clus1−vs−NON.clus1 in HNSC−TP RNASeq data

log2 fold change in expression level : [clus1−vs−NON.clus1]

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

Among total18361genes
all 8614 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3

KDELR3(1.82)
FKBP14(1.52)
PDIA5(1.36)
IGFBP1(1.33)
IL8(1.44)