clus1−vs−NON.clus1 in STES−TP RNASeq data
Among total18748genes
all 11408 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
GLI3(0.10)
WNT9A(0.13)
WNT7B(0.07)
FZD10(0.10)
WNT7A(0.08)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus1−vs−NON.clus1]
0
20
40
60
80
−10
−5
0
5
10