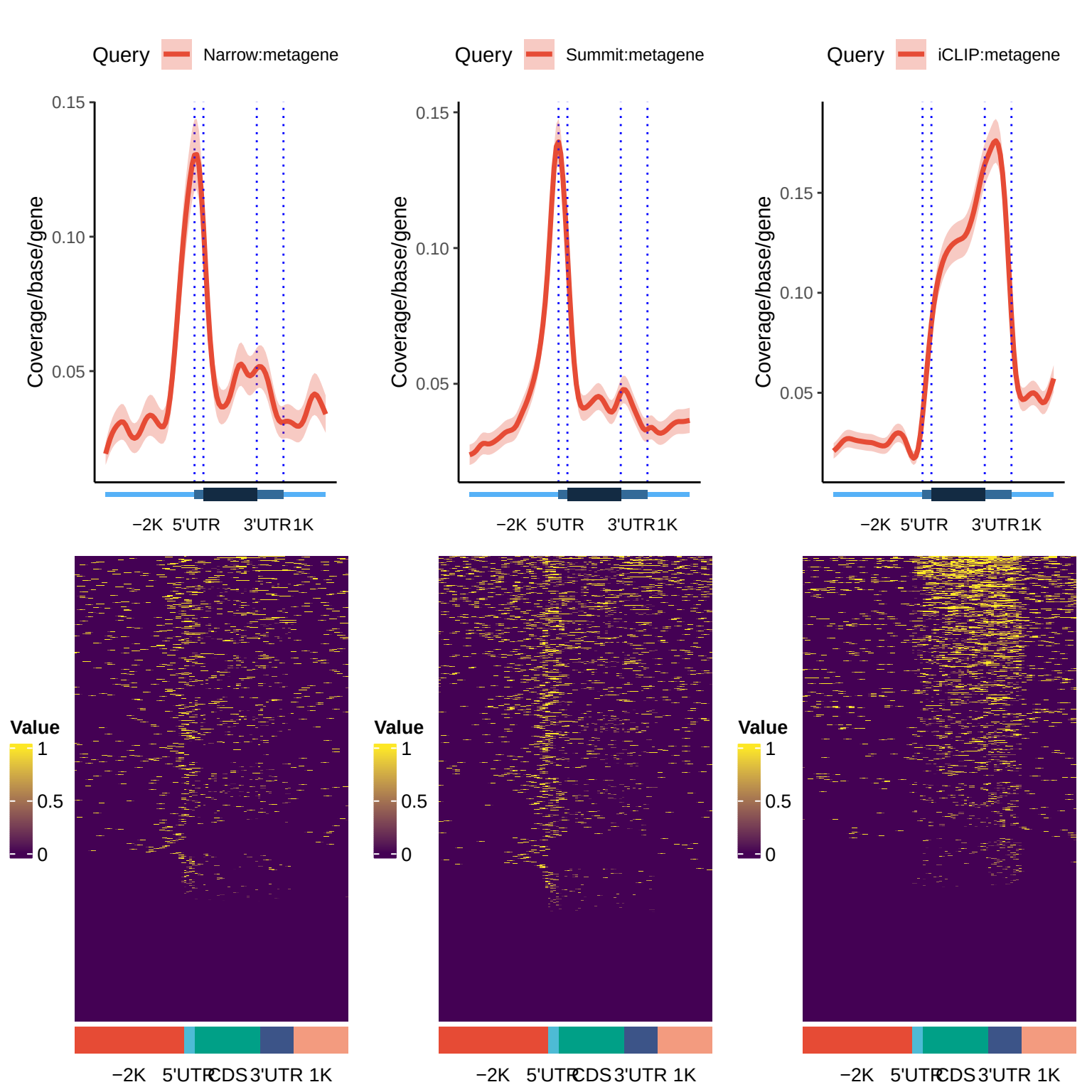
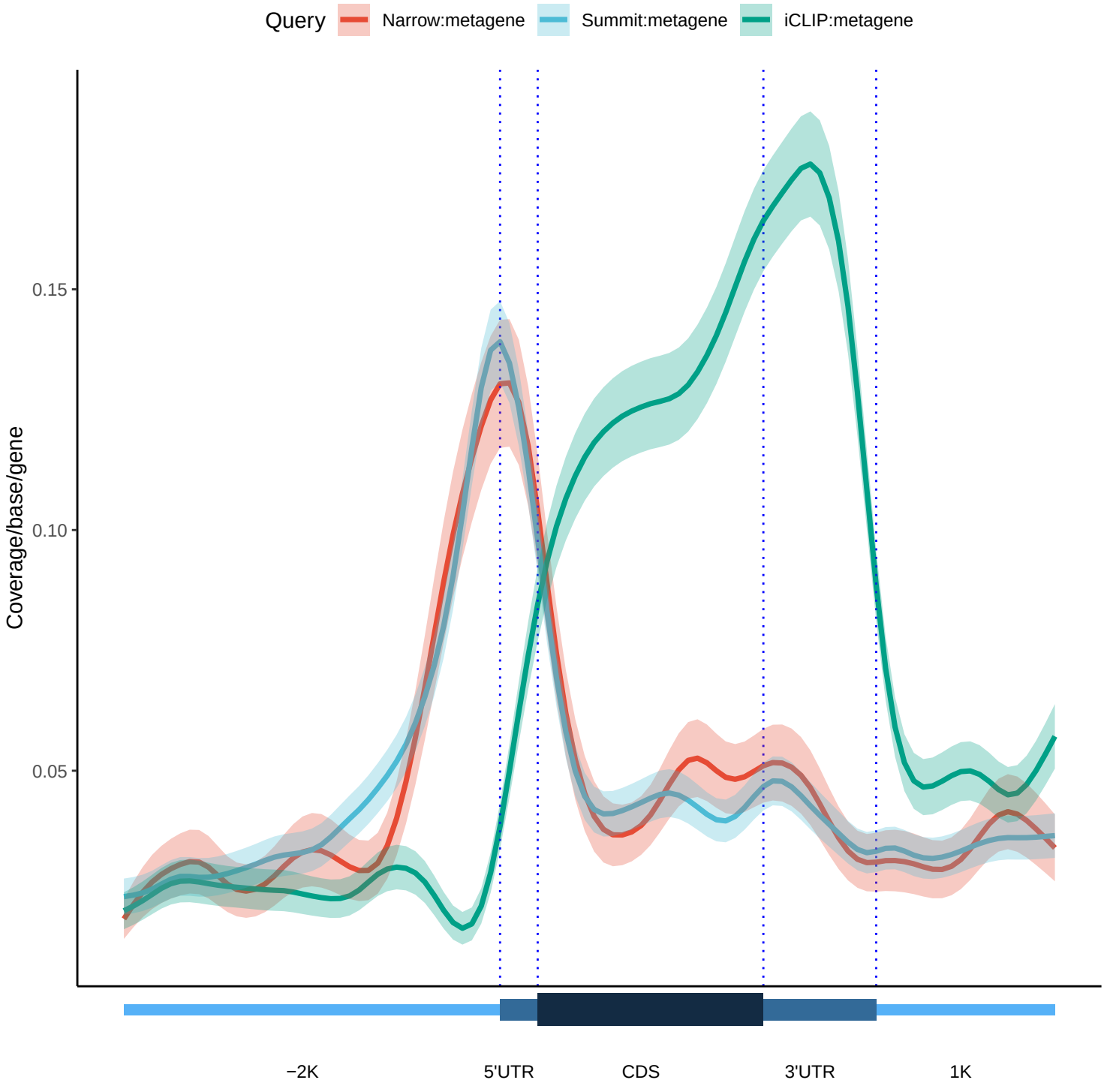

