Accurate cancer classification is critical for cancer treatment. Gene expression profile is expected to enable us to diagnose tumors precisely and systematically. Among a large number of genes, we need to identify some of them that are discriminative. Finding the minimum subset of genes that interact can help cancer diagnosis. We can expect that not all the genes are carrying relevant information for a particular classification task. The process of extracting only the important components is called gene or feature extraction. A common situation in gene-related classification problems is that there are thousands of genes with only hundreds of samples or less, i.e., the number of dimensions is much more than the number of samples. This creates a problem of over-fitting for many learning methods and raises an interesting question. How to reduce the dimensionality of the problem in extracting the gene signatures? ICA (Independent Component Analysis) defines a generative model in separating linear mixtures of independent source signals for the observed multivariate data. The compact ICA is based on the assumption that the latent independent components are as compact as possible. In this talk, a novel algorithm, based on PCA (Principal Component Analysis) and compact ICA, is presented for gene feature extraction. After the feature extraction, the nonlinear SVM (Support Vector Machine) is employed for classification. Performance of the method is illustrated using leukemia data.