Comparative analyses of fecal microbiota in Chinese isolated Yao population, minority Zhuang and rural Han by 16sRNA sequencing

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Figure 1S. The relationship between clean reads and OUT counts in the three ethnic groups.

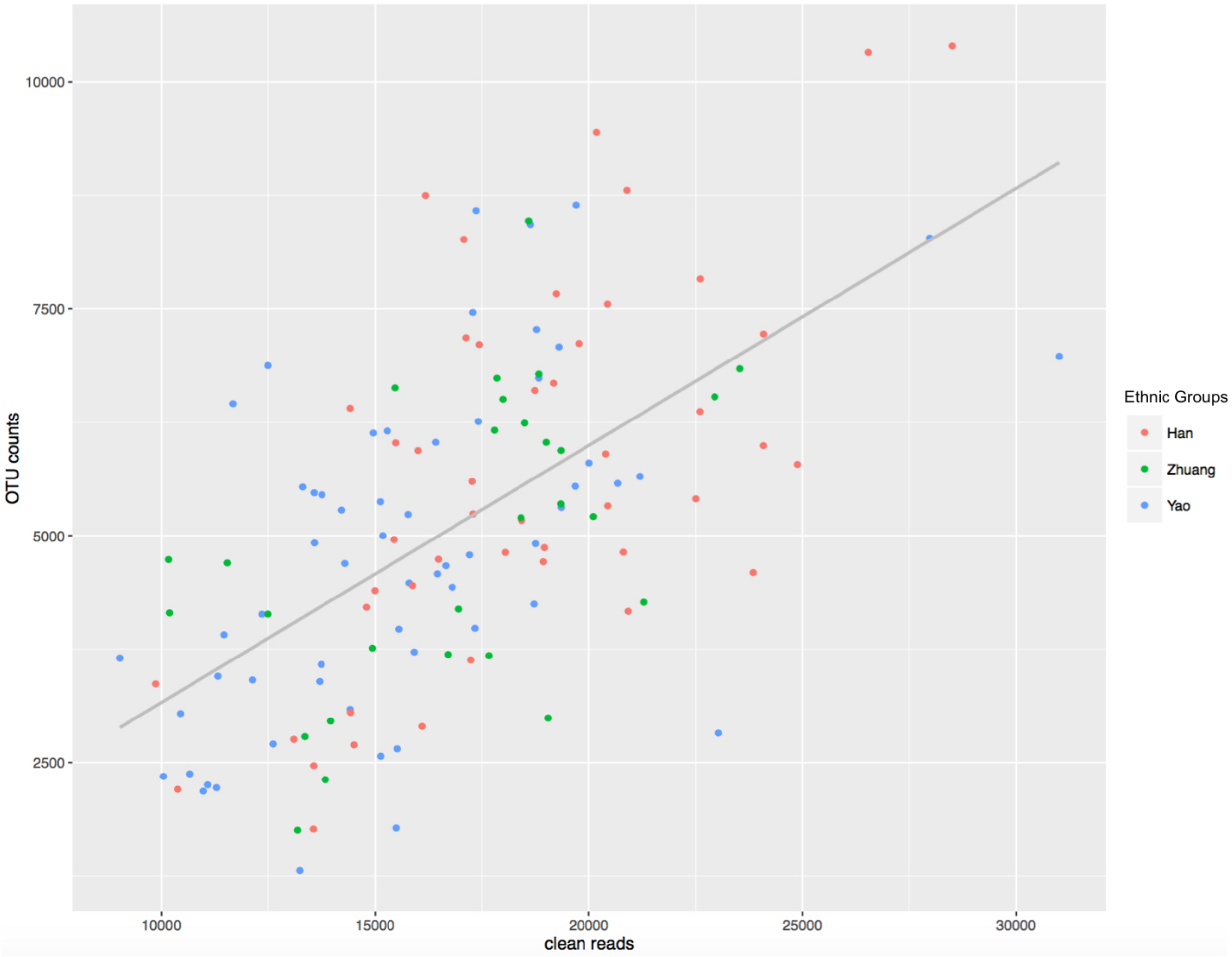
Figure 2S. The other alpha-diversity and beta-diversity analysis in three ethnic groups. (a) The Shannon index, PD_whole_tree and observed species at 4200 sequences per sample in the rarefaction curve; P was calculated from the analysis of variance. (b) The weighted Unifrac, Bray-curtis and Jensen-Shannon distance; P was calculated from the permutational multivariate analysis of variance.

