

	Low diversity (n=43)	High diversity (n=51)	p value
Age (years)	53.58 ± 12.72	55.09 ± 14.64	0.30
Weight (kg)	69.97 ± 12.69	72.35 ± 14.43	0.242
Height (cm)	171.16 ± 9.12	170.43 ± 7.167	0.301
BMI (kg/m²)	23.73 ± 2.77	24.79 ± 4.06	0.083
Stress Score (Scare 0 to 10)	5.18 ± 2.58	4.35 ± 2.8	0.066
DMF (Decayed, Missing, Filled)	14.65 ± 4.99	14.88 ± 5.59	0.83
Decayed (D)	0.37 ± 0.90	0.60 ± 1.078	0.121
Missing (M)	9.13 ± 3.04	8.72 ± 4.59	0.184
Filled (F)	5.55 ± 3.34	5.74 ± 4.28	0.382
Number of dental brushing/day	1.93 ± 0.59	2.07 ± 0.59	0.23
Score PAI	3.95 ± 1.13	3.41 ± 0.98	0.01
Diagnostic of severe peri apical diseases (PAI =5)	46.5 % (n=20)	15.6 % (n=8)	Odds Ratio : 4.592 IC 95% [1.6329 ; 14.0728]; p=0.001

Supplementary Table S1: Clinical and oral parameters based on the diversity score (data as mean ± SD). *p<0.05. **p<0.01. ****p<0.0001. unpaired Mann-Whitney test).

Relative abundance (%) in oral microbiota	Microbiota parameters among the High div (n=51)	PAI≤3	PAI >3	p value
	α-diversity by the Shannon index	1.96±0.83	1.57 ± 0.91	0.0370
Family	Burkholderiaceae	0.90±1.84	0.16±0.74	0.0012
	Flavobacteriaceae	1.03±4.48	0.34±1.34	0.18
	Pseudomonadaceae	8.40±21.49	10.18±22.21	0.22
Genus	Propionibacterium	0.00±0.00	0.41±0.92	<0.0001
	Prevotella7	1.39±5.02	2.14±4.64	0.17
	Capnocytophaga	0.84±3.95	0.33±1.34	0.36
	Butyrivibrio2	0.02±0.10	0.44±1.69	<0.0001
	Sphingomonas	0.87±1.63	0.44±1.69	0.0348
	Pseudomonas	8.40±21.49	10.18±22.21	0.22

Supplementary Table S2: Relative abundance (%) for taxonomic family and genus identified with significant differences in granuloma microbiota in the two groups among the high diversity samples. (data as mean ± SD. *p<0.05. **p<0.01. ***p<0.0001. unpaired Mann-Whitney test).

Relative abundance (%) in oral microbiota	Microbiota parameters among the High div (n=51)	HBP +	HBP -	p value
	α -diversity by the Shannon index	1.82 ± 0.93	1.45± 0.87	0.0434
	α -diversity by the Chao Index	92.66 ± 25.76	82.04 ± 19.07	0.045
Family	Actinomycetaceae	0.016±0.46	1.41±3.62	0.0025
	Corynebacteriaceae	0.02±0.07	0.54±1.65	0.0035
	Muribaculaceae	0.43±1.73	0.090.56	0.0914
	Sphingobacteriaceae	0.12±0.37	1.29±3.73	0.036
	ClostridialesvadinBB60group	0.96±2.81	0.15±1.09	0.0031
	Eubacteriaceae	0.008±0.03	0.21±0.85	0.38
	FamilyXIII_Uncertain	3.55±13.36	0.85±2.11	0.20
	Lachnospiraceae	0.88±1.60	0.0003±0.001	<0.0001
	Ruminococcaceae	0.50±1.50	0.0003±0.001	0.20
	Leptotrichiaceae	8.01e-005±0.0003	0.0003±0.001	0.68
	Desulfovibrionaceae_Uncertain	0.50±1.53	0.25±1.25	0.38
	Nesseriacae	0.13±0.38	0.25±1.25	0.84
Genus	Actinomyces	0.01±0.05	1.23±2.75	0.0023
	Corynebacterium	0.017±0.074	1.41±0.62	<0.0001
	Lawsonella	0.00±0.00	0.056±0.40	0.034
	Rothia	0.09±0.40	0.52±2.13	0.2302
	Pseudopropionibacterium	0.06±0.20	0.99±5.50	0.046
	Elizabethkingia	7.19±22.79	1.22±5.49	0.025
	Nubsella	0.11±0.37	0.84±2.76	0.089
	Streptococcus	0.23±0.80	0.91±2.79	0.073
	Pseudoramibacter	0.009±0.03	0.21±0.85	0.38
	Blautia	0.32±0.92	0.0008±0.002	0.19

	GCA_900066575	0.08±0.34	0.001±0.01	0.13
	Roseburia	0.11±0.27	0.0003±0.001	0.20
	Leptotrichia	8.02e-005±0.0003	0.0003±0.001	0.68
	Neisseria	0.05±0.22	0.44±1.62	0.0099
	Serratia	0.002±0.006	2.26±0.83	0.0060

Supplementary Table S3: Relative abundance (%) for taxonomic family and genus identified with significant differences in granuloma microbiota in the two groups among the high diversity samples. (data as mean ± SD. *p<0.05. **p<0.01. ***p<0.0001. unpaired Mann-Whitney test).

