



# A human gut microbial gene catalogue established by metagenomic sequencing

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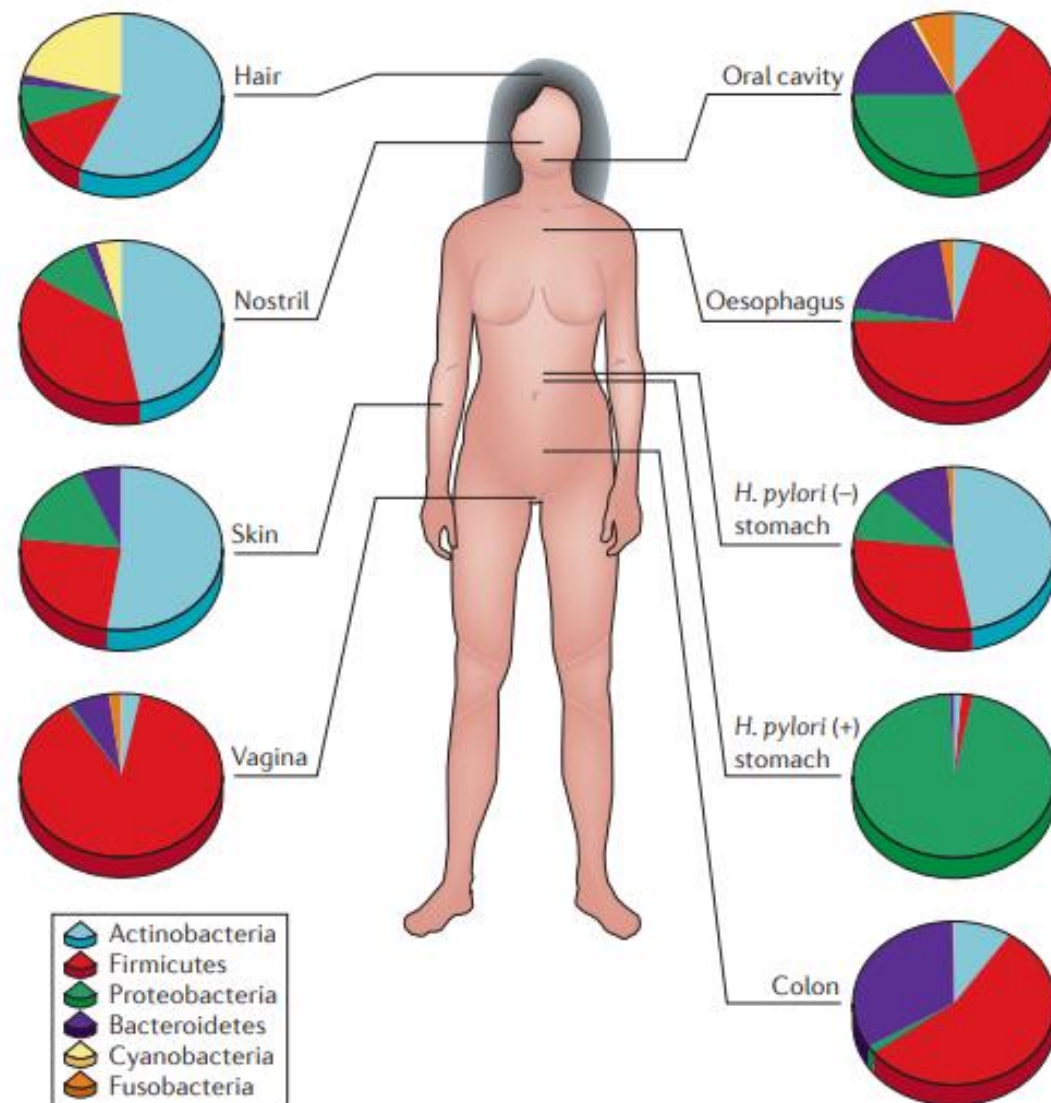
2021.12.02

华大生命科学研究院  
**BGI** • research

# Background

## 人类共生微生物

- 细胞数量：~100 万亿个细胞（人类细胞数量的10倍）
- 编码独特的基因数量：~人类基因的100倍
- 大多数微生物存在于肠道中，对人体生理和营养有着深远的影响
- 肠道微生物的改变可能与肠道疾病或肥胖相关联

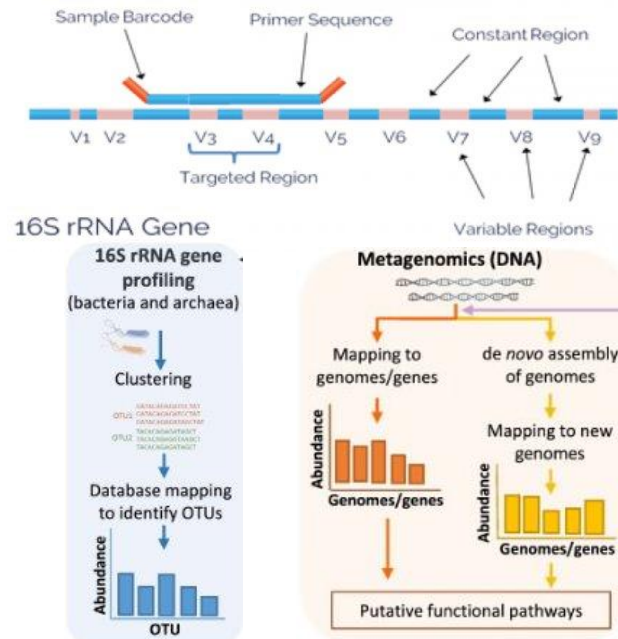


## 微生物群落的研究方法

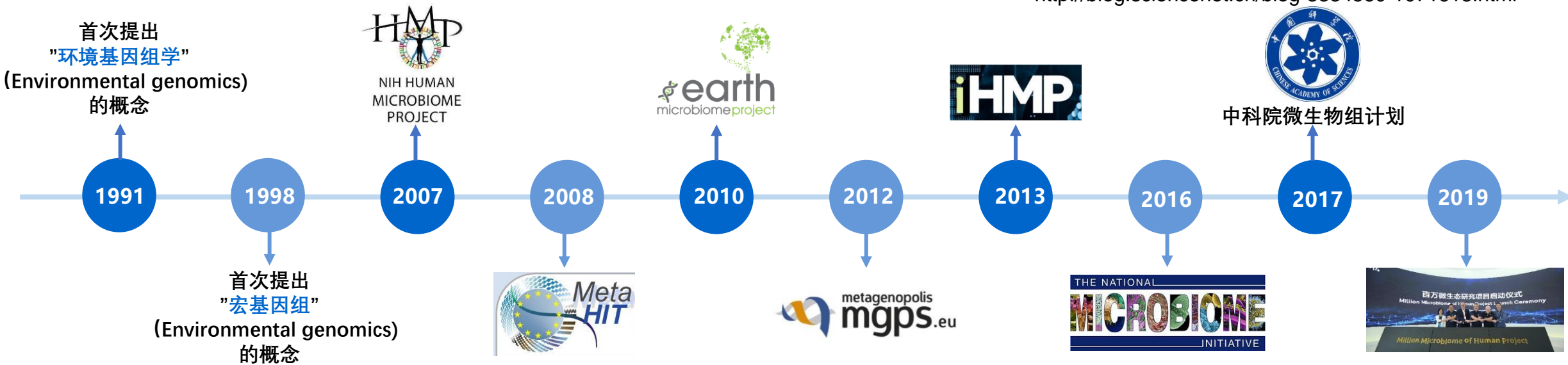
- 基于16S rRNA 基因序列的**扩增子测序**
- **宏基因组鸟枪法测序**

## MetaHIT（人类肠道宏基因组学）项目

- MetaHIT计划是由欧盟第七框架计划(FP7)资助的子项目之一，致力于建立人肠道微生物基因与人体健康和疾病的关系
- 聚集了来自学术界和工业界的 13 个合作伙伴，共计 8 个国家

