcaceae abundance positively correlates with BSS scores (r=−0.37, p=0.016), while *Bacteroides* populations increase in looser stools (r=0.43, p=0.004) (see online supplementary figure S2). Hence, the enhanced prevalence of the RB enterotype in the harder stool categories is driven by the samples with a high Ruminococcaceae:*Bacteroides* ratio, which would classify them as Ruminococcaceae enterotype according to the terminology originally suggested by Arumugam *et al*.[23] As even within a single enterotype low richness samples are more abundant in looser stool (see online supplementary figure S3), the richness signal is thus not a mere consequence of enterotype distribution across consistency scores. Although the identification of environmental factors shaping or contributing to enterotype stratification is still ongoing, the potentially diverging impact of diet has been emphasised previously.[5 30] More specifically, the occurrence of the P enterotype has been linked to a rural, fibre-rich diet.[5 31] As non-fermentable fibre consumption is thought to increase water content and plasticity of stool,[32] this observation fits with the increased prevalence of the P enterotype in the loose stool categories. However, the question whether dietary fibre consumption or the resulting changes in transit rate or water activity are driving *Prevotella* blooms, remains currently unanswered.

Stool consistency variation is associated with shifts in faecal microbiota composition at the level of community structure and

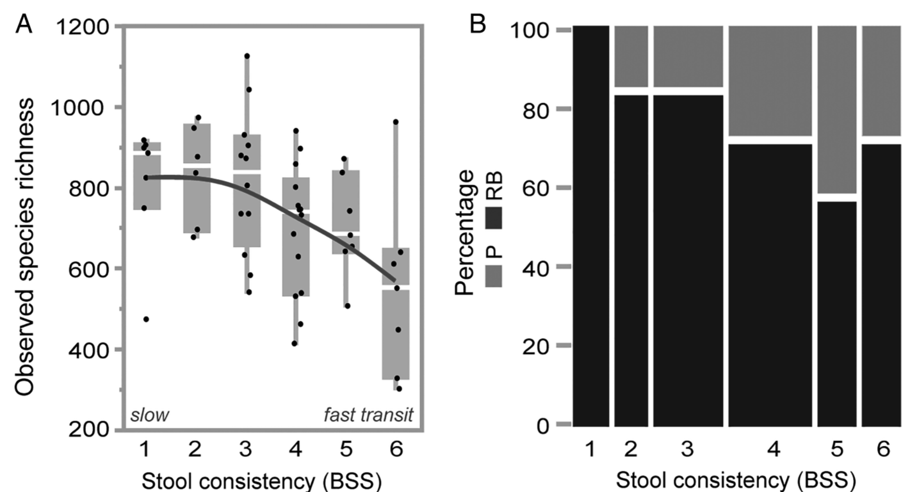

Figure 1 Stool consistency variation drives species richness and human enterotypes. Correlation between (A) observed species richness and stool consistency, defined by Bristol Stool Scale (BSS) (Spearman's correlation, r=−0.45, p=0.0007) and (B) enterotype distribution and stool consistency (BSS); Blue: Ruminococcaceae-*Bacteroides* (RB) enterotype (r=−0.88, p=0.019), green: P enterotype (r=0.88, p=0.019).

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Table 1 Genera abundances significantly correlated with stool consistency

Genus	Total data set r	Total data set q Value	RB enterotype r	RB enterotype q Value	P enterotype r	P enterotype q Value
Akkermansia	−0.504	0.0722	−0.528	0.0342	−0.078	0.6696
Bacteroides	0.177	0.6134	0.460	0.0718	−0.048	0.7803
Butyricimonas	−0.348	0.0722	−0.406	0.0718	−0.264	0.8620
Methanobrevibacter	−0.126	0.0722	−0.095	0.0718	−0.134	0.7978
Methanosphaera	−0.305	0.0966	−0.307	0.1318	NA	NA
Odoribacter	−0.094	0.0966	−0.048	0.2232	−0.284	0.8551
Oxalobacter	−0.424	0.0722	−0.460	0.0350	−0.051	0.6127

Genera abundances significantly correlated with stool consistency (BSS) (q<0.1) in the total data set, the RB enterotype, or the P enterotype. Spearman's rank order correlation with Benjamini-Hochberg false discovery rate correction.
BSS, Bristol Stool Scale; NA, not assigned; RB, Ruminococcaceae-Bacteroides.

diversity, and it correlates with abundance gradients of individual genera (see online supplementary table S3). Within the RB enterotype, *Methanobrevibacter* and *Akkermansia* populations increase with stool firmness (and are thus more prevalent in slow transit individuals). A similar observation can be made for *Oxalobacter* and *Butyricimonas*, while *Bacteroides* is more abundant in loose stools (see online supplementary figure S4). Most of these associations remain significant in the total data set (see table 1 and online supplementary figure S5) or when applying a more stringent taxonomic assignment (see online supplementary table S4).

The increased abundance of methanogens such as *Methanobrevibacter* in harder stools confirms previous reports of elevated methane production in constipated individuals.[33] It has been suggested that methane plays an active role in the delay of transit by slowing down intestinal motility.[34] Moreover, hydrogen removal through methane production alters the whole of gut fermentation processes, which could potentially affect colon peristalsis.[33] Alternatively, increased abundance could reflect the fitness of a genus to grow in conditions of slowed-down intestinal transit. As firmer stool consistencies correspond with reduced ecosystem water activity, associated fluctuations in microbial abundances could also result from species-specific resistance to water stress.

The human colon ecosystem is an open, nutrient-rich and continuous-flow environment. In order to avoid washout, the residing bacteria can either reproduce at a sufficiently high growth rate or attach to or colonise host tissues.[35] Hence, transit time may act as a selective force on gut bacterial growth rates. Indeed, higher fluctuations in nutrient availability and microbiota population size induced by decreased colon transit time would be the text-book selection pressure for fast growing bacteria, outgrowing their slow growing counterparts whenever resources are available (r-selection).[36] Also enhanced water activity and the associated increase of nutrient mobility in loose stools will contribute to the selective force imposed by accelerated transit. Indications for the suggested correlation between bacterial growth rates and rates of passage come from in vitro work with continuous flow fermenters[37–39]—where dilution rates determine pace of growth of the bacteria cultured—and in vivo observations of higher faecal bacterial biomass associated with shorter transit times.[40 41] To assess this hypothesis, we estimated each sample's microbiota growth potential as the average of the maxGR[25] (see methods) of the genera, weighted by their abundance in the sample (based on de novo OTU as well as closed reference OTU assignment; online supplementary table S5). We find that microbiota growth potential is indeed positively correlated with stool score, and hence colon transit time, in the RB enterotype (r=0.34, p=0,028; figure 2). However, this correlation is absent in the P enterotype (figure 2). Strikingly, the average growth rate of the P enterotype samples is lower than the one of the RB samples (median microbiota growth potential 0.38/h vs 0.52/h, respectively, Wilcoxon $p<10^{-4}$; online supplementary figure S6). This is largely driven by the higher abundance of relatively slow-growing *Prevotella* spp in these samples (median relative abundance of *Prevotella* of 0.48671 vs 0.00026 in the P-enterotype and RB-enterotype, respectively). On one hand, the absence of correlation between growth rate and colon transit time in the P enterotype could suggest that species in this enterotype resort to an alternative strategy to avoid washout, namely a higher degree of adherence to host tissues. The fact that *Prevotella* is indeed able to bind collagen and degrade mucin oligosaccharides support this hypothesis.[42 43] Alternatively, our results could indicate that stool consistency and hence water activity in *Prevotella* individuals are independent of accelerated transit, and mainly reflect increased faecal water-binding capacity, for example, related to fibre consumption. Overall, as faeces and library dilution series have been shown not to affect compositional readouts in 16S amplicon analyses[44]—and the results obtained are thus not due to technical issues arising from the variation in water content—our results hint to transit time as one of the determining selective forces on microbial life-strategies.

