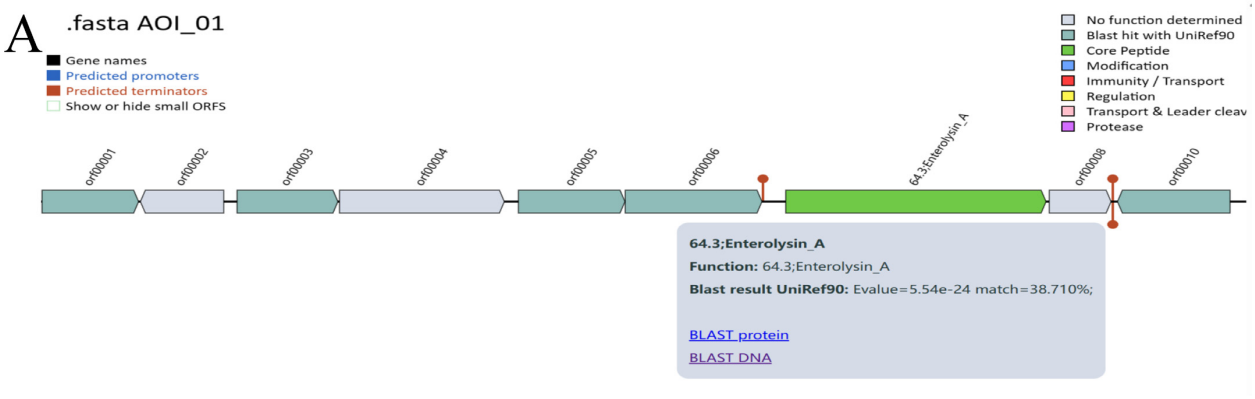
Table S1: Assembly of L. salivarius GX118 genome.

Attribute	Indicators of GX118
Genome size (bp)	2,034,343
Gene number	2,005
Gene length/Genome(%)	88.63
Sequence GC%	32.63
N50	127,744
Number of tRNA	66
Gls number	10
Number of Prophage	13
Number of T3PKS	1
Number of lassopeptide	7
Number of CRISPR loci	2

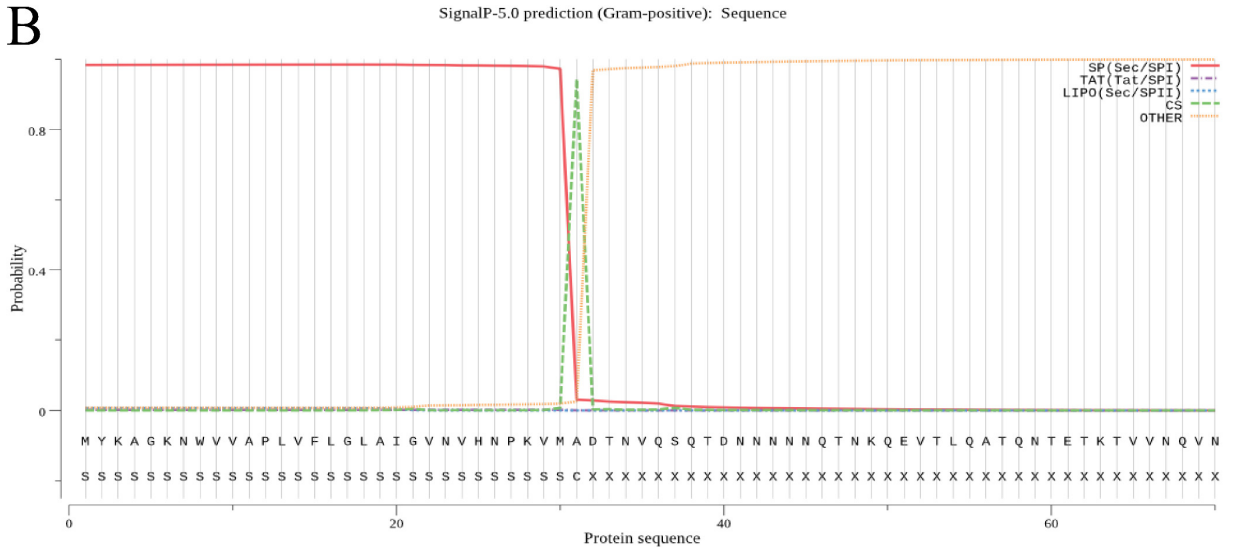
Table S2: The statistical estimates of alpha diversity of gut microbiota.

Group	Shannon	Simpson	Chao1	ACE
CK7	1.79±0.72	0.42±0.19	484.34±212.04^{ab}	503.08±217.08^{ab}
A7	3.47±0.76	0.76±0.19	529.43±276.42^{ab}	482.11±182.38^{ab}
B7	2.64±1.02	0.59±0.24	329.96±140.39^{a}	335.84±140.76^{a}
CK14	2.55±1.86	0.55±0.41	370.73±109.83^{a}	389.06±107.22^{a}
A14	1.71±1.08	0.41±0.32	451.58±79.84^{ab}	477.18±70.83^{ab}
B14	1.65±0.55	0.32±0.12	329.61±125.76^{a}	341.35±132.99^{a}
CK21	1.89±1.80	0.39±0.41	362.97±150.40^{a}	373.86±147.62^{a}
A21	3.09±1.54	0.61±0.29	771.02±407.06^{b}	791.28±403.33^{b}
B21	2.33±1.34	0.50±0.28	395.98±157.77^{ab}	418.14±166.85^{a}

