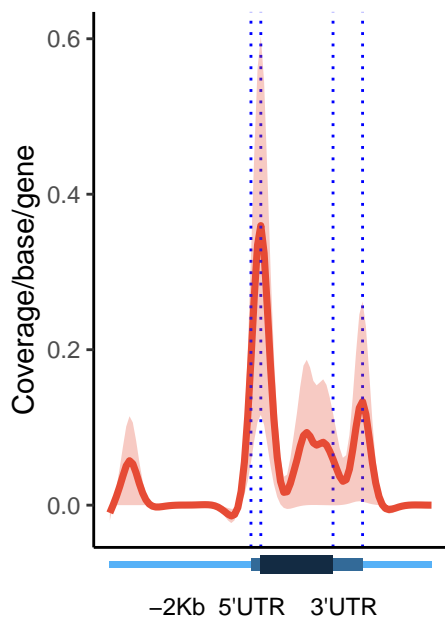
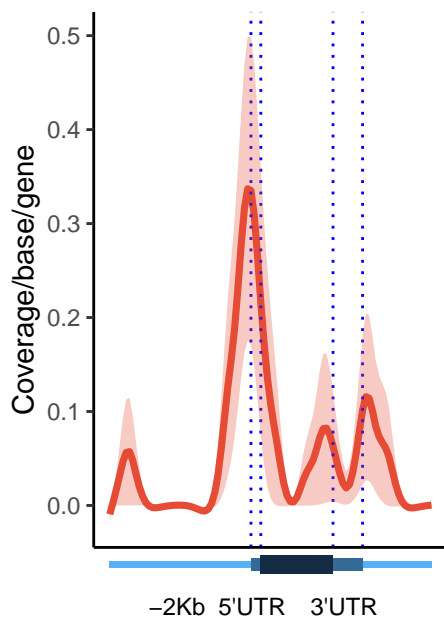


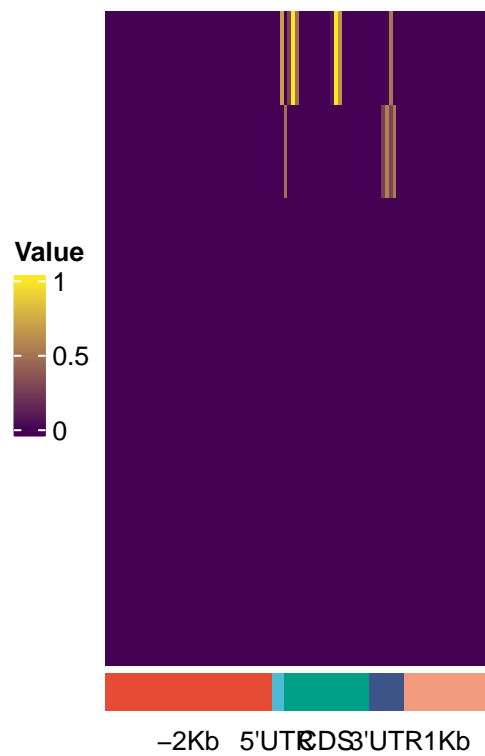
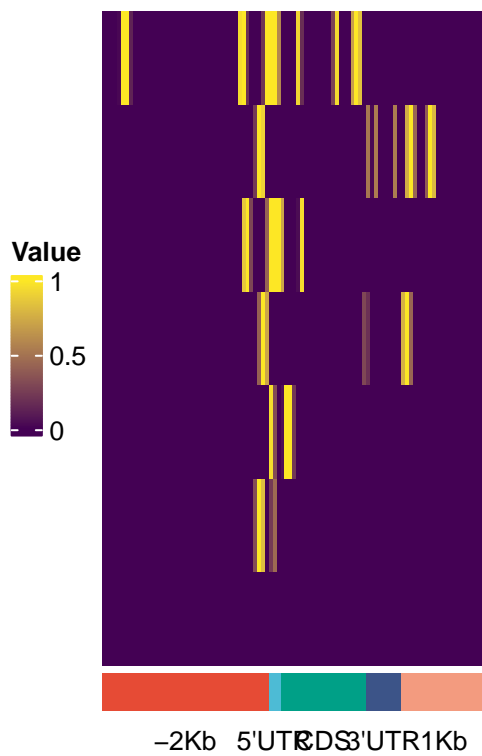
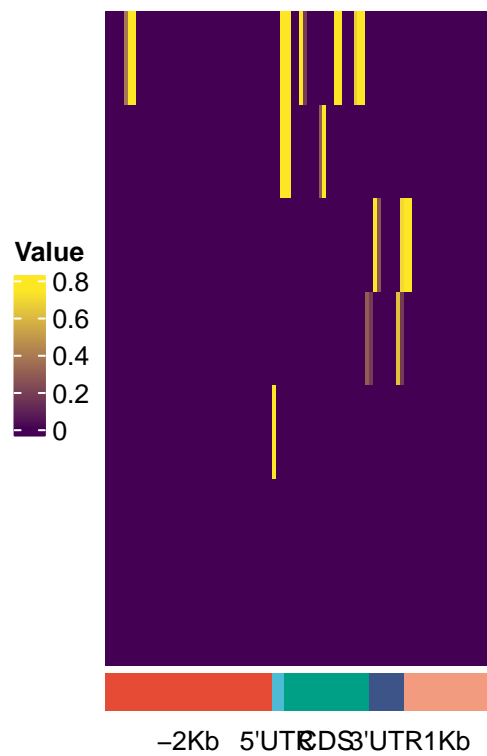
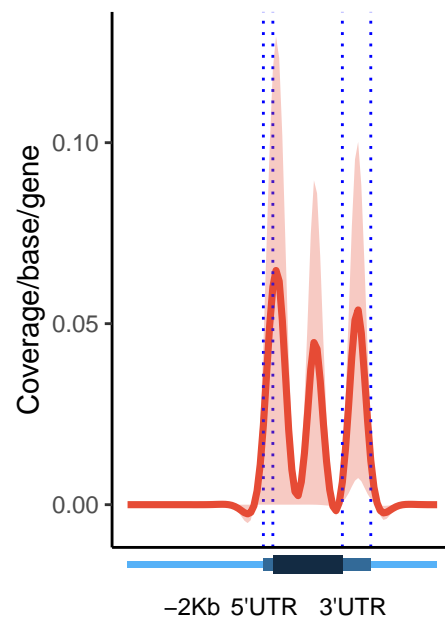
NarrowPeak:metagene



