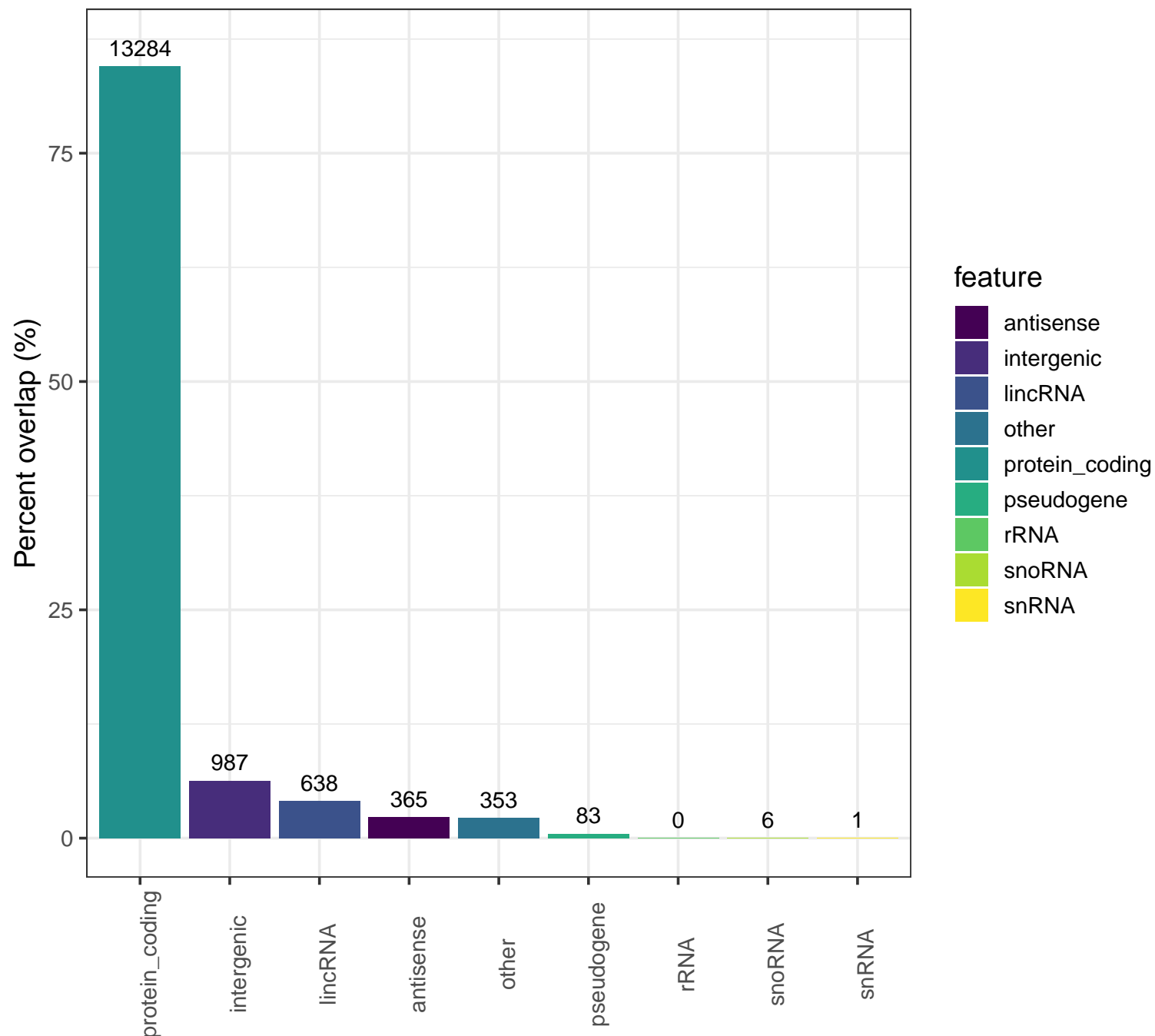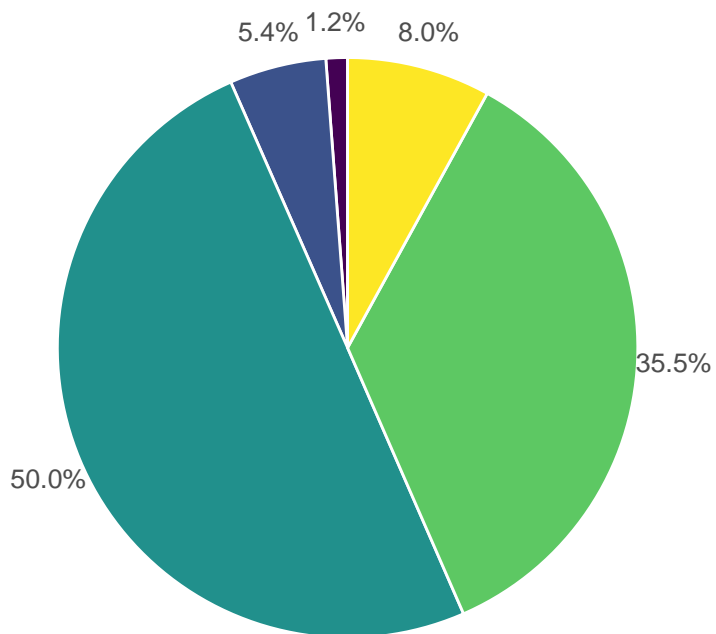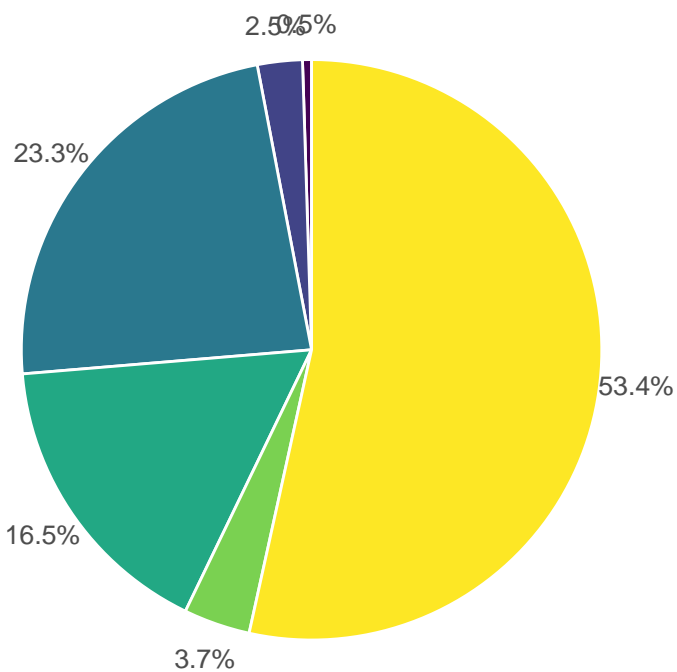Annotation of peaks to all type of genes
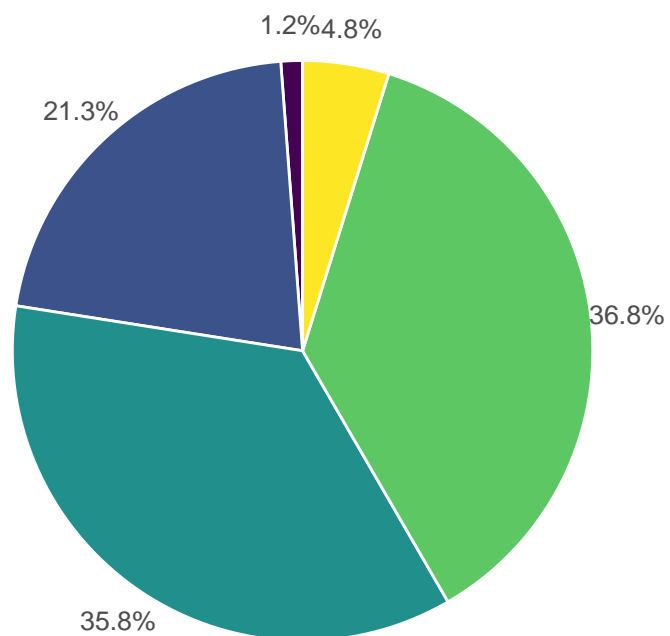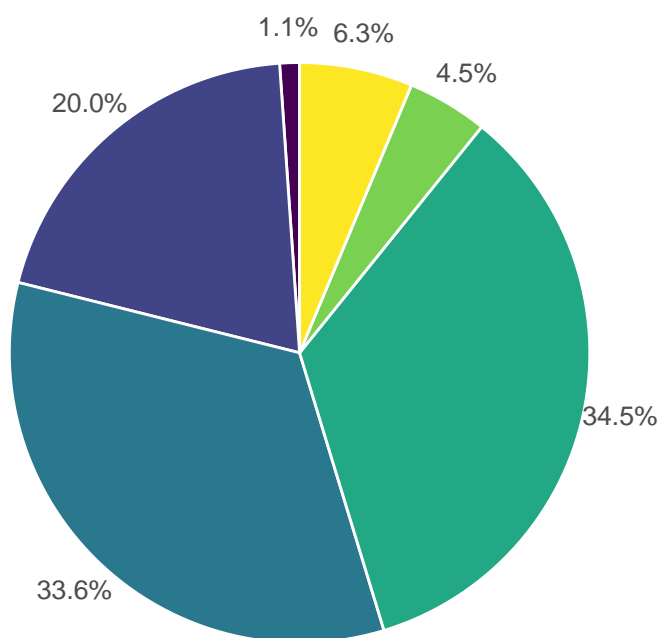(Total number of peaks = 15717)

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
importParams: list(offset = 0, fix_width = 100, fix_point = "center", norm = FALSE, useScore
= FALSE, outRle = TRUE, 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