clus1−vs−NON.clus1 in LUAD−TP RNASeq data
Among total18300genes
all 11715 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
MAPK10(4.11)
ERBB4(4.42)
SHC3(2.54)
CAMK2A(2.52)
ARG2(1.72)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus1−vs−NON.clus1]
0
10
20
30
40
50
−4
−2
0
2
4