clus5−vs−NON.clus5 in PAAD−TP RNASeq data

Legend:
- ○ Among total18457genes
- ● all 5855 sig genes
- ○ top 5 core enriched genes
- -- sig level:(−log10(0.05)==1.3

significance of gene : [−log10(ebayes_fit$p.val)]

log2 fold change in expression level : [clus5−vs−NON.clus5]

Labeled points: NTRK3(3.14), NGFR(3.97), NGF(2.31), CAMK2A(2.34), FASLG(2.14)