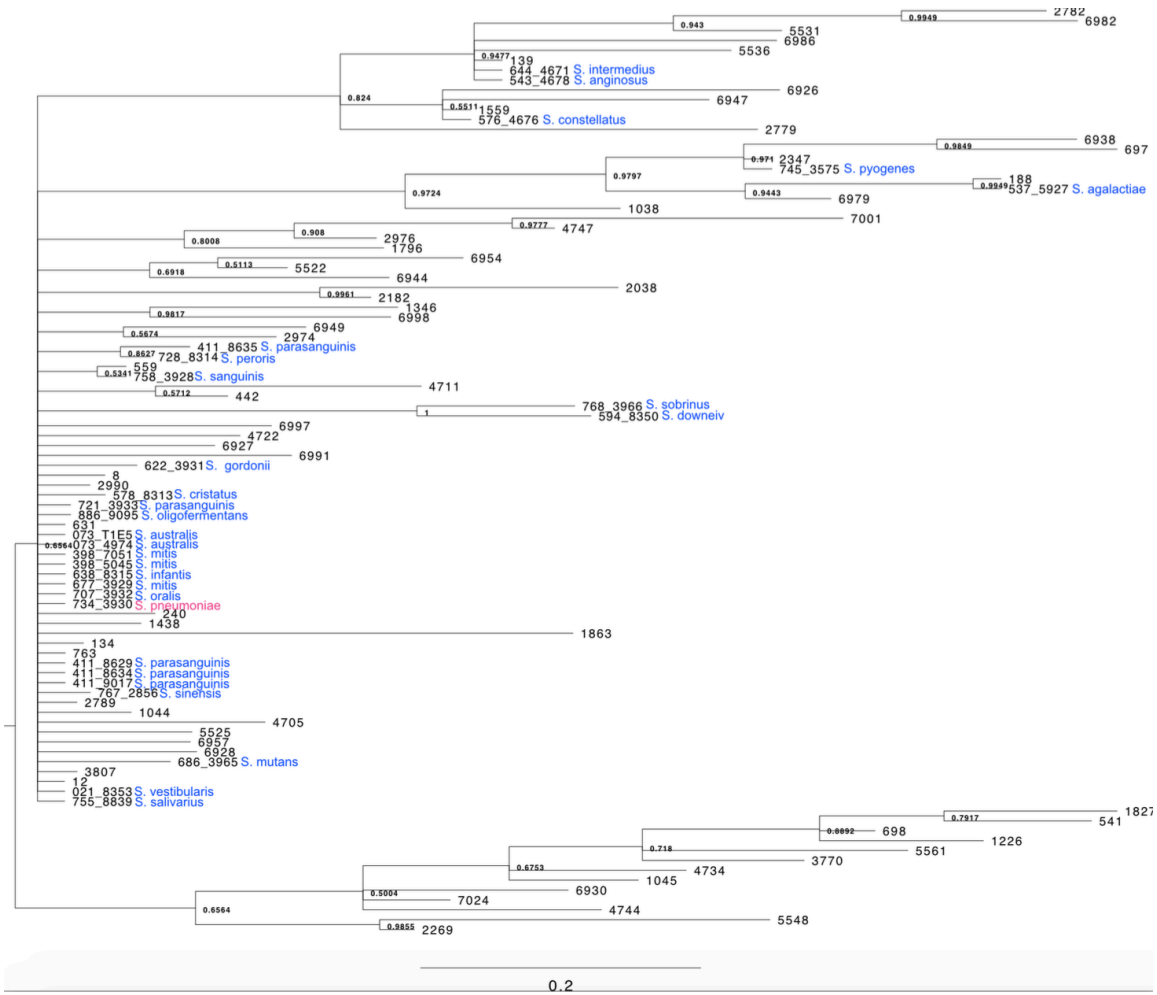


Supplementary Figures

Supplementary Table 1: Statistical analyses conducted on PCoA plots between young, mid-age and old mice at each time point throughout colonization⁴.

