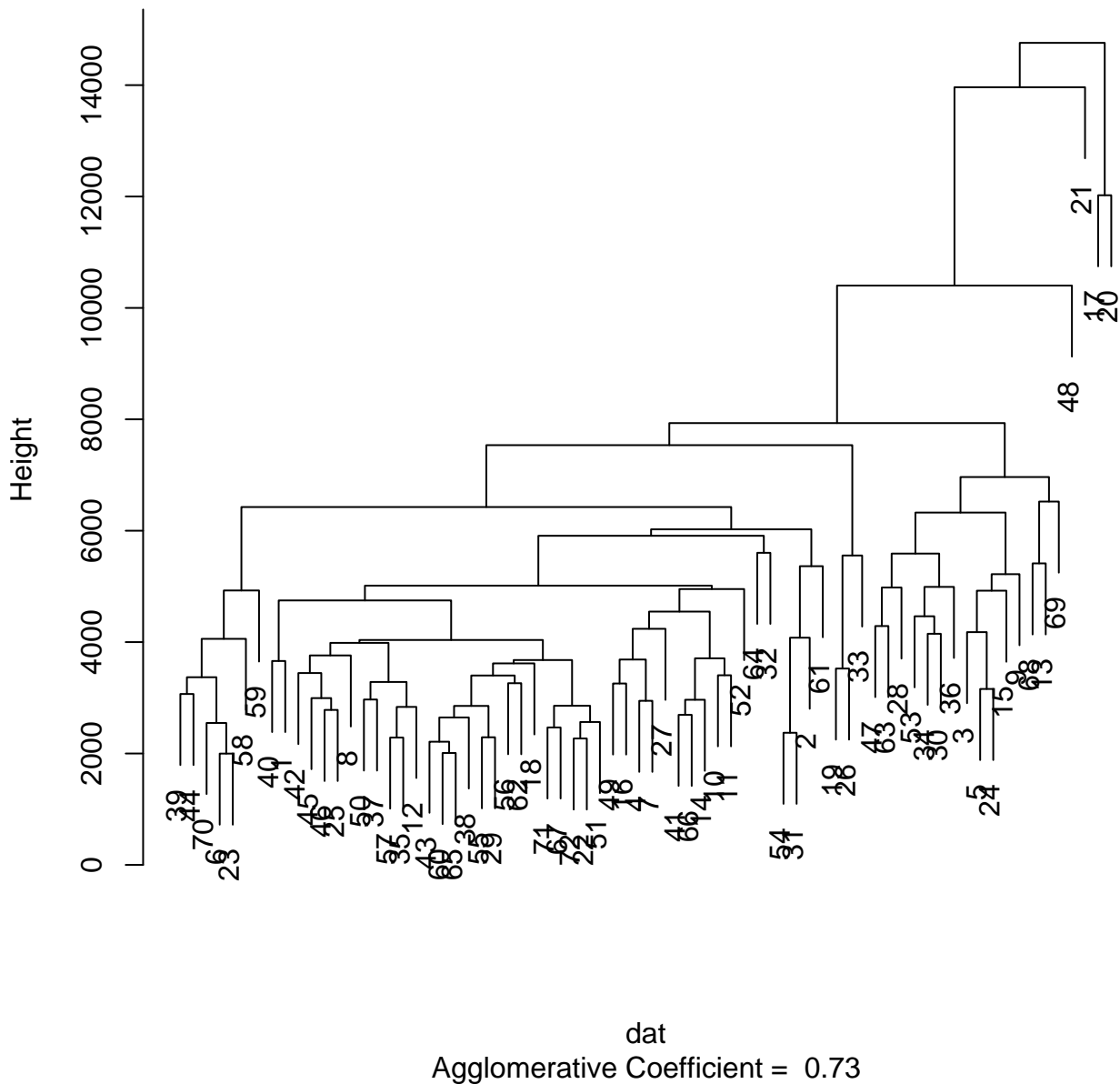
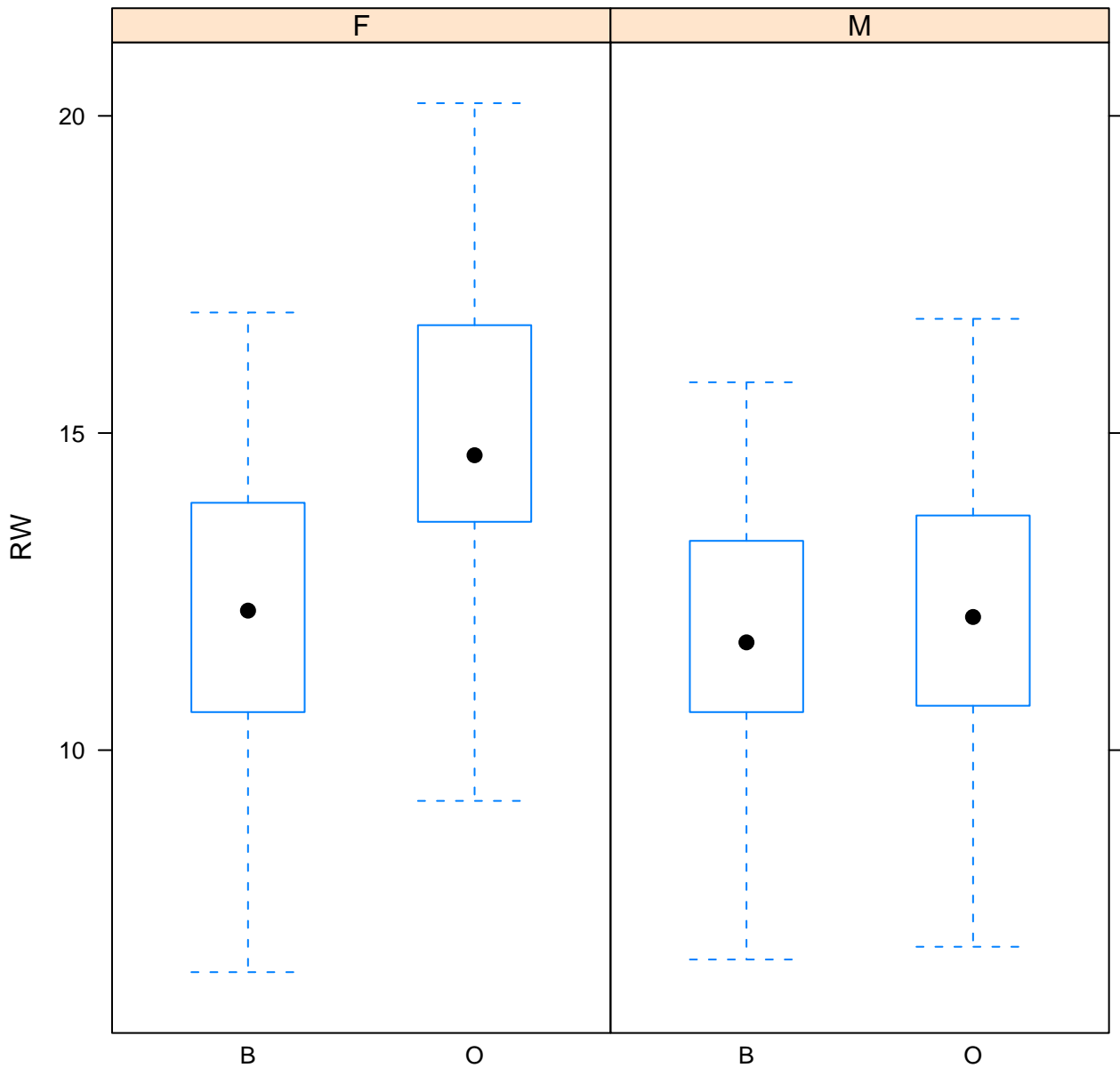
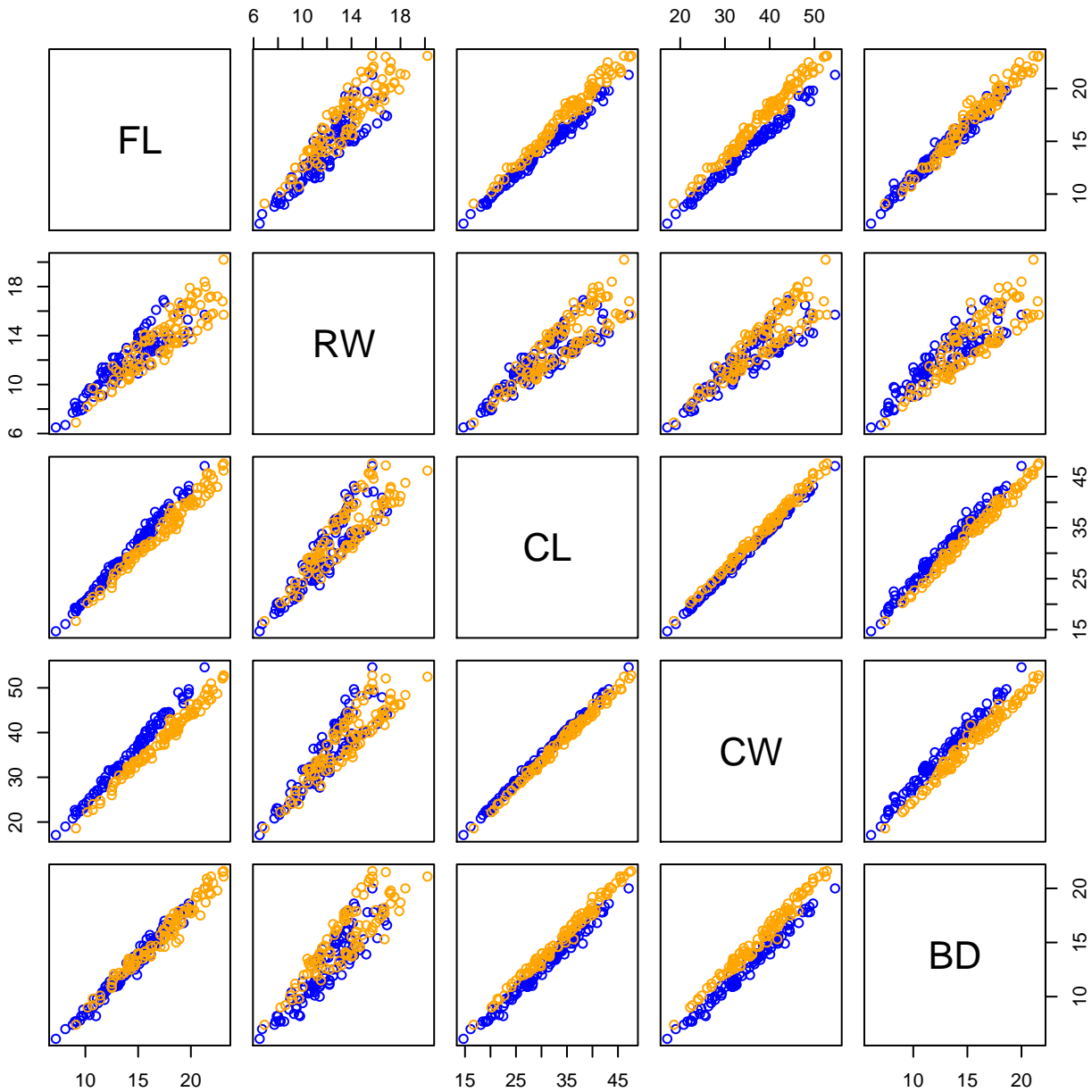
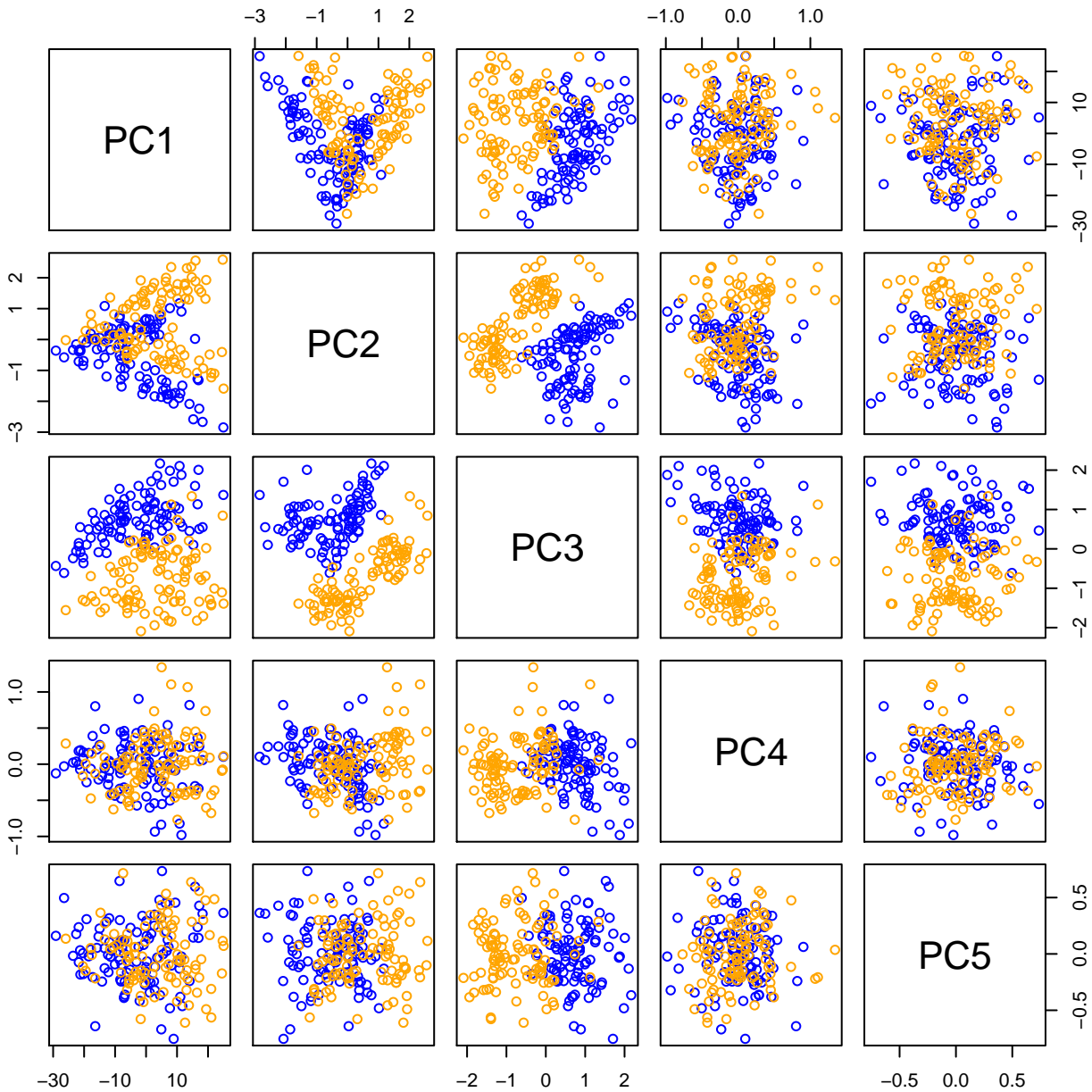