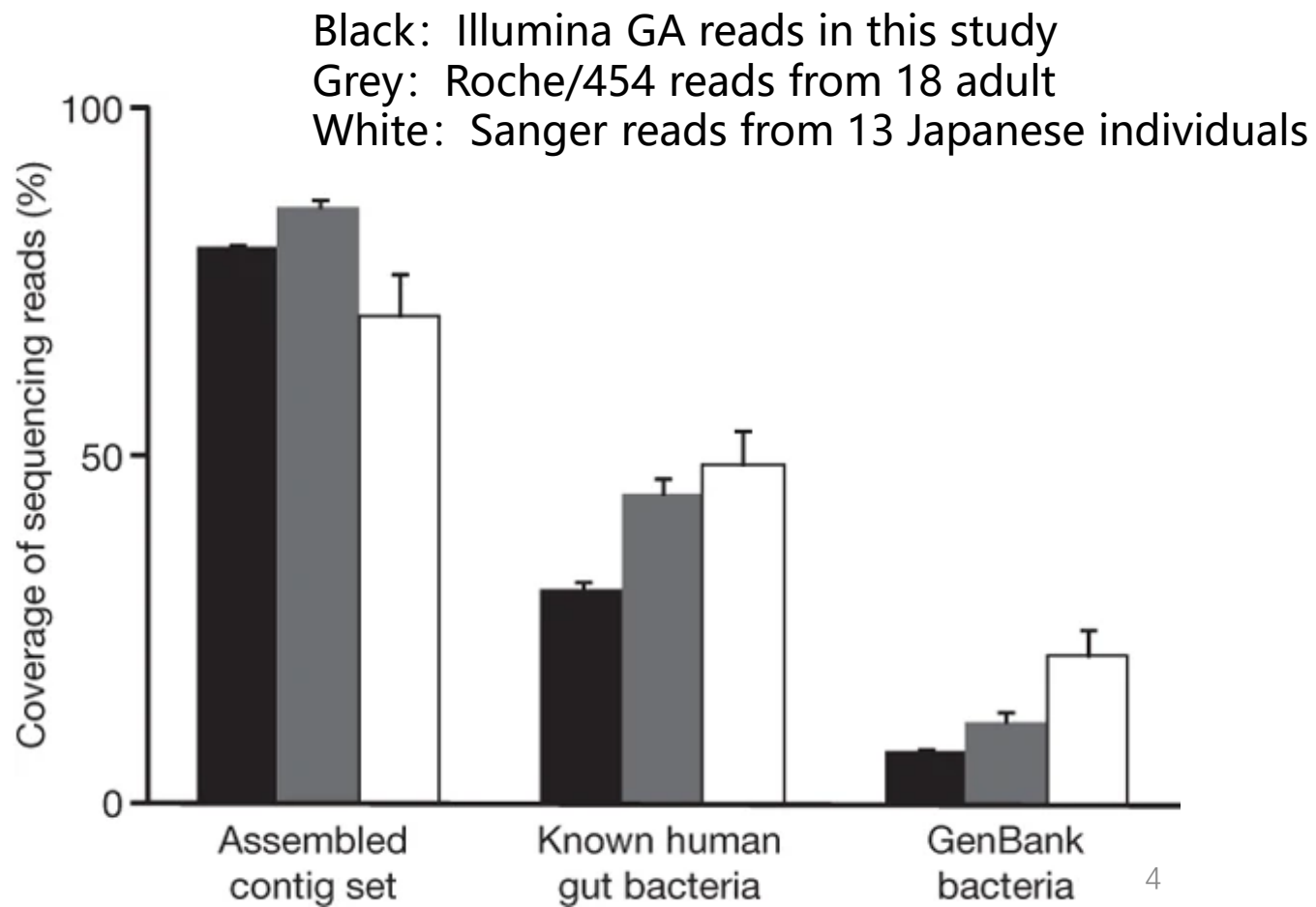
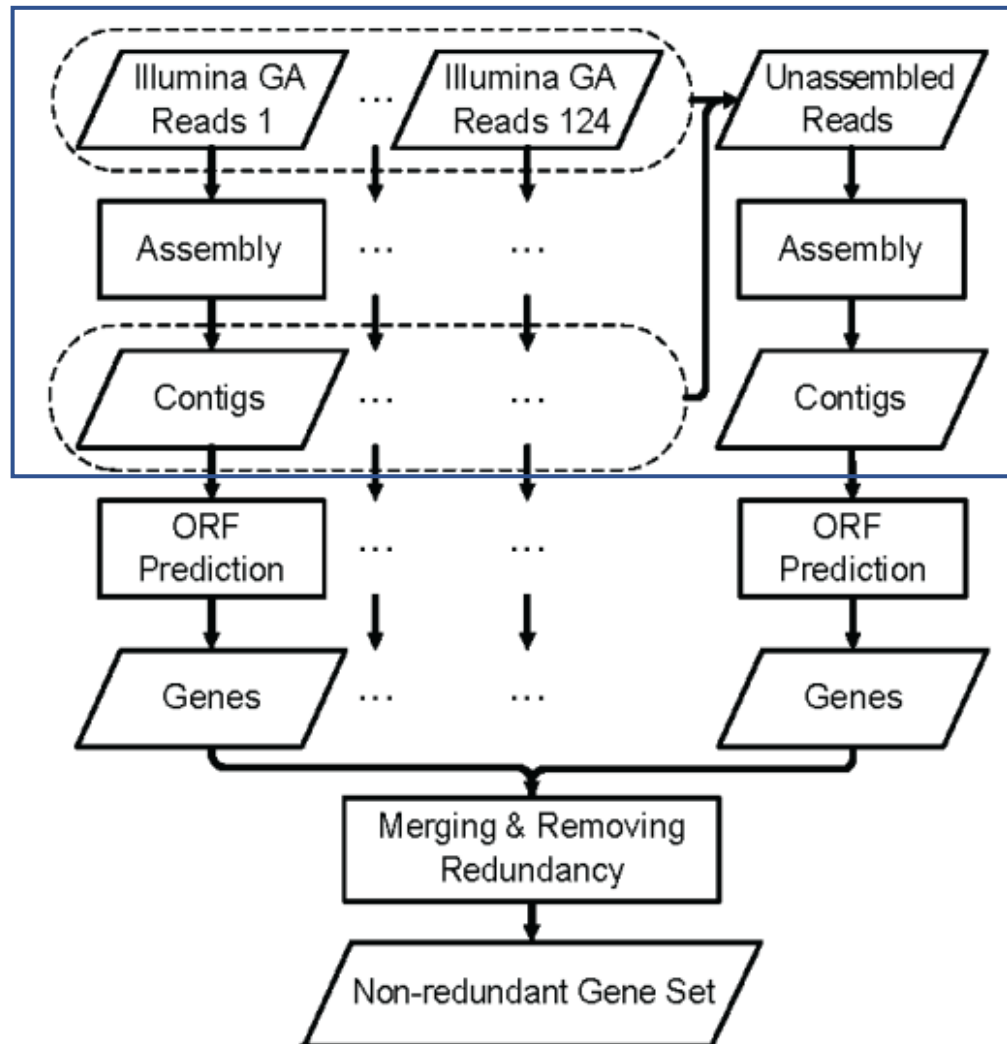