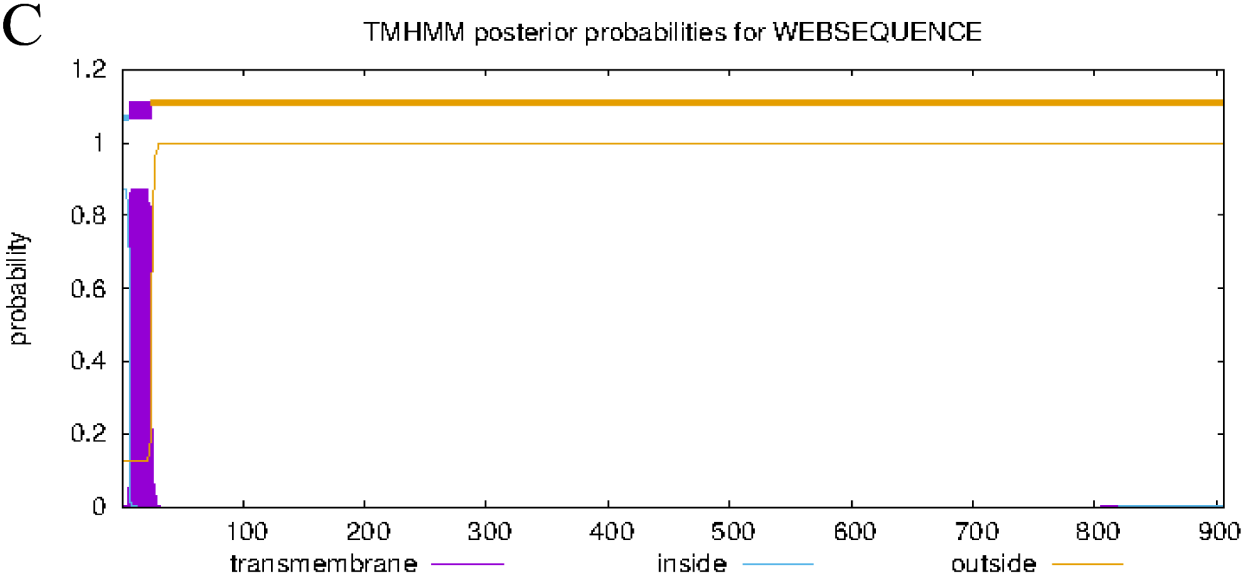
A


.fasta AOI_01
Gene names
Predicted promoters
Predicted terminators
Show or hide small ORFS
No function determined
Blast hit with UniRef90
Core Peptide
Modification
Immunity / Transport
Regulation
Transport & Leader cleav
Protease
orf00001
orf00002
orf00003
orf00004
orf00005
orf00006
64.3;Enterolysin_A
orf00008
orf00010
64.3;Enterolysin_A
Function: 64.3;Enterolysin_A
Blast result UniRef90: Evalue=5.54e-24 match=38.710%;
BLAST protein
BLAST DNA

B


SignalP-5.0 prediction (Gram-positive): Sequence
SP(Sec/SPI)
TAT(Tat/SPI)
LIPO(Sec/SPII)
CS
OTHER
Probability
0.8
0.4
0
M Y K A G K N W V V A P L V F L G L A I G V N V H N P K V M A D T N V Q S Q T D N N N N N Q T N K Q E V T L Q A T Q N T E T K T V V N Q V N
S S S S S S S S S S S S S S S S S S S S S S S S S S S S C X X X X X X X X X X X X X X X X X X X X X X X X X X X X X X X X X X X X X X X
0
20
40
60
Protein sequence

C


TMHMM posterior probabilities for WEBSEQUENCE
probability
1.2
1
0.8
0.6
0.4
0.2
0
100
200
300
400
500
600
700
800
900
transmembrane
inside
outside

D

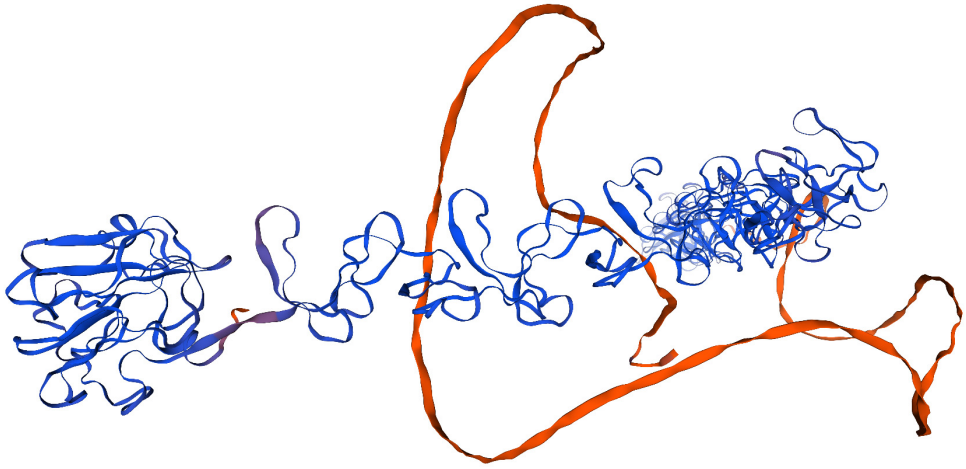


Figure S1: GX118 Bacteriocin Characteristics. (A) BAGEL4 software predicts bacteriocins. (B) Signal peptide prediction. (C) Transmembrane helix signalling. (D) Tertiary structural model of Enterolysin A.

