

# Targeting keystone species helps restore the dysbiosis of butyrate-producing bacteria in non-alcoholic fatty liver disease

Dingfeng Wu<sup>1, 2, #</sup>, Lei Liu<sup>2, #</sup>, Na Jiao<sup>1, 3, #</sup>, Yida Zhang<sup>4</sup>, Li Yang<sup>5</sup>, Chuan Tian<sup>2</sup>,  
Ping Lan<sup>3, 6</sup>, Lixin Zhu<sup>3, 6, 7, \*</sup>, Rohit Loomba<sup>8, \*</sup>, Ruixin Zhu<sup>2, 9, \*</sup>

<sup>1</sup>National Clinical Research Center for Child Health, the Children's Hospital, Zhejiang University School of Medicine, Hangzhou 310058, Zhejiang, P. R. China.

<sup>2</sup>The Shanghai Tenth People's Hospital, School of Life Sciences and Technology, Tongji University, Shanghai 200072, P. R. China.

<sup>3</sup>Guangdong Institute of Gastroenterology, Guangdong Provincial Key Laboratory of Colorectal and Pelvic Floor Diseases, the Sixth Affiliated Hospital, Sun Yat-sen University, Guangzhou 510655, P.R. China.

<sup>4</sup>Department of Biomedical Informatics, Harvard Medical School, Boston, MA 02215, United States.

<sup>5</sup>State Key Laboratory of Biotherapy, West China Hospital, Sichuan University and Collaborative Innovation Center, Chengdu, Sichuan, P.R.China.

<sup>6</sup>Department of Gastroenterology, the Sixth Affiliated Hospital of Sun Yat-sen University, Guangzhou 510655, P.R.China.

<sup>7</sup>Digestive Diseases and Nutrition Center, Department of Pediatrics, the State University of New York at Buffalo, Buffalo, NY14214, United States.

<sup>8</sup>NAFLD Research Center, Division of Gastroenterology and Epidemiology, Department of Medicine, University of California San Diego, La Jolla, California 92093, United States.

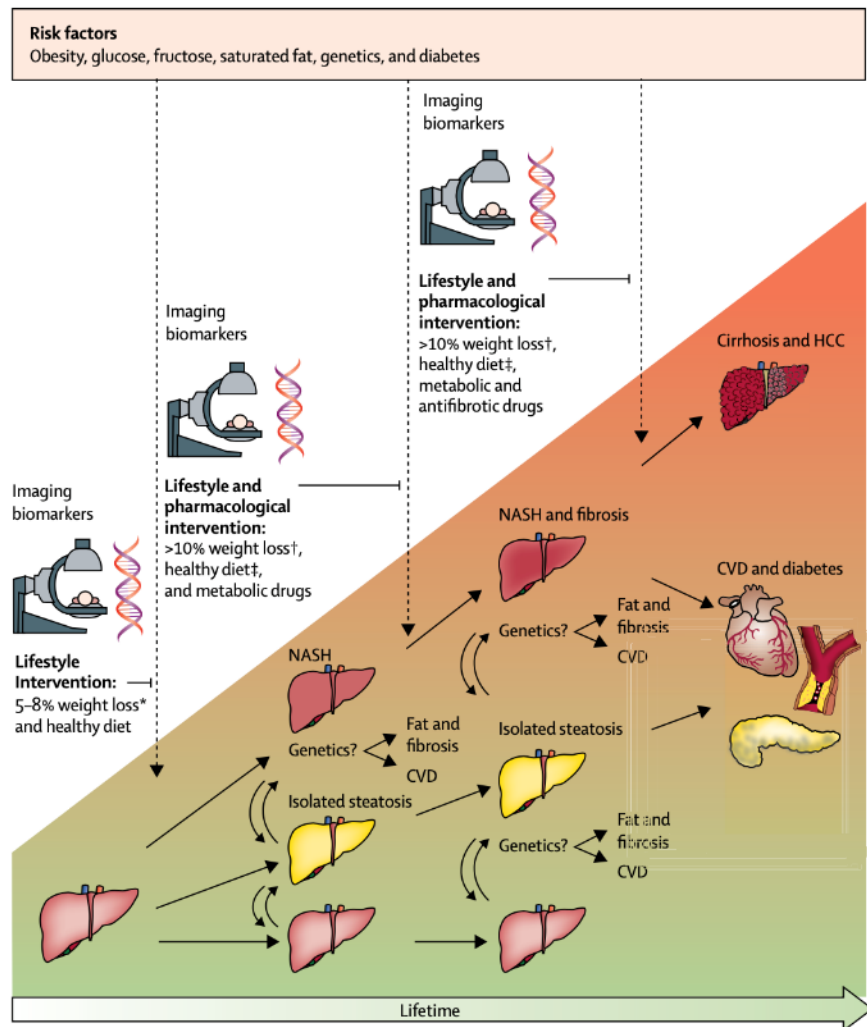
<sup>9</sup>Research Institute, GloriousMed Clinical Laboratory Co., Ltd., Shanghai 201318, P. R.China.



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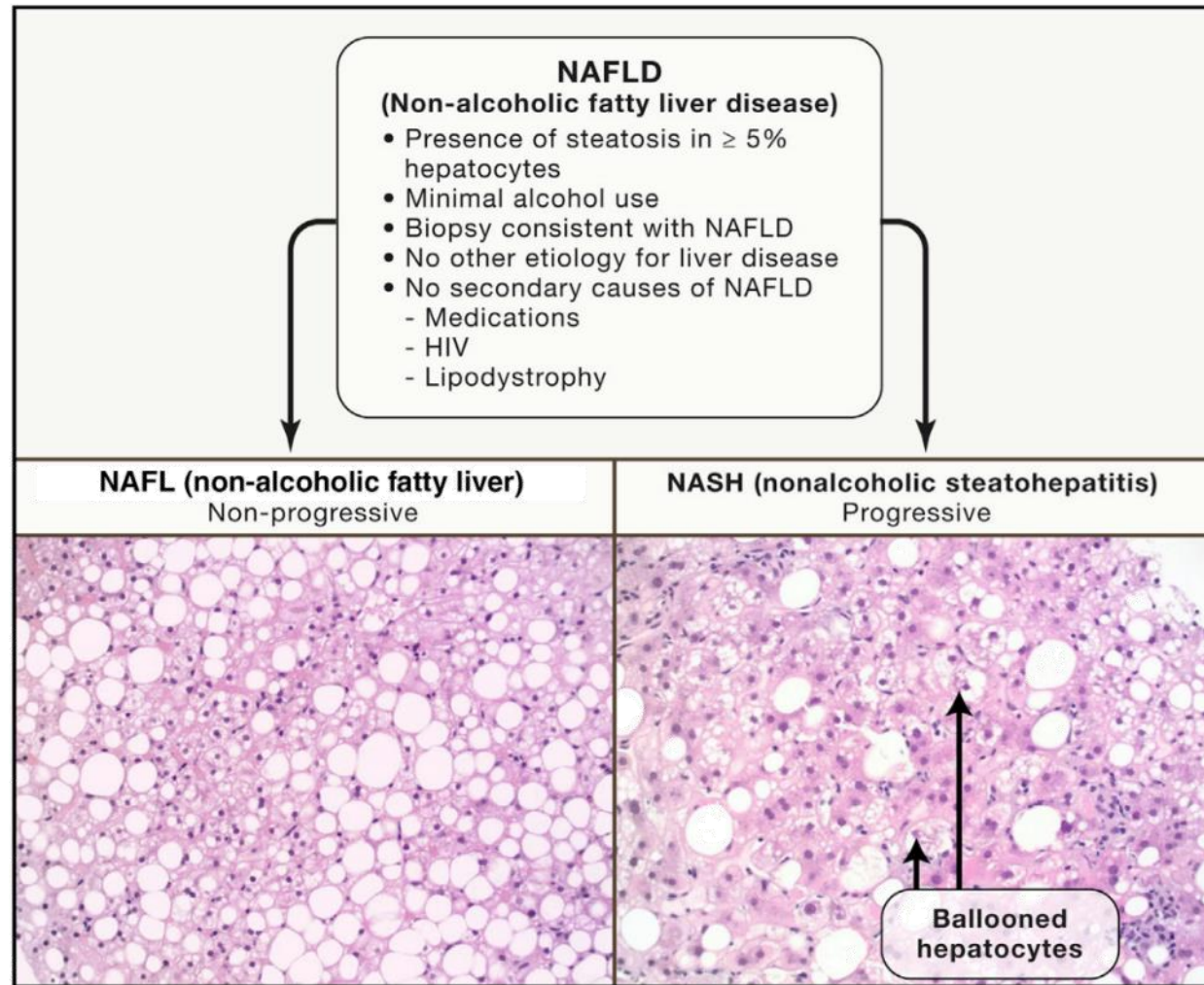
# Introduction

## Natural history of NAFLD



Stefan, N., et al. The Lancet Diabetes & Endocrinology. 2019.

