

Supplementary Tables.

Table S1

Classification of the study groups and clinical characteristics of the participants.

Group	Number	Age, median [Q1, Q3]	Probing depth	Bone loss thresholds	Probing/suppuration
HI	10	60.0 [58.0, 64.75]	0 mm	0 mm	N
PI	10	57.5 [49.5, 69.75]	≥6 mm	≥3 mm	Y
PI-HTN	10	71.5 [62.75, 77.5]	≥6 mm	≥3 mm	Y
PI-DM	10	65.5 [58.75, 67.5]	≥6 mm	≥3 mm	Y
PI-OP	10	67.5 [66.25, 69.75]	≥6 mm	≥3 mm	Y
Total	50	66.0 [58.5, 70.0]	–	–	–

6 **Table S2**

7 Primer sequences used in this study.

Oligo Name	Sequence (5'-3')
<i>LCN2</i>	F: CCACCTCAGACCTGATCCCA R: CCCCTGGAATTGGTTGTCCTG
<i>PDK1</i>	F: GGATTGCCCATATCACGTCTTT R: TCCCGTAACCCTCTAGGGAATA
<i>NUCB2</i>	F: ATGAGGTGGAGGACCATCCTG R: TGGTTCTATCTTCGCACTTTCC
<i>MS4A6A</i>	F: TGTGGCATGATGGTATTGAGC R: AGGGTCCTATGAATGGGTAAGC
<i>LAMC1</i>	F: GGACTCCGCCCAGGAATA R: ACTTGAGACGCACATAGGTGA
<i>CASP4</i>	F: TCTGCGGAACTGTGCATGATG R: TGTGTGATGAAGATAGAGCCCAT
<i>CLEC3B</i>	F: CCCAGACGAAGACCTTCCAC R: CGCAGGTACTCATAACAGGGC
<i>TEAD3</i>	F: TGGACCCTCTCAGGACATCAA R: CCAGGGGCTCATAACTGCTG
<i>FGFBP1</i>	F: CTTACAGCAAAGTGGTCTCA R: GACACAGGAAAATTCATGGTCCA
<i>RPL17</i>	F: TTCCGACGTTACAATGGTGGA R: TCTGCGTTTTTAAGCATGTGC
<i>β-actin (ACTB)</i>	F: GACTTAGTTGCGTTACACCCTTTCTTG R: CTGTCACCTTCACCGTTCCAGTTTT

Table S3. TMM- and CPM-normalized expression values used for Figure 1.

a. PI-HTN versus HI

Gene symbol	HI	PI-HTN	Entrez ID	Biotype
VSIG10L2	3.686277	0.000000	338667	protein_coding
RPS6KA6	3.077505	0.000000	27330	protein_coding
MT4	2.927025	0.000000	84560	protein_coding
LCE2A	2.911077	0.000000	353139	protein_coding
CAPN6	3.338252	0.000000	827	protein_coding
INSM1	3.239533	0.000000	3642	protein_coding
KIAA1522	4.373830	1.208557	57648	protein_coding
PYHIN1	0.000000	3.624257	149628	protein_coding
PDK2	3.974148	1.021566	5164	protein_coding
SPINK8	0.000000	0.000000	646424	protein_coding
IQGAP2	0.586574	4.800993	10788	protein_coding
PRSS22	2.441344	6.640939	64063	protein_coding
ARHGAP15	0.586574	3.613259	55843	protein_coding
DUSP5	2.173682	5.588104	1847	protein_coding
LCN2	1.225154	6.078595	3934	protein_coding
ADGRF1	0.503922	4.288520	266977	protein_coding
NR4A2	0.416246	3.424832	4929	protein_coding
ZNF641	3.147241	3.193350	121274	protein_coding
NUCB2	5.385535	8.848318	4925	protein_coding
IL19	0.000000	4.056507	29949	protein_coding
APLN	0.115849	3.020983	8862	protein_coding
FFAR2	0.000000	2.899499	2867	protein_coding
ABTB2	0.586574	3.462088	25841	protein_coding
TRR-CCG1-1	0.000000	3.117543	100189365	tRNA
TMC5	0.000000	3.265371	79838	protein_coding
PLXNC1	1.776007	5.085930	10154	protein_coding
GPR68	4.194389	3.373612	8111	protein_coding
MED4	5.781722	5.806608	29079	protein_coding
CCDC144BP	0.738899	3.779895	284047	transcribed_pseudogene
PDK1	2.942800	7.752480	5163	protein_coding

