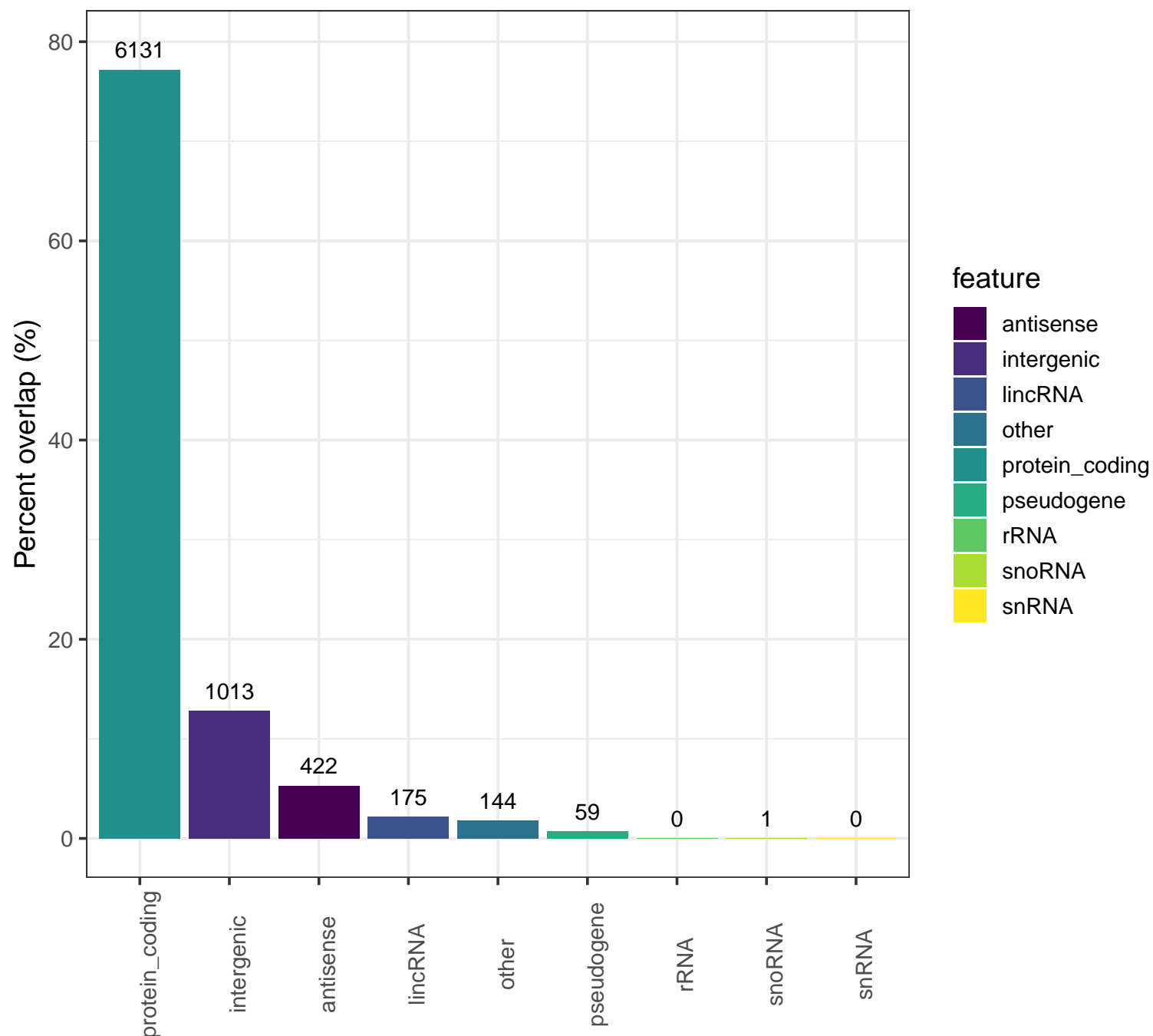
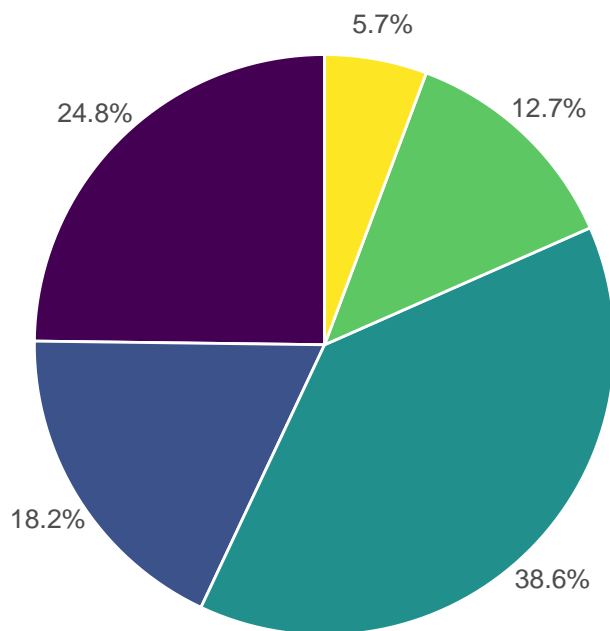
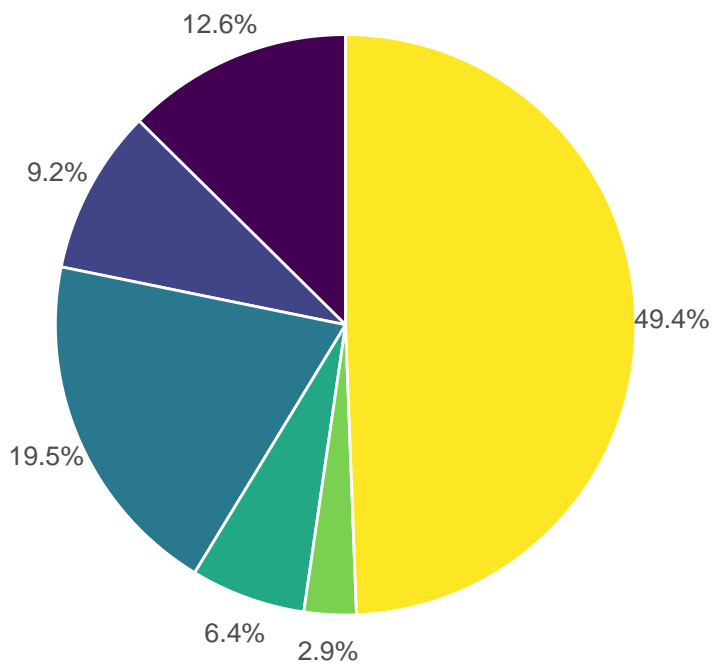


