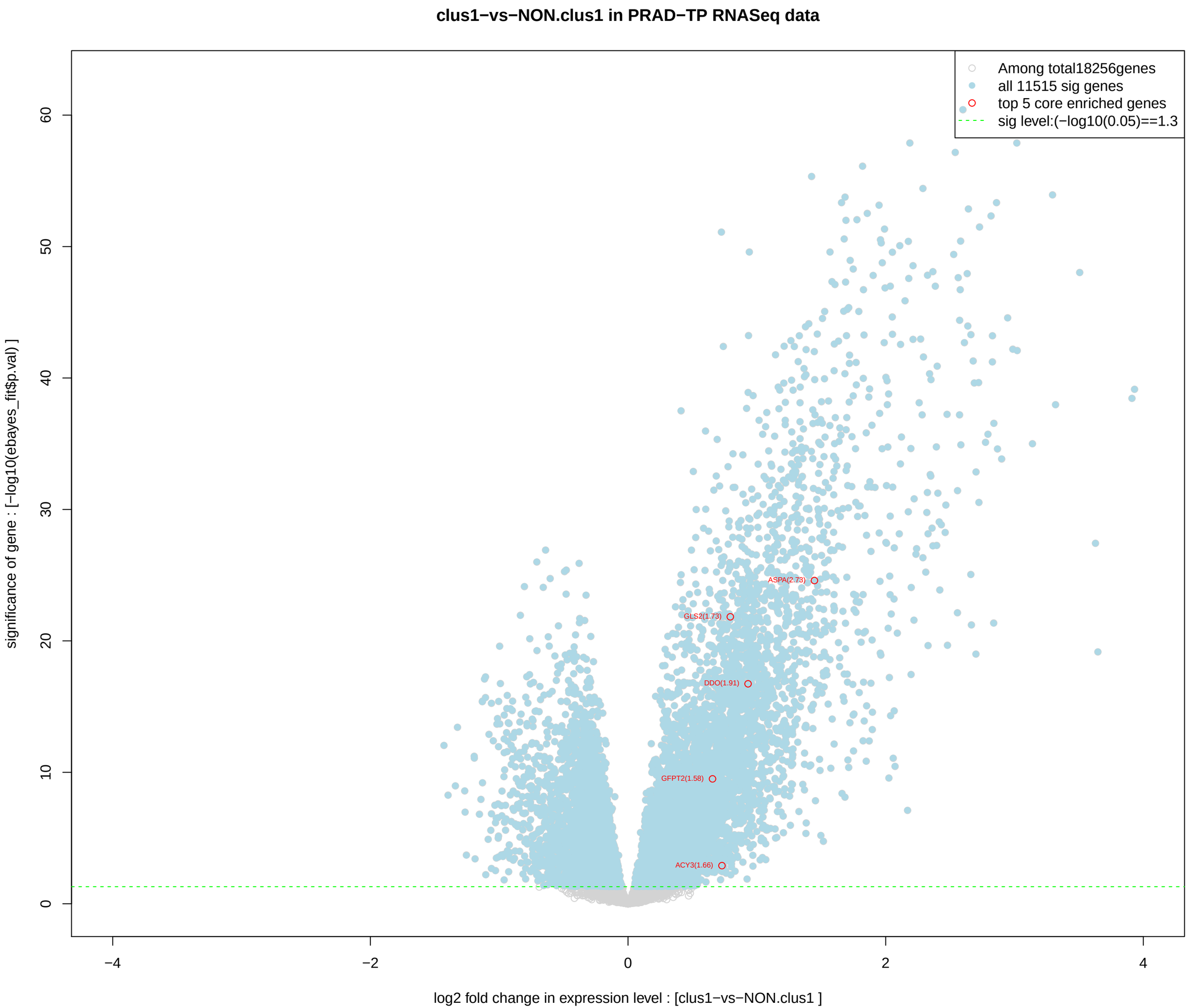
clus1−vs−NON.clus1 in PRAD−TP RNASeq data
Among total18256genes
all 11515 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
ASPA(2.73)
GLS2(1.73)
DDO(1.91)
GFPT2(1.58)
ACY3(1.66)
significance of gene : [−log10(ebayes_fit$p.val) ]
log2 fold change in expression level : [clus1−vs−NON.clus1 ]
0
10
20
30
40
50
60
−4
−2
0
2
4