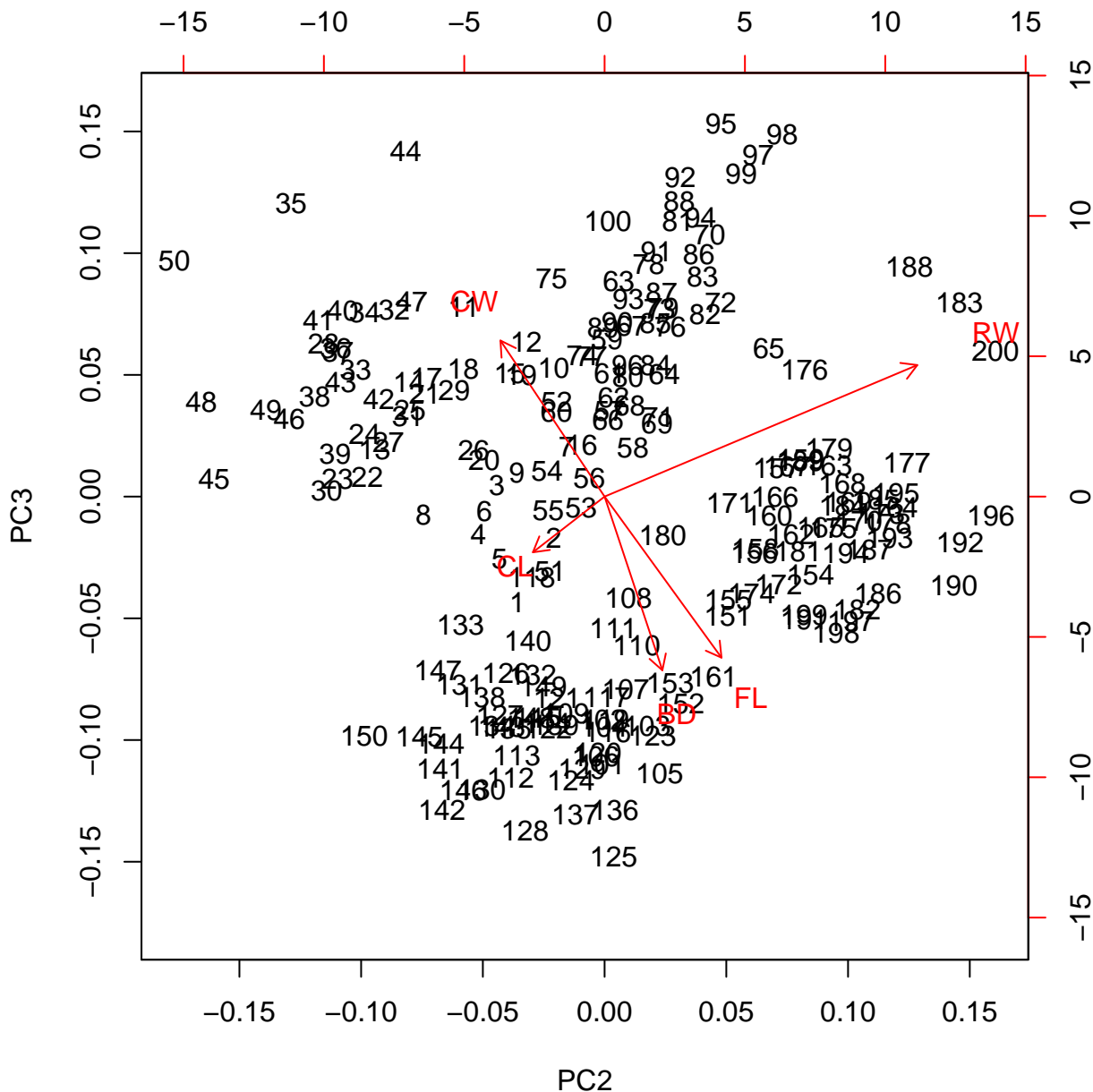
Dendrogram of `cluster::agnes(x = dat, metric = metric, stand = stand, method = keep.diss = keep.diss, keep.data = keep.data)`

