CHIP-seq

zqq

2019/9/27

```
library("ChIPseeker")
```

```
##
```

```
## ChIPseeker v1.18.0  For help: https://guangchuangyu.github.io/ChIPseeker
##
## If you use ChIPseeker in published research, please cite:
## Guangchuang Yu, Li-Gen Wang, Qing-Yu He. ChIPseeker: an R/Bioconductor package for ChIP peak annotation, comparison and visualization. Bioinformatics 2015, 31(14):2382-2383
```

```
library("org.Mm.eg.db")
```

```
## Loading required package: AnnotationDbi
```

```
## Loading required package: stats4
```

```
## Loading required package: BiocGenerics
```

```
## Loading required package: parallel
```

```
##
## Attaching package: 'BiocGenerics'
```

```
## The following objects are masked from 'package:parallel':
##
##     clusterApply, clusterApplyLB, clusterCall, clusterEvalQ,
##     clusterExport, clusterMap, parApply, parCapply, parLapply,
##     parLapplyLB, parRapply, parSapply, parSapplyLB
```

```
## The following objects are masked from 'package:stats':
##
##     IQR, mad, sd, var, xtabs
```

```
## The following objects are masked from 'package:base':
##
##     anyDuplicated, append, as.data.frame, basename, cbind,
##     colMeans, colnames, colSums, dirname, do.call, duplicated,
##     eval, evalq, Filter, Find, get, grep, grepl, intersect,
##     is.unsorted, lapply, lengths, Map, mapply, match, mget, order,
##     paste, pmax, pmax.int, pmin, pmin.int, Position, rank, rbind,
##     Reduce, rowMeans, rownames, rowSums, sapply, setdiff, sort,
##     table, tapply, union, unique, unsplit, which, which.max,
##     which.min
```

