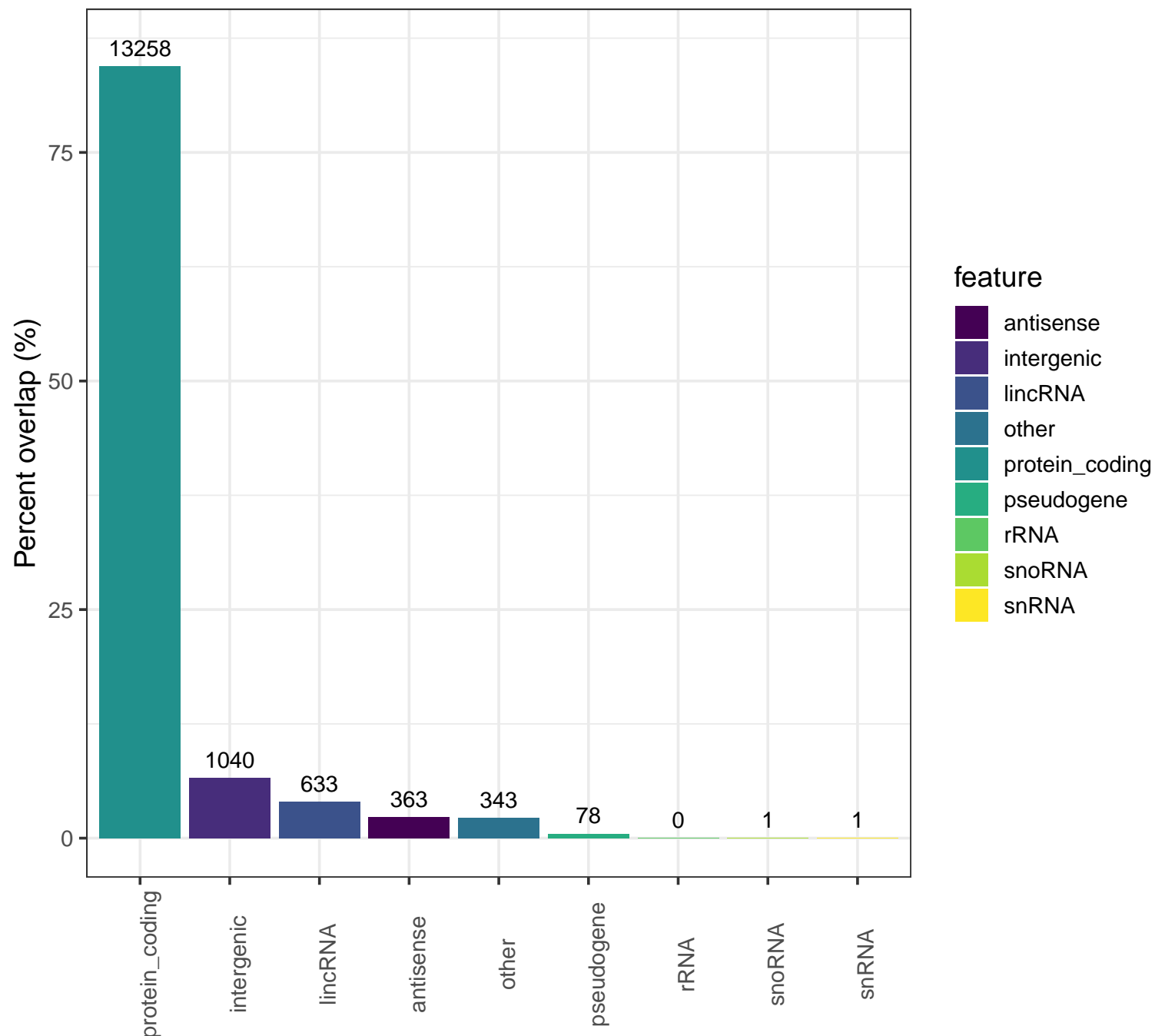
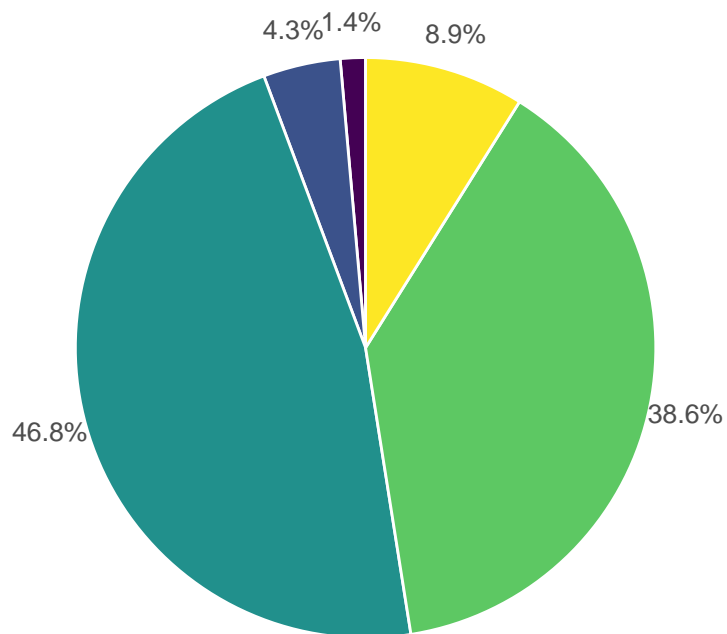
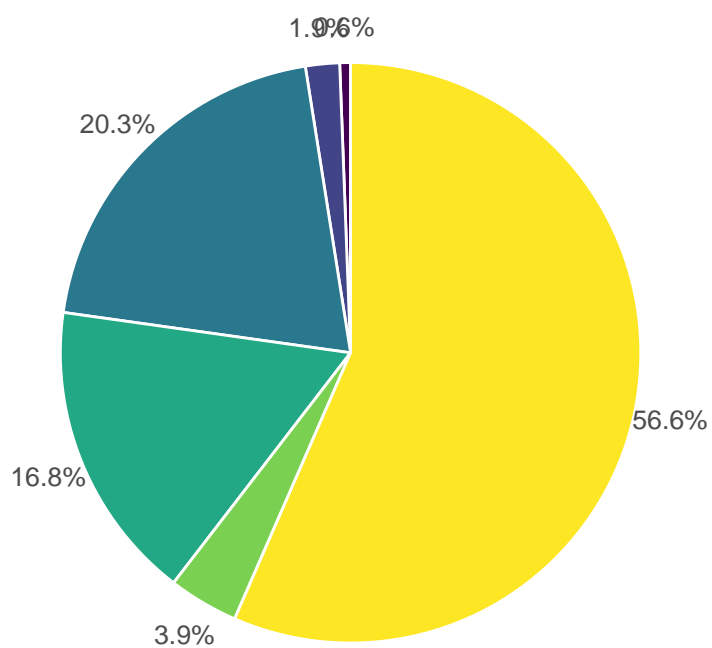


