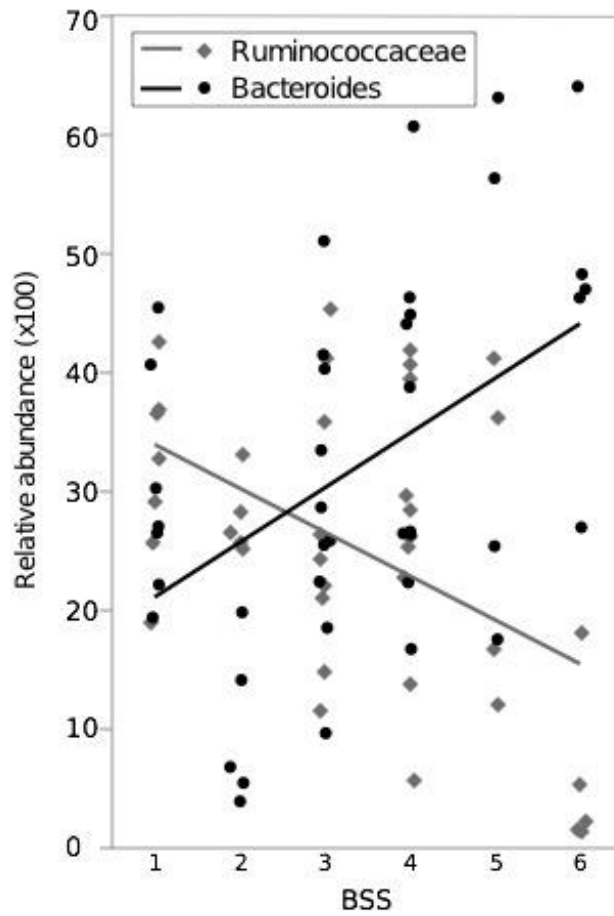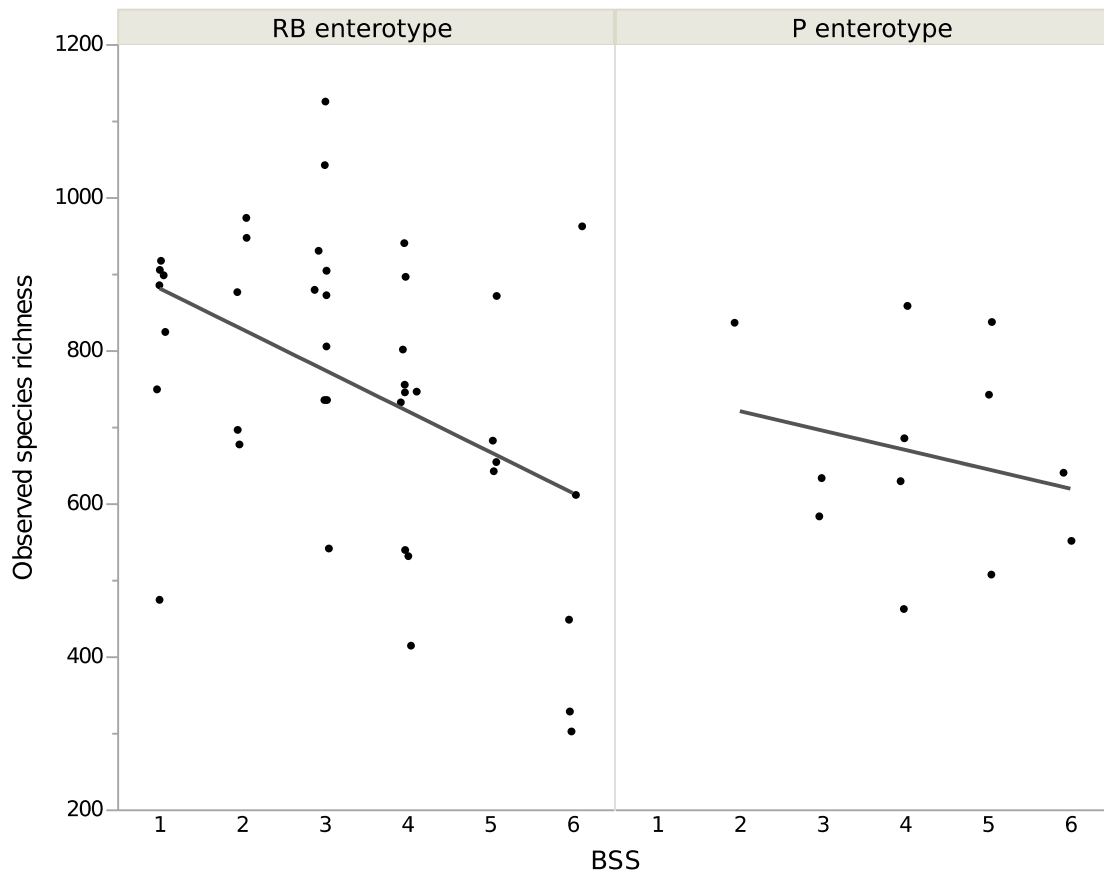Supplementary Figure 1: Correlation between stool consistency and the Firmicutes/Bacteroidetes and Prevotellaceae/Bacteroidetes abundance ratios.

