

Non-differential gut microbes contribute to hypertension and its severity through co-abundances: A multi-regional prospective cohort study

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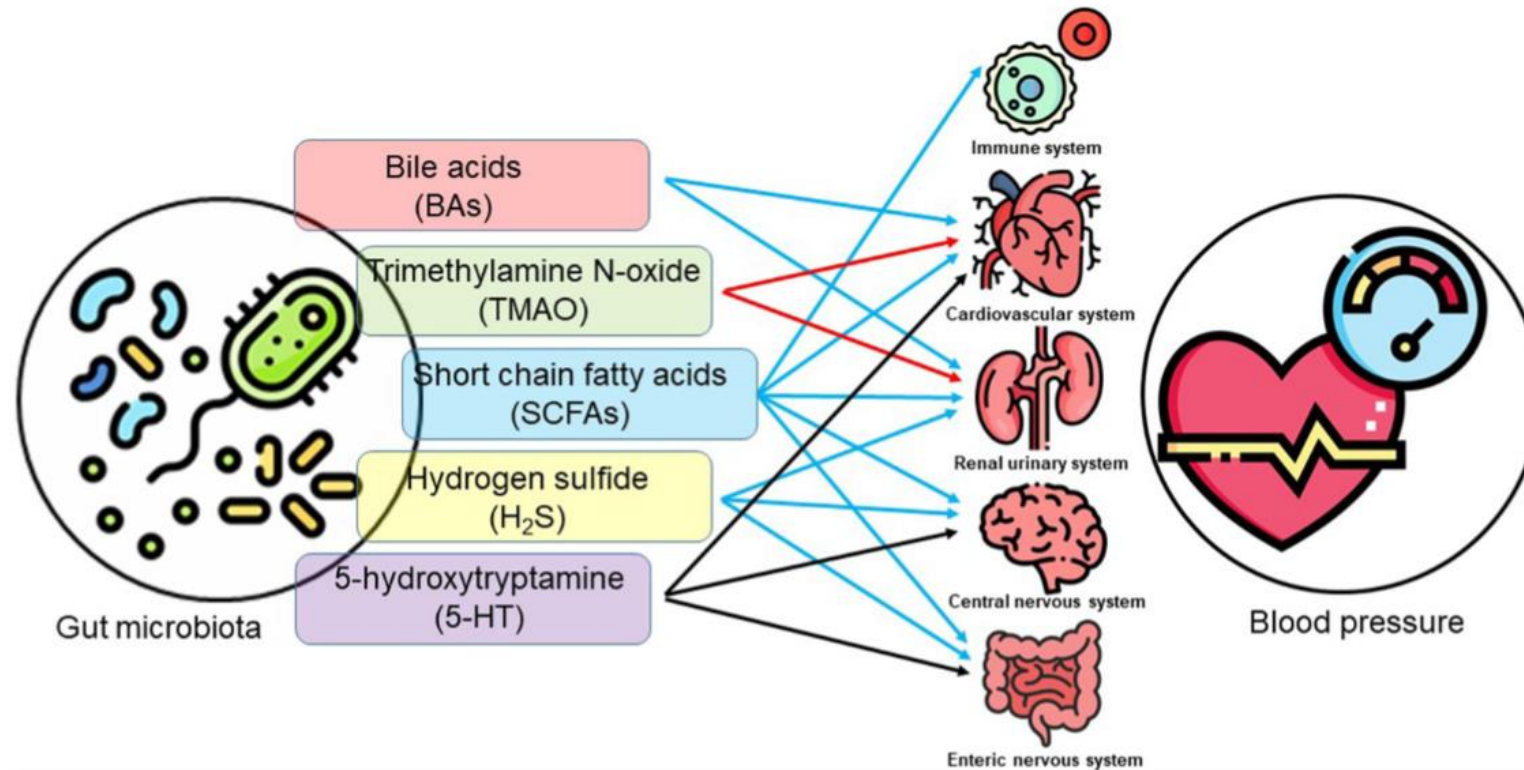
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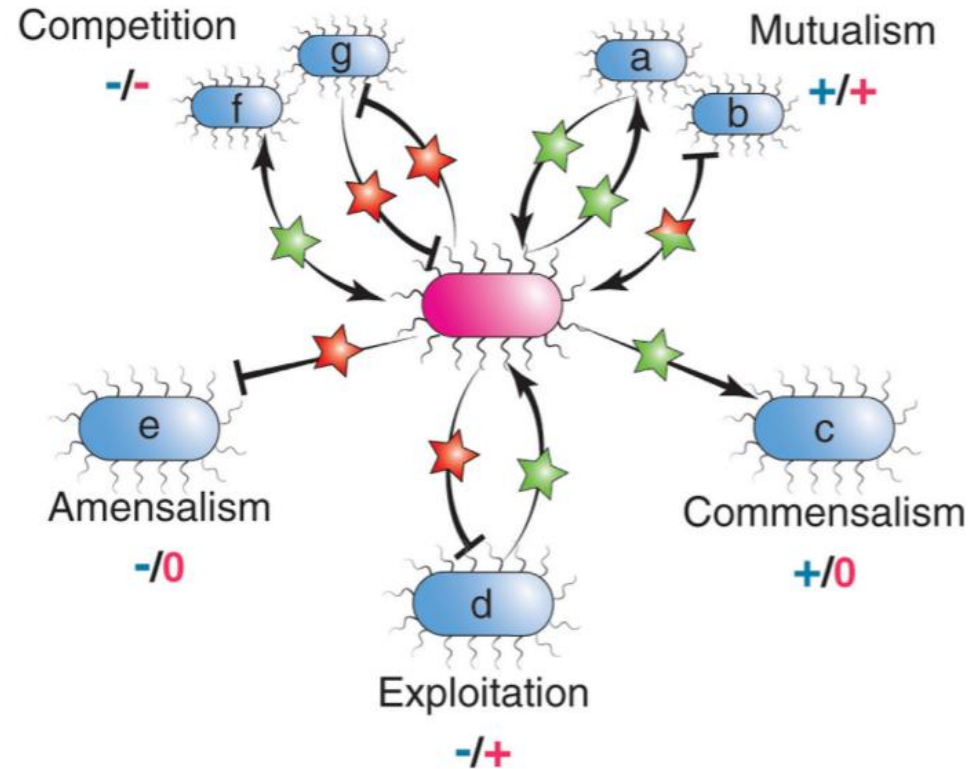