The results of the present study indicate that major alterations in species richness or community composition could partially be reflecting variation in stool consistency, hampering the identification, and affecting robustness and reproducibility of disease markers. While constipation and or diarrhoea are often seen as indicators of a dysbiotic colon microbiota potentially contributing to disease symptoms, onset or evolvement, stool consistency or transit time are not always taken into account as confounders. We illustrate this concern using a recent study by Scheperjans *et al*[45] evaluating the role of the microbiota in Parkinson's disease. The authors detected a lower abundance of

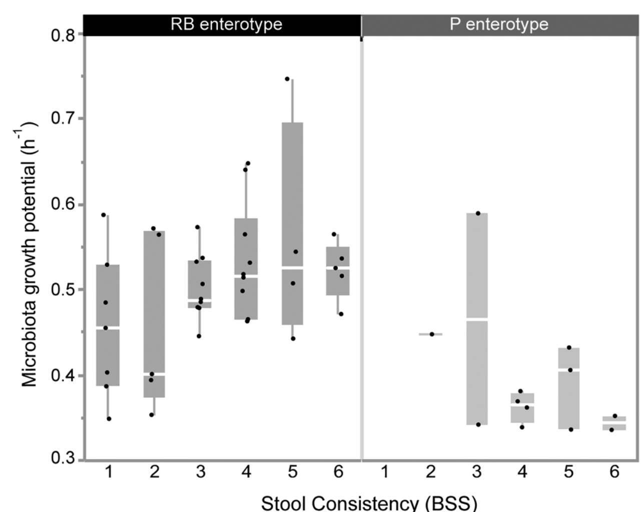

Figure 2 Microbiota growth potential correlates to faster intestinal transit in the Ruminococcaceae-*Bacteroides* (RB) enterotype. Microbiota growth potential over stool consistency (Bristol Stool Scale (BSS)), which is proposed as a proxy for transit time, in the RB-enterotype (r=0.34, p=0.028).

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Prevotellaceae combined with an increased Ruminococcaceae population in patients compared with healthy controls. However, as constipation has been reported as an early symptom of Parkinson's disease[46] and given the overlap between the microbiome signal observed and our findings of BSS-associated fluctuations in microbial abundances, there might be a risk that the microbiota signature proposed is a mere consequence of stool consistency differences between healthy and diseased individuals. To their credit, the authors did include the Wexner constipation score in the study—yet this score is primarily focused on long-term assessment of severe constipation (ie, extreme BSS 1) and would not compensate for day-to-day variation in BSS in patients as well as controls.[47] Inclusion of stool consistency records or colon transit time measurements as a confounder would have allowed better disentangling of signals exclusively associated to the disease and those associated to stool consistency.

CONCLUSION

Together, our results demonstrate a profound association between stool consistency and all major readouts of gut microbiota composition. As increased colon transit time has been linked to enhanced proteolytic fermentation[48–50] and associated production of potentially deleterious metabolites, the observed negative correlation between BSS-assessed passage rate and microbiome richness as reported here challenges the currently dominating view of high richness being directly associated to host health. Furthermore, we here identify gut microbial compositional differences with stool consistency on community scale and genus level and evaluate a hypothesised biological mechanism of how transit time might shape the gut microbiota through selective pressure on microbial life-strategies. Although longitudinal studies combining stool score records and direct transit time measurements are necessary to consolidate the observed correlations and proposed hypotheses, the strength of the associations between BSS and species richness, enterotypes and community composition emphasise the crucial importance of stool consistency assessment and confounder analysis in gut microbiota research and clinical studies.

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Contributors DV participated in data collection, performed the analyses and wrote the paper. GF designed the study, collected the data and participated in data analysis and writing of the paper. SVS participated in data analysis and writing of the paper. RT performed data preprocessing. MJ collected the data, participated in study design and writing of the paper. JR participated in study design and writing of the paper and was responsible for overall study coordination.

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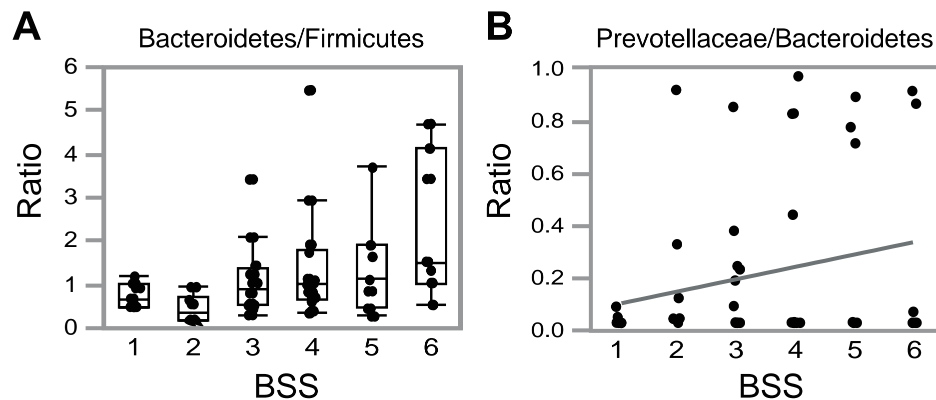
Supplementary Figures & Tables

