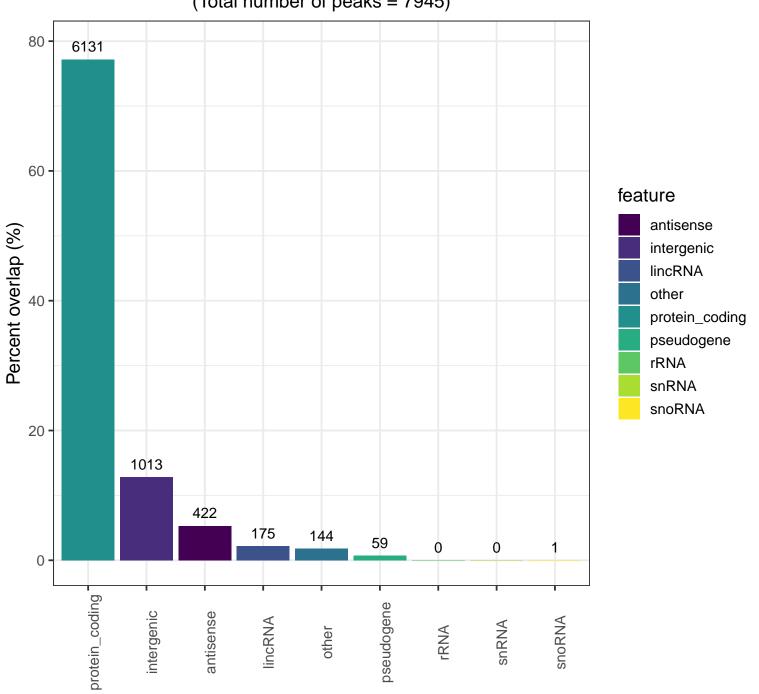
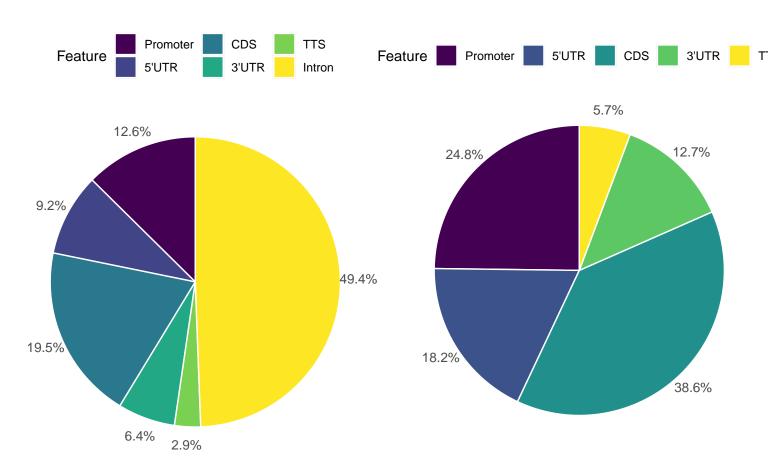
## Annotation of peaks to all type of genes

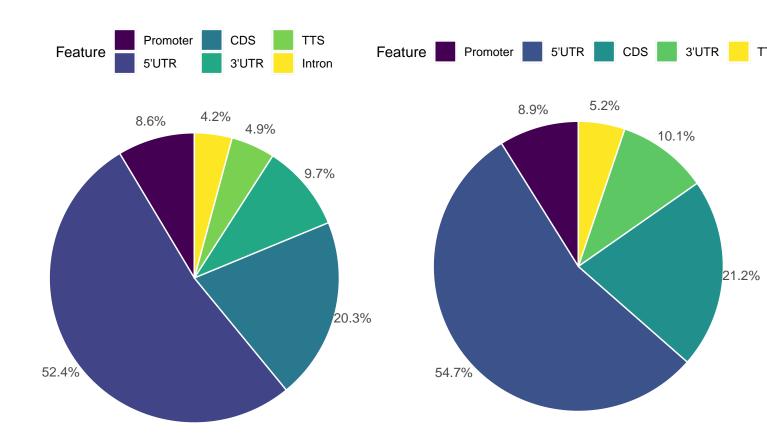
(Total number of peaks = 7945)



## **Absolute counts**



## Length-normalized counts



## Plotting parameters:

functionName: "plot\_peak\_annotation"

peakFile: c(SummitPeak =

"C:/GREENBLATT/Rscripts/GenomicPlot\_gh/inst/extdata/test\_chip\_peak\_chr19.bed")

gtfFile: "C:/GREENBLATT/Rscripts/GenomicPlot\_gh/inst/extdata/gencode.v19.annotation\_chr19.gtf"

importParams: list(offset = 0, fix\_width = 100, fix\_point = "center", norm = FALSE, useScore

= FALSE, outRle = FALSE, useSizeFactor = FALSE, genome = "hg19")

fiveP: -2000

dsTSS: 200

threeP: 1000

outPrefix: "test\_plot\_peak\_annotation1" verbose: FALSE

simple: FALSE

hw: c(8, 8)

nc: 2