Background



- The gut microbiota is closely related to hypertension and regulates blood pressure through different mechanisms
- Previous studies have primarily focused on microbial diversity and abundance difference

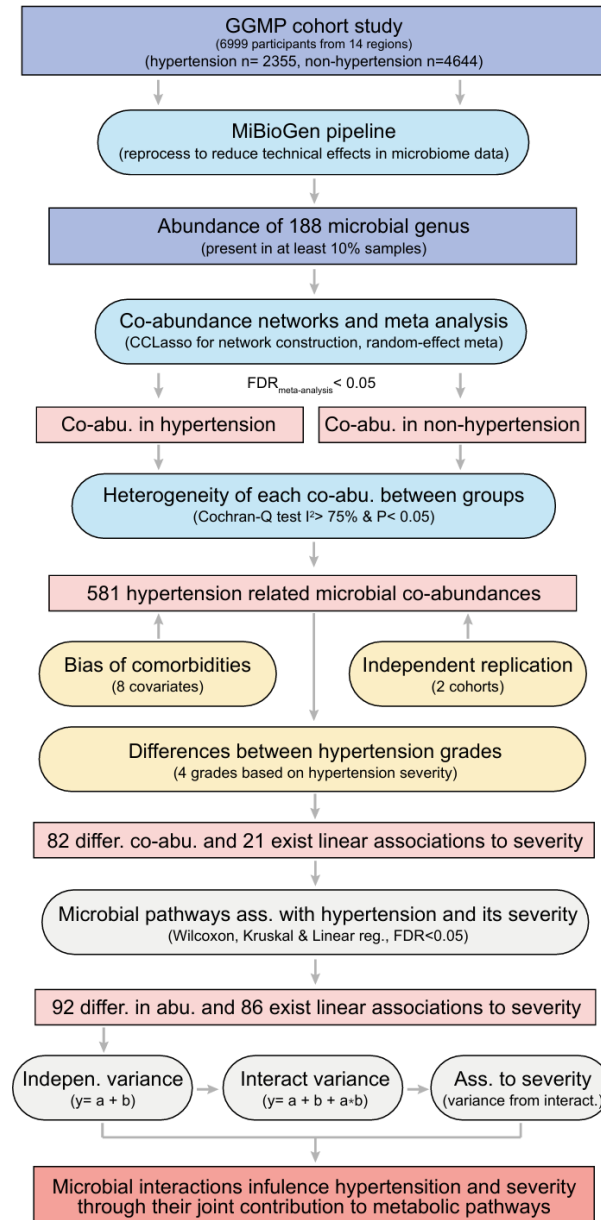
Background



- There are various microbe-microbe interactions, which affect the structure of microbiome and host health