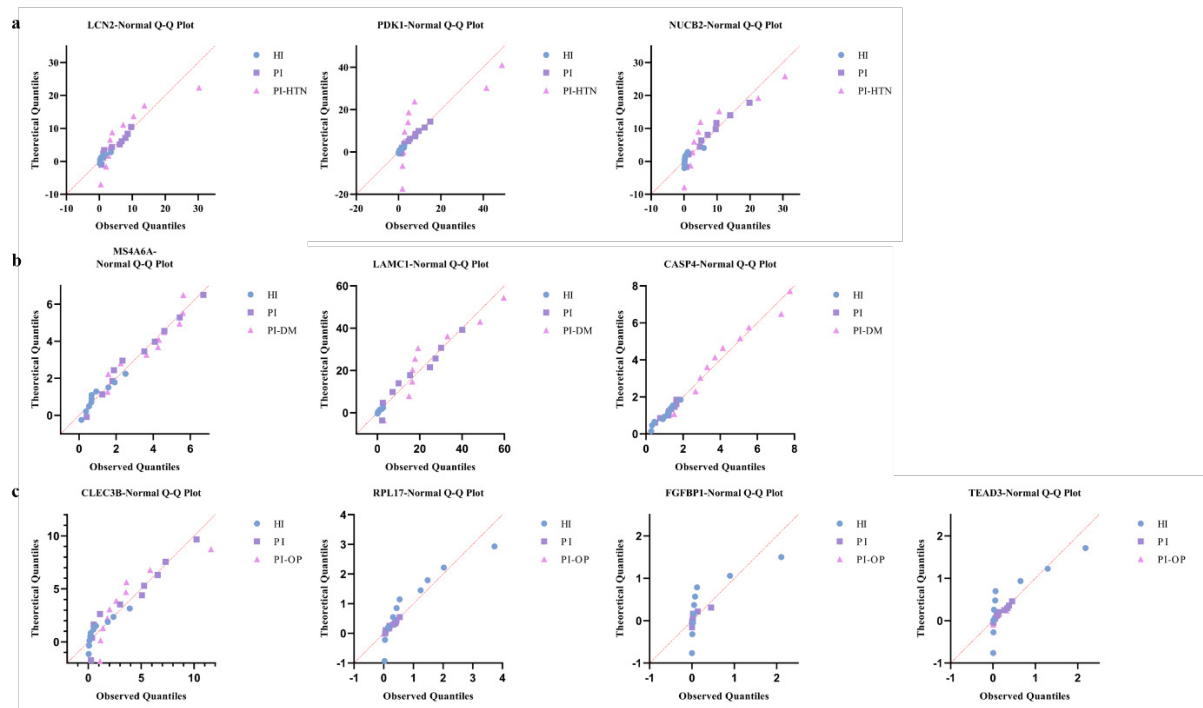
Gene symbol	HI	PI-DM	Entrez ID	Biotype
LOC124900335	6.796659	1.207073	124900335	lncRNA
TTYH3	0.000000	5.808696	80727	protein_coding
TRABD	0.000000	5.119527	80305	protein_coding
RCN1	0.000000	5.526885	5954	protein_coding
PLBD2	0.000000	5.067926	196463	protein_coding
GBP4	0.000000	5.941607	115361	protein_coding
COPB2	0.000000	5.916820	9276	protein_coding
EBP	0.000000	5.067926	10682	protein_coding
SDF4	0.251302	5.880960	51150	protein_coding
OSTC	0.251302	5.863771	58505	protein_coding
LAMC1	0.251302	6.221789	3915	protein_coding
HAX1	0.251302	5.389507	10456	protein_coding
ATRAID	0.251302	5.677123	51374	protein_coding
EIF2S1	0.251302	5.386502	1965	protein_coding
SSH1	0.465256	5.564607	54434	protein_coding
SLCO2B1	0.000000	5.471225	11309	protein_coding
SLC39A11	0.000000	5.306067	201266	protein_coding
PFKP	0.000000	5.334420	5214	protein_coding
PAFAH2	1.629050	3.798297	5051	protein_coding
MS4A6A	0.000000	6.378261	64231	protein_coding
LPCAT3	0.000000	5.101309	10162	protein_coding
LAMTOR2	0.000000	5.179802	28956	protein_coding
HLA-DRB6	0.465256	6.691245	3128	transcribed_pseudogene
HCK	0.000000	5.056624	3055	protein_coding
GLB1	0.000000	5.197061	2720	protein_coding
E2F3	0.000000	5.389507	1871	protein_coding
DRAM1	0.000000	5.383489	55332	protein_coding
DNASE2	0.465256	6.397798	1777	protein_coding
CASP4	0.000000	5.953843	837	protein_coding
CCL8	0.000000	5.309245	6355	protein_coding