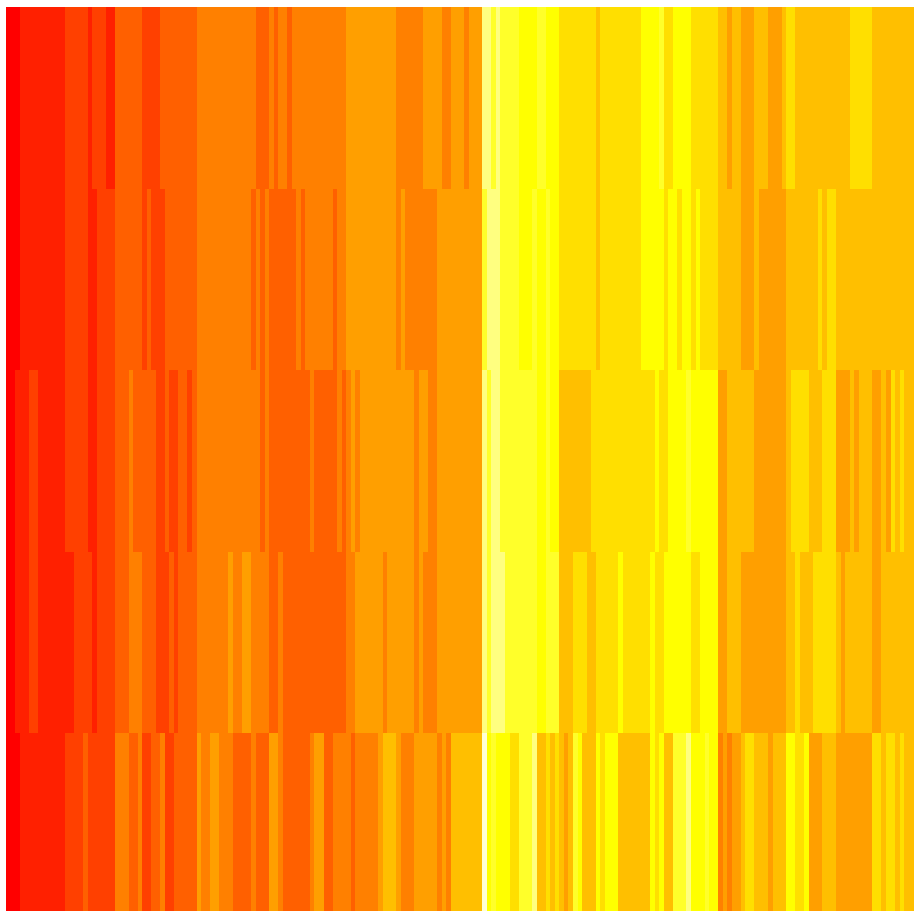
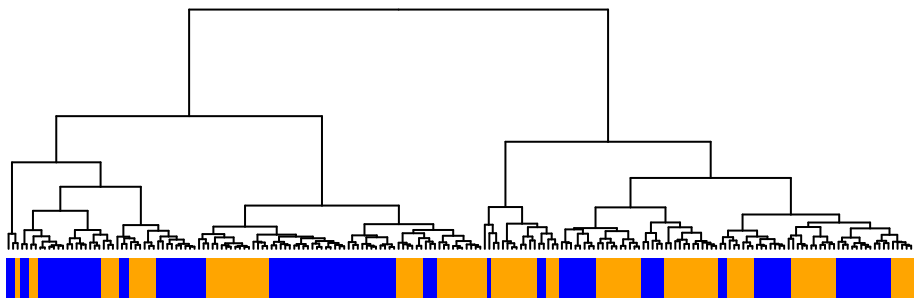










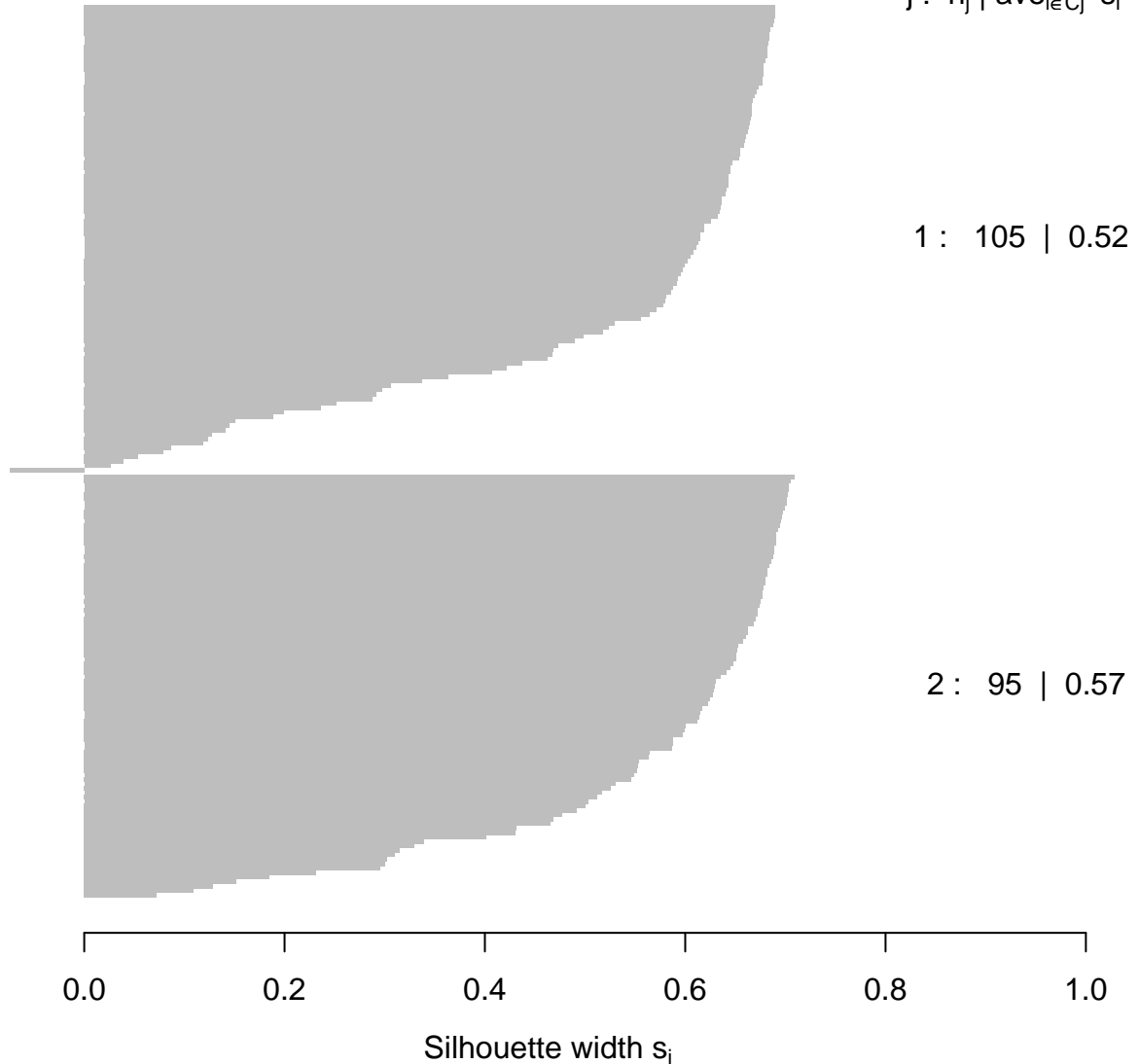


Gene names (e.g., LOC100000000, LOC100000001, etc.) are listed along the bottom of the heatmap, corresponding to the rows of data.

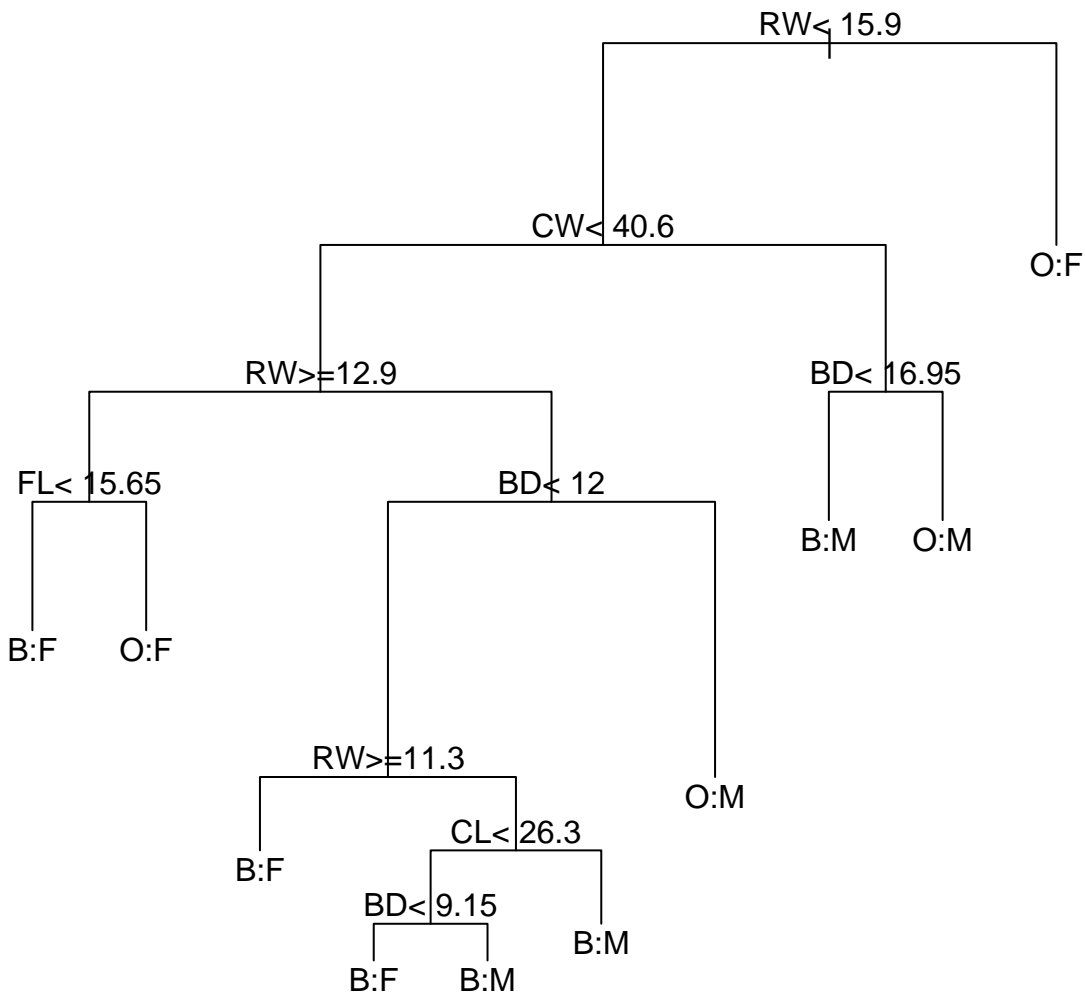
Silhouette plot of (x = tr, dist = dist(X))

