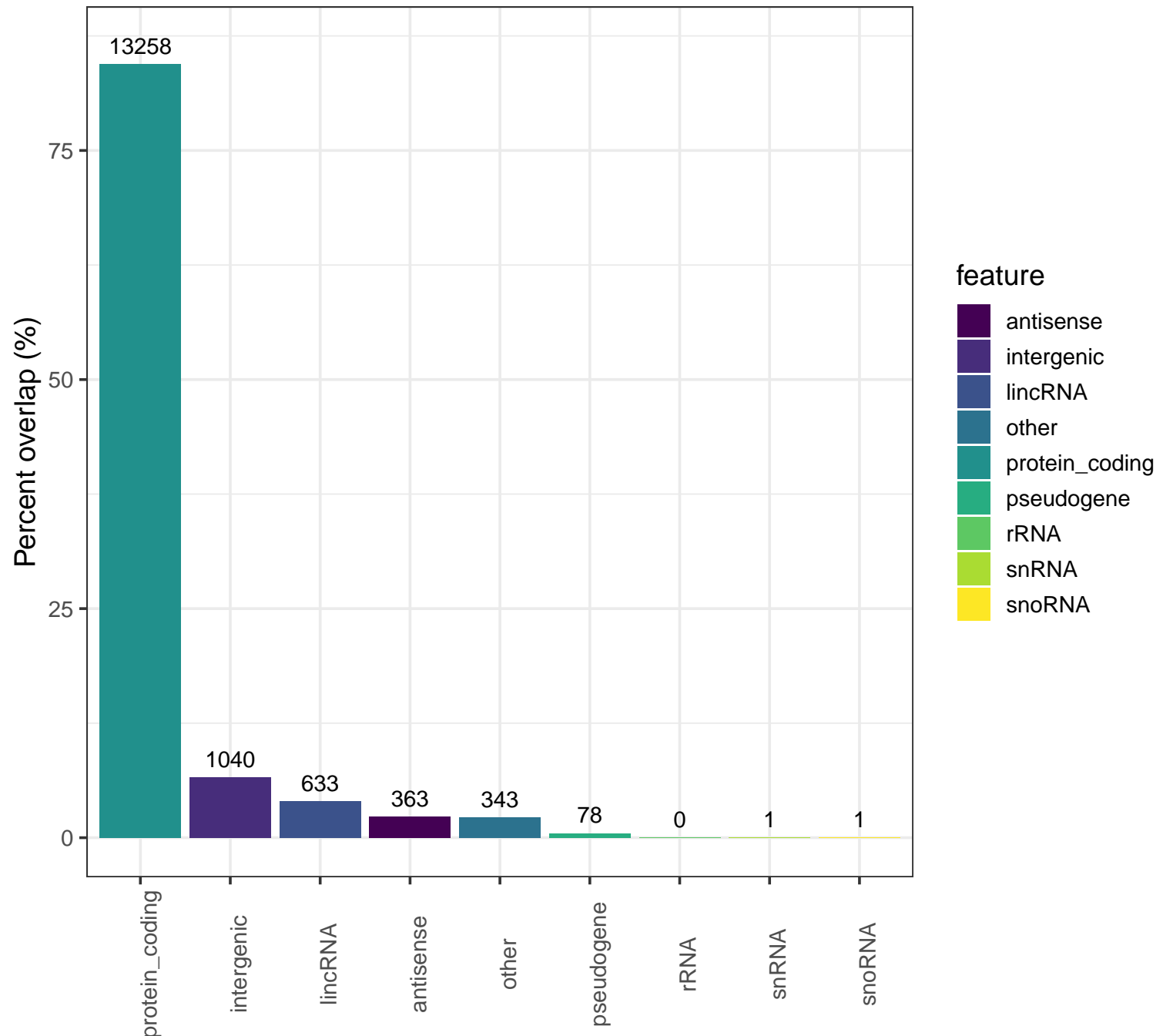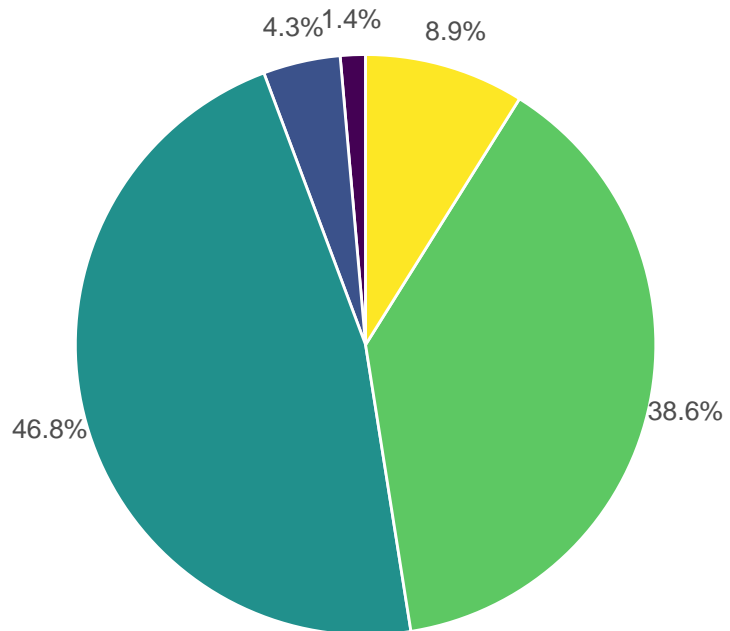