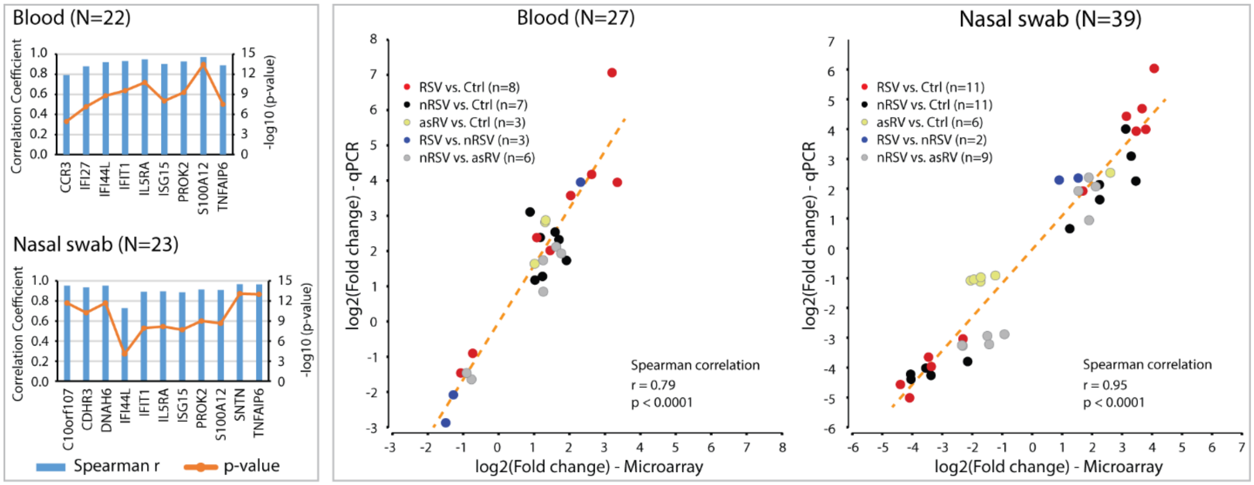
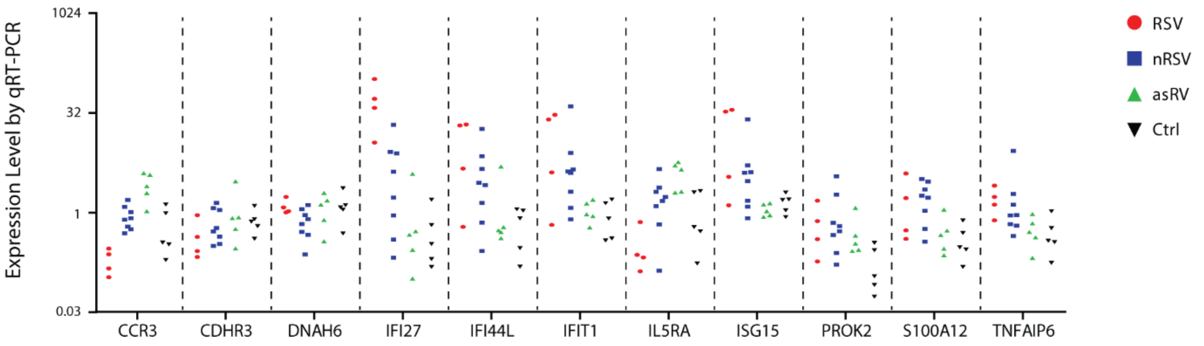

A Signal correlation

B Fold change correlation


C Blood Samples

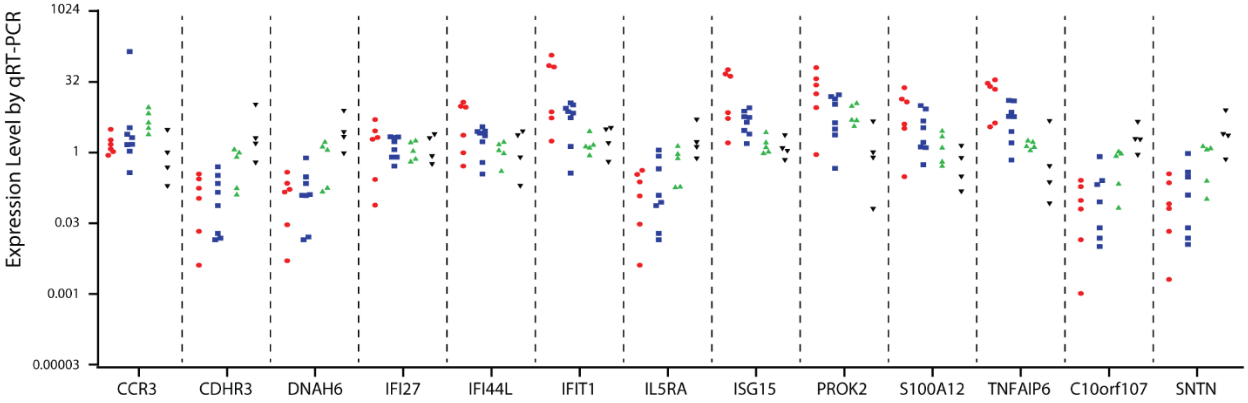

D Nasal Samples

Figure S7. RT-qPCR validation. RT-qPCR assays were performed on 11 genes for blood samples and 13 genes for nasal samples, each of which showed a significant difference in microarray mean signal intensity in at least 1 of the 5 comparisons between the subject groups. Panel A shows the signal correlation between RT-qPCR and microarray for each gene using the Spearman correlation test. Panel B shows the correlation between signal fold-change measured by RT-qPCR and microarray. In Panels A and B, each gene is represented by a dot. Each gene was analyzed separately for each of 5 between-group comparisons, which are indicated with different colors. Only comparisons that showed differential expression are displayed. RT-qPCR data is shown in Panel C for blood and Panel D for nasal samples.