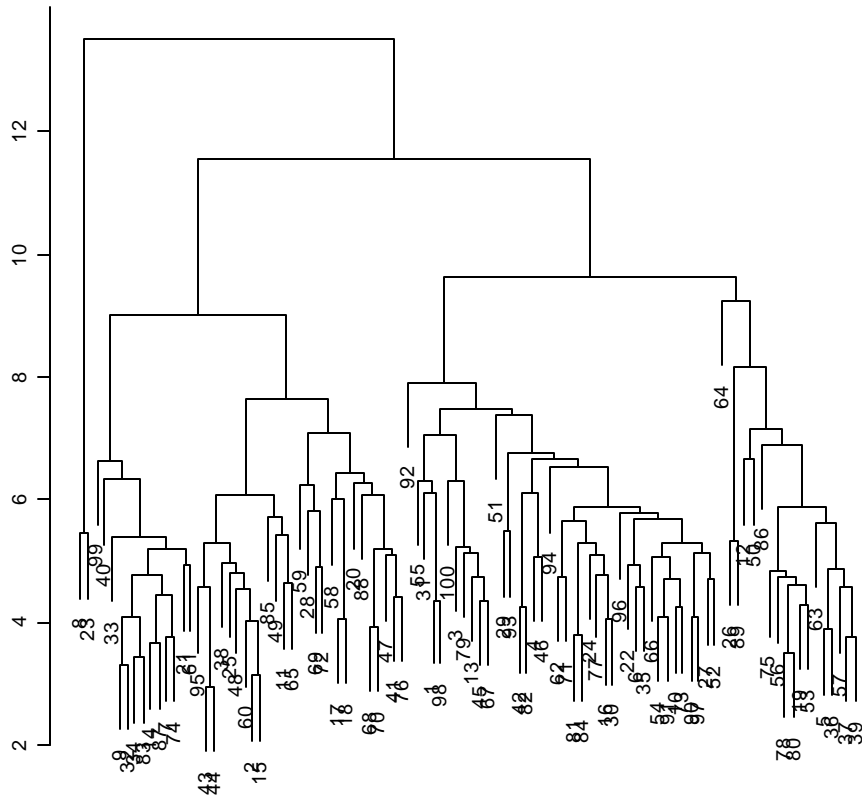


Figure 9.1 Tree dendrograms using the (i) average linkage (ii) complete linkage criteria for a dataset with two tumors.

(i) Average Linkage



(ii) Complete Linkage

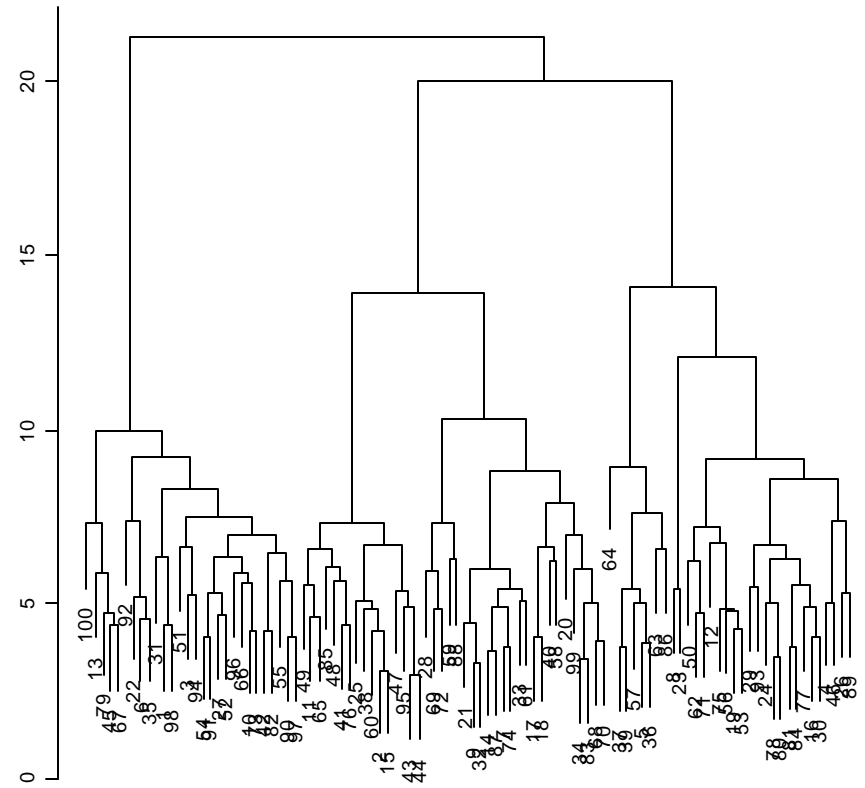


Figure 9.2 Clusters of samples for a dataset with two tumors.