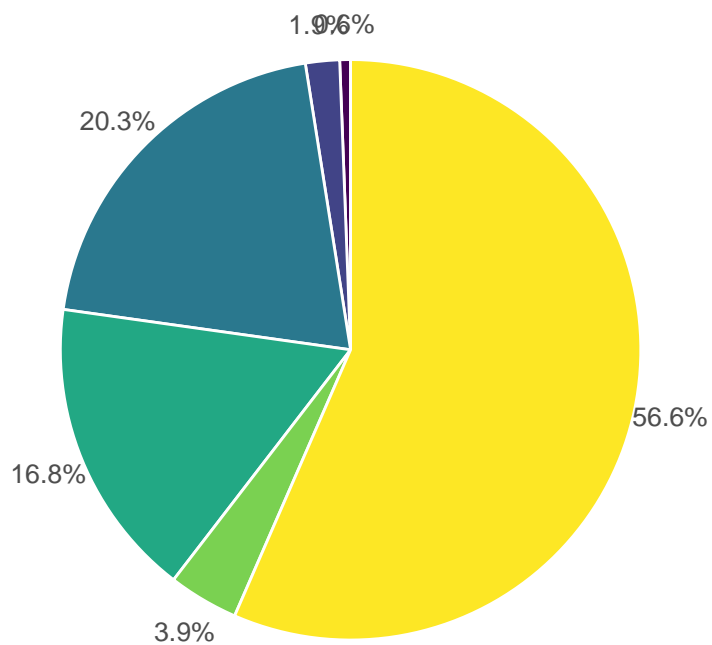Annotation of peaks to all type of genes
(Total number of peaks = 15717)

