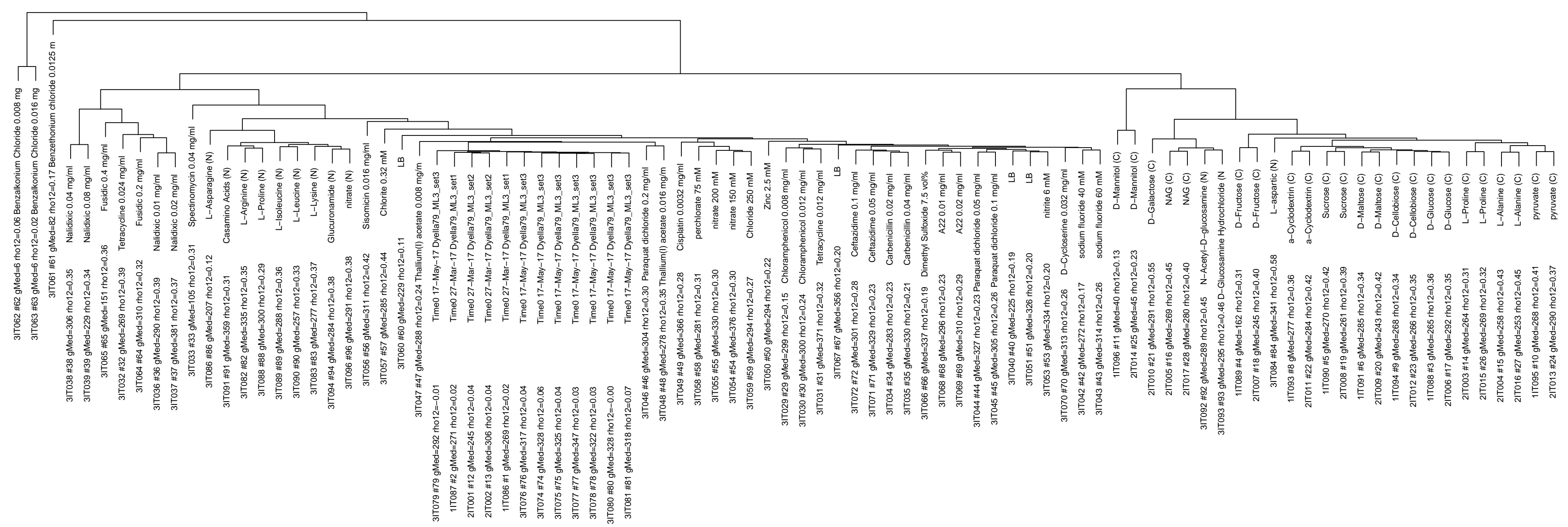


Height

0.0
0.1
0.2
0.3
0.4



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