```
## Loading required package: Biobase
```

```
## Welcome to Bioconductor
##
##     Vignettes contain introductory material; view with
##     'browseVignettes()'. To cite Bioconductor, see
##     'citation("Biobase")', and for packages 'citation("pkgname")'.
```

```
## Loading required package: IRanges
```

```
## Loading required package: S4Vectors
```

```
##
## Attaching package: 'S4Vectors'
```

```
## The following object is masked from 'package:base':
##
##     expand.grid
```

```
##
## Attaching package: 'IRanges'
```

```
## The following object is masked from 'package:grDevices':
##
##     windows
```

```
##
```

```
library("TxDb.Mmusculus.UCSC.mm10.knownGene")
```

```
## Loading required package: GenomicFeatures
```

```
## Loading required package: GenomeInfoDb
```

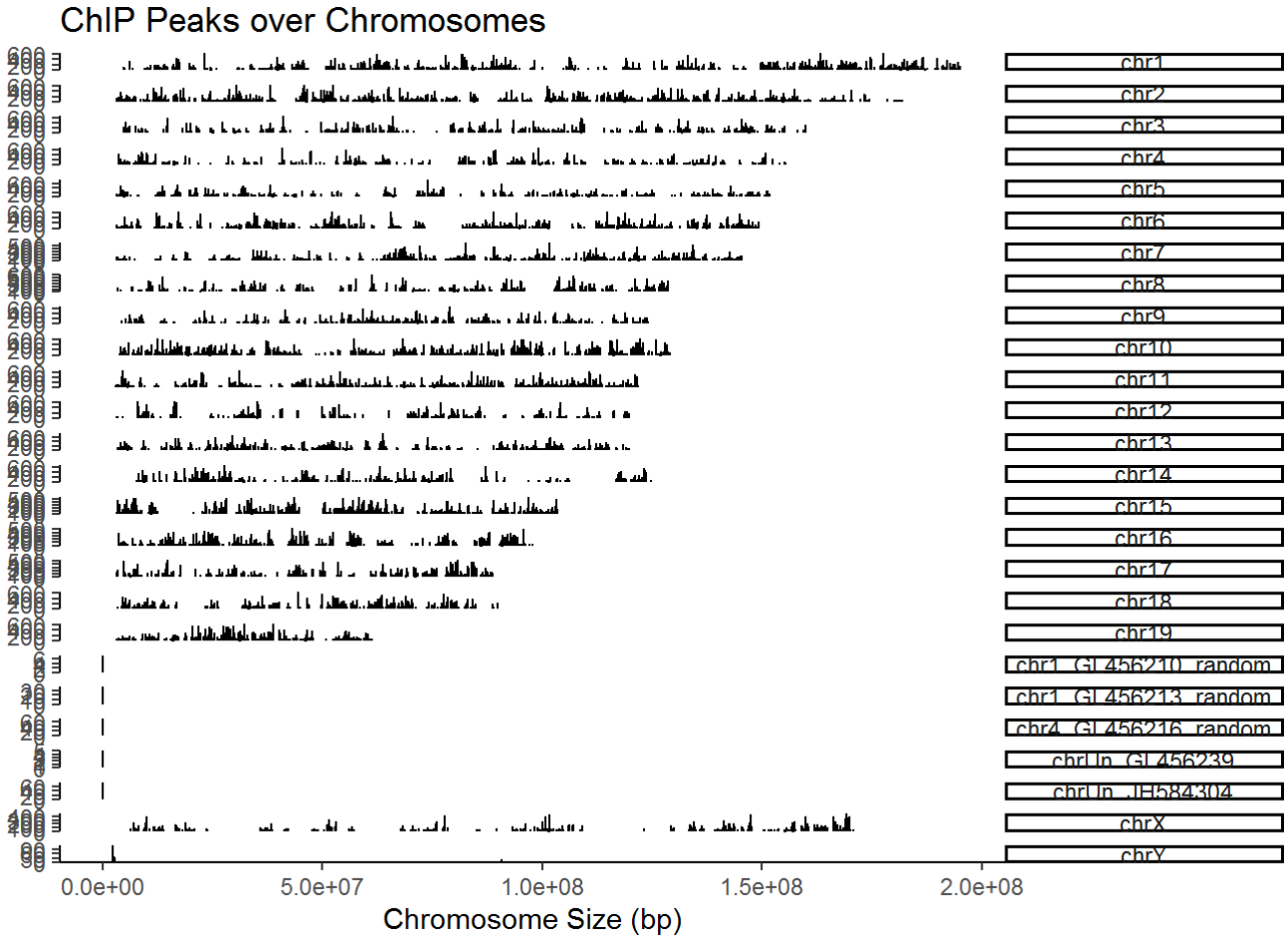
```
## Loading required package: GenomicRanges
```

```
library("clusterProfiler")
```

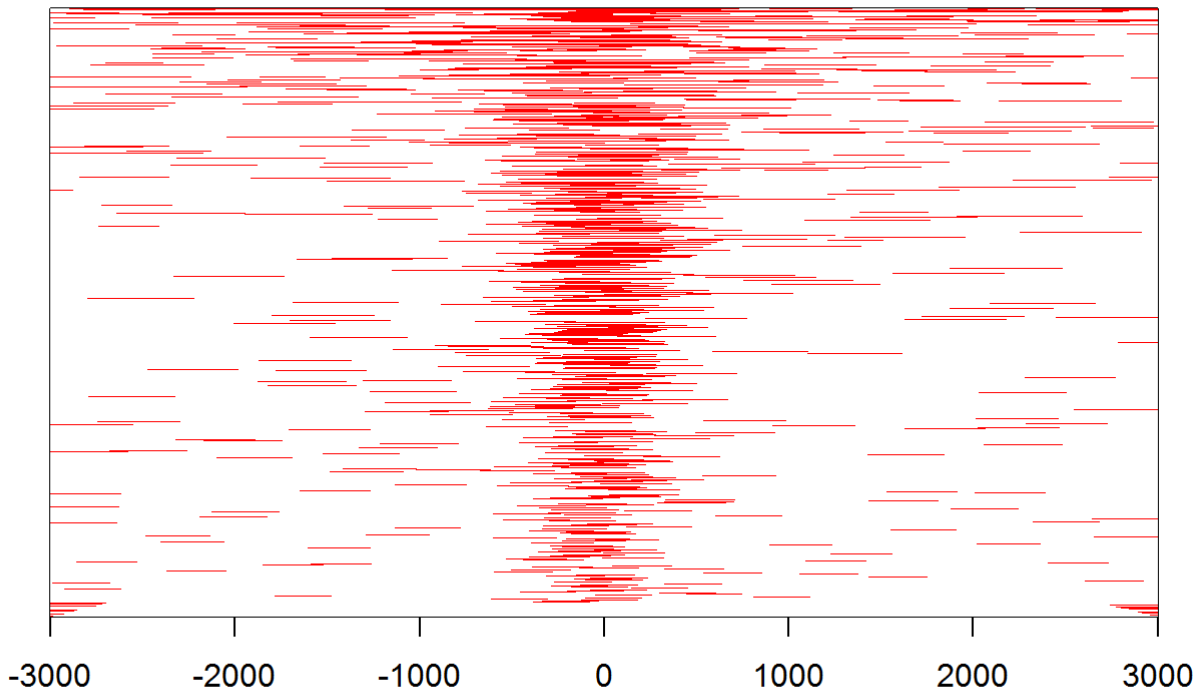
```
## clusterProfiler v3.10.1  For help: https://guangchuangyu.github.io/software/clusterProfiler
##
## If you use clusterProfiler in published research, please cite:
## Guangchuang Yu, Li-Gen Wang, Yanyan Han, Qing-Yu He. clusterProfiler: an R package for compa
ring biological themes among gene clusters. OMICS: A Journal of Integrative Biology. 2012, 16
(5):284-287.
