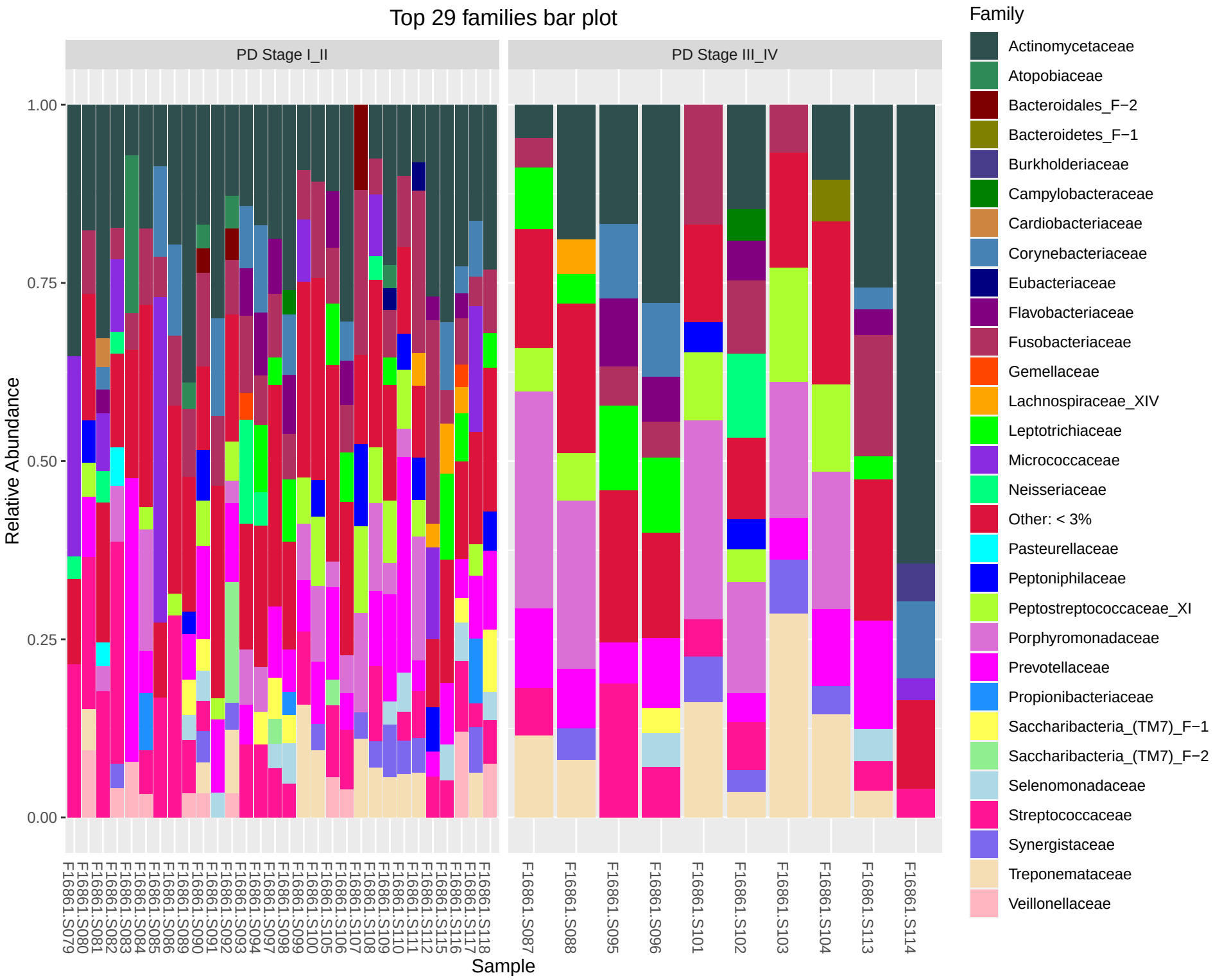
Top 29 families bar plot
PD Stage I_II
PD Stage III_IV
Relative Abundance
1.00
0.75
0.50
0.25
0.00
Sample
F16861.S079
F16861.S080
F16861.S081
F16861.S082
F16861.S083
F16861.S084
F16861.S085
F16861.S086
F16861.S089
F16861.S090
F16861.S091
F16861.S092
F16861.S093
F16861.S094
F16861.S097
F16861.S098
F16861.S099
F16861.S100
F16861.S105
F16861.S106
F16861.S107
F16861.S108
F16861.S109
F16861.S110
F16861.S111
F16861.S112
F16861.S115
F16861.S116
F16861.S117
F16861.S118
F16861.S087
F16861.S088
F16861.S095
F16861.S096
F16861.S101
F16861.S102
F16861.S103
F16861.S104
F16861.S113
F16861.S114
Family
Actinomycetaceae
Atopobiaceae
Bacteroidales_F−2
Bacteroidetes_F−1
Burkholderiaceae
Campylobacteraceae
Cardiobacteriaceae
Corynebacteriaceae
Eubacteriaceae
Flavobacteriaceae
Fusobacteriaceae
Gemellaceae
Lachnospiraceae_XIV
Leptotrichiaceae
Micrococcaceae
Neisseriaceae
Other: < 3%
Pasteurellaceae
Peptoniphilaceae
Peptostreptococcaceae_XI
Porphyromonadaceae
Prevotellaceae
Propionibacteriaceae
Saccharibacteria_(TM7)_F−1
Saccharibacteria_(TM7)_F−2
Selenomonadaceae
Streptococcaceae
Synergistaceae
Treponemataceae
Veillonellaceae