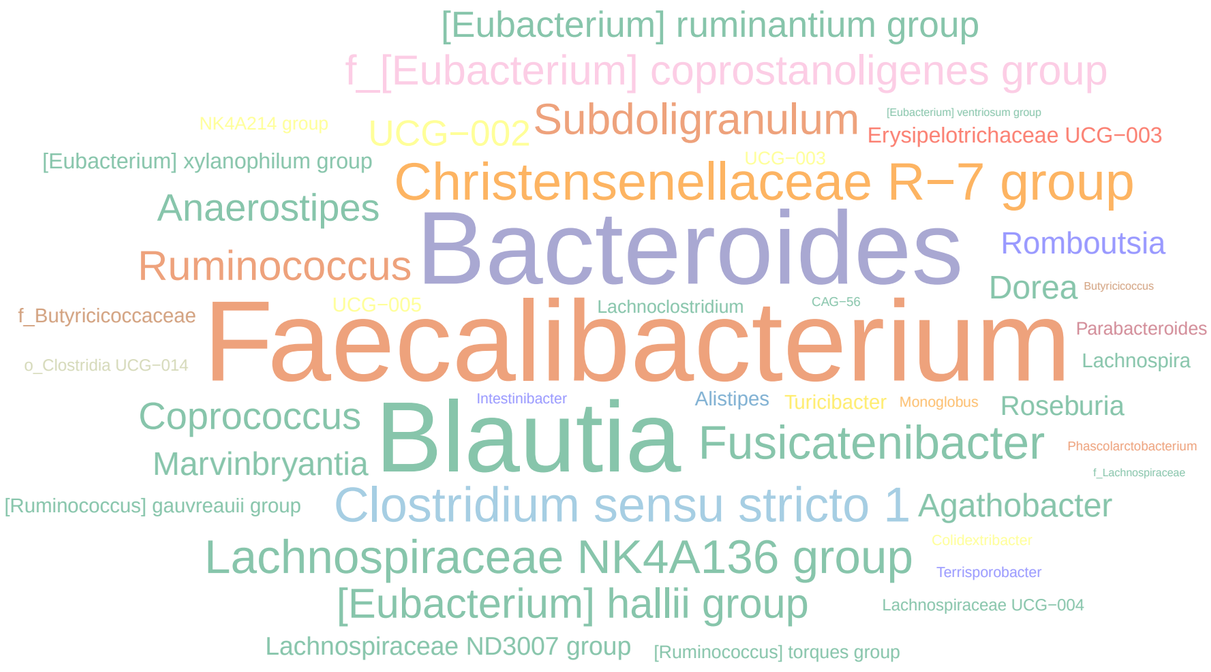
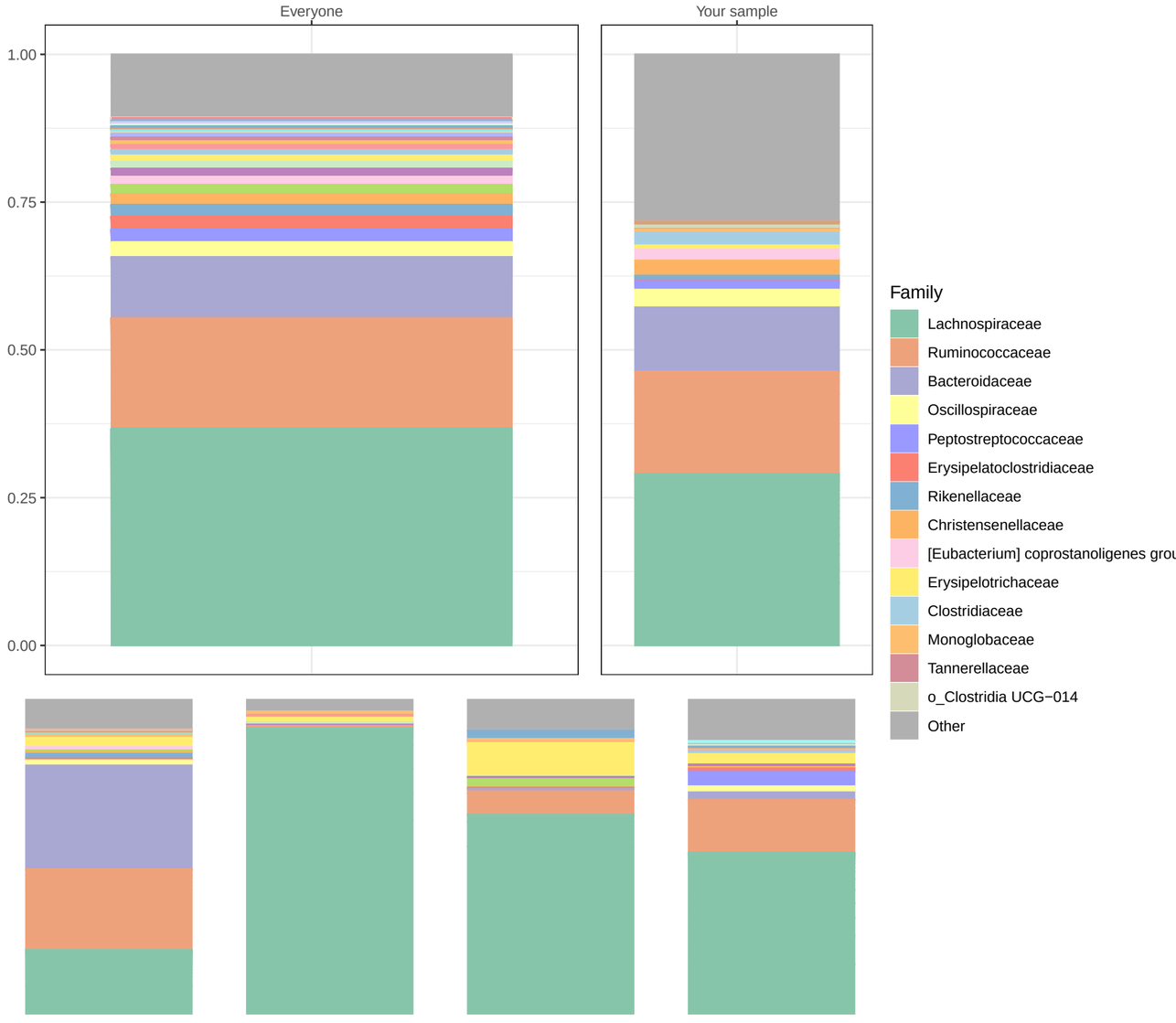

[Eubacterium] ruminantium group
f_[Eubacterium] coprostanoligenes group
NK4A214 group
UCG−002
Subdoligranulum
[Eubacterium] ventriosum group
Erysipelotrichaceae UCG−003
[Eubacterium] xylanophilum group
UCG−003
Christensenellaceae R−7 group
Anaerostipes
Bacteroides
Romboutsia
Ruminococcus
Dorea
Butyricicoccus
f_Butyricicoccaceae
UCG−005
Lachnoclostridium
CAG−56
Parabacteroides
o_Clostridia UCG−014
Faecalibacterium
Lachnospira
Intestinibacter
Alistipes
Turicibacter
Monoglobus
Roseburia
Coprococcus
Blautia
Fusicatenibacter
Phascolarctobacterium
Marvinbryantia
f_Lachnospiraceae
[Ruminococcus] gauvreauii group
Clostridium sensu stricto 1
Agathobacter
Colidextribacter
Lachnospiraceae NK4A136 group
Terrisporobacter
[Eubacterium] hallii group
Lachnospiraceae UCG−004
Lachnospiraceae ND3007 group
[Ruminococcus] torques group


Everyone
Your sample
1.00
0.75
0.50
0.25
0.00
Family
Lachnospiraceae
Ruminococcaceae
Bacteroidaceae
Oscillospiraceae
Peptostreptococcaceae
Erysipelatoclostridiaceae
Rikenellaceae
Christensenellaceae
[Eubacterium] coprostanoligenes grou
Erysipelotrichaceae
Clostridiaceae
Monoglobaceae
Tannerellaceae
o_Clostridia UCG−014
Other