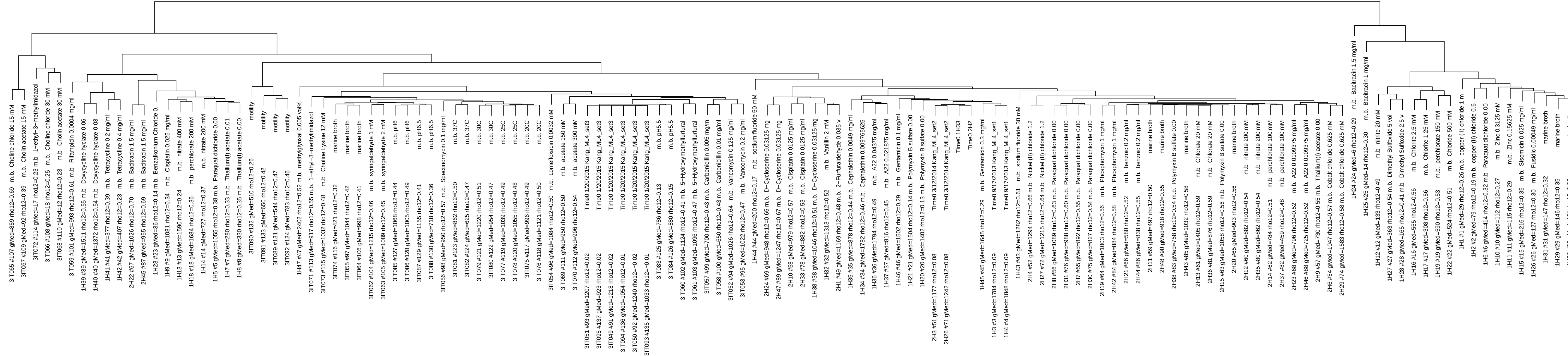
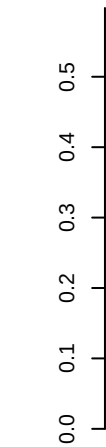




```
as.dist(1 - cor(log2(1 + fit$gN[fit$gN$locusId %in% fit$genesUs
hclust(*, "complete")
```