Figure 5A KAT2B signals display

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04/15/2022

Contents

```
require(dplyr)
require(GenomicRanges)

load("./ZFP3.annotated.sites.RData")

require(EnsDb.Hsapiens.v86)
require(ChIPpeakAnno)
require(GenomicRanges)

ZFP3.peaks.regions = GRanges(seqnames = "chr3",
                             ranges   = IRanges(start = 20039523,
                                                end   = 20041522))

ZFP3.peaks.regions
```

```
## GRanges object with 1 range and 0 metadata columns:
##       seqnames            ranges strand
##          <Rle>         <IRanges>  <Rle>
##   [1]     chr3 20039523-20041522      *
##   -------
##   seqinfo: 1 sequence from an unspecified genome; no seqlengths
```

```
hg38.genomeAxis.track <- Gviz::GenomeAxisTrack()

require(ensembldb)
require(EnsDb.Hsapiens.v86)
edb <- EnsDb.Hsapiens.v86
seqlevelsStyle(edb) <- "UCSC"

require(Gviz)
```

```
## Loading required package: Gviz

## Loading required package: grid

##
## Attaching package: 'Gviz'
```

```
## The following object is masked from 'package:AnnotationFilter':
##
##     feature
```

```
require(ggplotify)
```

```
## Loading required package: ggplotify
```

```
## Warning: package 'ggplotify' was built under R version 4.1.2
```

```
hg38.geneRegion.track <- Gviz::GeneRegionTrack(ensembldb::getGeneRegionTrackForGviz(edb,
                                                                                    chromosome = seqnames(ZFP3.peaks.regions)
                                                                                    ),
                                               name = "Genes Model",
                                               transcriptAnnotation = "symbol",
                                               background.title = "brown",
                                               fill = "#777777")

ZFP3.ChIP.H293.track <- Gviz::DataTrack(range = rtracklayer::import.bw("./ENCFF655DZE.bigWig",
                                                                       which = ZFP3.peaks.regions),
                        genome = "hg38", type = "l", col = "#E6A024",
                        groups = factor(1, levels = seq(1,10)),
                        name = "ZFP3 ChIP-seq signals (HEK293 cells)", ylim = c(0, 8500))

ZFP3.ChIP.SKN.track <- Gviz::DataTrack(range = rtracklayer::import.bw("./ENCFF774MKP.bigWig",
                                                                      which = ZFP3.peaks.regions),
                        genome = "hg38", type = "l", col = "#5BB4E5",
                        groups = factor(2, levels = seq(1,10)),
                        name = "ZFP3 ChIP-seq signal (SK-N-SH cells)", ylim = c(0, 8500))

ZFP3.ChIP.tracks <- Gviz::OverlayTrack(trackList=list(ZFP3.ChIP.H293.track,
                                                      ZFP3.ChIP.SKN.track
                                                     ))


DNase.H293.track <- Gviz::DataTrack(range = rtracklayer::import.bw("DNase-seq signals/ENCFF529BOG.H293T
                                                                   which = ZFP3.peaks.regions),
                        genome = "hg38", type = "l", col = "#E6A024",
                        groups = factor(3, levels = seq(1,10)),
                        name = "DNase-seq signals (HEK293 cells)", ylim = c(0, 6))


DNase.SKN.track <- Gviz::DataTrack(range = rtracklayer::import.bw("DNase-seq signals/ENCFF280RMA.SKN.bi
                                                                  which = ZFP3.peaks.regions),
                        genome = "hg38", type = "l", col = "#5BB4E5",
                        groups = factor(4, levels = seq(1,10)),
                        name = "DNase-seq signals (SK-N-SH cells)", ylim = c(0, 6))


DNase.tracks <- Gviz::OverlayTrack(trackList=list(DNase.H293.track,
                                                  DNase.SKN.track
                                                  ))
```

```
H3K27ac.H293.track <- Gviz::DataTrack(range = rtracklayer::import.bw("Chromatin signals/ENCFF157TGK.HEK
                                                                    which = ZFP3.peaks.regions),
                      genome = "hg38", type = "l", col = "#E6A024",
                      groups = factor(5, levels = seq(1,10)),
                      name = "H3K27ac signals (HEK293 cells)", ylim = c(0, 200))


H3K27ac.SKN.track <- Gviz::DataTrack(range = rtracklayer::import.bw("Chromatin signals/ENCFF287KJY.SKN.
                                                                    which = ZFP3.peaks.regions),
                      genome = "hg38", type = "l", col = "#5BB4E5",
                      groups = factor(6, levels = seq(1,10)),
                      name = "H3K27ac signals (SK-N-SH cells)", ylim = c(0, 200))


H3K27ac.tracks <- Gviz::OverlayTrack(trackList=list(H3K27ac.H293.track,
                                                    H3K27ac.SKN.track))

H3K4me3.H293.track <- Gviz::DataTrack(range = rtracklayer::import.bw("Chromatin signals/ENCFF315TAU.HEK
                                                                    which = ZFP3.peaks.regions),
                      genome = "hg38", type = "l", col = "#E6A024",
                      groups = factor(7, levels = seq(1,10)),
                      name = "H3K4me3 signals (HEK293 cells)", ylim = c(0, 380))


H3K4me3.SKN.track <- Gviz::DataTrack(range = rtracklayer::import.bw("Chromatin signals/ENCFF943FNS.SKN.
                                                                    which = ZFP3.peaks.regions),
                      genome = "hg38", type = "l", col = "#5BB4E5",
                      groups = factor(8, levels = seq(1,10)),
                      name = "H3K4me3 signals (SK-N-SH cells)", ylim = c(0, 380))


H3K4me3.tracks <- Gviz::OverlayTrack(trackList=list(H3K4me3.H293.track,
                                                    H3K4me3.SKN.track))

H3K4me1.H293.track <- Gviz::DataTrack(range = rtracklayer::import.bw("Chromatin signals/ENCFF003LZR.HEK
                                                                    which = ZFP3.peaks.regions),
                      genome = "hg38", type = "l", col = "#E6A024",
                      groups = factor(9, levels = seq(1,10)),
                      name = "H3K4me1 signals (HEK293 cells)", ylim = c(0, 20))

H3K4me1.SKN.track <- Gviz::DataTrack(range = rtracklayer::import.bw("Chromatin signals/ENCFF056LYG.SKN.
                                                                    which = ZFP3.peaks.regions),
                      genome = "hg38", type = "l", col = "#5BB4E5",
                      groups = factor(10, levels = seq(1,10)),
                      name = "H3K4me3 signals (SK-N-SH cells)", ylim = c(0, 20))

H3K4me1.tracks <- Gviz::OverlayTrack(trackList=list(H3K4me1.H293.track,
                                                    H3K4me1.SKN.track))

H3K9me3.H293.track <- Gviz::DataTrack(range = rtracklayer::import.bw("Chromatin signals/ENCFF758LNF.HEK
                                                                    which = ZFP3.peaks.regions),
                      genome = "hg38", type = "l", col = "#E6A024",
                      groups = factor("HEK293", levels = c("HEK293", "SK-N-SH")),
```

```
                    name = "H3K9me3 signals (HEK293 cells)", ylim = c(0, 10))

H3K9me3.SKN.track <- Gviz::DataTrack(range = rtracklayer::import.bw("Chromatin signals/ENCFF655EVA.SKN.
                                                                    which = ZFP3.peaks.regions),
                    genome = "hg38", type = "l", col = "#5BB4E5",
                    groups = factor("SK-N-SH", levels = c("HEK293", "SK-N-SH")),
                    name = "H3K9me3 signals (SK-N-SH cells)", ylim = c(0, 10))

H3K9me3.tracks <- Gviz::OverlayTrack(trackList=list(H3K9me3.H293.track,
                                                    H3K9me3.SKN.track))
```

