clus1−vs−NON.clus1 in THYM−TP RNASeq data
Among total18283genes
all 9492 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
WNT5A(0.08)
MECOM(0.18)
CCNA1(0.13)
WNT2B(0.13)
FGF5(0.18)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus1−vs−NON.clus1]
0
5
10
15
20
25
30
35
−5
0
5