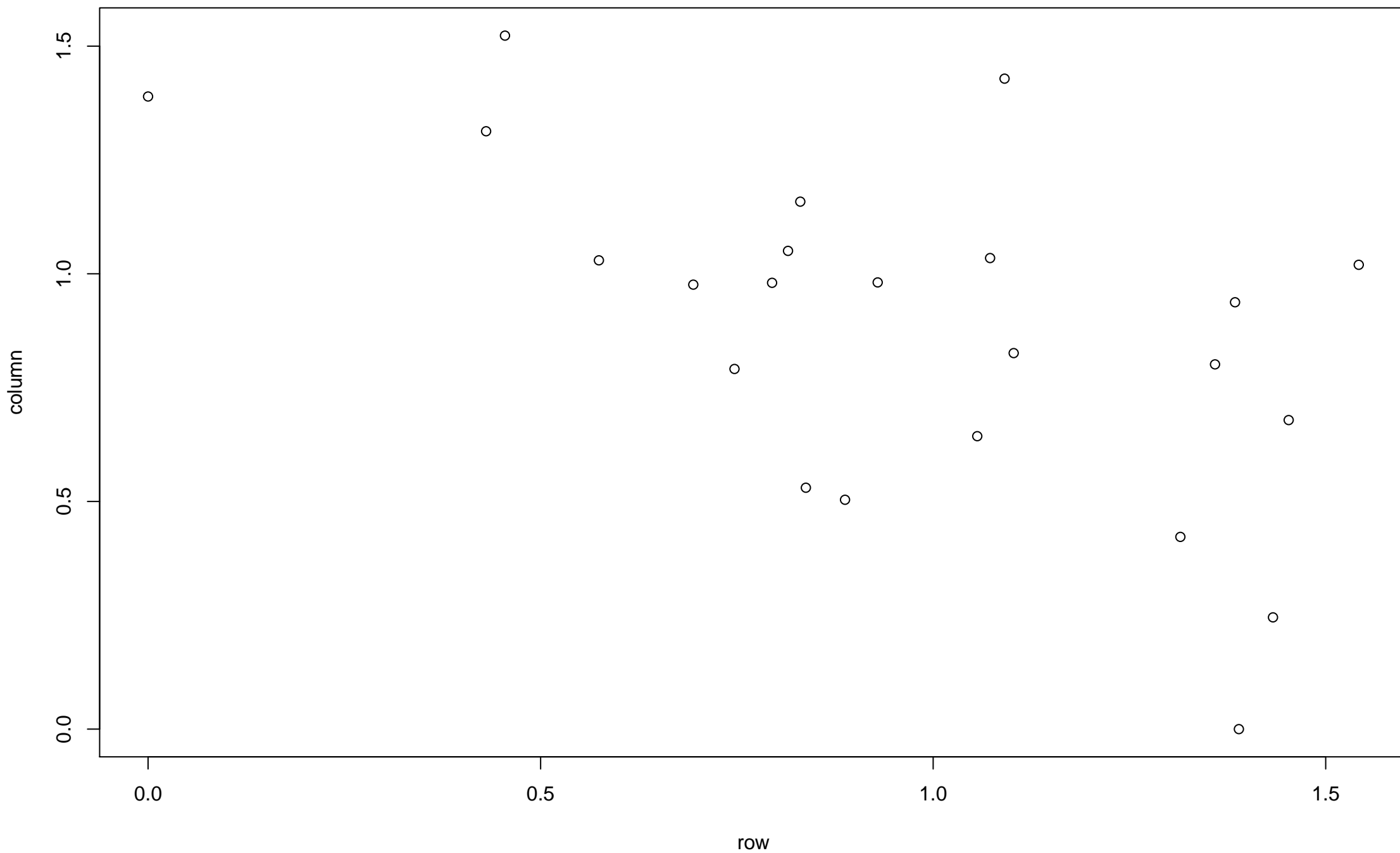
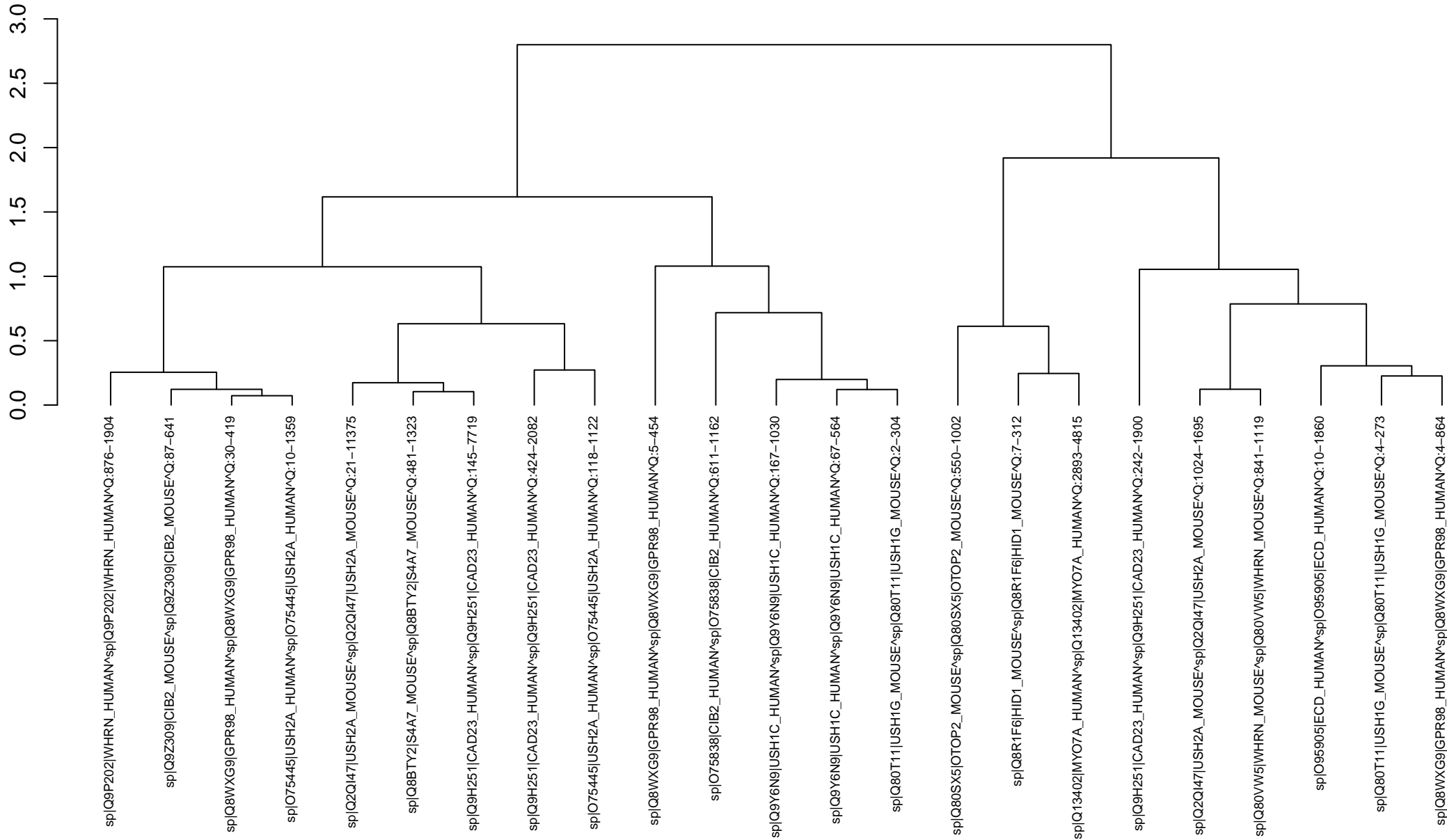


Gene expression pairwise correlation distance



Cluster Dendrogram

Height



as.dist(cor_dist_matrix)
hclust (*, "ward.D2")

