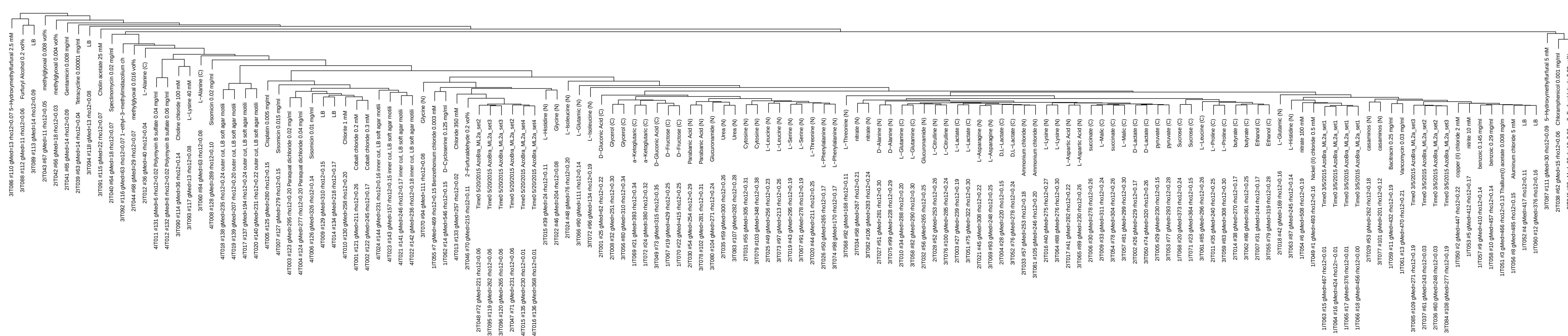
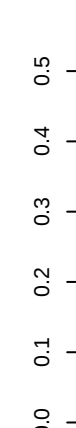


Height



as.dist(1 - cor(log2(1 + fit\$gNfit\$gN\$locusD %in% fit\$genesUsed, hclust(\*, "complete")