

Supplementary Figure 1: Taxonomic Hits Distribution of Five (CP+S) patients sample: The charts represent the distribution of taxa using a contigLCA algorithm finding a single consensus taxonomic entity at Phylum level on each individual sample.

Supplementary Figure 2: Taxonomic Hits Distribution of Five (CP+S) patients sample: The charts represent the distribution of taxa using a contigLCA algorithm finding a single consensus taxonomic entity at genus level on each individual sample.

Supplementary Figure 3: Taxonomic Hits Distribution of Five (S) Control sample: The charts represent the distribution of taxa using a contigLCA algorithm finding a single consensus taxonomic entity at Phylum level on each individual sample.

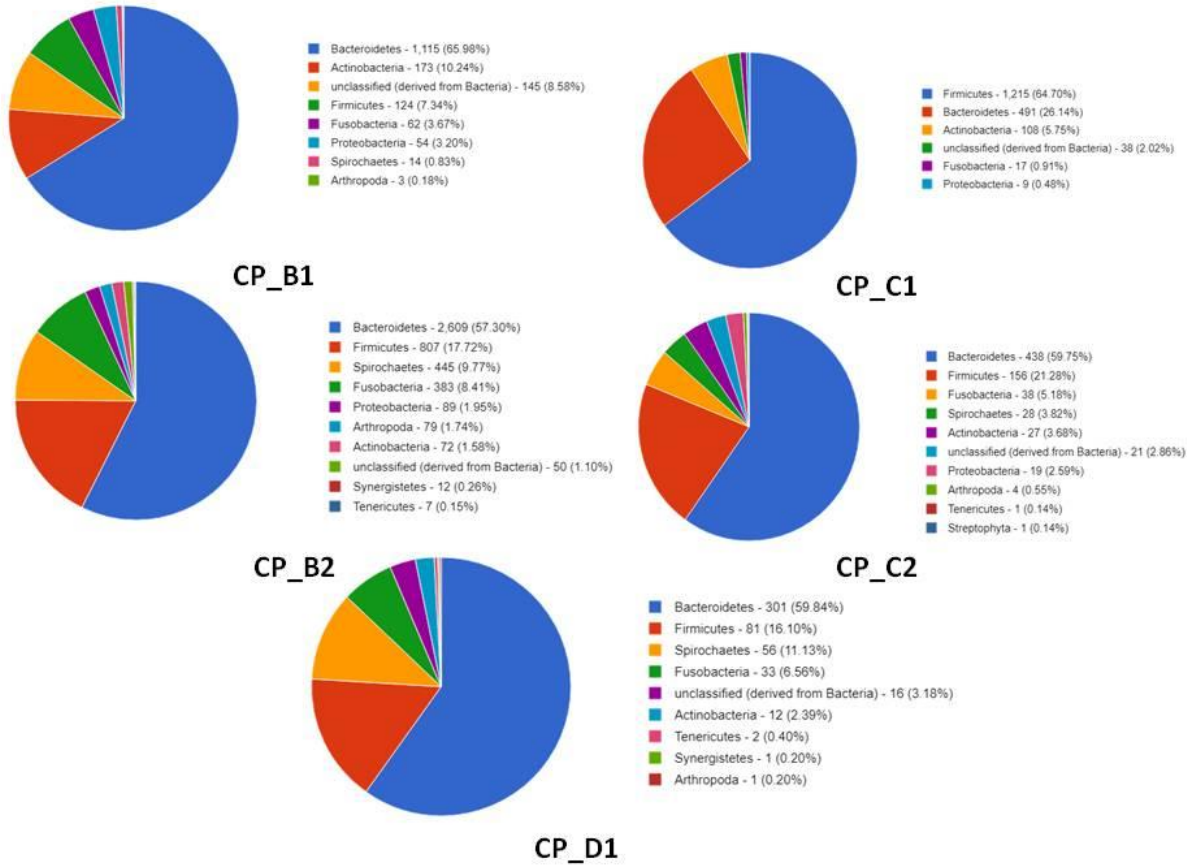
Supplementary Figure 4: Taxonomic Hits Distribution of Five (S) Control sample: The charts represent the distribution of taxa using a contigLCA algorithm finding a single consensus taxonomic entity at genus level on each individual sample.

Supplementary Figure 5: Alpha diversity of five control (a) and experimental (b) samples: The above images show the range of α -diversity values. The min, max, and mean values are shown, with the standard deviation ranges (σ and 2σ) in different shades. The α -diversity of this metagenome is shown in red.