Figure 3S. The relative proportions of genus presence in the three ethnic groups. (a) The pattern of the median proportions of genus presence. (b) The presence proportions of two significant genera; p was calculated from Fisher's exact test.

Figure 4S. The LEfSe results by comparison of the Zhuang and Han groups. (a) The linear discriminant analysis. (b) The cladograms report. Prefixes represent abbreviations for the taxonomic rank of each taxa: phylum (p__), class (c__), etc.

Figure 5S. The importance and distribution of serum biomarkers in the three ethnic groups. (a) The importance of each biomarker in random forest classification; * indicates the significant biomarkers from the Kruskal-Wallis rank-sum test. (b) The distribution of the significant biomarkers in routine blood tests and liver function; p was calculated from the Kruskal-Wallis rank-sum test. The bars between the groups indicate $p<0.05$ after multiple comparisons following a significant Kruskal-Wallis test.

Figure. 1S



10000
7500
5000
2500
OTU counts
10000
15000
20000
25000
30000
clean reads
Ethnic Groups
Han
Zhuang
Yao

Figure. 2S

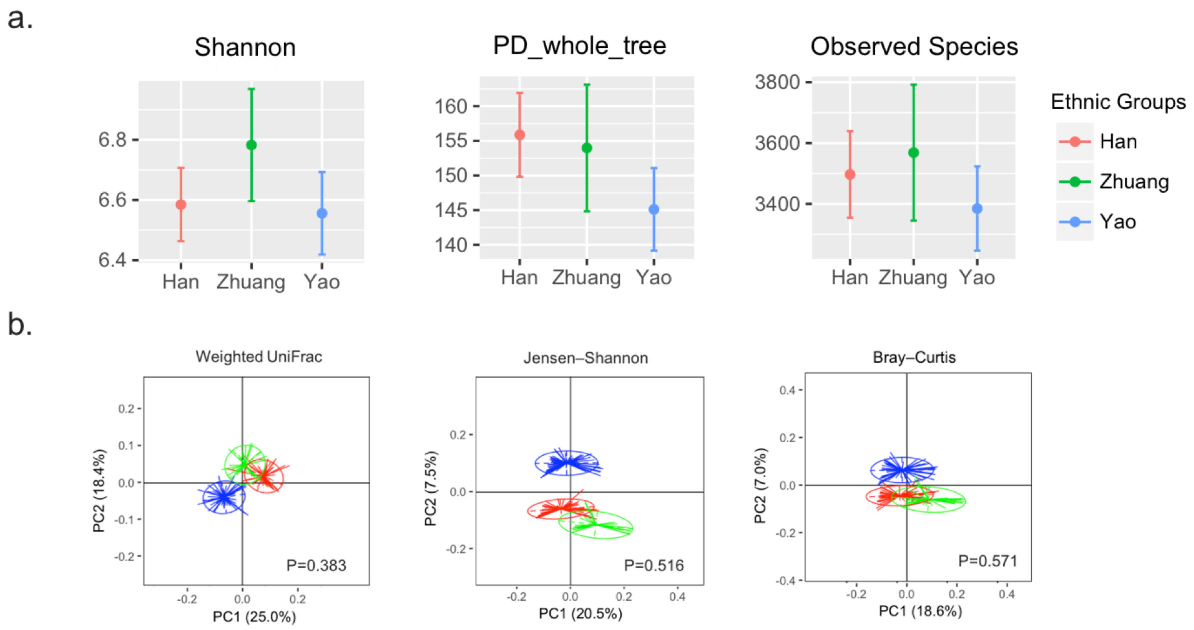

a.
Shannon
6.8
6.6
6.4
Han
Zhuang
Yao
PD_whole_tree
160
155
150
145
140
Han
Zhuang
Yao
Observed Species
3800
3600
3400
Han
Zhuang
Yao
Ethnic Groups
Han
Zhuang
Yao
b.
Weighted UniFrac
PC2 (18.4%)
0.2
0.1
0.0
-0.1
-0.2
-0.2
0.0
0.2
PC1 (25.0%)
P=0.383
Jensen–Shannon
PC2 (7.5%)
0.2
0.0
-0.2
-0.2
0.0
0.2
0.4
PC1 (20.5%)
P=0.516
Bray–Curtis
PC2 (7.0%)
0.4
0.2
0.0
-0.2
-0.4
-0.2
0.0
0.2
0.4
PC1 (18.6%)
P=0.571

