

Supplementary Materials

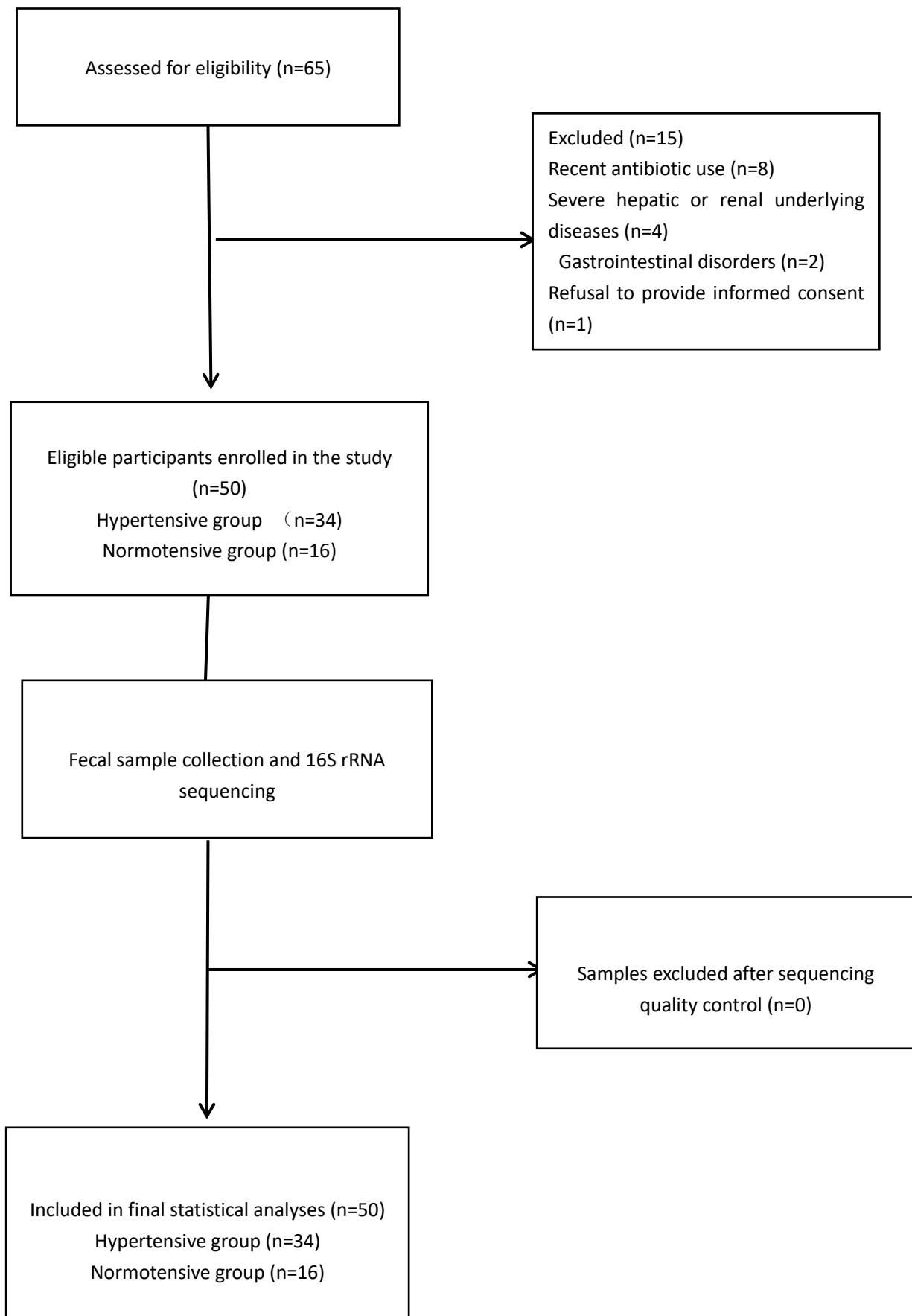


Figure S1. Participant-flow diagram of the cross-sectional case-control study. A total of 65 individuals from the Chaoshan region were assessed for eligibility between July 2017 and July 2018. Of these, 15 were excluded (8 for recent antibiotic use within 4 weeks, 4 for significant liver or kidney disease, 2 for gastrointestinal disorders, and 1 declined participation), leaving 50 enrolled participants (34 hypertensive, 16 normotensive). All 50 samples were successfully sequenced and passed quality control; no sample was excluded after sequencing.