Annotation of peaks to all type of genes

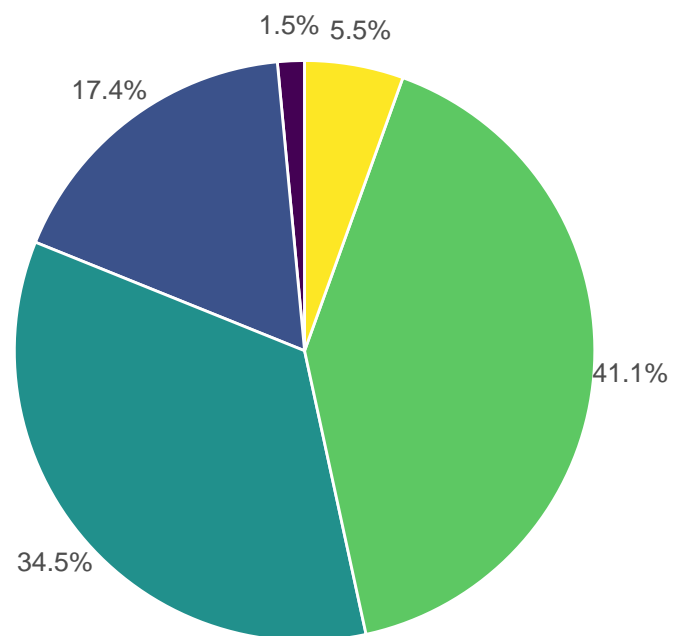
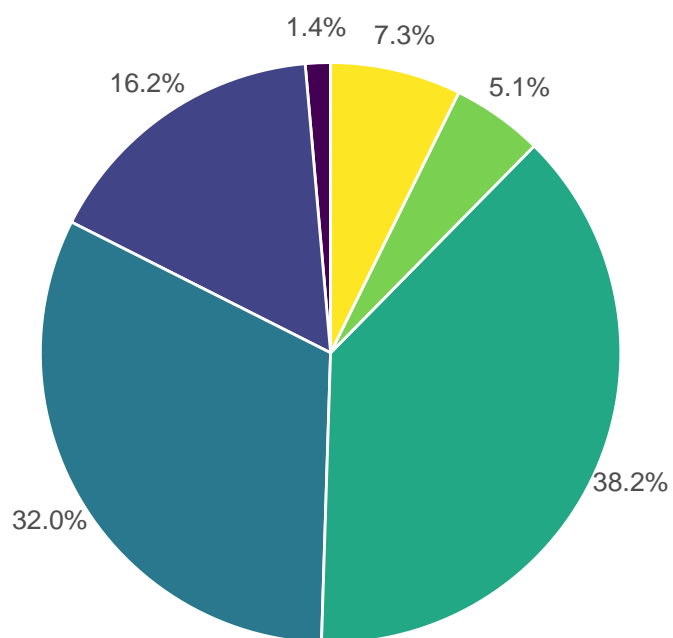
(Total number of peaks = 15717)



Absolute counts



Length-normalized counts



Plotting parameters:

```
functionName: "plot_peak_annotation"  
peakFile: c(iCLIPPeak =  
"C:/Users/greenblatt/AppData/Local/Programs/R/R-4.2.1/library/GenomicPlot/extdata/test_clip_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 = 21, fix_point = "center", norm = FALSE, useScore =  
FALSE, outRle = FALSE, useSizeFactor = FALSE, genome = "hg19")  
fiveP: -1000  
dsTSS: 0  
threeP: 2000  
simple: FALSE  
outPrefix: "test_plot_peak_annotation2"  
verbose: FALSE  
hw: c(8, 8)  
nc: 2
```