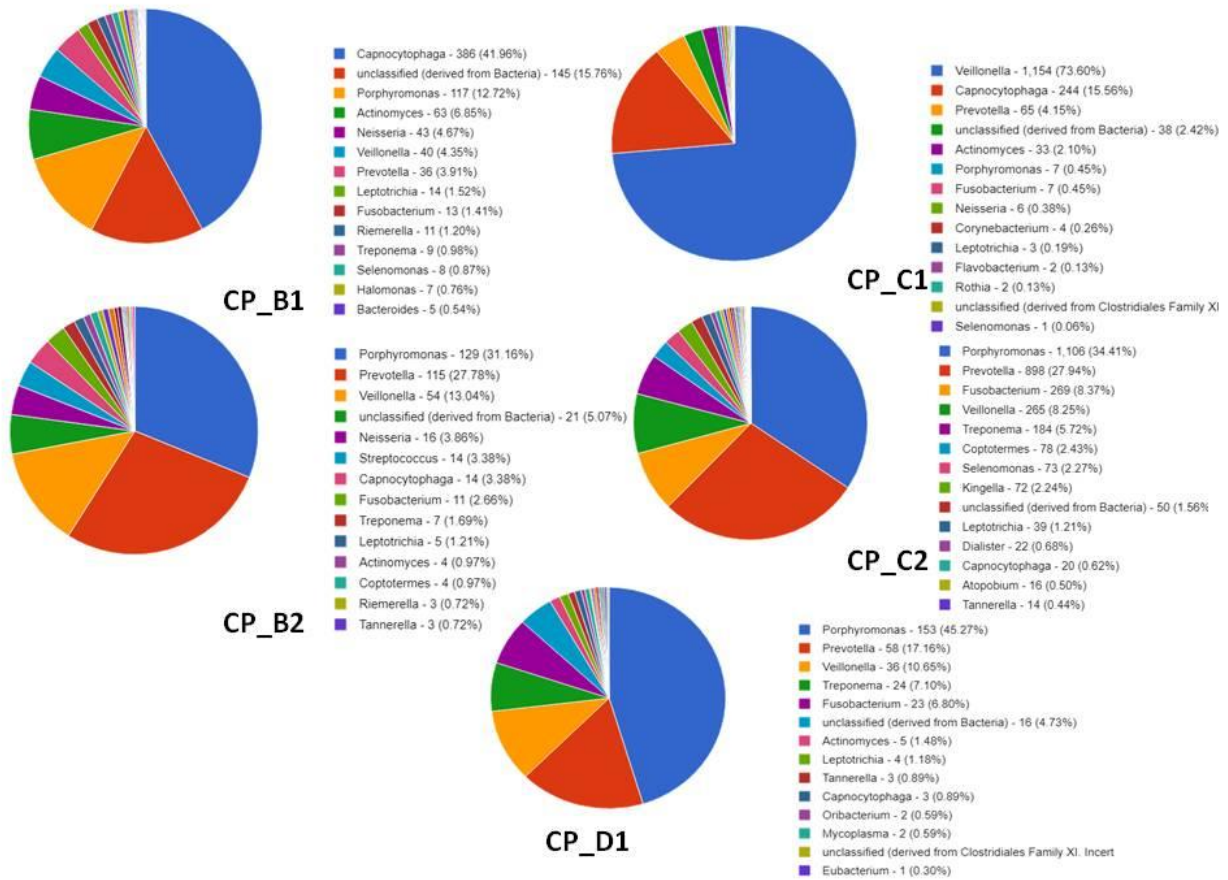
Supplementary Figure 6: Rarefaction curve of five control (a) and experimental (b) samples: The plot shows the rarefaction curve of the total number of annotated species richness per sample as a function of the number of sequences sampled.

Supplementary Table 1: Screening of 30 Chronic Periodontitis (CP) patients where, five patients (CP_B1, CP_B2, CP_C1, CP_C2, CP_D1) with the history of smoking and tobacco chewing, bleeding on probing, Periodontal pockets ≥ 5 mm and having Clinical attachment loss (CAL) were selected as experimental group (CP+S). Five patients of corresponding age group (CP_6, CP_7, CP_8, CP_15, CP_20) with the history of no smoking and tobacco chewing, bleeding on probing, Periodontal pockets ≥ 5 mm and having Clinical attachment loss (CAL) were included as control group. Raw reads and filtered consensus sequences (CCS) obtained after demultiplexing of barcoded individual samples.

