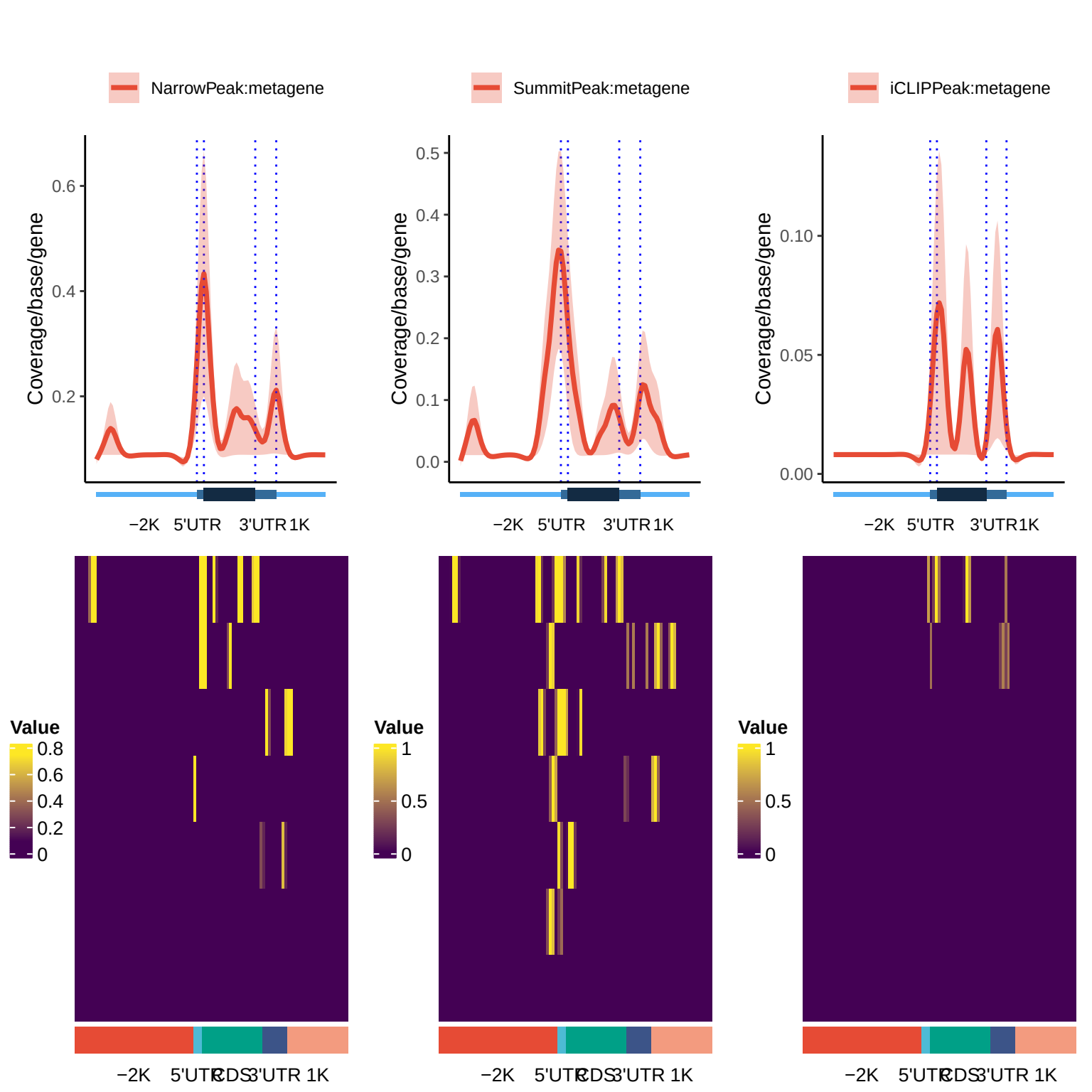
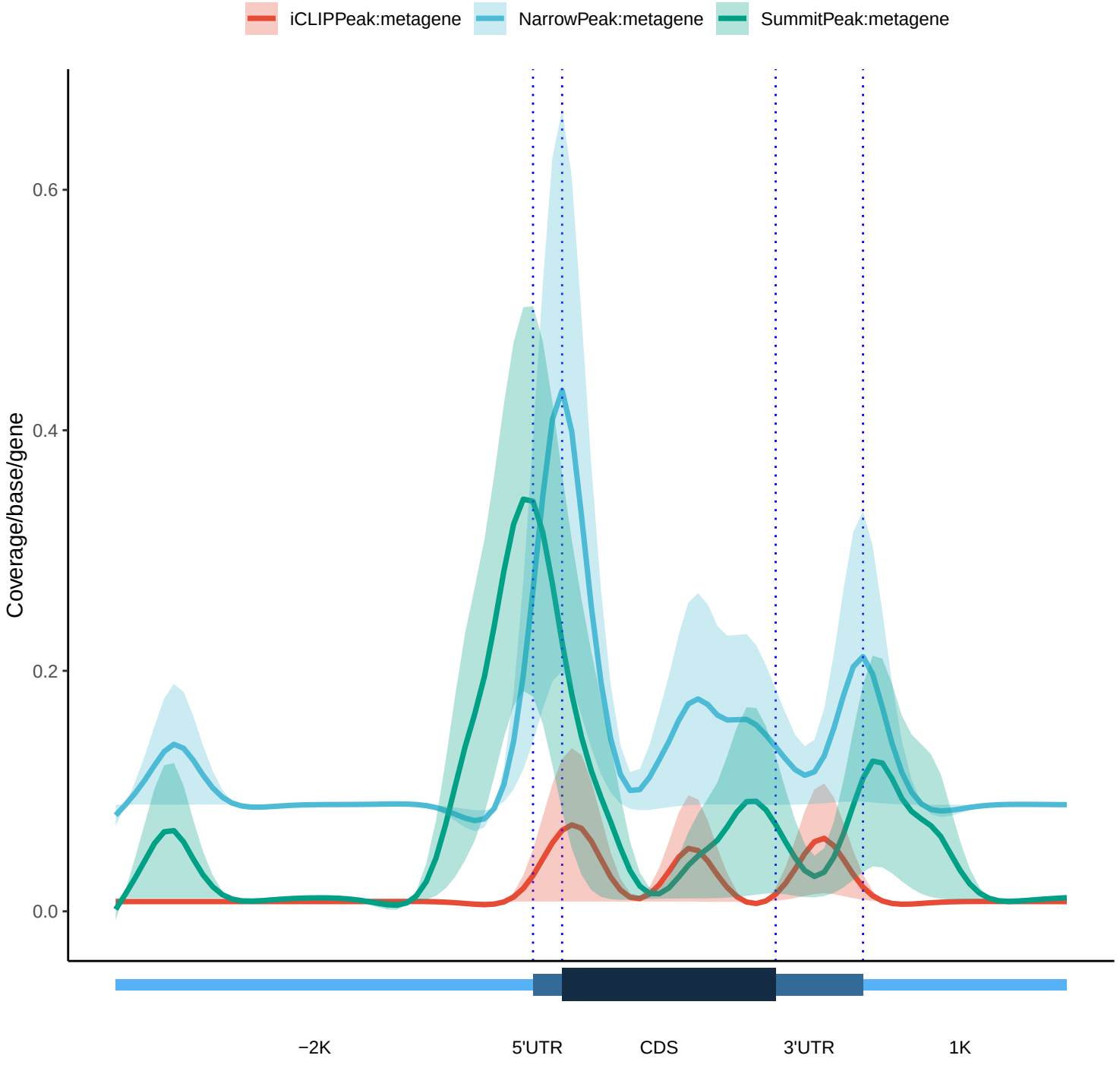

