**File S2: Supplementary Figures**

**Figure S1. PCR-RFLP analysis of *TNFB* +252A/G polymorphism on 2.0 % agarose gel electrophoresis:** lanes: 1, 3, 4, 5 & 7 show homozygous (GG) genotypes; lane: 2 shows homozygous (AA) genotype; lane: 6 shows heterozygous (AG) genotype.

**Figure S2. TaqMan end point fluoroscence analysis for *TNFB* C/A; (Thr26Asn) polymorphism** using dual color hydrolysis probes (FAM and VIC) by LightCycler®480Real-Time PCR protocol.The three genotypes identified as: AA, AC and CC, based on fluorescence with Channel 465-510 (FAM for ‘A’ allele) and Channel 536-580 (VIC for ‘C’ allele). A no-template control (NTC) was used with each SNP genotyping assay (shown as grey spot).

**Figure S3. Melt curve analysis of *TNFB*, *ICAM1* and *GAPDH* showing specific amplification.**

**Figure S4. Relative gene expression of *TNFB* and *ICAM1* with respect to *TNFB* exon 3 C/A in controls and vitiligo patients:**

**(A)** Expression of *TNFB* mRNA with respect to *TNFB* exon 3C/A in 166 vitiligo patients and 175 controls using Mann-Whitney Wilcoxon test [Mean∆Cp ± SEM: Controls CC vs Patients CC: 8.102 ± 0.1747 vs 7.678 ± 0.2379 (*p=*0.168); Controls CA vs Patients CA: 7.761 ± 0.0952 vs 7.028 ± 0.3376 (*p=*0.039); Controls AA vs Patients AA: 6.918 ± 0.2808 vs 5.217 ± 0.5087 (*p=*0.015) (*NS* = non-significant)].

**(B)** Expression of *ICAM1* mRNA with respect to *TNFB* exon 3C/A in 166 vitiligo patients and 175 controls using Mann-Whitney Wilcoxon test [Mean∆Cp ± SEM: Controls CC vs Patients CC: 8.767 ± 0.2267 vs 8.133 ± 0.2658 (*p=*0.074); Controls CA vs Patients CA: 8.494 ± 0.2434 vs 7.225 ± 0.2729 (*p=*0.001); Controls AA vs Patients AA: 8.007 ± 0.3297 vs 6.327 ± 0.4397 (*p=*0.005).

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