Supplementary information to the manuscript:

Different gut microbial communities correlate with efficacy of albendazole-ivermectin against soil-transmitted helminthiases

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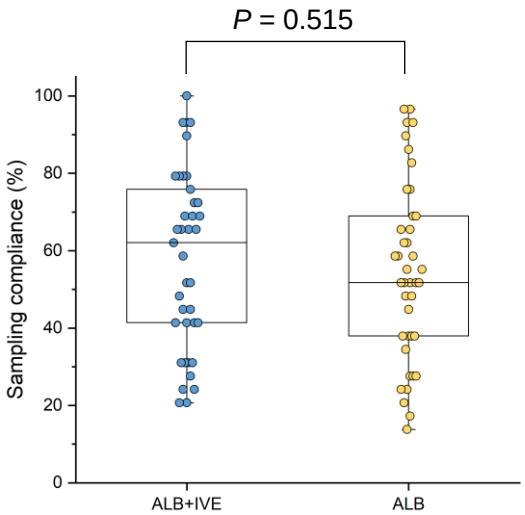
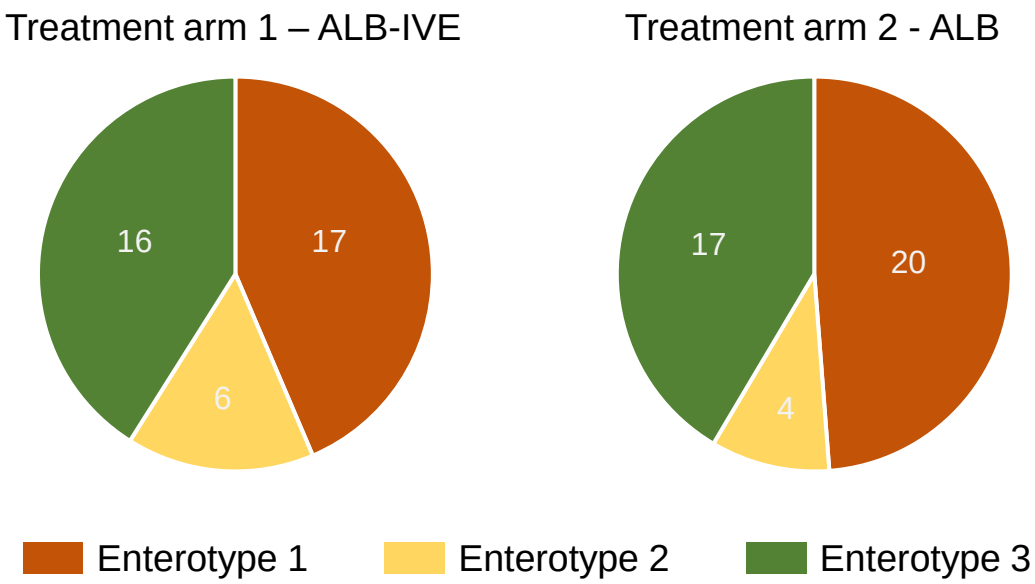
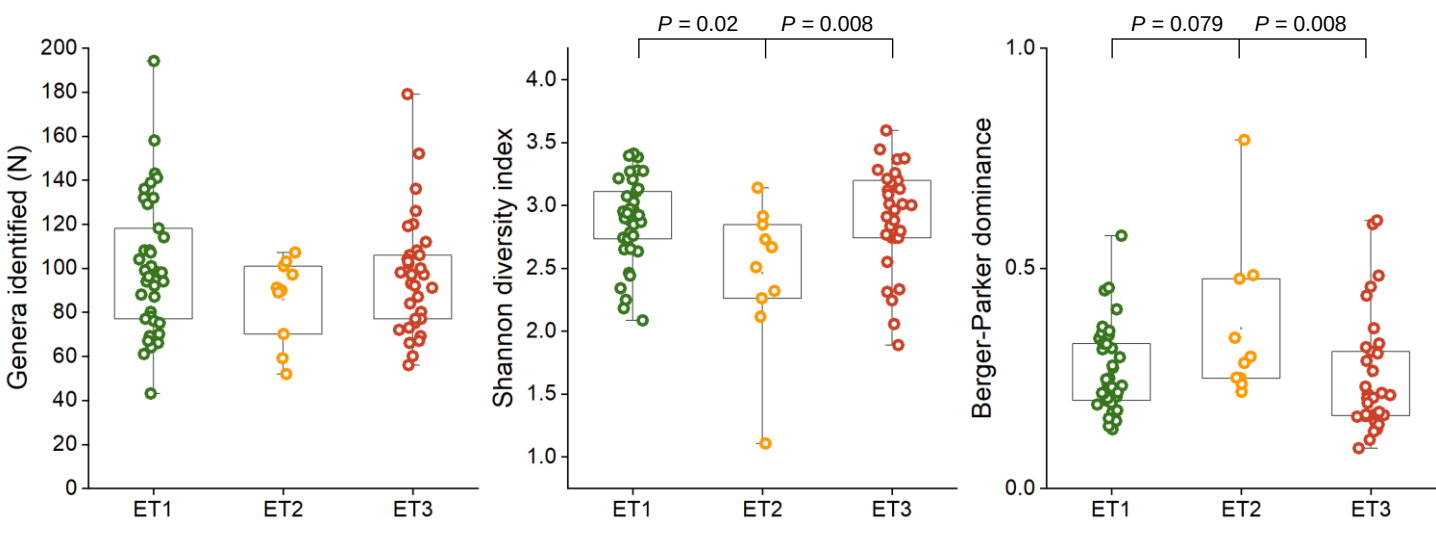


