

The top CNV component has the followinfg trio-states. Where ‘1’ indicates a deletion and order is F, M, O.

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

GRanges with 4 ranges and 0 metadata columns:

	seqnames	ranges	strand
	<Rle>	<IRanges>	<Rle>
comp1883	chr7	[141435189, 141439888]	*
comp1994	chr8	[39356825, 39370186]	*
comp2009	chr8	[39476659, 39497557]	*
comp2610	chr11	[55204004, 55209499]	*

seqlengths:

chr1	chr1_random	chr2 ...	chrY	chrM
247249719	1663265	242951149 ...	57772954	16571

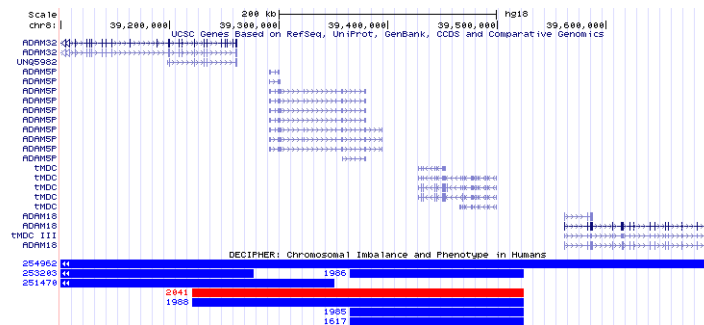
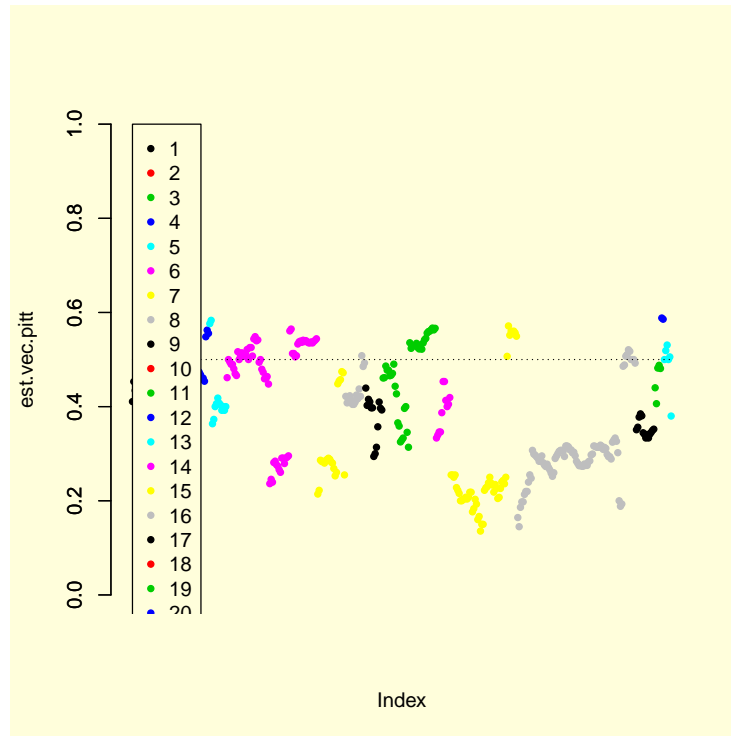
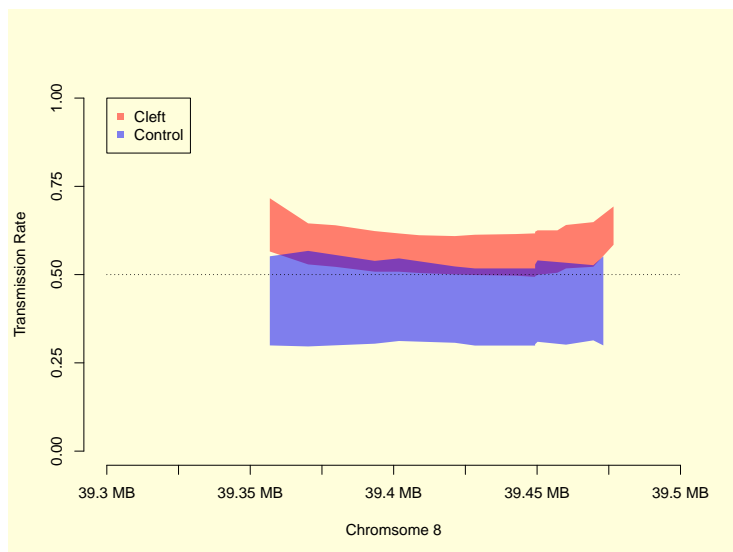


Figure 1: UCSC Genome Browser at chromosome 8 locus.



