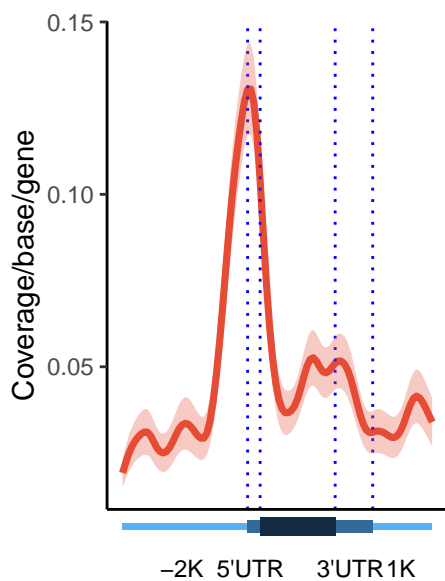
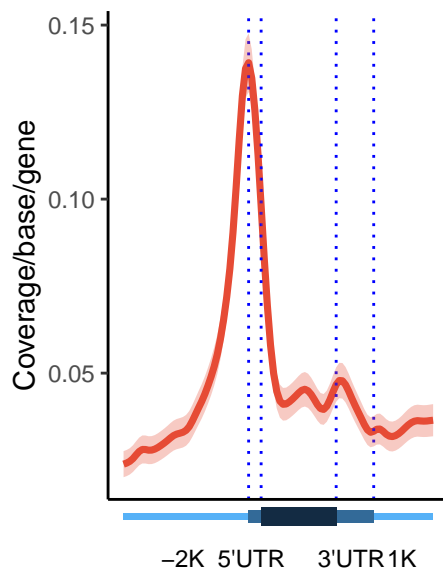