NarrowPeak:metagene
SummitPeak:metagene
iCLIPPeak:metagene
Coverage/base/gene
0.6
0.4
0.2
0.5
0.3
0.1
0.0
0.10
0.05
0.00
−2K
5'UTR
3'UTR
1K
Value
0.8
0.6
0.4
0.2
0
1
0.5
CDS


iCLIPPeak:metagene
NarrowPeak:metagene
SummitPeak:metagene
Coverage/base/gene
0.6
0.4
0.2
0.0
−2K
5'UTR
CDS
3'UTR
1K

Plotting parameters:

functionName: "plot_5parts_metagene"
queryFiles: c(NarrowPeak =
"C:/Users/greenblatt/AppData/Local/R/win−library/4.3/GenomicPlot/extdata/test_chip_peak_chr19.narrowPeak",
SummitPeak =
"C:/Users/greenblatt/AppData/Local/R/win−library/4.3/GenomicPlot/extdata/test_chip_peak_chr19.bed",
iCLIPPeak =
"C:/Users/greenblatt/AppData/Local/R/win−library/4.3/GenomicPlot/extdata/test_clip_peak_chr19.bed")
gFeatures_list: as.list(environment())[["gFeatures_list"]]
inputFiles: NULL
importParams: 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: NULL
rmOutlier: 0
Ylab: "Coverage/base/gene"
hw: c(8, 8)
nc: 2