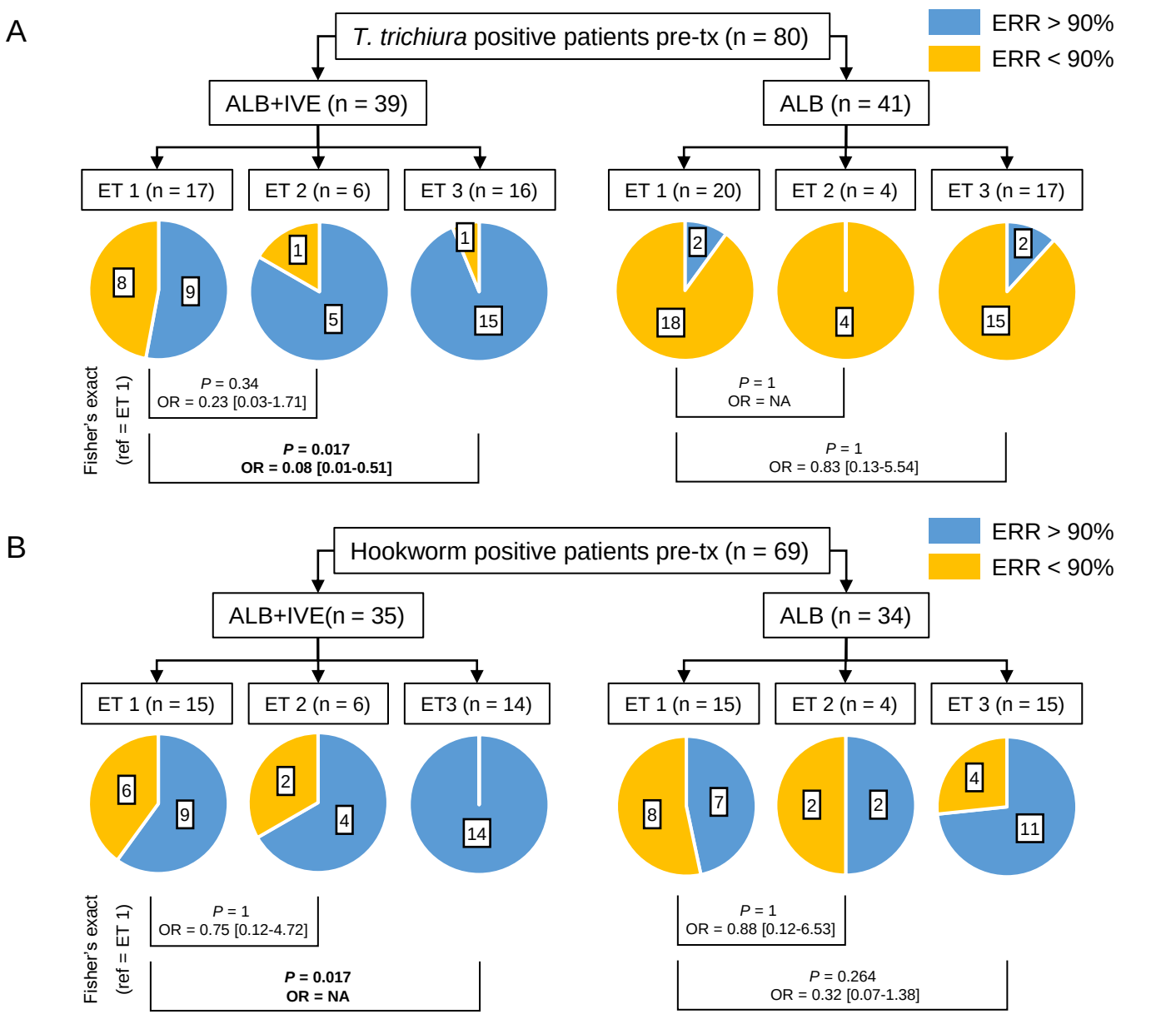
Supplementary figure 1. Sampling compliance, by treatment arm. A two-sided Mann-Whitney test was used to compare sampling compliance between the monotherapy arm (n=41) and the combination therapy arm (n=39). The lower and upper bound of each box represent the 25th and 75th percentiles, respectively, and the line within indicates the median. The whiskers represent the minimum and maximum values.