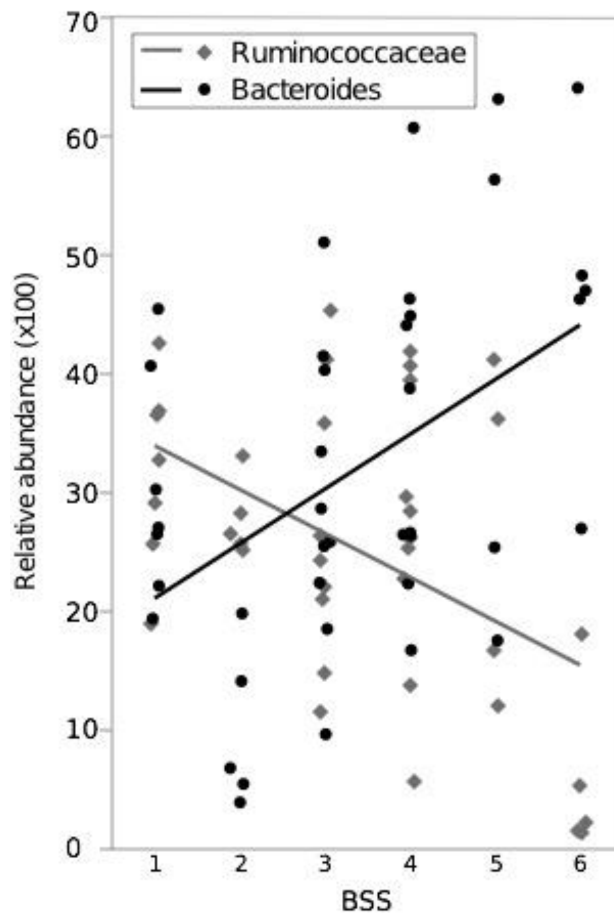
Figures S1-S6

Tables S1-S5



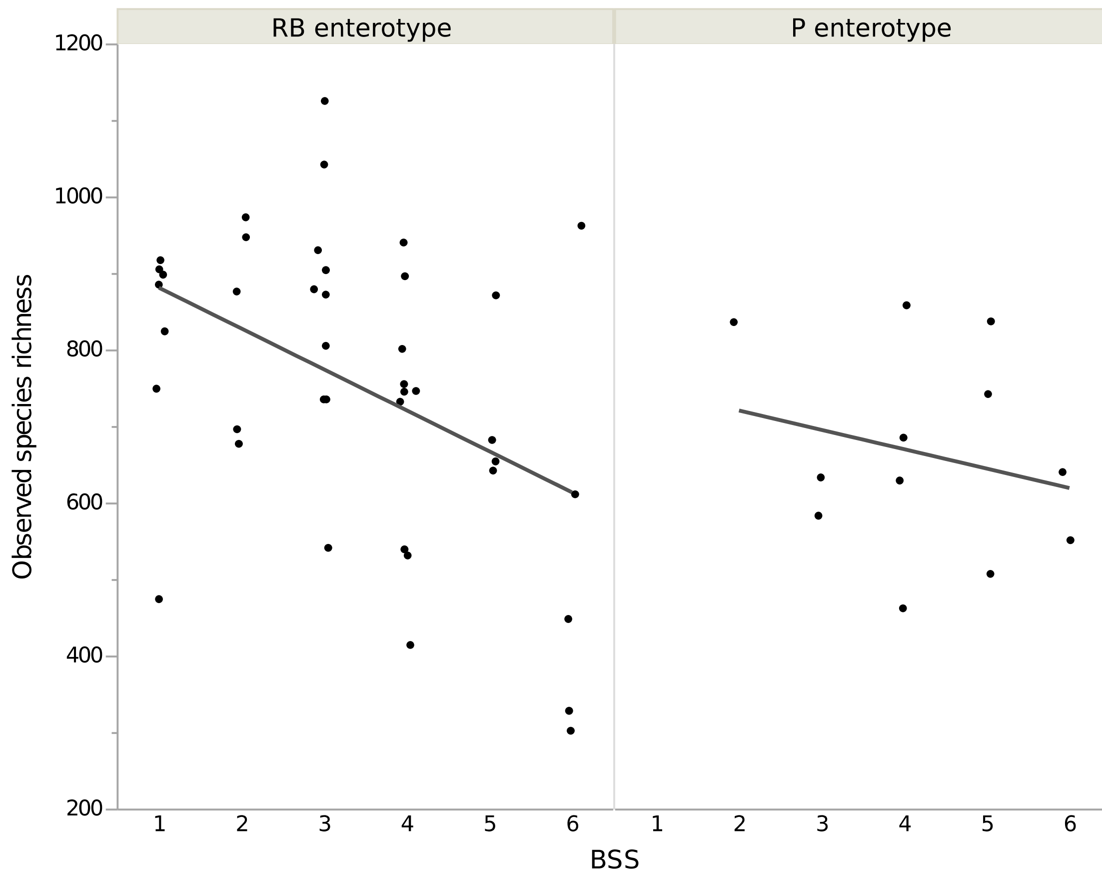
Supplementary Figure 1: Correlation between stool consistency and the Firmicutes/Bacteroidetes and Prevotellaceae/Bacteroidetes abundance ratios.

Both the Firmicutes/Bacteroidetes and Prevotellaceae/Bacteroidetes abundance ratios were proposed before as alternative to enterotyping. A) The Firmicutes/Bacteroidetes abundance ratio is significantly correlated with stool consistency (BSS) (rho=0.42, p-value=0.001). B) The Prevotellaceae/Bacteroidetes abundance ratio clearly separates the Prevotella-enterotype samples from the others and does not correlate with stool consistency (BSS) (rho=-0.04, p-value=0.77).



Supplementary Figure 2: Ruminococcaceae and *Bacteroides* abundance show opposite correlations with stool consistency in the RB enterotype.

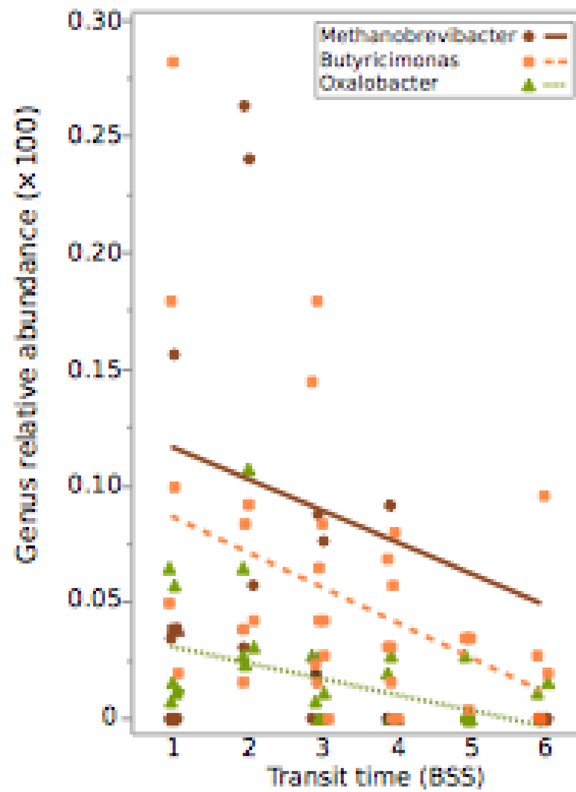
Correlation between stool consistency and the relative abundances of Ruminococcaceae (BSS) (rho=-0.37, p-value=0.016) and of *Bacteroides* (rho=0.43, p-value=0.004) in the RB-enterotype.

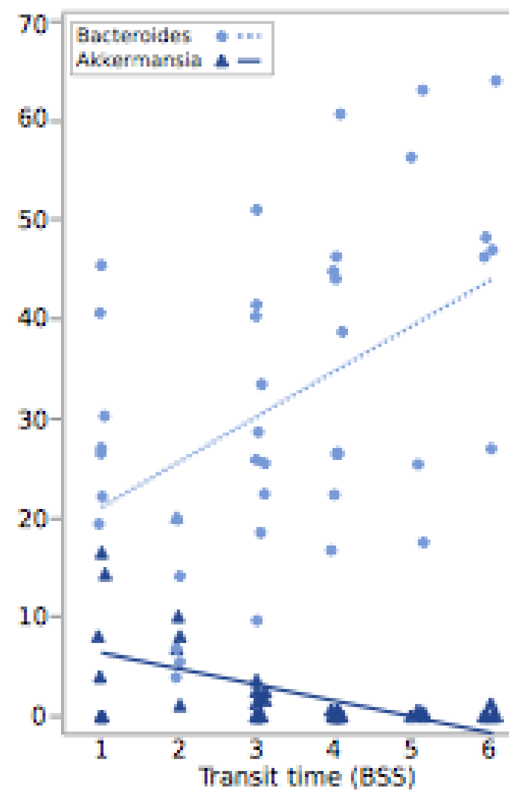


Supplementary Figure 3: Within an enterotype, low richness samples are more abundant with faster transit. Correlation between observed species richness and stool consistency (BSS) in the RB enterotype (rho= -0.43, p-value=0.004) and the P enterotype (rho= -0.12, p-value=0.7).

