

Data S1. Measurements of clinical parameters. All of the clinical parameters were measured by standardized procedures. A total of three readings of BP were recorded using a mercury sphygmomanometer with a 5-min resting period and the mean was taken as the final measurement. Blood samples were drawn following a fasting period of 12 h for the detection of fasting blood glucose level.

Figure S1. Rarefaction curves used to estimate richness among the hypertension and control groups at the 97% similarity level. OTU, operational taxonomic unit.

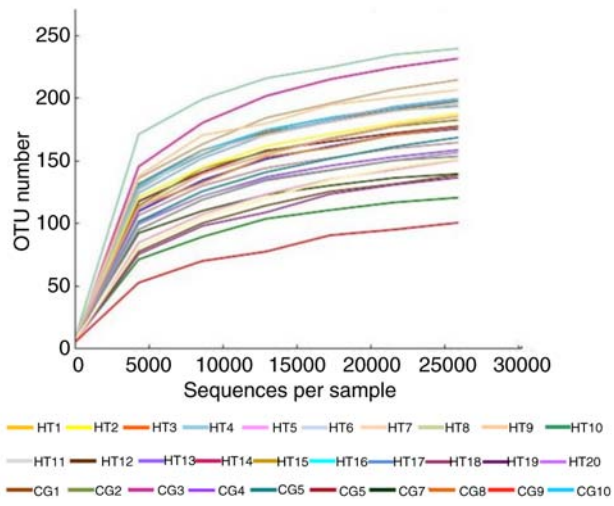


Table SI. World Health Organization/International Society of Hypertension blood pressure classification, including three grades of hypertension.

Blood pressure	Grade 1	Grade 2	Grade 3
SBP, mm Hg	140-159	160-179	≥180
DBP, mm Hg	90-99	100-109	≥110

SBP, systolic blood pressure; DBP, diastolic blood pressure.

Table SII. Detailed phenotype information for 50 patients with grade 3 hypertension and 30 sex-, age- and body weight-matched healthy controls.