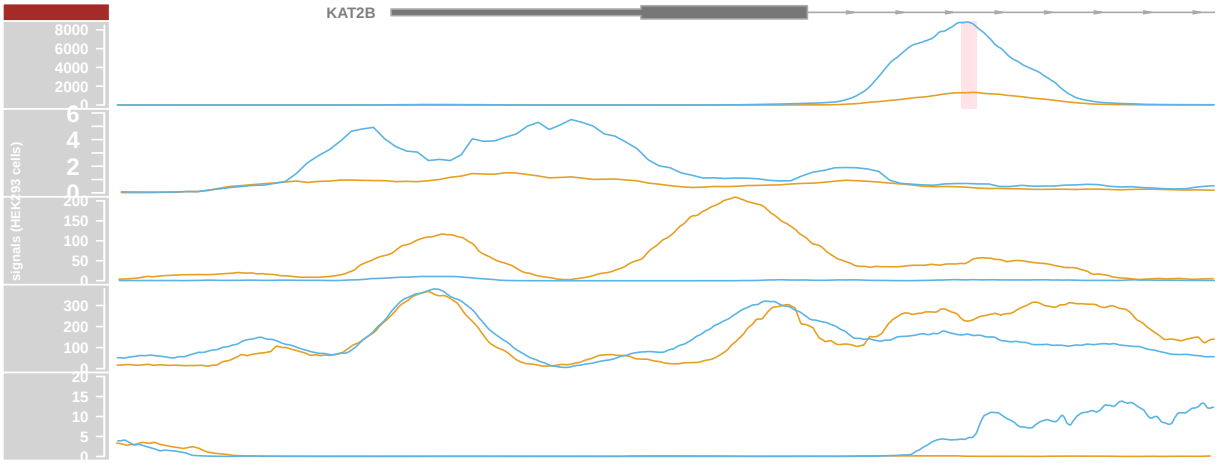
```
ZFP3.highlight.sites <- subset(ZFP3.annotated.sites, gene_name == "KAT2B") %>%
                        subset(predicted.Full.Energy < (-7))

highlightBox <-          Gviz::HighlightTrack(trackList = list(ZFP3.ChIP.tracks),
                                              start     = start(ZFP3.highlight.sites),
                                              end       = end(ZFP3.highlight.sites),
                                              chromosome= seqnames(ZFP3.highlight.sites), col = NA

                                     )


as.ggplot(function(){
  ZFP3.peaks.regions %>%
  Gviz::plotTracks(trackList = list(hg38.geneRegion.track,
                                    highlightBox,
                                    DNase.tracks,
                                    H3K27ac.tracks,
                                    H3K4me3.tracks,
                                    H3K4me1.tracks
                                   ),
                                    collapseTranscripts = "longest",
                                    chromosome = as.character(seqnames(.)),
                                    from = start(.),
                                    to =   end(.),
                                    window = -1,
                                    windowSize = 10,
                                    reverseStrand = FALSE, legend = FALSE)
}) -> plot.KAT2B

plot.KAT2B
```




```
#ggsave("KAT2B tracks.svg", height = 2.8, width = 8)
```