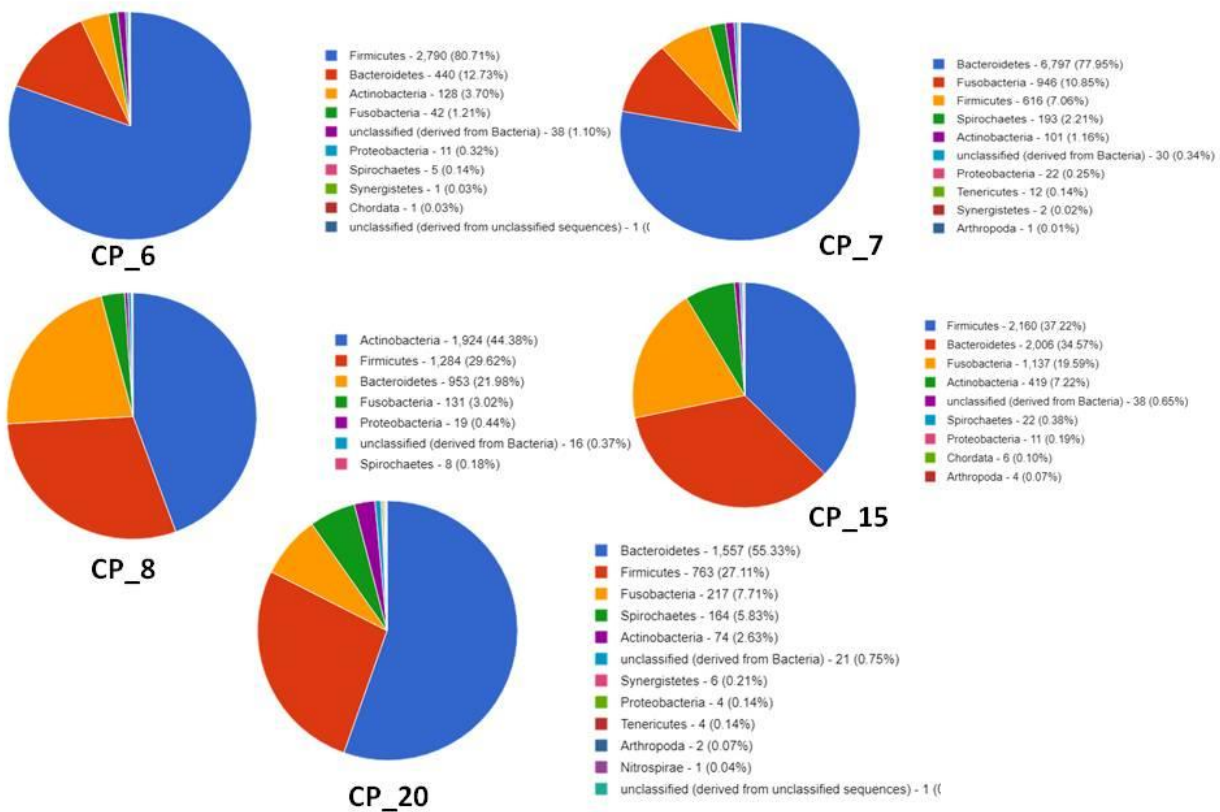
Group	Sample	Age	Raw Reads	Filtered Reads
Control (CP without smoking)	CP6	50	18441	12727
	CP7	60	22446	18378
	CP8	60	14842	7825
	CP15	55	14778	10887
	CP20	66	11332	5860
Experimental (CP with Smoking)	CP_D1	60	12658	1379
	CP_B1	42	21749	19564
	CP_B2	50	15976	10155
	CP_C1	47	14342	5197
	CP_C2	67	16982	7194
Total Reads			163546	99166



