clus2−vs−NON.clus2 in LUAD−TP RNASeq data
Among total18300genes
all 10864 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
MAOA(0.35)
DDC(0.19)
ASPA(0.52)
ALDH3A1(0.21)
ABP1(0.27)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus2−vs−NON.clus2]
0
10
20
30
40
−4
−2
0
2
4