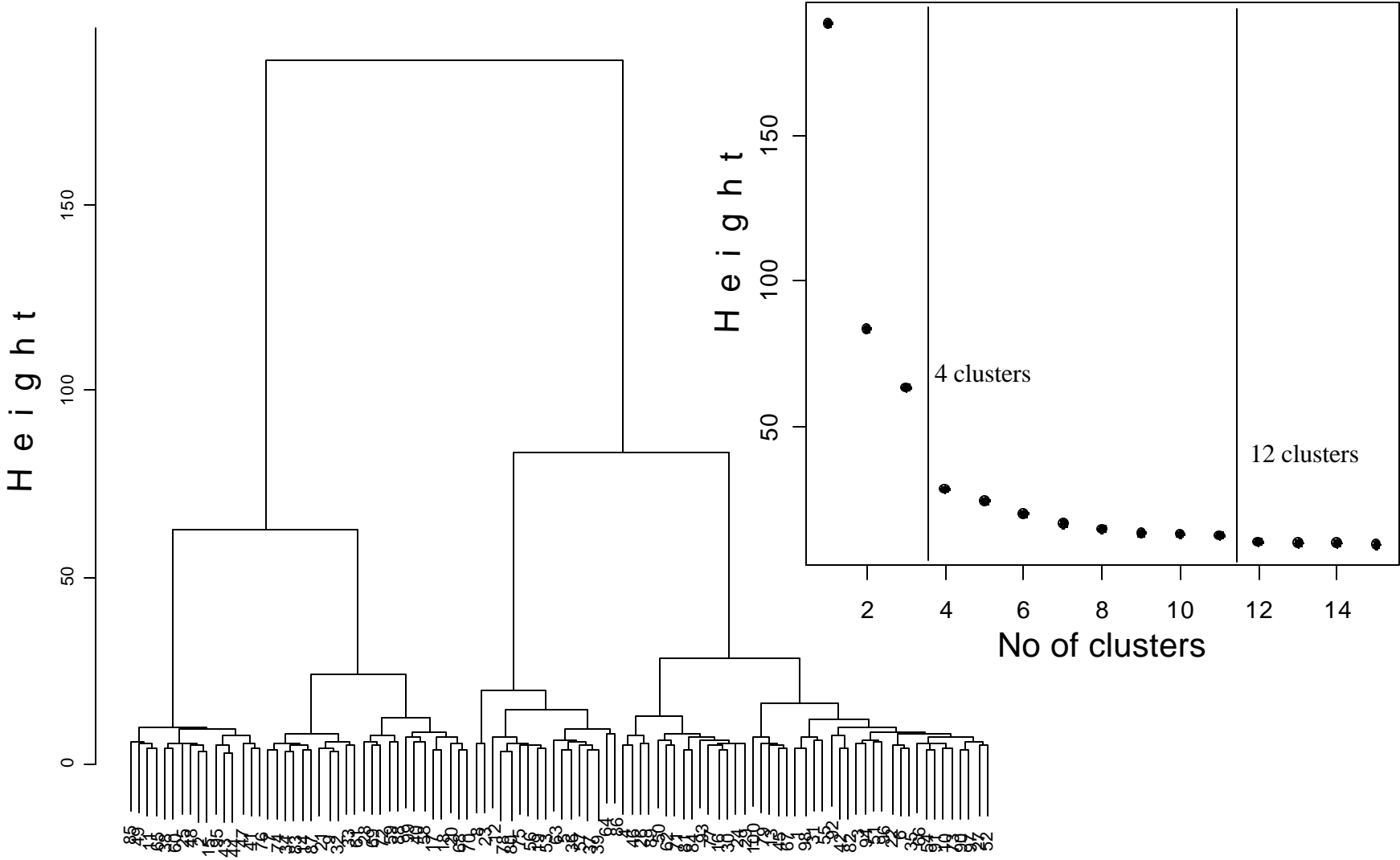


Figure 9.3 Average profiles of the 12 clusters obtained using Ward's method.

