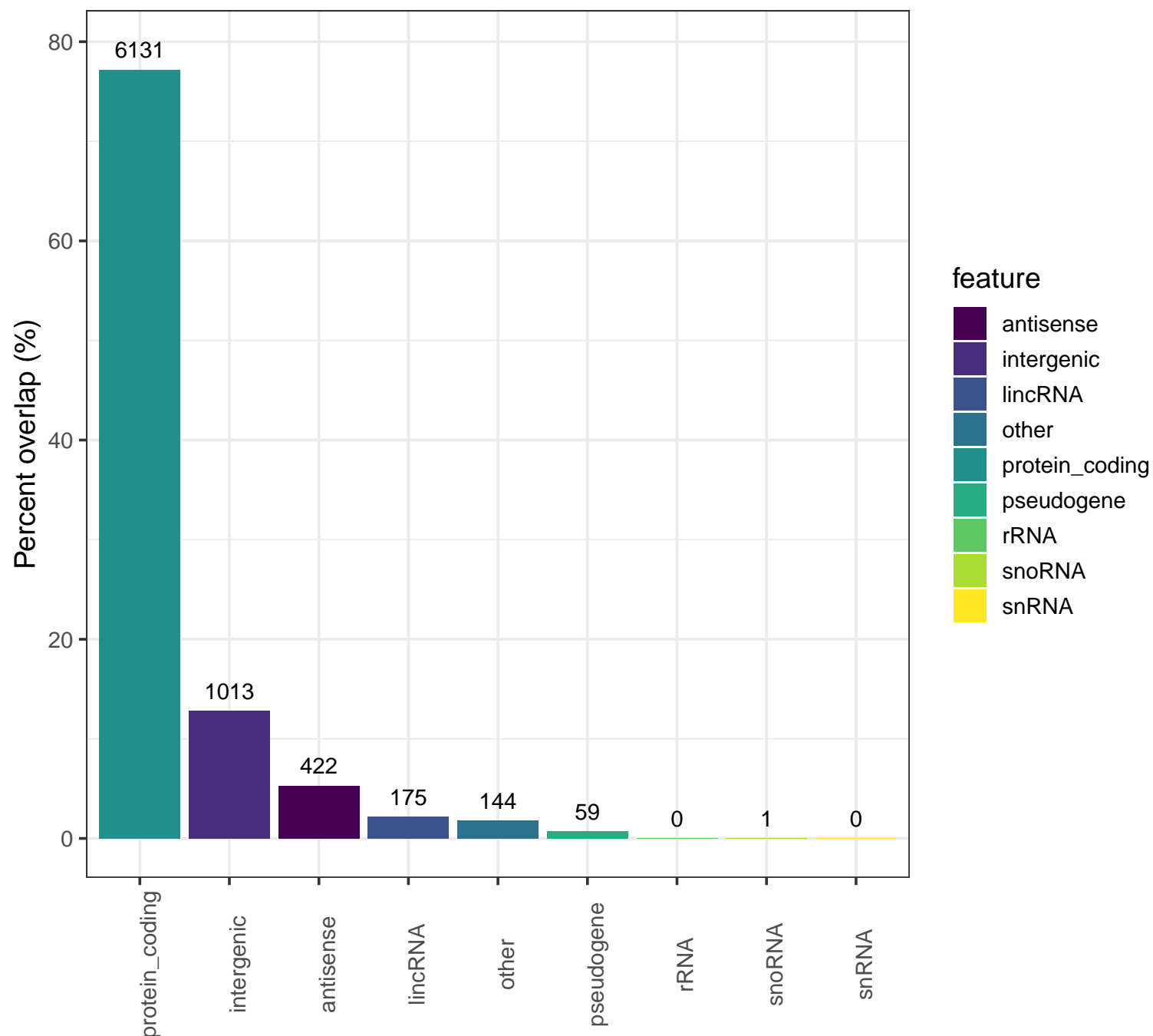
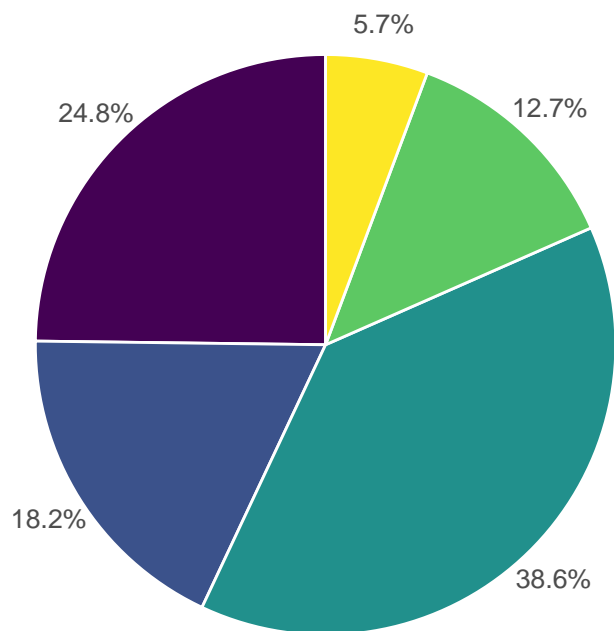
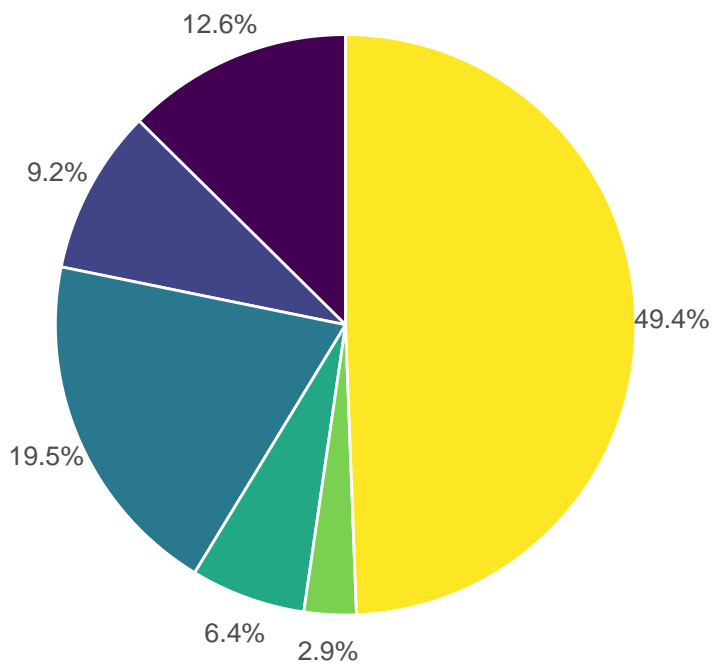