Results

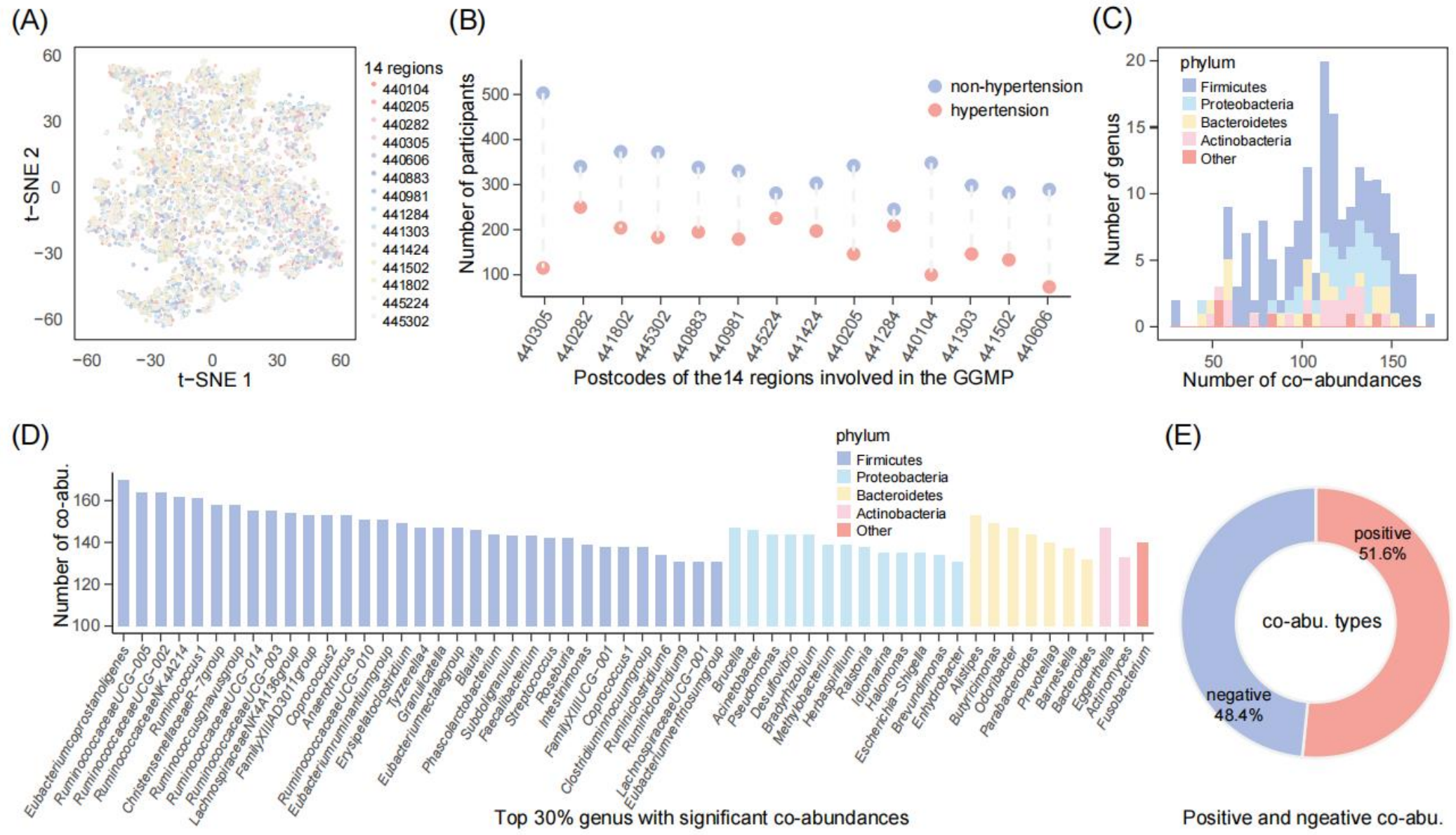


Overview of the study design and analysis workflow



Results

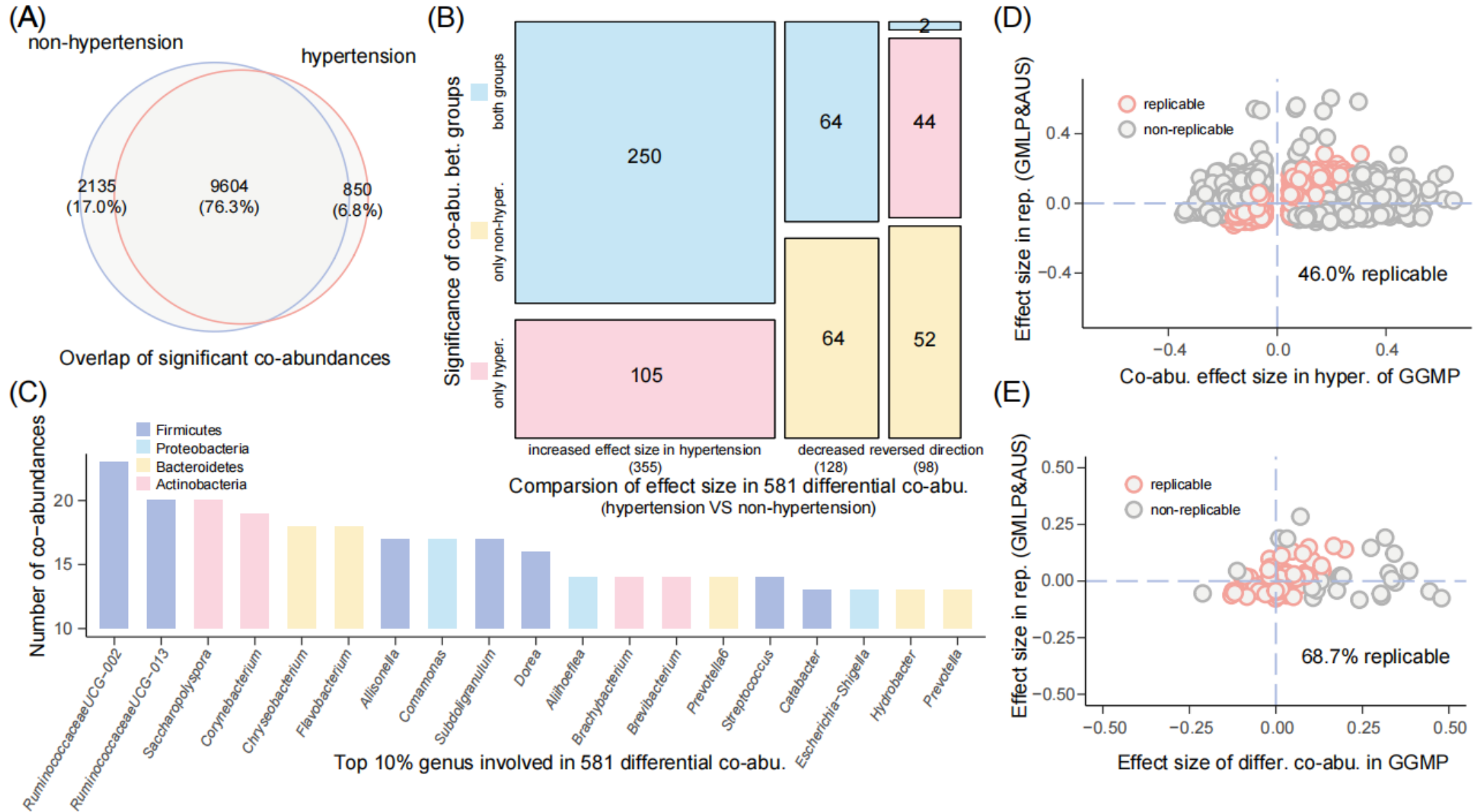
Inter-microbial interactions as reflected by co-abundances in hypertension



Positive and negative co-abu.

