

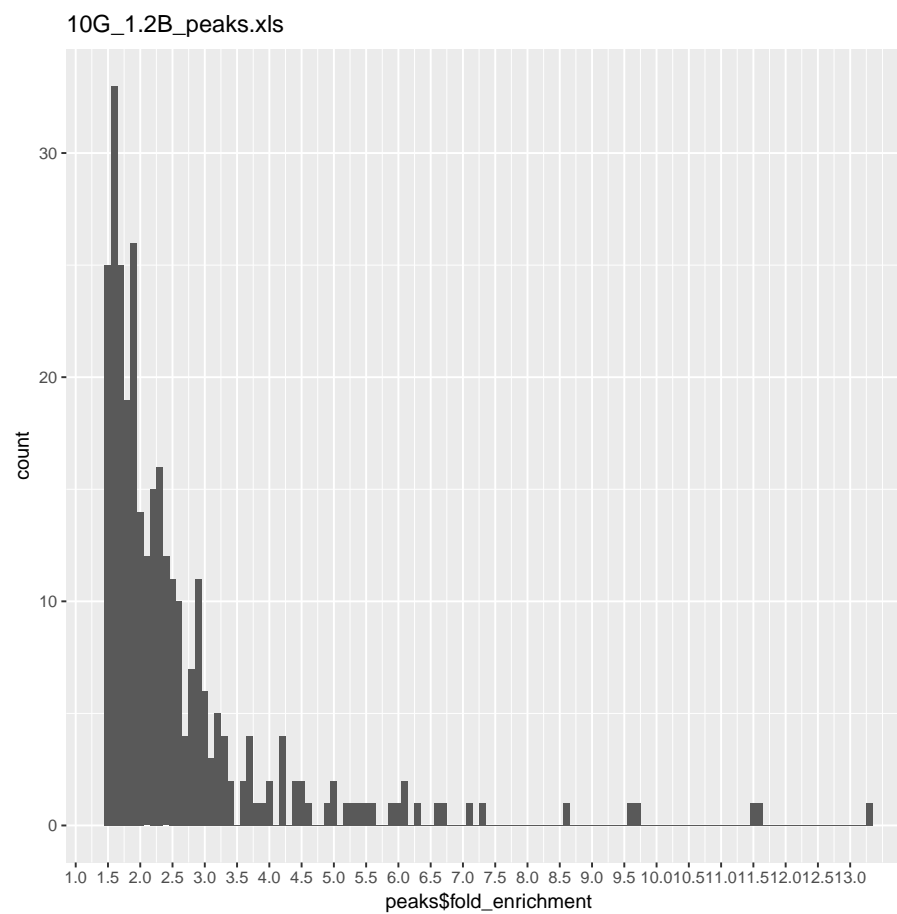
Load libraries:

```
library(ggplot2)
```

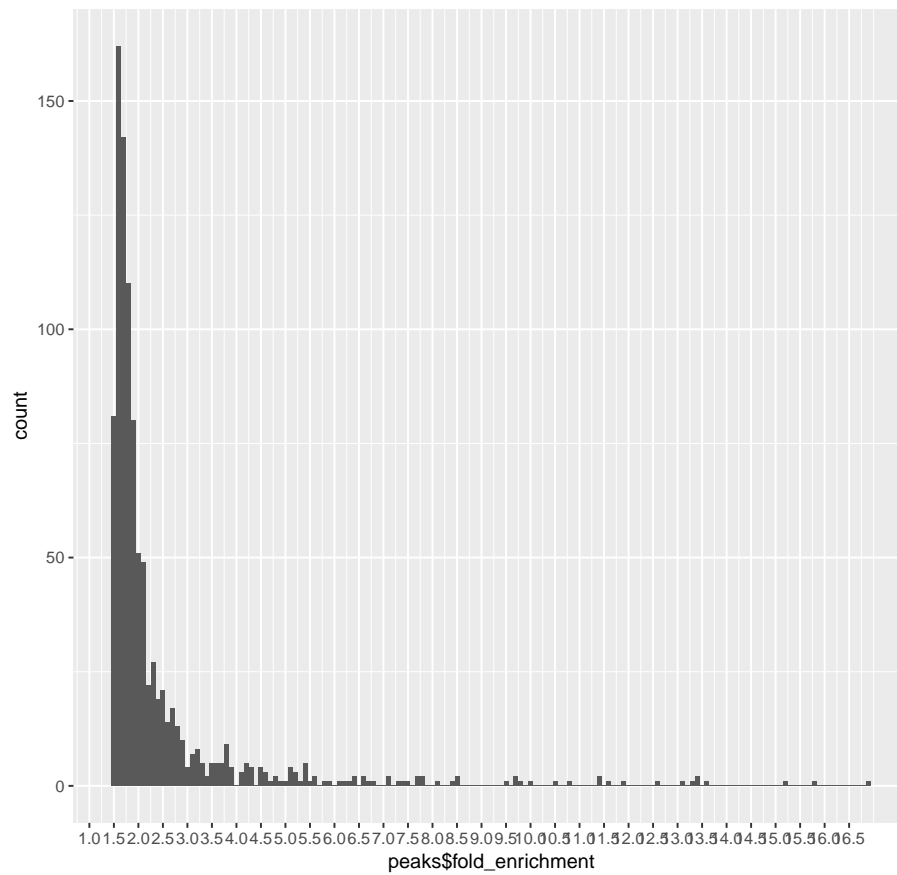
Plot fold-enrichment histogram:

```
path <- "/home/lucas/ISGlobal/Chip_Seq/DATA/Aligns/q5/Narrow_fe15/XLS/"
files <- list.files(path = "/home/lucas/ISGlobal/Chip_Seq/DATA/Aligns/q5/Narrow_fe15/XLS", pattern = "*.xls")

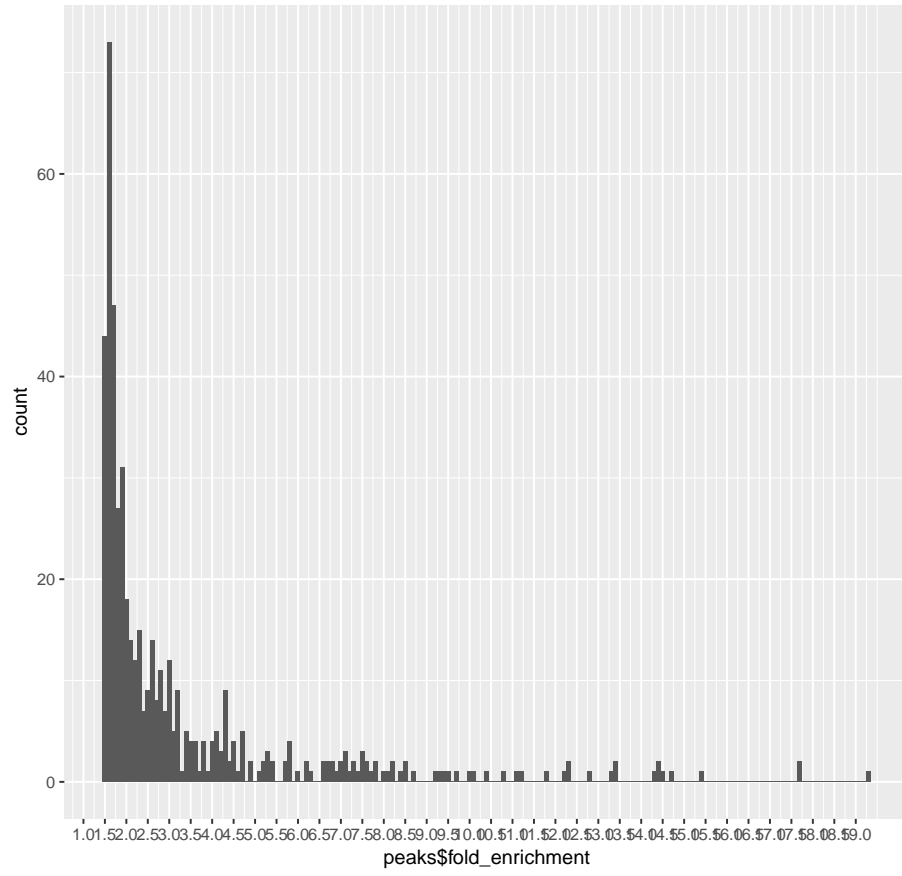
for (file in files){
  peaks <- read.table(paste0(path,file), header = TRUE, fileEncoding = "UTF-8")
  print(qplot(peaks$fold_enrichment, geom="histogram", binwidth = 0.1) + scale_x_continuous(breaks = 1:13))
}
```



