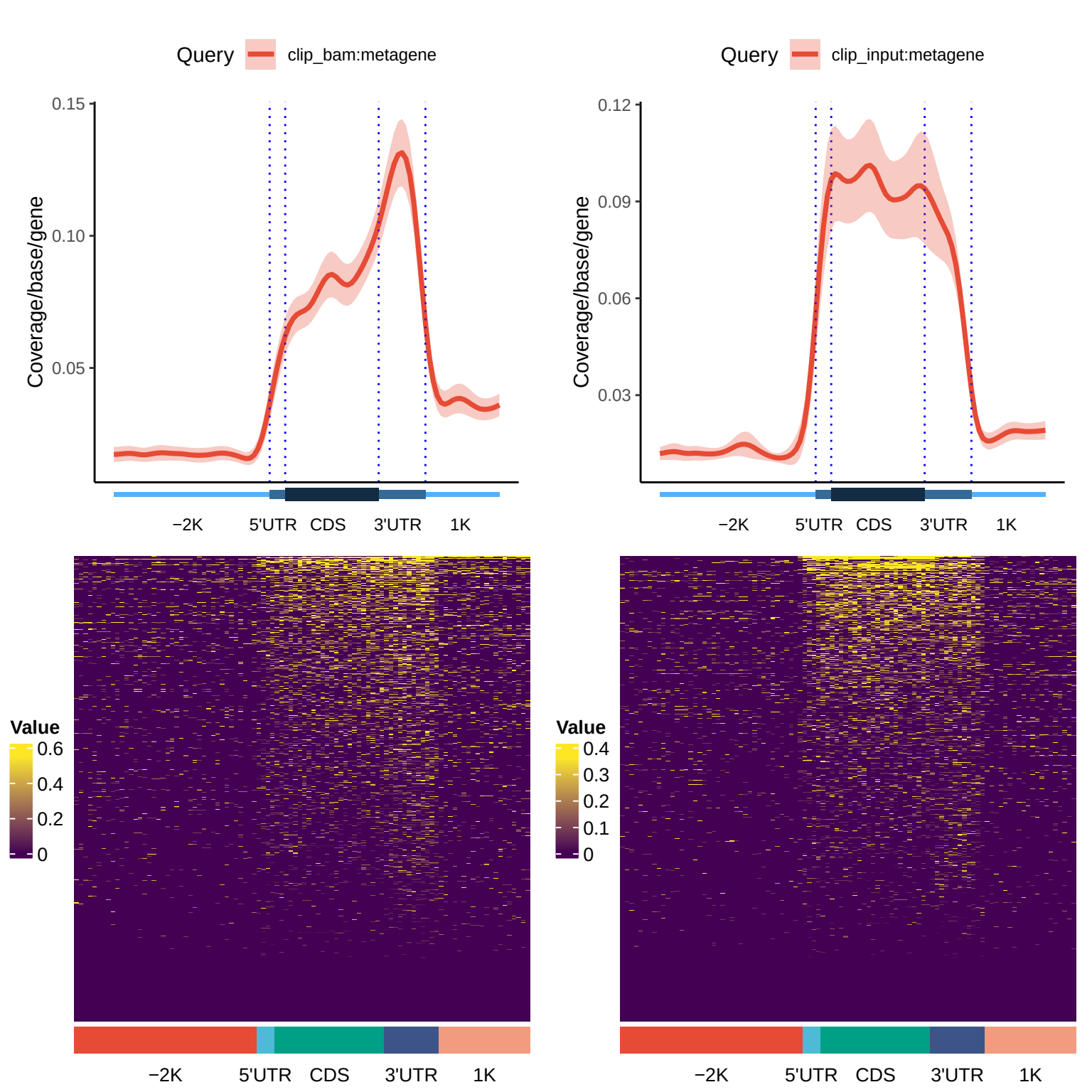
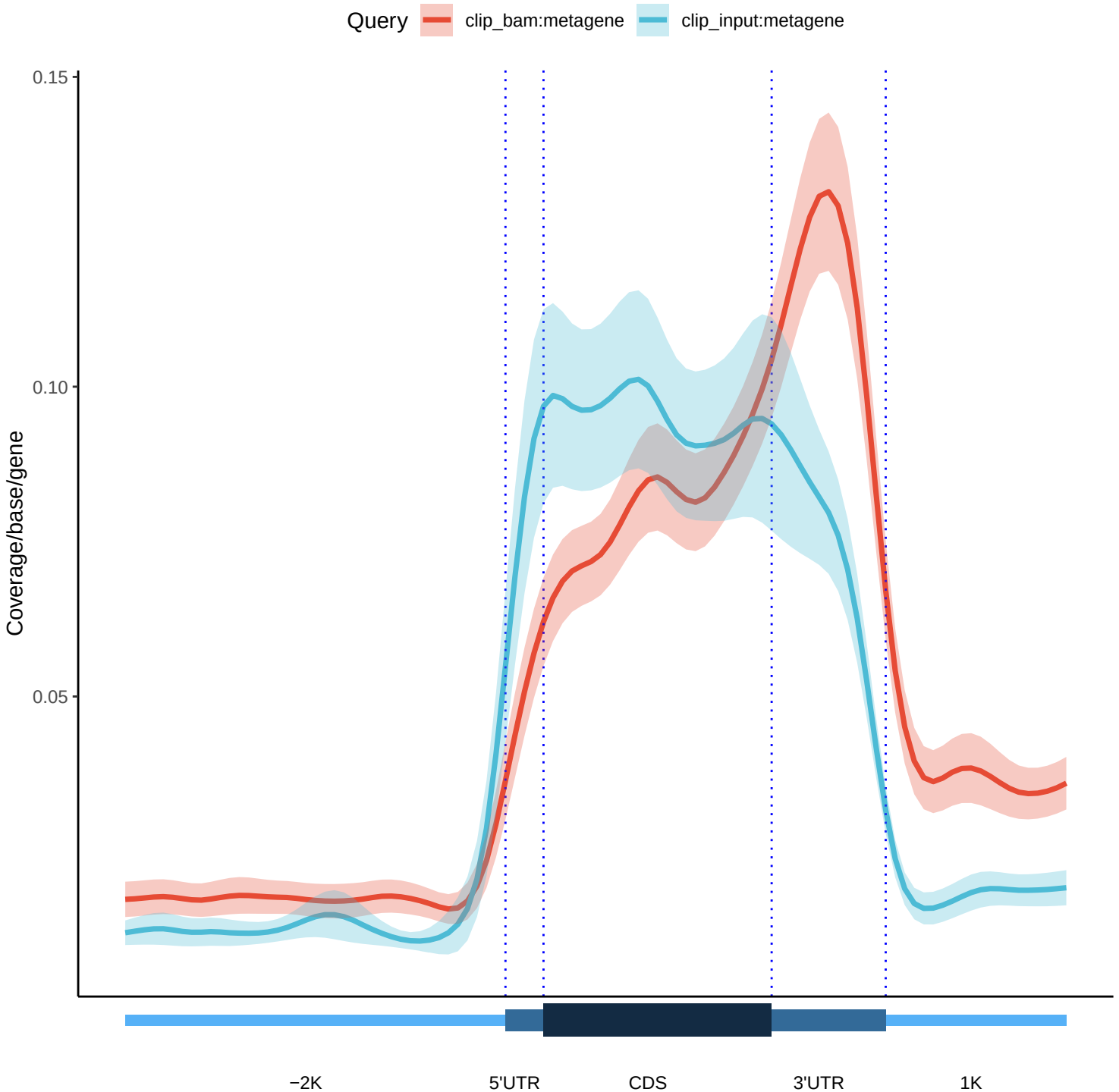