```

```
bcat1 <- readPeakFile("F:/CHIP-seq/bCat1_peaks.narrowPeak")
txdb <- TxDb.Mmusculus.UCSC.mm10.knownGene
```

```
covplot(bcat1,weightCol=5)
```

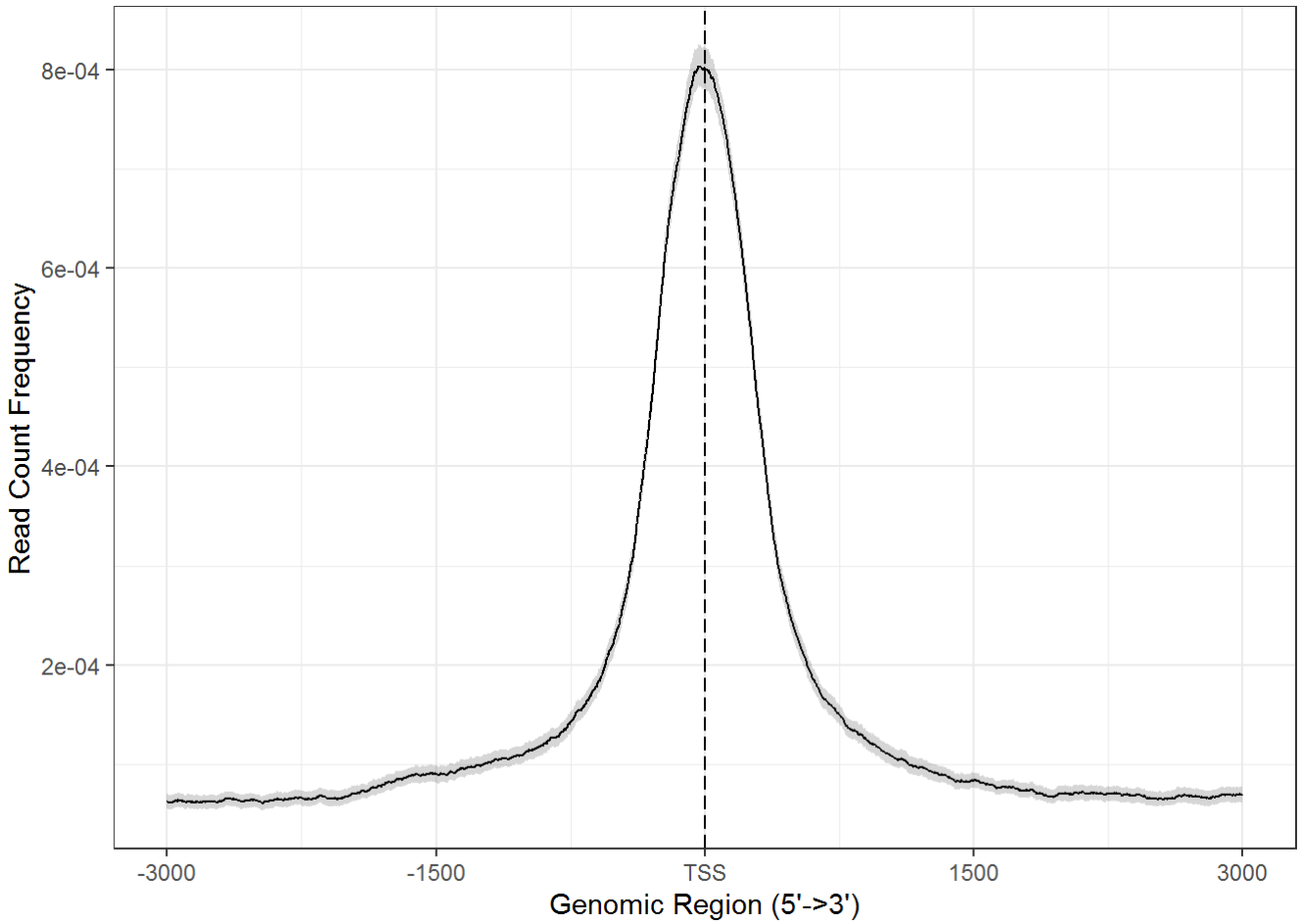



```
promoter <- getPromoters(TxDb=txdb, upstream=3000, downstream=3000)
tagMatrix <- getTagMatrix(bcat1, windows=promoter)