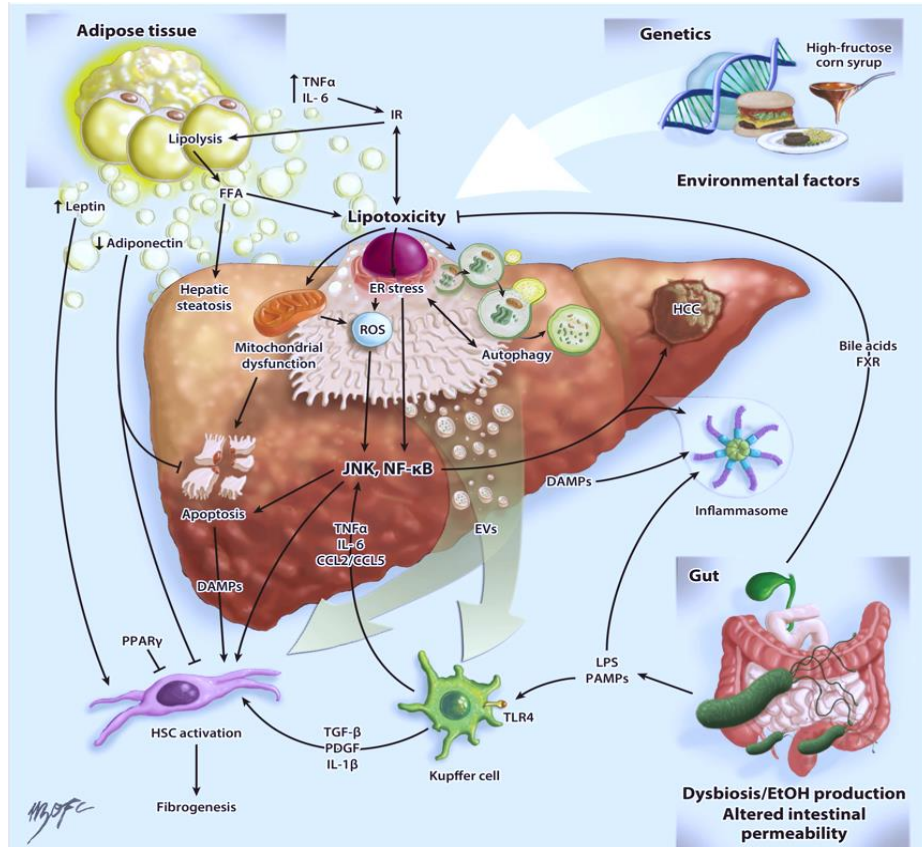
## Histologic features of NAFLD



Loomba R, et al. Cell. 2021.

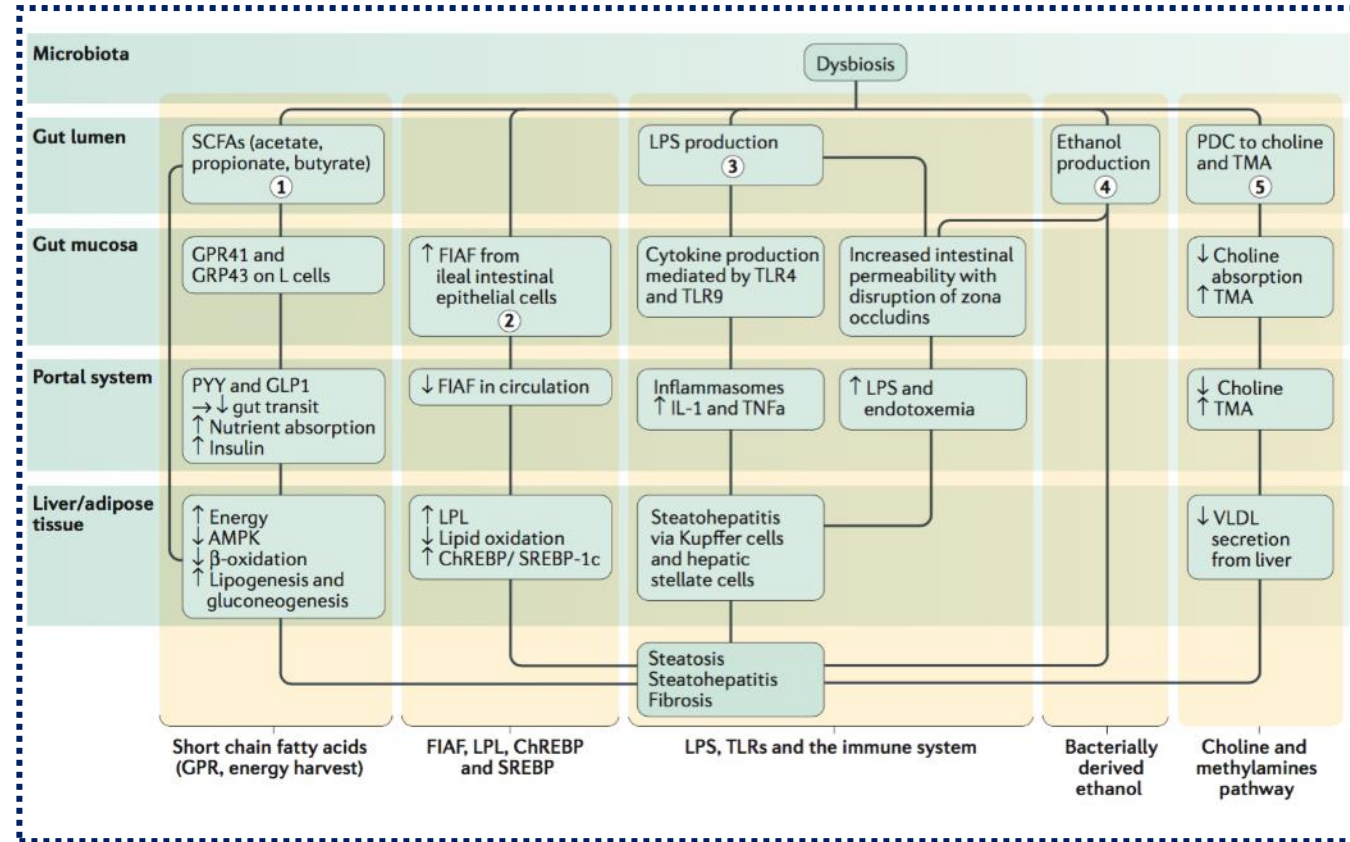
# Introduction

## Multiple hit hypothesis for the development of NAFLD



Buzzetti E, et. al. Metabolism, 2016.