A

B

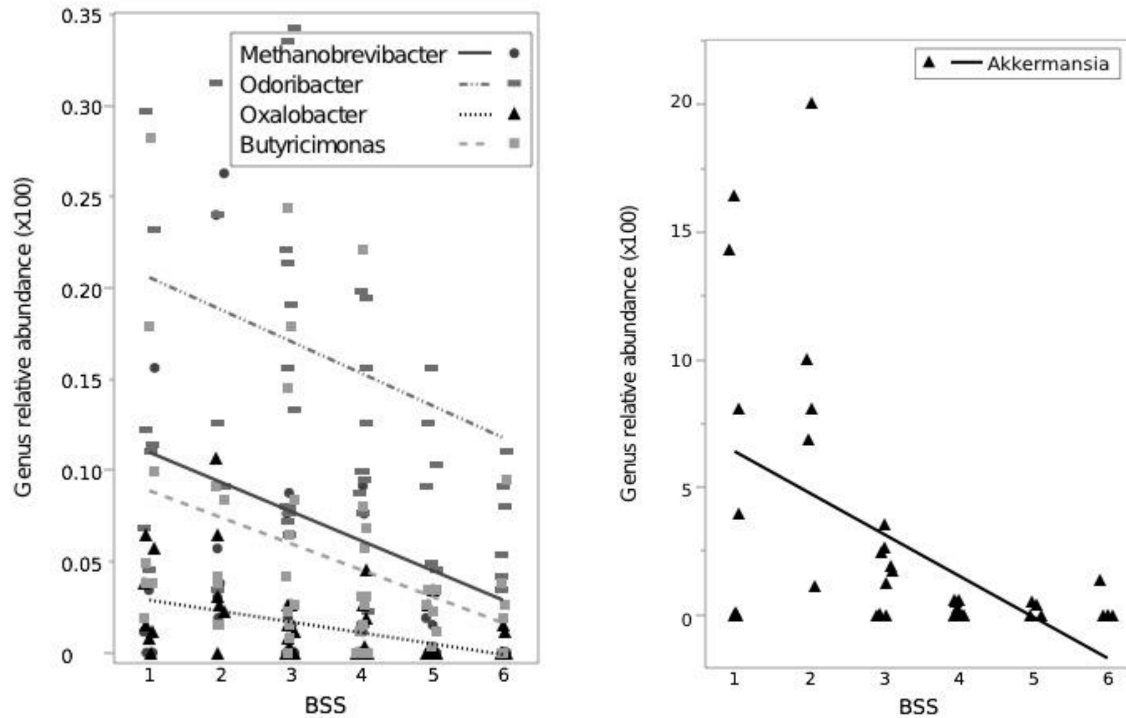




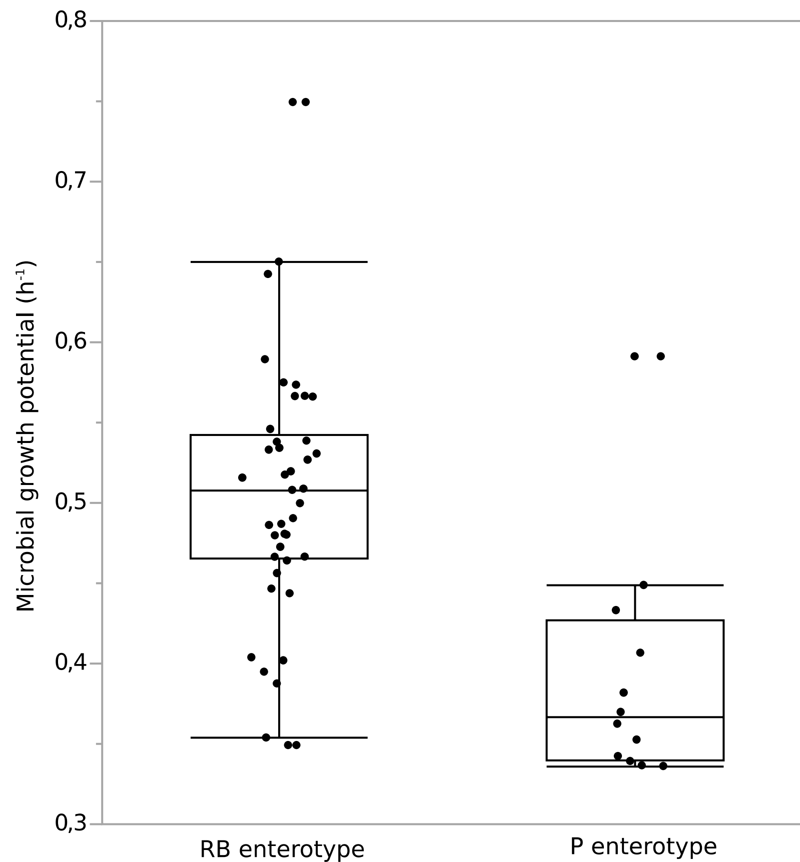
Supplementary Figure 4: Genera significantly correlated with stool consistency in the Ruminococcaceae-Bacteroides enterotype. A) Relative abundance of *Methanobrevibacter*, *Oxalobacter* and *Butyricimonas* in the RB-enterotype (respectively, rho=-0.10, q-value=0.072; rho=-0.46, q-value=0.035; rho=-0.41, q-value=0.072). B) Relative abundance of *Akkermansia* and *Bacteroides* in the RB-enterotype (respectively: rho=0.46, q-value=0.072; rho=-0.53, q-value=0.034).

A

B

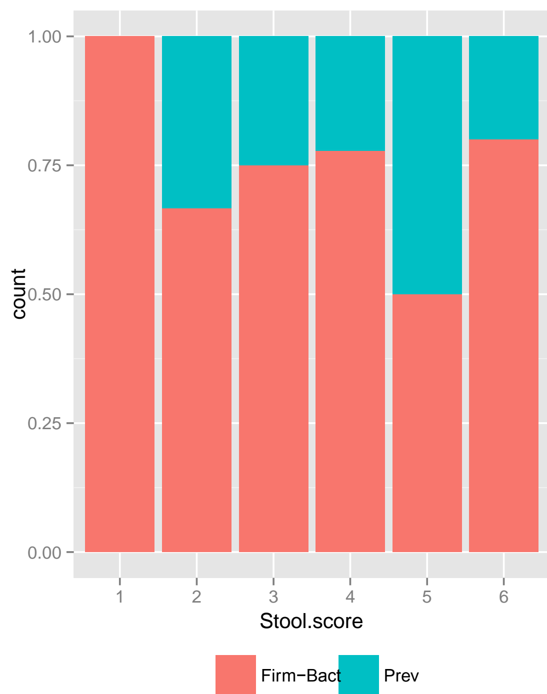


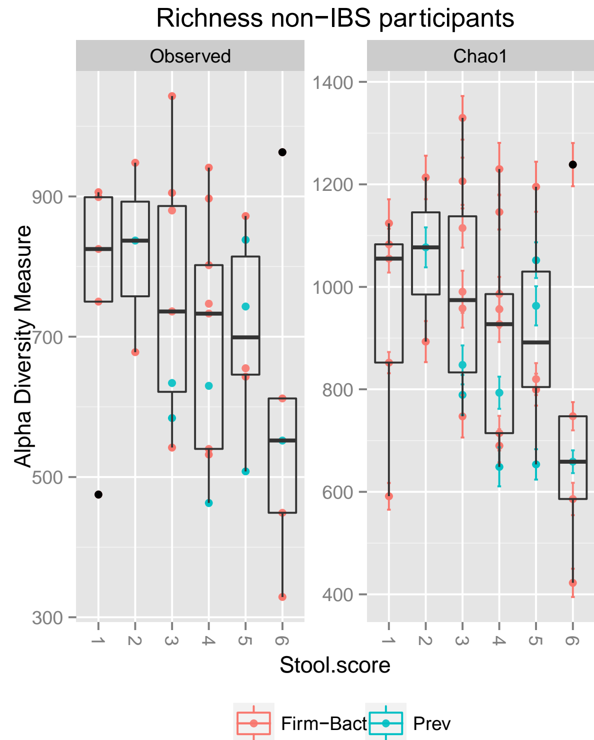
Supplementary Figure 5: Genera abundances significantly correlated with stool consistency in the total dataset. A) Relative abundance of *Methanobrevibacter*, *Oxalobacter*, *Butyricimonas* and *Odoribacter* in the total dataset (respectively: rho=-0.10, q-value=0.072; rho=-0.46, q-value=0.035; rho=-0.41, q-value=0.072). B) Relative abundance of *Akkermansia* in the total dataset (rho=0.50, q-value=0.072).



Supplementary Figure 6: Microbiota growth potential in the RB- and P enterotype. On average, microbiota growth potentials of the P enterotype samples are lower than those of the RB samples (median microbiota growth potential 0.38 h^{-1} vs. 0.52 h^{-1}, respectively). Significance of differences in microbiota growth potential between enterotypes was assessed by Wilcoxon signed rank test (p-value<10^{-4}).