tagHeatmap(tagMatrix, xlim=c(-3000, 3000), color="red")
```




```
plotAvgProf(tagMatrix, xlim=c(-3000, 3000),
            conf=0.95,resample = 1000,
            xlab="Genomic Region (5'->3')", ylab = "Read Count Frequency")
```

```
## >> Running bootstrapping for tag matrix...        2019-09-27 17:13:25
```



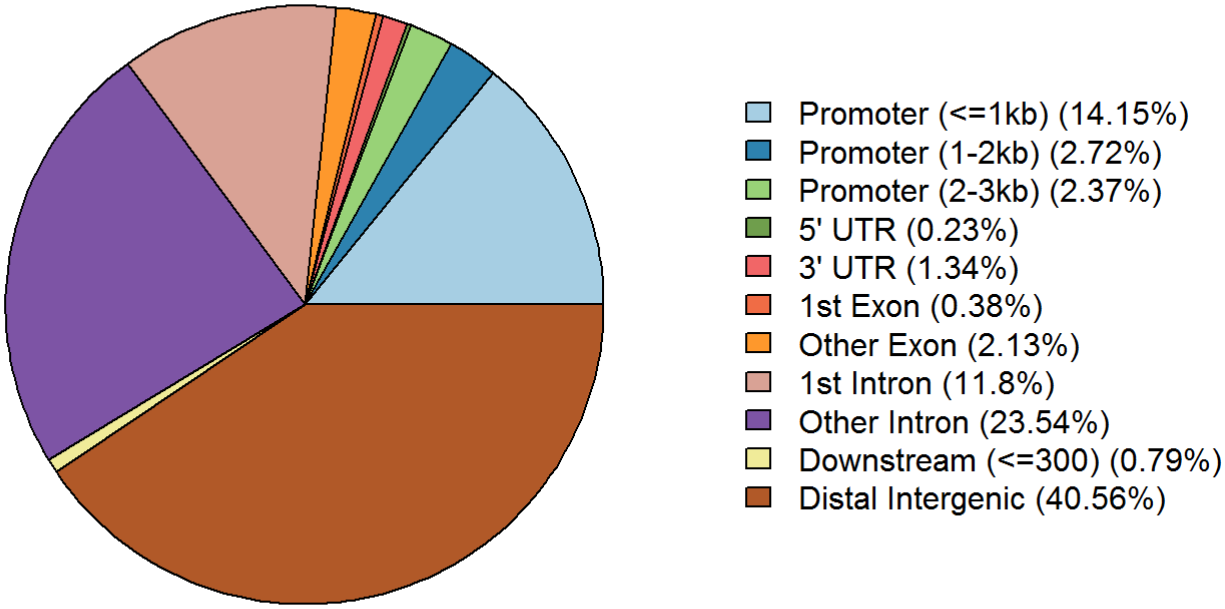

```
