
clus4−vs−NON.clus4 in THCA−TP RNASeq data
Among total17971genes
all 9688 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
NEURL(2.44)
HEY2(1.88)
DTX1(1.60)
MAMLD1(2.09)
DTX4(2.13)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus4−vs−NON.clus4]
0
10
20
30
40
50
−4
−2
0
2
4