Statistical analysis for viral load (baseline and 4 weeks) and other clinical features were done using GraphPad Prism software v 5.03 statistical package. Parametric and non-parametric t-tests were carried out and P<0.05 was considered significant. For flow cytometry results, Cellquest software (BD Biosciences, USA) was used. Analysis of up-regulated and down-regulated genes was done using web based online software RT^2 Profiler PCR array data analysis version 3.5 software. To check interactions and associations between different genes, string software available online was used.