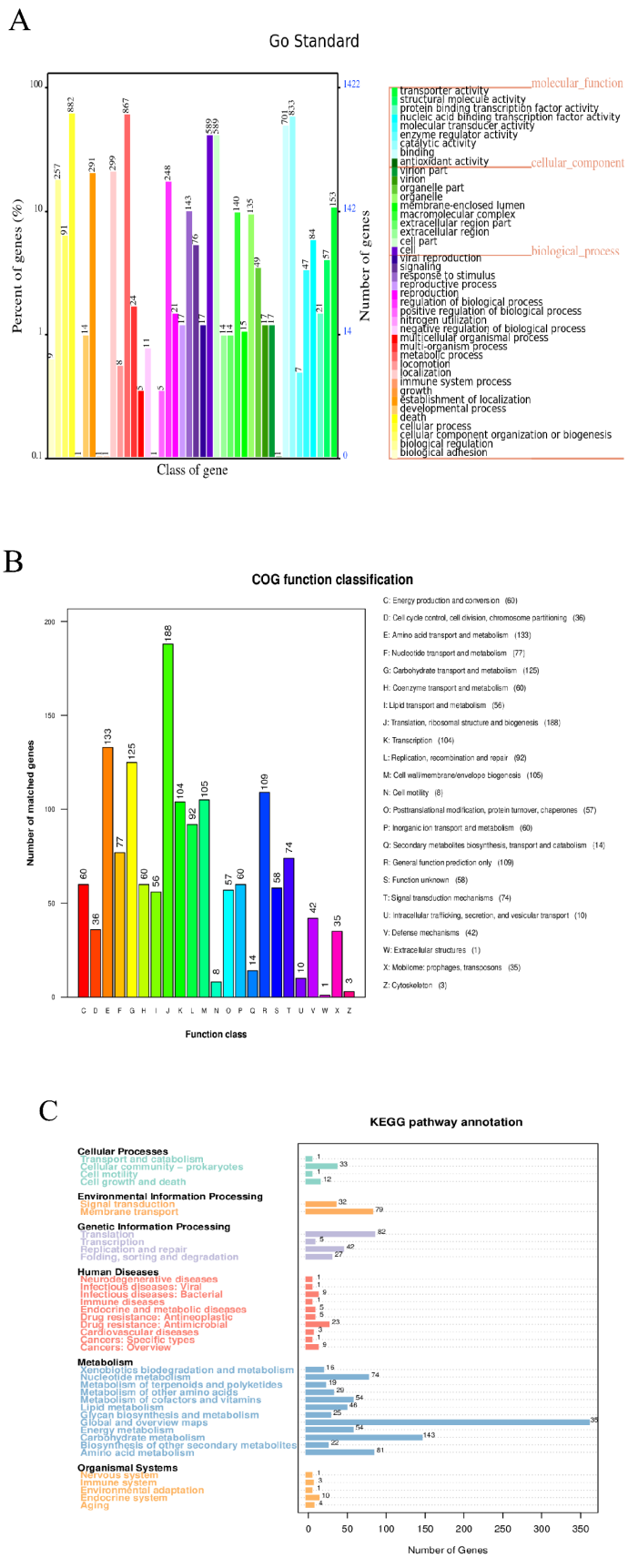
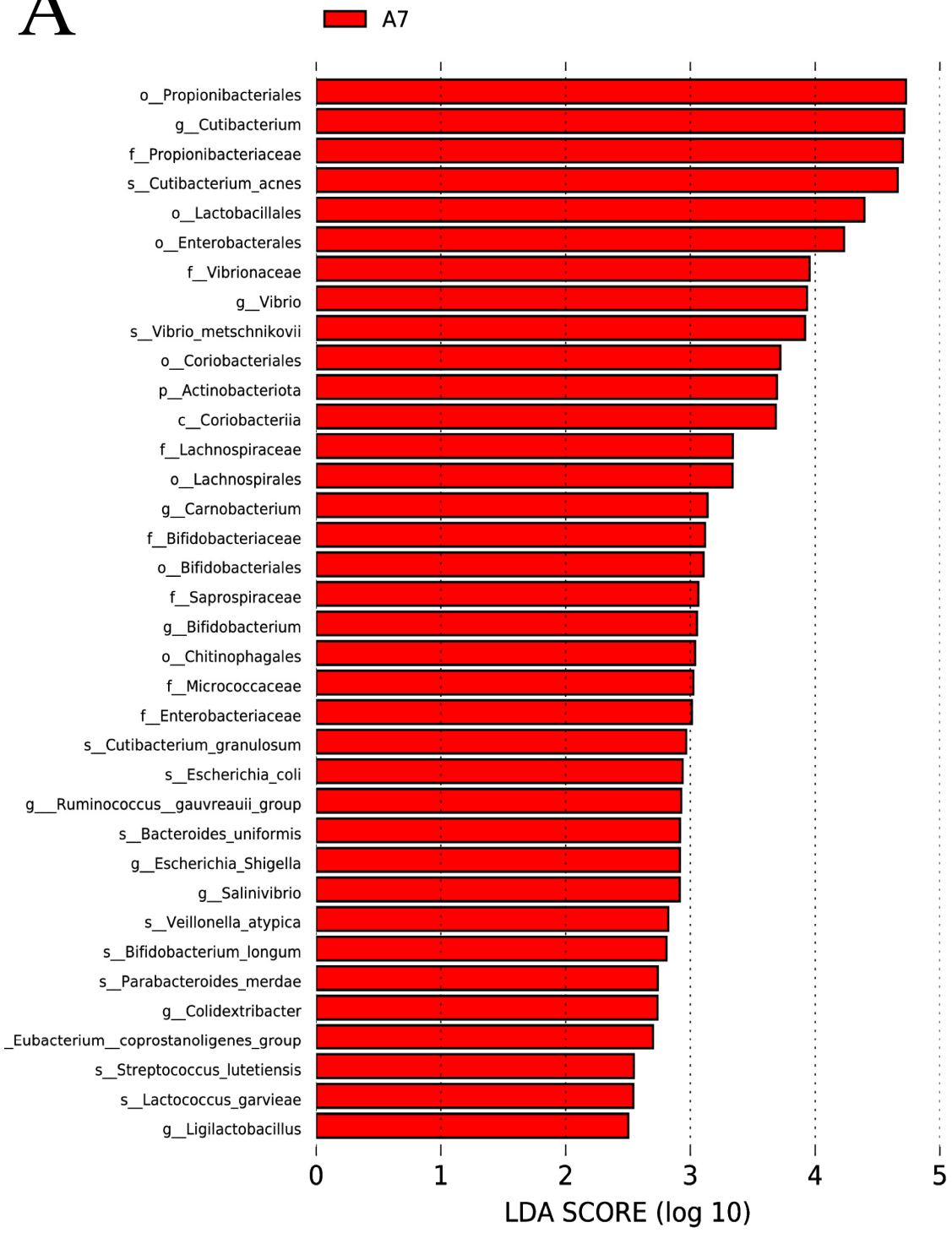
