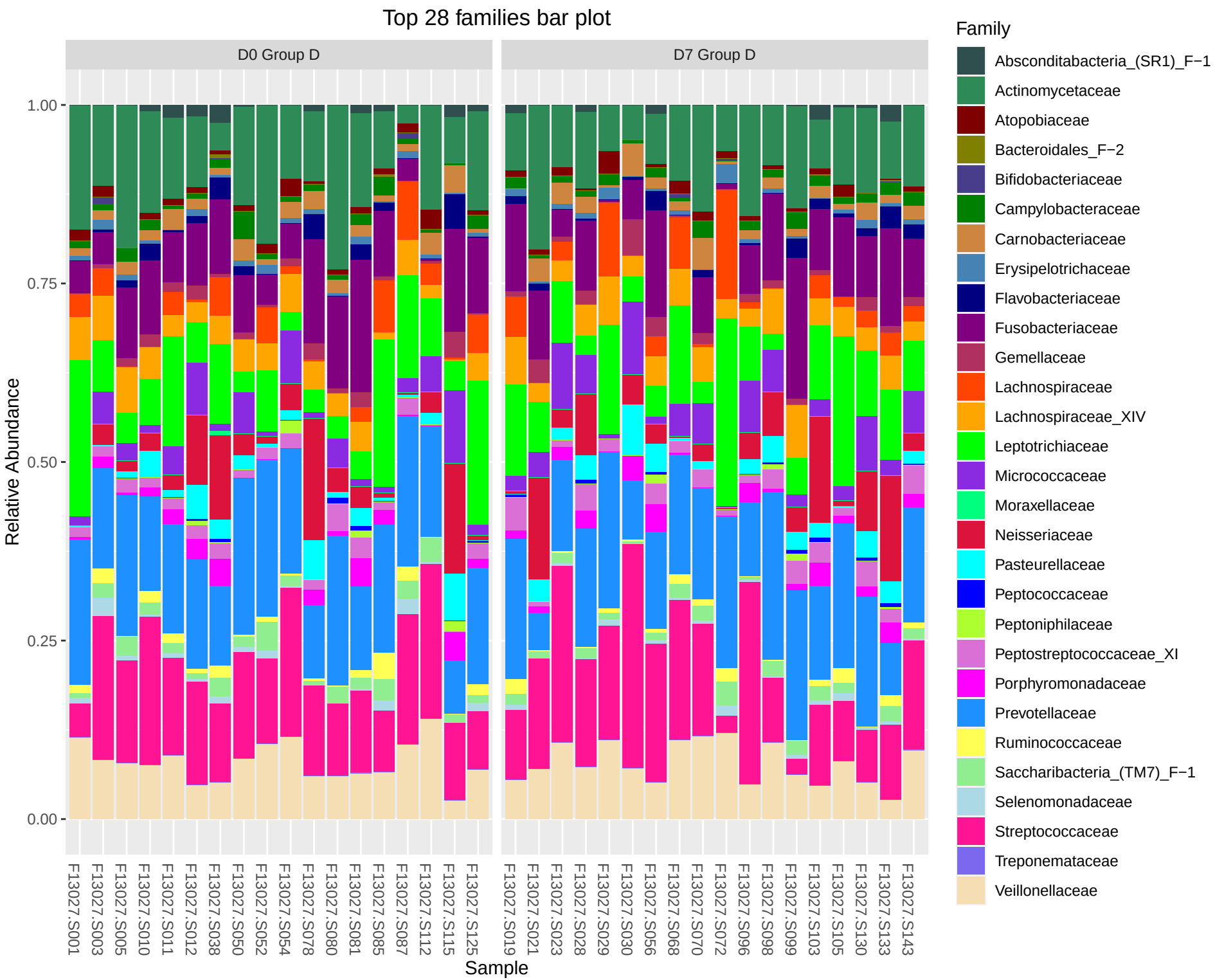
Top 28 families bar plot
D0 Group D
D7 Group D
Relative Abundance
1.00
0.75
0.50
0.25
0.00
F13027.S001
F13027.S003
F13027.S005
F13027.S010
F13027.S011
F13027.S012
F13027.S038
F13027.S050
F13027.S052
F13027.S054
F13027.S078
F13027.S080
F13027.S081
F13027.S085
F13027.S087
F13027.S112
F13027.S115
F13027.S125
F13027.S019
F13027.S021
F13027.S023
F13027.S028
F13027.S029
F13027.S030
F13027.S056
F13027.S068
F13027.S070
F13027.S072
F13027.S096
F13027.S098
F13027.S099
F13027.S103
F13027.S105
F13027.S130
F13027.S133
F13027.S143
Sample
Family
Absconditabacteria_(SR1)_F−1
Actinomycetaceae
Atopobiaceae
Bacteroidales_F−2
Bifidobacteriaceae
Campylobacteraceae
Carnobacteriaceae
Erysipelotrichaceae
Flavobacteriaceae
Fusobacteriaceae
Gemellaceae
Lachnospiraceae
Lachnospiraceae_XIV
Leptotrichiaceae
Micrococcaceae
Moraxellaceae
Neisseriaceae
Pasteurellaceae
Peptococcaceae
Peptoniphilaceae
Peptostreptococcaceae_XI
Porphyromonadaceae
Prevotellaceae
Ruminococcaceae
Saccharibacteria_(TM7)_F−1
Selenomonadaceae
Streptococcaceae
Treponemataceae
Veillonellaceae