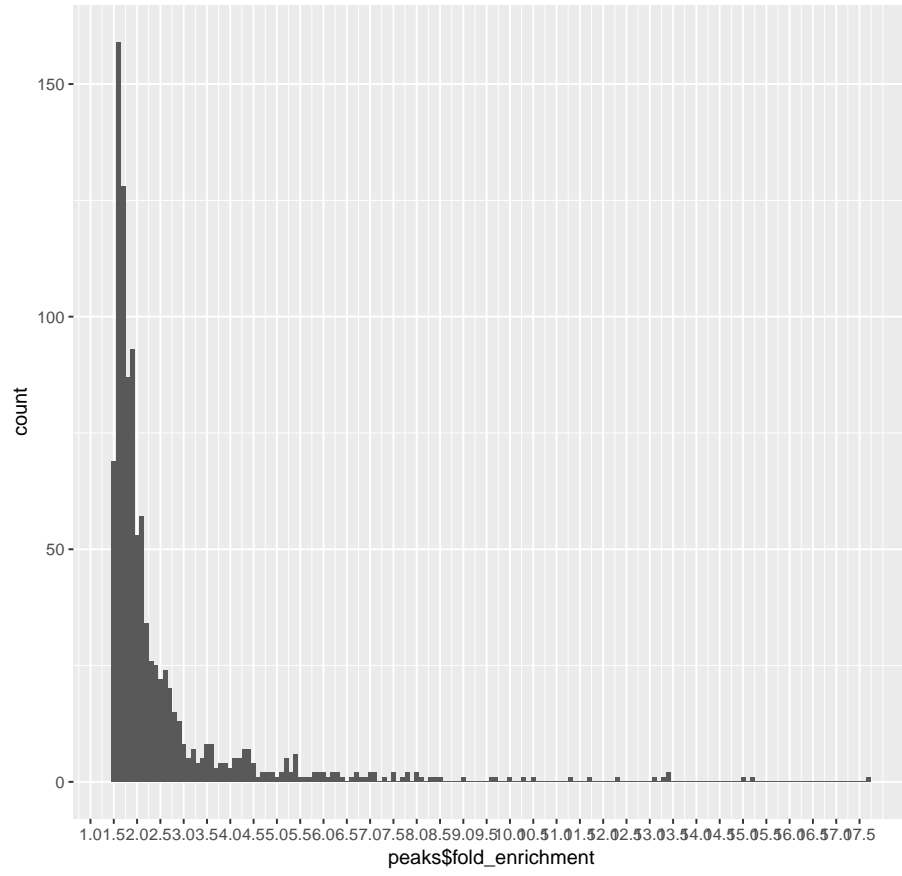
10G_A7K9_peaks.xls



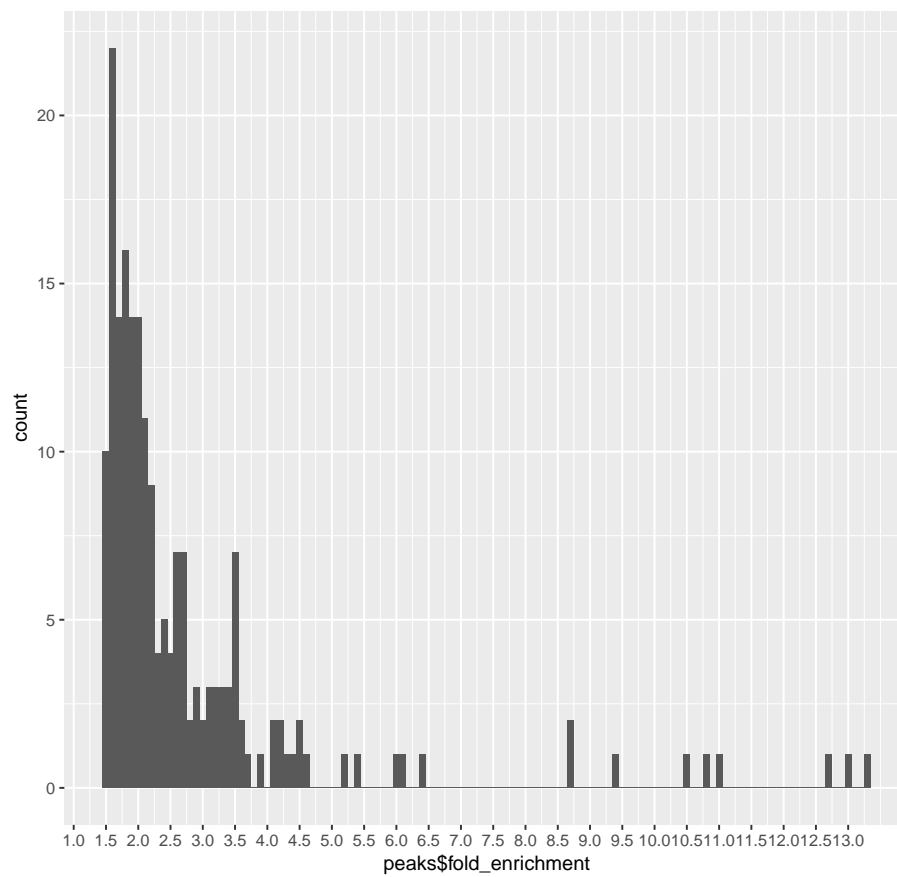
10G_C2_peaks.xls



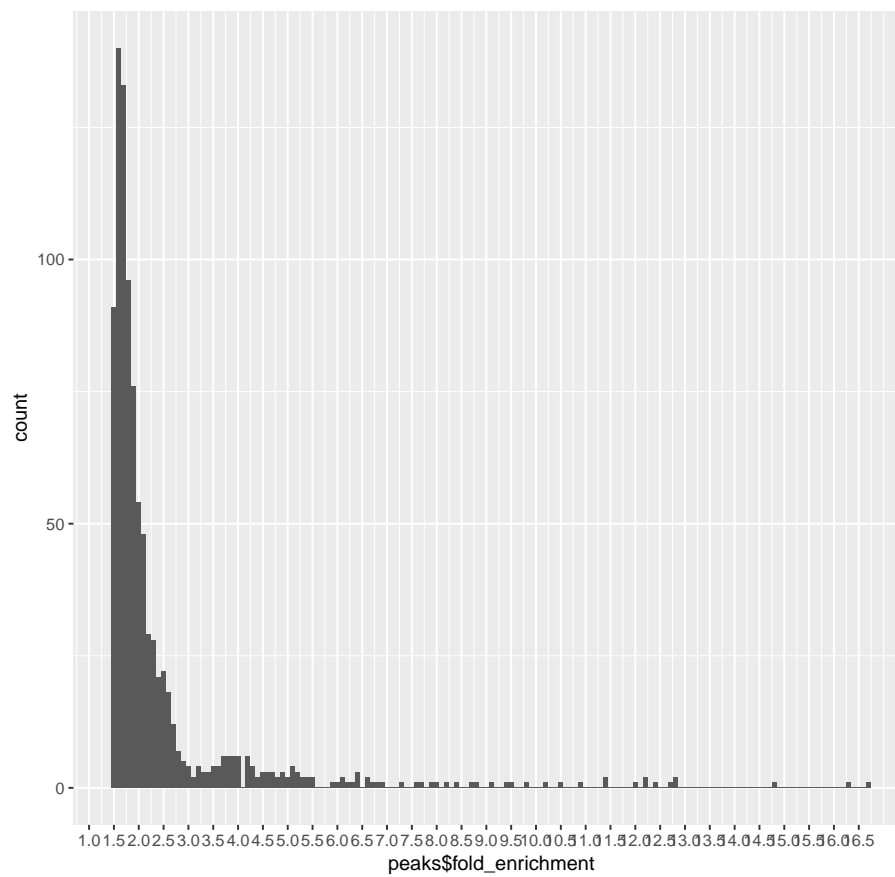