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).
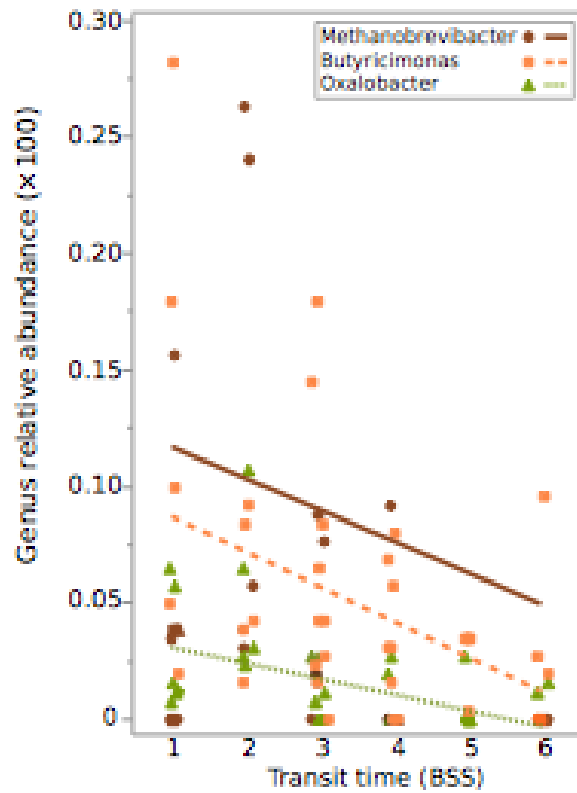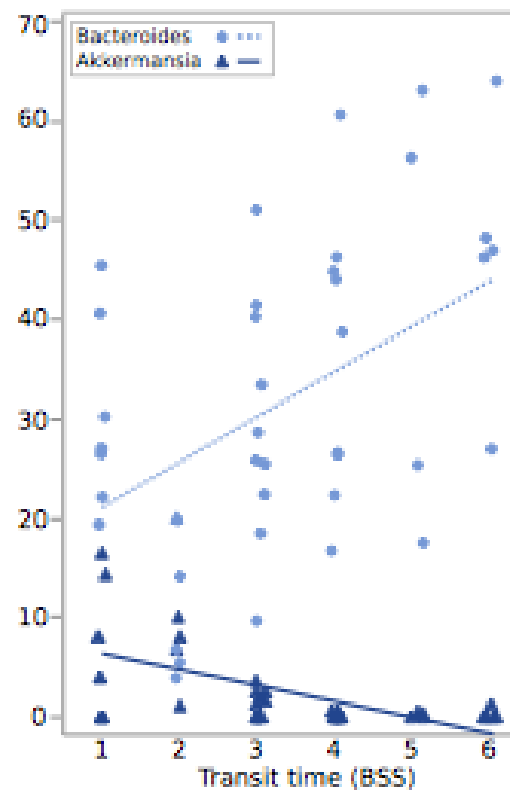
Supplementary Figure 4: Genera significantly correlated with stool consistency in the Ruminococcaceae-Bacteroides enterotype. A) Relative abundance of *Methanobrevibacter*, *Oxalobacter* and *Butyricimonas* in the RB-enterotype (respectively, rho=-0.10, q-value=0.072; rho=-0.46, q-value=0.035; rho=-0.41, 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