Query
Narrow:metagene
Summit:metagene
iCLIP:metagene
Coverage/base/gene
0.15
0.10
0.05
−2K
5'UTR
3'UTR
1K
Value
1
0.5
0
CDS


Query
Narrow:metagene
Summit:metagene
iCLIP:metagene
Coverage/base/gene
0.15
0.10
0.05
−2K
5'UTR
CDS
3'UTR
1K

Plotting parameters:

functionName: "plot_5parts_metagene"
queryFiles: c(Narrow =
"C:/GREENBLATT/Rscripts/GenomicPlot_gh/inst/extdata/test_chip_peak_chr19.narrowPeak",
Summit =
"C:/GREENBLATT/Rscripts/GenomicPlot_gh/inst/extdata/test_chip_peak_chr19.bed",
iCLIP =
"C:/GREENBLATT/Rscripts/GenomicPlot_gh/inst/extdata/test_clip_peak_chr19.bed")
gFeatures_list: as.list(environment())[["gFeatures_list"]]
inputFiles: NULL
handleInputParams: list(offset = 0, fix_width = 100, fix_point = "center", norm = FALSE, useScore
= FALSE, outRle = TRUE, useSizeFactor = FALSE, genome = "hg19")
verbose: FALSE
transform: NA
smooth: TRUE
scale: FALSE
stranded: TRUE
outPrefix: "test_plot_5parts_metagene1"
heatmap: TRUE
heatRange: c(0, 1)
rmOutlier: TRUE
Ylab: "Coverage/base/gene"
hw: c(8, 8)
nc: 2