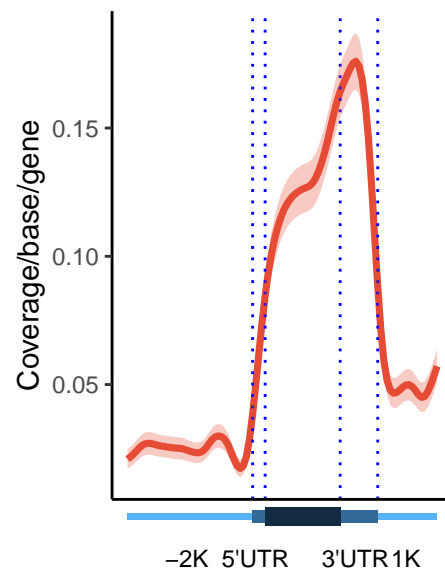
NarrowPeak:metagene



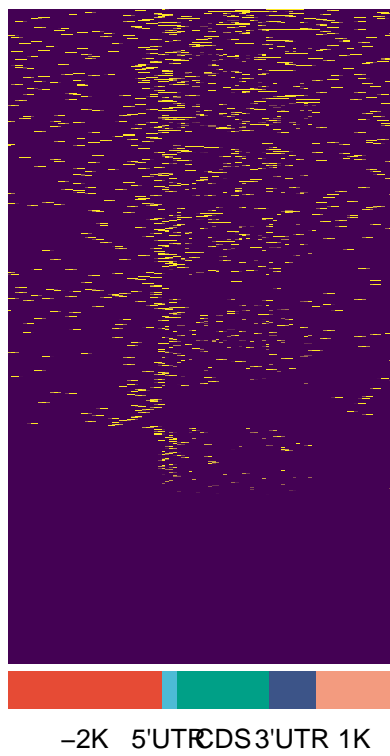
SummitPeak:metagene



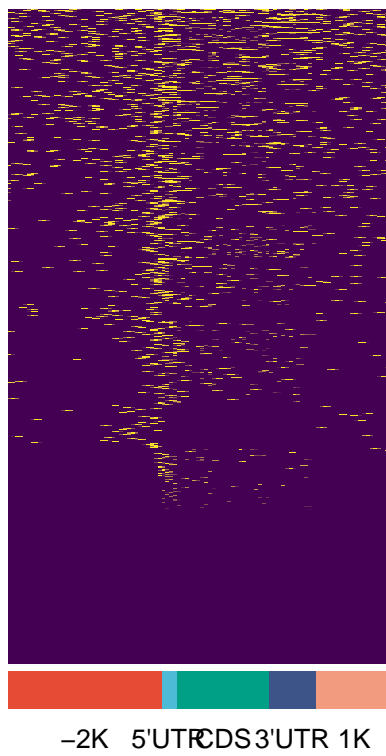
iCLIPPeak:metagene



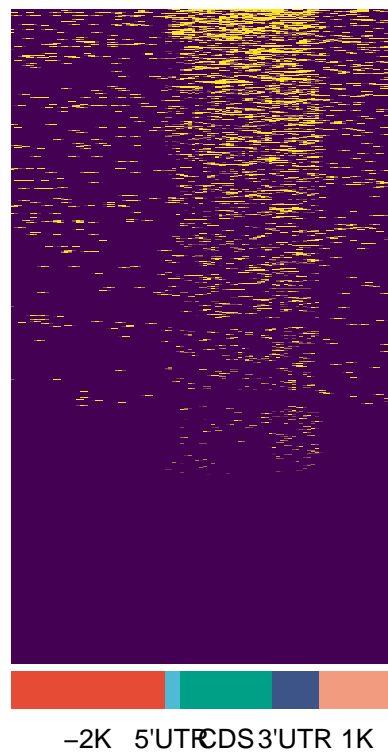
Value  
0.8  
0.6  
0.4  
0.2  
0



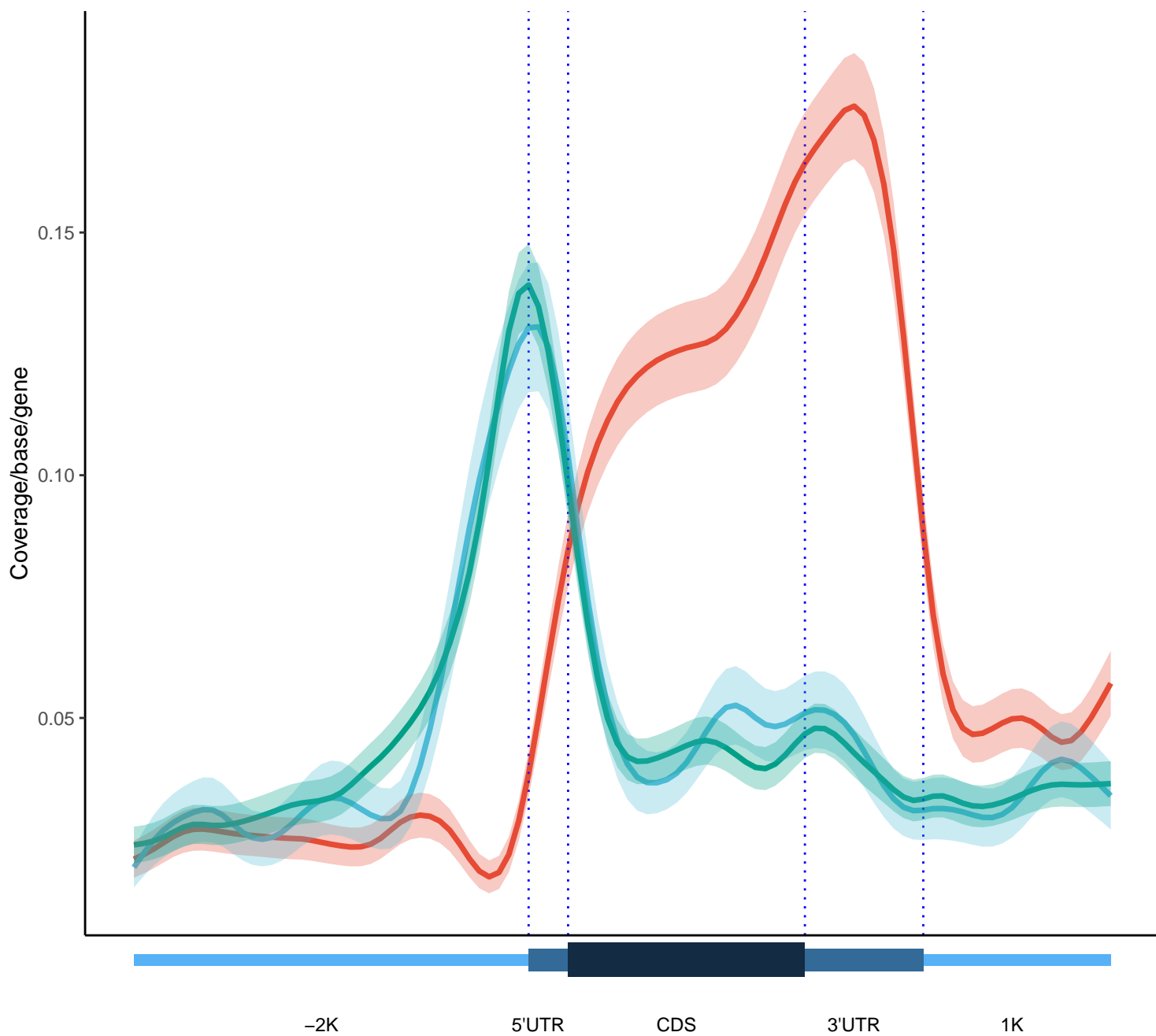
Value  
1  
0.5  
0



Value  
1  
0.5  
0



iCLIPPeak:metagene    NarrowPeak:metagene    SummitPeak:metagene



Plotting parameters:

```
functionName: "plot_5parts_metagene"  
queryFiles: c(NarrowPeak =  
C:/Users/greenblatt/AppData/Local/Programs/R/R-4.2.1/library/GenomicPlot/extdata/test_chip_peak_chr19.narrowPeak  
SummitPeak =  
"C:/Users/greenblatt/AppData/Local/Programs/R/R-4.2.1/library/GenomicPlot/extdata/test_chip_peak_chr19.bed",  
iCLIPPeak =  
"C:/Users/greenblatt/AppData/Local/Programs/R/R-4.2.1/library/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
```