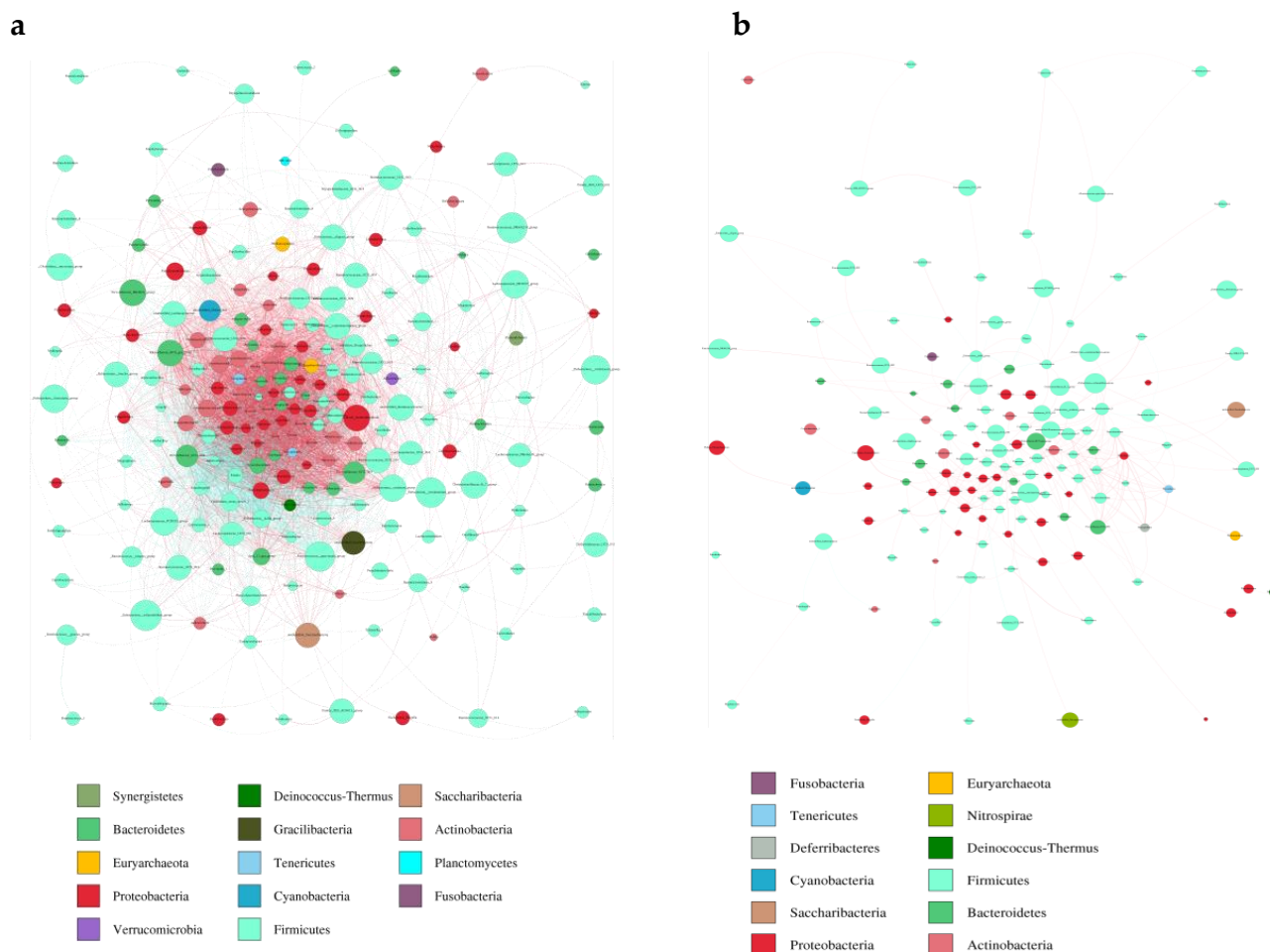


Figure S2. Microbial co-occurrence network analysis. Interaction networks of microbial species at the genus level in (a) normotensive (n = 16) and (b) hypertensive (n = 34) groups. Networks were constructed based on Spearman correlations ($|r| > 0.6$, $p < 0.05$). Node size represents relative abundance; edge color represents positive (red) or negative (green) correlations. These networks are descriptive and were not statistically compared between groups.