clus1−vs−NON.clus1 in PRAD−TP RNASeq data
Among total18256genes
all 11515 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
CHP2(8.10)
GRIN2A(3.01)
DRD1(3.02)
CALML3(5.01)
NOS1(3.86)
significance of gene : [−log10(ebayes_fit$p.val) ]
log2 fold change in expression level : [clus1−vs−NON.clus1 ]
0
10
20
30
40
50
60
−4
−2
0
2
4