n = 200

2 clusters C_j
 $j : n_j \mid \text{ave}_{i \in C_j} s_i$

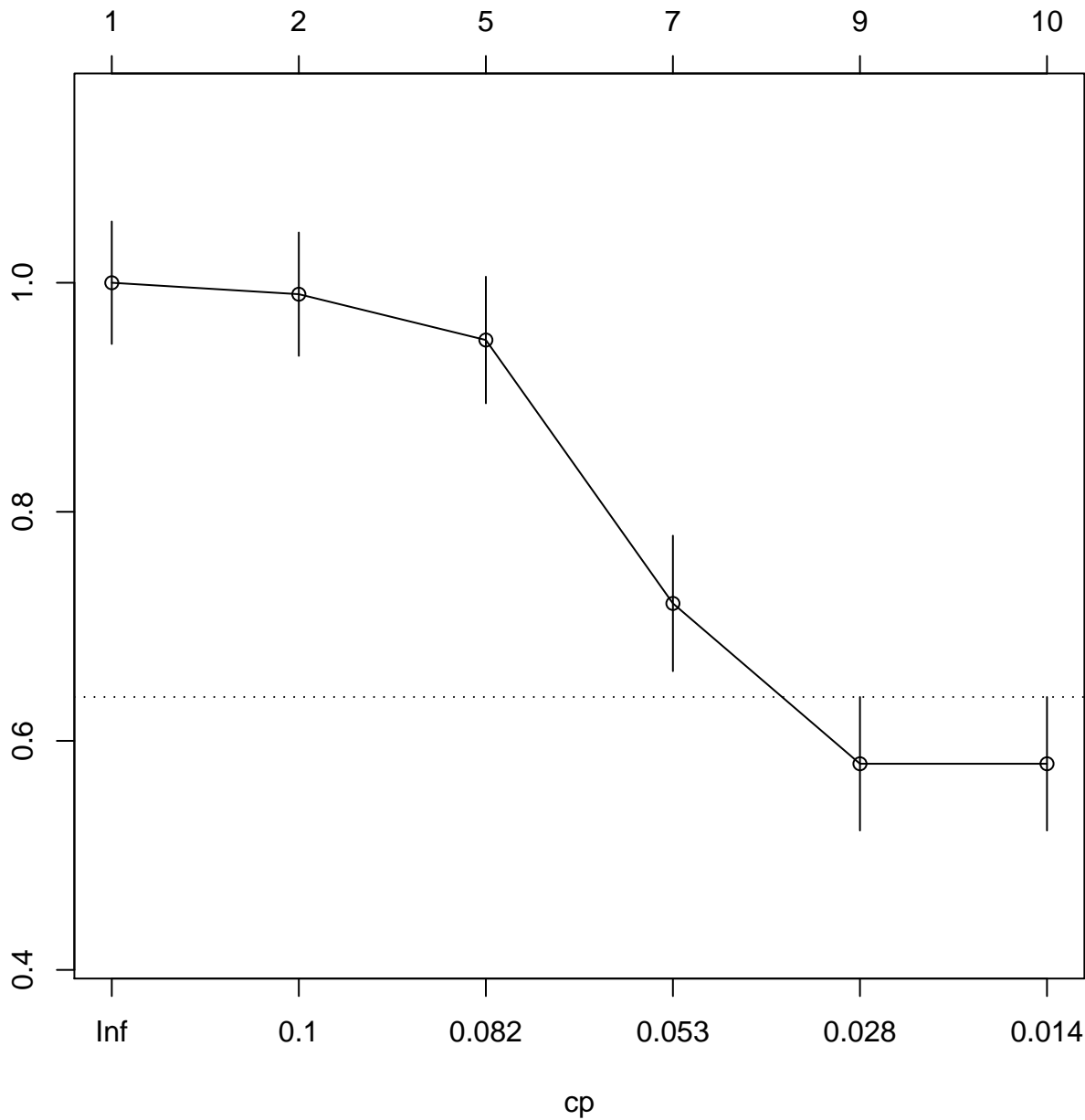


Average silhouette width : 0.55

