
SUPPLEMENTARY TABLE

Table S1. Significance of PCoA of Jaccard and BrayCurtis diversities

Jaccard/Bray-Curtis

	Female						Male					
	Young		Mid		Old		Young		Mid		Old	
	PC1	PC2	PC1	PC2	PC1	PC2	PC1	PC2	PC1	PC2	PC1	PC2
None vs low	n.s. n.s.	# n.s.	n.s. n.s.	n.s. *	n.s. n.s.	** *	n.s. n.s.	n.s. *	** n.s.	n.s. n.s.	# #	n.s. n.s.
None vs high	n.s. n.s.	n.s. n.s.	n.s. n.s.	n.s. n.s.	n.s. n.s.	** **	n.s. n.s.	** n.s.	** **	n.s. n.s.	n.s. n.s.	n.s. n.s.
Low vs high	n.s. n.s.	n.s. n.s.	n.s. n.s.	n.s. *	n.s. n.s.	n.s. n.s.	n.s. n.s.	* *	n.s. **	n.s. n.s.	# #	n.s. n.s.

p < 0.1; * p < 0.05; ** p < 0.01

SUPPLEMENTARY FIGURES

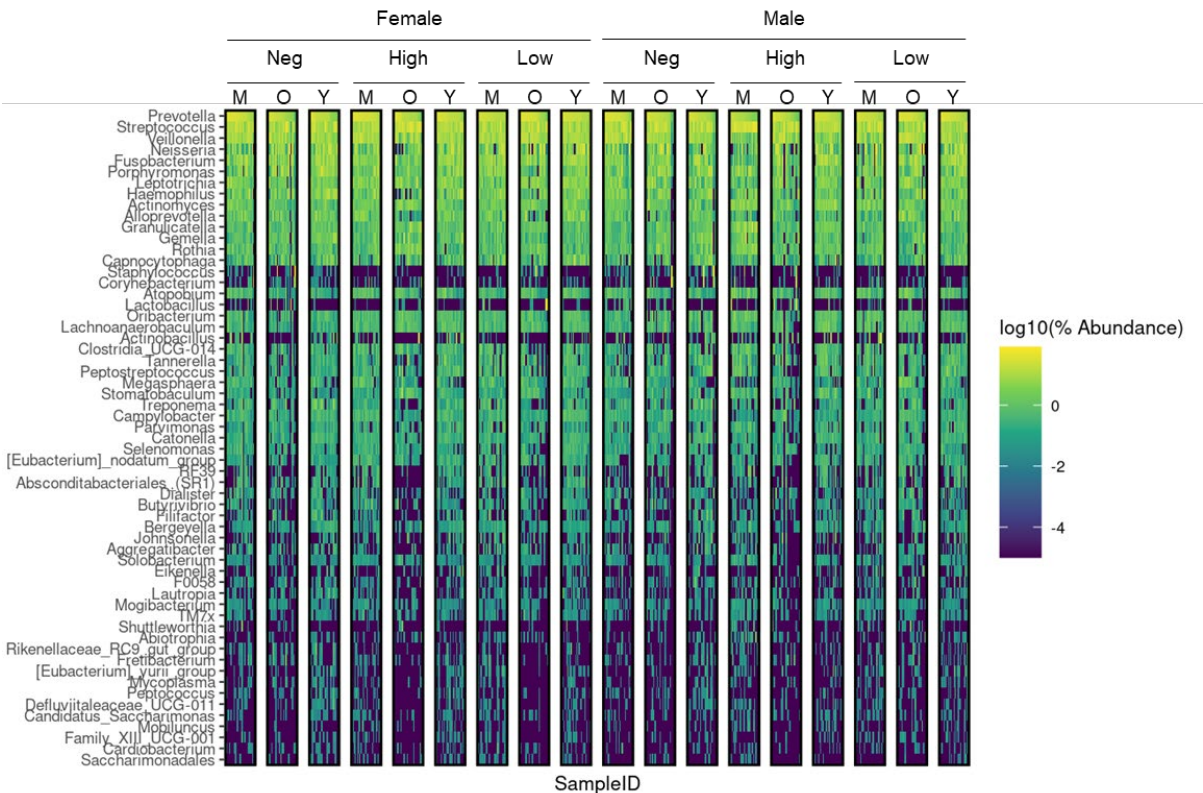


Figure S1. Heatmap of genera by groups (logarithmic abundance values). Features were selected if present in the microbiome core, i.e. genera present in at least 50% of samples with a relative abundance of at least 0.1%, of at least one of the 18 groups and sorted by mean abundance averaged on all samples. Samples are sorted by abundance of the most abundant genus (*Prevotella*).

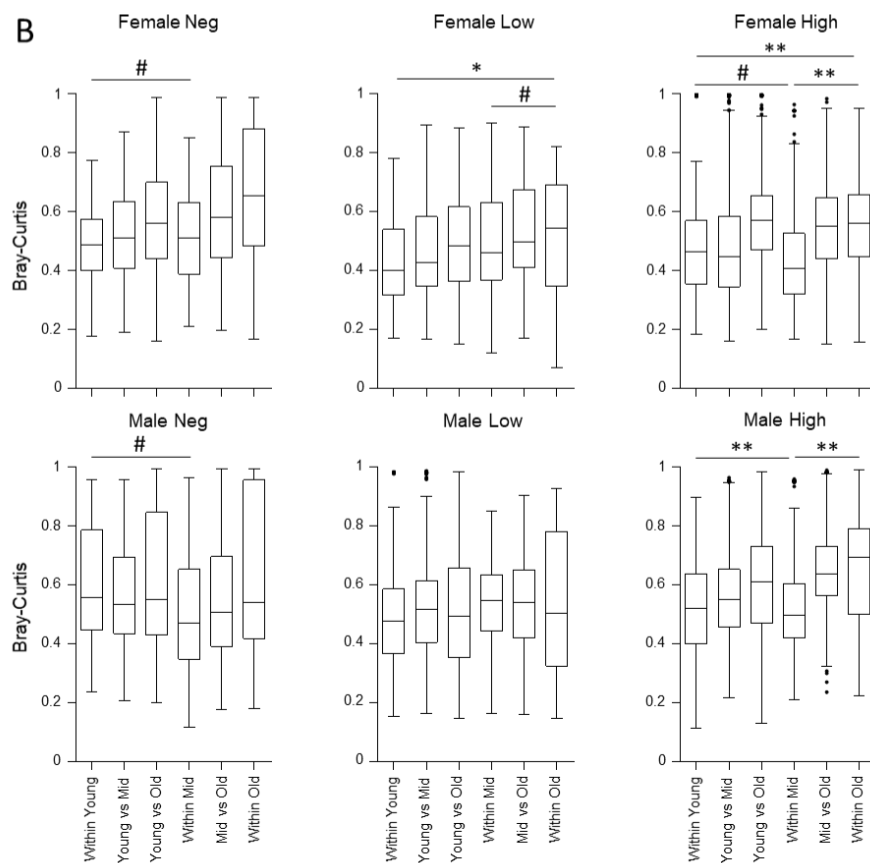
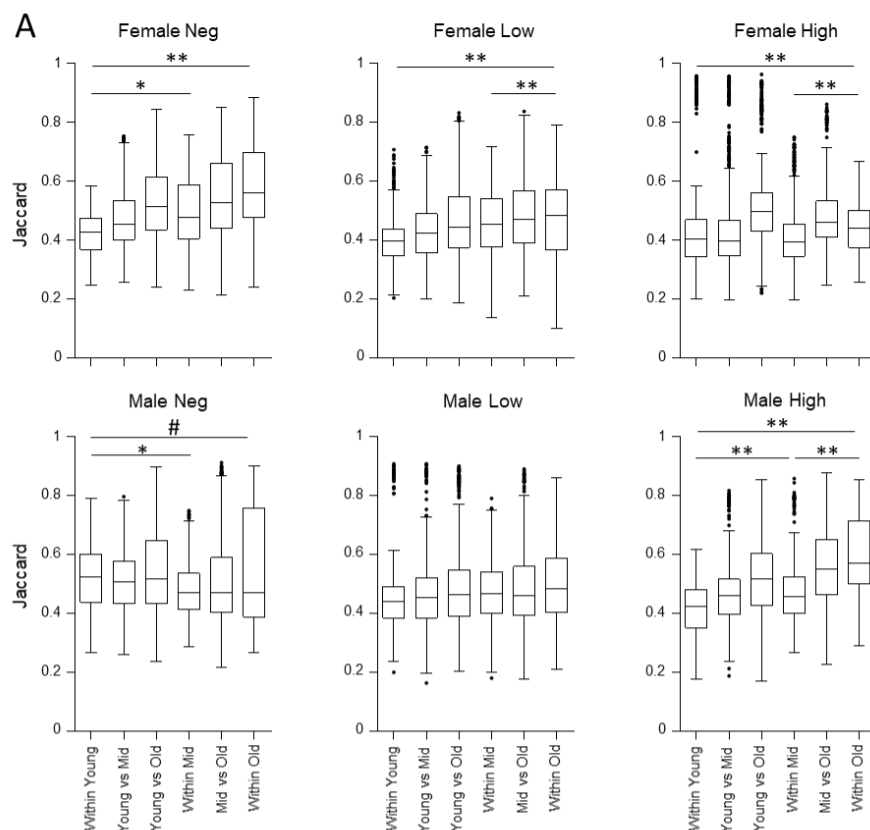


