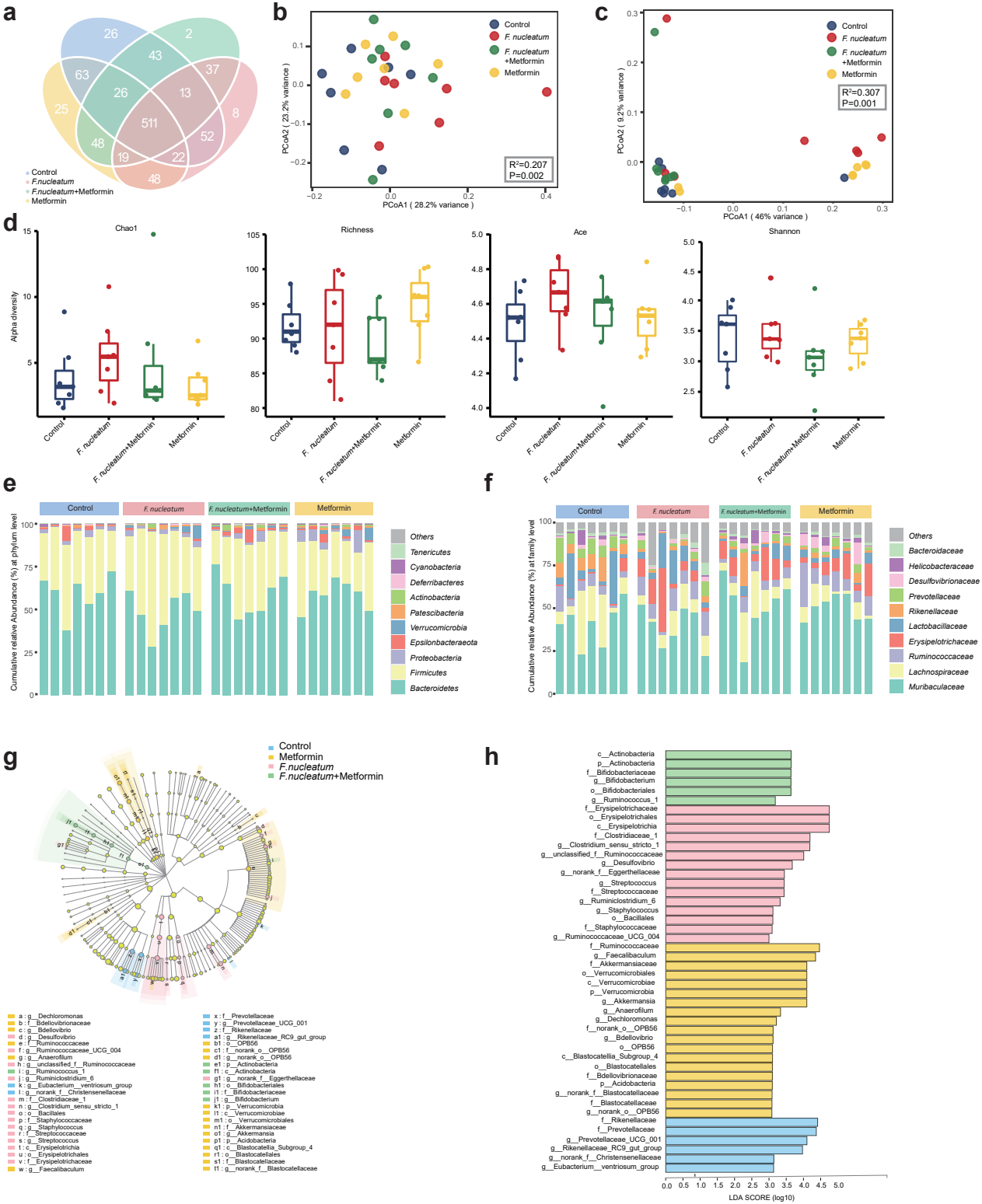
a
26
2
43
63
37
26
13
25
8
511
48
52
19
22
48
Control
F.nucleatum
F.nucleatum+Metformin
Metformin
b
Control
F. nucleatum
F. nucleatum +Metformin
Metformin
R²=0.207
P=0.002
PCoA1 (28.2% variance)
PCoA2 (23.2% variance)
c
Control
F. nucleatum
F. nucleatum +Metformin
Metformin
R²=0.307
P=0.001
PCoA1 (46% variance)
PCoA2 (9.2% variance)
d
Chao1
Richness
Ace
Shannon
Alpha diversity
Control
F. nucleatum
F. nucleatum+Metformin
Metformin
e
Control
F. nucleatum
F. nucleatum+Metformin
Metformin
Cumulative relative Abundance (%) at phylum level
Others
Tenericutes
Cyanobacteria
Deferribacteres
Actinobacteria
Patescibacteria
Verrucomicrobia
Epsilonbacteraeota
Proteobacteria
Firmicutes
Bacteroidetes
f
Control
F. nucleatum
F. nucleatum+Metformin
Metformin
Cumulative relative Abundance (%) at family level
Others
Bacteroidaceae
Helicobacteraceae
Desulfovibrionaceae
Prevotellaceae
Rikenellaceae
Lactobacillaceae
Erysipelotrichaceae
Ruminococcaceae
Lachnospiraceae
Muribaculaceae
g
Control
Metformin
F.nucleatum
F.nucleatum+Metformin
a : g__Dechloromonas
b : f__Bdellovibrionaceae
c : g__Bdellovibrio
d : g__Desulfovibrio
e : f__Ruminococcaceae
f : g__Ruminococcaceae_UCG_004
g : g__Anaerofilum
h : g__unclassified_f__Ruminococcaceae
i : g__Ruminococcus_1
j : g__Ruminiclostridium_6
k : g__Eubacterium__ventriosum_group
l : g__norank_f__Christensenellaceae
m : f__Clostridiaceae_1
n : g__Clostridium_sensu_stricto_1
o : o__Bacillales
p : f__Staphylococcaceae
q : g__Staphylococcus
r : f__Streptococcaceae
s : g__Streptococcus
t : c__Erysipelotrichia
u : o__Erysipelotrichales
