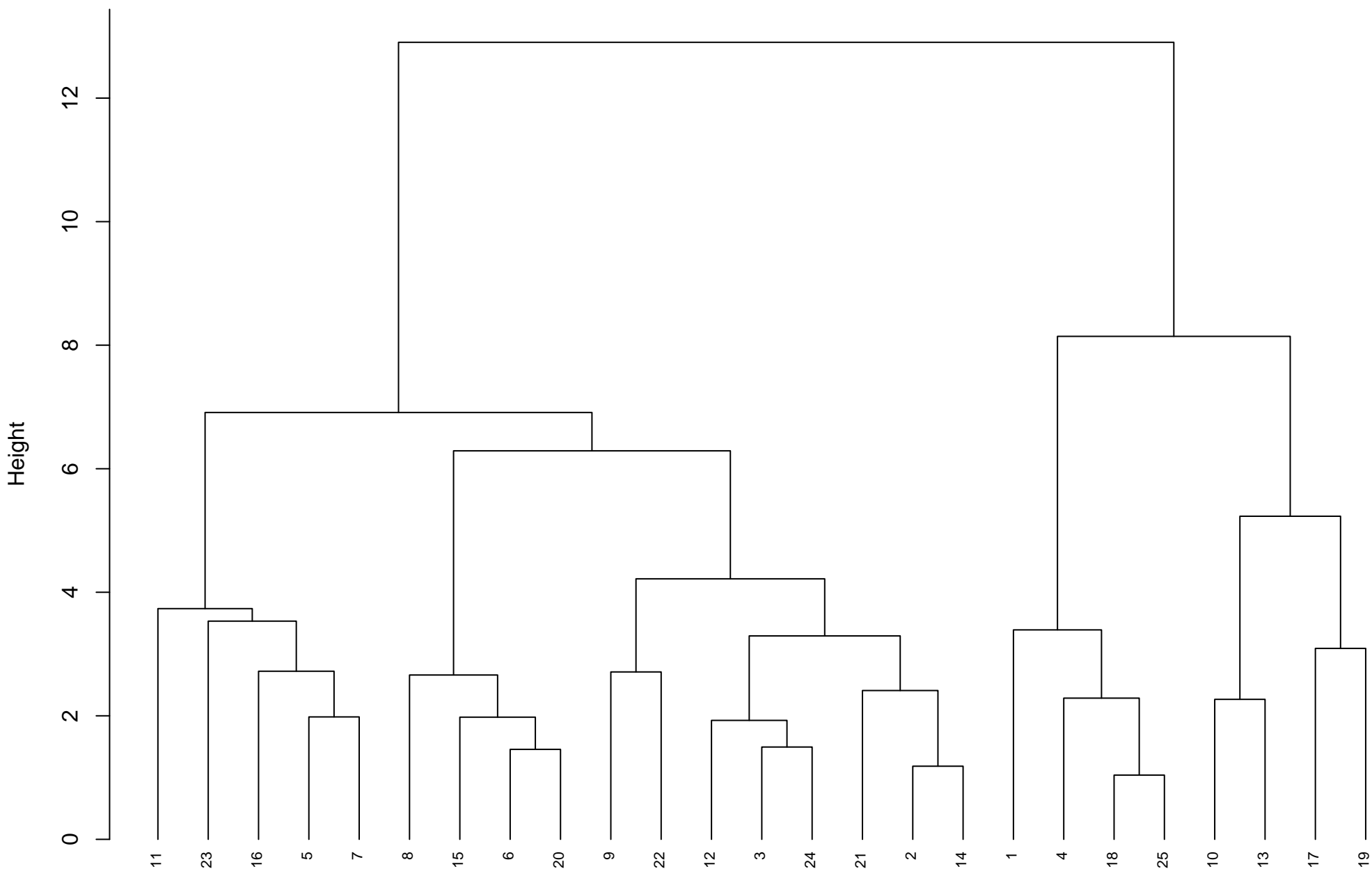


Cluster Dendrogram



dist(proteinIntakeScaled, method = "euclidean")
hclust (*, "ward.D2")