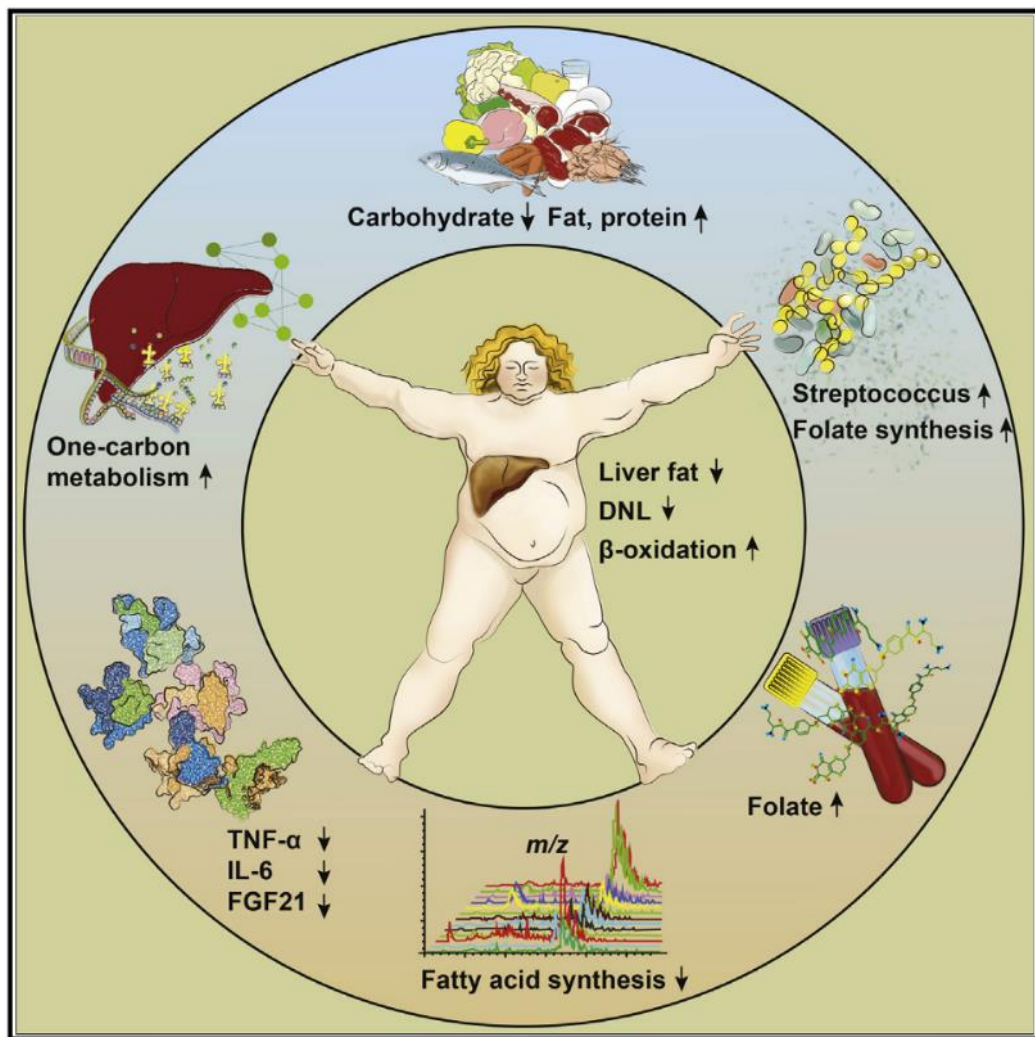
## Key mechanistic pathways involved in the gut–liver axis in NAFLD progression



Leung C, et. al. Nature Reviews Gastroenterology & Hepatology, 2016.

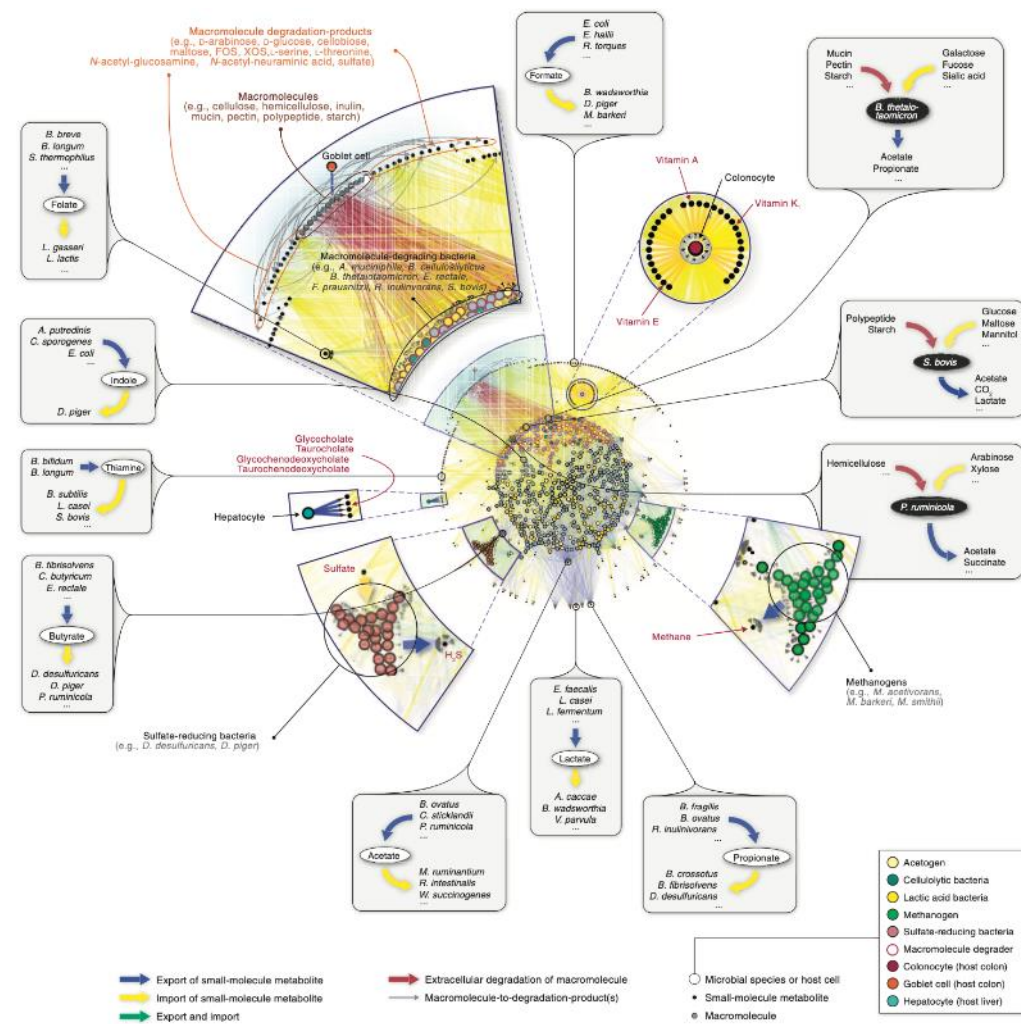
# Introduction

## Treatment targeted gut microbiota



Mardinoglu A, et. al. Cell Metab. 2018.

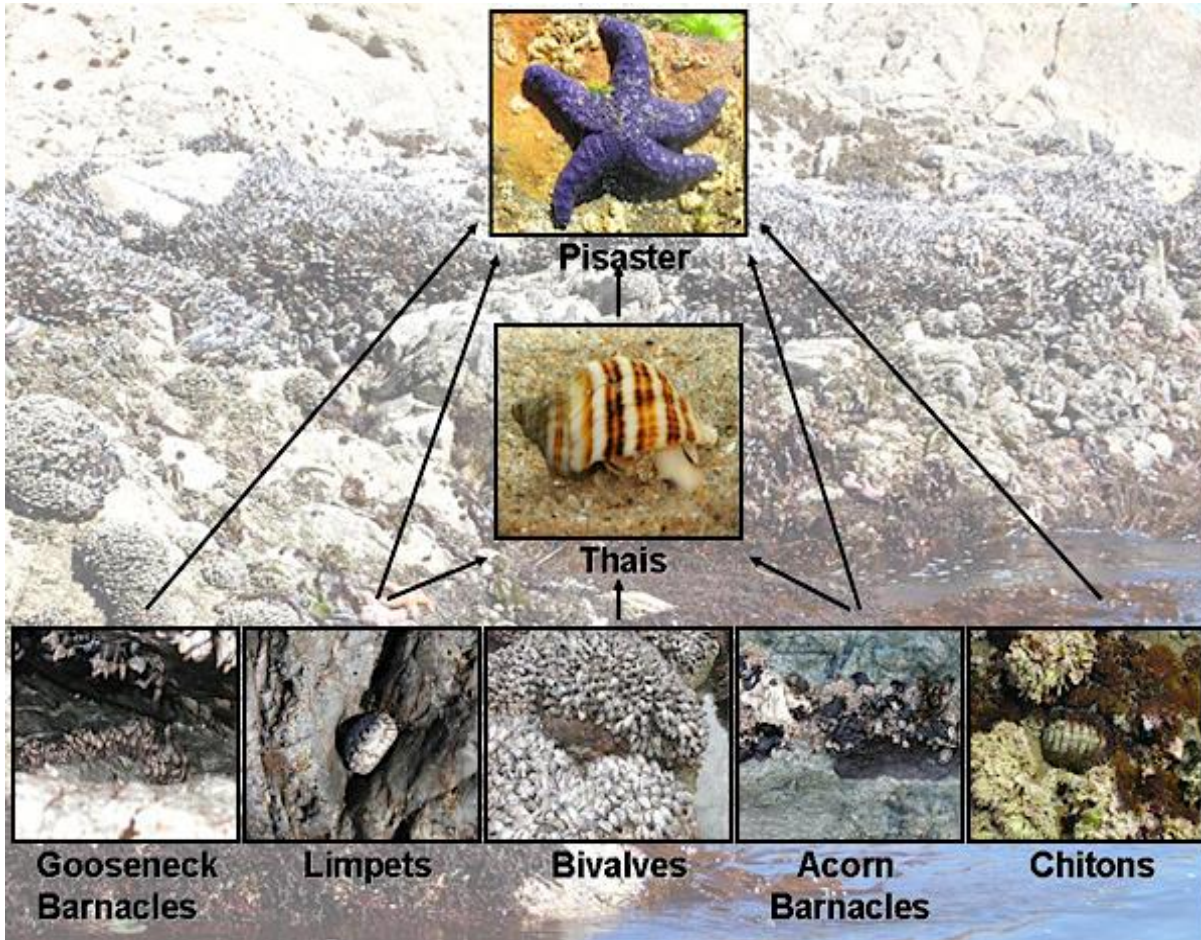
## Structural complexity of the microecosystem



Sung J, et. al. Nat Commun. 2017.  
Tarantino G, et. al. Future Microbiol. 2015.