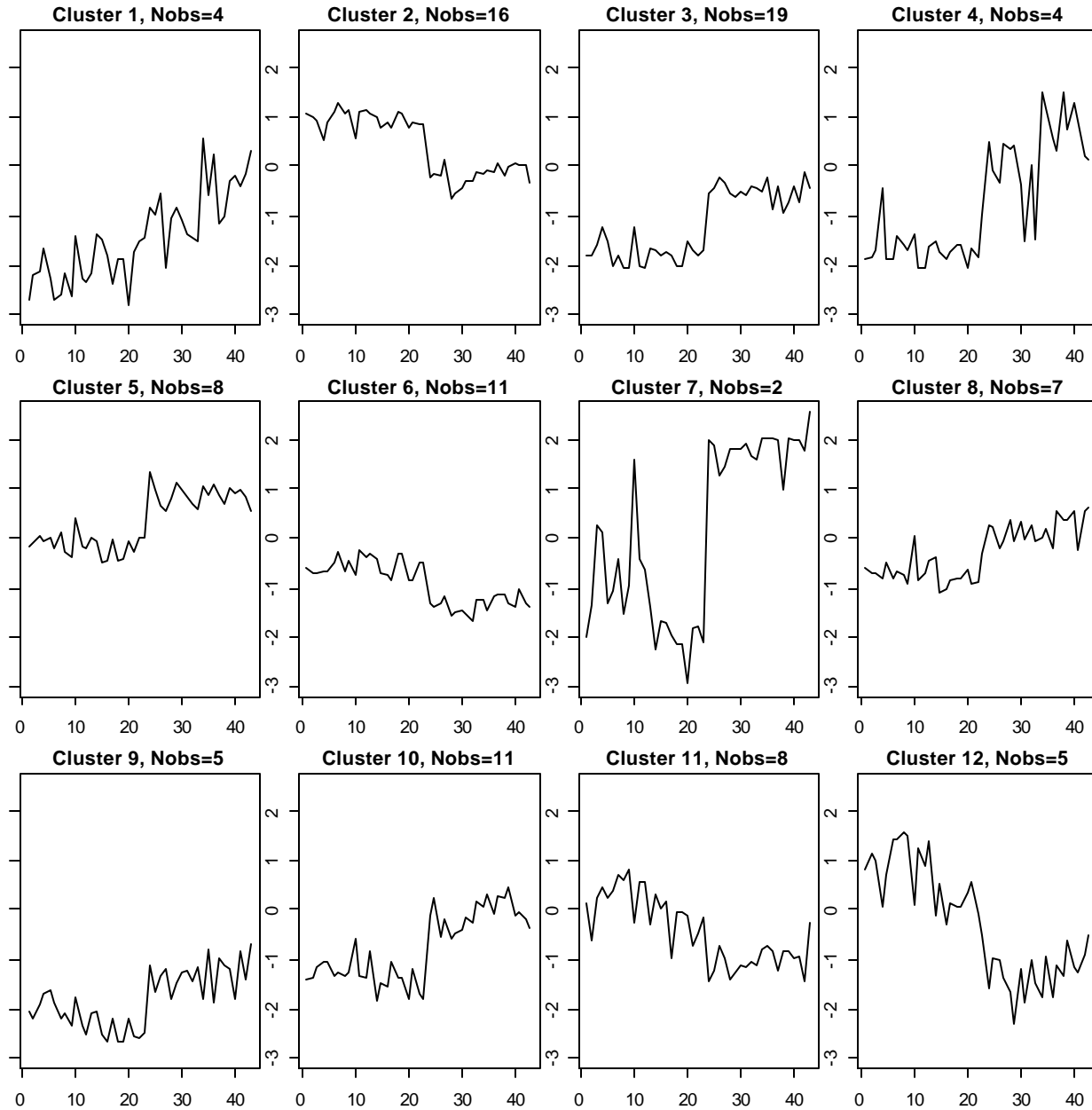


Figure 9.5 Microarray graph summarizing the gene clusters and the sample clusters. The main panel is the image plot of the intensities for the 100×43 array. The horizontal and vertical bars on the top and left side of the main image indicate the clustering of genes and samples respectively. The right panel shows the twelve cluster profiles on a normalized scale from zero to one. Finally, the lower panel shows the color scale for the main image.

