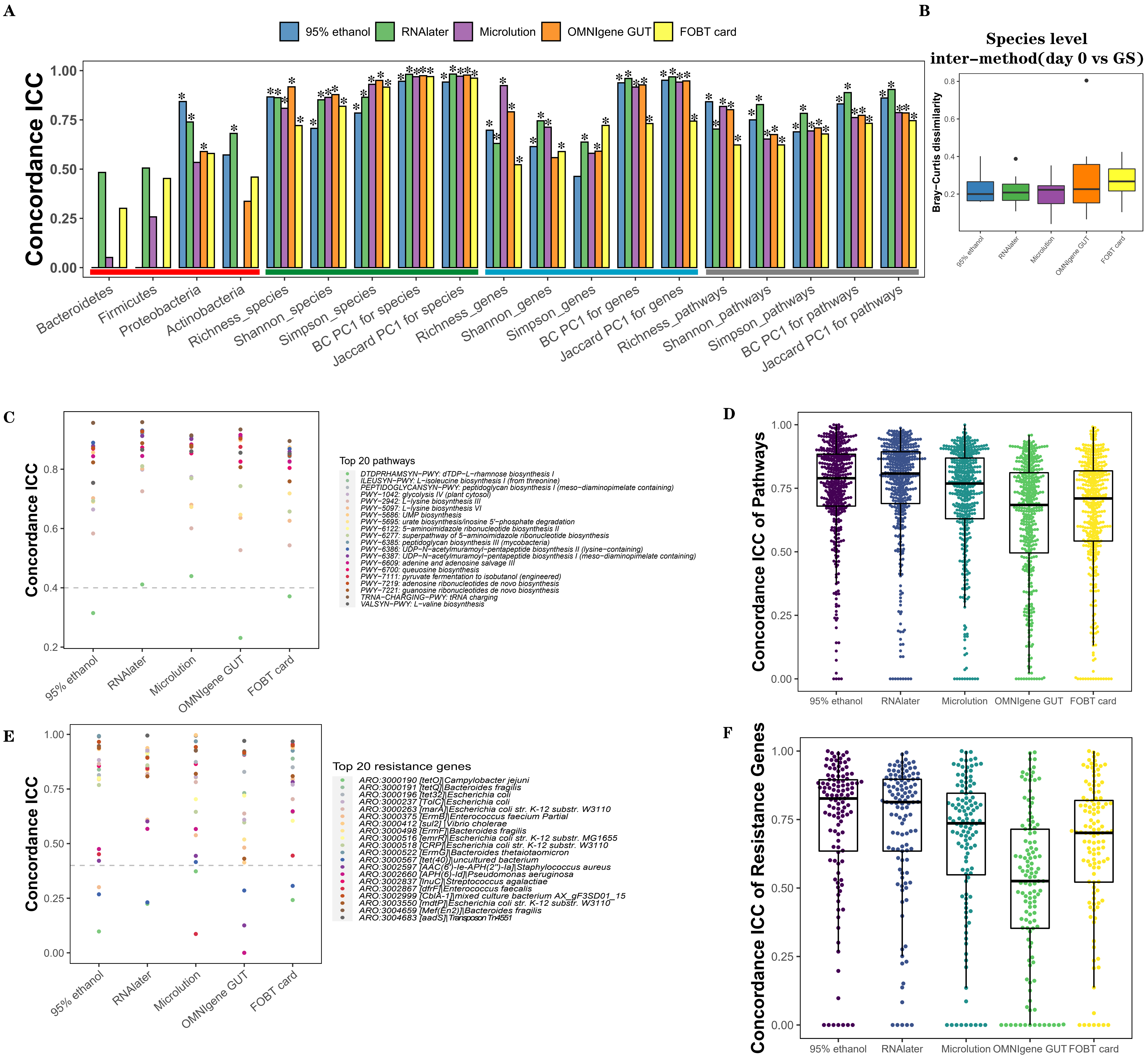
A
95% ethanol
RNAlater
Microlution
OMNIgene GUT
FOBT card
Concordance ICC
1.00
0.75
0.50
0.25
0.00
Bacteroidetes
Firmicutes
Proteobacteria
Actinobacteria
Richness_species
Shannon_species
Simpson_species
BC PC1 for species
Jaccard PC1 for species
Richness_genes
Shannon_genes
Simpson_genes
BC PC1 for genes
Jaccard PC1 for genes
Richness_pathways
Shannon_pathways
Simpson_pathways
BC PC1 for pathways
Jaccard PC1 for pathways
B
Species level
inter−method(day 0 vs GS)
Bray−Curtis dissimilarity
0.8
0.6
0.4
0.2
95% ethanol
RNAlater
Microlution
OMNIgene GUT
FOBT card
C
Concordance ICC
0.8
0.6
0.4
0.2
95% ethanol
RNAlater
Microlution
OMNIgene GUT
FOBT card
Top 20 pathways
DTDPRHAMSYN−PWY: dTDP−L−rhamnose biosynthesis I
ILEUSYN−PWY: L−isoleucine biosynthesis I (from threonine)
PEPTIDOGLYCANSYN−PWY: peptidoglycan biosynthesis I (meso−diaminopimelate containing)
PWY−1042: glycolysis IV (plant cytosol)
PWY−2942: L−lysine biosynthesis III
PWY−5097: L−lysine biosynthesis VI
PWY−5686: UMP biosynthesis
PWY−5695: urate biosynthesis/inosine 5'−phosphate degradation
PWY−6122: 5−aminoimidazole ribonucleotide biosynthesis II
PWY−6277: superpathway of 5−aminoimidazole ribonucleotide biosynthesis
PWY−6385: peptidoglycan biosynthesis III (mycobacteria)
PWY−6386: UDP−N−acetylmuramoyl−pentapeptide biosynthesis II (lysine−containing)
PWY−6387: UDP−N−acetylmuramoyl−pentapeptide biosynthesis I (meso−diaminopimelate containing)
PWY−6609: adenine and adenosine salvage III
PWY−6700: queuosine biosynthesis
