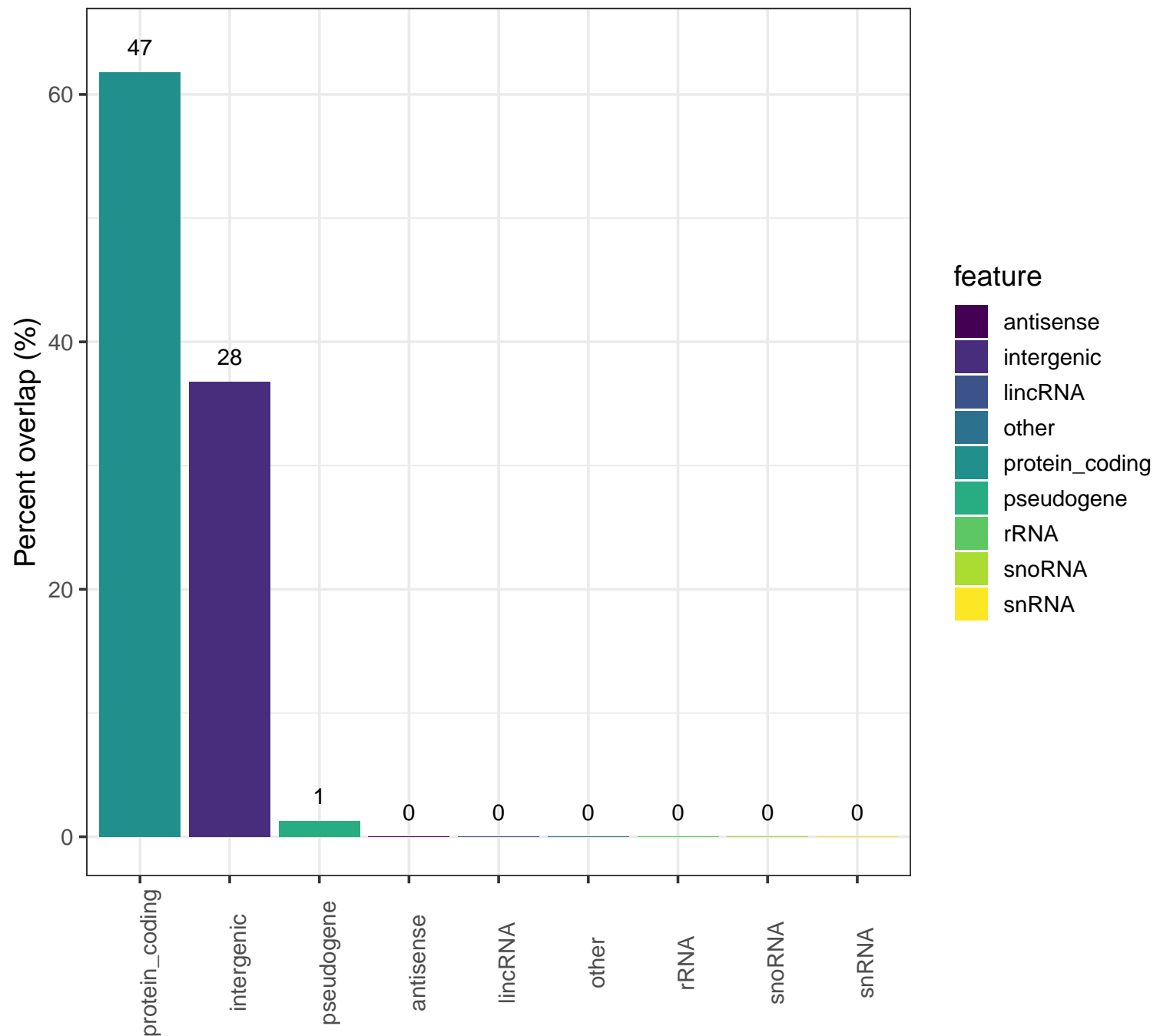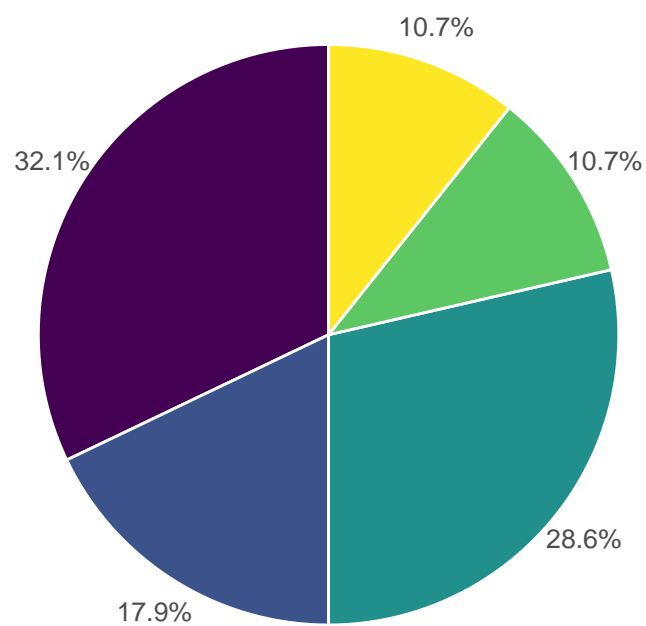**Annotation of peaks to all type of genes**
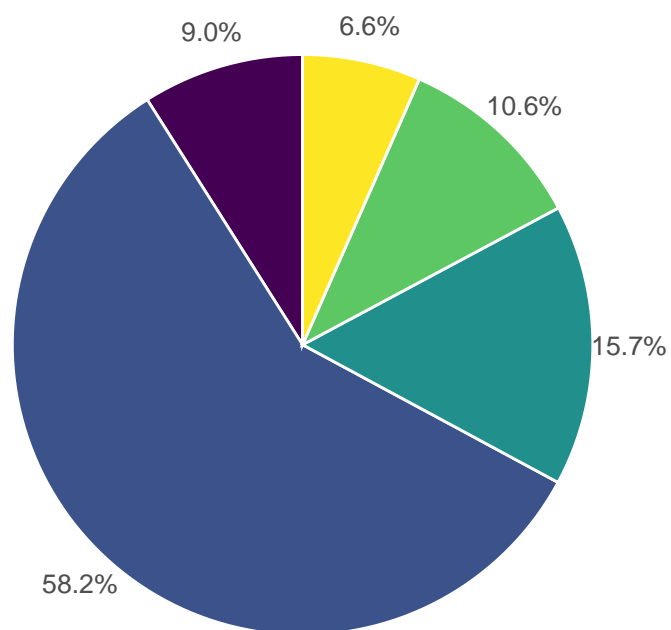(Total number of peaks = 76)