10G_E5K9_peaks.xls



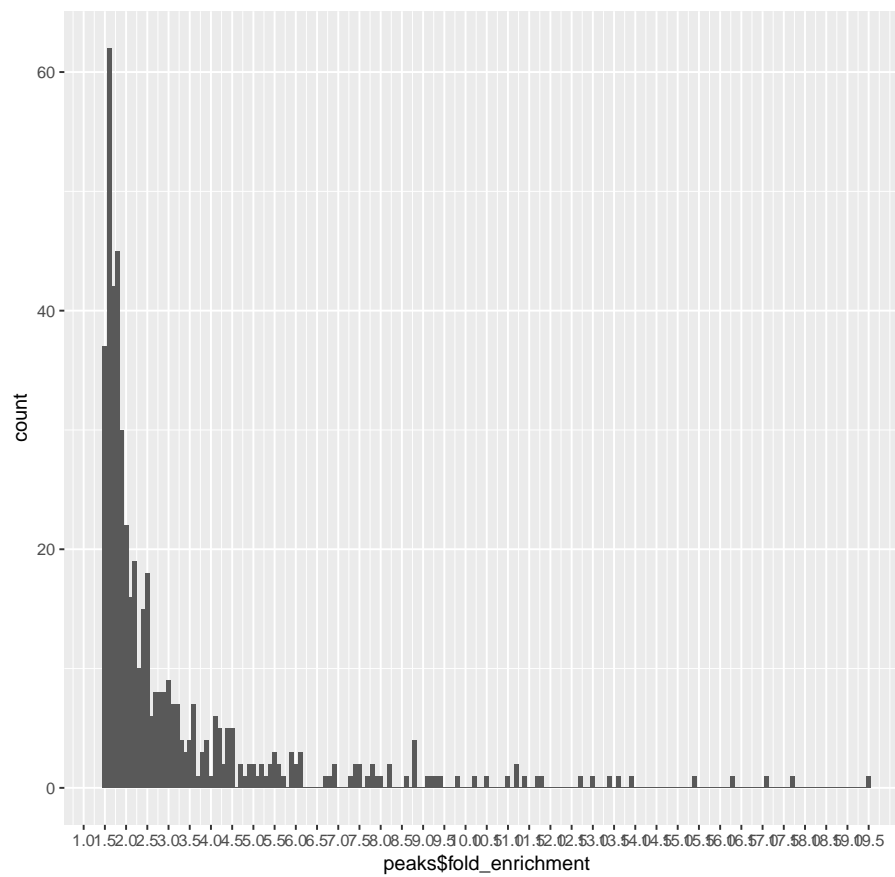
1.2B_10G_peaks.xls

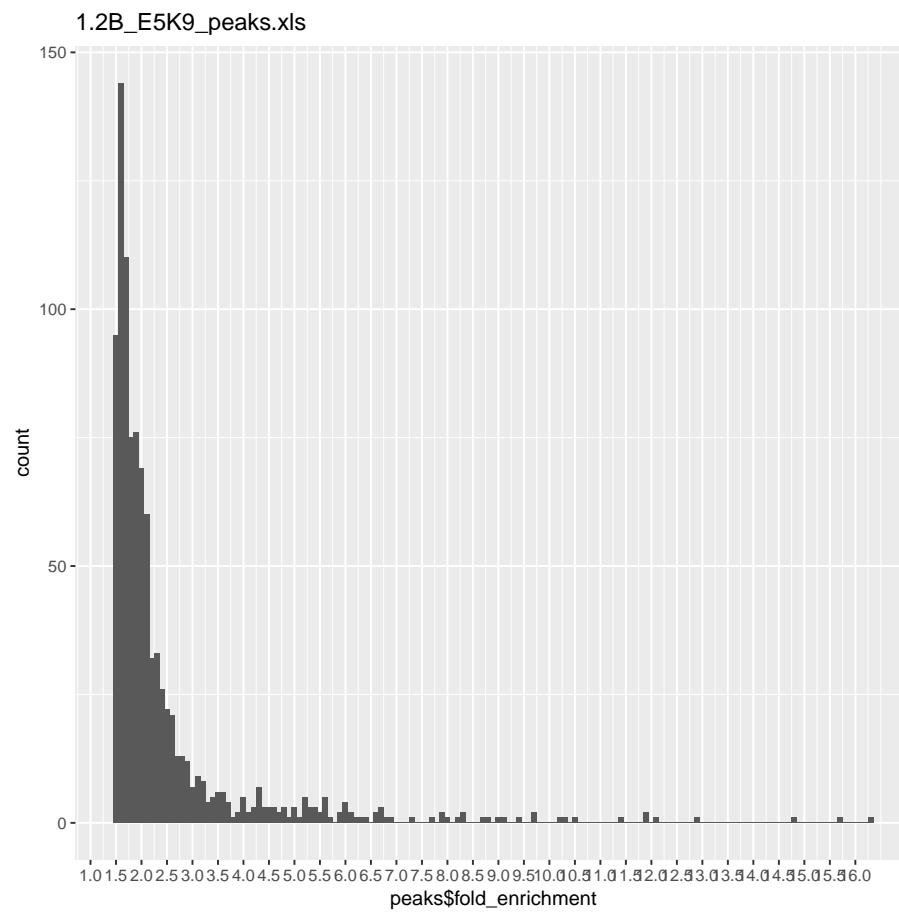


1.2B_A7K9_peaks.xls