Figure. 3S

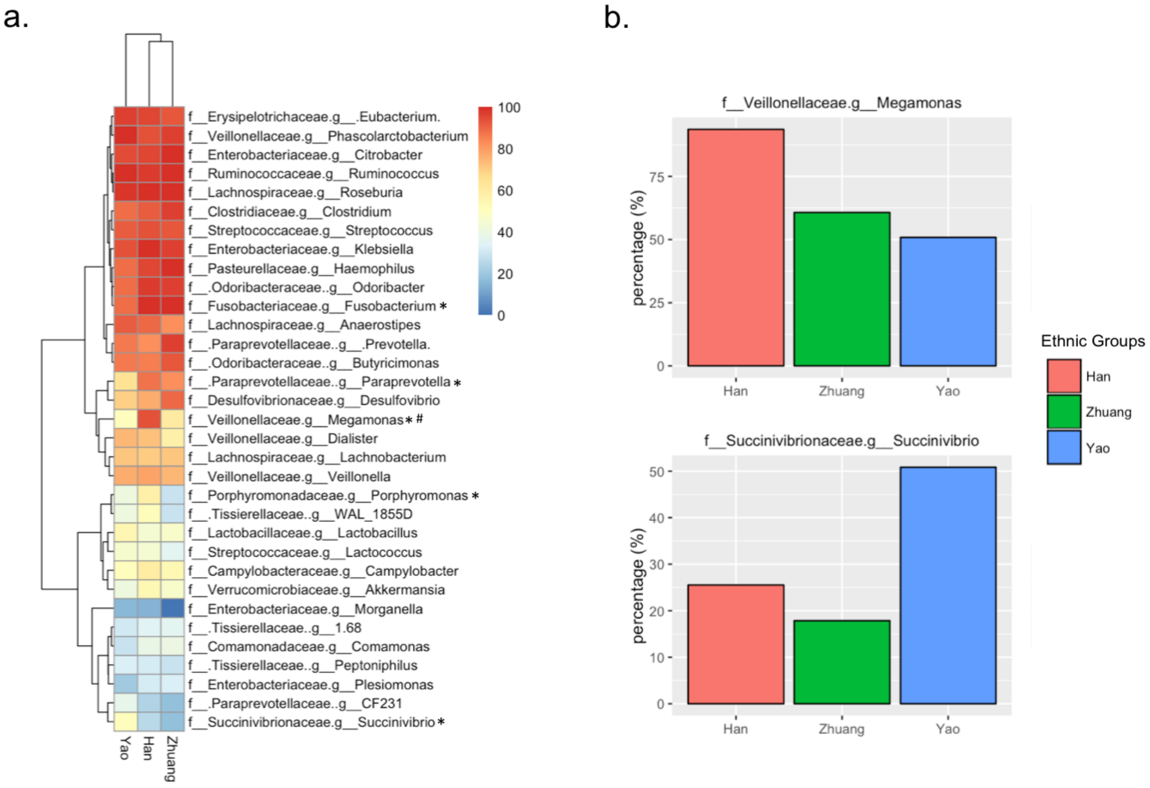

a.
100
80
60
40
20
0
f__Erysipelotrichaceae.g__.Eubacterium.
f__Veillonellaceae.g__Phascolarctobacterium
f__Enterobacteriaceae.g__Citrobacter
f__Ruminococcaceae.g__Ruminococcus
f__Lachnospiraceae.g__Roseburia
f__Clostridiaceae.g__Clostridium
f__Streptococcaceae.g__Streptococcus
f__Enterobacteriaceae.g__Klebsiella
f__Pasteurellaceae.g__Haemophilus
f__.Odoribacteraceae..g__Odoribacter
f__Fusobacteriaceae.g__Fusobacterium *
f__Lachnospiraceae.g__Anaerostipes
f__.Paraprevotellaceae..g__.Prevotella.
f__.Odoribacteraceae..g__Butyricimonas
f__.Paraprevotellaceae..g__Paraprevotella *
f__Desulfovibrionaceae.g__Desulfovibrio
f__Veillonellaceae.g__Megamonas * #
f__Veillonellaceae.g__Dialister
f__Lachnospiraceae.g__Lachnobacterium
f__Veillonellaceae.g__Veillonella
f__Porphyromonadaceae.g__Porphyromonas *
f__.Tissierellaceae..g__WAL_1855D
f__Lactobacillaceae.g__Lactobacillus
f__Streptococcaceae.g__Lactococcus
f__Campylobacteraceae.g__Campylobacter
f__Verrucomicrobiaceae.g__Akkermansia
f__Enterobacteriaceae.g__Morganella
f__.Tissierellaceae..g__1.68
f__Comamonadaceae.g__Comamonas
f__.Tissierellaceae..g__Peptoniphilus
f__Enterobacteriaceae.g__Plesiomonas
f__.Paraprevotellaceae..g__CF231
f__Succinivibrionaceae.g__Succinivibrio *
Yao
Han
Zhuang
b.
f__Veillonellaceae.g__Megamonas
percentage (%)
75
50
25
0
Han
Zhuang
Yao
Ethnic Groups
Han
Zhuang
Yao
f__Succinivibrionaceae.g__Succinivibrio
percentage (%)
50
40
30
20
10
0
Han
Zhuang
Yao