v : f__Erysipelotrichaceae
w : g__Faecalibaculum
x : f__Prevotellaceae
y : g__Prevotellaceae_UCG_001
z : f__Rikenellaceae
a1 : g__Rikenellaceae_RC9_gut_group
b1 : o__OPB56
c1 : f__norank_o__OPB56
d1 : g__norank_o__OPB56
e1 : p__Actinobacteria
f1 : c__Actinobacteria
g1 : g__norank_f__Eggerthellaceae
h1 : o__Bifidobacteriales
i1 : f__Bifidobacteriaceae
j1 : g__Bifidobacterium
k1 : p__Verrucomicrobia
l1 : c__Verrucomicrobiae
m1 : o__Verrucomicrobiales
n1 : f__Akkermansiaceae
o1 : g__Akkermansia
p1 : p__Acidobacteria
q1 : c__Blastocatella_Subgroup_4
r1 : o__Blastocatellales
s1 : f__Blastocatellaceae
t1 : g__norank_f__Blastocatellaceae
h
c__Actinobacteria
p__Actinobacteria
f__Bifidobacteriaceae
g__Bifidobacterium
o__Bifidobacteriales
g__Ruminococcus_1
f__Erysipelotrichaceae
o__Erysipelotrichales
c__Erysipelotrichia
f__Clostridiaceae_1
g__Clostridium_sensu_stricto_1
g__unclassified_f__Ruminococcaceae
g__Desulfovibrio
g__norank_f__Eggerthellaceae
g__Streptococcus
f__Streptococcaceae
g__Ruminiclostridium_6
g__Staphylococcus
o__Bacillales
f__Staphylococcaceae
g__Ruminococcaceae_UCG_004
f__Ruminococcaceae
g__Faecalibaculum
f__Akkermansiaceae
o__Verrucomicrobiales
c__Verrucomicrobiae
p__Verrucomicrobia
g__Akkermansia
g__Anaerofilum
g__Dechloromonas
f__norank_o__OPB56
g__Bdellovibrio
o__OPB56
c__Blastocatellia_Subgroup_4
o__Blastocatellales
f__Bdellovibrionaceae
p__Acidobacteria
g__norank_f__Blastocatellaceae
f__Blastocatellaceae
g__norank_o__OPB56
f__Rikenellaceae
f__Prevotellaceae
g__Prevotellaceae_UCG_001
g__Rikenellaceae_RC9_gut_group
g__norank_f__Christensenellaceae
g__Eubacterium__ventriosum_group
LDA SCORE (log10)