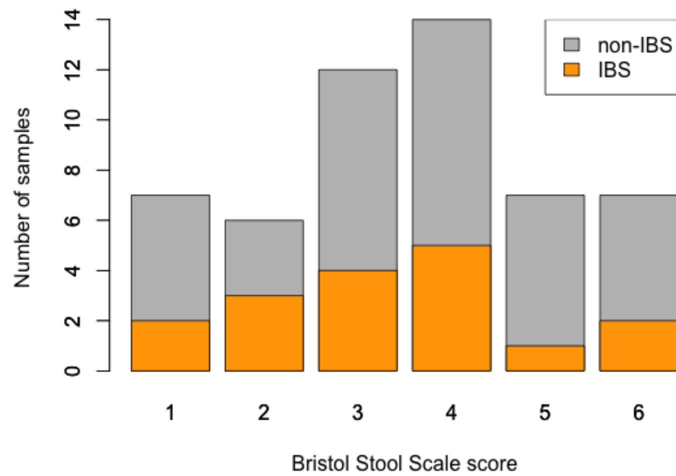
Supplementary Figure 7: Characteristics of the non-IBS cohort. Distribution of the enterotypes of the non-IBS participants over the BSS scores (A), Observed and estimated richness of the non-IBS participants over BSS scores (B), and distribution of the non-IBS participants and IBS patients over the BSS scores (C).





A. Distribution of the enterotypes over BSS scores in non-IBS participants.

B. Observed and estimated richness over BSS scores in non-IBS participants.

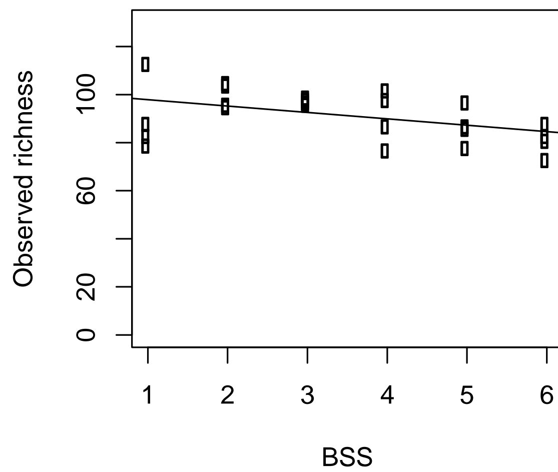


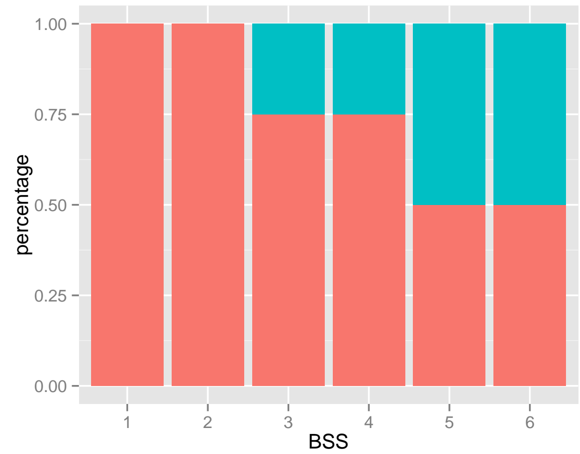
C. Distribution of the non-IBS participants and IBS patients over the BSS scores.

Supplementary Figure 8: Characteristics of a male cohort. A male cohort of 24 individuals - fulfilling the inclusion criteria as in the main cohort - with BSS stool scores equally distributed over the BSS scores (4 samples / BSS category) was analyzed for observed and estimated richness over BSS scores (A), and the distribution of the enterotypes over the BSS scores (B).

Fecal samples were frozen at −20°C immediately after collection by the participants. After frozen transport to a collection point in their neighborhood and subsequent transport on dry ice, samples were stored at −80°C within 72 hours after delivery at the collection point until DNA extraction. Samples were extracted using the PowerMicrobiome RNA isolation kit (Mobio), with the following adjustments to the protocol: (1) an incubation step of 10 minutes at 90°C after bead beating, (2) Steps to remove DNA were not executed.

The V4 region of the 16S rRNA gene was amplified with primer pair 515F and 806R, with single multiplex identifier (MID) and adaptors as described by Kozich *et al.* [1]. Sequencing was performed using Illumina MiSeq sequencer and sequencing kit MiSeq V2 to produce 250 bp pair-end reads. After de-multiplexing, fastq sequences were merged using FLASH [2] software with default parameters, and successfully combined reads were filtered based on quality (>90% of nucleotides must have quality score 30 or higher for every read) using Fastx tool kit (http://hannonlab.cshl.edu/fastx_toolkit/). Chimeras were removed using UCHIME [3] and each sample was standardized to 3,000 reads using random selection of reads. The taxonomy of reads was determined using RDP classifier [4] and taxonomy tables for phylum to genus level were created using Perl scripts.





A Richness over BSS in 24 male individuals.

B Enterotypes Ruminococcaceae-Bacteroides (Red) and Prevotella (Blue) over BSS in 24 male individuals.

Supplementary Table 1. Description of the 53 individuals (indiv.) in this study: age, self-reported dietary restrictions (diet), digestive system disorders as reported by their GI and their self-indicated sample Bristol Stool Scale (BSS) score. None of the participants ingested diarrhea inhibitors, laxatives or probiotics in the week prior to sample collection, nor antibiotics within the three months before sampling. None of the participants had inflammatory bowel disease (IBD). Some reported irritable bowel syndrome (IBS), celiac disease (indiv. 6), gallstones, lactose intolerance and other gastrointestinal problems. One participant was diabetic (indiv. 16).

	Diet	BSS	Age	Digestive system disorders
1	Vegetarian	4	50	IBS
2	NA	3	26	no digestive system disorder
3	None	5	49	no digestive system disorder
4	None	2	45	IBS
5	None	6	27	IBS
6	Glutenfree diet	3	33	other digestive system disorder (no IBD)
7	Vegetarian	1	44	no digestive system disorder
8	Lactosefree diet	6	46	IBS
9	None	2	53	no digestive system disorder
10	Vegetarian	5	38	no digestive system disorder
11	None	3	34	IBS

12	None	1	50	no digestive system disorder
13	Flexitarian	4	27	no digestive system disorder
14	None	4	35	other digestive system disorder (no IBD)
15	Vegetarian	4	46	no digestive system disorder
16	low salt diet	3	43	no digestive system disorder
17	Vegetarian	5	20	no digestive system disorder
18	Vegetarian	6	43	no digestive system disorder
19	Flexitarian	6	43	no digestive system disorder
20	None	4	39	no digestive system disorder
21	None	5	25	no digestive system disorder
22	None	4	44	no digestive system disorder
23	None	3	28	IBS
24	Vegetarian	6	22	no digestive system disorder
25	Protein diet	6	43	other digestive system disorder (no IBD)
26	None	5	39	IBS
27	Glutenfree diet	1	55	other digestive system disorder (no IBD)
28	None	3	23	no digestive system disorder
29	None	3	28	no digestive system disorder
30	None	1	52	no digestive system disorder
31	None	2	52	other digestive system disorder (no IBD)
32	low salt diet	4	45	no digestive system disorder
33	None	1	48	no digestive system disorder
34	Lactosefree diet	4	32	IBS
35	None	2	47	IBS
36	Vegetarian	4	31	no digestive system disorder
37	None	3	47	no digestive system disorder
38	None	5	47	no digestive system disorder
39	Flexitarian	3	35	no digestive system disorder
40	None	2	46	no digestive system disorder
41	weight loss diet	3	28	IBS
42	None	4	25	no digestive system disorder
43	None	3	42	IBS
44	None	4	45	IBS
45	None	6	40	no digestive system disorder
46	Lactosefree diet	4	42	IBS
47	None	1	55	IBS
48	None	1	50	IBS
49	Glutenfree diet	2	55	IBS
50	Vegetarian	3	30	no digestive system disorder
51	Lactosefree diet	4	40	IBS
52	None	5	27	no digestive system disorder
53	None	4	36	no digestive system disorder

Supplementary Table 2. Enterotyping of the 53 samples. Clustering of the samples into enterotypes was performed by either PAM clustering with JSD distance or Dirichlet multinomial mixtures.