Figure S2. Beta diversity analysis of nasopharyngeal microbiome. Boxplots of Jaccard (A) and Bray-Curtis (B) beta diversity indexes evaluating sample distances within or between age groups for each combination of viral load and gender. Significance among within-distances was evaluated by applying a pairwise PermAnova test to the 18 groups. # $p < 0.1$; * $p < 0.05$; ** $p < 0.01$. BH-FDR correction.

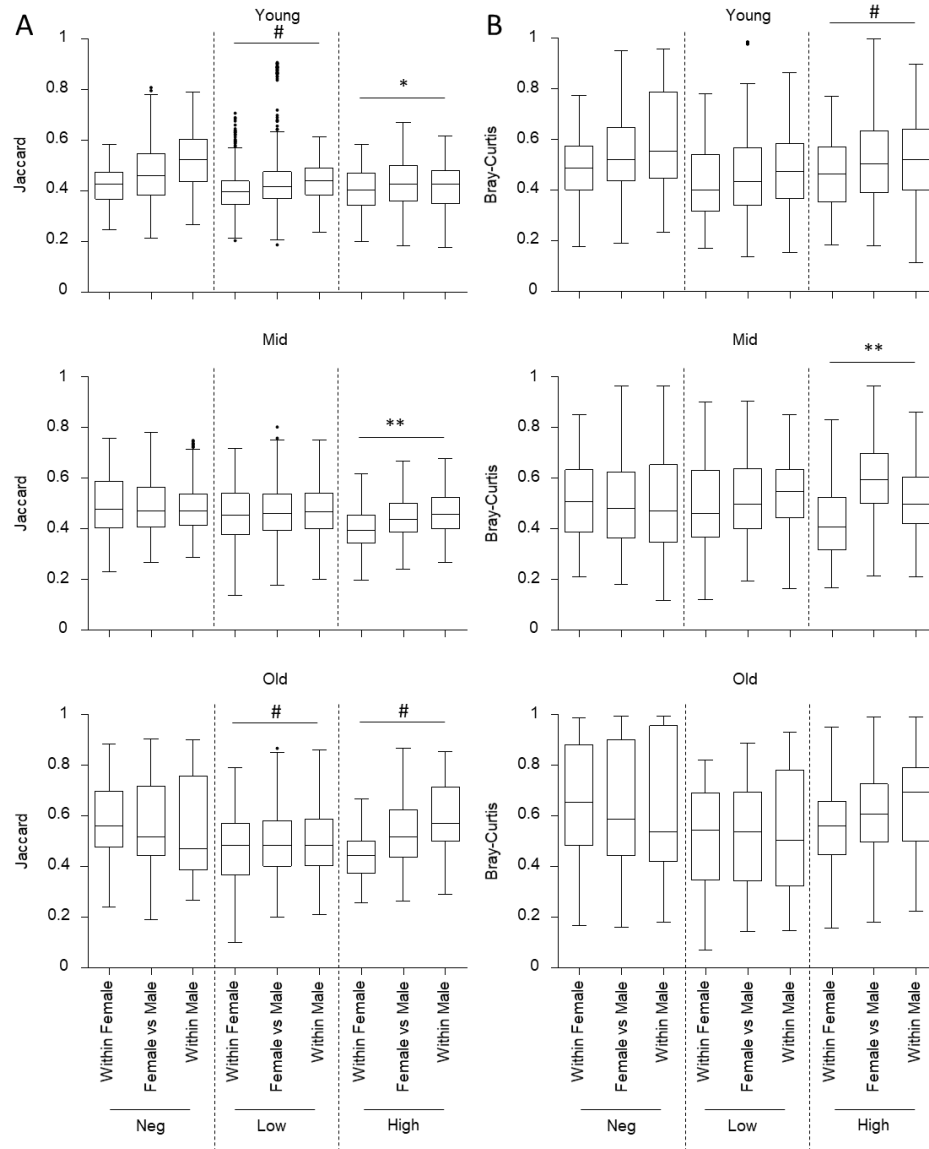
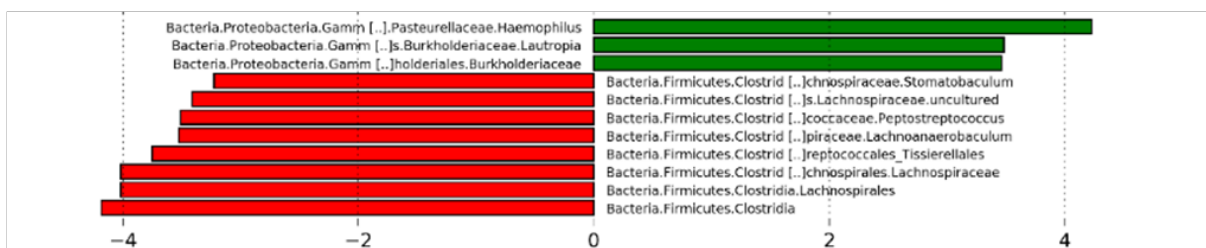
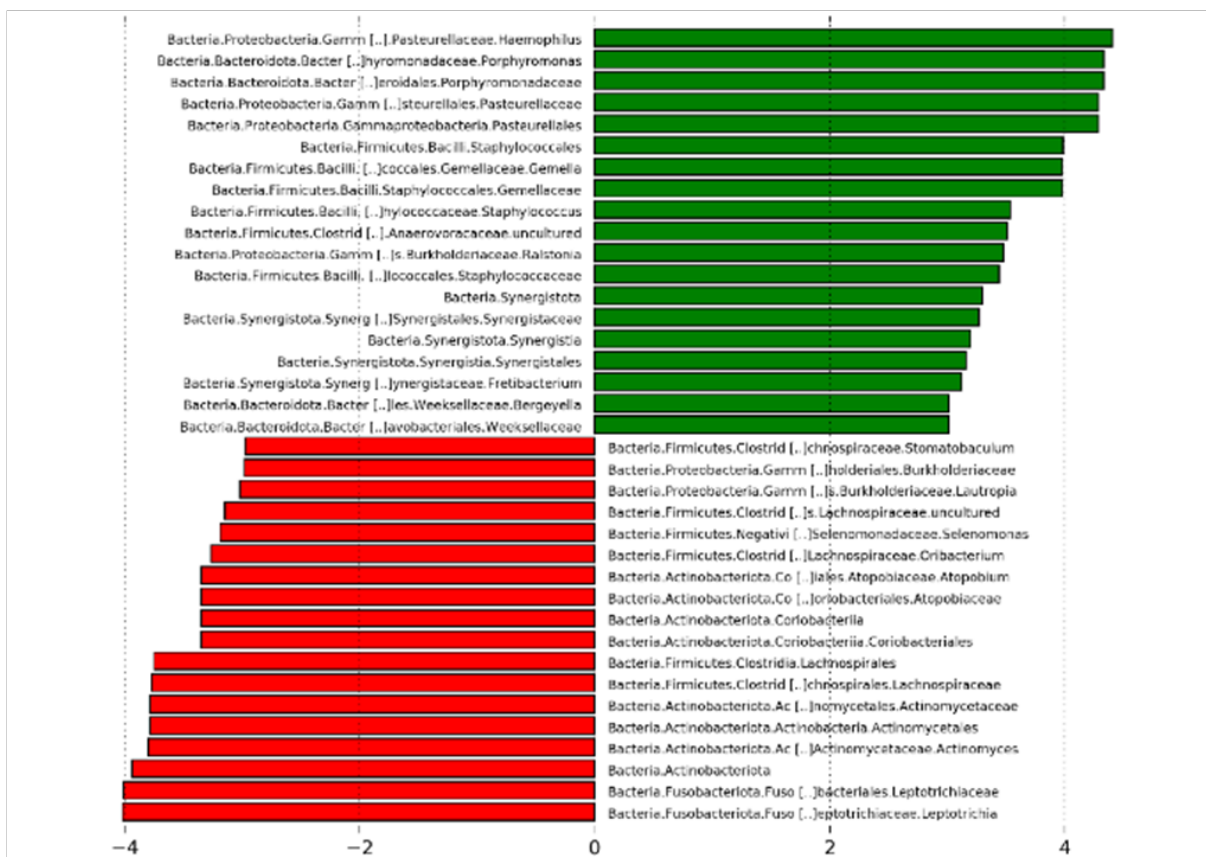
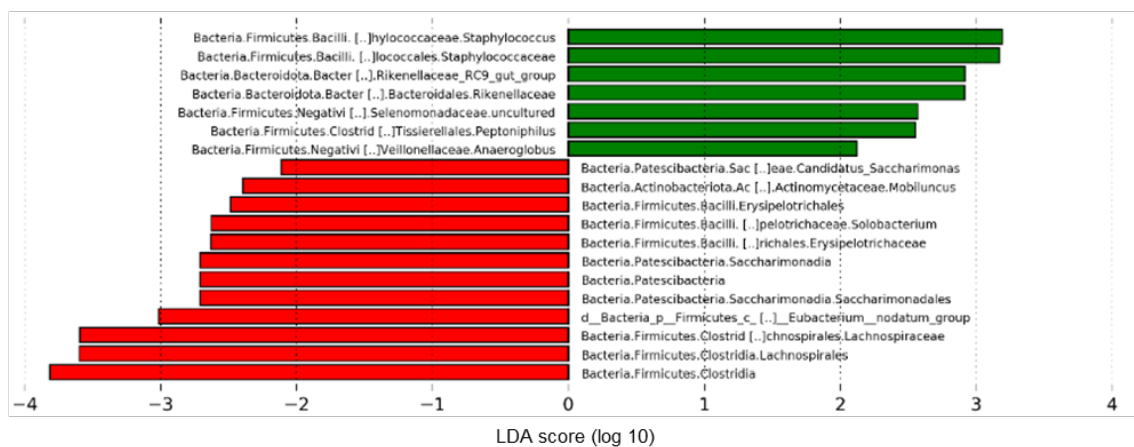
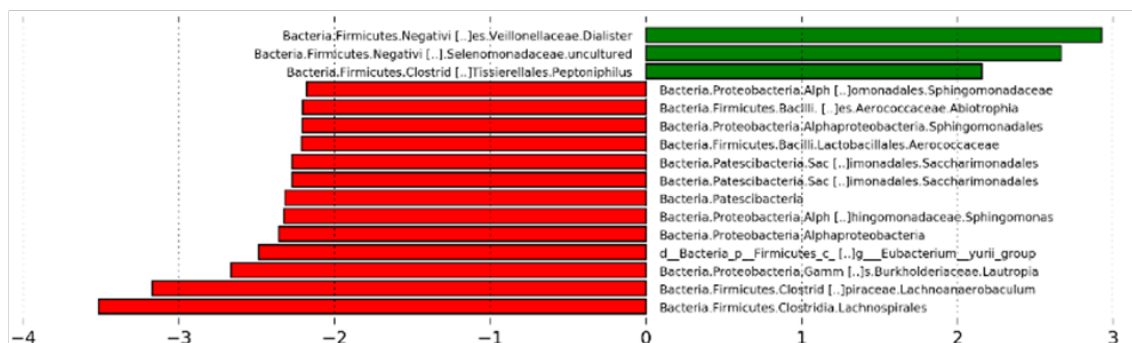


