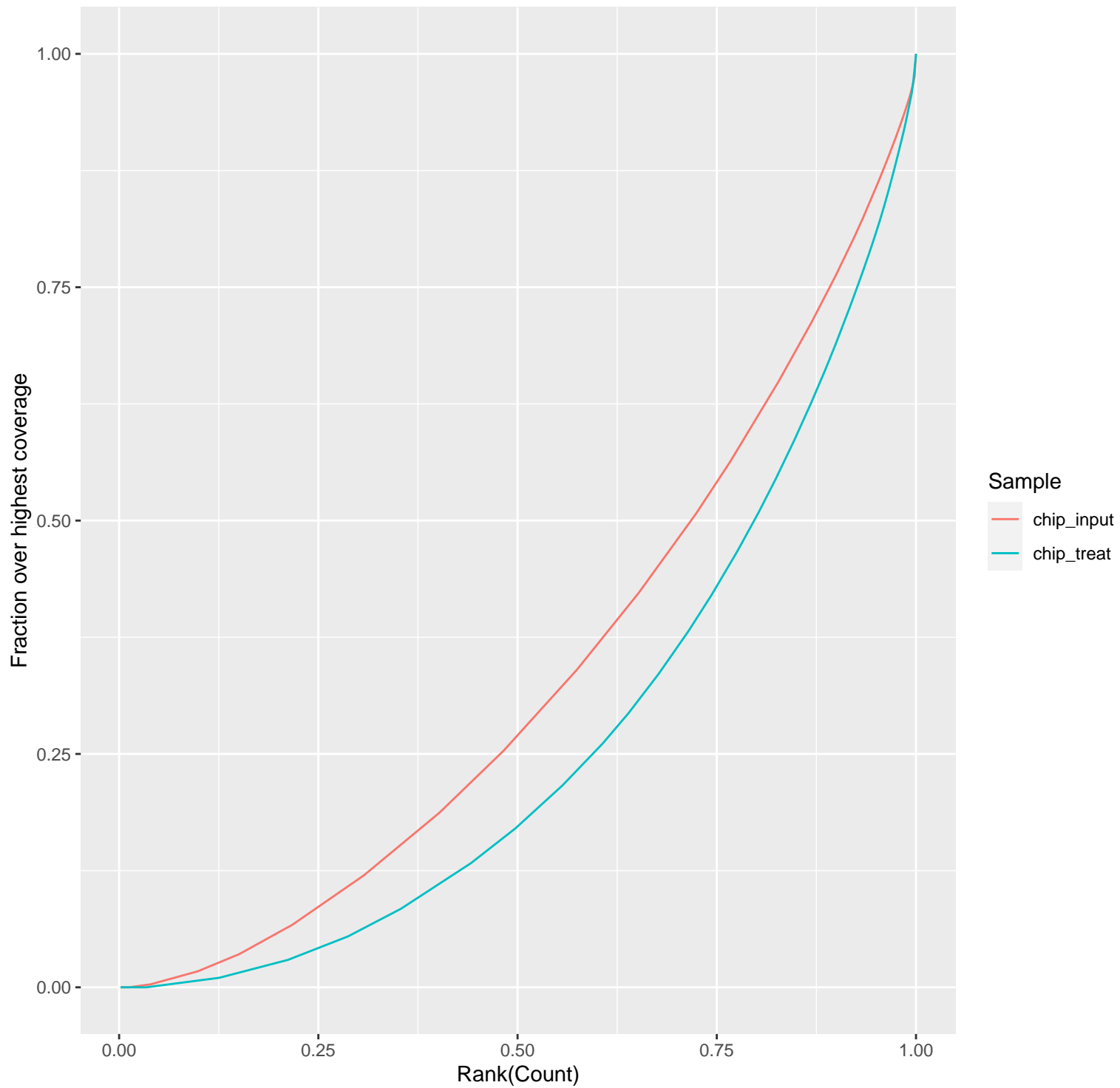


Binned read counts distribution: bin size = 1e+05



chip_treat

0.45

1

chip_input

1

0.45

chip_input

chip_treat

$\log_2(\text{CPM}/\text{bin})$, bin size = $1\text{e}+05$

0 2 4 6 8 10 12

chip_input