<http://blog.sciencenet.cn/blog-3334560-1071618.html>

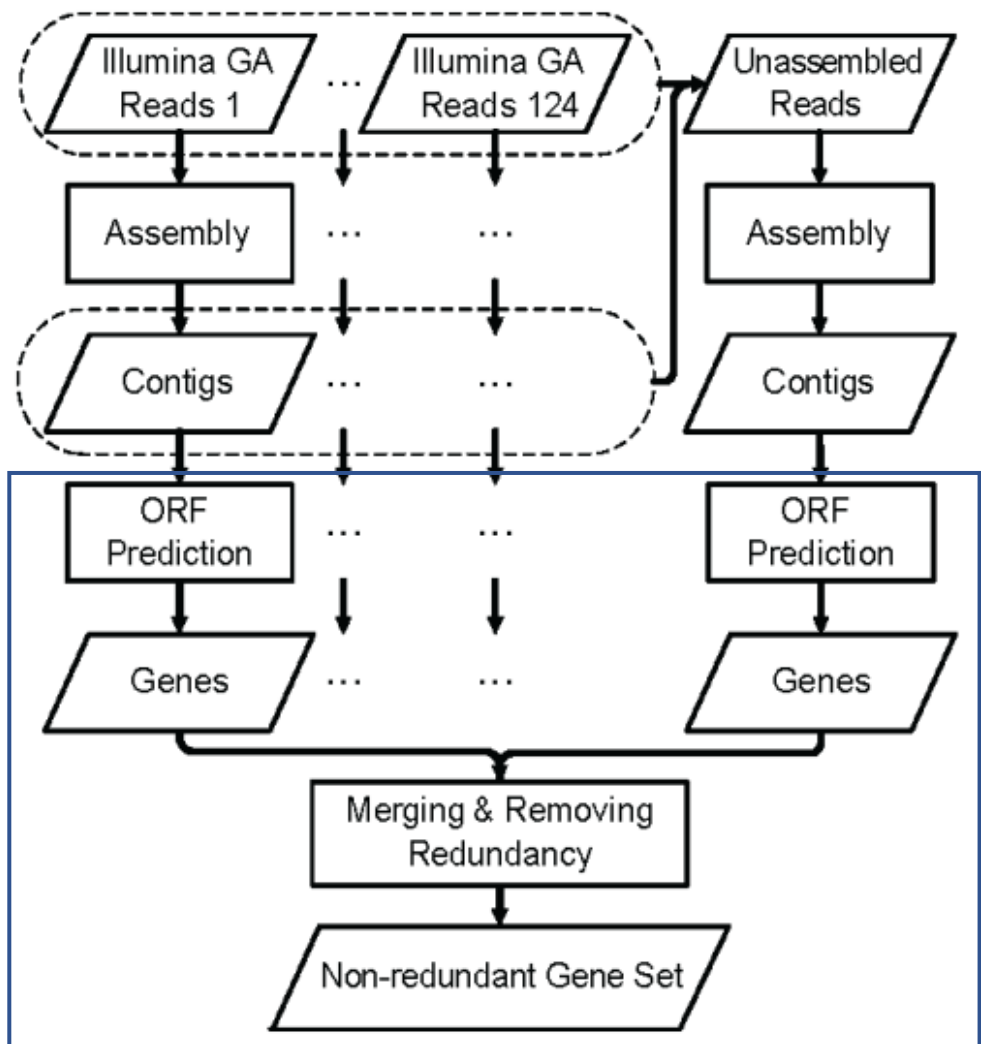


## Metagenomic sequencing of gut microbiomes

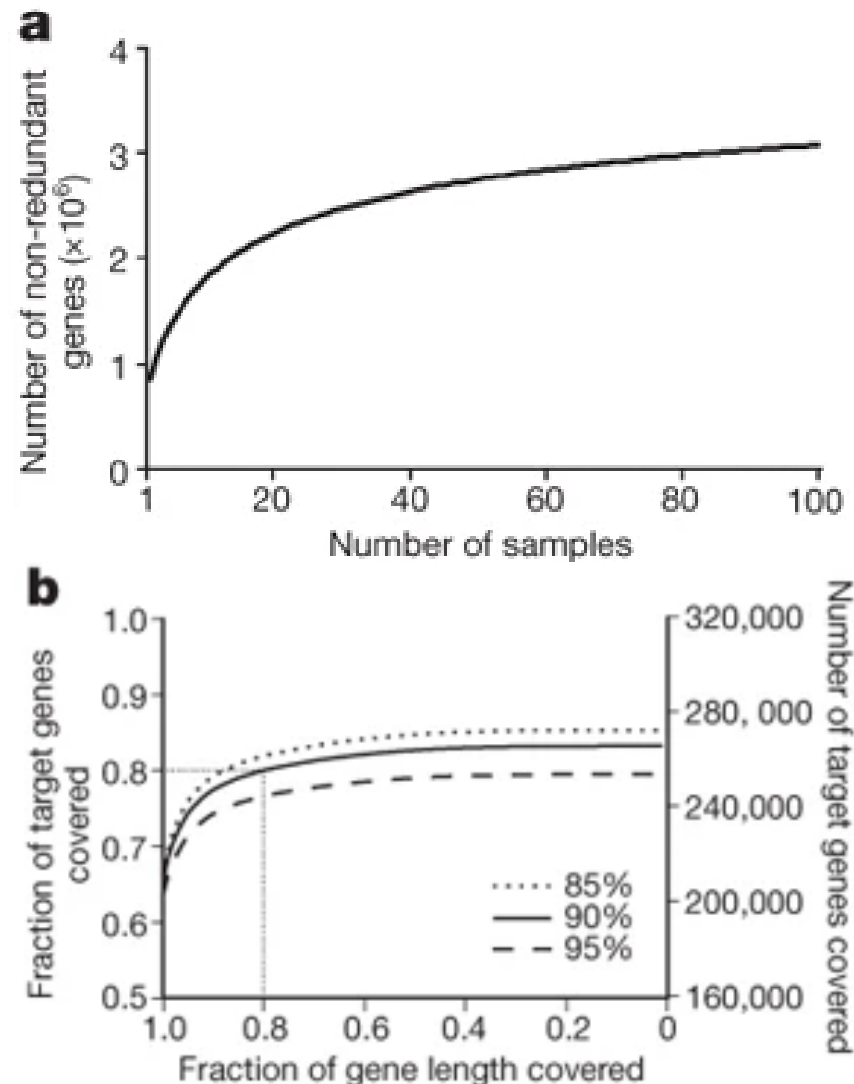
- 丹麦和西班牙的 124 名健康、超重、肥胖以及炎症性肠病 (IBD) 患者的粪便样本



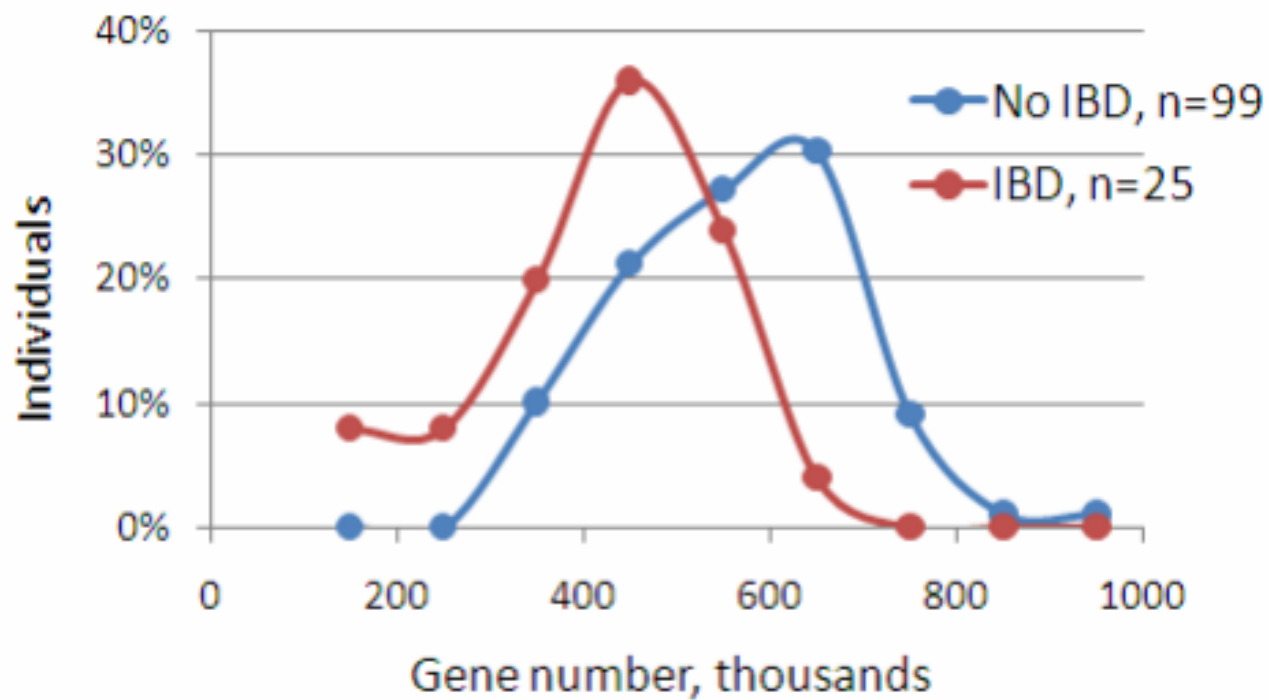
## A gene catalogue of the human gut microbiome



- 3,299,822 的非冗余ORF



## A gene catalogue of the human gut microbiome

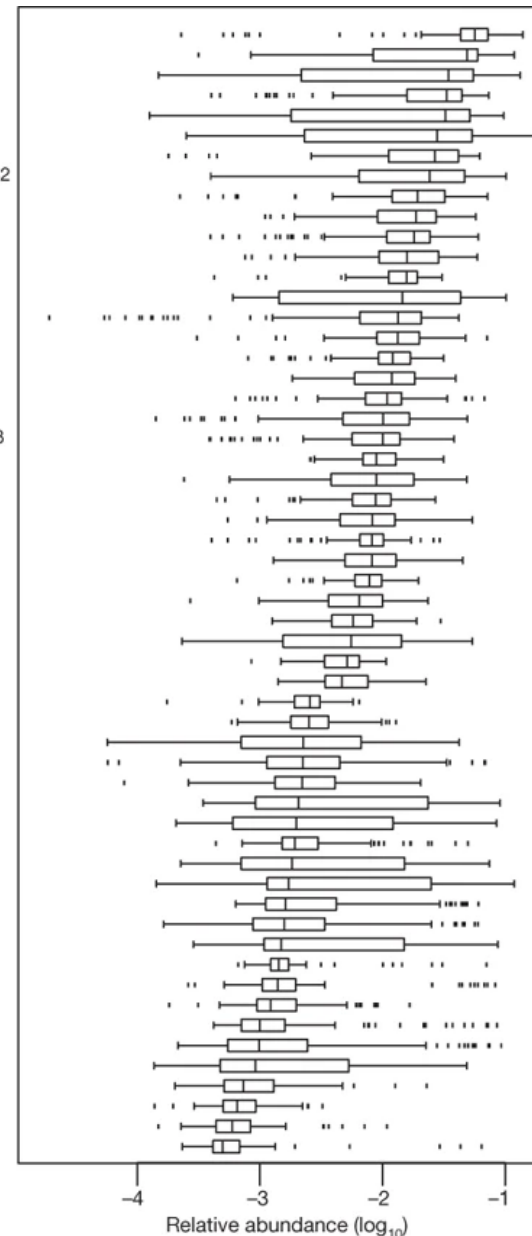




## Common bacterial core

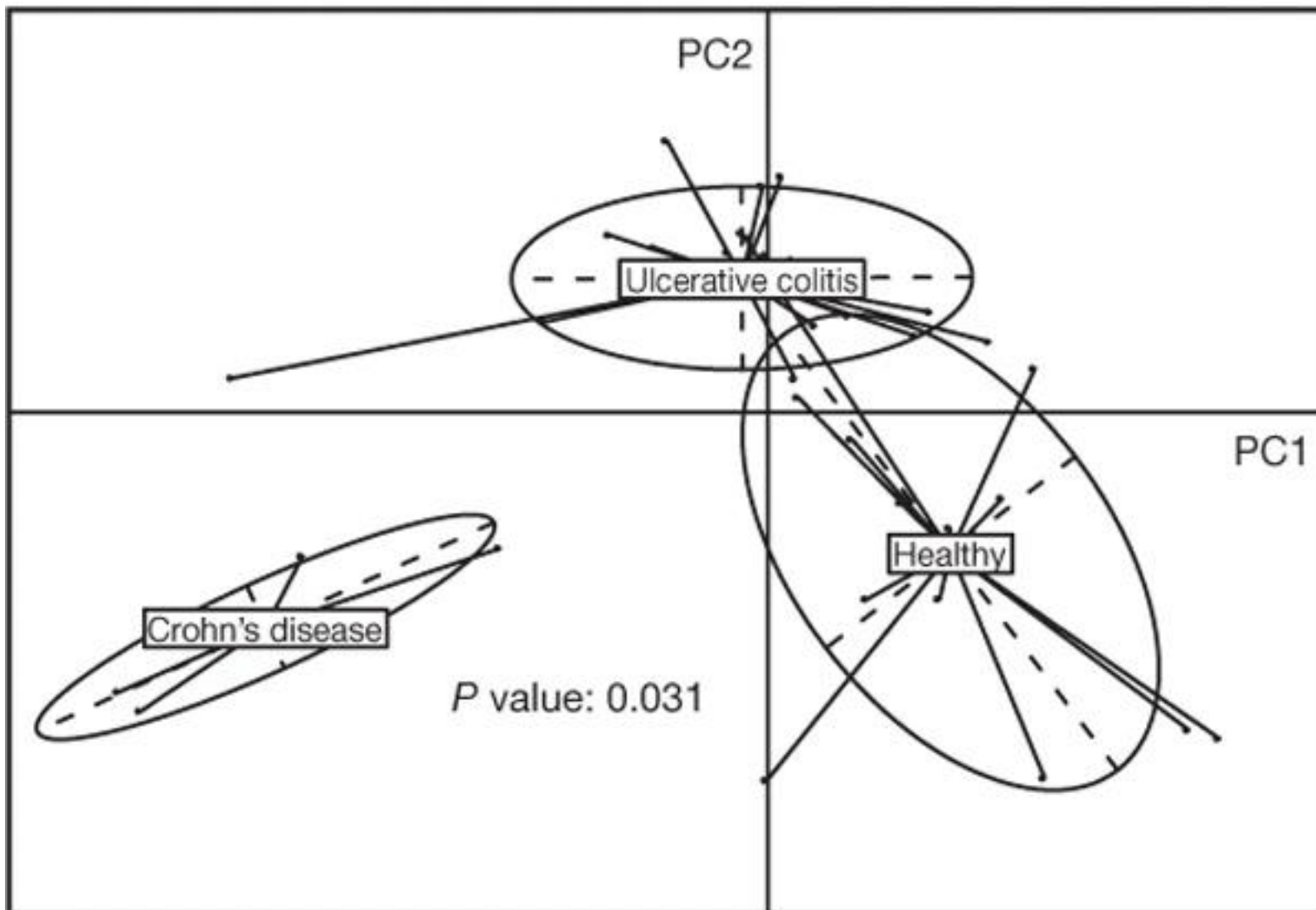
- 深度宏基因组测序提供了探索队列中是否存在一组共同微生物物种（共同核心）的机会。
- 在所有个体中检测到 18 个物种， $\geq 90\%$ 的个体中检测到57个物种。
- 个体中微生物物种丰度的可变性会极大地影响共同核心的识别。
- 与先前研究一致，拟杆菌门和厚壁菌门的丰度最高。

