```
> 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)
```

The top 3 CNV components have the followinfg trio-states. Where '1' indicates a deletion and order is F, M, O.

```
$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
```

The CNV components with signiifcant p-values (Bonferroni) are given below.

```
GRanges with 16 ranges and 0 metadata columns:
           seqnames                  ranges strand
              <Rle>               <IRanges>  <Rle>
  comp1994     chr8 [39356825, 39370186]        *
  comp1995     chr8 [39370187, 39379683]        *
  comp1996     chr8 [39379684, 39393417]        *
  comp1997     chr8 [39393418, 39401865]        *
  comp1998     chr8 [39401866, 39408899]        *
      ...      ...                    ...      ...
  comp2005     chr8 [39450168, 39457081]        *
  comp2006     chr8 [39457082, 39460087]        *
  comp2007     chr8 [39460088, 39469612]        *
  comp2008     chr8 [39469613, 39476658]        *
```
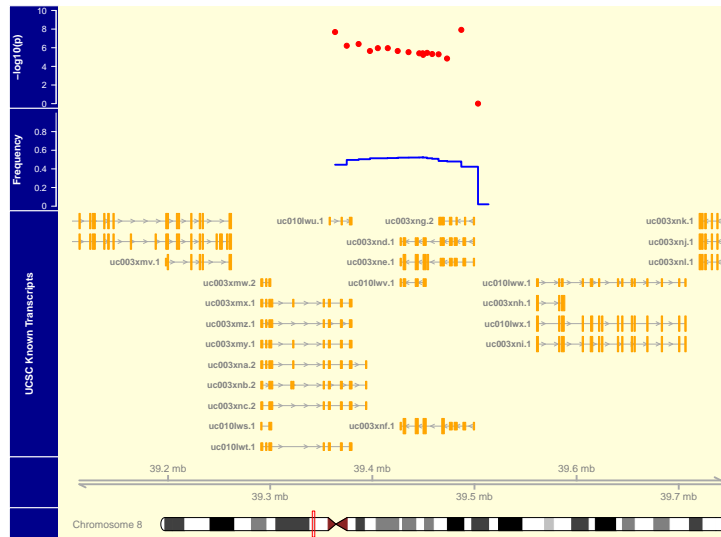
Figure 1: Red: $-\log_{10} p$-values for each CNV component that has at least **five** "0/1" mating pairs. Null hypothesis is transmission rate of $\frac{1}{2}$, and alternative hypothesis is "one-sided." Blue: The frequency of CNV component in the parents. Yellow: Gene tracks, labeled by transcript.

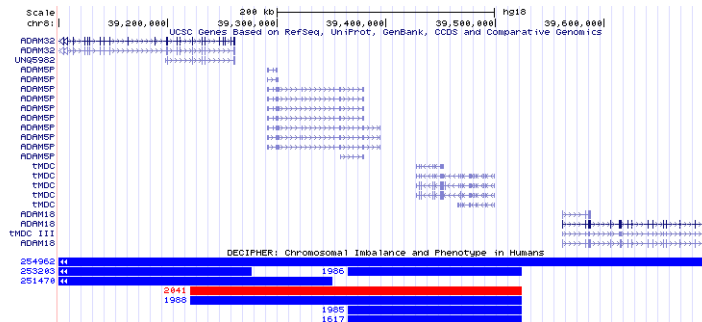Figure 2: UCSC Genome Browser at chromosome 8 locus.

```
   comp2009      chr8 [39476659, 39497557]        *
   ---
   seqlengths:
             chr1   chr1_random            chr2 ...              chrY          chrM
        247249719       1663265       242951149 ...          57772954         16571
```

All CNV components are contiguous and the total width is 140.7 kB.

```
function (object)
{
    if (sum(object[c("101", "011", "100", "010")], na.rm = TRUE) >=
        5) {
        T <- sum(object[c("101", "011")], na.rm = TRUE)
        U <- sum(object[c("100", "010")], na.rm = TRUE)
        return(binom.test(x = T, n = T + U, p = 0.5, alternative = "greater")$p.value)
    }
    else {
        return(NA)
    }
}
<environment: namespace:trioClasses>

> gr.deletion.pitt <- gr.pitt[values(gr.pitt)$numsnp >= 10 &
    values(gr.pitt)$cn %in% 0:1]
> sum(countOverlaps(gr.deletion.pitt, reduce(locus)))

[1] 417
```