









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 = FALSE, 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