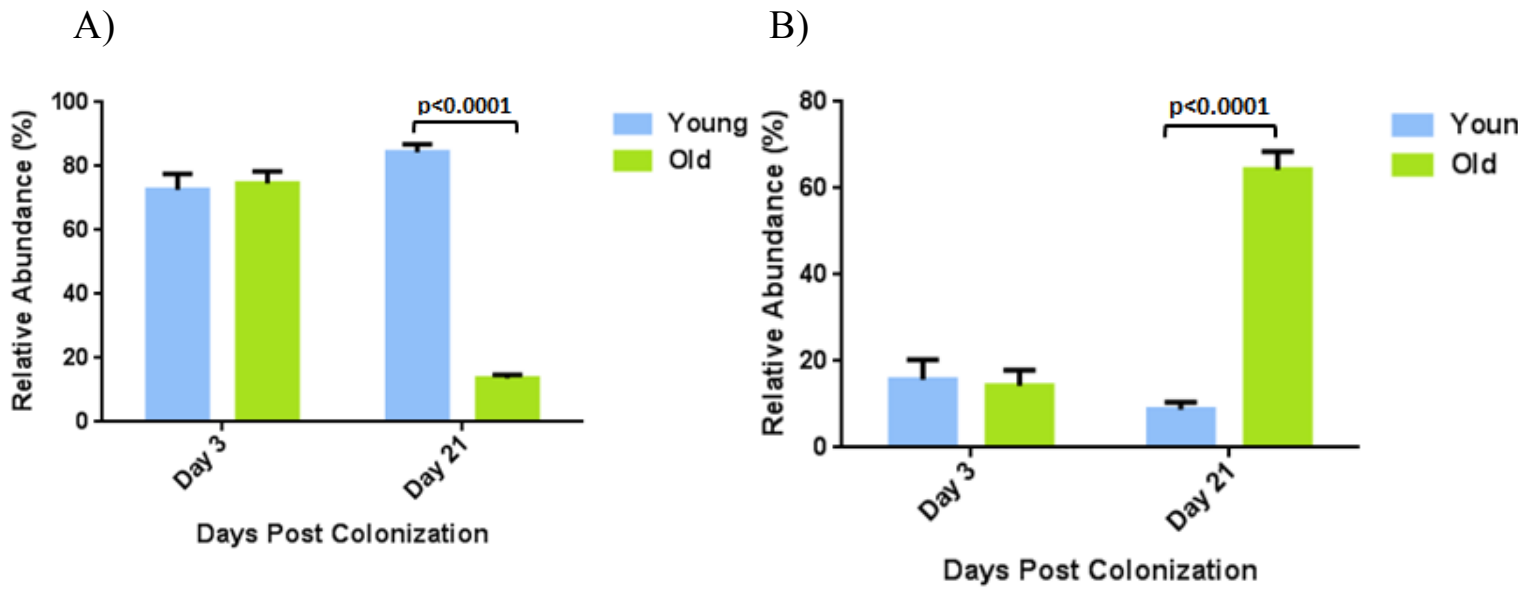
	Bray-Curtis
Day 0	0.04
Day 3	0.001
Day 14	0.014
Day 21	0.008

⁴Statistical significance was determined using PERMANOVA in R phyloseq. The p values indicated in the table describe the statistical difference between the three age groups at each time point. This was calculated using the ADONIS function, which conducts a permutational multivariate analysis of variance within the samples using distance matrices. $p < 0.05$ was considered to be significant.



