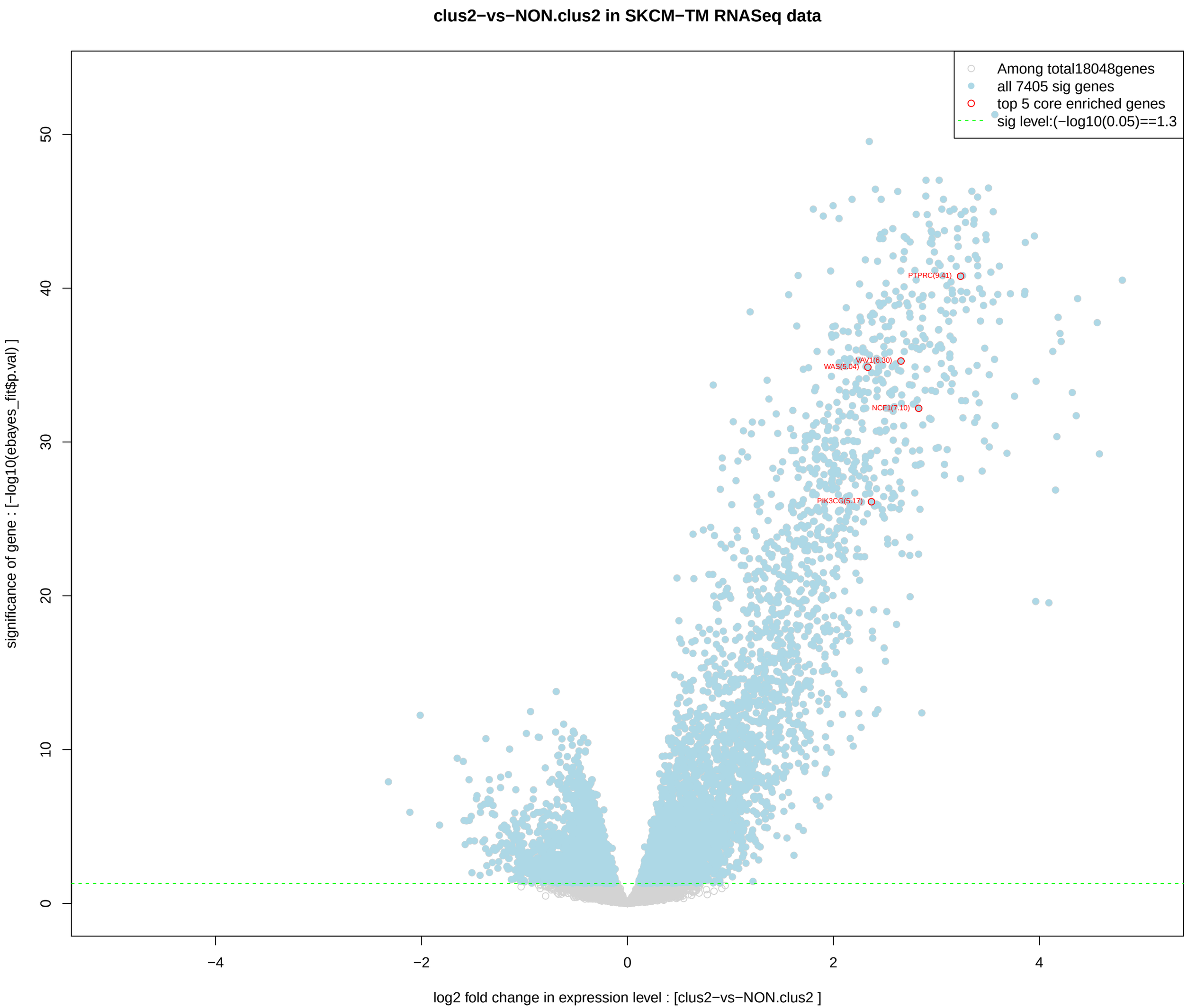
clus2−vs−NON.clus2 in SKCM−TM RNASeq data
Among total18048genes
all 7405 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
PTPRC(9.41)
VAV1(6.30)
WAS(5.04)
NCF1(7.10)
PIK3CG(5.17)
significance of gene : [−log10(ebayes_fit$p.val)]
0
10
20
30
40
50
−4
−2
0
2
4
log2 fold change in expression level : [clus2−vs−NON.clus2]