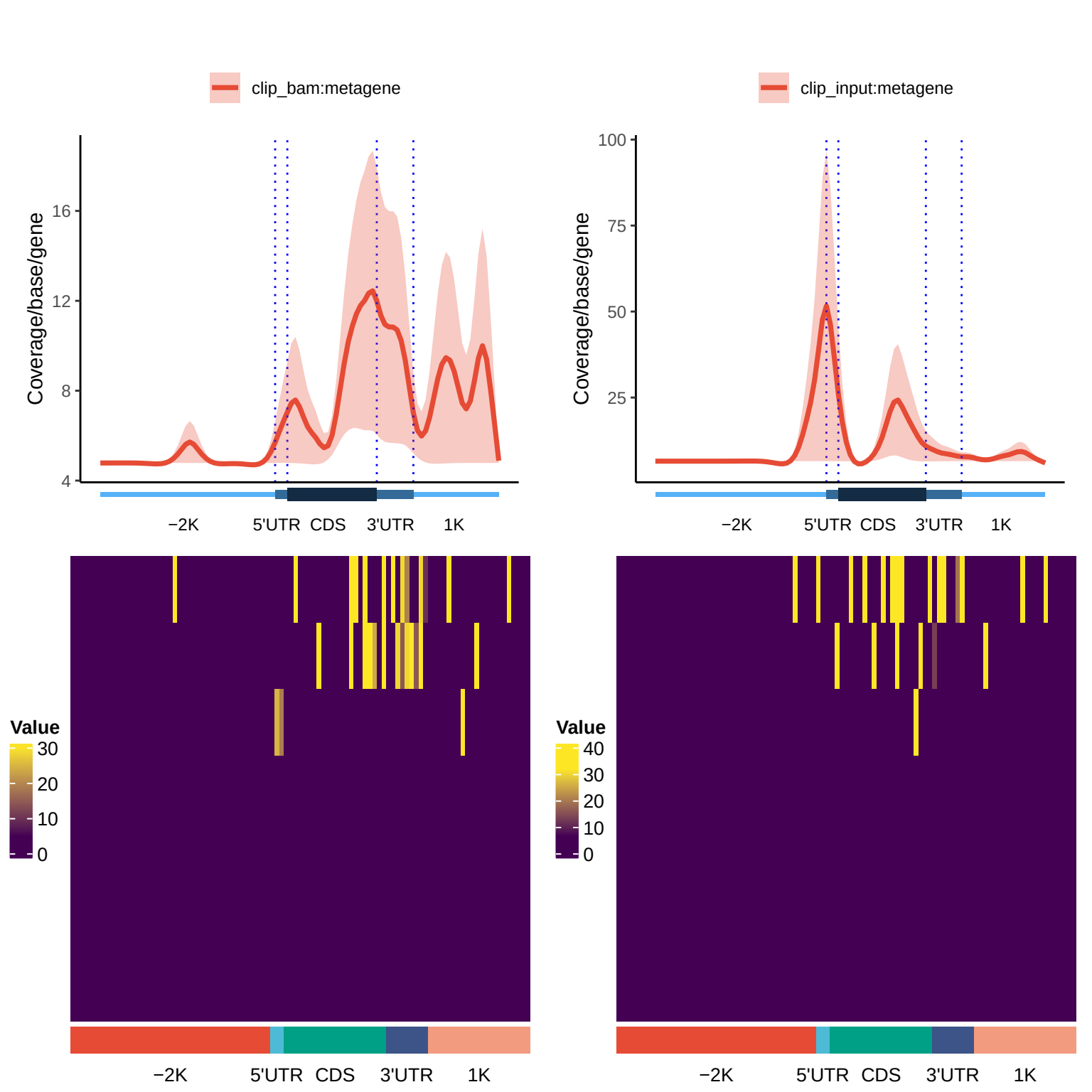
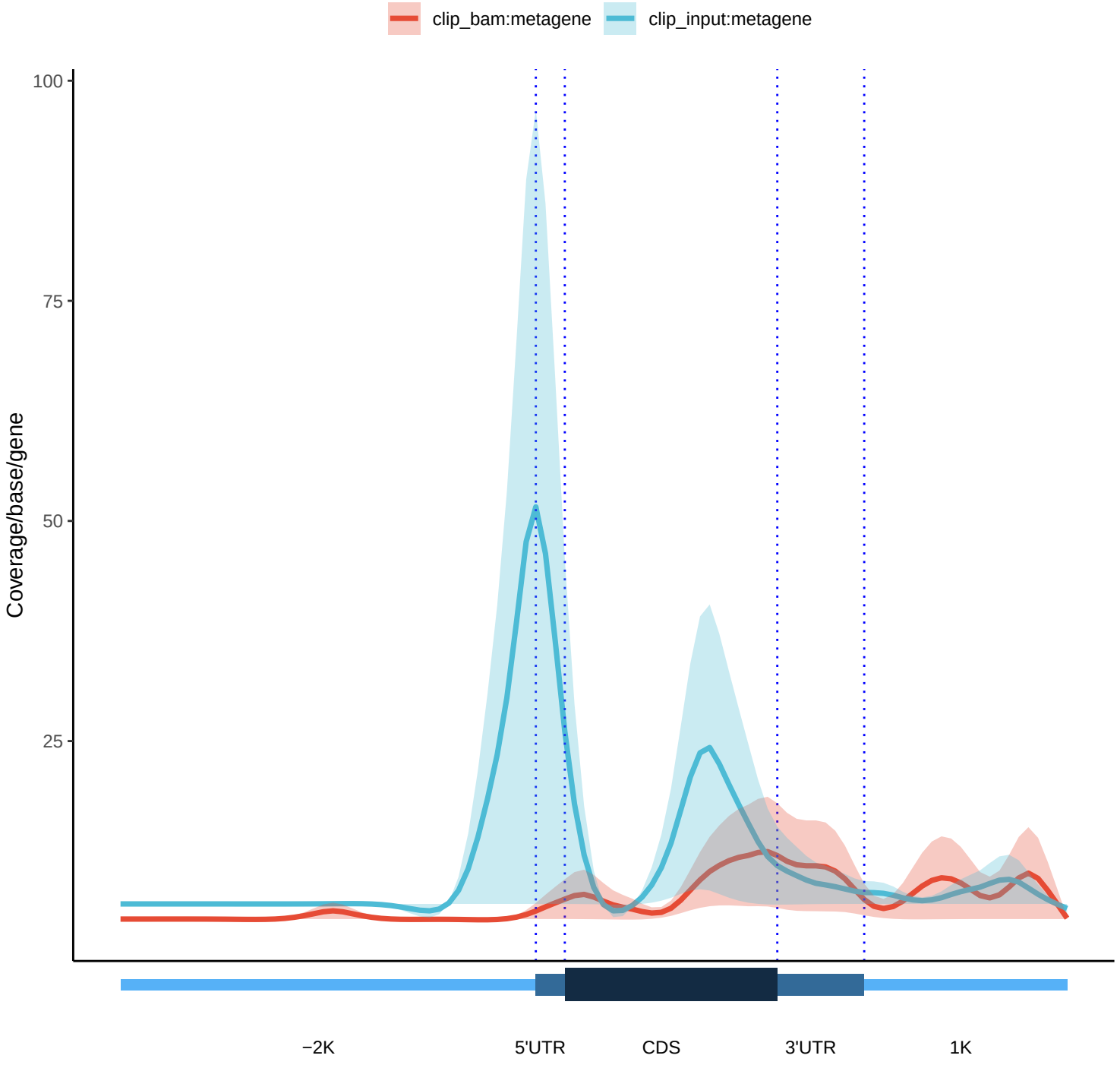