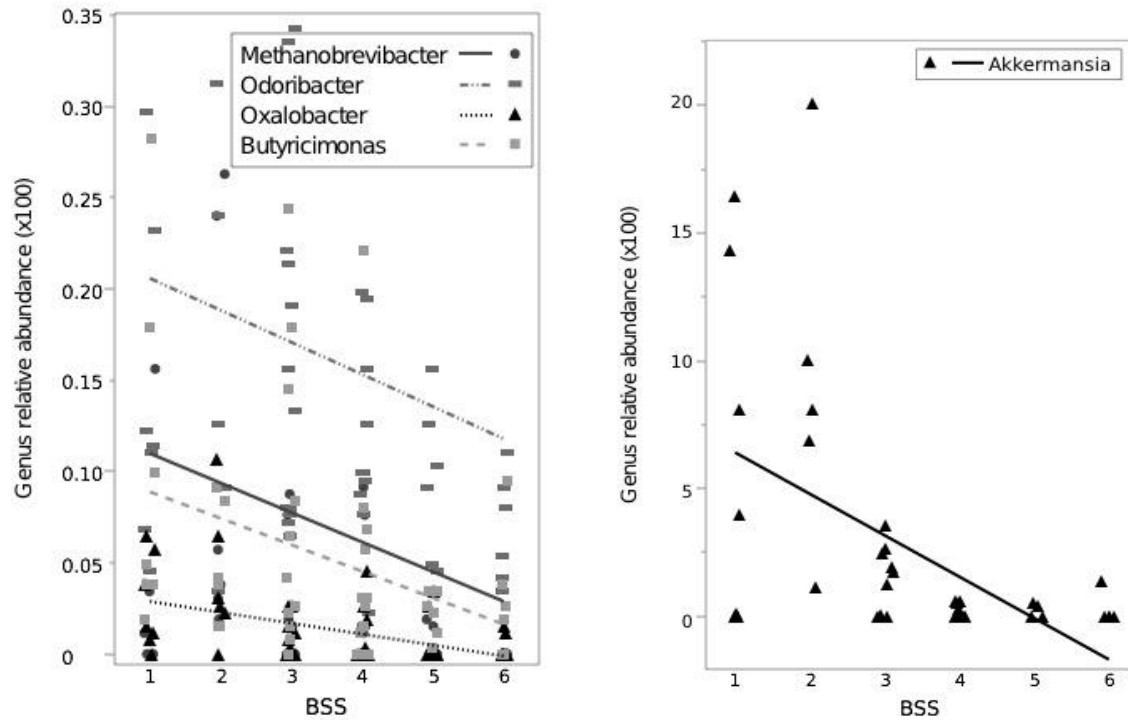
Supplementary Figure 5: Genera abundances significantly correlated with stool consistency in the total dataset. A) Relative abundance of *Methanobrevibacter*, *Oxalobacter*, *Butyricimonas* and *Odoribacter* in the total dataset (respectively: rho=-0.10, q-value=0.072; rho=-0.46, q-value=0.035; rho=-0.41, q-value=0.072). B) Relative abundance of *Akkermansia* in the total dataset (rho=0.50, q-value=0.072).
