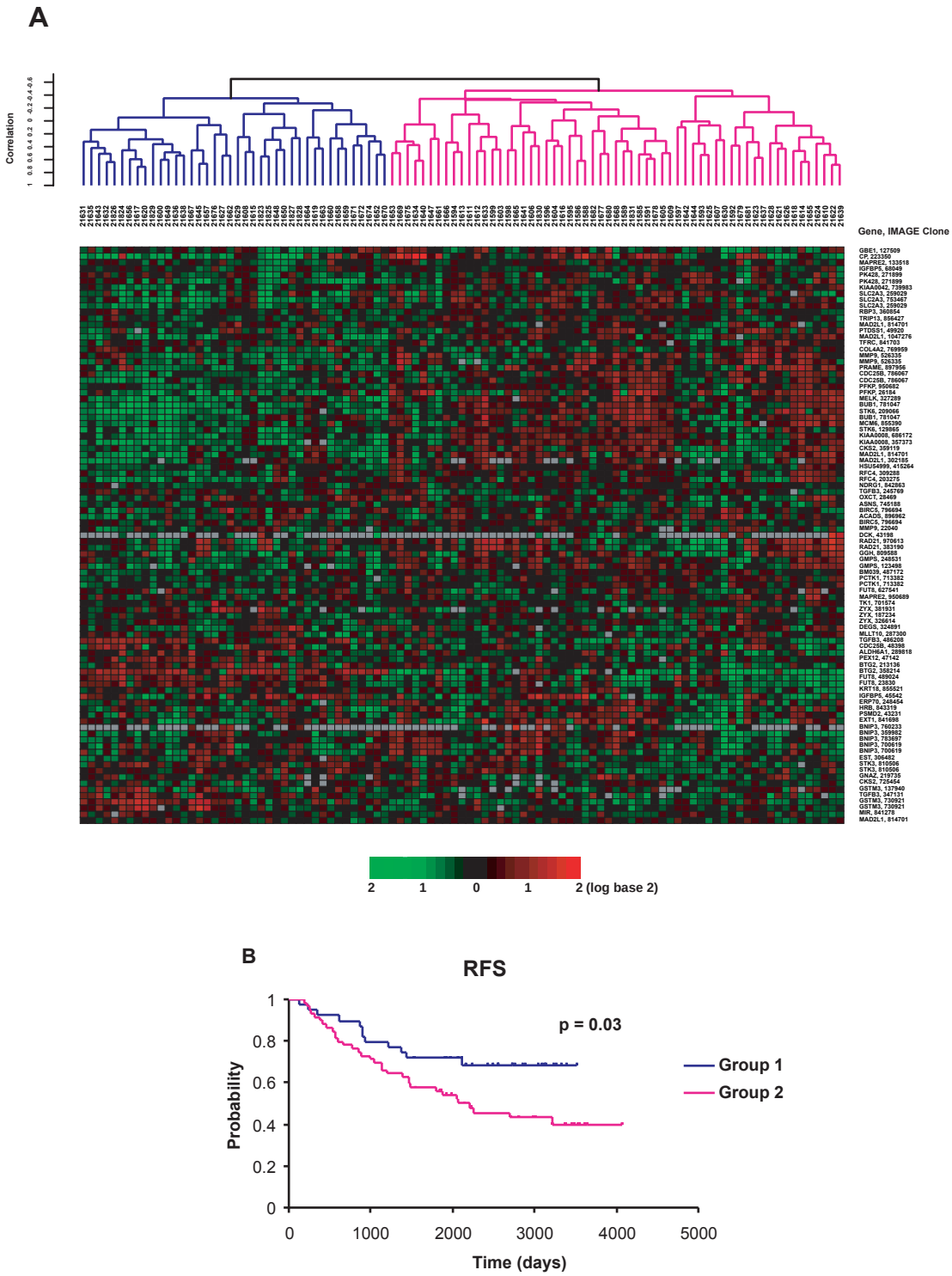
Figure 3



(A) Hierarchical clustering analysis of 93 probes elements overlapping between the prognostic gene list of Van't Veer et al previously reported and our cDNA microarray. Each row represents a single gene and each column represents a tumor specimen. Red and green bars indicate the amount by which the log base 2 ratio of expression falls above (red) or below (green) the median log base 2 ratio for that gene across all tumors, where expression ratio is calculated as the expression in a breast tumor as compared to Universal Human Reference (UHR) (Stratagene). Black bars indicate expression ratios approximately equal to the median expression ratio for the gene across the tumors, and gray bars indicate missing or filter-excluded data. (B) The tumor specimens could be separated into two main clusters based on the differences in gene expression with distinct relapse-free survival (RFS) as has been assessed by Kaplan Meier analysis.