clus2−vs−NON.clus2 in LUAD−TP RNASeq data

x-axis: log2 fold change in expression level : [clus2−vs−NON.clus2]

y-axis: significance of gene : [−log10(ebayes_fit$p.val)]

Legend:
- ○ Among total18300genes
- ● all 10864 sig genes
- ○ top 5 core enriched genes
- - - - sig level:(−log10(0.05)==1.3

Labeled points:
- PLA2G10(0.19)
- PLA2G1B(0.18)
- PLA2G3(0.31)
- PLA2G4E(0.46)
- PLA2G2A(0.47)