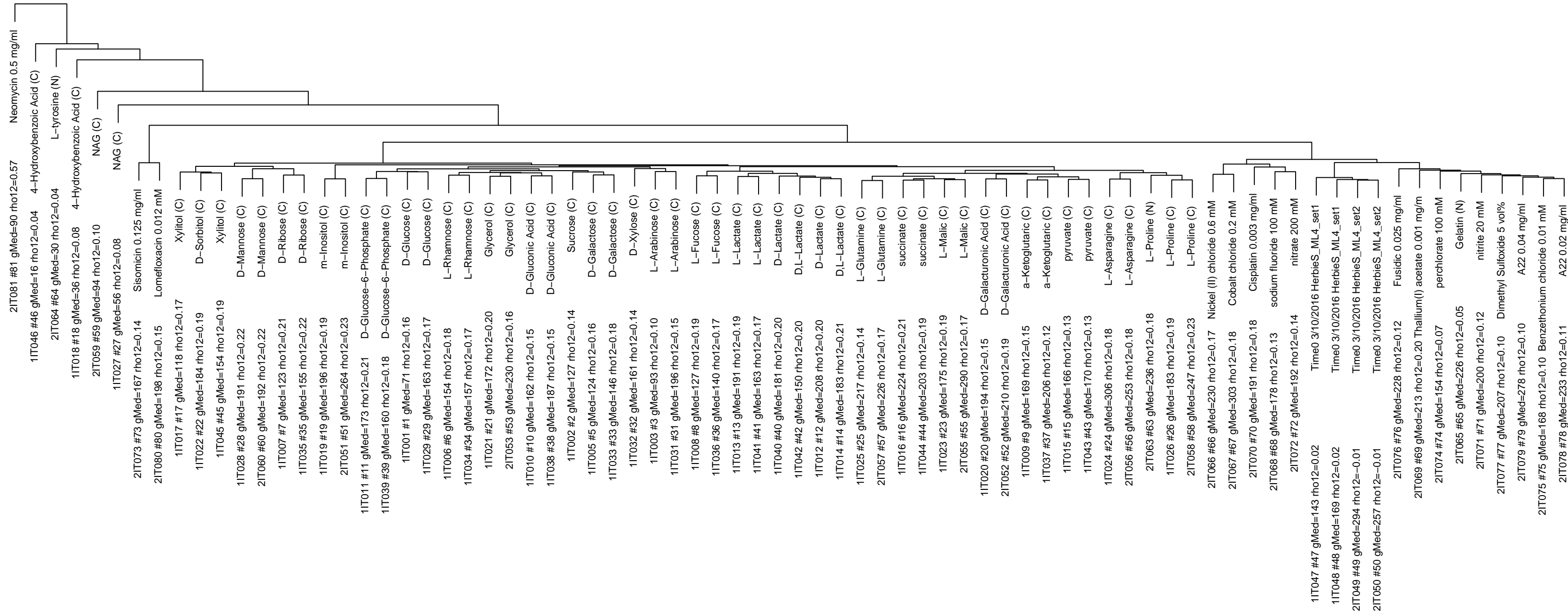


Height

0.0 0.1 0.2 0.3 0.4 0.5 0.6 0.7



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