Participant	JSD (2)	DMM (2)	JSD (3)
1	P	F-B	R
2	F-B	F-B	B
3	P	P	P
4	F-B	F-B	R
5	P	P	P
6	F-B	F-B	B
7	F-B	F-B	R
8	F-B	F-B	B
9	F-B	F-B	R
10	P	P	P
11	F-B	F-B	B
12	F-B	F-B	R
13	F-B	F-B	B
14	F-B	F-B	B
15	F-B	F-B	B
16	F-B	F-B	R
17	F-B	F-B	B
18	P	P	P
19	F-B	F-B	B
20	P	P	P
21	F-B	F-B	B
22	P	P	P
23	F-B	F-B	B
24	F-B	F-B	B
25	F-B	F-B	B
26	F-B	F-B	B
27	F-B	F-B	B
28	F-B	F-B	B
29	P	P	P
30	F-B	F-B	B
31	P	P	P
32	F-B	F-B	B
33	F-B	F-B	R
34	P	P	P
35	F-B	F-B	R
36	F-B	F-B	B
37	P	P	P
38	P	P	P
39	F-B	F-B	B

40	F-B	F-B	R
41	F-B	F-B	B
42	F-B	F-B	B
43	F-B	F-B	R
44	F-B	F-B	B
45	F-B	F-B	B
46	F-B	F-B	B
47	F-B	F-B	B
48	F-B	F-B	B
49	F-B	F-B	R
50	F-B	F-B	B
51	F-B	F-B	B
52	F-B	F-B	B
53	F-B	F-B	B

PAM clustering was performed as originally described on http://enterotyping.embl.de were used. The dataset separated optimally into two clusters as determined by the Calinski-Harabasz index and clusters were assigned the enterotype Ruminoccoccaceae-Bacteroides or Prevotella, based on the taxa dominating the enterotype as in the original article of Arumugam *et al.* (2011). Additionally we clustered the dataset with the same method into three enterotypes, and named them as in the original article Ruminococcaceae (R), Bacteroides (B) and Prevotella (P), again based on the taxa dominating the enterotype.

Clustering of the dataset with Dirichlet multinomial mixtures (DMM) was performed using the DirichletMultinomial 1.6.0 package in R. Laplace was used to penalize model complexity and indicated an optimal separation of the dataset into two clusters. Naming of the clusters was identical as with the PAM clustering method. All except one sample got assigned the same enterotype as with the PAM clustering method

Supplementary Table 3. Non-parametric Spearman correlation between stool consistency (BSS) and genera abundances, after multiple testing correction (Benjamini-Hochberg, q-values). Dataset with de novo OTU assignment.

		N samples	total dataset		RB enterotype		P enterotype	
Phylum	**Genus**		rho	q_value	rho	q_value	rho	q_value
Firmicutes	[Eubacterium]	30	-0.28	0.4072	-0.401	0.1434	0.048	0.9925
Bacteroidetes	[Prevotella]	13	0.018	0.9628	0.106	0.8861	-0.246	0.8279
Firmicutes	[Ruminococcus]	53	0.028	0.6905	0.144	0.9519	-0.541	0.1487
Firmicutes	5-7N15	4	0.016	0.4768	0.047	0.5447	NA	NA
Proteobacteria	Acetobacter	1	0.041	0.929	0.067	0.7842	NA	NA
Firmicutes	Acidaminococcus	10	-0.099	0.9124	-0.11	0.3811	0.199	0.7594
Actinobacteria	Actinomyces	15	-0.022	0.6905	0.069	0.9242	-0.451	0.6991
Actinobacteria	Adlercreutzia	7	-0.213	0.4104	-0.178	0.5447	-0.48	0.3926
Proteobacteria	Aggregatibacter	6	0.112	0.8738	0.09	0.5787	0.453	0.3656
Verrucomicrobia	Akkermansia	41	-0.504	0.0722	-0.528	0.0342	-0.078	0.6696
Firmicutes	Anaerococcus	1	-0.232	0.4104	-0.238	0.3726	NA	NA
Firmicutes	Anaerostipes	47	-0.272	0.334	-0.202	0.5667	-0.366	0.7978
Firmicutes	Anaerotruncus	23	-0.214	0.4426	-0.188	0.5667	-0.118	0.7803
Bacteroidetes	Bacteroides	53	0.177	0.6134	0.46	0.0718	-0.048	0.7803
Actinobacteria	Bifidobacterium	43	-0.073	0.9628	-0.044	0.9519	0.234	0.6145
Proteobacteria	Bilophila	48	-0.106	0.6905	-0.077	0.7795	0.26	0.8375
Firmicutes	Blautia	53	0.253	0.8072	0.448	0.1401	-0.341	0.6127
Firmicutes	Bulleidia	5	-0.088	0.9784	0.106	0.4879	-0.638	0.1489
Bacteroidetes	Butyricimonas	44	-0.348	0.0722	-0.406	0.0718	-0.264	0.862

Firmicutes	Butyrivibrio	2	0.028	0.9735	0.057	0.9416	NA	NA
Proteobacteria	Campylobacter	4	0.08	0.4072	0.115	0.2232	NA	NA
Firmicutes	Catenibacterium	6	0.039	0.6394	-0.033	0.9416	0.154	0.8279
Firmicutes	cc_115	21	-0.351	0.334	-0.35	0.2228	-0.084	0.8375
Bacteroidetes	CF231	2	-0.05	0.9735	-0.035	0.9416	NA	NA
Firmicutes	Christensenella	7	-0.09	0.4426	-0.045	0.6214	-0.394	0.4488
Firmicutes	Clostridium	48	-0.183	0.169	-0.166	0.1693	-0.246	0.8375
Actinobacteria	Collinsella	39	-0.122	0.4072	-0.064	0.4028	-0.456	0.6991
Firmicutes	Coprobacillus	11	0.169	0.9628	0.225	0.7795	NA	NA
Firmicutes	Coprococcus	53	-0.112	0.8053	-0.07	0.7842	-0.407	0.6991
Firmicutes	Dehalobacterium	24	-0.278	0.2954	-0.28	0.2232	0.043	0.5769
Proteobacteria	Desulfovibrio	30	-0.121	0.588	-0.26	0.3726	-0.102	0.6696
Firmicutes	Dialister	31	0.166	0.6904	0.015	0.9288	0.34	0.4888
Firmicutes	Dorea	53	-0.16	0.169	-0.113	0.3722	-0.288	0.1618
Actinobacteria	Eggerthella	9	0.006	0.6922	0.022	0.6372	0.194	0.7004
Firmicutes	Faecalibacterium	53	-0.08	0.6898	-0.059	0.5787	0.112	0.7247
Fusobacteria	Fusobacterium	10	0.221	0.9505	0.269	0.6417	-0.324	0.4888
Proteobacteria	Haemophilus	39	0.232	0.2843	0.302	0.1434	0.338	0.6696
Firmicutes	Holdemania	28	-0.032	0.6898	0.013	0.7842	0.131	0.8375
Firmicutes	Lachnobacterium	15	-0.122	0.9628	-0.086	0.7145	-0.065	0.8551
Firmicutes	Lachnospira	52	0.179	0.8072	0.272	0.5667	-0.291	0.2688
Firmicutes	Lactobacillus	17	0.102	0.6111	0.113	0.5667	0.175	0.9292
Firmicutes	Lactococcus	10	-0.049	0.5836	0.098	0.9288	-0.583	0.2897
Firmicutes	Megamonas	4	0.164	0.4104	-0.035	0.9242	0.401	0.2688