Figure. S4

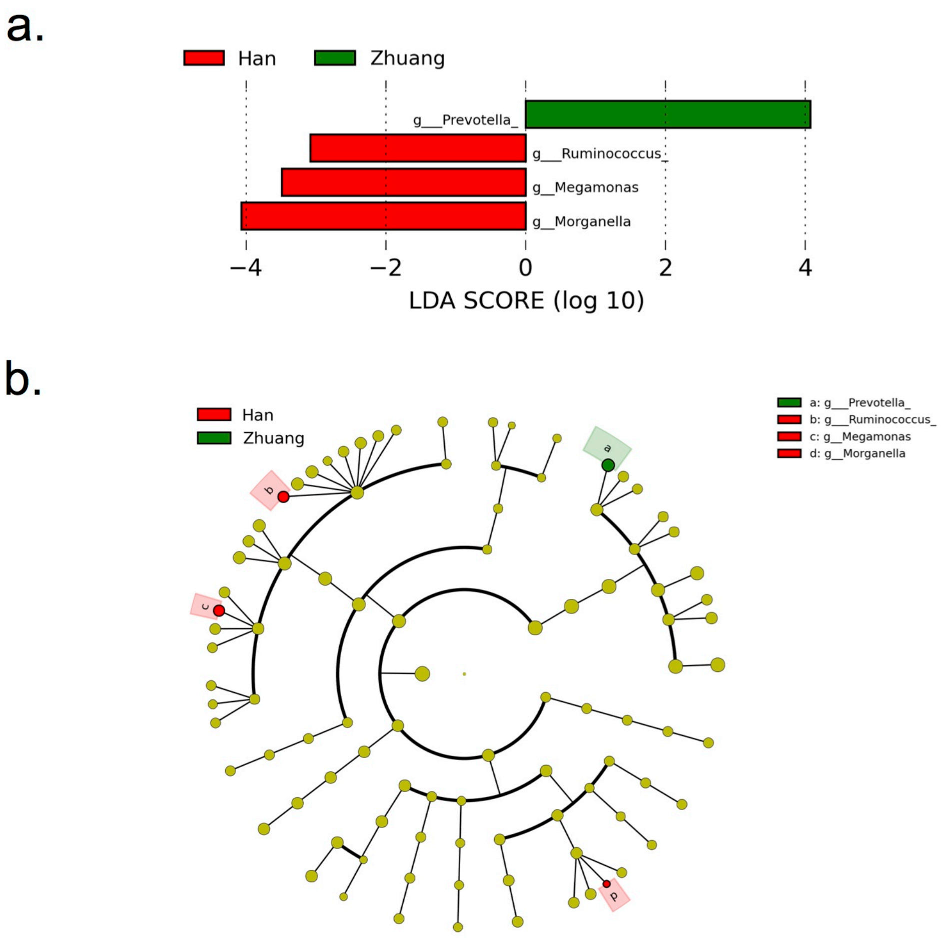
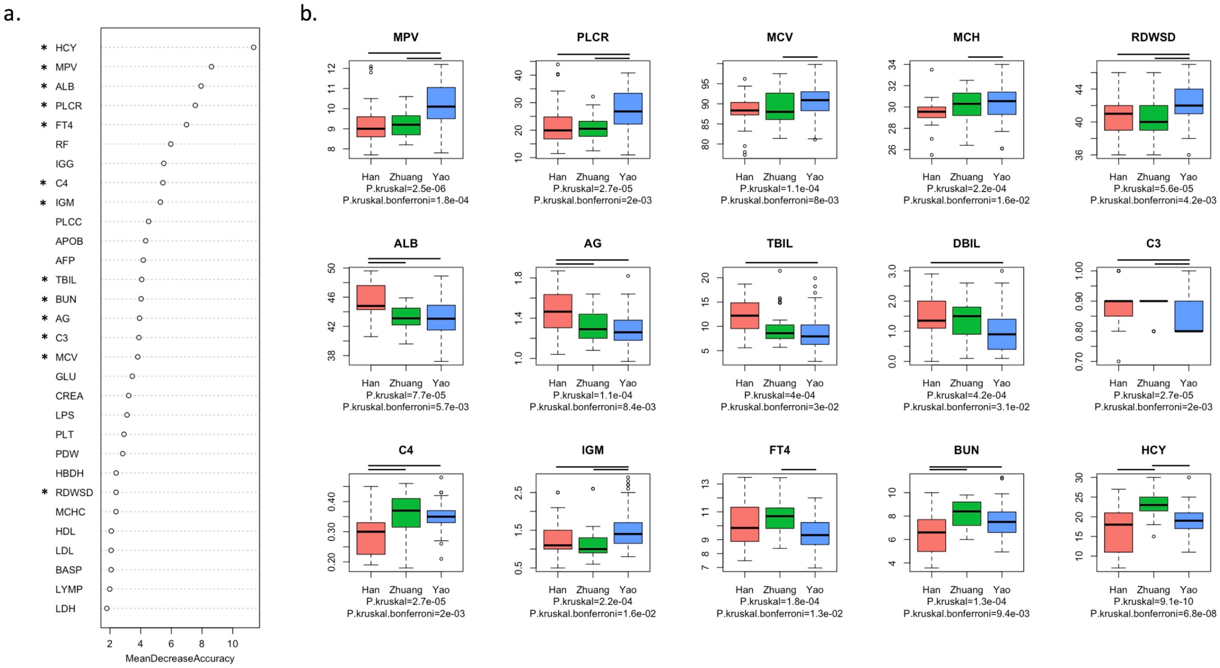