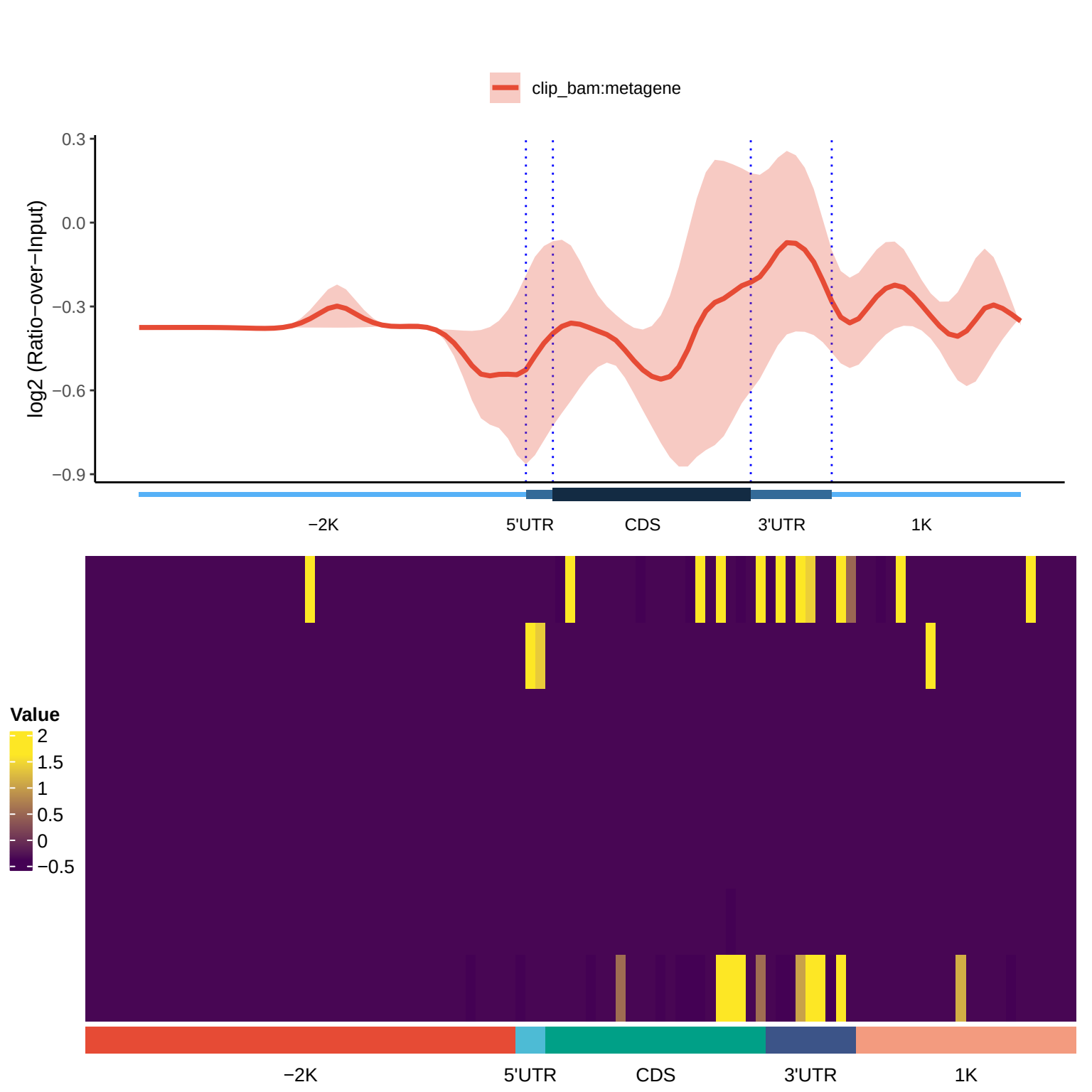