Gene symbol	HI	PI-OP	Entrez ID	Biotype
GLB1L	1.888840	5.436638	79411	protein_coding
CLEC3B	1.607867	5.137845	7123	protein_coding
LOC124905123	0.113594	3.893690	124905123	lncRNA
SBSN	10.306358	6.751758	374897	protein_coding
SPRR2E	12.385276	8.537336	6704	protein_coding
CASTOR2	5.294871	1.815827	729438	protein_coding
DIPK2A	4.478926	0.623054	205428	protein_coding
SERPINB2	5.038569	0.238840	5055	protein_coding
MRPS22	5.020476	1.485653	56945	protein_coding
SERPINB11	5.059984	1.176519	89778	protein_coding
WDR48	4.586142	0.782556	57599	protein_coding
GRPEL2	4.357344	0.238840	134266	protein_coding
RCL1	4.119694	0.238840	10171	protein_coding
RPL6	8.164415	4.451876	6128	protein_coding
PPL	7.449850	3.422551	5493	protein_coding
RPL17	8.916427	4.760559	6139	protein_coding
PRSS3	6.555533	3.067260	5646	protein_coding
PTPRF	8.884773	3.470206	5792	protein_coding
TTC39A	3.961792	0.000000	22996	protein_coding
S100A8	14.777236	11.104032	6279	protein_coding
HTT	4.615366	1.056766	3064	protein_coding
CLDN17	3.630747	0.000000	26285	protein_coding
AK4	3.532034	0.000000	205	protein_coding
CDKN3	4.166516	0.000000	1033	protein_coding
TEAD3	3.931129	0.443700	7005	protein_coding
FH	5.774517	1.575546	2271	protein_coding
KLK7	8.055350	2.257288	5650	protein_coding
TMEM106B	5.118991	1.575546	54664	protein_coding
ATP10B	5.446210	1.887782	23120	protein_coding
FGFBP1	7.330097	3.746638	9982	protein_coding

17 **Note:** Values are presented as TMM- and CPM-normalized expression values on a log₂ scale. For each group,
18 RNA from three individual samples was pooled before library preparation, resulting in one RNA-seq library per
19 group. HI, healthy implant; PI, peri-implantitis; HTN, hypertension; DM, diabetes mellitus; OP, osteoporosis.

Supplementary Figure

Figure S1. Normal Q–Q plots for RT-qPCR validation data.



Normal Q–Q plots showing the distribution of RT-qPCR data for *LCN2*, *PDK1*, *NUCB2*, *MS4A6A*, *LAMC1*, *CASP4*, *CLEC3B*, *RPL17*, *FGFBP1*, and *TEAD3* across the corresponding study groups. Normality was assessed using the Shapiro–Wilk test as described in the Statistical Analysis section. Each group included 10 independent biological samples.