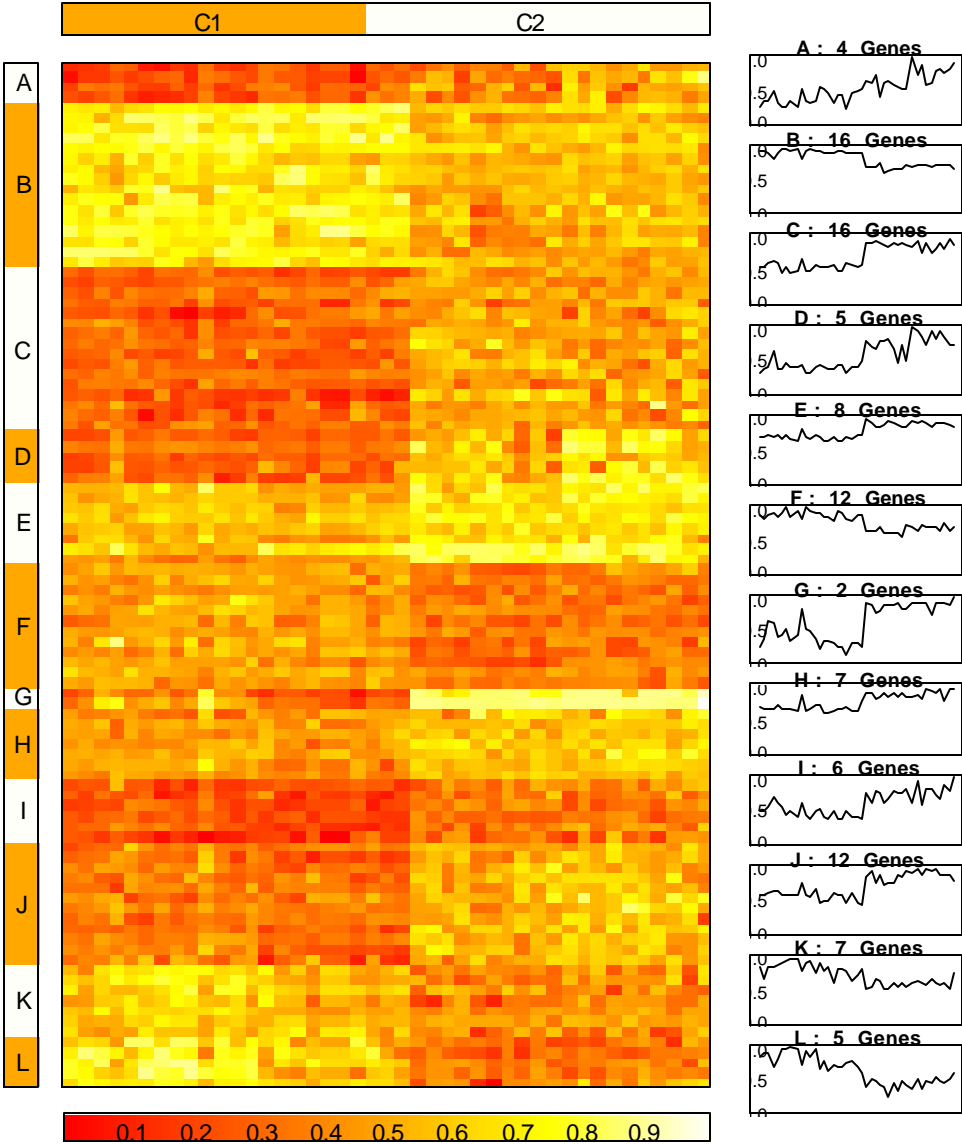


Figure 9.6 Principal components of the top 100 genes - PC2 versus PC1.

