clus3−vs−NON.clus3 in GBMLGG−TP RNASeq data

significance of gene : [−log10(ebayes_fit$p.val)]

log2 fold change in expression level : [clus3−vs−NON.clus3]

Among total18307genes
all 14306 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3

FCGR2A(0.31)
NCF4(0.42)
FCGR2C(0.29)
NCF1(0.38)
IL10(0.38)