clus1−vs−NON.clus1 in MESO−TP RNASeq data
Among total18193genes
all 5063 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
SSR1(1.42)
TRAM1(1.48)
SEC11C(1.49)
FAM153A(3.27)
RPS4Y1(2.36)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus1−vs−NON.clus1]
0
5
10
15
−6
−4
−2
0
2
4
6