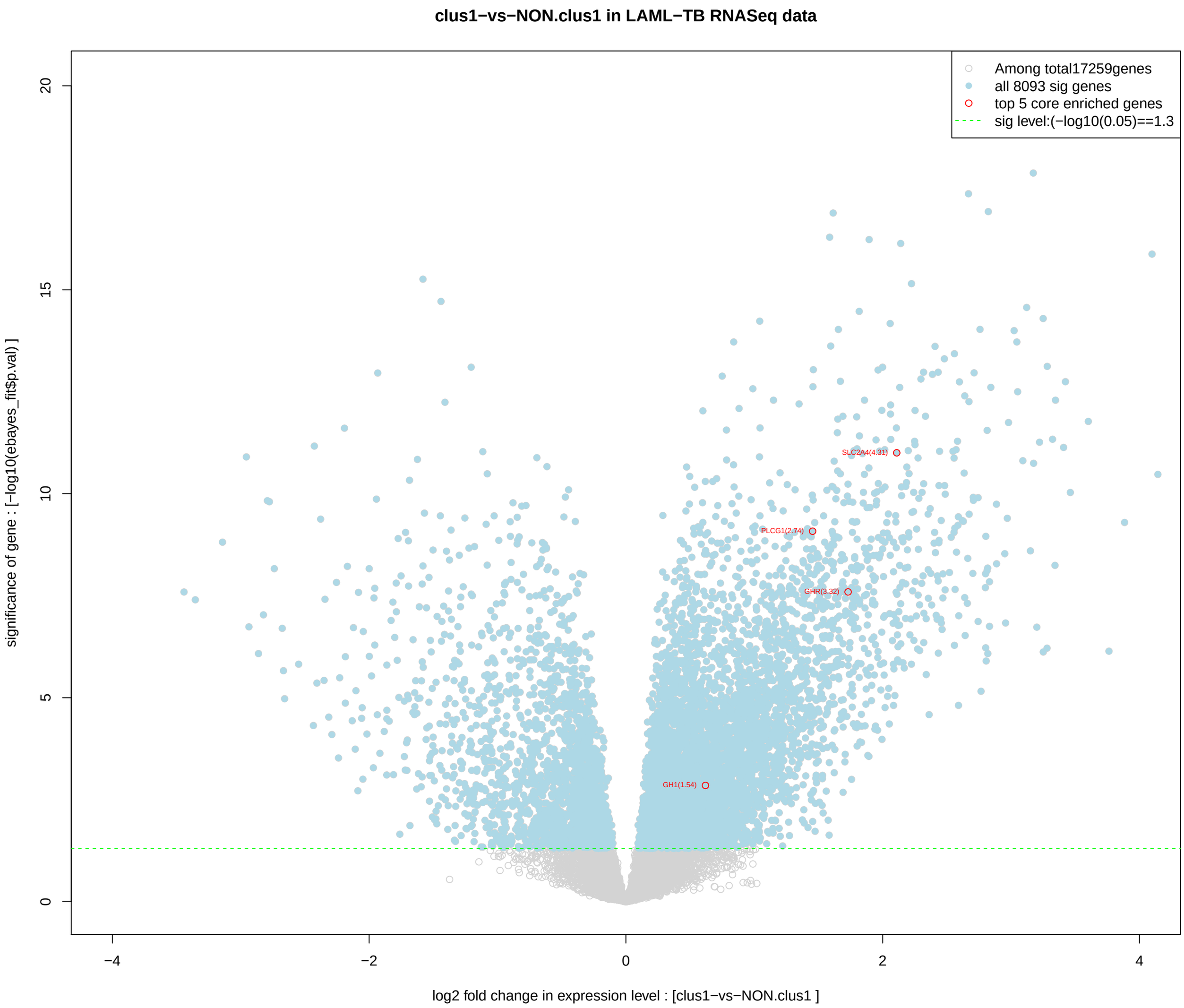
clus1−vs−NON.clus1 in LAML−TB RNASeq data
Among total17259genes
all 8093 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
SLC2A4(4.31)
PLCG1(2.74)
GHR(3.32)
GH1(1.54)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus1−vs−NON.clus1]
0
5
10
15
20
−4
−2
0
2
4