a.
Han
Zhuang
g___Prevotella_
g___Ruminococcus_
g__Megamonas
g__Morganella
−4
−2
0
2
4
LDA SCORE (log 10)
b.
Han
Zhuang
a: g___Prevotella_
b: g___Ruminococcus_
c: g__Megamonas
d: g__Morganella
a
b
c
d

Figure. S5


a.
* HCY
* MPV
* ALB
* PLCR
* FT4
RF
IGG
* C4
* IGM
PLCC
APOB
AFP
* TBIL
* BUN
* AG
* C3
* MCV
GLU
CREA
LPS
PLT
PDW
HBDH
* RDWSD
MCHC
HDL
LDL
BASP
LYMP
LDH
2 4 6 8 10
MeanDecreaseAccuracy
b.
MPV
Han Zhuang Yao
P.kruskal=2.5e-06
P.kruskal.bonferroni=1.8e-04
PLCR
Han Zhuang Yao
P.kruskal=2.7e-05
P.kruskal.bonferroni=2e-03
MCV
Han Zhuang Yao
P.kruskal=1.1e-04
P.kruskal.bonferroni=8e-03
MCH
Han Zhuang Yao
P.kruskal=2.2e-04
P.kruskal.bonferroni=1.6e-02
RDWSD
Han Zhuang Yao
P.kruskal=5.6e-05
P.kruskal.bonferroni=4.2e-03
ALB
Han Zhuang Yao
P.kruskal=7.7e-05
P.kruskal.bonferroni=5.7e-03
AG
Han Zhuang Yao
P.kruskal=1.1e-04
P.kruskal.bonferroni=8.4e-03
TBIL
Han Zhuang Yao
P.kruskal=4e-04
P.kruskal.bonferroni=3e-02
DBIL
Han Zhuang Yao
P.kruskal=4.2e-04
P.kruskal.bonferroni=3.1e-02
C3
Han Zhuang Yao
P.kruskal=2.7e-05
P.kruskal.bonferroni=2e-03
C4
Han Zhuang Yao
P.kruskal=2.7e-05
P.kruskal.bonferroni=2e-03
IGM
Han Zhuang Yao
P.kruskal=2.2e-04
P.kruskal.bonferroni=1.6e-02
FT4
Han Zhuang Yao
P.kruskal=1.8e-04
P.kruskal.bonferroni=1.3e-02
BUN
Han Zhuang Yao
P.kruskal=1.3e-04
P.kruskal.bonferroni=9.4e-03
HCY
Han Zhuang Yao
P.kruskal=9.1e-10
P.kruskal.bonferroni=6.8e-08