*Bacteroides uniformis*  
*Alistipes putredinis*  
*Parabacteroides merdae*  
*Dorea longicatena*  
*Ruminococcus bromii* L2-63  
*Bacteroides caccae*  
*Clostridium* sp. SS2-1  
*Bacteroides thetaiotaomicron* VPI-5482  
*Eubacterium hallii*  
*Ruminococcus torques* L2-14  
*Unknown* sp. SS3 4  
*Ruminococcus* sp. SR1 5  
*Faecalibacterium prausnitzii* SL3 3  
*Ruminococcus lactaris*  
*Collinsella aerofaciens*  
*Dorea formicigenerans*  
*Bacteroides vulgatus* ATCC 8482  
*Roseburia intestinalis* M50 1  
*Bacteroides* sp. 2\_1\_7  
*Eubacterium siraeum* 70 3  
*Parabacteroides distasonis* ATCC 8503  
*Bacteroides* sp. 9\_1\_42FAA  
*Bacteroides ovatus*  
*Bacteroides* sp. 4\_3\_47FAA  
*Bacteroides* sp. 2\_2\_4  
*Eubacterium rectale* M104 1  
*Bacteriodes xylanisolvans* XB1A  
*Coprococcus comes* SL7 1  
*Bacteroides* sp. D1  
*Bacteroides* sp. D4  
*Eubacterium ventriosum*  
*Bacteroides dorei*  
*Ruminococcus obeum* A2-162  
*Subdoligranulum variabile*  
*Bacteroides capillosus*  
*Streptococcus thermophilus* LMD-9  
*Clostridium leptum*  
*Holdemania filiformis*  
*Bacteroides stercoris*  
*Coprococcus eutactus*  
*Clostridium* sp. M62 1  
*Bacteroides eggerthii*  
*Butyrivibrio crossotus*  
*Bacteroides finegoldii*  
*Parabacteroides johnsonii*  
*Clostridium* sp. L2-50  
*Clostridium nexile*  
*Bacteroides pectinophilus*  
*Anaerotruncus colihominis*  
*Ruminococcus gnavus*  
*Bacteroides intestinalis*  
*Bacteroides fragilis* 3\_1\_12  
*Clostridium asparagiforme*  
*Enterococcus faecalis* TX0104  
*Clostridium scindens*  
*Blautia hansenii*