Results

Hundreds of interactions among gut microbes vary in hypertension

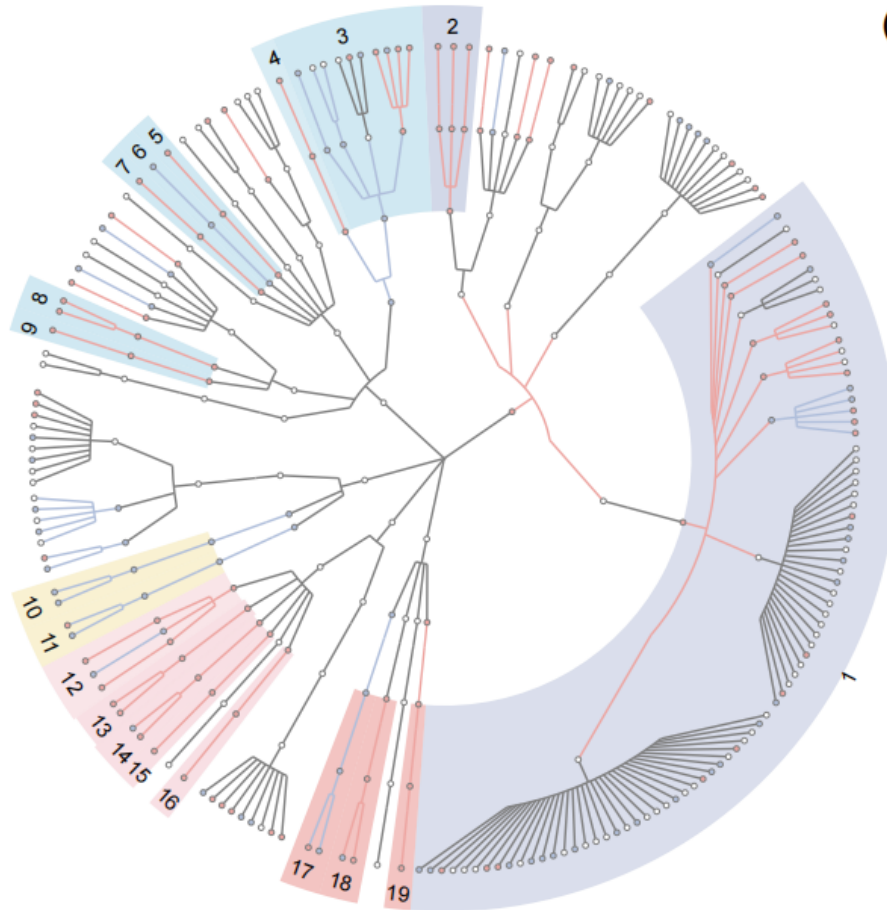


Results

Nearly half of the gut microbes display non-significance in abundance but dominate hypertension-related interactions

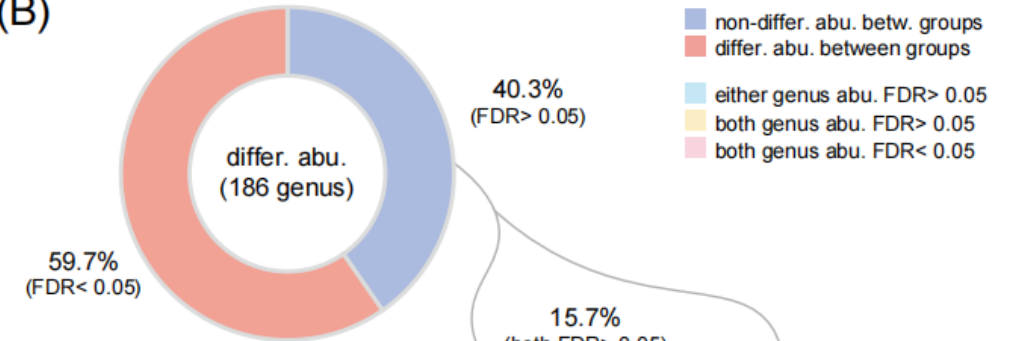
(A)

- phylum
- Firmicutes
 - Proteobacteria
 - Bacteroidetes
 - Actinobacteria
 - Other
- order
- Clostridiales
 - Bacillales
 - Burkholderiales
 - Neisseriales
 - Xanthomonadales
 - Chromatiales
 - Alteromonadales
 - Sphingomonadales
 - Caulobacteriales
 - Sphingobacteriales
 - Flavobacteriales
 - Micrococcales
 - Corynebacteriales
 - Pseudonocardiales
 - Streptosporangiales
 - Actinomycetales
 - Synergistales
 - Fusobacteriales
 - Methanobacteriales
- abu. lower in hyper.
- abu. higher in hyper.
- abu. non-differ.