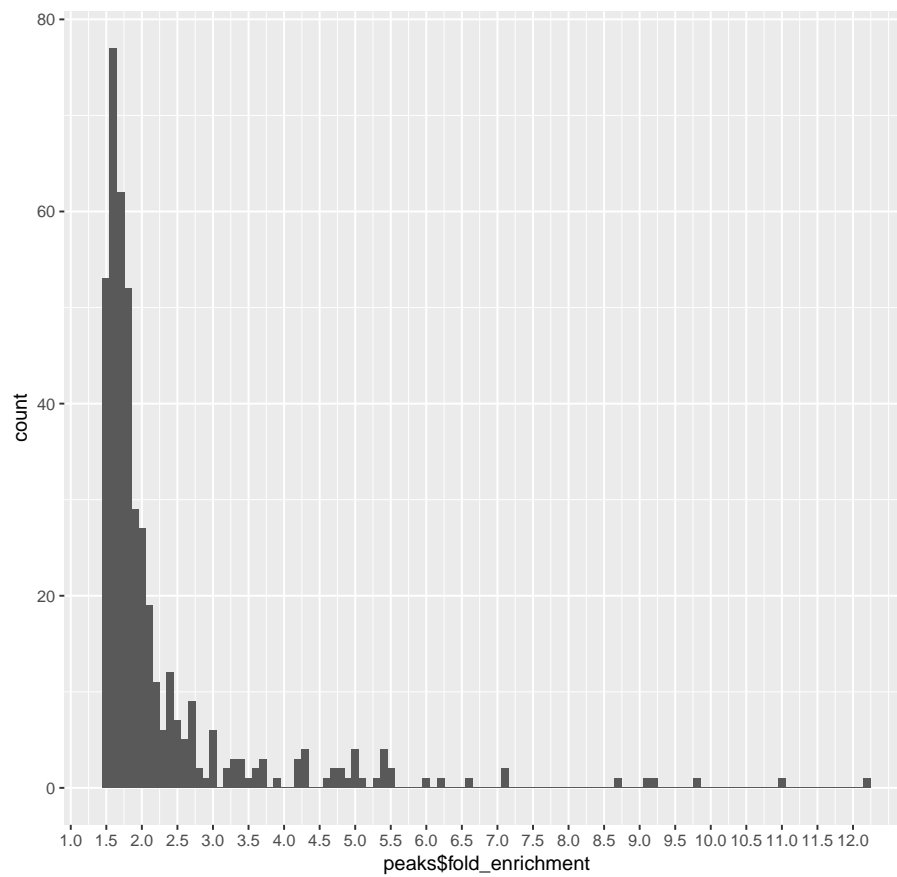


1.2B_C2_peaks.xls

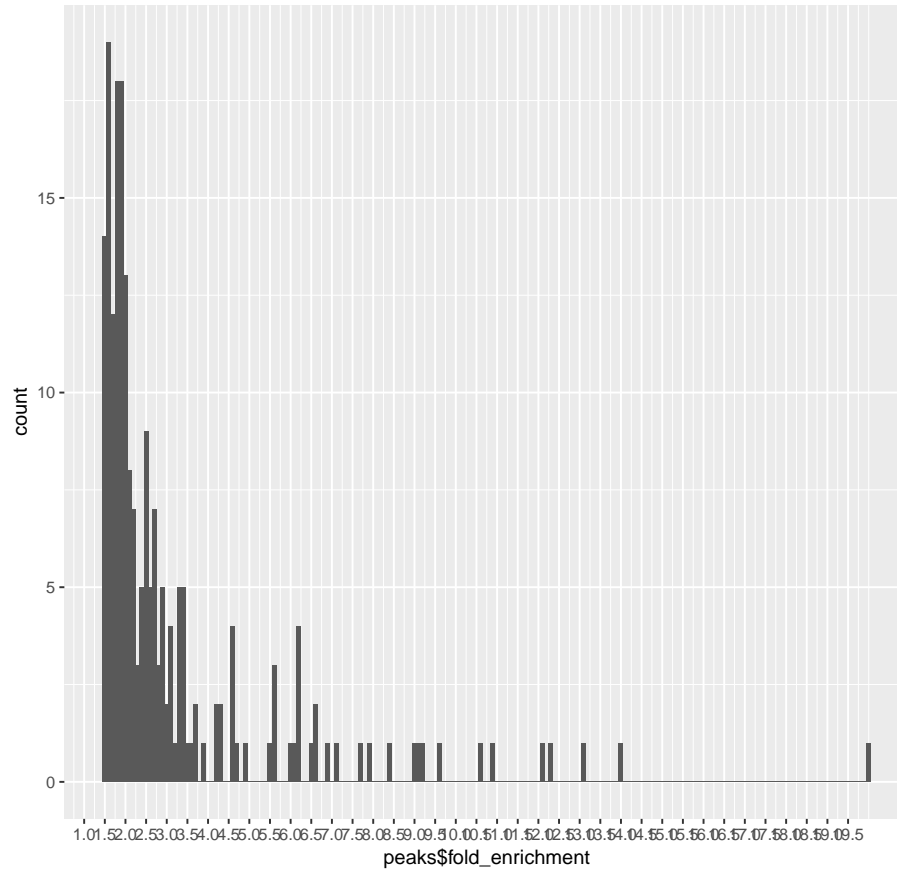


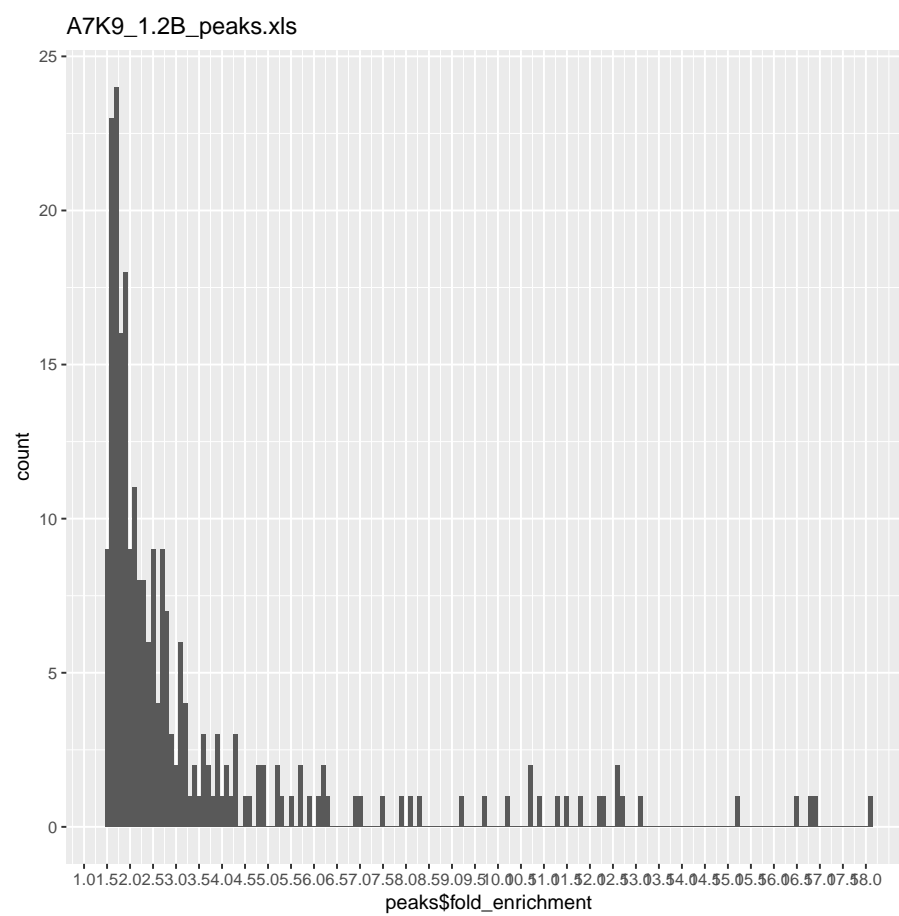