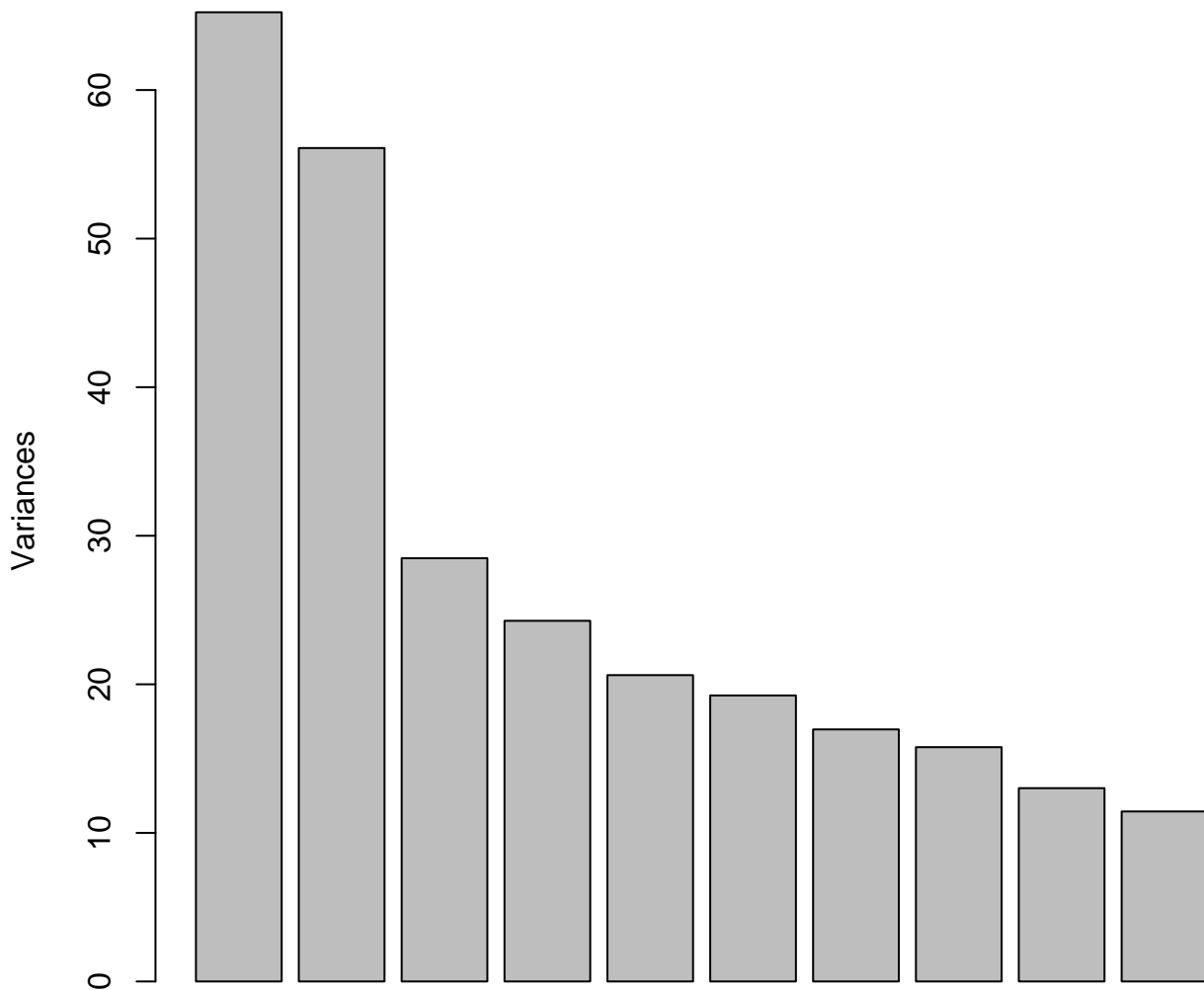


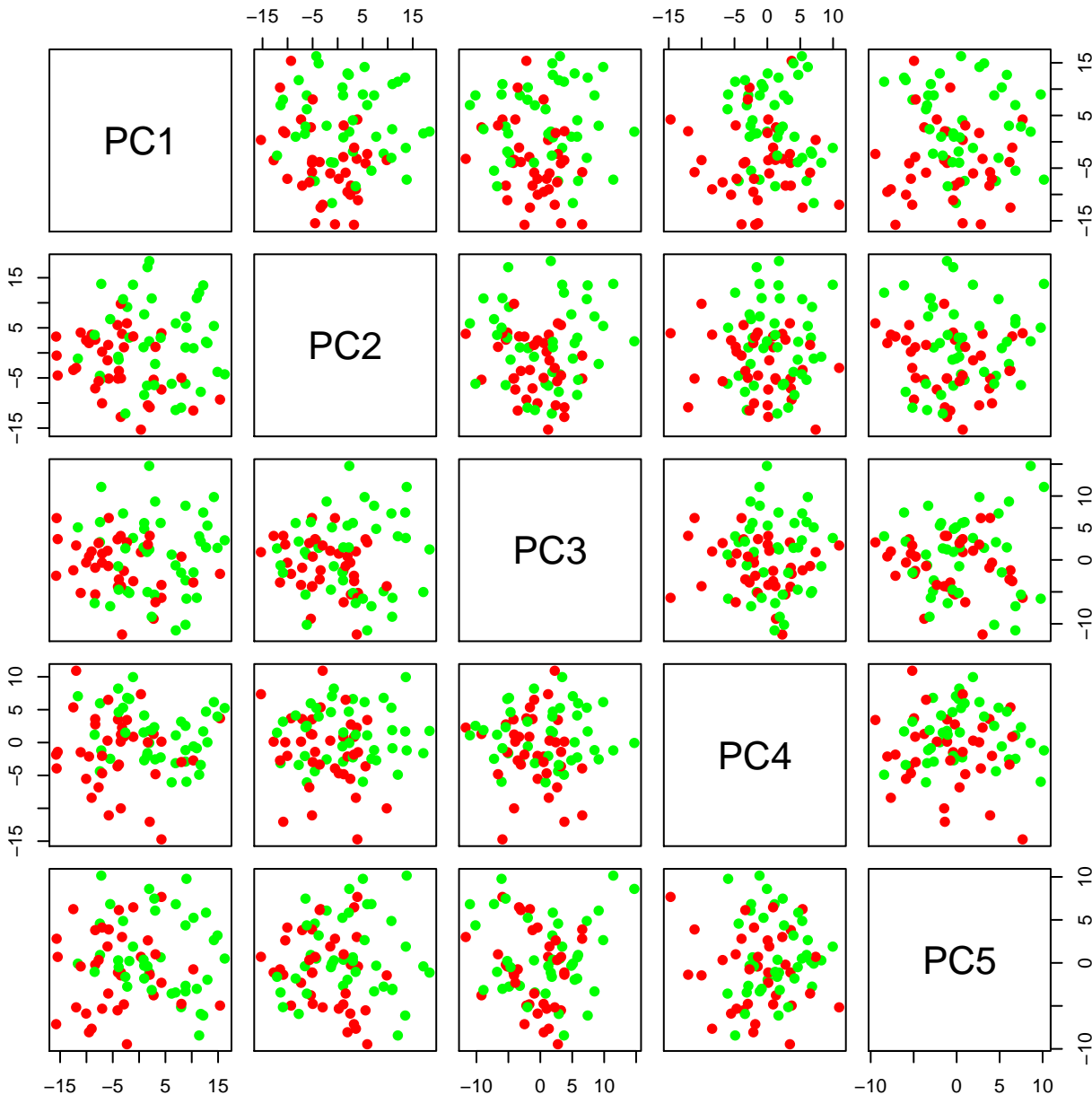
size of tree

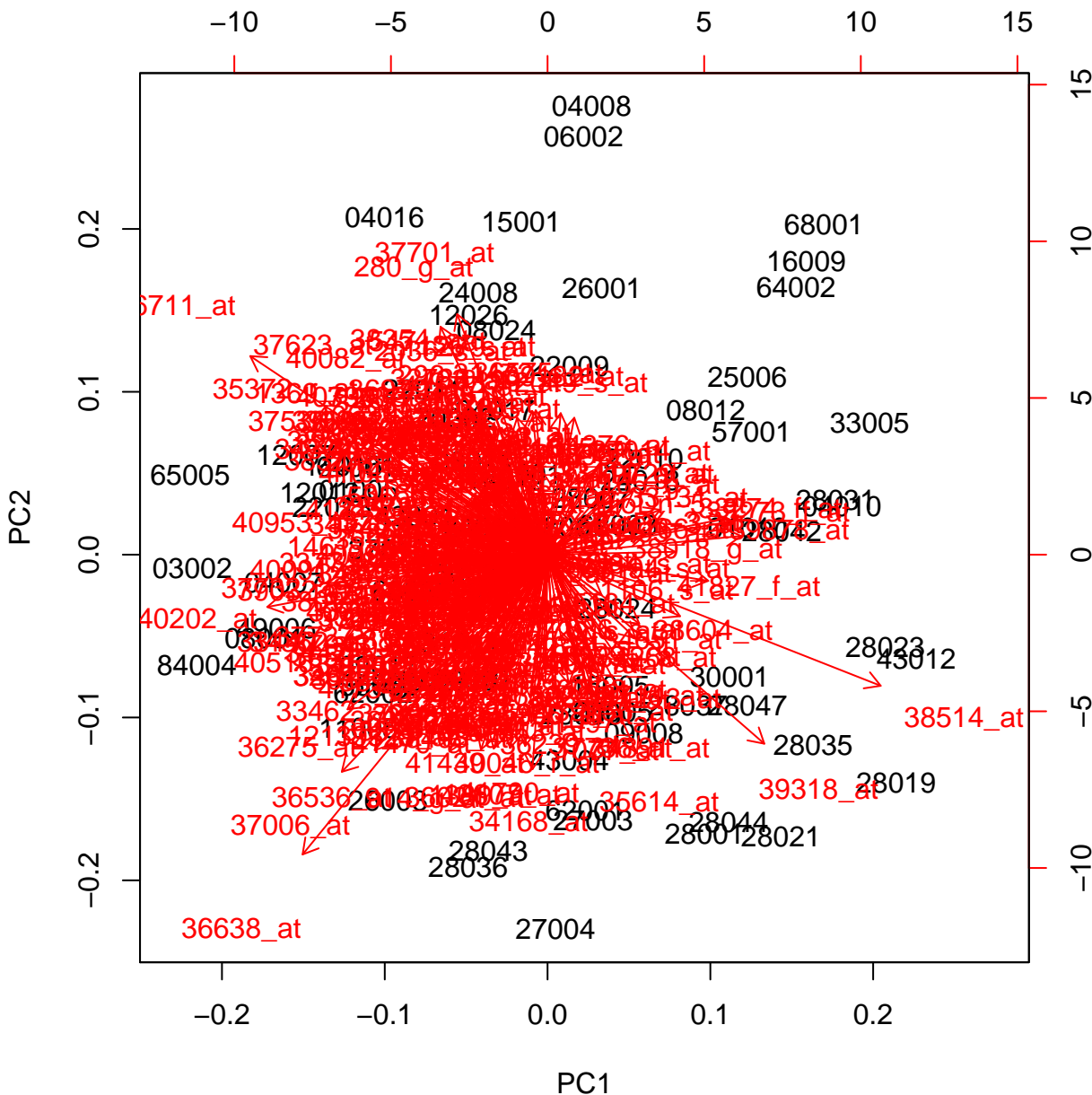