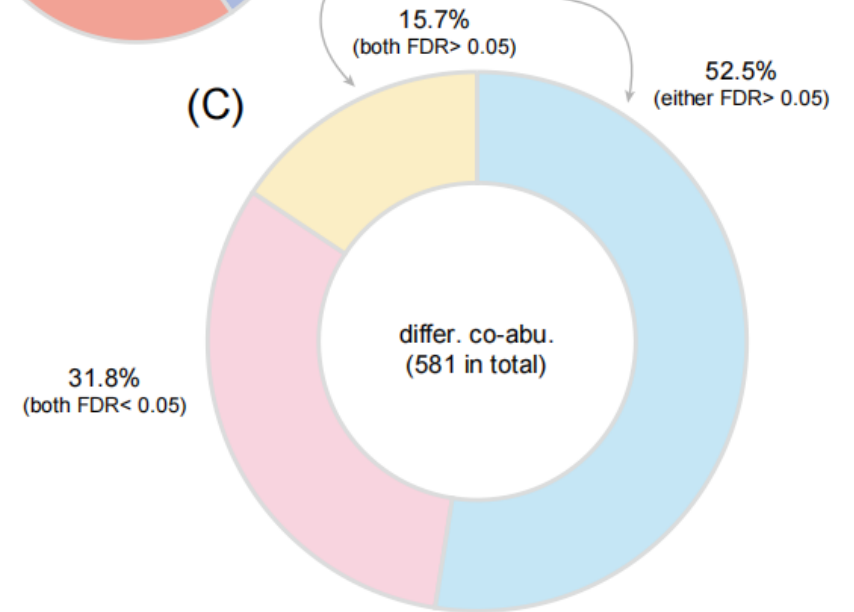


Distribution of 186 genus involved in 581 hypertension-related co-abu.

(B)

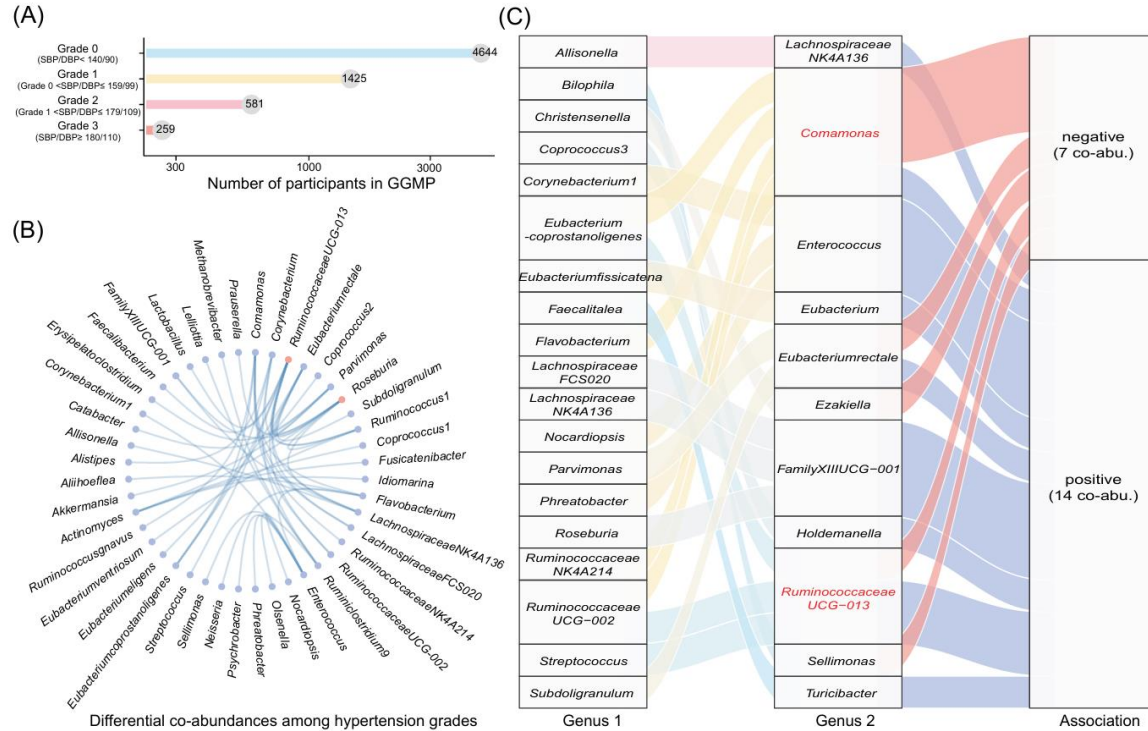


(C)