Absolute counts
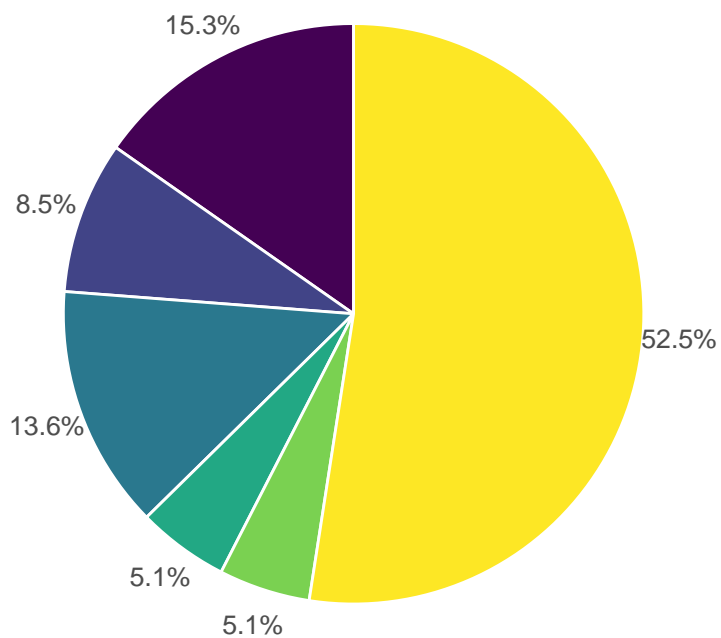
Length−normalized counts

Legend (left)		
Promoter	CDS	TTS
5'UTR	3'UTR	Intron

Left pie chart:
- 8.6%
- 4.1%
- 6.3%
- 10.1%
- 15.1%
- 55.8%

Legend (right)				
Promoter	5'UTR	CDS	3'UTR	TTS

Right pie chart:
- 9.0%
- 6.6%
- 10.6%
- 15.7%
- 58.2%
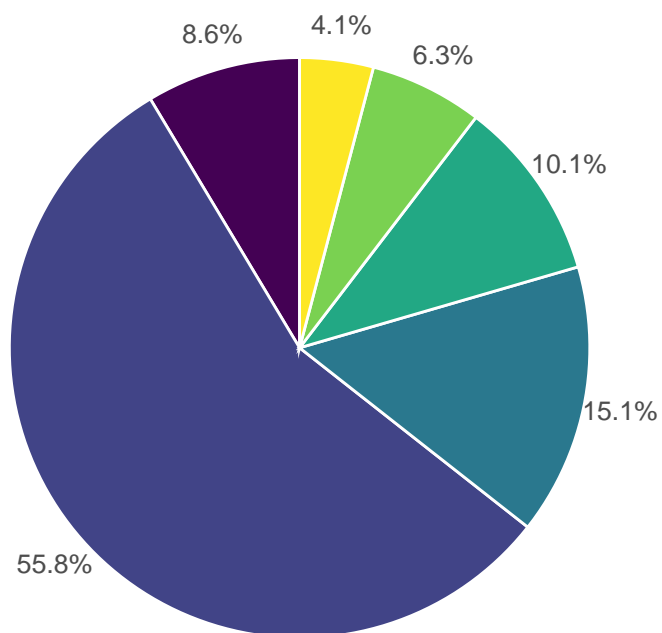
Plotting parameters:

functionName: "plot_peak_annotation"
peakFile: c(SummitPeak =
"C:/Users/greenblatt/AppData/Local/R/win−library/4.3/GenomicPlot/extdata/test_chip_peak_chr19.bed")
gtfFile: "C:/Users/greenblatt/AppData/Local/R/win−library/4.3/GenomicPlot/extdata/gencode.v19.annotation_chr19.gtf"
importParams: list(offset = 0, fix_width = 100, fix_point = "center", norm = FALSE, useScore
= FALSE, outRle = TRUE, 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