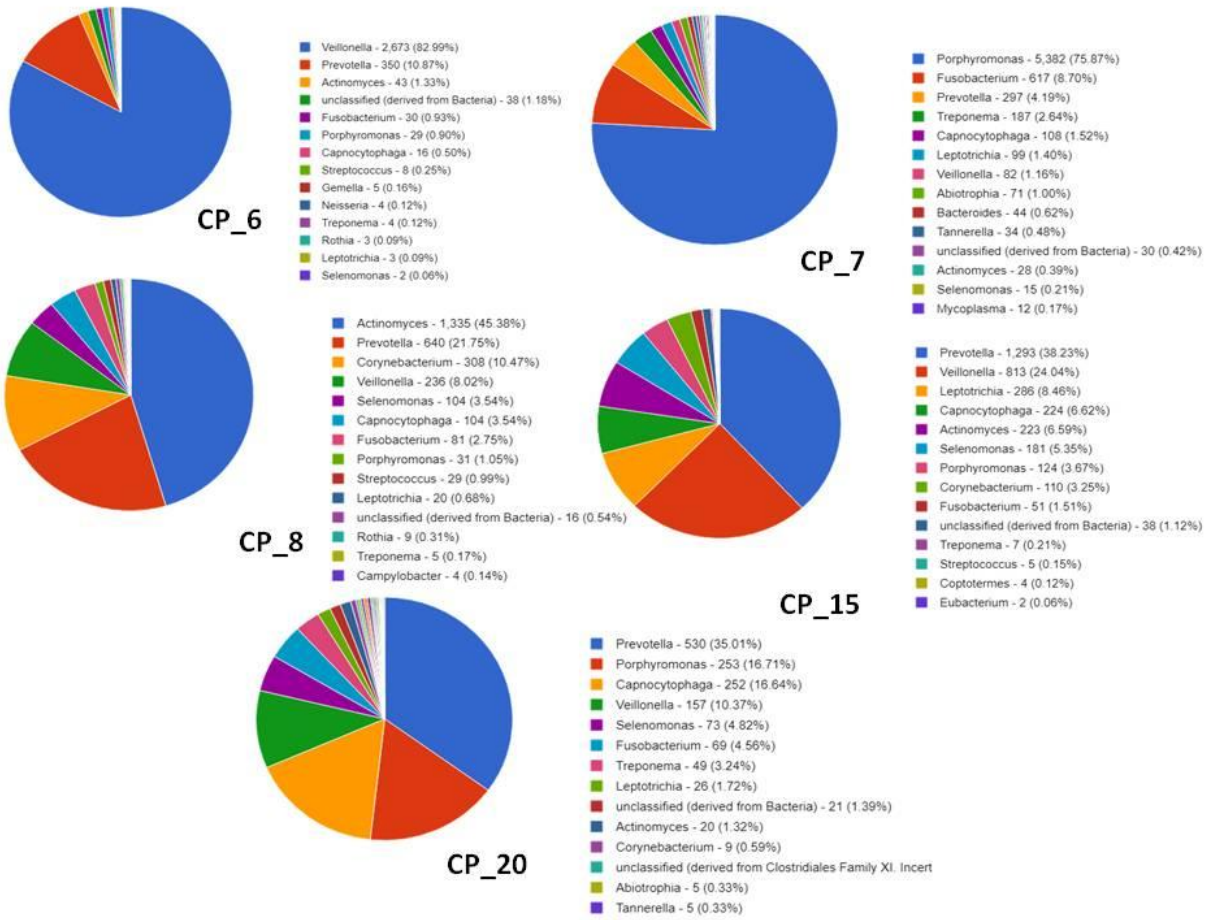
Supplementary Figure 1



Supplementary Figure 2



Supplementary Figure 3



Supplementary Figure 4



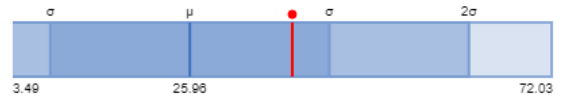
CP-6: The α -diversity of this data set is 10 species.



CP_7: The α -diversity of this data set is 13 species.



CP-8: The α -diversity of this data set is 28 species.



CP_15: The α -diversity of this data set is 39 species.

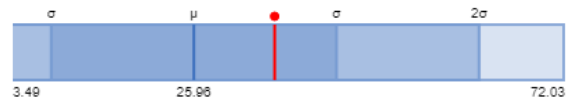


CP-20: The α -diversity of this data set is 72 species.

(a)



CP-B1: The α -diversity of this data set is 7 species.



CP_B2: The α -diversity of this data set is 36 species.



CP_C1: The α -diversity of this data set is 12 species.