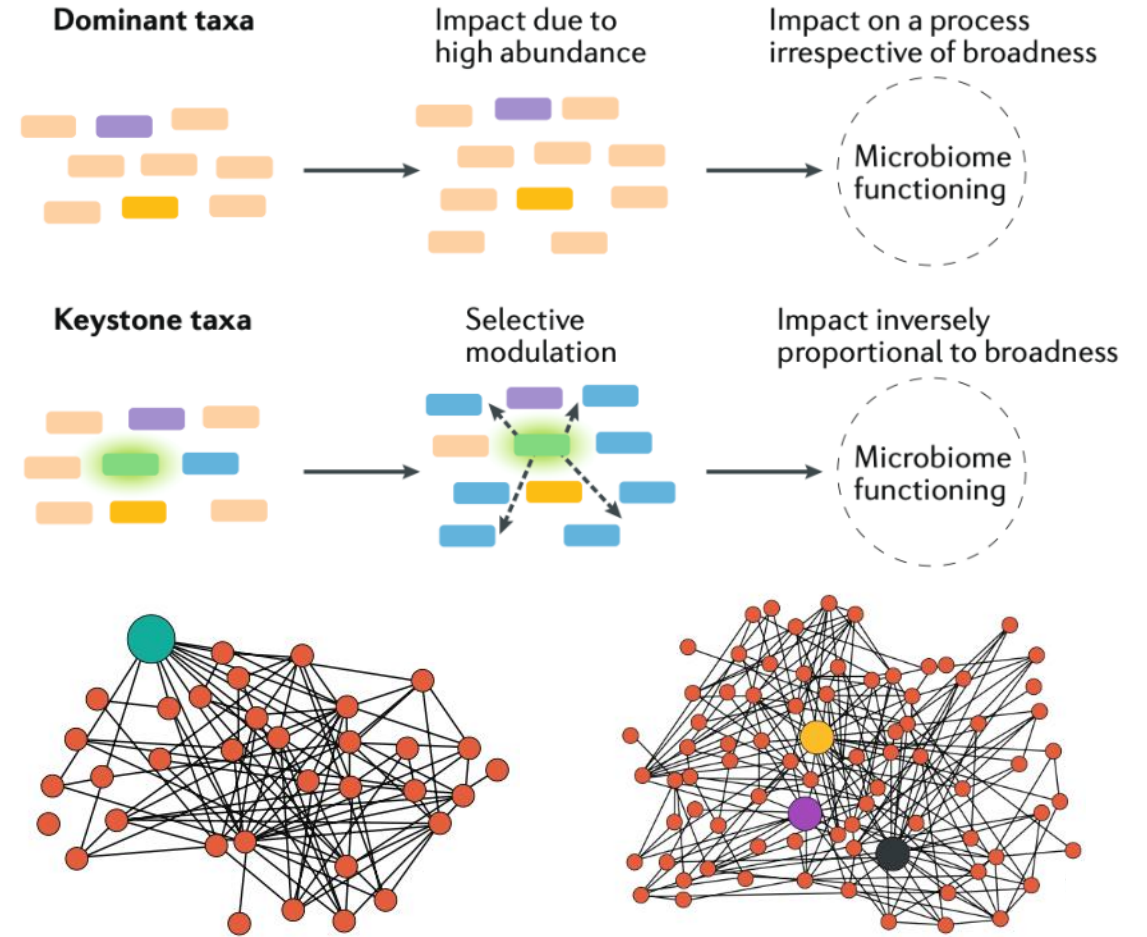
# Introduction

## Keystone species in food web



Stephen C. et. al. Nature Education Knowledge. 2010

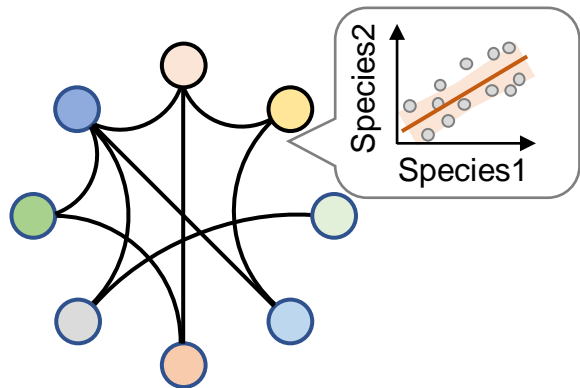
## Keystone species in microbial interaction network



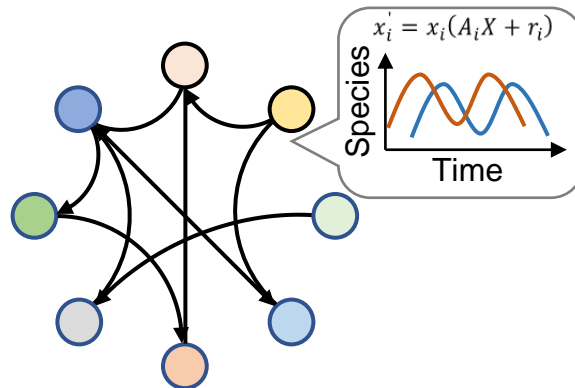
Banerjee S. et. al. Nat Rev Microbiol. 2018.

# Introduction

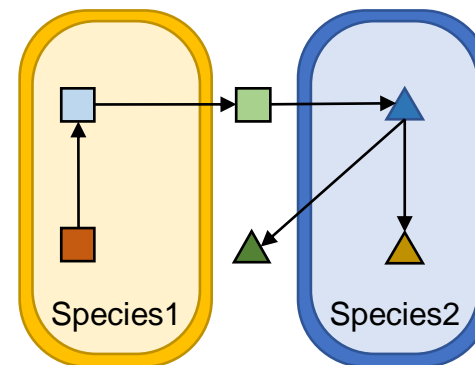
## Common microecosystem modeling methods



