Plotting parameters:

functionName: "plot_bam_correlation"
bamfiles: c(chip_input =
"C:/Users/greenblatt/AppData/Local/R/win−library/4.3/GenomicPlot/extdata/chip_input_chr19.bam",
chip_treat =
"C:/Users/greenblatt/AppData/Local/R/win−library/4.3/GenomicPlot/extdata/chip_treat_chr19.bam")
binSize: 1e+05
outPrefix: "test_plot_bam_correlation"
importParams: list(offset = 0, fix_width = 150, fix_point = "start", norm = FALSE, useScore =
FALSE, outRle = FALSE, useSizeFactor = FALSE, genome = "hg19")
verbose: FALSE
hw: c(8, 8)
nc: 2