

## Supplementary Materials

Males

(a)

metabogram components

positive

negative

12345671234567

MICROBIOTA

Enterobacteriaceae0.360.960.400.440.350.570.670.870.390.470.350.720.980.49

Staphylococcus0.400.850.600.040.470.930.510.090.130.320.050.150.060.67

Enterococcus0.580.240.210.210.240.690.950.420.280.880.410.930.350.97

Aerobic bacteria0.520.280.410.960.560.650.090.310.310.240.250.260.550.68

Anaerobic bacteria0.790.880.960.420.380.730.430.580.600.910.360.510.350.39

Hemolytic aerobic bacteria0.460.600.550.990.590.300.360.330.180.690.140.160.620.95

Hemolytic anaerobic bacteria0.920.770.970.460.440.140.100.180.080.750.070.450.690.83

Lactobacillus0.770.780.770.630.920.650.660.240.750.550.590.080.300.13

Citrate-assimilating Enterobacteria0.360.270.350.750.210.100.320.480.740.270.670.850.330.47

Bifidobacteria0.650.020.470.740.410.160.000.290.250.130.190.510.170.69

Sulfite-reducing Clostridia0.600.140.080.620.260.870.110.600.740.500.260.810.760.76

Yeasts0.120.0020.010.050.050.0010.950.720.0040.250.030.020.300.06

Bacteroides0.840.170.020.540.600.020.800.330.260.130.840.110.860.92

Antagonistic activity of Bifidobacteria0.440.990.460.380.860.150.370.060.140.090.280.160.120.71

Females

(b)

metabogram components

positive

negative

12345671234567

MICROBIOTA

Enterobacteriaceae0.060.850.410.110.420.950.280.170.140.550.180.320.080.23

Staphylococcus0.110.660.690.770.540.730.850.470.270.630.460.860.530.23

Enterococcus0.250.670.470.500.910.890.740.410.630.510.780.820.480.17

Aerobic bacteria0.350.890.820.380.980.990.350.470.270.530.220.440.160.46

Anaerobic bacteria0.730.500.360.730.430.220.300.570.780.340.720.190.820.69

Hemolytic aerobic bacteria0.360.800.950.480.690.840.340.440.290.440.160.560.140.42

Hemolytic anaerobic bacteria0.830.670.610.720.430.300.620.520.940.940.820.530.600.72

Lactobacillus0.130.640.750.510.480.850.340.300.740.390.830.800.420.46

Citrate-assimilating Enterobacteria0.060.080.200.220.520.600.370.570.520.080.570.710.590.57

Bifidobacteria0.140.830.500.190.730.240.380.070.110.130.160.380.130.92

Sulfite-reducing Clostridia0.080.890.830.280.210.110.670.140.470.280.440.230.190.41

Yeasts0.450.950.230.180.200.310.200.310.610.200.910.160.280.66

Bacteroides0.240.820.450.180.820.060.140.090.010.730.020.040.090.97

Antagonistic activity of Bifidobacteria0.100.700.470.060.370.670.630.090.080.420.050.810.070.91

**Figure S1.** p-Values for the correlation of gut microorganism levels (assessed by a culture-based method) with the metabogram components calculated for healthy individuals and individuals with various degrees of body weight deviation. The p-value tests the hypothesis of no correlation against the alternative hypothesis of a nonzero correlation. P-values <0.05 (rejection of the hypothesis that no correlation exists) are selected by the red color. Data is presented for males (**a**) and females (**b**).