Co-occurrence networks

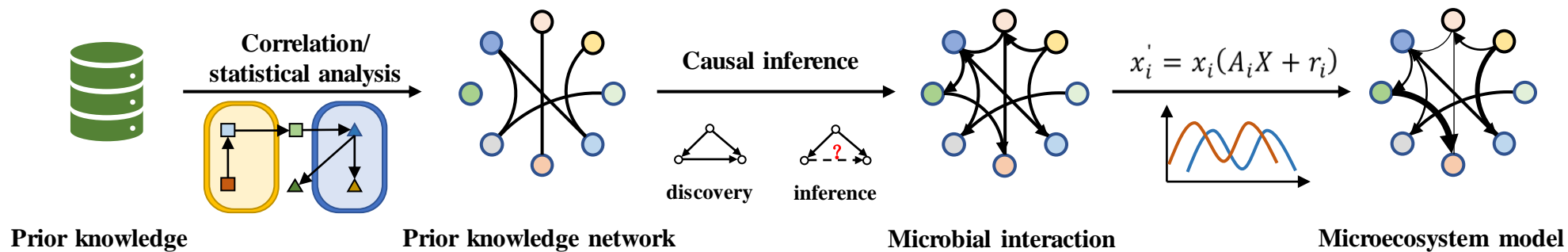


Population dynamic models



Metabolic models

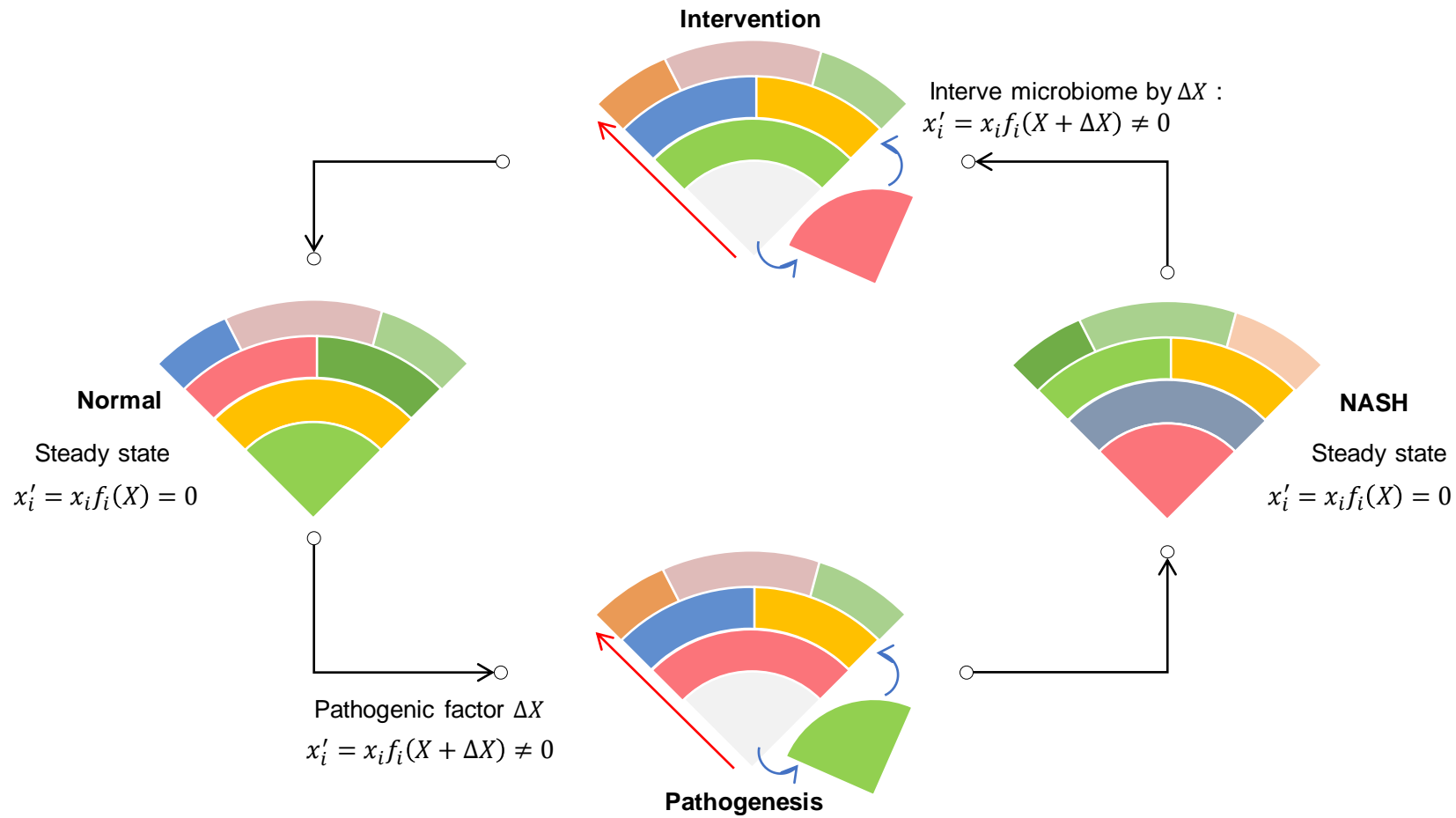
## Microecosystem modeling based on causality theory



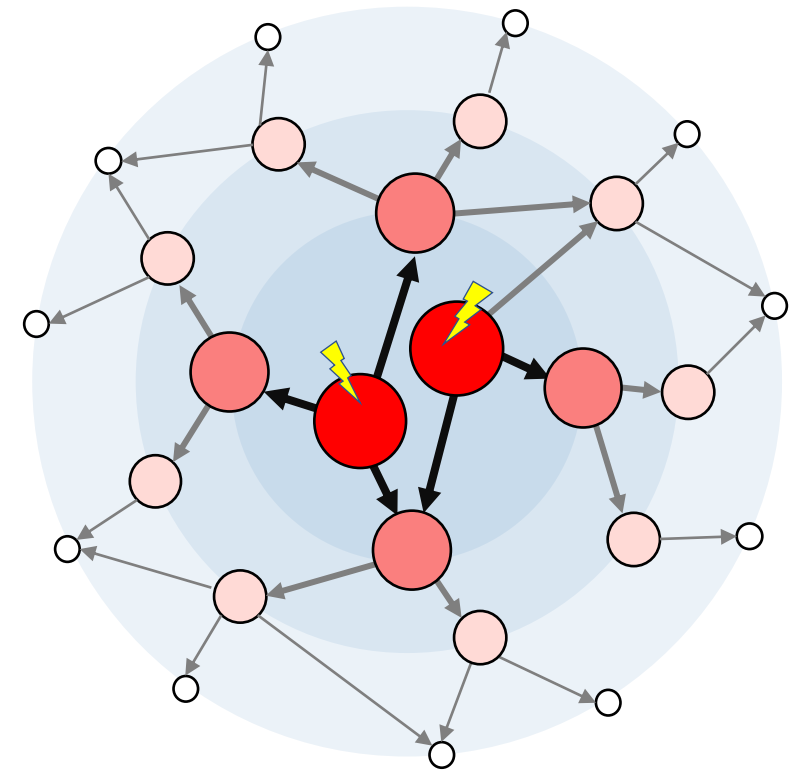
Faust K, et al. PLoS computational biology, 2012.  
Judea Pearl, et. al. 《The Book of Why》 . 2020

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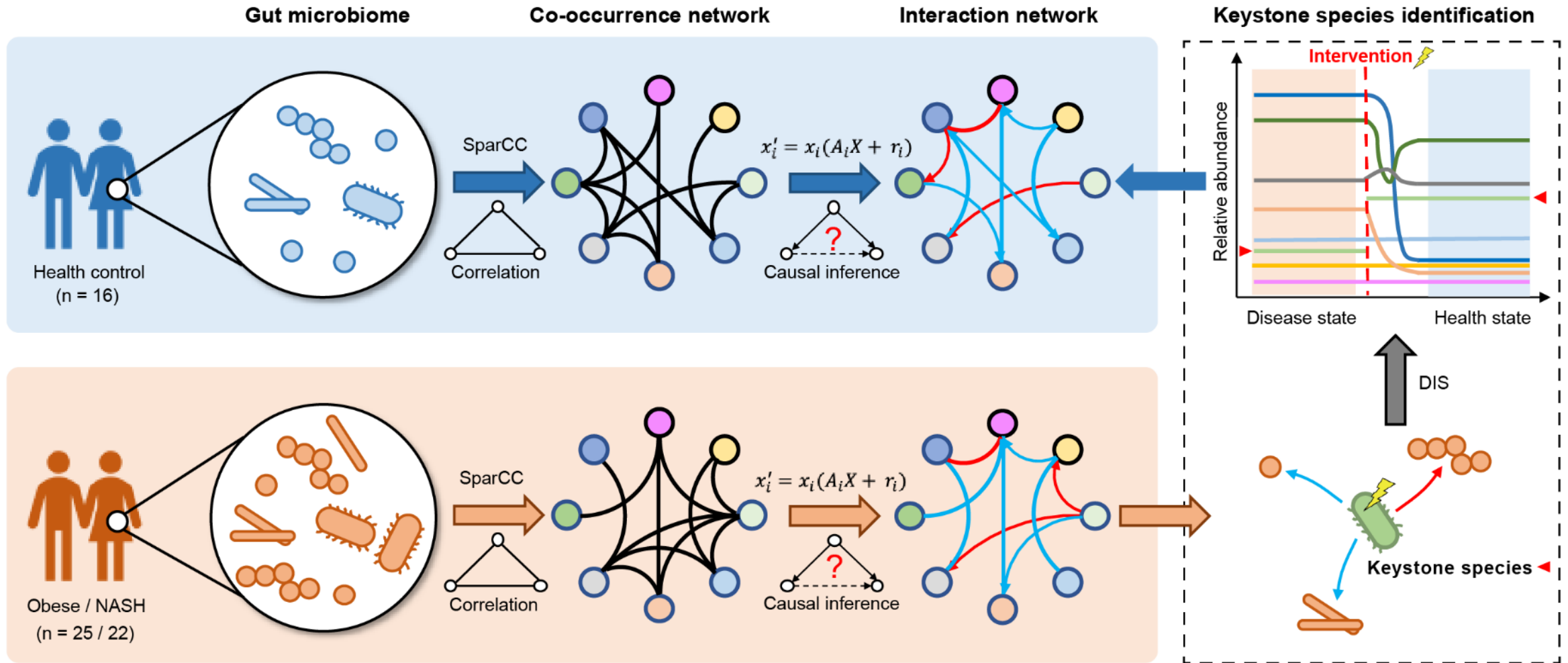
## Dynamic intervention simulation