X-val Relative Error

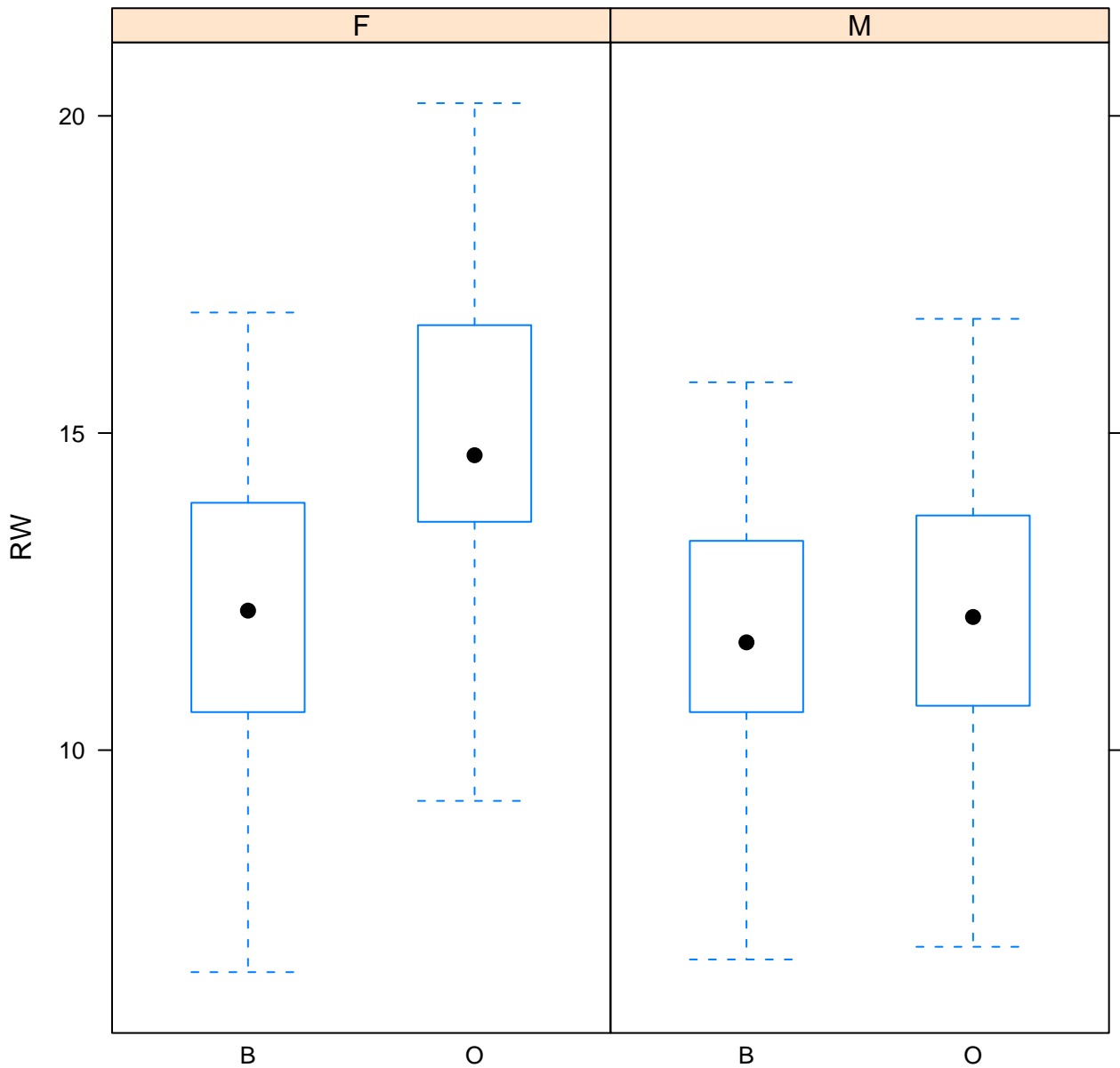


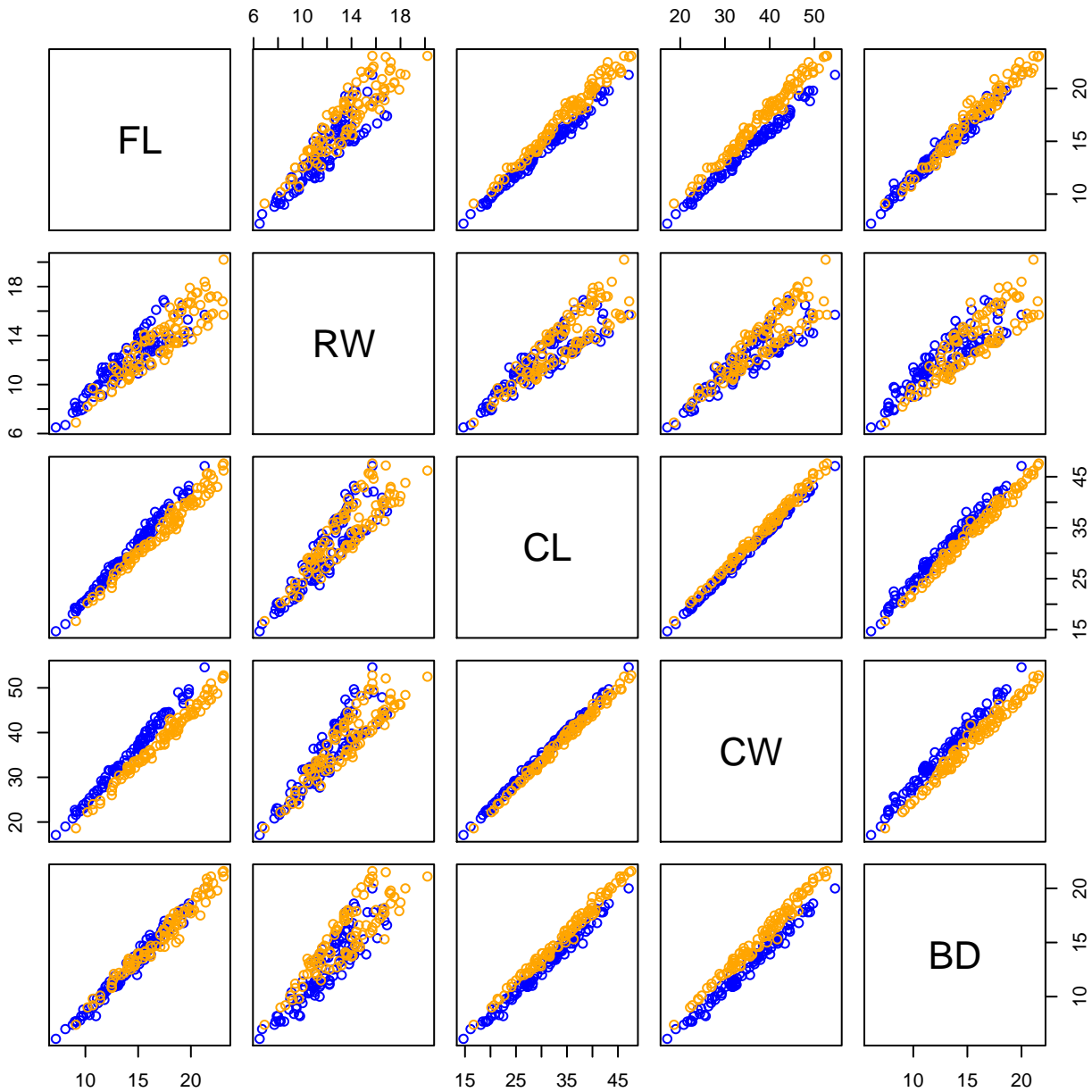
PCg

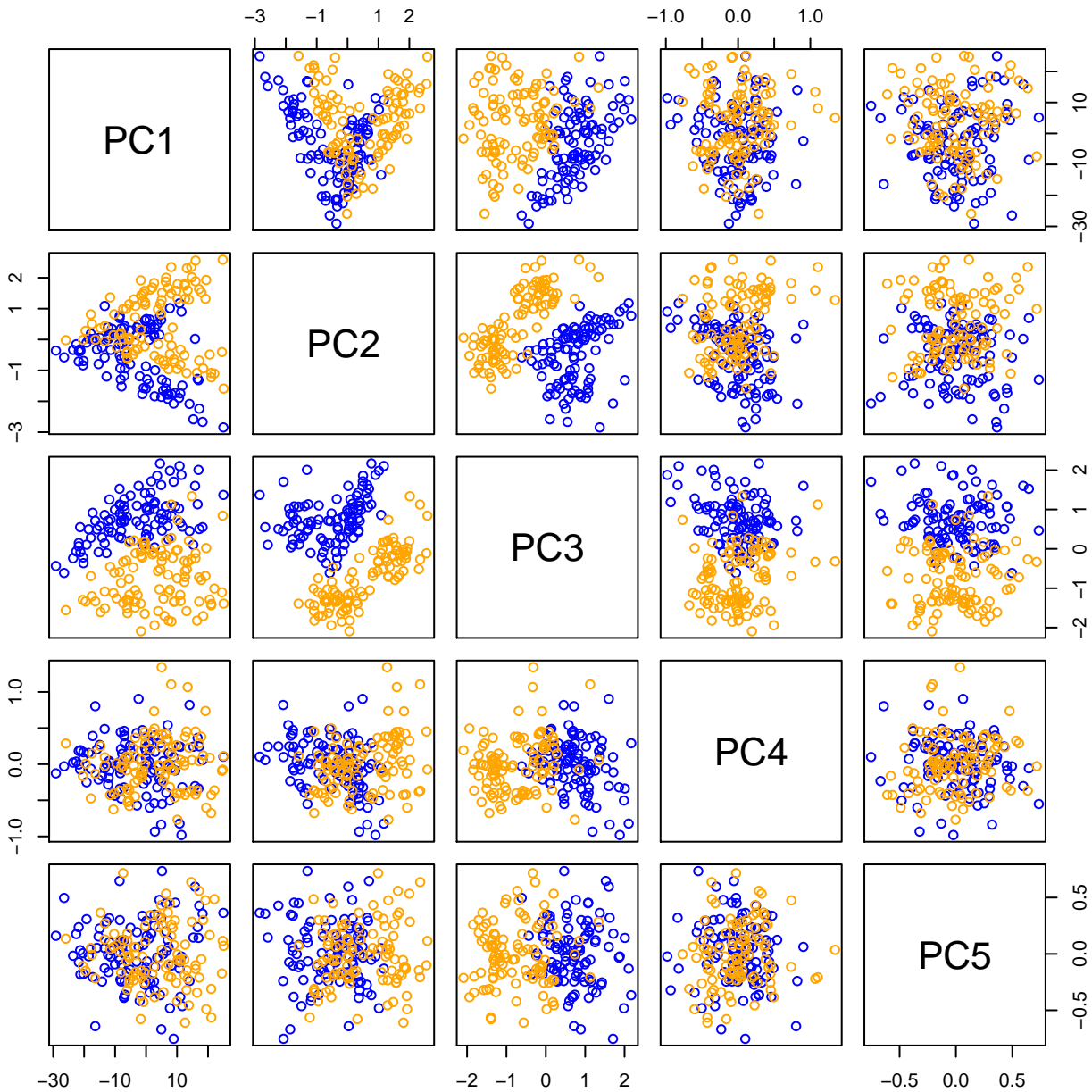


