

Plotting parameters:

```
txdb: new("TxDb", .xData = <environment>)
treat: c(query = "C:/GREENBLATT/Rscripts/GenomicPlot/inst/extdata/treat_chr19.bam")
control: c(input = "C:/GREENBLATT/Rscripts/GenomicPlot/inst/extdata/input_chr19.bam")
feature: alist[["feature"]]
param: list(offset = -1, fix_width = 0, fix_point = "start", norm = TRUE, useScore =
FALSE, outRle = TRUE, useSizeFactor = FALSE, genome = "hg19")
```