Sample ID	Sex	Age, years	Weight, kg	Current SBP, mmHg	Current DBP, mmHg	Disease duration, years	FBG, mmol/l	TC, mmol/l	TG, mmol/l	HDL, mmol/l	LDL, mmol/l
HT1	F	64	75	190	109	2	4.96	5.34	1.02	1.38	3.49
HT2	F	66	73	160	81	3	4.77	4.54	2.01	0.94	2.36
HT3	F	65	66	180	110	3	5.23	6.72	2.02	0.67	0.94
HT4	M	67	81	180	100	5	5.17	4.4	1.3	1.4	2.4
HT5	F	70	67	190	110	2	4.08	4.53	1.26	1.1	2.8
HT6	F	69	70	180	100	3	4.28	4.6	2.5	0.7	3.3
HT7	M	47	79	189	100	1	6.67	3.98	1.5	0.88	2.6
HT8	M	61	82	160	100	1	5.16	3.37	2.16	0.53	1.97
HT9	M	74	78	210	110	3	6.11	3.72	0.73	0.82	2.3
HT10	F	57	74	180	110	1	3.64	3.7	3.05	0.7	2.33
HT11	M	40	69	160	105	2	5.07	4.36	1.85	1.13	2.6
HT12	M	60	80	180	110	2	4.62	3.8	1.3	0.86	2.38
HT13	F	71	75	189	105	3	3.91	3.59	1.2	0.96	2.1
HT14	M	74	74	200	120	4	5.36	2.7	1.49	0.73	1.54
HT15	M	62	72	240	120	3	5.34	3.6	0.9	1	2
HT16	F	78	65	180	110	2	6.22	2.7	1	0.98	1.29
HT17	F	54	75	180	100	3	5.18	4.54	1.4	1.25	2.76
HT18	M	53	70	160	108	2	7.53	4.47	1.97	0.8	2.94
HT19	F	53	65	157	100	2	4.66	4.36	0.93	0.87	2.89
HT20	M	40	75	180	110	3	4.82	4.07	2.1	0.98	2.37
HT21	F	64	58	200	110	5	5.79	4.29	1.99	0.94	2.7
HT22	F	74	47	180	160	3	5.27	5.03	1.58	1.76	2.7
HT23	M	49	64	180	110	6	5.74	3.64	1.9	1.13	1.78
HT24	F	48	58	190	110	5	4.89	2.9	0.8	0.9	1.5
HT25	F	64	62	170	100	2	4.18	3.27	1.4	0.93	1.8
HT26	F	52	58	170	105	2	4.9	4.28	0.94	1.12	2.67
HT27	F	74	60	189	105	2	6.64	5.28	1.33	1.18	3.23
HT28	M	56	69	182	100	1	6	3.39	1.06	0.84	1.9
HT29	F	77	61	150	100	4	4.23	3.04	1.5	0.8	1.6
HT30	M	63	65	180	105	3	4.37	4.01	2.01	1.01	2.41
HT31	M	72	58	172	100	3	4.8	4.7	0.46	1.26	2.9
HT32	M	61	67	160	100	4	5.47	3.02	0.7	0.99	1.5
HT33	M	74	76	175	105	2	5.24	3.26	1.72	1.07	1.7
HT34	F	54	57	180	115	3	3.74	3.89	0.87	1.44	1.98
HT35	F	72	60	180	105	4	4.2	3.06	1.04	0.96	1.48
HT36	M	48	72	180	110	2	4.38	3.38	0.99	0.96	1.83
HT37	M	86	63	170	100	3	4.11	5.52	1.3	1.04	3.86
HT38	F	48	54	204	102	6	5.55	4.37	1.96	0.94	2.67
HT39	M	55	78	185	105	3	4.11	4.4	2.11	1.07	1.7
HT40	M	67	69	180	100	2	4.55	4.7	1.01	1.44	2.3
HT41	M	70	71	175	110	2	4.38	3.5	1.89	0.96	0.9
HT42	F	60	52	170	105	5	5.78	3.04	1.3	1.1	3.5
HT43	M	72	68	200	120	4	4.87	4.7	1.5	1.3	2.4
HT44	M	72	71	190	109	4	5.99	4.28	0.8	1.43	2.4
HT45	M	68	70	160	105	3	5.9	3.37	1.73	1.17	2.5
HT46	M	54	75	190	110	3	5.1	4.38	2.2	1.25	2.1
HT47	M	50	78	190	100	3	3.89	5.52	0.98	0.8	2
HT48	M	65	69	170	100	2	5.88	3.02	0.94	1.37	1.9
HT49	M	59	75	180	110	3	4.98	4.54	1.88	0.98	2.3
HT50	M	75	70	170	110	4	5.21	4.53	2.43	1.18	1.7
CG1	M	55	74	125	87	-	4.68	5.05	0.9	0.96	3.34
CG2	M	74	72	110	80	-	3.47	4.31	1.2	1.09	2.37
CG3	F	66	59	120	80	-	4.14	4.62	0.7	1.17	1.99
CG4	M	57	75	112	77	-	5.06	3.48	0.77	1.25	1.97

Table SII. Continued.