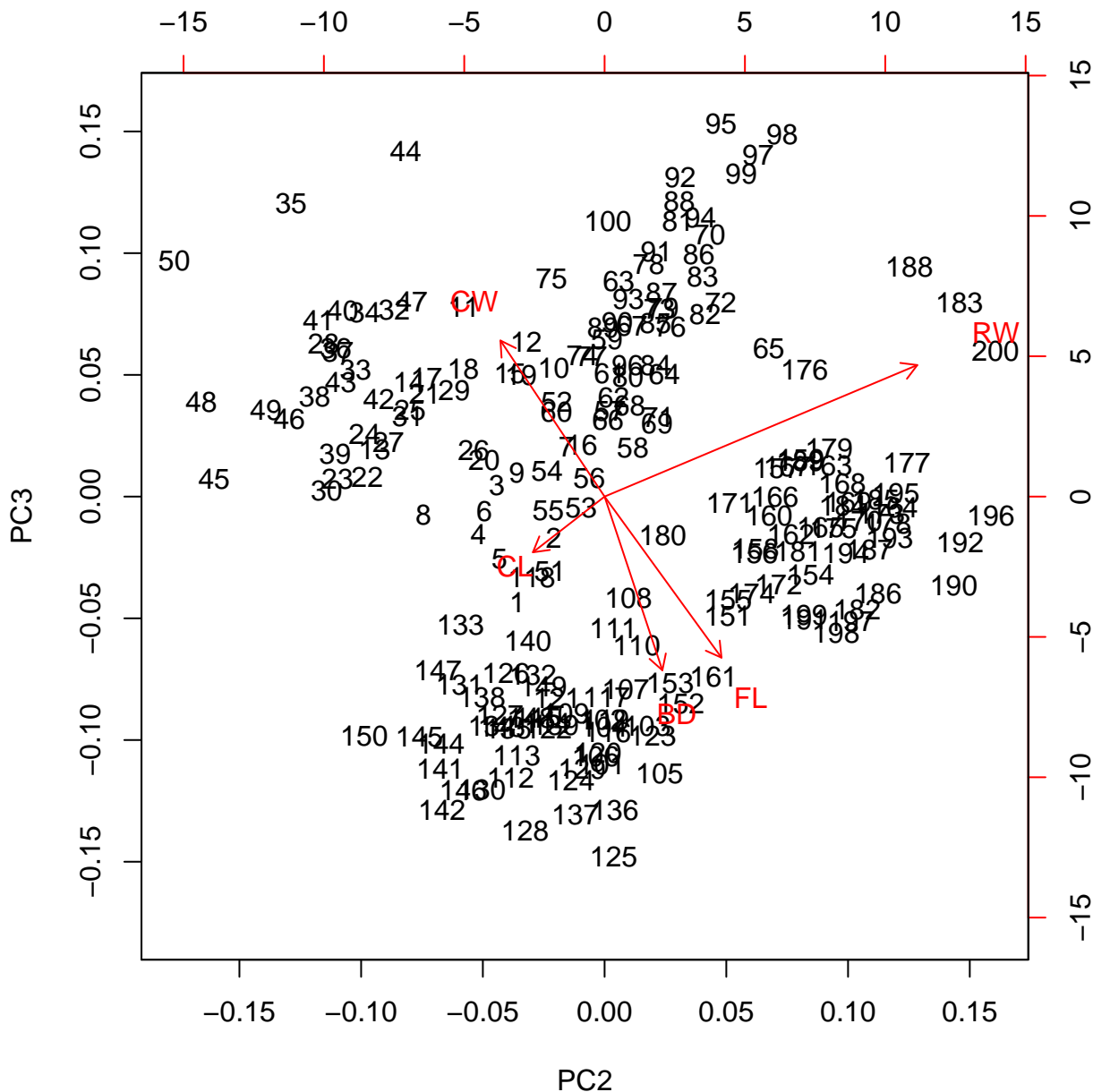


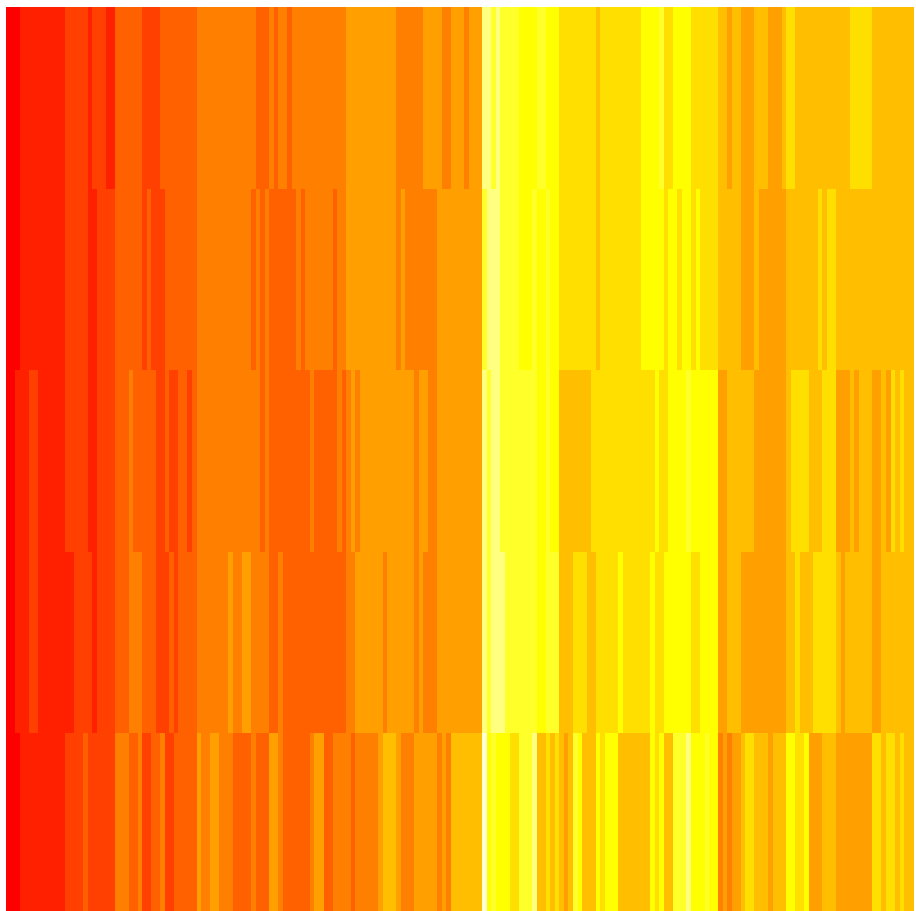
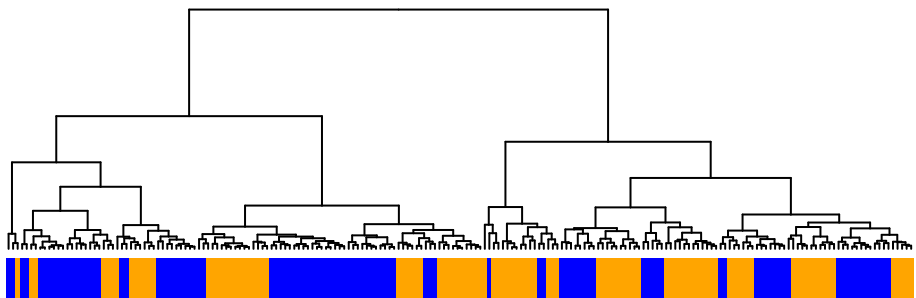