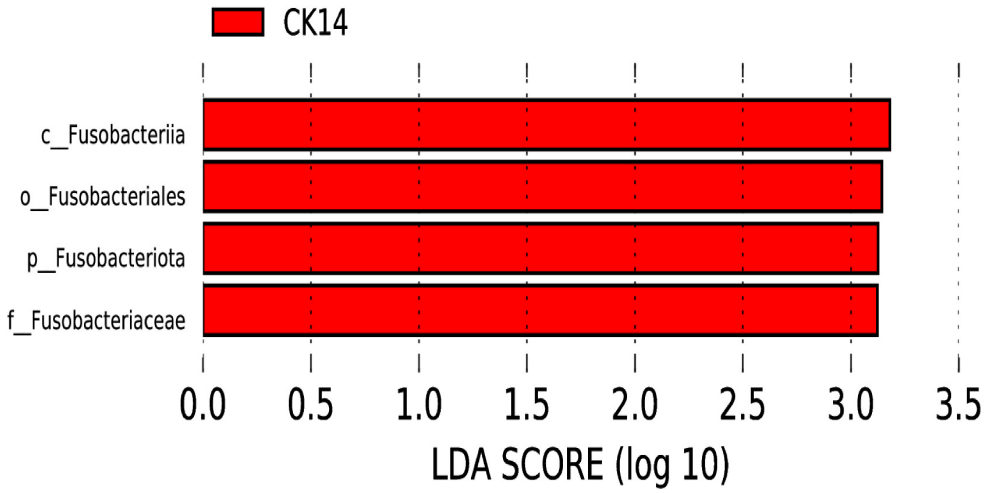