# Result

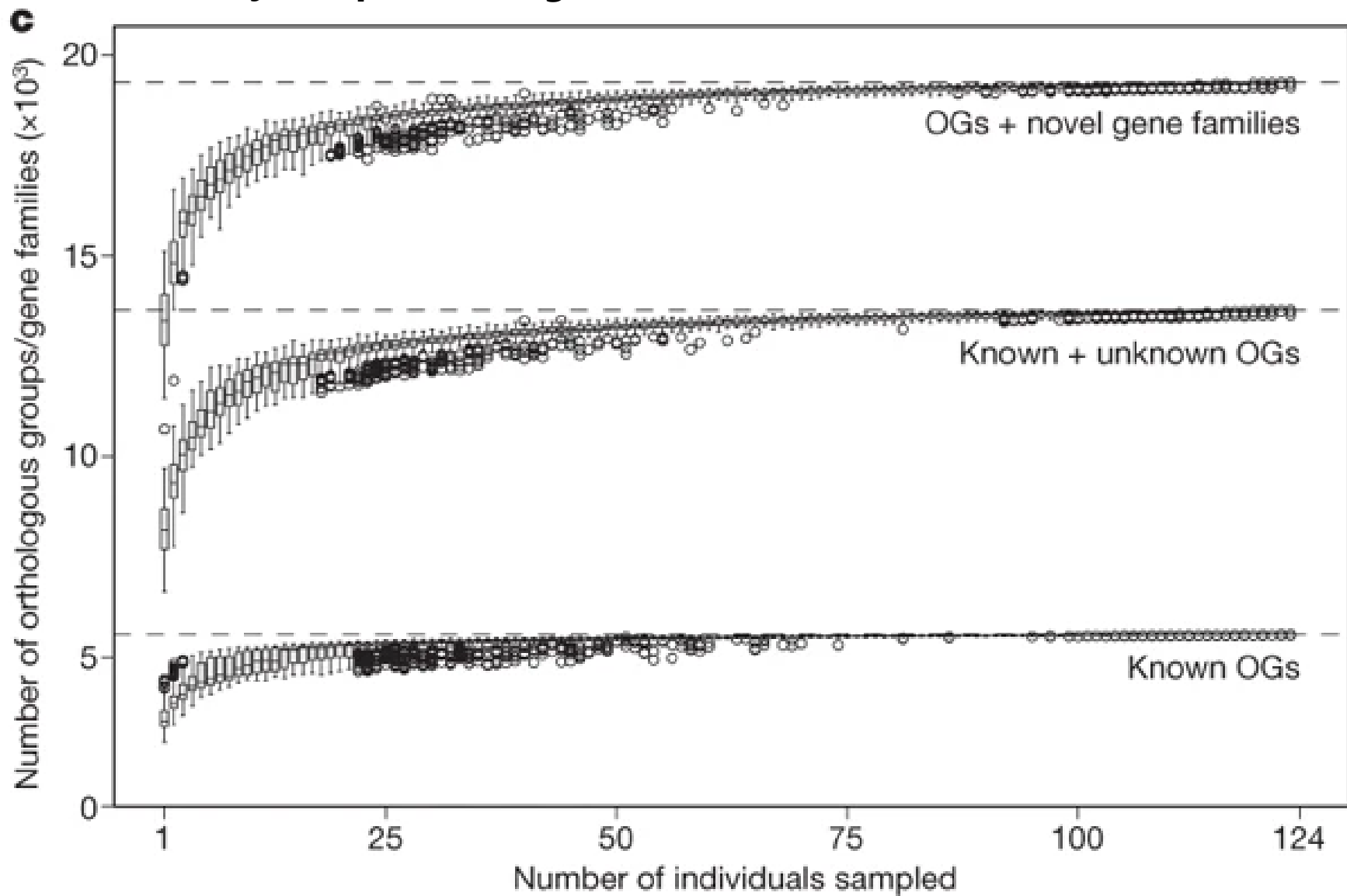
## Common bacterial core





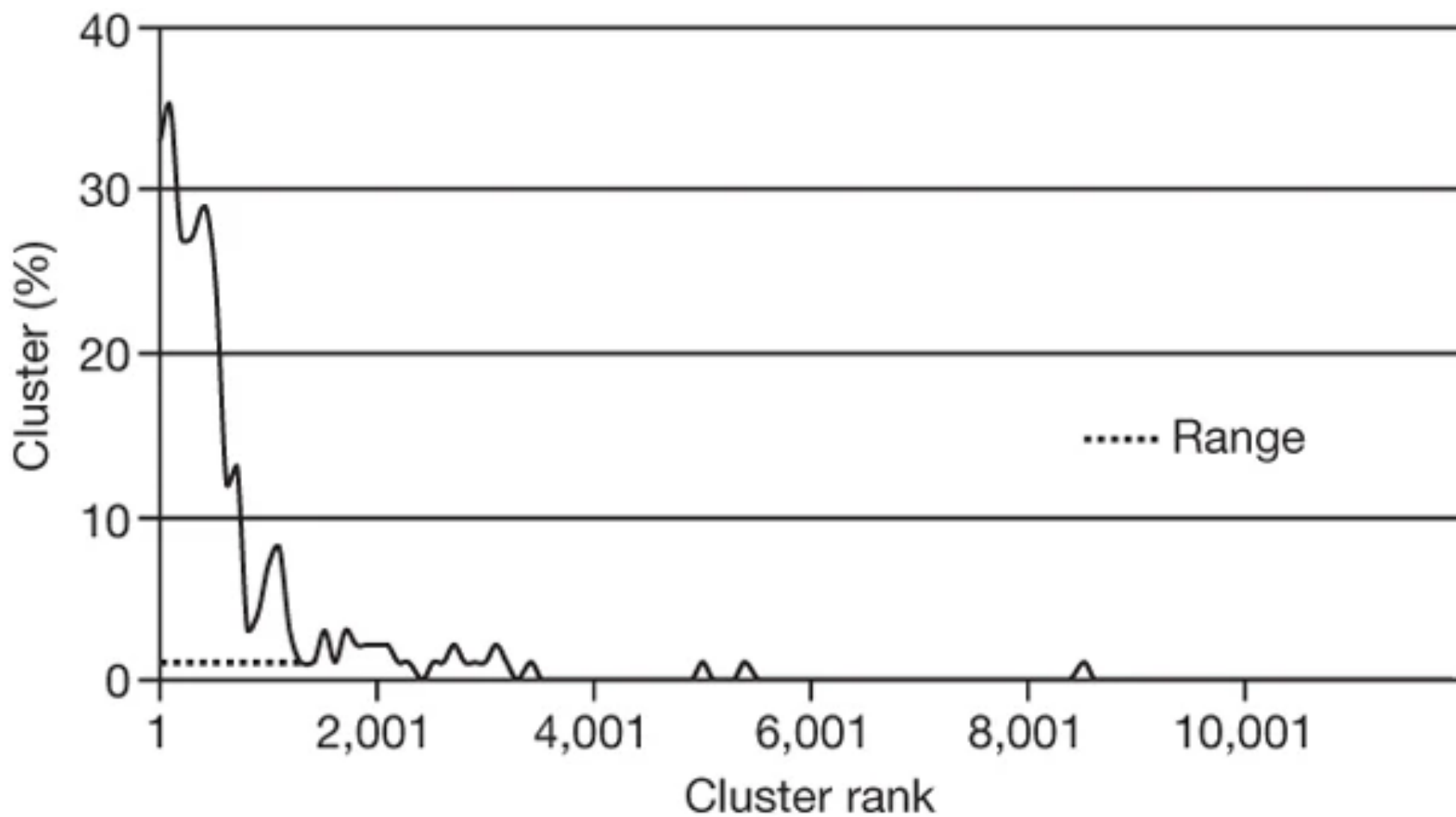
# Result

## Functions encoded by the prevalent gene set



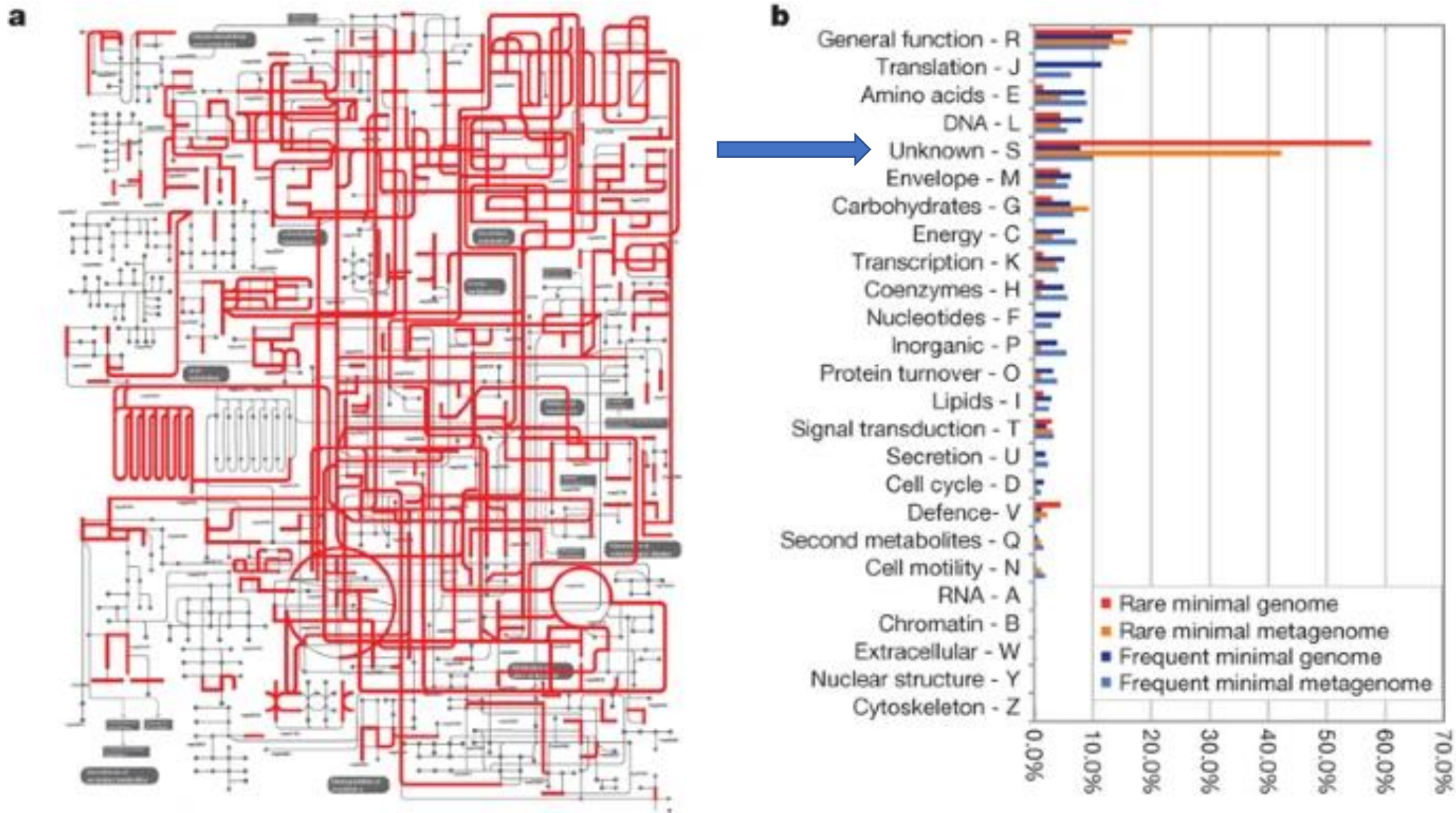
## Bacterial functions important for life in the gut

