Tabla S4. Methodological and results description of studies assessing polymorphonuclears (PMNs) cells or subcomponents (neutrophils) differential gene expression

Authors	Subject/ Population	Comparison	Cell Type(s)/ Source	Methylation/ Expression Technique	Main Results	Systemic Biomarkers meth/mRNA
Wright HJ et al., 2008 [30]	19 Patientes with periodontitis (19, 36- 61 years) (baseline and 3 months after periodontal treatment*)	19 Age- and gender-matched periodontally healthy control subjects (37– 62 years)	Neutrophils (discontinuous Percoll gradient isolation)/ peripheral blood	HG_U133A microarrays (Affymetrix) semi-quantitative RT-PCR	Pairwise analysis of hybri dization data indicated that of the 5680 genes detected as being present in both targets, 163 genes (2.87% of detected genes) were 2-fold or greater differentially expressed between healthy and periodontitis patient samples. 14 were more highly expressed in neutrophils from healthy patients than those with periodontitis (age- and gender-matched) 149 were upregulated in periodontitis patient neutrophils relative to healthy patients. RT-PCR analysis The gene expression data confirmed that transcript levels for all six genes (MX1, IFIT4, G1P2, IFIT1, CIG5, and IFI44-like) were increased.	↑ mRNA *MX1*, *IFIT4*, *G1P2*, *IFIT1*, *CIG5*, and *IFI44-like*
Iwata T et al., 2009 [31]	36 patients with periodontitis (age range: 16 to 41 years)	36 systemically healthy control subjects (n = 36; age range: 21 to 39 years)	PMNs discontinuous gradient	RT-qPCR	Compared to healthy PMNs, Periodontitis PMNs expressed significantly more CP mRNA.	↑ mRNA *CP*

HG, Human genome; CP, ceruloplasmin. Green arrow ↑denote increase in mRNA expression.