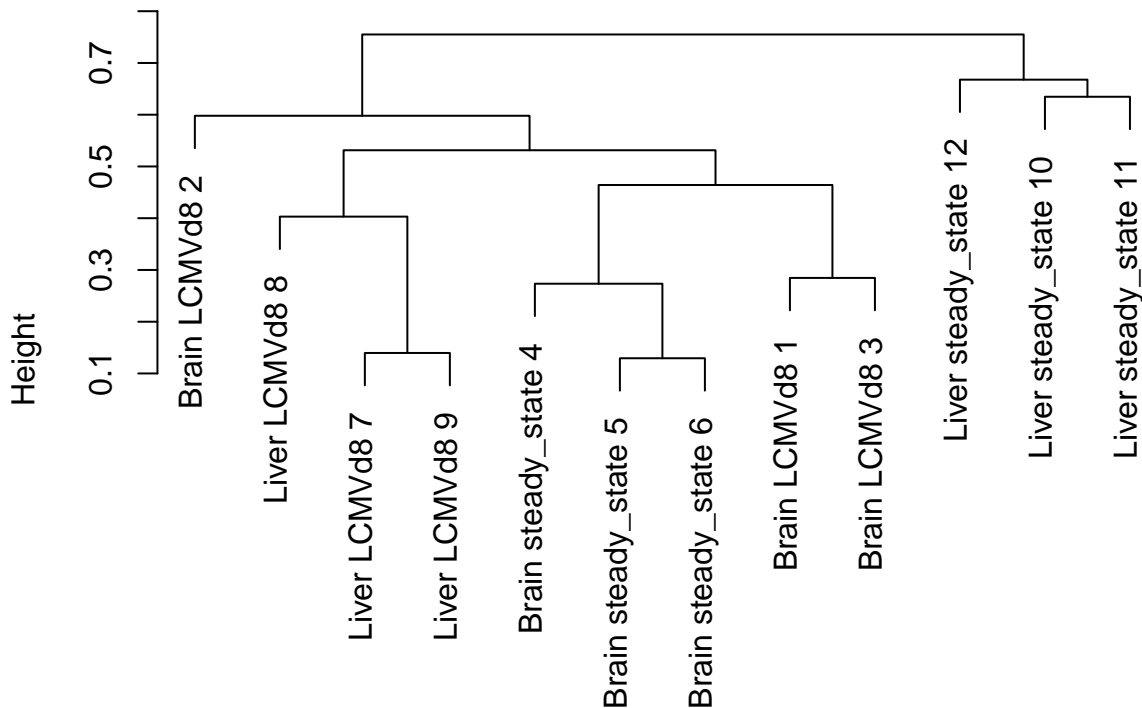


Cluster Dendrogram



as.dist(1 - corr_spearman)
hclust (*, "complete")