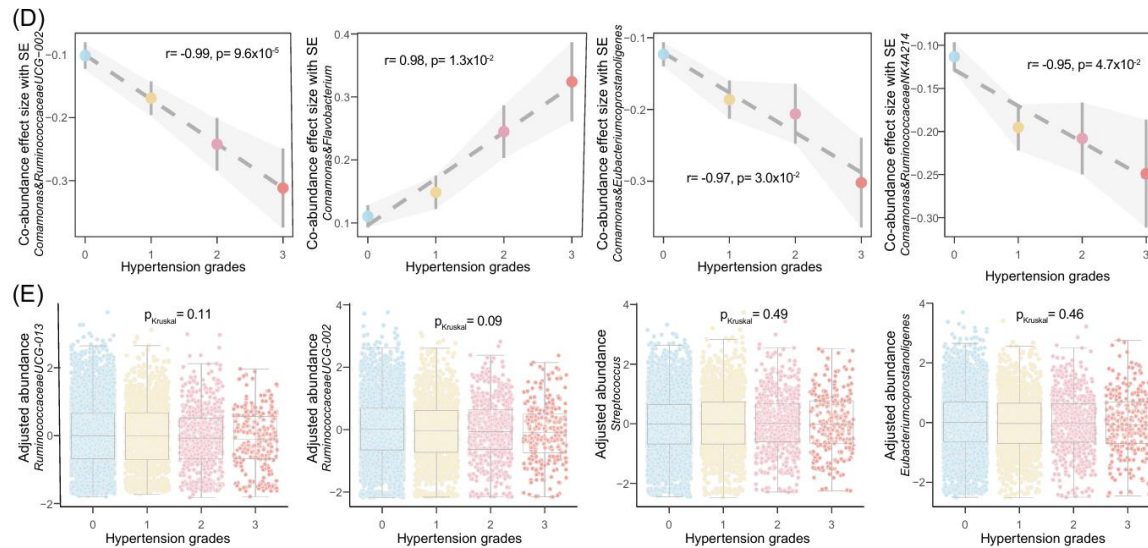


Non-differ. genus involved in hypertension-related co-abu.