Annotation of peaks to all type of genes

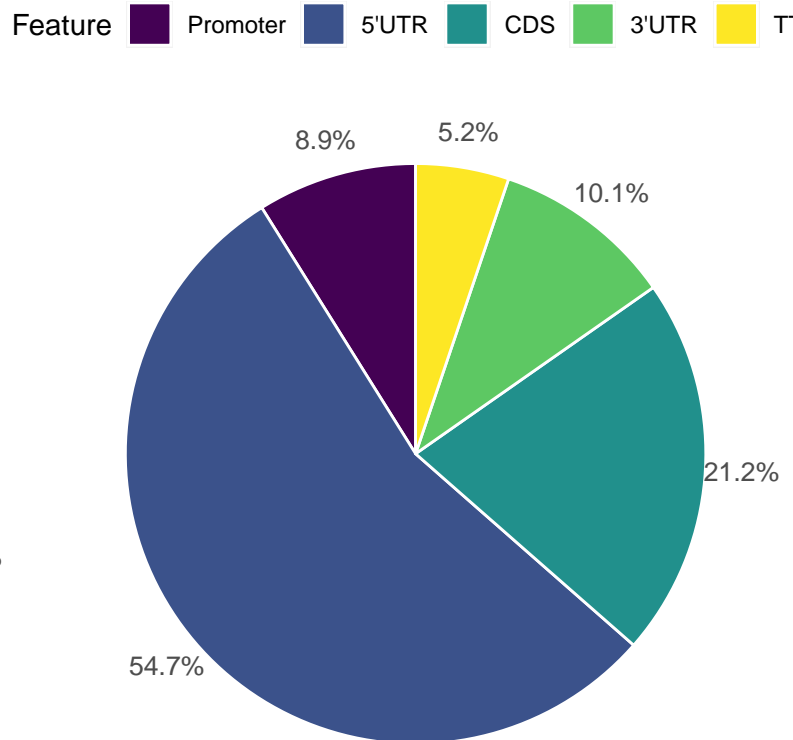
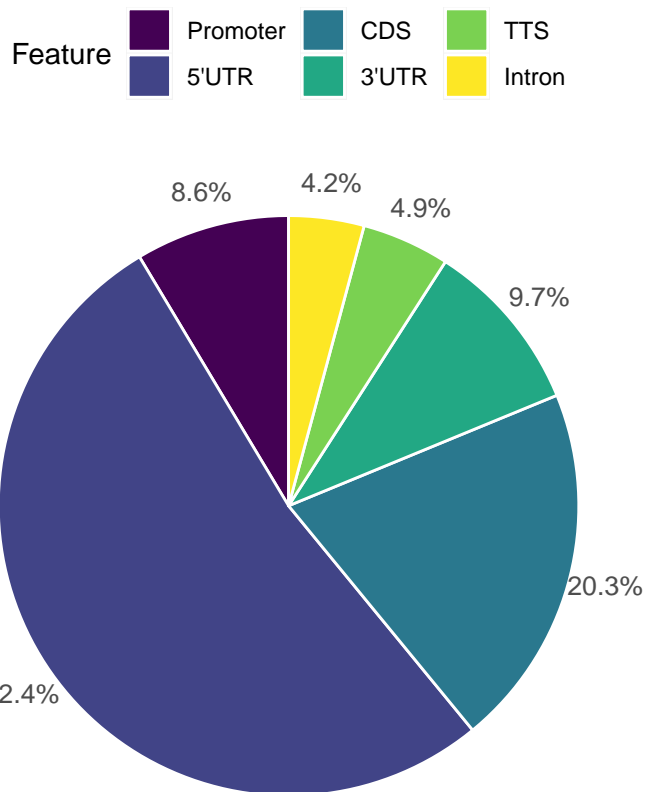
(Total number of peaks = 7945)



Absolute counts



Length-normalized counts



Plotting parameters:

```
functionName: "plot_peak_annotation"  
peakFile: c(SummitPeak =  
  "C:/GREENBLATT/Rscripts/GenomicPlot_gh/inst/extdata/test_chip_peak_chr19.bed")  
gtfFile: "C:/GREENBLATT/Rscripts/GenomicPlot_gh/inst/extdata/gencode.v19.annotation_chr19.gtf"  
importParams: list(offset = 0, fix_width = 100, fix_point = "center", norm = FALSE, useScore  
  = FALSE, outRle = FALSE, useSizeFactor = FALSE, genome = "hg19")  
  fiveP: -2000  
  dsTSS: 200  
  threeP: 1000  
  simple: FALSE  
outPrefix: "test_plot_peak_annotation1"  
verbose: FALSE  
  hw: c(8, 8)  
  nc: 2
```