Firmicutes	Megasphaera	2	0.009	0.9735	0.067	0.7842	-0.324	0.4888
Euryarchaeota	Methanobrevibacter	21	-0.126	0.0722	-0.095	0.0718	-0.134	0.7978
Euryarchaeota	Methanosphaera	4	-0.305	0.0966	-0.307	0.1318	NA	NA
Firmicutes	Mitsuokella	3	0.133	0.8072	0.044	0.9416	0.194	0.7004
Proteobacteria	Neisseria	4	0.169	0.6905	0.231	0.5667	0	0
Bacteroidetes	Odoribacter	51	-0.094	0.0966	-0.048	0.2232	-0.284	0.8551
Firmicutes	Oribacterium	2	-0.006	0.9735	0.023	0.9416	NA	NA
Firmicutes	Oscillospira	53	-0.237	0.1502	-0.22	0.2028	-0.107	0.4888
Proteobacteria	Oxalobacter	25	-0.424	0.0722	-0.46	0.035	-0.051	0.6127
Firmicutes	p-75-a5	1	-0.05	0.8701	NA	NA	-0.324	0.4888
Bacteroidetes	Parabacteroides	51	-0.012	0.4072	0.051	0.5447	-0.101	0.7456
Bacteroidetes	Paraprevotella	24	0.124	0.9735	0.142	0.9679	0.222	0.8639
Firmicutes	Pediococcus	2	0.095	0.4426	0.27	0.3726	-0.065	0.8551
Firmicutes	Peptococcus	6	-0.038	0.9966	-0.017	0.8874	-0.206	0.8639
Firmicutes	Peptoniphilus	2	-0.149	0.4318	-0.139	0.483	NA	NA
Firmicutes	Peptostreptococcus	2	0.04	0.9784	0.074	0.9519	NA	NA
Firmicutes	Phascolarctobacterium	31	-0.057	0.9735	-0.004	0.8053	-0.369	0.4888
Bacteroidetes	Porphyromonas	11	-0.274	0.4104	-0.29	0.3617	0.03	0.862
Bacteroidetes	Prevotella	50	0.265	0.9735	-0.153	0.1463	0.342	0.4749
Proteobacteria	Proteus	1	0.223	0.4104	0.27	0.3726	NA	NA
Proteobacteria	Pseudomonas	2	-0.041	0.9735	-0.021	0.9416	NA	NA
Firmicutes	Pseudoramibacter_ Eubacterium	4	-0.038	0.9628	-0.002	0.9519	NA	NA
Proteobacteria	Ralstonia	1	0.041	0.929	0.067	0.7842	NA	NA

Firmicutes	rc4-4	16	-0.125	0.6134	-0.085	0.4028	-0.49	0.7803
Firmicutes	RFN20	1	-0.141	0.5836	-0.136	0.5787	NA	NA
Bacteroidetes	Rikenella	2	0.05	0.4426	0.078	0.3726	NA	NA
Firmicutes	Roseburia	53	0.208	0.4426	0.299	0.1434	-0.458	0.2593
Actinobacteria	Rothia	1	-0.232	0.4104	-0.238	0.3726	NA	NA
Firmicutes	Ruminococcus	53	-0.215	0.371	-0.211	0.2232	0.252	0.704
Proteobacteria	Serratia	8	-0.024	0.9735	-0.03	0.7909	0.128	0.7978
Actinobacteria	Slackia	8	-0.339	0.334	-0.338	0.3621	NA	NA
Fusobacteria	Sneathia	1	-0.232	0.4104	-0.238	0.3726	NA	NA
Firmicutes	Streptococcus	43	0.308	0.4072	0.385	0.3609	-0.124	0.9715
Firmicutes	Succiniclasticum	8	-0.13	0.9735	-0.108	0.9679	-0.569	0.6127
Proteobacteria	Succinivibrio	3	-0.141	0.5836	-0.136	0.5787	-0.594	0.3608
Proteobacteria	Sutterella	51	0.082	0.929	0.155	0.5828	0.063	0.9925
Firmicutes	Turicibacter	20	-0.086	0.7467	-0.043	0.9242	-0.456	0.59
Euryarchaeota	vadinCA11	3	-0.245	0.334	-0.239	0.3609	NA	NA
Actinobacteria	Varibaculum	2	-0.075	0.4318	-0.061	0.483	NA	NA
Firmicutes	Veillonella	32	0.266	0.5706	0.33	0.3726	0.071	1
Firmicutes	WAL_1855D	12	-0.243	0.8053	-0.248	0.7795	0.096	0.8551
Bacteroidetes	YRC22	2	0.166	0.7076	NA	NA	0.228	0.8375

Supplementary Table 4. Non-parametric Spearman correlation between stool consistency (BSS) and genera abundances, after multiple testing correction (Benjamini-Hochberg, q-values). Dataset with closed reference OTU assignment. Abundance of key organisms *Methanobrevibacter* and *Akkermansia* are significantly correlated with stool consistency (BSS) with this more stringent OTU assignment. The same can be said about *Butyricimonas* and *Cloacibacillus.* The genera *Oxalobacter* and *Bacteroides* are however not significantly correlated with stool consistency (BSS) in this dataset.

			total dataset		**RB enterotype**		**P enterotype**	
Phylum	**Genus**	**N samples**	**rho**	**q value**	**rho**	**q value**	**rho**	**q value**
Firmicutes	[Eubacterium]	29	-0,31	0,4236	-0,31	0,4236	0,08	0,8924
Bacteroidetes	[Prevotella]	10	0,02	0,8382	0,02	0,8382	-0,24	0,9667
Firmicutes	[Ruminococcus]	53	-0,14	0,5865	-0,14	0,5865	-0,34	0,2966
Firmicutes	02d06	5	0,20	0,4821	0,20	0,4821	0,19	0,6694
Firmicutes	57N15	3	0,02	0,9536	0,02	0,9536	NA	NA
Proteobacteria	Acetobacter	1	0,04	0,8900	0,04	0,8900	NA	NA
Firmicutes	Acidaminococcus	8	-0,09	0,7537	-0,09	0,7537	0,20	0,6556
Proteobacteria	Actinobacillus	2	0,19	0,4821	0,19	0,4821	NA	NA
Actinobacteria	Actinomyces	15	-0,07	0,8382	-0,07	0,8382	-0,58	0,2966
Actinobacteria	Adlercreutzia	5	-0,14	0,5022	-0,14	0,5022	NA	NA
Proteobacteria	Aggregatibacter	5	0,17	0,9475	0,17	0,9475	0,45	0,3780
Verrucomicrobia	Akkermansia	40	-0,51	0,0793	-0,51	0,0793	-0,07	0,5603

Firmicutes	Anaerococcus	1	-0,23	0,4222	-0,23	0,4222	NA	NA
Firmicutes	Anaerostipes	46	-0,24	0,2421	-0,24	0,2421	-0,52	0,7483
Firmicutes	Anaerotruncus	25	0,21	0,2421	0,21	0,2421	-0,19	0,9687
Bacteroidetes	Bacteroides	53	0,19	0,5145	0,19	0,5145	-0,08	0,5992
Actinobacteria	Bifidobacterium	44	-0,08	0,9550	-0,08	0,9550	0,21	0,6556
Proteobacteria	Bilophila	47	-0,12	0,6700	-0,12	0,6700	0,26	0,8159
Firmicutes	Blautia	53	0,16	0,8634	0,16	0,8634	-0,44	0,6694
Firmicutes	Bulleidia	3	-0,06	0,9475	-0,06	0,9475	-0,58	0,2966
Bacteroidetes	Butyricimonas	42	-0,35	0,0793	-0,35	0,0793	-0,26	0,7483
Proteobacteria	Campylobacter	4	0,08	0,3384	0,08	0,3384	NA	NA
Firmicutes	Catenibacterium	6	0,06	0,6027	0,06	0,6027	0,16	0,8390
Firmicutes	cc_115	26	-0,38	0,2000	-0,38	0,2000	-0,02	0,9667
Firmicutes	Christensenella	10	-0,25	0,2900	-0,25	0,2900	-0,06	0,8416
Synergistetes	Cloacibacillus	6	-0,22	0,0793	-0,22	0,0793	NA	NA
Firmicutes	Clostridium	53	-0,15	0,2165	-0,15	0,2165	0,09	0,8416
Actinobacteria	Collinsella	39	-0,07	0,9475	-0,07	0,9475	-0,54	0,6694
Firmicutes	Coprobacillus	10	-0,10	0,6999	-0,10	0,6999	NA	NA
Firmicutes	Coprococcus	53	0,06	0,5145	0,06	0,5145	-0,58	0,7483
Firmicutes	Dehalobacterium	20	-0,28	0,3633	-0,28	0,3633	0,09	0,5603
Proteobacteria	Desulfovibrio	28	-0,11	0,5022	-0,11	0,5022	-0,06	0,6556
Firmicutes	Dialister	31	0,15	0,5865	0,15	0,5865	0,29	0,6556
Firmicutes	Dorea	53	0,02	0,2652	0,02	0,2652	-0,27	0,1935