A7_E5_fe15_peaks.xls

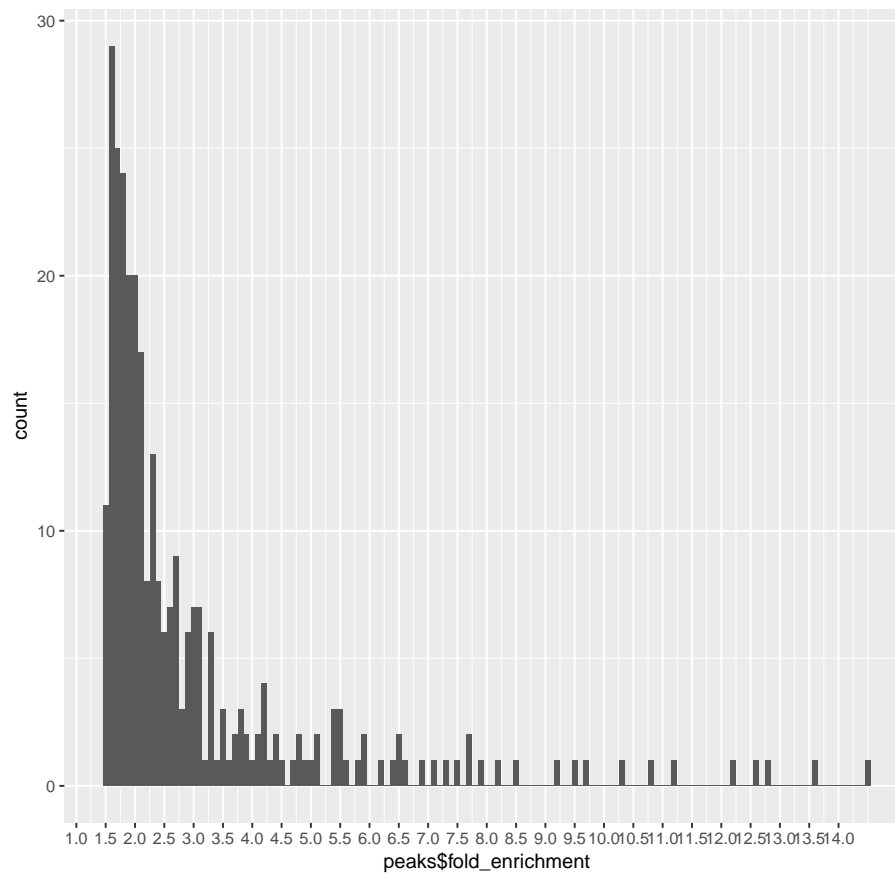


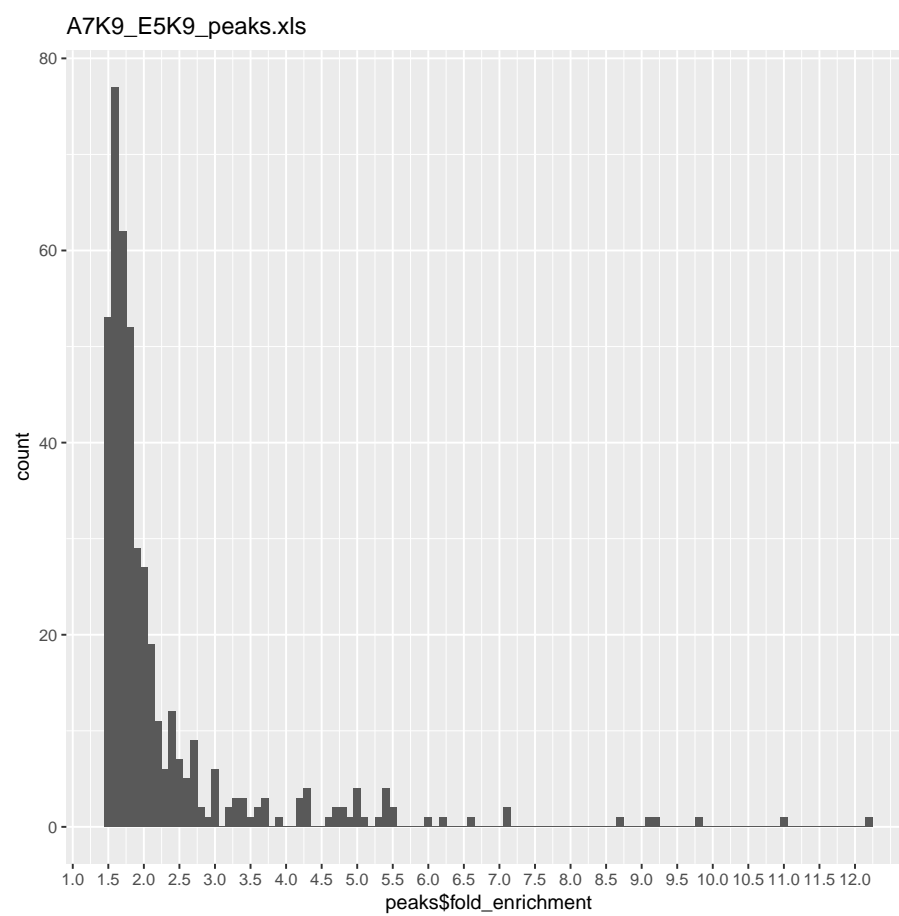
A7K9_10G_peaks.xls



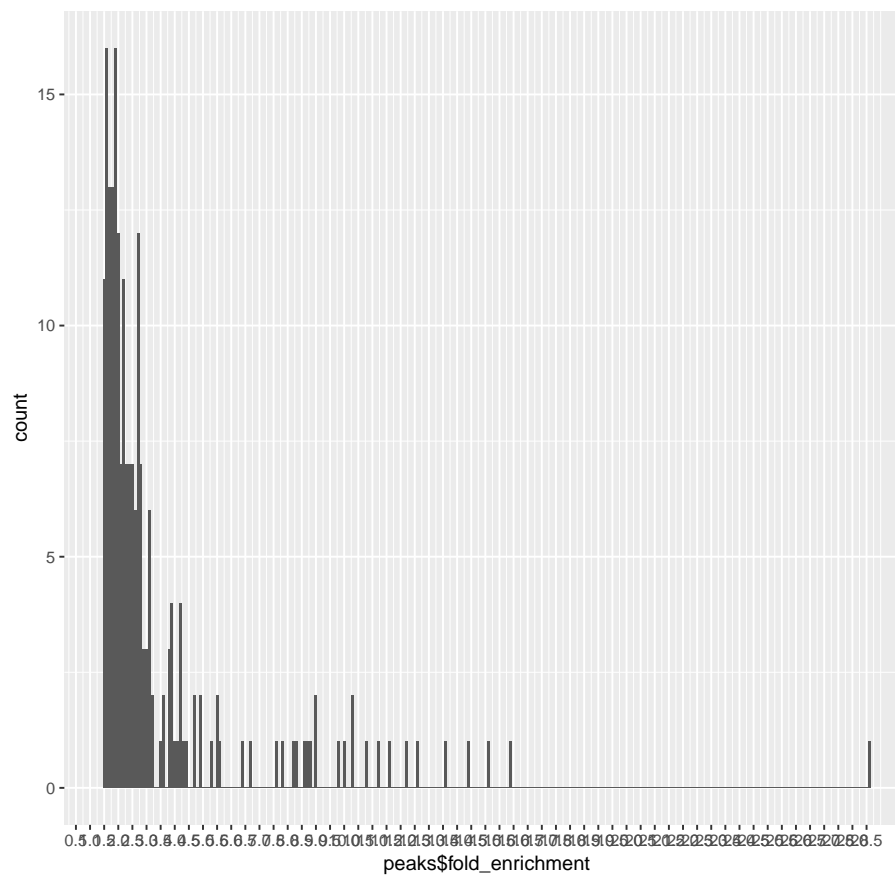