Males (a)														
metabogram components														
MICROBIOME	positive							negative						
	1	2	3	4	5	6	7	1	2	3	4	5	6	7
Total bacteria	0.91	0.26	0.20	0.48	0.53	0.91	0.48	0.92	0.74	0.22	0.69	0.96	0.51	0.37
<i>Lactobacillus</i> spp.	0.69	0.90	0.90	0.14	0.27	0.97	0.54	0.36	0.97	0.09	0.24	0.32	0.47	0.12
<i>Bifidobacterium</i> spp.	1.00	0.42	0.20	0.61	0.59	0.83	0.25	0.26	0.77	0.98	0.44	0.09	0.48	0.03
<i>Escherichia coli</i>	0.53	0.11	0.47	0.16	0.58	0.43	0.07	0.08	0.32	0.19	0.05	0.70	0.10	0.42
<i>Bacteroides fragilis</i> group	0.83	0.21	0.16	0.23	0.64	0.84	0.65	0.76	0.69	0.25	0.90	0.61	0.35	0.72
<i>Faecalibacterium prausnitzii</i>	0.92	0.16	0.26	0.64	0.56	0.62	0.09	0.08	0.64	0.72	0.22	0.10	0.18	0.23
<i>Klebsiella pneumoniae</i>	0.21	0.20	0.25	0.66	0.52	0.25	0.30	0.17	0.70	0.50	0.78	0.57	0.43	0.42
<i>Escherichia coli</i> enteropathogenic	0.58	0.18	0.39	0.98	0.94	0.08	0.10	0.63	0.90	0.65	0.28	0.47	0.81	0.66
<i>Enterococcus</i> spp.	0.86	0.88	0.83	0.13	0.07	0.97	0.47	0.12	0.35	0.03	0.07	0.28	0.12	0.72
<i>Bacteroides thetaiotaomicron</i>	0.54	0.79	0.90	0.64	0.81	0.12	0.94	0.96	0.28	0.26	0.39	0.49	0.83	0.37
<i>Clostridium perfringens</i>	0.99	0.21	0.02	0.53	0.23	0.73	0.15	0.88	0.95	0.91	0.36	0.68	0.67	0.89
<i>Enterobacter</i> spp. and <i>Citrobacter</i> spp.	0.70	0.34	0.72	0.17	0.44	0.52	0.36	0.27	0.61	0.15	0.20	0.89	0.22	0.43
<i>Parvimonas micra</i>	0.83	0.48	0.51	0.47	0.91	0.07	0.72	0.82	0.05	0.36	0.14	0.11	0.32	0.43
<i>B. fragilis</i> group / <i>F. prausnitzii</i> ratio	0.50	0.67	0.51	0.22	0.59	0.49	0.17	0.20	0.69	0.57	0.48	0.33	0.10	0.43

  

Females (b)														
metabogram components														
MICROBIOME	positive							negative						
	1	2	3	4	5	6	7	1	2	3	4	5	6	7
Total bacteria	0.97	0.07	0.13	0.75	0.90	0.39	0.73	0.71	0.57	0.92	0.80	0.98	0.73	0.63
<i>Lactobacillus</i> spp.	0.95	0.95	0.85	0.46	0.14	0.30	0.34	0.91	0.22	0.62	0.42	0.18	0.57	0.37
<i>Bifidobacterium</i> spp.	0.26	0.59	0.86	0.61	0.48	0.37	0.53	0.97	0.85	0.97	0.90	0.74	0.50	0.37
<i>Escherichia coli</i>	0.55	0.80	0.70	0.42	0.40	0.49	0.28	0.77	0.50	0.63	0.55	0.41	0.86	0.37
<i>Bacteroides fragilis</i> group	0.51	0.24	0.34	0.66	0.83	0.97	0.42	0.54	0.99	0.68	0.64	0.40	0.59	0.63
<i>Faecalibacterium prausnitzii</i>	0.16	0.90	0.46	0.49	0.55	0.50	0.71	0.90	0.60	0.13	0.89	0.25	0.83	0.40
<i>Klebsiella pneumoniae</i>	0.02	0.10	0.14	0.68	0.90	0.23	0.89	0.25	0.23	0.54	0.53	0.63	0.81	0.65
<i>Enterococcus</i> spp.	0.05	0.56	0.17	0.21	0.16	0.65	0.64	0.89	0.33	0.64	0.55	0.68	0.69	0.41
<i>Bacteroides thetaiotaomicron</i>	0.17	0.29	0.28	0.82	0.01	0.05	0.84	0.85	0.48	0.09	0.34	0.32	0.72	0.62
<i>Enterobacter</i> spp. and <i>Citrobacter</i> spp.	0.36	0.41	0.35	0.29	0.68	0.13	0.30	0.76	0.09	0.75	0.24	0.20	0.99	0.43
<i>Fusobacterium nucleatum</i>	0.53	0.65	0.72	0.32	0.55	0.95	0.37	0.19	0.52	0.37	0.34	0.71	0.13	0.98
<i>Parvimonas micra</i>	0.62	0.97	0.16	0.004	0.57	0.31	0.01	0.07	0.001	0.26	0.0003	0.05	0.01	0.91
<i>B. fragilis</i> group / <i>F. prausnitzii</i> ratio	0.94	0.59	0.76	0.84	0.26	0.23	0.65	0.72	0.86	0.30	0.76	0.19	0.73	0.50