Figure S2 Gene function annotation of GX1118: (A) GO database annotations. (B) COG Functional Classification. (C) Classification of KEGG metabolic pathways.

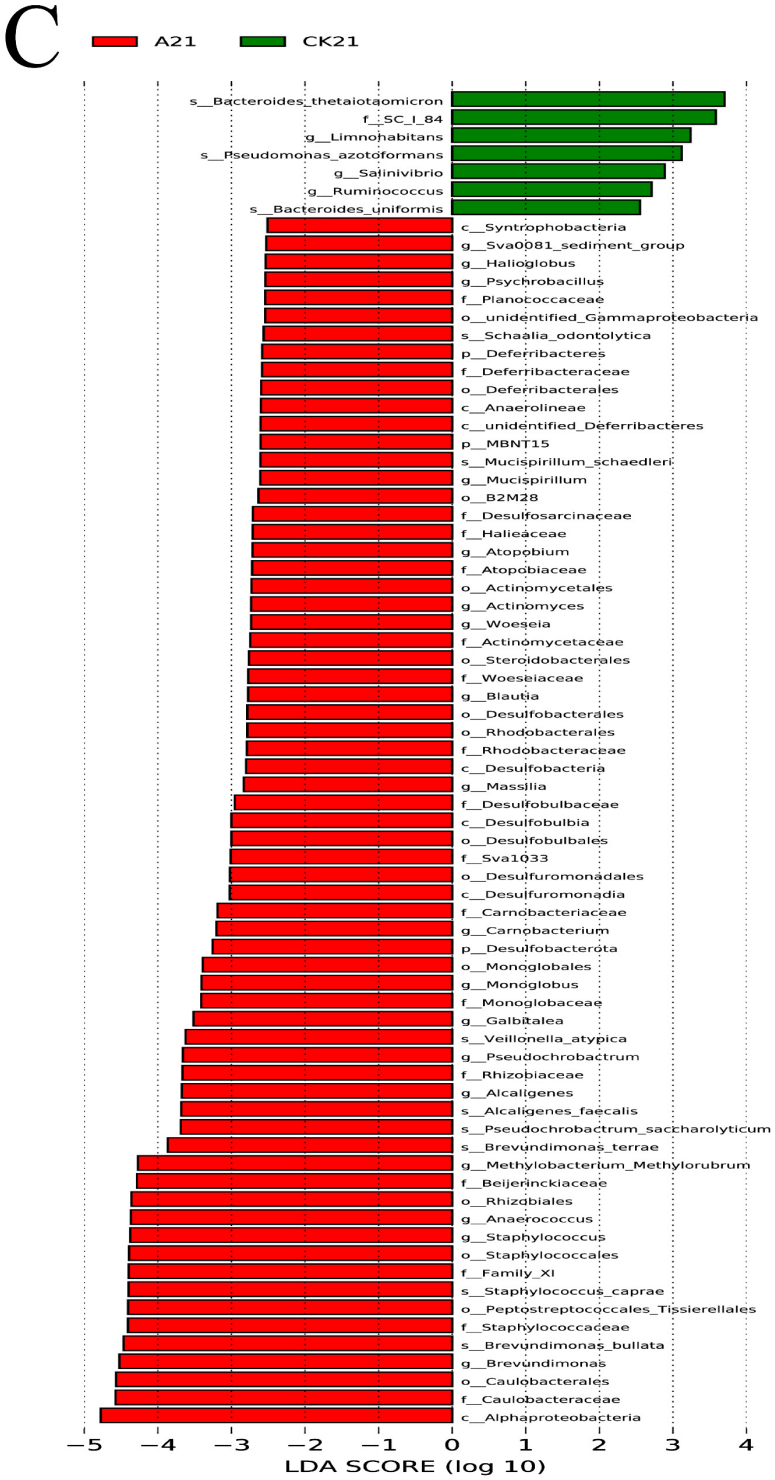
A


A7
o__Propionibacteriales
g__Cutibacterium
f__Propionibacteriaceae
s__Cutibacterium_acnes
o__Lactobacillales
o__Enterobacterales
f__Vibrionaceae
g__Vibrio
s__Vibrio_metschnikovii
o__Coriobacteriales
p__Actinobacteriota
c__Coriobacteriia
f__Lachnospiraceae
o__Lachnospirales
g__Carnobacterium
f__Bifidobacteriaceae
o__Bifidobacteriales
f__Saprospiraceae
g__Bifidobacterium
o__Chitinophagales
f__Micrococcaceae
f__Enterobacteriaceae
s__Cutibacterium_granulosum
s__Escherichia_coli
g__Ruminococcus_gauvreauii_group
s__Bacteroides_uniformis
g__Escherichia_Shigella
g__Salinivibrio
s__Veillonella_atypica
s__Bifidobacterium_longum
s__Parabacteroides_merdae
g__Colidextribacter
_Eubacterium__coprostanoligenes_group
s__Streptococcus_lutetiensis
s__Lactococcus_garvieae
g__Ligilactobacillus
0
1
2
3
4
5
LDA SCORE (log 10)