A7K9_C2_peaks.xls

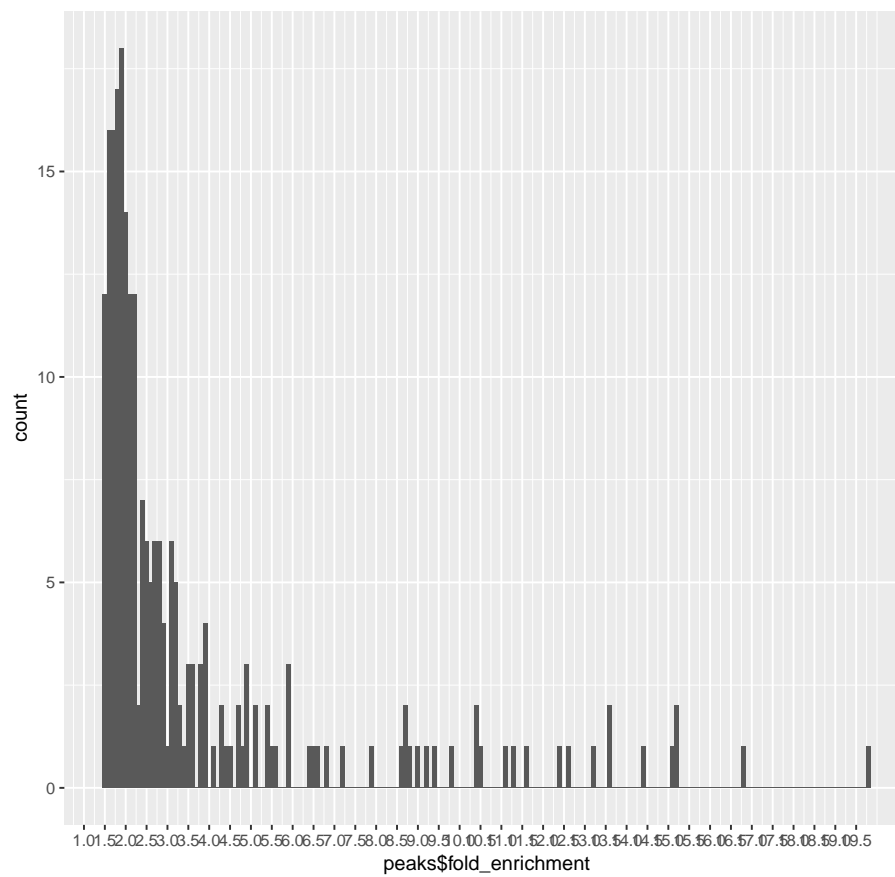




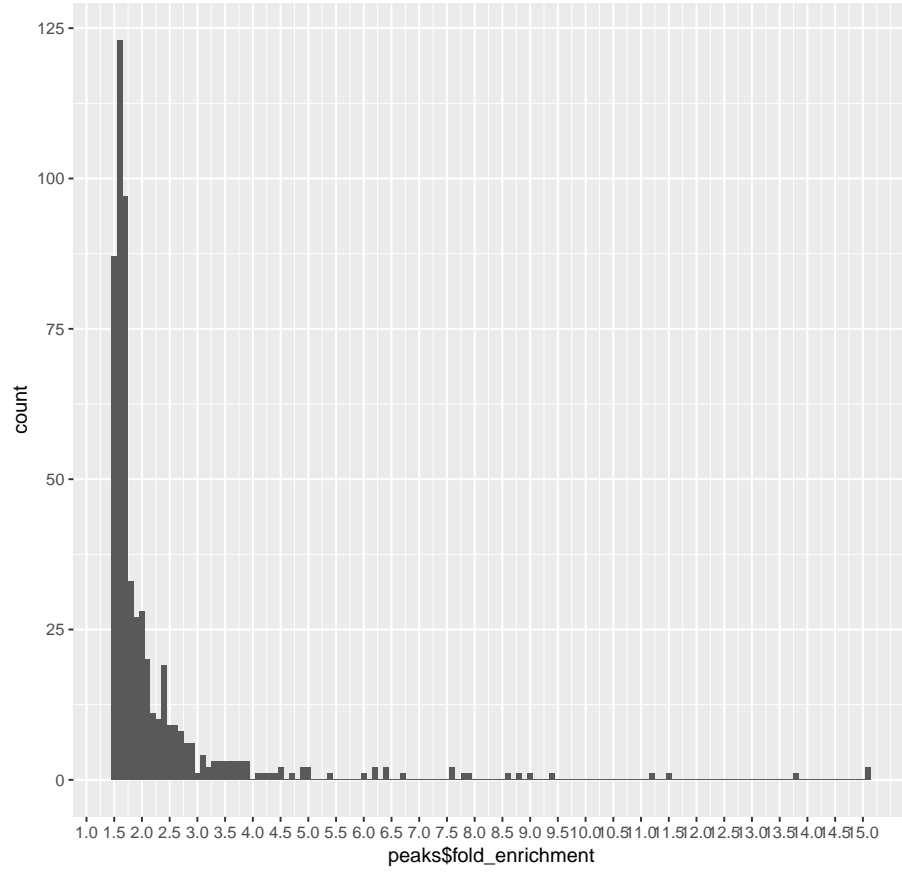
C2_10G_peaks.xls