GRanges with 3 ranges and 0 metadata columns:

	seqnames	ranges	strand
	<Rle>	<IRanges>	<Rle>
[1]	chr7	[141407267, 141441259]	*
[2]	chr8	[39341981, 39518214]	*
[3]	chr11	[55124465, 55216671]	*

seqlengths:

chr1	chr1_random	chr2 ...	chrY	chrM
247249719	1663265	242951149 ...	57772954	16571

```
> freq.beaty <- colSums(cnv(fe.beaty))/2/nrow(cnv(fe.beaty))
> freq.pitt <- colSums(cnv(fe.pitt))/2/nrow(cnv(fe.pitt))
> freq.beaty[index.1.beaty]
```

```
comp1883
0.1023152
```

```
> freq.pitt[index.1.pitt]
```

```
comp1645
0.116408
```

```
> freq.beaty[index.2.beaty]
```

```
comp1994
0.3278566
```

```

> freq.pitt[index.2.pitt]

comp1793
0.2577605

> freq.beaty[index.3.beaty]

comp2009
0.3188947

> freq.pitt[index.3.pitt]

comp1805
0.2588692

> freq.beaty[index.4.beaty]

comp2610
0.1467513

> freq.pitt[index.4.pitt]

comp2356
0.154102

> summary(freq.beaty[index.1.full.beaty])

      Min.   1st Qu.   Median     Mean   3rd Qu.     Max.
0.0003734 0.0067210 0.1070000 0.0690100 0.1131000 0.1135000

> summary(freq.pitt[index.1.full.pitt])

      Min.   1st Qu.   Median     Mean   3rd Qu.     Max.
0.001109 0.016210 0.121400 0.081830 0.129200 0.129700

> summary(freq.beaty[index.2.full.beaty])

      Min.   1st Qu.   Median     Mean   3rd Qu.     Max.
0.0003734 0.3359000 0.3574000 0.2984000 0.3620000 0.3645000

> summary(freq.pitt[index.2.full.pitt])

      Min.   1st Qu.   Median     Mean   3rd Qu.     Max.
0.0005543 0.2633000 0.2716000 0.2352000 0.2752000 0.2788000

> summary(freq.beaty[index.3.full.beaty])

      Min.   1st Qu.   Median     Mean   3rd Qu.     Max.
0.0007468 0.1822000 0.2110000 0.1940000 0.2255000 0.2274000

```

```

> summary(freq.pitt[index.3.full.pitt])

      Min.   1st Qu.   Median     Mean   3rd Qu.     Max.
0.0005543 0.1818000 0.1924000 0.1795000 0.1973000 0.2040000

> trioClasses:::trans.tab

function (object)
{
  T <- sum(object[c("101", "011", "122", "212", "111", "112",
    "112")], na.rm = TRUE)
  U <- sum(object[c("100", "010", "121", "211", "111", "110",
    "110")], na.rm = TRUE)
  if (T + U >= 50) {
    return(binom.test(x = T, n = T + U, p = 0.5, alternative = "greater")$p.value)
  }
  else {
    return(NA)
  }
}
<environment: namespace:trioClasses>

> trioClasses:::trans.rate

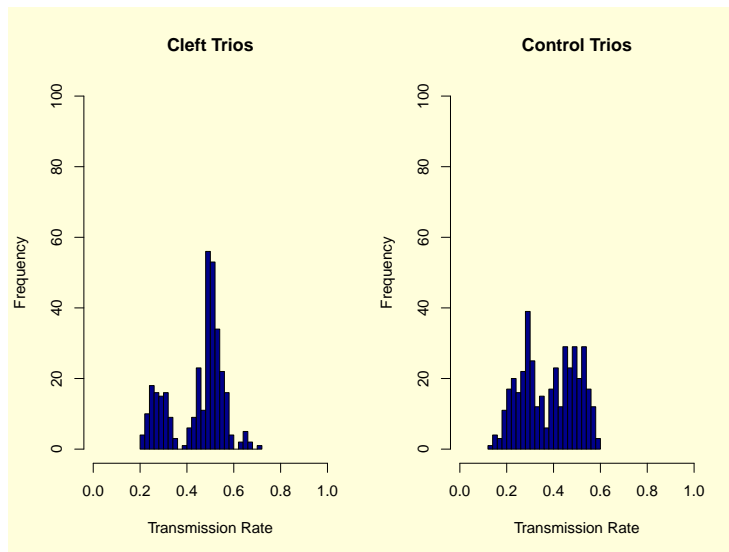
function (object)
{
  T <- sum(object[c("101", "011", "122", "212", "111", "112",
    "112")], na.rm = TRUE)
  U <- sum(object[c("100", "010", "121", "211", "111", "110",
    "110")], na.rm = TRUE)
  if (T + U >= 50) {
    return(binom.test(x = T, n = T + U, p = 0.5))
  }
  else {
    return(NA)
  }
}
<environment: namespace:trioClasses>

```

Methods

Cleft Data Description

- Performed 336 tests.
- *PennCNV* joint HMM
- european, MAD < 0.3, non-WGA, aux \neq 1



- coverage > 10
- 14857 hemi/homozygous deletions identified in 445 trios
- 4288 CNV components
 - Common (> 0.01): 660
 - Rare: 3628
- Construct trio-states for all CNV components
 - 0,1,2 variable for normal, hemizygous and homozygous, respectively
- $T + U > 50$
- count transmissions and perform `binom.test` (See “trans.tab”)