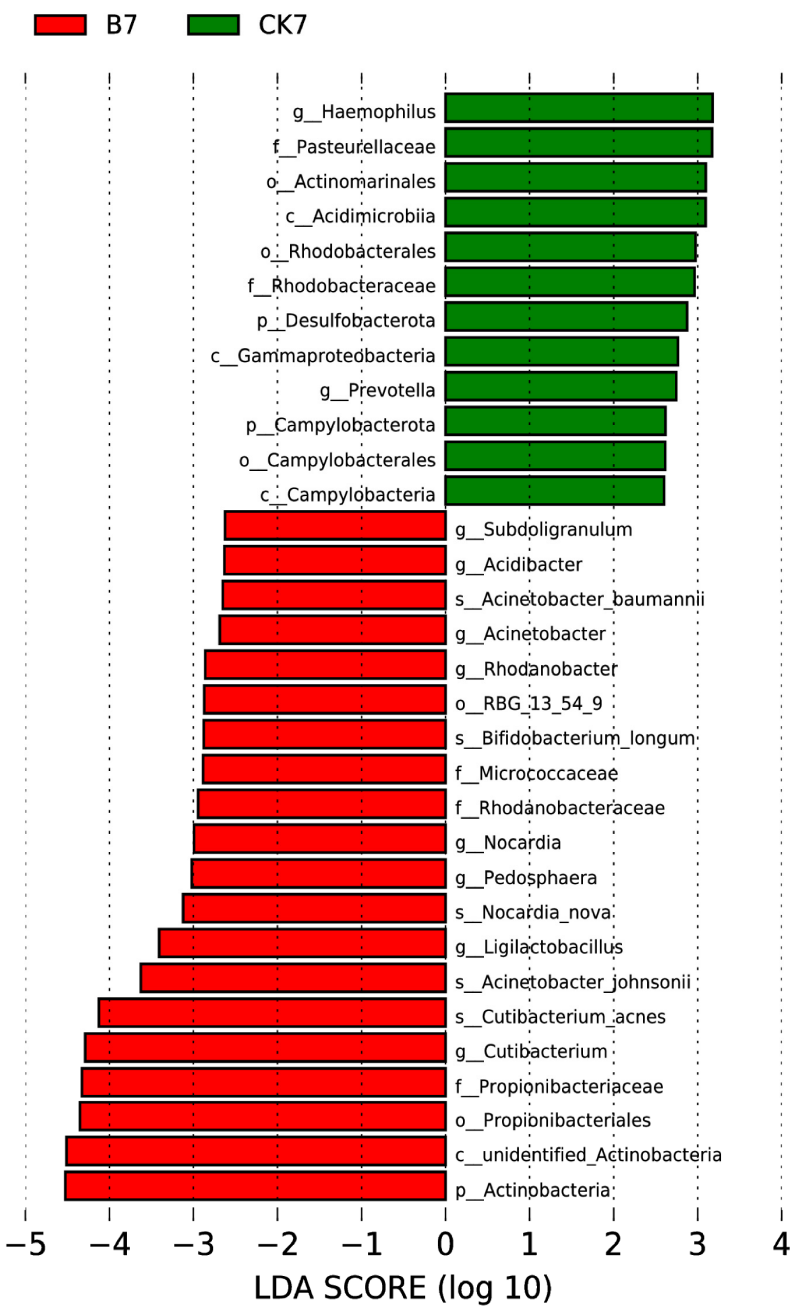
B

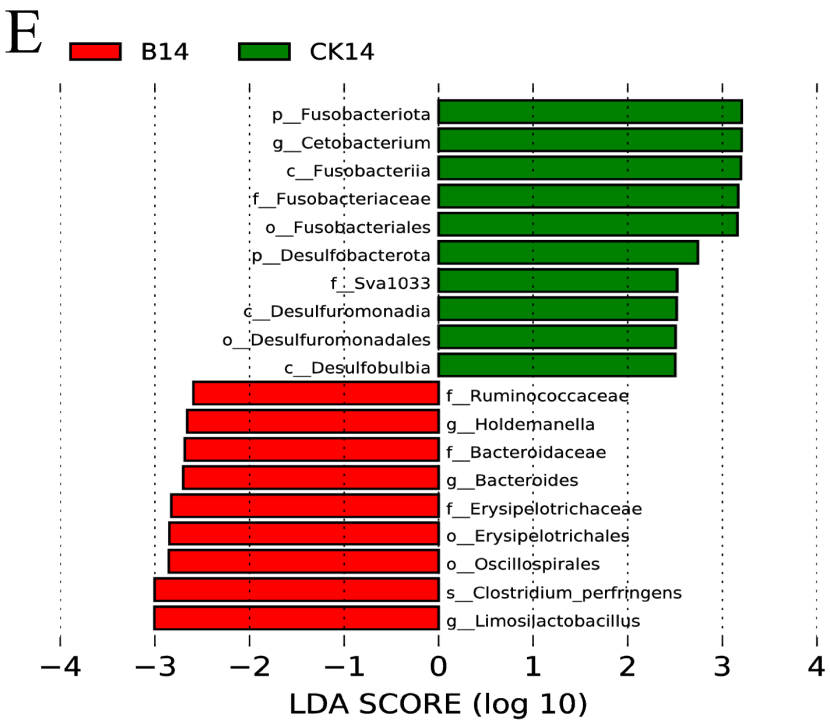

CK14
c__Fusobacteriia
o__Fusobacteriales
p__Fusobacteriota
f__Fusobacteriaceae
0.0
0.5
1.0
1.5
2.0
2.5
3.0
3.5
LDA SCORE (log 10)

C


A21
CK21
s__Bacteroides_thetaiotaomicron
f__SC_I_84
g__Limnohabitans
s__Pseudomonas_azotoformans
g__Sajinivibrio
g__Ruminococcus
s__Bacteroides_uniformis
c__Syntrophobacteria
g__Sva0081_sediment_group
g__Halioglobus
g__Psychrobacillus
f__Planococcaceae
o__unidentified_Gammaproteobacteria
s__Schaalia_odontolytica
p__Deferribacteres
f__Deferribacteraceae
o__Deferribacterales
c__Anaerolineae
c__unidentified_Deferribacteres
p__MBNT15
s__Mucispirillum_schaedleri
g__Mucispirillum
o__B2M28
f__Desulfosarcinaceae
f__Halieaceae
g__Atopobium
f__Atopobiaceae
o__Actinomycetales
g__Actinomyces
g__Woeseia
f__Actinomycetaceae
o__Steroidobacterales
f__Woeseiaceae
g__Blautia
o__Desulfobacterales
o__Rhodobacterales
f__Rhodobacteraceae
c__Desulfobacteria
g__Massilia
f__Desulfobulbaceae
c__Desulfobulbia
o__Desulfobulbales
f__Sva1033
o__Desulfuromonadales
c__Desulfuromonadia
f__Carnobacteriaceae
g__Carnobacterium
p__Desulfobacterota
o__Monoglobales
g__Monoglobus
f__Monoglobaceae
g__Galbitalea
s__Veillonella_atypica
g__Pseudochrobactrum
f__Rhizobiaceae
g__Alcaligenes
s__Alcaligenes_faecalis
s__Pseudochrobactrum_saccharolyticum
s__Brevundimonas_terrae
g__Methylobacterium_Methylorubrum
f__Beijerinckiaceae
o__Rhizobiales
g__Anaerococcus
g__Staphylococcus
o__Staphylococcales
f__Family_XI
s__Staphylococcus_caprae
o__Peptostreptococcales_Tissierellales
f__Staphylococcaceae
s__Brevundimonas_bullata
g__Brevundimonas
o__Caulobacterales
f__Caulobacteraceae
c__Alphaproteobacteria
−5
−4
−3
−2
−1
0
1
2
3
4
LDA SCORE (log 10)

D


B7
CK7
g__Haemophilus
f__Pasteurellaceae
o__Actinomarinales
c__Acidimicrobiia
o__Rhodobacterales
f__Rhodobacteraceae
p__Desulfobacterota
c__Gammaproteobacteria
g__Prevotella
p__Campylobacterota
o__Campylobacterales
c__Campylobacteria
g__Subdoligranulum
g__Acidibacter
s__Acinetobacter_baumannii
g__Acinetobacter
g__Rhodanobacter
o__RBG_13_54_9
s__Bifidobacterium_longum
f__Micrococcaceae
f__Rhodanobacteraceae
g__Nocardia
g__Pedosphaera
s__Nocardia_nova
g__Ligilactobacillus
s__Acinetobacter_johnsonii
s__Cutibacterium_acnes
g__Cutibacterium
f__Propionibacteriaceae
o__Propionibacteriales
c__unidentified_Actinobacteria
p__Actinobacteria
−5
−4
−3
−2
−1
0
1
2
3
4
LDA SCORE (log 10)


E
B14
CK14
p__Fusobacteriota
g__Cetobacterium
c__Fusobacteriia
f__Fusobacteriaceae
o__Fusobacteriales
p__Desulfobacterota
f__Sva1033
c__Desulfuromonadia
o__Desulfuromonadales
c__Desulfobulbia
f__Ruminococcaceae
g__Holdemanella
f__Bacteroidaceae
g__Bacteroides
f__Erysipelotrichaceae
o__Erysipelotrichales
o__Oscillospirales
s__Clostridium_perfringens
g__Limosilactobacillus
−4
−3
−2
−1
0
1
2
3
4
LDA SCORE (log 10)