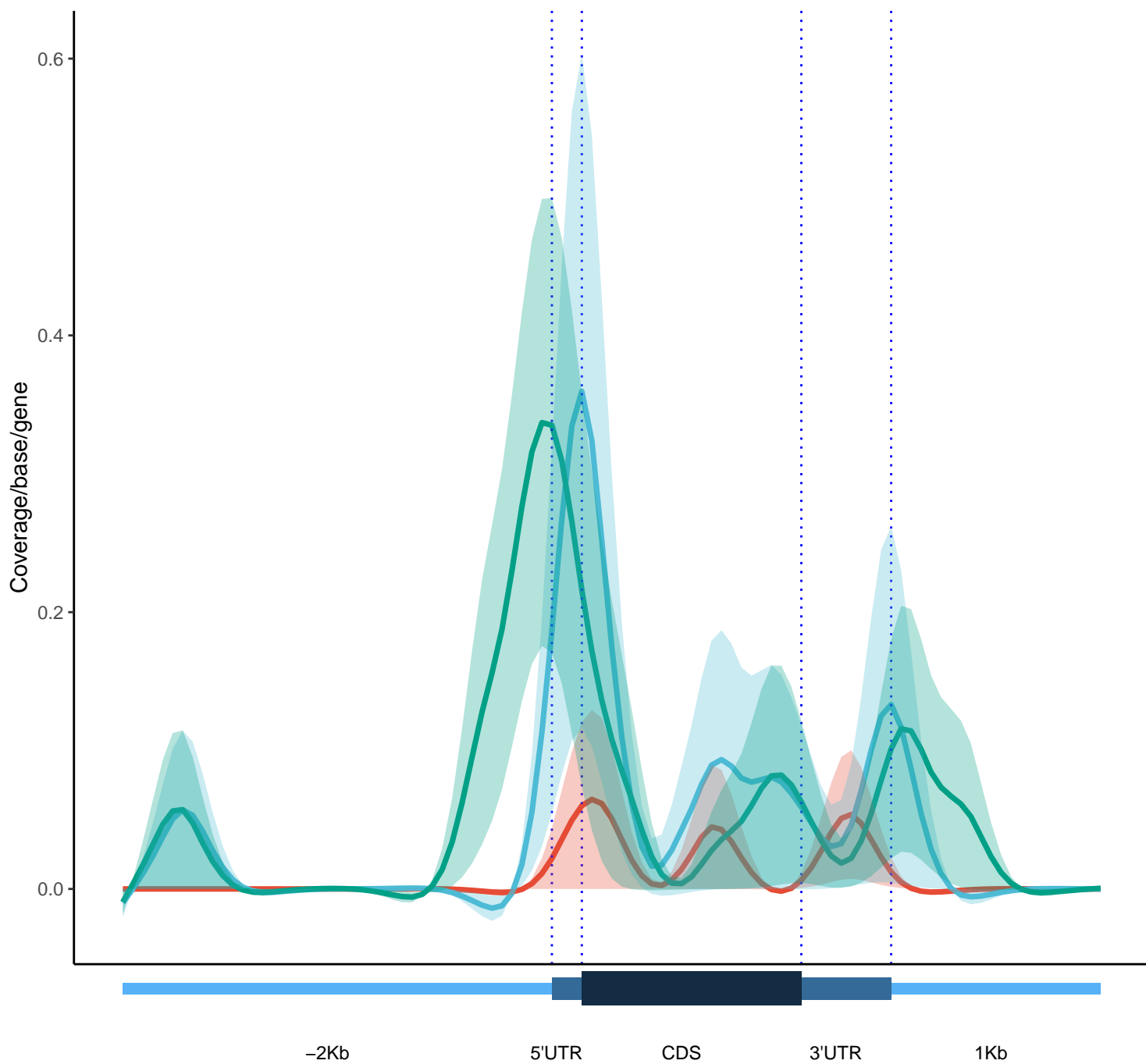
SummitPeak:metagene



iCLIPPeak:metagene



iCLIPPeak:metagene NarrowPeak:metagene SummitPeak:metagene



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, saveRds = 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
```