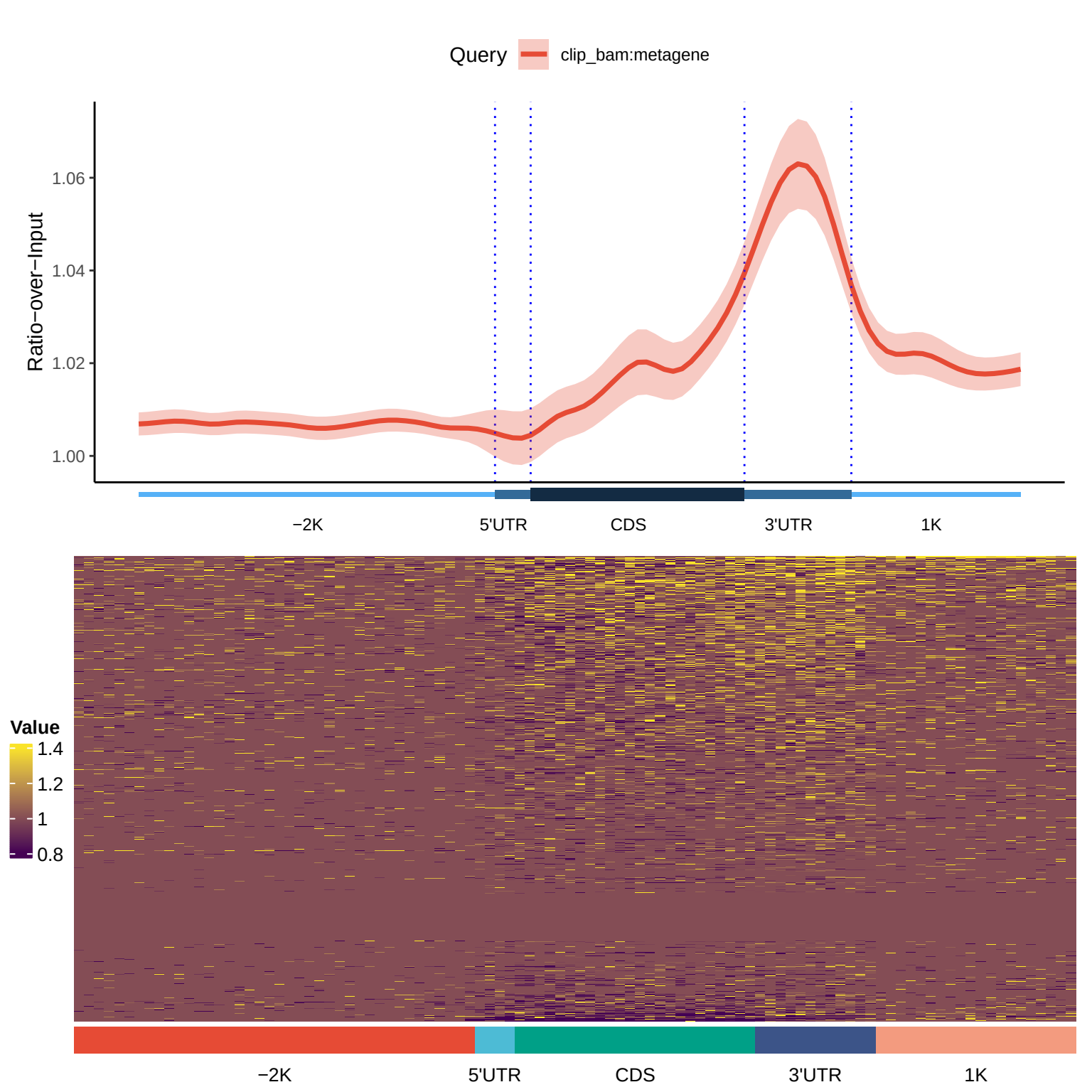

