```
> options(width = 75, continue = " ")
> library("Gviz")
> library("trioClasses")
> data("cnv", package = "trioClasses")
> data("pedigrees", package = "CleftCNVAssoc")
> se <- SummarizedExperiment(assays = SimpleList(cnv = t(cnv.obj$cnv.mat)),
     colData = DataFrame(id = rownames(cnv.obj$cnv.mat), row.names = rownames(cnv.obj$cnv.ma
     rowData = cnv.obj$cmp.gr)
> beaty.trios <- MinimumDistance:::trios(beaty.pedigree)
> beaty.ped <- DataFrame(famid = do.call("rbind", strsplit(beaty.trios$O,
     "_"))[, 1], id = beaty.trios$O, fid = beaty.trios$F,
     mid = beaty.trios$M, sex = NA, dx = NA)
> ped <- PedClass(beaty.ped)
> fe <- FamilyExperiment(se, pedigree = ped)

> fe.parents <- fe[, colnames(fe) %in% parents(fe)]

> freq.vec <- colSums(cnv(fe.parents))/nrow(cnv(fe.parents))

> trioAssay <- trioClasses:::TrioAssay(fe, type = "cnv")
> trioStates <- with(trioAssay, matrix(paste0(F, M, O), nrow = nrow(O),
     ncol = ncol(O)))
> dimnames(trioStates) <- dimnames(trioAssay$O)

> table.list <- apply(trioStates, 2, "table")

> trans.vec <- as(lapply(table.list, trioClasses:::trans.tab),
     "numeric")
> head(table.list[which(trans.vec <= 0.05/length(trans.vec))])

$comp1994

000 001 010 011 100 101 110 111
149   7  26  57  28  71   5 102

$comp1995

000 001 010 011 100 101 110 111
116   5  30  63  38  75   9 109

$comp1996

000 001 010 011 100 101 110 111
113   5  30  64  37  74  11 111

$comp1997
```

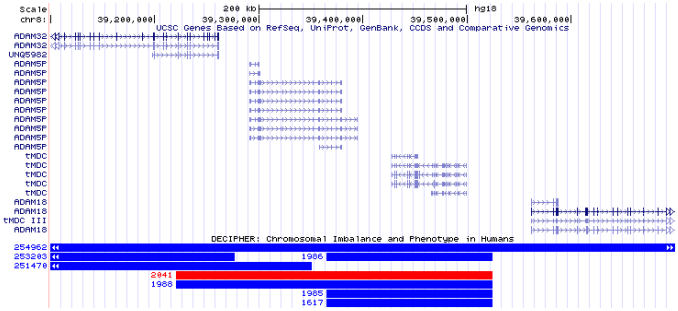
```
000 001 010 011 100 101 110 111
109   5  30  64  39  71  12 115

$comp1998

000 001 010 011 100 101 110 111
109   5  30  64  38  72  12 115

$comp1999

000 001 010 011 100 101 110 111
108   5  30  63  38  73  12 116
```


Scale
200 kb
hg18
chr8:
39,200,000
39,300,000
39,400,000
39,500,000
39,600,000
UCSC Genes Based on RefSeq, UniProt, GenBank, CCDS and Comparative Genomics
ADAM32
ADAM32
UNQ5982
ADAM5P
ADAM5P
ADAM5P
ADAM5P
ADAM5P
ADAM5P
ADAM5P
ADAM5P
ADAM5P
ADAM5P
tMDC
tMDC
tMDC
tMDC
tMDC
ADAM18
ADAM18
tMDC III
ADAM18
DECIPHER: Chromosomal Imbalance and Phenotype in Humans
264962
253203
251470
1986
2041
1988
1985
1617

```
> chr <- 8
> gr.cnp <- cnv.obj$cmp.gr
> gr.cnp.chr <- gr.cnp[as.logical(seqnames(gr.cnp) == paste0("chr",
    chr))]
> p.vec <- trans.vec
> p.vec.chr <- p.vec[as.logical(seqnames(gr.cnp) == paste0("chr",
    chr))]
> freq.vec.chr <- freq.vec[as.logical(seqnames(gr.cnp) == paste0("chr",
    chr))]
> library("TxDb.Hsapiens.UCSC.hg18.knownGene")
> TranscriptDb <- TxDb.Hsapiens.UCSC.hg18.knownGene
> atrack <- AnnotationTrack(reduce(gr.cnp.chr), name = "CNP comp.",
    fill = "darkgreen")
> gtrack <- GenomeAxisTrack()
> dtrack <- DataTrack(range = gr.cnp.chr, data = -log10(p.vec.chr),
    type = "p", cex = 1, name = "-log10(p)", ylim = c(0,
        10), col = "red")
> dtrack2 <- DataTrack(range = gr.cnp.chr, data = ifelse(freq.vec.chr >
    0.01, freq.vec.chr, NA), type = "s", col = "blue", cex = 1,
    name = "Frequency", ylim = c(0, 1), lwd = 2)
> itrack <- IdeogramTrack(genome = "hg18", chromosome = paste0("chr",
    chr), lty = 1, lwd = 1)
> grtrack <- GeneRegionTrack(TranscriptDb, genome = "hg18",
    chromosome = chr, name = "UCSC Known Transcripts", showId = TRUE)
> fud <- 5e+05/2
> plotTracks(list(dtrack, dtrack2, grtrack, gtrack, itrack),
    background.panel = "#FFFEDB", background.title = "darkblue",
    from = 39356825 - fud, to = 39497557 + fud)
```

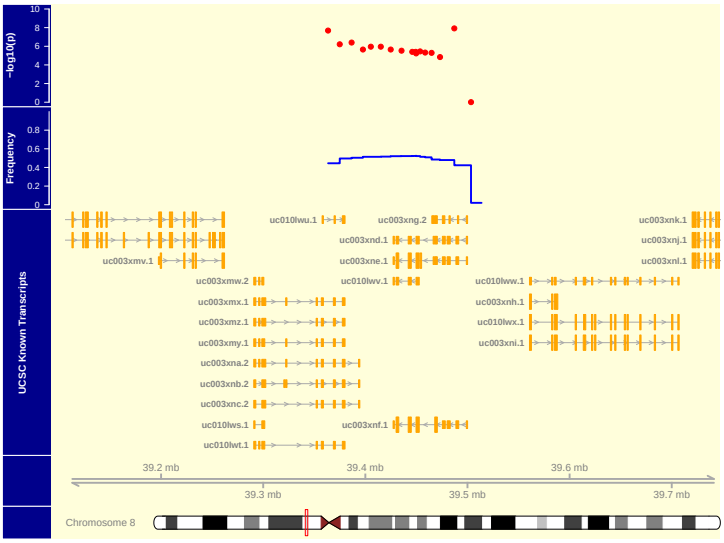


Figure 1: Foo!