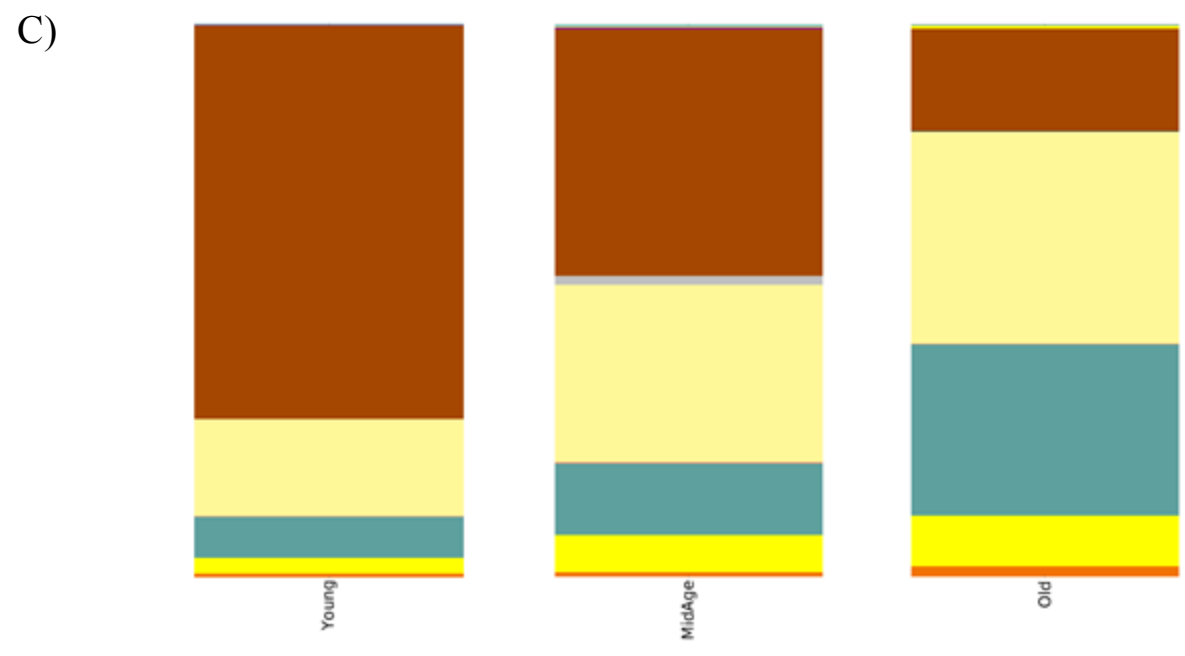
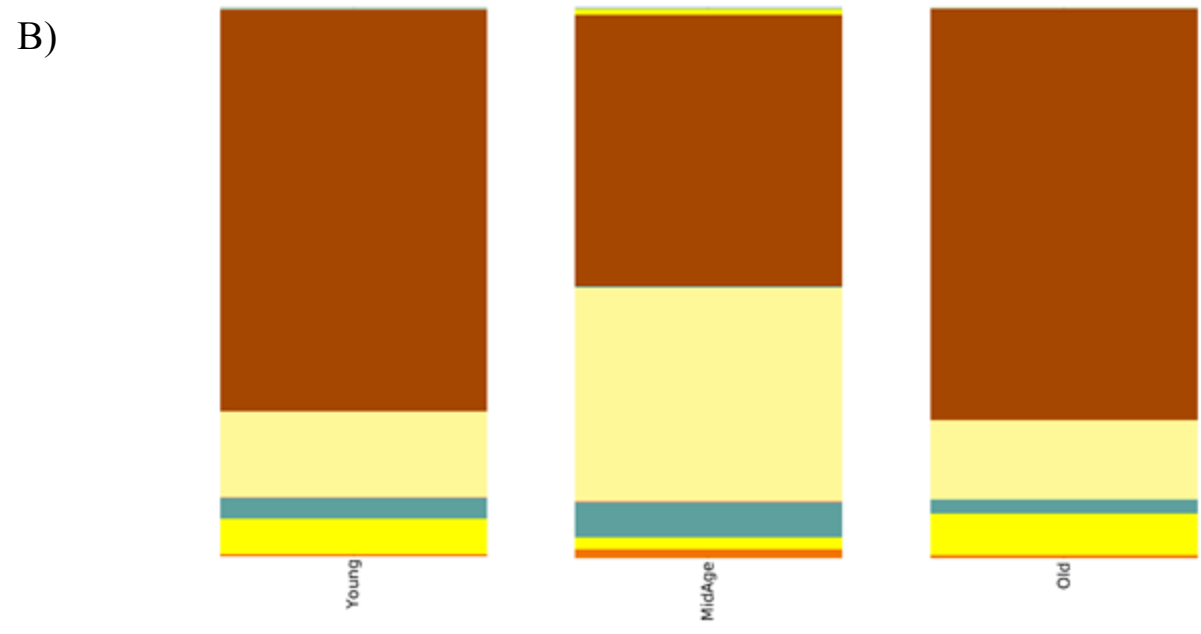
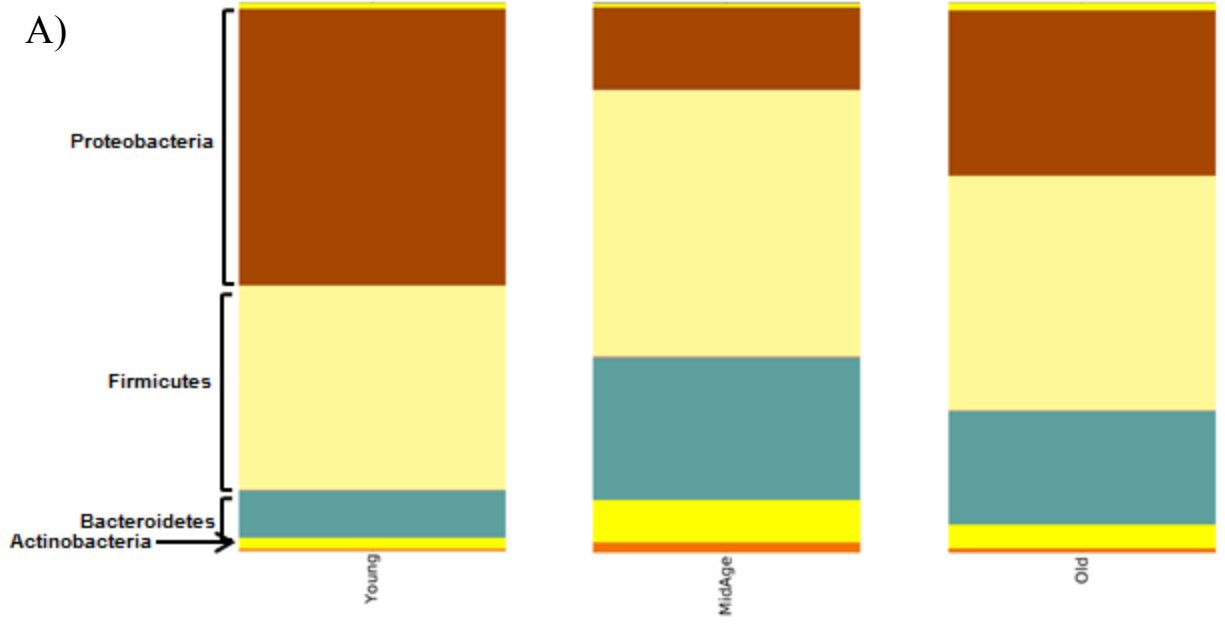
Supplementary Figure 1: OTUs representing specific species within the *Streptococcus* genus.

