**clus2−vs−NON.clus2 in LUSC−TP RNASeq data**

Legend:
- ○ Among total18496genes
- ● all 12406 sig genes
- ○ top 5 core enriched genes
- --- sig level:(−log10(0.05)==1.3

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

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

Labeled points:
- PPP2R2B(4.10)
- PPP2R2C(3.72)
- PRKAA2(2.36)
- PRKAG3(1.78)
- MLXIPL(1.86)