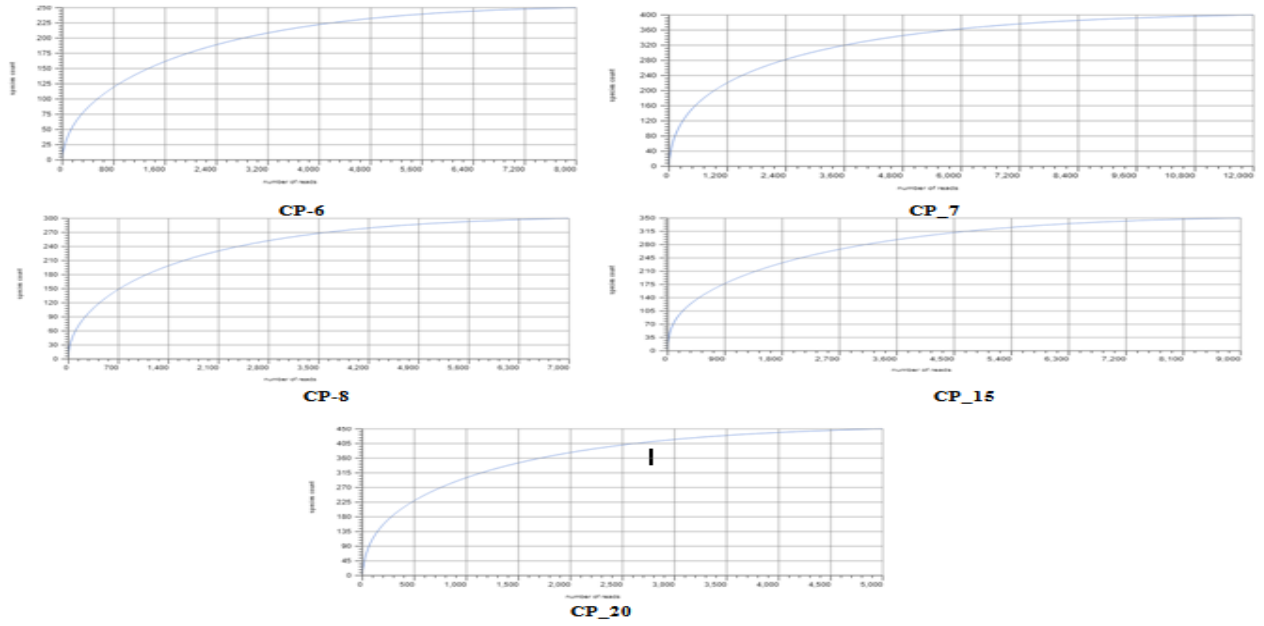
CP_C2: The α -diversity of this data set is 10 species.



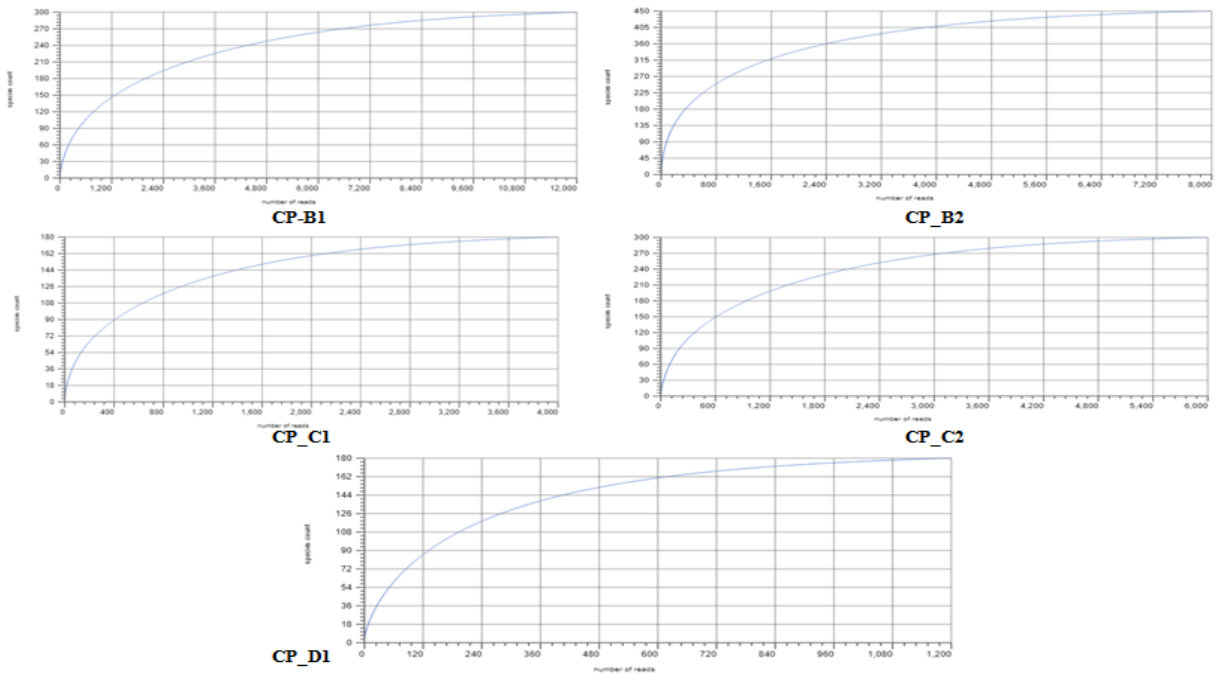
CP_D1: The α -diversity of this data set is 20 species.

(b)

Supplementary Figure 5



(a)



(b)

Supplementary Figure 6