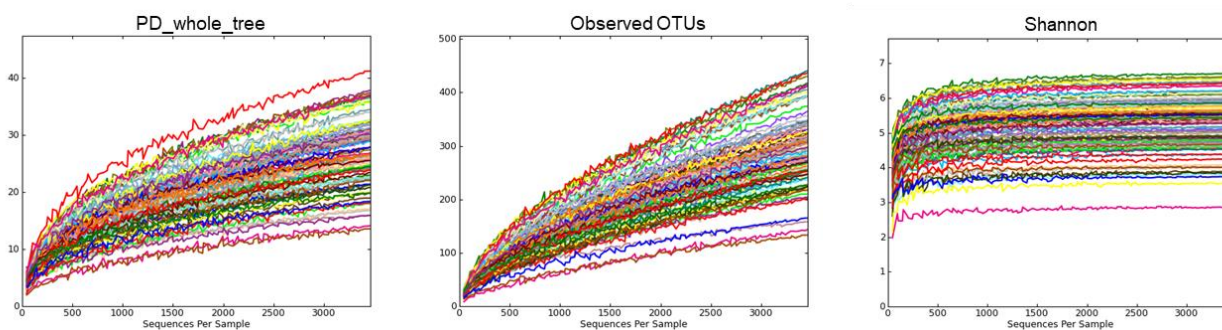
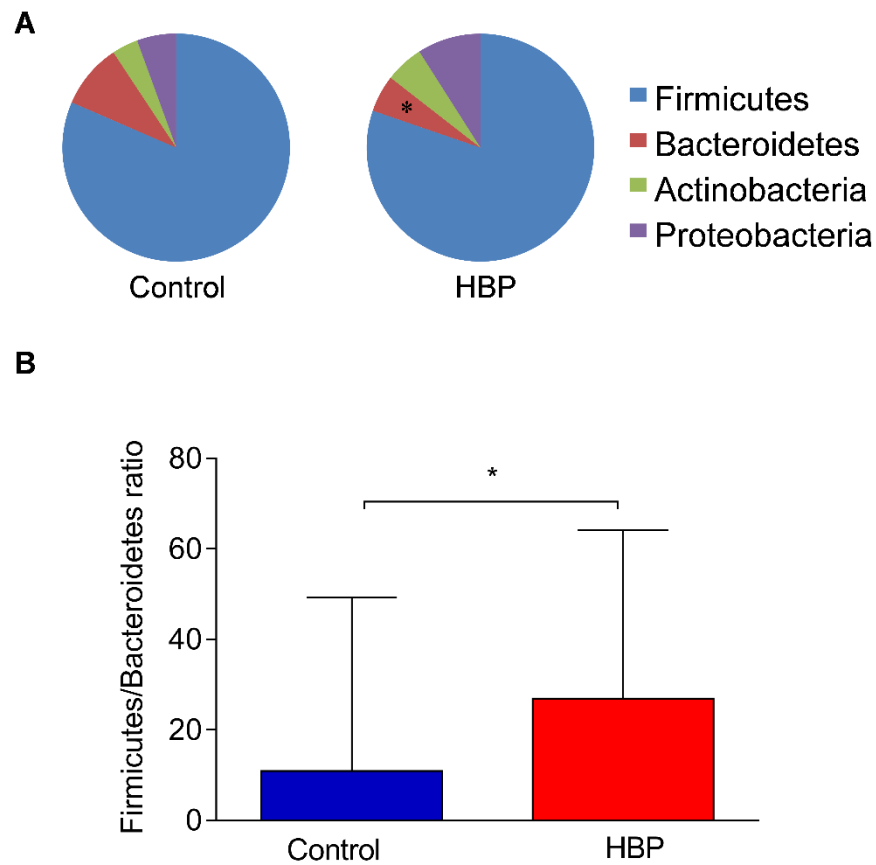