Figure S3. Beta diversity analysis of nasopharyngeal microbiome. Boxplots of Jaccard (A) and Bray-Curtis (B) beta diversity indexes evaluating sample distances within or between gender groups for each combination of viral load and age. Significance among within-distances was evaluated by applying a pairwise PerMANOVA test to the 18 groups. # $p < 0.1$; * $p < 0.05$; ** $p < 0.01$. BH-FDR correction.

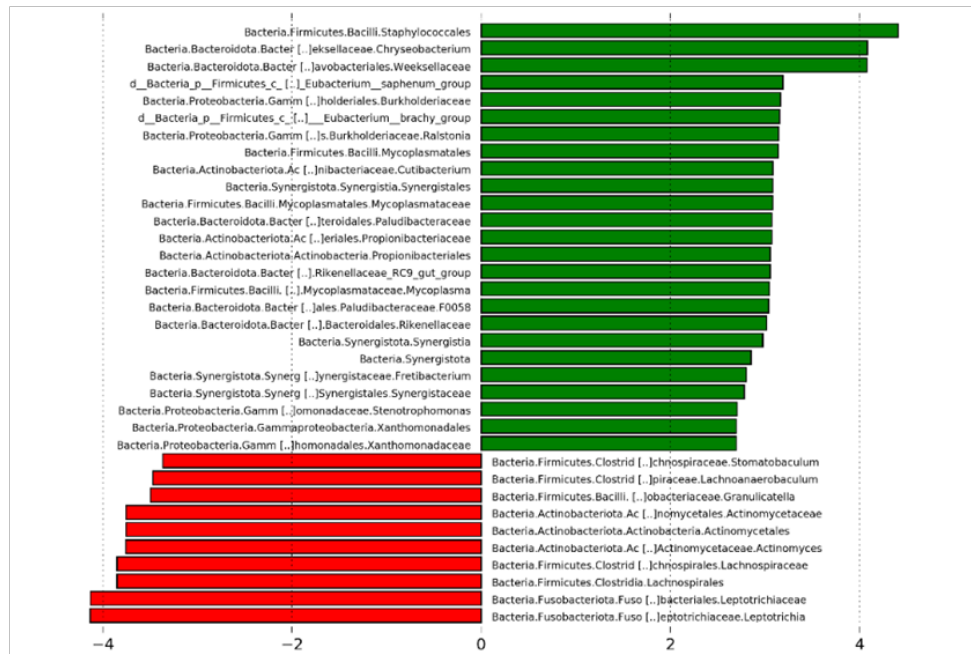


LDA score (log 10)

