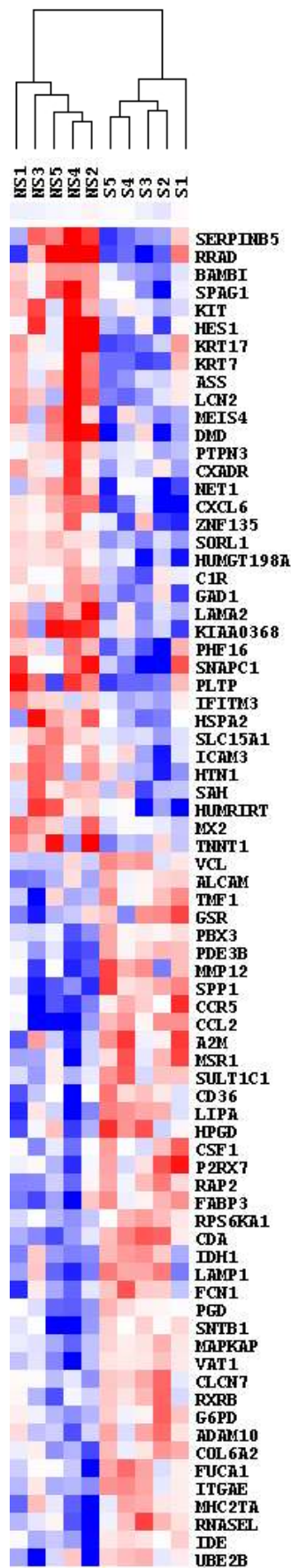


Supplemental Figure 2



**Supplemental Figure 2.** Cluster analysis of gene expression levels in smokers and non-smokers.

The normalized, log-transformed expression levels for the 75 genes that were differentially expressed in smokers and non-smokers were evaluated using the Cluster program (16) and subjected to hierarchical complete linkage clustering by both individual and gene. The resulting cluster was visualized with the TreeView (16) program. Genes expressed above average level are represented in *red*; genes expressed below average level are represented in *blue*. Average levels across all arrays are represented in *white*. The intensity of the *red* and *blue* squares indicates the degree of up- or down-regulation with respect to the average. Non-smokers are labeled as *NS* followed by an individual number, and smokers are labeled as *S* followed by an individual number. As expected, since these genes were selected because their expression levels were altered in smokers compared to non-smokers, the smokers and non-smokers clearly segregate. The 35 genes that are up-regulated in non-smokers are all on the top portion of the cluster, while the 40 genes that are up-regulated in smokers are all in the bottom portion of the cluster. Genes are labeled using the gene symbols, as in Tables I and II.