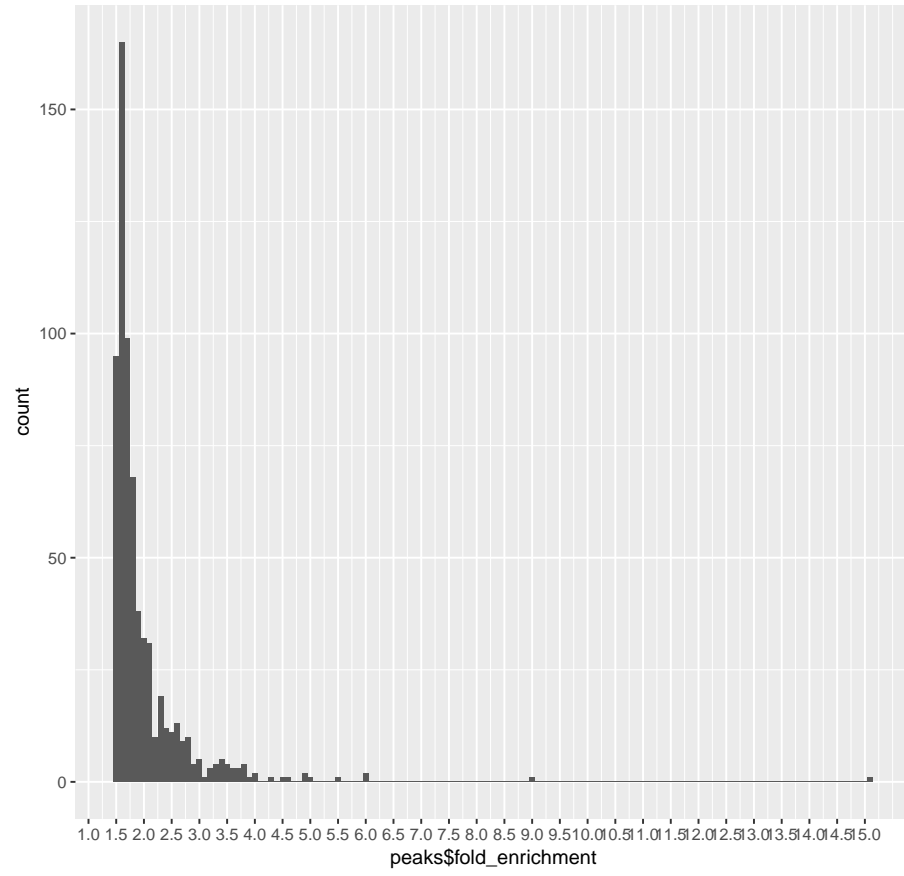
C2_1.2B_peaks.xls



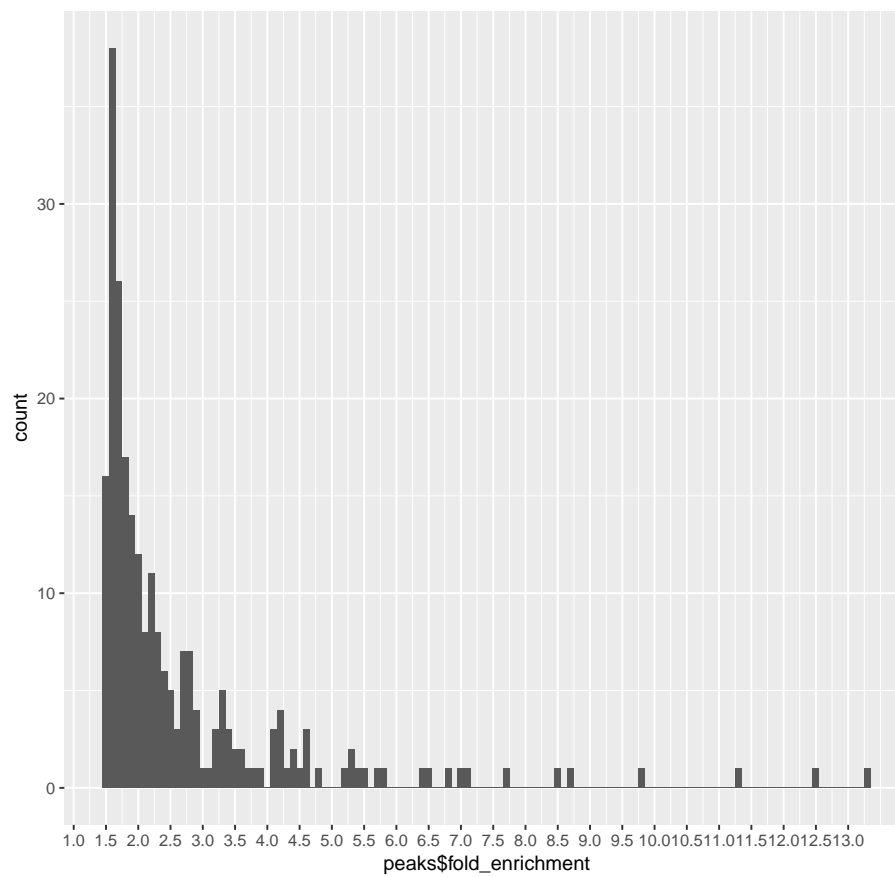
C2_A7K9_peaks.xls



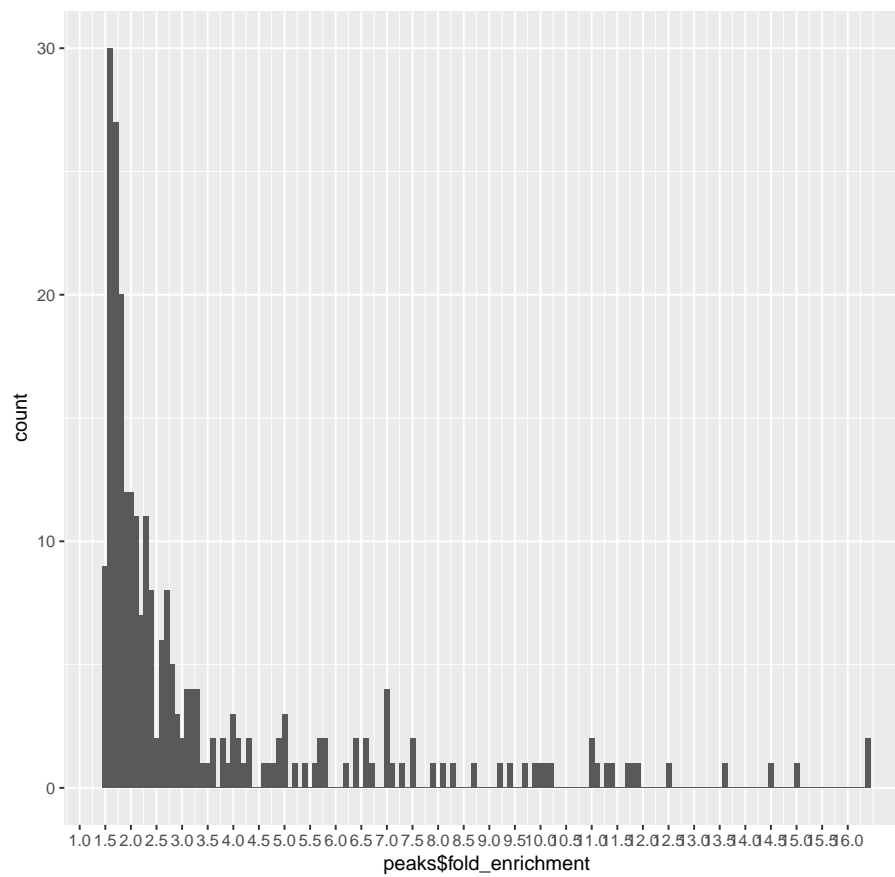
