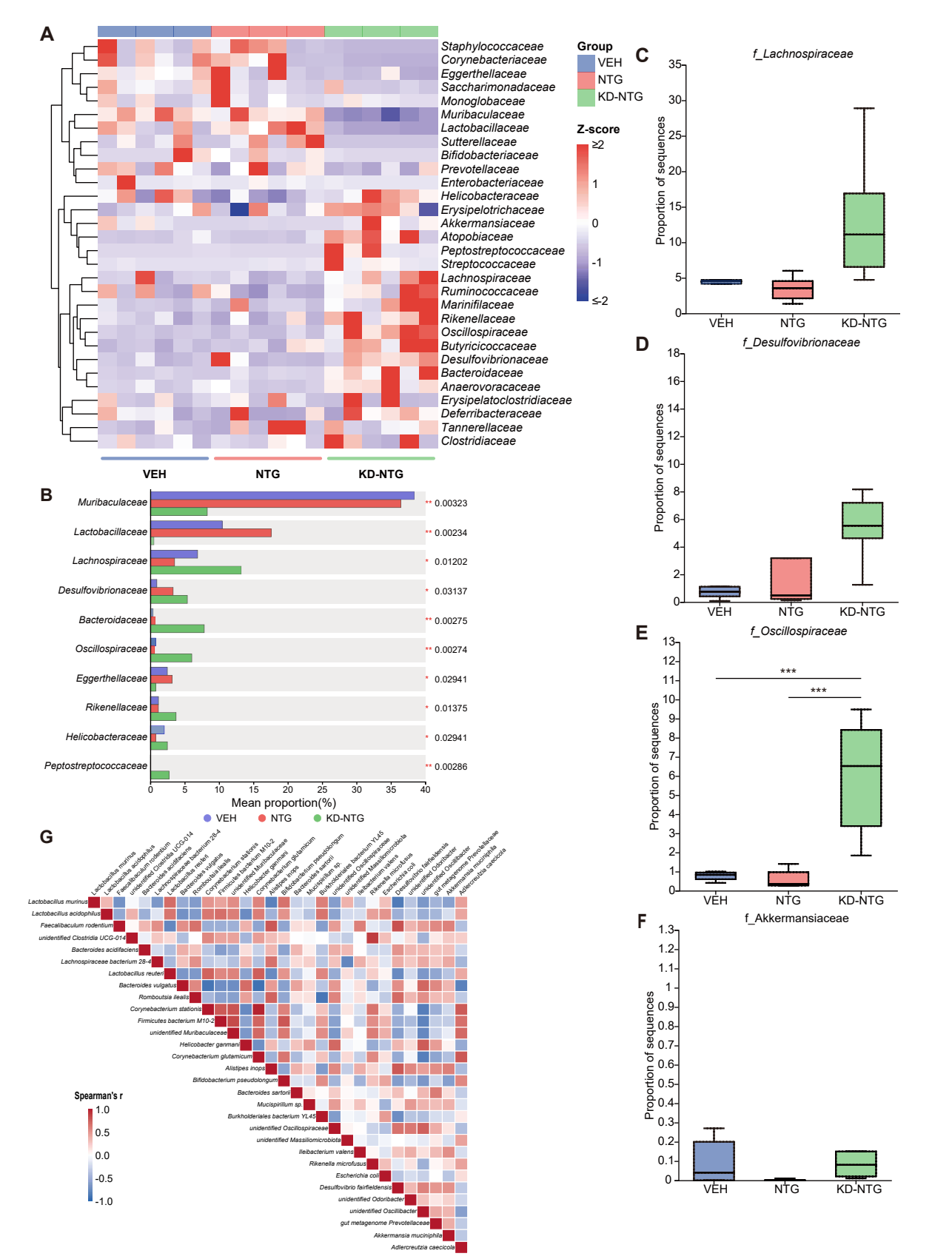
A
Staphylococcaceae
Corynebacteriaceae
Eggerthellaceae
Saccharimonadaceae
Monoglobaceae
Muribaculaceae
Lactobacillaceae
Sutterellaceae
Bifidobacteriaceae
Prevotellaceae
Enterobacteriaceae
Helicobacteraceae
Erysipelotrichaceae
Akkermansiaceae
Atopobiaceae
Peptostreptococcaceae
Streptococcaceae
Lachnospiraceae
Ruminococcaceae
Marinifilaceae
Rikenellaceae
Oscillospiraceae
Butyricicoccaceae
Desulfovibrionaceae
Bacteroidaceae
Anaerovoracaceae
Erysipelatoclostridiaceae
Deferribacteraceae
Tannerellaceae
Clostridiaceae
VEH
NTG
KD-NTG
Group
VEH
NTG
KD-NTG
Z-score
≥2
1
0
-1
≤-2
B
Muribaculaceae ** 0.00323
Lactobacillaceae ** 0.00234
Lachnospiraceae * 0.01202
Desulfovibrionaceae * 0.03137
Bacteroidaceae ** 0.00275
Oscillospiraceae ** 0.00274
Eggerthellaceae * 0.02941
Rikenellaceae * 0.01375
Helicobacteraceae * 0.02941
Peptostreptococcaceae ** 0.00286
0 5 10 15 20 25 30 35 40
Mean proportion(%)
VEH
NTG
KD-NTG
C
f_Lachnospiraceae
Proportion of sequences
0 5 10 15 20 25 30 35
VEH
NTG
KD-NTG
D
f_Desulfovibrionaceae
Proportion of sequences
0 2 4 6 8 10 12 14 16 18
VEH
NTG
KD-NTG
E
f_Oscillospiraceae
***
***
Proportion of sequences
0 1 2 3 4 5 6 7 8 9 10 11 12 13
VEH
NTG
KD-NTG
F
f_Akkermansiaceae
Proportion of sequences
0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 1 1.1 1.2 1.3
VEH
NTG
KD-NTG
G
Lactobacillus murinus
Lactobacillus acidophilus
Faecalibaculum rodentium
unidentified Clostridia UCG-014
Bacteroidales bacterium 28-4
Lachnospiraceae bacterium 28-4
Lactobacillus reuteri
Bacteroides vulgatus
Romboutsia ilealis
Corynebacterium stationis
Firmicutes bacterium M10-2
unidentified Muribaculaceae
Helicobacter ganmani
Corynebacterium glutamicum
Alistipes inops
Bifidobacterium pseudolongum
Bacteroides sartorii
Mucispirillum sp.
Burkholderiales bacterium YL45
unidentified Oscillospiraceae
unidentified Massilimicrobiota
Ileibacterium valens
Rikenella microfusus
Escherichia coli
Desulfovibrio fairfieldensis
unidentified Odoribacter
unidentified Oscillibacter
gut metagenome Prevotellaceae
Akkermansia muciniphila
Adlercreutzia caecicola
Spearman's r
1.0
0.5
0.0
-0.5
-1.0