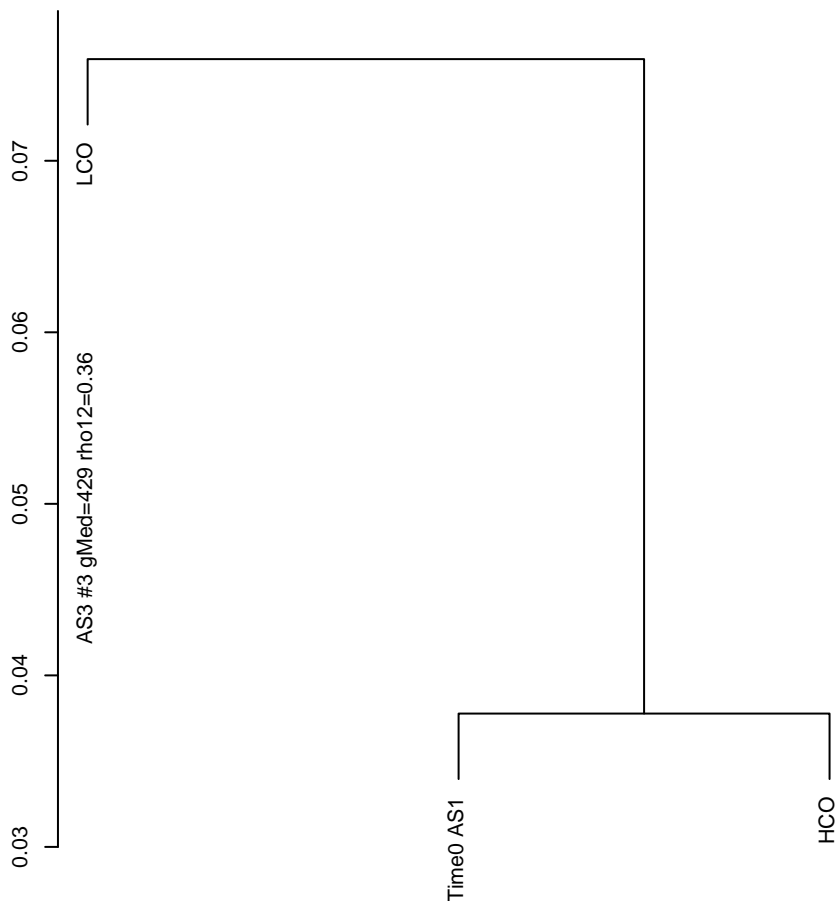


Height



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