## Dynamic changes during intervention

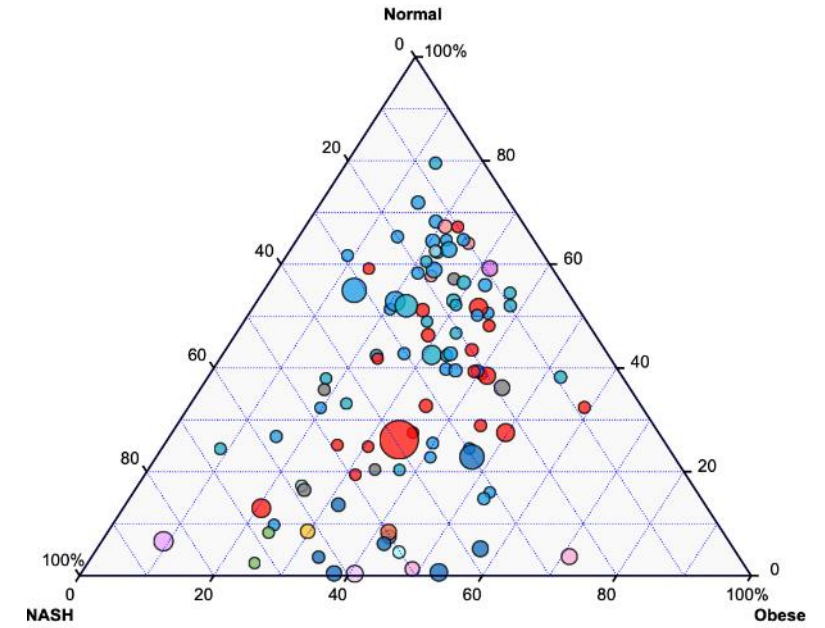
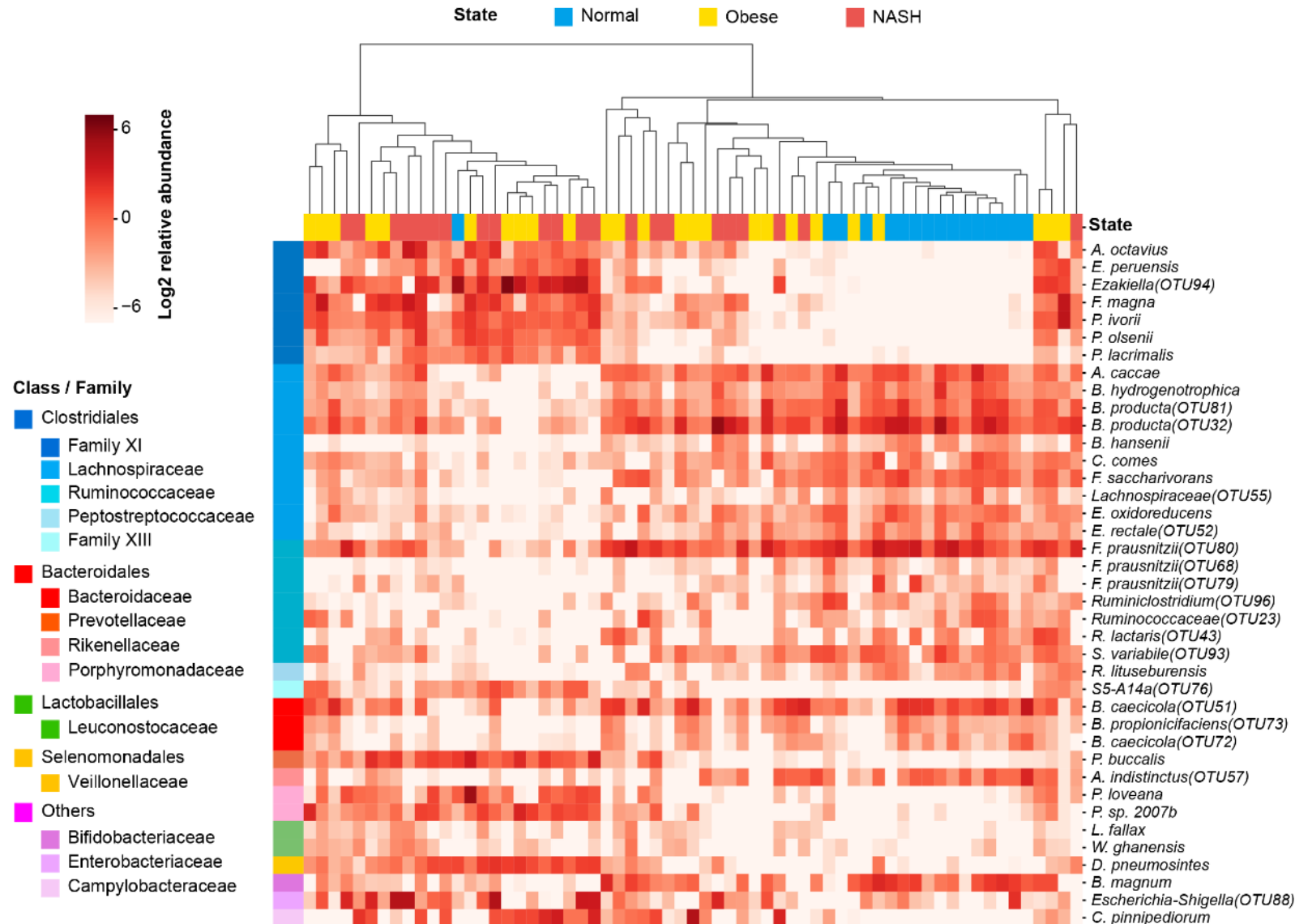