PWY−7111: pyruvate fermentation to isobutanol (engineered)
PWY−7219: adenosine ribonucleotides de novo biosynthesis
PWY−7221: guanosine ribonucleotides de novo biosynthesis
TRNA−CHARGING−PWY: tRNA charging
VALSYN−PWY: L−valine biosynthesis
D
Concordance ICC of Pathways
1.00
0.75
0.50
0.25
0.00
95% ethanol
RNAlater
Microlution
OMNIgene GUT
FOBT card
E
Concordance ICC
1.00
0.75
0.50
0.25
0.00
95% ethanol
RNAlater
Microlution
OMNIgene GUT
FOBT card
Top 20 resistance genes
ARO:3000190 [tetO]|Campylobacter jejuni
ARO:3000191 [tetQ]|Bacteroides fragilis
ARO:3000196 [tet32]|Escherichia coli
ARO:3000237 [TolC]|Escherichia coli
ARO:3000263 [marA]|Escherichia coli str. K-12 substr. W3110
ARO:3000375 [ErmB]|Enterococcus faecium Partial
ARO:3000412 [sul2] |Vibrio cholerae
ARO:3000498 [ErmF]|Bacteroides fragilis
ARO:3000516 [emrR]|Escherichia coli str. K-12 substr. MG1655
ARO:3000518 [CRP]|Escherichia coli str. K-12 substr. W3110
ARO:3000522 [ErmG]|Bacteroides thetaiotaomicron
ARO:3000567 [tet(40)]|uncultured bacterium
ARO:3002597 [AAC(6')-Ie-APH(2'')-Ia]|Staphylococcus aureus
ARO:3002660 [APH(6)-Id]|Pseudomonas aeruginosa
ARO:3002837 [lnuC]|Streptococcus agalactiae
ARO:3002867 [dfrF]|Enterococcus faecalis
ARO:3002999 [CblA-1]|mixed culture bacterium AX_gF3SD01_15
ARO:3003550 [mdtP]|Escherichia coli str. K-12 substr. W3110
ARO:3004659 [Mef(En2)]|Bacteroides fragilis
ARO:3004683 [aadS]|Transposon Tn4551
F
Concordance ICC of Resistance Genes
1.00
0.75
0.50
0.25
0.00
95% ethanol
RNAlater
Microlution
OMNIgene GUT
FOBT card