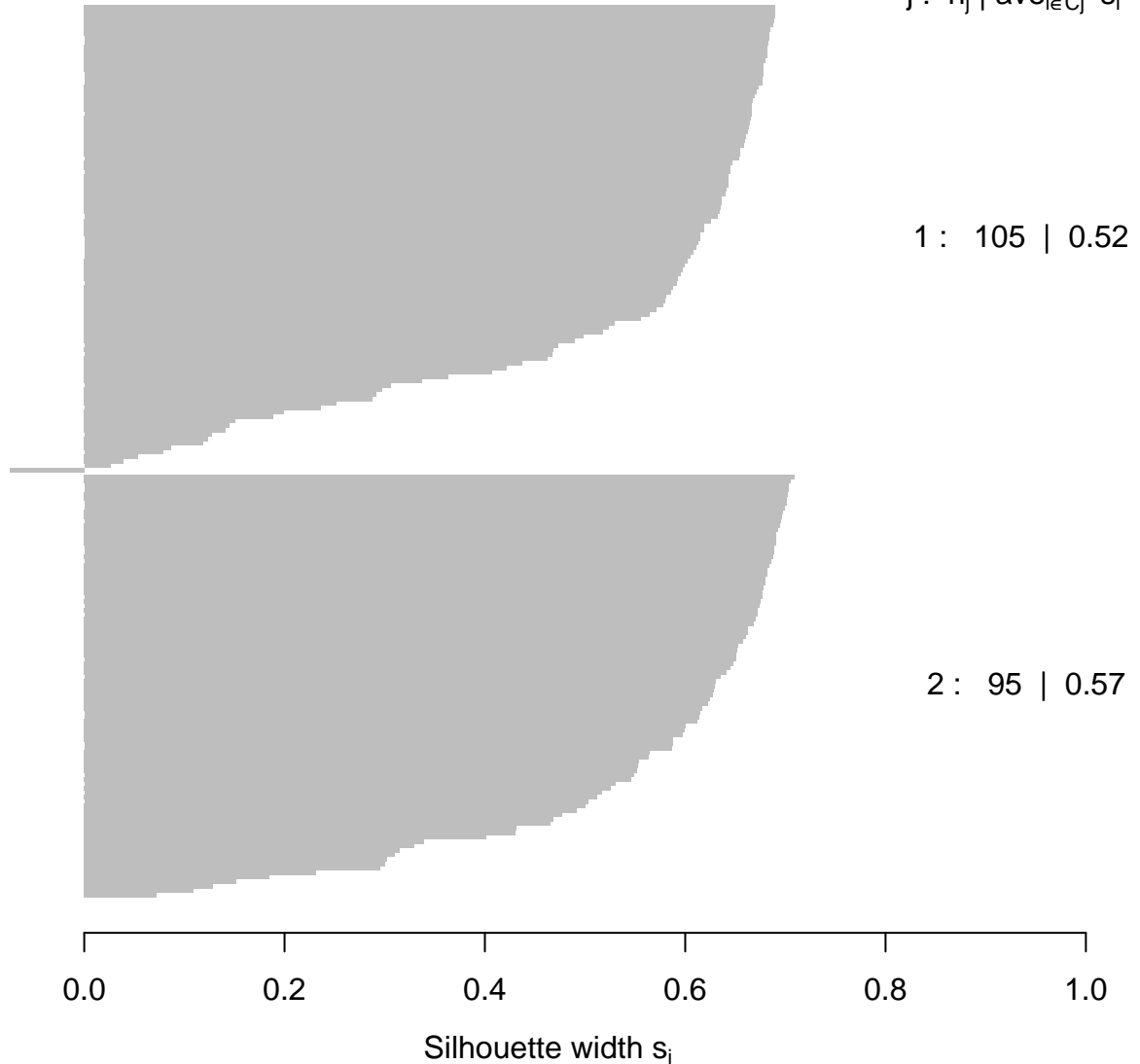


Gene names (e.g., LOC100000000, LOC100000001, etc.) are listed along the bottom of the heatmap, corresponding to the rows of data.

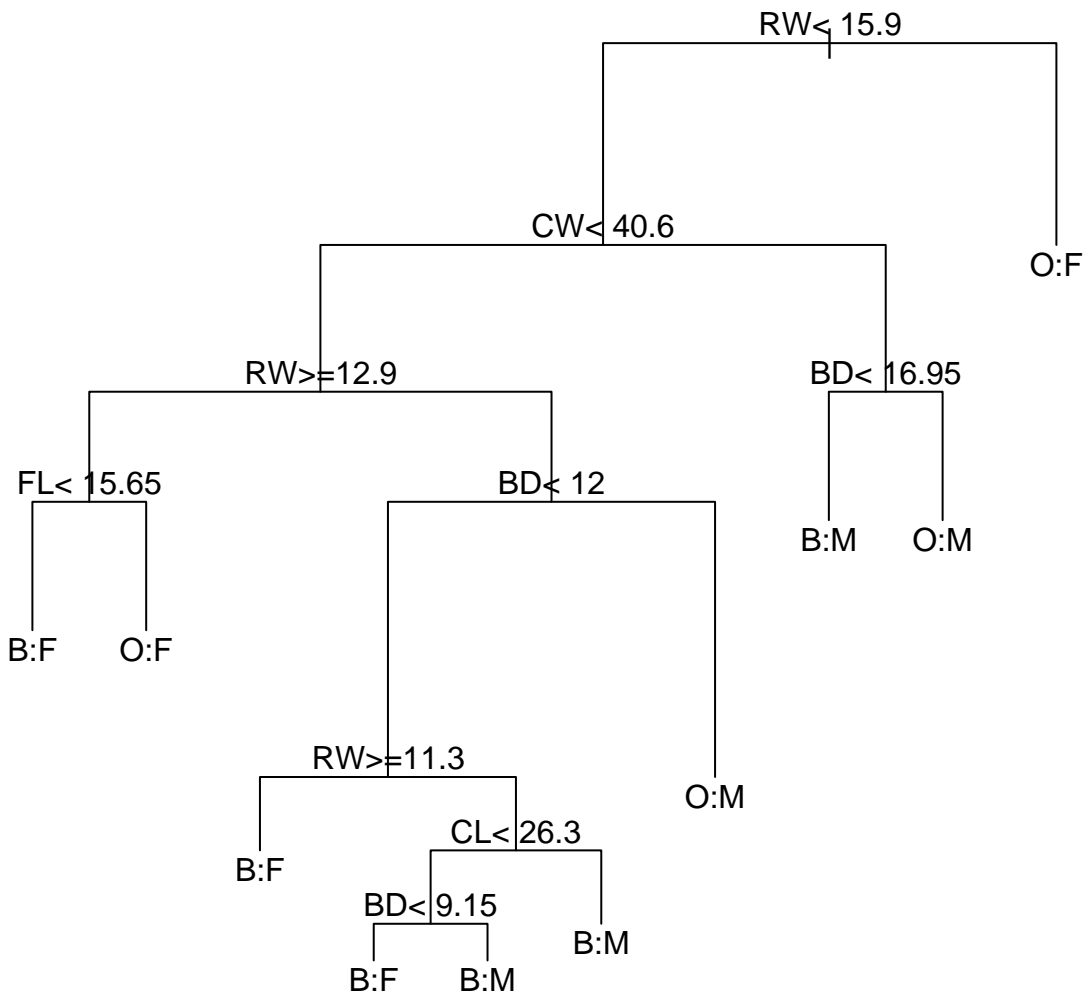
Silhouette plot of (x = tr, dist = dist(X))

n = 200

2 clusters C_j
 $j : n_j \mid \text{ave}_{i \in C_j} s_i$

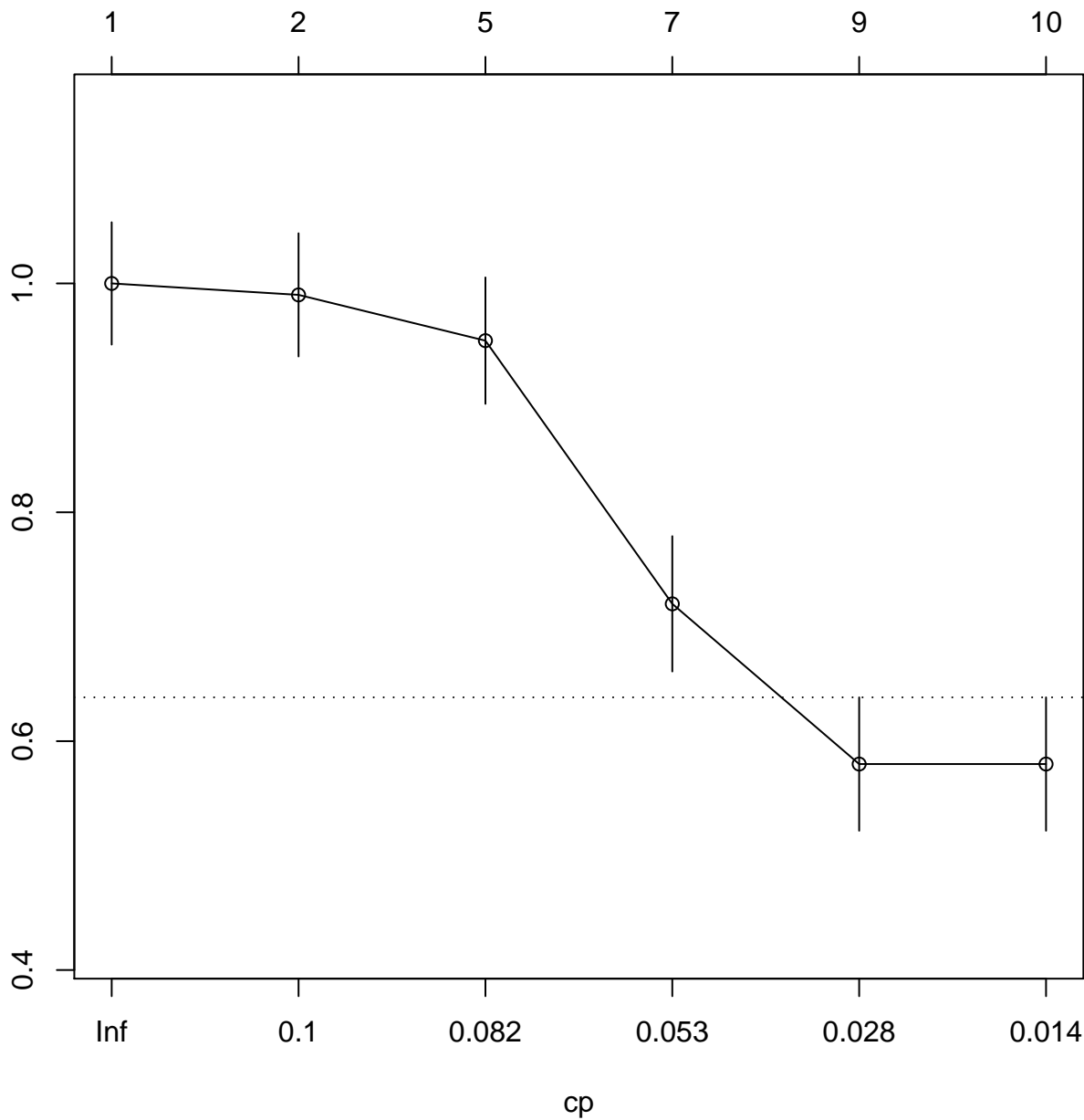


Average silhouette width : 0.55



size of tree

X-val Relative Error



PCg