Absolute counts
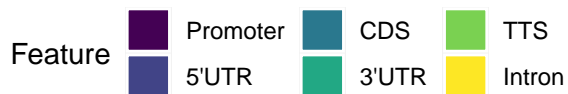
Length−normalized counts

Feature			
Promoter	CDS	TTS
5'UTR	3'UTR	Intron

Feature				
Promoter	5'UTR	CDS	3'UTR	T...

Left pie chart: 1.4%, 7.3%, 16.2%, 5.1%, 32.0%, 38.2%

Right pie chart: 1.5%, 5.5%, 17.4%, 41.1%, 34.5%
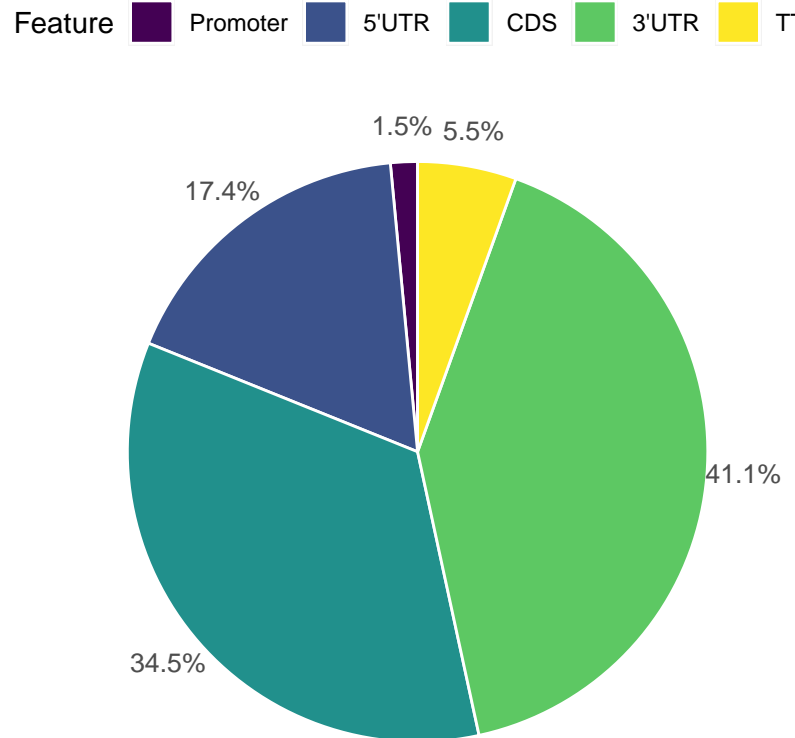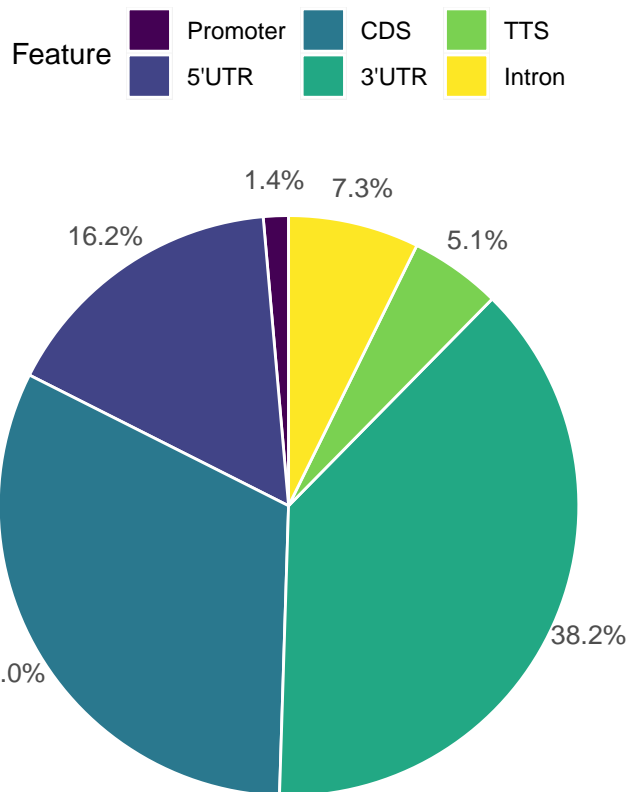
Plotting parameters:

functionName: "plot_peak_annotation"
peakFile: c(iCLIPPeak =
"C:/GREENBLATT/Rscripts/GenomicPlot_gh/inst/extdata/test_clip_peak_chr19.bed")
gtfFile: "C:/GREENBLATT/Rscripts/GenomicPlot_gh/inst/extdata/gencode.v19.annotation_chr19.gtf"
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