## Supplementary Material

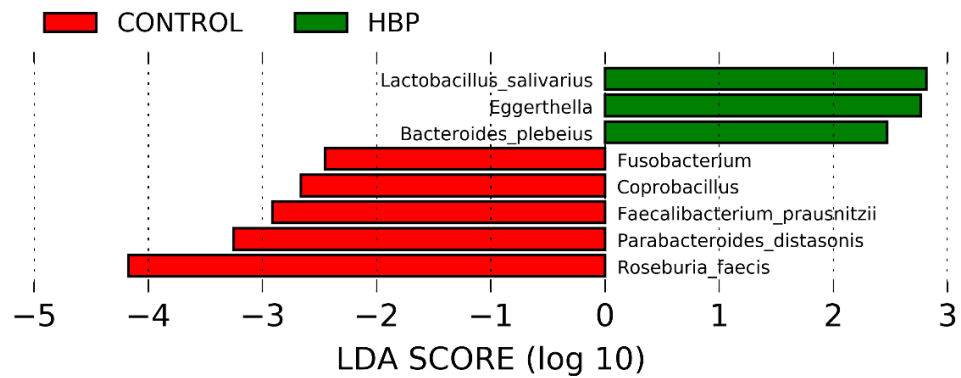
### Supplementary Figures



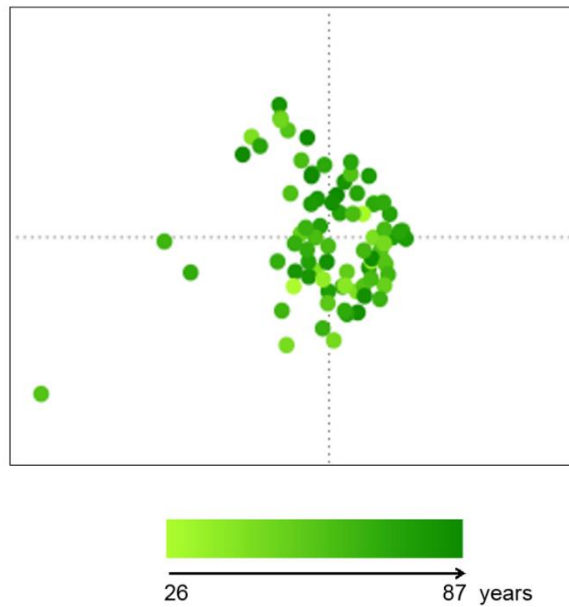
**Supplementary Figure 1. Rarefaction curves.** The following metrics were used: phylogenetic diversity (PD\_whole\_tree), the number of observed OTUs and the Shannon index. Curves are color-coded by subject.



**Supplementary Figure 2. Phylum-level gut microbiota composition in hypertensive (HBP) and normotensive (control) subjects. A.** Pie charts summarizing the relative abundance of the four most abundant phyla in HBP subjects and controls. **B.** Firmicutes/Bacteroidetes ratio. \*,  $p=0.03$ , Mann-Whitney U test.



**Supplementary Figure 3. Intestinal microbiota species potentially driving the separation between hypertensive (HBP) and normotensive (control) subjects.** Linear discriminant analysis (LDA) effect size (LEfSe) analysis. LDA scores indicate differentially represented species between groups (the logarithmic threshold for discriminative features was set to 2.0). For *Eggerthella*, *Fusobacterium* and *Coprobacillus*, the species were unclassified.



**Supplementary Figure 4. The gut microbiota dysbiosis in a cohort of Brazilian hypertensive subjects is independent of age.** Principal Coordinates Analysis of the weighted UniFrac distances for hypertensive and control subjects. Dots are colored by subject age (see the color gradient at the bottom). See also Figure 1B.

## Supplementary Tables

**Supplementary Table 1.** Frequency of macronutrients intake in high blood pressure group (HBP) and control group (Control).

	Macronutrient		
	Protein	Fat	Carbohydrate
Total	19%	28%	53%
Control	17%	26%	57%
HBP	19%	30%	51%

**Supplementary Table 2.** Summary of published studies on human gut microbiota and hypertension. Only research articles based on next-generation sequencing technologies were considered. Genus-level differences between hypertensive (case) and normotensive (control) subjects or associations with blood pressure are reported. Results consistent with our study are highlighted in bold.