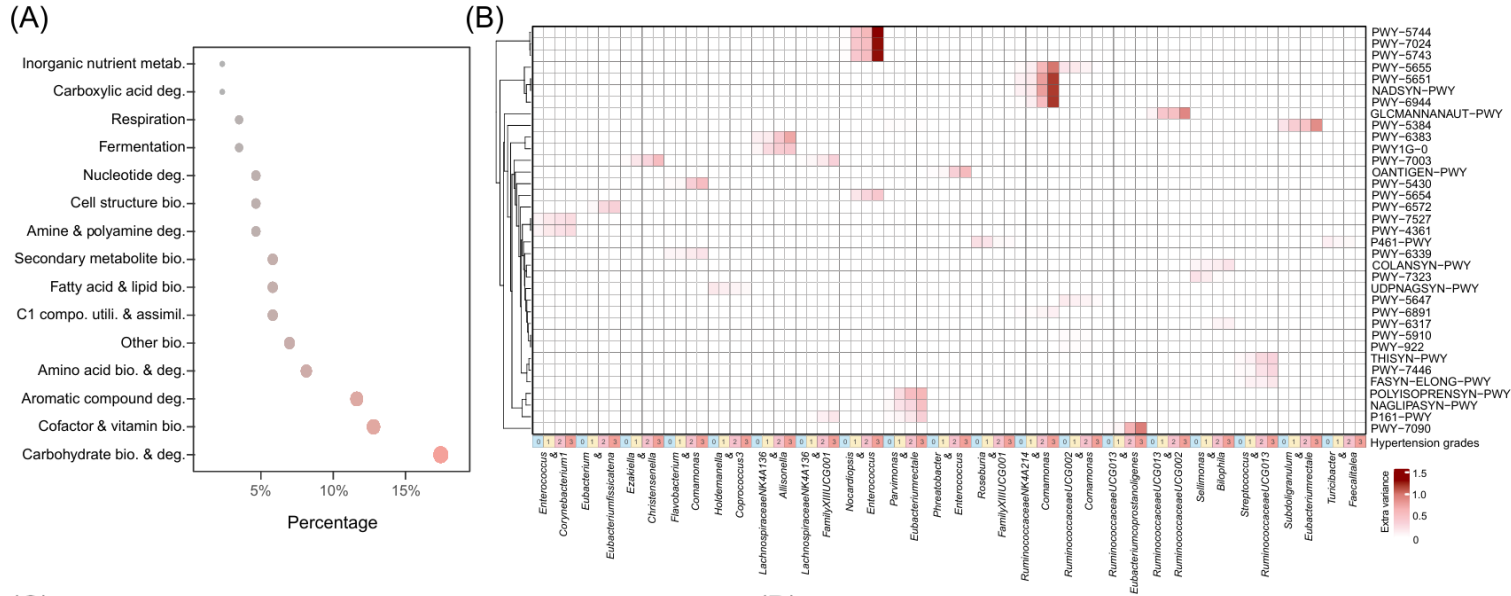
Results



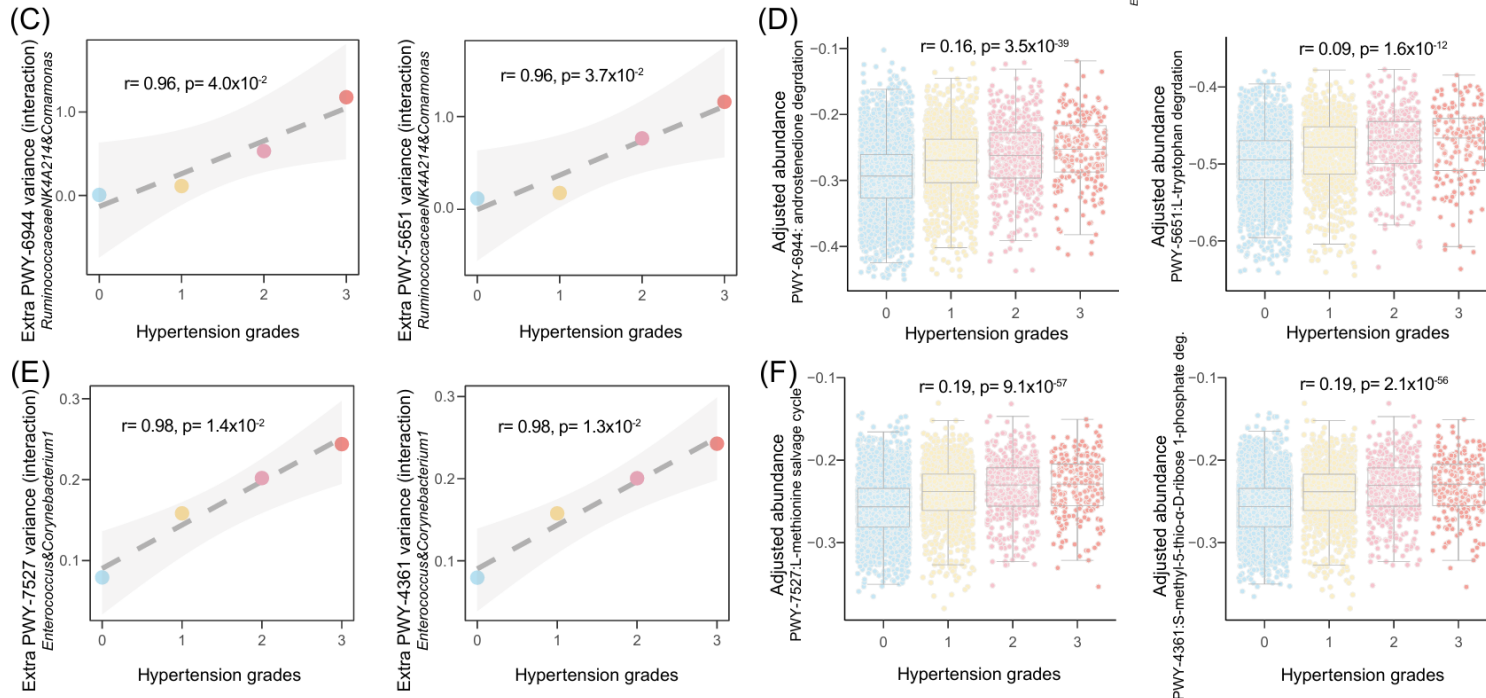
The microbial interaction strength associated with hypertension severity



Results



Microbial interactions may influence hypertension severity through jointly contributing to metabolic pathways





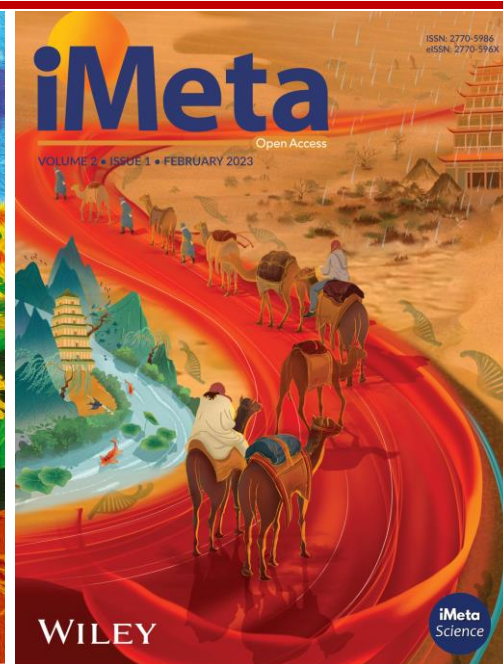
Summary

- ❑ Gut microbial co-abundances differ between hypertensive and non-hypertensive participants;
- ❑ Non-differential gut microbes dominate hypertension-related co-abundances;
- ❑ The strength of gut microbial co-abundances is associated with hypertension severity;
- ❑ Microbial interactions contribute additional variance to hypertension-related microbial metabolic pathways.

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