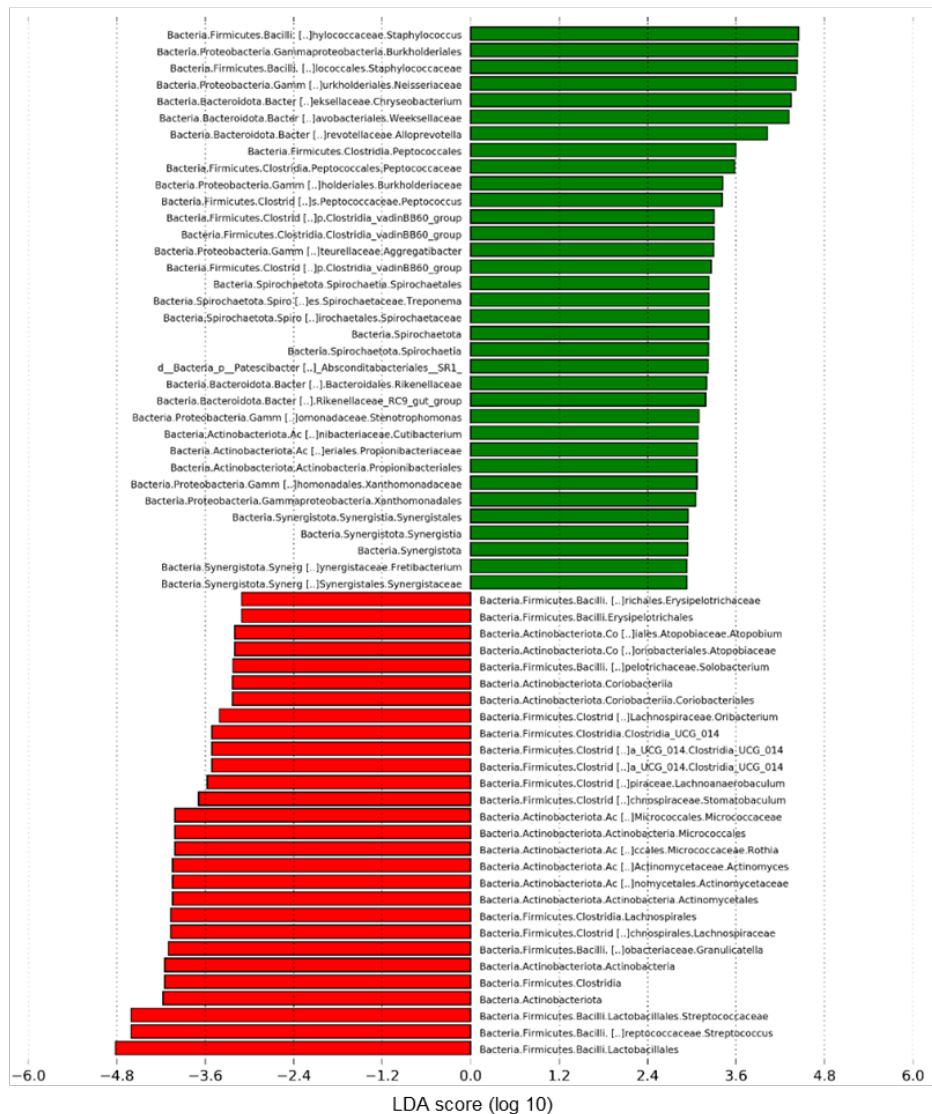


Old female

Low
None



High
None



LDA score (log 10)

Figure S4. Differential abundance analysis between age groups in females. The histograms of the linear discriminant analysis (LDA) scores are computed for genera significantly associated with low or high (red), or negative (None) viral load groups in young, mid and old females. LefSe has been applied with default alpha values for the analysis of variance (ANOVA) and Wilcoxon tests (0.05), and the LDA effect size has been evaluated by setting the absolute value of the logarithmic LDA threshold equal to 3.5. Other LefSe parameters have been set to the default.