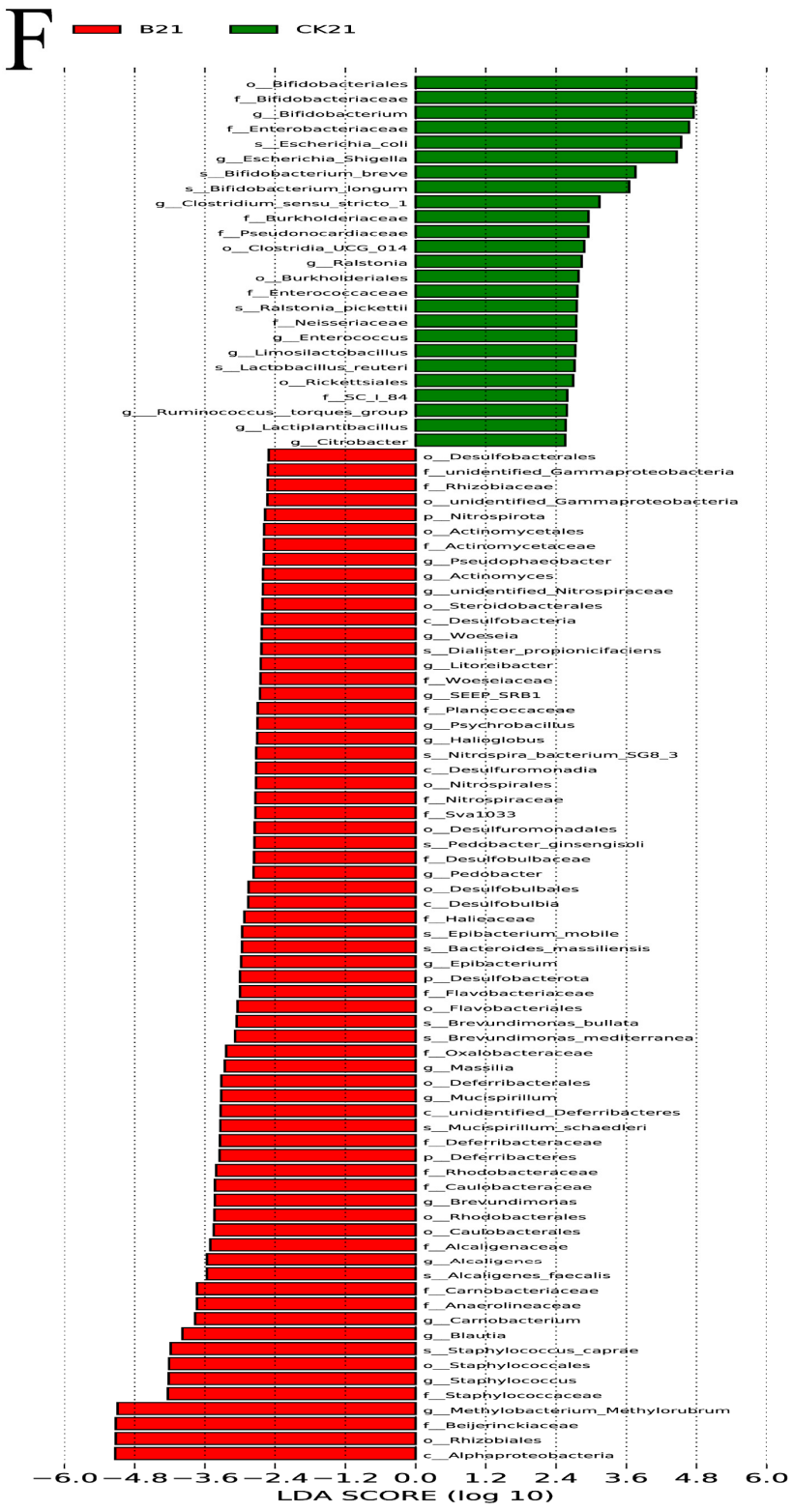


Figure S3: LEfSe analysis for differential abundant microbiota (LDA > 3, $P < 0.05$). A7, A14 and A21: supplementation of 10^7 cfu/ml GX118 per kilogram diet at day 7, day 14 and day 21, respectively; B7, B14 and B21: supplementation of 10^9 cfu/ml GX118 per kilogram diet at day 7, day 14 and day 21, respectively, CK: control group.

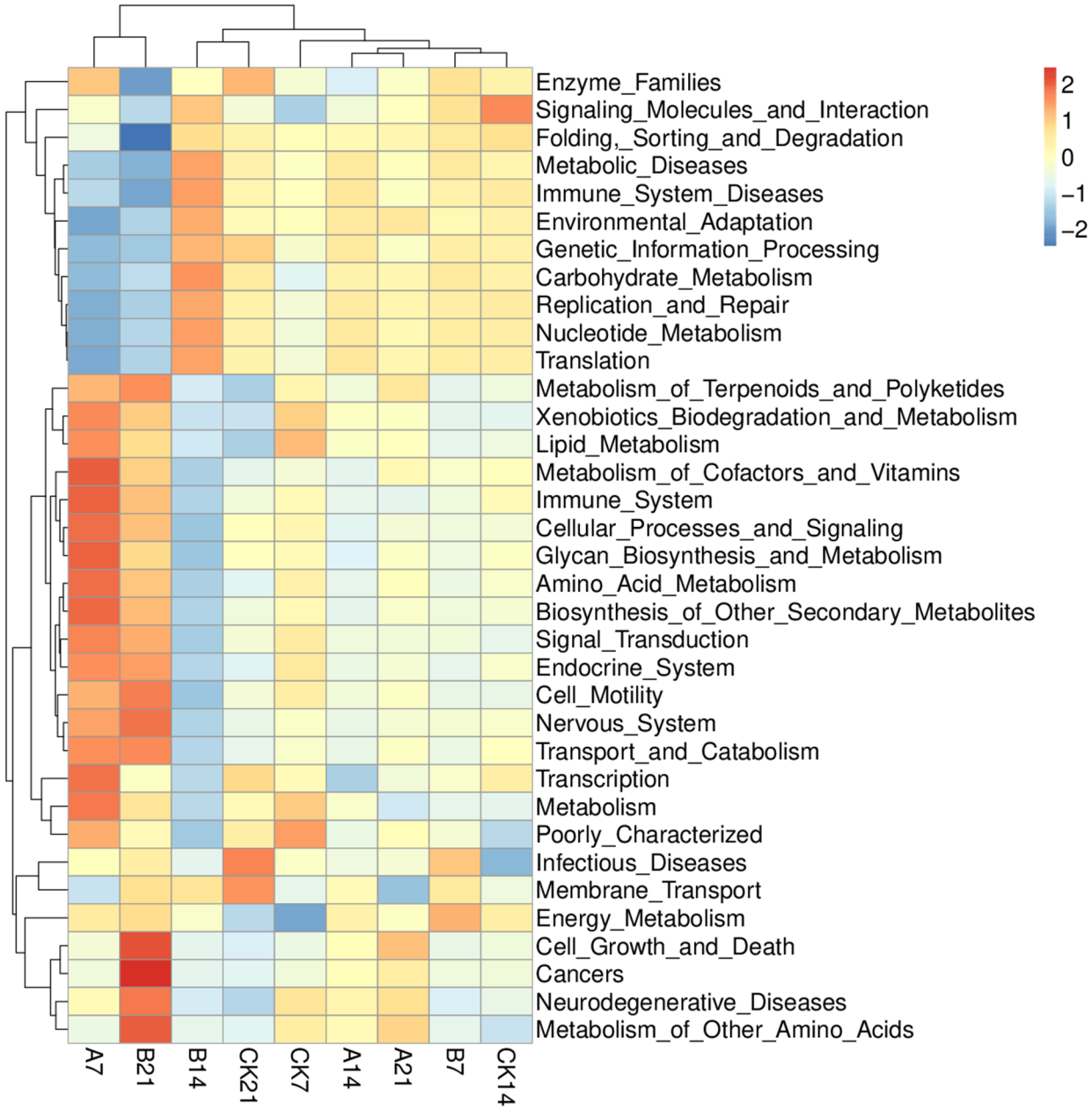


Figure S4 KEGG pathway of gut microbiota predicted by Tax4Fun analysis (First 35 predicted pathways). A7, A14 and A21: supplementation of 10^7 cfu/ml GX118 per kilogram diet at day 7, day 14 and day 21, respectively; B7, B14 and B21: supplementation of 10^9 cfu/ml GX118 per kilogram diet at day 7, day 14 and day 21, respectively, CK: control group.