C2_E5K9_peaks.xls



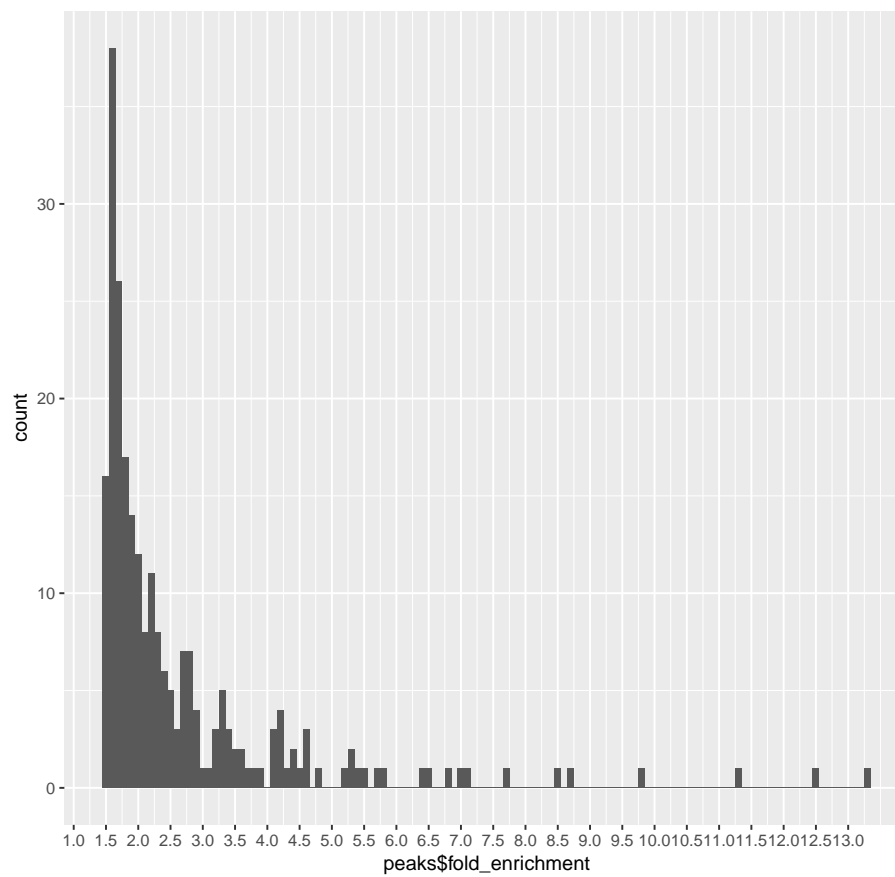
E5_A7_fe15_peaks.xls



E5K9_1.2B_peaks.xls



E5K9_A7K9_peaks.xls



E5K9_C2_peaks.xls

