Plotting parameters:

functionName: "plot_3parts_metagene"
queryFiles: c(chip_bam =
"C:/Users/greenblatt/AppData/Local/Programs/R/R−4.2.1/library/GenomicPlot/extdata/chip_treat_chr19.bam")
gFeatures: as.list(environment())[["gFeatures"]]
inputFiles: c(chip_input =
"C:/Users/greenblatt/AppData/Local/Programs/R/R−4.2.1/library/GenomicPlot/extdata/chip_input_chr19.bam")
scale: FALSE
verbose: FALSE
Ylab: "Coverage/base/gene"
importParams: list(offset = 0, fix_width = 150, fix_point = "start", norm = TRUE, useScore =
FALSE, outRle = TRUE, useSizeFactor = TRUE, genome = "hg19")
smooth: TRUE
stranded: TRUE
outPrefix: "test_plot_3parts_metagene"
heatmap: TRUE
rmOutlier: 0
heatRange: NULL
transform: NA
hw: c(8, 8)
nc: 2