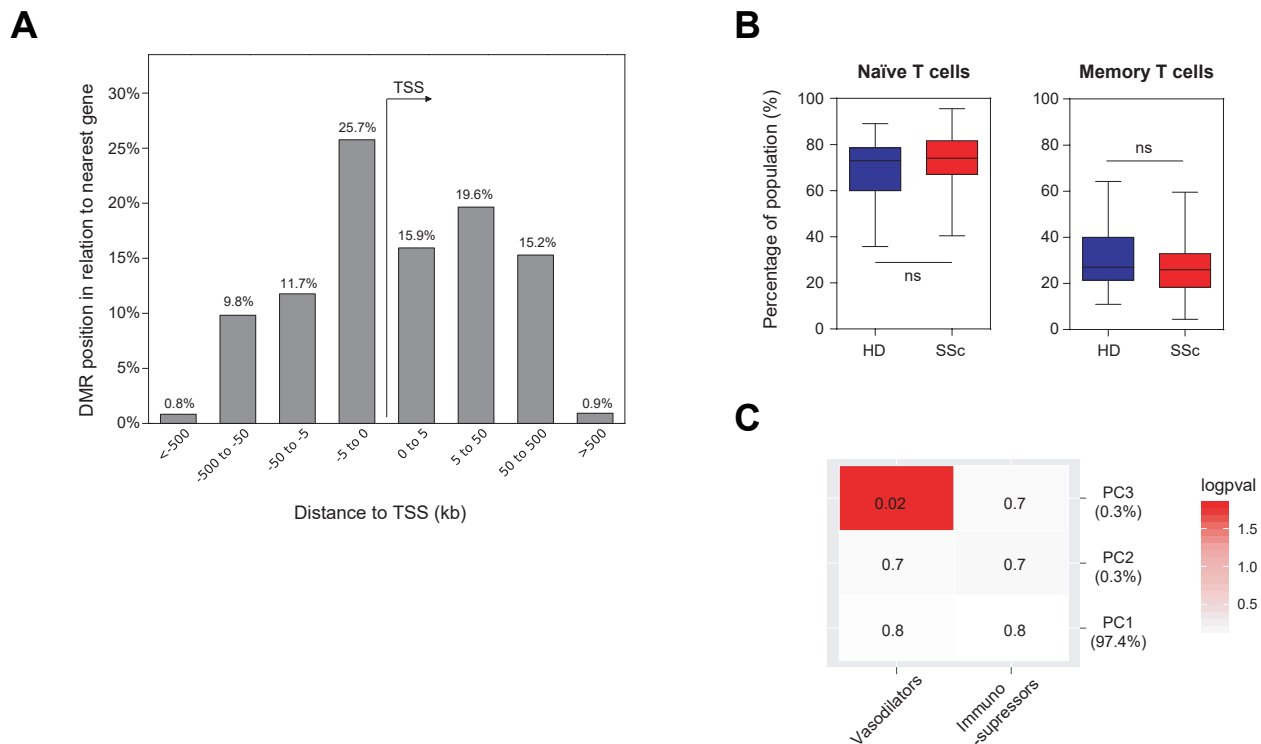


Figure S2



Additional file 5: Figure S2. (A) Bar graph representing the genomic distribution of identified DMRs in relation to transcription start site (TSS) as mapped utilizing the GREAT online tool. (B) Deconvolution analysis of CD4+ T cell gene expression utilizing the Absolute Immune Signal (ABIS) online tool. (C) Wilcoxon signed-rank test of variables in which patients were treated with vasodilators (n = 14) and/or immunosuppressive therapy (n = 21) and their association with the first three principal components (PC) identified for SSc-associated DEGs. Percentage represents the percentage of contribution of each PC to total variance.