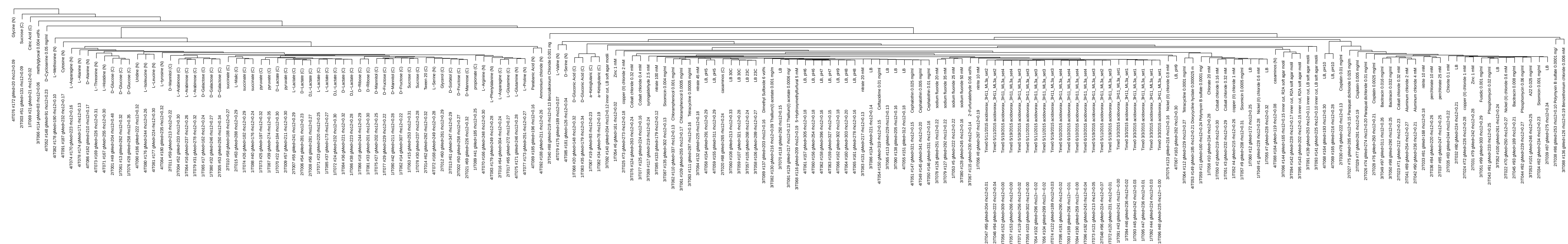
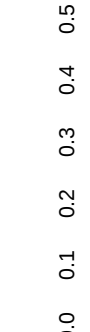


Height



as.dist(1 - cor(log2(1 + fit\$N(fit\$S,locusid) %in% fit\$genesUsed, hclust(*, "complete"))