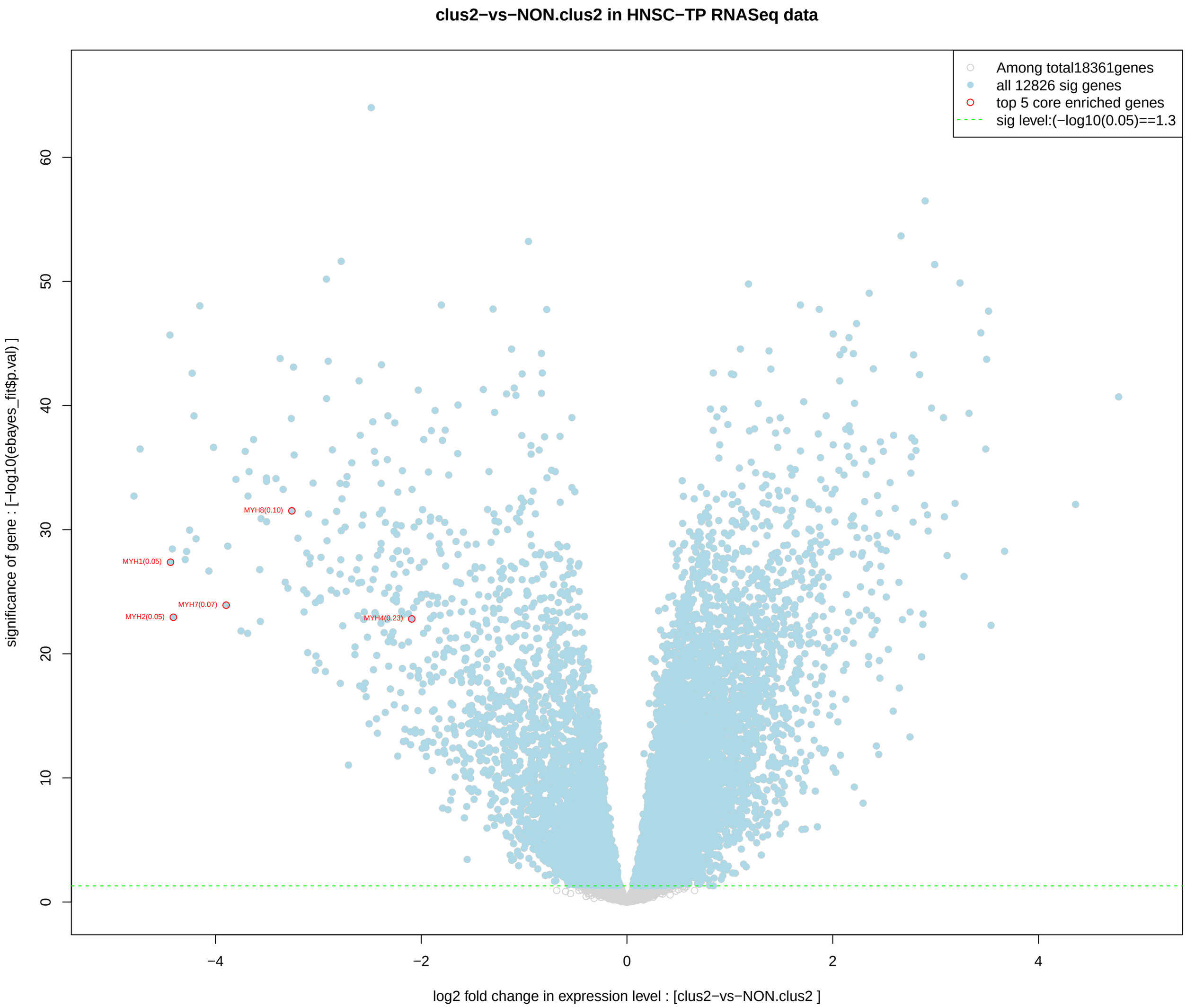
clus2−vs−NON.clus2 in HNSC−TP RNASeq data
Among total18361genes
all 12826 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
MYH8(0.10)
MYH1(0.05)
MYH7(0.07)
MYH2(0.05)
MYH4(0.23)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus2−vs−NON.clus2]
0
10
20
30
40
50
60
−4
−2
0
2
4