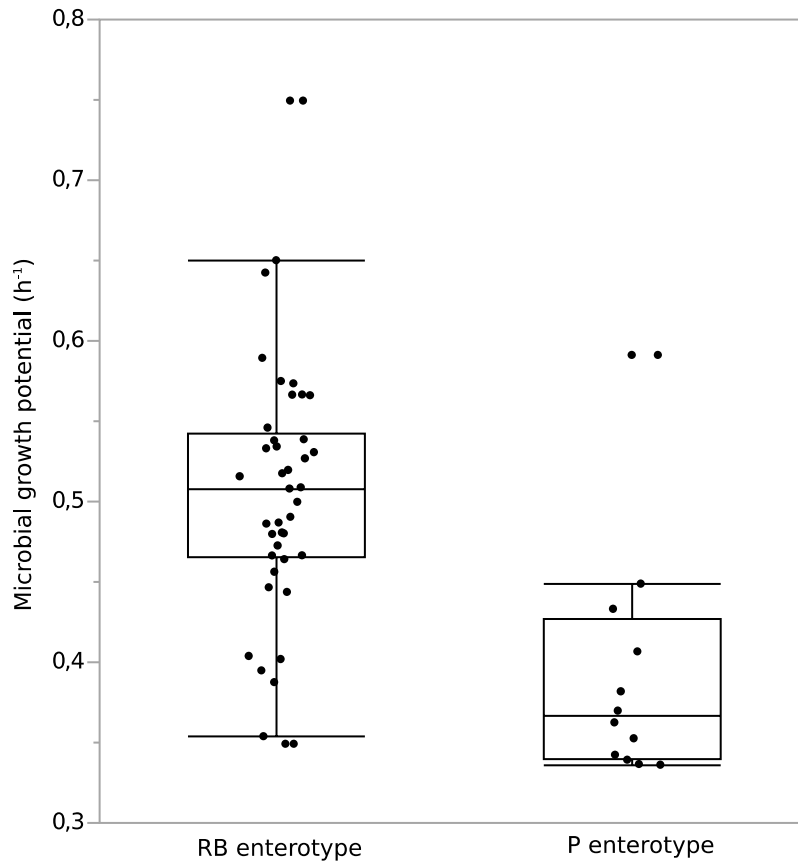
Supplementary Figure 6: Microbiota growth potential in the RB- and P enterotype. On average, microbiota growth potentials of the P enterotype samples are lower than those of the RB samples (median microbiota growth potential 0.38 h^{-1} vs. 0.52 h^{-1}, respectively). Significance of differences in microbiota 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).
