

Supplementary data

Table S1 Sequencing of PCR amplicons slashed from DGGE gel profile and recognition linking to BLAST database

Bacterial Genus (Bands sequencing)	Female		Male	
	HTN (n=14)	CG (n=10)	HTN (n=13)	CG (n=15)
Phylum Bacteroidetes				
<i>Genus Prevotella</i>	4 (28.57 %)	0	3 (23.07%)	2 (13.3%)
<i>Genus Barnesiella</i>	0	1 (10.0 %)	0	0
<i>Bacteroides vulgatus</i>	1 (7.14 %)	2 (20.0 %)	0	1 (6.66 %)
<i>Genus Bacteroides</i>	3 (21.42 %)	2 (20.0 %)	1 (7.69%)	4 (26.6 %)
Phylum Firmicutes				
<i>Genus Megasphaera</i>	2 (14.28 %)	0	1 (7.69%)	1 (6.66 %)
<i>Genus Clostridium</i>	2 (14.28 %)	0	3 (23.07%)	3 (20%)
<i>Genus Faecalibacterium</i>	0	4 (40.0 %)	2 (15.38%)	1 (6.66 %)
<i>Genus Dialister</i>	1 (7.14%)	1 (10.0 %)	0	2 (13.3%)
Phylum Proteobacteria				
<i>Escherichia coli</i>	1 (7.14%)	0	2 (15.38%)	1 (6.66 %)
Phylum Actinobacteria				
<i>Genus Propionibacterium</i>	0	0	1 (7.69%)	0

Table S2 Gut microbial phylotypes from High-throughput sequencing results

Taxonomy	Female			Male		
	HTN	CG	P value	HTN	CG	P value
Phyla						
Bacteroidetes	0.541913	0.621701	0.07	0.575993	0.709759	0.03
Firmicutes	0.347729	0.291117	0.05	0.353574	0.222718	0.04
Proteobacteria	0.094756	0.080988	0.71	0.040186	0.045247	0.69
Actinobacteria	0.013353	0.030586	0.64	0.022936	0.019008	0.63
Fusobacteria	0.000984	0.000434	0.30	0.006061	0.002542	0.43
Verrucomicrobia	0	9.65E-05	0.001	0.000207	0	0.001
Spirochaetes	0.000347	0	0.05	0.000165	0.000122	0.47
Synergistetes	8.69E-05	0	0.01	0.000102	0.00018	0.34
Cyanobacteria	0.000111	1.93E-05	0.08	9.83E-05	0.000161	0.51
Saccharibacteria	7.24E-05	0	0.02	1.4E-05	1.29E-05	0.81
Family						
Bacteroidaceae	0.386336	0.480783	0.57	0.308158	0.447655	0.013
Prevotellaceae	0.123876	0.002259	0.022	0.209471	0.187862	0.96
Veillonellaceae	0.138319	0.017943	0.026	0.098076	0.059654	0.378
Ruminococcaceae	0.06914	0.196626	0.938	0.149932	0.093764	0.045
Lachnospiraceae	0.064783	0.059397	0.291	0.06056	0.051643	0.235
Bifidobacteriaceae	0.012842	0.029428	0.679	0.022255	0.018776	0.625
Enterobacteriaceae	0.035325	0.045576	0.311	0.012954	0.022167	0.249
Alcaligenaceae	0.049682	0.034293	0.194	0.020034	0.01895	0.645
Peptostreptococcaceae	0.03339	0.001824	0.02	0.005226	0.01128	0.353
Acidaminococcaceae	0.02786	0.011466	0.006	0.026435	0.002188	0.044
Genera						
Bacteroides	0.386336	0.480783	0.57	0.308158	0.447655	0.013
Prevotella_9	0.103583	0.002104	0.012	0.192572	0.181279	0.84
Megamonas	0.000449	0.00027	0.067	0.066022	0.025732	0.013
Megasphaera	0.091219	0.00029	0.017	0.011003	0.00278	0.154
Faecalibacterium	0.033525	0.085901	0.428	0.054931	0.041348	0.285
Ruminococcus_2	0.000584	0.004585	0.019	0.026491	0.009523	0.177
Bifidobacterium	0.012822	0.029428	0.68	0.022245	0.018776	0.625
Dialister	0.015554	0.002133	0.183	0.020114	0.030326	0.773
Parasutterella	0.043196	0.019139	0.086	0.016805	0.006106	0.23
[Eubacterium]_rectale_g	0.01038	0.024448	0.849	0.029415	0.020584	0.212

Table S3 The composition of significantly divergent gut microbial species from High-throughput sequencing analysis

Taxonomy	Female			Male		
	HTN	CG	P value	HTN	CG	P value
<i>Bacteroides_plebeius</i>	0.088434	0.132461	0.70	0.014787	0.079157	0.02
<i>Bacteroides_uniformis</i>	0.023188	0.076674	0.07	0.015899	0.096814	0.01
<i>Phascolarctobacterium_faecium</i>	0.027763	0.006061	0.01	0.020757	0.002046	0.03
<i>Bifidobacterium_adolescentis</i>	0.000748	0.009217	0.004	0.008529	0.006209	0.68
<i>Bacteroides_caccae</i>	0.009131	0.010771	0.04	0.010199	0.006763	0.37
<i>Clostridium_perfringens</i>	2.9E-05	0.000154	0.004	0.002773	0.000148	0.13
<i>Roseburia_inulinivorans</i>	0.000888	0.007731	0.002	0.005163	0.004678	0.63
<i>Anaerostipes_hadrus</i>	0.00291	0.000859	0.01	0.00146	0.000444	0.20
<i>Faecalibacterium_prausnitzii</i>	0	8.69E-05	0.001	3.51E-06	0.000476	0.0001