# Study design



# Results

## Abundance changes of the gut microbial species in obesity and NASH.

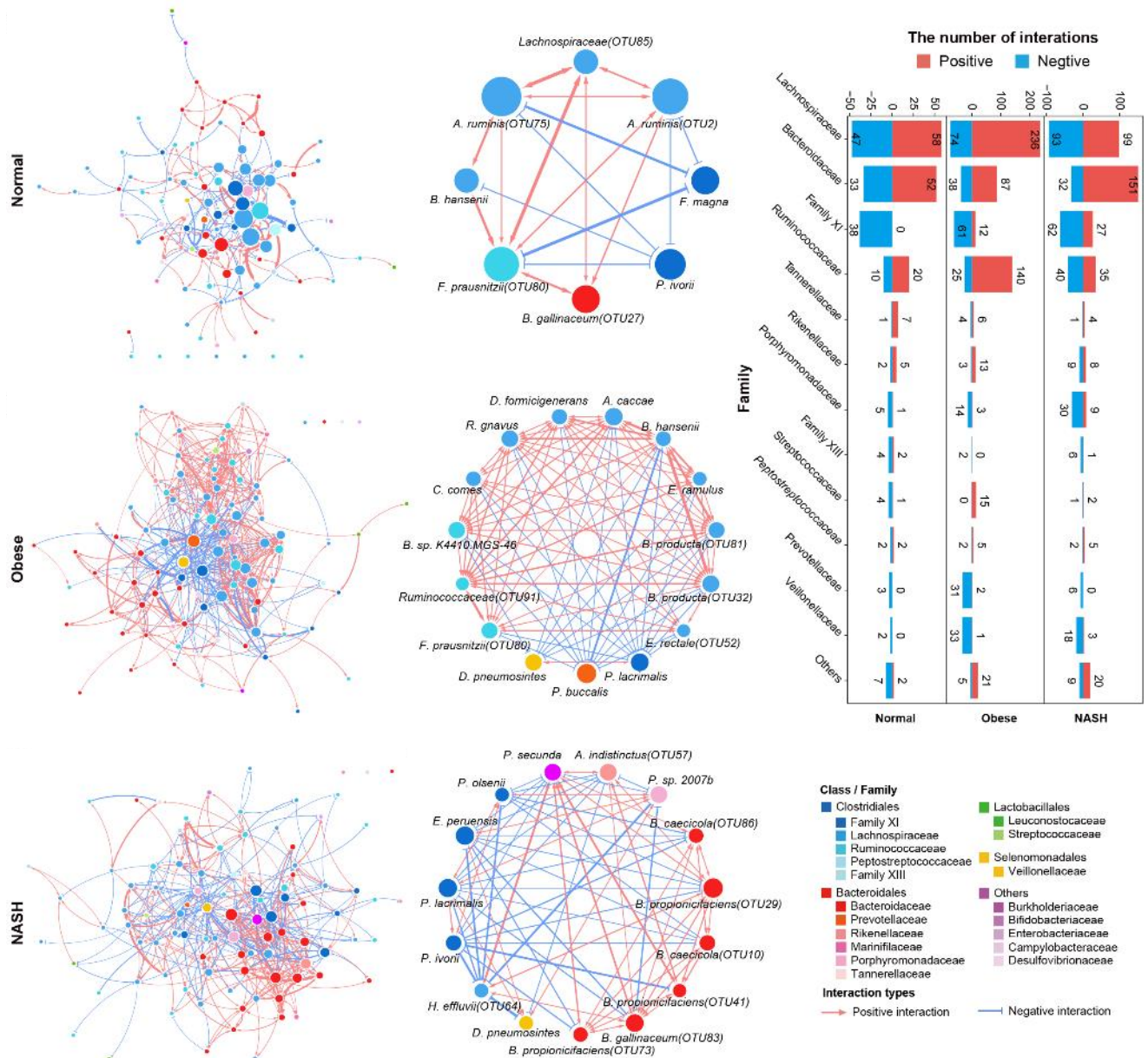


Decreased abundances in family:

- **Lachnospiraceae**
- **Ruminococcaceae**

# Results

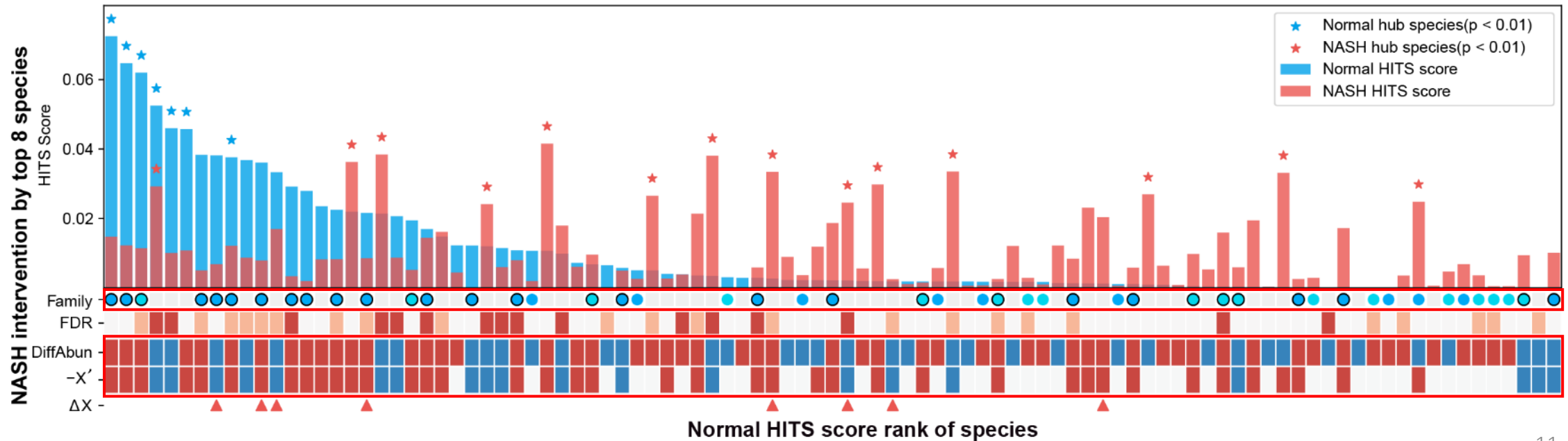
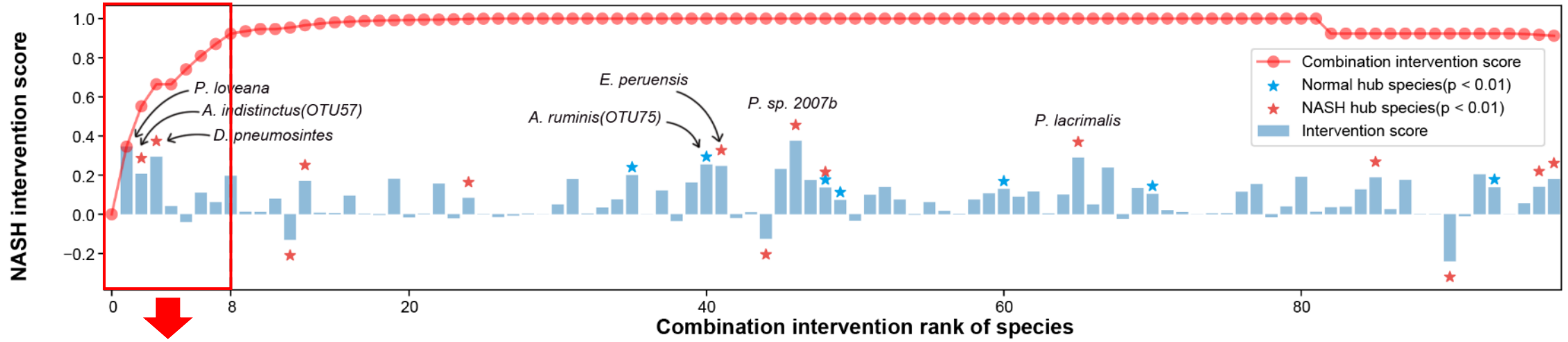
Distinct patterns of the microbial interactions in the gut of normal, obese and NASH subjects.



The gut microbiome of normal, obese and NASH groups exhibited distinct patterns of microbial interactions.

# Results

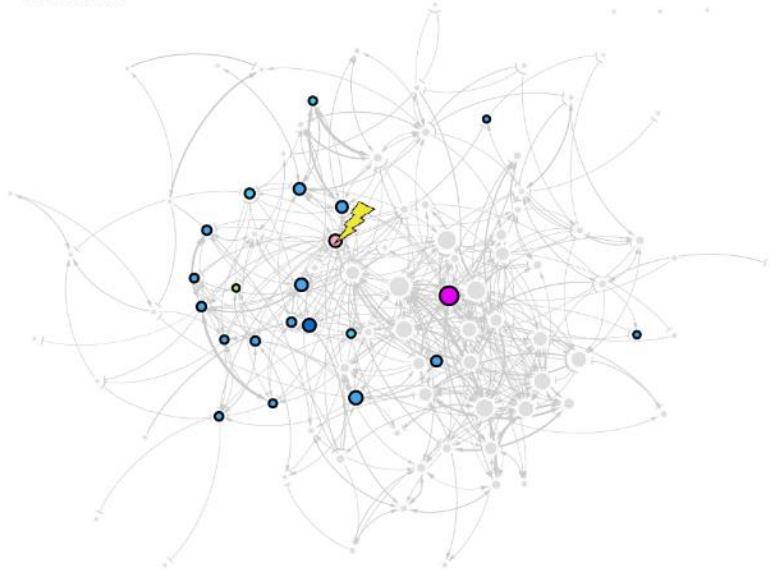
Keystone species of NASH drive the changes of the diseased gut microbiome toward a normal microbiome.