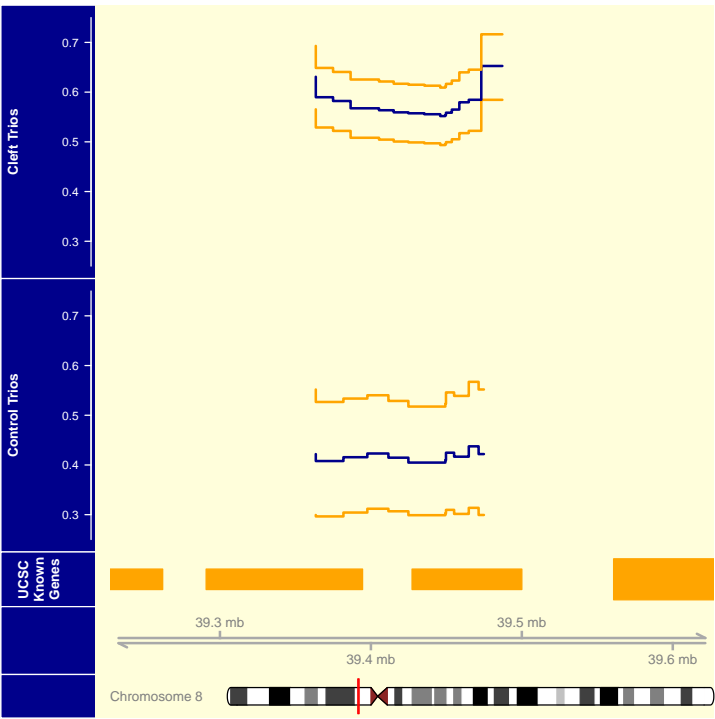


Figure 2:

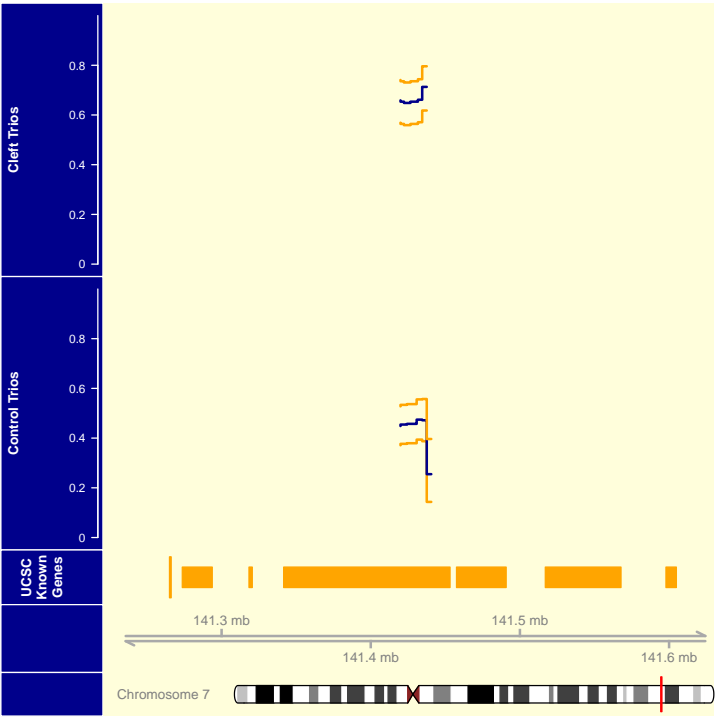


Figure 3:

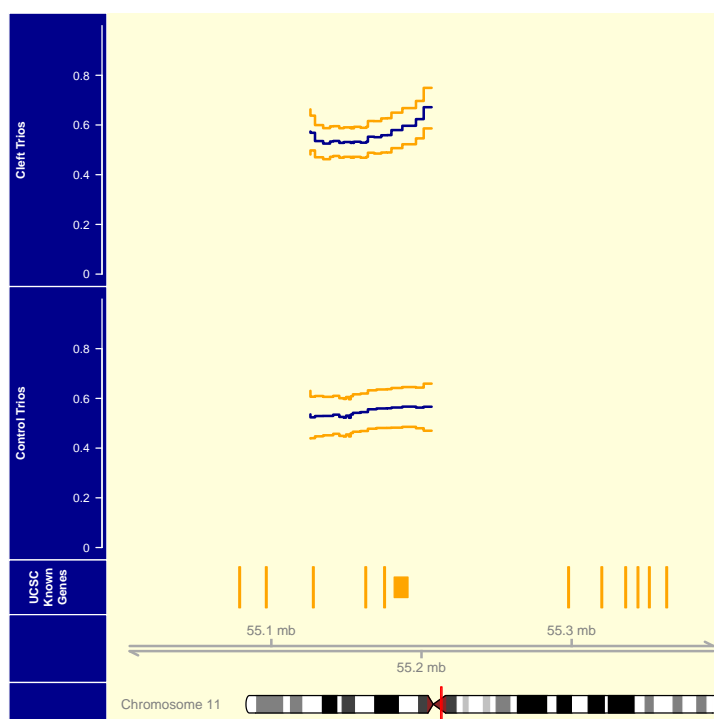


Figure 4: