









Plotting parameters:

```
functionName: "plot_start_end"
                                      queryFiles: c(clip_bam =
"C:/Users/greenblatt/AppData/Local/Programs/R/R-4.2.1/library/GenomicPlot/extdata/treat_chr19.bam")
                                      inputFiles: c(clip_input =
"C:/Users/greenblatt/AppData/Local/Programs/R/R-4.2.1/library/GenomicPlot/extdata/input_chr19.bam")
                                         centerFiles: "intron"
                             txdb: new("TxDb", .xData = <environment>)
      importParams: list(offset = -1, fix_width = 0, fix_point = "start", norm = TRUE, useScore =
                 FALSE, outRle = TRUE, useSizeFactor = FALSE, genome = "hg19")
                                             binSize: 10
                                             insert: 100
                                          verbose: FALSE
                                    ext: c(-500, 200, -200, 500)
                                     hl: c(-100, 100, -100, 100)
                                          stranded: TRUE
                                           scale: FALSE
                                           smooth: TRUE
                                            rmOutlier: 0
                                   outPrefix: "test plot start end"
                                           transform: NA
                                            shade: TRUE
                                    Ylab: "Coverage/base/gene"
                                             hw: c(8, 8)
                                                nc: 2
```