Table S1. Classes of chromatin modification enzymes examined in this study.

DNA Methyltransferases								
DNMT1	DNMT3A	DNMT3B						
DNA & Histone Demethylases								
KDM1A (KDM1) (LSD1)	KDM5B	KDM5C	KDM4A	KDM4C	KDM6B (JmjD3)	MBD2		
Histone Acetyltransferases								
ATF2 (CREB2)	CDYL	CIITA	CSRP2BP	ESCO1	ESCO2	HAT1	KAT2A (GCN5L2)	KAT2B (PCAF)
KAT5	KAT8 (MYST1)	KAT7 (MYST2)	KAT6A (MYST3)	KAT6B (MYST4)	NCOA1	NCOA3	NCOA6	
Histone Deacetylases								
HDAC1	HDAC2	HDAC3	HDAC4	HDAC5	HDAC6	HDAC7	HDAC8	HDAC9
HDAC10	HDAC11							
Histone Methyltransferases								
CARM1 (PRMT4)	DOT1L	EHMT2	KMT2A	KMT2C	PRMT1	PRMT2	PRMT3	
PRMT5	PRMT6	PRMT7	PRMT8	SETDB2	SMYD3	SUV39H1		
SET Domain Proteins (Histone Methyltransferase Activity)								
ASH1L	KMT2C	KMT2E	NSD1	SETD1A	SETD1B	SETD2	SETD3	SETD4
SETD5	SETD6	SETD7	SETD8	SETDB1	SUV39H1	SUV420H1	WHSC1	
Histone Phosphorylation								
AURKA	AURKB	AURKC	NEK6	PAK1	RPS6KA3	RPS6KA5		
Histone Ubiquitination								
DZIP3	MYSM1	RNF2	RNF20	UBE2A	UBE2B	USP16	USP21	USP22

Table S2. Chromatin modification enzymes showing significant transcriptional alterations in periodontal disease.

Altered enzymes in periodontally-involved tissue	**Fold expression**
DNA Methyltransferases	
DNMT3A	-2.5095
DNMT3B	-2.3956
DNA & Histone Demethylases	
KDM5C	-2.0033
KDM6B	-2.6471
Histone Acetyltransferases	
ESCO1	2.1489
ESCO2	2.1654
KAT2A	-2.933
KAT5	-2.0006
NCOA6	-2.3545
CIITA	-2.2383
CSRP2BP	-2.1176
Histone Methyltransferases	
KMT2A	-2.394
PRMT2	-2.044
PRMT7	-2.0942
PRMT8	-9.059
SET Domain Proteins (Histone Methyltransferase Activity)	
SETD4	2.4176
Histone Deacetylases	
HDAC10	-3.0051
HDAC11	-5.519
HDAC4	-3.5318
HDAC5	-2.4715
HDAC7	-2.4562
HDAC9	-2.5854
Histone Phosphorylation	
AURKB	2.2762
NEK6	-2.3076
Histone Ubiquitination	
RNF20	-2.2711

* Numerical values represent fold expression level in diseased tissue versus healthy controls.

Table S3. Chromatin modification enzymes showing significant transcriptional alterations in *Td*-challenged PDL cells.

Altered enzymes in *T. denticola*-challenged PDL cells	**Fold expression***
DNA Methyltransferases	
DNMT3B	-2.2
DNA & Histone Demethylases	
KDM4A	-2.24
KDM4C	-2.04
KDM5C	-2.1
Histone Acetyltransferases	
CSRP2BP	-2.38
KAT2B	-2.67
KAT6A	-2.28
KAT6B	-2.07
NCOA1	-2.4
Histone Methyltransferases	
EHMT2	-3.44
PRMT5	-2
PRMT6	-2
SETDB2	-2
SMYD3	-2.24
SUV39H1	-2.47
SET Domain Proteins (Histone Methyltransferase Activity)	
SETD2	-2.06
SETD8	-2.43
SETDB1	-2.21
SUV420H1	-2.05
WHSC1	-2.04
Histone Deacetylases	
HDAC10	-2.09
HDAC4	-2.43
HDAC6	-2.03
Histone Phosphorylation	
AURKB	-5.57
Histone Ubiquitination	
RNF20	-2.09
USP22	-2.04

* Numerical values represent fold expression level in challenged versus control PDL cells.