Query
clip_bam:metagene
Coverage/base/gene
0.15
0.10
0.05
−2K
5'UTR
CDS
3'UTR
1K
Query
clip_input:metagene
Coverage/base/gene
0.12
0.09
0.06
0.03
−2K
5'UTR
CDS
3'UTR
1K
Value
0.6
0.4
0.2
0
−2K
5'UTR
CDS
3'UTR
1K
Value
0.4
0.3
0.2
0.1
0
−2K
5'UTR
CDS
3'UTR
1K


Query
clip_bam:metagene
clip_input:metagene
0.15
0.10
0.05
Coverage/base/gene
−2K
5'UTR
CDS
3'UTR
1K


Query
clip_bam:metagene
Ratio−over−Input
1.06
1.04
1.02
1.00
−2K
5'UTR
CDS
3'UTR
1K
Value
1.4
1.2
1
0.8
−2K
5'UTR
CDS
3'UTR
1K

Plotting parameters:

functionName: "plot_5parts_metagene"
queryFiles: c(clip_bam =
"C:/GREENBLATT/Rscripts/GenomicPlot_gh/inst/extdata/treat_chr19.bam")
gFeatures_list: as.list(environment())[["gFeatures_list"]]
inputFiles: c(clip_input =
"C:/GREENBLATT/Rscripts/GenomicPlot_gh/inst/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: NA
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