clus3−vs−NON.clus3 in HNSC−TP RNASeq data
Among total18361genes
all 13069 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
PRKAA2(0.12)
MLXIPL(0.30)
PRKAR2B(0.47)
GCK(0.45)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus3−vs−NON.clus3]
0
10
20
30
40
50
−4
−2
0
2
4