A phylogenetic tree based on the representative sequence from each OTU. The phylogeny was contracted using the *Streptococcus* reference sequences from HOMO. The tree was created using Mr Bayes to 100 million generations using the GRT+I+V evolutionary model. Any numerical node label corresponds with the OTU number; all human oral microbiome database (HOMO) reference sequences are named in colour, with *S. pneumoniae* in pink.

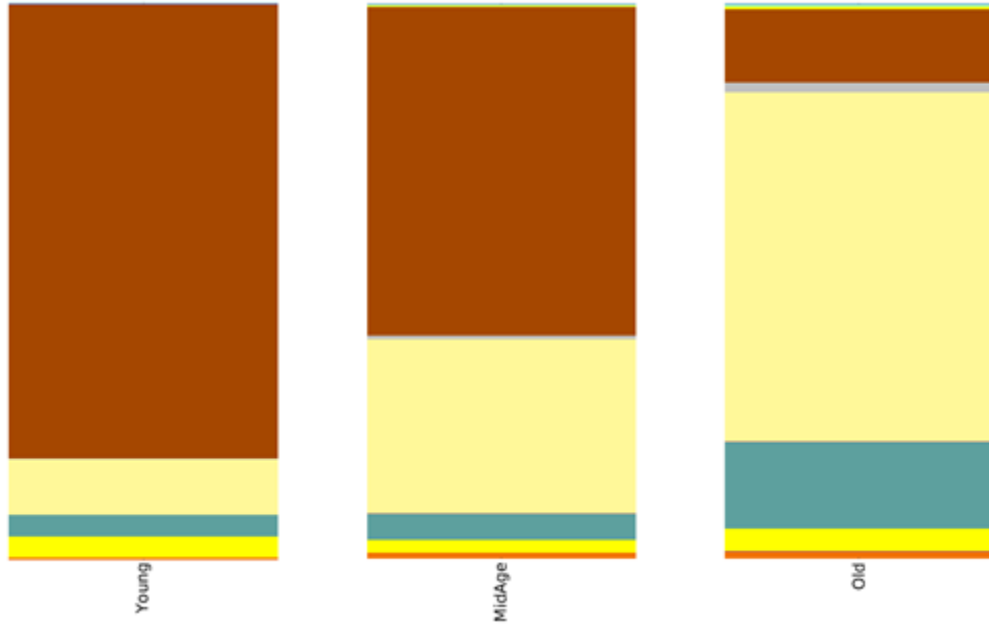


Supplementary Figure 2: OTUs representing the A) Proteobacteria and B) Firmicutes phylum differences within the young and old microbiome post-colonization with *S. pneumoniae*.

Relative abundances were calculated using QIIME analyses of the OTUs representing the phylum of interest in young and old mice at day 3 and 21 (n=4-7/group). Values are the mean +/- SEM of samples within each category. Statistical significance was determined using multiple t-test where appropriate. $p < 0.05$ was considered to be significant.



D)



Supplementary Figure 3: Bacterial communities within the URT are altered in response to pneumococcal colonization in young, mid-age and old mice.

Averaged taxa summary plot of all the samples within the particular group [n=3-9/group]. Major bacterial groups are labeled according to phylum. The height of the bar represents the relative abundance of the associated genus within the a) Day 0 (control) mice, b) Day 3 post-colonization mice, c) Day 14 post-colonization and d) Day 21 post-colonization mice.