*Bacillus subtilis*

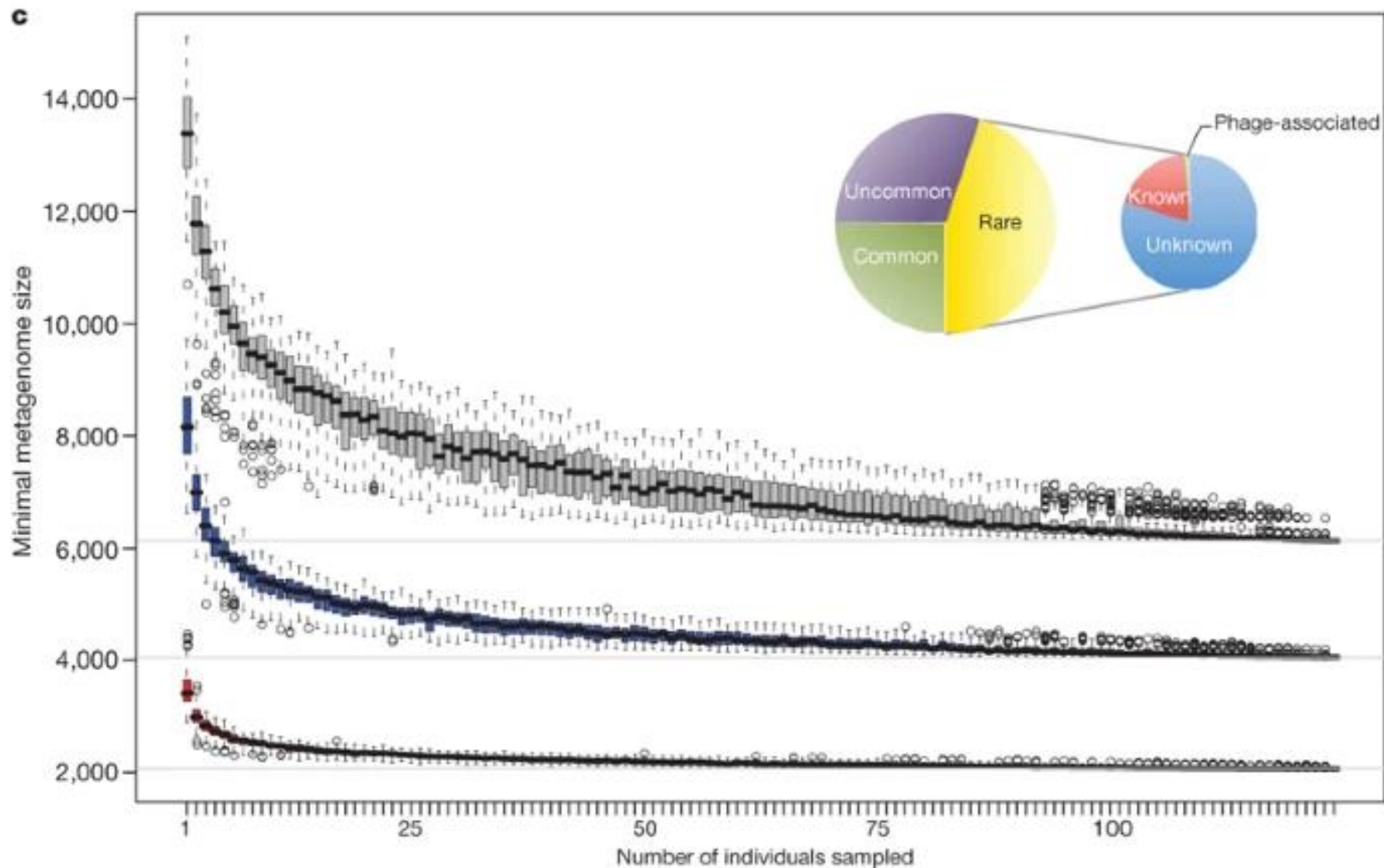


# Result

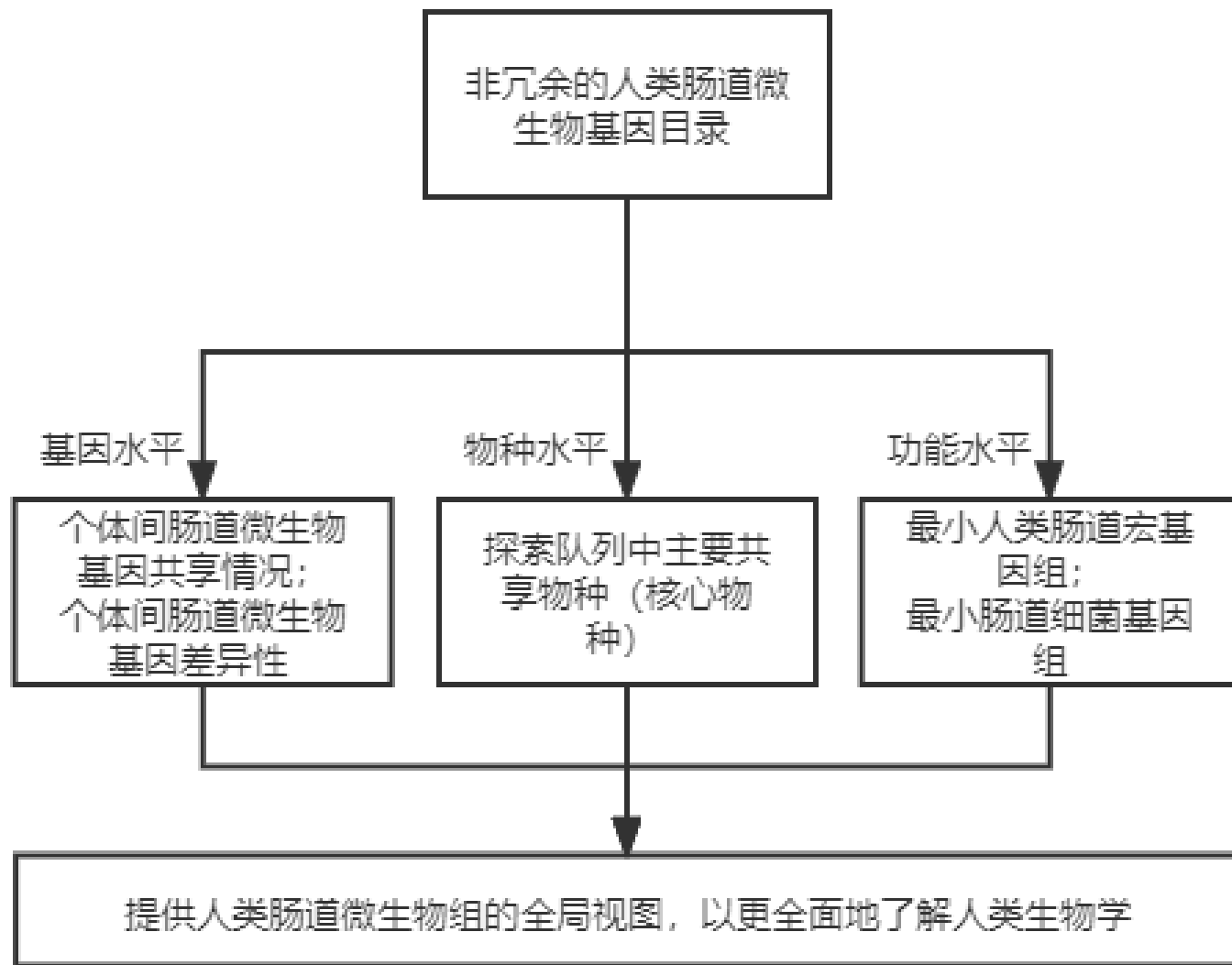
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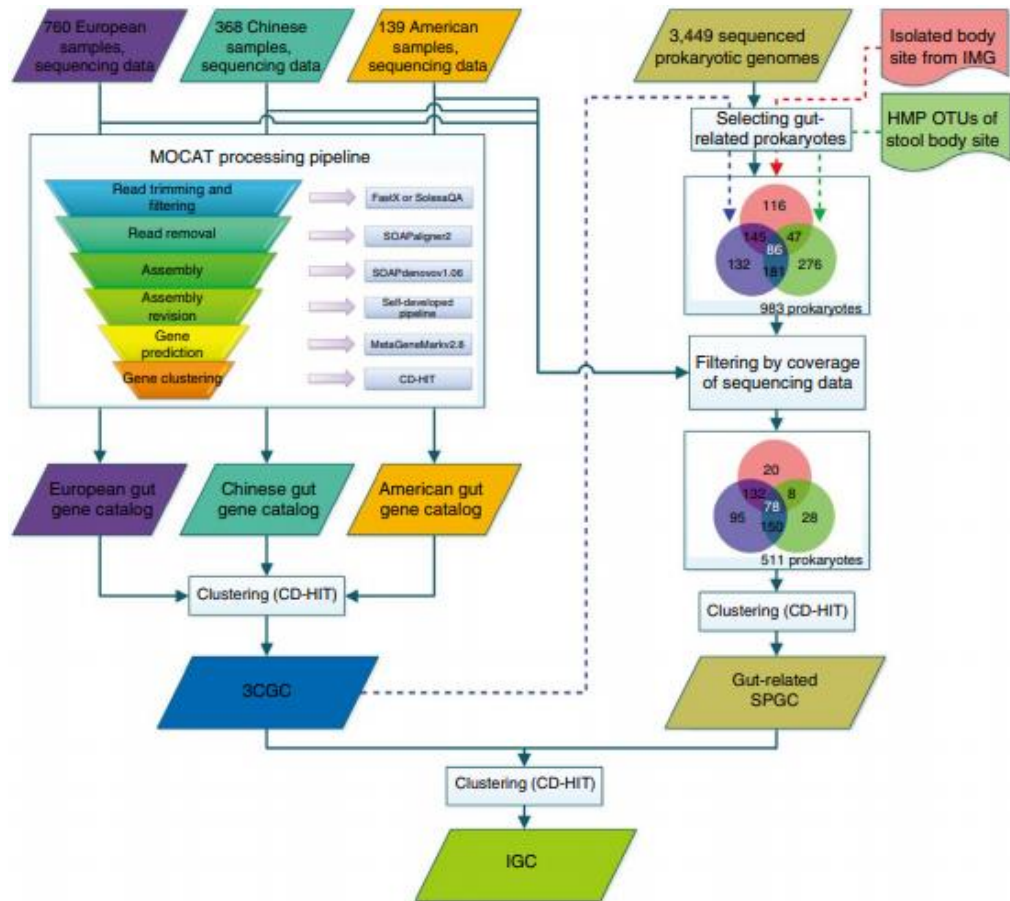


# Discussion

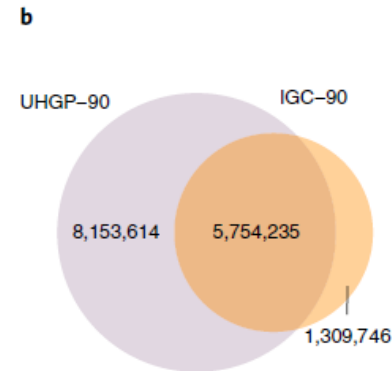
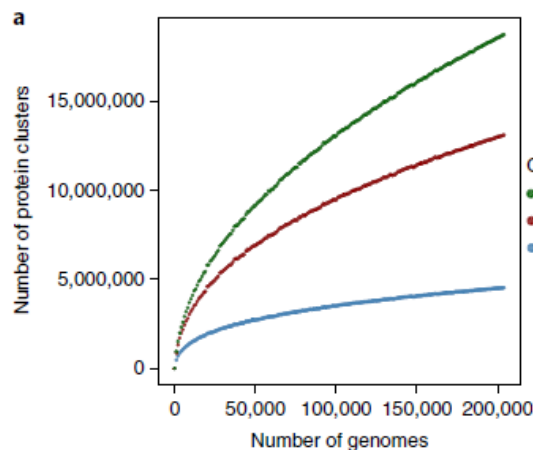
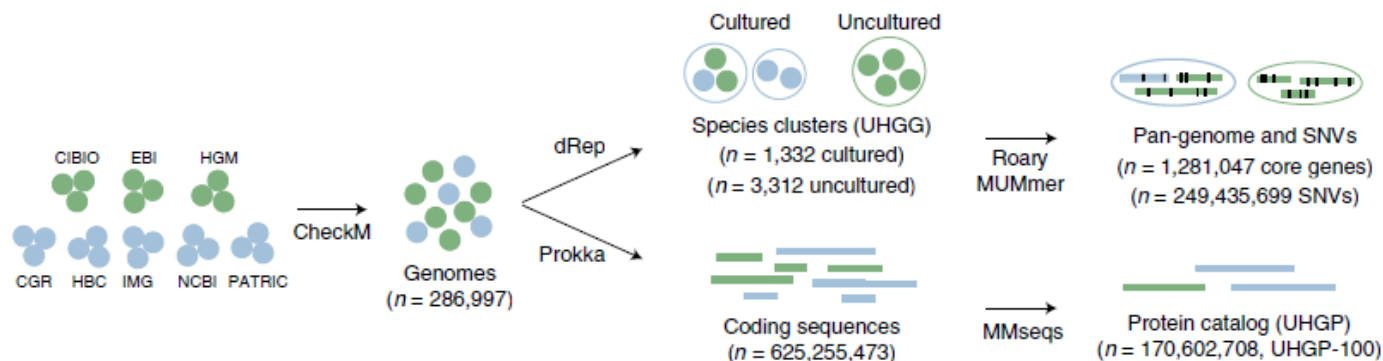


