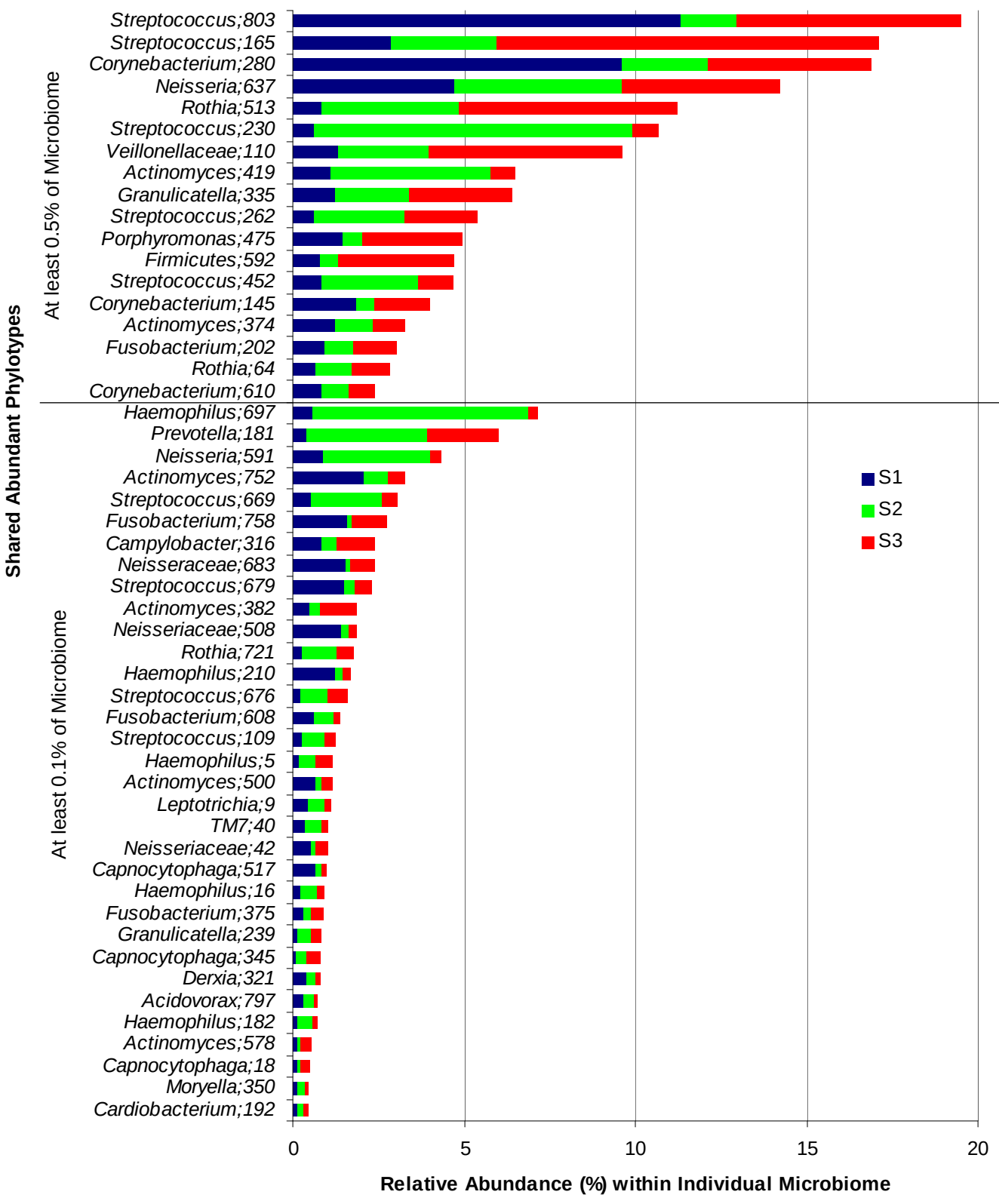
Shared Abundant Phylotypes
At least 0.5% of Microbiome
At least 0.1% of Microbiome
Streptococcus;803
Streptococcus;165
Corynebacterium;280
Neisseria;637
Rothia;513
Streptococcus;230
Veillonellaceae;110
Actinomyces;419
Granulicatella;335
Streptococcus;262
Porphyromonas;475
Firmicutes;592
Streptococcus;452
Corynebacterium;145
Actinomyces;374
Fusobacterium;202
Rothia;64
Corynebacterium;610
Haemophilus;697
Prevotella;181
Neisseria;591
Actinomyces;752
Streptococcus;669
Fusobacterium;758
Campylobacter;316
Neisseraceae;683
Streptococcus;679
Actinomyces;382
Neisseriaceae;508
Rothia;721
Haemophilus;210
Streptococcus;676
Fusobacterium;608
Streptococcus;109
Haemophilus;5
Actinomyces;500
Leptotrichia;9
TM7;40
Neisseriaceae;42
Capnocytophaga;517
Haemophilus;16
Fusobacterium;375
Granulicatella;239
Capnocytophaga;345
Derxia;321
Acidovorax;797
Haemophilus;182
Actinomyces;578
Capnocytophaga;18
Moryella;350
Cardiobacterium;192
S1
S2
S3
0
5
10
15
20
Relative Abundance (%) within Individual Microbiome