Annotation of peaks to all type of genes

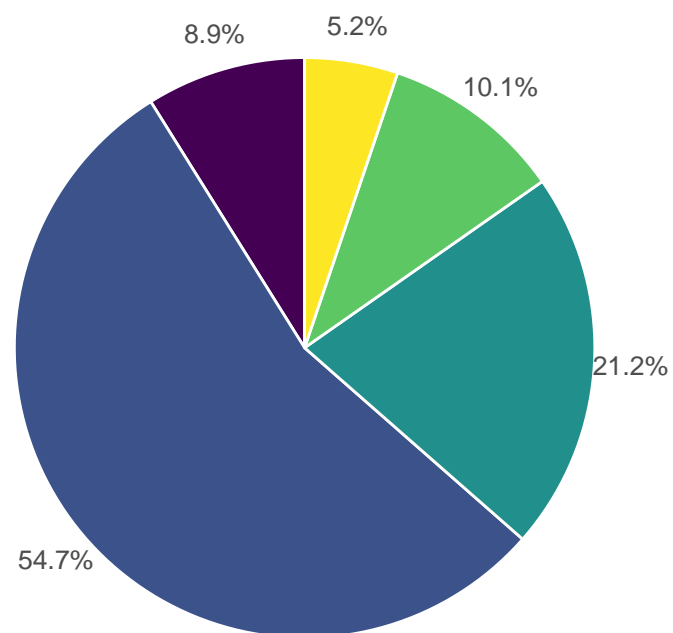
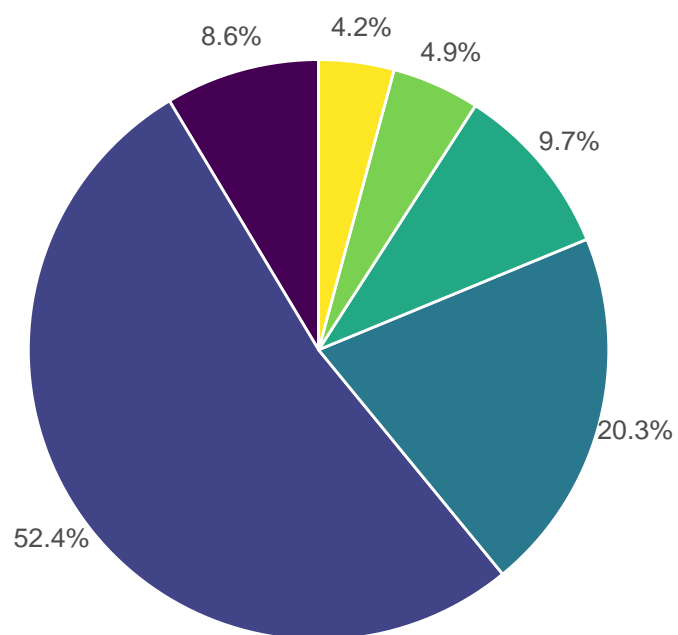
(Total number of peaks = 7945)



Absolute counts



Length-normalized counts



Plotting parameters:

```
functionName: "plot_peak_annotation"  
peakFile: c(SummitPeak =  
"C:/Users/greenblatt/AppData/Local/Programs/R/R-4.2.1/library/GenomicPlot/extdata/test_chip_peak_chr19.bed")  
e: "C:/Users/greenblatt/AppData/Local/Programs/R/R-4.2.1/library/GenomicPlot/extdata/gencode.v19.annotation_chr19.bed")  
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
```