
clus1−vs−NON.clus1 in PRAD−TP RNASeq data
Among total18256genes
all 9890 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
PAK3(3.04)
ACTA1(5.54)
DMD(2.02)
NRG2(2.14)
NRG1(1.92)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus1−vs−NON.clus1]
0
5
10
15
20
25
30
−3
−2
−1
0
1
2
3