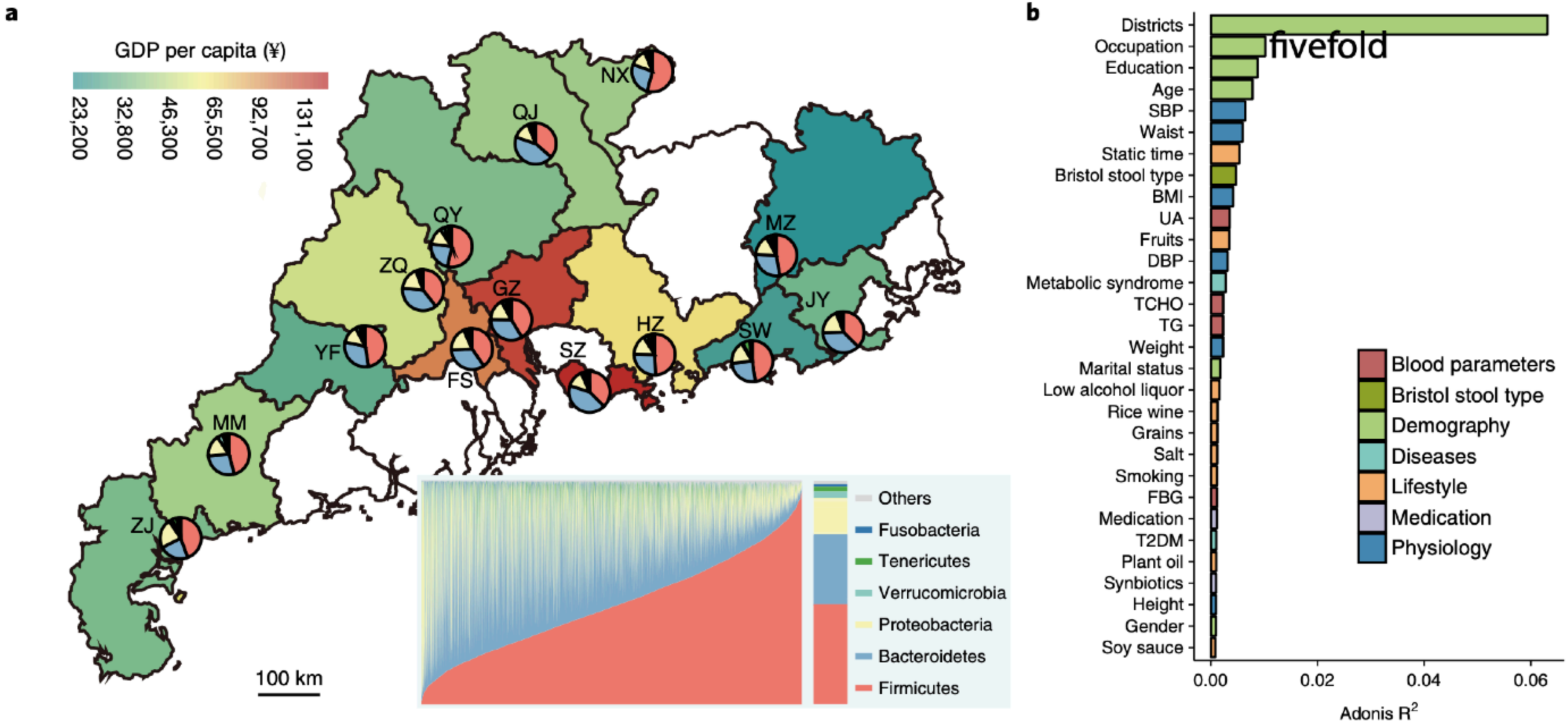
Limitação


a
GDP per capita (¥)
23,200
32,800
46,300
65,500
92,700
131,100
NX
QJ
QY
ZQ
GZ
MZ
JY
HZ
SW
YF
SZ
FS
MM
ZJ
100 km
Others
Fusobacteria
Tenericutes
Verrucomicrobia
Proteobacteria
Bacteroidetes
Firmicutes
b
fivefold
Districts
Occupation
Education
Age
SBP
Waist
Static time
Bristol stool type
BMI
UA
Fruits
DBP
Metabolic syndrome
TCHO
TG
Weight
Marital status
Low alcohol liquor
Rice wine
Grains
Salt
Smoking
FBG
Medication
T2DM
Plant oil
Synbiotics
Height
Gender
Soy sauce
Blood parameters
Bristol stool type
Demography
Diseases
Lifestyle
Medication
Physiology
0.00
0.02
0.04
0.06
Adonis R²

LETTERS
https://doi.org/10.1038/s41591-018-0164-x

nature medicine

Corrected: Author Correction

Regional variation limits applications of healthy gut microbiome reference ranges and disease models

Yan He[1,16], Wei Wu[2,3,16], Hui-Min Zheng[1,2,16], Pan Li[1,2,16], Daniel McDonald[4], Hua-Fang Sheng[1], Mu-Xuan Chen[1], Zi-Hui Chen[3], Gui-Yuan Ji[3], Zhong-Dai-Xi Zheng[2], Prabhakar Mujagond[5], Xiao-Jiao Chen[1], Zu-Hua Rong[1,2], Peng Chen[6], Li-Yi Lyu[7], Xian Wang[7], Chong-Bin Wu[7], Nan Yu[1], Yan-Jun Xu[8], Jia Yin[9], Jeroen Raes[10,11,12], Rob Knight[4,13,14], Wen-Jun Ma[3*] and Hong-Wei Zhou[1,2,15*]

In conclusion, our data reinforce the need to use consistent sampling protocols to build localized reference baselines for gut microbiota. The applicability of disease models in new populations must be explicitly tested rather than assumed. The populations used to generate healthy reference data and train disease models must therefore be clearly stated when performing gut microbiome analyses, especially when intended for clinical use.

Limitação

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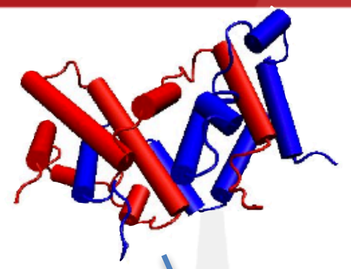
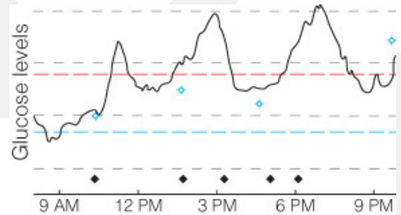
Observar e criar hipótese

- IFN-gamma atrapalha o metabolismo de glicose.
- Diabetes tipo 2 é um desequilíbrio no metabolismo.
- Akkermansia muciniphila associada à diabetes.
- Inflamação associada à diabetes.

"Chronic inflammation impairs metabolic homeostasis and is intimately correlated with the pathogenesis of type 2 diabetes. The pro-inflammatory cytokine IFN-gamma is an integral part of the metabolic inflammation circuit and contributes significantly to metabolic dysfunction. The underlying mechanism, however, remains largely unknown."





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Interferon gamma (IFN-γ) disrupts energy expenditure and metabolic homeostasis by suppressing SIRT1 transcription

Ping Li[1,6], Yuhao Zhao[1,6], Xiaoyan Wu[2,6], Minjie Xia[1], Mingming Fang[1,4], Yasumasa Iwasaki[5], Jiahao Sha[1], Qi Chen[1], Yong Xu[1,*] and Aiguo Shen[3,*]

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