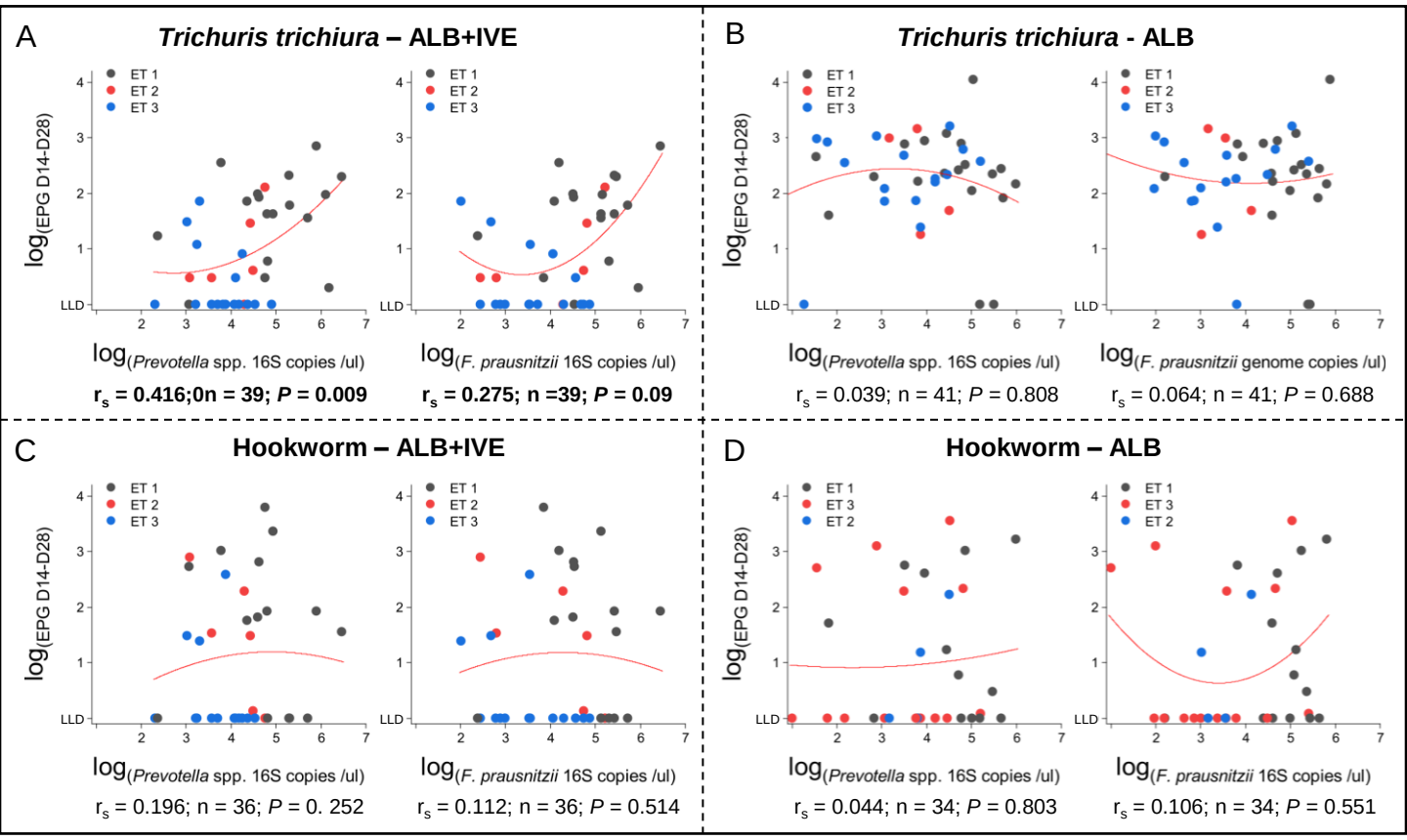
Supplementary figure 2. Proportion of each enterotype, by treatment arm. ALB = albendazole; IVE = ivermectin.



