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)
FCER1A(5.98)
MS4A2(3.86)
PLA2G1B(4.85)
CSF2(2.12)
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