Sample ID	Sex	Age, years	Weight, kg	Current SBP, mmHg	Current DBP, mmHg	Disease duration, years	FBG, mmol/l	TC, mmol/l	TG, mmol/l	HDL, mmol/l	LDL, mmol/l
CG5	F	75	62	123	68	-	4.68	5.72	1.3	0.8	2.3
CG6	F	72	60	134	79	-	4.85	5.82	1.4	1.37	2.33
CG7	M	77	70	127	88	-	4.78	4.87	1.3	0.98	1.54
CG8	M	70	58	127	82	-	5.28	3.54	1.22	1.18	2
CG9	M	73	67	120	80	-	4.7	3.97	0.8	0.84	1.29
CG10	F	76	64	117	70	-	3.14	4.62	1	1.09	1.5
CG11	M	72	58	120	80	-	4.08	2.28	1	1.26	1.7
CG12	F	40	62	116	84	-	3.89	4.67	0.9	0.99	1.5
CG13	F	47	58	102	70	-	5.27	5.23	0.9	1.07	1.5
CG14	F	64	60	108	60	-	3.91	4.99	1.2	1.44	2.3
CG15	F	61	69	125	76	-	5	5.69	0.8	0.96	0.94
CG16	M	49	69	129	74	-	4.22	3.74	1.3	1.1	1.29
CG17	M	65	62	120	80	-	4.15	3.79	1.3	1.3	1.6
CG18	F	74	58	120	80	-	4.63	3.7	1.2	1.43	1.8
CG19	M	65	60	115	80	-	3.47	4.67	0.98	0.78	2.4
CG20	M	60	69	110	80	-	3.88	5.2	1.6	1	2.4
CG21	M	58	61	115	80	-	3.21	3.97	0.9	0.87	2.5
CG22	F	55	59	120	75	-	3.33	3.34	1	0.95	2.1
CG23	M	63	68	120	80	-	4.25	4.87	1.5	1.18	2
CG24	F	50	67	120	80	-	3.9	3.89	0.9	1.53	1.9
CG25	F	47	76	120	80	-	3.91	2.54	0.9	1.4	1
CG26	F	45	61	125	90	-	3.5	3.44	1.9	1.4	1.8
CG27	F	52	64	125	80	-	4.53	3.7	0.7	1	2.1
CG28	M	60	70	135	80	-	4.08	4.21	0.98	1	1.7
CG29	M	44	76	120	89	-	5.31	4.62	1.73	1.01	2.3
CG30	M	49	72	120	80	-	3.47	5.74	0.9	0.8	0.9

SBP, systolic blood pressure; DBP, diastolic blood pressure; FBG, fasting blood glucose; HDL, high density lipoprotein; LDL, low density lipoprotein; TG, triglycerides; TC, total cholesterol; F, female; M, male; HT, hypertension; CG, control group.

Table SIII. Sequence identities of PCR amplicons derived from denaturing gradient gel electrophoresis gels based on the Basic Local Alignment Search Tool database.

Bacteria (band sequencing)	HTN (n=45) (%)	CG (n=40) (%)
Phylum Bacteroidetes		
Genus <i>Prevotella</i>	11 (24.44)	5 (12.5)
Genus <i>Alistipes</i>	3 (6.66)	1 (2.5)
<i>Bacteroides vulgatus</i>	2 (4.44)	5 (12.5)
Genus <i>Bacteroides</i>	5 (11.11)	7 (17.5)
Phylum Firmicutes		
Genus <i>Clostridium</i>	4 (8.88)	7 (17.5)
Genus <i>Dialister</i>	3 (6.66)	2 (5.00)
Genus <i>Faecalibacterium</i>	5 (11.11)	6 (15.00)
Genus <i>Megasphaera</i>	2 (4.44)	1 (2.5)
Phylum Proteobacteria		
<i>Escherichia coli</i>	4 (8.88)	2 (5.00)
Genus <i>Klebsiella</i>	1 (2.22)	2 (5.00)
Phylum Actinobacteria		
Genus <i>Propionibacterium</i>	2 (4.44)	0
Uncultured bacterium	3 (6.66)	2 (5.00)

HTN, hypertension; CG, control group.

Table SIV. Gut microbial phylotypes from high-throughput sequencing.

Taxon	HTN (mean)	CG (mean)	P-value
Phyla			
Bacteroidetes	0.480521	0.664536	0.002
Firmicutes	0.414503	0.250077	0.001
Proteobacteria	0.075405	0.059544	0.939
Actinobacteria	0.016173	0.023639	0.628
Fusobacteria	0.006731	0.001699	0.085
Verrucomicrobia	1.03x10 ⁻⁴	3.86x10 ⁻⁵	0.113
Spirochaetes	0.000304	7.34x10 ⁻⁵	0.022
Synergistetes	0.000121	0.000108	0.983
Cyanobacteria	0.000126	0.000104	0.726
Tenericutes	5.91975x10 ⁻⁵	6.18x10 ⁻⁵	0.763
Family			
Bacteroidaceae	0.297388	0.460906	0.071
Prevotellaceae	0.137297	0.113621	0.04
Veillonellaceae	0.142331	0.04297	0.02
Ruminococcaceae	0.134378	0.134909	0.115
Lachnospiraceae	0.071024	0.054745	0.043
Bifidobacteriaceae	0.022909	0.023037	0.54
Enterobacteriaceae	0.026804	0.03153	0.378
Alcaligenaceae	0.038427	0.025087	0.052
Peptostreptococcaceae	2.10x10 ⁻²	0.007497	0.042
Fusobacteriaceae	0.01134	0.000403	0.001
Genera			
<i>Bacteroides</i>	0.297388	0.460906	0.071
<i>Prevotella_9</i>	0.145742	0.109609	0.041
<i>Megamonas</i>	0.048411	0.015547	0.147
<i>Megasphaera</i>	0.055177	0.001784	0.003
<i>Faecalibacterium</i>	0.053015	0.059169	0.24
<i>Ruminococcus_2</i>	0.019499	0.007548	0.129
<i>Bifidobacterium</i>	0.022891	0.023037	0.542
<i>Dialister</i>	0.022137	0.019049	0.738
<i>Parasutterella</i>	0.033871	0.01132	0.011
<i>Escherichia-Shigella</i>	2.10x10 ⁻²	0.004807	0.038