peakAnno <- annotatePeak(bcat1, tssRegion=c(-3000, 3000),


TxDb=txdb, annoDb="org.Mm.eg.db")
```

```
## >> preparing features information...      2019-09-27 17:13:27
## >> identifying nearest features...        2019-09-27 17:13:28
## >> calculating distance from peak to TSS...   2019-09-27 17:13:29
## >> assigning genomic annotation...        2019-09-27 17:13:29
## >> adding gene annotation...          2019-09-27 17:13:38
```

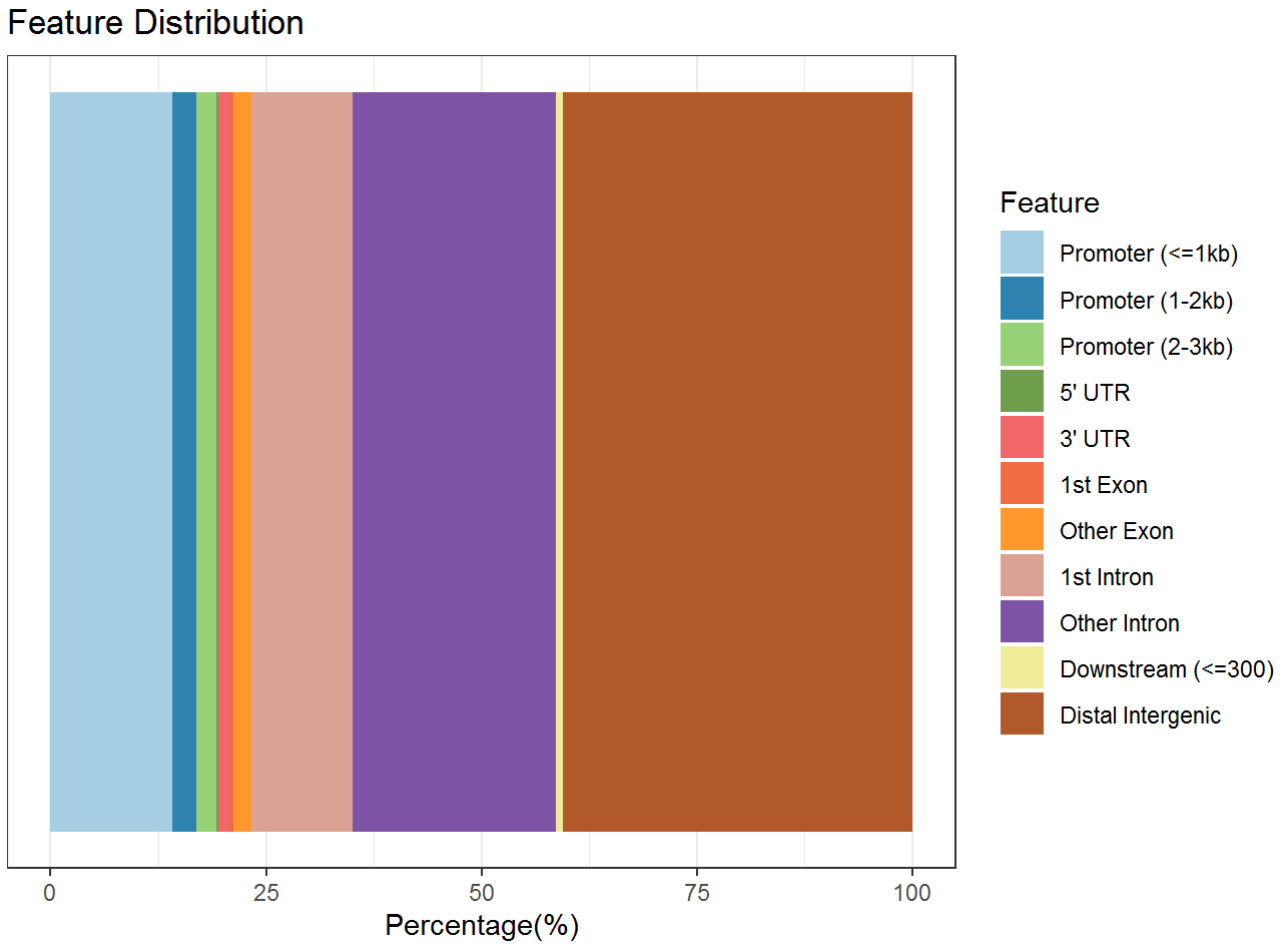
```
## 'select()' returned 1:many mapping between keys and columns
```

```
## >> assigning chromosome lengths           2019-09-27 17:13:38
## >> done...                    2019-09-27 17:13:38
```

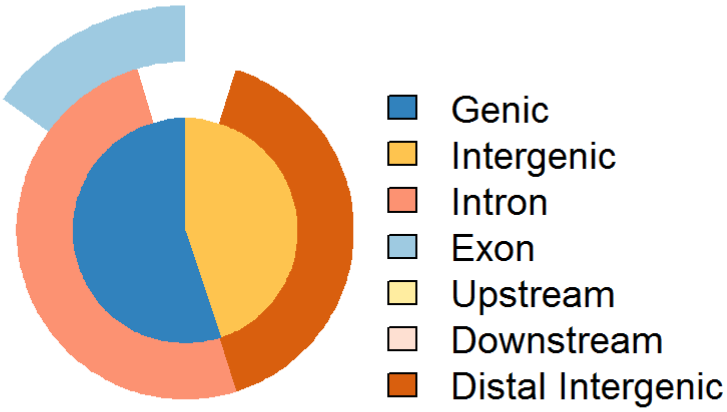