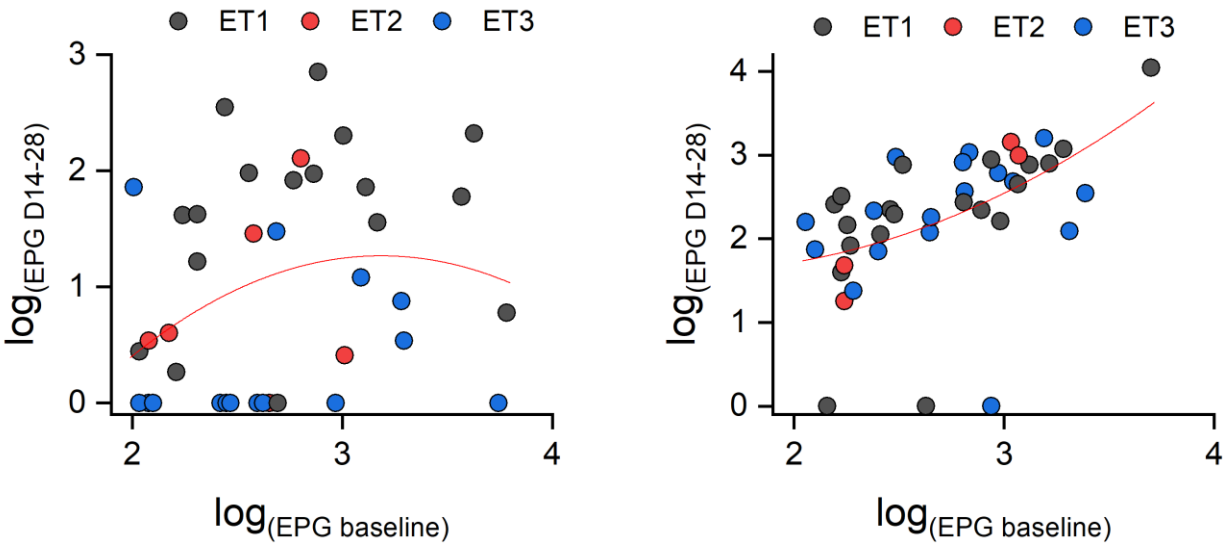
Supplementary figure 3. Alpha diversity indices, by enterotype. Group comparison between enterotype 1 (ET1; n=37), enterotype 2 (ET2; n=10), and enterotype 3 (ET3; n=33) was performed with a Kruskal-Wallis test and adjusted for multiple testing bias using the Bonferroni procedure. The lower and upper bound of each box represent the 25th and 75th percentiles, respectively, and the line within indicates the median. The whiskers represent the minimum and maximum values.



Supplementary figure 4. Association between egg reduction rate (ERR) and pre-treatment enterotype (ET), by treatment arm. A. Association between treatment outcome of *Trichuris trichiura* and ET at baseline. **B.** Association measured between treatment outcome of hookworm and ET before treatment. Egg reduction rate is the ratio of average eggs per gram (EPG) of stool between days 14-28 post-treatment and pre-treatment EPG. The threshold for treatment success is an ERR equal or above 90%. The Fisher's exact tests were two-sided and the 95% confidence interval of the odd ratios is shown in bracket. Labels on the pie charts represent the number of patients in each group. n = number of patients; OR = odds ratios.



Supplementary figure 5. Correlation between average eggs per gram of stool counts from days 14 to 28 and copy number of *Prevotella* and *Faecalibacterium prausnitzii,* measured by qPCR. Significance of the Spearman correlation was calculated using a two-sided test. r_s = Spearman correlation coefficient; EPG = eggs per gram of stool; ET(1-3) = enterotypes 1 to 3; ALB+IVE = albendazole and ivermectin; ALB = albendazole.



