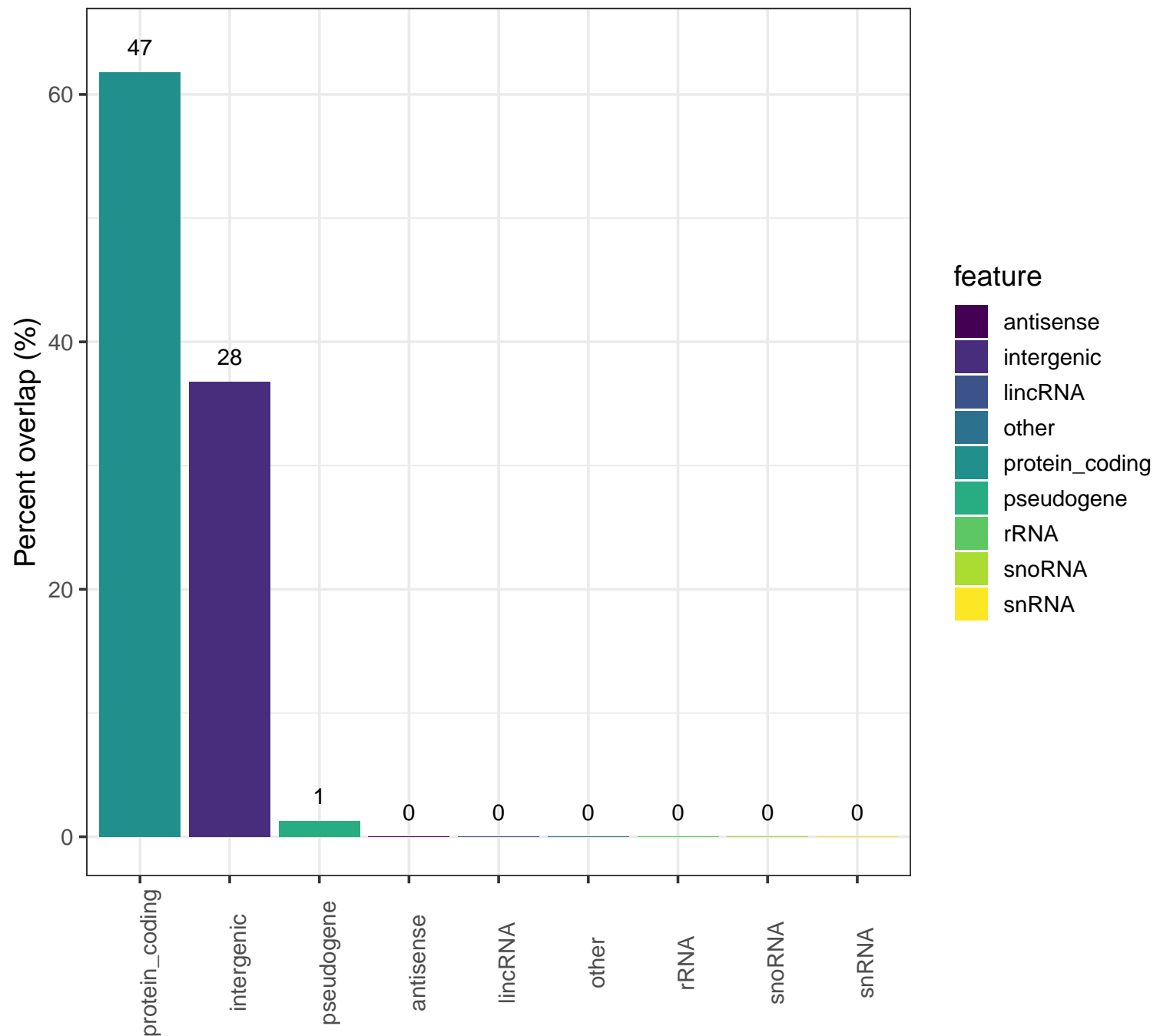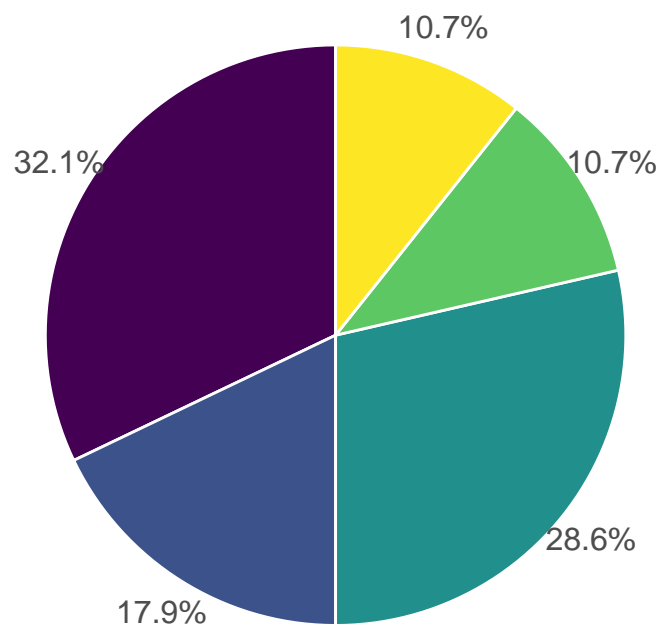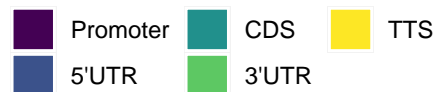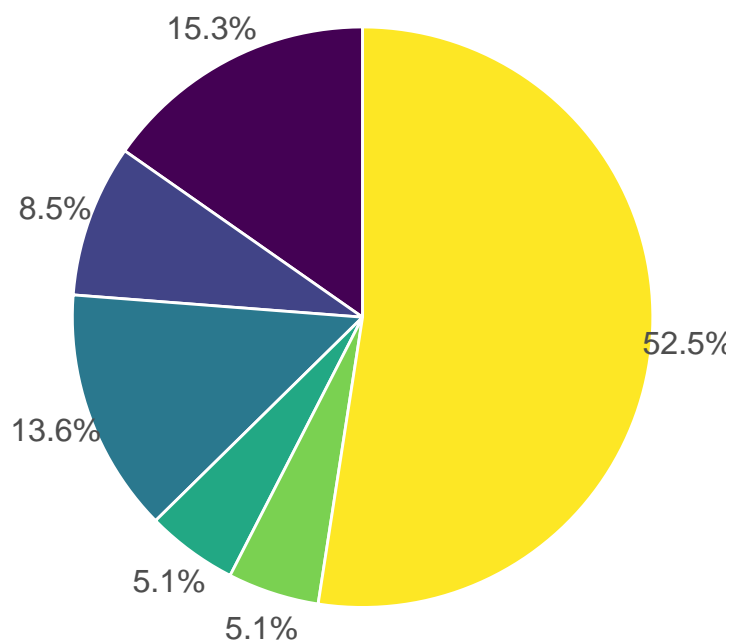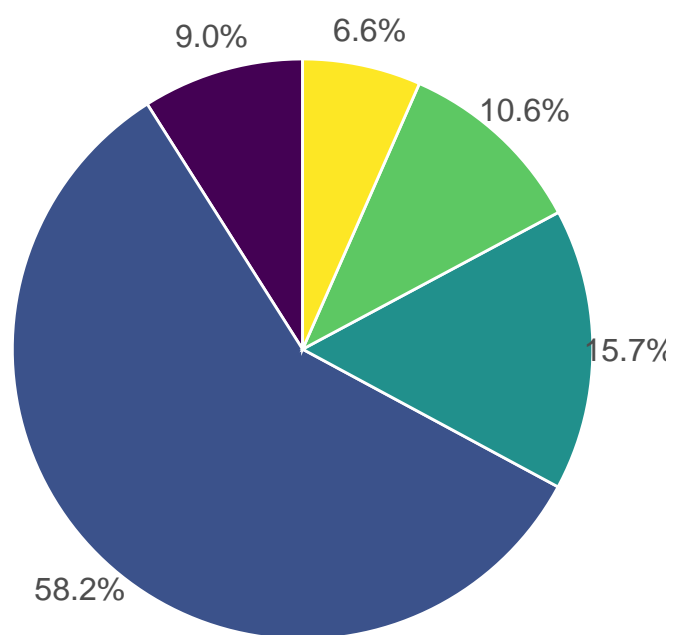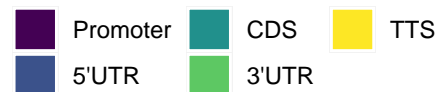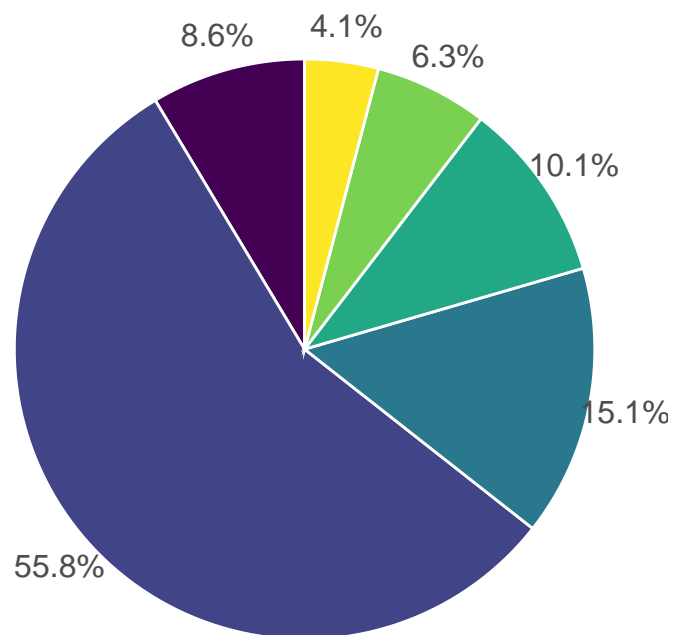Annotation of peaks to all type of genes
(Total number of peaks = 76)

Absolute counts

Length−normalized counts

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, saveRds = FALSE, genome =
"hg19")
fiveP: −2000
dsTSS: 200
threeP: 1000
simple: FALSE
outPrefix: "test_plot_peak_annotation1"
verbose: FALSE
hw: c(8, 8)
nc: 2