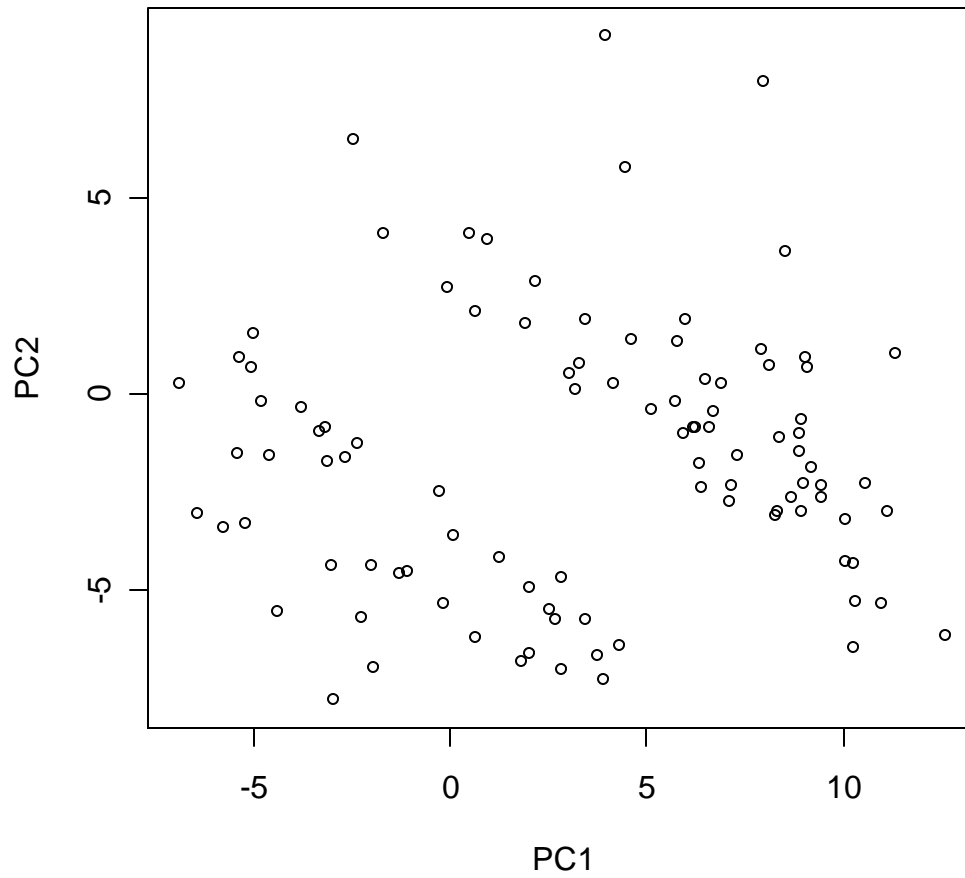


Figure 9.7 Scree plot

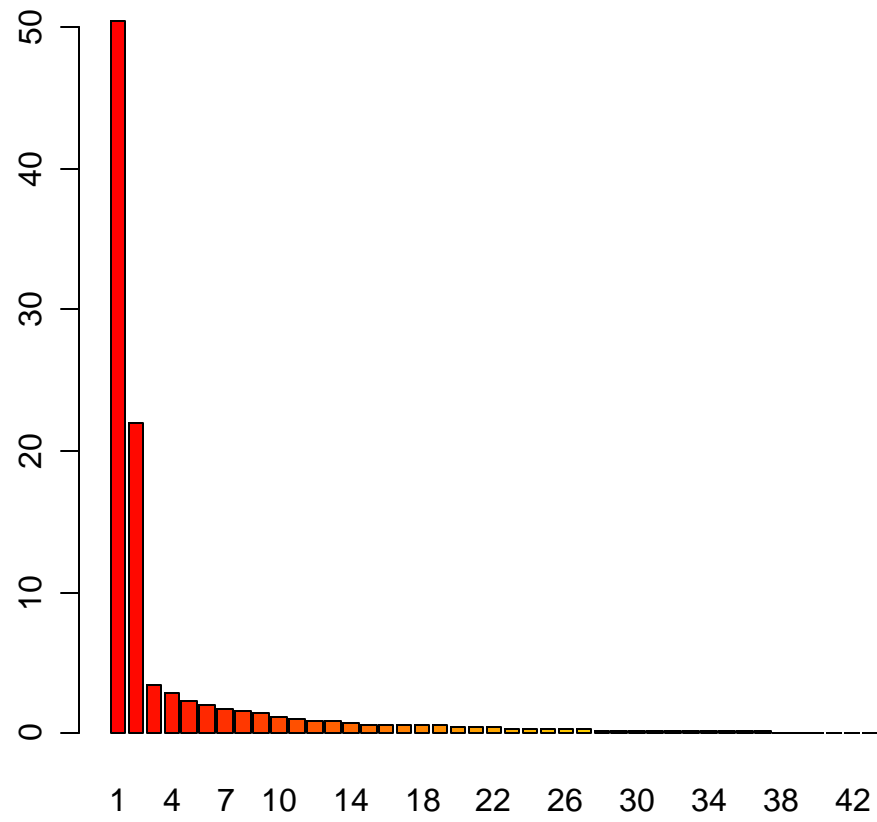


Figure 9.8 Biplot of the first two principal components.