Actinobacteria	Eggerthella	8	0,04	0,4962	0,04	0,4962	NA	NA
Firmicutes	Enterococcus	4	0,20	0,5691	0,20	0,5691	-0,17	0,9667
Proteobacteria	Erwinia	3	-0,04	0,9145	-0,04	0,9145	-0,32	0,5172
Firmicutes	Faecalibacterium	53	-0,11	0,5022	-0,11	0,5022	-0,07	0,8416
Fusobacteria	Fusobacterium	5	0,22	0,9475	0,22	0,9475	-0,32	0,5172
Firmicutes	Granulicatella	9	0,14	0,5022	0,14	0,5022	-0,10	0,9667
Proteobacteria	Haemophilus	39	0,23	0,3377	0,23	0,3377	0,21	0,6548
Firmicutes	Holdemania	28	-0,08	0,4229	-0,08	0,4229	0,00	0,9667
Proteobacteria	Klebsiella	1	-0,05	0,8382	-0,05	0,8382	-0,32	0,5172
Firmicutes	Lachnobacterium	31	-0,20	0,9475	-0,20	0,9475	-0,03	0,8416
Firmicutes	Lachnospira	51	-0,14	0,9115	-0,14	0,9115	-0,33	0,5827
Firmicutes	Lactobacillus	16	0,04	0,9550	0,04	0,9550	-0,06	0,5603
Firmicutes	Lactococcus	9	-0,01	0,5022	-0,01	0,5022	-0,58	0,2966
Firmicutes	Megamonas	4	0,19	0,4229	0,19	0,4229	0,50	0,2966
Firmicutes	Megasphaera	2	0,01	0,9550	0,01	0,9550	-0,32	0,5172
Euryarchaeota	Methanobrevibacter	24	-0,12	0,0793	-0,12	0,0793	-0,22	0,3780
Euryarchaeota	Methanomassiliicoccus	6	-0,27	0,4962	-0,27	0,4962	-0,06	0,8416
Euryarchaeota	Methanosphaera	3	-0,24	0,2421	-0,24	0,2421	NA	NA
Firmicutes	Mitsuokella	3	0,13	0,8209	0,13	0,8209	0,19	0,6694
Proteobacteria	Neisseria	4	0,17	0,5865	0,17	0,5865	NA	NA
Bacteroidetes	Odoribacter	51	-0,34	0,1764	-0,34	0,1764	-0,14	0,8416
Firmicutes	Oribacterium	5	-0,21	0,9755	-0,21	0,9755	0,24	0,2966

Firmicutes	Oscillospira	53	-0,21	0,2421	-0,21	0,2421	-0,33	0,6694
Proteobacteria	Oxalobacter	24	-0,40	0,1764	-0,40	0,1764	-0,01	0,7483
Firmicutes	p-75-a5	1	-0,05	0,8382	-0,05	0,8382	-0,32	0,5172
Bacteroidetes	Parabacteroides	50	-0,04	0,2421	-0,04	0,2421	-0,16	0,6556
Bacteroidetes	Paraprevotella	24	0,12	0,9475	0,12	0,9475	0,21	0,9667
Firmicutes	Pediococcus	1	0,04	0,8900	0,04	0,8900	0,27	0,8416
Firmicutes	Peptococcus	5	-0,05	0,8015	-0,05	0,8015	-0,19	0,5848
Firmicutes	Phascolarctobacterium	33	-0,05	0,8558	-0,05	0,8558	-0,39	0,6342
Bacteroidetes	Porphyromonas	7	-0,27	0,6027	-0,27	0,6027	-0,06	0,8416
Bacteroidetes	Prevotella	50	0,27	0,9475	0,27	0,9475	0,36	0,5172
Proteobacteria	Proteus	1	0,22	0,4222	0,22	0,4222	NA	NA
Proteobacteria	Pseudomonas	2	-0,14	0,6700	-0,14	0,6700	NA	NA
Firmicutes	Pseudoramibacter - Eubacterium	1	-0,23	0,4222	-0,23	0,4222	NA	NA
Proteobacteria	Ralstonia	1	0,04	0,8900	0,04	0,8900	NA	NA
Firmicutes	rc4-4	16	-0,11	0,9475	-0,11	0,9475	-0,61	0,4392
Bacteroidetes	Rikenella	2	0,05	0,4821	0,05	0,4821	NA	NA
Firmicutes	Roseburia	53	0,27	0,2421	0,27	0,2421	-0,61	0,1913
Actinobacteria	Rothia	3	-0,09	0,6602	-0,09	0,6602	NA	NA
Firmicutes	Ruminococcus	53	-0,24	0,2950	-0,24	0,2950	-0,02	0,6556
Proteobacteria	Salmonella	3	0,00	0,9414	0,00	0,9414	-0,32	0,5172
Firmicutes	Sarcina	6	-0,23	0,5611	-0,23	0,5611	0,19	0,6694
Proteobacteria	Serratia	8	0,04	0,8900	0,04	0,8900	-0,12	0,7665

Actinobacteria	Slackia	10	-0,31	0,2421	-0,31	0,2421	NA	NA
Firmicutes	SMB53	17	0,18	0,6700	0,18	0,6700	-0,54	0,2966
Fusobacteria	Sneathia	3	-0,23	0,8382	-0,23	0,8382	-0,06	0,8416
Firmicutes	Streptococcus	45	0,32	0,2421	0,32	0,2421	-0,15	0,8416
Firmicutes	Succiniclasticum	7	-0,13	0,9791	-0,13	0,9791	-0,56	0,5992
Proteobacteria	Succinivibrio	3	-0,14	0,2421	-0,14	0,2421	-0,58	0,2966
Proteobacteria	Sutterella	51	0,09	0,7517	0,09	0,7517	0,04	0,8416
Firmicutes	Turicibacter	21	-0,05	0,8128	-0,05	0,8128	0,08	0,7920
Euryarchaeota	vadinCA11	3	-0,22	0,2638	-0,22	0,2638	NA	NA
Actinobacteria	Varibaculum	2	-0,05	0,9550	-0,05	0,9550	NA	NA
Firmicutes	Veillonella	30	0,27	0,4962	0,27	0,4962	0,21	0,7665
Firmicutes	WAL_1855D	6	-0,24	0,4620	-0,24	0,4620	NA	NA
Bacteroidetes	YRC22	2	0,16	0,7094	0,16	0,7094	0,20	0,8416

Supplementary Table 5. Correlations of growth rate and stool consistency on the dataset with closed reference OTU assignment. The difference between the median microbiota growth potential

	RB enterotype	**P enterotype**
Correlation of microbiota growth potential with stool consistency score (BSS)	rho= 0.35, p-value= 0.023	rho= 0.47, p-value= 0.12
Median microbiota growth potential	0.37 h^{-1} *	0.51 h^{-1} *

Median relative abundance of Prevotella	0.48314	0.00034

* Wilcoxon test p-value $< 10^{-4}$