Plotting parameters:

functionName: "plot_locus_with_random"
queryFiles: c(clip_bam =
"C:/Users/greenblatt/AppData/Local/Programs/R/R−4.2.1/library/GenomicPlot/extdata/treat_chr19.bam")
centerFiles: c(iCLIPPeak =
Users/greenblatt/AppData/Local/Programs/R/R−4.2.1/library/GenomicPlot/extdata/test_clip_peak_chr19.b
txdb: new("TxDb", .xData = <environment>)
ext: c(−500, 500)
hl: c(−100, 100)
shade: TRUE
importParams: list(offset = −1, fix_width = 0, fix_point = "start", norm = TRUE, useScore =
FALSE, outRle = TRUE, useSizeFactor = FALSE, genome = "hg19")
verbose: FALSE
smooth: TRUE
transform: NA
binSize: 10
refPoint: "center"
Xlab: "Center"
Ylab: "Coverage/base/gene"
inputFiles: c(clip_input =
"C:/Users/greenblatt/AppData/Local/Programs/R/R−4.2.1/library/GenomicPlot/extdata/input_chr19.bam")
stranded: TRUE
scale: FALSE
outPrefix: "test_plot_locus_with_random"
rmOutlier: 0
n_random: 1
hw: c(8, 8)
statsMethod: "wilcox.test"
nc: 2