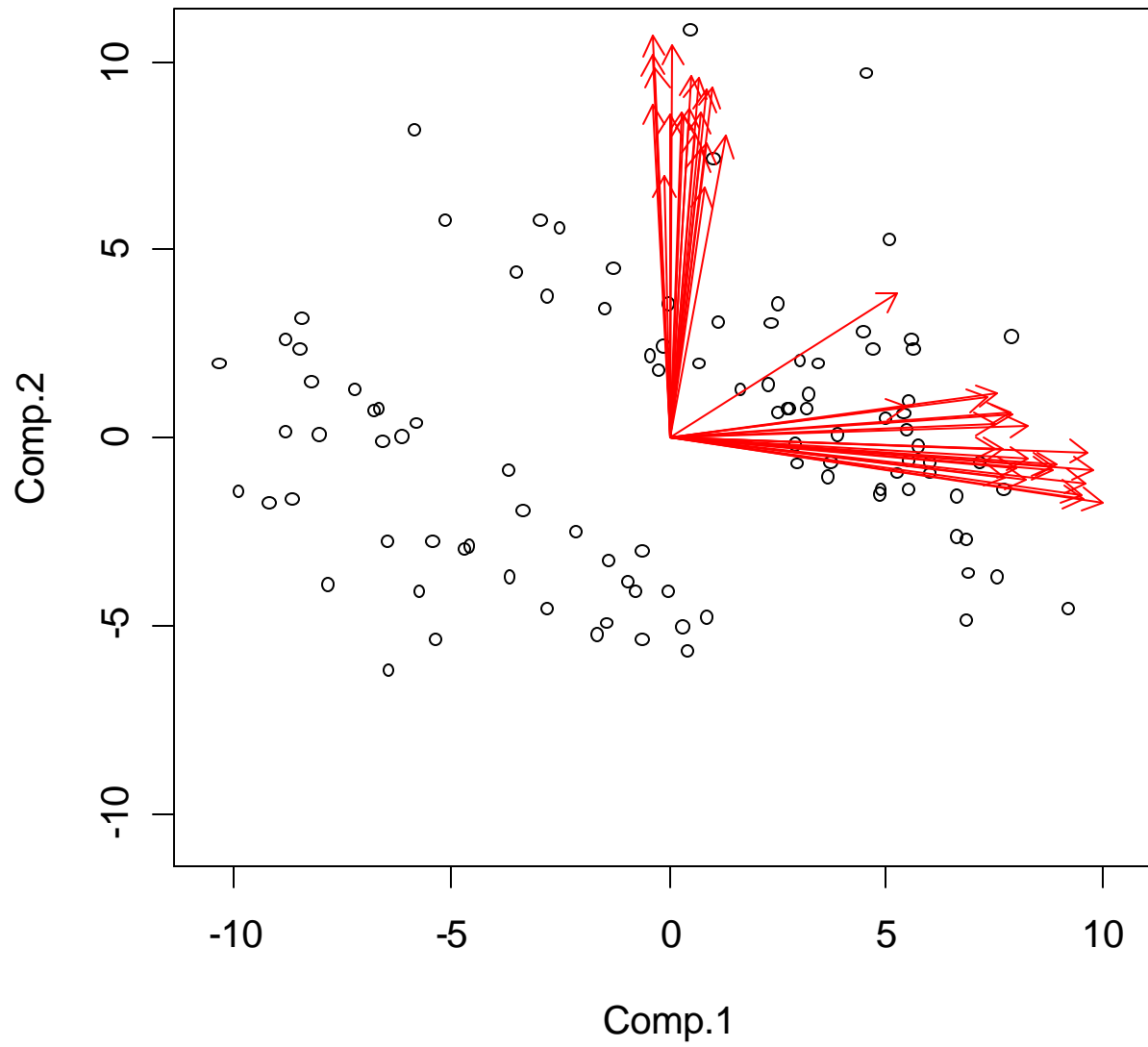


Figure 9.9 Biplot of the first two factors after Varimax rotation.