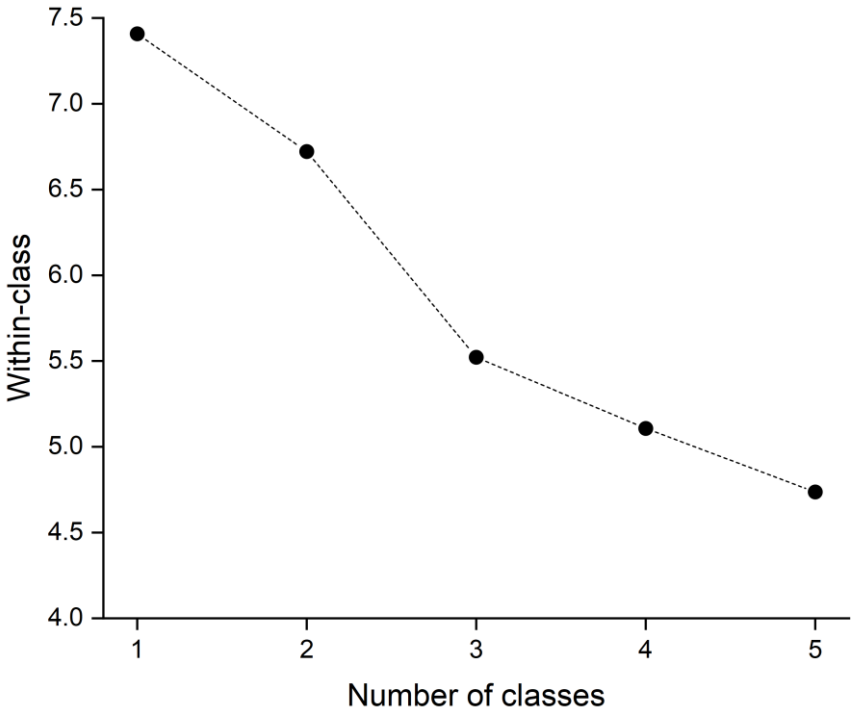
r_s = 0.257; n = 39; *P* = 0.115

r_s = 0.633; n = 41; *P* < 0.0001

Supplementary figure 6. Spearman correlation between average *T. trichiura* eggs per gram (EPG) of stool counts from days 14 to 28 and baseline (pre-treatment) EPG, by treatment arm. The left half includes patients who received albendazole and ivermectin while the right half includes patients who received only albendazole. Significance of the Spearman correlation was calculated using a two-sided test. r_s = Spearman correlation coefficient; EPG = eggs per gram of stool.

Supplementary figure 7. Comparison of KEGG pathways abundances between enterotype 1 (ET1; n=17), enterotype 2 (ET2; n=6), and enterotype 3 (ET3; n=16).

A Kruskal-Wallis test was used to compare medians for each pathway, and the resulting P-value was adjusted using the Benjamini-Hochberg procedure (Q-value) to account for multiple testing bias. The lower and upper bound of each box represent the 25th and 75th percentiles, respectively, and the line within indicates the median. The whiskers represent 1.5 times the interquartile range.



Supplementary figure 8. Evolution of inertia during k-means clustering.

Supplementary table 1. Shotgun sequencing depth.

Patient_ID	Shotgun sequencing depth (M sequences)
8764	8.5
8842	7
8946	13.3
8985	10
8999	5.5
9023	6
9951	5.6
9952	6.3
9959	11.4
9960	5.6
A0872	7.6
A0875	7.9
A0885	4.6
A0944	6.8
A1001	9.4
A1025	7.2
A1032	9.6
A1033	7.9
A1042	7.4
A1073	5.2
A1091	8.4
A1172	4.4
A1174	9.6
A1191	6.4
A1221	10.3
A1242	6.3
A1244	7.7
A1261	6.7
A1272	7.9
A1276	8.6
A1291	9.9
A1301	5.5
A1332	5
A1341	5.3
A1344	6.6
A1362	5.7
A1382	5.3
A1393	6.5
A1482	7.3

Supplementary table 2. Spearman correlation between community metrics and sequencing depth to assess bias related to low sequencing coverage. A value in bold indicates a significant correlation ($P < 0.05$) measured using a two-sided test.