## 人类肠道微生物基因目录的后续研究

Integrated non-redundant gene catalog (IGC): 9.9M



The Unified Human Gastrointestinal Protein (UHGP) catalog





# 对TEDDY 儿童早期肠道微生物组随时间发展的研究

## 《Temporal development of the gut microbiome in early childhood from the TEDDY study》

第五组：林晓倩、李灵讷、刘旭东、于华新、李文曦

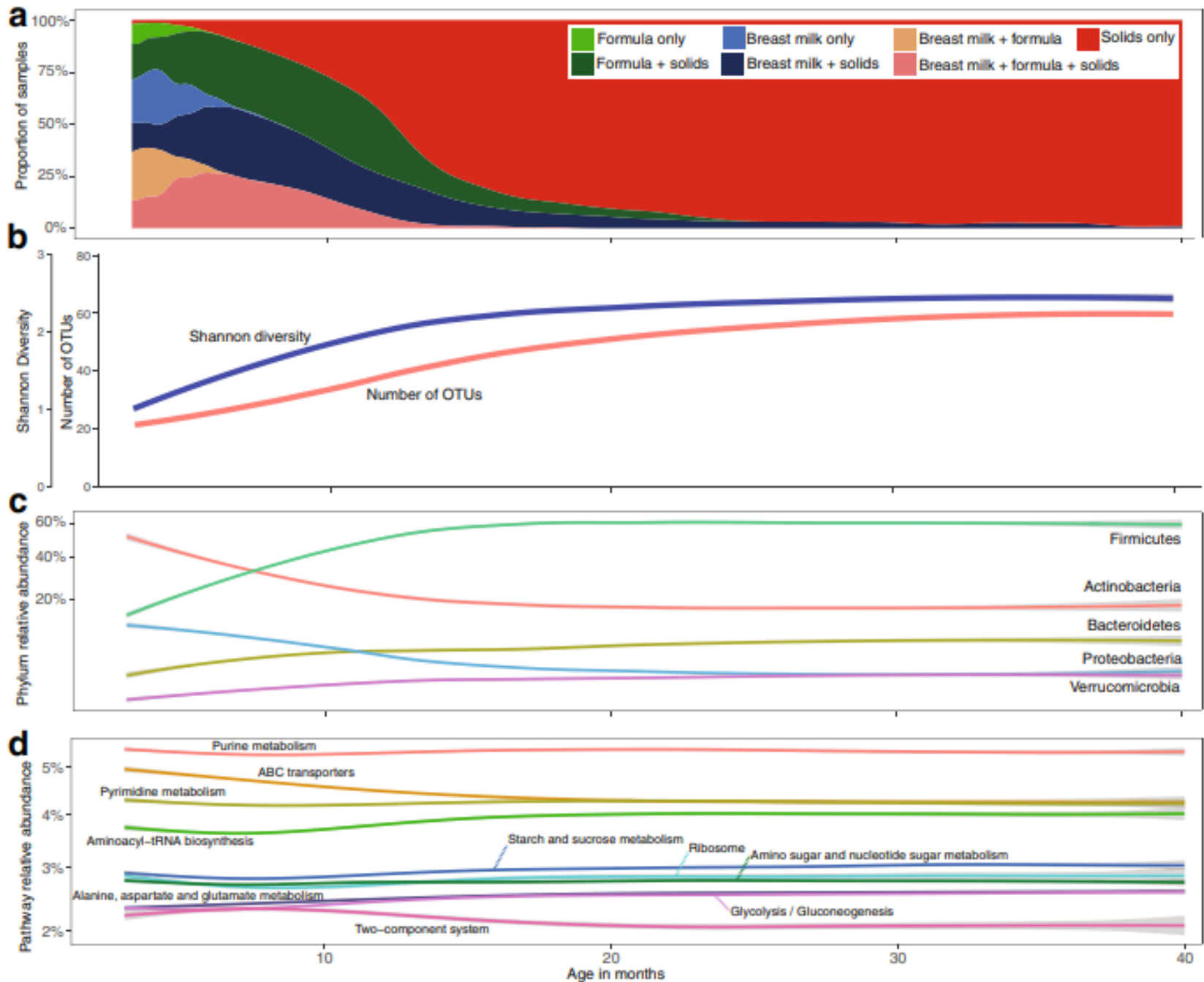
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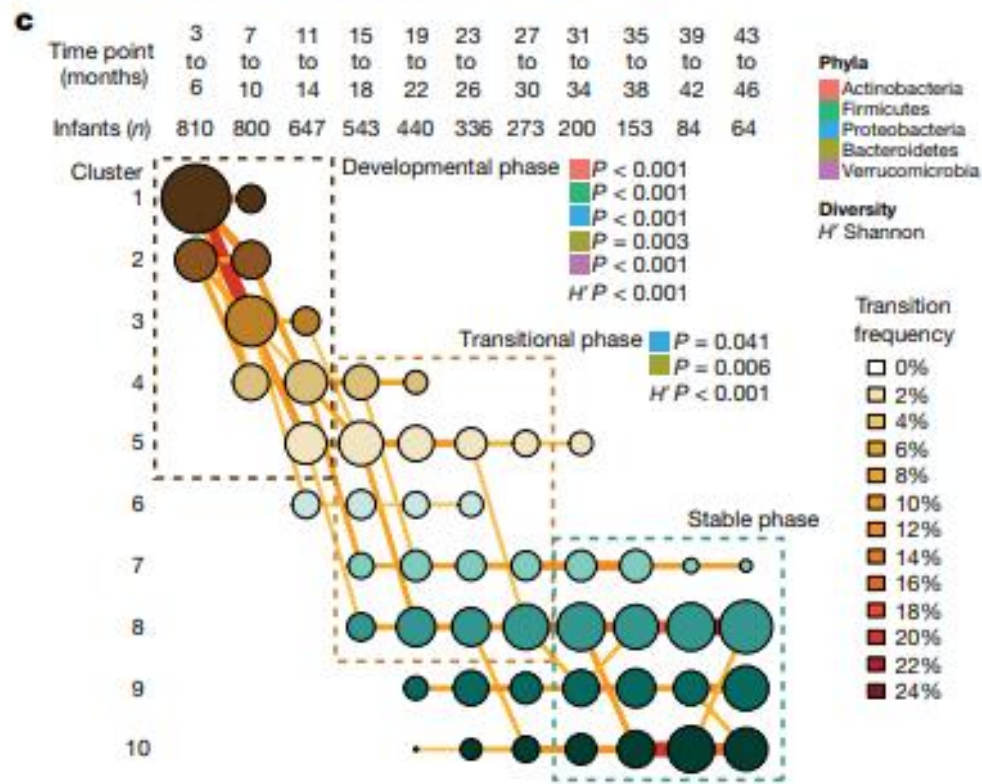
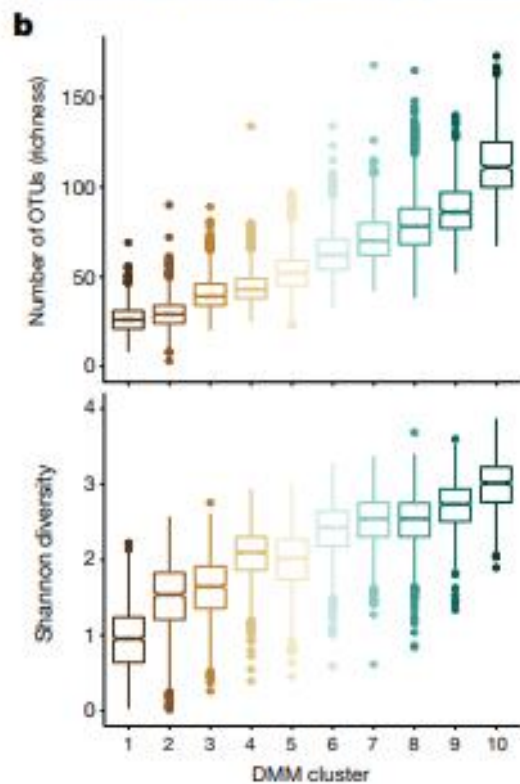
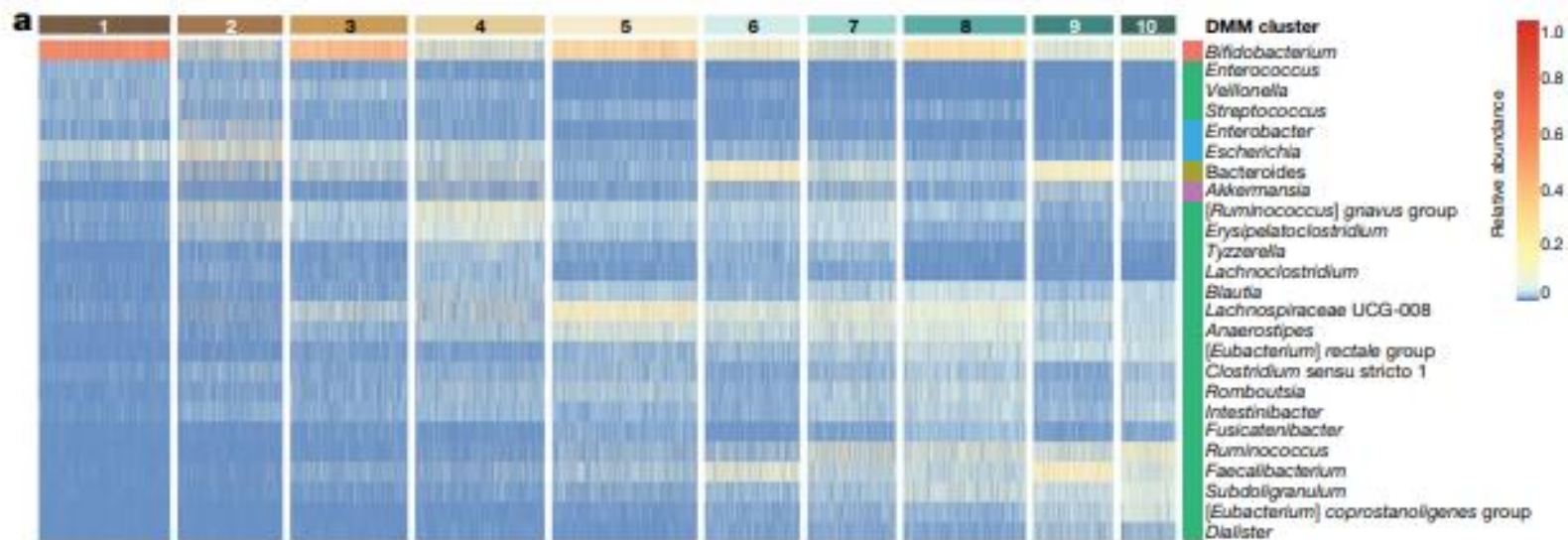
## TEDDY : The Environmental Determinants of Diabetes in the Young (TEDDY) study