clip_bam:metagene
clip_input:metagene
Coverage/base/gene
16
12
8
4
100
75
50
25
−2K
5'UTR
CDS
3'UTR
1K
Value
30
20
10
0
40


clip_bam:metagene
clip_input:metagene
100
75
50
25
Coverage/base/gene
−2K
5'UTR
CDS
3'UTR
1K


clip_bam:metagene
log2 (Ratio−over−Input)
0.3
0.0
−0.3
−0.6
−0.9
−2K
5'UTR
CDS
3'UTR
1K
Value
2
1.5
1
0.5
0
−0.5
−2K
5'UTR
CDS
3'UTR
1K

Plotting parameters:

functionName: "plot_5parts_metagene"
queryFiles: c(clip_bam =
"C:/Users/greenblatt/AppData/Local/R/win−library/4.3/GenomicPlot/extdata/treat_chr19.bam")
gFeatures_list: as.list(environment())[["gFeatures_list"]]
inputFiles: c(clip_input =
"C:/Users/greenblatt/AppData/Local/R/win−library/4.3/GenomicPlot/extdata/input_chr19.bam")
importParams: list(offset = −1, fix_width = 0, fix_point = "start", norm = TRUE, useScore =
FALSE, outRle = TRUE, useSizeFactor = FALSE, genome = "hg19")
verbose: FALSE
transform: "log2"
smooth: TRUE
scale: FALSE
stranded: TRUE
outPrefix: "test_plot_5parts_metagene2"
heatmap: TRUE
heatRange: NULL
rmOutlier: 0
Ylab: "Coverage/base/gene"
hw: c(8, 8)
nc: 2