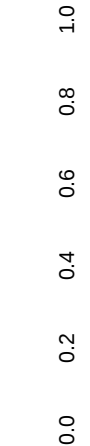


Height



as.dist(1 - cor(log2(1 + fit\$N[fit\$Sglucosid %in% fit\$genesUsed, hclust("c", 0.0001), complete))