已有基础：婴儿期到儿童期的微生物组发展取决于一系列因素，在此期间微生物-免疫串扰被认为与晚年疾病（持续性胰岛自身免疫和 1 型糖尿病）有关

研究意义：本研究前还没有研究对生命早期微生物组进行大数据、多中心人群的广泛研究

OTU  
(Operational  
Taxonomic Unit )  
即**分类操作单元**，  
是在系统发生学研究或群体遗传学研究中，为了便于进行分析，人为给某一个分类单元（品系，种，属，分组等）设置的同一标志。





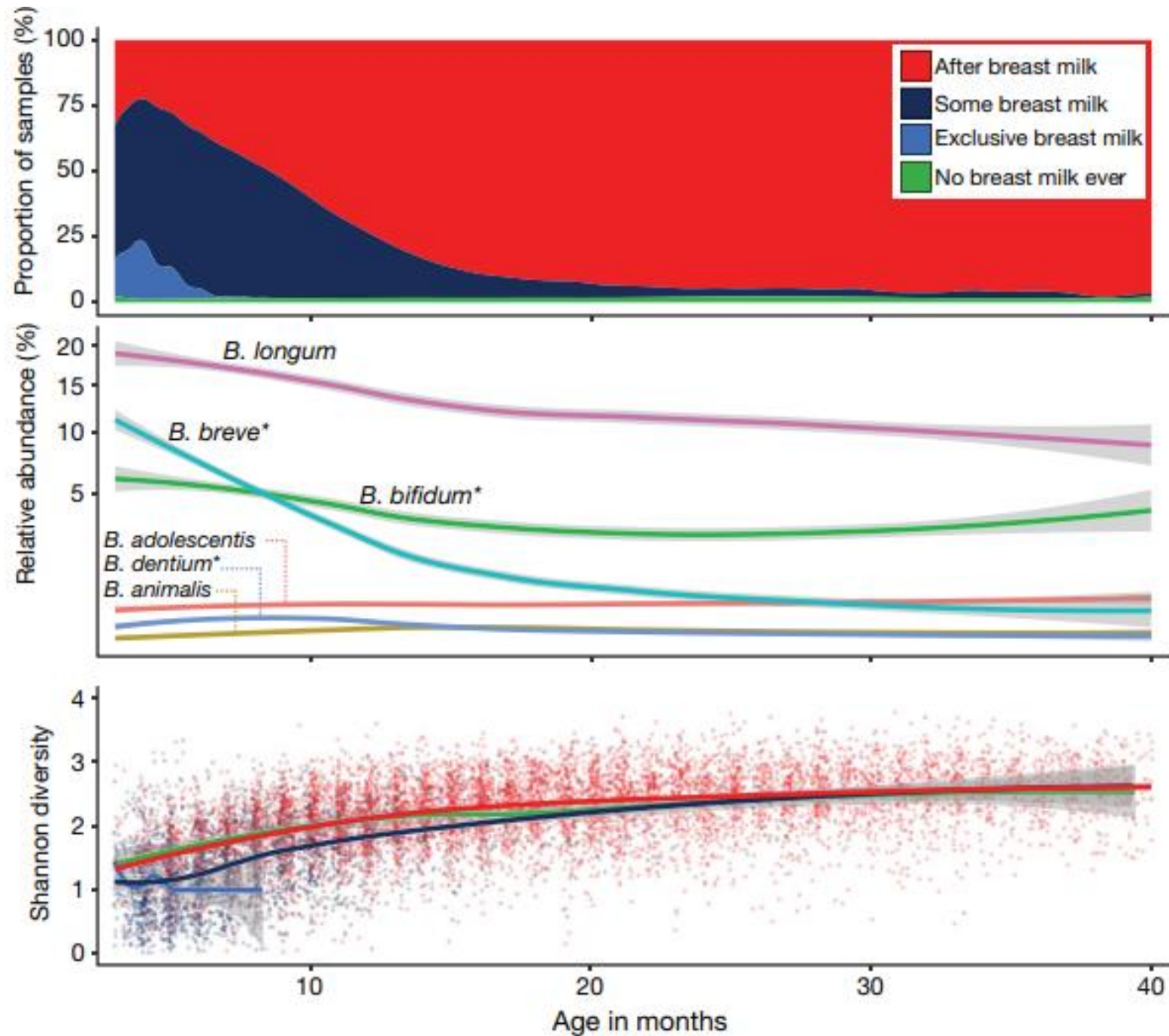
at the genus level

at the species level

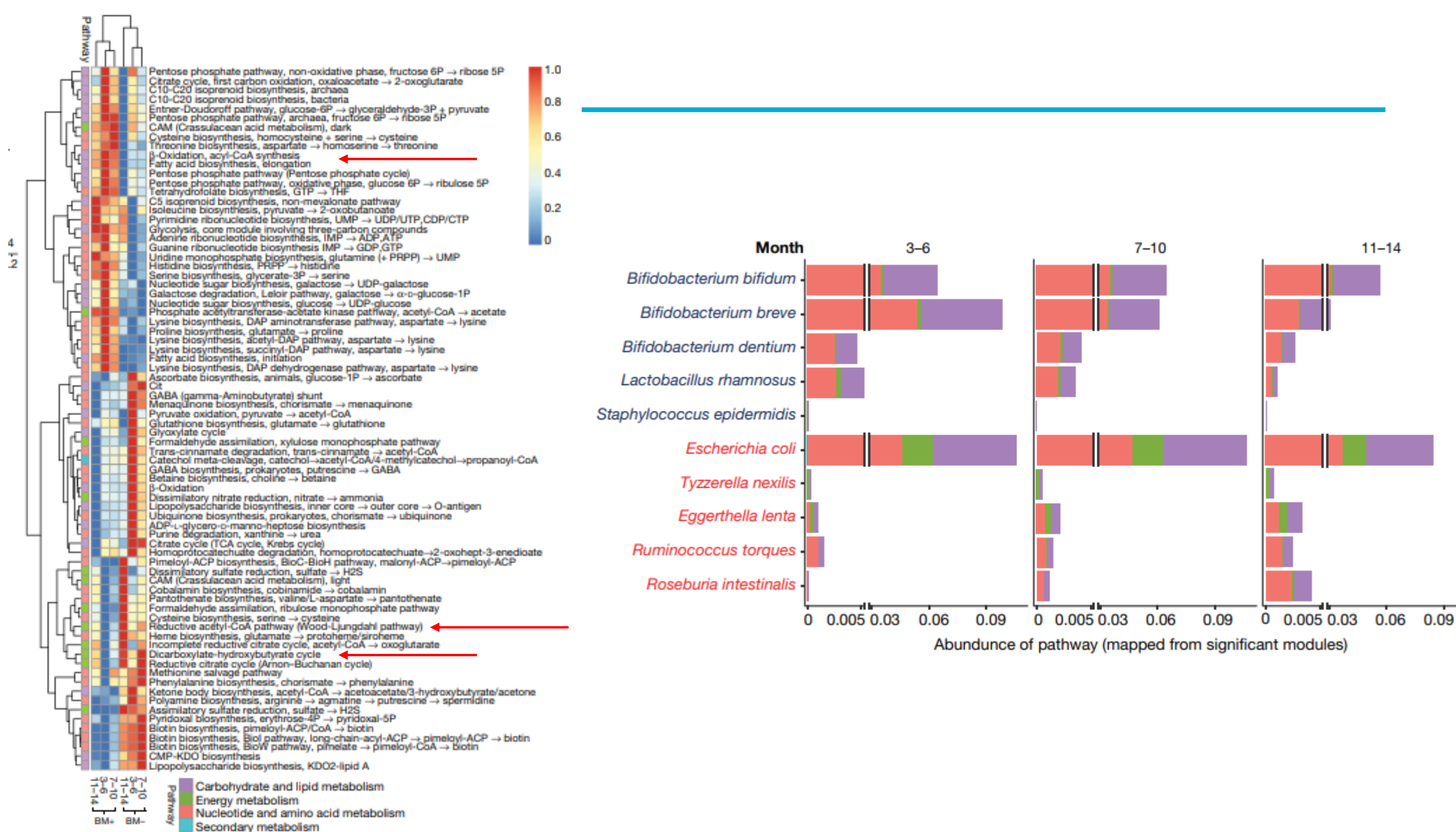
Functional  
metagenomic  
capacity at the  
module level











# THANKS

OMICS FOR ALL

基因科技造福人类