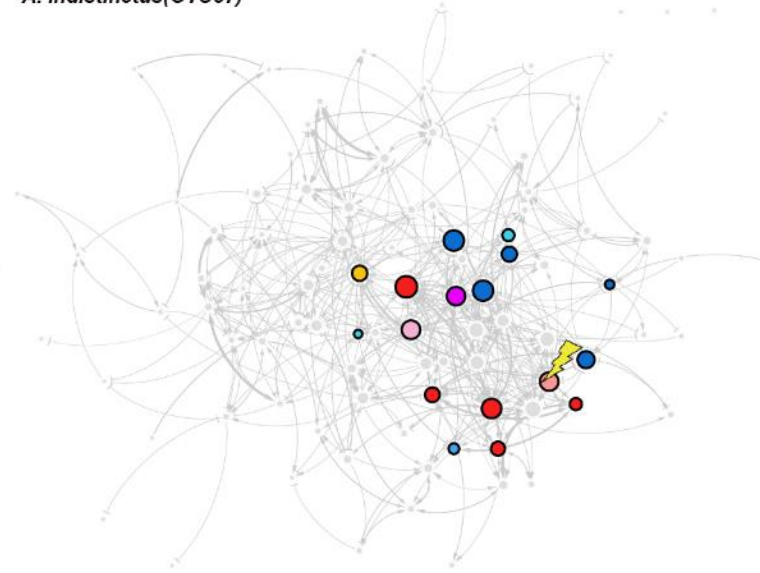
# Results

Keystone species of NASH drive the changes of the diseased gut microbiome toward a normal microbiome.

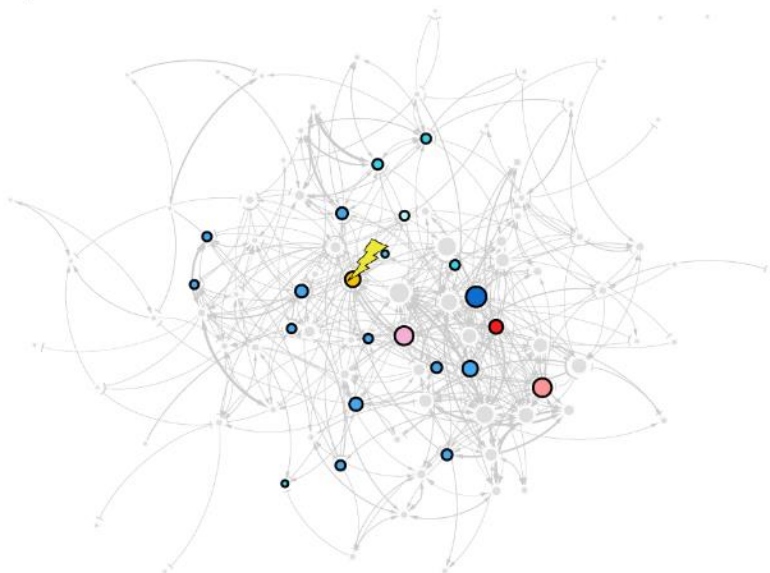
*P. loveana*



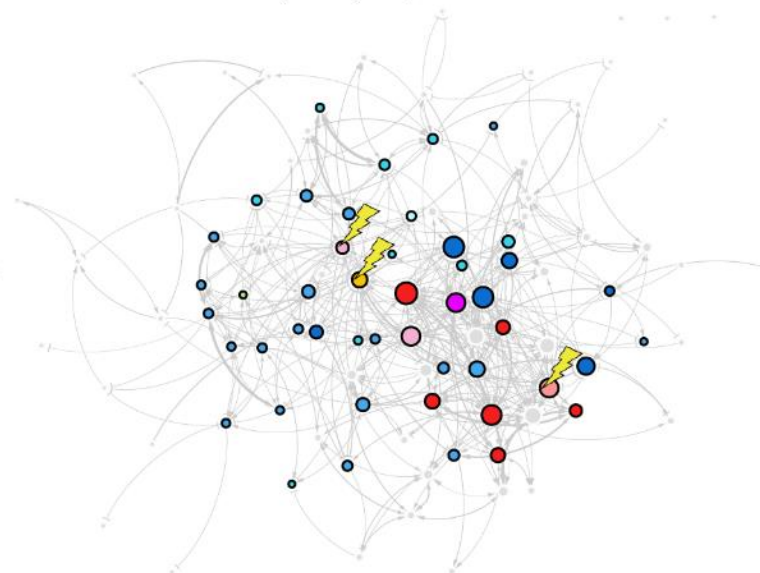
*A. indistinctus(OTU57)*



*D. pneumosintes*



*P. loveana + A. indistinctus(OTU57) + D. pneumosintes*



Class / Family

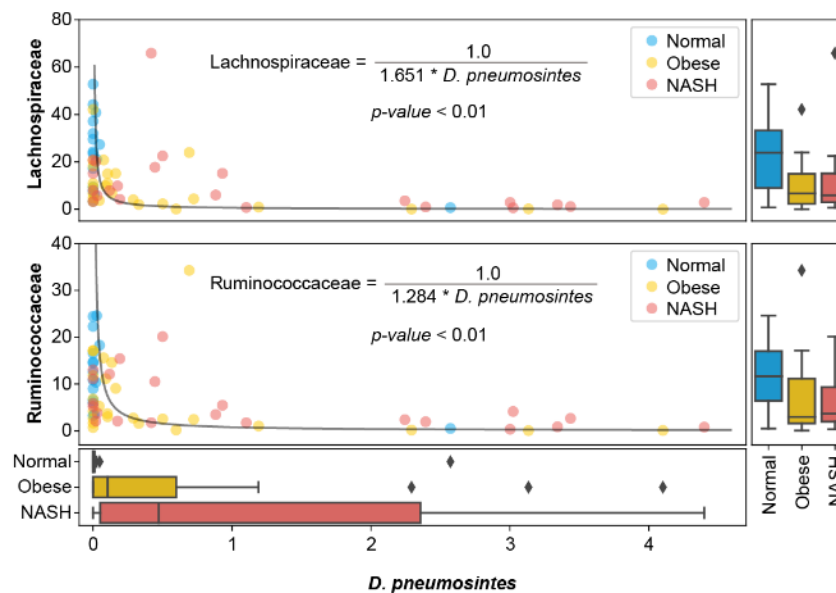
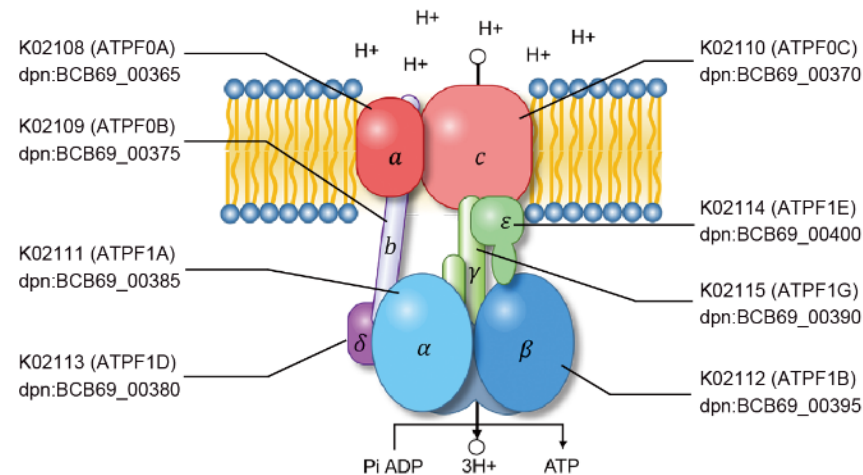
- Clostridiales
  - Family XI
  - Lachnospiraceae
  - Ruminococcaceae
  - Peptostreptococcaceae
  - Family XIII
- Bacteroidales
  - Bacteroidaceae
  - Prevotellaceae
  - Rikenellaceae
  - Marinifilaceae
  - Porphyromonadaceae
  - Tannerellaceae
- Lactobacillales
  - Leuconostocaceae
  - Streptococcaceae
- Selenomonadales
  - Veillonellaceae
- Others
  - Burkholderiaceae
  - Bifidobacteriaceae
  - Enterobacteriaceae
  - Campylobacteraceae
  - Desulfovibrionaceae

⚡ Intervention target species

○ Affected species

# Results

## Potential mechanisms for the keystone species to impact the NASH microbiome.



# Summary

- The dysbiosis of butyrate-producing bacteria is a critical factor contributing to the development of NAFLD.
- Causal algorithm intergraded with ecological theory and dynamic intervention simulation could mine microbial keystone species from metagenomic data.
- Keystone species of NASH, such as *P. loveana*, *A. indistinctus* and *D. pneumosintes*, provided potential precise intervention strategies for NAFLD treatment.

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