```
plotAnnoPie(peakAnno)
```



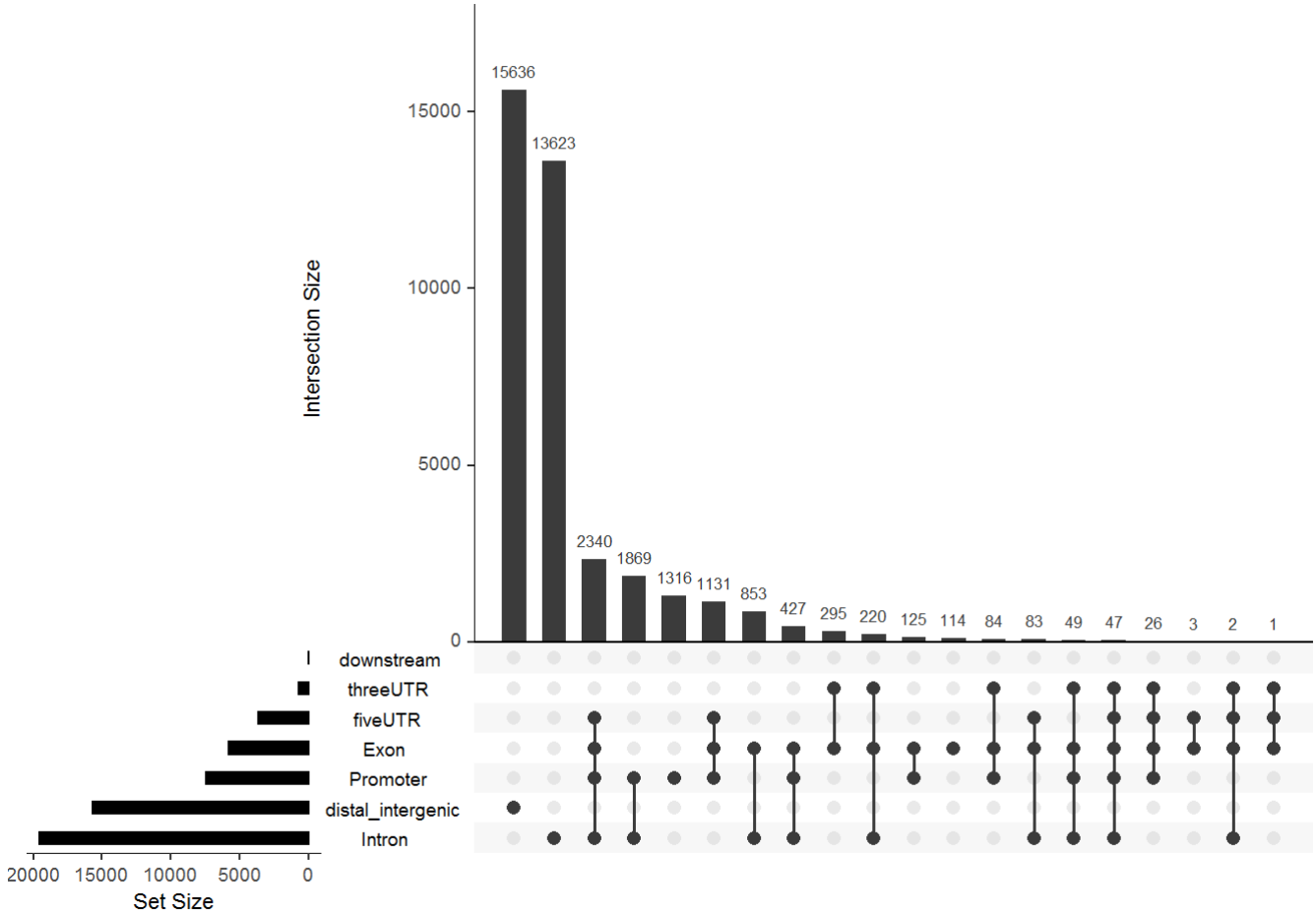

```
plotAnnoBar(peakAnno)
```

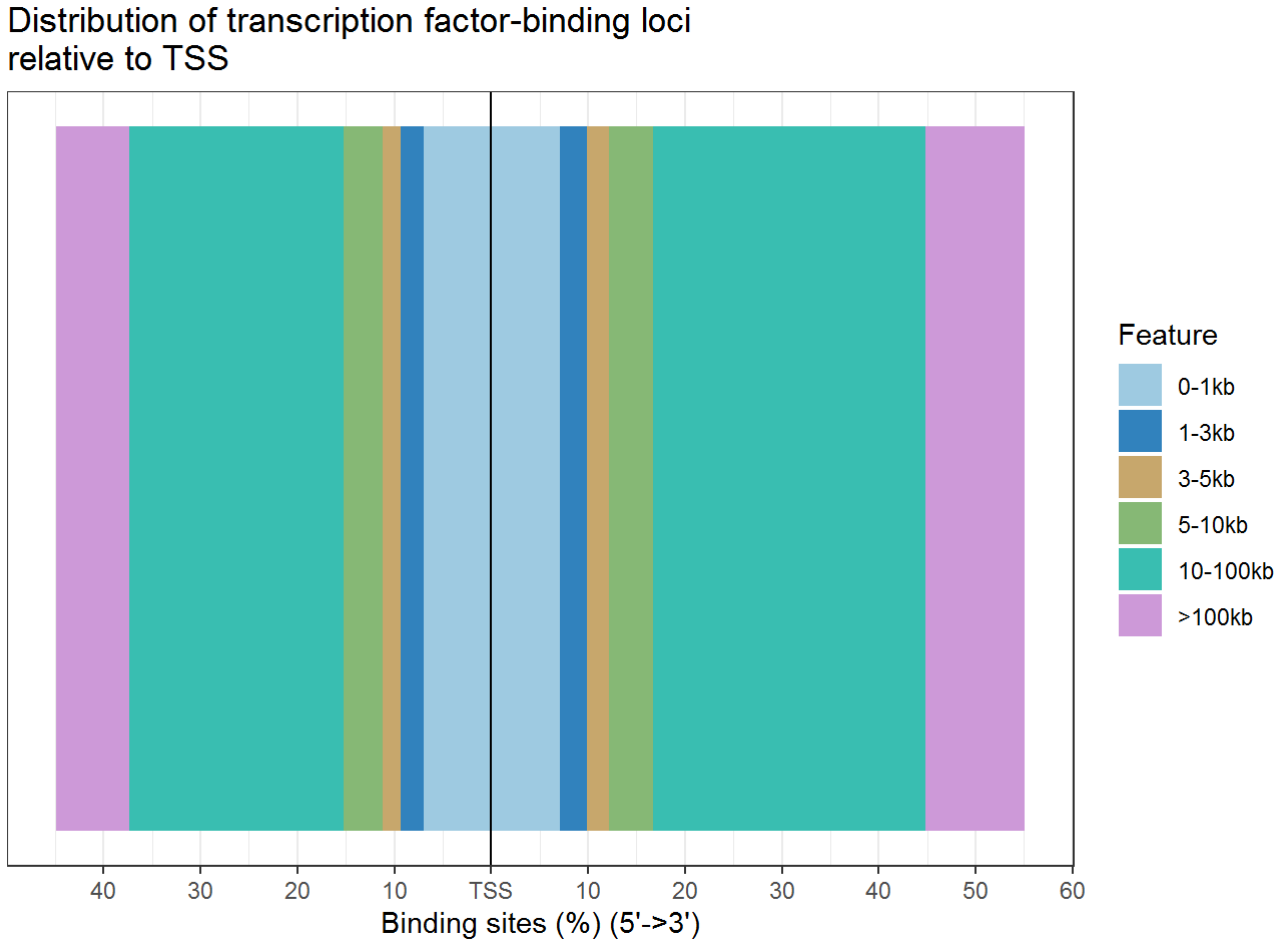


```
vennpie(peakAnno)
```




```
upsetplot(peakAnno)
```




```
plotDistToTSS(peakAnno,
              title="Distribution of transcription factor-binding loci\nrelative to TSS")
```