clus3−vs−NON.clus3 in LUAD−TP RNASeq data
Among total18300genes
all 10473 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
FGA(30.51)
FGB(34.91)
F7(4.02)
F2(3.99)
FGG(15.15)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus3−vs−NON.clus3]
0
10
20
30
40
50
−6
−4
−2
0
2
4
6