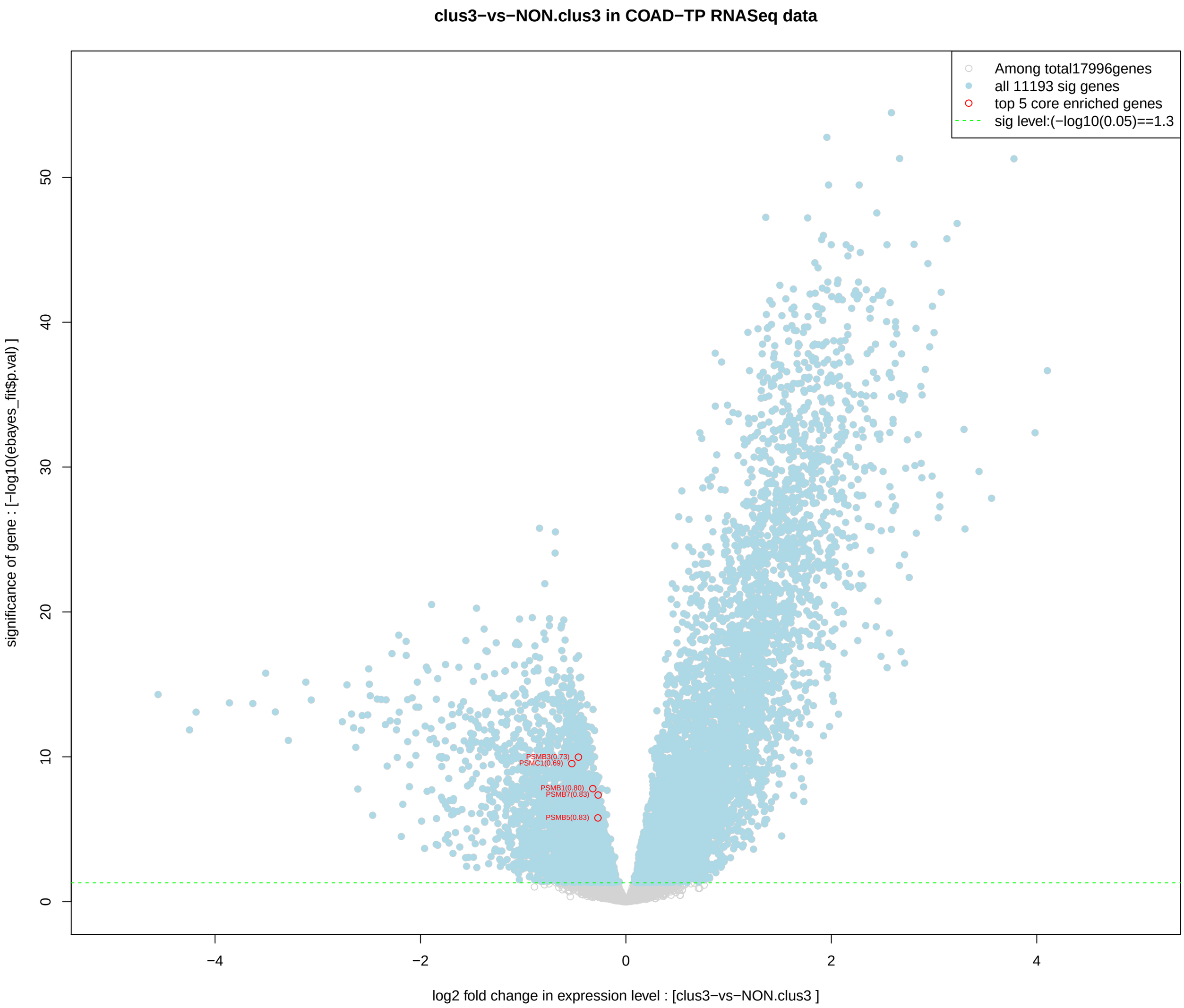
clus3−vs−NON.clus3 in COAD−TP RNASeq data
Among total17996genes
all 11193 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
PSMB3(0.73)
PSMC1(0.69)
PSMB1(0.80)
PSMB7(0.83)
PSMB5(0.83)
significance of gene : [−log10(ebayes_fit$p.val) ]
log2 fold change in expression level : [clus3−vs−NON.clus3 ]
0
10
20
30
40
50
−4
−2
0
2
4