Cluster Dendrogram

Height
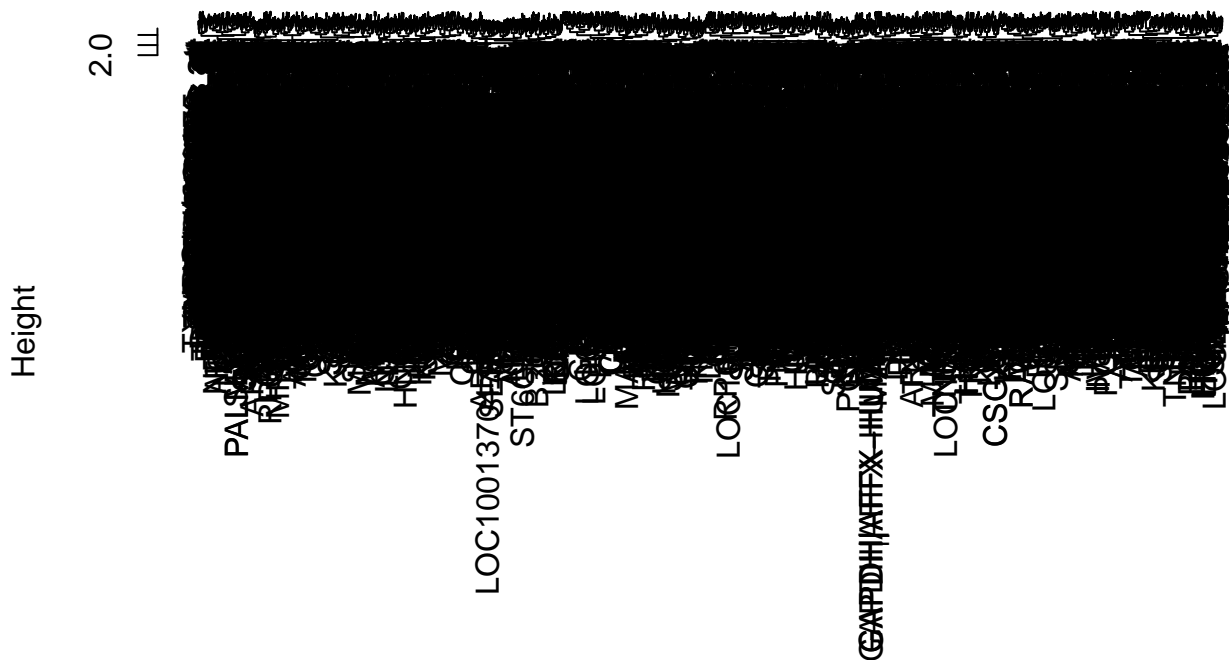
as.dist(gene.cor)
hclust (*, "complete")