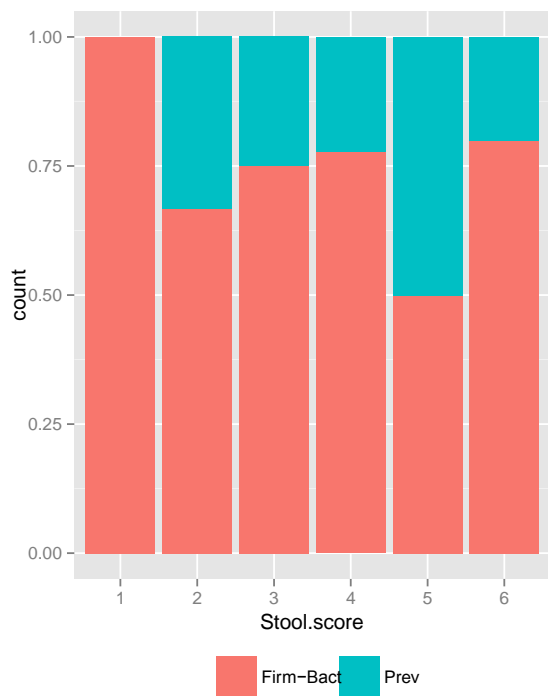
A. Distribution of the enterotypes over BSS scores in non-IBS participants.
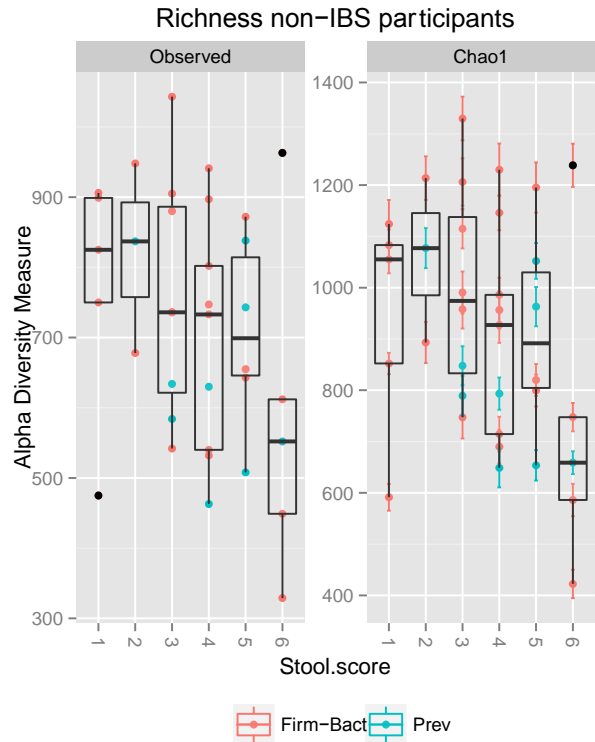
B. Observed and estimated richness over BSS scores in non-IBS participants.
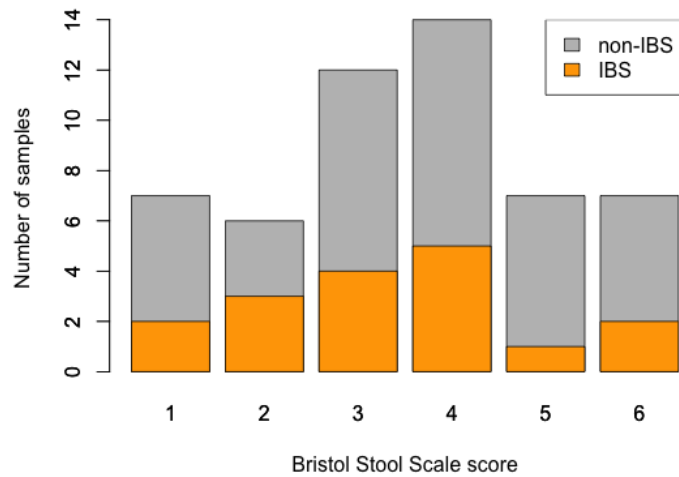
C. Distribution of the non-IBS participants and IBS patients over the BSS scores.

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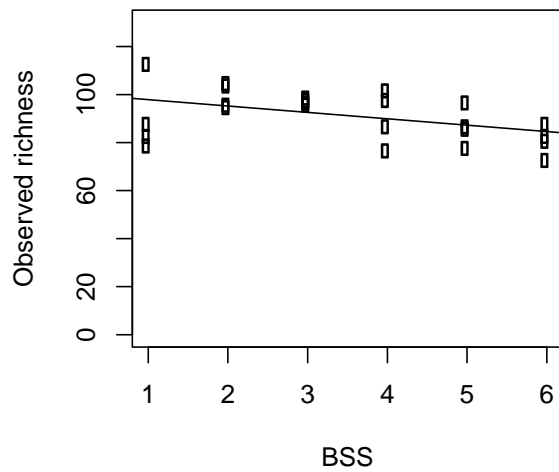
A Richness over BSS in 24 male individuals.
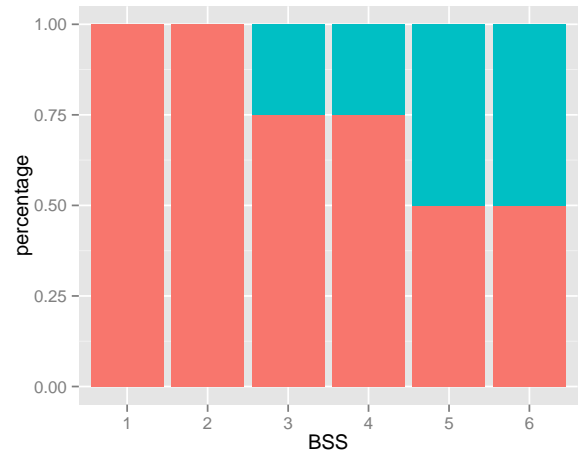
B Enterotypes Ruminococcaceae-Bacteroides (Red) and Prevotella (Blue) over BSS in 24 male individuals.

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.

Phylum	Genus	N samples	total dataset		RB enterotype		P enterotype	
			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.

Phylum	Genus	N samples	total dataset		RB enterotype		P enterotype	
			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

Phylum	Genus							
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}