**Figure S2.** p-Values for the correlation of gut microorganism levels (assessed by a real-time PCR analysis) with the metabogram components calculated for healthy individuals and individuals with various degrees of body weight deviation. The p-value tests the hypothesis of no correlation against the alternative hypothesis of a nonzero correlation. P-values <0.05 (rejection of the hypothesis that no correlation exists) are selected by the red color. Data is presented for males (a) and females (b).

**Table S3.** Statistical data for gut microbiota test results calculated for males and females separately.

		Males		Females	
		mean	st.d.	mean	st.d.
Culture-based method	Enterobacteriaceae	6.97	1.08	7.30	1.01
	Staphylococcus	5.50	1.02	5.82	1.47
	Coagulase Positive Staphylococci	-	-	-	-
	Enterococcus	6.12	0.78	6.13	1.16
	Aerobic bacteria	7.62	0.82	7.86	0.84
	Anaerobic bacteria	10.04	0.84	9.44	0.98
	Hemolytic aerobic bacteria	7.25	0.86	7.42	1.35
	Hemolytic anaerobic bacteria	8.99	1.24	8.56	1.26
	Lactobacillus	7.20	0.92	7.21	1.11
	citrate-assimilating enterobacteria	6.22	0.93	5.92	0.71
	Bifidobacteria	8.68	0.85	8.61	1.09
	Sulfite-reducing Clostridia	7.16	0.99	7.22	0.88
	Yeasts	3.12	0.85	3.06	1.18
	Bacteroides	8.89	1.04	8.13	1.37
	Antagonistic activity of Bifidobacteria	4.30	0.22	4.17	0.16
	Total bacteria	13.55	0.62	13.83	0.40
	Lactobacillus spp.	8.75	1.11	8.73	1.10
	Bifidobacterium spp.	12.32	1.05	12.68	0.67
	Escherichia coli	9.43	0.99	10.07	0.68
	Bacteroides fragilis group	13.32	0.82	13.50	0.42
Real-time PCR analysis	Faecalibacterium prausnitzii	12.05	0.76	12.25	0.35
	Klebsiella pneumoniae	1.36	2.62	2.62	3.25
	Klebsiella oxytoca	0.38	1.60	1.05	2.46
	Candida spp.	-	-	-	-
	Staphylococcus aureus	-	-	-	-
	Escherichia coli enteropathogenic	2.93	3.46	-	-
	Enterococcus spp.	6.55	3.22	6.17	2.59
	Bacteroides thetaiotaomicron	10.05	2.78	6.55	5.05
	Clostridium difficile	-	-	-	-
	Clostridium perfringens	2.36	3.52	1.55	3.69
	Proteus vulgaris and Proteus mirabilis	-	-	-	-
	Enterobacter spp. and Citrobacter spp.	8.95	0.96	9.54	0.85
	Fusobacterium nucleatum	-	-	2.70	4.04
	Parvimonas micra	6.51	3.66	6.96	3.33
	Salmonella spp.	-	-	-	-
	Shigella spp.	-	-	-	-
	B. fragilis group / F. prausnitzii ratio	125.47	387.36	23.45	22.17