Number of subjects and characteristics <sup>a</sup>	Geographical origin	Positively associated with or increased in relative abundance in hypertension	Negatively associated with or decreased in relative abundance in hypertension	Ref.
99 cases (53.6 yrs, 6.1%) 41 controls (53.7 yrs, 21.9%)	Tangshan, China	<i>Prevotella</i> , <i>Klebsiella</i> , <i>Porphyromonas</i> , and <i>Actinomyces</i>	<i>Faecalibacterium</i> , <i>Bacteroides</i> , <i>Oscillibacter</i> , <b><i>Roseburia</i></b> , <i>Bifidobacterium</i> , <b><i>Coprococcus</i></b> , and <i>Butyrivibrio</i>	Li et al., 2017
60 cases (57.0 yrs, 41.7%) 60 controls (56.0 yrs, 46.7%)	Harbin, China	<i>Klebsiella</i> , <i>Clostridium</i> , <i>Streptococcus</i> , <i>Parabacteroides</i> , <b><i>Eggerthella</i></b> , <i>Salmonella</i> , <b><i>Bacteroides</i></b> , <i>Sutterella</i> , and <i>Pyramidobacter</i>	<i>Faecalibacterium</i> , <b><i>Roseburia</i></b> , <i>Synergistetes</i> , <b><i>Bacteroides</i></b> , <i>Megasphaera</i> , and <i>Aeromicrobium</i>	Yan et al., 2017
22 cases (NA) 18 controls (NA)	Florida, US	<i>Alistipes</i> , <i>Ruminococcus</i> , and <i>Eubacterium</i>	<b><i>Bacteroides</i></b>	Kim et al., 2018
62 cases (69.3 yrs, 53.2%) 67 controls (69.5 yrs, 61.0%)	Beijing, China	<i>Alistipes</i> , <b><i>Bacteroides</i></b> , <i>Barnesiella</i> , <i>Butyricimonas</i> , <i>Christensenella</i> , <i>Clostridium sensu stricto</i> , <i>Cosenzaea</i> , <i>Desulfovibrio</i> , <i>Dialister</i> , <i>Eisenbergiella</i> , <i>Faecalitalea</i> , <i>Megasphaera</i> , <i>Microvirgula</i> , <i>Mitsuokella</i> , <i>Parabacteroides</i> , <i>Proteiniborus</i> , and <i>Terrisporobacter</i>	<i>Acidaminobacter</i> , <i>Adlercreutzia</i> , <i>Anaerotruncus</i> , <i>Asteroleplasma</i> , <i>Bulleidia</i> , <i>Cellulosilyticum</i> , <i>Clostridium III</i> , <b><i>Clostridium IV</i></b> , <b><i>Clostridium XIVa</i></b> , <i>Coprobacter</i> , <i>Enterococcus</i> , <i>Enterorhabdus</i> , <i>Flavonifractor</i> , <i>Gemmiger</i> , <i>Guggenheimella</i> , <i>Intestinimonas</i> , <b><i>Lachnospiracea incertae sedis</i></b> , <i>Lactivibrio</i> , <i>Lactobacillus</i> , <i>Macellibacteroides</i> , <i>Marvinbryantia</i> , <i>Olsenella</i> , <i>Paraprevotella</i> , <i>Parasutterella</i> , <i>Phascolarctobacterium</i> , <i>Prevotella</i> , <i>Romboutsia</i> , <i>Ruminococcus</i> ,	Dan et al., 2019

			<i>Sporobacter</i> , <i>Sporobacterium</i> , <i>Sutterella</i> , <i>Vampirovibrio</i> , <i>Veillonella</i> , and <i>Victivallis</i>	
38 cases (52.5 yrs, 0%) 9 controls (46.2 yrs, 0%)	Liège, Belgium	<i>Clostridium sensu stricto</i>	<b>Ruminococcaceae*</b> , and <i>Clostridiales*</i>	Huart et al., 2019
63 cases (58.4 yrs, 44.4%) 42 controls (59.3 yrs, 59.5%)	Xinxiang county, China	<i>Tyzzelerella</i> , <i>Enterobacter</i> , <i>Actinobacillus</i> , <i>Sutterella</i> , <i>Parasutterella</i> , <i>Paenibacillus</i> , <i>Prevotella</i> , <i>Vibrio</i> , <i>Holdemanella</i> , <i>Dongia</i> , <i>Romboutsia</i> , <i>Flavonifractor</i> , and <i>Glutamicibacter</i>	<i>Chitinibacter</i> , <b><i>Bacteroides</i></b> , <i>Faecalitalea</i> , <b><i>Dorea</i></b> , <i>Phascolarctobacterium</i> , <i>Pediococcus</i> , <i>Lachnospira</i> , <i>Megamonas</i> , <b><i>Faecalibacterium</i></b> , <b><i>Fusobacterium</i></b> , <i>Terrimonas</i> , and <i>Erysipelatoclostridium</i>	Li et al., 2019
20 cases (NA) 10 controls (NA)	Shaanxi, China	<i>Prevotella</i> , <i>Megasphaera</i> , <i>Parasutterella</i> , <i>Phascolarctobacterium</i> , and <i>Escherichia-Shigella</i>	<b><i>Faecalibacterium</i></b>	Mushtaq et al., 2019
186 cases (NA) 343 controls (NA)	Birmingham, Chicago, Minneapolis, Oakland, US	<i>Veillonella</i> , <i>Robinsoniella</i> , and <i>Catabacter</i>	<i>Akkermansia</i> , <i>Ruminococcus</i> , <i>Anaerovorax</i> , <i>Sporobacter</i> , <i>Asaccharobacter</i>	Sun et al., 2019

<sup>a</sup> Mean age and percentage of females are shown in brackets.

NA, not available.

\*, unclassified OTU reported at higher taxonomic level.

## Supplementary References

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