HTN, hypertension; CG, control group.

Table SV. Gut microbial taxa at species level from high-throughput sequencing.

Species	HTN (mean)	CG (mean)	P-value
<i>Bacteroides_plebeius</i>	0.047628	0.100478728	0.192
<i>Bacteroides_uniformis</i>	0.019609811	0.088757625	0.016
<i>Bacteroides_vulgatus</i>	0.034309	0.054632847	0.538
<i>Bacteroides_dorei</i>	0.040148766	0.031225388	0.595
<i>Bacteroides_stercoris</i>	0.038906	0.062481662	0.79
<i>Bacteroides_eggerthii</i>	0.013968033	9.38x10 ⁻⁴	0.113
<i>Bacteroides_ovatus</i>	0.022652	0.019095051	0.139
<i>Bacteroides_coprocola</i>	0.0128021	0.011354336	0.831
<i>Phascolarctobacterium_faecium</i>	0.026217	0.003652228	0.03
<i>Ruminococcus_sp._5_1_39BFAA</i>	0.007371	0.001042391	0.11
<i>Bifidobacterium_adolescentis</i>	0.006635	0.007412555	0.975
<i>Parabacteroides_merdae</i>	0.012702	0.014419736	0.957
<i>Bacteroides_caccae</i>	0.007711	0.008366149	0.362
<i>Bifidobacterium_pseudocatenulatum</i>	0.006728	0.008462667	0.477
<i>Fusobacterium_varium</i>	0.004159	1.48x10 ⁻³	0.307
<i>Bacteroides_massiliensis</i>	0.002324	8.88x10 ⁻⁵	0.099
<i>Clostridium_perfringens</i>	0.002044	0.000150568	0.111
<i>Lactobacillus_salivarius</i>	2.00x10 ⁻³	1.93035x10 ⁻⁵	0.096
<i>Roseburia_inulinivorans</i>	0.003816951	0.005899158	0.31
<i>Bacteroides_cellulosilyticus</i>	0.0026	0.001590611	0.288
<i>Bacteroides_fragilis</i>	0.003403	0.001567447	0.207
<i>Coprococcus_eutactus</i>	0.001791	0.000347464	0.178
<i>Parabacteroides_sp._SB4</i>	0.001606054	5.40499x10 ⁻⁵	0.10
<i>Bacteroides_clarus</i>	0.002625	2.75x10 ⁻³	0.407
<i>Anaerostipes_hadrus</i>	0.00155942	8.45x10 ⁻⁴	0.406
<i>Lactobacillus_reuteri</i>	0.001307	3.86071x10 ⁻⁶	0.095
<i>Sutterella_wadsworthensis</i>	0.000342	0.001833835	0.34
<i>[Clostridium]_leptum</i>	0.001467	0.000277971	0.133
<i>Faecalibacterium_prausnitzii</i>	2.5738x10 ⁻⁶	0.000320439	0.001
<i>Parabacteroides_distasonis</i>	0.004422	0.004358737	0.09
<i>Bacteroides_xylanisolvens</i>	0.001169	0.002536484	0.186
<i>Fusobacterium_sp._RMA_1065</i>	0.000241938	0.000189175	0.059

HTN, hypertension; CG, control group.