clus2−vs−NON.clus2 in READ−TP RNASeq data

log2 fold change in expression level : [clus2−vs−NON.clus2]

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

Among total18090genes
all 791 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3

PTK2B(1.66)
PRKCB(1.97)
GNAQ(1.45)
SOS1(1.30)
MAP3K1(1.26)