			Taxonomic features			**Functional features**	
	Spearman correlation matrix	Sequencing depth ($log10_{sequenced\ reads}$)	Taxa (N)	Shannon diversity	Berger-Parker dominance	Number of Kegg Orthology terms identified	Complete metabolic pathways (>99% confidence)
	Sequencing depth ($log10_{sequenced\ reads}$)	**1**	0.097	-0.243	0.091	0.057	0.149
Taxonomic features	Taxa (N)	0.097	**1**	**0.551**	**-0.425**	0.089	0.189
	Shannon diversity	-0.243	**0.551**	**1**	**-0.853**	-0.051	**0.322**
	Berger-Parker dominance	0.091	**-0.425**	**-0.853**	**1**	0.188	-0.278
Functional features	Number of Kegg Orthology terms identified	0.057	0.089	-0.051	0.188	**1**	**0.449**
	Complete metabolic pathways (>99% confidence)	0.149	0.189	**0.322**	-0.278	**0.449**	**1**

Supplementary table 3. 16S and taxon-specific qPCR primers and conditions

Bacterial 16S

Primer	Primer sequence
F	5-TCCTACGGGAGGCAGCAGT-3
R	5-GGACTACCAGGGTATCTAATCCTGTT-3
probe	(FAM)-CGTATTACCGCGGCTGCTGGCAC-(NFQ-MGB)

Master mix		
Taqman Mix	1X	5
F primer	0.3 uM	1
R primer	0.3 uM	1
Probe	0.2 uM	1
DNA		2

Cycling conditions		
	← 45 cycles →	
95°C	95°C	
10 min	15 sec	60°C
		1 min

FAEC

Primer	Primer sequence
F	5-TGTAAACTCCTGTTGTTGAGGAAGATAA-3
R	5-GCGCTCCCTTTACACCCA-3
probe	(HEX)-CAAGGAAGTGACGGCTAACTACGTGCCAG-(NFQ-MGB)

Master mix		
Taqman Mix	1X	5
F primer	0.3 uM	1
R primer	0.3 uM	1
Probe	0.2 uM	1
DNA		2

Cycling conditions		
	← 45 cycles →	
95°C	95°C	
10 min	15 sec	60°C
		1 min

PREV

Primer	Primer sequence
F	5-CCAGCCAAGTAGCGTGCA-3
R	5-TGGACCTTCCGTATTACCGC-3
probe	(FAM)-AATAAGGACCGGCTAATTCCGTGCCAG-(NFQ-MGB)

Master mix		
Taqman Mix	1X	5
F primer	0.3 uM	1
R primer	0.3 uM	1
Probe	0.2 uM	1
DNA		2

Cycling conditions		
	← 45 cycles →	
95°C	95°C	
10 min	15 sec	60°C
		1 min

ESCH

Primer	Primer sequence
F	5-CATGCCGCGTGTATGAAGAA-3
R	5-CGGGTAACGTCAATGAGCAAA-3
probe	(CY5)-TATTAACTTTACTCCCTTCCTCCCCGCTGAA-(NFQ-MGB)

Master mix		
Taqman Mix	1X	5
F primer	0.3 uM	1
R primer	0.3 uM	1
Probe	0.2 uM	1
DNA		2

Cycling conditions		
	← 45 cycles →	
95°C	95°C	
10 min	15 sec	60°C
		1 min

Supplementary table 4. Correlation of enterotype-relevant taxa at the genus level between 16S rRNA gene sequencing and shallow shotgun sequencing. A value in bold indicates a significant correlation (P < 0.05) measured using a two-sided test.

Genus	Spearman correlation	*P*-value
Prevotella	**0.512**	**0.001**
Faecalibacterium	**0.737**	**<0.0001**
Escherichia	**0.838**	**<0.0001**
Roseburia	**0.301**	**0.063**
Eubacterium	**0.468**	**0.003**
Ruminococcus	**0.361**	**0.025**
Fusicatenibacter	0.2	0.222
Veillonella	**0.664**	**<0.0001**

Supplementary table 5. Spearman correlation of relative abundances of *Prevotella*, *Faecalibacterium*, and *Escherichia* genera between sequencing (16S rRNA gene and shallow shotgun sequencing) and qPCR-derived values (ratio of target density over total bacteria density). A value in bold indicates a significant correlation (P < 0.05) measured using a two-sided test.

		measured by qPCR (ratio of target density over 16S density)					
		Prevotella	*P*-value	*Faecalibacterium*	*P*-value	*Escherichia*	*P*-value
measured by 16S rRNA gene sequencing	*Prevotella*	**0.538**	**0**				
	Faecalibacterium			**0.639**	**<0.0001**		
	Escherichia					**0.838**	**<0.0001**
measured by shallow shotgun sequencing	*Prevotella*	**0.895**	**<0.0001**				
	Faecalibacterium			**0.737**	**<0.0001**		
	Escherichia					**0.965**	**<0.0001**