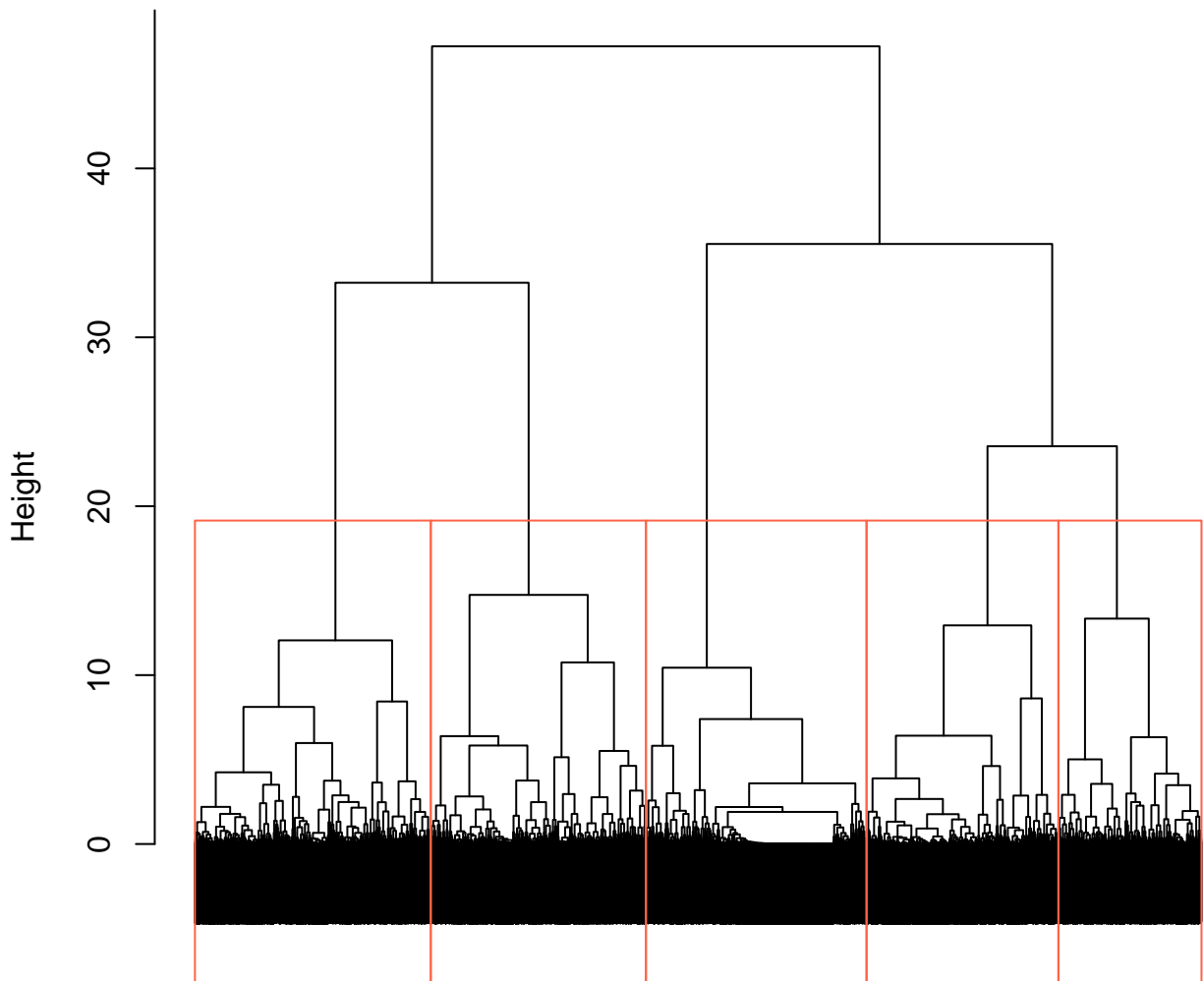


Dendrogramme Ag=ward.D2, Cor=pearson



Genes
`hclust(*, "ward.D2")`