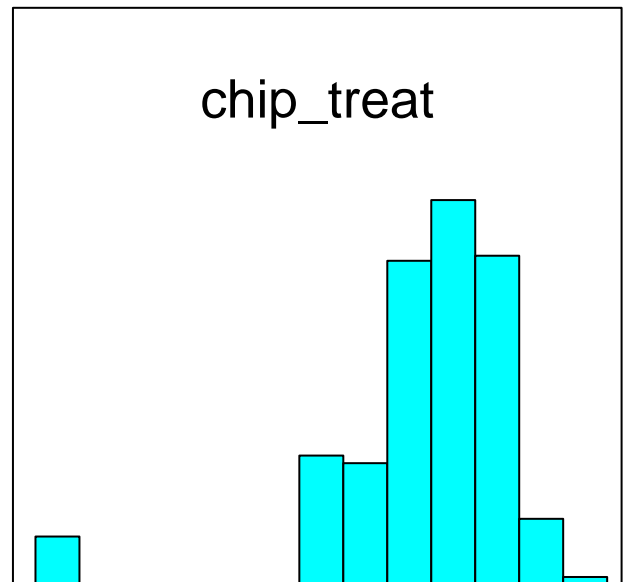
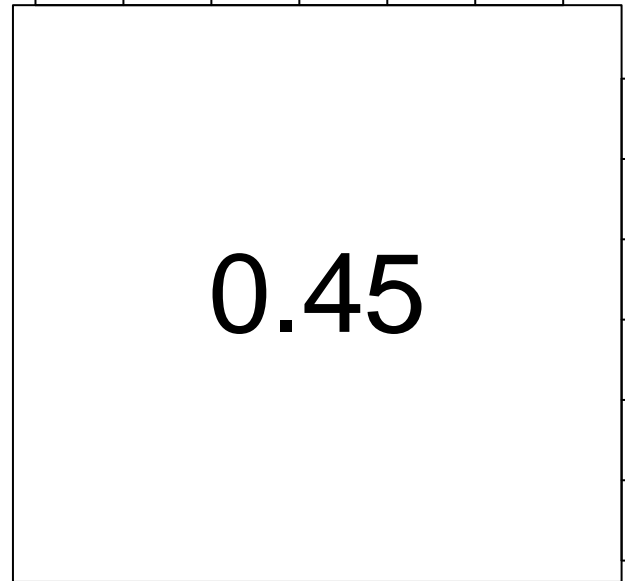
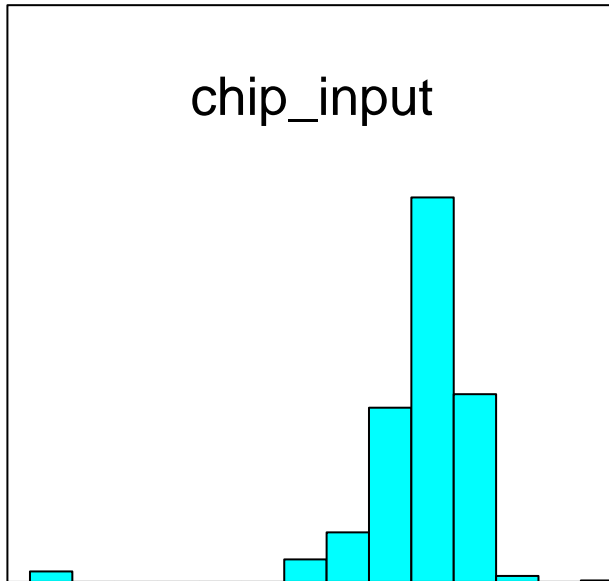
0.45

12
10
8
6
4
2
0

12
10
8
6
4
2
0

chip_treat

0 2 4 6 8 10 12



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
```