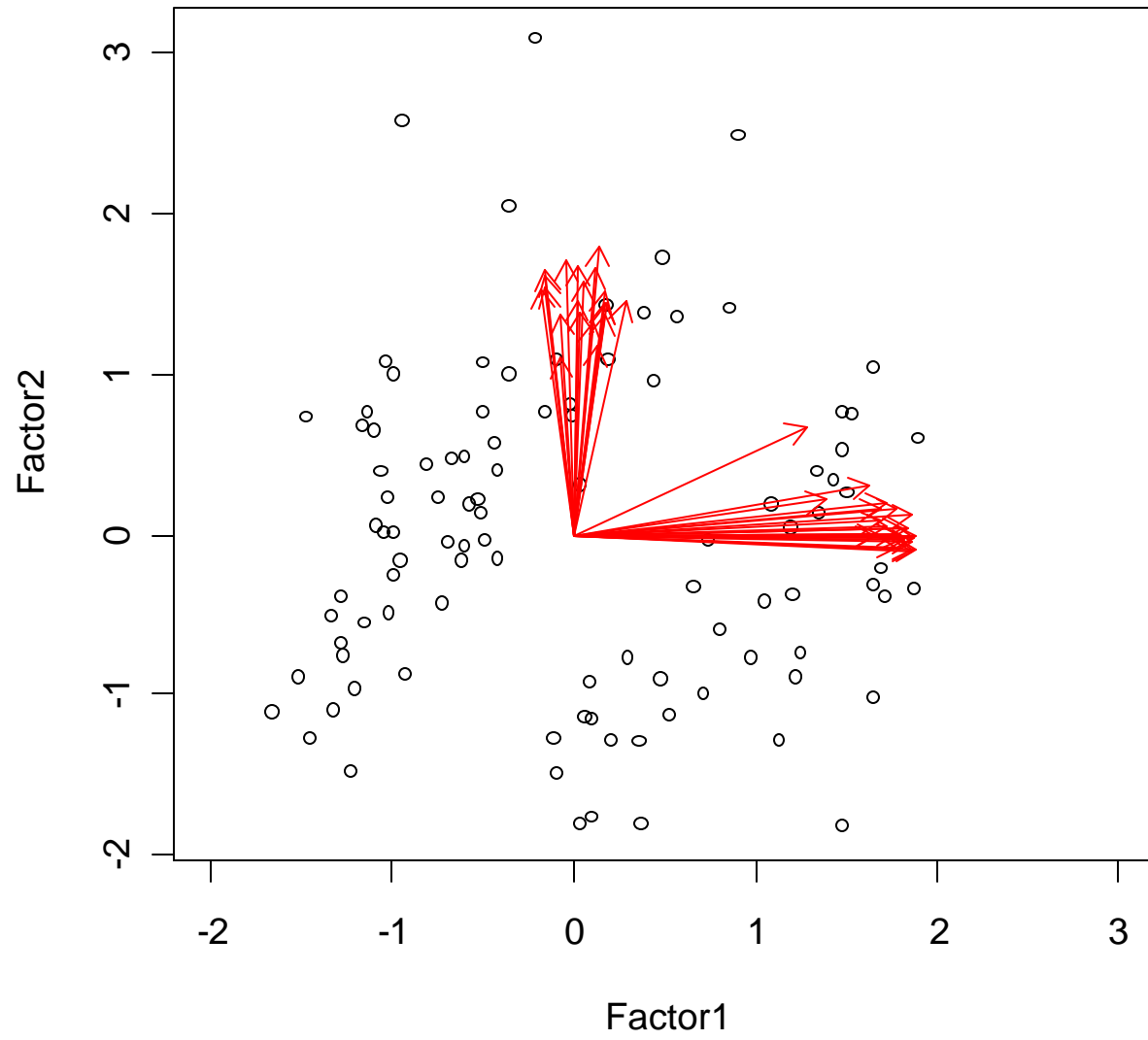


Figure 9.10 Ggobi display finding four clusters of tumors using the PP index on the set of 63 cases. The main panel shows the two dimensional projection selected by the PP index with the four clusters in different colors and glyphs. The top left panel shows the main controls and the left bottom panel displays the controls and the graph of the PP index that is been optimized. The graph shows the index value for a sequence of projection ending at the current one.

