clus1−vs−NON.clus1 in UCEC−TP RNASeq data
Among total18525genes
all 12503 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
L1CAM(21.00)
EPHB2(4.01)
ROBO3(2.77)
DPYSL5(4.20)
EPHB1(3.05)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus1−vs−NON.clus1]
0
20
40
60
80
100
−6
−4
−2
0
2
4
6